The Regulation of Meiotic Recombination by DNA Damage Response Proteins

A thesis submitted for the degree of

Doctor of Philosophy in Biochemistry

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Statement

I hereby declare that this thesis has not been and will not be, submitted in whole or in part to another University for the award of any other degree.

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Acknowledgements

Summary

Homologous recombination (HR) is a vital aspect of meiotic cell division, required for the correct segregation of chromosomes, and generation of genetic diversity. DNA double strand breaks (DSBs) are formed by Spo11 and repaired by HR to produce crossovers (COs) between homologous chromosomes. DSBs and COs are subject to interference to ensure even spacing of recombination events. The DNA damage response checkpoint, mediated by Mec1 and Tel1, is partly responsible for the regulation of HR and its outcomes.

To investigate HR outcomes, hybrid budding yeast containing ~65,000 variants were induced to undergo meiosis and the resulting spores were sequenced. Recombination events were categorized via comparison to the parental genomes, using a custom-designed bioinformatic pipeline.

Changes in recombination event type and distribution were examined in Mec1 and Tel1 mutants, revealing that these proteins are required to limit Spo11-DSB formation, reduce DSB clustering and maintain DSB interference, and to promote CO formation and mediate CO interference, likely by altering the ratio of interfering to non-interfering CO formation.

An activator of Mec1, Rad24, is shown to have a meiotic recombination phenotype similar to that of the Mec1 mutant, but displays an increase in event length, and a reduction in CO interference and CO formation. The roles of Mec1, Tel1 and Rad24 are further examined by testing genetic interaction with factors that influence the outcome of meiotic recombination. Separable roles of Mec1 and Rad24 are also identified by examining the different effects of prophase extension on these strains.

During these analyses, it is determined that the mismatch repair protein Msh2 has opposing roles in both improving and reducing spore survival in hybrids, and in the promotion of interfering CO formation.

Collectively, this study reveals the consequences of the loss of important DNA damage sensor proteins on the meiotic genome, at a high resolution conferred by the use of deep-sequencing and bioinformatic tools.

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Figure 9.2.   Overlapping and separate roles of checkpoint proteins in controlling meiotic recombination.

List of Abbreviations

AA: Amino acid

bp: base pairs

°C: Degrees Centigrade

CDK: Cyclin dependent kinase

CO: Crossover

CWC: Chromosome without a Crossover

dCO: double crossover

DDR: DNA Damage Response

dHJ: double Holliday Junction

D-loop: Displacement loop

DNA: Deoxyribonucleic acid

dNTP: deoxynucleoside triphosphate

dNCO: double non-crossover

DSB: Double strand break

dsDNA: double stranded DNA

h: hours

hDNA: Heteroduplex DNA

HR: Homologous Recombination

HU: Hydroxyurea

Indel: insertion/deletion

IED/ICD/IND: Inter-Event/CO/NCO distance

JM: Joint molecule

Kb: Kilobases

KS: Kolmogorov-Smirnov

M: Molar

Mb: Megabases

Ml: millilitres

mM: millimolar

MMR: Mismatch repair

mtDNA: mitochondrial DNA

µl: microlitre

NCO: Non-crossover

ng: nanogram

OM: Octad *msh2Δ*

OMT: Octad *msh2Δ tel1Δ*

RFC: Replication factor C

RMM: Rec114, Mer2, Mei4

SC: Synaptonemal complex

SDSA: Synthesis-dependent strand annealing

SNP: Small Nucleotide Polymorphism

ssDNA: Single-stranded DNA

TCMM: Tetrad pCLB2-MEC1 *msh2Δ*

TCMN: Tetrad pCLB2-MEC1 Ndt80-arrest

TN: Tetrad Ndt80-arrest

TRM: Tetrad *rad24Δ msh2Δ*

TRMS: Tetrad *rad24Δ msh2Δ sml1Δ*

TRN: Tetrad *rad24Δ* Ndt80-arrest

TRS: Tetrad *rad24Δ sml1Δ*

TW: Tetrad wild-type

WT: Wild type

ZMM: Zip1, Zip2, Zip3, Zip4, Mer3, Msh4, Msh5

Chapter 1.

Introduction

<div align="center">**Chapter 1. Introduction**</div>

1.1. Meiosis

Meiosis is a specialized form of eukaryotic cell division that produces haploid gametes from a diploid parent. Haploid gametes are required for sexual reproduction, and include animal eggs and sperm, plant pollen and ova, and fungal spores.

Eukaryotic vegetative growth is characterized by alternation of chromosome replication and segregation, maintaining a diploid genome (Figure 1.1). In meiosis, a reduction in ploidy is achieved by the occurrence of two sequential chromosome segregation events, first segregating homologous chromosomes in Meiosis I, followed by sister chromatids in Meiosis II (Figure 1.2). DNA replication is regulated by Cdk levels; in G1 when Cdk activity is low, prereplicative complexes are formed at replication origins, and an increase in Cdk levels in late G1 initiates DNA replication (Tanaka & Araki, 2010). In meiosis, a second replication phase is skipped because Cdk activity is maintained at a high levels in between the two divisions (Holt *et al.*, 2007).

To achieve chromosome segregation, spindle fibres attach to the kinetochore, a protein structure that links microtubules and centromeres. During mitosis, sister chromatid kinetochores must be orientated such that they attach to opposite poles of the cell. However, in Meiosis I, sister kinetochores must attach to the same pole, while homologs must attach to opposite poles. In Meiosis II, sister kinetochores must attach to opposite poles as in mitosis. In *Saccharomyces cerevisiae*, a single microtubule attaches to each kinetochore, and the protein complex monopolin, which clamps microtubule binding sites, is required for monopolar orientation of sister kinetochores in meiosis I (Tóth *et al.*, 2000; Rabitsch *et al.*, 2003).

In order for correct segregation of chromosomes to occur, chromosome pairs must be connected to each other, ensuring proper orientation on the spindle apparatus (reviewed in Miller *et al.*, 2013). As in mitotic cell division, sister chromatids are joined by sister chromatid cohesion which is established during duplication of the diploid genome in premeiotic S phase (reviewed in Nasmyth & Haering, 2009). In contrast, homologous chromosomes must become connected by chiasmata during meiotic prophase (Figure 1.3).
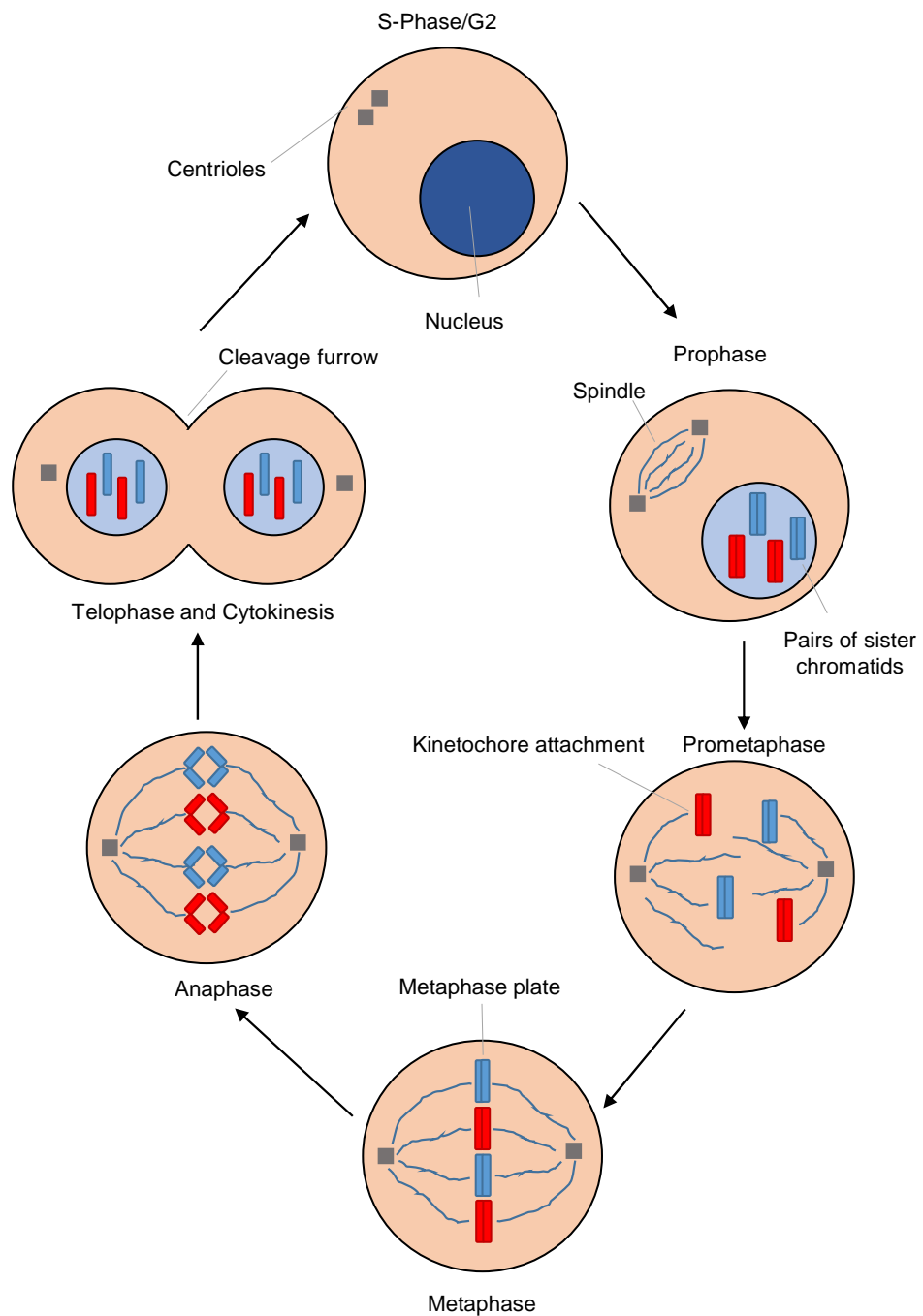
Figure 1.1. Simple representation of the stages of mitosis.

S-Phase/G2: Cell growth, centrioles and chromosomes duplicate.
Prophase: Chromosomes condense, centrioles move to opposite sides of the cell, microtubules are assembled.
Prometaphase: The nuclear envelope disintegrates and microtubules can attach to kinetochores.
Metaphase: Chromosomes line up on the metaphase plate and become connected to spindle fibres.
Anaphase: Sister chromatids are pulled apart.
Telophase & cytokinesis: Chromosomes decondense and the nuclear envelope reforms.
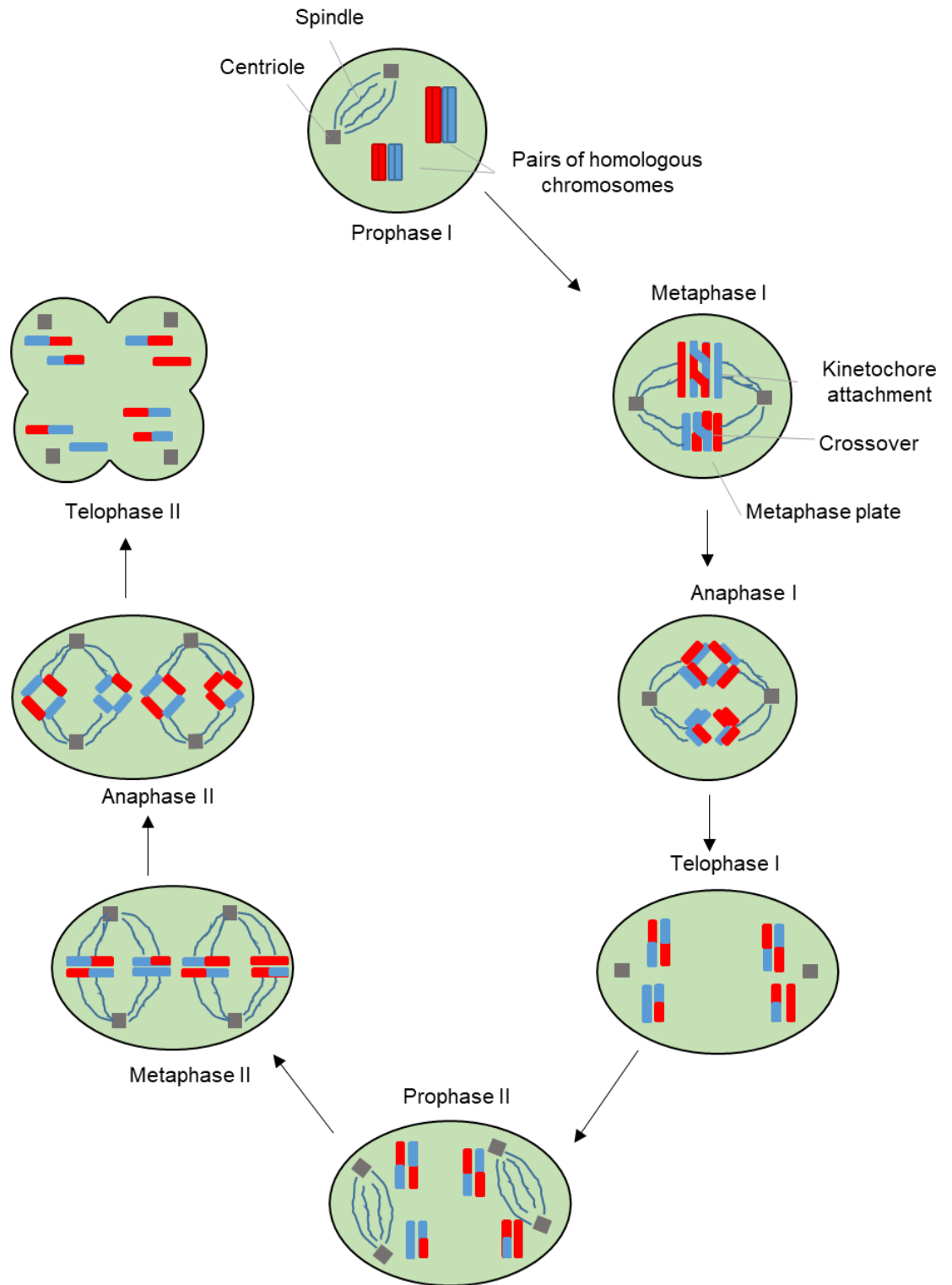
Figure 1.2. Simple representation of the stages of meiosis.

Prophase I: Homologous chromosomes pair up and crossovers form.
Metaphase I: Homologous chromosomes line up on the metaphase plate and are connected to spindle fibres.
Anaphase I: Homologous chromosomes are pulled apart.
Telophase I & cytokinesis: Cytoplasm divides to form two separate cells.
Prophase II: A new spindle forms in each separate cell.
Metaphase II: Chromosomes line up on the metaphase plate.
Anaphase II: sister chromatids are separated.
Telophase II & cytokinesis: The nuclear envelope reforms, cytoplasm divides to form a total of four separate haploid cells.
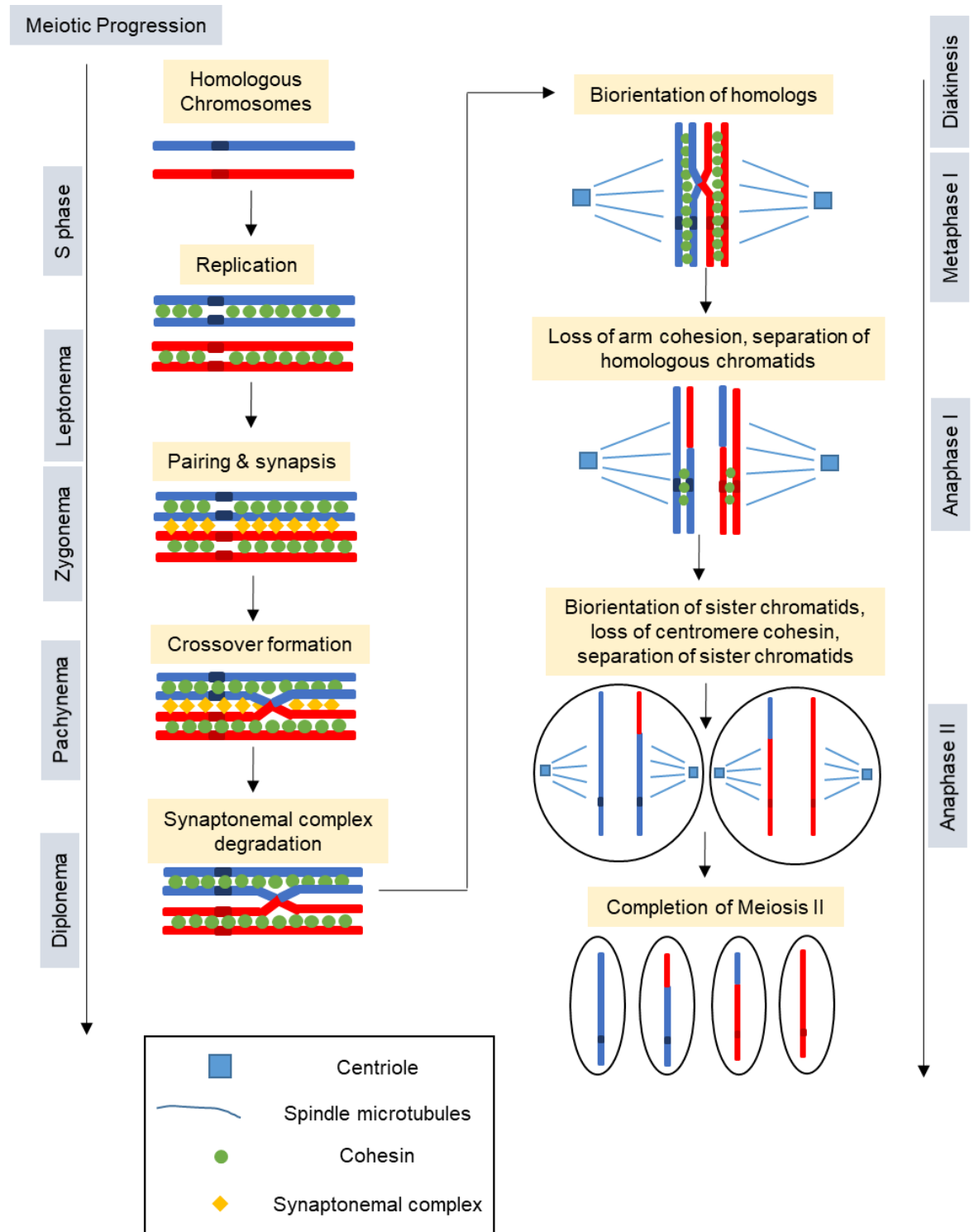
Figure 1.3. Simple representation of the chromosomal events of meiosis.

The main stages are shown for a single pair of homologous chromosomes (red and blue). Green circles indicate cohesin complexes connecting sister chromatids. Yellow diamonds represent the synaptonemal complex. Darker patches on chromosomes are kinetochores/centromeres. The blue structure represents the spindle, with a square as the centriole and lines as microtubules.

A CO establishes a physical link between homologues. A crossover between homologues in conjunction with cohesion establishes a physical connection, and allows orientation on the meiotic spindle.

1.2. Homologue Pairing and separation

Several factors contribute to the process of homologue pairing. During the meiotic prophase of many organisms, chromosomes are arranged in a bouquet formation, where telomeres become attached to the nuclear envelope (Harper *et al.*, 2004). In *S. cerevisiae*, vigorous chromosome movement occurs during prophase I, led by telomere clustering near spindle pole bodies and powered by actin filaments; this facilitates the pairing of homologous chromosomes (Scherthan et al., 2007; Conrad *et al.*, 2008, Koszul *et al.*, 2008). Homologous chromosomes become paired along their entire length and are stabilized by the synaptonemal complex, a structure consisting of two parallel lateral regions and a central element. A diverse group of proteins known as ZMM proteins, including Zip1, Zip2 and Zip3, localize on chromosomes during meiotic prophase I, promoting initiation of the synaptonemal complex (Sym *et al.*, 1993). In *S. cerevisiae*, Zip1 forms the transverse filament component of the synaptonemal complex (Sym *et al.* 1993). Dependent on Zip2, Zip1 localizes to Zip2/Zip3 foci, then begins polymerization along the length of the yeast SC during pachytene (Chua & Roeder, 1998, Agarwal & Roeder, 2000).

In most organisms, homologous chromosomes are held together by homologous recombination events which form chiasmata and are resolved into crossovers (COs), resulting in a reciprocal exchange of chromosome arms. The formation of noncrossover (NCO) products between homologous chromosomes also contributes to their stable pairing, though not as much as CO formation (Peoples-Holst & Burgess, 2005). Meiotic recombination is thus important to the process of homologue recognition and juxtaposition, and additionally essential to exchange genetic diversity in offspring, as it causes a reshuffling of maternal and paternal alleles, although there is also the potential to homogenize alleles by gene conversion.

The SC requires meiotic recombination to occur for its formation in yeast and mice (Loidl *et al.*, 1994, Baudat *et al.*, 2000, Romanienko & Camerini-Otero 2000) but not in *Drosophila melanogaster* or *Caenorhabditis elegans* (Dernburg *et al* 1998, McKim *et al.*, 1998). In *S. cerevisiae*, Zip3 and the proline isomerase Fpr3 ensure that DSB formation precedes synapsis initiation (MacQueen & Roeder, 2009).

The SC is also required for efficient CO formation in most organisms (reviewed in Zickler & Kleckner, 2015). The SC can also limit CO formation (Chen *et al.* 2008). The decision between CO or NCO formation occurs before the formation of a stable strand invasion intermediate, well before HJ resolution (Hunter & Kleckner, 2001). The evidence for this is as follows: in the absence of various CO-promoting ZMM proteins, DSBs and NCO products occur efficiently and with normal timing (Borner *et al.*, 2004). Synaptonemal complex polymerisation is

promoted at synapsis initiation complexes (SICs), which contain ZMM proteins and are associated with CO events (Agarwal & Roeder, 2000; Chua & Roeder, 1998). Like Class I CO events, SICs display interference (Fung *et al.*, 2004; Wang *et al.*, 2015). However, in mutants such as *tel1Δ*, *zip1Δ*, *msh2Δ* and *sgs1Δ*, CO interference is reduced but SIC distribution is unaffected (Anderson *et al.*, 2015; Fung *et al.*, 2004). A model has been suggested to explain this in which DSBs are designated to become COs or NCOs, with SICs marking future interfering CO sites. Mutants disrupting the formation of the SIC-marked COs cause non-interfering COs to form instead, meaning the initial CO/NCO decision is not altered (Fung *et al.*, 2004; Anderson *et al.*, 2015).

In *C. elegans*, pairing of homologous chromosomes is achieved via pairing centres found on each chromosomes, although meiotic recombination does also occur (Tsai & McKee 2011). In *D. melanogaster* males, pairing also occurs via pairing centres and is thought to occur early before meiosis, allowing accurate segregation without meiotic recombination (Hawley, 2002). In *Bombyx mori* females, there is also no meiotic recombination, and instead a long-lived synaptonemal complex is formed and persists throughout meiosis, indicating that the synaptonemal complex allows accurate homologue segregation (Rasmussen *et al*., 1977).

In mitosis, the cohesin complex must be removed to allow sister chromatid separation during metaphase (reviewed in Nasmyth & Haering, 2009). Cohesin is removed by cleavage of the Scc1 subunit, or by phosphorylation (Uhlmann *et al.*, 1999). In meiosis I, the presence of sister chromatid cohesion is also necessary to hold homologous chromosomes, themselves connected by chiasmata, together. To allow homologs to separate in anaphase I, cohesin must be removed, but must also remain in order to prevent sister chromatid separation. Thus, cohesion is only removed from chromosome arms, but cohesion at centromeres is protected until anaphase II. A meiosis-specific cohesin subunit, Rec8, replaces Scc1, and the protein Shugoshin is responsible for centromere protection (Watanabe & Nurse, 1999; Kitajima *et al.*, 2004).

1.3. Homologous Recombination

While homologous recombination (HR) is employed during the mitotic cell cycle to repair accidental DNA breakage, HR is initiated in meiosis by the deliberate activity of Spo11, which forms DNA double strand breaks (DSBs) (Keeney, 2001). Spo11-DSBs can only be repaired by HR, in contrast to the mitotic cell cycle, where DSBs can be repaired by either HR or non-homologous end joining (NHEJ) (reviewed in Symington & Gautier, 2011; Lieber, 2010).

In budding yeast, it has been estimated that 140–220 DSBs result in ~95 COs per meiosis (Mancera *et al.*, 2008). Each DSB undergoes 5` resection, producing a 3` single-stranded DNA (ssDNA) end, which is able to search for a double-stranded homologous repair template into which it can invade, in conjunction with the strand invasion proteins (RecA homologs) Rad51 and Dmc1 (Neale & Keeney, 2006).

While recombination preferentially occurs with the identical sister chromatid in mitosis, meiotic recombination is biased towards occurring with the homologous chromosomes (Hollingsworth, 2010; Kadyk & Hartwell, 1992; Bzymek *et al.*, 2010). This bias is essential to hold homologous chromosomes together during metaphase I. Rad51 is expressed in mitosis and meiosis, and when alone, promotes strand invasion into the sister chromatid; when in combination with the meiosis-specific Dmc1, both proteins promote interhomologue recombination (Cloud *et al.*, 2012). Interhomologue bias is also established in meiosis by the repression of Rad51 by two meiosis-specific factors, the kinase complex Red1/Hop1/Mek1 and by Hed1, which interacts with Rad51 (Busygina *et al.*, 2008; Niu *et al.*, 2009).

The even distribution of CO events among chromosomes is ensured by CO interference (Carpenter & Sandler, 1974; Bishop & Zickler, 2004; reviewed in Berchowitz & Copenhaver, 2010). CO interference is thought to be important in meiosis because it causes the limited number of chiasmata occurring to be spread out evenly among the chromosomes. An even distribution of CO events helps to ensure that even the smallest chromosomes will have at least one chiasma, the 'obligate CO' needed for proper chromosome segregation (Shinohara *et al.*, 2008; reviewed in Egel, 1995). In this way, CO interference contributes to CO assurance, the process which promotes the occurrence of at least one CO per chromosome. In addition, Spo11 DSBs are subject to DSB interference, in *cis* and *trans* (Zhang *et al.*, 2011; Garcia *et al.*, 2014).

1.4. Structure and Function of Spo11

In *S. cerevisiae*, Spo11 forms DNA DSBs in meiotic prophase I (Keeney *et al.*, 1997), catalyzing DSB formation via a topoisomerase-like reaction (Bergerat *et al.*, 1997). Spo11 is highly conserved, appearing to be present in all sequenced eukaryotic genomes (Ramesh *et al.*, 2005), having DSB-forming equivalents in *C. elegans*, *D. melanogaster*, *Mus musculus*, *Schizosaccharomyces pombe*, and *Arabidopsis thaliana* (Dernberg *et al* 1998; McKim and Hayashi-Hagihara 1998; Baudat *et al.*, 2000; Steiner *et al.*, 2002; Grelon *et al.*, 2001).

Spo11 is related to DNA topoisomerases, the purpose of which is to resolve topological issues in DNA, such as supercoiling and intertwining of DNA molecules, by breaking and rejoining DNA strands (reviewed in Champoux 2001). There are two categories of topoisomerase, I and

II, which break single and double strands of DNA respectively. To carry out their role, topoisomerases contain a tyrosine residue that can attack a phosphorus in DNA, forming a tyrosyl phosphodiester link on the DNA and severing the DNA backbone. Another DNA strand can then pass through the break in order to resolve tangles, after which the cleavage reaction is reversed to reseal the DNA strand.

Spo11 is most closely related to Archaeal Topoisomerase VI, which is a Type II topoisomerase and an A^2B^2 heterotetramer (Bergerat *et al.*, 1997). The A subunit contains the catalytic domain and a Toprim metal binding domain, and the B subunit contains an ATP-binding domain. Cleavage by the A subunit is dependent on the presence of the B subunit and ATP (Buhler *et al.*, 1998). *S. cerevisiae* Spo11 is biochemically and structurally similar to the TopoVIA subunit (Diaz *et al.*, 2002; Nag *et al.*, 2005). Like TopoVIA, Spo11 cleaves DNA to leave a two-nucleotide 5' overhang (Buhler *et al.*, 2001; Liu *et al.*, 1995). Recently, a conserved protein family was identified in plants and animals with a strong structural similarity to the TopoVIB subunit (the TOPOVIB-like family) (Robert, *et al.*, 2016; Vrielynck et al., 2016). In *S. cerevisiae*, Rec102 shares sequence similarity and predicted structure with TopoVIB, and is known to form a complex with Spo11 and be required for meiotic DSB formation (Kee & Keeney, 2001; Bhargava *et al.*, 1991).

Based on structure and function analyses of Spo11 and TopoVIA (Nichols *et al.*, 1999; Diaz *et al.*, 2002), Spo11 is thought to dimerize via an interaction between the catalytic tyrosine of one Spo11 and the metal binding pocket on the other, forming two active sites on either side of the duplex. Next, in a topoisomerase-like reaction, the tyrosine residues perform a nucleophilic attack on the DNA, producing a DSB with Spo11 remaining covalently attached to the 5' ends. Unlike the topoisomerase reaction, the covalent attachment is not reversed but instead Spo11 remains bound and must be removed by the endonuclease activity of Mre11. Sae2, the functional homologue of CtIP, appears to be required to activate Mre11 endonuclease (Neale *et al.*, 2005; Cannavo & Cejka, 2014; Lengsfeld *et al.*, 2007). Mre11 endonuclease nicks the 5' strand up to 300 nucleotides away from the DSB, enabling 5'-3' resection by Exo1 away from the DSB and 3'-5' resection by the exonuclease activity of Mre11 back towards the DSB, leaving a short oligonucleotide with Spo11 attached (Garcia *et al.*, 2011). Normal meiotic resection occurs between ~200 to ~2000 nt away from Spo11-DSB hotspot centres, with a mean of 822 nt (Mimitou *et al.*, 2016). Resection must be limited because excessive levels of ssDNA can induce mutations and cell death (Ngo & Lydall, 2010; Yang *et al.*, 2008).

1.5. Spo11 accessory factors

While Spo11 is the catalyst of DSB formation, it requires at least nine other proteins for its activity. These form four complexes, Spo11-Ski8, Rec102-Rec104, Mei4-Mer2-Rec114, and Mre11-Rad50-Xrs2 (reviewed in Keeney, 2008).

Ski8 directly interacts with Spo11, and is required for the interaction between Spo11 and Rec104 (Arora *et al.* 2004); thus its role may be to bridge interactions between proteins. Ski8 is not meiosis-specific but has a very different role in vegetative growth, where it is involved in RNA metabolism (Araki *et al.*, 2001). During meiosis, Ski8 relocalizes from the cytoplasm to the nucleus (Arora *et al.* 2004), where it is required for DSB formation (Gardiner *et al.*, 1997).

The Mre11-Rad50-Xrs2 (MRX) complex has roles in vegetative and meiotic DNA repair, telomere maintenance and DNA damage checkpoint signalling (reviewed in Assenmacher & Hopfner 2004; Krogh & Symington, 2004). Unique to *S. cerevisiae*, the MRX complex is required for both DSB formation and DSB processing. Mre11 has both single-strand endonuclease and 3'→5' exonuclease activities, and endonuclease-dead Mre11 mutants cause DSBs to accumulate with Spo11 covalently attached to the DNA ends (Moreau *et al.*, 1999), indicating that Mre11 is required for the removal of Spo11 from DSB ends (Neale *et al.*, 2005). Mre11 has been shown to bind to sites of DSB formation in *S. cerevisiae* (Borde *et al.*, 2004). Rad50 is an ATP-binding protein and is structurally related to the Structural Maintenance of Chromosomes (SMC) proteins. In *S. cerevisiae*, Xrs2 interacts with Mre11 and with the checkpoint/telomere maintenance kinase Tel1 (Shima *et al.*, 2005).

As mentioned above, Rec102 appears to act as the equivalent of the TopoVIB subunit for Spo11, which is similar to TopoVIA. Rec102 physically interacts with Rec104 (Jiao *et al.*, 2003). Rec102 and Rec104 are both required for Spo11 dimerization, chromatin binding and localization to DSB hotspots (Prieler *et al.*, 2005; Sasanuma *et al.*, 2007).

Mer2, Rec114 and Mei4 associate together and colocalize on meiotic chromosomes (Li *et al.*, 2006). Mer2 is phosphorylated during meiosis by the cyclin-dependent kinase Cdc28, an event that may be part of the mechanism controlling the timing of meiotic DSB formation (Henderson *et al.*, 2006). Rec114 is required for both the association of Spo11 and Mre11 with hotspot sequences, and for Spo11 dimerization (Borde *et al.*, 2004; Prieler *et al.*, 2005; Sasanuma *et al.*, 2007).

1.6. Location of Spo11-DSBs

Spo11 does not form DSBs randomly, but displays preferences for certain sites known as DSB hotspots (Lichten & Goldman, 1995). In most mammals, hotspots are determined by PRDM9, a H3K4 methyltransferase with a zinc finger domain. An amino acid sequence in the zinc finger domain determines the consensus sequence to which PRDM9 binds, which varies between PRDM9 alleles and thus alters DSB patterns in different individuals (Baudat *et al.*, 2010).

In *S. cerevisiae*, hotspots do not have any conserved sequence, but have a correlation with nucleosome-depleted regions such as promoters, indicating a need for chromatin accessibility (Figure 1.4) (Pan *et al.*, 2011, Ohta *et al.*, 1994, Wu & Lichten, 1994). Other factors influencing chromatin accessibly such as transcription factors and chromatin remodelers also influence DSB activity (Petes, 2001). Spo11 hotspots also correlate with the methylation of histone H3 at lysine 4 (Sollier *et al.*, 2004). In *S. cerevisiae*, H3K4me3 is known to interact with Spp1, which itself interacts with the DSB protein Mer2 (Sommermeyer *et al.*, 2013; Acquaviva *et al.*, 2012). Spp1 is a part of the COMPASS complex, which is responsible for the methylation of lysine 4 of histone H3 (Dehe *et al.* 2006).

In meiosis, chromosomes appear in the form of a series of chromatin loops on a structural axis, which contains meiosis-specific proteins such as Red1, Hop1 and the cohesin Rec8 (reviewed in Kleckner, 2006). Meiotic DSBs preferentially occur within loops (Blat *et al.*, 2002; Glynn *et al.*, 2004; Kugou *et al.*, 2009; Pan *et al.*, 2011), but proteins needed for DSB formation (Rec114, Mer2, and Mei4) and repair (Rad51 and Dmc1), occur primarily on the axis (Panizza *et al.*, 2011; Tarsounas *et al.*, 1999; Blat *et al.*, 2002). Thus, it is thought that either prior to, or because of, DSB formation, DSB sites on chromatin loops become linked to the axis; this is known as the 'Tethered-loop axis model' (Figure 1.5) (Blat *et al.*, 2002; Kleckner, 2006; Panizza *et al.*, 2011). The tethering most likely occurs prior to DSB formation because many DSB proteins are enriched on the axis (Panizza *et al.*, 2011). The mechanism for loop tethering may be explained by the physical interaction between Spp1, Mer3 and H3K4me3 (Acquaviva *et al.*, 2012; Sommermeyer *et al.*, 2013). Spp1 may simultaneously interact with Mer3 and H4K4me3, bringing chromatin loops closer to the DSB proteins enriched on the chromosome axis (Acquaviva *et al.*, 2012)
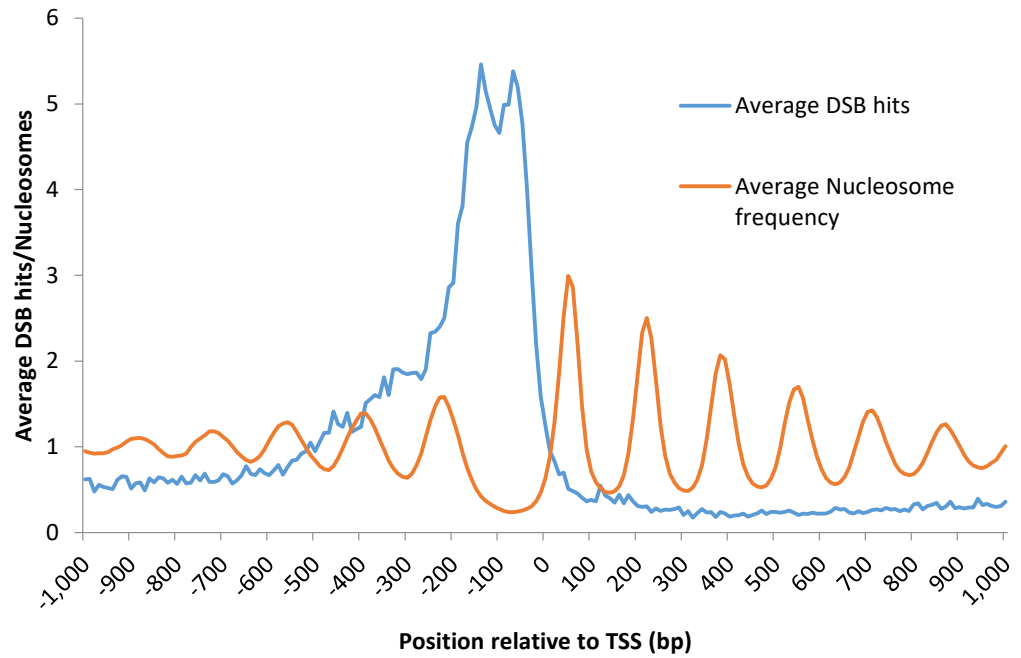
Figure 1.4. Comparison of average frequency of nucleosome occupancy and Spo11-DSB hits around piled-up gene transcription start sites.

Spo11-DSB data is from Pan *et al*., 2011.

Nucleosome location data is from Kent *et al*., 2011.

Gene TSS data is from Xu *et al*., 2009 and includes 5171 gene TSSs from *S. cerevisiae*.
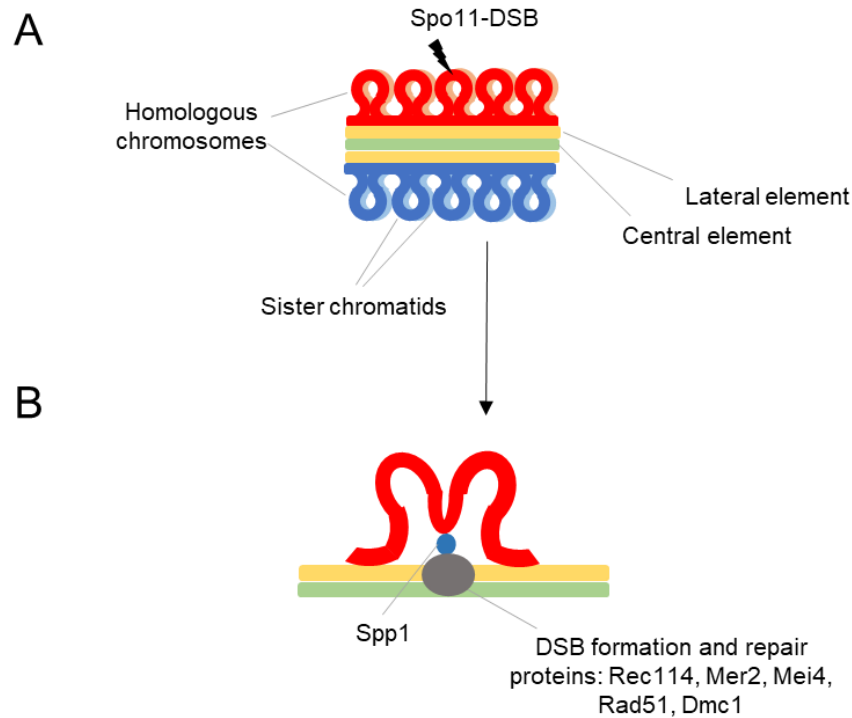
Figure 1.5. Simple representation of the tethered-loop axis model of the synaptonemal complex and Spo11-DSB tethering. A) In the tethered-loop axis model, sister chromatid loop arrays are attached to an axis of structural proteins. Meiotic DSBs preferentially occur within loops, but proteins needed for DSB formation (Rec114, Mer2, and Mei4) and repair (Rad51 and Dmc1) occur primarily on the axis. **B)** The tethered-loop axis model suggests that immediately before or after DSB formation, DSB sites on chromatin loops become linked to the axis. Loop tethering may be enacted by the dual interaction of Spp1 with Mer3 at the DSB site and H4K4me3 on the axis.

1.7. Timing of Spo11-DSB formation

The timing of DSB formation in *S. cerevisiae* is strictly controlled, only occurring within a small window of time during Prophase I division (Padmore *et al.*, 1991). The transition between prophase and metaphase is controlled by the activation of Ndt80, which occurs after DSB repair is completed and itself activates a cascade of proteins causing meiotic commitment (Prugar *et al.*, 2017; reviewed in Winter, 2012). Spo11 forms foci on chromatin as early as leptonema (Prieler *et al.*, 2005), and DSB proteins persist on chromosomes after DSB formation is complete (Kee *et al.*, 2004; Prieler *et al.*, 2005; Li *et al.*, 2006).

DSB formation is negatively regulated by ATM/Tel1 (Lange *et al.*, 2011; Garcia *et al.*, 2014; Anderson *et al.*, 2015). Both Tel1 and Mec1 also downregulate the Spo11-accessory factor Rec114 upon meiotic DSB formation via phosphorylation (Carballo *et al.*, 2013).

The DSB formation phase appears to be concluded by the formation of the SC (Thacker *et al.*, 2014). SC formation, when assayed by presence of Zip1, is strongly correlated with a reduction in the presence of Hop1, dependent on Pch2 (Borner *et al.*, 2008). As a target of Mec1/Tel1, the absence of Hop1 means Mec1/Tel1 signal can no longer be transduced, and remaining meiotic DSBs are repaired by a Dmc1-independent inter-sister repair pathway (Carballo *et al.*, 2008).

As mentioned previously, DSB formation is directly regulated by the Cdc28(CDK)-dependent phosphorylation of Mer2 in meiosis (Smith *et al.*, 2001; Henderson *et al.*, 2006), linking DSB formation to premeiotic DNA replication, which requires a low level of Cdc28 (Benjamin *et al.*, 2003; Shuster & Byers, 1989; Stuart & Wittenberg, 1998). Specifically, there is evidence that DSB formation is coordinated to occur after DNA replication. In order to take advantage of sister chromatid cohesion in homologue pairing, DSBs must only occur after replication has completed. In a *CDC6* mutant, DSBs can form prior to replication fork passage in Spo11 (Hochwagen *et al.*, 2005), but in normal *S. cerevisiae* cells, DNA replication and DSB formation are closely connected (Baudat & Keeney 2001; Smith *et al.*, 2001; Borde *et al.*, 2000). In the latter study, it was found that DSBs form ~90 minutes after local replication.

1.8. DSB processing

DSB end resection enables HR by providing a ssDNA tail that can invade a matching region on another chromosome for use as a repair template. The processes of searching for a homologue and strand invasion are facilitated in meiosis by the cooperative activity of the RecA homologs Rad51 and Dmc1 (Brown & Bishop, 2015). Rad51 and Dmc1 form a nucleoprotein filament with the ssDNA, and catalyse strand exchange (Hong *et al.*, 2001).

In vegetative DSB repair, Rad51 alone is responsible for catalyzing strand exchange (Shinohara *et al.*, 1992). However, during meiosis in *S. cerevisiae* (but not other organisms), Rad51 activity is inhibited by Hed1 (Busygina *et al.*, 2008), and instead the meiosis-specific Dmc1 is predominantly responsible for strand exchange (Bishop *et al.*, 1992; Cloud *et al.*, 2012). Rad51 still has a meiotic role in promoting Dmc1 assembly and homologue bias (Cloud *et al.*, 2012; Lao *et al.*, 2013).

The binding of the MRX complex to DSB sites also activates the checkpoint kinase Tel1, via an interaction with Xrs2 (Nakada *et al.*, 2003). Tel1 detects and is activated by blunt and protein conjugated DSB ends (Usui *et al.*, 2001). Tel1 in turn activates Sae2 via phosphorylation, promoting the initiation of resection (Cartagena-Lirola *et al.*, 2006; Terasawa *et al.*, 2008). The initiation of DSB resection by the MRX complex also facilitates the DNA damage response

(DDR), as the resulting RPA-coated ssDNA activates Mec1 (Jazayeri *et al.*, 2006; Shiotani & Zou, 2009; Zou & Elledge, 2003). Mec1 also activates Sae2 in a positive feedback loop (Cartagena-Lirola *et al.*, 2006).

Tel1 and Mec1 activation initiates the DNA damage response (DDR) network, which coordinates responses to damaged DNA by regulating DNA repair and cell cycle arrest in mitosis and meiosis (Figure 1.6) (Shinohara *et al.*, 2003; Finn *et al.*, 2012; Ciccia & Elledge, 2010; Carballo & Cha, 2007). Another important sensor of DNA damage is the checkpoint clamp, composed of Ddc1/Rad9, Mec3/Hus1 and Rad17/Rad1 (known as the 9-1-1 clamp, based on the numeric component of the mammalian protein names). The clamp is loaded onto DSB sites by Rad24 (Rad17), which acts in combination with Replication Factor C (RFC) (Kondo *et al.*, 2001; Melo *et al.*, 2001). The 9-1-1 complex activates Mec1 directly via an interaction with the C terminal of Ddc1 (Navadgi-Patil & Burgers, 2011). In meiosis, both the 9-1-1 clamp and the clamp loader Rad24 prevent excessive resection (Gray *et al.*, 2013). In mitosis, 9-1-1 inhibits DSB resection, but Rad24 appears to promote resection (Ngo & Lydall, 2015; Aylon & Kupiec, 2003). ATR is also activated in response to unsynapsed meiotic chromatin by the cofactors BRCA1 and TOPBP1 (Royo *et al.*, 2013).

When a ssDNA end invades into a homologous duplex, it anneals to one strand and displaces the other, producing a displacement loop (D-loop), or joint molecule (JM) (Figure 1.7) (Hunter & Kleckner, 2001). This JM may be dissolved to form a NCO by synthesis-dependent strand annealing (SDSA), where after the invading strand is extended by DNA synthesis, the D-loop is disrupted by helicases, freeing the newly-synthesized strand to anneal back to the other end of the DSB (Allers & Lichten, 2001). Alternatively, the D-loop can mature into an intermediate known as a Holliday junction (HJ), in which the second ssDNA end from the DSB is captured so that both recombining DNA strands are covalently-linked by a four-way junction (Schwacha & Kleckner, 1994; 1995). HJ-containing joint molecules need to be resolved in order to allow chromosome segregation, and in meiosis, are resolved to form mostly CO, but occasionally NCO, products (Allers & Lichten, 2001; Borner *et al.*, 2004).
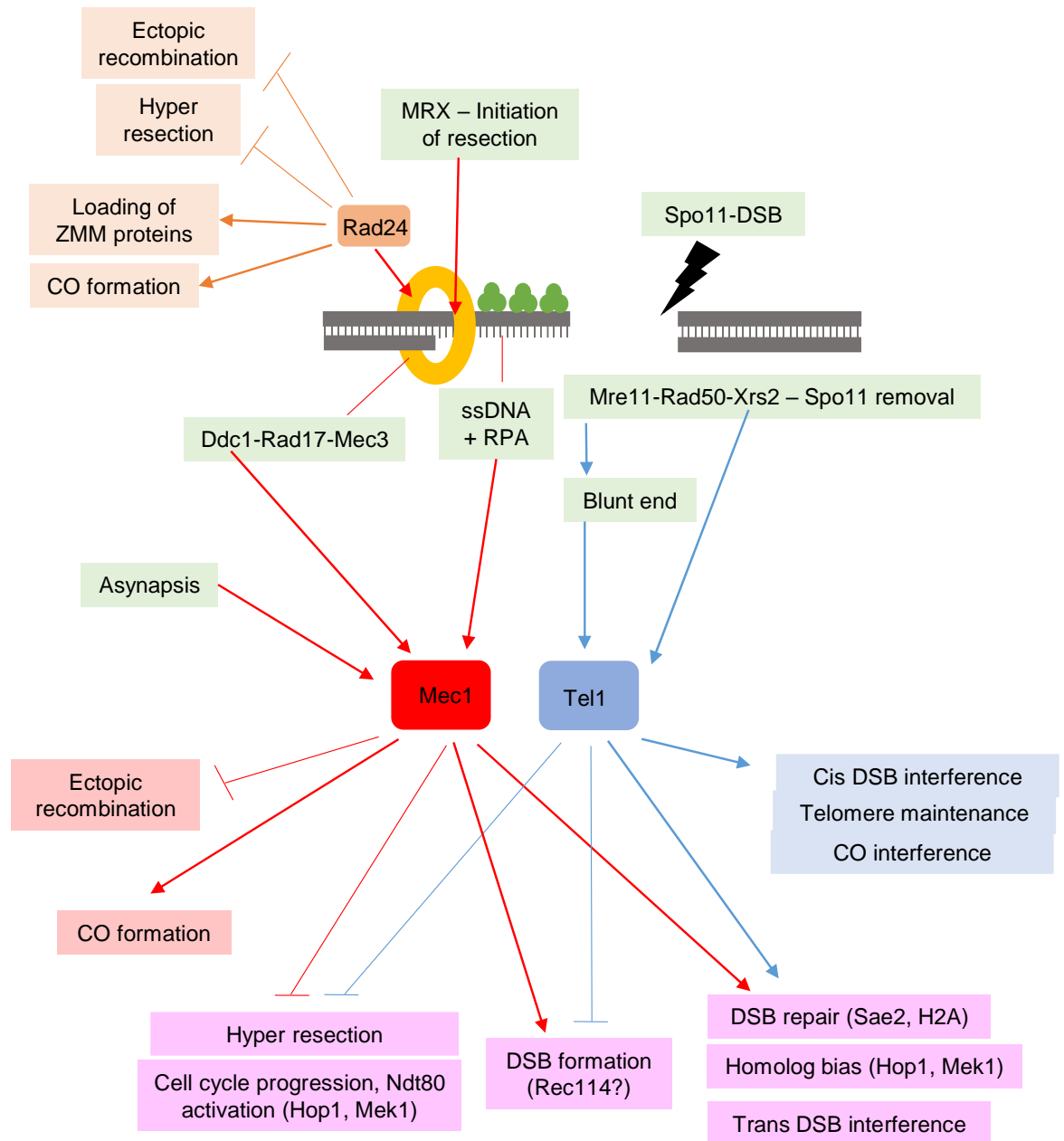
Figure 1.6. Key roles of DNA damage checkpoint proteins in meiotic prophase. Signalling pathways for the activation and activities of Mec1 and Tel1 in meiotic prophase. In addition, roles of Rad24 that are separable from roles of Mec1 are given. Green boxes contain activating factors, while important meiotic prophase activities of Mec1 are given in red, Tel1 in blue, Rad24 in orange and overlapping roles of Mec1 and Tel1 in purple.
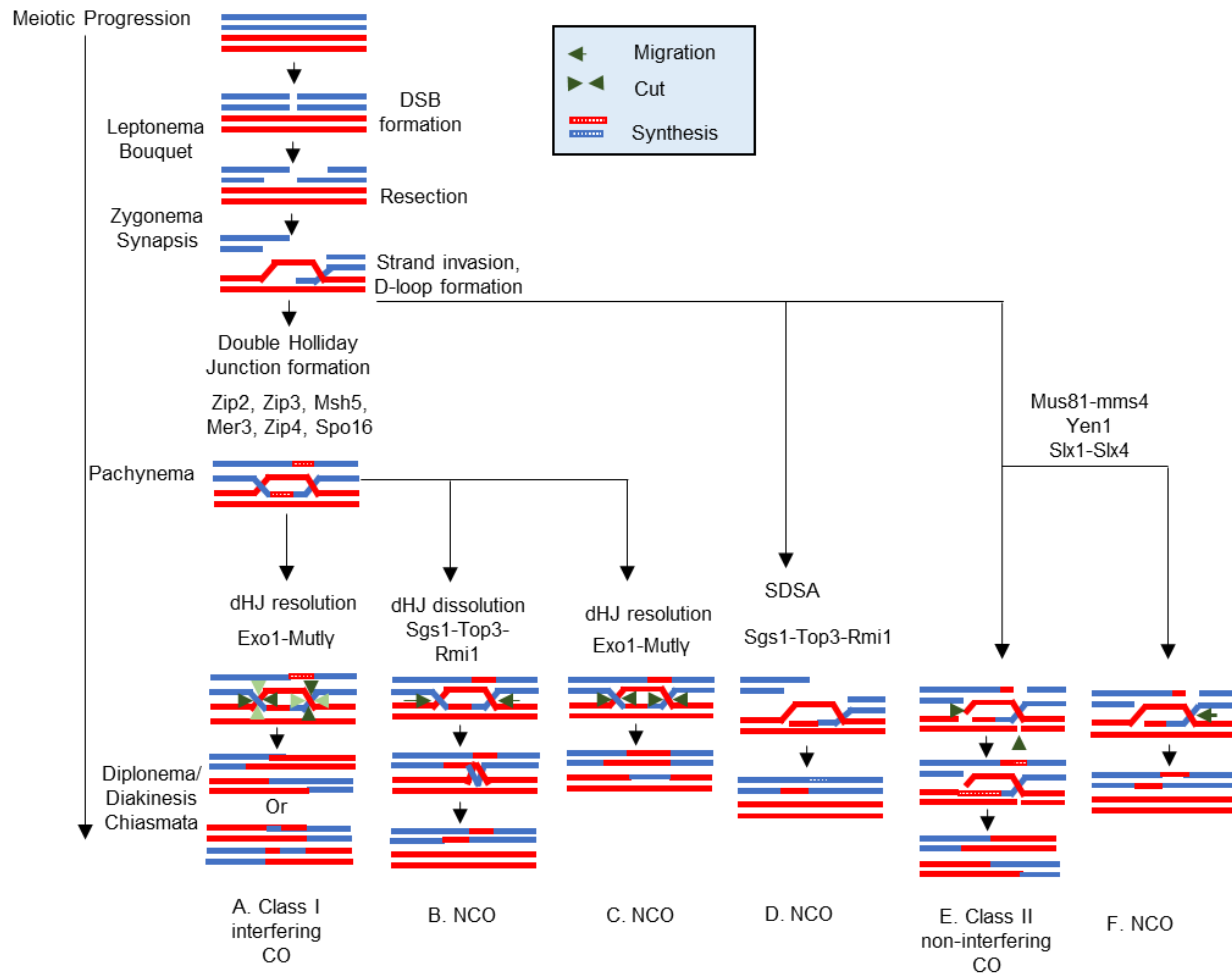
Figure 1.7. Models of meiotic CO and NCO formation in *S. cerevisiae* as described by Paques and Haber, 1999. For simplicity, only two homologous DNA molecules are represented, one red and one blue. The appropriate stage of meiosis is given for each progression in HR. This only applies to the leftmost path, as other outcomes may occur later or earlier.

A. Canonical dHJ resolution: After 3' end invasion, a stable SEI intermediate is formed and is processed into a dHJ. dHJ resolution can lead to a CO if the four nicks (arrowheads) cleave four different DNA strands. The darker and lighter coloured arrowhead pairs illustrate two possible resolutions. Of the final CO patterns, the top corresponds to resolution by the darker arrowheads, and the bottom CO pattern corresponds to resolution by the lighter arrowheads.

B. dHJ dissolution: After 3' end invasion, a stable SEI intermediate is formed and is processed into a dHJ, but the dHJ is dissolved by the combined action of Sgs1 helicase and Top3 topoisomerase, producing an NCO with two hDNA tracts in a trans configuration on the same chromatid.

C. dHJ resolution: After 3' end invasion, a stable SEI intermediate is formed and is processed into a dHJ, the resolution of which can lead to NCO if the four nicks affect only two DNA strands.

D. SDSA: After strand invasion, the invading 3' end is extended by DNA synthesis. The intermediate is dismantled and the DSB repaired by annealing of the ends and gap repair.

E. dHJ-independent CO: After 3' end invasion, an unstable intermediate is formed. A structure-specific endonuclease such as Mus81 can process this intermediate into a CO.

F. dHJ/SDSA-independent NCO: After 3' end invasion, an unstable intermediate is formed. A structure-specific endonuclease such as Mus81 can process this intermediate into an NCO.

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1.9. HJ-resolution in *S. cerevisiae*

The first HJ-resolving endonuclease, prokaryotic RuvC, was identified 30 years ago (West *et al.*, 1997), however the lack of sequence conservation between prokaryotic and eukaryotic resolvases meant that the discovery of a eukaryotic resolvase did not follow quickly.

In *S. cerevisiae*, four distinct endonucleases capable of resolving JMs *in vitro* have been identified: Mus81-Mms4 (Boddy *et al.*, 2001), Slx1–Slx4 (Fricke & Brill, 2003), Yen1 (Ip *et al.*, 2008), and Exo1-MutLγ (Zakharyevich *et al.*, 2012), which together account for essentially all JM resolution *in vivo* (Figure 1.7) (Zakharyevich *et al.*, 2012). All four of these resolvases have meiotic roles, but Mus81-Mms4 and Yen1 are also important for mitotic CO resolution (Ho *et al.*, 2010).

The majority of COs are formed by the resolvase action of the MutLγ complex, in combination with Exo1 nuclease and Sgs1, an ortholog of Bloom's helicase (Zakharyevich *et al.*, 2012). Exo1- MutLγ acts late in recombination (Zakharyevich *et al.*, 2010). Zakharyevich *et al.*, 2012 found that an *mms4Δ slx4Δ yen1Δ* triple mutant had a WT level of NCOs and around 70% of WT CO levels, though chromosome segregation failed in this strain, likely due to remaining unresolved JMs. Nevertheless this indicates that MutLγ is responsible for resolving ~70% of COs, and that dHJ resolution by MutLγ rarely or never produces NCOs. The second most prolific resolvase is Mus81, which acts with Mms4(Eme1). This pathway accounts for somewhere between 10-40% of COs (de los Santos, 2003). In some species such as *S. pombe*, Mus81 is the main CO resolvase (Smith *et al.*, 2003). Osman et al., 2003

Finally, Yen1 (GEN1) and Slx1-Slx4 (BTBD12) normally account for only a small subset of COs; *yen1Δ*, *slx1Δ* and *slx4Δ* single mutants all show slight or no defects in meiotic recombination. In fact, Slx1-Slx4 resolvase activity is not normally detectable during meiosis (Matos *et al.*, 2011). However, in the absence of other CO resolution pathways, Yen1 and Slx1-Slx4 appear to play a more important role in recombination. In an *mms4Δ* background, the loss of Yen1 has a much more severe effect, reducing CO levels by ~21% and resulting in the inability to produce viable spores (Zakharyevich *et al.*, 2012). A similar effect is seen in an *sgs1Δ* background, where the loss of Slx4 or Slx1 causes meiotic catastrophe and an increase in unresolved JMs, although this does not cause a reduction in the levels of CO or NCO products (Zakharyevich *et al.*, 2012). These observations suggest that Yen1 and Slx1-Slx4 act as 'backup' resolvases, essential for the resolution of some types of JM in the absence of the main CO resolution pathways. Yen1 also acts as a backup for Mus81 in mitotic CO resolution (Ho *et al.*, 2010).

Unlike MutLγ, dHJ cleavage mediated by Mus81-Mms4, Yen1 or Slx1-Slx4 can yield NCOs as well as COs. This is evident from the fact that in the absence of Sgs1, which is normally responsible for early NCO formation, there are still joint molecules formed that are resolved, without bias, into COs and NCOs (De Muyt *et al.*, 2012). However, these COs and NCOs are dependent on Mus81-Mms4, Slx1-Slx4 and Yen1 (Zakharyevich *et al.*, 2012).

Mus81-Mms4 is activated in meiosis I by the polo-like kinase, Cdc5 (Matos *et al.*, 2011). Expression of Yen1 is induced in late meiosis (Chu & Herskowitz, 1998), and Yen1p must also be activated by dephosphorylation, which occurs during the metaphase II to anaphase II transition (Matos *et al.*, 2011). Also, Yen1 is able to cleave a wide variety of DNA substrates including HJs, 5′-flaps, and replication fork structures (Matos *et al.*, 2011). Thus, Yen1 is able to resolve any persistent joint molecules that were not processed by other resolvases before the second meiotic division. It has been suggested that the purpose of the late activation of Yen1 in vegetative cells is to allow most joint molecules to be dissolved rather than resolved, preventing an excessive number of COs from forming; however, this has not been shown to be the case for meiotic cells (Blanco *et al.*, 2014).

In the process of SDSA, joint molecules are dismantled by branch migration and decatenation to form NCOs by the action of the STR(BTR) complex, composed of Sgs1(BLM), type-I topoisomerase Top3(TOPIIIα), and specificity factor Rmi1(RMI1–RMI2) (Cejka *et al.*, 2010). Thus, Sgs1 is involved in both a pro- and anti- CO pathway, promoting COs via Exo1-MutLγ, and preventing COs by removing aberrant recombination intermediates (Jessop *et al.,* 2006). NCOs are formed by the STR complex early in the cell cycle, which is thought to be important to limit the formation of COs in cycling cells, which could cause a loss of heterozygosity if occurring in excess (Blanco *et al.*, 2014).

1.10. ZMM proteins promote the formation of Class I interfering COs

Originally identified in Drosophila, CO interference is a phenomenon where CO events occur further apart than would be expected from a random distribution (Sturtevant 1913; Sturtevant 1915). CO interference has been documented in many species (Zhao *et al.,* 1995). CO interference is thought to be important in meiosis because it causes the limited number of chiasmata occurring to be spread out evenly among the chromosomes. This helps to ensure that even the smallest chromosomes will have at least one chiasma (known as the 'obligate CO') needed for proper chromosome segregation (reviewed in Egel, 1995). The obligate CO is thought to be ensured by the interference-dependent pathway during the CO/NCO decision step, before single-end invasion (Allers & Lichten 2001; Hunter & Kleckner, 2001). CO homeostasis ensures that, if DSB numbers are reduced, COs are maintained at the expense of NCOs (Martini

et al. 2006; Zanders & Alani, 2009). In *S. cerevisiae*, loss of CO interference due to Zip1 or Tam1 deletion causes an increase in chromosome nondisjunction (Sym & Roeder 1994; Chua & Roeder 1997). Spreading out CO events, whether spatially or temporally, may also be beneficial to prevent the repair processes from overlapping (e.g. resection tracts running into each other), although this may be more applicable to DSB interference.

However, not all COs display interference. In *S. cerevisiae*, there are at least two distinct classes of COs. Class I COs exhibit interference and are dependent upon Msh4/Msh5 activity (Novak *et al.*, 2001), and Class II COs do not display interference and are dependent upon Mus81/Mms4, Yen1 or Slx1-Slx4 activity (Figure 1.7) (de los Santos, 2003). The interfering pathway is meiosis specific, while the non-interfering pathway is very similar to mitotic DSB repair (Kohl & Sekelsky, 2013).

Msh4 and Msh5 are homologs of MutS (Hollingsworth *et al.*, 1995; Snowden *et al.*, 2004), a bacterial protein that identifies mismatches and forms a repair complex with MutL and MutH. The Msh4/Msh5 heterodimer is only required for meiotic functions, as opposed to standard mismatch repair (Hollingsworth *et al.* 1995). Msh4 and Msh5 are members of a group of proteins known as ZMMs, a meiosis-specific, functionally diverse set of proteins, which promote the formation of dHJs (Lynn *et al.*, 2007) and their biased resolution into Class I COs (Chen *et al.*, 2015). The ZMM proteins are important for the maintenance of both CO assurance and CO interference in meiosis (Shinohara *et al.*, 2008). ZMM proteins localize on chromosomes during meiotic prophase-I, promoting initiation of the synaptonemal complex (Sym *et al.*, 1993). Other ZMM proteins are Zip1, Zip2, Zip3, Mer3, Spo22/Zip4, and Spo16.

Zip3 is a putative SUMO/Ubiquitin E3 ligase (Cheng *et al.*, 2006), which binds DNA close to DSBs and promotes local assembly of other ZMM proteins (Serrentino *et al.*, 2013). Zip2 colocalizes with Zip3 at discrete foci and promotes initiation of chromosome synapsis. Zip1 forms the transverse filament component of the synaptonemal complex (Sym *et al.* 1993). Dependent on Zip2, Zip1 localizes to Zip2/Zip3 foci, then begins polymerization along the length of the yeast SC during pachytene (Chua & Roeder, 1998, Agarwal & Roeder, 2000). Spo16 works together with Spo22 in a subcomplex which facilitates Zip1 polymerization from recombination sites (Shinohara *et al.*, 2008). Finally, Mer3 is a 5'-3' DNA helicase, able to unwind various double-stranded substrates (Nakagawa *et al.* 2001). All ZMM mutants show a reduction in crossing over, and in most ZMM mutants, residual COs show a loss of interference; however, Spo16 and Spo22 mutants show a normal interference distribution (Shinohara *et al.*, 2008).

Not all organisms have separate classes of COs. In *S. pombe*, ~80-95% of COs are resolved by Mus81-Eme1, and there is no CO interference (Cromie *et al.*, 2006; Smith *et al.*, 2003; Osman *et al.*, 2003; Boddy *et al.,* 2001). On the other hand, *C. elegans* COs are dependent on Msh4-Msh5, and interference is absolute, with exactly one CO per bivalent (Meneely *et al.*, 2002).

1.11. Influence of DSB interference on CO interference

CO interference could in theory be a reflection of DSB interference. However, the observation that NCO events do not display interference, suggests this is not the case (Mortimer & Fogel, 1974; Getz *et al.*, 2008; Mancera *et al.*, 2008). In contrast, COs and NCOs appear to display weak positive interference as assayed by a genome wide survey (Mancera *et al.*, 2008), but not when assaying single loci (Mortimer & Fogel, 1974; Malkova *et al.*, 2004; Getz *et al.*, 2008).

The extent to which DSBs interfere with each other is not well understood, but the insertion of a strong artificial hotspot in *S. cerevisiae* has been observed to decrease DSB formation in a ~60kb region around the hotspot (Ohta *et al.*, 1999; Wu & Lichten, 1995; Fan *et al.,* 1997). However, this may actually may be a reflection of DSB competition, a phenomenon thought to arise upstream of DSB formation due to limited availability of pro-recombination factors for the formation of DSBs occurring within the same chromatin loop (Cooper *et al.,* 2016). Nonetheless, if the reduction in DSB formation after insertion of a strong hotspot were caused by DSB interference, the short range would not be enough to explain CO interference over much larger distances.

1.12. Roles of Mec1 and Tel1 in the DNA damage response

Tel1[ATM] and Mec1[ATR] are serine/threonine kinases with many functions in both mitosis and meiosis, including monitoring of DNA damage repair, checkpoint regulation, genome duplication and cell cycle progression (Figure 1.6) (Cha *et al.*, 2002; Harper & Elledge, 2007; Carballo & Cha, 2007).

The functions of Tel1[ATM] and Mec1[ATR] have been well-studied in the context of *S. cerevisiae* meiotic prophase. In meiotic prophase, programmed DSBs are formed by Spo11. With the yeast 911 complex (Rad17, Mec3, and Ddc1), its loader Rad24 and the MRX complex as damage sensors (Hochwagen & Amon, 2006), unresected DSBs cause activation of Tel1 (Usui *et al.*, 2001), and unrepaired ssDNA produced by the resection of DSBs activates Mec1 (Lydall *et al.*, 2011). The accumulation of unrepaired DSBs causes Tel1 and Mec1 to trigger meiotic arrest as part of the meiotic checkpoint response (Lydall *et al.*, 1996). The meiotic checkpoint monitors meiotic events and halts cell cycle progression if necessary, ensuring that cells do not exit

prophase before the process of DSB repair is complete (Lydall *et al.*, 1996; Carballo *et al.*, 2008).

In addition, Tel1 and Mec1 modulate DSB frequency in an antagonistic manner. Tel1 negatively regulates DSB formation in mammals, flies and yeast (Lange *et al.*, 2011; Joyce *et al.*, 2011; Gray *et al.*, 2011), while Mec1 positively regulates DSB formation in yeast via the checkpoint dependent extension of meiotic prophase length (Gray *et al.*, 2011).

As kinases, Tel1 and Mec1 carry out many of their functions via the phosphorylation of other proteins including histone H2A, which has roles in DNA replication (Cheng *et al.*, 2013); Zip1, the main component of the SC central element (Falk *et al.*, 2010; Sym *et al.*, 1993), and two meiosis-specific components of the axial element, Hop1, required for chromosome synapsis, and Mek1, another serine/threonine kinase and paralog of Dun1 (Smith & Roeder, 1997; Hollingsworth *et al.*, 1990; Rockmill & Roeder, 1991; Carballo *et al.*, 2008; Usui *et al.*, 2001; Carballo *et al.*, 2008; Penedos *et al.*, 2015). Mec1 and Tel1 downregulate the Spo11-accessory protein Rec114 via phosphorylation, affecting DSB formation (Carballo *et al.*, 2013).

To implement meiotic checkpoint arrest, Tel1 and Mec1 utilize Hop1 and Mek1 as adaptor and effector kinases, respectively (Carballo *et al.*, 2008). Tel1/Mec1 also phosphorylate proteins involved in DNA repair during vegetative growth, such as RPA, Sae2 (Carballo & Cha, 2007; Chen *et al.*, 2010; Cartagena-Lirola *et al.*, 2006) and histone H2A, which triggers a DNA damage response (Szilard *et al.*, 2010) in addition to having roles in premeiotic DNA replication.

Another important meiotic activity of Tel1/Mec1 is to promote interhomologue bias in meiotic DSB repair, which takes place preferentially between homologous chromosomes, as opposed to the sister chromatids preferred in mitosis (Schwacha & Kleckner, 1994; Collins & Newlon, 1994). As with the implementation of checkpoint arrest, homologue bias processes are initiated by Tel1/Mec1 phosphorylation of Hop1, leading to activation of Mek1, which then phosphorylates further downstream proteins such as Rad54 (Carballo *et al.*, 2008; Goldfarb & Lichten, 2010; Niu *et al.*, 2009). Mek1 indirectly promotes interhomolog strand invasion by Dmc1 via its downregulation of Rad51 (Prugar *et al.*, 2017). Mec1 and Tel1 also act to destabilize centromere pairing that occurs without homology via phosphorylation of Zip1, which mediates nonhomologous centromere coupling (Falk et al., 2010; Tsubouchi & Roeder, 2005).

It should be noted that while there is a degree of redundancy in the functions of Mec1 and Tel1, their contributions are not necessarily identical in all cases. Tel1 and Mec1 work through independent pathways to phosphorylate Hop1, with Mec1 activated by Rad17 and ssDNA (Lydall *et al.*, 1996), while Tel1 works with Pch2 ATPase and MRX component Xrs2 (Wu & Burgess, 2006).

Of the two kinases, Tel1 appears to be much less important for survival. The homozygous deletion of $MEC1^{ATR}$ is inviable in yeast (Giaever *et al.*, 2002) and mice (Brown & Baltimore, 2000; de Klein *et al.*, 2000). However, *TEL1* deletion has only a minor effect on spore viability in yeast, reducing it from ~97% to ~93% (Chapter 3, Figure 3.7). Even the conditional Mec1 mutant P_{CLB2}-MEC1 which is only suppressed during meiosis has a lower spore viability of ~58%. Despite the modest effect on viability, ATM mouse mutants and tefu fly mutants have been shown to display increased rates of recombination initiation, unrepaired DSBs and apoptosis (Joyce *et al.,* 2011; Lange *et al.,* 2011; Barchi *et al.,* 2005; Di Giacomo *et al.,* 2005; Barchi *et al.,* 2008). In humans, ATM defects cause the disease ataxia telangiectasia, which among other symptoms includes infertility, indicating that ATM has a role in human meiotic DSB repair. In addition, when the overall DSB level is low, Tel1 is required in yeast for efficient resection of DSBs and maintenance of homologue bias (Joshi *et al.*, 2015).

1.13. Regulation of Sml1 activity by Mec1

Mec1 deletion is inviable in *S. cerevisiae*, but the deletion of Sml1 (Suppressor of Mec1 Lethality) restores the cell viability of *mec1Δ* in both meiosis and mitosis, though *sml1Δ* does not compensate for the checkpoint or transcriptional functions of Mec1 (Zhao *et al.*, 1998).

Sml1 inhibits dNTP synthesis post-translationally by binding directly to the ribonucleotide reductase (RNR) subunit Rnr1 (Zhao *et al.*, 1998). RNR catalyzes the conversion of NDP to dNDP, the rate-limiting step of dNTP synthesis, thus controlling dNTP pool levels and affecting genetic fidelity and cell viability (Reichard, 1988).

RNR activity is strictly regulated during DNA replication and repair (Figure 1.8). During S-phase and after DNA damage, Sml1 is inactivated by Dun1 phosphorylation (Zhao & Rothstein, 2002). As a result, *dun1Δ* yeast take longer to complete DNA replication, and are sensitive to DNA-damaging agents (Zhao & Rothstein, 2002).

In mitosis, Dun1 is activated by Rad53 (Chen *et al.*, 2006), and Rad53 is in turn activated by phosphorylation via Mec1 and Tel1 (Sanchez *et al.*, 1996). Rad53 and Dun1 are therefore the

mitotic equivalents of meiotic Hop1 and Mek1 respectively, though it is not known whether Mek1 performs the same roles as Dun1 in Sml1 regulation (Carballo *et al.*, 2008). Mec1, Rad53 and Dun1 also affect RNR activity by upregulating the transcription of RNR genes (Huang & Elledge, 1997). Dun1 upregulates transcription of the *RNR* genes by relieving the transcriptional repression of the Crt1 protein (Elledge *et al.*, 1992; Huang *et al.*, 1998). In this way, dNTP levels can be controlled in response to DNA damage.

Deletion of Sml1 therefore rescues the inviable phenotype of *mec1Δ* in two ways, first by relieving the requirement for Mec1-mediated inactivation of Sml1, and secondly by increasing dNTP levels (Huang & Elledge, 1997) by releasing RNR suppression, allowing DNA repair to be more efficient in the absence of the DDR checkpoint.
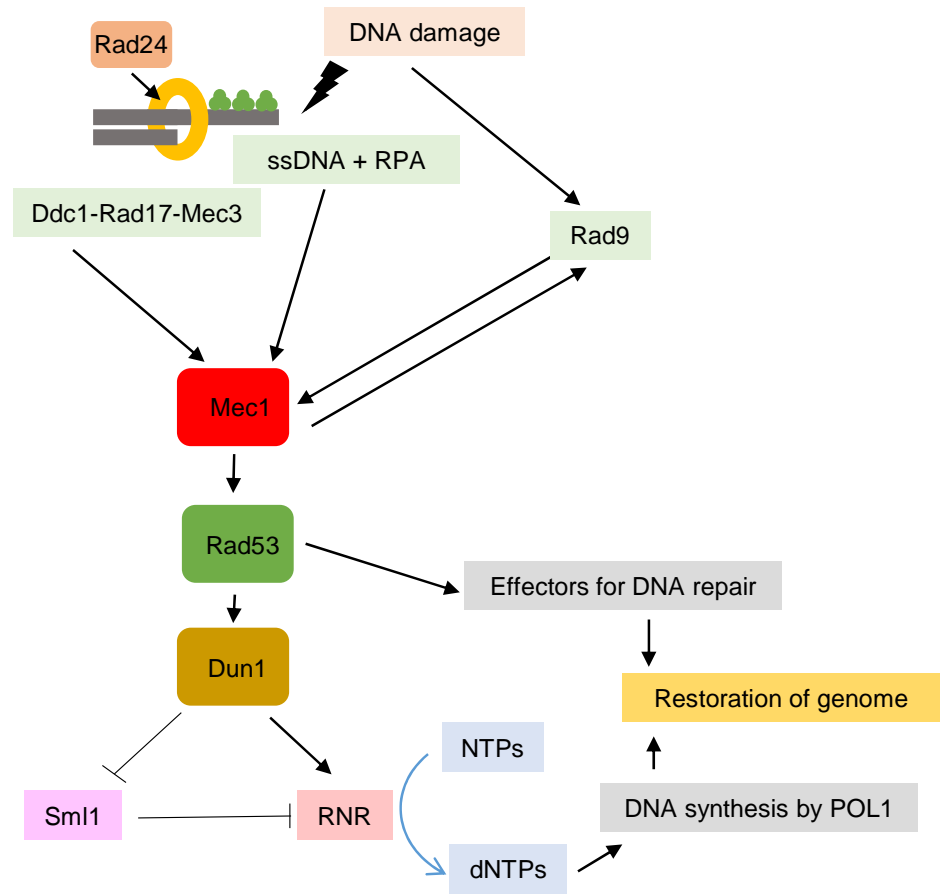
Figure 1.8. The role of Sml1 in the mitotic response to DNA damage. Sml1 represses ribonucleotide reductase activity, which is needed to produce dNTPs. In response to DNA damage during vegetative cell growth, Mec1 activation causes repression of Sml1 activity via Rad53 and Dun1, allowing the production of more dNTPs which facilitate DNA repair. In the absence of Mec1, Sml1 is no longer repressed and so can continue to inhibit RNR, reducing the number of dNTPs available for DNA damage repair. Multiple DNA damage sensors activate Mec1, including RPA-bound ssDNA, the Ddc1-Rad17-Mec3 clamp loaded by Rad24-RFC, and Rad9. Rad9 is hyper phosphorylated by Mec1 in response to DNA damage, and the activated Rad9 then enhances Mec1 phosphorylation of Rad53 (Emili, 1998; Sweeney et al., 2005). Thus, the loss of Rad24 alone is predicted to only partly reduce Sml1 repression.

1.14. Role of Mec1 and Rad24 in CO formation

One of the functions of the DNA damage response proteins Mec1 and Rad24 is the promotion of CO formation (Grushcow *et al.*, 1999). This study found that checkpoint mutants *rad24Δ* and *mec1-1 smlX* had an approximately twofold decrease in interhomologue recombinants using the *HIS4::LEU2* assay, likely due to loss of ability to arrest meiosis in response to impaired meiotic recombination. The similar phenotype in both mutants suggests that Rad24 indirectly promotes CO formation as a consequence of Mec1 activation, rather than acting separately. However, it has recently been discovered that Rad24 is necessary for loading ZMM proteins, and interacts physically with Zip3, independent of Mec1 (Shinohara *et al.*, 2015). This indicates that Rad24 may promote the loading of ZMM proteins at sites of future COs.

Rad24 also has a meiotic role in limiting DSB resection, which was not seen in a Mec1 mutant (Gray e*t al*., 2013). This observation is counter to one suggesting Rad24 is important for promoting resection of vegetative DSBs (Ngo & Lydall, 2015). This discrepancy may be explained by the fact that Rad9 recruitment is required for vegetative DSB resection regulation, and Rad9 is not required for checkpoint activation in meiosis (Lydall *et al*., 1996). The mechanism of Rad24 resection regulation may be via the loading of the 9-1-1 clamp, which provides a physical barrier to resection.

1.15. Roles of Mec1 and Rad24 in CO and DSB interference

There has been very little investigation into the roles of Mec1 and Rad24 in DSB or CO interference. Mec1 has been shown to be a mediator of *trans* DSB interference via tetrad analysis at the *HIS4::LEU2* hotspot (Zhang *et al.*, 2011). A reduction in DSB interference can be indicated by an increase in concerted Spo11-DSB formation; while a *tel1Δ* mutant had an increase in double-cuts (closely juxtaposed DSBs), a *rad24Δ* mutant did not (Garcia *et al.*, 2014). However, this measurement was only made at a few loci, which may not reflect the genome-wide situation.

1.16. Evidence for a role in DSB interference for Tel1

DSBs do not occur independently, but are subject to interference among the four chromatids. This interference occurs in *cis* (adjacent on the same chromatid), and *trans* (between chromatids). All DSBs are proposed to be constrained to occur only once per pair, and some to occur only once per quartet, indicating communication between homologous chromosomes. This *trans* inhibition effect spreads for some distance along the chromosome, likely contributing to even spacing of DSBs (Zhang *et al.*, 2011).

Mec1 and Tel1 have been shown to be mediators of *trans* DSB interference via tetrad analysis at the *HIS4::LEU2* hotspot, showing that DSB formation is no longer constrained to occur only once per quartet of chromatids in Tel1 and Mec1 mutants (Zhang *et al.*, 2011).

Tel1 has also been shown to mediate *cis* DSB interference (Garcia *et al.*, 2014). This study utilized a method of monitoring recombination by Southern blot analysis of DNA extracted from cells undergoing meiosis. By assessment of the frequency of multiple cleavages among four chromosomes, this study found that over large distances (~150 kb), DSBs tend to form independently of each other regardless of Tel1 presence, as in Zhang *et al.* (2011). However, over a range of 10-70 kb, interference was lost in the absence of Tel1. An estimation of interference was obtained by measuring the frequencies of coincident DSB formation (double-cuts) at the *HIS4::LEU2* and *ARE1* loci and comparing them to the values that would be expected if DSB formation was random. Intriguingly, over very short distances (<10 kb), loss of Tel1 was found to cause concerted DSB formation, an activity known as DSB clustering or negative interference. According to the tethered-loop axis model, Spo11-DSB catalysis is triggered by the tethering of small chromatin loops to the chromosome axis (Panizza, *et al.,* 2011; Blat *et al.*, 2002). An anticorrelation was identified between negative interference and chromosome axis component RMM, suggesting that the clustering domains are confined within chromatin loop domains. In contrast, the downregulation of the Mec1 branch of the DDR checkpoint pathway, enacted by deletion of Rad24, did not have a significant effect on double-cut frequencies at these loci.

1.17. Evidence for a role in CO interference for Tel1

The occurrence of a CO event reduces the chance of another CO event occurring in proximity, a phenomenon known as CO interference. The majority of COs in yeast display interference and are formed by the activity of Msh4/Msh5, but Class II COs formed by the activity of Mus81, Yen1 or Slx1-Slx4 do not (Novak *et al.*, 2001; de los Santos, 2003).

It has been shown that Tel1 has a role in CO interference, specifically by limiting ZMM-independent recombination, i.e. reduces the number of Class II COs but does not affect the number of Class I COs (Anderson *et al.*, 2015). This study used whole-genome mapping of recombination products in eight MMR-proficient *tel1Δ* hybrid tetrads, along with six *tel1Δ zip3Δ* tetrads. The parental strains were S96 and YJM789, which have about 65,000 polymorphisms giving a median resolution of 81 bp. The study also found that *tel1Δ* increases recombination levels for both COs and NCOs, correlating with the increased levels of DSB

formation shown by Garcia *et al.* (2015), and that the distribution of all detectable recombination events was altered in *tel1Δ*, supporting a role for Tel1 in DSB interference (Anderson *et al.*, 2015). However, their use of recombination products as indicators of DSB locations is imperfect as not all DSBs produce detectable recombination products, especially in MMR-proficient backgrounds which disguise NCO numbers (Martini *et al.*, 2011).

The number and distribution of Zip3 foci in *tel1Δ* is not significantly different to WT, suggesting normal interference in Class I COs. In addition, CO number is less affected by *ZIP3* deletion in *tel1Δ* than in WT. The percentage of all detected events that are COs is ~72% in WT and ~39% in *zip3Δ*, but there is a smaller decrease between *tel1Δ* (~67%) and *tel1Δ zip3Δ* (~49%), indicating that COs are less dependent on Zip3 in the absence of Tel1 (Anderson *et al.*, 2015).

1.18. The role of Ndt80 in meiosis

NDT80 was identified in a general screen for mutants defective in spore formation (Xu *et al.*, 1995). It is a meiosis-specific transcription factor for genes with middle sporulation elements (MSEs), and is required for pachytene exit and meiotic progression. *NDT80* expression is an important step in meiosis, and it is highly regulated. The initial transcription of *NDT80* is caused by protein kinase Ime2, after which Ndt80 causes a positive feedback loop by binding to its own promoter (which also contains an MSE) and enhancing its own transcription, ensuring irreversible meiotic commitment (Chu and Herskowitz, 1998). The normal activation of *NDT80* likely takes place somewhere between 4-5 hours into meiosis, since this is when WT and *NDT80* phenotypes begin to diverge (Xu *et al.*, 1995). Ndt80 is also subject to posttranslational regulation, as it must be phosphorylated before it can act as a transcription factor. Premature meiotic expression causes Ndt80 to accumulate in non-phosphorylated state until it is modified by Ime2 (Sopko *et al.*, 2002).

The meiotic recombination checkpoint inactivates Ndt80 in response to DNA damage via Mek1 (Prugar *et al.*, 2017). High levels of Mek1 activation correspond to low levels of Ndt80 activation. As DSBs are repaired, Mek1 activity is reduced until Ndt80 activation is allowed (Prugar *et al.*, 2017). This is important to prevent cells from exiting meiotic prophase before recombination is complete. The DDR checkpoint is also thought to repress NDT80 transcription via Sum1 (Lindgren *et al.*, 2000; Pak & Segall, 2002). Sum1 is a transcriptional repressor which, like Ndt80, binds to MSEs (Xie *et al.*, 1999). Sum1 levels decrease over the course of meiosis, but the decrease is halted during checkpoint arrest (Lindgren *et al.*, 2000).

ndt80Δ yeast arrest in meiotic prophase with fully synapsed chromosomes and unresolved dHJs (Allers & Lichten, 2001). Spindle pole bodies are duplicated but do not separate. SCs appear at the same time as in a wild-type strain (~4 h), but continue to accumulate and persist for at least 15 hours. There is some evidence that the SCs would eventually decay at later time points. Around 55% of *NDT80*-arrested cells were found to contain large Zip1 polycomplexes (aggregates of SC material) (Bhuiyan *et al.*, 2002). A *HIS4::LEU2* locus assay showed that the *ndt80Δ* mutant exhibits normal levels of DSB formation, but only 50% of the wild-type level of COs (Xu *et al.*, 1995). However, this assay was only performed at one particular locus.

1.19. Spo11 hypomorph alleles

The importance of Spo11-DSBs to the timing of meiosis can be investigated by using hypomorphic Spo11 (hypo-*spo11*) alleles. *SPO11-HA3-His6* ('*Spo11-HA*') has a C terminal epitope (haemagglutinin) tag, a total of 33 amino acids in length. *Spo11-HA* is reported to reduce the formation of Spo11-DSBs by 11-50% (Martini *et al.*, 2006). Spore viability is also slightly reduced, by ~2% compared to WT. The reason for this is unknown, but it may be that the tag physically interferes with Spo11 activity.

spo11-D290A has a point mutation occurring in a putative Toprim domain, thought to be involved in DSB catalysis via the coordination of Mg2+ (Diaz *et al.*, 2002). Under standard conditions, *spo11-D290A* only has a mild recombination defect phenotype (spore viability of ~87%), but if sensitized by other conditions, the defects become much more severe e.g. sporulation at the low temperature of 16°C gives a viability of ~2% (Martini *et al.*, 2006; Diaz *et al.*, 2002).

Interestingly, the *spo11-D290A* and *spo11-HA* alleles also cause a synergistic decrease in spore viability when combined: HA-tagged *spo11-D290A* has a spore viability of 19.3% and reduced DSB formation, which suggests the tag and the point mutation affect Spo11 activity in different ways (Diaz *et al.*, 2002).

1.20. Interaction between Ndt80, Spo11 and Rad24

Wild type SK1 budding yeast strains have a spore viability of ~97%. The deletion of the DDR checkpoint protein Rad24 reduces spore viability to ~25%, and this can be rescued to ~50% by an 8 hour prophase arrest mediated by transient *NDT80* repression (Gray *et al.* 2013). Budding yeast with a hypo-*spo11* allele, such as *spo11-HA* or *D290A*, do not have significantly decreased viability compared to WT. Surprisingly, when hypo-*Spo11* is combined with *rad24Δ*, a synergistic reduction in viability to just 5% is observed. Interestingly, in the *rad24Δ* hypo-*spo11* strains, eight hours of *NDT80*-mediated prophase arrest improves spore viability to ~70%

(Gray *et al.*, 2013). Similarly, P$_{CLB2}$-MEC1, a conditional Mec1 allele expressed only in mitosis, has a spore viability of ~50%, and when combined with hypo-*spo11*, this drops to ~7% (Gray *et al.*, 2013).

A possible explanation for the mechanism of the rescue of spore viability in *rad24Δ* and hypo-*spo11* is simply that the prophase arrest allows more time for DSBs to be formed and repaired (Gray *et al.*, 2013). For *rad24Δ*, the prophase arrest essentially replaces the function of the checkpoint, restoring the cell cycle arrest that is lost in the absence of Rad24. For the hypo-*spo11*, the arrest allows more time for the less efficient protein to make DSBs. However, it is important to note that spore viability is not restored to WT levels, so there are additional deleterious effects of the *rad24Δ* and hypo-*spo11* mutations that are not rescued by the arrest.

The recruitment of Mec1 to DSBs requires the formation of RPA-coated ssDNA via resection of the DSB (Clerici *et al.*, 2014). Thus, inefficient DSB formation due to a hypo-*spo11* allele is expected to cause a weaker checkpoint response, as would the loss of Rad24. A synergistic reduction in DSB signal also occurs in *rad24Δ* hypo-*spo11* strains, which can be rescued by transiently extending meiotic prophase (Gray *et al.*, 2013). This explains why the combination of *rad24Δ* and hypo-*spo11* causes a greater reduction in spore viability than either alone.

Since Ndt80 expression is likely repressed during checkpoint arrest, a weakened checkpoint response is expected to cause precocious Ndt80 expression, leading to an early exit from meiotic prophase and reducing the amount of time available for DSB formation by the already-inefficient hypo-*spo11*. This explains why prophase arrest is more beneficial to spore viability than expected in a *rad24Δ* hypo-*spo11* background.

However, it is unclear why spore viability in rad24Δ hypo-Spo11 is higher than that of *rad24Δ* when prophase is extended to 8 h. It is possible that one contributing factor to the lower spore viability of *rad24Δ* +8 h is an excessive number of DSBs, which is rescued by a hypo-*spo11* allele. Thus, *rad24Δ* viability is negatively affected by both too few DSBs (hypo-*spo11*) and by too many DSBs (extended prophase), though having too few DSBs is more deleterious than having too many. This implies that Rad24 has a role in controlling DSB number.

1.21. Assaying Meiotic recombination

In order to better understand the processes controlling recombination events, it is desirable to monitor changes in the frequency and distribution of various types of events in mutant strains for genes of interest. To study recombination event outcomes and positioning, a system is needed to allow the formation, detection and categorization of recombination events. During *S. cerevisiae* meiosis, a diploid cell divides into four haploid spores (a tetrad), which can be separated physically and cultured separately. The genotype of each spore can then be examined to reconstruct recombination events. In the absence of recombination, markers will show a continuous Mendelian segregation pattern (2:2). COs are identified as the junction between two different 2:2 segregations, which indicate a reciprocal exchange. There may also be gene conversion tracts associated with COs, appearing as non-Mendelian (3:1) segregation of markers around the reciprocal exchange. 3:1 patterns observed without a reciprocal exchange indicate the presence of a NCO.

Historically, recombination could only be detected at a small number of loci with nutritional or antibiotic resistance markers (Papazian, 1952). For example, the *leu2-R* and *leu2-K* mutations can be utilized, which occur in the *LEU2* coding sequence and eliminate either the EcoRI or KpnI restriction sites at nucleotides 1295 and 909 (Lichten *et al.*, 1986). Diploids heterozygous for *leu2-R* and *leu2-K* may produce *LEU2* recombinants, which are detected by assaying for auxotrophy.

However, this method can only give a narrow view of a few loci, and very little information is discovered about the recombination events in a single cell. It is possible that the few loci examined are not representative of the average of all loci. To examine, genome wide and at high spatial resolution, as many recombination events as possible in a single meiosis, polymorphisms must be present at many thousands of loci. The established method is to mate two highly divergent yeast strains, producing a hybrid diploid naturally heterozygous for tens of thousands of alleles (Winzeler *et al.*, 1998). For example, the genomes of SK1 and S288c strains are composed of ~0.7% polymorphisms, and an S96xYJM789 hybrid cross contains 0.6% variants (Martini *et al.*, 2011; Anderson *et al.*, 2011).

After sporulation of the hybrid diploid, the recombination outcomes in each resultant tetrad can be detected by the use of microarrays or high-throughput sequencing to genotype single-nucleotide polymorphisms (SNPs) and insertions/deletions (indels), allowing the determination of the regions of the genome derived from each parent. This information allows recombination events to be reconstructed (Chapter 4, Figure 4.1).

This approach allows detection of most recombination events in a single meiosis, allowing the frequency and distribution of events in a single cell to be examined. It is still not possible to detect any events occurring between sister chromatids, since both chromatids have identical sequences; however, these events are thought to be rare in wild type meiosis because most repair happens between homologs (Schwacha & Kleckner, 1997; Kim *et al.*, 2010). In addition, NCOs may be missed if they occur between markers, or if they result in restoration of the original genotype rather than conversion, both of which prevent the detection of parental polymorphism exchanges.

Polymorphisms occurring in repetitive regions such as rDNA, telomeres, and Ty-element containing regions are not considered due to the difficulty of pinpointing their genomic locations. Thus, any recombination events occurring in repetitive regions will not be detected, though such events are rare in a WT background (Petes & Botstein, 1977; Pan *et al.*, 2011). DSBs formed in repetitive regions can cause ectopic recombination leading to genome rearrangement (reviewed in Sasaki *et al.*, 2010).

An example of a study utilizing microarray hybridization to detect recombination events genome wide comes from Mancera *et al.*, 2008. This study used an S288c/YJM789 hybrid budding yeast strain, with ~52,000 SNP markers (median distance between markers 78 bp, when repetitive regions are excluded). Genomic DNA from all four products of fifty-one wild-type yeast meioses was hybridized to high-density microarrays tiling the genomes of S288c and YJM789. In this method, genotypes are inferred from the hybridization intensities of the probes covering each polymorphism. The high density of markers used allowed detection of both the CO and the shorter NCO gene conversion tracts. However, it is likely that many NCOs are missed by this method due to occurring between markers, or because MMR has restored the original genotype. In addition, this study only looked at SNP-type polymorphisms, excluding information from indels (Mancera *et al.*, 2008).

An example of a study utilizing high throughput sequencing to detect recombination outcomes comes from Anderson *et al.*, 2011. This used an S96xYJM789 hybrid cross, with ~60,000 SNPs and ~6,000 indels (median distance between markers 56 bp). Sequencing on the Illumina platform requires the preparation of a library of ssDNA fragments, which are immobilized on a flow cell and amplified to form clusters. Fluorescent nucleotides are then added and clusters are imaged to determine which fluorophore, and thus which nucleotide, was used in synthesis. The output of nucleotides allows reconstruction of the sequence of the DNA in the cluster. The DNA sequences can then be aligned to the parental genomes to detect polymorphisms. This method

typically gives a higher resolution of recombination event data than microarray hybridization due to higher coverage of the yeast genome.

In the study by Anderson *et al.*, 2011, the read lengths were 36-43bp long and 27x average coverage of the yeast genome was obtained. Reads of this short length need stringent alignment criteria as allowing mismatches can result in incorrect mapping. From this data they were able to obtain information on both simple CO and NCO events and more complex recombination events such as clusters of multiple COs and/or NCOs. The method described by Anderson *et al.* was subsequently used to examine recombination in S96xYJM789 strains heterozygous for hypo-*spo11* alleles, finding that reduced Spo11 activity causes significantly longer gene conversion tracts associated with COs (Rockmill *et al.*, 2012).

In addition, Oke *et al.*, 2014 utilized the method to quantify recombination in *sgs1* and *mms4-md* mutants, finding an increase in aberrant recombination in both. In *sgs1*, there were more multichromatid events (3-4 chromatids), while in *mms4-md*, increased scarring (frequent genome changes) was detected near recombination events occurring on 1-2 chromatids. The authors explain both as multiple strand invasions from complex repair of a single DSB, however the same patterns could be produced by the repair of multiple DSBs.

It is important to note that any method relying on 4-spore viable tetrads for genomic analysis is potentially susceptible to bias; in a severe mutation with a low percentage of 4-spore viables, the recombination events may not be representative of the population but instead represent an extreme case. Also, particularly deleterious recombination events cannot be captured e.g. ectopic recombination that produces acentric/dicentric chromosomes will result in cell death.

A bias has only been previously shown when sporulation was very inefficient (0.4% tetrads formed) as in the *zip1* mutant (Chen *et al.*, 2008). In this case, high levels of CO formation were detected in *zip1* mutant strains via sequencing tetrads, but not by genetic and physical data, indicating that only cells with an unusually high number of COs managed to sporulate and thus were able to be dissected and sequenced. However, COs near centromeres were shown to be increased by both methods (Chen *et al.*, 2008).

1.22. Caveats of whole-genome recombination assays

Using whole-genome mapping of recombination products means that almost all recombination from an individual meiosis can be detected, allowing detailed examination of the relationships between events across the entire genome. However, there are caveats to this method.

Firstly, exact DSB locations cannot be determined, only approximated by event locations. Since not every DSB produces a visible recombination event, many DSBs will not be represented at all by recombination event data. Around 15-30% of meiotic DSBs are thought to repair with the sister chromatid (Schwacha & Kleckner, 1997).

Based on the proportion of CO events that occur without detectable conversion tracts, ~14% of NCO events are predicted to occur between markers in the WT strain (Martini *et al.*, 2011), although this is only correct if conversion tract lengths are equal between CO and NCO products. In addition, based on the number of NCO events composed only of hDNA, ~30% of NCOs are estimated to be restored to the original genotype by mismatch repair (Chapter 5, section 5.2.1). These issues in pinpointing DSB locations may be expected to affect measurements of DSB interference. However, the calculated strength of DSB interference has been found to be mostly constant regardless of event density, assuming that the undetectable events occur uniformly in the genome (Zhang *et al.*, 2014; Anderson *et al.*, 2015).

Secondly, when examining recombination genome-wide, fewer events will be detected per hotspot. Roughly 150-250 events are detected in most meioses, so it is unlikely that any given hotspot of interest will contain an event in a single meiosis, let alone multiple events between samples. This means that any event occurring at a hotspot may not be representative of recombination activity generally at that hotspot. In contrast, a detailed analysis of recombination at one hotspot using Southern blot analysis of DNA extracted from cells undergoing meiosis represents an average of tens of millions of meiotic recombination events at that locus (Garcia *et al.*, 2014). However, since this an average, it is not possible to know the exact nature of any individual recombination event, unlike NGS marker analysis. Thus, both methods have specific advantages in this case.

Thirdly, as described above, this analysis cannot be done in backgrounds with a very low spore viability, since all four products of recombination are required. Southern blot analysis can be used to view recombination without culturing the spores, so can be done in any background including mutants with a severe inviable spore phenotype. In addition, backgrounds with a borderline spore viability (very low but still occasionally produces four viable spores) may produce a selection bias. For example, a strain with 2% of tetrads containing four viable spores

has 98% of meioses result in failure, but only the 2% of successful meioses are being assayed, which may not be representative of the failed meioses.

1.23. Recombination is impaired in a hybrid diploid

The high number of polymorphisms between SK1 and S288c make this cross desirable for high resolution genotyping. However, there is also a decrease in spore viability associated with increasing sequence divergence (Liti *et al.*, 2006). This is known as hybrid incompatibility and is caused by the action of MMR proteins preventing recombination between divergent sequences, a protective activity that reduces chromosomal rearrangements (Myung *et al.*, 2001), but also enforces reproductive barriers between species (Hunter *et al.*, 1996). Increasing sequence divergence is also associated with decreasing efficiency of hDNA formation in mitotic and meiotic cells (Datta *et al.*, 1997; Chen & Jinks-Robertson, 1999), thought to be because MMR proteins detect and reject hDNA intermediates that contain mismatches.

Thus, the high amount of heterozygosity between SK1 and S288c could affect meiotic recombination, affecting both recombination outcomes and locations due to highly diverse regions being selected against by the MMR proteins. However, in wild *S. cerevisiae* populations, most individuals are heterozygous (reviewed in Mortimer 2000; Borts & Haber, 1987), indicating that outbreeding is common; thus, a heterozygous cross may be more representative of wild type conditions than a homozygous cross, discounting the inbreeding that occurs during colony germination.

There is a known incompatibility between SK1 and S288c *MLH1* and *PMS1* alleles (Heck *et al.*, 2005), *MLH1-PMS1* being vital for post replicative MMR as the primary MLH heterodimer in *S. cerevisiae*. When the S288c allele of *MLH1* was combined with the SK1 allele of *PMS1*, an approximately 100-fold higher mutation rate was observed, along with a reduction in longterm fitness in the progeny derived from crossing S288c and SK1 strains (Heck *et al.*, 2005). However, Martini *et al.*, 2011 found that the fraction of COs associated with conversion tracts found in a WT SK1xS288c hybrid was comparable to that found in YJM789 x S288c hybrid (which does not have the *MLH1-PMS1* incompatibility), indicating that the partial MMR defect in SK1 xS288c hybrids has a negligible effect (assuming that the YJM789xS288c cross does not itself produce another unknown MMR defect).

1.24. The use of MMR-deficient strains increases meiotic recombination rate and allows observation of post-meiotic segregation

During homologous recombination, the pairing of complementary DNA between donor and recipient strands produces heteroduplex DNA (hDNA) with mismatches at heterozygous positions (White *et al.*, 1985; Williamson *et al.*, 1985; Bishop *et al.*, 1987; Allers & Lichten, 2001). The mismatches are usually repaired by MMR machinery to give either gene conversion or restoration of the original genotype, producing 3:1 or 2:2 segregation patterns respectively.

If any mismatches remain unrepaired (by chance or due to a deficiency of the MMR system), the semi-conservative nature of DNA replication means that the alleles will segregate during the first mitotic division. This phenomenon, known as post-meiotic segregation (PMS), has implications for inheritance patterns, causing non-Mendelian inheritance ratios for simple traits, and mosaicism in multicellular organisms where the first zygotic division produces cells with different alleles (Surtees *et al.*, 2004; Leslie & Watt, 1984).

A simple way to observe PMS in fungi is by the formation of sectored colonies grown from a single spore when PMS has occurred in markers conferring a phenotype (Esposito, 1971). However, the implications of PMS for inheritance merit a genome-wide investigation as well as single loci. In order to detect PMS on a wide scale, it is necessary to allow each spore of a tetrad to germinate and undergo one mitotic division, then score genetic markers in the resulting eight cells (an octad).

By this method, each of the dissected spores is allowed to germinate and divide mitotically, and the resulting cells separated to give four pairs of mother and daughter cells per tetrad. The genotypes of mother and daughter cells are compared in order to identify markers where PMS occurred. This essentially allows reconstruction of the post-meiotic sequence of the eight individual DNA strands from the four chromatids of the diploid hybrid. Thus in addition to the usual Mendelian 2:2 and non-Mendelian 1:3 marker segregation patterns encountered in tetrads, octads can display 5:3 patterns, indicating half-conversion tracts which can be associated with either COs or NCOs.

Previous genome wide studies of PMS include Mancera *et al.*, 2011. This study examined post-meiotic segregation in four octads, genotyping using tiling microarrays in the same way as in Mancera *et al.*, 2008. However, this was in a MMR-proficient background, relying on mismatches being left unrepaired by chance. Nonetheless, PMS events were detected in nearly 10% of recombination events (with equal relative frequency in COs and NCOs).

However, a much higher level of PMS was detected by Martini *et al.*, 2011, using microarray tiling for genotyping in a SK1 x S288c hybrid MMR-deficient background, providing a genome-wide view of hDNAs associated with COs and NCOs. This study found that 83% of events contain 5:3 or 3:5 segregation patterns, indicating PMS. The SK1 x S288c cross contains ~62000 sequence polymorphisms with a median inter-marker distance of 77 bp, and few regions longer than 10kb devoid of polymorphisms. These characteristics are desirable for high-resolution genotyping.

SK1 and S288c have a relatively high sequence divergence of around 0.7%, but the hybrid undergoes meiosis efficiently and has a spore viability of around ~70%, reduced to ~63% in the absence of MMR. The S288cxSK1 hybrid strain sporulates efficiently (88%), much like a pure SK1 strain (Laureau *et al.* 2016).

In order to reveal hDNA intermediates, Martini *et al.*, 2011 chose to inactivate MMR via the disruption of the MutS homolog *MSH2* because Msh2 covers a wide scope of mismatch recognition, but unlike the MutL homologues *MLH1* or *MLH3*, which can promote meiotic CO formation (Hunter & Borts, 1997; Al-Sweel *et al.*, 2017), it does not affect meiotic recombination in the absence of DNA polymorphisms (Hunter *et al.*, 1996). However, it was observed that in the presence of DNA polymorphisms, the absence of Msh2 increased CO numbers from ~73 to ~92 (Martini *et al.*, 2011). In *msh2Δ* the COs were properly distributed, with all chromosomes having at least one CO, a median distance between COs that was not significantly different than that in the WT hybrid, and a positive correlation between CO numbers and chromosome size (Martini *et al.*, 2011). In fact, this correlation is even stronger in *msh2Δ* than WT, suggesting that the presence of polymorphisms slightly affects CO distribution. Since Msh2 only reduces CO numbers in the presence of polymorphisms, this suggests that the polymorphisms are the cause of the CO reduction via the action of Msh2. It may be the case that MMR proficiency causes DSBs in variant-rich regions to be repaired with the sister chromatid, which would produce an undetectable event. This is supported by the fact that meiotic DSBs are repaired with the sister chromatid if they form at a locus lacking homology (Goldfarb & Lichten, 2010).

The deletion of Msh2 causes a reduction in spore viability, which may be at least partly due to unrepaired mutations accumulated during vegetative growth of the SK1 and S288c haploids, and/or the hybrid diploid. Though *msh2Δ*-mediated MMR deficiency reduces spore viability in WT and *tel1Δ* backgrounds, it improves spore viability in DDR checkpoint-deficient hybrid backgrounds, as discussed in Chapter 3.

1.25. Bioinformatic solutions for detection and classification of recombination genome-wide

In order to analyse recombination events genome-wide, it is necessary to have a list of variants and the parental genotypes at each position, a method of identifying recombination products and a way to consistently deal with the classification of simple and complex events.

To extract a list of polymorphisms, sequencing data from hybrids can be aligned to one or both parental genomes. There are many existing programs that can be used for alignment, including Bowtie2 (Langmead *et al.*, 2009) and BWA (Li & Durbin, 2010).

To detect SNPs and indels in this aligned data, it is necessary to identify locations where the read sequences differ from a known reference genome (e.g. van Oeveren & Janssen, 2009). However, apparent variants can occur due to sequencing or alignment error, so a quality score threshold can be used which will depend on read depth and proportions of reads with the variant, so rare variants can be ignored (Li *et al.*, 2008; Li *et al.*, 2009). Programs exist for this purpose e.g. LAGAN (Brudno *et al.*, 2003) or GATK (McKenna *et al.*, 2010).

The genotype of each spore at each position can then be determined by comparing the number of sequencing reads that match the reference sequence for each parent. For example, Laureau *et al.* 2016, used a system where an 'S288c' genotype was assigned at each position if at least 95% of the reads displayed the S288c allele, 'SK1' if at least 75% of reads exhibited the SK1 allele, or 'heterozygous' if 25-95% of the reads were S288c and 5-75% were SK1. The reason for the biased threshold towards S288c was due to the fact that this study only aligned reads once, to the S288c reference.

Once all the spores from a single meiosis have been genotyped, recombination events must be detected and classified from this information. Due to the large number of markers involved, it is not possible to manually annotate every event, so the process of identifying, classifying and describing each event can be automated. The output can then be manually checked to ensure that the program is working as expected, and to deal with any unusual recombination events that may have escaped classification.

Programs exist for this purpose; for example, Anderson *et al.*, 2011 describes a package of programs called 'ReCombine' which is able to classify recombination events from microarray or sequencing data, including 'GenotypeCaller' to determine the genotype for each SNP and indel, and 'CrossOver' which detects various types of recombination events including COs,

NCOs, and GCs, classifies them into categories, and reports event frequency, distribution and conversion tract length. Via GenotypeCaller, genotypes for each polymorphism are provisionally assigned twice, once for each parent, and the two calls are reconciled. Information from each spore in a tetrad is then combined, producing a binary table which can be analyzed by CrossOver. Any polymorphisms that were not genotyped in all four spores are discarded, as it is not possible to determine the nature of any event that occurred at a particular marker location if fewer than four spores can be genotyped at that locus. However, the ReCombine package has no capacity to analyse PMS in octad data. In addition, 4:0 segregation patterns are removed because they may represent mitotic recombination events. This quality control step was also carried out in Martini *et al.*, 2011, who additionally discounted events that were identified from only one marker. However, it is possible that 4:0 segregation patterns could be produced by meiotic recombination, caused by complex event repair or the presence of multiple DSBs. These are expected to be rare in WT, but could be increased in mutants that have lost meiotic recombination control.

1.26. General aims of this project

1. To better understand the role of Rad24 and Mec1 in meiosis, and where those roles may differ.

2. To refine a method to assay recombination events genome-wide.

3. To use this method to analyse recombination levels in wild type and checkpoint mutants.

4. To use high resolution event location data to analyse CO and DSB interference processes in wild type and checkpoint mutants.

Chapter 2.

Methods

Chapter 2. Methods

2.1. Strain creation

All *Saccharomyces cerevisiae* strains used in this study are derivatives of SK1 (Kane and Roth, 1974), S288c (Mortimer and Johnston, 1986), or BY4741, a derivative of S288c (Brachmann *et al.*, 1998). All hybrid yeast strains were derived from a cross of haploid SK1 and S288c or BY4741 parents. Strain genotypes are listed in Table 2.1.

Gene disruptions for *rad24Δ::HphMX*, *msh2Δ::kanMX6*, *mus81Δ::kanMX6* and *tel1Δ::HphMX* were performed by PCR mediated gene replacement using pFA6a-*kanMX6* or pFA6-*hphMX* plasmids (Longtine *et al.*, 1998; Goldstein & McCusker, 1999).

P$_{CLB2}$-*MEC1* strains were created by replacing the natural *MEC1* promoter with the mitosis-specific *CLB2* promoter using pFA6a-*natMX4-PCLB2-3HA* plasmid as a template (Gray *et al.*, 2013; Grandin & Reed, 1993).

The *spo11-HA* allele is produced by tagging *SPO11* with the *HA3-His6*::*kanMX4* epitope (Diaz *et al.*, 2002).

The *spo11-D290A*::*kanMX4* allele is made with a point mutation at the natural *SPO11* locus (Diaz *et al.*, 2002).

The *P$_{GAL}$-NDT80*::*TRP1* allele has the natural *NDT80* promoter replaced by the *GAL1-10* promoter, and strains include a *GAL4*::*ER* chimeric transactivator for β-oestradiol-induced expression (Benjamin *et al.*, 2003).

The *cdc20-1*::*kanMX4* allele is made with a point mutation at the natural *CDC20* locus (Hartwell *et al.*, 1973).

Table 2.1. *S. cerevisiae* **strains used in this study.**

Strain	Background	Mat	Genotype
MJ512	SK1	α	*ho::LYS2 lys2Δ ura3Δ leu2Δ arg4Δ*
MJ513	SK1	a	*ho::LYS2 lys2Δ leu2Δ arg4Δ*
MJ600	S288c	α	*ho::LYS2 lys2Δ ade8Δ*
MJ631	S288c	a	*ho::LYS2 lys2Δ ade8Δ*
MJ43	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ::hisG trp1Δ::hisG his4XΔ::LEU2 nuc1ΔΔ::LEU2 PGAL1-NDT80::TRP1 ura3::pGPD1-GAL4(848)-ER::URA3*
MC42	S288c	a	*ho::LYS2 lys2Δ ade8Δ ndt80ΔΔ::Kan*
MC25	SK1	a	*ho::LYS2 lys2Δ arg4Δ leu2Δ msh2Δ::Kan*
MC26	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ msh2Δ::Kan*
MC51	S288c	α	*ho::LYS2 lys2Δ ade8Δ msh2Δ::Kan*
MC49	S288c	a	*ho::LYS2 lys2Δ ade8Δ msh2Δ::Kan*
MC214	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan*
MC215	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan*
MC230	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan msh2Δ::Kan*
MC231	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan msh2Δ::Kan*
MC254	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ mlh3ΔΔ::KanMX6*
MC255	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ mlh3ΔΔ::KanMX6*
MC264	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ yen1Δ::hphMX*
MC265	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ yen1Δ::hphMX*
MC271	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ mlh3Δ::KanMX6 mus81Δ::KanMX6*
MC272	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ mlh3Δ::KanMX6 mus81Δ::KanMX6*
MC267	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ yen1Δ::hphMX mus81Δ::KanMX6*
MC268	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ yen1Δ::hphMX mus81Δ::KanMX6*
MC277	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ yen1Δ::hphMX mlh3Δ::KanMX6*
MC278	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ yen1Δ::hphMX mlh3Δ::KanMX6*
MC17	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4*
MC18	SK1	α	*ho::LYS2 lys2Δ URA3 arg4Δ leu2Δ rad24Δ::HphMX4*
MC19	S288c	a	*ho::LYS2 ade8Δ rad24Δ::HphMX4*
MC20	S288c	α	*ho::LYS2 ade8Δ rad24Δ::HphMX4*
MC31	BY474	a	*ho::LYS2 lys2Δ his4 ura3Δ leu2Δ rad24Δ::HphMX4*
MC32	BY474	α	*ho::LYS2 lys2Δ his4 ura3Δ leu2Δ rad24Δ::HphMX4*
MC107	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 msh2Δ::Kan*
MC105	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 msh2Δ::Kan*
MC202	S288c	a	*ho::LYS2 ade8Δ rad24Δ::HphMX4 msh2Δ::Kan*
MC203	S288c	α	*ho::LYS2 ade8Δ rad24Δ::HphMX4 msh2Δ::Kan*
MC223	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan rad24::hphMX*
MC222	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan rad24::hphMX*
MC227	S288c	α	*ho::LYS2 lys2Δ ade8Δ mus81Δ::Kan rad24::hphMX*
MC247	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ rad24Δ::HphMX4 mlh3Δ::KanMX6*
MC248	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ rad24Δ::HphMX4 mlh3Δ::KanMX6*
MC251	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 yen1Δ::hphMX*
MC252	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 yen1Δ::hphMX*
MC262	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 mlh3Δ::KanMX6 yen1Δ::hphMX*
MC263	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 mlh3Δ::KanMX6 yen1Δ::hphMX*
MC257	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ rad24Δ::HphMX4 mus81Δ::KanMX6 mlh3Δ::KanMX6*
MC258	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ rad24Δ::HphMX4 mus81Δ::KanMX6 mlh3Δ::KanMX6*
MC101	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 sml1Δ::URA3*
MC103	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 sml1Δ::URA3*
MC59	BY474	a	*ho::LYS2 lys2Δ his4 ura3Δ leu2Δ sml1Δ::URA3 rad24Δ::HphMX4*
MC61	BY474	α	*ho::LYS2 lys2Δ his4 ura3Δ leu2Δ sml1Δ::URA3 rad24Δ::HphMX4*
MC273	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 yen1Δ::hphMX mus81Δ::KanMX6*
MC274	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ rad24Δ::HphMX4 yen1Δ::hphMX mus81Δ::KanMX6*
MC190	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ msh2Δ::Kan rad24::HphMX4 sml1Δ::URA3*
MC193	BY474	a	*ho::LYS2 lys2Δ his4 ura3Δ leu2Δ msh2Δ::Kan rad24::HphMX4 sml1Δ::URA3*

Table 2.1. continued. *S. cerevisiae* **strains used in this study.**

Strain	Background	Mat	Genotype
MC21	SK1	A	*ho::LYS2 lys2Δ arg4Δ leu2Δ tel1Δ::HphMX4*
MC22	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ tel1Δ::HphMX4*
MC23	S288c	a	*ho::LYS2 ade8Δ tel1Δ::HphMX4*
MC24	S288c	α	*ho::LYS2 ade8Δ tel1Δ::HphMX4*
MC234	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan tel1Δ::HphMX4*
MC235	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan tel1Δ::HphMX4*
MC29	SK1	a	*ho::LYS2 lys2Δ arg4Δ leu2Δ tel1Δ::HphMX4 msh2Δ::Kan*
MC30	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ tel1Δ::HphMX4 msh2Δ::Kan*
MC53	S288c	a	*ho::LYS2 lys2Δ ade8Δ msh2Δ::Kan tel1Δ::HphMX4*
MC55	S288c	α	*ho::LYS2 lys2Δ ade8Δ msh2Δ::Kan tel1Δ::HphMX4*
VG120	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 ade2-bglPCLB2-MEC1::Kan*
VG121	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 ade2-bglPCLB2-MEC1::Kan*
MC152	S288c	a	*ho::LYS2 lys2Δ ade8Δ PCLB2-MEC1::Kan*
MC153	S288c	α	*ho::LYS2 lys2Δ ade8Δ PCLB2-MEC1::Kan*
MC163	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG nuc1Δ::LEU2PCLB2-MEC1::Kan msh2Δ::Kan*
MC164	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG nuc1Δ::LEU2 his4XΔ::LEU2PCLB2-MEC1::Kan msh2Δ::Kan*
MC171	S288c	a	*ho::LYS2 lys2Δ ade8Δ PCLB2-MEC1::Kan msh2::HphMX4*
MC172	S288c	α	*ho::LYS2 lys2Δ ade8Δ PCLB2-MEC1::Kan msh2::HphMX4*
MC243	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan PCLB2-MEC1::Kan*
MC242	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ mus81Δ::Kan PCLB2-MEC1::Kan*
MC281	SK1		*ho::LYS2 lys2Δ arg4Δ leu2Δ his4B/X::LEU2 nuc1Δ::LEU2 trp1Δ::hisG ura3Δ::pGPD1-GAL4(848)-ER::URA3 PCLB2-MEC1::Kan Spo11(D290A)::kanMX4*
MC282	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ his4B/X::LEU2 nuc1Δ::LEU2 trp1Δ::hisG ura3Δ::PGPD1-GAL4(848)-ER::URA3 PCLB2-MEC1::Kan Spo11(D290A)::kanMX4*
MC2	SK1	a	*ho::LYS2 lys2Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 trp1Δ::hisG ura3Δ::PGPD1-GAL4(848)-ER::URA3 PCLB2-MEC1::Kan PGALNDT80::TRP1*
MC3	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 trp1Δ::hisG ura3Δ::PGPD1-GAL4(848)-ER::URA3 PCLB2-MEC1::Kan PGALNDT80::TRP1*
MC198	S288c	α	*ho::LYS2 lys2Δ ade8Δ PCLB2-MEC1::Kan ndt80Δ::Kan*
MC211	SK1	a	*ho::LYS2 lys2Δ arg4Δ leu2Δ his4XΔ::LEU2 nuc1Δ::LEU2 trp1Δ::hisG ura3Δ::PGPD1-GAL4(848)-ER::URA3 PCLB2-MEC1::Kan PGAL-NDT80::TRP1 Spo11(D290A)::kanMX4*
MC212	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ his4XΔ::LEU2 nuc1Δ::LEU2 trp1Δ::hisG ura3Δ::PGPD1-GAL4(848)-ER::URA3 PCLB2-MEC1::Kan PGAL-NDT80::TRP1 Spo11(D290A)::kanMX4*
MJ846	SK1	a/α	*ho::LYS2/" lys2Δ/" arg4Δ-nsp/" leu2Δ::hisG/" trp1Δ::hisG/" his4XΔ::LEU2/" nuc1Δ::LEU2/" ura3Δ::PGPD1-GAL4(848)-ER::URA3/"PGAL-NDT80::TRP1/"*
MJ892	SK1	a/α	*ho::LYS2/" lys2Δ/" ura3Δ/" arg4Δ-nsp/" leu2Δ-?/" trp1Δ::hisG/" his4B/X::LEU2/" nuc1Δ::LEU2/" ura3Δ::PGPD1-GAL4(848)-ER::URA3/"PGAL1NDT80::TRP1/" spo11(D290A)::kanMX/"*
MJ847	SK1	a/α	*ho::LYS2/" lys2Δ/" arg4Δ-nsp/" leu2Δ::hisG/" trp1Δ::hisG/" his4XΔ::LEU2/" nuc1Δ::LEU2/" ura3Δ::PGPD1-GAL4(848)-ER::URA3/"PGAL-NDT80::TRP1/" SPO11-HA3His6::KanMX4/"*
MC207	SK1	a	*ho::LYS2 lys2Δ arg4Δ leu2Δ trp1Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 msh2Δ::Kan ura3Δ::PGPD1-GAL4*
MC208	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ trp1Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 msh2Δ::Kan ura3Δ::PGPD1-GAL4*
MC239	S288c	α	*ho::LYS2 ade8Δ rad24Δ::HphMX4 ndt80Δ::Kan msh2Δ::Kan*
MJ835	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ::hisG trp1Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 ura3Δ::PGPD1-GAL4(848)-ER::URA3 PGAL-NDT80::TRP1 rad24Δ::hphMX*
MC89	S288c	a	*ho::LYS2 ade8Δ rad24Δ::HphMX4 ndt80Δ::Kan*
MC120	SK1	a	*ho::LYS2 lys2Δ trp1Δ::hisG arg4Δ leu2Δ his4XΔ::LEU2 nuc1Δ::LEU2 sml1Δ::URA3 ura3Δ::PGPD1-GAL4*
MC122	SK1	α	*ho::LYS2 lys2Δ trp1Δ::hisG arg4Δ leu2Δ his4XΔ::LEU2 nuc1Δ::LEU2 sml1Δ::URA3 ura3Δ::PGPD1-GAL4*
MC139	BY474	α	*ho::LYS2 lys2Δ his4 ura3Δ leu2Δ ndt80Δ::Kan rad24Δ::HphMX4 sml1Δ::URA3*
MJ848	SK1	a/α	*ho::LYS2/" lys2Δ/" arg4Δ/" leu2Δ::hisG/" trp1Δ::hisG/" his4XΔ::LEU2/" nuc1Δ::LEU2/" ura3Δ::PGPD1-GAL4(848)-ER::URA3/"PGAL-NDT80::TRP1/" rad24Δ::hphMX/"*
MJ913	SK1	a/α	*ho::LYS2/" lys2Δ/" arg4Δ/" leu2Δ::hisG/" trp1Δ::hisG/" his4B/X::LEU2/" nuc1Δ::LEU2/" ura3Δ::PGPD1-GAL4(848)-ER::URA3/"PGAL-NDT80::TRP1/" spo11(D290A)::kanMX4/" rad24Δ::hphMX/"*
MJ850	SK1	a/α	*ho::LYS2/" lys2Δ/" arg4Δ/" leu2Δ::hisG/" trp1Δ::hisG/" his4XΔ::LEU2/" nuc1Δ::LEU2/" ura3Δ::PGPD1-GAL4(848)-ER::URA3/"PGAL-NDT80::TRP1/" rad24Δ::hphMX/" SPO11-HA3His6::KanMX4/"*
MC142	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 cdc20-1::Kan rad24Δ::HphMX4*
MC143	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 cdc20-1::Kan rad24Δ::HphMX4*
MC132	SK1	a	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 cdc20-1::Kan*
MC133	SK1	α	*ho::LYS2 lys2Δ ura3Δ arg4Δ leu2Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 cdc20-1::Kan*
MC288	SK1	a	*ho::LYS2 lys2Δ arg4Δ leu2Δ trp1Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 ura3Δ::PGPD1-GAL4(848)-ER::URA3 PGAL-NDT80::TRP mus81Δ::Kan rad24Δ::HphMX4*
MC289	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ trp1Δ::hisG his4XΔ::LEU2 and/or nuc1Δ::LEU2 ura3Δ::PGPD1-GAL4(848)-ER::URA3 PGAL-NDT80::TRP mus81Δ::Kan rad24Δ::HphMX4*
MC286	SK1	a	*ho::LYS2 lys2Δ arg4Δ leu2Δ trp1Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 ura3Δ::PGPD1-GAL4(848)-ER::URA3 PGAL-NDT80::TRP mus81Δ::Kan*
MC287	SK1	α	*ho::LYS2 lys2Δ arg4Δ leu2Δ trp1Δ::hisG his4XΔ::LEU2 nuc1Δ::LEU2 ura3Δ::PGPD1-GAL4(848)-ER::URA3 PGAL-NDT80::TRP mus81Δ::Kan*

2.2. Yeast growth media

YPD: 1% BD Bacto Yeast Extract, 2% BD Bacto Peptone, 0.5 mM Adenine and 0.4 mM Uracil are added to 90% of the required volume in double distilled water and autoclaved. Once cooled, 20% D-Glucose is added to a final concentration of 2% and to bring the total to 100% of the required volume. For YPD plates, 2% Bacto Agar is added prior to autoclaving and D-glucose addition.

YPA: 1% BD Bacto Yeast Extract, 2% BD Bacto peptone, and 1% potassium acetate are added to the required volume and autoclaved.

Drug selection plates for marker selection and strain genotyping are made by producing YPD as above and adding the relevant drug to the final concentrations listed in Table 2.2. For plates, 2% Bacto Agar is added prior to autoclaving.

Table 2.2. Drug concentrations.

Drug	Final Concentration
G418	200 µg/ml
Hygromycin	300 µg/ml

Drop-out liquids and plates for marker selection and strain genotyping are made as follows: 0.675% Yeast Nitrogen Base with ammonium sulphate, 2% Glucose and the relevant amino acids are combined to the final concentrations listed in Table 2.2. For plates, 2% Bacto Agar is added prior to autoclaving.

Table 2.3. Amino acid concentrations.

Amino Acid	Final Concentration
Adenine Sulphate	0.02%
Arginine	0.02%
Aspartic Acid	0.1%
Histidine	0.02%
Leucine	0.06%
Lysine	0.03%
Methionine	0.02%
Phenylalanine	0.05%
Threonine	0.2%
Tryptophan	0.02%
Tyrosine	0.03%
Uracil	0.02%

2.3. Yeast Transformation

A single colony of cells is inoculated into 4 ml of YPD and grown overnight at 30 °C. Cell density is measured and 50 ml of YPD is inoculated to a cell density (OD600) of 5×10^6 cells/ml and grown to a cell density of 2×10^7 cells/ml. Cells are spun for 5 minutes at 3,000 $\times$g. The supernatant is aspirated and the pellet is resuspended in 50 ml double distilled water and spun again for 5 minutes at 3,000 $\times$g. The supernatant is aspirated and the pellet is resuspended in 1 ml of 100 mM lithium acetate, transferred to 1.5 ml tubes and spun at 1,000 $\times$g for 1 minute. The lithium acetate is aspirated and the pellet is resuspended in a volume of 100 mM lithium acetate necessary to give a cell density of 2×10^9 cells/ml. 50 µl of cells per transformation are transferred to 1.5ml tubes. Tubes are spun at 4,600 $\times$g for 1 minute, lithium acetate aspirated and 360 µl transformation mix (33.3% PEG, 100 mM Lithium Acetate, 0.28 mg/ml single stranded carrier DNA (salmon sperm), between 0.1-10 µg transformation DNA fragment) is added to each tube.

Tubes are vortexed until the pellet is resuspended, then incubated at 30°C for 30 minutes. Tubes are transferred to 42°C for 22 minutes to heat shock cells then spun for 15 seconds at 4,600 $\times$g and the transformation mix is aspirated. Pellets are resuspended in 1 ml YPD and incubated for 2 hours to allow recovery. 200µl of cells are then spread onto selection plates and grown for 48-72 hours to allow identification of transformants.

2.4. Spot tests for resistance to UV light and Hydroxyurea

Hydroxyurea plates are made by adding HU in the amount required for the desired concentration to YPD+Agar before pouring plates.

For exponentially growing yeast, an overnight saturated YPD culture is measured for cell density and diluted in YPD to a cell density (OD600) of 5×10^6 cells/ml and grown to a cell density of 3×10^7 cells/ml. Cultures are diluted to a cell density (OD600) of 5×10^6 cells/ml again in double distilled water, then serially diluted to produce 1/10, 1/100, 1/1,000 and 1/10,000 dilutions. 5µl of each dilution is spotted onto plates.

For hydroxyurea exposure, YPD plates containing 25, 50 or 100 mM HU are used, plus a control YPD plate. Spots are allowed the dry and the plates incubated at 30°C for 2 days.

For UV light exposure, four YPD plates are used. Spots are allowed to dry, then plates are immediately exposed to 25 J/m^2, 50 J/m^2 or 75 J/m^2 of UV light, plus one untreated control. Plates are incubated at 30°C for 2 days.

2.5. Meiotic timecourses with *NDT80* or *cdc20-1* arrest

Strains are taken from -80 °C storage, streaked onto YPD plates and incubated at 30 °C for 2 days. For SK1 diploids, a single colony is inoculated into 4 ml YPD and incubated at 30 °C at 250 rpm for 24 hours. For hybrid crosses, haploid parents are mated in 1 ml YPD for 8 hours, after which an additional 3ml YPD is added and the cells are grown for a further 16 hours.

Cell density is measured and inoculated to a density of (OD600) 0.2 into 30 ml YPA. The culture is incubated at 250 rpm at 30°C for 14 hours. Cells are collected by centrifugation at 6,000 ×g for 3 minutes, resuspended in 30 ml double distilled water, re-spun and then resuspended in 30 ml pre-warmed sporulation media (2% potassium acetate, 5 µg/ml Adenine, 5 µg/ml Arginine, 5 µg/ml Histidine, 15 µg/ml Leucine, 5 µg/ml Tryptophan, 5 µg/ml Uracil). The culture is then incubated at 30°C at 250 rpm for the duration of the time course with samples taken at relevant time points.

For the P_{GAL}-*NDT80* experiments, synchronized cultures were split after the required amount of time (3-12 h) in 2% potassium acetate, and one fraction induced to sporulate by addition of beta-oestradiol to a final concentration of 2 mM. Cultures were then incubated to a total of 48 h at 30 °C prior to dissection.

For the *CDC20-1* experiments, synchronized cultures were split after 8 h at 37 °C in 2% potassium acetate, and one fraction induced to sporulate by transfer to 30 °C. Cultures were then incubated to a total of 48 h prior to dissection.

2.6. Sporulation Efficiency

4 μl of meiotic culture is taken after 48 hours, added to a slide, cover slip placed on top, and scored under a microscope for cells that have not formed tetrads and those that have. Percentages are calculated to give the sporulation efficiency.

2.7. Dissection of tetrads/octads to assay spore viability and for sequencing hybrids

To assay spore viability, 50 μl of sporulated cells in sporulation media are incubated with Zymolyase 100T (10 mM Sucrose, 0.7% Glucose, 1 mM HEPES pH 7.5, 1 mg Zymolyase 100T) at a final concentration of 4 μg/ml in a 150 mM sodium phosphate buffer at 37 °C for 15 min. 15μl of digested cells is pipetted onto a YPD plate and allowed to dry before tetrad dissection. Dissected spores were incubated for 2 days at 30°C on YPD and scored for percentage viability per strain and viable spores per tetrad.

To produce hybrid spores for sequencing, SK1 x S288c and SK1xBY4741 haploid parents were mated for 8–14 hours on YPD plates. Haploid are mated freshly on each occasion and not propagated as diploids, in order to reduce mitotic recombination. Sporulation was induced and tetrads were dissected after 72 hours in 2% potassium acetate. For octads, spores were allowed to grow for 4-8 hours on YPD plates until they had completed one division, after which mother and daughter cells were separated. Colonies were grown for 16 hours in liquid YPD for DNA isolation.

Only tetrads giving four viable spores, and octads giving eight viable progeny, are considered for genotyping by Next Generation Sequencing.

2.8. Genomic DNA Preparation

4 ml of overnight saturated YPD culture is spun down at 1,750 ×g for 3 minutes and washed once with double distilled water. The pellet is resuspended in 0.5 ml sphaeroplasting buffer (1 M Sorbitol, 100 mM Sodium Phosphate Buffer pH 7.5, 100 mM EDTA, 1% 2-Mercaptoethanol, 0.25 mg/ml Zymolyase 100T) and transferred to 2 ml tubes, then incubated at 37°C for 30 minutes.

If the sample is to be sequenced, 0.5 ml of Triton mix (5% Triton X-100, 0.1M EDTA, 0.1M Tris-HCl pH 7.5) is added, the sample vortexed and incubated at room temperature for 5 minutes with intermittent inversion. The sample is spun down at 20,000 ×g for 5 minutes and the supernatant aspirated. The pellet is resuspended in 0.5 ml sphaeroplasting buffer.

The cells are lysed with the addition of 100 μl lysis buffer (3% SDS, 0.1 M EDTA, 1 mg/ml Proteinase K) and incubation at 60°C for 1 hour. Samples allowed to cool and then 800 μl of Phenol/Chloroform/Isoamyl alcohol (25:24:1) is added. Samples are vigorously mixed, rested for

5 minutes, then mixed again and spun down at 20,000 ×g for 5 minutes. Approximately 450 µl of the aqueous phase is removed into a clean 1.5 ml tube. 50 µl 3 M NaAc pH 5.2 is added, mixed in and then 550 µl 100% Ethanol is added, mixed in and the sample is spun down for 1 minute at 20,000 ×g. The supernatant is aspirated and the pellet washed with 1 ml 70 % Ethanol, spun for 1 minute at 20,000 ×g, aspirated again and allowed to dry for approximately 10 minutes. The pellet is then dissolved in 450 µl 1xTE (10 mM Tris Base·HCl pH 8.0, 1 mM EDTA pH 8.0). 50 µl of 1 mg/ml RNAse A in 1xTE is added, mixed and incubated at 37°C for 2 hours, with additional mixing every 30 minutes. DNA is precipitated by adding 30 µl 3 M NaAc pH 5.2, mixing, then adding 700µl of 100% ethanol and mixing. The sample is spun for 1 minute at 20,000 ×g, aspirated and the pellet washed in 70% ethanol then spun again for 1 minute at 20,000 ×g. The pellet is allowed to dry for approximately 10 minutes and dissolved in 200 µl of 1xTE. The sample is incubated overnight at 4°C to aid dissolution.

2.9. Preparation of samples for sequencing

Samples of genomic DNA are defrosted and diluted 1/10 with 1xTE. The DNA concentration is measured using the Qubit High Sensitivity dsDNA Assay. The sample is diluted again and re-measured until the concentration is between 0.2-0.3 ng/µl.

The diluted samples are input into the Nextera XT workflow according to the Best Practises recommended by Illumina.

The Nextera transposome is used to tagment genomic DNA, which fragments and tags the DNA with adapter sequences in a single step. 5µl of ~0.2 ng/µl DNA is transferred to a PCR tube and 5 µl Amplicon Tagment Mix (ATM) is added. Samples are spun at 280 ×g for 1 minute and incubated at 55 °C for 5 minutes. 5 µl of Neutralise Tagmentation (NT) is added and the samples incubated at room temperature for 5 minutes.

To amplify libraries and add indexing adapters, 5 µl of an Index 1 (i7) adapter and 5 µl of an Index 2 (i5) adapter is added to each sample. A different combination is used for each sample to allow demultiplexing. 15µl of Nextera PCR Master is added to each sample, mixed and spun at 280 ×g for 1 minute. The samples are placed in a thermal cycler with pre-heated lid and the following program is run:

> 72 °C for 3 minutes
> 95 °C for 30 seconds
> 12 cycles of [95 °C for 10 seconds, 55 °C for 30 seconds, 72 °C for 30 seconds]
> 72 °C for 5 minutes

To purify library DNA and remove short library fragments, 30 µl of AMPure XP magnetic beads are added to each sample and shaken at 1,800 rpm for 2 minutes. Samples are incubated at room temperature for 5 minutes and placed on a magnetic stand for 2 minutes. The supernatant is removed and the samples washed with 200 µl fresh 80% Ethanol. After 30 seconds the ethanol is removed and the wash step repeated with another 200 µl of 80% ethanol. After 30 seconds the ethanol is removed and the beads allowed to air dry for 15 minutes. 52.5 µl Resuspension Buffer is added to each sample and shaken at 1,800 rpm for 2 minutes, then incubated at room temperature for 2 minutes. Samples are placed on a magnetic stand for 2 minutes and 50 µl of supernatant is removed and transferred to fresh PCR tubes.

To check the fragment length distribution and concentration of the purified libraries, 1 µl of undiluted library is run on an Agilent Technology 2100 Bioanalyzer using a High Sensitivity DNA chip.

To normalize the quantity of each library, 20 µl of supernatant is transferred to a new tube. Library Normalization Additives and Library Normalization Beads are combined in a ratio of 6.5:1 to give a total volume sufficient to add 45 µl to each sample. 45 µl of the mixture is added to each sample and shaken at 1,800 rpm for 30 minutes. Samples are placed on a magnetic stand for 2 minutes and the supernatant is removed. Samples are washed with 45 µl of Library Normalization Wash, shaken at 1,800 rpm for 5 minutes, placed on a magnetic stand for 2 minutes and supernatant removed. The wash step is repeated with the addition of 45 µl of Library Normalization Wash, sample is shaken at 1,800 rpm for 5 minutes, placed on a magnetic stand for 2 minutes and supernatant removed. 30 µl of freshly prepared 0.1 N NaOH is added to each sample and shaken at 1800 rpm for 5 minutes. Samples are placed on a magnetic stand for 2 minutes and 30 µl of supernatant is removed to fresh tubes containing 30 µl of Library Normalization Storage Buffer, then centrifuged at 1,000 ×g for 1 minute.

To denature and dilute a PhiX library for use as a sequencing control, 2 µl of 10 nM PhiX library is mixed with 3 µl of 10 mM Tris-Cl, pH 8.5 with 0.1% Tween 20 in a 1.5 ml tube. 5 µl of freshly made 0.2 N NaOH is added, the sample mixed and spun down at 280 × g for 1 minute, then incubated at room temperature for 5 minutes. 990 µl prechilled hybridization buffer is added to give a 20 pM PhiX library.

To pool samples for sequencing, 5 µl of each sample is combined into a 1.5 ml tube and mixed. 24 µl of the mix is transferred to a tube containing 570 µl hybridization buffer. The mix is boiled at 96°C for 2 minutes and placed in ice water for 5 minutes. 6 µl of denatured PhiX control (final

concentration 1%) is added to the library, mixed well and then loaded into a MiSeq reagent cartridge.

2.10. Alignment of paired-end reads

Paired read files are aligned using bowtie2 (Langmead *et al.*, 2009) to the S288c reference genome (version R64-2-1_20150113 (Engel *et al.*, 2013). Also included in the reference file are sequences from the yeast mitochondrial (GenBank: KP263414.1 [Foury *et al.*, 1998]) and 2μ plasmid (GenBank: V01323.1 [Hartley & Donelson, 1980]). In addition, paired read files are aligned to a custom-made SK1 genome. The reference files are formatted with the bowtie2-build command.

To optimize the alignment for long reads and tolerance of mismatches expected in the hybrid genome, the bowtie2 alignment is performed with the following settings:

-X 1000: Allows paired reads to map up to 1,000 bp apart. The default is 500, which may not be appropriate for long sequenced fragments.

--local: Allows bowtie2 to trim off mismatching bases at the ends of reads, if the rest of the fragment is a good match. This is useful for mapping long reads as they commonly have poor quality reads at the end.

--mp 5,1: Reduces the mismatch penalty by 1. This may help with mapping of reads containing SNPs and indels.

-D 20 -R 3 -N 1 -L 20 -i S,1,0.50: These options increase the likelihood that bowtie2 will report the correct alignment for a read that aligns in many places. Bowtie2 uses multiseed alignment, creating small 'seed' oligonucleotides from each read to speed up searching for a match. To make the mapping more sensitive, options can be turned on that allow a mismatch in a seed (-N), decrease the length of the seed (-L), alter the interval between extracted seeds (-i), and specify how many times bowtie2 will re-seed repetitive seeds (-R) and try consecutive seed extension attempts before moving on (-D), using the alignments found so far.

--dovetail: Allows paired reads that dovetail each other to be considered concordant. This does not affect alignment, but makes the reported fragment lengths more accurate.

--rg-id 1 --rg PU:1 --rg LB:1 --rg SM:1 --rg PL:1 Optional fields which do not affect alignment but are required for downsteam processing.

The alignment produces a SAM file, which is then converted into a sorted BAM file using the Samtools view command (Li *et al.*, 2009), for downstream processing.

2.11. Detection of SNPs and indels and creation of SK1 genome

Once sequences from hybrid spores have been aligned, SNP and indel type polymorphisms were detected using the GenomeAnalysisToolkit function HaplotypeCaller (Van der Auwera *et al.*

2013). The S288c reference sequence used is the same as the one used for the initial alignment (version R64-2-1_20150113 (Engel *et al.*, 2013).

The program 'VariantCaller' by Tim Cooper (personal communication) was then run, which combined the GATK calls from 120 samples, and calculated the call frequency, total read depth and averaged variant read-depth:total read-depth ratios for each variant. Variants were filtered for a call-freq between 45-55% of spores, a total read-depth spanning the site of >250 and where 95% or more of the reads at that site contained the variant. The final variant list was then used to automatically produce a custom 'SK1' genome, using the S288c genome as a backbone and converting any SNP or indel positions into the newly-detected SK1 equivalent.

2.12. Genotype calling in tetrads and octads

The PySamStats module 'variation' (Miles & Mattioni, 2016) is run on the sorted BAM file for each sequenced spore. This produces a list of the number of reads containing an A, C, T, G, insertion or deletion for each genomic position specified in the reference, in .txt format. The S288c reference sequence used is the same as the one used for the initial alignment (version R64-2-1_20150113 (Engel *et al.*, 2013).

In order to isolate only SNP and indel reads, VariantIsolator.R (available in appendix) is run on each .txt file using the data from the variant table produced by the GATK analysis. VariantIsolator is run twice, once for each parent, because the genomic positions of variants are different.

To call genotypes at each variant positions, VariantCaller.R (available in appendix) is run twice on each sample for comparison to each parent. Thus, one call is made using S288c as the reference genome and SK1 as the variant, and the other with SK1 as the reference and S288c as the variant. The program VariantCaller examines the makeup of the reads at each position and assigns genotypes according to the following rules:

All positions must have a read depth of at least 5 in order to pass the read depth threshold.

A SNP is called as having the variant genotype if 70% or more of reads at that position match the variant, or as the reference genotype if 90% of reads match the reference. If the variant and reference reads are above 90% of all reads *and* within 70% of each other, the position is called heteroduplex.

Insertions and deletions are called as having the variant genotype if 30% or more of reads at that position match the variant. This low threshold is used because the alignment of indel sequences is biased towards the reference sequence, which means that they are unlikely to be erroneously called as matching the variant genotype. In addition, if the indel is longer than 20bp the threshold is reduced to 20% because the increased length will make it harder to align. There is also a reduced 20% threshold when there are more than 10 reads matching the variant. This is because reads are unlikely to be recorded as having an insertion or deletion if there is not one present, so having >10 indel reads increases the confidence.

To be called as the reference genotype, at least 95% of reads must match the reference sequence, and there must be fewer than 2 reads matching the variant call. This is because even if there is an indel, there are usually reference reads recorded as well due to the difficulty in alignment, so the presence of more than one variant read reduces confidence in the ability to correctly call the position as reference.

Indel positions technically can be called as heteroduplex, but it is uncommon and they are discarded later in the pipeline.

Each indel is called as both an insertion and a deletion depending on which parental genotype it is being compared to. When the indel is called as a deletion, each base of the deletion is called separately. The calls for the separate bases must then be collapsed into a single call. This process has another set of rules for calling, based on the length of the deletion. If there is at least one reference call and at least one variant call within the same deletion, the deletion is discarded. Otherwise, both reference and variant calls are evaluated by the same rules (Table 2.4).

Table 2.4. Deletion calling rules

Length of deletion (bp)	Required percentage of bases called for pass
1	100
2-5	40
6-10	33
11-20	25
21-50	16
51-100	10
>100	5

If an octad is being analysed, each of the eight progeny are processed. If a tetrad is being analysed, the four spores are processed and the data for each spore is duplicated in order to appear as an octad, in order to simplify downstream processing.

In octads and MMR-proficient tetrads, SNPs called as heteroduplex are discarded. However, in MMR-deficient tetrads, heteroduplex calls are converted. For each position with a heteroduplex call, the original 'mother' is converted to SK1 and the duplicated 'daughter' to S288c. This is an arbitrary choice since it is impossible to know which should have which call, assuming there is no bias in the directionality of the repair.

Finally, the genotype calls against each parent are combined using the program 'Combining_SK1_S288c.R' (available in appendix). The rules for this are that if one call is SK1 and the other S288c, there is a conflict and the position is discarded; if both calls are the same, that call is used; if there is only one call, with the other unable to be called due to low read depth or ambiguity, the lone call is used; if neither was able to be called, the position is discarded.

The genotype call is converted into a binary signal, either 1 for S288c or 0 for SK1. Two files are produced from this, one containing final binary calls for each variant, which is compatible with the event calling script (the binary file); and one containing both the binary calls and the raw SK1 and S288c read depths, which is used to produce visualizations of recombination events (the gr2 file).

2.13. Event Calling

Using the binarized input, chromosomes are split into segments with the same segregation pattern by the program 'Annotation.py' (authored by Marie-Claude Marsolier, unpublished work). Each segment has information recorded about the limits of the upstream 'start' interval and downstream 'stop' interval and the genotypic pattern of the eight progeny, for example [1, 1, 0, 0, 0, 0, 1, 1]. The spores are always arranged in the same order 1, 2, 3, 4, 5, 6, 7, 8 with mother/daughter couples. Also recorded is the segment type, which will be 1:7, 2:6, 2:6*, 3:5, 4:4, 4:4*, 5:3, 6:2, 6:2* or 7:1 as described in Martini *et al.* (2011). The first number corresponds to the number of spores with the S288c genotype.

Next, events are called using the chromosome segments listed in the Annotation file and the 'Event Caller' program (authored by Marie-Claude Marsolier, personal communication). This determines recombination events as being a set of segments located between two 4:4 segments longer than 1.5 kb. If these two 4:4 segments have the same pattern, the event is an NCO, and if the two 4:4 segments have different patterns, then the event is a CO. The program produces a file recording information about each recombination event including the limits of the upstream 'start' interval and downstream 'stop' interval, the types of the segments composing the event, the number of chromatids involved in the event and the length of the event.

2.14. Subclassification of events

Events are automatically subclassified by the program Event_Sorter (available in appendix). Classes are based on those described in Martini *et al.* (2011).

According to the rules of this program, NCOs are subcategorized into four groups:

Group 1: Changes on one chromatid, no trans hDNA

Group 2: Changes on one chromatid, and trans hDNA (occurrences of separate 5:3 or 3:5 patterns from different chromatids)

Group 3: Changes on two non-sister chromatids.

Group 0: Changes on two sister chromatids or 3 or 4 chromatids.

Within each group, there are also separate classes, as detailed below and in Figure 2.1.

<u>Group 1</u>

Class 1: 5:3 only

Class 2: 3:5 only

Class 3: 5:3 with restoration and/or conversion tract (4:4, 6:2)

Class 4: 3:5 with restoration and/or conversion tract (4:4, 6:2)

Class 10: 6:2 only

Class 10.1: 2:6 only

Class 7: One 6:2 plus other

Class 8: One 2:6 plus other

Class 9: Anything else

<u>Group 2</u>

Class 11: 5:3_5:3a

Class 12: 3:5_3:5a

Class 13: 5:3_5:3a plus other patterns NOT in the middle of the trans hDNA

Class 14: 3:5_3:5a plus other patterns NOT in the middle of the trans hDNA

Class 15: 5:3_4:4_5:3a (trans het with restoration tract gap in the middle)

Class 16: 3:5_4:4_3:5a

Class 17: 5:3_4:4_5:3a plus other patterns NOT in the middle of the trans hDNA

Class 18: 3:5_4:4_3:5a plus other patterns NOT in the middle of the trans hDNA

Class 19: 5:3_6:2_5:3a (trans het with conversion tract gap in the middle)

Class 20: 3:5_2:6_3:5a

Class 21: 5:3_6:2_5:3a plus other patterns NOT in the middle of the trans hDNA

Class 22: 3:5_2:6_3:5a plus other patterns NOT in the middle of the trans hDNA

Class 23: Anything else

<u>Group 3</u>

Class 31: contains 4:4i (symmetrical heteroduplex)

Class 30: anything else

COs are also subcategorized into four groups:

Group 1: No trans hDNA or incompatible hDNA

Group 2: trans hDNA is present, but no incompatible hDNA

Group 3: Events with incompatible hDNA (containing both [5:3 or 6:2 segments] and [3:5 or 2:6 segments].

Group 0: Events involving more than 2 chromatids.

Within each group, there are also separate classes, as detailed below and in Figure 2.2.

<u>Group 1</u>

Class 100: 4:4aCO: just CO, no associated patterns

Class 1: (5:3)_(4:4aCO): CO with hDNA tract

Class 2: (3:5)_(4:4aCO): CO with hDNA tract

Class 3: (5:3)_(4:4)_(4:4aCO): Characteristic pattern of hDNA, restoration tract, then CO, thought to be caused by resection from break to give hDNA, branch migration to give 4:4, then the actual CO.

Class 4: (4:4aCO)_(5:3)_(4:4a): Same as above but in opposite direction.

Class 5: (3:5)_(4:4)_(4:4aCO)

Class 6: (4:4aCO)_(3:5)_(4:4a)

Class 7: (5:3)_(6:2)_(4:4aCO) Characteristic pattern of hDNA, conversion tract, then CO, thought to be caused by resection from break to give hDNA, branch migration to give 6:2, then the actual CO.

Class 8: (6:2)_(5:3)_(4:4aCO) Same as above but in opposite direction.

Class 9: (3:5)_(2:6)_(4:4aCO)

Class 10: (2:6)_(3:5)_(4:4aCO)

Class 11: contains 4:4i: where the 4:4 pattern is actually produced by symmetrical heteroduplex on different chromatids.

Class 15: (6:2)_(4:4aCO) (CO with conversion tract)

Class 16: (2:6)_(4:4aCO) (CO with conversion tract)

Class 12: Anything else

<u>Group 2</u>

Class 30: adjacent 5:3 5:3a, plus any other patterns

Class 31: adjacent 3:5 3:5a, plus any other patterns

Class 32: non-adjacent trans hDNA i.e. have conversion or restoration tract in between

<u>Group 3</u>

Class 21: contains 4:4i

Class 20: any other

Finally, Group 0 is composed of events that show signs of complexity or difficulty in classification.

Group 0

Class 1 = NCO involving 2_sis, 3 or 4 chromatids

Class 2= Crossover involving 3 or 4 chromatids

Class 3= Contains multiple different 4:4 patterns indicating possibly of multiple COs

Class 4= Type 'U' events: cannot classify due to occurrence at the end of the chromosome – never returns to 4:4 pattern.

The sorted event tables and gr2 files for each meiosis can be combined into master tables using the script 'Event table combiner.R' (available in appendix).

Group 1
Class 1/2

Group 1
Class 3/4

Group 1
Class 7/8

Group 1
Class 10/10.1

Group 2
Class 11/12

Group 2
Class 13/14

Group 2
Class 15/16

Group 2
Class 17/18

Group 2
Class 21/22
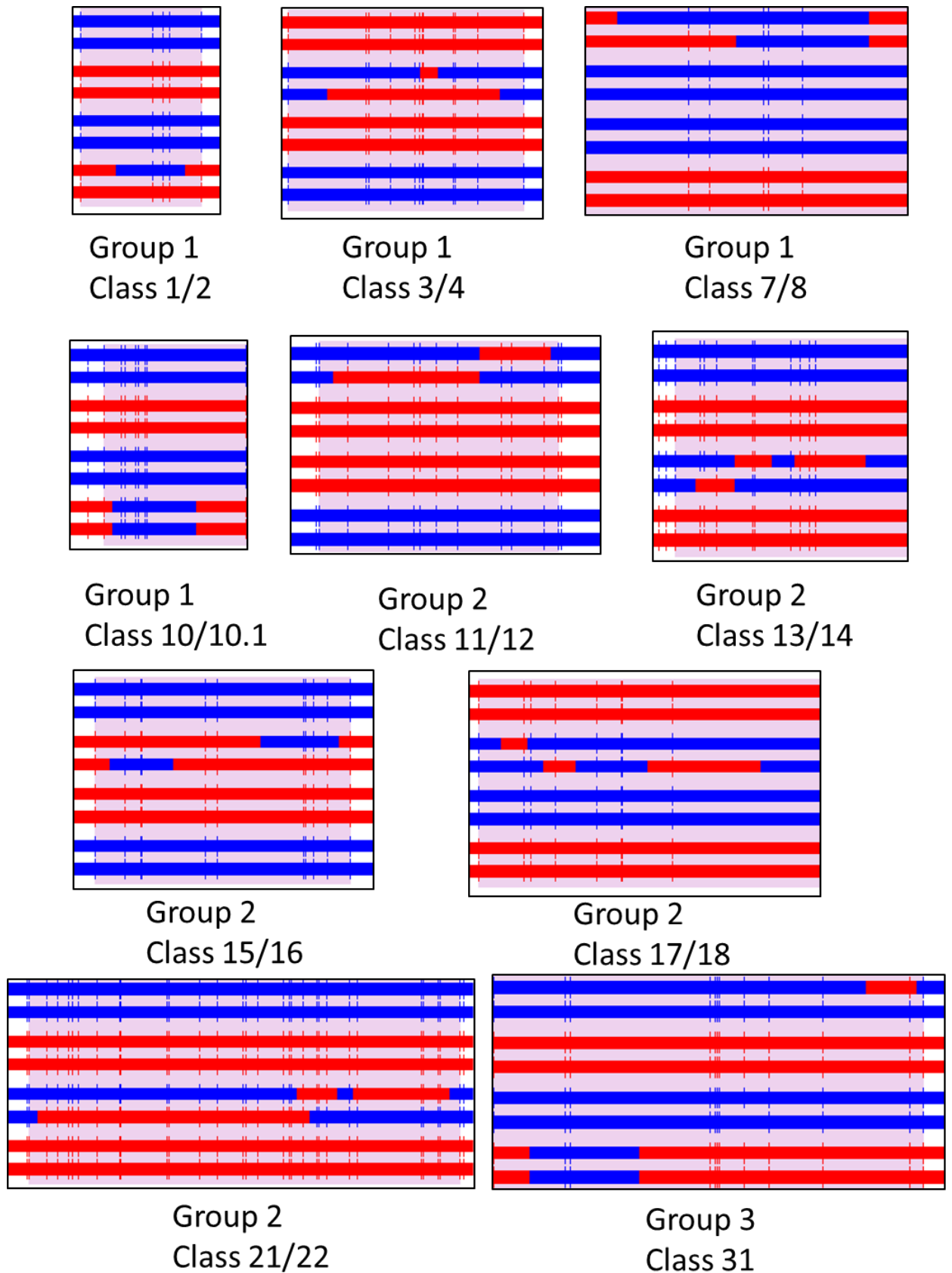
Group 3
Class 31

Figure 2.1. Examples of events matching NCO groups and classes. A representative example event for each category is shown. Event length does not affect categorization. The red and blue lines correspond to the eight strands of DNA present during meiotic recombination, four from each parent. Vertical ticks correspond to called polymorphism positions. The different colours represent homologous chromosomes from the different parents of the hybrid. The purple background highlights the NCO event region.
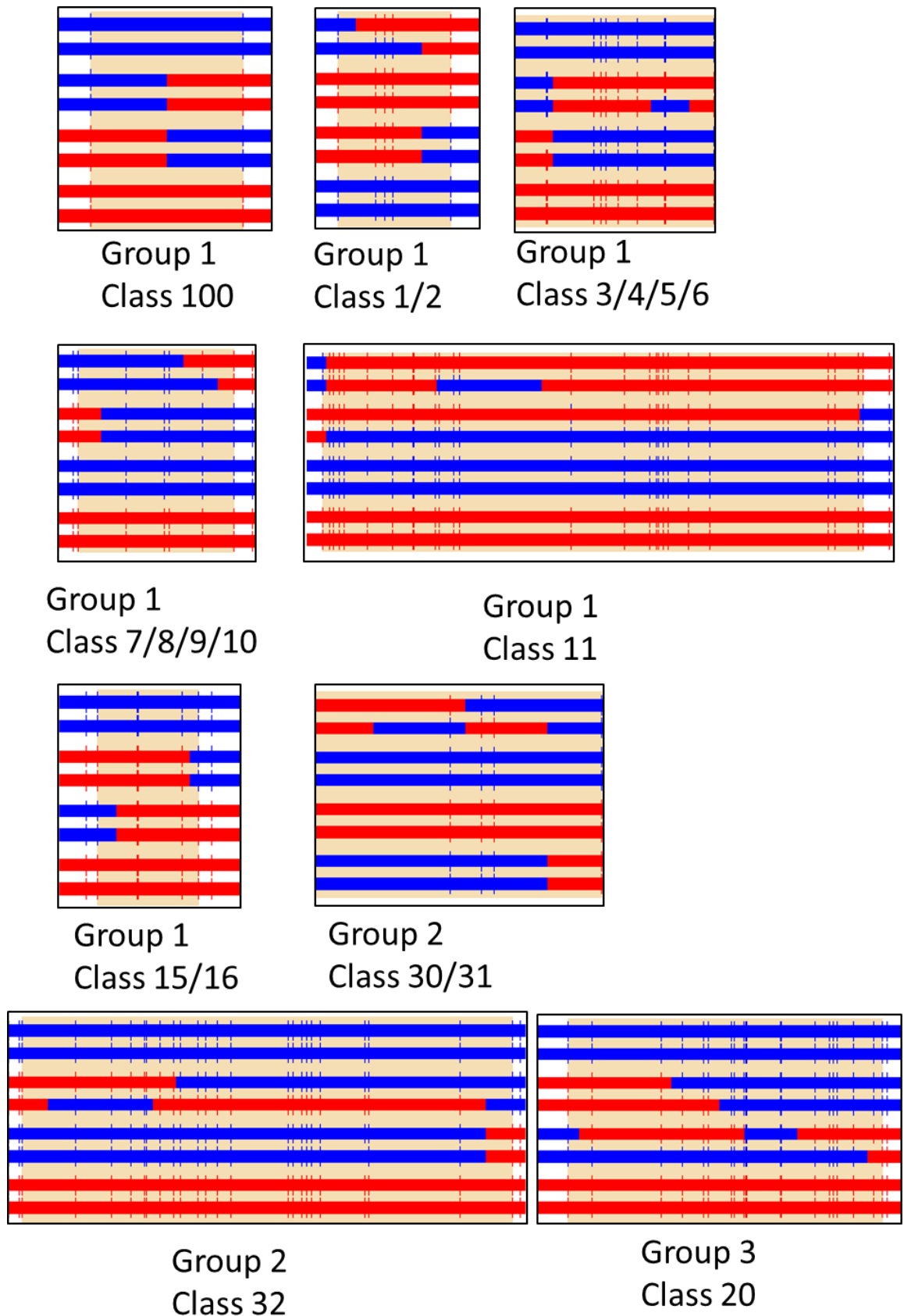
Figure 2.2. Examples of events matching CO groups and classes. A representative example event for each category is shown. Event length does not affect categorization. The red and blue lines correspond to the eight strands of DNA present during meiotic recombination, four from each parent. Vertical ticks correspond to called polymorphism positions. The different colours represent homologous chromosomes from the different parents of the hybrid. The orange background highlights the CO event region.

2.15. Event Imaging

Using the sorted event table and gr2 imaging file for each meiosis, recombination event regions can be imaged using the script 'Event_Imager' (available in appendix). Alongside the event, the Spo11 profile and hotspot strength values (Pan *et al.*, 2011), Rec114/Mer2/Mei1 (RMM) profile (Panizza *et al.*, 2011), Rec8 peaks (Ito *et al.*, 2014), and transcribed regions (Nagalakshmi *et al.*, 2008) are plotted.

2.16. Manual Annotation of Events

Event tables and images are inspected manually to ensure correct classification. Events in Group 0 in particular are scrutinized as they are difficult to correctly classify automatically.

For Class 1 (NCOs involving 2_sis, 3 or 4 chromatids), the event is marked as being produced by two Spo11-DSBs. If the event is composed solely of a 8:0 segregation pattern, the event is marked as mitotic and there are no Spo11-DSBs considered to have occurred. Also, events occurring in the same place across multiple samples are likely to be caused by a variant table error.

For Class 2 events (COs involving 3 or 4 chromatids): These are usually a CO and an NCO, but occasionally double COs, which are unambiguous because all four chromosomes swap over. Either way, the event is categorized as being produced by two Spo11-DSBs.

For Class 3 events (more than two different 4:4 regions – potential double CO): These are usually not actually double COs according to the 1.5kb threshold, but have a different 4:4 pattern occurring within the event caused by a complex CO/NCO or multiple NCOs. Events are only considered to be double COs if the event involves all four chromatids in a double reciprocal exchange, or if the two different 4:4 segments are more than 1.5kb apart. Usually, if the 4:4 segments are >1.5 kb apart, the two COs will be considered separate anyway. However, if another event or other pattern changes occur on different chromatids in between, they will 'interrupt' the threshold. So, the two CO regions are more than 1.5kb apart, but the automatic categorization could not detect this due to the presence of another pattern on a different chromatid occurring within 1.5kb of both 4:4 patterns, obscuring the event boundaries.

It is possible that a double crossover could occur where one or both chromatids are shared, but it is not possible to say for certain, so the threshold value of 1.5kb is used. The threshold means that some dCOs will be miscategorised as not dCOs, and some non-dCOs miscategorised as dCOs, but on average it should give a representative result.

Any events that were automatically categorized as double COs, but do not fulfil the criteria according to manual inspection, are re-annotated as either one CO and 1+ NCOs (common for 3-chromatid events), or 2+ NCOs (common for 2-chromatid events). In either case, the event is still

considered to have occurred from two separate Spo11-DSBs, due to the inherent incompatibility of the heteroduplex tracts; in order to create the 4:4 pattern, the event must have separate DSBs on multiple chromatids.

2.17. Removal of false events

Apparent 'events' that are actually caused by variant table errors are easily spotted because they will occur in the same place across multiple samples. The offending variants are removed from the event table and event calling is repeated. Common types of false event include:

8-0s: A unique event solely composed of 8:0 or 0:8 positions could be mitotic, but if it appears in multiple samples, it is a table error.

False hDNA: In *msh2Δ* tetrads which have undergone heteroduplex calling to produce an 'octad', occasionally variants occurring in repetitive regions like subtelomeres may be detected as hDNA, when actually they are duplicates. So in these samples, events composed solely of heteroduplex and occurring in the same place across multiple samples are considered to be table errors.

False 4:4: This occurs if the actual S288c strain used has a different DNA sequence from the reference S288c. The variant table is made by comparing real samples to the S288c reference, so any differences are assigned to SK1. However, if the SK1 actually matches the S288c reference and the S288c does not, it causes a switched position. For these positions, the variants can be swapped back over to the correct parental genotypes.

2.18. Inter-event distance simulations: independence and interference

This analysis was performed and authored by Tim Cooper (personal communication).

To show the hypothetical distribution of events along the chromosomes, simulated data is produced for a given event count. For comparison to experimental data, simulated datasets are produced for each genotype. Data from separate samples from the same genotype is aggregated.

To simulate inter-event distance (IED) data under conditions of interference or independence, virtual events occur sequentially on simulated chromosomes and either have no influence on the following events (independence simulation) or apply an interference window that reduces the chance of another event occurring within it, with a size based on best-fit gamma parameters (interference simulation). If simulated events occur within 1.5kb, the two events will be merged so the final observed event count will be identical to the experimental data.

To quantify the strength of inter-event interference, the best fit to a gamma distribution is determined for the experimental inter-event distribution. A gamma distribution is a continuous probability distribution that is observed in the intervals between successive independent events,

and so can be used to describe the distances between recombination events (McPeek and Speed, 1995; Zhao *et al.*, 1995).

A gamma distribution function has a shape factor, α, and a scale factor, β. For recombination events, α corresponds to the strength of interference. A value of 1 indicates an exponential distribution i.e. no interference. Values > 1 indicate interference, with higher values corresponding to stronger interference.

β describes the distance over which the shape designated by α is stretched, thus indicating the range of the interference. It is also affected by the number of data points, so is higher in strains with more events.

A one-sample Kolmogorov–Smirnov test (section 2.20) is utilized to determine whether the experimental inter-event distribution is significantly different from the best fit gamma distribution.

2.19. Mixture modelling

This analysis was performed and authored by Tim Cooper (personal communication).

Experimental inter-CO distance data is expected to contain a random component (Class II COs) and an interfering component (Class I COs). The two components can be separated into two gamma distributions, based on the expectation that one component will display no interference (α=1) and the other will display interference (α>1). Initial parameter estimates are provided and the two gamma-components are iteratively corrected until they fit the experimental data.

A two-sample Kolmogorov–Smirnov test (section 2.20) is utilized to determine whether the experimental inter-event distribution is significantly different from the two-component system.

2.20. Kolmogorov–Smirnov test

The Kolmogorov–Smirnov test is a nonparametric test used to compare continuous probability distributions, either one sample against a hypothetical distribution (one-sample K-S test) or two samples (two-sample K-S test). This test can thus be used to compare inter-event distance cumulative frequency distributions between samples or to compare a sample to a hypothetical gamma distribution.

One Sample: A one-sample Kolmogorov-Smirnov-test is used to compare an inter-event distance distribution from experimental data to a theoretical gamma distribution.

Two Sample: A two-sample KS-test is used to compare two inter-event distributions derived from experimental data.

2.21. T-test (independent samples)

To compare data from independent samples with unequal sample sizes (e.g. the number of double crossovers in each meiosis per genotype), two-sample two-tailed T-tests were carried out, with the assumption of equal or unequal variances depending on the result of an F-test Two-Sample for Variances (see 2.22). For samples with unequal variances, a Welch's T-test is used. The tests are carried out using the function in Microsoft Excel.

2.22. F-test

An F-test was used to determine whether two populations have the same variance. The tests are carried out using the function in Microsoft Excel.

2.23. One-way ANOVA

A one-way ANOVA was carried out to test if the value of a single parametric variable (e.g. the number of double crossovers in each meiosis) differs significantly between three genotypes. The test is carried out using an online tool (http://astatsa.com/OneWay_Anova_with_TukeyHSD)

2.23. Tukey Test

After using an ANOVA to determine that there is a significant difference, the Tukey test is used to determine exactly which pairs of means are significantly different. The test is carried out using an online tool (http://astatsa.com/OneWay_Anova_with_TukeyHSD)

Chapter 3.

Spore viability in the absence of the DNA damage response and mismatch repair

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Chapter 3. Spore viability in the absence of the

DNA damage response and mismatch repair

</div>

3.1. Introduction

3.1.1. General Introduction

In meiotic prophase, around 200 DSBs are formed by Spo11 before the cell enters metaphase I. The transition between prophase and metaphase is controlled by *NDT80* activation, a meiosis-specific transcription factor which activates a cascade of proteins causing pachytene exit and meiotic progression. In order to ensure that DSBs are repaired before this occurs, the DNA damage response checkpoint arrests cell cycle progression in pachytene in response to the presence of unresected DSBs and unrepaired ssDNA. Key checkpoint proteins include the kinases Tel1^{ATM} and Mec1^{ATR}, and Rad24^{Rad17}, an activator of Mec1.

The importance of Spo11-DSBs to the timing of meiosis can be investigated by using hypomorphic *SPO11* alleles (hypo-*spo11*). *SPO11-HA3-His6* ('*spo11-HA* ') has a tag composed of three copies of a C terminal epitope (haemagglutinin), a total of 33 amino acids in length, and six histidine residues. *spo11-HA* is reported to reduce the formation of Spo11-DSBs by 11-50% (Martini *et al.*, 2006). Spore viability is also slightly reduced, by ~2% compared to WT. The reason for this is unknown, but it may be that the tag physically interferes with Spo11 activity. *spo11-D290A* has a point mutation occurring in a putative Toprim domain, thought to be involved in DSB catalysis via the coordination of Mg2$^+$ (Diaz *et al.*, 2002). Under standard conditions, *spo11-D290A* only has a mild recombination defect phenotype (spore viability of ~87%), but if sensitized by other conditions, the defects become much more severe (e.g. sporulation at 16°C gives a viability of ~2%: Martini *et al.*, 2006; Diaz *et al.*, 2002). The *spo11-D290A* and spo11-HA alleles cause a greater decrease in spore viability when combined: HA-tagged *spo11-D290A* has a spore viability of 19.3% and reduced DSB formation, which suggests the tag and the point mutation affect Spo11 activity in different ways (Diaz *et al.*, 2002).

3.1.2. The relationship between DSB formation, DNA damage response and meiotic progression

Wild type SK1 budding yeast strains have a spore viability of ~97%. The deletion of the DDR checkpoint protein Rad24 reduces spore viability to ~25%, and this can be rescued to ~50% by an 8 hour prophase arrest mediated by transient *NDT80* repression (Gray *et al.* 2013).

Budding yeast with a hypo-*spo11* allele, such as *spo11-HA* or *D290A*, do not have significantly decreased viability compared to WT. Surprisingly, when hypo-*spo11* is combined with *rad24Δ*, a synergistic reduction in viability to just 5% is seen. Interestingly, in the *rad24Δ* hypo-*spo11* strains, eight hours of *NDT80*-mediated prophase arrest improves spore viability to ~70% (Gray *et al.*, 2013). Similarly, P_{CLB2}-*MEC1*, a conditional Mec1 allele expressed only in mitosis, has a spore viability of ~50%, and when combined with hypom-*spo11,* this drops to ~7% (Gray *et al.*, 2013), but whether P_{CLB2}-*MEC1* viability can also be rescued by prophase arrest has not been examined.

3.1.3. NDT80 prophase arrest system

The release from *NDT80* prophase arrest is enacted via induction of the *GAL* promoter with beta-estradiol, a *GAL* promoter having been placed upstream of the *NDT80* coding sequence. GAL transcription is induced by a chimeric transcription factor consisting of an estradiol binding domain fused with Gal4 (Benjamin *et al.*, 2003). Gal4-ER thus activates transcription only in the presence of estradiol, which causes strong expression of any GAL-controlled genes, including the *GAL* family of galactose metabolism genes. This increase in GAL-gene transcription during meiosis could cause decondensation of chromosomes, which may explain the observed abnormalities e.g. the increased presence of polycomplexes (Bhuiyan *et al.*, 2002).

3.1.4. Aims of this investigation

These observations provoked the following ideas;

1. Whether there was a correlation between prophase length and spore viability.
2. What would be the maximum and minimum length of prophase required to observe a rescue effect.
3. If prolonging prophase in Mec1 mutants would also increase spore viability, as Rad24 and Mec1 function in the same DDR pathway.
4. Whether the rescue was specific to *NDT80* prophase arrest, or cell cycle arrest generally.

3.2. Results

3.2.1. The spore viabilities of *rad24Δ* and hypo-*spo11* mutants positively correlate with time in *NDT80* prophase arrest

It has been shown that the spore viability of *rad24Δ* and hypo-*spo11* strains can be rescued by transient *NDT80* prophase arrest (Gray *et al*., 2013). To investigate the impact of varying the length of time cells are held in meiotic prophase, a meiotic timecourse was carried out on *rad24Δ* and *rad24Δ hypo-spo11* diploid strains, as described in Methods Section 2.5. The release from *NDT80* prophase arrest is enacted via induction of the *GAL* promoter with beta-estradiol, a *GAL* promoter having been placed upstream of the *NDT80* coding sequence. A chimeric transcription factor is used, consisting of an estradiol binding domain fused with Gal4 (Benjamin *et al.*, 2003). Gal4-ER thus activates transcription only in the presence of estradiol. The estradiol induction causes strong expression of any *GAL*-controlled genes, including the *GAL* family of galactose metabolism genes.

Sporulation is induced in diploid cells via transfer to 2% potassium acetate solution, and *NDT80* expression, and therefore exit from prophase and meiotic progression, is triggered by the addition of β-estradiol at timepoints taken each hour between 3-12 hours. In order to determine whether the phenotype is unique to a particular *SPO11* allele or to *spo11* hypomorphs generally, two different hypomorphic alleles (*spo11-HA* and *spo11-D290A*) are used, as in Gray *et al.,* 2013. Samples were incubated at 30 ºC for 48 hours to allow the completion of sporulation, then dissected and scored for the number of surviving spores.

The viability of the *rad24Δ* strain at 8 hours recapitulated that from Gray *et al.,* who reported ~54% viability, while this experiment showed ~59% these are within 95% confidence limits (Figure 3.1A). [Similarly, the non-arrested viabilities of *rad24Δ* and P_{CLB2}-*MEC1* were reported to be 27% and 52% respectively in Gray *et al*. (2013), but are here observed at 22% and 58% respectively (data not shown)]. Between 3 and 8 hours of prophase arrest, the viability of the *rad24Δ* strain steadily increases from 22% to 60%, with no substantial further improvement from extending the time beyond 8 h (Figure 3.1A). For the *rad24Δ hypo-spo11* strains, a similar trend of viability improving with increasing prophase length is observed, and no appreciable additional improvement to viability is gained from extending prophase to longer than 8 h. However, it is interesting to note that both *rad24Δ hypo-spo11* strains are less viable than *rad24Δ* when *NDT80* is induced earlier (3-4 h) and more viable when *NDT80* is induced later (6-12 h). In addition, at early timepoints, 3-4 h, *rad24Δ spo11-HA* has a slightly higher spore viability than *rad24Δ spo11-D290A*; at later timepoints, the viabilities are indistinguishable. This is explored further in Section 3.2.3.

A simple explanation for the mechanism of rescue by prophase arrest is that for *rad24Δ*, the arrest essentially replaces the function of the checkpoint, restoring the cell cycle arrest that Rad24 is involved in maintaining. The arrest also allows more time for the less efficient *hypo-spo11* protein to make DSBs. The recruitment of Mec1 to DSBs requires the formation of RPA-coated ssDNA via resection of the DSB (Clerici *et al.*, 2014). Thus, inefficient DSB formation due to a hypomorphic *spo11* allele is expected to cause a weaker checkpoint response, as would the loss of Rad24. This explains why the combination of *rad24Δ* and hypo-*spo11* causes a greater reduction in spore viability than either alone (Gray *et al.*, 2015).

Since Ndt80 expression is likely repressed during checkpoint arrest, a weakened checkpoint response is expected to cause precocious Ndt80 expression, leading to an early exit from meiotic prophase and reducing the amount of time available for DSB formation by the already-inefficient hypo-*spo11*. This explains why prophase arrest is more beneficial to spore viability than expected in a *rad24Δ* hypo-*spo11* background. This agrees with the hypothesis that activation of the DDR checkpoint represses *NDT80* transcription and activation (Lindgren *et al.*, 2000; Pak and Segall, 2002; Prugar *et al.*, 2017).

However, it is unclear why spore viability in *rad24Δ hypo-spo11* is higher than that of *rad24Δ* when prophase is extended to 8 h. It is possible that one contributing factor to the lower spore viability of *rad24Δ* +8 h is an excessive number of DSBs, which is rescued by a hypo-*spo11* allele. Thus, *rad24Δ* viability is negatively affected by both too few DSBs (hypo-*spo11*) and by too many DSBs (extended prophase), though having too few DSBs is more deleterious than having too many. This implies that Rad24 has a role in controlling DSB numbers, though this is likely to occur indirectly via the activation of Mec1. It is also important to note that the spore viability of arrested *rad24Δ hypo-spo11* is not restored to WT levels, so there are additional deleterious effects of the *rad24Δ* and hypo-*spo11* mutations that are not rescued by the arrest.
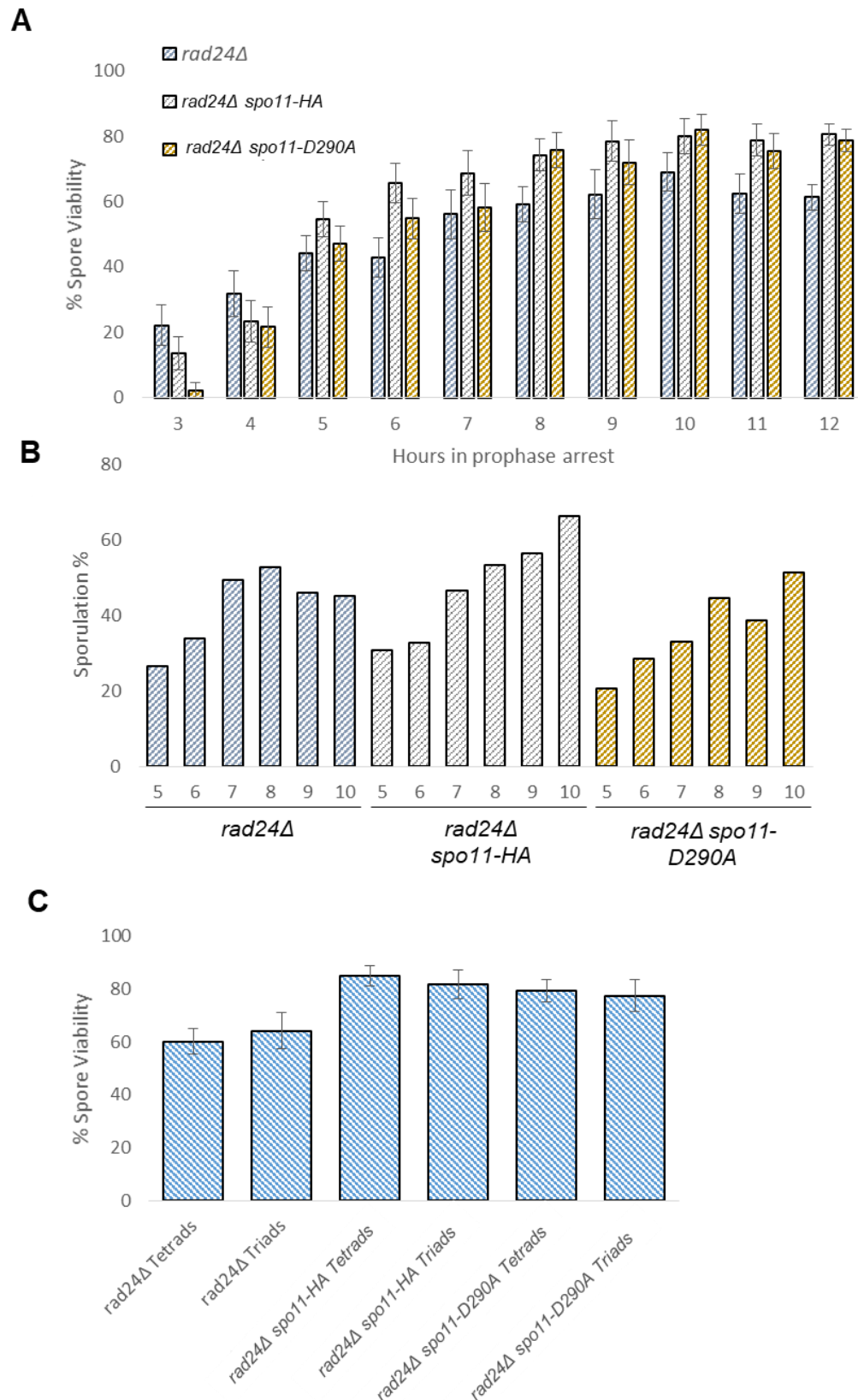
Figure 3.1. Effects of prophase arrest on spore viability and sporulation efficiency. All error bars are 95% confidence intervals. Strains are detailed in Table 2.1, raw data is available in Table S1. **A)** Comparison between the spore viability of, and the effect of changing the amount of time spent in prophase arrest on, *rad24Δ* and *rad24Δ* hypo-*spo11* strains. **B)** Length of *NDT80* prophase arrest compared to sporulation efficiency of *rad24Δ* and *rad24Δ* hypo-*spo11* cultures. **C)** Comparison of tetrad and triad viability in *rad24Δ* and *rad24Δ* hypo-*spo11* strains, after 12h prophase arrest.

3.2.2. Use of the *NDT80* prophase arrest and release system causes sporulation defects

The SK1 strain is a highly efficient sporulator; after 24 h in sporulation medium, ~80% of cells in an SK1 culture will have sporulated (Deutschbauer & Davis, 2005). However, it was observed that prophase-arrested *rad24Δ* and *rad24Δ* hypo-*spo11* cells exhibited relatively inefficient sporulation, ranging from 20-60% and which was partly alleviated by increasing prophase length (Figure 3.1B). This may be due to the high rate of *NDT80* transcription induced by the Gal4-ER construct in response to β-estradiol; Ndt80 overexpression has been shown to reduce the overall efficiency of sporulation in wild-type SK1 strains (Tung *et al.*, 2000).

In addition, only ~1/5 of the cells that sporulated produced tetrads, the remainder produced triads or dyads (data not shown). In order to assess whether there was a systematic bias caused by the low number of tetrads available to select for dissection, the spore viability of triads from samples arrested for 12h was assessed. Tetrad and triad viability were not significantly different in both *rad24Δ* and *rad24Δ* hypo-*spo11* backgrounds (Figure 3.1C). This indicates that the tetrads are not a biased population. In addition, the size of the spores in tetrads and triads was consistent, suggesting that they are all haploid cells. Thus it seems likely that triads are simply tetrads that have failed to package a spore, rather than having one pair of spores failing to correctly undergo Meiosis II.

NDT80 induces transcription of many genes encoding proteins that are directly involved in spore assembly (Chu *et al.*, 1998; Primig *et al.*, 2000). For example, one *NDT80*-induced gene is *ADY3* (*A*ccumulates *DY*ads), which as the name suggests, when mutated leads to an increase in asci with fewer than four spores due to a failure to form mature spore walls (Rabitsch *et al.*, 2001). Excessive or inappropriately timed *NDT80* expression could thus cause failure in spore packaging or spore wall formation.
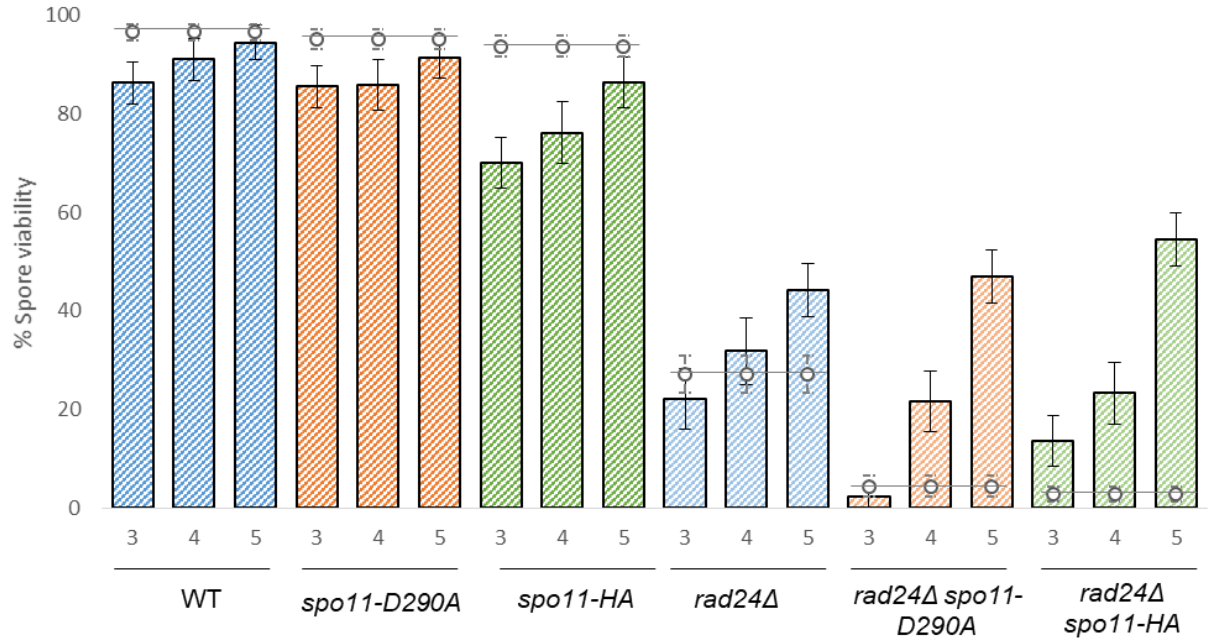
Figure 3.2. A comparison of *rad24Δ* strains and *RAD24* strains with 3-5 hours of prophase and hypo-*spo11*. Error bars are 95% confidence limits. Strains are detailed in Table 2.1, raw data is available in Table S1. White circles with grey error bars represent the spore viabilities of equivalent non-arrested strains reported by Gray *et al.*, 2013.

3.2.3. Early induction of *NDT80* in *RAD24* strains

Interestingly, the viability of *rad24Δ*, *rad24Δ spo11-HA* and *rad24Δ spo11-D290A* strains after 3 hours of arrest (~22%, ~13%, ~2% respectively) is similar to the viability of the non-inducible strains reported by Gray *et al.* (~27%, ~4%, ~3% respectively). Since spore viability is similar in *rad24Δ* whether *NDT80* expression is deliberately induced early or not, this suggests that *NDT80* is activated early anyway in the checkpoint mutants. This agrees with the hypothesis that the DDR checkpoint represses *NDT80* transcription (Lindgren *et al.*, 2000; Pak and Segall, 2002).

Wild type and *hypo-spo11* yeast do not have significantly different spore viabilities (Gray *et al.,* 2011). However, when hypo-*spo11* is combined with *rad24Δ*, there is a synergistic reduction in spore viability, suggesting that inefficient formation of DSBs is especially deleterious in checkpoint-deficient strains. This has been explained by the low DSB signal from the hypo-*spo11* being unable to trigger the DDR checkpoint in the absence of *rad24Δ*, and thus unable to inhibit *NDT80* transcription. If this is the case, the effect of *rad24Δ* in *hypo-spo11* backgrounds might be recapitulated by inducing an early exit from prophase in *RAD24 hypo-spo11* strains.

To test this idea, the *NDT80* induction system was utilized to cause early exit from prophase, instead of increasing prophase length. The normal activation of *NDT80* likely takes place somewhere between 4-5 hours into meiosis, since this is when WT and *NDT80* phenotypes begin to diverge (Xu *et al.*, 1995). Meiotic timecourses were carried out as previously described (Methods section 2.5) on *RAD24+ SPO11+*, *spo11-HA* and *D290A* strains, with *NDT80* induction at 3, 4 and 5 hours. Earlier timepoints could not be used because the cells do not efficiently sporulate.

In checkpoint proficient yeast, all strains have their spore viabilities reduced by the early exit from prophase when induced after 3 or 4 hours (Figure 3.2). A prophase length of 5 hours is sufficient to restore WT and *spo11-D290A* strains to a level of spore viability comparable with a non-arrested strain. However, the viability of *spo11-HA* after 5 hours is still significantly lower than its non-arrested equivalent. Also, *spo11-HA* shows the greatest improvement in viability between 3-5 hours, indicating that it benefits the most from the arrest. This is probably because *spo11-HA* has a more severe phenotype than *spo11-D290A*.

However, even when prophase length is only 3 hours, the checkpoint proficient yeast have a much higher viability than their *rad24Δ* equivalents, indicating that either *NDT80* is induced even earlier than 3h in checkpoint mutants, or that there are other deleterious effects of *rad24Δ* not related to the early exit from prophase. By contrast, in checkpoint deficient yeast, a prophase

length of just 4 hours is sufficient to raise the spore viability not just equivalent to, but higher than, that of the equivalent non-arrested strain (Figure 3.2).

The presence of a hypo-*spo11* allele is more deleterious to *rad24Δ* spore viability with a 3 h prophase, but advantageous after 6 h+ (Figure 3.1A). The *rad24Δ hypo-spo11* strains both benefit more from increased arrest time than *rad24Δ* alone, showing a greater improvement as prophase is extended (Figure 3.2). Thus, *spo11-HA rad24Δ* and *RAD24* strains both show a greater improvement than *SPO11* equivalents when prophase is extended, but the same is only true for *spo11-D290A* when checkpoint deficient. This can be explained by the fact that *spo11-HA* has a more severe phenotype, while the more proficient *spo11-D290A* can make more DSBs in the shortened prophase. However, with a 3 h prophase, *rad24Δ spo11-D290A* experiences a greater loss of viability than *rad24Δ spo11-HA*. This suggests that *spo11-D290A* is more deleterious than *spo11-HA* only under the specific conditions of a 3h prophase and checkpoint deficiency.

Overall, these results indicate that an early exit from prophase has a more severe effect on hypo-spo11 strains, in both *RAD24* and *rad24Δ* backgrounds. This is likely because the reduced activity of Spo11 makes it unable to form sufficient DSBs in the reduced timeframe, consistent with conclusions from Gray *et al*., 2013.
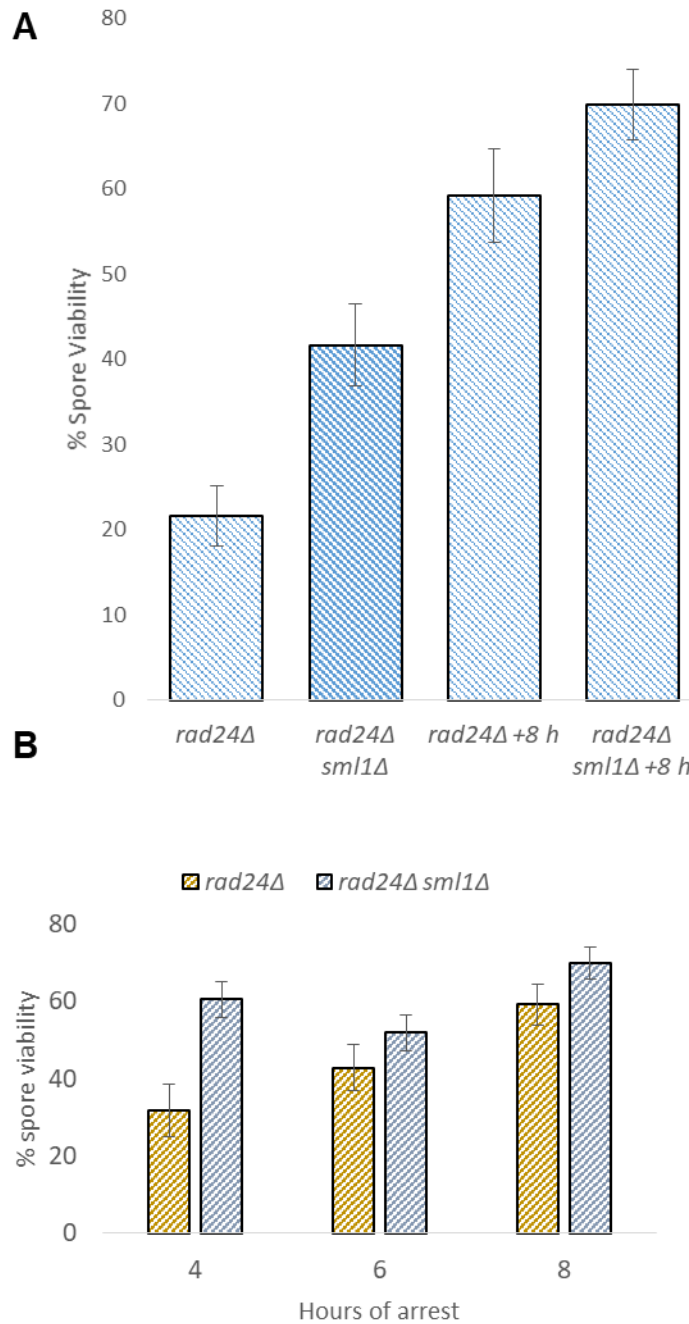
Figure 3.4. The effect of Sml1 deletion on the spore viability of Rad24 mutants.
All error bars are 95% confidence limits. Strains are detailed in Table 2.1, raw data is available in Table S1. **A)** Comparison of spore viability in *rad24Δ* strains with or without *sml1Δ* and/or prophase extension. **B)** Comparison of the effect of different prophase lengths on *rad24Δ* and *rad24Δ sml1Δ* SK1 strains.

3.2.4. The viability of P_{CLB2}-*MEC1* is not affected by *NDT80* prophase arrest

The homozygous deletion of $MEC1^{ATR}$ is inviable in yeast (Giaever *et al.*, 2002) and mice (Brown and Baltimore, 2000; de Klein *et al.*, 2000). In order to examine the function of Mec1 in meiosis, the promoter of *CLB2* can be used to create a conditional mutant where *MEC1* transcription is suppressed during meiotic prophase. P_{CLB2}-*MEC1* yeast have a spore viability of 52-58%, substantially higher than the 22-27% seen in *rad24Δ* (Gray *et al.*, 2013).

Since Mec1 and Rad24 function in the same DNA damage response pathway, it was thought that extending prophase length via *NDT80* block and release may also rescue the viability of Mec1 mutants. To test this idea, the spore viability of P_{CLB2}-*MEC1* strains was scored after varying times of arrest in the *NDT80* block-and-release system. It was found that the spore viability of P_{CLB2}-*MEC1* with eight hours of *NDT80* block and release was not distinguishable from that of a non-arrested strain (Figure 3.3A). Other timepoints were also taken, demonstrating no notable change in spore viability with 4 to 10 hours of arrest (Figure 3.3B).

When P_{CLB2}-*MEC1* is combined with the hypomorphic *spo11-HA*, spore viability drops to 9%; a synergistic effect like that seen in *rad24Δ spo11-HA* (Gray *et al.*, 2013). To discover if P_{CLB2}-*MEC1* would also have a synergistic relationship with the *spo11-D290A* allele, the spore viability of a P_{CLB2}-*MEC1 spo11-D290A* was tested (Figure 3.3C).

Here, a similarity is seen between *rad24Δ* and $_{PCLB2}$-*MEC1* phenotypes, in that both have spore viability reduced by the presence of a hypomorphic Spo11 allele. Also, for both checkpoint mutants, the *spo11-HA* allele reduces viability to around 0.2x of the starting value (P_{CLB2}-*MEC1*: 58% to 7%, *rad24Δ*: 27% to 5% (Gray *et al.*, 2013)). However, the *spo11-D290A* allele is slightly less deleterious to P_{CLB2}-*MEC1* than to *rad24Δ*, reducing *rad24Δ* viability by 0.2x, but P_{CLB2}-*MEC1* viability only by 0.4x (P_{CLB2}-*MEC1*: 58% to 17%, *rad24Δ*: 27% to 3% [Gray *et al.*, 2013]).

It was reasoned that under the combined sensitising effects of a hypomorphic spo11 and P_{CLB2}-*MEC1*, prophase arrest may now rescue spore viability. It was found that *NDT80* prophase arrest does rescue the viability of P_{CLB2}-*MEC1 spo11-D290A*, but unlike with *rad24Δ* the rescue is not time dependent – roughly the same viability is observed between 4-10 hours (Figure 3.3C). Interestingly, at most timepoints the viability of P_{CLB2}-*MEC1 spo11-D290A* is generally not substantially different to that of P_{CLB2}-*MEC1*. This is unlike the situation in *rad24Δ spo11-D290A*, where *NDT80* prophase arrest raises spore viability above that of *rad24Δ*. This suggests that the arrest is only rescuing the hypomorphic Spo11 aspect of the phenotype, and P_{CLB2}-*MEC1* is still the limiting factor in preventing the spore viability from improving further. Thus

hypo-spo11 alleles may have a synergistic effect in decreasing viability when combined with P_{CLB2}-*MEC1*, but not in increasing viability in response to prophase arrest, unlike in *rad24Δ*. This suggests that unlike in *rad24Δ*, the P_{CLB2}-*MEC1* spore viability phenotype is entirely unrelated to prophase length. In *rad24Δ*, most of the loss of spore viability is explained by a reduced prophase length, but not all.

P_{CLB2}-*MEC1* yeast is more viable than *rad24Δ* to begin with (52-58% vs 22-25%), but the viability of *rad24Δ* is higher than that of P_{CLB2}-*MEC1* when both checkpoint mutants have a hypomorphic Spo11 allele and a prophase length of >=6 h (e.g. 83% in *rad24Δ spo11-D290A* +10 h, 60% in P_{CLB2}-*MEC1 spo11-D290A* +10 h). The reason why *rad24Δ* viability surpasses that of P_{CLB2}-*MEC1* under these specific circumstances may be that *rad24Δ* is less tolerant of an excessive number of DSBs than P_{CLB2}-*MEC1*. A reduced number of DSBs due to hypomorphic Spo11 is deleterious for both checkpoint mutants, but an increased number of DSBs due to extended prophase is only deleterious to *rad24Δ*. This implies that Rad24 has some role in controlling recombination event quantities or qualities separate to those of Mec1.

A more simple explanation for the observed differences between *rad24Δ* and P_{CLB2}-*MEC1* may be that it is due to the use of a meiotic knockout of Mec1. Mec1 is still able to perform its roles in the mitotic cell cycle, unlike *rad24Δ*; perhaps some of the reduced viability observed in *rad24Δ* spores is due to death during germination and vegetative growth, which would have been prevented in P_{CLB2}-*RAD24*. Also, the *CLB2*-promoter may affect Mec1 expression in mitosis, causing Mec1 to be expressed at inappropriate times, in inappropriate quantities. This may contribute to the observation that P_{CLB2}-*MEC1* spore viability is not rescued by a longer prophase. Alternatively, it may be that the meiotic knockout of Mec1 is incomplete; there may still be some MEC1 protein present by the time DSBs are being formed. In P_{CLB2}-*MEC1,* DSBs are seen from 2 hours after entry into meiosis, at which time the amount of Mec1 is low, but there is still some Mec1 present until around 3 hours (Gray *et al.*, Figures 3A & S4). Regardless, during the bulk of DSB formation and repair, there should be little or no Mec1 protein present.

3.2.5. *SML1* deletion rescues *rad24Δ* spore viability

Mec1 deletion is inviable in *S. cerevisiae*, but the deletion of Sml1 (Suppressor of Mec1 Lethality) restores the cell viability of *mec1Δ* in both meiosis and mitosis, though *sml1Δ* does not compensate for the checkpoint or transcriptional functions of Mec1 (Zhao *et al.*, 1998).

Sml1 inhibits dNTP synthesis post-translationally by binding directly to the ribonucleotide reductase (RNR) subunit Rnr1 (Zhao *et al.*, 1998). RNR catalyses the conversion of NDP to

dNDP, the rate-limiting step of dNTP synthesis, thus controlling dNTP pool levels and affecting genetic fidelity and cell viability (Reichard, 1988). RNR activity is strictly regulated during DNA replication and repair. During S-phase and after DNA damage, Sml1 is inactivated by Dun1 phosphorylation (Zhao and Rothstein 2002). As a result, *dun1Δ* yeast take longer to complete DNA replication, and are sensitive to DNA-damaging agents (Zhao and Rothstein 2002). Dun1 is activated by Rad53 (Chen *et al.*, 2006), and Rad53 is in turn activated by phosphorylation via Mec1 and Tel1 (Sanchez *et al.*, 1996). Mec1, Rad53 and Dun1 also affect RNR activity by upregulating the transcription of RNR genes (Huang & Elledge 1997). Dun1 upregulates transcription of the *RNR* genes by relieving the transcriptional repression of the Crt1 protein (Elledge *et al.*, 1992; Huang *et al.*, 1998). In this way, dNTP levels can be controlled in response to DNA damage.

Deletion of Sml1 therefore rescues the inviable phenotype of *mec1Δ* in two ways, first by relieving the requirement for Mec1-mediated inactivation of Sml1, and secondly by increasing dNTP levels (Huang & Elledge, 1997) by releasing RNR suppression, allowing DNA repair to be more efficient in the absence of the DDR checkpoint.

Since Rad24 is an activator of Mec1, this raised the question of whether Sml1 deletion would also rescue *rad24Δ*, in mitosis and meiosis. To examine meiotic rescue, the spore viability of a *rad24Δ sml1Δ* strain was measured and found to be twice as high as in *rad24Δ* alone (Figure 3.4A). However, the rescue effect of *sml1Δ* on *rad24Δ* was not as substantial as that of 8 h prophase arrest, which was 50% more beneficial than *sml1Δ* to *rad24Δ* viability.
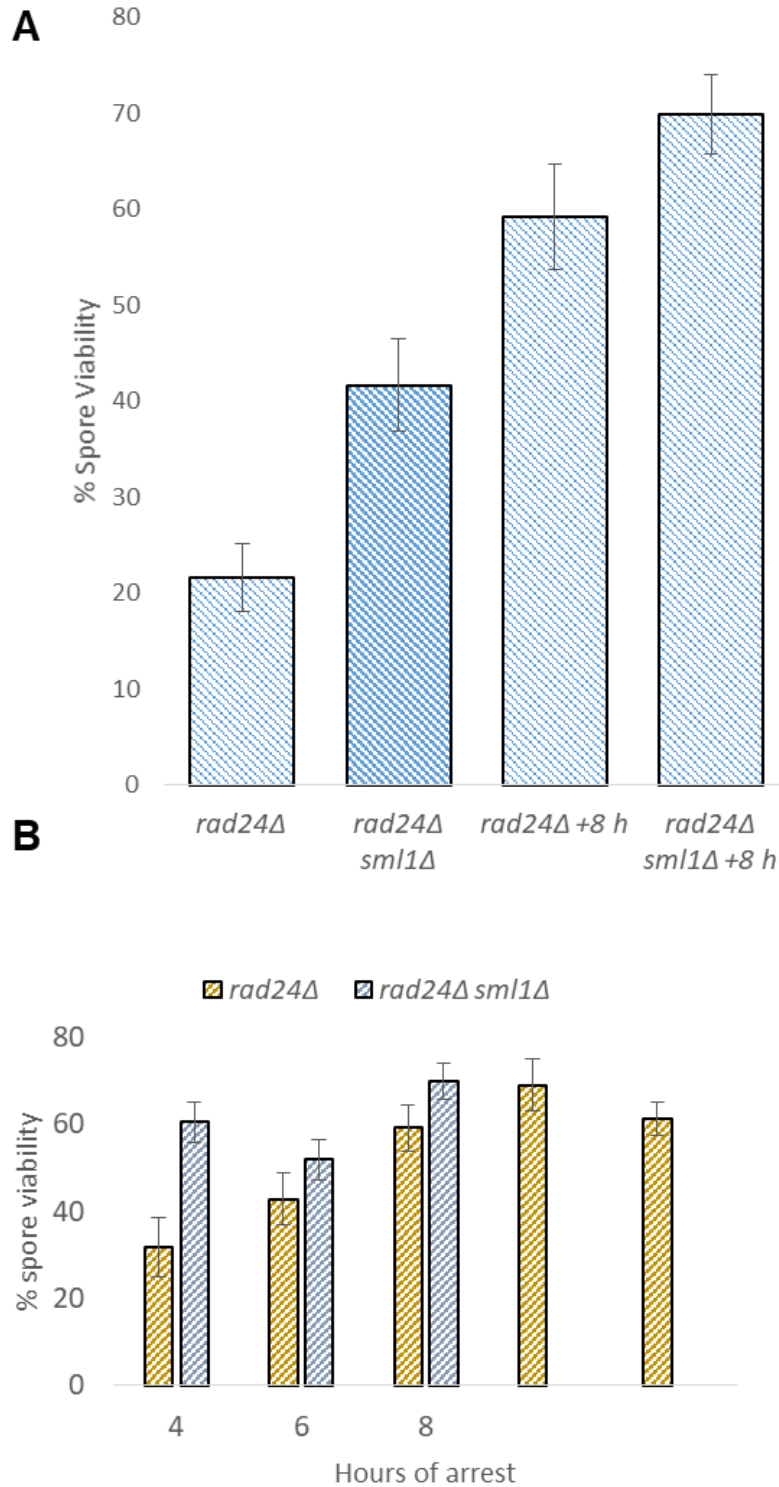
Figure 3.4. The effect of Sml1 deletion on the spore viability of Rad24 mutants.
All error bars are 95% confidence limits. Strains are detailed in Table 2.1, raw data is available in Table S1. **A)** Comparison of spore viability in *rad24Δ* strains with or without *sml1Δ* and/or prophase extension. **B)** Comparison of the effect of different prophase lengths on *rad24Δ* and *rad24Δ sml1Δ* SK1 strains.

3.2.6. The deletion of *SML1* and prophase arrest rescue the viability of *rad24Δ* by different mechanisms

rad24Δ spore viability can be rescued by both *sml1Δ* and by transient prophase arrest. To observe the relationship between the two forms of rescue, the viabilities of *rad24Δ*, *rad24Δ sml1Δ*, *rad24Δ* 8 h *NDT80* prophase arrest, and *rad24Δ sml1Δ* 8 h *NDT80* prophase arrest were compared in an SK1 background (Figure 3.4A). A deletion of Sml1 increases *rad24Δ* viability from ~20% to ~40%, while *NDT80* prophase arrest increases it to 60%. However, *sml1Δ* deletion combined with *NDT80* prophase arrest gave a viability of 70%, suggesting that the two forms of rescue together improve *rad24Δ* viability more than either does alone, and supporting the idea that each rescues *rad24Δ* viability by a separate mechanism.

To determine whether this synergistic effect with *sml1Δ* effect would be observed for different prophase lengths, the spore viability of *rad24Δ sml1Δ* was tested with 4 and 6 h prophase (Figure 3.4B). This revealed that the largest difference in viability between *rad24Δ* and *rad24Δ sml1Δ* is with a 4 h prophase, so *sml1Δ* is particularly protective of *rad24Δ* viability when prophase is shortened. These data support the idea that *sml1Δ* and *NDT80* prophase arrest rescue *rad24Δ* via different mechanisms. The most likely explanation is that *sml1Δ* increases the number of available nucleotides for repair as it is no longer inhibiting RNR, and *NDT80* gives the cells more time to make/repair DSBs.

3.2.7. Different *S. cerevisiae* strains display significantly altered spore viabilities in checkpoint-deficient backgrounds

To test if *rad24Δ* has the same effect on spore viability in different strain backgrounds, the viabilities of SK1 and S288c *rad24Δ* yeast were compared (Figure 3.5A). This revealed that the spore viability of *rad24Δ* was higher in an S288c background than in SK1, but the S288c strain received less benefit from *SML1* deletion. To see if S288c always has a higher spore viability than SK1, the viabilities of other mutants were scored (Figure 3.5B). In most backgrounds tested, S288c spore viability was not substantially different to that of SK1. However, along with *rad24Δ*, P_{CLB2}-*MEC1* was also noticeably less viable in SK1 than in S288c. This suggests that the loss of DDR response checkpoint proteins is more deleterious to SK1 than to S288c yeast. This may be related to the fact that SK1 is a much more efficient sporulator than S288c; 90% of SK1 yeast, but only 10% of S288c yeast, sporulate after 48 hours (Deutschbauer & Davis, 2005). A possible explanation is that in SK1, sporulation may continue despite errors in segregation, producing more defective tetrads able to be assayed, but in S288c, sporulation may be more likely to fail entirely if there are any errors in chromosome segregation, meaning that fewer defective tetrads are produced.
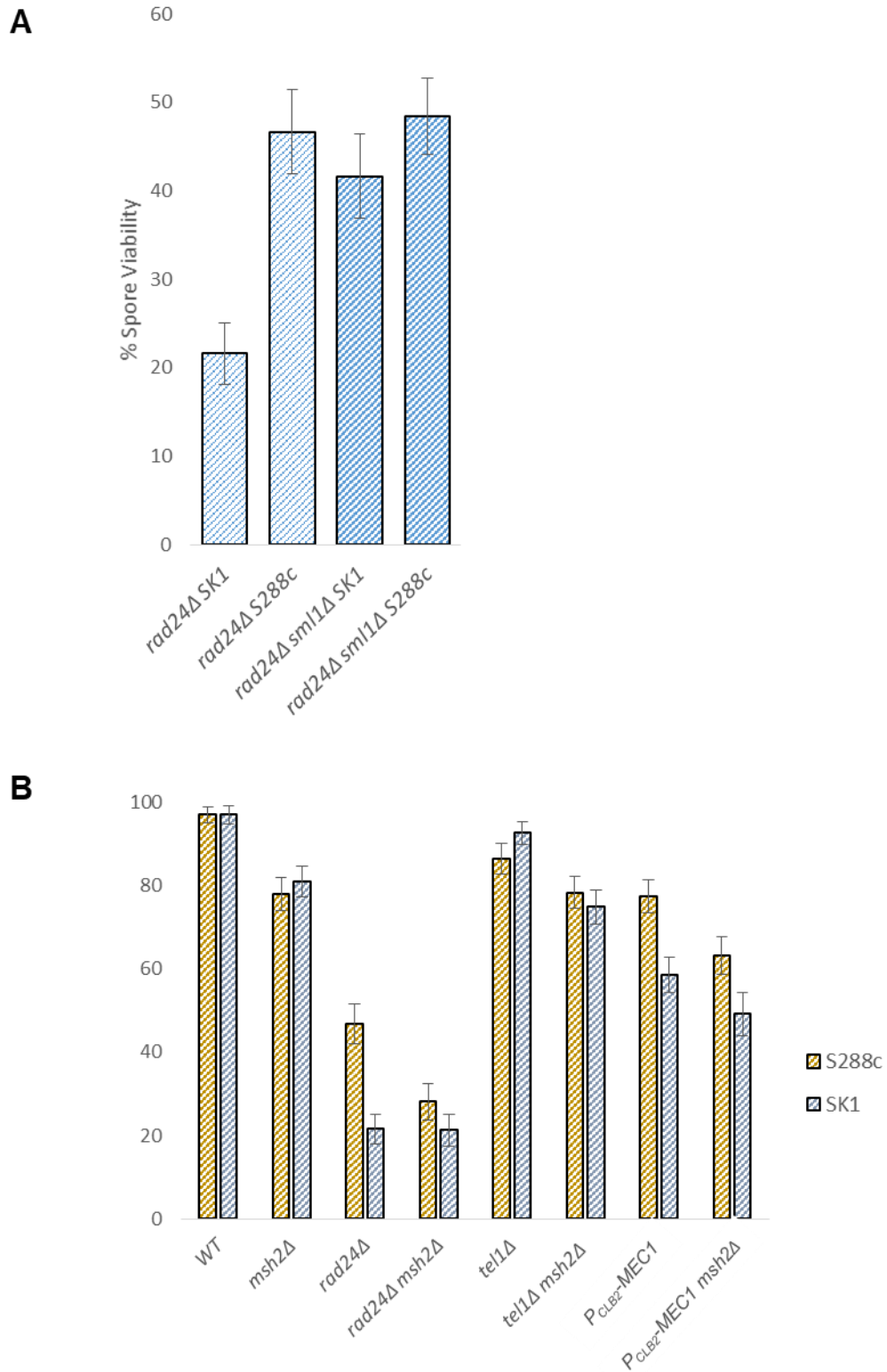
Figure 3.5. Differences in spore viability observed in SK1 and S288c strains. All error bars are 95% confidence limits. Strains are detailed in Table 2.1, raw data is available in Table S1. **A)** Comparison of spore viability of *rad24Δ* and *rad24Δsml1Δ* yeast in SK1 and S288c backgrounds. **B)** Comparison between spore viability in pure SK1 and S288c strains. Error bars are 95% confidence limits.

3.2.8. *sml1Δ* rescues *rad24Δ* viability in cycling cells when exposed to UV damage but not hydroxyurea

It has been shown that *sml1Δ* rescues *rad24Δ* spore viability in meiosis. *SML1* deletion is known to rescue *mec1Δ* in mitosis (Zhao *et al.*, 1998), so it was reasoned that *sml1Δ* should also rescue *rad24Δ* in mitosis. To test this idea, spot tests were carried out on *rad24Δ* strains with acute exposure to UV light or chronic exposure to hydroxyurea. *rad24* mutant strains have decreased resistance to UV damage (Paulovich *et al.*, 1998). Hydroxyurea, like *SML1*, is an inhibitor of RNR, so exposing *rad24Δ* yeast to HU may abrogate the rescue effect of *sml1Δ*. Both SK1 and S288c backgrounds were tested because SK1 haploid cells tend to clump together and do not spread out well for the spot test, and because S288c *rad24Δ* is naturally more viable than SK1 *rad24Δ* (Figure 3.5A), so may give a different result.

It was found that *rad24Δ* yeast viability is reduced when exposed to acute doses of 25, 50 and 75 J/m^2 of UV, with the reduction proportional to the dose received; and that *sml1Δ* rescues the viability of UV-exposed *rad24Δ* yeast, though not to WT levels (Figure 3.6A). This result demonstrates that *sml1Δ* rescues *rad24Δ* UV damage sensitivity phenotype in mitosis, in both SK1 and S288c backgrounds. Spot tests were also carried out in the presence of 25, 50 and 100 mM HU (Figure 3.6B). In both backgrounds, *sml1Δ* appears to rescue viability slightly in both *rad24Δ* and WT. However, it is not a strong rescue. It may be that, while *SML1* and HU are both inhibitors of RNR, HU is a much more potent inhibitor and so its presence is not compensated for by a lack of *sml1Δ*; or it may be due to the fact that the HU exposure is chronic, while the UV exposure is acute.
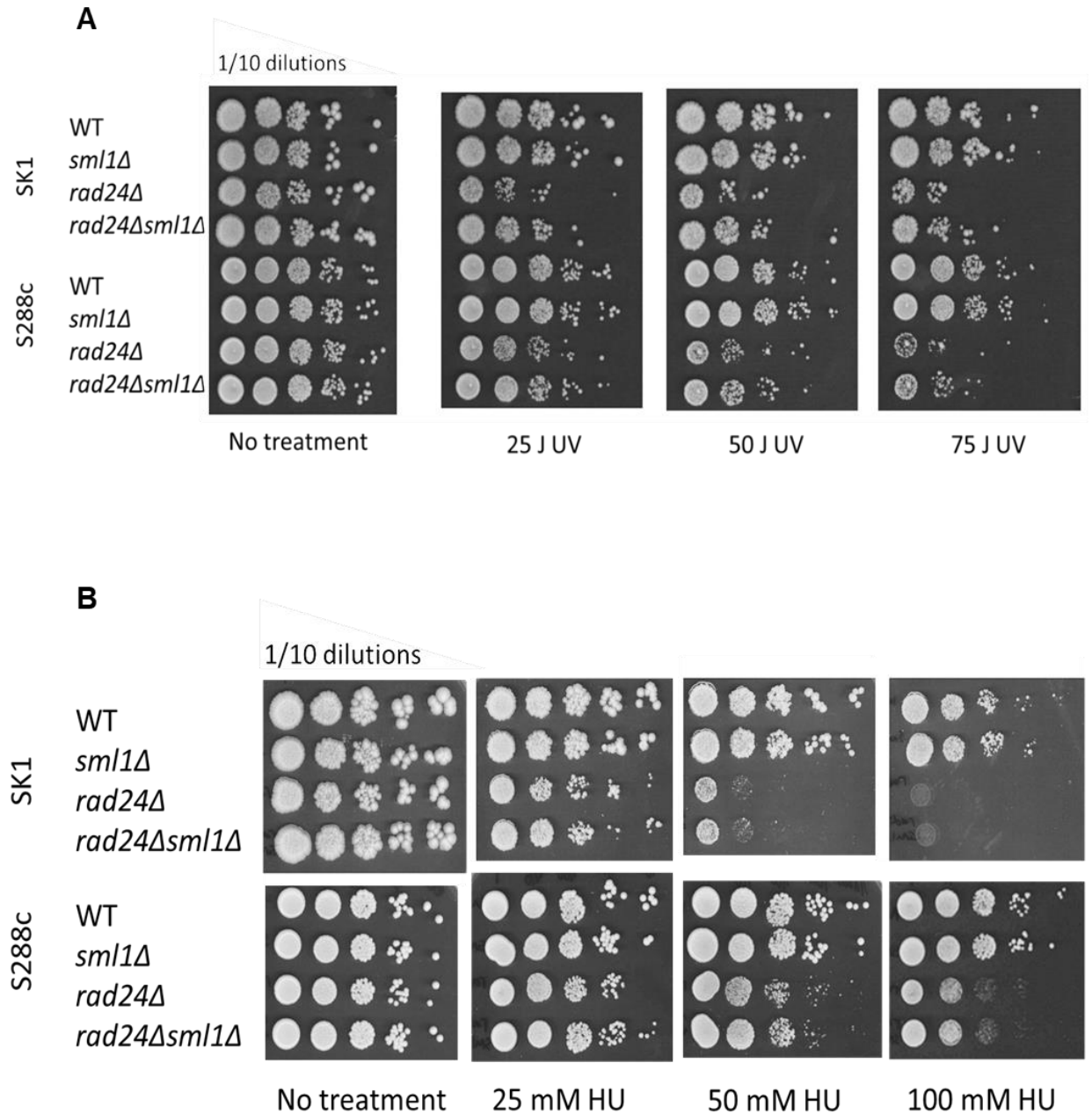
Figure 3.6. Spot tests carried out on WT, *rad24Δ*, *sml1Δ* and *rad24Δsml1Δ* strains in both SK1 and S288c backgrounds. Strains are detailed in Table 2.1. **A)** Serial dilutions spotted onto a YPD plate, then exposed to UV radiation. **B)** Serial dilutions spotted onto a YPD plate containing hydroxyurea.

3.2.9. Effect of metaphase arrest on *rad24Δ* spore viability

It has been shown that *rad24Δ* spore viability is rescued by transient prophase arrest mediated by *NDT80* repression. If the mechanism of this rescue is simply that it gives the cells more time to make and repair DSBs, then other methods of prophase arrest should work similarly to transient *NDT80* prophase arrest.

Another protein that can be targeted to cause cell cycle arrest is Cdc5 (Polo-like kinase), an important cell cycle kinase needed for pachytene exit in mitosis and meiosis (Clyne *et al.*, 2003). However, the meiotic function of Cdc5 requires activation by *NDT80* (Sourirajan and Lichten, 2008), so the functions of Ndt80 and Cdc5 may be too similar for Cdc5 arrest to be a proper control. Also, *cdc5* mutant cells show some evidence of entry into metaphase, so Cdc5 activity may not be absolutely required for meiotic progression beyond pachytene (Clyne *et al.*, 2003). Cdc5 arrest was also examined in Gray *et al.*, (2013) where it was found to have little effect on measured DSB frequency at *HIS4::LEU2*, unlike *NDT80* prophase arrest.

Another candidate is *CDC20*, which is responsible for the transition to anaphase via activation of the Anaphase Promoting Complex, so *CDC20* mutants arrest at the end of metaphase. *CDC20* is also essential for mitosis, so it is not possible to use an inducible knockout as with *NDT80*. Instead, a temperature sensitive mutant can be utilized: *cdc20-1*, which is degraded at 37 °C. The strain can be arrested and released by putting the sporulating culture at 37 °C for 8 hours, then moving to 30°C to release. However, exposure to the higher temperature of 37 °C causes prophase arrest in A364A yeast (Byers and Goetsch, 1982). This may not be the case for SK1 as it is a very proficient sporulator, but if so, the temperature-related arrest may also rescue spore viability.

To discover whether *rad24Δ* spore viability could be rescued by metaphase arrest, the *cdc20-1* allele was introduced into SK1 strains. To test the system, *cdc20-1* cultures were inoculated into SPM and placed at 37 °C. After 8 hours, samples were taken and placed at 30 °C for an additional 40 hours. These showed evidence of sporulation, while the cultures left at 37 °C for 48 hours did not, indicating that the allele is functioning as expected (data not shown). Additionally, the spore viability of 8-hour-arrested *cdc20-1* was examined to see if viability is affected by the arrest (Figure 3.7). The viability was indistinguishable from WT, so 8 hours of *cdc20-1* arrest does not have an effect on spore viability. To see the effect of the temperature shift on *rad24Δ*, this strain was also exposed to 8 hours at 37 °C. The 8 hour incubation at 37° C slightly reduced *rad24Δ* spore viability, so if the temperature shift does induce prophase arrest, it is not beneficial to spore viability (Figure 3.7). A high temperature is known to have other

effects on the events and timing of the cell cycle (Vanoni *et al*., 1984; Börner *et al*., 2004 & 2008), which may be deleterious to spore viability.

Finally, the spore viability of a *rad24Δ* strain with 8 h of *cdc20-1* arrest was indistinguishable from the non-arrested *rad24Δ* strain. This shows that 8 h of metaphase arrest did not improve viability of a *cdc20-1 rad24Δ* SK1 strain, while in contrast, 8 h of prophase arrest triples the viability of *rad24Δ* (Figure 3.7).

Since spore viability is restored by *NDT80*, but not *cdc20-1* arrest, it suggests that specifically prophase length, rather than the length of meiosis generally, is important to the viability of *rad24Δ* yeast, and that the rescue is not an indirect consequence of the onset of anaphase I caused by the *NDT80*-dependent transcriptional cascade. This agrees with the result from Gray *et al.* (2013) regarding *CDC5*-mediated arrest.
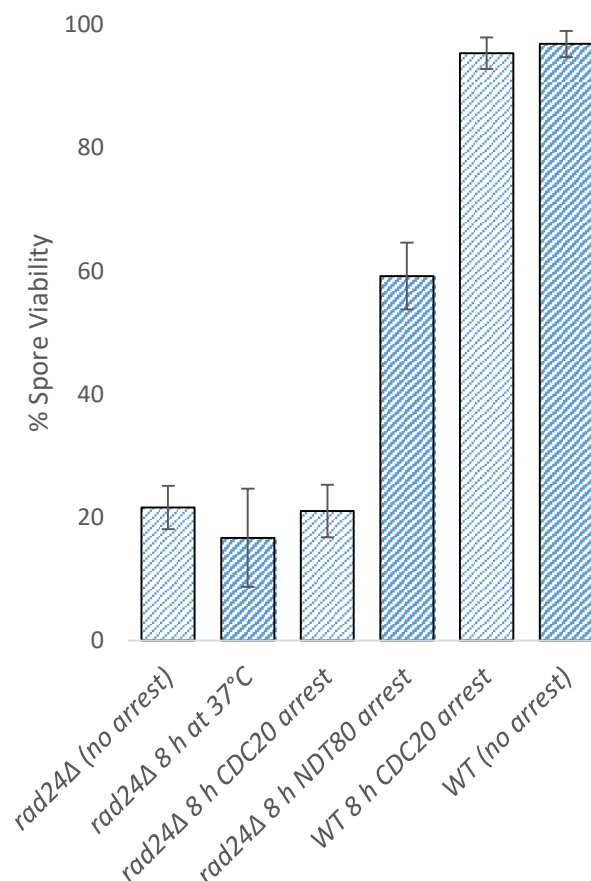
Figure 3.7. Comparison of effect of *NDT80* arrest and *CDC20* arrest on viability of WT and *rad24Δ* strains. Error bars are 95% confidence limits.

3.2.10. The mismatch repair protein Msh2 has both negative and positive effects on spore viability

During meiotic recombination, it is important for strand invasion to occur into a homologous sequence in order to prevent ectopic recombination. One likely role of the mismatch repair (MMS) protein Msh2, a MutS homolog, is to detect and reject mismatched DNA intermediates formed during strand invasion. Msh2 localizes to DSB repair donor and recipient sequences, and is enriched in the presence of sequence polymorphism (Sugawara *et al.*, 1997; Evans *et al.*, 2000). Rejection of mismatched strand invasion intermediates is important in order to prevent recombination with non-allelic sequences. However, MMR also acts as a barrier to recombination between populations with many DNA polymorphisms. In *S. cerevisiae,* increasing sequence divergence reduces the efficiency of hDNA formation, in mitotic cells (Datta *et al.*, 1997; Chen & Jinks-Robinson, 1999). These studies both utilized an inverted repeat assay system with the recombination substrates ranging in identity from 74% to 100% (Datta *et al.*, 1997) or 82% to 100% (Chen & Jinks-Robinson, 1999) in order to score recombination rates in in both wild-type and MMR-deficient strains. Even a single mismatch reduces the recombination rate by 4x, and additional mismatches reduce the recombination rate exponentially with increasing sequence divergence (Datta *et al.*, 1997). Substrates with 99.7% sequence identity recombined 4.1x less efficiently than the 100% control substrates (Datta *et al.*, 1997), so a similar relationship may be expected to be seen between *S. cerevisiae* SK1 and S288c sequences which have around 99.3% sequence identity. Therefore, MMR-proficient SK1xS288c hybrid yeast should undergo a higher rate of strand invasion rejection during recombination. In contrast, for MMR-deficient strains the effect of sequence divergence on recombination rates was inconspicuous unless the identity was lower than 91% (Datta *et al.*, 1997). This suggests that the inhibitory effect of sequence divergence on recombination can be entirely explained by MMR activity, if the sequence divergence is less than 10%; however, with higher divergence, another factor is negatively affecting the recombination process (Datta *et al.*, 1997). This suggests that in *msh2Δ* SK1xS288c hybrids (~0.7% divergence on average), there should be little reduction in recombination.

If strand invasion into a mismatching sequence does occur, heteroduplex DNA (hDNA) will be formed (Allers & Lichten, 2001). hDNA tracts formed during MMR-deficient meiotic recombination are 65% longer than in a MMR-proficient strain, indicating that the MMR machinery may interfere with the extension, as well as the formation, of heteroduplex recombination intermediates (Chen & Jinks-Robinson, 1999). The mismatches in an hDNA tract will be recognized and repaired by the Msh2-Msh6 or Msh2-Msh3 complexes, causing restoration or conversion of the genetic markers within the hDNA depending on how the mismatches are repaired. Msh2–Msh6 is responsible for the repair of single-base mispairs and

single-base indels (Marsischky *et al.*, 1996). Msh2–Msh3 repairs both single base indels and larger indels (Marsischky *et al.*, 1996; Kolodner, 1996). Thus, the loss of Msh2 during meiotic recombination is expected to have major effects on the efficiency of strand invasion, ectopic recombination and presence of mismatched DNA.

To observe the effect of Msh2 deletion on spore viability in pure SK1 backgrounds, strains of interest were scored for spore viability in the presence or absence of Msh2 activity (Figure 3.8A). In pure SK1 strains, WT, *tel1Δ* and P_{CLB2}-*MEC1* all experience reduced viability as a result of Msh2 deletion, possibly due to increased ectopic recombination or unrepaired mismatches in DNA after meiosis. However, this is not the case for a *rad24Δ* strain, which seems unaffected by the loss of mismatch repair. This may be because *rad24Δ* already has an increase in ectopic recombination (Gray *et al.*, 2013), so additional ectopic recombination caused by *msh2Δ* may not have a noticeable effect. However, *mec1Δ* also causes an increase in ectopic recombination (Grushcow *et al.*, 1999), and is affected by *msh2Δ* deletion, so the occurrence of ectopic recombination cannot solely explain why *rad24Δ* is unaffected by *msh2Δ*.

Hybrid SK1xS288c yeast have a spore viability reduced by about 20% compared to that of either pure parental strain (Figure 3.8B). To observe the effect of Msh2 deletion on spore viability in hybrid SK1xS288c backgrounds, strains of interest were scored for spore viability in the presence or absence of Msh2 activity (Figure 3.8C). This revealed that deletion of Msh2 is less deleterious in hybrid SK1xS288c strains than in pure SK1 strains, with a reduction by ~16% and ~21% of the starting value in SK1 WT and *tel1Δ* respectively, but only ~11% and ~8% in hybrid WT and *tel1Δ* (compare Figure 3.8A and 3.8C). This is likely because MMR-proficient strains are more likely to reject strand invasion into mismatched sequences, which are more common in hybrids. However, the *msh2Δ* still has an overall negative effect on spore viability in hybrids, probably due to the other roles of MMR in repairing mismatches and preventing ectopic recombination.

In contrast, it was found that in checkpoint mutant hybrids, *msh2Δ* has an overall beneficial effect on spore viability. In *rad24Δ* hybrids, MMR-deficiency improves spore viability by 8x, while in P_{CLB2}-*MEC1*, spore viability is improved 4.5x (Figure 3.8 A and C). This may be due to the fact that one role of Mec1 and Rad24 is to promote CO formation; the loss of either protein produces half as many CO molecules compared to the WT (Grushcow *et al.*, 1999). Therefore, the loss of the checkpoint is expected to decrease CO levels, as well as overall DSB numbers (Gray *et al.*, 2013). If there are fewer CO-destined DSBs in these backgrounds, it becomes more important for strand invasion to be successful. As with the pure SK1 strains, it may be the case that *rad24Δ* and P_{CLB2}-*MEC1* experience fewer deleterious effects from *msh2Δ* than WT and

tel1Δ because Rad24 and Mec1 mutants already have higher levels of ectopic recombination (Grushcow *et al.*, 1999; Gray *et al.*, 2013).

Overall, these results show that MMR-deficiency has both a positive and negative effect on spore viability. Generally the negative effect outweighs any positive effects, but in backgrounds where it is more important for strand invasion to be successful, *msh2Δ* can have an overall neutral or positive effect on spore viability.

3.2.11. In SK1xS288c hybrids, both *rad24Δ* and P*CLB2*-*MEC1* are rescued by prophase extension

To examine the effect of prophase extension on hybrid checkpoint mutant spore viability, hybrid Rad24 and Mec1 mutants were scored for spore viability with different prophase lengths (Figure 3.9A). This showed that both *rad24Δ* and *rad24Δ sml1Δ* hybrid spore viabilities are rescued by *NDT80* prophase arrest, and the viability improves further with increased arrest time, which is the same result as seen in the pure SK1 equivalent strains (Figure 3.4B). However, unlike in pure SK1, the *rad24Δ sml1Δ* hybrid strain does not have a viability distinguishable from that of *rad24Δ* alone after 8 h or 10 h prophase, so the two forms of rescue no longer produce a strong synergistic effect like that observed in Figure 3.4A. Surprisingly, the P*CLB2*-*MEC1* hybrid is rescued by prophase arrest, despite this not being the case in the pure SK1 background (Figure 3.3B). This may be because the arrest is rescuing the deleterious effects of being a hybrid, rather than the Mec1 phenotype.
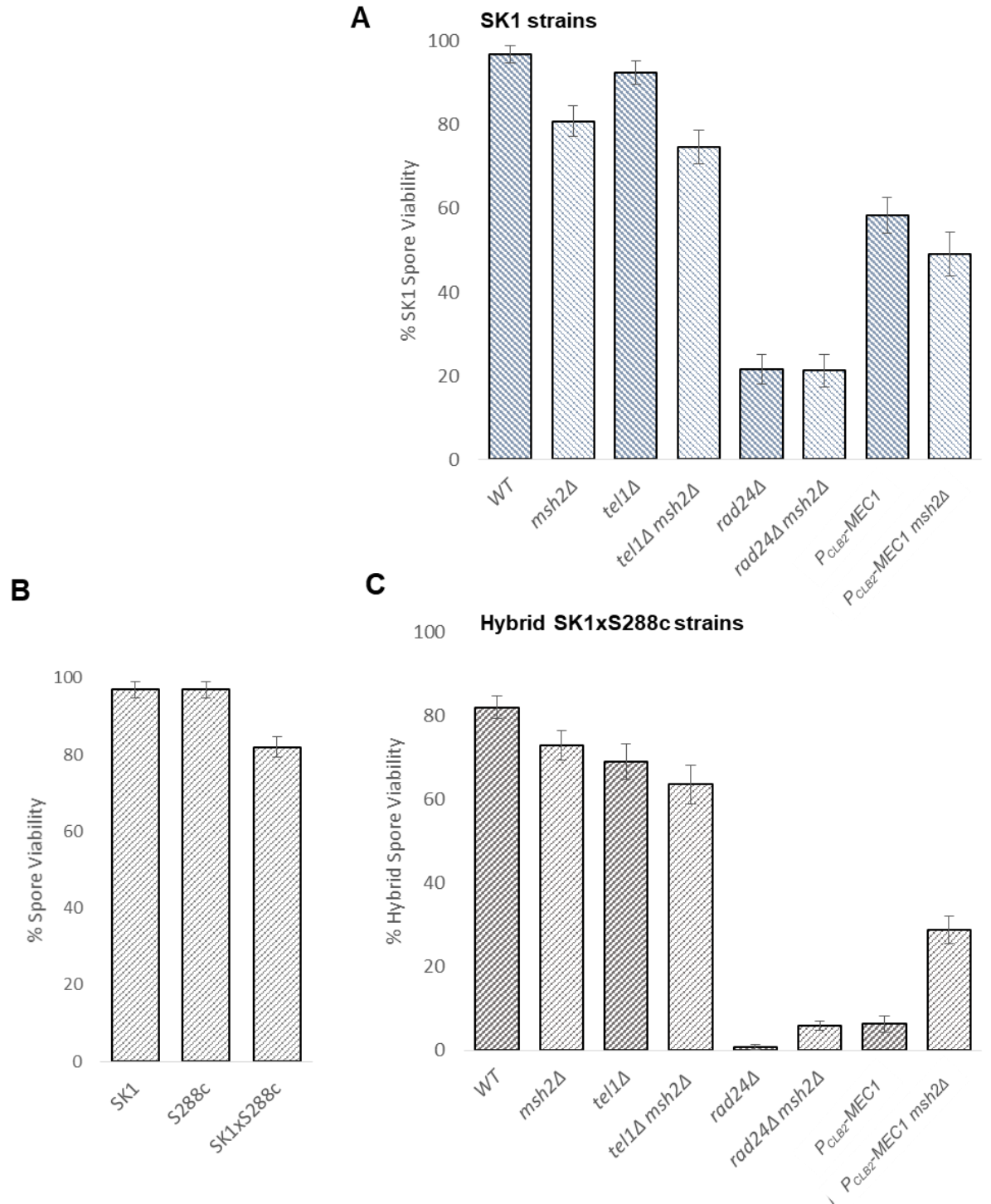
Figure 3.8. Comparison of pure and hybrid spore viabilities. All error bars are 95% confidence limits. Strains are detailed in Table 2.1, raw data is available in Table S1. **A)** Comparison of spore viability in SK1 strains with and without mismatch repair proficiency. **B)** Comparison of spore viability in WT SK1, S288c and SK1xS288c hybrid strains. **C)** Comparison of spore viability in hybrid SK1xS288c strains with and without mismatch repair proficiency.
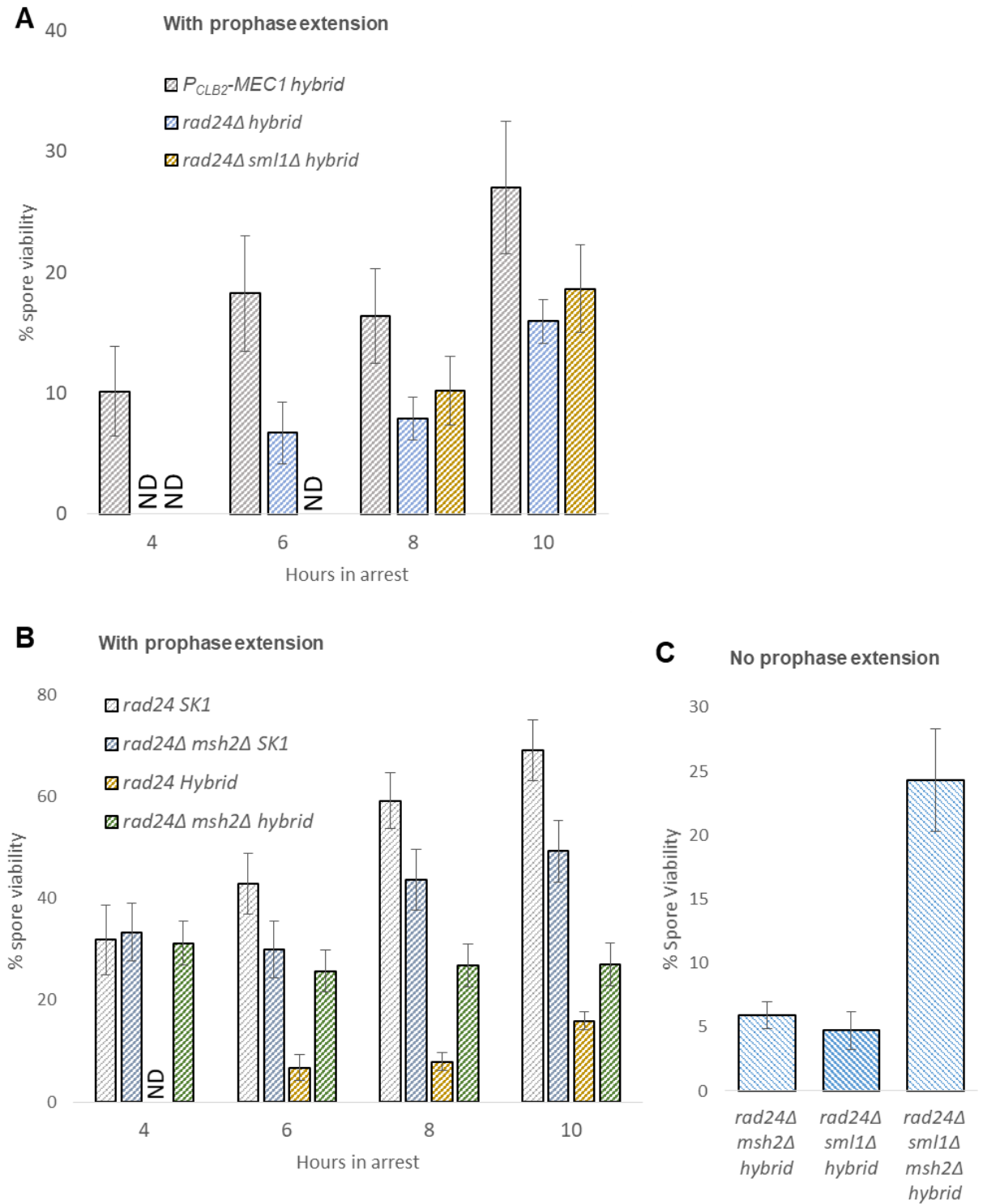
Figure 3.9. Effects of prophase arrest, SML1 mutation and MMR deficiency on the spore viability hybrid strains. Strains are detailed in Table 2.1, raw data is available in Table S1. Error bars are 95% confidence limits. ND: not determined. **A)** Comparison of the effect of different prophase lengths on the spore viability of SK1xS288c hybrids. **B)** Comparison of the effect of changing prophase length on spore viability in *rad24Δ* and *rad24Δ msh2Δ* SK1 and hybrid strains. **C)** Comparison of spore viability in *rad24Δ* hybrid strains with *msh2Δ*, *sml1Δ* or both.

3.2.12. The benefits of *msh2Δ* in *rad24Δ* hybrids are additive to those of *sml1Δ* and prolonged prophase

Prophase arrest rescues the viability of *rad24Δ* SK1 and hybrid strains. To determine whether the rescue has an additive effect with that of *msh2Δ*, spore viability was scored in *rad24Δ* and *rad24Δ msh2Δ* SK1 and hybrid backgrounds with altered prophase lengths (Figure 3.9B). After 4 h arrest, the viability of *rad24Δ* and *rad24Δ msh2Δ* is similar, around 30%. However, by 10 h of arrest the *rad24Δ* strain viability is 70%, an improvement of 2.3x from the starting value, while the *rad24Δ msh2Δ* has only gone up to 45%, an improvement of 1.5%. Therefore, though *msh2Δ* deletion did not affect the viability of a *rad24Δ* pure strain, the loss of Msh2 does partially negate the benefits of *NDT80* prophase arrest in *rad24Δ*.

In a *rad24Δ* hybrid strain, viability is rescued by both *msh2Δ* and *NDT80* prophase arrest. While the *NDT80* prophase arrest rescue is dependent on the exact amount of time spent arrested, when combined with *msh2Δ* the amount of time does not make a difference, with viability not showing a substantial change between 4-10 h (Figure 3.9B). The *rad24Δ msh2Δ* hybrid has a viability similar to that of *rad24Δ* and *rad24Δ msh2Δ* pure SK1 strains, indicating that the two forms of rescue have overcome the deleterious effect of being a hybrid; however, unlike the pure SK1 strains, the *rad24Δ msh2Δ* hybrid does not show further improvement from longer prophase, so by 10 h the viabilities of the pure strains are much higher.

Both *sml1Δ* and *msh2Δ* rescue spore viability of *rad24Δ* in a hybrid background. To see if there is a relationship between the two forms of rescue, spore viability was assayed in a *rad24Δ msh2Δ sml1Δ* hybrid background (Figure 3.9C). This revealed that the combination of msh2Δ and *sml1Δ* produces a synergistic effect on *rad24Δ* hybrid viability. In a *rad24Δ* hybrid, *msh2Δ* and *sml1Δ* both improve spore viability from almost 0 to around 5%. However, a triple mutant has a viability of around 25%, meaning that the two forms of rescue have a highly synergistic effect (Figure 3.9C).

3.3. Discussion

The loss of Rad24 is highly deleterious to spore survival in both pure SK1 and hybrid SK1xS288c strains (Figure 3.8). It was observed that 8 hours of extended prophase rescued the spore viability of *rad24Δ* SK1 strains (Gray *et al*., 2013). To further investigate this, the relationship between prophase length and spore viability was examined in *rad24Δ* and P_{CLB2}-*MEC1* SK1 and hybrid strains. In addition, other ways in which the *rad24Δ* and P_{CLB2}-*MEC1* meiotic phenotype can be rescued were examined to help inform on the roles of Rad24 in meiosis and where they may differ from Mec1.

3.3.1. Effect of prophase extension in Rad24 and Mec1 mutants

The rescue of *rad24Δ* spore viability by *NDT80* prophase arrest is thought to be because the arrest restores part of the natural function of the meiotic checkpoint (Gray *et al*., 2013). Presumably via its role in the activation of Mec1 by the 9-1-1 clamp, Rad24 activity is important for the inhibition of Ndt80 activation, as Mec1 activity inactivates Ndt80 via Mek1 until DSBs are repaired (Prugar *et al*., 2017). However, the spore viability of P_{CLB2}-*MEC1* is not affected by prophase extension in a pure SK1 background, suggesting that Mec1 activity is not important to inactivate *NDT80*. In contrast, P_{CLB2}-*MEC1* spore viability is rescued by prophase extension in an SK1xS288c hybrid background (Figure 3.9). This discrepancy may be explained by the difference in recombination event numbers between pure and hybrid strains. Hybrid strains are thought to have fewer recombination events than pure strains due to the activity of Msh2, which rejects strand invasion into mismatched sequences (Sugawara *et al*., 1997; Evans *et al*., 2000). The increase in recombination event numbers in *msh2Δ* hybrids compared to WT indicates that recombination event formation is reduced in MMR-proficient hybrids (Datta *et al*., 1999; Chen & Jinks-Robinson, 1998). This suggests that prophase arrest is more helpful in backgrounds with fewer recombination events; this is supported by the fact that hypomorphic Spo11 alleles have a synergistic negative effect on spore viability in combination with *rad24Δ* and P_{CLB2}-*MEC1*, suggesting that the slower/reduced DSB formation of the hypomorphic Spo11 is particularly deleterious in checkpoint deficient backgrounds. One reason why *rad24Δ* is more deleterious to spore viability than P_{CLB2}-*MEC1* may be because Rad24 and Mec1 mutants have different effects on recombination event numbers; this is examined further in Chapter 7.

Interestingly, while the spore viability of *rad24Δ* is much lower than that of P_{CLB2}-*MEC1* (Table 9.1), when prophase is extended to 10 h, *rad24Δ* spore viability is higher than that of P_{CLB2}-*MEC1* (70% vs 60%). Since P_{CLB2}-*MEC1* viability is not affected at all by prophase length, this indicates that there is a factor negatively affecting spore viability in the absence of Mec1 that does not occur in *rad24Δ*.

3.3.2. Effect of *sml1Δ* and *msh2Δ* in Rad24 and Mec1 mutants

SK1 and hybrid *rad24Δ* spores are rescued by Sml1 deletion, which is well established as a method of rescuing *mec1Δ*. Mec1 activity indirectly deactivates Sml1, which is an inhibitor of Rnr1, which produces dNTPs; therefore, it is likely that the rescue is due to the presence of more nucleotides readily available for DSB repair, allowing repair to occur faster. As Rad24 activity is needed to activate Mec1, the absence of Rad24 means that Sml1 is expected to have a higher level of activity in meiosis than in WT.

Deletion of *msh2Δ* has no effect on pure SK1 *rad24Δ* (though it does partly negate the rescue effect of NDT80 prophase arrest (Figure 3.9))*,* despite having a negative effect on WT, *tel1Δ* and P*_{CLB2}*-*MEC1* spore viability (Figure 3.8). In SK1xS288c hybrids, *msh2Δ* has a positive effect on *rad24Δ* spore viability similar to that of *sml1Δ*, with both raising spore survival from <1% to around 5%. Removing both Sml1 and Msh2 raises *rad24Δ* spore viability to ~25%, a much larger increase in viability than expected. A possible explanation is that *rad24Δ* has low CO numbers, which are boosted by *msh2Δ* (though not to WT levels), but not affected by *sml1Δ*, which does not affect CO numbers but only their repair. Similarly to *rad24Δ*, P*_{CLB2}*-*MEC1* is affected negatively by *msh2Δ* in a pure SK1 background, but affected positively in a hybrid background; however, the improvement is not as great as that seen in *rad24Δ*. An explanation for these observations is that the increase in the efficiency of strand invasion in *msh2Δ* improves recombination event counts in checkpoint mutants, but in order to complete the repair, it is highly beneficial to have a large pool of dNTPs.

Having many dNTPs available may also reduce the amount of time taken for *de novo* DNA synthesis during repair, since a given base is more likely to be readily available; this would be particularly helpful when MMR is inactive and so unable to repair mistakes that could occur.

NDT80 prophase arrest and *msh2Δ* also interact in hybrids to give a higher viability than either rescue alone (Figure 3.9), but the time-dependence is removed. This suggests that the increased success rate of strand invasion in the absence of *msh2Δ* means that even a short prophase is sufficient to allow DSB to form.

Essentially, the checkpoint functions that are lost in *rad24Δ* can be 'reconstructed' by prophase arrest and Sml1 deletion, providing the aspects of DSB formation and repair that would normally be ensured by Rad24 activity. However, the viability of *rad24Δ* with prophase arrest and *sml1Δ* is still lower than WT, which may relate to other roles of Rad24 such as controlling resection distance and reducing ectopic recombination (Gray *et al.*, 2013).

3.3.3. Spo11-DSB levels in *rad24Δ*

While low DSB/CO numbers may be a source of *rad24Δ* meiotic defects, there is also an indication that high levels of Spo11-DSBs may also be deleterious to *rad24Δ*, because in pure SK1, the highest *rad24Δ* viabilities are seen when 10 h of *NDT80* prophase extension is combined with *hypo-spo11*, allowing the viability to reach a level of around 80%, while 10 h of *NDT80* prophase extension alone improves viability to ~69%. An excessively high number of DSBs may be deleterious to *rad24Δ* because there are not enough dNTPs to repair all the breaks. The effect of having few dNTPs can be observed by comparing the spore viabilities of *rad24Δ sml1Δ* + 8 h which has a spore viability of ~70%, which is lower than the ~75% viability of *rad24Δ* + hypo-*spo11* +8 h, but higher than the ~60% viability of *rad24Δ* +8 h. This suggests that the presence of addition dNTPs may help to repair an increased number of DSBs. In addition, unlike in pure SK1, the *rad24Δ sml1Δ* hybrid strain does not have a substantially different viability than *rad24Δ* after 8h or 10h prophase, meaning the two forms of rescue no longer produce a strong synergistic effect. This may be because the hybrid has fewer recombination events due to rejection of strand invasion by MMR proteins (Chapter 5, Figure 5.1; Sugawara *et al.*, 1997; Evans *et al.*, 2000; Datta *et al.*, 1999; Chen & Jinks-Robinson, 1998), so there is a reduced need for dNTPs.

3.3.4. Closing statement

As a whole, the results shown in this chapter demonstrate that the deleterious *rad24Δ* phenotype can be rescued in multiple ways, such as having more nucleotides present via *sml1Δ*, restoration of at least four hours of prophase extension in both SK1 and hybrid backgrounds, hypomorphic Spo11 alleles in combination with extended prophase, and by *msh2Δ* in hybrid, but not SK1, backgrounds (Figures 3.1, 3.4, 3.8, 3.9). In addition, P_{CLB2}-*MEC1* spore viability can be rescued by *msh2Δ* and prophase extension, but only if hybrid, not pure SK1. To further investigate the meiotic roles of Rad24 and Mec1, and to identify where these roles may differ, genome-wide analysis of recombination was performed in Rad24 and Mec1 mutants. This is discussed in Chapter 7.

Chapter 4.

Development of lab and bioinformatics methods for generating and analyzing recombination event data

Chapter 4. Development of lab and bioinformatics methods for generating and analyzing recombination event data

4.1. Introduction

4.1.1. General introduction

In order to better understand the processes controlling recombination events, it is desirable to monitor changes in the frequency and distribution of various types of events in mutant strains for genes of interest. To study recombination event outcomes and positioning, a system is needed to allow the formation, detection and categorization of recombination events.

To accomplish this, the established method is to mate two highly divergent yeast strains, producing a hybrid diploid naturally heterozygous for tens of thousands of alleles (Winzeler *et al.*, 1998). After sporulation of the hybrid diploid, the recombination outcomes in each resultant tetrad can be detected by the use of high-throughput sequencing to genotype single-nucleotide polymorphisms (SNPs) and insertions/deletions (indels), allowing the determination of the regions of the genome derived from each parent and reconstruction of recombination events. This approach allows detection of most recombination events in a single meiosis, allowing the frequency and distribution of events in a single cell to be examined. Notably, recombination occurring between sister chromatids or in repetitive regions cannot be detected by this method, but such events are rare in wild-type meiosis (Schwacha & Kleckner, 1997; Kim *et al.*, 2010; Petes and Botstein, 1977; Pan *et al.*, 2011).

4.1.2. The use of MMR-deficient strains increases meiotic recombination rate and allows observation of post-meiotic segregation

During homologous recombination, the pairing of complementary DNA between donor and recipient strands produces heteroduplex DNA (hDNA) with mismatches at heterozygous positions (White *et al.*, 1985; Williamson *et al.*, 1985; Bishop *et al.*, 1987; Allers & Lichten, 2001). The mismatches are usually repaired by MMR machinery to give either gene conversion or restoration of the original genotype, producing 3:1 or 2:2 segregation patterns respectively.

In order to reveal hDNA intermediates, MMR can be inactivated via the disruption of *MSH2*. If any mismatches remain unrepaired, the alleles will segregate during the first mitotic division. This phenomenon is known as post-meiotic segregation (PMS). In order to detect PMS on a wide scale, it is necessary to allow each spore of a tetrad to germinate and undergo one mitotic division, then score genetic markers in the resulting eight cells (an octad). This essentially allows reconstruction of the post-meiotic sequence of the eight individual DNA strands from the four chromatids of the diploid hybrid.

4.1.3. Bioinformatic solutions for detection and classification of recombination genome-wide

In order to analyse recombination events genome-wide, it is necessary to have a list of variants and the parental genotypes at each position, a method of identifying recombination products and a way to consistently deal with the classification of simple and complex events. To extract a list of polymorphisms, sequencing data from hybrids can be aligned to one or both parental genomes. There are many existing programs that can be used for alignment, including Bowtie (Langmead *et al.*, 2009) and BWA (Li & Durbin, 2010). To detect SNPs and indels in this aligned data, it is necessary to identify locations where the read sequences differ from a known reference genome (e.g. van Oeveren & Janssen, 2009). The genotype of each spore at each position can then be determined by comparing the number of sequencing reads that match the reference sequence for each parent. Once all the spores from a single meiosis have been genotyped, recombination events must be detected and classified from this information.

4.1.4. Characteristics of an SK1 x S288c hybrid cross

An SK1 x S288c hybrid cross has a relatively high sequence divergence of around 0.7%, containing ~62,000 sequence polymorphisms with a median inter-marker distance of 77 bp (when excluding repetitive regions). There are few (11) regions longer than 10kb devoid of polymorphisms (Laureau *et al.*, 2016). These characteristics are desirable for high-resolution genotyping. The hybrid undergoes meiosis efficiently and has a spore viability of around ~70%, reduced to ~63% in the absence of MMR. Though *msh2Δ*-mediated MMR deficiency reduces spore viability in WT and *tel1Δ* backgrounds, it improves spore viability in DDR checkpoint-deficient hybrid backgrounds (discussed in Chapter 3).

4.1.5. Aims of this investigation

There are many established methods for characterizing recombination events genome wide. However, there is scope to improve upon these methods, and adapt them for new lines of investigation. The aims of this project are:

1. To create a dedicated SNP and indel list tailored for the SK1 and S288c strains used in this investigation.

2. To reconstruct an 'SK1' genome using S288c scaffolding and the detected variants.

3. To create a data analysis pipeline that compares to both parental genomes to establish the genotype of each detected variant.

4. To create a pipeline that can handle the heteroduplex DNA found in *msh2Δ* tetrads, as well as *msh2Δ* octads and *MSH2* tetrads. This is important for getting the most out of low-viability crosses. The octad protocol is not suitable for all backgrounds as some very rarely produce 4-spore viable tetrads (Table S1).

5. To create a pipeline optimized for long reads and relatively low read depths.

4.2. Results

4.2.1. Strategy for maximizing sequencing data

In order to examine recombination genome wide, hybrid SK1xS288c diploids were sporulated and tetrad dissected as detailed in Methods (the sequencing and analysis workflow is also summarized in Figure 4.1). To produce octads for the analysis of PMS, an additional round of dissection was carried out on *msh2Δ* strains after the first mitotic division. One concern was that this mechanical interference with actively dividing cells may reduce their viability. To test this, the viability of *msh2Δ* tetrads and octads was compared (Figure 4.2). The spore viability of *msh2Δ* octads and tetrads were not found to be noticeably different, indicating that the mechanical separation of mitotically dividing cells does not affect their viability.

Genomic DNA was prepared from colonies derived from each tetrad spore or octad progeny, diluted to ~0.2ng/µl and prepared for sequencing as according to the Nextera XT protocol. By this method, genomic DNA is 'tagmented' by an enzyme that simultaneously fragments the DNA and adds in adapter sequences, then PCR amplified with indexed primers. By using different indexes for each sample, many samples can be sequenced together and demultiplexed. Samples are paired-end sequenced on the Illumina MiSeq platform (Methods Section 2.9).

The Nextera XT protocol recommends 12 cycles of PCR. Increasing the number of cycles may produce more material for sequencing, but carries a risk of biasing the read population towards whichever reads were amplified early. However, no strong correlation between the number of cycles and duplication rate of sequenced reads was observed (Figure 4.3A).

After PCR amplification, a clean-up step is carried out with magnetic beads; this also serves to select for certain size fragments. Adding fewer beads selects for longer DNA fragments, which affects the read lengths of the final output (Figure 4.3B). However, selecting for long reads means less DNA is carried though the clean-up step, affecting cluster density (Figure 4.3C). In addition, reads longer than 600bp will not be sequenced completely. This means that overall, more sequence data is produced when short fragments are retained, despite not fulfilling the potential read lengths and being counter to the recommendation of the Nextera XT protocol.

SK1   S288c

X

Hybrid

1. Sporulation produces tetrad

2. First mitotic division produces octad

3. Extract genomic DNA, prepare with Nextera XT: fragment, add indexes, amplify

A
G
A
T
C

4. Sequence DNA on Illumina Miseq

5. Bowtie2 alignment to S288c reference- permits mismatches to preserve SK1 sequences

S288c Reference   Sequenced spore data

Pos	S288c	SK1
1	A	G
2	T	A
3	-	Ins
4	C	T
5	Del	-

6. GATK detection of SNPs and indels from sequencing data

7. Generate "SK1" genome, perform alignment to "SK1" genome

S288c Reference   SK1 Reference

Pos	Call 1	Call 2	Final
1	c	c	c
2	c	-	c
3	c	c	c
4	k	-	k
5	h	h	h
6	k	c	-

8. Using the variants detected by GATK, compare reads matching each parent to make genotype call. Resolve calls against S288c and SK1 for final list

Pos 1a 1b 2a 2b 3a 3b 4a 4b
1	c c k k c c k k
2	c c k k c c k k
3	c c k k c c k k
4	k k c c c c k k
5	**h h** c c c c k k

9. Combine called spores from a tetrad or octad [c=S288c call, k=SK1 call, h=heteroduplex call]

Pos 1a 1b 2a 2b 3a 3b 4a 4b
1	c c k k c c k k
2	c c k k c c k k
3	c c k k c c k k
4	k k c c c c k k
5	**c k** c c c c k k

10. In *msh2Δ* tetrads, resolve heteroduplex calls into S288c and SK1

11. Input into Event Caller (authored by Marie-Claude Marsolier). Examine recombination events, analyse properties.

CO: between 1 and 3

Event length

Complex: CO between 3 and 4 and NCO on 2

1a
1b
2a
2b
3a
3b
4a
4b

NCO: between 3 and 4 with **heteroduplex tract**

A   B

Inter-event distance = B–A

Sequenced sample types

MSH2 Tetrad

msh2Δ Octad

msh2Δ Tetrad   *msh2Δ* "Octad"

Figure 4.1. Workflow for genome-wide analysis of recombination.
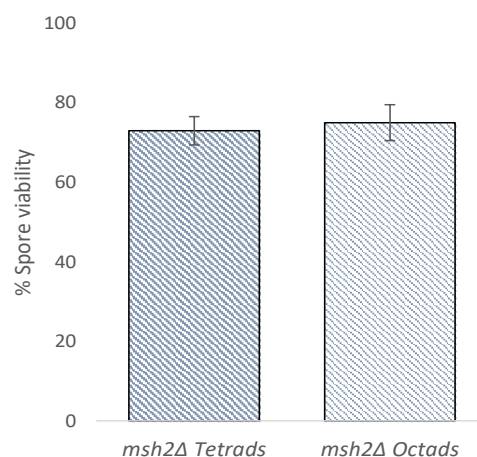
Figure 4.2. The average spore viability of *msh2Δ* tetrads and *msh2Δ* octads. Error bars are 95% confidence limits.
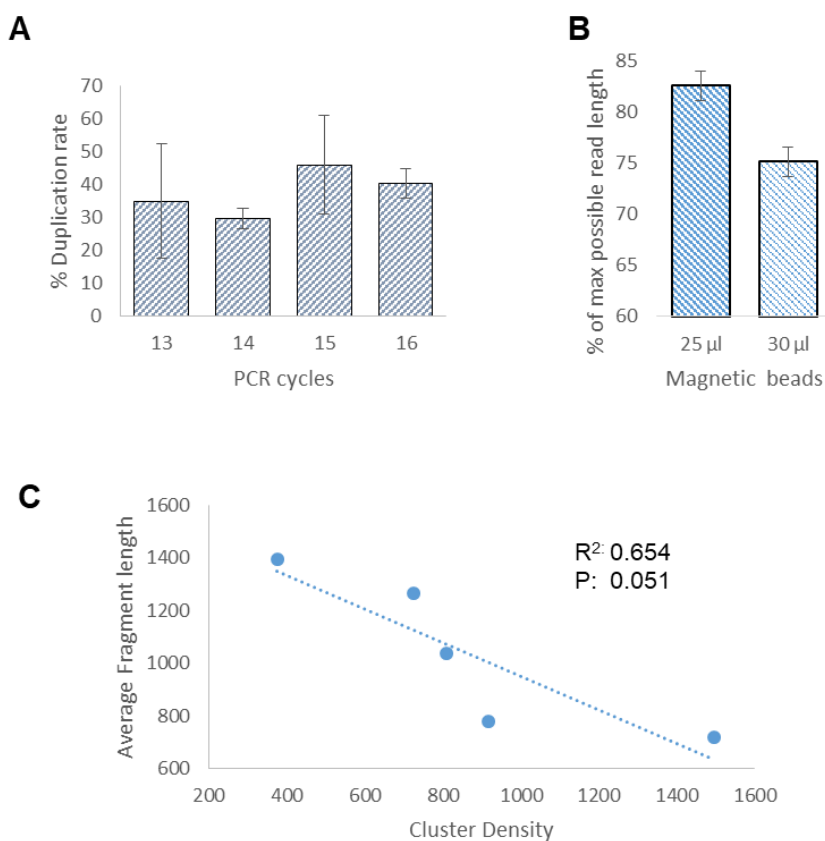
Figure 4.3. Quality control of sequencing sample preparation. All error bars are 95% confidence limits. A) Relationship between duplication rate of sequenced reads and the number of PCR cycles. Duplication rate corresponds to non-unique read start positions, so e.g. 20% duplication rate means 1/5 read start positions occurred more than once. **B)** The average read length of sequencing runs expressed as a % of the maximum possible read length (300bp or 75bp), depending on whether samples were cleaned up with 25µl or 30µl of magnetic beads (a ratio of PCR product to volume of beads of 9:5 or 3:2, respectively). **C)** The effect of the average size of DNA fragments after PCR clean-up on cluster density of the sequencing run. Fragment lengths were measured on a Bioanalyzer.

4.2.2. Reduction of contamination by 2µ plasmid and mitochondrial DNA

An undesirably large number of sequenced reads were found to align to the 2µ plasmid or mitochondrial genomes. In an attempt to reduce this contamination, an additional step was added to the standard genomic prep involving treatment with Triton X-100 (a nonionic surfactant) after sphaeroplasting. This was intended to open small holes in the cell and nuclear membranes, allowing small plasmids and mitochondria to exit but not the bulky genomic DNA. This was a partial success; comparing samples prepared by the new and old method shows that the amounts of both 2µ plasmid and mtDNA have been reduced on average, although they are still undesirably high (Figure 4.4).

Sequencing results suggest that the average haploid yeast cell contains 146 copies of the 2µ plasmid. This is higher than the published amount of 50 to 100 copies (Zakian *et al.*, 1979), which suggests that the protocol is biased towards 2µ plasmids somehow, possibly because plasmid DNA has a higher stability than genomic DNA in storage. On the other hand, sequencing suggests an average of only 2 mtDNA copies, compared to a normal range of 20-30 mitochondria per yeast cell (Visser *et al.*, 1995). This may be because mtDNA is not contained in the nucleosome, and so is more likely to be lost during the genomic prep. Petite colonies were not observed among hybrid spores (data not shown), so they are not expected to have mitochondrial defects.
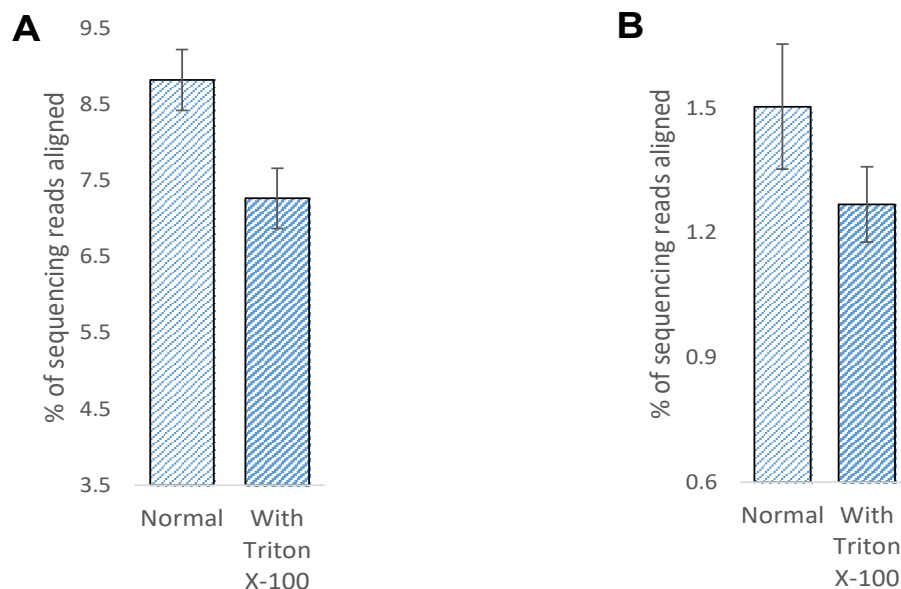
Figure 4.4. Reduction of contamination in sequenced DNA. Error bars are 95% confidence limits. **A)** Comparison of the average number of sequenced reads that align to the 2-micron plasmid sequence, in samples prepared with or without an additional treatment with Triton X-100. **B)** Comparison of the average number of sequenced reads that align to the mtDNA sequence, in samples prepared with or without an additional treatment with Triton X-100.

4.2.3. Detection of polymorphisms and creation of SK1 genome

The S288c strain has the status of being the first eukaryotic genome ever sequenced (Goffeau *et al.*, 1996), and has since been regularly improved upon to give a reliable and thorough sequence. In contrast, the SK1 genome has only been partially sequenced, and is missing detail from repetitive regions (Liti *et al.*, 2009). To overcome this issue, data from sequenced tetrads was first aligned to the S288c genome only (Engel *et al.*, 2013). Also included in the reference file are sequences from the yeast mitochondrial (Foury *et al.*, 1998) and 2µ plasmid (Hartley & Donelson, 1980), a small high-copy plasmid present in *S. cerevisiae* (Nelson and Fangman, 1979).

The sequenced reads in this study are up to 300bp long, unlike most previous studies which have used reads of up to 100bp (e.g. Anderson *et al.*, 2011; Laureau *et al.*, 2016). Since an SK1 variant will appear on average once every ~77bp (when excluding repetitive regions), a 300bp read may contain several SK1 type alleles. During alignment, these would be treated as mismatches and reduce the success of alignment. To preserve SK1 sequences, a high sensitivity bowtie2 alignment was used with a reduced mismatch penalty (detailed in methods). This permits >99% of reads to be mapped in most samples (data not shown). This will also preserve sequencing errors, so a good read depth is needed to dilute any miscalls.

To detect SNPs and indels in the aligned data, it is necessary to identify locations where the read sequences differ from a known reference genome (e.g. van Oeveren & Janssen, 2009). However, apparent variants can occur due to sequencing or alignment error, so a quality score threshold can be used which will depend on read depth and proportions of reads with the variant, so rare variants can be ignored (Li *et al.*, 2008; Li *et al.*, 2009).

SNP and indel type polymorphisms were discovered and genotyped using the GenomeAnalysisToolkit function HaplotypeCaller (DePristo *et al.* 2011). The calls from 120 samples were combined and the call frequency, total read depth and averaged variant read-depth:total read-depth ratios were calculated. Variants were filtered according to custom filtering parameters for a call-frequency between 45-55% of spores, a total read depth spanning the site of >250 and where 95% or more of the reads at that site contained the variant. Variants occurring in repetitive regions such as subtelomeres are also removed. This is performed using the script 'VariantCalling' authored by Tim Cooper (Methods section 2.11).

The final robust list of 64582 SNPs and 3947 indels has a median distance of 81bp and a mean distance of 169bp between polymorphisms, when excluding repetitive regions of the genome (Figure 4.5). If only SNPs were considered and not indels, the median distance would be 87bp

and the mean 180bp, which shows that the indels have a beneficial effect on marker density even though there are 16x fewer indels than SNPs.

The variant table was then used to create an 'SK1' genome by substituting each polymorphism detected into the S288c reference genome. Each sequenced sample was then realigned to this 'SK1' genome. During the second alignment, it is still necessary to tolerate mismatches because if there are reads that span a recombination event, there may be polymorphisms from both parents present within one read. Thus a very strict alignment would discard reads covering these junctions.
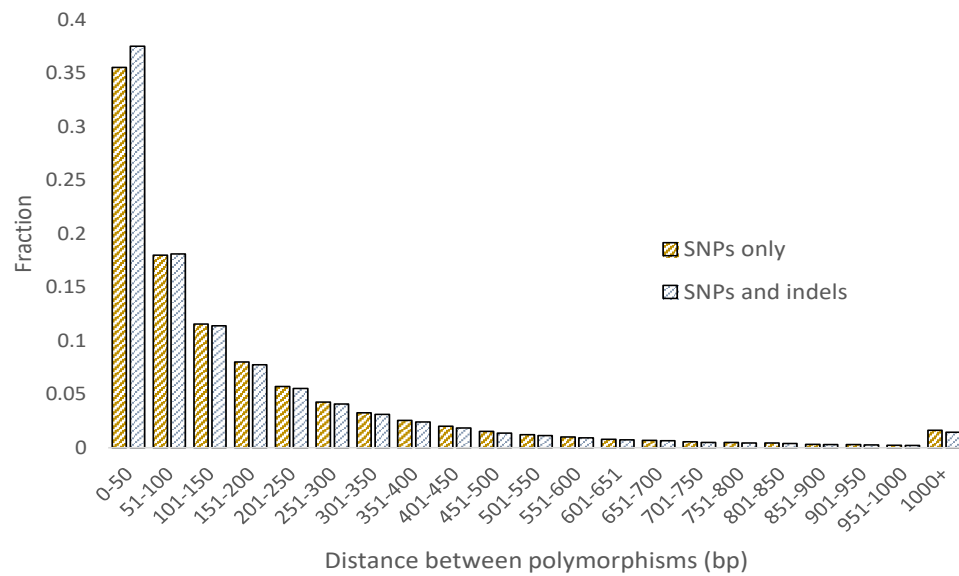
Figure 4.5 Comparison of the distribution of distances between polymorphisms
Distances between polymorphisms in the variant table are plotted for when both the 64582 SNPs and 3947 indels are considered, or when the SNPS alone are considered.

4.2.4. SNP calling

In order to extract the number of reads matching each base, or an insertion or deletion, at each genomic position, the PySamStat module 'variation' (Miles & Mattioni, 2016) is run on each sample. These are then compared to the list of parental variants in order to make a call for each polymorphism, using a set of custom scripts authored by myself (available in Appendix). Variant calling is performed twice, once against each parental variant list, and the two lists are reconciled. Rules for calling are detailed in Methods section 2.12.

A genotype will only be assigned for positions with 5 or more reads. This is similar to Laureau *et al.* (2016), who used a limit of 6 or more. There are different calling thresholds for SNPs and indels, because indels are harder to align and so usually have a lower reported read depth than the surrounding positions. However, alignments are not likely to falsely report the presence of an indel, so even a low number of reads can be trusted to be accurate. Thus, SNP reads are required to have a 75% match for a variant call, and 90% for a reference call; indels need a 30% match for a variant call, 95% for a reference call.

The variant caller script also produces a statistics file containing various useful stats e.g. the number of positions that failed the read depth threshold, number of variants called S288c or SK1 etc. This helps give feedback on the validity of the rules, informing e.g. if there is a bias in calling.

At most positions, it is easy to make an unambiguous call as reads will only match one parental genotype. There are occasionally some positions that consistently appear as segregating 4:0 across multiple tetrads; these are considered unreliable and are removed to improve the accuracy of the variant table.

If a mixture of SK1 and S288c-type reads are detected at a SNP position, it is marked as 'heteroduplex'. This occurs if total SNP reads are >90% of all reads, and S288c and SK1 reads are each between 20%-70% of all reads. This is similar to the thresholds used by Laureau *et al.*, (2016) which required 25-95% S288c reads and 5-75% SK1 reads for a heterozygous call.
Indels cannot be called heteroduplex, because it is hard to be certain if there is truly a mixture of reads. Due to the difficulty in alignment of sequences containing indels, there is always a reference bias for these positions.

4.2.5. Heteroduplex calling in *msh2Δ* tetrads

In most samples, positions with a heteroduplex call are then discarded before event calling, because *msh2Δ* octads and *MSH2* tetrads are not expected to have hDNA. However, in *msh2Δ* tetrads, it is possible to convert hDNA calls into separate SK1 and S288c calls, as a reconstruction of what would have been seen if it were possible to perform octad dissection in a low-viability background. By this method, calls for each spore in a tetrad are combined into one file and duplicated to produce eight columns. Positions that were called as heteroduplex will be assigned as S288c in the original column and SK1 in the duplicated column. From this, almost all the information that would have been available in an octad can be accessed. The features that can be observed in the different types of meiotic products are summarized in Table 4.1.

Table 4.1. Comparison of recombination event features that can be seen in the different types of sequenced tetrad. hDNA tracts are regions where the inherited parental variant differs between DNA strands of a chromosome. Duplications are regions of consecutive variant positions where a roughly 50:50 mixture of reads containing the different parental SNPs is detected. Trans hDNA is when the genotype changes between DNA strands or chromosomes, but the same overall segregation pattern is seen. Incompatible hDNA is a hDNA pattern that cannot be explained by a single DSB.

Feature	*msh2Δ* octads	msh2Δ tetrads	Tetrads
hDNA tracts	Yes	Yes	No
Duplications	Yes	No	Yes
Trans hDNA	Yes	No	No
COs with incompatible hDNA indicating a separate NCO	Yes	Yes	No

The ability to detect hDNA in *msh2Δ* tetrads is an advantage of the use of sequencing over the use of DNA-chip arrays, because mixed hybridization would be difficult to achieve in that system. Thus when using DNA-chip arrays for hDNA analysis it would be necessary to use octads, which would greatly increase the difficultly of examination of mutants with a low spore viability, as the probability of successfully isolating a viable octad is low in those backgrounds.

To assess the effectiveness of this system of heteroduplex reconstruction, *msh2Δ* octad data can be converted into 'mock tetrads' by summing the reads from each pair of mother-daughter spores to give an output resembling that of a *msh2Δ* tetrad, with a mixture of reads at heteroduplex positions. The mock tetrad can then be processed as if it were a tetrad, without heteroduplex calling, or with the heteroduplex calling to give a 'mock octad'. The results of this comparison are shown in Figure 4.6A. This shows that, between the different ways of calling genotypes, the number of COs detected is not greatly affected, but the number of NCOs is severely reduced when

heteroduplex calling is not performed on *msh2Δ* tetrads. When heteroduplex calling is carried out, the number of NCOs detected as slightly higher than the number seen in the true octad, though not significantly so (T-test, P=0.298 [Methods 2.21]). These extra 'NCOs' could be duplications, as discussed in section 4.2.6, or errors, as discussed in section 4.2.7.

One limitation of heteroduplex calling is that in true octads, it is possible to see occurrences of trans hDNA in NCOs, where there are two 5:3 sections occurring on different strands or chromatids (Figure 4.6B). These are of interest because usually the original Spo11-DSB occurred in the middle of the trans hDNA (Martini *et al.*, 2011). This means it is possible to work out which strand of the original chromatid was 3' and which was 5', because resection occurs 5' to 3'. Thus, there is less information available in *msh2Δ* tetrads about Spo11-DSB positioning and strand directionality.

4.2.6. Presence of potential duplications

Occasionally, unique 'heteroduplex' SNP calls are observed in octads or *MSH2* tetrads, even though there should not be occurring in these backgrounds (an example is shown in Figure 4.6C). These calls most likely represent duplications occurring during recombination. If an SK1-type allele is broken and copies from an S288c sequence, but invades in the wrong place, it may end up with two copies of the same sequence, once from each parent. The duplications are not always associated with a detected recombination event, meaning that they could represent undetected NCOs. It is interesting to examine these duplications as they represent a loss of control in meiotic recombination; e.g. they occur more frequently in *tel1Δmsh2Δ* octads than in *msh2Δ* octads (Chapter 6, Section 6.2.6). However, if these duplications occur in *msh2Δ* tetrads, they would be indistinguishable from hDNA caused by PMS, so cannot be detected separately.

4.2.7. Errors in heteroduplex calling

Occasionally, there are some positions that are called as heteroduplex across multiple tetrads; these are considered unreliable and are removed to improve the accuracy of the variant table. It is likely that these positions are from naturally duplicated regions of the genome, as they are most commonly found in the subtelomeres. If one copy of a repeated gene is different between SK1 and S288c but the other is not, when reads are aligned by bowtie2, they are randomly assigned to the wrong copy of the gene, indicating that there is a polymorphism but it is not possible to pinpoint where it occurs with simple alignment.
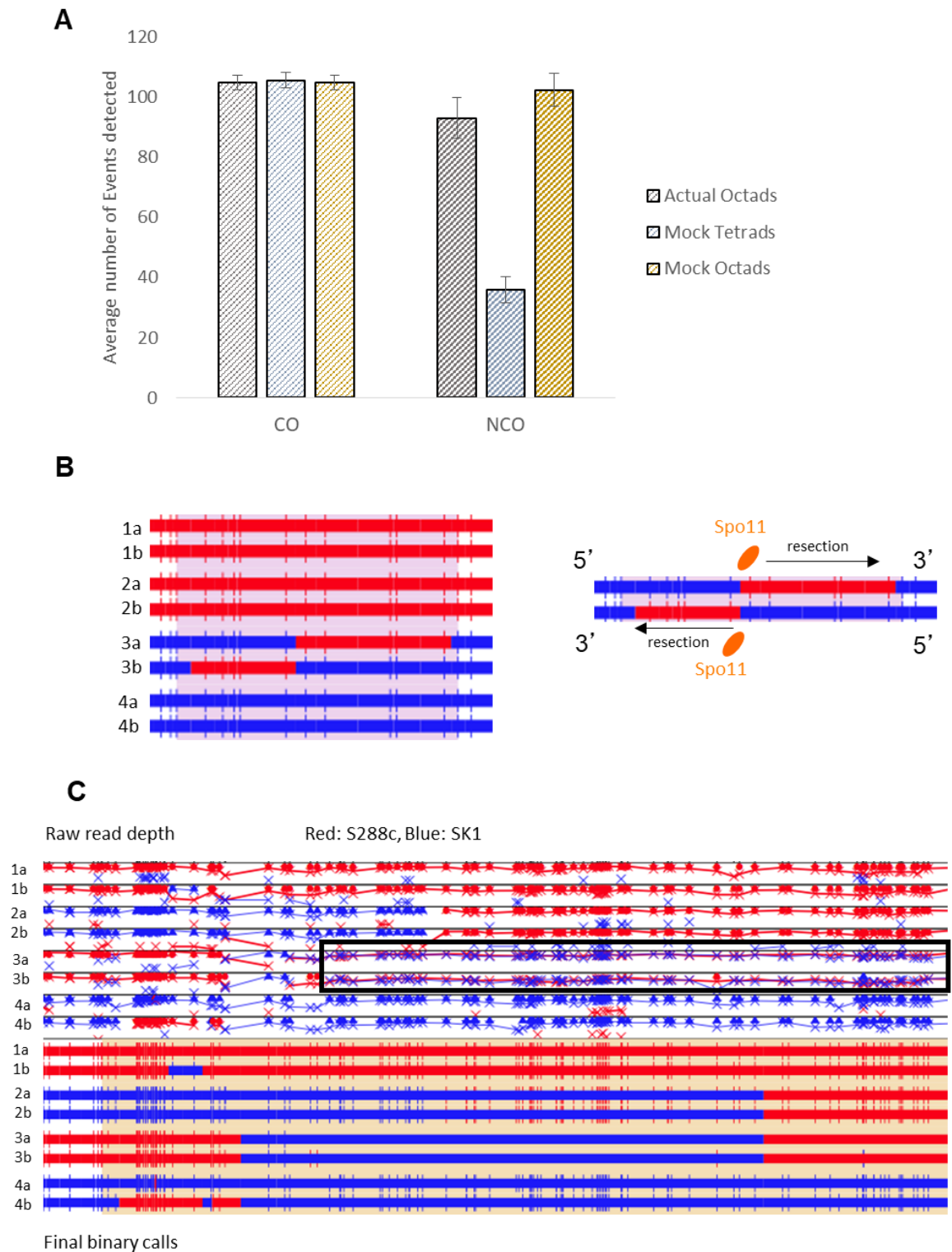
Figure 4.6. Considerations for heteroduplex calling. Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. **A)** Comparison of the number of events detected as CO or NCO in actual octads, mock tetrads and mock octads. Error bars are 95% confidence limits. **B)** Example of a *trans* hDNA tract, occurring on chromatid 1. *trans* hDNA can also occur between two different chromatids. **C)** Example of a suspected duplication in a *tel1Δ msh2Δ* octad. From the raw read depth, it is apparent that there is a mixture of SK1 and S288c type reads occurring on chromatid 3 (black box), close to a CO event between 3 and 4. However, in the final binary calls, these positions have been discarded.

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4.2.8. Variant call reconciliation

Once variant calling is complete, all members of an octad or tetrad are combined into one file. If any member lacks a call at one position, the position is removed. In addition, indels with a 4:0 segregation patterns are removed because the difficulty of indel calling means that they may not be real.

To reconcile calls made against each parent, each position is tested to see if the two calls agree, or disagree. If there is a clash, the position will be removed. If only one parental alignment has successfully called the position, this call will be used (a system similar to that described in Anderson *et al.*, 2011). From this step, a binary file is produced that is compatible with event analysis programs authored by Marie-Claude Marsolier (personal communication).

The overall number of variant positions discarded due to an inability to unambiguously call a genotype at that position is reduced at higher read depths (Figure 4.7). On average, samples from this study have 27x read depth and 8.11% of variants removed. In comparison, additional sequencing data from four *msh2Δ* octads was provided by Bertrand Llorente, which had an average read depth of 75x and 0.62% of variants removed. However, there is a lot of variation; samples with the same read depth may have different numbers of unambiguously called variants. In addition, even very high read depth samples have some variants removed, for reasons unrelated to read depth such as heteroduplex calling, alignment error or mutation.

It is important to note that variant removal only affects the potential to see all recombination events, and does not necessarily mean than a significant number of events are missed. Even in samples with a lot of variants removed, there are typically a similar number of events detected to that of higher-read depth samples of the same genotype (Figure 4.14). In particular, the number of COs detected is unlikely to change with higher read depth because COs are very unambiguous due to the reciprocal exchange of markers.
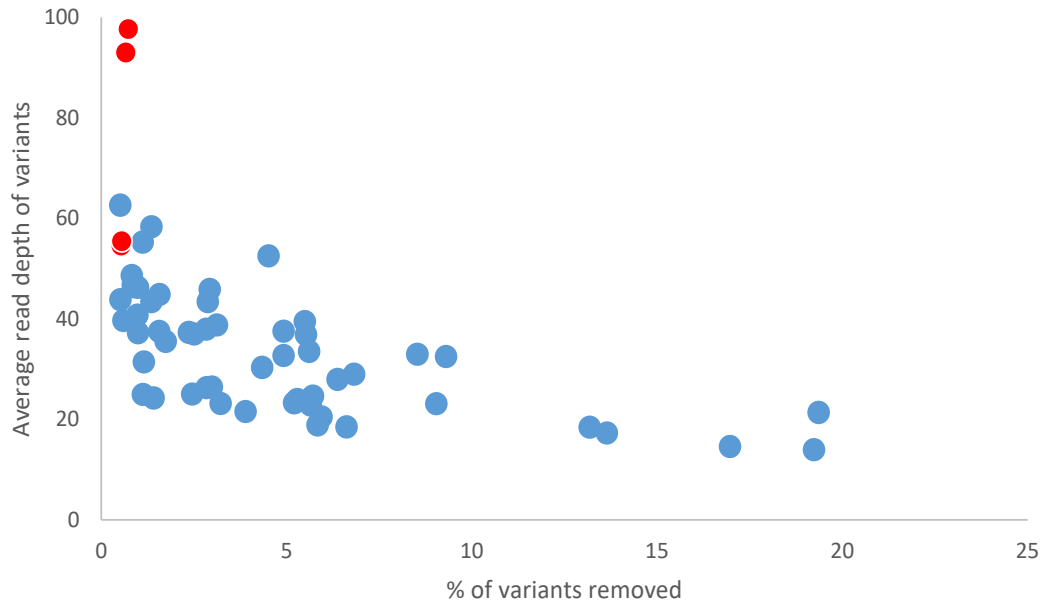
Figure 4.7. Percentage of variant positions removed in each sample compared to the average read depth of variant positions for each sample. Blue dots are original data, red dots represent data provided by the Llorente lab.

4.2.9. MMR incompatibility

It is known that there is an incompatibility between SK1 and S288c *MLH1* and *PMS1* alleles, affecting MMR processes and causing a higher mutation rate in the progeny that inherit the combination of alleles (Heck *et al.,* 2005). *MLH1-PMS1* is vital for post replicative MMR, being the primary *MLH* heterodimer in *Saccharomyces cerevisiae*. A single SNP in each gene is responsible for the incompatibility: in Mlh1, amino acid 761 is Asp in S288c, but Gly in SK1; and in Pms1, amino acid 818 is Arg in S288c, but the equivalent position is Lys in SK1. When the S288c allele of *MLH1* was combined with the SK1 allele of *PMS1*, an approximately 100-fold higher mutation rate was observed (Heck et al, 2005). Sequencing shows that these polymorphisms are present between the S288c and SK1 strains used in the experiments described in this project, so around 1 in 4 spores produced should have the incompatible combination. These spores may then have accumulated additional mutations during normal growth before being sequenced, potentially introducing apparent noncrossover events. However, unless a mutation occurred at a known polymorphism location, coincidentally converting the genotype at that location from that of one parent to the other, it would not be detected. Also, most of the sequenced samples lack Msh2 anyway, so this mismatch defect would not affect them additionally. Finally, the fraction of COs associated with conversion tracts in a WT SK1xS288c hybrid was comparable to that found in a YJM789 x S288C hybrid, indicating that the partial MMR defect has a negligible effect (Martini *et al.*, 2011).

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4.2.10 Event categorization

The scripts for event categorization described in this section were authored by Marie-Claude Marsolier (Methods section 2.13). In order to detect recombination events, the chromosomes of the spores are first segmented into regions of homogeneous genotypic patterns, i.e. each change in the segregation pattern is a separate segment. Next, recombination events are considered as a set of segments occurring within a set distance of each other (the merging threshold), located between regions of 4:4 (Mendelian) segregation. In the absence of recombination, markers will show a continuous Mendelian segregation pattern (2:2). COs are identified as the junction between two different 2:2 segregations, which indicate a reciprocal exchange. There may also be gene conversion tracts associated with COs, appearing as non-Mendelian (3:1) segregation of markers around the reciprocal exchange. 3:1 patterns observed without a reciprocal exchange indicate the presence of a NCO. In addition to the usual Mendelian 2:2 and non-Mendelian 1:3 marker segregation patterns encountered in tetrads, octads can display 5:3 patterns, indicating half-conversion tracts which can be associated with either COs or NCOs.

The event detecting script outputs a file containing the event start and stop positions (the minimum and maximum possible are reported based on the last SNP to change and the first SNP to not change); the length of the event, which is estimated from the distance between the midpoints of the start and stop intervals; the type of event e.g. 5:3_4:4_3:5 means that the event is composed of 3 segments of different segregation patterns; the number of chromatids involved in the event, and the number of variants that were called as part of the event.

A higher merging threshold means that events may be merged when they should be considered separate; a lower threshold may cause the opposite. Originally, a 5kb merging threshold was used, meaning that pattern changes occurring within 5kb of each other would not be considered as separate events (Martini *et al.*, 2011). However, after extensive analysis of heteroduplex patterns, the authors now consider 1.5kb to be most representative of the situation in *msh2Δ* octads (Bertrand Llorente, personal communication). This threshold allows the majority of events to be correctly called, based on existing data on event numbers in WT and the occurrence of segregation patterns incompatible with a single DSB. However, this may not be the case in all backgrounds. If a loss of CO or DSB interference has occurred, DSB clustering may be observed, meaning that multiple events will occur close together. These events will not be resolved if the distance between them is shorter than the merging threshold. Even if the merging threshold is not appropriate in all backgrounds, it is still necessary to use the same threshold for all analyses to avoid introducing a bias. Different genotypes can then be compared for other characteristics to identify clustering. For example, if tetrads analyzed with a 1.5kb merging limit have many more events detected than if they were analyzed at 5kb, it suggests that there were a lot of events that are close together in

this background. For all analyzed genotypes, reducing the limit from 5kb to 1.5kb increases the number of events detected as separate, but most checkpoint mutants have a larger increase than WTs (Figure 4.8). In most cases, the number of NCOs is more heavily affected than the number of COs when the threshold is changed. Other examples suggestive of clustering are the occurrence of long events that may be merged events, and an increase in the proportion of events affecting multiple chromosomes.
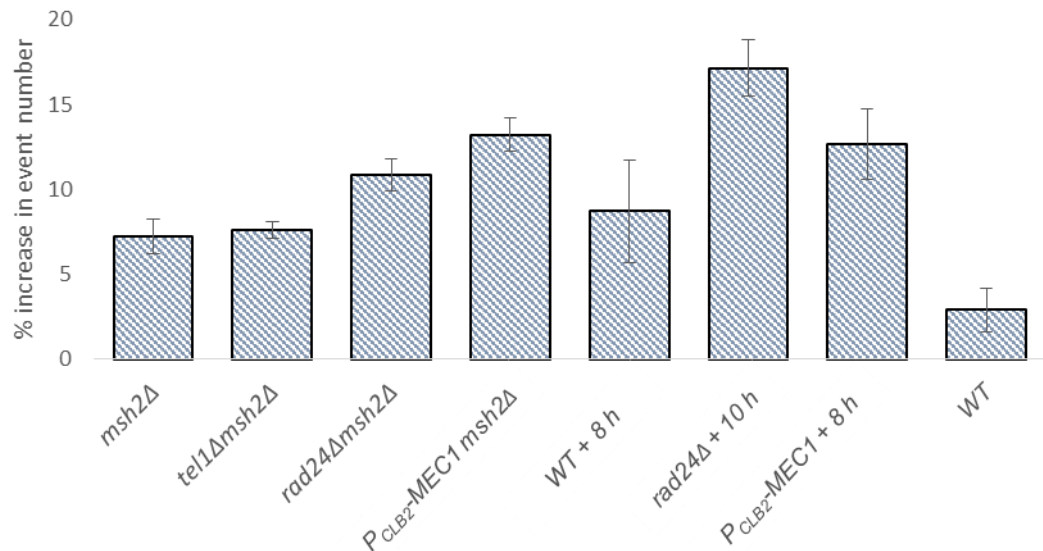
Figure 4.8. The percentage increase in the number of separate events called when the merging threshold is reduced from 5000bp to 1500bp, across different genotypes.
Strains with 8 or 10 hours of NDT80-mediated prophase extension are named with '+ 8/10 h'.

4.2.11. Subcategorization of events and manual annotation

In addition to the higher categories of CO or NCO categories, recombination events can be subcategorized based on certain signatures that may give clues as to how they were formed. The event categorizes are based on those described by Martini *et al.*, 2011. As such, many categories depend upon the presence of hDNA, so fewer classes are available for the MMR-proficient strains. The classification system is described in Methods section 2.14. For both COs and NCOs, there are four groups which are composed of multiple classes. Categorizing events in this manner is helpful because certain patterns may be indicative of different repair methods. Generally, Group 1 contains simple events, Groups 2 and 3 contain events with signatures suggestive of different complex repair processes (such as repair of nicks and double-stranded gaps, template switches between non-sister and sister chromatids, and HJ branch migration), and Group 0 contains events with signatures suggestive of multiple DSBs. Some models for how certain complex signatures may have been formed are shown in Figures 4.9 and 4.10. However, there are many ambiguous cases where it is not possible to be certain exactly how an event was formed. For example,

segments of 6:2 or 2:6 segregation were originally not predicted to occur in *msh2Δ* octads as these conversion tracts were thought to be a result of mismatch repair only (Martini *et al.*, 2011). However, around 19% of CO and NCO events in *msh2Δ* octads display segments of 6:2 or 2:6 (e.g. Figure 4.11A). It is likely that these segments result from the repair of gaps, which could arise from two close Spo11-DSBs on the same chromatid or from the removal of a 3' end after invasion of a homologous sequence, e.g. the formation of a nick during topological processing of a dHJ (Figure 4.10, E and H). In such ambiguous cases, the scenario involving fewer DSBs is chosen for the purpose of the categorization, but an increase in such events could still be suggestive of increased DSB formation.

CO events:

CO events are usually associated with conversion, restoration or hDNA tracts, caused by resection and dHJ migration. However, these patterns could also be caused by an adjacent NCO. It is possible to differentiate CO-associated tracts from separate CO and NCO pairs because the broken chromatid can be identified based on which DNA strands had a pattern change, since the broken strands will copy from an intact donor. Usually, patterns are consistent with a single break, i.e. all show the same directionality of repair (e.g. only 3:5 and 2:6, or only 5:3 and 6:2). If patterns of different directionalities occur, e.g. 5:3 then 3:5, this indicates that more than one chromatid was broken. However, it does not mean that both breaks were formed by Spo11 activity; the second break could have occurred during DSB repair (Figure 4.10G). Thus, these events are only considered to be formed by two Spo11 breaks if the CO and potential NCO occur on different chromatids (Group 0 Class 2; e.g. Figure 4.11C). Otherwise, COs with hDNA patterns incompatible with a 1-break scenario on the same chromatids as the CO are sorted into Group 3 (e.g. Figure 4.11B). Again, in these ambiguous cases, the scenario involving fewer DSBs is chosen; however, Group 3 COs could conceivably be produced by concerted DSB formation.

Figure 4.9. Models of meiotic NCO formation
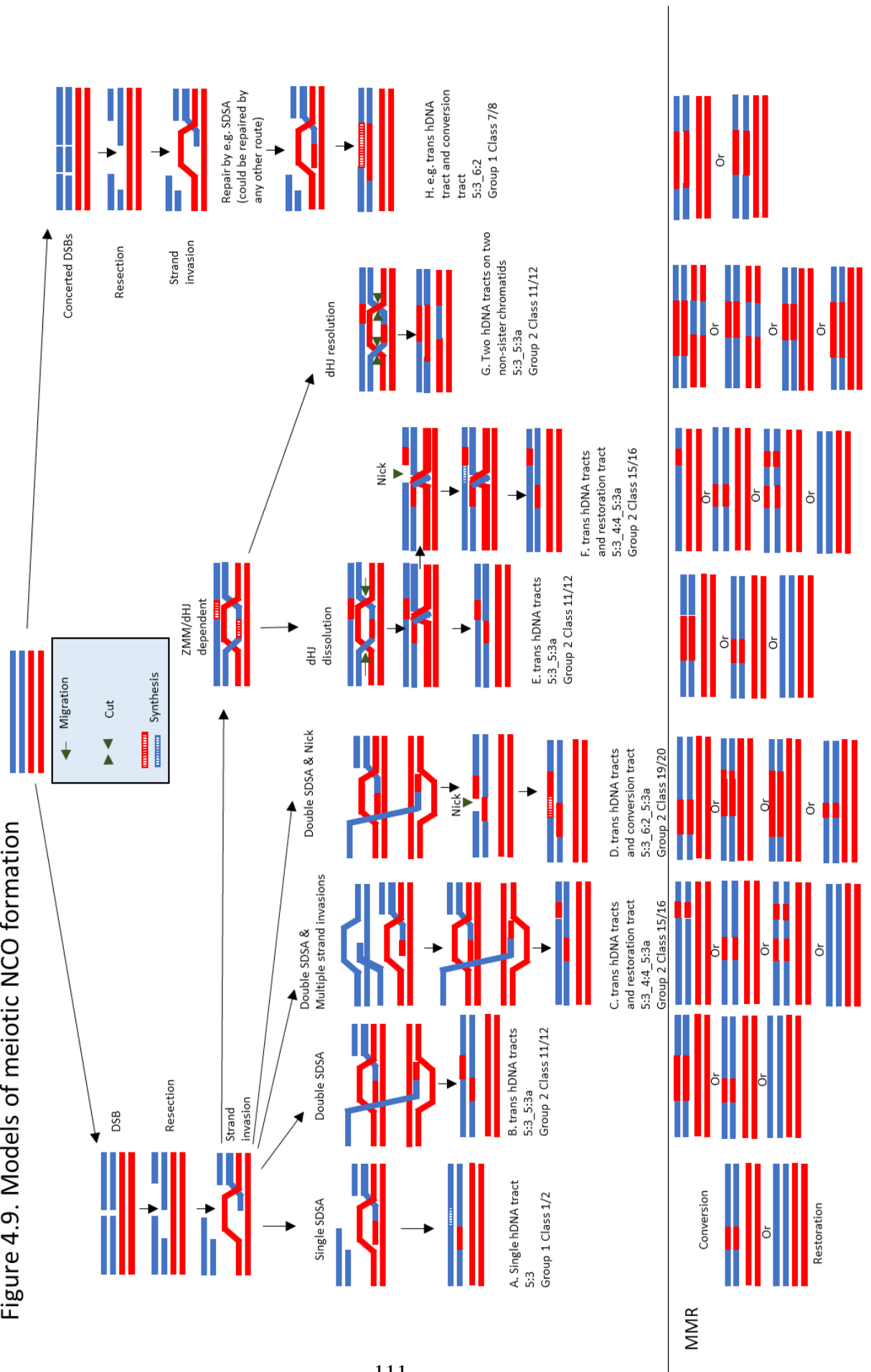
Figure 4.9. Models of meiotic NCO formation. For simplicity, only two homologous DNA molecules are represented, one red and one blue, unless necessary to represent template switching/multiple strand invasions. Note that nicks and multiple strand invasions could happen in combination with other pathways to produce more complex patterns. The notation 5:3_5:3a stands for two consecutive hDNA tracts producing the same overall segregation pattern but affecting different strands. This is called 'trans hDNA' if the affected strands are on the same chromatid, but the hDNA tracts can also be produced on two non-sister chromatids by dHJ resolution. **A)** SDSA (Paques and Haber, 1999): After strand invasion, the invading 3' end is extended by DNA synthesis. The intermediate is dismantled and the DSB repaired by annealing of the ends and gap repair. This pathway generates NCOs with only one hDNA tract. **B)** Double SDSA (Martini et al., 2011): Both ends of the DSB engage in two independent SDSA reactions, generating a NCO with two hDNA tracts in a trans configuration on the same chromatid. **C)** Double SDSA & template switching (Martini et al., 2011): During double SDSA, one end first invades the sister chromatid followed by a non-sister chromatid. The other end invades the non-sister chromatid as usual. Annealing of the two ends leads to the formation of a trans hDNA pattern separated by a 4:4 tract. **D)** Double SDSA & nick formation: After strand invasion, a nick is formed in the 3' end. Double SDSA occurs as usual and the nick is filled in with information copied from the non-sister chromatid, producing a conversion tract. **E)** dHJ dissolution (Paques and Haber, 1999): After 3' end invasion, a stable SEI intermediate is formed and is processed into a dHJ, but the dHJ is dissolved by the combined action of Sgs1 helicase and Top3 topoisomerase, producing an NCO with two hDNA tracts in a trans configuration on the same chromatid. **F)** dHJ dissolution and nick (Martini et al., 2011) During dHJ dissolution, a nick is formed during the topological processing of the junction. Nick translation generates a 4:4 restoration tract. **G)** dHJ resolution (Paques and Haber, 1999): After 3' end invasion, a stable SEI intermediate is formed and is processed into a dHJ, the resolution of which can lead to NCO if the four nicks affect only two DNA strands. **H)** Double DSB. Two close DSBs occur on the same chromatid, and the DNA in between is lost. Resection and strand invasion happen normally and the break is repaired by any method, with additional gap repair producing a conversion tract. The example shows repair by SDSA (as in A). **I)** Effect of MMR: Each image is a possible outcome of the repair pathway shown directly above it, after mismatch repair has converted or restored hDNA tracts. Note that the invading 3' end may be converted or restored during strand invasion instead of post-repair.

Figure 4.10. Models of meiotic CO formation
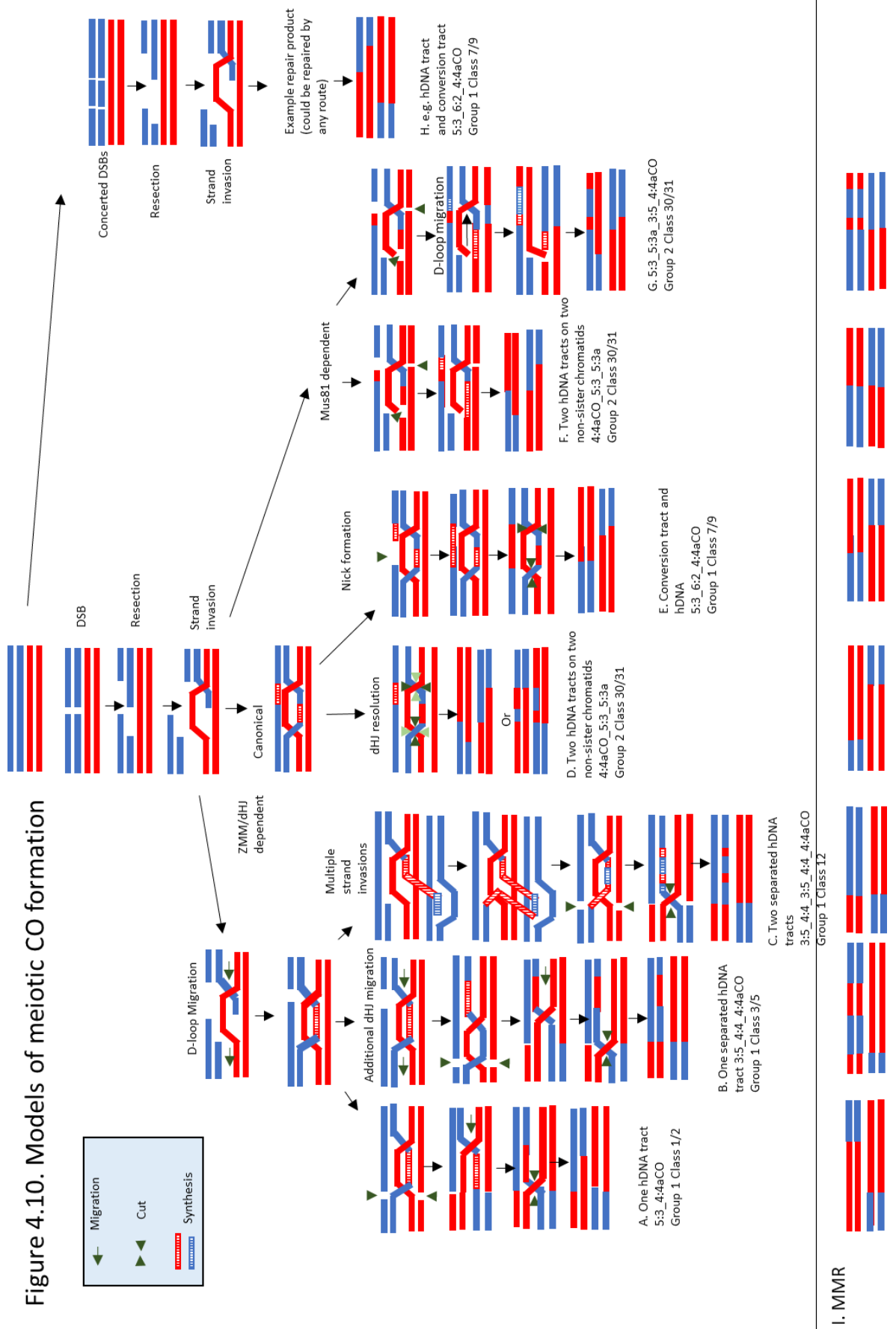
Figure 4.10. Models for meiotic CO formation. For simplicity, only two homologous DNA molecules are represented, one red and one blue, unless necessary to represent template switching/multiple strand invasions. Note that nicks and multiple strand invasions could happen in combination with other pathways to produce more complex patterns. The notation 5:3_5:3a stands for two consecutive hDNA tracts producing the same overall segregation pattern but affecting different strands. This is called 'trans hDNA' if the affected strands are on the same chromatid, but the hDNA tracts can also be produced on two non-sister chromatids by dHJ resolution. **A)** D-loop migration (Martini et al., 2011): Concurrent with DNA synthesis at the invading end, D-loop migration (horizontal green arrows) occurs in the same direction. Migration of the D-loop can potentially completely erase the first hDNA formed after strand invasion, leaving hDNA on only 1 side of the event. **B)** dHJ migration (Martini et al., 2011): As above, but with dHJ migration away from the invasion point after dHJ formation forming an additional restoration tract. The two-step resolution process shown is speculative and as equally probable as a one-step resolution process for two close HJs. **C)** dHJ migration and multiple strand invasion (Martini et al., 2011): The invading end undergoes template switching between non-sister and sister chromatids, generating an alternating strand transfer pattern on a single chromatid. **D)** Canonical dHJ resolution (Paques and Haber, 1999): After 3' end invasion, a stable SEI intermediate is formed and is processed into a dHJ. dHJ resolution can lead to a CO if the four nicks (arrowheads) cleave four different DNA strands. The darker and lighter coloured arrowhead pairs illustrate two possible resolutions. Of the final CO patterns, the top corresponds to resolution by the darker arrowheads, and the bottom CO pattern corresponds to resolution by the lighter arrowheads. Both contain two hDNA tracts distributed on the two non-sister chromatids involved in the repair reaction. **E)** dHJ with nick: An unrepaired nick is formed before or during the topological processing of a dHJ. Nick translation generates a conversion tract. **F)** dHJ-independent (Pagues and Haber, 1999): After 3' end invasion, an unstable intermediate is formed. A structure-specific endonuclease such as Mus81 can process this intermediate into a CO with two hDNA tracts distributed between the non-sister chromatids. **G)** D-loop migration coupled with endonuclease processing by e.g. Mus81 (Martini et al., 2011): First end invasion produces a HJ. Close by, DNA is cut by a nuclease such as the structure-specific endonuclease Mus81. DNA synthesis is initiated at the nick, using the invading strand as a template due to HJ branch migration. Under this scenario, a 5:3 segregation tract is partially inverted to become a 3:5 tract. **H)** Double DSB. Two close DSBs occur on the same chromatid, and the DNA in between is lost. Resection and strand invasion happen normally and the break is repaired by any method, with additional gap repair producing a conversion tract. The example shows repair by the canonical DSB resolution (as in D). **I)** Effect of MMR: Each image is a possible outcome of the repair pathway shown directly above it, after mismatch repair has converted or restored hDNA tracts. Only one example outcome is shown, not all possible combinations. Note that the invading 3' end may be converted or restored during strand invasion instead of post-repair. CO events are almost always detectable due to reciprocal exchange, but a bias towards conversion tracts means that more information about events can be detected.

NCO Events:

For NCOs, hDNA patterns can give an idea of the pathway in which they were formed. Technically, NCOs can be formed by SDSA, dHJ dissolution or by dHJ resolution; however, the number of meiotic NCOs produced by dHJ resolution is seemingly negligible because removal of MutLγ complex components does not affect NCO numbers (Zakharyevich *et al.*, 2012). NCOs likely to have been formed by SDSA usually have a simple signature of a 5:3 or 3:5 tract (e.g. Figure 4.12A, Figure 4.9A). Using hDNA patterns, it is also possible to identify NCOs that could have been formed by dHJ dissolution. NCO Group 2 classes all contain trans hDNA on a single chromatid (e.g. Figure 4.12B). Trans hDNA is when the same overall segregation pattern is repeated, e.g. 5:3 5:3, but the actual altered chromatids or strands are different. When this occurs on a single chromatid, this means that the two DNA strands must have each been broken separately, potentially by dissolution of a dHJ (Figure 4.9, E). However, these patterns could also be produced by the occurrence of double SDSA, i.e. both resected ends have undergone strand invasion into a homologous chromosome and copied the sequence (Figure 4.9B). A preliminary finding from the Llorente lab is that a DSB hotspot site is usually found in the middle of the two trans hDNA segments, which points towards the majority of these events being produced by double SDSA rather than dHJ dissolution (Bertrand Llorente & Marie-Claude Marsolier, personal communication).

Within Group 0, there are more specific classes which are strongly suggestive of a loss of DSB or CO interference. For example, 4:0 or 8:0 segregation of markers strongly indicates the occurrence of multiple events in proximity to other events, which should normally be prevented by DSB interference (e.g. Figure 4.13). Another example is the double crossovers (dCOs), which are defined here as COs occurring on different chromosomes within 1.5kb of each other (Figure 4.14A). Double COs could also occur between the same two chromatids or sharing one chromatid, but they cannot be distinguished from a combination of a CO and an NCO or two NCOs. In these ambiguous cases, the scenario with fewer COs is favoured. So, if a double reciprocal exchange occurs with less than 1.5kb between the exchanges, it is classified as 1 CO & 1 NCO if occurring on three chromatids with one overall reciprocal exchange, and as 2 NCOs if on 2 chromatids (Figure 4.14B). The number of four-chromatid dCOs can be used to estimate how many three- and two-chromatid dCOs there should be, assuming that double DSBs are equally likely to be resolved as COs regardless of which chromosomes they occur on. For example, a meiosis with 5 four-chromatid dCOs would be predicted to have 10 three-chromatid dCOs and five 2-chromatid dCOs.

The existence of the double NCO group means that there is a class of complex NCOs occurring on two non-sister chromatids, in this special case of both non-sisters having a conversion tract in

the same place indicating that both have been broken. Usually, NCOs that affect two non-sister chromatids are not considered to be produced by more than one Spo11-DSB, but the signature of an apparent 4:4 double reciprocal exchange within 1.5kb is incompatible with a 1-DSB scenario and not explainable by either double SDSA or by dHJ resolution/dissolution.

Initially, events are automatically categorized by the script 'Event_Sorter' (Methods section 2.14, script available in appendix). Events are also manually inspected in order to check their classification, because it is not always possible to correctly categorize them automatically. In particular, events with signatures indicating complexity or clustering may require manual annotation, based on the presence of segregation patterns that are very unlikely to have been produced by the repair of one DSB. These multiple-DSB signatures include NCOs with changes on two sister chromatids, which indicates two separate NCOs because another chromatid must have been involved for the repair; COs involving 3 chromatids, which can be produced by 1 CO and 1 NCO; COs involving 4 chromatids, which can also be 1 CO and 1 NCO but also possibly double COs; and events with heteroduplex tracts that are incompatible with a 1-DSB scenario, i.e. events containing segments with both 5:3 or 6:2 *and* 3:5 or 2:6 segregation patterns. These incompatible heteroduplex tracts indicate that the identities of the donor and recipient chromatids are not consistent within the event region. If events are likely to be formed from more than one DSB, they are split into the component events (rules are detailed in Methods section 2.14).

To determine whether the manual annotation process significantly affects event numbers, the average number of COs and NCOs classified for each genotype before and after annotation are compared in Figure 4.15. This analysis shows that CO numbers generally do not change, but NCOs show a small increase in some backgrounds (these increases were not found to be significant according to a T-test [Methods section 2.21]).
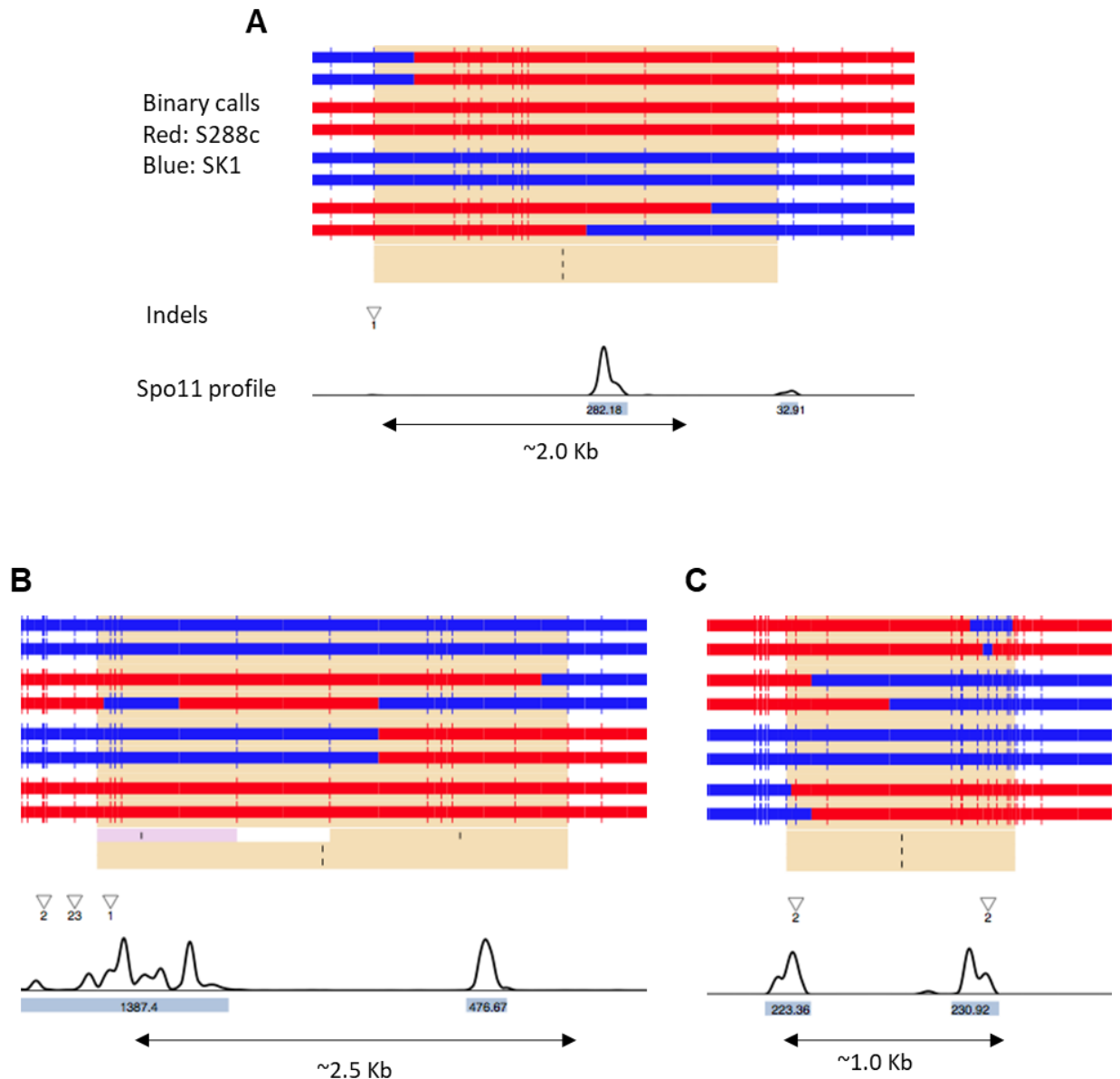
Figure 4.11. A selection of example CO events from *msh2Δ* octads.
Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan *et al.*, 2011). **A)** CO Group 1 class 8: A CO showing a pattern of hDNA, conversion tract, reciprocal exchange. **B)** CO Group 3 class 20: A CO associated with hDNA incompatible with a single DSB occurring on the same chromatid. **C)** CO Group 0 Class 2: A CO associated with an NCO occurring on a different chromatid.
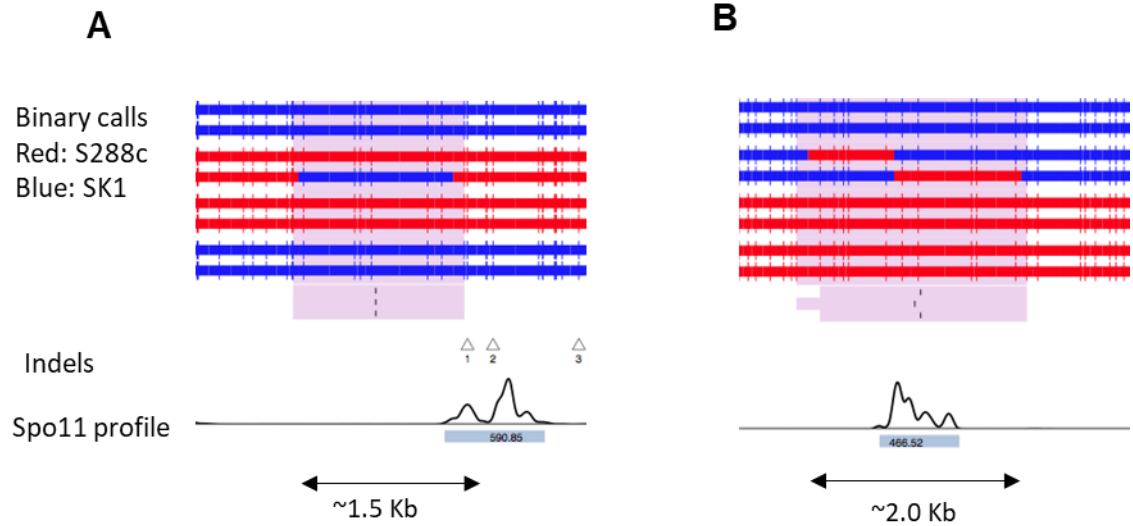
Figure 4.12. A selection of example NCO events from *msh2Δ* octads.
Recombination events were mapped in hybrid strains by detection of SK1 (blue) or
S288c (red) markers. The region of interest is plotted as eight horizontal lines
corresponding to the eight strands of DNA present in the original hybrid diploid, with
vertical tick marks indicating called variant positions. The event region is indicated by
the orange or purple box. Indel markers are indicated by triangles with the length of the
indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each
hotspot below (Pan *et al.*, 2011). **A)** NCO Group 1 class 2: A simple NCO formed by
SDSA. **B)** NCO Group 2 class 11: An NCO containing trans hDNA, formed by either
double SDSA or dHJ resolution.
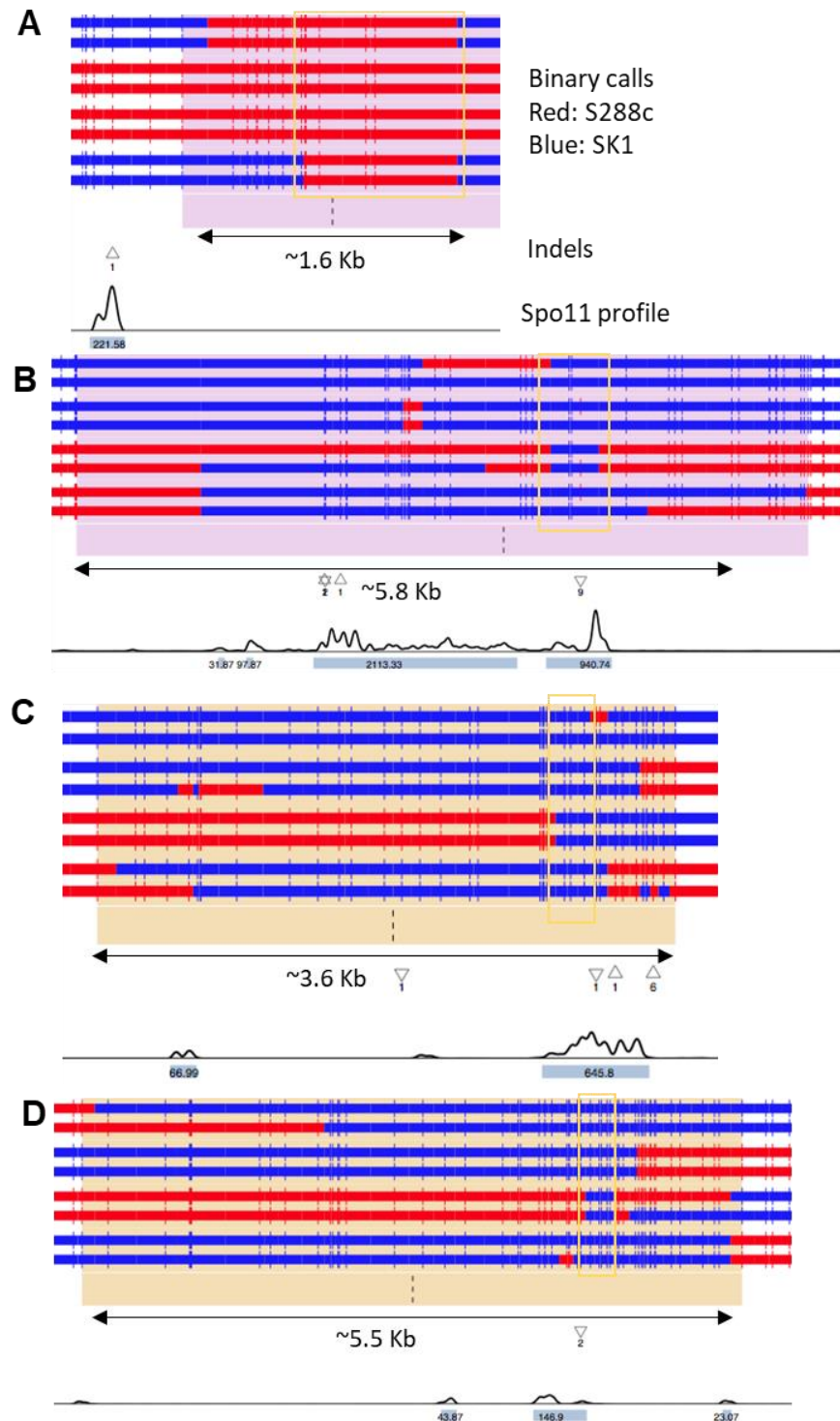
Figure 4.13. A selection of example events from *msh2Δ* octads containing 8:0 or 0:8 segments. Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan *et al.*, 2011). The segments of interest are highlighted in yellow. **A)** Affects two sister chromatids, likely caused by two NCOs. **B)** Affects all four chromatids, but no reciprocal exchange. Could be 2-4 NCOs. **C)** Affects all four chromatids and has one reciprocal exchange. Likely 1 CO, 1NCO. **D)** Affects all four chromatids and has a double reciprocal exchange. Double CO.

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A

Binary calls
Red: S288c
Blue: SK1

Spo11 profile

1489.9   170.57

~2.5 Kb

B

128.86   480.8   278.89   89.51

~3.0 Kb
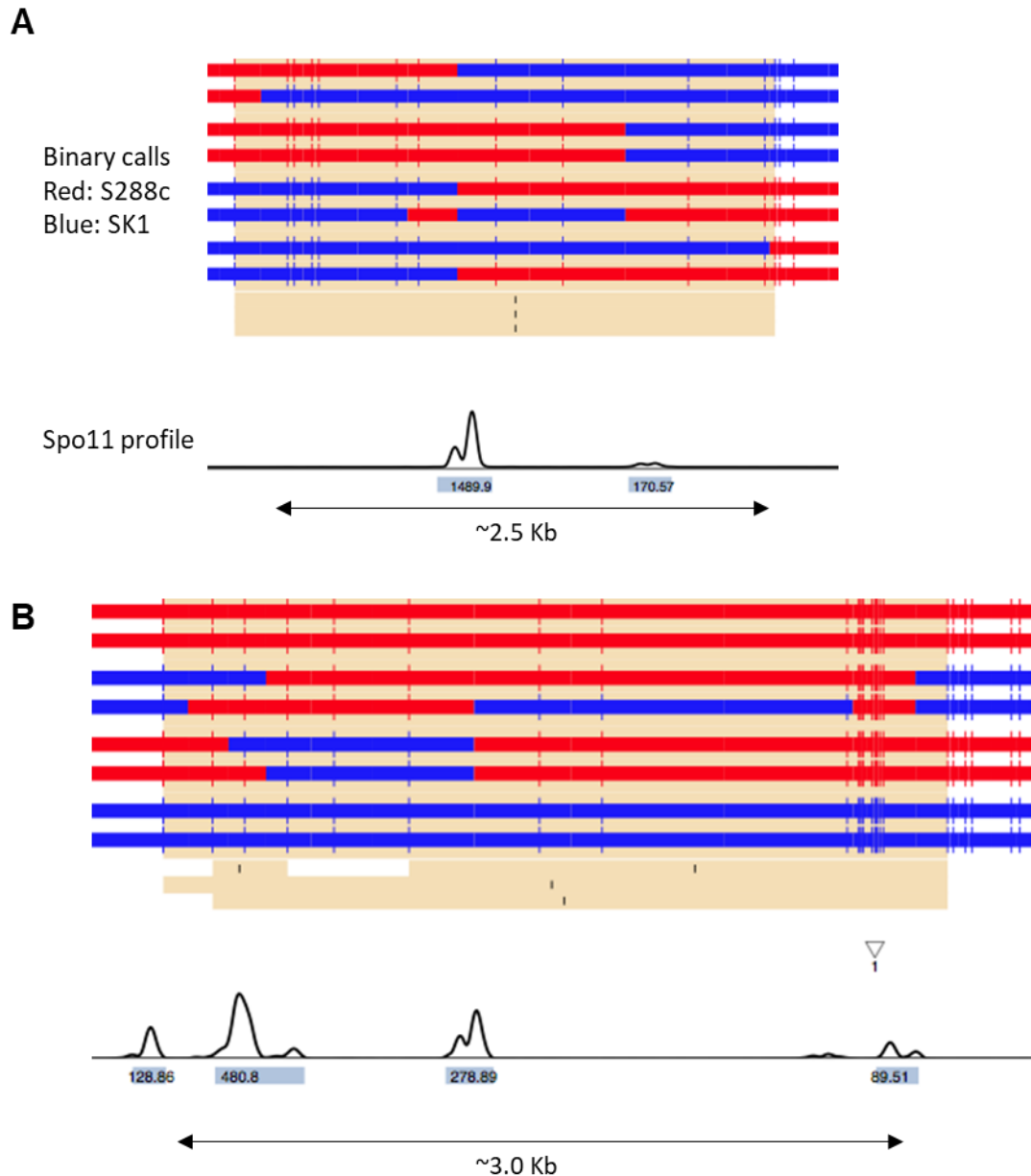
Figure 4.14. A selection of example dCO events from *msh2Δ* octads.
Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan *et al.*, 2011). **A)** CO Group 0 class 2: A dCO involving all four chromatids in a double reciprocal exchange. **B)** Group 0 Class 3: Has a 4:4 pattern suggestive of a double CO, but occurring on the same two chromatids within 1.5kb, so considered to be two NCOs.
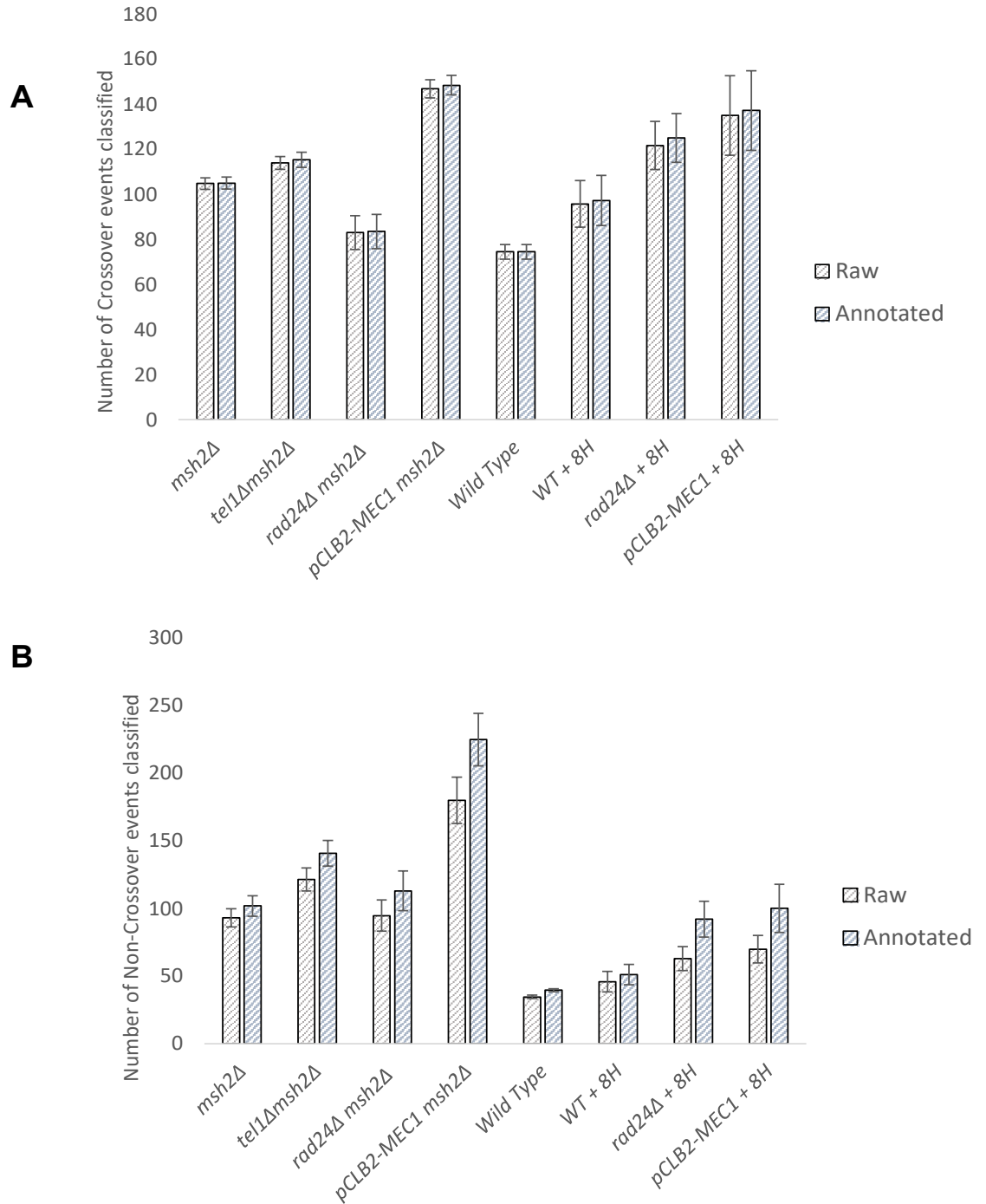
Figure 4.15. Comparison of the average number of recombination events classified for each genotype before and after manual annotation. Error bars are 95% confidence limits. Comparison of average **A**) CO and **B**) NCO numbers.

4.2.12. Quality control of detected recombination events

To help inform on whether the detected events are real, and whether they might be made up of separate events, Spo11-DSB hotspot data from Pan *et al.* (2011) can be used. If an event is detected in a DSB-cold region, there is less confidence in its legitimacy, though it is certainly possible for real events to occur in such locations; 11% of uniquely mapped Spo11-oligos occur away from hotspots (Pan *et al.*, 2011). If multiple DSB hotspots occur within an event boundary, it may suggest that there are two separate DSBs occurring within the event.

The number of variants that are called within an event is also helpful to determine the accuracy of event calling. Originally, Martini *et al.* discounted 1-SNP events as they may not be real, and instead caused by sequencing or alignment errors. The authors no longer recommend this, but there is still a reduced confidence in the validity of events composed of only one variant (Bertrand Llorente, personal communication). However, events that cover only a few variants may simply be occurring in areas of relatively low variant density, as opposed to events that occur in regions of high SNP variant density but are still only composed of one variant change, so it is important to take the SNP density of the event region into account.

Overall, events with few variant changes that occur in areas of high variant density, and low Spo11-DSB signal are less likely to be real. Still, these events are not currently removed from event tables in this analysis. Events are only discarded if they occur with the same characteristics and in the same place across multiple samples, as this suggests an error in the variant table. The offending variants are removed from the table.

Events are also removed if they are suspected of being caused by mitotic, rather than meiotic, recombination. This is done for events composed solely of a 4:0 segregation pattern. Those containing a 4:0 segment, but also other segments or a CO, are retained. It is possible for 4:0 patterns to be produced by meiotic recombination, caused by complex event repair or the presence of multiple DSBs. These are expected to be rare in WT, but could be increased in mutants that have lost meiotic recombination control. Others (Martini *et al.*, 2011; Anderson *et al.*, 2011) routinely remove all variant positions with 4:0 segregation patterns, discarding information about event complexity.

To ascertain whether reproducible results can be obtained from analysis of sequencing data obtained from different experiments, use of sequencing data from four SK1xS288c *msh2Δ* octads from the Llorente lab (distinct from the four *msh2Δ* octads analyzed by microarray in Martini *et al.*, 2011) was kindly provided to allow comparison with data from the nine *msh2Δ* octads sequenced in this project. This revealed that when using the pipeline described in this chapter,

both sets of *msh2Δ* octads have similar overall event numbers (Figure 4.16A), and proportions of event in each subgroup (Figure 4.16B,C). In addition, both sets of *msh2Δ* octads have an overall similar proportion of events suspected to be formed by DSB clusters (overall number of events in Group 0, Figure 4.16D). In terms of event lengths, the mid length of COs was very similar for both sets of *msh2Δ* octads (Figure 4.16E), although there were more short NCOs in the Llorente data (Figure 4.16F).

The similarity of results from the two sets of *msh2Δ* octads suggests that firstly, the higher read depth of the Llorente samples does not make a significant difference to the number of events called, and secondly, that for this experiment, results are generally consistent between samples produced by different laboratories. This suggests that the pipeline is valid and strengthens confidence in the results.
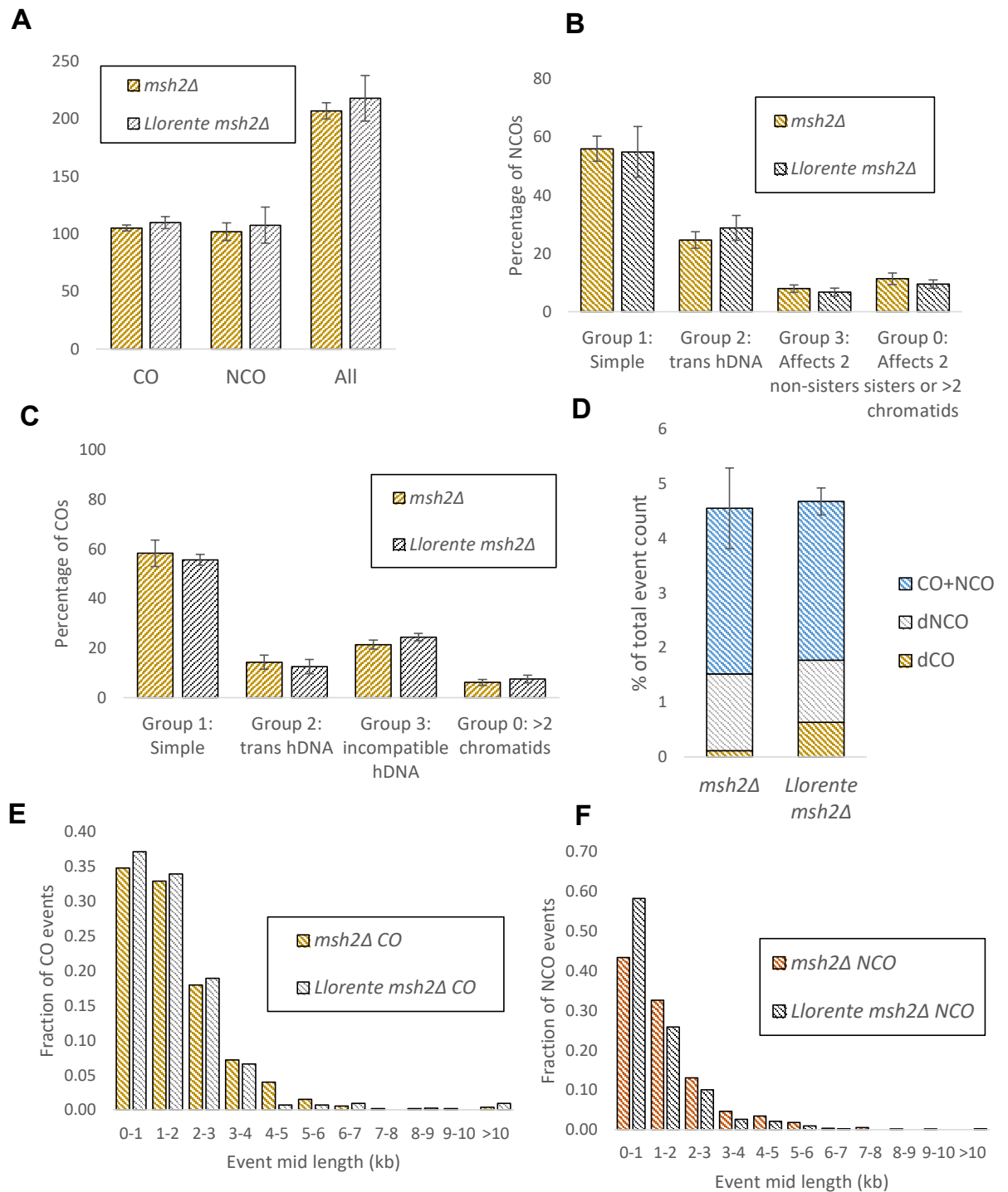
Figure 4.16. Comparison of the data output observed from the nine *msh2Δ* octads produced in this study and four from the Llorente lab. Error bars are 95% confidence limits. **A)** Comparison of average CO and NCO numbers per octad. **B)** Average percentage of NCOs in each group. **C)** Average percentage of COs in each group. **D)** Comparison of the average percentage of events thought to be DSB clusters (overall Group 0), with sublevels indicating whether the clusters were thought to be a double CO, double NCO or CO and NCO. **E)** Comparison of the average fraction of CO events occurring within each length category. **F)** Comparison of the average fraction of NCO events occurring within each length category.

4.3. Discussion

In order to determine the roles of various factors in the regulation of meiotic recombination, it is necessary to view characteristics of meiotic recombination genome-wide in a single meiosis. While there are many established methods for characterizing recombination events genome wide, there is scope to improve upon these methods and tailor them for a specific dataset.

4.3.1. Advantages of sequencing over microarray for marker detection

Genome-wide recombination assays have been used previously to examine recombination in *msh2Δ* octads (Martini *et al.*, 2011). Martini *et al.* used microarray hybridisation for genotyping. Deep sequencing provides a higher resolution of polymorphisms than microarray hybridisation, because sequencing is capable of interrogating the entire genome, without depending on pre-selected targets. This means that the SNPs of interest must be decided in advance and cannot be determined from the data itself, unlike with deep sequencing (Section 4.2.3). In addition, with sequenced samples it is simple to repeatedly align the same sample with different settings in order to optimise quality and quantity of reads, which is helpful when aligning against a sequence expected to contain mismatches. DNA fragments containing polymorphisms from both parents are particularly of interest as they cover the junction of recombining strands. To obtain a similar effect in microarray analysis, the entire hybridization would have to be repeated with different conditions, and it would still be difficult to detect fragments containing polymorphisms from both parents. Additionally, more recombination events may be detected via sequencing compared to microarray analysis. The authors of Martini *et al.* (2011) used sequencing to analyse recombination in a further four *msh2Δ* octads, finding an average of 107 NCOs and 109 COs per meiosis (Section 4.2.12) compared to an average of only 84.5 NCOs and 92 COs in the microarray analysis. While the *msh2Δ* octads were different in each analysis, the samples were obtained, prepared and analysed in the same way except for the method of detecting markers, so the results should be similar.

Finally, hDNA can be detected in *msh2Δ* tetrads via sequencing, but not via microarray (discussed in Section 4.2.5). The ability to use *msh2Δ* tetrads rather than octads is thus advantageous for strains with very low spore viability.

4.3.2. Adjustments to marker numbers, event resolution and event classification

Previous analysis of *msh2Δ* octads has only used SNP markers, disregarding indels (Martini *et al.*, 2011). The use of indels improves the resolution of genotyping, decreasing the median distance between markers to 81bp from 87bp if SNPs alone are used (Figure 4.5). In addition,

during classification of recombination products, pattern changes within 5kb of each other were considered to be part of the same event (Martini et al., 2011). However, the authors subsequently found that many events incompatible with a 1-DSB scenario occur closer than 5kb by careful examination of hDNA tracts associated with recombination in MMR-deficient backgrounds, and thus recommend a 1.5kb merging limit (Bertrand Llorente & Marie-Claude Marsolier, personal communication). Thus, the 1.5 kb merging limit used in the data presented here is advantageous for detailed examination of the distance between recombination events.

Finally, previous studies (e.g. Martini *et al.*, 2011; Anderson *et al.*, 2011) also discount events containing 4:0 tracts as being caused by pre-meiotic recombination, even though they could potentially be caused by two overlapping DSBs, suggesting a loss of trans DSB interference. In an MMR-deficient background, the ability to see a greater variety of pattern changes via hDNA analysis means that 4:0 events can be categorized as meiotic or mitotic with more certainty, depending on whether they are associated with other pattern changes.

4.3.3 Closing statement

This chapter describes how a new bioinformatics pipeline was designed, differing from previously published methods in several ways, including that it is optimized for long reads and lower read depths; uses a dedicated list of both SNPs and indels produced for the specific SK1 and S288c strains used in this investigation; is capable of analyzing heteroduplex DNA found in *msh2Δ* tetrads, as well as *msh2Δ* octads and *MSH2* tetrads. Overall, though recombination has been previously assayed genome-wide in *msh2Δ* octads, this study offers distinct advantages over preceding ones in terms of marker and event resolution and detection. Taken together, the results shown in the chapter indicate that this optimized analysis method can be used with confidence to examine recombination in genotypes of interest.

Chapter 5.

Effect of MMR deficiency and prolonged prophase on meiotic recombination in WT hybrid crosses

Chapter 5. Effect of MMR deficiency and prolonged prophase on meiotic recombination in WT hybrid crosses

5.1. Introduction

5.1.1. General introduction

Meiotic recombination is important for correct disjunction of chromosomes, fertility and genetic diversity. To understand the process of meiotic recombination, it is desirable to catalogue the types and distribution of recombination events in a wild type meiosis. However, it is not possible to detect recombination events with high resolution in a 'true WT' because it is necessary to use hybrids with many polymorphisms in order to visualize the events.

A high sequence divergence between homologous chromosomes reduces spore viability, due to the action of MMR proteins preventing recombination between divergent sequences (Liti *et al.*, 2006). This is a protective activity that reduces chromosomal rearrangements (Myung *et al.*, 2001), but also enforces reproductive barriers between species (Hunter *et al.*, 1996). Increasing sequence divergence is also associated with decreasing efficiency of hDNA formation in mitotic and meiotic cells (Datta *et al.*, 1997; Chen & Jinks-Robertson, 1999), thought to be because MMR proteins detect and reject hDNA intermediates that contain mismatches.

MMR can be disrupted by the deletion of proteins such as Msh2 and Mlh1, homologues of MutS and MutL respectively (Reenan and Kolodner, 1992; Hunter & Borts, 1997). Both cover a wide scope of mismatch recognition, but since Mlh1 can promote meiotic CO formation (Hunter & Borts, 1997), and Msh2 does not affect meiotic recombination in the absence of polymorphisms (Hunter *et al.*, 1996), a hybrid *msh2Δ* strain can be used to compare to a WT hybrid in order to determine the effect of MMR deficiency on recombination in a hybrid.

Due to the potential bias against recombination occurring in regions containing polymorphisms in a WT hybrid, meiotic recombination in a MMR-deficient hybrid may be considered to be more similar to a non-hybrid WT. However, the loss of Msh2 activity also leads to an increase in unrepaired mutations, strand invasion into ectopic regions of the genome, and a decrease in spore viability in most backgrounds (Chapter 3, Figure 3.8 B and C).

Spo11 DSBs are formed during meiotic prophase, so the length of the prophase may affect the types, frequency and distribution of recombination events. Using the *NDT80* arrest and release system (Chapter 1, Figure 1.9) in a WT hybrid can allow examination of events in a WT strain with an elongated prophase. An extended prophase is known to increase the viability of hybrid

checkpoint mutants (Chapter 3, Figure 3.10A), so sequencing strains of this background may help to understand how the arrest is rescuing spore viability.

5.1.2. Aims of this section

1. To establish a baseline for 'wild-type' recombination that can be used for comparisons, by using high-resolution sequencing data to examine features of meiotic recombination in wild type, MMR deficient and prophase arrested hybrid strains.

2. To determine whether these 'wild type' backgrounds have differences in recombination to each other, and if so, to understand why.

5.2. Results

5.2.1. The number of detected recombination events in hybrids is altered by prophase arrest and MMR deficiency

To acquire information on the quality and quantity of meiotic recombination in a 'wild-type' background, hybrid SK1xS288c tetrads or octads were produced in WT, WT + 8 h of prophase arrest, or *msh2Δ* backgrounds. The normal activation of *NDT80* likely takes place somewhere between 4-5 hours into meiosis (Xu *et al.*, 1995), so the WT + 8 h strain could be considered to have 3-4 extra hours in prophase. The individual spores were sequenced and the data analyzed as detailed in Chapter 4. Raw data is available in the appendix (Table S2).

To see if prophase extension and MMR deficiency have an effect on the number of recombination events detected, CO and NCO numbers were compared across backgrounds (Table 5.1, Figure 5.1A).

The WT hybrid strain has an average of ~74 COs detected per meiosis, which is very close to the average of ~73 COs reported previously (Martini *et al.*, 2011). In contrast, an average of ~40 NCOs per meiosis were detected in the WT hybrid strain vs ~27 reported by Martini *et al.*, 2011. This disparity in NCO numbers could be related to the use of microarrays to view marker changes, which may give a lower NCO estimate than that obtained by sequencing due to the lower resolution of the method.

It is not possible to measure recombination in a homozygous background by marker analysis, since no markers will be different; however, ~86 COs have been detected genetically in a S96xYJM789 hybrid WT background, with a sequence difference of 0.6% (Chen *et al.*, 2008). This is higher than the number of COs detected in an SK1xS288c hybrid background, which has ~0.7% sequence divergence, suggesting that the presence of polymorphisms may be inhibitory to recombination.

Table 5.1. Data summary for recombination events detected in WT, *msh2Δ* and prophase arrested backgrounds.

Separate samples for each genotype are shown. TW: Wild type tetrad, TN: NDT80 arrest tetrad, OM: *msh2Δ* octad. Columns contain the number of COs, NCOs and Undetermined (U) events detected, the overall number of events, the number of chromosomes without COs (CWCs), the identity of the CWCs, the number of double COs closer than 1.5kb (dCOs), the number of events containing an 8:0/0:8 or 7:1/1:7 segment, the number of COs without a detectable conversion tract, and the number of NCOs that were composed only of hDNA.

Meiosis	CO	NCO	U	Total	CO:NCO	CWCs Frequency	CWCs Identity	dCO number	8:0	7:1	COs without tracts	NCOs hDNA only
Wild Type												
Average	**74.5±3**	**39.5±1**	**0.3**	**114.3±4**	**1:0.53**			**0**	**0.8**		**12.8**	
TW1	68	39	1	108	1:0.57	2	Chr 1, 6	0	1	-	11	-
TW2	83	42	0	125	1:0.51	1	Chr 1	0	0	-	15	-
TW3	76	40	0	116	1:0.53	0	-	0	1	-	13	-
TW4	71	37	0	108	1:0.52	0	-	0	1	-	12	-
WT + 8 h												
Average	**97.3±11**	**51.0±8**	**0.5**	**148.8±19**	**1:0.52**			**1.5**	**2.5**		**20.5**	
TN1	70	34	0	104	1:0.49	0	-	0	1	-	11	-
TN2	90	43	0	133	1:0.48	0	-	1	1	-	23	-
TN3	121	61	1	183	1:0.50	0	-	4	5	-	29	-
TN4	108	66	1	175	1:0.61	0	-	1	3	-	19	-
msh2Δ												
Average	**105.0±3**	**101.8±8**	**0**	**206.8±7**	**1:0.98**			**0.2**	**0.1**	**0.4**	**14.9**	**64.1**
OM1	116	109	0	225	1:0.94	0	-	0	0	0	13	45
OM2	100	125	0	225	1:1.25	0	-	0	0	0	8	69
OM3	95	100	0	195	1:1.05	0	-	0	0	0	18	50
OM4	105	98	0	203	1:0.93	0	-	1	0	1	11	50
OM5	98	79	0	177	1:0.81	0	-	0	0	0	19	41
OM6	116	65	0	181	1:0.56	0	-	1	1	0	22	37
OM7	98	139	0	237	1:1.42	0	-	0	0	1	11	70
OM8	107	113	0	220	1:1.06	0	-	0	0	2	21	62
OM9	110	88	0	198	1:0.80	0	-	0	0	0	10	45

Figure 5.1. Quantity of recombination events detected in WT, MMR deficient and prophase extension strains. Strain details are given in Table 2.1, raw event data is available in Table S2. **A**) Average number of CO and NCO events. Error bars are 95% confidence limits. **B**) Density of COs and **C**) NCOs per Mbp. The average number of CO/NCO events per chromosome is divided by the average total CO/NCO count, then divided by the chromosome length in Mbp. Dotted lines are linear regressions. R^2: WT CO 0.16, NCO 0.01; WT + 8 h CO 0.36, NCO 0.40; *msh2Δ* CO 0.54, NCO 0.20.

When the WT strain has prophase extended to 8 hours, the number of detected events increases to ~97 COs and ~51 NCOs per meiosis. A possible explanation for this is that the longer prophase allows more DSBs to be formed and repaired, helping to overcome the less efficient strand invasion caused by the presence of polymorphisms in a *MSH2* background (Sugawara *et al.*, 1997; Evans *et al.*, 2000; Goldfarb & Lichten, 2010). The ratio of COs to NCOs is not altered by the prophase arrest, with 1.85 COs for every NCO in WT and 1.9 with prophase arrest.

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The number of observed NCOs is likely to be an underestimate of the real frequency, due to events occurring in regions without markers, short event lengths and, in MMR-proficient strains, restoration (Mancera *et al.*, 2008). The percentage of observed COs that occur between markers and thus have no detectable conversion tract can be used to estimate the number of NCOs that may be invisible due to falling between markers. In the WT hybrid, an average of 17% of COs had no associated conversion tract (Table 5.1), so the corrected estimate of the number of NCOs for the WT hybrid is 48. In the WT hybrid with extended prophase, 21.1% of COs had no associated conversion tract, so the corrected number of NCOs in this background is 64.6. However, these estimates assume that GC tracts are of a similar length in CO and NCO events, while in fact NCOs tend to be shorter (Figure 5.3), meaning that the true number of undetectable NCOs is likely higher.

In the MMR-deficient *msh2Δ* strain, an average of 105 COs are detected, which is considerably higher than WT but within error limits of the amount detected in WT+ 8 h, and an average of 101 NCOs which is substantially higher than both the other backgrounds. In addition, 32% of COs fell between markers, indicating that an additional average of 43 NCOs may have occurred in marker free regions and thus were undetectable.

Functional MMR can prevent recombination in variant rich regions from using a homologous chromatid, instead promoting repair using the sister chromatid and producing undetectable recombination events (Goldfarb & Lichten, 2010). Therefore, the increased event numbers observed in *msh2Δ* compared to WT may be at least partly because strand invasion into sequences containing polymorphisms is less likely to be rejected when MMR is not functioning.

MMR can also produce invisible NCOs by restoring parental information, meaning that NCOs are easier to detect in the *msh2Δ* strain because heteroduplex tracts are not repaired. An average of 52 NCOs per meiosis in the *msh2Δ* background were composed of only a single hDNA tract. If the strain was MMR-proficient with no bias towards conversion or restoration, it could be assumed that 50% of these events would have been repaired to give a conversion tract and 50% to a restoration tract, meaning that around 26 events would become invisible. If this logic is applied to the NCO count in the WT hybrid, the corrected total would be 66, which is still much lower than the number of NCOs detected in *msh2Δ*. This suggests that in the WT hybrid there may be a bias towards conversion, or that there may be a significant amount of repair with the sister chromatid, both of which would mask the total number of NCOs detected.

While almost twice as many CO events were detected than NCO events in MMR-proficient backgrounds, the CO to NCO ratio is almost 1:1 in *msh2Δ*. The larger disparity in NCO numbers

than in CO numbers between MMR-proficient and deficient strains (Table 5.1) suggests that the reason for lower event counts in MMR-proficient strains is primarily explained by a bias towards conversion, since this only masks NCO numbers, while repair with the sister chromatid can hide both potential COs and NCOs.

Conflictingly, an average of only 84.5 NCOs and 92 COs were detected in an SK1xS288c *msh2Δ* background using microarrays to detect markers (Martini *et al.*, 2011). However, when a further four *msh2*Δ octads produced by this lab were analyzed via sequencing for marker detection, an average of 107 NCOs and 109 COs were detected per meiosis (Chapter 4, Figure 4.16A), which is very similar to the frequency observed in the data presented here. This indicates that the lower event counts in the original *msh2*Δ octads compared to the sequenced *msh2*Δ octads from the Llorente group were caused by the lower resolution of the microarray method for event detection.

In total, an average of 114 recombination events are detected in a WT hybrid, 148 in a WT hybrid with extended prophase, and 206 in *msh2Δ*. Based on an estimate of ~160-200 Spo11-DSBs per cell (Pan *et al.*, 2011), the *msh2Δ* genotype may enable the observation of the event counts most comparable to those of a non-hybrid strain, suggesting that the low level of NCOs observed in WT hybrids mainly results from Msh2 activity. Based on this, Msh2 activity appears to reduce overall recombination by 1.8x when the sequence divergence is ~0.7% as in SK1xS288c.

The estimate of a 1.8x reduction in recombination with 0.7% sequence divergence is slightly lower than expected, given the reduction in recombination rate by 4.1x at 0.3% divergence reported by Datta *et al.*, 1999. However, that was measured at a single, artificially constructed locus by using an inverted repeat of the *HIS3* gene with different point mutations, inserted at the *URA3* locus and assayed via return to growth.

5.2.2. Relationship between chromosome length and recombination

In WT meiosis, there is a negative correlation between chromosome length and the density of DSB formation, dependent on Zip3 (Thacker *et al.*, 2014). To see if this is affected by prophase arrest or MMR deficiency, the relationship between chromosome length and fraction of all detected COs or NCOs that occurred on that chromosome was examined in WT, prophase arrested and *msh2Δ* strains (Figures 5.1B&C). All backgrounds tested displayed negative correlation between chromosome length and CO or NCO density, indicating that prophase arrest and MMR deficiency do not affect CO event distribution among chromosomes.

The skew in CO numbers towards short chromosomes is due to crossover assurance, a phenomenon in which meiotic COs are distributed so that each chromosome has at least one CO, which is believed to help prevent nondisjunction of chromosomes (Shinohara *et al.*, 2008; reviewed in Egel, 1995). However, in the WT background, three chromosomes without a CO were observed among the four assayed tetrads (Table 5.1). The chromosomes were Chr VI and Chr I twice, the two shortest chromosomes. In contrast, all chromosomes had at least one crossover in the prophase arrested and *msh2Δ* strains. This suggests that the low number of COs in the WT hybrid affects crossover assurance. Alternatively, the length of prophase or MMR proficiency may be important factors in crossover assurance.

5.2.3. The complexity of detected recombination events in WT, prophase arrest and MMR deficient backgrounds

Recombination events in each strain were categorized further as described in Section 4.2.10 (Table 5.2 and Figure 5.2A, B). The event categories are based on those described by Martini *et al.*, 2011. As such, many categories depend upon the presence of hDNA, which does not apply to the MMR-proficient strains. Thus, WT and *msh2Δ* strains cannot be directly compared because fewer categories are available in WT; however, the WT and prophase arrested strains generally have similar proportions of event types to each other. This indicates that prophase arrest does not strongly affect the complexity of DSB repair. The only notable difference between WT, prophase arrest and MMR deficient strains is in the proportion of CO and NCO events occurring in Group 0, which contains 'complex events'. These events, including NCOs on 2 sister chromatids or 2 non-sister chromatids with a 4:4 segment, and COs or NCOs affecting 3 or 4 chromatids, are considered to be complex because they are likely to have been caused by two close DSBs.

It should be noted that these two close DSBs are not necessarily both Spo11-DSBs, because during the repair of a Spo11-DSB, a second DSB could be caused by enzymatic nicking. Complex conversion tracts have also been proposed to be caused by multiple rounds of strand invasion into different chromatids and extension from different templates (Oke *et al.*, 2014).

The proportions of all detected COs and NCOs that were classified into Group 0 can be compared (Table 5.2; Figure 5.2A, B). The proportion of all COs sorted into Group 0 is similar in all backgrounds, but there is slightly higher proportion of Group 0 NCOs in WT and prophase arrest compared to *msh2Δ*. However, the reason why *msh2Δ* appears to have a somewhat low proportion of complex NCOs is likely to be because it is easier to detect simple NCOs in an MMR-deficient background than in an MMR-proficient background. Thus, the WT and WT+ 8 h strains appear to have a higher proportion of complex NCOs only because simple NCOs are harder to detect in

these backgrounds. This would not apply to COs, because their detected is facilitated by the presence of a reciprocal exchange of chromosome arms.

In addition, the proportion of all recombination events classified into Group 0 was compared, equivalent to the number of suspected DSB clusters (Figure 5.2C). This differs from looking at the proportion of COs or NCOs in Group 0 as in Figure 5.2A&B, in that each cluster contains two events which are not counted separately in Figure 5.2C. Overall, all strains had a similar percentage of events occurring in Group 0, i.e. in each strain, approximately 5% of all recombination events are thought to be produced by DSB clusters. Within those clusters, the proportion of different cluster types were roughly equal across strains, with the majority of clusters being composed of a CO and a NCO for all strains (Figure 5.2C).

Previously, 2.6% of COs were reported to have a non-overlapping NCO partner on a third spore, and 0.6% had an additional CO partner involving the other two spores (Mancera et al., 2008). Here, 4.36% of COs had a non-overlapping NCO partner on a third spore, but none had an additional CO partner involving the other two spores. The increase in CO+NCO clusters detected here may be due to the improved ability to detect NCO events by sequencing compared to microarray marker analysis.

Within the Group 0 (complex events) category, one specific category of events is those containing a 4:0 or 8:0 segregation of markers, which is a strong indication of multiple events. The occurrence is generally low in wild type strains, with ~0.7% and ~0.17% of events occurring with 4:0 segments per meiosis in WT and prophase arrest, respectively, and ~0.3% of events occurring with 8:0 or 7:1 segments in *msh2Δ* (Table 5.1).

Another specific subcategory is double COs, defined as a double reciprocal exchange involving all four chromatids within 1.5kb. No double COs were detected in WT, 2 dCOs in nine *msh2Δ* octads, and 6 dCOs in four prophase arrest tetrads (Table 5.1). As described in Section 4.2.11, the composition of an event cluster can be ambiguous. In such cases, the outcome with fewer COs is favoured; e.g. an event that could conceivably be a double CO or a CO + NCO, will be categorized as the latter. However, it is possible that some CO + NCO and double NCO clusters could be double CO events. The number of definite, four-chromatid dCOs is an indicator of how many three- and two-chromatid dCOs there may be. The true number of dCOs should be four times as high, if it is assumed that double DSBs are equally likely to be resolved as COs regardless of which chromosomes they occur on and that COs are equally distributed among the four chromatids (in terms of both initiating DSB and repair donor). Under these circumstances, ¼ of double COs would involve all four chromatids, ½ would involve 3 chromatids (indistinguishable

from 1 CO + 1 NCO) and ¼ would involve two chromatids (indistinguishable from double NCO). This means that the number of dCOs reported here is likely an underestimate, and some CO+NCO or NCO+NCO clusters may actually be dCOs, giving revised estimates of 24 dCOs in four WT + 8 h tetrads, and eight in nine *msh2Δ* octads. (Original, not corrected, values are shown in Figure 5.2C).

Table 5.2. Data summary of the percentage of CO and NCO events in each group and class, detected in WT, *msh2Δ* and prophase arrested backgrounds. A short description of the characteristics of each group and class is given.

Crossover Groups		*msh2Δ*	*Llorente msh2Δ*	*WT*	*WT +8H*
		%	%	%	%
Group 1: Simple - no trans hDNA or incompatible hDNA					
Total		58.21	55.59	92.95	89.97
Class 1	(5:3)_(4:4aCO) - CO with hDNA tract	4.76	6.15		
Class 2	(3:5)_(4:4aCO) - CO with hDNA tract	4.76	4.78		
Class 3	(5:3)_(4:4)_(4:4aCO) - hDNA, restoration tract, CO pattern	0.85	1.37		
Class 4	(4:4aCO)_(5:3)_(4:4a) - Same as above but in opposite direction.	0.63	0.46		
Class 5	(3:5)_(4:4)_(4:4aCO) - hDNA, restoration tract, CO pattern	0.21	0.91		
Class 6	(4:4aCO)_(3:5)_(4:4a) - Same as above but in opposite direction.	0.85	1.14		
Class 7	(5:3)_(6:2)_(4:4aCO) - hDNA, conversion tract, CO pattern	1.59	0.91		
Class 8	(6:2)_(5:3)_(4:4aCO) - Same as above but in opposite direction.	1.80	0.23		
Class 9	(3:5)_(2:6)_(4:4aCO) - hDNA, conversion tract, CO pattern	1.80	3.19		
Class 10	(2:6)_(3:5)_(4:4aCO) - Same as above but in opposite direction.	2.12	2.05		
Class 11	Contains 4:4i (symmetrical hDNA)	1.59	2.05		
Class 12	Anything else	10.90	11.16	5.37	9.51
Class 15	(6:2)_(4:4aCO) - CO with conversion tract	5.93	3.87	33.22	26.48
Class 16	(2:6)_(4:4aCO) - CO with conversion tract	6.35	3.42	37.25	32.90
Class 100	4:4aCO: CO in marker-sparse region	14.07	13.90	17.11	21.08
Group 2: Presence of trans hDNA, but not incompatible hDNA					
Total		14.29	12.53	0	0
Class 30	adjacent 5:3 5:3a, plus any other segments	2.86	3.19		
Class 31	adjacent 3:5 3:5a, plus any other segments	3.60	1.37		
Class 32	non-adjacent trans hDNA i.e. have conversion or restoration tract in between	7.83	7.97		
Group 3: Presence of incompatible hDNA					
Total		21.37	24.37	2.68	1.8
Class 20	Contains 4:4i (symmetrical hDNA)	19.15	22.32	2.68	1.8
Class 21	Anything else	2.22	2.05		
Group 0: Multiple Spo11-DSBs: Affects 3 or 4 chromatids					
Total		6.14	7.52	4.37	8.22
Class 2	CO ± NCO involving 3 or 4 chromatids	5.4	6.61	4.03	4.88
Class 3	CO ± NCO involving 3 or 4 chromatids, contains different 4:4 patterns	0.74	0.91	0.34	3.34

Noncrossover Groups		*msh2Δ*	*Llorente msh2Δ*	*WT*	*WT +8H*
		%	%	%	%
Group 1: SDSA-like: Affects one chromatid, no trans hDNA					
Total		55.99	54.9	80.38	85.78
Class 1	5:3 - composed of hDNA only	19.10	22.56		
Class 2	3:5 - composed of hDNA only	21.29	20.23		
Class 3	5:3_6:2_5:3 or 5:3_4:4_5:3 - Conversion/restoration tract between hDNA	2.40	2.33		
Class 4	3:5_6:2_3:5 or 3:5_4:4_3:5 - Conversion/restoration tract between hDNA	2.07	1.16		
Class 7	6:2 plus any other segments	2.73	3.26	0.63	1.96
Class 8	2:6 plus any other segments	3.38	2.56	1.27	0.98
Class 10	6:2 - composed of conversion tract only	2.73	0.47	36.71	47.06
Class 10.1	2:6 - composed of conversion tract only	2.29	2.33	41.77	35.78
Group 2: dHJ-dissolution-like: Affects one chromatid, has trans hDNA					
Total		24.67	28.84	0	0
Class 11	5:3_5:3a - two 5:3 patterns on different strands	4.91	5.12		
Class 12	3:5_3:5a - two 3:5 patterns on different strands	3.82	6.28		
Class 13	5:3_5:3a plus other segments NOT in the middle of the trans hDNA	1.31	1.86		
Class 14	3:5_3:5a plus other segments NOT in the middle of the trans hDNA	1.86	1.86		
Class 15	5:3_4:4_5:3a - restoration tract in the middle of trans hDNA	3.49	4.42		
Class 16	3:5_4:4_3:5a - restoration tract in the middle of trans hDNA	3.93	3.95		
Class 17	5:3_4:4_5:3a plus other segments NOT in the middle of the trans hDNA	1.53	1.16		
Class 18	3:5_4:4_3:5a plus other segments NOT in the middle of the trans hDNA	0.98	0.70		
Class 19	5:3_6:2_5:3a - conversion tract in the middle of trans hDNA	0.87	1.40		
Class 20	3:5_2:6_3:5a - conversion tract in the middle of trans hDNA	0.87	0.23		
Class 21	5:3_6:2_5:3a plus other segments NOT in the middle of the trans hDNA	0.44	0		
Class 22	3:5_2:6_3:5a plus other segments NOT in the middle of the trans hDNA	0.22	0		
Class 23	Anything else	0.44	1.86		
Group 3: Affects two non-sister chromatids					
Total		7.97	6.74	2.53	1.96
Class 30	Contains 4:4i (symmetrical heteroduplex)	4.69	1.86	2.53	1.96
Class 31	Anything else	3.28	4.88		
Group 0: Multiple Spo11-DSBs: Affects two sister, 3 or 4 chromatids					
Total		11.35	9.54	17.09	13.23
Class 1	NCO involving 2_sis, 3 or 4 chromatids	2.40	2.79	1.27	2.94
Class 2	NCO+CO involving 3 or 4 chromatids	5.13	5.35	7.59	7.35
Class 3	NCO±CO involving 3 or 4 chromatids, contains different 4:4 patterns	3.82	1.40	8.23	2.94
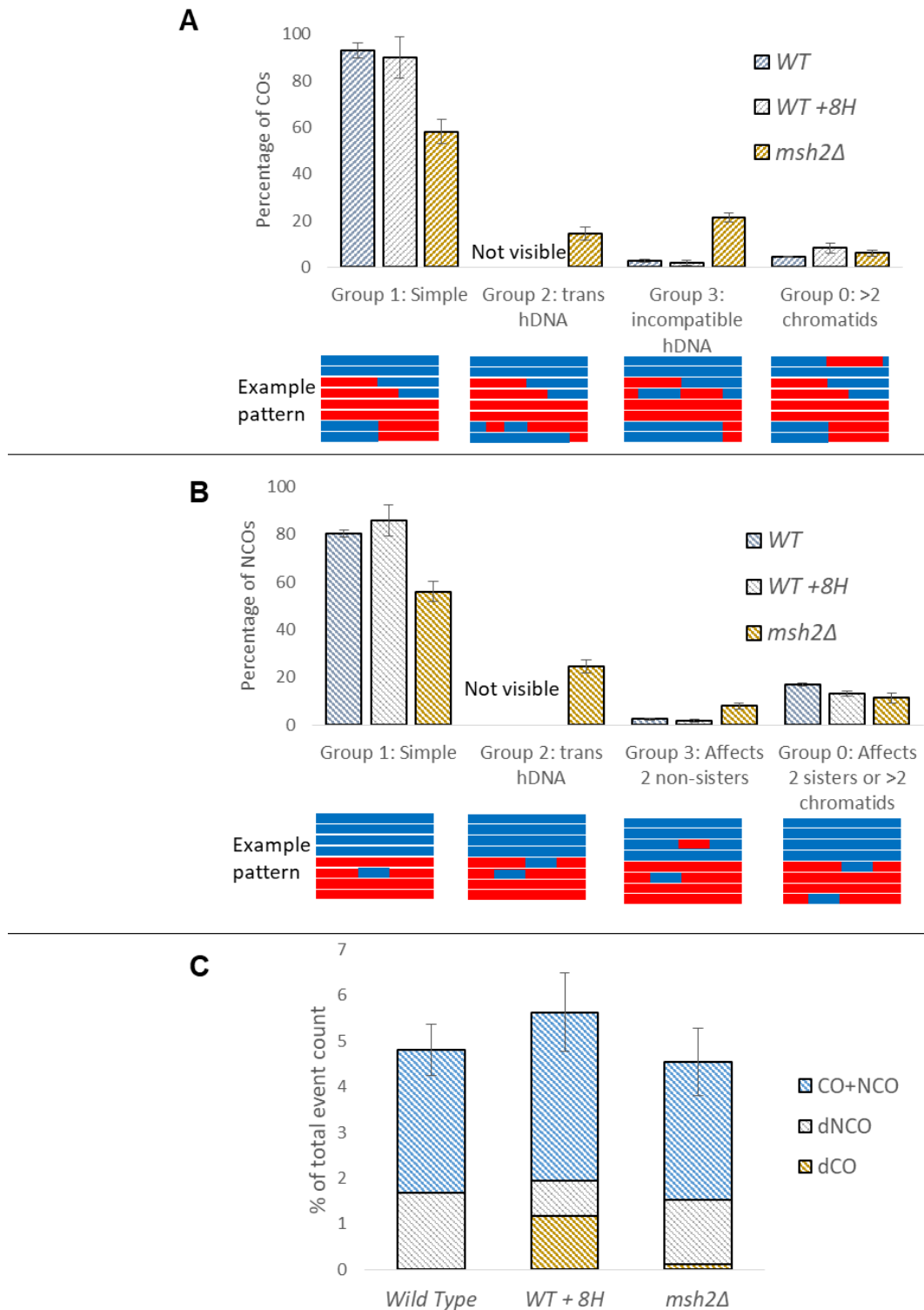
Figure 5.2. Categories of recombination events detected in WT, MMR deficient and prophase extension strains. Error bars are 95% confidence limits. Strain details are given in Table 2.1, raw event data is available in Table S2. A simple example event for each category is shown directly beneath the X-axis, with the red and blue lines corresponding to the eight strands of DNA present during meiotic recombination, four from each parent. **A)** Average percentage of COs and **B)** NCOs in each group. Group 2 is not available in MMR-proficient strains. **C)** Comparison of the average percentage of events thought to be DSB clusters (overall Group 0), with sublevels indicating whether the clusters were inferred to be a double CO, double NCO or CO plus NCO.

5.2.4. The length of detected recombination events in WT, prophase arrest and MMR deficient backgrounds

The length of recombination event tracts could be indicative of the extent of D-loop/dHJ migration and/or resection (Chapter 4, Figure 4.9/4.10), as longer resection or migration distances are predicted to correspond to longer tracts of marker changes. The length of recombination events is also an indicator of event complexity, because apparent long events can be produced by two separate events occuring nearby and overlapping.

Using marker changes to detect recombination events means that the exact start and end of an event cannot be pinpointed, only the locations of the two markers flanking a genotype change at each end of the event. Thus, event length can be reported as the maximum (the difference in the coordinates between the two outer flanking markers), the minimum (the different between the inner flanking markers), or the mid length, which is the difference between the midpoints between the two sets of flanking markers (Figure 5.3A). Generally, the mid length is preferred because on average, it is most likely to approximate the true event length. However, events occuring in areas of low polymorphism density may have poor correlation between mid length estimates and the true event length.

To examine event lengths in WT, MMR deficient and extended prophase strains, event mid lengths were categorized into bins, and mean and median values are also reported (Figure 5.3B & C). Compared to WT hybrids, WT with extended prophase had a general trend towards longer events, having a higher proportion of events with a length >8kb than WT. This may be caused by clustering of separate events, longer conversion tracts or dHJ migration. However, since the trend is seen in both COs and NCOs, it is unlikely that it is caused by dHJ migration since most NCOs are not formed from dHJ resolution in meiosis (Zakharyevich *et al.*, 2012). Nevertheless, it is possible that NCOs displaying trans hDNA on a single chromatid could be formed by dHJ resolution (Martini *et al.*, 2011); if there was a greater occurrence of these events in prophase-arrested strains, it could suggest that more NCO events are produced by dHJ resolution in this background. However, this category (NCO Group 2) is not visible in MMR-proficient strains because hDNA is not detected. Testing this hypothesis would require analysis of recombination events in a *msh2Δ* strain with prophase arrest.

In contrast, both COs and NCOs tended to have shorter lengths in *msh2Δ* than in WT. However, there are also some events in *msh2Δ* with a length >8kb, which is not seen in WT. The higher proportion of short events is probably at least partly explained by the fact that it is easier to detect short NCO events in a *msh2Δ* background due to the presence of hDNA tracts, although short CO events should be detectable in any background due to the reciprocal exchange. The detection of

longer events could be partly caused by the increased information available about event boundaries due to hDNA tract detection.

To determine whether long events represent DSB cluster events, event length distributions were plotted separately for DSB cluster events and non-cluster events (Figure 5.4). In WT, a general trend is seen for both COs and NCOs where the longest events are mostly clusters, and the shorter events are mostly non-clusters. However, there are some short clusters and long non-clusters. Similarly, the WT strain with prophase arrest long events that are mostly, but not always, DSB clusters. However, all of the shortest events are non-clusters. In stark contrast, in *msh2Δ*, all of the longest events are non-clusters. Overall, these results suggest that in WT, the main cause of long event lengths is the merging of two separate events, although not all long events can be explained in this way. However, in an MMR-deficient strain, long event lengths are not well explained by DSB clustering, despite all three strains having similar levels of DSB clusters (Figure 5.2C) (discussed in Section 9.8).
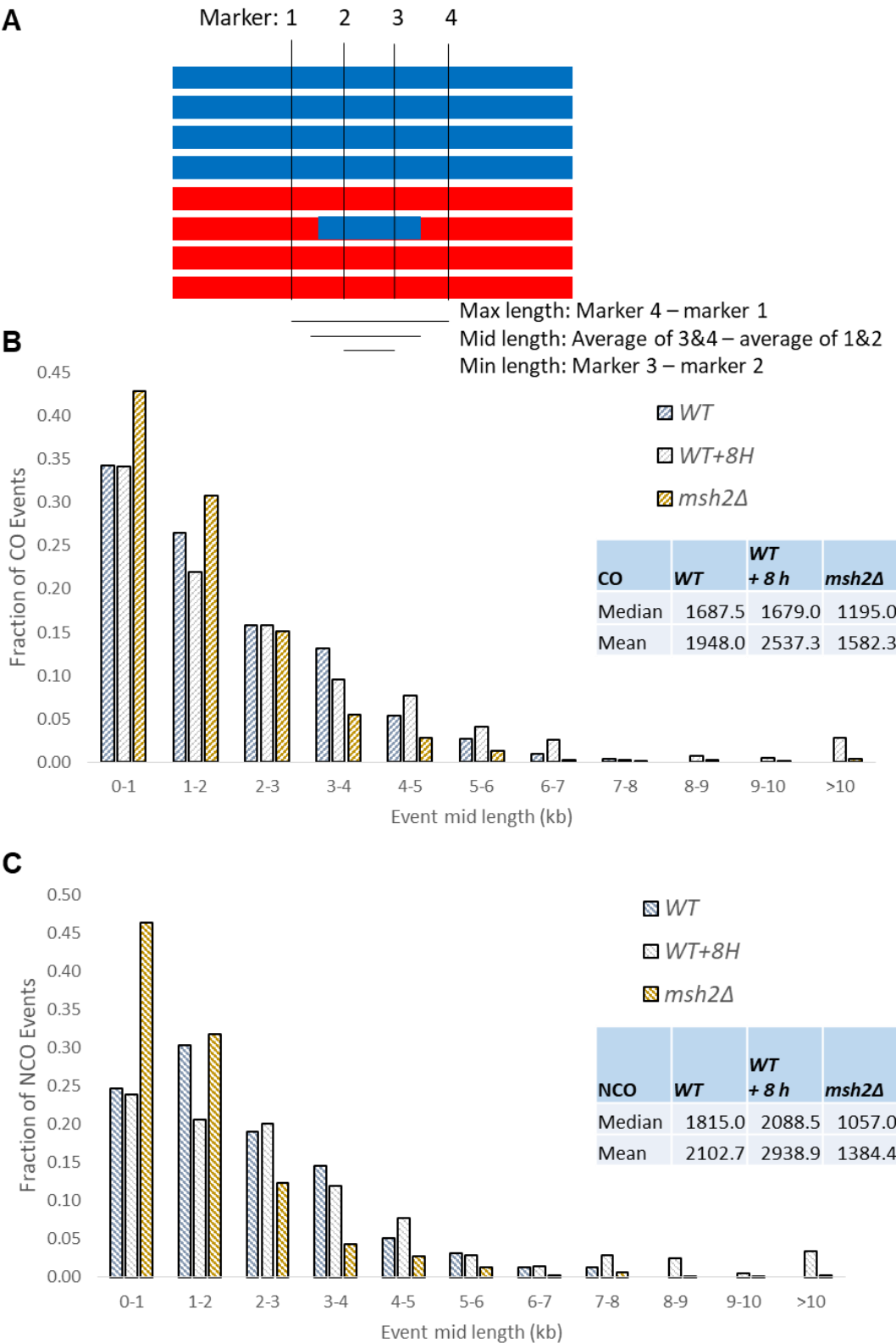
Figure 5.3. Mid length estimates for recombination events detected in WT, MMR deficient and prophase extension strains. Strain details are given in Table 2.1, raw event data is available in Table S2. Insert tables contain the median and mean lengths in bp. **A)** Diagram illustrating how the mid length estimate is calculated. Mid length estimate of **B)** CO and **C)** NCO events.
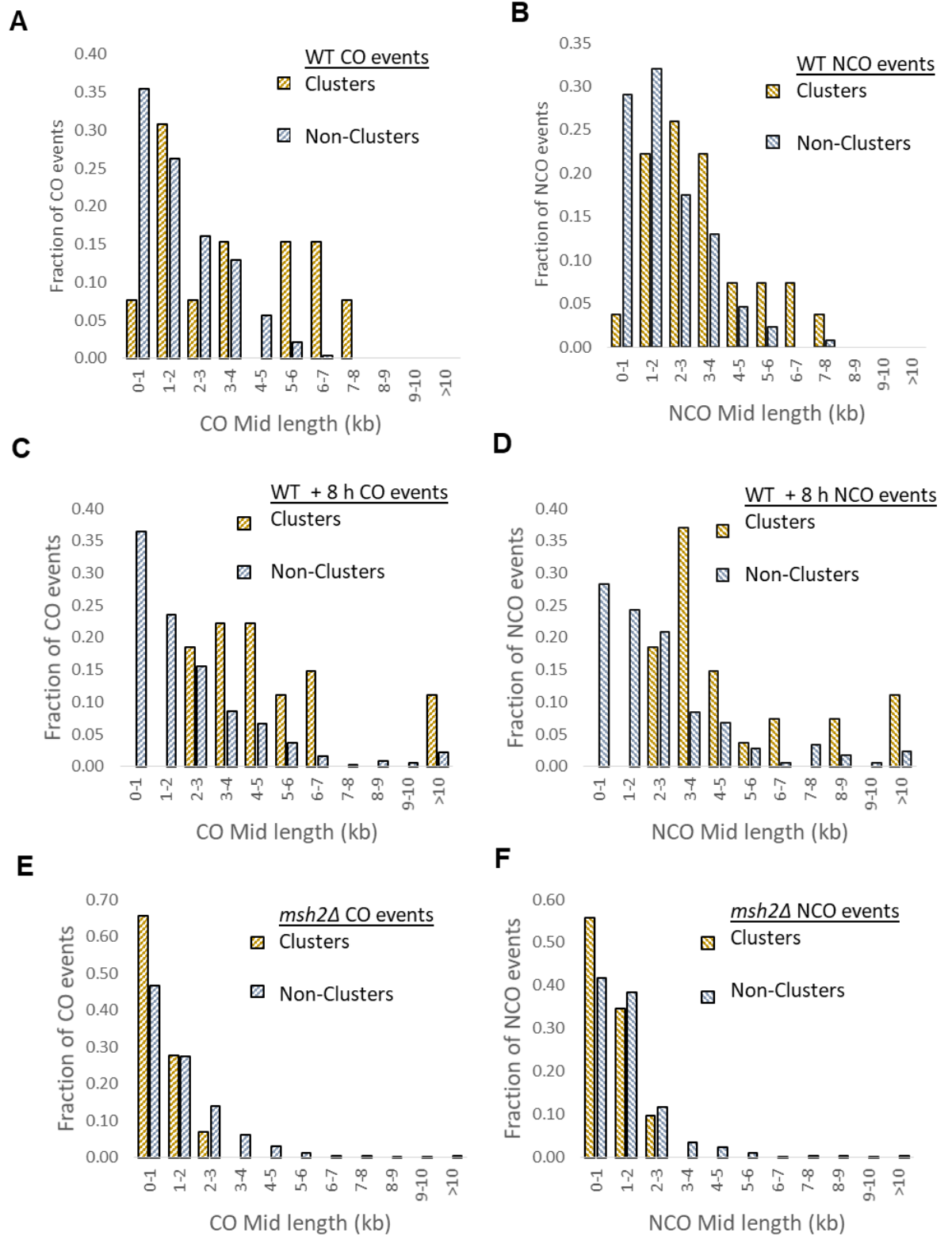
Figure 5.4. Comparison of mid length estimates in single-DSB and DSB-cluster events detected in WT, MMR deficient and prophase extension strains. Strain details are given in Table 2.1, raw event data is available in Table S2. Mid length estimate of cluster/non-clusters of: **A)** CO events in WT, **B)** NCO events in WT, **C)** CO events in WT+8 h, **D)** NCO events in WT+8 h, **E)** CO events in *msh2Δ*, **F)** NCO events in *msh2Δ*.

5.2.5. Presence of potential duplications and deletions in WT, prophase extended and MMR deficient backgrounds

Occasionally, unique 'heteroduplex' SNP calls are seen in individual spore members of an octad or MSH2 tetrad, even though they are not expected to be present in these backgrounds. One possible explanation is that these calls may actually represent duplications occurring during recombination. If an SK1-type allele is broken and copies from an S288c sequence, but invades in the wrong place, it may end up with two copies of the same sequence, once from each parent. The duplications are not always associated with a detected recombination event, suggesting that they could represent undetected NCOs. An example of a potential duplication is shown in Figure 5.5A. In addition, potential deletions can be detected in a similar way by looking for unique adjacent polymorphisms that have a low read depth, suggesting that a section of DNA could be missing in that spore clone. However, these could also be caused a by low sequencing depth of the region in question.

Potential duplications and deletions were examined in WT, extended prophase and *msh2Δ* backgrounds (Table 5.3, Figure 5.5B&C, Figure 5.6A&B). Potential duplications and deletions were only counted if they covered at least two consecutive SNPs.

In a WT background, an average of 2 potential duplications and 1.25 deletions were detected per meiosis, each covering relatively few SNPs and having short potential lengths (Table 5.3, Figure 5.5B&C, Figure 5.6A&B). When prophase is extended, the average number of potential duplications and deletions detected per meiosis is unchanged (2.5 and 1.25 respectively), but the average length of the duplications is somewhat increased, with one having a length of over 900bp; however, due to the low number of samples it is not possible to say if this is significant. In contrast, the MMR deficient strain has an average of 6.6 duplications and 8.3 deletions. The potential duplications in *msh2Δ* contain an average of 3.2 adjacent SNPs, increasing confidence in their calling. The average lengths are increased compared to those in WT, with two duplications over 1000bp long and 5 deletions over 200bp.

Overall, the validity of the deletions is uncertain, as they tend to be short and cover few SNPs (Table 5.3). In addition, the detection of potential deletions is based on an absence of data, so deletions may just be regions with low read depth. However, the potential duplications tend to contain more adjacent SNPs, and are based on the presence of heteroduplex reads, increasing confidence in their validity. It should be noted, however, that deletion lengths may be expected to be shorter than duplications, as long deletions are less likely to be tolerated by the cell. The number of duplications that are not associated with an identified event gives an indication that there may have been additional NCOs occurring during meiosis that are not otherwise reported because they produced a mixture of markers that cannot be called as one genotype or the other.
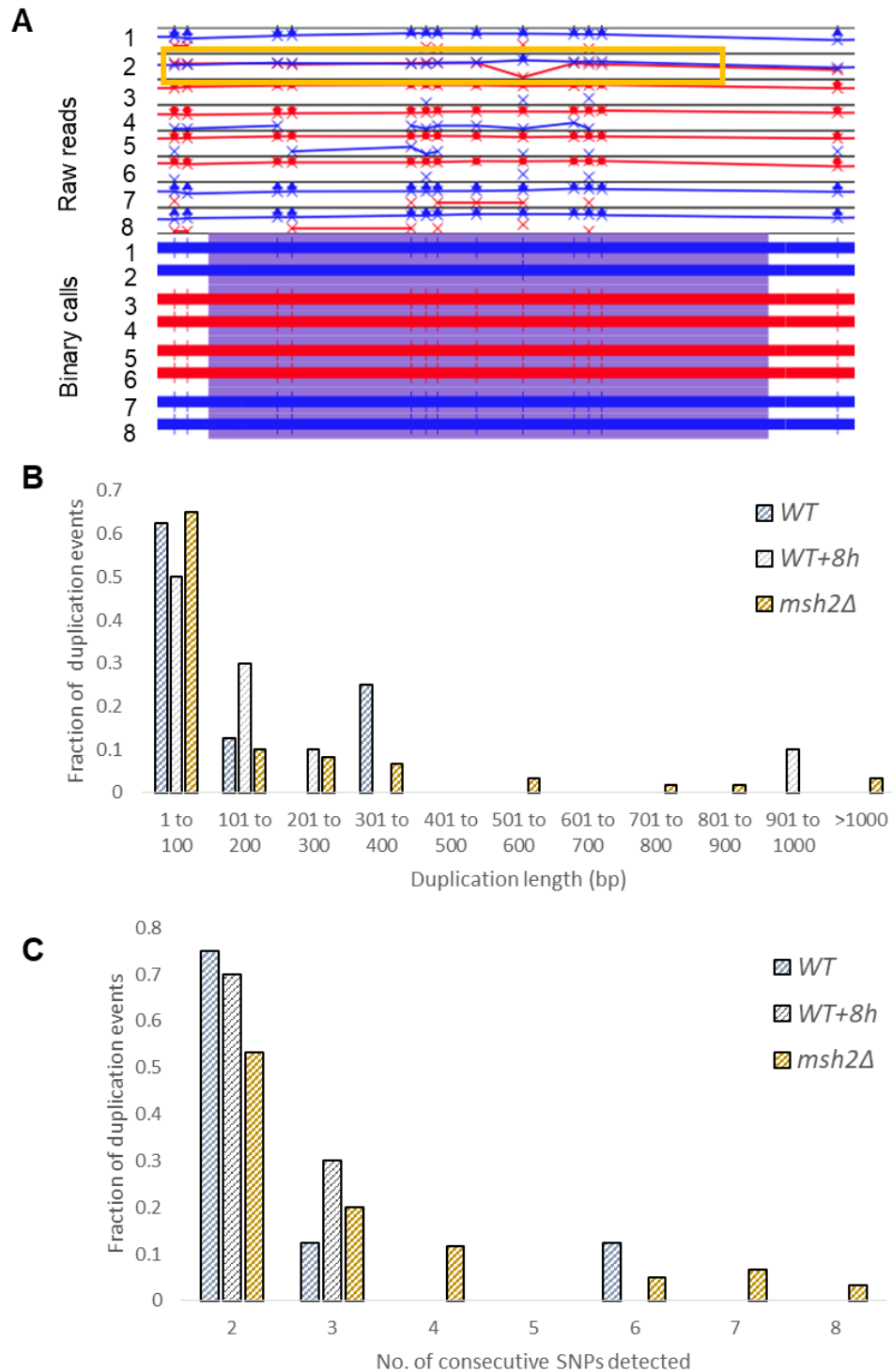
Figure 5.5. Length of potential duplications detected in WT, MMR deficient and prophase extension strains.

Regions of hDNA were mapped by detection of mixed SK1 (blue) and S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The hDNA region is indicated by the purple box. **A)** An example duplication from a msh2 octad, containing 8 SNPs and with a length of 1081bp. Raw reads indicate the frequency of reads containing SK1 or S288c type polymorphisms detected at each position; these are translated into binary calls, which can only be SK1 or S288c. The yellow box highlights the suspected duplication, which can be seen to contain both SK1 and S288c reads. In the binary calls, these positions are discarded. **B)** Length of potential duplications in bp, **C)** Number of consecutive SNPs in potential duplications.

Table 5.3. Data summary for potential duplications and deletions detected in WT, *msh2Δ* and prophase arrested backgrounds. Only duplications and deletions containing at least two SNPs are included.

Genotype (repeats)	Duplications			Deletions		
	Total detected	Mean no. of SNPs	Mean length (bp)	Total detected	Mean no. of SNPs	Mean length (bp)
WT (4)	8	2.6	121.9	5	2.0	41.0
WT + 8 h (4)	10	2.3	199.2	5	2.0	22.6
msh2Δ (9)	60	3.2	165.3	75	2.1	59.1

A
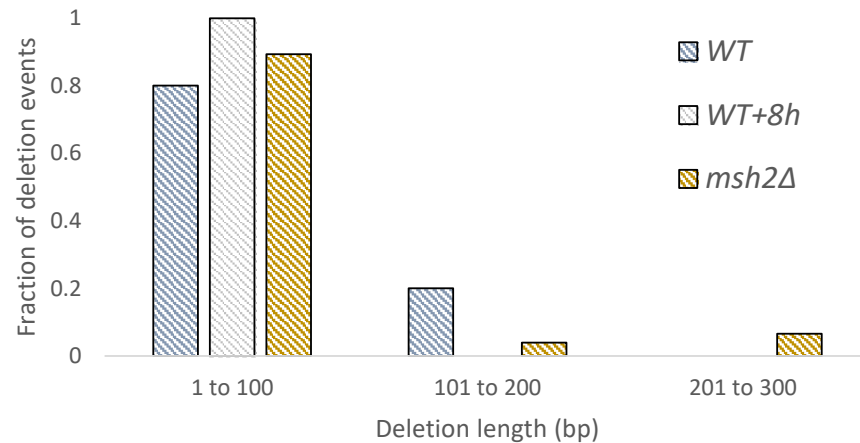
B
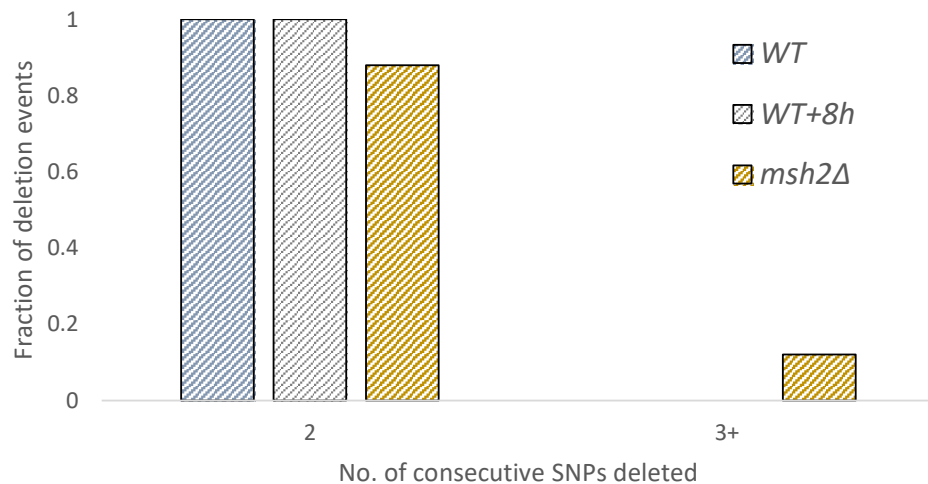
Figure 5.6. Length of potential deletions detected in WT, MMR deficient and prophase extension strains. Potential deletions were detected by looking for consecutive SNPS with low read depth. **A)** Length of potential deletions in bp. *pCLB2-MEC1* +8 h is not shown because no potential deletions were detected. **B)** Number of consecutive SNPs in potential deletions.

5.2.6. Distribution of recombination events in relation to centromeres and telomeres

Normally, recombination is suppressed from occurring near centromeres and telomeres (Petes & Botstein, 1977; Pan *et al.*, 2011). DSBs formed in repetitive regions can cause ectopic recombination leading to genome rearrangement (reviewed in Sasaki *et al.*, 2010). In particular, CO formation is repressed near centromeres (Lambie & Roeder, 1986) and telomeres (Rockmill et al., 2006). The formation of CO events in centromeres and telomeres has consequences for chromosome segregation (Ross et al., 1996; Barton et al., 2003).

It is not possible to detect whether any recombination events occur within centromeres or telomeres using marker mapping, because it is difficult to accurately map reads to repetitive DNA. However, the proximity of events to the region of interest can be measured.

The proximity of recombination events to the nearest telomere to centromeres was measured in WT, extended prophase and *msh2Δ* backgrounds, ranked and plotted as a fraction of total events (Figure 5.7).

In all backgrounds, the frequency of CO event formation is reduced close to the telomeres and centromeres, with very few events occurring within 10kb. This indicates that the mechanisms preventing recombination near these regions is functioning normally in these backgrounds. However, WT + 8 h has a slightly increased fraction of recombination events occurring close to telomeres, but not centromeres, compared to WT or *msh2Δ*. This suggests that there may be a slight loss of the repression of DSB formation near telomeres when prophase is extended. This may be because the overall number of recombination events is increased when prophase is extended, and DSB events tend to 'spread' towards the ends of chromosomes due to DSB interference mechanisms, which mean that middle regions of chromosomes have a higher probability of being under the effects of interference than end regions.

For all strains, the majority of recombination events that do occur close to telomeres and centromeres are NCOs rather than COs (Figure 5.7 C,D). This suggests that the repression of CO formation near these regions is intact when prophase is extended or MMR inactivated.
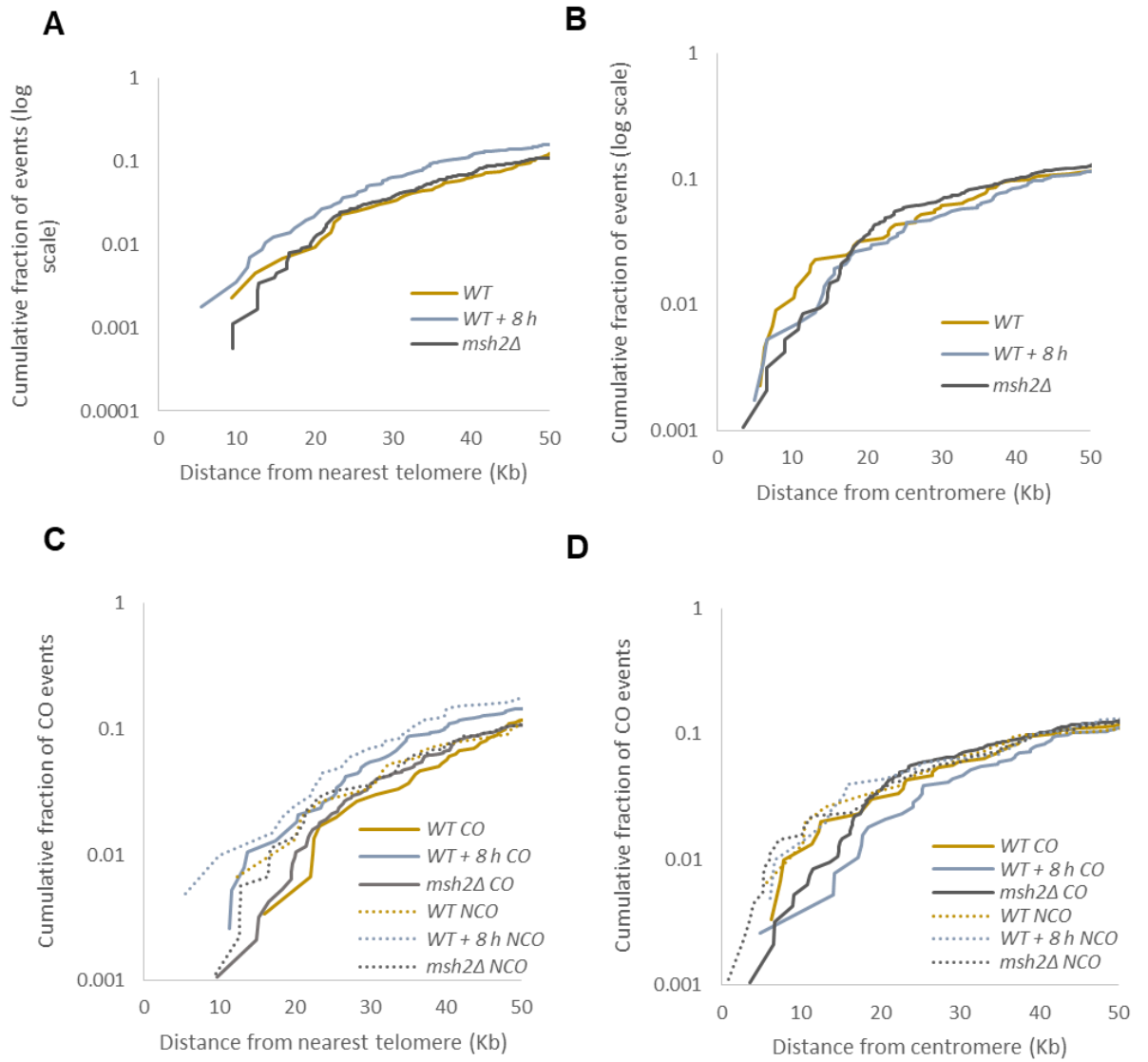
Figure 5.7. Distance between telomeres or centromeres and recombination events detected in WT, MMR deficient and prophase extension strains. For each event, the distance to the centromere or nearest telomere is calculated and plotted against a cumulative fraction of events. **A)** Distance between telomeres and all events. This includes 'U' events which cannot be called a CO or NCO due to occurrence close to the telomeres. **B)** Distance between centromeres and all events. **C)** Distance between telomeres and CO or NCO events. **D)** Distance between centromeres and CO or NCO events.

5.2.7. The distribution of CO events shows evidence of interference

During meiosis, the formation of a CO event reduces the likelihood of another CO occurring nearby. This process (interference) is thought to ensure that events are spread out more evenly along the chromosome. The degree of interference between events can be estimated by measuring the distance between event midpoints and comparing the distributions. The distribution of inter-CO distances gives an indication of CO interference; for example, an increase in short distances between events indicates a loss of interference.

The inter-event distance data shown in this section and the following is from non-annotated samples, meaning that any DSB clusters are treated as a single event (double CO and CO+NCO are considered to be one CO, and double NCO is considered to be one NCO). One consequence of this is that there are no inter-event distances shorter than 1.5 Kb in the non-annotated data, as this is the event merging threshold. The reason for the use of non-annotated data is in order to allow comparisons between experimental data and simulated data that displays random or non-random patterns. While simulated events are merged with the same 1.5 Kb limit used for experimental data, DSB clusters cannot be distinguished in the simulated data, so the experimental data needs to match this format for the purpose of comparison.

Inter-CO distances were calculated for the WT, prophase arrest and *msh2Δ* strains, arranged in order from smallest to largest and plotted as cumulative fraction of total events against inter-CO distance (ICD) size on a log scale (Figure 5.8). In the WT, prophase arrest and MMR-deficient backgrounds, CO interference is expected to be present as the mutations are not currently known to affect this process.

In order to determine whether the experimental inter-event distance distributions are distinct from a random distribution, simulated data is produced for the appropriate event counts to show the hypothetical distribution of events along the chromosomes under conditions of independence (Methods section 2.18; Tim Cooper, personal communication). To simulate IED data under conditions of interference or independence, virtual events occur sequentially on simulated chromosomes and either have no influence on the following events (independence simulation) or apply an interference window that reduces the chance of another event occurring within it, with a size based on the gamma parameters (interference simulation). Since the experimental data was analyzed with a 1.5kb merging threshold between events, this is also done for simulated events so the final observed event count will be identical to the experimental data. Because inter-event distances are strongly influenced by the number of events, and this varies between octads/tetrads, data for each genotype must be plotted separately, with its own simulated datasets that match the number of events.

For crossovers (Figure 5.8), experimental inter-CO distance distributions in all cases deviate from the random simulation (compare blue (experimental) and orange (random simulation). The experimental data is shifted to the right, indicating that there are fewer short inter-CO distances than expected. This means that CO events are occurring further apart than would be expected if events were occurring independently, suggesting the presence of CO interference.

Visually, interference appears to be stronger in the *msh2Δ* strain in comparison to the MMR-proficient strains; the deviation in the experimental data from a random simulation is larger. However, experimental IED distributions cannot be directly compared because the number of events is different in each background. Instead, to quantify the strength of CO interference in each strain, the best fit to a gamma distribution can be determined. A gamma distribution is a continuous probability distribution that is observed in the intervals between successive independent events, and so can be used to describe the distances between recombination events (McPeek and Speed, 1995; Zhao *et al.*, 1995). A gamma distribution function has a shape factor, α, and a scale factor, β. For recombination events, α corresponds to the strength of interference. A value of 1 indicates an exponential distribution i.e. no interference. Values > 1 indicate interference, with higher values corresponding to stronger interference. β describes the distance over which the shape designated by α is stretched, thus indicating the range of the interference. It is also affected by the number of data points, so is lower in strains with more events. Experimentally obtained inter-CO distances from WT cells have been shown to be well fit by a gamma distribution, indicating the presence of CO interference (Chen *et al.*, 2008). Calculated gamma parameters are presented in Table 5.4.

The α values were similar for WT (1.39) and prophase arrested (1.46) strains, suggesting that CO interference has a similar strength in both backgrounds despite the different CO counts. Previous studies have used the same method to quantify the strength of interference in WT strains, finding α values of 1.9 and 2.0 (Chen *et al.*, 2008; Rockmill *et al.*, 2013). The reason why these studies found WT CO interference to be somewhat stronger may be related to the fact that they utilized a different hybrid strain background (S96 x YJM789). Alternatively, the relatively low sample size in the data presented here may be showing an incomplete picture of interference, so ideally more data from WT and prophase arrested samples should be obtained. In contrast, inter-CO distances in *msh2Δ* were best described by a gamma function with an α value of 2.44, suggesting that interference is stronger in this background than in the MMR-proficient background.

A Kolmogorov-Smirnov test (Methods section 2.20) was utilized to determine whether the experimental inter-CO distribution was significantly different from the best fit gamma

distribution, revealing that in all cases they were significantly different (low P-values in Table 5.4), indicating that inter-CO distributions cannot be well described by a gamma distribution. The best fit gamma function for each background also was used to produce simulated IED data. Simulated IED data was plotted alongside experimental data to give a visual indication of the goodness of fit to the 'best fit' gamma parameters (Figure 5.8, grey lines). This shows that there is a particularly poor fit for the shortest inter-CO distances, with the experimental data shifted to the left compared to the gamma distribution, meaning that more short distances are occurring than expected. This suggests that there are many events occurring that do not display interference; this may be caused by the presence of Class II (non-interfering) COs, as discussed in section 5.2.10.
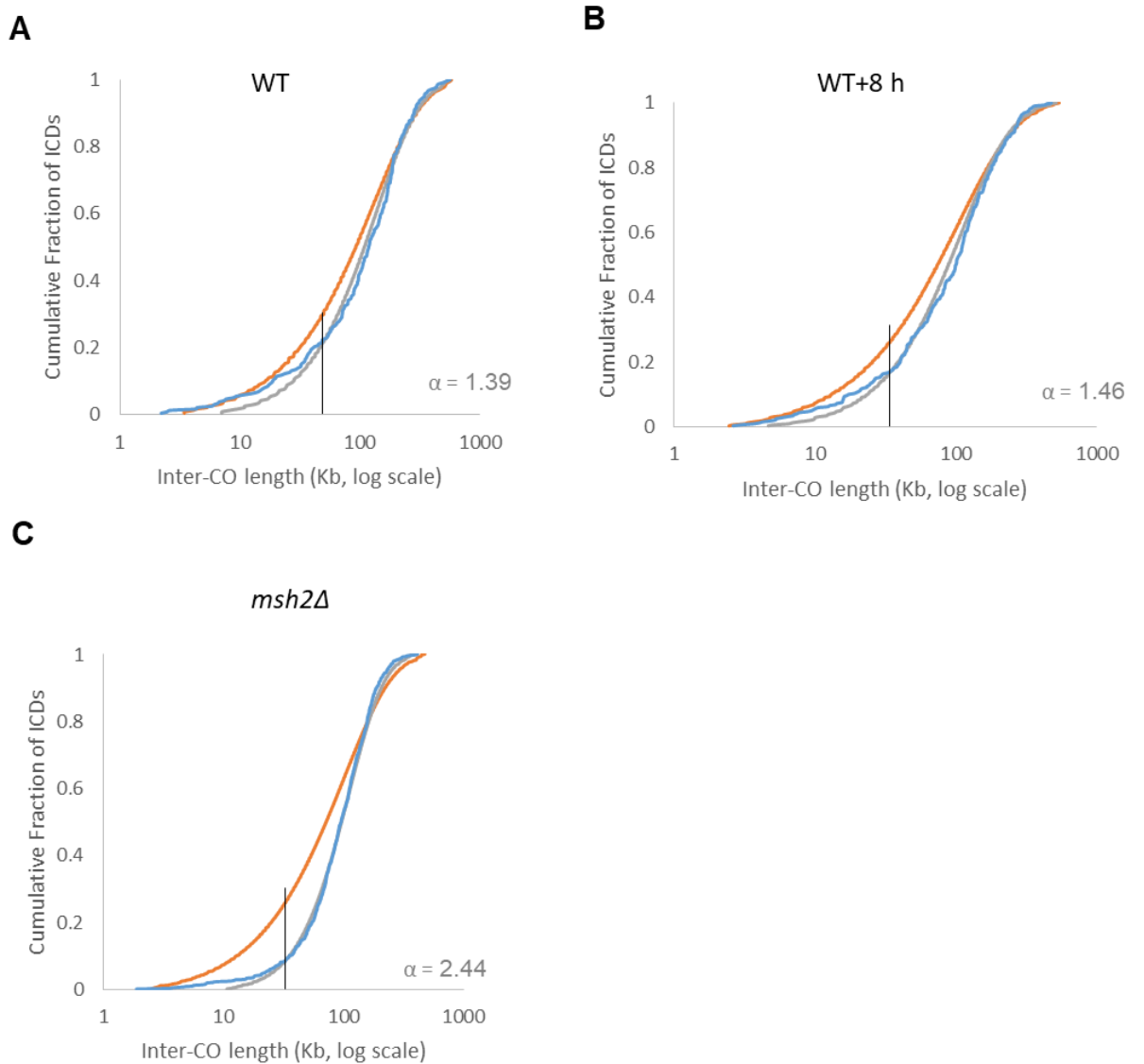
Figure 5.8. Distribution of distances between crossover events observed in WT, MMR deficient and prophase extension strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-CO distance (ICD) in **A)** WT, **B)** WT + 8 h, **C)** *msh2Δ*.

Table 5.4. Gamma parameters.

Best-fit gamma parameters are given for the inter-event distribution for each aggregate genotype and event type. The number following the genotype indicates how many samples were included in the aggregate. N indicates the total number of recombination events (CO, NCO or both) included in the analysis. The shape factor, α, corresponds to the strength of interference: A value of 1 indicates an exponential distribution i.e. no interference. Values > 1 indicate interference, with higher values corresponding to stronger interference. The scale factor, β describes the distance over which the shape designated by α is stretched, thus indicating the range of the interference. It is also affected by the number of data points, so is lower in strains with more events. A one-sample Kolmogorov–Smirnov test is utilized to determine whether the experimental inter-event distribution is significantly different from the theoretical best fit gamma distribution, with the reported P-value indicating whether the difference was significant. If the value is <0.05, the difference is considered significant (red).

Genotype (repeats) Crossovers	N	Best fit gamma α value	Best fit gamma β value	(P)
WT (4)	237	1.39	100429	0.0217
WT+8 h (4)	319	1.46	79142	0.0245
msh2Δ (9)	799	2.44	44056	0.0036
Non-Crossovers	N	α	β	(P)
WT (4)	85	1.24	165657	0.0146
WT+8 h (4)	123	0.96	186147	0.9732
msh2Δ (9)	698	1.21	87998	0.0861
Total events	N	α	β	(P)
WT (4)	375	1.36	73799	0.0123
WT+8 h (4)	504	1.1	72010	0.0011
msh2Δ (9)	1636	1.57	36542	0.0001

5.2.8. The distribution of NCO events does not shows evidence of interference

In contrast to CO events, NCOs do not display interference. This was first shown for single loci (Mortimer & Fogel, 1974) and reiterated by a genome wide survey (Mancera *et al.*, 2008).

In order to determine whether NCO events display interference in WT, prophase-arrested and MMR-deficient backgrounds, inter-NCO distances were plotted as described for inter-CO distances in Section 5.2.7 (Figure 5.9). In these backgrounds, NCO interference is not expected to be present. If interference is present, events should occur further apart than would be expected if event placement was random. As described for CO events, simulated datasets for events occurring under conditions of independence were produced for the appropriate event counts.

For noncrossovers (Figure 5.9), the experimental inter-NCO distance plots are visually a good match to the random simulation (compare blue (experimental) and orange (random simulation).

The best match is seen in *msh2Δ*; the other backgrounds have more noise in the data due to the low NCO counts, but still show a random distribution. This is as expected as NCOs are known to not display interference in yeast.

The best fit to a gamma distribution was found for inter-NCO event distances (Table 5.4), producing α values of 1.24, 0.96, and 1.21 for WT, WT+ 8h and *msh2Δ* respectively, all of which indicate low or no interference between NCO events, as predicted. A Kolmogorov-Smirnov test was utilized to determine whether the experimental inter-NCO distribution was significantly different from the best fit gamma distribution, revealing that even the best-fit for the WT distribution was still significantly different (P-values in Table 5.4), indicating that WT inter-NCO distributions cannot be well described by a gamma distribution. However, the best-fit gamma distributions for WT +8h and *msh2Δ* are not significantly different from experimental data, indicating that the calculated gamma values are a good description of the strength of NCO interference in these backgrounds.
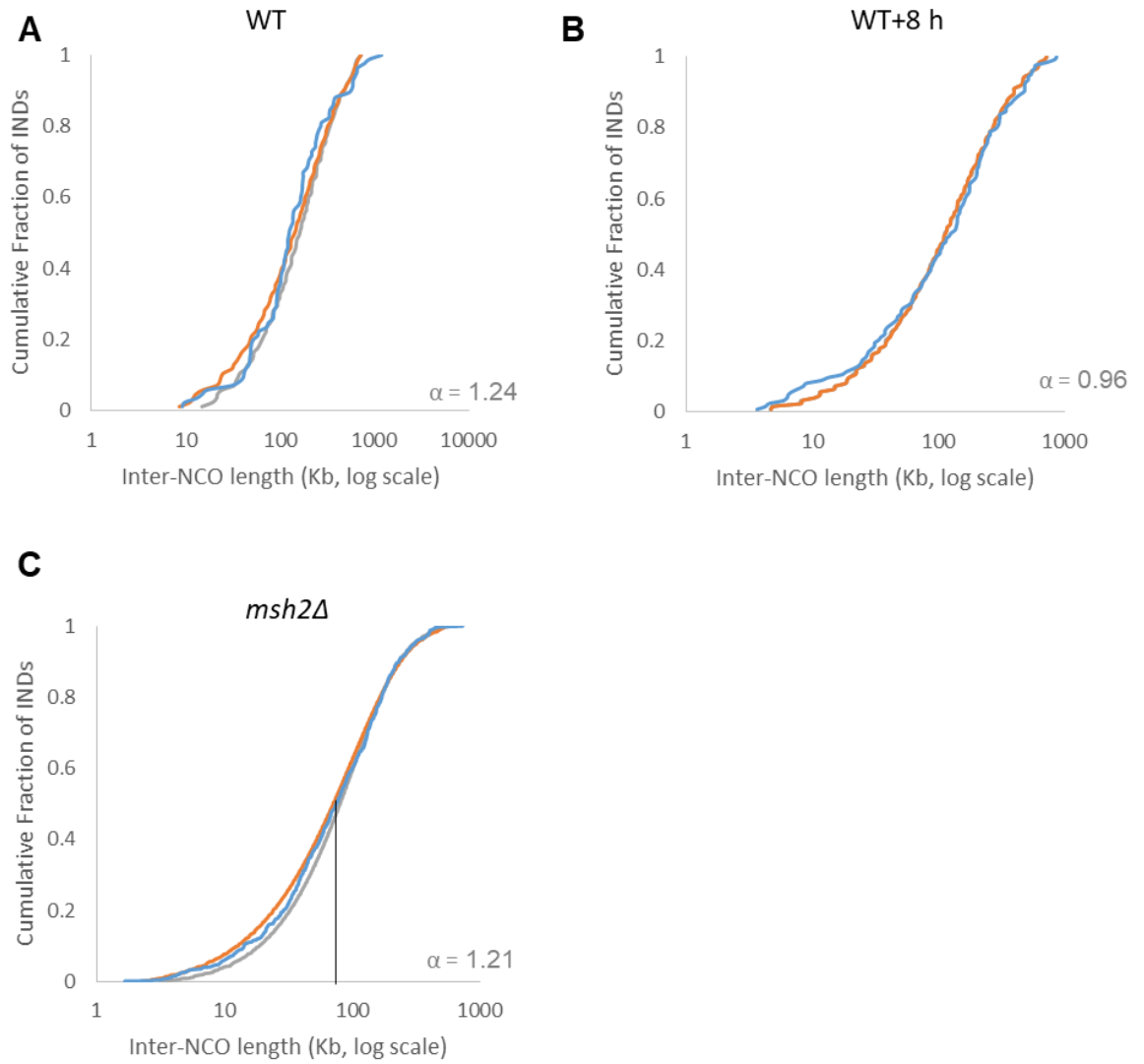
Figure 5.9. Distribution of distances between noncrossover events observed in WT, MMR deficient and prophase extension strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-NCO distance (IND) in **A)** WT, **B)** WT + 8 h, **C)** *msh2Δ*.

5.2.9. The distribution of all recombination events shows some evidence of DSB interference

The occurrence of a DSB is known to reduce further DSB formation nearby in *cis* and in *trans*, a phenomenon known as DSB interference. To give an approximate measure of DSB interference, the distance between any type of event is used as an equivalent of inter-DSB distance. This is an imperfect measure for two reasons. Firstly, event midpoints are not necessarily where the DSB was located; this would disproportionally affect strain backgrounds with increased event lengths. Secondly, many recombination events occur invisibly. Around 15-30% of meiotic DSBs are thought to repair with the sister chromatid (Schwacha & Kleckner, 1997). In addition, in the WT strain, ~16% of NCO events are predicted to occur between markers, and ~30% of NCOs are estimated to be restored to the original genotype by mismatch repair (Section 5.2.1). However, the issue of genotype restoration should in theory not affect the strength of interference (assuming that the undetectable events occur uniformly in the genome), because interference has been found to be mostly constant regardless of event density (Zhang *et al.*, 2014; Anderson *et al.*, 2015).

Inter-event distances were calculated for the WT, prophase arrest and *msh2Δ* strains, and plotted alongside simulated datasets for events occurring under conditions of independence as described for inter-CO distances in Section 5.2.7 (Figure 5.10). In WT, prophase arrest and *msh2Δ* strains, DSB interference is expected to be present because the *msh2Δ* and *ndt80* mutations are not currently known to affect these processes. If interference is present, events should occur further apart than would be expected if event placement was random.

Both WT and *msh2Δ* inter-event distributions have a convincing deviation away from the random distribution, indicating that events are occurring further apart than would be expected by random chance. However, there is a tendency towards randomness over short distances (Figure 5.8, A &C). The prophase arrested WT strain has a similarly-shaped, but more exaggerated, curve, with a high tendency towards randomness over short distances, but evidence of interference over a long range (Figure 5.8B).

In order to quantify the strength of "DSB" interference for each genotype, the best fit gamma parameters were found for inter-event intervals from WT, prophase arrested and *msh2Δ* strains as described in Methods Section 2.18 and Section 5.2.7 (Table 5.4). The inter-event distributions were best described by gamma distributions with α values of 1.36, 1.1 and 1.57 for WT, WT+8 h and *msh2Δ* respectively. This suggests that both WT and *msh2Δ* display interference in event positioning, but events in prophase-arrested WT tend to be randomly placed. However, since event midpoints do not necessarily correspond to DSB locations, this does not mean that DSB interference is definitely lost under conditions of prophase arrest. In addition, the results of a Kolmogorov-Smirnov test used to compare the best-fit gamma distribution with the experimental

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distribution showed that in all cases the distributions were significantly different (low P-values in Table 5.4). This indicates that inter-event distributions cannot be well described by a gamma distribution.

In a WT background, the α value for DSB interference was found to be 0.37 by Anderson *et al.*, 2015, which is much lower than the value calculated here and indicative of negative interference. This may be related to the fact that Anderson et al. used a slightly different strain background (S96 x YJM789) and a higher event merging threshold of 5 Kb, which would reduce the ability to resolve closely-occurring events.

One reason why inter-event interference may not be a good estimate for DSB interference is that it may be influenced by CO interference due to CO-CO intervals present in the data, which are known to display interference (Section 5.2.7). In addition, if event positions are a good approximation of DSBs, NCO events should display some interference caused by the underlying DSB interference. However, this may be prevented by CO events occurring in between NCO events.

These ideas have been investigated previously using a simulation where DSB interference was established entirely independently of CO interference (Anderson *et al.*, 2015).
The model revealed that a complete loss of CO interference only slightly reduces the interference among all detectable events, with the reduction not being comparable to that observed in mutants that lose DSB interference such as *tel1Δ*, *zip3Δ*, *msh4Δ*, and *sgs1Δ* (Anderson et al., 2015). However, the experimentally-observed lack of interference between NCOs was not predicted by the model, suggesting that DSB interference may be at least partly influenced by DSB suppression near COs.
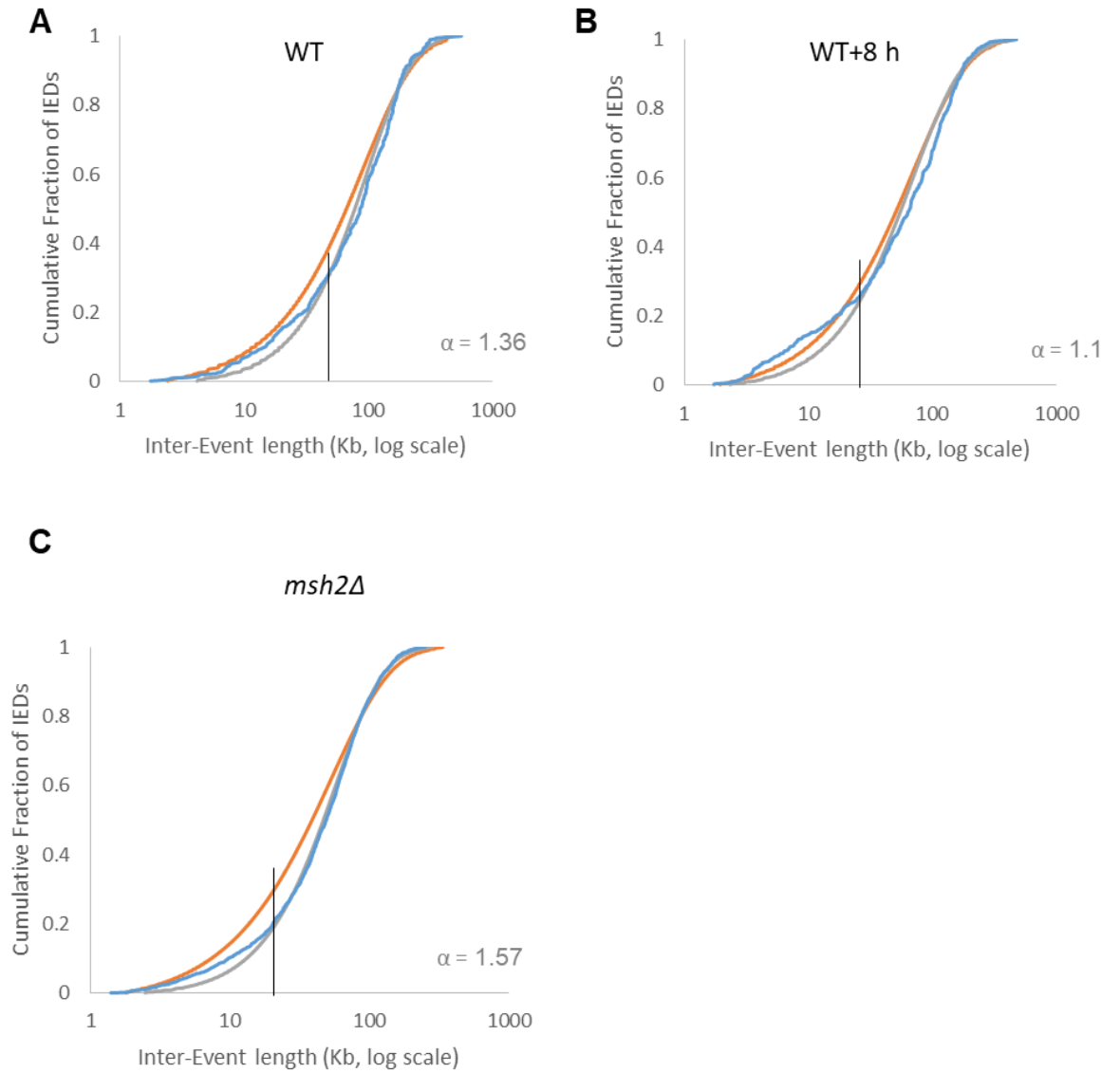
Figure 5.10. Distribution of distances between all recombination events observed in WT, MMR deficient and prophase extension strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-event distance (IED) in **A)** WT, **B)** WT + 8 h, **C)** *msh2Δ*.

5.2.10. MMR-deficient meiotic recombination is predicted to have a lower proportion of Class II COs than WT

There are two distinct classes of CO event in *S. cerevisiae* meiosis: Class I COs exhibit interference and are dependent upon Msh4/Msh5 activity (Novak *et al.*, 2001), and Class II COs do not display interference and are dependent upon Mus81/Mms4, Yen1 or Slx1-Slx4 activity (de los Santos, 2003). A potential explanation for an apparent loss of CO interference is an increase in the proportion of COs that are non-interfering, rather than a reduction in the interference displayed by Class I events. The normal ratio of Class I to II is somewhere around 70:30 (Zakharyevich *et al.*, 2012; de los Santos, 2003).

Thus, the distribution of CO events can be viewed as having two components, a distribution of non-random, interfering events and a distribution of random, non-interfering events. Based on the expectation of a two-component distribution, it is possible to separate out the two using mixture modelling. Each dataset was split into an interfering and a non-interfering subset, which are inferred to be equivalent to Class I and Class II COs. This analysis was performed and authored by Tim Cooper (personal communication) (Methods section 2.19). Based on the expectation that one component will display no interference ($\alpha=1$) and the other will display interference ($\alpha>1$), this system takes initial parameter estimates and iteratively corrects the two gamma-components until they fit the experimental data.

It was observed that *msh2Δ* appears to have much stronger CO interference than WT (Section 5.2.7). A potential explanation is that *msh2Δ* may have a reduction in Class II CO formation. To be able to predict the proportions of Class I/II COs in these backgrounds, two-component analysis was carried out on these strains (Table 5.5). The ability of the two-component system to describe experimental data was analyzed via a Kolmogorov-Smirnov test. In comparison to the poor fit of a single gamma distribution to inter-CO distances (Table 5.4), a large improvement for all genotypes is seen when a mixed-fit is used, with none of the distributions significantly different to the experimentally observed data (compare P-values in Tables 5.4 and 5.5).

The results of this analysis show that the WT strain is predicted to have ~67% Class I to ~33% Class II COs, which is in accord with what is expected from the literature (Zakharyevich *et al.*, 2012; de los Santos, 2003). Extending prophase does not affect the ratio, with ~66% Class I and ~34% Class II in the prophase arrest WT background. In contrast, *msh2Δ* is predicted to have ~77% Class I COs and ~23% Class II, suggesting that *msh2Δ* is predicted to have about two-thirds the proportion of Type II COs compared to WT or WT+8 h arrest. However, because more COs occur in *msh2Δ* than WT, there is actually the same absolute number of Class II COs predicted in WT and *msh2Δ* (24.5 vs 24.7 respectively). This suggests that the reason for the shift in

proportions in *msh2Δ* is not due to the occurrence of fewer Class II COs, but of more Class I COs. This suggests that Msh2 is an anti-Class I CO factor, which may be related to the anti-recombinogenic activity of MMR in hybrid backgrounds (Hunter *et al.*, 1996), if this affects crossovers formed by the ZMM pathway disproportionately to those formed by other pathways. To test this hypothesis, Class II COs can be suppressed via the deletion of Mus81, the main resolvase responsible for their formation. This is discussed in Chapter 8.

Table 5.5. Percentage of COs that do not appear to show interference in sequenced strain backgrounds.

Mixture modelling results are given for each genotype. The strength of interference in the non-random population is given by α1 and is expected to be >1. The strength of interference in the random population is given by α2 and is expected to be ~1. The scale factors, β1 and β2 describe the distance over which the shapes designated by α1 or α2 respectively are stretched, thus indicating the range of the interference. The overall proportion of CO events that are thought to occur with random or non-random placement is given, which allows a predicted total number of Class I and Class II COs to be calculated from the overall CO count. A two-sample Kolmogorov–Smirnov test is utilized to determine whether the experimental inter-event distribution is significantly different from the two-component system, with the significance indicated by the reported P-value. A value of >0.05 is considered to show no significant difference.

Genotype (repeats)	α1	α2	β1	β2	Non-random proportion (%)	Random proportion (%)	Predicted mean number of Class I COs	Predicted mean number of Class II COs	P
WT (4)	3.78	1.06	37696	107930	67.1	32.9	50	24.5	0.7
WT +8 h (4)	3.22	1.4	47109	32856	66	34	64.1	33.15	1
msh2Δ (9)	3.84	1.21	29877	68155	76.5	23.5	80.3	24.7	0.9

5.3. Discussion

5.3.1. The effect of the mismatch repair protein Msh2 on meiotic recombination

The loss of the mismatch protein Msh2 is deleterious to spore viability in SK1 and hybrid SK1xS288c WT strains (Chapter 3, Figure 3.7A, B). However, deletion of *MSH2* is less deleterious in hybrid SK1xS288c strains than in pure SK1 strains. Msh2 is thought to detect and reject mismatched DNA intermediates formed during strand invasion (Sugawara *et al.*, 1997; Evans *et al.*, 2000), something that is more likely to occur in hybrid strains. The absence of Msh2 allows more recombination events to form in hybrids (Figure 5.1), supporting an anti-recombination role for Msh2 when sequences are diverged. The reduced recombination event frequency in *MSH2* hybrids may contribute to the lowered spore viability (Figure 3.8).

Msh2 appears to be an anti-Class I factor, as the increase in CO number in *msh2Δ* compared to WT appears to be entirely made up of Class I COs, causing an apparent increase in the strength of CO interference as the distribution of CO events matches gamma distributions with higher alpha values in *msh2Δ* (Figure 5.8, Table 5.5). *msh2Δ* also increases NCO counts compared to WT. This is at least partly because they are easier to detect because hDNA can be seen when sequencing. However, even when accounting for events detected in *msh2Δ* that are composed of hDNA only, the WT strain is still predicted to have fewer than *msh2Δ* (Section 5.2.1).

Overall, these results show that MMR-deficiency has both a positive and negative effect on spore viability in hybrid strains. The negative effect is presumably due to the occurrence of unrepaired mismatches and increased ectopic recombination due to lack of fidelity in strand invasion. The positive effect is due to the increase of event counts of COs and NCOs, specifically Class I COs. In most backgrounds, the negative effect outweighs any positive effects to give an overall decrease in viability, but in backgrounds where it is more important for strand invasion to be successful, *msh2Δ* can have an overall neutral or positive effect on spore viability (Figure 3.8).

It is possible that deleting *MSH2* in hybrids effectively restores the situation that would be seen in a WT pure background (in terms of CO/NCO counts), though with some negative effects due to unrepaired mismatches etc. However, whether the increase in CO and NCO counts would be seen in a pure SK1 strain cannot be determined by using the marker analysis method to assay recombination as there are no different markers.

5.3.2. Effect of prophase arrest

Recombination was assayed genome-wide in hybrid yeast with around 3-4 extra hours of prophase, mediated by *NDT80* block and release (Xu *et al.*, 1995). The WT + 8 h cells had an increase in CO and NCO events compared to WT. Prophase arrest cells also have longer CO and

NCO events and an increase in the percentage of recombination events that appear to be DSB clusters compared to WT or *msh2Δ*. WT and WT + 8 h cells have similar proportions of COs that appear to be placed randomly or subject to interference, indicating that the increase in CO formation caused by the extended prophase does not favour Class I or Class II in particular.

Increased prophase length is more beneficial to hybrid spore survival than *msh2Δ*, perhaps because a lack of MMR means that mutations cannot be repaired and ectopic recombination is increased due to the inability to reject strand invasion into non-homologous regions, while *NDT80* arrest does not produce many effects that persist after *NDT80* induction (Allers & Lichten, 2001; Bhuiyan *et al.*, 2002). However, the prophase arrest does slightly reduce hybrid viability (~82% to ~70%) (Table 5.6).

Table 5.6. Summary of basic recombination characteristics across strains.
Spore viability was originally shown in Figures 3.1A, 3.8, 3.9. WT + 8 h is from Gray *et al.*, 2013. DSB cluster formation originally shown in Figure 5.2. CO/NCO formation originally reported in Table 5.1. Event mid length median shown in Figure 5.3.
Best fit alpha values are from Table 5.4. (It should be noted that the best fit alpha value was still significantly different from the actual CO distribution in most cases). The Class I and II percentages and numbers are from Table 5.5.

	WT	WT + 8 h	*msh2Δ*
Spore viability % (SK1)	97	94	81
Spore viability % (SK1xS288c hybrid)	82	70	73
Average CO number	74.5	97.3	105
Average NCO number	39.5	51	101.8
Median NCO mid length (bp)	1815	2089	1057
Median CO mid length (bp)	1688	1679	1195
% of events that are DSB clusters	4.8	5.6	4.6
Best fit α value (CO interference)	1.18	1.46	2.44
Class I/Class II CO percentage	67.1/ 32.9	66/ 34	76.5/ 23.5
Class I/Class II CO number (predicted)	50/ 24.5	64.1/ 33.2	80.3/ 24.7

5.3.3 Closing Statement

In this chapter, high-resolution sequencing data was used to examine features of meiotic recombination in wild type, MMR deficient and prophase arrested hybrid strains. This allowed a baseline for 'wild-type' recombination to be established, which can be used for comparisons. In addition, it was found that the three 'wild type' backgrounds have some significantly different features of recombination to each other (Table 5.6).

Chapter 6.

The role of the DDR kinase Tel1 in

regulation of meiotic recombination

Chapter 6. The role of the DDR kinase Tel1 in regulation of meiotic recombination

6.1. Introduction

6.1.1. Roles of Tel1 in the DNA damage response

Tel1[ATM] kinase has many functions in meiosis, including monitoring of DNA damage repair, checkpoint regulation, and cell cycle progression (Cha *et al.*, 2002; Harper & Elledge, 2007; Carballo & Cha, 2007). In *S. cerevisiae* meiotic prophase, programmed DSBs are formed by Spo11. The accumulation of unresected DSBs cause activation of Tel1 (Usui *et al.*, 2001). The meiotic checkpoint monitors meiotic events and halts cell cycle progression if necessary, ensuring that cells do not exit prophase before the process of DSB repair is complete (Lydall *et al.*, 1996; Carballo *et al.*, 2008). Tel1 negatively regulates DSB formation in mammals, flies and yeast (Lange *et al.*, 2011; Joyce *et al.*, 2011; Gray *et al.*, 2011). An increase in Spo11-oligonucleotide complex formation has been observed in *tel1* deletion and kinase dead mutant yeast (Mohibullah & Keeney, 2017). Tel1 also has a role in telomere maintenance, producing a DNA damage response when telomeres are damaged in vegetative cells (Lustig & Petes, 1985; Eckert-Boulet & Lisby, 2010). Atm-/- mouse spermatocytes have been observed to have aberrant telomere bouquet formation, with altered timing and occurrence of chromosome polarization (Pandita *et al.*, 1999). *TEL1* deletion has only a minor effect on spore viability in yeast, reducing it from ~97% to ~93% (Chapter 3, Figure 3.7). In addition, when the overall DSB level is low, Tel1 is required in yeast for efficient resection of DSBs and maintenance of homolog bias (Joshi *et al.*, 2015).

6.1.2. Evidence for a role in DSB interference for Tel1

DSBs do not occur independently, but are subject to interference among the four chromatids. This interference occurs in *cis* (adjacent on the same chromatid), and *trans* (between chromatids). Tel1 has been shown to be a mediator of trans DSB interference via tetrad analysis at the *HIS4::LEU2* hotspot, showing that DSB formation is no longer constrained to occur only once per quartet of chromatids in *TEL1* mutants (Zhang *et al.*, 2011).

Tel1 also mediates DSB interference in *cis* (Garcia *et al.*, 2014). This study found that over a range of 10 kb-70 kb, interference was lost in the absence of Tel1. Intriguingly, over very short distances (<10 kb), loss of Tel1 was found to cause concerted DSB formation, an activity known as DSB clustering or negative interference (Garcia *et al.*, 2014).

6.1.3. Evidence for a role in CO interference for Tel1

The occurrence of a CO event reduces the chance of another CO event occurring in proximity, a phenomenon known as CO interference. The majority of COs in yeast display interference and are formed by the activity of Msh4/Msh5, but Class II COs formed by the activity of Mus81, Yen1 or Slx1-Slx4 do not (Novak *et al.*, 2001; de los Santos, 2003).

It has been shown by whole-genome mapping of recombination products in eight *tel1Δ* hybrid tetrads that Tel1 has a role in CO interference, specifically by limiting ZMM-independent recombination, i.e. Tel1 reduces the number of Class II COs but does not affect the number of Class I COs (Anderson *et al.*, 2015). This study also found that *tel1Δ* increases recombination levels for both COs and NCOs, correlating with the increased levels of DSB formation shown by Garcia *et al.* (2015), and that the distribution of all detectable recombination events was altered in *tel1Δ*, supporting a role for Tel1 in DSB interference (Anderson *et al.*, 2015).

However, Anderson *et al.* (2015) used MMR proficient strains, which greatly reduces the number of NCOs that can be detected as well as the amount of information about e.g. length, complexity that can be gathered for each event (Martini *et al.*, 2011). In addition, during classification of recombination products, pattern changes within 5kb of each other were considered to be part of the same event. This limit was based on previous analysis by the authors of wild-type tetrads showing that events occurring 5 kb have properties that suggest they originated from a single DSB (Anderson *et al.*, 2011). However, by careful examination of hDNA tracts associated with recombination in MMR-deficient backgrounds, others have found that many events incompatible with a 1-DSB scenario occur closer than 5kb, and thus recommend a 1.5kb merging limit (Bertrand Llorente & Marie-Claude Marsolier, personal communication). In addition, a 5kb limit may mask the detection of event clustering at short range, such as that described by Garcia *et al.* (2015). In order to view close-range recombination event formation in higher resolution, and to enable detection of more events in greater detail, it is worthwhile to repeat event analysis in a *tel1* deletion strain, with MMR deficiency and a 1.5kb event merging threshold.

6.1.4. Aims of this investigation

1. To map recombination events in MMR-deficient *tel1Δ* octads via deep sequencing and marker analysis.
2. To observe the effects of *tel1Δ* on recombination event quantity and quality.
3. To determine whether CO and DSB interference are altered in *tel1Δ*.

6.2. Results

6.2.1. Tel1 deletion increases numbers of detected recombination events in hybrids

To observe the effect of *tel1Δ* on meiotic recombination, nine *msh2Δ* and ten *tel1Δ msh2Δ* hybrid SK1xS288c octads were produced. The deletion of MMR protein Msh2 from a *tel1Δ* hybrid reduces spore viability only slightly from ~69% to ~63% (Chapter 3, Figure 3.8), making this strain background an excellent candidate for octad analysis. The individual spores were sequenced and the data analyzed as detailed in Chapter 4. Raw data is available in the appendix (Table S2).

To observe the effect of *tel1Δ* on the numbers of recombination events detected, CO and NCO numbers were compared across *tel1Δmsh2Δ* and *msh2Δ* backgrounds (Figure 6.1A; Table 6.1). Upon the loss of Tel1, CO numbers experienced a slight increase from ~105 to ~115 (~1.1x) while NCO events had a more dramatic increase from ~102 to ~141 (~1.4x). This agrees with the observation of increased DSB levels from Garcia *et al.* (2015). Additionally, in the MMR-proficient tetrads analyzed by Anderson *et al.* (2015), *tel1Δ* caused an increase in CO numbers from ~98 in WT to ~115 (~1.15x), and NCO numbers from ~35 in WT to ~58 (~1.8x). Thus detected CO numbers are very similar between MMR-proficient and -deficient strains, but many more NCOs are detected when MMR is not functioning.

An average of 52 NCOs detected in a *msh2Δ* background and 64 NCOs in a *tel1Δ msh2Δ* background were composed only of hDNA (Table 6.1). If hDNA tracts are equally likely to be repaired as restoration or conversion, then 50% of these events would be visible in a MMR-proficient background. However, the disparity in NCO counts between the MMR deficient strains described here and the MMR-proficient strains from Anderson *et al.* is too high to be explained purely in terms of invisible hDNA. This is probably because MMR proficiency reduces the number of events repaired with the homologous chromosome in a hybrid background, due to rejection of mismatches during strand invasion (Goldfarb & Lichten, 2010). This may also explain why the increase in NCO levels in *tel1Δ* is not proportional between the two backgrounds, with a 38% increase in NCO number in the MMR-deficient strain and a 60% increase in the MMR-proficient strain.

In addition, *tel1Δ* alters the ratio of CO:NCO formation from almost 1:1 in *msh2Δ* to 1:1.4 in *tel1Δ msh2Δ*, indicating that Tel1 may have a role in dictating repair pathway choice, or that there is a maximum limit on CO formation under homeostatic control (Martini *et al*., 2006). This suggests that the excess DSB formed in a *tel1Δ* background (Garcia *et al*., 2015) may be more likely to be repaired as NCOs than COs.

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The number of NCOs is likely to be an underestimate caused by events occurring in regions without markers (Mancera *et al.*, 2008). The percentage of observed COs that occur between markers and thus have no detectable conversion tract can be used to estimate the number of NCOs that may be invisible due to falling between markers (assuming that NCO and CO events are of similar lengths; NCOs are generally shorter (Section 6.2.5), so these numbers are likely underestimates). An average of 15% COs in *msh2Δ* and 18% in *tel1Δ msh2Δ* had no associated conversion tracts (Table 6.1). Based on this, an additional 15 and 25 NCOs are predicted to have occurred in regions without markers, in *msh2Δ* and *tel1Δ msh2Δ* respectively.

Table 6.1. Data summary for recombination events detected in *msh2Δ and tel1Δ msh2Δ* backgrounds.

Separate samples for each genotype are shown. OM: *msh2Δ* octad, OMT: *tel1Δ msh2Δ* octad. Columns contain the number of COs, NCOs and Undetermined (U) events detected, the overall number of events, the number of chromosomes without COs (CWCs), the identity of the CWCs, the number of double COs closer than 1.5kb (dCOs), the number of events containing an 8:0/0:8 or 7:1/1:7 segment, the number of COs without a detectable conversion tract, and the number of NCOs that were composed only of hDNA.

Meiosis	CO	NCO	U	Total	CO:NCO	CWC frequency	CWC identity	dCO number	8:0	7:1	COs without tracts	NCOs hDNA only
msh2Δ												
Average	**105.0±3**	**101.8±8**	**0**	**206.8±7**	**1:0.98**			**0.2**	**0.1**	**0.4**	**14.7**	**52.1**
OM1	116	109	0	225	1:0.94	0	-	0	0	0	13	45
OM2	100	125	0	225	1:1.25	0	-	0	0	0	8	69
OM3	95	100	0	195	1:1.05	0	-	0	0	0	18	50
OM4	105	98	0	203	1:0.93	0	-	1	0	1	11	50
OM5	98	79	0	177	1:0.81	0	-	0	0	0	19	41
OM6	116	65	0	181	1:0.56	0	-	1	1	0	22	37
OM7	98	139	0	237	1:1.42	0	-	0	0	1	11	70
OM8	107	113	0	220	1:1.06	0	-	0	0	2	21	62
OM9	110	88	0	198	1:0.80	0	-	0	0	0	10	45
tel1Δ msh2Δ												
Average	**115.3±3**	**140.7±10**	**1.1**	**257.1±12**	**1:1.22**			**1.3**	**0.8**	**4.4**	**15.9**	**64.1**
OMT1	136	188	6	330	1:1.38	0	-	4	1	7	23	101
OMT2	118	92	2	212	1:0.78	0	-	1	0	2	26	48
OMT3	104	113	0	217	1:1.09	0	-	0	0	2	14	50
OMT4	112	168	1	281	1:1.50	0	-	0	0	3	14	77
OMT5	128	145	0	273	1:1.13	0	-	3	1	7	20	54
OMT6	110	143	1	254	1:1.30	0	-	1	0	3	14	76
OMT7	106	130	0	236	1:1.23	0	-	0	1	4	13	68
OMT8	110	107	0	217	1:0.97	0	-	1	1	2	12	47
OMT9	122	157	0	279	1:1.29	0	-	2	2	4	12	52
OMT10	107	164	1	272	1:1.53	0	-	1	2	10	11	68
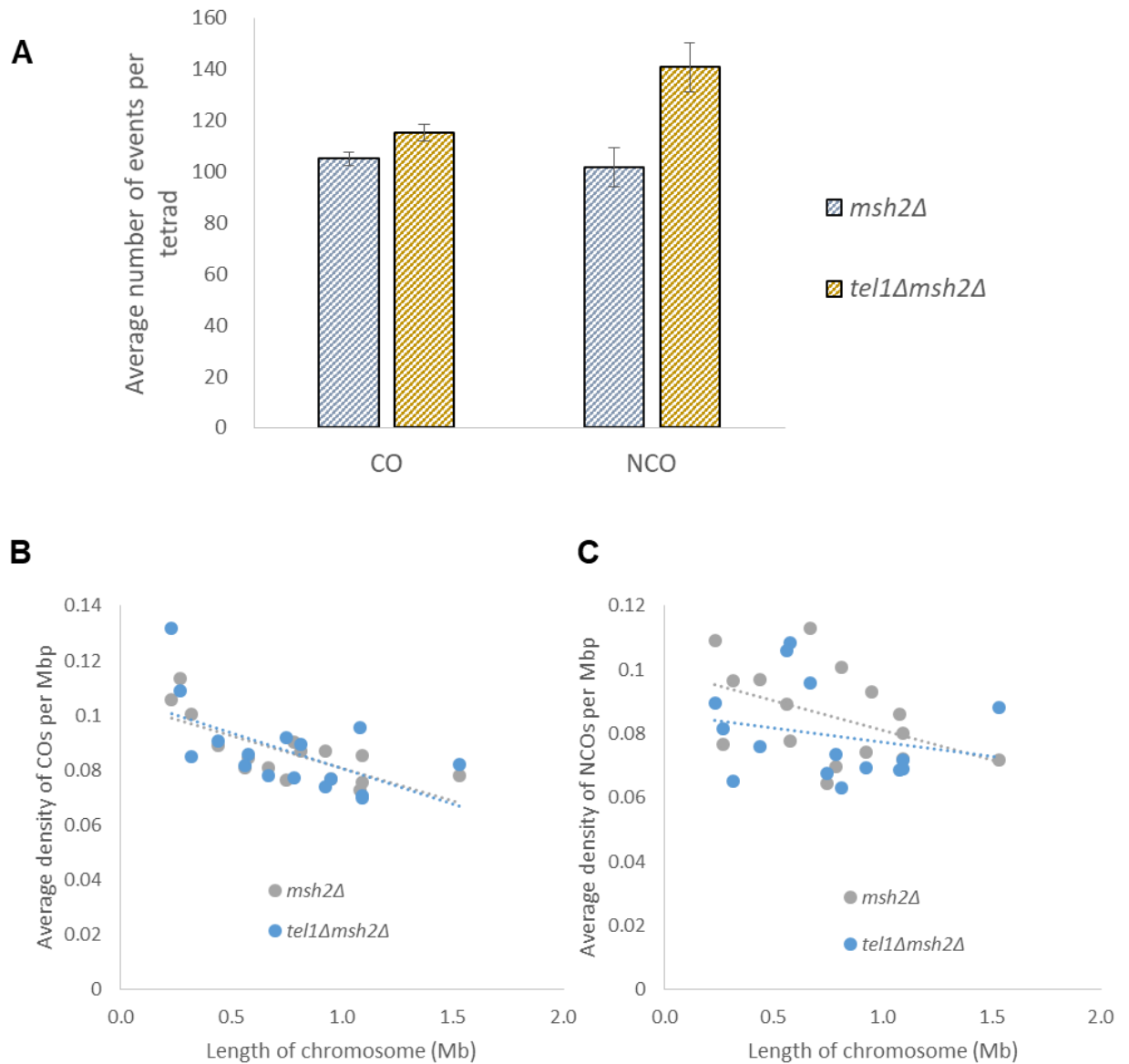
Figure 6.1. Quantity of recombination events detected in *msh2Δ* and *tel1Δ msh2Δ* strains.
Strain details are given in Table 2.1, raw event data is available in Table S2. **A**) Average
number of CO and NCO events. Error bars are 95% confidence limits. **B**) Density of COs and **C**.
NCOs per Mbp. The average number of CO/NCO events per chromosome is divided by the
average total CO/NCO count, then divided by the chromosome length in Mbp. Dotted lines are
linear regressions. R^2: *msh2Δ* CO 0.54, NCO 0.20; *tel1Δ msh2Δ* CO 0.35, NCO 0.05.

6.2.2. Relationship between chromosome length and recombination

In WT and *msh2Δ* meiosis, there is a negative correlation between chromosome length and the density of DSB formation, dependent on Zip3 (Thacker *et al.*, 2014; Chapter 5, Section 5.2.2). To see if this is affected by *tel1Δ*, the relationship between chromosome length and fraction of all detected COs or NCOs that occurred on that chromosome was examined in *tel1Δ msh2Δ* (Figure 6.1B&C). In *msh2Δ* and *tel1Δ msh2Δ*, there is a negative correlation between chromosome length and CO and NCO density, suggesting that *tel1Δ* does not affect this relationship. In addition, there were no chromosomes without at least one CO in every *msh2Δ* and *tel1Δ msh2Δ* octad tested, suggesting that there is no defect in crossover assurance.

6.2.3. Tel1 affects the complexity of detected recombination events

Recombination events in each strain were categorized further as described in Section 4.2.10 (Table 6.2 and Figure 6.2A,B). Similar analysis was performed on *tel1Δ* tetrads by Anderson *et al.* (2015), but events could not be categorized in as much detail in their analysis due to the inability to detect hDNA tracts. Due to this, proportions of events in each category cannot be directly compared between these studies.

Compared to *msh2Δ* cells, *tel1Δ msh2Δ* cells have a lower proportion of events classified into CO Group 3 (~21% and ~17% respectively) and NCO Group 2 (~25% and ~16% respectively), both of which contain events with patterns indicative of complex repair (Figure 6.2 A,B). CO Group 3 is composed of COs associated with hDNA patterns that suggest of the occurrence of another DSB, but constrained to the same chromatids as the CO, and so the second DSB is considered to be a consequence of complex repair e.g. multiple strand invasions (as detailed in Chapter 4 Section 4.2.11). NCO Group 2 is composed of NCOs containing trans hDNA patterns on the same chromatid, which are thought to be formed by double SDSA (Martini *et al.*, 2011).

Another difference between *msh2Δ* and *tel1Δ msh2Δ* was in the proportion of recombination events in Group 0. This group contains events with signatures suggesting that they are composed of multiple separate Spo11-DSBs, including NCOs on 2 sister chromatids or 2 non-sister chromatids with a 4:4 segment, and COs or NCOs affecting three or four chromatids. A significantly higher proportion of all individual detected COs (~13% and ~6% respectively) and NCOs (~18 and ~11% respectively) are involved in an event cluster in *tel1Δ msh2Δ* compared to *msh2Δ* (Figure 6.2A, B). Thus, while *tel1Δ* reduces the proportion of events that have signatures of complex repair, there is an increase in events with signatures indicative of multiple DSBs.

Table 6.2. Data summary of the percentage of CO and NCO events in each group and class, detected in *msh2Δ and tel1Δ msh2Δ* backgrounds. A short description of the characteristics of each group and class is given.

Crossover Groups			msh2Δ	tel1Δ msh2Δ
Group 1: Simple - no trans hDNA or incompatible hDNA			%	%
Total			58.21	56.73
Class 1	(5:3)_(4:4aCO) - CO with hDNA tract		4.76	4.51
Class 2	(3:5)_(4:4aCO) - CO with hDNA tract		4.76	4.60
Class 3	(5:3)_(4:4)_(4:4aCO) - hDNA, restoration tract, CO pattern		0.85	0.61
Class 4	(4:4aCO)_(5:3)_(4:4a) - Same as above but in opposite direction.		0.63	0.43
Class 5	(3:5)_(4:4)_(4:4aCO) - hDNA, restoration tract, CO pattern		0.21	1.04
Class 6	(4:4aCO)_(3:5)_(4:4a) - Same as above but in opposite direction.		0.85	0.26
Class 7	(5:3)_(6:2)_(4:4aCO) - hDNA, conversion tract, CO pattern		1.59	1.91
Class 8	(6:2)_(5:3)_(4:4aCO) - Same as above but in opposite direction.		1.80	1.65
Class 9	(3:5)_(2:6)_(4:4aCO) - hDNA, conversion tract, CO pattern		1.80	2.25
Class 10	(2:6)_(3:5)_(4:4aCO) - Same as above but in opposite direction.		2.12	1.91
Class 11	Contains 4:4i (symmetrical hDNA)		1.59	2.17
Class 12	Anything else		10.90	9.37
Class 15	(6:2)_(4:4aCO) - CO with conversion tract		5.93	6.68
Class 16	(2:6)_(4:4aCO) - CO with conversion tract		6.35	5.55
Class 100	4:4aCO: CO in marker-sparse region		14.07	13.79
Group 2: Presence of trans hDNA, but not incompatible hDNA				
Total			14.29	12.92
Class 30	adjacent 5:3 5:3a, plus any other segments		2.86	2.25
Class 31	adjacent 3:5 3:5a, plus any other segments		3.60	3.04
Class 32	non-adjacent trans hDNA i.e. have conversion or restoration tract in between		7.83	7.63
Group 3: Presence of incompatible hDNA				
Total			21.37	17.00
Class 20	Contains 4:4i (symmetrical hDNA)		19.15	14.31
Class 21	Anything else		2.22	2.69
Group 0: Multiple Spo11-DSBs: Affects 3 or 4 chromatids				
Total			6.14	13.35
Class 2	CO ± NCO involving 3 or 4 chromatids		5.40	10.49
Class 3	CO ± NCO involving 3 or 4 chromatids, contains different 4:4 patterns		0.74	2.86
Noncrossover Groups			msh2Δ	tel1Δ msh2Δ
Group 1: SDSA-like: Affects one chromatid, no trans hDNA			%	%
Total			55.99	58.78
Class 1	5:3 - composed of hDNA only		19.10	19.55
Class 2	3:5 - composed of hDNA only		21.29	19.97
Class 3	5:3_6:2_5:3 or 5:3_4:4_5:3 - Conversion/restoration tract between hDNA		2.40	2.13
Class 4	3:5_6:2_3:5 or 3:5_4:4_3:5 - Conversion/restoration tract between hDNA		2.07	2.35
Class 7	6:2 plus any other segments		2.73	3.62
Class 8	2:6 plus any other segments		3.38	3.84
Class 10	6:2 - composed of conversion tract only		2.73	3.13
Class 10.1	2:6 - composed of conversion tract only		2.29	4.19
Group 2: dHJ-dissolution-like: Affects one chromatid, has trans hDNA				
Total			24.67	15.85
Class 11	5:3_5:3a - two 5:3 patterns on different strands		4.91	2.27
Class 12	3:5_3:5a - two 3:5 patterns on different strands		3.82	2.77
Class 13	5:3_5:3a plus other segments NOT in the middle of the trans hDNA		1.31	1.21
Class 14	3:5_3:5a plus other segments NOT in the middle of the trans hDNA		1.86	0.71
Class 15	5:3_4:4_5:3a - restoration tract in the middle of trans hDNA		3.49	2.70
Class 16	3:5_4:4_3:5a - restoration tract in the middle of trans hDNA		3.93	2.06
Class 17	5:3_4:4_5:3a plus other segments NOT in the middle of the trans hDNA		1.53	1.21
Class 18	3:5_4:4_3:5a plus other segments NOT in the middle of the trans hDNA		0.98	0.71
Class 19	5:3_6:2_5:3a - conversion tract in the middle of trans hDNA		0.87	0.43
Class 20	3:5_2:6_3:5a - conversion tract in the middle of trans hDNA		0.87	0.36
Class 21	5:3_6:2_5:3a plus other segments NOT in the middle of the trans hDNA		0.44	0.14
Class 22	3:5_2:6_3:5a plus other segments NOT in the middle of the trans hDNA		0.22	0.28
Class 23	Anything else		0.44	1.00
Group 3: Affects two non-sister chromatids				
Total			7.97	6.89
Class 30	Contains 4:4i (symmetrical heteroduplex)		4.69	4.05
Class 31	Anything else		3.28	2.84
Group 0: Multiple Spo11-DSBs: Affects two sister, 3 or 4 chromatids				
Total			11.35	18.48
Class 1	NCO involving 2_sis, 3 or 4 chromatids		2.40	7.68
Class 2	NCO+CO involving 3 or 4 chromatids		5.13	7.32
Class 3	NCO±CO involving 3 or 4 chromatids, contains different 4:4 patterns		3.82	3.48
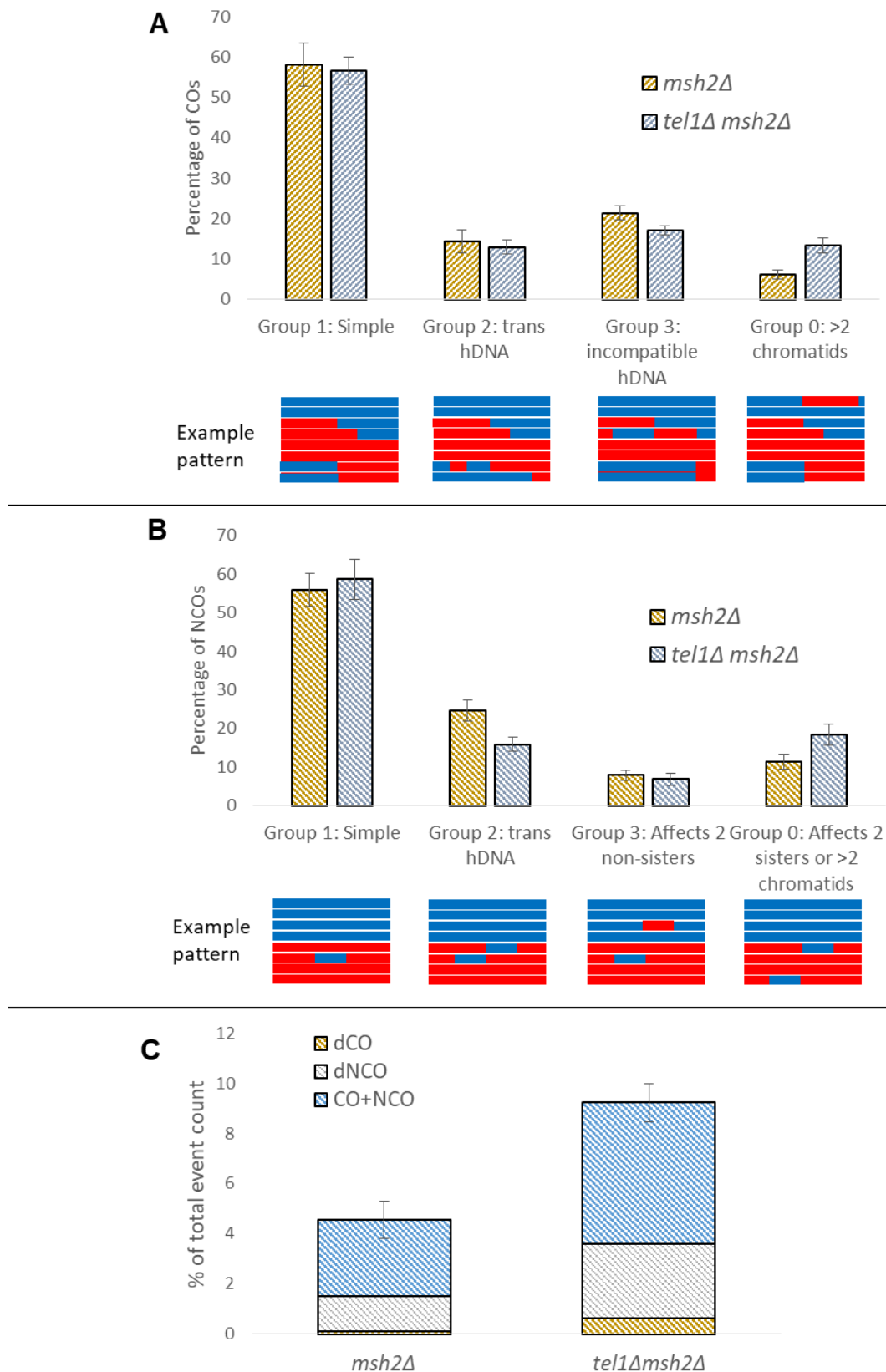
Figure 6.2. Categories of recombination events detected in *msh2Δ* and *tel1Δ msh2Δ* strains. Error bars are 95% confidence limits. Strain details are given in Table 2.1, raw event data is available in Table S2. A simple example event for each category is shown directly beneath the X-axis, with the red and blue lines corresponding to the eight strands of DNA present during meiotic recombination, four from each parent. **A)** Average percentage of COs and **B)** NCOs in each group. **C)** Comparison of the average percentage of events thought to be DSB clusters (overall Group 0), with sublevels indicating whether the clusters were inferred to be a double CO, double NCO or CO plus NCO.

In addition, the proportion of all recombination events classified into Group 0 (equivalent to the number of suspected DSB clusters) was compared between *msh2Δ* and *tel1Δ msh2Δ* strains (Figure 6.2C). (This differs from looking at the proportion of COs or NCOs in Group 0 as in Figure 6.2A&B, in that each cluster contains two events each of which are not counted separately in Figure 6.2C). The percentage of all detected recombination events that were classified as being a DSB cluster is 4.6% in *msh2Δ* and 9.2% in *tel1Δ msh2Δ*. A cluster of two DSBs can resolve into a double CO, CO + NCO or double NCO event; this categorization is done manually (Section 4.2.11). Within those clusters, the proportion of different cluster types (double CO, CO + NCO or double NCO) were roughly equal in each strain, with the majority of clusters being composed of a CO and a NCO for both strains (Figure 6.2C).

In analysis by Anderson *et al.* (2015), complex events accounted for ~14% of all events in WT, and ~22% in *tel1Δ*. These higher values are likely due to the fact that Anderson *et al.* (2015) used an event merging threshold of 5kb, compared to the 1.5kb used in this study. A lower merging threshold has a different advantage for event cluster analysis, in that any clusters that would be detected with a 5kb threshold can be resolved down further so that more detail can be revealed about the component events and the distance between them, allowing interference interactions over short distances to be analysed (Section 5.2.7). With a threshold of 1.5kb (as used here), any remaining clusters are those with events so close that they cannot be disentangled computationally at any reasonable threshold, and so can only be manually categorized.

Of particular interest are double CO clusters (defined as a double reciprocal exchange involving all four chromatids within 1.5kb). Among the nine octads tested, there were two dCOs in *msh2Δ*; in *tel1Δ msh2Δ*, there were fourteen detected among ten octads (Table 6.1). The number of double crossovers is significantly higher in *tel1Δ msh2Δ* than in *msh2Δ* (T-test, P=0.0454). It is expected that dCO events should be a rare occurrence under conditions of crossover interference, suggesting a loss of CO interference in *tel1Δ*. Examples of dCO events observed in *tel1Δ msh2Δ* octads are shown in Figure 6.3. As described in Section 4.2.11, the composition of an event cluster can be ambiguous. In such cases, the outcome with fewer COs is favoured; e.g. an event that could conceivably be a double CO or a CO + NCO, will be categorized as the latter. However, it is possible that some CO + NCO and double NCO clusters could be double CO events. The number of definite, four-chromatid dCOs is an indicator of how many three- and two-chromatid dCOs there may be. The true number of dCOs should be four times as high, if it is assumed that double DSBs are equally likely to be resolved as COs regardless of which chromosomes they occur on and that COs are equally distributed among the four chromatids (in terms of both initiating DSB and repair donor). Under these circumstances, ¼ of double COs would involve all four chromatids, ½ would involve 3 chromatids (indistinguishable from 1 CO + 1 NCO) and ¼

would involve two chromatids (indistinguishable from double NCO). This means that the number of dCOs reported here is likely an underestimate, and some CO+NCO or NCO+NCO clusters may actually be dCOs, giving revised estimates of eight dCOs in nine *msh2Δ* octads and 56 in ten *tel1Δmsh2Δ* octads.
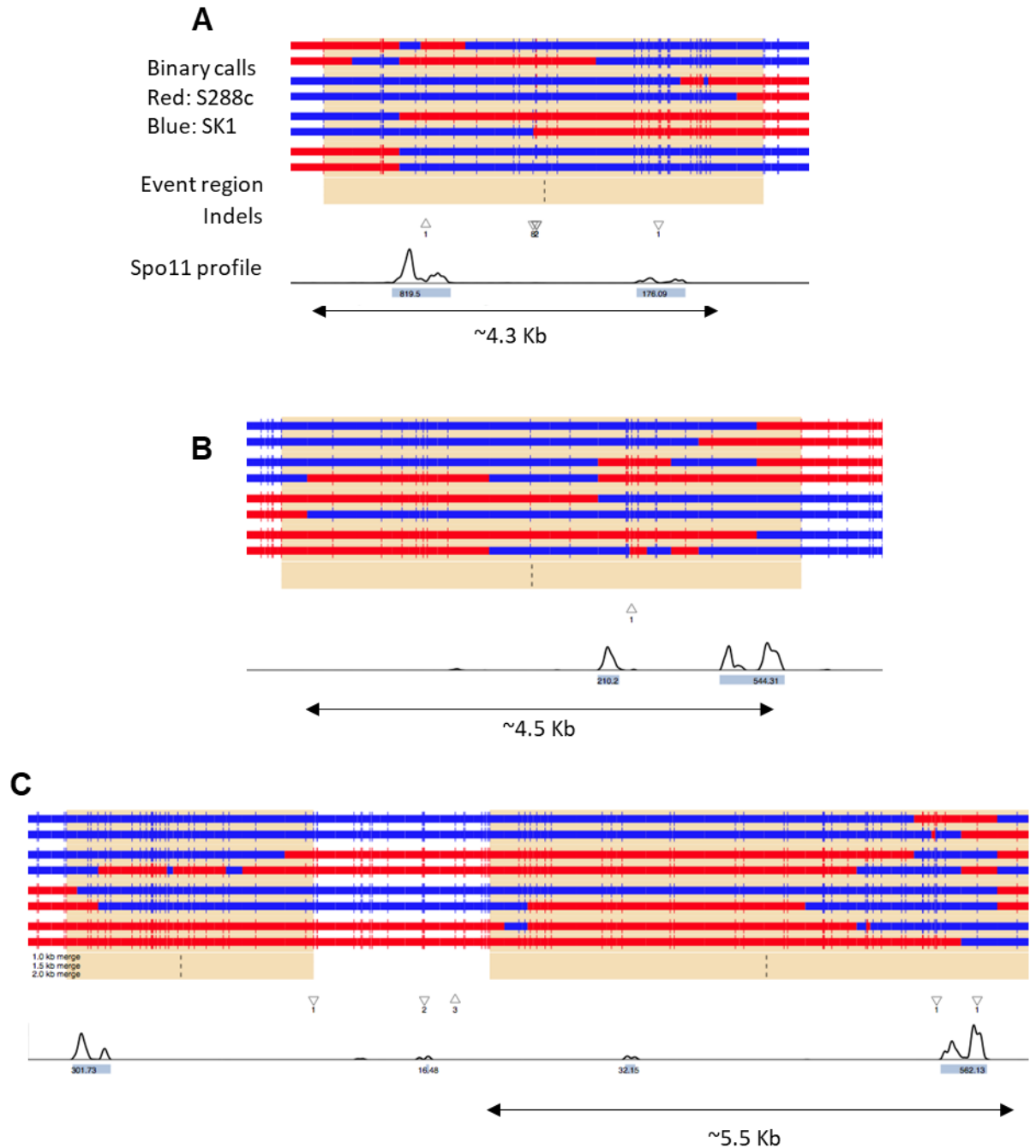
Figure 6.3. Examples of four-chromatid double COs detected in *tel1Δ msh2Δ* strains.
Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan et al., 2011). **A)** and **B)**, examples of double COs, determined by the fact that a double reciprocal exchange occurs between all four chromatids. In **C)** another CO occurs to the left of the double CO, though outside the 1.5kb merging threshold.

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Another specific category of events within Group 0 are events containing a 4:0 or 8:0/7:1 segregation of markers, which is a strong indication of multiple DSB events. Out of nine *msh2Δ* octads, one event contained an 8:0 segment and four contained 7:1 segments (Table 6.1). In contrast, ten *tel1Δ msh2Δ* octads contained a total of nine events with an 8:0 segment (examples shown in Figure 6.4), and 44 events with a 7:1 segment. When only counting events containing an 8:0 if they are associated with at least one other different segment, a significantly higher number of events with an 8:0 or 7:1 segment are seen in *tel1Δ msh2Δ* than in *msh2Δ* (T-test, P=0.001 [Methods 2.21]). This is suggestive of a loss of *trans* DSB interference in *tel1Δ*, as these patterns may be produced by the formation of two DSBs on different chromatids at the same position.

In MMR-proficient tetrads, segments of 7:1 segregation are not visible, but analysis of events containing 4:0 tracts is included in Anderson *et al*. (2015). However, these events are discounted as being caused by pre-meiotic recombination, because the majority of 4:0 tracts detected in WT and *tel1Δ* tetrads had perfect overlap, meaning that the two gene conversion tracts begin or end at the same markers on the different chromatids (Anderson *et al*., 2015). The authors suggest that this indicates an increase in premeiotic recombination in *tel1Δ,* which are then replicated in premeiotic S phase. However, in data from octads presented here, the single 8:0 event detected from the *msh2Δ* octads did not have perfect overlap, and in 9 events containing an 8:0 segment from *tel1Δ msh2Δ* octads, only one had perfect overlap. Overall, there were no mitotic-like 8:0 events in *msh2Δ* octads, and ~10% of 8:0 events were mitotic-like in *tel1Δ msh2Δ* octads, different to the situation observed in MMR-proficient tetrads. The reason why fewer premeiotic-like events were detected in octad samples may be due to a difference in the sporulation protocol, as the amount of time mated haploids are allowed to spend propagating as a diploid may influence the amount of premeiotic recombination seen. Alternatively, the ability to view hDNA tracts in octads may mean that some events that could have become apparent 8:0s due to genotype conversion during NCO repair instead became other patterns such as 7:1 or symmetrical hDNA. In an MMR-deficient background, the ability to observe a greater variety of pattern changes via hDNA analysis means that 4:0 events can be categorized as meiotic or mitotic with more certainty.

Another potential group of DSB cluster events are events containing a conversion tract (6:2 or 2:6). This is discussed in the following section.
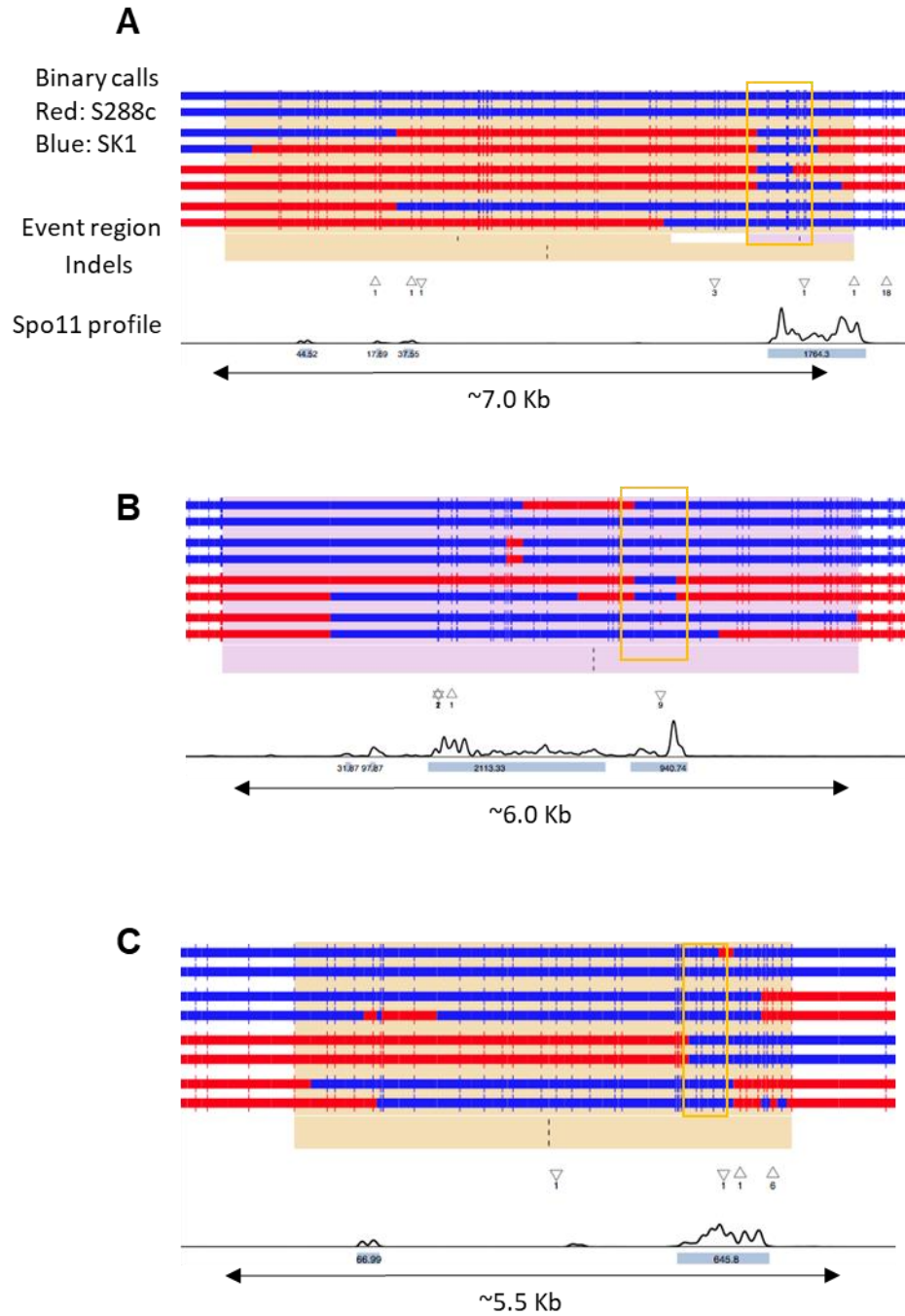
Figure 6.4. Examples of different event types containing 8:0 segments detected in *tel1Δ msh2Δ* strains. Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan et al., 2011). The yellow box highlights the 8:0 segment. **A)** A CO and NCO cluster, determined by the occurrence of one overall reciprocal exchange. **B)** An NCO cluster, determined by the absence of an overall reciprocal exchange. **C)** A double CO cluster, determined by the double reciprocal exchange involving all four chromatids.

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6.2.4. 6:2/2:6 conversion tracts observed in MMR-deficient recombination may represent DSB clusters

In MMR-deficient backgrounds, conversion tracts are not expected to arise because they are thought to be a result of mismatch repair only (Martini *et al.*, 2011). However, around 19% of CO and NCO events in *msh2Δ* octads contain segments with 6:2 or 2:6 segregation patterns, hereafter referred to as 'conversion segments' (examples shown in Figure 6.5). Conversion segments could occur alone or as part of other segregation pattern changes within an event. It is likely that these conversion segments result from the repair of gaps, which could arise from 1) two close Spo11-DSBs on the same chromatid or 2) from the removal of a 3' end after invasion of a homologous sequence, e.g. the formation of a nick during topological processing of a dHJ (Chapter 4, Figure 4.9 D, H and Figure 4.10 E, H). In such ambiguous cases, the scenario involving fewer DSBs is chosen for the purpose of the categorization. Thus, events containing 6:2 segments are not automatically categorized as DSB clusters in the current pipeline (Section 4.2.11), but an increase in such events could still be suggestive of adjacent DSB formation.

Interestingly, the possibility that a significant number of recombination events may be initiated by the formation of a gap is reminiscent of the model of meiotic recombination proposed by Szostak *et al.* (1983), which proposed that recombination events are initiated by DSBs which are enlarged into double-strand gaps by exonuclease action. Such ideas were based on observations of 6:2 segregation in fungi and efficient repair of restriction enzyme induced gaps on a plasmid.

In addition, segments of 8:0 segregation can be considered to be two overlapping conversion tracts, meaning that these could also be produced by concerted DSB formation, although there would have to be four Spo11-DSBs arising on a pair of sister chromatids. As mentioned in Section 6.2.3, segments of 8:0 segregation are increased in *tel1Δ msh2Δ* compared to *msh2Δ*.

Concerted DSB formation has been observed in both WT and *tel1Δ* strains, supporting the possibility that many recombination events are initiated by a double DSB (Garcia *et al.*, 2015; Dominic Johnson, personal communication). Concerted DSB formation has been suggested to occur within a single chromatin loop domain that has been primed for DSB formation (Garcia *et al.*, 2015).

Analysis of conversion segments can only be done in MMR-deficient backgrounds because MMR activity produces many 6:2/2:6 signatures which will obscure any conversion tracts produced by multiple DSBs (Chapter 4, Figure 4.9 I, 4.10 I).
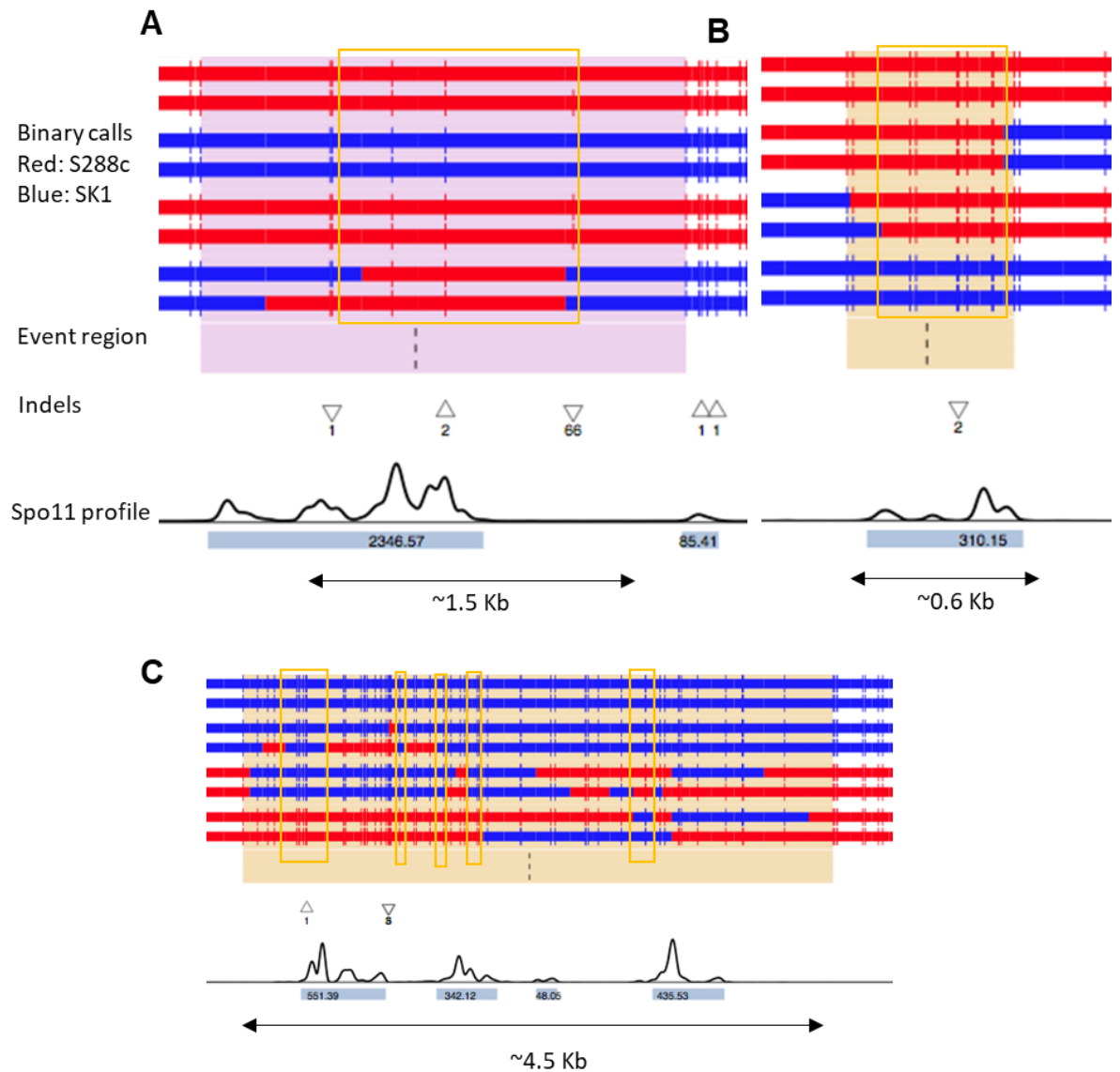
Figure 6.5. Examples of different event types containing 6:2 segments detected in *tel1Δ msh2Δ* strains.

Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan *et al*., 2011). The yellow box highlights the 6:2 segment. **A)** An NCO containing a 6:2 segment. **B)** A CO containing a 6:2 segment. **D)** A CO and NCO cluster containing numerous small 6:2 patches.

To investigate this phenomenon in more detail, the occurrence of events containing a conversion segment was examined in *msh2Δ* and *tel1Δ msh2Δ* hybrids (Figure 6.6A). On average, *msh2Δ* octads contained ~80 events (39% of all events) that have at least one conversion segment, while *tel1Δ msh2Δ* octads had ~107 (42% of all events). In both backgrounds, conversion segments were more frequently observed as part of CO events than NCO events (Figure 6.6B). In *msh2Δ*, 52.4% of all COs and 23.6% of all NCOs contained a conversion segment, while in *tel1Δ msh2Δ*, 57.2% of all COs and 29.1% of all NCOs contained a conversion segment.

As previously mentioned, conversion segments could be produced by concerted DSBs or by nicking during repair. Because the occurrence of multiple DSBs in proximity is expected to be relatively rare, events containing multiple separate conversion segments may be more likely to be caused by nicking during repair (e.g. Figure 6.5C) (as they would otherwise necessitate the formation of two close DSBs per segment). By contrast, events containing a single conversion segment may be more likely to be caused by concerted DSB formation (e.g. Figure 6.5A,B).

The number of conversion segments that occurred as part of an event that contained either a single or multiple conversion segments was compared in *msh2Δ* and *tel1Δ msh2Δ* (Figure 6.6 C). For both strains, the majority (~66-68%) of conversion segments occurred as part of an event containing only one conversion segment.

If single-conversion segment events are produced by concerted DSBs, they may be expected to occur in strong Spo11 hotspots, or spanning multiple hotspots. If multiple-conversion segment events are produced by nicking, they may be expected to be shorter in length, because the nicking enzyme should cause relatively little degradation, and few markers will be converted during repair of the single strand break.

Using Spo11 location data from Pan *et al.* (2011), the observed and expected values of Spo11 hits for a conversion segment region can be calculated. The number of Spo11 hits for each genomic position is normalized by dividing by the total number of Spo11 hits and multiplying by the number of reads, to obtain Spo11 hits per million reads (HpM). For each segment, the maximum possible coordinates are taken (i.e. the position before the next marker with a different segregation pattern), and Spo11 HpM is summed for that region. The expected value is obtained by multiplying the genomic average number of hits per bp by the maximum length of the conversion segment. The DSB landscape is known to be altered across large chromosomal domains in *tel1Δ* during early meiosis, but at sub-kb size scales, Spo11-oligos tend to map to hotspots similar to WT in location and width (Mohibullah & Keeney, 2017).

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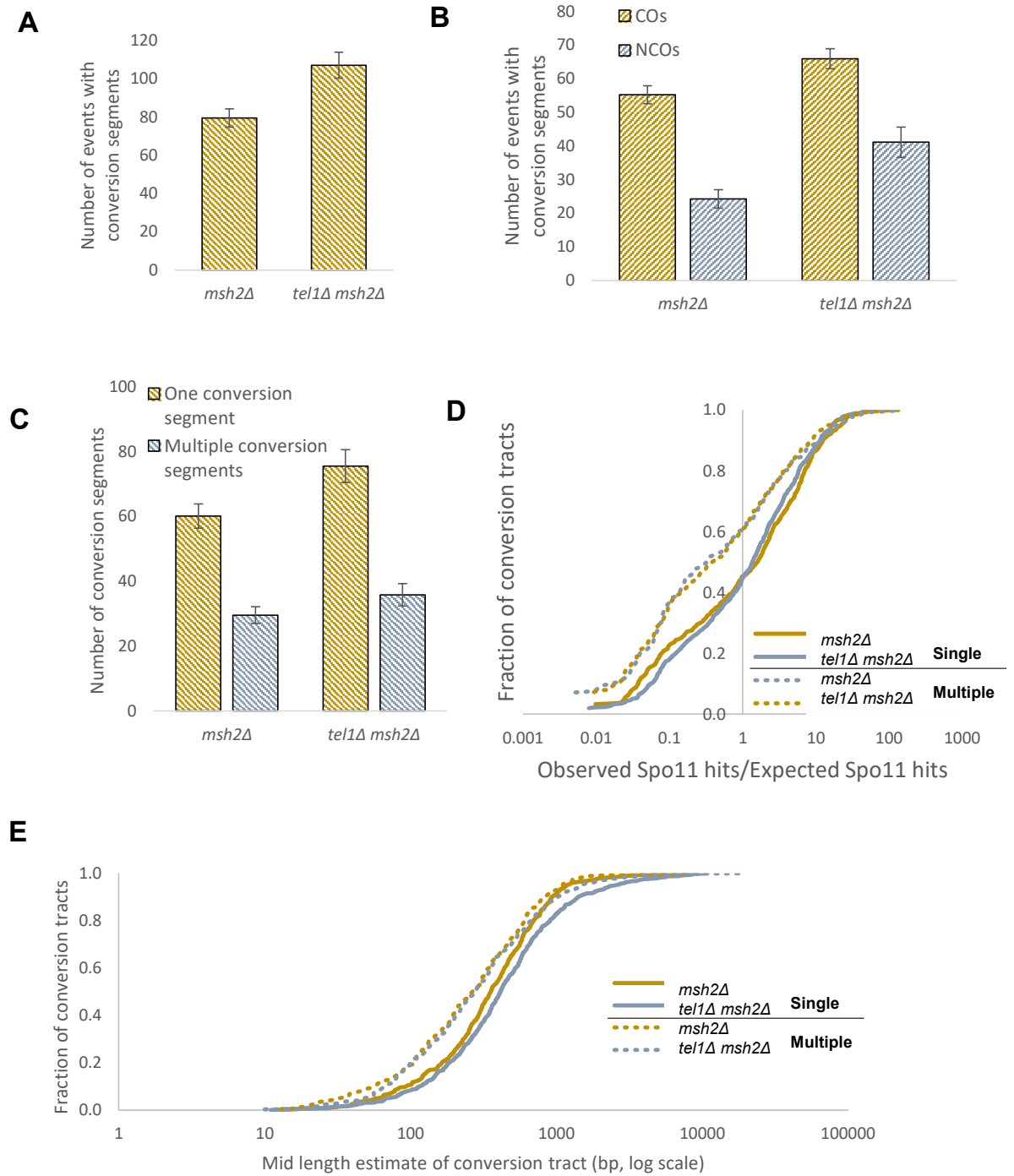
Figure 6.6. Comparison of conversion segment features detected in *msh2Δ* and *tel1Δ msh2Δ* strains. A) Average number of events containing at least one conversion segment. **B**) Average number of CO and NCO events containing at least one conversion segment. **C**) Average number of conversion segments that are part of an event with a single conversion segment, or with multiple conversion segments. **D**) Cumulative fraction of events with single or multiple conversion segments with an increasing observed Spo11 hits/expected Spo11 hits ratio. **E**) Cumulative fraction of events with single or multiple conversion segments with an increasing mid length estimate.

To determine whether there is evidence supporting the idea that events containing multiple conversion segments are not produced by multiple Spo11-DSBs, the relationship between conversion segment length and DSB frequency was examined. The mid length estimate and the ratio of the observed and expected numbers of Spo11 HpM was calculated for each segment, and plotted separately for segments occurring in events with single or multiple conversion segments (Figure 6.6D&E).

For both *msh2Δ* and *tel1Δ msh2Δ*, conversion segments that occur as part of events with multiple conversion segments are shorter than those occurring in events with a single conversion segment. In addition, conversion segments from events containing only one conversion segment are more likely to have a higher than expected number of Spo11 hits in the vicinity; for single conversion segments, 40% of segments have an observed/expected ratio <1, while 60% of multiple-segment-event conversion segments have an observed/expected ratio of <1.

These results suggest that there is some evidence that there are two groups of conversion-tracts: 1), those that occur in hotter regions, have longer lengths and occur in isolation, and 2), those that occur in colder regions, have shorter lengths and occur in multiples. The two groups are predicted to generally correspond to the local formation of multiple Spo11-DSBs on the same chromatid and 3' nicking during repair, respectively (although there is likely some crossover between the two). The reasoning for this is that events in hotter regions are thought to be more likely to have multiple DSBs, while those in colder regions are predicted to have fewer DSBs; events with multiple conversion segments are less likely to be produced by multiple DSBs because each additional conversion segment would require the formation of another two Spo11-DSBs, which should be limited by DSB interference; and enzymatic nicking is expected to produce shorter conversion segments due to causing little degradation of DNA.

However, there is no particular difference in the formation of either group between *msh2Δ* and *tel1Δ msh2Δ*; this is counter to observations from Garcia *et al.* (2014) that indicate that concerted DSB formation is increased in *tel1Δ*. This may be due to the fact that conversion segments occurring within complex (Group 0) events are not included in this analysis, because conversion segments can be 'interrupted' by pattern changes on different chromatids. Complex events are thought to be produced by DSB clusters (although not necessarily occurring on the same chromatid), and are increased in *tel1Δ msh2Δ* (Section 6.2.3).

6.2.5. Recombination event length is altered in *tel1Δ*

The length of recombination event tracts could be indicative of the extent of D-loop/dHJ migration and/or resection (Chapter 4, Figure 4.9/4.10), as longer resection or migration distances are predicted to correspond to longer tracts of marker changes. The length of recombination events is also an indicator of event complexity, because apparent long events can be produced by two separate events occuring nearby and overlapping. Using marker changes to detect recombination events means that the exact start and end of an event cannot be pinpointed, only the locations of the two markers flanking a genotype change at each end of the event. Thus, event length can be reported as the maximum (the difference in the coordinates between the two outer flanking markers), the minimum (the different between the inner flanking markers), or the mid length, which is the difference between the midpoints between the two sets of flanking markers (Chapter 5, Figure 5.3A). Generally, the mid length is preferred because on average, it is most likely to approximate the true event length. However, events occuring in areas of low polymorphism density may have poor correlation between mid length estimates and the true event length.

To compare event lengths in *msh2Δ* and *tel1Δ msh2Δ*, event mid lengths were categorized into bins and plotted; median and mean lengths are also reported (Figure 6.7A & B). Compared to *msh2Δ*, *tel1Δ msh2Δ* event lengths are increased for both COs and NCOs. Of particular interest, the proportion of very long events (>10kb) is increased in *tel1Δ msh2Δ* (~2% of COs and ~1% of NCOs, compared to none in *msh2Δ*). Some examples of very long events observed in *tel1Δ msh2Δ* are shown in Figure 6.6C & D. This subset of very long events may represent event clustering, increased resection or dHJ migration. Since both CO and NCO lengths are increased, it is unlikely to be caused by dHJ migration because most, if not all, NCOs are formed by SDSA (Zakharyevich *et al.*, 2012). However, D-loop migration could still occur during NCO formation, which could contribute to event length (Martini et al., 2011).

To determine whether events thought to be composed of multiple DSBs were longer than those thought to be produced by a single DSB (Section 4.2.11), event lengths were compared between single-DSB and DSB cluster events (Figure 6.8) (This differs from Figure 6.7, in which DSB cluster events are separated into their component events and thus their lengths are counted twice). This shows that in *msh2Δ*, all the longest events are produced by non-clusters, and clusters tend to be short in length (discussed in Section 9.8). In contrast, almost all long events are produced by clusters in *tel1Δ msh2Δ*, though there are also some short clusters. Non-cluster COs in *tel1Δ msh2Δ* are also slightly longer than non-cluster COs in *msh2Δ*. This indicates that the increased event lengths observed in *tel1Δ msh2Δ* are almost entirely explainable by the increase in DSB cluster events observed in Section 6.2.3.
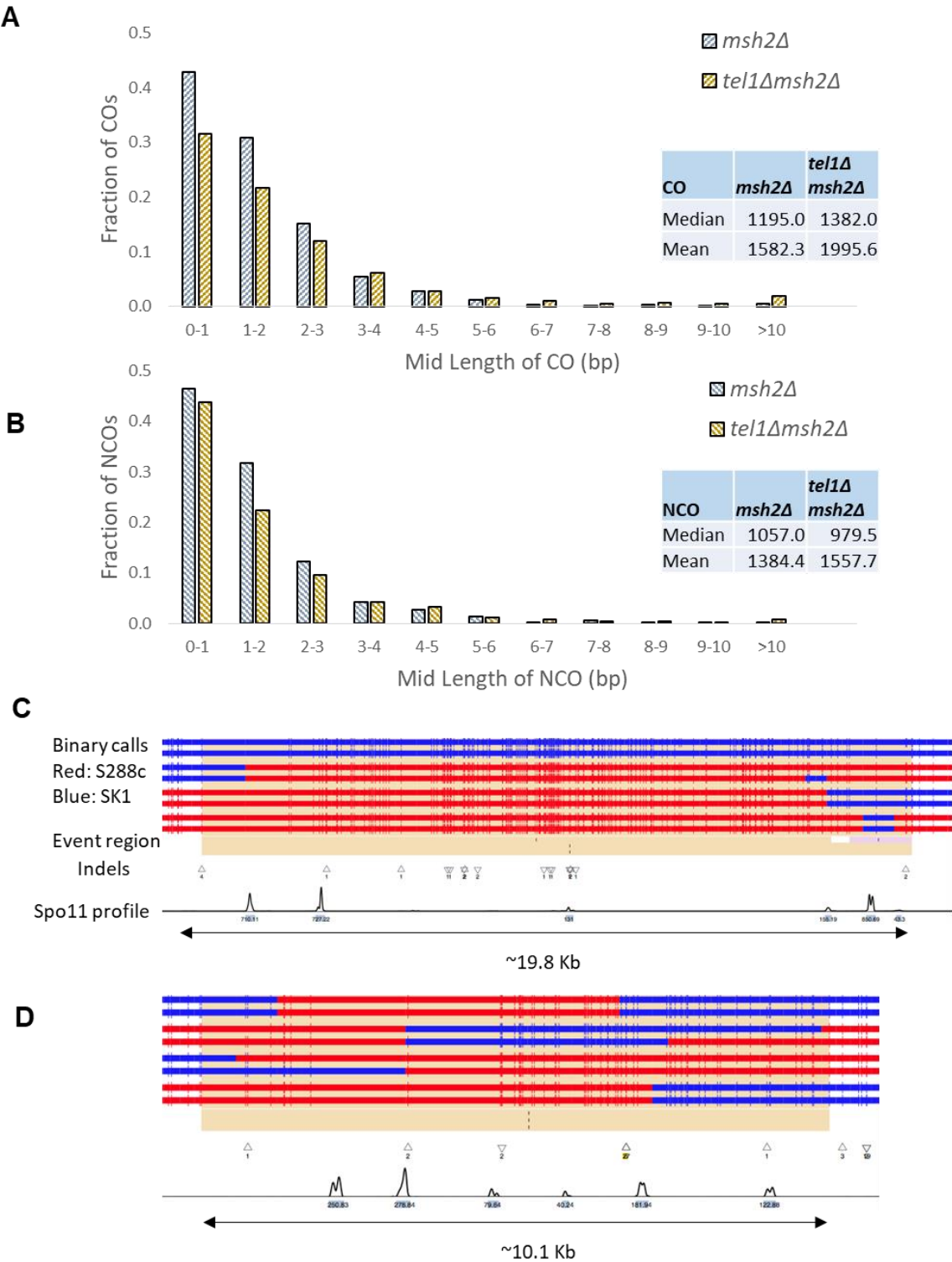
Figure 6.7. Mid length estimates of recombination events detected in *msh2Δ* and *tel1Δ msh2Δ* strains. Strain details are given in Table 2.1, raw event data is available in Table S2. Histogram of mid length estimate of A) CO and B) NCO events. Insert tables contain median and mean length in bp. Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan *et al*., 2011). C) A CO and NCO cluster with a mid length estimate of 19867bp. D) A double CO with a mid length estimate of 10083bp.

A

B

C

D
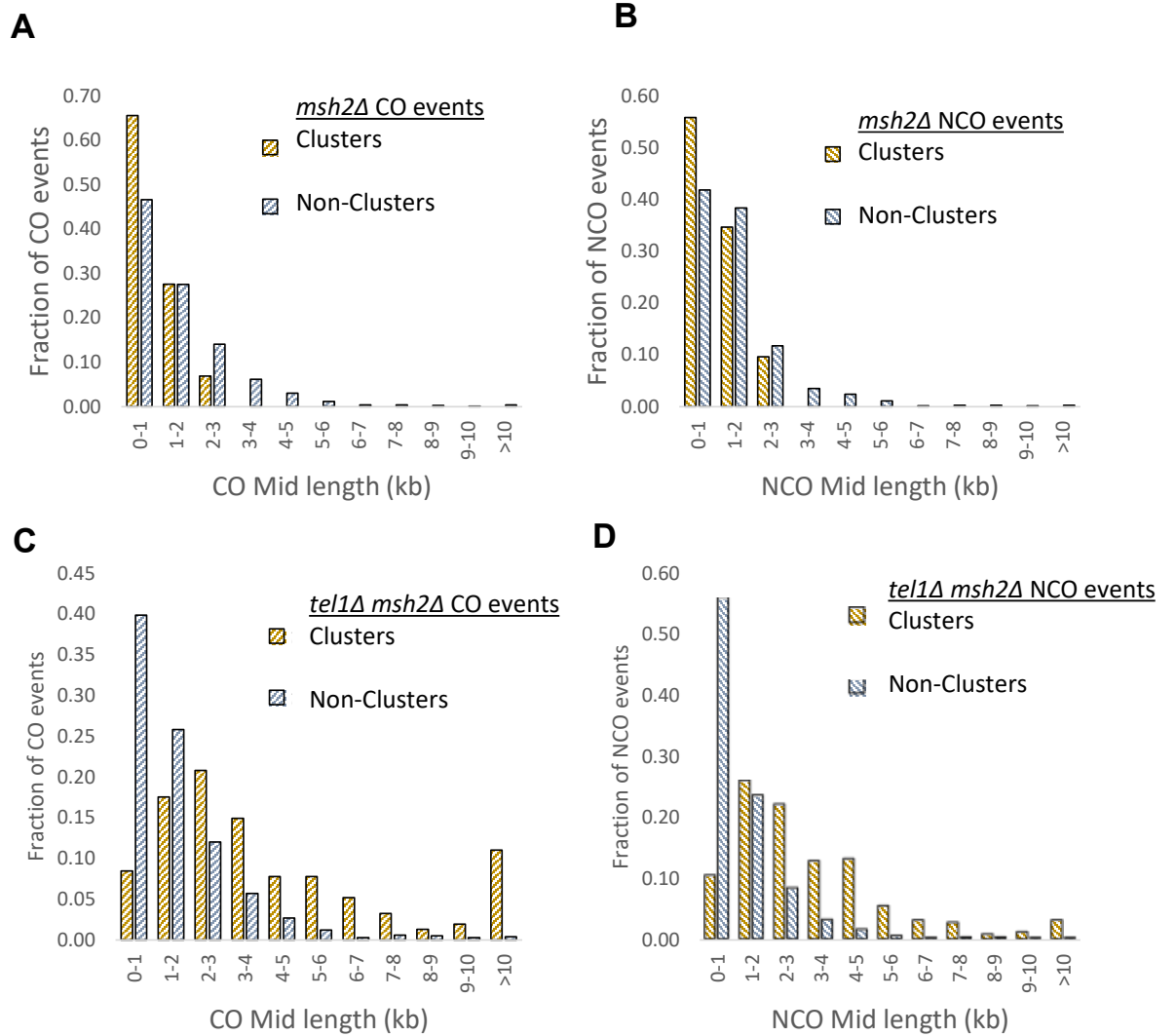
Figure 6.8. Comparison of mid length estimates in single-DSB and DSB-cluster events detected in *msh2Δ* and *tel1Δ msh2Δ* strains. Mid length estimate of cluster/non-cluster of: **A)** CO events in *msh2Δ*, **B)** NCO events in *msh2Δ*, **C)** CO events in *tel1Δ msh2Δ*, **D)** NCO events in *tel1Δ msh2Δ*.

6.2.6. Presence of potential duplications is increased in *tel1Δ*

It is possible to detect what appear to be novel duplications in the post meiotic genome (described in Chapter 4 Section 4.2.6). These duplications may or may not be associated with a detected recombination event, meaning that they could represent additional NCOs occurring during meiosis that were not detected because they produced a mixture of markers that could not called as one genotype or the other. Examples of potential duplications identified in *tel1Δ msh2Δ* data are presented in Figure 6.9A&B.

To test whether duplications are more likely to occur or have different lengths in *tel1Δ*, duplications were examined in *msh2Δ* and *tel1Δ msh2Δ* backgrounds (Table 6.3, Figure 6.9C&D). Duplications were only counted if they covered at least two consecutive SNPs. While the *msh2Δ* strain has an average of 6.6 duplications per cell covering an average of 3.2 adjacent SNPs, the *tel1Δmsh2Δ* strain had an average of 8.8 duplications per cell covering an average of 4.4 SNPs. The distribution of duplication lengths shows that duplications tend to be longer in *tel1Δ* in terms of both bp and SNPs, including an increase in the proportion of duplications >1kb in length and those converting >10 consecutive SNPs. This observation is noteworthy because duplications may be formed during complex repair of a DSB, for example multiple strand invasions into the same sequence on different chromatids could result in the same region being copied twice with different polymorphisms.

Alternatively, gene duplications can be caused by ectopic recombination (reviewed in Zhang, 2003). Ectopic recombination most commonly occurs during repair of DSBs formed in repetitive regions. Spo11-DSBs do not normally form in these regions (Pan *et al.*, 2011), so an increase in ectopic recombination may reflect an increase in recombination in, or close to, repetitive regions (reviewed in Sasaki *et al.*, 2010), although markers occurring in repetitive regions are not used in this analysis (Section 4.2.3). Overall, since Tel1, unlike Mec1 and Rad24, is not known to have a role in preventing ectopic recombination, it seems most likely that the increase in duplications in *tel1Δ* are caused by complex DSB repair.
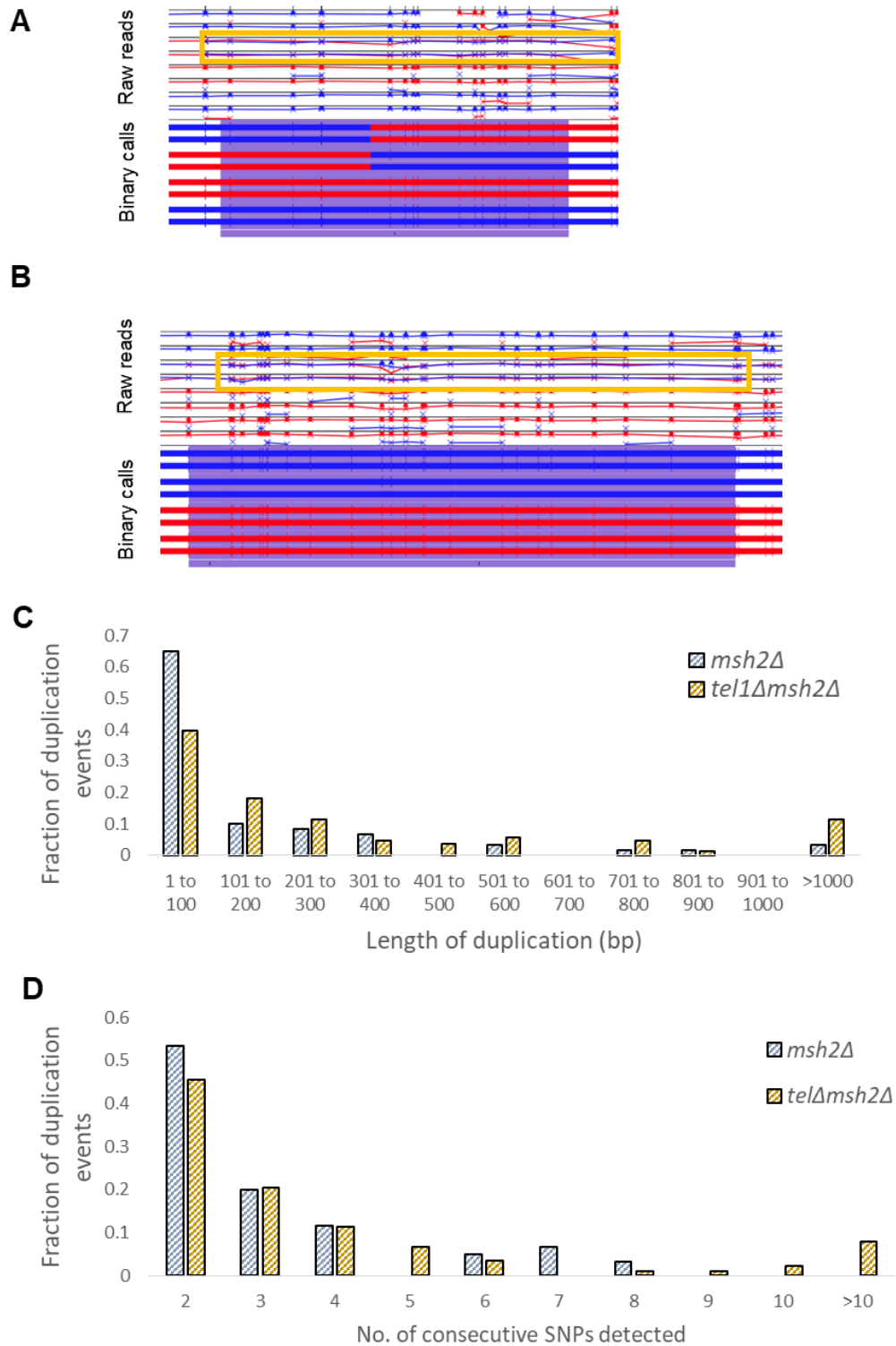
Figure 6.9. Length of potential duplications detected in *msh2Δ* and *tel1Δ msh2Δ* strains. Regions of hDNA were mapped by detection of mixed SK1 (blue) and S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The hDNA region is indicated by the purple box. **A)** An example duplication from a *tel1Δ msh2Δ* octad associated with a CO, containing 17 SNPs and with a length of 2683bp. The yellow box highlights the suspected duplication, which can be seen to contain both SK1 and S288c reads. In the binary calls, these positions are discarded. Discarded positions are highlighted by a purple box. **B)** An example duplication from a tel1Δmsh2Δ octad that is not associated with a detected recombination event, containing 11 SNPs and with a length of 2047 bp. **C)** Length of potential duplications in bp, **D)** Number of consecutive SNPs in potential duplications.

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Table 6.3. Data summary for potential duplications and deletions detected in *msh2Δ and* *tel1Δ msh2Δ* **backgrounds.** Only duplications and deletions containing at least two SNPs are included.

Genotype (repeats)	Duplications			Deletions		
	Total detected	Mean no. of SNPs	Mean length (bp)	Total detected	Mean no. of SNPs	Mean length (bp)
msh2Δ (9)	60	3.2	165.3	75	2.1	59.1
tel1Δ msh2Δ (10)	88	4.4	432	71	2.1	63.4

Similarly, novel deletions may be detectable by looking for adjacent SNPs with low read depth. However, these could also simply represent areas that did not receive much sequencing coverage. In addition, the presence of deletions is based on the absence of data, while duplications are based on the presence of heteroduplex calls, meaning there is less confidence in the accuracy of the deletions.

Potential deletions in *msh2Δ* and *tel1Δ msh2Δ* were examined (Figure 6.10, Table 6.3), revealing that all were very short in length, and there was no difference between the genotypes, unlike the duplications. This suggests that the potential deletions are a technical artefact, because deletions are based on the absence of data, cover few markers, have short lengths and are not altered between genotypes, as opposed to duplications, which are based on the presence of data, can have long lengths and cover many markers, and display altered characteristics between genotypes. However, it should be noted that deletions are likely to be shorter in length than duplications, because longer deletions may not be tolerated by the cell.

Overall, *tel1Δ* appears to have no effect on the rate of deletion occurrence, though the limitations of this analysis mean this is not definitive.

A
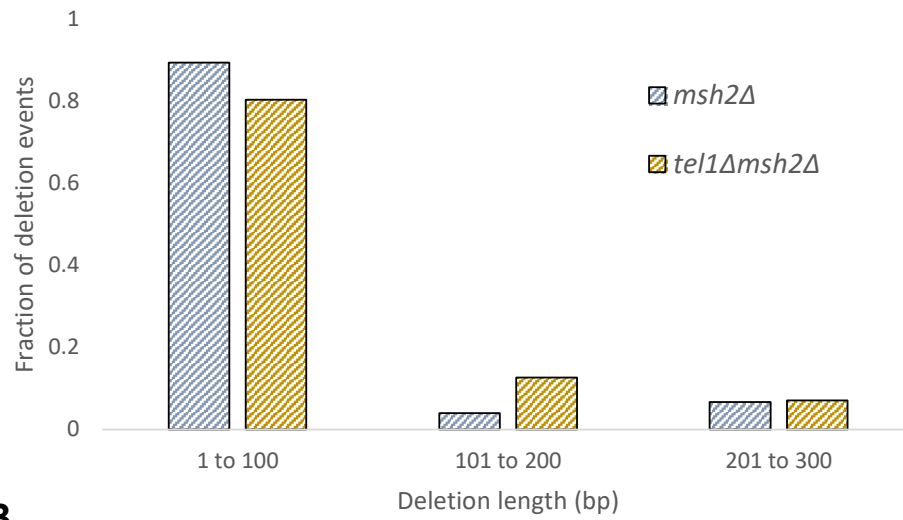
B
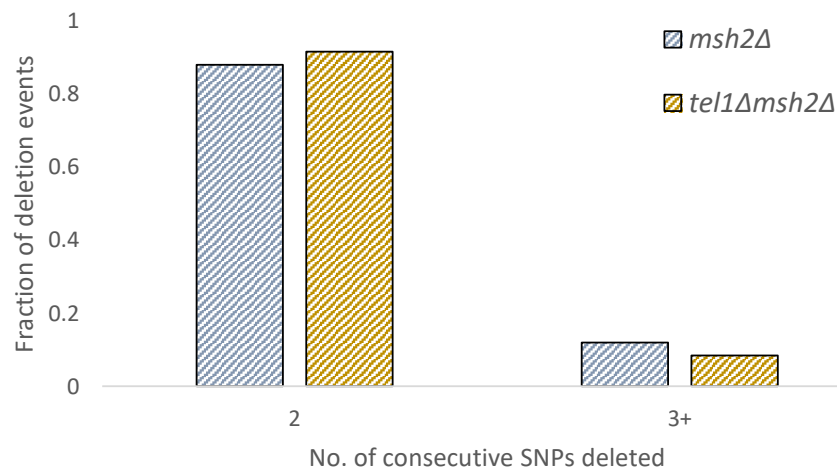
Figure 6.10. Length of potential deletions detected in *msh2Δ* and *tel1Δ msh2Δ* strains.
Potential deletions were detected by looking for consecutive SNPS with low read depth. **A)** Length of potential deletions in bp. **B)** Number of consecutive SNPs in potential deletions.

6.2.7. Distribution of recombination events in relation to centromeres and telomeres

Normally, recombination is suppressed from occurring near centromeres and telomeres (Petes & Botstein, 1977; Pan *et al.*, 2011). DSBs formed in repetitive regions can cause ectopic recombination leading to genome rearrangement (reviewed in Sasaki *et al.*, 2010). In particular, CO formation is repressed near centromeres (Lambie & Roeder, 1986) and telomeres (Rockmill et al., 2006). The formation of CO events in centromeres and telomeres has consequences for chromosome segregation (Ross et al., 1996; Barton et al., 2003).

It is not possible to detect whether any recombination events occur within centromeres or telomeres using marker mapping, because it is difficult to accurately map reads to repetitive DNA, and because centromeres are very short in *S. cerevisiae (*100-200bp) (Mortimer and Schild, 1980). However, the proximity of events to the region of interest can be measured. To see if the mechanisms preventing recombination near these regions is functioning normally, the proximity of recombination events to telomeres and centromeres in *msh2Δ* and *tel1Δ msh2Δ* backgrounds was measured (Figure 6.11). This analysis includes 'unclassified' events, which cannot be classified as CO or NCO because they occur towards the end of the region covered by the variant table (i.e. are subtelomeric), so never return to a 4:4 segregation pattern. Since only one endpoint can be seen for an unclassified event, it is not certain how far into the repetitive subtelomeric region it may extend.

In both backgrounds, the frequency of all recombination event formation (including unclassified events) is reduced close to telomeres and centromeres (Figure 6.11A&B) and of events that do occur close to these regions, there are more NCO events than CO events (excluding unclassified events) (Figure 6.11 C&D). There is not a noticeable difference between *tel1Δ msh2Δ* and *msh2Δ*. However, out of 10 *tel1Δ msh2Δ* octads, a total of 11 "unclassified" events were detected, while no such events were observed in *msh2Δ* octads. This suggests that while events are equally likely to occur in non-repetitive regions that are close to telomeres in *msh2Δ* and *tel1Δ msh2Δ*, they are still more likely to extend into the repetitive subtelomeric region in *tel1Δ msh2Δ*. This may represent a partial loss of control over event positioning in subtelomeric regions in *tel1Δ*. This could be related to the fact that Tel1 is known to have a role in telomere maintenance, producing a DNA damage response when telomeres are damaged (Lustig & Petes, 1985; Eckert-Boulet & Lisby, 2010). In addition, it has been observed that Spo11-oligo frequencies are initially lower than expected in *tel1Δ* near telomeres and centromeres, but the levels increase over the course of meiosis, suggesting that the suppression of DSBs in these regions seen in WT is initially functional, but the accumulation of DSBs over time overcomes the suppression in *tel1Δ* (Mohibullah & Keeney, 2017).
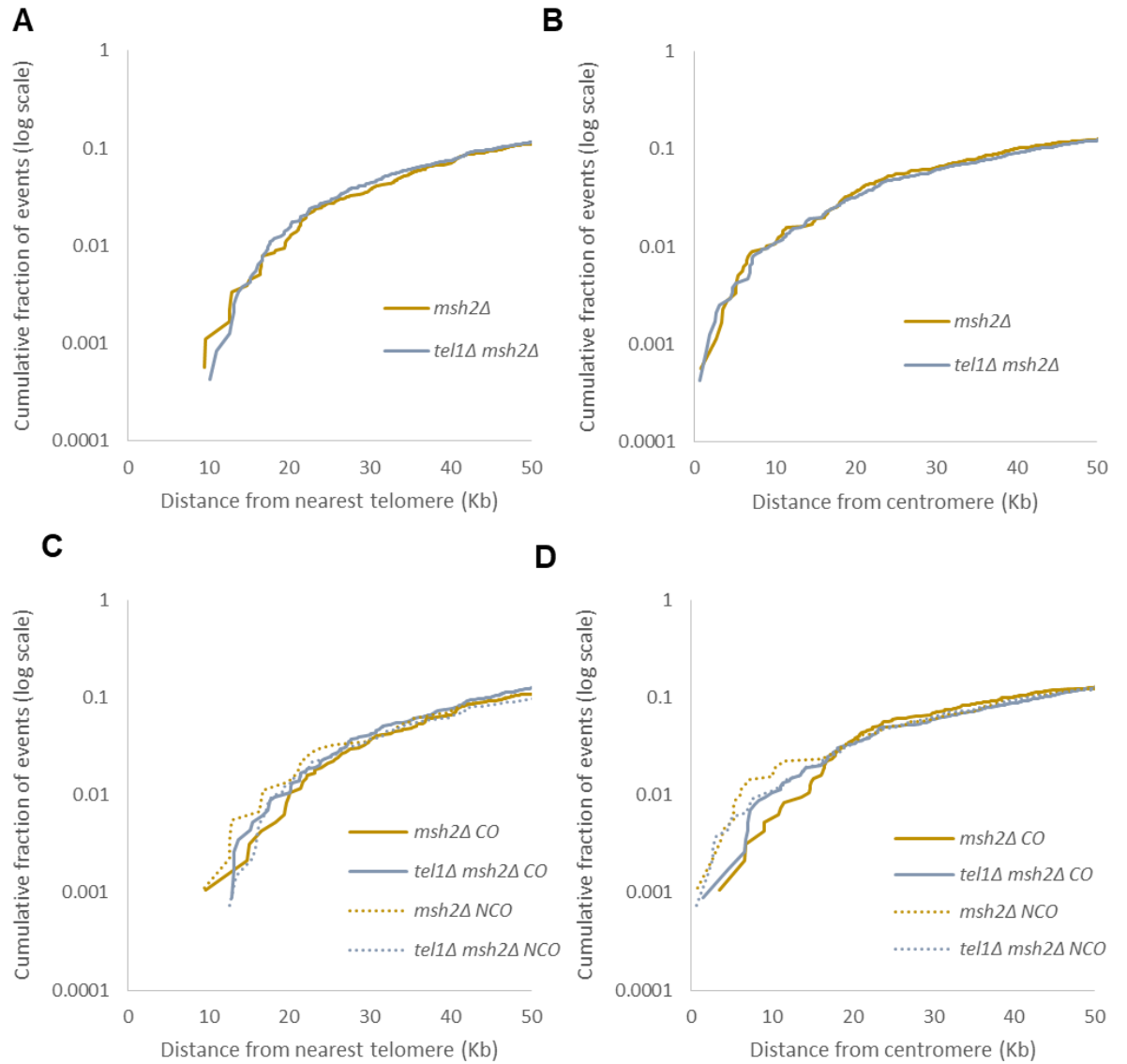
Figure 6.11. Distance between telomeres or centromeres and recombination events detected in *msh2Δ* and *tel1Δ msh2Δ* strains. For each event, the distance to the centromere or nearest telomere is calculated and plotted against a cumulative fraction of events. **A)** Distance between telomeres and all events. This includes 'U' events which cannot be called a CO or NCO due to occurrence close to the telomeres. **B)** Distance between centromeres and all events. **C)** Distance between telomeres and CO or NCO events. **D)** Distance between centromeres and CO or NCO events.

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6.2.8. The distribution of CO events shows evidence of loss of interference between COs in *tel1Δ*

The occurrence of a CO is known to reduce further CO formation nearby, a phenomenon known as CO interference. The degree of interference between COs can be estimated by measuring the distance between event midpoints and comparing the distributions (as described in Chapter 5, Section 5.2.7).

Inter-CO distances were calculated for *msh2Δ* and *tel1Δ msh2Δ* strains, arranged in order from smallest to largest and plotted as cumulative fraction of total events against inter-CO distance size on a log scale (Figure 6.12). If interference is present, events should occur further apart than would be expected if event placement was random. In order to determine whether the experimental inter-event distance distributions are distinct from a random distribution, simulated data is produced for the appropriate event counts to show the hypothetical distribution of events along the chromosomes under conditions of independence (Methods section 2.18; Tim Cooper, personal communication).

In *msh2Δ*, experimental inter-CO distance distributions deviate greatly from the random simulation, with the experimental data shifted to the right, indicating that there are fewer short inter-CO distances than expected (Figure 6.12, compare blue (experimental data) and orange (random simulation). This means that CO events are occurring further apart than would be expected if events were occurring independently, suggesting the presence of CO interference. In *tel1Δ msh2Δ*, inter-CO distances also deviate from the random simulation, but not as strongly as in *msh2Δ*.

In order to quantify the strength of CO interference for each genotype, the best fit gamma parameters were found for inter-CO intervals from *msh2Δ* strains (as described in Chapter 5, Section 5.2.7 and in Methods section 2.18 (analysis performed by Tim Cooper)). Calculated gamma parameters are shown in Table 6.4. Inter-CO distances in *msh2Δ* were best described by a gamma function with an α value of 2.44, while *tel1Δ msh2Δ* CO distribution was best fit by a gamma curve with α=2.03, suggesting that the strength of CO interference is reduced in *tel1Δ*. However, even the best-fit gamma distributions are not a good fit for the experimental data, according to the results of a Kolmogorov-Smirnov test used to determine whether the distributions are significantly different (P-values in Table 6.4). This indicates that inter-CO distributions cannot be well described by a gamma distribution.

The best fit gamma function for each background was also used to produce simulated IED data (as described in Chapter 5, section 5.2.7). Simulated IED data was plotted alongside experimental

data to give a visual indication of the goodness of fit to the 'best fit' gamma parameters (Figure 6.12, grey lines). This shows that in both *msh2Δ* and *tel1Δ msh2Δ*, there is a particularly poor fit for the shortest inter-CO distances (shorter than ~27kb*)*, with the experimental data shifted to the left in comparison to the gamma distribution, indicating that that more short distances are occurring than expected, in agreement with the results of the KS test. This suggests that there are many events occurring that do not display interference; this may be caused by the presence of Class II (non-interfering) COs, as discussed in section 6.2.10.

The value of α was calculated as 2.0 in WT and 1.6 in *tel1Δ* by Anderson *et al.* (2015). The reason why interference values are higher in the *msh2Δ* strains is likely because the proportion of COs that display interference (Class I) is increased in *msh2Δ* compared to WT (Chapter 5, Section 5.2.10); discounting this influence, the difference in interference strength between WT and *tel1Δ* from Anderson *et al.* is proportional to the difference between *msh2Δ* and *tel1Δ msh2Δ*.
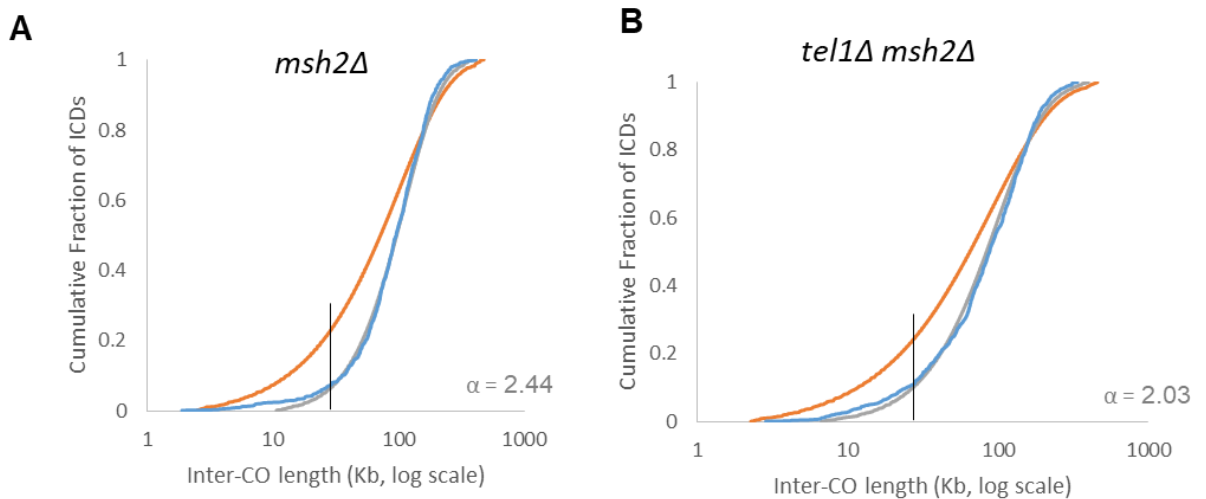
Figure 6.12. Distribution of distances between crossover events observed in *msh2Δ* and *tel1Δ msh2Δ* strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-CO distance (ICD) in **A)** *msh2Δ*, **B)** *tel1Δ msh2Δ*.

Table 6.4. Gamma parameters

Best-fit gamma parameters are given for the inter-event distribution for each aggregate genotype and event type. The number following the genotype indicates how many samples were included in the aggregate. N indicates the total number of recombination events (CO, NCO or both) included in the analysis. The shape factor, α, corresponds to the strength of interference: A value of 1 indicates an exponential distribution i.e. no interference. Values > 1 indicate interference, with higher values corresponding to stronger interference. The scale factor, β describes the distance over which the shape designated by α is stretched, thus indicating the range of the interference. A one-sample Kolmogorov–Smirnov test is utilized to determine whether the experimental inter-event distribution is significantly different from the theoretical best fit gamma distribution, with the reported P-value indicating whether the difference was significant. If the value is <0.05, the difference is considered significant (red).

Genotype (repeats) Crossovers	N	Best fit gamma α value	Best fit gamma β value	(P)
msh2Δ (9)	799	2.44	44056	0.0036
tel1Δmsh2Δ (10)	979	2.03	48931	0.0004
Non-Crossovers	N	α	β	(P)
msh2Δ (9)	698	1.21	87998	0.0861
tel1Δmsh2Δ (10)	1057	1.11	73646	0.0586
Total events	N	α	β	(P)
msh2Δ (9)	1636	1.57	36542	0.0001
tel1Δmsh2Δ (10)	2204	1.31	36386	0.0005

6.2.9. The distribution of NCO events does not show evidence of interference

In contrast to CO events, NCOs do not display interference (Mancera *et al.*, 2008). In order to determine whether this is affected by Tel1, inter-NCO distances were plotted as described for inter-CO distances, alongside simulated datasets for events occurring under conditions of independence (Figure 6.13). In both backgrounds, the experimental inter-NCO distance plots are a good match to the random simulation (Figure 6.13, compare blue (experimental) and orange (random simulation). This is as expected as NCOs are known to not display interference in yeast.

The best fit to a gamma distribution was found for inter-NCO event distances (Table 6.4), producing α values of 1.21 and 1.11 for *msh2Δ* and *tel1Δ msh2Δ* respectively, both of which indicate low or no interference between NCO events, as predicted. A Kolmogorov-Smirnov test was utilized to determine whether the experimental inter-NCO distribution was significantly different from the best fit gamma distribution, revealing they were not (P-values in Table 5.4), indicating that the calculated gamma values are a good description of the strength of NCO interference in these backgrounds.
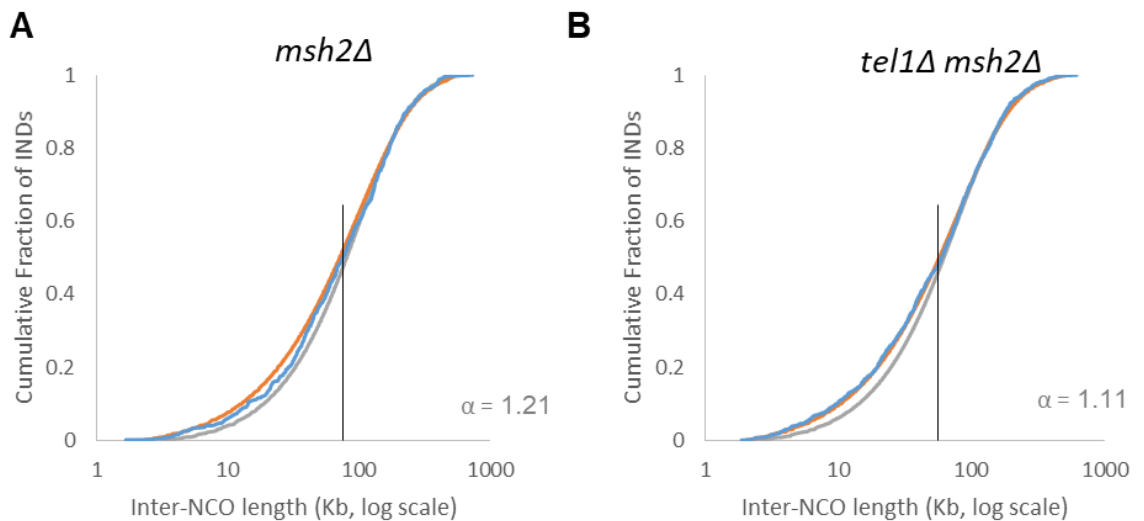
Figure 6.13. Distribution of distances between noncrossover events observed in *msh2Δ* and *tel1Δ msh2Δ* strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-NCO distance (IND) in **A)** *msh2Δ*, **B)** *tel1Δ msh2Δ*.

6.2.10. The distribution of all recombination events shows some evidence of DSB interference loss in *tel1Δ msh2Δ*

In addition to CO interference, DSBs also reduce the likelihood of another DSB occurring nearby in *cis* and in *trans*, a phenomenon known as DSB interference. For an estimate of DSB interference, the distribution of all events is examined, although this is not precise because event midpoints do not always correspond to DSB locations. In addition, there may be additional DSBs repaired to form NCOs that are not detected due to occurring in regions without markers, or due to being repaired as a restoration tract in an MMR-proficient strain (as detailed in Chapter 5, section 5.2.9). In addition, recombination events that are repaired with the sister chromatid cannot be detected.

In order to estimate DSB interference in *tel1Δ*, inter-event distances were calculated for the *tel1Δ msh2Δ* and *msh2Δ* strains, arranged in order from smallest to largest and plotted as cumulative fraction of total events against IED size on a log scale, alongside simulated datasets for events occurring under conditions of independence as described for inter-CO distances (Figure 6.14). If DSB interference is present, events should occur further apart than would be expected if event placement was random.

While the *msh2Δ* inter-event distribution deviates to the right from the random distribution, indicating that there are fewer short distances than expected, the *tel1Δ msh2Δ* inter-event distribution is well-described by a random distribution (Figure 6.14A&B, compare blue and orange lines), indicating that events are mostly randomly placed in *tel1Δ*.

In order to quantify the strength of DSB interference for each genotype, the best fit gamma parameters were found for inter-event intervals from *tel1Δ msh2Δ* and *msh2Δ* strains (as described in Chapter 5, Section 5.2.7 and in Methods section 2.18 (analysis performed by Tim Cooper)). Calculated gamma parameters are shown in Table 6.4.

The distribution of recombination events in *msh2Δ* is best described by a gamma distribution of α=1.57, and in *tel1Δ msh2Δ,* by α=1.31, indicating a decrease in inter-event interference in *tel1Δ*. However, the results of a Kolmogorov-Smirnov test to compare the experimental and gamma distributions show that these best-fit gamma distributions were still significantly different to the experimental data (P-values in Table 6.4). This indicates that inter-event distributions cannot be well described by a gamma distribution.

The best-fit gamma distributions were plotted alongside the experimental data to allow a visual examination of the goodness-of-fit (Figure 6.14, grey lines). This shows that the fit is poor for

both inter-event distance distributions, which deviate to the left of the best fit gamma distribution for distances shorter than ~17 Kb in *msh2Δ* and ~31Kb in *tel1Δ msh2Δ*, indicating that more short distances are occurring than expected.

In WT and *tel1Δ*, inter-event distance distributions were found to be best described by α values of 0.37 and 0.21 by Anderson *et al.* (2015). These much lower values may be due to the fact that fewer events can be detected in MMR-proficient backgrounds, meaning that a less complete picture of DSB interference can be revealed from this data. Alternatively, it could be due to the slightly different strain background, or the higher event merging threshold used in the analysis by Anderson *et al.* Nonetheless, both this study and that of Anderson et al are in agreement in that they show a decrease in DSB interference in *tel1Δ*.

Overall, these results suggest that DSB interference is reduced in *tel1Δ*, in agreement with findings from Garcia *et al.*, 2014. However, it should be emphasized again that event midpoint distributions do not necessarily correspond to DSB locations. In addition, inter-event interference may be influenced by CO interference due to CO-CO intervals present in the data, which are known to display interference that is reduced in *tel1Δ* (Section 6.2.8).
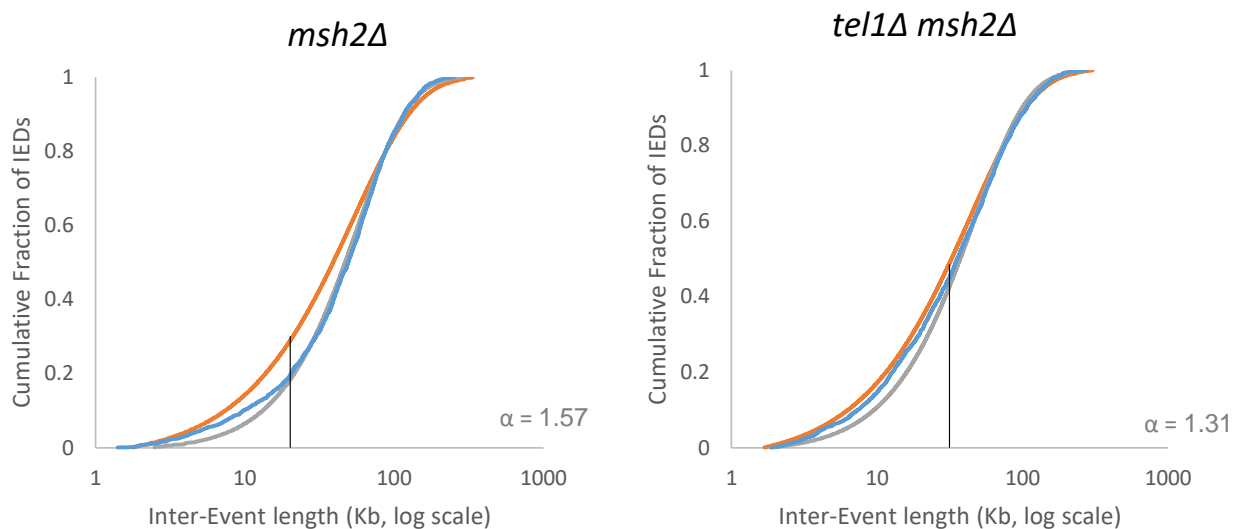
Figure 6.14. Distribution of distances between all recombination events observed in *msh2Δ* and *tel1Δ msh2Δ* strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-event distance in **A)** *msh2Δ,* **B)** *tel1Δ msh2Δ.*

6.2.11. The proportion of Class I and Class II COs is predicted to be altered in *tel1Δ*

There are two distinct classes of CO event in *S. cerevisiae* meiosis: Class I COs exhibit interference and are dependent upon Msh4/Msh5 activity (Novak *et al.*, 2001), and Class II COs do not display interference and are dependent upon Mus81/Mms4, Yen1 or Slx1-Slx4 activity (de los Santos, 2003). The normal ratio of Class I to II is estimated to be 70:30 (Zakharyevich *et al.*, 2012; de los Santos, 2003). Based on the expectation of a two-component distribution, it is possible to separate out an interfering and a non-interfering subset, which are inferred to be equivalent to Class I and Class II COs (as described in Section 5.2.10; Methods section 2.19). This analysis was performed and authored by Tim Cooper (personal communication).

It was observed that *tel1Δ msh2Δ* cells appear to have reduced CO interference compared to *msh2Δ* (Section 6.2.8). A potential explanation is that *tel1Δ msh2Δ* may have a reduction in Class I CO formation, or an increase in Class II CO formation. To be able to predict the proportions of Class I/II COs in these backgrounds, two-component analysis was carried out on these strains (Table 6.5). The ability of the two-component system to describe experimental data was analyzed via a Kolmogorov-Smirnov test. In comparison to the poor fit of a single gamma distribution to inter-CO distances (Table 6.4), a large improvement for all genotypes is seen when a mixed-fit is used, with none of the fitted distributions significantly different to the experimentally observed data (compare P-values in Tables 6.4 and 6.5).

The predictions from the two-component analysis are that *msh2Δ* should have ~77% Class I COs and ~23% Class II, while *tel1Δ msh2Δ* should have ~67% Class I and ~33% Class II, indicating that the ratio is shifted towards Class II non-interfering events in *tel1Δ*. When taking into account the differing event numbers for each background, the average number of Class I COs is not predicted to change much between the two strains, with ~80 in *msh2Δ* and ~77 in *tel1Δ msh2Δ*. However, the average number of Class II COs is predicted to increase from ~25 to ~38 when Tel1 is deleted. This suggests that the increase in CO number seen in *tel1Δ msh2Δ* compared to *msh2Δ* (Figure 6.1A) may be caused by an increase in Class II CO formation without any change in Class I CO formation. To test this hypothesis, Class II CO formation can be reduced by the deletion of Mus81, the main resolvase responsible for their formation. This is discussed in Chapter 8.

This conclusion is supported by the findings of Anderson *et al.* (2015), who reported that a larger share of COs in *tel1Δ* is ZMM-independent. Zip3 deletion reduced the proportion of events repaired as COs from 72% to 39% in WT, but a more modest reduction from 67% to 49% was seen in *tel1Δ,* suggesting that CO formation is less dependent on Zip3 in *tel1Δ*. In addition, the number and distribution of Zip3 foci in *tel1Δ* was not significantly different to WT, suggesting normal interference in Class I COs (Anderson *et al.*, 2015).

Table 6.5. Percentage of COs that do not appear to show interference in sequenced strain backgrounds.

Mixture modelling results are given for each genotype. The strength of interference in the non-random population is given by $\alpha 1$ and is expected to be >1. The strength of interference in the random population is given by $\alpha 2$ and is expected to be ~1. The scale factors, $\beta 1$ and $\beta 2$ describe the distance over which the shapes designated by $\alpha 1$ or $\alpha 2$ respectively are stretched, thus indicating the range of the interference. The overall proportion of CO events that are thought to occur with random or non-random placement is given, which allows a predicted total number of Class I and Class II COs to be calculated from the overall CO count. A two-sample Kolmogorov–Smirnov test is utilized to determine whether the experimental inter-event distribution is significantly different from the two-component system, with the significance indicated by the reported P-value. A value of >0.05 is considered to show no significant difference.

Genotype (repeats)	$\alpha 1$	$\alpha 2$	$\beta 1$	$\beta 2$	Non-random proportion (%)	Random proportion (%)	Predicted mean number of Class I COs	Predicted mean number of Class II COs	P
msh2Δ (9)	3.84	1.21	29877	68155	76.5	23.5	80.3	24.7	0.9
tel1Δ msh2Δ (10)	4.45	1.97	28187	23104	67.4	32.6	77.7	37.6	0.9

6.3. Discussion

6.3.1. Comparison of genome-wide sequencing in MMR-proficient and MMR-deficient *tel1Δ* hybrids

Here, recombination is examined in *tel1Δ msh2Δ* meiosis genome-wide, revealing that Tel1 has roles in limiting NCO and CO (especially Class II) formation (Figure 6.1), and reduces CO and potentially DSB formation (Figure 6.12 and 6.14), causing more DSB/CO cluster events to form (Figure 6.2), which produce long complex events (Figure 6.8), supporting previous work showing an increase in Spo11 double-cuts in *tel1Δ* (Garcia *et al.*, 2015). These features have also been noted previously in genome-wide assays of recombination in *tel1Δ* meiosis (Anderson *et al.*, 2015). However, MMR proficient strains were used, which greatly reduces the number of NCOs that can be detected as well as the amount of information about e.g. length, complexity that can be gathered for each event (Martini *et al.*, 2011). MMR-deficient hybrids may also be more representative of recombination in a pure SK1 background than MMR-proficient hybrids, due to the rejection of strand invasion into mismatching sequences by Msh2 (Sugawara *et al.*, 1997; Evans *et al.*, 2000; Datta et al., 1999; Chen & Jinks-Robinson, 1998). In addition, during classification of recombination products, pattern changes within 5kb of each other were considered to be part of the same event (Anderson *et al.*, 2015). This limit was based on previous analysis by the authors of wild-type tetrads showing that events occurring 5 kb have properties that suggest they originated from a single DSB (Anderson *et al.*, 2011). By careful examination of hDNA tracts associated with recombination in MMR-deficient backgrounds, others have found that many events incompatible with a 1-DSB scenario occur closer than 5kb, and thus recommend a 1.5kb merging limit (Bertrand Llorente & Marie-Claude Marsolier, personal communication). In addition, a 5kb limit may mask the detection of event clustering at short range as described by Garcia *et al.*, 2015. Thus, the 1.5 kb merging limit used in the data presented here is advantageous for detailed examination of the distance between recombination events.

Anderson *et al.* (2015) does include analysis of events containing 4:0 tracts, unlike previous studies (e.g. Martini *et al.*, 2011; Anderson *et al.*, 2011) which discount these events as being caused by pre-meiotic recombination, even though they could potentially be caused by two overlapping NCOs. However, events composed solely of 4:0 tracts are included as well as 4:0 segments associated with other pattern changes, which are more likely to have arisen during meiosis. In an MMR-deficient background, the ability to see a greater variety of pattern changes via hDNA analysis means that 4:0 events can be categorized as meiotic or mitotic with more certainty. In the data presented here, 8:0 and 4:0 events are only kept if they are associated with other pattern changes. In addition, segments of 7:1 segregation can also be seen in *msh2Δ* octads, which are likely produced by the same processes as 8:0 segments such as double initiation on sister chromatids. An increase in 7:1 segments is seen between *msh2Δ* and *tel1Δ msh2Δ* (Section

6.2.3), which would not be possible to see in the MMR-proficient strains of Anderson *et al.* (2015). In addition, 6:2 segments are visible in *msh2Δ* octads that may be indicative of concerted DSB formation (Section 6.2.4); while these would also be present in tetrads, they would be indistinguishable from 6:2 segments produced by MMR.

6.3.2. Closing Statement

Previously, recombination has been assayed genome-wide in *tel1Δ* tetrads (Anderson et al., 2015). However, recombination has not been assayed in a MMR-deficient *tel1Δ* background. In this chapter, the role of Tel1 in controlling recombination event quantity and quality, CO and DSB interference are revealed by analysis of recombination event mapping in MMR-deficient *tel1Δ* octads via deep sequencing and marker analysis. This study offers distinct advantages over preceding ones in terms of marker and event resolution and detection.

Chapter 7.

Separable roles of Mec1 and Rad24 in regulation of meiotic recombination

Chapter 7. Separable roles of Mec1 and Rad24 in regulation of meiotic recombination

7.1. Introduction

7.1.1. Roles of Mec1 and Rad24 in the DNA damage response

Mec1^{ATR} is a kinase which functions in meiosis to monitor DNA damage repair, activate checkpoints and regulate cell cycle progression (Cha *et al.*, 2002; Harper & Elledge, 2007; Carballo & Cha, 2007). In meiotic prophase, programmed DSBs are formed by Spo11. With the yeast 9-1-1 clamp complex (Rad17, Mec3, and Ddc1), its loader Rad24 and the MRX complex as damage sensors (Hochwagen & Amon, 2006), unrepaired ssDNA produced by the resection of Spo11-DSBs activates Mec1 (Lydall *et al.*, 2011). The accumulation of unrepaired DSBs causes Mec1 to trigger meiotic arrest as part of the meiotic checkpoint response (Lydall *et al.*, 1996). The meiotic checkpoint monitors meiotic events and halts cell cycle progression if necessary, ensuring that cells do not exit prophase before the process of DSB repair is complete (Lydall *et al.*, 1996; Carballo *et al.*, 2008).

Mec1 positively regulates DSB formation in yeast (Gray *et al.*, 2011), and both Mec1 and Rad24 promote CO formation (Grushcow *et al.*, 1999), likely due to the loss of the ability to arrest meiosis in response to impaired meiotic recombination. The interaction between Mec1 and the 9-1-1 complex is also important for other Mec1 functions such as Hop1 phosphorylation, which is important for homolog bias and chiasma formation (Cheng *et al.*, 2013).

Mec1^{ATR} deletion is inviable in yeast (Giaever *et al.*, 2002), but P_{CLB2}-*MEC1*, a conditional Mec1 allele expressed only in mitosis, supports vegetative growth and has a spore viability of ~50% compared to ~97% in WT. However, the use of this mitosis-specific promoter could potentially affect the mitotic or meiotic behaviour of Mec1. Potentially, Mec1 could be expressed at inappropriate times, or in inappropriate quantities. In addition, the meiotic knockout of *MEC1* could be incomplete, causing Mec1 protein to be present during meiotic prophase at the time when Spo11-DSBs are being formed. In P_{CLB2}-*MEC1*, DSBs are seen from 2 hours after entry into meiosis, at which time the amount of Mec1 is low, but there is still some Mec1 present until around 3 hours (Gray *et al.*, 2013). Nevertheless, during the bulk of DSB formation and repair, there is expected to be little or no Mec1 protein present.

The deletion of Sml1 restores the cell viability of *mec1Δ*, though *sml1Δ* does not compensate for the checkpoint functions of Mec1 (Zhao *et al.*, 1998). Sml1 inhibits dNTP synthesis (Zhao *et al.*, 1998), and is inactivated by phosphorylation initiated by Mec1 via Rad53 and Dun1 (Zhao and Rothstein 2002; Chen *et al.*, 2006, Sanchez *et al.*, 1996). Deletion of Sml1 rescues *mec1Δ* by relieving the requirement for Mec1-mediated inactivation of Sml1, and by increasing dNTP levels

(Huang & Elledge, 1997) by releasing ribonucleotide reductase suppression, allowing DNA repair to be more efficient in the absence of the DDR checkpoint. *mec1Δ sml1Δ* strains have a spore viability of 30-50% (Lydall *et al.*, 1996, Carballo & Cha, 2007).

It was not previously known if Rad24 activity was important for Sml1 inactivation, however *sml1Δ* was found to double *rad24Δ* spore viability (Chapter 3, Figure 3.4A) and also rescue *rad24Δ* cell viability after UV treatment (Figure 3.6A), suggesting that Rad24 has a role in Sml1 inactivation.

7.1.2. Roles of Mec1 and Rad24 in CO and DSB interference

DSBs do not occur independently, but are subject to interference among the four chromatids. This interference occurs in *cis* (adjacent on the same chromatid), and *trans* (between chromatids) (Zhang *et al.*, 2011). CO events also display interference (Sturtevant 1913; Zhao *et al.,* 1995). There has been very little investigation into the roles of Mec1 and Rad24 in DSB or CO interference. Mec1 has been shown to be a mediator of *trans* DSB interference via tetrad analysis at the *HIS4::LEU2* hotspot (Zhang *et al.*, 2011). A reduction in DSB interference can be indicated by an increase in concerted Spo11-DSB formation; while a *tel1Δ* mutant had an increase in double-cuts (closely juxtaposed DSBs), a *rad24Δ* mutant did not (Garcia *et al.*, 2014). However, this measurement was only made at a few loci, which may not reflect the genome-wide situation.

7.1.3. Differences and similarities in Rad24 and Mec1 meiotic behaviour

Despite functioning in the same DDR pathway, Mec1 and Rad24 are known to have some separable functions. Rad24 spore viability can be rescued to ~50% by prophase extension mediated by *NDT80* repression and release, but P_{CLB2}-*MEC1* viability is not affected by *NDT80* prophase extension (Chapter 3, Figure 3A&B; Gray *et al.* 2013). In addition, Rad24 is necessary for loading ZMM proteins, and interacts physically with Zip3, independently of Mec1 (Shinohara *et al.*, 2015). This indicates that Rad24 may promote the loading of ZMM proteins at sites of future COs. Finally, a high degree of hyper-resection at Spo11-DSBs is visible in *rad24Δ* and *rad17Δ* cells; some hyper-resection is also seen in P_{CLB2}-*MEC1*, but not to the same extent as in *rad24Δ* (Gray *et al.*, 2013; Kayleigh Wardell, personal communication).

Rad24 may enact its role in regulating resection distance by loading the 9-1-1 clamp, which has been proposed to act as a physical barrier to resection (Kayleigh Wardell, personal communication). Alternatively or additionally, the effect on resection may be because Rad24 and Rad17 are involved in activating Mec1, which may then prevent resection by e.g. deactivation of

Sae2 (Cartagena-Lirola *et al.*, 2006) or Exo1 (Morin *et al.*, 2008). The 9-1-1 complex inhibits resection by promoting the recruitment of Rad9 near mitotic DSBs (Ngo & Lydall, 2015); however, this may not be the case for meiotic DSBs, because Rad9 is not required for checkpoint activation in meiosis (Lydall *et al.*, 1996).

rad24Δ strains also have an increase in ectopic recombination, which may be related to hyper-resection as the longer resection tracts uncover more ssDNA that could potentially pair with a non-allelic region (Gray *et al.*, 2013; Grushcow et al., 1999).

7.1.4. Genome-wide analysis of recombination in *rad24Δ* and *P$_{CLB2}$-MEC1* is confounded by low spore viability

In order to examine the roles of Rad24 and Mec1 in recombination rate, CO formation and interference between COs and DSBs, hybrid spores can be sequenced for marker analysis. However, both *rad24Δ* and *P$_{CLB2}$-MEC1* are more severely affected by being a hybrid than other backgrounds (Chapter 3, Figure 3.7A). This is likely because the rate of meiotic recombination is affected by sequence divergence; since meiotic recombination is already likely to be reduced in *rad24Δ* and *P$_{CLB2}$-MEC1*, any further reductions may be particularly deleterious. The very low spore viability of the hybrids (*rad24Δ* 0.73%, *P$_{CLB2}$-MEC1* 6%) makes these strains unsuitable for tetrad or octad analysis. However, the spore viability can be rescued in a variety of ways.

The mismatch repair protein Msh2 is responsible for detecting and rejecting mismatched DNA intermediates formed during strand invasion. Msh2 deletion is deleterious to spore viability in most pure or hybrid backgrounds (Chapter 3, Figure 3.7B&C). However, in *rad24Δ* and *P$_{CLB2}$-MEC1* hybrids, *msh2Δ* has an overall beneficial effect on spore viability. This is likely because strand invasion is more likely to be successful in the absence of Msh2 meaning that more recombination events can occur. The rejection of mismatched strand invasion intermediates is potentially important in order to prevent recombination with non-allelic sequences; however, in *RAD24* and *MEC1* mutants already have an increase in ectopic recombination (Gray *et al.*, 2013; Grushcow *et al.*, 1999), so there may not be a significant change in the probability that recombination will occur ectopically without MMR. Alternatively, the two factors could cause a synergistic increase in ectopic formation, but this is outweighed by the positive effects of *msh2Δ* such that there is an overall increase in viability.

As with non-hybrid strains, the spore viabilities of *rad24Δ* hybrids are rescued by *sml1Δ* and by *NDT80* prophase arrest (Chapter 3, Figure 3.9). Unlike the non-hybrid strain, *P$_{CLB2}$-MEC1* hybrids are also rescued by *NDT80* prophase arrest. Thus, using *msh2Δ*, *NDT80* prophase arrest and/or

sml1Δ in these backgrounds can improve viability enough to allow tetrad analysis, though not high enough for octad analysis. Instead, heteroduplex DNA information in *msh2Δ* tetrads is partially retained by harvesting entire sectored colonies and looking for variants present in a roughly 50:50 ratio (Chapter 4, Section 4.2.5).

Since some of the deleterious effects of *rad24Δ* and P_{CLB2}-*MEC1* are presumably abrogated by the rescues, meiotic recombination in the rescued strains may not resemble that of non-rescued checkpoint mutants; for example, if the rescue is increasing DSB or CO formation, then the number of recombination events detected will not be representative of the non-rescued phenotype. However, by assaying multiple different rescue backgrounds, a more complete picture can be uncovered by observing differences and similarities between them.

It is important to note that because only surviving spores can be assayed, spores with particularly deleterious occurrences such as dicentric/acentric chromosome formation from ectopic recombination can never be sequenced. Since only very few sets of four spores survive, the recombination events may not be representative of the population but instead represent extreme cases. However, a bias has only been previously shown for a *ZIP1* mutant with very inefficient sporulation (0.4%) (Chen *et al.*, 2008).

7.1.5. Aims of this investigation

1. To assay meiotic recombination genome wide in *rad24Δ* and P_{CLB2}-*MEC1* backgrounds, in order to establish the roles of these proteins in meiotic recombination.
2. To look for differences and similarities between Rad24 and Mec1 activity.
3. To utilise different rescue backgrounds to obtain a more complete picture of recombination in non-rescued checkpoint mutants.

7.2. Results

7.2.1. Alterations in CO and NCO numbers in *rad24Δ* and *P_{CLB2}-MEC1*

To assay recombination event formation in P_{CLB2}-*MEC1* and *rad24Δ* backgrounds, hybrid tetrads were obtained, sequenced and analysed as described in Chapter 4. For both backgrounds, six *msh2Δ* tetrads and six *NDT80* prophase extension tetrads were assayed. The length of prophase arrest was 8 hours for P_{CLB2}-*MEC1* tetrads, but 10 hours for *rad24Δ* tetrads to improve their lower spore viability. The normal activation of *NDT80* likely takes place somewhere between 4-5 hours into meiosis (Xu *et al.*, 1995), so the P_{CLB2}-*MEC1* + 8 h and *rad24Δ* + 10 h strains could be considered to have 3-4 or 5-6 extra hours in prophase, respectively. In addition, one *rad24Δ sml1Δ* tetrad and two *rad24Δ sml1Δ msh2Δ* tetrads were sequenced. These were not used for most analyses due to having fewer repeats. Raw data is available in the appendix (Table S2).

To determine whether CO and NCO numbers are altered in checkpoint mutants, and if the results are different in *msh2Δ* and *NDT80* prophase-arrest backgrounds, event numbers were examined in these strains (Figure 7.1; Table 7.1).

The *rad24Δ msh2Δ* tetrads had on average fewer COs than *msh2Δ* (~83.5 vs ~105); however, the P_{CLB2}-*MEC1 msh2Δ* tetrads had a much higher average of 134.7 COs (Figure 7.1A). *rad24Δ msh2Δ* tetrads had an average of ~113 NCOs, similar to the ~101 NCOs seen in WT and within 95% confidence intervals; P_{CLB2}-*MEC1 msh2Δ* again had a much higher average of ~213 NCOs (Figure 7.1A). Overall, P_{CLB2}-*MEC1 msh2Δ* had a dramatic 1.75x fold increase in total recombination event numbers compared to the *msh2Δ* control, something that was not observed in *rad24Δ msh2Δ*.

The almost 1:1 ratio of CO:NCO detection observed in *msh2Δ* is altered to 1:1.35 in *rad24Δ msh2Δ* and to 1:1.58 in P_{CLB2}-*MEC1 msh2Δ* (Figure 7.1C). Since both checkpoint mutants skew the ratio in favour of NCOs, this supports the idea that both Mec1 and Rad24 are important for promoting CO formation; alternatively, it could be that there is a limit on the number of COs that can form, so any excessive DSBs must be resolved as NCOs.

Overall, these results indicate that Mec1 meiotic activity may be important for limiting both CO and NCO numbers (but primarily NCO numbers), while Rad24 is responsible for promoting CO formation, but has no significant effect on NCO frequency. This suggests that Mec1 may be more important for controlling DSB frequency, whereas Rad24 is more involved in controlling CO frequency.

Table 7.1. Data summary for recombination events detected in *msh2Δ, P_{CLB2}-MEC1 msh2Δ,* rad24Δ msh2Δ, WT+8 h, P_{CLB2}-MEC1 +8 h, rad24Δ +10 h, rad24Δ msh2Δ sml1Δ* and *rad24Δ sml1Δ* backgrounds.

Separate samples for each genotype are shown. TN: Ndt80 arrest tetrad, OM: *msh2Δ* octad, TRM: *rad24Δ msh2Δ* tetrad, TCMM: *P_{CLB2}-MEC1 msh2Δ* tetrad, *TRN: rad24Δ +10 h* tetrad, TCMN: *P_{CLB2}-MEC1 +8 h* tetrad, *TRS: rad24Δ sml1Δ* tetrad, TRMS: *rad24Δ msh2Δ sml1Δ* tetrad. Columns contain the number of COs, NCOs and Undetermined (U) events detected, the overall number of events, the number of chromosomes without COs (CWCs), the identity of the CWCs, the number of double COs closer than 1.5kb (dCOs), the number of events containing an 8:0/0:8 or 7:1/1:7 segment, the number of COs without a detectable conversion tract, and the number of NCOs that were composed only of hDNA.

Meiosis	CO	NCO	U	Total	CO:NCO	CWCs Frequency	CWCs Identity	dCO number	8:0	7:1	COs without tracts	NCOs hDNA only
msh2Δ												
Average	**105.0±3**	**101.8±8**	**0**	**206.8±7**	**1:0.98**			**0.2**	**0.1**	**0.4**	**14.9**	**64.1**
OM1	116	109	0	225	1:0.94	0	-	0	0	0	13	45
OM2	100	125	0	225	1:1.25	0	-	0	0	0	8	69
OM3	95	100	0	195	1:1.05	0	-	0	0	0	18	50
OM4	105	98	0	203	1:0.93	0	-	1	0	1	11	50
OM5	98	79	0	177	1:0.81	0	-	0	0	0	19	41
OM6	116	65	0	181	1:0.56	0	-	1	1	0	22	37
OM7	98	139	0	237	1:1.42	0	-	0	0	1	11	70
OM8	107	113	0	220	1:1.06	0	-	0	0	2	21	62
OM9	110	88	0	198	1:0.80	0	-	0	0	0	10	45
rad24Δ msh2Δ												
Average	**83.5±8**	**113.0±15**	**0.67**	**197.2±21**	**1:1.35**			**0.5**	**0.7**	**2.0**	**8.8**	**44.2**
TRM1	54	53	0	107	1:0.98	2	Chr 5, 15	0	0	0	12	32
TRM2	86	121	0	207	1:1.41	1	Chr 1	1	2	4	5	43
TRM3	104	159	0	263	1:1.53	0	-	0	2	5	8	68
TRM4	82	130	1	213	1:1.59	2	Chr 6, 8	1	0	1	13	41
TRM5	102	96	2	200	1:0.94	1	Chr 8	1	0	1	10	30
TRM6	73	119	1	193	1:1.63	0	-	0	0	1	5	51
P_{CLB2}-MEC1 msh2Δ												
Average	**134.7±14**	**213.8±19**	**1**	**349.5±30**	**1:1.67**			**1.5**	**3.2**	**5.3**	**22.3**	**56.7**
TCMM4	66	159	0	225	1:2.41	1	Chr 8	1	1	1	11	48
TCMM8	145	230	1	376	1:1.59	0	-	0	4	6	30	58
TCMM15	137	196	1	334	1:1.43	0	-	0	1	5	19	61
TCMM16	144	211	1	356	1:1.47	0	-	3	3	5	21	42
TCMM18	162	190	2	354	1:1.17	0	-	2	5	4	38	30
TCMM19	154	297	1	452	1:1.93	0	-	3	5	11	15	101
WT + 8 h												
Average	**97.3±11**	**51.0±8**	**0.5**	**148.8±19**	**1:0.52**			**1.5**	**2.5**	**-**	**20.5**	**-**
TN1	70	34	0	104	1:0.49	0	-	0	1	-	11	-
TN2	90	43	0	133	1:0.48	0	-	1	1	-	23	-
TN3	121	61	1	183	1:0.50	0	-	4	5	-	29	-
TN4	108	66	1	175	1:0.61	0	-	1	3	-	19	-
rad24Δ + 10 h												
Average	**125.0±11**	**92.0±13**	**1.5**	**218.5±22**	**1:0.73**			**3.0**	**9.3**	**-**	**25.3**	**-**
TRN1	146	112	4	262	1:0.77	0	-	3	17	-	28	-
TRN2	142	68	2	212	1:0.48	0	-	3	7	-	38	-
TRN4	107	70	0	177	1:0.65	1	Chr 6	6	7	-	20	-
TRN10	155	130	3	288	1:0.84	0	-	2	13	-	23	-
TRN11	87	52	0	139	1:0.60	1	Chr 6	0	6	-	26	-
TRN20	113	120	0	233	1:1.06	0	-	4	6	-	17	-
P_{CLB2}-MEC1 + 8 h												
Average	**126.8±18**	**90.7±17**	**1**	**218.5±35**	**1:0.69**			**3**	**15.8**		**22.3**	
TCMN1	196	143	0	339	1:0.73	0	-	2	21	-	26	-
TCMN2	97	51	0	148	1:0.53	0	-	1	9	-	28	-
TCMN3	135	88	0	223	1:0.65	0	-	2	15	-	23	-
TCMN4	106	79	2	187	1:0.75	0	-	3	7	-	16	-
TCMN5	152	139	3	294	1:0.91	0	-	3	32	-	30	-
TCMN6	75	44	1	120	1:0.59	1	Chr 1	6	11	-	11	-
rad24Δ sml1Δ												
TRS10	34	15	3	52	1:0.44	6	Chr 1, 5, 8, 11, 12, 14	2	8	-	7	-
rad24Δ sml1Δ msh2Δ												
TRMS1	92	73	0	165	1:0.79	1	Chr 3	0	2	1	10	46
TRMS2	61	26	0	87	1:0.43	2	Chr 3, 8	0	1	0	9	19
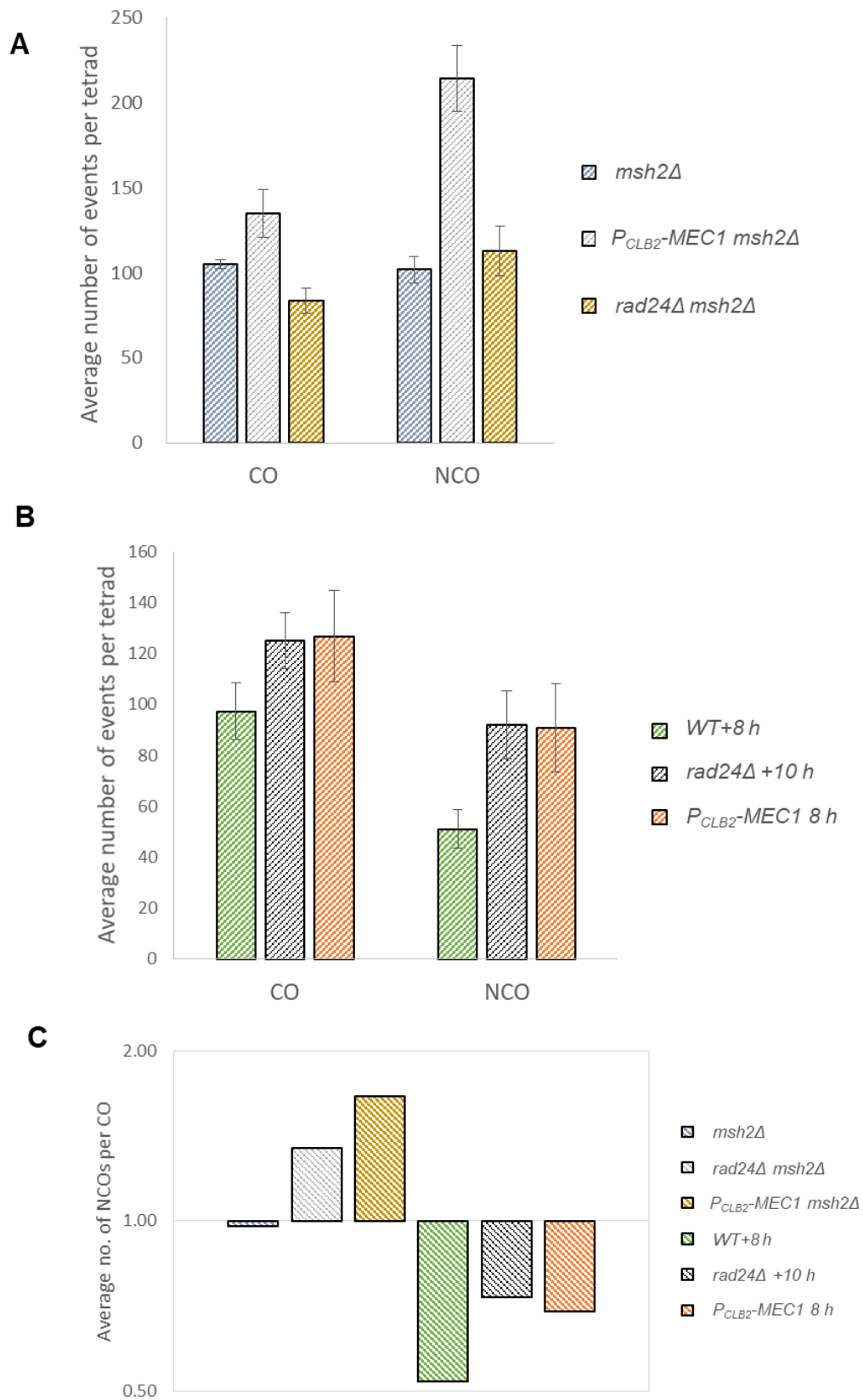
Figure 7.1. Quantity of recombination events detected in Msh2 deficient and prophase arrested *rad24Δ* and *P*$_{CLB2}$*-MEC1* strains. All error bars are 95% confidence limits. Strain details are given in Table 2.1, raw event data is available in Table S2. Average number of CO and NCO events per tetrad in **A**) Msh2 deficient strains, **B**) prophase arrest strains. C) CO: NCO ratio for all strains, plotted as average no. of NCOs per CO.

Msh2 deficient strains

Prophase extension strains
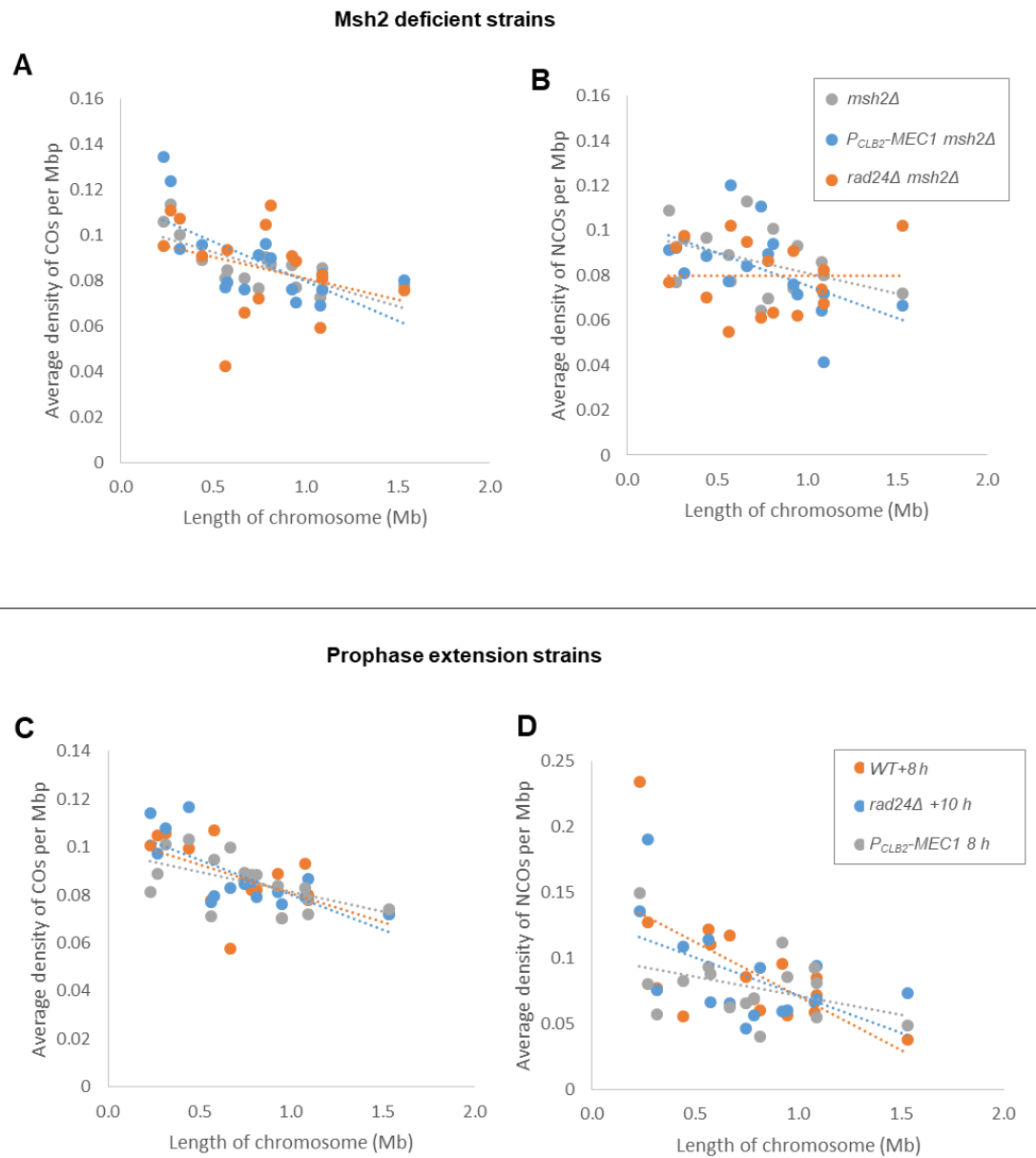
Figure 7.2. Density of recombination events detected in Msh2 deficient or prophase arrested *rad24Δ* and *P_CLB2*-*MEC1* strains. Strain details are given in Table 2.1, raw event data is available in Table S2. The average number of CO/NCO events per chromosome is divided by the average total CO/NCO count, then divided by the chromosome length in Mbp. Density of **A)** COs and **B)** NCOs per Mbp in MMR-deficient strains; **C)** COs and **D)** NCOs per Mbp in prophase-extension strains. Dotted lines are linear regressions. R^2: *msh2Δ* CO 0.54, NCO 0.20; *rad24Δ msh2Δ* CO 0.12, NCO 0.01; *P_CLB2*-*MEC1 msh2Δ* CO 0.45, NCO 0.31; WT + 8 h CO 0.36, NCO 0.40; *rad24Δ* + 10 h CO 0.31, NCO 0.15; *P_CLB2*-*MEC1* + 8 h CO 0.55, NCO 0.31.

By contrast, the effect of *NDT80* prophase extension abrogated many of the differences observed between *rad24Δ* and P_{CLB2}-*MEC1* in the *msh2Δ* background. For example, the *rad24Δ* +*10 h* and P_{CLB2}-*MEC1*+*8 h* tetrads had very similar average counts for COs (~125 and ~126.8 respectively) and NCOs (~92 and ~90.7 respectively). However, both were significantly higher than the WT+*8 h* control (~97.3 COs and ~51 NCOs), an overall ~1.5x increase in recombination event formation (Figure 7.1B).

In the *NDT80* prophase extension WT, a CO:NCO ratio of 1:0.52 is observed, which is increased to 1:0.74 in *rad24Δ* and 1:0.72 in P_{CLB2}-*MEC1* (Figure 7.1C). As with the *msh2Δ* strains, both checkpoint mutants show a disproportionate increase in NCO formation, suggesting a role in the promotion of CO formation, or that there is a maximum limit on CO formation due to CO homeostasis (Martini et al., 2006). The *NDT80* prophase-arrested strains have fewer NCOs per CO than their *msh2Δ* equivalents, likely due to the ability to detect more NCOs in a *msh2Δ* background (Chapter 5, Section 5.2.1).

Overall, these results indicate that when prophase is extended, both Rad24 and Mec1 have an equal role in limiting the amount of CO and NCO events formed, but are more important for limiting NCOs than COs, and so perhaps are both involved in controlling DSB frequency and promoting CO formation.

The event counts in *msh2Δ* compared to *NDT80* prophase extension backgrounds seem contradictory for *rad24Δ* but not for P_{CLB2}-*MEC1*. This may be related to the fact that, in non-hybrids, only *rad24Δ* is rescued by *NDT80* prophase arrest and P_{CLB2}-*MEC1* is unaffected. In addition, while P_{CLB2}-*MEC1* yeast is more viable than *rad24Δ* (~60% vs ~22%), the viability of *rad24Δ* is higher than that of P_{CLB2}-*MEC1* when *rad24Δ* has a hypomorphic Spo11 allele and a prophase length of >=6h (e.g. ~83% in *rad24Δ spo11-D290A* +10 h, ~60% in P_{CLB2}-*MEC1 or* P_{CLB2}-*MEC1 +10 h spo11-D290A*) (Chapter 3, Figures 3.1A and 3.3B). The reason why *rad24Δ* viability surpasses that of P_{CLB2}-*MEC1* under these specific circumstances may be that *rad24Δ* is less tolerant of an excessive number of DSBs than P_{CLB2}-*MEC1*, so hypomorphic Spo11 activity is advantageous under these circumstances. A possible explanation for this is that *rad24Δ* may have a loss of DSB and/or CO interference, causing any excessive DSBs to form deleterious clusters, while P_{CLB2}-*MEC1* may have more normal interference, meaning that extra recombination events are still properly spaced. This is discussed further in Section 7.2.8.

The number of NCOs is likely to be an underestimate caused by events occurring in regions without markers (Mancera *et al.*, 2008). The percentage of observed COs that occur between markers and thus have no detectable conversion tract can be used to estimate the number of NCOs

that may be invisible due to falling between markers. An average of 10.5% of COs in *rad24Δ msh2Δ*, 16.6% in *P_{CLB2}-MEC1 msh2Δ*, 20.2% in *rad24Δ +10 h* and 17.6% in *P_{CLB2}-MEC1 +8 h* had no associated conversion tracts (Table 7.1). Based on this, an additional 12, 35, 19 and 16 NCOs are estimated to have occurred in regions without markers, in *rad24Δ msh2Δ*, *P_{CLB2}-MEC1 msh2Δ*, *rad24Δ+10 h* and *P_{CLB2}-MEC1+8 h* respectively.

In addition, the number of NCOs detected in MMR-deficient strains that were composed only of hDNA can be used to estimate the number of NCOs that may have occurred in MMR-proficient strains but were repaired invisibly to restoration tracts by MMR. In the MMR-deficient strains, an average of ~38.9% and ~26.6% of NCOs in *rad24Δ* and *P_{CLB2}-MEC1* respectively were composed of hDNA patterns only (Table 7.1). Assuming that in MMR-proficient strains, half of such events are repaired to a conversion and half are restored, an additional 18 and 12 undetected NCOs are predicted to have occurred in *rad24Δ+10 h* and *P_{CLB2}-MEC1+8 h* strains respectively. Overall, the estimated invisible NCO counts for each strain raise the overall NCO count from ~113 to ~125 in *rad24Δ msh2Δ*, from ~214 to ~248 in *P_{CLB2}-MEC1 msh2Δ*, from ~92 to ~129 in *rad24Δ + 10 h*, and from ~91 to ~119 in *P_{CLB2}-MEC1 + 8 h*. The estimated NCO counts are now similar in both *rad24Δ* strains and in *P_{CLB2}-MEC1+8 h*, but are still much higher in *P_{CLB2}-MEC1 msh2Δ*. This suggests that there is a particularly high amount of DSB formation in this background, with the excess all becoming NCOs due to CO homeostasis, or that NCOs are favoured over COs. This may also be the case in *P_{CLB2}-MEC1 + 8 h*, but the rejection of strand invasion into mismatched sequences by Msh2 may cause more potential NCOs to be repaired with the sister chromatid.

A single *rad24Δ sml1Δ* tetrad was also sequenced. This tetrad displayed highly abnormal meiotic recombination, with only 34 COs and 15 NCOs detected (Table 7.1). This supports the idea that *sml1Δ* rescues the *rad24Δ* phenotype by boosting nucleotide pools for efficient repair, rather than actually increasing event numbers, unlike either *msh2Δ* or *NDT80* prophase extension. Thus, the *rad24Δ sml1Δ* tetrad probably best represents the true *rad24Δ* phenotype out of all the rescue strains (at least in terms of event numbers), but unfortunately the viability was too low to sequence enough tetrads for further analysis.

Two *rad24Δ msh2Δ sml1Δ* tetrads were also sequenced; the two repeats were quite variable, with one having 92 COs and 73 NCOs, while the other had 61 COs and 26 NCOs (Table 7.1). These features are generally similar to those of *rad24Δ msh2Δ* tetrads.

7.2.2. Loss of CO assurance in *rad24Δ*

In WT, *msh2Δ* and WT+ 8 h meiosis, there is a negative correlation between chromosome length and the density of DSB formation, dependent on Zip3 (Thacker *et al.*, 2014; Chapter 5, Section 5.2.2). To determine whether this correlation is affected by Mec1 or Rad24 deficiency, the relationship between chromosome length and CO and NCO number was examined in *NDT80* prophase-extended and *msh2Δ* checkpoint mutant strains (Figure 7.2). In all of the backgrounds examined, the density of both COs and NCOs decreases with chromosome size, indicating that the checkpoint mutant strains have a normal relationship between DSB/CO formation and chromosome length.

Normally, meiotic COs are distributed so that each chromosome has at least one CO, which helps prevent nondisjunction of chromosomes. Crossover assurance is the name for the observation that every chromosome gets a CO, regardless of length. However, many chromosomes without COs were observed in *rad24Δ* strains (Table 7.1). Among the six *rad24Δ msh2Δ* tetrads, two had two chromosomes without COs, and two had one chromosome without a CO. The chromosomes affected were Chr 1, 5, 6, 15 and 8 twice. Most of these are among the shortest chromosomes, but Chr 15 is the third longest. This suggests that the low number of COs in *rad24Δ msh2Δ* affects crossover assurance, or that *rad24Δ* directly regulates CO assurance independently of CO numbers. In *rad24Δ* +10 h strains, only two out of six tetrads had one chromosome without a CO, which was the short Chr 6 in both cases (Table 7.1). This suggests that crossover assurance is more reliable in *rad24Δ* when prophase is extended, perhaps due to the ~1.5x increase in CO frequency observed in *rad24Δ* + 10 h vs *rad24Δ msh2Δ*, which could simply mean that there are enough events for each chromosome to receive one by chance. The formation of noncrossover products between homologous chromosomes also contributes to their stable pairing, though not as much as CO formation (Peoples-Holst & Burgess, 2005). All the CO-less chromosomes in *rad24Δ msh2Δ* has at least one NCO event; however, neither of the ones in *rad24Δ* + 10 h had an NCO.

Among P_{CLB2}-*MEC1* strains, chromosomes without COs were infrequent. Only one out of six P_{CLB2}-*MEC1* tetrads had a chromosome without a detected CO (or NCO), Chr 8, and one out of six P_{CLB2}-*MEC1* +8 h tetrads had a chromosome without a CO (but two NCOs), Chr 1. However, these cases may not represent a loss of crossover assurance. Examination of recombination in these two specific tetrads (known as 'TCMM4' and 'TCMN6', for '**T**etrad P_{CLB2}-*MEC1* *msh2Δ*/**N**dt80' revealed some unusual features not seen in other P_{CLB2}-*MEC1* tetrads. The chromosome 8 apparently without a CO in the P_{CLB2}-*MEC1* *msh2Δ* TCMM4 appears to actually have undergone a mitotic duplication of the S288c copy prior to sporulation. This is apparent because from the final tetrad, two spores had normal S288c chromosomes and two had mixed reads for almost the entire length of chromosome 8, indicating that they had two copies of the

chromosome, one from each parent (Figure 7.3A). Thus, no COs could be detected on this chromosome, but some could have occurred invisibly. In addition, the P_{CLB2}-*MEC1* +*8 h* tetrad TCMN6 had a number of partial chromosome conversions; two spores contain chromosomes where a substantial portion has been converted to the other parental genotype, which must have occurred prior to meiotic S phase, or only one copy would have been converted (Figure 7.3B). Approximately half of Chr 4, two-fifths of Chr 7 and one quarter of Chr 10 have been converted to entirely S288c, SK1 or S288c sequence respectively. The unaffected portions of each chromosome display normal meiotic recombination, with both COs and NCOs evident. However, the chromosome without a CO in this tetrad, Chr 1, did not have a partial conversion, so this may still represent a loss of CO assurance.

The observation that mitotic duplication events have occurred in P_{CLB2}-*MEC1* may be related to the use of the *CLB2* promoter, which could potentially affect Mec1 expression during mitotic growth, causing Mec1 to be expressed at inappropriate times, or in inappropriate quantities.
The single *rad24Δ sml1Δ* tetrad had six chromosomes lacking a CO, Chrs 1, 5, 8, 11, 12 and 14, most of which are not especially short. This tetrad likely represents a unique case. Out of 196 dissected tetrads, only one four spore viable was obtained. If all *rad24Δ sml1Δ* tetrads have so many chromosomes without COs, it is likely that this surviving tetrad was 'lucky' in that all chromosomes fortuitously segregated correctly. Each of the chromosomes without a CO in *rad24Δ sml1Δ* also lacked any detectable NCOs, so NCO formation did not contribute to homolog pairing either. Of the two *rad24Δ msh2Δ sml1Δ* tetrads, one had one chromosome without a CO, but two NCOs (Chr 3), while the other had two chromosomes without COs or NCOs (Chr 3 and 8).
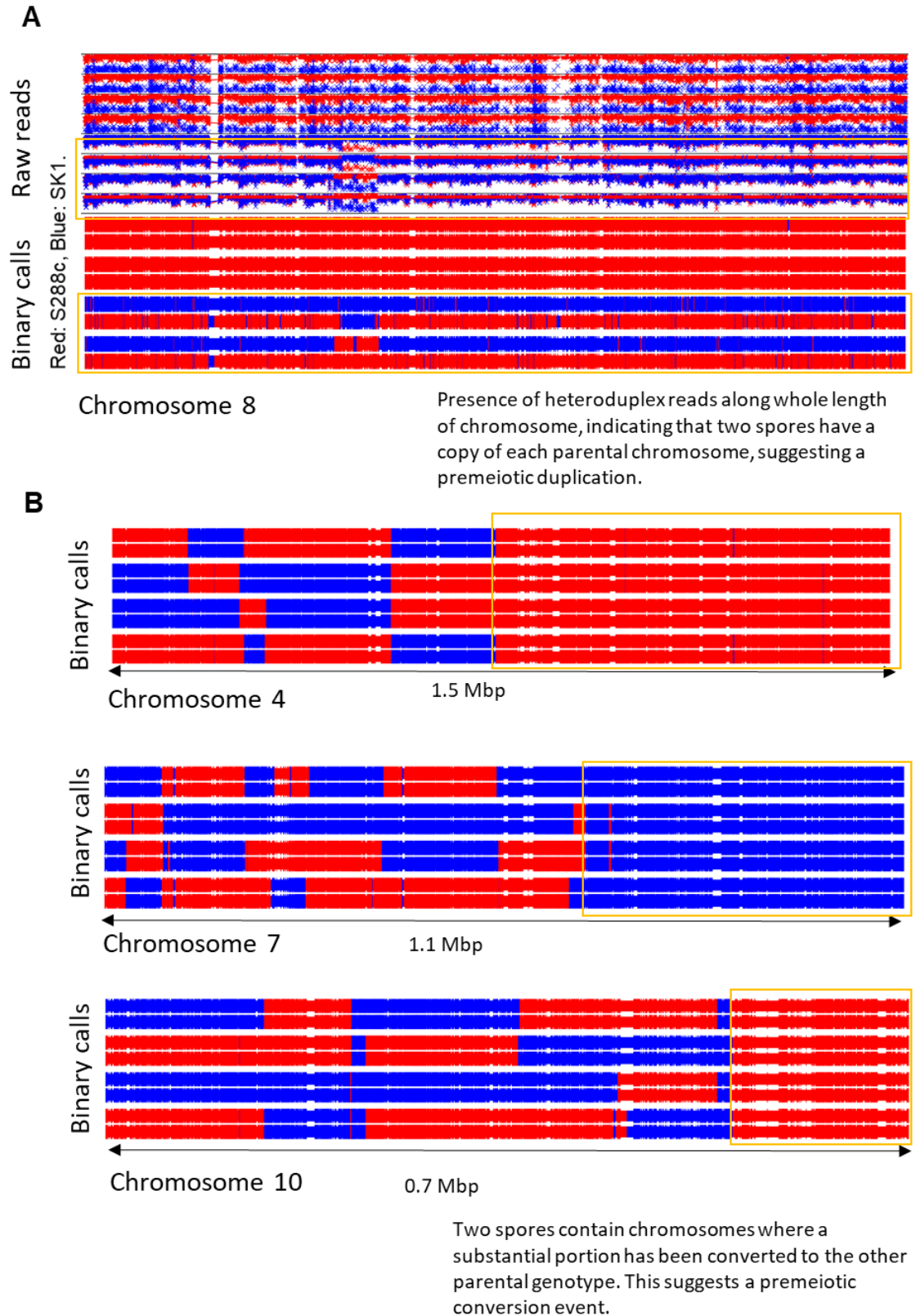
Figure 7.3. Abnormal mitotic recombination events in P_{CLB2}-*MEC1* strains. Whole chromosome recombination patterns were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight horizontal lines corresponding to the eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. **A)** A duplication of S288c Chr 8 in a P_{CLB2}-*MEC1 msh2Δ* tetrad (TCMM4); **B)** partial chromosome conversions on Chr 4, 7 and 10 in a P_{CLB2}-*MEC1* +10 h tetrad (TCMN6). Raw reads indicate the frequency of reads containing SK1 or S288c type polymorphisms detected at each position; these are translated into binary calls, which can only be SK1 or S288c.

Rad24 is known to interact with Zip3, independently of Mec1 (Shinohara et al., 2015), so this may explain the difference between Rad24 and Mec1 in establishing the relationship between chromosome length and recombination event density. However, the *NDT80* prophase-arrested *rad24Δ* strain did not display such a defect. This suggests that prophase length, and/or the lower CO count observed in *rad24Δ msh2Δ* compared to *rad24Δ* +10 h (Figure 7.1), may be important for establishing the relationship between chromosome length and DSB/CO numbers in the absence of the Rad24-Zip3 interaction.

Alternatively, the increased incidence of chromosomes without crossovers among *rad24Δ* strains may simply be related to low CO counts, because the tetrads with the lowest CO counts are also those most likely to have a chromosome without a CO (Figure 7.4). Since P_{CLB2}-*MEC1* strains tend to have higher CO counts than *rad24Δ* strains, they may be expected to have fewer chromosomes without COs, just by chance.
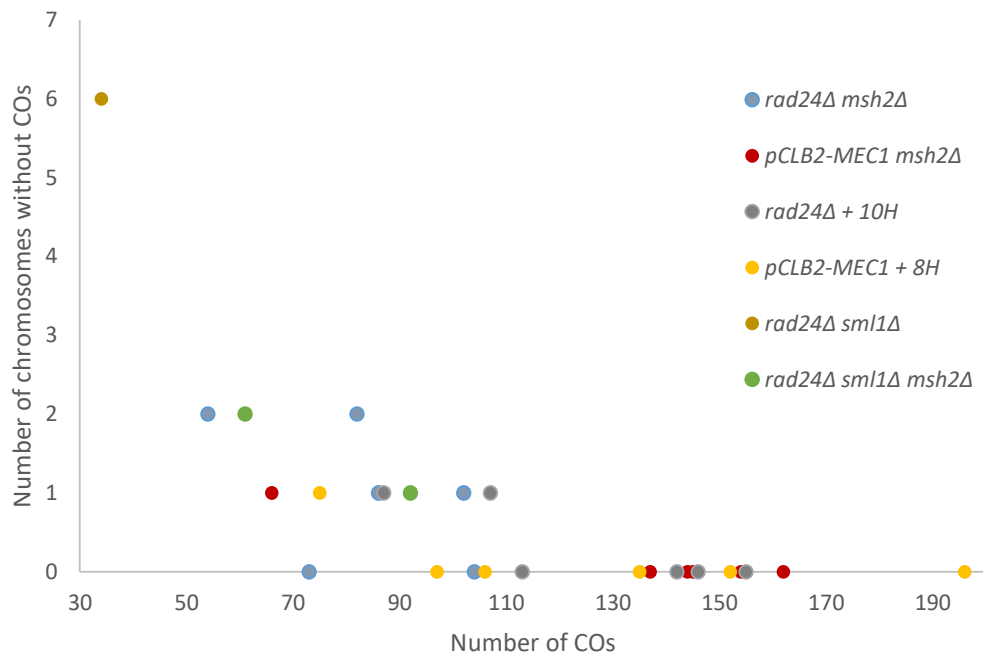
Figure 7.4. Relationship between CO number and the number of chromosomes without COs in *rad24Δ* and *pCLB2-MEC1* strains. The number of COs detected in each meiosis is plotted against the number of chromosomes lacking a CO in that meiosis.

7.2.3. The complexity of detected recombination events is altered in checkpoint mutants

Recombination events in each strain were categorized further as described in Chapter 4, Section 4.2.9 (Table 7.2, Figure 7.5, Figure 7.6). Briefly, Group 1 contains events with simple signatures, Groups 2 and 3 events with signatures indicative of complex repair, and Group 0 contains events likely to be part of a cluster of Spo11-DSBs occurring closer than 1.5kb.

For the MMR-proficient *NDT80* prophase extension strains, events could not be categorized in full detail due to the inability to detect hDNA tracts (Group 2 COs and NCOs, which contain *trans* hDNA [symmetrical hDNA patterns on the same or different chromatids], cannot be seen). Due to this, proportions of events in each category cannot be compared between the *msh2Δ* and *NDT80* prophase arrest backgrounds.

In addition, because the MMR-deficient strains were tetrads rather than octads, the ability to detect *trans* hDNA on the same chromatid is lost because there is no strand information (as discussed in Chapter 4, Section 4.2.5), meaning that no NCOs composed of *trans* hDNA will be detected (however, trans hDNA on different chromatids can be seen, as in CO Group 2). To allow proper comparison with the *rad24Δ msh2Δ* and *P_{CLB2}-MEC1 msh2Δ* tetrads, the *msh2Δ* octads were reanalysed as 'mock tetrads' summing the reads from each pair of mother-daughter spores to give an output resembling that of a *msh2Δ* tetrad, with a mixture of reads at heteroduplex positions. Another way in which *msh2Δ* octads and tetrads differ is in the ability to detect duplications causing the presence of mixed reads, which will instead be categorized as NCOs (as discussed in Section 4.2.6). This is discussed further in Section 7.2.7.

In the MMR-deficient strains, there was a reduced proportion of COs detected in *P_{CLB2}-MEC1* and *rad24Δ msh2Δ* that displayed signatures of complex repair (Groups 2 and 3), and an increased proportion of COs likely to have occurred as part of a cluster of Spo11-DSBs (Group 0) (Figure 7.5A). In *rad24Δ msh2Δ*, the proportion of COs classified as being part of DSB cluster was also increased, though not to the same extent as in *P_{CLB2}-MEC1 msh2Δ*.

For both *rad24Δ msh2Δ* and *P_{CLB2}-MEC1 msh2Δ*, there was a lower proportion of simple NCOs (Group 1) and a higher proportion of NCOs occurring as part of a cluster of Spo11-DSBs (Group 0) (Figure 7.5B). Note that in *msh2Δ* tetrads, any NCO events that would have displayed *trans* hDNA in an octad, and thus be sorted into Group 2, would be sorted into Group 1 instead, so the decrease in Group 1 NCOs could also reflect a reduction in Group 2 NCOs.

Table 7.2. Data summary of the percentage of CO and NCO events in each group and class.

For events detected in *msh2Δ*, *P_{CLB2}-MEC1 msh2Δ*, *rad24Δ msh2Δ*, *WT+8 h*, *P_{CLB2}-MEC1 +8 h*, and *rad24Δ +10 h* backgrounds. A short description of the characteristics of each group and class is given.

Crossover Groups		msh2Δ as tetrad %	pCLB2-MEC1 msh2Δ %	rad24Δ msh2Δ %	rad24Δ msh2Δ sml1Δ %	WT %	WT +8H %	pCLB2-MEC1 +8H %	rad24Δ +10H %
Group 1: Simple - no trans hDNA or incompatible hDNA									
Total		61.54	64.24	59.49	57.16	92.95	89.97	74.51	74.79
Class 1	(5:3)_(4:4aCO) - CO with hDNA tract	4.45	2.1	5.19	2.12				
Class 2	(3:5)_(4:4aCO) - CO with hDNA tract	4.24	2.72	3.19	3.17				
Class 3	(5:3)_(4:4)_(4:4aCO) - hDNA, restoration tract, CO pattern	0.74	0.25	0	0				
Class 4	(4:4aCO)_(5:3)_(4:4a) - Same as above but in opposite direction.	0.74	0.25	0.8	0				
Class 5	(3:5)_(4:4)_(4:4aCO) - hDNA, restoration tract, CO pattern	0.11	0.37	0.2	0				
Class 6	(4:4aCO)_(3:5)_(4:4a) - Same as above but in opposite direction.	0.95	1.11	0.4	0				
Class 7	(5:3)_(6:2)_(4:4aCO) - hDNA, conversion tract, CO pattern	1.48	1.49	2	2.12				
Class 8	(6:2)_(5:3)_(4:4aCO) - Same as above but in opposite direction.	1.8	0.87	1.6	0				
Class 9	(3:5)_(2:6)_(4:4aCO) - hDNA, conversion tract, CO pattern	2.01	0.5	1.4	1.06				
Class 10	(2:6)_(3:5)_(4:4aCO) - Same as above but in opposite direction.	2.33	2.1	2.79	2.12				
Class 11	Contains 4:4i (symmetrical hDNA)	1.8	0.62	2.2	1.06				
Class 12	Anything else	16	16.34	15.97	19.05	5.37	9.51	8.02	9.73
Class 15	(6:2)_(4:4aCO) - CO with conversion tract	5.61	9.16	4.59	8.47	33.22	26.48	22.6	22.53
Class 16	(2:6)_(4:4aCO) - CO with conversion tract	6.36	9.78	8.58	7.41	37.25	32.9	26.41	22.4
Class 100	4:4aCO: CO in marker-sparse region	12.92	16.58	10.58	10.58	17.11	21.08	17.48	20.13
Group 2: Presence of trans hDNA, but not incompatible hDNA									
Total		9.53	3.83	9.38	4.23	0	0	0	0
Class 30	adjacent 5:3 5:3a, plus any other segments	2.22	1.11	2.79	0				
Class 31	adjacent 3:5 3:5a, plus any other segments	1.91	0.62	1.2	1.06				
Class 32	non-adjacent trans hDNA i.e. have conversion or restoration tract in between	5.4	2.1	5.39	3.17				
Group 3: Presence of incompatible hDNA									
Total		22.56	12.5	18.57	11.64	2.68	1.8	5.78	5.73
Class 20	Contains 4:4i (symmetrical hDNA)	20.02	11.63	16.57	11.64	2.68	1.8	5.78	5.73
Class 21	Anything else	2.54	0.87	2	0				
Group 0: Multiple Spo11-DSBs: Affects 3 or 4 chromatids									
Total		6.35	19.43	12.57	26.98	4.37	8.22	19.71	19.46
Class 2	CO ± NCO involving 3 or 4 chromatids	5.61	14.23	9.58	11.64	4.03	4.88	14.06	10.93
Class 3	CO ± NCO involving 3 or 4 chromatids, contains different 4:4 patterns	0.74	5.2	2.99	15.34	0.34	3.34	5.65	8.53
Noncrossover Groups		msh2Δ as tetrad %	pCLB2-MEC1 msh2Δ %	rad24Δ msh2Δ %	rad24Δ msh2Δ sml1Δ %	WT %	WT +8H %	pCLB2-MEC1 +8H %	rad24Δ +10H %
Group 1: SDSA-like: Affects one chromatid, no trans hDNA									
Total		79.94	68.04	67.1	63.23	80.38	85.78	60.29	52.73
Class 1	5:3 - composed of hDNA only	20.76	12.7	19.62	17.65				
Class 2	3:5 - composed of hDNA only	23.67	13.09	18.58	13.97				
Class 3	5:3_6:2_5:3 or 5:3_4:4_5:3 - Conversion/restoration tract between hDNA	8.93	3.66	2.36	4.41				
Class 4	3:5_6:2_3:5 or 3:5_4:4_3:5 - Conversion/restoration tract between hDNA	8.83	3.51	4.87	0.74				
Class 7	6:2 plus any other segments	4.91	5.69	3.24	1.47	0.63	1.96	0.92	2.54
Class 8	2:6 plus any other segments	5.32	6.24	5.16	4.41	1.27	0.98	1.47	2.36
Class 10	6:2 - composed of conversion tract only	4.01	11.38	6.19	11.76	36.71	47.06	23.71	21.92
Class 10.1	2:6 - composed of conversion tract only	3.51	11.77	7.08	8.82	41.77	35.78	34.19	25.91
Group 2: dHJ-dissolution-like: Affects one chromatid, has trans hDNA									
This group not applicable to tetrads		0	0	0	0	0	0	0	0
Group 3: Affects two non-sister chromatids									
Total		7.82	5.69	8.85	8.82	2.53	1.96	2.94	3.26
Class 30	Contains 4:4i (symmetrical heteroduplex)	4.51	4.75	6.34	7.35	2.53	1.96	2.94	3.26
Class 31	Anything else	3.31	0.94	2.51	1.47				
Group 0: Multiple Spo11-DSBs: Affects two sister, 3 or 4 chromatids									
Total		12.24	26.26	24.04	30.88	17.09	13.23	36.76	44.02
Class 1	NCO involving 2_sis, 3 or 4 chromatids	3.41	7.79	6.49	15.44	1.27	2.94	9.56	7.25
Class 2	NCO+CO involving 3 or 4 chromatids	5.12	8.81	6.19	7.72	7.59	7.35	15.99	12.68
Class 3	NCO±CO involving 3 or 4 chromatids, contains different 4:4 patterns	3.71	9.66	11.36	7.72	8.23	2.94	11.21	24.09
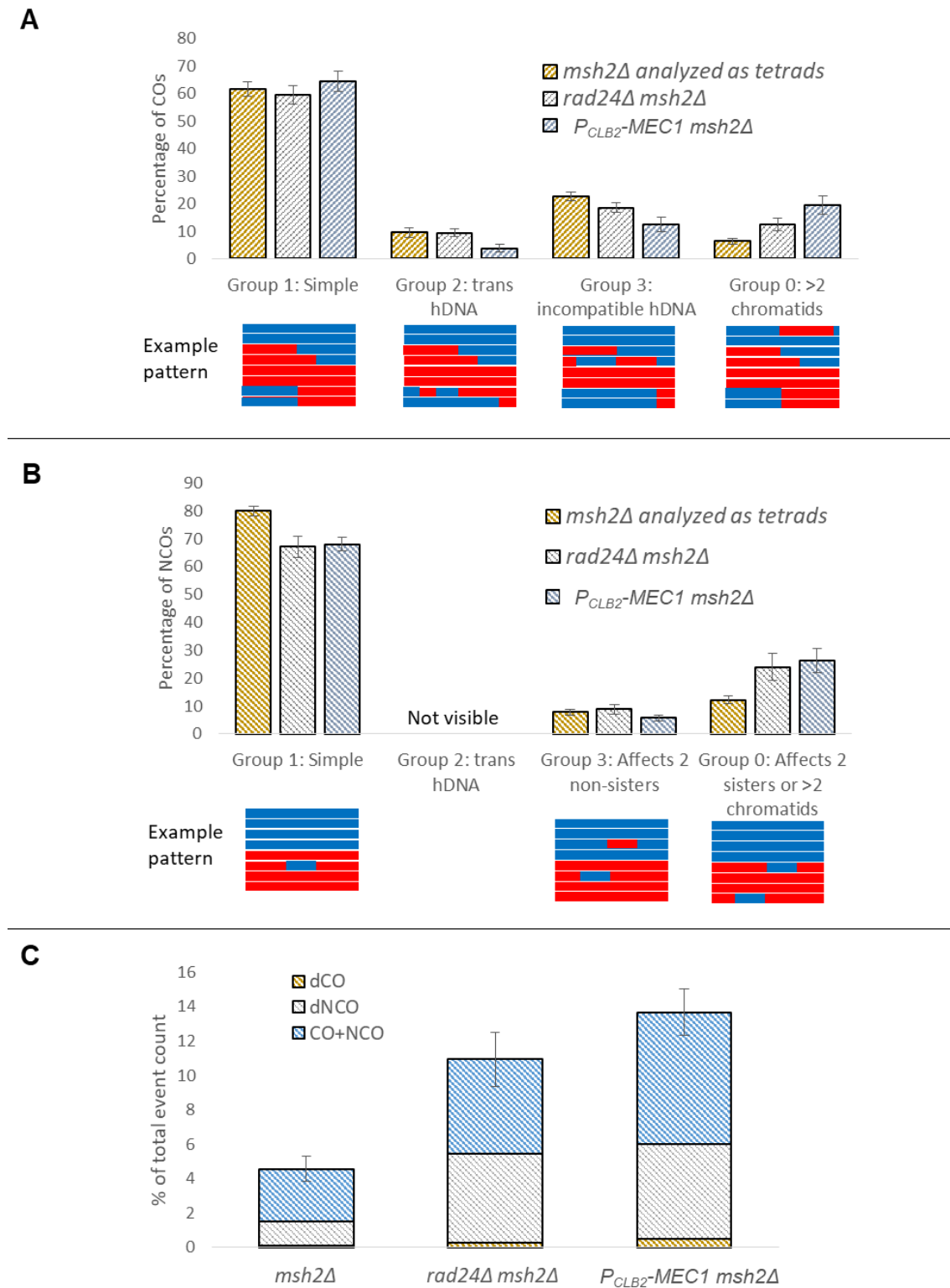
Figure 7.5. Categories of recombination events detected in Msh2-deficient *rad24Δ* and P_{CLB2}-MEC1 strains. Error bars are 95% confidence limits. Strain details are given in Table 2.1, raw event data is available in Table S2. A simple example event for each category is shown directly beneath the X-axis, with the red and blue lines corresponding to the eight strands of DNA present during meiotic recombination, four from each parent. **A)** Average percentage of COs and **B)** NCOs in each group. Group 2 NCOs are not possible to detect in msh2Δ tetrads, and will instead appear as Group 1 NCOs. **C)** Comparison of the average percentage of events thought to be DSB clusters (overall Group 0), with sublevels indicating whether the clusters were inferred to be a double CO, double NCO or CO plus NCO.
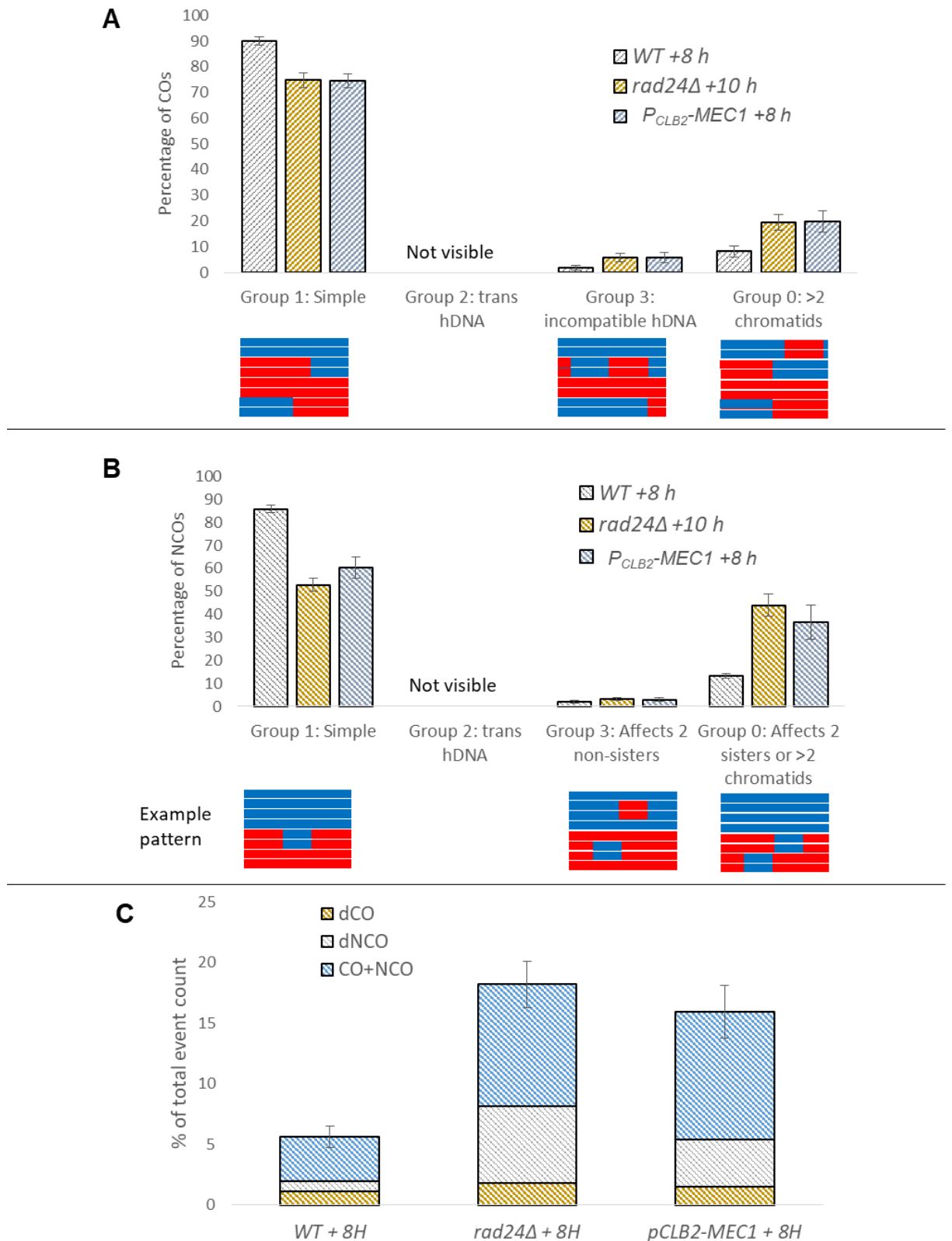
Figure 7.6. Categories of recombination events detected in *rad24Δ* and *P~CLB2~-MEC1* strains with prophase extension. Error bars are 95% confidence limits. Strain details are given in Table 2.1, raw event data is available in Table S2. A simple example event for each category is shown directly beneath the X-axis, with the red and blue lines corresponding to the eight strands of DNA present during meiotic recombination, four from each parent. **A)** Average percentage of COs and **B)** NCOs in each group. Group 2 is not available in MMR-proficient strains. **C)** Comparison of the average percentage of events thought to be DSB clusters (overall Group 0), with sublevels indicating whether the clusters were inferred to be a double CO, double NCO or CO plus NCO.

In the MMR-proficient *NDT80* prophase extension strains, P_{CLB2}-*MEC1 +8 h* and *rad24Δ +10 h* displayed very similar proportions of subcategories for both COs and NCOs (Figure 7.5A,B). Both had a reduced proportion of simple NCOs (Group 1), but an increase in complex repair (Group 3) and NCOs occurring in DSB clusters (Group 0). For COs, both checkpoint mutants had a reduction in the proportion of simple-signature COs (Group 1) and an increase in COs occurring in DSB clusters (Group 0). Note that Group 2 is not available in MMR-proficient backgrounds, so events with this signature of complex repair will be likely categorized into Group 1.

The main conclusion from this analysis is that in all four checkpoint mutant backgrounds, there was a higher proportion of CO and NCO events occurring as part of a DSB cluster compared to the relevant WT control. To examine this further, the proportion of all recombination events classified into Group 0 was compared, equivalent to the number of suspected DSB clusters (Figure 7.5C, 7.6C). This differs from looking at the proportion of COs or NCOs in Group 0, in that each cluster contains two events which are not counted separately.

The percentage of all detected recombination events that were classified as being a DSB cluster was ~4.6% in *msh2Δ*, ~13.7% in P_{CLB2}-*MEC1 msh2Δ* and ~10.9% in *rad24Δ msh2Δ*, with the mean values for *rad24Δ* and P_{CLB2}-*MEC1* being within 95% confidence intervals (Figure 7.5C). Similarly for *NDT80* prophase-arrest strains, ~5.6% of WT+*8 h* events occurred as part of a DSB cluster, compared to ~15.9% of p_{CLB2}-MEC+*8 h* and ~18.1% of *rad24Δ+10 h* events (Figure 7.6C). Again, the mean values for *rad24Δ* and P_{CLB2}-*MEC1* were within 95% confidence intervals. The proportion of clusters classified as double CO, double NCO or CO+NCO is roughly equal across strains, with CO + NCO clusters being most commonly observed.

Double COs are defined here as a double reciprocal exchange involving all four chromatids within 1.5kb. Among nine octads tested, there were 2 dCOs in *msh2Δ*; in P_{CLB2}-*MEC1 msh2Δ*, there were nine detected among six tetrads, and in *rad24Δ msh2Δ*, three in six tetrads. The results of a one-way ANOVA [Methods 2.23] indicate a significant difference between sample means (P=0.028). The results of a post-hoc Tukey test [Methods 2.24] indicate that the number of dCOs in P_{CLB2}-*MEC1 msh2Δ* is significantly higher than the number in *msh2Δ* (P<0.05), though not significantly higher than the number in *rad24Δ msh2Δ*, and the number in *rad24Δ msh2Δ* is not significantly higher than in *msh2Δ*. Double COs are expected to be a rare occurrence under conditions of crossover interference, suggesting a loss of CO interference in P_{CLB2}-*MEC1 msh2Δ*.

For *NDT80* prophase arrest strains, there were six dCOs detected in four tetrads in WT+*8 h*, seventeen in six P_{CLB2}-*MEC1+8 h* tetrads and eighteen in six *rad24Δ+10 h* tetrads. However, the

means for each were not significantly different to each other according to a one-way ANOVA (P=0.4285 [Methods 2.23]).

The number of definite, four-chromatid dCOs can be used to estimate how many three- and two-chromatid dCOs there should be (as described in Chapter 5, section 5.2.3). The true number of dCOs should be four times as high, if it is assumed that double DSBs are equally likely to be resolved as COs regardless of which chromosomes they occur on and that COs are equally distributed among the four chromatids (in terms of both initiating DSB and repair donor). Under these circumstances, ¼ of double COs would involve all four chromatids, ½ would involve 3 chromatids (indistinguishable from 1 CO + 1 NCO) and ¼ would involve two chromatids (indistinguishable from double NCO). This means that the number of dCOs reported here is likely an underestimate, and some CO+NCO or NCO+NCO clusters may actually be dCOs, giving revised estimates of eight dCOs in nine *msh2Δ* octads, 36 in six *P_{CLB2}-MEC1 msh2Δ* tetrads and 12 in six *rad24Δ msh2Δ* tetrads; 24 dCOs in four WT + 8 h tetrads, 68 in six *P_{CLB2}-MEC1* + 8 h, and 72 in six *rad24Δ* + 10 h tetrads.

Another specific category of event within Group 0 are those containing a 4:0, 8:0 or 7:1 segregation of markers, which is a strong indication of multiple events. Events containing a 4:0 or 8:0 segment are only counted if they are associated with at least one other different segment (i.e. do not have perfect overlap), else they are considered possibly to be mitotic in origin.

In *msh2Δ*, one 8:0 and four 7:1 events were observed in nine octads, while *rad24Δ msh2Δ* had four 8:0 and twelve 7:1 events in six tetrads, *P_{CLB2}-MEC1 msh2Δ* displayed nineteen 8:0 and thirty-two 7:1 events across six tetrads (Table 7.1). These numbers are significantly higher than *msh2Δ* for both *rad24Δ* and *P_{CLB2}-MEC1* (T-test, P=0.019 and 2×10^{-6} respectively), and in addition, *P_{CLB2}-MEC1 msh2Δ* also has significantly more than *rad24Δ msh2Δ* (T-test, P=0.006). Among *NDT80* prophase arrest trains, WT+8 h had ten 4:0 events in four tetrads, while *rad24Δ+10 h* had fifty-six 4:0 events in six tetrads and *P_{CLB2}-MEC1+8 h* had ninety-five 4:0 events in six tetrads. The frequencies of 4:0 events observed in both *rad24Δ+10 h* and *P_{CLB2}-MEC1+8 h* were significantly higher than the frequency observed in WT+*8 h* (P=0.014 and P=0.025, respectively), but the frequencies observed in *rad24Δ+10 h* and *P_{CLB2}-MEC1+8 h* were not significantly different from each other.

An increase in such events is strongly suggestive of a loss of *trans* DSB interference, as two DSBs must have formed at the same location on different chromatids, so these results are suggestive of DSB interference loss in *P_{CLB2}-MEC1 msh2Δ*, *rad24Δ+10 h* and *P_{CLB2}-MEC1+8 h*. The difference observed between *NDT80* prophase-arrest and MMR-deficient strains may be simply due to the

increased ability to detect such events in the absence of Msh2, since 7:1 segments could be converted to either 4:0 or 3:1 events by MMR.

Another potential indication of DSB cluster formation is the presence of 6:2 or 2:6 segregation patterns in MMR-deficient strains, as described in Chapter 6, Section 6.2.4. This is discussed in the following section.

7.2.4. Conversion tracts observed in MMR-deficient recombination may represent DSB clusters

In an MMR-deficient background, 6:2 or 2:6 segregation patterns ('conversion segments') are thought to result from the repair of gaps, which could arise either from two close Spo11-DSBs on the same chromatid or from the removal of a 3' end after invasion of a homologous sequence, e.g. the formation of a nick during topological processing of a dHJ (Chapter 4, Figure 4.9 D, H and Figure 4.10 E, H). Thus, an increase in such events could be suggestive of increased DSB formation, or increased nicking (as discussed in Chapter 6, Section 6.2.4).

In addition, segments of 8:0 segregation could be considered to essentially be two overlapping conversion tracts, meaning that these could also be produced by concerted DSB formation, although there would have to be four close Spo11-DSBs. As discussed in the previous section, segments of 8:0 segregation are increased in *rad24Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ* compared to *msh2Δ*.

Analysis of conversion segments can only be done in Msh2-deficient backgrounds because MMR activity produces many 6:2/2:6 signatures which would obscure any conversion tracts produced by multiple DSBs (Figure 4.9 I, 4.10 I).

The occurrence of events containing a conversion segment was examined in *msh2Δ*, P_{CLB2}-*MEC1 msh2Δ* and *rad24Δ msh2Δ* (Figure 7.7A). On average, *msh2Δ* octads contained ~80 events that have at least one conversion segment events (39% of all events), *rad24Δ msh2Δ* tetrads had an increase to ~98 (50% of all events), and P_{CLB2}-*MEC1 msh2Δ* tetrads had an increase to ~196 (56% of all events).

While in *msh2Δ*, conversion segments were more frequently observed as part of CO events than NCO events, there is an increase in the number of NCOs containing a conversion segment in *rad24Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ* (Figure 7.7B). This is not simply due to the increase in NCO numbers in the mutant strains, because in *msh2Δ*, ~52.4% of all COs and ~23.6% of all NCOs contained a conversion segment, while in *rad24Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ*

respectively, ~65.3%/~67.6% of all COs and ~38.9%/ ~49.6 of all NCOs contained a conversion segment. This indicates that the loss of Rad24 or Mec1 activity increases the probability that a conversion segment will occur as part of an NCO event as opposed to a CO event.

Conversion segments could be produced by concerted DSBs on the same chromatid or by nicking during repair. Since multiple DSBs occurring in proximity is expected to be a rare occurrence, events containing multiple separate conversion segments may be more likely to be caused by nicking during repair (as they would otherwise necessitate the formation of four or more close DSBs), and events containing a single conversion segment may be more likely to be caused by concerted DSB formation.

The number of conversion segments that were part of an event that contained a single or multiple conversion segments was compared in *msh2Δ*, *P$_{CLB2}$-MEC1 msh2Δ* and *rad24Δ msh2Δ* (Figure 7.7 C). For both *msh2Δ* and *P$_{CLB2}$-MEC1 msh2Δ* strains, the majority (~67% and ~61% respectively) of conversion segments occurred as part of an event containing only one conversion segment. However, in *rad24Δ msh2Δ*, there was a roughly equal number (within 95% confidence intervals) of conversion segments occurring as part of an event containing one or multiple conversion segments.

As explained in Chapter 6 Section 6.2.4., if single-conversion segment events are produced by concerted DSBs, they may be expected to occur in strong Spo11 hotspots, or spanning multiple hotspots. If multiple-conversion segment events are produced by nicking, they may be expected to be shorter in length, because the nicking enzyme should cause relatively little degradation, and few markers will be converted during repair of the single strand break.

Using Spo11 location data from Pan *et al.* (2011), the observed and expected values of Spo11 hits for a conversion segment region can be calculated, as described in Chapter 6, Section 6.2.4. To examine differences in conversion segment length and heat, the medium length estimate and the ratio of the observed and expected numbers of Spo11 HpM was calculated for each segment, and plotted separately for segments occurring in events with single or multiple conversion segments (Figure 7.7 D&E).

For all three strains, conversion segments from events containing only one conversion segment are more likely to have a higher than expected number of Spo11 hits in the vicinity; for single conversion segments, ~40% of segments in *msh2Δ* and *P$_{CLB2}$-MEC1 msh2Δ* and ~50% of segments in *rad24Δ msh2Δ* have an observed/expected ratio <1, while ~60% of multiple-segment-event conversion segments have an observed/expected ratio of <1 (Figure 7.7D).

For all three strains, conversion segments that occur as part of events with multiple conversion segments are likely to be slightly shorter than those occurring in events with a single conversion segment (Figure 7.7E). In addition, for conversion segments in both single-segment or multiple-segment events, P_{CLB2}-*MEC1 msh2Δ* tends to have conversion segments that are on average around 100bp longer than those observed in *msh2Δ*, while *rad24Δ msh2Δ* tends to have segments around 50bp longer than *msh2Δ*.
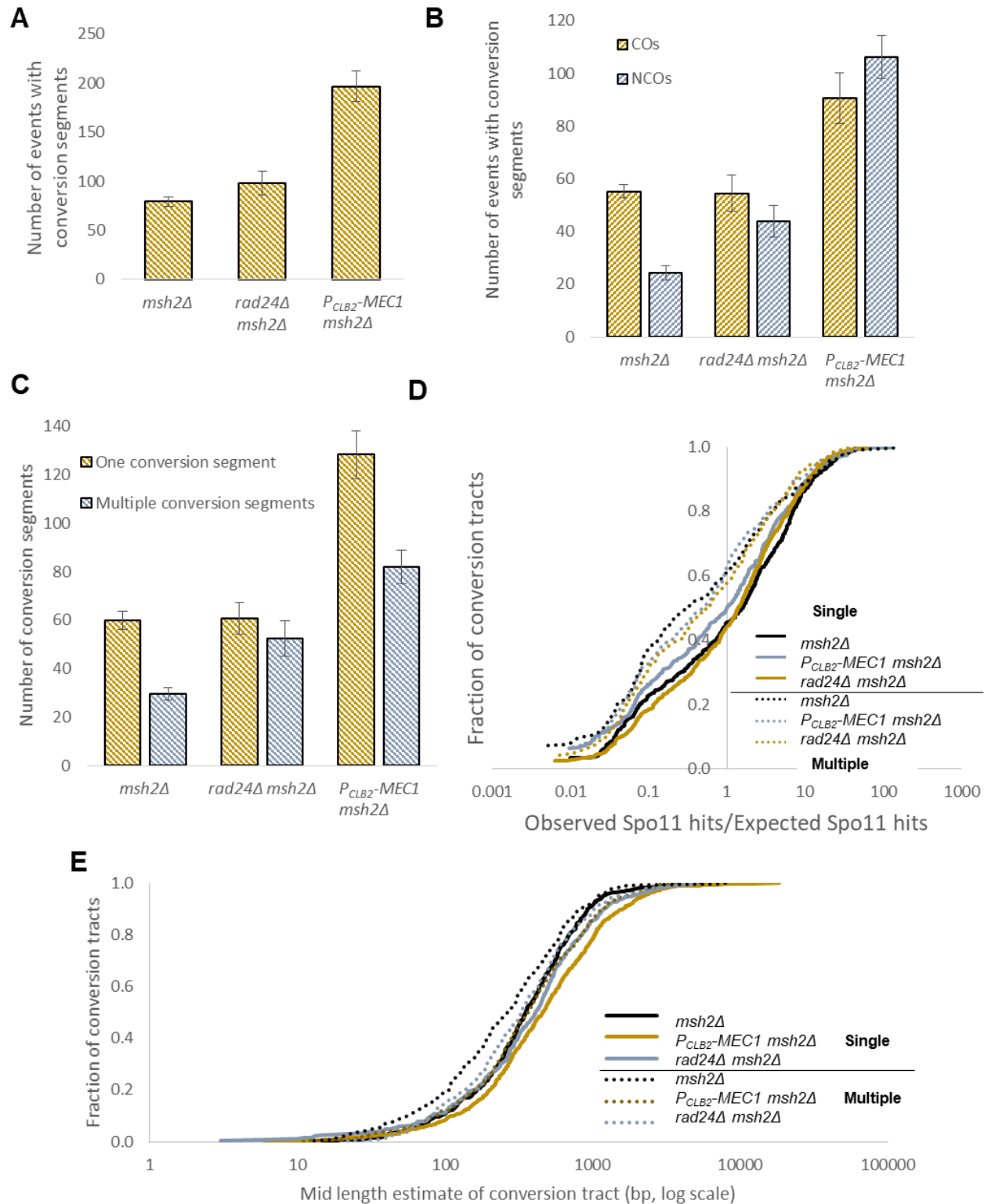
Figure 7.7. Comparison of conversion segment features detected in *msh2Δ*, *P$_{CLB2}$-MEC1 msh2Δ* and *rad24Δ msh2Δ* strains. A) Average number of events containing at least one conversion segment. **B)** Average number of CO and NCO events containing at least one conversion segment. **C)** Average number of conversion segments that are part of an event with a single conversion segment, or with multiple conversion segments. **D)** Cumulative fraction of events with single or multiple conversion segments with an increasing observed Spo11 hits/expected Spo11 hits ratio. **E)** Cumulative fraction of events with single or multiple conversion segments with an increasing mid length estimate.

As with the analysis performed in *tel1Δ* strains (Chapter 6, Section 6.2.4), these results suggest that there is some evidence that there are two groups of conversion-tracts: 1), those that occur in hotter regions, have longer lengths and occur in isolation, and 2), those that occur in colder regions, have shorter lengths and occur in multiples. The two groups are predicted to generally correspond to the local formation of multiple Spo11-DSBs on the same chromatid and 3' nicking during repair, respectively (although there is likely some overlap between the two). The reasoning for this is that events in hotter regions are expected to be more likely to have multiple DSBs, while those in colder regions are expected to have fewer DSBs; events with multiple conversion segments are less likely to be produced by multiple DSBs because each additional conversion segment would require the formation of another two Spo11-DSBs, which should be limited by DSB interference (although this may be reduced or missing in the mutants); and enzymatic nicking is expected to produce shorter conversion segments due to causing little degradation of DNA.

There is no particular difference in the formation of either group between *msh2Δ* and *P$_{CLB2}$-MEC1 msh2Δ*, but *rad24Δ msh2Δ* appears to have slightly more conversion segments occurring in events containing multiple conversion segments, and also conversion segments occurring in events with a single conversion segment tend to occur in slightly colder regions; this may indicate that *rad24Δ msh2Δ* is more likely to have conversion tracts produced by 3' nicking during repair than the other strains.

It should also be noted that conversion segments occurring within complex (Group 0) events are not included in this analysis, because conversion segments can be 'interrupted' by pattern changes on different chromatids, meaning that the overall segregation pattern may not reflect the true nature of a 6:2 segment (e.g. a single 6:2 segment may appear to be composed of separate 6:2 segments interrupted by other patterns, or to have a shorter length). Complex events are also thought to be produced by DSB clusters (although not necessarily occurring on the same chromatid, unlike those that may produce 6:2 segments), and are increased in both *rad24Δ msh2Δ* and *P$_{CLB2}$-MEC1 msh2Δ* (Section 7.2.3).

7.2.5. Event length is altered in checkpoint mutants

The length of recombination event tracts may be indicative of the extent of D-loop/dHJ migration and/or resection (Chapter 4, Figure 4.9/4.10), because longer resection or migration distances are predicted to correspond to longer tracts of marker changes. The length of a recombination event may also be an indicator of event complexity, because long events can be produced by two separate events occuring nearby and overlapping.

To compare event lengths in *msh2Δ* strains, event mid lengths were categorized into bins (Figure 7.8 A&B). Event mid lengths are used rather than the maximum or minimum length, because on average, they are most likely to approximate the true event length (as described in Chapter 5, Section 5.2.4, Figure 5.3A). The median and mean event mid lengths are also given in Figure 7.8. Compared to *msh2Δ*, both *rad24Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ* have an increase in CO lengths, but more so in *rad24Δ msh2Δ*. NCO event lengths do not differ much between the strains, but *rad24Δ msh2Δ* has some very long (>10kb) NCOs, unlike *msh2Δ* and P_{CLB2}-*MEC1 msh2Δ*. A long event example is shown in Figure 7.8C.

Event lengths in *NDT80* prophase extension strains were also examined (Figure 7.9 A&B). Here, a striking increase in the proportion of very long CO and NCO events, including those >10kb long, is observed in both *rad24Δ+10 h* and P_{CLB2}-*MEC1+8 h* compared to WT+*8 h*. Again, CO and NCO lengths in *rad24Δ+10 h* are also longer than those in P_{CLB2}-*MEC1+8 h*. Some long event examples are shown in Figure 7.10.

It was previously found that the *NDT80*-arrest WT strain has somewhat increased event lengths compared to *msh2Δ* (Chapter 5, Figure 5.3 A and B), which suggests that event lengths may increase during *NDT80* prophase arrest (possibly because of continuing resection or D-loop migration). If so, this phenotype may be exacerbated by the loss of the checkpoint proteins. Alternatively, long events may represent DSB clusters, where overlapping recombination signatures (up to 1.5kb apart) merge into a single apparently large recombination event, or Msh2 activity may contribute to event length somehow. Since both CO and NCO lengths are increased in *rad24Δ msh2Δ*, *rad24Δ+10 h* and P_{CLB2}-*MEC1+8 h*, the increased length is unlikely to be caused by dHJ migration because most, if not all, NCOs are formed by SDSA. However, only CO, and not NCO, lengths are increased in P_{CLB2}-*MEC1 msh2Δ*, so dHJ migration is a possible explanation for this change.
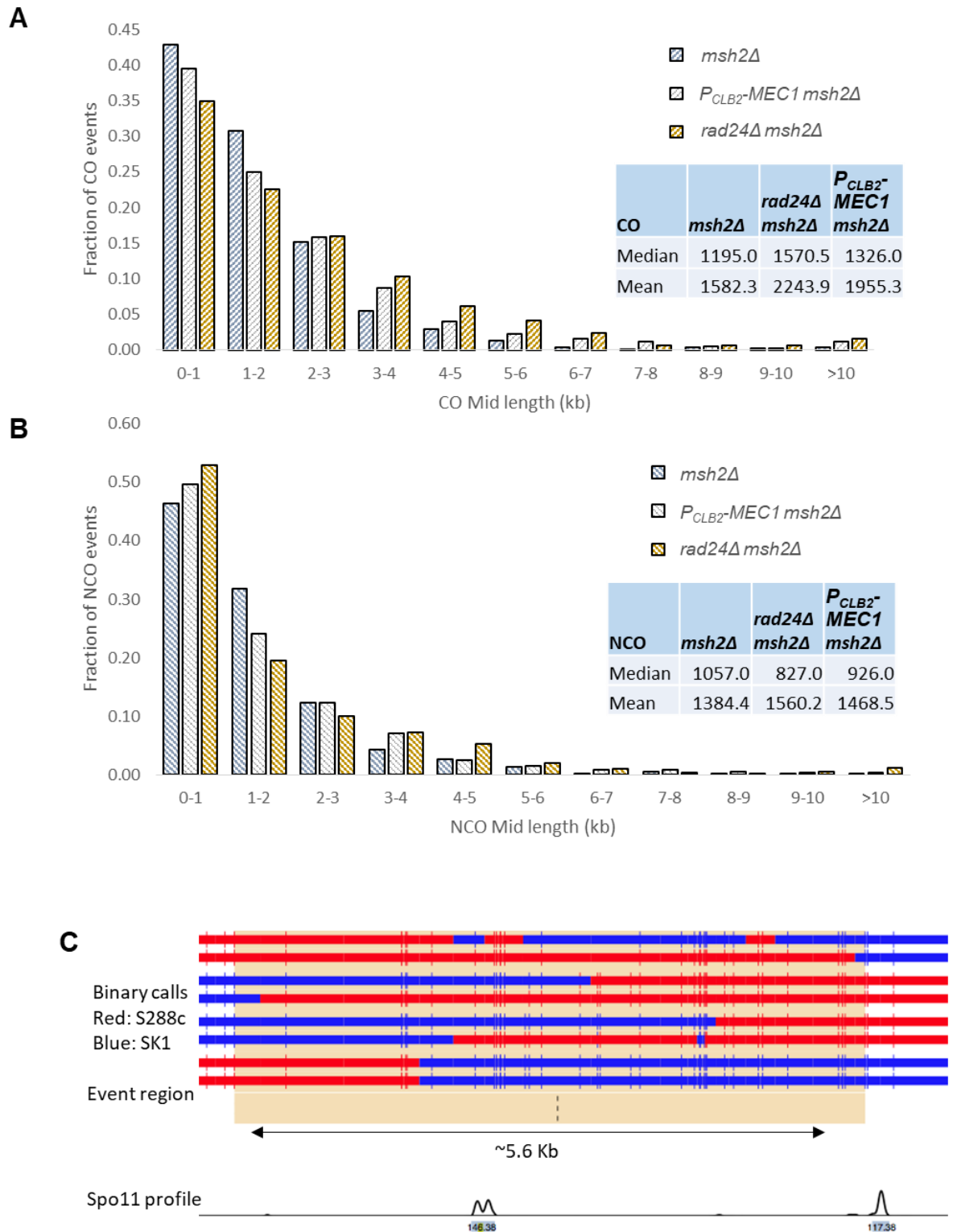
Figure 7.8. Mid length estimates of recombination events detected in Msh2 deficient *rad24Δ* and *P_CLB2*-*MEC1* strains. Strain details are given in Table 2.1, raw event data is available in Table S2. Histogram of mid length estimates for **A)** CO and **B)** NCO events. **C)** An example of a 5598bp event in a *rad24Δ msh2Δ* tetrad, in this case actually two COs occurring in proximity. Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan *et al*., 2011).

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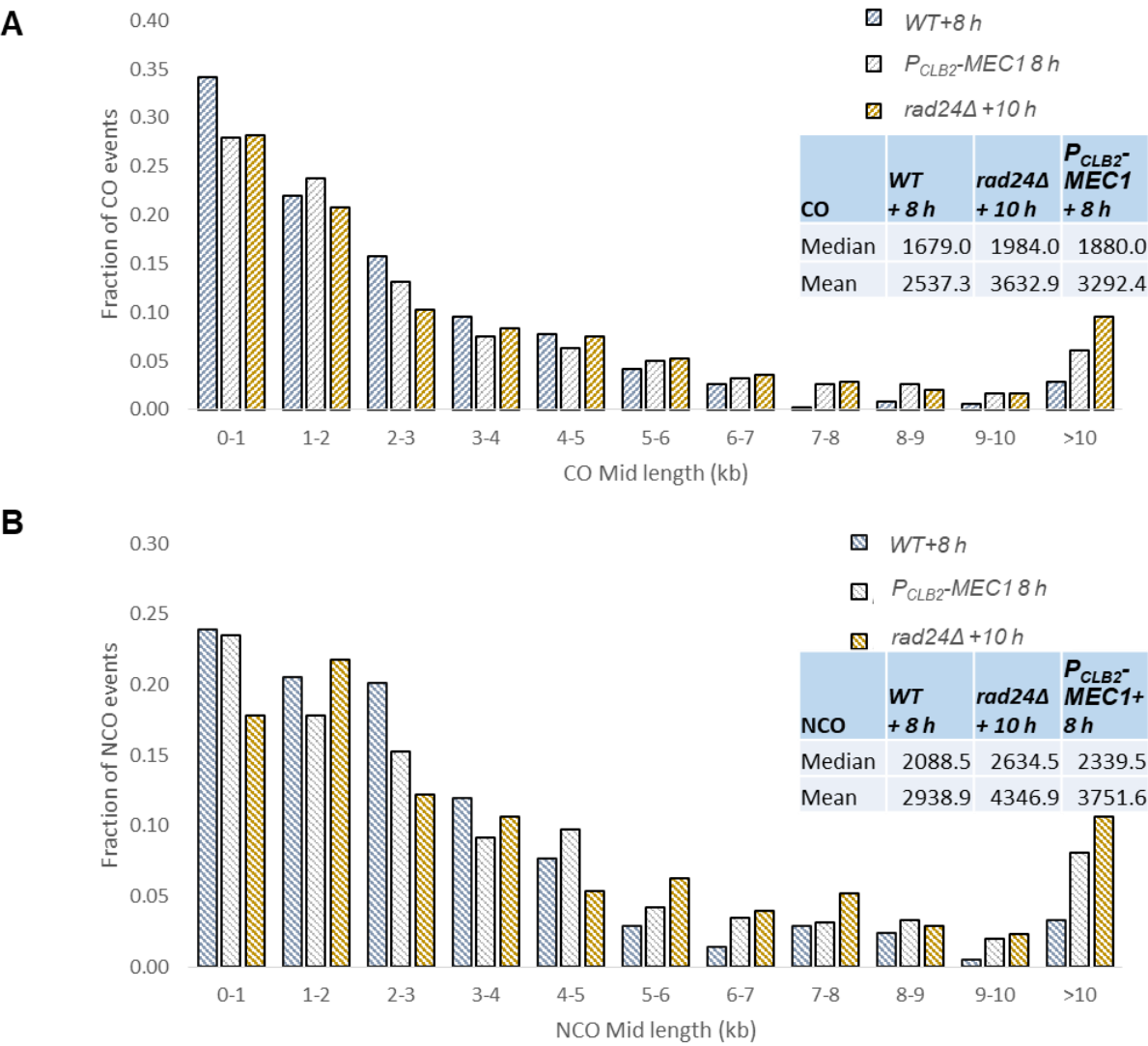
Figure 7.9. Mid length estimates of recombination events detected in *rad24Δ* and *P_CLB2*-MEC1 strains with prophase extension. Strain details are given in Table 2.1, raw event data is available in Table S2. Histogram of mid length estimates for **A)** CO and **B)** NCO events.
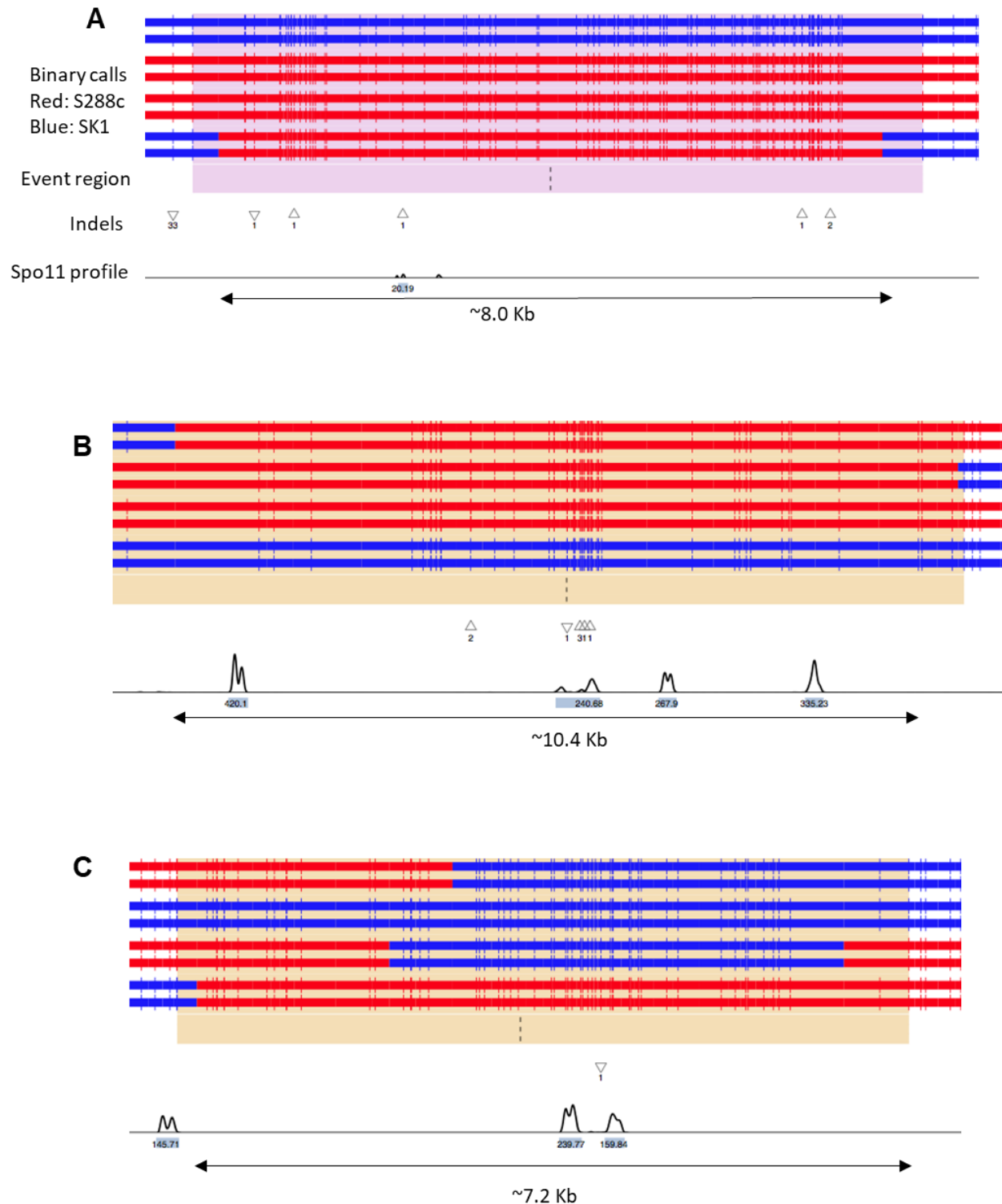
Figure 7.10. Example long recombination events detected in *rad24Δ* with prophase extension. Recombination events were mapped in hybrid strains by detection of SK1 (blue) or S288c (red) markers. The region of interest is plotted as eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The event region is indicated by the orange or purple box. Indel markers are indicated by triangles with the length of the indel below. A 100bp-smoothed DSB profile is plotted in black with the strength of each hotspot below (Pan *et al*., 2011). **A)** A simple NCO with a mid length estimate of 7939bp. **B)** A simple CO with a mid length estimate of 10435bp. **C)** A DSB cluster event, in this case annotated as a CO and a NCO due to the overall single reciprocal exchange within 1.5kb, with a mid length estimate of 7206bp.

DSB cluster events are defined by the occurrence of signatures indicative of multiple DSBs which have occurred to so close together they cannot be distinguished and have merged into one event (Section 4.2.11). Since DSB cluster formation increases in the checkpoint mutant backgrounds (Figure 7.5, 7.6), this may be expected to cause an increase in apparently long events that are actually two events are merged into one. To determine whether if DSB clusters disproportionately contribute to long event categories, the lengths of single-DSB and DSB-cluster events were compared (Figure 7.11, 7.12). This analysis shows that in *msh2Δ*, DSB cluster events actually tend to be relatively short, and the longest events are all single-DSB events (Figure 7.11, A&B). However, in both *P_CLB2-MEC1 msh2Δ* and *rad24Δ msh2Δ*, DSB cluster events tend to be the longest events and non-clusters the shortest (Figure 7.11, C-F). Thus, in the *msh2Δ* background, the increase in event lengths observed in checkpoint mutants is likely to be explained by the increase in DSB cluster formation, which is consistent with a loss of DSB and/or CO interference.

In the *NDT80* prophase extension WT, DSB cluster events tend to be the longest events and non-clusters the shortest, though there are some very long events that do not appear to be clusters (Figure 7.12, A&B). In both *rad24Δ+10 h* and *P_CLB2-MEC1+8 h*, the majority of long events are DSB cluster events and most short events are single-DSB events. However, there are some long non-cluster CO and NCO events, including those over >10kb in length, as well as some very short DSB cluster events (Figure 7.12, C-F).

Thus, the greatly increased event lengths observed in *rad24Δ* and *P_CLB2-MEC1* strains with extended prophase (Figure 7.9) are mostly, but not entirely, explainable by increased DSB cluster formation, as there are still some long non-clusters that are not seen in the control. An explanation involving continuing DSB resection during prophase arrest is also plausible because *rad24Δ* and *P_CLB2-MEC1* are known to have increased DSB resection compared to WT (Gray *et al.*, 2013; Kayleigh Wardell, personal communication). Normal meiotic resection occurs between ~200 to ~2000 nt away from hotspot centres, with a mean of 822 nt (Mimitou *et al.*, 2016). Estimates based on gel migration distances put *rad24Δ* resection up to 3.9x further than WT, and *P_CLB2-MEC1* up to 2.3x further (Kayleigh Wardell, personal communication). This correlates with the observation that in *NDT80* prophase arrested backgrounds, *rad24Δ* has longer COs and NCOs than *P_CLB2-MEC1*, and *P_CLB2-MEC1 msh2Δ* has longer COs and NCOs than WT, although does not prove that distant resection is the cause of the long events.
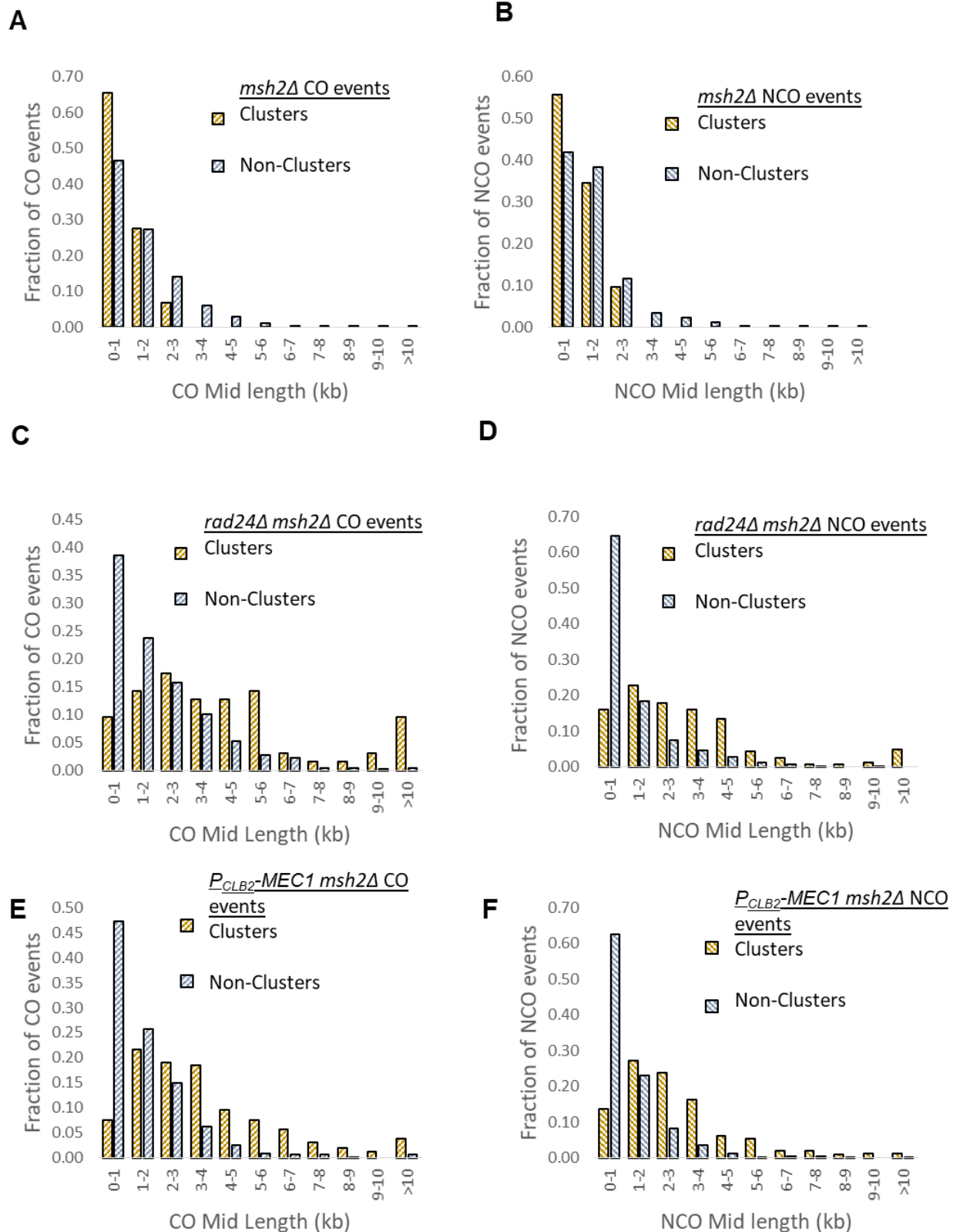
Figure 7.11. Comparison of mid length estimates in single-DSB and DSB-cluster events detected in Msh2 deficient *rad24Δ* and *P$_{CLB2}$-MEC1* strains. Strain details are given in Table 2.1, raw event data is available in Table S2. Mid length estimate of cluster/non-cluster of: **A)** CO events in *msh2Δ*, **B)** NCO events in *msh2Δ*, **C)** CO events in *rad24Δ msh2Δ* **D)** NCO events in *rad24Δ msh2Δ* **E)** CO events in *P$_{CLB2}$-MEC1 msh2Δ*, **F)** NCO events in *P$_{CLB2}$-MEC1 msh2Δ*.
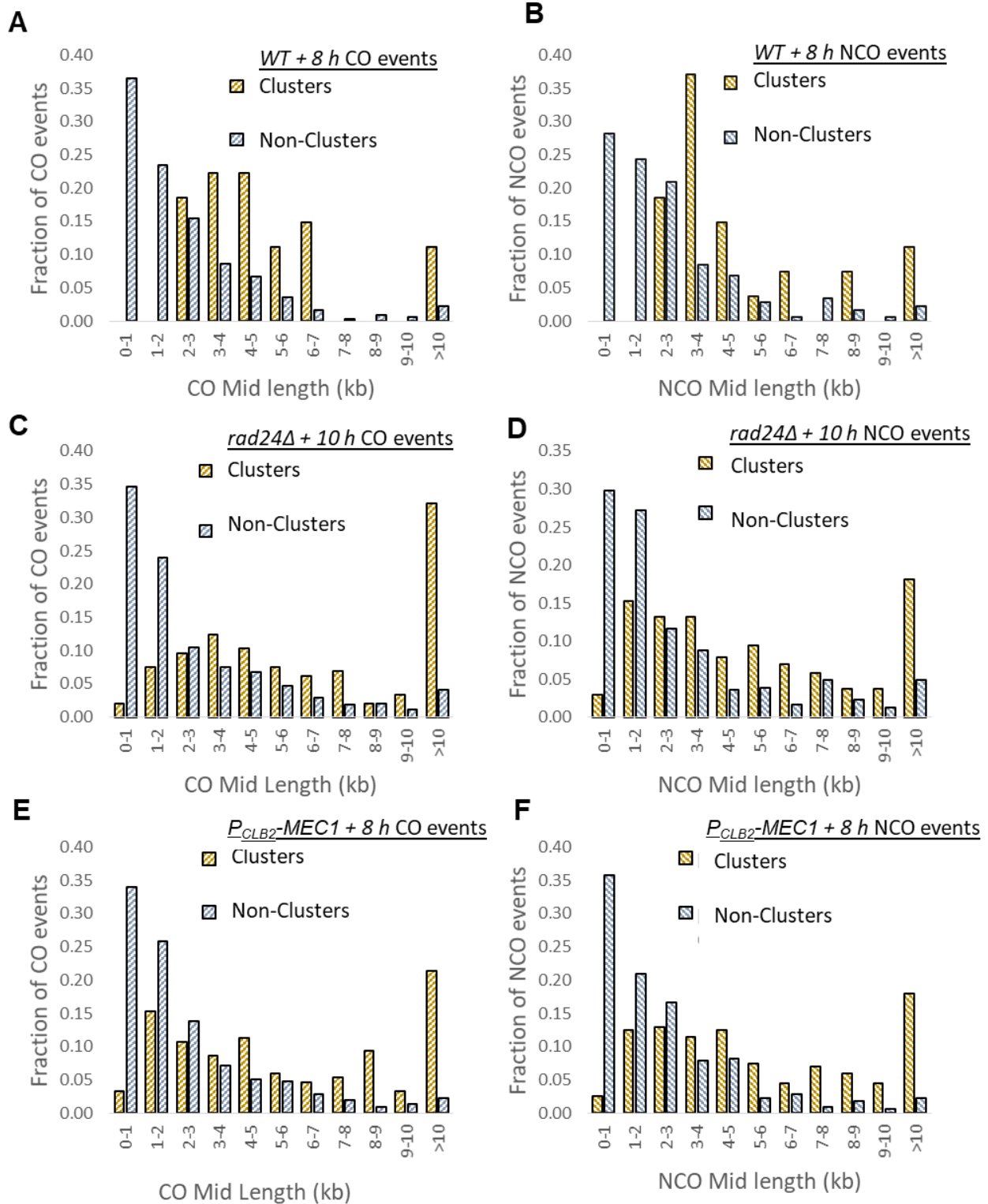
Figure 7.12. Comparison of mid length estimates in single-DSB and DSB-cluster events detected in prophase-extension *rad24Δ* and *P_{CLB2}-MEC1* strains. Strain details are given in Table 2.1, raw event data is available in Table S2. Mid length estimate of cluster/non-cluster of: A) CO events in WT+8 h, B) NCO events in WT+8 h, C) CO events in *rad24Δ* +10 h, D) NCO events in *rad24Δ* +10 h, E) CO events in *P_{CLB2}-MEC1* +8 h, F) NCO events in *P_{CLB2}-MEC1* +8 h.

It has been proposed that Rad24 activity provides a physical barrier to resection, as it is responsible for loading the 9-1-1 clamp at DSB sites (Kayleigh Wardell, personal communication). Mutants of the 9-1-1 component, Rad17, show a hyper-resection phenotype identical to that of *rad24Δ* (Shinohara *et al.*, 2003). In addition, Rad24 and Rad17 are involved in the activation of Mec1, which may regulate resection by deactivating Sae2, or in another way. Thus, all three proteins contribute to resection regulation, but the contributions of Rad24 and Rad17 appear larger than those of Mec1.

The increase in resection in Rad24 and Mec1 mutants is a possible explanation for the increase in ectopic recombination seen in these backgrounds (Gray *et al.*, 2013; Grushcow *et al.*, 1999), as the longer resection tracts uncover more ssDNA that could potentially pair with a non-allelic region. A comparison of ectopic recombination frequencies in the sequenced spores could provide evidence for this connection; however, ectopic recombination is difficult to measure by this method because it is highly deleterious and likely to cause cell death due to the formation of acentric and dicentric chromosomes, meaning that affected spores cannot be sequenced. On the other hand, small-scale occurrences of ectopic recombination are not as deleterious, and could cause signatures such as duplications, something that is discussed in the next section.

7.2.6. Increase in potential duplications in *rad24Δ* and P_{CLB2}-*MEC1 NDT80* prophase extension backgrounds

It is possible to detect what appear to be novel duplications in the post meiotic genome (as discussed in section Chapter 4, Section 4.2.6). These duplications may or may not be associated with a detected recombination event, meaning that they could represent additional NCOs occurring during meiosis that were not detected by the pipeline because they produced a mixture of markers which could not be called as one genotype or the other. An example duplication associated with a CO identified in a P_{CLB2}-*MEC1+8 h* tetrad is shown in Figure 7.13A.

To determine whether duplications are more likely to occur or have different lengths in checkpoint mutants, duplications were examined in P_{CLB2}-*MEC1+8 h* and *rad24Δ+10 h* backgrounds (Table 7.3, Figure 7.13B&C). Duplications were only counted if they covered at least two consecutive SNPs.

In *rad24Δ+10 h*, there were considerably more duplications detected than in WT+*8 h* (average of 7 vs 2.5), and they tended to contain more consecutive SNPs and be slightly longer in length, with one in ten duplications being >10kb in length. In P_{CLB2}-*MEC1*, there were more duplications than in WT (average of 3.2 vs 2.5), but fewer than in *rad24Δ +10 h*. However, the P_{CLB2}-*MEC1* duplications tended to be much longer than WT or *rad24Δ*, with one in five duplications being

longer than 10kb in length, and also contained more consecutive SNPs on average which increases confidence in their validity. It should be noted that some large whole chromosome or partial chromosome duplications were also observed in P_{CLB2}-*MEC1* strains (Section 7.2.2, Figure 7.3A&B), although these are thought to be mitotic in origin, due to affecting both sister chromatids.

The presence of duplications is important because they may be formed during complex repair of a DSB. For example, multiple strand invasions into the same sequence on different chromatids could result in the same region being copied twice with different polymorphisms. Alternatively, gene duplications can be caused by ectopic recombination (reviewed in Zhang, 2003). Ectopic recombination most commonly occurs during repair of DSBs formed in repetitive regions. Spo11-DSBs do not normally form in these regions (Pan *et al.*, 2011), so an increase in ectopic recombination may reflect an increase in recombination in repetitive regions (reviewed in Sasaki *et al.*, 2010).

Duplications cannot be detected separately in *msh2Δ* tetrads, because all mixed reads are converted into apparent hDNA and so duplications will be analysed as normal NCOs (Chapter 4, Section 4.2.5). (This is not wholly undesirable, because the duplications are likely to have been caused by a Spo11 break repaired as a complex NCO). When *msh2Δ* octads are reanalysed as if they were tetrads, they gain an average of 9 NCOs (Figure 4.6A); *msh2Δ* octads have an average of 6.7 duplications, so most of the new apparent NCOs in *msh2Δ* tetrads are likely to actually be duplications. This could partly explain why *rad24Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ* have an increase in NCO formation in relation to CO formation. For example, the large increase in NCO formation seen in P_{CLB2}-*MEC1 msh2Δ* could in fact represent an increase in duplication formation, but NCOs and duplications are indistinguishable due to both producing ~50:50 mixed reads in *msh2Δ* tetrads. This cannot be confirmed without performing octad analysis in these backgrounds however, which is not trivial due to the low viability of the strains.

A

B

C
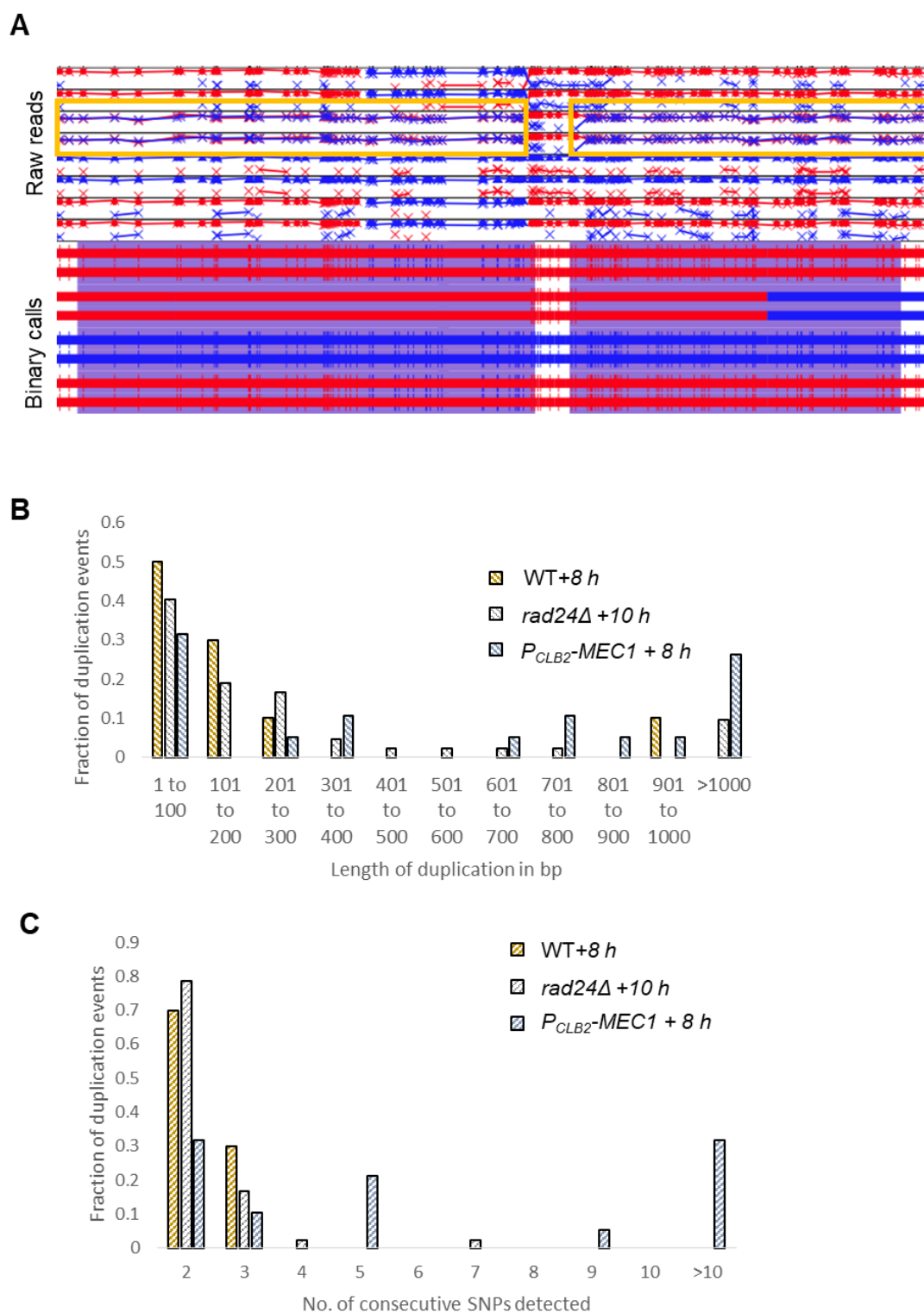
Figure 7.13. Length of potential duplications detected in *rad24Δ* and *P_{CLB2}-MEC1* strains with prophase extension. Regions of hDNA were mapped by detection of mixed SK1 (blue) and S288c (red) markers. The region of interest is plotted as eight strands of DNA present in the original hybrid diploid, with vertical tick marks indicating called variant positions. The hDNA region is indicated by the purple box. **A)** An example duplication associated with a CO event, from a P_{CLB2}-*MEC1* +8 h tetrad, containing 48 SNPs and with a length of 3336bp. Raw reads indicate the frequency of reads containing SK1 or S288c type polymorphisms detected at each position; these are translated into binary calls, which can only be SK1 or S288c. The yellow box highlights the suspected duplication, which can be seen to contain both SK1 and S288c reads. In the binary calls, these positions are discarded. **B)** Length of potential duplications in bp, **C)** Number of consecutive SNPs in potential duplications.

Table 7.3. Data summary for potential duplications and deletions detected in $msh2\Delta$, P_{CLB2}-$MEC1$ $msh2\Delta$, $rad24\Delta$ $msh2\Delta$, $WT+8$ h, P_{CLB2}-$MEC1$ $+8$ h and $rad24\Delta$ $+10$ h tetrads. Only duplications and deletions containing at least two SNPs are included.

Genotype (repeats)	Duplications			Deletions		
	Total detected	Mean no. of SNPs	Mean length (bp)	Total detected	Mean no. of SNPs	Mean length (bp)
WT + 8 h (4)	10	2.3	199.2	5	2.0	41.0
rad24Δ +10 h (6)	42	2.3	278.7	5	2.0	22.6
P_{CLB2}-MEC1 + 8 h (6)	19	10.9	827.4	0	0	0
msh2Δ (9)	60	3.2	165.3	75	2.1	59.1
rad24Δ msh2Δ (6)	NA	NA	NA	4	2	17.3
P_{CLB2}-MEC1 msh2Δ (6)	NA	NA	NA	12	2.1	9.83

Similarly, novel deletions may be detectable by looking for adjacent SNPs with low read depth. However, these could also simply represent areas that, for some reason, did not receive much sequencing coverage. In addition, the presence of deletions is based on the absence of data, while duplications are based on the presence of heteroduplex calls, meaning there is less confidence in the accuracy of the deletion calls.

Nonetheless, potential deletions in *NDT80* prophase-arrested and MMR-deficient checkpoint mutant strains were examined (Figure 7.14, Table 7.3), revealing that all were very short in length, and there was no difference between the genotypes, unlike the duplications. This suggests that the potential deletions are a technical artefact. However, it should be noted that deletions are likely to be shorter in length than duplications, because longer deletions would not be well tolerated by the cell, suggesting that at least some may be real.

A
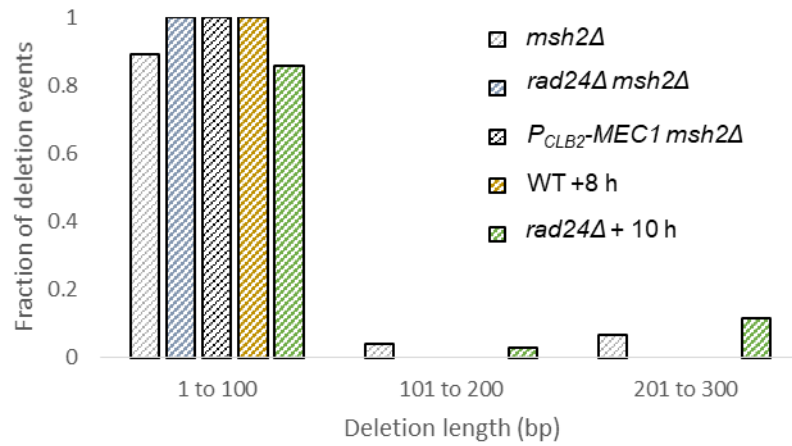
B
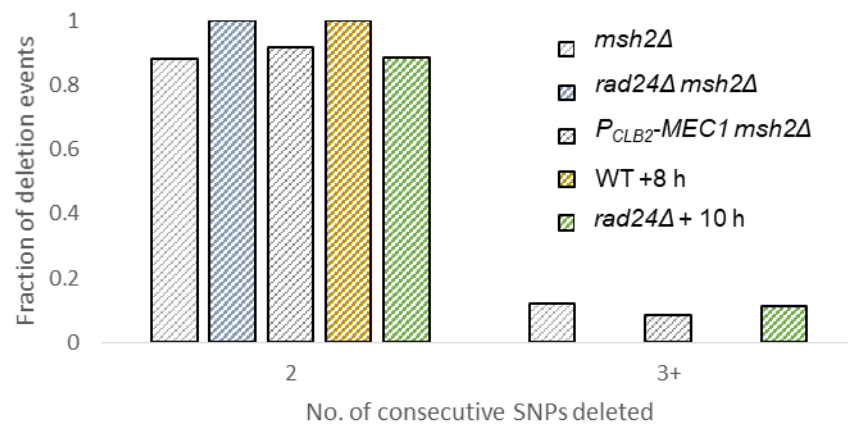
Figure 7.14. Length of potential deletions detected in *rad24Δ* and *P_{CLB2}-MEC1* strains with prophase extension and Msh2 deficiency. Potential deletions were detected by looking for consecutive SNPS with low read depth. **A)** Length of potential deletions in bp. *P_{CLB2}-MEC1* +8 h is not shown because no potential deletions were detected. **B)** Number of consecutive SNPs in potential deletions.

7.2.7. Distribution of recombination events in relation to centromeres and telomeres

Normally, recombination is suppressed from occurring near centromeres and telomeres (Petes & Botstein, 1977; Pan *et al.*, 2011). In particular, CO formation is repressed near centromeres (Lambie & Roeder, 1986) and telomeres (Rockmill *et al.*, 2006).

To determine whether the mechanisms preventing recombination near centromeres and telomeres is functioning normally in the mutant strains, the proximity of all recombination events to telomeres and centromeres was measured in MMR-deficient and *NDT80* prophase arrested P_{CLB2}-*MEC1* and *rad24Δ* backgrounds (Figures 7.15, 7.16). The frequency of recombination event formation is reduced close to the telomeres and centromeres to a similar degree in *rad24Δ* strains and their relevant controls, with very few events occurring within 10kb (Figure 7.15 A, B; 7.16 A, B). CO events also tend to occur further from telomeres and centromeres than NCOs in *rad24Δ* backgrounds and their controls (Figure 7.15 C, D; 7.16 C, D). This indicates that the mechanisms preventing recombination near these regions is functioning normally in a *rad24Δ* background.

However, there are some abnormalities in the P_{CLB2}-MEC1 strains. In P_{CLB2}-MEC1 + 8 h, there is an increase in the proportion of COs occurring near the centromere (Figure 7.16 B, D). The suppression of CO formation near centromeres is eliminated in the absence of kinetochore assembly (Lambie *et al.*, 1988). Mec1 has a role in the destabilization of centromere pairing that occurs without homology via phosphorylation of Zip1 (Falk et al., 2010); incorrect centromere pairing in the absence of Mec1 may affect kinetochore assembly, reducing CO suppression near centromeres. Strangely, this is not seen in the P_{CLB2}-*MEC1 msh2Δ* strain, suggesting that the phenomenon may be related to prophase length or Msh2 activity in combination with Mec1 deficiency.

In P_{CLB2}-*MEC1 msh2Δ*, there is an increase in the proportion of NCOs that occur near subtelomeric regions (Figure 7.15A, C); this suggests that the increased number of NCOs formed in P_{CLB2}-MEC1 are also more likely to form in subtelomeric regions. This could be related to DSB spreading, a phenomenon where DSB interference increases the probability that DSBs will occur towards the ends of the chromosomes, as central regions become more likely to have a DSB in proximity than outer regions; this would have a more visible effect in a strain with an increased DSB formation.
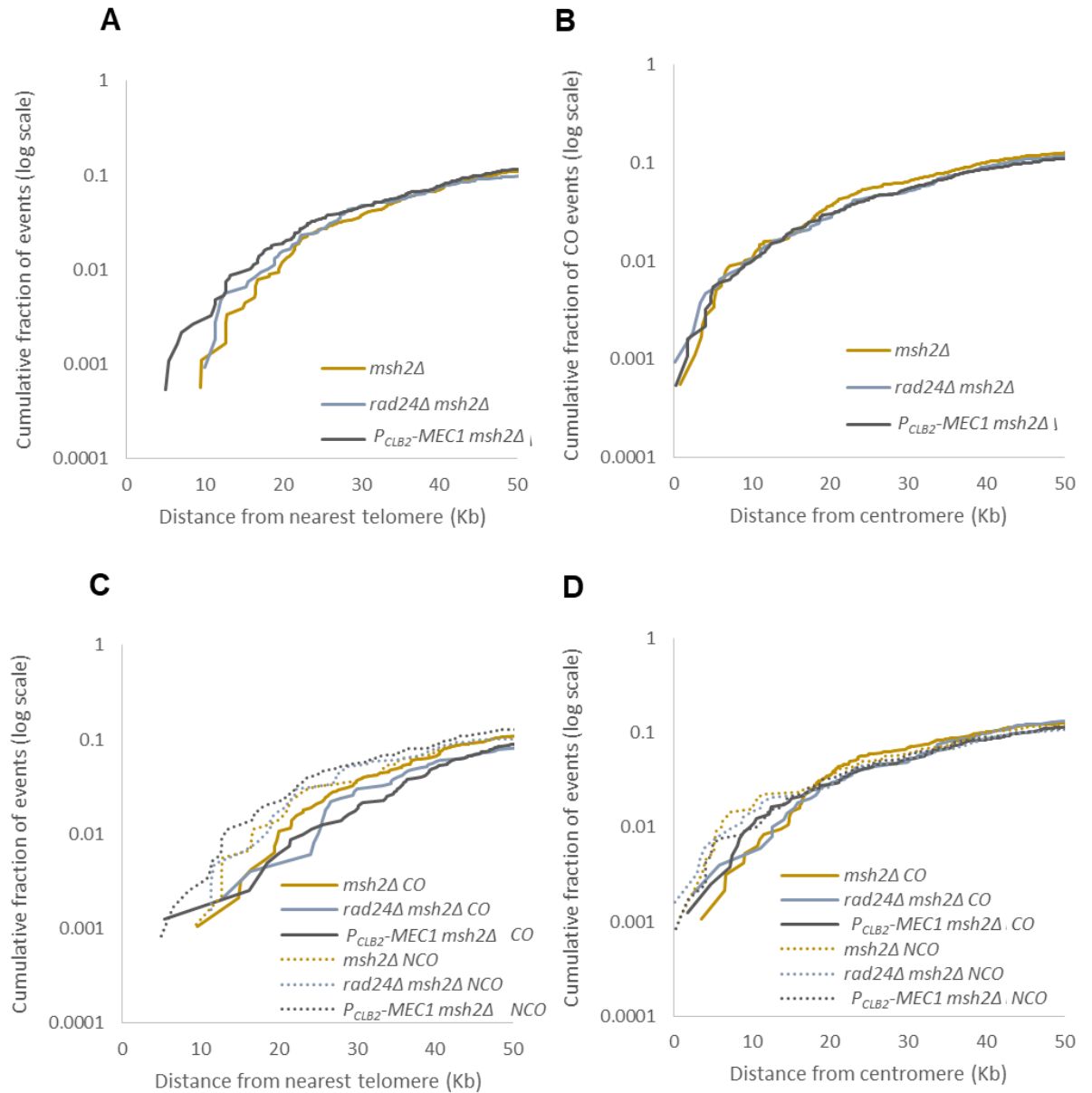
Figure 7.15. Distance between telomeres or centromeres and recombination events detected in Msh2 deficient *rad24Δ* and *P_CLB2-MEC1* strains. For each event, the distance to the centromere or nearest telomere is calculated and plotted against a cumulative fraction of events. **A)** Distance between telomeres and all events. This includes 'U' events which cannot be called a CO or NCO due to occurrence close to the telomeres. **B)** Distance between centromeres and all events. **C)** Distance between telomeres and CO or NCO events. **D)** Distance between centromeres and CO or NCO events.
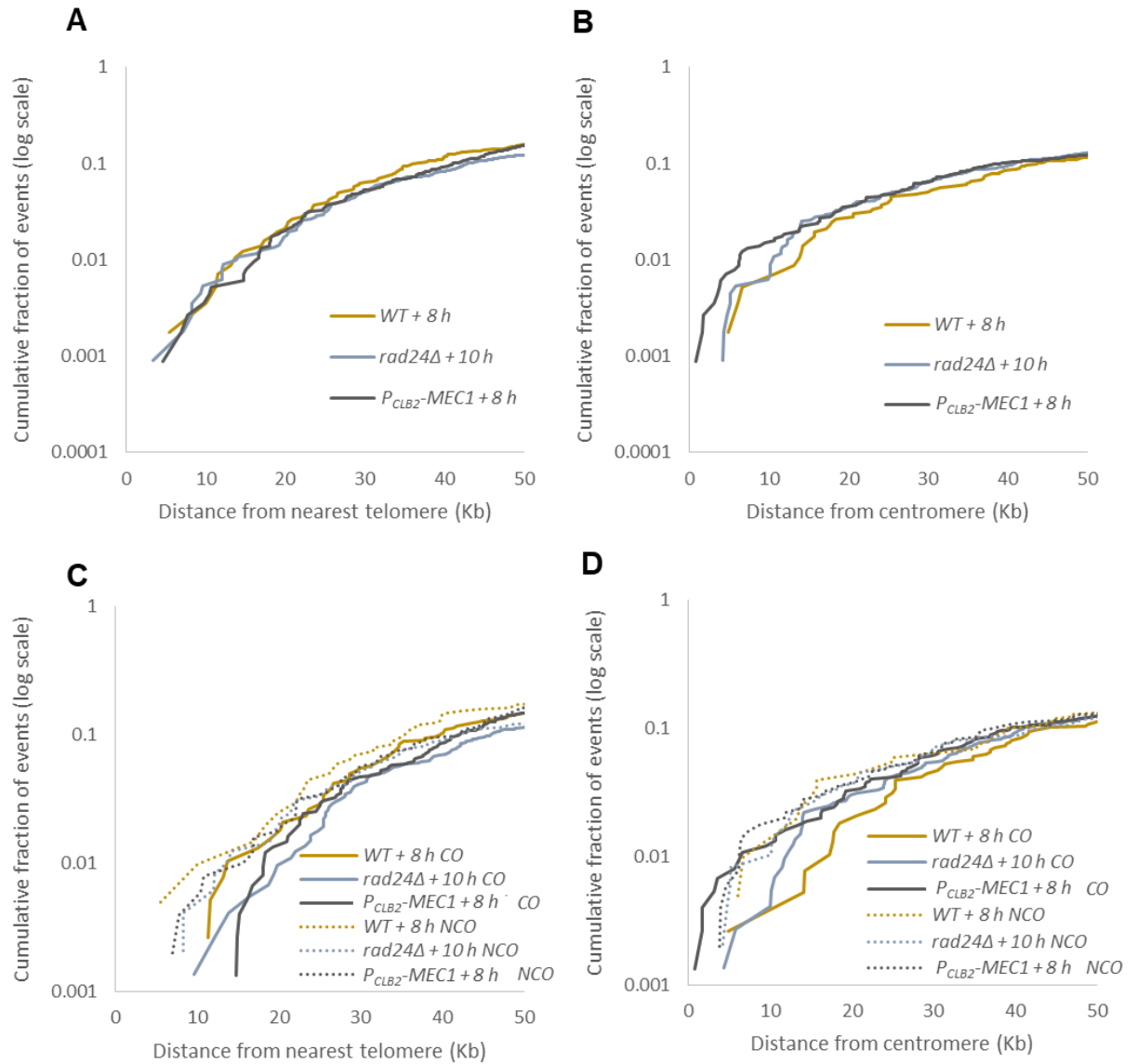
Figure 7.16. Distance between telomeres or centromeres and recombination events detected in *rad24Δ* and *P_{CLB2}-MEC1* strains with prophase extension. For each event, the distance to the centromere or nearest telomere is calculated and plotted against a cumulative fraction of events. **A)** Distance between telomeres and all events. This includes 'U' events which cannot be called a CO or NCO due to occurrence close to the telomeres. **B)** Distance between centromeres and all events. **C)** Distance between telomeres and CO or NCO events. **D)** Distance between centromeres and CO or NCO events.

7.2.8. The distribution of CO events shows evidence of interference loss in checkpoint mutants

The occurrence of a CO is known to reduce further CO formation nearby, a phenomenon known as CO interference (Sturtevant 1913; Sturtevant 1915). The degree of interference between COs can be estimated by measuring the distance between event midpoints and comparing the distributions (as described in Chapter 5, Section 5.2.7).

Inter-CO distances were calculated for MMR-deficient and *NDT80* prophase arrested P_{CLB2}-*MEC1* and *rad24Δ* strains, arranged in order from smallest to largest and plotted as cumulative fraction of total CO events against IED size on a log scale (Figure 7.17). If interference is present, events should occur further apart than would be expected if event placement was random. In order to determine whether the experimental inter-event distance distributions are distinct from a random distribution, simulated data is produced for the appropriate event counts to show the hypothetical distribution of events along the chromosomes under conditions of independence (Methods Section 2.18; Tim Cooper, personal communication).

In *msh2Δ* and WT+*8 h*, experimental inter-CO distance distributions deviate from the random simulation, with the distribution being shifted to the right (Figure 7.17A&B, compare blue (experimental) and orange (random simulation). This distinctive shape indicates that CO events are occurring further apart than would be expected if events were occurring independently, indicating the presence of CO interference. As discussed in Chapter 5, Section 5.2.10, CO interference is stronger in *msh2Δ* than in WT, likely due to an increased presence of Class I (interfering) COs.

In P_{CLB2}-*MEC1 msh2Δ*, inter-CO distances are not well-described by a random simulation, indicating the presence of CO interference (Figure 7.17E, compare blue (experimental) and orange (random simulation)). However, there is a tendency towards a random distribution for closely-spaced events, suggesting some loss of interference (this is also seen in *msh2Δ* and WT+ 8 h, but with a slightly weaker skew towards a random distribution). Similarly, *NDT80* prophase-arrested P_{CLB2}-*MEC1* also displays inter-CO distances that do not quite match a random distribution. However, as with other strains, they are shifted towards the random distribution for closely-spaced events (Figure 7.17F, compare blue (experimental) and orange (random simulation)).

In a *rad24Δ msh2Δ* background, inter-CO distances are again not well-described by a random distribution, but tend towards randomness for closely-spaced events (Figure 7.17C, compare blue (experimental) and orange (random simulation)). In contrast, the *NDT80* prophase-arrested

rad24Δ strain demonstrates and almost complete loss of CO interference; the distribution of inter-CO distances closely matches a random distribution for medium-long range distances (50kb+) (Figure 7.17D, compare blue (experimental) and orange (random simulation)). Notably, over short distances, events are clustered more closely than expected by chance (negative interference), indicated by the blue line crossing the orange line).

In order to quantify the strength of CO interference for each genotype, the best fit gamma parameters were found for inter-CO intervals (as described in Chapter 5, Section 5.2.7 and in Methods section I (analysis performed by Tim Cooper). Calculated gamma parameters are shown in Table 7.4.

Inter-CO distances in *msh2Δ* were best described by a gamma function with an α value of 2.44, while WT+*8 h* CO distribution was best fit by a gamma curve with α=1.46, indicating that the apparent strength of CO interference is increased upon *MSH2* deletion.

The best-fit gamma distributions for both P_{CLB2}-*MEC1 msh2Δ* and P_{CLB2}-*MEC1* + 8 h have lower α values than their appropriate controls, supporting a loss of interference in these strains. The apparent strength of interference in the *NDT80* prophase-arrested Mec1 mutant is lower than in the MMR-deficient Mec1 mutant (α=1.20 vs 1.65), but this is likely to be related to the fact that *msh2Δ* displays stronger interference than *NDT80* prophase-arrested backgrounds. Overall, these results indicate that in P_{CLB2}-*MEC1*, there is a reduction in CO interference, and to a similar extent in both MMR-deficient and *NDT80* prophase-extension backgrounds.

In a *rad24Δ msh2Δ* background, the inter-CO distances are best described by a gamma distribution with α=1.60, meaning that CO interference in *rad24Δ msh2Δ* is similar to P_{CLB2}-*MEC1 msh2Δ*. The *NDT80* prophase-arrested *rad24Δ* strain is best described by an α value of 1.07, suggesting a loss of CO interference in this strain.

However, even the best-fit gamma distributions are not a good fit for the experimental data, according to the results of a Kolmogorov-Smirnov test (Methods section 2.20) used to determine whether the two distributions are significantly different (P-values in Table 7.4). This indicates that inter-CO distributions cannot be well described by a gamma distribution (except for P_{CLB2}-MEC1 +8 h, where P=0.0542).

The best fit gamma function for each background was also used to produce simulated IED data as described in Chapter 5, section 5.2.7. Simulated IED data was plotted alongside experimental data to give a visual indication of the goodness of fit of the experimental data to the 'best fit' gamma parameters (Figure 7.17, grey lines).

In all strains, there is a particularly poor fit for the shortest inter-CO distances, with the experimental data shifted to the left in comparison to the best-fit gamma distribution, which indicates that there are more short distances occurring than expected. This suggests that there are many events occurring that do not display interference; this may be caused by the presence of Class II (non-interfering) COs, as discussed in section 7.2.11.

In *msh2Δ*, *P*$_{CLB2}$*-MEC1 msh2Δ* and in *tel1Δ msh2Δ* (see Chapter 6), inter-CO distances shorter than ~25-27kb are poorly described by the best-fit gamma distribution (Figure 7.17A, E, Figure 6.12B, point at which blue and grey lines deviate), though the strength of CO interference is lower in *P*$_{CLB2}$*-MEC1 msh2Δ* than in *tel1Δ msh2Δ* (α=1.65 vs 2.03). In *rad24Δ msh2Δ,* the range is 46kb, a much wider range than observed for other backgrounds, and the α value of 1.60 is lower than in *tel1Δ msh2Δ. NDT80* prophase-arrested *P*$_{CLB2}$*-MEC1* has a slightly wider range (~32kb) of poorly-fitting inter-CO distances than MMR-deficient *P*$_{CLB2}$*-MEC1*. The reason for this disparity may be explained by a difference in the ratio of Class I/Class II CO formation (discussed in Section 7.2.11).

The observation that CO interference is reduced in *P*$_{CLB2}$*-MEC1* and *rad24Δ* strains may help to explain why these mutants have low viability. CO clustering means that COs are not properly spread out along the chromosomes, potentially causing non disjunction of chromosomes, which is increased in *rad24Δ* (Section 7.2.2). This may also be partly explained by the reduced CO count seen in *rad24Δ msh2Δ*, because if there are not enough COs to go around, an increase in CO-less chromosomes is expected.

When the overall CO count is high, the effect of reduced CO interference loss may be counteracted, ensuring that all chromosomes are still likely to receive a CO. However, *rad24Δ* + 10 h has an increase in CO events compared to WT + 8 h, yet still has some CO-less chromosomes, which may be caused by the complete loss of CO interference in this strain.
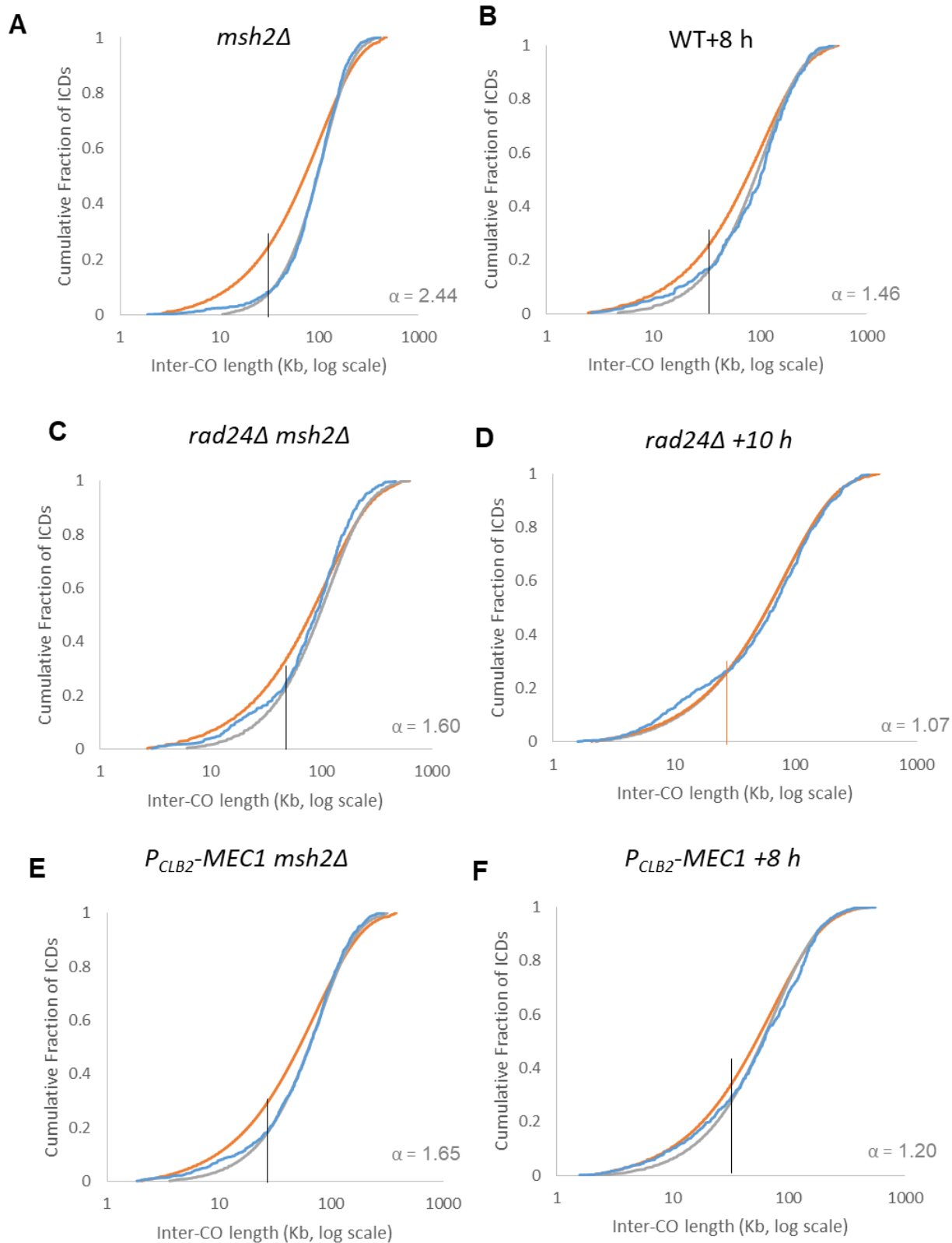
Figure 7.17. Distribution of distances between crossover events observed in Msh2 deficient and prophase extension checkpoint mutant strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-CO distance (ICD) in **A)** *msh2Δ*, **B)** WT + 8 h, **C)** *rad24Δ msh2Δ*, **D)** *rad24Δ +10 h*, **E)** P_{CLB2}-*MEC1 msh2Δ*, **F)** P_{CLB2}-*MEC1 +8 h*.

Table 7.4. Gamma parameters

Best-fit gamma parameters are given for the inter-event distribution for each aggregate genotype and event type. The number following the genotype indicates how many samples were included in the aggregate. N indicates the total number of recombination events (CO, NCO or both) included in the analysis. The shape factor, α, corresponds to the strength of interference: A value of 1 indicates an exponential distribution i.e. no interference. Values > 1 indicate interference, with higher values corresponding to stronger interference. The scale factor, β describes the distance over which the shape designated by α is stretched, thus indicating the range of the interference. A one-sample Kolmogorov–Smirnov test is utilized to determine whether the experimental inter-event distribution is significantly different from the theoretical best fit gamma distribution, with the reported P-value indicating whether the difference was significant. If the value is <0.05, the difference is considered significant (red).

Genotype (repeats) Crossovers	N	Best fit gamma α value	Best fit gamma β value	(P)
msh2Δ (9)	799	2.44	44056	0.0036
rad24Δmsh2Δ (6)	408	1.60	65725	0.0580
P$_{CLB2}$-MEC1 msh2Δ (5)	654	1.65	44833	0.0375
WT+8 h (4)	319	1.46	79142	0.0245
rad24Δ +10 h (6)	636	1.07	81728	0.0025
P$_{CLB2}$-MEC1 +8 h (5)	595	1.20	68504	0.0542
Non-Crossovers	N	α	β	(P)
msh2Δ (9)	698	1.21	87998	0.0861
rad24Δmsh2Δ (6)	474	1.06	88589	0.7754
P$_{CLB2}$-MEC1 msh2Δ (5)	820	1.02	59296	0.0501
WT+8 h (4)	123	0.96	186147	0.9732
rad24Δ +10 h (6)	287	1.02	134129	0.4625
P$_{CLB2}$-MEC1 +8 h (5)	273	0.95	133785	0.0558
Total events	N	α	β	(P)
msh2Δ (9)	1636	1.57	36542	0.0001
rad24Δmsh2Δ (6)	974	1.11	50168	0.1302
P$_{CLB2}$-MEC1 msh2Δ (5)	1560	1.24	28006	0.0001
WT+8 h (4)	504	1.10	72010	0.0011
rad24Δ +10 h (6)	1022	0.98	60137	0.0001
P$_{CLB2}$-MEC1 +8 h (5)	949	1.05	52784	0.0075

7.2.9. The distribution of NCO events does not show evidence of interference

In contrast to CO events, NCOs do not display interference (Mancera *et al.*, 2008). In order to determine whether this was affected by checkpoint mutations, inter-NCO distances were plotted as described for inter-CO distances, alongside simulated datasets for events occurring under conditions of independence (Figure 7.18). In all backgrounds, the experimental inter-NCO distance plots are a good match to the random simulation (Figure 7.18, compare blue (experimental) and orange (random simulation); suggesting that NCOs are randomly distributed. The best fit to a gamma distribution was found for inter-NCO event distances (Table 7.4), producing α values close to 1 for all strains, also indicative of low or no interference between NCO events, as predicted. A Kolmogorov-Smirnov test was utilized to determine whether the experimental inter-NCO distribution was significantly different from the best fit gamma distribution, revealing that they were not (P-values >0.05 in Table 5.4), indicating that the calculated gamma values are a good description of the strength of NCO interference in these backgrounds.
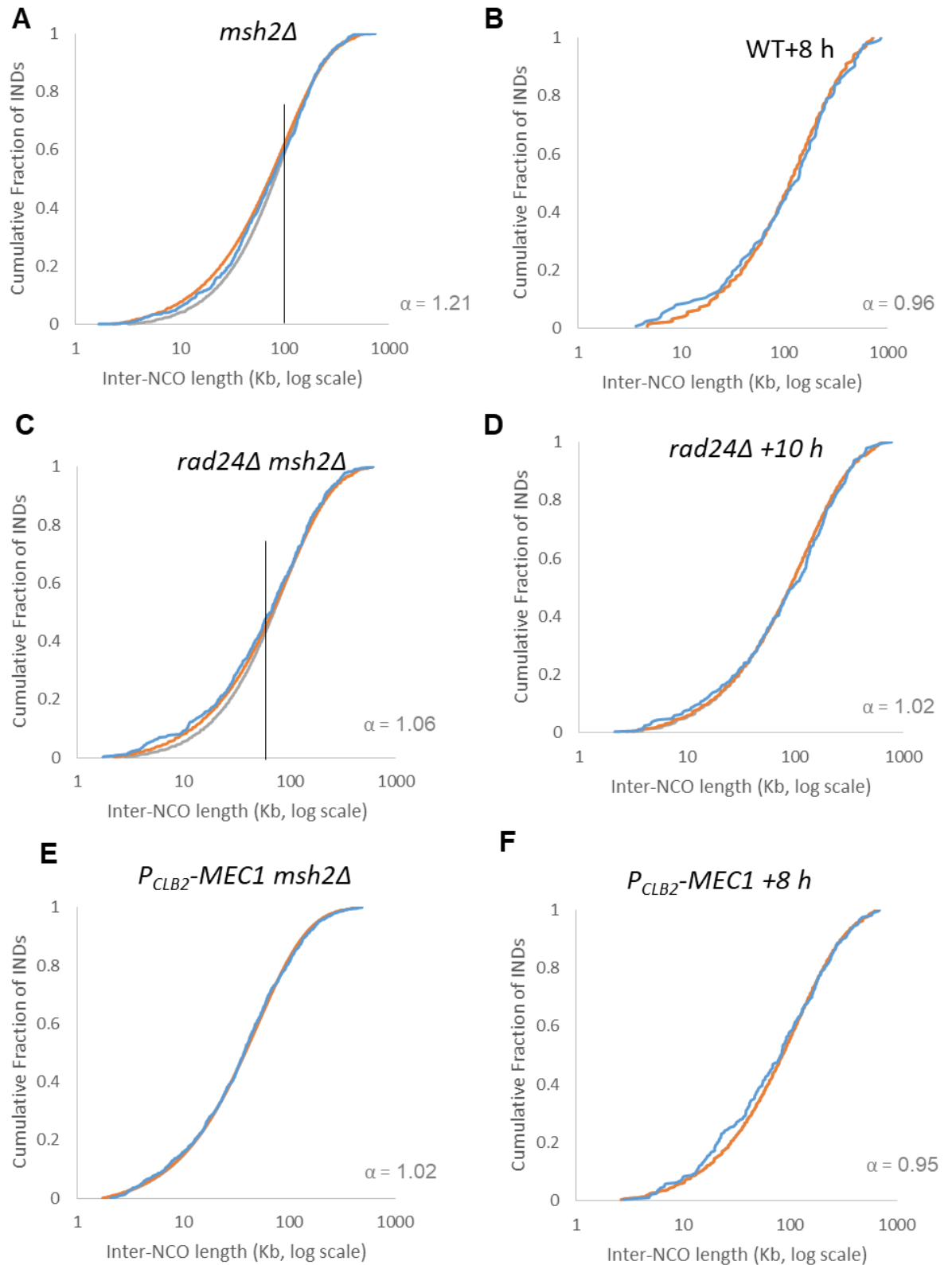
Figure 7.18. Distribution of distances between noncrossover events observed in Msh2 deficient and prophase extension checkpoint mutant strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-NCO distance (IND) in **A)** *msh2Δ*, **B)** WT + 8 h, **C)** *rad24Δ msh2Δ*, **D)** *rad24Δ +10 h*, **E)** P_{CLB2}-*MEC1 msh2Δ*, **F)** P_{CLB2}-*MEC1* +8 h.

7.2.10. The distribution of all recombination events may show evidence of DSB interference loss in DDR mutants

In addition to CO interference, DSBs also reduce the likelihood of another DSB occurring nearby in *cis* and in *trans*, a phenomenon known as DSB interference (Zhang *et al*., 2012; Garcia *et al*., 2014). For an estimate of DSB interference, the distribution of all events is examined, although this is not precise because event midpoints do not always correspond to DSB locations; this may disproportionately affect strains that tend to have long event lengths. In addition, there may be additional DSBs repaired to form NCOs that are not detected due to occurring in regions without markers, or being repaired as a restoration tract in an MMR-proficient strain, and CO or NCO events that are not detected due to being repaired with the sister chromatid (as detailed in Chapter 5, section 5.2.9).

In order to estimate DSB interference in checkpoint mutants, inter-event distances were calculated for the *NDT80* prophase-extension and MMR-deficient *rad24Δ* and P_{CLB2}-*MEC1* strains, arranged in order from smallest to largest and plotted as cumulative fraction of total events against IED size on a log scale, alongside simulated datasets for events occurring under conditions of independence as described for inter-CO distances (Figure 7.19). If DSB interference is present, events should occur further apart than would be expected if event placement was random.

While the *msh2Δ* inter-event distribution deviates to the right from the random distribution, indicating that there are fewer short distances than expected, both the P_{CLB2}-*MEC1 msh2Δ* and *rad24Δ msh2Δ* inter-event distribution are well-described by a random distribution, with only few IEDs occurring closer than expected in P_{CLB2}-*MEC1* (Figure 7.19A-C, compare blue and orange lines), indicating that events are mostly randomly placed in P_{CLB2}-*MEC1* and *rad24Δ*. Similarly to their MMR-deficient equivalents, *NDT80* prophase-arrested *rad24Δ* and P_{CLB2}-*MEC1* strains also display inter-event distance distributions that are well-described by a random distribution. Notably, *rad24Δ+10 h* in particular shows negative interference (DSB clustering) at distances between 4.5-32kb. However, the WT+*8 h* inter-event distribution also mostly matches a random distribution, so this may be mostly related to the increased prophase length rather than *rad24Δ*.

In order to quantify the strength of inter-event interference for each genotype, the best fit gamma parameters were found for inter-event intervals from *msh2Δ, rad24Δ msh2Δ and P_{CLB2}-MEC1 msh2Δ* strains as described for CO events (Methods section 2.18). Calculated gamma parameters are shown in Table 7.4. The α value corresponds to the strength of the interference, with a value of 1 corresponding to a random distribution and values >1 indicating interference.

Inter-event distances in *msh2Δ* are best described by a gamma distribution with α=1.57, while the distribution of events in P_{CLB2}-*MEC1 msh2Δ* and *rad24Δ msh2Δ* are best described by gamma

distributions with $\alpha=1.24$ and $\alpha=1.11$, respectively, suggesting a loss of DSB interference in both checkpoint mutants. Similarly, α values of 1.1, 1.05 and 0.98 were obtained for WT+*8 h*, P_{CLB2}-*MEC1*+*8 h* and *rad24Δ+10 h* respectively, suggesting a loss of DSB interference in the checkpoint mutants.

However, for all strains except *rad24Δ msh2Δ*, the results of a Kolmogorov-Smirnov test to compare the experimental and gamma distributions show that the best-fit gamma distributions are still significantly different to the experimental data (P-values in Table 7.4). This indicates that inter-event distributions in most strains cannot be well described by a gamma distribution.

To provide a visual indication of the goodness of fit, the gamma distributions were used to produce simulated inter-event distance matching the specified parameters, which was plotted to allow comparison with the original data (Figure 7.19, grey lines). For all strains, the gamma distributions are particularly poor fits for the shortest IEDs, which tend to be more randomly placed (Figure 7.19, compare blue and grey lines).

Overall, these results suggest that DSB interference is reduced in P_{CLB2}-*MEC1*, and reduced further in *rad24Δ*, for both MMR-deficient and *NDT80* prophase-arrested backgrounds. However, it should be emphasized again that event midpoint distributions do not necessarily correspond to DSB locations. In addition, inter-event interference may be influenced by CO interference due to CO-CO intervals present within the data, which are known to display interference that is reduced in checkpoint mutants (Section 7.2.8). Overall, because strains generally lose inter-event interference to a similar extent as CO interference, loss of inter-event interference is probably primarily due to the loss of CO interference, rather than reflecting a reduction in DSB interference.
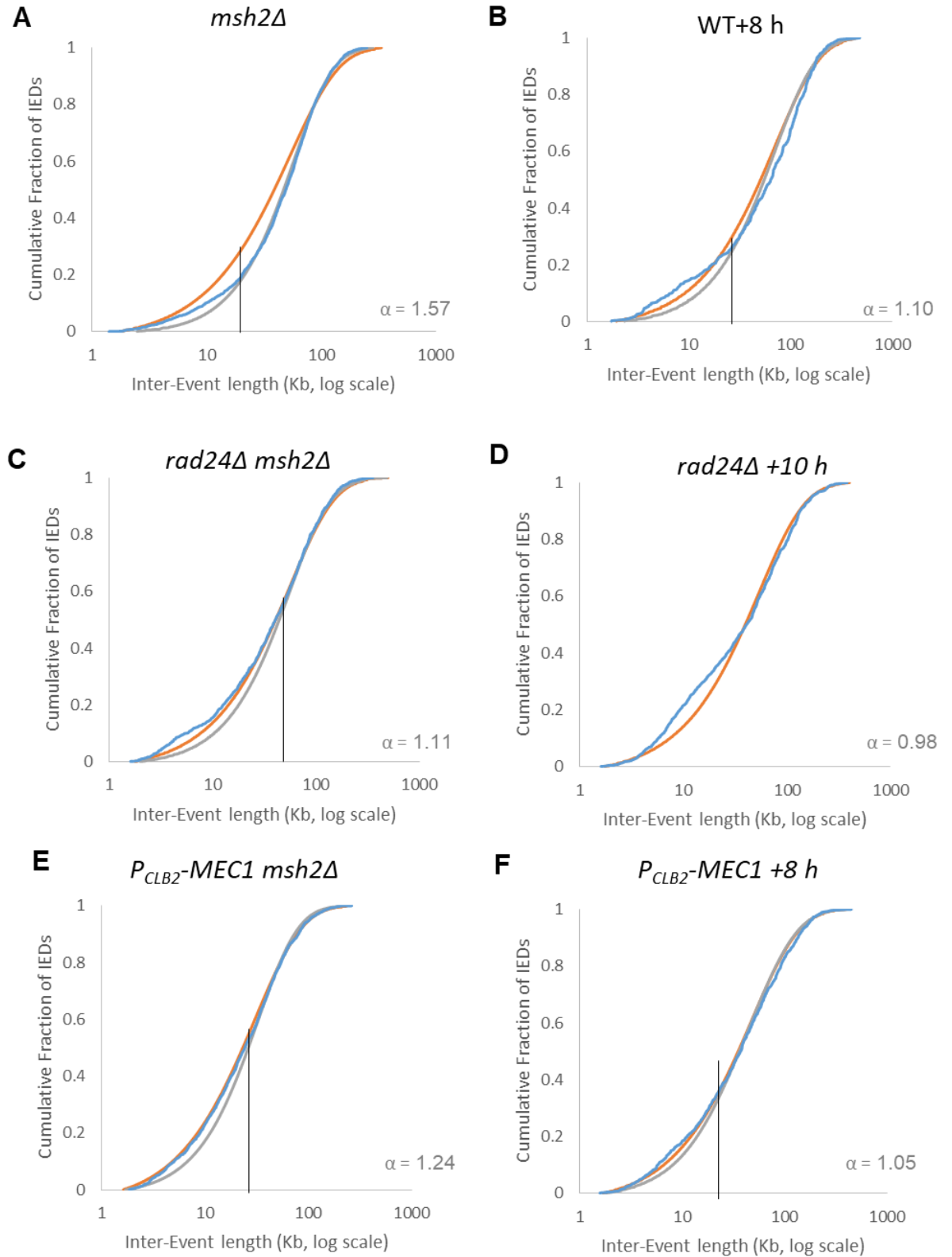
Figure 7.19. Distribution of distances between all recombination events observed in Msh2 deficient and prophase extension checkpoint mutant strains. Both experimental and simulated data are plotted. Blue: Experimental data, Orange: Random simulation, Grey: Best-fit gamma for experimental data, with strength given by α. Vertical black line indicates where deviation between experimental and best-fit gamma begins. Inter-event distance (IED) in **A)** *msh2Δ*, **B)** WT + 8 h, **C)** *rad24Δ msh2Δ*, **D)** *rad24Δ +10 h*, **E)** P_{CLB2}-*MEC1 msh2Δ*, **F)** P_{CLB2}-*MEC1* +8 h.

7.2.11. Mixture modelling predicts proportion of Class I and Class II COs in *rad24Δ* and *P_CLB2-MEC1*

There are two distinct classes of CO event in *S. cerevisiae* meiosis: Class I COs exhibit interference and are dependent upon Msh4/Msh5 activity (Novak *et al.*, 2001), and Class II COs do not display interference and are dependent upon Mus81/Mms4, Yen1 or Slx1-Slx4 activity (de los Santos, 2003). The normal ratio of Class I to II is somewhere around 70:30 (Zakharyevich *et al.*, 2012; de los Santos, 2003). Based on the expectation of a two-component distribution, it is possible to separate out an interfering and a non-interfering subset, which are inferred to be equivalent to Class I and Class II COs (as described in Section 5.2.10). This analysis was authored and performed by Tim Cooper (Methods section 2.19).

It was observed that both MMR-deficient and *NDT80* prophase arrested checkpoint mutants appear to have reduced CO interference (Section 7.2.8), which could be explained by a decrease in Class I CO formation or by an increase in Class II CO formation. To be able to predict the proportions of Class I/II COs in these backgrounds, two-component analysis was carried out on these strains (Table 7.5).

It should be noted that, due to the high degree of randomness in CO distribution observed in these strains, results from the mixture modelling analysis are unreliable for the *rad24Δ msh2Δ* and *rad24Δ +10 h* strains. In fact, since the distribution of events in *rad24Δ +10 h* appears to be totally random, it cannot be successfully separated into two components, because there is no major non-random component.

The ability of the two-component system to describe experimental data was analysed via a Kolmogorov-Smirnov test. In comparison to the poor fit of a single gamma distribution to inter-CO distances (Table 7.4), a large improvement for all genotypes is observed when a mixed-fit is used, with none of the distributions significantly different to the experimentally observed data (compare P-values in Tables 7.4 and 7.5).

The results from the two-component analysis indicate that both MMR-deficient and *NDT80* prophase arrested *P_CLB2-MEC1* strains appear to have a striking increase in the predicted number of Class II COs, compared to the appropriate WT control (Table 7.5). *NDT80* prophase-arrested *P_CLB2-MEC1* is expected to have ~64 Class I COs and ~63 Class II COs, compared to ~64 Class I COs and ~33 Class II COs expected in the *NDT80* prophase-arrested WT. Thus Class I CO formation does not appear to be altered in *P_CLB2-MEC1*, but Class II CO formation is greatly increased. Indeed, the increased CO count observed in *P_CLB2-MEC1* appears to be entirely accounted for by Class II COs.

On the other hand, P_{CLB2}-*MEC1 msh2Δ* is predicted to have ~71 Class I COs and ~64 Class II COs, compared to ~80 Class I COs and ~25 Class II COs in *msh2Δ*. While Class II CO formation is again apparently increased when Mec1 is inactive, Class I CO formation appears to be slightly reduced. Since it was previously observed that Msh2 appears to have anti-Class I CO activity (discussed in Chapter 5, Section 5.2.10), loss of Mec1 activity appears to slightly abrogate this phenotype, though not completely, since P_{CLB2}-*MEC1 msh2Δ* has more Class I COs than its *NDT80* prophase-arrested counterpart.

Interestingly, both the MMR-deficient and *NDT80* prophase arrested P_{CLB2}-*MEC1* strains have very similar predicted proportions for the random and non-random components (52.7%/47.3% compared to 50.7%/49.4%, respectively). Thus, the ratio of Class I: Class II in P_{CLB2}-*MEC1* is roughly 50:50, regardless of the method used to rescue spore viability.

Similarly to the P_{CLB2}-*MEC1* strains, both *rad24Δ* strains are predicted to have a dramatic increase in Class II CO formation compared to the relevant WT controls. However, unlike in the Mec1 mutants, the predicted number of Class I COs is substantially reduced. *rad24Δ msh2Δ* and *rad24Δ + 10 h* are expected to have only around ~10% Class I CO formation, meaning they are predicted to have 7 and 13 Class I COs on average, respectively. It may seem contradictory for *rad24Δ msh2Δ* and *rad24Δ* + 10 h to have a similar level of Class I CO formation, considering that the latter appears to have a total loss of CO interference, while the former retains some (Figure 7.17). However, the CO-CO intervals identified by mixture modelling that appear to show interference in *rad24Δ* + 10 h have a very low β value (1984) compared to that of *rad24Δ msh2Δ* (18994); this indicates that the range of the interference is very narrow in *rad24Δ* + 10 h (Methods Section 2.18). In addition, the results of mixture modelling only offer a prediction of the proportion of CO-CO intervals that appear to show interference, and are by no means definitive.

Both *rad24Δ* strains are also predicted to have a greater number of Class II COs than their P_{CLB2}-*MEC1* equivalent, with ~76 and ~111 in *rad24Δ msh2Δ/rad24Δ+10 h* respectively, compared to ~64 and ~63 in P_{CLB2}-*MEC1 msh2Δ/P_{CLB2}-MEC1+8 h* respectively. In addition, since both *rad24Δ msh2Δ* and *rad24Δ* + 10 h strains have a similar level of predicted Class I formation, it appears that *rad24Δ* is able to abrogate the Class I–promoting phenotype of *msh2Δ* (Section 5.2.10).

The observation that most COs in *NDT80* prophase-arrested *rad24Δ* appear to be Class II non-interfering COs could be explained by the use of the *NDT80* system rather than the lack of Rad24 activity. However, in other backgrounds, *NDT80* arrest does not seem to promote more Class II COs. In WT strains, the number of Class II COs predicted to form is identical between arrested and non-arrested backgrounds (Chapter 4, Section 5.2.10). In addition, P_{CLB2}-*MEC1+8 h* and P_{CLB2}-*MEC1 msh2Δ* also have identical predicted CO numbers; the only thing that changes

between these pairs of strains is the predicted Class I CO numbers. Thus, the reason for the random CO distribution in *rad24Δ* is not caused by the prophase arrest alone, though the arrest conditions likely promote continued Class II CO formation when Rad24 is absent.

Overall, these results suggest an explanation for why P_{CLB2}-*MEC1* strains have overall higher numbers of COs than their *rad24Δ* equivalents; both have an increase in Class II COs, but only *rad24Δ* has a reduction in Class I COs. This explanation is supported by the observation from Shinohara *et al.,* 2015, which suggests that Rad24, but not Mec1, is normally involved in promoting Class I COs. To test this hypothesis, further Class II CO formation can be reduced by the deletion of Mus81, the main resolvase responsible for their formation. This idea is investigated further in Chapter 8.

Table 7.5. Percentage of COs that do not appear to show interference in sequenced strain backgrounds.

Mixture modelling results are given for each genotype. The strength of interference in the non-random population is given by α1 and is expected to be >1. The strength of interference in the random population is given by α2 and is expected to be ~1. The scale factors, β1 and β2 describe the distance over which the shapes designated by α1 or α2 respectively are stretched, thus indicating the range of the interference. The overall proportion of CO events that are thought to occur with random or non-random placement is given, which allows a predicted total number of Class I and Class II COs to be calculated from the overall CO count. A two-sample Kolmogorov–Smirnov test is utilized to determine whether the experimental inter-event distribution is significantly different from the two-component system, with the significance indicated by the reported P-value. A value of >0.05 is considered to show no significant difference.

Genotype (repeats)	α1	α2	β1	β2	Non-random proportion (%)	Random proportion (%)	Predicted mean number of Class I COs	Predicted mean number of Class II COs	P
msh2Δ (9)	3.84	1.21	29877	68155	76.5	23.5	80.3	24.7	0.9
rad24ΔmshΔ (6)	4.25	1.34	18994	75454	8.5	91.5	7.0	76.4	0.9
P_{CLB2}-*MEC1 msh2Δ (5)*	3.56	1.37	35114	27035	52.7	47.3	71.0	63.7	1
WT +8 h (4)	3.22	1.40	47109	32856	66.0	34.0	64.1	33.2	1
rad24Δ+10 h (6)	4.12	1.41	1984	63394	10.9	89.1	13.6	111.3	1
P_{CLB2}-*MEC1 +8 h (5)*	3.25	1.29	39718	24840	50.7	49.4	64.2	62.6	0.9

7.3. Discussion

7.3.1 The meiotic roles of Rad24 and Mec1

Previously, it was found that *rad24Δ* SK1 and SK1xS288c spore viability was rescued by *NDT80* prophase arrest and *sml1Δ*, and hybrid *rad24Δ* by *msh2Δ* (Chapter 3). However, only hybrid, not SK1, P_{CLB2}-*MEC1* yeast were rescued by *NDT80* prophase arrest. It was thought that the low spore viability in *rad24Δ* and P_{CLB2}-*MEC1* hybrids is caused by low numbers of CO events, which is exacerbated in hybrid backgrounds due to the increase in strand rejection by Msh2. In order to investigate these ideas further, recombination events were sequenced genome wide in Rad24 and Mec1 mutants. This revealed that *rad24Δ* has lower CO counts than Mec1 strains (Table 7.6). In addition, a *rad24Δ sml1Δ* meiosis had only 34 COs (Table 7.1), while *rad24Δ msh2Δ* had ~84 COs, *rad24Δ msh2Δ sml1Δ* had ~76.5 and *rad24Δ* + 10 h had ~125. This suggests that *rad24Δ* has low CO numbers, which are boosted by *msh2Δ* (though not to WT levels), but not affected by *sml1*Δ. This supports the idea that the low spore viability in *rad24Δ* is due to low CO counts, which are improved by *msh2Δ* and *NDT80* prophase arrest in hybrids, but not by *sml1Δ* which does not affect CO numbers but only their repair. In addition, *rad24Δ* has fewer CO and NCO events than P_{CLB2}-MEC1, in both MMR-deficient and *NDT80* prophase-extension backgrounds (Table 9.1). This suggests that Rad24 contributes more to ensuring DSB and/or CO formation than Mec1, perhaps via its role in Class I CO formation by interaction with Zip3 and its role in loading ZMM proteins (Section 7.2.11; Shinohara *et al.*, 2015). Alternatively, this could be because Mec1 also has a role in limiting DSB formation via phosphorylation of Rec114 after DSB formation (Carballo *et al.*, 2013), so the absence of Mec1 boosts DSB formation.

Mec1 activity inactivates NDT80 via Mek1 until DSBs are repaired (Prugar *et al.*, 2017). Via its role in the activation of Mec1, Rad24 activity is presumably also important for the inhibition of NDT80 activation. The spore viability of P_{CLB2}-*MEC1* is not affected by prophase extension in a pure SK1 background, but is rescued in an SK1xS288c hybrid background (Chapter 3, Figure 3.9). This may be explained by a reduction in recombination event numbers in hybrid strains, which are thought to have fewer recombination events than pure strains due to the activity of Msh2, which rejects strand invasion into mismatched sequences (Sugawara *et al.*, 1997; Evans *et al.*, 2000). DSB processing leads to the activation of Mec1 due to the formation of RPA-bound ssDNA (Zou & Elledge, 2003), so strains with low rates of DSB formation will also have a reduced level of Mec1 activation. Thus, the lower levels of recombination and spore viability seen in *rad24Δ* compared to P_{CLB2}-*MEC1* can be explained as follows: The absence of Mec1 means there is no Mec1-mediated inhibition of Ndt80, causing a shorter prophase and fewer DSBs, but Rad24 is still present to promote the formation of Class I COs. In the absence of Rad24, there is a reduction in Class I CO formation, and Mec1-mediated inhibition of Ndt80 is weakened because

Mec1 activation by the 9-1-1 clamp and RPA-coated ssDNA is reduced, leading to the formation of fewer DSBs and fewer CO events.

7.3.2. Influence of CO interference and CO numbers on spore viability and CO assurance in *rad24Δ*

The observation that CO interference is reduced in *rad24Δ* strains may also help to explain why these mutants have low viability. CO clustering means that COs are not properly spread out along the chromosomes, potentially causing non disjunction of chromosomes, which is increased in *rad24Δ* (Section 7.2.2). Many chromosomes without COs are seen in *rad24Δ sml1Δ* and *rad24Δ msh2Δ* strains, which also have low spore viability, few COs and reduced CO interference (Tables 7.1, 9.1); this raises the possibility that a lack of CO interference may cause non-disjunction of chromosomes. However, *rad24Δ* + 10 h has an increase in CO events and a greater loss of CO interference compared to *rad24Δ msh2Δ*, but a lower number of chromosomes without COs, indicating that the strength of CO interference is less important than the overall CO number for ensuring that all chromosomes receive a CO event (CO assurance). This suggests that the loss of CO interference observed in *rad24Δ* does not greatly affect spore viability, because while chromosome non disjunction due to lack of CO formation is likely a major contributor to spore viability, this seems to be mainly affected by CO number rather than CO interference. Thus, the role of Rad24 in promoting Class I CO formation appears to be more important to boost CO numbers rather than to maintain CO interference, at least in terms of spore survival.

7.3.3. Differences and similarities between recombination in *msh2Δ* and *NDT80* prophase-arrested *rad24Δ* and P_{CLB2}-*MEC1* backgrounds

For WT, *rad24Δ* and P_{CLB2}-*MEC1* strains, recombination was assayed genome-wide in both *msh2Δ* and *NDT80* prophase-extension backgrounds. Recombination in *NDT80* prophase arrested and *msh2Δ* versions of strains can be compared, but any differences may be only due to the difference in Msh2 proficiency or due to the difference in prophase length, so the contribution of each factor is uncertain. *msh2Δ* strains are expected to have 4-5 hours of prophase (Xu *et al.*, 1995). Ideally, recombination characteristics would be compared between *msh2Δ* and *msh2Δ* with *NDT80* prophase arrest strain versions. Alternatively, characteristics could be compared between WT and *NDT80* prophase arrest versions of strains, but four-spore-viable tetrads cannot be obtained from *rad24Δ* hybrids without the rescue effect of prophase arrest of *msh2Δ*.

Key recombination characteristics were compared between *msh2Δ* and *NDT80* prophase arrest strains (Table 7.6). Generally, the spore viability of *NDT80* prophase arrest strains is higher than *msh2Δ* strains, except in P_{CLB2}-*MEC1* hybrids. Usually, *msh2Δ* strains have more CO and NCO

events, except for *rad24Δ NDT80* prophase arrest, which has more COs than *rad24Δ msh2Δ*. The increase in NCO events in *msh2Δ* is at least partly because of the ability to detect hDNA in *msh2Δ* backgrounds. In all cases, *NDT80* prophase arrest strains have longer CO and NCO events, while *msh2Δ* strains have an increase in the percentage of recombination events that appear to be DSB clusters. The distribution of CO events matches gamma distributions with higher alpha values in *msh2Δ*, suggesting stronger CO interference than in *NDT80* prophase arrest strains. This may be explained by the higher percentage of COs that are predicted to be Class I interfering COs, in comparison to Class II non-interfering COs, in *msh2Δ* strains.

Increased prophase length is more beneficial to cell survival than *msh2Δ*, perhaps because a lack of MMR means that mutations cannot be repaired and ectopic recombination is increased due to the inability to reject strand invasion into non-homologous regions, while Ndt80 arrest does not produce many effects that persist after Ndt80 induction (Allers & Lichten, 2001; Bhuiyan *et al.*, 2002). In *NDT80* prophase arrest strains, events occur in lower numbers and with weaker CO interference than *msh2Δ*; however, this is probably because of the effect of *msh2Δ* rather than the effect of prophase length, because *msh2Δ* has an increase in Class I COs, boosting CO numbers and increasing the strength of interference.

Table 7.6. Summary of basic recombination characteristics in *rad24Δ* **and** *P_CLB2-MEC1* strains. To highlight differences between *msh2Δ* and *NDT80*-arrest version of WT, *rad24Δ* and *pCLB2-MEC1* strains. For each pair of strains, the *NDT80* prophase arrest version is on the left and the MMR deficient version on the right. For each characteristic, the red coloured box indicates the strain with the highest value (for the final two categories, the highest percentage and number of Class I COs). Spore viability was originally shown in Figures 3.1A, 3.8, 3.9. WT + 8 h is from Gray *et al.*, 2013. DSB cluster formation originally shown in Figure 7.5, 7.6. CO/NCO formation originally reported in Table 7.1. Event mid length median shown in Figure 7.8, 7.9. Best fit alpha values are from Table 7.4. (It should be noted that the best fit alpha value was still significantly different from the actual CO distribution in most cases). The Class I and II percentages and numbers are from Table 7.5.

	WT + 8 h	*msh2Δ*	*rad24Δ* + 10 h	*rad24Δ msh2Δ*	*P_CLB2-MEC1* + 8 h	*P_CLB2-MEC1 msh2Δ*
Spore viability % (SK1)	94	81	69	21	58	49
Spore viability % (SK1xS288c hybrid)	70	73	16	6	16	29
Average CO number	97.3	105	125	83.5	126.8	134.7
Average NCO number	51	101.8	92	113	90.7	213.8
Median NCO mid length (bp)	2089	1057	2635	827	2340	926
Median CO mid length (bp)	1679	1195	1984	1571	1880	1326
% of events that are DSB clusters	5.6	4.6	18.2	10.9	15.9	13.7
Best fit α value (CO interference)	1.46	2.44	1.07	1.60	1.20	1.65
Class I/Class II CO percentage	66/ 34	76.5/ 23.5	10.9/ 89.1	8.5/ 91.5	50.7/ 49.4	52.7/ 47.3
Class I/Class II CO number (predicted)	64.1/ 33.2	80.3/ 24.7	13.6/ 111.3	7/ 76.4	64.2/ 62.6	71/ 63.7

7.3.4. Closing Statement

In this chapter, the roles of Rad24 and Mec1 proteins are established via the analysis of meiotic recombination genome wide in *rad24Δ* and *P_{CLB2}-MEC1* backgrounds. In particular, differences and similarities between Rad24 and Mec1 activity are examined. The analysis is repeated in two different rescue backgrounds in order to account for any effects produced by the rescue mechanism.

Overall, these results suggest that the main cause of the low spore viability of *rad24Δ* and *P_{CLB2}-MEC1* is a reduction in Spo11-DSB formation (likely due to the loss of the meiotic checkpoint), and a resultant reduction in CO formation, which is particularly severe in *rad24Δ* due to the role of Rad24 in promoting Class I CO formation. Increasing the number of DSBs that are formed and repaired via prophase arrest, or via increasing the efficiency of strand invasion into homologous chromosomes via *msh2Δ*, improves *rad24Δ* and *P_{CLB2}-MEC1* hybrid viability.

Chapter 8.

The effect of resolvase pathway choice on spore viability and CO interference in DDR and MMR mutants

Chapter 8. The effect of resolvase pathway choice on spore viability and CO interference in DDR and MMR mutants

8.1. Introduction

8.1.1. CO resolution in *S. cerevisiae*

In *S. cerevisiae*, there are at least four distinct endonucleases capable of resolving JMs in vitro: Mus81-Mms4 (Boddy *et al.*, 2001), Slx1–Slx4 (Fricke and Brill, 2003), Yen1 (Ip *et al.*, 2008), and Exo1-MutLγ (Zakharyevich *et al.*, 2012), which together account for essentially all JM resolution in vivo (Zakharyevich *et al.*, 2012). Around 70% of COs, and few or no NCOs, are formed by the MutLγ complex, in combination with Exo1 nuclease and Sgs1 helicase (Zakharyevich *et al.*, 2012). The Mus81-Mms4 pathway accounts for somewhere between 10-40% of COs (de los Santos, 2003). Yen1 and Slx1-Slx4 do not usually account for many COs. However, in the absence of other CO resolution pathways, Yen1 and Slx1-Slx4 appear to play a more important role in recombination (Zakharyevich *et al.*, 2012).

8.1.2. ZMM proteins promote the formation of Class I interfering COs

Crossover interference is a phenomenon where CO events occur further apart than would be expected from a random distribution (Sturtevant 1913; Sturtevant 1915). However, interference is only exhibited in Class I COs, which are dependent upon Msh4/Msh5 activity (Novak *et al.*, 2001). Class II COs do not display interference and are dependent upon Mus81/Mms4, Yen1 or Slx1-Slx4 activity (de los Santos, 2003). Msh4 and Msh5 are ZMM proteins, which promote the biased resolution of dHJs into Class I COs (Chen *et al.*, 2015) and are important for the maintenance of crossover interference in meiosis (Shinohara *et al.*, 2008). Another ZMM protein is Zip3, which binds DNA close to DSBs and promotes local assembly of other ZMM proteins (Serrentino *et al.*, 2013). It has recently been discovered that Rad24 is necessary for loading ZMM proteins, and interacts physically with Zip3, independent of Mec1. This indicates that Rad24 may promote the loading of ZMM proteins at sites of future Class I COs (Shinohara *et al.*, 2015).

8.1.3. Mixture modelling predicts the percentage of Class II COs

The distribution of CO events can be viewed as having two components, a distribution of non-random, interfering events and a distribution of random, non-interfering events (previously discussed in Chapter 5 section 5.2.10, Chapter 6 section 6.2.11, Chapter 7 section 7.2.11). Based on the expectation of a two-component distribution, it is possible to separate out random and non-random components of inter-CO distance distributions using mixture modelling. The system for this analysis was authored by Tim Cooper (Methods section 2.19). The random distribution is

inferred to be equivalent to Class I interfering COs, and the non-random distribution to Class II non-interfering COs. Different strain backgrounds have differing ratios, as shown in Table 8.1.

8.1.4. Aims of this investigation

Mixture modelling predicts a certain percentage of Class II COs in each background. Because Mus81 is the major Class II pathway, strains predicted to have more Class II COs are expected to have a larger drop in viability when Mus81 is deleted. In this chapter this idea is explored in two ways.

1. To measure the effect of the loss of the major Class II CO pathway resolvase Mus81 in various backgrounds.

2. To examine the effect of single and double mutants of Mus81, Mlh3 and Yen1 in WT and *rad24Δ* backgrounds, to discover the relationship between the resolvases and the role they play in *rad24Δ* viability.

Table 8.1. Percentage of COs that do not appear to show interference in sequenced strain backgrounds.

Mixture model results per genotype. The strength of interference in the non-random population is given by α1 and is expected to be >1. The strength of interference in the random population is given by α2 and is expected to be ~1.

Genotype (repeats)	α1	α2	Non-random proportion (%)	Random proportion (%)	Predicted mean number of Class I COs	Predicted mean number of Class II COs
WT (4)	3.78	1.06	67.1	32.9	50	24.5
WT +8h (4)	3.22	1.4	66	34	64.1	33.15
msh2Δ (9)	3.84	1.21	76.5	23.5	80.3	24.7
tel1Δ msh2Δ (10)	4.45	1.97	67.4	32.6	77.7	37.6
P$_{CLB2}$-MEC1 mshΔ (5)	3.56	1.37	52.7	47.3	71	63.7
P$_{CLB2}$-MEC1 +8 h (5)	3.25	1.29	50.7	49.4	64.2	62.6
rad24ΔmshΔ (6)	4.25	1.34	8.5	91.5	7	76.4
rad24Δ+10 h (6)	4.12	1.41	10.9	89.1	13.6	111.3

8.2. Results

8.2.1. Deletion of Mus81 reduces spore viability in all strains except *rad24Δ*

Genome-wide analysis of recombination events suggests that there is a loss of CO interference in checkpoint mutants, and this may be caused by an increase in the proportion of Class II COs. To observe the effect of removing the main Class II CO pathway on spore viability, a deletion of Mus81 is used.

mus81Δ yeast have been reported to have a spore viability of 40% (de los Santos *et al.*, 2003), 38.7% (Chen *et al.*, 2016) and ~50% (Matos *et al.*, 2011). The *mus81Δ* strain used here had a spore viability of ~55%, compared to a WT viability of ~96% (Figure 8.1). This is somewhat higher than previous reported values for *mus81Δ* viability, which may be due to variation in sporulation conditions.

Considering that Mus81 is responsible for resolving only 10-40% of COs, the large drop in viability is surprising compared to the 71.7-79% spore viability observed in *mlh3Δ*, which abolishes ~70% of COs (Nishant *et al.*, 2008; Brown *et al.*, 2013). This suggests that there are some joint molecule structures that cannot be resolved by anything other than Mus81. *mus81Δ* viability may also be lower than other resolvases because Mms4 is required for crossovers between short chromosomes (de los Santos, 2003).

In addition, since Mus81 is also functional in mitotic recombination (Ho *et al.*, 2010), that may also be affecting viability of the germinating spores. However, it has been previously shown that using a meiotic depletion allele of *MMS4* gives a similar sporulation defect to that of a complete *MMS4* knockout, so if there is a build-up of repair intermediates from the preceding mitoses, it does not have a significant effect on the following meiosis (Matos *et al.*, 2011).

In *WT, msh2Δ, tel1Δ* and P_{CLB2}-*MEC1* mutant strains, the loss of Mus81 reduces spore viability (Figure 8.1). In order to determine if the spore viability reduction is as expected based on the WT values, the expected viability of a double mutant can be calculated and compared to the actual viability (Table 8.2). If the viability is lower than expected, this indicates that the loss of Mus81 activity is particularly severe to this mutant. If viability is higher than expected, this suggests that the mutant strain may have already lost some Mus81 function or is able to compensate for its absence. If viability is as expected based on WT values, then there is no indication of any relationship between the gene of interest and Mus81 activity.
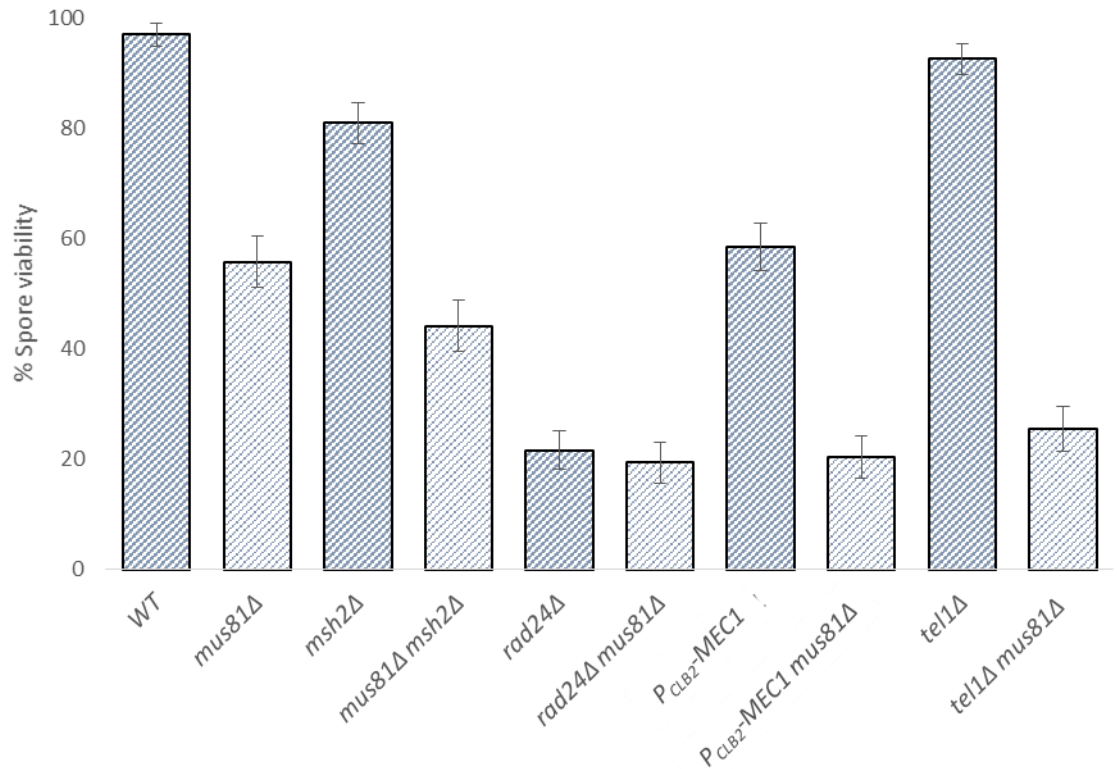
Figure 8.1. Spore viability in strains with and without Mus81 activity. All error bars represent 95% confidence limits.

Table 8.2. Observed and expected spore viabilities of *mus81Δ* strains. The expected spore viability is calculated by working out the percentage change in spore viability from WT for each single mutant, then combining the change for the relevant single mutants to work out the expected for the double mutant.

Genotype	No. tetrads dissected	Observed Spore viability %	Expected Spore viability of double mutants %	Observed/ Expected ratio
WT	64	96.88		
mus81Δ	110	55.68		
rad24Δ	132	21.59		
rad24Δ mus81Δ	110	19.32	12.4	1.56
msh2Δ	110	73.0		
msh2Δmus81Δ	110	44.1	40.6	1.09
tel1Δ	87	92.5		
tel1Δmus81Δ	109	25.5	51.5	0.50
P_{CLB2}-MEC1	130	58.5		
P_{CLB2}-MEC1 mus81Δ	108	20.4	32.6	0.63
mlh3Δ	110	89.09		
mus81Δ mlh3Δ	107	59.58	51.2	1.16

The *msh2Δ* strain was predicted to have ~24% Class II COs, compared to ~33% in WT (Table 8.1). However, the actual average number of Class II COs is not expected to change between strains, with both WT and *msh2Δ* having ~25 Class II COs; only the number of Class I COs is altered. The viability of the *msh2Δ mus81Δ* strain was ~44%, which is exactly as expected based on the viabilities of the *msh2Δ* and *mus81Δ* single mutants (Table 8.2). This indicates that *msh2Δ* spore viability is affected by the loss of Mus81 activity to the same degree as WT, supporting the conclusion that the number of Class II COs is unaffected by loss of Msh2 activity.

The *tel1Δ msh2Δ* strain was predicted to have ~33% Class II COs, giving an average of 38 Class II COs per octad, an increase compared to the *msh2Δ* control (Table 8.1). The spore viability of *tel1Δ mus81Δ* was 50% lower than expected based on the viability of *tel1Δ* and *mus81Δ* single mutants (Table 8.2), indicating that Class II COs are more important for successful meiosis in *tel1Δ* than in WT, as their spore viability is disproportionately affected by the loss of Mus81 activity. This supports the conclusion that *tel1Δ msh2Δ* has a greater number of Class II COs, which was also predicted by Anderson *et al.*, 2015.

Both *NDT80* prophase-arrested and MMR-deficient P_{CLB2}-*MEC1* strains were predicted to have a roughly 50:50 ratio of Class I to Class II, and were expected to have 63-64 Class II each, a significant increase compared to the *NDT80* prophase-arrested and MMR deficient wild types (Table 8.1). P_{CLB2}-*MEC1 mus81Δ* spore viability was around 37% lower than expected based on the spore viabilities of the P_{CLB2}-*MEC1* and *mus81Δ* single mutants, indicating that Class II COs are more important for successful meiosis in P_{CLB2}-*MEC1* than in WT (Table 8.2). This supports the conclusion that P_{CLB2}-*MEC1* strains have a greater number of Class II COs than WT strains, as their spore viability is disproportionately affected by the loss of Mus81 activity. However, the P_{CLB2}-*MEC1 msh2Δ* strain was also predicted to have a greater number and proportion of Class II COs than *tel1Δ msh2Δ* strain, but *tel1Δ mus81Δ* spore viability was reduced more than that of P_{CLB2}-*MEC1 mus81Δ*. This indicates that even though P_{CLB2}-*MEC1 msh2Δ* had more Class II COs, and fewer Class I COs, than *tel1Δ msh2Δ*, the Class II COs were not as important to successful meiosis in P_{CLB2}-*MEC1* as in *tel1Δ*. This may be because the P_{CLB2}-*MEC1 msh2Δ* strain has more COs in total than *tel1Δ msh2Δ*, so is less affected by a reduction in CO numbers.

Lack of Mus81 is expected to impact spore viability partly due to the presence of unresolvable joint molecules; the increase in recombination events seen in *tel1Δ* and P_{CLB2}-*MEC1* meioses may mean that this is the cause of their greater loss of viability, rather than being due to the reduction in Class II COs formation. However, *msh2Δ* meioses also have an increase in recombination, but are not disproportionally affected by *mus81Δ*, which indicates that complex repair of aberrant

joint molecules is not impacting spore viability disproportionately in strains with increased recombination activity.

Both MMR-deficient and *NDT80* prophase arrested *rad24Δ* strains were predicted to have few Class I COs, with only ~10% of COs predicted to be Class I (Table 8.1). This conclusion was supported by the observation that Rad24 interacts with Zip3, which promotes Class I CO formation (Shinohara *et al.*, 2015). Thus, deletion of *mus81Δ* was expected to have a severe effect on *rad24Δ* spore viability. However, *rad24Δ mus81Δ* had a much higher spore viability than expected based on the viabilities of the *rad24Δ* and *mus81Δ* single mutants, indicating that Class II COs are not as important to *rad24Δ* spore viability as in WT (Table 8.2). This also indicates that Class II COs are less vital to a successful meiosis in *rad24Δ* than in P_{CLB2}-*MEC1*, despite the two proteins being in the same DDR pathway.

A possible explanation for the spore viability of *rad24Δ mus81Δ* being higher than expected may be because *rad24Δ* has already lost some Mus81 function, and so is not affected further by its deletion. Alternatively, *rad24Δ* may be able to compensate for the loss of Mus81 more effectively than WT, with other resolvases able to rescue spore viability. Since the sequenced *rad24Δ* strains are either MMR-deficient or with 10 h of *NDT80* prophase arrest, it may be that Class II CO proportions are only elevated under these circumstances, and so the effect of *mus81Δ* is not seen in *rad24Δ* alone. Finally, the results could be affected by bias – since only successfully sporulated cells can be dissected, the spore viability is skewed towards situations where meiosis was completed, which could be unusual. To investigate some of these ideas, the effect of removing the action of other resolvases on *rad24Δ* viability was tested (Section 8.2.3) and the viability of *rad24Δ mus81Δ* with *NDT80* prophase arrest was assayed (Section 8.2.4).

8.2.2. Contribution of resolvases to WT spore viability

To investigate the individual and combined contributions of different resolvases in meiosis, the spore viability of *yen1Δ*, *mlh3Δ* and *mus81Δ* single and double mutants was assayed (Figure 8.2A, Table 8.3). The ~93% viability of the *yen1Δ* strain is in line with the measurement of ~95% by Matos *et al.*, 2011, which was about the same as their WT. Yen1 is also functional in mitotic CO resolution (Ho *et al.*, 2010), so survival defects in this background could be due to mitotic, as well as meiotic, recombination failure. A *mus81Δ yen1Δ* strain was also created, but its sporulation was too inefficient for dissection. *mus81Δ yen1Δ* viability was previously found to be ~2.5% (Matos *et al.*, 2011). This result is in line with conclusions that Yen1 resolvase activity is redundant with that of Mus81.

Of the MutLγ components, it was decided to use a deletion of Mlh3 rather than Mlh1, because *mlh3Δ* has a lower rate of spontaneous mitotic mutation (Brown, 2013). As mentioned for *mus81Δ* in the previous section, the *mlh3Δ* strain is also healthier than expected (89%, Figure 8.2) given reported values of 71.7% (Nishant *et al.*, 2008) and 79% (Brown *et al.* 2013) for *mlh3Δ*, and 81% (Hoffmann *et al.*, 2003) and 68% (Argueso *et al.*, 2004) for *mlh1Δ*. This may be due to variation in sporulation conditions.

The combination of *mus81Δ* and *mlh3Δ* is surprisingly healthy (~59% spore viability), considering that both major CO pathways are lost. This suggests that the backup resolvase pathways Yen1 and Slx1-Slx4 are able to compensate effectively for the loss of both Mus81 and Mlh3.

It is important to note that *mlh3Δ* may not necessarily completely lose interference. Synaptonemal complex initiation sites also display interference, even in the absence of CO interference (Fung *et al.*, 2004), and are established by the ZMM proteins far upstream of dHJ resolution, so interfering CO sites may have already been determined when Mlh1-Mlh3 acts (Argueso *et al.*, 2004). However, this is only a concern if the pre-determined interfering CO sites are able to be used to complete CO formation. Since COs are reduced by ~70% in *mlh1Δ*, it seems unlikely that many residual Class I COs are formed by other resolvases. Instead, the pre-determined CO sites may be dissolved by Sgs1, which has a role in removing aberrant recombination intermediates (Jessop *et al.*, 2006). *sgs1Δ* alleviates the crossover defect of *mlh3Δ* mutants (Oh *et al.*, 2007). In addition, it would not be fair to compare the *mus81Δ* phenotype to that of ZMM mutants, because the ZMM proteins have other roles in addition to maintaining CO interference. For example, Zip1, as the transverse filament protein, is a major part of the synaptonemal complex, and its mutation is much more severe than *mlh3Δ*. *zip1Δ* has a spore viability of 48.4%, and 17% when combined with *mus81Δ* (Chen *et al.*, 2016).
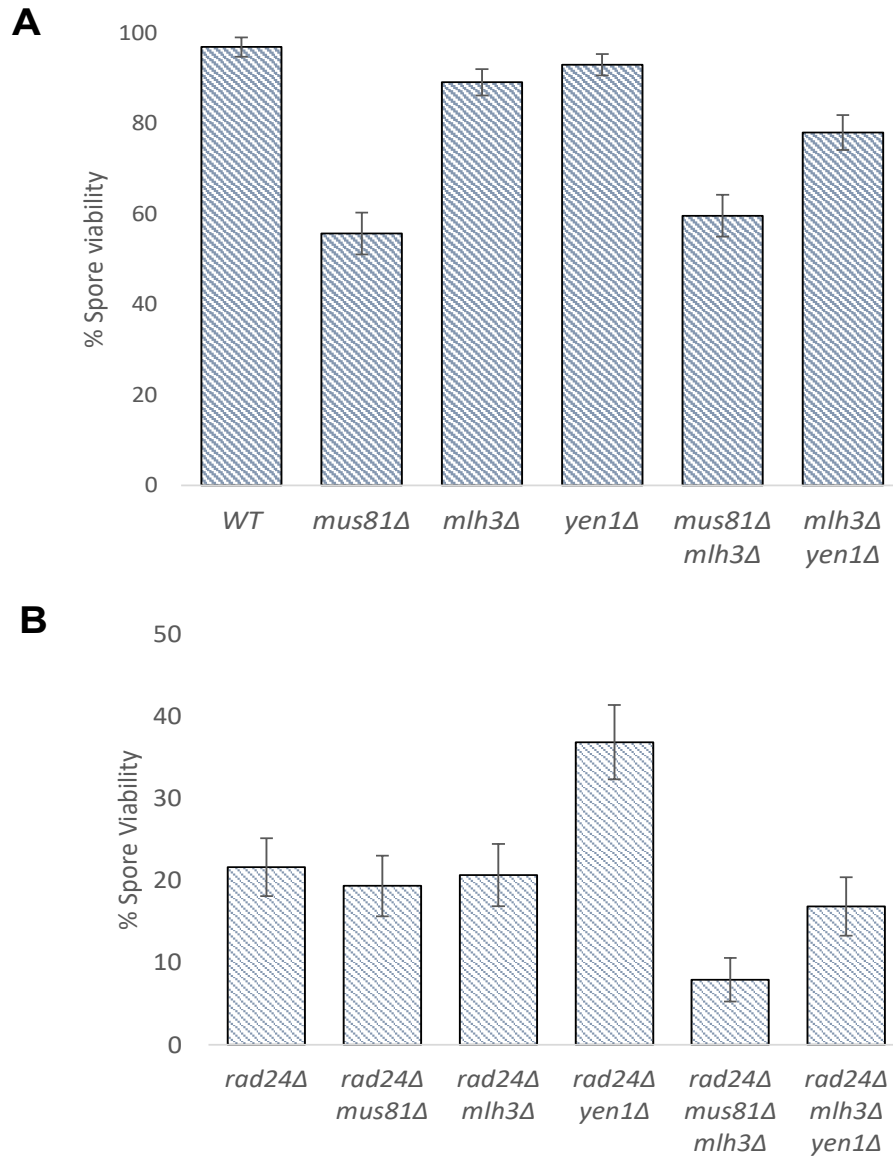
Figure 8.2. Spore viability in resolvase mutants. All error bars represent 95% confidence limits. Spore viabilities of various resolvase single and double mutants in **A**) a *RAD24* background, **B**) a *rad24Δ* background.

Genotype	No. Tetrads dissected	Observed % Spore viability	Expected % viability of double/triple mutants	Observed/ Expected ratio
WT	64	96.88		
mus81Δ	110	55.68		
mlh3Δ	110	89.09		
yen1Δ	110	92.95		
mus81Δ mlh3Δ	107	59.58	51.2	1.16
mlh3Δyen1Δ	110	77.95	85.49	0.91
mus81Δyen1Δ	0	-	53.43	-
rad24Δ	132	21.59		
rad24Δ mus81Δ	110	19.32	12.4	1.56
rad24Δ mlh3Δ	109	20.64	19.9	1.04
rad24Δ yen1Δ	110	36.82	20.7	1.78
rad24Δ mus81Δ mlh3Δ	98	7.91	11.4	0.69
rad24Δ mlh3Δ yen1Δ	107	16.82	19.05	0.88
rad24Δ mus81Δ yen1Δ	0	-	11.91	-

Table 8.3. Observed vs expected spore viabilities of *rad24Δ* strains. For the triple mutants, the expected value was calculated using the viabilities of the three relevant singles rather than the doubles.

8.2.3. Contribution of resolvases to *rad24Δ* spore viability

Due to the unexpected result of *mus81Δ* not having much effect on *rad24Δ* viability, the effect of other resolvase mutations on *rad24Δ* spore viability was also tested (Figure 8.2B), and compared to expected values based on single mutant spore viabilities (Table 8.3). This shows that *rad24Δ* is very tolerant of the loss of any single resolvase (Mus81, Mlh3 or Yen1), and loss of both Mlh3 and Yen1, none of which produce a significant effect on *rad24Δ* spore viability. Since the number of ZMM foci in *rad24Δ* is reduced by 2/3 (Shinohara *et al.*, 2013), Mlh1-Mlh3 activity is not expected to be vital to *rad24Δ* spore survival. In contrast, removal of both Mus81 and Yen1 or Mus81 and Mlh3 has a significant effect on *rad24Δ* spore viability. In *rad24Δ mus81Δ yen1Δ*, sporulation efficiency was too low to test viability. The few tetrads present were composed of very small, pale spores. This is the same as in *mus81Δ yen1Δ* backgrounds, affirming Yen1's role in acting as a backup for Mus81 and suggesting that the reason for meiotic failure in *rad24Δ mus81Δ yen1Δ* is due to the presence of joint molecules that cannot be resolved.

The combination of *mus81Δ* and *mlh3Δ* reduces *rad24Δ* viability from 21% to 8%. However, in a WT background, *mus81Δ mlh3Δ* does not reduce viability any more than *mus81Δ* alone. This suggests that *rad24Δ* is less tolerant of the loss of both major resolvases than *RAD24*^{+} backgrounds. Since CO numbers are reduced in *rad24Δ* strains (Chapter 7, Table 7.1), it may be that *rad24Δ* does not have a high requirement for resolvases due to having few dHJs to resolve.

Overall, in *rad24Δ*, the loss of any single resolvase is not deleterious. This suggests that Yen1 and Mlh3 activity can compensate for a lack of Mus81, and Mus81 can make up for absence of both Mlh3 and Yen1. However, losing another resolvase on top of *mus81Δ* is more deleterious, suggesting that Mus81 is the resolvase most important to spore viability in *rad24Δ*.

Taken together, these results suggest that the reason why *rad24Δ* is more tolerant to *mus81Δ* than WT is that it is able to use the Yen1 and Mlh1/Mlh3 pathways to compensate for the loss of Mus81-mediated COs more effectively than WT, perhaps because it has few CO events to begin with. Thus, *rad24Δ* is not negatively affected by *mus81Δ* unless it has also lost Mlh3 or Yen1, while WT is not affected by the loss of Mlh3 if it has already lost Mus81.

An explanation for why *rad24Δ* is resistant to the loss of any single resolvase could be because it forms fewer COs, so is less reliant on any particular resolvase. This agrees with the observation that *rad24Δ msh2Δ* and *rad24Δ sml1Δ* sequenced tetrads have fewer COs than WT (Chapter 7, Section 7.2.1).

The reason why *rad24Δ mus81Δ* viability is dependent on *mlh3Δ* may be because the number of ZMM foci in *rad24Δ* is reduced by 2/3 in *rad24Δ*, so the remaining 1/3 of Class I COs have increased importance to *rad24Δ* viability in the absence of Mus81. The decreased number of COs observed in sequenced *rad24Δ msh2Δ* and *rad24Δ sml1Δ* tetrads supports the idea that *rad24Δ* is more reliant on residual COs.

Surprisingly, the deletion of Yen1 improves the spore viability of *rad24Δ*, by about 15%. Yen1 activity is known to be deleterious when uncontrolled; a constitutively activated form of Yen1 causes increased sensitivity to DNA-damaging agent methyl methanesulfonate (MMS) and an increase in mitotic CO numbers at the expense of NCO products, causing a loss of heterozygosity (Blanco *et al.*, 2014). This seems unlikely to be a factor in the health of *rad24Δ*, because it has a reduced number of meiotic COs based on sequencing data from *rad24Δ msh2Δ* and *rad24Δ sml1Δ*. So, if Yen1 is activated at an inappropriate time in *rad24Δ* meiosis, it would be expected to improve CO numbers and thus be beneficial to survival. Yen1 is normally subject to strict spatial and temporal control in meiosis and mitosis. In mitotic S-phase, Yen1p is subject to phosphorylation mediated by the cyclin-dependent kinase Cdk1. This has the dual effect of both excluding Yen1p from the nucleus and reducing the efficiency of DNA binding (Blanco *et al.*, 2014). In anaphase, Yen1p is activated by Cdc14 phosphatase, which dephosphorylates Yen1p, allowing it to efficiently bind DNA and causing it to relocalize to the nucleus (Blanco *et al.*, 2014). The levels of Yen1 remain fairly constant throughout meiosis, but its HJ resolvase activity is not observed until the start of anaphase II transition, when it is activated by desphosphorylation

(Matos *et al.*, 2011). It is not clear whether Cdk1 and Cdc14 have the same roles in regulating Yen1p in meiosis as in mitosis. Yen1 does have some phosphorylation sites matching the consensus target sequences for Mec1, which could indicate a connection with Rad24 (Blanco *et al.*, 2014). If Mec1 is at least partly responsible for phosphorylating Yen1, the reduced activity of Mec1 in *rad24Δ* could potentially lead to inappropriate activity of Yen1p. However, Mec1-mediated activation of the DDR checkpoint is known to inhibit Cdk1 activity in mitosis. The lethal effects of Mec1 mutations can be alleviated by a decrease in Cdk1 activity, indicating that certain Cdk1 activities are detrimental in the absence of the DDR (Manfrini *et al.*, 2012). Also, MMS treatment during G1 delays the transcription of *CLN1* and *CLN2*, cyclins which bind Cdk1; this alleviated by Mec1 mutation (Sidorova and Breeden, 1997). If this also applies in meiosis, it would be expected that lower activity of Mec1 due to lack of Rad24 would cause higher activity of Cdk1, and thus lower activity of Yen1p.

Overall, it seems most likely that the reason for Yen1 activity being deleterious in *rad24Δ* is due to inappropriately early activation of Yen1, as *rad24Δ* is known to have abnormal cell cycle timing due to its short prophase; however, the exact details of when Yen1 is activated in *rad24Δ* are unclear.

8.2.3. *rad24Δ* spore viability is no longer rescued by 8h of *NDT80* prophase arrest in the absence of Mus81 activity.

In contrast to *rad24Δ msh2Δ* and *rad24Δ sml1Δ*, sequenced *rad24Δ* tetrads with 10 h of *NDT80* prophase arrest had an increased number of COs compared to WT, and those COs displayed no interference (Chapter 7, Sections 7.2.1 and 7.2.8). It was thought that the increase in CO number may be caused by the formation of Class II COs during the arrest. To test this idea, *NDT80* prophase arrest and release was carried out on a *rad24Δ mus81Δ* strain.

In *mus81Δ*, transient prophase arrest mediated by *NDT80* block-and-release reduces spore viability from ~55% to ~33% (Figure 8.1 and Figure 8.3). This effect is independent of the length of the *NDT80* prophase arrest, with the same results seen for 4 and 8 hours. Since Mus81 is activated by Cdc5, and Cdc5 expression is controlled by Ndt80 (De Muyt *et al.*, 2012; Matos *et al.*, 2011; Allers & Lichten, 2001), Mus81 is not active during prophase arrest. Thus, it is not necessarily expected that there should be a difference in spore viability between *mus81Δ* and prophase-arrested *mus81Δ*. Yen1 is also not active during meiotic prophase (Matos *et al.*, 2011), so a possible explanation is that there may be a build-up of joint molecules that cannot be processed by either Mus81 or Yen1 during the prophase arrest. Once *NDT80* is induced, Mus81 will become active and able to resolve the build-up of joint molecules, but if Mus81 is not present, Yen1 activity is insufficient to compensate. However, the negative effect on spore viability does

not increase with prophase length, so any build-up of unresolvable joint molecules does not continue beyond 4 hours into prophase.

The spore viability of *rad24Δ* is normally rescued by 8 h of *NDT80* prophase arrest, going from ~21% to ~59% (Chapter 3, Figure 3.1). However, in the absence of Mus81, *rad24Δ* is no longer rescued by the extension of prophase (Figure 8.3). Based on the *rad24Δ* +8 h spore viability of ~59% and a *mus81Δ* viability of ~55%, *rad24Δ mus81Δ* +8 h is expected to have a viability of ~33%, but it is actually around 10% (Table 8.3). This shows that the rescue of *rad24Δ* by *NDT80* prophase extension is dependent on the activity of Mus81. Combined with the observations that there is an increase in CO numbers in sequenced *rad24Δ* +10 h tetrads (Chapter 7, Section 7.2.1), and these COs do not display interference (Chapter 7, Section 7.2.8), this suggests the additional COs formed during prophase arrest are Class II COs. In addition, it has been previously show that *rad24Δ* strains arrested in prophase for 8 hours do not experience a significant increase in ZMM foci compared to non-arrested *rad24Δ* (Shinohara *et al*., 2015). This supports the idea that the increase in CO numbers in *rad24Δ* +10 h is due to the formation of additional Class II COs, not Class I COs.

While the difference in spore viability between *rad24Δ* and *rad24Δ mus81Δ* was negligible (Figure 8.1), *rad24Δ mus81Δ* +8 h has a viability significantly lower than that of *rad24Δ* +8 h (Figure 8.3). This indicates that the loss of *mus81Δ* is not deleterious to *rad24Δ* unless prophase is extended. It may be the case that *rad24Δ* is normally resistant to the loss of *mus81Δ* because it has fewer COs, so is less reliant on any particular resolvase. However, when CO numbers are increased by *NDT80* prophase arrest, *rad24Δ* requires Mus81 activity for the timely resolution of joint molecules.

In addition, because *msh2Δ* normally rescues the spore viability of *rad24Δ* SK1xS288c hybrids (but not pure SK1 strains), and these *rad24Δ msh2Δ* hybrids are predicted to have mostly Class II COs, a hybrid *rad24Δ msh2Δ mus81Δ* strain was assayed for spore viability. However, the sporulation efficiency was extremely low, rendering tetrad dissection difficult. Nonetheless, out of 31 successfully dissected tetrads, not a single viable spore was produced (Table S1). This supports the idea that the additional COs formed in a *msh2Δ* background are all or mostly Class II in *rad24Δ*.
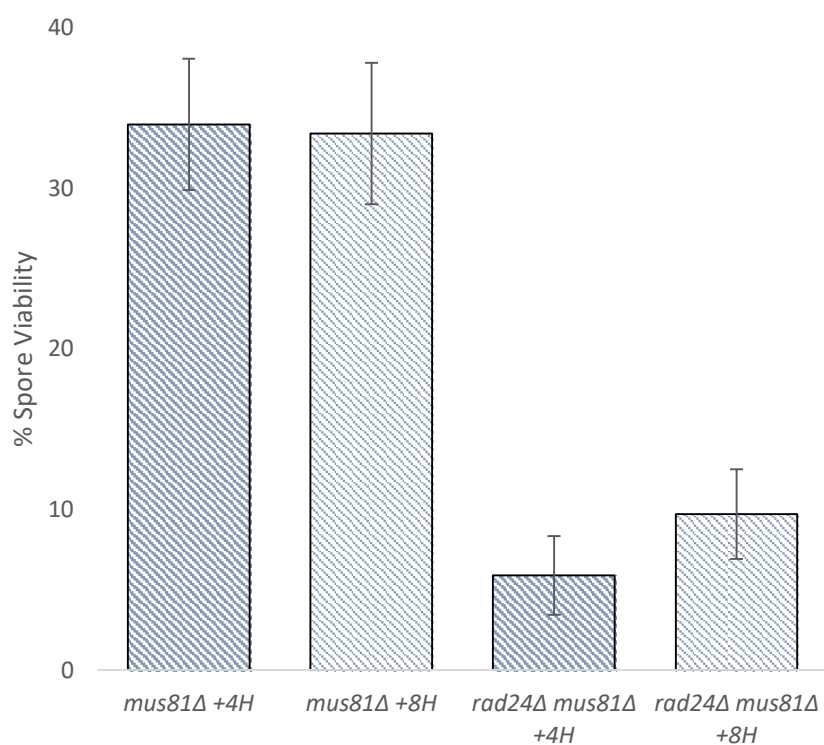
Figure 8.3. Effect of 4 or 8 hours of prophase arrest on the spore viability of *mus81Δ* and *rad24Δ mus81Δ* yeast. All error bars represent 95% confidence limits.

8.3. Discussion

8.3.1 Effect of different proteins on Class I/II ratio

CO events can be Class I, which display interference (Novak *et al.*, 2001), or Class II, which do not interfere and are primarily formed by Mus81 activity (de los Santos, 2003). By predicting the percentage of COs that display interference or not by mixture modelling (Sections 5.2.10, 6.2.11, 7.2.11) and by removing *mus81Δ* activity (Section 8.2.1), information about the roles of Mec1, Tel1, Rad24 and Msh2 in determining the ratio of Class I/II formation can be obtained.

In most strains, the results of mixture modelling and Mus81 deletion are in agreement, in terms of the importance of Class II CO formation for each strain. The spore viability of *tel1Δ* and P_{CLB2}-*MEC1* strains are affected more than WT strains by *mus81Δ* (Table 8.2), indicating that they are more reliant on Class II COs than WT strains; the results of mixture modelling also predict a large increase in Class II CO formation and small reduction in Class I CO formation in *tel1Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ* compared to *msh2Δ* (Table 8.1). This suggests that Mec1 and Tel1 are pro Class I and/or anti Class II factors, though this is likely an indirect activity as they are not known to interact with any relevant proteins, unlike Rad24 (Figure 8.4). In addition, mixture modelling predicts an increase in Class I formation in *msh2Δ* but no change in Class II formation; the loss of Mus81 affects *msh2Δ* to the same degree as a WT strain, indicating that *msh2Δ* is not more reliant on Class II CO formation than WT, and that Msh2 is an anti-class I CO factor, possibly by disproportionately rejecting strand invasion at sites for future Class I COs rather than Class II COs (Figure 8.4).

In contrast, while *rad24Δ* strains are predicted to have few or no Class I COs, and instead mainly Class II COs (Section 7.2.11), the deletion of Mus81 does not affect spore viability at all (Chapter 8, Figure 8.1). This may be explained by the fact that the sequenced *rad24Δ* strains also had prophase extension or *msh2Δ* deletion, while the *rad24Δ mus81Δ* strain did not. The *NDT80* prophase arrest and MMR deficiency are thought to improve *rad24Δ* viability by increasing CO numbers (Chapter 7, Section 7.2.1), which may increase the need for Mus81 activity for the timely resolution of joint molecules. When observing the effect of *mus81Δ* on prophase-arrested *rad24Δ* or *rad24Δ msh2Δ*, it was found that a *rad24Δ msh2Δ mus81Δ* triple mutant had low sporulation efficiency and produced no viable spores. In addition, *rad24Δ* no longer experienced a rescue effect from prophase arrest in the absence of Mus81, and in fact, *rad24Δ mus81Δ* +8 h has a viability substantially lower than that of *rad24Δ* (Chapter 8, Figure 8.3). This suggests that *msh2Δ* and prophase extension likely rescue *rad24Δ* viability by allowing the formation of additional Class II COs, because Class I COs form infrequently in *rad24Δ* (Figure 8.4). In the absence of these conditions, the formation of any CO events may be so infrequent that the presence or

absence of Mus81 makes no difference (assuming the presence of other resolvases; the additional absence of Yen1 or Mlh3 has a more severe effect (Section 8.2.3)).

In addition, it has been previously show that *rad24Δ* strains arrested in prophase for 8 hours do not experience a significant increase in ZMM foci compared to non-arrested *rad24Δ* (Shinohara *et al.*, 2015). This supports the idea that the increase in CO numbers in *rad24Δ* +10 h is due to the formation of additional Class II COs, not Class I COs.

CO numbers are also affected by DSB formation levels, since DSBs are the precursors of COs. The absence of Msh2, Mec1 or Tel1 in meiosis increases the number of recombination events detected, suggesting that they are anti-DSB factors (Figures 5.1, 6.1, 7.1). In support of this latter conclusion, *tel1Δ* strains have been directly shown to have increase in DSB formation (Garcia *et al.*, 2015; Mohibullah *et al.*, 2017). The absence of Rad24 decreases recombination event formation in a *msh2Δ*, but not *NDT80* prophase arrest, background (Figure 7.1). However, Mec1 and Rad24 are also known to be pro-DSB factors due to their role in the meiotic checkpoint (Gray *et al.*, 2013) indicating that these proteins have both positive and negative effects on DSB formation.

The resolution of Class II COs occurs after meiotic prophase, as Mus81 is indirectly activated by Ndt80 via Cdc5 (Matos *et al.*, 2011; Sourirajan and Lichten, 2008), and Yen1 activation occurs in late meiosis (Chu & Herskowitz, 1998; Matos *et al.*, 2011). However, the DDR response checkpoint occurs during meiotic prophase. For this reason, the increase in Class II CO formation in the absence of Mec1, Tel1 or Rad24 is likely not because these proteins normally inhibit Class II formation, but that they normally promote Class I formation. In absence of the checkpoint proteins, recombination events that would have ordinarily become Class I COs have to become Class II COs or NCOs instead. This is further supported by the fact that Yen1 is able to cleave a wide variety of DNA substrates, suggesting that its role is to resolve any persistent joint molecules that were not processed by other resolvases before the second meiotic division (Matos *et al.*, 2011). In addition, Mus81 is needed to resolve aberrant JMs such as single Holliday junctions, intersister JMs, multichromatid (3 or 4 chromatid) JMs, and JMs containing two chromatids where one has undergone crossing over (Oh *et al.*, 2008).
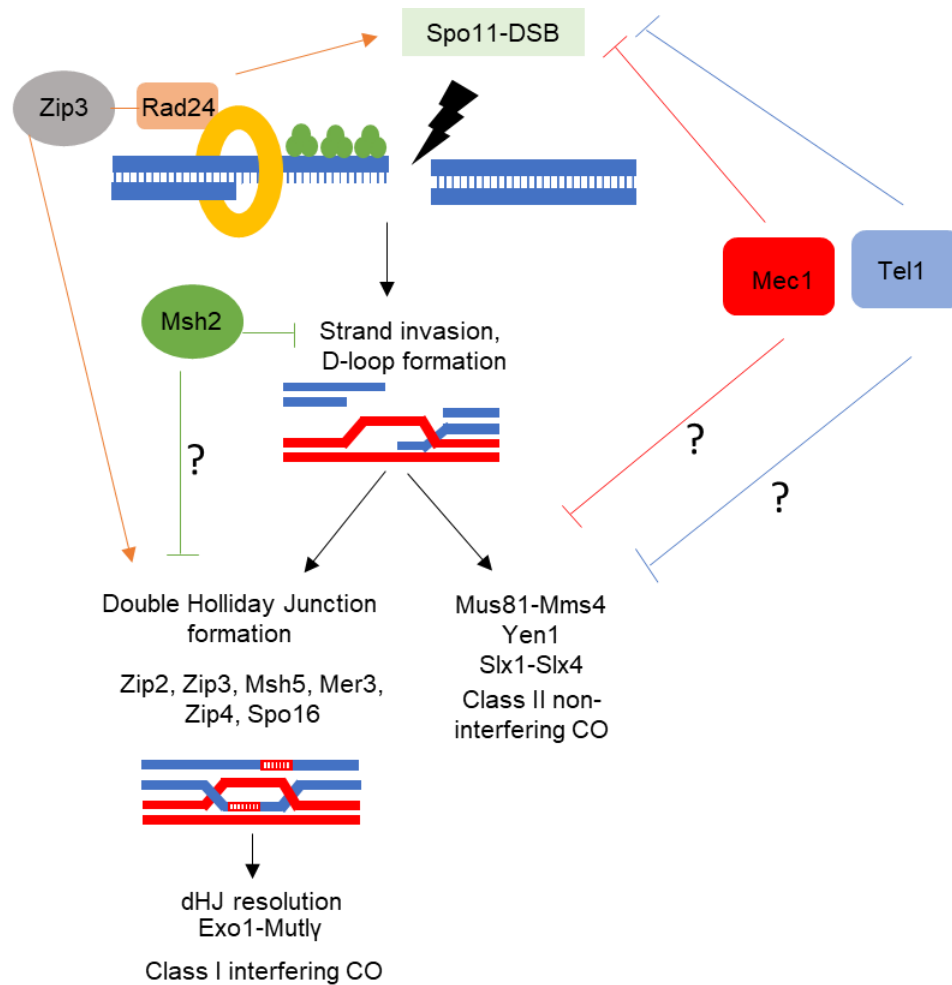
Figure 8.4. Model of Class I /Class II pathway influences

Spo11-DSBs can be repaired to produce CO or NCO products. After strand invasion and D-loop formation, CO events can be formed by either dHJ formation and resolution, or via a structure specific endonuclease (Paques and Haber, 1999). These pathways produce interfering and non-interfering COs respectively. Rad24 influences CO formation by promoting the Class I CO pathway via the loading of ZMM proteins (Shinohara et al., 2015). In addition, Rad24 also indirectly promotes CO formation by increasing DSB formation due to its role in the meiotic checkpoint (Gray *et al.*, 2013; Chapter 7, Section 7.2.1). In the absence of Msh2, more recombination events are detected (Chapter 5, Section 5.2.1). Msh2 inhibits strand invasion into mismatching sequences, which likely reduces recombination between homologous chromosomes in hybrids. In *msh2Δ*, an increase in Class I Co formation is observed without a change in Class II CO numbers, indicating that Msh2 activity is an anti-class I CO factor, perhaps by disproportionately rejecting strand invasion at sites for future Class I COs. The absence of either Mec1 or Tel1 in meiosis increases the number of recombination events detected, indicating that they are anti-DSB factors. Both are also known to be pro-DSB factors however (Garcia *et al.,* 2015; Gray *et al.*, 2013), indicating that they have positive and negative effects on DSB formation. Absence of Mec1 or Tel1 also produces a large increase in Class II CO formation, but only a slight reduction in Class I CO formation. This suggests that Mec1 and Tel1 are pro Class I/anti Class II factors.

8.3.2. Closing Statement

In this chapter, the effect of the loss of the major Class II CO pathway resolvase Mus81 in various backgrounds is measured by assaying spore viability. In addition, the effect of single and double mutants of *mus81*, *mlh3* and *yen1* in WT and *rad24Δ* backgrounds is examined, to discover the relationship between the resolvases and the role they play in *rad24Δ* viability.

Overall, these results show that in silico models can predict the ratio of Class I: Class II CO formation, and these predictions are largely supported by the *in vivo* effects of removing Class II CO formation. The results support an anti-Class I CO role for Msh2, and a pro-Class I and/or anti-Class II role for Mec1, Tel1 and Rad24. In addition, *rad24Δ* spore viability is not reliant on any particular resolvase, likely because it has so few CO events. The rescue effect of prophase extension and *msh2Δ* on *rad24Δ* strains is abrogated by loss of Mus81, indicating that Class II CO formation is integral to the mechanism of rescue by these methods.

Chapter 9.

Discussion

Chapter 9. Discussion

9.1. Overview

Previous investigations into the roles of the DDR checkpoint proteins Tel1, Mec1 and Rad24 during meiotic recombination have demonstrated an increase in DSB formation and loss of DSB interference in *tel1Δ* at some single loci (Garcia *et al.*, 2015), a reduction in DSB formation in P_{CLB2}-*MEC1* at single loci and rescue of spore viability by *NDT80* prophase extension in *rad24Δ* (Gray *et al.*, 2013).

To further investigate the roles of these DDR proteins in regulation of meiotic recombination, recombination events were analysed genome-wide in individual meioses. Methods for mapping meiotic recombination genome wide from sequencing data have been established, but required improvements and customization to accommodate the relatively long reads and lower read depths generated by the MiSeq platform, and to use the polymorphism markers present in the strains used in this investigation (Chapter 4). In addition, the analysis pipeline was updated so that heteroduplex DNA present in *msh2Δ* tetrads could be analysed, alongside *msh2Δ* octads and *MSH2* tetrads (Chapter 4).

The high resolution event location data produced by this method was used to determine various characteristics of meiotic recombination in wild type, *msh2Δ*, *NDT80* prophase-extension and checkpoint mutant hybrids, including CO and DSB interference processes (Chapters 5-7). The conclusions drawn about changes in CO interference were further substantiated by removing most Class II COs from each strain via *mus81Δ* and observing the effect on spore survival (Chapter 8).

An important aim was to understand where the roles of Rad24 and Mec1 in meiosis may differ, which was investigated in two ways. Firstly, by comparing the effect of the absence of each protein on meiotic recombination by the genome-wide survey (Chapter 7), and secondly by examining the differences in spore viability and rescue by *NDT80* prophase arrest between each mutant (Chapter 3).

9.2. Development and quality control of a customized pipeline for recombination event analysis

In Chapter 4, a new bioinformatics pipeline was designed, differing from previously published methods in several ways, including that it is optimized for long reads (300bp) and relatively low read depths (~27x); uses a dedicated list of both SNPs and indels produced for the specific SK1

and S288c strains used in this investigation; and is capable of analysing heteroduplex DNA found in *msh2Δ* tetrads, as well as *msh2Δ* octads and *MSH2* tetrads.

Overall, though recombination has been assayed genome-wide in *msh2Δ* octads, this updated study offers distinct advantages over preceding ones in terms of marker detection and recombination event resolution. For example, deep sequencing provides a higher resolution of polymorphisms than microarray hybridisation, because sequencing is capable of interrogating the entire genome, without depending on pre-selected targets. This means that the polymorphisms of interest can be determined from the data itself (Section 4.2.3). In addition, hDNA can be detected in *msh2Δ* tetrads via sequencing, but not via microarray (discussed in Section 4.2.5). Finally, during classification of recombination products, pattern changes falling within only 1.5kb of each other were considered to be part of the same event, compared to the up to 5kb limit used in previous studies (e.g. Martini *et al.*, 2011). The reduced threshold of 1.5kb was determined by detailed analysis of heteroduplex DNA patterns in recombination events, allowing the identification of events that must have been produced by multiple Spo11-DSBs (Bertrand Llorente and Marie-Claude Marsolier, personal communication). This is advantageous for detailed examination of the distance between recombination events, which may enable the detection of event clustering at short range, as proposed to arise in *tel1Δ* mutants (Garcia *et al.*, 2015).

9.3. Analysis of recombination genome-wide in wild type meiosis

In Chapter 5, high-resolution sequencing data was used to examine features of meiotic recombination in wild type, MMR deficient and *NDT80* prophase-extended hybrid strains. Such analyses provided a baseline for 'wild-type' recombination to be established, which can be used for comparisons. In addition, it was determined that the three 'wild type' backgrounds have some substantially different features of recombination to each other (Table 5.6).

Genome-wide recombination assaying in *msh2Δ* hybrids reveals an increased CO and NCO count compared to the $MSH2^+$ wildtype control (Chapter 5, Figure 5.1). The increase in recombination supports the idea that Msh2 has a role in rejecting strand invasion during recombination, which would be more of an issue in the hybrid diploids due to the numerous mismatches (~68,500) spread across the genome. *msh2Δ* also increases NCO counts compared to WT. This is at least partly because they are easier to detect because hDNA can be detected in *msh2Δ*. However, even when accounting for events detected in *msh2Δ* that are composed of hDNA only, the WT strain is still predicted to have fewer than *msh2Δ,* suggesting that Msh2 suppresses both CO and NCO formation (Section 5.2.1). In agreement with these observations,

it was found that *msh2Δ* is less deleterious to hybrid strains than to pure SK1 strains, and even rescues the viability of *rad24Δ* and P_{CLB2}-*MEC1* hybrids (Figure 3.8B).

Collectively, these data suggest a role for Msh2 in rejecting strand invasion into mismatched sequences, something that is more likely to occur in hybrids.

Extended prophase also increases the number of CO and NCO events detected, but not as much as *msh2Δ* (Chapter 5, section 5.2.1). Prophase-extended strains also have longer CO and NCO events than *msh2Δ* or WT, suggesting that recombination event tracts may continue to be lengthened by e.g. resection or joint molecule migration, while in prophase arrest.

In WT, *NDT80* prophase-extension and *msh2Δ* strains, CO events occur further apart than expected from a random distribution, indicating the presence of CO interference. The distributions of CO events in WT and WT + 8 h are best fit by gamma distributions with α=1.39 and 1.46 respectively, while in *msh2Δ*, the best-fit gamma distribution has α=2.44, suggesting stronger CO interference than in WT or *NDT80* prophase arrest strains. This may be explained by the higher percentage of COs that are predicted to be Class I interfering COs, in comparison to Class II non-interfering COs, in *msh2Δ* strains. Increased prophase length is more beneficial to cell survival than *msh2Δ*, perhaps because a lack of MMR means that mutations cannot be repaired, or because ectopic recombination is increased due to the inability to reject strand invasion into non-homologous regions. By contrast, extending prophase may provide more time to complete accurate recombination, and has only minor impacts on recombination and spore viability (Allers & Lichten, 2001; Bhuiyan *et al.*, 2002; Table 9.1).

Table 9.1. Summary of basic recombination characteristics across strains.

Spore viability was originally shown in Figures 3.1A, 3.3A, 3.8, 3.9.

DSB cluster formation originally shown in Figures 5.2, 6.2, 7.5, 7.6.

CO/NCO formation originally reported in Table 5.1, 6.1, 7.1.

Event lengths originally reported in Figures 5.3, 6.7, 7.8, 7.9.

Best fit alpha values are from Table 5.4, 6.4, 7.4.

It should be noted that the best fit alpha value was still significantly different from the actual CO distribution in most cases.

The Class I and II percentages and numbers are from Table 5.5, 6.5, 7.5.

	WT	*WT + 8 h*	*msh2Δ*	*rad24Δ + 10 h*	*rad24Δ msh2Δ*	*P$_{CLB2}$- MEC1 + 8 h*	*P$_{CLB2}$- MEC1 msh2Δ*	*tel1Δ msh2Δ*
Spore viability % (SK1)	97	94	81	69	21	58	49	75
Spore viability % (SK1xS288c hybrid)	82	70	73	16	6	16	29	64
Average CO number	74.5	97.3	105.0	125.0	83.5	126.8	134.7	115.3
Average NCO number	39.5	51.0	101.8	92.0	113.0	90.7	213.8	140.7
Median NCO mid length (bp)	1815	2089	1057	2635	827	2340	926	980
Median CO mid length (bp)	1688	1679	1195	1984	1571	1880	1326	1382
% of events that are DSB clusters	4.8	5.6	4.6	18.2	10.9	15.9	13.7	9.2
Best fit α value (CO interference)	1.2	1.5	2.4	1.1	1.6	1.2	1.7	1.9
Class I/Class II CO percentage	67.1/ 32.9	66.0/ 34.0	76.5/ 23.5	10.9/ 89.1	8.5/ 91.5	50.7/ 49.4	52.7/ 47.3	67.4/ 32.6
Class I/Class II CO number (predicted)	50.0/ 24.5	64.1/ 33.2	80.3/ 24.7	13.6/ 111.3	7.0/ 76.4	64.2/ 62.6	71.0/ 63.7	77.7/ 37.6

9.4. Analysis of recombination genome wide in *tel1Δ*

Previously, recombination has been assayed genome-wide in *tel1Δ* tetrads (Anderson *et al.*, 2015), but not in a MMR-deficient *tel1Δ* background. In Chapter 6, the deep sequencing methods that I developed were used to investigate the effects that *tel1Δ* has on recombination event quantity and quality, and CO and DSB interference. Tel1 is found to have roles in controlling CO and NCO event formation, levels of DSB cluster formation, and CO interference, likely via controlling the ratio of Class I/II CO formation (Figure 9.1). This study offers distinct advantages over preceding ones in terms of marker and event resolution and detection.

The use of MMR deficient strains greatly increases the number of NCOs that can be detected, as well as the amount of information about e.g. length and complexity that can be gathered for each event (Martini *et al.*, 2011). For example, an increase in 7:1 segments is observed upon *tel1Δ* (Section 6.2.3), something that is impossible to detect in the MMR-proficient strains used by Anderson *et al.*, 2015. These events are of particular interest because they represent cases where recombination has occurred on two sister chromatids at the same location, suggesting a loss of *trans* DSB interference, which is known to be reduced in *tel1Δ* (Zhang *et al*., 2011). In addition, segments of 6:2 segregation may represent DSB cis interference loss, as they could be formed by the occurrence of two close Spo11-DSBs. Such segments would be visible in *MSH2+* as well as *msh2Δ* cells, but since 6:2 segments are also produced by MMR activity, any 6:2 segments formed by concerted Spo11-DSB formation would be occluded in the former. MMR-deficient hybrids may also be more representative of recombination in a pure SK1 background than MMR-proficient hybrids, due to the rejection of strand invasion into mismatching sequences by Msh2 (Sugawara *et al.*, 1997; Evans *et al.*, 2000; Datta *et al.*, 1999; Chen & Jinks-Robinson, 1998). However, in wild *S. cerevisiae* populations, most individuals are heterozygous (reviewed in Mortimer 2000; Borts & Haber, 1987), so a heterozygous cross may be more representative of wild type conditions than homozygous strains.
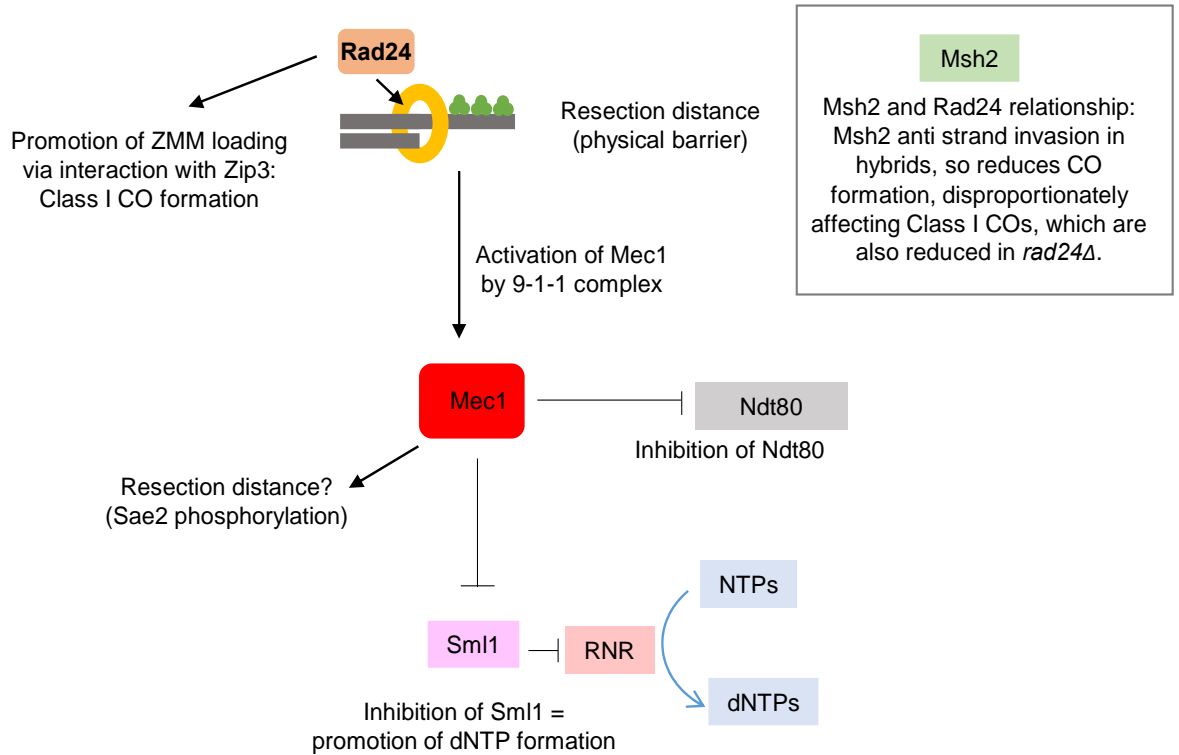
Figure 9.1. Model of Rad24 and Mec1 meiotic roles

In response to DNA damage initiated by Spo11, Rad24 loads the 9-1-1 clamp at the DSB site and promotes loading of ZMM proteins, likely via an interaction with Zip3 (Shinohara et al., 2015). ZMM proteins are required for Class I interfering CO formation. Rad24 contributes to the activation of Mec1 via the 9-1-1 complex. Mec1 activation inhibits NDT80 activation, stalling meiotic progress (Prugar et al., 2017). Mec1 also inhibits Sml1 activity via Dun1, promoting the formation of dNTPs which contribute to DNA repair. Mec1 also limits resection distance, possibly via Sae2 phosphorylation. Rad24 also contributes to resection distance, likely via the 9-1-1 clamp which may act as a physical barrier to resection.

9.5. Separable contributions of Rad24 and Mec1 to outcomes of meiosis

9.5.1 Meiotic recombination

The roles of Rad24 and Mec1 proteins are investigated via the analysis of meiotic recombination signatures genome wide in *rad24Δ* and *P_{CLB2}-MEC1* backgrounds (Chapter 7). In order to carry out this analysis, the spore viability of the hybrid checkpoint mutants must be improved by prophase extension or *msh2Δ* to allow collection of four-spore viable tetrads. Since these rescue methods may affect the recombination event outcomes, the analysis is repeated in two different rescue backgrounds to help reduce any bias and obtain a more complete picture of the effect of Mec1 and Rad24 on meiotic recombination.

rad24Δ has fewer CO and NCO events than *P_{CLB2}-MEC1*, in both MMR-deficient and *NDT80* prophase-extension backgrounds (Table 9.1). This suggests that Rad24 contributes more to ensuring DSB formation than Mec1. Most residual COs in *rad24Δ* are distributed randomly, showing a loss of interference (Chapter 7, Figure 7.17); this could be due to a reduction in Class I CO formation. A loss of CO interference is also observed in *P_{CLB2}-MEC1*, but to a lesser extent. In addition, unlike Mec1, Rad24 has a physical interaction with Zip3, and has a role in loading ZMM proteins at sites of future Class I COs (Shinohara *et al.*, 2015).

Alternatively, the disparity in recombination event numbers between Rad24 and Mec1 could be because Mec1 has a role in limiting DSB formation via phosphorylation of Rec114 (Carballo *et al.*, 2013). DSB processing leads to the activation of Mec1 due to the formation of RPA-bound ssDNA (Zou & Elledge, 2003), thus strains with low rates of DSB formation will also have a reduced level of Mec1 activation. In the absence of Rad24*,* Mec1 activation is reduced in two ways: by the reduction of ssDNA formation and by the lack of a clamp loader to load the 9-1-1 clamp (Figure 9.1), affecting the role of Mec1 in processes such as Ndt80 inhibition, meaning that fewer recombination events can occur before the end of prophase. The scarcity of recombination events is exacerbated by the reduction in Class I CO formation caused by *rad24Δ*. In contrast, in the absence of Mec1, Mec1 activities are removed entirely e.g. there is no Mec1-mediated inhibition of Ndt80, but CO formation is not strongly affected because Rad24 is still present to promote the formation of Class I COs.

9.5.2 Spore viability

Loss of Rad24 and Mec1 activity greatly impacts spore viability. In Chapter 3, ways in which the *rad24Δ* and *P_{CLB2}-MEC1* meiotic phenotype can be rescued were examined to help inform on the roles of Rad24 in meiosis and where they may differ from Mec1. It was found that the deleterious *rad24Δ* phenotype can be rescued in multiple ways, such as having more nucleotides present via

sml1Δ, restoration of at least four hours of prophase arrest in both SK1 and hybrid backgrounds (Figure 3.4, 3.9), and reductions in Spo11 activity in combination with extended prophase (Gray *et al.*, 2013). The relationship between prophase length and spore viability of DDR mutants is also investigated, showing a positive correlation for up to 12 hours of prophase. In addition, as noted above, in hybrid, but not SK1, backgrounds, *msh2Δ* also improves viability (Figure 3.8). Finally, P_{CLB2}-*MEC1* spore viability can be rescued by *msh2Δ* and *NDT80* prophase extension, but only if hybrid, not pure SK1 (Figures 3.3, 3.8, 3.9). The rescue of *rad24Δ* and P_{CLB2}-*MEC1* hybrid spore viability is unexpected because *msh2Δ* is deleterious to WT strains. This suggests that a main cause of low viability in *mec1* and *rad24* mutant hybrids is the reduced recombination event formation due to Msh2 activity (Figure 9.1).

Overall, these results suggest that the main cause of the low spore viability of *rad24Δ and P_{CLB2}-MEC1* is a reduction in Spo11-DSB formation (likely due to the loss of the meiotic checkpoint, and in hybrids, the rejection of strand invasion by Msh2), and a resultant reduction in CO formation, which is particularly severe in *rad24Δ* due to the role of Rad24 in promoting Class I CO formation. Increasing the number of DSBs that are formed and repaired via *NDT80* prophase extension, or via increasing the efficiency of strand invasion into homologous chromosomes via *msh2Δ*, improves *rad24Δ* and P_{CLB2}-*MEC1* hybrid viability. This suggests that in WT meiosis, the DDR checkpoint is important to delay prophase exit in order to promote DSB formation and repair.

Mec1 is known to inactivate Ndt80 via Mek1 until DSBs are repaired (Prugar *et al.*, 2017). As an activator of Mec1, it is logical that Rad24 is therefore also important for the inhibition of Ndt80 activation (Figure 9.1). This model likely explains why *rad24Δ* spore viability is rescued by transient *NDT80* repression, which is thought to restore part of the natural function of the meiotic checkpoint. Intriguingly, the spore viability of P_{CLB2}-*MEC1* is not affected by *NDT80* prophase extension in a pure SK1 background, but is rescued in an SK1xS288c hybrid background (Figure 3.9). An explanation for this discrepancy may be that while both Mec1 and Rad24 are important to inhibit Ndt80, early induction of Ndt80 is only a problem for spore survival if recombination event numbers are low. Thus, *rad24Δ* is rescued by *NDT80* prophase extension, because *rad24Δ* has fewer CO events due to its influence on Class I CO formation, and hybrid P_{CLB2}-*MEC1* are rescued because they have fewer recombination events due to the activity of Msh2, which rejects strand invasion into mismatched sequences (Sugawara *et al.*, 1997; Evans *et al.*, 2000). The latter is likely to cause an increased level of inter-sister repair – something which may be exacerbated by the absence of Mec1, which is known to have a role in ensuring inter-homologue bias. The conclusion that prophase extension is more helpful in backgrounds with fewer recombination events is supported by the fact that hypo-*spo11* alleles have a synergistic negative effect on spore

viability in combination with *rad24Δ* and *P_{CLB2}-MEC1*, suggesting that the slower/reduced DSB formation of the hypo-*spo11* is particularly deleterious in checkpoint deficient backgrounds. An increase in DSB/CO formation is important to spore viability because the formation of COs between homologous chromosomes is essential to ensure correct disjunction of chromosomes during meiosis. Chromosomes without COs are more likely to divide incorrectly, leading to aneuploidy and cell death (reviewed in Egel, 1995).

9.5.3 Efficient DSB repair

Sml1 is an inhibitor of RNR, which is needed for dNTPs synthesis, required for repair of DNA damage (Zhao *et al.*, 1998; Reichard, 1988). Survival of *rad24Δ* spores can be improved via deletion of Sml1, likely due to the role of Rad24 in activating Mec1, which indirectly inactivates Sml1 (Figure 9.1), especially in combination with *msh2Δ* and/or *NDT80* prophase arrest. A *rad24Δ sml1Δ* meiosis had only 32 COs (Table 7.1), compared to averages of 84 and 125 COs in *rad24Δ msh2Δ* and *rad24Δ* + 10 h respectively. In addition, 61 and 92 COs were detected in two *rad24Δ msh2Δ sml1Δ* meioses, similar numbers to those observed in *rad24Δ msh2Δ* (which range from 54-104 CO events), suggesting that *msh2Δ* increases CO event formation in *rad24Δ,* but *sml1Δ* does not. Thus, *sml1Δ* likely does not affect recombination event formation, but may increase the efficiency of their repair due to the increase in dNTP numbers, and so is particularly beneficial in the *msh2Δ* background where the levels of event formation are increased but there is limited time to repair them due to the early induction of Ndt80. While *NDT80* prophase extension is highly beneficial to *rad24Δ* spore viability, it is even more beneficial when combined with a hypo-*spo11* allele, suggesting that excessively high levels of Spo11-DSBs may be deleterious to *rad24Δ*. It is possible that this is because there are too few dNTPs available for repair of the increased DSBs, due to the lower activation of Mec1, and thus loss of Sml1 inactivation, in *rad24Δ* + 10 h.

Having many dNTPs available could also potentially reduce the number of mismatches formed during the repair, because the correct base is more likely to be available; this would then be particularly helpful when MMR is inactive and so unable to repair mismatches. In vegetatively growing yeast with a point mutation in RNR that results in an increase in dCTP and dTTP, but not dATP or dGTP, an increase in mutation rate is observed (~14x), which is greatly exacerbated by the deletion of *MSH2* (an additional ~40x) (Buckland *et al.*, 2014; Watt *et al.*, 2016). This suggests that elevated dNTP production increases mutation rate in the absence of MMR, but specifically when dNTP pools are biased, which may reduce the probability that the correct base is available. A different effect may be observed if dNTP pools are uniformly increased, as would be the case in *sml1Δ*.

9.6. The contribution of CO resolvases to meiotic success in the absence of DDR and MMR proteins

CO events detected via recombination event analysis can be divided into those that show Class I– or Class II–like behaviour, by separating out those that are distributed randomly and those that appear to show CO interference (Sections 5.2.10, 6.2.11, 7.2.11). This analysis is complemented by observing the effect of the loss of the major Class II CO pathway resolvase Mus81 on spore viability in various backgrounds (Section 8.2.1).

For *msh2Δ*, *tel1Δ* and P_{CLB2}-*MEC1* strains, the results of each analysis are coherent. P_{CLB2}-*MEC1* and *tel1Δ* both have a greater reduction in spore viability on *mus81Δ* than WT (Table 8.1), which agrees with analysis suggesting they have an increase in Class II CO formation (Tables 6.5, 7.5). In contrast, Msh2 appears to be an anti-Class I factor, as *msh2Δ* is affected by *mus81Δ* to the same extent as WT (Table 8.1), and the increase in CO number in *msh2Δ* compared to WT appears to be entirely made up of Class I COs, with no change in Class II CO number (Table 5.5). However, the results of each analysis are not coherent for *rad24Δ* strains, which are unaffected by *mus81Δ* (Table 8.1) but appear to have almost no Class I CO formation (Table 7.5). However, *rad24Δ* strains are affected by *mus81Δ* when prophase is extended or MMR is deficient (as in the sequenced tetrads), indicating that Class II CO formation may only be increased in *rad24Δ* under these circumstances.

9.7. Contribution of Mec1 and Tel1 to meiotic recombination

While Tel1 and Mec1 have many overlapping roles in meiotic recombination (Figure 9.2), the contribution of each protein is not equal. For both SK1 and hybrid strains, loss of Mec1 is more deleterious to spore viability than loss of Tel1, in agreement with previous findings that Tel1/ATM is less vital to survival than Mec1/ATR (Morrow *et al.*, 1995; de Klein *et al.*, 2000).

Both Mec1 and Tel1 are proposed to downregulate DSB formation via Rec114 phosphorylation (Carballo *et al.*, 2012). Mec1 also promotes DSB formation indirectly via the inhibition of Ndt80 (Gray *et al.*, 2013; Prugar *et al.*, 2017). Significantly more CO and NCO events are detected in P_{CLB2}-*MEC1* than in *tel1Δ* (Table 9.1). This is counter to previous observations suggesting that both P_{CLB2}-*MEC1* and *tel1Δ* have an approximately twofold increase in DSB formation: DSB signal at the *LEU2::HISG* hotspot, measured by Southern blotting after 3 hours of meiosis, is increased from ~6% in WT to ~12.5% in P_{CLB2}-*MEC1* (Gray et al., 2013), and from 2-3% in WT to 4-6% in *tel1Δ* (Garcia et al., 2014). A *tel1Δ* strain has also been found to have on average, 2.2x more Spo11-oligos than WT (Mohibullah et al., 2017). However, these studies only assay the

products of DSB formation and not recombination. It could be the case that excessive DSBs are formed, but are not detected in the outcomes of recombination. For example, DSBs may be more likely to be repaired with the sister chromatid due to loss of homolog bias, which Mec1 and Tel1 are known to have roles in (Schwacha & Kleckner, 1994; Collins & Newlon, 1994). If the role of Tel1 in maintaining homologue bias is more vital than that of Mec1, this could explain why the increase in DSB formation in *tel1Δ* is not reflected in detected recombination event numbers, but is for Mec1.

Tel1-deficient strains have on average longer NCO and CO events than Mec1-deficient strains. However, P_{CLB2}-*MEC1* have a higher percentage of events that are formed from multiple DSBs than *tel1Δ*. This seems counterintuitive considering that long event lengths in *msh2Δ* strains are almost entirely explained by DSB clustering (Sections 6.2.5, 7.2.5). However, when observing the range of DSB cluster lengths across strains, it can be seen that in *tel1Δ*, a higher proportion of DSB cluster events have long lengths (Figure 7.11, 6.8). For example, 11% of CO-containing DSB clusters in *tel1Δ*, but only 4% in P_{CLB2}-*MEC1*, are >10kb in length. This suggests that there is a higher proportion of DSB clusters with very long lengths in *tel1Δ* than in P_{CLB2}-*MEC1*.

P_{CLB2}-*MEC1* appears to have lost CO interference to a higher degree than *tel1Δ*, likely because P_{CLB2}-*MEC1* also has fewer Class I COs and more Class II COs than *tel1Δ*. Tel1 has been previously shown to be involved in CO interference and to influence the ratio of Class I/II CO formation (Anderson *et al.*, 2015), but Mec1 has not previously been implicated in these processes.
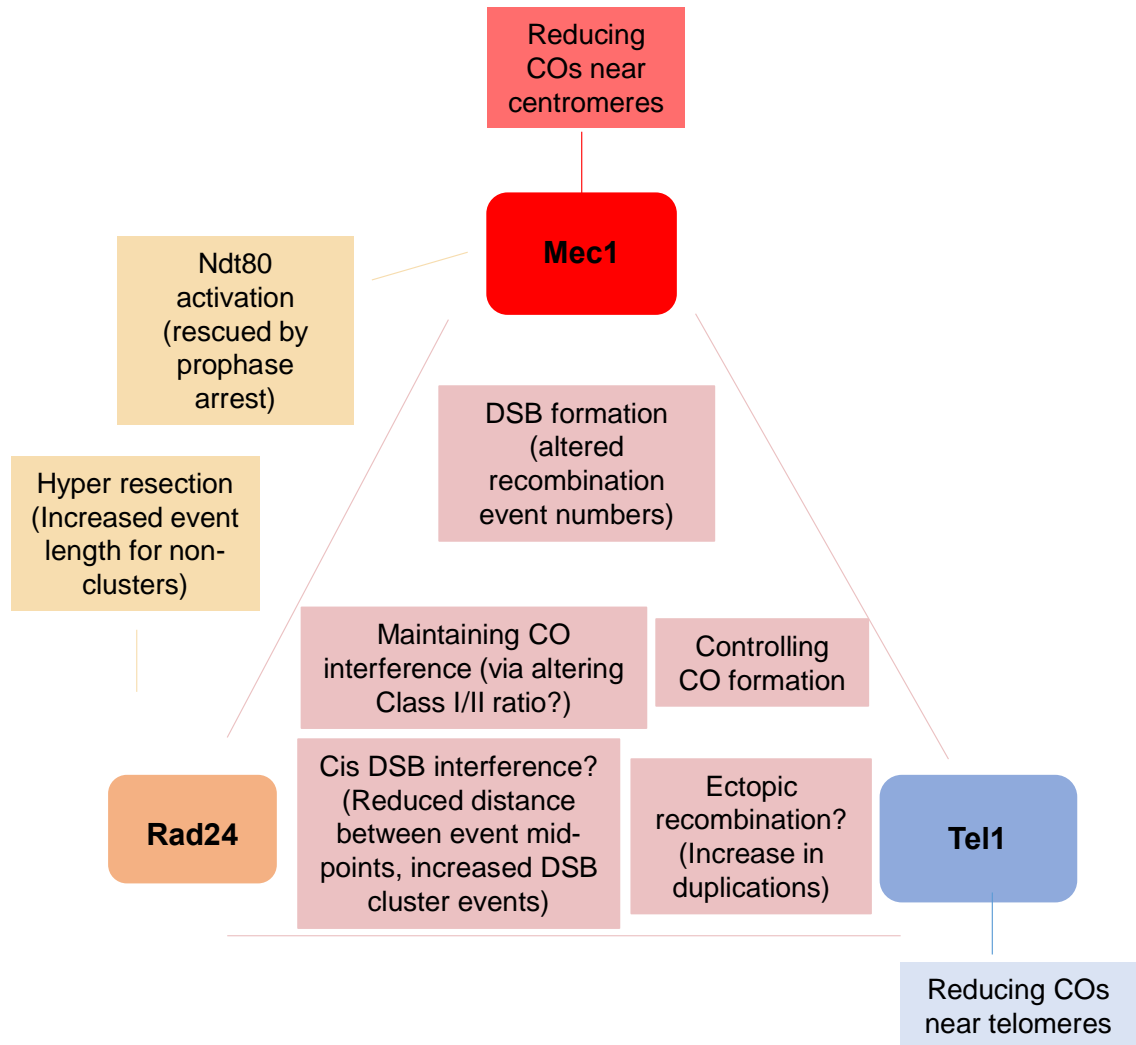
Figure 9.2. Overlapping and separate roles of checkpoint proteins in controlling meiotic recombination.

Roles of the DDR proteins Mec1, Tel1, and Rad24 in meiotic recombination, as interpreted from the results of genome-wide recombination assays. Red indicates Mec1-specific roles; blue, Tel1 specific; yellow, roles shared by Mec1 and Rad24, and pink, roles shared by all three.

9.8. Increase in recombination event length observed in mutants is mostly explainable by an increase in DSB cluster events

The amount of genetic change associated with a recombination event was investigated by comparing mid length estimates, which are calculated as the difference between the midpoints between the first and last SNPs to display an altered segregation pattern in a recombination event (Figure 5.3). It should be noted that the mid length may be an overestimate in areas of low SNP density, but on average is expected to be more accurate than the minimum or maximum possible lengths.

The mid length estimate of CO and NCO events is increased in WT+8 h (Figure 5.3), *tel1Δ msh2Δ* (Figure 6.7), *rad24Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ* (Figure 7.8), *rad24Δ* +10 h and P_{CLB2}-*MEC1* +8 h (Figure 7.9), compared to the WT and *msh2Δ* controls, which do not have highly different event lengths to each other. Overall, *rad24Δ* + 10 h has the highest proportion of long events of any background. Possible explanations for an increase in event length include an increase in D-loop or dHJ migration (Figure 4.9, 4.10), an increase in DSB resection distance, or the merging of two separate DSB repair events.

An increase in dHJ migration would be expected to primarily affect the length of CO events, since the number of NCOs formed from dHJ resolution is thought to be low or none (Zakharyevich *et al.*, 2012). However, both CO and NCO event lengths are increased in the strains mentioned above, so dHJ migration alone is not a satisfactory explanation. Nonetheless, D-loop migration could occur during NCO formation.

Examining the length of single-DSB and DSB-cluster events separately revealed that most long events in *tel1Δ msh2Δ* (Figure 6.8), *rad24Δ msh2Δ* and P_{CLB2}-*MEC1 msh2Δ* (Figure 7.11) were DSB cluster events, indicating that the primary reason for an increase in event length observed in these strains is that there is an increase in DSB clustering. However, there are a few short DSB cluster events and long non-cluster events in these strains.

In WT+ 8 h (Figure 5.3), the majority of long events were DSB clusters, with a few long non-clusters but no short DSB clusters. In *rad24Δ* +10 h and P_{CLB2}-*MEC1* + 8 h, while most long events were again DSB clusters, there was also an increase in the proportion of long non-clusters, and in short DSB clusters (Figure 7.12). This suggests that while most of the increase in event length can be explained by DSB clustering in *rad24Δ* and P_{CLB2}-*MEC1* with prophase extension, this is not sufficient to explain the increase in the length of non-clusters. The most likely explanation for this is resection distance, because hyper resection has been previously observed in *rad24Δ* and P_{CLB2}-*MEC1* (Gray *et al.*, 2013; Kayleigh Wardell, personal communication).

Excessive resection may disproportionately affect *NDT80* prophase-arrested strains due to the increased time available for DSB repair, suggesting that DSB resection is continuing during the time spent in prophase arrest.

Curiously, DSB cluster events tend to be short compared to non-clusters in *msh2Δ* (Figure 5.4). Shorter NCO events are also found more often in *msh2Δ* backgrounds (Figure 5.3), likely because hDNA is visible, allowing short NCOs composed entirely of hDNA to be detected. On the other hand, short COs should be detectable in any background due to the reciprocal exchange of chromosome arms, so *msh2Δ* strains may be expected to display longer CO events due to the increased detail provided by hDNA analysis. However, CO event lengths also tend to be shorter in *msh2Δ* compared to WT and *NDT80* prophase-extension backgrounds (Figure 5.3). Potentially, because one likely role of Msh2 is to reject strand invasion into mismatching sequences (Chapter 5, Figure 5.1; Sugawara *et al.*, 1997; Evans *et al.*, 2000; Datta *et al.*, 1999; Chen & Jinks-Robinson, 1998), the absence of *msh2Δ* may mean that less homology is needed for successful strand invasion, and thus less resection is needed for homology searching, causing faster initiation of DSB repair and contributing to the occurrence of shorter event lengths in *msh2Δ* backgrounds compared to WT and *NDT80* prophase-extension backgrounds. Alternatively, the distance between DSBs that produce clusters in *msh2Δ* may generally be smaller than in other backgrounds; shorter cluster events may be produced by DSBs occurring within the same hotspot, while longer events result from DSB clusters between adjacent hotspots.

9.9. Future Work

This work has revealed the consequences of the loss of important DDR and MMR proteins on the meiotic genome, at a high resolution conferred by the use of next generation sequencing and new bioinformatic tools. However, there are a number of ways in which it can be extended.

In order to determine the reproducibility of results, it is desirable to sequence additional WT and WT + 8 h tetrads, because data from only four of each was acquired. In addition, these strains in particular tend to have very low event counts, which means that more data needs to be acquired to confirm the reproducibility of CO event distributions for interference measurements.

Another strain that would be useful to sequence for event analysis would be a *msh2Δ* hybrid with *NDT80* prophase extension. This would be helpful to reconcile some of the differences observed between *msh2Δ* and *NDT80* prophase extension strains, such as the different levels of DSB cluster formation. The increased information about recombination events from hDNA would also be useful. For example, it would reveal more about the nature of the very long events observed in

NDT80 prophase arrest strains that are not DSB clusters. Increasing detail within the hDNA patterns of these events would help to determine how they are formed.

For existing datasets, additional data analysis is planned:

Analysis of recombination events with regards to Spo11-DSB positions and hotspot strength information from Pan *et al.*, 2011 and Mohibullah *et al.*, 2017, will help to determine the most likely position of the originating DSB for each event, and which events may have been produced by multiple DSBs. Currently, suspected DSB cluster events have been manually annotated without considering the DSB peaks, so as not to bias the data. This means that it can be tested whether events annotated with more than 1 DSB tend to contain multiple and/or strong hotspots. Previously, an anticorrelation between concerted DSB formation and Rec114, Mer2 and Mei4 (RMM) axis proteins was observed (Garcia *et al.*, 2014), suggesting that concerted DSBs occur within the same chromatin loop, and that Tel1 is involved in maintaining DSB interference/suppression within loops. Because this phenomenon was observed at only a few single loci, it would be advantageous to determine whether the same phenomenon is present for recombination genome wide. Previously-annotated DSB cluster events (events with more than one DSB within 1.5kb) can be tested for whether they are disproportionately contained within loops (determined by absence of RMM) or tend to cross loop boundaries (determined by Rec8 peaks) (Panizza *et al.*, 2011; Ito *et al.*, 2014).

In *msh2Δ* strains, tracts of 6:2 or 2:6 conversion were observed, which was not predicted as these tracts were thought to be produced by gene conversion (Sections 6.2.4, 7.2.4). These may represent occurrences of concerted DSB formation on the same chromatid. To study these events further, the occurrence and strength of DSB hotspots and the correlation with chromatin loops and axis will be examined.

Ectopic recombination is known to be increased in *rad24* and *mec1* mutants (Gray *et al.*, 2013; Grushcow *et al.*, 1999). Ectopic recombination is difficult to observe in sequencing data because any given read will simply map to the correct region of the genome. However, sequences from different regions of the genome that are contained within the same pair of reads may be detectable. To detect this, paired end reads that map discordantly can be isolated and analysed for whether they occur uniquely and frequently in a certain location, indicating that ectopic recombination has occurred in that region.

9.10. Closing Statement

Collectively, these analyses permit a genome-wide and high-resolution view of meiotic recombination processes, revealing information about the roles of Mec1, Tel1, Rad24 and Msh2 in the regulation of meiotic recombination event quality, quantity and location, and the effect that this has on ensuring spore survival.

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Genotype	Cross	Background	Tetrads	Mean viability	95% conf	4 spores	95% conf	3 spores	95% conf	2 spores	95% conf	1 spore	95% conf	0 spores	95% conf
WT	MJ512xMJ513	SK1	64	96.88	2.13	92.19	6.58	3.13	4.26	4.69	5.18	0.00	0.00	0.00	0.00
WT	MJ600xMJ631	S288c	72	96.88	2.01	88.89	7.26	9.72	6.84	4.17	4.62	0.00	0.00	29.17	10.50
WT	MJ600xMJ513	SK1xS288c	197	81.98	2.68	13.45	2.38	6.85	1.76	3.55	1.29	0.51	0.50	0.63	0.55
WT + 10 h	MJ43xMC42	SK1xS288c	86	70.35	4.83	36.05	10.15	25.58	9.22	25.58	9.22	9.30	6.14	3.49	3.88
msh2Δ	MC25xMC26	SK1	110	80.91	3.67	15.00	3.34	3.18	1.64	4.55	1.95	2.27	1.39	0.00	0.00
msh2Δ	MC49xMC50	S288c	105	77.86	3.97	47.62	9.55	26.67	8.46	18.10	7.36	4.76	4.07	2.86	3.19
msh2Δ Tetrads	MC49xMC26	SK1xS288c	149	72.99	3.56	10.07	2.42	6.38	1.96	5.37	1.81	2.85	1.34	0.34	0.46
msh2Δ Octads	MC49xMC26	SK1xS288c	87	75.00	4.55	36.78	10.13	33.33	9.91	24.14	8.99	4.60	4.40	1.15	2.24
mus81Δ	MC214xMC215	SK1	110	55.68	4.64	17.27	7.06	27.27	8.32	25.45	8.14	20.91	7.60	9.09	5.37
mus81Δ msh2Δ	MC230xMC231	SK1	110	44.09	4.64	13.64	6.41	20.00	7.48	19.09	7.34	23.64	7.94	23.64	7.94
mlh3Δ	MC254xMC255	SK1	110	89.09	2.91	81.82	7.21	3.64	3.50	9.09	5.37	0.00	0.00	5.45	4.24
yen1Δ	MC264xMC265	SK1	110	92.95	2.39	89.09	5.83	0.00	0.00	6.36	4.56	2.73	3.04	1.82	2.50
mus81Δ mlh3Δ	MC271xMC272	SK1	107	59.58	4.65	26.17	8.33	28.04	8.51	19.63	7.53	10.28	5.75	15.89	6.93
mus81Δ yen1Δ	MC267xMC268	SK1	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
mlh3Δ yen1Δ	MC277xMC278	SK1	110	77.95	3.87	64.55	8.94	4.55	3.89	19.09	7.34	1.82	2.50	10.00	5.61
rad24Δ	MC17xMC18	SK1	132	21.59	3.51	7.58	4.51	5.30	3.82	17.42	6.47	5.30	3.82	64.39	8.17
rad24Δ	MC19xMC20	S288c	106	46.70	4.75	12.26	6.24	17.92	7.30	29.25	8.66	25.47	8.29	15.09	6.82
rad24Δ	MC31xMC32	BY474	197	46.70	3.48	14.21	4.88	20.30	5.62	22.84	5.86	23.35	5.91	19.29	5.51
rad24Δ	MC17xMC20	SK1xS288c	240	0.73	0.54	0.00	0.00	0.00	0.00	0.00	0.00	2.92	2.13	97.08	2.13
rad24Δ msh2Δ	MC105xMC106	SK1	107	21.26	3.88	9.35	5.52	5.61	4.36	21.50	7.78	24.30	8.13	59.81	9.29
rad24Δ msh2Δ	MC202xMC203	S288c	102	28.19	4.37	2.94	3.28	11.76	6.25	18.63	7.56	28.43	8.75	38.24	9.43
rad24Δ msh2Δ	MC105xMC203	SK1xS288c	462	5.90	1.07	1.30	1.03	2.38	1.39	8.87	2.59	21.00	3.71	66.45	4.31
rad24Δ mus81Δ	MC222xMC223	SK1	110	19.32	3.69	0.00	0.00	7.27	4.85	20.91	7.60	13.64	6.41	58.18	9.22
rad24Δ mus81Δ	MC222xMC227	SK1XS288c	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
rad24Δ mlh3Δ	MC247xMC248	SK1	109	20.64	3.80	6.42	4.60	3.67	3.53	13.76	6.47	18.35	7.27	57.80	9.27
rad24Δ yen1Δ	MC251xMC252	SK1	110	36.82	4.51	12.73	6.23	11.82	6.03	21.82	7.72	17.27	7.06	36.36	8.99
rad24Δ mlh3Δ yen1Δ	MC262xMC263	SK1	107	16.82	3.54	2.80	3.13	6.54	4.69	9.35	5.52	17.76	7.24	63.55	9.12
rad24Δ mus81Δ mlh3Δ	MC257xMC258	SK1	98	7.91	2.67	1.02	1.99	0.00	0.00	9.18	5.72	9.18	5.72	80.61	7.83
rad24Δ sml1Δ	MC101xMC102	SK1	102	41.67	4.78	18.63	7.56	13.73	6.68	21.57	7.98	7.84	5.22	38.24	9.43
rad24Δ sml1Δ	MC59xMC60	BY474	131	48.47	4.28	15.27	6.16	22.90	7.20	19.85	6.83	24.43	7.36	17.56	6.52
rad24Δ mus81Δ yen1Δ	MC273xMC274	SK1	5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00

Genotype	Cross	Background	N												
rad24Δ sml1Δ	MC101xMC61	SK1xBY474	196	4.72	1.48	0.51	1.00	0.51	1.00	4.08	2.77	7.14	3.61	87.76	4.59
rad24Δ sml1Δ msh2Δ	MC190xMC193	SK1xBY474	110	24.32	4.01	5.45	4.24	6.36	4.56	13.64	6.41	29.09	8.49	45.45	9.31
tel1Δ	MC21xMC22	SK1	87	92.53	2.76	82.76	10.34	2.30	3.45	1.15	7.94	6.40	3.15	3.83	2.24
tel1Δ	MC23xMC24	S288c	86	86.34	3.63	63.95	10.15	20.93	8.60	12.79	7.06	1.16	2.27	1.16	2.27
tel1Δ	MC21xMC24	SK1xS288c	109	69.04	4.34	33.94	8.89	26.61	8.30	24.77	8.10	11.01	5.88	3.67	3.53
tel1Δ mus81Δ	MC234xMC235	SK1	109	25.46	4.09	1.83	2.52	11.01	5.88	12.84	6.28	35.78	9.00	38.53	9.14
tel1Δ msh2Δ	MC29xMC30	SK1	109	74.77	4.08	59.63	9.21	6.42	4.60	15.60	6.81	10.09	5.65	8.26	5.17
tel1Δ msh2Δ	MC53xMC54	S288c	116	78.23	3.75	57.76	8.99	15.52	6.59	14.66	6.44	6.03	4.33	6.03	4.33
tel1Δ msh2Δ Tetrads	MC53xMC30	SK1xS288c	105	63.57	4.60	24.76	8.26	28.57	8.64	26.67	8.46	16.19	7.05	3.81	3.66
tel1Δ msh2Δ Octads 2%glucose	MC53xMC30	SK1xS288c	130	60.19	4.21	20.00	6.88	30.77	7.93	26.92	7.62	14.62	6.07	7.69	4.58
tel1Δ msh2Δ Octads 5%glucose	MC53xMC30	SK1xS288c	76	64.47	10.76	21.05	18.33	31.58	20.90	31.58	20.90	15.79	16.40	0.00	0.00
PCLB2-MEC1	VG120xVG121	SK1	130	58.46	4.24	21.54	7.07	32.31	8.04	15.38	6.20	20.00	6.88	10.77	5.33
PCLB2-MEC1	MC152xMC153	S288c	110	77.27	3.92	62.50	10.12	30.68	9.64	21.59	8.60	1.14	2.21	9.09	6.01
PCLB2-MEC1	VG120xMC153	SK1xS288c	153	6.37	1.94	1.31	1.80	0.65	1.28	4.58	3.31	9.15	4.57	84.31	5.76
PCLB2-MEC1 msh2Δ	MC163xMC164	SK1	88	49.15	5.22	19.32	8.25	23.86	8.91	14.77	7.41	18.18	8.06	23.86	8.91
PCLB2-MEC1 msh2Δ	MC171xMC172	S288c	111	63.06	4.49	30.63	8.58	25.23	8.08	19.82	7.42	14.41	6.53	9.91	5.56
PCLB2-MEC1 msh2Δ	MC163xMC172	SK1xS288c	176	28.84	3.35	3.41	2.68	10.80	4.58	17.61	5.63	34.09	7.00	34.09	7.00
PCLB2-MEC1 mus81Δ	MC243xMC242	SK1	108	20.37	3.80	1.85	2.54	3.70	3.56	14.81	6.70	33.33	8.89	46.30	9.40
PCLB2-MEC1 Spo11-D290A	MC281xMC282	SK1	88	17.05	3.93	6.82	5.27	4.55	4.35	9.09	6.01	9.09	6.01	70.45	9.53
PCLB2-MEC1 + 4 h	MC2xMC3	SK1	88	49.15	5.22	12.50	6.91	28.41	9.42	18.18	8.06	25.00	9.05	15.91	7.64
PCLB2-MEC1 + 6 h	MC2xMC3	SK1	86	54.07	5.27	19.77	8.42	23.26	8.93	23.26	8.93	20.93	8.60	12.79	7.06
PCLB2-MEC1 + 8 h	MC2xMC3	SK1	84	57.74	5.28	17.86	8.19	30.95	9.89	25.00	9.26	16.67	7.97	9.52	6.28
PCLB2-MEC1 + 10 h	MC2xMC3	SK1	86	48.55	5.28	12.79	7.06	19.77	8.42	30.23	9.71	23.26	8.93	13.95	7.32
PCLB2-MEC1 + 12 h	MC2xMC3	SK1	53	51.89	6.73	16.98	10.11	32.08	12.57	15.09	9.64	13.21	9.12	22.64	11.27
PCLB2-MEC1 +4 h	MC2xMC198	SK1xS288c	64	10.16	3.70	1.56	3.04	1.56	3.04	3.13	4.26	23.44	10.38	70.31	11.19
PCLB2-MEC1 +6 h	MC2xMC198	SK1xS288c	63	18.25	4.77	0.00	0.00	6.35	6.02	14.29	8.64	25.40	10.75	53.97	12.31
PCLB2-MEC1 +8 h	MC2xMC198	SK1xS288c	87	16.38	3.89	2.30	3.15	4.60	4.40	9.20	6.07	24.14	8.99	59.77	10.30
PCLB2-MEC1 +10 h	MC2xMC198	SK1xS288c	63	26.98	5.48	4.76	5.26	6.35	6.02	19.05	9.70	31.75	11.49	38.10	11.99
PCLB2-MEC1 D290A + 4 h	MC211xMC212	SK1	61	73.36	5.55	37.70	12.16	31.15	11.62	19.67	9.98	9.84	7.47	1.64	3.19
PCLB2-MEC1 D290A + 6 h	MC211xMC212	SK1	86	60.47	5.17	24.42	9.08	31.40	9.81	18.60	8.22	12.79	7.06	12.79	7.06
PCLB2-MEC1 D290A + 8 h	MC211xMC212	SK1	85	60.29	5.20	25.88	9.31	31.76	9.90	15.29	7.65	11.76	6.85	15.29	7.65

PCLB2-MEC1 D290A + 10 h	MC211xMC212	SK1	87	60.63	5.13	31.03	9.72	21.84	8.68	17.24	7.94	18.39	8.14	11.49	6.70
WT + 3 h	MJ846	SK1	64	86.33	4.21	75.00	10.61	7.81	6.58	9.38	7.14	3.13	4.26	4.69	5.18
WT + 4 h	MJ846	SK1	42	91.07	4.31	80.95	11.88	11.90	9.79	2.38	4.61	0.00	0.00	4.76	6.44
WT + 5 h	MJ846	SK1	41	94.51	3.49	85.37	10.82	7.32	7.97	7.32	7.97	0.00	0.00	0.00	0.00
Spo11-D290A +3 h	MJ892	SK1	64	85.55	4.31	67.19	11.50	12.50	8.10	17.19	9.24	1.56	3.04	1.56	3.04
Spo11-D290A +4 h	MJ892	SK1	44	85.80	5.16	72.73	13.16	9.09	8.49	11.36	9.38	2.27	4.40	4.55	6.15
Spo11-D290A +5 h	MJ892	SK1	44	91.48	4.13	79.55	11.92	11.36	9.38	6.82	7.45	0.00	0.00	2.27	4.40
Spo11-HA +3 h	MJ847	SK1	77	70.13	5.11	51.95	11.16	11.69	7.18	16.88	8.37	3.90	4.32	15.58	8.10
Spo11-HA +4 h	MJ847	SK1	44	76.14	6.30	54.55	14.71	11.36	9.38	25.00	12.79	2.27	4.40	6.82	7.45
Spo11-HA +5 h	MJ847	SK1	44	86.36	5.07	72.73	13.16	6.82	7.45	15.91	10.81	2.27	4.40	2.27	4.40
rad24Δ msh2Δ + 4 h	MC207xMC208	SK1	66	33.33	5.69	4.55	5.03	18.18	9.31	15.15	8.65	30.30	11.09	31.82	11.24
rad24Δ msh2Δ + 6 h	MC207xMC208	SK1	78	30.00	5.57	1.54	2.99	9.23	7.04	27.69	10.88	30.77	11.22	30.77	11.22
rad24Δ msh2Δ + 8 h	MC207xMC208	SK1	66	43.56	5.98	13.64	8.28	13.64	8.28	27.27	10.74	24.24	10.34	21.21	9.86
rad24Δ msh2Δ + 10 h	MC207xMC208	SK1	66	49.24	6.03	7.58	6.38	24.24	10.34	34.85	11.50	24.24	10.34	9.09	6.94
rad24Δ msh2Δ +4 h	MC239xMC207	SK1xS288c	109	31.19	4.35	4.59	3.93	10.09	5.65	24.77	8.10	26.61	8.30	33.94	8.89
rad24Δ msh2Δ +6 h	MC239xMC207	SK1xS288c	110	25.68	4.08	1.82	2.50	7.27	4.85	17.27	7.06	39.09	9.12	34.55	8.89
rad24Δ msh2Δ +8 h	MC239xMC207	SK1xS288c	110	26.82	4.14	3.64	3.50	4.55	3.89	20.00	7.48	39.09	9.12	32.73	8.77
rad24Δ msh2Δ +10 h	MC239xMC207	SK1xS288c	110	27.05	4.15	6.36	4.56	5.45	4.24	20.91	7.60	24.55	8.04	42.73	9.24
rad24Δ +6 h	MJ835xMC89	SK1xS288c	93	6.72	2.54	0.00	0.00	4.30	4.12	1.08	2.10	11.83	6.56	82.80	7.67
rad24Δ +8 h	MJ835xMC89	SK1xS288c	218	7.91	1.79	0.46	0.90	0.92	1.27	4.59	2.78	17.89	5.09	76.15	5.66
rad24Δ +10 h	MJ835xMC89	SK1xS288c	269	15.94	1.82	1.86	1.61	2.60	1.90	13.38	4.07	17.84	4.58	64.31	5.73
rad24Δ sml1Δ +4 h	MC120xMC122	SK1	109	60.55	4.59	34.86	8.95	26.61	8.30	19.27	7.40	11.93	6.08	16.51	6.97
rad24Δ sml1Δ +6 h	MC120xMC122	SK1	107	51.87	4.73	27.10	8.42	17.76	7.24	28.04	8.51	17.76	7.24	18.69	7.39
rad24Δ sml1Δ +8 h	MC120xMC122	SK1	117	69.87	4.16	43.59	8.99	27.35	8.08	17.09	6.82	14.53	6.39	5.98	4.30
rad24Δ sml1Δ +8 h	MC120xMC139	SK1xBY474	110	10.23	2.83	0.00	0.00	0.91	1.77	10.91	5.83	16.36	6.91	71.82	8.41
rad24Δ sml1Δ +10 h	MC120xMC139	SK1xBY474	110	18.64	3.64	0.00	0.00	4.55	3.89	14.55	6.59	31.82	8.70	49.09	9.34
rad24Δ +3 h	MJ848	SK1	43	22.09	6.20	9.30	8.68	6.98	7.61	6.98	7.61	16.28	11.03	60.47	14.61
rad24Δ +4 h	MJ848	SK1	44	31.82	6.88	4.55	6.15	18.18	11.40	20.45	11.92	13.64	10.14	43.18	14.64
rad24Δ +5 h	MJ848	SK1	82	44.21	5.37	9.76	6.42	18.29	8.37	35.37	10.35	12.20	7.08	24.39	9.29
rad24Δ +6 h	MJ848	SK1	66	42.80	5.97	9.09	6.94	15.15	8.65	36.36	11.61	16.67	8.99	22.73	10.11
rad24Δ +7 h	MJ848	SK1	41	56.10	7.60	19.51	12.13	26.83	13.56	24.39	13.15	17.07	11.52	12.20	10.02
rad24Δ +8 h	MJ848	SK1	84	59.18	5.42	15.48	7.73	26.19	9.40	28.57	9.66	25.00	9.26	4.76	4.55
rad24Δ +9 h	MJ848	SK1	41	62.20	7.42	24.39	13.15	26.83	13.56	26.83	13.56	17.07	11.52	4.88	6.59

rad24Δ +10 h	MJ848	SK1	59	69.07	5.90	35.59	12.22	22.03	10.58	28.81	11.56	10.17	7.71	3.39	4.62
rad24Δ +11 h	MJ848	SK1	64	62.50	5.93	23.44	10.38	34.38	11.64	18.75	9.56	15.63	8.90	7.81	6.58
rad24Δ +12 h	MJ848	SK1	165	61.34	3.91	17.58	5.81	23.03	6.42	33.94	7.22	13.94	5.28	11.52	4.87
rad24Δ Spo11-D290A +3 h	MJ913	SK1	44	2.27	2.20	0.00	0.00	0.00	0.00	4.55	6.15	0.00	0.00	95.45	6.15
rad24Δ Spo11-D290A +4 h	MJ913	SK1	44	21.59	6.08	4.55	6.15	2.27	4.40	25.00	12.79	11.36	9.38	56.82	14.64
rad24Δ Spo11-D290A +5 h	MJ913	SK1	83	46.99	5.37	15.66	7.82	16.87	8.06	27.71	9.63	19.28	8.49	20.48	8.68
rad24Δ Spo11-D290A +6 h	MJ913	SK1	62	54.84	6.19	20.97	10.13	22.58	10.41	25.81	10.89	16.13	9.16	14.52	8.77
rad24Δ Spo11-D290A +7 h	MJ913	SK1	43	58.14	7.37	30.23	13.73	13.95	10.36	27.91	13.41	13.95	10.36	13.95	10.36
rad24Δ Spo11-D290A +8 h	MJ913	SK1	63	75.79	5.29	41.27	12.16	28.57	11.16	23.81	10.52	4.76	5.26	1.59	3.09
rad24Δ Spo11-D290A +9 h	MJ913	SK1	41	71.95	6.88	39.02	14.93	21.95	12.67	29.27	13.93	7.32	7.97	2.44	4.72
rad24Δ Spo11-D290A +10 h	MJ913	SK1	61	81.97	4.82	47.54	12.53	37.70	12.16	11.48	8.00	1.64	3.19	1.64	3.19
rad24Δ Spo11-D290A +11 h	MJ913	SK1	63	75.40	5.32	50.79	12.35	23.81	10.52	11.11	7.76	4.76	5.26	9.52	7.25
rad24Δ Spo11-D290A +12 h	MJ913	SK1	149	78.65	3.48	24.83	6.94	44.30	7.98	19.46	6.36	10.74	4.97	0.67	1.31
rad24Δ Spo11-HA +3 h	MJ850	SK1	44	13.64	5.07	4.55	6.15	0.00	0.00	15.91	10.81	4.55	6.15	75.00	12.79
rad24Δ Spo11-HA +4 h	MJ850	SK1	44	23.30	6.25	11.36	9.38	2.27	4.40	15.91	10.81	9.09	8.49	61.36	14.39
rad24Δ Spo11-HA +5 h	MJ850	SK1	83	54.52	5.36	31.33	9.98	14.46	7.57	19.28	8.49	10.84	6.69	24.10	9.20
rad24Δ Spo11-HA +6 h	MJ850	SK1	59	65.68	6.06	40.68	12.53	18.64	9.94	18.64	9.94	6.78	6.41	15.25	9.17
rad24Δ Spo11-HA +7 h	MJ850	SK1	44	68.75	6.85	45.45	14.71	15.91	10.81	15.91	10.81	13.64	10.14	9.09	8.49
rad24Δ Spo11-HA +8 h	MJ850	SK1	73	74.32	5.01	45.21	11.42	24.66	9.89	17.81	8.78	6.85	5.79	5.48	5.22
rad24Δ Spo11-HA +9 h	MJ850	SK1	43	78.49	6.14	46.51	14.91	32.56	14.01	11.63	9.58	6.98	7.61	2.33	4.50
rad24Δ Spo11-HA +10 h	MJ850	SK1	54	80.09	5.33	66.67	12.57	3.70	5.04	18.52	10.36	5.56	6.11	5.56	6.11
rad24Δ Spo11-HA +11 h	MJ850	SK1	65	78.85	4.96	50.77	12.15	26.15	10.68	12.31	7.99	9.23	7.04	1.54	2.99
rad24Δ Spo11-HA +12 h	MJ850	SK1	154	80.59	3.24	35.71	7.57	43.51	7.83	10.39	4.82	5.19	3.51	5.19	3.51
rad24 CDC20-1 +8 h @37oC	MC142xMC143	SK1	88	21.02	4.26	0.85	0.96	2.56	1.65	1.99	1.46	5.97	2.47	13.64	3.59
CDC20-1 +8 h @37oC	MC132xMC133	SK1	65	95.38	2.55	22.31	5.06	1.15	1.30	1.15	1.30	0.38	0.75	0.00	0.00
rad24Δ +8 h @37oC	MC17xMC18	SK1	21	16.67	7.97	0.00	0.00	1.19	2.32	3.57	3.97	5.95	5.06	14.29	7.48
rad24Δ mus81Δ +8 h		SK1	108	9.72	2.79	0.00	0.00	1.85	2.54	2.78	3.10	27.78	8.45	67.59	8.83
rad24Δ mus81Δ +4 h		SK1	89	5.90	2.45	1.12	2.19	0.00	0.00	4.49	4.30	10.11	6.26	84.27	7.56
mus81Δ +8 h		SK1	110	33.41	4.41	3.64	3.50	17.27	7.06	21.82	7.72	23.64	7.94	33.64	8.83
mus81Δ +4 h		SK1	128	33.98	4.10	6.25	4.19	10.94	5.41	23.44	7.34	31.25	8.03	28.13	7.79

id	Meiosis	Genotype	chr	start5	start3	stop5	stop3	chromatids	len_min	len_mid	len_max	groupe	classe	LSB	LCO	LNCO	type
112	BOM1	BOM	7	951785	951834	951845	951926	1	12	76	140	1	1	1	0	1	05:03
237	BOM1	BOM	15	931168	931340	931340	931409	1	1	121	240	1	1	1	0	1	05:03
34	BOM1	BOM	4	163443	163447	163455	163695	1	9	130	251	1	1	1	0	1	05:03
114	BOM1	BOM	7	993849	994015	994032	994097	1	18	133	247	1	1	1	0	1	05:03
56	BOM1	BOM	4	930409	930421	930421	930813	1	1	202	403	1	1	1	0	1	05:03
16	BOM1	BOM	2	549839	550124	550142	550241	1	19	210	401	1	1	1	0	1	05:03
75	BOM1	BOM	5	45963	46022	46098	46310	1	77	212	346	1	1	1	0	1	05:03
205	BOM1	BOM	13	732051	732373	732395	732528	1	23	250	476	1	1	1	0	1	05:03
76	BOM1	BOM	5	69083	69209	69243	69568	1	35	260	484	1	1	1	0	1	05:03
5	BOM1	BOM	1	138499	138650	138650	139076	1	1	289	576	1	1	1	0	1	05:03
227	BOM1	BOM	15	360812	360995	360995	361461	1	1	325	648	1	1	1	0	1	05:03
196	BOM1	BOM	13	119087	119306	119476	119630	1	171	357	542	1	1	1	0	1	05:03
46	BOM1	BOM	4	444672	445249	445249	445472	1	1	400	799	1	1	1	0	1	05:03
144	BOM1	BOM	10	379811	380369	380369	380706	1	1	448	894	1	1	1	0	1	05:03
115	BOM1	BOM	7	1011203	1011474	1011510	1012069	1	37	451	865	1	1	1	0	1	05:03
69	BOM1	BOM	4	1459261	1459669	1459669	1460259	1	1	499	997	1	1	1	0	1	05:03
218	BOM1	BOM	14	323136	323238	323606	323787	1	369	510	650	1	1	1	0	1	05:03
18	BOM1	BOM	2	651616	652362	652467	652587	1	106	538	970	1	1	1	0	1	05:03
146	BOM1	BOM	10	465282	465795	465816	466454	1	22	597	1171	1	1	1	0	1	05:03
63	BOM1	BOM	4	1270457	1270902	1270902	1271755	1	1	649	1297	1	1	1	0	1	05:03
57	BOM1	BOM	4	960101	960464	960787	961189	1	324	706	1087	1	1	1	0	1	05:03
198	BOM1	BOM	13	281241	282022	282022	282723	1	1	741	1481	1	1	1	0	1	05:03
159	BOM1	BOM	11	317104	317375	317831	318297	1	457	825	1192	1	1	1	0	1	05:03
174	BOM1	BOM	12	398507	398570	399414	399454	1	845	896	946	1	1	1	0	1	05:03
86	BOM1	BOM	5	460411	461582	461594	462226	1	13	914	1814	1	1	1	0	1	05:03
37	BOM1	BOM	4	225248	226059	226209	227127	1	151	1015	1878	1	1	1	0	1	05:03
118	BOM1	BOM	8	111246	111464	112492	112829	1	1029	1306	1582	1	1	1	0	1	05:03
31	BOM1	BOM	4	52141	52534	54490	55084	1	1957	2450	2942	1	1	1	0	1	05:03
36	BOM1	BOM	4	212746	213315	215967	216258	1	2653	3082	3511	1	1	1	0	1	05:03
8	BOM1	BOM	1	202856	202897	202977	203031	1	81	128	174	1	2	1	0	1	03:05
128	BOM1	BOM	9	138710	138723	138762	139068	1	40	199	357	1	2	1	0	1	03:05
35	BOM1	BOM	4	176273	176423	176519	176588	1	97	206	314	1	2	1	0	1	03:05
41	BOM1	BOM	4	266029	266113	266302	266398	1	190	279	368	1	2	1	0	1	03:05
163	BOM1	BOM	11	384228	384363	384363	384792	1	1	282	563	1	2	1	0	1	03:05
91	BOM1	BOM	6	74705	74753	74992	75055	1	240	295	349	1	2	1	0	1	03:05
170	BOM1	BOM	12	259471	260086	260086	260298	1	1	414	826	1	2	1	0	1	03:05
82	BOM1	BOM	5	237481	238122	238122	238396	1	1	458	914	1	2	1	0	1	03:05
133	BOM1	BOM	9	248675	248948	249032	249546	1	85	478	870	1	2	1	0	1	03:05
73	BOM1	BOM	5	26594	26638	27119	27260	1	482	574	665	1	2	1	0	1	03:05
240	BOM1	BOM	16	54755	55257	55562	55604	1	306	577	848	1	2	1	0	1	03:05
103	BOM1	BOM	7	375036	375227	375494	375933	1	268	582	896	1	2	1	0	1	03:05
94	BOM1	BOM	6	202731	202970	203253	203623	1	284	588	891	1	2	1	0	1	03:05
247	BOM1	BOM	16	539197	539336	539891	539931	1	556	645	733	1	2	1	0	1	03:05
230	BOM1	BOM	15	553518	554715	554715	554820	1	1	651	1301	1	2	1	0	1	03:05
108	BOM1	BOM	7	784625	785199	785318	785828	1	120	661	1202	1	2	1	0	1	03:05
61	BOM1	BOM	4	1078458	1078855	1079258	1079450	1	404	698	991	1	2	1	0	1	03:05
206	BOM1	BOM	13	752521	752958	752958	753954	1	1	717	1432	1	2	1	0	1	03:05
184	BOM1	BOM	12	757131	757763	758099	758246	1	337	726	1114	1	2	1	0	1	03:05
152	BOM1	BOM	11	99646	100443	100670	101183	1	228	882	1536	1	2	1	0	1	03:05
64	BOM1	BOM	4	1335831	1337219	1337219	1337684	1	1	927	1852	1	2	1	0	1	03:05
124	BOM1	BOM	8	487644	488458	488588	489445	1	131	966	1800	1	2	1	0	1	03:05
1	BOM1	BOM	1	43565	43691	44588	44675	1	898	1004	1109	1	2	1	0	1	03:05
106	BOM1	BOM	7	599815	599896	600706	601348	1	811	1172	1532	1	2	1	0	1	03:05
113	BOM1	BOM	7	972322	972898	973354	974385	1	457	1260	2062	1	2	1	0	1	03:05
221	BOM1	BOM	14	673326	674407	674690	676085	1	284	1521	2758	1	2	1	0	1	03:05
155	BOM1	BOM	11	140833	141109	141122	143878	1	14	1529	3044	1	2	1	0	1	03:05
132	BOM1	BOM	9	185865	188629	188877	188919	1	249	1651	3053	1	2	1	0	1	03:05
49	BOM1	BOM	4	628602	629487	630674	631576	1	1188	2081	2973	1	2	1	0	1	03:05
50	BOM1	BOM	4	645102	652022	652241	652907	1	220	4012	7804	1	2	1	0	1	03:05

121	BOM1	BOM	8	316015	317153	317992	318122	1	840	1473	2106	1	3	1	0	1 5:3_4:4_5:3
167	BOM1	BOM	12	45294	46479	47654	48661	1	1176	2271	3366	1	3	1	0	1 5:3_4:4_5:3
244	BOM1	BOM	16	294452	294899	296393	297021	1	1495	2032	2568	1	3	1	0	1 5:3_4:4_5:3_4:4_5:3
23	BOM1	BOM	3	39281	39525	40294	40374	1	770	931	1092	1	3	1	0	1 5:3_6:2_5:3_6:2_5:3_6:2_5:3
42	BOM1	BOM	4	313728	313860	314015	314500	1	156	464	771	1	4	1	0	1 3:5_2:6_3:5
125	BOM1	BOM	8	517036	517336	517499	518179	1	164	653	1142	1	4	1	0	1 3:5_4:4_3:5
71	BOM1	BOM	4	1476514	1476956	1479784	1480113	1	2829	3214	3598	1	4	1	0	1 5:3_4:4_3:5
214	BOM1	BOM	14	184882	184944	185309	185417	1	366	450	534	1	7	1	0	1 5:3_6:2
181	BOM1	BOM	12	714641	714966	715622	715772	1	657	894	1130	1	7	1	0	1 6:2_5:3
79	BOM1	BOM	5	187705	187805	189254	189662	1	1450	1703	1956	1	7	1	0	1 6:2_5:3
201	BOM1	BOM	13	492116	492266	492388	492749	1	123	378	632	1	7	1	0	1 5:3_6:2_5:3_6:2
96	BOM1	BOM	6	254081	254393	255417	255483	1	1025	1213	1401	1	7	1	0	1 5:3_4:4_5:3_6:2
160	BOM1	BOM	11	327998	328028	329482	329573	1	1455	1515	1574	1	7	1	0	1 6:2_5:3_4:4_5:3
67	BOM1	BOM	4	1409336	1409468	1412942	1413914	1	3475	4026	4577	1	7	1	0	1 5:3_6:2_5:3_6:2_5:3_6:2
217	BOM1	BOM	14	316782	316808	317360	317738	1	553	754	955	1	8	1	0	1 3:5_2:6
199	BOM1	BOM	13	396483	396553	397289	397850	1	737	1052	1366	1	8	1	0	1 2:6_3:5
74	BOM1	BOM	5	42646	42708	43260	43494	1	553	700	847	1	8	1	0	1 2:6_4:4_3:5_4:4_2:6
14	BOM1	BOM	2	356462	356648	356648	356805	1	1	172	342	1	10.1	1	0	1 02:06
78	BOM1	BOM	5	160729	160912	160912	161191	1	1	231	461	1	10.1	1	0	1 02:06
209	BOM1	BOM	14	40306	40397	40430	41146	1	34	437	839	1	10.1	1	0	1 02:06
65	BOM1	BOM	4	1385671	1385846	1386016	1386524	1	171	512	852	1	10.1	1	0	1 02:06
232	BOM1	BOM	15	684419	684893	685067	685601	1	175	678	1181	1	10.1	1	0	1 02:06
211	BOM1	BOM	14	68234	68498	68923	69145	1	426	668	910	2	11	1	0	1 5:3_5:3a
223	BOM1	BOM	15	68535	68903	69357	69484	1	455	702	948	2	11	1	0	1 5:3_5:3a
250	BOM1	BOM	16	833382	833507	834395	834534	1	889	1020	1151	2	11	1	0	1 5:3_5:3a
161	BOM1	BOM	11	368313	369378	369878	370412	1	501	1300	2098	2	11	1	0	1 5:3_5:3a
6	BOM1	BOM	1	141984	142779	143679	143822	1	901	1369	1837	2	11	1	0	1 5:3_5:3a
231	BOM1	BOM	15	558128	558487	559768	560108	1	1282	1631	1979	2	11	1	0	1 5:3_5:3a
22	BOM1	BOM	2	800055	800115	800316	800859	1	202	503	803	2	12	1	0	1 3:5_3:5a
153	BOM1	BOM	11	114400	114572	114933	115293	1	362	627	892	2	12	1	0	1 3:5_3:5a
186	BOM1	BOM	12	827928	828244	828622	828844	1	379	647	915	2	12	1	0	1 3:5_3:5a
40	BOM1	BOM	4	254856	255187	255722	255870	1	536	775	1013	2	12	1	0	1 3:5_3:5a
157	BOM1	BOM	11	216709	216788	217514	217814	1	727	916	1104	2	12	1	0	1 3:5_3:5a
80	BOM1	BOM	5	201006	201879	202285	202470	1	407	935	1463	2	12	1	0	1 3:5_3:5a
20	BOM1	BOM	2	701832	701871	702673	703042	1	803	1006	1209	2	12	1	0	1 3:5_3:5a
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55	BOM1	BOM	4	855461	855709	856679	857591	1	971	1550	2129	2	12	1	0	1 3:5_3:5a
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44	BOM1	BOM	4	402050	402371	403830	403952	1	1460	1681	1901	2	13	1	0	1 5:3_4:4_5:3_5:3a
39	BOM1	BOM	4	240657	240792	243004	243234	1	2213	2395	2576	2	13	1	0	1 5:3_6:2_5:3_5:3a
84	BOM1	BOM	5	334460	334676	335812	335874	1	1137	1275	1413	2	13	1	0	1 6:2_5:3_4:4_5:3_5:3a
207	BOM1	BOM	13	795946	796038	798333	798592	1	2296	2471	2645	2	14	1	0	1 3:5_4:4_3:5_3:5a
235	BOM1	BOM	15	824928	825148	826879	827016	1	1732	1910	2087	2	14	1	0	1 3:5_3:5a_4:4_2:6_3:5a
183	BOM1	BOM	12	747180	747358	747982	748236	1	625	840	1055	2	15	1	0	1 5:3_4:4_5:3a
215	BOM1	BOM	14	199873	199979	200718	201078	1	740	972	1204	2	15	1	0	1 5:3_4:4_5:3a
97	BOM1	BOM	7	17261	17428	18259	18394	1	832	982	1132	2	15	1	0	1 5:3_4:4_5:3a
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123	BOM1	BOM	8	463706	463786	464855	465244	1	1070	1304	1537	2	15	1	0	1 5:3_4:4_5:3a
131	BOM1	BOM	9	169256	169294	170681	170921	1	1388	1526	1664	2	15	1	0	1 5:3_4:4_5:3a
127	BOM1	BOM	9	124830	125455	126608	127338	1	1154	1831	2507	2	15	1	0	1 5:3_4:4_5:3a
101	BOM1	BOM	7	165523	166667	167983	168156	1	1317	1975	2632	2	15	1	0	1 5:3_4:4_5:3a
202	BOM1	BOM	13	535437	535671	536671	536833	1	1001	1198	1395	2	16	1	0	1 3:5_4:4_3:5a
12	BOM1	BOM	2	269653	269904	270387	271598	1	484	1214	1944	2	16	1	0	1 3:5_4:4_3:5a
251	BOM1	BOM	16	842086	842864	843720	843861	1	857	1316	1774	2	16	1	0	1 3:5_4:4_3:5a
52	BOM1	BOM	4	721365	721724	723150	723345	1	1427	1703	1979	2	16	1	0	1 3:5_4:4_3:5a
139	BOM1	BOM	10	34093	36217	37127	37895	1	911	2356	3801	2	16	1	0	1 3:5_4:4_3:5a
116	BOM1	BOM	8	20117	20294	20993	21004	1	700	793	886	2	17	1	0	1 5:3_4:4_5:3a_6:2
45	BOM1	BOM	4	423595	423759	424131	424226	1	373	502	630	2	18	1	0	1 2:6_3:5_4:4_3:5a
85	BOM1	BOM	5	377471	377999	379332	379879	1	1334	1871	2407	2	18	1	0	1 2:6_3:5_4:4_3:5_4:4_3:5a
194	BOM1	BOM	13	76522	77019	77482	77676	1	464	809	1153	2	20	1	0	1 3:5_2:6_3:5a

180	BOM1	BOM	12	611812	611864	612358	612475	1	495	579	662	2	23	1	0	1	3:5_2:6_4:4_3:5a
177	BOM1	BOM	12	539092	539598	540258	540405	1	661	987	1312	2	23	1	0	1	5:3_6:2_4:4_5:3a
102	BOM1	BOM	7	170211	170880	171571	171676	1	692	1078	1464	2	23	1	0	1	5:3_6:2_4:4_5:3a
59	BOM1	BOM	4	1010910	1011237	1011970	1012387	1	734	1105	1476	2	23	1	0	1	3:5_2:6_4:4_3:5a
241	BOM1	BOM	16	131754	131951	133388	133624	1	1438	1654	1869	2	23	1	0	1	5:3_4:4_6:2_5:3a_4:4_5:3a
156	BOM1	BOM	11	176780	177108	179509	179637	2_nonsis		2402	2629	2856	3	30	1	0	1	3:5_3:5a_2:6_3:5b
25	BOM1	BOM	3	56432	57568	59465	59925	2_nonsis		1898	2695	3492	3	31	1	0	1	4:4ai_3:5
140	BOM1	BOM	10	100496	101045	101339	101966	2_nonsis		295	882	1469	3	31	1	0	1	4:4ai_4:4bi_5:3
88	BOM1	BOM	5	523260	523683	525834	526150	2_nonsis		2152	2521	2889	3	31	1	0	1	3:5_4:4ai_3:5a_4:4ai
66	BOM1	BOM	4	1400232	1400438	1402144	1402695	2_nonsis		1707	2085	2462	3	31	1	0	1	5:3_4:4_4:4ai_5:3_5:3a
2	BOM1	BOM	1	80077	80554	82379	83613	2_nonsis		1826	2681	3535	3	31	1	0	1	4:4ai_5:3_4:4ai_5:3_5:3a
11	BOM1	BOM	2	212886	213058	218557	218624	2_nonsis		5500	5619	5737	3	31	1	0	1	4:4ai_3:5_4:4ai_5:3_5:3a_5:3b
90	BOM1	BOM	6	35993	36224	38359	38588	2_nonsis		2136	2365	2594	3	31	1	0	1	4:4ai_3:5_4:4ai_5:3_5:3a_6:2_5:3a
213	BOM1	BOM	14	121220	121385	124154	124235	2_nonsis		2770	2892	3014	3	31	1	0	1	5:3_6:2_5:3_6:2_5:3_6:2_5:3a_4:4ai_3:5
164	BOM1	BOM	11	433175	433506	437754	437891	2_nonsis		4249	4482	4715	3	31	1	0	1	4:4ai_3:5_2:6_3:5_2:6_3:5a_4:4_3:5a_5:3_3:5_3:5a_4:4ai
182	BOM1	BOM	12	717181	717475	717475	717529	2_nonsis		1	174	347	1	1	1	1	0	(5:3)_(4:4aCO)
242	BOM1	BOM	16	135194	135326	135326	135618	2_nonsis		1	212	423	1	1	1	1	0	(5:3)_(4:4aCO)
203	BOM1	BOM	13	556437	557365	557425	557517	2_nonsis		61	570	1079	1	1	1	1	0	(5:3)_(4:4aCO)
70	BOM1	BOM	4	1464680	1465187	1465397	1465791	2_nonsis		211	661	1110	1	1	1	1	0	(5:3)_(4:4aCO)
212	BOM1	BOM	14	70909	71495	72005	72122	2_nonsis		511	862	1212	1	1	1	1	0	(5:3)_(4:4aCO)
151	BOM1	BOM	11	77827	78581	79874	80353	2_nonsis		1294	1910	2525	1	1	1	1	0	(5:3)_(4:4aCO)
135	BOM1	BOM	9	289127	292353	292446	292870	2_nonsis		94	1918	3742	1	1	1	1	0	(5:3)_(4:4aCO)
117	BOM1	BOM	8	45102	46055	47072	48088	2_nonsis		1018	2002	2985	1	1	1	1	0	(5:3)_(4:4aCO)
150	BOM1	BOM	11	32124	33673	34686	35136	2_nonsis		1014	2013	3011	1	1	1	1	0	(5:3)_(4:4aCO)
138	BOM1	BOM	10	21859	22066	22066	22158	2_nonsis		1	150	298	1	2	1	1	0	(3:5)_(4:4aCO)
141	BOM1	BOM	10	155705	156143	156143	156360	2_nonsis		1	328	654	1	2	1	1	0	(3:5)_(4:4aCO)
225	BOM1	BOM	15	154165	154173	154173	156059	2_nonsis		1	947	1893	1	2	1	1	0	(3:5)_(4:4aCO)
200	BOM1	BOM	13	487831	489569	489569	490109	2_nonsis		1	1139	2277	1	2	1	1	0	(3:5)_(4:4aCO)
51	BOM1	BOM	4	698788	699229	699280	699436	2_nonsis		52	350	647	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
195	BOM1	BOM	13	113641	114304	115471	115959	2_nonsis		1168	1743	2317	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
166	BOM1	BOM	11	616404	616917	618540	618631	2_nonsis		1624	1925	2226	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
110	BOM1	BOM	7	847727	847980	848688	849134	2_nonsis		709	1058	1406	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
10	BOM1	BOM	2	115894	116084	116947	117293	2_nonsis		864	1131	1398	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
24	BOM1	BOM	3	41852	42410	43346	43513	2_nonsis		937	1299	1660	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
179	BOM1	BOM	12	606928	607451	607458	607531	2_nonsis		8	305	602	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
21	BOM1	BOM	2	742150	742220	742660	742690	2_nonsis		441	490	539	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
239	BOM1	BOM	16	45800	45974	46435	46547	2_nonsis		462	604	746	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
30	BOM1	BOM	4	43482	46115	46818	47365	2_nonsis		704	2293	3882	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
107	BOM1	BOM	7	605648	605710	606561	606799	2_nonsis		852	1001	1150	1	11	1	1	0	(4:4ai)_(3:5)_(4:4bCO)
192	BOM1	BOM	13	18814	20392	21881	22318	2_nonsis		1490	2497	3503	1	11	1	1	0	(4:4ai)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4bCO)_(3:5)_(2:6)_(4:4b)
27	BOM1	BOM	3	218655	218906	219723	219844	2_nonsis		818	1003	1188	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
216	BOM1	BOM	14	237756	237804	238429	238793	2_nonsis		626	831	1036	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
158	BOM1	BOM	11	298637	298924	299201	300874	2_nonsis		278	1257	2236	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
234	BOM1	BOM	15	774457	774673	776223	776725	2_nonsis		1551	1909	2267	1	12	1	1	0	(3:5)_(2:6)_(4:4)_(4:4aCO)
246	BOM1	BOM	16	476851	477152	478714	479396	2_nonsis		1563	2054	2544	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
149	BOM1	BOM	10	723717	723783	725123	725433	2_nonsis		1341	1528	1715	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)
15	BOM1	BOM	2	452218	452891	454336	454401	2_nonsis		1446	1814	2182	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
47	BOM1	BOM	4	480846	480887	482676	482955	2_nonsis		1790	1949	2108	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
252	BOM1	BOM	16	876719	876797	876914	877898	2_nonsis		118	648	1178	1	15	1	1	0	(6:2)_(4:4aCO)
109	BOM1	BOM	7	798380	798397	798848	799244	2_nonsis		452	658	863	1	15	1	1	0	(6:2)_(4:4aCO)
193	BOM1	BOM	13	73368	74014	74014	74346	2_nonsis		1	489	977	1	16	1	1	0	(2:6)_(4:4aCO)
172	BOM1	BOM	12	322903	323570	323570	324050	2_nonsis		1	574	1146	1	16	1	1	0	(2:6)_(4:4aCO)
62	BOM1	BOM	4	1241519	1242168	1242241	1242658	2_nonsis		74	606	1138	1	16	1	1	0	(2:6)_(4:4aCO)
228	BOM1	BOM	15	362851	363553	363824	364095	2_nonsis		272	758	1243	1	16	1	1	0	(2:6)_(4:4aCO)
147	BOM1	BOM	10	503880	504158	504158	506424	2_nonsis		1	1272	2543	1	16	1	1	0	(2:6)_(4:4aCO)
17	BOM1	BOM	2	625298	626092	627055	627259	2_nonsis		964	1462	1960	1	16	1	1	0	(2:6)_(4:4aCO)
168	BOM1	BOM	12	124421	124596	124421	124596	2_nonsis		0	87	174	1	100	1	1	0	(4:4aCO)
53	BOM1	BOM	4	770352	770770	770352	770770	2_nonsis		0	209	417	1	100	1	1	0	(4:4aCO)
220	BOM1	BOM	14	547958	548436	547958	548436	2_nonsis		0	239	477	1	100	1	1	0	(4:4aCO)
233	BOM1	BOM	15	686985	687587	686985	687587	2_nonsis		0	301	601	1	100	1	1	0	(4:4aCO)

13	BOM1	BOM	2	354720	355349	354720	355349	2_nonsis	0	314	628	1	100	1	1	0 (4:4aCO)
58	BOM1	BOM	4	963777	964418	963777	964418	2_nonsis	0	320	640	1	100	1	1	0 (4:4aCO)
222	BOM1	BOM	14	705870	706528	705870	706528	2_nonsis	0	329	657	1	100	1	1	0 (4:4aCO)
187	BOM1	BOM	12	866643	867405	866643	867405	2_nonsis	0	381	761	1	100	1	1	0 (4:4aCO)
111	BOM1	BOM	7	948202	949014	948202	949014	2_nonsis	0	406	811	1	100	1	1	0 (4:4aCO)
243	BOM1	BOM	16	291355	292215	291355	292215	2_nonsis	0	430	859	1	100	1	1	0 (4:4aCO)
134	BOM1	BOM	9	255654	256581	255654	256581	2_nonsis	0	463	926	1	100	1	1	0 (4:4aCO)
238	BOM1	BOM	15	996896	997902	996896	997902	2_nonsis	0	503	1005	1	100	1	1	0 (4:4aCO)
19	BOM1	BOM	2	695479	697455	695479	697455	2_nonsis	0	988	1975	1	100	1	1	0 (4:4aCO)
154	BOM1	BOM	11	138050	140833	138050	140833	2_nonsis	0	1391	2782	1	100	1	1	0 (4:4aCO)
148	BOM1	BOM	10	596891	601293	596891	601293	2_nonsis	0	2201	4401	1	100	1	1	0 (4:4aCO)
188	BOM1	BOM	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0 (4:4aCO)
176	BOM1	BOM	12	439126	439413	441152	441612	2_nonsis	1740	2113	2485	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
189	BOM1	BOM	12	1000203	1000542	1001464	1001833	2_nonsis	923	1276	1629	2	30	1	1	0 (6:2)_(5:3)_(5:3a)_(4:4aCO)
32	BOM1	BOM	4	104069	104854	106899	107966	2_nonsis	2046	2971	3896	2	30	1	1	0 (4:4aCO)_(5:3)_(5:3a)_(4:4a)
99	BOM1	BOM	7	75778	76021	76989	77983	2_nonsis	969	1587	2204	2	30	1	1	0 (5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
191	BOM1	BOM	12	1055872	1056105	1057759	1058607	2_nonsis	1655	2195	2734	2	30	1	1	0 (5:3)_(6:2)_(5:3)_(5:3a)_(4:4aCO)
245	BOM1	BOM	16	381280	381362	381840	381920	2_nonsis	479	559	639	2	31	1	1	0 (3:5)_(5:3a)_(4:4aCO)
72	BOM1	BOM	4	1488904	1489717	1490210	1490249	2_nonsis	494	919	1344	2	31	1	1	0 (3:5)_(2:6)_(3:5)_(5:3a)_(4:4aCO)
142	BOM1	BOM	10	235976	236393	236674	236901	2_nonsis	282	603	924	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
83	BOM1	BOM	5	330953	332219	332482	332992	2_nonsis	264	1151	2038	2	32	1	1	0 (3:5)_(2:6)_(5:3a)_(4:4aCO)
145	BOM1	BOM	10	384052	384310	385510	385772	2_nonsis	1201	1460	1719	2	32	1	1	0 (3:5)_(2:6)_(5:3a)_(4:4aCO)
95	BOM1	BOM	6	247354	247915	249213	249459	2_nonsis	1299	1702	2104	2	32	1	1	0 (5:3)_(4:4aCO)_(5:3a)_(4:4a)
98	BOM1	BOM	7	22405	23215	24468	25442	2_nonsis	1254	2145	3036	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
100	BOM1	BOM	7	82858	84285	85628	86297	2_nonsis	1344	2391	3438	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
185	BOM1	BOM	12	788874	789356	791142	794003	2_nonsis	1787	3458	5128	2	32	1	1	0 (3:5)_(4:4)_(5:3a)_(4:4aCO)
190	BOM1	BOM	12	1009719	1011169	1012226	1013592	2_nonsis	1058	2465	3872	2	32	1	1	0 (5:3)_(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
226	BOM1	BOM	15	309144	309237	311489	312220	2_nonsis	2253	2664	3075	2	32	1	1	0 (5:3)_(4:4)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
130	BOM1	BOM	9	157619	157961	160764	161147	2_nonsis	2804	3166	3527	2	32	1	1	0 (6:2)_(5:3)_(4:4aCO)_(5:3a)_(5:3)_(4:4a)
169	BOM1	BOM	12	233075	234128	235352	235684	2_nonsis	1225	1917	2608	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
236	BOM1	BOM	15	890409	890957	892736	892829	2_nonsis	1780	2100	2419	2	32	1	1	0 (5:3)_(6:2)_(5:3)_(4:4)_(4:4aCO)_(5:3a)_(4:4a)
178	BOM1	BOM	12	600676	601080	604223	604825	2_nonsis	3144	3646	4148	2	32	1	1	0 (3:5)_(2:6)_(3:5)_(4:4aCO)_(5:3a)_(2:6)_(5:3a)_(4:4a)
87	BOM1	BOM	5	473950	474020	476027	476048	2_nonsis	2008	2053	2097	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(2:6)_(3:5a)_(2:6)_(4:4)_(3:5b)_(4:4aCO)
224	BOM1	BOM	15	112140	112969	117525	123864	2_nonsis	4557	8140	11723	2	32	1	1	0 (5:3)_(4:4aCO)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4a)_(5:3b)_(4:4a)
26	BOM1	BOM	3	135329	136159	137021	137201	2_nonsis	863	1367	1871	3	20	1	1	0 (6:2)_(2:6)_(4:4aCO)
219	BOM1	BOM	14	412609	413686	414025	415775	2_nonsis	340	1753	3165	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
60	BOM1	BOM	4	1061165	1061318	1062037	1062818	2_nonsis	720	1186	1652	3	20	1	1	0 (2:6)_(3:5)_(5:3)_(4:4aCO)
120	BOM1	BOM	8	238630	238746	239033	239430	2_nonsis	288	544	799	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(5:3)_(4:4aCO)
9	BOM1	BOM	2	75576	75822	77073	77094	2_nonsis	1252	1385	1517	3	20	1	1	0 (3:5)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
197	BOM1	BOM	13	227027	227957	228901	229206	2_nonsis	945	1562	2178	3	20	1	1	0 (2:6)_(4:4aCO)_(2:6)_(5:3)_(4:4a)
162	BOM1	BOM	11	377390	377792	379287	379301	2_nonsis	1496	1703	1910	3	20	1	1	0 (3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)
77	BOM1	BOM	5	70969	71501	73131	73474	2_nonsis	1631	2068	2504	3	20	1	1	0 (4:4aCO)_(5:3)_(4:4a)_(3:5)_(4:4a)
129	BOM1	BOM	9	141022	141141	143092	143302	2_nonsis	1952	2116	2279	3	20	1	1	0 (3:5)_(2:6)_(4:4aCO)_(5:3)_(4:4a)
105	BOM1	BOM	7	436065	436337	438470	438674	2_nonsis	2134	2371	2608	3	20	1	1	0 (2:6)_(4:4aCO)_(5:3)_(6:2)_(4:4a)
204	BOM1	BOM	13	700620	700942	702308	702452	2_nonsis	1367	1599	1831	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(4:4)_(5:3)_(4:4aCO)
54	BOM1	BOM	4	848136	848341	849796	850164	2_nonsis	1456	1742	2027	3	20	1	1	0 (6:2)_(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
104	BOM1	BOM	7	398049	398572	399836	400713	2_nonsis	1265	1964	2663	3	20	1	1	0 (2:6)_(4:4)_(5:3)_(3:5)_(4:4)_(4:4aCO)
38	BOM1	BOM	4	231260	231400	233237	233528	2_nonsis	1838	2053	2267	3	20	1	1	0 (5:3)_(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
249	BOM1	BOM	16	700101	700285	703359	703434	2_nonsis	3075	3204	3332	3	20	1	1	0 (5:3)_(4:4)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
92	BOM1	BOM	6	85636	85688	87512	87585	2_nonsis	1825	1887	1948	3	20	1	1	0 (2:6)_(4:4aCO)_(6:2)_(5:3)_(4:4a)_(5:3a)_(4:4a)
143	BOM1	BOM	10	347630	347852	349631	350244	2_nonsis	1780	2197	2613	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(5:3)_(6:2)_(5:3)_(4:4aCO)
165	BOM1	BOM	11	573486	573513	576522	576947	2_nonsis	3010	3235	3460	3	20	1	1	0 (5:3)_(4:4)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
136	BOM1	BOM	9	357298	357540	360876	360955	2_nonsis	3337	3497	3656	3	20	1	1	0 (2:6)_(3:5)_(4:4aCO)_(5:3)_(4:4a)_(5:3a)_(4:4a)
208	BOM1	BOM	13	850650	851409	854292	854948	2_nonsis	2884	3591	4297	3	20	1	1	0 (3:5)_(5:3a)_(2:6)_(3:5a)_(4:4)_(5:3)_(4:4aCO)
93	BOM1	BOM	6	193973	194109	195471	195636	2_nonsis	1363	1513	1662	3	20	1	1	0 (6:2)_(5:3)_(6:2)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
175	BOM1	BOM	12	416464	416793	419081	419132	2_nonsis	2289	2478	2667	3	20	1	1	0 (3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)_(3:5a)_(2:6)_(3:5a)_(4:4a)
43	BOM1	BOM	4	372201	372238	375384	375458	2_nonsis	3147	3202	3256	3	20	1	1	0 (2:6)_(4:4)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(6:2)_(5:3a)_(4:4a)
7	BOM1	BOM	1	180509	180583	181957	182519	2_nonsis	1375	1692	2009	3	20	1	1	0 (3:5)_(2:6)_(4:4)_(3:5)_(4:4)_(4:4)_(2:6)_(4:4)_(5:3)_(2:6)_(4:4aCO)
173	BOM1	BOM	12	340008	340119	341926	341974	2_nonsis	1808	1887	1965	3	21	1	1	0 (4:4ai)_(3:5)_(4:4)_(2:6)_(6:2)_(4:4bCO)
81	BOM1	BOM	5	223802	224276	230208	230344	2_nonsis	5933	6237	6541	3	21	1	1	0 (5:3)_(4:4)_(3:5)_(5:3)_(3:5)_(2:6)_(3:5)_(4:4ai)_(3:5)_(4:4bCO)_(3:5)_(4:4b)

28	BOM1	BOM	3	224261	224961	226498	228130	2_sis		1538	2703	3868	0	1	2	0	2 (6:2i)_(5:3)_(5:3a)_(4:4)_(5:3b)_(4:4)
68	BOM1	BOM	4	1446792	1446979	1447313	1447694	2_sis		335	618	901	0	1	2	0	2 (3:5)_(4:4)_(3:5a)_(4:4)
137	BOM1	BOM	9	412645	415204	416627	416694	2_sis		1424	2736	4048	0	1	2	0	2 (6:2i)_(5:3)_(4:4)
3	BOM1	BOM	1	90516	90665	95139	95169	3	4475	4564	4652	0	2	2	1	1 (5:3)_(4:4aCO)_(3:5)_(4:4a)
29	BOM1	BOM	4	34237	34987	39986	40439	4	5000	5601	6201	0	2	2	1	1 (5:3)_(4:4ai)_(5:3)_(5:3a)_(6:2i)_(5:3b)_(4:4ai)_(4:4bCO)_(3:5)_(4:4b)
33	BOM1	BOM	4	137047	137547	139926	140600	3	2380	2966	3552	0	2	2	1	1 (6:2)_(2:6)_(5:3)_(6:2)_(4:4)_(4:4aCO)
48	BOM1	BOM	4	613630	613738	617421	617533	3	3684	3793	3902	0	2	2	1	1 (3:5)_(2:6)_(3:5)_(4:4)_(3:5)_(4:4ai)_(3:5a)_(2:6)_(3:5b)_(3:5c)_(4:4bi)_(3:5d)_(4:4cCO)_(5:3)_(4:4c)
119	BOM1	BOM	8	140123	142800	144393	144688	3	1594	3079	4564	0	2	2	1	1 (4:4aCO)_(2:6)_(2:6ai)_(3:5)_(4:4a)_(3:5)_(4:4a)
122	BOM1	BOM	8	360186	360415	362567	362829	4	2153	2398	2642	0	2	2	1	1 (3:5)_(4:4)_(3:5)_(5:3)_(4:4ai)_(4:4bi)_(4:4cCO)
126	BOM1	BOM	9	98294	98932	99653	99715	3	722	1071	1420	0	2	2	1	1 (4:4ai)_(5:3)_(4:4)_(4:4bCO)
248	BOM1	BOM	16	642789	643790	644963	645571	3	1174	1978	2781	0	2	2	1	1 (5:3)_(4:4)_(4:4aCO)
4	BOM1	BOM	1	129075	129476	130975	132066	4	1500	2245	2990	0	3	2	2	0 (3:5)_(6:2i)_(4:4aCO)_(6:2ai)_(5:3)_(4:4bCO)
368	BOM1	BOM	7	1042643	1043244	1064130	1090940	3	20887	34592	48296	0	4	1	NA	NA 2:6_2:6
69	BOM2	BOM	6	119127	119224	119229	119266	1	6	72	138	1	1	1	0	1 05:03
78	BOM2	BOM	7	156075	156105	156105	156252	1	1	89	176	1	1	1	0	1 05:03
102	BOM2	BOM	8	297072	297365	297365	297421	1	1	175	348	1	1	1	0	1 05:03
15	BOM2	BOM	2	419495	419604	419604	419859	1	1	182	363	1	1	1	0	1 05:03
91	BOM2	BOM	7	766129	766363	766363	766502	1	1	187	372	1	1	1	0	1 05:03
192	BOM2	BOM	14	427295	427451	427451	427715	1	1	210	419	1	1	1	0	1 05:03
178	BOM2	BOM	13	517348	517743	517743	517791	1	1	222	442	1	1	1	0	1 05:03
10	BOM2	BOM	2	292212	292254	292401	292524	1	148	230	311	1	1	1	0	1 05:03
73	BOM2	BOM	7	48448	48835	48835	49026	1	1	289	577	1	1	1	0	1 05:03
87	BOM2	BOM	7	581464	581660	581814	581949	1	155	320	484	1	1	1	0	1 05:03
195	BOM2	BOM	14	715182	715380	715430	715791	1	51	330	608	1	1	1	0	1 05:03
220	BOM2	BOM	16	320885	321573	321573	321586	1	1	351	700	1	1	1	0	1 05:03
81	BOM2	BOM	7	271853	272144	272144	272568	1	1	358	714	1	1	1	0	1 05:03
19	BOM2	BOM	3	40637	40987	41096	41289	1	110	381	651	1	1	1	0	1 05:03
52	BOM2	BOM	4	1352454	1353241	1353245	1353261	1	5	406	806	1	1	1	0	1 05:03
34	BOM2	BOM	4	497463	498138	498138	498305	1	1	421	841	1	1	1	0	1 05:03
40	BOM2	BOM	4	722085	722407	722687	722776	1	281	486	690	1	1	1	0	1 05:03
43	BOM2	BOM	4	945712	946425	946452	946721	1	28	518	1008	1	1	1	0	1 05:03
113	BOM2	BOM	9	165195	166074	166141	166175	1	68	524	979	1	1	1	0	1 05:03
169	BOM2	BOM	12	1014227	1014332	1014670	1014976	1	339	544	748	1	1	1	0	1 05:03
222	BOM2	BOM	16	404106	404554	404667	405120	1	114	564	1013	1	1	1	0	1 05:03
180	BOM2	BOM	13	540798	541071	541511	541716	1	441	679	917	1	1	1	0	1 05:03
100	BOM2	BOM	8	190024	190339	190671	191072	1	333	690	1047	1	1	1	0	1 05:03
163	BOM2	BOM	12	623566	623758	623971	624838	1	214	743	1271	1	1	1	0	1 05:03
143	BOM2	BOM	11	513454	514126	514315	514792	1	190	764	1337	1	1	1	0	1 05:03
48	BOM2	BOM	4	1268647	1269918	1269918	1270457	1	1	905	1809	1	1	1	0	1 05:03
165	BOM2	BOM	12	778158	779222	779607	780114	1	386	1171	1955	1	1	1	0	1 05:03
214	BOM2	BOM	16	56155	56290	56290	63220	1	1	3533	7064	1	1	1	0	1 05:03
22	BOM2	BOM	3	77849	77866	77866	77900	1	1	26	50	1	2	1	0	1 03:05
109	BOM2	BOM	9	117336	117411	117411	117413	1	1	39	76	1	2	1	0	1 03:05
225	BOM2	BOM	16	678652	678709	678709	678816	1	1	82	163	1	2	1	0	1 03:05
144	BOM2	BOM	11	581803	581827	581827	582019	1	1	108	215	1	2	1	0	1 03:05
13	BOM2	BOM	2	393237	393340	393340	393507	1	1	135	269	1	2	1	0	1 03:05
12	BOM2	BOM	2	382571	382644	382823	382880	1	180	244	308	1	2	1	0	1 03:05
201	BOM2	BOM	15	231814	232193	232193	232303	1	1	245	488	1	2	1	0	1 03:05
90	BOM2	BOM	7	650898	651268	651268	651425	1	1	264	526	1	2	1	0	1 03:05
139	BOM2	BOM	11	340714	340743	340811	341198	1	69	276	483	1	2	1	0	1 03:05
174	BOM2	BOM	13	236240	236370	236410	236819	1	41	310	578	1	2	1	0	1 03:05
77	BOM2	BOM	7	123839	124322	124322	124460	1	1	311	620	1	2	1	0	1 03:05
99	BOM2	BOM	8	121987	122169	122169	122633	1	1	323	645	1	2	1	0	1 03:05
70	BOM2	BOM	6	155336	155718	155718	155985	1	1	325	648	1	2	1	0	1 03:05
127	BOM2	BOM	10	317305	317491	317491	317989	1	1	342	683	1	2	1	0	1 03:05
106	BOM2	BOM	9	41664	41898	41980	42365	1	83	392	700	1	2	1	0	1 03:05
45	BOM2	BOM	4	1055678	1055799	1056079	1056232	1	281	417	553	1	2	1	0	1 03:05
57	BOM2	BOM	5	209424	209789	209789	210347	1	1	462	922	1	2	1	0	1 03:05
116	BOM2	BOM	9	248675	248948	249032	249546	1	85	478	870	1	2	1	0	1 03:05
121	BOM2	BOM	9	380279	380666	380999	381073	1	334	564	793	1	2	1	0	1 03:05

112	BOM2	BOM	9	160585	160764	161147	161384	1	384	591	798	1	2	1	0	1 03:05
216	BOM2	BOM	16	106600	107304	107496	107754	1	193	673	1153	1	2	1	0	1 03:05
153	BOM2	BOM	12	252779	252885	253274	253791	1	390	701	1011	1	2	1	0	1 03:05
186	BOM2	BOM	14	39652	40306	40430	41146	1	125	809	1493	1	2	1	0	1 03:05
64	BOM2	BOM	5	460411	461582	461594	462226	1	13	914	1814	1	2	1	0	1 03:05
142	BOM2	BOM	11	477203	477776	477776	479195	1	1	996	1991	1	2	1	0	1 03:05
75	BOM2	BOM	7	97616	98124	98613	100362	1	490	1618	2745	1	2	1	0	1 03:05
110	BOM2	BOM	9	136083	136100	137266	138115	1	1167	1599	2031	1	3	1	0	1 5:3_4:4_5:3
97	BOM2	BOM	8	84777	84820	85033	85109	1	214	273	331	1	4	1	0	1 3:5_2:6_3:5
209	BOM2	BOM	15	638644	639033	639159	639225	1	127	354	580	1	7	1	0	1 6:2_5:3
149	BOM2	BOM	12	115422	116205	116613	116647	1	409	817	1224	1	7	1	0	1 5:3_6:2
122	BOM2	BOM	9	396753	396773	397178	397230	1	406	441	476	1	7	1	0	1 6:2_4:4_6:2
157	BOM2	BOM	12	301472	301852	302144	302282	1	293	551	809	1	7	1	0	1 5:3_4:4_6:2
50	BOM2	BOM	4	1332857	1333408	1334142	1334337	1	735	1107	1479	1	8	1	0	1 3:5_2:6
187	BOM2	BOM	14	51050	51868	52659	52850	1	792	1296	1799	1	8	1	0	1 2:6_4:4_3:5
170	BOM2	BOM	12	1022675	1022756	1024168	1024747	1	1413	1742	2071	1	8	1	0	1 3:5_4:4_2:6
31	BOM2	BOM	4	302250	303051	303504	303806	1	454	1005	1555	1	8	1	0	1 2:6_4:4_3:5_4:4_3:5
160	BOM2	BOM	12	514832	514961	514961	515064	1	1	116	231	1	10.1	1	0	1 02:06
66	BOM2	BOM	5	512058	512295	512664	512863	1	370	587	804	2	11	1	0	1 5:3_5:3a
162	BOM2	BOM	12	573671	573804	574726	574950	1	923	1101	1278	2	11	1	0	1 5:3_5:3a
168	BOM2	BOM	12	1001464	1001833	1003348	1004176	1	1516	2114	2711	2	11	1	0	1 5:3_5:3a
154	BOM2	BOM	12	258730	259051	261119	261578	1	2069	2458	2847	2	11	1	0	1 5:3_5:3a
11	BOM2	BOM	2	323214	323896	324185	324220	1	290	648	1005	2	12	1	0	1 3:5_3:5a
68	BOM2	BOM	6	106222	106492	107042	107101	1	551	715	878	2	12	1	0	1 3:5_3:5a
82	BOM2	BOM	7	370641	370822	371625	372033	1	804	1098	1391	2	12	1	0	1 3:5_3:5a
118	BOM2	BOM	9	281719	281795	283713	284253	1	1919	2226	2533	2	12	1	0	1 3:5_3:5a
141	BOM2	BOM	11	428081	428986	429656	429690	1	671	1140	1608	2	13	1	0	1 5:3_5:3a_6:2
8	BOM2	BOM	2	63243	63284	65309	65480	1	2026	2131	2236	2	13	1	0	1 5:3_5:3a_4:4_5:3a
196	BOM2	BOM	15	39607	39768	41050	41221	1	1283	1448	1613	2	14	1	0	1 3:5_3:5a_2:6
156	BOM2	BOM	12	289291	289538	290328	290359	1	791	929	1067	2	14	1	0	1 3:5_3:5a_4:4_3:5a
85	BOM2	BOM	7	442874	442935	444107	444236	1	1173	1267	1361	2	14	1	0	1 3:5_3:5a_2:6_3:5a
115	BOM2	BOM	9	175960	176421	177853	178160	1	1433	1816	2199	2	14	1	0	1 3:5_4:4_3:5_3:5a
7	BOM2	BOM	2	27832	28538	29377	36302	1	840	4655	8469	2	14	1	0	1 3:5_3:5a_4:4_2:6
103	BOM2	BOM	8	360504	360630	360746	360898	1	117	255	393	2	15	1	0	1 5:3_4:4_5:3a
199	BOM2	BOM	15	185951	186289	186970	187008	1	682	869	1056	2	15	1	0	1 5:3_4:4_5:3a
59	BOM2	BOM	5	325958	326031	327059	327079	1	1029	1075	1120	2	15	1	0	1 5:3_4:4_5:3a
217	BOM2	BOM	16	113385	114050	114957	115228	1	908	1375	1842	2	15	1	0	1 5:3_4:4_5:3a
2	BOM2	BOM	1	75520	76205	77433	77528	1	1229	1618	2007	2	15	1	0	1 5:3_4:4_5:3a
203	BOM2	BOM	15	295281	295611	297107	297302	1	1497	1759	2020	2	15	1	0	1 5:3_4:4_5:3a
146	BOM2	BOM	12	20699	20715	21252	21693	1	538	766	993	2	16	1	0	1 3:5_4:4_3:5a
152	BOM2	BOM	12	233075	234128	234633	234668	1	506	1049	1592	2	16	1	0	1 3:5_4:4_3:5a
35	BOM2	BOM	4	538829	538864	539680	540228	1	817	1108	1398	2	16	1	0	1 3:5_4:4_3:5a
177	BOM2	BOM	13	513553	513778	514431	515212	1	654	1156	1658	2	16	1	0	1 3:5_4:4_3:5a
158	BOM2	BOM	12	387156	387519	388930	388950	1	1412	1603	1793	2	16	1	0	1 3:5_4:4_3:5a
207	BOM2	BOM	15	533520	533636	534200	536230	1	565	1637	2709	2	16	1	0	1 3:5_4:4_3:5a
41	BOM2	BOM	4	834537	834720	836436	836558	1	1717	1869	2020	2	16	1	0	1 3:5_4:4_3:5a
61	BOM2	BOM	5	335262	335310	335874	336237	1	565	770	974	2	18	1	0	1 2:6_3:5_4:4_3:5a
80	BOM2	BOM	7	196769	196840	198003	198476	1	1164	1435	1706	2	19	1	0	1 5:3_6:2_5:3a
108	BOM2	BOM	9	99043	99647	99846	100355	1	200	756	1311	2	23	1	0	1 5:3_4:4_6:2_5:3a
86	BOM2	BOM	7	472321	472609	473748	473949	2_nonsis	1140	1384	1627	3	30	1	0	1 5:3_5:3a
25	BOM2	BOM	3	211204	211348	213768	213849	2_nonsis	2421	2533	2644	3	30	1	0	1 3:5_4:4_3:5a_5:3_5:3a
136	BOM2	BOM	11	99646	100443	100670	101183	2_nonsis	228	882	1536	3	31	1	0	1 4:4ai
29	BOM2	BOM	4	155900	156500	156591	157148	2_nonsis	92	670	1247	3	31	1	0	1 4:4ai_3:5
23	BOM2	BOM	3	117992	118273	118751	119120	2_nonsis	479	803	1127	3	31	1	0	1 4:4ai_3:5_3:5a
44	BOM2	BOM	4	1013843	1013924	1014713	1015229	2_nonsis	790	1088	1385	3	31	1	0	1 5:3_4:4_4:4ai
123	BOM2	BOM	10	34093	36217	37127	37895	2_nonsis	911	2356	3801	3	31	1	0	1 4:4ai_5:3_6:2_5:3
36	BOM2	BOM	4	550672	550699	552846	553583	2_nonsis	2148	2529	2910	3	31	1	0	1 3:5_4:4_2:6_5:3_4:4ai
107	BOM2	BOM	9	53832	54480	56514	57063	2_nonsis	2035	2633	3230	3	31	1	0	1 5:3_4:4_5:3a_4:4ai_5:3a_2:6
172	BOM2	BOM	13	77019	77135	77135	77482	2_nonsis	1	232	462	1	1	1	1	0 (5:3)_(4:4aCO)
72	BOM2	BOM	6	239066	239639	239639	239696	2_nonsis	1	315	629	1	1	1	1	0 (5:3)_(4:4aCO)

135	BOM2	BOM	11	71211	71541	71541	71930	2_nonsis	1	360	718	1	1	1	1	0	(5:3)_(4:4aCO)
6	BOM2	BOM	2	24379	24823	24920	25246	2_nonsis	98	482	866	1	1	1	1	0	(5:3)_(4:4aCO)
227	BOM2	BOM	16	841702	842073	842086	842864	2_nonsis	14	588	1161	1	1	1	1	0	(5:3)_(4:4aCO)
166	BOM2	BOM	12	836343	837497	837595	837962	2_nonsis	99	859	1618	1	1	1	1	0	(5:3)_(4:4aCO)
125	BOM2	BOM	10	187746	188331	188961	189017	2_nonsis	631	951	1270	1	1	1	1	0	(5:3)_(4:4aCO)
17	BOM2	BOM	2	703264	703780	704282	704922	2_nonsis	503	1080	1657	1	1	1	1	0	(5:3)_(4:4aCO)
111	BOM2	BOM	9	141514	141703	141703	141911	2_nonsis	1	199	396	1	2	1	1	0	(3:5)_(4:4aCO)
26	BOM2	BOM	3	223339	223676	223676	224009	2_nonsis	1	335	669	1	2	1	1	0	(3:5)_(4:4aCO)
224	BOM2	BOM	16	676361	676691	676743	677025	2_nonsis	53	358	663	1	2	1	1	0	(3:5)_(4:4aCO)
190	BOM2	BOM	14	204995	205138	205208	205814	2_nonsis	71	445	818	1	2	1	1	0	(3:5)_(4:4aCO)
185	BOM2	BOM	13	873246	874942	875718	876530	2_nonsis	777	2030	3283	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
20	BOM2	BOM	3	51650	52350	53316	53891	2_nonsis	967	1604	2240	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
51	BOM2	BOM	4	1347683	1349666	1350213	1350342	2_nonsis	548	1603	2658	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
129	BOM2	BOM	10	466454	467010	467589	469453	2_nonsis	580	1789	2998	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
228	BOM2	BOM	16	921117	921154	921490	921713	2_nonsis	337	466	595	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
171	BOM2	BOM	12	1032869	1033274	1034221	1034264	2_nonsis	948	1171	1394	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
62	BOM2	BOM	5	397892	398975	399399	400005	2_nonsis	425	1269	2112	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
89	BOM2	BOM	7	617675	617861	618236	618272	2_nonsis	376	486	596	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
4	BOM2	BOM	1	107970	108457	108718	108763	2_nonsis	262	527	792	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
49	BOM2	BOM	4	1300388	1300582	1302220	1302530	2_nonsis	1639	1890	2141	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
9	BOM2	BOM	2	220055	220122	220817	227201	2_nonsis	696	3921	7145	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
197	BOM2	BOM	15	83853	84190	84388	84463	2_nonsis	199	404	609	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
120	BOM2	BOM	9	338050	338086	338465	338670	2_nonsis	380	500	619	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
175	BOM2	BOM	13	306097	306566	307804	308296	2_nonsis	1239	1719	2198	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
28	BOM2	BOM	4	33135	33253	34987	35378	2_nonsis	1735	1989	2242	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
27	BOM2	BOM	3	260698	261312	263025	264441	2_nonsis	1714	2728	3742	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
179	BOM2	BOM	13	538839	539007	539282	539498	2_nonsis	276	467	658	1	11	1	1	0	(5:3)_(4:4ai)_(4:4bCO)
132	BOM2	BOM	10	661017	661171	662479	663134	2_nonsis	1309	1713	2116	1	11	1	1	0	(4:4ai)_(3:5)_(4:4bCO)
117	BOM2	BOM	9	267764	268176	268278	268466	2_nonsis	103	402	701	1	11	1	1	0	(3:5)_(4:4ai)_(3:5)_(4:4bCO)
14	BOM2	BOM	2	416426	417214	417468	417889	2_nonsis	255	859	1462	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
184	BOM2	BOM	13	798261	798332	798889	799519	2_nonsis	558	908	1257	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
93	BOM2	BOM	7	914816	915691	916059	916953	2_nonsis	369	1253	2136	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
114	BOM2	BOM	9	170156	170408	171637	171711	2_nonsis	1230	1392	1554	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
210	BOM2	BOM	15	770868	771765	772232	773455	2_nonsis	468	1527	2586	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
16	BOM2	BOM	2	535775	535946	536146	536197	2_nonsis	201	311	421	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
67	BOM2	BOM	6	73933	74035	75475	76048	2_nonsis	1441	1778	2114	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
182	BOM2	BOM	13	661888	662059	663903	663987	2_nonsis	1845	1972	2098	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
226	BOM2	BOM	16	681542	681719	684164	685433	2_nonsis	2446	3168	3890	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4aCO)
98	BOM2	BOM	8	93770	96126	98284	98376	2_nonsis	2159	3382	4605	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
202	BOM2	BOM	15	284521	284983	285663	286242	2_nonsis	681	1201	1720	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
188	BOM2	BOM	14	86514	86730	88100	88950	2_nonsis	1371	1903	2435	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(4:4aCO)
38	BOM2	BOM	4	615449	615581	616214	616380	2_nonsis	634	782	930	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
53	BOM2	BOM	4	1435091	1435647	1436962	1437126	2_nonsis	1316	1675	2034	1	12	1	1	0	(4:4aCO)_(6:2)_(5:3)_(4:4a)_(5:3)_(4:4a)
183	BOM2	BOM	13	683958	684171	684171	684406	2_nonsis	1	224	447	1	15	1	1	0	(6:2)_(4:4aCO)
134	BOM2	BOM	11	34159	34378	34444	34686	2_nonsis	67	297	526	1	15	1	1	0	(6:2)_(4:4aCO)
71	BOM2	BOM	6	203253	203623	204061	204282	2_nonsis	439	734	1028	1	15	1	1	0	(6:2)_(4:4aCO)
213	BOM2	BOM	16	49049	49169	49169	50572	2_nonsis	1	762	1522	1	15	1	1	0	(6:2)_(4:4aCO)
3	BOM2	BOM	1	92891	93563	93563	94472	2_nonsis	1	791	1580	1	15	1	1	0	(6:2)_(4:4aCO)
130	BOM2	BOM	10	570822	573135	573135	573950	2_nonsis	1	1564	3127	1	15	1	1	0	(6:2)_(4:4aCO)
92	BOM2	BOM	7	801970	802249	802249	802512	2_nonsis	1	271	541	1	16	1	1	0	(2:6)_(4:4aCO)
60	BOM2	BOM	5	332482	332992	332992	333114	2_nonsis	1	316	631	1	16	1	1	0	(2:6)_(4:4aCO)
88	BOM2	BOM	7	609958	610218	610674	611145	2_nonsis	457	822	1186	1	16	1	1	0	(2:6)_(4:4aCO)
181	BOM2	BOM	13	588927	589273	588927	589273	2_nonsis	0	173	345	1	100	1	1	0	(4:4aCO)
58	BOM2	BOM	5	225841	226347	225841	226347	2_nonsis	0	253	505	1	100	1	1	0	(4:4aCO)
39	BOM2	BOM	4	719896	720645	719896	720645	2_nonsis	0	374	748	1	100	1	1	0	(4:4aCO)
221	BOM2	BOM	16	371914	372742	371914	372742	2_nonsis	0	414	827	1	100	1	1	0	(4:4aCO)
79	BOM2	BOM	7	192332	193477	192332	193477	2_nonsis	0	572	1144	1	100	1	1	0	(4:4aCO)
194	BOM2	BOM	14	701618	702991	701618	702991	2_nonsis	0	686	1372	1	100	1	1	0	(4:4aCO)
193	BOM2	BOM	14	542443	543829	542443	543829	2_nonsis	0	693	1385	1	100	1	1	0	(4:4aCO)
105	BOM2	BOM	8	484090	485522	484090	485522	2_nonsis	0	716	1431	1	100	1	1	0	(4:4aCO)

223	BOM2	BOM	16	465383	466824	465383	466824	2_nonsis		0	720	1440	1	100	1	1	0	(4:4aCO)
76	BOM2	BOM	7	100529	102955	100529	102955	2_nonsis		0	1213	2425	1	100	1	1	0	(4:4aCO)
137	BOM2	BOM	11	235115	238513	235115	238513	2_nonsis		0	1699	3397	1	100	1	1	0	(4:4aCO)
24	BOM2	BOM	3	171207	174943	171207	174943	2_nonsis		0	1868	3735	1	100	1	1	0	(4:4aCO)
131	BOM2	BOM	10	601293	609171	601293	609171	2_nonsis		0	3939	7877	1	100	1	1	0	(4:4aCO)
54	BOM2	BOM	4	1505138	1505479	1506992	1507780	2_nonsis		1514	2078	2641	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
147	BOM2	BOM	12	28820	29085	30375	30558	2_nonsis		1291	1514	1737	2	30	1	1	0	(5:3)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
42	BOM2	BOM	4	923952	924026	925318	925618	2_nonsis		1293	1479	1665	2	30	1	1	0	(5:3)_(5:3a)_(4:4)_(6:2)_(4:4)_(4:4aCO)
191	BOM2	BOM	14	364020	364611	366762	367502	2_nonsis		2152	2817	3481	2	30	1	1	0	(6:2)_(4:4aCO)_(6:2)_(5:3)_(5:3a)_(4:4a)
200	BOM2	BOM	15	220116	220335	221206	221576	2_nonsis		872	1166	1459	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
124	BOM2	BOM	10	69523	69580	70072	70786	2_nonsis		493	878	1262	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
74	BOM2	BOM	7	53982	54056	55107	55263	2_nonsis		1052	1166	1280	2	32	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
215	BOM2	BOM	16	74885	74937	76316	76413	2_nonsis		1380	1454	1527	2	32	1	1	0	(3:5)_(4:4aCO)_(3:5a)_(4:4a)_(3:5a)_(4:4a)
133	BOM2	BOM	10	704861	704987	706608	707018	2_nonsis		1622	1889	2156	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4)_(5:3)_(4:4aCO)
150	BOM2	BOM	12	135409	135677	137012	137313	2_nonsis		1336	1620	1903	2	32	1	1	0	(3:5)_(4:4ai)_(4:4bCO)_(2:6)_(4:4b)_(3:5a)_(4:4b)
176	BOM2	BOM	13	387879	388308	392173	392209	2_nonsis		3866	4098	4329	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(4:4)_(2:6)_(3:5)_(2:6)_(3:5b)_(4:4aCO)_(3:5b)_(4:4a)_(3:5b)_(4:4a)
212	BOM2	BOM	15	1061185	1061339	1061899	1061951	2_nonsis		561	663	765	3	20	1	1	0	(6:2)_(3:5)_(4:4aCO)
148	BOM2	BOM	12	98655	99028	100126	100150	2_nonsis		1099	1297	1494	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
104	BOM2	BOM	8	380348	380530	381058	381424	2_nonsis		529	802	1075	3	20	1	1	0	(2:6)_(3:5)_(5:3)_(4:4aCO)
101	BOM2	BOM	8	236251	237146	237633	238170	2_nonsis		488	1203	1918	3	20	1	1	0	(6:2)_(5:3)_(3:5)_(4:4aCO)
198	BOM2	BOM	15	91592	91686	93175	93845	2_nonsis		1490	1871	2252	3	20	1	1	0	(2:6)_(4:4aCO)_(5:3)_(4:4a)
37	BOM2	BOM	4	573947	574093	575468	577551	2_nonsis		1376	2490	3603	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
56	BOM2	BOM	5	124517	124905	125756	125939	2_nonsis		852	1137	1421	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(5:3)_(4:4aCO)
173	BOM2	BOM	13	165218	166349	167027	167431	2_nonsis		679	1446	2212	3	20	1	1	0	(5:3)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
159	BOM2	BOM	12	414993	415537	417465	417575	2_nonsis		1929	2255	2581	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
218	BOM2	BOM	16	169911	170076	172192	172402	2_nonsis		2117	2304	2490	3	20	1	1	0	(3:5)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
30	BOM2	BOM	4	160479	160731	163327	163439	2_nonsis		2597	2778	2959	3	20	1	1	0	(5:3)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
161	BOM2	BOM	12	560519	561781	563822	564068	2_nonsis		2042	2795	3548	3	20	1	1	0	(3:5)_(3:5a)_(3:5)_(5:3)_(4:4aCO)
46	BOM2	BOM	4	1059380	1059396	1062037	1062818	2_nonsis		2642	3040	3437	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(3:5)_(4:4aCO)
119	BOM2	BOM	9	329125	332459	333581	334640	2_nonsis		1123	3319	5514	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(5:3)_(4:4a)
96	BOM2	BOM	8	10261	10615	11625	11689	2_nonsis		1011	1219	1427	3	20	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)_(5:3)_(4:4a)
65	BOM2	BOM	5	489897	490102	491262	491327	2_nonsis		1161	1295	1429	3	20	1	1	0	(2:6)_(5:3)_(3:5)_(4:4aCO)_(5:3a)_(4:4a)
219	BOM2	BOM	16	213190	213534	215126	215175	2_nonsis		1593	1789	1984	3	20	1	1	0	(4:4aCO)_(2:6)_(6:2)_(4:4a)_(5:3)_(4:4a)
206	BOM2	BOM	15	494326	494461	496163	496422	2_nonsis		1703	1899	2095	3	20	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(6:2)_(4:4aCO)
140	BOM2	BOM	11	379301	379423	381058	381640	2_nonsis		1636	1987	2338	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)_(2:6)_(3:5a)_(4:4a)
47	BOM2	BOM	4	1078009	1078458	1079984	1080788	2_nonsis		1527	2153	2778	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
145	BOM2	BOM	11	606370	606560	609738	610232	2_nonsis		3179	3520	3861	3	20	1	1	0	(5:3)_(4:4)_(6:2)_(5:3a)_(3:5)_(4:4aCO)
32	BOM2	BOM	4	312186	312250	313644	313728	2_nonsis		1395	1468	1541	3	20	1	1	0	(2:6)_(3:5)_(5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
94	BOM2	BOM	7	1009812	1010365	1012544	1012661	2_nonsis		2180	2514	2848	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(4:4aCO)_(3:5)_(3:5a)_(4:4a)
33	BOM2	BOM	4	408894	410728	412574	413313	2_nonsis		1847	3133	4418	3	20	1	1	0	(5:3)_(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
84	BOM2	BOM	7	410531	411461	414265	414479	2_nonsis		2805	3376	3947	3	20	1	1	0	(3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
138	BOM2	BOM	11	258771	258873	260530	260745	2_nonsis		1658	1816	1973	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
5	BOM2	BOM	1	178682	178989	180747	180881	2_nonsis		1759	1979	2198	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(5:3)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
126	BOM2	BOM	10	208377	208641	211991	212108	2_nonsis		3351	3541	3730	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(3:5a)_(4:4aCO)_(3:5b)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4a)
151	BOM2	BOM	12	210240	210476	212081	212681	2_nonsis		1606	2023	2440	3	21	1	1	0	(4:4ai)_(5:3)_(2:6)_(4:4bCO)
1	BOM2	BOM	1	32989	33040	36898	37019	2_nonsis		3859	3944	4029	3	21	1	1	0	(5:3)_(3:5)_(5:3)_(4:4ai)_(3:5)_(4:4bCO)
189	BOM2	BOM	14	195358	195766	199432	199570	2_nonsis		3667	3939	4211	3	21	1	1	0	(3:5)_(4:4ai)_(5:3)_(6:2)_(5:3)_(4:4)_(4:4bi)_(5:3)_(4:4cCO)
63	BOM2	BOM	5	441963	442012	443395	449846	2_sis		1384	4633	7882	0	1	2	0	2	(5:3)_(4:4)_(6:2)_(4:4)
95	BOM2	BOM	7	1021077	1021490	1022816	1023234	2_sis		1327	1742	2156	0	1	2	0	2	(3:5)_(4:4)_(2:6i)_(3:5a)_(2:6a)_(3:5a)_(3:5b)_(4:4)
18	BOM2	BOM	2	741097	741197	744063	744356		3	2867	3063	3258	0	2	2	1	1	(3:5)_(4:4)_(2:6)_(3:5)_(2:6ai)_(1:7)_(2:6)_(2:6b)_(3:5a)_(4:4aCO)
21	BOM2	BOM	3	73255	73479	75546	75892		4	2068	2352	2636	0	2	2	1	1	(3:5)_(3:5a)_(3:5b)_(4:4aCO)_(5:3)_(4:4a)
55	BOM2	BOM	5	54453	55841	58346	58866		3	2506	3459	4412	0	2	2	1	1	(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)_(2:6i)_(4:4a)_(3:5)_(3:5a)_(4:4a)
83	BOM2	BOM	7	383348	383573	385570	386428		3	1998	2539	3079	0	2	2	1	1	(3:5)_(2:6)_(4:4aCO)_(5:3)_(4:4a)
164	BOM2	BOM	12	704793	704829	706966	707098		3	2138	2221	2304	0	2	2	1	1	(6:2)_(3:5)_(3:5a)_(2:6)_(4:4aCO)_(3:5b)_(4:4a)
167	BOM2	BOM	12	865078	866286	872401	872807		3	6116	6922	7728	0	2	2	1	1	(5:3)_(4:4ai)_(5:3)_(4:4)_(3:5)_(4:4bCO)
208	BOM2	BOM	15	585808	586076	592385	592588		4	6310	6545	6779	0	2	2	2	0	(3:5)_(4:4ai)_(3:5a)_(3:5)_(2:6)_(4:4ai)_(3:5b)_(5:3)_(5:3a)_(3:5b)_(4:4bCO)_(5:3b)_(4:4b)
211	BOM2	BOM	15	984651	984992	989690	991111		3	4699	5579	6459	0	2	2	1	1	(5:3)_(4:4aCO)_(2:6)_(3:5)_(4:4a)_(3:5a)_(4:4a)_(3:5b)_(4:4a)
128	BOM2	BOM	10	360767	360976	363678	363726		4	2703	2831	2958	0	3	2	2	0	(3:5)_(4:4ai)_(3:5a)_(5:3)_(4:4bCO)_(4:4ci)_(4:4dCO)
171	BOM3	BOM	16	921271	921352	921352	921490		1	1	110	218	1	1	1	0	1	05:03
30	BOM3	BOM	4	848136	848341	848341	848397		1	1	131	260	1	1	1	0	1	05:03

110	BOM3	BOM	12	363805	363912	363912	364089	1	1	142	283	1	1	1	0	1	05:03
43	BOM3	BOM	5	268597	268713	268713	268979	1	1	191	381	1	1	1	0	1	05:03
36	BOM3	BOM	4	1434754	1434866	1434996	1435091	1	131	234	336	1	1	1	0	1	05:03
97	BOM3	BOM	11	258604	258771	258943	259176	1	173	372	571	1	1	1	0	1	05:03
48	BOM3	BOM	5	560026	560290	560376	560686	1	87	373	659	1	1	1	0	1	05:03
156	BOM3	BOM	15	967611	967862	968047	968186	1	186	380	574	1	1	1	0	1	05:03
35	BOM3	BOM	4	1337910	1338084	1338366	1338448	1	283	410	537	1	1	1	0	1	05:03
92	BOM3	BOM	11	67700	67997	68250	68298	1	254	426	597	1	1	1	0	1	05:03
167	BOM3	BOM	16	644963	645571	645683	645731	1	113	440	767	1	1	1	0	1	05:03
39	BOM3	BOM	5	77697	77918	77918	78595	1	1	449	897	1	1	1	0	1	05:03
69	BOM3	BOM	8	16735	16788	17157	17359	1	370	497	623	1	1	1	0	1	05:03
148	BOM3	BOM	15	579028	579517	579517	580206	1	1	589	1177	1	1	1	0	1	05:03
71	BOM3	BOM	8	121618	121987	122169	122633	1	183	599	1014	1	1	1	0	1	05:03
164	BOM3	BOM	16	491133	491543	491568	492354	1	26	623	1220	1	1	1	0	1	05:03
61	BOM3	BOM	7	785318	785828	785907	786618	1	80	690	1299	1	1	1	0	1	05:03
93	BOM3	BOM	11	99646	100443	100670	101183	1	228	882	1536	1	1	1	0	1	05:03
4	BOM3	BOM	1	71008	71281	71673	72952	1	393	1168	1943	1	1	1	0	1	05:03
102	BOM3	BOM	11	569085	569468	571329	571639	1	1862	2208	2553	1	1	1	0	1	05:03
67	BOM3	BOM	8	10934	11006	11006	11100	1	1	83	165	1	2	1	0	1	03:05
89	BOM3	BOM	10	672728	672798	672815	672937	1	18	113	208	1	2	1	0	1	03:05
58	BOM3	BOM	7	584298	584414	584414	584527	1	1	115	228	1	2	1	0	1	03:05
115	BOM3	BOM	12	611994	612158	612306	612349	1	149	252	354	1	2	1	0	1	03:05
5	BOM3	BOM	1	184510	184921	184921	185150	1	1	320	639	1	2	1	0	1	03:05
59	BOM3	BOM	7	609958	610218	610218	610674	1	1	358	715	1	2	1	0	1	03:05
29	BOM3	BOM	4	836867	837275	837527	837572	1	253	479	704	1	2	1	0	1	03:05
46	BOM3	BOM	5	398975	399399	399399	400005	1	1	515	1029	1	2	1	0	1	03:05
16	BOM3	BOM	3	103955	104476	104476	105047	1	1	546	1091	1	2	1	0	1	03:05
169	BOM3	BOM	16	713201	713880	713959	714342	1	80	610	1140	1	2	1	0	1	03:05
17	BOM3	BOM	3	142499	143131	143316	143575	1	186	631	1075	1	2	1	0	1	03:05
105	BOM3	BOM	12	38737	39963	39963	40119	1	1	691	1381	1	2	1	0	1	03:05
11	BOM3	BOM	2	585909	586331	586331	587309	1	1	700	1399	1	2	1	0	1	03:05
107	BOM3	BOM	12	281289	282215	282385	282626	1	171	754	1336	1	2	1	0	1	03:05
130	BOM3	BOM	14	79165	79183	80071	80156	1	889	940	990	1	2	1	0	1	03:05
94	BOM3	BOM	11	116904	117207	118109	118487	1	903	1243	1582	1	2	1	0	1	03:05
87	BOM3	BOM	10	570822	573135	573950	574034	1	816	2014	3211	1	2	1	0	1	03:05
153	BOM3	BOM	15	829911	830506	830857	831051	1	352	746	1139	1	3	1	0	1	5:3_4:4_5:3
99	BOM3	BOM	11	355272	355411	356100	356125	1	690	771	852	1	3	1	0	1	5:3_6:2_5:3
28	BOM3	BOM	4	636201	636237	636465	636737	1	229	382	535	1	7	1	0	1	5:3_6:2
44	BOM3	BOM	5	311900	311969	311996	312007	1	28	67	106	1	8	1	0	1	2:6_3:5
22	BOM3	BOM	4	87296	87312	87353	87458	1	42	102	161	1	8	1	0	1	3:5_2:6
139	BOM3	BOM	14	631369	631510	631514	631593	1	5	114	223	1	10.1	1	0	1	02:06
13	BOM3	BOM	2	642483	642776	642776	643134	1	1	326	650	1	10.1	1	0	1	02:06
140	BOM3	BOM	14	635465	636275	636966	637234	1	692	1230	1768	2	11	1	0	1	5:3_5:3a
128	BOM3	BOM	13	797401	797456	798739	798826	1	1284	1354	1424	2	11	1	0	1	5:3_5:3a
41	BOM3	BOM	5	161191	161593	162567	163290	1	975	1537	2098	2	11	1	0	1	5:3_5:3a
100	BOM3	BOM	11	369378	369689	369878	370412	1	190	612	1033	2	12	1	0	1	3:5_3:5a
151	BOM3	BOM	15	633069	633360	633825	634186	1	466	791	1116	2	12	1	0	1	3:5_3:5a
75	BOM3	BOM	8	438697	439062	439686	439692	1	625	810	994	2	12	1	0	1	3:5_3:5a
86	BOM3	BOM	10	391429	391555	392346	392871	1	792	1117	1441	2	12	1	0	1	3:5_3:5a
62	BOM3	BOM	7	797674	797989	798848	799244	1	860	1215	1569	2	12	1	0	1	3:5_3:5a
18	BOM3	BOM	3	145735	145988	148041	148135	1	2054	2227	2399	2	12	1	0	1	3:5_3:5a
129	BOM3	BOM	13	915009	915182	916458	916492	1	1277	1380	1482	2	13	1	0	1	5:3_5:3a_6:2_5:3a
147	BOM3	BOM	15	478649	478679	480909	481143	1	2231	2362	2493	2	13	1	0	1	5:3_4:4_5:3_5:3a
27	BOM3	BOM	4	615060	615092	616750	616883	1	1659	1741	1822	2	14	1	0	1	2:6_3:5_3:5a
150	BOM3	BOM	15	619075	619398	619861	620063	1	464	726	987	2	15	1	0	1	5:3_4:4_5:3a
112	BOM3	BOM	12	424702	424898	425696	425939	1	799	1018	1236	2	15	1	0	1	5:3_4:4_5:3a
134	BOM3	BOM	14	273091	273306	274808	275212	1	1503	1812	2120	2	15	1	0	1	5:3_4:4_5:3a
162	BOM3	BOM	16	264726	264772	265153	265309	1	382	482	582	2	16	1	0	1	3:5_4:4_5:3a
165	BOM3	BOM	16	520404	520684	520832	521292	1	149	518	887	2	16	1	0	1	3:5_4:4_3:5a
56	BOM3	BOM	7	427318	427600	428728	428940	1	1129	1375	1621	2	17	1	0	1	5:3_4:4_5:3_4:4_5:3a

95	BOM3	BOM	11	194709	195050	196712	196848	1	1663	1901	2138	2	17	1	0	1 5:3_4:4_5:3a_4:4_5:3a
45	BOM3	BOM	5	334750	335065	336702	336936	1	1638	1912	2185	2	17	1	0	1 5:3_4:4_5:3_4:4_5:3a
122	BOM3	BOM	13	352695	353026	353814	354080	1	789	1087	1384	2	19	1	0	1 5:3_6:2_5:3a
154	BOM3	BOM	15	880027	880543	882343	882544	1	1801	2159	2516	2	19	1	0	1 5:3_6:2_5:3a
1	BOM3	BOM	1	31403	31635	32271	32511	1	637	872	1107	2	23	1	0	1 3:5_2:6_4:4_3:5a
135	BOM3	BOM	14	364611	364966	366581	366762	1	1616	1883	2150	2	23	1	0	1 3:5_4:4_2:6_4:4_3:5a
159	BOM3	BOM	16	72872	73338	76987	77082	2_nonsis	3650	3930	4209	3	30	1	0	1 5:3_3:5_4:4_5:3a_4:4_5:3a
98	BOM3	BOM	11	334135	334655	334655	334735	2_nonsis	1	300	599	3	31	1	0	1 4:4ai
144	BOM3	BOM	15	220116	220335	221206	221576	2_nonsis	872	1166	1459	3	31	1	0	1 4:4ai_4:4_3:5
20	BOM3	BOM	4	76974	77295	79321	79387	2_nonsis	2027	2220	2412	3	31	1	0	1 5:3_6:2_4:4ai_5:3a
127	BOM3	BOM	13	795107	795326	795326	795946	2_nonsis	1	420	838	1	1	1	1	0 (5:3)_(4:4aCO)
109	BOM3	BOM	12	320469	320997	320997	322903	2_nonsis	1	1217	2433	1	1	1	1	0 (5:3)_(4:4aCO)
101	BOM3	BOM	11	534234	534309	535712	536243	2_nonsis	1404	1706	2008	1	1	1	1	0 (5:3)_(4:4aCO)
143	BOM3	BOM	15	146419	147007	147007	150962	2_nonsis	1	2272	4542	1	1	1	1	0 (5:3)_(4:4aCO)
142	BOM3	BOM	15	94972	95393	95393	95966	2_nonsis	1	497	993	1	2	1	1	0 (3:5)_(4:4aCO)
66	BOM3	BOM	7	1045427	1045920	1045920	1046573	2_nonsis	1	573	1145	1	2	1	1	0 (3:5)_(4:4aCO)
126	BOM3	BOM	13	702605	703253	703549	703560	2_nonsis	297	626	954	1	2	1	1	0 (3:5)_(4:4aCO)
155	BOM3	BOM	15	920281	920643	921405	922090	2_nonsis	763	1286	1808	1	2	1	1	0 (3:5)_(4:4aCO)
117	BOM3	BOM	12	837962	840577	840682	843387	2_nonsis	106	2765	5424	1	2	1	1	0 (3:5)_(4:4aCO)
113	BOM3	BOM	12	496489	497835	498565	499674	2_nonsis	731	1958	3184	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
33	BOM3	BOM	4	1239399	1240123	1241519	1242168	2_nonsis	1397	2083	2768	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
80	BOM3	BOM	9	401375	402165	403510	403760	2_nonsis	1346	1865	2384	1	5	1	1	0 (3:5)_(4:4)_(4:4aCO)
116	BOM3	BOM	12	658054	658599	660046	660371	2_nonsis	1448	1882	2316	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
136	BOM3	BOM	14	415877	416164	416362	416620	2_nonsis	199	471	742	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
21	BOM3	BOM	4	84443	84518	84947	85442	2_nonsis	430	714	998	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
42	BOM3	BOM	5	236202	236672	237191	237481	2_nonsis	520	899	1278	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
31	BOM3	BOM	4	868578	868704	869992	870200	2_nonsis	1289	1455	1621	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
158	BOM3	BOM	16	40127	40351	40445	40527	2_nonsis	95	247	399	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
170	BOM3	BOM	16	828891	829002	829418	830004	2_nonsis	417	765	1112	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
88	BOM3	BOM	10	662479	663134	663739	663948	2_nonsis	606	1037	1468	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
146	BOM3	BOM	15	447606	447942	449353	449867	2_nonsis	1412	1836	2260	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
84	BOM3	BOM	10	290730	290883	291438	291807	2_nonsis	556	816	1076	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
114	BOM3	BOM	12	552323	552416	553063	553358	2_nonsis	648	841	1034	1	12	1	1	0 (6:2)_(5:3)_(6:2)_(4:4aCO)
10	BOM3	BOM	2	393237	393340	394726	394786	2_nonsis	1387	1468	1548	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
14	BOM3	BOM	2	694512	695405	697503	698250	2_nonsis	2099	2918	3737	1	12	1	1	0 (2:6)_(4:4aCO)_(3:5)_(4:4a)
131	BOM3	BOM	14	137862	138022	138984	139602	2_nonsis	963	1351	1739	1	12	1	1	0 (3:5)_(4:4)_(2:6)_(4:4)_(4:4aCO)
24	BOM3	BOM	4	300160	300204	302084	302250	2_nonsis	1881	1985	2089	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
70	BOM3	BOM	8	97715	98248	99909	101246	2_nonsis	1662	2596	3530	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4)_(4:4aCO)
168	BOM3	BOM	16	679712	679897	680837	681366	2_nonsis	941	1297	1653	1	12	1	1	0 (5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(4:4aCO)
37	BOM3	BOM	4	1447313	1447694	1448987	1449188	2_nonsis	1294	1584	1874	1	12	1	1	0 (3:5)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
76	BOM3	BOM	8	517036	517336	517376	517399	2_nonsis	41	202	362	1	15	1	1	0 (6:2)_(4:4aCO)
34	BOM3	BOM	4	1289490	1289885	1289885	1289939	2_nonsis	1	225	448	1	15	1	1	0 (6:2)_(4:4aCO)
111	BOM3	BOM	12	367857	367998	368038	368453	2_nonsis	41	318	595	1	15	1	1	0 (6:2)_(4:4aCO)
121	BOM3	BOM	13	141979	142186	142395	142575	2_nonsis	210	403	595	1	15	1	1	0 (6:2)_(4:4aCO)
149	BOM3	BOM	15	589303	589700	589839	590260	2_nonsis	140	548	956	1	15	1	1	0 (6:2)_(4:4aCO)
74	BOM3	BOM	8	435329	435693	435968	436433	2_nonsis	276	690	1103	1	15	1	1	0 (6:2)_(4:4aCO)
73	BOM3	BOM	8	361272	361539	361910	362504	2_nonsis	372	802	1231	1	15	1	1	0 (6:2)_(4:4aCO)
106	BOM3	BOM	12	159272	159591	159591	159665	2_nonsis	1	197	392	1	16	1	1	0 (2:6)_(4:4aCO)
50	BOM3	BOM	6	81532	81686	82058	82187	2_nonsis	373	514	654	1	16	1	1	0 (2:6)_(4:4aCO)
23	BOM3	BOM	4	177807	178219	178306	179632	2_nonsis	88	956	1824	1	16	1	1	0 (2:6)_(4:4aCO)
40	BOM3	BOM	5	123248	123378	123248	123378	2_nonsis	0	65	129	1	100	1	1	0 (4:4aCO)
72	BOM3	BOM	8	237328	237556	237328	237556	2_nonsis	0	114	227	1	100	1	1	0 (4:4aCO)
125	BOM3	BOM	13	675387	675697	675387	675697	2_nonsis	0	155	309	1	100	1	1	0 (4:4aCO)
15	BOM3	BOM	3	60997	61457	60997	61457	2_nonsis	0	230	459	1	100	1	1	0 (4:4aCO)
124	BOM3	BOM	13	559312	559794	559312	559794	2_nonsis	0	241	481	1	100	1	1	0 (4:4aCO)
8	BOM3	BOM	2	170868	171433	170868	171433	2_nonsis	0	282	564	1	100	1	1	0 (4:4aCO)
38	BOM3	BOM	5	30664	31247	30664	31247	2_nonsis	0	291	582	1	100	1	1	0 (4:4aCO)
12	BOM3	BOM	2	615005	615654	615005	615654	2_nonsis	0	324	648	1	100	1	1	0 (4:4aCO)
137	BOM3	BOM	14	440622	441276	440622	441276	2_nonsis	0	327	653	1	100	1	1	0 (4:4aCO)
26	BOM3	BOM	4	588711	589440	588711	589440	2_nonsis	0	364	728	1	100	1	1	0 (4:4aCO)

2	BOM3	BOM	1	64499	65365	64499	65365	2_nonsis		0	433	865	1	100	1	1	0 (4:4aCO)
103	BOM3	BOM	11	603048	604059	603048	604059	2_nonsis		0	505	1010	1	100	1	1	0 (4:4aCO)
90	BOM3	BOM	11	4775	5928	4775	5928	2_nonsis		0	576	1152	1	100	1	1	0 (4:4aCO)
157	BOM3	BOM	15	1002614	1003809	1002614	1003809	2_nonsis		0	597	1194	1	100	1	1	0 (4:4aCO)
19	BOM3	BOM	3	228130	230267	228130	230267	2_nonsis		0	1068	2136	1	100	1	1	0 (4:4aCO)
91	BOM3	BOM	11	46439	48790	46439	48790	2_nonsis		0	1175	2350	1	100	1	1	0 (4:4aCO)
138	BOM3	BOM	14	539950	542443	539950	542443	2_nonsis		0	1246	2492	1	100	1	1	0 (4:4aCO)
78	BOM3	BOM	9	185865	188629	185865	188629	2_nonsis		0	1382	2763	1	100	1	1	0 (4:4aCO)
79	BOM3	BOM	9	299287	302738	299287	302738	2_nonsis		0	1725	3450	1	100	1	1	0 (4:4aCO)
53	BOM3	BOM	7	58086	58485	59403	60729	2_nonsis		919	1781	2642	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
96	BOM3	BOM	11	229432	229903	232839	234299	2_nonsis		2937	3902	4866	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)_(3:5b)_(4:4a)
77	BOM3	BOM	9	54480	55071	56514	57063	2_nonsis		1444	2013	2582	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
161	BOM3	BOM	16	226160	226313	228253	228815	2_nonsis		1941	2298	2654	2	32	1	1	0 (5:3)_(4:4aCO)_(5:3a)_(4:4a)
145	BOM3	BOM	15	283744	284515	285663	286242	2_nonsis		1149	1823	2497	2	32	1	1	0 (4:4aCO)_(3:5)_(2:6)_(3:5a)_(4:4a)
104	BOM3	BOM	12	20715	20975	22811	22902	2_nonsis		1837	2012	2186	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
32	BOM3	BOM	4	1148075	1148435	1149565	1149761	2_nonsis		1131	1408	1685	2	32	1	1	0 (4:4ai)_(6:2)_(5:3)_(4:4bCO)_(5:3a)_(4:4b)
64	BOM3	BOM	7	807791	807996	809973	810159	2_nonsis		1978	2173	2367	2	32	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5a)_(3:5)_(4:4a)
49	BOM3	BOM	6	72559	73471	75475	76048	2_nonsis		2005	2747	3488	2	32	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4)_(3:5a)_(4:4aCO)
119	BOM3	BOM	12	1043537	1043638	1043701	1043895	2_nonsis		64	211	357	3	20	1	1	0 (3:5)_(6:2)_(4:4aCO)
7	BOM3	BOM	2	88022	88046	89785	90196	2_nonsis		1740	1957	2173	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
163	BOM3	BOM	16	359182	359890	361590	361807	2_nonsis		1701	2163	2624	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
54	BOM3	BOM	7	76149	76406	76620	76882	2_nonsis		215	474	732	3	20	1	1	0 (6:2)_(4:4aCO)_(2:6)_(4:4a)
118	BOM3	BOM	12	877274	877539	877999	878076	2_nonsis		461	631	801	3	20	1	1	0 (2:6)_(3:5)_(6:2)_(4:4aCO)
83	BOM3	BOM	10	246652	247233	247893	247938	2_nonsis		661	973	1285	3	20	1	1	0 (6:2)_(4:4)_(3:5)_(4:4aCO)
85	BOM3	BOM	10	363087	363678	364397	364524	2_nonsis		720	1078	1436	3	20	1	1	0 (6:2)_(5:3)_(2:6)_(4:4aCO)
133	BOM3	BOM	14	270187	270523	271443	271707	2_nonsis		921	1220	1519	3	20	1	1	0 (6:2)_(4:4aCO)_(3:5)_(4:4a)
25	BOM3	BOM	4	439479	439746	441071	441206	2_nonsis		1326	1526	1726	3	20	1	1	0 (3:5)_(4:4aCO)_(6:2)_(4:4a)
52	BOM3	BOM	7	23297	23450	24468	25442	2_nonsis		1019	1582	2144	3	20	1	1	0 (2:6)_(4:4)_(6:2)_(4:4aCO)
82	BOM3	BOM	10	102425	102662	104033	104395	2_nonsis		1372	1671	1969	3	20	1	1	0 (2:6)_(4:4aCO)_(6:2)_(4:4a)
152	BOM3	BOM	15	821737	822154	823983	824604	2_nonsis		1830	2348	2866	3	20	1	1	0 (5:3)_(2:6)_(3:5)_(4:4aCO)
81	BOM3	BOM	10	73391	73708	75075	75279	2_nonsis		1368	1628	1887	3	20	1	1	0 (2:6)_(4:4)_(2:6)_(5:3)_(4:4aCO)
65	BOM3	BOM	7	1011510	1012069	1013788	1013909	2_nonsis		1720	2059	2398	3	20	1	1	0 (5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)
9	BOM3	BOM	2	288304	288339	289409	289530	2_nonsis		1071	1148	1225	3	20	1	1	0 (3:5)_(5:3)_(6:2)_(4:4aCO)_(5:3)_(4:4a)
68	BOM3	BOM	8	13244	13408	14784	14833	2_nonsis		1377	1483	1588	3	20	1	1	0 (6:2)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
120	BOM3	BOM	13	70292	70356	74346	74436	2_nonsis		3991	4067	4143	3	20	1	1	0 (5:3)_(4:4)_(6:2)_(4:4)_(2:6)_(4:4aCO)
57	BOM3	BOM	7	432412	432654	434308	434403	2_nonsis		1655	1823	1990	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(3:5a)_(4:4)_(6:2)_(4:4aCO)
123	BOM3	BOM	13	388308	388416	390486	390597	2_nonsis		2071	2180	2288	3	20	1	1	0 (2:6)_(4:4)_(5:3)_(3:5)_(5:3)_(3:5)_(4:4a)
63	BOM3	BOM	7	800442	801373	803780	803951	2_nonsis		2408	2958	3508	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(3:5a)_(5:3)_(5:3a)_(4:4aCO)
55	BOM3	BOM	7	146193	146595	147855	148827	2_nonsis		1261	1947	2633	3	20	1	1	0 (3:5)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)_(5:3)_(4:4a)
166	BOM3	BOM	16	585037	585060	587432	587665	2_nonsis		2373	2500	2627	3	20	1	1	0 (5:3)_(4:4)_(3:5)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)
51	BOM3	BOM	6	235114	235342	237962	238279	2_nonsis		2621	2893	3164	3	20	1	1	0 (2:6)_(3:5)_(5:3)_(4:4)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
47	BOM3	BOM	5	463157	463255	465206	465425	2_nonsis		1952	2110	2267	3	21	1	1	0 (5:3)_(5:3a)_(3:5)_(4:4ai)_(5:3a)_(4:4bCO)
132	BOM3	BOM	14	197191	197707	198636	198795	2_sis		930	1267	1603	0	1	2	0	2 (5:3)_(4:4)_(5:3a)_(6:2)_(4:4)
3	BOM3	BOM	1	66178	66696	68959	69112		3	2264	2599	2933	0	2	2	1	1 (5:3)_(4:4ai)_(3:5)_(4:4bi)_(5:3a)_(2:6)_(4:4cCO)
6	BOM3	BOM	1	190636	190880	195750	195910		3	4871	5072	5273	0	2	2	1	1 (2:6)_(5:3)_(6:2i)_(5:3)_(3:5)_(4:4ai)_(4:4bCO)_(3:5)_(4:4b)
141	BOM3	BOM	14	715086	715182	716055	716316		3	874	1052	1229	0	2	2	1	1 (3:5)_(2:6)_(5:3a)_(4:4aCO)
160	BOM3	BOM	16	173291	173330	174906	175137		3	1577	1711	1845	0	2	2	1	1 (5:3)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
60	BOM3	BOM	7	621861	622133	625898	626137	2_nonsis		3766	4021	4275	0	3	2	0	2 (5:3)_(4:4aCO)_(4:4CO)_(3:5)_(4:4)_(3:5)_(3:5a)_(4:4)
343	BOM3	BOM	16	923175	923621	925093	948066		1	1473	13182	24890	0	4	1	NA	NA 5:3_6:2_5:3_6:2_5:3
2	BOM4	BOM	1	108718	108763	108763	108814		1	1	48	95	1	1	1	0	1 05:03
179	BOM4	BOM	16	339687	339729	339729	339833		1	1	73	145	1	1	1	0	1 05:03
72	BOM4	BOM	7	993849	994015	994032	994097		1	18	133	247	1	1	1	0	1 05:03
45	BOM4	BOM	5	42396	42646	42646	42708		1	1	156	311	1	1	1	0	1 05:03
137	BOM4	BOM	12	877274	877539	877560	877606		1	22	177	331	1	1	1	0	1 05:03
35	BOM4	BOM	4	807628	807907	807918	808086		1	12	235	457	1	1	1	0	1 05:03
166	BOM4	BOM	15	769092	769431	769458	769620		1	28	278	527	1	1	1	0	1 05:03
56	BOM4	BOM	6	225428	225457	225457	226036		1	1	304	607	1	1	1	0	1 05:03
186	BOM4	BOM	16	840488	840627	840627	841238		1	1	375	749	1	1	1	0	1 05:03
146	BOM4	BOM	13	509869	510245	510379	510599		1	135	432	729	1	1	1	0	1 05:03
173	BOM4	BOM	16	131951	132681	132693	132838		1	13	450	886	1	1	1	0	1 05:03

108	BOM4	BOM	11	80353	80724	80854	81244	1	131	511	890	1	1	1	0	1 05:03
32	BOM4	BOM	4	454193	454502	454502	455316	1	1	562	1122	1	1	1	0	1 05:03
99	BOM4	BOM	10	465816	466454	466454	467010	1	1	597	1193	1	1	1	0	1 05:03
115	BOM4	BOM	11	346941	347287	347376	348332	1	90	740	1390	1	1	1	0	1 05:03
77	BOM4	BOM	8	54591	55333	55477	56032	1	145	793	1440	1	1	1	0	1 05:03
168	BOM4	BOM	15	857961	859039	859217	859587	1	179	902	1625	1	1	1	0	1 05:03
106	BOM4	BOM	11	4775	5928	5999	6589	1	72	943	1813	1	1	1	0	1 05:03
123	BOM4	BOM	12	82663	82757	83596	83835	1	840	1006	1171	1	1	1	0	1 05:03
4	BOM4	BOM	1	167179	170726	170726	170945	1	1	1883	3765	1	1	1	0	1 05:03
129	BOM4	BOM	12	416803	416876	416876	416918	1	1	58	114	1	2	1	0	1 03:05
6	BOM4	BOM	1	198657	198664	198713	198815	1	50	104	157	1	2	1	0	1 03:05
119	BOM4	BOM	11	511186	511303	511327	511387	1	25	113	200	1	2	1	0	1 03:05
104	BOM4	BOM	10	675511	675536	675595	675709	1	60	129	197	1	2	1	0	1 03:05
16	BOM4	BOM	2	535946	536134	536146	536197	1	13	132	250	1	2	1	0	1 03:05
60	BOM4	BOM	7	371335	371489	371489	371625	1	1	145	289	1	2	1	0	1 03:05
107	BOM4	BOM	11	78639	78838	78838	79002	1	1	182	362	1	2	1	0	1 03:05
79	BOM4	BOM	8	97245	97536	97650	97715	1	115	292	469	1	2	1	0	1 03:05
145	BOM4	BOM	13	397289	397850	397850	397898	1	1	305	608	1	2	1	0	1 03:05
63	BOM4	BOM	7	494205	494624	494636	494870	1	13	339	664	1	2	1	0	1 03:05
93	BOM4	BOM	10	101339	101966	102081	102363	1	116	570	1023	1	2	1	0	1 03:05
143	BOM4	BOM	13	271372	271672	271672	272762	1	1	695	1389	1	2	1	0	1 03:05
5	BOM4	BOM	1	190031	190402	190880	191026	1	479	737	994	1	2	1	0	1 03:05
117	BOM4	BOM	11	450308	450894	451133	452719	1	240	1325	2410	1	2	1	0	1 03:05
114	BOM4	BOM	11	276968	277294	278406	278445	1	1113	1295	1476	1	3	1	0	1 5:3_4:4_5:3
20	BOM4	BOM	2	786528	786546	788596	789113	1	2051	2318	2584	1	3	1	0	1 5:3_6:2_5:3_4:4_5:3
164	BOM4	BOM	15	587316	587565	590260	590710	1	2696	3045	3393	1	3	1	0	1 5:3_4:4_5:3_4:4_5:3
25	BOM4	BOM	3	246581	246789	246853	247156	1	65	320	574	1	4	1	0	1 3:5_4:4_3:5
46	BOM4	BOM	5	98507	98854	99031	99091	1	178	381	583	1	7	1	0	1 6:2_5:3
75	BOM4	BOM	7	1050064	1050446	1051057	1051093	1	612	820	1028	1	7	1	0	1 6:2_5:3
52	BOM4	BOM	5	472245	472448	472577	472664	1	130	274	418	1	8	1	0	1 3:5_2:6
48	BOM4	BOM	5	210793	211386	212029	212585	1	644	1218	1791	1	8	1	0	1 3:5_4:4_2:6
14	BOM4	BOM	2	476602	476950	477015	477199	1	66	331	596	1	10	1	0	1 06:02
66	BOM4	BOM	7	626947	627440	627463	627706	1	24	391	758	1	10	1	0	1 06:02
73	BOM4	BOM	7	996426	996469	996469	996604	1	1	89	177	1	10.1	1	0	1 02:06
84	BOM4	BOM	9	55837	56514	56514	57063	1	1	613	1225	1	10.1	1	0	1 02:06
182	BOM4	BOM	16	552585	552953	553028	553046	1	76	268	460	2	11	1	0	1 5:3_5:3a
37	BOM4	BOM	4	955140	955230	955484	955574	1	255	344	433	2	11	1	0	1 5:3_5:3a
105	BOM4	BOM	10	703339	703431	703967	704056	1	537	627	716	2	11	1	0	1 5:3_5:3a
118	BOM4	BOM	11	456743	456866	457465	457579	1	600	718	835	2	11	1	0	1 5:3_5:3a
110	BOM4	BOM	11	177551	178198	178613	178752	1	416	808	1200	2	11	1	0	1 5:3_5:3a
62	BOM4	BOM	7	472321	472609	473448	473748	1	840	1133	1426	2	11	1	0	1 5:3_5:3a
121	BOM4	BOM	11	532742	533318	534234	534309	1	917	1242	1566	2	11	1	0	1 5:3_5:3a
9	BOM4	BOM	2	106396	107123	107917	108149	1	795	1274	1752	2	11	1	0	1 5:3_5:3a
11	BOM4	BOM	2	254899	255469	256767	256925	1	1299	1662	2025	2	11	1	0	1 5:3_5:3a
176	BOM4	BOM	16	230687	230837	231179	231457	1	343	556	769	2	12	1	0	1 3:5_3:5a
29	BOM4	BOM	4	184320	184727	185143	185244	1	417	670	923	2	12	1	0	1 3:5_3:5a
113	BOM4	BOM	11	231543	231603	231922	232567	1	320	672	1023	2	12	1	0	1 3:5_3:5a
130	BOM4	BOM	12	424702	424898	425404	425550	1	507	677	847	2	12	1	0	1 3:5_3:5a
92	BOM4	BOM	10	83057	83207	83804	83877	1	598	709	819	2	12	1	0	1 3:5_3:5a
90	BOM4	BOM	9	423651	424253	425064	425130	1	812	1145	1478	2	12	1	0	1 3:5_3:5a
69	BOM4	BOM	7	784625	785199	785907	786618	1	709	1351	1992	2	12	1	0	1 3:5_3:5a
43	BOM4	BOM	4	1420281	1420528	1423497	1423605	1	2970	3147	3323	2	13	1	0	1 5:3_5:3a_4:4_5:3a_6:2_5:3a
174	BOM4	BOM	16	163169	163239	164063	164740	1	825	1198	1570	2	15	1	0	1 5:3_4:4_5:3a
180	BOM4	BOM	16	350968	351571	353391	353535	1	1821	2194	2566	2	15	1	0	1 5:3_4:4_5:3a
94	BOM4	BOM	10	146738	146986	147143	147445	1	158	432	706	2	16	1	0	1 3:5_4:4_3:5a
169	BOM4	BOM	15	967885	968047	968991	969441	1	945	1250	1555	2	16	1	0	1 3:5_4:4_3:5a
111	BOM4	BOM	11	187243	187398	188875	188972	1	1478	1603	1728	2	16	1	0	1 3:5_4:4_3:5a
68	BOM4	BOM	7	746564	746615	748153	748214	1	1539	1594	1649	2	17	1	0	1 5:3_4:4_5:3a_4:4_5:3a
65	BOM4	BOM	7	609644	609701	609928	609958	1	228	271	313	2	19	1	0	1 5:3_6:2_5:3a
177	BOM4	BOM	16	267098	267298	267573	267749	1	276	463	650	2	19	1	0	1 5:3_6:2_5:3a

134	BOM4	BOM	12	659350	659916	660916	661444	1	1001	1547	2093	2	19	1	0	1	5:3_6:2_5:3a
163	BOM4	BOM	15	481588	481817	482608	483090	2_nonsis	792	1147	1501	3	30	1	0	1	3:5_3:5a_4:4_5:3
1	BOM4	BOM	1	33077	33147	34497	34515	2_nonsis	1351	1394	1437	3	30	1	0	1	5:3_6:2_4:4_3:5
124	BOM4	BOM	12	134715	134767	136834	137012	2_nonsis	2068	2182	2296	3	30	1	0	1	5:3_4:4_5:3_5:3a_5:3b
13	BOM4	BOM	2	465156	465417	468402	468870	2_nonsis	2986	3350	3713	3	30	1	0	1	5:3_4:4_5:3_4:4_3:5
120	BOM4	BOM	11	525645	526035	527432	527498	2_nonsis	1398	1625	1852	3	31	1	0	1	3:5_4:4ai_4:4_3:5a
97	BOM4	BOM	10	277465	277623	279207	279278	2_nonsis	1585	1699	1812	3	31	1	0	1	4:4ai_5:3_5:3a_5:3b
87	BOM4	BOM	9	122089	122282	122375	122588	2_nonsis	94	296	498	1	1	1	1	0	(5:3)_(4:4aCO)
159	BOM4	BOM	15	73362	73589	73589	74106	2_nonsis	1	372	743	1	1	1	1	0	(5:3)_(4:4aCO)
64	BOM4	BOM	7	528447	528489	528828	528993	2_nonsis	340	443	545	1	1	1	1	0	(5:3)_(4:4aCO)
112	BOM4	BOM	11	222033	223233	223330	223790	2_nonsis	98	927	1756	1	1	1	1	0	(5:3)_(4:4aCO)
151	BOM4	BOM	14	37063	37986	37986	39122	2_nonsis	1	1030	2058	1	1	1	1	0	(5:3)_(4:4aCO)
171	BOM4	BOM	15	1043151	1043361	1044558	1044705	2_nonsis	1198	1376	1553	1	1	1	1	0	(5:3)_(4:4aCO)
133	BOM4	BOM	12	602685	602909	602909	603057	2_nonsis	1	186	371	1	2	1	1	0	(3:5)_(4:4aCO)
27	BOM4	BOM	4	62205	62366	62366	62726	2_nonsis	1	261	520	1	2	1	1	0	(3:5)_(4:4aCO)
126	BOM4	BOM	12	269565	269839	269839	270392	2_nonsis	1	414	826	1	2	1	1	0	(3:5)_(4:4aCO)
138	BOM4	BOM	12	878875	879756	879756	880251	2_nonsis	1	688	1375	1	2	1	1	0	(3:5)_(4:4aCO)
109	BOM4	BOM	11	118487	119310	119339	120268	2_nonsis	30	905	1780	1	2	1	1	0	(3:5)_(4:4aCO)
51	BOM4	BOM	5	460411	461582	461594	462226	2_nonsis	13	914	1814	1	2	1	1	0	(3:5)_(4:4aCO)
8	BOM4	BOM	2	101289	101613	102815	103652	2_nonsis	1203	1783	2362	1	2	1	1	0	(3:5)_(4:4aCO)
3	BOM4	BOM	1	130975	132066	132066	135319	2_nonsis	1	2172	4343	1	2	1	1	0	(3:5)_(4:4aCO)
162	BOM4	BOM	15	429624	429729	430036	430667	2_nonsis	308	675	1042	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
175	BOM4	BOM	16	213597	213837	214358	214684	2_nonsis	522	804	1086	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
70	BOM4	BOM	7	877134	878070	878701	878834	2_nonsis	632	1166	1699	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
185	BOM4	BOM	16	686122	687687	689677	691459	2_nonsis	1991	3664	5336	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
157	BOM4	BOM	14	650114	650366	650687	650816	2_nonsis	322	512	701	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
141	BOM4	BOM	13	118473	118852	119306	119467	2_nonsis	455	724	993	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
76	BOM4	BOM	8	9426	9704	10615	10670	2_nonsis	912	1078	1243	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
103	BOM4	BOM	10	661626	662241	663534	663564	2_nonsis	1294	1616	1937	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
34	BOM4	BOM	4	681992	682073	682303	682509	2_nonsis	231	374	516	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
39	BOM4	BOM	4	1224954	1225088	1225088	1225292	2_nonsis	1	169	337	1	11	1	1	0	(4:4ai)_(4:4bCO)
54	BOM4	BOM	6	156102	156218	156218	156651	2_nonsis	1	275	548	1	11	1	1	0	(4:4ai)_(4:4bCO)
10	BOM4	BOM	2	196145	196404	196417	196581	2_nonsis	14	225	435	1	11	1	1	0	(4:4ai)_(3:5)_(4:4bCO)
49	BOM4	BOM	5	227105	227242	228774	228943	2_nonsis	1533	1685	1837	1	11	1	1	0	(4:4aCO)_(5:3)_(4:4bi)_(5:3)_(4:4a)
152	BOM4	BOM	14	117055	117101	117410	117759	2_nonsis	310	507	703	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
150	BOM4	BOM	13	860181	861184	861205	861520	2_nonsis	22	680	1338	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
28	BOM4	BOM	4	155900	156500	157148	157424	2_nonsis	649	1086	1523	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
36	BOM4	BOM	4	931376	931988	932535	933005	2_nonsis	548	1088	1628	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
42	BOM4	BOM	4	1414373	1414490	1415193	1416035	2_nonsis	704	1183	1661	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
139	BOM4	BOM	12	1009719	1011169	1011952	1012226	2_nonsis	784	1645	2506	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
165	BOM4	BOM	15	721121	721240	722724	723053	2_nonsis	1485	1708	1931	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
71	BOM4	BOM	7	959381	959587	959945	960299	2_nonsis	359	638	917	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
170	BOM4	BOM	15	985518	985891	986501	986764	2_nonsis	611	928	1245	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)
61	BOM4	BOM	7	384678	384785	385570	386428	2_nonsis	786	1268	1749	1	12	1	1	0	(6:2)_(4:4)_(5:3)_(4:4aCO)
128	BOM4	BOM	12	388010	388456	389584	389815	2_nonsis	1129	1467	1804	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
95	BOM4	BOM	10	159830	160491	161596	162223	2_nonsis	1106	1749	2392	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(4:4aCO)
86	BOM4	BOM	9	99043	99647	100450	102247	2_nonsis	804	2004	3203	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)
116	BOM4	BOM	11	400068	400341	401916	402660	2_nonsis	1576	2084	2591	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
40	BOM4	BOM	4	1289490	1289885	1291869	1292138	2_nonsis	1985	2316	2647	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(4:4aCO)
154	BOM4	BOM	14	331790	332278	335092	335197	2_nonsis	2815	3111	3406	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(6:2)_(4:4aCO)
58	BOM4	BOM	7	145098	145450	145516	145962	2_nonsis	67	465	863	1	15	1	1	0	(6:2)_(4:4aCO)
161	BOM4	BOM	15	288781	288918	289563	289728	2_nonsis	646	796	946	1	15	1	1	0	(6:2)_(4:4aCO)
23	BOM4	BOM	3	152439	152546	152546	152748	2_nonsis	1	155	308	1	16	1	1	0	(2:6)_(4:4aCO)
144	BOM4	BOM	13	332932	333053	333079	333250	2_nonsis	27	172	317	1	16	1	1	0	(2:6)_(4:4aCO)
26	BOM4	BOM	4	20444	20659	20785	20969	2_nonsis	127	326	524	1	16	1	1	0	(2:6)_(4:4aCO)
15	BOM4	BOM	2	479516	479752	479516	479752	2_nonsis	0	118	235	1	100	1	1	0	(4:4aCO)
30	BOM4	BOM	4	303504	303806	303504	303806	2_nonsis	0	151	301	1	100	1	1	0	(4:4aCO)
184	BOM4	BOM	16	677836	678266	677836	678266	2_nonsis	0	215	429	1	100	1	1	0	(4:4aCO)
53	BOM4	BOM	6	48712	49201	48712	49201	2_nonsis	0	244	488	1	100	1	1	0	(4:4aCO)
31	BOM4	BOM	4	369971	370499	369971	370499	2_nonsis	0	264	527	1	100	1	1	0	(4:4aCO)

17	BOM4	BOM	2	650619	651379	650619	651379	2_nonsis		0	380	759	1	100	1	1	0	(4:4aCO)
167	BOM4	BOM	15	803637	804529	803637	804529	2_nonsis		0	446	891	1	100	1	1	0	(4:4aCO)
156	BOM4	BOM	14	542443	543829	542443	543829	2_nonsis		0	693	1385	1	100	1	1	0	(4:4aCO)
155	BOM4	BOM	14	437581	439088	437581	439088	2_nonsis		0	753	1506	1	100	1	1	0	(4:4aCO)
140	BOM4	BOM	13	26922	28623	26922	28623	2_nonsis		0	850	1700	1	100	1	1	0	(4:4aCO)
101	BOM4	BOM	10	570822	573135	570822	573135	2_nonsis		0	1156	2312	1	100	1	1	0	(4:4aCO)
78	BOM4	BOM	8	93770	96126	93770	96126	2_nonsis		0	1178	2355	1	100	1	1	0	(4:4aCO)
59	BOM4	BOM	7	236277	241275	236277	241275	2_nonsis		0	2499	4997	1	100	1	1	0	(4:4aCO)
125	BOM4	BOM	12	212026	212081	212780	212801	2_nonsis		700	737	774	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
85	BOM4	BOM	9	95341	95580	96885	96924	2_nonsis		1306	1444	1582	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
149	BOM4	BOM	13	748055	748748	750177	751108	2_nonsis		1430	2241	3052	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
89	BOM4	BOM	9	306037	306523	308383	308815	2_nonsis		1861	2319	2777	2	30	1	1	0	(5:3)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
132	BOM4	BOM	12	510395	510423	511071	511197	2_nonsis		649	725	801	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
88	BOM4	BOM	9	177082	177586	178629	179273	2_nonsis		1044	1617	2190	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
38	BOM4	BOM	4	999431	999562	999724	999930	2_nonsis		163	331	498	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
135	BOM4	BOM	12	719618	719858	722079	722344	2_nonsis		2222	2474	2725	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
131	BOM4	BOM	12	490675	493339	494429	495002	2_nonsis		1091	2709	4326	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
74	BOM4	BOM	7	1022196	1022301	1023633	1023685	2_nonsis		1333	1411	1488	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(6:2)_(4:4aCO)
67	BOM4	BOM	7	629962	630335	631589	631912	2_nonsis		1255	1602	1949	2	32	1	1	0	(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
33	BOM4	BOM	4	549856	550499	551991	552102	2_nonsis		1493	1869	2245	2	32	1	1	0	(3:5)_(4:4)_(3:5)_(4:4)_(2:6)_(3:5a)_(4:4aCO)
188	BOM4	BOM	16	886812	887016	890080	890467	2_nonsis		3065	3360	3654	2	32	1	1	0	(6:2)_(5:3)_(6:2)_(5:3a)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
178	BOM4	BOM	16	279568	279637	279975	280422	2_nonsis		339	596	853	3	20	1	1	0	(5:3)_(2:6)_(4:4aCO)
80	BOM4	BOM	8	121618	121987	122674	122848	2_nonsis		688	959	1229	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
158	BOM4	BOM	14	709675	709906	710457	711379	2_nonsis		552	1128	1703	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
153	BOM4	BOM	14	197788	198236	198937	199403	2_nonsis		702	1158	1614	3	20	1	1	0	(3:5)_(6:2)_(4:4aCO)
102	BOM4	BOM	10	627178	627999	628891	629879	2_nonsis		893	1797	2700	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
147	BOM4	BOM	13	552466	553020	554456	555036	2_nonsis		1437	2003	2569	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
100	BOM4	BOM	10	489721	490750	492405	493019	2_nonsis		1656	2477	3297	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
22	BOM4	BOM	3	59925	60198	60997	61457	2_nonsis		800	1166	1531	3	20	1	1	0	(5:3)_(4:4aCO)_(2:6)_(4:4a)
83	BOM4	BOM	8	498566	498745	499853	500211	2_nonsis		1109	1377	1644	3	20	1	1	0	(5:3)_(6:2)_(3:5)_(4:4aCO)
12	BOM4	BOM	2	304001	304384	306376	306932	2_nonsis		1993	2462	2930	3	20	1	1	0	(3:5)_(5:3)_(6:2)_(4:4aCO)
160	BOM4	BOM	15	198105	198213	198772	199130	2_nonsis		560	792	1024	3	20	1	1	0	(3:5)_(2:6)_(4:4aCO)_(5:3)_(4:4a)
24	BOM4	BOM	3	224261	224961	225200	225673	2_nonsis		240	826	1411	3	20	1	1	0	(2:6)_(3:5)_(4:4)_(6:2)_(4:4aCO)
81	BOM4	BOM	8	225748	225911	227343	227411	2_nonsis		1433	1548	1662	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(5:3)_(4:4a)
44	BOM4	BOM	5	11847	12024	13645	13996	2_nonsis		1622	1885	2148	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
82	BOM4	BOM	8	361910	362504	364439	364600	2_nonsis		1936	2313	2689	3	20	1	1	0	(6:2)_(4:4)_(3:5)_(3:5a)_(4:4aCO)
148	BOM4	BOM	13	683655	683958	685884	686613	2_nonsis		1927	2442	2957	3	20	1	1	0	(5:3)_(4:4aCO)_(2:6)_(4:4a)
91	BOM4	BOM	10	51007	51976	53312	53513	2_nonsis		1337	1921	2505	3	20	1	1	0	(5:3)_(6:2)_(4:4)_(2:6)_(3:5)_(4:4aCO)
41	BOM4	BOM	4	1315764	1316569	1318539	1318597	2_nonsis		1971	2402	2832	3	20	1	1	0	(6:2)_(4:4aCO)_(3:5)_(4:4a)_(3:5a)_(4:4a)
96	BOM4	BOM	10	272315	272381	274782	275124	2_nonsis		2402	2605	2808	3	20	1	1	0	(3:5)_(3:5a)_(2:6)_(4:4aCO)_(5:3)_(4:4a)
122	BOM4	BOM	11	580815	581385	582336	582583	2_nonsis		952	1360	1767	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(6:2)_(5:3)_(4:4a)
183	BOM4	BOM	16	585958	586036	588931	588991	2_nonsis		2896	2964	3032	3	20	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4)_(2:6)_(3:5)_(4:4aCO)
142	BOM4	BOM	13	192291	192332	195330	195572	2_nonsis		2999	3140	3280	3	20	1	1	0	(3:5)_(4:4)_(3:5a)_(4:4)_(3:5)_(5:3)_(5:3a)_(4:4aCO)
181	BOM4	BOM	16	524743	525053	527574	528017	2_nonsis		2522	2898	3273	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
47	BOM4	BOM	5	123248	123378	124970	125141	2_nonsis		1593	1743	1892	3	21	1	1	0	(5:3)_(4:4)_(6:2)_(4:4ai)_(3:5)_(4:4bCO)
50	BOM4	BOM	5	376275	376375	378395	378586	2_nonsis		2021	2166	2310	3	21	1	1	0	(4:4ai)_(3:5)_(4:4bCO)_(5:3)_(6:2)_(5:3a)_(4:4b)
172	BOM4	BOM	16	66527	66703	69355	69402	2_nonsis		2653	2764	2874	3	21	1	1	0	(3:5)_(3:5a)_(4:4ai)_(4:4)_(5:3)_(5:3a)_(4:4bCO)
18	BOM4	BOM	2	695479	697455	716856	716927		3	19402	20425	21447	0	2	2	1	1	(0:8)_(2:6)_(4:4)_(5:3)_(6:2)_(0:8)_(4:4aCO)
19	BOM4	BOM	2	723663	723755	738241	738886		3	14487	14855	15222	0	2	2	2	0	(0:8)_(4:4)_(0:8)_(4:4aCO)
57	BOM4	BOM	7	20257	20512	22405	23215		3	1894	2426	2957	0	2	2	2	0	(5:3)_(5:3a)_(7:1)_(5:3b)_(4:4aCO)_(5:3b)_(6:2)_(5:3b)_(4:4a)
98	BOM4	BOM	10	359445	359702	361485	361643		3	1784	1991	2197	0	2	2	1	1	(2:6)_(4:4aCO)_(5:3)_(5:3a)_(4:4a)
136	BOM4	BOM	12	837543	837595	837595	837962		3	1	210	418	0	2	2	1	1	(4:4ai)_(4:4bCO)
187	BOM4	BOM	16	878578	878899	879550	879742		3	652	908	1163	0	2	2	1	1	(3:5)_(2:6i)_(1:7)_(0:8)_(4:4aCO)
7	BOM4	BOM	2	44210	44904	45959	46603	2_nonsis		1056	1724	2392	0	3	2	0	2	(5:3)_(4:4aCO)_(3:5)_(4:4CO)
55	BOM4	BOM	6	203253	203623	205576	205702	2_nonsis		1954	2201	2448	0	3	2	0	2	(5:3)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4CO)
205	OM1	OM	16	63201	63205	63205	63216		1	1	8	14	1	1	1	0	1	05:03
122	OM1	OM	10	360588	360746	360746	360767		1	1	90	178	1	1	1	0	1	05:03
105	OM1	OM	8	399043	399050	399050	399235		1	1	96	191	1	1	1	0	1	05:03
155	OM1	OM	13	51358	51433	51433	51596		1	1	119	237	1	1	1	0	1	05:03
103	OM1	OM	8	371268	371744	371744	371815		1	1	274	546	1	1	1	0	1	05:03

45	OM1	OM	4	787173	787632	787632	787723	1	1	275	549	1	1	1	0	1 05:03
37	OM1	OM	4	71525	71645	71743	72032	1	99	303	506	1	1	1	0	1 05:03
98	OM1	OM	8	98484	98622	98643	99089	1	22	313	604	1	1	1	0	1 05:03
174	OM1	OM	14	136113	136144	136375	136579	1	232	349	465	1	1	1	0	1 05:03
66	OM1	OM	6	43988	44192	44192	44748	1	1	380	759	1	1	1	0	1 05:03
49	OM1	OM	4	1015515	1016282	1016332	1016426	1	51	481	910	1	1	1	0	1 05:03
56	OM1	OM	5	15966	16323	16323	17065	1	1	550	1098	1	1	1	0	1 05:03
89	OM1	OM	7	635353	635861	635861	636660	1	1	654	1306	1	1	1	0	1 05:03
65	OM1	OM	5	509962	510678	510678	511287	1	1	663	1324	1	1	1	0	1 05:03
159	OM1	OM	13	228322	228901	229206	229539	1	306	761	1216	1	1	1	0	1 05:03
171	OM1	OM	14	32426	34396	34412	34467	1	17	1029	2040	1	1	1	0	1 05:03
24	OM1	OM	2	730662	730763	731596	731934	1	834	1053	1271	1	1	1	0	1 05:03
117	OM1	OM	10	146059	146367	147143	147445	1	777	1081	1385	1	1	1	0	1 05:03
109	OM1	OM	9	46174	46556	48252	48606	1	1697	2064	2431	1	1	1	0	1 05:03
166	OM1	OM	13	618075	618182	618182	618249	1	1	87	173	1	2	1	0	1 03:05
130	OM1	OM	11	20761	20824	20824	20955	1	1	97	193	1	2	1	0	1 03:05
137	OM1	OM	11	506430	506614	506614	506729	1	1	150	298	1	2	1	0	1 03:05
162	OM1	OM	13	496640	496721	496739	496955	1	19	167	314	1	2	1	0	1 03:05
115	OM1	OM	10	54311	54420	54420	54825	1	1	257	513	1	2	1	0	1 03:05
12	OM1	OM	2	350451	350900	350900	351083	1	1	316	631	1	2	1	0	1 03:05
62	OM1	OM	5	378395	378586	378586	379092	1	1	349	696	1	2	1	0	1 03:05
67	OM1	OM	6	55864	56533	56533	56854	1	1	495	989	1	2	1	0	1 03:05
110	OM1	OM	9	60879	61323	62057	62207	1	735	1031	1327	1	2	1	0	1 03:05
84	OM1	OM	7	442184	442299	443342	443602	1	1044	1231	1417	1	2	1	0	1 03:05
32	OM1	OM	3	238725	238995	239515	240922	1	521	1359	2196	1	2	1	0	1 03:05
79	OM1	OM	7	178509	179910	180364	181069	1	455	1507	2559	1	2	1	0	1 03:05
70	OM1	OM	6	158086	158256	159616	159744	1	1361	1509	1657	1	2	1	0	1 03:05
147	OM1	OM	12	439951	440042	440342	440952	1	301	651	1000	1	3	1	0	1 5:3_6:2_5:3
156	OM1	OM	13	101569	101681	102320	102554	1	640	812	984	1	3	1	0	1 5:3_4:4_5:3
26	OM1	OM	2	786902	787329	787939	788189	1	611	949	1286	1	3	1	0	1 5:3_6:2_5:3
20	OM1	OM	2	641433	641467	642776	643134	1	1310	1505	1700	1	3	1	0	1 5:3_4:4_5:3
74	OM1	OM	7	21041	21167	21543	21569	1	377	452	527	1	3	1	0	1 5:3_4:4_5:3_6:2_5:3
90	OM1	OM	7	701596	701914	703157	703857	1	1244	1752	2260	1	7	1	0	1 6:2_5:3
22	OM1	OM	2	679385	680044	681414	681557	1	1371	1771	2171	1	7	1	0	1 6:2_4:4_6:2
72	OM1	OM	6	229247	229320	230462	230627	1	1143	1261	1379	1	7	1	0	1 6:2_4:4_5:3_4:4_5:3
149	OM1	OM	12	601489	601624	603693	603907	1	2070	2244	2417	1	7	1	0	1 6:2_5:3_6:2_5:3_6:2
150	OM1	OM	12	644551	645338	645971	646705	1	634	1394	2153	1	8	1	0	1 3:5_2:6
184	OM1	OM	14	574949	575525	576383	577027	1	859	1468	2077	1	8	1	0	1 2:6_4:4_2:6
107	OM1	OM	8	516468	516616	517036	517336	1	421	644	867	1	8	1	0	1 2:6_3:5_2:6_3:5
203	OM1	OM	15	1070965	1071028	1071033	1071090	1	6	65	124	1	10	1	0	1 06:02
134	OM1	OM	11	369378	369689	369689	369878	1	1	250	499	1	10	1	0	1 06:02
18	OM1	OM	2	558042	558499	558499	558576	1	1	267	533	1	10	1	0	1 06:02
163	OM1	OM	13	540526	540798	540798	541071	1	1	273	544	1	10	1	0	1 06:02
206	OM1	OM	16	168076	169035	169035	169613	1	1	769	1536	1	10	1	0	1 06:02
136	OM1	OM	11	477776	479195	479195	479521	1	1	873	1744	1	10	1	0	1 06:02
14	OM1	OM	2	392022	392544	393197	393340	1	654	986	1317	1	10	1	0	1 06:02
178	OM1	OM	14	331699	331790	331790	332278	1	1	290	578	1	10.1	1	0	1 02:06
64	OM1	OM	5	461582	461594	461594	462226	1	1	322	643	1	10.1	1	0	1 02:06
69	OM1	OM	6	95849	96304	96305	96502	1	2	327	652	1	10.1	1	0	1 02:06
202	OM1	OM	15	986991	987247	987247	987667	1	1	338	675	1	10.1	1	0	1 02:06
192	OM1	OM	15	256235	256322	256457	256963	1	136	432	727	1	10.1	1	0	1 02:06
102	OM1	OM	8	369483	369871	369898	370655	1	28	600	1171	1	10.1	1	0	1 02:06
51	OM1	OM	4	1102674	1103455	1103488	1104014	1	34	687	1339	1	10.1	1	0	1 02:06
61	OM1	OM	5	318016	318309	318414	319404	1	106	747	1387	1	10.1	1	0	1 02:06
158	OM1	OM	13	169522	169808	169962	170932	1	155	782	1409	1	10.1	1	0	1 02:06
76	OM1	OM	7	55263	55957	55957	57501	1	1	1119	2237	1	10.1	1	0	1 02:06
44	OM1	OM	4	743651	743850	744435	745067	1	586	1001	1415	2	11	1	0	1 5:3_5:3a
41	OM1	OM	4	476888	477034	478019	478092	1	986	1095	1203	2	11	1	0	1 5:3_5:3a
75	OM1	OM	7	34992	35217	36018	36691	1	802	1250	1698	2	11	1	0	1 5:3_5:3a
4	OM1	OM	1	173222	173966	175578	175876	1	1613	2133	2653	2	11	1	0	1 5:3_5:3a

82	OM1	OM	7	345438	345471	347682	348496	1	2212	2635	3057	2	11	1	0	1 5:3_5:3a
126	OM1	OM	10	585466	586827	587861	589894	1	1035	2731	4427	2	11	1	0	1 5:3_5:3a
30	OM1	OM	3	207534	207705	208489	208699	1	785	975	1164	2	12	1	0	1 3:5_3:5a
13	OM1	OM	2	371746	372547	373488	373782	1	942	1489	2035	2	12	1	0	1 3:5_3:5a
215	OM1	OM	16	831160	831178	832685	832807	1	1508	1577	1646	2	12	1	0	1 3:5_3:5a
25	OM1	OM	2	767058	767298	768073	769699	1	776	1708	2640	2	12	1	0	1 3:5_3:5a
198	OM1	OM	15	586076	586304	588171	588409	1	1868	2100	2332	2	12	1	0	1 3:5_3:5a
175	OM1	OM	14	166733	167934	169998	170087	1	2065	2709	3353	2	12	1	0	1 3:5_3:5a
191	OM1	OM	15	242641	242848	243335	243831	1	488	839	1189	2	13	1	0	1 5:3_5:3a_4:4_5:3a
188	OM1	OM	15	108331	108945	109584	110892	1	640	1600	2560	2	14	1	0	1 3:5_3:5a_2:6
59	OM1	OM	5	183549	183864	184363	184684	1	500	817	1134	2	14	1	0	1 3:5_4:4_3:5_3:5a
179	OM1	OM	14	335707	335910	336414	336437	1	505	617	729	2	15	1	0	1 5:3_4:4_5:3a
85	OM1	OM	7	451346	451921	452589	452990	1	669	1156	1643	2	15	1	0	1 5:3_4:4_5:3a
10	OM1	OM	2	269036	269210	270207	270387	1	998	1174	1350	2	15	1	0	1 5:3_4:4_5:3a
210	OM1	OM	16	454587	454982	455955	456445	1	974	1416	1857	2	15	1	0	1 5:3_4:4_5:3a
77	OM1	OM	7	119177	119852	121176	121350	1	1325	1749	2172	2	15	1	0	1 5:3_4:4_5:3a
148	OM1	OM	12	445923	446046	447993	448167	1	1948	2096	2243	2	15	1	0	1 5:3_4:4_5:3a
196	OM1	OM	15	494089	494313	494956	495340	1	644	947	1250	2	16	1	0	1 3:5_4:4_3:5a
48	OM1	OM	4	1004000	1004480	1005656	1005728	1	1177	1452	1727	2	16	1	0	1 3:5_4:4_3:5a
23	OM1	OM	2	701354	701832	703042	703256	1	1211	1556	1901	2	16	1	0	1 3:5_4:4_3:5a
16	OM1	OM	2	466266	466523	467353	468345	1	831	1455	2078	2	17	1	0	1 5:3_4:4_5:3a_4:4_5:3a
73	OM1	OM	6	239066	239639	240385	240682	1	747	1181	1615	2	18	1	0	1 3:5_4:4_3:5a_4:4_3:5a
190	OM1	OM	15	205739	205841	208106	208220	1	2266	2373	2480	2	21	1	0	1 5:3_6:2_5:3a_4:4_5:3a
177	OM1	OM	14	307665	307785	311673	312312	1	3889	4268	4646	2	21	1	0	1 5:3_6:2_5:3_6:2_5:3_6:2_5:3a_6:2
145	OM1	OM	12	314478	314762	316496	316628	1	1735	1942	2149	2	22	1	0	1 3:5_4:4_3:5_2:6_3:5a
139	OM1	OM	11	614450	614538	615361	615437	2_nonsis	824	905	986	3	30	1	0	1 05:03
28	OM1	OM	3	96055	96799	97696	98578	2_nonsis	898	1710	2522	3	30	1	0	1 2:6_3:5
101	OM1	OM	8	267804	268308	272512	273164	2_nonsis	4205	4782	5359	3	30	1	0	1 3:5_2:6
86	OM1	OM	7	531741	532320	533847	533952	2_nonsis	1528	1869	2210	3	30	1	0	1 3:5_4:4_5:3
93	OM1	OM	7	848452	848688	850043	850236	2_nonsis	1356	1570	1783	3	30	1	0	1 5:3_3:5_4:4_3:5
6	OM1	OM	2	45075	45304	47900	47948	2_nonsis	2597	2735	2872	3	30	1	0	1 5:3_4:4_5:3a_5:3b
94	OM1	OM	7	913000	913222	915939	916059	2_nonsis	2718	2888	3058	3	30	1	0	1 3:5_5:3_4:4_5:3_3:5_5:3_5:3a
133	OM1	OM	11	316845	317019	317104	317375	2_nonsis	86	308	529	1	1	1	1	0 (5:3)_(4:4aCO)
57	OM1	OM	5	17824	18447	18447	18515	2_nonsis	1	346	690	1	1	1	1	0 (5:3)_(4:4aCO)
131	OM1	OM	11	73320	73701	73701	74074	2_nonsis	1	377	753	1	1	1	1	0 (5:3)_(4:4aCO)
120	OM1	OM	10	302207	302882	302943	303003	2_nonsis	62	429	795	1	1	1	1	0 (5:3)_(4:4aCO)
169	OM1	OM	13	820241	820753	821125	821368	2_nonsis	373	750	1126	1	1	1	1	0 (5:3)_(4:4aCO)
36	OM1	OM	4	68799	69384	69990	70167	2_nonsis	607	987	1367	1	1	1	1	0 (5:3)_(4:4aCO)
114	OM1	OM	9	424642	424776	424776	424866	2_nonsis	1	112	223	1	2	1	1	0 (3:5)_(4:4aCO)
11	OM1	OM	2	317892	318192	318225	318982	2_nonsis	34	562	1089	1	2	1	1	0 (3:5)_(4:4aCO)
152	OM1	OM	12	849651	854761	854846	855144	2_nonsis	86	2789	5492	1	2	1	1	0 (3:5)_(4:4aCO)
168	OM1	OM	13	772587	773055	773268	773415	2_nonsis	214	521	827	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
161	OM1	OM	13	456970	457507	458513	459192	2_nonsis	1007	1614	2221	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
142	OM1	OM	12	112405	112468	112663	112689	2_nonsis	196	240	283	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
7	OM1	OM	2	61810	62000	62445	62830	2_nonsis	446	733	1019	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
116	OM1	OM	10	66411	67353	70072	70786	2_nonsis	2720	3547	4374	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
121	OM1	OM	10	331024	332595	333136	333385	2_nonsis	542	1451	2360	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
52	OM1	OM	4	1241519	1242168	1242658	1246191	2_nonsis	491	2581	4671	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
187	OM1	OM	15	40593	40834	41221	41378	2_nonsis	388	586	784	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
141	OM1	OM	12	45294	47080	47204	48661	2_nonsis	125	1746	3366	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
157	OM1	OM	13	157807	159085	160280	160611	2_nonsis	1196	2000	2803	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
154	OM1	OM	13	45656	45908	46860	48814	2_nonsis	953	2055	3157	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
111	OM1	OM	9	166074	166116	169444	169471	2_nonsis	3329	3363	3396	1	11	1	1	0 (5:3)_(4:4ai)_(5:3)_(4:4bCO)
104	OM1	OM	8	378234	378579	378642	378942	2_nonsis	64	386	707	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
78	OM1	OM	7	139179	139322	139797	140188	2_nonsis	476	742	1008	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
29	OM1	OM	3	146470	146649	146949	147882	2_nonsis	301	856	1411	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
182	OM1	OM	14	487393	487663	488208	488587	2_nonsis	546	870	1193	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
88	OM1	OM	7	609614	609644	609958	610218	2_nonsis	315	459	603	1	12	1	1	0 (5:3)_(4:4aCO)_(5:3)_(4:4a)
118	OM1	OM	10	183834	184128	184439	184592	2_nonsis	312	535	757	1	12	1	1	0 (3:5)_(4:4aCO)_(3:5)_(4:4a)
55	OM1	OM	4	1509719	1509983	1510510	1511013	2_nonsis	528	911	1293	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)

195	OM1	OM	15	461434	461644	462267	462906	2_nonsis	624	1048	1471	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
185	OM1	OM	14	643259	643444	644271	644875	2_nonsis	828	1222	1615	1	12	1	1	0	(6:2)_(4:4)_(5:3)_(4:4aCO)
71	OM1	OM	6	204282	204454	205702	205793	2_nonsis	1249	1380	1510	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
193	OM1	OM	15	268456	269276	270526	270656	2_nonsis	1251	1725	2199	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(4:4aCO)
140	OM1	OM	11	619375	619475	620968	621343	2_nonsis	1494	1731	1967	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
165	OM1	OM	13	590865	591615	593072	593361	2_nonsis	1458	1977	2495	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
95	OM1	OM	7	948202	949014	950926	951196	2_nonsis	1913	2453	2993	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
167	OM1	OM	13	666220	666667	667511	667766	2_nonsis	845	1195	1545	1	12	1	1	0	(4:4aCO)_(5:3)_(4:4a)_(5:3)_(4:4a)
211	OM1	OM	16	497140	497162	498200	498617	2_nonsis	1039	1258	1476	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4)_(4:4aCO)
106	OM1	OM	8	510752	510778	512291	512682	2_nonsis	1514	1722	1929	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(4:4aCO)
127	OM1	OM	10	704056	704425	705938	706135	2_nonsis	1514	1796	2078	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
181	OM1	OM	14	410941	411667	412609	413686	2_nonsis	943	1844	2744	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
68	OM1	OM	6	88777	89605	91021	91098	2_nonsis	1417	1869	2320	1	12	1	1	0	(4:4aCO)_(5:3)_(4:4a)_(5:3)_(4:4a)
33	OM1	OM	3	272348	273723	276551	277187	2_nonsis	2829	3834	4838	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(4:4aCO)
207	OM1	OM	16	170349	170630	171270	171314	2_nonsis	641	803	964	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(3:5)_(4:4aCO)
144	OM1	OM	12	230218	230960	232561	233075	2_nonsis	1602	2229	2856	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(6:2)_(4:4a)
201	OM1	OM	15	985000	985377	985377	985518	2_nonsis	1	259	517	1	15	1	1	0	(6:2)_(4:4aCO)
63	OM1	OM	5	414243	414432	414642	414720	2_nonsis	211	344	476	1	15	1	1	0	(6:2)_(4:4aCO)
100	OM1	OM	8	195826	195949	196180	196402	2_nonsis	232	404	575	1	15	1	1	0	(6:2)_(4:4aCO)
47	OM1	OM	4	908967	909447	909447	909908	2_nonsis	1	471	940	1	15	1	1	0	(6:2)_(4:4aCO)
213	OM1	OM	16	677287	677647	677836	678266	2_nonsis	190	584	978	1	15	1	1	0	(6:2)_(4:4aCO)
80	OM1	OM	7	244757	245112	245422	245686	2_nonsis	311	620	928	1	15	1	1	0	(6:2)_(4:4aCO)
132	OM1	OM	11	172715	173133	173315	173801	2_nonsis	183	634	1085	1	15	1	1	0	(6:2)_(4:4aCO)
197	OM1	OM	15	510696	511001	511476	511568	2_nonsis	476	674	871	1	15	1	1	0	(6:2)_(4:4aCO)
50	OM1	OM	4	1044635	1044751	1045062	1045735	2_nonsis	312	706	1099	1	15	1	1	0	(6:2)_(4:4aCO)
208	OM1	OM	16	253297	253600	254117	254324	2_nonsis	518	772	1026	1	15	1	1	0	(6:2)_(4:4aCO)
19	OM1	OM	2	611338	611905	611905	613145	2_nonsis	1	904	1806	1	15	1	1	0	(6:2)_(4:4aCO)
53	OM1	OM	4	1268647	1269918	1269918	1270457	2_nonsis	1	905	1809	1	15	1	1	0	(6:2)_(4:4aCO)
17	OM1	OM	2	504535	504568	505298	506138	2_nonsis	731	1167	1602	1	15	1	1	0	(6:2)_(4:4aCO)
204	OM1	OM	16	29458	29604	29674	29749	2_nonsis	71	181	290	1	16	1	1	0	(2:6)_(4:4aCO)
43	OM1	OM	4	699938	700023	700170	700186	2_nonsis	148	198	247	1	16	1	1	0	(2:6)_(4:4aCO)
199	OM1	OM	15	670429	670593	670593	670904	2_nonsis	1	238	474	1	16	1	1	0	(2:6)_(4:4aCO)
194	OM1	OM	15	407171	407340	407340	407771	2_nonsis	1	300	599	1	16	1	1	0	(2:6)_(4:4aCO)
170	OM1	OM	13	838248	838336	838336	838867	2_nonsis	1	310	618	1	16	1	1	0	(2:6)_(4:4aCO)
151	OM1	OM	12	677815	677890	678194	678512	2_nonsis	305	501	696	1	16	1	1	0	(2:6)_(4:4aCO)
97	OM1	OM	8	81320	81666	81685	82351	2_nonsis	20	525	1030	1	16	1	1	0	(2:6)_(4:4aCO)
40	OM1	OM	4	410728	411048	411335	411785	2_nonsis	288	672	1056	1	16	1	1	0	(2:6)_(4:4aCO)
200	OM1	OM	15	806960	807123	807631	807840	2_nonsis	509	694	879	1	16	1	1	0	(2:6)_(4:4aCO)
214	OM1	OM	16	828891	829002	829418	830004	2_nonsis	417	765	1112	1	16	1	1	0	(2:6)_(4:4aCO)
172	OM1	OM	14	56038	57439	57439	57579	2_nonsis	1	771	1540	1	16	1	1	0	(2:6)_(4:4aCO)
21	OM1	OM	2	661374	662094	662444	666708	2_nonsis	351	2842	5333	1	16	1	1	0	(2:6)_(4:4aCO)
160	OM1	OM	13	287574	287682	287574	287682	2_nonsis	0	54	107	1	100	1	1	0	(4:4aCO)
38	OM1	OM	4	164096	164298	164096	164298	2_nonsis	0	101	201	1	100	1	1	0	(4:4aCO)
2	OM1	OM	1	61708	61999	61708	61999	2_nonsis	0	145	290	1	100	1	1	0	(4:4aCO)
209	OM1	OM	16	374857	375235	374857	375235	2_nonsis	0	189	377	1	100	1	1	0	(4:4aCO)
31	OM1	OM	3	225200	225631	225200	225631	2_nonsis	0	215	430	1	100	1	1	0	(4:4aCO)
146	OM1	OM	12	341070	341507	341070	341507	2_nonsis	0	218	436	1	100	1	1	0	(4:4aCO)
113	OM1	OM	9	303489	303983	303489	303983	2_nonsis	0	247	493	1	100	1	1	0	(4:4aCO)
212	OM1	OM	16	607028	607677	607028	607677	2_nonsis	0	324	648	1	100	1	1	0	(4:4aCO)
129	OM1	OM	11	19020	19855	19020	19855	2_nonsis	0	417	834	1	100	1	1	0	(4:4aCO)
27	OM1	OM	3	77900	78844	77900	78844	2_nonsis	0	472	943	1	100	1	1	0	(4:4aCO)
54	OM1	OM	4	1355944	1357024	1355944	1357024	2_nonsis	0	540	1079	1	100	1	1	0	(4:4aCO)
60	OM1	OM	5	256810	258361	256810	258361	2_nonsis	0	775	1550	1	100	1	1	0	(4:4aCO)
3	OM1	OM	1	130975	135319	130975	135319	2_nonsis	0	2172	4343	1	100	1	1	0	(4:4aCO)
46	OM1	OM	4	816853	817682	817919	818507	2_nonsis	238	946	1653	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
123	OM1	OM	10	398357	398746	399390	400622	2_nonsis	645	1455	2264	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
92	OM1	OM	7	799970	800086	803311	803780	2_nonsis	3226	3518	3809	2	31	1	1	0	(3:5)_(3:5a)_(3:5b)_(4:4aCO)
186	OM1	OM	14	689057	689310	690428	691118	2_nonsis	1119	1588	2057	2	31	1	1	0	(2:6)_(4:4aCO)_(3:5)_(3:5a)_(4:4a)
108	OM1	OM	9	37222	39367	42866	43949	2_nonsis	3500	5113	6726	2	31	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(3:5a)_(4:4aCO)
173	OM1	OM	14	116131	116459	118803	119128	2_nonsis	2345	2671	2996	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(4:4aCO)

119 OM1	OM	10	189441	190275	192156	192956	2_nonsis		1882	2698	3514	2	32	1	1	0 (5:3)_(4:4aCO)_(5:3a)_(4:4a)
42 OM1	OM	4	614321	614433	617533	617915	2_nonsis		3101	3347	3593	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
87 OM1	OM	7	559914	560083	560364	560455	2_nonsis		282	411	540	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
216 OM1	OM	16	921352	921490	921998	922220	2_nonsis		509	688	867	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
5 OM1	OM	1	184083	184235	184921	185150	2_nonsis		687	877	1066	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
180 OM1	OM	14	372088	372101	373375	373628	2_nonsis		1275	1407	1539	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
112 OM1	OM	9	175126	175167	176578	177082	2_nonsis		1412	1684	1955	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
125 OM1	OM	10	544523	545038	547200	547730	2_nonsis		2163	2685	3206	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
91 OM1	OM	7	733970	733979	734573	734668	2_nonsis		595	646	697	3	20	1	1	0 (2:6)_(5:3)_(2:6)_(4:4aCO)
58 OM1	OM	5	173989	174295	174794	175154	2_nonsis		500	832	1164	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(4:4aCO)
34 OM1	OM	4	61175	61275	62205	62366	2_nonsis		931	1061	1190	3	20	1	1	0 (3:5)_(6:2)_(5:3)_(4:4aCO)
99 OM1	OM	8	120445	121477	122655	122848	2_nonsis		1179	1791	2402	3	20	1	1	0 (5:3)_(3:5)_(6:2)_(4:4aCO)
164 OM1	OM	13	541852	542119	543392	543706	2_nonsis		1274	1564	1853	3	20	1	1	0 (6:2)_(4:4)_(6:2)_(3:5)_(4:4aCO)
39 OM1	OM	4	278692	280191	281647	281853	2_nonsis		1457	2309	3160	3	20	1	1	0 (2:6)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
183 OM1	OM	14	549663	550069	553809	554217	2_nonsis		3741	4147	4553	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
138 OM1	OM	11	573530	574134	577779	578230	2_nonsis		3646	4173	4699	3	20	1	1	0 (5:3)_(6:2)_(5:3)_(3:5)_(4:4aCO)
1 OM1	OM	1	36160	36898	38689	38888	2_nonsis		1792	2260	2727	3	20	1	1	0 (2:6)_(3:5)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
83 OM1	OM	7	427600	427741	431344	431867	2_nonsis		3604	3935	4266	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
189 OM1	OM	15	170203	170363	172081	172515	2_nonsis		1719	2015	2311	3	20	1	1	0 (3:5)_(4:4)_(3:5a)_(2:6)_(3:5)_(6:2)_(4:4aCO)
135 OM1	OM	11	428081	428986	429694	429883	2_nonsis		709	1255	1801	3	21	1	1	0 (4:4ai)_(5:3)_(3:5)_(4:4bCO)
8 OM1	OM	2	70638	70774	72233	72395	2_nonsis		1460	1608	1756	3	21	1	1	0 (5:3)_(4:4ai)_(3:5)_(2:6)_(3:5)_(4:4bCO)
35 OM1	OM	4	64539	64917	66855	67141	2_nonsis		1939	2270	2601	3	21	1	1	0 (5:3)_(4:4ai)_(3:5)_(2:6)_(3:5)_(4:4bCO)
9 OM1	OM	2	215989	216051	218741	219119		3	2691	2910	3129	0	2	2	1	1 (3:5)_(4:4ai)_(5:3)_(4:4bCO)
15 OM1	OM	2	430067	431229	435951	436119		3	4723	5387	6051	0	2	2	1	1 (3:5)_(3:5a)_(2:6)_(3:5)_(4:4)_(3:5)_(5:3)_(4:4aCO)
81 OM1	OM	7	271422	271683	273422	273707		3	1740	2012	2284	0	2	2	1	1 (3:5)_(4:4ai)_(4:4bCO)
143 OM1	OM	12	223258	223495	225620	225795		3	2126	2331	2536	0	2	2	1	1 (3:5)_(2:6)_(3:5)_(4:4)_(3:5a)_(4:4aCO)
176 OM1	OM	14	190429	190588	192780	193106		3	2193	2435	2676	0	2	2	1	1 (2:6)_(3:5)_(4:4ai)_(4:4bCO)
96 OM1	OM	7	1050064	1050446	1052107	1052468		3	1662	2033	2403	0	3	2	1	1 (2:6)_(4:4aCO)_(6:2)_(4:4bCO)
124 OM1	OM	10	453451	454963	455506	456781	2_nonsis		544	1937	3329	0	3	2	0	2 (3:5)_(4:4aCO)_(3:5a)_(4:4CO)
128 OM1	OM	10	722676	723534	725475	725492	2_nonsis		1942	2379	2815	0	3	2	0	2 (3:5)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4CO)_(5:3)_(4:4)
153 OM1	OM	12	1013592	1014017	1015598	1015774	2_nonsis		1582	1882	2181	0	3	2	0	2 (4:4aCO)_(2:6)_(3:5)_(4:4a)_(2:6)_(3:5a)_(4:4CO)
103 OM2	OM	9	160362	160453	160457	160514		1	5	78	151	1	1	1	0	1 05:03
204 OM2	OM	16	347463	347684	347684	347716		1	1	127	252	1	1	1	0	1 05:03
49 OM2	OM	4	1402857	1402868	1402910	1403082		1	43	134	224	1	1	1	0	1 05:03
143 OM2	OM	12	829264	829433	829433	829534		1	1	135	269	1	1	1	0	1 05:03
112 OM2	OM	10	360316	360588	360588	360746		1	1	215	429	1	1	1	0	1 05:03
86 OM2	OM	7	785318	785828	785828	785851		1	1	267	532	1	1	1	0	1 05:03
5 OM2	OM	2	193664	193715	193715	194226		1	1	281	561	1	1	1	0	1 05:03
164 OM2	OM	13	914620	915009	915009	915182		1	1	281	561	1	1	1	0	1 05:03
135 OM2	OM	12	260086	260298	260496	260584		1	199	348	497	1	1	1	0	1 05:03
92 OM2	OM	8	189521	190024	190024	190339		1	1	409	817	1	1	1	0	1 05:03
39 OM2	OM	4	635784	636201	636352	636465		1	152	416	680	1	1	1	0	1 05:03
152 OM2	OM	13	228322	228901	228901	229206		1	1	442	883	1	1	1	0	1 05:03
76 OM2	OM	7	304247	304566	304734	305050		1	169	486	802	1	1	1	0	1 05:03
189 OM2	OM	15	742445	742492	742716	743206		1	225	493	760	1	1	1	0	1 05:03
59 OM2	OM	5	326423	326990	327079	327363		1	90	515	939	1	1	1	0	1 05:03
100 OM2	OM	9	74241	74340	74723	75152		1	384	647	910	1	1	1	0	1 05:03
128 OM2	OM	11	629864	630615	630615	631180		1	1	658	1315	1	1	1	0	1 05:03
126 OM2	OM	11	521737	521933	522458	522560		1	526	674	822	1	1	1	0	1 05:03
56 OM2	OM	5	131558	132643	132767	133007		1	125	787	1448	1	1	1	0	1 05:03
35 OM2	OM	4	375458	375530	375932	376661		1	403	803	1202	1	1	1	0	1 05:03
33 OM2	OM	4	286258	287699	287699	288063		1	1	903	1804	1	1	1	0	1 05:03
95 OM2	OM	8	419057	419187	420099	420248		1	913	1052	1190	1	1	1	0	1 05:03
13 OM2	OM	2	477368	479516	479516	479752		1	1	1192	2383	1	1	1	0	1 05:03
120 OM2	OM	11	218177	218544	218976	220318		1	433	1287	2140	1	1	1	0	1 05:03
82 OM2	OM	7	590933	591242	592334	592660		1	1093	1410	1726	1	1	1	0	1 05:03
154 OM2	OM	13	388681	388700	388700	388702		1	1	11	20	1	2	1	0	1 03:05
160 OM2	OM	13	707030	707109	707109	707180		1	1	75	149	1	2	1	0	1 03:05
109 OM2	OM	10	79812	79831	79840	79972		1	10	85	159	1	2	1	0	1 03:05
54 OM2	OM	5	42217	42238	42280	42354		1	43	90	136	1	2	1	0	1 03:05

216	OM2	OM	16	775448	775673	775673	775730	1	1	141	281	1	2	1	0	1 03:05
199	OM2	OM	16	114414	114586	114586	114774	1	1	180	359	1	2	1	0	1 03:05
104	OM2	OM	9	195082	195274	195274	195521	1	1	220	438	1	2	1	0	1 03:05
198	OM2	OM	16	74885	74937	74937	75355	1	1	235	469	1	2	1	0	1 03:05
133	OM2	OM	12	198146	198396	198484	198532	1	89	237	385	1	2	1	0	1 03:05
107	OM2	OM	10	40683	41107	41107	41211	1	1	264	527	1	2	1	0	1 03:05
44	OM2	OM	4	888734	889122	889122	889358	1	1	312	623	1	2	1	0	1 03:05
147	OM2	OM	12	1001464	1001833	1001922	1002086	1	90	356	621	1	2	1	0	1 03:05
77	OM2	OM	7	356141	356393	356588	356663	1	196	359	521	1	2	1	0	1 03:05
119	OM2	OM	11	174125	174419	174509	174833	1	91	399	707	1	2	1	0	1 03:05
153	OM2	OM	13	273767	274088	274088	274730	1	1	482	962	1	2	1	0	1 03:05
206	OM2	OM	16	425481	425740	426048	426150	1	309	489	668	1	2	1	0	1 03:05
184	OM2	OM	15	487166	487809	487838	488123	1	30	493	956	1	2	1	0	1 03:05
6	OM2	OM	2	202580	202724	203030	203566	1	307	646	985	1	2	1	0	1 03:05
156	OM2	OM	13	511632	512090	512558	512572	1	469	704	939	1	2	1	0	1 03:05
61	OM2	OM	5	342945	343116	343350	344171	1	235	730	1225	1	2	1	0	1 03:05
70	OM2	OM	6	195471	195636	196194	196491	1	559	789	1019	1	2	1	0	1 03:05
66	OM2	OM	5	545109	545863	546141	546545	1	279	857	1435	1	2	1	0	1 03:05
177	OM2	OM	15	82218	82279	83069	83198	1	791	885	979	1	2	1	0	1 03:05
131	OM2	OM	12	124421	124596	124986	126014	1	391	992	1592	1	2	1	0	1 03:05
148	OM2	OM	12	1042570	1042844	1043701	1043895	1	858	1091	1324	1	2	1	0	1 03:05
170	OM2	OM	14	331067	331336	332371	332613	1	1036	1291	1545	1	2	1	0	1 03:05
75	OM2	OM	7	273422	273707	274448	275758	1	742	1539	2335	1	2	1	0	1 03:05
138	OM2	OM	12	521782	522608	522914	525267	1	307	1896	3484	1	2	1	0	1 03:05
144	OM2	OM	12	849651	854846	855154	856994	1	309	3826	7342	1	2	1	0	1 03:05
97	OM2	OM	8	483502	483796	484090	485522	1	295	1157	2019	1	3	1	0	1 5:3_6:2_5:3
50	OM2	OM	4	1417050	1417646	1418937	1419231	1	1292	1736	2180	1	3	1	0	1 5:3_6:2_5:3
83	OM2	OM	7	610674	611145	612267	612759	1	1123	1604	2084	1	4	1	0	1 3:5_4:4_3:5
37	OM2	OM	4	548255	548809	551587	551626	1	2779	3075	3370	1	4	1	0	1 3:5_4:4_3:5_2:6_3:5
207	OM2	OM	16	449172	450060	450430	450669	1	371	934	1496	1	7	1	0	1 5:3_6:2
45	OM2	OM	4	955335	955435	958717	959103	1	3283	3525	3767	1	7	1	0	1 6:2_5:3_4:4_5:3_4:4_5:3_4:4_5:3
81	OM2	OM	7	582077	582172	582429	582790	1	258	485	712	1	8	1	0	1 2:6_3:5
85	OM2	OM	7	732583	733373	733567	733673	1	195	642	1089	1	8	1	0	1 2:6_3:5
180	OM2	OM	15	220116	220335	220880	220974	1	546	702	857	1	8	1	0	1 3:5_4:4_2:6
57	OM2	OM	5	146641	146798	146798	146845	1	1	102	203	1	10	1	0	1 06:02
51	OM2	OM	4	1420794	1420932	1420941	1421025	1	10	120	230	1	10	1	0	1 06:02
14	OM2	OM	2	490619	490686	490686	491476	1	1	429	856	1	10	1	0	1 06:02
42	OM2	OM	4	820502	821075	821075	821822	1	1	660	1319	1	10.1	1	0	1 02:06
88	OM2	OM	7	912431	912560	913222	913393	1	663	812	961	2	11	1	0	1 5:3_5:3a
65	OM2	OM	5	540880	541003	541873	541980	1	871	985	1099	2	11	1	0	1 5:3_5:3a
10	OM2	OM	2	305500	305677	306376	306932	1	700	1066	1431	2	11	1	0	1 5:3_5:3a
90	OM2	OM	8	50050	50186	51314	51378	1	1129	1228	1327	2	11	1	0	1 5:3_5:3a
159	OM2	OM	13	674283	675083	675970	676095	1	888	1350	1811	2	11	1	0	1 5:3_5:3a
190	OM2	OM	15	816620	816745	818428	818557	1	1684	1810	1936	2	11	1	0	1 5:3_5:3a
26	OM2	OM	3	224038	224261	225710	226498	1	1450	1955	2459	2	11	1	0	1 5:3_5:3a
182	OM2	OM	15	315837	316312	316611	317034	1	300	748	1196	2	12	1	0	1 3:5_3:5a
167	OM2	OM	14	168712	169090	169784	169998	1	695	990	1285	2	12	1	0	1 3:5_3:5a
11	OM2	OM	2	323214	323896	324467	324761	1	572	1059	1546	2	12	1	0	1 3:5_3:5a
125	OM2	OM	11	515018	515114	516158	516240	1	1045	1133	1221	2	12	1	0	1 3:5_3:5a
158	OM2	OM	13	666220	666667	667766	668207	1	1100	1543	1986	2	12	1	0	1 3:5_3:5a
52	OM2	OM	4	1452723	1453451	1455354	1455507	1	1904	2344	2783	2	12	1	0	1 3:5_3:5a
116	OM2	OM	10	645177	645288	647196	647651	1	1909	2191	2473	2	14	1	0	1 3:5_4:4_3:5_3:5a
96	OM2	OM	8	437014	437680	439710	440297	1	2031	2657	3282	2	14	1	0	1 3:5_4:4_3:5_3:5a
188	OM2	OM	15	700514	700551	701772	701808	1	1222	1258	1293	2	14	1	0	1 3:5_2:6_3:5_3:5a_4:4_3:5a
93	OM2	OM	8	238630	238746	239033	239430	1	288	544	799	2	15	1	0	1 5:3_4:4_5:3a
212	OM2	OM	16	656563	656605	657509	657678	1	905	1010	1114	2	15	1	0	1 5:3_4:4_5:3a
195	OM2	OM	15	1010000	1010114	1010673	1011684	1	560	1122	1683	2	16	1	0	1 3:5_4:4_3:5a
215	OM2	OM	16	754107	754263	755318	755437	1	1056	1193	1329	2	16	1	0	1 3:5_4:4_3:5a
210	OM2	OM	16	609630	609903	610981	611302	1	1079	1375	1671	2	16	1	0	1 3:5_4:4_3:5a
63	OM2	OM	5	471690	471723	473209	473281	1	1487	1539	1590	2	16	1	0	1 3:5_4:4_3:5a

19	OM2	OM	2	734046	734409	735807	736128	1	1399	1740	2081	2	16	1	0	1 3:5_4:4_3:5a
17	OM2	OM	2	679385	680044	680726	681166	1	683	1232	1780	2	17	1	0	1 5:3_4:4_5:3a_6:2
73	OM2	OM	7	120933	120977	122047	122120	1	1071	1129	1186	2	17	1	0	1 5:3_4:4_5:3a_6:2_5:3a_6:2_5:3a
41	OM2	OM	4	769372	769508	771211	771632	1	1704	1982	2259	2	18	1	0	1 3:5_4:4_3:5a_4:4_3:5a
203	OM2	OM	16	286085	286209	287664	288762	1	1456	2066	2676	2	18	1	0	1 3:5_4:4_3:5a_2:6_3:5a
110	OM2	OM	10	294302	294332	296106	296529	1	1775	2001	2226	2	18	1	0	1 2:6_3:5_4:4_3:5_4:4_3:5a
181	OM2	OM	15	271047	271168	271758	271964	1	591	754	916	2	19	1	0	1 5:3_6:2_5:3a
209	OM2	OM	16	581896	582013	583481	583659	1	1469	1616	1762	2	19	1	0	1 5:3_6:2_5:3a
139	OM2	OM	12	587932	588394	589563	590028	1	1170	1633	2095	2	19	1	0	1 5:3_6:2_5:3a
9	OM2	OM	2	269029	269036	269987	270191	1	952	1057	1161	2	20	1	0	1 3:5_2:6_3:5a
98	OM2	OM	8	503996	505427	506192	506267	1	766	1518	2270	2	20	1	0	1 3:5_2:6_3:5a
68	OM2	OM	6	94545	94981	96991	97235	1	2011	2350	2689	2	21	1	0	1 5:3_6:2_5:3_6:2_5:3a
78	OM2	OM	7	421478	421561	424065	424176	1	2505	2601	2697	2	23	1	0	1 3:5_4:4_2:6_3:5a_4:4_3:5a_4:4_2:6_3:5a
136	OM2	OM	12	367546	367570	368453	368695	2_nonsis		884	1016	1148	3	30	1	0	1 3:5_6:2_3:5
22	OM2	OM	3	50664	51152	51650	52350	2_nonsis		499	1092	1685	3	30	1	0	1 5:3_4:4_3:5
175	OM2	OM	14	730427	730652	731562	732158	2_nonsis		911	1321	1730	3	30	1	0	1 5:3_5:3a_3:5
23	OM2	OM	3	94376	94470	96988	97369	2_nonsis		2519	2756	2992	3	30	1	0	1 5:3_5:3a_5:3b
129	OM2	OM	11	633545	633641	633641	634259	2_nonsis		1	357	713	3	31	1	0	1 4:4ai
161	OM2	OM	13	751553	751891	752521	753954	2_nonsis		631	1516	2400	3	31	1	0	1 5:3_4:4ai_5:3a
108	OM2	OM	10	52186	52869	54311	54420	2_nonsis		1443	1838	2233	3	31	1	0	1 5:3_4:4ai_3:5
145	OM2	OM	12	867405	869664	873021	873153	2_nonsis		3358	4553	5747	3	31	1	0	1 4:4ai_3:5_4:4ai
32	OM2	OM	4	263030	263811	270285	271431	2_nonsis		6475	7438	8400	3	31	1	0	1 4:4ai_3:5_3:5a
123	OM2	OM	11	401736	401769	403011	403407	2_nonsis		1243	1457	1670	3	31	1	0	1 3:5_4:4_4:4ai_5:3
30	OM2	OM	4	169331	170362	173380	174736	2_nonsis		3019	4212	5404	3	31	1	0	1 4:4ai_3:5_2:6_3:5_3:5a
101	OM2	OM	9	100450	102247	103227	103838	2_nonsis		981	2184	3387	3	31	1	0	1 3:5_2:6_3:5a_3:5b_4:4ai_5:3
3	OM2	OM	1	191704	191755	194625	194803	2_nonsis		2871	2985	3098	3	31	1	0	1 5:3_4:4_6:2_4:4_5:3a_4:4ai
15	OM2	OM	2	524315	524415	528294	528370	2_nonsis		3880	3967	4054	3	31	1	0	1 4:4ai_3:5_4:4_3:5_4:4_3:5a
89	OM2	OM	7	986883	986910	988550	988609	2_nonsis		1641	1683	1725	3	31	1	0	1 5:3_4:4_5:3a_4:4_3:5_4:4ai_6:2_5:3a
34	OM2	OM	4	314015	314500	314500	315175	2_nonsis		1	580	1159	1	1	1	1	0 (5:3)_(4:4aCO)
58	OM2	OM	5	184684	185983	185983	186070	2_nonsis		1	693	1385	1	1	1	1	0 (5:3)_(4:4aCO)
186	OM2	OM	15	604804	605119	605119	606232	2_nonsis		1	714	1427	1	1	1	1	0 (5:3)_(4:4aCO)
174	OM2	OM	14	652841	653557	653635	655138	2_nonsis		79	1188	2296	1	1	1	1	0 (5:3)_(4:4aCO)
21	OM2	OM	3	23149	23567	23887	25689	2_nonsis		321	1430	2539	1	1	1	1	0 (5:3)_(4:4aCO)
16	OM2	OM	2	585814	585909	585909	586331	2_nonsis		1	259	516	1	2	1	1	0 (3:5)_(4:4aCO)
162	OM2	OM	13	797688	798060	798090	798261	2_nonsis		31	302	572	1	2	1	1	0 (3:5)_(4:4aCO)
47	OM2	OM	4	1286871	1286949	1287125	1287842	2_nonsis		177	574	970	1	2	1	1	0 (3:5)_(4:4aCO)
121	OM2	OM	11	242705	243550	243838	244481	2_nonsis		289	1032	1775	1	2	1	1	0 (3:5)_(4:4aCO)
118	OM2	OM	11	28441	30068	30068	31754	2_nonsis		1	1657	3312	1	2	1	1	0 (3:5)_(4:4aCO)
202	OM2	OM	16	230335	230413	231052	231144	2_nonsis		640	724	808	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
69	OM2	OM	6	154357	154385	155718	155985	2_nonsis		1334	1481	1627	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
130	OM2	OM	12	95188	97490	97654	98056	2_nonsis		165	1516	2867	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
155	OM2	OM	13	411264	412303	412382	412745	2_nonsis		80	780	1480	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
150	OM2	OM	13	169522	169808	170002	170932	2_nonsis		195	802	1409	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
71	OM2	OM	6	244444	245103	246533	246625	2_nonsis		1431	1806	2180	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
192	OM2	OM	15	903669	903843	904346	904817	2_nonsis		504	826	1147	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
25	OM2	OM	3	162361	162686	163699	164093	2_nonsis		1014	1373	1731	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
62	OM2	OM	5	392326	392813	394083	394357	2_nonsis		1271	1651	2030	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
211	OM2	OM	16	612912	613008	613103	613637	2_nonsis		96	410	724	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
124	OM2	OM	11	491161	491399	491873	492251	2_nonsis		475	782	1089	1	11	1	1	0 (6:2)_(4:4)_(4:4ai)_(4:4bCO)
191	OM2	OM	15	825345	826024	826212	826624	2_nonsis		189	734	1278	1	12	1	1	0 (3:5)_(4:4aCO)_(3:5)_(4:4a)
12	OM2	OM	2	332548	332630	333382	334070	2_nonsis		753	1137	1521	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
29	OM2	OM	4	140835	141791	143253	143335	2_nonsis		1463	1981	2499	1	12	1	1	0 (5:3)_(4:4)_(6:2)_(4:4aCO)
165	OM2	OM	14	49011	49737	51868	52069	2_nonsis		2132	2595	3057	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
67	OM2	OM	6	51193	51257	51603	2_nonsis		347	451	554	1	12	1	1	0 (2:6)_(4:4)_(3:5)_(2:6)_(4:4aCO)
84	OM2	OM	7	694539	694708	695230	695342	2_nonsis		523	663	802	1	15	1	1	0 (6:2)_(4:4aCO)
53	OM2	OM	4	1474578	1475249	1475397	1475979	2_nonsis		149	775	1400	1	15	1	1	0 (6:2)_(4:4aCO)
134	OM2	OM	12	257669	257813	257813	258349	2_nonsis		1	340	679	1	16	1	1	0 (2:6)_(4:4aCO)
142	OM2	OM	12	826618	827343	827343	827901	2_nonsis		1	642	1282	1	16	1	1	0 (2:6)_(4:4aCO)
217	OM2	OM	16	829035	829198	829035	829198	2_nonsis		0	81	162	1	100	1	1	0 (4:4aCO)
72	OM2	OM	7	38848	39412	38848	39412	2_nonsis		0	282	563	1	100	1	1	0 (4:4aCO)

								2_nonsis									
7 OM2	OM	2	204536	205151	204536	205151	2_nonsis	0	307	614	1	100	1	1	0 (4:4aCO)
48 OM2	OM	4	1288775	1289394	1288775	1289394	2_nonsis	0	309	618	1	100	1	1	0 (4:4aCO)
114 OM2	OM	10	450678	451382	450678	451382	2_nonsis	0	352	703	1	100	1	1	0 (4:4aCO)
91 OM2	OM	8	186453	187527	186453	187527	2_nonsis	0	537	1073	1	100	1	1	0 (4:4aCO)
27 OM2	OM	3	252633	253903	252633	253903	2_nonsis	0	635	1269	1	100	1	1	0 (4:4aCO)
115 OM2	OM	10	570822	573135	570822	573135	2_nonsis	0	1156	2312	1	100	1	1	0 (4:4aCO)
178 OM2	OM	15	198700	198772	199186	199433	2_nonsis	415	574	732	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
43 OM2	OM	4	859708	859980	861727	862580	2_nonsis	1748	2310	2871	2	30	1	1	0 (6:2)_(5:3)_(5:3a)_(4:4aCO)
173 OM2	OM	14	558085	558811	559885	559919	2_nonsis	1075	1454	1833	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
197 OM2	OM	16	53429	53499	65675	66393	2_nonsis	12177	12570	12963	2	30	1	1	0 (4:4ai)_(5:3)_(5:3a)_(6:2)_(5:3a)_(4:4bCO)
196 OM2	OM	15	1053326	1053371	1055396	1055524	2_nonsis	2026	2112	2197	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)_(5:3a)_(6:2)_(5:3a)_(4:4a)
179 OM2	OM	15	203386	203506	205574	205723	2_nonsis	2069	2203	2336	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
106 OM2	OM	9	401375	402165	404802	405428	2_nonsis	2638	3345	4052	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
117 OM2	OM	10	704705	704768	707333	707549	2_nonsis	2566	2705	2843	2	31	1	1	0 (3:5)_(3:5a)_(4:4)_(3:5)_(4:4aCO)
18 OM2	OM	2	706449	706983	707509	708202	2_nonsis	527	1140	1752	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(4:4aCO)
132 OM2	OM	12	193985	194032	195201	195525	2_nonsis	1170	1355	1539	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
140 OM2	OM	12	627370	627543	628424	629441	2_nonsis	882	1476	2070	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
64 OM2	OM	5	521844	521857	523683	524394	2_nonsis	1827	2188	2549	2	32	1	1	0 (3:5)_(4:4aCO)_(3:5a)_(4:4a)
176 OM2	OM	15	40365	40497	41495	41838	2_nonsis	999	1236	1472	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(2:6)_(4:4aCO)
111 OM2	OM	10	331024	332595	333385	333992	2_nonsis	791	1879	2967	2	32	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5a)_(4:4a)
102 OM2	OM	9	136172	136619	138293	138305	2_nonsis	1675	1904	2132	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
36 OM2	OM	4	430899	430932	432803	432926	2_nonsis	1872	1949	2026	2	32	1	1	0 (3:5)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
94 OM2	OM	8	327083	327422	330227	330629	2_nonsis	2806	3176	3545	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(6:2)_(4:4aCO)
193 OM2	OM	15	941405	941706	944698	945099	2_nonsis	2993	3343	3693	2	32	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5a)_(4:4a)
8 OM2	OM	2	215181	215962	218741	219119	2_nonsis	2780	3359	3937	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(3:5b)_(4:4aCO)
169 OM2	OM	14	270133	270187	271256	271443	2_nonsis	1070	1190	1309	2	32	1	1	0 (5:3)_(4:4ai)_(5:3a)_(4:4bCO)_(6:2)_(4:4b)
187 OM2	OM	15	648434	648663	650442	650943	2_nonsis	1780	2144	2508	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4)_(6:2)_(4:4aCO)
172 OM2	OM	14	486092	486859	488598	488965	2_nonsis	1740	2306	2872	2	32	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5a)_(3:5)_(4:4a)
137 OM2	OM	12	514693	514832	517338	517614	2_nonsis	2507	2714	2920	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(4:4)_(5:3)_(6:2)_(4:4aCO)
99 OM2	OM	9	35774	35955	37222	39244	2_nonsis	1268	2369	3469	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4)_(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
87 OM2	OM	7	848688	849134	849797	849971	2_nonsis	664	973	1282	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
80 OM2	OM	7	523740	524713	524998	525413	2_nonsis	286	979	1672	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
163 OM2	OM	13	857842	858111	859063	859155	2_nonsis	953	1133	1312	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
20 OM2	OM	2	743899	744063	745085	745190	2_nonsis	1023	1157	1290	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
213 OM2	OM	16	677836	678266	679094	679573	2_nonsis	829	1283	1736	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
38 OM2	OM	4	615258	615413	616624	616689	2_nonsis	1212	1321	1430	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
2 OM2	OM	1	108814	108928	109735	110713	2_nonsis	808	1353	1898	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
171 OM2	OM	14	419770	420029	420961	421631	2_nonsis	933	1397	1860	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
218 OM2	OM	16	887709	888159	890080	890467	2_nonsis	1922	2340	2757	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
74 OM2	OM	7	197230	197465	198476	198752	2_nonsis	1012	1267	1521	3	20	1	1	0 (2:6)_(4:4aCO)_(5:3)_(4:4a)
24 OM2	OM	3	104476	105047	105854	106362	2_nonsis	808	1347	1885	3	20	1	1	0 (3:5)_(6:2)_(5:3)_(4:4aCO)
185 OM2	OM	15	493415	493846	494956	495340	2_nonsis	1111	1518	1924	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(4:4aCO)
151 OM2	OM	13	213451	213972	215661	215779	2_nonsis	1690	2009	2327	3	20	1	1	0 (3:5)_(4:4aCO)_(5:3)_(4:4a)
113 OM2	OM	10	391555	391631	393918	394217	2_nonsis	2288	2475	2661	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(4:4aCO)
79 OM2	OM	7	484957	485223	485842	486003	2_nonsis	620	833	1045	3	20	1	1	0 (5:3)_(3:5)_(2:6)_(3:5)_(4:4aCO)
122 OM2	OM	11	308042	308133	309188	309294	2_nonsis	1056	1154	1251	3	20	1	1	0 (5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)
40 OM2	OM	4	699280	699436	700752	700773	2_nonsis	1317	1405	1492	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
149 OM2	OM	13	24877	24997	26434	26922	2_nonsis	1438	1741	2044	3	20	1	1	0 (5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
205 OM2	OM	16	406571	406826	409553	409812	2_nonsis	2728	2984	3240	3	20	1	1	0 (3:5)_(6:2)_(4:4aCO)_(5:3)_(4:4a)
201 OM2	OM	16	224069	224569	227039	227828	2_nonsis	2471	3115	3758	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
1 OM2	OM	1	51371	51434	52858	52939	2_nonsis	1425	1496	1567	3	20	1	1	0 (5:3)_(4:4)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
141 OM2	OM	12	677132	677323	678817	678971	2_nonsis	1495	1667	1838	3	20	1	1	0 (3:5)_(4:4)_(3:5)_(4:4aCO)_(5:3)_(4:4a)
168 OM2	OM	14	210033	210155	211886	211934	2_nonsis	1732	1816	1900	3	20	1	1	0 (5:3)_(3:5)_(4:4)_(3:5)_(5:3)_(4:4aCO)
183 OM2	OM	15	443071	443358	444029	444178	2_nonsis	672	889	1106	3	20	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(5:3)_(3:5)_(4:4aCO)
127 OM2	OM	11	526209	526649	527758	528174	2_nonsis	1110	1537	1964	3	20	1	1	0 (5:3)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
157 OM2	OM	13	623510	623868	625844	625856	2_nonsis	1977	2161	2345	3	20	1	1	0 (5:3)_(4:4)_(3:5)_(2:6)_(4:4aCO)_(2:6)_(3:5a)_(4:4a)
60 OM2	OM	5	333453	333669	335874	336237	2_nonsis	2206	2495	2783	3	20	1	1	0 (2:6)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
208 OM2	OM	16	528017	528301	534749	535407	2_nonsis	6449	6919	7389	3	20	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(3:5a)_(5:3)_(6:2)_(4:4aCO)
166 OM2	OM	14	108948	109033	113360	113719	2_nonsis	4328	4549	4770	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
28 OM2	OM	4	28077	28487	30545	30752	2_nonsis	2059	2367	2674	3	20	1	1	0 (3:5)_(4:4)_(2:6)_(3:5)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)

4	OM2	OM	2	69355	69616	69901	70006	2_nonsis	286	468	650	3	21	1	1	0	(2:6)_(4:4ai)_(5:3)_(4:4bCO)
194	OM2	OM	15	966472	966571	968210	968244	2_nonsis	1640	1706	1771	3	21	1	1	0	(3:5)_(4:4ai)_(5:3)_(4:4ai)_(5:3a)_(4:4bCO)
214	OM2	OM	16	684164	685433	687708	687978	3	2276	3045	3813	0	1	2	0	2	(3:5)_(3:5a)_(6:2)_(4:4)
31	OM2	OM	4	183901	183975	185643	185762	3	1669	1765	1860	0	2	2	1	1	(5:3)_(4:4ai)_(5:3a)_(4:4bCO)
46	OM2	OM	4	1125228	1125275	1126330	1126356	3	1056	1092	1127	0	2	2	1	1	(5:3)_(5:3a)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)
55	OM2	OM	5	67311	67575	70022	70335	3	2448	2736	3023	0	2	2	1	1	(5:3)_(5:3a)_(3:5)_(5:3a)_(4:4aCO)
105	OM2	OM	9	267764	268176	268690	269349	3	515	1050	1584	0	2	2	1	1	(4:4aCO)_(5:3)_(4:4a)_(6:2i)_(5:3a)_(6:2a)_(5:3a)_(4:4a)
146	OM2	OM	12	952469	952886	955645	955822	3	2760	3056	3352	0	2	2	1	1	(5:3)_(3:5)_(2:6)_(3:5a)_(3:5)_(3:5b)_(4:4aCO)
200	OM2	OM	16	133867	133951	135687	136628	3	1737	2249	2760	0	2	2	1	1	(3:5)_(4:4ai)_(3:5a)_(2:6)_(5:3)_(4:4bCO)
176	OM3	OM	16	500988	501008	501008	501086	1	1	49	97	1	1	1	0	1	05:03
36	OM3	OM	4	1139520	1139804	1139804	1139987	1	1	234	466	1	1	1	0	1	05:03
182	OM3	OM	16	885455	885683	885683	885979	1	1	262	523	1	1	1	0	1	05:03
172	OM3	OM	16	168040	168073	168076	168575	1	4	269	534	1	1	1	0	1	05:03
132	OM3	OM	13	527316	527507	527507	527901	1	1	293	584	1	1	1	0	1	05:03
60	OM3	OM	7	810169	810199	810496	810523	1	298	326	353	1	1	1	0	1	05:03
178	OM3	OM	16	672209	672569	672668	672779	1	100	335	569	1	1	1	0	1	05:03
110	OM3	OM	12	124013	124317	124421	124596	1	105	344	582	1	1	1	0	1	05:03
32	OM3	OM	4	957502	957628	957628	958319	1	1	409	816	1	1	1	0	1	05:03
49	OM3	OM	6	182063	182307	182500	182752	1	194	441	688	1	1	1	0	1	05:03
64	OM3	OM	8	70138	70273	70542	70883	1	270	507	744	1	1	1	0	1	05:03
68	OM3	OM	8	276242	276840	276840	277301	1	1	530	1058	1	1	1	0	1	05:03
18	OM3	OM	3	102669	103556	103649	103757	1	94	591	1087	1	1	1	0	1	05:03
184	OM3	OM	16	920519	920779	921271	921352	1	493	663	832	1	1	1	0	1	05:03
100	OM3	OM	11	283904	284248	284656	284914	1	409	709	1009	1	1	1	0	1	05:03
27	OM3	OM	4	620963	621879	621894	622375	1	16	714	1411	1	1	1	0	1	05:03
89	OM3	OM	10	311129	311627	311915	312326	1	289	743	1196	1	1	1	0	1	05:03
170	OM3	OM	16	113385	114050	114414	114586	1	365	783	1200	1	1	1	0	1	05:03
119	OM3	OM	12	624838	625064	625064	627007	1	1	1085	2168	1	1	1	0	1	05:03
43	OM3	OM	5	321046	321126	321983	322493	1	858	1152	1446	1	1	1	0	1	05:03
3	OM3	OM	1	112136	113132	113326	114283	1	195	1171	2146	1	1	1	0	1	05:03
122	OM3	OM	12	835692	835791	836343	837497	1	553	1179	1804	1	1	1	0	1	05:03
147	OM3	OM	15	167546	168295	169333	169416	1	1039	1454	1869	1	1	1	0	1	05:03
153	OM3	OM	15	448955	448985	448985	449105	1	1	75	149	1	2	1	0	1	03:05
134	OM3	OM	13	695196	695300	695300	695427	1	1	116	230	1	2	1	0	1	03:05
86	OM3	OM	9	426906	427061	427061	427189	1	1	142	282	1	2	1	0	1	03:05
103	OM3	OM	11	369378	369689	369689	369878	1	1	250	499	1	2	1	0	1	03:05
77	OM3	OM	9	55071	55251	55362	55461	1	112	251	389	1	2	1	0	1	03:05
33	OM3	OM	4	965951	966501	966501	966530	1	1	290	578	1	2	1	0	1	03:05
127	OM3	OM	13	228146	228182	228322	228901	1	141	448	754	1	2	1	0	1	03:05
114	OM3	OM	12	286350	286840	286840	287319	1	1	485	968	1	2	1	0	1	03:05
92	OM3	OM	10	503037	503193	503352	503880	1	160	501	842	1	2	1	0	1	03:05
165	OM3	OM	15	942759	943167	943283	943688	1	117	523	928	1	2	1	0	1	03:05
25	OM3	OM	4	404690	404702	404996	405482	1	295	543	791	1	2	1	0	1	03:05
6	OM3	OM	2	27832	28538	28614	28912	1	77	578	1079	1	2	1	0	1	03:05
142	OM3	OM	14	605054	606035	606111	606283	1	77	653	1228	1	2	1	0	1	03:05
107	OM3	OM	11	565093	565270	565671	566185	1	402	747	1091	1	2	1	0	1	03:05
80	OM3	OM	9	185865	188629	188822	188845	1	194	1587	2979	1	2	1	0	1	03:05
179	OM3	OM	16	687978	688591	689677	691459	1	1087	2284	3480	1	2	1	0	1	03:05
137	OM3	OM	14	29547	32285	32426	34717	1	142	2656	5169	1	2	1	0	1	03:05
5	OM3	OM	1	190429	190558	190636	190880	1	79	265	450	1	3	1	0	1	5:3_4:4_5:3
101	OM3	OM	11	328709	329482	329590	330549	1	109	974	1839	1	3	1	0	1	5:3_6:2_5:3
12	OM3	OM	2	495218	495468	496048	496540	1	581	951	1321	1	4	1	0	1	3:5_4:4_3:5
74	OM3	OM	8	516015	516158	517376	517399	1	1219	1301	1383	1	4	1	0	1	3:5_2:6_3:5
162	OM3	OM	15	835656	836062	836505	836747	1	444	767	1090	1	7	1	0	1	5:3_6:2
34	OM3	OM	4	1007834	1008485	1008685	1009606	1	201	986	1771	1	7	1	0	1	5:3_6:2
106	OM3	OM	11	526688	527413	527758	528174	1	346	916	1485	1	7	1	0	1	5:3_4:4_5:3_6:2
76	OM3	OM	9	33062	33143	33434	33678	1	292	454	615	1	8	1	0	1	2:6_3:5
85	OM3	OM	9	421278	421475	421791	422134	1	317	586	855	1	8	1	0	1	3:5_2:6
130	OM3	OM	13	355571	355643	363140	363478	1	7498	7702	7906	1	8	1	0	1	3:5_2:6
113	OM3	OM	12	258730	259051	260496	260584	1	1446	1650	1853	2	11	1	0	1	5:3_5:3a

94	OM3	OM	10	705542	705639	706547	706608	1	909	987	1065	2	12	1	0	1	3:5_3:5a
116	OM3	OM	12	415898	416026	417083	417137	1	1058	1148	1238	2	12	1	0	1	3:5_3:5a
82	OM3	OM	9	268690	269349	270121	270435	1	773	1259	1744	2	12	1	0	1	3:5_3:5a
59	OM3	OM	7	784625	785199	785907	786618	1	709	1351	1992	2	12	1	0	1	3:5_3:5a
97	OM3	OM	11	88322	88618	90412	90586	1	1795	2029	2263	2	12	1	0	1	3:5_3:5a
171	OM3	OM	16	161519	161768	164063	164740	1	2296	2758	3220	2	12	1	0	1	3:5_3:5a
164	OM3	OM	15	929212	929593	932673	933245	1	3081	3557	4032	2	13	1	0	1	5:3_4:4_5:3_6:2_5:3_5:3a
56	OM3	OM	7	609903	609928	611145	611214	1	1218	1264	1310	2	14	1	0	1	3:5_3:5a_2:6_3:5a
47	OM3	OM	6	113619	113688	115088	115119	1	1401	1450	1499	2	14	1	0	1	3:5_4:4_3:5_3:5a
158	OM3	OM	15	732609	733385	733953	735184	1	569	1572	2574	2	14	1	0	1	3:5_4:4_3:5_3:5a
13	OM3	OM	2	514893	515049	515792	515871	1	744	861	977	2	15	1	0	1	5:3_4:4_5:3a
166	OM3	OM	15	967506	967611	968970	968991	1	1360	1422	1484	2	15	1	0	1	5:3_4:4_5:3a
163	OM3	OM	15	890957	891275	892523	892725	1	1249	1508	1767	2	15	1	0	1	5:3_4:4_5:3a
129	OM3	OM	13	346254	346559	347796	349796	1	1238	2390	3541	2	15	1	0	1	5:3_4:4_5:3a
63	OM3	OM	7	1016792	1017034	1019970	1020978	1	2937	3561	4185	2	15	1	0	1	5:3_4:4_5:3a
117	OM3	OM	12	554168	554190	554937	555282	1	748	931	1113	2	16	1	0	1	3:5_4:4_3:5a
75	OM3	OM	8	521408	521787	523245	523268	1	1459	1659	1859	2	16	1	0	1	3:5_4:4_3:5a
174	OM3	OM	16	371914	372742	374261	374470	1	1520	2038	2555	2	16	1	0	1	3:5_4:4_3:5a
20	OM3	OM	3	250253	250855	252633	253903	1	1779	2714	3649	2	16	1	0	1	3:5_4:4_3:5a
66	OM3	OM	8	194830	195121	196468	196529	1	1348	1523	1698	2	17	1	0	1	6:2_5:3_4:4_5:3a_4:4_5:3a
159	OM3	OM	15	761321	761947	763262	763613	1	1316	1804	2291	2	23	1	0	1	5:3_4:4_6:2_5:3a
1	OM3	OM	1	46375	46723	50024	50204	2_nonsis	3302	3565	3828	3	30	1	0	1	3:5_3:5a
40	OM3	OM	5	55841	55880	56829	57131	2_nonsis	950	1120	1289	3	30	1	0	1	3:5_3:5a_3:5b
70	OM3	OM	8	401408	401729	403805	404246	2_nonsis	2077	2457	2837	3	30	1	0	1	3:5_3:5a_3:5b
154	OM3	OM	15	478750	478915	481588	481817	2_nonsis	2674	2870	3066	3	30	1	0	1	5:3_5:3a_4:4_3:5
91	OM3	OM	10	458530	458980	461843	461906	2_nonsis	2864	3120	3375	3	30	1	0	1	3:5_5:3_4:4_5:3a
121	OM3	OM	12	815561	816037	820606	821384	2_nonsis	4570	5196	5822	3	30	1	0	1	6:2_5:3_6:2_4:4_3:5
155	OM3	OM	15	532110	532911	536230	538230	2_nonsis	3320	4720	6119	3	31	1	0	1	3:5_4:4ai
8	OM3	OM	2	180607	181279	182436	182643	2_nonsis	1158	1597	2035	3	31	1	0	1	5:3_4:4_4:4ai
95	OM3	OM	11	32124	33673	35505	35593	2_nonsis	1833	2651	3468	3	31	1	0	1	4:4ai_3:5_3:5a
83	OM3	OM	9	333081	333345	335079	336156	2_nonsis	1735	2405	3074	3	31	1	0	1	5:3_4:4_5:3a_4:4ai
96	OM3	OM	11	77827	78581	81388	81532	2_nonsis	2808	3256	3704	3	31	1	0	1	3:5_4:4_5:3_6:2_5:3_4:4ai_4:4_3:5a
67	OM3	OM	8	211004	211042	211042	211315	2_nonsis	1	156	310	1	1	1	1	0	(5:3)_(4:4aCO)
88	OM3	OM	10	192156	192956	192956	193023	2_nonsis	1	434	866	1	1	1	1	0	(5:3)_(4:4aCO)
157	OM3	OM	15	675019	675643	675643	675894	2_nonsis	1	438	874	1	1	1	1	0	(5:3)_(4:4aCO)
55	OM3	OM	7	523417	523732	523740	524713	2_nonsis	9	652	1295	1	1	1	1	0	(5:3)_(4:4aCO)
141	OM3	OM	14	425816	427278	427451	427715	2_nonsis	174	1036	1898	1	1	1	1	0	(5:3)_(4:4aCO)
143	OM3	OM	14	608001	610323	610323	610397	2_nonsis	1	1198	2395	1	1	1	1	0	(5:3)_(4:4aCO)
73	OM3	OM	8	510685	510752	511816	512259	2_nonsis	1065	1319	1573	1	1	1	1	0	(5:3)_(4:4aCO)
10	OM3	OM	2	426191	426299	427091	427568	2_nonsis	793	1085	1376	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
128	OM3	OM	13	306097	306566	306778	307008	2_nonsis	213	562	910	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
169	OM3	OM	16	105356	105755	106109	106351	2_nonsis	355	675	994	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
136	OM3	OM	13	880477	880820	881086	882052	2_nonsis	267	921	1574	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
54	OM3	OM	7	398049	398825	399032	399494	2_nonsis	208	826	1444	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
28	OM3	OM	4	725692	726379	726870	727318	2_nonsis	492	1059	1625	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
102	OM3	OM	11	355110	355272	355474	355535	2_nonsis	203	314	424	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
131	OM3	OM	13	485052	485130	485305	485712	2_nonsis	176	418	659	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
79	OM3	OM	9	169471	169640	170156	170408	2_nonsis	517	727	936	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
175	OM3	OM	16	444920	445378	445861	445985	2_nonsis	484	774	1064	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
140	OM3	OM	14	326722	327569	332884	333286	2_nonsis	5316	5940	6563	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
149	OM3	OM	15	189367	189822	193609	193685	2_nonsis	3788	4053	4317	1	11	1	1	0	(4:4ai)_(4:4bCO)
51	OM3	OM	7	66795	67477	69315	69578	2_nonsis	1839	2311	2782	1	11	1	1	0	(5:3)_(4:4)_(4:4ai)_(4:4bCO)
39	OM3	OM	4	1453865	1454543	1454648	1454951	2_nonsis	106	596	1085	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
111	OM3	OM	12	180421	180545	181518	181860	2_nonsis	316	706	1096	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
124	OM3	OM	12	1012226	1013592	1014017	1014198	2_nonsis	426	1199	1971	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
144	OM3	OM	14	651410	652054	652841	653557	2_nonsis	788	1467	2146	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
118	OM3	OM	12	567266	568114	568917	569539	2_nonsis	804	1538	2272	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
115	OM3	OM	12	318011	318672	319960	320465	2_nonsis	1289	1871	2453	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
133	OM3	OM	13	626104	626185	626430	627290	2_nonsis	246	716	1185	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
71	OM3	OM	8	422434	422538	423045	423870	2_nonsis	508	972	1435	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)

61	OM3	OM	7	847980	848452	849134	849405	2_nonsis	683	1054	1424	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
21	OM3	OM	4	19322	19376	20444	20659	2_nonsis	1069	1203	1336	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
24	OM3	OM	4	363860	365434	366072	366513	2_nonsis	639	1646	2652	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
146	OM3	OM	15	109584	110892	111855	111925	2_nonsis	964	1652	2340	1	12	1	1	0	(5:3)_(4:4aCO)_(5:3)_(4:4a)
78	OM3	OM	9	129907	130004	130049	130270	2_nonsis	46	204	362	1	15	1	1	0	(6:2)_(4:4aCO)
26	OM3	OM	4	550499	550672	550893	551387	2_nonsis	222	555	887	1	15	1	1	0	(6:2)_(4:4aCO)
81	OM3	OM	9	249032	249546	249546	250194	2_nonsis	1	581	1161	1	15	1	1	0	(6:2)_(4:4aCO)
99	OM3	OM	11	185334	185846	185846	186668	2_nonsis	1	667	1333	1	15	1	1	0	(6:2)_(4:4aCO)
19	OM3	OM	3	196331	196781	197306	197389	2_nonsis	526	792	1057	1	15	1	1	0	(6:2)_(4:4aCO)
41	OM3	OM	5	85103	85578	85693	86696	2_nonsis	116	854	1592	1	15	1	1	0	(6:2)_(4:4aCO)
183	OM3	OM	16	888536	888652	888868	888934	2_nonsis	217	307	397	1	16	1	1	0	(2:6)_(4:4aCO)
42	OM3	OM	5	234654	234744	234751	235773	2_nonsis	8	563	1118	1	16	1	1	0	(2:6)_(4:4aCO)
156	OM3	OM	15	607260	607371	607371	608818	2_nonsis	1	779	1557	1	16	1	1	0	(2:6)_(4:4aCO)
93	OM3	OM	10	631130	632972	632972	633146	2_nonsis	1	1008	2015	1	16	1	1	0	(2:6)_(4:4aCO)
125	OM3	OM	13	50955	51084	50955	51084	2_nonsis	0	64	128	1	100	1	1	0	(4:4aCO)
69	OM3	OM	8	328366	328590	328366	328590	2_nonsis	0	112	223	1	100	1	1	0	(4:4aCO)
173	OM3	OM	16	225893	226160	225893	226160	2_nonsis	0	133	266	1	100	1	1	0	(4:4aCO)
11	OM3	OM	2	493123	493536	493123	493536	2_nonsis	0	206	412	1	100	1	1	0	(4:4aCO)
35	OM3	OM	4	1011449	1011936	1011449	1011936	2_nonsis	0	243	486	1	100	1	1	0	(4:4aCO)
112	OM3	OM	12	253274	253791	253274	253791	2_nonsis	0	258	516	1	100	1	1	0	(4:4aCO)
177	OM3	OM	16	535437	535979	535437	535979	2_nonsis	0	271	541	1	100	1	1	0	(4:4aCO)
31	OM3	OM	4	926737	927283	926737	927283	2_nonsis	0	273	545	1	100	1	1	0	(4:4aCO)
90	OM3	OM	10	396063	396638	396063	396638	2_nonsis	0	287	574	1	100	1	1	0	(4:4aCO)
50	OM3	OM	6	225457	226036	225457	226036	2_nonsis	0	289	578	1	100	1	1	0	(4:4aCO)
58	OM3	OM	7	765415	766068	765415	766068	2_nonsis	0	326	652	1	100	1	1	0	(4:4aCO)
167	OM3	OM	15	1042440	1043118	1042440	1043118	2_nonsis	0	339	677	1	100	1	1	0	(4:4aCO)
120	OM3	OM	12	810333	811301	810333	811301	2_nonsis	0	484	967	1	100	1	1	0	(4:4aCO)
44	OM3	OM	5	362962	364031	362962	364031	2_nonsis	0	534	1068	1	100	1	1	0	(4:4aCO)
22	OM3	OM	4	133068	134651	133068	134651	2_nonsis	0	791	1582	1	100	1	1	0	(4:4aCO)
98	OM3	OM	11	141122	143878	141122	143878	2_nonsis	0	1378	2755	1	100	1	1	0	(4:4aCO)
145	OM3	OM	15	22043	39380	22043	39380	2_nonsis	0	8668	17336	1	100	1	1	0	(4:4aCO)
123	OM3	OM	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0	(4:4aCO)
108	OM3	OM	11	629129	629639	632117	632654	2_nonsis	2479	3002	3524	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
139	OM3	OM	14	293347	294319	295803	295990	2_nonsis	1485	2064	2642	2	30	1	1	0	(4:4aCO)_(5:3)_(5:3a)_(4:4a)
161	OM3	OM	15	802784	803471	804529	804694	2_nonsis	1059	1484	1909	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
148	OM3	OM	15	185107	185134	186970	187008	2_nonsis	1837	1869	1900	2	31	1	1	0	(3:5)_(3:5a)_(3:5b)_(4:4aCO)
29	OM3	OM	4	835164	835319	836867	837275	2_nonsis	1549	1830	2110	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4aCO)
4	OM3	OM	1	130254	130292	132066	135319	2_nonsis	1775	3420	5064	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(4:4aCO)
48	OM3	OM	6	173398	173500	174556	174682	2_nonsis	1057	1170	1283	2	32	1	1	0	(3:5)_(4:4aCO)_(2:6)_(3:5a)_(4:4a)
9	OM3	OM	2	299901	301455	302473	302626	2_nonsis	1019	1872	2724	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(2:6)_(4:4aCO)
65	OM3	OM	8	176184	176351	178314	178619	2_nonsis	1964	2199	2434	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(3:5b)_(4:4aCO)
160	OM3	OM	15	779309	779467	780072	780180	2_nonsis	606	738	870	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
53	OM3	OM	7	253383	253849	254422	254489	2_nonsis	574	840	1105	3	20	1	1	0	(3:5)_(6:2)_(4:4aCO)
138	OM3	OM	14	109914	110232	110961	111039	2_nonsis	730	927	1124	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
72	OM3	OM	8	455744	455850	457364	457544	2_nonsis	1515	1657	1799	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
126	OM3	OM	13	132751	132818	134000	136477	2_nonsis	1183	2454	3725	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
45	OM3	OM	5	452629	452746	452954	453437	2_nonsis	209	508	807	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(4:4aCO)
181	OM3	OM	16	812845	812990	813489	813633	2_nonsis	500	644	787	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(4:4aCO)
14	OM3	OM	2	701207	701303	702673	703042	2_nonsis	1371	1603	1834	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
57	OM3	OM	7	676875	677169	678883	679675	2_nonsis	1715	2257	2799	3	20	1	1	0	(5:3)_(6:2)_(3:5)_(4:4aCO)
2	OM3	OM	1	81841	82076	84046	84858	2_nonsis	1971	2494	3016	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(4:4aCO)
87	OM3	OM	10	69155	69275	69814	70030	2_nonsis	540	707	874	3	20	1	1	0	(2:6)_(3:5)_(5:3)_(3:5)_(4:4aCO)
152	OM3	OM	15	396447	396613	397394	397607	2_nonsis	782	971	1159	3	20	1	1	0	(2:6)_(5:3)_(4:4aCO)_(6:2)_(4:4a)
84	OM3	OM	9	374268	374496	375220	375595	2_nonsis	725	1026	1326	3	20	1	1	0	(6:2)_(3:5)_(5:3)_(3:5)_(4:4aCO)
151	OM3	OM	15	356119	356505	357367	357554	2_nonsis	863	1149	1434	3	20	1	1	0	(6:2)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
7	OM3	OM	2	86293	86416	87833	88022	2_nonsis	1418	1573	1728	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(6:2)_(4:4aCO)
180	OM3	OM	16	739738	739829	741423	741972	2_nonsis	1595	1914	2233	3	20	1	1	0	(6:2)_(5:3)_(4:4)_(3:5)_(4:4aCO)
52	OM3	OM	7	147249	147427	147855	148827	2_nonsis	429	1003	1577	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(5:3)_(6:2)_(4:4aCO)
30	OM3	OM	4	888734	889122	890417	890461	2_nonsis	1296	1511	1726	3	20	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(5:3)_(4:4aCO)
37	OM3	OM	4	1257459	1257868	1259982	1260032	2_nonsis	2115	2344	2572	3	20	1	1	0	(5:3)_(4:4)_(5:3a)_(6:2)_(3:5)_(4:4aCO)

38	OM3	OM	4	1334061	1334142	1335831	1337684	2_nonsis		1690	2656	3622	3	20	1	1	0 (5:3)_(6:2)_(4:4)_(5:3)_(2:6)_(4:4aCO)
135	OM3	OM	13	759962	760211	762993	763154	2_nonsis		2783	2987	3191	3	20	1	1	0 (5:3)_(6:2)_(5:3)_(4:4)_(3:5)_(2:6)_(3:5)_(5:3a)_(6:2)_(4:4aCO)_(5:3a)_(3:5)_(5:3a)_(4:4a)
23	OM3	OM	4	301375	301751	303260	303504	2_sis		1510	1819	2128	0	1	2	0	2 (5:3)_(5:3a)_(4:4)
150	OM3	OM	15	216181	216247	216499	217333	2_sis		253	702	1151	0	1	2	0	2 (3:5)_(2:6i)_(4:4)
168	OM3	OM	15	1056819	1056865	1058977	1059193	2_sis		2113	2243	2373	0	1	2	0	2 (5:3)_(5:3a)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4)
15	OM3	OM	2	735399	735582	739813	739882		4	4232	4357	4482	0	2	2	1	1 (4:4ai)_(6:2)_(4:4ai)_(5:3)_(4:4bi)_(5:3)_(6:2)_(5:3a)_(4:4ci)_(4:4dCO)
46	OM3	OM	6	95632	95746	97819	97944		3	2074	2193	2311	0	2	2	1	1 (6:2)_(4:4aCO)_(3:5)_(4:4a)
62	OM3	OM	7	938789	938924	940087	940564		3	1164	1469	1774	0	2	2	1	1 (5:3)_(4:4)_(3:5)_(4:4aCO)
105	OM3	OM	11	477203	477776	479195	479521		3	1420	1869	2317	0	2	2	1	1 (3:5)_(6:2)_(4:4aCO)
109	OM3	OM	12	85799	85916	88557	89489		3	2642	3166	3689	0	2	2	1	1 (5:3)_(4:4ai)_(4:4)_(6:2)_(4:4)_(3:5)_(6:2)_(4:4bCO)
16	OM3	OM	3	40637	40987	43107	43304	2_nonsis		2121	2394	2666	0	3	2	0	2 (5:3)_(4:4aCO)_(5:3)_(6:2)_(4:4CO)
17	OM3	OM	3	54721	55672	59465	59925	2_nonsis		3794	4499	5203	0	3	2	0	2 (3:5)_(2:6)_(4:4aCO)_(4:4CO)
104	OM3	OM	11	381058	381640	383538	383706	2_nonsis		1899	2273	2647	0	3	2	0	2 (5:3)_(4:4aCO)_(5:3)_(6:2)_(4:4CO)_(5:3a)_(4:4)
66	OM4	OM	7	584200	584249	584298	584414	1		50	132	213	1	1	1	0	1 05:03
135	OM4	OM	13	540798	541071	541071	541246	1		1	224	447	1	1	1	0	1 05:03
3	OM4	OM	1	71116	71281	71312	71535	1		32	225	418	1	1	1	0	1 05:03
115	OM4	OM	12	377594	377691	377750	378126	1		60	296	531	1	1	1	0	1 05:03
126	OM4	OM	13	29994	30303	30379	30523	1		77	303	528	1	1	1	0	1 05:03
129	OM4	OM	13	160280	160611	160785	160953	1		175	424	672	1	1	1	0	1 05:03
40	OM4	OM	4	1011449	1011936	1011970	1012387	1		35	486	937	1	1	1	0	1 05:03
14	OM4	OM	2	410015	410900	410900	410992	1		1	489	976	1	1	1	0	1 05:03
175	OM4	OM	16	74327	74884	74937	75355	1		54	541	1027	1	1	1	0	1 05:03
10	OM4	OM	2	192576	193122	193122	193664	1		1	544	1087	1	1	1	0	1 05:03
168	OM4	OM	15	848635	848657	849274	849337	1		618	660	701	1	1	1	0	1 05:03
185	OM4	OM	16	712507	713201	713201	713880	1		1	687	1372	1	1	1	0	1 05:03
8	OM4	OM	2	135796	135971	136348	136840	1		378	711	1043	1	1	1	0	1 05:03
112	OM4	OM	12	99653	100126	100583	100678	1		458	741	1024	1	1	1	0	1 05:03
5	OM4	OM	1	170726	170945	170945	172280	1		1	777	1553	1	1	1	0	1 05:03
80	OM4	OM	8	411072	411599	412127	412418	1		529	937	1345	1	1	1	0	1 05:03
102	OM4	OM	11	114199	114400	114933	115636	1		534	985	1436	1	1	1	0	1 05:03
104	OM4	OM	11	245116	246336	246873	247464	1		538	1443	2347	1	1	1	0	1 05:03
42	OM4	OM	4	1141710	1142883	1143838	1143894	1		956	1570	2183	1	1	1	0	1 05:03
88	OM4	OM	9	361353	361360	362523	363445	1		1164	1628	2091	1	1	1	0	1 05:03
167	OM4	OM	15	837247	837630	839012	839332	1		1383	1734	2084	1	1	1	0	1 05:03
20	OM4	OM	2	735240	735363	735363	735399	1		1	80	158	1	2	1	0	1 03:05
24	OM4	OM	3	153893	153973	153973	154067	1		1	87	173	1	2	1	0	1 03:05
13	OM4	OM	2	341632	341930	341973	342023	1		44	217	390	1	2	1	0	1 03:05
29	OM4	OM	4	159315	159567	159567	159777	1		1	231	461	1	2	1	0	1 03:05
19	OM4	OM	2	642483	642776	642776	643134	1		1	326	650	1	2	1	0	1 03:05
176	OM4	OM	16	214281	214333	214684	214724	1		352	397	442	1	2	1	0	1 03:05
180	OM4	OM	16	529035	529207	529418	529663	1		212	420	627	1	2	1	0	1 03:05
110	OM4	OM	12	22811	22902	23199	23393	1		298	440	581	1	2	1	0	1 03:05
11	OM4	OM	2	217015	217070	217109	218039	1		40	532	1023	1	2	1	0	1 03:05
178	OM4	OM	16	372742	373522	373522	373847	1		1	553	1104	1	2	1	0	1 03:05
2	OM4	OM	1	60267	60417	61084	61164	1		668	782	896	1	2	1	0	1 03:05
121	OM4	OM	12	690280	690475	690781	691605	1		307	816	1324	1	2	1	0	1 03:05
159	OM4	OM	15	442786	442914	443611	443738	1		698	825	951	1	2	1	0	1 03:05
63	OM4	OM	7	270608	270688	271853	272144	1		1166	1351	1535	1	2	1	0	1 03:05
111	OM4	OM	12	85595	85625	86634	87317	1		1010	1366	1721	1	2	1	0	1 03:05
44	OM4	OM	4	1270902	1271755	1272164	1272726	1		410	1117	1823	1	3	1	0	1 5:3_4:4_5:3
15	OM4	OM	2	503402	504535	505298	506138	1		764	1750	2735	1	4	1	0	1 3:5_4:4_3:5
22	OM4	OM	3	60704	60997	61457	61855	1		461	806	1150	1	7	1	0	1 5:3_6:2
155	OM4	OM	15	145798	146225	147007	150962	1		783	2973	5163	1	7	1	0	1 5:3_6:2
173	OM4	OM	15	1039293	1039487	1039586	1039607	1		100	207	313	1	8	1	0	1 2:6_3:5
60	OM4	OM	7	123330	123839	124322	124671	1		484	912	1340	1	8	1	0	1 3:5_2:6
170	OM4	OM	15	953320	953577	954310	954766	1		734	1090	1445	1	8	1	0	1 3:5_2:6
37	OM4	OM	4	820502	821075	821822	822225	1		748	1235	1722	1	8	1	0	1 2:6_3:5
142	OM4	OM	14	34396	34412	34917	37063	1		506	1586	2666	1	8	1	0	1 2:6_3:5
174	OM4	OM	16	56116	56137	64540	65675	1		8404	8981	9558	1	8	1	0	1 2:6_3:5_2:6_3:5
90	OM4	OM	10	68659	68967	68967	69094	1		1	218	434	1	10	1	0	1 06:02

144	OM4	OM	14	116892	116973	117253	117326	1	281	357	433	1	10	1	0	1	06:02
87	OM4	OM	9	249032	249546	249546	250194	1	1	581	1161	1	10.1	1	0	1	02:06
70	OM4	OM	7	766797	767046	767446	767698	1	401	651	900	2	11	1	0	1	5:3_5:3a
30	OM4	OM	4	177807	178219	178306	179632	1	88	956	1824	2	11	1	0	1	5:3_5:3a
32	OM4	OM	4	333754	334214	334954	335332	1	741	1159	1577	2	11	1	0	1	5:3_5:3a
172	OM4	OM	15	1024766	1025192	1026039	1026427	1	848	1254	1660	2	11	1	0	1	5:3_5:3a
138	OM4	OM	13	713980	715257	715953	715971	1	697	1344	1990	2	11	1	0	1	5:3_5:3a
122	OM4	OM	12	703815	703971	705221	705602	1	1251	1519	1786	2	11	1	0	1	5:3_5:3a
107	OM4	OM	11	472114	472789	474395	474932	1	1607	2212	2817	2	11	1	0	1	5:3_5:3a
147	OM4	OM	14	341067	341465	342273	342387	1	809	1064	1319	2	12	1	0	1	3:5_3:5a
38	OM4	OM	4	870568	870749	871483	878186	1	735	4176	7617	2	12	1	0	1	3:5_3:5a
120	OM4	OM	12	677323	677545	678541	678658	1	997	1166	1334	2	13	1	0	1	5:3_5:3a_4:4_5:3a
50	OM4	OM	5	233356	234239	234931	235495	1	693	1416	2138	2	14	1	0	1	3:5_2:6_3:5_3:5a
184	OM4	OM	16	699223	699663	703259	703359	1	3597	3866	4135	2	14	1	0	1	3:5_3:5a_2:6_3:5a
61	OM4	OM	7	190505	190661	191252	191348	1	592	717	842	2	15	1	0	1	5:3_4:4_5:3a
165	OM4	OM	15	769002	769092	769620	770027	1	529	777	1024	2	15	1	0	1	5:3_4:4_5:3a
131	OM4	OM	13	230470	230627	231947	232186	1	1321	1518	1715	2	15	1	0	1	5:3_4:4_5:3a
62	OM4	OM	7	225112	225550	226354	226711	1	805	1202	1598	2	16	1	0	1	3:5_4:4_3:5a
92	OM4	OM	10	128154	128296	129510	129833	1	1215	1447	1678	2	17	1	0	1	5:3_4:4_5:3a_6:2_5:3a
188	OM4	OM	16	840103	840263	841702	842073	1	1440	1705	1969	2	17	1	0	1	5:3_4:4_5:3a_4:4_5:3a
156	OM4	OM	15	215043	215265	216039	216075	1	775	903	1031	2	19	1	0	1	5:3_6:2_5:3a
99	OM4	OM	10	723948	724020	724519	724641	1	500	596	692	2	20	1	0	1	3:5_2:6_3:5a
166	OM4	OM	15	832326	832546	833472	833904	1	927	1252	1577	2	20	1	0	1	3:5_2:6_3:5a
157	OM4	OM	15	251789	252485	256152	256235	1	3668	4057	4445	2	20	1	0	1	3:5_2:6_3:5a
139	OM4	OM	13	797688	798060	798090	798261	2_nonsis	31	302	572	3	30	1	0	1	03:05
124	OM4	OM	12	860959	861841	861841	863244	2_nonsis	1	1143	2284	3	30	1	0	1	03:05
73	OM4	OM	7	1022499	1022816	1023277	1023633	2_nonsis	462	798	1133	3	30	1	0	1	3:5_5:3
105	OM4	OM	11	254966	255050	255714	256637	2_nonsis	665	1168	1670	3	30	1	0	1	5:3_3:5
57	OM4	OM	6	226919	227043	229991	230223	2_nonsis	2949	3126	3303	3	30	1	0	1	3:5_3:5a_3:5b
130	OM4	OM	13	191318	191452	192436	192717	2_nonsis	985	1192	1398	3	30	1	0	1	5:3_4:4_3:5_2:6
93	OM4	OM	10	314642	314885	317046	317150	2_nonsis	2162	2335	2507	3	30	1	0	1	5:3_4:4_2:6_3:5
171	OM4	OM	15	985932	986343	989301	989690	2_nonsis	2959	3358	3757	3	30	1	0	1	5:3_4:4_5:3a_3:5b
59	OM4	OM	7	72181	72738	76989	78426	2_nonsis	4252	5248	6244	3	30	1	0	1	5:3_4:4_5:3_4:4_5:3_5:3a_6:2
85	OM4	OM	9	53238	53717	54480	55071	2_nonsis	764	1298	1832	3	31	1	0	1	4:4ai_5:3_4:4ai_5:3a
108	OM4	OM	11	502040	502594	506842	506935	2_nonsis	4249	4572	4894	3	31	1	0	1	3:5_4:4ai_3:5_3:5a
69	OM4	OM	7	677412	678405	678405	678750	2_nonsis	1	669	1337	1	1	1	1	0	(5:3)_(4:4aCO)
125	OM4	OM	12	1009719	1011169	1011170	1011621	2_nonsis	2	952	1901	1	1	1	1	0	(5:3)_(4:4aCO)
163	OM4	OM	15	732609	733385	733953	735107	2_nonsis	569	1533	2497	1	1	1	1	0	(5:3)_(4:4aCO)
68	OM4	OM	7	633985	634428	634428	634525	2_nonsis	1	270	539	1	2	1	1	0	(3:5)_(4:4aCO)
25	OM4	OM	3	163371	163645	163699	164093	2_nonsis	55	388	721	1	2	1	1	0	(3:5)_(4:4aCO)
96	OM4	OM	10	471025	471532	471532	472011	2_nonsis	1	493	985	1	2	1	1	0	(3:5)_(4:4aCO)
106	OM4	OM	11	456155	456734	457094	457349	2_nonsis	361	777	1193	1	2	1	1	0	(3:5)_(4:4aCO)
82	OM4	OM	8	483502	483796	484090	485522	2_nonsis	295	1157	2019	1	2	1	1	0	(3:5)_(4:4aCO)
143	OM4	OM	14	79325	79763	80433	81575	2_nonsis	671	1460	2249	1	2	1	1	0	(3:5)_(4:4aCO)
51	OM4	OM	5	296971	297515	299873	300269	2_nonsis	2359	2828	3297	1	2	1	1	0	(3:5)_(4:4aCO)
23	OM4	OM	3	77505	77826	78844	78909	2_nonsis	1019	1211	1403	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
152	OM4	OM	14	646547	646799	647174	647815	2_nonsis	376	822	1267	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
27	OM4	OM	4	83687	83831	84518	84625	2_nonsis	688	813	937	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
78	OM4	OM	8	221372	221854	222996	223791	2_nonsis	1143	1781	2418	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
53	OM4	OM	5	521881	522010	522899	523260	2_nonsis	890	1134	1378	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
128	OM4	OM	13	119630	120376	120995	121603	2_nonsis	620	1296	1972	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
91	OM4	OM	10	77203	78874	79138	79551	2_nonsis	265	1306	2347	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
89	OM4	OM	9	398092	398246	398583	398957	2_nonsis	338	601	864	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
7	OM4	OM	2	110746	110917	112684	113236	2_nonsis	1768	2129	2489	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
186	OM4	OM	16	752508	752721	753173	753251	2_nonsis	453	598	742	1	11	1	1	0	(4:4ai)_(3:5)_(4:4bCO)
26	OM4	OM	3	222542	223339	223676	224009	2_nonsis	338	902	1466	1	11	1	1	0	(3:5)_(4:4ai)_(4:4bCO)
109	OM4	OM	11	590994	592478	592577	593181	2_nonsis	100	1143	2186	1	11	1	1	0	(3:5)_(4:4ai)_(4:4bCO)
16	OM4	OM	2	535946	536134	537210	537267	2_nonsis	1077	1199	1320	1	11	1	1	0	(4:4ai)_(5:3)_(4:4bCO)
98	OM4	OM	10	662479	663134	664330	664516	2_nonsis	1197	1617	2036	1	11	1	1	0	(4:4ai)_(4:4bCO)_(3:5)_(4:4b)
179	OM4	OM	16	408139	408347	408842	408889	2_nonsis	496	623	749	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)

34	OM4	OM	4	565322	565398	566007	566376	2_nonsis	610	832	1053	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
160	OM4	OM	15	480909	481143	482126	482383	2_nonsis	984	1229	1473	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
46	OM4	OM	4	1489808	1490210	1491321	1491574	2_nonsis	1112	1439	1765	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
132	OM4	OM	13	355503	355560	356924	362992	2_nonsis	1365	4427	7488	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
162	OM4	OM	15	578881	578915	579517	580333	2_nonsis	603	1027	1451	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4)_(4:4aCO)
49	OM4	OM	5	201006	201879	203706	203832	2_nonsis	1828	2327	2825	1	12	1	1	0	(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
55	OM4	OM	6	104114	105370	108071	108113	2_nonsis	2702	3350	3998	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4a)
146	OM4	OM	14	288926	289222	290461	291122	2_nonsis	1240	1718	2195	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(4:4aCO)
47	OM4	OM	5	24966	25188	27932	28151	2_nonsis	2745	2965	3184	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(5:3)_(2:6)_(4:4aCO)
75	OM4	OM	8	50351	50566	50566	50752	2_nonsis	1	201	400	1	15	1	1	0	(6:2)_(4:4aCO)
95	OM4	OM	10	394408	394692	394713	394810	2_nonsis	22	212	401	1	15	1	1	0	(6:2)_(4:4aCO)
97	OM4	OM	10	555723	556159	556159	556720	2_nonsis	1	499	996	1	15	1	1	0	(6:2)_(4:4aCO)
84	OM4	OM	9	41664	41898	41980	42365	2_nonsis	83	392	700	1	16	1	1	0	(2:6)_(4:4aCO)
140	OM4	OM	13	849562	851409	851409	851620	2_nonsis	1	1029	2057	1	16	1	1	0	(2:6)_(4:4aCO)
119	OM4	OM	12	624838	627007	627007	627201	2_nonsis	1	1182	2362	1	16	1	1	0	(2:6)_(4:4aCO)
103	OM4	OM	11	149388	152355	152355	154732	2_nonsis	1	2672	5343	1	16	1	1	0	(2:6)_(4:4aCO)
183	OM4	OM	16	656605	656677	656605	656677	2_nonsis	0	36	71	1	100	1	1	0	(4:4aCO)
145	OM4	OM	14	118803	119128	118803	119128	2_nonsis	0	162	324	1	100	1	1	0	(4:4aCO)
150	OM4	OM	14	483386	483741	483386	483741	2_nonsis	0	177	354	1	100	1	1	0	(4:4aCO)
74	OM4	OM	7	1050064	1050446	1050064	1050446	2_nonsis	0	191	381	1	100	1	1	0	(4:4aCO)
158	OM4	OM	15	288307	288781	288307	288781	2_nonsis	0	237	473	1	100	1	1	0	(4:4aCO)
100	OM4	OM	11	74916	75663	74916	75663	2_nonsis	0	373	746	1	100	1	1	0	(4:4aCO)
28	OM4	OM	4	106899	107966	106899	107966	2_nonsis	0	533	1066	1	100	1	1	0	(4:4aCO)
136	OM4	OM	13	556437	557517	556437	557517	2_nonsis	0	540	1079	1	100	1	1	0	(4:4aCO)
35	OM4	OM	4	625839	628602	625839	628602	2_nonsis	0	1381	2762	1	100	1	1	0	(4:4aCO)
123	OM4	OM	12	791142	794003	791142	794003	2_nonsis	0	1430	2860	1	100	1	1	0	(4:4aCO)
154	OM4	OM	15	22358	39380	22358	39380	2_nonsis	0	8511	17021	1	100	1	1	0	(4:4aCO)
39	OM4	OM	4	888611	888734	889358	889568	2_nonsis	625	791	956	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
1	OM4	OM	1	41481	41587	42257	42484	2_nonsis	671	837	1002	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
187	OM4	OM	16	830277	831160	832685	832807	2_nonsis	1526	2028	2529	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
189	OM4	OM	16	918448	918658	920048	920519	2_nonsis	1391	1731	2070	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(5:3a)_(5:3)_(4:4aCO)
127	OM4	OM	13	94190	94473	95911	96019	2_nonsis	1439	1634	1828	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)_(5:3b)_(4:4a)
81	OM4	OM	8	421075	421312	423045	423870	2_nonsis	1734	2264	2794	2	30	1	1	0	(5:3)_(5:3a)_(6:2)_(5:3a)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
117	OM4	OM	12	507531	508649	512083	513766	2_nonsis	3435	4835	6234	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(5:3a)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
71	OM4	OM	7	824168	824337	825852	826536	2_nonsis	1516	1942	2367	2	31	1	1	0	(3:5)_(5:3a)_(4:4aCO)
21	OM4	OM	2	790680	790744	792465	792968	2_nonsis	1722	2005	2287	2	31	1	1	0	(3:5)_(5:3a)_(4:4aCO)
141	OM4	OM	13	912584	912804	916816	917194	2_nonsis	4013	4311	4609	2	31	1	1	0	(3:5)_(4:4)_(3:5)_(4:3)_(3:5)_(2:6)_(3:5)_(5:3a)_(4:4aCO)_(3:5a)_(4:4a)_(3:5a)_(2:6)_(3:5a)_(4:4a)
94	OM4	OM	10	361124	361221	362546	362886	2_nonsis	1326	1544	1761	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4aCO)
164	OM4	OM	15	760366	761321	762399	762530	2_nonsis	1079	1621	2163	2	32	1	1	0	(3:5)_(4:4aCO)_(3:5a)_(4:4a)
118	OM4	OM	12	566615	567266	568917	569539	2_nonsis	1652	2288	2923	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
64	OM4	OM	7	351287	351684	352489	352538	2_nonsis	806	1028	1250	2	32	1	1	0	(4:4aCO)_(3:5)_(4:4a)_(3:5a)_(4:4a)
56	OM4	OM	6	168217	168241	169392	169586	2_nonsis	1152	1260	1368	2	32	1	1	0	(2:6)_(3:5)_(4:4aCO)_(3:5a)_(4:4a)
113	OM4	OM	12	252615	252766	254321	254610	2_nonsis	1556	1775	1994	2	32	1	1	0	(5:3)_(6:2)_(4:4)_(5:3a)_(4:4aCO)
9	OM4	OM	2	175526	175964	178099	178447	2_nonsis	2136	2528	2920	2	32	1	1	0	(5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
45	OM4	OM	4	1410189	1410611	1411672	1411690	2_nonsis	1062	1281	1500	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
149	OM4	OM	14	386641	386898	388348	388819	2_nonsis	1451	1814	2177	2	32	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
161	OM4	OM	15	519432	519516	521442	521727	2_nonsis	1927	2111	2294	2	32	1	1	0	(5:3)_(6:2)_(4:4aCO)_(5:3a)_(6:2)_(5:3a)_(4:4a)
86	OM4	OM	9	166646	166778	169788	169820	2_nonsis	3011	3092	3173	2	32	1	1	0	(3:5)_(4:4)_(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
18	OM4	OM	2	632170	632896	636372	636994	2_nonsis	3477	4150	4823	2	32	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
153	OM4	OM	14	719985	720135	723593	723962	2_nonsis	3459	3718	3976	2	32	1	1	0	(5:3)_(2:6)_(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
182	OM4	OM	16	595114	595421	596701	596886	2_nonsis	1281	1526	1771	2	32	1	1	0	(5:3)_(4:4ai)_(5:3)_(6:2)_(4:4bCO)_(5:3a)_(4:4b)_(5:3b)_(6:2)_(5:3b)_(4:4b)
116	OM4	OM	12	390693	390717	391232	391272	2_nonsis	516	547	578	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
31	OM4	OM	4	284557	285372	285631	285994	2_nonsis	260	848	1436	3	20	1	1	0	(3:5)_(6:2)_(4:4aCO)
79	OM4	OM	8	329634	330629	331868	331868	2_nonsis	1013	1623	2233	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
72	OM4	OM	7	936067	936350	936948	937376	2_nonsis	599	954	1308	3	20	1	1	0	(5:3)_(6:2)_(3:5)_(4:4aCO)
54	OM4	OM	6	43123	43673	45082	45201	2_nonsis	1410	1744	2077	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
41	OM4	OM	4	1055277	1055562	1057601	1058554	2_nonsis	2040	2658	3276	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(4:4aCO)
137	OM4	OM	13	590016	590250	593361	594254	2_nonsis	3112	3675	4237	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(4:4aCO)
33	OM4	OM	4	420755	420793	422107	422276	2_nonsis	1315	1418	1520	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)
36	OM4	OM	4	698347	698417	699938	700023	2_nonsis	1522	1599	1675	3	20	1	1	0	(5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)

148	OM4	OM	14	370839	371516	372919	373080	2_nonsis		1404	1822	2240	3	20	1	1	0 (5:3)_(3:5)_(2:6)_(3:5)_(4:4aCO)
151	OM4	OM	14	530418	530856	532165	532649	2_nonsis		1310	1770	2230	3	20	1	1	0 (2:6)_(4:4)_(5:3)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
58	OM4	OM	6	245505	245636	250075	251026	2_nonsis		4440	4970	5500	3	20	1	1	0 (5:3)_(6:2)_(5:3a)_(5:3b)_(4:4aCO)_(3:5)_(4:4a)
181	OM4	OM	16	534749	535407	535727	535979	2_nonsis		321	775	1229	3	21	1	1	0 (5:3)_(4:4ai)_(3:5)_(4:4bCO)
4	OM4	OM	1	129517	130254	130975	132066	2_nonsis		722	1635	2548	3	21	1	1	0 (5:3)_(4:4ai)_(3:5)_(4:4bCO)
67	OM4	OM	7	610674	611145	612759	612980	2_nonsis		1615	1960	2305	3	21	1	1	0 (5:3)_(6:2)_(4:4ai)_(3:5)_(4:4bCO)
52	OM4	OM	5	487689	488899	491327	491424	2_nonsis		2429	3082	3734	3	21	1	1	0 (4:4ai)_(5:3)_(4:4bCO)_(2:6)_(4:4b)
133	OM4	OM	13	395969	396257	397127	397143	2_nonsis		871	1022	1173	3	21	1	1	0 (5:3)_(4:4)_(5:3)_(4:4ai)_(5:3a)_(3:5)_(4:4bCO)
83	OM4	OM	8	516184	516318	519408	519682	3		3091	3294	3497	0	1	2	0	2 (5:3)_(5:3a)_(4:4ai)_(5:3a)_(4:4)_(2:6i)_(1:7)_(2:6i)_(3:5)_(4:4)
6	OM4	OM	2	60793	60945	63304	63831	3		2360	2699	3037	0	2	2	1	1 (3:5)_(4:4)_(5:3)_(4:4ai)_(5:3a)_(4:4bCO)
12	OM4	OM	2	286762	286855	288498	288671	3		1644	1776	1908	0	2	2	1	1 (3:5)_(4:4)_(5:3)_(4:4ai)_(3:5a)_(4:4bCO)
17	OM4	OM	2	598254	598328	601647	602361	3		3320	3713	4106	0	2	2	1	1 (3:5)_(4:4ai)_(5:3)_(5:3a)_(4:4bCO)
65	OM4	OM	7	427215	427318	429941	430559	4		2624	2984	3343	0	2	2	1	1 (3:5)_(4:4)_(3:5)_(5:3)_(3:5)_(4:4)_(5:3a)_(2:6)_(4:4)_(4:4ai)_(3:5a)_(4:4bCO)
76	OM4	OM	8	120445	121477	123006	123099	3		1530	2092	2653	0	2	2	1	1 (5:3)_(5:3a)_(2:6)_(3:5)_(4:4aCO)
77	OM4	OM	8	191304	191691	192892	195121	4		1202	2509	3816	0	2	2	1	1 (5:3)_(6:2i)_(6:2a)_(4:4aCO)
101	OM4	OM	11	93041	93302	98707	98834	3		5406	5599	5792	0	2	2	1	1 (5:3)_(4:4)_(3:5)_(3:5a)_(4:4aCO)
134	OM4	OM	13	482376	482500	486437	486464	4		3938	4013	4087	0	2	2	1	1 (3:5)_(4:4)_(3:5)_(3:5a)_(4:4ai)_(3:5b)_(4:4bCO)
169	OM4	OM	15	942317	942594	945099	945153	4		2506	2671	2835	0	2	2	2	0 (3:5)_(4:4ai)_(4:4bi)_(3:5a)_(4:4cCO)
177	OM4	OM	16	325596	325797	329617	329941	3		3821	4083	4344	0	2	2	1	1 (5:3)_(4:4)_(5:3)_(5:3a)_(6:2)_(5:3)_(4:4ai)_(5:3b)_(4:4bi)_(3:5)_(4:4cCO)
43	OM4	OM	4	1179125	1179516	1181771	1182010	2_nonsis		2256	2570	2884	0	3	2	0	2 (3:5)_(2:6)_(5:3a)_(4:4aCO)_(5:3a)_(5:3)_(4:4CO)
48	OM4	OM	5	45665	45963	47165	48256	2_nonsis		1203	1897	2590	0	3	2	0	2 (5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3b)_(4:4CO)
114	OM4	OM	12	326213	326929	328075	328990	3		1147	1962	2776	0	3	2	1	1 (4:4ai)_(3:5)_(4:4bCO)_(5:3)_(4:4cCO)
113	OM5	OM	12	399513	399563	399563	399644	1	1	66	130	1	1	1	0	1	05:03
119	OM5	OM	12	722507	722593	722594	722657	1	2	76	149	1	1	1	0	1	05:03
69	OM5	OM	8	58415	58524	58524	58620	1	1	103	204	1	1	1	0	1	05:03
101	OM5	OM	11	327663	327707	327707	327893	1	1	115	229	1	1	1	0	1	05:03
157	OM5	OM	15	638644	639033	639042	639159	1	10	262	514	1	1	1	0	1	05:03
141	OM5	OM	14	440622	441276	441276	441344	1	1	361	721	1	1	1	0	1	05:03
154	OM5	OM	15	550812	551128	551234	551437	1	107	366	624	1	1	1	0	1	05:03
144	OM5	OM	14	604250	604879	604879	605054	1	1	402	803	1	1	1	0	1	05:03
2	OM5	OM	1	67801	68551	68551	68621	1	1	410	819	1	1	1	0	1	05:03
55	OM5	OM	7	75728	75778	76149	76406	1	372	525	677	1	1	1	0	1	05:03
35	OM5	OM	4	841276	842028	842070	842326	1	43	546	1049	1	1	1	0	1	05:03
149	OM5	OM	15	128417	128530	128730	129347	1	201	565	929	1	1	1	0	1	05:03
136	OM5	OM	14	273306	273490	273928	274328	1	439	730	1021	1	1	1	0	1	05:03
155	OM5	OM	15	571716	572407	572520	573068	1	114	733	1351	1	1	1	0	1	05:03
72	OM5	OM	8	340958	341040	341515	342157	1	476	837	1198	1	1	1	0	1	05:03
108	OM5	OM	12	114242	114659	115422	116251	1	764	1386	2008	1	1	1	0	1	05:03
112	OM5	OM	12	318672	320465	320997	322903	1	533	2382	4230	1	1	1	0	1	05:03
106	OM5	OM	12	84153	84302	84302	84315	1	1	81	161	1	2	1	0	1	03:05
73	OM5	OM	8	375097	375221	375221	375658	1	1	281	560	1	2	1	0	1	03:05
176	OM5	OM	16	840482	840627	840627	841238	1	1	378	755	1	2	1	0	1	03:05
78	OM5	OM	8	524046	524210	524455	524576	1	246	388	529	1	2	1	0	1	03:05
38	OM5	OM	4	969384	969561	969561	970293	1	1	455	908	1	2	1	0	1	03:05
170	OM5	OM	16	425006	425302	425481	425740	1	180	457	733	1	2	1	0	1	03:05
66	OM5	OM	7	1050064	1050446	1050446	1051057	1	1	497	992	1	2	1	0	1	03:05
168	OM5	OM	16	297234	297543	297634	298155	1	92	506	920	1	2	1	0	1	03:05
39	OM5	OM	4	1049309	1050120	1050175	1050369	1	56	558	1059	1	2	1	0	1	03:05
151	OM5	OM	15	314514	315191	315191	315748	1	1	617	1233	1	2	1	0	1	03:05
139	OM5	OM	14	425816	427278	427295	427451	1	18	826	1634	1	2	1	0	1	03:05
99	OM5	OM	11	165754	166502	166774	167254	1	273	886	1499	1	2	1	0	1	03:05
123	OM5	OM	13	42127	43336	43336	44157	1	1	1015	2029	1	2	1	0	1	03:05
158	OM5	OM	15	648434	649497	649839	650136	1	343	1022	1701	1	2	1	0	1	03:05
127	OM5	OM	13	347586	347780	347796	349796	1	17	1113	2209	1	2	1	0	1	03:05
27	OM5	OM	4	91959	93521	93541	94320	1	21	1191	2360	1	2	1	0	1	03:05
75	OM5	OM	8	461318	462176	462825	463320	1	650	1326	2001	1	2	1	0	1	03:05
138	OM5	OM	14	399462	400449	400849	401240	1	401	1089	1777	1	3	1	0	1	5:3_4:4_5:3
1	OM5	OM	1	32883	32986	34170	34308	1	1185	1305	1424	1	4	1	0	1	3:5_2:6_4:4_3:5_4:4_3:5
19	OM5	OM	2	738015	738213	738241	738886	1	29	450	870	1	7	1	0	1	6:2_5:3
82	OM5	OM	9	154922	155270	155702	155792	1	433	651	869	1	7	1	0	1	6:2_5:3

86	OM5	OM	9	386347	386352	388703	388925	1	2352	2465	2577	1	7	1	0	1 5:3_4:4_6:2_4:4_6:2
36	OM5	OM	4	870200	870568	870950	884980	1	383	7581	14779	1	8	1	0	1 3:5_2:6
48	OM5	OM	5	187482	187519	187838	188435	1	320	636	952	1	8	1	0	1 3:5_4:4_2:6
94	OM5	OM	10	502163	502527	503880	504158	1	1354	1674	1994	1	8	1	0	1 3:5_4:4_2:6
6	OM5	OM	1	180726	180747	180747	180881	1	1	78	154	1	10	1	0	1 06:02
15	OM5	OM	2	595106	595246	595246	595346	1	1	120	239	1	10	1	0	1 06:02
171	OM5	OM	16	482417	482429	482429	482737	1	1	160	319	1	10	1	0	1 06:02
28	OM5	OM	4	263811	264197	264197	264290	1	1	240	478	1	10	1	0	1 06:02
163	OM5	OM	16	21007	21094	21105	21507	1	12	256	499	1	10	1	0	1 06:02
173	OM5	OM	16	678266	678517	678709	678816	1	193	371	549	1	10	1	0	1 06:02
130	OM5	OM	13	661888	662059	662059	662796	1	1	454	907	1	10	1	0	1 06:02
109	OM5	OM	12	167737	168861	168861	169124	1	1	694	1386	1	10	1	0	1 06:02
50	OM5	OM	5	409333	409394	409394	410947	1	1	807	1613	1	10	1	0	1 06:02
165	OM5	OM	16	128399	128926	130068	130597	1	1143	1670	2197	1	10	1	0	1 06:02
80	OM5	OM	9	96842	96860	96885	96924	1	26	54	81	1	10.1	1	0	1 02:06
10	OM5	OM	2	170152	170442	170442	170593	1	1	221	440	1	10.1	1	0	1 02:06
162	OM5	OM	15	967885	968186	968244	968286	1	59	230	400	1	10.1	1	0	1 02:06
83	OM5	OM	9	177082	177853	177853	178629	1	1	774	1546	1	10.1	1	0	1 02:06
77	OM5	OM	8	486569	486921	487644	488458	1	724	1306	1888	1	10.1	1	0	1 02:06
135	OM5	OM	14	182462	182621	182639	185309	1	19	1433	2846	1	10.1	1	0	1 02:06
62	OM5	OM	7	650898	651268	651484	651712	1	217	515	813	2	11	1	0	1 5:3_5:3a
7	OM5	OM	2	46916	47062	47612	47900	1	551	767	983	2	11	1	0	1 5:3_5:3a
93	OM5	OM	10	465816	466454	467199	467589	1	746	1259	1772	2	11	1	0	1 5:3_5:3a
58	OM5	OM	7	271422	271683	272568	273422	1	886	1443	1999	2	11	1	0	1 5:3_5:3a
146	OM5	OM	14	698696	698753	700405	700775	1	1653	1866	2078	2	11	1	0	1 5:3_5:3a
89	OM5	OM	10	285419	285967	287517	287913	1	1551	2022	2493	2	11	1	0	1 5:3_5:3a
45	OM5	OM	4	1476168	1476261	1477237	1477311	1	977	1060	1142	2	12	1	0	1 3:5_3:5a
42	OM5	OM	4	1333898	1334061	1335206	1335398	1	1146	1323	1499	2	14	1	0	1 3:5_4:4_3:5a
115	OM5	OM	12	509642	509817	510507	510559	1	691	804	916	2	15	1	0	1 5:3_4:4_5:3a
160	OM5	OM	15	780823	781222	782242	782356	1	1021	1277	1532	2	15	1	0	1 5:3_4:4_5:3a
32	OM5	OM	4	692787	692797	694033	694047	1	1237	1248	1259	2	16	1	0	1 3:5_4:4_3:5a
131	OM5	OM	13	723721	723996	724434	726144	1	439	1431	2422	2	16	1	0	1 3:5_4:4_3:5a
117	OM5	OM	12	602107	602186	603907	604090	1	1722	1852	1982	2	18	1	0	1 3:5_4:4_3:5a_2:6_3:5a
59	OM5	OM	7	410453	410531	413797	414265	1	3267	3539	3811	2	18	1	0	1 3:5_4:4_3:5a_4:4_2:6_3:5a_4:4_3:5a
167	OM5	OM	16	213837	214028	214963	215112	1	936	1105	1274	2	20	1	0	1 3:5_2:6_3:5a
26	OM5	OM	4	32409	32706	33397	34987	2_nonsis	692	1635	2577	3	30	1	0	1 2:6_6:2_5:3
20	OM5	OM	3	40637	41096	42419	42698	2_nonsis	1324	1692	2060	3	30	1	0	1 5:3_4:4_2:6_3:5
122	OM5	OM	12	1023437	1023823	1027573	1027717	2_nonsis	3751	4015	4279	3	30	1	0	1 5:3_5:3a_4:4_2:6
74	OM5	OM	8	421840	422434	424326	425219	2_nonsis	1893	2636	3378	3	31	1	0	1 5:3_4:4ai_5:3a_4:4_5:3a
116	OM5	OM	12	541773	542005	542005	542794	2_nonsis	1	511	1020	1	1	1	1	0 (5:3)_(4:4aCO)
120	OM5	OM	12	789373	789615	789623	791142	2_nonsis	9	889	1768	1	1	1	1	0 (5:3)_(4:4aCO)
172	OM5	OM	16	623041	623258	624882	625108	2_nonsis	1625	1846	2066	1	1	1	1	0 (5:3)_(4:4aCO)
16	OM5	OM	2	660972	662444	662444	666708	2_nonsis	1	2868	5735	1	1	1	1	0 (5:3)_(4:4aCO)
174	OM5	OM	16	696490	696582	696582	696879	2_nonsis	1	195	388	1	2	1	1	0 (3:5)_(4:4aCO)
64	OM5	OM	7	795505	795543	795662	795876	2_nonsis	120	245	370	1	2	1	1	0 (3:5)_(4:4aCO)
22	OM5	OM	3	100466	100585	100585	101527	2_nonsis	1	531	1060	1	2	1	1	0 (3:5)_(4:4aCO)
54	OM5	OM	6	244444	245484	245505	245636	2_nonsis	22	607	1191	1	2	1	1	0 (3:5)_(4:4aCO)
31	OM5	OM	4	501667	502245	502277	502877	2_nonsis	33	621	1209	1	2	1	1	0 (3:5)_(4:4aCO)
24	OM5	OM	3	249994	250855	250855	251323	2_nonsis	1	665	1328	1	2	1	1	0 (3:5)_(4:4aCO)
164	OM5	OM	16	106109	106450	106600	107304	2_nonsis	151	673	1194	1	2	1	1	0 (3:5)_(4:4aCO)
143	OM5	OM	14	539848	542443	542443	543829	2_nonsis	1	1991	3980	1	2	1	1	0 (3:5)_(4:4aCO)
63	OM5	OM	7	733453	733567	734928	736788	2_nonsis	1362	2348	3334	1	2	1	1	0 (3:5)_(4:4aCO)
4	OM5	OM	1	155505	158814	158870	159623	2_nonsis	57	2087	4117	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
30	OM5	OM	4	432487	432803	433470	434094	2_nonsis	668	1137	1606	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
102	OM5	OM	11	368313	369378	369878	370412	2_nonsis	501	1300	2098	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
169	OM5	OM	16	307685	308234	309089	309787	2_nonsis	856	1479	2101	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
148	OM5	OM	15	40057	40497	40593	40834	2_nonsis	97	437	776	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
18	OM5	OM	2	733887	733953	734046	734409	2_nonsis	94	308	521	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
161	OM5	OM	15	941405	941706	942317	942594	2_nonsis	612	900	1188	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
14	OM5	OM	2	539483	540265	540365	540546	2_nonsis	101	582	1062	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)

91	OM5	OM	10	360588	360746	361340	361485	2_nonsis	595	746	896	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
44	OM5	OM	4	1427252	1428300	1428864	1429122	2_nonsis	565	1217	1869	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
98	OM5	OM	11	91825	92069	92330	92948	2_nonsis	262	692	1122	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
56	OM5	OM	7	81306	81381	81435	82858	2_nonsis	55	803	1551	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
124	OM5	OM	13	70356	71137	71397	72027	2_nonsis	261	966	1670	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
104	OM5	OM	11	590023	590067	590994	592478	2_nonsis	928	1691	2454	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
87	OM5	OM	9	405428	405665	405973	406124	2_nonsis	309	502	695	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
90	OM5	OM	10	294619	294826	295430	295604	2_nonsis	605	795	984	1	12	1	1	0	(2:6)_(3:5)_(4:4)_(4:4aCO)
53	OM5	OM	6	93934	94545	95246	95308	2_nonsis	702	1038	1373	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
111	OM5	OM	12	314762	314849	315642	316064	2_nonsis	794	1048	1301	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)
33	OM5	OM	4	698788	699229	700250	700440	2_nonsis	1022	1337	1651	1	12	1	1	0	(5:3)_(6:2)_(4:4)_(4:4aCO)
34	OM5	OM	4	836051	836148	837527	837572	2_nonsis	1380	1450	1520	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
128	OM5	OM	13	387879	388308	389541	389574	2_nonsis	1234	1464	1694	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
92	OM5	OM	10	400808	401166	402577	402683	2_nonsis	1412	1643	1874	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
51	OM5	OM	5	461594	462614	463625	464078	2_nonsis	1012	1748	2483	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)
147	OM5	OM	14	761636	761851	763447	763540	2_nonsis	1597	1750	1903	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
47	OM5	OM	5	98381	98507	98507	98854	2_nonsis	1	237	472	1	15	1	1	0	(6:2)_(4:4aCO)
12	OM5	OM	2	344093	344182	344186	344668	2_nonsis	5	290	574	1	15	1	1	0	(6:2)_(4:4aCO)
52	OM5	OM	6	40189	40564	40564	40771	2_nonsis	1	291	581	1	15	1	1	0	(6:2)_(4:4aCO)
29	OM5	OM	4	353410	353682	353682	354016	2_nonsis	1	303	605	1	15	1	1	0	(6:2)_(4:4aCO)
11	OM5	OM	2	247069	247234	247399	247522	2_nonsis	166	309	452	1	15	1	1	0	(6:2)_(4:4aCO)
97	OM5	OM	11	19020	19563	19563	19855	2_nonsis	1	418	834	1	15	1	1	0	(6:2)_(4:4aCO)
37	OM5	OM	4	908967	909447	909447	909908	2_nonsis	1	471	940	1	15	1	1	0	(6:2)_(4:4aCO)
142	OM5	OM	14	470413	471767	471767	472546	2_nonsis	1	1067	2132	1	15	1	1	0	(6:2)_(4:4aCO)
118	OM5	OM	12	624838	627007	627007	627201	2_nonsis	1	1182	2362	1	15	1	1	0	(6:2)_(4:4aCO)
125	OM5	OM	13	214290	214378	214378	214530	2_nonsis	1	120	239	1	16	1	1	0	(2:6)_(4:4aCO)
23	OM5	OM	3	212528	212637	212637	212942	2_nonsis	1	207	413	1	16	1	1	0	(2:6)_(4:4aCO)
152	OM5	OM	15	394567	394716	394716	395073	2_nonsis	1	253	505	1	16	1	1	0	(2:6)_(4:4aCO)
150	OM5	OM	15	240538	241147	241147	241190	2_nonsis	1	326	651	1	16	1	1	0	(2:6)_(4:4aCO)
159	OM5	OM	15	737961	738026	738026	738617	2_nonsis	1	328	655	1	16	1	1	0	(2:6)_(4:4aCO)
96	OM5	OM	10	662479	663134	663134	663261	2_nonsis	1	391	781	1	16	1	1	0	(2:6)_(4:4aCO)
79	OM5	OM	9	28746	28937	29193	29619	2_nonsis	257	565	872	1	16	1	1	0	(2:6)_(4:4aCO)
70	OM5	OM	8	101512	102030	102030	103046	2_nonsis	1	767	1533	1	16	1	1	0	(2:6)_(4:4aCO)
103	OM5	OM	11	477203	477776	477776	479195	2_nonsis	1	996	1991	1	16	1	1	0	(2:6)_(4:4aCO)
95	OM5	OM	10	574799	576464	576551	576835	2_nonsis	88	1062	2035	1	16	1	1	0	(2:6)_(4:4aCO)
13	OM5	OM	2	429131	430040	431229	431663	2_nonsis	1190	1861	2531	1	16	1	1	0	(2:6)_(4:4aCO)
5	OM5	OM	1	166369	166571	166571	166571	2_nonsis	0	101	201	1	100	1	1	0	(4:4aCO)
88	OM5	OM	10	59791	60064	59791	60064	2_nonsis	0	136	272	1	100	1	1	0	(4:4aCO)
175	OM5	OM	16	832826	833262	832826	833262	2_nonsis	0	218	435	1	100	1	1	0	(4:4aCO)
145	OM5	OM	14	647174	647815	647174	647815	2_nonsis	0	320	640	1	100	1	1	0	(4:4aCO)
166	OM5	OM	16	147141	147862	147141	147862	2_nonsis	0	360	720	1	100	1	1	0	(4:4aCO)
8	OM5	OM	2	73943	74853	73943	74853	2_nonsis	0	455	909	1	100	1	1	0	(4:4aCO)
49	OM5	OM	5	267673	268597	267673	268597	2_nonsis	0	462	923	1	100	1	1	0	(4:4aCO)
68	OM5	OM	8	47072	48088	47072	48088	2_nonsis	0	508	1015	1	100	1	1	0	(4:4aCO)
129	OM5	OM	13	411264	412303	411264	412303	2_nonsis	0	519	1038	1	100	1	1	0	(4:4aCO)
71	OM5	OM	8	184323	185364	184323	185364	2_nonsis	0	520	1040	1	100	1	1	0	(4:4aCO)
121	OM5	OM	12	987417	988464	987417	988464	2_nonsis	0	523	1046	1	100	1	1	0	(4:4aCO)
153	OM5	OM	15	487028	488123	487028	488123	2_nonsis	0	547	1094	1	100	1	1	0	(4:4aCO)
140	OM5	OM	14	428883	430018	428883	430018	2_nonsis	0	567	1134	1	100	1	1	0	(4:4aCO)
100	OM5	OM	11	182573	183958	182573	183958	2_nonsis	0	692	1384	1	100	1	1	0	(4:4aCO)
76	OM5	OM	8	484090	485522	484090	485522	2_nonsis	0	716	1431	1	100	1	1	0	(4:4aCO)
17	OM5	OM	2	668082	669586	668082	669586	2_nonsis	0	752	1503	1	100	1	1	0	(4:4aCO)
134	OM5	OM	14	166583	168436	166583	168436	2_nonsis	0	926	1852	1	100	1	1	0	(4:4aCO)
57	OM5	OM	7	113828	116310	113828	116310	2_nonsis	0	1241	2481	1	100	1	1	0	(4:4aCO)
156	OM5	OM	15	574716	578388	574716	578388	2_nonsis	0	1836	3671	1	100	1	1	0	(4:4aCO)
9	OM5	OM	2	145486	146169	146891	147197	2_nonsis	723	1217	1710	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4ai)_(4:4bCO)
85	OM5	OM	9	332459	332503	333581	334640	2_nonsis	1079	1630	2180	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
133	OM5	OM	14	108312	108405	111039	111216	2_nonsis	2635	2769	2903	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)_(2:6)_(4:4a)_(3:5a)_(4:4a)
84	OM5	OM	9	274516	274938	275192	275372	2_nonsis	255	555	855	3	20	1	1	0	(2:6)_(5:3)_(4:4aCO)
65	OM5	OM	7	959381	959587	959945	960299	2_nonsis	359	638	917	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)

137	OM5	OM	14	317078	317360	317738	317977	2_nonsis	379	639	898	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
41	OM5	OM	4	1288090	1288209	1288775	1289394	2_nonsis	567	935	1303	3	20	1	1	0	(6:2)_(3:5)_(4:4aCO)
126	OM5	OM	13	342492	342513	343909	344475	2_nonsis	1397	1690	1982	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
67	OM5	OM	7	1056817	1057978	1059252	1059363	2_nonsis	1275	1910	2545	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
114	OM5	OM	12	403568	404007	404333	405334	2_nonsis	327	1046	1765	3	20	1	1	0	(3:5)_(4:4aCO)_(6:2)_(4:4a)
107	OM5	OM	12	94728	94846	95188	97572	2_nonsis	343	1593	2843	3	20	1	1	0	(2:6)_(6:2)_(5:3)_(4:4aCO)
3	OM5	OM	1	81731	81841	83613	84046	2_nonsis	1773	2044	2314	3	20	1	1	0	(3:5)_(2:6)_(5:3)_(4:4aCO)
46	OM5	OM	5	68996	69083	70969	71501	2_nonsis	1887	2196	2504	3	20	1	1	0	(2:6)_(5:3)_(3:5)_(4:4aCO)
81	OM5	OM	9	100355	102438	103227	104128	2_nonsis	790	2281	3772	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
132	OM5	OM	13	796811	796868	797379	797401	2_nonsis	512	551	589	3	20	1	1	0	(2:6)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
61	OM5	OM	7	608221	609405	610218	610674	2_nonsis	814	1633	2452	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)
25	OM5	OM	3	299527	299645	300560	300759	2_nonsis	916	1074	1231	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(5:3)_(3:5)_(4:4aCO)
60	OM5	OM	7	528501	528674	529644	529943	2_nonsis	971	1206	1441	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
105	OM5	OM	12	36167	36336	37611	37705	2_nonsis	1276	1407	1537	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)
40	OM5	OM	4	1165937	1166232	1169428	1169720	2_nonsis	3197	3490	3782	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(3:5)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(6:2)_(4:4a)_(5:3a)_(4:4a)
21	OM5	OM	3	46714	47161	48383	48702	2_nonsis	1223	1605	1987	3	21	1	1	0	(3:5)_(4:4ai)_(5:3)_(4:4bCO)
43	OM5	OM	4	1387223	1387436	1388150	1389010	2_nonsis	715	1251	1786	3	21	1	1	0	(6:2)_(4:4)_(3:5)_(4:4ai)_(4:4bCO)
110	OM5	OM	12	211226	212081	221668	223058	2_sis	9588	10710	11831	0	1	2	0	2	(3:5)_(4:4)_(3:5a)_(4:4)_(3:5a)_(2:6)_(3:5b)_(4:4)
76	OM6	OM	8	455850	455862	455862	455976	1	1	63	125	1	1	1	0	1 05:03
169	OM6	OM	16	339516	339687	339729	339833	1	43	180	316	1	1	1	0	1 05:03
146	OM6	OM	14	258013	258264	258264	258392	1	1	190	378	1	1	1	0	1 05:03
134	OM6	OM	13	706399	706931	707030	707109	1	100	405	709	1	1	1	0	1 05:03
16	OM6	OM	2	723102	723175	723454	723663	1	280	420	560	1	1	1	0	1 05:03
144	OM6	OM	14	196834	197191	197191	197707	1	1	437	872	1	1	1	0	1 05:03
117	OM6	OM	12	866496	866643	866643	867405	1	1	455	908	1	1	1	0	1 05:03
39	OM6	OM	4	1335831	1337219	1337219	1337684	1	1	927	1852	1	1	1	0	1 05:03
153	OM6	OM	14	764697	764741	764741	764938	1	1	121	240	1	2	1	0	1 03:05
18	OM6	OM	3	51405	51491	51491	51650	1	1	123	244	1	2	1	0	1 03:05
174	OM6	OM	16	681542	681719	681719	681810	1	1	134	267	1	2	1	0	1 03:05
91	OM6	OM	10	574034	574073	574091	574310	1	19	147	275	1	2	1	0	1 03:05
85	OM6	OM	10	67457	67697	67697	67836	1	1	190	378	1	2	1	0	1 03:05
156	OM6	OM	15	315837	316312	316312	316327	1	1	245	489	1	2	1	0	1 03:05
82	OM6	OM	9	350189	350470	350470	350705	1	1	258	515	1	2	1	0	1 03:05
100	OM6	OM	11	308234	308325	308425	308754	1	101	310	519	1	2	1	0	1 03:05
93	OM6	OM	10	663948	664155	664330	664516	1	176	372	567	1	2	1	0	1 03:05
43	OM6	OM	5	84810	85009	85103	85578	1	95	431	767	1	2	1	0	1 03:05
80	OM6	OM	9	165195	166074	166074	166116	1	1	461	920	1	2	1	0	1 03:05
172	OM6	OM	16	519523	519709	520162	520194	1	454	562	670	1	2	1	0	1 03:05
90	OM6	OM	10	465816	466454	466454	467010	1	1	597	1193	1	2	1	0	1 03:05
141	OM6	OM	14	76429	76856	77185	77306	1	330	603	876	1	2	1	0	1 03:05
138	OM6	OM	13	819611	819989	820241	820753	1	253	697	1141	1	2	1	0	1 03:05
4	OM6	OM	2	73943	74853	75084	75564	1	232	926	1620	1	2	1	0	1 03:05
109	OM6	OM	12	282626	283463	283731	284270	1	269	956	1643	1	2	1	0	1 03:05
24	OM6	OM	4	198376	198685	200025	200151	1	1341	1558	1774	1	2	1	0	1 03:05
104	OM6	OM	11	477776	479195	481321	482428	1	2127	3389	4651	1	2	1	0	1 03:05
99	OM6	OM	11	276968	277294	278448	278756	1	1155	1471	1787	1	3	1	0	1 5:3_4:4_5:3
167	OM6	OM	16	263635	263648	264796	266276	1	1149	1895	2640	1	3	1	0	1 5:3_4:4_5:3
28	OM6	OM	4	345209	345524	347623	347851	1	2100	2371	2641	1	3	1	0	1 5:3_4:4_5:3
26	OM6	OM	4	239643	239693	242094	242772	1	2402	2765	3128	1	3	1	0	1 5:3_4:4_5:3_6:2_5:3
132	OM6	OM	13	652413	652621	653063	653200	1	443	615	786	1	4	1	0	1 3:5_2:6_3:5
177	OM6	OM	16	888652	888868	891194	891335	1	2327	2505	2682	1	4	1	0	1 3:5_4:4_3:5
25	OM6	OM	4	202572	202761	202877	202902	1	117	223	329	1	7	1	0	1 6:2_5:3
151	OM6	OM	14	574949	575525	577067	577136	1	1543	1865	2186	1	8	1	0	1 3:5_2:6
96	OM6	OM	11	136761	137170	137170	137272	1	1	256	510	1	10	1	0	1 06:02
157	OM6	OM	15	322692	322741	323130	323552	1	390	625	859	2	11	1	0	1 5:3_5:3a
143	OM6	OM	14	182084	182303	182639	183060	1	337	656	975	2	11	1	0	1 5:3_5:3a
137	OM6	OM	13	809473	810028	811666	811677	1	1639	1921	2203	2	11	1	0	1 5:3_5:3a
111	OM6	OM	12	423416	423821	424138	424315	1	318	608	898	2	12	1	0	1 3:5_3:5a
127	OM6	OM	13	336845	337176	337732	337869	1	557	790	1023	2	12	1	0	1 3:5_3:5a
79	OM6	OM	9	153913	154387	155292	155480	1	906	1236	1566	2	12	1	0	1 3:5_3:5a

11	OM6	OM	2	481949	482720	483944	484110	1	1225	1693	2160	2	12	1	0	1 3:5_3:5a
15	OM6	OM	2	716467	716483	720010	720178	1	3528	3619	3710	2	12	1	0	1 3:5_3:5a
57	OM6	OM	6	168728	168886	169618	169635	1	733	820	906	2	13	1	0	1 5:3_6:2_5:3_5:3a
12	OM6	OM	2	513994	514468	515996	516344	1	1529	1939	2349	2	13	1	0	1 5:3_5:3a_4:4_5:3a
161	OM6	OM	15	700856	700946	701852	702223	1	907	1137	1366	2	14	1	0	1 3:5_3:5a_2:6_3:5a
101	OM6	OM	11	340285	340451	340811	341198	1	361	637	912	2	15	1	0	1 5:3_4:4_5:3a
71	OM6	OM	8	46457	47060	48508	48551	1	1449	1771	2093	2	15	1	0	1 5:3_4:4_5:3a
31	OM6	OM	4	599314	599388	599865	599964	1	478	564	649	2	16	1	0	1 3:5_4:4_3:5a
129	OM6	OM	13	434958	435813	436595	436769	1	783	1297	1810	2	16	1	0	1 3:5_4:4_3:5a
50	OM6	OM	5	348780	349106	350516	350543	1	1411	1587	1762	2	16	1	0	1 3:5_4:4_3:5a
46	OM6	OM	5	195975	196106	197502	197916	1	1397	1669	1940	2	16	1	0	1 3:5_4:4_3:5a
159	OM6	OM	15	494089	494313	496482	496659	1	2170	2370	2569	2	16	1	0	1 3:5_4:4_3:5a
45	OM6	OM	5	162008	162250	163835	163997	1	1586	1787	1988	2	19	1	0	1 5:3_6:2_5:3a
6	OM6	OM	2	82573	83659	84823	84862	1	1165	1727	2288	2	23	1	0	1 5:3_4:4_6:2_5:3a
175	OM6	OM	16	829002	829035	829418	830004	2_nonsis	384	693	1001	3	30	1	0	1 3:5_3:5a
29	OM6	OM	4	366072	366513	366913	367042	2_nonsis	401	685	969	3	30	1	0	1 5:3_5:3a_3:5
142	OM6	OM	14	85801	85831	88100	88950	2_nonsis	2270	2709	3148	3	30	1	0	1 5:3_6:2_5:3_5:3a
119	OM6	OM	13	11305	11831	13831	13907	2_nonsis	2001	2301	2601	3	31	1	0	1 4:4ai_5:3_4:4_5:3a
78	OM6	OM	9	82538	82899	82899	83067	2_nonsis	1	265	528	1	1	1	1	0 (5:3)_(4:4aCO)
152	OM6	OM	14	652238	652389	652419	652841	2_nonsis	31	317	602	1	1	1	1	0 (5:3)_(4:4aCO)
14	OM6	OM	2	642483	642776	642776	643134	2_nonsis	1	326	650	1	1	1	1	0 (5:3)_(4:4aCO)
35	OM6	OM	4	954963	955643	955755	956552	2_nonsis	113	851	1588	1	1	1	1	0 (5:3)_(4:4aCO)
108	OM6	OM	12	224270	225174	225645	225795	2_nonsis	472	998	1524	1	1	1	1	0 (5:3)_(4:4aCO)
5	OM6	OM	2	78234	78701	79464	79692	2_nonsis	764	1111	1457	1	1	1	1	0 (5:3)_(4:4aCO)
122	OM6	OM	13	99880	100124	101176	102104	2_nonsis	1053	1638	2223	1	1	1	1	0 (5:3)_(4:4aCO)
42	OM6	OM	5	26685	27044	27044	27119	2_nonsis	1	217	433	1	2	1	1	0 (3:5)_(4:4aCO)
72	OM6	OM	8	70542	70883	70883	71457	2_nonsis	1	458	914	1	2	1	1	0 (3:5)_(4:4aCO)
130	OM6	OM	13	476908	477780	477780	478087	2_nonsis	1	590	1178	1	2	1	1	0 (3:5)_(4:4aCO)
10	OM6	OM	2	409495	410015	410015	410900	2_nonsis	1	703	1404	1	2	1	1	0 (3:5)_(4:4aCO)
94	OM6	OM	11	19020	19563	20014	20275	2_nonsis	452	853	1254	1	2	1	1	0 (3:5)_(4:4aCO)
131	OM6	OM	13	574226	575064	575127	576259	2_nonsis	64	1048	2032	1	2	1	1	0 (3:5)_(4:4aCO)
124	OM6	OM	13	117651	120604	120995	121603	2_nonsis	392	2172	3951	1	2	1	1	0 (3:5)_(4:4aCO)
148	OM6	OM	14	416991	418723	420283	420526	2_nonsis	1561	2548	3534	1	2	1	1	0 (3:5)_(4:4aCO)
73	OM6	OM	8	121618	121987	122169	122633	2_nonsis	183	599	1014	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
120	OM6	OM	13	39438	40376	40511	41051	2_nonsis	136	874	1612	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
19	OM6	OM	3	102669	103556	103955	104476	2_nonsis	400	1103	1806	1	5	1	1	0 (3:5)_(4:4)_(4:4aCO)
65	OM6	OM	7	609958	610674	611214	611295	2_nonsis	541	939	1336	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
165	OM6	OM	15	985518	985891	986838	986894	2_nonsis	948	1162	1375	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
52	OM6	OM	5	465974	466823	467963	468715	2_nonsis	1141	1941	2740	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
22	OM6	OM	4	105121	105197	105348	105623	2_nonsis	152	327	501	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
13	OM6	OM	2	564041	565133	565389	565408	2_nonsis	257	812	1366	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
47	OM6	OM	5	212944	213244	214752	214893	2_nonsis	1509	1729	1948	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
27	OM6	OM	4	263030	263811	266878	267359	2_nonsis	3068	3698	4328	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
158	OM6	OM	15	410276	410471	410754	411250	2_nonsis	284	629	973	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
115	OM6	OM	12	678541	678650	678658	678971	2_nonsis	314	693	1072	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
128	OM6	OM	13	388416	388450	389307	389541	2_nonsis	858	991	1124	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
155	OM6	OM	15	267320	267756	268456	269276	2_nonsis	701	1328	1955	1	12	1	1	0 (6:2)_(4:4aCO)_(5:3)_(4:4a)
59	OM6	OM	6	228093	228299	230627	230867	2_nonsis	2329	2551	2773	1	12	1	1	0 (5:3)_(4:4aCO)_(6:2)_(4:4a)
38	OM6	OM	4	1278613	1278992	1279680	1279875	2_nonsis	689	975	1261	1	12	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
136	OM6	OM	13	772282	772333	774012	774331	2_nonsis	1680	1864	2048	1	12	1	1	0 (2:6)_(3:5)_(4:4)_(2:6)_(4:4aCO)
58	OM6	OM	6	189336	189828	191655	191860	2_nonsis	1828	2176	2523	1	12	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
63	OM6	OM	7	433234	433416	435261	435280	2_nonsis	1846	1946	2045	1	12	1	1	0 (2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
37	OM6	OM	4	1149128	1149251	1153171	1153699	2_nonsis	3921	4246	4570	1	12	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
103	OM6	OM	11	469355	469480	469561	469692	2_nonsis	82	209	336	1	15	1	1	0 (6:2)_(4:4aCO)
86	OM6	OM	10	146598	146986	147014	147143	2_nonsis	29	287	544	1	15	1	1	0 (6:2)_(4:4aCO)
64	OM6	OM	7	451921	452296	452296	452589	2_nonsis	1	334	667	1	15	1	1	0 (6:2)_(4:4aCO)
114	OM6	OM	12	616330	616917	616917	617208	2_nonsis	1	439	877	1	15	1	1	0 (6:2)_(4:4aCO)
97	OM6	OM	11	172151	172715	172715	173133	2_nonsis	1	491	981	1	15	1	1	0 (6:2)_(4:4aCO)
166	OM6	OM	16	65675	66393	66527	66703	2_nonsis	135	581	1027	1	15	1	1	0 (6:2)_(4:4aCO)
69	OM6	OM	7	911857	912297	912560	912779	2_nonsis	264	593	921	1	15	1	1	0 (6:2)_(4:4aCO)

61	OM6	OM	7	141481	141849	142398	142616	2_nonsis	550	842	1134	1	15	1	1	0	(6:2)_(4:4aCO)
20	OM6	OM	3	156517	156868	157515	157686	2_nonsis	648	908	1168	1	15	1	1	0	(6:2)_(4:4aCO)
160	OM6	OM	15	570484	570759	570759	571108	2_nonsis	1	312	623	1	16	1	1	0	(2:6)_(4:4aCO)
150	OM6	OM	14	531520	531611	531656	532165	2_nonsis	46	345	644	1	16	1	1	0	(2:6)_(4:4aCO)
164	OM6	OM	15	968047	968210	968476	968504	2_nonsis	267	362	456	1	16	1	1	0	(2:6)_(4:4aCO)
77	OM6	OM	8	462588	462676	462717	463320	2_nonsis	42	387	731	1	16	1	1	0	(2:6)_(4:4aCO)
48	OM6	OM	5	228943	229569	229569	229778	2_nonsis	1	418	834	1	16	1	1	0	(2:6)_(4:4aCO)
54	OM6	OM	6	39690	40189	40232	40564	2_nonsis	44	459	873	1	16	1	1	0	(2:6)_(4:4aCO)
40	OM6	OM	4	1394566	1394881	1394881	1395687	2_nonsis	1	561	1120	1	16	1	1	0	(2:6)_(4:4aCO)
75	OM6	OM	8	352905	353097	353343	354035	2_nonsis	247	688	1129	1	16	1	1	0	(2:6)_(4:4aCO)
9	OM6	OM	2	338226	338664	339083	339200	2_nonsis	420	697	973	1	16	1	1	0	(2:6)_(4:4aCO)
87	OM6	OM	10	272315	272728	272728	273972	2_nonsis	1	829	1656	1	16	1	1	0	(2:6)_(4:4aCO)
163	OM6	OM	15	761321	761947	762399	762530	2_nonsis	453	831	1208	1	16	1	1	0	(2:6)_(4:4aCO)
60	OM6	OM	7	92892	93381	93397	94650	2_nonsis	17	887	1757	1	16	1	1	0	(2:6)_(4:4aCO)
123	OM6	OM	13	104516	105255	105707	106249	2_nonsis	453	1093	1732	1	16	1	1	0	(2:6)_(4:4aCO)
107	OM6	OM	12	54071	54226	54071	54226	2_nonsis	0	77	154	1	100	1	1	0	(4:4aCO)
66	OM6	OM	7	640541	640786	640541	640786	2_nonsis	0	122	244	1	100	1	1	0	(4:4aCO)
67	OM6	OM	7	697261	697513	697261	697513	2_nonsis	0	126	251	1	100	1	1	0	(4:4aCO)
112	OM6	OM	12	568114	568449	568114	568449	2_nonsis	0	167	334	1	100	1	1	0	(4:4aCO)
33	OM6	OM	4	808258	808803	808258	808803	2_nonsis	0	272	544	1	100	1	1	0	(4:4aCO)
7	OM6	OM	2	150492	151117	150492	151117	2_nonsis	0	312	624	1	100	1	1	0	(4:4aCO)
17	OM6	OM	2	738241	738886	738241	738886	2_nonsis	0	322	644	1	100	1	1	0	(4:4aCO)
30	OM6	OM	4	375932	376661	375932	376661	2_nonsis	0	364	728	1	100	1	1	0	(4:4aCO)
140	OM6	OM	14	51050	51868	51050	51868	2_nonsis	0	409	817	1	100	1	1	0	(4:4aCO)
51	OM6	OM	5	359292	360247	359292	360247	2_nonsis	0	477	954	1	100	1	1	0	(4:4aCO)
36	OM6	OM	4	1063173	1064173	1063173	1064173	2_nonsis	0	500	999	1	100	1	1	0	(4:4aCO)
34	OM6	OM	4	894075	895202	894075	895202	2_nonsis	0	563	1126	1	100	1	1	0	(4:4aCO)
89	OM6	OM	10	391693	392871	391693	392871	2_nonsis	0	589	1177	1	100	1	1	0	(4:4aCO)
92	OM6	OM	10	577732	578943	577732	578943	2_nonsis	0	605	1210	1	100	1	1	0	(4:4aCO)
21	OM6	OM	3	252633	253903	252633	253903	2_nonsis	0	635	1269	1	100	1	1	0	(4:4aCO)
3	OM6	OM	1	170945	172280	170945	172280	2_nonsis	0	667	1334	1	100	1	1	0	(4:4aCO)
106	OM6	OM	11	634635	635970	634635	635970	2_nonsis	0	667	1334	1	100	1	1	0	(4:4aCO)
149	OM6	OM	14	439088	440569	439088	440569	2_nonsis	0	740	1480	1	100	1	1	0	(4:4aCO)
126	OM6	OM	13	222095	223597	222095	223597	2_nonsis	0	751	1501	1	100	1	1	0	(4:4aCO)
81	OM6	OM	9	240939	242535	240939	242535	2_nonsis	0	798	1595	1	100	1	1	0	(4:4aCO)
121	OM6	OM	13	42127	44157	42127	44157	2_nonsis	0	1015	2029	1	100	1	1	0	(4:4aCO)
145	OM6	OM	14	197788	200172	197788	200172	2_nonsis	0	1192	2383	1	100	1	1	0	(4:4aCO)
139	OM6	OM	13	889717	890524	892536	893651	2_nonsis	2013	2973	3933	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
173	OM6	OM	16	653303	653426	653932	653953	2_nonsis	507	578	649	2	30	1	1	0	(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
2	OM6	OM	1	121235	128637	130776	130897	2_nonsis	2140	5901	9661	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
98	OM6	OM	11	263873	263933	265522	265790	2_nonsis	1590	1711	1832	2	31	1	1	0	(3:5)_(4:4)_(3:5)_(3:5a)_(2:6)_(4:4aCO)
55	OM6	OM	6	87978	88329	91421	92092	2_nonsis	3093	3603	4113	2	31	1	1	0	(4:4ai)_(3:5)_(2:6)_(3:5)_(3:5a)_(3:5b)_(4:4bCO)
83	OM6	OM	9	405428	405665	405973	406124	2_nonsis	309	502	695	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4aCO)
1	OM6	OM	1	55793	55914	57455	57739	2_nonsis	1542	1744	1945	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
95	OM6	OM	11	74916	75663	77172	77759	2_nonsis	1510	2176	2842	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(2:6)_(4:4aCO)
70	OM6	OM	7	991617	991917	994032	994097	2_nonsis	2116	2298	2479	2	32	1	1	0	(4:4aCO)_(3:5)_(4:4a)_(3:5a)_(4:4a)
170	OM6	OM	16	425006	425302	427600	428058	2_nonsis	2299	2675	3051	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4)_(4:4aCO)
168	OM6	OM	16	312873	312892	316205	316676	2_nonsis	3314	3558	3802	2	32	1	1	0	(5:3)_(4:4)_(6:2)_(5:3a)_(4:4aCO)
23	OM6	OM	4	174905	175847	177807	178219	2_nonsis	1961	2637	3313	2	32	1	1	0	(5:3)_(4:4aCO)_(5:3a)_(4:4a)_(5:3a)_(4:4a)
32	OM6	OM	4	635526	635784	637466	637466	2_nonsis	1474	1707	1939	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
44	OM6	OM	5	119741	120378	122638	122728	2_nonsis	2261	2624	2986	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
171	OM6	OM	16	482069	482104	482429	482737	2_nonsis	326	497	667	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(4:4a)
84	OM6	OM	10	36445	36722	37127	37895	2_nonsis	406	928	1449	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
88	OM6	OM	10	315888	316551	317150	317223	2_nonsis	600	967	1334	3	20	1	1	0	(3:5)_(5:3)_(3:5a)_(4:4aCO)
154	OM6	OM	15	40365	40497	41470	41495	2_nonsis	974	1052	1129	3	20	1	1	0	(2:6)_(4:4aCO)_(5:3)_(4:4a)
68	OM6	OM	7	853206	853242	855067	855163	2_nonsis	1826	1891	1956	3	20	1	1	0	(3:5)_(2:6)_(5:3)_(4:4aCO)
105	OM6	OM	11	522458	522560	525240	525421	2_nonsis	2681	2822	2962	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(4:4aCO)
49	OM6	OM	5	298190	298538	299333	299795	2_nonsis	796	1200	1604	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
135	OM6	OM	13	715257	715590	716494	716783	2_nonsis	905	1215	1525	3	20	1	1	0	(3:5)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
162	OM6	OM	15	749079	749636	750300	751330	2_nonsis	665	1458	2250	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)

		OM	N	A	B	C	D	Type	K	V1	V2	V3					F	Label
147	OM6	OM	14	364966	365449	366762	367502	2_nonsis		1314	1925	2535	3	20	1	1	0	(3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)
74	OM6	OM	8	279897	280350	281430	282877	2_nonsis		1081	2030	2979	3	20	1	1	0	(5:3)_(5:3a)_(6:2)_(3:5)_(4:4aCO)
62	OM6	OM	7	197816	197942	199894	200351	2_nonsis		1953	2244	2534	3	20	1	1	0	(6:2)_(4:4)_(5:3)_(5:3)_(4:4aCO)
176	OM6	OM	16	839916	840103	842086	842864	2_nonsis		1984	2466	2947	3	20	1	1	0	(5:3)_(4:4)_(6:2)_(2:6)_(4:4aCO)
113	OM6	OM	12	600547	600676	602186	602338	2_nonsis		1511	1651	1790	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
56	OM6	OM	6	113910	114016	116186	116269	2_nonsis		2171	2265	2358	3	20	1	1	0	(3:5)_(4:4)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(4:4a)
8	OM6	OM	2	251742	251790	254006	254436	2_nonsis		2217	2455	2693	3	20	1	1	0	(3:5)_(2:6)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(4:4a)
116	OM6	OM	12	835509	835608	837962	840577	2_nonsis		2355	3711	5067	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)_(3:5a)_(2:6)_(3:5)_(4:4a)
41	OM6	OM	4	1442138	1442312	1443911	1444256	2_nonsis		1600	1859	2117	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4a)
133	OM6	OM	13	664149	664502	668408	668902	2_nonsis		3907	4330	4752	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
53	OM6	OM	5	491135	491222	491960	492293	2_nonsis		739	948	1157	3	21	1	1	0	(5:3)_(4:4ai)_(3:5)_(3:5a)_(4:4bCO)
125	OM6	OM	13	178780	179112	180040	181117	2_sis		929	1633	2336	0	1	2	0	2	(6:2)_(8:0)_(4:4)
110	OM6	OM	12	340821	340838	341070	341507		4	233	459	685	0	2	2	2	0	(3:5)_(2:6)_(4:4aCO)
118	OM6	OM	12	1012226	1013592	1014541	1014649		3	950	1686	2422	0	2	2	1	1	(3:5)_(3:5a)_(4:4aCO)
102	OM6	OM	11	369878	370412	370874	371565	2_nonsis		463	1075	1686	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4CO)
134	OM7	OM	11	506252	506430	506430	506614		1	1	181	361	1	1	1	0	1	05:03
126	OM7	OM	11	258873	259176	259177	259318		1	2	223	444	1	1	1	0	1	05:03
161	OM7	OM	13	95214	95277	95482	95516		1	206	254	301	1	1	1	0	1	05:03
39	OM7	OM	4	954530	954939	954985	955099		1	47	308	568	1	1	1	0	1	05:03
44	OM7	OM	4	1126843	1126921	1127082	1127449		1	162	384	605	1	1	1	0	1	05:03
142	OM7	OM	12	97654	98056	98056	98431		1	1	389	776	1	1	1	0	1	05:03
41	OM7	OM	4	1045146	1045288	1045482	1045735		1	195	392	588	1	1	1	0	1	05:03
22	OM7	OM	3	197057	197306	197389	197788		1	84	407	730	1	1	1	0	1	05:03
5	OM7	OM	1	175409	175578	175876	175963		1	299	426	553	1	1	1	0	1	05:03
103	OM7	OM	9	169471	169640	169820	170156		1	181	433	684	1	1	1	0	1	05:03
129	OM7	OM	11	333757	334135	334135	334655		1	1	449	897	1	1	1	0	1	05:03
183	OM7	OM	14	382904	383402	383575	383709		1	174	489	804	1	1	1	0	1	05:03
198	OM7	OM	15	486108	486243	486511	487028		1	269	594	919	1	1	1	0	1	05:03
173	OM7	OM	13	776909	777163	777598	777667		1	436	597	757	1	1	1	0	1	05:03
159	OM7	OM	13	15705	16224	16764	17138		1	541	987	1432	1	1	1	0	1	05:03
145	OM7	OM	12	341070	341507	342190	342448		1	684	1031	1377	1	1	1	0	1	05:03
2	OM7	OM	1	73855	73970	74786	75211		1	817	1086	1355	1	1	1	0	1	05:03
9	OM7	OM	2	126263	126565	126921	128153		1	357	1123	1889	1	1	1	0	1	05:03
98	OM7	OM	8	499040	499430	500464	500752		1	1035	1373	1711	1	1	1	0	1	05:03
47	OM7	OM	4	1240626	1241483	1242241	1242658		1	759	1395	2031	1	1	1	0	1	05:03
118	OM7	OM	10	570822	573135	573135	573950		1	1	1564	3127	1	1	1	0	1	05:03
216	OM7	OM	16	461367	462319	463723	464194		1	1405	2116	2826	1	1	1	0	1	05:03
190	OM7	OM	15	99650	99844	102107	102146		1	2264	2380	2495	1	1	1	0	1	05:03
196	OM7	OM	15	378043	378090	378090	378122		1	1	40	78	1	2	1	0	1	03:05
60	OM7	OM	5	335567	335661	335661	335687		1	1	60	119	1	2	1	0	1	03:05
63	OM7	OM	5	472577	472664	472664	472738		1	1	81	160	1	2	1	0	1	03:05
194	OM7	OM	15	316433	316591	316591	316611		1	1	89	177	1	2	1	0	1	03:05
91	OM7	OM	8	48709	48768	48768	48921		1	1	106	211	1	2	1	0	1	03:05
51	OM7	OM	4	1420714	1420794	1420794	1420932		1	1	109	217	1	2	1	0	1	03:05
74	OM7	OM	7	196917	196981	197001	197150		1	21	127	232	1	2	1	0	1	03:05
164	OM7	OM	13	303300	303354	303419	303491		1	66	128	190	1	2	1	0	1	03:05
215	OM7	OM	16	425451	425480	425481	425740		1	2	145	288	1	2	1	0	1	03:05
136	OM7	OM	11	565671	565988	565988	566185		1	1	257	513	1	2	1	0	1	03:05
100	OM7	OM	9	76162	76340	76381	76848		1	42	364	685	1	2	1	0	1	03:05
28	OM7	OM	4	164096	164298	164298	164984		1	1	444	887	1	2	1	0	1	03:05
76	OM7	OM	7	224665	225106	225112	225550		1	7	446	884	1	2	1	0	1	03:05
83	OM7	OM	7	597592	598397	598397	598538		1	1	473	945	1	2	1	0	1	03:05
38	OM7	OM	4	909447	909908	909908	910427		1	1	490	979	1	2	1	0	1	03:05
206	OM7	OM	16	21870	21970	22388	22478		1	419	513	607	1	2	1	0	1	03:05
199	OM7	OM	15	513637	514366	514405	514625		1	40	514	987	1	2	1	0	1	03:05
186	OM7	OM	14	464849	465005	465005	465885		1	1	518	1035	1	2	1	0	1	03:05
15	OM7	OM	2	490686	491476	491476	492001		1	1	658	1314	1	2	1	0	1	03:05
214	OM7	OM	16	371914	372742	372742	373291		1	1	689	1376	1	2	1	0	1	03:05
181	OM7	OM	14	240933	241136	241440	242111		1	305	741	1177	1	2	1	0	1	03:05
85	OM7	OM	7	640541	640849	640849	642042		1	1	751	1500	1	2	1	0	1	03:05

140	OM7	OM	12	37196	37375	38224	38338	1	850	996	1141	1	2	1	0	1	03:05
152	OM7	OM	12	727539	727901	728268	729242	1	368	1035	1702	1	2	1	0	1	03:05
185	OM7	OM	14	425816	427278	427451	427715	1	174	1036	1898	1	2	1	0	1	03:05
105	OM7	OM	9	257646	257823	258908	259266	1	1086	1353	1619	1	2	1	0	1	03:05
176	OM7	OM	14	52324	52659	53888	54162	1	1230	1534	1837	1	2	1	0	1	03:05
13	OM7	OM	2	371139	371446	372730	372954	1	1285	1550	1814	1	2	1	0	1	03:05
125	OM7	OM	11	225909	226549	227625	227937	1	1077	1552	2027	1	2	1	0	1	03:05
223	OM7	OM	16	892211	892306	893806	893821	1	1501	1555	1609	1	2	1	0	1	03:05
37	OM7	OM	4	865525	865546	867508	867984	1	1963	2211	2458	1	2	1	0	1	03:05
102	OM7	OM	9	160585	160764	162266	163812	1	1503	2365	3226	1	2	1	0	1	03:05
144	OM7	OM	12	317117	318011	319960	320465	1	1950	2649	3347	1	2	1	0	1	03:05
155	OM7	OM	12	837962	840577	840682	843387	1	106	2765	5424	1	2	1	0	1	03:05
71	OM7	OM	6	236578	236905	237488	237962	1	584	984	1383	1	3	1	0	1	5:3_6:2_5:3
137	OM7	OM	11	598922	599337	600144	600159	1	808	1022	1236	1	3	1	0	1	5:3_4:4_5:3
40	OM7	OM	4	968331	968466	969561	970293	1	1096	1529	1961	1	3	1	0	1	5:3_4:4_5:3
16	OM7	OM	2	516590	516896	519354	519405	1	2459	2637	2814	1	3	1	0	1	5:3_6:2_5:3
1	OM7	OM	1	30493	30516	30644	30662	1	129	149	168	1	3	1	0	1	5:3_4:4_6:2_5:3
132	OM7	OM	11	438489	439212	439879	439894	1	668	1036	1404	1	4	1	0	1	3:5_4:4_3:5
45	OM7	OM	4	1167232	1167361	1168770	1168940	1	1410	1559	1707	1	4	1	0	1	3:5_2:6_3:5
138	OM7	OM	11	612809	613087	614538	615121	1	1452	1882	2311	1	4	1	0	1	3:5_4:4_3:5
43	OM7	OM	4	1052845	1053051	1054662	1055183	1	1612	1975	2337	1	4	1	0	1	3:5_2:6_3:5
54	OM7	OM	5	11847	12024	13307	13446	1	1284	1441	1598	1	4	1	0	1	3:5_4:4_2:6_3:5
131	OM7	OM	11	434978	435357	437047	437157	1	1691	1935	2178	1	4	1	0	1	3:5_4:4_3:5_2:6_3:5
31	OM7	OM	4	341036	341381	341421	341782	1	41	393	745	1	7	1	0	1	5:3_6:2
84	OM7	OM	7	636413	636660	636810	637449	1	151	593	1035	1	7	1	0	1	6:2_5:3
158	OM7	OM	12	1053098	1053517	1054794	1055114	1	1278	1647	2015	1	7	1	0	1	5:3_6:2
154	OM7	OM	12	818577	819069	819834	820606	1	766	1397	2028	1	7	1	0	1	5:3_6:2_5:3_6:2
10	OM7	OM	2	160020	160143	160810	161687	1	668	1167	1666	1	8	1	0	1	3:5_2:6
165	OM7	OM	13	371760	371798	379248	379442	1	7451	7566	7681	1	8	1	0	1	3:5_2:6_4:4_2:6
6	OM7	OM	1	195324	195456	198699	198707	1	3244	3313	3382	1	8	1	0	1	3:5_2:6_3:5_2:6_3:5_2:6_3:5_2:6_3:5_2:6_3:5_2:6
148	OM7	OM	12	602479	602685	602685	602909	1	1	215	429	1	10.1	1	0	1	02:06
178	OM7	OM	14	116678	116796	117055	117101	1	260	341	422	2	11	1	0	1	5:3_5:3a
56	OM7	OM	5	33348	33706	34050	34247	1	345	622	898	2	11	1	0	1	5:3_5:3a
201	OM7	OM	15	733385	733489	733953	735184	1	465	1132	1798	2	11	1	0	1	5:3_5:3a
151	OM7	OM	12	679633	680510	681146	681539	1	637	1271	1905	2	11	1	0	1	5:3_5:3a
213	OM7	OM	16	358537	358849	360315	360607	1	1467	1768	2069	2	11	1	0	1	5:3_5:3a
121	OM7	OM	11	33673	34051	35874	36243	1	1824	2197	2569	2	11	1	0	1	5:3_5:3a
172	OM7	OM	13	741504	741880	744735	744855	1	2856	3103	3350	2	11	1	0	1	5:3_5:3a
49	OM7	OM	4	1318030	1318331	1321506	1322306	1	3176	3726	4275	2	11	1	0	1	5:3_5:3a
75	OM7	OM	7	201499	202039	205641	205751	1	3603	3927	4251	2	11	1	0	1	5:3_5:3a
149	OM7	OM	12	644551	645338	645971	646705	1	634	1394	2153	2	12	1	0	1	3:5_3:5a
42	OM7	OM	4	1049195	1049210	1050770	1050824	1	1561	1595	1628	2	12	1	0	1	3:5_3:5a
135	OM7	OM	11	523649	523718	525240	525421	1	1523	1647	1771	2	12	1	0	1	3:5_3:5a
79	OM7	OM	7	412771	412810	413503	413620	1	694	771	848	2	13	1	0	1	5:3_4:4_5:3_5:3a
80	OM7	OM	7	451346	451921	453324	453639	1	1404	1848	2292	2	13	1	0	1	5:3_5:3a_6:2_5:3a
130	OM7	OM	11	400972	401736	404440	404696	1	2705	3214	3723	2	13	1	0	1	5:3_4:4_5:3_5:3a
221	OM7	OM	16	810641	811565	815485	816173	1	3921	4726	5531	2	13	1	0	1	5:3_4:4_5:3_5:3a_4:4_5:3a_4:4_5:3a_6:2_5:3a
87	OM7	OM	7	795193	795253	796413	796586	1	1161	1277	1392	2	14	1	0	1	3:5_3:5a_2:6
182	OM7	OM	14	317977	318057	319911	321214	1	1855	2546	3236	2	14	1	0	1	3:5_3:5a_2:6_3:5a
24	OM7	OM	4	21450	21476	22513	22525	1	1038	1056	1074	2	14	1	0	1	3:5_4:4_3:5_2:6_3:5_3:5a
116	OM7	OM	10	380992	381023	381650	381896	1	628	766	903	2	15	1	0	1	5:3_4:4_5:3a
34	OM7	OM	4	714934	715058	716075	716118	1	1018	1101	1183	2	15	1	0	1	5:3_4:4_5:3a
205	OM7	OM	15	1024766	1025192	1026039	1026427	1	848	1254	1660	2	15	1	0	1	5:3_4:4_5:3a
210	OM7	OM	16	172192	172402	173535	174782	1	1134	1862	2589	2	15	1	0	1	5:3_4:4_5:3a
127	OM7	OM	11	267504	267528	272535	272996	1	5008	5250	5491	2	15	1	0	1	5:3_4:4_5:3a
12	OM7	OM	2	350797	350900	351335	351500	1	436	569	702	2	16	1	0	1	3:5_4:4_3:5a
171	OM7	OM	13	694524	694679	695300	695427	1	622	762	902	2	16	1	0	1	3:5_4:4_3:5a
212	OM7	OM	16	286085	286209	286979	287057	1	771	871	971	2	16	1	0	1	3:5_4:4_3:5a
209	OM7	OM	16	114414	114586	115228	115785	1	643	1007	1370	2	16	1	0	1	3:5_4:4_3:5a
48	OM7	OM	4	1278056	1278456	1279416	1279422	1	961	1163	1365	2	16	1	0	1	3:5_4:4_3:5a

177	OM7	OM	14	107852	108148	109033	109383	1	886	1208	1530	2	16	1	0	1 3:5_4:4_3:5a
167	OM7	OM	13	459508	459995	461290	461498	1	1296	1643	1989	2	16	1	0	1 3:5_4:4_3:5a
106	OM7	OM	9	266803	267668	268690	269349	1	1023	1784	2545	2	16	1	0	1 3:5_4:4_3:5a
57	OM7	OM	5	66291	67085	69243	69568	1	2159	2718	3276	2	17	1	0	1 6:2_5:3_4:4_5:3a
150	OM7	OM	12	675407	675924	678194	678512	1	2271	2688	3104	2	17	1	0	1 6:2_5:3_4:4_5:3_4:4_5:3_4:4_5:3a
68	OM7	OM	6	108920	109247	114918	115088	1	5672	5920	6167	2	17	1	0	1 5:3_4:4_5:3a_4:4_6:2_5:3a_6:2_5:3a_4:4_5:3a
108	OM7	OM	9	335079	336156	339115	340356	1	2960	4118	5276	2	18	1	0	1 3:5_2:6_3:5_4:4_3:5a
120	OM7	OM	10	704768	704861	705639	705848	1	779	929	1079	2	19	1	0	1 5:3_6:2_5:3a
110	OM7	OM	9	396773	396834	399240	399281	1	2407	2457	2507	2	19	1	0	1 5:3_6:2_5:3a
207	OM7	OM	16	45974	46114	46637	46780	1	524	665	805	2	20	1	0	1 3:5_2:6_3:5a
82	OM7	OM	7	527159	527396	528501	528674	1	1106	1310	1514	2	20	1	0	1 3:5_2:6_3:5a
20	OM7	OM	3	70158	70491	71427	71575	1	937	1177	1416	2	22	1	0	1 3:5_2:6_3:5_2:6_3:5a
94	OM7	OM	8	140123	142800	143949	144253	2_nonsis	1150	2640	4129	3	30	1	0	1 3:5_5:3_3:5
72	OM7	OM	7	19992	20130	21041	21167	2_nonsis	912	1043	1174	3	30	1	0	1 3:5_4:4_3:5_5:3_4:4_5:3_4:4_2:6_3:5a
92	OM7	OM	8	97245	97536	99112	99909	2_nonsis	1577	2120	2663	3	31	1	0	1 5:3_5:3a_4:4ai
220	OM7	OM	16	784177	784693	786663	787292	2_nonsis	1971	2543	3114	3	31	1	0	1 3:5_4:4ai_4:4bi_5:3_6:2_5:3
123	OM7	OM	11	99224	99633	99646	100670	2_nonsis	14	730	1445	1	1	1	1	0 (5:3)_(4:4aCO)
187	OM7	OM	14	606438	606872	606872	608001	2_nonsis	1	782	1562	1	1	1	1	0 (5:3)_(4:4aCO)
77	OM7	OM	7	247749	249983	250680	252024	2_nonsis	698	2486	4274	1	1	1	1	0 (5:3)_(4:4aCO)
21	OM7	OM	3	163699	164093	164277	165283	2_nonsis	185	884	1583	1	2	1	1	0 (3:5)_(4:4aCO)
99	OM7	OM	8	517036	517336	518620	518740	2_nonsis	1285	1494	1703	1	2	1	1	0 (3:5)_(4:4aCO)
114	OM7	OM	10	346858	347630	347951	348292	2_nonsis	322	878	1433	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
197	OM7	OM	15	457110	457531	458312	458549	2_nonsis	782	1110	1438	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
111	OM7	OM	10	58202	58607	60064	60979	2_nonsis	1458	2117	2776	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
26	OM7	OM	4	77883	78578	79621	79687	2_nonsis	1044	1424	1803	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
192	OM7	OM	15	270164	270370	270526	270656	2_nonsis	157	324	491	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
143	OM7	OM	12	233075	234128	234378	234633	2_nonsis	251	904	1557	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
52	OM7	OM	4	1463798	1464429	1465960	1466217	2_nonsis	1532	1975	2418	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
78	OM7	OM	7	306279	306537	306650	306793	2_nonsis	114	314	513	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
86	OM7	OM	7	766129	766363	766579	766797	2_nonsis	217	442	667	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
69	OM7	OM	6	172677	173376	173765	174112	2_nonsis	390	912	1434	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
174	OM7	OM	13	797223	797362	797456	797542	2_nonsis	95	207	318	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
208	OM7	OM	16	72392	72410	73929	74327	2_nonsis	1520	1727	1934	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
90	OM7	OM	7	1012544	1012661	1012874	1013000	2_nonsis	214	335	455	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
95	OM7	OM	8	189310	189521	190671	191072	2_nonsis	1151	1456	1761	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
153	OM7	OM	12	776373	777814	778158	779222	2_nonsis	345	1597	2848	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
146	OM7	OM	12	370090	370487	370966	371874	2_nonsis	480	1132	1783	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
73	OM7	OM	7	124322	124671	125090	125128	2_nonsis	420	613	805	1	12	1	1	0 (5:3)_(4:4aCO)_(5:3)_(4:4a)
211	OM7	OM	16	212773	213190	214028	214067	2_nonsis	839	1066	1293	1	12	1	1	0 (5:3)_(4:4aCO)_(6:2)_(4:4a)
170	OM7	OM	13	664811	665349	666220	666667	2_nonsis	872	1364	1855	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4aCO)
122	OM7	OM	11	80353	80724	81532	82469	2_nonsis	809	1462	2115	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
64	OM7	OM	5	540528	540683	541194	541873	2_nonsis	512	928	1344	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
113	OM7	OM	10	236674	236901	237784	238262	2_nonsis	884	1236	1587	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
109	OM7	OM	9	375595	375691	377556	378238	2_nonsis	1866	2254	2642	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(3:5)_(4:4a)
101	OM7	OM	9	90720	91277	93376	93546	2_nonsis	2100	2463	2825	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(6:2)_(5:3)_(4:4a)
218	OM7	OM	16	586133	586291	586309	586497	2_nonsis	19	191	363	1	15	1	1	0 (6:2)_(4:4aCO)
19	OM7	OM	3	40374	40637	40637	40987	2_nonsis	1	307	612	1	15	1	1	0 (6:2)_(4:4aCO)
70	OM7	OM	6	223659	224098	224098	224275	2_nonsis	1	308	615	1	15	1	1	0 (6:2)_(4:4aCO)
133	OM7	OM	11	479195	479521	479521	480070	2_nonsis	1	438	874	1	15	1	1	0 (6:2)_(4:4aCO)
180	OM7	OM	14	233897	234026	234026	234916	2_nonsis	1	510	1018	1	15	1	1	0 (6:2)_(4:4aCO)
203	OM7	OM	15	860391	861174	861195	861567	2_nonsis	22	599	1175	1	15	1	1	0 (6:2)_(4:4aCO)
11	OM7	OM	2	288990	289129	289129	289364	2_nonsis	1	187	373	1	16	1	1	0 (2:6)_(4:4aCO)
217	OM7	OM	16	520404	520684	520684	520828	2_nonsis	1	212	423	1	16	1	1	0 (2:6)_(4:4aCO)
33	OM7	OM	4	615975	616214	616434	616559	2_nonsis	221	402	583	1	16	1	1	0 (2:6)_(4:4aCO)
59	OM7	OM	5	224681	225229	225485	226347	2_nonsis	257	961	1665	1	16	1	1	0 (2:6)_(4:4aCO)
141	OM7	OM	12	94920	95188	94920	95188	2_nonsis	0	134	267	1	100	1	1	0 (4:4aCO)
81	OM7	OM	7	523417	523732	523417	523732	2_nonsis	0	157	314	1	100	1	1	0 (4:4aCO)
163	OM7	OM	13	236410	236819	236410	236819	2_nonsis	0	204	408	1	100	1	1	0 (4:4aCO)
200	OM7	OM	15	670513	671012	670513	671012	2_nonsis	0	249	498	1	100	1	1	0 (4:4aCO)
184	OM7	OM	14	424418	425075	424418	425075	2_nonsis	0	328	656	1	100	1	1	0 (4:4aCO)

124	OM7	OM	11	171261	172151	171261	172151	2_nonsis	0	445	889	1	100	1	1	0 (4:4aCO)
219	OM7	OM	16	689677	691459	689677	691459	2_nonsis	0	891	1781	1	100	1	1	0 (4:4aCO)
117	OM7	OM	10	568805	570822	568805	570822	2_nonsis	0	1008	2016	1	100	1	1	0 (4:4aCO)
4	OM7	OM	1	132066	135319	132066	135319	2_nonsis	0	1626	3252	1	100	1	1	0 (4:4aCO)
191	OM7	OM	15	147007	150962	147007	150962	2_nonsis	0	1977	3954	1	100	1	1	0 (4:4aCO)
156	OM7	OM	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0 (4:4aCO)
107	OM7	OM	9	274972	275112	275507	275789	2_nonsis	396	606	816	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
222	OM7	OM	16	887394	887495	889742	890080	2_nonsis	2248	2467	2685	2	30	1	1	0 (5:3)_(5:3a)_(6:2)_(5:3a)_(4:4ai)_(4:4bCO)
168	OM7	OM	13	494666	494984	498745	499915	2_nonsis	3762	4505	5248	2	30	1	1	0 (6:2)_(5:3)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
50	OM7	OM	4	1362965	1363089	1367355	1367748	2_nonsis	4267	4525	4782	2	30	1	1	0 (5:3)_(6:2)_(5:3)_(5:3a)_(5:3b)_(4:4aCO)
8	OM7	OM	2	73943	74920	76470	76676	2_nonsis	1551	2142	2732	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
175	OM7	OM	13	860181	861184	864272	864551	2_nonsis	3089	3729	4369	2	31	1	1	0 (3:5)_(3:5a)_(4:4)_(3:5b)_(4:4aCO)
36	OM7	OM	4	809670	810702	814490	814815	2_nonsis	3789	4467	5144	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
30	OM7	OM	4	319641	320177	321785	321844	2_nonsis	1609	1906	2202	2	31	1	1	0 (3:5)_(3:5a)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
202	OM7	OM	15	778024	779060	781184	781897	2_nonsis	2752	3312	3872	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)_(3:5a)_(3:5a)_(3:5b)_(4:4a)
55	OM7	OM	5	26638	26678	28312	28600	2_nonsis	1635	1798	1961	2	32	1	1	0 (3:5)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
139	OM7	OM	12	29131	29612	31221	31473	2_nonsis	1610	1976	2341	2	32	1	1	0 (5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
195	OM7	OM	15	346743	347366	349515	349564	2_nonsis	2150	2485	2820	2	32	1	1	0 (5:3)_(4:4aCO)_(5:3a)_(5:3b)_(4:4a)
188	OM7	OM	14	662512	665017	667685	668135	2_nonsis	2669	4146	5622	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(4:4)_(5:3)_(4:4aCO)
160	OM7	OM	13	54192	54469	56748	57144	2_nonsis	2280	2616	2951	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(4:4)_(3:5)_(4:4ai)_(3:5b)_(4:4bCO)
169	OM7	OM	13	560428	561397	561662	561993	2_nonsis	266	915	1564	3	20	1	1	0 (2:6)_(5:3)_(4:4aCO)
67	OM7	OM	6	102071	102489	103865	104114	2_nonsis	1377	1710	2042	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
61	OM7	OM	5	358357	359292	360556	361242	2_nonsis	1265	2075	2884	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
29	OM7	OM	4	230153	230663	233071	233134	2_nonsis	2409	2695	2980	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
204	OM7	OM	15	944698	945099	945647	945784	2_nonsis	549	817	1085	3	20	1	1	0 (6:2)_(5:3)_(3:5)_(4:4aCO)
53	OM7	OM	4	1497031	1497133	1498007	1498087	2_nonsis	875	965	1055	3	20	1	1	0 (5:3)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
193	OM7	OM	15	295611	296401	297608	297726	2_nonsis	1208	1661	2114	3	20	1	1	0 (5:3)_(6:2)_(4:4)_(2:6)_(4:4aCO)
119	OM7	OM	10	660786	661017	662479	663134	2_nonsis	1463	1905	2347	3	20	1	1	0 (5:3)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
115	OM7	OM	10	373437	373775	375392	375980	2_nonsis	1618	2080	2542	3	20	1	1	0 (6:2)_(2:6)_(4:4aCO)_(3:5)_(4:4a)
162	OM7	OM	13	163286	163391	167027	167431	2_nonsis	3637	3891	4144	3	20	1	1	0 (5:3)_(4:4)_(3:5)_(5:3a)_(4:4aCO)
89	OM7	OM	7	919531	919947	926465	926609	2_nonsis	6519	6798	7077	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)
93	OM7	OM	8	121477	121987	123099	123320	2_nonsis	1113	1478	1842	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(5:3)_(4:4aCO)
27	OM7	OM	4	145687	145805	148667	148986	2_nonsis	2863	3081	3298	3	20	1	1	0 (5:3)_(4:4aCO)_(3:5)_(4:4a)_(3:5a)_(4:4a)
104	OM7	OM	9	175175	175368	178629	179273	2_nonsis	3262	3680	4097	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)_(3:5)_(2:6)_(4:4a)
14	OM7	OM	2	457416	457610	458835	458919	2_nonsis	1226	1364	1502	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(4:4aCO)_(2:6)_(3:5)_(4:4a)
96	OM7	OM	8	279197	279622	281264	281430	2_nonsis	1643	1938	2232	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(3:5)_(4:4aCO)
18	OM7	OM	2	757908	758926	761970	762336	2_nonsis	3045	3736	4427	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)_(2:6)_(4:4a)_(3:5a)_(4:4a)
147	OM7	OM	12	514693	514832	519358	520183	2_nonsis	4527	5008	5489	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)
66	OM7	OM	6	74173	74254	78202	78568	2_nonsis	3949	4172	4394	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(4:4)_(3:5)_(2:6)_(3:5)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
179	OM7	OM	14	187434	187730	188341	188387	2_nonsis	612	782	952	3	21	1	1	0 (6:2)_(4:4ai)_(3:5)_(4:4bCO)
157	OM7	OM	12	952346	952469	955099	955168	2_nonsis	2631	2726	2821	3	21	1	1	0 (3:5)_(4:4ai)_(5:3)_(4:4bCO)
17	OM7	OM	2	597752	597781	600626	601097	2_nonsis	2846	3095	3344	3	21	1	1	0 (5:3)_(4:4ai)_(3:5)_(4:4bCO)_(3:5)_(4:4b)
88	OM7	OM	7	847512	847727	850043	850236	2_nonsis	2317	2520	2723	3	21	1	1	0 (5:3)_(6:2)_(5:3)_(4:4ai)_(4:4bCO)_(3:5)_(4:4b)
46	OM7	OM	4	1216449	1216848	1219165	1219718	2_nonsis	2318	2793	3268	3	21	1	1	0 (5:3)_(4:4)_(5:3)_(4:4ai)_(3:5)_(2:6)_(3:5)_(4:4bCO)
3	OM7	OM	1	129075	129476	130075	132066	2_sis	1500	2245	2990	0	1	2	0	2 (5:3)_(5:3a)_(6:2)_(4:4)
58	OM7	OM	5	155613	155858	160248	160729	3	4391	4753	5115	0	1	2	0	2 (3:5)_(4:4)_(3:5)_(3:5a)_(5:3)_(3:5b)_(4:4ai)_(3:5a)_(4:4)_(5:3)_(4:4)
128	OM7	OM	11	307466	307562	310373	310702	3	2812	3024	3235	0	1	2	0	2 (3:5)_(3:5a)_(2:6i)_(1:7)_(1:7a)_(2:6i)_(3:5b)_(4:4)
23	OM7	OM	3	212942	213185	218143	218655	3	4959	5336	5712	0	2	2	1	1 (6:2)_(5:3)_(2:6i)_(4:4ai)_(5:3a)_(4:4bCO)
25	OM7	OM	4	55084	55881	57910	58341	3	2030	2643	3256	0	2	2	1	1 (3:5)_(4:4aCO)_(3:5a)_(2:6)_(3:5a)_(2:6)_(4:4a)
32	OM7	OM	4	550699	550807	552354	552557	3	1548	1703	1857	0	2	2	1	1 (5:3)_(4:4)_(4:4aCO)_(5:3a)_(4:4a)
35	OM7	OM	4	788889	789368	794075	794507	3	4708	5163	5617	0	2	2	1	1 (5:3)_(5:3a)_(6:2)_(4:4aCO)
62	OM7	OM	5	397892	398975	400033	400481	3	1059	1824	2588	0	2	2	1	1 (6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
97	OM7	OM	8	372612	372964	377294	377321	4	4331	4520	4708	0	2	2	1	1 (3:5)_(2:6)_(3:5)_(4:4ai)_(2:6)_(3:5)_(3:5a)_(2:6ai)_(3:5b)_(2:6bi)_(3:5c)_(4:4bCO)
112	OM7	OM	10	156523	157046	159830	160491	3	2785	3376	3967	0	2	2	1	1 (3:5)_(2:6)_(3:5a)_(4:4aCO)_(5:3)_(4:4a)
189	OM7	OM	14	707765	708870	710457	711615	3	1588	2719	3849	0	2	2	1	1 (5:3)_(3:5)_(4:4ai)_(4:4bCO)
7	OM7	OM	2	37628	39234	45824	46603	3	6591	7783	8974	0	3	2	1	1 (5:3)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)_(6:2a)_(5:3b)_(6:2a)_(5:3b)_(4:4bCO)
65	OM7	OM	6	54605	54858	58295	58625	2_nonsis	3438	3729	4019	0	3	2	0	2 (5:3)_(4:4ai)_(4:4bCO)_(5:3a)_(6:2)_(4:4CO)
166	OM7	OM	13	405911	406116	411113	411264	3	4998	5175	5352	0	3	2	1	1 (4:4aCO)_(3:5)_(2:6)_(3:5)_(6:2)_(2:6)_(3:5a)_(4:4bCO)
72	OM8	OM	7	442184	442209	442209	442299	1	1	58	114	1	1	1	0	1 05:03
55	OM8	OM	5	311842	311900	311969	311996	1	70	112	153	1	1	1	0	1 05:03

197	OM8	OM	16	339114	339477	339486	339516	1	10	206	401	1	1	1	0	1	05:03
123	OM8	OM	12	65728	65992	66129	66235	1	138	322	506	1	1	1	0	1	05:03
73	OM8	OM	7	478509	478940	478995	479144	1	56	345	634	1	1	1	0	1	05:03
144	OM8	OM	13	159532	159727	159950	160037	1	224	364	504	1	1	1	0	1	05:03
61	OM8	OM	5	560026	560290	560376	560686	1	87	373	659	1	1	1	0	1	05:03
136	OM8	OM	12	677763	677890	677890	678512	1	1	375	748	1	1	1	0	1	05:03
24	OM8	OM	3	40637	40987	41096	41289	1	110	381	651	1	1	1	0	1	05:03
40	OM8	OM	4	654179	654729	654813	654890	1	85	398	710	1	1	1	0	1	05:03
88	OM8	OM	8	515162	515676	515688	516015	1	13	433	852	1	1	1	0	1	05:03
112	OM8	OM	11	165754	166502	166543	166672	1	42	480	917	1	1	1	0	1	05:03
92	OM8	OM	9	174391	174961	175175	175368	1	215	596	976	1	1	1	0	1	05:03
130	OM8	OM	12	253274	253791	253941	254321	1	151	599	1046	1	1	1	0	1	05:03
16	OM8	OM	2	492334	493122	493123	493536	1	2	602	1201	1	1	1	0	1	05:03
48	OM8	OM	4	1265447	1266696	1266696	1266824	1	1	689	1376	1	1	1	0	1	05:03
89	OM8	OM	8	517499	518179	518762	518911	1	584	998	1411	1	1	1	0	1	05:03
69	OM8	OM	7	270688	270975	271853	272144	1	879	1167	1455	1	1	1	0	1	05:03
160	OM8	OM	14	460076	462377	462386	462443	1	10	1188	2366	1	1	1	0	1	05:03
192	OM8	OM	16	154774	155088	155906	156518	1	819	1281	1743	1	1	1	0	1	05:03
129	OM8	OM	12	248700	248752	249826	250571	1	1075	1473	1870	1	1	1	0	1	05:03
126	OM8	OM	12	144379	144822	146111	146275	1	1290	1593	1895	1	1	1	0	1	05:03
180	OM8	OM	15	684419	685601	685875	687587	1	275	1721	3167	1	1	1	0	1	05:03
17	OM8	OM	2	541389	541474	541474	541477	1	1	44	87	1	2	1	0	1	03:05
21	OM8	OM	2	714536	714609	714609	714638	1	1	51	101	1	2	1	0	1	03:05
102	OM8	OM	10	323078	323243	323243	323333	1	1	128	254	1	2	1	0	1	03:05
194	OM8	OM	16	214068	214281	214281	214333	1	1	133	264	1	2	1	0	1	03:05
28	OM8	OM	3	197306	197389	197389	197578	1	1	136	271	1	2	1	0	1	03:05
118	OM8	OM	11	361983	362017	362231	362247	1	215	239	263	1	2	1	0	1	03:05
116	OM8	OM	11	283762	283904	283904	284248	1	1	243	485	1	2	1	0	1	03:05
195	OM8	OM	16	257730	257972	257972	258230	1	1	250	499	1	2	1	0	1	03:05
1	OM8	OM	1	34554	34991	34991	35059	1	1	253	504	1	2	1	0	1	03:05
178	OM8	OM	15	457110	457531	457548	457599	1	18	253	488	1	2	1	0	1	03:05
31	OM8	OM	3	236387	236702	236772	236946	1	71	315	558	1	2	1	0	1	03:05
49	OM8	OM	4	1296388	1296525	1296525	1297076	1	1	344	687	1	2	1	0	1	03:05
23	OM8	OM	3	16356	16705	16705	17092	1	1	368	735	1	2	1	0	1	03:05
172	OM8	OM	15	159092	159369	159369	159827	1	1	368	734	1	2	1	0	1	03:05
56	OM8	OM	5	328320	328370	328370	329070	1	1	375	749	1	2	1	0	1	03:05
104	OM8	OM	10	503352	503880	503880	504158	1	1	403	805	1	2	1	0	1	03:05
36	OM8	OM	4	266878	267359	267406	267874	1	48	522	995	1	2	1	0	1	03:05
184	OM8	OM	15	836747	837056	837247	837630	1	192	537	882	1	2	1	0	1	03:05
34	OM8	OM	4	93541	94320	94538	94649	1	219	663	1107	1	2	1	0	1	03:05
186	OM8	OM	15	967506	967611	968210	968244	1	600	669	737	1	2	1	0	1	03:05
182	OM8	OM	15	783046	784086	784086	784606	1	1	780	1559	1	2	1	0	1	03:05
125	OM8	OM	12	124986	126014	126014	126853	1	1	934	1866	1	2	1	0	1	03:05
169	OM8	OM	15	70751	70932	71365	72322	1	434	1002	1570	1	2	1	0	1	03:05
175	OM8	OM	15	267165	268222	268330	269276	1	109	1110	2110	1	2	1	0	1	03:05
5	OM8	OM	1	112136	113132	113326	114283	1	195	1171	2146	1	2	1	0	1	03:05
156	OM8	OM	14	293347	294505	294505	295803	1	1	1228	2455	1	2	1	0	1	03:05
83	OM8	OM	8	66280	66569	67460	68202	1	892	1407	1921	1	2	1	0	1	03:05
9	OM8	OM	2	36507	36690	37628	39234	1	939	1833	2726	1	2	1	0	1	03:05
132	OM8	OM	12	341070	341507	343213	343396	1	1707	2016	2325	1	2	1	0	1	03:05
6	OM8	OM	1	132066	135319	135325	136910	1	7	2425	4843	1	2	1	0	1	03:05
205	OM8	OM	16	857345	858788	861839	863244	1	3052	4475	5898	1	2	1	0	1	03:05
127	OM8	OM	12	181770	182125	182197	182242	1	73	272	471	1	3	1	0	1	5:3_4:4_5:3
167	OM8	OM	14	732856	732888	733411	733695	1	524	681	838	1	4	1	0	1	3:5_4:4_3:5
42	OM8	OM	4	833693	834320	835319	835444	1	1000	1375	1750	1	4	1	0	1	3:5_4:4_3:5
37	OM8	OM	4	272060	272298	272385	273003	1	88	515	942	1	7	1	0	1	6:2_5:3
45	OM8	OM	4	1032015	1032120	1032141	1033091	1	22	549	1075	1	7	1	0	1	6:2_5:3
158	OM8	OM	14	335395	335707	336158	336315	1	452	686	919	1	7	1	0	1	6:2_5:3
106	OM8	OM	10	640552	640718	641346	641571	1	629	824	1018	1	7	1	0	1	6:2_5:3
120	OM8	OM	11	513454	514126	514543	514792	1	418	878	1337	1	8	1	0	1	3:5_2:6

140	OM8	OM	12	1012226	1013592	1014017	1014198	1	426	1199	1971	1	8	1	0	1 3:5_2:6
19	OM8	OM	2	661374	662094	662444	666708	1	351	2842	5333	1	8	1	0	1 2:6_3:5
12	OM8	OM	2	306376	306932	307944	307989	1	1013	1313	1612	1	8	1	0	1 3:5_4:4_2:6
147	OM8	OM	13	309395	309424	310153	310534	1	730	934	1138	1	8	1	0	1 3:5_4:4_3:5_2:6
30	OM8	OM	3	224261	225200	225200	225631	1	1	685	1369	1	10	1	0	1 06:02
124	OM8	OM	12	95236	97490	97572	97654	1	83	1250	2417	1	10	1	0	1 06:02
201	OM8	OM	16	591009	591334	591382	591462	1	49	251	452	1	10.1	1	0	1 02:06
81	OM8	OM	7	1049349	1050057	1050064	1050446	1	8	552	1096	1	10.1	1	0	1 02:06
97	OM8	OM	9	422694	422857	423571	423632	1	715	826	937	2	11	1	0	1 5:3_5:3a
161	OM8	OM	14	486859	487177	488598	488965	1	1422	1764	2105	2	11	1	0	1 5:3_5:3a
111	OM8	OM	11	74916	75663	76124	76914	1	462	1230	1997	2	12	1	0	1 3:5_3:5a
58	OM8	OM	5	404063	404317	405271	406216	1	955	1554	2152	2	12	1	0	1 3:5_3:5a
96	OM8	OM	9	407232	407953	409125	409496	1	1173	1718	2263	2	12	1	0	1 3:5_3:5a
78	OM8	OM	7	847980	848452	849600	849797	1	1149	1483	1816	2	13	1	0	1 6:2_5:3_5:3a_4:4_6:2
62	OM8	OM	5	563348	563399	564974	565161	1	1576	1694	1812	2	13	1	0	1 5:3_5:3a_6:2_5:3a_6:2_5:3a_6:2_5:3a
162	OM8	OM	14	508321	508617	510300	510459	1	1684	1911	2137	2	14	1	0	1 3:5_3:5a_4:4_3:5a
14	OM8	OM	2	408107	408483	409364	409495	1	882	1135	1387	2	15	1	0	1 5:3_4:4_5:3a
52	OM8	OM	5	68996	69083	70022	70335	1	940	1139	1338	2	15	1	0	1 5:3_4:4_5:3a
176	OM8	OM	15	322819	323107	324679	325064	1	1573	1909	2244	2	15	1	0	1 5:3_4:4_5:3a
151	OM8	OM	13	618182	618249	619714	619995	1	1466	1639	1812	2	16	1	0	1 3:5_4:4_3:5a
198	OM8	OM	16	372742	373291	374857	375235	1	1567	2030	2492	2	16	1	0	1 3:5_4:4_3:5a
142	OM8	OM	13	28854	29616	30379	30523	1	764	1216	1668	2	17	1	0	1 5:3_6:2_5:3_4:4_5:3a
44	OM8	OM	4	1002178	1002467	1004000	1004480	1	1534	1918	2301	2	18	1	0	1 3:5_4:4_3:5a_2:6
67	OM8	OM	7	121571	121697	123330	123839	1	1634	1951	2267	2	18	1	0	1 3:5_4:4_3:5a_4:4_3:5a
115	OM8	OM	11	278448	278756	279830	280076	1	1075	1351	1627	2	19	1	0	1 5:3_6:2_5:3a
179	OM8	OM	15	493415	494313	494326	494732	2_nonsis	14	665	1316	3	30	1	0	1 05:03
133	OM8	OM	12	414993	416362	416803	417943	2_nonsis	442	1696	2949	3	30	1	0	1 03:05
164	OM8	OM	14	674690	676085	677207	677352	2_nonsis	1123	1892	2661	3	30	1	0	1 5:3_5:3a
26	OM8	OM	3	94591	95029	96988	97369	2_nonsis	1960	2369	2777	3	30	1	0	1 3:5_2:6
3	OM8	OM	1	74190	74538	75211	76205	2_nonsis	674	1344	2014	3	30	1	0	1 3:5_4:4_3:5a
190	OM8	OM	16	21112	21201	22826	26191	2_nonsis	1626	3352	5078	3	30	1	0	1 2:6_4:4_5:3
90	OM8	OM	9	55837	56514	58256	58630	2_nonsis	1743	2268	2792	3	31	1	0	1 2:6_4:4ai_4:4_3:5_4:4_3:5
109	OM8	OM	11	19607	19617	23532	27301	2_nonsis	3916	5805	7693	3	31	1	0	1 3:5_2:6_3:5_2:6_3:5_4:4_3:5_4:4ai
20	OM8	OM	2	708952	709993	712259	712456	2_nonsis	2267	2885	3503	3	31	1	0	1 3:5_4:4_3:5_3:5a_4:4ai_5:3_4:4ai_3:5a_4:4ai
50	OM8	OM	4	1318646	1318845	1318845	1319624	2_nonsis	1	489	977	1	1	1	1	0 (5:3)_(4:4aCO)
60	OM8	OM	5	539346	540205	540256	540509	2_nonsis	52	607	1162	1	1	1	1	0 (5:3)_(4:4aCO)
166	OM8	OM	14	707765	708870	708870	709317	2_nonsis	1	776	1551	1	1	1	1	0 (5:3)_(4:4aCO)
183	OM8	OM	15	825345	826024	826642	826798	2_nonsis	619	1036	1452	1	1	1	1	0 (5:3)_(4:4aCO)
207	OM8	OM	16	921352	921490	922622	922730	2_nonsis	1133	1255	1377	1	1	1	1	0 (5:3)_(4:4aCO)
110	OM8	OM	11	44603	45993	46439	48790	2_nonsis	447	2317	4186	1	1	1	1	0 (5:3)_(4:4aCO)
15	OM8	OM	2	489580	490532	490619	490686	2_nonsis	88	597	1105	1	2	1	1	0 (3:5)_(4:4aCO)
98	OM8	OM	10	34093	36217	36357	36445	2_nonsis	141	1246	2351	1	2	1	1	0 (3:5)_(4:4aCO)
64	OM8	OM	6	164557	166317	166317	167318	2_nonsis	1	1381	2760	1	2	1	1	0 (3:5)_(4:4aCO)
47	OM8	OM	4	1242169	1242241	1242241	1246191	2_nonsis	1	2011	4021	1	2	1	1	0 (3:5)_(4:4aCO)
10	OM8	OM	2	125843	126130	126565	126921	2_nonsis	436	757	1077	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
202	OM8	OM	16	652985	653303	653978	654370	2_nonsis	676	1030	1384	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
138	OM8	OM	12	828844	829206	829398	829421	2_nonsis	193	385	576	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
18	OM8	OM	2	595735	595927	596267	596654	2_nonsis	341	630	918	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
134	OM8	OM	12	534194	535113	535963	536245	2_nonsis	851	1451	2050	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
77	OM8	OM	7	832207	832717	833517	833796	2_nonsis	801	1195	1588	1	5	1	1	0 (3:5)_(4:4)_(4:4aCO)
143	OM8	OM	13	82357	83128	83176	83404	2_nonsis	49	548	1046	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
86	OM8	OM	8	256342	256905	257367	257823	2_nonsis	463	972	1480	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
157	OM8	OM	14	309823	310003	310729	311115	2_nonsis	727	1009	1291	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
153	OM8	OM	13	798333	798592	798739	798826	2_nonsis	148	320	492	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
168	OM8	OM	15	22358	39380	39893	40057	2_nonsis	514	9106	17698	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
117	OM8	OM	11	295309	296531	299201	300874	2_nonsis	2671	4118	5564	1	11	1	1	0 (5:3)_(4:4)_(4:4ai)_(4:4bCO)
13	OM8	OM	2	331827	332522	332548	332630	2_nonsis	27	415	802	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
103	OM8	OM	10	347951	348560	348792	348930	2_nonsis	233	606	978	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
185	OM8	OM	15	915096	915310	915759	915972	2_nonsis	450	663	875	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
41	OM8	OM	4	714714	714933	715715	715933	2_nonsis	783	1001	1218	1	12	1	1	0 (6:2)_(4:4aCO)_(5:3)_(4:4a)

54	OM8	OM	5	227640	227836	228774	228943	2_nonsis	939	1121	1302	1	12	1	1	0 (3:5)_(4:4)_(2:6)_(4:4aCO)
193	OM8	OM	16	176002	176140	177345	177590	2_nonsis	1206	1397	1587	1	12	1	1	0 (3:5)_(4:4)_(2:6)_(4:4aCO)
196	OM8	OM	16	308785	308999	310159	310530	2_nonsis	1161	1453	1744	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4aCO)
84	OM8	OM	8	120445	121477	122634	122655	2_nonsis	1158	1684	2209	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
145	OM8	OM	13	163519	164021	165218	166349	2_nonsis	1198	2014	2829	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4aCO)
99	OM8	OM	10	148569	149059	150714	151050	2_nonsis	1656	2068	2480	1	12	1	1	0 (4:4aCO)_(2:6)_(3:5)_(4:4a)
57	OM8	OM	5	400033	400481	402400	402722	2_nonsis	1920	2304	2688	1	12	1	1	0 (5:3)_(4:4)_(6:2)_(4:4aCO)
82	OM8	OM	8	21579	21612	22834	23105	2_nonsis	1223	1374	1525	1	12	1	1	0 (6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
71	OM8	OM	7	433234	433416	433556	433681	2_nonsis	141	294	446	1	15	1	1	0 (6:2)_(4:4aCO)
51	OM8	OM	4	1476514	1476956	1476956	1477116	2_nonsis	1	301	601	1	15	1	1	0 (6:2)_(4:4aCO)
204	OM8	OM	16	745157	746299	746299	746899	2_nonsis	1	871	1741	1	15	1	1	0 (6:2)_(4:4aCO)
189	OM8	OM	15	1042440	1043118	1043151	1044215	2_nonsis	34	904	1774	1	15	1	1	0 (6:2)_(4:4aCO)
206	OM8	OM	16	900472	900592	901342	901564	2_nonsis	751	921	1091	1	15	1	1	0 (6:2)_(4:4aCO)
163	OM8	OM	14	542443	543829	543829	544303	2_nonsis	1	930	1859	1	15	1	1	0 (6:2)_(4:4aCO)
76	OM8	OM	7	763413	763485	763517	763747	2_nonsis	33	183	333	1	16	1	1	0 (2:6)_(4:4aCO)
53	OM8	OM	5	79940	80081	80182	80303	2_nonsis	102	232	362	1	16	1	1	0 (2:6)_(4:4aCO)
135	OM8	OM	12	602685	602909	603077	603141	2_nonsis	169	312	455	1	16	1	1	0 (2:6)_(4:4aCO)
95	OM8	OM	9	377556	378238	378238	378456	2_nonsis	1	450	899	1	16	1	1	0 (2:6)_(4:4aCO)
122	OM8	OM	11	578824	578904	579153	579541	2_nonsis	250	483	716	1	16	1	1	0 (2:6)_(4:4aCO)
70	OM8	OM	7	325875	326015	326056	326922	2_nonsis	42	544	1046	1	16	1	1	0 (2:6)_(4:4aCO)
177	OM8	OM	15	425518	426767	426767	427406	2_nonsis	1	944	1887	1	16	1	1	0 (2:6)_(4:4aCO)
107	OM8	OM	10	660786	661017	660786	661017	2_nonsis	0	115	230	1	100	1	1	0 (4:4aCO)
101	OM8	OM	10	280699	281003	280699	281003	2_nonsis	0	152	303	1	100	1	1	0 (4:4aCO)
105	OM8	OM	10	542308	542637	542308	542637	2_nonsis	0	164	328	1	100	1	1	0 (4:4aCO)
91	OM8	OM	9	97151	97705	97151	97705	2_nonsis	0	277	553	1	100	1	1	0 (4:4aCO)
148	OM8	OM	13	311582	312171	311582	312171	2_nonsis	0	294	588	1	100	1	1	0 (4:4aCO)
29	OM8	OM	3	222542	223339	222542	223339	2_nonsis	0	398	796	1	100	1	1	0 (4:4aCO)
75	OM8	OM	7	639145	639946	639145	639946	2_nonsis	0	400	800	1	100	1	1	0 (4:4aCO)
11	OM8	OM	2	255862	256767	255862	256767	2_nonsis	0	452	904	1	100	1	1	0 (4:4aCO)
4	OM8	OM	1	109735	110713	109735	110713	2_nonsis	0	489	977	1	100	1	1	0 (4:4aCO)
137	OM8	OM	12	780728	781856	780728	781856	2_nonsis	0	564	1127	1	100	1	1	0 (4:4aCO)
46	OM8	OM	4	1079976	1081335	1079976	1081335	2_nonsis	0	679	1358	1	100	1	1	0 (4:4aCO)
113	OM8	OM	11	204194	205607	204194	205607	2_nonsis	0	706	1412	1	100	1	1	0 (4:4aCO)
199	OM8	OM	16	465383	466824	465383	466824	2_nonsis	0	720	1440	1	100	1	1	0 (4:4aCO)
2	OM8	OM	1	57739	59349	57739	59349	2_nonsis	0	805	1609	1	100	1	1	0 (4:4aCO)
66	OM8	OM	7	98613	100529	98613	100529	2_nonsis	0	958	1915	1	100	1	1	0 (4:4aCO)
93	OM8	OM	9	185865	188629	185865	188629	2_nonsis	0	1382	2763	1	100	1	1	0 (4:4aCO)
159	OM8	OM	14	401251	404051	401251	404051	2_nonsis	0	1400	2799	1	100	1	1	0 (4:4aCO)
7	OM8	OM	1	167179	170726	167179	170726	2_nonsis	0	1773	3546	1	100	1	1	0 (4:4aCO)
171	OM8	OM	15	154173	158356	154173	158356	2_nonsis	0	2091	4182	1	100	1	1	0 (4:4aCO)
68	OM8	OM	7	235967	241354	235967	241354	2_nonsis	0	2693	5386	1	100	1	1	0 (4:4aCO)
139	OM8	OM	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0 (4:4aCO)
155	OM8	OM	14	260618	261617	264607	265328	2_nonsis	2991	3850	4709	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
187	OM8	OM	15	987247	987667	988871	989690	2_nonsis	1205	1824	2442	2	31	1	1	0 (3:5)_(3:5a)_(2:6)_(4:4aCO)
114	OM8	OM	11	245116	246336	249723	250518	2_nonsis	3388	4395	5401	2	31	1	1	0 (3:5)_(2:6)_(3:5)_(3:5a)_(4:4ai)_(4:4bCO)
8	OM8	OM	2	27032	27154	29377	36302	2_nonsis	2224	5747	9269	2	31	1	1	0 (3:5)_(2:6)_(4:4ai)_(3:5)_(3:5a)_(2:6)_(3:5a)_(4:4bCO)_(3:5a)_(4:4b)
79	OM8	OM	7	906181	906494	906758	906845	2_nonsis	265	464	663	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
59	OM8	OM	5	490942	490952	491556	491806	2_nonsis	605	734	863	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
188	OM8	OM	15	1022391	1022673	1023697	1023785	2_nonsis	1025	1209	1393	2	32	1	1	0 (3:5)_(4:4aCO)_(3:5a)_(4:4a)
131	OM8	OM	12	260086	260298	262070	262322	2_nonsis	1773	2004	2235	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(4:4aCO)
63	OM8	OM	6	61904	62459	64252	64937	2_nonsis	1794	2413	3032	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
173	OM8	OM	15	170112	170199	178587	178731	2_nonsis	8389	8504	8618	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(4:4ai)_(4:4bCO)
33	OM8	OM	4	19455	19746	20444	20659	2_nonsis	699	951	1203	2	32	1	1	0 (5:3)_(4:4)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
65	OM8	OM	6	223558	224098	227043	227223	2_nonsis	2946	3305	3664	2	32	1	1	0 (4:4aCO)_(6:2)_(4:4a)_(5:3)_(6:2)_(5:3a)_(4:4a)
174	OM8	OM	15	258408	258436	261788	261915	2_nonsis	3353	3430	3506	2	32	1	1	0 (5:3)_(6:2)_(4:4)_(5:3a)_(4:4)_(5:3)_(6:2)_(4:4ai)_(4:4bCO)
22	OM8	OM	2	760599	760767	760960	761030	2_nonsis	194	312	430	3	20	1	1	0 (5:3)_(2:6)_(4:4aCO)
38	OM8	OM	4	482676	482955	483171	483225	2_nonsis	217	383	548	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
74	OM8	OM	7	598733	599081	599198	599515	2_nonsis	118	450	781	3	20	1	1	0 (5:3)_(2:6)_(4:4aCO)
27	OM8	OM	3	191932	192715	193828	196331	2_nonsis	1114	2756	4398	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
108	OM8	OM	11	13260	13310	14411	18399	2_nonsis	1102	3120	5138	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)

128	OM8	OM	12	215021	221295	223495	223519	2_nonsis	2201	5349	8497	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
150	OM8	OM	13	523390	523621	524320	524617	2_nonsis	700	963	1226	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
43	OM8	OM	4	925956	926065	926737	927283	2_nonsis	673	1000	1326	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
149	OM8	OM	13	407599	407663	408374	408897	2_nonsis	712	1005	1297	3	20	1	1	0	(3:5)_(4:4aCO)_(6:2)_(4:4a)
85	OM8	OM	8	187989	188673	189521	190024	2_nonsis	849	1442	2034	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
25	OM8	OM	3	48704	50099	51405	52350	2_nonsis	1307	2476	3645	3	20	1	1	0	(3:5)_(5:3)_(3:5)_(4:4aCO)
203	OM8	OM	16	675149	676046	676743	677025	2_nonsis	698	1287	1875	3	20	1	1	0	(6:2)_(4:4aCO)_(3:5)_(2:6)_(4:4a)
191	OM8	OM	16	73338	73929	75455	75694	2_nonsis	1527	1941	2355	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
100	OM8	OM	10	178616	179084	180354	180756	2_nonsis	1271	1705	2139	3	20	1	1	0	(3:5)_(3:5a)_(5:3)_(6:2)_(5:3)_(4:4aCO)
181	OM8	OM	15	761947	762072	763679	763784	2_nonsis	1608	1722	1836	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
87	OM8	OM	8	459589	459844	463473	463665	2_nonsis	3630	3853	4075	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(5:3)_(4:4aCO)
170	OM8	OM	15	103968	103993	106264	106364	2_nonsis	2272	2334	2395	3	21	1	1	0	(5:3)_(4:4ai)_(3:5)_(4:4ai)_(5:3a)_(4:4bCO)
121	OM8	OM	11	568041	568472	571329	571639	2_sis	2858	3228	3597	0	1	2	0	2	(5:3)_(7:1)_(5:3a)_(4:4)_(6:2)_(5:3a)_(4:4)_(5:3a)_(4:4)
32	OM8	OM	3	239515	240922	240922	241753	3	1	1119	2237	0	2	2	1	1	(4:4ai)_(4:4bCO)
39	OM8	OM	4	549856	550499	552354	552557	3	1856	2278	2700	0	2	2	1	1	(5:3)_(4:4)_(4:4aCO)_(3:5)_(4:4a)
80	OM8	OM	7	1011203	1011474	1012213	1012326	3	740	931	1122	0	2	2	1	1	(3:5)_(4:4ai)_(4:4bCO)
119	OM8	OM	11	400972	401736	403011	403407	3	1276	1855	2434	0	2	2	1	1	(3:5)_(4:4ai)_(4:4bCO)
154	OM8	OM	14	63403	64611	64800	65227	3	190	1007	1823	0	2	2	1	1	(4:4ai)_(7:1)_(4:4bCO)
165	OM8	OM	14	699152	700405	702991	703330	3	2587	3382	4177	0	2	2	1	1	(3:5)_(5:3)_(4:4aCO)
200	OM8	OM	16	525308	525445	527344	527574	3	1900	2083	2265	0	2	2	1	1	(5:3)_(4:4)_(2:6)_(4:4aCO)_(3:5)_(4:4a)
35	OM8	OM	4	184754	184859	186841	187054	3	1983	2141	2299	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(3:5)_(4:4bCO)
94	OM8	OM	9	267764	268176	269349	269523	3	1174	1466	1758	0	3	2	1	1	(4:4aCO)_(6:2)_(3:5)_(4:4bCO)
141	OM8	OM	12	1053098	1053478	1053841	1054279	2_nonsis	364	772	1180	0	3	2	0	2	(4:4aCO)_(5:3)_(4:4CO)
146	OM8	OM	13	202482	203305	204735	205670	2_nonsis	1431	2309	3187	0	3	2	0	2	(5:3)_(4:4aCO)_(4:4CO)
152	OM8	OM	13	750177	751108	752227	752515	2_nonsis	1120	1729	2337	0	3	2	0	2	(4:4aCO)_(4:4CO)_(3:5)_(4:4)
129	OM9	OM	12	677815	677890	677890	677900	1	1	43	84	1	1	1	0	1	05:03
11	OM9	OM	2	288081	288303	288339	288484	1	37	220	402	1	1	1	0	1	05:03
143	OM9	OM	13	561510	561662	561662	561993	1	1	242	482	1	1	1	0	1	05:03
71	OM9	OM	7	450034	450372	450372	450623	1	1	295	588	1	1	1	0	1	05:03
51	OM9	OM	4	1476514	1476956	1476956	1477116	1	1	301	601	1	1	1	0	1	05:03
117	OM9	OM	11	526649	526688	526688	527413	1	1	382	763	1	1	1	0	1	05:03
115	OM9	OM	11	445062	445342	445342	445854	1	1	396	791	1	1	1	0	1	05:03
98	OM9	OM	10	256465	256690	256992	257035	1	303	436	569	1	1	1	0	1	05:03
78	OM9	OM	7	950639	951537	951595	951635	1	59	527	995	1	1	1	0	1	05:03
122	OM9	OM	12	176946	177754	177778	178195	1	25	637	1248	1	1	1	0	1	05:03
84	OM9	OM	8	366783	367303	367303	368538	1	1	878	1754	1	1	1	0	1	05:03
182	OM9	OM	16	374470	374857	375235	376113	1	379	1011	1642	1	1	1	0	1	05:03
179	OM9	OM	16	214684	214724	215587	216380	1	864	1280	1695	1	1	1	0	1	05:03
120	OM9	OM	12	97490	98056	99028	99470	1	973	1476	1979	1	1	1	0	1	05:03
151	OM9	OM	14	319853	319911	321214	321588	1	1304	1519	1734	1	1	1	0	1	05:03
91	OM9	OM	9	204908	213470	213470	213953	1	1	4523	9044	1	1	1	0	1	05:03
70	OM9	OM	7	446220	446369	446399	446571	1	31	191	350	1	2	1	0	1	03:05
60	OM9	OM	6	72559	73353	73353	73471	1	1	456	911	1	2	1	0	1	03:05
162	OM9	OM	15	233742	233865	234124	234579	1	260	548	836	1	2	1	0	1	03:05
88	OM9	OM	9	68666	68857	68857	69789	1	1	562	1122	1	2	1	0	1	03:05
173	OM9	OM	15	1010523	1010592	1010673	1011684	1	82	621	1160	1	2	1	0	1	03:05
66	OM9	OM	7	166667	167076	167099	167889	1	24	623	1221	1	2	1	0	1	03:05
183	OM9	OM	16	382450	382832	383083	383599	1	252	700	1148	1	2	1	0	1	03:05
172	OM9	OM	15	977302	977581	977770	978537	1	190	712	1234	1	2	1	0	1	03:05
14	OM9	OM	2	414950	415547	415695	416297	1	149	748	1346	1	2	1	0	1	03:05
4	OM9	OM	2	39607	40029	40260	40882	1	232	753	1274	1	2	1	0	1	03:05
86	OM9	OM	8	515162	515676	516184	516318	1	509	832	1155	1	2	1	0	1	03:05
110	OM9	OM	11	95374	96187	96250	97113	1	64	901	1738	1	2	1	0	1	03:05
31	OM9	OM	4	215724	215967	216399	217109	1	433	909	1384	1	2	1	0	1	03:05
41	OM9	OM	4	784537	784809	785156	786657	1	348	1234	2119	1	2	1	0	1	03:05
15	OM9	OM	2	448188	448816	449152	450377	1	337	1263	2188	1	2	1	0	1	03:05
139	OM9	OM	13	369783	370224	370569	372277	1	346	1420	2493	1	2	1	0	1	03:05
8	OM9	OM	2	124617	124942	126263	126565	1	1322	1635	1947	1	2	1	0	1	03:05
32	OM9	OM	4	265338	265426	266878	267359	1	1453	1737	2020	1	2	1	0	1	03:05
104	OM9	OM	10	568363	570822	570822	573135	1	1	2386	4771	1	2	1	0	1	03:05

184	OM9	OM	16	435977	443833	444028	444118	1		196	4168	8140	1	2	1	0	1 03:05
35	OM9	OM	4	321997	324926	326210	326416	1		1285	2852	4418	1	3	1	0	1 5:3_6:2_5:3
76	OM9	OM	7	894109	894129	894550	894616	1		422	464	506	1	4	1	0	1 3:5_2:6_3:5
52	OM9	OM	4	1496573	1497025	1497214	1497535	1		190	576	961	1	4	1	0	1 3:5_4:4_3:5
85	OM9	OM	8	482724	482776	483502	483796	1		727	899	1071	1	4	1	0	1 3:5_4:4_3:5
188	OM9	OM	16	718964	719387	719419	719631	1		33	350	666	1	7	1	0	1 5:3_6:2
136	OM9	OM	13	178203	178325	179271	179346	1		947	1045	1142	1	7	1	0	1 6:2_4:4_5:3
57	OM9	OM	5	362296	362343	362389	362397	1		47	74	100	1	8	1	0	1 3:5_2:6
169	OM9	OM	15	770508	770539	770554	770868	1		16	188	359	1	8	1	0	1 3:5_2:6
6	OM9	OM	2	79121	79329	79359	80573	1		31	741	1451	1	8	1	0	1 2:6_3:5
124	OM9	OM	12	234668	234824	235891	235940	1		1068	1170	1271	1	8	1	0	1 2:6_3:5
100	OM9	OM	10	302207	302882	303316	303556	1		435	892	1348	2	11	1	0	1 5:3_5:3a
18	OM9	OM	2	624736	624805	625298	626092	1		494	925	1355	2	11	1	0	1 5:3_5:3a
125	OM9	OM	12	269839	270392	270995	271951	1		604	1358	2111	2	11	1	0	1 5:3_5:3a
160	OM9	OM	15	192333	192748	193911	195064	1		1164	1947	2730	2	11	1	0	1 5:3_5:3a
47	OM9	OM	4	1084839	1084860	1085100	1085571	1		241	486	731	2	12	1	0	1 3:5_3:5a
159	OM9	OM	15	108331	108945	109584	111554	1		640	1931	3222	2	12	1	0	1 3:5_3:5a
105	OM9	OM	10	622874	623040	624648	627140	1		1609	2937	4265	2	12	1	0	1 3:5_3:5a
185	OM9	OM	16	461367	462405	464201	464470	1		1797	2450	3102	2	13	1	0	1 5:3_4:4_5:3_5:3a
177	OM9	OM	16	104443	105356	105972	106107	1		617	1140	1663	2	14	1	0	1 3:5_3:5a_2:6_3:5a
114	OM9	OM	11	382140	382201	383133	383398	1		933	1095	1257	2	15	1	0	1 5:3_4:4_5:3a
106	OM9	OM	10	636028	636245	637574	637737	1		1330	1519	1708	2	15	1	0	1 5:3_4:4_5:3a
74	OM9	OM	7	623700	624442	625479	625898	1		1038	1618	2197	2	15	1	0	1 5:3_4:4_5:3a
146	OM9	OM	13	819141	819393	821494	822331	1		2102	2646	3189	2	15	1	0	1 5:3_4:4_5:3a
97	OM9	OM	10	235668	235976	236912	237017	1		937	1143	1348	2	16	1	0	1 3:5_4:4_3:5a
29	OM9	OM	4	158510	158749	159777	159930	1		1029	1224	1419	2	16	1	0	1 3:5_4:4_3:5a
181	OM9	OM	16	296144	296178	297234	297543	1		1057	1228	1398	2	16	1	0	1 3:5_4:4_3:5a
166	OM9	OM	15	519516	519651	520826	521084	1		1176	1372	1567	2	16	1	0	1 3:5_4:4_3:5a
95	OM9	OM	10	79138	79551	81028	81358	1		1478	1849	2219	2	16	1	0	1 3:5_4:4_3:5a
24	OM9	OM	3	212528	212637	214762	215005	1		2126	2301	2476	2	16	1	0	1 3:5_4:4_3:5a
175	OM9	OM	16	21970	21980	22826	26261	1		847	2569	4290	2	17	1	0	1 5:3_4:4_5:3a_5:3
45	OM9	OM	4	953912	954283	955620	956552	1		1338	1989	2639	2	17	1	0	1 5:3_4:4_5:3_4:4_5:3a
83	OM9	OM	8	341482	341488	343561	344834	1		2074	2713	3351	2	17	1	0	1 5:3_4:4_5:3a_4:4_5:3a
72	OM9	OM	7	473951	474708	479200	480192	1		4493	5367	6240	2	17	1	0	1 5:3_4:4_5:3_4:4_5:3a
149	OM9	OM	14	106295	106712	110232	110465	1		3521	3845	4169	2	21	1	0	1 5:3_4:4_5:3_6:2_5:3a_6:2_5:3a
121	OM9	OM	12	107894	107971	113758	113903	1		5788	5898	6008	2	23	1	0	1 5:3_4:4_6:2_5:3a
7	OM9	OM	2	119499	119918	122010	122996	2_nonsis		2093	2795	3496	3	30	1	0	1 5:3_3:5
109	OM9	OM	11	60173	62759	65282	66233	2_nonsis		2524	4292	6059	3	30	1	0	1 3:5_5:3
23	OM9	OM	3	152143	152240	155616	156252	2_nonsis		3377	3743	4108	3	30	1	0	1 3:5_4:4_3:5_5:3_3:5a_4:4_3:5b
92	OM9	OM	9	249032	249546	249546	250194	2_nonsis		1	581	1161	3	31	1	0	1 4:4ai
107	OM9	OM	10	724020	724234	724657	725433	2_nonsis		424	918	1412	3	31	1	0	1 3:5_4:4ai_3:5a
108	OM9	OM	11	49756	52588	55280	56302	2_nonsis		2693	4619	6545	3	31	1	0	1 3:5_4:4ai_3:5a
10	OM9	OM	2	212014	212764	218624	218666	2_nonsis		5861	6256	6651	3	31	1	0	1 4:4ai_3:5_3:5a
62	OM9	OM	6	211344	211545	214157	214378	2_nonsis		2613	2823	3033	3	31	1	0	1 5:3_4:4ai_6:2_5:3a_4:4_3:5
190	OM9	OM	16	785910	786015	786020	786518	2_nonsis		6	307	607	1	1	1	1	0 (5:3)_(4:4aCO)
90	OM9	OM	9	193298	193815	193815	194648	2_nonsis		1	675	1349	1	1	1	1	0 (5:3)_(4:4aCO)
180	OM9	OM	16	254117	254324	254813	255970	2_nonsis		490	1171	1852	1	1	1	1	0 (5:3)_(4:4aCO)
58	OM9	OM	5	400915	401106	402268	402321	2_nonsis		1163	1284	1405	1	1	1	1	0 (5:3)_(4:4aCO)
148	OM9	OM	14	22855	23245	23245	23459	2_nonsis		1	302	603	1	2	1	1	0 (3:5)_(4:4aCO)
61	OM9	OM	6	115494	115717	115810	116037	2_nonsis		94	318	542	1	2	1	1	0 (3:5)_(4:4aCO)
48	OM9	OM	4	1091591	1092239	1092239	1092561	2_nonsis		1	485	969	1	2	1	1	0 (3:5)_(4:4aCO)
155	OM9	OM	14	651410	652389	652419	652841	2_nonsis		31	731	1430	1	2	1	1	0 (3:5)_(4:4aCO)
21	OM9	OM	3	51650	52350	52919	53316	2_nonsis		570	1118	1665	1	2	1	1	0 (3:5)_(4:4aCO)
126	OM9	OM	12	320997	322903	322903	324050	2_nonsis		1	1527	3052	1	2	1	1	0 (3:5)_(4:4aCO)
99	OM9	OM	10	278411	279038	280099	280598	2_nonsis		1062	1624	2186	1	2	1	1	0 (3:5)_(4:4aCO)
135	OM9	OM	13	76243	76517	77135	77482	2_nonsis		619	929	1238	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
77	OM9	OM	7	914816	915691	917686	918119	2_nonsis		1996	2649	3302	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
39	OM9	OM	4	654816	654890	655473	656349	2_nonsis		584	1058	1532	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
113	OM9	OM	11	378458	379495	379888	380602	2_nonsis		394	1269	2143	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
65	OM9	OM	7	164429	164774	165175	165212	2_nonsis		402	592	782	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)

59	OM9	OM	5	525834	526150	526303	526638	2_nonsis	154	479	803	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
44	OM9	OM	4	936739	936980	937167	937517	2_nonsis	188	483	777	1	11	1	1	0 (2:6)_(4:4ai)_(4:4bCO)
103	OM9	OM	10	503037	503193	503352	503880	2_nonsis	160	501	842	1	11	1	1	0 (3:5)_(4:4ai)_(4:4bCO)
9	OM9	OM	2	194226	196404	196581	196633	2_nonsis	178	1292	2406	1	11	1	1	0 (5:3)_(4:4ai)_(4:4bCO)
127	OM9	OM	12	438989	439125	440042	440337	2_nonsis	918	1133	1347	1	11	1	1	0 (2:6)_(3:5)_(4:4ai)_(4:4bCO)
167	OM9	OM	15	612123	613660	616666	616760	2_nonsis	3007	3822	4636	1	11	1	1	0 (4:4ai)_(3:5)_(2:6)_(4:4bCO)
116	OM9	OM	11	514315	514543	515611	515680	2_nonsis	1069	1217	1364	1	12	1	1	0 (2:6)_(4:4)_(3:5)_(4:4aCO)
138	OM9	OM	13	339889	340680	341630	341834	2_nonsis	951	1448	1944	1	12	1	1	0 (5:3)_(6:2)_(5:3)_(4:4aCO)
163	OM9	OM	15	283744	284515	285557	285663	2_nonsis	1043	1481	1918	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
137	OM9	OM	13	226133	227957	228322	228901	2_nonsis	366	1567	2767	1	12	1	1	0 (3:5)_(2:6)_(3:5)_(4:4aCO)
16	OM9	OM	2	490686	491476	492334	493122	2_nonsis	859	1647	2435	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4aCO)
79	OM9	OM	8	73929	73993	74435	74477	2_nonsis	443	495	547	1	12	1	1	0 (3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
111	OM9	OM	11	264513	264611	265706	266888	2_nonsis	1096	1735	2374	1	12	1	1	0 (5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)
147	OM9	OM	13	861520	862065	863707	864551	2_nonsis	1643	2337	3030	1	12	1	1	0 (6:2)_(5:3)_(4:4aCO)_(6:2)_(4:4a)
142	OM9	OM	13	540526	540798	540798	541071	2_nonsis	1	273	544	1	15	1	1	0 (6:2)_(4:4aCO)
25	OM9	OM	3	224261	224961	225116	225200	2_nonsis	156	547	938	1	15	1	1	0 (6:2)_(4:4aCO)
161	OM9	OM	15	198772	199130	199186	199433	2_nonsis	57	359	660	1	16	1	1	0 (2:6)_(4:4aCO)
55	OM9	OM	5	321624	322875	322875	323078	2_nonsis	1	727	1453	1	16	1	1	0 (2:6)_(4:4aCO)
186	OM9	OM	16	503192	503873	504044	504597	2_nonsis	172	788	1404	1	16	1	1	0 (2:6)_(4:4CO)
101	OM9	OM	10	359445	359702	359445	359702	2_nonsis	0	128	256	1	100	1	1	(4:4aCO)
123	OM9	OM	12	231692	232046	231692	232046	2_nonsis	0	177	353	1	100	1	1	(4:4aCO)
38	OM9	OM	4	617533	617915	617533	617915	2_nonsis	0	191	381	1	100	1	1	(4:4aCO)
187	OM9	OM	16	653978	654370	653978	654370	2_nonsis	0	196	391	1	100	1	1	(4:4aCO)
150	OM9	OM	14	187803	188308	187803	188308	2_nonsis	0	252	504	1	100	1	1	(4:4aCO)
30	OM9	OM	4	199393	200025	199393	200025	2_nonsis	0	316	631	1	100	1	1	(4:4aCO)
73	OM9	OM	7	621311	622492	621311	622492	2_nonsis	0	590	1180	1	100	1	1	(4:4aCO)
82	OM9	OM	8	260343	261563	260343	261563	2_nonsis	0	610	1219	1	100	1	1	(4:4aCO)
49	OM9	OM	4	1254292	1256876	1254292	1256876	2_nonsis	0	1292	2583	1	100	1	1	(4:4aCO)
131	OM9	OM	12	822430	827343	822430	827343	2_nonsis	0	2456	4912	1	100	1	1	(4:4aCO)
93	OM9	OM	9	308018	308167	308908	310160	2_nonsis	742	1442	2141	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
157	OM9	OM	15	50464	52771	53357	54061	2_nonsis	587	2092	3596	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
22	OM9	OM	3	58033	59028	60704	60997	2_nonsis	1677	2320	2963	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
153	OM9	OM	14	506768	507599	509646	510203	2_nonsis	2048	2741	3434	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
132	OM9	OM	12	860959	861841	864291	864999	2_nonsis	2451	3245	4039	2	30	1	1	0 (5:3)_(4:4ai)_(5:3)_(5:3a)_(4:4bCO)
12	OM9	OM	2	354093	354317	356128	356462	2_nonsis	1812	2090	2368	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)_(5:3a)_(5:3b)_(4:4a)
176	OM9	OM	16	46435	46780	47566	48262	2_nonsis	787	1307	1826	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
158	OM9	OM	15	86647	88299	88659	89229	2_nonsis	361	1471	2581	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
54	OM9	OM	5	96491	97220	98283	98381	2_nonsis	1064	1477	1889	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
53	OM9	OM	5	26638	26678	28151	28312	2_nonsis	1474	1574	1673	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
80	OM9	OM	8	171347	172563	173412	173805	2_nonsis	850	1654	2457	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
26	OM9	OM	4	32706	32904	37123	37597	2_nonsis	4220	4555	4890	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
63	OM9	OM	6	231775	232381	234009	234589	2_nonsis	1629	2221	2813	2	31	1	1	0 (4:4aCO)_(3:5)_(3:5a)_(4:4a)
43	OM9	OM	4	854367	855322	857627	858176	2_nonsis	2306	3057	3808	2	31	1	1	0 (4:4ai)_(3:5)_(3:5a)_(4:4bCO)
102	OM9	OM	10	494603	494940	498958	499043	2_nonsis	4019	4229	4439	2	31	1	1	0 (3:5)_(4:4)_(3:5)_(3:5a)_(4:4aCO)
1	OM9	OM	1	67801	68551	69734	69998	2_nonsis	1184	1690	2196	2	31	1	1	0 (4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)_(2:6)_(3:5)_(3:5a)_(4:4a)
42	OM9	OM	4	826327	826825	827581	828045	2_nonsis	757	1237	1717	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
68	OM9	OM	7	379162	379420	380582	380720	2_nonsis	1163	1360	1557	2	32	1	1	0 (5:3)_(4:4ai)_(5:3a)_(4:4bCO)
118	OM9	OM	11	642394	642498	644727	645008	2_nonsis	2230	2422	2613	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
17	OM9	OM	2	566061	566265	568465	569235	2_nonsis	2201	2687	3173	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(4:4aCO)
56	OM9	OM	5	327079	327970	332391	332460	2_nonsis	4422	4901	5380	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
141	OM9	OM	13	491864	492749	494333	495115	2_nonsis	1585	2418	3250	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(2:6)_(4:4aCO)
164	OM9	OM	15	380023	380192	382531	383827	2_nonsis	2340	3072	3803	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(4:4)_(4:4aCO)
154	OM9	OM	14	536514	536751	538142	538315	2_nonsis	1392	1596	1800	2	32	1	1	0 (3:5)_(4:4aCO)_(2:6)_(3:5a)_(3:5b)_(4:4a)
20	OM9	OM	2	786053	786732	788501	789182	2_nonsis	1770	2449	3128	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)_(3:5b)_(4:4a)
37	OM9	OM	4	425304	425896	428969	428983	2_nonsis	3074	3376	3678	2	32	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
27	OM9	OM	4	59246	59321	62366	62726	2_nonsis	3046	3263	3479	2	32	1	1	0 (6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)_(5:3a)_(4:4a)
130	OM9	OM	12	707950	708595	711837	713312	2_nonsis	3243	4302	5361	2	32	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4ai)_(3:5a)_(4:4bCO)_(3:5a)_(4:4b)
67	OM9	OM	7	286802	287143	287729	288473	2_nonsis	587	1129	1670	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
94	OM9	OM	9	369589	370024	370992	371210	2_nonsis	969	1295	1620	3	20	1	1	0 (5:3)_(5:3)_(4:4aCO)
19	OM9	OM	2	633618	633876	635127	635445	2_nonsis	1252	1539	1826	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)

69	OM9	OM	7	391649	391859	393263	393326	2_nonsis		1405	1541	1676	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
89	OM9	OM	9	87717	87789	89380	89461	2_nonsis		1592	1668	1743	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
46	OM9	OM	4	1021040	1022238	1023685	1024279	2_nonsis		1448	2343	3238	3	20	1	1	0 (6:2)_(3:5)_(4:4aCO)
140	OM9	OM	13	444677	444908	445712	446574	2_nonsis		805	1351	1896	3	20	1	1	0 (5:3)_(4:4aCO)_(3:5)_(4:4a)
40	OM9	OM	4	769038	769356	770770	771211	2_nonsis		1415	1794	2172	3	20	1	1	0 (6:2)_(4:4)_(2:6)_(4:4aCO)
170	OM9	OM	15	780184	780221	782242	782356	2_nonsis		2022	2097	2171	3	20	1	1	0 (3:5)_(4:4aCO)_(5:3)_(4:4a)
13	OM9	OM	2	406115	406787	408724	408801	2_nonsis		1938	2312	2685	3	20	1	1	0 (3:5)_(4:4aCO)_(5:3)_(4:4a)
189	OM9	OM	16	772366	774130	775448	777332	2_nonsis		1319	3142	4965	3	20	1	1	0 (5:3)_(4:4aCO)_(2:6)_(4:4a)
156	OM9	OM	14	735112	735174	736111	736153	2_nonsis		938	989	1040	3	20	1	1	0 (3:5)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
50	OM9	OM	4	1419366	1419516	1420941	1421025	2_nonsis		1426	1542	1658	3	20	1	1	0 (3:5)_(5:3)_(3:5)_(2:6)_(4:4aCO)
174	OM9	OM	15	1047626	1047731	1048990	1049465	2_nonsis		1260	1549	1838	3	20	1	1	0 (3:5)_(5:3)_(3:5)_(5:3)_(4:4aCO)
152	OM9	OM	14	418511	419029	420283	420526	2_nonsis		1255	1635	2014	3	20	1	1	0 (5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)
34	OM9	OM	4	312701	313108	314500	315175	2_nonsis		1393	1933	2473	3	20	1	1	0 (5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
128	OM9	OM	12	611864	611994	613380	614564	2_nonsis		1387	2043	2699	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)
144	OM9	OM	13	695196	695427	697269	697465	2_nonsis		1843	2056	2268	3	20	1	1	0 (3:5)_(4:4)_(3:5a)_(5:3)_(4:4aCO)
112	OM9	OM	11	267528	268550	270178	270231	2_nonsis		1629	2166	2702	3	20	1	1	0 (6:2)_(4:4aCO)_(2:6)_(5:3)_(4:4a)
96	OM9	OM	10	140649	140994	142749	143550	2_nonsis		1756	2328	2900	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)_(6:2)_(4:4a)
5	OM9	OM	2	65975	66052	69901	70006	2_nonsis		3850	3940	4030	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
168	OM9	OM	15	652283	652485	653431	653618	2_nonsis		947	1141	1334	3	20	1	1	0 (2:6)_(4:4)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
119	OM9	OM	12	28820	29085	30768	30884	2_nonsis		1684	1874	2063	3	20	1	1	0 (5:3)_(5:3a)_(4:4)_(2:6)_(3:5)_(4:4aCO)
171	OM9	OM	15	906405	907000	908551	908634	2_nonsis		1552	1890	2228	3	20	1	1	0 (3:5)_(5:3)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
165	OM9	OM	15	454944	455108	458549	458585	2_nonsis		3442	3541	3640	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)_(3:5a)_(3:5)_(4:4a)
33	OM9	OM	4	268432	269350	272060	272298	2_nonsis		2711	3288	3865	3	20	1	1	0 (3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
87	OM9	OM	9	30858	31904	34648	34698	2_nonsis		2745	3292	3839	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
64	OM9	OM	7	47196	47512	48448	48835	2_nonsis		937	1288	1638	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)_(2:6)_(4:4a)
133	OM9	OM	12	940786	947200	949429	949489	2_nonsis		2230	5466	8702	3	21	1	1	0 (3:5)_(4:4ai)_(5:3)_(4:4bCO)_(5:3)_(4:4b)
145	OM9	OM	13	771109	771220	773689	774012	2_nonsis		2470	2686	2902	3	21	1	1	0 (5:3)_(4:4)_(5:3)_(4:4ai)_(3:5)_(4:4bCO)_(3:5a)_(4:4b)_(3:5a)_(4:4b)
2	OM9	OM	1	121235	128637	130975	132066		3	2339	6585	10830	0	2	2	1	1 (5:3)_(6:2)_(5:3a)_(3:5)_(3:5a)_(4:4aCO)
3	OM9	OM	1	190429	190558	193737	193807		4	3180	3279	3377	0	2	2	1	1 (5:3)_(6:2)_(5:3)_(4:4aCO)_(3:5)_(5:3a)_(4:4a)
28	OM9	OM	4	127476	129270	130537	130640		3	1268	2216	3163	0	2	2	1	1 (5:3)_(4:4ai)_(4:4bCO)
81	OM9	OM	8	191691	192435	196468	196529		3	4034	4436	4837	0	2	2	1	1 (3:5)_(2:6i)_(4:4ai)_(4:4bCO)_(5:3)_(6:2)_(5:3)_(4:4b)
134	OM9	OM	12	1025374	1025702	1027717	1028477		3	2016	2559	3102	0	2	2	1	1 (5:3)_(4:4)_(5:3)_(4:4ai)_(4:4bCO)_(3:5)_(4:4b)
178	OM9	OM	16	127908	127985	137386	137748		4	9402	9621	9839	0	2	2	1	1 (5:3)_(4:4)_(5:3)_(5:3a)_(4:4)_(5:3a)_(4:4)_(5:3a)_(4:4ai)_(4:4)_(3:5)_(4:4)_(5:3b)_(4:4bi)_(5:3b)_(5:3c)_(4:4cCO)
36	OM9	OM	4	373728	373922	375932	376867	2_nonsis		2011	2575	3138	0	3	2	0	2 (5:3)_(6:2)_(5:3a)_(4:4aCO)_(6:2)_(5:3a)_(4:4CO)
75	OM9	OM	7	795662	795876	798400	798821		3	2525	2842	3158	0	3	2	1	1 (6:2)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4bi)_(3:5)_(4:4cCO)
179	OMT1	OMT	11	361878	361983	361983	362017		1	1	70	138	1	1	1	0	1 05:03
281	OMT1	OMT	16	425940	426048	426048	426150		1	1	105	209	1	1	1	0	1 05:03
85	OMT1	OMT	4	1471301	1471484	1471484	1471524		1	1	112	222	1	1	1	0	1 05:03
153	OMT1	OMT	9	337914	337948	338050	338086		1	103	137	171	1	1	1	0	1 05:03
96	OMT1	OMT	5	386529	386588	386692	386715		1	105	145	185	1	1	1	0	1 05:03
189	OMT1	OMT	12	87687	87824	87825	88002		1	2	158	314	1	1	1	0	1 05:03
270	OMT1	OMT	16	46921	46996	47067	47208		1	72	179	286	1	1	1	0	1 05:03
13	OMT1	OMT	2	236188	236256	236256	236554		1	1	183	365	1	1	1	0	1 05:03
134	OMT1	OMT	8	17359	17641	17641	17751		1	1	196	391	1	1	1	0	1 05:03
175	OMT1	OMT	11	258604	258771	258873	258943		1	103	221	338	1	1	1	0	1 05:03
115	OMT1	OMT	7	80976	81268	81306	81381		1	39	222	404	1	1	1	0	1 05:03
95	OMT1	OMT	5	303778	304224	304224	304272		1	1	247	493	1	1	1	0	1 05:03
39	OMT1	OMT	3	95527	95697	95815	95935		1	119	263	407	1	1	1	0	1 05:03
280	OMT1	OMT	16	383387	383599	383599	383919		1	1	266	531	1	1	1	0	1 05:03
227	OMT1	OMT	13	797688	798060	798090	798261		1	31	302	572	1	1	1	0	1 05:03
38	OMT1	OMT	3	78909	79012	79170	79392		1	159	321	482	1	1	1	0	1 05:03
245	OMT1	OMT	14	678322	678661	678759	678891		1	99	334	568	1	1	1	0	1 05:03
10	OMT1	OMT	2	169893	170442	170442	170593		1	1	350	699	1	1	1	0	1 05:03
294	OMT1	OMT	16	840103	840263	840488	840627		1	226	375	523	1	1	1	0	1 05:03
235	OMT1	OMT	14	210033	210155	210474	210617		1	320	452	583	1	1	1	0	1 05:03
102	OMT1	OMT	5	517549	517944	517944	518464		1	1	458	914	1	1	1	0	1 05:03
128	OMT1	OMT	7	836443	837183	837183	837417		1	1	487	973	1	1	1	0	1 05:03
196	OMT1	OMT	12	388456	388801	388950	389347		1	150	520	890	1	1	1	0	1 05:03
159	OMT1	OMT	10	150714	151050	151245	151609		1	196	545	894	1	1	1	0	1 05:03
81	OMT1	OMT	4	1394566	1394881	1394881	1395687		1	1	561	1120	1	1	1	0	1 05:03

65	OMT1	OMT	4	719671	719728	719896	720645	1	169	571	973	1	1	1	0	1	05:03
73	OMT1	OMT	4	1109835	1110571	1110571	1111002	1	1	584	1166	1	1	1	0	1	05:03
192	OMT1	OMT	12	231106	231430	231692	232046	1	263	601	939	1	1	1	0	1	05:03
66	OMT1	OMT	4	814278	814490	814815	815156	1	326	602	877	1	1	1	0	1	05:03
28	OMT1	OMT	2	564884	565133	565601	565627	1	469	606	742	1	1	1	0	1	05:03
185	OMT1	OMT	11	626765	627471	627471	628158	1	1	697	1392	1	1	1	0	1	05:03
142	OMT1	OMT	8	323497	324669	324770	325071	1	102	838	1573	1	1	1	0	1	05:03
255	OMT1	OMT	15	206718	206822	207586	207629	1	765	838	910	1	1	1	0	1	05:03
133	OMT1	OMT	8	11695	12640	13001	13116	1	362	891	1420	1	1	1	0	1	05:03
284	OMT1	OMT	16	502118	503157	503192	503873	1	36	895	1754	1	1	1	0	1	05:03
75	OMT1	OMT	4	1128837	1129980	1129980	1130680	1	1	922	1842	1	1	1	0	1	05:03
181	OMT1	OMT	11	400521	400972	401769	401790	1	798	1033	1268	1	1	1	0	1	05:03
137	OMT1	OMT	8	189521	190024	190671	191072	1	648	1099	1550	1	1	1	0	1	05:03
114	OMT1	OMT	7	55263	55957	55957	57501	1	1	1119	2237	1	1	1	0	1	05:03
247	OMT1	OMT	14	715430	715791	716564	716912	1	774	1128	1481	1	1	1	0	1	05:03
93	OMT1	OMT	5	264105	264464	265681	266217	1	1218	1665	2111	1	1	1	0	1	05:03
25	OMT1	OMT	2	510710	512166	513202	513337	1	1037	1832	2626	1	1	1	0	1	05:03
62	OMT1	OMT	4	625839	628602	628602	629725	1	1	1943	3885	1	1	1	0	1	05:03
99	OMT1	OMT	5	443341	443369	443369	443373	1	1	16	31	1	2	1	0	1	03:05
108	OMT1	OMT	6	114205	114248	114251	114263	1	4	31	57	1	2	1	0	1	03:05
140	OMT1	OMT	8	238630	238746	238746	238799	1	1	85	168	1	2	1	0	1	03:05
290	OMT1	OMT	16	656605	656677	656677	656784	1	1	90	178	1	2	1	0	1	03:05
254	OMT1	OMT	15	198587	198700	198700	198772	1	1	93	184	1	2	1	0	1	03:05
259	OMT1	OMT	15	301153	301302	301302	301346	1	1	97	192	1	2	1	0	1	03:05
253	OMT1	OMT	15	162190	162324	162324	162386	1	1	98	195	1	2	1	0	1	03:05
267	OMT1	OMT	15	1037336	1037514	1037514	1037595	1	1	130	258	1	2	1	0	1	03:05
288	OMT1	OMT	16	609903	610056	610056	610223	1	1	160	319	1	2	1	0	1	03:05
15	OMT1	OMT	2	269653	269904	269904	269983	1	1	165	329	1	2	1	0	1	03:05
167	OMT1	OMT	10	568363	568755	568755	568805	1	1	221	441	1	2	1	0	1	03:05
68	OMT1	OMT	4	910968	911274	911343	911454	1	70	278	485	1	2	1	0	1	03:05
223	OMT1	OMT	13	625245	625844	625844	625856	1	1	306	610	1	2	1	0	1	03:05
274	OMT1	OMT	16	188250	188615	188703	188788	1	89	313	537	1	2	1	0	1	03:05
125	OMT1	OMT	7	616159	616580	616580	616811	1	1	326	651	1	2	1	0	1	03:05
232	OMT1	OMT	14	121988	122135	122278	122496	1	144	326	507	1	2	1	0	1	03:05
201	OMT1	OMT	12	540147	540219	540405	540621	1	187	330	473	1	2	1	0	1	03:05
161	OMT1	OMT	10	254503	254968	254968	255203	1	1	350	699	1	2	1	0	1	03:05
88	OMT1	OMT	5	15698	15888	15966	16323	1	79	352	624	1	2	1	0	1	03:05
198	OMT1	OMT	12	417373	417445	417665	417943	1	221	395	569	1	2	1	0	1	03:05
47	OMT1	OMT	4	52663	53011	53077	53471	1	67	437	807	1	2	1	0	1	03:05
87	OMT1	OMT	4	1518155	1518220	1518269	1519166	1	50	530	1010	1	2	1	0	1	03:05
53	OMT1	OMT	4	200220	200994	200994	201329	1	1	555	1108	1	2	1	0	1	03:05
98	OMT1	OMT	5	430305	430576	430899	431114	1	324	566	808	1	2	1	0	1	03:05
8	OMT1	OMT	2	159427	159926	160143	160403	1	218	597	975	1	2	1	0	1	03:05
49	OMT1	OMT	4	146582	147362	147377	147778	1	16	606	1195	1	2	1	0	1	03:05
120	OMT1	OMT	7	373958	374507	374973	375001	1	467	755	1042	1	2	1	0	1	03:05
207	OMT1	OMT	12	770488	770842	771112	771882	1	271	832	1393	1	2	1	0	1	03:05
141	OMT1	OMT	8	270370	271207	271207	272321	1	1	976	1950	1	2	1	0	1	03:05
33	OMT1	OMT	2	697503	698250	698250	699461	1	1	979	1957	1	2	1	0	1	03:05
243	OMT1	OMT	14	604250	604879	605054	606035	1	176	980	1784	1	2	1	0	1	03:05
190	OMT1	OMT	12	104468	105183	105323	106427	1	141	1050	1958	1	2	1	0	1	03:05
109	OMT1	OMT	6	166317	167037	167410	168102	1	374	1079	1784	1	2	1	0	1	03:05
238	OMT1	OMT	14	308673	309212	310003	310045	1	792	1082	1371	1	2	1	0	1	03:05
41	OMT1	OMT	3	209648	209856	210635	211159	1	780	1145	1510	1	2	1	0	1	03:05
244	OMT1	OMT	14	662512	665502	665502	665847	1	1	1668	3334	1	2	1	0	1	03:05
229	OMT1	OMT	14	41218	41680	42594	43912	1	915	1804	2693	1	2	1	0	1	03:05
146	OMT1	OMT	8	511414	511546	514601	515162	1	3056	3402	3747	1	2	1	0	1	03:05
249	OMT1	OMT	15	43376	43479	43753	43786	1	275	342	409	1	4	1	0	1	3:5_2:6_3:5
59	OMT1	OMT	4	521481	521536	522457	522598	1	922	1019	1116	1	4	1	0	1	3:5_4:4_3:5
234	OMT1	OMT	14	198636	198795	199738	199813	1	944	1060	1176	1	4	1	0	1	3:5_2:6_3:5
156	OMT1	OMT	10	79138	79551	80439	80673	1	889	1212	1534	1	4	1	0	1	3:5_4:4_3:5

177	OMT1	OMT	11	309310	309823	310861	310963	1	1039	1346	1652	1	4	1	0	1 3:5_4:4_3:5
293	OMT1	OMT	16	831601	831747	832034	832084	1	288	385	482	1	7	1	0	1 5:3_6:2
172	OMT1	OMT	11	178752	179179	179509	179637	1	331	608	884	1	7	1	0	1 5:3_6:2
77	OMT1	OMT	4	1251240	1251845	1252149	1252244	1	305	654	1003	1	7	1	0	1 5:3_6:2
197	OMT1	OMT	12	404007	404208	404333	405334	1	126	726	1326	1	7	1	0	1 5:3_6:2
258	OMT1	OMT	15	266279	266696	267756	267906	1	1061	1344	1626	1	7	1	0	1 5:3_6:2
129	OMT1	OMT	7	892549	892563	894129	894236	1	1567	1627	1686	1	7	1	0	1 5:3_6:2
106	OMT1	OMT	6	94981	95054	95232	95308	1	179	253	326	1	8	1	0	1 3:5_2:6
225	OMT1	OMT	13	737651	738269	739163	739584	1	895	1414	1932	1	8	1	0	1 3:5_2:6
180	OMT1	OMT	11	382201	382357	384068	384196	1	1712	1853	1994	1	8	1	0	1 2:6_3:5
43	OMT1	OMT	3	257993	258780	259910	260698	1	1131	1918	2704	1	8	1	0	1 3:5_2:6
213	OMT1	OMT	13	29826	29994	31154	35547	1	1161	3441	5720	1	8	1	0	1 2:6_3:5
184	OMT1	OMT	11	577779	578230	578230	578669	1	1	445	889	1	10	1	0	1 06:02
239	OMT1	OMT	14	350848	350864	355731	357348	1	4868	5684	6499	1	10	1	0	1 06:02
58	OMT1	OMT	4	506865	507130	507130	507490	1	1	313	624	1	10.1	1	0	1 02:06
173	OMT1	OMT	11	195050	195153	195825	196346	1	673	984	1295	1	10.1	1	0	1 02:06
170	OMT1	OMT	11	38739	38767	38767	41369	1	1	1315	2629	1	10.1	1	0	1 02:06
174	OMT1	OMT	11	201727	202124	203378	204194	1	1255	1861	2466	1	10.1	1	0	1 02:06
236	OMT1	OMT	14	288680	288926	289457	289633	1	532	742	952	2	11	1	0	1 5:3_5:3a
221	OMT1	OMT	13	423811	424537	425138	425898	1	602	1344	2086	2	11	1	0	1 5:3_5:3a
277	OMT1	OMT	16	241702	241882	243049	243556	1	1168	1511	1853	2	11	1	0	1 5:3_5:3a
144	OMT1	OMT	8	400335	400618	401862	402413	1	1245	1661	2077	2	11	1	0	1 5:3_5:3a
246	OMT1	OMT	14	689310	689558	691115	691292	1	1558	1770	1981	2	11	1	0	1 5:3_5:3a
273	OMT1	OMT	16	150219	150295	150413	150484	1	119	192	264	2	12	1	0	1 3:5_3:5a
40	OMT1	OMT	3	154645	154683	154902	155018	1	220	296	372	2	12	1	0	1 3:5_3:5a
282	OMT1	OMT	16	463723	464194	464400	464470	1	207	477	746	2	12	1	0	1 3:5_3:5a
111	OMT1	OMT	6	196194	196491	197027	197428	1	537	885	1233	2	12	1	0	1 3:5_3:5a
79	OMT1	OMT	4	1337684	1337715	1338585	1338669	1	871	928	984	2	12	1	0	1 3:5_3:5a
165	OMT1	OMT	10	465816	466454	467107	467162	1	654	1000	1345	2	12	1	0	1 3:5_3:5a
70	OMT1	OMT	4	930077	930409	931180	931376	1	772	1035	1298	2	12	1	0	1 3:5_3:5a
261	OMT1	OMT	15	586076	586304	587206	587265	1	903	1046	1188	2	12	1	0	1 3:5_3:5a
89	OMT1	OMT	5	30664	31247	31867	32276	1	621	1116	1611	2	12	1	0	1 3:5_3:5a
242	OMT1	OMT	14	551646	552035	552709	553315	1	675	1172	1668	2	12	1	0	1 3:5_3:5a
272	OMT1	OMT	16	83873	84641	85621	85729	1	981	1418	1855	2	12	1	0	1 3:5_3:5a
119	OMT1	OMT	7	337363	337618	338951	339102	1	1334	1536	1738	2	12	1	0	1 3:5_3:5a
24	OMT1	OMT	2	465471	465657	466266	466521	1	610	830	1049	2	13	1	0	1 5:3_6:2_5:3_5:3a
214	OMT1	OMT	13	44503	45656	46860	48814	1	1205	2758	4310	2	13	1	0	1 5:3_6:2_5:3_5:3a
74	OMT1	OMT	4	1125429	1126043	1126356	1126365	1	314	625	935	2	13	1	0	1 5:3_4:4_5:3_5:3a_6:2
286	OMT1	OMT	16	580936	581005	582043	582137	1	1039	1120	1200	2	13	1	0	1 5:3_5:3a_6:2_5:3a_6:2_4:4_5:3a
224	OMT1	OMT	13	644973	645040	645786	645859	1	747	816	885	2	15	1	0	1 5:3_4:4_5:3a
276	OMT1	OMT	16	227039	227828	228253	228815	1	426	1101	1775	2	15	1	0	1 5:3_4:4_5:3a
67	OMT1	OMT	4	847053	847395	848397	848940	1	1003	1445	1886	2	15	1	0	1 5:3_4:4_5:3a
123	OMT1	OMT	7	584200	584249	584527	584635	1	279	357	434	2	16	1	0	1 3:5_4:4_3:5a
219	OMT1	OMT	13	352513	352695	353429	353814	1	735	1018	1300	2	16	1	0	1 3:5_4:4_3:5a
84	OMT1	OMT	4	1432932	1433048	1435091	1435647	1	2044	2379	2714	2	16	1	0	1 3:5_4:4_3:5a
55	OMT1	OMT	4	312431	312518	313223	313308	1	706	791	876	2	18	1	0	1 2:6_3:5_4:4_3:5a
94	OMT1	OMT	5	290420	290513	292770	293965	1	2258	2901	3544	2	19	1	0	1 5:3_6:2_5:3a
117	OMT1	OMT	7	194553	195492	197465	197816	1	1974	2618	3262	2	22	1	0	1 3:5_4:4_3:5_2:6_3:5a
104	OMT1	OMT	6	16574	16654	17595	17653	1	942	1010	1078	2	22	1	0	1 3:5_2:6_3:5a_2:6_3:5a_4:4_3:5a
157	OMT1	OMT	10	103601	104033	104033	104395	2_nonsis	1	397	793	3	30	1	0	1 05:03
113	OMT1	OMT	7	41041	41301	41497	41833	2_nonsis	197	494	791	3	30	1	0	1 2:6_3:5
45	OMT1	OMT	3	289600	289803	290527	290957	2_nonsis	725	1041	1356	3	30	1	0	1 2:6_6:2
16	OMT1	OMT	2	275372	275968	277874	278630	2_nonsis	1907	2582	3257	3	30	1	0	1 5:3_5:3a
50	OMT1	OMT	4	163031	163324	170953	171661	2_nonsis	7630	8130	8629	3	30	1	0	1 2:6_3:5
264	OMT1	OMT	15	795711	796275	797043	797205	2_nonsis	769	1131	1493	3	30	1	0	1 5:3_4:4_3:5
291	OMT1	OMT	16	677796	677836	679575	679712	2_nonsis	1740	1828	1915	3	30	1	0	1 5:3_4:4_3:5a
200	OMT1	OMT	12	515064	515468	517114	517338	2_nonsis	1647	1960	2273	3	30	1	0	1 5:3_6:2_5:3a
44	OMT1	OMT	3	278462	279641	280071	281752	2_nonsis	1331	2310	3289	3	30	1	0	1 3:5_3:5a_3:5b
12	OMT1	OMT	2	214810	215068	219381	220055	2_nonsis	4314	4779	5244	3	30	1	0	1 5:3_6:2_5:3_3:5_3:5a
204	OMT1	OMT	12	634488	634506	636269	637193	2_nonsis	1764	2234	2704	3	30	1	0	1 3:5_4:4_3:5_4:4_3:5_3:5a

226	OMT1	OMT	13	772587	772883	775737	775955	2_nonsis	2855	3111	3367	3	30	1	0	1	3:5_3:5a_2:6_4:4_3:5b_3:5
150	OMT1	OMT	9	136028	136044	139273	139299	2_nonsis	3230	3250	3270	3	30	1	0	1	3:5_4:4_3:5_5:3_5:3a_4:4_3:5a
268	OMT1	OMT	15	1048488	1048836	1049902	1050066	2_nonsis	1067	1322	1577	3	31	1	0	1	4:4ai_5:3
27	OMT1	OMT	2	551607	552237	554757	555319	2_nonsis	2521	3116	3711	3	31	1	0	1	5:3_4:4ai
9	OMT1	OMT	2	162680	162986	164474	164851	2_nonsis	1489	1830	2170	3	31	1	0	1	4:4ai_3:5_3:5a
191	OMT1	OMT	12	167737	168861	170609	170795	2_nonsis	1749	2403	3057	3	31	1	0	1	4:4ai_3:5_3:5a
124	OMT1	OMT	7	609760	609887	610674	611145	2_nonsis	788	1086	1384	3	31	1	0	1	3:5_4:4ai_2:6_3:5a
32	OMT1	OMT	2	684271	684966	687872	689156	2_nonsis	2907	3896	4884	3	31	1	0	1	5:3_4:4ai_4:4_3:5
163	OMT1	OMT	10	378340	378557	380706	380992	2_nonsis	2150	2401	2651	3	31	1	0	1	3:5_4:4_3:5_4:4ai_5:3
279	OMT1	OMT	16	371706	371914	375235	376113	2_nonsis	3322	3864	4406	3	31	1	0	1	3:5_4:4ai_3:5a_4:4ai_2:6_3:5a
257	OMT1	OMT	15	260906	261194	261194	261299	2_nonsis	1	197	392	1	1	1	1	0	(5:3)_(4:4aCO)
231	OMT1	OMT	14	87215	87864	87864	88013	2_nonsis	1	399	797	1	1	1	1	0	(5:3)_(4:4aCO)
218	OMT1	OMT	13	317105	317648	317750	317836	2_nonsis	103	417	730	1	1	1	1	0	(5:3)_(4:4aCO)
131	OMT1	OMT	7	990718	990823	990823	991617	2_nonsis	1	450	898	1	1	1	1	0	(5:3)_(4:4aCO)
158	OMT1	OMT	10	143166	143550	143678	144098	2_nonsis	129	530	931	1	1	1	1	0	(5:3)_(4:4aCO)
212	OMT1	OMT	12	1054333	1054794	1055114	1055417	2_nonsis	321	702	1083	1	1	1	1	0	(5:3)_(4:4aCO)
138	OMT1	OMT	8	192892	194830	194830	195121	2_nonsis	1	1115	2228	1	1	1	1	0	(5:3)_(4:4aCO)
105	OMT1	OMT	6	30616	30827	30834	30954	2_nonsis	8	173	337	1	2	1	1	0	(3:5)_(4:4aCO)
250	OMT1	OMT	15	45210	46201	46201	46774	2_nonsis	1	782	1563	1	2	1	1	0	(3:5)_(4:4aCO)
78	OMT1	OMT	4	1268647	1269918	1269918	1270457	2_nonsis	1	905	1809	1	2	1	1	0	(3:5)_(4:4aCO)
166	OMT1	OMT	10	496029	497589	497879	497985	2_nonsis	291	1123	1955	1	2	1	1	0	(3:5)_(4:4aCO)
178	OMT1	OMT	11	321853	321982	322308	322974	2_nonsis	327	724	1120	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
122	OMT1	OMT	7	581660	581705	582429	582800	2_nonsis	725	932	1139	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
64	OMT1	OMT	4	674927	675634	675833	676252	2_nonsis	200	762	1324	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
275	OMT1	OMT	16	191256	191540	191750	191940	2_nonsis	211	447	683	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
265	OMT1	OMT	15	836747	837056	838315	838372	2_nonsis	1260	1442	1624	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
228	OMT1	OMT	13	903826	904006	904069	904131	2_nonsis	64	184	304	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
194	OMT1	OMT	12	273722	274041	274243	274580	2_nonsis	203	530	857	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
18	OMT1	OMT	2	306242	306376	307860	307919	2_nonsis	1485	1581	1676	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
260	OMT1	OMT	15	460871	461249	464547	464562	2_nonsis	3299	3495	3690	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
107	OMT1	OMT	6	97737	97814	98593	98654	2_nonsis	780	848	916	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
240	OMT1	OMT	14	425816	427278	427715	428693	2_nonsis	438	1657	2876	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
283	OMT1	OMT	16	487851	488388	489543	490095	2_nonsis	1156	1700	2243	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
154	OMT1	OMT	9	407232	407953	409496	409532	2_nonsis	1544	1922	2299	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
97	OMT1	OMT	5	395813	396138	397105	397401	2_nonsis	968	1278	1587	1	11	1	1	0	(4:4ai)_(2:6)_(4:4bCO)_(3:5)_(4:4b)
271	OMT1	OMT	16	72872	73338	74327	74884	2_nonsis	990	1501	2011	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
57	OMT1	OMT	4	430932	431592	431930	432137	2_nonsis	339	772	1204	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
263	OMT1	OMT	15	741984	742253	742716	743206	2_nonsis	464	843	1221	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
139	OMT1	OMT	8	235099	235912	236251	237146	2_nonsis	340	1193	2046	1	12	1	1	0	(3:5)_(2:6)_(4:4)_(4:4aCO)
202	OMT1	OMT	12	552850	553063	554218	554679	2_nonsis	1156	1492	1828	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
116	OMT1	OMT	7	90444	91031	91862	92820	2_nonsis	832	1604	2375	1	12	1	1	0	(5:3)_(6:2)_(4:4)_(4:4aCO)
295	OMT1	OMT	16	874996	875078	876811	876914	2_nonsis	1734	1826	1917	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
143	OMT1	OMT	8	331868	334431	335220	335465	2_nonsis	790	2193	3596	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
148	OMT1	OMT	9	36691	36702	39559	40190	2_nonsis	2858	3178	3498	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
61	OMT1	OMT	4	599518	599722	601683	602153	2_nonsis	1962	2298	2634	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(3:5)_(4:4aCO)
162	OMT1	OMT	10	300402	300732	302943	303003	2_nonsis	2212	2406	2600	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(4:4aCO)
80	OMT1	OMT	4	1347683	1349666	1350718	1350819	2_nonsis	1053	2094	3135	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
205	OMT1	OMT	12	638411	640114	642815	643838	2_nonsis	2702	4064	5426	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
121	OMT1	OMT	7	394219	394474	394474	394511	2_nonsis	1	146	291	1	15	1	1	0	(6:2)_(4:4aCO)
126	OMT1	OMT	7	671982	672059	672059	672419	2_nonsis	1	219	436	1	15	1	1	0	(6:2)_(4:4aCO)
118	OMT1	OMT	7	199894	200351	200351	200448	2_nonsis	1	277	553	1	15	1	1	0	(6:2)_(4:4aCO)
230	OMT1	OMT	14	51868	52069	52243	52297	2_nonsis	175	302	428	1	15	1	1	0	(6:2)_(4:4aCO)
48	OMT1	OMT	4	105853	106143	106143	106727	2_nonsis	1	437	873	1	15	1	1	0	(6:2)_(4:4aCO)
76	OMT1	OMT	4	1198548	1199289	1199413	1199588	2_nonsis	125	582	1039	1	15	1	1	0	(6:2)_(4:4aCO)
52	OMT1	OMT	4	196851	198376	198734	198778	2_nonsis	359	1143	1926	1	15	1	1	0	(6:2)_(4:4aCO)
248	OMT1	OMT	14	743089	743137	743262	743408	2_nonsis	126	222	318	1	16	1	1	0	(2:6)_(4:4aCO)
37	OMT1	OMT	3	74394	74577	74577	75202	2_nonsis	1	404	807	1	16	1	1	0	(2:6)_(4:4aCO)
127	OMT1	OMT	7	825066	825417	825444	825852	2_nonsis	28	407	785	1	16	1	1	0	(2:6)_(4:4aCO)
56	OMT1	OMT	4	366072	366513	366629	366913	2_nonsis	117	479	840	1	16	1	1	0	(2:6)_(4:4aCO)
11	OMT1	OMT	2	192576	193122	193122	193664	2_nonsis	1	544	1087	1	16	1	1	0	(2:6)_(4:4aCO)

								2_nonsis									
71	OMT1	OMT	4	1039132	1039385	1039385	1040424	2_nonsis	1	646	1291	1	16	1	1	0	(2:6)_(4:4aCO)
211	OMT1	OMT	12	1009719	1011169	1011170	1011621	2_nonsis	2	952	1901	1	16	1	1	0	(2:6)_(4:4aCO)
31	OMT1	OMT	2	640627	641071	642483	642776	2_nonsis	1413	1781	2148	1	16	1	1	0	(2:6)_(4:4aCO)
287	OMT1	OMT	16	591462	591540	591462	591540	2_nonsis	0	39	77	1	100	1	1	0	(4:4aCO)
269	OMT1	OMT	16	30747	30844	30747	30844	2_nonsis	0	48	96	1	100	1	1	0	(4:4aCO)
1	OMT1	OMT	1	77554	77737	77554	77737	2_nonsis	0	91	182	1	100	1	1	0	(4:4aCO)
252	OMT1	OMT	15	96983	97189	96983	97189	2_nonsis	0	103	205	1	100	1	1	0	(4:4aCO)
289	OMT1	OMT	16	623051	623258	623051	623258	2_nonsis	0	103	206	1	100	1	1	0	(4:4aCO)
54	OMT1	OMT	4	255481	255722	255481	255722	2_nonsis	0	120	240	1	100	1	1	0	(4:4aCO)
237	OMT1	OMT	14	300738	301119	300738	301119	2_nonsis	0	190	380	1	100	1	1	0	(4:4aCO)
217	OMT1	OMT	13	209542	209952	209542	209952	2_nonsis	0	205	409	1	100	1	1	0	(4:4aCO)
195	OMT1	OMT	12	341070	341507	341070	341507	2_nonsis	0	218	436	1	100	1	1	0	(4:4aCO)
151	OMT1	OMT	9	215186	215644	215186	215644	2_nonsis	0	229	457	1	100	1	1	0	(4:4aCO)
92	OMT1	OMT	5	225841	226347	225841	226347	2_nonsis	0	253	505	1	100	1	1	0	(4:4aCO)
262	OMT1	OMT	15	606336	606849	606336	606849	2_nonsis	0	256	512	1	100	1	1	0	(4:4aCO)
164	OMT1	OMT	10	421930	422597	421930	422597	2_nonsis	0	333	666	1	100	1	1	0	(4:4aCO)
82	OMT1	OMT	4	1415193	1416035	1415193	1416035	2_nonsis	0	421	841	1	100	1	1	0	(4:4aCO)
176	OMT1	OMT	11	291136	292055	291136	292055	2_nonsis	0	459	918	1	100	1	1	0	(4:4aCO)
256	OMT1	OMT	15	218142	219124	218142	219124	2_nonsis	0	491	981	1	100	1	1	0	(4:4aCO)
220	OMT1	OMT	13	411264	412303	411264	412303	2_nonsis	0	519	1038	1	100	1	1	0	(4:4aCO)
278	OMT1	OMT	16	345110	346505	345110	346505	2_nonsis	0	697	1394	1	100	1	1	0	(4:4aCO)
171	OMT1	OMT	11	125651	127396	125651	127396	2_nonsis	0	872	1744	1	100	1	1	0	(4:4aCO)
69	OMT1	OMT	4	915507	917310	915507	917310	2_nonsis	0	901	1802	1	100	1	1	0	(4:4aCO)
3	OMT1	OMT	1	187427	189825	187427	189825	2_nonsis	0	1199	2397	1	100	1	1	0	(4:4aCO)
168	OMT1	OMT	10	624648	627140	624648	627140	2_nonsis	0	1246	2491	1	100	1	1	0	(4:4aCO)
2	OMT1	OMT	1	104068	107245	104068	107245	2_nonsis	0	1588	3176	1	100	1	1	0	(4:4aCO)
35	OMT1	OMT	2	726633	726855	727581	727716	2_nonsis	727	905	1082	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
216	OMT1	OMT	13	167521	167925	172118	172478	2_nonsis	4194	4575	4956	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
36	OMT1	OMT	2	791057	791214	792210	792968	2_nonsis	997	1454	1910	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
251	OMT1	OMT	15	68200	68284	69841	69894	2_nonsis	1558	1626	1693	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
30	OMT1	OMT	2	632917	633067	636267	636372	2_nonsis	3201	3328	3454	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
208	OMT1	OMT	12	787510	787598	789373	789615	2_nonsis	1776	1940	2104	2	31	1	1	0	(3:5)_(3:5a)_(2:6)_(4:4aCO)
46	OMT1	OMT	4	20081	20103	20400	20444	2_nonsis	298	330	362	2	31	1	1	0	(2:6)_(3:5)_(3:5a)_(2:6)_(4:4aCO)
215	OMT1	OMT	13	68292	69113	72351	73368	2_nonsis	3239	4157	5075	2	31	1	1	0	(3:5)_(2:6)_(3:5)_(3:5a)_(4:4aCO)
101	OMT1	OMT	5	473281	473821	475154	475295	2_nonsis	1334	1674	2013	2	31	1	1	0	(3:5)_(2:6)_(3:5)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
241	OMT1	OMT	14	531399	531505	533533	533705	2_nonsis	2029	2167	2305	2	31	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(3:5)_(3:5a)_(4:4aCO)
6	OMT1	OMT	2	107438	107671	109488	110113	2_nonsis	1818	2246	2674	2	31	1	1	0	(3:5)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
132	OMT1	OMT	7	1011474	1011503	1013000	1013720	2_nonsis	1498	1872	2245	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
203	OMT1	OMT	12	566431	566615	578083	578714	2_nonsis	11469	11876	12282	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
112	OMT1	OMT	6	208668	209238	211344	211545	2_nonsis	2107	2492	2876	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3b)_(4:4a)
110	OMT1	OMT	6	176167	176296	177858	177999	2_nonsis	1563	1697	1831	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(5:3b)_(4:4aCO)_(5:3b)_(4:4a)
155	OMT1	OMT	10	32041	32051	37982	38095	2_nonsis	5932	5993	6053	2	32	1	1	0	(2:6)_(3:5)_(2:6)_(4:4)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
83	OMT1	OMT	4	1417050	1417646	1422082	1422450	2_nonsis	4437	4918	5399	2	32	1	1	0	(6:2)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
149	OMT1	OMT	9	42866	43748	47054	47493	2_nonsis	3307	3967	4626	2	32	1	1	0	(2:6)_(3:5)_(4:4)_(3:5)_(4:4ai)_(3:5a)_(4:4ai)_(4:4bCO)_(3:5b)_(3:5a)_(4:4b)
160	OMT1	OMT	10	189105	189246	189441	189631	2_nonsis	196	361	525	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
188	OMT1	OMT	12	36038	36125	37050	37123	2_nonsis	926	1005	1084	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
23	OMT1	OMT	2	451982	452218	453426	453575	2_nonsis	1209	1401	1592	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
182	OMT1	OMT	11	486704	487095	488294	488405	2_nonsis	1200	1450	1700	3	20	1	1	0	(3:5)_(6:2)_(5:3)_(4:4aCO)
210	OMT1	OMT	12	953141	953351	954772	954849	2_nonsis	1422	1565	1707	3	20	1	1	0	(3:5)_(6:2)_(5:3)_(4:4aCO)
130	OMT1	OMT	7	904249	904347	905710	906181	2_nonsis	1364	1648	1931	3	20	1	1	0	(3:5)_(4:4aCO)_(6:2)_(4:4a)
86	OMT1	OMT	4	1487095	1487794	1488904	1489717	2_nonsis	1111	1866	2621	3	20	1	1	0	(3:5)_(4:4)_(6:2)_(4:4aCO)
136	OMT1	OMT	8	121477	121618	123473	123592	2_nonsis	1856	1985	2114	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
199	OMT1	OMT	12	422565	423102	425324	425404	2_nonsis	2223	2531	2838	3	20	1	1	0	(5:3)_(5:3a)_(3:5)_(4:4aCO)
17	OMT1	OMT	2	287551	287818	290619	291653	2_nonsis	2802	3452	4101	3	20	1	1	0	(5:3)_(3:5)_(5:3a)_(4:4aCO)
186	OMT1	OMT	11	630615	631180	631559	632039	2_nonsis	380	902	1423	3	20	1	1	0	(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
285	OMT1	OMT	16	525053	525272	527456	527480	2_nonsis	2185	2306	2426	3	20	1	1	0	(5:3)_(4:4)_(5:3a)_(6:2)_(3:5)_(5:3b)_(4:4aCO)
206	OMT1	OMT	12	759015	759162	761502	761602	2_nonsis	2341	2464	2586	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
103	OMT1	OMT	5	525075	525798	527534	528932	2_nonsis	1737	2797	3856	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
233	OMT1	OMT	14	185896	186475	188016	188308	2_nonsis	1542	1977	2411	3	20	1	1	0	(5:3)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)_(3:5a)_(4:4a)
91	OMT1	OMT	5	65622	65697	68268	68547	2_nonsis	2572	2748	2924	3	21	1	1	0	(3:5)_(4:4)_(6:2)_(5:3)_(4:4ai)_(4:4bCO)

63	OMT1	OMT	4	662835	663783	667027	667309	2_nonsis		3245	3859	4473	3	21	1	1	0	(5:3)_(4:4ai)_(3:5)_(2:6)_(3:5)_(4:4bCO)
21	OMT1	OMT	2	390744	391464	395368	395476	2_nonsis		3905	4318	4731	3	21	1	1	0	(5:3)_(3:5)_(4:4ai)_(5:3)_(4:4ai)_(3:5a)_(4:4ai)_(3:5a)_(4:4bCO)
14	OMT1	OMT	2	250789	251134	252589	253219	2_sis		1456	1943	2429	0	1	2	0	2	(3:5)_(4:4)_(2:6i)_(3:5a)_(2:6i)_(3:5b)_(4:4)
19	OMT1	OMT	2	310393	310571	312167	312299	2_sis		1597	1751	1905	0	1	2	0	2	(5:3)_(5:3a)_(5:3b)_(4:4)
20	OMT1	OMT	2	350900	351083	352907	353413	2_sis		1825	2169	2512	0	1	2	0	2	(2:6i)_(3:5)_(4:4)
51	OMT1	OMT	4	174905	174996	174996	175763	2_sis		1	429	857	0	1	2	0	2	(6:2i)_(4:4)
60	OMT1	OMT	4	589456	589536	591129	591782	2_sis		1594	1960	2325	0	1	2	0	2	(3:5)_(4:4)_(2:6i)_(2:6a)_(4:4)
72	OMT1	OMT	4	1079984	1080788	1081335	1081779	2_sis		548	1171	1794	0	1	2	0	2	(2:6i)_(3:5)_(4:4)_(3:5)_(4:4)
187	OMT1	OMT	12	20616	20678	22902	23199	2_sis		2225	2404	2582	0	1	2	0	2	(5:3)_(4:4)_(6:2i)_(6:2a)_(4:4)
193	OMT1	OMT	12	250711	251635	255736	255818		3	4102	4604	5106	0	1	2	0	2	(3:5)_(4:4)_(3:5)_(6:2i)_(5:3)_(4:4)
5	OMT1	OMT	2	44210	44904	61179	61197		3	16276	16631	16986	0	2	2	1	1	(5:3)_(2:6)_(3:5)_(4:4ai)_(5:3a)_(5:3b)_(6:2i)_(5:3b)_(6:2i)_(5:3c)_(4:4bCO)
7	OMT1	OMT	2	112018	112335	117726	117972		4	5392	5673	5953	0	2	2	2	0	(3:5)_(5:3)_(4:4)_(2:6i)_(3:5a)_(2:6i)_(2:6ai)_(3:5b)_(2:6ai)_(3:5c)_(4:4ai)_(4:4bCO)
22	OMT1	OMT	2	430067	431229	433097	433196		3	1869	2499	3128	0	2	2	1	1	(5:3)_(4:4ai)_(3:5)_(4:4bCO)
29	OMT1	OMT	2	579131	579255	582680	583031		3	3426	3663	3899	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(5:3a)_(6:2i)_(5:3a)_(6:2i)_(5:3b)_(4:4aCO)
34	OMT1	OMT	2	700117	700495	704282	704922		3	3333	4069	4804	0	2	2	1	1	(5:3)_(4:4ai)_(6:2)_(6:2ai)_(5:3a)_(4:4bCO)_(5:3a)_(4:4b)
100	OMT1	OMT	5	459831	460003	463625	464078		3	3623	3935	4246	0	2	2	1	1	(5:3)_(4:4)_(7:1)_(4:4)_(8:0)_(5:3a)_(4:4aCO)
135	OMT1	OMT	8	54302	54591	58733	59498		3	4143	4669	5195	0	2	2	1	1	(3:5)_(4:4ai)_(2:6)_(6:2)_(5:3)_(4:4)_(2:6)_(3:5)_(4:4bCO)
145	OMT1	OMT	8	422434	422538	423045	423870		3	508	972	1435	0	2	2	1	1	(2:6i)_(1:7)_(4:4aCO)_(3:5)_(4:4a)
147	OMT1	OMT	8	516318	516468	518620	518743		3	2153	2289	2424	0	2	2	1	1	(5:3)_(6:2)_(7:1)_(3:5)_(3:5a)_(4:4aCO)
152	OMT1	OMT	9	266803	267668	269580	269763		3	1913	2436	2959	0	2	2	1	1	(3:5)_(2:6)_(1:7)_(2:6ai)_(3:5a)_(2:6b)_(6:2)_(4:4aCO)
169	OMT1	OMT	10	662479	663134	664569	664824		3	1436	1890	2344	0	2	2	1	1	(4:4ai)_(4:4)_(6:2)_(4:4bCO)
209	OMT1	OMT	12	827343	827901	831136	831658		4	3236	3775	4314	0	2	2	2	0	(3:5)_(2:6i)_(3:5a)_(2:6i)_(3:5b)_(2:6a)_(3:5c)_(2:6a)_(3:5c)_(4:4aCO)
222	OMT1	OMT	13	592777	593048	594694	595371		3	1647	2120	2593	0	2	2	1	1	(2:6i)_(3:5)_(4:4aCO)_(3:5a)_(4:4a)
292	OMT1	OMT	16	784177	784693	786161	786518		3	1469	1905	2340	0	2	2	1	1	(3:5)_(4:4)_(2:6)_(5:3)_(4:4aCO)_(3:5a)_(4:4a)
4	OMT1	OMT	2	26815	27032	37454	37628		4	10423	10618	10812	0	3	2	2	0	(4:4ai)_(3:5)_(4:4ai)_(5:3)_(5:3a)_(4:4bCO)_(5:3a)_(6:2)_(5:3b)_(4:4ci)_(5:3c)_(4:4dCO)
26	OMT1	OMT	2	530065	531256	540568	540838		4	9313	10043	10772	0	3	3	2	1	(5:3)_(7:1)_(6:2)_(4:4aCO)_(2:6)_(3:5)_(4:4bCO)
42	OMT1	OMT	3	216424	216599	230267	231791		4	13669	14518	15366	0	3	2	2	0	(6:2)_(1:7)_(2:6)_(1:7)_(2:6a)_(3:5)_(4:4aCO)_(6:2a)_(5:3)_(4:4bCO)
90	OMT1	OMT	5	38064	38431	42646	43035		3	4216	4593	4970	0	3	2	1	1	(5:3)_(4:4aCO)_(2:6)_(3:5a)_(4:4ci)_(3:5a)_(4:4CO)
183	OMT1	OMT	11	521737	521933	527630	527758		3	5698	5859	6020	0	3	2	0	2	(5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)_(5:3b)_(6:2)_(4:4b)
266	OMT1	OMT	15	987667	988081	989301	991111		3	1221	2332	3443	0	3	2	1	1	(5:3)_(5:3a)_(3:5)_(2:6)_(4:4aCO)_(4:4bCO)
296	OMT1	OMT	1	31403	31635	33328	33347		1	1694	1819	1943	0	4	1	NA	NA	3:5_2:6_3:5_4:4_3:5
333	OMT1	OMT	2	797248	797326	800937	813184	2_nonsis		3612	9774	15935	0	4	1	NA	NA	3:5_3:5_4:4_3:5
343	OMT1	OMT	3	292937	296463	303499	316620	2_sis		7037	15360	23682	0	4	1	NA	NA	5:3_6:2_7:1_5:3_6:2_5:3
453	OMT1	OMT	10	21758	21859	22895	22911	2_nonsis		1037	1095	1152	0	4	1	NA	NA	3:5_4:4*_4:4*_3:5_3:5_5:3
469	OMT1	OMT	10	725123	725433	725933	745751		1	0	10314	20627	0	4	1	NA	NA	
596	OMT1	OMT	16	920519	920779	925093	948066	2_nonsis		4315	15931	27546	0	4	1	NA	NA	4:4*_4:4_4:4*_5:3_4:4_5:3_6:2_5:3_4:4_5:3_4:4_5:3
219	OMT10	OMT	15	494326	494461	494461	494556		1	1	115	229	1	1	1	0	1	05:03
241	OMT10	OMT	16	785910	786015	786020	786161		1	6	128	250	1	1	1	0	1	05:03
166	OMT10	OMT	12	433420	433567	433567	433851		1	1	216	430	1	1	1	0	1	05:03
103	OMT10	OMT	8	108568	108672	108672	109025		1	1	229	456	1	1	1	0	1	05:03
21	OMT10	OMT	3	52371	52747	52792	52803		1	46	239	431	1	1	1	0	1	05:03
239	OMT10	OMT	16	645731	645899	645942	646173		1	44	243	441	1	1	1	0	1	05:03
171	OMT10	OMT	12	763412	763502	763666	763742		1	165	247	329	1	1	1	0	1	05:03
26	OMT10	OMT	4	20223	20376	20444	20659		1	69	252	435	1	1	1	0	1	05:03
56	OMT10	OMT	4	1295451	1295582	1295582	1295980		1	1	265	528	1	1	1	0	1	05:03
186	OMT10	OMT	13	513381	513415	513553	513778		1	139	268	396	1	1	1	0	1	05:03
202	OMT10	OMT	14	531611	531656	531656	532165		1	1	277	553	1	1	1	0	1	05:03
79	OMT10	OMT	6	207745	207760	207985	208075		1	226	278	329	1	1	1	0	1	05:03
183	OMT10	OMT	13	236240	236370	236410	236819		1	41	310	578	1	1	1	0	1	05:03
149	OMT10	OMT	11	437157	437524	437585	437754		1	62	329	596	1	1	1	0	1	05:03
95	OMT10	OMT	7	848688	849134	849134	849405		1	1	359	716	1	1	1	0	1	05:03
7	OMT10	OMT	2	70774	71161	71276	71395		1	116	368	620	1	1	1	0	1	05:03
52	OMT10	OMT	4	1188542	1188946	1188946	1189283		1	1	371	740	1	1	1	0	1	05:03
101	OMT10	OMT	8	16906	17120	17359	17641		1	240	487	734	1	1	1	0	1	05:03
46	OMT10	OMT	4	835164	835319	835444	836028		1	126	495	863	1	1	1	0	1	05:03
135	OMT10	OMT	10	360767	360976	361340	361485		1	365	541	717	1	1	1	0	1	05:03
105	OMT10	OMT	8	186876	187527	187695	187989		1	169	641	1112	1	1	1	0	1	05:03
54	OMT10	OMT	4	1270457	1270902	1270902	1271755		1	1	649	1297	1	1	1	0	1	05:03
50	OMT10	OMT	4	1110571	1111002	1111414	1111575		1	413	708	1003	1	1	1	0	1	05:03
215	OMT10	OMT	15	284521	284983	285417	285557		1	435	735	1035	1	1	1	0	1	05:03

53	OMT10	OMT	4	1260078	1260779	1261105	1261386	1	327	817	1307	1	1	1	0	1	05:03
211	OMT10	OMT	15	197183	197943	198230	198587	1	288	846	1403	1	1	1	0	1	05:03
200	OMT10	OMT	14	355731	357348	357375	357524	1	28	910	1792	1	1	1	0	1	05:03
152	OMT10	OMT	11	634259	634414	634635	635970	1	222	966	1710	1	1	1	0	1	05:03
197	OMT10	OMT	14	90644	90834	91563	91989	1	730	1037	1344	1	1	1	0	1	05:03
45	OMT10	OMT	4	802711	805658	805658	805687	1	1	1488	2975	1	1	1	0	1	05:03
209	OMT10	OMT	15	153405	153546	154173	156059	1	628	1641	2653	1	1	1	0	1	05:03
106	OMT10	OMT	8	206103	206439	207745	208403	1	1307	1803	2299	1	1	1	0	1	05:03
126	OMT10	OMT	10	83804	83877	85773	85992	1	1897	2042	2187	1	1	1	0	1	05:03
17	OMT10	OMT	2	662272	662444	662444	666708	1	1	2218	4435	1	1	1	0	1	05:03
157	OMT10	OMT	12	112012	112031	112068	112137	1	38	81	124	1	2	1	0	1	03:05
225	OMT10	OMT	15	768429	768642	768642	768676	1	1	124	246	1	2	1	0	1	03:05
36	OMT10	OMT	4	520944	521108	521126	521211	1	19	143	266	1	2	1	0	1	03:05
162	OMT10	OMT	12	278546	278659	278673	278823	1	15	146	276	1	2	1	0	1	03:05
38	OMT10	OMT	4	556617	556732	556732	556934	1	1	159	316	1	2	1	0	1	03:05
193	OMT10	OMT	13	759350	759582	759582	759679	1	1	165	328	1	2	1	0	1	03:05
180	OMT10	OMT	13	159532	159727	159757	159950	1	31	224	417	1	2	1	0	1	03:05
110	OMT10	OMT	8	360746	360898	360906	361205	1	9	234	458	1	2	1	0	1	03:05
22	OMT10	OMT	3	69091	69652	69652	69718	1	1	314	626	1	2	1	0	1	03:05
34	OMT10	OMT	4	462638	462986	463089	463263	1	104	364	624	1	2	1	0	1	03:05
164	OMT10	OMT	12	332162	332441	332524	332859	1	84	390	696	1	2	1	0	1	03:05
229	OMT10	OMT	15	1025392	1025498	1025760	1025986	1	263	428	593	1	2	1	0	1	03:05
182	OMT10	OMT	13	191318	191452	191569	192110	1	118	455	791	1	2	1	0	1	03:05
204	OMT10	OMT	14	586871	587725	587867	587867	1	1	498	995	1	2	1	0	1	03:05
163	OMT10	OMT	12	319960	320465	320469	320997	1	5	521	1036	1	2	1	0	1	03:05
86	OMT10	OMT	7	351684	351949	352206	352489	1	258	531	804	1	2	1	0	1	03:05
63	OMT10	OMT	5	41711	41961	42354	42396	1	394	539	684	1	2	1	0	1	03:05
111	OMT10	OMT	8	373732	373987	374065	374774	1	79	560	1041	1	2	1	0	1	03:05
25	OMT10	OMT	3	235472	236284	236387	236702	1	104	667	1229	1	2	1	0	1	03:05
212	OMT10	OMT	15	218142	219124	219136	219822	1	13	846	1679	1	2	1	0	1	03:05
228	OMT10	OMT	15	985518	985891	986501	986764	1	611	928	1245	1	2	1	0	1	03:05
146	OMT10	OMT	11	176780	177108	177551	178198	1	444	931	1417	1	2	1	0	1	03:05
55	OMT10	OMT	4	1288775	1289394	1289972	1290308	1	579	1056	1532	1	2	1	0	1	03:05
39	OMT10	OMT	4	628602	629487	629725	630640	1	239	1138	2037	1	2	1	0	1	03:05
145	OMT10	OMT	11	170362	170773	171261	172151	1	489	1139	1788	1	2	1	0	1	03:05
8	OMT10	OMT	2	73943	74853	75576	75822	1	724	1301	1878	1	2	1	0	1	03:05
2	OMT10	OMT	1	85751	87490	88008	90330	1	519	2549	4578	1	2	1	0	1	03:05
235	OMT10	OMT	16	519754	520090	520684	521292	1	595	1066	1537	1	3	1	0	1	5:3_6:2_5:3
23	OMT10	OMT	3	168300	169991	171207	174943	1	1217	3930	6642	1	4	1	0	1	3:5_4:4_3:5
65	OMT10	OMT	5	69243	69568	69789	70022	1	222	500	778	1	7	1	0	1	6:2_5:3
77	OMT10	OMT	6	155336	155718	156218	156651	1	501	908	1314	1	7	1	0	1	5:3_6:2
220	OMT10	OMT	15	584870	585188	586345	586852	1	1158	1570	1981	1	7	1	0	1	5:3_6:2
107	OMT10	OMT	8	233475	233495	235099	235912	1	1605	2021	2436	1	7	1	0	1	5:3_6:2
100	OMT10	OMT	7	1016792	1017034	1017880	1018075	1	847	1065	1282	1	7	1	0	1	5:3_4:4_6:2
233	OMT10	OMT	16	323900	324163	324535	325197	1	373	835	1296	1	7	1	0	1	6:2_4:4_5:3_6:2_5:3
51	OMT10	OMT	4	1166461	1166557	1166937	1167032	1	381	476	570	1	7	1	0	1	6:2_5:3_4:4_5:3_6:2_5:3
37	OMT10	OMT	4	524941	525488	526636	526651	1	1149	1429	1709	1	7	1	0	1	6:2_5:3_6:2_5:3_4:4_5:3_4:4_6:2_5:3_6:2
226	OMT10	OMT	15	943688	944039	945252	945621	1	1214	1573	1932	1	8	1	0	1	2:6_3:5
67	OMT10	OMT	5	195529	195746	202626	203184	1	6881	7268	7654	1	8	1	0	1	2:6_3:5
10	OMT10	OMT	2	290619	291653	293405	293501	1	1753	2317	2881	1	8	1	0	1	2:6_4:4_3:5
122	OMT10	OMT	9	273624	273888	275131	275192	1	1244	1406	1567	1	8	1	0	1	2:6_3:5_4:4_3:5
216	OMT10	OMT	15	302883	303066	304525	304796	1	1460	1686	1912	1	8	1	0	1	2:6_3:5_4:4_2:6
72	OMT10	OMT	5	486986	487184	490700	490942	1	3517	3736	3955	1	8	1	0	1	3:5_2:6_3:5_4:4_3:5_2:6_3:5_2:6
168	OMT10	OMT	12	500605	500833	500833	501707	1	1	551	1101	1	10	1	0	1	06:02
130	OMT10	OMT	10	220326	220622	220637	221804	1	16	747	1477	1	10	1	0	1	06:02
5	OMT10	OMT	1	187280	187411	187411	187414	1	1	67	133	1	10.1	1	0	1	02:06
189	OMT10	OMT	13	618075	618182	618182	618249	1	1	87	173	1	10.1	1	0	1	02:06
230	OMT10	OMT	16	22571	22695	22695	22824	1	1	127	252	1	10.1	1	0	1	02:06
43	OMT10	OMT	4	770058	770136	770136	770352	1	1	147	293	1	10.1	1	0	1	02:06
217	OMT10	OMT	15	412174	412390	412390	412522	1	1	174	347	1	10.1	1	0	1	02:06

140	OMT10	OMT	10	709147	709747	709747	711083		1	1	968	1935	1	10.1	1	0	1 02:06
121	OMT10	OMT	9	244304	244618	244765	244951		1	148	397	646	2	11	1	0	1 5:3_5:3a
153	OMT10	OMT	12	36477	36694	37050	37123		1	357	501	645	2	11	1	0	1 5:3_5:3a
148	OMT10	OMT	11	368313	369378	369689	369878		1	312	938	1564	2	11	1	0	1 5:3_5:3a
11	OMT10	OMT	2	296843	297226	298189	298678		1	964	1399	1834	2	11	1	0	1 5:3_5:3a
190	OMT10	OMT	13	675294	675387	675697	675922		1	311	469	627	2	12	1	0	1 3:5_3:5a
40	OMT10	OMT	4	674365	674440	675833	676252		1	1394	1640	1886	2	12	1	0	1 3:5_3:5a
98	OMT10	OMT	7	987011	987084	988045	988071		1	962	1011	1059	2	13	1	0	1 5:3_5:3a_6:2_5:3a
199	OMT10	OMT	14	345280	345668	346414	346690		1	747	1078	1409	2	13	1	0	1 5:3_6:2_5:3_5:3a
62	OMT10	OMT	5	14955	15170	17320	17368		1	2151	2282	2412	2	13	1	0	1 6:2_5:3_6:2_5:3_6:2_5:3_5:3a
73	OMT10	OMT	5	524497	524520	526303	526638		1	1784	1962	2140	2	14	1	0	1 2:6_3:5_3:5a_2:6_3:5a
154	OMT10	OMT	12	48757	49068	49545	49638		1	478	679	880	2	15	1	0	1 5:3_4:4_5:3a
47	OMT10	OMT	4	855763	856001	856679	857591		1	679	1253	1827	2	15	1	0	1 5:3_4:4_5:3a
32	OMT10	OMT	4	267874	268279	269406	269544		1	1128	1399	1669	2	15	1	0	1 5:3_4:4_5:3a
192	OMT10	OMT	13	721068	721309	721694	721833		1	386	575	764	2	16	1	0	1 3:5_4:4_3:5a
237	OMT10	OMT	16	609630	609903	610749	610825		1	847	1021	1194	2	16	1	0	1 3:5_4:4_3:5a
223	OMT10	OMT	15	745929	746313	747546	747612		1	1234	1458	1682	2	16	1	0	1 3:5_4:4_3:5a
69	OMT10	OMT	5	270072	270213	271703	271934		1	1491	1676	1861	2	16	1	0	1 3:5_4:4_3:5a
124	OMT10	OMT	10	22158	22350	24307	26108		1	1958	2954	3949	2	16	1	0	1 3:5_4:4_3:5a
29	OMT10	OMT	4	183023	183468	186001	186485		1	2534	2998	3461	2	16	1	0	1 3:5_4:4_3:5a
66	OMT10	OMT	5	73474	74196	76636	77002		1	2441	2984	3527	2	17	1	0	1 6:2_5:3_4:4_5:3a
88	OMT10	OMT	7	395416	395553	398049	398572		1	2497	2826	3155	2	17	1	0	1 5:3_4:4_5:3_4:4_5:3a
13	OMT10	OMT	2	444564	444664	445794	446007		1	1131	1287	1442	2	18	1	0	1 3:5_4:4_3:5_4:4_3:5a
194	OMT10	OMT	13	835125	837907	839353	839983		1	1447	3152	4857	2	18	1	0	1 5:3_4:4_3:5a_4:4_3:5a
227	OMT10	OMT	15	977533	977581	980032	981230		1	2452	3074	3696	2	18	1	0	1 3:5_2:6_4:4_3:5_4:4_3:5a_4:4_3:5a_2:6
15	OMT10	OMT	2	554757	555319	555805	556121		1	487	925	1363	2	19	1	0	1 5:3_6:2_5:3a
161	OMT10	OMT	12	259126	259210	261119	261578		1	1910	2181	2451	2	20	1	0	1 3:5_2:6_3:5a
179	OMT10	OMT	13	76522	77019	78923	79258		1	1905	2320	2735	2	21	1	0	1 5:3_6:2_5:3a_4:4_5:3a
128	OMT10	OMT	10	171829	172240	173515	173883		1	1276	1665	2053	2	23	1	0	1 5:3_4:4_6:2_5:3a
31	OMT10	OMT	4	262409	262808	266029	266113		1	3222	3463	3703	2	23	1	0	1 5:3_6:2_4:4_6:2_5:3a
221	OMT10	OMT	15	656165	656264	659154	660208		1	2891	3467	4042	2	23	1	0	1 5:3_4:4_6:2_5:3a_6:2_5:3a
109	OMT10	OMT	8	336133	336486	338239	338392	2_nonsis		1754	2006	2258	3	30	1	0	1 5:3_5:3a_5:3b
142	OMT10	OMT	11	14411	19020	21803	22806	2_nonsis		2784	5589	8394	3	30	1	0	1 6:2_5:3
118	OMT10	OMT	9	113159	113517	115941	116245	2_nonsis		2425	2755	3085	3	30	1	0	1 5:3_6:2_5:3_5:3a_5:3b
206	OMT10	OMT	14	661270	661348	665064	665097	2_nonsis		3717	3772	3826	3	30	1	0	1 5:3_4:4_3:5_3:5a_5:3
132	OMT10	OMT	10	240364	240782	246652	247233	2_nonsis		5871	6370	6868	3	30	1	0	1 3:5_2:6_3:5_2:6_3:5a
174	OMT10	OMT	12	947421	947519	949489	949843	2_nonsis		1971	2196	2421	3	30	1	0	1 5:3_6:2_5:3_6:2_4:4_6:2
99	OMT10	OMT	7	992475	992805	994272	994410	2_nonsis		1468	1701	1934	3	30	1	0	1 5:3_3:5_4:4_3:5_4:4_3:5_5:3a_6:2
236	OMT10	OMT	16	524220	524743	525053	525272	2_nonsis		311	681	1051	3	31	1	0	1 4:4ai
177	OMT10	OMT	13	15470	15705	17138	17364	2_nonsis		1434	1664	1893	3	31	1	0	1 3:5_4:4_3:5_4:4_3:5_4:4ai
184	OMT10	OMT	13	367523	367636	380209	380209	2_nonsis		12349	12517	12685	3	31	1	0	1 5:3_4:4_5:3_4:4_5:3_6:2_5:3_3:5_4:4ai
57	OMT10	OMT	4	1326110	1326543	1330877	1330885	2_nonsis		4335	4555	4774	3	31	1	0	1 3:5_4:4ai_5:3_4:4ai_3:5a_4:4ai_3:5a_5:3a_3:5a_4:4ai_3:5
114	OMT10	OMT	8	511816	512259	512291	512682	2_nonsis		33	449	865	1	1	1	1	0 (5:3)_(4:4aCO)
82	OMT10	OMT	7	127409	127838	127940	128210	2_nonsis		103	452	800	1	1	1	1	0 (5:3)_(4:4aCO)
120	OMT10	OMT	9	212207	213470	213470	213953	2_nonsis		1	873	1745	1	1	1	1	0 (5:3)_(4:4aCO)
205	OMT10	OMT	14	606872	608001	608001	610323	2_nonsis		1	1726	3450	1	1	1	1	0 (5:3)_(4:4aCO)
85	OMT10	OMT	7	248225	249983	250680	252024	2_nonsis		698	2248	3798	1	1	1	1	0 (5:3)_(4:4aCO)
113	OMT10	OMT	8	484090	485522	487338	487560	2_nonsis		1817	2643	3469	1	1	1	1	0 (5:3)_(4:4aCO)
141	OMT10	OMT	10	721671	721886	721886	722092	2_nonsis		1	211	420	1	2	1	1	0 (3:5)_(4:4aCO)
214	OMT10	OMT	15	246178	246679	246679	247071	2_nonsis		1	447	892	1	2	1	1	0 (3:5)_(4:4aCO)
185	OMT10	OMT	13	447619	448761	448761	449175	2_nonsis		1	778	1555	1	2	1	1	0 (3:5)_(4:4aCO)
75	OMT10	OMT	6	73471	73840	74753	74843	2_nonsis		914	1143	1371	1	2	1	1	0 (3:5)_(4:4aCO)
27	OMT10	OMT	4	43482	46115	46179	46608	2_nonsis		65	1595	3125	1	2	1	1	0 (3:5)_(4:4aCO)
117	OMT10	OMT	9	91970	92242	93903	94143	2_nonsis		1662	1917	2172	1	5	1	1	0 (3:5)_(4:4)_(4:4aCO)
156	OMT10	OMT	12	100126	100150	100682	100762	2_nonsis		533	584	635	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
59	OMT10	OMT	4	1445249	1445402	1447213	1447296	2_nonsis		1812	1929	2046	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
30	OMT10	OMT	4	196851	198376	199393	200025	2_nonsis		1018	2096	3173	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
68	OMT10	OMT	5	241522	241980	243892	244317	2_nonsis		1913	2354	2794	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
70	OMT10	OMT	5	413281	413862	414243	414432	2_nonsis		382	766	1150	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
81	OMT10	OMT	7	57501	57822	58485	59379	2_nonsis		664	1271	1877	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)

139	OMT10	OMT	10	637795	637967	638018	638343	2_nonsis	52	300	547	1	11	1	1	0 (4:4ai)_(5:3)_(4:4bCO)
44	OMT10	OMT	4	783406	783598	784297	784537	2_nonsis	700	915	1130	1	12	1	1	0 (3:5)_(2:6)_(4:4)_(4:4aCO)
232	OMT10	OMT	16	214963	215112	215587	216380	2_nonsis	476	946	1416	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4aCO)
203	OMT10	OMT	14	552429	552569	553315	553805	2_nonsis	747	1061	1375	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
3	OMT10	OMT	1	99374	99440	100840	101177	2_nonsis	1401	1602	1802	1	12	1	1	0 (5:3)_(4:4)_(6:2)_(4:4aCO)
93	OMT10	OMT	7	760939	761877	763227	763406	2_nonsis	1351	1909	2466	1	12	1	1	0 (5:3)_(4:4)_(6:2)_(4:4aCO)
198	OMT10	OMT	14	267621	268398	270547	270838	2_nonsis	2150	2683	3216	1	12	1	1	0 (3:5)_(4:4aCO)_(3:5)_(4:4a)
80	OMT10	OMT	6	220253	221384	222196	222477	2_nonsis	813	1518	2223	1	12	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
9	OMT10	OMT	2	83944	84352	84976	85339	2_nonsis	625	1010	1394	1	12	1	1	0 (6:2)_(5:3)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
218	OMT10	OMT	15	448985	449105	449105	449205	2_nonsis	1	110	219	1	15	1	1	0 (6:2)_(4:4aCO)
176	OMT10	OMT	12	1043157	1043284	1043701	1043895	2_nonsis	418	578	737	1	15	1	1	0 (6:2)_(4:4aCO)
201	OMT10	OMT	14	425816	427278	427278	427295	2_nonsis	1	740	1478	1	15	1	1	0 (6:2)_(4:4aCO)
147	OMT10	OMT	11	341772	342080	342621	342813	2_nonsis	542	791	1040	1	15	1	1	0 (6:2)_(4:4aCO)
131	OMT10	OMT	10	236615	236674	236674	236901	2_nonsis	1	143	285	1	16	1	1	0 (2:6)_(4:4aCO)
96	OMT10	OMT	7	958623	958749	958749	958930	2_nonsis	1	154	306	1	16	1	1	0 (2:6)_(4:4aCO)
20	OMT10	OMT	3	39123	39265	39281	39525	2_nonsis	17	209	401	1	16	1	1	0 (2:6)_(4:4aCO)
240	OMT10	OMT	16	677836	678266	678266	678517	2_nonsis	1	341	680	1	16	1	1	0 (2:6)_(4:4aCO)
136	OMT10	OMT	10	486009	486193	486432	486501	2_nonsis	240	366	491	1	16	1	1	0 (2:6)_(4:4aCO)
222	OMT10	OMT	15	701028	701208	701466	701569	2_nonsis	259	400	540	1	16	1	1	0 (2:6)_(4:4aCO)
208	OMT10	OMT	15	134063	135587	135770	136025	2_nonsis	184	1073	1961	1	16	1	1	0 (2:6)_(4:4aCO)
94	OMT10	OMT	7	807533	823555	823615	823674	2_nonsis	61	8101	16140	1	16	1	1	0 (2:6)_(4:4aCO)
170	OMT10	OMT	12	681146	681539	681146	681539	2_nonsis	0	196	392	1	100	1	1	0 (4:4aCO)
92	OMT10	OMT	7	612267	612759	612267	612759	2_nonsis	0	246	491	1	100	1	1	0 (4:4aCO)
181	OMT10	OMT	13	164532	165032	164532	165032	2_nonsis	0	250	499	1	100	1	1	0 (4:4aCO)
243	OMT10	OMT	16	879007	879511	879007	879511	2_nonsis	0	252	503	1	100	1	1	0 (4:4aCO)
35	OMT10	OMT	4	511815	512370	511815	512370	2_nonsis	0	277	554	1	100	1	1	0 (4:4aCO)
14	OMT10	OMT	2	531940	533263	531940	533263	2_nonsis	0	661	1322	1	100	1	1	0 (4:4aCO)
172	OMT10	OMT	12	789623	791142	789623	791142	2_nonsis	0	759	1518	1	100	1	1	0 (4:4aCO)
134	OMT10	OMT	10	331024	332595	331024	332595	2_nonsis	0	785	1570	1	100	1	1	0 (4:4aCO)
138	OMT10	OMT	10	601293	609171	601293	609171	2_nonsis	0	3939	7877	1	100	1	1	0 (4:4aCO)
207	OMT10	OMT	15	22358	39380	22358	39380	2_nonsis	0	8511	17021	1	100	1	1	0 (4:4aCO)
173	OMT10	OMT	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0 (4:4aCO)
115	OMT10	OMT	9	47519	47656	48252	48606	2_nonsis	597	842	1086	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
58	OMT10	OMT	4	1384944	1385143	1387436	1387907	2_nonsis	2294	2628	2962	2	30	1	1	0 (5:3)_(6:2)_(5:3)_(5:3a)_(4:4aCO)
160	OMT10	OMT	12	242568	242737	246534	246798	2_nonsis	3798	4014	4229	2	30	1	1	0 (5:3)_(6:2)_(5:3)_(5:3a)_(4:4aCO)
137	OMT10	OMT	10	567525	568041	573950	574034	2_nonsis	5910	6209	6508	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
87	OMT10	OMT	7	360287	360441	360942	361541	2_nonsis	502	878	1253	2	31	1	1	0 (3:5)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
127	OMT10	OMT	10	159135	159148	161596	162223	2_nonsis	2449	2768	3087	2	31	1	1	0 (3:5)_(3:5a)_(2:6)_(3:5a)_(4:4ai)_(4:4bCO)
90	OMT10	OMT	7	482421	483344	488836	489042	2_nonsis	5493	6057	6620	2	31	1	1	0 (2:6)_(3:5)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
76	OMT10	OMT	6	93664	93934	97372	97617	2_nonsis	3439	3696	3952	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
97	OMT10	OMT	7	968127	968214	973354	974385	2_nonsis	5141	5699	6257	2	32	1	1	0 (3:5)_(4:4ai)_(3:5a)_(4:4bCO)
123	OMT10	OMT	9	340507	340858	342462	342976	2_nonsis	1605	2037	2468	2	32	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
191	OMT10	OMT	13	696177	696333	699586	700248	2_nonsis	3254	3662	4070	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(4:4)_(5:3b)_(6:2)_(4:4aCO)
42	OMT10	OMT	4	719896	720645	723349	723451	2_nonsis	2705	3130	3554	2	32	1	1	0 (4:4ai)_(3:5)_(4:4bCO)_(3:5)_(4:4ai)_(2:6)_(3:5a)_(3:5b)_(4:4b)
178	OMT10	OMT	13	42127	43336	46860	48814	2_nonsis	3525	5106	6686	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(2:6)_(3:5a)_(4:4)_(2:6)_(3:5b)_(4:4aCO)
116	OMT10	OMT	9	53832	54480	55071	55251	2_nonsis	592	1005	1418	3	20	1	1	0 (3:5)_(6:2)_(4:4aCO)
144	OMT10	OMT	11	119339	120268	121106	121247	2_nonsis	839	1373	1907	3	20	1	1	0 (3:5)_(6:2)_(4:4aCO)
61	OMT10	OMT	4	1495680	1496054	1496573	1497025	2_nonsis	520	932	1344	3	20	1	1	0 (5:3)_(4:4)_(2:6)_(4:4aCO)
74	OMT10	OMT	5	557877	558441	559174	559301	2_nonsis	734	1079	1423	3	20	1	1	0 (5:3)_(3:5)_(6:2)_(4:4aCO)
89	OMT10	OMT	7	478509	478940	479689	480192	2_nonsis	750	1216	1682	3	20	1	1	0 (5:3)_(4:4)_(3:5)_(4:4aCO)
151	OMT10	OMT	11	562768	562948	564055	564676	2_nonsis	1108	1508	1907	3	20	1	1	0 (6:2)_(4:4)_(3:5)_(4:4aCO)
234	OMT10	OMT	16	372742	373291	375235	376113	2_nonsis	1945	2658	3370	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(4:4aCO)
169	OMT10	OMT	12	610934	611078	611779	611787	2_nonsis	702	777	852	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(6:2)_(4:4aCO)
1	OMT10	OMT	1	70497	70524	71535	71616	2_nonsis	1012	1065	1118	3	20	1	1	0 (6:2)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
242	OMT10	OMT	16	819509	820356	821711	822057	2_nonsis	1356	1952	2547	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)_(6:2)_(4:4a)
108	OMT10	OMT	8	322533	323234	324770	325071	2_nonsis	1537	2037	2537	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(5:3)_(4:4aCO)
19	OMT10	OMT	2	759221	759357	761529	761787	2_nonsis	2173	2369	2565	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
18	OMT10	OMT	2	718805	719463	721566	721863	2_nonsis	2104	2581	3057	3	20	1	1	0 (3:5)_(5:3)_(6:2)_(4:4aCO)
188	OMT10	OMT	13	552466	553020	555444	555852	2_nonsis	2425	2905	3385	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
78	OMT10	OMT	6	168241	168408	170209	170473	2_nonsis	1802	2017	2231	3	20	1	1	0 (3:5)_(4:4)_(2:6)_(5:3)_(5:3a)_(4:4aCO)

ID	Grp		n	s1	s2	s3	s4	num	label	v1	v2	v3	f1	f2	f3	f4	code	pattern
84	OMT10	OMT	7	206685	206716	209279	209637		2_nonsis	2564	2758	2951	3	20	1	1	0	(3:5)_(4:4)_(3:5a)_(6:2)_(5:3)_(4:4aCO)
104	OMT10	OMT	8	110685	111245	113512	114144		2_nonsis	2268	2863	3458	3	20	1	1	0	(6:2)_(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)
4	OMT10	OMT	1	141984	142779	145634	146539		2_nonsis	2856	3705	4554	3	20	1	1	0	(6:2)_(5:3)_(4:4)_(4:4aCO)_(3:5)_(4:4a)
33	OMT10	OMT	4	311119	311194	312701	313108		2_nonsis	1508	1748	1988	3	20	1	1	0	(5:3)_(4:4aCO)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4a)
159	OMT10	OMT	12	167737	168861	170342	170609		2_nonsis	1482	2177	2871	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(2:6)_(6:2)_(5:3)_(4:4aCO)
41	OMT10	OMT	4	697759	698151	700023	700151		2_nonsis	1873	2132	2391	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
238	OMT10	OMT	16	619088	619148	620773	620821		2_nonsis	1626	1679	1732	3	20	1	1	0	(2:6)_(3:5)_(4:4)_(3:5)_(4:4)_(2:6)_(3:5)_(5:3)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
213	OMT10	OMT	15	240538	241147	243831	244393		2_nonsis	2685	3270	3854	3	21	1	1	0	(6:2)_(5:3)_(4:4)_(5:3a)_(4:4ai)_(3:5)_(4:4bCO)
83	OMT10	OMT	7	197989	198003	201499	201788		2_nonsis	3497	3648	3798	3	21	1	1	0	(3:5)_(4:4)_(4:4ai)_(5:3)_(6:2)_(5:3)_(4:4bCO)
224	OMT10	OMT	15	753645	753808	755321	755705		2_nonsis	1514	1787	2059	3	21	1	1	0	(4:4ai)_(3:5)_(4:4bCO)_(5:3)_(4:4b)_(5:3)_(6:2)_(5:3a)_(4:4b)
133	OMT10	OMT	10	313030	313808	318240	318505		2_nonsis	4433	4954	5474	3	21	1	1	0	(5:3)_(4:4)_(5:3)_(4:4ai)_(5:3)_(4:4ai)_(4:4bCO)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4b)
60	OMT10	OMT	4	1476401	1476502	1477174	1477237	3		673	754	835	0	1	2	0	2	(5:3)_(6:2i)_(7:1)_(4:4ai)_(4:4)
71	OMT10	OMT	5	419827	420040	423233	423672		2_sis	3194	3519	3844	0	1	2	0	2	(5:3)_(5:3a)_(7:1)_(4:4)_(5:3b)_(4:4)_(5:3b)_(4:4)
91	OMT10	OMT	7	609044	609307	610674	611145		2_sis	1368	1734	2100	0	1	2	0	2	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(7:1)_(4:4ai)_(7:1)_(5:3a)_(4:4)
102	OMT10	OMT	8	46055	46220	50752	51058	3		4533	4768	5002	0	1	2	0	2	(5:3)_(6:2i)_(5:3a)_(5:3)_(6:2a)_(5:3a)_(6:2a)_(5:3a)_(6:2a)_(5:3a)_(4:4ai)_(4:4)
143	OMT10	OMT	11	90751	91192	92069	92108		2_sis	878	1117	1356	0	1	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4)
158	OMT10	OMT	12	154678	155252	157014	157169		2_sis	1763	2127	2490	0	1	2	0	2	(3:5)_(4:4)_(3:5a)_(4:4)
175	OMT10	OMT	12	1009719	1011169	1014670	1014976	3		3502	4379	5256	0	1	2	0	2	(5:3)_(6:2)_(7:1)_(6:2a)_(5:3a)_(6:2a)_(5:3a)_(4:4)
210	OMT10	OMT	15	169851	170112	171288	171805		2_sis	1177	1565	1953	0	1	2	0	2	(5:3)_(7:1)_(5:3a)_(6:2i)_(5:3b)_(4:4)
16	OMT10	OMT	2	649927	650411	651616	652362	3		1206	1820	2434	0	2	2	1	1	(6:2)_(5:3)_(2:6)_(4:4aCO)
24	OMT10	OMT	3	224038	224261	228130	230267	4		3870	5049	6228	0	2	2	1	1	(6:2)_(6:2a)_(7:1)_(5:3)_(4:4aCO)_(2:6)_(4:4a)
28	OMT10	OMT	4	122163	122341	130967	131084	3		8627	8774	8920	0	2	2	1	1	(6:2)_(5:3)_(4:4aCO)
48	OMT10	OMT	4	952018	952270	955755	955831	4		3486	3649	3812	0	2	2	1	1	(3:5)_(4:4ai)_(2:6)_(3:5a)_(2:6)_(0:8)_(1:7)_(2:6a)_(3:5b)_(4:4bCO)_(3:5b)_(4:4b)
49	OMT10	OMT	4	1105780	1106241	1108696	1109358	3		2456	3017	3577	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(4:4)_(5:3a)_(6:2)_(4:4aCO)
112	OMT10	OMT	8	449402	449894	462176	462297	3		12283	12589	12894	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(6:2ai)_(5:3)_(7:1)_(6:2)_(7:1)_(6:2)_(4:4aCO)
119	OMT10	OMT	9	137266	138115	143458	144100	4		5344	6089	6833	0	2	2	1	1	(4:4ai)_(5:3)_(4:4ai)_(4:4)_(3:5)_(2:6)_(3:5)_(2:6ai)_(3:5a)_(2:6ai)_(2:6b)_(3:5)_(2:6)_(3:5b)_(2:6)_(3:5b)_(3:5c)_(4:4bCO)
155	OMT10	OMT	12	85096	85270	88069	88362	3		2800	3033	3265	0	2	2	1	1	(5:3)_(5:3a)_(3:5)_(6:2i)_(5:3a)_(4:4ai)_(4:4bCO)
165	OMT10	OMT	12	340602	340616	344859	345042	3		4244	4342	4439	0	2	2	1	1	(6:2)_(5:3)_(5:3a)_(4:4aCO)
167	OMT10	OMT	12	446902	447260	448793	449654	3		1534	2143	2751	0	2	2	1	1	(7:1)_(5:3)_(4:4aCO)
187	OMT10	OMT	13	533975	534586	540798	541071	3		6213	6654	7095	0	2	2	1	1	(5:3)_(5:3a)_(4:4aCO)_(0:8)_(1:7)_(3:5)_(4:4a)
231	OMT10	OMT	16	107304	107496	108552	109014	3		1057	1383	1709	0	2	2	1	1	(3:5)_(4:4)_(4:4aCO)
6	OMT10	OMT	1	190031	190402	194169	194241	4		3768	3989	4209	0	3	2	1	1	(2:6)_(4:4)_(4:4aCO)_(3:5)_(5:3)_(3:5a)_(4:4bCO)
12	OMT10	OMT	2	311366	311639	313334	313427	3		1696	1878	2060	0	3	2	1	1	(3:5)_(4:4aCO)_(3:5a)_(4:4bCO)
64	OMT10	OMT	5	59555	60057	63585	63707		2_nonsis	3529	3840	4151	0	3	2	0	2	(3:5)_(4:4aCO)_(3:5a)_(4:4CO)_(3:5a)_(4:4)_(3:5a)_(4:4)_(3:5a)_(4:4)
125	OMT10	OMT	10	55650	56177	60064	60979	4		3888	4608	5328	0	3	2	2	0	(4:4ai)_(2:6i)_(3:5)_(4:4bCO)_(3:5)_(3:5a)_(3:5b)_(4:4cCO)
129	OMT10	OMT	10	183834	184128	187746	188331		2_nonsis	3619	4058	4496	0	3	2	0	2	(3:5)_(3:5a)_(2:6)_(5:3)_(4:4aCO)_(4:4bi)_(3:5a)_(4:4bi)_(3:5a)_(4:4CO)
150	OMT10	OMT	11	468315	468458	469831	470250		2_nonsis	1374	1654	1934	0	3	2	0	2	(5:3)_(4:4aCO)_(5:3a)_(4:4a)_(3:5)_(4:4CO)
195	OMT10	OMT	13	860181	861184	866753	867864	4		5570	6626	7682	0	3	2	1	1	(5:3)_(4:4aCO)_(5:3)_(3:5)_(5:3a)_(3:5b)_(4:4bi)_(3:5a)_(4:4bi)_(4:4cCO)_(3:5b)_(2:6)_(4:4di)_(3:5c)_(4:4eCO)
196	OMT10	OMT	14	78386	79032	80433	81575	3		1402	2295	3188	0	3	2	1	1	(6:2)_(4:4)_(5:3)_(2:6)_(4:4aCO)_(4:4bCO)
473	OMT10	OMT	16	19545	19582	20186	20220	1		605	640	674	0	4	1	NA	NA	2:6_3:5_2:6_3:5_2:6_3:5_4:4_3:5_4:4_3:5
138	OMT2	OMT	12	743917	744124	744124	744207	1		1	145	289	1	1	1	0	1	05:03
65	OMT2	OMT	5	15698	15888	15940	15966	1		53	160	267	1	1	1	0	1	05:03
144	OMT2	OMT	12	1056569	1056760	1056760	1056900	1		1	166	330	1	1	1	0	1	05:03
46	OMT2	OMT	4	936189	936221	936290	936485	1		70	183	295	1	1	1	0	1	05:03
189	OMT2	OMT	16	169696	169911	169911	170076	1		1	190	379	1	1	1	0	1	05:03
190	OMT2	OMT	16	213190	213534	213534	213597	1		1	204	406	1	1	1	0	1	05:03
105	OMT2	OMT	8	337281	337596	337596	337894	1		1	307	612	1	1	1	0	1	05:03
163	OMT2	OMT	14	122717	123158	123158	123338	1		1	311	620	1	1	1	0	1	05:03
71	OMT2	OMT	5	325661	325958	326031	326225	1		74	319	563	1	1	1	0	1	05:03
60	OMT2	OMT	4	1416976	1417050	1417050	1417646	1		1	335	669	1	1	1	0	1	05:03
26	OMT2	OMT	4	199393	200025	200025	200151	1		1	379	757	1	1	1	0	1	05:03
88	OMT2	OMT	7	397325	397929	397971	398049	1		43	383	723	1	1	1	0	1	05:03
67	OMT2	OMT	5	132767	133007	133078	133491	1		72	398	723	1	1	1	0	1	05:03
120	OMT2	OMT	10	523373	523995	523995	524341	1		1	484	967	1	1	1	0	1	05:03
125	OMT2	OMT	11	216046	216382	216709	216788	1		328	535	741	1	1	1	0	1	05:03
43	OMT2	OMT	4	841276	842028	842070	842326	1		43	546	1049	1	1	1	0	1	05:03
99	OMT2	OMT	8	67629	68025	68352	68508	1		328	603	878	1	1	1	0	1	05:03
40	OMT2	OMT	4	792642	793089	793254	793726	1		166	625	1083	1	1	1	0	1	05:03
28	OMT2	OMT	4	258755	258793	259198	259676	1		406	663	920	1	1	1	0	1	05:03
41	OMT2	OMT	4	806528	806564	807222	807409	1		659	770	880	1	1	1	0	1	05:03

134	OMT2	OMT	12	325937	326213	326981	327112	1	769	972	1174	1	1	1	0	1	05:03
63	OMT2	OMT	4	1488904	1489717	1490249	1490604	1	533	1116	1699	1	1	1	0	1	05:03
159	OMT2	OMT	13	897645	897755	899239	899812	1	1485	1826	2166	1	1	1	0	1	05:03
6	OMT2	OMT	2	50893	59500	59525	60420	1	26	4776	9526	1	1	1	0	1	05:03
95	OMT2	OMT	7	823555	823607	823734	823786	1	128	179	230	1	2	1	0	1	03:05
16	OMT2	OMT	2	527865	528054	528108	528212	1	55	201	346	1	2	1	0	1	03:05
152	OMT2	OMT	13	675294	675387	675387	675697	1	1	202	402	1	2	1	0	1	03:05
45	OMT2	OMT	4	911343	911454	911454	911813	1	1	235	469	1	2	1	0	1	03:05
79	OMT2	OMT	6	205970	206097	206097	206474	1	1	252	503	1	2	1	0	1	03:05
89	OMT2	OMT	7	412279	412400	412413	412771	1	14	253	491	1	2	1	0	1	03:05
173	OMT2	OMT	14	625861	626122	626122	626480	1	1	310	618	1	2	1	0	1	03:05
75	OMT2	OMT	5	536075	536455	536455	536698	1	1	312	622	1	2	1	0	1	03:05
38	OMT2	OMT	4	701739	702278	702278	702480	1	1	371	740	1	2	1	0	1	03:05
80	OMT2	OMT	6	207790	207823	208165	208303	1	343	428	512	1	2	1	0	1	03:05
37	OMT2	OMT	4	693728	693982	694241	694457	1	260	494	728	1	2	1	0	1	03:05
9	OMT2	OMT	2	191242	191470	191613	192398	1	144	650	1155	1	2	1	0	1	03:05
22	OMT2	OMT	3	146860	146949	147587	147882	1	639	830	1021	1	2	1	0	1	03:05
139	OMT2	OMT	12	776373	777814	777868	778158	1	55	920	1784	1	2	1	0	1	03:05
84	OMT2	OMT	7	271853	272144	272568	273422	1	425	997	1568	1	2	1	0	1	03:05
36	OMT2	OMT	4	587057	588381	588711	589440	1	331	1357	2382	1	2	1	0	1	03:05
102	OMT2	OMT	8	143727	143824	145105	145255	1	1282	1405	1527	1	2	1	0	1	03:05
110	OMT2	OMT	9	96388	96801	96885	96924	1	85	310	535	1	3	1	0	1	5:3_6:2_5:3
167	OMT2	OMT	14	318393	318591	318845	319024	1	255	443	630	1	3	1	0	1	5:3_6:2_5:3
109	OMT2	OMT	8	516318	516468	517036	517336	1	569	793	1017	1	3	1	0	1	5:3_6:2_5:3
7	OMT2	OMT	2	71569	71621	72420	73226	1	800	1228	1656	1	3	1	0	1	5:3_6:2_5:3
142	OMT2	OMT	12	954173	954521	955099	955168	1	579	787	994	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
197	OMT2	OMT	16	525636	525655	528017	528301	1	2363	2514	2664	1	3	1	0	1	5:3_4:4_5:3_6:2_5:3
150	OMT2	OMT	13	464785	464976	465931	466308	1	956	1239	1522	1	4	1	0	1	3:5_4:4_3:5
52	OMT2	OMT	4	1258442	1258657	1260078	1260779	1	1422	1879	2336	1	4	1	0	1	3:5_2:6_3:5
177	OMT2	OMT	15	230614	230706	232710	232797	1	2005	2094	2182	1	4	1	0	1	3:5_2:6_3:5_4:4_2:6_3:5
86	OMT2	OMT	7	309604	310446	310906	311141	1	461	999	1536	1	7	1	0	1	6:2_5:3
185	OMT2	OMT	15	1043807	1044044	1046807	1047359	1	2764	3158	3551	1	7	1	0	1	6:2_5:3
171	OMT2	OMT	14	539950	542443	546371	547464	1	3929	5721	7513	1	7	1	0	1	6:2_5:3
166	OMT2	OMT	14	267621	268398	270187	270523	1	1790	2346	2901	1	7	1	0	1	5:3_4:4_6:2
59	OMT2	OMT	4	1409468	1409615	1412047	1412326	1	2433	2645	2857	1	7	1	0	1	5:3_4:4_5:3_6:2
56	OMT2	OMT	4	1318539	1318597	1322553	1323143	1	3957	4280	4603	1	7	1	0	1	6:2_5:3_4:4_5:3
50	OMT2	OMT	4	1153966	1161539	1166609	1166645	1	5071	8875	12678	1	7	1	0	1	5:3_6:2_5:3_6:2
98	OMT2	OMT	8	16362	16671	17151	17157	1	481	638	794	1	8	1	0	1	3:5_2:6
181	OMT2	OMT	15	601325	601569	602638	603166	1	1070	1455	1840	1	8	1	0	1	3:5_2:6
148	OMT2	OMT	13	386530	386785	388416	388450	1	1632	1776	1919	1	8	1	0	1	3:5_2:6
77	OMT2	OMT	6	95746	95849	97636	97737	1	1788	1889	1990	1	8	1	0	1	3:5_2:6
117	OMT2	OMT	10	244325	244400	246451	246591	1	2052	2159	2265	1	8	1	0	1	3:5_2:6
195	OMT2	OMT	16	492354	493222	495265	495414	1	2044	2552	3059	1	8	1	0	1	2:6_3:5_2:6_3:5
1	OMT2	OMT	1	29354	29374	29996	30051	1	623	660	696	1	8	1	0	1	3:5_2:6_4:4_3:5_2:6
198	OMT2	OMT	16	536429	536720	536720	536802	1	1	187	372	1	10	1	0	1	06:02
108	OMT2	OMT	8	498868	499032	499040	499430	1	9	285	561	1	10.1	1	0	1	02:06
11	OMT2	OMT	2	356462	356648	356805	357199	1	158	447	736	1	10.1	1	0	1	02:06
199	OMT2	OMT	16	629722	630417	631326	631631	1	910	1409	1908	1	10.1	1	0	1	02:06
12	OMT2	OMT	2	359006	359116	362183	362354	1	3068	3208	3347	1	10.1	1	0	1	02:06
42	OMT2	OMT	4	812580	813568	816853	817682	1	3286	4194	5101	1	10.1	1	0	1	02:06
158	OMT2	OMT	13	873141	873246	875463	875718	1	2218	2397	2576	2	11	1	0	1	5:3_5:3a
17	OMT2	OMT	2	539483	539810	539825	540265	1	16	399	781	2	12	1	0	1	3:5_3:5a
193	OMT2	OMT	16	381121	381280	381960	382120	1	681	840	998	2	12	1	0	1	3:5_3:5a
18	OMT2	OMT	2	632170	632896	633960	635127	1	1065	2011	2956	2	12	1	0	1	3:5_3:5a
33	OMT2	OMT	4	403347	403449	406385	406667	1	2937	3128	3319	2	12	1	0	1	3:5_3:5a
160	OMT2	OMT	14	29547	30923	32426	34396	1	1504	3176	4848	2	12	1	0	1	3:5_3:5a
191	OMT2	OMT	16	308420	308669	311060	311427	1	2392	2699	3006	2	13	1	0	1	5:3_4:4_5:3_5:3a_4:4_5:3a
47	OMT2	OMT	4	953693	953912	955643	955755	1	1732	1897	2061	2	15	1	0	1	5:3_4:4_5:3a
113	OMT2	OMT	9	228903	229515	231138	232195	1	1624	2458	3291	2	15	1	0	1	5:3_4:4_5:3a
154	OMT2	OMT	13	742214	742337	745005	745236	1	2669	2845	3021	2	15	1	0	1	5:3_4:4_5:3a

184	OMT2	OMT	15	1037757	1038438	1039786	1039824		1	1349	1708	2066	2	16	1	0	1	3:5_4:4_3:5a
83	OMT2	OMT	7	197230	197465	201093	201499		1	3629	3949	4268	2	20	1	0	1	3:5_2:6_3:5a
103	OMT2	OMT	8	229106	229427	232747	233140		1	3321	3677	4033	2	23	1	0	1	2:6_3:5_2:6_4:4_3:5a
203	OMT2	OMT	16	919303	919423	923175	923621	2_nonsis		3753	4035	4317	3	30	1	0	1	2:6_3:5_4:4_3:5a_4:4_3:5a_2:6_3:5a_6:2_5:3_6:2_5:3_4:4_5:3
14	OMT2	OMT	2	434210	434430	436905	437154	2_nonsis		2476	2710	2943	3	31	1	0	1	4:4ai_5:3_4:4_5:3a
3	OMT2	OMT	1	112136	113132	115665	116327	2_nonsis		2534	3362	4190	3	31	1	0	1	3:5_4:4ai_3:5a_4:4ai
124	OMT2	OMT	11	211030	211408	211676	211843	2_nonsis		269	541	812	1	1	1	1	0	(5:3)_(4:4aCO)
53	OMT2	OMT	4	1268439	1268647	1268647	1269918	2_nonsis		1	740	1478	1	1	1	1	0	(5:3)_(4:4aCO)
27	OMT2	OMT	4	217557	218010	219340	221090	2_nonsis		1331	2432	3532	1	1	1	1	0	(5:3)_(4:4aCO)
97	OMT2	OMT	7	974457	974639	974639	974684	2_nonsis		1	114	226	1	2	1	1	0	(3:5)_(4:4aCO)
162	OMT2	OMT	14	116131	116459	116459	116676	2_nonsis		1	273	544	1	2	1	1	0	(3:5)_(4:4aCO)
143	OMT2	OMT	12	1027717	1028133	1028133	1028477	2_nonsis		1	380	759	1	2	1	1	0	(3:5)_(4:4aCO)
172	OMT2	OMT	14	605054	606035	606111	606283	2_nonsis		77	653	1228	1	2	1	1	0	(3:5)_(4:4aCO)
78	OMT2	OMT	6	129391	130480	130480	131200	2_nonsis		1	905	1808	1	2	1	1	0	(3:5)_(4:4aCO)
123	OMT2	OMT	11	53005	53905	53905	54957	2_nonsis		1	976	1951	1	2	1	1	0	(3:5)_(4:4aCO)
32	OMT2	OMT	4	375826	376661	377176	377306	2_nonsis		516	998	1479	1	2	1	1	0	(3:5)_(4:4aCO)
196	OMT2	OMT	16	520404	520684	521328	521940	2_nonsis		645	1090	1535	1	2	1	1	0	(3:5)_(4:4aCO)
96	OMT2	OMT	7	825444	825852	826641	826948	2_nonsis		790	1147	1503	1	2	1	1	0	(3:5)_(4:4aCO)
51	OMT2	OMT	4	1175004	1176543	1176920	1176974	2_nonsis		378	1174	1969	1	2	1	1	0	(3:5)_(4:4aCO)
58	OMT2	OMT	4	1380649	1381111	1381111	1383527	2_nonsis		1	1439	2877	1	2	1	1	0	(3:5)_(4:4aCO)
176	OMT2	OMT	15	196577	196695	196803	197183	2_nonsis		109	357	605	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
92	OMT2	OMT	7	592334	592660	594021	594391	2_nonsis		1362	1709	2056	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
164	OMT2	OMT	14	153222	153782	154853	155065	2_nonsis		1072	1457	1842	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
54	OMT2	OMT	4	1279680	1279875	1280622	1281921	2_nonsis		748	1494	2240	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
157	OMT2	OMT	13	860181	861184	864551	864888	2_nonsis		3368	4037	4706	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
61	OMT2	OMT	4	1452483	1452723	1455942	1458372	2_nonsis		3220	4554	5888	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
130	OMT2	OMT	12	29781	30008	30375	30558	2_nonsis		368	572	776	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
19	OMT2	OMT	2	641914	642165	642483	642776	2_nonsis		319	590	861	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
21	OMT2	OMT	3	136789	137021	137490	138018	2_nonsis		470	849	1228	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
200	OMT2	OMT	16	644568	644801	645942	646173	2_nonsis		1142	1373	1604	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
161	OMT2	OMT	14	86730	87215	89959	89998	2_nonsis		2745	3006	3267	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
73	OMT2	OMT	5	456087	456116	456801	456960	2_nonsis		686	779	872	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
192	OMT2	OMT	16	371914	372742	372742	373291	2_nonsis		1	689	1376	1	11	1	1	0	(4:4ai)_(4:4bCO)
155	OMT2	OMT	13	759081	759285	759679	759844	2_nonsis		395	579	762	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
20	OMT2	OMT	3	71310	71391	72034	72190	2_nonsis		644	762	879	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
68	OMT2	OMT	5	173645	173948	174794	175080	2_nonsis		847	1141	1434	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4aCO)
182	OMT2	OMT	15	738026	738211	739494	739749	2_nonsis		1284	1503	1722	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
90	OMT2	OMT	7	463843	464170	465028	466029	2_nonsis		859	1522	2185	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(4:4aCO)
81	OMT2	OMT	6	226919	227043	228617	229028	2_nonsis		1575	1842	2108	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
151	OMT2	OMT	13	494582	494666	495559	496159	2_nonsis		894	1235	1576	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4)_(4:4aCO)
126	OMT2	OMT	11	309188	309294	309310	309621	2_nonsis		17	225	432	1	15	1	1	0	(6:2)_(4:4aCO)
202	OMT2	OMT	16	883117	883214	883313	883526	2_nonsis		100	254	408	1	15	1	1	0	(6:2)_(4:4aCO)
175	OMT2	OMT	15	40497	40570	40593	41027	2_nonsis		24	277	529	1	15	1	1	0	(6:2)_(4:4aCO)
115	OMT2	OMT	10	50434	50613	50613	51007	2_nonsis		1	287	572	1	15	1	1	0	(6:2)_(4:4aCO)
149	OMT2	OMT	13	409894	410079	410172	410428	2_nonsis		94	314	533	1	15	1	1	0	(6:2)_(4:4aCO)
129	OMT2	OMT	11	578230	578669	578824	578904	2_nonsis		156	415	673	1	15	1	1	0	(6:2)_(4:4aCO)
2	OMT2	OMT	1	56786	57455	57455	57739	2_nonsis		1	477	952	1	15	1	1	0	(6:2)_(4:4aCO)
165	OMT2	OMT	14	209155	210033	210033	210155	2_nonsis		1	500	999	1	15	1	1	0	(6:2)_(4:4aCO)
69	OMT2	OMT	5	225841	226347	226500	226861	2_nonsis		154	587	1019	1	15	1	1	0	(6:2)_(4:4aCO)
57	OMT2	OMT	4	1349944	1350135	1350135	1351399	2_nonsis		1	728	1454	1	15	1	1	0	(6:2)_(4:4aCO)
24	OMT2	OMT	4	61275	62061	62366	62726	2_nonsis		306	878	1450	1	15	1	1	0	(6:2)_(4:4aCO)
169	OMT2	OMT	14	478186	479345	479609	479875	2_nonsis		265	977	1688	1	15	1	1	0	(6:2)_(4:4aCO)
66	OMT2	OMT	5	103937	104269	105345	105369	2_nonsis		1077	1254	1431	1	15	1	1	0	(6:2)_(4:4aCO)
104	OMT2	OMT	8	283683	283957	284440	285871	2_nonsis		484	1336	2187	1	15	1	1	0	(6:2)_(4:4aCO)
15	OMT2	OMT	2	487781	489580	489580	490532	2_nonsis		1	1376	2750	1	15	1	1	0	(6:2)_(4:4aCO)
132	OMT2	OMT	12	114144	114242	114242	114659	2_nonsis		1	258	514	1	16	1	1	0	(2:6)_(4:4aCO)
147	OMT2	OMT	13	195330	195572	195572	195860	2_nonsis		1	265	529	1	16	1	1	0	(2:6)_(4:4aCO)
39	OMT2	OMT	4	765017	765331	765398	765553	2_nonsis		68	302	535	1	16	1	1	0	(2:6)_(4:4aCO)
153	OMT2	OMT	13	720681	720893	721068	721309	2_nonsis		176	402	627	1	16	1	1	0	(2:6)_(4:4aCO)
180	OMT2	OMT	15	585323	585644	586076	586304	2_nonsis		433	707	980	1	16	1	1	0	(2:6)_(4:4aCO)

35	OMT2	OMT	4	539680	540228	540514	540965	2_nonsis		287	786	1284	1	16	1	1	0 (2:6)_(4:4aCO)
87	OMT2	OMT	7	346985	347223	347682	348496	2_nonsis		460	985	1510	1	16	1	1	0 (2:6)_(4:4aCO)
118	OMT2	OMT	10	394217	394408	394217	394408	2_nonsis		0	95	190	1	100	1	1	0 (4:4aCO)
116	OMT2	OMT	10	85363	85607	85363	85607	2_nonsis		0	122	243	1	100	1	1	0 (4:4aCO)
74	OMT2	OMT	5	491556	491806	491556	491806	2_nonsis		0	125	249	1	100	1	1	0 (4:4aCO)
121	OMT2	OMT	10	579770	580075	579770	580075	2_nonsis		0	152	304	1	100	1	1	0 (4:4aCO)
85	OMT2	OMT	7	288130	288473	288130	288473	2_nonsis		0	171	342	1	100	1	1	0 (4:4aCO)
49	OMT2	OMT	4	1088958	1089304	1088958	1089304	2_nonsis		0	173	345	1	100	1	1	0 (4:4aCO)
112	OMT2	OMT	9	176578	177082	176578	177082	2_nonsis		0	252	503	1	100	1	1	0 (4:4aCO)
94	OMT2	OMT	7	785318	785828	785318	785828	2_nonsis		0	255	509	1	100	1	1	0 (4:4aCO)
106	OMT2	OMT	8	365442	365964	365442	365964	2_nonsis		0	261	521	1	100	1	1	0 (4:4aCO)
128	OMT2	OMT	11	463071	463630	463071	463630	2_nonsis		0	279	558	1	100	1	1	0 (4:4aCO)
168	OMT2	OMT	14	382124	382693	382124	382693	2_nonsis		0	284	568	1	100	1	1	0 (4:4aCO)
174	OMT2	OMT	14	705870	706528	705870	706528	2_nonsis		0	329	657	1	100	1	1	0 (4:4aCO)
8	OMT2	OMT	2	124959	125762	124959	125762	2_nonsis		0	401	802	1	100	1	1	0 (4:4aCO)
179	OMT2	OMT	15	477802	478649	477802	478649	2_nonsis		0	423	846	1	100	1	1	0 (4:4aCO)
70	OMT2	OMT	5	310175	311096	310175	311096	2_nonsis		0	460	920	1	100	1	1	0 (4:4aCO)
146	OMT2	OMT	13	70356	71382	70356	71382	2_nonsis		0	513	1025	1	100	1	1	0 (4:4aCO)
48	OMT2	OMT	4	1000380	1001608	1000380	1001608	2_nonsis		0	614	1227	1	100	1	1	0 (4:4aCO)
93	OMT2	OMT	7	677169	678405	677169	678405	2_nonsis		0	618	1235	1	100	1	1	0 (4:4aCO)
82	OMT2	OMT	7	81435	82858	81435	82858	2_nonsis		0	711	1422	1	100	1	1	0 (4:4aCO)
76	OMT2	OMT	6	48712	50410	48712	50410	2_nonsis		0	849	1697	1	100	1	1	0 (4:4aCO)
5	OMT2	OMT	1	190880	192723	190880	192723	2_nonsis		0	921	1842	1	100	1	1	0 (4:4aCO)
119	OMT2	OMT	10	467589	469453	467589	469453	2_nonsis		0	932	1863	1	100	1	1	0 (4:4aCO)
140	OMT2	OMT	12	795275	798382	795275	798382	2_nonsis		0	1553	3106	1	100	1	1	0 (4:4aCO)
194	OMT2	OMT	16	400838	404554	400838	404554	2_nonsis		0	1858	3715	1	100	1	1	0 (4:4aCO)
145	OMT2	OMT	13	44503	48814	44503	48814	2_nonsis		0	2155	4310	1	100	1	1	0 (4:4aCO)
141	OMT2	OMT	12	892436	930472	892436	930472	2_nonsis		0	19018	38035	1	100	1	1	0 (4:4aCO)
30	OMT2	OMT	4	310698	312431	313644	313728	2_nonsis		1214	2122	3029	2	30	1	1	0 (5:3)_(4:4aCO)_(5:3)_(5:3a)_(4:4a)
44	OMT2	OMT	4	843869	843908	845628	845959	2_nonsis		1721	1905	2089	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)_(4:4bi)_(5:3a)_(4:4a)
62	OMT2	OMT	4	1476514	1476956	1479150	1479318	2_nonsis		2195	2499	2803	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
10	OMT2	OMT	2	258153	258313	258617	259158	2_nonsis		305	655	1004	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
170	OMT2	OMT	14	492521	492836	494368	494731	2_nonsis		1533	1871	2209	2	32	1	1	0 (3:5)_(4:4aCO)_(3:5a)_(4:4a)
4	OMT2	OMT	1	137336	138499	139277	141984	2_nonsis		779	2713	4647	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
186	OMT2	OMT	15	1058801	1058868	1060419	1060435	2_nonsis		1552	1593	1633	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(4:4)_(3:5a)_(2:6)_(3:5b)_(4:4aCO)
178	OMT2	OMT	15	265983	266696	268100	268222	2_nonsis		1405	1822	2238	2	32	1	1	0 (2:6)_(3:5)_(4:4aCO)_(2:6)_(4:4a)_(3:5a)_(4:4a)_(3:5)_(4:4a)
137	OMT2	OMT	12	602186	602338	602685	603057	2_nonsis		348	609	870	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
131	OMT2	OMT	12	97572	97654	98655	99028	2_nonsis		1002	1229	1455	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
31	OMT2	OMT	4	334709	334761	334954	335332	2_nonsis		194	408	622	3	20	1	1	0 (6:2)_(4:4)_(2:6)_(4:4aCO)
29	OMT2	OMT	4	271809	272060	272385	273003	2_nonsis		326	760	1193	3	20	1	1	0 (5:3)_(4:4)_(2:6)_(4:4aCO)
55	OMT2	OMT	4	1288090	1288209	1289394	1289490	2_nonsis		1186	1293	1399	3	20	1	1	0 (5:3)_(4:4)_(3:5)_(4:4aCO)
114	OMT2	OMT	9	338225	338465	340356	340507	2_nonsis		1892	2087	2281	3	20	1	1	0 (5:3)_(6:2)_(3:5)_(4:4aCO)
136	OMT2	OMT	12	533245	533365	536152	536245	2_nonsis		2788	2894	2999	3	20	1	1	0 (3:5)_(2:6)_(5:3)_(4:4aCO)
187	OMT2	OMT	16	46273	46282	47208	47273	2_nonsis		927	963	999	3	20	1	1	0 (3:5)_(2:6)_(3:5)_(5:3)_(4:4aCO)
127	OMT2	OMT	11	339536	340007	341413	341641	2_nonsis		1407	1756	2104	3	20	1	1	0 (3:5)_(2:6)_(5:3)_(4:4aCO)
13	OMT2	OMT	2	392522	392544	394376	394430	2_nonsis		1833	1870	1907	3	20	1	1	0 (3:5)_(2:6)_(4:4aCO)_(5:3)_(4:4a)
34	OMT2	OMT	4	408894	410728	412574	413313	2_nonsis		1847	3133	4418	3	20	1	1	0 (6:2)_(4:4)_(6:2)_(3:5)_(4:4aCO)
201	OMT2	OMT	16	804145	810641	812990	813147	2_nonsis		2350	5676	9001	3	20	1	1	0 (5:3)_(4:4)_(4:4aCO)_(3:5)_(4:4a)
107	OMT2	OMT	8	433873	434369	436695	436939	2_nonsis		2327	2696	3065	3	20	1	1	0 (3:5)_(4:4)_(6:2)_(5:3)_(6:2)_(4:4aCO)
111	OMT2	OMT	9	141332	141469	143302	143414	2_nonsis		1834	1958	2081	3	20	1	1	0 (3:5)_(2:6)_(5:3)_(4:4aCO)_(5:3)_(6:2)_(5:3)_(4:4a)
64	OMT2	OMT	5	11741	11756	14073	14175	2_nonsis		2318	2376	2433	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
183	OMT2	OMT	15	801084	801285	804884	805025	2_nonsis		3600	3770	3940	3	20	1	1	0 (5:3)_(5:3a)_(4:4)_(5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)
133	OMT2	OMT	12	208797	209042	212823	212873	2_nonsis		3782	3929	4075	3	20	1	1	0 (5:3)_(4:4)_(5:3)_(4:4)_(2:6)_(4:4aCO)_(3:5)_(4:4a)
188	OMT2	OMT	16	127009	127901	131951	132681	2_nonsis		4051	4861	5671	3	20	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)_(5:3)_(4:4a)_(6:2)_(4:4a)
100	OMT2	OMT	8	76095	76580	77625	78204	2_nonsis		1046	1577	2108	3	21	1	1	0 (5:3)_(4:4ai)_(2:6)_(3:5)_(4:4bCO)
156	OMT2	OMT	13	849562	850650	853802	854292	2_nonsis		3153	3941	4729	3	21	1	1	0 (5:3)_(4:4ai)_(3:5)_(2:6)_(3:5)_(4:4bCO)
23	OMT2	OMT	3	218655	218906	223676	224009		3	4771	5062	5353	0	2	2	1	1 (3:5)_(2:6)_(4:4)_(2:6)_(5:3)_(5:3a)_(4:4aCO)
25	OMT2	OMT	4	132259	132560	134836	135705		3	2277	2861	3445	0	2	2	1	1 (3:5)_(2:6)_(4:4ai)_(4:4bi)_(4:4cCO)
72	OMT2	OMT	5	334460	334676	335567	336936		3	892	1684	2475	0	2	2	1	1 (5:3)_(6:2)_(1:7)_(4:4aCO)
91	OMT2	OMT	7	575122	575955	576556	576979		3	602	1229	1856	0	2	2	1	1 (2:6i)_(4:4)_(4:4aCO)

122	OMT2	OMT	10	661626	663261	663948	664824	4	688	1943	3197	0	2	2	2	0	(1:7)_(2:6i)_(4:4aCO)
135	OMT2	OMT	12	341070	341507	341974	342190	3	468	794	1119	0	2	2	1	1	(2:6)_(4:4aCO)_(3:5)_(4:4a)
101	OMT2	OMT	8	96393	97160	99909	101246	2_nonsis	2750	3801	4852	0	3	2	1	1	(3:5)_(2:6)_(3:5)_(5:3)_(4:4ai)_(4:4bCO)_(4:4ai)_(3:5a)_(4:4CO)
223	OMT2	OMT	2	798886	799021	801020	813184	1	0	7149	14297	0	4	1	NA	NA	
364	OMT2	OMT	14	17935	18306	18838	19210	2_nonsis	533	904	1274	0	4	1	NA	NA	05:03
179	OMT3	OMT	15	832222	832326	832326	832546	1	1	162	323	1	1	1	0	1	05:03
28	OMT3	OMT	4	234361	234547	234547	234711	1	1	175	349	1	1	1	0	1	05:03
85	OMT3	OMT	8	319436	319609	319609	319904	1	1	234	467	1	1	1	0	1	05:03
197	OMT3	OMT	16	921352	921490	921490	921845	1	1	247	492	1	1	1	0	1	05:03
126	OMT3	OMT	12	553728	554116	554168	554190	1	53	257	461	1	1	1	0	1	05:03
33	OMT3	OMT	4	569606	569971	569971	570356	1	1	375	749	1	1	1	0	1	05:03
48	OMT3	OMT	4	1453865	1454543	1454543	1454648	1	1	392	782	1	1	1	0	1	05:03
94	OMT3	OMT	9	332503	333073	333081	333345	1	9	425	841	1	1	1	0	1	05:03
99	OMT3	OMT	10	195349	195849	195964	196239	1	116	503	889	1	1	1	0	1	05:03
131	OMT3	OMT	12	778158	779222	779222	779322	1	1	582	1163	1	1	1	0	1	05:03
170	OMT3	OMT	15	272726	273137	273461	273775	1	325	687	1048	1	1	1	0	1	05:03
57	OMT3	OMT	5	358357	359292	359292	360247	1	1	945	1889	1	1	1	0	1	05:03
39	OMT3	OMT	4	1000380	1001608	1001916	1002119	1	309	1024	1738	1	1	1	0	1	05:03
64	OMT3	OMT	6	211974	212097	212940	213216	1	844	1043	1241	1	1	1	0	1	05:03
192	OMT3	OMT	16	664567	664678	665441	665970	1	764	1083	1402	1	1	1	0	1	05:03
37	OMT3	OMT	4	921620	922016	922979	923047	1	964	1195	1426	1	1	1	0	1	05:03
185	OMT3	OMT	16	187323	187324	187324	187327	1	1	2	3	1	2	1	0	1	03:05
66	OMT3	OMT	7	23450	23509	23516	23602	1	8	80	151	1	2	1	0	1	03:05
175	OMT3	OMT	15	494556	494573	494573	494732	1	1	88	175	1	2	1	0	1	03:05
134	OMT3	OMT	12	1019126	1019156	1019199	1019284	1	44	101	157	1	2	1	0	1	03:05
113	OMT3	OMT	11	365937	366156	366174	366213	1	19	147	275	1	2	1	0	1	03:05
41	OMT3	OMT	4	1105249	1105534	1105534	1105561	1	1	156	311	1	2	1	0	1	03:05
6	OMT3	OMT	2	63891	64139	64139	64291	1	1	200	399	1	2	1	0	1	03:05
165	OMT3	OMT	14	724364	724486	724600	724671	1	115	211	306	1	2	1	0	1	03:05
96	OMT3	OMT	9	406436	406590	406596	406941	1	7	256	504	1	2	1	0	1	03:05
143	OMT3	OMT	13	460662	460753	460753	461207	1	1	273	544	1	2	1	0	1	03:05
91	OMT3	OMT	9	177586	177853	177853	178160	1	1	287	573	1	2	1	0	1	03:05
128	OMT3	OMT	12	711045	711067	711354	711432	1	288	337	386	1	2	1	0	1	03:05
19	OMT3	OMT	3	60997	61457	61457	61855	1	1	429	857	1	2	1	0	1	03:05
29	OMT3	OMT	4	362993	363511	363511	363860	1	1	434	866	1	2	1	0	1	03:05
1	OMT3	OMT	1	67801	68551	68621	68725	1	71	497	923	1	2	1	0	1	03:05
183	OMT3	OMT	15	1035181	1035608	1035815	1036058	1	208	542	876	1	2	1	0	1	03:05
55	OMT3	OMT	5	225229	225841	225841	226347	1	1	559	1117	1	2	1	0	1	03:05
74	OMT3	OMT	7	756484	756717	757121	757231	1	405	576	746	1	2	1	0	1	03:05
176	OMT3	OMT	15	511466	511476	511738	512726	1	263	761	1259	1	2	1	0	1	03:05
145	OMT3	OMT	13	576343	577768	577768	577948	1	1	803	1604	1	2	1	0	1	03:05
49	OMT3	OMT	4	1476168	1476261	1476956	1477116	1	696	822	947	1	2	1	0	1	03:05
100	OMT3	OMT	10	207695	208362	208641	209220	1	280	902	1524	1	2	1	0	1	03:05
157	OMT3	OMT	14	391752	392860	392860	393703	1	1	976	1950	1	2	1	0	1	03:05
35	OMT3	OMT	4	630640	631576	631885	632423	1	310	1046	1782	1	2	1	0	1	03:05
136	OMT3	OMT	13	41174	42127	42127	43336	1	1	1081	2161	1	2	1	0	1	03:05
167	OMT3	OMT	15	127669	128123	128730	129347	1	608	1143	1677	1	2	1	0	1	03:05
112	OMT3	OMT	11	363248	363372	364489	364596	1	1118	1233	1347	1	2	1	0	1	03:05
187	OMT3	OMT	16	214281	214333	214724	214866	1	392	488	584	1	3	1	0	1	5:3_4:4_5:3
31	OMT3	OMT	4	390756	391128	391712	392799	1	585	1314	2042	1	3	1	0	1	5:3_6:2_5:3
83	OMT3	OMT	8	227227	227323	228507	228696	1	1185	1327	1468	1	3	1	0	1	5:3_6:2_5:3
118	OMT3	OMT	12	36792	36833	38338	38565	1	1506	1639	1772	1	3	1	0	1	5:3_6:2_5:3
72	OMT3	OMT	7	626794	626892	626947	627440	1	56	351	645	1	4	1	0	1	3:5_4:4_3:5
142	OMT3	OMT	13	458051	458330	458513	459192	1	184	662	1140	1	4	1	0	1	3:5_4:4_3:5
182	OMT3	OMT	15	978665	978755	979457	979485	1	703	761	819	1	4	1	1	1	3:5_4:4_3:5
161	OMT3	OMT	14	577136	579044	579121	579520	1	78	1231	2383	1	4	1	0	1	3:5_2:6_3:5
88	OMT3	OMT	8	496531	496975	497336	497380	1	362	605	848	1	7	1	0	1	5:3_6:2
188	OMT3	OMT	16	245496	245843	246962	247112	1	1120	1368	1615	1	7	1	0	1	5:3_4:4_6:2
180	OMT3	OMT	15	942759	943167	944039	944698	1	873	1406	1938	1	7	1	0	1	6:2_4:4_5:3
117	OMT3	OMT	11	526649	526688	527413	527423	1	726	750	773	1	8	1	0	1	2:6_3:5

45	OMT3	OMT	4	1338669	1339080	1341826	1342306	1	2747	3192	3636	1	8	1	0	1	3:5_2:6
34	OMT3	OMT	4	617153	617276	617421	617533	1	146	263	379	1	10	1	0	1	06:02
138	OMT3	OMT	13	169522	169808	169808	169962	1	1	220	439	1	10.1	1	0	1	02:06
84	OMT3	OMT	8	236227	236251	236251	237146	1	1	460	918	1	10.1	1	0	1	02:06
15	OMT3	OMT	2	620548	621285	621285	621546	1	1	499	997	1	10.1	1	0	1	02:06
103	OMT3	OMT	10	568805	570822	570822	573135	1	1	2165	4329	1	10.1	1	0	1	02:06
158	OMT3	OMT	14	427295	427451	427715	428693	1	265	831	1397	2	11	1	0	1	5:3_5:3a
54	OMT3	OMT	5	211420	211559	212585	212818	1	1027	1212	1397	2	11	1	0	1	5:3_5:3a
11	OMT3	OMT	2	350378	350451	352907	353413	1	2457	2746	3034	2	11	1	0	1	5:3_5:3a
75	OMT3	OMT	7	797674	797989	798400	798821	1	412	779	1146	2	12	1	0	1	3:5_3:5a
109	OMT3	OMT	11	201271	201376	202339	202593	1	964	1143	1321	2	12	1	0	1	3:5_3:5a
194	OMT3	OMT	16	703890	704140	705306	705875	1	1167	1576	1984	2	12	1	0	1	3:5_3:5a
68	OMT3	OMT	7	190037	190333	191348	192332	1	1016	1655	2294	2	12	1	0	1	3:5_3:5a
154	OMT3	OMT	14	214918	215120	221010	221673	1	5891	6323	6754	2	13	1	0	1	5:3_5:3a_4:4_5:3a_4:4_5:3a_6:2_5:3a
160	OMT3	OMT	14	537552	537564	538564	538640	1	1001	1044	1087	2	15	1	0	1	5:3_4:4_5:3a
119	OMT3	OMT	12	86087	86291	88362	88422	1	2072	2203	2334	2	15	1	0	1	5:3_4:4_5:3a
189	OMT3	OMT	16	279259	279412	280470	281659	1	1059	1729	2399	2	16	1	0	1	3:5_4:4_3:5a
146	OMT3	OMT	13	667024	667065	669672	670228	1	2608	2906	3203	2	16	1	0	1	3:5_4:4_3:5a
196	OMT3	OMT	16	886812	887016	889543	889589	1	2528	2652	2776	2	17	1	0	1	5:3_4:4_5:3a_6:2_5:3a
181	OMT3	OMT	15	967263	967506	968504	968918	1	999	1327	1654	2	18	1	0	1	3:5_2:6_3:5_4:4_3:5a
7	OMT3	OMT	2	68834	69355	70774	71161	1	1420	1873	2326	2	19	1	0	1	5:3_6:2_5:3a
139	OMT3	OMT	13	208108	208467	209542	209890	1	1076	1429	1781	2	23	1	0	1	3:5_4:4_2:6_3:5a
53	OMT3	OMT	5	56000	56129	56829	57131	2_nonsis	701	916	1130	3	30	1	0	1	5:3_6:2
5	OMT3	OMT	1	187427	189816	190031	190402	2_nonsis	216	1595	2974	3	30	1	0	1	6:2_3:5_5:3
59	OMT3	OMT	5	490700	490942	492341	498773	2_nonsis	1400	4736	8072	3	30	1	0	1	5:3_4:4_3:5_2:6
121	OMT3	OMT	12	247140	247370	249353	249539	2_nonsis	1984	2191	2398	3	30	1	0	1	5:3_2:6_3:5_4:4_3:5a
76	OMT3	OMT	7	805722	806818	809973	810159	2_nonsis	3156	3796	4436	3	30	1	0	1	3:5_4:4_5:3_4:4_6:2
90	OMT3	OMT	9	171281	171632	175368	175738	2_nonsis	3737	4097	4456	3	30	1	0	1	2:6_3:5_2:6_3:5_2:6_3:5_3:5a
147	OMT3	OMT	13	688905	688991	689685	689746	2_nonsis	695	768	840	3	31	1	0	1	2:6_4:4ai_5:3_4:4ai
110	OMT3	OMT	11	284248	284656	289528	289859	2_nonsis	4873	5242	5610	3	31	1	0	1	3:5_4:4_3:5a_4:4ai
173	OMT3	OMT	15	479565	480090	481447	481588	2_nonsis	1358	1690	2022	3	31	1	0	1	3:5_3:5a_4:4ai_3:5a_5:3
12	OMT3	OMT	2	463842	464330	469344	474261	2_nonsis	5015	7717	10418	3	31	1	0	1	4:4ai_3:5_5:3_4:4_5:3_4:4ai_6:2_4:4ai_5:3_4:4ai
82	OMT3	OMT	8	138557	138587	138587	138887	2_nonsis	1	165	329	1	1	1	1	0	(5:3)_(4:4aCO)
101	OMT3	OMT	10	317305	317491	317491	317989	2_nonsis	1	342	683	1	1	1	1	0	(5:3)_(4:4aCO)
166	OMT3	OMT	15	90886	91370	91686	91777	2_nonsis	317	604	890	1	1	1	1	0	(5:3)_(4:4aCO)
191	OMT3	OMT	16	504044	504597	504597	505893	2_nonsis	1	925	1848	1	1	1	1	0	(5:3)_(4:4aCO)
93	OMT3	OMT	9	318469	319670	319670	320609	2_nonsis	1	1070	2139	1	1	1	1	0	(5:3)_(4:4aCO)
168	OMT3	OMT	15	203284	203344	204093	204904	2_nonsis	750	1185	1619	1	1	1	1	0	(5:3)_(4:4aCO)
2	OMT3	OMT	1	71312	71535	72952	73633	2_nonsis	1418	1869	2320	1	1	1	1	0	(5:3)_(4:4aCO)
63	OMT3	OMT	6	107101	107432	107432	107906	2_nonsis	1	403	804	1	2	1	1	0	(3:5)_(4:4aCO)
20	OMT3	OMT	3	77900	78705	78705	78844	2_nonsis	1	472	943	1	2	1	1	0	(3:5)_(4:4aCO)
162	OMT3	OMT	14	652389	652419	652841	653557	2_nonsis	423	795	1167	1	2	1	1	0	(3:5)_(4:4aCO)
98	OMT3	OMT	10	152637	154954	154973	154996	2_nonsis	20	1189	2358	1	2	1	1	0	(3:5)_(4:4aCO)
22	OMT3	OMT	3	226498	228130	228130	230267	2_nonsis	1	1885	3768	1	2	1	1	0	(3:5)_(4:4aCO)
3	OMT3	OMT	1	81604	81691	82379	83613	2_nonsis	689	1349	2008	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
80	OMT3	OMT	8	66569	67460	68532	68854	2_nonsis	1073	1679	2284	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
89	OMT3	OMT	9	40953	41223	41980	42365	2_nonsis	758	1085	1411	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
10	OMT3	OMT	2	340279	340534	341632	341930	2_nonsis	1099	1375	1650	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
56	OMT3	OMT	5	335262	335310	335687	335812	2_nonsis	378	464	549	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
104	OMT3	OMT	10	635321	635444	635710	635986	2_nonsis	267	466	664	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
193	OMT3	OMT	16	677287	677647	677836	678266	2_nonsis	190	584	978	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
108	OMT3	OMT	11	193829	194564	195507	195729	2_nonsis	944	1422	1899	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
137	OMT3	OMT	13	144771	145063	146198	149583	2_nonsis	1136	2974	4811	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
171	OMT3	OMT	15	275073	275191	275230	275863	2_nonsis	40	415	789	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
129	OMT3	OMT	12	745464	745552	746036	746372	2_nonsis	485	696	907	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
8	OMT3	OMT	2	146169	146217	146891	147197	2_nonsis	675	851	1027	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
60	OMT3	OMT	5	551411	551830	553226	553261	2_nonsis	1397	1623	1849	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
195	OMT3	OMT	16	842931	843042	843391	843720	2_nonsis	350	569	788	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
81	OMT3	OMT	8	74727	74846	75188	75639	2_nonsis	343	627	911	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(4:4aCO)
9	OMT3	OMT	2	310088	310328	310706	310972	2_nonsis	379	631	883	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)

79	OMT3	OMT	8	25677	25834	26825	27080	2_nonsis	992	1197	1402	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
116	OMT3	OMT	11	511387	511838	514315	514792	2_nonsis	2478	2941	3404	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
105	OMT3	OMT	10	697206	697486	701326	701478	2_nonsis	3841	4056	4271	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
69	OMT3	OMT	7	389105	389508	390472	390727	2_nonsis	965	1293	1621	1	12	1	1	0	(3:5)_(2:6)_(4:4aCO)_(3:5)_(4:4a)
71	OMT3	OMT	7	616811	617037	618272	618689	2_nonsis	1236	1557	1877	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(3:5)_(4:4aCO)
164	OMT3	OMT	14	694273	694765	694765	694868	2_nonsis	1	298	594	1	15	1	1	0	(6:2)_(4:4aCO)
123	OMT3	OMT	12	388010	388456	388456	388801	2_nonsis	1	396	790	1	15	1	1	0	(6:2)_(4:4aCO)
23	OMT3	OMT	3	289942	290527	290527	290957	2_nonsis	1	508	1014	1	15	1	1	0	(6:2)_(4:4aCO)
115	OMT3	OMT	11	476160	476611	476611	477203	2_nonsis	1	522	1042	1	15	1	1	0	(6:2)_(4:4aCO)
111	OMT3	OMT	11	315983	316401	317104	317375	2_nonsis	704	1048	1391	1	15	1	1	0	(6:2)_(4:4aCO)
186	OMT3	OMT	16	211075	212033	212526	212736	2_nonsis	494	1077	1660	1	15	1	1	0	(6:2)_(4:4aCO)
95	OMT3	OMT	9	385355	385422	385550	385711	2_nonsis	129	242	355	1	16	1	1	0	(2:6)_(4:4aCO)
70	OMT3	OMT	7	457721	457920	457920	458281	2_nonsis	1	280	559	1	16	1	1	0	(2:6)_(4:4aCO)
140	OMT3	OMT	13	221252	221642	221642	222095	2_nonsis	1	422	842	1	16	1	1	0	(2:6)_(4:4aCO)
125	OMT3	OMT	12	525539	525791	525539	525791	2_nonsis	0	126	251	1	100	1	1	0	(4:4aCO)
14	OMT3	OMT	2	568465	568762	568465	568762	2_nonsis	0	148	296	1	100	1	1	0	(4:4aCO)
144	OMT3	OMT	13	543392	543706	543392	543706	2_nonsis	0	157	313	1	100	1	1	0	(4:4aCO)
122	OMT3	OMT	12	319635	319960	319635	319960	2_nonsis	0	162	324	1	100	1	1	0	(4:4aCO)
73	OMT3	OMT	7	702791	703157	702791	703157	2_nonsis	0	183	365	1	100	1	1	0	(4:4aCO)
172	OMT3	OMT	15	413774	414171	413774	414171	2_nonsis	0	198	396	1	100	1	1	0	(4:4aCO)
25	OMT3	OMT	4	87619	88023	87619	88023	2_nonsis	0	202	403	1	100	1	1	0	(4:4aCO)
78	OMT3	OMT	7	1011510	1012069	1011510	1012069	2_nonsis	0	279	558	1	100	1	1	0	(4:4aCO)
27	OMT3	OMT	4	226209	227127	226209	227127	2_nonsis	0	459	917	1	100	1	1	0	(4:4aCO)
92	OMT3	OMT	9	297675	298626	297675	298626	2_nonsis	0	475	950	1	100	1	1	0	(4:4aCO)
159	OMT3	OMT	14	478186	479345	478186	479345	2_nonsis	0	579	1158	1	100	1	1	0	(4:4aCO)
130	OMT3	OMT	12	776373	777814	776373	777814	2_nonsis	0	720	1440	1	100	1	1	0	(4:4aCO)
163	OMT3	OMT	14	686681	688572	686681	688572	2_nonsis	0	945	1890	1	100	1	1	0	(4:4aCO)
135	OMT3	OMT	13	26434	28623	26434	28623	2_nonsis	0	1094	2188	1	100	1	1	0	(4:4aCO)
46	OMT3	OMT	4	1347683	1349666	1352299	1353241	2_nonsis	2634	4096	5557	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(5:3a)_(6:2)_(5:3b)_(4:4aCO)
21	OMT3	OMT	3	162694	163059	163371	163645	2_nonsis	313	632	950	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
50	OMT3	OMT	4	1488106	1488682	1490249	1490604	2_nonsis	1568	2033	2497	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
42	OMT3	OMT	4	1229336	1229391	1231118	1231256	2_nonsis	1728	1824	1919	2	31	1	1	0	(3:5)_(3:5a)_(2:6)_(3:5b)_(4:4aCO)
18	OMT3	OMT	2	773089	773889	778895	779836	2_nonsis	5007	5877	6746	2	31	1	1	0	(3:5)_(4:4)_(5:3)_(3:5a)_(4:4aCO)
44	OMT3	OMT	4	1296525	1297076	1306509	1306661	2_nonsis	9434	9785	10135	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)_(3:5a)_(4:4a)
38	OMT3	OMT	4	958717	959103	960570	960787	2_nonsis	1468	1769	2069	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(4:4aCO)
61	OMT3	OMT	6	40771	40841	42943	43072	2_nonsis	2103	2202	2300	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
43	OMT3	OMT	4	1267989	1268154	1271871	1271941	2_nonsis	3718	3835	3951	2	32	1	1	0	(5:3)_(6:2)_(3:5a)_(4:4aCO)
65	OMT3	OMT	6	224599	224792	226370	226615	2_nonsis	1579	1797	2015	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(4:4)_(4:4aCO)
156	OMT3	OMT	14	355289	355500	358643	358757	2_nonsis	3144	3306	3467	2	32	1	1	0	(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
169	OMT3	OMT	15	210403	210877	212020	212816	2_nonsis	1144	1778	2412	2	32	1	1	0	(3:5)_(4:4)_(3:5)_(4:4ai)_(3:5a)_(4:4bCO)
141	OMT3	OMT	13	430948	431689	434927	434958	2_nonsis	3239	3624	4009	2	32	1	1	0	(5:3)_(6:2)_(3:5a)_(4:4aCO)_(5:3a)_(4:4a)
149	OMT3	OMT	13	840464	840468	841905	842091	2_nonsis	1438	1532	1626	2	32	1	1	0	(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)_(5:3a)_(4:4a)
124	OMT3	OMT	12	447993	448167	450128	450178	2_nonsis	1962	2073	2184	2	32	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3a)_(5:3b)_(4:4aCO)
40	OMT3	OMT	4	1083252	1083381	1087412	1088864	2_nonsis	4032	4822	5611	2	32	1	1	0	(3:5)_(4:4)_(4:4ai)_(3:5a)_(4:4bCO)_(3:5a)_(4:4b)
4	OMT3	OMT	1	176948	178602	180361	180393	2_nonsis	1760	2602	3444	2	32	1	1	0	(3:5)_(2:6)_(4:4aCO)_(3:5a)_(2:6)_(3:5b)_(2:6)_(3:5b)_(4:4a)
127	OMT3	OMT	12	599905	600169	603216	603313	2_nonsis	3048	3228	3407	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)_(5:3b)_(6:2)_(5:3b)_(4:4a)
36	OMT3	OMT	4	847395	847524	848397	848940	2_nonsis	874	1209	1544	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
155	OMT3	OMT	14	262513	263036	264607	265328	2_nonsis	1572	2193	2814	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
190	OMT3	OMT	16	329617	329941	330571	331090	2_nonsis	631	1052	1472	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
13	OMT3	OMT	2	487454	487781	489580	490532	2_nonsis	1800	2439	3077	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(4:4a)
150	OMT3	OMT	14	51050	51868	53888	54162	2_nonsis	2021	2566	3111	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
174	OMT3	OMT	15	486327	486494	488163	488189	2_nonsis	1670	1766	1861	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)_(5:3)_(4:4a)
133	OMT3	OMT	12	992572	992595	994933	994942	2_nonsis	2339	2354	2369	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(6:2)_(4:4aCO)
152	OMT3	OMT	14	120530	121108	123158	123338	2_nonsis	2051	2429	2807	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
30	OMT3	OMT	4	365434	365716	367564	368207	2_nonsis	1849	2311	2772	3	20	1	1	0	(3:5)_(4:4)_(6:2)_(5:3)_(4:4)_(3:5a)_(4:4aCO)
62	OMT3	OMT	6	94545	94981	96991	97235	2_nonsis	2011	2350	2689	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(3:5)_(4:4aCO)
184	OMT3	OMT	16	27168	27460	29674	29749	2_nonsis	2215	2398	2580	3	20	1	1	0	(5:3)_(5:3a)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
120	OMT3	OMT	12	94920	97490	98655	99028	2_nonsis	1166	2637	4107	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(3:5)_(2:6)_(3:5)_(4:4aCO)
114	OMT3	OMT	11	367941	368071	370874	371565	2_nonsis	2804	3214	3623	3	21	1	1	0	(5:3)_(4:4ai)_(3:5)_(4:4bCO)
26	OMT3	OMT	4	198376	198685	200193	200220	2_nonsis	1509	1676	1843	3	21	1	1	0	(3:5)_(4:4ai)_(5:3)_(3:5)_(4:4bCO)

51	OMT3	OMT	5	12341	12413	13996	14061	2_nonsis	1584	1652	1719	3	21	1	1	0	(5:3)_(6:2)_(5:3)_(4:4ai)_(3:5)_(4:4ai)_(4:4bCO)
153	OMT3	OMT	14	132374	132585	137407	137422	2_nonsis	4823	4935	5047	3	21	1	1	0	(3:5)_(3:5a)_(4:4aCO)_(5:3)_(4:4bi)_(5:3)_(4:4a)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4a)
24	OMT3	OMT	4	60151	61039	62973	63046	3	1935	2415	2894	0	1	2	0	2	(3:5)_(4:4)_(3:5)_(2:6i)_(2:6ai)_(2:6bi)_(1:7)_(1:7a)_(3:5a)_(4:4)
47	OMT3	OMT	4	1410029	1410091	1411239	1411446	2_sis	1149	1283	1416	0	1	2	0	2	(5:3)_(6:2i)_(5:3a)_(4:4)
52	OMT3	OMT	5	23990	24079	27636	27869	2_sis	3558	3718	3878	0	1	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4)
77	OMT3	OMT	7	967869	968127	969533	969608	2_sis	1407	1573	1738	0	1	2	0	2	(3:5)_(4:4)_(3:5a)_(4:4)
151	OMT3	OMT	14	59823	59998	61469	62457	2_sis	1472	2053	2633	0	1	2	0	2	(5:3)_(5:3a)_(4:4)
16	OMT3	OMT	2	695479	697455	698250	699461	3	796	2389	3981	0	2	2	1	1	(4:4ai)_(3:5)_(6:2)_(4:4bCO)
17	OMT3	OMT	2	741732	741884	744640	745085	3	2757	3055	3352	0	2	2	1	1	(5:3)_(3:5)_(4:4ai)_(4:4bi)_(3:5a)_(2:6)_(3:5a)_(4:4cCO)
32	OMT3	OMT	4	549856	550499	550893	551387	3	395	963	1530	0	2	2	1	1	(3:5)_(2:6)_(4:4)_(4:4aCO)
58	OMT3	OMT	5	422255	422613	424029	424927	3	1417	2044	2671	0	2	2	1	1	(3:5)_(4:4)_(4:4ai)_(4:4bCO)
67	OMT3	OMT	7	74791	75209	76989	78426	3	1781	2708	3634	0	2	2	1	1	(5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)_(5:3a)_(6:2a)_(5:3b)_(4:4a)
86	OMT3	OMT	8	325184	325621	327422	327845	3	1802	2231	2660	0	2	2	1	1	(2:6i)_(3:5)_(3:5a)_(4:4aCO)
87	OMT3	OMT	8	461593	462176	462419	462588	3	244	619	994	0	2	2	1	1	(3:5)_(4:4ai)_(5:3)_(4:4bCO)
102	OMT3	OMT	10	461906	461975	471532	472011	3	9558	9831	10104	0	2	2	1	1	(6:2)_(4:4)_(5:3)_(4:4a)_(5:3a)_(5:3)_(4:4aCO)
106	OMT3	OMT	11	69942	69964	72294	72330	3	2331	2359	2387	0	2	2	1	1	(5:3)_(4:4ai)_(2:6)_(3:5)_(2:6)_(4:4)_(2:6)_(4:4bCO)_(5:3a)_(4:4b)
107	OMT3	OMT	11	85027	86234	89674	90100	3	3441	4257	5072	0	2	2	1	1	(5:3)_(6:2i)_(5:3a)_(6:2a)_(5:3a)_(4:4aCO)
132	OMT3	OMT	12	837497	837595	840682	843387	3	3088	4489	5889	0	2	2	1	1	(5:3)_(4:4ai)_(5:3a)_(4:4bCO)
148	OMT3	OMT	13	739584	740188	746108	746305	3	5921	6321	6720	0	2	2	1	1	(6:2)_(5:3)_(6:2)_(5:3)_(5:3a)_(6:2a)_(5:3a)_(4:4aCO)
177	OMT3	OMT	15	580351	580729	586345	586852	3	5617	6059	6500	0	2	2	1	1	(3:5)_(4:4)_(6:2)_(4:4aCO)
178	OMT3	OMT	15	769620	770027	771781	772232	3	1755	2183	2611	0	2	2	1	1	(6:2)_(7:1)_(4:4)_(2:6)_(4:4aCO)
97	OMT3	OMT	10	29806	29815	37127	37895	2_nonsis	7313	7701	8088	0	3	2	0	2	(3:5)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5b)_(4:4CO)
253	OMT4	OMT	16	339486	339516	339516	339687	1	1	101	200	1	1	1	0	1	05:03
202	OMT4	OMT	14	86180	86282	86282	86514	1	1	167	333	1	1	1	0	1	05:03
117	OMT4	OMT	9	270121	270435	270435	270588	1	1	234	466	1	1	1	0	1	05:03
171	OMT4	OMT	12	616917	617208	617302	617371	1	95	274	453	1	1	1	0	1	05:03
224	OMT4	OMT	15	273775	273944	273944	274324	1	1	275	548	1	1	1	0	1	05:03
228	OMT4	OMT	15	394716	395073	395093	395268	1	21	286	551	1	1	1	0	1	05:03
84	OMT4	OMT	7	208043	208356	208356	208622	1	1	290	578	1	1	1	0	1	05:03
16	OMT4	OMT	2	394726	394786	394786	395349	1	1	312	622	1	1	1	0	1	05:03
210	OMT4	OMT	14	301506	301548	301794	301887	1	247	314	380	1	1	1	0	1	05:03
190	OMT4	OMT	13	318454	318678	318678	319105	1	1	326	650	1	1	1	0	1	05:03
128	OMT4	OMT	10	253405	254075	254119	254247	1	45	443	841	1	1	1	0	1	05:03
46	OMT4	OMT	4	550672	550699	550893	551387	1	195	455	714	1	1	1	0	1	05:03
225	OMT4	OMT	15	284521	284983	285010	285417	1	28	462	895	1	1	1	0	1	05:03
242	OMT4	OMT	15	943688	944039	944039	944698	1	1	505	1009	1	1	1	0	1	05:03
114	OMT4	OMT	9	169820	170156	170432	170681	1	277	569	860	1	1	1	0	1	05:03
262	OMT4	OMT	16	801399	801614	801756	802415	1	143	579	1015	1	1	1	0	1	05:03
65	OMT4	OMT	5	80182	80303	80737	81049	1	435	651	866	1	1	1	0	1	05:03
119	OMT4	OMT	9	338670	339115	339115	340356	1	1	843	1685	1	1	1	0	1	05:03
179	OMT4	OMT	12	827343	827901	828345	828622	1	445	862	1278	1	1	1	0	1	05:03
39	OMT4	OMT	4	266113	266302	266878	267359	1	577	911	1245	1	1	1	0	1	05:03
207	OMT4	OMT	14	185798	185846	186921	186976	1	1076	1127	1177	1	1	1	0	1	05:03
21	OMT4	OMT	2	658797	659928	660237	660972	1	310	1242	2174	1	1	1	0	1	05:03
185	OMT4	OMT	12	1026889	1027477	1028477	1028782	1	1001	1447	1892	1	1	1	0	1	05:03
170	OMT4	OMT	12	572294	572662	573804	574096	1	1143	1472	1801	1	1	1	0	1	05:03
160	OMT4	OMT	12	138768	141153	141390	141933	1	238	1701	3164	1	1	1	0	1	05:03
258	OMT4	OMT	16	642789	643790	644963	645571	1	1174	1978	2781	1	1	1	0	1	05:03
118	OMT4	OMT	9	329125	332459	332503	333073	1	45	1996	3947	1	1	1	0	1	05:03
44	OMT4	OMT	4	465458	465495	465495	465563	1	1	53	104	1	2	1	0	1	03:05
93	OMT4	OMT	7	905148	905227	905266	905275	1	40	83	126	1	2	1	0	1	03:05
218	OMT4	OMT	14	736429	736458	736460	736619	1	3	96	189	1	2	1	0	1	03:05
24	OMT4	OMT	2	723175	723232	723232	723385	1	1	105	209	1	2	1	0	1	03:05
48	OMT4	OMT	4	617153	617276	617276	617367	1	1	107	213	1	2	1	0	1	03:05
154	OMT4	OMT	11	625985	626193	626193	626218	1	1	117	232	1	2	1	0	1	03:05
231	OMT4	OMT	15	533847	533983	533983	534085	1	1	119	237	1	2	1	0	1	03:05
248	OMT4	OMT	16	125867	125934	125970	126095	1	37	132	227	1	2	1	0	1	03:05
53	OMT4	OMT	4	1005614	1005656	1005728	1005839	1	73	149	224	1	2	1	0	1	03:05
87	OMT4	OMT	7	459382	459691	459691	459753	1	1	186	370	1	2	1	0	1	03:05
165	OMT4	OMT	12	412564	412603	412603	412966	1	1	201	401	1	2	1	0	1	03:05

129	OMT4	OMT	10	316551	316590	316590	317045	1	1	247	493	1	2	1	0	1	03:05
80	OMT4	OMT	6	115291	115411	115494	115717	1	84	255	425	1	2	1	0	1	03:05
72	OMT4	OMT	5	315416	315857	315857	315976	1	1	280	559	1	2	1	0	1	03:05
155	OMT4	OMT	11	630615	631180	631180	631232	1	1	309	616	1	2	1	0	1	03:05
23	OMT4	OMT	2	720615	720905	721088	721115	1	184	342	499	1	2	1	0	1	03:05
257	OMT4	OMT	16	564015	564521	564521	564703	1	1	344	687	1	2	1	0	1	03:05
112	OMT4	OMT	9	150789	151377	151394	151474	1	18	351	684	1	2	1	0	1	03:05
94	OMT4	OMT	7	936948	937376	937376	937670	1	1	361	721	1	2	1	0	1	03:05
19	OMT4	OMT	2	537354	537480	537549	538047	1	70	381	692	1	2	1	0	1	03:05
50	OMT4	OMT	4	721724	721991	722085	722407	1	95	389	682	1	2	1	0	1	03:05
89	OMT4	OMT	7	598733	599198	599198	599515	1	1	391	781	1	2	1	0	1	03:05
1	OMT4	OMT	1	45030	45198	45198	45831	1	1	401	800	1	2	1	0	1	03:05
111	OMT4	OMT	9	131341	131883	131891	132148	1	9	408	806	1	2	1	0	1	03:05
244	OMT4	OMT	15	1009095	1009862	1009862	1009919	1	1	412	823	1	2	1	0	1	03:05
221	OMT4	OMT	15	128417	128530	128730	129118	1	201	451	700	1	2	1	0	1	03:05
236	OMT4	OMT	15	662688	662842	662842	663595	1	1	454	906	1	2	1	0	1	03:05
41	OMT4	OMT	4	407286	407403	407403	408221	1	1	468	934	1	2	1	0	1	03:05
73	OMT4	OMT	5	417790	418504	418513	418792	1	10	506	1001	1	2	1	0	1	03:05
123	OMT4	OMT	10	22158	22350	22772	22827	1	423	546	668	1	2	1	0	1	03:05
20	OMT4	OMT	2	641467	641914	642356	642406	1	443	691	938	1	2	1	0	1	03:05
113	OMT4	OMT	9	159685	160007	160585	160764	1	579	829	1078	1	2	1	0	1	03:05
251	OMT4	OMT	16	222390	222598	222957	223697	1	360	833	1306	1	2	1	0	1	03:05
66	OMT4	OMT	5	83200	83329	83692	84562	1	364	863	1361	1	2	1	0	1	03:05
140	OMT4	OMT	11	179745	180215	180215	182377	1	1	1316	2631	1	2	1	0	1	03:05
159	OMT4	OMT	12	63076	63559	63859	65485	1	301	1355	2408	1	2	1	0	1	03:05
212	OMT4	OMT	14	404051	405175	405878	406133	1	704	1393	2081	1	2	1	0	1	03:05
173	OMT4	OMT	12	625064	627007	627370	627543	1	364	1421	2478	1	2	1	0	1	03:05
139	OMT4	OMT	11	166774	167254	168464	168746	1	1211	1591	1971	1	2	1	0	1	03:05
103	OMT4	OMT	8	280455	280619	281430	282877	1	812	1617	2421	1	2	1	0	1	03:05
255	OMT4	OMT	16	425481	425740	427238	427523	1	1499	1770	2041	1	2	1	0	1	03:05
10	OMT4	OMT	2	150492	151117	151407	151865	1	291	832	1372	1	3	1	0	1	5:3_4:4_5:3
206	OMT4	OMT	14	174664	174821	175274	176348	1	454	1069	1683	1	3	1	0	1	5:3_6:2_5:3
172	OMT4	OMT	12	622999	623416	623971	624838	1	556	1197	1838	1	3	1	0	1	5:3_6:2_5:3
145	OMT4	OMT	11	327707	327893	328709	329482	1	817	1296	1774	1	3	1	0	1	5:3_4:4_5:3
227	OMT4	OMT	15	356936	357029	358915	359878	1	1887	2414	2941	1	3	1	0	1	5:3_4:4_5:3
162	OMT4	OMT	12	198146	198396	198771	199043	1	376	636	896	1	4	1	0	1	3:5_2:6_3:5
60	OMT4	OMT	4	1271755	1271812	1272164	1272726	1	353	662	970	1	4	1	0	1	3:5_4:4_3:5
99	OMT4	OMT	8	116330	117152	117423	117631	1	272	786	1300	1	4	1	0	1	3:5_4:4_3:5
194	OMT4	OMT	13	529347	529948	530525	530917	1	578	1074	1569	1	7	1	0	1	6:2_5:3
106	OMT4	OMT	8	461593	462176	462825	463320	1	650	1188	1726	1	7	1	0	1	6:2_5:3
17	OMT4	OMT	2	483804	483939	492334	493122	1	8396	8857	9317	1	7	1	0	1	5:3_6:2
126	OMT4	OMT	10	194790	194922	195349	195849	1	428	743	1058	1	7	1	0	1	6:2_4:4_6:2
232	OMT4	OMT	15	544722	544812	546393	546837	1	1582	1848	2114	1	7	1	0	1	6:2_4:4_5:3
121	OMT4	OMT	9	382792	382906	384418	384629	1	1513	1675	1836	1	7	1	0	1	6:2_5:3_4:4_5:3
4	OMT4	OMT	1	129517	130254	130776	130897	1	523	951	1379	1	8	1	0	1	2:6_3:5
102	OMT4	OMT	8	260343	261563	261724	262100	1	162	959	1756	1	8	1	0	1	3:5_2:6
214	OMT4	OMT	14	575525	576199	577136	579044	1	938	2228	3518	1	8	1	0	1	3:5_2:6
141	OMT4	OMT	11	198458	198833	201727	202124	1	2895	3280	3665	1	8	1	0	1	3:5_2:6_4:4_2:6
56	OMT4	OMT	4	1083881	1083977	1083977	1084057	1	1	88	175	1	10	1	0	1	06:02
12	OMT4	OMT	2	216902	216962	217015	217070	1	54	111	167	1	10	1	0	1	06:02
58	OMT4	OMT	4	1162210	1162357	1162494	1162575	1	138	251	364	1	10	1	0	1	06:02
239	OMT4	OMT	15	802784	803471	803471	803637	1	1	427	852	1	10	1	0	1	06:02
27	OMT4	OMT	3	51491	51650	51650	52350	1	1	430	858	1	10	1	0	1	06:02
189	OMT4	OMT	13	241597	242042	242235	242692	1	194	644	1094	1	10	1	0	1	06:02
9	OMT4	OMT	2	140383	140643	141215	141553	1	573	871	1169	1	10	1	0	1	06:02
176	OMT4	OMT	12	719910	721257	721257	721983	1	1	1037	2072	1	10	1	0	1	06:02
180	OMT4	OMT	12	832633	833476	833540	834769	1	65	1100	2135	1	10	1	0	1	06:02
134	OMT4	OMT	10	631130	632972	633146	633240	1	175	1142	2109	1	10	1	0	1	06:02
219	OMT4	OMT	15	22358	39380	40593	40834	1	1214	9845	18475	1	10	1	0	1	06:02
187	OMT4	OMT	13	169412	169477	169477	169492	1	1	40	79	1	10.1	1	0	1	02:06

90	OMT4	OMT	7	706337	706391	706439	706722	1	49	217	384	1	10.1	1	0	1	02:06
211	OMT4	OMT	14	366158	366581	366581	366762	1	1	302	603	1	10.1	1	0	1	02:06
107	OMT4	OMT	8	465996	466004	466305	466322	1	302	314	325	1	10.1	1	0	1	02:06
149	OMT4	OMT	11	425593	425840	425991	426133	1	152	346	539	1	10.1	1	0	1	02:06
235	OMT4	OMT	15	653431	653618	653896	653929	1	279	388	497	1	10.1	1	0	1	02:06
69	OMT4	OMT	5	210793	211386	211559	211770	1	174	575	976	1	10.1	1	0	1	02:06
79	OMT4	OMT	6	105427	105934	106222	106492	1	289	677	1064	1	10.1	1	0	1	02:06
122	OMT4	OMT	9	405665	405821	406436	406590	1	616	770	924	1	10.1	1	0	1	02:06
241	OMT4	OMT	15	882131	882322	882911	883100	1	590	779	968	1	10.1	1	0	1	02:06
8	OMT4	OMT	2	121576	121643	126263	126921	1	4621	4983	5344	1	10.1	1	0	1	02:06
260	OMT4	OMT	16	751172	751586	752166	752508	1	581	958	1335	2	11	1	0	1	5:3_5:3a
54	OMT4	OMT	4	1011299	1011430	1012387	1012624	1	958	1141	1324	2	11	1	0	1	5:3_5:3a
183	OMT4	OMT	12	964591	964739	967302	969880	1	2564	3926	5288	2	11	1	0	1	5:3_5:3a
91	OMT4	OMT	7	801946	801970	802550	802904	1	581	769	957	2	12	1	0	1	3:5_3:5a
42	OMT4	OMT	4	410728	411048	411785	412382	1	738	1196	1653	2	12	1	0	1	3:5_3:5a
64	OMT4	OMT	5	40898	41432	42396	42646	1	965	1356	1747	2	12	1	0	1	3:5_3:5a
247	OMT4	OMT	16	119752	120748	121751	122624	1	1004	1938	2871	2	12	1	0	1	3:5_3:5a
259	OMT4	OMT	16	708937	708998	711113	711619	1	2116	2399	2681	2	13	1	0	1	6:2_5:3_5:3a_4:4_5:3a
203	OMT4	OMT	14	89837	89883	90956	91169	1	1074	1203	1331	2	14	1	0	1	3:5_3:5a_4:4_3:5a
13	OMT4	OMT	2	248159	248728	251548	251742	1	2821	3202	3582	2	14	1	0	1	2:6_3:5_2:6_3:5_3:5a
5	OMT4	OMT	1	175578	175849	176713	176948	1	865	1117	1369	2	14	1	0	1	3:5_2:6_3:5_2:6_3:5_3:5a
238	OMT4	OMT	15	781222	781633	782356	782474	1	724	988	1251	2	15	1	0	1	5:3_4:4_5:3a
25	OMT4	OMT	2	760365	760599	761454	761529	1	856	1010	1163	2	15	1	0	1	5:3_4:4_5:3a
168	OMT4	OMT	12	527518	527685	528671	528758	1	987	1113	1239	2	15	1	0	1	5:3_4:4_5:3a
222	OMT4	OMT	15	242267	242488	243831	244393	1	1344	1735	2125	2	15	1	0	1	5:3_4:4_5:3a
163	OMT4	OMT	12	266094	266454	267117	267423	1	664	996	1328	2	16	1	0	1	3:5_4:4_3:5a
250	OMT4	OMT	16	162602	162746	163739	163759	1	994	1075	1156	2	17	1	0	1	5:3_4:4_5:3_4:4_5:3a
137	OMT4	OMT	11	69153	69417	70711	70841	1	1295	1491	1687	2	17	1	0	1	5:3_6:2_5:3_4:4_5:3a
220	OMT4	OMT	15	82279	82570	83853	84190	1	1284	1597	1910	2	17	1	0	1	5:3_4:4_5:3a_6:2_5:3a
193	OMT4	OMT	13	527516	527588	527901	528307	1	314	552	790	2	19	1	0	1	5:3_6:2_5:3a
132	OMT4	OMT	10	567298	567353	568805	570822	1	1453	2488	3523	2	19	1	0	1	5:3_6:2_5:3a
209	OMT4	OMT	14	287606	287672	289222	289345	1	1551	1645	1738	2	23	1	0	1	3:5_4:4_2:6_3:5a
82	OMT4	OMT	7	71410	71649	74453	74566	1	2805	2980	3155	2	23	1	0	1	2:6_3:5_4:4_2:6_3:5a
52	OMT4	OMT	4	1000380	1001608	1002837	1003188	1	1230	2019	2807	2	23	1	0	1	3:5_2:6_4:4_3:5_2:6_4:4_3:5a
204	OMT4	OMT	14	111039	111216	114221	114314	1	3006	3140	3274	2	23	1	0	1	5:3_4:4_6:2_5:3a_4:4_5:3a_4:4_5:3a_6:2_5:3a
153	OMT4	OMT	11	597889	598496	599535	599900	2_nonsis	1040	1525	2010	3	30	1	0	1	05:03
70	OMT4	OMT	5	238122	238396	239816	239949	2_nonsis	1421	1624	1826	3	30	1	0	1	3:5_2:6
105	OMT4	OMT	8	404970	405293	406734	407300	2_nonsis	1442	1886	2329	3	30	1	0	1	2:6_3:5
75	OMT4	OMT	5	472577	472664	474569	474623	2_nonsis	1906	1976	2045	3	30	1	0	1	6:2_4:4_3:5
184	OMT4	OMT	12	1011170	1011621	1014437	1014538	2_nonsis	2817	3092	3367	3	30	1	0	1	3:5_2:6_3:5a
263	OMT4	OMT	16	894511	894610	896267	896434	2_nonsis	1658	1790	1922	3	30	1	0	1	5:3_2:6_5:3_3:5
85	OMT4	OMT	7	270374	270491	272144	272568	2_nonsis	1654	1924	2193	3	30	1	0	1	3:5_3:5a_3:5b_3:5a
200	OMT4	OMT	14	37986	39122	41680	42185	2_nonsis	2559	3379	4198	3	30	1	0	1	6:2_5:3_2:6_3:5_4:4_3:5
181	OMT4	OMT	12	867405	869664	875259	876120	2_nonsis	5596	7155	8714	3	30	1	0	1	3:5_5:3_3:5_4:4_2:6_3:5a
14	OMT4	OMT	2	287818	287997	292755	292797	2_nonsis	4759	4869	4978	3	30	1	0	1	3:5_4:4_3:5_4:4_5:3_4:4_5:3a_5:3_4:4_5:3
254	OMT4	OMT	16	381280	381362	381362	381840	2_nonsis	1	280	559	1	1	1	1	0	(5:3)_(4:4aCO)
77	OMT4	OMT	6	48712	49201	49483	49819	2_nonsis	283	695	1106	1	1	1	1	0	(5:3)_(4:4aCO)
169	OMT4	OMT	12	560519	561781	561781	562070	2_nonsis	1	776	1550	1	1	1	1	0	(5:3)_(4:4aCO)
208	OMT4	OMT	14	273928	274328	274808	275212	2_nonsis	481	882	1283	1	1	1	1	0	(5:3)_(4:4aCO)
62	OMT4	OMT	4	1505853	1506604	1506992	1507780	2_nonsis	389	1158	1926	1	1	1	1	0	(5:3)_(4:4aCO)
76	OMT4	OMT	5	483903	485006	485380	486292	2_nonsis	375	1382	2388	1	1	1	1	0	(5:3)_(4:4aCO)
136	OMT4	OMT	11	44603	45993	46439	48790	2_nonsis	447	2317	4186	1	1	1	1	0	(5:3)_(4:4aCO)
178	OMT4	OMT	12	822848	823217	823256	826618	2_nonsis	40	1905	3769	1	2	1	1	0	(3:5)_(4:4aCO)
216	OMT4	OMT	14	686681	688572	689582	689944	2_nonsis	1011	2137	3262	1	2	1	1	0	(3:5)_(4:4aCO)
57	OMT4	OMT	4	1152100	1152705	1153303	1161539	2_nonsis	599	5019	9438	1	2	1	1	0	(3:5)_(4:4aCO)
110	OMT4	OMT	9	41439	41532	42365	42595	2_nonsis	834	995	1155	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
226	OMT4	OMT	15	312575	312919	313126	313924	2_nonsis	208	778	1348	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
233	OMT4	OMT	15	586345	586852	587316	587565	2_nonsis	465	842	1219	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
120	OMT4	OMT	9	347702	348431	348958	349855	2_nonsis	528	1340	2152	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
59	OMT4	OMT	4	1261452	1262394	1263265	1263883	2_nonsis	872	1651	2430	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)

								2_nonsis									
243	OMT4	OMT	15	953577	954310	954766	955006	2_nonsis	457	943	1428	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
47	OMT4	OMT	4	591129	591782	592050	592072	2_nonsis	269	606	942	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
167	OMT4	OMT	12	509342	509612	510230	510340	2_nonsis	619	808	997	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
164	OMT4	OMT	12	300946	301171	302719	302764	2_nonsis	1549	1683	1817	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
166	OMT4	OMT	12	493339	493774	494429	495002	2_nonsis	656	1159	1662	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
67	OMT4	OMT	5	106188	106333	106607	106808	2_nonsis	275	447	619	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
100	OMT4	OMT	8	187989	188673	189221	189274	2_nonsis	549	917	1284	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
135	OMT4	OMT	10	639041	639365	641346	641571	2_nonsis	1982	2256	2529	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
157	OMT4	OMT	12	36792	36833	38737	39963	2_nonsis	1905	2538	3170	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
32	OMT4	OMT	3	249994	250855	259910	260698	2_nonsis	9056	9880	10703	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
188	OMT4	OMT	13	170932	171275	171896	172118	2_nonsis	622	904	1185	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
35	OMT4	OMT	4	29152	29441	30908	31112	2_nonsis	1468	1714	1959	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
142	OMT4	OMT	11	217298	217457	220881	221472	2_nonsis	3425	3799	4173	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
29	OMT4	OMT	3	83816	93230	94139	94175	2_nonsis	910	5634	10358	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
109	OMT4	OMT	8	511816	512259	513034	514468	2_nonsis	776	1714	2651	1	11	1	1	0	(6:2)_(5:3)_(4:4aii)_(4:4bCO)
256	OMT4	OMT	16	475802	476377	477361	477481	2_nonsis	985	1332	1678	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
38	OMT4	OMT	4	211460	211831	212746	213315	2_nonsis	916	1385	1854	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
74	OMT4	OMT	5	452590	452629	452954	453437	2_nonsis	326	586	846	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
22	OMT4	OMT	2	716328	716467	716927	717374	2_nonsis	461	753	1045	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)
191	OMT4	OMT	13	324736	325194	326120	326401	2_nonsis	927	1296	1664	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
26	OMT4	OMT	3	47306	48335	48704	50099	2_nonsis	370	1581	2792	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(4:4aCO)
151	OMT4	OMT	11	486704	487095	488665	489458	2_nonsis	1571	2162	2753	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
205	OMT4	OMT	14	144587	144778	145535	145554	2_nonsis	758	862	966	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
68	OMT4	OMT	5	189662	189983	190829	191462	2_nonsis	847	1323	1799	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
55	OMT4	OMT	4	1079059	1079189	1080869	1080944	2_nonsis	1681	1783	1884	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
7	OMT4	OMT	1	195910	196198	198713	198815	2_nonsis	2516	2710	2904	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
63	OMT4	OMT	5	27119	27260	27272	27604	2_nonsis	13	249	484	1	15	1	1	0	(6:2)_(4:4aCO)
33	OMT4	OMT	3	287614	288008	288099	288246	2_nonsis	92	362	631	1	15	1	1	0	(6:2)_(4:4aCO)
201	OMT4	OMT	14	79325	79763	79763	80071	2_nonsis	1	373	745	1	15	1	1	0	(6:2)_(4:4aCO)
97	OMT4	OMT	8	21033	21160	21541	21579	2_nonsis	382	464	545	1	15	1	1	0	(6:2)_(4:4aCO)
217	OMT4	OMT	14	713149	713326	713775	713826	2_nonsis	450	563	676	1	15	1	1	0	(6:2)_(4:4aCO)
116	OMT4	OMT	9	266255	266803	266803	267668	2_nonsis	1	707	1412	1	15	1	1	0	(6:2)_(4:4aCO)
83	OMT4	OMT	7	140806	140941	141481	141723	2_nonsis	541	729	916	1	15	1	1	0	(6:2)_(4:4aCO)
175	OMT4	OMT	12	703971	704793	705221	705602	2_nonsis	429	1030	1630	1	15	1	1	0	(6:2)_(4:4aCO)
252	OMT4	OMT	16	239686	239952	241053	241174	2_nonsis	1102	1295	1487	1	15	1	1	0	(6:2)_(4:4aCO)
36	OMT4	OMT	4	43482	46608	47467	48046	2_nonsis	860	2712	4563	1	15	1	1	0	(6:2)_(4:4aCO)
148	OMT4	OMT	11	389926	389996	393512	393589	2_nonsis	3517	3590	3662	1	15	1	1	0	(6:2)_(4:4aCO)
127	OMT4	OMT	10	211498	211638	211638	211656	2_nonsis	1	79	157	1	16	1	1	0	(2:6)_(4:4aCO)
213	OMT4	OMT	14	435509	435739	435739	435934	2_nonsis	1	213	424	1	16	1	1	0	(2:6)_(4:4aCO)
81	OMT4	OMT	6	167410	168102	168122	168217	2_nonsis	21	414	806	1	16	1	1	0	(2:6)_(4:4aCO)
2	OMT4	OMT	1	47896	48115	48591	48751	2_nonsis	477	666	854	1	16	1	1	0	(2:6)_(4:4aCO)
86	OMT4	OMT	7	452296	452589	452296	452589	2_nonsis	0	146	292	1	100	1	1	0	(4:4aCO)
18	OMT4	OMT	2	533263	533610	533263	533610	2_nonsis	0	173	346	1	100	1	1	0	(4:4aCO)
198	OMT4	OMT	13	840667	841022	840667	841022	2_nonsis	0	177	354	1	100	1	1	0	(4:4aCO)
240	OMT4	OMT	15	837247	837630	837247	837630	2_nonsis	0	191	382	1	100	1	1	0	(4:4aCO)
11	OMT4	OMT	2	170868	171433	170868	171433	2_nonsis	0	282	564	1	100	1	1	0	(4:4aCO)
215	OMT4	OMT	14	651410	652054	651410	652054	2_nonsis	0	322	643	1	100	1	1	0	(4:4aCO)
101	OMT4	OMT	8	222295	222996	222295	222996	2_nonsis	0	350	700	1	100	1	1	0	(4:4aCO)
195	OMT4	OMT	13	556437	557365	556437	557365	2_nonsis	0	464	927	1	100	1	1	0	(4:4aCO)
3	OMT4	OMT	1	112136	113132	112136	113132	2_nonsis	0	498	995	1	100	1	1	0	(4:4aCO)
104	OMT4	OMT	8	330227	331641	330227	331641	2_nonsis	0	707	1413	1	100	1	1	0	(4:4aCO)
158	OMT4	OMT	12	40119	41721	40119	41721	2_nonsis	0	801	1601	1	100	1	1	0	(4:4aCO)
6	OMT4	OMT	1	187427	189821	187427	189821	2_nonsis	0	1197	2393	1	100	1	1	0	(4:4aCO)
115	OMT4	OMT	9	185865	188629	185865	188629	2_nonsis	0	1382	2763	1	100	1	1	0	(4:4aCO)
182	OMT4	OMT	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0	(4:4aCO)
96	OMT4	OMT	7	1017034	1017661	1019116	1019203	2_nonsis	1456	1812	2168	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
124	OMT4	OMT	10	164772	164955	167814	168672	2_nonsis	2860	3380	3899	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
125	OMT4	OMT	10	179084	179602	181065	181281	2_nonsis	1464	1830	2196	2	30	1	1	0	(5:3)_(6:2)_(5:3)_(5:3a)_(4:4aCO)
246	OMT4	OMT	15	1041417	1042440	1043807	1044044	2_nonsis	1368	1997	2626	2	30	1	1	0	(4:4aCO)_(6:2)_(5:3)_(5:3a)_(4:4a)
144	OMT4	OMT	11	281006	281154	283904	284248	2_nonsis	2751	2996	3241	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)_(5:3b)_(4:4a)

28	OMT4	OMT	3	69745	70158	70491	70617	2_nonsis	334	603	871	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
230	OMT4	OMT	15	478915	479565	482126	482383	2_nonsis	2562	3015	3467	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
130	OMT4	OMT	10	360316	360588	362886	363087	2_nonsis	2299	2535	2770	2	31	1	1	0	(3:5)_(3:5a)_(4:4)_(2:6)_(4:4aCO)
229	OMT4	OMT	15	460815	460848	464113	464395	2_nonsis	3266	3423	3579	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)_(2:6)_(3:5a)_(4:4a)
34	OMT4	OMT	4	19746	19880	20444	20737	2_nonsis	565	778	990	2	32	1	1	0	(5:3)_(4:4aCO)_(5:3a)_(4:4a)
156	OMT4	OMT	11	641940	642207	643856	643871	2_nonsis	1650	1790	1930	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
223	OMT4	OMT	15	246022	246178	247462	248324	2_nonsis	1285	1793	2301	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
234	OMT4	OMT	15	636422	637574	638644	639033	2_nonsis	1071	1841	2610	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(4:4aCO)
147	OMT4	OMT	11	379888	380602	382357	382980	2_nonsis	1756	2424	3091	2	32	1	1	0	(2:6)_(3:5)_(4:4aCO)_(3:5a)_(4:4a)
30	OMT4	OMT	3	154278	154645	156960	157443	2_nonsis	2316	2740	3164	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(3:5b)_(4:4aCO)
45	OMT4	OMT	4	483545	483565	486079	486783	2_nonsis	2515	2876	3237	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4)_(4:4aCO)
152	OMT4	OMT	11	526688	527413	527498	527511	2_nonsis	86	454	822	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
249	OMT4	OMT	16	131754	131951	132915	133150	2_nonsis	965	1180	1395	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
31	OMT4	OMT	3	239394	239437	240922	241753	2_nonsis	1486	1922	2358	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
95	OMT4	OMT	7	1008097	1008259	1010365	1010428	2_nonsis	2107	2219	2330	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
71	OMT4	OMT	5	263992	264105	264738	264848	2_nonsis	634	745	855	3	20	1	1	0	(5:3)_(5:3a)_(3:5)_(4:4aCO)
43	OMT4	OMT	4	434256	435260	436026	436257	2_nonsis	767	1384	2000	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
161	OMT4	OMT	12	160531	160756	162922	163451	2_nonsis	2167	2543	2919	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(4:4a)
15	OMT4	OMT	2	323106	323214	324467	324761	2_nonsis	1254	1454	1654	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
197	OMT4	OMT	13	712889	713054	713980	715257	2_nonsis	927	1647	2367	3	20	1	1	0	(6:2)_(5:3)_(2:6)_(3:5)_(4:4aCO)
237	OMT4	OMT	15	735184	735517	738211	738617	2_nonsis	2695	3064	3432	3	20	1	1	0	(5:3)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
261	OMT4	OMT	16	785197	785578	786663	787292	2_nonsis	1086	1590	2094	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)_(5:3)_(4:4a)
199	OMT4	OMT	13	858111	859174	861520	862065	2_nonsis	2347	3150	3953	3	20	1	1	0	(3:5)_(4:4)_(3:5a)_(5:3)_(3:5b)_(4:4aCO)
192	OMT4	OMT	13	492378	492387	495115	495304	2_nonsis	2729	2827	2925	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
49	OMT4	OMT	4	697201	697575	700151	700170	2_nonsis	2577	2773	2968	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
174	OMT4	OMT	12	677014	677110	678971	679614	2_nonsis	1862	2231	2599	3	21	1	1	0	(5:3)_(4:4ai)_(3:5)_(4:4ai)_(4:4bCO)
143	OMT4	OMT	11	277809	277967	279367	279467	2_nonsis	1401	1529	1657	3	21	1	1	0	(3:5)_(4:4)_(3:5)_(4:4ai)_(5:3)_(4:4bCO)
37	OMT4	OMT	4	132892	133023	134836	135397	2_sis	1814	2159	2504	0	1	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4)
98	OMT4	OMT	8	23964	24334	26184	26675	2_sis	1851	2281	2710	0	1	2	0	2	(3:5)_(2:6i)_(1:7)_(2:6i)_(3:5a)_(2:6i)_(3:5a)_(2:6a)_(2:6bi)_(4:4)
108	OMT4	OMT	8	497380	497405	499040	499430	2_sis	1636	1843	2049	0	1	2	0	2	(5:3)_(5:3a)_(6:2)_(4:4)
131	OMT4	OMT	10	461975	462161	465816	466454	3	3656	4067	4478	0	1	2	0	2	(2:6)_(3:5)_(4:4ai)_(3:5a)_(2:6)_(4:4)
138	OMT4	OMT	11	80854	81244	81532	82469	2_sis	289	952	1614	0	1	2	0	2	(1:7)_(3:5)_(4:4)
150	OMT4	OMT	11	428081	428986	429005	429076	2_sis	20	507	994	0	1	2	0	2	(1:7)_(4:4)
196	OMT4	OMT	13	695123	695196	696571	697269	2_sis	1376	1761	2145	0	1	2	0	2	(3:5)_(2:6i)_(4:4)
245	OMT4	OMT	15	1038822	1038960	1039487	1039544	2_sis	528	625	721	0	1	2	0	2	(5:3)_(6:2)_(4:4)
40	OMT4	OMT	4	302250	303051	308617	308638	3	5567	5977	6387	0	2	2	1	1	(4:4ai)_(6:2)_(5:3)_(4:4bCO)_(3:5)_(4:4b)_(3:5a)_(4:4b)
51	OMT4	OMT	4	767007	767342	770058	770136	3	2717	2923	3128	0	2	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
61	OMT4	OMT	4	1418139	1418662	1421025	1421204	4	2364	2714	3064	0	2	2	1	1	(4:4ai)_(3:5)_(2:6)_(3:5)_(2:6)_(2:6ai)_(3:5)_(4:4bCO)
78	OMT4	OMT	6	86721	87400	95849	96304	3	8450	9016	9582	0	2	2	1	1	(4:4ai)_(6:2i)_(5:3)_(4:4ai)_(5:3a)_(4:4ai)_(5:3b)_(6:2a)_(4:4bCO)
88	OMT4	OMT	7	588549	588631	590933	591242	3	2303	2498	2692	0	2	2	1	1	(3:5)_(3:5a)_(4:4aCO)_(5:3)_(4:4a)
92	OMT4	OMT	7	846945	846990	850043	850236	3	3054	3172	3290	0	2	2	1	1	(5:3)_(6:2i)_(6:2a)_(5:3a)_(6:2b)_(5:3a)_(4:4aCO)
146	OMT4	OMT	11	351989	352346	355543	355649	3	3198	3429	3659	0	2	2	1	1	(5:3)_(4:4ai)_(3:5)_(2:6)_(3:5)_(3:5a)_(2:6a)_(3:5b)_(4:4bCO)
186	OMT4	OMT	13	25829	26166	26922	28623	3	757	1775	2793	0	2	2	1	1	(5:3)_(3:5)_(4:4aCO)
133	OMT4	OMT	10	570822	573135	584209	584647	3	11075	12450	13824	0	3	2	1	1	(5:3)_(6:2)_(4:4aCO)_(5:3a)_(6:2a)_(4:4bCO)
177	OMT4	OMT	12	745706	746036	747982	748236	2_nonsis	1947	2238	2529	0	3	1	1	0	(3:5)_(4:4aCO)_(3:5a)_(2:6)_(3:5a)_(4:4CO)_(3:5b)_(3:5c)_(4:4aCO)
449	OMT4	OMT	12	1053841	1054279	1059350	1078177	2_sis	5072	14704	24335	0	4	1	NA	NA	3:5_3:5_4:4_2:6
160	OMT5	OMT	12	603216	603313	603325	603374	1	13	85	157	1	1	1	0	1	05:03
210	OMT5	OMT	15	494326	494461	494461	494556	1	1	115	229	1	1	1	0	1	05:03
230	OMT5	OMT	16	236868	236925	236925	237102	1	1	117	233	1	1	1	0	1	05:03
99	OMT5	OMT	8	462176	462297	462297	462419	1	1	122	242	1	1	1	0	1	05:03
92	OMT5	OMT	8	143543	143727	143727	143824	1	1	141	280	1	1	1	0	1	05:03
98	OMT5	OMT	8	383099	383247	383257	383395	1	11	153	295	1	1	1	0	1	05:03
150	OMT5	OMT	12	166641	166909	166909	166947	1	1	153	305	1	1	1	0	1	05:03
79	OMT5	OMT	7	413051	413440	413440	413503	1	1	226	451	1	1	1	0	1	05:03
116	OMT5	OMT	10	236674	236901	237020	237032	1	120	239	357	1	1	1	0	1	05:03
238	OMT5	OMT	16	653426	653739	653824	653857	1	86	258	430	1	1	1	0	1	05:03
228	OMT5	OMT	16	150500	150643	150643	151045	1	1	273	544	1	1	1	0	1	05:03
175	OMT5	OMT	13	239896	240226	240226	240460	1	1	282	563	1	1	1	0	1	05:03
185	OMT5	OMT	13	692858	693184	693290	693352	1	107	300	493	1	1	1	0	1	05:03
48	OMT5	OMT	4	1434996	1435091	1435091	1435647	1	1	326	650	1	1	1	0	1	05:03

63	OMT5	OMT	5	491262	491327	491556	491806	1	230	387	543	1	1	1	0	1	05:03
17	OMT5	OMT	2	308083	308205	308422	308770	1	218	452	686	1	1	1	0	1	05:03
200	OMT5	OMT	14	560308	560362	560362	561334	1	1	513	1025	1	1	1	0	1	05:03
156	OMT5	OMT	12	509342	509612	509982	510120	1	371	574	777	1	1	1	0	1	05:03
80	OMT5	OMT	7	450034	450372	450623	451100	1	252	659	1065	1	1	1	0	1	05:03
164	OMT5	OMT	12	706112	706444	707098	707238	1	655	890	1125	1	1	1	0	1	05:03
176	OMT5	OMT	13	258060	258493	259094	259263	1	602	902	1202	1	1	1	0	1	05:03
171	OMT5	OMT	13	21556	21881	22567	22768	1	687	949	1211	1	1	1	0	1	05:03
188	OMT5	OMT	13	873246	874942	874942	875434	1	1	1094	2187	1	1	1	0	1	05:03
121	OMT5	OMT	10	337345	337436	337436	339657	1	1	1156	2311	1	1	1	0	1	05:03
6	OMT5	OMT	1	112136	113132	113326	114283	1	195	1171	2146	1	1	1	0	1	05:03
146	OMT5	OMT	12	27605	28820	29781	30008	1	962	1682	2402	1	1	1	0	1	05:03
110	OMT5	OMT	9	412645	415204	415643	415827	1	440	1811	3181	1	1	1	0	1	05:03
9	OMT5	OMT	2	50611	50820	50893	59500	1	74	4481	8888	1	1	1	0	1	05:03
16	OMT5	OMT	2	258153	258313	258313	258409	1	1	128	255	1	2	1	0	1	03:05
149	OMT5	OMT	12	109602	109677	109736	109886	1	60	172	283	1	2	1	0	1	03:05
60	OMT5	OMT	5	416514	416792	416815	416927	1	24	218	412	1	2	1	0	1	03:05
199	OMT5	OMT	14	487991	488208	488208	488587	1	1	298	595	1	2	1	0	1	03:05
151	OMT5	OMT	12	177778	178195	178195	178408	1	1	315	629	1	2	1	0	1	03:05
197	OMT5	OMT	14	417156	417610	417659	417758	1	50	326	601	1	2	1	0	1	03:05
212	OMT5	OMT	15	609608	609836	609993	610269	1	158	409	660	1	2	1	0	1	03:05
39	OMT5	OMT	4	730704	730734	730734	731588	1	1	442	883	1	2	1	0	1	03:05
192	OMT5	OMT	14	121889	121988	122278	122496	1	291	449	606	1	2	1	0	1	03:05
28	OMT5	OMT	3	235472	236284	236284	236387	1	1	458	914	1	2	1	0	1	03:05
88	OMT5	OMT	7	984677	984935	985232	985352	1	298	486	674	1	2	1	0	1	03:05
113	OMT5	OMT	10	99116	99941	99962	100224	1	22	565	1107	1	2	1	0	1	03:05
54	OMT5	OMT	5	267673	268597	268713	268979	1	117	711	1305	1	2	1	0	1	03:05
224	OMT5	OMT	16	67558	68036	68341	68882	1	306	815	1323	1	2	1	0	1	03:05
75	OMT5	OMT	7	254552	255756	255756	256325	1	1	887	1772	1	2	1	0	1	03:05
72	OMT5	OMT	7	165111	165175	165523	166667	1	349	952	1555	1	2	1	0	1	03:05
225	OMT5	OMT	16	82186	82464	83474	83873	1	1011	1349	1686	1	2	1	0	1	03:05
11	OMT5	OMT	2	74920	75084	76470	76676	1	1387	1571	1755	1	2	1	0	1	03:05
3	OMT5	OMT	1	56399	56786	57739	59349	1	954	1952	2949	1	2	1	0	1	03:05
140	OMT5	OMT	11	356064	356100	356315	356343	1	216	247	278	1	3	1	0	1	5:3_6:2_5:3
135	OMT5	OMT	11	80353	80724	80854	81244	1	131	511	890	1	3	1	0	1	5:3_4:4_5:3
132	OMT5	OMT	10	716692	716901	717538	717626	1	638	786	933	1	3	1	0	1	5:3_4:4_5:3_6:2_5:3
162	OMT5	OMT	12	657825	657860	657926	658005	1	67	123	179	1	4	1	0	1	3:5_2:6_3:5
214	OMT5	OMT	15	690299	690558	694301	694394	1	3744	3919	4094	1	4	1	0	1	3:5_4:4_3:5
240	OMT5	OMT	16	700509	702403	703434	703815	1	1032	2169	3305	1	4	1	0	1	3:5_2:6_3:5_4:4_3:5
126	OMT5	OMT	10	513875	515737	527538	528639	1	11802	13283	14763	1	7	1	0	1	5:3_6:2
159	OMT5	OMT	12	572946	573483	574950	575257	1	1468	1889	2310	1	7	1	0	1	5:3_4:4_6:2
221	OMT5	OMT	15	1048437	1048836	1049580	1049902	1	745	1105	1464	1	7	1	0	1	5:3_4:4_5:3_6:2
20	OMT5	OMT	2	515049	515130	515316	515610	1	187	374	560	1	8	1	0	1	3:5_2:6
201	OMT5	OMT	14	652054	652238	652419	652841	1	182	484	786	1	8	1	0	1	2:6_3:5
243	OMT5	OMT	16	900602	900649	901564	901586	1	916	950	983	1	8	1	0	1	3:5_2:6
207	OMT5	OMT	15	303222	303785	304796	304859	1	1012	1324	1636	1	8	1	0	1	2:6_3:5
161	OMT5	OMT	12	623758	623971	624838	627007	1	868	2058	3248	1	8	1	0	1	3:5_2:6
104	OMT5	OMT	9	232253	232425	232425	232621	1	1	184	367	1	10	1	0	1	06:02
139	OMT5	OMT	11	329686	329885	329955	330549	1	71	467	862	1	10	1	0	1	06:02
73	OMT5	OMT	7	197001	197230	197230	197989	1	1	494	987	1	10	1	0	1	06:02
58	OMT5	OMT	5	360556	361242	361243	361787	1	2	616	1230	1	10	1	0	1	06:02
127	OMT5	OMT	10	543291	543878	543880	544523	1	3	617	1231	1	10	1	0	1	06:02
102	OMT5	OMT	9	87789	88444	88448	89046	1	5	631	1256	1	10	1	0	1	06:02
223	OMT5	OMT	16	56116	56137	56137	56152	1	1	18	35	1	10.1	1	0	1	02:06
47	OMT5	OMT	4	1430578	1430819	1430819	1430837	1	1	130	258	1	10.1	1	0	1	02:06
130	OMT5	OMT	10	581638	581835	581835	581933	1	1	148	294	1	10.1	1	0	1	02:06
36	OMT5	OMT	4	595122	595155	595275	595314	1	121	156	191	1	10.1	1	0	1	02:06
56	OMT5	OMT	5	318564	318778	318778	319090	1	1	263	525	1	10.1	1	0	1	02:06
61	OMT5	OMT	5	461582	461594	461594	462226	1	1	322	643	1	10.1	1	0	1	02:06
27	OMT5	OMT	3	211617	212106	212106	212264	1	1	324	646	1	10.1	1	0	1	02:06

96	OMT5	OMT	8	235099	235973	235973	236137	1	1	519	1037	1	10.1	1	0	1	02:06
193	OMT5	OMT	14	146493	147100	147100	147716	1	1	612	1222	1	10.1	1	0	1	02:06
26	OMT5	OMT	3	163699	164093	164093	165982	1	1	1142	2282	1	10.1	1	0	1	02:06
77	OMT5	OMT	7	329667	330639	330839	331345	1	201	939	1677	2	11	1	0	1	5:3_5:3a
32	OMT5	OMT	4	271809	272060	272385	273003	1	326	760	1193	2	12	1	0	1	3:5_3:5a
85	OMT5	OMT	7	858731	859410	859955	860468	1	546	1141	1736	2	12	1	0	1	3:5_3:5a
219	OMT5	OMT	15	953190	953320	954766	955006	1	1447	1631	1815	2	12	1	0	1	3:5_3:5a
182	OMT5	OMT	13	605754	605794	606066	606299	1	273	409	544	2	13	1	0	1	5:3_4:4_5:3_5:3a
133	OMT5	OMT	11	68802	68824	69425	69662	1	602	731	859	2	13	1	0	1	5:3_6:2_5:3_5:3a
37	OMT5	OMT	4	670771	671025	672865	673237	1	1841	2153	2465	2	13	1	0	1	5:3_5:3a_4:4_5:3
42	OMT5	OMT	4	954954	954963	955755	956552	1	793	1195	1597	2	13	1	0	1	6:2_5:3_5:3a_6:2_5:3
2	OMT5	OMT	1	51522	51951	54508	54661	1	2558	2848	3138	2	14	1	0	1	3:5_3:5a_2:6_3:5a
115	OMT5	OMT	10	227032	227303	230075	230256	1	2773	2998	3223	2	14	1	0	1	3:5_4:4_3:5_4:4_3:5_3:5a
179	OMT5	OMT	13	392261	392366	392634	392778	1	269	393	516	2	15	1	0	1	5:3_4:4_5:3a
165	OMT5	OMT	12	758595	758853	759341	759438	1	489	666	842	2	15	1	0	1	5:3_4:4_5:3a
222	OMT5	OMT	15	1063605	1063818	1064615	1064799	1	798	996	1193	2	15	1	0	1	5:3_4:4_5:3a
112	OMT5	OMT	10	78874	79092	80055	80196	1	964	1143	1321	2	15	1	0	1	5:3_4:4_5:3a
97	OMT5	OMT	8	380348	380530	381642	381677	1	1113	1221	1328	2	15	1	0	1	5:3_4:4_5:3a
226	OMT5	OMT	16	105874	105972	107496	107754	1	1525	1702	1879	2	15	1	0	1	5:3_4:4_5:3a
57	OMT5	OMT	5	327452	327970	328370	329070	1	401	1009	1617	2	16	1	0	1	3:5_4:4_3:5a
181	OMT5	OMT	13	571457	571706	572658	572735	1	953	1115	1277	2	16	1	0	1	3:5_4:4_3:5a
234	OMT5	OMT	16	474750	475030	475802	476377	1	773	1200	1626	2	16	1	0	1	3:5_4:4_3:5a
71	OMT5	OMT	7	79203	80122	81435	82858	1	1314	2484	3654	2	16	1	0	1	3:5_4:4_3:5a
81	OMT5	OMT	7	609732	609750	610218	610674	1	469	705	941	2	17	1	0	1	5:3_4:4_5:3_4:4_5:3a
137	OMT5	OMT	11	259816	259883	263194	263873	1	3312	3684	4056	2	18	1	0	1	3:5_4:4_3:5a_4:4_3:5_4:4_3:5
87	OMT5	OMT	7	950426	950639	952505	952947	1	1867	2194	2520	2	21	1	0	1	5:3_4:4_5:3_6:2_5:3a_6:2_5:3a
12	OMT5	OMT	2	137392	137522	138346	138529	1	825	981	1136	2	23	1	0	1	5:3_6:2_4:4_5:3a
46	OMT5	OMT	4	1333898	1334061	1335206	1335398	1	1146	1323	1499	2	23	1	0	1	3:5_4:4_2:6_3:5a
109	OMT5	OMT	9	407232	407953	408224	408521	2_nonsis	272	780	1288	3	30	1	0	1	5:3_5:3a
50	OMT5	OMT	4	1478931	1479729	1480271	1480913	2_nonsis	543	1262	1981	3	30	1	0	1	6:2_5:3
55	OMT5	OMT	5	283424	284680	285062	285738	2_nonsis	383	1348	2313	3	30	1	0	1	5:3_6:2
189	OMT5	OMT	14	32426	34396	34917	37063	2_nonsis	522	2579	4636	3	30	1	0	1	5:3_5:3a
122	OMT5	OMT	10	359445	360186	361643	362386	2_nonsis	1458	2199	2940	3	30	1	0	1	2:6_4:4_5:3
194	OMT5	OMT	14	165982	166576	168436	168578	2_nonsis	1861	2228	2595	3	30	1	0	1	5:3_5:3a_5:3b
13	OMT5	OMT	2	146672	147197	148726	149389	2_nonsis	1530	2123	2716	3	30	1	0	1	2:6_4:4_2:6_3:5
107	OMT5	OMT	9	266803	267668	269349	269523	2_nonsis	1682	2201	2719	3	30	1	0	1	3:5_6:2_4:4_3:5a
211	OMT5	OMT	15	586076	586304	586907	587142	2_nonsis	604	835	1065	3	31	1	0	1	4:4ai_2:6
153	OMT5	OMT	12	320997	322903	326213	326929	2_nonsis	3311	4621	5931	3	31	1	0	1	3:5_4:4ai
158	OMT5	OMT	12	545416	545525	547047	547203	2_nonsis	1523	1655	1786	3	31	1	0	1	5:3_6:2_5:3a_4:4ai_3:5
172	OMT5	OMT	13	49588	49712	51433	51596	2_nonsis	1722	1865	2007	3	31	1	0	1	5:3_4:4_4:4ai_4:4_5:3a_6:2_5:3a
216	OMT5	OMT	15	736963	737103	737961	738617	2_nonsis	859	1256	1653	1	1	1	1	0	(5:3)_(4:4aCO)
90	OMT5	OMT	7	999847	999896	999896	1000147	2_nonsis	1	150	299	1	2	1	1	0	(3:5)_(4:4aCO)
244	OMT5	OMT	16	903504	903807	903807	904203	2_nonsis	1	350	698	1	2	1	1	0	(3:5)_(4:4aCO)
123	OMT5	OMT	10	391693	393423	393564	393918	2_nonsis	142	1183	2224	1	2	1	1	0	(3:5)_(4:4aCO)
34	OMT5	OMT	4	395767	396458	396700	397411	2_nonsis	243	943	1643	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
187	OMT5	OMT	13	860181	861184	862092	862695	2_nonsis	909	1711	2513	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
31	OMT5	OMT	4	218815	219142	219340	220878	2_nonsis	199	1131	2062	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
147	OMT5	OMT	12	52409	53039	54071	54226	2_nonsis	1033	1425	1816	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
76	OMT5	OMT	7	270975	271422	271853	272144	2_nonsis	432	800	1168	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
144	OMT5	OMT	11	633026	633545	634635	635970	2_nonsis	1091	2017	2943	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
191	OMT5	OMT	14	113233	113311	113360	113719	2_nonsis	50	268	485	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
154	OMT5	OMT	12	338130	338262	338685	339496	2_nonsis	424	895	1365	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
232	OMT5	OMT	16	296393	297021	297634	298155	2_nonsis	614	1188	1761	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
93	OMT5	OMT	8	159136	159406	159599	159887	2_nonsis	194	472	750	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
203	OMT5	OMT	15	39466	39499	40834	41027	2_nonsis	1336	1448	1560	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
91	OMT5	OMT	8	21033	21160	21727	22121	2_nonsis	568	828	1087	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
190	OMT5	OMT	14	87215	87864	88100	88950	2_nonsis	237	986	1734	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
53	OMT5	OMT	5	223022	223802	223802	224528	2_nonsis	1	753	1505	1	11	1	1	0	(4:4ai)_(4:4bCO)
59	OMT5	OMT	5	378075	378265	379092	379332	2_nonsis	828	1042	1256	1	11	1	1	0	(4:4ai)_(5:3)_(4:4bCO)
236	OMT5	OMT	16	493304	493377	499073	499388	2_nonsis	5697	5890	6083	1	11	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(4:4ai)_(4:4bCO)

100	OMT5	OMT	8	479332	480039	487338	487560	2_nonsis	7300	7764	8227	1	11	1	1	0	(5:3)_(4:4)_(5:3)_(4:4ai)_(6:2)_(4:4bCO)_(5:3)_(6:2)_(4:4b)
24	OMT5	OMT	3	37180	37525	38022	38178	2_nonsis	498	748	997	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
239	OMT5	OMT	16	664861	665235	665970	666185	2_nonsis	736	1030	1323	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
21	OMT5	OMT	2	572025	572093	573399	573446	2_nonsis	1307	1364	1420	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
142	OMT5	OMT	11	527758	528174	529197	529548	2_nonsis	1024	1407	1789	1	12	1	1	0	(5:3)_(6:2)_(4:4)_(4:4aCO)
40	OMT5	OMT	4	850697	850922	851427	853136	2_nonsis	506	1472	2438	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
62	OMT5	OMT	5	467203	467312	469007	469292	2_nonsis	1696	1892	2088	1	12	1	1	0	(5:3)_(4:4)_(3:5)_(4:4aCO)
35	OMT5	OMT	4	545483	546251	547565	548255	2_nonsis	1315	2043	2771	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
117	OMT5	OMT	10	278411	279038	281006	281289	2_nonsis	1969	2423	2877	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
245	OMT5	OMT	16	910123	910771	918999	919303	2_nonsis	8229	8704	9179	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
41	OMT5	OMT	4	931988	932298	934184	934358	2_nonsis	1887	2128	2369	1	12	1	1	0	(5:3)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
231	OMT5	OMT	16	258986	259333	264524	264575	2_nonsis	5192	5390	5588	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
33	OMT5	OMT	4	356968	357312	359534	360404	2_nonsis	2223	2829	3435	1	12	1	1	0	(3:5)_(2:6)_(4:4)_(3:5)_(2:6)_(3:5)_(4:4aCO)
22	OMT5	OMT	2	702600	702673	702673	703042	2_nonsis	1	221	441	1	15	1	1	0	(6:2)_(4:4aCO)
183	OMT5	OMT	13	619353	619660	619714	619822	2_nonsis	55	262	468	1	15	1	1	0	(6:2)_(4:4aCO)
145	OMT5	OMT	12	21995	22201	22201	22811	2_nonsis	1	408	815	1	15	1	1	0	(6:2)_(4:4aCO)
217	OMT5	OMT	15	795711	796275	796356	796472	2_nonsis	82	421	760	1	15	1	1	0	(6:2)_(4:4aCO)
218	OMT5	OMT	15	891508	891758	891830	892334	2_nonsis	73	449	825	1	15	1	1	0	(6:2)_(4:4aCO)
134	OMT5	OMT	11	74103	74603	74756	74916	2_nonsis	154	483	812	1	15	1	1	0	(6:2)_(4:4aCO)
235	OMT5	OMT	16	490450	490554	491133	491543	2_nonsis	580	836	1092	1	15	1	1	0	(6:2)_(4:4aCO)
86	OMT5	OMT	7	914107	914538	914816	915691	2_nonsis	279	931	1583	1	15	1	1	0	(6:2)_(4:4aCO)
220	OMT5	OMT	15	1011684	1011803	1011803	1013810	2_nonsis	1	1063	2125	1	15	1	1	0	(6:2)_(4:4aCO)
131	OMT5	OMT	10	637980	638018	639365	640236	2_nonsis	1348	1802	2255	1	15	1	1	0	(6:2)_(4:4aCO)
69	OMT5	OMT	6	225457	226036	229247	229247	2_nonsis	2058	2924	3789	1	15	1	1	0	(6:2)_(4:4aCO)
204	OMT5	OMT	15	135770	136025	136025	136228	2_nonsis	1	229	457	1	16	1	1	0	(2:6)_(4:4aCO)
184	OMT5	OMT	13	686613	686772	686772	687199	2_nonsis	1	293	585	1	16	1	1	0	(2:6)_(4:4aCO)
143	OMT5	OMT	11	567633	567960	568041	568283	2_nonsis	82	366	649	1	16	1	1	0	(2:6)_(4:4aCO)
198	OMT5	OMT	14	424418	425075	425075	425369	2_nonsis	1	476	950	1	16	1	1	0	(2:6)_(4:4aCO)
43	OMT5	OMT	4	1084062	1084839	1084864	1085054	2_nonsis	26	509	991	1	16	1	1	0	(2:6)_(4:4aCO)
174	OMT5	OMT	13	235798	236240	236240	236819	2_nonsis	1	511	1020	1	16	1	1	0	(2:6)_(4:4aCO)
70	OMT5	OMT	7	23450	23509	23642	24468	2_nonsis	134	576	1017	1	16	1	1	0	(2:6)_(4:4aCO)
173	OMT5	OMT	13	76243	76517	77019	77135	2_nonsis	503	697	891	1	16	1	1	0	(2:6)_(4:4aCO)
152	OMT5	OMT	12	232561	233075	233075	234128	2_nonsis	1	784	1566	1	16	1	1	0	(2:6)_(4:4aCO)
229	OMT5	OMT	16	213597	214067	214963	216380	2_nonsis	897	1840	2782	1	16	1	1	0	(2:6)_(4:4aCO)
68	OMT5	OMT	6	203845	204006	212520	212940	2_nonsis	8515	8805	9094	1	16	1	1	0	(2:6)_(4:4aCO)
138	OMT5	OMT	11	308786	309009	308786	309009	2_nonsis	0	111	222	1	100	1	1	0	(4:4aCO)
84	OMT5	OMT	7	784372	784625	784372	784625	2_nonsis	0	126	252	1	100	1	1	0	(4:4aCO)
148	OMT5	OMT	12	100782	101108	100782	101108	2_nonsis	0	163	325	1	100	1	1	0	(4:4aCO)
136	OMT5	OMT	11	164565	164899	164565	164899	2_nonsis	0	167	333	1	100	1	1	0	(4:4aCO)
178	OMT5	OMT	13	387879	388308	387879	388308	2_nonsis	0	214	428	1	100	1	1	0	(4:4aCO)
242	OMT5	OMT	16	876278	876719	876278	876719	2_nonsis	0	220	440	1	100	1	1	0	(4:4aCO)
23	OMT5	OMT	2	736314	736876	736314	736876	2_nonsis	0	281	561	1	100	1	1	0	(4:4aCO)
169	OMT5	OMT	12	990920	991691	990920	991691	2_nonsis	0	385	770	1	100	1	1	0	(4:4aCO)
108	OMT5	OMT	9	377342	378238	377342	378238	2_nonsis	0	448	895	1	100	1	1	0	(4:4aCO)
83	OMT5	OMT	7	677412	678405	677412	678405	2_nonsis	0	496	992	1	100	1	1	0	(4:4aCO)
25	OMT5	OMT	3	74577	76009	74577	76009	2_nonsis	0	716	1431	1	100	1	1	0	(4:4aCO)
167	OMT5	OMT	12	859351	860959	859351	860959	2_nonsis	0	804	1607	1	100	1	1	0	(4:4aCO)
202	OMT5	OMT	14	674690	676368	674690	676368	2_nonsis	0	839	1677	1	100	1	1	0	(4:4aCO)
67	OMT5	OMT	6	85688	87400	85688	87400	2_nonsis	0	856	1711	1	100	1	1	0	(4:4aCO)
45	OMT5	OMT	4	1301405	1303168	1301405	1303168	2_nonsis	0	881	1762	1	100	1	1	0	(4:4aCO)
141	OMT5	OMT	11	368313	370529	368313	370529	2_nonsis	0	1108	2215	1	100	1	1	0	(4:4aCO)
213	OMT5	OMT	15	658496	660722	658496	660722	2_nonsis	0	1113	2225	1	100	1	1	0	(4:4aCO)
4	OMT5	OMT	1	59659	61999	59659	61999	2_nonsis	0	1170	2339	1	100	1	1	0	(4:4aCO)
128	OMT5	OMT	10	544523	547200	544523	547200	2_nonsis	0	1338	2676	1	100	1	1	0	(4:4aCO)
49	OMT5	OMT	4	1455942	1459261	1455942	1459261	2_nonsis	0	1659	3318	1	100	1	1	0	(4:4aCO)
106	OMT5	OMT	9	249546	250194	251980	252174	2_nonsis	1787	2207	2627	2	31	1	1	0	(3:5)_(3:5a)_(4:4ai)_(4:4bCO)
111	OMT5	OMT	10	33525	34030	38250	38373	2_nonsis	4221	4534	4847	2	31	1	1	0	(3:5)_(4:4)_(2:6)_(3:5)_(3:5a)_(2:6)_(3:5)_(4:4ai)_(4:4bCO)
124	OMT5	OMT	10	458442	458980	460257	460723	2_nonsis	1278	1779	2280	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
101	OMT5	OMT	8	514601	517336	517418	518179	2_nonsis	83	1830	3577	2	32	1	1	0	(3:5)_(4:4aCO)_(3:5a)_(4:4a)
14	OMT5	OMT	2	193664	193715	198241	198355	2_nonsis	4527	4609	4690	2	32	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(4:4)_(5:3a)_(4:4aCO)

18	OMT5	OMT	2	434210	434484	435236	435650	2_nonsis	753	1096	1439	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
206	OMT5	OMT	15	245153	245875	246679	247071	2_nonsis	805	1361	1917	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
209	OMT5	OMT	15	478915	479565	480144	482383	2_nonsis	580	2024	3467	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
186	OMT5	OMT	13	713194	713353	716386	716783	2_nonsis	3034	3311	3588	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
241	OMT5	OMT	16	731859	732035	732750	732897	2_nonsis	716	877	1037	3	20	1	1	0	(3:5)_(6:2)_(5:3)_(4:4aCO)
205	OMT5	OMT	15	215043	215265	216270	216376	2_nonsis	1006	1169	1332	3	20	1	1	0	(3:5)_(5:3)_(6:2)_(4:4aCO)
30	OMT5	OMT	4	162718	162819	163967	164298	2_nonsis	1149	1364	1579	3	20	1	1	0	(3:5)_(3:5)_(5:3)_(4:4aCO)
82	OMT5	OMT	7	613998	614457	615842	616159	2_nonsis	1386	1773	2160	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
177	OMT5	OMT	13	321916	322143	323763	324584	2_nonsis	1621	2144	2667	3	20	1	1	0	(6:2)_(4:4)_(3:5)_(4:4aCO)
157	OMT5	OMT	12	533081	533245	535113	535533	2_nonsis	1869	2160	2451	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(4:4aCO)
10	OMT5	OMT	2	71395	71420	72233	72346	2_nonsis	814	882	950	3	20	1	1	0	(5:3)_(3:5)_(2:6)_(3:5)_(4:4aCO)
233	OMT5	OMT	16	427730	428058	429173	429236	2_nonsis	1116	1311	1505	3	20	1	1	0	(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
215	OMT5	OMT	15	700551	700804	702553	702696	2_nonsis	1750	1947	2144	3	20	1	1	0	(3:5)_(5:3)_(6:2)_(5:3)_(4:4aCO)
78	OMT5	OMT	7	397325	397929	400713	401117	2_nonsis	2785	3288	3791	3	20	1	1	0	(5:3)_(5:3a)_(4:4)_(3:5)_(4:4aCO)
103	OMT5	OMT	9	102536	102597	104545	104638	2_nonsis	1949	2025	2101	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
237	OMT5	OMT	16	584400	584447	586546	586768	2_nonsis	2100	2234	2367	3	20	1	1	0	(3:5)_(5:3)_(4:4)_(5:3a)_(4:4a)_(5:3)_(4:4a)
44	OMT5	OMT	4	1270902	1272147	1274074	1274743	2_nonsis	1928	2884	3840	3	20	1	1	0	(3:5)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
170	OMT5	OMT	12	1030457	1030472	1033418	1033763	2_nonsis	2947	3126	3305	3	20	1	1	0	(5:3)_(3:5)_(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
66	OMT5	OMT	6	53398	54604	55480	55864	2_nonsis	877	1671	2465	3	21	1	1	0	(3:5)_(4:4ai)_(5:3)_(4:4bCO)
196	OMT5	OMT	14	232241	232438	235424	236810	2_nonsis	2987	3778	4568	3	21	1	1	0	(3:5)_(4:4ai)_(5:3)_(3:5a)_(2:6)_(4:4bCO)
5	OMT5	OMT	1	70999	71116	74786	75211	2_nonsis	3671	3941	4211	3	21	1	1	0	(6:2)_(4:4ai)_(3:5)_(4:4ai)_(3:5)_(4:4bCO)
64	OMT5	OMT	5	550011	550177	551411	551830	2_nonsis	1235	1527	1818	3	21	1	1	0	(4:4ai)_(5:3)_(4:4ai)_(3:5)_(4:4ai)_(3:5)_(4:4ai)_(5:3)_(4:4bCO)_(5:3)_(4:4b)
246	OMT5	OMT	16	921047	921116	924291	924915	2_nonsis	3176	3522	3867	3	21	1	1	0	(5:3)_(4:4)_(4:4ai)_(3:5)_(4:4bCO)_(3:5)_(4:4b)_(3:5)_(2:6)_(3:5)_(4:4b)
8	OMT5	OMT	1	180747	180881	183101	183881	2_sis	2221	2677	3133	0	1	2	0	2	(5:3)_(7:1)_(7:1a)_(5:3a)_(6:2)_(5:3a)_(4:4)
95	OMT5	OMT	8	230913	230956	232174	232258	2_sis	1219	1282	1344	0	1	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4)_(5:3b)_(4:4)
105	OMT5	OMT	9	247495	247508	247508	247526	2_sis	1	16	30	0	1	2	0	2	(2:6i)_(4:4)
119	OMT5	OMT	10	315587	315842	316590	317045	2_sis	749	1103	1457	0	1	2	0	2	(7:1)_(7:1a)_(4:4)
120	OMT5	OMT	10	330191	330470	334204	334468	3	3735	4006	4276	0	1	2	0	2	(5:3)_(4:4)_(5:3)_(6:2i)_(4:4ai)_(4:4)
7	OMT5	OMT	1	121235	128637	130975	132066	3	2339	6585	10830	0	2	2	1	1	(3:5)_(4:4aCO)_(4:4bi)_(3:5a)_(2:6)_(4:4a)
15	OMT5	OMT	2	252036	254006	255862	257565	3	1857	3693	5528	0	2	2	1	1	(5:3)_(4:4aCO)
19	OMT5	OMT	2	447949	448135	455204	455563	3	7070	7342	7613	0	2	2	1	1	(3:5)_(3:5a)_(2:6i)_(3:5a)_(2:6i)_(3:5a)_(4:4ai)_(4:4)_(3:5)_(4:4)_(3:5)_(4:4)_(4:4ai)_(3:5b)_(4:4bCO)
29	OMT5	OMT	4	55881	57157	62366	62726	3	5210	6027	6844	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(4:4)_(6:2)_(6:2a)_(4:4aCO)
38	OMT5	OMT	4	698788	699229	699938	700023	3	710	972	1234	0	2	2	1	1	(5:3)_(5:3a)_(4:4aCO)
51	OMT5	OMT	5	65210	65418	69083	69209	3	3666	3832	3998	0	2	2	1	1	(3:5)_(4:4ai)_(3:5)_(5:3)_(4:4bCO)
52	OMT5	OMT	5	98283	98854	117889	118141	4	19036	19447	19857	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(4:4ai)_(4:4)_(5:3)_(2:6)_(6:2a)_(7:1)_(4:4bCO)
65	OMT5	OMT	6	30616	30827	32620	32663	3	1794	1920	2046	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
94	OMT5	OMT	8	192892	194830	195949	196156	3	1120	2192	3263	0	2	2	1	1	(7:1)_(7:1a)_(7:1b)_(8:0)_(5:3)_(6:2i)_(5:3a)_(4:4aCO)
114	OMT5	OMT	10	195349	196239	197119	204724	3	881	5128	9374	0	2	2	1	1	(3:5)_(4:4ai)_(4:4bCO)
118	OMT5	OMT	10	301236	301476	303151	303215	3	1676	1827	1978	0	2	2	1	1	(2:6)_(3:5)_(4:4ai)_(4:4bCO)_(4:4ai)_(4:4b)
125	OMT5	OMT	10	469702	472011	485198	485447	4	13188	14466	15744	0	2	2	2	0	(1:7)_(3:5)_(4:4aCO)
129	OMT5	OMT	10	570822	573135	574799	576464	4	1665	3653	5641	0	2	2	1	1	(7:1)_(6:2i)_(5:3)_(6:2a)_(5:3a)_(3:5)_(4:4aCO)
163	OMT5	OMT	12	677014	677110	678541	679614	3	1432	2016	2599	0	2	2	1	1	(5:3)_(3:5)_(2:6i)_(1:7)_(2:6a)_(4:4aCO)
166	OMT5	OMT	12	836343	840577	840682	843387	4	106	3575	7043	0	2	2	2	0	(3:5)_(4:4aCO)
180	OMT5	OMT	13	538176	538772	543143	543227	3	4372	4711	5050	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(4:4ai)_(3:5)_(4:4bCO)_(3:5)_(5:3a)_(4:4b)
195	OMT5	OMT	14	216026	216647	216919	218712	3	273	1479	2685	0	2	2	1	1	(5:3)_(5:3a)_(4:4aCO)
227	OMT5	OMT	16	130145	130597	133624	133867	3	3028	3375	3721	0	2	2	1	1	(3:5)_(3:5a)_(2:6)_(4:4aCO)
1	OMT5	OMT	1	28696	28844	32652	32883	3	3809	3998	4186	0	3	2	1	1	(3:5)_(2:6)_(4:4)_(3:5)_(2:6)_(3:5)_(4:4)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(4:4bCO)
74	OMT5	OMT	7	223151	224665	226711	229846	2_nonsis	2047	4371	6694	0	3	2	0	2	(3:5)_(2:6)_(4:4aCO)_(4:4bi)_(4:4CO)
89	OMT5	OMT	7	991998	992205	994782	994829	3	2578	2704	2830	0	3	2	1	1	(3:5)_(4:4)_(4:4aCO)_(3:5a)_(4:4bCO)_(3:5a)_(4:4b)
168	OMT5	OMT	12	938923	939652	951524	951540	4	11873	12245	12616	0	3	2	2	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)_(5:3b)_(3:5)_(4:4bCO)
208	OMT5	OMT	15	416094	416506	418252	418353	3	1747	2003	2258	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(2:6)_(4:4bCO)
221	OMT6	OMT	16	187312	187323	187323	187327	1	1	8	14	1	1	1	0	1	05:03
32	OMT6	OMT	4	202761	202877	202877	202902	1	1	71	140	1	1	1	0	1	05:03
177	OMT6	OMT	13	388416	388450	388450	388681	1	1	133	264	1	1	1	0	1	05:03
226	OMT6	OMT	16	529035	529207	529207	529318	1	1	142	282	1	1	1	0	1	05:03
231	OMT6	OMT	16	754351	754681	754681	754744	1	1	197	392	1	1	1	0	1	05:03
166	OMT6	OMT	12	759015	759188	759288	759341	1	101	213	325	1	1	1	0	1	05:03
162	OMT6	OMT	12	568114	568449	568449	568546	1	1	216	431	1	1	1	0	1	05:03
145	OMT6	OMT	11	519020	519160	519160	519513	1	1	247	492	1	1	1	0	1	05:03
61	OMT6	OMT	5	41545	41566	41711	41961	1	146	281	415	1	1	1	0	1	05:03

89	OMT6	OMT	7	766129	766363	766502	766579	1	140	295	449	1	1	1	0	1	05:03
159	OMT6	OMT	12	514832	514961	514961	515468	1	1	318	635	1	1	1	0	1	05:03
35	OMT6	OMT	4	307984	308058	308257	308500	1	200	358	515	1	1	1	0	1	05:03
146	OMT6	OMT	11	523472	523649	523718	524191	1	70	394	718	1	1	1	0	1	05:03
203	OMT6	OMT	15	371158	371479	371632	371824	1	154	410	665	1	1	1	0	1	05:03
214	OMT6	OMT	15	987247	987667	987667	988081	1	1	417	833	1	1	1	0	1	05:03
23	OMT6	OMT	3	95967	96019	96055	96799	1	37	434	831	1	1	1	0	1	05:03
201	OMT6	OMT	15	226694	227513	227538	227560	1	26	446	865	1	1	1	0	1	05:03
43	OMT6	OMT	4	622991	623053	623197	623798	1	145	476	806	1	1	1	0	1	05:03
164	OMT6	OMT	12	721257	721788	721984	722023	1	197	481	765	1	1	1	0	1	05:03
186	OMT6	OMT	14	198937	199403	199570	199738	1	168	484	800	1	1	1	0	1	05:03
187	OMT6	OMT	14	240441	240587	240933	241136	1	347	521	694	1	1	1	0	1	05:03
148	OMT6	OMT	11	604404	605465	605465	605622	1	1	609	1217	1	1	1	0	1	05:03
98	OMT6	OMT	7	1048158	1048356	1048437	1049349	1	82	636	1190	1	1	1	0	1	05:03
223	OMT6	OMT	16	321586	321864	322313	322652	1	450	758	1065	1	1	1	0	1	05:03
130	OMT6	OMT	10	547820	548463	548463	549376	1	1	778	1555	1	1	1	0	1	05:03
178	OMT6	OMT	13	495304	495559	496159	496520	1	601	908	1215	1	1	1	0	1	05:03
92	OMT6	OMT	7	896389	896765	897484	897531	1	720	931	1141	1	1	1	0	1	05:03
197	OMT6	OMT	14	733303	733411	734296	734519	1	886	1051	1215	1	1	1	0	1	05:03
229	OMT6	OMT	16	618638	618915	619974	620007	1	1060	1214	1368	1	1	1	0	1	05:03
144	OMT6	OMT	11	498225	499168	499999	500101	1	832	1354	1875	1	1	1	0	1	05:03
28	OMT6	OMT	4	62366	62726	63846	64139	1	1121	1447	1772	1	1	1	0	1	05:03
154	OMT6	OMT	12	279533	280412	281289	282215	1	878	1780	2681	1	1	1	0	1	05:03
85	OMT6	OMT	7	398049	398572	400713	401117	1	2142	2605	3067	1	1	1	0	1	05:03
113	OMT6	OMT	9	247495	247522	247522	247526	1	1	16	30	1	2	1	0	1	03:05
184	OMT6	OMT	14	187825	187884	187910	188016	1	27	109	190	1	2	1	0	1	03:05
206	OMT6	OMT	15	533847	533983	533983	534085	1	1	119	237	1	2	1	0	1	03:05
127	OMT6	OMT	10	459351	459420	459431	459643	1	12	152	291	1	2	1	0	1	03:05
211	OMT6	OMT	15	797043	797205	797205	797362	1	1	160	318	1	2	1	0	1	03:05
80	OMT6	OMT	7	269180	269232	269232	269505	1	1	163	324	1	2	1	0	1	03:05
34	OMT6	OMT	4	301751	301888	301888	302084	1	1	167	332	1	2	1	0	1	03:05
95	OMT6	OMT	7	990505	990538	990659	990718	1	122	167	212	1	2	1	0	1	03:05
190	OMT6	OMT	14	400901	400998	401015	401240	1	18	178	338	1	2	1	0	1	03:05
205	OMT6	OMT	15	511001	511101	511101	511376	1	1	188	374	1	2	1	0	1	03:05
66	OMT6	OMT	5	342731	342945	342945	343116	1	1	193	384	1	2	1	0	1	03:05
42	OMT6	OMT	4	619930	620254	620254	620359	1	1	215	428	1	2	1	0	1	03:05
81	OMT6	OMT	7	271683	271853	271853	272144	1	1	231	460	1	2	1	0	1	03:05
51	OMT6	OMT	4	1108150	1108456	1108511	1108662	1	56	284	511	1	2	1	0	1	03:05
17	OMT6	OMT	2	727268	727326	727581	727716	1	256	352	447	1	2	1	0	1	03:05
230	OMT6	OMT	16	678816	679094	679119	679573	1	26	391	756	1	2	1	0	1	03:05
208	OMT6	OMT	15	682981	683158	683410	683562	1	253	417	580	1	2	1	0	1	03:05
65	OMT6	OMT	5	238975	239168	239238	239782	1	71	439	806	1	2	1	0	1	03:05
151	OMT6	OMT	12	49831	50099	50287	50531	1	189	444	699	1	2	1	0	1	03:05
173	OMT6	OMT	13	82207	82357	82357	83128	1	1	461	920	1	2	1	0	1	03:05
210	OMT6	OMT	15	760366	760705	760705	761321	1	1	478	954	1	2	1	0	1	03:05
16	OMT6	OMT	2	724953	725168	725454	725631	1	287	482	677	1	2	1	0	1	03:05
142	OMT6	OMT	11	345623	345918	345918	346598	1	1	488	974	1	2	1	0	1	03:05
125	OMT6	OMT	10	337582	338042	338042	338561	1	1	490	978	1	2	1	0	1	03:05
218	OMT6	OMT	16	85516	85599	85729	86390	1	131	502	873	1	2	1	0	1	03:05
29	OMT6	OMT	4	78578	78587	78945	79228	1	359	504	649	1	2	1	0	1	03:05
219	OMT6	OMT	16	164740	165213	165244	165730	1	32	511	989	1	2	1	0	1	03:05
48	OMT6	OMT	4	1001692	1001907	1002178	1002467	1	272	523	774	1	2	1	0	1	03:05
37	OMT6	OMT	4	387000	387021	387397	387713	1	377	545	712	1	2	1	0	1	03:05
25	OMT6	OMT	3	210245	210441	210635	211159	1	195	554	913	1	2	1	0	1	03:05
78	OMT6	OMT	7	96337	96869	97109	97316	1	241	610	978	1	2	1	0	1	03:05
118	OMT6	OMT	10	36445	36722	37127	37895	1	406	928	1449	1	2	1	0	1	03:05
8	OMT6	OMT	2	217109	218039	218624	218666	1	586	1071	1556	1	2	1	0	1	03:05
129	OMT6	OMT	10	526176	526730	527538	528639	1	809	1636	2462	1	2	1	0	1	03:05
116	OMT6	OMT	9	406124	406436	408110	408224	1	1675	1887	2099	1	2	1	0	1	03:05
9	OMT6	OMT	2	288339	288484	288990	289129	1	507	648	789	1	3	1	0	1	5:3_6:2_5:3

91	OMT6	OMT	7	892563	893054	894236	894312	1	1183	1466	1748	1	3	1	0	1 5:3_4:4_5:3
225	OMT6	OMT	16	431840	432048	432288	432333	1	241	367	492	1	4	1	0	1 3:5_2:6_3:5
55	OMT6	OMT	4	1398960	1399211	1399679	1399937	1	469	723	976	1	4	1	0	1 5:3_2:6_3:5
133	OMT6	OMT	10	690126	690711	692187	692358	1	1477	1854	2231	1	4	1	0	1 3:5_4:4_3:5_4:4_3:5
106	OMT6	OMT	8	400960	401190	402986	403215	1	1797	2026	2254	1	4	1	0	1 3:5_2:6_3:5_4:4_3:5
170	OMT6	OMT	12	1043284	1043537	1043701	1043895	1	165	388	610	1	7	1	0	1 5:3_6:2
122	OMT6	OMT	10	257310	257383	257831	257958	1	449	548	647	1	7	1	0	1 6:2_5:3
104	OMT6	OMT	8	235099	235912	235973	236137	1	62	550	1037	1	7	1	0	1 5:3_6:2
72	OMT6	OMT	6	94545	95140	95460	95585	1	321	680	1039	1	7	1	0	1 5:3_6:2
181	OMT6	OMT	13	777598	777667	778144	779842	1	478	1361	2243	1	7	1	0	1 5:3_6:2
53	OMT6	OMT	4	1333678	1333799	1334562	1334981	1	764	1033	1302	1	7	1	0	1 5:3_4:4_5:3_4:4_6:2
49	OMT6	OMT	4	1005047	1005151	1005358	1005567	1	208	364	519	1	8	1	0	1 3:5_2:6
195	OMT6	OMT	14	651410	652054	652419	652841	1	366	898	1430	1	8	1	0	1 2:6_3:5
100	OMT6	OMT	8	97715	98248	99112	99909	1	865	1529	2193	1	8	1	0	1 2:6_3:5
193	OMT6	OMT	14	577067	579044	579894	580292	1	851	2038	3224	1	8	1	0	1 2:6_3:5
175	OMT6	OMT	13	352695	353026	353260	353329	1	235	434	633	1	10	1	0	1 06:02
21	OMT6	OMT	3	52371	52418	52418	52747	1	1	188	375	1	10.1	1	0	1 02:06
111	OMT6	OMT	9	215186	215644	215644	215993	1	1	404	806	1	10.1	1	0	1 02:06
215	OMT6	OMT	15	1006918	1007685	1009862	1009919	1	2178	2589	3000	1	10.1	1	0	1 02:06
135	OMT6	OMT	11	30068	31754	33673	34051	1	1920	2951	3982	1	10.1	1	0	1 02:06
58	OMT6	OMT	4	1497628	1497856	1498087	1498561	1	232	582	932	2	11	1	0	1 5:3_5:3a
94	OMT6	OMT	7	919139	919329	919947	920266	1	619	873	1126	2	11	1	0	1 5:3_5:3a
84	OMT6	OMT	7	393263	393326	394550	394643	1	1225	1302	1379	2	11	1	0	1 5:3_5:3a
63	OMT6	OMT	5	201006	201879	203238	203277	1	1360	1815	2270	2	11	1	0	1 5:3_5:3a
71	OMT6	OMT	6	45217	45521	45896	45926	1	376	542	708	2	12	1	0	1 3:5_3:5a
41	OMT6	OMT	4	599865	599964	600480	600632	1	517	642	766	2	12	1	0	1 3:5_3:5a
22	OMT6	OMT	3	76009	76939	78909	79012	1	1971	2487	3002	2	12	1	0	1 3:5_3:5a
228	OMT6	OMT	16	590589	590724	591899	592129	1	1176	1358	1539	2	13	1	0	1 5:3_5:3a_4:4_5:3a_4:4_5:3a
3	OMT6	OMT	1	107970	108457	108928	109735	1	472	1118	1764	2	14	1	0	1 3:5_2:6_3:5_3:5a
40	OMT6	OMT	4	568816	568833	578452	578566	1	9620	9685	9749	2	14	1	0	1 3:5_3:5a_4:4_3:5_4:4_3:5a
90	OMT6	OMT	7	847980	848452	849134	849405	1	683	1054	1424	2	15	1	0	1 5:3_4:4_5:3a
149	OMT6	OMT	12	28820	29085	30008	30375	1	924	1239	1554	2	15	1	0	1 5:3_4:4_5:3a
138	OMT6	OMT	11	263151	263194	265522	265706	1	2329	2442	2554	2	16	1	0	1 3:5_4:4_3:5a
212	OMT6	OMT	15	867663	868024	870449	871008	1	2426	2885	3344	2	16	1	0	1 3:5_4:4_3:5a
222	OMT6	OMT	16	214068	214281	215286	215587	1	1006	1262	1518	2	17	1	0	1 5:3_4:4_5:3a_6:2
54	OMT6	OMT	4	1388273	1388378	1389437	1389786	1	1060	1286	1512	2	17	1	0	1 5:3_4:4_5:3a_6:2
121	OMT6	OMT	10	172240	172657	175309	175369	1	2653	2891	3128	2	17	1	0	1 5:3_4:4_5:3a_6:2_5:3a
68	OMT6	OMT	5	490456	490516	492341	498773	1	1826	5071	8316	2	19	1	0	1 5:3_6:2_5:3a
56	OMT6	OMT	4	1435868	1436177	1436962	1437126	1	786	1022	1257	2	20	1	0	1 3:5_2:6_3:5a
2	OMT6	OMT	1	93563	94472	95748	96047	2_nonsis	1277	1880	2483	3	30	1	0	1 5:3_5:3a
157	OMT6	OMT	12	423854	424103	425696	425939	2_nonsis	1594	1839	2084	3	30	1	0	1 6:2_5:3_3:5
101	OMT6	OMT	8	120445	121477	122169	122633	2_nonsis	693	1440	2187	3	30	1	0	1 6:2_4:4_5:3_2:6
202	OMT6	OMT	15	285417	285557	287386	288164	2_nonsis	1830	2288	2746	3	31	1	0	1 4:4ai_5:3
199	OMT6	OMT	15	168268	168295	168885	169317	2_nonsis	591	820	1048	3	31	1	0	1 5:3_4:4ai_3:5
189	OMT6	OMT	14	391590	391752	393787	394167	2_nonsis	2036	2306	2576	3	31	1	0	1 5:3_4:4ai_5:3a
158	OMT6	OMT	12	509982	510120	511389	511536	2_nonsis	1270	1412	1553	3	31	1	0	1 5:3_4:4ai_3:5_3:5a
140	OMT6	OMT	11	283904	284248	285383	287276	2_nonsis	1136	2254	3371	3	31	1	0	1 5:3_5:3a_4:4ai_3:5
141	OMT6	OMT	11	307722	307855	309294	309310	2_nonsis	1440	1514	1587	3	31	1	0	1 5:3_4:4ai_3:5_5:3_4:4_5:3a
161	OMT6	OMT	12	553728	554116	556056	556208	2_nonsis	1941	2210	2479	3	31	1	0	1 2:6_3:5_2:6_3:5a_2:6_4:4ai
227	OMT6	OMT	16	532161	532319	532319	532708	2_nonsis	1	274	546	1	1	1	1	0 (5:3)_(4:4aCO)
64	OMT6	OMT	5	236202	236672	236672	237191	2_nonsis	1	495	988	1	1	1	1	0 (5:3)_(4:4aCO)
109	OMT6	OMT	9	37068	37170	37222	39244	2_nonsis	53	1114	2175	1	1	1	1	0 (5:3)_(4:4aCO)
6	OMT6	OMT	2	71161	71276	71276	71395	2_nonsis	1	117	233	1	2	1	1	0 (3:5)_(4:4aCO)
167	OMT6	OMT	12	828244	828345	828345	828622	2_nonsis	1	189	377	1	2	1	1	0 (3:5)_(4:4aCO)
180	OMT6	OMT	13	603797	603987	603987	604354	2_nonsis	1	279	556	1	2	1	1	0 (3:5)_(4:4aCO)
7	OMT6	OMT	2	117726	117972	117972	118304	2_nonsis	1	289	577	1	2	1	1	0 (3:5)_(4:4aCO)
52	OMT6	OMT	4	1296388	1296525	1296525	1297076	2_nonsis	1	344	687	1	2	1	1	0 (3:5)_(4:4aCO)
62	OMT6	OMT	5	160248	160729	161767	162008	2_nonsis	1039	1399	1759	1	2	1	1	0 (3:5)_(4:4aCO)
132	OMT6	OMT	10	596468	596891	596891	601293	2_nonsis	1	2413	4824	1	2	1	1	0 (3:5)_(4:4aCO)
93	OMT6	OMT	7	906630	906758	908884	909136	2_nonsis	2127	2316	2505	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)

10	OMT6	OMT	2	342041	342236	342723	343406	2_nonsis	488	926	1364	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
196	OMT6	OMT	14	698753	699116	700166	700405	2_nonsis	1051	1351	1651	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
156	OMT6	OMT	12	416026	416228	417575	417641	2_nonsis	1348	1481	1614	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
86	OMT6	OMT	7	609044	609405	610218	610674	2_nonsis	814	1222	1629	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
76	OMT6	OMT	7	57501	57822	58485	60729	2_nonsis	664	1946	3227	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
213	OMT6	OMT	15	892334	892523	892736	892829	2_nonsis	214	354	494	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
153	OMT6	OMT	12	223541	223716	224139	224193	2_nonsis	424	538	651	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
44	OMT6	OMT	4	721991	722687	722776	723150	2_nonsis	90	624	1158	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
69	OMT6	OMT	5	545109	545863	545863	546069	2_nonsis	1	480	959	1	11	1	1	0	(4:4ai)_(4:4bCO)
182	OMT6	OMT	13	830002	830235	830613	831156	2_nonsis	379	766	1153	1	11	1	1	0	(4:4ai)_(5:3)_(4:4bCO)
57	OMT6	OMT	4	1475979	1476168	1477311	1477505	2_nonsis	1144	1335	1525	1	11	1	1	0	(4:4ai)_(4:4bCO)_(6:2)_(5:3)_(4:4b)
97	OMT6	OMT	7	1011510	1012069	1014216	1014432	2_nonsis	2148	2535	2921	1	11	1	1	0	(4:4ai)_(3:5)_(2:6)_(4:4bCO)_(3:5)_(4:4b)
26	OMT6	OMT	3	246853	247156	248853	249269	2_nonsis	1698	2057	2415	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
155	OMT6	OMT	12	368695	368748	370768	370966	2_nonsis	2021	2146	2270	1	12	1	1	0	(6:2)_(4:4)_(5:3)_(4:4aCO)
110	OMT6	OMT	9	141141	141212	141990	141990	2_nonsis	700	774	848	1	12	1	1	0	(2:6)_(3:5)_(4:4aCO)_(2:6)_(4:4a)
96	OMT6	OMT	7	999433	999807	1000659	1000855	2_nonsis	853	1137	1421	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(3:5)_(4:4a)
73	OMT6	OMT	6	173398	173500	174951	175060	2_nonsis	1452	1557	1661	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4a)
33	OMT6	OMT	4	296339	296793	299200	299792	2_nonsis	2408	2930	3452	1	12	1	1	0	(3:5)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
5	OMT6	OMT	1	191818	192170	192170	192196	2_nonsis	1	189	377	1	15	1	1	0	(6:2)_(4:4aCO)
124	OMT6	OMT	10	302207	302882	302882	302892	2_nonsis	1	343	684	1	15	1	1	0	(6:2)_(4:4aCO)
131	OMT6	OMT	10	550333	550587	550609	551032	2_nonsis	23	361	698	1	15	1	1	0	(6:2)_(4:4aCO)
188	OMT6	OMT	14	258883	258967	259408	259493	2_nonsis	442	526	609	1	15	1	1	0	(6:2)_(4:4aCO)
77	OMT6	OMT	7	76882	76989	76989	77983	2_nonsis	1	551	1100	1	15	1	1	0	(6:2)_(4:4aCO)
79	OMT6	OMT	7	142176	142353	142710	142935	2_nonsis	358	558	758	1	15	1	1	0	(6:2)_(4:4aCO)
235	OMT6	OMT	16	912387	912564	912647	913446	2_nonsis	84	571	1058	1	15	1	1	0	(6:2)_(4:4aCO)
120	OMT6	OMT	10	122256	122391	123026	123360	2_nonsis	636	870	1103	1	15	1	1	0	(6:2)_(4:4aCO)
70	OMT6	OMT	6	36660	36739	37375	38086	2_nonsis	637	1031	1425	1	15	1	1	0	(6:2)_(4:4aCO)
105	OMT6	OMT	8	352905	353097	354125	354571	2_nonsis	1029	1347	1665	1	15	1	1	0	(6:2)_(4:4aCO)
172	OMT6	OMT	13	79258	79575	79575	79713	2_nonsis	1	228	454	1	16	1	1	0	(2:6)_(4:4aCO)
209	OMT6	OMT	15	725534	725550	725863	726404	2_nonsis	314	592	869	1	16	1	1	0	(2:6)_(4:4aCO)
160	OMT6	OMT	12	522914	525267	525539	525791	2_nonsis	273	1575	2876	1	16	1	1	0	(2:6)_(4:4aCO)
46	OMT6	OMT	4	870568	870950	870950	884980	2_nonsis	1	7206	14411	1	16	1	1	0	(2:6)_(4:4aCO)
60	OMT6	OMT	5	27272	27604	27272	27604	2_nonsis	0	166	331	1	100	1	1	0	(4:4aCO)
99	OMT6	OMT	8	17157	17641	17157	17641	2_nonsis	0	242	483	1	100	1	1	0	(4:4aCO)
174	OMT6	OMT	13	164532	165032	164532	165032	2_nonsis	0	250	499	1	100	1	1	0	(4:4aCO)
45	OMT6	OMT	4	835444	836028	835444	836028	2_nonsis	0	292	583	1	100	1	1	0	(4:4aCO)
217	OMT6	OMT	16	73338	73929	73338	73929	2_nonsis	0	295	590	1	100	1	1	0	(4:4aCO)
82	OMT6	OMT	7	349285	349962	349285	349962	2_nonsis	0	338	676	1	100	1	1	0	(4:4aCO)
224	OMT6	OMT	16	348815	349538	348815	349538	2_nonsis	0	361	722	1	100	1	1	0	(4:4aCO)
38	OMT6	OMT	4	407403	408221	407403	408221	2_nonsis	0	409	817	1	100	1	1	0	(4:4aCO)
200	OMT6	OMT	15	218142	219124	218142	219124	2_nonsis	0	491	981	1	100	1	1	0	(4:4aCO)
103	OMT6	OMT	8	186453	187527	186453	187527	2_nonsis	0	537	1073	1	100	1	1	0	(4:4aCO)
191	OMT6	OMT	14	425816	427278	425816	427278	2_nonsis	0	731	1461	1	100	1	1	0	(4:4aCO)
31	OMT6	OMT	4	196851	198376	196851	198376	2_nonsis	0	762	1524	1	100	1	1	0	(4:4aCO)
4	OMT6	OMT	1	132066	135319	132066	135319	2_nonsis	0	1626	3252	1	100	1	1	0	(4:4aCO)
134	OMT6	OMT	11	23532	27301	23532	27301	2_nonsis	0	1884	3768	1	100	1	1	0	(4:4aCO)
30	OMT6	OMT	4	144344	144733	146582	147362	2_nonsis	1850	2434	3017	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
18	OMT6	OMT	2	744519	744640	745895	746171	2_nonsis	1256	1454	1651	2	30	1	1	0	(5:3)_(5:3a)_(4:4)_(5:3)_(4:4aCO)
171	OMT6	OMT	12	1051488	1053098	1055717	1055872	2_nonsis	2620	3502	4383	2	30	1	1	0	(5:3)_(5:3a)_(4:4)_(5:3b)_(4:4aCO)
137	OMT6	OMT	11	94121	94372	101564	102604	2_nonsis	7193	7838	8482	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
27	OMT6	OMT	4	51098	51199	53011	53077	2_nonsis	1813	1896	1978	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
185	OMT6	OMT	14	189445	189694	192676	192780	2_nonsis	2983	3159	3334	2	31	1	1	0	(3:5)_(3:5a)_(4:4ai)_(4:4bCO)
88	OMT6	OMT	7	733088	733373	734123	734330	2_nonsis	751	996	1241	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
192	OMT6	OMT	14	537564	537637	539848	539903	2_nonsis	2212	2275	2338	2	32	1	1	0	(3:5)_(2:6)_(5:3a)_(4:4aCO)
165	OMT6	OMT	12	753571	754314	757131	757763	2_nonsis	2818	3505	4191	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
19	OMT6	OMT	2	790890	791057	795035	795146	2_nonsis	3979	4117	4255	2	32	1	1	0	(3:5)_(4:4ai)_(3:5a)_(4:4bCO)
50	OMT6	OMT	4	1021040	1021881	1026927	1027140	2_nonsis	5047	5573	6099	2	32	1	1	0	(3:5)_(4:4ai)_(3:5a)_(4:4bCO)
13	OMT6	OMT	2	656699	657139	662444	666708	2_nonsis	5306	7657	10008	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
234	OMT6	OMT	16	840627	841238	844218	857345	2_nonsis	2981	9849	16717	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
24	OMT6	OMT	3	156289	156517	158345	158451	2_nonsis	1829	1995	2161	2	32	1	1	0	(3:5)_(4:4)_(2:6)_(3:5a)_(4:4aCO)

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18
117	OMT6	OMT	9	424253	424322	425170	425239	2_nonsis	849	917	985	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
150	OMT6	OMT	12	36477	36694	37762	37937	2_nonsis	1069	1264	1459	2	32	1	1	0	(3:5)_(4:4ai)_(2:6)_(4:4bCO)_(3:5a)_(4:4b)
152	OMT6	OMT	12	85270	85385	87470	87559	2_nonsis	2086	2187	2288	2	32	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
233	OMT6	OMT	16	830277	831160	834629	834822	2_nonsis	3470	4007	4544	2	32	1	1	0	(5:3)_(4:4ai)_(5:3a)_(6:2)_(5:3a)_(4:4bCO)
179	OMT6	OMT	13	513425	513553	517743	518064	2_nonsis	4191	4415	4638	2	32	1	1	0	(3:5)_(4:4)_(3:5a)_(2:6)_(4:4)_(3:5)_(4:4aCO)
36	OMT6	OMT	4	380668	381268	382830	383033	2_nonsis	1563	1964	2364	2	32	1	1	0	(3:5)_(4:4ai)_(3:5a)_(2:6)_(3:5a)_(4:4bCO)_(3:5a)_(4:4b)
14	OMT6	OMT	2	697503	699461	702673	703042	2_nonsis	3213	4376	5538	2	32	1	1	0	(4:4ai)_(5:3)_(6:2)_(5:3a)_(6:2)_(4:4bCO)_(5:3a)_(6:2)_(4:4b)
12	OMT6	OMT	2	531940	533263	538606	538919	2_nonsis	5344	6161	6978	2	32	1	1	0	(3:5)_(4:4)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
176	OMT6	OMT	13	355563	355571	355763	356149	2_nonsis	193	389	585	3	20	1	1	0	(3:5)_(6:2)_(4:4aCO)
87	OMT6	OMT	7	670175	670263	670598	670804	2_nonsis	336	482	628	3	20	1	1	0	(6:2)_(3:5)_(4:4aCO)
20	OMT6	OMT	3	41451	41571	42419	42698	2_nonsis	849	1048	1246	3	20	1	1	0	(2:6)_(5:3)_(4:4aCO)
147	OMT6	OMT	11	527758	528174	529197	529548	2_nonsis	1024	1407	1789	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
143	OMT6	OMT	11	434756	434978	436087	436826	2_nonsis	1110	1590	2069	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
47	OMT6	OMT	4	926737	927283	930409	930813	2_nonsis	3127	3601	4075	3	20	1	1	0	(2:6)_(5:3)_(4:4aCO)
75	OMT6	OMT	6	226238	226370	227223	227351	2_nonsis	854	983	1112	3	20	1	1	0	(5:3)_(6:2)_(3:5)_(4:4aCO)
216	OMT6	OMT	15	1064466	1064500	1065462	1065522	2_nonsis	963	1009	1055	3	20	1	1	0	(6:2)_(5:3)_(3:5)_(4:4aCO)
112	OMT6	OMT	9	237295	237441	238957	239011	2_nonsis	1517	1616	1715	3	20	1	1	0	(6:2)_(2:6)_(3:5)_(4:4aCO)
194	OMT6	OMT	14	628490	629955	631369	631514	2_nonsis	1415	2219	3023	3	20	1	1	0	(5:3)_(3:5)_(2:6)_(4:4aCO)
119	OMT6	OMT	10	68659	68967	69814	70030	2_nonsis	848	1109	1370	3	20	1	1	0	(5:3)_(3:5)_(5:3)_(4:4)_(4:4aCO)
11	OMT6	OMT	2	392022	392314	393604	393708	2_nonsis	1291	1488	1685	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(5:3)_(4:4aCO)
128	OMT6	OMT	10	466454	467010	467589	469453	2_nonsis	580	1789	2998	3	20	1	1	0	(6:2)_(2:6)_(3:5)_(4:4)_(4:4aCO)
67	OMT6	OMT	5	458865	458964	460411	461582	2_nonsis	1448	2082	2716	3	20	1	1	0	(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
126	OMT6	OMT	10	389963	390467	392346	392871	2_nonsis	1880	2394	2907	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(3:5a)_(4:4aCO)
15	OMT6	OMT	2	715932	716328	718805	719463	2_nonsis	2478	3004	3530	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)_(3:5a)_(4:4a)
114	OMT6	OMT	9	337352	337478	340356	340507	2_nonsis	2879	3017	3154	3	20	1	1	0	(6:2)_(5:3)_(6:2)_(3:5)_(4:4aCO)
204	OMT6	OMT	15	492629	492865	494573	494732	2_nonsis	1709	1906	2102	3	20	1	1	0	(5:3)_(4:4)_(6:2)_(4:4)_(2:6)_(4:4aCO)_(6:2)_(4:4a)
163	OMT6	OMT	12	710710	710866	711432	711547	2_nonsis	567	702	836	3	21	1	1	0	(4:4ai)_(5:3)_(4:4ai)_(3:5)_(4:4bCO)
168	OMT6	OMT	12	953884	954049	955645	955822	2_nonsis	1597	1767	1937	3	21	1	1	0	(3:5)_(2:6)_(5:3)_(2:6)_(4:4ai)_(5:3)_(4:4bCO)
1	OMT6	OMT	1	77152	77433	82099	82230	2_sis	4667	4872	5077	0	1	2	0	2	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(5:3a)_(4:4)
59	OMT6	OMT	5	18839	18992	18992	19001	2_sis	1	81	161	0	1	2	0	2	(1:7)_(4:4)
83	OMT6	OMT	7	382993	383186	388627	389082	3	5442	5765	6088	0	1	2	0	2	(5:3)_(6:2i)_(7:1)_(6:2i)_(7:1)_(7:1a)_(6:2ai)_(5:3a)_(6:2ai)_(4:4ai)_(4:4)
123	OMT6	OMT	10	290730	290883	291981	292117	2_sis	1099	1243	1386	0	1	2	0	2	(3:5)_(2:6i)_(4:4)_(3:5a)_(2:6a)_(3:5a)_(4:4)
183	OMT6	OMT	14	79763	80071	81857	82092	3	1787	2058	2328	0	1	2	0	2	(3:5)_(3:5a)_(4:4)
39	OMT6	OMT	4	546573	547556	551775	551991	3	4220	4819	5417	0	2	2	1	1	(5:3)_(3:5)_(5:3a)_(4:4aCO)_(5:3a)_(4:4bi)_(3:5a)_(4:4a)
102	OMT6	OMT	8	140123	142800	160782	161874	3	17983	19867	21750	0	2	2	1	1	(6:2)_(5:3)_(4:4aCO)_(2:6)_(4:4a)
108	OMT6	OMT	8	515688	516015	519135	519269	4	3121	3351	3580	0	2	2	2	0	(3:5)_(5:3)_(6:2i)_(3:5a)_(3:5b)_(4:4aCO)_(3:5b)_(4:4a)
169	OMT6	OMT	12	1001464	1001833	1003348	1004257	3	1516	2154	2792	0	2	2	1	1	(3:5)_(4:4ai)_(3:5)_(5:3)_(4:4bCO)
207	OMT6	OMT	15	586076	586304	589303	589700	3	3000	3312	3623	0	2	2	1	1	(3:5)_(5:3)_(6:2)_(5:3a)_(4:4ai)_(6:2ai)_(5:3b)_(6:2ai)_(5:3b)_(4:4bCO)
220	OMT6	OMT	16	175137	175312	176684	177089	3	1373	1662	1951	0	2	2	1	1	(6:2)_(4:4aCO)_(3:5)_(4:4a)
232	OMT6	OMT	16	811809	811842	813201	813489	3	1360	1520	1679	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
74	OMT6	OMT	6	203623	203665	213776	214043	3	10112	10266	10419	0	3	2	1	2	(2:6)_(3:5)_(4:4aCO)_(5:3)_(6:2i)_(5:3a)_(6:2ai)_(5:3b)_(4:4bCO)
107	OMT6	OMT	8	420572	420823	424326	425219	3	3504	4075	4646	0	3	2	0	0	(4:4ai)_(4:4bCO)_(5:3)_(4:4b)_(3:5)_(4:4ai)_(3:5a)_(4:4ci)_(4:4CO)
115	OMT6	OMT	9	384418	384629	395522	395890	3	10894	11183	11471	0	3	2	1	1	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)_(3:5)_(2:6)_(2:6a)_(3:5a)_(4:4bCO)
136	OMT6	OMT	11	67187	67304	71541	71930	3	4238	4490	4742	0	3	2	0	2	(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)_(2:6)_(3:5)_(2:6)_(3:5a)_(4:4CO)_(2:6)_(1:7)_(2:6ai)_(3:5b)_(2:6ai)_(2:6b)_(2:6ai)_(3:5b)_(2:6ci)_(3:5c)_(4:4)
139	OMT6	OMT	11	278119	278179	279467	279551	2_nonsis	1289	1360	1431	0	3	2	0	2	(2:6)_(3:5)_(5:3a)_(6:2)_(4:4aCO)_(4:4bi)_(5:3b)_(4:4CO)
198	OMT6	OMT	15	107690	108214	109424	109584	3	1211	1552	1893	0	3	2	1	1	(4:4aCO)_(3:5)_(5:3)_(4:4bCO)
241	OMT6	OMT	1	198713	198815	203111	230218	1	0	15752	31504	0	4	1	NA	NA	
46	OMT7	OMT	4	1058864	1059094	1059127	1059179	1	34	174	314	1	1	1	0	1	05:03
183	OMT7	OMT	14	559202	559420	559472	559575	1	53	213	372	1	1	1	0	1	05:03
6	OMT7	OMT	1	189970	190025	190031	190402	1	7	219	431	1	1	1	0	1	05:03
88	OMT7	OMT	8	17157	17359	17359	17641	1	1	242	483	1	1	1	0	1	05:03
73	OMT7	OMT	6	228617	229028	229028	229247	1	1	315	629	1	1	1	0	1	05:03
17	OMT7	OMT	2	392544	392785	392785	393180	1	1	318	635	1	1	1	0	1	05:03
64	OMT7	OMT	5	441591	441625	441963	442012	1	339	380	420	1	1	1	0	1	05:03
80	OMT7	OMT	7	190333	190505	190661	191102	1	157	463	768	1	1	1	0	1	05:03
130	OMT7	OMT	11	270852	271065	271321	271548	1	257	476	695	1	1	1	0	1	05:03
115	OMT7	OMT	10	421930	422597	422597	422897	1	1	484	966	1	1	1	0	1	05:03
119	OMT7	OMT	10	579112	579350	579671	579770	1	322	490	657	1	1	1	0	1	05:03
126	OMT7	OMT	11	82733	83549	83549	83733	1	1	500	999	1	1	1	0	1	05:03
184	OMT7	OMT	14	585226	585962	585996	586230	1	35	519	1003	1	1	1	0	1	05:03

206	OMT7	OMT	16	279975	280422	280470	280994	1	49	534	1018	1	1	1	0	1 05:03
136	OMT7	OMT	11	427874	428081	428081	428986	1	1	556	1111	1	1	1	0	1 05:03
101	OMT7	OMT	9	249032	249546	249546	250194	1	1	581	1161	1	1	1	0	1 05:03
132	OMT7	OMT	11	328709	329482	329686	329885	1	205	690	1175	1	1	1	0	1 05:03
51	OMT7	OMT	4	1416384	1416431	1417050	1417646	1	620	941	1261	1	1	1	0	1 05:03
27	OMT7	OMT	3	102669	103556	103955	104476	1	400	1103	1806	1	1	1	0	1 05:03
171	OMT7	OMT	13	755564	757086	757281	757815	1	196	1223	2250	1	1	1	0	1 05:03
104	OMT7	OMT	9	332503	333073	333581	334640	1	509	1323	2136	1	1	1	0	1 05:03
79	OMT7	OMT	7	178509	179910	180364	181036	1	455	1491	2526	1	1	1	0	1 05:03
182	OMT7	OMT	14	510479	510728	512000	512400	1	1273	1597	1920	1	1	1	0	1 05:03
168	OMT7	OMT	13	686772	687199	688379	689370	1	1181	1889	2597	1	1	1	0	1 05:03
157	OMT7	OMT	13	41174	42127	43336	44157	1	1210	2096	2982	1	1	1	0	1 05:03
147	OMT7	OMT	12	279509	279533	281289	282215	1	1757	2231	2705	1	1	1	0	1 05:03
208	OMT7	OMT	16	337160	337250	337250	337348	1	1	94	187	1	2	1	0	1 03:05
59	OMT7	OMT	5	68996	69083	69083	69209	1	1	107	212	1	2	1	0	1 03:05
55	OMT7	OMT	4	1502380	1502449	1502449	1502604	1	1	112	223	1	2	1	0	1 03:05
103	OMT7	OMT	9	315163	315261	315283	315406	1	23	133	242	1	2	1	0	1 03:05
97	OMT7	OMT	9	85758	85860	85860	86070	1	1	156	311	1	2	1	0	1 03:05
211	OMT7	OMT	16	499073	499315	499315	499388	1	1	158	314	1	2	1	0	1 03:05
19	OMT7	OMT	2	454566	454753	454753	454884	1	1	159	317	1	2	1	0	1 03:05
58	OMT7	OMT	5	53618	53693	53785	53876	1	93	175	257	1	2	1	0	1 03:05
172	OMT7	OMT	13	798333	798592	798593	798732	1	2	200	398	1	2	1	0	1 03:05
202	OMT7	OMT	16	22388	22478	22571	22695	1	94	200	306	1	2	1	0	1 03:05
133	OMT7	OMT	11	385427	385473	385688	385714	1	216	251	286	1	2	1	0	1 03:05
7	OMT7	OMT	1	198299	198699	198713	198815	1	15	265	515	1	2	1	0	1 03:05
216	OMT7	OMT	16	687708	687978	687978	688591	1	1	442	882	1	2	1	0	1 03:05
95	OMT7	OMT	8	488465	488588	488588	489445	1	1	490	979	1	2	1	0	1 03:05
193	OMT7	OMT	15	487166	487809	487838	488123	1	30	493	956	1	2	1	0	1 03:05
15	OMT7	OMT	2	306376	306932	307032	307275	1	101	500	898	1	2	1	0	1 03:05
56	OMT7	OMT	5	33002	33344	33706	33782	1	363	571	779	1	2	1	0	1 03:05
9	OMT7	OMT	2	216250	216513	217015	217070	1	503	661	819	1	2	1	0	1 03:05
128	OMT7	OMT	11	204194	205481	205481	205607	1	1	707	1412	1	2	1	0	1 03:05
35	OMT7	OMT	4	413995	414381	414726	415078	1	346	714	1082	1	2	1	0	1 03:05
116	OMT7	OMT	10	461843	461906	462595	462605	1	690	726	761	1	2	1	0	1 03:05
28	OMT7	OMT	3	186028	186237	186237	187655	1	1	814	1626	1	2	1	0	1 03:05
180	OMT7	OMT	14	404051	404995	405175	405600	1	181	865	1548	1	2	1	0	1 03:05
191	OMT7	OMT	15	233865	234020	234731	235143	1	712	995	1277	1	2	1	0	1 03:05
141	OMT7	OMT	12	86634	87286	88002	88069	1	717	1076	1434	1	2	1	0	1 03:05
93	OMT7	OMT	8	267649	267804	268308	269395	1	505	1125	1745	1	2	1	0	1 03:05
178	OMT7	OMT	14	274328	274637	275457	275934	1	821	1213	1605	1	2	1	0	1 03:05
24	OMT7	OMT	3	55716	56210	56432	58033	1	223	1270	2316	1	2	1	0	1 03:05
187	OMT7	OMT	14	709906	710457	711379	711615	1	923	1316	1708	1	2	1	0	1 03:05
34	OMT7	OMT	4	408894	410728	411189	411335	1	462	1451	2440	1	2	1	0	1 03:05
135	OMT7	OMT	11	400521	400972	401916	402660	1	945	1542	2138	1	2	1	0	1 03:05
189	OMT7	OMT	15	71365	72322	73362	73589	1	1041	1632	2223	1	2	1	0	1 03:05
176	OMT7	OMT	14	185896	186475	186992	187346	1	518	984	1449	1	3	1	0	1 5:3_4:4_5:3
74	OMT7	OMT	6	239696	239766	240682	240940	1	917	1080	1243	1	3	1	0	1 5:3_4:4_5:3
146	OMT7	OMT	12	259051	259126	260496	260584	1	1371	1452	1532	1	3	1	0	1 5:3_4:4_5:3
48	OMT7	OMT	4	1090145	1090269	1093048	1093368	1	2780	3001	3222	1	3	1	0	1 5:3_6:2_5:3
164	OMT7	OMT	13	456970	457507	459508	459995	1	2002	2513	3024	1	3	1	0	1 5:3_4:4_5:3_4:4_5:3
76	OMT7	OMT	7	72181	72738	73362	73438	1	625	941	1256	1	4	1	0	1 3:5_4:4_3:5
16	OMT7	OMT	2	313868	314198	315318	315655	1	1121	1454	1786	1	4	1	0	1 3:5_2:6_3:5
100	OMT7	OMT	9	215644	215993	216106	216122	1	114	296	477	1	7	1	0	1 5:3_6:2
30	OMT7	OMT	3	225088	225116	225200	225631	1	85	314	542	1	7	1	0	1 6:2_5:3
214	OMT7	OMT	16	677836	678266	678816	679094	1	551	904	1257	1	7	1	0	1 6:2_5:3
38	OMT7	OMT	4	549856	550499	550893	551387	1	395	963	1530	1	7	1	0	1 5:3_6:2
11	OMT7	OMT	2	256767	256925	257565	258058	1	641	966	1290	1	7	1	0	1 6:2_5:3
137	OMT7	OMT	11	469355	469480	469719	469831	1	240	358	475	1	8	1	0	1 2:6_3:5
83	OMT7	OMT	7	384239	384425	384678	384785	1	254	400	545	1	8	1	0	1 2:6_3:5
71	OMT7	OMT	6	169022	169147	169663	169872	1	517	683	849	1	8	1	0	1 3:5_2:6

131	OMT7	OMT	11	308754	308786	310035	310373		1	1250	1434	1618	1	8	1	0	1 2:6_3:5
218	OMT7	OMT	16	827752	827895	829386	829418		1	1492	1579	1665	1	8	1	0	1 3:5_2:6
152	OMT7	OMT	12	778158	779222	780728	781856		1	1507	2602	3697	1	8	1	0	1 3:5_2:6
174	OMT7	OMT	13	870588	871217	873246	874942		1	2030	3192	4353	1	8	1	0	1 3:5_2:6
159	OMT7	OMT	13	168722	168744	169808	169962		1	1065	1152	1239	1	8	1	0	1 3:5_2:6_3:5_2:6
181	OMT7	OMT	14	495101	495222	496505	496570		1	1284	1376	1468	1	8	1	0	1 2:6_3:5_4:4_3:5
215	OMT7	OMT	16	681914	682109	682109	682384		1	1	235	469	1	10	1	0	1 06:02
23	OMT7	OMT	3	39861	40089	40205	40294		1	117	275	432	1	10	1	0	1 06:02
67	OMT7	OMT	5	523260	523683	523683	524394		1	1	567	1133	1	10	1	0	1 06:02
12	OMT7	OMT	2	290619	291653	292193	292212		1	541	1067	1592	1	10	1	0	1 06:02
196	OMT7	OMT	15	638644	639033	639042	639159		1	10	262	514	1	10.1	1	0	1 02:06
143	OMT7	OMT	12	107971	108813	108813	109073		1	1	551	1101	1	10.1	1	0	1 02:06
145	OMT7	OMT	12	252885	253274	253791	253941		1	518	787	1055	2	11	1	0	1 5:3_5:3a
96	OMT7	OMT	9	53238	53717	54480	55071		1	764	1298	1832	2	11	1	0	1 5:3_5:3a
42	OMT7	OMT	4	754071	754974	755547	756152		1	574	1327	2080	2	11	1	0	1 5:3_5:3a
41	OMT7	OMT	4	720645	721283	722085	722687		1	803	1422	2041	2	11	1	0	1 5:3_5:3a
166	OMT7	OMT	13	477118	477780	478673	479146		1	894	1461	2027	2	11	1	0	1 5:3_5:3a
203	OMT7	OMT	16	52375	52500	53945	54119		1	1446	1595	1743	2	11	1	0	1 5:3_5:3a
36	OMT7	OMT	4	423787	423847	424526	424905		1	680	899	1117	2	12	1	0	1 3:5_3:5a
65	OMT7	OMT	5	460411	461582	462226	462614		1	645	1424	2202	2	12	1	0	1 3:5_3:5a
94	OMT7	OMT	8	421507	421639	422992	423045		1	1354	1446	1537	2	13	1	0	1 5:3_6:2_5:3_5:3a
111	OMT7	OMT	10	290542	290669	292319	292331		1	1651	1720	1788	2	13	1	0	1 5:3_4:4_5:3_5:3a_4:4_5:3a
200	OMT7	OMT	15	930310	930799	931340	931409		1	542	820	1098	2	15	1	0	1 5:3_4:4_5:3a
61	OMT7	OMT	5	193949	194375	194773	195341		1	399	895	1391	2	15	1	0	1 5:3_4:4_5:3a
45	OMT7	OMT	4	1054109	1054225	1055277	1055562		1	1053	1253	1452	2	16	1	0	1 3:5_4:4_3:5a
127	OMT7	OMT	11	91402	91565	92653	92948		1	1089	1317	1545	2	16	1	0	1 3:5_4:4_3:5a
207	OMT7	OMT	16	306755	307244	308420	308781		1	1177	1601	2025	2	16	1	0	1 3:5_4:4_3:5a
69	OMT7	OMT	6	95849	96304	97819	97944		1	1516	1805	2094	2	16	1	0	1 3:5_4:4_3:5a
1	OMT7	OMT	1	66178	66696	71673	72952		1	4978	5876	6773	2	17	1	0	1 5:3_4:4_5:3a_6:2
163	OMT7	OMT	13	433952	434151	437392	437945		1	3242	3617	3992	2	18	1	0	1 3:5_4:4_3:5a_4:4_3:5a
155	OMT7	OMT	12	1009719	1011169	1012226	1013592		1	1058	2465	3872	2	20	1	0	1 3:5_2:6_3:5a
26	OMT7	OMT	3	71427	71575	75892	76009		1	4318	4450	4581	2	20	1	0	1 3:5_2:6_3:5a
169	OMT7	OMT	13	715257	715590	716783	718679		1	1194	2308	3421	2	22	1	0	1 3:5_2:6_3:5a_4:4_3:5a
204	OMT7	OMT	16	93759	93996	95802	95982		1	1807	2015	2222	2	23	1	0	1 5:3_4:4_6:2_4:4_5:3a
5	OMT7	OMT	1	179247	179614	181957	182519		1	2344	2808	3271	2	23	1	0	1 3:5_4:4_3:5_4:4_2:6_3:5_2:6_4:4_3:5a
68	OMT7	OMT	5	546617	546721	548081	548258	2_nonsis		1361	1501	1640	3	30	1	0	1 3:5_5:3
77	OMT7	OMT	7	80976	81268	82858	84285	2_nonsis		1591	2450	3308	3	30	1	0	1 5:3_5:3a_5:3
31	OMT7	OMT	4	148667	148986	149689	149839	2_nonsis		704	938	1171	3	31	1	0	1 3:5_3:5a_4:4ai
129	OMT7	OMT	11	247692	247882	248806	249447	2_nonsis		925	1340	1754	1	1	1	1	0 (5:3)_(4:4aCO)
149	OMT7	OMT	12	610061	610216	610216	610430	2_nonsis		1	185	368	1	2	1	1	0 (3:5)_(4:4aCO)
102	OMT7	OMT	9	254357	254748	254765	256673	2_nonsis		18	1167	2315	1	2	1	1	0 (3:5)_(4:4aCO)
153	OMT7	OMT	12	789623	791142	791142	794003	2_nonsis		1	2190	4379	1	2	1	1	0 (3:5)_(4:4aCO)
50	OMT7	OMT	4	1341641	1341684	1343357	1343581	2_nonsis		1674	1807	1939	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
72	OMT7	OMT	6	203253	203623	204676	204767	2_nonsis		1054	1284	1513	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
118	OMT7	OMT	10	557648	558226	559033	559588	2_nonsis		808	1374	1939	1	5	1	1	0 (3:5)_(4:4)_(4:4aCO)
13	OMT7	OMT	2	294230	295028	295912	296774	2_nonsis		885	1714	2543	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
173	OMT7	OMT	13	852220	852413	853001	853271	2_nonsis		589	820	1050	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
18	OMT7	OMT	2	397849	397984	398452	399052	2_nonsis		469	836	1202	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
148	OMT7	OMT	12	340365	340527	341070	341507	2_nonsis		544	843	1141	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
63	OMT7	OMT	5	439039	439206	439545	439909	2_nonsis		340	605	869	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
198	OMT7	OMT	15	720440	720518	720799	721121	2_nonsis		282	481	680	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
2	OMT7	OMT	1	91629	92384	93563	94472	2_nonsis		1180	2011	2842	1	11	1	1	0 (4:4ai)_(4:4bCO)
81	OMT7	OMT	7	197001	197150	197465	197816	2_nonsis		316	565	814	1	11	1	1	0 (5:3)_(4:4ai)_(4:4bCO)
140	OMT7	OMT	12	29085	29131	29612	29773	2_nonsis		482	585	687	1	11	1	1	0 (4:4ai)_(3:5)_(4:4bCO)
25	OMT7	OMT	3	60704	60997	61457	61855	2_nonsis		461	806	1150	1	11	1	1	0 (3:5)_(4:4ai)_(4:4bCO)
123	OMT7	OMT	10	703893	703967	705542	705639	2_nonsis		1576	1661	1745	1	11	1	1	0 (2:6)_(4:4ai)_(4:4bCO)
167	OMT7	OMT	13	554421	555036	556437	557365	2_nonsis		1402	2173	2943	1	11	1	1	0 (5:3)_(4:4ai)_(5:3)_(4:4bCO)
220	OMT7	OMT	16	887709	888159	888652	888868	2_nonsis		494	826	1158	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
217	OMT7	OMT	16	731037	731859	732154	732711	2_nonsis		296	985	1673	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
150	OMT7	OMT	12	657926	658005	658599	659350	2_nonsis		595	1009	1423	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)

37	OMT7	OMT	4	526111	526117	526594	526633	2_nonsis	478	500	521	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
54	OMT7	OMT	4	1495580	1495680	1497214	1497535	2_nonsis	1535	1745	1954	1	12	1	1	0 (5:3)_(4:4)_(5:3)_(4:4aCO)
209	OMT7	OMT	16	374470	374857	376312	377062	2_nonsis	1456	2024	2591	1	12	1	1	0 (3:5)_(4:4)_(2:6)_(4:4aCO)
43	OMT7	OMT	4	834537	834720	836588	836867	2_nonsis	1869	2099	2329	1	12	1	1	0 (6:2)_(4:4aCO)_(5:3)_(4:4a)
105	OMT7	OMT	9	410521	410692	412645	415204	2_nonsis	1954	3318	4682	1	12	1	1	0 (6:2)_(4:4aCO)_(5:3)_(4:4a)
195	OMT7	OMT	15	601325	601569	602638	603166	2_nonsis	1070	1455	1840	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
161	OMT7	OMT	13	352374	352504	354080	354247	2_nonsis	1577	1725	1872	1	12	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
175	OMT7	OMT	14	145227	145293	147100	147466	2_nonsis	1808	2023	2238	1	12	1	1	0 (3:5)_(2:6)_(4:4)_(2:6)_(4:4aCO)
10	OMT7	OMT	2	248159	248659	250789	251134	2_nonsis	2131	2553	2974	1	12	1	1	0 (5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
33	OMT7	OMT	4	366072	366513	369582	369971	2_nonsis	3070	3484	3898	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
49	OMT7	OMT	4	1167232	1167361	1168188	1168767	2_nonsis	828	1181	1534	1	12	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(4:4)_(4:4aCO)
53	OMT7	OMT	4	1476514	1476956	1478129	1478319	2_nonsis	1174	1489	1804	1	12	1	1	0 (6:2)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(4:4a)
70	OMT7	OMT	6	114541	114707	116045	116186	2_nonsis	1339	1492	1644	1	12	1	1	0 (6:2)_(5:3)_(4:4aCO)_(5:3)_(6:2)_(5:3)_(4:4a)
158	OMT7	OMT	13	141979	142186	142206	142395	2_nonsis	21	218	415	1	15	1	1	0 (6:2)_(4:4aCO)
144	OMT7	OMT	12	183955	184185	184414	184588	2_nonsis	230	431	632	1	15	1	1	0 (6:2)_(4:4aCO)
39	OMT7	OMT	4	591782	592050	592527	593211	2_nonsis	478	953	1428	1	15	1	1	0 (6:2)_(4:4aCO)
186	OMT7	OMT	14	658861	658915	658915	659022	2_nonsis	1	81	160	1	16	1	1	0 (2:6)_(4:4aCO)
138	OMT7	OMT	11	532742	533318	533318	533844	2_nonsis	1	551	1101	1	16	1	1	0 (2:6)_(4:4aCO)
160	OMT7	OMT	13	229786	230470	230627	230928	2_nonsis	158	650	1141	1	16	1	1	0 (2:6)_(4:4aCO)
8	OMT7	OMT	2	16749	17715	17715	18175	2_nonsis	1	713	1425	1	16	1	1	0 (2:6)_(4:4aCO)
60	OMT7	OMT	5	157999	158386	158931	159422	2_nonsis	546	984	1422	1	16	1	1	0 (2:6)_(4:4aCO)
142	OMT7	OMT	12	104468	105183	105323	106427	2_nonsis	141	1050	1958	1	16	1	1	0 (2:6)_(4:4aCO)
32	OMT7	OMT	4	172175	172830	173380	174831	2_nonsis	551	1603	2655	1	16	1	1	0 (2:6)_(4:4aCO)
154	OMT7	OMT	12	884813	885146	884813	885146	2_nonsis	0	166	332	1	100	1	1	0 (4:4aCO)
112	OMT7	OMT	10	338042	338561	338042	338561	2_nonsis	0	259	518	1	100	1	1	0 (4:4aCO)
44	OMT7	OMT	4	926737	927283	926737	927283	2_nonsis	0	273	545	1	100	1	1	0 (4:4aCO)
205	OMT7	OMT	16	112536	113385	112536	113385	2_nonsis	0	424	848	1	100	1	1	0 (4:4aCO)
87	OMT7	OMT	7	914816	915691	914816	915691	2_nonsis	0	437	874	1	100	1	1	0 (4:4aCO)
151	OMT7	OMT	12	728268	729242	728268	729242	2_nonsis	0	487	973	1	100	1	1	0 (4:4aCO)
139	OMT7	OMT	11	634635	635970	634635	635970	2_nonsis	0	667	1334	1	100	1	1	0 (4:4aCO)
75	OMT7	OMT	7	55957	57501	55957	57501	2_nonsis	0	772	1543	1	100	1	1	0 (4:4aCO)
29	OMT7	OMT	3	190177	191741	190177	191741	2_nonsis	0	782	1563	1	100	1	1	0 (4:4aCO)
107	OMT7	OMT	10	51007	52869	51007	52869	2_nonsis	0	931	1861	1	100	1	1	0 (4:4aCO)
99	OMT7	OMT	9	185865	188629	185865	188629	2_nonsis	0	1382	2763	1	100	1	1	0 (4:4aCO)
179	OMT7	OMT	14	401251	404051	401251	404051	2_nonsis	0	1400	2799	1	100	1	1	0 (4:4aCO)
21	OMT7	OMT	2	662444	666708	662444	666708	2_nonsis	0	2132	4263	1	100	1	1	0 (4:4aCO)
66	OMT7	OMT	5	474031	474077	474191	474245	2_nonsis	115	164	213	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
122	OMT7	OMT	10	696365	696739	697206	697486	2_nonsis	468	794	1120	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
52	OMT7	OMT	4	1420155	1420281	1421025	1421204	2_nonsis	745	897	1048	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
185	OMT7	OMT	14	605054	606283	608001	610323	2_nonsis	1719	3494	5268	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
106	OMT7	OMT	10	40239	40575	41803	42451	2_nonsis	1229	1720	2211	2	30	1	1	0 (4:4ai)_(5:3)_(5:3a)_(4:4bCO)
156	OMT7	OMT	13	20392	20497	22318	22495	2_nonsis	1822	1962	2102	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
22	OMT7	OMT	2	741732	741884	742721	743655	2_nonsis	838	1380	1922	2	31	1	1	0 (3:5)_(3:5a)_(2:6)_(4:4aCO)_(2:6)_(4:4a)_(3:5a)_(4:4a)
84	OMT7	OMT	7	436628	437973	438333	438433	2_nonsis	361	1083	1804	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(4:4aCO)
98	OMT7	OMT	9	98932	99043	100355	100450	2_nonsis	1313	1415	1517	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
20	OMT7	OMT	2	583514	583825	585548	585769	2_nonsis	1724	1989	2254	2	32	1	1	0 (3:5)_(4:4aCO)_(3:5a)_(4:4a)
124	OMT7	OMT	11	10753	13039	14406	14411	2_nonsis	1368	2513	3657	2	32	1	1	0 (5:3)_(4:4aCO)_(5:3a)_(4:4a)
113	OMT7	OMT	10	348930	349396	351617	352052	2_nonsis	2222	2672	3121	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
199	OMT7	OMT	15	846635	846762	848406	848537	2_nonsis	1645	1773	1901	2	32	1	1	0 (3:5)_(4:4)_(3:5a)_(4:4ai)_(4:4bCO)
108	OMT7	OMT	10	79138	79551	87390	87652	2_nonsis	7840	8177	8513	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(3:5b)_(4:4aCO)
86	OMT7	OMT	7	809329	809973	811276	811285	2_nonsis	1304	1630	1955	2	32	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
188	OMT7	OMT	14	735047	735112	737420	737636	2_nonsis	2309	2449	2588	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
201	OMT7	OMT	15	987247	987667	989690	991111	2_nonsis	2024	2944	3863	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
177	OMT7	OMT	14	255895	256217	259694	259989	2_nonsis	3478	3786	4093	2	32	1	1	0 (3:5)_(2:6)_(4:4aCO)_(4:4bi)_(3:5a)_(4:4a)
120	OMT7	OMT	10	631130	632972	636506	637392	2_nonsis	3535	4898	6261	2	32	1	1	0 (5:3)_(4:4aCO)_(5:3a)_(4:4a)_(5:3)_(4:4a)
117	OMT7	OMT	10	467589	469453	469702	470533	2_nonsis	250	1597	2943	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
92	OMT7	OMT	8	240468	240738	245011	245056	2_nonsis	4274	4431	4587	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
213	OMT7	OMT	16	638483	638684	639081	639173	2_nonsis	398	544	689	3	20	1	1	0 (6:2)_(4:4)_(2:6)_(4:4aCO)
109	OMT7	OMT	10	110925	111085	111408	111784	2_nonsis	324	591	858	3	20	1	1	0 (5:3)_(2:6)_(5:3)_(4:4aCO)
190	OMT7	OMT	15	185134	185240	186679	186762	2_nonsis	1440	1534	1627	3	20	1	1	0 (2:6)_(6:2)_(5:3)_(4:4aCO)

4	OMT7	OMT	1	137336	138499	144826	145634	2_nonsis		6328	7313	8297	3	20	1	1	0	(5:3)_(3:5)_(3:5a)_(4:4aCO)
219	OMT7	OMT	16	839313	839436	839916	840103	2_nonsis		481	635	789	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(6:2)_(4:4aCO)
197	OMT7	OMT	15	640649	640991	642471	642646	2_nonsis		1481	1739	1996	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)_(6:2)_(4:4a)
210	OMT7	OMT	16	443521	443526	445448	445861	2_nonsis		1923	2131	2339	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)
165	OMT7	OMT	13	471264	472484	475252	476241	2_nonsis		2769	3873	4976	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)
40	OMT7	OMT	4	700440	700614	701137	701178	2_nonsis		524	631	737	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(6:2)_(5:3)_(4:4aCO)
134	OMT7	OMT	11	390798	391848	393359	393512	2_nonsis		1512	2113	2713	3	20	1	1	0	(6:2)_(5:3)_(4:4)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
82	OMT7	OMT	7	324572	324601	326922	326953	2_nonsis		2322	2351	2380	3	20	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)_(2:6)_(3:5)_(4:4a)
47	OMT7	OMT	4	1077529	1077787	1079984	1080788	2_nonsis		2198	2728	3258	3	20	1	1	0	(5:3)_(4:4)_(6:2)_(5:3a)_(4:4aCO)_(2:6)_(4:4a)
192	OMT7	OMT	15	479565	480090	482608	483090	2_nonsis		2519	3022	3524	3	20	1	1	0	(3:5)_(3:5a)_(2:6)_(4:4)_(6:2)_(5:3)_(4:4aCO)
162	OMT7	OMT	13	408001	408347	409194	409543	2_nonsis		848	1195	1541	3	21	1	1	0	(5:3)_(4:4ai)_(2:6)_(4:4bCO)
14	OMT7	OMT	2	299901	301455	301964	302062		3	510	1335	2160	0	1	2	0	2	(1:7)_(4:4ai)_(2:6i)_(3:5)_(4:4)
212	OMT7	OMT	16	525636	525655	526860	527307	2_sis		1206	1438	1670	0	1	2	0	2	(8:0)_(5:3)_(6:2)_(4:4)
3	OMT7	OMT	1	128756	129063	129517	130254		3	455	976	1497	0	2	2	1	1	(4:4ai)_(5:3)_(7:1)_(4:4bCO)
57	OMT7	OMT	5	39651	40307	42708	43035		3	2402	2893	3383	0	2	2	1	1	(3:5)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(7:1)_(6:2a)_(4:4a)
62	OMT7	OMT	5	377471	377999	378395	378586		3	397	756	1114	0	2	2	1	1	(3:5)_(4:4aCO)_(6:2)_(3:5a)_(4:4a)
78	OMT7	OMT	7	165317	165523	170880	171278		4	5358	5659	5960	0	2	2	1	1	(3:5)_(4:4aCO)_(3:5a)_(4:4bi)_(4:4a)
85	OMT7	OMT	7	622492	622738	629428	629474		3	6691	6836	6981	0	2	2	1	1	(5:3)_(4:4aCO)_(5:3a)_(3:5)_(2:6i)_(1:7)_(2:6i)_(3:5a)_(4:4a)
90	OMT7	OMT	8	159136	159406	160782	161715		4	1377	1978	2578	0	2	2	1	1	(3:5)_(2:6i)_(3:5a)_(4:4aCO)
91	OMT7	OMT	8	187695	187989	190024	190339		3	2036	2340	2643	0	2	2	1	1	(5:3)_(4:4aCO)_(3:5)_(4:4a)
114	OMT7	OMT	10	391162	391247	391693	392346		3	447	815	1183	0	2	2	1	1	(5:3)_(6:2i)_(4:4)_(2:6)_(4:4aCO)
121	OMT7	OMT	10	662479	663134	665076	665938		3	1943	2701	3458	0	2	2	1	1	(3:5)_(2:6i)_(3:5a)_(5:3)_(4:4ai)_(5:3)_(4:4ai)_(4:4bCO)
170	OMT7	OMT	13	730533	731517	731841	731964		3	325	878	1430	0	2	2	1	1	(5:3)_(4:4ai)_(2:6)_(4:4bCO)
89	OMT7	OMT	8	114924	115401	123473	123592		4	8073	8370	8667	0	3	2	1	1	(5:3)_(4:4)_(5:3)_(5:3a)_(4:4ai)_(3:5)_(4:4bCO)_(5:3a)_(4:4ci)_(4:4dCO)_(2:6)_(4:4eCO)_(5:3b)_(6:2)_(5:3b)_(5:3c)_(4:4dCO)
110	OMT7	OMT	10	235235	235337	241123	241420		3	5787	5986	6184	0	3	2	1	1	(3:5)_(4:4aCO)_(5:3)_(3:5a)_(2:6)_(4:4a)_(6:2)_(4:4bCO)
125	OMT7	OMT	11	65282	66233	70579	70690		3	4347	4877	5407	0	3	2	1	1	(5:3)_(4:4)_(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(5:3b)_(6:2)_(4:4bCO)
194	OMT7	OMT	15	501040	501220	503975	504672		3	2756	3194	3631	0	3	2	0	2	(4:4ai)_(5:3)_(4:4bCO)_(5:3)_(6:2i)_(6:2ai)_(4:4CO)
80	OMT8	OMT	7	492175	492247	492247	492317		1	1	71	141	1	1	1	0	1	05:03
110	OMT8	OMT	10	361124	361221	361221	361340		1	1	108	215	1	1	1	0	1	05:03
40	OMT8	OMT	4	1036768	1036886	1036886	1037061		1	1	147	292	1	1	1	0	1	05:03
189	OMT8	OMT	16	370453	370707	370710	370796		1	4	173	342	1	1	1	0	1	05:03
58	OMT8	OMT	5	316361	316556	316681	316709		1	126	237	347	1	1	1	0	1	05:03
150	OMT8	OMT	13	321686	321801	321916	322143		1	116	286	456	1	1	1	0	1	05:03
159	OMT8	OMT	14	197788	198236	198236	198384		1	1	298	595	1	1	1	0	1	05:03
60	OMT8	OMT	5	342057	342537	342537	342667		1	1	305	609	1	1	1	0	1	05:03
122	OMT8	OMT	11	315394	315610	315844	315867		1	235	354	472	1	1	1	0	1	05:03
92	OMT8	OMT	8	190339	190671	190671	191072		1	1	367	732	1	1	1	0	1	05:03
52	OMT8	OMT	5	152335	152616	152858	153026		1	243	467	690	1	1	1	0	1	05:03
23	OMT8	OMT	4	105348	105623	105853	106143		1	231	513	794	1	1	1	0	1	05:03
29	OMT8	OMT	4	592527	593211	593463	593517		1	253	621	989	1	1	1	0	1	05:03
73	OMT8	OMT	7	165317	165523	165523	166667		1	1	675	1349	1	1	1	0	1	05:03
147	OMT8	OMT	13	166364	166589	167027	167431		1	439	753	1066	1	1	1	0	1	05:03
102	OMT8	OMT	9	193298	193815	193815	195082		1	1	892	1783	1	1	1	0	1	05:03
65	OMT8	OMT	6	51193	51257	52024	52738		1	768	1156	1544	1	1	1	0	1	05:03
46	OMT8	OMT	4	1417050	1417646	1419516	1419978		1	1871	2399	2927	1	1	1	0	1	05:03
132	OMT8	OMT	12	245980	246315	248700	248752		1	2386	2579	2771	1	1	1	0	1	05:03
22	OMT8	OMT	4	83626	83684	83687	83831		1	4	104	204	1	2	1	0	1	03:05
144	OMT8	OMT	13	17843	17913	17955	18080		1	43	140	236	1	2	1	0	1	03:05
162	OMT8	OMT	14	465885	465982	465982	466168		1	1	142	282	1	2	1	0	1	03:05
85	OMT8	OMT	7	939718	939793	939794	940048		1	2	166	329	1	2	1	0	1	03:05
118	OMT8	OMT	11	155185	155453	155453	155667		1	1	241	481	1	2	1	0	1	03:05
105	OMT8	OMT	9	360178	360413	360460	360682		1	48	276	503	1	2	1	0	1	03:05
32	OMT8	OMT	4	643929	643973	643973	644532		1	1	302	602	1	2	1	0	1	03:05
34	OMT8	OMT	4	836867	837275	837275	837527		1	1	330	659	1	2	1	0	1	03:05
124	OMT8	OMT	11	352373	352793	352843	353048		1	51	363	674	1	2	1	0	1	03:05
54	OMT8	OMT	5	182381	182827	182827	183157		1	1	388	775	1	2	1	0	1	03:05
127	OMT8	OMT	11	535712	536243	536243	536702		1	1	495	989	1	2	1	0	1	03:05
93	OMT8	OMT	8	232321	232501	232747	233140		1	247	533	818	1	2	1	0	1	03:05
120	OMT8	OMT	11	260152	260236	260745	260953		1	510	655	800	1	2	1	0	1	03:05
36	OMT8	OMT	4	861257	861707	861727	862580		1	21	672	1322	1	2	1	0	1	03:05

178	OMT8	OMT	15	787005	787105	787600	787943	1	496	717	937	1	2	1	0	1	03:05
10	OMT8	OMT	2	531601	531940	531940	533263	1	1	831	1661	1	2	1	0	1	03:05
188	OMT8	OMT	16	310732	310795	311442	311970	1	648	943	1237	1	2	1	0	1	03:05
160	OMT8	OMT	14	389775	391590	391590	391752	1	1	989	1976	1	2	1	0	1	03:05
15	OMT8	OMT	2	757029	757438	757908	758568	1	471	1005	1538	1	2	1	0	1	03:05
62	OMT8	OMT	5	482316	483903	483903	485006	1	1	1345	2689	1	2	1	0	1	03:05
76	OMT8	OMT	7	352964	355166	355292	356141	1	127	1652	3176	1	2	1	0	1	03:05
43	OMT8	OMT	4	1203967	1205010	1206115	1206306	1	1106	1722	2338	1	2	1	0	1	03:05
13	OMT8	OMT	2	662444	666708	666849	668076	1	142	2887	5631	1	2	1	0	1	03:05
164	OMT8	OMT	14	525960	526397	529097	529112	1	2701	2926	3151	1	2	1	0	1	03:05
26	OMT8	OMT	4	212036	212222	212267	212746	1	46	378	709	1	3	1	0	1	5:3_6:2_5:3
8	OMT8	OMT	2	454753	454884	455916	456385	1	1033	1332	1631	1	3	1	0	1	5:3_6:2_5:3
125	OMT8	OMT	11	379560	379623	381721	382140	1	2099	2339	2579	1	3	1	0	1	5:3_4:4_6:2_5:3
95	OMT8	OMT	8	387911	388397	389979	390041	1	1583	1856	2129	1	4	1	0	1	3:5_4:4_3:5
79	OMT8	OMT	7	424734	424942	426675	426969	1	1734	1984	2234	1	4	1	0	1	3:5_4:4_3:5
68	OMT8	OMT	6	226238	226370	228617	229028	1	2248	2519	2789	1	4	1	0	1	3:5_2:6_4:4_3:5_4:4_3:5
19	OMT8	OMT	3	93455	93872	94376	94470	1	505	760	1014	1	7	1	0	1	5:3_6:2
69	OMT8	OMT	6	241984	242028	245875	246259	1	3848	4061	4274	1	7	1	0	1	6:2_5:3
111	OMT8	OMT	10	391555	391631	391693	392346	1	63	427	790	1	8	1	0	1	2:6_3:5
194	OMT8	OMT	16	621480	622057	623258	623271	1	1202	1496	1790	1	8	1	0	1	2:6_3:5
61	OMT8	OMT	5	399399	400005	401106	401545	1	1102	1624	2145	1	8	1	0	1	2:6_3:5
193	OMT8	OMT	16	619292	619388	620007	620016	1	620	672	723	1	8	1	0	1	2:6_3:5_2:6_3:5
129	OMT8	OMT	11	561779	561959	561959	562081	1	1	151	301	1	10	1	0	1	06:02
27	OMT8	OMT	4	215724	215967	215967	216258	1	1	267	533	1	10	1	0	1	06:02
38	OMT8	OMT	4	962545	962923	963004	963556	1	82	546	1010	1	10.1	1	0	1	02:06
9	OMT8	OMT	2	495085	495218	495703	495960	1	486	680	874	2	11	1	0	1	5:3_5:3a
91	OMT8	OMT	8	181132	181682	182092	182246	1	411	762	1113	2	12	1	0	1	3:5_3:5a
72	OMT8	OMT	7	122622	123330	123839	124322	1	510	1105	1699	2	12	1	0	1	3:5_3:5a
45	OMT8	OMT	4	1268439	1268647	1270457	1270902	1	1811	2137	2462	2	12	1	0	1	3:5_3:5a
64	OMT8	OMT	6	24251	24494	26058	26127	1	1565	1720	1875	2	14	1	0	1	3:5_3:5a_4:4_3:5a
166	OMT8	OMT	14	641631	641859	643444	643651	1	1586	1803	2019	2	14	1	0	1	3:5_3:5a_4:4_3:5a
55	OMT8	OMT	5	190829	191462	192221	192670	1	760	1300	1840	2	15	1	0	1	5:3_4:4_5:3a
96	OMT8	OMT	8	450359	450521	451172	452903	1	652	1598	2543	2	15	1	0	1	5:3_4:4_5:3a
185	OMT8	OMT	16	133150	133177	134518	135194	1	1342	1693	2043	2	15	1	0	1	5:3_4:4_5:3a
157	OMT8	OMT	14	116131	116459	117208	117253	1	750	936	1121	2	16	1	0	1	3:5_4:4_3:5a
108	OMT8	OMT	10	302207	302882	303556	303606	1	675	1037	1398	2	16	1	0	1	3:5_4:4_3:5a
182	OMT8	OMT	15	987247	987667	988671	988871	1	1005	1314	1623	2	16	1	0	1	3:5_4:4_3:5a
99	OMT8	OMT	9	87283	87642	89179	89302	1	1538	1778	2018	2	16	1	0	1	3:5_4:4_3:5a
171	OMT8	OMT	15	169772	169851	171849	172081	1	1999	2154	2308	2	16	1	0	1	3:5_4:4_3:5a
59	OMT8	OMT	5	334750	335065	337748	337825	1	2684	2879	3074	2	17	1	0	1	5:3_4:4_5:3a_4:4_5:3a
190	OMT8	OMT	16	425006	425377	428691	428845	1	3315	3577	3838	2	17	1	0	1	5:3_4:4_5:3a_4:4_5:3a
121	OMT8	OMT	11	262447	262597	264863	264974	1	2267	2397	2526	2	18	1	0	1	3:5_4:4_3:5a_4:4_3:5a
170	OMT8	OMT	15	159827	160743	164383	164556	1	3641	4185	4728	2	18	1	0	1	3:5_4:4_3:5a_2:6_3:5a
4	OMT8	OMT	2	83713	83944	85339	85504	2_nonsis	1396	1593	1790	3	30	1	0	1	3:5_2:6_3:5a_3:5b
21	OMT8	OMT	4	19119	19143	19746	19880	2_nonsis	604	682	760	3	31	1	0	1	5:3_4:4ai_2:6
12	OMT8	OMT	2	626092	626455	628807	629013	2_nonsis	2353	2637	2920	3	31	1	0	1	5:3_4:4ai_4:4_3:5
134	OMT8	OMT	12	257813	258349	261119	261578	2_nonsis	2771	3268	3764	3	31	1	0	1	4:4ai_4:4_5:3_5:3a
148	OMT8	OMT	13	235798	236240	239896	240226	2_nonsis	3657	4042	4427	3	31	1	0	1	5:3_4:4ai_5:3a_4:4ai_5:3a_5:3b
181	OMT8	OMT	15	953577	954766	958901	959058	2_nonsis	4136	4808	5480	3	31	1	0	1	6:2_5:3_4:4ai_5:3a_6:2_5:3
196	OMT8	OMT	16	785578	785712	785737	785910	2_nonsis	26	179	331	1	1	1	1	0	(5:3)_(4:4aCO)
33	OMT8	OMT	4	699436	699549	699549	699810	2_nonsis	1	187	373	1	1	1	1	0	(5:3)_(4:4aCO)
177	OMT8	OMT	15	738211	738617	738654	739134	2_nonsis	38	480	922	1	1	1	1	0	(5:3)_(4:4aCO)
14	OMT8	OMT	2	704282	704922	704939	705275	2_nonsis	18	505	992	1	1	1	1	0	(5:3)_(4:4aCO)
113	OMT8	OMT	10	580119	580576	580666	581143	2_nonsis	91	557	1023	1	1	1	1	0	(5:3)_(4:4aCO)
168	OMT8	OMT	15	40057	40365	40834	41027	2_nonsis	470	720	969	1	1	1	1	0	(5:3)_(4:4aCO)
28	OMT8	OMT	4	363511	363860	363860	365434	2_nonsis	1	962	1922	1	1	1	1	0	(5:3)_(4:4aCO)
24	OMT8	OMT	4	125573	126283	126408	127476	2_nonsis	126	1014	1902	1	1	1	1	0	(5:3)_(4:4aCO)
39	OMT8	OMT	4	1002837	1003188	1003188	1003263	2_nonsis	1	213	425	1	2	1	1	0	(3:5)_(4:4aCO)
126	OMT8	OMT	11	491399	491562	491562	491862	2_nonsis	1	232	462	1	2	1	1	0	(3:5)_(4:4aCO)
112	OMT8	OMT	10	393918	394217	394217	394408	2_nonsis	1	245	489	1	2	1	1	0	(3:5)_(4:4aCO)

63	OMT8	OMT	5	499930	500606	500606	501719	2_nonsis	1	895	1788	1	2	1	1	0 (3:5)_(4:4aCO)
103	OMT8	OMT	9	239821	240376	240939	242535	2_nonsis	564	1639	2713	1	2	1	1	0 (3:5)_(4:4aCO)
31	OMT8	OMT	4	625839	629487	629725	630640	2_nonsis	239	2520	4800	1	2	1	1	0 (3:5)_(4:4aCO)
84	OMT8	OMT	7	936948	937376	937863	938065	2_nonsis	488	802	1116	1	3	1	1	0 (5:3)_(4:4)_(4:4aCO)
156	OMT8	OMT	14	51050	51868	52925	53465	2_nonsis	1058	1736	2414	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
165	OMT8	OMT	14	531399	531505	531656	532165	2_nonsis	152	459	765	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
100	OMT8	OMT	9	96801	96831	97151	97705	2_nonsis	321	612	903	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
173	OMT8	OMT	15	393958	394357	394716	395073	2_nonsis	360	737	1114	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
11	OMT8	OMT	2	579647	579929	580868	581091	2_nonsis	940	1192	1443	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
136	OMT8	OMT	12	572662	572946	576339	576551	2_nonsis	3394	3641	3888	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
18	OMT8	OMT	3	61855	61894	62698	63052	2_nonsis	805	1001	1196	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
56	OMT8	OMT	5	222293	222394	226861	227104	2_nonsis	4468	4639	4810	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
94	OMT8	OMT	8	319904	320071	320927	321084	2_nonsis	857	1018	1179	1	11	1	1	0 (4:4ai)_(5:3)_(4:4bCO)
119	OMT8	OMT	11	184809	185334	185846	186668	2_nonsis	513	1186	1858	1	11	1	1	0 (4:4ai)_(5:3)_(4:4bCO)
70	OMT8	OMT	7	55263	55957	57501	57822	2_nonsis	1545	2052	2558	1	11	1	1	0 (5:3)_(4:4ai)_(4:4bCO)
82	OMT8	OMT	7	798046	798196	799970	800086	2_nonsis	1775	1907	2039	1	11	1	1	0 (6:2)_(4:4)_(5:3)_(4:4ai)_(4:4bCO)
20	OMT8	OMT	3	204750	207459	211504	211982	2_nonsis	4046	5639	7231	1	11	1	1	0 (4:4ai)_(3:5)_(4:4bCO)_(3:5)_(2:6)_(4:4b)
141	OMT8	OMT	12	884813	885146	885458	885745	2_nonsis	313	622	931	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
158	OMT8	OMT	14	184992	185309	185896	186475	2_nonsis	588	1035	1482	1	12	1	1	0 (2:6)_(3:5)_(2:6)_(4:4aCO)
152	OMT8	OMT	13	457932	458330	459995	460145	2_nonsis	1666	1939	2212	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
7	OMT8	OMT	2	418592	419139	419931	420076	2_nonsis	793	1138	1483	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4a)
78	OMT8	OMT	7	411573	412208	413620	413728	2_nonsis	1413	1784	2154	1	12	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
146	OMT8	OMT	13	159018	159085	161406	161572	2_nonsis	2322	2438	2553	1	12	1	1	0 (5:3)_(4:4)_(5:3)_(4:4)_(6:2)_(4:4aCO)
81	OMT8	OMT	7	609325	609405	611510	612267	2_nonsis	2106	2524	2941	1	12	1	1	0 (5:3)_(4:4)_(5:3)_(4:4)_(6:2)_(4:4)_(4:4aCO)
180	OMT8	OMT	15	845688	845796	845840	846014	2_nonsis	45	185	325	1	15	1	1	0 (6:2)_(4:4aCO)
109	OMT8	OMT	10	305635	305904	305977	306157	2_nonsis	74	298	521	1	15	1	1	0 (6:2)_(4:4aCO)
35	OMT8	OMT	4	858862	859191	859191	859510	2_nonsis	1	324	647	1	15	1	1	0 (6:2)_(4:4aCO)
175	OMT8	OMT	15	542952	543498	543498	543780	2_nonsis	1	414	827	1	15	1	1	0 (6:2)_(4:4aCO)
5	OMT8	OMT	2	192441	192576	193122	193664	2_nonsis	547	885	1222	1	15	1	1	0 (6:2)_(4:4aCO)
104	OMT8	OMT	9	307779	307943	308018	308167	2_nonsis	76	232	387	1	16	1	1	0 (2:6)_(4:4aCO)
186	OMT8	OMT	16	202594	202808	202948	203064	2_nonsis	141	305	469	1	16	1	1	0 (2:6)_(4:4aCO)
77	OMT8	OMT	7	384425	384641	384832	385141	2_nonsis	192	454	715	1	16	1	1	0 (2:6)_(4:4aCO)
184	OMT8	OMT	16	73338	73929	73929	74327	2_nonsis	1	495	988	1	16	1	1	0 (2:6)_(4:4aCO)
71	OMT8	OMT	7	66795	67477	67477	68133	2_nonsis	1	669	1337	1	16	1	1	0 (2:6)_(4:4aCO)
117	OMT8	OMT	11	99224	99633	99646	100670	2_nonsis	14	730	1445	1	16	1	1	0 (2:6)_(4:4aCO)
145	OMT8	OMT	13	110245	110807	110970	111909	2_nonsis	164	914	1663	1	16	1	1	0 (2:6)_(4:4aCO)
192	OMT8	OMT	16	497758	497958	497758	497958	2_nonsis	0	100	199	1	100	1	1	(4:4aCO)
30	OMT8	OMT	4	595713	596055	595713	596055	2_nonsis	0	171	341	1	100	1	1	(4:4aCO)
174	OMT8	OMT	15	413774	414171	413774	414171	2_nonsis	0	198	396	1	100	1	1	(4:4aCO)
155	OMT8	OMT	13	820241	820753	820241	820753	2_nonsis	0	256	511	1	100	1	1	(4:4aCO)
123	OMT8	OMT	11	328709	329482	328709	329482	2_nonsis	0	386	772	1	100	1	1	(4:4aCO)
138	OMT8	OMT	12	703971	704829	703971	704829	2_nonsis	0	429	857	1	100	1	1	(4:4aCO)
130	OMT8	OMT	12	88557	89489	88557	89489	2_nonsis	0	466	931	1	100	1	1	(4:4aCO)
163	OMT8	OMT	14	478186	479345	478186	479345	2_nonsis	0	579	1158	1	100	1	1	(4:4aCO)
167	OMT8	OMT	14	701618	702991	701618	702991	2_nonsis	0	686	1372	1	100	1	1	(4:4aCO)
191	OMT8	OMT	16	465383	466824	465383	466824	2_nonsis	0	720	1440	1	100	1	1	(4:4aCO)
16	OMT8	OMT	2	768073	769699	768073	769699	2_nonsis	0	813	1625	1	100	1	1	(4:4aCO)
2	OMT8	OMT	1	121235	128637	121235	128637	2_nonsis	0	3701	7401	1	100	1	1	(4:4aCO)
25	OMT8	OMT	4	146582	147362	147846	147986	2_nonsis	485	944	1403	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
114	OMT8	OMT	10	701848	702817	703332	703339	2_nonsis	516	1003	1490	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
187	OMT8	OMT	16	267749	267830	269309	270158	2_nonsis	1480	1944	2408	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
48	OMT8	OMT	5	12629	12704	14598	14893	2_nonsis	1895	2079	2263	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
169	OMT8	OMT	15	146419	147007	151304	151369	2_nonsis	4298	4624	4949	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
183	OMT8	OMT	15	1039487	1039544	1039824	1040442	2_nonsis	281	618	954	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
6	OMT8	OMT	2	322968	323106	324220	324467	2_nonsis	1115	1307	1498	2	32	1	1	0 (3:5)_(4:4ai)_(3:5a)_(4:4bCO)
51	OMT8	OMT	5	120418	120588	124517	124905	2_nonsis	3930	4208	4486	2	32	1	1	0 (3:5)_(4:4ai)_(3:5a)_(4:4bCO)
139	OMT8	OMT	12	821384	822226	826618	827343	2_nonsis	4393	5176	5958	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
151	OMT8	OMT	13	333862	334198	335383	335404	2_nonsis	1186	1364	1541	2	32	1	1	0 (3:5)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
107	OMT8	OMT	10	135953	135988	137367	137481	2_nonsis	1380	1454	1527	2	32	1	1	0 (3:5)_(4:4)_(2:6)_(3:5a)_(4:4aCO)
89	OMT8	OMT	8	68905	69088	70273	70286	2_nonsis	1186	1283	1380	2	32	1	1	0 (5:3)_(4:4)_(5:3)_(4:4aCO)_(5:3a)_(4:4a)

44	OMT8	OMT	4	1206428	1212811	1214386	1214533	2_nonsis		1576	4840	8104	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
75	OMT8	OMT	7	269232	269505	272144	272568	2_nonsis		2640	2988	3335	2	32	1	1	0	(2:6)_(3:5)_(2:6)_(3:5a)_(2:6)_(3:5)_(4:4aCO)
88	OMT8	OMT	8	52328	52566	56032	56225	2_nonsis		3467	3682	3896	2	32	1	1	0	(3:5)_(4:4ai)_(3:5a)_(4:4bCO)_(3:5a)_(4:4ai)_(4:4b)
197	OMT8	OMT	16	918763	918769	922391	922477	2_nonsis		3623	3668	3713	2	32	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
142	OMT8	OMT	12	948003	948176	955168	955348	2_nonsis		6993	7169	7344	2	32	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
83	OMT8	OMT	7	807540	807662	811131	811176	2_nonsis		3470	3553	3635	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(2:6)_(3:5b)_(4:4aCO)_(3:5b)_(4:4a)_(3:5a)_(4:4a)
74	OMT8	OMT	7	195912	196275	196468	196504	2_nonsis		194	393	591	3	20	1	1	0	(5:3)_(5:3)_(4:4aCO)
161	OMT8	OMT	14	425816	427278	427295	427451	2_nonsis		18	826	1634	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
1	OMT8	OMT	1	60445	60774	61451	61708	2_nonsis		678	970	1262	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
131	OMT8	OMT	12	196991	197276	198396	198410	2_nonsis		1121	1270	1418	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
41	OMT8	OMT	4	1129980	1130680	1132014	1132218	2_nonsis		1335	1786	2237	3	20	1	1	0	(5:3)_(6:2)_(4:4aCO)
143	OMT8	OMT	12	1014976	1015108	1016012	1016099	2_nonsis		905	1014	1122	3	20	1	1	0	(6:2)_(4:4)_(3:5)_(4:4aCO)
49	OMT8	OMT	5	67809	68268	69243	69568	2_nonsis		976	1367	1758	3	20	1	1	0	(3:5)_(5:3)_(3:5)_(4:4aCO)
176	OMT8	OMT	15	682254	682436	683845	683929	2_nonsis		1410	1542	1674	3	20	1	1	0	(2:6)_(3:5)_(4:4aCO)_(5:3)_(4:4a)
57	OMT8	OMT	5	309648	309961	311789	311837	2_nonsis		1829	2009	2188	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
154	OMT8	OMT	13	797587	797644	798889	799519	2_nonsis		1246	1589	1931	3	20	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
53	OMT8	OMT	5	159422	159475	161191	161593	2_nonsis		1717	1944	2170	3	20	1	1	0	(5:3)_(5:3a)_(4:4)_(3:5)_(5:3b)_(4:4aCO)
153	OMT8	OMT	13	671402	672472	675294	675387	2_nonsis		2823	3404	3984	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4a)
101	OMT8	OMT	9	149380	149501	152184	152243	2_nonsis		2684	2773	2862	3	20	1	1	0	(2:6)_(4:4)_(3:5)_(4:4)_(3:5a)_(4:4aCO)_(5:3)_(4:4a)
195	OMT8	OMT	16	675149	676046	678816	679094	2_nonsis		2771	3358	3944	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
67	OMT8	OMT	6	220148	221384	224098	224275	2_nonsis		2715	3421	4126	3	20	1	1	0	(6:2)_(5:3)_(6:2)_(3:5)_(2:6)_(4:4aCO)_(5:3a)_(4:4a)
98	OMT8	OMT	8	505727	505776	507281	507567	2_nonsis		1506	1673	1839	3	20	1	1	0	(5:3)_(4:4)_(5:3a)_(6:2)_(4:4)_(6:2)_(4:4aCO)_(3:5)_(4:4a)
50	OMT8	OMT	5	72502	72694	76382	76636	2_nonsis		3689	3911	4133	3	21	1	1	0	(3:5)_(5:3)_(4:4ai)_(5:3)_(6:2)_(4:4bCO)
3	OMT8	OMT	1	190031	190402	194625	194803	2_nonsis		4224	4498	4771	3	21	1	1	0	(6:2)_(5:3)_(4:4ai)_(3:5)_(2:6)_(3:5)_(4:4bCO)
17	OMT8	OMT	3	51491	51650	52919	53316		3	1270	1547	1824	0	1	2	0	2	(3:5)_(4:4)_(5:3)_(5:3a)_(4:4)
86	OMT8	OMT	7	967722	967869	968811	969304	2_sis		943	1262	1581	0	1	2	0	2	(5:3)_(6:2i)_(5:3)_(4:4)
115	OMT8	OMT	11	34051	34159	35874	36243		3	1716	1954	2191	0	1	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4ai)_(5:3b)_(6:2)_(4:4)
116	OMT8	OMT	11	67187	67304	70711	70841		3	3408	3531	3653	0	1	2	0	2	(4:4ai)_(3:5)_(2:6)_(4:4bi)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4)
179	OMT8	OMT	15	795030	795362	797043	797205	2_sis		1682	1928	2174	0	1	2	0	2	(3:5)_(2:6i)_(2:6a)_(4:4)
37	OMT8	OMT	4	955335	955435	960570	960787		3	5136	5294	5451	0	2	2	1	1	(3:5)_(4:4)_(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
42	OMT8	OMT	4	1168188	1168767	1168770	1168958		3	4	387	769	0	2	2	1	1	(5:3)_(4:4aCO)
47	OMT8	OMT	4	1433731	1433930	1434367	1434455		3	438	581	723	0	2	2	1	1	(5:3)_(3:5)_(4:4aCO)
66	OMT8	OMT	6	95326	95387	95632	95746		3	246	333	419	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(4:4aCO)
87	OMT8	OMT	7	1049349	1050057	1051093	1051991		3	1037	1839	2641	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(5:3b)_(4:4aCO)
90	OMT8	OMT	8	122169	122633	122674	122848		3	42	360	678	0	2	2	1	1	(4:4ai)_(4:4bCO)
97	OMT8	OMT	8	461593	462297	463854	464156		3	1558	2060	2562	0	2	2	1	1	(0:8)_(1:7)_(3:5)_(2:6i)_(3:5)_(4:4aCO)
106	OMT8	OMT	9	386051	386090	387314	387368		3	1225	1271	1316	0	2	2	1	1	(5:3)_(4:4ai)_(5:3)_(6:2)_(5:3a)_(4:4bCO)_(5:3b)_(4:4b)
128	OMT8	OMT	11	557299	558102	559707	560658		3	1606	2482	3358	0	2	2	1	1	(3:5)_(4:4ai)_(5:3)_(4:4ai)_(5:3)_(4:4bCO)_(3:5a)_(4:4ci)_(4:4b)
135	OMT8	OMT	12	339496	340008	341507	341678		4	1500	1841	2181	0	2	2	2	0	(5:3)_(2:6)_(3:5)_(4:4aCO)
137	OMT8	OMT	12	611203	611744	613380	614136		3	1637	2285	2932	0	2	2	1	1	(3:5)_(4:4)_(3:5)_(2:6)_(1:7)_(4:4)_(5:3)_(4:4)_(4:4aCO)
140	OMT8	OMT	12	835509	835608	837543	837595		3	1936	2011	2085	0	2	2	1	1	(3:5)_(3:5a)_(3:5b)_(4:4aCO)
172	OMT8	OMT	15	215808	215865	217521	218142		3	1657	1995	2333	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(6:2i)_(5:3a)_(4:4aCO)
133	OMT8	OMT	12	250711	251635	255317	255485	2_nonsis		3683	4228	4773	0	3	2	0	2	(3:5)_(3:5a)_(4:4aCO)_(3:5a)_(4:4bi)_(4:4CO)
149	OMT8	OMT	13	283368	283562	288558	289245		3	4997	5437	5876	0	3	2	1	1	(5:3)_(4:4aCO)_(5:3a)_(5:3b)_(4:4bCO)_(4:4ci)_(4:4b)
11	OMT9	OMT	1	196623	196686	196686	196738	1		1	58	114	1	1	1	0	1	05:03
74	OMT9	OMT	5	264585	264668	264738	264848	1		71	167	262	1	1	1	0	1	05:03
138	OMT9	OMT	10	549846	550041	550041	550237	1		1	196	390	1	1	1	0	1	05:03
139	OMT9	OMT	10	633240	633350	633463	633743	1		114	308	502	1	1	1	0	1	05:03
93	OMT9	OMT	7	217121	217417	217461	217697	1		45	310	575	1	1	1	0	1	05:03
76	OMT9	OMT	5	318778	319090	319090	319404	1		1	313	625	1	1	1	0	1	05:03
237	OMT9	OMT	16	171075	171270	171314	171708	1		45	339	632	1	1	1	0	1	05:03
69	OMT9	OMT	4	1422008	1422082	1422082	1422760	1		1	376	751	1	1	1	0	1	05:03
236	OMT9	OMT	16	138435	138747	138809	139202	1		63	415	766	1	1	1	0	1	05:03
20	OMT9	OMT	2	492226	492334	492334	493122	1		1	448	895	1	1	1	0	1	05:03
63	OMT9	OMT	4	1135519	1136116	1136171	1136363	1		56	450	843	1	1	1	0	1	05:03
66	OMT9	OMT	4	1270902	1271755	1271755	1271812	1		1	455	909	1	1	1	0	1	05:03
128	OMT9	OMT	9	405428	405665	405973	406124	1		309	502	695	1	1	1	0	1	05:03
216	OMT9	OMT	14	603874	604244	604244	604879	1		1	503	1004	1	1	1	0	1	05:03
46	OMT9	OMT	4	302250	303051	303140	303260	1		90	550	1009	1	1	1	0	1	05:03
112	OMT9	OMT	8	142863	143543	143727	143824	1		185	573	960	1	1	1	0	1	05:03

243	OMT9	OMT	16	285465	286085	286391	286502	1	307	672	1036	1	1	1	0	1	05:03
73	OMT9	OMT	5	178287	178671	179143	179281	1	473	733	993	1	1	1	0	1	05:03
189	OMT9	OMT	13	166876	167027	167521	167925	1	495	772	1048	1	1	1	0	1	05:03
177	OMT9	OMT	12	819834	820606	820606	821384	1	1	775	1549	1	1	1	0	1	05:03
64	OMT9	OMT	4	1180090	1181300	1181437	1181528	1	138	788	1437	1	1	1	0	1	05:03
116	OMT9	OMT	8	281264	281430	281430	282877	1	1	807	1612	1	1	1	0	1	05:03
252	OMT9	OMT	16	678266	678517	679119	679575	1	603	956	1308	1	1	1	0	1	05:03
136	OMT9	OMT	10	401166	401242	402145	402267	1	904	1002	1100	1	1	1	0	1	05:03
41	OMT9	OMT	4	159777	159930	161136	162357	1	1207	1893	2579	1	1	1	0	1	05:03
22	OMT9	OMT	2	556121	556210	556210	556272	1	1	76	150	1	2	1	0	1	03:05
122	OMT9	OMT	9	82899	83067	83067	83104	1	1	103	204	1	2	1	0	1	03:05
60	OMT9	OMT	4	955335	955435	955435	955755	1	1	210	419	1	2	1	0	1	03:05
31	OMT9	OMT	3	51209	51405	51491	51650	1	87	264	440	1	2	1	0	1	03:05
211	OMT9	OMT	14	405600	405841	405878	406133	1	38	285	532	1	2	1	0	1	03:05
140	OMT9	OMT	10	639041	639365	639365	639986	1	1	473	944	1	2	1	0	1	03:05
79	OMT9	OMT	5	461594	462226	462226	462614	1	1	510	1019	1	2	1	0	1	03:05
48	OMT9	OMT	4	361942	362378	362378	362993	1	1	526	1050	1	2	1	0	1	03:05
194	OMT9	OMT	13	433720	433878	434234	434450	1	357	543	729	1	2	1	0	1	03:05
113	OMT9	OMT	8	151206	151383	151824	152076	1	442	656	869	1	2	1	0	1	03:05
154	OMT9	OMT	12	27605	28820	28820	29085	1	1	740	1479	1	2	1	0	1	03:05
203	OMT9	OMT	14	39652	40306	40430	41146	1	125	809	1493	1	2	1	0	1	03:05
221	OMT9	OMT	15	218142	219124	219136	219822	1	13	846	1679	1	2	1	0	1	03:05
119	OMT9	OMT	8	470864	471244	471607	472204	1	364	852	1339	1	2	1	0	1	03:05
89	OMT9	OMT	7	93397	94650	94650	95130	1	1	867	1732	1	2	1	0	1	03:05
4	OMT9	OMT	1	73970	74190	74786	75211	1	597	919	1240	1	2	1	0	1	03:05
130	OMT9	OMT	10	21859	22066	22895	22911	1	830	941	1051	1	2	1	0	1	03:05
168	OMT9	OMT	12	424103	424315	425059	425314	1	745	978	1210	1	2	1	0	1	03:05
36	OMT9	OMT	3	220112	221651	221877	222524	1	227	1319	2411	1	2	1	0	1	03:05
178	OMT9	OMT	12	822848	823217	823256	826618	1	40	1905	3769	1	2	1	0	1	03:05
43	OMT9	OMT	4	222020	222257	224854	225140	1	2598	2859	3119	1	2	1	0	1	03:05
91	OMT9	OMT	7	147249	147427	147698	148827	1	272	925	1577	1	3	1	0	1	5:3_6:2_5:3
164	OMT9	OMT	12	341507	341678	342190	342448	1	513	727	940	1	4	1	0	1	3:5_2:6_3:5
225	OMT9	OMT	15	619075	619398	620962	621636	1	1565	2063	2560	1	4	1	0	1	3:5_2:6_3:5
161	OMT9	OMT	12	231692	232046	232561	233075	1	516	949	1382	1	4	1	0	1	3:5_4:4_2:6_3:5
99	OMT9	OMT	7	625898	626137	629962	630335	1	3826	4131	4436	1	4	1	0	1	3:5_4:4_3:5_4:4_3:5_2:6_3:5
233	OMT9	OMT	16	19590	19596	21363	21404	1	1768	1791	1813	1	4	1	0	1	3:5_2:6_3:5_2:6_3:5_4:4_3:5_4:4_3:5
107	OMT9	OMT	7	1009812	1010365	1010428	1011166	1	64	709	1353	1	7	1	0	1	5:3_6:2
126	OMT9	OMT	9	332503	333073	333581	334640	1	509	1323	2136	1	7	1	0	1	5:3_6:2
238	OMT9	OMT	16	173018	173053	173981	174782	1	929	1346	1763	1	7	1	0	1	5:3_6:2
68	OMT9	OMT	4	1295582	1295980	1300582	1300834	1	4603	4927	5251	1	7	1	0	1	6:2_5:3
87	OMT9	OMT	7	19850	19896	20580	20692	1	685	763	841	1	7	1	0	1	6:2_4:4_6:2_4:4_6:2
131	OMT9	OMT	10	130065	130174	130263	130584	1	90	304	518	1	8	1	0	1	3:5_2:6
232	OMT9	OMT	15	1043361	1043801	1050821	1051046	1	7021	7353	7684	1	8	1	0	1	2:6_3:5
191	OMT9	OMT	13	251286	251609	252379	252532	1	771	1008	1245	1	8	1	0	1	2:6_4:4_2:6
27	OMT9	OMT	2	727085	727268	727435	728481	1	1168	1282	1395	1	8	1	0	1	3:5_4:4_2:6
67	OMT9	OMT	4	1278056	1278456	1279422	1279680	1	967	1295	1623	1	8	1	0	1	3:5_4:4_2:6
133	OMT9	OMT	10	293368	293436	294827	294918	1	1392	1471	1549	1	8	1	0	1	2:6_4:4_2:6
148	OMT9	OMT	11	264974	265409	266175	266189	1	767	991	1214	1	8	1	0	1	2:6_4:4_2:6_3:5
3	OMT9	OMT	1	67801	68551	70621	70999	1	2071	2634	3197	1	8	1	0	1	2:6_3:5_4:4_3:5
241	OMT9	OMT	16	254454	254494	254494	254696	1	1	121	241	1	10	1	0	1	06:02
157	OMT9	OMT	12	124230	124317	124421	124596	1	105	235	365	1	10	1	0	1	06:02
35	OMT9	OMT	3	210517	210635	210635	211159	1	1	321	641	1	10	1	0	1	06:02
9	OMT9	OMT	1	180982	181085	181334	181491	1	250	379	508	1	10	1	0	1	06:02
212	OMT9	OMT	14	424418	425075	425075	425369	1	1	476	950	1	10	1	0	1	06:02
81	OMT9	OMT	5	544734	545025	545025	545863	1	1	565	1128	1	10	1	0	1	06:02
195	OMT9	OMT	13	464785	464976	465435	465476	1	460	575	690	1	10	1	0	1	06:02
176	OMT9	OMT	12	778158	779222	779222	779322	1	1	582	1163	1	10	1	0	1	06:02
196	OMT9	OMT	13	467817	467994	468499	468637	1	506	663	819	1	10	1	0	1	06:02
229	OMT9	OMT	15	907801	907843	908551	908634	1	709	771	832	1	10	1	0	1	06:02
97	OMT9	OMT	7	588633	588807	589377	589637	1	571	787	1003	1	10	1	0	1	06:02

173	OMT9	OMT	12	610920	611078	611812	611994	1	735	904	1073	1	10	1	0	1 06:02
158	OMT9	OMT	12	127531	128653	130739	130857	1	2087	2706	3325	1	10	1	0	1 06:02
160	OMT9	OMT	12	180683	180796	183318	183574	1	2523	2707	2890	1	10	1	0	1 06:02
18	OMT9	OMT	2	350135	350166	350178	350376	1	13	127	240	1	10.1	1	0	1 02:06
183	OMT9	OMT	12	1058624	1058732	1058785	1058831	1	54	130	206	1	10.1	1	0	1 02:06
47	OMT9	OMT	4	317913	318023	318317	318659	1	295	520	745	1	10.1	1	0	1 02:06
108	OMT9	OMT	7	1013720	1013788	1014216	1014432	1	429	570	711	1	10.1	1	0	1 02:06
32	OMT9	OMT	3	65580	66138	66375	66729	1	238	693	1148	1	10.1	1	0	1 02:06
55	OMT9	OMT	4	699549	699810	700440	700614	1	631	848	1064	1	10.1	1	0	1 02:06
62	OMT9	OMT	4	1126095	1126171	1127082	1127449	1	912	1133	1353	1	10.1	1	0	1 02:06
244	OMT9	OMT	16	371914	372742	373422	373522	1	681	1144	1607	1	10.1	1	0	1 02:06
104	OMT9	OMT	7	913393	913982	914538	915691	1	557	1427	2297	1	10.1	1	0	1 02:06
78	OMT9	OMT	5	458086	458181	460225	460341	1	2045	2150	2254	1	10.1	1	0	1 02:06
214	OMT9	OMT	14	488208	488587	490406	490766	1	1820	2189	2557	1	10.1	1	0	1 02:06
53	OMT9	OMT	4	644966	645102	645102	652022	1	1	3528	7055	1	10.1	1	0	1 02:06
246	OMT9	OMT	16	475496	475562	475802	476379	1	241	562	882	2	11	1	0	1 5:3_5:3a
39	OMT9	OMT	4	46608	46818	48267	48349	1	1450	1595	1740	2	11	1	0	1 5:3_5:3a
151	OMT9	OMT	11	566023	566185	567633	567960	1	1449	1693	1936	2	11	1	0	1 5:3_5:3a
57	OMT9	OMT	4	753858	754044	755801	756152	1	1758	2026	2293	2	11	1	0	1 5:3_5:3a
94	OMT9	OMT	7	244757	245112	245422	245686	1	311	620	928	2	12	1	0	1 3:5_5:3a
110	OMT9	OMT	8	97715	98248	98643	99089	1	396	885	1373	2	15	1	0	1 5:3_4:4_5:3a
209	OMT9	OMT	14	219410	220323	220950	221010	1	628	1114	1599	2	15	1	0	1 5:3_4:4_5:3a
250	OMT9	OMT	16	637334	638483	639362	639417	1	880	1481	2082	2	15	1	0	1 5:3_4:4_5:3a
146	OMT9	OMT	11	230455	230765	231922	232567	1	1158	1635	2111	2	15	1	0	1 5:3_4:4_5:3a
70	OMT9	OMT	4	1486166	1487095	1488106	1488682	1	1012	1764	2515	2	15	1	0	1 5:3_4:4_5:3a
169	OMT9	OMT	12	509219	509342	511071	511197	1	1730	1854	1977	2	15	1	0	1 5:3_4:4_5:3a
19	OMT9	OMT	2	487454	487781	489580	490532	1	1800	2439	3077	2	15	1	0	1 5:3_4:4_5:3a
187	OMT9	OMT	13	91733	91890	94190	94473	1	2301	2520	2739	2	15	1	0	1 5:3_4:4_5:3a
106	OMT9	OMT	7	983164	983358	986049	986380	1	2692	2954	3215	2	15	1	0	1 5:3_4:4_5:3a
115	OMT9	OMT	8	185625	186453	191248	191304	1	4796	5237	5678	2	15	1	0	1 5:3_4:4_5:3a
54	OMT9	OMT	4	678799	679210	680288	680316	1	1079	1298	1516	2	16	1	0	1 3:5_4:4_3:5a
135	OMT9	OMT	10	389413	389929	391693	392871	1	1765	2611	3457	2	17	1	0	1 6:2_5:3_4:4_5:3a
155	OMT9	OMT	12	65523	65606	67821	68071	1	2216	2382	2547	2	17	1	0	1 5:3_6:2_5:3_4:4_5:3a
247	OMT9	OMT	16	481833	482069	483961	485045	1	1893	2552	3211	2	17	1	0	1 5:3_4:4_5:3a_6:2_5:3a
13	OMT9	OMT	2	145486	145751	150492	151117	1	4742	5186	5630	2	17	1	0	1 5:3_6:2_5:3_4:4_5:3a_4:4_5:3a
103	OMT9	OMT	7	839712	839880	843717	843816	1	3838	3971	4103	2	18	1	0	1 3:5_4:4_3:5_2:6_3:5_4:4_3:5a
98	OMT9	OMT	7	609044	609307	610674	611145	1	1368	1734	2100	2	22	1	0	1 3:5_4:4_3:5_2:6_3:5_2:6_3:5a
40	OMT9	OMT	4	86606	87227	94649	95033	1	7423	7925	8426	2	23	1	0	1 5:3_4:4_6:2_5:3a
248	OMT9	OMT	16	492354	493222	493470	494188	2_nonsis	249	1041	1833	3	30	1	0	1 03:05
193	OMT9	OMT	13	407191	407557	408374	408897	2_nonsis	818	1262	1705	3	30	1	0	1 5:3_4:4_3:5
24	OMT9	OMT	2	633129	633214	635127	635445	2_nonsis	1914	2115	2315	3	30	1	0	1 3:5_2:6_5:3
83	OMT9	OMT	6	50137	50410	51257	51370	2_nonsis	848	1040	1232	3	30	1	0	1 3:5_5:3_6:2_5:3
120	OMT9	OMT	8	515162	515676	516811	516908	2_nonsis	1136	1441	1745	3	30	1	0	1 3:5_2:6_4:4_5:3
199	OMT9	OMT	13	792254	793043	798090	798261	2_nonsis	5048	5527	6006	3	30	1	0	1 3:5_2:6_4:4_2:6
117	OMT9	OMT	8	384631	384685	391351	392078	2_nonsis	6667	7057	7446	3	31	1	0	1 4:4ai_2:6
184	OMT9	OMT	13	26922	28623	31858	35547	2_nonsis	3236	5930	8624	3	31	1	0	1 5:3_4:4ai_5:3
92	OMT9	OMT	7	165317	165523	171282	171503	2_nonsis	5760	5973	6185	3	31	1	0	1 6:2_4:4ai_5:3_4:4ai
174	OMT9	OMT	12	689527	689587	692181	692874	2_nonsis	2595	2971	3346	3	31	1	0	1 5:3_6:2_4:4_5:3_4:4ai
59	OMT9	OMT	4	935099	935138	938591	939572	2_nonsis	3454	3963	4472	3	31	1	0	1 4:4ai_3:5_4:4ai_3:5a_4:4_3:5a
96	OMT9	OMT	7	351015	351063	351063	351287	2_nonsis	1	136	271	1	1	1	1	0 (5:3)_(4:4aCO)
33	OMT9	OMT	3	148171	148238	148271	148481	2_nonsis	34	172	309	1	1	1	1	0 (5:3)_(4:4aCO)
25	OMT9	OMT	2	642776	643134	643176	643272	2_nonsis	43	269	495	1	1	1	1	0 (5:3)_(4:4aCO)
90	OMT9	OMT	7	114793	116310	116310	116629	2_nonsis	1	918	1835	1	1	1	1	0 (5:3)_(4:4aCO)
185	OMT9	OMT	13	41174	42127	42127	43336	2_nonsis	1	1081	2161	1	1	1	1	0 (5:3)_(4:4aCO)
170	OMT9	OMT	12	520933	521221	521782	522608	2_nonsis	562	1118	1674	1	1	1	1	0 (5:3)_(4:4aCO)
231	OMT9	OMT	15	1040442	1040775	1041177	1042440	2_nonsis	403	1200	1997	1	1	1	1	0 (5:3)_(4:4aCO)
235	OMT9	OMT	16	130647	130793	131951	132681	2_nonsis	1159	1596	2033	1	1	1	1	0 (5:3)_(4:4aCO)
206	OMT9	OMT	14	122278	122496	124329	124634	2_nonsis	1834	2095	2355	1	1	1	1	0 (5:3)_(4:4aCO)
156	OMT9	OMT	12	81147	81186	81207	81387	2_nonsis	22	131	239	1	2	1	1	0 (3:5)_(4:4aCO)
149	OMT9	OMT	11	353289	353522	353522	353672	2_nonsis	1	192	382	1	2	1	1	0 (3:5)_(4:4aCO)

123	OMT9	OMT	9	94596	94804	94919	95341	2_nonsis	116	430	744	1	2	1	1	0	(3:5)_(4:4aCO)
219	OMT9	OMT	15	40365	40497	40834	41027	2_nonsis	338	500	661	1	2	1	1	0	(3:5)_(4:4aCO)
37	OMT9	OMT	3	288455	289600	289600	289803	2_nonsis	1	674	1347	1	2	1	1	0	(3:5)_(4:4aCO)
166	OMT9	OMT	12	382702	382931	384821	385142	2_nonsis	1891	2165	2439	1	2	1	1	0	(3:5)_(4:4aCO)
127	OMT9	OMT	9	377342	377556	378456	379276	2_nonsis	901	1417	1933	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
210	OMT9	OMT	14	306527	307339	308436	308655	2_nonsis	1098	1613	2127	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
42	OMT9	OMT	4	196851	198376	200220	200994	2_nonsis	1845	2994	4142	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
220	OMT9	OMT	15	195722	196238	196803	197183	2_nonsis	566	1013	1460	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
61	OMT9	OMT	4	1005257	1005358	1006922	1007012	2_nonsis	1565	1660	1754	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
175	OMT9	OMT	12	713180	713312	715886	715955	2_nonsis	2575	2675	2774	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
208	OMT9	OMT	14	188016	188308	191916	192676	2_nonsis	3609	4134	4659	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
254	OMT9	OMT	16	811965	812355	812845	812990	2_nonsis	491	758	1024	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
242	OMT9	OMT	16	278394	278872	279975	280422	2_nonsis	1104	1566	2027	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
7	OMT9	OMT	1	137336	138499	139404	141984	2_nonsis	906	2777	4647	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
163	OMT9	OMT	12	282215	282385	283463	284270	2_nonsis	1079	1567	2054	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
179	OMT9	OMT	12	835509	835608	843387	844293	2_nonsis	7780	8282	8783	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
16	OMT9	OMT	2	288339	288484	288498	288671	2_nonsis	15	173	331	1	11	1	1	0	(4:4ai)_(4:4bCO)
65	OMT9	OMT	4	1241519	1242658	1242658	1246191	2_nonsis	1	2336	4671	1	11	1	1	0	(4:4ai)_(4:4bCO)
147	OMT9	OMT	11	248004	248274	248310	248487	2_nonsis	37	260	482	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
118	OMT9	OMT	8	421840	422434	422538	422684	2_nonsis	105	474	843	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
111	OMT9	OMT	8	120445	121477	122169	122633	2_nonsis	693	1440	2187	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
249	OMT9	OMT	16	576041	576179	576653	576758	2_nonsis	475	596	716	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(4:4aCO)
165	OMT9	OMT	12	348259	348314	349138	349585	2_nonsis	825	1075	1325	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
132	OMT9	OMT	10	145019	145102	146059	146367	2_nonsis	958	1153	1347	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(4:4aCO)
245	OMT9	OMT	16	380674	380758	381840	381920	2_nonsis	1083	1164	1245	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
12	OMT9	OMT	2	71395	71420	72420	73226	2_nonsis	1001	1416	1830	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
51	OMT9	OMT	4	566007	566376	567474	567804	2_nonsis	1099	1448	1796	1	12	1	1	0	(5:3)_(6:2)_(4:4)_(4:4aCO)
182	OMT9	OMT	12	1030614	1030831	1031842	1032807	2_nonsis	1012	1602	2192	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
152	OMT9	OMT	11	580815	581481	582756	582855	2_nonsis	1276	1658	2039	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
105	OMT9	OMT	7	918156	918499	919947	920105	2_nonsis	1449	1699	1948	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
255	OMT9	OMT	16	905685	905754	907043	907815	2_nonsis	1290	1710	2129	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
134	OMT9	OMT	10	313986	314406	315888	316551	2_nonsis	1483	2024	2564	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)
230	OMT9	OMT	15	955553	956028	958391	958713	2_nonsis	2364	2762	3159	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
180	OMT9	OMT	12	887437	891755	892436	930472	2_nonsis	682	21858	43034	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
49	OMT9	OMT	4	365434	365716	366629	366913	2_nonsis	914	1196	1478	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)
56	OMT9	OMT	4	703059	703137	703905	706032	2_nonsis	769	1871	2972	1	12	1	1	0	(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
223	OMT9	OMT	15	302184	302514	304796	304859	2_nonsis	2283	2479	2674	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4a)
201	OMT9	OMT	13	894275	895607	898462	898537	2_nonsis	2856	3559	4261	1	12	1	1	0	(2:6)_(3:5)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)
205	OMT9	OMT	14	76137	76429	76429	76856	2_nonsis	1	360	718	1	15	1	1	0	(6:2)_(4:4aCO)
228	OMT9	OMT	15	905482	905729	905751	906405	2_nonsis	23	473	922	1	15	1	1	0	(6:2)_(4:4aCO)
102	OMT9	OMT	7	797366	797622	798046	798196	2_nonsis	425	627	829	1	15	1	1	0	(6:2)_(4:4aCO)
144	OMT9	OMT	11	77827	78581	79688	79772	2_nonsis	1108	1526	1944	1	15	1	1	0	(6:2)_(4:4aCO)
143	OMT9	OMT	11	14411	18399	18399	19020	2_nonsis	1	2305	4608	1	15	1	1	0	(6:2)_(4:4aCO)
72	OMT9	OMT	5	159624	159875	159882	160010	2_nonsis	8	197	385	1	16	1	1	0	(2:6)_(4:4aCO)
198	OMT9	OMT	13	715590	715643	715953	715971	2_nonsis	311	346	380	1	16	1	1	0	(2:6)_(4:4aCO)
129	OMT9	OMT	9	409125	409496	409916	410027	2_nonsis	421	661	901	1	16	1	1	0	(2:6)_(4:4aCO)
240	OMT9	OMT	16	226631	226745	227039	227828	2_nonsis	295	746	1196	1	16	1	1	0	(2:6)_(4:4aCO)
197	OMT9	OMT	13	644092	644367	645425	645754	2_nonsis	1059	1360	1661	1	16	1	1	0	(2:6)_(4:4aCO)
192	OMT9	OMT	13	387879	388308	387879	388308	2_nonsis	0	214	428	1	100	1	1	0	(4:4aCO)
213	OMT9	OMT	14	435934	436363	435934	436363	2_nonsis	0	214	428	1	100	1	1	0	(4:4aCO)
125	OMT9	OMT	9	267668	268176	267668	268176	2_nonsis	0	254	507	1	100	1	1	0	(4:4aCO)
114	OMT9	OMT	8	181132	181682	181132	181682	2_nonsis	0	275	549	1	100	1	1	0	(4:4aCO)
28	OMT9	OMT	2	736314	736876	736314	736876	2_nonsis	0	281	561	1	100	1	1	0	(4:4aCO)
251	OMT9	OMT	16	648799	649375	648799	649375	2_nonsis	0	288	575	1	100	1	1	0	(4:4aCO)
239	OMT9	OMT	16	219029	219860	219029	219860	2_nonsis	0	415	830	1	100	1	1	0	(4:4aCO)
50	OMT9	OMT	4	504204	505041	504204	505041	2_nonsis	0	418	836	1	100	1	1	0	(4:4aCO)
204	OMT9	OMT	14	46932	49011	46932	49011	2_nonsis	0	1039	2078	1	100	1	1	0	(4:4aCO)
145	OMT9	OMT	11	152355	154732	152355	154732	2_nonsis	0	1188	2376	1	100	1	1	0	(4:4aCO)
215	OMT9	OMT	14	539950	542443	539950	542443	2_nonsis	0	1246	2492	1	100	1	1	0	(4:4aCO)
8	OMT9	OMT	1	167179	170726	167179	170726	2_nonsis	0	1773	3546	1	100	1	1	0	(4:4aCO)

186	OMT9	OMT	13	51256	51335	53537	53642	2_nonsis		2203	2294	2385	2	30	1	1	0 (6:2)_(5:3)_(5:3a)_(4:4aCO)
52	OMT9	OMT	4	584012	584486	587057	588381	2_nonsis		2572	3470	4368	2	30	1	1	0 (6:2)_(5:3)_(5:3a)_(4:4aCO)_(5:3a)_(6:2)_(4:4a)
45	OMT9	OMT	4	294427	295520	296339	296793	2_nonsis		820	1593	2365	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
181	OMT9	OMT	12	1022570	1022675	1025374	1025702	2_nonsis		2700	2916	3131	2	31	1	1	0 (3:5)_(4:4)_(3:5)_(3:5a)_(4:4aCO)
26	OMT9	OMT	2	703042	703256	708952	709993	2_nonsis		5697	6324	6950	2	31	1	1	0 (4:4ai)_(3:5)_(4:4ai)_(3:5)_(3:5a)_(4:4bCO)
207	OMT9	OMT	14	146493	146563	148331	148607	2_nonsis		1769	1941	2113	2	32	1	1	0 (5:3)_(4:4ai)_(5:3a)_(4:4bCO)
38	OMT9	OMT	4	32706	32904	34987	35378	2_nonsis		2084	2378	2671	2	32	1	1	0 (3:5)_(2:6)_(3:5a)_(4:4aCO)
234	OMT9	OMT	16	82464	82826	85601	85621	2_nonsis		2776	2966	3156	2	32	1	1	0 (3:5)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
188	OMT9	OMT	13	103361	104510	107248	107332	2_nonsis		2739	3355	3970	2	32	1	1	0 (5:3)_(4:4)_(5:3a)_(4:4ai)_(4:4bCO)
5	OMT9	OMT	1	104068	107245	109735	110713	2_nonsis		2491	4568	6644	2	32	1	1	0 (3:5)_(4:4aCO)_(2:6)_(3:5a)_(4:4a)
58	OMT9	OMT	4	864727	865291	870568	871373	2_nonsis		5278	5962	6645	2	32	1	1	0 (4:4ai)_(5:3)_(6:2)_(5:3a)_(4:4ai)_(4:4bCO)
1	OMT9	OMT	1	31848	31975	37019	37294	2_nonsis		5045	5245	5445	2	32	1	1	0 (6:2)_(5:3)_(6:2)_(5:3a)_(6:2)_(5:3)_(4:4aCO)
153	OMT9	OMT	12	16338	16487	16757	17014	2_nonsis		271	473	675	3	20	1	1	0 (2:6)_(5:3)_(4:4aCO)
226	OMT9	OMT	15	656264	656389	657204	657250	2_nonsis		816	901	985	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)
121	OMT9	OMT	9	53091	53103	53832	54480	2_nonsis		730	1059	1388	3	20	1	1	0 (5:3)_(2:6)_(4:4aCO)
137	OMT9	OMT	10	464438	465021	465816	466454	2_nonsis		796	1406	2015	3	20	1	1	0 (6:2)_(2:6)_(4:4aCO)
217	OMT9	OMT	14	674690	676368	677207	677352	2_nonsis		840	1751	2661	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
34	OMT9	OMT	3	156517	156868	158627	158956	2_nonsis		1760	2099	2438	3	20	1	1	0 (3:5)_(5:3)_(4:4aCO)
17	OMT9	OMT	2	347935	348121	348478	348625	2_nonsis		358	524	689	3	20	1	1	0 (6:2)_(4:4aCO)_(2:6)_(4:4a)
80	OMT9	OMT	5	473893	473950	474470	474506	2_nonsis		521	567	612	3	20	1	1	0 (5:3)_(4:4)_(3:5)_(4:4aCO)
253	OMT9	OMT	16	739009	739133	740090	740140	2_nonsis		958	1044	1130	3	20	1	1	0 (3:5)_(4:4)_(6:2)_(4:4aCO)
150	OMT9	OMT	11	492262	493124	493667	494125	2_nonsis		544	1203	1862	3	20	1	1	0 (4:4aCO)_(2:6)_(5:3)_(4:4a)
227	OMT9	OMT	15	769458	769620	770868	771765	2_nonsis		1249	1778	2306	3	20	1	1	0 (2:6)_(4:4)_(6:2)_(4:4aCO)
142	OMT9	OMT	10	706608	707018	707655	707903	2_nonsis		638	966	1294	3	20	1	1	0 (2:6)_(4:4)_(5:3)_(6:2)_(4:4aCO)
77	OMT9	OMT	5	392867	393024	395011	395075	2_nonsis		1988	2098	2207	3	20	1	1	0 (2:6)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
162	OMT9	OMT	12	257813	258349	260323	260496	2_nonsis		1975	2329	2682	3	20	1	1	0 (3:5)_(2:6)_(4:4aCO)_(5:3)_(4:4a)
82	OMT9	OMT	5	548562	549247	550834	551094	2_nonsis		1588	2060	2531	3	20	1	1	0 (5:3)_(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
29	OMT9	OMT	2	770910	771544	776367	777303	2_nonsis		4824	5608	6392	3	20	1	1	0 (5:3)_(6:2)_(5:3)_(2:6)_(3:5)_(4:4aCO)
222	OMT9	OMT	15	256152	256235	259967	260183	2_nonsis		3733	3882	4030	3	20	1	1	0 (2:6)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(3:5)_(4:4aCO)
141	OMT9	OMT	10	642510	643441	643859	643946	2_nonsis		419	927	1435	3	21	1	1	0 (2:6)_(5:3)_(4:4ai)_(4:4bCO)
6	OMT9	OMT	1	128756	129063	130975	132066	2_nonsis		1913	2611	3309	3	21	1	1	0 (3:5)_(4:4ai)_(5:3)_(4:4bCO)
159	OMT9	OMT	12	142500	143093	144379	144822	2_nonsis		1287	1804	2321	3	21	1	1	0 (2:6)_(5:3)_(4:4ai)_(3:5)_(4:4bCO)
190	OMT9	OMT	13	177865	178128	179582	179588	2_nonsis		1455	1589	1722	3	21	1	1	0 (5:3)_(4:4)_(2:6)_(4:4ai)_(5:3)_(4:4bCO)
167	OMT9	OMT	12	388010	388456	392866	392954	2_nonsis		4411	4677	4943	3	21	1	1	0 (3:5)_(4:4ai)_(5:3)_(4:4bCO)_(5:3)_(4:4ai)_(3:5)_(2:6)_(4:4b)
23	OMT9	OMT	2	559930	560167	567682	567814	2_nonsis		7516	7700	7883	3	21	1	1	0 (5:3)_(6:2)_(5:3)_(4:4)_(4:4ai)_(3:5)_(4:4ai)_(3:5a)_(4:4ai)_(5:3a)_(4:4bCO)
10	OMT9	OMT	1	187427	189825	194436	194475		4	4612	5830	7047	0	1	2	0	2 (1:7)_(3:5)_(2:6i)_(3:5a)_(0:8)_(2:6a)_(3:5b)_(4:4)
14	OMT9	OMT	2	160143	160403	164419	164851	2_sis		4017	4362	4707	0	1	2	0	2 (2:6)_(3:5)_(4:4)_(2:6a)_(4:4)
75	OMT9	OMT	5	281237	281289	284190	284613	2_sis		2902	3139	3375	0	1	2	0	2 (3:5)_(3:5a)_(4:4)
85	OMT9	OMT	6	108920	109247	110820	110943		3	1574	1798	2022	0	1	2	0	2 (5:3)_(4:4)_(5:3)_(4:4ai)_(5:3a)_(4:4ai)_(3:5)_(4:4bi)_(4:4)
88	OMT9	OMT	7	53419	53732	55957	57501	2_sis		2226	3154	4081	0	1	2	0	2 (3:5)_(2:6)_(3:5)_(4:4)_(2:6)_(3:5)_(3:5a)_(4:4)
101	OMT9	OMT	7	696994	697261	700278	700504	2_sis		3018	3264	3509	0	1	2	0	2 (3:5)_(4:4)_(3:5)_(4:4)_(3:5)_(3:5a)_(3:5a)_(4:4)
171	OMT9	OMT	12	572662	572946	574950	575257		3	2005	2300	2594	0	1	2	0	2 (2:6)_(4:4)_(3:5)_(4:4)_(5:3)_(4:4)
202	OMT9	OMT	13	900142	901050	902696	902762		3	1647	2133	2619	0	1	2	0	2 (6:2)_(4:4)_(5:3)_(5:3a)_(4:4)
2	OMT9	OMT	1	57739	59349	61708	61999		3	2360	3310	4259	0	2	2	1	1 (2:6)_(3:5)_(3:5a)_(4:4aCO)
21	OMT9	OMT	2	504994	505129	506237	506715		3	1109	1415	1720	0	2	2	1	1 (3:5)_(4:4ai)_(2:6i)_(4:4bCO)
30	OMT9	OMT	2	789369	789930	792210	792968		3	2281	2940	3598	0	2	2	1	1 (3:5)_(4:4)_(1:7)_(2:6)_(4:4aCO)
44	OMT9	OMT	4	235676	235902	241206	241406		4	5305	5517	5729	0	2	2	2	0 (3:5)_(2:6)_(3:5a)_(2:6)_(0:8)_(2:6)_(1:7)_(3:5b)_(4:4aCO)
71	OMT9	OMT	5	38064	38431	45019	45548		3	6589	7036	7483	0	2	2	1	1 (4:4ai)_(3:5)_(4:4bi)_(5:3)_(5:3a)_(3:5a)_(4:4bi)_(2:6)_(5:3b)_(6:2)_(5:3b)_(4:4cCO)
84	OMT9	OMT	6	52838	53398	54858	55242		4	1461	1932	2403	0	2	2	2	0 (3:5)_(2:6)_(4:4aCO)
86	OMT9	OMT	6	129391	130480	132667	133039		3	2188	2918	3647	0	2	2	1	1 (2:6)_(6:2)_(5:3)_(4:4aCO)
109	OMT9	OMT	8	13244	13408	17641	17751		3	4234	4370	4506	0	2	2	1	1 (6:2)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
172	OMT9	OMT	12	593059	599206	605228	605250		3	6023	9107	12190	0	2	2	1	1 (5:3)_(4:4)_(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)_(5:3a)_(4:4a)
200	OMT9	OMT	13	826214	826499	828228	828274		3	1730	1895	2059	0	2	2	1	1 (3:5)_(4:4aCO)_(3:5a)_(4:4a)
15	OMT9	OMT	2	189673	190032	191613	192289	2_nonsis		1582	2099	2615	0	3	2	0	2 (5:3)_(4:4ai)_(4:4bCO)_(6:2)_(4:4b)_(4:4CO)
95	OMT9	OMT	7	270975	271422	272568	273422		3	1147	1797	2446	0	3	2	1	1 (2:6)_(3:5)_(4:4aCO)_(6:2)_(4:4bCO)
100	OMT9	OMT	7	632060	632357	639145	639946		3	6789	7337	7885	0	3	2	1	1 (5:3)_(4:4aCO)_(3:5)_(4:4a)_(5:3a)_(4:4bCO)
124	OMT9	OMT	9	244951	245022	252174	252259		4	7153	7230	7307	0	3	2	1	1 (3:5)_(2:6)_(1:7)_(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
218	OMT9	OMT	14	722025	722231	724724	725092	2_nonsis		2494	2780	3066	0	3	2	0	2 (4:4aCO)_(5:3)_(6:2)_(4:4CO)
224	OMT9	OMT	15	479565	480144	487166	487809		3	7023	7633	8243	0	3	2	1	1 (2:6)_(4:4)_(3:5)_(2:6a)_(4:4aCO)_(5:3)_(6:2)_(4:4bCO)_(2:6)_(4:4b)
137	TCMM15	TCMM	10	265324	265353	265353	265422		1	1	49	97	1	1	1	0	1 05:03

66	TCMM15	TCMM	5	62815	62818	62818	62914	1	1	50	98	1	1	1	0	1	05:03
242	TCMM15	TCMM	14	531520	531611	531611	531656	1	1	68	135	1	1	1	0	1	05:03
72	TCMM15	TCMM	5	378075	378265	378297	378395	1	33	176	319	1	1	1	0	1	05:03
181	TCMM15	TCMM	12	568114	568449	568449	568546	1	1	216	431	1	1	1	0	1	05:03
249	TCMM15	TCMM	14	722231	722345	722345	722690	1	1	230	458	1	1	1	0	1	05:03
100	TCMM15	TCMM	7	730599	731008	731064	731073	1	57	265	473	1	1	1	0	1	05:03
262	TCMM15	TCMM	15	586304	586345	586345	586852	1	1	274	547	1	1	1	0	1	05:03
171	TCMM15	TCMM	12	74294	74484	74484	74872	1	1	289	577	1	1	1	0	1	05:03
246	TCMM15	TCMM	14	643651	643956	643956	644271	1	1	310	619	1	1	1	0	1	05:03
166	TCMM15	TCMM	11	489458	489975	489975	490084	1	1	313	625	1	1	1	0	1	05:03
130	TCMM15	TCMM	10	58607	59185	59202	59484	1	18	447	876	1	1	1	0	1	05:03
138	TCMM15	TCMM	10	268513	269086	269086	269458	1	1	473	944	1	1	1	0	1	05:03
224	TCMM15	TCMM	13	759679	759844	760211	760322	1	368	505	642	1	1	1	0	1	05:03
191	TCMM15	TCMM	12	818015	818577	818577	819069	1	1	527	1053	1	1	1	0	1	05:03
283	TCMM15	TCMM	16	640589	640976	640976	641895	1	1	653	1305	1	1	1	0	1	05:03
19	TCMM15	TCMM	2	633960	635127	635127	635445	1	1	743	1484	1	1	1	0	1	05:03
44	TCMM15	TCMM	4	667986	669064	669064	669601	1	1	808	1614	1	1	1	0	1	05:03
56	TCMM15	TCMM	4	1048403	1049195	1049309	1050120	1	115	916	1716	1	1	1	0	1	05:03
272	TCMM15	TCMM	16	106600	107304	107754	108114	1	451	982	1513	1	1	1	0	1	05:03
280	TCMM15	TCMM	16	492354	493222	493470	494188	1	249	1041	1833	1	1	1	0	1	05:03
127	TCMM15	TCMM	9	380809	380958	381607	382331	1	650	1086	1521	1	1	1	0	1	05:03
23	TCMM15	TCMM	2	746171	747838	747838	748391	1	1	1110	2219	1	1	1	0	1	05:03
189	TCMM15	TCMM	12	763502	763595	764623	764781	1	1029	1154	1278	1	1	1	0	1	05:03
183	TCMM15	TCMM	12	644135	644551	645452	645754	1	902	1260	1618	1	1	1	0	1	05:03
267	TCMM15	TCMM	15	1008443	1009862	1010523	1010592	1	662	1405	2148	1	1	1	0	1	05:03
217	TCMM15	TCMM	13	575127	576259	576343	577948	1	85	1453	2820	1	1	1	0	1	05:03
88	TCMM15	TCMM	7	109784	112158	112158	112793	1	1	1505	3008	1	1	1	0	1	05:03
208	TCMM15	TCMM	13	328760	328866	330411	330819	1	1546	1802	2058	1	1	1	0	1	05:03
2	TCMM15	TCMM	1	167179	170726	170945	172280	1	220	2660	5100	1	1	1	0	1	05:03
155	TCMM15	TCMM	11	84295	84308	84308	84350	1	1	28	54	1	2	1	0	1	03:05
203	TCMM15	TCMM	13	209285	209422	209449	209542	1	28	142	256	1	2	1	0	1	03:05
158	TCMM15	TCMM	11	225480	225609	225609	225834	1	1	177	353	1	2	1	0	1	03:05
30	TCMM15	TCMM	3	254715	254961	254961	255150	1	1	218	434	1	2	1	0	1	03:05
70	TCMM15	TCMM	5	263386	263549	263633	263748	1	85	223	361	1	2	1	0	1	03:05
174	TCMM15	TCMM	12	221524	221668	221668	222010	1	1	243	485	1	2	1	0	1	03:05
76	TCMM15	TCMM	5	475694	475964	476027	476183	1	64	276	488	1	2	1	0	1	03:05
277	TCMM15	TCMM	16	404106	404634	404634	404667	1	1	281	560	1	2	1	0	1	03:05
46	TCMM15	TCMM	4	693401	693728	693728	694033	1	1	316	631	1	2	1	0	1	03:05
20	TCMM15	TCMM	2	642483	642776	642776	643134	1	1	326	650	1	2	1	0	1	03:05
290	TCMM15	TCMM	16	911898	912387	912387	912564	1	1	333	665	1	2	1	0	1	03:05
145	TCMM15	TCMM	10	470777	471025	471025	471532	1	1	378	754	1	2	1	0	1	03:05
31	TCMM15	TCMM	3	262264	262830	262830	263025	1	1	381	760	1	2	1	0	1	03:05
42	TCMM15	TCMM	4	460852	461027	461027	461615	1	1	382	762	1	2	1	0	1	03:05
73	TCMM15	TCMM	5	409394	409516	409528	410181	1	13	400	786	1	2	1	0	1	03:05
287	TCMM15	TCMM	16	696953	697060	697067	697775	1	8	415	821	1	2	1	0	1	03:05
26	TCMM15	TCMM	3	77866	77900	77900	78705	1	1	420	838	1	2	1	0	1	03:05
5	TCMM15	TCMM	2	44210	44904	44974	45075	1	71	468	864	1	2	1	0	1	03:05
52	TCMM15	TCMM	4	886289	887179	887179	887504	1	1	608	1214	1	2	1	0	1	03:05
250	TCMM15	TCMM	14	731064	731177	731562	732158	1	386	740	1093	1	2	1	0	1	03:05
7	TCMM15	TCMM	2	116257	116476	116947	117293	1	472	754	1035	1	2	1	0	1	03:05
212	TCMM15	TCMM	13	452181	453503	453503	453745	1	1	782	1563	1	2	1	0	1	03:05
168	TCMM15	TCMM	11	559244	559385	559707	560658	1	323	868	1413	1	2	1	0	1	03:05
32	TCMM15	TCMM	3	272348	273723	273985	274039	1	263	977	1690	1	2	1	0	1	03:05
231	TCMM15	TCMM	14	75675	76137	77017	77179	1	881	1192	1503	1	2	1	0	1	03:05
117	TCMM15	TCMM	8	496013	496308	497380	497537	1	1073	1298	1523	1	2	1	0	1	03:05
8	TCMM15	TCMM	2	123320	123635	124617	124942	1	983	1302	1621	1	2	1	0	1	03:05
244	TCMM15	TCMM	14	551646	552259	552709	553805	1	451	1305	2158	1	2	1	0	1	03:05
153	TCMM15	TCMM	11	51558	52399	53005	53905	1	607	1477	2346	1	2	1	0	1	03:05
230	TCMM15	TCMM	13	842091	842866	844197	844367	1	1332	1804	2275	1	2	1	0	1	03:05
228	TCMM15	TCMM	13	810028	810085	812787	813019	1	2703	2847	2990	1	2	1	0	1	03:05

114	TCMM15	TCMM	8	340650	340958	341299	341482	1	342	587	831	1	3	1	0	1	5:3_6:2_5:3
68	TCMM15	TCMM	5	241522	241980	242472	242481	1	493	726	958	1	3	1	0	1	5:3_4:4_5:3
161	TCMM15	TCMM	11	308325	308425	309294	309310	1	870	927	984	1	3	1	0	1	5:3_6:2_5:3
193	TCMM15	TCMM	12	883503	884813	885216	885247	1	404	1074	1743	1	3	1	0	1	5:3_6:2_5:3
253	TCMM15	TCMM	15	103244	103443	104628	104808	1	1186	1375	1563	1	3	1	0	1	5:3_4:4_5:3
205	TCMM15	TCMM	13	239896	240460	241597	242103	1	1138	1672	2206	1	3	1	0	1	5:3_4:4_5:3
123	TCMM15	TCMM	9	235511	236044	237506	237799	1	1463	1875	2287	1	3	1	0	1	5:3_4:4_5:3
50	TCMM15	TCMM	4	866436	867508	868704	869191	1	1197	1976	2754	1	3	1	0	1	5:3_6:2_5:3
119	TCMM15	TCMM	9	36103	36166	36801	36833	1	636	683	729	1	3	1	0	1	5:3_6:2_5:3_4:4_5:3
54	TCMM15	TCMM	4	925130	925318	926065	926246	1	748	932	1115	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
172	TCMM15	TCMM	12	178813	179029	181545	181615	1	2517	2659	2801	1	3	1	0	1	5:3_4:4_5:3_6:2_5:3
187	TCMM15	TCMM	12	689626	689793	692181	692874	1	2389	2818	3247	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
179	TCMM15	TCMM	12	389953	390142	392292	392407	1	2151	2302	2453	1	3	1	0	1	5:3_4:4_5:3_6:2_5:3_6:2_5:3
182	TCMM15	TCMM	12	602479	603057	603216	603313	1	160	497	833	1	4	1	0	1	3:5_2:6_3:5
235	TCMM15	TCMM	14	301618	301887	302316	302384	1	430	598	765	1	4	1	0	1	3:5_4:4_3:5
78	TCMM15	TCMM	5	522421	522685	523260	523683	1	576	919	1261	1	4	1	0	1	3:5_2:6_3:5
271	TCMM15	TCMM	16	100143	100432	101603	101698	1	1172	1363	1554	1	4	1	0	1	3:5_4:4_3:5
206	TCMM15	TCMM	13	281241	282022	283234	283250	1	1213	1611	2008	1	4	1	0	1	3:5_4:4_3:5
40	TCMM15	TCMM	4	368207	368620	369971	370499	1	1352	1822	2291	1	4	1	0	1	3:5_4:4_3:5
150	TCMM15	TCMM	10	639365	640236	641631	642317	1	1396	2174	2951	1	4	1	0	1	3:5_2:6_3:5
219	TCMM15	TCMM	13	603074	603083	605479	605741	1	2397	2532	2666	1	4	1	0	1	3:5_4:4_3:5
92	TCMM15	TCMM	7	267480	268323	270975	272568	1	2653	3870	5087	1	4	1	0	1	3:5_4:4_3:5
21	TCMM15	TCMM	2	649354	649588	650619	651379	1	1032	1528	2024	1	4	1	0	1	3:5_2:6_4:4_3:5
210	TCMM15	TCMM	13	392003	392080	393147	393355	1	1068	1210	1351	1	4	1	0	1	3:5_2:6_3:5_4:4_3:5
223	TCMM15	TCMM	13	703990	704416	706935	707030	1	2520	2780	3039	1	4	1	0	1	3:5_4:4_3:5_4:4_3:5
93	TCMM15	TCMM	7	276637	276866	279435	279857	1	2570	2895	3219	1	4	1	0	1	3:5_2:6_3:5_2:6_3:5
94	TCMM15	TCMM	7	295907	296177	299630	299804	1	3454	3675	3896	1	4	1	0	1	3:5_4:4_3:5_2:6_3:5
84	TCMM15	TCMM	6	210590	210664	210721	210741	1	58	104	150	1	7	1	0	1	6:2_5:3
220	TCMM15	TCMM	13	610293	610441	610501	610660	1	61	214	366	1	7	1	0	1	6:2_5:3
284	TCMM15	TCMM	16	646670	647349	647471	647721	1	123	587	1050	1	7	1	0	1	5:3_6:2
167	TCMM15	TCMM	11	493193	493438	493667	494359	1	230	698	1165	1	7	1	0	1	5:3_6:2
81	TCMM15	TCMM	6	80049	80232	80386	81527	1	155	816	1477	1	7	1	0	1	5:3_6:2
162	TCMM15	TCMM	11	321714	321765	323019	323096	1	1255	1318	1381	1	7	1	0	1	6:2_5:3
48	TCMM15	TCMM	4	816853	817682	818507	818791	1	826	1382	1937	1	7	1	0	1	6:2_5:3
157	TCMM15	TCMM	11	180504	182377	184295	184364	1	1919	2889	3859	1	7	1	0	1	5:3_6:2
134	TCMM15	TCMM	10	158376	158721	159201	160491	1	481	1298	2114	1	7	1	0	1	6:2_4:4_6:2
285	TCMM15	TCMM	16	657450	657485	659091	659254	1	1607	1705	1803	1	7	1	0	1	5:3_6:2_4:4_6:2
141	TCMM15	TCMM	10	331024	332595	334468	334858	1	1874	2854	3833	1	7	1	0	1	6:2_5:3_4:4_5:3
227	TCMM15	TCMM	13	797048	797146	800264	800350	1	3119	3210	3301	1	7	1	0	1	5:3_4:4_6:2_5:3_4:4_6:2
97	TCMM15	TCMM	7	485256	485313	485316	485387	1	4	67	130	1	8	1	0	1	2:6_3:5
132	TCMM15	TCMM	10	135693	135754	135996	136071	1	243	310	377	1	8	1	0	1	2:6_3:5
149	TCMM15	TCMM	10	633240	633350	633743	634423	1	394	788	1182	1	8	1	0	1	2:6_3:5
258	TCMM15	TCMM	15	295611	296401	296804	296918	1	404	855	1306	1	8	1	0	1	3:5_2:6
139	TCMM15	TCMM	10	302943	303003	303882	304262	1	880	1099	1318	1	8	1	0	1	2:6_3:5
75	TCMM15	TCMM	5	415894	416514	417310	417511	1	797	1207	1616	1	8	1	0	1	3:5_2:6
108	TCMM15	TCMM	8	99909	101246	102468	102818	1	1223	2066	2908	1	8	1	0	1	2:6_3:5
216	TCMM15	TCMM	13	560428	561397	563317	563599	1	1921	2546	3170	1	8	1	0	1	2:6_3:5
247	TCMM15	TCMM	14	673326	674407	678144	678306	1	3738	4359	4979	1	8	1	0	1	3:5_2:6
86	TCMM15	TCMM	7	18028	18259	18693	18901	1	435	654	872	1	8	1	0	1	3:5_4:4_2:6
164	TCMM15	TCMM	11	462930	462985	464192	464456	1	1208	1367	1525	1	8	1	0	1	2:6_4:4_3:5
195	TCMM15	TCMM	12	954849	955099	956854	957115	1	1756	2011	2265	1	8	1	0	1	2:6_4:4_2:6_3:5_2:6_3:5
274	TCMM15	TCMM	16	187312	187323	187323	187327	1	1	8	14	1	10	1	0	1	06:02
58	TCMM15	TCMM	4	1095230	1095364	1095365	1095467	1	2	119	236	1	10	1	0	1	06:02
229	TCMM15	TCMM	13	831458	831576	831576	832164	1	1	353	705	1	10	1	0	1	06:02
218	TCMM15	TCMM	13	587969	588588	588597	588927	1	10	484	957	1	10	1	0	1	06:02
188	TCMM15	TCMM	12	710116	710420	710710	710866	1	291	520	749	1	10	1	0	1	06:02
82	TCMM15	TCMM	6	95585	95627	95746	96802	1	120	668	1216	1	10	1	0	1	06:02
245	TCMM15	TCMM	14	559694	559885	560362	561323	1	478	1053	1628	1	10	1	0	1	06:02
3	TCMM15	TCMM	1	198604	198618	198618	198648	1	1	22	43	1	10.1	1	0	1	02:06
104	TCMM15	TCMM	7	905148	905227	905227	905266	1	1	59	117	1	10.1	1	0	1	02:06

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64	TCMM15	TCMM	5	18839	18992	18992	19005	1	1	83	165	1	10.1	1	0	1	02:06
159	TCMM15	TCMM	11	248004	248274	248274	248487	1	1	242	482	1	10.1	1	0	1	02:06
279	TCMM15	TCMM	16	474526	474750	474750	475030	1	1	252	503	1	10.1	1	0	1	02:06
226	TCMM15	TCMM	13	793469	793604	793734	794088	1	131	375	618	1	10.1	1	0	1	02:06
51	TCMM15	TCMM	4	870568	870950	870950	871373	1	1	403	804	1	10.1	1	0	1	02:06
106	TCMM15	TCMM	8	11695	12627	12627	12640	1	1	473	944	1	10.1	1	0	1	02:06
15	TCMM15	TCMM	2	371554	371746	371746	372547	1	1	497	992	1	10.1	1	0	1	02:06
113	TCMM15	TCMM	8	329634	330227	330227	330660	1	1	513	1025	1	10.1	1	0	1	02:06
238	TCMM15	TCMM	14	425816	427715	427715	428693	1	1	1439	2876	1	10.1	1	0	1	02:06
80	TCMM15	TCMM	6	76860	77256	78202	78568	2_nonsis	947	1327	1707	3	30	1	0	1	2:6_4:4_6:2
240	TCMM15	TCMM	14	476731	476810	478186	479345	2_nonsis	1377	1995	2613	3	30	1	0	1	3:5_2:6_3:5a
142	TCMM15	TCMM	10	357628	358552	361124	362386	2_nonsis	2573	3665	4757	3	30	1	0	1	5:3_6:2_5:3a
136	TCMM15	TCMM	10	256465	256690	258301	258658	2_nonsis	1612	1902	2192	3	30	1	0	1	6:2_5:3_4:4_3:5
207	TCMM15	TCMM	13	315598	316408	318454	318678	2_nonsis	2047	2563	3079	3	30	1	0	1	5:3_4:4_5:3_2:6_3:5
22	TCMM15	TCMM	2	735807	736128	739563	739770	2_nonsis	3436	3699	3962	3	30	1	0	1	6:2_5:3_4:4_2:6_3:5
65	TCMM15	TCMM	5	32276	33002	36958	37041	2_nonsis	3957	4361	4764	3	30	1	0	1	3:5_4:4_3:5_4:4_5:3
9	TCMM15	TCMM	2	143613	144820	146169	146217	2_nonsis	1350	1977	2603	3	31	1	0	1	3:5_5:3_3:5_5:3a_4:4ai
198	TCMM15	TCMM	13	10941	11831	13964	14063	2_nonsis	2134	2628	3121	3	31	1	0	1	4:4ai_5:3_6:2_5:3a_4:4_5:3a
199	TCMM15	TCMM	13	77135	77482	81243	81354	2_nonsis	3762	3990	4218	3	31	1	0	1	5:3_6:2_5:3_6:2_5:3a_4:4ai_5:3_4:4_5:3
36	TCMM15	TCMM	4	139293	139499	139926	140600	2_nonsis	428	867	1306	1	1	1	1	0	(5:3)_(4:4aCO)
147	TCMM15	TCMM	10	568805	570822	570822	573135	2_nonsis	1	2165	4329	1	1	1	1	0	(5:3)_(4:4aCO)
170	TCMM15	TCMM	11	629864	630615	633026	633545	2_nonsis	2412	3046	3680	1	1	1	1	0	(5:3)_(4:4aCO)
201	TCMM15	TCMM	13	118473	118891	118891	119087	2_nonsis	1	307	613	1	2	1	1	0	(3:5)_(4:4aCO)
109	TCMM15	TCMM	8	112829	112944	112966	113512	2_nonsis	23	353	682	1	2	1	1	0	(3:5)_(4:4aCO)
143	TCMM15	TCMM	10	394408	394692	394810	395209	2_nonsis	119	460	800	1	2	1	1	0	(3:5)_(4:4aCO)
209	TCMM15	TCMM	13	382384	383224	383224	383408	2_nonsis	1	512	1023	1	2	1	1	0	(3:5)_(4:4aCO)
200	TCMM15	TCMM	13	114535	115183	115471	115959	2_nonsis	289	856	1423	1	2	1	1	0	(3:5)_(4:4aCO)
204	TCMM15	TCMM	13	235798	236410	236833	237159	2_nonsis	424	892	1360	1	2	1	1	0	(3:5)_(4:4aCO)
131	TCMM15	TCMM	10	95205	96041	96432	96721	2_nonsis	392	954	1515	1	2	1	1	0	(3:5)_(4:4aCO)
83	TCMM15	TCMM	6	176446	177023	177753	177798	2_nonsis	731	1041	1351	1	2	1	1	0	(3:5)_(4:4aCO)
29	TCMM15	TCMM	3	228130	230267	230267	231791	2_nonsis	1	1831	3660	1	2	1	1	0	(3:5)_(4:4aCO)
278	TCMM15	TCMM	16	423985	424230	425006	425740	2_nonsis	777	1266	1754	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
63	TCMM15	TCMM	4	1450894	1451664	1452723	1453499	2_nonsis	1060	1832	2604	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
112	TCMM15	TCMM	8	325071	325184	326185	326461	2_nonsis	1002	1196	1389	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
16	TCMM15	TCMM	2	448827	449152	449588	450377	2_nonsis	437	993	1549	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
163	TCMM15	TCMM	11	381058	381640	382201	383052	2_nonsis	562	1278	1993	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
243	TCMM15	TCMM	14	545517	545697	547792	547958	2_nonsis	2096	2268	2440	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
266	TCMM15	TCMM	15	953577	954310	954766	955162	2_nonsis	457	1021	1584	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
115	TCMM15	TCMM	8	358468	359669	360186	360415	2_nonsis	518	1232	1946	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
289	TCMM15	TCMM	16	899499	899836	900827	901564	2_nonsis	992	1528	2064	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
194	TCMM15	TCMM	12	941016	947200	948612	948698	2_nonsis	1413	4547	7681	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
241	TCMM15	TCMM	14	501363	501440	501631	501828	2_nonsis	192	328	464	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
74	TCMM15	TCMM	5	413281	413862	414190	414243	2_nonsis	329	645	961	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
96	TCMM15	TCMM	7	452589	452990	453324	453639	2_nonsis	335	692	1049	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
10	TCMM15	TCMM	2	181425	181705	185478	185922	2_nonsis	3774	4135	4496	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
53	TCMM15	TCMM	4	893442	893751	893982	895202	2_nonsis	232	996	1759	1	11	1	1	0	(4:4ai)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4bCO)
110	TCMM15	TCMM	8	190339	191248	191304	191691	2_nonsis	57	704	1351	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
101	TCMM15	TCMM	7	732382	733088	733429	733453	2_nonsis	342	706	1070	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
111	TCMM15	TCMM	8	266994	267185	267804	268308	2_nonsis	620	967	1313	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
39	TCMM15	TCMM	4	343448	344216	345017	345134	2_nonsis	802	1244	1685	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
180	TCMM15	TCMM	12	548783	548969	549297	549472	2_nonsis	329	509	688	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(4:4aCO)
273	TCMM15	TCMM	16	133388	133624	134038	134203	2_nonsis	415	615	814	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(4:4aCO)
49	TCMM15	TCMM	4	835164	835319	836051	836148	2_nonsis	733	858	983	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
79	TCMM15	TCMM	6	28318	28390	29526	29691	2_nonsis	1137	1255	1372	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
43	TCMM15	TCMM	4	549856	550499	551775	551991	2_nonsis	1277	1706	2134	1	12	1	1	0	(3:5)_(2:6)_(4:4)_(4:4aCO)
28	TCMM15	TCMM	3	145988	146420	148171	148238	2_nonsis	1752	2001	2249	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)
118	TCMM15	TCMM	8	516184	516318	517036	517336	2_nonsis	719	935	1151	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
41	TCMM15	TCMM	4	440689	440889	441738	441971	2_nonsis	850	1066	1281	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
256	TCMM15	TCMM	15	218142	219124	220974	221075	2_nonsis	1851	2392	2932	1	12	1	1	0	(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)
37	TCMM15	TCMM	4	239328	239462	241406	241613	2_nonsis	1945	2115	2284	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4)_(6:2)_(4:4aCO)

								2_nonsis									
60	TCMM15	TCMM	4	1256179	1256876	1258968	1259896	2_nonsis	2093	2905	3716	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)_(3:5)_(4:4a)
25	TCMM15	TCMM	3	38178	38318	40205	40294	2_nonsis	1888	2002	2115	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(2:6)_(3:5)_(4:4a)
57	TCMM15	TCMM	4	1062818	1062952	1063008	1063031	2_nonsis	57	135	212	1	15	1	1	0	(6:2)_(4:4aCO)
35	TCMM15	TCMM	4	30545	30752	30752	30908	2_nonsis	1	182	362	1	15	1	1	0	(6:2)_(4:4aCO)
55	TCMM15	TCMM	4	1005358	1005567	1005839	1006075	2_nonsis	273	495	716	1	15	1	1	0	(6:2)_(4:4aCO)
45	TCMM15	TCMM	4	673982	674236	674519	674711	2_nonsis	284	506	728	1	15	1	1	0	(6:2)_(4:4aCO)
18	TCMM15	TCMM	2	552727	552889	560167	561765	2_nonsis	7279	8158	9037	1	15	1	1	0	(6:2)_(4:4aCO)
11	TCMM15	TCMM	2	198241	198355	198475	198501	2_nonsis	121	190	259	1	16	1	1	0	(2:6)_(4:4aCO)
62	TCMM15	TCMM	4	1396824	1397034	1397034	1397492	2_nonsis	1	334	667	1	16	1	1	0	(2:6)_(4:4aCO)
59	TCMM15	TCMM	4	1232377	1232436	1232773	1232950	2_nonsis	338	455	572	1	16	1	1	0	(2:6)_(4:4aCO)
263	TCMM15	TCMM	15	744706	745114	745265	745547	2_nonsis	152	496	840	1	16	1	1	0	(2:6)_(4:4aCO)
107	TCMM15	TCMM	8	54302	54591	54591	55333	2_nonsis	1	516	1030	1	16	1	1	0	(2:6)_(4:4aCO)
95	TCMM15	TCMM	7	370897	371489	371625	372033	2_nonsis	137	636	1135	1	16	1	1	0	(2:6)_(4:4aCO)
122	TCMM15	TCMM	9	192389	193262	193298	193815	2_nonsis	37	731	1425	1	16	1	1	0	(2:6)_(4:4aCO)
47	TCMM15	TCMM	4	730199	730652	730734	731588	2_nonsis	83	736	1388	1	16	1	1	0	(2:6)_(4:4aCO)
148	TCMM15	TCMM	10	622874	623040	623040	624389	2_nonsis	1	758	1514	1	16	1	1	0	(2:6)_(4:4aCO)
124	TCMM15	TCMM	9	266255	267764	267764	268176	2_nonsis	1	961	1920	1	16	1	1	0	(2:6)_(4:4aCO)
152	TCMM15	TCMM	11	48808	49402	49402	51203	2_nonsis	1	1198	2394	1	16	1	1	0	(2:6)_(4:4aCO)
197	TCMM15	TCMM	12	1009719	1014198	1014227	1014332	2_nonsis	30	2321	4612	1	16	1	1	0	(2:6)_(4:4aCO)
27	TCMM15	TCMM	3	79797	91287	91287	93455	2_nonsis	1	6829	13657	1	16	1	1	0	(2:6)_(4:4aCO)
213	TCMM15	TCMM	13	465295	465435	465295	465435	2_nonsis	0	70	139	1	100	1	1	0	(4:4aCO)
61	TCMM15	TCMM	4	1311986	1312365	1311986	1312365	2_nonsis	0	189	378	1	100	1	1	0	(4:4aCO)
87	TCMM15	TCMM	7	75209	75611	75209	75611	2_nonsis	0	201	401	1	100	1	1	0	(4:4aCO)
281	TCMM15	TCMM	16	497162	497602	497162	497602	2_nonsis	0	220	439	1	100	1	1	0	(4:4aCO)
265	TCMM15	TCMM	15	917763	918228	917763	918228	2_nonsis	0	232	464	1	100	1	1	0	(4:4aCO)
154	TCMM15	TCMM	11	74103	74603	74103	74603	2_nonsis	0	250	499	1	100	1	1	0	(4:4aCO)
102	TCMM15	TCMM	7	848452	849134	848452	849134	2_nonsis	0	341	681	1	100	1	1	0	(4:4aCO)
105	TCMM15	TCMM	7	914816	915691	914816	915691	2_nonsis	0	437	874	1	100	1	1	0	(4:4aCO)
190	TCMM15	TCMM	12	783530	784454	783530	784454	2_nonsis	0	462	923	1	100	1	1	0	(4:4aCO)
259	TCMM15	TCMM	15	477802	478750	477802	478750	2_nonsis	0	474	947	1	100	1	1	0	(4:4aCO)
1	TCMM15	TCMM	1	66696	67715	66696	67715	2_nonsis	0	509	1018	1	100	1	1	0	(4:4aCO)
233	TCMM15	TCMM	14	163952	165064	163952	165064	2_nonsis	0	556	1111	1	100	1	1	0	(4:4aCO)
38	TCMM15	TCMM	4	314015	315175	314015	315175	2_nonsis	0	580	1159	1	100	1	1	0	(4:4aCO)
156	TCMM15	TCMM	11	130226	131399	130226	131399	2_nonsis	0	586	1172	1	100	1	1	0	(4:4aCO)
90	TCMM15	TCMM	7	166667	167889	166667	167889	2_nonsis	0	611	1221	1	100	1	1	0	(4:4aCO)
248	TCMM15	TCMM	14	701618	702991	701618	702991	2_nonsis	0	686	1372	1	100	1	1	0	(4:4aCO)
239	TCMM15	TCMM	14	440622	442256	440622	442256	2_nonsis	0	817	1633	1	100	1	1	0	(4:4aCO)
196	TCMM15	TCMM	12	972928	974574	972928	974574	2_nonsis	0	823	1645	1	100	1	1	0	(4:4aCO)
144	TCMM15	TCMM	10	467589	469453	467589	469453	2_nonsis	0	932	1863	1	100	1	1	0	(4:4aCO)
286	TCMM15	TCMM	16	676743	677025	678599	679573	2_nonsis	1575	2202	2829	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
186	TCMM15	TCMM	12	681614	681851	682536	682671	2_nonsis	686	871	1056	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
176	TCMM15	TCMM	12	258730	259126	260749	261053	2_nonsis	1624	1973	2322	2	31	1	1	0	(3:5)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
116	TCMM15	TCMM	8	416109	416265	417114	417265	2_nonsis	850	1003	1155	2	31	1	1	0	(3:5)_(3:5a)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
133	TCMM15	TCMM	10	146059	146367	147143	147927	2_nonsis	777	1322	1867	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
177	TCMM15	TCMM	12	284957	285577	288686	288976	2_nonsis	3110	3564	4018	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
4	TCMM15	TCMM	2	16009	16380	20568	21007	2_nonsis	4189	4593	4997	2	32	1	1	0	(3:5)_(4:4)_(4:4aCO)_(3:5a)_(4:4a)
151	TCMM15	TCMM	10	708177	708302	710013	711083	2_nonsis	1712	2309	2905	2	32	1	1	0	(5:3)_(6:2)_(5:3)_(4:4ai)_(5:3a)_(4:4bCO)
234	TCMM15	TCMM	14	254149	254281	257904	257986	2_nonsis	3624	3730	3836	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(4:4aCO)
17	TCMM15	TCMM	2	489580	490532	493942	494538	2_nonsis	3411	4184	4957	2	32	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
288	TCMM15	TCMM	16	699663	700042	700309	700480	2_nonsis	268	542	816	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
270	TCMM15	TCMM	16	88282	88336	88834	89075	2_nonsis	499	646	792	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
165	TCMM15	TCMM	11	469480	469538	469831	470250	2_nonsis	294	532	769	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(4:4aCO)
261	TCMM15	TCMM	15	572419	572520	573378	573534	2_nonsis	859	987	1114	3	20	1	1	0	(6:2)_(4:4aCO)_(3:5)_(4:4a)
69	TCMM15	TCMM	5	254694	254754	256048	256159	2_nonsis	1295	1380	1464	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
282	TCMM15	TCMM	16	636736	638483	639081	639173	2_nonsis	599	1518	2436	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
184	TCMM15	TCMM	12	647512	647752	649258	649837	2_nonsis	1507	1916	2324	3	20	1	1	0	(6:2)_(2:6)_(3:5)_(4:4aCO)
260	TCMM15	TCMM	15	485588	485898	487028	487809	2_nonsis	1131	1676	2220	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(2:6)_(4:4aCO)
98	TCMM15	TCMM	7	515701	516816	518580	519356	2_nonsis	1765	2710	3654	3	20	1	1	0	(6:2)_(4:4)_(3:5)_(2:6)_(4:4aCO)
236	TCMM15	TCMM	14	333286	334339	335395	335707	2_nonsis	1057	1739	2420	3	20	1	1	0	(2:6)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
33	TCMM15	TCMM	3	277871	278153	281752	283221	2_nonsis	3600	4475	5349	3	20	1	1	0	(3:5)_(3:5a)_(4:4aCO)_(3:5a)_(5:3)_(4:4a)

ID	Sample		n	v1	v2	v3	v4	type	X	a	b	c	d	e	f	g	h	pattern
12	TCMM15	TCMM	2	267510	268100	269653	271598	2_nonsis		1554	2821	4087	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(3:5)_(2:6)_(4:4aCO)
67	TCMM15	TCMM	5	184684	185983	188495	188861	2_nonsis		2513	3345	4176	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(5:3)_(3:5a)_(4:4aCO)
140	TCMM15	TCMM	10	315888	316590	319398	320192	2_nonsis		2809	3556	4303	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(5:3)_(4:4aCO)
268	TCMM15	TCMM	15	1049756	1049902	1051958	1052288	2_nonsis		2057	2294	2531	3	21	1	1	0	(5:3)_(4:4)_(3:5)_(4:4ai)_(5:3a)_(4:4bCO)
252	TCMM15	TCMM	15	68988	69357	71365	72322	2_nonsis		2009	2671	3333	3	21	1	1	0	(5:3)_(4:4)_(4:4ai)_(2:6)_(4:4ai)_(6:2)_(5:3)_(6:2)_(4:4bCO)
71	TCMM15	TCMM	5	335461	336936	343350	344171	2_nonsis		6415	7562	8709	3	21	1	1	0	(5:3)_(4:4ai)_(2:6)_(5:3a)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4bCO)
34	TCMM15	TCMM	4	21075	21083	23155	23241	2_sis		2073	2119	2165	0	1	2	0	2	(3:5)_(4:4)_(3:5a)_(4:4)_(3:5a)_(2:6)_(4:4)_(3:5a)_(2:6)_(3:5a)_(4:4)
146	TCMM15	TCMM	10	526176	526730	526730	527538	2_sis		1	681	1361	0	1	2	0	2	(2:6i)_(4:4)
173	TCMM15	TCMM	12	183955	184185	189603	190285		3	5419	5874	6329	0	1	2	0	2	(2:6i)_(4:4)_(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4)
185	TCMM15	TCMM	12	657926	658599	659350	660046	2_sis		752	1436	2119	0	1	2	0	2	(3:5)_(3:5a)_(4:4)
222	TCMM15	TCMM	13	665811	666112	667496	668902		3	1385	2238	3090	0	1	2	0	2	(5:3)_(4:4ai)_(1:7)_(4:4)
269	TCMM15	TCMM	16	46435	46551	46551	46637	2_sis		1	101	201	0	1	2	0	2	(2:6i)_(4:4)
6	TCMM15	TCMM	2	69355	69616	71161	71276		3	1546	1733	1920	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(4:4aCO)
13	TCMM15	TCMM	2	295912	296774	301951	301964		3	5178	5615	6051	0	2	2	1	1	(3:5)_(4:4ai)_(3:5a)_(4:4bCO)_(5:3)_(4:4b)_(5:3)_(4:4b)_(5:3)_(4:4b)_(5:3a)_(4:4b)
14	TCMM15	TCMM	2	306376	306932	307275	307459		3	344	713	1082	0	2	2	1	1	(2:6)_(1:7)_(4:4)_(4:4aCO)
77	TCMM15	TCMM	5	490952	491135	492341	498773		3	1207	4514	7820	0	2	2	1	1	(3:5)_(3:5a)_(2:6)_(3:5b)_(2:6)_(4:4aCO)
85	TCMM15	TCMM	6	221860	221864	222940	223531		3	1077	1374	1670	0	2	2	1	1	(3:5)_(4:4)_(4:4aCO)
91	TCMM15	TCMM	7	193769	194505	197465	197816		3	2961	3504	4046	0	2	2	1	1	(3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)_(6:2)_(4:4a)
99	TCMM15	TCMM	7	675850	676025	680390	681013		3	4366	4764	5162	0	2	2	1	1	(6:2)_(4:4)_(4:4ai)_(3:5)_(5:3)_(4:4bCO)_(5:3)_(6:2a)_(5:3)_(4:4b)
103	TCMM15	TCMM	7	879687	879882	881223	882479		3	1342	2067	2791	0	2	2	1	1	(3:5)_(4:4)_(3:5a)_(2:6)_(3:5a)_(4:4ai)_(4:4bCO)
120	TCMM15	TCMM	9	51326	51375	55251	56514		4	3877	4532	5187	0	2	2	1	1	(5:3)_(3:5)_(2:6)_(4:4aCO)
125	TCMM15	TCMM	9	281888	281969	285554	285709		3	3586	3703	3820	0	2	2	1	1	(3:5)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5b)_(4:4aCO)
126	TCMM15	TCMM	9	345656	345745	347647	347702		3	1903	1974	2045	0	2	2	1	1	(3:5)_(4:4)_(5:3)_(4:4)_(5:3a)_(4:4aCO)
128	TCMM15	TCMM	10	21670	21859	34093	36217		3	12235	13391	14546	0	2	2	1	1	(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5a)_(2:6a)_(3:5a)_(4:4a)
129	TCMM15	TCMM	10	51007	51976	53592	53842		3	1617	2226	2834	0	2	2	1	1	(3:5)_(4:4ai)_(5:3)_(4:4bCO)
169	TCMM15	TCMM	11	589828	589969	590994	592478		3	1026	1838	2649	0	2	2	1	1	(4:4ai)_(3:5)_(4:4bCO)
175	TCMM15	TCMM	12	224270	225226	229623	230005		3	4398	5066	5734	0	2	2	1	1	(5:3)_(5:3a)_(4:4aCO)_(5:3)_(6:2)_(5:3)_(4:4a)
178	TCMM15	TCMM	12	339496	340008	341688	341926		3	1681	2055	2429	0	2	2	1	1	(5:3)_(5:3a)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
202	TCMM15	TCMM	13	168229	168773	171275	171292		3	2503	2783	3062	0	2	2	1	1	(3:5)_(4:4)_(1:7)_(3:5)_(3:5a)_(4:4aCO)
211	TCMM15	TCMM	13	424897	425033	427114	428830		3	2082	3007	3932	0	2	2	1	1	(3:5)_(4:4aCO)_(4:4bi)_(4:4a)
215	TCMM15	TCMM	13	539007	539282	543392	543706		4	4111	4405	4698	0	2	2	1	1	(2:6i)_(3:5)_(2:6i)_(3:5a)_(3:5b)_(4:4aCO)_(3:5b)_(2:6a)_(3:5b)_(4:4a)
221	TCMM15	TCMM	13	645101	645268	646966	647164		3	1699	1881	2062	0	2	2	1	1	(2:6)_(0:8)_(4:4aCO)
225	TCMM15	TCMM	13	772587	772812	773689	774661		3	878	1476	2073	0	2	2	1	1	(5:3)_(4:4)_(4:4aCO)
232	TCMM15	TCMM	14	102906	103068	104411	104767		3	1344	1602	1860	0	2	2	1	1	(5:3)_(5:3a)_(4:4aCO)
237	TCMM15	TCMM	14	407287	408111	414025	415775		3	5915	7201	8487	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)_(6:2)_(4:4a)_(5:3a)_(4:4a)
255	TCMM15	TCMM	15	198230	198700	200443	201256		3	1744	2385	3025	0	2	2	1	1	(5:3)_(6:2)_(4:4aCO)_(2:6i)_(4:4a)
257	TCMM15	TCMM	15	264557	264752	268456	269276		3	3705	4212	4718	0	2	2	1	1	(5:3)_(4:4ai)_(3:5)_(2:6)_(4:4bCO)_(3:5a)_(4:4b)
275	TCMM15	TCMM	16	207823	208076	214358	214888		3	6283	6674	7064	0	2	2	1	1	(3:5)_(4:4)_(3:5)_(4:4)_(2:6)_(6:2)_(7:1)_(6:2)_(5:3)_(6:2a)_(4:4aCO)
24	TCMM15	TCMM	2	786546	786589	787596	787803	2_nonsis		1008	1132	1256	0	3	2	0	2	(3:5)_(5:3)_(4:4aCO)_(5:3)_(4:4bi)_(4:4CO)
89	TCMM15	TCMM	7	118134	119177	122499	122514		4	3323	3851	4379	0	3	2	1	1	(6:2)_(4:4aCO)_(5:3)_(4:4bCO)_(5:3a)_(5:3)_(6:2)_(4:4b)_(5:3b)_(4:4b)
121	TCMM15	TCMM	9	139714	139937	143092	143414		3	3156	3428	3699	0	3	2	1	1	(5:3)_(6:2)_(4:4aCO)_(6:2a)_(5:3a)_(4:4a)_(2:6)_(3:5)_(4:4b)_(6:2a)_(5:3a)_(6:2a)_(4:4cCO)
135	TCMM15	TCMM	10	234413	234627	237403	237740		3	2777	3052	3326	0	3	2	1	1	(3:5)_(2:6)_(3:5a)_(5:3)_(4:4aCO)_(3:5b)_(4:4a)_(3:5b)_(5:3c)_(4:4CO)
160	TCMM15	TCMM	11	264372	264393	265409	265522	2_nonsis		1017	1083	1149	0	3	2	0	2	(6:2)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4CO)
192	TCMM15	TCMM	12	874541	875066	880574	880934		4	5509	5951	6392	0	3	2	1	1	(5:3)_(4:4ai)_(4:4bi)_(4:4ai)_(2:6)_(3:5)_(2:6)_(4:4cCO)_(5:3a)_(4:4dCO)
214	TCMM15	TCMM	13	508768	509203	510876	511205	2_nonsis		1674	2055	2436	0	3	2	0	2	(3:5)_(4:4aCO)_(6:2)_(4:4CO)
251	TCMM15	TCMM	14	754799	754814	754814	754815	2_nonsis		1	8	15	0	3	2	0	2	(4:4aCO)_(4:4CO)
254	TCMM15	TCMM	15	190009	191548	193911	195064		3	2364	3709	5054	0	3	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4aCO)_(7:1)_(5:3)_(3:5)_(4:4CO)
264	TCMM15	TCMM	15	830857	831592	833083	833356	2_nonsis		1492	1995	2498	0	3	2	0	2	(5:3)_(4:4aCO)_(5:3a)_(4:4CO)
276	TCMM15	TCMM	16	312892	313236	316205	316676	2_nonsis		2970	3377	3783	0	3	2	0	2	(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4bi)_(3:5)_(4:4CO)
369	TCMM15	TCMM	6	15012	15279	18345	18537	NA		3067	3296	3524	0	4	1	NA	NA	4:4_3:5_4:4_3:5
136	TCMM16	TCMM	8	12663	12670	12670	12721		1	1	29	57	1	1	1	0	1	05:03
8	TCMM16	TCMM	2	71825	71828	71828	72018		1	1	97	192	1	1	1	0	1	05:03
89	TCMM16	TCMM	5	378046	378074	378075	378297		1	2	126	250	1	1	1	0	1	05:03
126	TCMM16	TCMM	7	277224	277283	277346	277418		1	64	129	193	1	1	1	0	1	05:03
276	TCMM16	TCMM	15	544813	544924	544976	545061		1	53	150	247	1	1	1	0	1	05:03
299	TCMM16	TCMM	16	431840	432048	432085	432226		1	38	212	385	1	1	1	0	1	05:03
305	TCMM16	TCMM	16	538649	538784	538784	539088		1	1	220	438	1	1	1	0	1	05:03
162	TCMM16	TCMM	10	157921	158024	158168	158223		1	145	223	301	1	1	1	0	1	05:03
177	TCMM16	TCMM	10	705235	705450	705542	705639		1	93	248	403	1	1	1	0	1	05:03
283	TCMM16	TCMM	15	768090	768428	768428	768642		1	1	276	551	1	1	1	0	1	05:03

50	TCMM16	TCMM	4	198376	198685	198778	198878	1	94	298	501	1	1	1	0	1	05:03
60	TCMM16	TCMM	4	784537	784809	784809	785140	1	1	302	602	1	1	1	0	1	05:03
284	TCMM16	TCMM	15	807285	807291	807631	807840	1	341	448	554	1	1	1	0	1	05:03
262	TCMM16	TCMM	14	719201	719586	719874	719985	1	289	536	783	1	1	1	0	1	05:03
194	TCMM16	TCMM	12	17679	17745	18183	18460	1	439	610	780	1	1	1	0	1	05:03
161	TCMM16	TCMM	10	90733	91114	91264	92203	1	151	810	1469	1	1	1	0	1	05:03
285	TCMM16	TCMM	15	819625	820504	820842	820906	1	339	810	1280	1	1	1	0	1	05:03
104	TCMM16	TCMM	6	129074	129176	129391	130480	1	216	811	1405	1	1	1	0	1	05:03
233	TCMM16	TCMM	13	691343	691745	692123	692624	1	379	830	1280	1	1	1	0	1	05:03
98	TCMM16	TCMM	5	559301	559558	560376	560686	1	819	1102	1384	1	1	1	0	1	05:03
51	TCMM16	TCMM	4	221175	222017	222257	223377	1	241	1221	2201	1	1	1	0	1	05:03
96	TCMM16	TCMM	5	521007	521844	522739	522899	1	896	1394	1891	1	1	1	0	1	05:03
255	TCMM16	TCMM	14	437581	439088	439088	440569	1	1	1494	2987	1	1	1	0	1	05:03
271	TCMM16	TCMM	15	216181	216247	216247	216270	1	1	45	88	1	2	1	0	1	03:05
196	TCMM16	TCMM	12	54244	54357	54357	54748	1	1	252	503	1	2	1	0	1	03:05
37	TCMM16	TCMM	3	50664	51152	51152	51209	1	1	273	544	1	2	1	0	1	03:05
143	TCMM16	TCMM	8	450572	450770	450770	451138	1	1	283	565	1	2	1	0	1	03:05
80	TCMM16	TCMM	5	106918	107341	107341	107574	1	1	328	655	1	2	1	0	1	03:05
90	TCMM16	TCMM	5	439545	439909	439909	440398	1	1	427	852	1	2	1	0	1	03:05
234	TCMM16	TCMM	13	696571	697269	697269	697465	1	1	447	893	1	2	1	0	1	03:05
72	TCMM16	TCMM	4	1427252	1427658	1427686	1428259	1	29	518	1006	1	2	1	0	1	03:05
68	TCMM16	TCMM	4	1278056	1278456	1278613	1278992	1	158	547	935	1	2	1	0	1	03:05
281	TCMM16	TCMM	15	732609	733385	733489	733608	1	105	552	998	1	2	1	0	1	03:05
82	TCMM16	TCMM	5	132643	132762	133078	133491	1	317	582	847	1	2	1	0	1	03:05
158	TCMM16	TCMM	10	57356	58202	58202	58607	1	1	626	1250	1	2	1	0	1	03:05
301	TCMM16	TCMM	16	452203	453010	453106	453873	1	97	883	1669	1	2	1	0	1	03:05
142	TCMM16	TCMM	8	428824	429261	429603	430273	1	343	896	1448	1	2	1	0	1	03:05
296	TCMM16	TCMM	16	354279	354478	355469	355495	1	992	1104	1215	1	2	1	0	1	03:05
13	TCMM16	TCMM	2	201456	201932	202580	203030	1	649	1111	1573	1	2	1	0	1	03:05
74	TCMM16	TCMM	5	18839	23192	23192	23309	1	1	2235	4469	1	2	1	0	1	03:05
288	TCMM16	TCMM	15	968047	968186	968504	968918	1	319	595	870	1	3	1	0	1	5:3_6:2_5:3
215	TCMM16	TCMM	13	30303	30379	31154	31858	1	776	1165	1554	1	3	1	0	1	5:3_4:4_5:3
36	TCMM16	TCMM	2	799093	799230	800316	800859	1	1087	1426	1765	1	3	1	0	1	5:3_6:2_5:3
167	TCMM16	TCMM	10	282456	282525	283650	284198	1	1126	1434	1741	1	3	1	0	1	5:3_6:2_5:3
298	TCMM16	TCMM	16	381362	381922	383310	383387	1	1389	1707	2024	1	3	1	0	1	5:3_4:4_5:3
250	TCMM16	TCMM	14	293224	293332	296142	296290	1	2811	2938	3065	1	3	1	0	1	5:3_6:2_4:4_5:3
239	TCMM16	TCMM	13	775628	776036	777554	777598	1	1519	1744	1969	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
79	TCMM16	TCMM	5	100108	100213	100307	101018	1	95	502	909	1	4	1	0	1	3:5_4:4_3:5
267	TCMM16	TCMM	15	82066	82213	83327	83622	1	1115	1335	1555	1	4	1	0	1	3:5_2:6_3:5
130	TCMM16	TCMM	7	482042	482318	484452	484780	1	2135	2436	2737	1	4	1	0	1	3:5_4:4_3:5
44	TCMM16	TCMM	3	259910	260698	263025	264441	1	2328	3429	4530	1	4	1	0	1	3:5_2:6_4:4_3:5
39	TCMM16	TCMM	3	70158	70770	72190	72786	1	1421	2024	2627	1	4	1	0	1	3:5_4:4_2:6_4:4_3:5
309	TCMM16	TCMM	16	825143	825536	827895	828087	1	2360	2652	2943	1	4	1	0	1	3:5_2:6_3:5_2:6_3:5
266	TCMM16	TCMM	15	52771	52863	56223	56332	1	3361	3461	3560	1	4	1	0	1	3:5_2:6_3:5_4:4_3:5
293	TCMM16	TCMM	16	105972	106107	106450	106600	1	344	486	627	1	7	1	0	1	6:2_5:3
32	TCMM16	TCMM	2	718548	718601	718700	719463	1	100	507	914	1	7	1	0	1	6:2_5:3
102	TCMM16	TCMM	6	56854	58110	58653	58715	1	544	1202	1860	1	7	1	0	1	6:2_5:3
66	TCMM16	TCMM	4	1141710	1142883	1143495	1143696	1	613	1299	1985	1	7	1	0	1	6:2_5:3
260	TCMM16	TCMM	14	557698	557959	559202	559575	1	1244	1560	1876	1	7	1	0	1	5:3_6:2
81	TCMM16	TCMM	5	122439	122503	123598	123734	1	1096	1195	1294	1	7	1	0	1	6:2_4:4_6:2
35	TCMM16	TCMM	2	761081	761108	763117	763218	1	2010	2073	2136	1	7	1	0	1	6:2_5:3_6:2
31	TCMM16	TCMM	2	711439	711554	713038	713451	1	1485	1748	2011	1	7	1	0	1	5:3_6:2_5:3_6:2
24	TCMM16	TCMM	2	513202	513337	516896	517356	1	3560	3857	4153	1	7	1	0	1	5:3_6:2_4:4_6:2
189	TCMM16	TCMM	11	523718	524191	524346	524511	1	156	474	792	1	8	1	0	1	2:6_3:5
113	TCMM16	TCMM	6	244444	245103	245286	245484	1	184	612	1039	1	8	1	0	1	3:5_2:6
101	TCMM16	TCMM	6	53398	54858	55242	55864	1	385	1425	2465	1	8	1	0	1	3:5_2:6
112	TCMM16	TCMM	6	229838	229991	231344	231638	1	1354	1577	1799	1	8	1	0	1	3:5_2:6
214	TCMM16	TCMM	12	1051488	1053478	1054333	1054794	1	856	2081	3305	1	8	1	0	1	3:5_2:6
178	TCMM16	TCMM	11	74916	75663	76124	76914	1	462	1230	1997	1	8	1	0	1	2:6_4:4_2:6
30	TCMM16	TCMM	2	699878	700005	701871	702521	1	1867	2255	2642	1	8	1	0	1	2:6_4:4_2:6

95	TCMM16	TCMM	5	498820	498872	500606	501719	1	1735	2317	2898	1	8	1	0	1 3:5_4:4_3:5_2:6
264	TCMM16	TCMM	14	741976	742112	744080	744202	1	1969	2097	2225	1	8	1	0	1 3:5_4:4_2:6_3:5_2:6
231	TCMM16	TCMM	13	650997	651148	654624	654748	1	3477	3614	3750	1	8	1	0	1 3:5_4:4_3:5_4:4_3:5_2:6
290	TCMM16	TCMM	16	55962	56116	56116	56137	1	1	88	174	1	10	1	0	1 06:02
151	TCMM16	TCMM	9	93376	93546	93555	93577	1	10	105	200	1	10	1	0	1 06:02
275	TCMM16	TCMM	15	533847	533983	533983	534085	1	1	119	237	1	10	1	0	1 06:02
119	TCMM16	TCMM	7	80976	81268	81306	81381	1	39	222	404	1	10	1	0	1 06:02
292	TCMM16	TCMM	16	103016	103137	103137	103486	1	1	235	469	1	10	1	0	1 06:02
107	TCMM16	TCMM	6	190849	191180	191180	191409	1	1	280	559	1	10	1	0	1 06:02
252	TCMM16	TCMM	14	365449	365642	365824	365847	1	183	290	397	1	10	1	0	1 06:02
245	TCMM16	TCMM	14	40397	40430	40430	41146	1	1	375	748	1	10	1	0	1 06:02
295	TCMM16	TCMM	16	228043	228253	228253	228815	1	1	386	771	1	10	1	0	1 06:02
59	TCMM16	TCMM	4	721724	721991	722085	722407	1	95	389	682	1	10	1	0	1 06:02
127	TCMM16	TCMM	7	333791	334340	334340	334584	1	1	397	792	1	10	1	0	1 06:02
206	TCMM16	TCMM	12	568653	568917	568917	569539	1	1	443	885	1	10	1	0	1 06:02
236	TCMM16	TCMM	13	746108	746305	746448	746979	1	144	507	870	1	10	1	0	1 06:02
23	TCMM16	TCMM	2	492334	493122	493123	493536	1	2	602	1201	1	10	1	0	1 06:02
170	TCMM16	TCMM	10	500414	500582	500582	501650	1	1	618	1235	1	10	1	0	1 06:02
164	TCMM16	TCMM	10	192156	192956	193023	193406	1	68	659	1249	1	10	1	0	1 06:02
277	TCMM16	TCMM	15	552117	553236	553236	553518	1	1	701	1400	1	10	1	0	1 06:02
116	TCMM16	TCMM	7	22405	23215	23509	23516	1	295	703	1110	1	10	1	0	1 06:02
258	TCMM16	TCMM	14	530856	531399	531656	532165	1	258	783	1308	1	10	1	0	1 06:02
149	TCMM16	TCMM	9	60879	61323	61787	62057	1	465	821	1177	1	10	1	0	1 06:02
106	TCMM16	TCMM	6	172677	173376	173765	174112	1	390	912	1434	1	10	1	0	1 06:02
241	TCMM16	TCMM	13	814511	814574	815081	815882	1	508	939	1370	1	10	1	0	1 06:02
304	TCMM16	TCMM	16	502118	503157	503314	503873	1	158	956	1754	1	10	1	0	1 06:02
183	TCMM16	TCMM	11	273206	273474	273882	274746	1	409	974	1539	1	10	1	0	1 06:02
213	TCMM16	TCMM	12	1031842	1032807	1033274	1033418	1	468	1022	1575	1	10	1	0	1 06:02
147	TCMM16	TCMM	9	37222	39244	39244	39277	1	1	1028	2054	1	10	1	0	1 06:02
118	TCMM16	TCMM	7	55263	55957	55957	57501	1	1	1119	2237	1	10	1	0	1 06:02
302	TCMM16	TCMM	16	469730	470217	470860	471369	1	644	1141	1638	1	10	1	0	1 06:02
186	TCMM16	TCMM	11	458003	458672	459513	459567	1	842	1203	1563	1	10	1	0	1 06:02
42	TCMM16	TCMM	3	225710	226498	226498	228130	1	1	1210	2419	1	10	1	0	1 06:02
210	TCMM16	TCMM	12	710635	710704	712040	712581	1	1337	1641	1945	1	10	1	0	1 06:02
85	TCMM16	TCMM	5	317416	317740	319090	319404	1	1351	1669	1987	1	10	1	0	1 06:02
235	TCMM16	TCMM	13	713980	715257	716494	716783	1	1238	2020	2802	1	10	1	0	1 06:02
172	TCMM16	TCMM	10	518880	519660	521093	521645	1	1434	2099	2764	1	10	1	0	1 06:02
310	TCMM16	TCMM	16	888652	888868	890698	891130	1	1831	2154	2477	1	10	1	0	1 06:02
91	TCMM16	TCMM	5	443341	443369	443369	443371	1	1	15	29	1	10.1	1	0	1 02:06
55	TCMM16	TCMM	4	524228	524258	524258	524264	1	1	18	35	1	10.1	1	0	1 02:06
191	TCMM16	TCMM	11	571283	571301	571301	571323	1	1	20	39	1	10.1	1	0	1 02:06
46	TCMM16	TCMM	4	20376	20400	20400	20444	1	1	34	67	1	10.1	1	0	1 02:06
226	TCMM16	TCMM	13	388681	388700	388700	388751	1	1	35	69	1	10.1	1	0	1 02:06
87	TCMM16	TCMM	5	355008	355019	355038	355237	1	20	124	228	1	10.1	1	0	1 02:06
132	TCMM16	TCMM	7	605710	605793	605833	605941	1	41	136	230	1	10.1	1	0	1 02:06
17	TCMM16	TCMM	2	321553	321773	321773	321857	1	1	152	303	1	10.1	1	0	1 02:06
229	TCMM16	TCMM	13	605965	606066	606066	606299	1	1	167	333	1	10.1	1	0	1 02:06
273	TCMM16	TCMM	15	446616	446899	446899	447004	1	1	194	387	1	10.1	1	0	1 02:06
254	TCMM16	TCMM	14	417156	417610	417610	417659	1	1	252	502	1	10.1	1	0	1 02:06
62	TCMM16	TCMM	4	814278	814490	814490	814815	1	1	269	536	1	10.1	1	0	1 02:06
20	TCMM16	TCMM	2	392022	392314	392522	392544	1	209	365	521	1	10.1	1	0	1 02:06
171	TCMM16	TCMM	10	503352	503880	503880	504158	1	1	403	805	1	10.1	1	0	1 02:06
166	TCMM16	TCMM	10	278226	278337	278337	279038	1	1	406	811	1	10.1	1	0	1 02:06
199	TCMM16	TCMM	12	197459	197675	197801	198146	1	127	407	686	1	10.1	1	0	1 02:06
238	TCMM16	TCMM	13	759082	759285	759582	759679	1	298	447	596	1	10.1	1	0	1 02:06
123	TCMM16	TCMM	7	120395	120656	120977	121054	1	322	490	658	1	10.1	1	0	1 02:06
146	TCMM16	TCMM	8	516616	516651	517036	517336	1	386	553	719	1	10.1	1	0	1 02:06
187	TCMM16	TCMM	11	461467	462364	462364	462779	1	1	656	1311	1	10.1	1	0	1 02:06
144	TCMM16	TCMM	8	470287	470706	470864	471466	1	159	669	1178	1	10.1	1	0	1 02:06
120	TCMM16	TCMM	7	82858	84285	84285	84308	1	1	725	1449	1	10.1	1	0	1 02:06

45	TCMM16	TCMM	3	281752	283214	283214	283221	1	1	735	1468	1	10.1	1	0	1	02:06
135	TCMM16	TCMM	7	1048437	1049349	1049349	1050057	1	1	810	1619	1	10.1	1	0	1	02:06
93	TCMM16	TCMM	5	473893	473950	474722	474860	1	773	870	966	1	10.1	1	0	1	02:06
219	TCMM16	TCMM	13	164532	165032	165218	166349	1	187	1002	1816	1	10.1	1	0	1	02:06
224	TCMM16	TCMM	13	251736	251941	252532	253248	1	592	1052	1511	1	10.1	1	0	1	02:06
103	TCMM16	TCMM	6	80386	81527	82058	82187	1	532	1166	1800	1	10.1	1	0	1	02:06
97	TCMM16	TCMM	5	540205	540256	541194	541873	1	939	1303	1667	1	10.1	1	0	1	02:06
220	TCMM16	TCMM	13	190411	190535	191569	192110	1	1035	1367	1698	1	10.1	1	0	1	02:06
76	TCMM16	TCMM	5	31867	32276	33706	33782	1	1431	1673	1914	1	10.1	1	0	1	02:06
221	TCMM16	TCMM	13	194107	194499	195968	196000	1	1470	1681	1892	1	10.1	1	0	1	02:06
88	TCMM16	TCMM	5	356837	357566	358357	360247	1	792	2101	3409	1	10.1	1	0	1	02:06
261	TCMM16	TCMM	14	686681	688572	690428	691115	1	1857	3145	4433	1	10.1	1	0	1	02:06
265	TCMM16	TCMM	15	46903	47322	47652	47740	2_nonsis	331	584	836	3	30	1	0	1	05:03
202	TCMM16	TCMM	12	387927	388010	388801	388930	2_nonsis	792	897	1002	3	30	1	0	1	5:3_2:6
115	TCMM16	TCMM	7	10242	11635	11737	12020	2_nonsis	103	940	1777	3	30	1	0	1	3:5_5:3
21	TCMM16	TCMM	2	426669	426888	430067	431229	2_nonsis	3180	3870	4559	3	30	1	0	1	2:6_3:5
18	TCMM16	TCMM	2	323214	323896	324761	325371	2_nonsis	866	1511	2156	3	30	1	0	1	5:3_6:2_5:3_6:2
148	TCMM16	TCMM	9	54480	55071	56514	57063	2_nonsis	1444	2013	2582	3	30	1	0	1	3:5_4:4_3:5_6:2
287	TCMM16	TCMM	15	930026	930118	931901	932032	2_nonsis	1784	1895	2005	3	30	1	0	1	5:3_4:4_6:2_4:4_2:6
243	TCMM16	TCMM	13	856401	856957	863229	863412	2_nonsis	6273	6642	7010	3	30	1	0	1	5:3_4:4_5:3_4:4_6:2_2:6
1	TCMM16	TCMM	1	41278	41481	45831	46030	2_nonsis	4351	4551	4751	3	30	1	0	1	5:3_4:4_3:5_2:6_3:5_2:6_3:5
176	TCMM16	TCMM	10	664516	664569	664824	665027	2_nonsis	256	383	510	3	31	1	0	1	4:4ai_3:5
175	TCMM16	TCMM	10	660786	661017	662479	663134	2_nonsis	1463	1905	2347	3	31	1	0	1	3:5_4:4ai_3:5a_2:6_3:5a_2:6
4	TCMM16	TCMM	1	82379	83613	83613	84046	2_nonsis	1	834	1666	1	1	1	1	0	(5:3)_(4:4aCO)
163	TCMM16	TCMM	10	160511	161023	161251	162223	2_nonsis	229	970	1711	1	1	1	1	0	(5:3)_(4:4aCO)
65	TCMM16	TCMM	4	1139381	1139520	1140165	1141284	2_nonsis	646	1274	1902	1	1	1	1	0	(5:3)_(4:4aCO)
168	TCMM16	TCMM	10	323004	323077	323823	324913	2_nonsis	747	1328	1908	1	1	1	1	0	(5:3)_(4:4aCO)
28	TCMM16	TCMM	2	624805	626092	626092	626455	2_nonsis	1	825	1649	1	2	1	1	0	(3:5)_(4:4aCO)
83	TCMM16	TCMM	5	212029	212818	213929	214752	2_nonsis	1112	1917	2722	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
16	TCMM16	TCMM	2	291653	292193	293099	293297	2_nonsis	907	1275	1643	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
188	TCMM16	TCMM	11	520682	521362	522153	522458	2_nonsis	792	1284	1775	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
150	TCMM16	TCMM	9	75941	76162	77594	78985	2_nonsis	1433	2238	3043	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
278	TCMM16	TCMM	15	582005	582071	582149	582404	2_nonsis	79	239	398	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
225	TCMM16	TCMM	13	339889	340680	341020	341111	2_nonsis	341	781	1221	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
257	TCMM16	TCMM	14	517494	517634	518686	518907	2_nonsis	1053	1233	1412	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
218	TCMM16	TCMM	13	120376	120604	120947	120995	2_nonsis	344	481	618	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
181	TCMM16	TCMM	11	230455	230765	231038	231246	2_nonsis	274	532	790	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
63	TCMM16	TCMM	4	930421	930813	931180	931376	2_nonsis	368	661	954	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
185	TCMM16	TCMM	11	351348	351443	351989	352346	2_nonsis	547	772	997	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
140	TCMM16	TCMM	8	373732	373987	374794	375059	2_nonsis	808	1067	1326	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
69	TCMM16	TCMM	4	1298219	1298337	1299214	1299598	2_nonsis	878	1128	1378	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
41	TCMM16	TCMM	3	191932	192715	193107	193828	2_nonsis	393	1144	1895	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
77	TCMM16	TCMM	5	44999	45019	46098	46310	2_nonsis	1080	1195	1310	1	12	1	1	0	(5:3)_(4:4aCO)_(6:2)_(4:4a)
223	TCMM16	TCMM	13	224339	224490	225618	225831	2_nonsis	1129	1310	1491	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
232	TCMM16	TCMM	13	667065	667456	668408	668902	2_nonsis	953	1395	1836	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
242	TCMM16	TCMM	13	848560	848643	849562	850650	2_nonsis	920	1505	2089	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)
19	TCMM16	TCMM	2	330203	330450	331827	332522	2_nonsis	1378	1848	2318	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
246	TCMM16	TCMM	14	59823	59998	61469	62457	2_nonsis	1472	2053	2633	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
268	TCMM16	TCMM	15	134063	135587	136572	137220	2_nonsis	986	2071	3156	1	12	1	1	0	(2:6)_(3:5)_(4:4)_(4:4aCO)
133	TCMM16	TCMM	7	787089	787750	789553	789609	2_nonsis	1804	2162	2519	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
54	TCMM16	TCMM	4	315175	316669	318317	318659	2_nonsis	1649	2566	3483	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(4:4aCO)
200	TCMM16	TCMM	12	257195	257291	258349	258577	2_nonsis	1059	1220	1381	1	12	1	1	0	(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
117	TCMM16	TCMM	7	44898	45371	46634	46860	2_nonsis	1264	1613	1961	1	12	1	1	0	(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
173	TCMM16	TCMM	10	581428	581638	583178	583223	2_nonsis	1541	1668	1794	1	12	1	1	0	(4:4aCO)_(4:4a)_(6:2)_(4:4a)
11	TCMM16	TCMM	2	171495	171570	173028	173659	2_nonsis	1459	1811	2163	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
48	TCMM16	TCMM	4	121990	122142	124765	125066	2_nonsis	2624	2850	3075	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(5:3)_(4:4aCO)
38	TCMM16	TCMM	3	57568	58033	60633	60687	2_nonsis	2601	2860	3118	1	12	1	1	0	(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
10	TCMM16	TCMM	2	79359	79464	82087	82573	2_nonsis	2624	2919	3213	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
99	TCMM16	TCMM	6	37078	37375	40232	40564	2_nonsis	2858	3172	3485	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(5:3)_(4:4aCO)
57	TCMM16	TCMM	4	652241	652907	654780	654813	2_nonsis	1874	2223	2571	1	12	1	1	0	(3:5)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)

47	TCMM16	TCMM	4	32904	33027	35807	37096	2_nonsis	2781	3486	4191	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
156	TCMM16	TCMM	9	420530	420788	426627	426906	2_nonsis	5840	6108	6375	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
2	TCMM16	TCMM	1	50840	51095	57455	59349	2_nonsis	6361	7435	8508	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4)_(3:5)_(4:4)_(3:5)_(4:4)_(3:5)_(4:4)_(4:4aCO)
34	TCMM16	TCMM	2	742150	742220	742220	742472	2_nonsis	1	161	321	1	15	1	1	0	(6:2)_(4:4aCO)
282	TCMM16	TCMM	15	738026	738211	738211	738617	2_nonsis	1	296	590	1	15	1	1	0	(6:2)_(4:4aCO)
270	TCMM16	TCMM	15	195644	195722	195722	196238	2_nonsis	1	297	593	1	15	1	1	0	(6:2)_(4:4aCO)
217	TCMM16	TCMM	13	51141	51256	51433	51596	2_nonsis	178	316	454	1	15	1	1	0	(6:2)_(4:4aCO)
111	TCMM16	TCMM	6	225457	226036	226036	226238	2_nonsis	1	391	780	1	15	1	1	0	(6:2)_(4:4aCO)
129	TCMM16	TCMM	7	449895	450034	450372	450623	2_nonsis	339	533	727	1	15	1	1	0	(6:2)_(4:4aCO)
128	TCMM16	TCMM	7	398572	398825	399032	399494	2_nonsis	208	565	921	1	15	1	1	0	(6:2)_(4:4aCO)
15	TCMM16	TCMM	2	270387	271598	271598	271912	2_nonsis	1	763	1524	1	15	1	1	0	(6:2)_(4:4aCO)
155	TCMM16	TCMM	9	338670	339115	339305	340356	2_nonsis	191	938	1685	1	15	1	1	0	(6:2)_(4:4aCO)
137	TCMM16	TCMM	8	67460	67629	68532	68854	2_nonsis	904	1149	1393	1	15	1	1	0	(6:2)_(4:4aCO)
307	TCMM16	TCMM	16	656677	656784	657714	658289	2_nonsis	931	1271	1611	1	15	1	1	0	(6:2)_(4:4aCO)
160	TCMM16	TCMM	10	79840	79972	81028	81358	2_nonsis	1057	1287	1517	1	15	1	1	0	(6:2)_(4:4aCO)
58	TCMM16	TCMM	4	679489	679624	680813	681125	2_nonsis	1190	1413	1635	1	15	1	1	0	(6:2)_(4:4aCO)
279	TCMM16	TCMM	15	624475	624868	625595	626602	2_nonsis	728	1427	2126	1	15	1	1	0	(6:2)_(4:4aCO)
272	TCMM16	TCMM	15	340588	341353	341821	343279	2_nonsis	469	1580	2690	1	15	1	1	0	(6:2)_(4:4aCO)
259	TCMM16	TCMM	14	539950	542443	542443	543829	2_nonsis	1	1940	3878	1	15	1	1	0	(6:2)_(4:4aCO)
297	TCMM16	TCMM	16	373351	373419	375235	376113	2_nonsis	1817	2289	2761	1	15	1	1	0	(6:2)_(4:4aCO)
248	TCMM16	TCMM	14	116678	116796	116796	116881	2_nonsis	1	102	202	1	16	1	1	0	(2:6)_(4:4aCO)
208	TCMM16	TCMM	12	602479	602685	602685	602909	2_nonsis	1	215	429	1	16	1	1	0	(2:6)_(4:4aCO)
26	TCMM16	TCMM	2	585814	585909	585909	586331	2_nonsis	1	259	516	1	16	1	1	0	(2:6)_(4:4aCO)
192	TCMM16	TCMM	11	594186	594303	594303	594718	2_nonsis	1	266	531	1	16	1	1	0	(2:6)_(4:4aCO)
110	TCMM16	TCMM	6	212520	212940	212940	213216	2_nonsis	1	348	695	1	16	1	1	0	(2:6)_(4:4aCO)
274	TCMM16	TCMM	15	461434	461644	461696	462083	2_nonsis	53	351	648	1	16	1	1	0	(2:6)_(4:4aCO)
230	TCMM16	TCMM	13	645786	645859	646181	646241	2_nonsis	323	389	454	1	16	1	1	0	(2:6)_(4:4aCO)
159	TCMM16	TCMM	10	60064	60979	61260	61449	2_nonsis	282	833	1384	1	16	1	1	0	(2:6)_(4:4aCO)
195	TCMM16	TCMM	12	51800	51952	52504	53039	2_nonsis	553	896	1238	1	16	1	1	0	(2:6)_(4:4aCO)
198	TCMM16	TCMM	12	194811	195201	195645	196197	2_nonsis	445	915	1385	1	16	1	1	0	(2:6)_(4:4aCO)
247	TCMM16	TCMM	14	65652	66215	67101	67383	2_nonsis	887	1309	1730	1	16	1	1	0	(2:6)_(4:4aCO)
157	TCMM16	TCMM	10	34093	36217	36357	36722	2_nonsis	141	1385	2628	1	16	1	1	0	(2:6)_(4:4aCO)
291	TCMM16	TCMM	16	73338	73929	74937	75355	2_nonsis	1009	1513	2016	1	16	1	1	0	(2:6)_(4:4aCO)
92	TCMM16	TCMM	5	460225	460411	461594	462226	2_nonsis	1184	1592	2000	1	16	1	1	0	(2:6)_(4:4aCO)
121	TCMM16	TCMM	7	91862	92820	93397	94650	2_nonsis	578	1683	2787	1	16	1	1	0	(2:6)_(4:4aCO)
184	TCMM16	TCMM	11	291136	292055	293072	293792	2_nonsis	1018	1837	2655	1	16	1	1	0	(2:6)_(4:4aCO)
237	TCMM16	TCMM	13	748748	750177	751553	751891	2_nonsis	1377	2260	3142	1	16	1	1	0	(2:6)_(4:4aCO)
53	TCMM16	TCMM	4	310900	310948	313308	313436	2_nonsis	2361	2448	2535	1	16	1	1	0	(2:6)_(4:4aCO)
201	TCMM16	TCMM	12	293464	293839	296236	296997	2_nonsis	2398	2965	3532	1	16	1	1	0	(2:6)_(4:4aCO)
222	TCMM16	TCMM	13	203948	204520	221642	223597	2_nonsis	17123	18386	19648	1	16	1	1	0	(2:6)_(4:4aCO)
61	TCMM16	TCMM	4	806292	806407	806292	806407	2_nonsis	0	57	114	1	100	1	1	0	(4:4aCO)
109	TCMM16	TCMM	6	210967	211149	210967	211149	2_nonsis	0	91	181	1	100	1	1	0	(4:4aCO)
67	TCMM16	TCMM	4	1253334	1253523	1253334	1253523	2_nonsis	0	94	188	1	100	1	1	0	(4:4aCO)
300	TCMM16	TCMM	16	450160	450384	450160	450384	2_nonsis	0	112	223	1	100	1	1	0	(4:4aCO)
71	TCMM16	TCMM	4	1420281	1420528	1420281	1420528	2_nonsis	0	123	246	1	100	1	1	0	(4:4aCO)
308	TCMM16	TCMM	16	718964	719293	718964	719293	2_nonsis	0	164	328	1	100	1	1	0	(4:4aCO)
139	TCMM16	TCMM	8	219461	219876	219461	219876	2_nonsis	0	207	414	1	100	1	1	0	(4:4aCO)
205	TCMM16	TCMM	12	532084	532555	532084	532555	2_nonsis	0	235	470	1	100	1	1	0	(4:4aCO)
25	TCMM16	TCMM	2	537549	538047	537549	538047	2_nonsis	0	249	497	1	100	1	1	0	(4:4aCO)
122	TCMM16	TCMM	7	117612	118134	117612	118134	2_nonsis	0	261	521	1	100	1	1	0	(4:4aCO)
174	TCMM16	TCMM	10	636506	637056	636506	637056	2_nonsis	0	275	549	1	100	1	1	0	(4:4aCO)
256	TCMM16	TCMM	14	483894	484452	483894	484452	2_nonsis	0	279	557	1	100	1	1	0	(4:4aCO)
70	TCMM16	TCMM	4	1394881	1395699	1394881	1395699	2_nonsis	0	409	817	1	100	1	1	0	(4:4aCO)
134	TCMM16	TCMM	7	914816	915691	914816	915691	2_nonsis	0	437	874	1	100	1	1	0	(4:4aCO)
204	TCMM16	TCMM	12	512877	513766	512877	513766	2_nonsis	0	444	888	1	100	1	1	0	(4:4aCO)
64	TCMM16	TCMM	4	994719	995637	994719	995637	2_nonsis	0	459	917	1	100	1	1	0	(4:4aCO)
253	TCMM16	TCMM	14	394349	395338	394349	395338	2_nonsis	0	494	988	1	100	1	1	0	(4:4aCO)
78	TCMM16	TCMM	5	85578	86696	85578	86696	2_nonsis	0	559	1117	1	100	1	1	0	(4:4aCO)
153	TCMM16	TCMM	9	184053	185865	184053	185865	2_nonsis	0	906	1811	1	100	1	1	0	(4:4aCO)
138	TCMM16	TCMM	8	140123	142800	140123	142800	2_nonsis	0	1338	2676	1	100	1	1	0	(4:4aCO)

ID			n					type										descriptor
29	TCMM16	TCMM	2	662444	666712	662444	666712	2_nonsis		0	2134	4267	1	100	1	1	0	(4:4aCO)
86	TCMM16	TCMM	5	335065	335254	336702	336936	2_nonsis		1449	1660	1870	2	30	1	1	0	(5:3)_(6:2)_(5:3)_(5:3a)_(4:4aCO)
303	TCMM16	TCMM	16	492354	493222	495673	496633	2_nonsis		2452	3365	4278	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
49	TCMM16	TCMM	4	157958	158137	158816	158898	2_nonsis		680	810	939	3	20	1	1	0	(5:3)_(4:4aCO)_(2:6)_(4:4a)
105	TCMM16	TCMM	6	160108	160471	161501	161527	2_nonsis		1031	1225	1418	3	20	1	1	0	(6:2)_(4:4aCO)_(3:5)_(4:4a)
145	TCMM16	TCMM	8	482359	482489	484090	485522	2_nonsis		1602	2382	3162	3	20	1	1	0	(2:6)_(4:4aCO)_(5:3)_(4:4a)
169	TCMM16	TCMM	10	364569	364721	367642	368244	2_nonsis		2922	3298	3674	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
294	TCMM16	TCMM	16	149586	150295	151045	151173	2_nonsis		751	1169	1586	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(2:6)_(4:4aCO)
209	TCMM16	TCMM	12	618891	619230	619971	620772	2_nonsis		742	1311	1880	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(6:2)_(4:4aCO)
108	TCMM16	TCMM	6	194182	194304	197027	197428	2_nonsis		2724	2985	3245	3	20	1	1	0	(6:2)_(5:3)_(3:5)_(4:4)_(4:4aCO)
211	TCMM16	TCMM	12	747817	747822	749136	749273	2_nonsis		1315	1385	1455	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(4:4)_(2:6)_(4:4aCO)
7	TCMM16	TCMM	1	187427	189816	192196	192723	2_nonsis		2381	3838	5295	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(4:4)_(2:6)_(4:4aCO)
207	TCMM16	TCMM	12	572946	573483	574950	575257	2_nonsis		1468	1889	2310	3	20	1	1	0	(2:6)_(3:5)_(4:4)_(2:6)_(4:4)_(6:2)_(4:4aCO)
56	TCMM16	TCMM	4	551775	551991	553867	554904	2_nonsis		1877	2503	3128	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
251	TCMM16	TCMM	14	317977	318057	319911	321214	2_nonsis		1855	2546	3236	3	20	1	1	0	(5:3)_(6:2)_(4:4)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
289	TCMM16	TCMM	15	1018270	1018471	1020208	1020336	2_nonsis		1738	1902	2065	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(5:3)_(5:3)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
131	TCMM16	TCMM	7	584249	584298	586267	586992	2_nonsis		1970	2356	2742	3	20	1	1	0	(2:6)_(4:4)_(3:5)_(4:4)_(2:6)_(4:4)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
14	TCMM16	TCMM	2	256942	257565	259235	259417	2_sis		1671	2073	2474	0	1	2	0	2	(3:5)_(4:4)_(2:6)_(4:4)
22	TCMM16	TCMM	2	448827	449152	449416	449588	2_sis		265	513	760	0	1	2	0	2	(1:7)_(3:5)_(4:4)
52	TCMM16	TCMM	4	269895	270285	273764	273899		3	3480	3742	4003	0	1	2	0	2	(6:2)_(4:4)_(3:5)_(3:5a)_(2:6)_(4:4)
100	TCMM16	TCMM	6	41791	42233	44192	44668	2_sis		1960	2418	2876	0	1	2	0	2	(5:3)_(4:4)_(5:3)_(4:4)_(6:2)_(4:4)
114	TCMM16	TCMM	6	262930	263216	264395	264419		3	1180	1334	1488	0	1	2	0	2	(6:2)_(4:4)_(3:5)_(4:4ai)_(5:3)_(3:5)_(2:6)_(4:4)
203	TCMM16	TCMM	12	507075	507492	507492	508294	2_sis		1	610	1218	0	1	2	0	2	(2:6i)_(4:4)
311	TCMM16	TCMM	16	921161	921247	923175	923621	2_sis		1929	2194	2459	0	1	2	0	2	(6:2a)_(4:4)_(6:2a)_(4:4)
3	TCMM16	TCMM	1	66696	67476	71535	71601		3	4060	4482	4904	0	2	2	1	1	(3:5)_(2:6)_(0:8)_(2:6)_(4:4)_(2:6)_(3:5a)_(2:6)_(4:4aCO)
5	TCMM16	TCMM	1	91044	91629	92891	94472		3	1263	2345	3427	0	2	2	1	1	(2:6)_(2:6ai)_(4:4aCO)
33	TCMM16	TCMM	2	734046	734409	740026	740164		3	5618	5868	6117	0	2	2	1	1	(5:3)_(6:2)_(5:3a)_(4:4)_(6:2a)_(6:2bi)_(5:3a)_(6:2)_(4:4aCO)
40	TCMM16	TCMM	3	91287	93230	93230	93455		3	1	1084	2167	0	2	2	1	1	(5:3)_(4:4aCO)
84	TCMM16	TCMM	5	228943	229119	230421	230583		3	1303	1471	1639	0	2	2	1	1	(2:6)_(0:8)_(2:6)_(4:4aCO)
94	TCMM16	TCMM	5	489026	489879	492329	498796		3	2451	6110	9769	0	2	2	1	1	(2:6)_(4:4)_(0:8)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
165	TCMM16	TCMM	10	235019	235177	238463	238738		3	3287	3503	3718	0	2	2	1	1	(2:6)_(4:4)_(6:2)_(4:4aCO)_(5:3)_(4:4a)
182	TCMM16	TCMM	11	247931	247951	249447	249660		3	1497	1613	1728	0	2	2	1	1	(5:3)_(6:2)_(7:1)_(6:2a)_(7:1)_(6:2a)_(5:3a)_(4:4aCO)
190	TCMM16	TCMM	11	526688	527413	528213	528273		3	801	1193	1584	0	2	2	1	1	(6:2)_(2:6)_(2:6a)_(4:4aCO)
193	TCMM16	TCMM	11	628847	629063	633026	633545		3	3964	4331	4697	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)
197	TCMM16	TCMM	12	114144	114659	116274	116312		3	1616	1892	2167	0	2	2	1	1	(6:2)_(2:6)_(4:4aCO)
212	TCMM16	TCMM	12	1008786	1008873	1011621	1014017		3	2749	3990	5230	0	2	2	1	1	(2:6)_(5:3)_(4:4aCO)
216	TCMM16	TCMM	13	41174	43336	43336	44157		3	1	1492	2982	0	2	2	1	1	(5:3)_(4:4aCO)
228	TCMM16	TCMM	13	588927	589273	593072	594254		3	3800	4563	5326	0	2	2	1	1	(2:6)_(3:5)_(4:4aCO)_(2:6a)_(3:5a)_(3:5)_(4:4a)
249	TCMM16	TCMM	14	252203	254039	261617	261794		4	7579	8585	9590	0	2	2	1	1	(2:6)_(4:4)_(3:5)_(4:4)_(3:5)_(4:4)_(3:5a)_(2:6a)_(6:2)_(4:4aCO)
263	TCMM16	TCMM	14	734887	734975	737804	737846		3	2830	2894	2958	0	2	2	1	1	(6:2)_(7:1)_(6:2)_(4:4aCO)
269	TCMM16	TCMM	15	186289	186571	187911	188321		3	1341	1686	2031	0	2	2	1	1	(1:7)_(2:6)_(1:7)_(3:5)_(4:4aCO)
286	TCMM16	TCMM	15	866689	866753	868909	869133		3	2157	2300	2443	0	2	2	1	1	(2:6)_(4:4)_(5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
6	TCMM16	TCMM	1	121235	128637	130975	132066		4	2339	6585	10830	0	3	2	2	0	(6:2)_(5:3)_(4:4)_(4:4aCO)_(4:4bCO)
9	TCMM16	TCMM	2	74920	75084	76470	76676	2_nonsis		1387	1571	1755	0	3	2	0	2	(4:4aCO)_(5:3)_(4:4CO)_(3:5)_(4:4)
12	TCMM16	TCMM	2	176636	177287	182892	182901	2_nonsis		5606	5935	6264	0	3	2	0	2	(4:4ai)_(3:5)_(4:4ai)_(5:3)_(4:4bCO)_(4:4b)_(5:3)_(5:3a)_(4:4CO)
27	TCMM16	TCMM	2	617107	617606	620548	621285	2_nonsis		2943	3560	4177	0	3	2	0	2	(4:4aCO)_(5:3)_(4:4CO)_(3:5)_(2:6)_(4:4aCO)
43	TCMM16	TCMM	3	248549	248853	254715	254941		3	5863	6127	6391	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(5:3)_(6:2)_(4:4CO)_(4:4aCO)_(5:3)_(6:2)_(4:4bCO)_(3:5)_(4:4b)
73	TCMM16	TCMM	4	1492673	1492990	1494247	1495338	2_nonsis		1258	1961	2664	0	3	2	0	2	(4:4aCO)_(5:3)_(6:2)_(4:4CO)
75	TCMM16	TCMM	5	26313	26322	28694	29872	2_nonsis		2373	2966	3558	0	3	2	0	2	(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4CO)
124	TCMM16	TCMM	7	140941	141046	143073	143359		4	2028	2223	2417	0	3	2	2	0	(6:2)_(4:4aCO)_(6:2a)_(4:4bCO)
125	TCMM16	TCMM	7	264928	265218	272144	272568		4	6927	7283	7639	0	3	2	2	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4bCO)
141	TCMM16	TCMM	8	422684	422786	423045	423870		3	260	723	1185	0	3	2	1	1	(4:4aCO)_(2:6)_(4:4bCO)
152	TCMM16	TCMM	9	174391	174961	181677	182837	2_nonsis		6717	7581	8445	0	3	2	0	2	(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4CO)
154	TCMM16	TCMM	9	268278	268466	269580	269763		3	1115	1300	1484	0	3	2	1	1	(4:4aCO)_(2:6)_(4:4a)_(4:4CO)
179	TCMM16	TCMM	11	79100	79688	81532	82469		3	1845	2607	3368	0	3	2	0		(2:6)_(3:5)_(4:4aCO)_(5:3)_(4:4CO)
180	TCMM16	TCMM	11	84611	85003	94473	94945		3	9471	9902	10333	0	3	2	1	1	(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4)_(3:5)_(2:6)_(4:4)_(2:6)_(3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
227	TCMM16	TCMM	13	496739	496955	503136	504775		3	6182	7109	8035	0	3	2	1	1	(5:3)_(4:4aCO)_(6:2)_(4:4a)_(3:5)_(3:5a)_(2:6)_(3:5)_(3:5a)_(5:3a)_(4:4bCO)
240	TCMM16	TCMM	13	798090	798332	799763	800212	2_nonsis		1432	1777	2121	0	3	2	0	2	(4:4aCO)_(5:3)_(4:4CO)_(2:6)_(4:4)
244	TCMM16	TCMM	14	20559	21301	24857	25137		4	3557	4067	4577	0	3	2	2	0	(5:3)_(4:4)_(5:3a)_(6:2)_(6:2a)_(4:4aCO)_(4:4CO)
280	TCMM16	TCMM	15	701028	701208	703124	703302	2_nonsis		1917	2095	2273	0	3	2	0		(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)_(2:6)_(4:4CO)

306	TCMM16	TCMM	16	651191	651827	654661	655575	3	2835	3609	4383	0	3	2	1	1	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(7:1)_(6:2)_(7:1)_(6:2a)_(4:4aCO)_(5:3a)_(4:4CO)
410	TCMM16	TCMM	6	15012	15279	16574	16654 NA		1296	1469	1641	0	4	1 NA	NA		4:4_5:3_4:4_5:3_6:2
87	TCMM18	TCMM	5	62818	62914	62914	63004	1	1	93	185	1	1	1	0	1	05:03
11	TCMM18	TCMM	2	71825	71828	71828	72018	1	1	97	192	1	1	1	0	1	05:03
30	TCMM18	TCMM	2	742472	742660	742660	742690	1	1	109	217	1	1	1	0	1	05:03
244	TCMM18	TCMM	14	138172	138230	138230	138404	1	1	116	231	1	1	1	0	1	05:03
282	TCMM18	TCMM	16	46780	46831	46871	46996	1	41	128	215	1	1	1	0	1	05:03
157	TCMM18	TCMM	9	40140	40190	40190	40512	1	1	186	371	1	1	1	0	1	05:03
106	TCMM18	TCMM	6	78069	78202	78202	78568	1	1	250	498	1	1	1	0	1	05:03
32	TCMM18	TCMM	3	41571	41852	41852	42410	1	1	420	838	1	1	1	0	1	05:03
131	TCMM18	TCMM	7	763517	765005	765005	765055	1	1	769	1537	1	1	1	0	1	05:03
138	TCMM18	TCMM	7	905275	905694	906181	906494	1	488	853	1218	1	1	1	0	1	05:03
177	TCMM18	TCMM	10	190298	191257	191621	192156	1	365	1111	1857	1	1	1	0	1	05:03
147	TCMM18	TCMM	8	167785	168208	168879	170402	1	672	1644	2616	1	1	1	0	1	05:03
35	TCMM18	TCMM	3	79797	93230	93230	93455	1	1	6829	13657	1	1	1	0	1	05:03
45	TCMM18	TCMM	4	27258	27277	27277	27377	1	1	60	118	1	2	1	0	1	03:05
24	TCMM18	TCMM	2	593091	593127	593127	593215	1	1	62	123	1	2	1	0	1	03:05
276	TCMM18	TCMM	15	808101	808141	808141	808281	1	1	90	179	1	2	1	0	1	03:05
289	TCMM18	TCMM	16	171860	171885	171885	172109	1	1	125	248	1	2	1	0	1	03:05
300	TCMM18	TCMM	16	560045	560053	560053	560312	1	1	134	266	1	2	1	0	1	03:05
54	TCMM18	TCMM	4	611969	612171	612171	612253	1	1	142	283	1	2	1	0	1	03:05
186	TCMM18	TCMM	10	639041	639136	639136	639365	1	1	162	323	1	2	1	0	1	03:05
149	TCMM18	TCMM	8	293075	293153	293153	293443	1	1	184	367	1	2	1	0	1	03:05
125	TCMM18	TCMM	7	531741	531976	531976	532147	1	1	203	405	1	2	1	0	1	03:05
46	TCMM18	TCMM	4	84518	84625	84632	84947	1	8	218	428	1	2	1	0	1	03:05
16	TCMM18	TCMM	2	275372	275994	275994	276052	1	1	340	679	1	2	1	0	1	03:05
165	TCMM18	TCMM	9	199527	199623	199628	200296	1	6	387	768	1	2	1	0	1	03:05
8	TCMM18	TCMM	1	151333	151919	151919	152233	1	1	450	899	1	2	1	0	1	03:05
242	TCMM18	TCMM	14	88100	88974	88974	89169	1	1	535	1068	1	2	1	0	1	03:05
75	TCMM18	TCMM	4	1270457	1270902	1270902	1271755	1	1	649	1297	1	2	1	0	1	03:05
81	TCMM18	TCMM	4	1409083	1409336	1409794	1410029	1	459	702	945	1	2	1	0	1	03:05
292	TCMM18	TCMM	16	245496	245843	246558	246962	1	716	1091	1465	1	3	1	0	1	5:3_4:4_5:3
202	TCMM18	TCMM	12	259126	260086	260749	261053	1	664	1295	1926	1	3	1	0	1	5:3_6:2_5:3
115	TCMM18	TCMM	6	248365	248816	249213	249566	1	398	799	1200	1	4	1	0	1	3:5_4:4_3:5
94	TCMM18	TCMM	5	317359	317416	318564	318778	1	1149	1284	1418	1	4	1	0	1	3:5_2:6_3:5
117	TCMM18	TCMM	7	41041	41301	43400	43798	1	2100	2428	2756	1	4	1	0	1	3:5_2:6_3:5
135	TCMM18	TCMM	7	840315	840622	840852	841693	1	231	804	1377	1	7	1	0	1	6:2_5:3
126	TCMM18	TCMM	7	609044	609307	609958	610218	1	652	913	1173	1	7	1	0	1	5:3_6:2
159	TCMM18	TCMM	9	67395	68149	69035	69770	1	887	1631	2374	1	7	1	0	1	5:3_6:2
263	TCMM18	TCMM	15	107138	107387	109106	109424	1	1720	2003	2285	1	7	1	0	1	5:3_6:2
262	TCMM18	TCMM	15	90886	91370	91557	91592	1	188	447	705	1	7	1	0	1	6:2_4:4_6:2
306	TCMM18	TCMM	16	885210	885444	885979	886611	1	536	968	1400	1	7	1	0	1	6:2_4:4_6:2
239	TCMM18	TCMM	13	906418	906551	907700	907728	1	1150	1230	1309	1	7	1	0	1	6:2_4:4_6:2
86	TCMM18	TCMM	5	56829	57131	58183	58866	1	1053	1545	2036	1	7	1	0	1	6:2_5:3_6:2
128	TCMM18	TCMM	7	623527	623695	625479	625898	1	1785	2078	2370	1	7	1	0	1	6:2_5:3_4:4_6:2_5:3
183	TCMM18	TCMM	10	526176	526730	526799	527538	1	70	716	1361	1	8	1	0	1	3:5_2:6
133	TCMM18	TCMM	7	798380	798397	799262	799613	1	866	1049	1232	1	8	1	0	1	2:6_3:5
182	TCMM18	TCMM	10	521093	521645	523373	524003	1	1729	2319	2909	1	8	1	0	1	3:5_2:6
296	TCMM18	TCMM	16	414884	415343	418090	418435	1	2748	3149	3550	1	8	1	0	1	2:6_3:5
218	TCMM18	TCMM	12	855154	856994	857516	857614	1	523	1491	2459	1	8	1	0	1	4:4_3:5
203	TCMM18	TCMM	12	263065	264597	265441	265975	1	845	1877	2909	1	8	1	0	1	3:5_4:4_2:6
211	TCMM18	TCMM	12	632381	632910	636269	637193	1	3360	4086	4811	1	8	1	0	1	2:6_4:4_2:6
209	TCMM18	TCMM	12	611078	611179	612564	612630	1	1386	1469	1551	1	8	1	0	1	3:5_2:6_3:5_2:6
173	TCMM18	TCMM	10	59308	59484	61260	61449	1	1777	1959	2140	1	8	1	0	1	3:5_4:4_3:5_2:6
288	TCMM18	TCMM	16	150295	150413	153125	153659	1	2713	3038	3363	1	8	1	0	1	2:6_4:4_2:6_4:4_2:6
247	TCMM18	TCMM	14	224132	224654	226114	226134	1	1461	1731	2001	1	8	1	0	1	3:5_4:4_3:5_2:6_3:5_2:6
299	TCMM18	TCMM	16	523494	523583	530472	530807	1	6890	7101	7312	1	8	1	0	1	2:6_3:5_2:6_3:5_2:6_4:4_2:6_3:5_2:6_3:5_4:4_2:6
168	TCMM18	TCMM	9	285060	285202	285229	285322	1	28	145	261	1	10	1	0	1	06:02
130	TCMM18	TCMM	7	689803	690018	690039	690131	1	22	175	327	1	10	1	0	1	06:02
228	TCMM18	TCMM	13	236410	236819	236819	236833	1	1	212	422	1	10	1	0	1	06:02

264	TCMM18	TCMM	15	189367	189653	189700	189822	1	48	251	454	1	10	1	0	1	06:02
109	TCMM18	TCMM	6	157416	157760	157828	157884	1	69	268	467	1	10	1	0	1	06:02
9	TCMM18	TCMM	1	190031	190402	190429	190558	1	28	277	526	1	10	1	0	1	06:02
274	TCMM18	TCMM	15	770102	770118	770280	770508	1	163	284	405	1	10	1	0	1	06:02
23	TCMM18	TCMM	2	535775	535946	536146	536197	1	201	311	421	1	10	1	0	1	06:02
160	TCMM18	TCMM	9	93058	93207	93376	93546	1	170	329	487	1	10	1	0	1	06:02
47	TCMM18	TCMM	4	100723	101068	101199	101273	1	132	341	549	1	10	1	0	1	06:02
90	TCMM18	TCMM	5	201879	202172	202285	202470	1	114	352	590	1	10	1	0	1	06:02
57	TCMM18	TCMM	4	770058	770136	770136	770770	1	1	356	711	1	10	1	0	1	06:02
136	TCMM18	TCMM	7	848688	849134	849134	849405	1	1	359	716	1	10	1	0	1	06:02
56	TCMM18	TCMM	4	690964	691222	691222	691713	1	1	375	748	1	10	1	0	1	06:02
60	TCMM18	TCMM	4	794075	794507	794676	794820	1	170	457	744	1	10	1	0	1	06:02
63	TCMM18	TCMM	4	909447	909908	909908	910427	1	1	490	979	1	10	1	0	1	06:02
233	TCMM18	TCMM	13	482522	482985	482985	483557	1	1	518	1034	1	10	1	0	1	06:02
103	TCMM18	TCMM	6	27212	27436	27810	28033	1	375	598	820	1	10	1	0	1	06:02
217	TCMM18	TCMM	12	808452	809313	809313	809749	1	1	649	1296	1	10	1	0	1	06:02
166	TCMM18	TCMM	9	258908	259266	259788	259858	1	523	736	949	1	10	1	0	1	06:02
67	TCMM18	TCMM	4	1034904	1035084	1035697	1035811	1	614	760	906	1	10	1	0	1	06:02
192	TCMM18	TCMM	11	218728	218804	218976	220318	1	173	881	1589	1	10	1	0	1	06:02
97	TCMM18	TCMM	5	358357	359292	359292	360247	1	1	945	1889	1	10	1	0	1	06:02
112	TCMM18	TCMM	6	208668	209238	209430	210544	1	193	1034	1875	1	10	1	0	1	06:02
139	TCMM18	TCMM	7	916059	917004	917454	917686	1	451	1039	1626	1	10	1	0	1	06:02
7	TCMM18	TCMM	1	112136	113132	113326	114283	1	195	1171	2146	1	10	1	0	1	06:02
297	TCMM18	TCMM	16	425481	425740	426505	427075	1	766	1180	1593	1	10	1	0	1	06:02
65	TCMM18	TCMM	4	1013721	1013843	1014713	1015229	1	871	1189	1507	1	10	1	0	1	06:02
225	TCMM18	TCMM	13	75576	75773	77019	77135	1	1247	1403	1558	1	10	1	0	1	06:02
196	TCMM18	TCMM	11	339266	339499	340783	340811	1	1285	1415	1544	1	10	1	0	1	06:02
200	TCMM18	TCMM	12	27605	28820	29612	29773	1	793	1480	2167	1	10	1	0	1	06:02
172	TCMM18	TCMM	9	358980	359077	360460	360682	1	1384	1543	1701	1	10	1	0	1	06:02
180	TCMM18	TCMM	10	407487	407535	407535	411303	1	1	1908	3815	1	10	1	0	1	06:02
251	TCMM18	TCMM	14	412406	412417	412417	412447	1	1	21	40	1	10.1	1	0	1	02:06
194	TCMM18	TCMM	11	278363	278388	278406	278445	1	19	50	81	1	10.1	1	0	1	02:06
205	TCMM18	TCMM	12	412590	412603	412603	412803	1	1	107	212	1	10.1	1	0	1	02:06
25	TCMM18	TCMM	2	595518	595625	595625	595735	1	1	109	216	1	10.1	1	0	1	02:06
241	TCMM18	TCMM	14	82362	82505	82505	82667	1	1	153	304	1	10.1	1	0	1	02:06
124	TCMM18	TCMM	7	529630	529644	529644	529943	1	1	157	312	1	10.1	1	0	1	02:06
303	TCMM18	TCMM	16	724951	725136	725147	725262	1	12	161	310	1	10.1	1	0	1	02:06
44	TCMM18	TCMM	3	299645	299933	299933	300032	1	1	194	386	1	10.1	1	0	1	02:06
280	TCMM18	TCMM	15	968476	968504	968504	968918	1	1	221	441	1	10.1	1	0	1	02:06
151	TCMM18	TCMM	8	404521	404866	404866	404970	1	1	225	448	1	10.1	1	0	1	02:06
66	TCMM18	TCMM	4	1022417	1022660	1022660	1022874	1	1	229	456	1	10.1	1	0	1	02:06
266	TCMM18	TCMM	15	234124	234579	234579	234673	1	1	275	548	1	10.1	1	0	1	02:06
41	TCMM18	TCMM	3	242663	242917	242917	243218	1	1	278	554	1	10.1	1	0	1	02:06
13	TCMM18	TCMM	2	164995	165049	165178	165525	1	130	330	529	1	10.1	1	0	1	02:06
245	TCMM18	TCMM	14	201732	201876	201973	202301	1	98	333	568	1	10.1	1	0	1	02:06
96	TCMM18	TCMM	5	349434	349710	349715	350100	1	6	336	665	1	10.1	1	0	1	02:06
104	TCMM18	TCMM	6	32918	32931	33340	33496	1	410	494	577	1	10.1	1	0	1	02:06
187	TCMM18	TCMM	10	649035	649585	649660	649976	1	76	508	940	1	10.1	1	0	1	02:06
4	TCMM18	TCMM	1	70621	70999	71116	71673	1	118	585	1051	1	10.1	1	0	1	02:06
261	TCMM18	TCMM	15	79764	79906	80423	80449	1	518	601	684	1	10.1	1	0	1	02:06
271	TCMM18	TCMM	15	478915	479565	479565	480144	1	1	615	1228	1	10.1	1	0	1	02:06
254	TCMM18	TCMM	14	586560	586773	586871	587725	1	99	632	1164	1	10.1	1	0	1	02:06
294	TCMM18	TCMM	16	282512	282651	282651	283933	1	1	711	1420	1	10.1	1	0	1	02:06
291	TCMM18	TCMM	16	227039	227828	228043	228253	1	216	715	1213	1	10.1	1	0	1	02:06
238	TCMM18	TCMM	13	866753	867864	867864	868389	1	1	818	1635	1	10.1	1	0	1	02:06
80	TCMM18	TCMM	4	1394881	1395687	1396041	1396310	1	355	892	1428	1	10.1	1	0	1	02:06
101	TCMM18	TCMM	5	540528	540683	541194	541873	1	512	928	1344	1	10.1	1	0	1	02:06
152	TCMM18	TCMM	8	444367	444619	445557	445735	1	939	1153	1367	1	10.1	1	0	1	02:06
38	TCMM18	TCMM	3	190177	191932	192715	193066	1	784	1836	2888	1	10.1	1	0	1	02:06
253	TCMM18	TCMM	14	539950	542443	542443	543829	1	1	1940	3878	1	10.1	1	0	1	02:06

ID			n	p1	p2	p3	p4	type	v1	v2	v3	a	b	c	d	e	code
164	TCMM18	TCMM	9	184053	185865	185865	188629	1	1	2288	4575	1	10.1	1	0	1	02:06
287	TCMM18	TCMM	16	127009	127901	130145	130597	1	2245	2916	3587	1	10.1	1	0	1	02:06
14	TCMM18	TCMM	2	205559	205766	209271	209402	1	3506	3674	3842	1	10.1	1	0	1	02:06
188	TCMM18	TCMM	10	658094	658862	658912	660402	2_nonsis	51	1179	2307	3	30	1	0	1	05:03
134	TCMM18	TCMM	7	835169	836201	837577	837741	2_nonsis	1377	1974	2571	3	30	1	0	1	6:2_5:3
108	TCMM18	TCMM	6	114541	114707	115810	116037	2_nonsis	1104	1300	1495	3	30	1	0	1	2:6_4:4_6:2
249	TCMM18	TCMM	14	311614	311670	316253	316782	2_nonsis	4584	4876	5167	3	30	1	0	1	6:2_4:4_2:6_4:4_2:6_3:5_2:6
82	TCMM18	TCMM	4	1415081	1416035	1418139	1418662	2_nonsis	2105	2843	3580	3	31	1	0	1	3:5_4:4_2:6_4:4_4:4ai
298	TCMM18	TCMM	16	495977	496633	499388	499617	2_nonsis	2756	3198	3639	3	31	1	0	1	6:2_5:3_2:6_3:5_4:4ai_6:2_4:4_5:3_4:4_5:3
272	TCMM18	TCMM	15	558497	559459	559768	560108	2_nonsis	310	960	1610	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
285	TCMM18	TCMM	16	104784	105755	106109	106600	2_nonsis	355	1085	1815	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
260	TCMM18	TCMM	15	75017	75243	75710	75779	2_nonsis	468	615	761	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
91	TCMM18	TCMM	5	234931	235495	235773	235812	2_nonsis	279	580	880	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
105	TCMM18	TCMM	6	72559	73471	74705	74753	2_nonsis	1235	1714	2193	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
176	TCMM18	TCMM	10	179749	180268	183834	184212	2_nonsis	3567	4015	4462	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
120	TCMM18	TCMM	7	232997	235967	236277	241275	2_nonsis	311	4294	8277	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
143	TCMM18	TCMM	7	1018075	1018655	1019597	1019728	2_nonsis	943	1298	1652	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
137	TCMM18	TCMM	7	895181	895701	897158	897290	2_nonsis	1458	1783	2108	1	11	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4ai)_(4:4bCO)
195	TCMM18	TCMM	11	281006	281154	281307	281630	2_nonsis	154	389	623	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
267	TCMM18	TCMM	15	265983	266279	266759	266963	2_nonsis	481	730	979	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
268	TCMM18	TCMM	15	302514	302730	303222	303785	2_nonsis	493	882	1270	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
69	TCMM18	TCMM	4	1113566	1113753	1114225	1114859	2_nonsis	473	883	1292	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
146	TCMM18	TCMM	8	163731	164274	165835	165867	2_nonsis	1562	1849	2135	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
50	TCMM18	TCMM	4	196186	196482	198685	198734	2_nonsis	2204	2376	2547	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
277	TCMM18	TCMM	15	939870	940002	940839	941405	2_nonsis	838	1186	1534	1	12	1	1	0	(5:3)_(4:4aCO)_(5:3)_(4:4a)
110	TCMM18	TCMM	6	170473	170899	171501	172334	2_nonsis	603	1232	1860	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
150	TCMM18	TCMM	8	400642	400960	401862	402413	2_nonsis	903	1337	1770	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
31	TCMM18	TCMM	2	784336	784573	785908	786053	2_nonsis	1336	1526	1716	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
34	TCMM18	TCMM	3	66729	66765	68058	68556	2_nonsis	1294	1560	1826	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
189	TCMM18	TCMM	10	705235	705450	707333	707549	2_nonsis	1884	2099	2313	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
220	TCMM18	TCMM	12	875066	875233	877476	877539	2_nonsis	2244	2358	2472	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
210	TCMM18	TCMM	12	623971	624838	627370	627543	2_nonsis	2533	3052	3571	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(4:4aCO)
74	TCMM18	TCMM	4	1261105	1261386	1263883	1264743	2_nonsis	2498	3068	3637	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
158	TCMM18	TCMM	9	53832	54480	57153	57568	2_nonsis	2674	3205	3735	1	12	1	1	0	(6:2)_(4:4)_(5:3)_(4:4aCO)
40	TCMM18	TCMM	3	223676	224009	226498	230267	2_nonsis	2490	4540	6590	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
42	TCMM18	TCMM	3	248853	249269	249994	250253	2_nonsis	726	1063	1399	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(3:5)_(4:4aCO)
116	TCMM18	TCMM	6	251816	252064	253044	253284	2_nonsis	981	1224	1467	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
1	TCMM18	TCMM	1	36160	36524	38361	38490	2_nonsis	1838	2084	2329	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4)_(4:4aCO)
163	TCMM18	TCMM	9	168244	168511	171065	171083	2_nonsis	2555	2697	2838	1	12	1	1	0	(4:4aCO)_(3:5)_(4:4a)_(2:6)_(4:4a)
98	TCMM18	TCMM	5	411277	413233	415894	416514	2_nonsis	2662	3949	5236	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(4:4aCO)
70	TCMM18	TCMM	4	1124620	1125098	1129980	1130680	2_nonsis	4883	5471	6059	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(3:5)_(4:4aCO)
295	TCMM18	TCMM	16	359182	359890	362178	362269	2_nonsis	2289	2688	3086	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
19	TCMM18	TCMM	2	482984	483713	485863	487113	2_nonsis	2151	3140	4128	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)
118	TCMM18	TCMM	7	73941	74322	74612	74791	2_nonsis	291	570	849	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
270	TCMM18	TCMM	15	466340	466702	469093	469522	2_nonsis	2392	2787	3181	1	12	1	1	0	(2:6)_(3:5)_(4:4)_(2:6)_(3:5)_(2:6)_(4:4)_(4:4aCO)
281	TCMM18	TCMM	15	1017032	1017296	1020208	1020336	2_nonsis	2913	3108	3303	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)_(3:5)_(4:4a)
170	TCMM18	TCMM	9	308908	310223	311461	311839	2_nonsis	1239	2085	2930	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
132	TCMM18	TCMM	7	774621	774677	774766	774937	2_nonsis	90	203	315	1	15	1	1	0	(6:2)_(4:4aCO)
141	TCMM18	TCMM	7	968274	968486	968486	968708	2_nonsis	1	217	433	1	15	1	1	0	(6:2)_(4:4aCO)
175	TCMM18	TCMM	10	146738	146986	147014	147143	2_nonsis	29	217	404	1	15	1	1	0	(6:2)_(4:4aCO)
190	TCMM18	TCMM	11	19902	19942	20014	20275	2_nonsis	73	223	372	1	15	1	1	0	(6:2)_(4:4aCO)
5	TCMM18	TCMM	1	73490	73633	73733	73855	2_nonsis	101	233	364	1	15	1	1	0	(6:2)_(4:4aCO)
123	TCMM18	TCMM	7	383665	383867	383908	384183	2_nonsis	42	280	517	1	15	1	1	0	(6:2)_(4:4aCO)
36	TCMM18	TCMM	3	109320	109704	109776	109851	2_nonsis	73	302	530	1	15	1	1	0	(6:2)_(4:4aCO)
88	TCMM18	TCMM	5	101365	102020	102020	102185	2_nonsis	1	410	819	1	15	1	1	0	(6:2)_(4:4aCO)
250	TCMM18	TCMM	14	381889	382124	382139	382693	2_nonsis	16	410	803	1	15	1	1	0	(6:2)_(4:4aCO)
265	TCMM18	TCMM	15	199186	199433	199433	200443	2_nonsis	1	629	1256	1	15	1	1	0	(6:2)_(4:4aCO)
304	TCMM18	TCMM	16	726715	727099	727505	727667	2_nonsis	407	679	951	1	15	1	1	0	(6:2)_(4:4aCO)
221	TCMM18	TCMM	12	878875	879756	879756	880251	2_nonsis	1	688	1375	1	15	1	1	0	(6:2)_(4:4aCO)
127	TCMM18	TCMM	7	611358	612267	612267	612759	2_nonsis	1	701	1400	1	15	1	1	0	(6:2)_(4:4aCO)

								2_nonsis									
256	TCMM18	TCMM	14	613459	614988	615001	615141	2_nonsis	14	848	1681	1	15	1	1	0	(6:2)_(4:4aCO)
111	TCMM18	TCMM	6	198468	199207	199247	200419	2_nonsis	41	996	1950	1	15	1	1	0	(6:2)_(4:4aCO)
72	TCMM18	TCMM	4	1137630	1137761	1138406	1138987	2_nonsis	646	1001	1356	1	15	1	1	0	(6:2)_(4:4aCO)
216	TCMM18	TCMM	12	780728	781856	781856	782839	2_nonsis	1	1056	2110	1	15	1	1	0	(6:2)_(4:4aCO)
43	TCMM18	TCMM	3	285783	286611	287188	287614	2_nonsis	578	1204	1830	1	15	1	1	0	(6:2)_(4:4aCO)
22	TCMM18	TCMM	2	531940	533263	533263	535193	2_nonsis	1	1627	3252	1	15	1	1	0	(6:2)_(4:4aCO)
278	TCMM18	TCMM	15	943283	943688	945153	945177	2_nonsis	1466	1680	1893	1	15	1	1	0	(6:2)_(4:4aCO)
301	TCMM18	TCMM	16	609204	609390	609390	609523	2_nonsis	1	160	318	1	16	1	1	0	(2:6)_(4:4aCO)
290	TCMM18	TCMM	16	214358	214684	214684	214724	2_nonsis	1	183	365	1	16	1	1	0	(2:6)_(4:4aCO)
89	TCMM18	TCMM	5	161593	161767	161767	162008	2_nonsis	1	208	414	1	16	1	1	0	(2:6)_(4:4aCO)
201	TCMM18	TCMM	12	183955	184185	184185	184390	2_nonsis	1	218	434	1	16	1	1	0	(2:6)_(4:4aCO)
10	TCMM18	TCMM	2	45307	45660	45660	45824	2_nonsis	1	259	516	1	16	1	1	0	(2:6)_(4:4aCO)
226	TCMM18	TCMM	13	160037	160135	160280	160611	2_nonsis	146	360	573	1	16	1	1	0	(2:6)_(4:4aCO)
259	TCMM18	TCMM	15	41221	41378	41495	41838	2_nonsis	118	367	616	1	16	1	1	0	(2:6)_(4:4aCO)
121	TCMM18	TCMM	7	253383	253849	253916	254261	2_nonsis	68	473	877	1	16	1	1	0	(2:6)_(4:4aCO)
93	TCMM18	TCMM	5	247750	247981	248412	248444	2_nonsis	432	563	693	1	16	1	1	0	(2:6)_(4:4aCO)
275	TCMM18	TCMM	15	774203	774251	774747	774866	2_nonsis	497	580	662	1	16	1	1	0	(2:6)_(4:4aCO)
179	TCMM18	TCMM	10	323823	325190	325190	325369	2_nonsis	1	773	1545	1	16	1	1	0	(2:6)_(4:4aCO)
129	TCMM18	TCMM	7	640541	640786	640849	642042	2_nonsis	64	782	1500	1	16	1	1	0	(2:6)_(4:4aCO)
235	TCMM18	TCMM	13	661764	662059	662603	662796	2_nonsis	545	788	1031	1	16	1	1	0	(2:6)_(4:4aCO)
51	TCMM18	TCMM	4	396700	397411	397411	398408	2_nonsis	1	854	1707	1	16	1	1	0	(2:6)_(4:4aCO)
197	TCMM18	TCMM	11	394215	394878	395389	395440	2_nonsis	512	868	1224	1	16	1	1	0	(2:6)_(4:4aCO)
234	TCMM18	TCMM	13	559794	560210	560428	561397	2_nonsis	219	911	1602	1	16	1	1	0	(2:6)_(4:4aCO)
51	TCMM18	TCMM	4	503996	505427	505427	505984	2_nonsis	1	994	1987	1	16	1	1	0	(2:6)_(4:4aCO)
6	TCMM18	TCMM	1	79085	79449	80077	80554	2_nonsis	629	1049	1468	1	16	1	1	0	(2:6)_(4:4aCO)
231	TCMM18	TCMM	13	410428	410894	411264	412303	2_nonsis	371	1123	1874	1	16	1	1	0	(2:6)_(4:4aCO)
27	TCMM18	TCMM	2	695479	697455	697503	699461	2_nonsis	49	2015	3981	1	16	1	1	0	(2:6)_(4:4aCO)
83	TCMM18	TCMM	4	1433600	1433731	1435647	1435868	2_nonsis	1917	2092	2267	1	16	1	1	0	(2:6)_(4:4aCO)
161	TCMM18	TCMM	9	139714	139937	142621	142688	2_nonsis	2685	2829	2973	1	16	1	1	0	(2:6)_(4:4aCO)
68	TCMM18	TCMM	4	1095082	1095364	1095467	1102243	2_nonsis	104	3632	7160	1	16	1	1	0	(2:6)_(4:4aCO)
140	TCMM18	TCMM	7	927341	927609	932723	933365	2_nonsis	5115	5569	6023	1	16	1	1	0	(2:6)_(4:4aCO)
84	TCMM18	TCMM	4	1498007	1498087	1498007	1498087	2_nonsis	0	40	79	1	100	1	1	0	(4:4aCO)
100	TCMM18	TCMM	5	522810	522899	522810	522899	2_nonsis	0	44	88	1	100	1	1	0	(4:4aCO)
144	TCMM18	TCMM	8	76827	76976	76827	76976	2_nonsis	0	74	148	1	100	1	1	0	(4:4aCO)
76	TCMM18	TCMM	4	1293522	1293708	1293522	1293708	2_nonsis	0	93	185	1	100	1	1	0	(4:4aCO)
222	TCMM18	TCMM	12	949229	949418	949229	949418	2_nonsis	0	94	188	1	100	1	1	0	(4:4aCO)
26	TCMM18	TCMM	2	650411	650619	650411	650619	2_nonsis	0	104	207	1	100	1	1	0	(4:4aCO)
248	TCMM18	TCMM	14	257643	257904	257643	257904	2_nonsis	0	130	260	1	100	1	1	0	(4:4aCO)
58	TCMM18	TCMM	4	781986	782410	781986	782410	2_nonsis	0	212	423	1	100	1	1	0	(4:4aCO)
243	TCMM18	TCMM	14	122717	123158	122717	123158	2_nonsis	0	220	440	1	100	1	1	0	(4:4aCO)
33	TCMM18	TCMM	3	57568	58033	57568	58033	2_nonsis	0	232	464	1	100	1	1	0	(4:4aCO)
283	TCMM18	TCMM	16	72872	73338	72872	73338	2_nonsis	0	233	465	1	100	1	1	0	(4:4aCO)
213	TCMM18	TCMM	12	723739	724217	723739	724217	2_nonsis	0	239	477	1	100	1	1	0	(4:4aCO)
12	TCMM18	TCMM	2	82087	82573	82087	82573	2_nonsis	0	243	485	1	100	1	1	0	(4:4aCO)
204	TCMM18	TCMM	12	319960	320465	319960	320465	2_nonsis	0	252	504	1	100	1	1	0	(4:4aCO)
148	TCMM18	TCMM	8	207052	207624	207052	207624	2_nonsis	0	286	571	1	100	1	1	0	(4:4aCO)
71	TCMM18	TCMM	4	1135519	1136116	1135519	1136116	2_nonsis	0	298	596	1	100	1	1	0	(4:4aCO)
64	TCMM18	TCMM	4	931376	931988	931376	931988	2_nonsis	0	306	611	1	100	1	1	0	(4:4aCO)
92	TCMM18	TCMM	5	237481	238122	237481	238122	2_nonsis	0	320	640	1	100	1	1	0	(4:4aCO)
52	TCMM18	TCMM	4	549856	550499	549856	550499	2_nonsis	0	321	642	1	100	1	1	0	(4:4aCO)
28	TCMM18	TCMM	2	701871	702521	701871	702521	2_nonsis	0	325	649	1	100	1	1	0	(4:4aCO)
236	TCMM18	TCMM	13	810963	811653	810963	811653	2_nonsis	0	345	689	1	100	1	1	0	(4:4aCO)
273	TCMM18	TCMM	15	624868	625559	624868	625559	2_nonsis	0	345	690	1	100	1	1	0	(4:4aCO)
240	TCMM18	TCMM	14	49011	49737	49011	49737	2_nonsis	0	363	725	1	100	1	1	0	(4:4aCO)
224	TCMM18	TCMM	13	43336	44157	43336	44157	2_nonsis	0	410	820	1	100	1	1	0	(4:4aCO)
279	TCMM18	TCMM	15	965240	966067	965240	966067	2_nonsis	0	413	826	1	100	1	1	0	(4:4aCO)
119	TCMM18	TCMM	7	129484	130374	129484	130374	2_nonsis	0	445	889	1	100	1	1	0	(4:4aCO)
18	TCMM18	TCMM	2	428064	428982	428064	428982	2_nonsis	0	459	917	1	100	1	1	0	(4:4aCO)
223	TCMM18	TCMM	13	41174	42127	41174	42127	2_nonsis	0	476	952	1	100	1	1	0	(4:4aCO)

246	TCMM18	TCMM	14	221973	222978	221973	222978	2_nonsis		0	502	1004	1	100	1	1	0	(4:4aCO)
174	TCMM18	TCMM	10	98106	99116	98106	99116	2_nonsis		0	505	1009	1	100	1	1	0	(4:4aCO)
17	TCMM18	TCMM	2	316189	317232	316189	317232	2_nonsis		0	521	1042	1	100	1	1	0	(4:4aCO)
185	TCMM18	TCMM	10	577732	578943	577732	578943	2_nonsis		0	605	1210	1	100	1	1	0	(4:4aCO)
252	TCMM18	TCMM	14	414025	415775	414025	415775	2_nonsis		0	875	1749	1	100	1	1	0	(4:4aCO)
227	TCMM18	TCMM	13	219863	221642	219863	221642	2_nonsis		0	889	1778	1	100	1	1	0	(4:4aCO)
181	TCMM18	TCMM	10	467589	469453	467589	469453	2_nonsis		0	932	1863	1	100	1	1	0	(4:4aCO)
184	TCMM18	TCMM	10	570822	573135	570822	573135	2_nonsis		0	1156	2312	1	100	1	1	0	(4:4aCO)
219	TCMM18	TCMM	12	857770	860959	857770	860959	2_nonsis		0	1594	3188	1	100	1	1	0	(4:4aCO)
169	TCMM18	TCMM	9	299287	302738	299287	302738	2_nonsis		0	1725	3450	1	100	1	1	0	(4:4aCO)
122	TCMM18	TCMM	7	305233	305542	305542	305956	2_nonsis		261	492	722	3	20	1	1	0	(5:3)_(2:6)_(4:4aCO)
206	TCMM18	TCMM	12	415537	415898	416464	416793	2_nonsis		567	911	1255	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
114	TCMM18	TCMM	6	245286	245484	246293	246533	2_nonsis		810	1028	1246	3	20	1	1	0	(2:6)_(5:3)_(4:4)_(4:4aCO)
198	TCMM18	TCMM	11	567633	567960	569085	569468	2_nonsis		1126	1480	1834	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
15	TCMM18	TCMM	2	255743	255862	258071	258313	2_nonsis		2210	2390	2569	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
258	TCMM18	TCMM	14	710457	711379	713465	713685	2_nonsis		2087	2657	3227	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
79	TCMM18	TCMM	4	1364167	1364482	1366837	1366906	2_nonsis		2356	2547	2738	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
20	TCMM18	TCMM	2	499070	499985	501576	501897	2_nonsis		1592	2209	2826	3	20	1	1	0	(5:3)_(6:2)_(4:4aCO)_(2:6)_(3:5)_(5:3)_(4:4a)
286	TCMM18	TCMM	16	114774	114957	117204	117756	2_nonsis		2248	2615	2981	3	20	1	1	0	(6:2)_(3:5)_(4:4)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
95	TCMM18	TCMM	5	330953	332219	334331	334460	2_nonsis		2113	2810	3506	3	20	1	1	0	(6:2)_(2:6)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
3	TCMM18	TCMM	1	59659	60198	62679	62754	2_sis		2482	2788	3094	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(3:5)_(4:4)
39	TCMM18	TCMM	3	211159	211204	213542	213768	2_sis		2339	2474	2608	0	1	2	0	2	(6:2)_(4:4)_(6:2)_(7:1)_(6:2)_(4:4)
49	TCMM18	TCMM	4	106899	107966	110696	111349		3	2731	3590	4449	0	1	2	0	2	(6:2)_(2:6)_(0:8)_(2:6)_(4:4)
62	TCMM18	TCMM	4	891889	892825	894075	895202		3	1251	2282	3312	0	1	2	0	2	(7:1)_(4:4)_(3:5)_(4:4)_(3:5)_(4:4)
73	TCMM18	TCMM	4	1167961	1168078	1169278	1169426	2_sis		1201	1333	1464	0	1	2	0	2	(6:2)_(6:2a)_(4:4)_(6:2a)_(4:4)
199	TCMM18	TCMM	12	21252	21693	22811	22902	2_sis		1119	1384	1649	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
229	TCMM18	TCMM	13	353026	353180	353429	353814	2_sis		250	519	787	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
302	TCMM18	TCMM	16	663708	664041	665472	665513	2_sis		1432	1618	1804	0	1	2	0	2	(2:6)_(4:4)_(6:2a)_(4:4)
21	TCMM18	TCMM	2	513641	513994	515130	515157		3	1137	1326	1515	0	2	2	1	1	(4:4aCO)_(3:5)_(4:4a)
29	TCMM18	TCMM	2	731564	731596	736946	737232		3	5351	5509	5667	0	2	2	1	1	(6:2)_(4:4)_(5:3)_(3:5)_(4:4)_(5:3)_(2:6)_(3:5)_(4:4aCO)
37	TCMM18	TCMM	3	156517	156868	156868	157443		3	1	463	925	0	2	2	1	1	(3:5)_(4:4aCO)
48	TCMM18	TCMM	4	104069	104854	105623	105784		3	770	1242	1714	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)
55	TCMM18	TCMM	4	679655	680244	684395	685013		4	4152	4755	5357	0	2	2	1	1	(6:2)_(5:3)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
59	TCMM18	TCMM	4	783598	783897	784537	784809		3	641	926	1210	0	2	2	1	1	(4:4aCO)_(2:6)_(4:4a)
61	TCMM18	TCMM	4	832054	832844	837953	838644		3	5110	5850	6589	0	2	2	1	1	(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4)_(3:5)_(4:4)_(4:4aCO)
77	TCMM18	TCMM	4	1295582	1295980	1296525	1297076		3	546	1020	1493	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
113	TCMM18	TCMM	6	219786	220148	226036	226238		3	5889	6170	6451	0	2	2	1	1	(6:2)_(4:4aCO)_(3:5)_(4:4a)_(2:6)_(4:4a)_(2:6a)_(4:4a)
142	TCMM18	TCMM	7	1011510	1012069	1012874	1013000		3	806	1148	1489	0	2	2	1	1	(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
145	TCMM18	TCMM	8	120445	121618	123814	124092		3	2197	2922	3646	0	2	2	1	1	(4:4aCO)_(6:2)_(6:2a)_(4:4a)
156	TCMM18	TCMM	9	35118	35226	36971	36978		3	1746	1803	1859	0	2	2	1	1	(2:6)_(3:5)_(3:5a)_(6:2)_(4:4)_(6:2)_(4:4aCO)_(2:6a)_(4:4a)_(3:5b)_(4:4a)
162	TCMM18	TCMM	9	160170	160514	161651	161738		3	1138	1353	1567	0	2	2	1	1	(7:1)_(5:3)_(4:4aCO)_(5:3a)_(4:4a)
167	TCMM18	TCMM	9	268278	268466	271556	271960		3	3091	3386	3681	0	2	2	1	1	(6:2)_(4:4)_(2:6)_(3:5)_(4:4)_(4:4aCO)
171	TCMM18	TCMM	9	336673	337083	338670	339115		3	1588	2015	2441	0	2	2	1	1	(5:3)_(6:2)_(4:4)_(5:3)_(6:2a)_(5:3a)_(4:4aCO)
191	TCMM18	TCMM	11	34159	34378	35136	35505		3	759	1052	1345	0	2	2	1	1	(6:2)_(4:4)_(4:4aCO)
193	TCMM18	TCMM	11	230455	230837	231603	232567		3	767	1439	2111	0	2	2	1	1	(3:5)_(4:4)_(3:5a)_(5:3)_(4:4aCO)
232	TCMM18	TCMM	13	472484	473000	473172	473320		3	173	504	835	0	2	2	1	1	(3:5)_(5:3)_(4:4aCO)
255	TCMM18	TCMM	14	598176	602658	606111	606283		3	3454	5780	8106	0	2	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4a)
257	TCMM18	TCMM	14	659022	661270	662512	665017		3	1243	3619	5994	0	2	2	1	1	(8:0)_(6:2)_(8:0)_(6:2a)_(4:4aCO)
305	TCMM18	TCMM	16	840263	840416	843391	843720		3	2976	3216	3456	0	2	2	1	1	(2:6)_(1:7)_(2:6)_(0:8)_(2:6)_(4:4aCO)
2	TCMM18	TCMM	1	42635	42684	45030	45831		3	2347	2771	3195	0	3	2	0	2	(6:2)_(4:4aCO)_(5:3)_(4:4bCO)_(5:3)_(4:4b)_(4:4CO)
53	TCMM18	TCMM	4	556934	556996	559582	559935	2_nonsis		2587	2794	3000	0	3	2	0	2	(4:4aCO)_(2:6)_(3:5)_(2:6)_(4:4CO)
78	TCMM18	TCMM	4	1300582	1300834	1303188	1303306	2_nonsis		2355	2539	2723	0	3	2	0	2	(4:4aCO)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4CO)
85	TCMM18	TCMM	5	41961	42216	46383	46589		3	4168	4398	4627	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)
99	TCMM18	TCMM	5	502911	502995	509962	510678	2_nonsis		6968	7367	7766	0	3	2	0	2	(5:3)_(4:4aCO)_(4:4CO)_(6:2)_(5:3)_(6:2)_(5:3)_(3:5)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4)
102	TCMM18	TCMM	5	544042	544296	546141	546545	2_nonsis		1846	2174	2502	0	3	2	0	2	(3:5)_(4:4aCO)_(2:6)_(4:4CO)
107	TCMM18	TCMM	6	80386	81527	82679	83125		3	1153	1946	2738	0	3	2	1	1	(4:4aCO)_(6:2)_(4:4bCO)
153	TCMM18	TCMM	8	497211	497276	498771	499032	2_nonsis		1496	1658	1820	0	3	2	0	2	(6:2)_(4:4aCO)_(5:3)_(6:2)_(4:4CO)
178	TCMM18	TCMM	10	235976	236393	236674	236901		3	282	603	924	0	3	2	1	1	(6:2)_(4:4aCO)_(4:4bCO)
207	TCMM18	TCMM	12	570914	571412	574096	574439		4	2685	3105	3524	0	3	2	2	0	(2:6)_(6:2)_(4:4aCO)_(4:4bCO)_(8:0)_(6:2a)_(6:2b)_(4:4b)
208	TCMM18	TCMM	12	584201	584485	585365	586011	2_nonsis		881	1345	1809	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)

212	TCMM18	TCMM	12	674080	674152	679633	680510	3	5482	5956	6429	0	3	2	1	1	(6:2)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4CO)_(4:4bCO)
214	TCMM18	TCMM	12	744566	744885	753571	754314	3	8687	9217	9747	0	3	2	0	2	(3:5)_(4:4aCO)_(4:4bCO)_(2:6)_(4:4CO)_(2:6)_(4:4)_(3:5a)_(2:6a)_(3:5a)_(2:6a)_(4:4)
215	TCMM18	TCMM	12	762220	762817	763199	763325 2_nonsis		383	744	1104	0	3	2	0	2	(4:4aCO)_(4:4CO)
230	TCMM18	TCMM	13	385945	386206	388450	388702 2_nonsis		2245	2501	2756	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)_(6:2)_(4:4)_(6:2)_(4:4)
237	TCMM18	TCMM	13	856957	857240	859155	859920	4	1916	2439	2962	0	3	2	2	0	(4:4aCO)_(6:2)_(4:4bCO)
269	TCMM18	TCMM	15	438163	438791	441487	441731 2_nonsis		2697	3132	3567	0	3	2	1	1	(4:4aCO)_(6:2)_(4:4CO)_(3:5)_(4:4aCO)_(6:2)_(4:4a)
293	TCMM18	TCMM	16	255611	255970	257972	258230	3	2003	2311	2618	0	3	2	1	1	(6:2)_(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
316	TCMM18	TCMM	1	192723	193131	203038	230218	1	0	18747	37494	0	4	1	NA	NA	
615	TCMM18	TCMM	16	924011	924094	925093	948066	1	1000	12527	24054	0	4	1	NA	NA	2:6_4:4_2:6_4:4_2:6
131	TCMM19	TCMM	7	780065	780103	780103	780122	1	1	29	56	1	1	1	0	1	05:03
145	TCMM19	TCMM	8	12640	12663	12670	12721	1	8	44	80	1	1	1	0	1	05:03
47	TCMM19	TCMM	3	128174	128224	128224	128266	1	1	46	91	1	1	1	0	1	05:03
371	TCMM19	TCMM	16	231042	231052	231052	231144	1	1	51	101	1	1	1	0	1	05:03
115	TCMM19	TCMM	6	210590	210664	210664	210721	1	1	66	130	1	1	1	0	1	05:03
243	TCMM19	TCMM	11	642656	642703	642703	642801	1	1	73	144	1	1	1	0	1	05:03
260	TCMM19	TCMM	12	680988	681097	681097	681146	1	1	79	157	1	1	1	0	1	05:03
99	TCMM19	TCMM	5	311423	311515	311515	311716	1	1	147	292	1	1	1	0	1	05:03
322	TCMM19	TCMM	14	779204	779247	779247	779510	1	1	153	305	1	1	1	0	1	05:03
116	TCMM19	TCMM	6	234593	234694	234694	234904	1	1	156	310	1	1	1	0	1	05:03
32	TCMM19	TCMM	2	568465	568762	568762	568783	1	1	159	317	1	1	1	0	1	05:03
231	TCMM19	TCMM	11	350945	351226	351226	351268	1	1	162	322	1	1	1	0	1	05:03
82	TCMM19	TCMM	4	1266824	1266952	1266952	1267153	1	1	165	328	1	1	1	0	1	05:03
64	TCMM19	TCMM	4	505462	505577	505577	505795	1	1	167	332	1	1	1	0	1	05:03
296	TCMM19	TCMM	14	187434	187730	187730	187769	1	1	168	334	1	1	1	0	1	05:03
257	TCMM19	TCMM	12	510433	510495	510600	510745	1	106	209	311	1	1	1	0	1	05:03
382	TCMM19	TCMM	16	458912	458958	458958	459330	1	1	209	417	1	1	1	0	1	05:03
189	TCMM19	TCMM	9	360460	360682	360722	360876	1	41	228	415	1	1	1	0	1	05:03
355	TCMM19	TCMM	15	815746	816176	816176	816215	1	1	235	468	1	1	1	0	1	05:03
273	TCMM19	TCMM	13	336425	336566	336695	336784	1	130	244	358	1	1	1	0	1	05:03
310	TCMM19	TCMM	14	532165	532649	532649	532670	1	1	253	504	1	1	1	0	1	05:03
97	TCMM19	TCMM	5	250573	250605	250692	251006	1	88	260	432	1	1	1	0	1	05:03
337	TCMM19	TCMM	15	351333	351470	351607	351787	1	138	296	453	1	1	1	0	1	05:03
300	TCMM19	TCMM	14	278430	278571	278757	278850	1	187	303	419	1	1	1	0	1	05:03
93	TCMM19	TCMM	5	182242	182338	182381	182827	1	44	314	584	1	1	1	0	1	05:03
121	TCMM19	TCMM	7	170880	171278	171278	171569	1	1	345	688	1	1	1	0	1	05:03
128	TCMM19	TCMM	7	667659	667672	667843	668222	1	172	367	562	1	1	1	0	1	05:03
95	TCMM19	TCMM	5	198865	198962	199227	199337	1	266	369	471	1	1	1	0	1	05:03
20	TCMM19	TCMM	2	202227	202580	202580	203030	1	1	402	802	1	1	1	0	1	05:03
278	TCMM19	TCMM	13	695793	695805	696177	696333	1	373	456	539	1	1	1	0	1	05:03
117	TCMM19	TCMM	6	244268	244360	244444	245103	1	85	460	834	1	1	1	0	1	05:03
96	TCMM19	TCMM	5	236202	236672	236672	237191	1	1	495	988	1	1	1	0	1	05:03
360	TCMM19	TCMM	15	954766	955006	955483	955552	1	478	632	785	1	1	1	0	1	05:03
185	TCMM19	TCMM	9	192389	193262	193298	193815	1	37	731	1425	1	1	1	0	1	05:03
330	TCMM19	TCMM	15	227759	228291	228291	229235	1	1	738	1475	1	1	1	0	1	05:03
160	TCMM19	TCMM	8	277301	278461	278461	278994	1	1	847	1692	1	1	1	0	1	05:03
318	TCMM19	TCMM	14	718033	718741	719201	719304	1	461	866	1270	1	1	1	0	1	05:03
236	TCMM19	TCMM	11	492262	493124	493438	494125	1	315	1089	1862	1	1	1	0	1	05:03
212	TCMM19	TCMM	10	449329	450386	450678	451382	1	293	1173	2052	1	1	1	0	1	05:03
326	TCMM19	TCMM	15	170583	170921	171849	172081	1	929	1213	1497	1	1	1	0	1	05:03
172	TCMM19	TCMM	8	505427	505776	506810	506933	1	1035	1270	1505	1	1	1	0	1	05:03
15	TCMM19	TCMM	2	73943	74853	75576	75822	1	724	1301	1878	1	1	1	0	1	05:03
101	TCMM19	TCMM	5	334750	335065	336237	336549	1	1173	1486	1798	1	1	1	0	1	05:03
5	TCMM19	TCMM	1	81306	81604	82379	83613	1	776	1541	2306	1	1	1	0	1	05:03
325	TCMM19	TCMM	15	128123	128405	129671	130049	1	1267	1596	1925	1	1	1	0	1	05:03
53	TCMM19	TCMM	4	52141	52663	53890	54185	1	1228	1636	2043	1	1	1	0	1	05:03
308	TCMM19	TCMM	14	487880	487935	489468	489631	1	1534	1642	1750	1	1	1	0	1	05:03
106	TCMM19	TCMM	5	413862	414190	415484	415894	1	1295	1663	2031	1	1	1	0	1	05:03
384	TCMM19	TCMM	16	474526	474750	476380	476646	1	1631	1875	2119	1	1	1	0	1	05:03
389	TCMM19	TCMM	16	663036	663543	665235	665344	1	1693	2000	2307	1	1	1	0	1	05:03
291	TCMM19	TCMM	14	60029	60034	60034	60050	1	1	11	20	1	2	1	0	1	03:05

365	TCMM19	TCMM	16	46435	46551	46551	46594	1	1	80	158	1	2	1	0	1 03:05
63	TCMM19	TCMM	4	387157	387371	387371	387397	1	1	120	239	1	2	1	0	1 03:05
341	TCMM19	TCMM	15	494461	494556	494573	494732	1	18	144	270	1	2	1	0	1 03:05
42	TCMM19	TCMM	2	798886	799021	799048	799164	1	28	153	277	1	2	1	0	1 03:05
41	TCMM19	TCMM	2	760365	760599	760599	760767	1	1	201	401	1	2	1	0	1 03:05
381	TCMM19	TCMM	16	443763	443833	443969	444028	1	137	201	264	1	2	1	0	1 03:05
301	TCMM19	TCMM	14	303243	303460	303486	303631	1	27	207	387	1	2	1	0	1 03:05
256	TCMM19	TCMM	12	507075	507492	507492	507531	1	1	228	455	1	2	1	0	1 03:05
347	TCMM19	TCMM	15	712306	712727	712727	712794	1	1	244	487	1	2	1	0	1 03:05
200	TCMM19	TCMM	10	180789	181065	181065	181281	1	1	246	491	1	2	1	0	1 03:05
232	TCMM19	TCMM	11	357937	358323	358323	358455	1	1	259	517	1	2	1	0	1 03:05
353	TCMM19	TCMM	15	783046	783587	783587	783594	1	1	274	547	1	2	1	0	1 03:05
23	TCMM19	TCMM	2	321773	321857	322002	322182	1	146	277	408	1	2	1	0	1 03:05
39	TCMM19	TCMM	2	740362	740429	740429	740972	1	1	305	609	1	2	1	0	1 03:05
31	TCMM19	TCMM	2	536197	536637	536700	536754	1	64	310	556	1	2	1	0	1 03:05
281	TCMM19	TCMM	13	768312	768463	768463	768951	1	1	320	638	1	2	1	0	1 03:05
210	TCMM19	TCMM	10	391657	391693	391693	392346	1	1	345	688	1	2	1	0	1 03:05
151	TCMM19	TCMM	8	122169	122634	122674	122848	1	41	360	678	1	2	1	0	1 03:05
374	TCMM19	TCMM	16	301952	302336	302336	302673	1	1	361	720	1	2	1	0	1 03:05
372	TCMM19	TCMM	16	272485	273202	273202	273221	1	1	368	735	1	2	1	0	1 03:05
344	TCMM19	TCMM	15	633360	633825	633825	634186	1	1	413	825	1	2	1	0	1 03:05
130	TCMM19	TCMM	7	745891	745981	746194	746541	1	214	432	649	1	2	1	0	1 03:05
211	TCMM19	TCMM	10	423783	424402	424406	424695	1	5	458	911	1	2	1	0	1 03:05
240	TCMM19	TCMM	11	571639	571872	571872	572586	1	1	474	946	1	2	1	0	1 03:05
289	TCMM19	TCMM	14	22397	22855	22855	23459	1	1	531	1061	1	2	1	0	1 03:05
83	TCMM19	TCMM	4	1289490	1289885	1289972	1290507	1	88	552	1016	1	2	1	0	1 03:05
229	TCMM19	TCMM	11	245116	245907	245907	246336	1	1	610	1219	1	2	1	0	1 03:05
129	TCMM19	TCMM	7	704403	704949	704949	705631	1	1	614	1227	1	2	1	0	1 03:05
354	TCMM19	TCMM	15	813043	813776	813794	814261	1	19	618	1217	1	2	1	0	1 03:05
81	TCMM19	TCMM	4	1257459	1257868	1258312	1258318	1	445	652	858	1	2	1	0	1 03:05
321	TCMM19	TCMM	14	770920	771471	771733	772160	1	263	751	1239	1	2	1	0	1 03:05
252	TCMM19	TCMM	12	346127	346167	346884	347086	1	718	838	958	1	2	1	0	1 03:05
89	TCMM19	TCMM	4	1458516	1459261	1459261	1460259	1	1	872	1742	1	2	1	0	1 03:05
133	TCMM19	TCMM	7	855522	856876	856876	857340	1	1	909	1817	1	2	1	0	1 03:05
35	TCMM19	TCMM	2	629782	630035	630469	631243	1	435	948	1460	1	2	1	0	1 03:05
140	TCMM19	TCMM	7	1021077	1021490	1022196	1022301	1	707	965	1223	1	2	1	0	1 03:05
304	TCMM19	TCMM	14	414025	415877	415877	416164	1	1	1070	2138	1	2	1	0	1 03:05
59	TCMM19	TCMM	4	266398	266488	267406	267874	1	919	1197	1475	1	2	1	0	1 03:05
196	TCMM19	TCMM	10	121522	122256	123026	123360	1	771	1304	1837	1	2	1	0	1 03:05
176	TCMM19	TCMM	9	40593	40898	41980	42365	1	1083	1427	1771	1	2	1	0	1 03:05
254	TCMM19	TCMM	12	404333	405334	406201	406472	1	868	1503	2138	1	2	1	0	1 03:05
155	TCMM19	TCMM	8	159599	159887	160782	161874	1	896	1585	2274	1	2	1	0	1 03:05
363	TCMM19	TCMM	16	22695	22824	22826	26191	1	3	1749	3495	1	2	1	0	1 03:05
171	TCMM19	TCMM	8	485522	485864	487338	487560	1	1475	1756	2037	1	2	1	0	1 03:05
286	TCMM19	TCMM	13	831222	831576	832607	834662	1	1032	2236	3439	1	2	1	0	1 03:05
214	TCMM19	TCMM	10	544322	544484	546603	546746	1	2120	2272	2423	1	2	1	0	1 03:05
343	TCMM19	TCMM	15	594122	594439	594454	601255	1	16	3574	7132	1	2	1	0	1 03:05
11	TCMM19	TCMM	2	29377	36302	36837	37454	1	536	4306	8076	1	2	1	0	1 03:05
234	TCMM19	TCMM	11	434756	434978	435882	436087	1	905	1118	1330	1	3	1	0	1 5:3_4:4_5:3
368	TCMM19	TCMM	16	159167	159487	160357	160565	1	871	1134	1397	1	3	1	0	1 5:3_6:2_5:3
33	TCMM19	TCMM	2	592641	592744	593500	594298	1	757	1207	1656	1	3	1	0	1 5:3_6:2_5:3
198	TCMM19	TCMM	10	149152	149570	150493	150662	1	924	1217	1509	1	3	1	0	1 5:3_6:2_5:3
271	TCMM19	TCMM	13	229786	230470	231382	231506	1	913	1316	1719	1	3	1	0	1 5:3_4:4_5:3
361	TCMM19	TCMM	15	966621	966892	968244	968286	1	1353	1509	1664	1	3	1	0	1 5:3_4:4_5:3
379	TCMM19	TCMM	16	425006	425451	426505	427075	1	1055	1562	2068	1	3	1	0	1 5:3_4:4_5:3
167	TCMM19	TCMM	8	416601	416745	418214	418349	1	1470	1609	1747	1	3	1	0	1 5:3_6:2_5:3
54	TCMM19	TCMM	4	76974	77295	78644	78945	1	1350	1660	1970	1	3	1	0	1 5:3_6:2_5:3
227	TCMM19	TCMM	11	224634	225480	226659	227319	1	1180	1932	2684	1	3	1	0	1 5:3_4:4_5:3
188	TCMM19	TCMM	9	337621	337673	339305	340356	1	1633	2184	2734	1	3	1	0	1 5:3_6:2_5:3
241	TCMM19	TCMM	11	573530	574134	575852	576495	1	1719	2342	2964	1	3	1	0	1 5:3_4:4_5:3

159	TCMM19	TCMM	8	267804	268308	274996	275150	1	6689	7017	7345	1	3	1	0	1	5:3_6:2_5:3
259	TCMM19	TCMM	12	676756	677005	677890	677900	1	886	1015	1143	1	3	1	0	1	5:3_6:2_5:3_6:2_5:3
352	TCMM19	TCMM	15	778024	779060	780184	780631	1	1125	1866	2606	1	3	1	0	1	5:3_6:2_5:3_4:4_5:3
213	TCMM19	TCMM	10	461507	461623	463641	464252	1	2019	2382	2744	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
9	TCMM19	TCMM	1	160074	166245	167179	170726	1	935	5793	10651	1	3	1	0	1	5:3_6:2_5:3_6:2_5:3
49	TCMM19	TCMM	3	224261	224961	225116	225200	1	156	547	938	1	4	1	0	1	3:5_2:6_3:5
338	TCMM19	TCMM	15	396805	397231	398023	398146	1	793	1067	1340	1	4	1	0	1	3:5_2:6_3:5
158	TCMM19	TCMM	8	259528	259588	260343	261563	1	756	1395	2034	1	4	1	0	1	3:5_4:4_3:5
168	TCMM19	TCMM	8	422798	422992	424326	425219	1	1335	1878	2420	1	4	1	0	1	3:5_4:4_3:5
146	TCMM19	TCMM	8	20318	20573	22253	22430	1	1681	1896	2111	1	4	1	0	1	3:5_4:4_3:5
250	TCMM19	TCMM	12	302004	302144	304381	304627	1	2238	2430	2622	1	4	1	0	1	3:5_4:4_3:5
108	TCMM19	TCMM	5	451413	451710	454403	454697	1	2694	2989	3283	1	4	1	0	1	3:5_4:4_3:5
246	TCMM19	TCMM	12	230218	230960	233075	234378	1	2116	3138	4159	1	4	1	0	1	3:5_4:4_2:6_3:5
164	TCMM19	TCMM	8	348462	348790	350566	350845	1	1777	2080	2382	1	4	1	0	1	3:5_2:6_3:5_4:4_3:5
73	TCMM19	TCMM	4	919279	919709	922174	922223	1	2466	2705	2943	1	4	1	0	1	3:5_4:4_3:5_4:4_3:5
247	TCMM19	TCMM	12	258577	259051	265441	265975	1	6391	6894	7397	1	4	1	0	1	3:5_4:4_2:6_3:5_2:6_3:5_2:6_3:5
295	TCMM19	TCMM	14	137123	137209	140190	140230	1	2982	3044	3106	1	4	1	0	1	3:5_4:4_3:5_4:4_2:6_3:5_2:6_3:5_4:4_3:5
152	TCMM19	TCMM	8	126142	126148	126397	126572	1	250	340	429	1	7	1	0	1	6:2_5:3
144	TCMM19	TCMM	7	1063290	1063368	1063846	1064130	1	479	659	839	1	7	1	0	1	6:2_5:3
203	TCMM19	TCMM	10	256690	256880	257445	257831	1	566	853	1140	1	7	1	0	1	6:2_5:3
395	TCMM19	TCMM	16	895354	895642	896575	896727	1	934	1153	1372	1	7	1	0	1	5:3_6:2
197	TCMM19	TCMM	10	136384	136623	138413	138706	1	1791	2056	2321	1	7	1	0	1	5:3_6:2
180	TCMM19	TCMM	9	93058	93207	93376	93546	1	170	329	487	1	7	1	0	1	6:2_4:4_6:2
150	TCMM19	TCMM	8	107008	107309	107606	107993	1	298	641	984	1	7	1	0	1	5:3_4:4_6:2
87	TCMM19	TCMM	4	1420155	1420281	1421240	1421307	1	960	1056	1151	1	7	1	0	1	6:2_4:4_6:2
313	TCMM19	TCMM	14	604879	605054	606872	608001	1	1819	2470	3121	1	7	1	0	1	6:2_4:4_5:3
165	TCMM19	TCMM	8	374065	374774	375825	375930	1	1052	1458	1864	1	7	1	0	1	5:3_6:2_5:3_6:2
175	TCMM19	TCMM	9	34985	35111	37068	37170	1	1958	2071	2184	1	7	1	0	1	6:2_5:3_4:4_5:3_6:2_5:3_6:2_5:3_6:2_5:3_6:2
348	TCMM19	TCMM	15	733489	733608	733667	733898	1	60	234	408	1	8	1	0	1	3:5_2:6
174	TCMM19	TCMM	9	32347	32528	33034	33054	1	507	607	706	1	8	1	0	1	2:6_3:5
56	TCMM19	TCMM	4	157958	158137	158965	158981	1	829	926	1022	1	8	1	0	1	3:5_2:6
391	TCMM19	TCMM	16	730292	730534	731036	731859	1	503	1035	1566	1	8	1	0	1	3:5_2:6
369	TCMM19	TCMM	16	170349	170630	171422	171708	1	793	1076	1358	1	8	1	0	1	2:6_3:5
71	TCMM19	TCMM	4	812667	813172	814114	814278	1	943	1277	1610	1	8	1	0	1	2:6_3:5
335	TCMM19	TCMM	15	290268	290790	291910	292246	1	1121	1549	1977	1	8	1	0	1	2:6_3:5
16	TCMM19	TCMM	2	99228	99630	102116	102386	1	2487	2822	3157	1	8	1	0	1	2:6_3:5
2	TCMM19	TCMM	1	57739	59349	62361	62648	1	3013	3961	4908	1	8	1	0	1	3:5_2:6
239	TCMM19	TCMM	11	558102	558496	567076	567430	1	8581	8954	9327	1	8	1	0	1	3:5_2:6
68	TCMM19	TCMM	4	654086	654167	655491	656349	1	1325	1794	2262	1	8	1	0	1	3:5_4:4_3:5_2:6_3:5_2:6
90	TCMM19	TCMM	5	15888	15940	17824	18174	1	1885	2085	2285	1	8	1	0	1	3:5_4:4_3:5_4:4_3:5_2:6
221	TCMM19	TCMM	11	10753	13039	14273	14406	1	1235	2444	3652	1	8	1	0	1	3:5_4:4_3:5_2:6_3:5_2:6
370	TCMM19	TCMM	16	187312	187323	187323	187324	1	1	6	11	1	10	1	0	1	06:02
126	TCMM19	TCMM	7	625898	626137	626137	626170	1	1	136	271	1	10	1	0	1	06:02
309	TCMM19	TCMM	14	525575	525857	525857	525960	1	1	193	384	1	10	1	0	1	06:02
387	TCMM19	TCMM	16	538649	538784	538784	539088	1	1	220	438	1	10	1	0	1	06:02
223	TCMM19	TCMM	11	135691	136140	136140	136171	1	1	240	479	1	10	1	0	1	06:02
182	TCMM19	TCMM	9	117717	117795	117809	118304	1	15	301	586	1	10	1	0	1	06:02
222	TCMM19	TCMM	11	74103	74603	74603	74756	1	1	327	652	1	10	1	0	1	06:02
283	TCMM19	TCMM	13	809325	809473	809473	810028	1	1	352	702	1	10	1	0	1	06:02
312	TCMM19	TCMM	14	552035	552259	552429	552569	1	171	352	533	1	10	1	0	1	06:02
13	TCMM19	TCMM	2	60478	60545	60793	60945	1	249	358	466	1	10	1	0	1	06:02
169	TCMM19	TCMM	8	455368	455642	455862	455976	1	221	414	607	1	10	1	0	1	06:02
205	TCMM19	TCMM	10	332735	332945	333136	333385	1	192	421	649	1	10	1	0	1	06:02
220	TCMM19	TCMM	10	705865	705917	706135	706547	1	219	450	681	1	10	1	0	1	06:02
156	TCMM19	TCMM	8	236191	236227	236251	237146	1	25	490	954	1	10	1	0	1	06:02
306	TCMM19	TCMM	14	452428	452892	453029	453469	1	138	589	1040	1	10	1	0	1	06:02
364	TCMM19	TCMM	16	28409	28513	29041	29091	1	529	605	681	1	10	1	0	1	06:02
177	TCMM19	TCMM	9	45259	45367	46102	46131	1	736	804	871	1	10	1	0	1	06:02
226	TCMM19	TCMM	11	218804	218858	218976	220318	1	119	816	1513	1	10	1	0	1	06:02
228	TCMM19	TCMM	11	241707	242410	242410	243550	1	1	922	1842	1	10	1	0	1	06:02

219	TCMM19	TCMM	10	700864	701241	701601	702817		1	361	1157	1952	1	10	1	0	1 06:02
111	TCMM19	TCMM	5	517549	517944	522900	523260		1	4957	5334	5710	1	10	1	0	1 06:02
186	TCMM19	TCMM	9	247495	247508	247508	247522		1	1	14	26	1	10.1	1	0	1 02:06
51	TCMM19	TCMM	4	22448	22481	22481	22513		1	1	33	64	1	10.1	1	0	1 02:06
285	TCMM19	TCMM	13	828291	828323	828323	828384		1	1	47	92	1	10.1	1	0	1 02:06
358	TCMM19	TCMM	15	849274	849337	849337	849390		1	1	58	115	1	10.1	1	0	1 02:06
85	TCMM19	TCMM	4	1341577	1341639	1341693	1341749		1	55	113	171	1	10.1	1	0	1 02:06
75	TCMM19	TCMM	4	976876	977181	977181	977275		1	1	200	398	1	10.1	1	0	1 02:06
394	TCMM19	TCMM	16	888239	888536	888536	888652		1	1	207	412	1	10.1	1	0	1 02:06
377	TCMM19	TCMM	16	352228	352381	352499	352575		1	119	233	346	1	10.1	1	0	1 02:06
65	TCMM19	TCMM	4	521269	521409	521536	521623		1	128	241	353	1	10.1	1	0	1 02:06
276	TCMM19	TCMM	13	421952	422261	422261	422449		1	1	249	496	1	10.1	1	0	1 02:06
201	TCMM19	TCMM	10	189105	189441	189441	189631		1	1	263	525	1	10.1	1	0	1 02:06
79	TCMM19	TCMM	4	1235870	1236152	1236284	1236427		1	133	345	556	1	10.1	1	0	1 02:06
142	TCMM19	TCMM	7	1042643	1043244	1043244	1043695		1	1	526	1051	1	10.1	1	0	1 02:06
102	TCMM19	TCMM	5	342057	342537	342731	342945		1	195	541	887	1	10.1	1	0	1 02:06
162	TCMM19	TCMM	8	322176	322381	322533	323234		1	153	605	1057	1	10.1	1	0	1 02:06
153	TCMM19	TCMM	8	143824	143930	144393	144688		1	464	664	863	1	10.1	1	0	1 02:06
385	TCMM19	TCMM	16	487851	488388	488388	489307		1	1	728	1455	1	10.1	1	0	1 02:06
72	TCMM19	TCMM	4	915507	916363	916363	917683		1	1	1088	2175	1	10.1	1	0	1 02:06
331	TCMM19	TCMM	15	238440	238504	241259	241438		1	2756	2877	2997	1	10.1	1	0	1 02:06
143	TCMM19	TCMM	7	1046648	1046925	1049349	1050057		1	2425	2917	3408	1	10.1	1	0	1 02:06
191	TCMM19	TCMM	10	21859	22066	24307	26108		1	2242	3245	4248	1	10.1	1	0	1 02:06
17	TCMM19	TCMM	2	140643	140850	141579	142181	2_nonsis	730	1134	1537	3	30	1	0	1 6:2_5:3
263	TCMM19	TCMM	12	772380	774096	775537	777814	2_nonsis	1442	3438	5433	3	30	1	0	1 2:6_5:3
25	TCMM19	TCMM	2	360531	360769	361468	361594	2_nonsis	700	881	1062	3	30	1	0	1 5:3_4:4_3:5
60	TCMM19	TCMM	4	300521	300921	302084	302250	2_nonsis	1164	1446	1728	3	30	1	0	1 5:3_4:4_6:2
18	TCMM19	TCMM	2	149872	150200	151407	151865	2_nonsis	1208	1600	1992	3	30	1	0	1 3:5_5:3_3:5
94	TCMM19	TCMM	5	193949	194375	195765	195830	2_nonsis	1391	1636	1880	3	30	1	0	1 2:6_3:5_5:3
217	TCMM19	TCMM	10	636506	637392	639365	640236	2_nonsis	1974	2852	3729	3	30	1	0	1 5:3_6:2_5:3a
88	TCMM19	TCMM	4	1423727	1424231	1427252	1427658	2_nonsis	3022	3476	3930	3	30	1	0	1 3:5_5:3_3:5
123	TCMM19	TCMM	7	355292	356141	359148	359394	2_nonsis	3008	3555	4101	3	30	1	0	1 6:2_5:3_3:5
113	TCMM19	TCMM	6	76126	76268	77181	77256	2_nonsis	914	1022	1129	3	30	1	0	1 2:6_4:4_6:2_5:3
323	TCMM19	TCMM	15	42859	43012	45210	46201	2_nonsis	2199	2770	3341	3	30	1	0	1 2:6_3:5_2:6_3:5a
316	TCMM19	TCMM	14	706575	707137	711379	711615	2_nonsis	4243	4641	5039	3	30	1	0	1 5:3_6:2_4:4_3:5
138	TCMM19	TCMM	7	951700	951733	952025	952040	2_nonsis	293	316	339	3	30	1	0	1 2:6_4:4_6:2_4:4_2:6
378	TCMM19	TCMM	16	383083	383310	384917	385830	2_nonsis	1608	2177	2746	3	30	1	0	1 2:6_4:4_5:3_4:4_5:3
139	TCMM19	TCMM	7	969753	969826	977494	978531	2_nonsis	7669	8223	8777	3	30	1	0	1 5:3_4:4_5:3_4:4_2:6
233	TCMM19	TCMM	11	381058	381640	385769	385778	2_nonsis	4130	4425	4719	3	30	1	0	1 6:2_4:4_3:5_4:4_3:5_4:4_2:6_3:5
351	TCMM19	TCMM	15	769620	770027	774457	774673	2_nonsis	4431	4742	5052	3	30	1	0	1 2:6_3:5_2:6_3:5_2:6_3:5a_2:6_3:5a
183	TCMM19	TCMM	9	149380	149501	152419	152956	2_nonsis	2919	3247	3575	3	30	1	0	1 5:3_3:5_3:5a_4:4_3:5_2:6_3:5_4:4_3:5
317	TCMM19	TCMM	14	714903	715086	716522	716912	2_nonsis	1437	1723	2008	3	31	1	0	1 4:4ai_3:5_3:5a
194	TCMM19	TCMM	10	77203	78874	80439	80673	2_nonsis	1566	2518	3469	3	31	1	0	1 4:4ai_3:5_4:4_3:5a_4:4_3:5a
218	TCMM19	TCMM	10	680328	680733	689090	689592	2_nonsis	8358	8811	9263	3	31	1	0	1 5:3_4:4ai_3:5_5:3_6:2_5:3a_4:4ai
279	TCMM19	TCMM	13	698569	698988	698988	699056	2_nonsis	1	244	486	1	1	1	1	0 (5:3)_(4:4aCO)
26	TCMM19	TCMM	2	452218	452891	452891	453095	2_nonsis	1	439	876	1	1	1	1	0 (5:3)_(4:4aCO)
22	TCMM19	TCMM	2	295058	295631	295912	296073	2_nonsis	282	648	1014	1	1	1	1	0 (5:3)_(4:4aCO)
376	TCMM19	TCMM	16	340194	340409	341647	341700	2_nonsis	1239	1372	1505	1	1	1	1	0 (5:3)_(4:4aCO)
38	TCMM19	TCMM	2	695479	697455	697455	698250	2_nonsis	1	1386	2770	1	1	1	1	0 (5:3)_(4:4aCO)
187	TCMM19	TCMM	9	289127	292446	292446	292870	2_nonsis	1	1872	3742	1	1	1	1	0 (5:3)_(4:4aCO)
70	TCMM19	TCMM	4	801845	801939	802711	805658	2_nonsis	773	2293	3812	1	1	1	1	0 (5:3)_(4:4aCO)
58	TCMM19	TCMM	4	263811	264106	264106	264197	2_nonsis	1	193	385	1	2	1	1	0 (3:5)_(4:4aCO)
392	TCMM19	TCMM	16	784888	785578	785578	785712	2_nonsis	1	412	823	1	2	1	1	0 (3:5)_(4:4aCO)
109	TCMM19	TCMM	5	499930	500567	500567	501719	2_nonsis	1	895	1788	1	2	1	1	0 (3:5)_(4:4aCO)
36	TCMM19	TCMM	2	633960	635127	635880	636267	2_nonsis	754	1530	2306	1	2	1	1	0 (3:5)_(4:4aCO)
216	TCMM19	TCMM	10	577732	578943	579361	579663	2_nonsis	419	1175	1930	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
327	TCMM19	TCMM	15	192748	193685	193911	194961	2_nonsis	227	1220	2212	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
209	TCMM19	TCMM	10	386527	387413	388253	388388	2_nonsis	841	1351	1860	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
288	TCMM19	TCMM	13	887934	888376	889638	889717	2_nonsis	1263	1523	1782	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
225	TCMM19	TCMM	11	162073	162583	162828	163173	2_nonsis	246	673	1099	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)

292	TCMM19	TCMM	14	81857	82092	83228	83675	2_nonsis	1137	1477	1817	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
287	TCMM19	TCMM	13	864888	866108	866477	867864	2_nonsis	370	1673	2975	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
157	TCMM19	TCMM	8	248649	248808	250465	250575	2_nonsis	1658	1792	1925	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
349	TCMM19	TCMM	15	735184	735517	735678	735877	2_nonsis	162	427	692	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
319	TCMM19	TCMM	14	739169	739459	739738	739896	2_nonsis	280	503	726	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
314	TCMM19	TCMM	14	608001	610323	610397	611511	2_nonsis	75	1792	3509	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
7	TCMM19	TCMM	1	118997	119350	121235	128637	2_nonsis	1886	5763	9639	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
383	TCMM19	TCMM	16	463723	464194	464194	464400	2_nonsis	1	339	676	1	11	1	1	0	(4:4ai)_(4:4bCO)
253	TCMM19	TCMM	12	395350	395431	395850	395986	2_nonsis	420	528	635	1	11	1	1	0	(4:4ai)_(3:5)_(4:4bCO)
199	TCMM19	TCMM	10	156143	156360	161251	161596	2_nonsis	4892	5172	5452	1	11	1	1	0	(4:4ai)_(5:3)_(6:2)_(5:3)_(4:4bCO)_(5:3)_(4:4b)
215	TCMM19	TCMM	10	573135	573950	574310	574412	2_nonsis	361	819	1276	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
266	TCMM19	TCMM	12	1028782	1030239	1030472	1030577	2_nonsis	234	1014	1794	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
258	TCMM19	TCMM	12	571412	571899	572946	573483	2_nonsis	1048	1559	2070	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
69	TCMM19	TCMM	4	781475	781568	784537	784809	2_nonsis	2970	3152	3333	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
77	TCMM19	TCMM	4	1150675	1150691	1151034	1151759	2_nonsis	344	714	1083	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
362	TCMM19	TCMM	15	1048196	1048227	1048953	1048990	2_nonsis	727	760	793	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
154	TCMM19	TCMM	8	150894	150909	151824	152274	2_nonsis	916	1148	1379	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
14	TCMM19	TCMM	2	69901	70006	71420	71553	2_nonsis	1415	1533	1651	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
122	TCMM19	TCMM	7	250680	252024	252806	253122	2_nonsis	783	1612	2441	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
293	TCMM19	TCMM	14	87215	88013	89169	89494	2_nonsis	1157	1718	2278	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(4:4aCO)
261	TCMM19	TCMM	12	683018	683405	684785	685228	2_nonsis	1381	1795	2209	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)
311	TCMM19	TCMM	14	537806	538122	539848	539903	2_nonsis	1727	1912	2096	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)
178	TCMM19	TCMM	9	53832	54480	55837	56514	2_nonsis	1358	2020	2681	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
43	TCMM19	TCMM	3	50269	51152	52919	53316	2_nonsis	1768	2407	3046	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(4:4aCO)
270	TCMM19	TCMM	13	218113	218127	219863	221252	2_nonsis	1737	2438	3138	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4aCO)
125	TCMM19	TCMM	7	580060	580178	582987	583179	2_nonsis	2810	2964	3118	1	12	1	1	0	(5:3)_(4:4)_(6:2)_(4:4aCO)
134	TCMM19	TCMM	7	886106	886758	887887	888005	2_nonsis	1130	1514	1898	1	12	1	1	0	(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
324	TCMM19	TCMM	15	107138	107387	108945	109088	2_nonsis	1559	1754	1949	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
62	TCMM19	TCMM	4	356226	356562	358197	358230	2_nonsis	1636	1820	2003	1	12	1	1	0	(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
390	TCMM19	TCMM	16	694969	695201	697067	697775	2_nonsis	1867	2336	2805	1	12	1	1	0	(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
3	TCMM19	TCMM	1	69112	69280	70621	71116	2_nonsis	1342	1673	2003	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
34	TCMM19	TCMM	2	606623	607563	609547	610045	2_nonsis	1985	2703	3421	1	12	1	1	0	(3:5)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)
342	TCMM19	TCMM	15	586345	586852	590260	590710	2_nonsis	3409	3887	4364	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
302	TCMM19	TCMM	14	338162	338424	342499	342707	2_nonsis	4076	4310	4544	1	12	1	1	0	(4:4aCO)_(5:3)_(6:2)_(5:3)_(4:4a)_(5:3)_(4:4a)
166	TCMM19	TCMM	8	394959	395132	399021	399235	2_nonsis	3890	4083	4275	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
248	TCMM19	TCMM	12	282385	283463	290479	290784	2_nonsis	7017	7708	8398	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
206	TCMM19	TCMM	10	338561	338643	338643	339206	2_nonsis	1	323	644	1	15	1	1	0	(6:2)_(4:4aCO)
84	TCMM19	TCMM	4	1322306	1322553	1322553	1323143	2_nonsis	1	419	836	1	15	1	1	0	(6:2)_(4:4aCO)
66	TCMM19	TCMM	4	551387	551638	551991	552102	2_nonsis	354	534	714	1	15	1	1	0	(6:2)_(4:4aCO)
120	TCMM19	TCMM	7	125147	125177	125333	125513	2_nonsis	157	261	365	1	16	1	1	0	(2:6)_(4:4aCO)
265	TCMM19	TCMM	12	931517	931804	931890	931997	2_nonsis	87	283	479	1	16	1	1	0	(2:6)_(4:4aCO)
277	TCMM19	TCMM	13	610928	611569	611569	611899	2_nonsis	1	486	970	1	16	1	1	0	(2:6)_(4:4aCO)
100	TCMM19	TCMM	5	328370	329070	329109	329730	2_nonsis	40	700	1359	1	16	1	1	0	(2:6)_(4:4aCO)
307	TCMM19	TCMM	14	456295	456437	458514	458618	2_nonsis	2078	2200	2322	1	16	1	1	0	(2:6)_(4:4aCO)
329	TCMM19	TCMM	15	213659	214699	216499	217333	2_nonsis	1801	2737	3673	1	16	1	1	0	(2:6)_(4:4aCO)
303	TCMM19	TCMM	14	373799	373925	373799	373925	2_nonsis	0	63	125	1	100	1	1	0	(4:4aCO)
24	TCMM19	TCMM	2	331580	331804	331580	331804	2_nonsis	0	112	223	1	100	1	1	0	(4:4aCO)
74	TCMM19	TCMM	4	947412	947805	947412	947805	2_nonsis	0	196	392	1	100	1	1	0	(4:4aCO)
118	TCMM19	TCMM	6	248365	248816	248365	248816	2_nonsis	0	225	450	1	100	1	1	0	(4:4aCO)
380	TCMM19	TCMM	16	428065	428562	428065	428562	2_nonsis	0	248	496	1	100	1	1	0	(4:4aCO)
78	TCMM19	TCMM	4	1174453	1174994	1174453	1174994	2_nonsis	0	270	540	1	100	1	1	0	(4:4aCO)
137	TCMM19	TCMM	7	948202	949014	948202	949014	2_nonsis	0	406	811	1	100	1	1	0	(4:4aCO)
290	TCMM19	TCMM	14	37986	39122	37986	39122	2_nonsis	0	568	1135	1	100	1	1	0	(4:4aCO)
230	TCMM19	TCMM	11	293792	295309	293792	295309	2_nonsis	0	758	1516	1	100	1	1	0	(4:4aCO)
315	TCMM19	TCMM	14	674690	676368	674690	676368	2_nonsis	0	839	1677	1	100	1	1	0	(4:4aCO)
357	TCMM19	TCMM	15	841378	843188	841378	843188	2_nonsis	0	905	1809	1	100	1	1	0	(4:4aCO)
57	TCMM19	TCMM	4	196851	198685	196851	198685	2_nonsis	0	917	1833	1	100	1	1	0	(4:4aCO)
224	TCMM19	TCMM	11	141109	143878	141109	143878	2_nonsis	0	1384	2768	1	100	1	1	0	(4:4aCO)
48	TCMM19	TCMM	3	171207	174943	171207	174943	2_nonsis	0	1868	3735	1	100	1	1	0	(4:4aCO)
264	TCMM19	TCMM	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0	(4:4aCO)

ID								Type										Composition
294	TCMM19	TCMM	14	122217	122278	122717	123158	2_nonsis		440	690	940	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
4	TCMM19	TCMM	1	73733	73855	77494	77528	2_nonsis		3640	3717	3794	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(5:3a)_(6:2)_(4:4aCO)
346	TCMM19	TCMM	15	700551	700804	700968	701028	2_nonsis		165	321	476	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
298	TCMM19	TCMM	14	235424	236810	240009	240414	2_nonsis		3200	4095	4989	2	31	1	1	0	(2:6)_(3:5)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)_(4:4bi)_(3:5a)_(4:4bi)_(4:4a)
141	TCMM19	TCMM	7	1027359	1027579	1029881	1029980	2_nonsis		2303	2462	2620	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
91	TCMM19	TCMM	5	53899	54237	57281	57855	2_nonsis		3045	3500	3955	2	32	1	1	0	(3:5)_(4:4)_(3:5)_(4:4ai)_(3:5a)_(4:4bCO)
114	TCMM19	TCMM	6	157416	157884	159955	160108	2_nonsis		2072	2382	2691	2	32	1	1	0	(5:3)_(6:2)_(4:4)_(6:2)_(4:4)_(5:3a)_(4:4aCO)
163	TCMM19	TCMM	8	326640	326679	329295	329634	2_nonsis		2617	2805	2993	2	32	1	1	0	(2:6)_(3:5)_(2:6)_(3:5a)_(4:4aCO)_(2:6)_(3:5a)_(4:4a)
76	TCMM19	TCMM	4	1045146	1045482	1062037	1062818	2_nonsis		16556	17114	17671	2	32	1	1	0	(5:3)_(4:4)_(4:4ai)_(5:3a)_(4:4bCO)_(5:3a)_(6:2)_(5:3a)_(6:2)_(5:3)_(6:2)_(4:4b)
52	TCMM19	TCMM	4	46608	46818	47365	47467	2_nonsis		548	703	858	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
280	TCMM19	TCMM	13	715257	715590	716317	716783	2_nonsis		728	1127	1525	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
170	TCMM19	TCMM	8	460801	461318	463473	463665	2_nonsis		2156	2510	2863	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
50	TCMM19	TCMM	3	266002	266699	267793	267916	2_nonsis		1095	1504	1913	3	20	1	1	0	(2:6)_(5:3)_(3:5)_(4:4aCO)
268	TCMM19	TCMM	13	111909	112670	113641	114304	2_nonsis		972	1683	2394	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(4:4aCO)
350	TCMM19	TCMM	15	745265	745659	747125	747490	2_nonsis		1467	1846	2224	3	20	1	1	0	(3:5)_(5:3)_(5:3a)_(4:4aCO)
334	TCMM19	TCMM	15	285010	285417	287386	288164	2_nonsis		1970	2562	3153	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(4:4aCO)
249	TCMM19	TCMM	12	291386	293464	295063	295222	2_nonsis		1600	2718	3835	3	20	1	1	0	(5:3)_(4:4aCO)_(3:5)_(4:4a)
29	TCMM19	TCMM	2	489241	489580	492226	492334	2_nonsis		2647	2870	3092	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(4:4aCO)
375	TCMM19	TCMM	16	309089	309787	310159	310530	2_nonsis		373	907	1440	3	20	1	1	0	(3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)
275	TCMM19	TCMM	13	406917	407179	409194	409543	2_nonsis		2016	2321	2625	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(2:6)_(4:4aCO)
192	TCMM19	TCMM	10	53843	54311	56177	56675	2_nonsis		1867	2349	2831	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(3:5)_(4:4aCO)
112	TCMM19	TCMM	6	37552	38102	40232	40564	2_nonsis		2131	2571	3011	3	20	1	1	0	(2:6)_(3:5)_(2:6)_(6:2)_(4:4aCO)
272	TCMM19	TCMM	13	298845	300558	302628	303266	2_nonsis		2071	3246	4420	3	20	1	1	0	(6:2)_(5:3)_(3:5)_(6:2)_(4:4aCO)
55	TCMM19	TCMM	4	103533	104069	106899	107966	2_nonsis		2831	3632	4432	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
119	TCMM19	TCMM	7	75686	75728	79203	80122	2_nonsis		3476	3956	4435	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(5:3)_(4:4aCO)
67	TCMM19	TCMM	4	610896	611056	612573	612828	2_nonsis		1518	1725	1931	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
262	TCMM19	TCMM	12	769396	769555	770890	771882	2_nonsis		1336	1911	2485	3	20	1	1	0	(3:5)_(2:6)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
44	TCMM19	TCMM	3	60354	60633	62698	63052	2_nonsis		2066	2382	2697	3	20	1	1	0	(5:3)_(3:5)_(2:6)_(4:4)_(3:5)_(4:4aCO)
242	TCMM19	TCMM	11	619045	619085	621619	621733	2_nonsis		2535	2611	2687	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
92	TCMM19	TCMM	5	60891	60924	61974	62815	2_nonsis		1051	1487	1923	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)_(6:2)_(5:3)_(4:4a)
366	TCMM19	TCMM	16	53945	54119	55625	56116	2_nonsis		1507	1839	2170	3	20	1	1	0	(3:5)_(5:3)_(6:2)_(4:4)_(3:5)_(4:4)_(4:4aCO)
299	TCMM19	TCMM	14	273306	273490	275457	275934	2_nonsis		1968	2298	2627	3	20	1	1	0	(5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
359	TCMM19	TCMM	15	919749	920281	922957	923092	2_nonsis		2677	3010	3342	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
179	TCMM19	TCMM	9	87283	87642	90521	90599	2_nonsis		2880	3098	3315	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)_(6:2)_(4:4a)
86	TCMM19	TCMM	4	1406566	1406793	1410669	1411239	2_nonsis		3877	4275	4672	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)_(2:6)_(3:5)_(4:4a)
367	TCMM19	TCMM	16	132693	132838	137962	138601	2_nonsis		5125	5516	5907	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(4:4)_(3:5)_(4:4aCO)
132	TCMM19	TCMM	7	829946	829998	834267	835147	2_nonsis		4270	4735	5200	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
333	TCMM19	TCMM	15	267950	268100	272275	272573	2_nonsis		4176	4399	4622	3	20	1	1	0	(5:3)_(4:4)_(3:5)_(4:4aCO)_(3:5a)_(4:4a)_(3:5a)_(4:4a)_(3:5a)_(5:3a)_(2:6)_(4:4a)_(3:5a)_(2:6)_(3:5a)_(4:4a)
267	TCMM19	TCMM	13	20392	20497	22318	22495	2_nonsis		1822	1962	2102	3	21	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4bi)_(4:4a)_(3:5)_(4:4a)
336	TCMM19	TCMM	15	315191	315748	321368	321655	2_nonsis		5621	6042	6463	3	21	1	1	0	(3:5)_(4:4ai)_(5:3)_(4:4bCO)_(5:3)_(4:4ai)_(3:5)_(4:4ai)_(4:4b)
103	TCMM19	TCMM	5	367125	367786	372487	372822	2_nonsis		4702	5199	5696	3	21	1	1	0	(4:4ai)_(5:3)_(4:4ai)_(5:3)_(3:5)_(3:5a)_(3:5)_(4:4bCO)_(5:3a)_(4:4b)
251	TCMM19	TCMM	12	336007	336315	343120	343396	2_nonsis		6806	7097	7388	3	21	1	1	0	(5:3)_(6:2)_(5:3)_(4:4ai)_(3:5)_(3:5a)_(4:4bCO)_(5:3a)_(4:4b)_(5:3a)_(4:4b)
10	TCMM19	TCMM	1	179796	179942	182519	183881		3	2578	3331	4084	0	1	2	0	2	(2:6)_(4:4)_(5:3)_(5:3a)_(5:3)_(4:4)
12	TCMM19	TCMM	2	44210	44904	49603	49789		3	4700	5139	5578	0	1	2	0	2	(5:3)_(4:4)_(3:5)_(4:4)_(6:2)_(4:4)_(5:3a)_(3:5)_(4:4)
27	TCMM19	TCMM	2	465690	465714	465714	465795	2_sis		1	53	104	0	1	2	0	2	(6:2i)_(4:4)
61	TCMM19	TCMM	4	321785	321836	321836	321844	2_sis		1	30	58	0	1	2	0	2	(6:2i)_(4:4)
105	TCMM19	TCMM	5	409531	410181	411277	412632	2_sis		1097	2099	3100	0	1	2	0	2	(6:2)_(7:1)_(5:3)_(4:4)
107	TCMM19	TCMM	5	439285	439545	440923	441329	2_sis		1379	1711	2043	0	1	2	0	2	(5:3)_(6:2)_(4:4)
127	TCMM19	TCMM	7	634549	634898	637771	637913	2_sis		2874	3119	3363	0	1	2	0	2	(5:3)_(4:4)_(6:2)_(4:4)
161	TCMM19	TCMM	8	291336	291357	291357	291367		3	1	16	30	0	1	2	0	2	(2:6)_(4:4)
193	TCMM19	TCMM	10	59239	59484	60064	60979	2_sis		581	1160	1739	0	1	2	0	2	(3:5)_(3:5a)_(4:4)
204	TCMM19	TCMM	10	279361	279703	281056	281289	2_sis		1354	1641	1927	0	1	2	0	2	(3:5)_(4:4)_(3:5a)_(3:5)_(4:4)
208	TCMM19	TCMM	10	375038	375069	376315	376343	2_sis		1247	1276	1304	0	1	2	0	2	(2:6)_(4:4)_(3:5)_(4:4)_(3:5a)_(4:4)
237	TCMM19	TCMM	11	505564	505715	506729	506760	2_sis		1015	1105	1195	0	1	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4)
244	TCMM19	TCMM	12	21869	21957	23981	25985	2_sis		2025	3070	4115	0	1	2	0	2	(6:2)_(4:4)_(6:2)_(7:1)_(6:2)_(5:3)_(4:4)_(5:3)_(4:4)
245	TCMM19	TCMM	12	222227	222430	225447	225620	2_sis		3018	3205	3392	0	1	2	0	2	(3:5)_(4:4)_(3:5)_(2:6i)_(1:7)_(3:5a)_(4:4)
269	TCMM19	TCMM	13	168885	169412	170002	170932	2_sis		591	1319	2046	0	1	2	0	2	(3:5)_(4:4)_(3:5a)_(4:4)
284	TCMM19	TCMM	13	818603	818759	819776	819989	2_sis		1018	1202	1385	0	1	2	0	2	(3:5)_(2:6i)_(3:5)_(4:4)
297	TCMM19	TCMM	14	221673	221973	224991	225318	2_sis		3019	3332	3644	0	1	2	0	2	(3:5)_(3:5a)_(4:4)_(3:5a)_(4:4)
305	TCMM19	TCMM	14	417659	417758	418123	418195	2_sis		366	451	535	0	1	2	0	2	(2:6i)_(3:5)_(4:4)

#	Sample	Assay	Chr	Start1	Start2	End1	End2	Cat	V1	V2	V3	c0	cA	cB	cC	cD	Annotation
328	TCMM19	TCMM	15	198105	198213	199433	200443	2_sis	1221	1779	2337	0	1	2	0	2	(3:5)_(1:7)_(2:6)_(4:4)
332	TCMM19	TCMM	15	256152	256235	257554	257615	2_sis	1320	1391	1462	0	1	2	0	2	(2:6)_(0:8)_(1:7)_(3:5)_(4:4)
340	TCMM19	TCMM	15	477077	477610	478915	479565	2_sis	1306	1897	2487	0	1	2	0	2	(3:5)_(4:4)_(2:6i)_(4:4)
8	TCMM19	TCMM	1	132066	135319	144406	145634	4	9088	11328	13567	0	2	2	1	1	(6:2)_(5:3)_(3:5)_(5:3a)_(3:5)_(4:4aCO)_(3:5)_(4:4bi)_(4:4a)
21	TCMM19	TCMM	2	207220	207859	218624	219197	4	10766	11371	11976	0	2	2	1	1	(6:2)_(7:1)_(8:0)_(7:1)_(8:0)_(6:2)_(5:3)_(6:2ai)_(5:3)_(4:4ai)_(4:4bi)_(3:5)_(2:6)_(4:4ci)_(4:4dCO)
30	TCMM19	TCMM	2	497645	497990	502305	502581	3	4316	4626	4935	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
37	TCMM19	TCMM	2	662444	666712	668082	669586	3	1371	4256	7141	0	2	2	1	1	(5:3)_(4:4aCO)_(2:6)_(4:4a)
80	TCMM19	TCMM	4	1240123	1240299	1242658	1246191	3	2360	4214	6067	0	2	2	1	1	(4:4aCO)_(5:3)_(4:4a)
98	TCMM19	TCMM	5	278802	279481	284680	285018	3	5200	5708	6215	0	2	2	1	1	(3:5)_(4:4)_(5:3)_(4:4)_(4:4aCO)_(3:5a)_(4:4a)_(3:5a)_(4:4a)
104	TCMM19	TCMM	5	377471	377999	379332	379879	3	1334	1871	2407	0	2	2	1	1	(6:2)_(5:3)_(4:4aCO)
110	TCMM19	TCMM	5	504481	505113	511509	511800	3	6397	6858	7318	0	2	2	1	1	(6:2)_(4:4)_(3:5)_(2:6)_(3:5)_(2:6ai)_(3:5a)_(6:2)_(5:3)_(4:4aCO)
124	TCMM19	TCMM	7	458458	458629	463348	463843	3	4720	5052	5384	0	2	2	1	1	(5:3)_(4:4)_(3:5)_(4:4)_(2:6)_(4:4)_(4:4aCO)_(3:5a)_(4:4a)
135	TCMM19	TCMM	7	904221	904249	906758	906845	3	2510	2567	2623	0	2	2	1	1	(3:5)_(3:5a)_(4:4ai)_(2:6)_(5:3)_(4:4ai)_(5:3a)_(3:5a)_(2:6)_(4:4bCO)
136	TCMM19	TCMM	7	914538	914816	915939	916059	4	1124	1322	1520	0	2	2	2	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
147	TCMM19	TCMM	8	23857	23964	27080	27293	3	3117	3276	3435	0	2	2	1	1	(5:3)_(4:4aCO)_(7:1)_(8:0)_(5:3a)_(4:4a)
148	TCMM19	TCMM	8	33397	33844	36592	36778	3	2749	3065	3380	0	2	2	1	1	(3:5)_(4:4)_(2:6)_(4:4)_(1:7)_(2:6ai)_(3:5a)_(5:3)_(4:4aCO)
149	TCMM19	TCMM	8	67460	67629	70434	70542	3	2806	2944	3081	0	2	2	1	1	(2:6)_(3:5)_(4:4)_(2:6a)_(4:4aCO)_(2:6a)_(4:4a)
173	TCMM19	TCMM	8	518458	518620	522909	523061	3	4290	4446	4602	0	2	2	1	1	(3:5)_(4:4)_(3:5)_(4:4)_(2:6)_(0:8)_(1:7)_(2:6a)_(4:4aCO)_(3:5a)_(4:4a)_(3:5a)_(4:4a)
190	TCMM19	TCMM	9	396557	396639	398583	398957	3	1945	2172	2399	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3a)_(4:4)_(6:2a)_(4:4aCO)
202	TCMM19	TCMM	10	235976	236393	236615	236901	3	223	574	924	0	2	2	1	1	(2:6i)_(4:4aCO)
207	TCMM19	TCMM	10	358755	359101	366482	366671	3	7382	7649	7915	0	2	2	1	1	(3:5)_(4:4)_(4:4ai)_(5:3)_(6:2)_(5:3a)_(3:5a)_(5:3a)_(3:5a)_(4:4bCO)
235	TCMM19	TCMM	11	475733	475940	479195	479521	3	3256	3522	3787	0	2	2	1	1	(5:3)_(4:4ai)_(5:3)_(4:4ai)_(3:5)_(2:6)_(3:5a)_(4:4bCO)
282	TCMM19	TCMM	13	795326	795946	798889	799519	3	2944	3568	4192	0	2	2	1	1	(2:6)_(3:5)_(5:3)_(6:2)_(5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(5:3a)_(3:5)_(4:4a)
339	TCMM19	TCMM	15	432006	433358	433558	434027	3	1	1011	2020	0	2	2	1	1	(5:3)_(4:4aCO)
345	TCMM19	TCMM	15	650943	651516	658010	658322	3	6495	6937	7378	0	2	2	1	1	(6:2)_(4:4)_(5:3)_(4:4ai)_(6:2ai)_(7:1)_(6:2b)_(5:3a)_(4:4bCO)
356	TCMM19	TCMM	15	822183	823421	826212	826624	3	2792	3616	4440	0	2	2	1	1	(4:4ai)_(5:3)_(3:5)_(4:4bCO)
373	TCMM19	TCMM	16	276934	277322	278394	278872	3	1073	1505	1937	0	2	2	1	1	(6:2)_(4:4)_(6:2a)_(5:3)_(4:4aCO)
386	TCMM19	TCMM	16	496835	497162	502118	503157	4	4957	5639	6321	0	2	2	1	1	(3:5)_(4:4)_(2:6)_(0:8)_(1:7)_(2:6a)_(3:5a)_(5:3)_(2:6b)_(2:6ci)_(3:5b)_(2:6b)_(4:4aCO)
388	TCMM19	TCMM	16	636736	638483	640119	640589	3	1637	2745	3852	0	2	2	1	1	(3:5)_(5:3)_(3:5a)_(4:4ai)_(4:4bCO)
1	TCMM19	TCMM	1	32989	33040	45198	45831	4	12159	12500	12841	0	3	2	2	0	(3:5)_(2:6)_(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)_(5:3)_(6:2i)_(5:3)_(3:5a)_(4:4bCO)
6	TCMM19	TCMM	1	103577	103866	112136	113132	3	8271	8913	9554	0	3	2	1	1	(5:3)_(6:2)_(5:3a)_(5:3b)_(4:4aCO)_(4:4CO)_(5:3)_(5:3c)_(4:4bCO)
19	TCMM19	TCMM	2	157617	158200	160020	160143	3	1821	2173	2525	0	3	2	1	1	(4:4aCO)_(5:3)_(4:4a)_(3:5)_(2:6)_(3:5a)_(4:4bCO)
28	TCMM19	TCMM	2	474402	475397	476602	476950	2_nonsis	1206	1877	2547	0	3	2	0	2	(6:2)_(4:4aCO)_(2:6)_(4:4CO)
40	TCMM19	TCMM	2	742220	742472	745298	745349	3	2827	2978	3128	0	3	2	0	2	(3:5)_(2:6)_(4:4)_(2:6a)_(4:4aCO)_(3:5a)_(4:4CO)
181	TCMM19	TCMM	9	111631	111711	115136	115941	3	3426	3868	4309	0	3	2	1	1	(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4bCO)
184	TCMM19	TCMM	9	159685	160007	168511	169256	3	8505	9038	9570	0	3	2	1	1	(6:2)_(4:4)_(5:3)_(5:3a)_(5:3)_(6:2a)_(5:3)_(4:4)_(4:4aCO)_(3:5)_(4:4a)_(2:6)_(4:4CO)_(2:6)_(5:3b)_(4:4bCO)
195	TCMM19	TCMM	10	89273	90197	98106	99116	3	7910	8876	9842	0	3	2	1	1	(3:5)_(4:4aCO)_(2:6)_(3:5a)_(4:4bCO)_(3:5a)_(2:6)_(3:5a)_(4:4b)
238	TCMM19	TCMM	11	525008	525421	527534	527598	4	2114	2352	2589	0	3	2	2	0	(6:2)_(5:3)_(4:4aCO)_(3:5)_(5:3a)_(4:4bCO)
274	TCMM19	TCMM	13	396864	397127	398818	398916	2_nonsis	1692	1872	2051	0	3	2	0	2	(2:6)_(3:5)_(4:4aCO)_(5:3)_(6:2)_(4:4CO)
320	TCMM19	TCMM	14	743441	743682	745944	746165	2_nonsis	2263	2493	2723	0	3	2	0	2	(3:5)_(4:4aCO)_(2:6)_(3:5)_(4:4bi)_(3:5)_(4:4bi)_(3:5a)_(2:6)_(4:4CO)
393	TCMM19	TCMM	16	880945	881165	881834	882467	2_nonsis	670	1096	1521	0	3	2	0	2	(4:4aCO)_(2:6)_(6:2)_(4:4CO)
515	TCMM19	TCMM	7	9430	9885	12326	12853	NA	2442	2932	3422	0	4	1	NA	NA	4:4_3:5_4:4
88	TCMM4	TCMM	7	778013	778064	778064	778073	1	1	30	59	1	1	1	1	1	05:03
79	TCMM4	TCMM	7	140207	140223	140227	140416	1	5	107	208	1	1	1	0	1	05:03
58	TCMM4	TCMM	4	1412352	1412444	1412444	1412726	1	1	187	373	1	1	1	0	1	05:03
163	TCMM4	TCMM	13	807655	807742	807924	807956	1	183	242	300	1	1	1	0	1	05:03
157	TCMM4	TCMM	13	451375	451502	451502	451971	1	1	298	595	1	1	1	0	1	05:03
39	TCMM4	TCMM	4	550699	550893	550893	551387	1	1	344	687	1	1	1	0	1	05:03
188	TCMM4	TCMM	15	522252	522596	522596	523000	1	1	374	747	1	1	1	0	1	05:03
174	TCMM4	TCMM	14	487880	487935	487991	488587	1	57	382	706	1	1	1	0	1	05:03
17	TCMM4	TCMM	2	649588	649927	649927	650411	1	1	412	822	1	1	1	0	1	05:03
110	TCMM4	TCMM	10	323078	323243	323333	323823	1	91	418	744	1	1	1	0	1	05:03
112	TCMM4	TCMM	10	359859	360186	360316	360588	1	131	430	728	1	1	1	0	1	05:03
71	TCMM4	TCMM	6	41791	42233	42346	42943	1	114	633	1151	1	1	1	0	1	05:03
211	TCMM4	TCMM	16	871620	871663	871860	872872	1	198	725	1251	1	1	1	0	1	05:03
205	TCMM4	TCMM	16	501709	502118	502118	503192	1	1	742	1482	1	1	1	0	1	05:03
31	TCMM4	TCMM	3	191932	192715	193107	193600	1	393	1030	1667	1	1	1	0	1	05:03
111	TCMM4	TCMM	10	330470	331024	331024	332595	1	1	1063	2124	1	1	1	0	1	05:03
55	TCMM4	TCMM	4	1288209	1288775	1289490	1289885	1	716	1196	1675	1	1	1	0	1	05:03
42	TCMM4	TCMM	4	769508	769848	770770	771211	1	923	1313	1702	1	1	1	0	1	05:03

5	TCMM4	TCMM	1	113326	114283	114824	115629	1	542	1422	2302	1	1	1	0	1	05:03
33	TCMM4	TCMM	3	243219	246581	246581	246789	1	1	1785	3569	1	1	1	0	1	05:03
176	TCMM4	TCMM	14	525271	525274	525274	525277	1	1	3	5	1	2	1	0	1	03:05
34	TCMM4	TCMM	4	21075	21083	21083	21086	1	1	6	10	1	2	1	0	1	03:05
129	TCMM4	TCMM	11	267712	267738	267738	267822	1	1	55	109	1	2	1	0	1	03:05
29	TCMM4	TCMM	3	148041	148135	148135	148171	1	1	65	129	1	2	1	0	1	03:05
90	TCMM4	TCMM	7	897158	897290	897290	897315	1	1	79	156	1	2	1	0	1	03:05
96	TCMM4	TCMM	9	102536	102597	102597	102706	1	1	85	169	1	2	1	0	1	03:05
38	TCMM4	TCMM	4	240005	240165	240165	240185	1	1	90	179	1	2	1	0	1	03:05
22	TCMM4	TCMM	2	787620	787638	787638	787803	1	1	92	182	1	2	1	0	1	03:05
115	TCMM4	TCMM	10	459643	459858	459858	459864	1	1	111	220	1	2	1	0	1	03:05
210	TCMM4	TCMM	16	769908	770049	770049	770162	1	1	127	253	1	2	1	0	1	03:05
60	TCMM4	TCMM	4	1429855	1430016	1430016	1430118	1	1	132	262	1	2	1	0	1	03:05
12	TCMM4	TCMM	2	460270	460340	460385	460520	1	46	148	249	1	2	1	0	1	03:05
103	TCMM4	TCMM	10	147613	147905	147905	147927	1	1	157	313	1	2	1	0	1	03:05
133	TCMM4	TCMM	11	565671	565988	565988	566023	1	1	176	351	1	2	1	0	1	03:05
126	TCMM4	TCMM	11	83795	84171	84171	84187	1	1	196	391	1	2	1	0	1	03:05
16	TCMM4	TCMM	2	564884	565189	565189	565389	1	1	253	504	1	2	1	0	1	03:05
185	TCMM4	TCMM	15	467407	467641	467641	467927	1	1	260	519	1	2	1	0	1	03:05
168	TCMM4	TCMM	14	154539	154853	154853	155065	1	1	263	525	1	2	1	0	1	03:05
140	TCMM4	TCMM	12	278673	278823	278861	279188	1	39	277	514	1	2	1	0	1	03:05
134	TCMM4	TCMM	11	575852	576492	576492	576495	1	1	322	642	1	2	1	0	1	03:05
183	TCMM4	TCMM	15	271388	271422	271727	271758	1	306	338	369	1	2	1	0	1	03:05
21	TCMM4	TCMM	2	744063	744356	744519	744640	1	164	370	576	1	2	1	0	1	03:05
26	TCMM4	TCMM	3	77900	78844	79012	79096	1	169	682	1195	1	2	1	0	1	03:05
171	TCMM4	TCMM	14	433271	434561	434561	435509	1	1	1119	2237	1	2	1	0	1	03:05
178	TCMM4	TCMM	14	772480	776872	776872	776904	1	1	2212	4423	1	2	1	0	1	03:05
137	TCMM4	TCMM	11	594186	594303	597106	597150	1	2804	2884	2963	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
124	TCMM4	TCMM	10	704426	704499	705014	705235	1	516	662	808	1	4	1	0	1	3:5_2:6_3:5
158	TCMM4	TCMM	13	601760	603029	603221	603486	1	193	959	1725	1	4	1	0	1	3:5_2:6_3:5
3	TCMM4	TCMM	1	47206	47518	48286	48591	1	769	1077	1384	1	4	1	0	1	3:5_2:6_3:5
135	TCMM4	TCMM	11	580815	581385	582336	582622	1	952	1379	1806	1	4	1	0	1	3:5_2:6_3:5_4:4_3:5
152	TCMM4	TCMM	13	286996	287260	287338	287411	1	79	247	414	1	7	1	0	1	6:2_5:3
77	TCMM4	TCMM	6	238279	238329	238462	238877	1	134	366	597	1	7	1	0	1	6:2_5:3
204	TCMM4	TCMM	16	492354	493222	493304	493377	1	83	553	1022	1	7	1	0	1	5:3_6:2
109	TCMM4	TCMM	10	313030	313808	313986	314624	1	179	886	1593	1	7	1	0	1	5:3_6:2
206	TCMM4	TCMM	16	525308	525445	526263	526602	1	819	1056	1293	1	7	1	0	1	6:2_5:3_6:2
92	TCMM4	TCMM	7	911599	911857	913222	913982	1	1366	1874	2382	1	7	1	0	1	6:2_5:3_6:2
18	TCMM4	TCMM	2	679385	680726	681557	682449	1	832	1948	3063	1	7	1	0	1	6:2_4:4_5:3
156	TCMM4	TCMM	13	405840	406116	408001	408347	1	1886	2196	2506	1	7	1	0	1	6:2_5:3_6:2
122	TCMM4	TCMM	10	646775	646861	648638	649585	1	1778	2294	2809	1	7	1	0	1	6:2_4:4_6:2
40	TCMM4	TCMM	4	555346	555365	557710	557899	1	2346	2449	2552	1	7	1	0	1	6:2_4:4_5:3
97	TCMM4	TCMM	9	171578	171632	172074	172693	1	443	779	1114	1	7	1	0	1	5:3_6:2_4:4_6:2
14	TCMM4	TCMM	2	525492	525674	526931	527102	1	1258	1434	1609	1	7	1	0	1	5:3_6:2_5:3_6:2
173	TCMM4	TCMM	14	479932	480082	481081	481350	1	1000	1209	1417	1	7	1	0	1	5:3_6:2_5:3_6:2_5:3_6:2
141	TCMM4	TCMM	12	504004	504031	504236	504665	1	206	433	660	1	8	1	0	1	3:5_2:6
166	TCMM4	TCMM	14	116131	116459	116678	116796	1	220	442	664	1	8	1	0	1	3:5_2:6
106	TCMM4	TCMM	10	195849	195964	196239	196517	1	276	472	667	1	8	1	0	1	2:6_3:5
153	TCMM4	TCMM	13	336381	336424	336845	337176	1	422	608	794	1	8	1	0	1	2:6_3:5
102	TCMM4	TCMM	10	143678	144558	144800	145019	1	243	792	1340	1	8	1	0	1	3:5_2:6
82	TCMM4	TCMM	7	433416	433556	433865	434126	1	310	510	709	1	8	1	0	1	2:6_4:4_3:5
130	TCMM4	TCMM	11	327663	327707	328373	328613	1	667	808	949	1	8	1	0	1	2:6_4:4_3:5
132	TCMM4	TCMM	11	492262	493124	495036	495081	1	1913	2366	2818	1	8	1	0	1	3:5_4:4_2:6
145	TCMM4	TCMM	12	721788	721983	724901	725366	1	2919	3248	3577	1	8	1	0	1	2:6_3:5_2:6
91	TCMM4	TCMM	7	904347	904567	908162	908324	1	3596	3786	3976	1	8	1	0	1	2:6_4:4_2:6
70	TCMM4	TCMM	6	16574	16654	16824	17029	1	171	313	454	1	8	1	0	1	3:5_2:6_3:5_2:6
155	TCMM4	TCMM	13	355271	355413	356149	356409	1	737	937	1137	1	8	1	0	1	2:6_3:5_2:6_3:5
208	TCMM4	TCMM	16	656563	656605	659469	660498	1	2865	3400	3934	1	8	1	0	1	2:6_4:4_3:5_4:4_2:6
52	TCMM4	TCMM	4	1198548	1199289	1206115	1206306	1	6827	7292	7757	1	8	1	0	1	2:6_3:5_2:6_3:5_2:6
197	TCMM4	TCMM	16	63198	63205	63205	63234	1	1	18	35	1	10	1	0	1	06:02

1	TCMM4	TCMM	1	32989	33040	33048	33070		1	9	45	80	1	10	1	0	1 06:02
47	TCMM4	TCMM	4	1056079	1056232	1056242	1056383		1	11	157	303	1	10	1	0	1 06:02
98	TCMM4	TCMM	9	215993	216106	216122	216326		1	17	175	332	1	10	1	0	1 06:02
9	TCMM4	TCMM	2	338226	338408	338408	338664		1	1	219	437	1	10	1	0	1 06:02
180	TCMM4	TCMM	15	153615	153774	153774	154056		1	1	221	440	1	10	1	0	1 06:02
203	TCMM4	TCMM	16	431492	431631	431787	431837		1	157	251	344	1	10	1	0	1 06:02
186	TCMM4	TCMM	15	480909	481143	481143	481447		1	1	269	537	1	10	1	0	1 06:02
101	TCMM4	TCMM	10	21371	21499	21670	21758		1	172	279	386	1	10	1	0	1 06:02
53	TCMM4	TCMM	4	1266546	1266696	1266696	1267153		1	1	304	606	1	10	1	0	1 06:02
117	TCMM4	TCMM	10	523373	523995	523995	524003		1	1	315	629	1	10	1	0	1 06:02
63	TCMM4	TCMM	5	67575	67809	67809	68268		1	1	347	692	1	10	1	0	1 06:02
170	TCMM4	TCMM	14	350057	350461	350601	350676		1	141	380	618	1	10	1	0	1 06:02
119	TCMM4	TCMM	10	579770	580075	580119	580576		1	45	425	805	1	10	1	0	1 06:02
66	TCMM4	TCMM	5	301647	302478	302478	302509		1	1	431	861	1	10	1	0	1 06:02
107	TCMM4	TCMM	10	236674	236901	237213	237403		1	313	521	728	1	10	1	0	1 06:02
64	TCMM4	TCMM	5	85693	86861	86861	86888		1	1	598	1194	1	10	1	0	1 06:02
7	TCMM4	TCMM	1	129075	129476	129517	130254		1	42	610	1178	1	10	1	0	1 06:02
182	TCMM4	TCMM	15	268456	269276	269497	269591		1	222	678	1134	1	10	1	0	1 06:02
43	TCMM4	TCMM	4	830619	830754	831259	831876		1	506	881	1256	1	10	1	0	1 06:02
69	TCMM4	TCMM	5	516553	516748	517321	517944		1	574	982	1390	1	10	1	0	1 06:02
121	TCMM4	TCMM	10	636506	637056	637795	637967		1	740	1100	1460	1	10	1	0	1 06:02
125	TCMM4	TCMM	11	80353	80724	81532	82469		1	809	1462	2115	1	10	1	0	1 06:02
138	TCMM4	TCMM	12	94920	97490	97654	98431		1	165	1838	3510	1	10	1	0	1 06:02
199	TCMM4	TCMM	16	187312	187324	187324	187327		1	1	8	14	1	10.1	1	0	1 02:06
93	TCMM4	TCMM	7	939184	939208	939212	939290		1	5	55	105	1	10.1	1	0	1 02:06
144	TCMM4	TCMM	12	677763	677815	677815	677890		1	1	64	126	1	10.1	1	0	1 02:06
202	TCMM4	TCMM	16	359989	360040	360040	360123		1	1	67	133	1	10.1	1	0	1 02:06
212	TCMM4	TCMM	16	899969	900008	900042	900148		1	35	107	178	1	10.1	1	0	1 02:06
76	TCMM4	TCMM	6	205702	205793	205793	205932		1	1	115	229	1	10.1	1	0	1 02:06
73	TCMM4	TCMM	6	97372	97617	97617	97630		1	1	129	257	1	10.1	1	0	1 02:06
160	TCMM4	TCMM	13	661764	661888	661888	662059		1	1	148	294	1	10.1	1	0	1 02:06
67	TCMM4	TCMM	5	327059	327079	327079	327363		1	1	152	303	1	10.1	1	0	1 02:06
150	TCMM4	TCMM	13	177865	178128	178203	178325		1	76	268	459	1	10.1	1	0	1 02:06
94	TCMM4	TCMM	7	958623	958930	958955	959157		1	26	280	533	1	10.1	1	0	1 02:06
87	TCMM4	TCMM	7	650278	650477	650623	650709		1	147	289	430	1	10.1	1	0	1 02:06
68	TCMM4	TCMM	5	342057	342537	342537	342667		1	1	305	609	1	10.1	1	0	1 02:06
189	TCMM4	TCMM	15	586076	586304	586345	586852		1	42	409	775	1	10.1	1	0	1 02:06
179	TCMM4	TCMM	15	93175	93845	93845	94096		1	1	461	920	1	10.1	1	0	1 02:06
20	TCMM4	TCMM	2	740518	740972	741197	741235		1	226	471	716	1	10.1	1	0	1 02:06
148	TCMM4	TCMM	12	989846	990344	990547	990749		1	204	553	902	1	10.1	1	0	1 02:06
25	TCMM4	TCMM	3	73479	74002	74202	74394		1	201	558	914	1	10.1	1	0	1 02:06
4	TCMM4	TCMM	1	61164	61414	61708	61999		1	295	565	834	1	10.1	1	0	1 02:06
190	TCMM4	TCMM	15	605119	606232	606232	606336		1	1	609	1216	1	10.1	1	0	1 02:06
146	TCMM4	TCMM	12	809313	809749	809989	810333		1	241	630	1019	1	10.1	1	0	1 02:06
207	TCMM4	TCMM	16	533457	533820	534401	534572		1	582	848	1114	1	10.1	1	0	1 02:06
35	TCMM4	TCMM	4	163031	163327	163967	164298		1	641	954	1266	1	10.1	1	0	1 02:06
143	TCMM4	TCMM	12	624838	627007	627007	627201		1	1	1182	2362	1	10.1	1	0	1 02:06
61	TCMM4	TCMM	5	18839	18992	18992	23192		1	1	2177	4352	1	10.1	1	0	1 02:06
56	TCMM4	TCMM	4	1341826	1342306	1345379	1345632		1	3074	3440	3805	1	10.1	1	0	1 02:06
100	TCMM4	TCMM	9	388227	388673	388673	389156	2_nonsis	1	465	928	3	30	1	0	1 05:03
78	TCMM4	TCMM	7	10242	11635	11737	12020	2_nonsis	103	940	1777	3	30	1	0	1 3:5_5:3
128	TCMM4	TCMM	11	244570	245116	245907	246807	2_nonsis	792	1514	2236	3	30	1	0	1 3:5_5:3
51	TCMM4	TCMM	4	1126921	1127082	1127836	1127919	2_nonsis	755	876	997	3	30	1	0	1 6:2_5:3_6:2
45	TCMM4	TCMM	4	888734	889358	890461	890830	2_nonsis	1104	1600	2095	3	30	1	0	1 2:6_3:5_5:3
120	TCMM4	TCMM	10	631130	632972	633743	634423	2_nonsis	772	2032	3292	3	30	1	0	1 2:6_4:4_6:2
191	TCMM4	TCMM	15	608818	608958	609836	609993	2_nonsis	879	1027	1174	3	30	1	0	1 3:5_2:6_4:4_2:6
159	TCMM4	TCMM	13	624027	624297	627290	627607	2_nonsis	2994	3287	3579	3	30	1	0	1 5:3_4:4_5:3_5:3a_6:2
23	TCMM4	TCMM	3	41571	41852	43618	43868	2_nonsis	1767	2032	2296	3	31	1	0	1 5:3_4:4_6:2_4:4_6:2_5:3a_4:4ai
167	TCMM4	TCMM	14	117901	118803	118803	119174	2_nonsis	1	637	1272	1	1	1	1	0 (5:3)_(4:4aCO)
200	TCMM4	TCMM	16	222957	224069	224069	224707	2_nonsis	1	875	1749	1	1	1	1	0 (5:3)_(4:4aCO)

65	TCMM4	TCMM	5	213929	214752	214752	215059	2_nonsis	1	565	1129	1	2	1	1	0	(3:5)_(4:4aCO)
19	TCMM4	TCMM	2	695479	697455	697503	698250	2_nonsis	49	1410	2770	1	2	1	1	0	(3:5)_(4:4aCO)
89	TCMM4	TCMM	7	784625	785199	785318	785851	2_nonsis	120	673	1225	1	3	1	1	0	(5:3)_(4:4)_(4:4aCO)
48	TCMM4	TCMM	4	1057601	1058554	1059396	1059445	2_nonsis	843	1343	1843	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
99	TCMM4	TCMM	9	332503	333073	335079	336156	2_nonsis	2007	2830	3652	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
108	TCMM4	TCMM	10	291106	291152	291438	291807	2_nonsis	287	494	700	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
74	TCMM4	TCMM	6	183406	183476	183881	184083	2_nonsis	406	541	676	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
194	TCMM4	TCMM	15	843195	843305	846762	846878	2_nonsis	3458	3570	3682	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
41	TCMM4	TCMM	4	698508	698668	699938	700023	2_nonsis	1271	1393	1514	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
59	TCMM4	TCMM	4	1419261	1419516	1420794	1420932	2_nonsis	1279	1475	1670	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
127	TCMM4	TCMM	11	93041	93302	94945	95374	2_nonsis	1644	1988	2332	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
81	TCMM4	TCMM	7	426969	427020	428940	429278	2_nonsis	1921	2115	2308	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
10	TCMM4	TCMM	2	345288	346363	347935	348121	2_nonsis	1573	2203	2832	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
192	TCMM4	TCMM	15	619647	619861	620962	621636	2_nonsis	1102	1545	1988	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(4:4aCO)
195	TCMM4	TCMM	15	967263	967506	969660	969713	2_nonsis	2155	2302	2449	1	12	1	1	0	(2:6)_(3:5)_(4:4)_(6:2)_(3:5)_(4:4aCO)
50	TCMM4	TCMM	4	1103339	1103455	1106292	1106884	2_nonsis	2838	3191	3544	1	12	1	1	0	(6:2)_(5:3)_(4:4)_(4:4aCO)
113	TCMM4	TCMM	10	380369	380706	383067	383417	2_nonsis	2362	2705	3047	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(4:4aCO)
151	TCMM4	TCMM	13	190186	190411	193159	194053	2_nonsis	2749	3308	3866	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(4:4)_(2:6)_(4:4aCO)
201	TCMM4	TCMM	16	286979	287057	287130	287198	2_nonsis	74	146	218	1	15	1	1	0	(6:2)_(4:4aCO)
72	TCMM4	TCMM	6	93077	93192	93404	93664	2_nonsis	213	400	586	1	15	1	1	0	(6:2)_(4:4aCO)
175	TCMM4	TCMM	14	502322	503261	503261	503609	2_nonsis	1	644	1286	1	15	1	1	0	(6:2)_(4:4aCO)
184	TCMM4	TCMM	15	274382	274550	275191	275863	2_nonsis	642	1061	1480	1	15	1	1	0	(6:2)_(4:4aCO)
161	TCMM4	TCMM	13	682560	683622	683958	685502	2_nonsis	337	1639	2941	1	15	1	1	0	(6:2)_(4:4aCO)
32	TCMM4	TCMM	3	198539	201185	201258	202229	2_nonsis	74	1882	3689	1	15	1	1	0	(6:2)_(4:4aCO)
104	TCMM4	TCMM	10	150493	150662	161596	162223	2_nonsis	10935	11332	11729	1	15	1	1	0	(6:2)_(4:4aCO)
84	TCMM4	TCMM	7	533747	533847	533847	533952	2_nonsis	1	103	204	1	16	1	1	0	(2:6)_(4:4aCO)
131	TCMM4	TCMM	11	457094	457349	457446	457465	2_nonsis	98	234	370	1	16	1	1	0	(2:6)_(4:4aCO)
198	TCMM4	TCMM	16	163301	163406	163478	163732	2_nonsis	73	252	430	1	16	1	1	0	(2:6)_(4:4aCO)
8	TCMM4	TCMM	1	180161	180219	180509	180583	2_nonsis	291	356	421	1	16	1	1	0	(2:6)_(4:4aCO)
46	TCMM4	TCMM	4	955335	955435	955686	956552	2_nonsis	252	734	1216	1	16	1	1	0	(2:6)_(4:4aCO)
139	TCMM4	TCMM	12	233075	234128	234378	234633	2_nonsis	251	904	1557	1	16	1	1	0	(2:6)_(4:4aCO)
57	TCMM4	TCMM	4	1382859	1383592	1385846	1385858	2_nonsis	2255	2627	2998	1	16	1	1	0	(2:6)_(4:4aCO)
2	TCMM4	TCMM	1	38120	38361	38120	38361	2_nonsis	0	120	240	1	100	1	1	0	(4:4aCO)
187	TCMM4	TCMM	15	482608	483090	482608	483090	2_nonsis	0	241	481	1	100	1	1	0	(4:4aCO)
6	TCMM4	TCMM	1	116905	117399	116905	117399	2_nonsis	0	247	493	1	100	1	1	0	(4:4aCO)
13	TCMM4	TCMM	2	491476	492001	491476	492001	2_nonsis	0	262	524	1	100	1	1	0	(4:4aCO)
28	TCMM4	TCMM	3	101597	102360	101597	102360	2_nonsis	0	381	762	1	100	1	1	0	(4:4aCO)
136	TCMM4	TCMM	11	590994	592577	590994	592577	2_nonsis	0	791	1582	1	100	1	1	0	(4:4aCO)
37	TCMM4	TCMM	4	173074	174736	173074	174736	2_nonsis	0	831	1661	1	100	1	1	0	(4:4aCO)
116	TCMM4	TCMM	10	467589	469453	467589	469453	2_nonsis	0	932	1863	1	100	1	1	0	(4:4aCO)
147	TCMM4	TCMM	12	811301	813365	811301	813365	2_nonsis	0	1032	2063	1	100	1	1	0	(4:4aCO)
165	TCMM4	TCMM	14	32426	34569	32426	34569	2_nonsis	0	1071	2142	1	100	1	1	0	(4:4aCO)
177	TCMM4	TCMM	14	682580	686654	682580	686654	2_nonsis	0	2037	4073	1	100	1	1	0	(4:4aCO)
105	TCMM4	TCMM	10	171357	171829	173479	173515	2_nonsis	1651	1904	2157	2	30	1	1	0	(5:3)_(5:3a)_(6:2)_(4:4aCO)
196	TCMM4	TCMM	15	986894	986977	989301	991111	2_nonsis	2325	3271	4216	2	30	1	1	0	(5:3)_(5:3a)_(4:4)_(5:3a)_(4:4)_(4:4aCO)
193	TCMM4	TCMM	15	660805	661531	661971	662027	2_nonsis	441	831	1221	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
172	TCMM4	TCMM	14	449114	449640	452892	453029	2_nonsis	3253	3584	3914	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
49	TCMM4	TCMM	4	1090283	1090578	1091591	1091826	2_nonsis	1014	1278	1542	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
36	TCMM4	TCMM	4	167826	170953	171817	172830	2_nonsis	865	2934	5003	3	20	1	1	0	(5:3)_(2:6)_(4:4aCO)
181	TCMM4	TCMM	15	206545	206718	207320	207397	2_nonsis	603	727	851	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
95	TCMM4	TCMM	7	1041395	1041814	1043244	1043695	2_nonsis	1431	1865	2299	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(4:4aCO)
11	TCMM4	TCMM	2	406787	407477	411233	411750	2_nonsis	3757	4360	4962	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
209	TCMM4	TCMM	16	663321	663543	664160	664567	2_nonsis	618	932	1245	3	20	1	1	0	(5:3)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
86	TCMM4	TCMM	7	642373	642480	644388	645493	2_nonsis	1909	2514	3119	3	20	1	1	0	(5:3)_(6:2)_(4:4)_(2:6)_(4:4aCO)
54	TCMM4	TCMM	4	1275069	1275148	1278056	1278456	2_nonsis	2909	3148	3386	3	20	1	1	0	(3:5)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
30	TCMM4	TCMM	3	171207	174943	179122	180127	2_nonsis	4180	6550	8919	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(5:3)_(4:4aCO)
62	TCMM4	TCMM	5	26549	26594	33348	34050	2_nonsis	6755	7128	7500	3	20	1	1	0	(6:2)_(5:3)_(6:2)_(4:4)_(5:3)_(5:3a)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
75	TCMM4	TCMM	6	191945	192279	193039	193175	2_sis	761	995	1229	0	1	2	0	2	(6:2)_(4:4)_(5:3)_(4:4)
85	TCMM4	TCMM	7	611358	611515	611515	612267	2_sis	1	455	908	0	1	2	0	2	(6:2i)_(4:4)
118	TCMM4	TCMM	10	524618	526730	527538	528639	2_sis	809	2415	4020	0	1	2	0	2	(3:5)_(2:6)_(4:4)

142	TCMM4	TCMM	12	507075	507492	507531	508294	3	40	629	1218	0	1	2	0	2	(2:6i)_(5:3)_(4:4)
44	TCMM4	TCMM	4	842070	842326	845136	845227	3	2811	2984	3156	0	2	2	1	1	(2:6)_(4:4)_(2:6)_(6:2)_(4:4aCO)_(2:6a)_(4:4a)
83	TCMM4	TCMM	7	448887	449525	452589	452990	3	3065	3584	4102	0	2	2	1	1	(3:5)_(2:6)_(4:4)_(3:5)_(5:3)_(6:2)_(4:4aCO)
154	TCMM4	TCMM	13	340906	341020	343482	343909	3	2463	2733	3002	0	2	2	1	1	(2:6)_(4:4)_(3:5)_(6:2)_(5:3)_(6:2)_(4:4aCO)
162	TCMM4	TCMM	13	741880	742214	747492	747874	3	5279	5636	5993	0	2	2	1	1	(2:6)_(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(2:6)_(4:4a)
169	TCMM4	TCMM	14	288198	288680	289457	289633	3	778	1106	1434	0	2	2	1	1	(6:2)_(8:0)_(4:4aCO)_(5:3)_(4:4a)
15	TCMM4	TCMM	2	554757	555319	556857	557651	2_nonsis	1539	2216	2893	0	3	2	0	2	(2:6)_(4:4)_(4:4aCO)_(5:3)_(4:4CO)
80	TCMM4	TCMM	7	195912	196275	199024	199690	4	2750	3264	3777	0	3	2	0	2	(4:4aCO)_(3:5)_(4:4a)_(2:6)_(1:7)_(2:6)_(4:4CO)_(2:6ai)_(3:5a)_(4:4bCO)
114	TCMM4	TCMM	10	391693	392346	394217	394408	3	1872	2293	2714	0	3	2	0	2	(4:4aCO)_(3:5)_(4:4bCO)_(3:5)_(4:4b)
123	TCMM4	TCMM	10	666742	667389	667686	667942	2_nonsis	298	749	1199	0	3	2	0	2	(4:4aCO)_(5:3)_(3:5)_(4:4CO)
149	TCMM4	TCMM	13	69113	70292	70356	71137	2_nonsis	65	1044	2023	0	3	2	0	2	(4:4aCO)_(4:4CO)
164	TCMM4	TCMM	13	851409	851822	855302	855635	3	3481	3853	4225	0	3	2	2	0	(4:4aCO)_(6:2)_(4:4a)_(3:5)_(3:5a)_(3:5)_(3:5a)_(4:4bCO)
67	TCMM8	TCMM	4	1224626	1224630	1224630	1224684	1	1	29	57	1	1	1	0	1	05:03
156	TCMM8	TCMM	9	183552	183567	183567	183795	1	1	122	242	1	1	1	0	1	05:03
5	TCMM8	TCMM	1	101193	101198	101198	101547	1	1	177	353	1	1	1	0	1	05:03
145	TCMM8	TCMM	8	319609	319904	319904	320071	1	1	231	461	1	1	1	0	1	05:03
153	TCMM8	TCMM	9	96388	96801	96801	96860	1	1	236	471	1	1	1	0	1	05:03
336	TCMM8	TCMM	16	920877	921047	921154	921247	1	108	239	369	1	1	1	0	1	05:03
328	TCMM8	TCMM	16	537122	537410	537410	537617	1	1	248	494	1	1	1	0	1	05:03
270	TCMM8	TCMM	14	465885	465982	466168	466216	1	187	259	330	1	1	1	0	1	05:03
327	TCMM8	TCMM	16	497602	497758	497758	498200	1	1	299	597	1	1	1	0	1	05:03
201	TCMM8	TCMM	11	393512	393589	393718	394215	1	130	416	702	1	1	1	0	1	05:03
37	TCMM8	TCMM	4	115646	116157	116157	116482	1	1	418	835	1	1	1	0	1	05:03
254	TCMM8	TCMM	14	122172	122216	122564	122677	1	349	427	504	1	1	1	0	1	05:03
2	TCMM8	TCMM	1	67729	68551	68551	68621	1	1	446	891	1	1	1	0	1	05:03
187	TCMM8	TCMM	10	666742	667126	667152	667627	1	27	456	884	1	1	1	0	1	05:03
103	TCMM8	TCMM	5	560376	560715	561069	561108	1	355	543	731	1	1	1	0	1	05:03
127	TCMM8	TCMM	7	470658	470964	470964	471870	1	1	606	1211	1	1	1	0	1	05:03
242	TCMM8	TCMM	13	477118	478087	478297	478448	1	211	770	1329	1	1	1	0	1	05:03
19	TCMM8	TCMM	2	248980	250316	250316	250537	1	1	779	1556	1	1	1	0	1	05:03
95	TCMM8	TCMM	5	408950	409183	409528	410181	1	346	788	1230	1	1	1	0	1	05:03
218	TCMM8	TCMM	12	253791	253941	254610	254773	1	670	826	981	1	1	1	0	1	05:03
169	TCMM8	TCMM	10	159201	160491	160511	160930	1	21	875	1728	1	1	1	0	1	05:03
228	TCMM8	TCMM	12	863244	864291	864291	864999	1	1	878	1754	1	1	1	0	1	05:03
206	TCMM8	TCMM	11	590994	592478	592577	593181	1	100	1143	2186	1	1	1	0	1	05:03
283	TCMM8	TCMM	15	190009	191548	191548	192333	1	1	1162	2323	1	1	1	0	1	05:03
205	TCMM8	TCMM	11	582622	582756	583946	584258	1	1191	1413	1635	1	1	1	0	1	05:03
210	TCMM8	TCMM	11	635970	636244	638139	638298	1	1896	2112	2327	1	1	1	0	1	05:03
227	TCMM8	TCMM	12	837962	840577	840682	843387	1	106	2765	5424	1	1	1	0	1	05:03
108	TCMM8	TCMM	6	76048	76053	76053	76126	1	1	39	77	1	2	1	0	1	03:05
47	TCMM8	TCMM	4	345524	345541	345541	345638	1	1	57	113	1	2	1	0	1	03:05
247	TCMM8	TCMM	13	804802	804888	804888	804916	1	1	57	113	1	2	1	0	1	03:05
310	TCMM8	TCMM	16	22544	22571	22571	22695	1	1	76	150	1	2	1	0	1	03:05
175	TCMM8	TCMM	10	284198	284309	284309	284375	1	1	89	176	1	2	1	0	1	03:05
40	TCMM8	TCMM	4	159284	159315	159315	159567	1	1	142	282	1	2	1	0	1	03:05
97	TCMM8	TCMM	5	439255	439285	439285	439545	1	1	145	289	1	2	1	0	1	03:05
219	TCMM8	TCMM	12	278546	278659	278673	278823	1	15	146	276	1	2	1	0	1	03:05
323	TCMM8	TCMM	16	426150	426395	426395	426505	1	1	178	354	1	2	1	0	1	03:05
101	TCMM8	TCMM	5	490952	491135	491135	491327	1	1	188	374	1	2	1	0	1	03:05
32	TCMM8	TCMM	3	153706	153719	153719	154234	1	1	264	527	1	2	1	0	1	03:05
321	TCMM8	TCMM	16	378890	378909	378909	379426	1	1	268	535	1	2	1	0	1	03:05
306	TCMM8	TCMM	15	985932	986343	986343	986501	1	1	285	568	1	2	1	0	1	03:05
93	TCMM8	TCMM	5	326423	326990	327059	327079	1	70	363	655	1	2	1	0	1	03:05
167	TCMM8	TCMM	10	113314	113443	113443	114082	1	1	384	767	1	2	1	0	1	03:05
263	TCMM8	TCMM	14	301506	301548	301887	301978	1	340	406	471	1	2	1	0	1	03:05
256	TCMM8	TCMM	14	188387	189221	189221	189381	1	1	497	993	1	2	1	0	1	03:05
81	TCMM8	TCMM	5	39304	39651	39651	40307	1	1	502	1002	1	2	1	0	1	03:05
186	TCMM8	TCMM	10	641346	641571	641631	642317	1	61	516	970	1	2	1	0	1	03:05
68	TCMM8	TCMM	4	1265921	1266546	1266696	1266824	1	151	527	902	1	2	1	0	1	03:05
311	TCMM8	TCMM	16	39420	39693	39840	40351	1	148	539	930	1	2	1	0	1	03:05

278	TCMM8	TCMM	15	55428	55437	55845	56223	1	409	602	794	1	2	1	0	1	03:05
179	TCMM8	TCMM	10	526176	526730	526730	527538	1	1	681	1361	1	2	1	0	1	03:05
21	TCMM8	TCMM	2	265831	266338	266358	267213	1	21	701	1381	1	2	1	0	1	03:05
142	TCMM8	TCMM	8	181049	181082	181744	182078	1	663	846	1028	1	2	1	0	1	03:05
141	TCMM8	TCMM	8	174093	174717	175253	175365	1	537	904	1271	1	2	1	0	1	03:05
320	TCMM8	TCMM	16	371914	372742	373291	373351	1	550	993	1436	1	2	1	0	1	03:05
54	TCMM8	TCMM	4	727318	727624	728057	728918	1	434	1017	1599	1	2	1	0	1	03:05
277	TCMM8	TCMM	15	39810	39886	41378	41470	1	1493	1576	1659	1	2	1	0	1	03:05
157	TCMM8	TCMM	9	205094	210741	210741	210751	1	1	2829	5656	1	2	1	0	1	03:05
51	TCMM8	TCMM	4	542170	542225	542914	543278	1	690	899	1107	1	3	1	0	1	5:3_4:4_5:3
80	TCMM8	TCMM	4	1490715	1490879	1491912	1492309	1	1034	1314	1593	1	3	1	0	1	5:3_4:4_5:3
233	TCMM8	TCMM	12	1053841	1054279	1055872	1056105	1	1594	1929	2263	1	3	1	0	1	5:3_4:4_5:3
34	TCMM8	TCMM	3	261331	262264	263025	264441	1	762	1936	3109	1	3	1	0	1	5:3_4:4_5:3
237	TCMM8	TCMM	13	262219	262578	263835	264337	1	1258	1688	2117	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
75	TCMM8	TCMM	4	1391941	1391986	1394881	1395687	1	2896	3321	3745	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3_4:4_5:3
272	TCMM8	TCMM	14	534658	535369	538640	539186	1	3272	3900	4527	1	3	1	0	1	5:3_4:4_5:3_4:4_6:2_5:3_4:4_5:3
246	TCMM8	TCMM	13	793076	793469	793752	794088	1	284	648	1011	1	4	1	0	1	3:5_4:4_3:5
307	TCMM8	TCMM	15	1019122	1019282	1019806	1020132	1	525	767	1009	1	4	1	0	1	3:5_4:4_3:5
191	TCMM8	TCMM	10	723534	723550	724337	724397	1	788	825	862	1	4	1	0	1	3:5_2:6_3:5_2:6_3:5
55	TCMM8	TCMM	4	750125	750698	751490	751579	1	793	1123	1453	1	4	1	0	1	3:5_2:6_3:5_4:4_3:5
122	TCMM8	TCMM	7	140207	140227	144484	144500	1	4258	4275	4292	1	4	1	0	1	3:5_4:4_3:5_2:6_4:4_3:5_4:4_2:6_3:5_4:4_2:6_4:4_3:5
313	TCMM8	TCMM	16	50846	50873	50951	50992	1	79	112	145	1	7	1	0	1	6:2_5:3
165	TCMM8	TCMM	10	31505	31566	31686	31756	1	121	186	250	1	7	1	0	1	6:2_5:3
135	TCMM8	TCMM	8	10615	10670	10795	10934	1	126	222	318	1	7	1	0	1	5:3_6:2
76	TCMM8	TCMM	4	1421908	1421954	1422450	1422760	1	497	674	851	1	7	1	0	1	5:3_6:2
199	TCMM8	TCMM	11	308325	308425	309009	309090	1	585	675	764	1	7	1	0	1	6:2_5:3
190	TCMM8	TCMM	10	704627	704699	705235	705450	1	537	680	822	1	7	1	0	1	5:3_6:2
289	TCMM8	TCMM	15	311489	312220	312575	312919	1	356	893	1429	1	7	1	0	1	6:2_5:3
286	TCMM8	TCMM	15	231231	232193	232797	233424	1	605	1399	2192	1	7	1	0	1	5:3_6:2
220	TCMM8	TCMM	12	340695	341678	342709	343120	1	1032	1728	2424	1	7	1	0	1	6:2_5:3
7	TCMM8	TCMM	1	111180	113132	113326	114652	1	195	1833	3471	1	7	1	0	1	6:2_5:3
88	TCMM8	TCMM	5	192670	192683	192792	192820	1	110	130	149	1	7	1	0	1	6:2_4:4_6:2
194	TCMM8	TCMM	11	92193	92251	92441	92653	1	191	325	459	1	7	1	0	1	6:2_4:4_6:2
217	TCMM8	TCMM	12	247833	248314	248752	249052	1	439	829	1218	1	7	1	0	1	5:3_4:4_6:2
309	TCMM8	TCMM	15	1047912	1047968	1048990	1049465	1	1023	1288	1552	1	7	1	0	1	6:2_4:4_5:3
195	TCMM8	TCMM	11	116904	117207	118487	119310	1	1281	1843	2405	1	7	1	0	1	6:2_4:4_5:3
253	TCMM8	TCMM	14	116459	116678	117410	117759	1	733	1016	1299	1	7	1	0	1	6:2_5:3_4:4_5:3
264	TCMM8	TCMM	14	307920	308304	310209	310493	1	1906	2239	2572	1	7	1	0	1	6:2_4:4_5:3_6:2
78	TCMM8	TCMM	4	1467260	1467745	1469510	1469852	1	1766	2179	2591	1	7	1	0	1	5:3_6:2_4:4_5:3_6:2_5:3_6:2
106	TCMM8	TCMM	6	34741	34967	36660	36739	1	1694	1846	1997	1	7	1	0	1	6:2_5:3_6:2_5:3_6:2_5:3_4:4_5:3
216	TCMM8	TCMM	12	234128	234194	234378	234633	1	185	345	504	1	8	1	0	1	3:5_2:6
255	TCMM8	TCMM	14	138230	138404	138539	138817	1	136	361	586	1	8	1	0	1	2:6_3:5
116	TCMM8	TCMM	6	226919	227043	227223	228092	1	181	677	1172	1	8	1	0	1	3:5_2:6
240	TCMM8	TCMM	13	434413	434538	434776	435813	1	239	819	1399	1	8	1	0	1	2:6_3:5
18	TCMM8	TCMM	2	201932	202108	202227	203566	1	120	877	1633	1	8	1	0	1	2:6_3:5
91	TCMM8	TCMM	5	270473	271135	271703	271934	1	569	1015	1460	1	8	1	0	1	3:5_2:6
117	TCMM8	TCMM	6	239854	240289	241206	241690	1	918	1377	1835	1	8	1	0	1	2:6_3:5
6	TCMM8	TCMM	1	107970	108718	108814	110713	1	97	1420	2742	1	8	1	0	1	2:6_3:5
92	TCMM8	TCMM	5	309648	309961	311423	311716	1	1463	1765	2067	1	8	1	0	1	3:5_2:6
143	TCMM8	TCMM	8	185625	186453	187989	188673	1	1537	2292	3047	1	8	1	0	1	3:5_2:6
138	TCMM8	TCMM	8	74101	74246	74632	74705	1	387	495	603	1	8	1	0	1	3:5_4:4_2:6
111	TCMM8	TCMM	6	118346	118792	119127	119229	1	336	609	882	1	8	1	0	1	2:6_4:4_2:6
62	TCMM8	TCMM	4	1078009	1078458	1078881	1079059	1	424	737	1049	1	8	1	0	1	2:6_3:5_2:6
66	TCMM8	TCMM	4	1216099	1216309	1217501	1217807	1	1193	1450	1707	1	8	1	0	1	2:6_4:4_2:6
98	TCMM8	TCMM	5	460008	460131	461594	462614	1	1464	2035	2605	1	8	1	0	1	2:6_3:5_2:6
244	TCMM8	TCMM	13	608323	608383	610501	611332	1	2119	2564	3008	1	8	1	0	1	2:6_3:5_2:6
110	TCMM8	TCMM	6	114275	114340	114707	115088	1	368	590	812	1	8	1	0	1	2:6_3:5_2:6_3:5
72	TCMM8	TCMM	4	1343357	1343962	1345079	1345315	1	1118	1538	1957	1	8	1	0	1	3:5_2:6_3:5_2:6
302	TCMM8	TCMM	15	899806	900141	903846	903919	1	3706	3909	4112	1	8	1	0	1	2:6_3:5_4:4_3:5
12	TCMM8	TCMM	1	198604	198630	198630	198648	1	1	22	43	1	10	1	0	1	06:02

45	TCMM8	TCMM	4	264106	264197	264197	264290		1	1	92	183	1	10	1	0	1 06:02
63	TCMM8	TCMM	4	1092561	1092723	1092723	1092764		1	1	102	202	1	10	1	0	1 06:02
15	TCMM8	TCMM	2	137272	137392	137392	137522		1	1	125	249	1	10	1	0	1 06:02
172	TCMM8	TCMM	10	236615	236674	236674	236901		1	1	143	285	1	10	1	0	1 06:02
99	TCMM8	TCMM	5	475154	475295	475308	475496		1	14	178	341	1	10	1	0	1 06:02
203	TCMM8	TCMM	11	523152	523472	523472	523649		1	1	249	496	1	10	1	0	1 06:02
281	TCMM8	TCMM	15	161509	161586	161586	162027		1	1	259	517	1	10	1	0	1 06:02
296	TCMM8	TCMM	15	637574	637797	637797	638136		1	1	281	561	1	10	1	0	1 06:02
86	TCMM8	TCMM	5	118179	118197	118211	118734		1	15	285	554	1	10	1	0	1 06:02
299	TCMM8	TCMM	15	700551	700804	700948	701028		1	145	311	476	1	10	1	0	1 06:02
57	TCMM8	TCMM	4	843009	843125	843125	843647		1	1	319	637	1	10	1	0	1 06:02
82	TCMM8	TCMM	5	41961	42646	42646	42708		1	1	374	746	1	10	1	0	1 06:02
322	TCMM8	TCMM	16	394211	394424	394442	395015		1	19	411	803	1	10	1	0	1 06:02
196	TCMM8	TCMM	11	177551	178198	178268	178399		1	71	459	847	1	10	1	0	1 06:02
316	TCMM8	TCMM	16	166118	166274	166465	166927		1	192	500	808	1	10	1	0	1 06:02
43	TCMM8	TCMM	4	229868	230128	230153	230893		1	26	525	1024	1	10	1	0	1 06:02
16	TCMM8	TCMM	2	139079	139949	140021	140131		1	73	562	1051	1	10	1	0	1 06:02
102	TCMM8	TCMM	5	544734	545109	545109	545863		1	1	565	1128	1	10	1	0	1 06:02
334	TCMM8	TCMM	16	840627	841449	841571	841702		1	123	599	1074	1	10	1	0	1 06:02
262	TCMM8	TCMM	14	288573	288680	289222	289345		1	543	657	771	1	10	1	0	1 06:02
326	TCMM8	TCMM	16	456671	456724	456878	458489		1	155	986	1817	1	10	1	0	1 06:02
87	TCMM8	TCMM	5	162474	162567	163290	163835		1	724	1042	1360	1	10	1	0	1 06:02
250	TCMM8	TCMM	13	872837	873141	873246	874942		1	106	1105	2104	1	10	1	0	1 06:02
28	TCMM8	TCMM	2	790813	790890	792247	792968		1	1358	1756	2154	1	10	1	0	1 06:02
177	TCMM8	TCMM	10	465816	467589	467589	469453		1	1	1819	3636	1	10	1	0	1 06:02
149	TCMM8	TCMM	8	465769	465801	465801	465803		1	1	17	33	1	10.1	1	0	1 02:06
230	TCMM8	TCMM	12	877560	877606	877625	877699		1	20	79	138	1	10.1	1	0	1 02:06
305	TCMM8	TCMM	15	984011	984169	984169	984206		1	1	98	194	1	10.1	1	0	1 02:06
317	TCMM8	TCMM	16	198355	198637	198637	198653		1	1	149	297	1	10.1	1	0	1 02:06
154	TCMM8	TCMM	9	102496	102536	102597	102742		1	62	154	245	1	10.1	1	0	1 02:06
118	TCMM8	TCMM	6	245159	245286	245286	245484		1	1	163	324	1	10.1	1	0	1 02:06
104	TCMM8	TCMM	6	17252	17394	17399	17582		1	6	168	329	1	10.1	1	0	1 02:06
234	TCMM8	TCMM	13	14857	14911	15055	15133		1	145	210	275	1	10.1	1	0	1 02:06
314	TCMM8	TCMM	16	74885	74937	74937	75355		1	1	235	469	1	10.1	1	0	1 02:06
290	TCMM8	TCMM	15	410084	410118	410276	410471		1	159	273	386	1	10.1	1	0	1 02:06
50	TCMM8	TCMM	4	443547	443924	443924	444097		1	1	275	549	1	10.1	1	0	1 02:06
147	TCMM8	TCMM	8	379789	379863	379863	380348		1	1	280	558	1	10.1	1	0	1 02:06
139	TCMM8	TCMM	8	76095	76580	76580	76673		1	1	289	577	1	10.1	1	0	1 02:06
259	TCMM8	TCMM	14	256273	256778	256789	256857		1	12	298	583	1	10.1	1	0	1 02:06
300	TCMM8	TCMM	15	745265	745547	745659	745778		1	113	313	512	1	10.1	1	0	1 02:06
74	TCMM8	TCMM	4	1385858	1385998	1386016	1386524		1	19	342	665	1	10.1	1	0	1 02:06
60	TCMM8	TCMM	4	954985	955099	955335	955686		1	237	469	700	1	10.1	1	0	1 02:06
192	TCMM8	TCMM	11	21787	21803	21803	22806		1	1	510	1018	1	10.1	1	0	1 02:06
258	TCMM8	TCMM	14	205874	206853	206892	207121		1	40	643	1246	1	10.1	1	0	1 02:06
41	TCMM8	TCMM	4	171661	171817	172175	172830		1	359	764	1168	1	10.1	1	0	1 02:06
304	TCMM8	TCMM	15	980032	981230	981571	981575		1	342	942	1542	1	10.1	1	0	1 02:06
94	TCMM8	TCMM	5	342057	342537	343263	343350		1	727	1010	1292	1	10.1	1	0	1 02:06
129	TCMM8	TCMM	7	640432	640541	640849	642144		1	309	1010	1711	1	10.1	1	0	1 02:06
236	TCMM8	TCMM	13	219620	221252	221252	221642		1	1	1011	2021	1	10.1	1	0	1 02:06
25	TCMM8	TCMM	2	623818	624009	624805	625298		1	797	1138	1479	1	10.1	1	0	1 02:06
35	TCMM8	TCMM	4	19281	19322	21255	21300		1	1934	1976	2018	1	10.1	1	0	1 02:06
10	TCMM8	TCMM	1	173966	174674	174674	175307	2_nonsis		1	671	1340	3	30	1	0	1 03:05
30	TCMM8	TCMM	3	79797	91287	93230	93455	2_nonsis		1944	7801	13657	3	30	1	0	1 2:6_5:3
105	TCMM8	TCMM	6	31880	31946	32447	32524	2_nonsis		502	573	643	3	30	1	0	1 6:2_3:5_2:6
65	TCMM8	TCMM	4	1161819	1161892	1163376	1163436	2_nonsis		1485	1551	1616	3	30	1	0	1 6:2_4:4_2:6
170	TCMM8	TCMM	10	162540	162711	164155	164308	2_nonsis		1445	1606	1767	3	30	1	0	1 6:2_4:4_3:5
266	TCMM8	TCMM	14	340939	340966	342707	342782	2_nonsis		1742	1792	1842	3	30	1	0	1 5:3_6:2_5:3a
164	TCMM8	TCMM	9	406124	406436	408110	408224	2_nonsis		1675	1887	2099	3	30	1	0	1 2:6_3:5_2:6
229	TCMM8	TCMM	12	873300	874112	875259	876120	2_nonsis		1148	1984	2819	3	30	1	0	1 6:2_4:4_2:6
49	TCMM8	TCMM	4	407403	408374	411785	412382	2_nonsis		3412	4195	4978	3	30	1	0	1 6:2_4:4_2:6

3	TCMM8	TCMM	1	70621	70999	71616	71673	2_nonsis	618	835	1051	3	30	1	0	1 6:2_5:3_4:4_3:5
33	TCMM8	TCMM	3	208489	209380	211617	212942	2_nonsis	2238	3345	4452	3	30	1	0	1 2:6_4:4_5:3_6:2
176	TCMM8	TCMM	10	330001	330191	333992	334125	2_nonsis	3802	3963	4123	3	30	1	0	1 3:5_2:6_4:4_6:2
152	TCMM8	TCMM	9	55251	56514	58630	58961	2_nonsis	2117	2913	3709	3	30	1	0	1 6:2_5:3_6:2_5:3_6:2
288	TCMM8	TCMM	15	282006	282038	288307	288781	2_nonsis	6270	6522	6774	3	30	1	0	1 5:3_4:4_5:3_6:2_4:4_6:2_5:3_4:4_2:6
120	TCMM8	TCMM	7	35217	35543	46050	46197	2_nonsis	10508	10744	10979	3	30	1	0	1 6:2_5:3_6:2_5:3_6:2_5:3_4:4_5:3_6:2_4:4_3:5
107	TCMM8	TCMM	6	45217	45870	46872	46998	2_nonsis	1003	1392	1780	3	31	1	0	1 3:5_4:4ai
53	TCMM8	TCMM	4	635784	636465	636465	636737	2_nonsis	1	477	952	1	1	1	1	0 (5:3)_(4:4aCO)
162	TCMM8	TCMM	9	370178	370386	370388	370992	2_nonsis	3	408	813	1	2	1	1	0 (3:5)_(4:4aCO)
293	TCMM8	TCMM	15	499294	499626	499626	500197	2_nonsis	1	452	902	1	2	1	1	0 (3:5)_(4:4aCO)
200	TCMM8	TCMM	11	372458	372830	372830	373379	2_nonsis	1	461	920	1	2	1	1	0 (3:5)_(4:4aCO)
70	TCMM8	TCMM	4	1333898	1334061	1334389	1335206	2_nonsis	329	818	1307	1	2	1	1	0 (3:5)_(4:4aCO)
174	TCMM8	TCMM	10	275597	275984	276704	277465	2_nonsis	721	1294	1867	1	2	1	1	0 (3:5)_(4:4aCO)
9	TCMM8	TCMM	1	155505	159623	159724	159877	2_nonsis	102	2237	4371	1	2	1	1	0 (3:5)_(4:4aCO)
13	TCMM8	TCMM	2	44210	44904	45075	45660	2_nonsis	172	811	1449	1	6	1	1	0 (4:4aCO)_(3:5)_(4:4a)
168	TCMM8	TCMM	10	153254	154954	155705	156143	2_nonsis	752	1820	2888	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
188	TCMM8	TCMM	10	675595	675709	676590	677087	2_nonsis	882	1187	1491	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
64	TCMM8	TCMM	4	1105249	1105561	1105780	1106241	2_nonsis	220	606	991	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
38	TCMM8	TCMM	4	124765	125066	125172	125573	2_nonsis	107	457	807	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
319	TCMM8	TCMM	16	348398	348431	348815	349538	2_nonsis	385	762	1139	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
238	TCMM8	TCMM	13	265689	266099	266262	267158	2_nonsis	164	816	1468	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
202	TCMM8	TCMM	11	401916	402660	403407	403558	2_nonsis	748	1195	1641	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
193	TCMM8	TCMM	11	32124	33673	34444	34686	2_nonsis	772	1667	2561	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
89	TCMM8	TCMM	5	194646	194693	195341	195356	2_nonsis	649	679	709	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
285	TCMM8	TCMM	15	216399	217333	217521	218142	2_nonsis	189	966	1742	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
292	TCMM8	TCMM	15	486327	486494	487166	487809	2_nonsis	673	1077	1481	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
171	TCMM8	TCMM	10	204730	205042	205946	206436	2_nonsis	905	1305	1705	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
248	TCMM8	TCMM	13	810229	810415	811756	812113	2_nonsis	1342	1613	1883	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
46	TCMM8	TCMM	4	280191	280598	282024	283030	2_nonsis	1427	2133	2838	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
136	TCMM8	TCMM	8	64197	64748	65412	65566	2_nonsis	665	1017	1368	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4aCO)
42	TCMM8	TCMM	4	211933	212036	212746	213315	2_nonsis	711	1046	1381	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
52	TCMM8	TCMM	4	550893	551387	552102	552354	2_nonsis	716	1088	1460	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
115	TCMM8	TCMM	6	213776	214043	214589	215586	2_nonsis	547	1178	1809	1	12	1	1	0 (2:6)_(3:5)_(2:6)_(4:4aCO)
159	TCMM8	TCMM	9	253488	253992	254765	255654	2_nonsis	774	1470	2165	1	12	1	1	0 (2:6)_(3:5)_(2:6)_(4:4aCO)
252	TCMM8	TCMM	14	49737	50444	51868	52069	2_nonsis	1425	1878	2331	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
39	TCMM8	TCMM	4	129270	129783	131512	131875	2_nonsis	1730	2167	2604	1	12	1	1	0 (6:2)_(4:4)_(5:3)_(4:4aCO)
189	TCMM8	TCMM	10	683353	683820	685208	686511	2_nonsis	1389	2273	3157	1	12	1	1	0 (3:5)_(4:4aCO)_(3:5)_(4:4a)
155	TCMM8	TCMM	9	129907	130294	132269	132429	2_nonsis	1976	2249	2521	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4)_(4:4aCO)
260	TCMM8	TCMM	14	260618	261617	264607	265328	2_nonsis	2991	3850	4709	1	12	1	1	0 (3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
211	TCMM8	TCMM	12	29131	29612	30884	30930	2_nonsis	1273	1536	1798	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)_(5:3)_(6:2)_(4:4a)
22	TCMM8	TCMM	2	322122	322182	324185	324220	2_nonsis	2004	2051	2097	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
125	TCMM8	TCMM	7	350649	351015	352964	355166	2_nonsis	1950	3233	4516	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
279	TCMM8	TCMM	15	93845	94096	97478	97910	2_nonsis	3383	3724	4064	1	12	1	1	0 (6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
119	TCMM8	TCMM	6	263658	263716	265792	265986	2_nonsis	2077	2202	2327	1	12	1	1	0 (6:2)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(4:4a)_(5:3)_(4:4a)
303	TCMM8	TCMM	15	953320	953577	956617	956880	2_nonsis	3041	3300	3559	1	12	1	1	0 (5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(4:4aCO)
132	TCMM8	TCMM	7	902661	903030	905275	905694	2_nonsis	2246	2639	3032	1	12	1	1	0 (6:2)_(4:4aCO)_(5:3)_(6:2)_(5:3)_(4:4a)_(5:3)_(4:4a)_(5:3)_(4:4a)
133	TCMM8	TCMM	7	994015	994032	994032	994097	2_nonsis	1	41	81	1	15	1	1	0 (6:2)_(4:4aCO)
126	TCMM8	TCMM	7	440241	440359	440359	440438	2_nonsis	1	99	196	1	15	1	1	0 (6:2)_(4:4aCO)
331	TCMM8	TCMM	16	696490	696582	696582	696879	2_nonsis	1	195	388	1	15	1	1	0 (6:2)_(4:4aCO)
17	TCMM8	TCMM	2	162271	162420	162420	162680	2_nonsis	1	205	408	1	15	1	1	0 (6:2)_(4:4aCO)
231	TCMM8	TCMM	12	949489	949843	949843	949938	2_nonsis	1	225	448	1	15	1	1	0 (6:2)_(4:4aCO)
241	TCMM8	TCMM	13	474938	475013	475160	475252	2_nonsis	148	231	313	1	15	1	1	0 (6:2)_(4:4aCO)
297	TCMM8	TCMM	15	670961	671534	671534	671818	2_nonsis	1	429	856	1	15	1	1	0 (6:2)_(4:4aCO)
130	TCMM8	TCMM	7	670175	670263	670598	670804	2_nonsis	336	482	628	1	15	1	1	0 (6:2)_(4:4aCO)
100	TCMM8	TCMM	5	488899	489026	489026	489879	2_nonsis	1	490	979	1	15	1	1	0 (6:2)_(4:4aCO)
148	TCMM8	TCMM	8	423045	423870	423870	424191	2_nonsis	1	573	1145	1	15	1	1	0 (6:2)_(4:4aCO)
282	TCMM8	TCMM	15	181640	182622	182738	182884	2_nonsis	117	680	1243	1	15	1	1	0 (6:2)_(4:4aCO)
221	TCMM8	TCMM	12	370487	370966	370966	371874	2_nonsis	1	694	1386	1	15	1	1	0 (6:2)_(4:4aCO)
48	TCMM8	TCMM	4	349591	350046	350462	350645	2_nonsis	417	735	1053	1	15	1	1	0 (6:2)_(4:4aCO)
131	TCMM8	TCMM	7	833796	834010	834267	835147	2_nonsis	258	804	1350	1	15	1	1	0 (6:2)_(4:4aCO)

318	TCMM8	TCMM	16	279235	279259	279975	280422	2_nonsis	717	952	1186	1	15	1	1	0	(6:2)_(4:4aCO)
207	TCMM8	TCMM	11	595509	596220	597223	597399	2_nonsis	1004	1447	1889	1	15	1	1	0	(6:2)_(4:4aCO)
274	TCMM8	TCMM	14	605054	606283	606872	608001	2_nonsis	590	1768	2946	1	15	1	1	0	(6:2)_(4:4aCO)
61	TCMM8	TCMM	4	1066006	1066159	1067784	1068162	2_nonsis	1626	1891	2155	1	15	1	1	0	(6:2)_(4:4aCO)
223	TCMM8	TCMM	12	521782	522608	522914	525267	2_nonsis	307	1896	3484	1	15	1	1	0	(6:2)_(4:4aCO)
1	TCMM8	TCMM	1	57455	57739	59349	59659	2_nonsis	1611	1907	2203	1	15	1	1	0	(6:2)_(4:4aCO)
181	TCMM8	TCMM	10	570822	573950	574412	574799	2_nonsis	463	2220	3976	1	15	1	1	0	(6:2)_(4:4aCO)
225	TCMM8	TCMM	12	731012	732527	732527	736073	2_nonsis	1	2531	5060	1	15	1	1	0	(6:2)_(4:4aCO)
324	TCMM8	TCMM	16	431787	431837	431840	432226	2_nonsis	4	221	438	1	16	1	1	0	(2:6)_(4:4aCO)
276	TCMM8	TCMM	14	711379	711615	711615	711951	2_nonsis	1	286	571	1	16	1	1	0	(2:6)_(4:4aCO)
90	TCMM8	TCMM	5	250692	251006	251036	251267	2_nonsis	31	303	574	1	16	1	1	0	(2:6)_(4:4aCO)
56	TCMM8	TCMM	4	770352	770770	770770	771211	2_nonsis	1	430	858	1	16	1	1	0	(2:6)_(4:4aCO)
239	TCMM8	TCMM	13	355195	355271	355763	356149	2_nonsis	493	723	953	1	16	1	1	0	(2:6)_(4:4aCO)
291	TCMM8	TCMM	15	425274	425464	425518	426767	2_nonsis	55	774	1492	1	16	1	1	0	(2:6)_(4:4aCO)
112	TCMM8	TCMM	6	121761	122971	122971	123435	2_nonsis	1	837	1673	1	16	1	1	0	(2:6)_(4:4aCO)
31	TCMM8	TCMM	3	136159	136789	137256	137490	2_nonsis	468	899	1330	1	16	1	1	0	(2:6)_(4:4aCO)
85	TCMM8	TCMM	5	111137	111209	111137	111209	2_nonsis	0	36	71	1	100	1	1	0	(4:4aCO)
298	TCMM8	TCMM	15	675019	675258	675019	675258	2_nonsis	0	119	238	1	100	1	1	0	(4:4aCO)
151	TCMM8	TCMM	8	505427	505727	505427	505727	2_nonsis	0	150	299	1	100	1	1	0	(4:4aCO)
173	TCMM8	TCMM	10	270332	270695	270332	270695	2_nonsis	0	181	362	1	100	1	1	0	(4:4aCO)
257	TCMM8	TCMM	14	197788	198236	197788	198236	2_nonsis	0	224	447	1	100	1	1	0	(4:4aCO)
144	TCMM8	TCMM	8	276840	277301	276840	277301	2_nonsis	0	230	460	1	100	1	1	0	(4:4aCO)
197	TCMM8	TCMM	11	179745	180215	179745	180215	2_nonsis	0	235	469	1	100	1	1	0	(4:4aCO)
69	TCMM8	TCMM	4	1296525	1297076	1296525	1297076	2_nonsis	0	275	550	1	100	1	1	0	(4:4aCO)
280	TCMM8	TCMM	15	146419	147007	146419	147007	2_nonsis	0	294	587	1	100	1	1	0	(4:4aCO)
333	TCMM8	TCMM	16	812552	813147	812552	813147	2_nonsis	0	297	594	1	100	1	1	0	(4:4aCO)
295	TCMM8	TCMM	15	517314	518019	517314	518019	2_nonsis	0	352	704	1	100	1	1	0	(4:4aCO)
59	TCMM8	TCMM	4	929368	930077	929368	930077	2_nonsis	0	354	708	1	100	1	1	0	(4:4aCO)
198	TCMM8	TCMM	11	224634	225480	224634	225480	2_nonsis	0	423	845	1	100	1	1	0	(4:4aCO)
325	TCMM8	TCMM	16	453010	453873	453010	453873	2_nonsis	0	431	862	1	100	1	1	0	(4:4aCO)
243	TCMM8	TCMM	13	556437	557365	556437	557365	2_nonsis	0	464	927	1	100	1	1	0	(4:4aCO)
24	TCMM8	TCMM	2	586331	587309	586331	587309	2_nonsis	0	489	977	1	100	1	1	0	(4:4aCO)
267	TCMM8	TCMM	14	391752	392860	391752	392860	2_nonsis	0	554	1107	1	100	1	1	0	(4:4aCO)
140	TCMM8	TCMM	8	171347	172563	171347	172563	2_nonsis	0	608	1215	1	100	1	1	0	(4:4aCO)
329	TCMM8	TCMM	16	591899	593126	591899	593126	2_nonsis	0	613	1226	1	100	1	1	0	(4:4aCO)
335	TCMM8	TCMM	16	880945	882337	880945	882337	2_nonsis	0	696	1391	1	100	1	1	0	(4:4aCO)
36	TCMM8	TCMM	4	60151	62061	60151	62061	2_nonsis	0	955	1909	1	100	1	1	0	(4:4aCO)
224	TCMM8	TCMM	12	625064	627007	625064	627007	2_nonsis	0	971	1942	1	100	1	1	0	(4:4aCO)
180	TCMM8	TCMM	10	568805	570822	568805	570822	2_nonsis	0	1008	2016	1	100	1	1	0	(4:4aCO)
11	TCMM8	TCMM	1	187427	189821	187427	189821	2_nonsis	0	1197	2393	1	100	1	1	0	(4:4aCO)
161	TCMM8	TCMM	9	299287	302738	299287	302738	2_nonsis	0	1725	3450	1	100	1	1	0	(4:4aCO)
275	TCMM8	TCMM	14	651410	655138	651410	655138	2_nonsis	0	1864	3727	1	100	1	1	0	(4:4aCO)
273	TCMM8	TCMM	14	539950	543829	539950	543829	2_nonsis	0	1939	3878	1	100	1	1	0	(4:4aCO)
26	TCMM8	TCMM	2	662444	666712	662444	666712	2_nonsis	0	2134	4267	1	100	1	1	0	(4:4aCO)
183	TCMM8	TCMM	10	596891	601293	596891	601293	2_nonsis	0	2201	4401	1	100	1	1	0	(4:4aCO)
226	TCMM8	TCMM	12	802287	808209	802287	808209	2_nonsis	0	2961	5921	1	100	1	1	0	(4:4aCO)
212	TCMM8	TCMM	12	85916	86081	87580	87661	2_nonsis	1500	1622	1744	2	30	1	1	0	(5:3)_(5:3a)_(6:2)_(4:4aCO)
160	TCMM8	TCMM	9	267764	268176	268690	269349	2_nonsis	515	1050	1584	2	30	1	1	0	(6:2)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
58	TCMM8	TCMM	4	848977	849478	851043	851602	2_nonsis	1566	2095	2624	2	30	1	1	0	(6:2)_(4:4)_(5:3)_(5:3a)_(6:2)_(4:4aCO)
14	TCMM8	TCMM	2	71636	72018	75084	75564	2_nonsis	3067	3497	3927	2	32	1	1	0	(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
83	TCMM8	TCMM	5	51944	53297	53899	54237	2_nonsis	603	1448	2292	2	32	1	1	0	(5:3)_(4:4aCO)_(5:3a)_(4:4a)_(6:2)_(4:4a)
158	TCMM8	TCMM	9	244951	245022	247894	248675	2_nonsis	2873	3298	3723	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(6:2)_(4:4aCO)
204	TCMM8	TCMM	11	526209	526649	526688	527413	2_nonsis	40	622	1203	3	20	1	1	0	(6:2)_(3:5)_(4:4aCO)
114	TCMM8	TCMM	6	201959	202421	202731	203115	2_nonsis	311	733	1155	3	20	1	1	0	(2:6)_(5:3)_(4:4aCO)
23	TCMM8	TCMM	2	495085	495218	496048	496540	2_nonsis	831	1143	1454	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
269	TCMM8	TCMM	14	432420	433148	435934	436363	2_nonsis	2787	3365	3942	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
124	TCMM8	TCMM	7	245686	247666	249983	250183	2_nonsis	2318	3407	4496	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
215	TCMM8	TCMM	12	225332	225447	225921	225953	2_nonsis	475	548	620	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
146	TCMM8	TCMM	8	342786	343035	343561	344320	2_nonsis	527	1030	1533	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
134	TCMM8	TCMM	7	1050064	1050446	1051093	1051973	2_nonsis	648	1278	1908	3	20	1	1	0	(6:2)_(4:4aCO)_(3:5)_(4:4a)

332	TCMM8	TCMM	16	784177	784888	785737	785910	2_nonsis		850	1291	1732	3	20	1	1	0	(5:3)_(2:6)_(3:5)_(4:4aCO)
166	TCMM8	TCMM	10	68967	69094	71182	71728	2_nonsis		2089	2425	2760	3	20	1	1	0	(3:5)_(5:3)_(6:2)_(4:4aCO)
163	TCMM8	TCMM	9	397090	397178	398583	398957	2_nonsis		1406	1636	1866	3	20	1	1	0	(6:2)_(5:3)_(4:4aCO)_(2:6)_(4:4a)
184	TCMM8	TCMM	10	628891	629879	633425	633463	2_nonsis		3547	4059	4571	3	20	1	1	0	(4:4aCO)_(5:3)_(4:4a)_(2:6)_(4:4a)
330	TCMM8	TCMM	16	654661	656181	656861	657485	2_nonsis		681	1752	2823	3	20	1	1	0	(3:5)_(2:6)_(4:4aCO)_(5:3)_(6:2)_(4:4a)
287	TCMM8	TCMM	15	264752	264924	267577	267756	2_nonsis		2654	2829	3003	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(2:6)_(4:4)_(4:4aCO)
121	TCMM8	TCMM	7	120395	120656	123330	123839	2_nonsis		2675	3059	3443	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(6:2)_(4:4aCO)
251	TCMM8	TCMM	14	21451	21949	24616	24781	2_nonsis		2668	2999	3329	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(5:3)_(3:5a)_(4:4aCO)
44	TCMM8	TCMM	4	238635	238826	242772	242997	2_nonsis		3947	4154	4361	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)_(3:5)_(4:4a)_(2:6)_(3:5)_(2:6)_(4:4a)_(3:5)_(4:4a)
4	TCMM8	TCMM	1	80077	80554	82379	83613		3	1826	2681	3535	0	1	2	0	2	(6:2)_(5:3)_(7:1)_(6:2a)_(8:0)_(6:2a)_(4:4)_(2:6)_(4:4)
79	TCMM8	TCMM	4	1476514	1477174	1479403	1479729	2_sis		2230	2722	3214	0	1	2	0	2	(5:3)_(4:4)_(6:2)_(4:4)
96	TCMM8	TCMM	5	411277	412632	414642	414720	2_sis		2011	2727	3442	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
150	TCMM8	TCMM	8	493409	493855	497537	497907	2_sis		3683	4090	4497	0	1	2	0	2	(3:5)_(2:6)_(4:4)_(2:6a)_(4:4)
8	TCMM8	TCMM	1	128637	129476	130975	132066		3	1500	2464	3428	0	2	2	1	1	(3:5)_(4:4aCO)_(3:5a)_(4:4a)
20	TCMM8	TCMM	2	255862	256941	259438	265684		3	2498	6160	9821	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
73	TCMM8	TCMM	4	1364750	1365372	1367355	1367748		3	1984	2491	2997	0	2	2	1	1	(6:2i)_(7:1)_(6:2i)_(5:3)_(4:4aCO)_(7:1)_(5:3)_(4:4a)
109	TCMM8	TCMM	6	93934	94545	95308	95627		3	764	1228	1692	0	2	2	1	1	(3:5)_(2:6)_(0:8)_(1:7)_(4:4aCO)
113	TCMM8	TCMM	6	196563	196793	198468	199207		3	1676	2160	2643	0	2	2	1	1	(6:2)_(4:4aCO)
123	TCMM8	TCMM	7	225112	225889	226151	226711		3	263	931	1598	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(4:4aCO)
128	TCMM8	TCMM	7	608090	608216	611358	611510		3	3143	3281	3419	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(4:4aCO)_(6:2)_(4:4a)_(5:3a)_(4:4a)
185	TCMM8	TCMM	10	636506	637392	639365	640236		3	1974	2852	3729	0	2	2	1	1	(2:6)_(4:4)_(4:4aCO)_(3:5)_(4:4a)_(3:5a)_(2:6a)_(4:4a)
208	TCMM8	TCMM	11	613247	613583	616950	617457		3	3368	3789	4209	0	2	2	1	1	(6:2)_(5:3)_(6:2)_(8:0)_(6:2)_(8:0)_(6:2a)_(4:4aCO)
213	TCMM8	TCMM	12	139322	140166	140300	141153		3	135	983	1830	0	2	2	1	1	(2:6)_(4:4)_(4:4aCO)
232	TCMM8	TCMM	12	1011952	1014017	1014227	1014332		3	211	1295	2379	0	2	2	1	1	(2:6)_(4:4aCO)
249	TCMM8	TCMM	13	857787	857842	862092	862695		4	4251	4579	4907	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(3:5)_(2:6)_(3:5)_(4:4aCO)
261	TCMM8	TCMM	14	270838	271001	273928	274637		3	2928	3363	3798	0	2	2	1	1	(6:2)_(3:5)_(4:4aCO)_(2:6)_(3:5)_(2:6)_(4:4a)
268	TCMM8	TCMM	14	394167	394349	395338	395701		3	990	1262	1533	0	2	2	1	1	(5:3)_(3:5)_(4:4aCO)
301	TCMM8	TCMM	15	781222	781633	782356	782474		3	724	988	1251	0	2	2	1	1	(2:6)_(4:4)_(2:6a)_(4:4aCO)
308	TCMM8	TCMM	15	1023212	1023785	1026039	1026427		3	2255	2735	3214	0	2	2	1	1	(2:6)_(3:5)_(2:6)_(4:4aCO)_(6:2)_(4:4a)
312	TCMM8	TCMM	16	46114	46273	47566	48262		3	1294	1721	2147	0	2	2	1	1	(6:2)_(4:4)_(3:5)_(2:6)_(4:4aCO)
315	TCMM8	TCMM	16	159167	159487	159707	159936		3	221	495	768	0	2	2	1	1	(5:3)_(4:4)_(4:4aCO)
27	TCMM8	TCMM	2	735096	735582	736946	737232		3	1365	1750	2135	0	3	2	0	2	(3:5)_(2:6)_(4:4aCO)_(4:4CO)
29	TCMM8	TCMM	3	38857	39123	39861	40089		3	739	985	1231	0	3	2	0	2	(3:5)_(1:7)_(4:4aCO)_(2:6)_(4:4CO)
71	TCMM8	TCMM	4	1341496	1341514	1341514	1341520	2_nonsis		1	12	23	0	3	2	0	2	(4:4aCO)_(4:4CO)
77	TCMM8	TCMM	4	1431919	1432329	1435091	1435647		3	2763	3245	3727	0	3	2	1	1	(2:6)_(3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4CO)_(6:2)_(4:4bCO)
84	TCMM8	TCMM	5	57281	57855	70969	71501		4	13115	13667	14219	0	3	2	1	1	(6:2)_(5:3)_(6:2)_(4:4)_(6:2a)_(4:4)_(6:2a)_(4:4)_(2:6)_(3:5)_(2:6)_(1:7)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(2:6a)_(3:5a)_(0:8)_(4:4aCO)_(2:6a)_(4:4bCO)_(4:4aCO)
137	TCMM8	TCMM	8	67629	68025	72171	72247	2_nonsis		4147	4382	4617	0	3	2	0	2	(5:3)_(4:4)_(5:3)_(3:5)_(4:4ai)_(4:4bCO)_(4:4CO)
178	TCMM8	TCMM	10	500582	501650	503352	503880	2_nonsis		1703	2500	3297	0	3	2	0	2	(3:5)_(4:4ai)_(4:4bCO)_(2:6)_(4:4CO)
182	TCMM8	TCMM	10	580104	580583	584062	584131	2_nonsis		3480	3753	4026	0	3	2	0	2	(6:2)_(5:3)_(4:4aCO)_(5:3a)_(4:4CO)_(5:3a)_(4:4)
209	TCMM8	TCMM	11	624274	624461	628158	628202		3	3698	3813	3927	0	3	2	1	1	(5:3)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(6:2)_(5:3a)_(4:4bCO)
214	TCMM8	TCMM	12	184588	185813	188360	188452	2_nonsis		2548	3206	3863	0	3	2	0	2	(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)_(5:3)_(4:4CO)
222	TCMM8	TCMM	12	510803	511071	514581	514693	2_nonsis		3511	3700	3889	0	3	2	0	2	(6:2)_(4:4aCO)_(5:3)_(4:4CO)
235	TCMM8	TCMM	13	202482	203606	203948	204520	2_nonsis		343	1190	2037	0	3	2	0	2	(4:4aCO)_(4:4CO)
245	TCMM8	TCMM	13	771775	771796	774012	774661		3	2217	2551	2885	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)_(6:2)_(4:4aCO)_(5:3)_(6:2)_(4:4bCO)
265	TCMM8	TCMM	14	317360	317738	318591	318794		3	854	1144	1433	0	3	2	0	2	(3:5)_(4:2)_(2:6)_(4:4aCO)_(2:6)_(4:4CO)
271	TCMM8	TCMM	14	489765	490190	490766	491097		3	577	954	1331	0	3	2	1	1	(4:4aCO)_(5:3)_(3:5)_(4:4bi)_(4:4cCO)
284	TCMM8	TCMM	15	193911	194961	196577	196695	2_nonsis		1617	2200	2783	0	3	2	0	2	(5:3)_(4:4)_(5:3)_(4:4)_(4:4aCO)_(6:2)_(4:4CO)
294	TCMM8	TCMM	15	501502	502195	504786	505006		3	2592	3048	3503	0	3	2	0	2	(2:6)_(4:4)_(5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4CO)
590	TCMM8	TCMM	13	913943	914143	917449	924431		3	3307	6897	10487	0	4	1	NA	NA	5:3_6:2_5:3_7:1_5:3_6:2*_4:4_5:3_6:2*_5:3_6:2_5:3_6:2
97	TCMN1	TCMN	7	293303	294083	296376	296534		1	2294	2762	3230	1	7	1	0	1	6:2_4:4_6:2
70	TCMN1	TCMN	5	465974	466898	469569	470253		1	2672	3475	4278	1	7	1	0	1	6:2_4:4_6:2
54	TCMN1	TCMN	4	1333527	1333678	1333678	1333799		1	1	136	271	1	10	1	0	1	06:02
79	TCMN1	TCMN	6	210742	210967	210967	211149		1	1	204	406	1	10	1	0	1	06:02
85	TCMN1	TCMN	6	262930	263216	263216	263436		1	1	253	505	1	10	1	0	1	06:02
227	TCMN1	TCMN	13	468637	468937	468937	469276		1	1	320	638	1	10	1	0	1	06:02
58	TCMN1	TCMN	4	1496573	1497025	1497133	1497214		1	109	375	640	1	10	1	0	1	06:02
205	TCMN1	TCMN	12	784477	784820	784820	785227		1	1	375	749	1	10	1	0	1	06:02
83	TCMN1	TCMN	6	249889	249944	250075	251006		1	132	624	1116	1	10	1	0	1	06:02
191	TCMN1	TCMN	12	180860	181545	181616	182125		1	72	668	1264	1	10	1	0	1	06:02
112	TCMN1	TCMN	7	924899	925190	925313	926236		1	124	730	1336	1	10	1	0	1	06:02

128	TCMN1	TCMN	8	267804	268308	268308	269395	1	1	796	1590	1	10	1	0	1 06:02
160	TCMN1	TCMN	10	207747	208362	208641	209220	1	280	876	1472	1	10	1	0	1 06:02
171	TCMN1	TCMN	11	7067	7529	8031	8317	1	503	876	1249	1	10	1	0	1 06:02
89	TCMN1	TCMN	7	76620	76882	76989	78426	1	108	957	1805	1	10	1	0	1 06:02
49	TCMN1	TCMN	4	846137	847005	847053	848136	1	49	1024	1998	1	10	1	0	1 06:02
230	TCMN1	TCMN	13	668408	668902	669832	670228	1	931	1375	1819	1	10	1	0	1 06:02
198	TCMN1	TCMN	12	369919	370090	370966	371874	1	877	1416	1954	1	10	1	0	1 06:02
180	TCMN1	TCMN	11	504362	504740	505937	506135	1	1198	1485	1772	1	10	1	0	1 06:02
156	TCMN1	TCMN	10	119064	119720	120394	121384	1	675	1497	2319	1	10	1	0	1 06:02
247	TCMN1	TCMN	14	761636	761851	763402	763447	1	1552	1681	1810	1	10	1	0	1 06:02
259	TCMN1	TCMN	15	729941	730011	731576	731874	1	1566	1749	1932	1	10	1	0	1 06:02
172	TCMN1	TCMN	11	98834	99633	101183	101384	1	1551	2050	2549	1	10	1	0	1 06:02
189	TCMN1	TCMN	12	124317	124421	126014	126853	1	1594	2065	2535	1	10	1	0	1 06:02
11	TCMN1	TCMN	2	86293	86416	88022	89351	1	1607	2332	3057	1	10	1	0	1 06:02
93	TCMN1	TCMN	7	159705	161545	162215	164025	1	671	2495	4319	1	10	1	0	1 06:02
133	TCMN1	TCMN	8	491435	491810	494116	494183	1	2307	2527	2747	1	10	1	0	1 06:02
81	TCMN1	TCMN	6	236256	236557	239066	239639	1	2510	2946	3382	1	10	1	0	1 06:02
114	TCMN1	TCMN	7	965717	966356	968737	969304	1	2382	2984	3586	1	10	1	0	1 06:02
127	TCMN1	TCMN	8	253019	253492	256342	256905	1	2851	3368	3885	1	10	1	0	1 06:02
192	TCMN1	TCMN	12	184588	185813	189070	189603	1	3258	4136	5014	1	10	1	0	1 06:02
280	TCMN1	TCMN	16	350221	350341	354840	355341	1	4500	4810	5119	1	10	1	0	1 06:02
210	TCMN1	TCMN	12	1007701	1008390	1012226	1013592	1	3837	4864	5890	1	10	1	0	1 06:02
208	TCMN1	TCMN	12	822848	823256	826618	829421	1	3363	4968	6572	1	10	1	0	1 06:02
3	TCMN1	TCMN	1	88008	90330	95552	95748	1	5223	6481	7739	1	10	1	0	1 06:02
57	TCMN1	TCMN	4	1475397	1476168	1482150	1483110	1	5983	6848	7712	1	10	1	0	1 06:02
1	TCMN1	TCMN	1	41987	42103	42103	42115	1	1	64	127	1	10.1	1	0	1 02:06
264	TCMN1	TCMN	15	978537	978614	978614	978665	1	1	64	127	1	10.1	1	0	1 02:06
270	TCMN1	TCMN	16	64053	64204	64204	64299	1	1	123	245	1	10.1	1	0	1 02:06
27	TCMN1	TCMN	3	148271	148481	148481	148587	1	1	158	315	1	10.1	1	0	1 02:06
221	TCMN1	TCMN	13	235740	235798	235798	236240	1	1	250	499	1	10.1	1	0	1 02:06
196	TCMN1	TCMN	12	301472	301852	301852	302004	1	1	266	531	1	10.1	1	0	1 02:06
50	TCMN1	TCMN	4	863685	863843	863843	864219	1	1	267	533	1	10.1	1	0	1 02:06
109	TCMN1	TCMN	7	839712	839880	839900	840315	1	21	312	602	1	10.1	1	0	1 02:06
254	TCMN1	TCMN	15	466340	466702	466762	467008	1	61	364	667	1	10.1	1	0	1 02:06
235	TCMN1	TCMN	14	43912	44757	44757	44844	1	1	466	931	1	10.1	1	0	1 02:06
77	TCMN1	TCMN	6	184083	184225	184483	184798	1	259	487	714	1	10.1	1	0	1 02:06
104	TCMN1	TCMN	7	599725	599815	599896	600628	1	82	492	902	1	10.1	1	0	1 02:06
64	TCMN1	TCMN	5	65418	65622	65985	66105	1	364	525	686	1	10.1	1	0	1 02:06
96	TCMN1	TCMN	7	288805	289212	289440	289648	1	229	536	842	1	10.1	1	0	1 02:06
288	TCMN1	TCMN	16	712507	713201	713201	713880	1	1	687	1372	1	10.1	1	0	1 02:06
291	TCMN1	TCMN	16	892106	892211	892709	892994	1	499	693	887	1	10.1	1	0	1 02:06
23	TCMN1	TCMN	3	96055	96799	96988	97369	1	190	752	1313	1	10.1	1	0	1 02:06
61	TCMN1	TCMN	4	1520098	1521369	1521427	1521711	1	59	836	1612	1	10.1	1	0	1 02:06
223	TCMN1	TCMN	13	331787	332507	332932	333053	1	426	846	1265	1	10.1	1	0	1 02:06
170	TCMN1	TCMN	10	709369	709746	709747	711083	1	2	858	1713	1	10.1	1	0	1 02:06
211	TCMN1	TCMN	12	1028477	1028782	1028782	1030239	1	1	881	1761	1	10.1	1	0	1 02:06
204	TCMN1	TCMN	12	629690	629914	630568	630870	1	655	917	1179	1	10.1	1	0	1 02:06
135	TCMN1	TCMN	9	33227	33678	34273	34525	1	596	947	1297	1	10.1	1	0	1 02:06
177	TCMN1	TCMN	11	374411	375794	375794	376307	1	1	948	1895	1	10.1	1	0	1 02:06
76	TCMN1	TCMN	6	152137	153281	153344	153974	1	64	950	1836	1	10.1	1	0	1 02:06
215	TCMN1	TCMN	13	91960	92531	92531	93961	1	1	1001	2000	1	10.1	1	0	1 02:06
113	TCMN1	TCMN	7	944010	944981	945166	946206	1	186	1191	2195	1	10.1	1	0	1 02:06
31	TCMN1	TCMN	3	230267	231791	231858	232833	1	68	1317	2565	1	10.1	1	0	1 02:06
56	TCMN1	TCMN	4	1347683	1349666	1350213	1350342	1	548	1603	2658	1	10.1	1	0	1 02:06
32	TCMN1	TCMN	3	235472	236284	236961	238082	1	678	1644	2609	1	10.1	1	0	1 02:06
121	TCMN1	TCMN	8	73929	73993	75768	76067	1	1776	1957	2137	1	10.1	1	0	1 02:06
141	TCMN1	TCMN	9	246806	246926	248675	249032	1	1750	1988	2225	1	10.1	1	0	1 02:06
148	TCMN1	TCMN	9	368217	368576	370178	370992	1	1603	2189	2774	1	10.1	1	0	1 02:06
88	TCMN1	TCMN	7	54056	54723	55957	57501	1	1235	2340	3444	1	10.1	1	0	1 02:06
218	TCMN1	TCMN	13	138042	138343	140328	140757	1	1986	2350	2714	1	10.1	1	0	1 02:06

159	TCMN1	TCMN	10	148569	149059	151245	151609		1	2187	2613	3039	1	10.1	1	0	1	02:06
78	TCMN1	TCMN	6	201959	203115	205431	205702		1	2317	3030	3742	1	10.1	1	0	1	02:06
145	TCMN1	TCMN	9	329125	334329	334775	334877		1	447	3099	5751	1	10.1	1	0	1	02:06
66	TCMN1	TCMN	5	122503	122997	126071	126254		1	3075	3413	3750	1	10.1	1	0	1	02:06
226	TCMN1	TCMN	13	445712	446574	449412	450562		1	2839	3844	4849	1	10.1	1	0	1	02:06
279	TCMN1	TCMN	16	307847	308140	311970	312483		1	3831	4233	4635	1	10.1	1	0	1	02:06
87	TCMN1	TCMN	7	46634	46860	50656	51330		1	3797	4246	4695	1	10.1	1	0	1	02:06
130	TCMN1	TCMN	8	372612	372964	377086	377259		1	4123	4385	4646	1	10.1	1	0	1	02:06
25	TCMN1	TCMN	3	133913	134648	138345	139189		1	3698	4487	5275	1	10.1	1	0	1	02:06
80	TCMN1	TCMN	6	225130	225428	229991	230223		1	4564	4828	5092	1	10.1	1	0	1	02:06
286	TCMN1	TCMN	16	515535	516710	524743	525272		1	8034	8885	9736	1	10.1	1	0	1	02:06
166	TCMN1	TCMN	10	568805	572936	574799	578943	2_nonsis		1864	6001	10137	3	30	1	0	1	2:6_6:2
263	TCMN1	TCMN	15	957717	957993	959820	960152	2_nonsis		1828	2131	2434	3	30	1	0	1	2:6_4:4_6:2
184	TCMN1	TCMN	11	614318	614450	617753	618317	2_nonsis		3304	3651	3998	3	30	1	0	1	6:2_2:6_6:2
241	TCMN1	TCMN	14	388819	389266	392860	393703	2_nonsis		3595	4239	4883	3	30	1	0	1	2:6_6:2_2:6
7	TCMN1	TCMN	1	190429	190880	194952	195144	2_nonsis		4073	4394	4714	3	30	1	0	1	6:2_4:4_2:6
169	TCMN1	TCMN	10	651682	652362	656567	656822	2_nonsis		4206	4673	5139	3	30	1	0	1	6:2_2:6_4:4_2:6
14	TCMN1	TCMN	2	252423	252499	252589	253219	2_nonsis		91	443	795	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
176	TCMN1	TCMN	11	276275	276893	276968	277294	2_nonsis		76	547	1018	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
265	TCMN1	TCMN	15	1006391	1007049	1007685	1008443	2_nonsis		637	1344	2051	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
248	TCMN1	TCMN	15	44801	45210	46201	46903	2_nonsis		992	1547	2101	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
18	TCMN1	TCMN	2	527102	527601	528108	528212	2_nonsis		508	809	1109	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
74	TCMN1	TCMN	6	113910	114171	115119	115151	2_nonsis		949	1095	1240	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
229	TCMN1	TCMN	13	663189	663903	664811	665349	2_nonsis		909	1534	2159	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
199	TCMN1	TCMN	12	392012	392046	393632	394020	2_nonsis		1587	1797	2007	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
84	TCMN1	TCMN	6	254411	254477	256222	256299	2_nonsis		1746	1817	1887	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
290	TCMN1	TCMN	16	778795	779145	780767	780924	2_nonsis		1623	1876	2128	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
95	TCMN1	TCMN	7	183038	183709	185240	185280	2_nonsis		1532	1887	2241	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
100	TCMN1	TCMN	7	443342	443602	445067	446059	2_nonsis		1466	2091	2716	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
73	TCMN1	TCMN	6	29993	30249	32259	32355	2_nonsis		2011	2186	2361	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
157	TCMN1	TCMN	10	135448	135579	137767	138413	2_nonsis		2189	2577	2964	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
123	TCMN1	TCMN	8	99112	99909	104568	105227	2_nonsis		4660	5387	6114	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
155	TCMN1	TCMN	10	81409	81757	88033	88303	2_nonsis		6277	6585	6893	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
246	TCMN1	TCMN	14	724364	724425	728369	729511	2_nonsis		3945	4546	5146	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)_(6:2)_(4:4a)
33	TCMN1	TCMN	3	273452	273723	273788	273881	2_nonsis		66	247	428	1	15	1	1	0	(6:2)_(4:4aCO)
55	TCMN1	TCMN	4	1335206	1335398	1335398	1335831	2_nonsis		1	313	624	1	15	1	1	0	(6:2)_(4:4aCO)
46	TCMN1	TCMN	4	775671	775941	776086	776259	2_nonsis		146	367	587	1	15	1	1	0	(6:2)_(4:4aCO)
152	TCMN1	TCMN	9	407154	407232	407232	407953	2_nonsis		1	400	798	1	15	1	1	0	(6:2)_(4:4aCO)
16	TCMN1	TCMN	2	497990	498089	498404	498575	2_nonsis		316	450	584	1	15	1	1	0	(6:2)_(4:4aCO)
34	TCMN1	TCMN	3	275423	275765	275817	276449	2_nonsis		53	539	1025	1	15	1	1	0	(6:2)_(4:4aCO)
281	TCMN1	TCMN	16	366380	366595	367091	367109	2_nonsis		497	613	728	1	15	1	1	0	(6:2)_(4:4aCO)
63	TCMN1	TCMN	5	46984	47089	47165	48256	2_nonsis		77	674	1271	1	15	1	1	0	(6:2)_(4:4aCO)
212	TCMN1	TCMN	13	44503	45656	45656	45908	2_nonsis		1	703	1404	1	15	1	1	0	(6:2)_(4:4aCO)
283	TCMN1	TCMN	16	444920	445448	445985	446142	2_nonsis		538	880	1221	1	15	1	1	0	(6:2)_(4:4aCO)
117	TCMN1	TCMN	7	982112	982548	983164	983358	2_nonsis		617	931	1245	1	15	1	1	0	(6:2)_(4:4aCO)
40	TCMN1	TCMN	4	151093	152053	152269	152758	2_nonsis		217	941	1664	1	15	1	1	0	(6:2)_(4:4aCO)
126	TCMN1	TCMN	8	248808	249226	249527	250465	2_nonsis		302	979	1656	1	15	1	1	0	(6:2)_(4:4aCO)
39	TCMN1	TCMN	4	106143	106727	106899	107966	2_nonsis		173	998	1822	1	15	1	1	0	(6:2)_(4:4aCO)
60	TCMN1	TCMN	4	1505853	1506604	1506992	1507780	2_nonsis		389	1158	1926	1	15	1	1	0	(6:2)_(4:4aCO)
119	TCMN1	TCMN	7	1016232	1017661	1017661	1018655	2_nonsis		1	1212	2422	1	15	1	1	0	(6:2)_(4:4aCO)
140	TCMN1	TCMN	9	240376	242535	242863	243088	2_nonsis		329	1520	2711	1	15	1	1	0	(6:2)_(4:4aCO)
110	TCMN1	TCMN	7	843110	843717	844986	845098	2_nonsis		1270	1629	1987	1	15	1	1	0	(6:2)_(4:4aCO)
285	TCMN1	TCMN	16	459333	460996	461367	462342	2_nonsis		372	1690	3008	1	15	1	1	0	(6:2)_(4:4aCO)
15	TCMN1	TCMN	2	269036	269402	270387	271598	2_nonsis		986	1774	2561	1	15	1	1	0	(6:2)_(4:4aCO)
274	TCMN1	TCMN	16	106600	107304	108552	109014	2_nonsis		1249	1831	2413	1	15	1	1	0	(6:2)_(4:4aCO)
249	TCMN1	TCMN	15	125806	126267	127669	128123	2_nonsis		1403	1860	2316	1	15	1	1	0	(6:2)_(4:4aCO)
6	TCMN1	TCMN	1	166820	166931	167179	170726	2_nonsis		249	2077	3905	1	15	1	1	0	(6:2)_(4:4aCO)
234	TCMN1	TCMN	14	39652	40306	42185	42326	2_nonsis		1880	2277	2673	1	15	1	1	0	(6:2)_(4:4aCO)
252	TCMN1	TCMN	15	323813	323974	325987	326413	2_nonsis		2014	2307	2599	1	15	1	1	0	(6:2)_(4:4aCO)
2	TCMN1	TCMN	1	80554	80715	82379	83613	2_nonsis		1665	2362	3058	1	15	1	1	0	(6:2)_(4:4aCO)

217	TCMN1	TCMN	13	98310	98939	100803	101176	2_nonsis	1865	2365	2865	1	15	1	1	0	(6:2)_(4:4aCO)
245	TCMN1	TCMN	14	637457	639165	640431	640932	2_nonsis	1267	2371	3474	1	15	1	1	0	(6:2)_(4:4aCO)
151	TCMN1	TCMN	9	390275	393280	393280	395260	2_nonsis	1	2493	4984	1	15	1	1	0	(6:2)_(4:4aCO)
239	TCMN1	TCMN	14	207358	207879	210240	210438	2_nonsis	2362	2721	3079	1	15	1	1	0	(6:2)_(4:4aCO)
30	TCMN1	TCMN	3	223339	228130	228130	230267	2_nonsis	1	3464	6927	1	15	1	1	0	(6:2)_(4:4aCO)
67	TCMN1	TCMN	5	187071	187243	190541	190754	2_nonsis	3299	3491	3682	1	15	1	1	0	(6:2)_(4:4aCO)
101	TCMN1	TCMN	7	450623	451100	454212	454910	2_nonsis	3113	3700	4286	1	15	1	1	0	(6:2)_(4:4aCO)
236	TCMN1	TCMN	14	49011	49737	52925	53465	2_nonsis	3189	3821	4453	1	15	1	1	0	(6:2)_(4:4aCO)
220	TCMN1	TCMN	13	194821	195330	196123	202482	2_nonsis	794	4227	7660	1	15	1	1	0	(6:2)_(4:4aCO)
202	TCMN1	TCMN	12	565625	566307	570142	570914	2_nonsis	3836	4562	5288	1	15	1	1	0	(6:2)_(4:4aCO)
45	TCMN1	TCMN	4	589875	590328	596055	597058	2_nonsis	5728	6455	7182	1	15	1	1	0	(6:2)_(4:4aCO)
243	TCMN1	TCMN	14	503261	504296	510838	511502	2_nonsis	6543	7392	8240	1	15	1	1	0	(6:2)_(4:4aCO)
207	TCMN1	TCMN	12	803833	808209	813365	814017	2_nonsis	5157	7670	10183	1	15	1	1	0	(6:2)_(4:4aCO)
284	TCMN1	TCMN	16	447002	448559	456671	458489	2_nonsis	8113	9800	11486	1	15	1	1	0	(6:2)_(4:4aCO)
237	TCMN1	TCMN	14	103068	103902	117410	117759	2_nonsis	13509	14100	14690	1	15	1	1	0	(6:2)_(4:4aCO)
24	TCMN1	TCMN	3	103649	103757	103813	103955	2_nonsis	57	181	305	1	16	1	1	0	(2:6)_(4:4aCO)
115	TCMN1	TCMN	7	972982	973057	973111	973354	2_nonsis	55	213	371	1	16	1	1	0	(2:6)_(4:4aCO)
71	TCMN1	TCMN	5	498820	499353	499353	499401	2_nonsis	1	291	580	1	16	1	1	0	(2:6)_(4:4aCO)
287	TCMN1	TCMN	16	623051	623271	623271	623671	2_nonsis	1	310	619	1	16	1	1	0	(2:6)_(4:4aCO)
42	TCMN1	TCMN	4	228508	228806	228806	229191	2_nonsis	1	342	682	1	16	1	1	0	(2:6)_(4:4aCO)
136	TCMN1	TCMN	9	47054	47493	47656	47766	2_nonsis	164	438	711	1	16	1	1	0	(2:6)_(4:4aCO)
122	TCMN1	TCMN	8	77306	77625	77625	78204	2_nonsis	1	449	897	1	16	1	1	0	(2:6)_(4:4aCO)
53	TCMN1	TCMN	4	1270902	1271755	1271812	1271871	2_nonsis	58	513	968	1	16	1	1	0	(2:6)_(4:4aCO)
224	TCMN1	TCMN	13	399473	399941	399941	400537	2_nonsis	1	532	1063	1	16	1	1	0	(2:6)_(4:4aCO)
35	TCMN1	TCMN	4	38202	38924	38924	39272	2_nonsis	1	535	1069	1	16	1	1	0	(2:6)_(4:4aCO)
163	TCMN1	TCMN	10	374415	375038	375163	375392	2_nonsis	126	551	976	1	16	1	1	0	(2:6)_(4:4aCO)
276	TCMN1	TCMN	16	193383	193773	193788	194710	2_nonsis	16	671	1326	1	16	1	1	0	(2:6)_(4:4aCO)
185	TCMN1	TCMN	11	619794	620047	620500	620816	2_nonsis	454	738	1021	1	16	1	1	0	(2:6)_(4:4aCO)
158	TCMN1	TCMN	10	144558	144958	145341	145726	2_nonsis	384	776	1167	1	16	1	1	0	(2:6)_(4:4aCO)
278	TCMN1	TCMN	16	303354	304561	304734	304831	2_nonsis	174	825	1476	1	16	1	1	0	(2:6)_(4:4aCO)
244	TCMN1	TCMN	14	546237	546338	546598	547766	2_nonsis	261	895	1528	1	16	1	1	0	(2:6)_(4:4aCO)
125	TCMN1	TCMN	8	185625	186453	186453	187527	2_nonsis	1	951	1901	1	16	1	1	0	(2:6)_(4:4aCO)
233	TCMN1	TCMN	13	860181	861184	861205	862065	2_nonsis	22	953	1883	1	16	1	1	0	(2:6)_(4:4aCO)
91	TCMN1	TCMN	7	91031	91449	91862	92820	2_nonsis	414	1101	1788	1	16	1	1	0	(2:6)_(4:4aCO)
94	TCMN1	TCMN	7	168156	169165	169612	170211	2_nonsis	448	1251	2054	1	16	1	1	0	(2:6)_(4:4aCO)
182	TCMN1	TCMN	11	558690	559170	559707	560658	2_nonsis	538	1253	1967	1	16	1	1	0	(2:6)_(4:4aCO)
131	TCMN1	TCMN	8	448997	449277	450359	450521	2_nonsis	1083	1303	1523	1	16	1	1	0	(2:6)_(4:4aCO)
255	TCMN1	TCMN	15	468364	468561	469548	470004	2_nonsis	988	1314	1639	1	16	1	1	0	(2:6)_(4:4aCO)
105	TCMN1	TCMN	7	642731	643019	643019	645676	2_nonsis	1	1473	2944	1	16	1	1	0	(2:6)_(4:4aCO)
256	TCMN1	TCMN	15	487028	487809	488859	488996	2_nonsis	1051	1509	1967	1	16	1	1	0	(2:6)_(4:4aCO)
165	TCMN1	TCMN	10	464438	465282	465795	467010	2_nonsis	514	1543	2571	1	16	1	1	0	(2:6)_(4:4aCO)
181	TCMN1	TCMN	11	534319	535346	536243	536702	2_nonsis	898	1640	2382	1	16	1	1	0	(2:6)_(4:4aCO)
197	TCMN1	TCMN	12	346698	346884	348364	348561	2_nonsis	1481	1672	1862	1	16	1	1	0	(2:6)_(4:4aCO)
275	TCMN1	TCMN	16	141675	141867	143532	143626	2_nonsis	1666	1808	1950	1	16	1	1	0	(2:6)_(4:4aCO)
106	TCMN1	TCMN	7	703857	705631	706439	706722	2_nonsis	809	1837	2864	1	16	1	1	0	(2:6)_(4:4aCO)
203	TCMN1	TCMN	12	625064	627007	627543	628274	2_nonsis	537	1873	3209	1	16	1	1	0	(2:6)_(4:4aCO)
209	TCMN1	TCMN	12	983190	986295	986469	986946	2_nonsis	175	1965	3755	1	16	1	1	0	(2:6)_(4:4aCO)
52	TCMN1	TCMN	4	1056739	1057249	1058864	1059094	2_nonsis	1616	1985	2354	1	16	1	1	0	(2:6)_(4:4aCO)
150	TCMN1	TCMN	9	384922	385024	387056	387285	2_nonsis	2033	2198	2362	1	16	1	1	0	(2:6)_(4:4aCO)
179	TCMN1	TCMN	11	471663	472114	474020	474395	2_nonsis	1907	2319	2731	1	16	1	1	0	(2:6)_(4:4aCO)
103	TCMN1	TCMN	7	557181	557367	559498	559914	2_nonsis	2132	2432	2732	1	16	1	1	0	(2:6)_(4:4aCO)
29	TCMN1	TCMN	3	210635	211159	212063	214762	2_nonsis	905	2516	4126	1	16	1	1	0	(2:6)_(4:4aCO)
190	TCMN1	TCMN	12	168352	168861	171076	171335	2_nonsis	2216	2599	2982	1	16	1	1	0	(2:6)_(4:4aCO)
262	TCMN1	TCMN	15	897794	898703	900879	900929	2_nonsis	2177	2656	3134	1	16	1	1	0	(2:6)_(4:4aCO)
174	TCMN1	TCMN	11	168746	169345	171261	172151	2_nonsis	1917	2661	3404	1	16	1	1	0	(2:6)_(4:4aCO)
51	TCMN1	TCMN	4	866041	866146	868704	869203	2_nonsis	2559	2860	3161	1	16	1	1	0	(2:6)_(4:4aCO)
167	TCMN1	TCMN	10	582845	583178	585466	586827	2_nonsis	2289	3135	3981	1	16	1	1	0	(2:6)_(4:4aCO)
134	TCMN1	TCMN	8	521047	521132	524576	524611	2_nonsis	3445	3504	3563	1	16	1	1	0	(2:6)_(4:4aCO)
72	TCMN1	TCMN	5	500606	501719	504481	505113	2_nonsis	2763	3635	4506	1	16	1	1	0	(2:6)_(4:4aCO)
102	TCMN1	TCMN	7	473951	474282	477384	478308	2_nonsis	3103	3730	4356	1	16	1	1	0	(2:6)_(4:4aCO)

258	TCMN1	TCMN	15	659154	660208	662842	664181	2_nonsis		2635	3831	5026	1	16	1	1	0	(2:6)_(4:4aCO)
277	TCMN1	TCMN	16	195918	196451	200515	200755	2_nonsis		4065	4451	4836	1	16	1	1	0	(2:6)_(4:4aCO)
260	TCMN1	TCMN	15	795030	795362	799553	800155	2_nonsis		4192	4658	5124	1	16	1	1	0	(2:6)_(4:4aCO)
44	TCMN1	TCMN	4	582739	583013	587057	588381	2_nonsis		4045	4843	5641	1	16	1	1	0	(2:6)_(4:4aCO)
153	TCMN1	TCMN	9	412588	412645	417395	417709	2_nonsis		4751	4936	5120	1	16	1	1	0	(2:6)_(4:4aCO)
168	TCMN1	TCMN	10	589894	590704	590704	601293	2_nonsis		1	5700	11398	1	16	1	1	0	(2:6)_(4:4aCO)
47	TCMN1	TCMN	4	825422	831279	831279	837275	2_nonsis		1	5927	11852	1	16	1	1	0	(2:6)_(4:4aCO)
183	TCMN1	TCMN	11	587530	587779	593181	594179	2_nonsis		5403	6026	6648	1	16	1	1	0	(2:6)_(4:4aCO)
161	TCMN1	TCMN	10	233724	233805	240364	240782	2_nonsis		6560	6809	7057	1	16	1	1	0	(2:6)_(4:4aCO)
108	TCMN1	TCMN	7	796858	798046	805722	806818	2_nonsis		7677	8818	9959	1	16	1	1	0	(2:6)_(4:4aCO)
289	TCMN1	TCMN	16	775448	775673	775448	775673	2_nonsis		0	112	224	1	100	1	1	0	(4:4aCO)
266	TCMN1	TCMN	15	1031754	1032017	1031754	1032017	2_nonsis		0	131	262	1	100	1	1	0	(4:4aCO)
17	TCMN1	TCMN	2	515316	515610	515316	515610	2_nonsis		0	147	293	1	100	1	1	0	(4:4aCO)
111	TCMN1	TCMN	7	898107	898653	898107	898653	2_nonsis		0	273	545	1	100	1	1	0	(4:4aCO)
173	TCMN1	TCMN	11	106973	107555	106973	107555	2_nonsis		0	291	581	1	100	1	1	0	(4:4aCO)
222	TCMN1	TCMN	13	237159	237882	237159	237882	2_nonsis		0	361	722	1	100	1	1	0	(4:4aCO)
216	TCMN1	TCMN	13	96022	96832	96022	96832	2_nonsis		0	405	809	1	100	1	1	0	(4:4aCO)
271	TCMN1	TCMN	16	66527	67491	66527	67491	2_nonsis		0	482	963	1	100	1	1	0	(4:4aCO)
116	TCMN1	TCMN	7	979753	980911	979753	980911	2_nonsis		0	579	1157	1	100	1	1	0	(4:4aCO)
187	TCMN1	TCMN	12	38737	39963	38737	39963	2_nonsis		0	613	1225	1	100	1	1	0	(4:4aCO)
48	TCMN1	TCMN	4	844304	845613	844304	845613	2_nonsis		0	654	1308	1	100	1	1	0	(4:4aCO)
272	TCMN1	TCMN	16	77509	78895	77509	78895	2_nonsis		0	693	1385	1	100	1	1	0	(4:4aCO)
282	TCMN1	TCMN	16	421124	422575	421124	422575	2_nonsis		0	725	1450	1	100	1	1	0	(4:4aCO)
10	TCMN1	TCMN	2	67361	68817	67361	68817	2_nonsis		0	728	1455	1	100	1	1	0	(4:4aCO)
26	TCMN1	TCMN	3	141799	143316	141799	143316	2_nonsis		0	758	1516	1	100	1	1	0	(4:4aCO)
59	TCMN1	TCMN	4	1503574	1505138	1503574	1505138	2_nonsis		0	782	1563	1	100	1	1	0	(4:4aCO)
188	TCMN1	TCMN	12	40119	41721	40119	41721	2_nonsis		0	801	1601	1	100	1	1	0	(4:4aCO)
267	TCMN1	TCMN	15	1069426	1071028	1069426	1071028	2_nonsis		0	801	1601	1	100	1	1	0	(4:4aCO)
206	TCMN1	TCMN	12	800672	802287	800672	802287	2_nonsis		0	807	1614	1	100	1	1	0	(4:4aCO)
154	TCMN1	TCMN	10	26958	28612	26958	28612	2_nonsis		0	827	1653	1	100	1	1	0	(4:4aCO)
144	TCMN1	TCMN	9	320712	323343	320712	323343	2_nonsis		0	1315	2630	1	100	1	1	0	(4:4aCO)
37	TCMN1	TCMN	4	43482	46608	43482	46608	2_nonsis		0	1563	3125	1	100	1	1	0	(4:4aCO)
195	TCMN1	TCMN	12	262367	265975	262367	265975	2_nonsis		0	1804	3607	1	100	1	1	0	(4:4aCO)
5	TCMN1	TCMN	1	131303	135319	131303	135319	2_nonsis		0	2008	4015	1	100	1	1	0	(4:4aCO)
228	TCMN1	TCMN	13	469552	473747	469552	473747	2_nonsis		0	2097	4194	1	100	1	1	0	(4:4aCO)
4	TCMN1	TCMN	1	121235	128637	121235	128637	2_nonsis		0	3701	7401	1	100	1	1	0	(4:4aCO)
240	TCMN1	TCMN	14	235424	235706	240152	240414	2_nonsis		4447	4718	4989	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
164	TCMN1	TCMN	10	377800	378111	383067	383417	2_nonsis		4957	5287	5616	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
200	TCMN1	TCMN	12	404478	405334	413032	413115	2_nonsis		7699	8168	8636	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
68	TCMN1	TCMN	5	220166	220626	221827	222207	2_nonsis		1202	1621	2040	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
28	TCMN1	TCMN	3	165706	165982	167541	167741	2_nonsis		1560	1797	2034	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
162	TCMN1	TCMN	10	367642	368244	370407	371132	2_nonsis		2164	2827	3489	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
178	TCMN1	TCMN	11	403561	404302	406489	407067	2_nonsis		2188	2847	3505	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
186	TCMN1	TCMN	11	629639	629864	632117	633545	2_nonsis		2254	3080	3905	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
273	TCMN1	TCMN	16	88834	89075	93022	93712	2_nonsis		3948	4413	4877	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
43	TCMN1	TCMN	4	367564	368207	372757	372821	2_nonsis		4551	4904	5256	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
257	TCMN1	TCMN	15	505622	505999	514857	516270	2_nonsis		8859	9753	10647	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
292	TCMN1	TCMN	16	912647	913446	915200	915973	2_nonsis		1755	2540	3325	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
69	TCMN1	TCMN	5	385850	385956	391914	392090	2_nonsis		5959	6099	6239	3	20	1	1	0	(2:6)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
142	TCMN1	TCMN	9	280331	280761	292870	296453	2_nonsis		12110	14116	16121	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
175	TCMN1	TCMN	11	211408	211676	213763	213930	2_nonsis		2088	2305	2521	3	20	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(2:6)_(4:4a)
238	TCMN1	TCMN	14	155435	155903	161474	161874	2_nonsis		5572	6005	6438	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
124	TCMN1	TCMN	8	135729	135947	139506	141400	2_sis		3560	4615	5670	0	1	2	0	2	(2:6)_(0:8)_(4:4)
139	TCMN1	TCMN	9	158276	160453	165039	165195	2_sis		4587	5753	6918	0	1	2	0	2	(2:6)_(4:4)_(2:6)_(4:4)
194	TCMN1	TCMN	12	252885	253274	256406	256727	2_sis		3133	3487	3841	0	1	2	0	2	(0:8)_(2:6)_(4:4)
232	TCMN1	TCMN	13	828518	828927	829545	830002	2_sis		619	1051	1483	0	1	2	0	2	(0:8)_(2:6)_(4:4)
253	TCMN1	TCMN	15	408540	408953	415035	415710	2_sis		6083	6626	7169	0	1	2	0	2	(2:6)_(0:8)_(2:6a)_(4:4)
8	TCMN1	TCMN	2	26161	27032	28960	35660		3	1929	5714	9498	0	2	2	1	1	(8:0)_(4:4aCO)
9	TCMN1	TCMN	2	44047	44210	48762	49603		3	4553	5054	5555	0	2	2	1	1	(6:2)_(4:4)_(2:6)_(6:2a)_(4:4aCO)
12	TCMN1	TCMN	2	113452	113971	120585	121110		3	6615	7136	7657	0	2	2	1	1	(8:0)_(6:2)_(8:0)_(6:2)_(4:4aCO)

20	TCMN1	TCMN	2	783892	784213	786589	789930	3	2377	4207	6037	0	2	2	1	1	(2:6)_(2:6a)_(0:8)_(2:6a)_(0:8)_(4:4aCO)
22	TCMN1	TCMN	3	71310	71391	79460	79758	3	8070	8259	8447	0	2	2	1	1	(2:6)_(4:4)_(2:6)_(0:8)_(2:6a)_(6:2)_(4:4aCO)
38	TCMN1	TCMN	4	57910	58341	62205	62366	3	3865	4160	4455	0	2	2	1	1	(2:6)_(6:2)_(8:0)_(4:4aCO)
62	TCMN1	TCMN	5	40898	41432	45019	45548	4	3588	4119	4649	0	2	2	1	1	(2:6)_(6:2)_(8:0)_(6:2a)_(4:4aCO)
75	TCMN1	TCMN	6	116839	118034	123435	123676	3	5402	6119	6836	0	2	2	1	1	(2:6)_(4:4aCO)_(6:2)_(4:4a)
82	TCMN1	TCMN	6	241206	241524	243667	243783	3	2144	2360	2576	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
86	TCMN1	TCMN	7	40619	40984	43798	44099	3	2815	3147	3479	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
90	TCMN1	TCMN	7	79203	80122	85628	86321	3	5507	6312	7117	0	2	2	1	1	(6:2)_(8:0)_(6:2)_(4:4aCO)
98	TCMN1	TCMN	7	321824	322208	331760	332360	3	9553	10044	10535	0	2	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4a)
120	TCMN1	TCMN	8	36778	37084	38190	38418	3	1107	1373	1639	0	2	2	1	1	(6:2)_(4:4)_(2:6)_(4:4aCO)
137	TCMN1	TCMN	9	54480	55071	57173	57568	3	2103	2595	3087	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)
143	TCMN1	TCMN	9	296453	297675	299287	302738	3	1613	3949	6284	0	2	2	1	1	(2:6)_(4:4aCO)
147	TCMN1	TCMN	9	359494	359599	363925	364352	4	4327	4592	4857	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(2:6)_(4:4aCO)
193	TCMN1	TCMN	12	199043	199425	201727	202093	3	2303	2676	3049	0	2	2	1	1	(6:2)_(8:0)_(4:4aCO)
213	TCMN1	TCMN	13	71397	71867	73368	75046	3	1502	2575	3648	0	2	2	1	1	(2:6)_(4:4aCO)
214	TCMN1	TCMN	13	83417	83709	83964	84058	3	256	448	640	0	2	2	1	1	(6:2)_(4:4aCO)
219	TCMN1	TCMN	13	145063	146198	146198	149583	3	1	2260	4519	0	2	2	1	1	(2:6)_(4:4aCO)
231	TCMN1	TCMN	13	795326	795946	800977	801034	3	5032	5370	5707	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
268	TCMN1	TCMN	16	34674	35338	43958	44051	3	8621	8999	9376	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
293	TCMN1	TCMN	16	918448	918658	920048	920779	3	1391	1861	2330	0	2	2	1	1	(6:2)_(4:4aCO)_(2:6)_(0:8)_(2:6)_(4:4a)
13	TCMN1	TCMN	2	123008	123103	125786	125843	2_nonsis	2684	2759	2834	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4CO)_(6:2)_(4:4aCO)
19	TCMN1	TCMN	2	659928	660972	668082	669586	3	7111	8384	9657	0	3	2	0	2	(6:2)_(6:2a)_(4:4aCO)_(4:4CO)
21	TCMN1	TCMN	3	40637	40987	43346	43513	4	2360	2618	2875	0	3	2	2	0	(2:6)_(4:4aCO)_(4:4bCO)_(2:6a)_(4:4b)
36	TCMN1	TCMN	4	41360	41423	43075	43335	3	1653	1814	1974	0	3	2	1	1	(2:6)_(4:4aCO)_(4:4bCO)
41	TCMN1	TCMN	4	154129	155368	167826	169331	3	12459	13830	15201	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)
65	TCMN1	TCMN	5	103937	104269	105493	105743	2_nonsis	1225	1515	1805	0	3	2	1	1	(6:2)_(4:4aCO)_(4:4CO)_(4:4aCO)
92	TCMN1	TCMN	7	93397	94650	94650	96070	3	1	1337	2672	0	3	2	1	1	(4:4aCO)_(4:4bCO)
107	TCMN1	TCMN	7	763517	765055	768165	768310	4	3111	3952	4792	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(2:6a)_(4:4bCO)
129	TCMN1	TCMN	8	326461	327083	329634	330227	3	2552	3159	3765	0	3	2	1	1	(4:4aCO)_(8:0)_(6:2)_(4:4CO)_(6:2)_(4:4aCO)
132	TCMN1	TCMN	8	483502	483796	488588	489445	4	4793	5368	5942	0	3	2	0	2	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)
138	TCMN1	TCMN	9	98294	98672	100530	102247	2_nonsis	1859	2906	3952	0	3	2	0	2	(2:6)_(4:4)_(2:6)_(4:4aCO)_(4:4CO)
146	TCMN1	TCMN	9	338145	338225	348958	349855	4	10734	11222	11709	0	3	2	1	1	(2:6)_(4:4)_(6:2)_(2:6a)_(4:4aCO)_(6:2a)_(8:0)_(6:2)_(4:4bCO)_(6:2)_(4:4CO)
149	TCMN1	TCMN	9	382403	382459	383079	383427	3	621	822	1023	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
201	TCMN1	TCMN	12	538633	539092	547203	548297	3	8112	8888	9663	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)
225	TCMN1	TCMN	13	406917	408897	410894	411113	4	1998	3097	4195	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2a)_(4:4bCO)
242	TCMN1	TCMN	14	416620	416832	420961	421631	3	4130	4570	5010	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
250	TCMN1	TCMN	15	190009	191548	192333	193685	2_nonsis	786	2231	3675	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4CO)
251	TCMN1	TCMN	15	199130	199433	214878	215265	4	15446	15790	16134	0	3	2	2	0	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)_(6:2a)_(4:4b)
261	TCMN1	TCMN	15	838603	839012	840426	840781	3	1415	1796	2177	0	3	2	1	1	(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
269	TCMN1	TCMN	16	46921	46996	48911	48928	3	1916	1961	2006	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)
129	TCMN2	TCMN	15	900141	900879	905801	906405	1	4923	5593	6263	1	8	1	0	1	2:6_4:4_2:6
123	TCMN2	TCMN	15	216376	216399	216399	216499	1	1	62	122	1	10	1	0	1	06:02
68	TCMN2	TCMN	9	30609	30632	30632	30845	1	1	118	235	1	10	1	0	1	06:02
11	TCMN2	TCMN	2	476602	476950	477263	477343	1	314	527	740	1	10	1	0	1	06:02
61	TCMN2	TCMN	8	10046	10240	10670	10789	1	431	587	742	1	10	1	0	1	06:02
14	TCMN2	TCMN	2	673785	674021	676125	676899	1	2105	2609	3113	1	10	1	0	1	06:02
47	TCMN2	TCMN	5	521881	523683	525075	525798	1	1393	2655	3916	1	10	1	0	1	06:02
1	TCMN2	TCMN	1	68551	71312	71616	73633	1	305	2693	5081	1	10	1	0	1	06:02
136	TCMN2	TCMN	16	649916	650861	653932	654370	1	3072	3763	4453	1	10	1	0	1	06:02
17	TCMN2	TCMN	2	714638	715332	718805	719463	1	3474	4149	4824	1	10	1	0	1	06:02
25	TCMN2	TCMN	4	126408	127476	131084	131276	1	3609	4238	4867	1	10	1	0	1	06:02
79	TCMN2	TCMN	10	377800	378111	384523	385172	1	6413	6892	7371	1	10	1	0	1	06:02
26	TCMN2	TCMN	4	173074	173380	180800	181678	1	7421	8012	8603	1	10	1	0	1	06:02
70	TCMN2	TCMN	9	92966	92996	92996	92999	1	1	17	32	1	10.1	1	0	1	02:06
49	TCMN2	TCMN	6	82265	82465	82465	82648	1	1	192	382	1	10.1	1	0	1	02:06
37	TCMN2	TCMN	4	1279422	1279680	1280121	1280319	1	442	669	896	1	10.1	1	0	1	02:06
101	TCMN2	TCMN	13	21556	21881	22318	22495	1	438	688	938	1	10.1	1	0	1	02:06
100	TCMN2	TCMN	12	1011952	1012226	1012226	1013592	1	1	820	1639	1	10.1	1	0	1	02:06
2	TCMN2	TCMN	1	130776	130897	131303	132066	1	407	848	1289	1	10.1	1	0	1	02:06
130	TCMN2	TCMN	15	942759	943167	943688	944039	1	522	901	1279	1	10.1	1	0	1	02:06

127	TCMN2	TCMN	15	660805	661971	662365	662487	1	395	1038	1681	1	10.1	1	0	1	02:06
67	TCMN2	TCMN	8	513034	514468	515162	515676	1	695	1668	2641	1	10.1	1	0	1	02:06
34	TCMN2	TCMN	4	847053	848136	848341	850484	1	206	1818	3430	1	10.1	1	0	1	02:06
87	TCMN2	TCMN	11	308425	308754	310373	310507	1	1620	1851	2081	1	10.1	1	0	1	02:06
102	TCMN2	TCMN	13	26434	26922	28623	28695	1	1702	1981	2260	1	10.1	1	0	1	02:06
110	TCMN2	TCMN	13	627290	627607	629399	629793	1	1793	2148	2502	1	10.1	1	0	1	02:06
128	TCMN2	TCMN	15	786510	786645	788305	789501	1	1661	2326	2990	1	10.1	1	0	1	02:06
82	TCMN2	TCMN	10	718719	720598	720763	723650	1	166	2548	4930	1	10.1	1	0	1	02:06
138	TCMN2	TCMN	16	709031	709506	711691	712507	1	2186	2831	3475	1	10.1	1	0	1	02:06
119	TCMN2	TCMN	14	455102	456295	458618	459935	1	2324	3578	4832	1	10.1	1	0	1	02:06
66	TCMN2	TCMN	8	470753	470864	475549	475984	1	4686	4958	5230	1	10.1	1	0	1	02:06
12	TCMN2	TCMN	2	510710	512166	518451	518569	1	6286	7072	7858	1	10.1	1	0	1	02:06
59	TCMN2	TCMN	7	635861	636413	643019	645676	1	6607	8211	9814	1	10.1	1	0	1	02:06
120	TCMN2	TCMN	14	536942	537303	545697	545731	1	8395	8592	8788	1	10.1	1	0	1	02:06
93	TCMN2	TCMN	12	565625	566307	574726	574950	1	8420	8872	9324	1	10.1	1	0	1	02:06
137	TCMN2	TCMN	16	683285	684164	692741	693047	1	8578	9170	9761	1	10.1	1	0	1	02:06
107	TCMN2	TCMN	13	404381	404404	427114	428830	1	22711	23580	24448	1	10.1	1	0	1	02:06
27	TCMN2	TCMN	4	289475	290079	294427	295520	2_nonsis	4349	5197	6044	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
113	TCMN2	TCMN	13	801823	801852	803211	803536	2_nonsis	1360	1536	1712	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
42	TCMN2	TCMN	5	233356	234239	235495	235642	2_nonsis	1257	1771	2285	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
126	TCMN2	TCMN	15	630587	632823	634307	634570	2_nonsis	1485	2734	3982	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
29	TCMN2	TCMN	4	385243	385363	385586	385750	2_nonsis	224	365	506	1	15	1	1	0	(6:2)_(4:4aCO)
104	TCMN2	TCMN	13	83417	83709	83964	84058	2_nonsis	256	448	640	1	15	1	1	0	(6:2)_(4:4aCO)
90	TCMN2	TCMN	11	612809	613087	613259	613583	2_nonsis	173	473	773	1	15	1	1	0	(6:2)_(4:4aCO)
140	TCMN2	TCMN	16	858788	859250	859250	860233	2_nonsis	1	723	1444	1	15	1	1	0	(6:2)_(4:4aCO)
9	TCMN2	TCMN	2	340843	341186	341632	341930	2_nonsis	447	767	1086	1	15	1	1	0	(6:2)_(4:4aCO)
65	TCMN2	TCMN	8	461593	461762	461762	463767	2_nonsis	1	1087	2173	1	15	1	1	0	(6:2)_(4:4aCO)
24	TCMN2	TCMN	4	122512	123344	123436	124765	2_nonsis	93	1173	2252	1	15	1	1	0	(6:2)_(4:4aCO)
75	TCMN2	TCMN	10	22158	22350	22914	24205	2_nonsis	565	1306	2046	1	15	1	1	0	(6:2)_(4:4aCO)
139	TCMN2	TCMN	16	795316	796263	797247	797530	2_nonsis	985	1599	2213	1	15	1	1	0	(6:2)_(4:4aCO)
132	TCMN2	TCMN	16	108114	108552	109647	110433	2_nonsis	1096	1707	2318	1	15	1	1	0	(6:2)_(4:4aCO)
41	TCMN2	TCMN	5	199337	200053	201006	201879	2_nonsis	954	1748	2541	1	15	1	1	0	(6:2)_(4:4aCO)
73	TCMN2	TCMN	9	299287	302738	302738	302793	2_nonsis	1	1753	3505	1	15	1	1	0	(6:2)_(4:4aCO)
5	TCMN2	TCMN	2	36837	39234	39607	40029	2_nonsis	374	1783	3191	1	15	1	1	0	(6:2)_(4:4aCO)
112	TCMN2	TCMN	13	748748	750177	751108	751553	2_nonsis	932	1868	2804	1	15	1	1	0	(6:2)_(4:4aCO)
89	TCMN2	TCMN	11	518221	518577	520682	521296	2_nonsis	2106	2590	3074	1	15	1	1	0	(6:2)_(4:4aCO)
76	TCMN2	TCMN	10	95205	96041	98106	99116	2_nonsis	2066	2988	3910	1	15	1	1	0	(6:2)_(4:4aCO)
30	TCMN2	TCMN	4	550893	551387	553867	554904	2_nonsis	2481	3246	4010	1	15	1	1	0	(6:2)_(4:4aCO)
15	TCMN2	TCMN	2	695479	699461	701832	702521	2_nonsis	2372	4707	7041	1	15	1	1	0	(6:2)_(4:4aCO)
62	TCMN2	TCMN	8	122169	122633	126792	128125	2_nonsis	4160	5058	5955	1	15	1	1	0	(6:2)_(4:4aCO)
13	TCMN2	TCMN	2	658507	658797	662444	666708	2_nonsis	3648	5924	8200	1	15	1	1	0	(6:2)_(4:4aCO)
81	TCMN2	TCMN	10	635321	640236	643946	644548	2_nonsis	3711	6469	9226	1	15	1	1	0	(6:2)_(4:4aCO)
7	TCMN2	TCMN	2	248980	250316	259158	259235	2_nonsis	8843	9549	10254	1	15	1	1	0	(6:2)_(4:4aCO)
99	TCMN2	TCMN	12	887437	891755	930773	931517	2_nonsis	39019	41549	44079	1	15	1	1	0	(6:2)_(4:4aCO)
35	TCMN2	TCMN	4	907845	908202	908284	908478	2_nonsis	83	358	632	1	16	1	1	0	(2:6)_(4:4aCO)
53	TCMN2	TCMN	6	218261	218594	218751	219393	2_nonsis	158	645	1131	1	16	1	1	0	(2:6)_(4:4aCO)
125	TCMN2	TCMN	15	546837	547266	547477	547969	2_nonsis	212	672	1131	1	16	1	1	0	(2:6)_(4:4aCO)
50	TCMN2	TCMN	6	110959	111466	111948	111956	2_nonsis	483	740	996	1	16	1	1	0	(2:6)_(4:4aCO)
108	TCMN2	TCMN	13	559794	560428	560428	561397	2_nonsis	1	802	1602	1	16	1	1	0	(2:6)_(4:4aCO)
122	TCMN2	TCMN	15	109584	110892	110892	111208	2_nonsis	1	812	1623	1	16	1	1	0	(2:6)_(4:4aCO)
36	TCMN2	TCMN	4	1076035	1077398	1077428	1077787	2_nonsis	31	891	1751	1	16	1	1	0	(2:6)_(4:4aCO)
51	TCMN2	TCMN	6	113910	114171	114918	115088	2_nonsis	748	963	1177	1	16	1	1	0	(2:6)_(4:4aCO)
28	TCMN2	TCMN	4	314500	315119	315175	316669	2_nonsis	57	1113	2168	1	16	1	1	0	(2:6)_(4:4aCO)
115	TCMN2	TCMN	14	215285	216026	216647	216919	2_nonsis	622	1128	1633	1	16	1	1	0	(2:6)_(4:4aCO)
134	TCMN2	TCMN	16	447002	448559	448839	448989	2_nonsis	281	1134	1986	1	16	1	1	0	(2:6)_(4:4aCO)
118	TCMN2	TCMN	14	439088	440569	440622	441344	2_nonsis	54	1155	2255	1	16	1	1	0	(2:6)_(4:4aCO)
96	TCMN2	TCMN	12	715235	715595	716777	716852	2_nonsis	1183	1400	1616	1	16	1	1	0	(2:6)_(4:4aCO)
18	TCMN2	TCMN	2	794237	794296	795692	795756	2_nonsis	1397	1458	1518	1	16	1	1	0	(2:6)_(4:4aCO)
83	TCMN2	TCMN	11	80353	80724	81532	82469	2_nonsis	809	1462	2115	1	16	1	1	0	(2:6)_(4:4aCO)
91	TCMN2	TCMN	12	51956	53039	54071	54226	2_nonsis	1033	1651	2269	1	16	1	1	0	(2:6)_(4:4aCO)

106	TCMN2	TCMN	13	315598	316408	317836	318108	2_nonsis		1429	1969	2509	1	16	1	1	0	(2:6)_(4:4aCO)
46	TCMN2	TCMN	5	489026	489879	491556	491806	2_nonsis		1678	2229	2779	1	16	1	1	0	(2:6)_(4:4aCO)
114	TCMN2	TCMN	14	78386	79032	80433	81575	2_nonsis		1402	2295	3188	1	16	1	1	0	(2:6)_(4:4aCO)
133	TCMN2	TCMN	16	245496	245843	248123	249056	2_nonsis		2281	2920	3559	1	16	1	1	0	(2:6)_(4:4aCO)
116	TCMN2	TCMN	14	230681	230897	233897	234026	2_nonsis		3001	3173	3344	1	16	1	1	0	(2:6)_(4:4aCO)
98	TCMN2	TCMN	12	882746	883237	885989	886838	2_nonsis		2753	3422	4091	1	16	1	1	0	(2:6)_(4:4aCO)
22	TCMN2	TCMN	3	240922	241753	243219	246581	2_nonsis		1467	3563	5658	1	16	1	1	0	(2:6)_(4:4aCO)
38	TCMN2	TCMN	4	1352299	1353241	1355944	1357024	2_nonsis		2704	3714	4724	1	16	1	1	0	(2:6)_(4:4aCO)
77	TCMN2	TCMN	10	197119	197244	197272	204724	2_nonsis		29	3817	7604	1	16	1	1	0	(2:6)_(4:4aCO)
43	TCMN2	TCMN	5	360556	361242	364465	365762	2_nonsis		3224	4215	5205	1	16	1	1	0	(2:6)_(4:4aCO)
95	TCMN2	TCMN	12	688789	689216	693687	693756	2_nonsis		4472	4719	4966	1	16	1	1	0	(2:6)_(4:4aCO)
92	TCMN2	TCMN	12	119524	120550	124986	126014	2_nonsis		4437	5463	6489	1	16	1	1	0	(2:6)_(4:4aCO)
58	TCMN2	TCMN	7	584527	584635	589840	590527	2_nonsis		5206	5603	5999	1	16	1	1	0	(2:6)_(4:4aCO)
39	TCMN2	TCMN	5	39651	40307	45665	46022	2_nonsis		5359	5865	6370	1	16	1	1	0	(2:6)_(4:4aCO)
31	TCMN2	TCMN	4	667858	667986	667858	667986	2_nonsis		0	64	127	1	100	1	1	0	(4:4aCO)
105	TCMN2	TCMN	13	172679	172925	172679	172925	2_nonsis		0	123	245	1	100	1	1	0	(4:4aCO)
84	TCMN2	TCMN	11	91796	92069	91796	92069	2_nonsis		0	136	272	1	100	1	1	0	(4:4aCO)
16	TCMN2	TCMN	2	713038	713316	713038	713316	2_nonsis		0	139	277	1	100	1	1	0	(4:4aCO)
33	TCMN2	TCMN	4	765017	765331	765017	765331	2_nonsis		0	157	313	1	100	1	1	0	(4:4aCO)
10	TCMN2	TCMN	2	373012	373340	373012	373340	2_nonsis		0	164	327	1	100	1	1	0	(4:4aCO)
40	TCMN2	TCMN	5	98507	98854	98507	98854	2_nonsis		0	173	346	1	100	1	1	0	(4:4aCO)
45	TCMN2	TCMN	5	398975	399399	398975	399399	2_nonsis		0	212	423	1	100	1	1	0	(4:4aCO)
4	TCMN2	TCMN	2	24379	24823	24379	24823	2_nonsis		0	222	443	1	100	1	1	0	(4:4aCO)
111	TCMN2	TCMN	13	746448	746979	746448	746979	2_nonsis		0	265	530	1	100	1	1	0	(4:4aCO)
44	TCMN2	TCMN	5	388982	389531	388982	389531	2_nonsis		0	274	548	1	100	1	1	0	(4:4aCO)
78	TCMN2	TCMN	10	372633	373437	372633	373437	2_nonsis		0	402	803	1	100	1	1	0	(4:4aCO)
85	TCMN2	TCMN	11	119339	120268	119339	120268	2_nonsis		0	464	928	1	100	1	1	0	(4:4aCO)
8	TCMN2	TCMN	2	304384	305499	304384	305499	2_nonsis		0	557	1114	1	100	1	1	0	(4:4aCO)
54	TCMN2	TCMN	7	122622	123839	122622	123839	2_nonsis		0	608	1216	1	100	1	1	0	(4:4aCO)
88	TCMN2	TCMN	11	374411	375794	374411	375794	2_nonsis		0	691	1382	1	100	1	1	0	(4:4aCO)
109	TCMN2	TCMN	13	576343	577768	576343	577768	2_nonsis		0	712	1424	1	100	1	1	0	(4:4aCO)
97	TCMN2	TCMN	12	791142	793555	791142	793555	2_nonsis		0	1206	2412	1	100	1	1	0	(4:4aCO)
64	TCMN2	TCMN	8	331868	334431	331868	334431	2_nonsis		0	1281	2562	1	100	1	1	0	(4:4aCO)
72	TCMN2	TCMN	9	185865	188629	185865	188629	2_nonsis		0	1382	2763	1	100	1	1	0	(4:4aCO)
23	TCMN2	TCMN	4	43482	46608	43482	46608	2_nonsis		0	1563	3125	1	100	1	1	0	(4:4aCO)
3	TCMN2	TCMN	1	132066	135319	132066	135319	2_nonsis		0	1626	3252	1	100	1	1	0	(4:4aCO)
55	TCMN2	TCMN	7	226711	230011	226711	230011	2_nonsis		0	1650	3299	1	100	1	1	0	(4:4aCO)
20	TCMN2	TCMN	3	171207	174943	171207	174943	2_nonsis		0	1868	3735	1	100	1	1	0	(4:4aCO)
121	TCMN2	TCMN	14	682580	686654	682580	686654	2_nonsis		0	2037	4073	1	100	1	1	0	(4:4aCO)
103	TCMN2	TCMN	13	31154	35547	31154	35547	2_nonsis		0	2196	4392	1	100	1	1	0	(4:4aCO)
48	TCMN2	TCMN	6	53398	58238	53398	58238	2_nonsis		0	2420	4839	1	100	1	1	0	(4:4aCO)
80	TCMN2	TCMN	10	590704	601293	590704	601293	2_nonsis		0	5294	10588	1	100	1	1	0	(4:4aCO)
124	TCMN2	TCMN	15	250259	250527	251789	252485	2_nonsis		1263	1744	2225	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
131	TCMN2	TCMN	15	996702	996896	997902	999293	2_nonsis		1007	1799	2590	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
6	TCMN2	TCMN	2	202227	202580	205157	205382	2_nonsis		2578	2866	3154	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
56	TCMN2	TCMN	7	266087	266369	274448	275758	2_nonsis		8080	8875	9670	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
52	TCMN2	TCMN	6	207080	207279	210514	210544	2_sis		3236	3350	3463	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
57	TCMN2	TCMN	7	392382	392993	406503	407307	2_sis		13511	14218	14924	0	1	2	0	2	(2:6)_(0:8)_(2:6)_(4:4)
135	TCMN2	TCMN	16	458958	460996	472825	473286	2_sis		11830	13079	14327	0	1	2	0	2	(2:6)_(0:8)_(2:6)_(4:4)
21	TCMN2	TCMN	3	204750	207459	212063	214762		3	4605	7308	10011	0	2	2	1	1	(0:8)_(4:4aCO)
32	TCMN2	TCMN	4	706032	706601	714483	714588		3	7883	8219	8555	0	2	2	1	1	(8:0)_(6:2)_(2:6)_(4:4aCO)
63	TCMN2	TCMN	8	139506	141400	151824	152076		3	10425	11497	12569	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
71	TCMN2	TCMN	9	173732	174345	184053	185865		3	9709	10921	12132	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
74	TCMN2	TCMN	9	390275	393280	398583	398957		3	5304	6993	8681	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
94	TCMN2	TCMN	12	674199	674615	683018	683405		3	8404	8805	9205	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
117	TCMN2	TCMN	14	401251	404051	404051	404995		3	1	1872	3743	0	2	2	2	0	(8:0)_(4:4aCO)
60	TCMN2	TCMN	7	880548	881223	888005	888305	2_nonsis		6783	7270	7756	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2)_(4:4CO)
100	TCMN2	TCMN	9	323883	324390	326071	326249		1	1682	2024	2365	1	7	1	0	1	6:2_4:4_6:2
51	TCMN3	TCMN	5	23494	23976	34985	36820		1	11010	12168	13325	1	7	1	0	1	6:2_4:4_6:2
131	TCMN3	TCMN	12	394339	394373	397495	398071		1	3123	3427	3731	1	8	1	0	1	2:6_4:4_2:6

167	TCMN3	TCMN	15	97199	97478	97478	97910		1	1	356	710	1	10	1	0	1 06:02
17	TCMN3	TCMN	2	439035	439486	439486	440337	1	1	651	1301	1	10	1	0	1 06:02
152	TCMN3	TCMN	13	858111	859063	859063	859920	1	1	905	1808	1	10	1	0	1 06:02
101	TCMN3	TCMN	9	338670	339115	339305	340356	1	191	938	1685	1	10	1	0	1 06:02
149	TCMN3	TCMN	13	695850	697269	697520	697993	1	252	1197	2142	1	10	1	0	1 06:02
106	TCMN3	TCMN	10	192156	192956	193406	194259	1	451	1277	2102	1	10	1	0	1 06:02
88	TCMN3	TCMN	8	198762	199794	200500	200720	1	707	1332	1957	1	10	1	0	1 06:02
119	TCMN3	TCMN	11	189718	190193	191290	191390	1	1098	1385	1671	1	10	1	0	1 06:02
12	TCMN3	TCMN	2	183084	184932	185478	186753	1	547	2108	3668	1	10	1	0	1 06:02
47	TCMN3	TCMN	4	1421768	1421908	1423727	1424231	1	1820	2141	2462	1	10	1	0	1 06:02
114	TCMN3	TCMN	10	535930	539012	539012	540433	1	1	2252	4502	1	10	1	0	1 06:02
172	TCMN3	TCMN	15	246178	247071	248980	249136	1	1910	2434	2957	1	10	1	0	1 06:02
121	TCMN3	TCMN	11	442302	442829	445342	445854	1	2514	3033	3551	1	10	1	0	1 06:02
159	TCMN3	TCMN	14	410443	410941	414025	415788	1	3085	4215	5344	1	10	1	0	1 06:02
13	TCMN3	TCMN	2	196745	198355	202227	202580	1	3873	4854	5834	1	10	1	0	1 06:02
96	TCMN3	TCMN	9	128732	129806	133870	135647	1	4065	5490	6914	1	10	1	0	1 06:02
55	TCMN3	TCMN	5	207710	208304	219608	219959	1	11305	11777	12248	1	10	1	0	1 06:02
3	TCMN3	TCMN	1	78802	78910	79085	79449	1	176	411	646	1	10.1	1	0	1 02:06
61	TCMN3	TCMN	6	16654	16725	17029	17210	1	305	430	555	1	10.1	1	0	1 02:06
178	TCMN3	TCMN	15	778005	778022	778024	779060	1	3	529	1054	1	10.1	1	0	1 02:06
87	TCMN3	TCMN	8	160782	161715	161715	161874	1	1	546	1091	1	10.1	1	0	1 02:06
71	TCMN3	TCMN	7	216479	216869	217121	217417	1	253	595	937	1	10.1	1	0	1 02:06
158	TCMN3	TCMN	14	407287	408111	408124	408508	1	14	617	1220	1	10.1	1	0	1 02:06
63	TCMN3	TCMN	6	95387	95460	95460	96667	1	1	640	1279	1	10.1	1	0	1 02:06
146	TCMN3	TCMN	13	524991	525537	525744	526308	1	208	762	1316	1	10.1	1	0	1 02:06
160	TCMN3	TCMN	14	427295	427451	427715	428693	1	265	831	1397	1	10.1	1	0	1 02:06
2	TCMN3	TCMN	1	54508	54661	55327	55508	1	667	833	999	1	10.1	1	0	1 02:06
6	TCMN3	TCMN	1	129517	130254	130776	130897	1	523	951	1379	1	10.1	1	0	1 02:06
14	TCMN3	TCMN	2	289723	289906	290619	291653	1	714	1322	1929	1	10.1	1	0	1 02:06
9	TCMN3	TCMN	2	40882	40992	41298	43330	1	307	1377	2447	1	10.1	1	0	1 02:06
98	TCMN3	TCMN	9	268278	269349	270121	270435	1	773	1465	2156	1	10.1	1	0	1 02:06
112	TCMN3	TCMN	10	489721	490750	491023	492405	1	274	1479	2683	1	10.1	1	0	1 02:06
194	TCMN3	TCMN	16	875078	876719	876914	877898	1	196	1508	2819	1	10.1	1	0	1 02:06
7	TCMN3	TCMN	1	138907	139263	139277	141984	1	15	1546	3076	1	10.1	1	0	1 02:06
165	TCMN3	TCMN	15	15782	15886	17484	17634	1	1599	1725	1851	1	10.1	1	0	1 02:06
35	TCMN3	TCMN	4	545047	545265	546573	547556	1	1309	1909	2508	1	10.1	1	0	1 02:06
168	TCMN3	TCMN	15	98981	99650	101052	101400	1	1403	1911	2418	1	10.1	1	0	1 02:06
185	TCMN3	TCMN	16	117927	118110	119752	120748	1	1643	2232	2820	1	10.1	1	0	1 02:06
156	TCMN3	TCMN	14	285483	286688	288680	288926	1	1993	2718	3442	1	10.1	1	0	1 02:06
45	TCMN3	TCMN	4	1288775	1289394	1291853	1291869	1	2460	2777	3093	1	10.1	1	0	1 02:06
37	TCMN3	TCMN	4	630640	631885	635136	635208	1	3252	3910	4567	1	10.1	1	0	1 02:06
46	TCMN3	TCMN	4	1343357	1343581	1347437	1347683	1	3857	4091	4325	1	10.1	1	0	1 02:06
77	TCMN3	TCMN	7	448887	449525	454212	454910	1	4688	5355	6022	1	10.1	1	0	1 02:06
142	TCMN3	TCMN	13	345829	346005	351095	351608	1	5091	5435	5778	1	10.1	1	0	1 02:06
130	TCMN3	TCMN	12	323570	325206	330320	330526	1	5115	6035	6955	1	10.1	1	0	1 02:06
41	TCMN3	TCMN	4	927283	927319	933019	933755	1	5701	6086	6471	1	10.1	1	0	1 02:06
136	TCMN3	TCMN	12	832633	833476	840682	843387	1	7207	8980	10753	1	10.1	1	0	1 02:06
177	TCMN3	TCMN	15	680588	680779	690558	690678	1	9780	9935	10089	1	10.1	1	0	1 02:06
105	TCMN3	TCMN	10	171357	171764	181820	182087	1	10057	10393	10729	1	10.1	1	0	1 02:06
190	TCMN3	TCMN	16	653426	653739	658323	658481	2_nonsis	4585	4820	5054	3	30	1	0	1 6:2_2:6
84	TCMN3	TCMN	7	1007272	1007947	1017661	1018655	2_nonsis	9715	10549	11382	3	30	1	0	1 6:2_2:6
169	TCMN3	TCMN	15	111249	111554	112140	112969	2_nonsis	587	1153	1719	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
126	TCMN3	TCMN	12	51956	53039	53575	54071	2_nonsis	537	1326	2114	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
139	TCMN3	TCMN	12	1009719	1011169	1011952	1012226	2_nonsis	784	1645	2506	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
176	TCMN3	TCMN	15	612123	613660	614674	614917	2_nonsis	1015	1904	2793	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
143	TCMN3	TCMN	13	354882	355195	356625	356924	2_nonsis	1431	1736	2041	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
127	TCMN3	TCMN	12	119524	120550	121567	122138	2_nonsis	1018	1816	2613	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
59	TCMN3	TCMN	5	526303	526638	528932	529325	2_nonsis	2295	2658	3021	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
21	TCMN3	TCMN	2	627055	627481	630094	630469	2_nonsis	2614	3014	3413	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
103	TCMN3	TCMN	10	31838	31900	34903	35185	2_nonsis	3004	3175	3346	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)

97	TCMN3	TCMN	9	210959	212207	215186	215644	2_nonsis	2980	3832	4684	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
166	TCMN3	TCMN	15	56753	56980	59664	59868	2_nonsis	2685	2900	3114	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
141	TCMN3	TCMN	13	222095	223597	229786	230470	2_nonsis	6190	7282	8374	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
148	TCMN3	TCMN	13	677217	677238	677238	677418	2_nonsis	1	101	200	1	15	1	1	0	(6:2)_(4:4aCO)
82	TCMN3	TCMN	7	619415	619777	619787	620023	2_nonsis	11	309	607	1	15	1	1	0	(6:2)_(4:4aCO)
95	TCMN3	TCMN	9	93903	94143	94263	94456	2_nonsis	121	337	552	1	15	1	1	0	(6:2)_(4:4aCO)
163	TCMN3	TCMN	14	745944	746165	746431	746539	2_nonsis	267	431	594	1	15	1	1	0	(6:2)_(4:4aCO)
29	TCMN3	TCMN	4	83831	84443	84518	84625	2_nonsis	76	435	793	1	15	1	1	0	(6:2)_(4:4aCO)
23	TCMN3	TCMN	2	757908	758568	758608	758926	2_nonsis	41	529	1017	1	15	1	1	0	(6:2)_(4:4aCO)
138	TCMN3	TCMN	12	998854	999870	999870	1000003	2_nonsis	1	575	1148	1	15	1	1	0	(6:2)_(4:4aCO)
73	TCMN3	TCMN	7	350649	351015	351287	351684	2_nonsis	273	654	1034	1	15	1	1	0	(6:2)_(4:4aCO)
187	TCMN3	TCMN	16	195285	195615	195918	196451	2_nonsis	304	735	1165	1	15	1	1	0	(6:2)_(4:4aCO)
151	TCMN3	TCMN	13	810229	810415	810963	811653	2_nonsis	549	986	1423	1	15	1	1	0	(6:2)_(4:4aCO)
18	TCMN3	TCMN	2	477199	477343	477368	479516	2_nonsis	26	1171	2316	1	15	1	1	0	(6:2)_(4:4aCO)
22	TCMN3	TCMN	2	739892	740026	741235	741285	2_nonsis	1210	1301	1392	1	15	1	1	0	(6:2)_(4:4aCO)
109	TCMN3	TCMN	10	390521	390617	391693	392058	2_nonsis	1077	1307	1536	1	15	1	1	0	(6:2)_(4:4aCO)
91	TCMN3	TCMN	8	513034	514468	515162	515676	2_nonsis	695	1668	2641	1	15	1	1	0	(6:2)_(4:4aCO)
15	TCMN3	TCMN	2	292680	292748	294230	295028	2_nonsis	1483	1915	2347	1	15	1	1	0	(6:2)_(4:4aCO)
145	TCMN3	TCMN	13	507502	508576	509691	510245	2_nonsis	1116	1929	2742	1	15	1	1	0	(6:2)_(4:4aCO)
72	TCMN3	TCMN	7	343687	343768	345521	345912	2_nonsis	1754	1989	2224	1	15	1	1	0	(6:2)_(4:4aCO)
94	TCMN3	TCMN	9	87283	87642	89500	89756	2_nonsis	1859	2166	2472	1	15	1	1	0	(6:2)_(4:4aCO)
175	TCMN3	TCMN	15	487166	487809	489366	489971	2_nonsis	1558	2181	2804	1	15	1	1	0	(6:2)_(4:4aCO)
31	TCMN3	TCMN	4	200994	201329	203329	203389	2_nonsis	2001	2198	2394	1	15	1	1	0	(6:2)_(4:4aCO)
8	TCMN3	TCMN	1	151919	152233	153182	155505	2_nonsis	950	2268	3585	1	15	1	1	0	(6:2)_(4:4aCO)
26	TCMN3	TCMN	3	68233	68852	70785	71079	2_nonsis	1934	2390	2845	1	15	1	1	0	(6:2)_(4:4aCO)
192	TCMN3	TCMN	16	751611	752166	754744	755194	2_nonsis	2579	3081	3582	1	15	1	1	0	(6:2)_(4:4aCO)
113	TCMN3	TCMN	10	528639	529735	532916	534212	2_nonsis	3182	4377	5572	1	15	1	1	0	(6:2)_(4:4aCO)
133	TCMN3	TCMN	12	593059	599905	600676	601080	2_nonsis	772	4396	8020	1	15	1	1	0	(6:2)_(4:4aCO)
90	TCMN3	TCMN	8	288884	289659	293740	293780	2_nonsis	4082	4489	4895	1	15	1	1	0	(6:2)_(4:4aCO)
4	TCMN3	TCMN	1	108928	110856	114283	114652	2_nonsis	3428	4576	5723	1	15	1	1	0	(6:2)_(4:4aCO)
195	TCMN3	TCMN	16	884283	884616	889742	890080	2_nonsis	5127	5462	5796	1	15	1	1	0	(6:2)_(4:4aCO)
180	TCMN3	TCMN	15	946536	946808	952140	952654	2_nonsis	5333	5725	6117	1	15	1	1	0	(6:2)_(4:4aCO)
58	TCMN3	TCMN	5	469424	469569	476465	476681	2_nonsis	6897	7077	7256	1	15	1	1	0	(6:2)_(4:4aCO)
132	TCMN3	TCMN	12	498457	499674	506259	507075	2_nonsis	6586	7602	8617	1	15	1	1	0	(6:2)_(4:4aCO)
118	TCMN3	TCMN	11	98834	99224	109640	110327	2_nonsis	10417	10955	11492	1	15	1	1	0	(6:2)_(4:4aCO)
107	TCMN3	TCMN	10	284309	284375	284375	284867	2_nonsis	1	279	557	1	16	1	1	0	(2:6)_(4:4aCO)
147	TCMN3	TCMN	13	527901	528307	528368	528469	2_nonsis	62	315	567	1	16	1	1	0	(2:6)_(4:4aCO)
32	TCMN3	TCMN	4	289365	289475	289475	290079	2_nonsis	1	357	713	1	16	1	1	0	(2:6)_(4:4aCO)
85	TCMN3	TCMN	8	46274	46457	46457	47060	2_nonsis	1	393	785	1	16	1	1	0	(2:6)_(4:4aCO)
34	TCMN3	TCMN	4	539680	540228	540228	540514	2_nonsis	1	417	833	1	16	1	1	0	(2:6)_(4:4aCO)
181	TCMN3	TCMN	15	1000015	1000082	1000334	1000780	2_nonsis	253	509	764	1	16	1	1	0	(2:6)_(4:4aCO)
108	TCMN3	TCMN	10	323823	324913	324924	325190	2_nonsis	12	689	1366	1	16	1	1	0	(2:6)_(4:4aCO)
74	TCMN3	TCMN	7	379162	379420	379937	380073	2_nonsis	518	714	910	1	16	1	1	0	(2:6)_(4:4aCO)
150	TCMN3	TCMN	13	778675	779631	779842	780034	2_nonsis	212	785	1358	1	16	1	1	0	(2:6)_(4:4aCO)
153	TCMN3	TCMN	13	862092	862695	863229	863412	2_nonsis	535	927	1319	1	16	1	1	0	(2:6)_(4:4aCO)
183	TCMN3	TCMN	16	38867	39420	39840	40527	2_nonsis	421	1040	1659	1	16	1	1	0	(2:6)_(4:4aCO)
76	TCMN3	TCMN	7	443602	443639	444683	444932	2_nonsis	1045	1187	1329	1	16	1	1	0	(2:6)_(4:4aCO)
66	TCMN3	TCMN	7	55263	55957	55957	57822	2_nonsis	1	1280	2558	1	16	1	1	0	(2:6)_(4:4aCO)
128	TCMN3	TCMN	12	221668	222046	223075	223258	2_nonsis	1030	1310	1589	1	16	1	1	0	(2:6)_(4:4aCO)
154	TCMN3	TCMN	14	30923	32285	32426	34396	2_nonsis	142	1807	3472	1	16	1	1	0	(2:6)_(4:4aCO)
36	TCMN3	TCMN	4	625839	628602	628602	629487	2_nonsis	1	1824	3647	1	16	1	1	0	(2:6)_(4:4aCO)
92	TCMN3	TCMN	9	46189	46556	48252	48606	2_nonsis	1697	2057	2416	1	16	1	1	0	(2:6)_(4:4aCO)
102	TCMN3	TCMN	9	422571	422694	424776	424866	2_nonsis	2083	2189	2294	1	16	1	1	0	(2:6)_(4:4aCO)
33	TCMN3	TCMN	4	311602	311752	314015	314500	2_nonsis	2264	2581	2897	1	16	1	1	0	(2:6)_(4:4aCO)
184	TCMN3	TCMN	16	49169	50572	52500	53686	2_nonsis	1929	3223	4516	1	16	1	1	0	(2:6)_(4:4aCO)
38	TCMN3	TCMN	4	768390	769038	772698	773522	2_nonsis	3661	4396	5131	1	16	1	1	0	(2:6)_(4:4aCO)
79	TCMN3	TCMN	7	520227	521004	525413	525947	2_nonsis	4410	5065	5719	1	16	1	1	0	(2:6)_(4:4aCO)
10	TCMN3	TCMN	2	73943	74853	79464	79692	2_nonsis	4612	5180	5748	1	16	1	1	0	(2:6)_(4:4aCO)
86	TCMN3	TCMN	8	137028	137997	142863	143543	2_nonsis	4867	5691	6514	1	16	1	1	0	(2:6)_(4:4aCO)
125	TCMN3	TCMN	12	23981	25369	31473	32690	2_nonsis	6105	7407	8708	1	16	1	1	0	(2:6)_(4:4aCO)

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188	TCMN3	TCMN	16	379426	379885	389187	389519	2_nonsis		9303	9698	10092	1	16	1	1	0	(2:6)_(4:4aCO)
144	TCMN3	TCMN	13	469552	473747	482985	485052	2_nonsis		9239	12369	15499	1	16	1	1	0	(2:6)_(4:4aCO)
173	TCMN3	TCMN	15	286975	287386	314073	314395	2_nonsis		26688	27054	27419	1	16	1	1	0	(2:6)_(4:4aCO)
157	TCMN3	TCMN	14	319024	319149	319024	319149	2_nonsis		0	62	124	1	100	1	1	0	(4:4aCO)
193	TCMN3	TCMN	16	758616	758824	758616	758824	2_nonsis		0	104	207	1	100	1	1	0	(4:4aCO)
78	TCMN3	TCMN	7	458629	458878	458629	458878	2_nonsis		0	124	248	1	100	1	1	0	(4:4aCO)
11	TCMN3	TCMN	2	121643	121908	121643	121908	2_nonsis		0	132	264	1	100	1	1	0	(4:4aCO)
42	TCMN3	TCMN	4	937167	937517	937167	937517	2_nonsis		0	175	349	1	100	1	1	0	(4:4aCO)
43	TCMN3	TCMN	4	1077428	1077787	1077428	1077787	2_nonsis		0	179	358	1	100	1	1	0	(4:4aCO)
39	TCMN3	TCMN	4	777671	778122	777671	778122	2_nonsis		0	225	450	1	100	1	1	0	(4:4aCO)
44	TCMN3	TCMN	4	1283592	1284111	1283592	1284111	2_nonsis		0	259	518	1	100	1	1	0	(4:4aCO)
68	TCMN3	TCMN	7	116629	117199	116629	117199	2_nonsis		0	285	569	1	100	1	1	0	(4:4aCO)
120	TCMN3	TCMN	11	238513	239211	238513	239211	2_nonsis		0	349	697	1	100	1	1	0	(4:4aCO)
54	TCMN3	TCMN	5	77918	78787	77918	78787	2_nonsis		0	434	868	1	100	1	1	0	(4:4aCO)
64	TCMN3	TCMN	6	151218	152137	151218	152137	2_nonsis		0	459	918	1	100	1	1	0	(4:4aCO)
19	TCMN3	TCMN	2	479752	480693	479752	480693	2_nonsis		0	470	940	1	100	1	1	0	(4:4aCO)
49	TCMN3	TCMN	4	1513338	1514440	1513338	1514440	2_nonsis		0	551	1101	1	100	1	1	0	(4:4aCO)
122	TCMN3	TCMN	11	481321	482428	481321	482428	2_nonsis		0	553	1106	1	100	1	1	0	(4:4aCO)
140	TCMN3	TCMN	13	37125	38744	37125	38744	2_nonsis		0	809	1618	1	100	1	1	0	(4:4aCO)
24	TCMN3	TCMN	3	18173	20235	18173	20235	2_nonsis		0	1031	2061	1	100	1	1	0	(4:4aCO)
129	TCMN3	TCMN	12	320997	323570	320997	323570	2_nonsis		0	1286	2572	1	100	1	1	0	(4:4aCO)
99	TCMN3	TCMN	9	320712	323343	320712	323343	2_nonsis		0	1315	2630	1	100	1	1	0	(4:4aCO)
25	TCMN3	TCMN	3	65580	68233	65580	68233	2_nonsis		0	1326	2652	1	100	1	1	0	(4:4aCO)
117	TCMN3	TCMN	11	23532	27301	23532	27301	2_nonsis		0	1884	3768	1	100	1	1	0	(4:4aCO)
50	TCMN3	TCMN	5	18839	23192	18839	23192	2_nonsis		0	2176	4352	1	100	1	1	0	(4:4aCO)
116	TCMN3	TCMN	10	697654	705639	697654	705639	2_nonsis		0	3992	7984	1	100	1	1	0	(4:4aCO)
28	TCMN3	TCMN	3	238082	238725	239004	239394	2_nonsis		280	796	1311	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
80	TCMN3	TCMN	7	581660	581705	582429	582987	2_nonsis		725	1026	1326	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
174	TCMN3	TCMN	15	423370	423571	424455	424779	2_nonsis		885	1147	1408	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
5	TCMN3	TCMN	1	116905	117399	118997	119344	2_nonsis		1599	2019	2438	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
179	TCMN3	TCMN	15	814706	814826	817513	818089	2_nonsis		2688	3035	3382	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
115	TCMN3	TCMN	10	622386	622799	624648	627140	2_nonsis		1850	3302	4753	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
161	TCMN3	TCMN	14	475211	475712	478186	479609	2_nonsis		2475	3436	4397	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
89	TCMN3	TCMN	8	211042	211315	218189	218688	2_nonsis		6875	7260	7645	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
162	TCMN3	TCMN	14	644875	646799	655324	655447	2_nonsis		8526	9549	10571	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
191	TCMN3	TCMN	16	694716	694965	704396	705129	2_nonsis		9432	9922	10412	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
56	TCMN3	TCMN	5	378586	379092	381978	382688	2_nonsis		2887	3494	4101	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
60	TCMN3	TCMN	5	543765	544042	550011	550177	2_nonsis		5970	6191	6411	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
67	TCMN3	TCMN	7	65309	66501	73684	73727	2_nonsis		7184	7801	8417	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(6:2)_(4:4aCO)
155	TCMN3	TCMN	14	199570	199738	211003	211753	2_nonsis		11266	11724	12182	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4)_(2:6)_(4:4aCO)
20	TCMN3	TCMN	2	484159	485003	498959	499985	2_sis		13957	14891	15825	0	1	2	0	2	(2:6)_(0:8)_(2:6a)_(4:4)
52	TCMN3	TCMN	5	40898	41432	48594	49397	2_sis		7163	7831	8498	0	1	2	0	2	(8:0)_(6:2)_(4:4)
1	TCMN3	TCMN	1	30662	30669	42257	42484		3	11589	11705	11821	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
16	TCMN3	TCMN	2	327003	327596	328340	328525		3	745	1133	1521	0	2	2	1	1	(4:4aCO)_(2:6)_(4:4a)
27	TCMN3	TCMN	3	215020	215336	223339	228130		3	8004	10557	13109	0	2	2	1	1	(2:6)_(4:4)_(0:8)_(2:6)_(4:4aCO)
40	TCMN3	TCMN	4	807222	816386	840697	842326		4	24312	29708	35103	0	2	2	1	1	(6:2)_(0:8)_(2:6)_(4:4aCO)
53	TCMN3	TCMN	5	68996	69083	76382	76636		3	7300	7470	7639	0	2	2	1	1	(8:0)_(6:2)_(4:4)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
57	TCMN3	TCMN	5	424029	424927	426333	429823		3	1407	3600	5793	0	2	2	1	1	(6:2)_(4:4aCO)
62	TCMN3	TCMN	6	45521	45740	59811	61005		3	14072	14778	15483	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
65	TCMN3	TCMN	6	216669	216972	232697	233456		4	15726	16256	16786	0	2	2	1	1	(2:6)_(2:6a)_(0:8)_(2:6)_(2:6b)_(4:4aCO)
69	TCMN3	TCMN	7	122622	123839	124460	124671		3	622	1335	2048	0	2	2	1	1	(0:8)_(4:4aCO)
70	TCMN3	TCMN	7	201093	201499	209671	210401		3	8173	8740	9307	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
83	TCMN3	TCMN	7	845918	846464	846750	851797		3	287	3083	5878	0	2	2	1	1	(0:8)_(4:4aCO)
110	TCMN3	TCMN	10	406334	407487	407535	411303		3	49	2509	4968	0	2	2	1	1	(6:2)_(4:4aCO)
135	TCMN3	TCMN	12	697961	701229	709102	709117		3	7874	9515	11155	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
137	TCMN3	TCMN	12	867405	869664	873155	873227		3	3492	4657	5821	0	2	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4a)
164	TCMN3	TCMN	14	761147	761193	762860	763294		3	1668	1907	2146	0	2	2	1	1	(2:6)_(4:4aCO)
170	TCMN3	TCMN	15	149247	149394	153615	153774		3	4222	4374	4526	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)
171	TCMN3	TCMN	15	156059	157101	168885	169317		3	11785	12521	13257	0	2	2	1	1	(6:2)_(8:0)_(6:2)_(4:4aCO)
182	TCMN3	TCMN	15	1034400	1034658	1043807	1044139		4	9150	9444	9738	0	2	2	1	1	(2:6)_(4:4)_(6:2)_(2:6a)_(4:4aCO)

30	TCMN3	TCMN	4	173380	174736	177160	177756	3	2425	3400	4375	0	3	2	1	1 (4:4aCO)_(2:6)_(4:4bCO)
48	TCMN3	TCMN	4	1444364	1444445	1458516	1459261	3	14072	14484	14896	0	3	2	1	1 (2:6)_(4:4aCO)_(2:6)_(4:4bCO)
81	TCMN3	TCMN	7	613734	613788	617292	617675 2_nonsis		3505	3723	3940	0	3	2	0	2 (4:4aCO)_(6:2)_(4:4CO)
93	TCMN3	TCMN	9	49641	51046	63202	63470	4	12157	12993	13828	0	3	2	2	0 (6:2)_(6:2a)_(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
104	TCMN3	TCMN	10	151846	152040	158376	158721	4	6337	6606	6874	0	3	2	2	0 (0:8)_(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
111	TCMN3	TCMN	10	464438	465282	472296	484073	4	7015	13325	19634	0	3	2	1	1 (8:0)_(4:4aCO)_(6:2)_(4:4a)_(2:6)_(4:4bCO)
124	TCMN3	TCMN	11	629129	629639	639711	641421 2_nonsis		10073	11182	12291	0	3	2	0	2 (6:2)_(4:4aCO)_(6:2)_(4:4CO)
134	TCMN3	TCMN	12	693267	693579	694951	696350	3	1373	2228	3082	0	3	2	1	1 (6:2)_(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
186	TCMN3	TCMN	16	139609	139660	142047	142339 2_nonsis		2388	2559	2729	0	3	2	0	2 (2:6)_(4:4)_(4:4aCO)_(2:6)_(4:4CO)
189	TCMN3	TCMN	16	649916	650861	651959	652093 2_nonsis		1099	1638	2176	0	3	2	0	2 (6:2)_(4:4aCO)_(4:4CO)_(4:4aCO)
169	TCMN4	TCMN	16	910123	910771	912589	912647	1	1819	2171	2523	1	8	1	0	1 2:6_4:4_2:6
57	TCMN4	TCMN	6	46998	47804	49483	50137	1	1680	2409	3138	1	8	1	0	1 2:6_4:4_2:6
104	TCMN4	TCMN	11	469271	469355	469355	469480	1	1	105	208	1	10	1	0	1 06:02
100	TCMN4	TCMN	11	265409	265522	265522	265706	1	1	149	296	1	10	1	0	1 06:02
40	TCMN4	TCMN	4	1291676	1291853	1291853	1292138	1	1	231	461	1	10	1	0	1 06:02
89	TCMN4	TCMN	10	42694	42739	42745	43261	1	7	287	566	1	10	1	0	1 06:02
24	TCMN4	TCMN	4	49108	49497	49666	49881	1	170	471	772	1	10	1	0	1 06:02
56	TCMN4	TCMN	6	16574	16654	17029	17210	1	376	506	635	1	10	1	0	1 06:02
87	TCMN4	TCMN	10	36853	37127	37127	37895	1	1	521	1041	1	10	1	0	1 06:02
3	TCMN4	TCMN	1	91629	92566	92566	92743	1	1	557	1113	1	10	1	0	1 06:02
33	TCMN4	TCMN	4	654890	655011	655491	656349	1	481	970	1458	1	10	1	0	1 06:02
156	TCMN4	TCMN	15	1002614	1003809	1004312	1004474	1	504	1182	1859	1	10	1	0	1 06:02
77	TCMN4	TCMN	8	283683	283957	284440	285871	1	484	1336	2187	1	10	1	0	1 06:02
46	TCMN4	TCMN	4	1485012	1486166	1486166	1487794	1	1	1391	2781	1	10	1	0	1 06:02
29	TCMN4	TCMN	4	263030	263811	264290	265338	1	480	1394	2307	1	10	1	0	1 06:02
145	TCMN4	TCMN	15	448080	448955	449944	450086	1	990	1498	2005	1	10	1	0	1 06:02
155	TCMN4	TCMN	15	986838	986894	988081	988671	1	1188	1510	1832	1	10	1	0	1 06:02
103	TCMN4	TCMN	11	385892	386072	386882	388314	1	811	1616	2421	1	10	1	0	1 06:02
79	TCMN4	TCMN	8	387002	387439	388791	388948	1	1353	1649	1945	1	10	1	0	1 06:02
144	TCMN4	TCMN	15	311489	312220	313126	313924	1	907	1671	2434	1	10	1	0	1 06:02
51	TCMN4	TCMN	5	104648	105087	106918	107341	1	1832	2262	2692	1	10	1	0	1 06:02
118	TCMN4	TCMN	12	658599	659350	661927	662311	1	2578	3145	3711	1	10	1	0	1 06:02
102	TCMN4	TCMN	11	345918	346598	349940	350196	1	3343	3810	4277	1	10	1	0	1 06:02
15	TCMN4	TCMN	2	678799	679276	682449	683592	1	3174	3983	4792	1	10	1	0	1 06:02
65	TCMN4	TCMN	7	605025	605491	611358	612267	1	5868	6555	7241	1	10	1	0	1 06:02
59	TCMN4	TCMN	6	249053	250075	257686	261543	1	7612	10051	12489	1	10	1	0	1 06:02
8	TCMN4	TCMN	1	198604	198618	198618	198639	1	1	18	34	1	10.1	1	0	1 02:06
152	TCMN4	TCMN	15	849274	849337	849337	849390	1	1	58	115	1	10.1	1	0	1 02:06
150	TCMN4	TCMN	15	826642	826798	826798	826879	1	1	119	236	1	10.1	1	0	1 02:06
31	TCMN4	TCMN	4	443292	443491	443491	443547	1	1	128	254	1	10.1	1	0	1 02:06
101	TCMN4	TCMN	11	333757	334135	334135	334655	1	1	449	897	1	10.1	1	0	1 02:06
20	TCMN4	TCMN	3	107312	108225	108293	108503	1	69	630	1190	1	10.1	1	0	1 02:06
117	TCMN4	TCMN	12	567266	567957	568114	568449	1	158	670	1182	1	10.1	1	0	1 02:06
69	TCMN4	TCMN	7	801373	801946	802249	802512	1	304	721	1138	1	10.1	1	0	1 02:06
25	TCMN4	TCMN	4	133023	133068	133068	134550	1	1	764	1526	1	10.1	1	0	1 02:06
109	TCMN4	TCMN	12	92960	93301	93954	94031	1	654	862	1070	1	10.1	1	0	1 02:06
81	TCMN4	TCMN	8	494825	494966	495688	496308	1	723	1103	1482	1	10.1	1	0	1 02:06
98	TCMN4	TCMN	11	231038	231246	231922	232606	1	677	1122	1567	1	10.1	1	0	1 02:06
17	TCMN4	TCMN	2	693243	694151	694512	695405	1	362	1262	2161	1	10.1	1	0	1 02:06
154	TCMN4	TCMN	15	940023	940429	941715	942129	1	1287	1696	2105	1	10.1	1	0	1 02:06
54	TCMN4	TCMN	5	526303	526638	527534	528932	1	897	1763	2628	1	10.1	1	0	1 02:06
147	TCMN4	TCMN	15	630587	632023	632823	633360	1	801	1787	2772	1	10.1	1	0	1 02:06
123	TCMN4	TCMN	13	25508	25638	26922	27948	1	1285	1862	2439	1	10.1	1	0	1 02:06
167	TCMN4	TCMN	16	812552	812762	814215	814896	1	1454	1899	2343	1	10.1	1	0	1 02:06
112	TCMN4	TCMN	12	253274	253791	255522	255647	1	1732	2052	2372	1	10.1	1	0	1 02:06
141	TCMN4	TCMN	15	136572	137220	138847	139359	1	1628	2207	2786	1	10.1	1	0	1 02:06
14	TCMN4	TCMN	2	499985	500498	502627	503196	1	2130	2670	3210	1	10.1	1	0	1 02:06
64	TCMN4	TCMN	7	542283	542388	545099	545143	1	2712	2786	2859	1	10.1	1	0	1 02:06
26	TCMN4	TCMN	4	154129	155368	157554	157843	1	2187	2950	3713	1	10.1	1	0	1 02:06
126	TCMN4	TCMN	13	235304	235740	238534	238681	1	2795	3086	3376	1	10.1	1	0	1 02:06

86	TCMN4	TCMN	9	415873	416339	419168	419420	1		2830	3188	3546	1	10.1	1	0	1 02:06
111	TCMN4	TCMN	12	181616	182125	184588	185813	1		2464	3330	4196	1	10.1	1	0	1 02:06
9	TCMN4	TCMN	2	45824	46603	49999	50569	1		3397	4071	4744	1	10.1	1	0	1 02:06
42	TCMN4	TCMN	4	1419516	1419978	1423727	1424231	1		3750	4232	4714	1	10.1	1	0	1 02:06
34	TCMN4	TCMN	4	673875	673951	678460	678773	1		4510	4704	4897	1	10.1	1	0	1 02:06
11	TCMN4	TCMN	2	379629	379974	383960	385751	1		3987	5054	6121	1	10.1	1	0	1 02:06
159	TCMN4	TCMN	16	70600	71375	77995	78895	1		6621	7458	8294	1	10.1	1	0	1 02:06
75	TCMN4	TCMN	8	206103	206439	208566	208748	2_nonsis	2128	2386	2644	3	30	1	0	1 6:2_2:6
10	TCMN4	TCMN	2	322610	322823	324761	325371	2_nonsis	1939	2350	2760	3	30	1	0	1 6:2_4:4_2:6
120	TCMN4	TCMN	12	791142	793555	795275	798382	2_nonsis	1721	4480	7239	3	30	1	0	1 2:6_6:2_4:4_2:6
97	TCMN4	TCMN	11	165754	166502	167778	168140	2_nonsis	1277	1831	2385	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
157	TCMN4	TCMN	15	1014090	1015192	1018794	1019036	2_nonsis	3603	4274	4945	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
138	TCMN4	TCMN	14	747445	747531	754802	755545	2_nonsis	7272	7686	8099	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
139	TCMN4	TCMN	15	40057	40697	41495	41838	2_nonsis	799	1290	1780	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
107	TCMN4	TCMN	11	625303	625924	626765	627471	2_nonsis	842	1505	2167	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
148	TCMN4	TCMN	15	733608	733667	735184	735517	2_nonsis	1518	1713	1908	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
82	TCMN4	TCMN	9	87283	87642	89179	89302	2_nonsis	1538	1778	2018	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
70	TCMN4	TCMN	7	805147	805562	807540	807662	2_nonsis	1979	2247	2514	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
52	TCMN4	TCMN	5	307383	308000	309961	310175	2_nonsis	1962	2377	2791	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
72	TCMN4	TCMN	7	1016792	1017661	1019728	1019751	2_nonsis	2068	2513	2958	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
43	TCMN4	TCMN	4	1450894	1451664	1453499	1454543	2_nonsis	1836	2742	3648	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
142	TCMN4	TCMN	15	151910	152407	155250	156059	2_nonsis	2844	3496	4148	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
158	TCMN4	TCMN	16	34674	35338	41399	42125	2_nonsis	6062	6756	7450	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
28	TCMN4	TCMN	4	230153	230663	233966	234088	2_nonsis	3304	3619	3934	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
146	TCMN4	TCMN	15	451948	452278	452536	452641	2_nonsis	259	476	692	1	15	1	1	0 (6:2)_(4:4aCO)
36	TCMN4	TCMN	4	752863	752908	752995	753858	2_nonsis	88	541	994	1	15	1	1	0 (6:2)_(4:4aCO)
73	TCMN4	TCMN	8	21160	21541	21727	22121	2_nonsis	187	574	960	1	15	1	1	0 (6:2)_(4:4aCO)
83	TCMN4	TCMN	9	272261	272369	272672	273183	2_nonsis	304	613	921	1	15	1	1	0 (6:2)_(4:4aCO)
45	TCMN4	TCMN	4	1482150	1483110	1483110	1483402	2_nonsis	1	626	1251	1	15	1	1	0 (6:2)_(4:4aCO)
32	TCMN4	TCMN	4	620943	621879	621894	622375	2_nonsis	16	724	1431	1	15	1	1	0 (6:2)_(4:4aCO)
129	TCMN4	TCMN	13	695850	697269	697269	697465	2_nonsis	1	808	1614	1	15	1	1	0 (6:2)_(4:4aCO)
113	TCMN4	TCMN	12	282626	283463	283731	284270	2_nonsis	269	956	1643	1	15	1	1	0 (6:2)_(4:4aCO)
125	TCMN4	TCMN	13	164304	165032	165218	166349	2_nonsis	187	1116	2044	1	15	1	1	0 (6:2)_(4:4aCO)
137	TCMN4	TCMN	14	700775	701567	701618	702991	2_nonsis	52	1134	2215	1	15	1	1	0 (6:2)_(4:4aCO)
161	TCMN4	TCMN	16	179634	180404	180992	181434	2_nonsis	589	1194	1799	1	15	1	1	0 (6:2)_(4:4aCO)
16	TCMN4	TCMN	2	685681	686221	686757	687872	2_nonsis	537	1364	2190	1	15	1	1	0 (6:2)_(4:4aCO)
132	TCMN4	TCMN	14	37986	39122	40430	41146	2_nonsis	1309	2234	3159	1	15	1	1	0 (6:2)_(4:4aCO)
93	TCMN4	TCMN	10	406334	407487	407535	411303	2_nonsis	49	2509	4968	1	15	1	1	0 (6:2)_(4:4aCO)
6	TCMN4	TCMN	1	166369	166429	167179	170726	2_nonsis	751	2554	4356	1	15	1	1	0 (6:2)_(4:4aCO)
163	TCMN4	TCMN	16	532319	532708	534749	535407	2_nonsis	2042	2565	3087	1	15	1	1	0 (6:2)_(4:4aCO)
121	TCMN4	TCMN	12	821384	822252	823256	826618	2_nonsis	1005	3119	5233	1	15	1	1	0 (6:2)_(4:4aCO)
85	TCMN4	TCMN	9	327096	329125	329125	333581	2_nonsis	1	3243	6484	1	15	1	1	0 (6:2)_(4:4aCO)
108	TCMN4	TCMN	12	38737	39963	42908	43069	2_nonsis	2946	3639	4331	1	15	1	1	0 (6:2)_(4:4aCO)
60	TCMN4	TCMN	7	199894	200351	205307	205559	2_nonsis	4957	5311	5664	1	15	1	1	0 (6:2)_(4:4aCO)
27	TCMN4	TCMN	4	195474	196150	200994	201329	2_nonsis	4845	5350	5854	1	15	1	1	0 (6:2)_(4:4aCO)
2	TCMN4	TCMN	1	77737	78187	84046	84858	2_nonsis	5860	6490	7120	1	15	1	1	0 (6:2)_(4:4aCO)
164	TCMN4	TCMN	16	668392	669691	675149	676046	2_nonsis	5459	6556	7653	1	15	1	1	0 (6:2)_(4:4aCO)
92	TCMN4	TCMN	10	263723	264165	270332	270695	2_nonsis	6168	6570	6971	1	15	1	1	0 (6:2)_(4:4aCO)
115	TCMN4	TCMN	12	341688	341926	341926	341974	2_nonsis	1	143	285	1	16	1	1	0 (2:6)_(4:4aCO)
91	TCMN4	TCMN	10	260627	260920	260920	261113	2_nonsis	1	243	485	1	16	1	1	0 (2:6)_(4:4aCO)
106	TCMN4	TCMN	11	567076	567430	567633	567960	2_nonsis	204	544	883	1	16	1	1	0 (2:6)_(4:4aCO)
110	TCMN4	TCMN	12	144822	145042	145416	145780	2_nonsis	375	666	957	1	16	1	1	0 (2:6)_(4:4aCO)
13	TCMN4	TCMN	2	487183	487454	487781	488751	2_nonsis	328	948	1567	1	16	1	1	0 (2:6)_(4:4aCO)
124	TCMN4	TCMN	13	37125	38744	38744	39077	2_nonsis	1	976	1951	1	16	1	1	0 (2:6)_(4:4aCO)
47	TCMN4	TCMN	4	1505853	1506604	1506992	1507780	2_nonsis	389	1158	1926	1	16	1	1	0 (2:6)_(4:4aCO)
134	TCMN4	TCMN	14	204995	205138	205874	206853	2_nonsis	737	1297	1857	1	16	1	1	0 (2:6)_(4:4aCO)
136	TCMN4	TCMN	14	531656	532165	532945	533519	2_nonsis	781	1322	1862	1	16	1	1	0 (2:6)_(4:4aCO)
50	TCMN4	TCMN	5	77697	77918	79059	79231	2_nonsis	1142	1338	1533	1	16	1	1	0 (2:6)_(4:4aCO)
19	TCMN4	TCMN	3	94376	94470	96055	96799	2_nonsis	1586	2004	2422	1	16	1	1	0 (2:6)_(4:4aCO)
116	TCMN4	TCMN	12	563822	564068	565625	566307	2_nonsis	1558	2021	2484	1	16	1	1	0 (2:6)_(4:4aCO)

39	TCMN4	TCMN	4	1267153	1267740	1268647	1270902	2_nonsis		908	2328	3748	1	16	1	1	0	(2:6)_(4:4aCO)
96	TCMN4	TCMN	11	14411	19020	19020	19563	2_nonsis		1	2576	5151	1	16	1	1	0	(2:6)_(4:4aCO)
133	TCMN4	TCMN	14	158538	159120	161474	161874	2_nonsis		2355	2845	3335	1	16	1	1	0	(2:6)_(4:4aCO)
151	TCMN4	TCMN	15	833472	833904	837247	837630	2_nonsis		3344	3751	4157	1	16	1	1	0	(2:6)_(4:4aCO)
84	TCMN4	TCMN	9	308908	310160	311839	314742	2_nonsis		1680	3757	5833	1	16	1	1	0	(2:6)_(4:4aCO)
135	TCMN4	TCMN	14	353111	353474	356935	357348	2_nonsis		3462	3849	4236	1	16	1	1	0	(2:6)_(4:4aCO)
168	TCMN4	TCMN	16	880884	881834	885979	886611	2_nonsis		4146	4936	5726	1	16	1	1	0	(2:6)_(4:4aCO)
49	TCMN4	TCMN	5	68268	68547	73131	74196	2_nonsis		4585	5256	5927	1	16	1	1	0	(2:6)_(4:4aCO)
68	TCMN4	TCMN	7	771558	772420	777630	777952	2_nonsis		5211	5802	6393	1	16	1	1	0	(2:6)_(4:4aCO)
48	TCMN4	TCMN	5	24628	24661	30664	31247	2_nonsis		6004	6311	6618	1	16	1	1	0	(2:6)_(4:4aCO)
23	TCMN4	TCMN	4	18805	18882	26111	26523	2_nonsis		7230	7474	7717	1	16	1	1	0	(2:6)_(4:4aCO)
61	TCMN4	TCMN	7	248225	249983	257078	257715	2_nonsis		7096	8293	9489	1	16	1	1	0	(2:6)_(4:4aCO)
12	TCMN4	TCMN	2	459961	460243	468402	468870	2_nonsis		8160	8534	8908	1	16	1	1	0	(2:6)_(4:4aCO)
119	TCMN4	TCMN	12	697759	697961	708261	708383	2_nonsis		10301	10462	10623	1	16	1	1	0	(2:6)_(4:4aCO)
30	TCMN4	TCMN	4	305599	306893	316669	317220	2_nonsis		9777	10699	11620	1	16	1	1	0	(2:6)_(4:4aCO)
160	TCMN4	TCMN	16	79797	82464	96592	98464	2_nonsis		14129	16398	18666	1	16	1	1	0	(2:6)_(4:4aCO)
78	TCMN4	TCMN	8	334431	334860	351073	351418	2_nonsis		16214	16600	16986	1	16	1	1	0	(2:6)_(4:4aCO)
76	TCMN4	TCMN	8	237328	237556	237328	237556	2_nonsis		0	114	227	1	100	1	1	0	(4:4aCO)
35	TCMN4	TCMN	4	750901	751203	750901	751203	2_nonsis		0	151	301	1	100	1	1	0	(4:4aCO)
90	TCMN4	TCMN	10	147143	147445	147143	147445	2_nonsis		0	151	301	1	100	1	1	0	(4:4aCO)
38	TCMN4	TCMN	4	899764	900294	899764	900294	2_nonsis		0	265	529	1	100	1	1	0	(4:4aCO)
53	TCMN4	TCMN	5	524520	525075	524520	525075	2_nonsis		0	277	554	1	100	1	1	0	(4:4aCO)
74	TCMN4	TCMN	8	104568	105227	104568	105227	2_nonsis		0	329	658	1	100	1	1	0	(4:4aCO)
95	TCMN4	TCMN	10	589894	590704	589894	590704	2_nonsis		0	405	809	1	100	1	1	0	(4:4aCO)
55	TCMN4	TCMN	5	539346	540205	539346	540205	2_nonsis		0	429	858	1	100	1	1	0	(4:4aCO)
105	TCMN4	TCMN	11	498054	499168	498054	499168	2_nonsis		0	557	1113	1	100	1	1	0	(4:4aCO)
166	TCMN4	TCMN	16	770637	771861	770637	771861	2_nonsis		0	612	1223	1	100	1	1	0	(4:4aCO)
62	TCMN4	TCMN	7	274448	275758	274448	275758	2_nonsis		0	655	1309	1	100	1	1	0	(4:4aCO)
71	TCMN4	TCMN	7	951675	953718	951675	953718	2_nonsis		0	1021	2042	1	100	1	1	0	(4:4aCO)
122	TCMN4	TCMN	12	964739	967075	964739	967075	2_nonsis		0	1168	2335	1	100	1	1	0	(4:4aCO)
7	TCMN4	TCMN	1	187280	189706	187280	189706	2_nonsis		0	1213	2425	1	100	1	1	0	(4:4aCO)
88	TCMN4	TCMN	10	39393	42694	39393	42694	2_nonsis		0	1650	3300	1	100	1	1	0	(4:4aCO)
18	TCMN4	TCMN	2	695479	699461	695479	699461	2_nonsis		0	1991	3981	1	100	1	1	0	(4:4aCO)
130	TCMN4	TCMN	13	713980	715257	715971	716317	2_nonsis		715	1526	2336	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
41	TCMN4	TCMN	4	1295582	1295980	1297076	1297562	2_nonsis		1097	1538	1979	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
127	TCMN4	TCMN	13	257640	257811	259263	259663	2_nonsis		1453	1738	2022	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
80	TCMN4	TCMN	8	459885	460708	461762	463854	2_nonsis		1055	2512	3968	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
21	TCMN4	TCMN	3	148589	149594	149594	151925	2_sis		1	1668	3335	0	1	2	0	2	(0:8)_(4:4)
44	TCMN4	TCMN	4	1474507	1475249	1477994	1478129	2_sis		2746	3184	3621	0	1	2	0	2	(6:2)_(8:0)_(6:2a)_(4:4)
1	TCMN4	TCMN	1	33892	33996	42527	42554		4	8532	8597	8661	0	2	2	1	1	(6:2)_(2:6)_(0:8)_(2:6a)_(4:4aCO)
4	TCMN4	TCMN	1	112136	114283	117940	118997		3	3658	5259	6860	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
5	TCMN4	TCMN	1	121235	128637	132066	135319		4	3430	8757	14083	0	2	2	2	0	(2:6)_(0:8)_(4:4aCO)
37	TCMN4	TCMN	4	837953	840598	847053	848136		3	6456	8319	10182	0	2	2	1	1	(2:6)_(2:6a)_(2:6)_(4:4aCO)
58	TCMN4	TCMN	6	77256	77340	77619	77922		3	280	473	665	0	2	2	1	1	(6:2)_(2:6)_(4:4aCO)
66	TCMN4	TCMN	7	622492	622738	629248	629428		3	6611	6773	6935	0	2	2	1	1	(2:6)_(4:4)_(2:6a)_(4:4aCO)
114	TCMN4	TCMN	12	320469	320997	322903	323570		3	1907	2504	3100	0	2	2	1	1	(2:6)_(2:6a)_(4:4aCO)
131	TCMN4	TCMN	13	866477	866753	889183	889570		3	22431	22762	23092	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
140	TCMN4	TCMN	15	83853	84190	89846	90174		4	5657	5989	6320	0	2	2	1	1	(2:6)_(6:2)_(8:0)_(6:2a)_(4:4aCO)
143	TCMN4	TCMN	15	184291	184504	199433	201256		3	14930	15947	16964	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
153	TCMN4	TCMN	15	890957	891275	892334	892523		3	1060	1313	1565	0	2	2	1	1	(2:6)_(4:4)_(2:6a)_(4:4aCO)
94	TCMN4	TCMN	10	465795	467010	467589	469453		3	580	2119	3657	0	3	2	1	1	(2:6)_(4:4aCO)_(4:4bCO)
99	TCMN4	TCMN	11	245116	246336	253608	254095		4	7273	8126	8978	0	3	2	2	0	(6:2)_(4:4aCO)_(6:2a)_(4:4bCO)
128	TCMN4	TCMN	13	535437	535671	541246	541397		3	5576	5768	5959	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4bCO)
149	TCMN4	TCMN	15	810411	810751	822183	823421		3	11433	12221	13009	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
162	TCMN4	TCMN	16	194832	195093	198834	198912	2_nonsis		3742	3911	4079	0	3	2	2	0	(6:2)_(4:4aCO)_(2:6)_(4:4CO)
165	TCMN4	TCMN	16	747971	748400	748650	749484	2_nonsis		251	882	1512	0	3	2	0	2	(4:4aCO)_(4:4CO)
229	TCMN4	TCMN	6	261543	265223	265223	270161		1	0	4309	8617	0	4	1	NA	NA	
340	TCMN4	TCMN	16	920048	920779	925093	948066		1	0	14009	28017	0	4	1	NA	NA	
62	TCMN5	TCMN	5	200070	200245	204261	204525		1	4017	4236	4454	1	7	1	0	1	6:2_4:4_6:2
165	TCMN5	TCMN	12	515064	515666	516236	516783		1	571	1145	1718	1	8	1	0	1	2:6_4:4_2:6

37	TCMN5	TCMN	4	441971	442320	444672	445249	1	2353	2815	3277	1	8	1	0	1	2:6_4:4_2:6
72	TCMN5	TCMN	6	218127	218244	221542	221657	1	3299	3414	3529	1	8	1	0	1	2:6_4:4_2:6
130	TCMN5	TCMN	10	43681	44482	51007	51976	1	6526	7410	8294	1	8	1	0	1	2:6_4:4_2:6
11	TCMN5	TCMN	2	327936	327972	327989	328054	1	18	68	117	1	10	1	0	1	06:02
235	TCMN5	TCMN	16	653824	653857	653932	654370	1	76	311	545	1	10	1	0	1	06:02
94	TCMN5	TCMN	7	909752	910360	910360	910494	1	1	371	741	1	10	1	0	1	06:02
223	TCMN5	TCMN	15	889642	889988	890036	890409	1	49	408	766	1	10	1	0	1	06:02
194	TCMN5	TCMN	14	189046	189221	189445	189694	1	225	436	647	1	10	1	0	1	06:02
121	TCMN5	TCMN	9	41980	42365	42595	42679	1	231	465	698	1	10	1	0	1	06:02
182	TCMN5	TCMN	13	437392	437945	437945	438469	1	1	539	1076	1	10	1	0	1	06:02
31	TCMN5	TCMN	4	145096	145686	145805	146231	1	120	627	1134	1	10	1	0	1	06:02
169	TCMN5	TCMN	12	679180	679614	679633	680510	1	20	675	1329	1	10	1	0	1	06:02
229	TCMN5	TCMN	16	69892	70402	70600	71375	1	199	841	1482	1	10	1	0	1	06:02
119	TCMN5	TCMN	8	438307	438697	439148	439617	1	452	881	1309	1	10	1	0	1	06:02
10	TCMN5	TCMN	2	251134	252027	252499	252589	1	473	964	1454	1	10	1	0	1	06:02
87	TCMN5	TCMN	7	448887	449525	450034	450372	1	510	997	1484	1	10	1	0	1	06:02
204	TCMN5	TCMN	14	498514	499188	499366	500627	1	179	1146	2112	1	10	1	0	1	06:02
222	TCMN5	TCMN	15	864480	864723	865407	866653	1	685	1429	2172	1	10	1	0	1	06:02
206	TCMN5	TCMN	14	576688	579044	579121	579520	1	78	1455	2831	1	10	1	0	1	06:02
214	TCMN5	TCMN	15	269468	269497	271047	271168	1	1551	1625	1699	1	10	1	0	1	06:02
21	TCMN5	TCMN	2	778544	778890	780187	781183	1	1298	1968	2638	1	10	1	0	1	06:02
86	TCMN5	TCMN	7	428152	428408	429941	430559	1	1534	1970	2406	1	10	1	0	1	06:02
203	TCMN5	TCMN	14	460625	462377	463310	463775	1	934	2042	3149	1	10	1	0	1	06:02
109	TCMN5	TCMN	8	120445	121477	123006	123099	1	1530	2092	2653	1	10	1	0	1	06:02
33	TCMN5	TCMN	4	166022	166634	167826	169331	1	1193	2251	3308	1	10	1	0	1	06:02
78	TCMN5	TCMN	7	76620	76882	79203	80122	1	2322	2912	3501	1	10	1	0	1	06:02
65	TCMN5	TCMN	5	519704	521844	523683	524394	1	1840	3265	4689	1	10	1	0	1	06:02
136	TCMN5	TCMN	10	305004	305635	308559	308682	1	2925	3301	3677	1	10	1	0	1	06:02
183	TCMN5	TCMN	13	455851	456415	459508	459995	1	3094	3619	4143	1	10	1	0	1	06:02
90	TCMN5	TCMN	7	830690	830766	834267	835147	1	3502	3979	4456	1	10	1	0	1	06:02
15	TCMN5	TCMN	2	498959	499985	503402	504535	1	3418	4497	5575	1	10	1	0	1	06:02
43	TCMN5	TCMN	4	805658	805687	807222	816386	1	1536	6132	10727	1	10	1	0	1	06:02
129	TCMN5	TCMN	9	419432	419479	419479	419544	1	1	56	111	1	10.1	1	0	1	02:06
77	TCMN5	TCMN	7	47968	47998	47998	48191	1	1	112	222	1	10.1	1	0	1	02:06
2	TCMN5	TCMN	1	44150	44384	44384	44588	1	1	219	437	1	10.1	1	0	1	02:06
131	TCMN5	TCMN	10	53592	53842	53843	54311	1	2	360	718	1	10.1	1	0	1	02:06
97	TCMN5	TCMN	7	936416	936948	936948	937376	1	1	480	959	1	10.1	1	0	1	02:06
209	TCMN5	TCMN	15	72322	72737	72842	73180	1	106	482	857	1	10.1	1	0	1	02:06
60	TCMN5	TCMN	5	25332	25874	25929	26265	1	56	494	932	1	10.1	1	0	1	02:06
102	TCMN5	TCMN	7	1021857	1022119	1022470	1022499	1	352	497	641	1	10.1	1	0	1	02:06
100	TCMN5	TCMN	7	1006262	1006307	1006778	1006862	1	472	536	599	1	10.1	1	0	1	02:06
59	TCMN5	TCMN	4	1498969	1499708	1499760	1500051	1	53	567	1081	1	10.1	1	0	1	02:06
9	TCMN5	TCMN	2	246613	246942	247399	247522	1	458	683	908	1	10.1	1	0	1	02:06
193	TCMN5	TCMN	14	166733	167934	168003	168178	1	70	757	1444	1	10.1	1	0	1	02:06
57	TCMN5	TCMN	4	1360167	1361014	1361086	1361801	1	73	853	1633	1	10.1	1	0	1	02:06
74	TCMN5	TCMN	6	232697	233456	234009	234160	1	554	1008	1462	1	10.1	1	0	1	02:06
239	TCMN5	TCMN	16	887552	887933	888652	888868	1	720	1018	1315	1	10.1	1	0	1	02:06
80	TCMN5	TCMN	7	162215	164025	164025	164428	1	1	1107	2212	1	10.1	1	0	1	02:06
29	TCMN5	TCMN	4	95036	96116	96674	96799	1	559	1161	1762	1	10.1	1	0	1	02:06
76	TCMN5	TCMN	7	43798	44099	44898	45371	1	800	1186	1572	1	10.1	1	0	1	02:06
178	TCMN5	TCMN	13	166349	167027	168134	168774	1	1108	1766	2424	1	10.1	1	0	1	02:06
127	TCMN5	TCMN	9	376613	377236	378238	379276	1	1003	1833	2662	1	10.1	1	0	1	02:06
13	TCMN5	TCMN	2	340843	341186	342723	343245	1	1538	1970	2401	1	10.1	1	0	1	02:06
116	TCMN5	TCMN	8	330660	331641	331868	334431	1	228	1999	3770	1	10.1	1	0	1	02:06
142	TCMN5	TCMN	10	623220	624389	624648	627140	1	260	2090	3919	1	10.1	1	0	1	02:06
189	TCMN5	TCMN	14	20559	21301	22855	23245	1	1555	2120	2685	1	10.1	1	0	1	02:06
163	TCMN5	TCMN	12	494429	495002	496489	497835	1	1488	2447	3405	1	10.1	1	0	1	02:06
99	TCMN5	TCMN	7	985524	985797	987893	988358	1	2097	2465	2833	1	10.1	1	0	1	02:06
63	TCMN5	TCMN	5	429823	429972	432416	432695	1	2445	2658	2871	1	10.1	1	0	1	02:06
38	TCMN5	TCMN	4	451867	452236	454502	455316	1	2267	2858	3448	1	10.1	1	0	1	02:06

58	TCMN5	TCMN	4	1364514	1364750	1369029	1369744		1	4280	4755	5229	1	10.1	1	0	1 02:06
155	TCMN5	TCMN	11	633641	634414	638298	641421		1	3885	5832	7779	1	10.1	1	0	1 02:06
52	TCMN5	TCMN	4	1228404	1228584	1234670	1235372		1	6087	6527	6967	1	10.1	1	0	1 02:06
118	TCMN5	TCMN	8	407637	407923	424326	425219		1	16404	16993	17581	1	10.1	1	0	1 02:06
111	TCMN5	TCMN	8	157612	158110	163422	163731	2_nonsis		5313	5716	6118	3	30	1	0	1 6:2_2:6
34	TCMN5	TCMN	4	173380	174736	179903	180800	2_nonsis		5168	6294	7419	3	30	1	0	1 2:6_6:2
20	TCMN5	TCMN	2	750883	752417	775579	777303	2_nonsis		23163	24791	26419	3	30	1	0	1 2:6_6:2
108	TCMN5	TCMN	8	76095	76580	78270	79037	2_nonsis		1691	2316	2941	3	30	1	0	1 6:2_4:4_2:6
213	TCMN5	TCMN	15	240239	240519	244803	245153	2_nonsis		4285	4599	4913	3	30	1	0	1 2:6_6:2_4:4_2:6
151	TCMN5	TCMN	11	531608	531920	532520	532628	2_nonsis		601	810	1019	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
117	TCMN5	TCMN	8	378642	378942	379863	380348	2_nonsis		922	1314	1705	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
124	TCMN5	TCMN	9	240376	242535	242863	243088	2_nonsis		329	1520	2711	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
81	TCMN5	TCMN	7	173276	173856	174975	175590	2_nonsis		1120	1717	2313	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
217	TCMN5	TCMN	15	484571	485571	487028	487166	2_nonsis		1458	2026	2594	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
240	TCMN5	TCMN	16	916877	917110	922391	922477	2_nonsis		5282	5441	5599	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
167	TCMN5	TCMN	12	650767	657027	660916	661444	2_nonsis		3890	7283	10676	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
123	TCMN5	TCMN	9	141990	142169	143302	143414	2_nonsis		1134	1279	1423	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
159	TCMN5	TCMN	12	176622	176833	178408	178716	2_nonsis		1576	1835	2093	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
231	TCMN5	TCMN	16	227039	227828	232560	232568	2_nonsis		4733	5131	5528	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
201	TCMN5	TCMN	14	397399	397432	401251	404051	2_nonsis		3820	5236	6651	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
171	TCMN5	TCMN	12	766775	767243	769888	770182	2_nonsis		2646	3026	3406	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4)_(4:4aCO)
184	TCMN5	TCMN	13	467764	467817	467817	467994	2_nonsis		1	115	229	1	15	1	1	0 (6:2)_(4:4aCO)
180	TCMN5	TCMN	13	391888	391938	392080	392165	2_nonsis		143	210	276	1	15	1	1	0 (6:2)_(4:4aCO)
85	TCMN5	TCMN	7	424734	424942	424942	425181	2_nonsis		1	224	446	1	15	1	1	0 (6:2)_(4:4aCO)
132	TCMN5	TCMN	10	56885	57032	57144	57356	2_nonsis		113	292	470	1	15	1	1	0 (6:2)_(4:4aCO)
98	TCMN5	TCMN	7	965717	965888	965888	966356	2_nonsis		1	320	638	1	15	1	1	0 (6:2)_(4:4aCO)
188	TCMN5	TCMN	13	887633	887824	887934	888376	2_nonsis		111	427	742	1	15	1	1	0 (6:2)_(4:4aCO)
82	TCMN5	TCMN	7	266087	266369	266369	266948	2_nonsis		1	431	860	1	15	1	1	0 (6:2)_(4:4aCO)
158	TCMN5	TCMN	12	128659	129489	129489	129657	2_nonsis		1	499	997	1	15	1	1	0 (6:2)_(4:4aCO)
22	TCMN5	TCMN	3	37180	37525	37687	38022	2_nonsis		163	502	841	1	15	1	1	0 (6:2)_(4:4aCO)
126	TCMN5	TCMN	9	373284	373728	373971	374268	2_nonsis		244	614	983	1	15	1	1	0 (6:2)_(4:4aCO)
186	TCMN5	TCMN	13	667511	667766	667766	668902	2_nonsis		1	696	1390	1	15	1	1	0 (6:2)_(4:4aCO)
238	TCMN5	TCMN	16	772693	773280	773283	774130	2_nonsis		4	720	1436	1	15	1	1	0 (6:2)_(4:4aCO)
35	TCMN5	TCMN	4	255481	255722	256213	256518	2_nonsis		492	764	1036	1	15	1	1	0 (6:2)_(4:4aCO)
84	TCMN5	TCMN	7	396713	397929	398049	398572	2_nonsis		121	990	1858	1	15	1	1	0 (6:2)_(4:4aCO)
179	TCMN5	TCMN	13	260820	261191	261864	262219	2_nonsis		674	1036	1398	1	15	1	1	0 (6:2)_(4:4aCO)
181	TCMN5	TCMN	13	426590	426949	427114	428830	2_nonsis		166	1203	2239	1	15	1	1	0 (6:2)_(4:4aCO)
161	TCMN5	TCMN	12	280412	281289	281896	282215	2_nonsis		608	1205	1802	1	15	1	1	0 (6:2)_(4:4aCO)
19	TCMN5	TCMN	2	746171	748391	748391	748916	2_nonsis		1	1373	2744	1	15	1	1	0 (6:2)_(4:4aCO)
137	TCMN5	TCMN	10	328971	329323	330470	330974	2_nonsis		1148	1575	2002	1	15	1	1	0 (6:2)_(4:4aCO)
174	TCMN5	TCMN	12	1031618	1032807	1033895	1034027	2_nonsis		1089	1749	2408	1	15	1	1	0 (6:2)_(4:4aCO)
66	TCMN5	TCMN	5	526150	526303	527534	528932	2_nonsis		1232	2007	2781	1	15	1	1	0 (6:2)_(4:4aCO)
199	TCMN5	TCMN	14	326497	326545	328483	328646	2_nonsis		1939	2044	2148	1	15	1	1	0 (6:2)_(4:4aCO)
83	TCMN5	TCMN	7	389105	389508	391279	391475	2_nonsis		1772	2071	2369	1	15	1	1	0 (6:2)_(4:4aCO)
192	TCMN5	TCMN	14	109033	109383	112128	112194	2_nonsis		2746	2953	3160	1	15	1	1	0 (6:2)_(4:4aCO)
26	TCMN5	TCMN	3	251945	252079	255168	255891	2_nonsis		3090	3518	3945	1	15	1	1	0 (6:2)_(4:4aCO)
68	TCMN5	TCMN	6	51370	51603	53398	58238	2_nonsis		1796	4332	6867	1	15	1	1	0 (6:2)_(4:4aCO)
147	TCMN5	TCMN	11	218976	220318	224634	225480	2_nonsis		4317	5410	6503	1	15	1	1	0 (6:2)_(4:4aCO)
6	TCMN5	TCMN	2	67361	68817	73472	73641	2_nonsis		4656	5468	6279	1	15	1	1	0 (6:2)_(4:4aCO)
140	TCMN5	TCMN	10	445855	446477	452919	453420	2_nonsis		6443	7004	7564	1	15	1	1	0 (6:2)_(4:4aCO)
232	TCMN5	TCMN	16	270630	271083	281703	281895	2_nonsis		10621	10943	11264	1	15	1	1	0 (6:2)_(4:4aCO)
233	TCMN5	TCMN	16	284937	285327	296393	297021	2_nonsis		11067	11575	12083	1	15	1	1	0 (6:2)_(4:4aCO)
215	TCMN5	TCMN	15	387208	387907	400124	400317	2_nonsis		12218	12663	13108	1	15	1	1	0 (6:2)_(4:4aCO)
5	TCMN5	TCMN	1	197812	197867	197983	198013	2_nonsis		117	159	200	1	16	1	1	0 (2:6)_(4:4aCO)
149	TCMN5	TCMN	11	355272	355411	355474	355535	2_nonsis		64	163	262	1	16	1	1	0 (2:6)_(4:4aCO)
105	TCMN5	TCMN	8	14965	15038	15239	15293	2_nonsis		202	265	327	1	16	1	1	0 (2:6)_(4:4aCO)
122	TCMN5	TCMN	9	44979	45096	45096	45530	2_nonsis		1	276	550	1	16	1	1	0 (2:6)_(4:4aCO)
145	TCMN5	TCMN	11	79100	79688	79772	79796	2_nonsis		85	390	695	1	16	1	1	0 (2:6)_(4:4aCO)
177	TCMN5	TCMN	13	163286	163391	163519	164021	2_nonsis		129	432	734	1	16	1	1	0 (2:6)_(4:4aCO)
230	TCMN5	TCMN	16	72506	72844	72872	73929	2_nonsis		29	726	1422	1	16	1	1	0 (2:6)_(4:4aCO)

226	TCMN5	TCMN	15	1041487	1042440	1042440	1043118	2_nonsis	1	816	1630	1	16	1	1	0 (2:6)_(4:4aCO)
212	TCMN5	TCMN	15	221112	221192	221900	222314	2_nonsis	709	955	1201	1	16	1	1	0 (2:6)_(4:4aCO)
216	TCMN5	TCMN	15	408540	409273	409753	410084	2_nonsis	481	1012	1543	1	16	1	1	0 (2:6)_(4:4aCO)
196	TCMN5	TCMN	14	197191	197707	198392	198574	2_nonsis	686	1034	1382	1	16	1	1	0 (2:6)_(4:4aCO)
198	TCMN5	TCMN	14	288680	288926	289819	289920	2_nonsis	894	1067	1239	1	16	1	1	0 (2:6)_(4:4aCO)
39	TCMN5	TCMN	4	510697	511129	511815	512370	2_nonsis	687	1180	1672	1	16	1	1	0 (2:6)_(4:4aCO)
164	TCMN5	TCMN	12	499857	500275	500833	501707	2_nonsis	559	1204	1849	1	16	1	1	0 (2:6)_(4:4aCO)
79	TCMN5	TCMN	7	117199	117612	118134	119177	2_nonsis	523	1250	1977	1	16	1	1	0 (2:6)_(4:4aCO)
211	TCMN5	TCMN	15	123921	124780	125570	125806	2_nonsis	791	1338	1884	1	16	1	1	0 (2:6)_(4:4aCO)
120	TCMN5	TCMN	8	503996	505427	505984	506159	2_nonsis	558	1360	2162	1	16	1	1	0 (2:6)_(4:4aCO)
128	TCMN5	TCMN	9	393280	395260	395260	396306	2_nonsis	1	1513	3025	1	16	1	1	0 (2:6)_(4:4aCO)
25	TCMN5	TCMN	3	220112	221651	221877	223339	2_nonsis	227	1727	3226	1	16	1	1	0 (2:6)_(4:4aCO)
30	TCMN5	TCMN	4	115646	116157	117449	117831	2_nonsis	1293	1739	2184	1	16	1	1	0 (2:6)_(4:4aCO)
50	TCMN5	TCMN	4	1127082	1127449	1128837	1129980	2_nonsis	1389	2143	2897	1	16	1	1	0 (2:6)_(4:4aCO)
49	TCMN5	TCMN	4	1051761	1054524	1055277	1055562	2_nonsis	754	2277	3800	1	16	1	1	0 (2:6)_(4:4aCO)
4	TCMN5	TCMN	1	176948	178602	180161	180219	2_nonsis	1560	2415	3270	1	16	1	1	0 (2:6)_(4:4aCO)
113	TCMN5	TCMN	8	217536	218189	220206	220708	2_nonsis	2018	2595	3171	1	16	1	1	0 (2:6)_(4:4aCO)
154	TCMN5	TCMN	11	622708	623698	625985	626193	2_nonsis	2288	2886	3484	1	16	1	1	0 (2:6)_(4:4aCO)
96	TCMN5	TCMN	7	930638	930881	932540	935766	2_nonsis	1660	3394	5127	1	16	1	1	0 (2:6)_(4:4aCO)
190	TCMN5	TCMN	14	42360	42594	45407	46489	2_nonsis	2814	3471	4128	1	16	1	1	0 (2:6)_(4:4aCO)
112	TCMN5	TCMN	8	204203	204657	207745	208403	2_nonsis	3089	3644	4199	1	16	1	1	0 (2:6)_(4:4aCO)
225	TCMN5	TCMN	15	984169	984206	987667	988081	2_nonsis	3462	3687	3911	1	16	1	1	0 (2:6)_(4:4aCO)
224	TCMN5	TCMN	15	940023	940429	944039	944698	2_nonsis	3611	4143	4674	1	16	1	1	0 (2:6)_(4:4aCO)
135	TCMN5	TCMN	10	298271	298682	302943	303003	2_nonsis	4262	4497	4731	1	16	1	1	0 (2:6)_(4:4aCO)
237	TCMN5	TCMN	16	700285	702403	707796	708162	2_nonsis	5394	6635	7876	1	16	1	1	0 (2:6)_(4:4aCO)
221	TCMN5	TCMN	15	820504	820842	829444	829911	2_nonsis	8603	9005	9406	1	16	1	1	0 (2:6)_(4:4aCO)
187	TCMN5	TCMN	13	826921	827091	826921	827091	2_nonsis	0	85	169	1	100	1	1	0 (4:4aCO)
91	TCMN5	TCMN	7	838500	838743	838500	838743	2_nonsis	0	121	242	1	100	1	1	0 (4:4aCO)
7	TCMN5	TCMN	2	120122	120369	120122	120369	2_nonsis	0	123	246	1	100	1	1	0 (4:4aCO)
51	TCMN5	TCMN	4	1133503	1133759	1133503	1133759	2_nonsis	0	128	255	1	100	1	1	0 (4:4aCO)
162	TCMN5	TCMN	12	342190	342448	342190	342448	2_nonsis	0	129	257	1	100	1	1	0 (4:4aCO)
104	TCMN5	TCMN	7	1063846	1064130	1063846	1064130	2_nonsis	0	142	283	1	100	1	1	0 (4:4aCO)
197	TCMN5	TCMN	14	259694	259989	259694	259989	2_nonsis	0	147	294	1	100	1	1	0 (4:4aCO)
45	TCMN5	TCMN	4	922382	922757	922382	922757	2_nonsis	0	187	374	1	100	1	1	0 (4:4aCO)
134	TCMN5	TCMN	10	251884	252286	251884	252286	2_nonsis	0	201	401	1	100	1	1	0 (4:4aCO)
16	TCMN5	TCMN	2	567077	567676	567077	567676	2_nonsis	0	299	598	1	100	1	1	0 (4:4aCO)
36	TCMN5	TCMN	4	306893	307571	306893	307571	2_nonsis	0	339	677	1	100	1	1	0 (4:4aCO)
168	TCMN5	TCMN	12	666935	667631	666935	667631	2_nonsis	0	348	695	1	100	1	1	0 (4:4aCO)
12	TCMN5	TCMN	2	333434	334196	333434	334196	2_nonsis	0	381	761	1	100	1	1	0 (4:4aCO)
146	TCMN5	TCMN	11	203378	204194	203378	204194	2_nonsis	0	408	815	1	100	1	1	0 (4:4aCO)
176	TCMN5	TCMN	13	68292	69113	68292	69113	2_nonsis	0	410	820	1	100	1	1	0 (4:4aCO)
88	TCMN5	TCMN	7	477384	478308	477384	478308	2_nonsis	0	462	923	1	100	1	1	0 (4:4aCO)
114	TCMN5	TCMN	8	277301	278461	277301	278461	2_nonsis	0	580	1159	1	100	1	1	0 (4:4aCO)
3	TCMN5	TCMN	1	82379	83613	82379	83613	2_nonsis	0	617	1233	1	100	1	1	0 (4:4aCO)
185	TCMN5	TCMN	13	576343	577768	576343	577768	2_nonsis	0	712	1424	1	100	1	1	0 (4:4aCO)
53	TCMN5	TCMN	4	1237229	1238791	1237229	1238791	2_nonsis	0	781	1561	1	100	1	1	0 (4:4aCO)
219	TCMN5	TCMN	15	664631	666379	664631	666379	2_nonsis	0	874	1747	1	100	1	1	0 (4:4aCO)
191	TCMN5	TCMN	14	46932	49011	46932	49011	2_nonsis	0	1039	2078	1	100	1	1	0 (4:4aCO)
42	TCMN5	TCMN	4	703905	706032	703905	706032	2_nonsis	0	1063	2126	1	100	1	1	0 (4:4aCO)
207	TCMN5	TCMN	14	652841	655138	652841	655138	2_nonsis	0	1148	2296	1	100	1	1	0 (4:4aCO)
89	TCMN5	TCMN	7	643019	645676	643019	645676	2_nonsis	0	1328	2656	1	100	1	1	0 (4:4aCO)
148	TCMN5	TCMN	11	293792	296531	293792	296531	2_nonsis	0	1369	2738	1	100	1	1	0 (4:4aCO)
1	TCMN5	TCMN	1	39162	41987	39162	41987	2_nonsis	0	1412	2824	1	100	1	1	0 (4:4aCO)
205	TCMN5	TCMN	14	554217	557562	554217	557562	2_nonsis	0	1672	3344	1	100	1	1	0 (4:4aCO)
144	TCMN5	TCMN	11	14411	19020	14411	19020	2_nonsis	0	2304	4608	1	100	1	1	0 (4:4aCO)
27	TCMN5	TCMN	3	291220	296463	291220	296463	2_nonsis	0	2621	5242	1	100	1	1	0 (4:4aCO)
156	TCMN5	TCMN	12	51956	53039	54357	54748	2_nonsis	1319	2055	2791	3	20	1	1	0 (6:2)_(2:6)_(4:4aCO)
125	TCMN5	TCMN	9	329125	334329	336223	336673	2_nonsis	1895	4721	7547	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
208	TCMN5	TCMN	14	765330	765537	766008	766895	2_nonsis	472	1018	1564	3	20	1	1	0 (2:6)_(4:4aCO)_(6:2)_(4:4a)
195	TCMN5	TCMN	14	192780	193276	194143	194260	2_nonsis	868	1174	1479	3	20	1	1	0 (6:2)_(4:4)_(2:6)_(4:4aCO)

ID			n	p1	p2	p3	p4	type	j	v1	v2	v3						composition
8	TCMN5	TCMN	2	166607	166703	167650	167794	2_nonsis		948	1067	1186	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(6:2)_(4:4aCO)
17	TCMN5	TCMN	2	662444	666708	668082	669586	2_sis		1375	4258	7141	0	1	2	0	2	(0:8)_(2:6)_(2:6a)_(4:4)
32	TCMN5	TCMN	4	156591	157148	160731	161006	2_sis		3584	3999	4414	0	1	2	0	2	(2:6)_(0:8)_(2:6)_(4:4)
44	TCMN5	TCMN	4	844304	845613	848136	850484	2_sis		2524	4352	6179	0	1	2	0	2	(6:2)_(8:0)_(4:4)
47	TCMN5	TCMN	4	951669	952018	960570	960787	2_sis		8553	8835	9117	0	1	2	0	2	(2:6)_(0:8)_(2:6)_(4:4)
64	TCMN5	TCMN	5	472756	472959	475154	475295	2_sis		2196	2367	2538	0	1	2	0	2	(2:6)_(0:8)_(2:6)_(4:4)
70	TCMN5	TCMN	6	129176	129391	130480	131237	2_sis		1090	1575	2060	0	1	2	0	2	(2:6)_(8:0)_(4:4)
101	TCMN5	TCMN	7	1009263	1009276	1016792	1017661		3	7517	7957	8397	0	1	2	0	2	(6:2)_(4:4)_(0:8)_(2:6)_(4:4)
106	TCMN5	TCMN	8	31980	32029	34675	34710	2_sis		2647	2688	2729	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
150	TCMN5	TCMN	11	525008	525645	529197	529548	2_sis		3553	4046	4539	0	1	2	0	2	(6:2)_(8:0)_(6:2)_(4:4)
172	TCMN5	TCMN	12	1007084	1007701	1011621	1013592		3	3921	5214	6507	0	1	2	0	2	(2:6)_(8:0)_(4:4)
202	TCMN5	TCMN	14	424418	425075	433271	434561		3	8197	9170	10142	0	1	2	0	2	(2:6)_(0:8)_(2:6)_(6:2)_(4:4)
227	TCMN5	TCMN	15	1059960	1060063	1063605	1063818	2_sis		3543	3700	3857	0	1	2	0	2	(6:2)_(8:0)_(6:2)_(4:4)
14	TCMN5	TCMN	2	479752	480693	484159	485003		3	3467	4359	5250	0	2	2	1	1	(6:2)_(6:2a)_(4:4aCO)
23	TCMN5	TCMN	3	57568	58033	59925	60354		3	1893	2339	2785	0	2	2	1	1	(2:6)_(0:8)_(4:4aCO)
28	TCMN5	TCMN	4	75223	76111	78945	79107		3	2835	3359	3883	0	2	2	1	1	(8:0)_(6:2)_(4:4aCO)
40	TCMN5	TCMN	4	548255	548809	555783	556617		3	6975	7668	8361	0	2	2	1	1	(2:6)_(4:4)_(2:6)_(4:4)_(2:6a)_(4:4aCO)
41	TCMN5	TCMN	4	698417	698508	703137	703208		4	4630	4710	4790	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
46	TCMN5	TCMN	4	924351	924464	929665	930059		3	5202	5455	5707	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
54	TCMN5	TCMN	4	1270457	1270902	1282347	1283112		3	11446	12050	12654	0	2	2	1	1	(2:6)_(4:4)_(0:8)_(2:6a)_(0:8)_(2:6a)_(4:4aCO)
55	TCMN5	TCMN	4	1328369	1329703	1338084	1338120		3	8382	9066	9750	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
56	TCMN5	TCMN	4	1341051	1341287	1347017	1347437		3	5731	6058	6385	0	2	2	1	1	(2:6)_(4:4)_(0:8)_(2:6)_(4:4aCO)
67	TCMN5	TCMN	6	25366	25514	29751	29945		3	4238	4408	4578	0	2	2	1	1	(2:6)_(2:6a)_(4:4)_(2:6a)_(4:4)_(2:6a)_(0:8)_(2:6)_(4:4aCO)
73	TCMN5	TCMN	6	223291	223531	227351	227543		3	3821	4036	4251	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
75	TCMN5	TCMN	6	244444	245103	250075	251006		4	4973	5767	6561	0	2	2	1	1	(0:8)_(2:6)_(0:8)_(2:6a)_(4:4aCO)
92	TCMN5	TCMN	7	846740	851797	853451	853758		4	1655	4336	7017	0	2	2	2	0	(0:8)_(4:4aCO)_(6:2)_(2:6)_(4:4a)
110	TCMN5	TCMN	8	139506	141400	141400	142863		3	1	1679	3356	0	2	2	1	1	(6:2)_(4:4aCO)
115	TCMN5	TCMN	8	279197	279622	283226	283558		3	3605	3983	4360	0	2	2	1	1	(8:0)_(4:4)_(6:2)_(4:4aCO)
133	TCMN5	TCMN	10	191621	192156	193406	194259		3	1251	1944	2637	0	2	2	1	1	(6:2)_(4:4)_(4:4aCO)
138	TCMN5	TCMN	10	355564	355601	362546	362886		3	6946	7134	7321	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
139	TCMN5	TCMN	10	384523	385172	398997	399390		4	13826	14346	14866	0	2	2	1	1	(6:2)_(4:4)_(2:6)_(0:8)_(2:6a)_(4:4aCO)
143	TCMN5	TCMN	10	707903	708090	709746	711083		3	1657	2418	3179	0	2	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4a)
152	TCMN5	TCMN	11	569085	569468	592577	593181		3	23110	23603	24095	0	2	2	1	1	(6:2)_(8:0)_(4:4aCO)
157	TCMN5	TCMN	12	95188	98056	100782	101108		4	2727	4323	5919	0	2	2	2	0	(8:0)_(4:4aCO)
160	TCMN5	TCMN	12	256406	256727	262367	265975		3	5641	7605	9568	0	2	2	1	1	(2:6)_(2:6a)_(0:8)_(4:4aCO)
166	TCMN5	TCMN	12	566431	566615	567266	568114		3	652	1167	1682	0	2	2	1	1	(6:2)_(4:4)_(4:4aCO)
170	TCMN5	TCMN	12	719910	721257	721257	721983		3	1	1037	2072	0	2	2	1	1	(2:6)_(4:4aCO)
220	TCMN5	TCMN	15	763727	764378	765404	766151		3	1027	1725	2423	0	2	2	1	1	(2:6)_(4:4aCO)
228	TCMN5	TCMN	16	22826	26114	68341	68882		4	42228	44142	46055	0	2	2	1	1	(6:2)_(8:0)_(6:2)_(2:6)_(4:4aCO)
234	TCMN5	TCMN	16	458660	458912	470217	470860		3	11306	11753	12199	0	2	2	1	1	(6:2)_(2:6)_(4:4aCO)
236	TCMN5	TCMN	16	679119	679573	682384	682729		3	2812	3211	3609	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)
18	TCMN5	TCMN	2	684988	685165	701832	702521		4	16668	17100	17532	0	3	2	2	0	(2:6)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(2:6a)_(4:4bCO)
24	TCMN5	TCMN	3	71752	71885	79797	83502		3	7913	9831	11749	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(0:8)_(2:6a)_(4:4bCO)
69	TCMN5	TCMN	6	87634	87949	94545	94981	2_nonsis		6597	6972	7346	0	3	2	0	2	(6:2)_(4:4aCO)_(2:6)_(4:4CO)
71	TCMN5	TCMN	6	192445	192534	199343	201607		3	6810	7986	9161	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)
93	TCMN5	TCMN	7	877161	878070	880304	880399	2_nonsis		2235	2736	3237	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4CO)
95	TCMN5	TCMN	7	914816	915691	920266	920986		3	4576	5373	6169	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)
103	TCMN5	TCMN	7	1024337	1025033	1039298	1039425		3	14266	14677	15087	0	3	2	1	1	(2:6)_(4:4aCO)_(4:4bCO)
107	TCMN5	TCMN	8	45102	46055	56808	57698		3	10754	11675	12595	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6a)_(0:8)_(2:6b)_(0:8)_(2:6)_(4:4CO)
141	TCMN5	TCMN	10	553415	554502	558676	558889	2_nonsis		4175	4824	5473	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4CO)
153	TCMN5	TCMN	11	606908	608039	611219	612138	2_nonsis		3181	4205	5229	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4CO)_(2:6)_(4:4aCO)
173	TCMN5	TCMN	12	1015108	1015543	1017718	1018933	2_nonsis		2176	3000	3824	0	3	2	1	1	(4:4aCO)_(4:4CO)_(6:2)_(4:4aCO)
175	TCMN5	TCMN	13	40511	41051	50109	50514		3	9059	9531	10002	0	3	2	1	1	(4:4aCO)_(2:6)_(4:4bCO)
210	TCMN5	TCMN	15	85011	85161	95393	95966		3	10233	10594	10954	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2a)_(2:6)_(4:4CO)
218	TCMN5	TCMN	15	574716	577841	590260	590710		3	12420	14207	15993	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)
384	TCMN5	TCMN	10	718719	720598	725123	745751		1	0	13516	27031	0	4	1	NA	NA	
430	TCMN5	TCMN	13	908047	908906	917449	924431	NA		8544	12464	16383	0	4	1	NA	NA	6:2_4:4_6:2_8:0_6:2
451	TCMN5	TCMN	15	40057	40834	40057	40834		1	0	388	776	0	4	1	NA	NA	
97	TCMN6	TCMN	14	135855	135879	135879	135908		1	1	27	52	1	10	1	0	1	06:02
123	TCMN6	TCMN	15	1045508	1045539	1045539	1045615		1	1	54	106	1	10	1	0	1	06:02

131	TCMN6	TCMN	16	664160	664567	664567	664678		1	1	259	517	1	10	1	0	1 06:02
130	TCMN6	TCMN	16	621160	621301	621480	622057		1	180	538	896	1	10	1	0	1 06:02
115	TCMN6	TCMN	15	484571	485571	485588	485898		1	18	672	1326	1	10	1	0	1 06:02
80	TCMN6	TCMN	12	679180	679614	679633	680510		1	20	675	1329	1	10	1	0	1 06:02
59	TCMN6	TCMN	9	347270	348431	348726	348958		1	296	992	1687	1	10	1	0	1 06:02
28	TCMN6	TCMN	5	460411	461582	461877	462226		1	296	1055	1814	1	10	1	0	1 06:02
51	TCMN6	TCMN	8	235099	235912	236251	237146		1	340	1193	2046	1	10	1	0	1 06:02
104	TCMN6	TCMN	14	651098	652238	652841	655138		1	604	2322	4039	1	10	1	0	1 06:02
37	TCMN6	TCMN	7	91862	92820	94650	95130		1	1831	2549	3267	1	10	1	0	1 06:02
118	TCMN6	TCMN	15	605119	606232	609553	609608		1	3322	3905	4488	1	10	1	0	1 06:02
73	TCMN6	TCMN	11	566212	566530	570049	570688		1	3520	3998	4475	1	10	1	0	1 06:02
86	TCMN6	TCMN	13	390393	390486	390486	390597		1	1	102	203	1	10.1	1	0	1 02:06
124	TCMN6	TCMN	16	162337	162602	162602	162746		1	1	205	408	1	10.1	1	0	1 02:06
40	TCMN6	TCMN	7	197001	197150	197230	197465		1	81	272	463	1	10.1	1	0	1 02:06
78	TCMN6	TCMN	12	645780	645971	645971	646705		1	1	463	924	1	10.1	1	0	1 02:06
44	TCMN6	TCMN	7	361880	362105	362105	363325		1	1	723	1444	1	10.1	1	0	1 02:06
98	TCMN6	TCMN	14	166733	167934	168003	168178		1	70	757	1444	1	10.1	1	0	1 02:06
117	TCMN6	TCMN	15	520372	520499	521161	521442		1	663	866	1069	1	10.1	1	0	1 02:06
42	TCMN6	TCMN	7	253383	253849	254552	255756		1	704	1538	2372	1	10.1	1	0	1 02:06
93	TCMN6	TCMN	14	30923	32285	32426	34396		1	142	1807	3472	1	10.1	1	0	1 02:06
105	TCMN6	TCMN	14	686681	688572	689310	689558		1	739	1808	2876	1	10.1	1	0	1 02:06
35	TCMN6	TCMN	7	44099	44898	46197	46424		1	1300	1812	2324	1	10.1	1	0	1 02:06
67	TCMN6	TCMN	11	124424	125000	125651	127396		1	652	1812	2971	1	10.1	1	0	1 02:06
64	TCMN6	TCMN	10	465795	467010	467589	469453		1	580	2119	3657	1	10.1	1	0	1 02:06
7	TCMN6	TCMN	2	144991	145073	147245	147314		1	2173	2248	2322	1	10.1	1	0	1 02:06
8	TCMN6	TCMN	2	158200	158707	160618	160810		1	1912	2261	2609	1	10.1	1	0	1 02:06
72	TCMN6	TCMN	11	531920	532520	534319	535346		1	1800	2613	3425	1	10.1	1	0	1 02:06
88	TCMN6	TCMN	13	447619	448761	450640	451369		1	1880	2815	3749	1	10.1	1	0	1 02:06
108	TCMN6	TCMN	15	100319	100603	103524	103968		1	2922	3285	3648	1	10.1	1	0	1 02:06
4	TCMN6	TCMN	2	66717	66852	68834	72096		1	1983	3681	5378	1	10.1	1	0	1 02:06
126	TCMN6	TCMN	16	352228	352381	356245	356407		1	3865	4022	4178	1	10.1	1	0	1 02:06
33	TCMN6	TCMN	6	215867	216669	221934	222095		1	5266	5747	6227	1	10.1	1	0	1 02:06
21	TCMN6	TCMN	4	271809	272060	273273	273764	2_nonsis		1214	1584	1954	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
114	TCMN6	TCMN	15	407771	408436	410084	410118	2_nonsis		1649	1998	2346	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
100	TCMN6	TCMN	14	256273	256857	256857	256929	2_nonsis		1	328	655	1	15	1	1	0 (6:2)_(4:4aCO)
58	TCMN6	TCMN	9	260488	260891	261499	261805	2_nonsis		609	963	1316	1	15	1	1	0 (6:2)_(4:4aCO)
70	TCMN6	TCMN	11	204194	205481	205840	206732	2_nonsis		360	1449	2537	1	15	1	1	0 (6:2)_(4:4aCO)
55	TCMN6	TCMN	9	52260	53016	53717	54480	2_nonsis		702	1461	2219	1	15	1	1	0 (6:2)_(4:4aCO)
99	TCMN6	TCMN	14	216026	216647	216919	218712	2_nonsis		273	1479	2685	1	15	1	1	0 (6:2)_(4:4aCO)
127	TCMN6	TCMN	16	474370	474526	475802	476377	2_nonsis		1277	1642	2006	1	15	1	1	0 (6:2)_(4:4aCO)
119	TCMN6	TCMN	15	662842	664181	664631	666379	2_nonsis		451	1994	3536	1	15	1	1	0 (6:2)_(4:4aCO)
30	TCMN6	TCMN	5	524520	525075	526712	527126	2_nonsis		1638	2122	2605	1	15	1	1	0 (6:2)_(4:4aCO)
9	TCMN6	TCMN	2	192576	193122	194226	195735	2_nonsis		1105	2132	3158	1	15	1	1	0 (6:2)_(4:4aCO)
56	TCMN6	TCMN	9	153913	154387	156304	156711	2_nonsis		1918	2358	2797	1	15	1	1	0 (6:2)_(4:4aCO)
22	TCMN6	TCMN	4	313461	313566	315175	316669	2_nonsis		1610	2409	3207	1	15	1	1	0 (6:2)_(4:4aCO)
25	TCMN6	TCMN	5	235812	236202	238396	238975	2_nonsis		2195	2679	3162	1	15	1	1	0 (6:2)_(4:4aCO)
110	TCMN6	TCMN	15	144479	144655	147007	147540	2_nonsis		2353	2707	3060	1	15	1	1	0 (6:2)_(4:4aCO)
10	TCMN6	TCMN	2	290619	291653	294230	295028	2_nonsis		2578	3493	4408	1	15	1	1	0 (6:2)_(4:4aCO)
26	TCMN6	TCMN	5	256810	258361	261062	261627	2_nonsis		2702	3759	4816	1	15	1	1	0 (6:2)_(4:4aCO)
43	TCMN6	TCMN	7	273707	274428	278975	279315	2_nonsis		4548	5078	5607	1	15	1	1	0 (6:2)_(4:4aCO)
53	TCMN6	TCMN	8	321084	321902	327083	327845	2_nonsis		5182	5971	6760	1	15	1	1	0 (6:2)_(4:4aCO)
89	TCMN6	TCMN	13	588661	588927	594694	595371	2_nonsis		5768	6239	6709	1	15	1	1	0 (6:2)_(4:4aCO)
65	TCMN6	TCMN	10	469702	470610	472296	484073	2_nonsis		1687	8029	14370	1	15	1	1	0 (6:2)_(4:4aCO)
113	TCMN6	TCMN	15	391650	392258	401076	401767	2_nonsis		8819	9468	10116	1	15	1	1	0 (6:2)_(4:4aCO)
125	TCMN6	TCMN	16	259430	259987	260098	260252	2_nonsis		112	467	821	1	16	1	1	0 (2:6)_(4:4aCO)
39	TCMN6	TCMN	7	193477	193769	193769	194505	2_nonsis		1	514	1027	1	16	1	1	0 (2:6)_(4:4aCO)
34	TCMN6	TCMN	7	36018	36691	37058	37087	2_nonsis		368	718	1068	1	16	1	1	0 (2:6)_(4:4aCO)
57	TCMN6	TCMN	9	252448	253199	253199	253992	2_nonsis		1	772	1543	1	16	1	1	0 (2:6)_(4:4aCO)
77	TCMN6	TCMN	12	507075	507492	507531	508649	2_nonsis		40	807	1573	1	16	1	1	0 (2:6)_(4:4aCO)
116	TCMN6	TCMN	15	487166	487809	488381	488504	2_nonsis		573	955	1337	1	16	1	1	0 (2:6)_(4:4aCO)

92	TCMN6	TCMN	13	830613	831156	831576	832164	2_nonsis		421	986	1550	1	16	1	1	0	(2:6)_(4:4aCO)
101	TCMN6	TCMN	14	345121	345280	346206	346414	2_nonsis		927	1110	1292	1	16	1	1	0	(2:6)_(4:4aCO)
18	TCMN6	TCMN	4	164298	164984	165551	166022	2_nonsis		568	1146	1723	1	16	1	1	0	(2:6)_(4:4aCO)
16	TCMN6	TCMN	3	189052	190177	190177	191741	2_nonsis		1	1345	2688	1	16	1	1	0	(2:6)_(4:4aCO)
63	TCMN6	TCMN	10	382565	383067	384052	384310	2_nonsis		986	1365	1744	1	16	1	1	0	(2:6)_(4:4aCO)
47	TCMN6	TCMN	7	526419	526675	528501	528674	2_nonsis		1827	2041	2254	1	16	1	1	0	(2:6)_(4:4aCO)
45	TCMN6	TCMN	7	374606	374962	376592	377296	2_nonsis		1631	2160	2689	1	16	1	1	0	(2:6)_(4:4aCO)
54	TCMN6	TCMN	8	381693	382565	384685	385098	2_nonsis		2121	2763	3404	1	16	1	1	0	(2:6)_(4:4aCO)
81	TCMN6	TCMN	12	826618	830392	831136	831658	2_nonsis		745	2892	5039	1	16	1	1	0	(2:6)_(4:4aCO)
128	TCMN6	TCMN	16	504597	505893	508709	508976	2_nonsis		2817	3598	4378	1	16	1	1	0	(2:6)_(4:4aCO)
74	TCMN6	TCMN	11	628847	629063	632654	633545	2_nonsis		3592	4145	4697	1	16	1	1	0	(2:6)_(4:4aCO)
69	TCMN6	TCMN	11	168746	169345	173133	173315	2_nonsis		3789	4179	4568	1	16	1	1	0	(2:6)_(4:4aCO)
68	TCMN6	TCMN	11	160799	161178	165087	165249	2_nonsis		3910	4180	4449	1	16	1	1	0	(2:6)_(4:4aCO)
41	TCMN6	TCMN	7	226711	230011	232615	232997	2_nonsis		2605	4445	6285	1	16	1	1	0	(2:6)_(4:4aCO)
87	TCMN6	TCMN	13	432244	432613	436769	437012	2_nonsis		4157	4462	4767	1	16	1	1	0	(2:6)_(4:4aCO)
94	TCMN6	TCMN	14	80433	81575	85405	85712	2_nonsis		3831	4555	5278	1	16	1	1	0	(2:6)_(4:4aCO)
96	TCMN6	TCMN	14	114676	114732	119295	119414	2_nonsis		4564	4651	4737	1	16	1	1	0	(2:6)_(4:4aCO)
121	TCMN6	TCMN	15	938699	939507	943688	944698	2_nonsis		4182	5090	5998	1	16	1	1	0	(2:6)_(4:4aCO)
48	TCMN6	TCMN	7	622133	622186	627463	627883	2_nonsis		5278	5514	5749	1	16	1	1	0	(2:6)_(4:4aCO)
31	TCMN6	TCMN	6	49483	50137	53398	58238	2_nonsis		3262	6008	8754	1	16	1	1	0	(2:6)_(4:4aCO)
20	TCMN6	TCMN	4	264197	264290	264197	264290	2_nonsis		0	46	92	1	100	1	1	0	(4:4aCO)
120	TCMN6	TCMN	15	757318	757677	757318	757677	2_nonsis		0	179	358	1	100	1	1	0	(4:4aCO)
11	TCMN6	TCMN	2	489897	490532	489897	490532	2_nonsis		0	317	634	1	100	1	1	0	(4:4aCO)
61	TCMN6	TCMN	10	159830	160491	159830	160491	2_nonsis		0	330	660	1	100	1	1	0	(4:4aCO)
91	TCMN6	TCMN	13	748055	748748	748055	748748	2_nonsis		0	346	692	1	100	1	1	0	(4:4aCO)
15	TCMN6	TCMN	2	797893	798747	797893	798747	2_nonsis		0	427	853	1	100	1	1	0	(4:4aCO)
109	TCMN6	TCMN	15	123921	124780	123921	124780	2_nonsis		0	429	858	1	100	1	1	0	(4:4aCO)
14	TCMN6	TCMN	2	746171	748391	746171	748391	2_nonsis		0	1110	2219	1	100	1	1	0	(4:4aCO)
32	TCMN6	TCMN	6	199339	201607	199339	201607	2_nonsis		0	1134	2267	1	100	1	1	0	(4:4aCO)
111	TCMN6	TCMN	15	192333	196238	192333	196238	2_nonsis		0	1952	3904	1	100	1	1	0	(4:4aCO)
27	TCMN6	TCMN	5	309648	309961	316361	316681	2_nonsis		6401	6717	7032	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
1	TCMN6	TCMN	1	121235	128637	129517	130254		3	881	4950	9018	0	1	2	0	2	(0:8)_(6:2)_(4:4)
85	TCMN6	TCMN	13	379442	379637	388700	388702	2_sis		9064	9162	9259	0	1	2	0	2	(2:6)_(0:8)_(4:4)_(2:6)_(4:4)
23	TCMN6	TCMN	4	557710	557899	557899	558895		4	1	593	1184	0	2	2	2	0	(8:0)_(4:4aCO)
36	TCMN6	TCMN	7	82858	85120	85628	86297		4	509	1974	3438	0	2	2	2	0	(8:0)_(4:4aCO)
50	TCMN6	TCMN	8	141400	142863	143727	143824		3	865	1644	2423	0	2	2	1	1	(2:6)_(0:8)_(4:4aCO)
62	TCMN6	TCMN	10	235668	235976	249099	249294		4	13124	13375	13625	0	2	2	1	1	(8:0)_(0:8)_(4:4aCO)
79	TCMN6	TCMN	12	657536	657602	661444	661750		3	3843	4028	4213	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
82	TCMN6	TCMN	12	874541	875035	881235	882746		3	6201	7203	8204	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
83	TCMN6	TCMN	12	892436	930472	892436	930472		4	0	19018	38035	0	2	2	2	0	(4:4aCO)
84	TCMN6	TCMN	13	72351	73368	81243	81991		4	7876	8758	9639	0	2	2	2	0	(8:0)_(4:4aCO)
95	TCMN6	TCMN	14	89494	89776	91169	91989		4	1394	1944	2494	0	2	2	2	0	(8:0)_(4:4aCO)
112	TCMN6	TCMN	15	252891	253882	255268	256152		3	1387	2324	3260	0	2	2	2	0	(8:0)_(4:4aCO)
13	TCMN6	TCMN	2	666849	668076	669668	669956	2_nonsis		1593	2350	3106	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)
210	TCMN6	TCMN	12	31473	32690	31473	32690	NA		0	608	1216	0	4	1	NA	NA	
84	TN1	TN	14	559022	559202	559202	559420		1	1	199	397	1	10	1	0	1	06:02
3	TN1	TN	2	195960	196145	196145	196362		1	1	201	401	1	10	1	0	1	06:02
9	TN1	TN	3	211504	211617	211617	211982		1	1	239	477	1	10	1	0	1	06:02
93	TN1	TN	15	722554	722838	722838	723053		1	1	250	498	1	10	1	0	1	06:02
100	TN1	TN	16	832084	832297	832535	832685		1	239	420	600	1	10	1	0	1	06:02
82	TN1	TN	14	370839	371516	371658	372088		1	143	696	1248	1	10	1	0	1	06:02
21	TN1	TN	4	1278613	1278992	1279422	1279680		1	431	749	1066	1	10	1	0	1	06:02
91	TN1	TN	15	477802	478649	478915	479565		1	267	1015	1762	1	10	1	0	1	06:02
64	TN1	TN	12	604223	604915	606088	606112		1	1174	1531	1888	1	10	1	0	1	06:02
27	TN1	TN	6	46998	47804	49258	49483		1	1455	1970	2484	1	10	1	0	1	06:02
72	TN1	TN	13	145373	145748	146198	149583		1	451	2330	4209	1	10	1	0	1	06:02
35	TN1	TN	7	591242	591949	594432	594587		1	2484	2914	3344	1	10	1	0	1	06:02
52	TN1	TN	10	557590	557648	560603	560828		1	2956	3097	3237	1	10	1	0	1	06:02
41	TN1	TN	8	37931	37944	42065	42238		1	4122	4214	4306	1	10	1	0	1	06:02
43	TN1	TN	9	32569	32674	36872	36921		1	4199	4275	4351	1	10	1	0	1	06:02

58	TN1	TN	11	502693	502906	507899	508337		1	4994	5319	5643	1	10	1	0	1	06:02
61	TN1	TN	12	224592	225174	225332	225620		1	159	593	1027	1	10.1	1	0	1	02:06
55	TN1	TN	11	225909	226549	226659	227319		1	111	760	1409	1	10.1	1	0	1	02:06
18	TN1	TN	4	794075	794507	794820	795302		1	314	770	1226	1	10.1	1	0	1	02:06
4	TN1	TN	2	335092	337090	337090	337453		1	1	1181	2360	1	10.1	1	0	1	02:06
44	TN1	TN	9	52260	53016	53717	54480		1	702	1461	2219	1	10.1	1	0	1	02:06
81	TN1	TN	14	365847	366158	368183	368877		1	2026	2528	3029	1	10.1	1	0	1	02:06
57	TN1	TN	11	474020	474395	476611	477203		1	2217	2700	3182	1	10.1	1	0	1	02:06
94	TN1	TN	15	801555	802374	804694	804884		1	2321	2825	3328	1	10.1	1	0	1	02:06
32	TN1	TN	7	195692	195804	198476	198752		1	2673	2866	3059	1	10.1	1	0	1	02:06
14	TN1	TN	4	373089	373363	375932	376661		1	2570	3071	3571	1	10.1	1	0	1	02:06
86	TN1	TN	14	760406	760949	763742	763922		1	2794	3155	3515	1	10.1	1	0	1	02:06
26	TN1	TN	5	541194	541518	544392	545025		1	2875	3353	3830	1	10.1	1	0	1	02:06
97	TN1	TN	16	244939	245420	248123	249056		1	2704	3410	4116	1	10.1	1	0	1	02:06
67	TN1	TN	12	803833	808209	810333	811301		1	2125	4796	7467	1	10.1	1	0	1	02:06
90	TN1	TN	15	427719	428753	430036	430667	2_nonsis		1284	2116	2947	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
50	TN1	TN	10	461089	461507	461975	462161	2_nonsis		469	770	1071	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
36	TN1	TN	7	610218	610674	612267	612759	2_nonsis		1594	2067	2540	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
79	TN1	TN	14	74669	75232	77185	77306	2_nonsis		1954	2295	2636	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
96	TN1	TN	16	131325	131623	134518	135194	2_nonsis		2896	3382	3868	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
5	TN1	TN	2	430067	431229	434210	434300	2_nonsis		2982	3607	4232	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
89	TN1	TN	15	216181	216247	220880	220974	2_nonsis		4634	4713	4792	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
69	TN1	TN	12	832387	832594	837962	840577	2_nonsis		5369	6779	8189	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
34	TN1	TN	7	415307	415568	415592	415703	2_nonsis		25	210	395	1	15	1	1	0	(6:2)_(4:4aCO)
47	TN1	TN	10	140425	140646	140649	140994	2_nonsis		4	286	568	1	15	1	1	0	(6:2)_(4:4aCO)
68	TN1	TN	12	819713	819771	819834	820606	2_nonsis		64	478	892	1	15	1	1	0	(6:2)_(4:4aCO)
66	TN1	TN	12	783055	783530	783530	784218	2_nonsis		1	582	1162	1	15	1	1	0	(6:2)_(4:4aCO)
60	TN1	TN	12	66129	66235	66714	66854	2_nonsis		480	602	724	1	15	1	1	0	(6:2)_(4:4aCO)
98	TN1	TN	16	496835	497140	497758	497958	2_nonsis		619	871	1122	1	15	1	1	0	(6:2)_(4:4aCO)
49	TN1	TN	10	236912	237017	238135	238262	2_nonsis		1119	1234	1349	1	15	1	1	0	(6:2)_(4:4aCO)
70	TN1	TN	12	964739	967075	967075	967302	2_nonsis		1	1282	2562	1	15	1	1	0	(6:2)_(4:4aCO)
87	TN1	TN	15	83362	83622	84553	85000	2_nonsis		932	1285	1637	1	15	1	1	0	(6:2)_(4:4aCO)
59	TN1	TN	11	532742	533318	534319	535346	2_nonsis		1002	1803	2603	1	15	1	1	0	(6:2)_(4:4aCO)
38	TN1	TN	7	936948	937376	939318	939675	2_nonsis		1943	2335	2726	1	15	1	1	0	(6:2)_(4:4aCO)
71	TN1	TN	12	1009719	1011169	1012226	1013592	2_nonsis		1058	2465	3872	1	15	1	1	0	(6:2)_(4:4aCO)
85	TN1	TN	14	710457	711615	713465	713685	2_nonsis		1851	2539	3227	1	15	1	1	0	(6:2)_(4:4aCO)
11	TN1	TN	4	83389	83626	86165	86337	2_nonsis		2540	2744	2947	1	15	1	1	0	(6:2)_(4:4aCO)
45	TN1	TN	9	185865	188629	190035	190142	2_nonsis		1407	2842	4276	1	15	1	1	0	(6:2)_(4:4aCO)
7	TN1	TN	2	782581	783142	786053	786204	2_nonsis		2912	3267	3622	1	15	1	1	0	(6:2)_(4:4aCO)
30	TN1	TN	6	195471	195636	198468	199207	2_nonsis		2833	3284	3735	1	15	1	1	0	(6:2)_(4:4aCO)
39	TN1	TN	7	966356	966466	970088	970143	2_nonsis		3623	3705	3786	1	15	1	1	0	(6:2)_(4:4aCO)
37	TN1	TN	7	802249	802512	805722	806818	2_nonsis		3211	3890	4568	1	15	1	1	0	(6:2)_(4:4aCO)
95	TN1	TN	15	913489	914118	917763	918228	2_nonsis		3646	4192	4738	1	15	1	1	0	(6:2)_(4:4aCO)
33	TN1	TN	7	269551	269881	274448	275758	2_nonsis		4568	5387	6206	1	15	1	1	0	(6:2)_(4:4aCO)
92	TN1	TN	15	638364	638644	638644	639033	2_nonsis		1	335	668	1	16	1	1	0	(2:6)_(4:4aCO)
15	TN1	TN	4	552557	552846	552846	553583	2_nonsis		1	513	1025	1	16	1	1	0	(2:6)_(4:4aCO)
28	TN1	TN	6	73933	74035	74485	74647	2_nonsis		451	582	713	1	16	1	1	0	(2:6)_(4:4aCO)
99	TN1	TN	16	760748	760865	761136	761833	2_nonsis		272	678	1084	1	16	1	1	0	(2:6)_(4:4aCO)
83	TN1	TN	14	468958	469102	469170	470301	2_nonsis		69	706	1342	1	16	1	1	0	(2:6)_(4:4aCO)
63	TN1	TN	12	430703	431555	431739	431957	2_nonsis		185	719	1253	1	16	1	1	0	(2:6)_(4:4aCO)
51	TN1	TN	10	544523	545038	545233	546078	2_nonsis		196	875	1554	1	16	1	1	0	(2:6)_(4:4aCO)
16	TN1	TN	4	630640	631885	631885	632423	2_nonsis		1	892	1782	1	16	1	1	0	(2:6)_(4:4aCO)
31	TN1	TN	7	59403	60729	60729	61349	2_nonsis		1	973	1945	1	16	1	1	0	(2:6)_(4:4aCO)
20	TN1	TN	4	1250653	1251183	1251845	1252116	2_nonsis		663	1063	1462	1	16	1	1	0	(2:6)_(4:4aCO)
25	TN1	TN	5	490102	490231	491262	491424	2_nonsis		1032	1177	1321	1	16	1	1	0	(2:6)_(4:4aCO)
17	TN1	TN	4	726870	727318	728057	728918	2_nonsis		740	1394	2047	1	16	1	1	0	(2:6)_(4:4aCO)
75	TN1	TN	13	576343	577768	577948	579159	2_nonsis		181	1498	2815	1	16	1	1	0	(2:6)_(4:4aCO)
74	TN1	TN	13	304685	304946	306097	306566	2_nonsis		1152	1516	1880	1	16	1	1	0	(2:6)_(4:4aCO)
73	TN1	TN	13	181240	182183	183219	184027	2_nonsis		1037	1912	2786	1	16	1	1	0	(2:6)_(4:4aCO)
77	TN1	TN	13	850650	851409	853271	853565	2_nonsis		1863	2389	2914	1	16	1	1	0	(2:6)_(4:4aCO)

65	TN1	TN	12	708261	708383	710710	710866	2_nonsis		2328	2466	2604	1	16	1	1	0	(2:6)_(4:4aCO)
78	TN1	TN	14	32426	34396	34917	37063	2_nonsis		522	2579	4636	1	16	1	1	0	(2:6)_(4:4aCO)
56	TN1	TN	11	368313	369378	371814	372140	2_nonsis		2437	3132	3826	1	16	1	1	0	(2:6)_(4:4aCO)
19	TN1	TN	4	818791	819541	822719	823198	2_nonsis		3179	3793	4406	1	16	1	1	0	(2:6)_(4:4aCO)
62	TN1	TN	12	338685	339496	342709	343120	2_nonsis		3214	3824	4434	1	16	1	1	0	(2:6)_(4:4aCO)
29	TN1	TN	6	171501	172334	175597	175923	2_nonsis		3264	3843	4421	1	16	1	1	0	(2:6)_(4:4aCO)
6	TN1	TN	2	659928	660972	662444	666708	2_nonsis		1473	4126	6779	1	16	1	1	0	(2:6)_(4:4aCO)
8	TN1	TN	3	162694	163059	167541	167741	2_nonsis		4483	4765	5046	1	16	1	1	0	(2:6)_(4:4aCO)
13	TN1	TN	4	196851	198376	202229	202572	2_nonsis		3854	4787	5720	1	16	1	1	0	(2:6)_(4:4aCO)
48	TN1	TN	10	197272	204724	205745	206436	2_nonsis		1022	5093	9163	1	16	1	1	0	(2:6)_(4:4aCO)
40	TN1	TN	8	20117	20294	20117	20294	2_nonsis		0	88	176	1	100	1	1	0	(4:4aCO)
54	TN1	TN	11	223790	224066	223790	224066	2_nonsis		0	138	275	1	100	1	1	0	(4:4aCO)
24	TN1	TN	5	376468	376801	376468	376801	2_nonsis		0	166	332	1	100	1	1	0	(4:4aCO)
22	TN1	TN	5	67809	68268	67809	68268	2_nonsis		0	229	458	1	100	1	1	0	(4:4aCO)
23	TN1	TN	5	215491	216124	215491	216124	2_nonsis		0	316	632	1	100	1	1	0	(4:4aCO)
53	TN1	TN	11	204194	205481	204194	205481	2_nonsis		0	643	1286	1	100	1	1	0	(4:4aCO)
42	TN1	TN	8	141400	142863	141400	142863	2_nonsis		0	731	1462	1	100	1	1	0	(4:4aCO)
80	TN1	TN	14	216919	218712	216919	218712	2_nonsis		0	896	1792	1	100	1	1	0	(4:4aCO)
2	TN1	TN	1	187280	189706	187280	189706	2_nonsis		0	1213	2425	1	100	1	1	0	(4:4aCO)
10	TN1	TN	3	212063	214762	212063	214762	2_nonsis		0	1349	2698	1	100	1	1	0	(4:4aCO)
46	TN1	TN	9	289127	292353	289127	292353	2_nonsis		0	1613	3225	1	100	1	1	0	(4:4aCO)
12	TN1	TN	4	125172	125573	130967	131084		3	5395	5653	5911	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
1	TN1	TN	1	57739	59349	61451	61708		3	2103	3036	3968	0	3	2	1	1	(2:6)_(4:4)_(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
76	TN1	TN	13	778647	779631	783789	784138		3	4159	4825	5490	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
88	TN1	TN	15	180685	180906	184609	185107		3	3704	4063	4421	0	3	2	1	1	(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
112	TN2	TN	15	82066	82183	84553	85000		1	2371	2652	2933	1	7	1	0	1	6:2_4:4_6:2
10	TN2	TN	2	491476	492001	494596	494992		1	2596	3056	3515	1	7	1	0	1	6:2_4:4_6:2
39	TN2	TN	7	122622	123839	129484	130374		1	5646	6699	7751	1	7	1	0	1	6:2_4:4_6:2
5	TN2	TN	1	198604	198630	198630	198648		1	1	22	43	1	10	1	0	1	06:02
29	TN2	TN	5	216211	216261	216261	216469		1	1	129	257	1	10	1	0	1	06:02
110	TN2	TN	14	754799	754802	754802	755545		1	1	373	745	1	10	1	0	1	06:02
117	TN2	TN	15	919749	920281	920281	920643		1	1	447	893	1	10	1	0	1	06:02
45	TN2	TN	7	586087	586177	586177	586992		1	1	453	904	1	10	1	0	1	06:02
91	TN2	TN	13	434658	434927	434958	435813		1	32	593	1154	1	10	1	0	1	06:02
64	TN2	TN	10	317989	318240	318628	318819		1	389	609	829	1	10	1	0	1	06:02
121	TN2	TN	16	298955	299549	300071	300401		1	523	984	1445	1	10	1	0	1	06:02
53	TN2	TN	8	245056	245608	246309	246363		1	702	1004	1306	1	10	1	0	1	06:02
54	TN2	TN	8	351889	352905	353343	354035		1	439	1292	2145	1	10	1	0	1	06:02
59	TN2	TN	9	172074	172693	173732	174345		1	1040	1655	2270	1	10	1	0	1	06:02
88	TN2	TN	13	282738	283144	284491	284713		1	1348	1661	1974	1	10	1	0	1	06:02
106	TN2	TN	14	495918	496505	497369	498514		1	865	1730	2595	1	10	1	0	1	06:02
41	TN2	TN	7	268323	269104	270608	270688		1	1505	1935	2364	1	10	1	0	1	06:02
2	TN2	TN	1	104068	107245	107538	108457		1	294	2341	4388	1	10	1	0	1	06:02
44	TN2	TN	7	578137	578374	580425	581017		1	2052	2466	2879	1	10	1	0	1	06:02
87	TN2	TN	13	166349	167027	168885	169477		1	1859	2493	3127	1	10	1	0	1	06:02
42	TN2	TN	7	351287	351684	352964	355166		1	1281	2580	3878	1	10	1	0	1	06:02
31	TN2	TN	5	415894	416514	418874	419038		1	2361	2752	3143	1	10	1	0	1	06:02
71	TN2	TN	11	46439	48790	49756	51512		1	967	3020	5072	1	10	1	0	1	06:02
80	TN2	TN	12	414993	415537	418481	418904		1	2945	3428	3910	1	10	1	0	1	06:02
43	TN2	TN	7	430869	431116	432076	432412		1	961	1252	1542	1	10.1	1	0	1	02:06
111	TN2	TN	15	54339	55102	55845	56223		1	744	1314	1883	1	10.1	1	0	1	02:06
36	TN2	TN	6	161261	161767	162872	163447		1	1106	1646	2185	1	10.1	1	0	1	02:06
50	TN2	TN	8	69180	69741	70883	71625		1	1143	1794	2444	1	10.1	1	0	1	02:06
32	TN2	TN	5	466898	467203	468838	469111		1	1636	1924	2212	1	10.1	1	0	1	02:06
55	TN2	TN	8	388949	390446	391559	392078		1	1114	2121	3128	1	10.1	1	0	1	02:06
94	TN2	TN	13	737651	737933	739584	740463		1	1652	2232	2811	1	10.1	1	0	1	02:06
90	TN2	TN	13	385180	387028	388995	389031		1	1968	2909	3850	1	10.1	1	0	1	02:06
25	TN2	TN	4	1475397	1476168	1479784	1480271		1	3617	4245	4873	1	10.1	1	0	1	02:06
70	TN2	TN	11	19942	19981	22806	27301		1	2826	5092	7358	1	10.1	1	0	1	02:06
67	TN2	TN	10	618846	621779	624648	627140		1	2870	5582	8293	1	10.1	1	0	1	02:06

114	TN2	TN	15	511443	511466	511738	512726	2_nonsis	273	778	1282	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
79	TN2	TN	12	320997	322903	324050	325206	2_nonsis	1148	2678	4208	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
18	TN2	TN	4	262409	262808	264290	265338	2_nonsis	1483	2206	2928	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
52	TN2	TN	8	188873	189026	189310	189521	2_nonsis	285	466	647	1	15	1	1	0	(6:2)_(4:4aCO)
19	TN2	TN	4	740221	741463	741463	741683	2_nonsis	1	731	1461	1	15	1	1	0	(6:2)_(4:4aCO)
107	TN2	TN	14	542443	543829	543829	544303	2_nonsis	1	930	1859	1	15	1	1	0	(6:2)_(4:4aCO)
85	TN2	TN	12	1017718	1018933	1019284	1019357	2_nonsis	352	995	1638	1	15	1	1	0	(6:2)_(4:4aCO)
122	TN2	TN	16	478714	479396	480004	480360	2_nonsis	609	1127	1645	1	15	1	1	0	(6:2)_(4:4aCO)
74	TN2	TN	11	524346	524511	525645	526035	2_nonsis	1135	1412	1688	1	15	1	1	0	(6:2)_(4:4aCO)
23	TN2	TN	4	1385147	1385256	1386524	1386851	2_nonsis	1269	1486	1703	1	15	1	1	0	(6:2)_(4:4aCO)
62	TN2	TN	9	393280	395260	395260	396306	2_nonsis	1	1513	3025	1	15	1	1	0	(6:2)_(4:4aCO)
97	TN2	TN	13	840667	841022	842091	842866	2_nonsis	1070	1634	2198	1	15	1	1	0	(6:2)_(4:4aCO)
13	TN2	TN	2	798747	798886	801020	801218	2_nonsis	2135	2303	2470	1	15	1	1	0	(6:2)_(4:4aCO)
123	TN2	TN	16	636736	638483	640119	640589	2_nonsis	1637	2745	3852	1	15	1	1	0	(6:2)_(4:4aCO)
105	TN2	TN	14	427715	428693	430407	431640	2_nonsis	1715	2820	3924	1	15	1	1	0	(6:2)_(4:4aCO)
37	TN2	TN	6	203172	204006	206548	206614	2_nonsis	2543	2992	3441	1	15	1	1	0	(6:2)_(4:4aCO)
28	TN2	TN	5	210793	211386	213929	214752	2_nonsis	2544	3251	3958	1	15	1	1	0	(6:2)_(4:4aCO)
120	TN2	TN	16	155661	156518	160357	160565	2_nonsis	3840	4372	4903	1	15	1	1	0	(6:2)_(4:4aCO)
125	TN2	TN	16	896727	896834	902268	902643	2_nonsis	5435	5675	5915	1	15	1	1	0	(6:2)_(4:4aCO)
60	TN2	TN	9	274413	274516	280761	280877	2_nonsis	6246	6355	6463	1	15	1	1	0	(6:2)_(4:4aCO)
1	TN2	TN	1	61708	61999	68551	71312	2_nonsis	6553	8078	9603	1	15	1	1	0	(6:2)_(4:4aCO)
81	TN2	TN	12	460709	490608	490675	493339	2_nonsis	68	16349	32629	1	15	1	1	0	(6:2)_(4:4aCO)
73	TN2	TN	11	383538	383706	383706	383913	2_nonsis	1	188	374	1	16	1	1	0	(2:6)_(4:4aCO)
33	TN2	TN	5	523683	524394	524394	524497	2_nonsis	1	407	813	1	16	1	1	0	(2:6)_(4:4aCO)
72	TN2	TN	11	228576	229432	229432	229903	2_nonsis	1	664	1326	1	16	1	1	0	(2:6)_(4:4aCO)
22	TN2	TN	4	1079984	1080788	1080869	1081335	2_nonsis	82	716	1350	1	16	1	1	0	(2:6)_(4:4aCO)
96	TN2	TN	13	811756	812562	812787	813019	2_nonsis	226	744	1262	1	16	1	1	0	(2:6)_(4:4aCO)
61	TN2	TN	9	340858	341514	341515	342354	2_nonsis	2	749	1495	1	16	1	1	0	(2:6)_(4:4aCO)
78	TN2	TN	12	259210	260086	260323	260496	2_nonsis	238	762	1285	1	16	1	1	0	(2:6)_(4:4aCO)
46	TN2	TN	7	676875	677169	677412	678405	2_nonsis	244	887	1529	1	16	1	1	0	(2:6)_(4:4aCO)
27	TN2	TN	5	155958	156904	157328	157488	2_nonsis	425	977	1529	1	16	1	1	0	(2:6)_(4:4aCO)
11	TN2	TN	2	547559	548176	548443	549466	2_nonsis	268	1087	1906	1	16	1	1	0	(2:6)_(4:4aCO)
66	TN2	TN	10	467589	469453	469520	469702	2_nonsis	68	1090	2112	1	16	1	1	0	(2:6)_(4:4aCO)
57	TN2	TN	8	469169	469438	470287	470706	2_nonsis	850	1193	1536	1	16	1	1	0	(2:6)_(4:4aCO)
21	TN2	TN	4	1012978	1013721	1013983	1015229	2_nonsis	263	1257	2250	1	16	1	1	0	(2:6)_(4:4aCO)
12	TN2	TN	2	717754	717945	718805	719463	2_nonsis	861	1285	1708	1	16	1	1	0	(2:6)_(4:4aCO)
109	TN2	TN	14	749073	749402	750473	750670	2_nonsis	1072	1334	1596	1	16	1	1	0	(2:6)_(4:4aCO)
89	TN2	TN	13	301274	303266	303638	303755	2_nonsis	373	1427	2480	1	16	1	1	0	(2:6)_(4:4aCO)
77	TN2	TN	12	233075	234128	234824	235352	2_nonsis	697	1487	2276	1	16	1	1	0	(2:6)_(4:4aCO)
113	TN2	TN	15	294448	294529	295611	296401	2_nonsis	1083	1518	1952	1	16	1	1	0	(2:6)_(4:4aCO)
49	TN2	TN	7	997225	999392	999433	1000433	2_nonsis	42	1625	3207	1	16	1	1	0	(2:6)_(4:4aCO)
86	TN2	TN	13	84059	84178	85411	86109	2_nonsis	1234	1642	2049	1	16	1	1	0	(2:6)_(4:4aCO)
103	TN2	TN	14	270838	271707	272956	273091	2_nonsis	1250	1751	2252	1	16	1	1	0	(2:6)_(4:4aCO)
51	TN2	TN	8	122169	122633	123878	124457	2_nonsis	1246	1767	2287	1	16	1	1	0	(2:6)_(4:4aCO)
48	TN2	TN	7	914107	914517	916059	917004	2_nonsis	1543	2220	2896	1	16	1	1	0	(2:6)_(4:4aCO)
101	TN2	TN	14	78386	79032	80433	81575	2_nonsis	1402	2295	3188	1	16	1	1	0	(2:6)_(4:4aCO)
30	TN2	TN	5	241522	241980	243892	244317	2_nonsis	1913	2354	2794	1	16	1	1	0	(2:6)_(4:4aCO)
100	TN2	TN	14	32426	34717	34917	37063	2_nonsis	201	2419	4636	1	16	1	1	0	(2:6)_(4:4aCO)
69	TN2	TN	10	676590	677087	678760	679959	2_nonsis	1674	2521	3368	1	16	1	1	0	(2:6)_(4:4aCO)
8	TN2	TN	2	293630	293954	295912	296774	2_nonsis	1959	2551	3143	1	16	1	1	0	(2:6)_(4:4aCO)
102	TN2	TN	14	102722	102793	106004	106090	2_nonsis	3212	3290	3367	1	16	1	1	0	(2:6)_(4:4aCO)
124	TN2	TN	16	830004	830277	833382	833734	2_nonsis	3106	3418	3729	1	16	1	1	0	(2:6)_(4:4aCO)
17	TN2	TN	4	145805	146216	149689	149839	2_nonsis	3474	3754	4033	1	16	1	1	0	(2:6)_(4:4aCO)
93	TN2	TN	13	673402	673803	677418	677544	2_nonsis	3616	3879	4141	1	16	1	1	0	(2:6)_(4:4aCO)
84	TN2	TN	12	822539	826618	826618	830392	2_nonsis	1	3927	7852	1	16	1	1	0	(2:6)_(4:4aCO)
82	TN2	TN	12	609572	609824	613380	614456	2_nonsis	3557	4220	4883	1	16	1	1	0	(2:6)_(4:4aCO)
15	TN2	TN	3	208795	208954	215020	215336	2_nonsis	6067	6304	6540	1	16	1	1	0	(2:6)_(4:4aCO)
6	TN2	TN	2	23707	24209	36837	39607	2_nonsis	12629	14264	15899	1	16	1	1	0	(2:6)_(4:4aCO)
20	TN2	TN	4	928988	929454	928988	929454	2_nonsis	0	233	465	1	100	1	1	0	(4:4aCO)
63	TN2	TN	10	84062	84655	84062	84655	2_nonsis	0	296	592	1	100	1	1	0	(4:4aCO)

95	TN2	TN	13	795326	795946	795326	795946	2_nonsis		0	310	619	1	100	1	1	0	(4:4aCO)
119	TN2	TN	16	47566	48262	47566	48262	2_nonsis		0	348	695	1	100	1	1	0	(4:4aCO)
115	TN2	TN	15	617162	617892	617162	617892	2_nonsis		0	365	729	1	100	1	1	0	(4:4aCO)
56	TN2	TN	8	421693	422434	421693	422434	2_nonsis		0	370	740	1	100	1	1	0	(4:4aCO)
99	TN2	TN	13	861205	862065	861205	862065	2_nonsis		0	430	859	1	100	1	1	0	(4:4aCO)
116	TN2	TN	15	803637	804529	803637	804529	2_nonsis		0	446	891	1	100	1	1	0	(4:4aCO)
83	TN2	TN	12	810333	811301	810333	811301	2_nonsis		0	484	967	1	100	1	1	0	(4:4aCO)
58	TN2	TN	9	62207	63202	62207	63202	2_nonsis		0	497	994	1	100	1	1	0	(4:4aCO)
76	TN2	TN	12	124986	126014	124986	126014	2_nonsis		0	514	1027	1	100	1	1	0	(4:4aCO)
38	TN2	TN	7	118134	119177	118134	119177	2_nonsis		0	521	1042	1	100	1	1	0	(4:4aCO)
104	TN2	TN	14	333286	334339	333286	334339	2_nonsis		0	526	1052	1	100	1	1	0	(4:4aCO)
7	TN2	TN	2	255862	257565	255862	257565	2_nonsis		0	851	1702	1	100	1	1	0	(4:4aCO)
98	TN2	TN	13	858111	859920	858111	859920	2_nonsis		0	904	1808	1	100	1	1	0	(4:4aCO)
3	TN2	TN	1	108928	110856	108928	110856	2_nonsis		0	964	1927	1	100	1	1	0	(4:4aCO)
9	TN2	TN	2	404173	406111	404173	406111	2_nonsis		0	969	1937	1	100	1	1	0	(4:4aCO)
40	TN2	TN	7	232997	235967	232997	235967	2_nonsis		0	1485	2969	1	100	1	1	0	(4:4aCO)
14	TN2	TN	3	171207	174943	171207	174943	2_nonsis		0	1868	3735	1	100	1	1	0	(4:4aCO)
108	TN2	TN	14	682580	686654	682580	686654	2_nonsis		0	2037	4073	1	100	1	1	0	(4:4aCO)
34	TN2	TN	6	53398	58238	53398	58238	2_nonsis		0	2420	4839	1	100	1	1	0	(4:4aCO)
68	TN2	TN	10	635321	640236	635321	640236	2_nonsis		0	2457	4914	1	100	1	1	0	(4:4aCO)
24	TN2	TN	4	1407535	1412849	1407535	1412849	2_nonsis		0	2657	5313	1	100	1	1	0	(4:4aCO)
75	TN2	TN	11	594987	595260	597889	598496	2_sis		2630	3069	3508	0	1	2	0	2	(6:2)_(8:0)_(6:2)_(4:4)
4	TN2	TN	1	187062	189746	191617	193131		3	1872	3970	6068	0	2	2	1	1	(2:6)_(4:4aCO)
16	TN2	TN	4	60151	60639	62829	62973		4	2191	2506	2821	0	2	2	2	0	(2:6)_(4:4aCO)
26	TN2	TN	5	24670	24749	27272	27604		3	2524	2729	2933	0	2	2	1	1	(6:2)_(4:4)_(4:4aCO)
35	TN2	TN	6	93404	93664	96991	97235		3	3328	3579	3830	0	2	2	1	1	(6:2)_(6:2a)_(4:4aCO)
47	TN2	TN	7	796858	798046	798848	800148		3	803	2046	3289	0	2	2	1	1	(2:6)_(4:4aCO)
65	TN2	TN	10	407535	411303	413049	414104		3	1747	4158	6568	0	2	2	1	1	(6:2)_(4:4aCO)
92	TN2	TN	13	591615	592775	595371	595605		3	2597	3293	3989	0	3	2	1	1	(4:4aCO)_(2:6)_(4:4bCO)
118	TN2	TN	15	1002614	1003809	1008443	1009862	2_nonsis		4635	5941	7247	0	3	1	1	0	(2:6)_(4:4aCO)_(4:4CO)_(2:6)_(4:4aCO)
6	TN3	TN	1	198618	198621	198621	198648		1	1	15	29	1	10	1	0	1	06:02
163	TN3	TN	16	126620	126726	126726	126838		1	1	109	217	1	10	1	0	1	06:02
91	TN3	TN	10	461089	461507	461507	461623		1	1	267	533	1	10	1	0	1	06:02
129	TN3	TN	13	168885	169464	169464	169477		1	1	296	591	1	10	1	0	1	06:02
76	TN3	TN	9	26499	26507	26801	26833		1	295	314	333	1	10	1	0	1	06:02
4	TN3	TN	1	181197	181334	181491	181752		1	158	356	554	1	10	1	0	1	06:02
44	TN3	TN	5	456429	456505	456801	456960		1	297	414	530	1	10	1	0	1	06:02
173	TN3	TN	16	887552	888159	888239	888536		1	81	532	983	1	10	1	0	1	06:02
35	TN3	TN	4	1497628	1497856	1498087	1498561		1	232	582	932	1	10	1	0	1	06:02
160	TN3	TN	16	39420	39693	39840	40527		1	148	627	1106	1	10	1	0	1	06:02
102	TN3	TN	11	224634	225480	225609	225834		1	130	665	1199	1	10	1	0	1	06:02
156	TN3	TN	15	825345	826024	826212	826624		1	189	734	1278	1	10	1	0	1	06:02
30	TN3	TN	4	1273954	1274074	1274743	1274867		1	670	791	912	1	10	1	0	1	06:02
139	TN3	TN	14	39652	40306	40430	41146		1	125	809	1493	1	10	1	0	1	06:02
13	TN3	TN	2	484159	485003	485567	485863		1	565	1134	1703	1	10	1	0	1	06:02
61	TN3	TN	7	785907	786618	787089	787750		1	472	1157	1842	1	10	1	0	1	06:02
47	TN3	TN	5	533244	534911	535145	535342		1	235	1166	2097	1	10	1	0	1	06:02
85	TN3	TN	10	35185	35365	36583	36722		1	1219	1378	1536	1	10	1	0	1	06:02
99	TN3	TN	11	118109	118487	119339	120268		1	853	1506	2158	1	10	1	0	1	06:02
79	TN3	TN	9	183089	183795	184053	185865		1	259	1517	2775	1	10	1	0	1	06:02
3	TN3	TN	1	155505	158814	158870	159623		1	57	2087	4117	1	10	1	0	1	06:02
94	TN3	TN	10	623220	624389	624648	627140		1	260	2090	3919	1	10	1	0	1	06:02
101	TN3	TN	11	125651	127396	127396	129862		1	1	2106	4210	1	10	1	0	1	06:02
121	TN3	TN	12	572294	572662	574950	575257		1	2289	2626	2962	1	10	1	0	1	06:02
107	TN3	TN	11	627471	628158	632117	632654		1	3960	4571	5182	1	10	1	0	1	06:02
134	TN3	TN	13	755812	757200	761318	761436		1	4119	4871	5623	1	10	1	0	1	06:02
14	TN3	TN	2	491216	491476	496540	497133		1	5065	5491	5916	1	10	1	0	1	06:02
43	TN3	TN	5	443341	450195	453437	454403		1	3243	7152	11061	1	10	1	0	1	06:02
90	TN3	TN	10	315888	316551	323333	323823		1	6783	7359	7934	1	10	1	0	1	06:02
147	TN3	TN	15	100319	100603	107690	108214		1	7088	7491	7894	1	10	1	0	1	06:02

25	TN3	TN	4	402050	402371	408894	410728	1	6524	7601	8677	1	10	1	0	1 06:02
105	TN3	TN	11	534319	535346	546863	546903	1	11518	12051	12583	1	10	1	0	1 06:02
52	TN3	TN	7	23297	23450	23602	23642	1	153	249	344	1	10.1	1	0	1 02:06
164	TN3	TN	16	131951	132681	132855	132909	1	175	566	957	1	10.1	1	0	1 02:06
72	TN3	TN	8	120247	120364	120445	121477	1	82	656	1229	1	10.1	1	0	1 02:06
40	TN3	TN	5	228115	228711	229119	229265	1	409	779	1149	1	10.1	1	0	1 02:06
143	TN3	TN	14	530856	531399	531656	532165	1	258	783	1308	1	10.1	1	0	1 02:06
111	TN3	TN	12	38338	38565	38737	39963	1	173	899	1624	1	10.1	1	0	1 02:06
11	TN3	TN	2	332654	332940	333434	334196	1	495	1018	1541	1	10.1	1	0	1 02:06
65	TN3	TN	8	9169	9385	10670	10789	1	1286	1453	1619	1	10.1	1	0	1 02:06
55	TN3	TN	7	268323	269104	270374	270491	1	1271	1719	2167	1	10.1	1	0	1 02:06
104	TN3	TN	11	400972	401736	403011	403407	1	1276	1855	2434	1	10.1	1	0	1 02:06
106	TN3	TN	11	567076	567430	569085	569468	1	1656	2024	2391	1	10.1	1	0	1 02:06
71	TN3	TN	8	98484	98622	99909	101246	1	1288	2025	2761	1	10.1	1	0	1 02:06
83	TN3	TN	9	329125	333581	333581	334329	1	1	2602	5203	1	10.1	1	0	1 02:06
166	TN3	TN	16	193788	194710	196727	197567	1	2018	2898	3778	1	10.1	1	0	1 02:06
174	TN3	TN	16	917515	918199	920877	921047	1	2679	3105	3531	1	10.1	1	0	1 02:06
159	TN3	TN	15	1053414	1053882	1057536	1057626	1	3655	3933	4211	1	10.1	1	0	1 02:06
126	TN3	TN	12	956371	956584	960131	961196	1	3548	4186	4824	1	10.1	1	0	1 02:06
171	TN3	TN	16	844218	857345	857345	858788	1	1	7285	14569	1	10.1	1	0	1 02:06
45	TN3	TN	5	465974	466823	473281	474191	1	6459	7338	8216	1	10.1	1	0	1 02:06
115	TN3	TN	12	242737	243937	252072	252507	1	8136	8953	9769	1	10.1	1	0	1 02:06
167	TN3	TN	16	294083	294452	303354	304351	1	8903	9585	10267	1	10.1	1	0	1 02:06
119	TN3	TN	12	460709	490608	490675	493339	1	68	16349	32629	1	10.1	1	0	1 02:06
123	TN3	TN	12	867405	870134	872807	873021	2_nonsis	2674	4145	5615	3	30	1	0	1 2:6_6:2
161	TN3	TN	16	54119	54725	55474	55562	2_nonsis	750	1096	1442	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
95	TN3	TN	10	627141	627999	628891	629879	2_nonsis	893	1815	2737	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
29	TN3	TN	4	1078009	1078458	1080788	1080869	2_nonsis	2331	2595	2859	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
142	TN3	TN	14	425890	427278	428883	430018	2_nonsis	1606	2867	4127	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
151	TN3	TN	15	511738	512726	516270	517169	2_nonsis	3545	4488	5430	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
38	TN3	TN	5	61280	61456	63253	63373	2_nonsis	1798	1945	2092	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
28	TN3	TN	4	730704	731588	733663	734357	2_nonsis	2076	2864	3652	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
128	TN3	TN	13	163519	164021	167027	167444	2_nonsis	3007	3466	3924	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
169	TN3	TN	16	674314	674569	678816	679094	2_nonsis	4248	4514	4779	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
120	TN3	TN	12	516236	516783	520933	521221	2_nonsis	4151	4568	4984	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
63	TN3	TN	7	908884	909136	919947	920105	2_nonsis	10812	11016	11220	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
109	TN3	TN	12	23199	23393	23393	23475	2_nonsis	1	138	275	1	15	1	1	0 (6:2)_(4:4aCO)
89	TN3	TN	10	285555	285967	286028	286125	2_nonsis	62	316	569	1	15	1	1	0 (6:2)_(4:4aCO)
54	TN3	TN	7	164025	164428	164429	164774	2_nonsis	2	375	748	1	15	1	1	0 (6:2)_(4:4aCO)
118	TN3	TN	12	386700	387140	387156	387519	2_nonsis	17	418	818	1	15	1	1	0 (6:2)_(4:4aCO)
58	TN3	TN	7	446910	447534	447534	447761	2_nonsis	1	426	850	1	15	1	1	0 (6:2)_(4:4aCO)
67	TN3	TN	8	38662	38887	39238	39521	2_nonsis	352	605	858	1	15	1	1	0 (6:2)_(4:4aCO)
136	TN3	TN	13	810415	810832	810963	811653	2_nonsis	132	685	1237	1	15	1	1	0 (6:2)_(4:4aCO)
66	TN3	TN	8	25945	26177	27080	27293	2_nonsis	904	1126	1347	1	15	1	1	0 (6:2)_(4:4aCO)
155	TN3	TN	15	820906	821660	822183	823421	2_nonsis	524	1519	2514	1	15	1	1	0 (6:2)_(4:4aCO)
74	TN3	TN	8	393074	393364	394728	394959	2_nonsis	1365	1625	1884	1	15	1	1	0 (6:2)_(4:4aCO)
154	TN3	TN	15	772232	773455	774457	774673	2_nonsis	1003	1722	2440	1	15	1	1	0 (6:2)_(4:4aCO)
117	TN3	TN	12	326213	326929	328075	328990	2_nonsis	1147	1962	2776	1	15	1	1	0 (6:2)_(4:4aCO)
150	TN3	TN	15	446025	446514	448080	448955	2_nonsis	1567	2248	2929	1	15	1	1	0 (6:2)_(4:4aCO)
8	TN3	TN	2	67361	68817	68834	72096	2_nonsis	18	2376	4734	1	15	1	1	0 (6:2)_(4:4aCO)
110	TN3	TN	12	25985	28820	29781	30008	2_nonsis	962	2492	4022	1	15	1	1	0 (6:2)_(4:4aCO)
19	TN3	TN	3	63929	64304	65580	68233	2_nonsis	1277	2790	4303	1	15	1	1	0 (6:2)_(4:4aCO)
168	TN3	TN	16	430826	431177	433373	434269	2_nonsis	2197	2820	3442	1	15	1	1	0 (6:2)_(4:4aCO)
68	TN3	TN	8	46274	46457	49378	49451	2_nonsis	2922	3049	3176	1	15	1	1	0 (6:2)_(4:4aCO)
92	TN3	TN	10	463257	463428	465795	467010	2_nonsis	2368	3060	3752	1	15	1	1	0 (6:2)_(4:4aCO)
56	TN3	TN	7	343251	343639	346294	346793	2_nonsis	2656	3099	3541	1	15	1	1	0 (6:2)_(4:4aCO)
127	TN3	TN	13	49898	50109	53276	53532	2_nonsis	3168	3401	3633	1	15	1	1	0 (6:2)_(4:4aCO)
152	TN3	TN	15	589839	590260	593587	594122	2_nonsis	3328	3805	4282	1	15	1	1	0 (6:2)_(4:4aCO)
96	TN3	TN	10	631130	635210	635321	640236	2_nonsis	112	4609	9105	1	15	1	1	0 (6:2)_(4:4aCO)
2	TN3	TN	1	121235	128637	129517	130254	2_nonsis	881	4950	9018	1	15	1	1	0 (6:2)_(4:4aCO)

86	TN3	TN	10	61449	61680	66738	67153	2_nonsis	5059	5381	5703	1	15	1	1	0	(6:2)_(4:4aCO)
133	TN3	TN	13	671402	672472	677544	678210	2_nonsis	5073	5940	6807	1	15	1	1	0	(6:2)_(4:4aCO)
75	TN3	TN	8	398452	398985	404521	404866	2_nonsis	5537	5975	6413	1	15	1	1	0	(6:2)_(4:4aCO)
153	TN3	TN	15	652513	654602	659154	660208	2_nonsis	4553	6124	7694	1	15	1	1	0	(6:2)_(4:4aCO)
48	TN3	TN	5	538885	539082	546617	546721	2_nonsis	7536	7686	7835	1	15	1	1	0	(6:2)_(4:4aCO)
57	TN3	TN	7	388315	388627	398572	399494	2_nonsis	9946	10562	11178	1	15	1	1	0	(6:2)_(4:4aCO)
158	TN3	TN	15	1047512	1047566	1047626	1047731	2_nonsis	61	140	218	1	16	1	1	0	(2:6)_(4:4aCO)
135	TN3	TN	13	765900	766029	766042	766186	2_nonsis	14	150	285	1	16	1	1	0	(2:6)_(4:4aCO)
114	TN3	TN	12	164945	165084	165084	165412	2_nonsis	1	234	466	1	16	1	1	0	(2:6)_(4:4aCO)
93	TN3	TN	10	470777	471195	471195	471532	2_nonsis	1	378	754	1	16	1	1	0	(2:6)_(4:4aCO)
130	TN3	TN	13	216954	217030	217312	217508	2_nonsis	283	418	553	1	16	1	1	0	(2:6)_(4:4aCO)
172	TN3	TN	16	885683	885979	885979	886611	2_nonsis	1	464	927	1	16	1	1	0	(2:6)_(4:4aCO)
146	TN3	TN	15	71043	71268	71365	72322	2_nonsis	98	688	1278	1	16	1	1	0	(2:6)_(4:4aCO)
88	TN3	TN	10	189655	190275	190298	191249	2_nonsis	24	809	1593	1	16	1	1	0	(2:6)_(4:4aCO)
23	TN3	TN	4	199393	200025	200220	200994	2_nonsis	196	898	1600	1	16	1	1	0	(2:6)_(4:4aCO)
53	TN3	TN	7	55957	57501	57855	58033	2_nonsis	355	1215	2075	1	16	1	1	0	(2:6)_(4:4aCO)
60	TN3	TN	7	609044	609405	610218	610674	2_nonsis	814	1222	1629	1	16	1	1	0	(2:6)_(4:4aCO)
112	TN3	TN	12	72514	72811	73852	74146	2_nonsis	1042	1337	1631	1	16	1	1	0	(2:6)_(4:4aCO)
64	TN3	TN	7	1011203	1012213	1012425	1013720	2_nonsis	213	1365	2516	1	16	1	1	0	(2:6)_(4:4aCO)
21	TN3	TN	3	239515	240922	240922	242663	2_nonsis	1	1574	3147	1	16	1	1	0	(2:6)_(4:4aCO)
78	TN3	TN	9	84138	85680	86442	86586	2_nonsis	763	1605	2447	1	16	1	1	0	(2:6)_(4:4aCO)
81	TN3	TN	9	267764	268176	269580	269763	2_nonsis	1405	1702	1998	1	16	1	1	0	(2:6)_(4:4aCO)
36	TN3	TN	5	25332	25874	27272	27604	2_nonsis	1399	1835	2271	1	16	1	1	0	(2:6)_(4:4aCO)
73	TN3	TN	8	126792	128125	129265	129586	2_nonsis	1141	1967	2793	1	16	1	1	0	(2:6)_(4:4aCO)
27	TN3	TN	4	599029	599103	600978	601683	2_nonsis	1876	2265	2653	1	16	1	1	0	(2:6)_(4:4aCO)
34	TN3	TN	4	1478319	1478581	1480517	1480913	2_nonsis	1937	2265	2593	1	16	1	1	0	(2:6)_(4:4aCO)
42	TN3	TN	5	393630	393855	396138	396428	2_nonsis	2284	2541	2797	1	16	1	1	0	(2:6)_(4:4aCO)
59	TN3	TN	7	592271	592334	594933	595174	2_nonsis	2600	2751	2902	1	16	1	1	0	(2:6)_(4:4aCO)
140	TN3	TN	14	58317	58553	61007	61469	2_nonsis	2455	2803	3151	1	16	1	1	0	(2:6)_(4:4aCO)
165	TN3	TN	16	149586	150219	152472	152993	2_nonsis	2254	2830	3406	1	16	1	1	0	(2:6)_(4:4aCO)
15	TN3	TN	2	661374	662094	662444	666708	2_nonsis	351	2842	5333	1	16	1	1	0	(2:6)_(4:4aCO)
97	TN3	TN	10	658912	660402	663134	663261	2_nonsis	2733	3541	4348	1	16	1	1	0	(2:6)_(4:4aCO)
113	TN3	TN	12	111878	111976	115422	116205	2_nonsis	3447	3887	4326	1	16	1	1	0	(2:6)_(4:4aCO)
33	TN3	TN	4	1463190	1463798	1467260	1467803	2_nonsis	3463	4038	4612	1	16	1	1	0	(2:6)_(4:4aCO)
145	TN3	TN	14	752591	753318	756919	757068	2_nonsis	3602	4039	4476	1	16	1	1	0	(2:6)_(4:4aCO)
10	TN3	TN	2	215181	215962	219381	220055	2_nonsis	3420	4147	4873	1	16	1	1	0	(2:6)_(4:4aCO)
131	TN3	TN	13	282738	283144	287574	287682	2_nonsis	4431	4687	4943	1	16	1	1	0	(2:6)_(4:4aCO)
37	TN3	TN	5	43260	43494	48594	49908	2_nonsis	5101	5874	6647	1	16	1	1	0	(2:6)_(4:4aCO)
32	TN3	TN	4	1420608	1420794	1427252	1427658	2_nonsis	6459	6754	7049	1	16	1	1	0	(2:6)_(4:4aCO)
17	TN3	TN	2	780187	781183	794651	794800	2_nonsis	13469	14041	14612	1	16	1	1	0	(2:6)_(4:4aCO)
137	TN3	TN	13	837907	838133	837907	838133	2_nonsis	0	113	225	1	100	1	1	0	(4:4aCO)
9	TN3	TN	2	107438	107671	107438	107671	2_nonsis	0	116	232	1	100	1	1	0	(4:4aCO)
132	TN3	TN	13	494333	494582	494333	494582	2_nonsis	0	124	248	1	100	1	1	0	(4:4aCO)
22	TN3	TN	4	24937	25195	24937	25195	2_nonsis	0	129	257	1	100	1	1	0	(4:4aCO)
103	TN3	TN	11	398547	398874	398547	398874	2_nonsis	0	163	326	1	100	1	1	0	(4:4aCO)
7	TN3	TN	2	47244	47612	47244	47612	2_nonsis	0	184	367	1	100	1	1	0	(4:4aCO)
41	TN3	TN	5	232874	233255	232874	233255	2_nonsis	0	190	380	1	100	1	1	0	(4:4aCO)
108	TN3	TN	12	20228	20609	20228	20609	2_nonsis	0	190	380	1	100	1	1	0	(4:4aCO)
87	TN3	TN	10	76754	77140	76754	77140	2_nonsis	0	193	385	1	100	1	1	0	(4:4aCO)
46	TN3	TN	5	526712	527126	526712	527126	2_nonsis	0	207	413	1	100	1	1	0	(4:4aCO)
51	TN3	TN	6	237488	237962	237488	237962	2_nonsis	0	237	473	1	100	1	1	0	(4:4aCO)
98	TN3	TN	11	48808	49402	48808	49402	2_nonsis	0	297	593	1	100	1	1	0	(4:4aCO)
26	TN3	TN	4	502277	502877	502277	502877	2_nonsis	0	300	599	1	100	1	1	0	(4:4aCO)
141	TN3	TN	14	205208	205814	205208	205814	2_nonsis	0	303	605	1	100	1	1	0	(4:4aCO)
69	TN3	TN	8	54591	55333	54591	55333	2_nonsis	0	371	741	1	100	1	1	0	(4:4aCO)
148	TN3	TN	15	112140	112969	112140	112969	2_nonsis	0	414	828	1	100	1	1	0	(4:4aCO)
124	TN3	TN	12	875259	876120	875259	876120	2_nonsis	0	430	860	1	100	1	1	0	(4:4aCO)
62	TN3	TN	7	789735	790683	789735	790683	2_nonsis	0	474	947	1	100	1	1	0	(4:4aCO)
18	TN3	TN	3	43877	45058	43877	45058	2_nonsis	0	590	1180	1	100	1	1	0	(4:4aCO)
100	TN3	TN	11	121247	122945	121247	122945	2_nonsis	0	849	1697	1	100	1	1	0	(4:4aCO)

12	TN3	TN	2	385751	387602	385751	387602	2_nonsis		0	925	1850	1	100	1	1	0 (4:4aCO)
162	TN3	TN	16	64540	66393	64540	66393	2_nonsis		0	926	1852	1	100	1	1	0 (4:4aCO)
144	TN3	TN	14	686681	688572	686681	688572	2_nonsis		0	945	1890	1	100	1	1	0 (4:4aCO)
138	TN3	TN	14	32426	34396	32426	34396	2_nonsis		0	985	1969	1	100	1	1	0 (4:4aCO)
80	TN3	TN	9	185865	188629	185865	188629	2_nonsis		0	1382	2763	1	100	1	1	0 (4:4aCO)
82	TN3	TN	9	299287	302738	299287	302738	2_nonsis		0	1725	3450	1	100	1	1	0 (4:4aCO)
16	TN3	TN	2	695479	699461	695479	699461	2_nonsis		0	1991	3981	1	100	1	1	0 (4:4aCO)
122	TN3	TN	12	849651	854846	849651	854846	2_nonsis		0	2597	5194	1	100	1	1	0 (4:4aCO)
125	TN3	TN	12	892436	930472	892436	930472	2_nonsis		0	19018	38035	1	100	1	1	0 (4:4aCO)
170	TN3	TN	16	783719	783796	784888	785197	2_nonsis		1093	1285	1477	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
31	TN3	TN	4	1407535	1412849	1418139	1418662	2_nonsis		5291	8209	11126	3	20	1	1	0 (6:2)_(2:6)_(4:4aCO)
24	TN3	TN	4	234944	235604	245765	246213	2_nonsis		10162	10715	11268	3	20	1	1	0 (2:6)_(4:4)_(6:2)_(4:4aCO)
70	TN3	TN	8	58733	59498	62455	62601	2_sis		2958	3413	3867	0	1	2	0	2 (6:2)_(4:4)_(6:2a)_(4:4)
1	TN3	TN	1	66696	67476	77554	77737		4	10079	10560	11040	0	2	2	1	1 (6:2)_(8:0)_(6:2a)_(8:0)_(6:2a)_(4:4aCO)
5	TN3	TN	1	187280	189706	191617	193131		3	1912	3881	5850	0	2	2	1	1 (8:0)_(6:2)_(4:4aCO)
49	TN3	TN	6	63394	64252	96814	96853		3	32563	33011	33458	0	2	2	1	1 (0:8)_(2:6)_(4:4)_(2:6a)_(4:4)_(6:2)_(4:4aCO)
116	TN3	TN	12	320997	322903	324050	325206		3	1148	2678	4208	0	2	2	1	1 (6:2)_(8:0)_(6:2a)_(4:4aCO)
149	TN3	TN	15	211687	213206	215550	215808		3	2345	3233	4120	0	2	2	1	1 (6:2)_(4:4aCO)
157	TN3	TN	15	941405	942129	954766	955006		4	12638	13119	13600	0	2	2	1	1 (6:2)_(6:2a)_(4:4aCO)
39	TN3	TN	5	106822	106918	112437	113066		4	5520	5882	6243	0	3	2	2	0 (2:6)_(4:4aCO)_(6:2)_(4:4bCO)
50	TN3	TN	6	190264	190849	194606	195375		4	3758	4434	5110	0	3	2	2	0 (4:4aCO)_(8:0)_(4:4a)_(6:2)_(4:4bCO)
77	TN3	TN	9	39559	40140	40593	40898	2_nonsis		454	896	1338	0	3	1	2	-1 (2:6)_(4:4aCO)_(4:4CO)
84	TN3	TN	9	404802	405428	405945	405973	2_nonsis		518	844	1170	0	3	1	2	-1 (4:4aCO)_(6:2)_(4:4CO)
301	TN3	TN	12	1057759	1058607	1059378	1078177		1	0	10209	20417	1	NA	NA		
16	TN4	TN	3	63052	63257	63929	64304		1	673	962	1251	1	7	1	0	1 6:2_4:4_6:2
98	TN4	TN	11	517983	518221	519160	519513		1	940	1235	1529	1	8	1	0	1 2:6_4:4_2:6
55	TN4	TN	6	262295	262470	266918	266983		1	4449	4568	4687	1	8	1	0	1 2:6_4:4_2:6
18	TN4	TN	3	101152	101285	101285	101527		1	1	188	374	1	10	1	0	1 06:02
138	TN4	TN	14	739169	739459	739477	739640		1	19	245	470	1	10	1	0	1 06:02
114	TN4	TN	12	1019768	1020076	1020245	1020463		1	170	432	694	1	10	1	0	1 06:02
54	TN4	TN	6	232697	233456	233456	233643		1	1	473	945	1	10	1	0	1 06:02
61	TN4	TN	7	385570	386428	386428	387199		1	1	815	1628	1	10	1	0	1 06:02
141	TN4	TN	15	109106	109424	109584	110892		1	161	973	1785	1	10	1	0	1 06:02
130	TN4	TN	13	900142	901050	901535	901903		1	486	1123	1760	1	10	1	0	1 06:02
30	TN4	TN	4	771211	772626	772698	773522		1	73	1192	2310	1	10	1	0	1 06:02
84	TN4	TN	10	219354	220326	220637	221804		1	312	1381	2449	1	10	1	0	1 06:02
142	TN4	TN	15	132713	134063	134063	135587		1	1	1437	2873	1	10	1	0	1 06:02
1	TN4	TN	1	60915	61084	62361	62648		1	1278	1505	1732	1	10	1	0	1 06:02
6	TN4	TN	2	125843	126130	126921	128153		1	792	1551	2309	1	10	1	0	1 06:02
117	TN4	TN	13	69113	70163	71382	71390		1	1220	1748	2276	1	10	1	0	1 06:02
10	TN4	TN	2	335092	337090	337786	338226		1	697	1915	3133	1	10	1	0	1 06:02
35	TN4	TN	4	1079984	1080788	1082232	1082379		1	1445	1920	2394	1	10	1	0	1 06:02
136	TN4	TN	14	643444	643651	644271	646799		1	621	1988	3354	1	10	1	0	1 06:02
37	TN4	TN	4	1277377	1278056	1279875	1280061		1	1820	2252	2683	1	10	1	0	1 06:02
139	TN4	TN	14	762860	763294	765537	765758		1	2244	2571	2897	1	10	1	0	1 06:02
49	TN4	TN	5	438396	438684	440923	441329		1	2240	2586	2932	1	10	1	0	1 06:02
143	TN4	TN	15	136228	136572	138847	139359		1	2276	2703	3130	1	10	1	0	1 06:02
60	TN4	TN	7	270046	270374	272568	273422		1	2195	2785	3375	1	10	1	0	1 06:02
44	TN4	TN	5	67085	67131	69789	70022		1	2659	2798	2936	1	10	1	0	1 06:02
67	TN4	TN	7	913393	913982	916059	916953		1	2078	2819	3559	1	10	1	0	1 06:02
111	TN4	TN	12	835791	836156	837962	840577		1	1807	3296	4785	1	10	1	0	1 06:02
104	TN4	TN	12	277961	278475	281289	281896		1	2815	3375	3934	1	10	1	0	1 06:02
2	TN4	TN	1	111180	112136	116905	117399		1	4770	5494	6218	1	10	1	0	1 06:02
78	TN4	TN	8	496308	496975	503996	505427		1	7022	8070	9118	1	10	1	0	1 06:02
58	TN4	TN	7	196910	196914	196914	196917		1	1	4	6	1	10.1	1	0	1 02:06
46	TN4	TN	5	131490	131495	131495	131499		1	1	5	8	1	10.1	1	0	1 02:06
125	TN4	TN	13	574226	574746	574746	575064		1	1	419	837	1	10.1	1	0	1 02:06
38	TN4	TN	4	1420281	1420528	1420794	1420932		1	267	459	650	1	10.1	1	0	1 02:06
83	TN4	TN	10	84062	84655	84848	85363		1	194	747	1300	1	10.1	1	0	1 02:06
113	TN4	TN	12	1011952	1012226	1012226	1013592		1	1	820	1639	1	10.1	1	0	1 02:06

56	TN4	TN	7	17649	18259	18693	18901	1	435	843	1251	1	10.1	1	0	1	02:06
69	TN4	TN	7	985834	987319	987319	987893	1	1	1030	2058	1	10.1	1	0	1	02:06
13	TN4	TN	2	678799	679276	680044	680219	1	769	1094	1419	1	10.1	1	0	1	02:06
103	TN4	TN	12	211226	212081	212873	213037	1	793	1302	1810	1	10.1	1	0	1	02:06
82	TN4	TN	10	26202	26529	26958	28612	1	430	1420	2409	1	10.1	1	0	1	02:06
23	TN4	TN	3	262154	262264	263025	264441	1	762	1524	2286	1	10.1	1	0	1	02:06
63	TN4	TN	7	396713	397929	398572	399494	1	644	1712	2780	1	10.1	1	0	1	02:06
122	TN4	TN	13	352513	352695	354466	354798	1	1772	2028	2284	1	10.1	1	0	1	02:06
107	TN4	TN	12	490675	493339	493890	494326	1	552	2101	3650	1	10.1	1	0	1	02:06
120	TN4	TN	13	229786	230470	232186	232627	1	1717	2279	2840	1	10.1	1	0	1	02:06
21	TN4	TN	3	224791	228130	228130	230267	1	1	2738	5475	1	10.1	1	0	1	02:06
159	TN4	TN	16	161519	161768	164063	164740	1	2296	2758	3220	1	10.1	1	0	1	02:06
157	TN4	TN	16	117204	117756	119752	120748	1	1997	2770	3543	1	10.1	1	0	1	02:06
166	TN4	TN	16	643795	644568	646670	647322	1	2103	2815	3526	1	10.1	1	0	1	02:06
123	TN4	TN	13	356463	356625	356625	362992	1	1	3265	6528	1	10.1	1	0	1	02:06
148	TN4	TN	15	491483	492036	495462	495679	1	3427	3811	4195	1	10.1	1	0	1	02:06
95	TN4	TN	11	68184	68250	72330	72431	1	4081	4164	4246	1	10.1	1	0	1	02:06
53	TN4	TN	6	156790	156928	161527	161720	1	4600	4765	4929	1	10.1	1	0	1	02:06
89	TN4	TN	10	523373	523974	527538	529735	1	3565	4963	6361	1	10.1	1	0	1	02:06
128	TN4	TN	13	675970	676095	689746	690170	1	13652	13926	14199	1	10.1	1	0	1	02:06
129	TN4	TN	13	858111	859063	861205	862065	2_nonsis	2143	3048	3953	3	30	1	0	1	2:6_6:2
86	TN4	TN	10	263244	263508	270752	272069	2_nonsis	7245	8035	8824	3	30	1	0	1	2:6_6:2
80	TN4	TN	9	141514	141703	156029	156304	2_nonsis	14327	14558	14789	3	30	1	0	1	2:6_6:2
133	TN4	TN	14	195358	195766	196345	196819	2_nonsis	580	1020	1460	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
135	TN4	TN	14	397680	397986	398966	399462	2_nonsis	981	1381	1781	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
64	TN4	TN	7	437349	438009	440241	440359	2_nonsis	2233	2621	3009	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
33	TN4	TN	4	1019664	1020939	1022238	1023685	2_nonsis	1300	2660	4020	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
25	TN4	TN	4	84947	85442	88345	88760	2_nonsis	2904	3358	3812	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
47	TN4	TN	5	330953	332219	344307	345204	2_nonsis	12089	13170	14250	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
140	TN4	TN	15	40057	40697	41957	42031	2_nonsis	1261	1617	1973	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
24	TN4	TN	3	274124	274173	275765	275817	2_nonsis	1593	1643	1692	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
137	TN4	TN	14	697058	697554	699152	700166	2_nonsis	1599	2353	3107	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
168	TN4	TN	16	830277	831160	834185	834395	2_nonsis	3026	3572	4117	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
27	TN4	TN	4	353682	354016	358348	358389	2_nonsis	4333	4520	4706	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
87	TN4	TN	10	392871	393423	397607	398093	2_nonsis	4185	4703	5221	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
92	TN4	TN	10	708349	708426	713263	713502	2_nonsis	4838	4995	5152	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
57	TN4	TN	7	162215	164025	168582	169165	2_nonsis	4558	5754	6949	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
100	TN4	TN	12	28820	29085	38338	38565	2_nonsis	9254	9499	9744	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
52	TN4	TN	6	18862	18920	18920	19068	2_nonsis	1	103	205	1	15	1	1	0	(6:2)_(4:4aCO)
28	TN4	TN	4	480096	480135	480231	480345	2_nonsis	97	173	248	1	15	1	1	0	(6:2)_(4:4aCO)
154	TN4	TN	15	977155	977302	977302	977533	2_nonsis	1	189	377	1	15	1	1	0	(6:2)_(4:4aCO)
150	TN4	TN	15	717433	717973	717973	718015	2_nonsis	1	291	581	1	15	1	1	0	(6:2)_(4:4aCO)
5	TN4	TN	2	58787	59164	59199	59500	2_nonsis	36	374	712	1	15	1	1	0	(6:2)_(4:4aCO)
134	TN4	TN	14	264607	265328	265328	265388	2_nonsis	1	391	780	1	15	1	1	0	(6:2)_(4:4aCO)
50	TN4	TN	5	461594	461877	461877	462614	2_nonsis	1	510	1019	1	15	1	1	0	(6:2)_(4:4aCO)
156	TN4	TN	16	39840	40527	40527	40910	2_nonsis	1	535	1069	1	15	1	1	0	(6:2)_(4:4aCO)
127	TN4	TN	13	619660	619714	620208	620381	2_nonsis	495	608	720	1	15	1	1	0	(6:2)_(4:4aCO)
32	TN4	TN	4	886289	887150	887179	887504	2_nonsis	30	622	1214	1	15	1	1	0	(6:2)_(4:4aCO)
20	TN4	TN	3	210517	210635	211617	211982	2_nonsis	983	1224	1464	1	15	1	1	0	(6:2)_(4:4aCO)
160	TN4	TN	16	228253	228815	229768	229960	2_nonsis	954	1330	1706	1	15	1	1	0	(6:2)_(4:4aCO)
45	TN4	TN	5	72694	72790	73131	75084	2_nonsis	342	1366	2389	1	15	1	1	0	(6:2)_(4:4aCO)
167	TN4	TN	16	686122	687687	687978	688591	2_nonsis	292	1380	2468	1	15	1	1	0	(6:2)_(4:4aCO)
26	TN4	TN	4	196851	198376	198878	199316	2_nonsis	503	1484	2464	1	15	1	1	0	(6:2)_(4:4aCO)
106	TN4	TN	12	421117	421364	422565	423102	2_nonsis	1202	1593	1984	1	15	1	1	0	(6:2)_(4:4aCO)
161	TN4	TN	16	305812	306080	307505	307579	2_nonsis	1426	1596	1766	1	15	1	1	0	(6:2)_(4:4aCO)
91	TN4	TN	10	624648	627140	627141	627999	2_nonsis	2	1676	3350	1	15	1	1	0	(6:2)_(4:4aCO)
164	TN4	TN	16	459333	460996	461367	462319	2_nonsis	372	1679	2985	1	15	1	1	0	(6:2)_(4:4aCO)
51	TN4	TN	5	564664	564705	566388	566434	2_nonsis	1684	1727	1769	1	15	1	1	0	(6:2)_(4:4aCO)
42	TN4	TN	4	1506992	1507780	1508751	1509719	2_nonsis	972	1849	2726	1	15	1	1	0	(6:2)_(4:4aCO)
165	TN4	TN	16	463723	464194	465383	466824	2_nonsis	1190	2145	3100	1	15	1	1	0	(6:2)_(4:4aCO)

132	TN4	TN	14	78386	79032	80433	81575	2_nonsis	1402	2295	3188	1	15	1	1	0	(6:2)_(4:4aCO)
7	TN4	TN	2	138346	138529	140964	141015	2_nonsis	2436	2552	2668	1	15	1	1	0	(6:2)_(4:4aCO)
101	TN4	TN	12	124986	126014	127531	128653	2_nonsis	1518	2592	3666	1	15	1	1	0	(6:2)_(4:4aCO)
40	TN4	TN	4	1465791	1466217	1467260	1470646	2_nonsis	1044	2949	4854	1	15	1	1	0	(6:2)_(4:4aCO)
76	TN4	TN	8	379353	379789	382565	383029	2_nonsis	2777	3226	3675	1	15	1	1	0	(6:2)_(4:4aCO)
151	TN4	TN	15	720799	721121	723552	725550	2_nonsis	2432	3591	4750	1	15	1	1	0	(6:2)_(4:4aCO)
59	TN4	TN	7	223151	224665	226711	230011	2_nonsis	2047	4453	6859	1	15	1	1	0	(6:2)_(4:4aCO)
8	TN4	TN	2	206083	207171	211332	211895	2_nonsis	4162	4987	5811	1	15	1	1	0	(6:2)_(4:4aCO)
85	TN4	TN	10	223465	225236	229307	229619	2_nonsis	4072	5113	6153	1	15	1	1	0	(6:2)_(4:4aCO)
131	TN4	TN	13	910045	910304	914143	916782	2_nonsis	3840	5288	6736	1	15	1	1	0	(6:2)_(4:4aCO)
145	TN4	TN	15	283315	283744	290268	290790	2_nonsis	6525	7000	7474	1	15	1	1	0	(6:2)_(4:4aCO)
31	TN4	TN	4	775671	775941	776086	776259	2_nonsis	146	367	587	1	16	1	1	0	(2:6)_(4:4aCO)
17	TN4	TN	3	72190	72786	72786	73095	2_nonsis	1	453	904	1	16	1	1	0	(2:6)_(4:4aCO)
152	TN4	TN	15	861195	861567	861653	862224	2_nonsis	87	558	1028	1	16	1	1	0	(2:6)_(4:4aCO)
99	TN4	TN	11	626218	626428	626765	627471	2_nonsis	338	795	1252	1	16	1	1	0	(2:6)_(4:4aCO)
65	TN4	TN	7	622738	623479	623527	624442	2_nonsis	49	876	1703	1	16	1	1	0	(2:6)_(4:4aCO)
155	TN4	TN	15	1058879	1058977	1059744	1059916	2_nonsis	768	902	1036	1	16	1	1	0	(2:6)_(4:4aCO)
12	TN4	TN	2	675106	676110	676125	676899	2_nonsis	16	904	1792	1	16	1	1	0	(2:6)_(4:4aCO)
34	TN4	TN	4	1075642	1075812	1075948	1077398	2_nonsis	137	946	1755	1	16	1	1	0	(2:6)_(4:4aCO)
144	TN4	TN	15	141147	141631	141631	143222	2_nonsis	1	1038	2074	1	16	1	1	0	(2:6)_(4:4aCO)
118	TN4	TN	13	164304	165032	165218	166349	2_nonsis	187	1116	2044	1	16	1	1	0	(2:6)_(4:4aCO)
97	TN4	TN	11	515018	515114	516391	516569	2_nonsis	1278	1414	1550	1	16	1	1	0	(2:6)_(4:4aCO)
121	TN4	TN	13	307804	308296	309490	309570	2_nonsis	1195	1480	1765	1	16	1	1	0	(2:6)_(4:4aCO)
75	TN4	TN	8	259045	259495	260343	261563	2_nonsis	849	1683	2517	1	16	1	1	0	(2:6)_(4:4aCO)
68	TN4	TN	7	950639	951196	951675	953718	2_nonsis	480	1779	3078	1	16	1	1	0	(2:6)_(4:4aCO)
43	TN4	TN	5	27272	27604	28694	29872	2_nonsis	1091	1845	2599	1	16	1	1	0	(2:6)_(4:4aCO)
105	TN4	TN	12	320997	322903	323570	324050	2_nonsis	668	1860	3052	1	16	1	1	0	(2:6)_(4:4aCO)
15	TN4	TN	3	50269	51152	52418	52747	2_nonsis	1267	1872	2477	1	16	1	1	0	(2:6)_(4:4aCO)
96	TN4	TN	11	226659	227480	228576	229432	2_nonsis	1097	1935	2772	1	16	1	1	0	(2:6)_(4:4aCO)
66	TN4	TN	7	794643	795956	796858	798046	2_nonsis	903	2153	3402	1	16	1	1	0	(2:6)_(4:4aCO)
14	TN4	TN	2	797893	798747	800316	800758	2_nonsis	1570	2217	2864	1	16	1	1	0	(2:6)_(4:4aCO)
36	TN4	TN	4	1261452	1262394	1263883	1264743	2_nonsis	1490	2390	3290	1	16	1	1	0	(2:6)_(4:4aCO)
158	TN4	TN	16	151184	151370	153677	153797	2_nonsis	2308	2460	2612	1	16	1	1	0	(2:6)_(4:4aCO)
19	TN4	TN	3	204750	207459	208954	209143	2_nonsis	1496	2944	4392	1	16	1	1	0	(2:6)_(4:4aCO)
124	TN4	TN	13	568585	568895	572476	572646	2_nonsis	3582	3821	4060	1	16	1	1	0	(2:6)_(4:4aCO)
79	TN4	TN	9	48626	48813	52260	53016	2_nonsis	3448	3919	4389	1	16	1	1	0	(2:6)_(4:4aCO)
77	TN4	TN	8	461762	463767	466551	466922	2_nonsis	2785	3972	5159	1	16	1	1	0	(2:6)_(4:4aCO)
90	TN4	TN	10	566114	566519	568805	572936	2_nonsis	2287	4554	6821	1	16	1	1	0	(2:6)_(4:4aCO)
109	TN4	TN	12	757131	757763	762049	762111	2_nonsis	4287	4633	4979	1	16	1	1	0	(2:6)_(4:4aCO)
4	TN4	TN	2	27441	27663	28960	35642	2_nonsis	1298	4749	8200	1	16	1	1	0	(2:6)_(4:4aCO)
119	TN4	TN	13	221642	222095	226133	227957	2_nonsis	4039	5177	6314	1	16	1	1	0	(2:6)_(4:4aCO)
163	TN4	TN	16	447002	448559	453873	454184	2_nonsis	5315	6248	7181	1	16	1	1	0	(2:6)_(4:4aCO)
149	TN4	TN	15	587565	588022	594499	600811	2_nonsis	6478	9862	13245	1	16	1	1	0	(2:6)_(4:4aCO)
102	TN4	TN	12	209847	209884	209847	209884	2_nonsis	0	18	36	1	100	1	1	0	(4:4aCO)
41	TN4	TN	4	1493916	1494247	1493916	1494247	2_nonsis	0	165	330	1	100	1	1	0	(4:4aCO)
88	TN4	TN	10	467199	467589	467199	467589	2_nonsis	0	195	389	1	100	1	1	0	(4:4aCO)
71	TN4	TN	7	1008259	1008695	1008259	1008695	2_nonsis	0	218	435	1	100	1	1	0	(4:4aCO)
48	TN4	TN	5	436763	437266	436763	437266	2_nonsis	0	251	502	1	100	1	1	0	(4:4aCO)
108	TN4	TN	12	616330	616917	616330	616917	2_nonsis	0	293	586	1	100	1	1	0	(4:4aCO)
153	TN4	TN	15	913489	914118	913489	914118	2_nonsis	0	314	628	1	100	1	1	0	(4:4aCO)
9	TN4	TN	2	323214	323896	323214	323896	2_nonsis	0	341	681	1	100	1	1	0	(4:4aCO)
62	TN4	TN	7	388315	389082	388315	389082	2_nonsis	0	383	766	1	100	1	1	0	(4:4aCO)
70	TN4	TN	7	992385	993196	992385	993196	2_nonsis	0	405	810	1	100	1	1	0	(4:4aCO)
29	TN4	TN	4	766047	767007	766047	767007	2_nonsis	0	480	959	1	100	1	1	0	(4:4aCO)
147	TN4	TN	15	489366	490345	489366	490345	2_nonsis	0	489	978	1	100	1	1	0	(4:4aCO)
22	TN4	TN	3	258915	259910	258915	259910	2_nonsis	0	497	994	1	100	1	1	0	(4:4aCO)
94	TN4	TN	11	32124	33673	32124	33673	2_nonsis	0	774	1548	1	100	1	1	0	(4:4aCO)
116	TN4	TN	13	37125	38744	37125	38744	2_nonsis	0	809	1618	1	100	1	1	0	(4:4aCO)
126	TN4	TN	13	575127	577768	575127	577768	2_nonsis	0	1320	2640	1	100	1	1	0	(4:4aCO)
72	TN4	TN	7	1046941	1050057	1046941	1050057	2_nonsis	0	1558	3115	1	100	1	1	0	(4:4aCO)

3	TN4	TN	1	132066	135319	132066	135319	2_nonsis		0	1626	3252	1	100	1	1	0	(4:4aCO)
93	TN4	TN	11	23532	27301	23532	27301	2_nonsis		0	1884	3768	1	100	1	1	0	(4:4aCO)
39	TN4	TN	4	1423134	1423374	1424231	1424583	2_nonsis		858	1153	1448	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
162	TN4	TN	16	309089	309787	314461	314704	2_nonsis		4675	5145	5614	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
146	TN4	TN	15	442786	442914	443923	444015	2_nonsis		1010	1119	1228	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
115	TN4	TN	13	12902	13242	21556	21881	2_nonsis		8315	8647	8978	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
73	TN4	TN	8	15653	16157	17751	18086	2_sis		1595	2014	2432	0	1	2	0	2	(6:2)_(8:0)_(4:4)
11	TN4	TN	2	499985	500498	506915	507219		3	6418	6826	7233	0	2	2	1	1	(2:6)_(4:4)_(2:6a)_(4:4aCO)
74	TN4	TN	8	33105	33337	37198	37339		3	3862	4048	4233	0	2	2	1	1	(8:0)_(6:2)_(8:0)_(6:2a)_(4:4aCO)
81	TN4	TN	9	292870	296453	299287	302738		4	2835	6351	9867	0	2	2	2	0	(6:2)_(8:0)_(6:2a)_(4:4aCO)
110	TN4	TN	12	821384	822252	826618	829421		3	4367	6202	8036	0	2	2	1	1	(6:2)_(2:6)_(6:2a)_(4:4aCO)
112	TN4	TN	12	1001464	1001833	1009719	1011169	2_nonsis		7887	8796	9704	0	3	2	0	2	(6:2)_(4:4aCO)_(2:6)_(4:4CO)
337	TN4	TN	16	917515	918199	925093	948066		1	0	15275	30550	0	4	1	NA	NA	
33	TRM1	TRM	7	363968	364007	364007	364128		1	1	80	159	1	1	1	0	1	05:03
5	TRM1	TRM	2	71825	71828	71828	72018		1	1	97	192	1	1	1	0	1	05:03
104	TRM1	TRM	16	785712	785737	785737	785910		1	1	99	197	1	1	1	0	1	05:03
19	TRM1	TRM	4	924351	924464	924464	924561		1	1	105	209	1	1	1	0	1	05:03
22	TRM1	TRM	4	1019082	1019195	1019208	1019310		1	14	121	227	1	1	1	0	1	05:03
61	TRM1	TRM	11	429005	429076	429143	429210		1	68	136	204	1	1	1	0	1	05:03
93	TRM1	TRM	15	662208	662245	662365	662487		1	121	200	278	1	1	1	0	1	05:03
59	TRM1	TRM	11	340811	341198	341198	341302		1	1	246	490	1	1	1	0	1	05:03
101	TRM1	TRM	16	663036	663321	663321	663543		1	1	254	506	1	1	1	0	1	05:03
67	TRM1	TRM	12	606928	607451	607458	607531		1	8	305	602	1	1	1	0	1	05:03
37	TRM1	TRM	7	611510	611515	611515	612267		1	1	379	756	1	1	1	0	1	05:03
21	TRM1	TRM	4	963556	963777	963777	964418		1	1	431	861	1	1	1	0	1	05:03
50	TRM1	TRM	10	335305	335788	335788	336181		1	1	438	875	1	1	1	0	1	05:03
27	TRM1	TRM	5	100108	100307	100307	101018		1	1	455	909	1	1	1	0	1	05:03
87	TRM1	TRM	14	515028	515081	515537	515602		1	457	515	573	1	1	1	0	1	05:03
12	TRM1	TRM	3	103955	104476	104476	105047		1	1	546	1091	1	1	1	0	1	05:03
20	TRM1	TRM	4	959563	959874	960101	960464		1	228	564	900	1	1	1	0	1	05:03
49	TRM1	TRM	10	26958	26988	26988	28612		1	1	827	1653	1	1	1	0	1	05:03
30	TRM1	TRM	6	35993	36288	37375	37482		1	1088	1288	1488	1	1	1	0	1	05:03
36	TRM1	TRM	7	545277	545279	545279	545319		1	1	21	41	1	2	1	0	1	03:05
17	TRM1	TRM	4	681992	682085	682094	682121		1	10	69	128	1	2	1	0	1	03:05
45	TRM1	TRM	9	254153	254261	254261	254315		1	1	81	161	1	2	1	0	1	03:05
25	TRM1	TRM	5	18839	18930	18949	19001		1	20	91	161	1	2	1	0	1	03:05
73	TRM1	TRM	13	388416	388450	388450	388681		1	1	133	264	1	2	1	0	1	03:05
16	TRM1	TRM	4	636352	636465	636465	636737		1	1	193	384	1	2	1	0	1	03:05
75	TRM1	TRM	13	438816	438970	438970	439214		1	1	199	397	1	2	1	0	1	03:05
32	TRM1	TRM	7	140227	140416	140416	140631		1	1	202	403	1	2	1	0	1	03:05
94	TRM1	TRM	15	977995	978537	978665	978755		1	129	444	759	1	2	1	0	1	03:05
91	TRM1	TRM	15	271047	271168	271422	271727		1	255	467	679	1	2	1	0	1	03:05
18	TRM1	TRM	4	769038	769356	769508	769848		1	153	481	809	1	2	1	0	1	03:05
66	TRM1	TRM	12	340839	341507	341688	341926		1	182	634	1086	1	2	1	0	1	03:05
26	TRM1	TRM	5	19005	23151	23160	23192		1	10	2098	4186	1	2	1	0	1	03:05
24	TRM1	TRM	4	1062037	1062818	1063052	1063171		1	235	684	1133	1	3	1	0	1	5:3_4:4_5:3
86	TRM1	TRM	14	372616	372745	374157	374306		1	1413	1551	1689	1	3	1	0	1	5:3_6:2_5:3
65	TRM1	TRM	11	571259	571283	571329	571639		1	47	213	379	1	7	1	0	1	6:2_5:3
8	TRM1	TRM	2	305677	305801	307032	307275		1	1232	1415	1597	1	7	1	0	1	5:3_6:2
56	TRM1	TRM	10	634739	635210	637464	637737		1	2255	2626	2997	1	7	1	0	1	6:2_5:3_4:4_5:3
57	TRM1	TRM	10	662479	663134	663948	664155		1	815	1245	1675	1	8	1	0	1	2:6_4:4_2:6
42	TRM1	TRM	8	93770	96126	98643	99089		1	2518	3918	5318	1	8	1	0	1	2:6_3:5_2:6_3:5
72	TRM1	TRM	13	169412	169464	169464	169477		1	1	33	64	1	10	1	0	1	06:02
79	TRM1	TRM	13	589414	589588	589588	589690		1	1	138	275	1	10	1	0	1	06:02
39	TRM1	TRM	7	892212	892452	892452	892541		1	1	165	328	1	10	1	0	1	06:02
103	TRM1	TRM	16	742152	742296	742684	743518		1	389	877	1365	1	10	1	0	1	06:02
92	TRM1	TRM	15	481860	482126	486511	487028		1	4386	4777	5167	1	10	1	0	1	06:02
10	TRM1	TRM	2	541389	541474	541474	541477		1	1	44	87	1	10.1	1	0	1	02:06
69	TRM1	TRM	12	936676	937242	937414	937738		1	173	617	1061	1	10.1	1	0	1	02:06
2	TRM1	TRM	1	187427	189825	190031	190402	2_nonsis		207	1591	2974	3	30	1	0	1	2:6_3:5

ID	Grp		n	v1	v2	v3	v4	type	x	a	b	c	d	e	f	g	desc
96	TRM1	TRM	16	371406	371706	373422	373522	2_nonsis		1717	1916	2115	3	30	1	0	1 3:5_4:4_6:2
99	TRM1	TRM	16	516982	517099	519038	519153	2_nonsis		1940	2055	2170	3	30	1	0	1 3:5_4:4_5:3_6:2_4:4_6:2
64	TRM1	TRM	11	568347	568472	568472	568685	2_nonsis		1	169	337	1	1	1	1	0 (5:3)_(4:4aCO)
98	TRM1	TRM	16	514359	514583	514728	515057	2_nonsis		146	422	697	1	2	1	1	0 (3:5)_(4:4aCO)
11	TRM1	TRM	3	41852	42410	42419	42698	2_nonsis		10	428	845	1	2	1	1	0 (3:5)_(4:4aCO)
44	TRM1	TRM	8	301054	301804	301804	303274	2_nonsis		1	1110	2219	1	2	1	1	0 (3:5)_(4:4aCO)
84	TRM1	TRM	14	318794	318845	319268	319642	2_nonsis		424	636	847	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
68	TRM1	TRM	12	645780	645971	647512	647752	2_nonsis		1542	1757	1971	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
77	TRM1	TRM	13	509359	509691	511256	511585	2_nonsis		1566	1896	2225	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
62	TRM1	TRM	11	510240	510698	510755	510872	2_nonsis		58	345	631	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
1	TRM1	TRM	1	69403	69677	70071	70228	2_nonsis		395	610	824	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
90	TRM1	TRM	14	770920	771471	772272	772448	2_nonsis		802	1165	1527	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
3	TRM1	TRM	1	192723	193131	195144	195324	2_nonsis		2014	2307	2600	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
31	TRM1	TRM	6	114541	114707	114918	115088	2_nonsis		212	379	546	1	11	1	1	0 (4:4ai)_(5:3)_(4:4bCO)
78	TRM1	TRM	13	513425	513778	514088	514095	2_nonsis		311	490	669	1	12	1	1	0 (3:5)_(4:4aCO)_(2:6)_(4:4a)
13	TRM1	TRM	3	155018	155616	156517	156868	2_nonsis		902	1376	1849	1	12	1	1	0 (3:5)_(2:6)_(3:5)_(4:4aCO)
29	TRM1	TRM	6	32886	32901	33496	33797	2_nonsis		596	753	910	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(4:4)_(4:4aCO)
85	TRM1	TRM	14	342917	343407	345744	345915	2_nonsis		2338	2668	2997	1	12	1	1	0 (4:4aCO)_(5:3)_(6:2)_(4:4a)_(5:3)_(4:4a)
83	TRM1	TRM	14	109914	110232	112194	112491	2_nonsis		1963	2270	2576	1	12	1	1	0 (5:3)_(4:4aCO)_(6:2)_(5:3)_(4:4a)_(6:2)_(5:3)_(4:4a)
43	TRM1	TRM	8	254647	254816	255648	256020	2_nonsis		833	1103	1372	1	15	1	1	0 (6:2)_(4:4aCO)
6	TRM1	TRM	2	235113	235877	235882	236188	2_nonsis		6	540	1074	1	16	1	1	0 (2:6)_(4:4aCO)
80	TRM1	TRM	13	591615	592775	592777	593048	2_nonsis		3	718	1432	1	16	1	1	0 (2:6)_(4:4aCO)
7	TRM1	TRM	2	250316	250537	251134	251548	2_nonsis		598	915	1231	1	16	1	1	0 (2:6)_(4:4aCO)
4	TRM1	TRM	2	47244	47612	47971	48762	2_nonsis		360	939	1517	1	16	1	1	0 (2:6)_(4:4aCO)
81	TRM1	TRM	13	684406	685502	685884	686613	2_nonsis		383	1295	2206	1	16	1	1	0 (2:6)_(4:4aCO)
38	TRM1	TRM	7	614580	615404	616159	616580	2_nonsis		756	1378	1999	1	16	1	1	0 (2:6)_(4:4aCO)
74	TRM1	TRM	13	410660	410894	410660	410894	2_nonsis		0	117	233	1	100	1	1	0 (4:4aCO)
23	TRM1	TRM	4	1020648	1020939	1020648	1020939	2_nonsis		0	145	290	1	100	1	1	0 (4:4aCO)
52	TRM1	TRM	10	458980	459291	458980	459291	2_nonsis		0	155	310	1	100	1	1	0 (4:4aCO)
100	TRM1	TRM	16	524220	524743	524220	524743	2_nonsis		0	261	522	1	100	1	1	0 (4:4aCO)
55	TRM1	TRM	10	559033	559588	559033	559588	2_nonsis		0	277	554	1	100	1	1	0 (4:4aCO)
70	TRM1	TRM	12	938923	939652	938923	939652	2_nonsis		0	364	728	1	100	1	1	0 (4:4aCO)
97	TRM1	TRM	16	376312	377062	376312	377062	2_nonsis		0	375	749	1	100	1	1	0 (4:4aCO)
47	TRM1	TRM	9	339305	340356	339305	340356	2_nonsis		0	525	1050	1	100	1	1	0 (4:4aCO)
14	TRM1	TRM	3	228130	230267	228130	230267	2_nonsis		0	1068	2136	1	100	1	1	0 (4:4aCO)
54	TRM1	TRM	10	504158	506424	504158	506424	2_nonsis		0	1133	2265	1	100	1	1	0 (4:4aCO)
89	TRM1	TRM	14	662512	665017	662512	665017	2_nonsis		0	1252	2504	1	100	1	1	0 (4:4aCO)
48	TRM1	TRM	9	412645	415204	412645	415204	2_nonsis		0	1279	2558	1	100	1	1	0 (4:4aCO)
53	TRM1	TRM	10	467589	469453	471532	472163	2_nonsis		2080	3327	4573	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
34	TRM1	TRM	7	373766	373940	378538	379046	2_nonsis		4599	4939	5279	2	32	1	1	0 (5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)
51	TRM1	TRM	10	440160	440847	443517	444241	2_nonsis		2671	3376	4080	2	32	1	1	0 (5:3)_(6:2)_(5:3a)_(6:2)_(4:4ai)_(4:4bCO)
71	TRM1	TRM	12	953059	953141	954772	954849	2_nonsis		1632	1711	1789	2	32	1	1	0 (2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
102	TRM1	TRM	16	739738	739829	740140	740246	2_nonsis		312	410	507	3	20	1	1	0 (5:3)_(4:4aCO)_(3:5)_(4:4a)
9	TRM1	TRM	2	458640	458701	459961	460243	2_nonsis		1261	1432	1602	3	20	1	1	0 (6:2)_(4:4)_(2:6)_(4:4aCO)
46	TRM1	TRM	9	275972	276080	277526	277693	2_nonsis		1447	1584	1720	3	20	1	1	0 (3:5)_(4:4)_(5:3)_(4:4aCO)
40	TRM1	TRM	7	900753	902479	903790	904076	2_nonsis		1312	2317	3322	3	20	1	1	0 (6:2)_(4:4aCO)_(2:6)_(4:4a)
95	TRM1	TRM	16	214684	214724	216696	217014	2_nonsis		1973	2151	2329	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
41	TRM1	TRM	7	974457	974639	977122	977277	2_nonsis		2484	2652	2819	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
82	TRM1	TRM	13	789974	790001	792254	793043	2_nonsis		2254	2661	3068	3	20	1	1	0 (5:3)_(6:2)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
88	TRM1	TRM	14	517634	517889	527330	527794	2_nonsis		9442	9801	10159	3	20	1	1	0 (5:3)_(3:5)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4a)
60	TRM1	TRM	11	399626	399800	405007	405343	2_nonsis		5208	5462	5716	3	21	1	1	0 (4:4ai)_(3:5)_(4:4ai)_(5:3)_(5:3a)_(3:5)_(4:4ai)_(4:4bCO)
35	TRM1	TRM	7	426211	426538	430810	431116	2_nonsis		4273	4589	4904	3	21	1	1	0 (2:6)_(3:5)_(2:6)_(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(6:2)_(5:3a)_(4:4a)_(4:4bi)_(4:4a)_(6:2)_(5:3a)_(5:3)_(6:2)_(4:4a)
58	TRM1	TRM	11	98452	98488	100670	101183		3	2183	2457	2730	0	2	2	1	1 (3:5)_(3:5a)_(4:4aCO)
76	TRM1	TRM	13	490109	490393	491864	492116		3	1472	1739	2006	0	2	2	1	1 (3:5)_(4:4)_(3:5a)_(4:4aCO)
15	TRM1	TRM	4	550893	551387	552354	552846		3	968	1460	1952	0	3	2	1	1 (4:4aCO)_(3:5)_(4:4bCO)_(3:5a)_(4:4b)
63	TRM1	TRM	11	513097	513249	516391	516569		3	3143	3307	3471	0	3	2	1	1 (2:6)_(4:4)_(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(5:3)_(4:4bCO)
11	TRM2	TRM	2	465690	465714	465714	465795		1	1	53	104	1	1	1	0	1 05:03
140	TRM2	TRM	13	420582	420683	420683	420689		1	1	54	106	1	1	1	0	1 05:03
83	TRM2	TRM	7	826948	827004	827004	827066		1	1	59	117	1	1	1	0	1 05:03
117	TRM2	TRM	11	618772	618816	618845	619007		1	30	132	234	1	1	1	0	1 05:03

98	TRM2	TRM	9	407953	408110	408110	408224	1	1	136	270	1	1	1	0	1	05:03
118	TRM2	TRM	12	157806	158132	158132	158461	1	1	328	654	1	1	1	0	1	05:03
177	TRM2	TRM	16	729469	729729	729729	730141	1	1	336	671	1	1	1	0	1	05:03
131	TRM2	TRM	12	818577	819282	819282	819432	1	1	428	854	1	1	1	0	1	05:03
41	TRM2	TRM	4	1079984	1080788	1080788	1080869	1	1	443	884	1	1	1	0	1	05:03
119	TRM2	TRM	12	252885	253274	253274	253791	1	1	453	905	1	1	1	0	1	05:03
81	TRM2	TRM	7	763747	765005	765005	765055	1	1	654	1307	1	1	1	0	1	05:03
12	TRM2	TRM	2	503402	504535	504587	504755	1	53	703	1352	1	1	1	0	1	05:03
110	TRM2	TRM	11	171261	172151	172151	172715	1	1	727	1453	1	1	1	0	1	05:03
99	TRM2	TRM	10	26958	26988	26988	28612	1	1	827	1653	1	1	1	0	1	05:03
54	TRM2	TRM	5	201879	202172	202626	203184	1	455	880	1304	1	1	1	0	1	05:03
120	TRM2	TRM	12	299532	300182	300539	300946	1	358	886	1413	1	1	1	0	1	05:03
16	TRM2	TRM	3	38022	38178	38857	39123	1	680	890	1100	1	1	1	0	1	05:03
160	TRM2	TRM	15	660805	661531	661971	662174	1	441	905	1368	1	1	1	0	1	05:03
73	TRM2	TRM	7	463111	463843	464314	464972	1	472	1166	1860	1	1	1	0	1	05:03
32	TRM2	TRM	4	748324	748386	749531	749726	1	1146	1274	1401	1	1	1	0	1	05:03
25	TRM2	TRM	4	523139	523141	523141	523161	1	1	11	21	1	2	1	0	1	03:05
1	TRM2	TRM	1	203038	203105	203111	203117	1	7	43	78	1	2	1	0	1	03:05
93	TRM2	TRM	9	138346	138455	138455	138490	1	1	72	143	1	2	1	0	1	03:05
152	TRM2	TRM	15	216270	216376	216399	216499	1	24	126	228	1	2	1	0	1	03:05
44	TRM2	TRM	4	1219901	1219991	1219991	1220176	1	1	138	274	1	2	1	0	1	03:05
91	TRM2	TRM	9	73686	73841	73899	73949	1	59	161	262	1	2	1	0	1	03:05
113	TRM2	TRM	11	231246	231464	231543	231603	1	80	218	356	1	2	1	0	1	03:05
114	TRM2	TRM	11	317104	317375	317375	317549	1	1	223	444	1	2	1	0	1	03:05
70	TRM2	TRM	7	344550	344881	344881	345010	1	1	230	459	1	2	1	0	1	03:05
158	TRM2	TRM	15	627675	627997	627997	628281	1	1	303	605	1	2	1	0	1	03:05
121	TRM2	TRM	12	372738	373260	373260	373385	1	1	324	646	1	2	1	0	1	03:05
170	TRM2	TRM	16	474750	475211	475211	475484	1	1	367	733	1	2	1	0	1	03:05
79	TRM2	TRM	7	702791	703157	703157	703857	1	1	533	1065	1	2	1	0	1	03:05
166	TRM2	TRM	16	104784	105356	105527	105755	1	172	571	970	1	2	1	0	1	03:05
146	TRM2	TRM	14	184449	184629	184992	185309	1	364	612	859	1	2	1	0	1	03:05
88	TRM2	TRM	8	254816	255648	255648	256087	1	1	636	1270	1	2	1	0	1	03:05
82	TRM2	TRM	7	800442	801373	801373	801844	1	1	701	1401	1	2	1	0	1	03:05
23	TRM2	TRM	4	452728	452771	453092	453903	1	322	748	1174	1	2	1	0	1	03:05
45	TRM2	TRM	4	1277186	1277374	1278056	1278456	1	683	976	1269	1	2	1	0	1	03:05
36	TRM2	TRM	4	931988	932298	933019	933755	1	722	1244	1766	1	2	1	0	1	03:05
103	TRM2	TRM	10	402004	402145	403036	404816	1	892	1852	2811	1	2	1	0	1	03:05
66	TRM2	TRM	7	147855	148827	149109	151606	1	283	2017	3750	1	2	1	0	1	03:05
10	TRM2	TRM	2	350797	350900	351335	351500	1	436	569	702	1	3	1	0	1	5:3_6:2_5:3
124	TRM2	TRM	12	514581	514693	515666	515811	1	974	1102	1229	1	3	1	0	1	5:3_4:4_5:3
34	TRM2	TRM	4	811642	811697	814278	814490	1	2582	2715	2847	1	3	1	0	1	5:3_4:4_5:3_4:4_5:3
159	TRM2	TRM	15	656887	657104	657959	658010	1	856	989	1122	1	4	1	0	1	3:5_2:6_3:5
42	TRM2	TRM	4	1093378	1093591	1094698	1095022	1	1108	1376	1643	1	4	1	0	1	3:5_4:4_3:5
46	TRM2	TRM	4	1332047	1332400	1334981	1335206	1	2582	2870	3158	1	4	1	0	1	3:5_4:4_3:5
105	TRM2	TRM	10	488230	488779	493019	494265	1	4241	5138	6034	1	4	1	0	1	3:5_2:6_3:5
84	TRM2	TRM	7	909136	909541	913000	913222	1	3460	3773	4085	1	4	1	0	1	3:5_4:4_3:5_4:4_2:6_3:5
128	TRM2	TRM	12	601825	601834	603154	603159	1	1321	1327	1333	1	4	1	0	1	3:5_2:6_4:4_3:5_2:6_4:4_3:5
27	TRM2	TRM	4	599722	599821	600037	600120	1	217	307	397	1	7	1	0	1	6:2_5:3
21	TRM2	TRM	4	330814	330985	332115	332376	1	1131	1346	1561	1	7	1	0	1	6:2_5:3
102	TRM2	TRM	10	389963	390467	392871	393423	1	2405	2932	3459	1	7	1	0	1	6:2_5:3_4:4_5:3
72	TRM2	TRM	7	448887	449549	452296	452589	1	2748	3225	3701	1	7	1	0	1	5:3_4:4_5:3_4:4_6:2
2	TRM2	TRM	2	71420	71553	72420	73226	1	868	1337	1805	1	7	1	0	1	6:2_4:4_6:2_5:3_6:2_5:3
126	TRM2	TRM	12	522914	525267	525800	526016	1	534	1818	3101	1	8	1	0	1	2:6_4:4_2:6
29	TRM2	TRM	4	652176	653010	660498	660681	1	7489	7997	8504	1	8	1	0	1	2:6_3:5_2:6_3:5_2:6_3:5_2:6_3:5_2:6_3:5_2:6
57	TRM2	TRM	5	443371	443378	443378	443383	1	1	6	11	1	10	1	0	1	06:02
78	TRM2	TRM	7	669985	670014	670014	670080	1	1	48	94	1	10	1	0	1	06:02
77	TRM2	TRM	7	627896	627924	627934	628012	1	11	63	115	1	10	1	0	1	06:02
30	TRM2	TRM	4	699436	699549	699549	699810	1	1	187	373	1	10	1	0	1	06:02
38	TRM2	TRM	4	993391	993416	993571	993715	1	156	240	323	1	10	1	0	1	06:02
109	TRM2	TRM	11	99224	99633	99646	100670	1	14	730	1445	1	10	1	0	1	06:02

132	TRM2	TRM	12	823217	826618	826618	827343	1	1	2063	4125	1	10	1	0	1	06:02
43	TRM2	TRM	4	1163374	1163376	1163376	1163379	1	1	3	4	1	10.1	1	0	1	02:06
52	TRM2	TRM	5	131479	131495	131495	131499	1	1	10	19	1	10.1	1	0	1	02:06
139	TRM2	TRM	13	388681	388700	388700	388702	1	1	11	20	1	10.1	1	0	1	02:06
37	TRM2	TRM	4	966228	966303	966303	966390	1	1	81	161	1	10.1	1	0	1	02:06
112	TRM2	TRM	11	202124	202182	202188	202339	1	7	111	214	1	10.1	1	0	1	02:06
169	TRM2	TRM	16	328786	329095	329095	329314	1	1	264	527	1	10.1	1	0	1	02:06
142	TRM2	TRM	13	830613	831156	832164	832607	2_nonsis	1009	1501	1993	3	30	1	0	1	3:5_3:5a
156	TRM2	TRM	15	545340	546162	547477	547969	2_nonsis	1316	1972	2628	3	30	1	0	1	6:2_5:3_5:3a
141	TRM2	TRM	13	773634	774011	776252	776333	2_nonsis	2242	2470	2698	3	30	1	0	1	6:2_4:4_3:5
137	TRM2	TRM	13	175894	176006	181240	182183	2_nonsis	5235	5762	6288	3	30	1	0	1	3:5_2:6_3:5a
150	TRM2	TRM	14	738960	739015	740460	740592	2_nonsis	1446	1539	1631	3	30	1	0	1	3:5_2:6_4:4_5:3
101	TRM2	TRM	10	275984	276470	280699	281003	2_nonsis	4230	4624	5018	3	30	1	0	1	5:3_4:4_2:6_5:3
95	TRM2	TRM	9	210959	212207	216122	216326	2_nonsis	3916	4641	5366	3	30	1	0	1	5:3_4:4_5:3_4:4_2:6
107	TRM2	TRM	10	701848	702981	705639	705848	2_nonsis	2659	3329	3999	3	30	1	0	1	3:5_2:6_4:4_2:6_4:4_5:3
133	TRM2	TRM	13	39174	39438	42127	44157	2_nonsis	2690	3836	4982	3	31	1	0	1	5:3_4:4ai_5:3
168	TRM2	TRM	16	284937	285327	287422	288762	2_nonsis	2096	2960	3824	3	31	1	0	1	3:5_2:6_3:5_4:4ai_4:4_3:5
165	TRM2	TRM	15	908551	908634	911484	911625	2_nonsis	2851	2962	3073	3	31	1	0	1	5:3_6:2_5:3a_6:2_5:3_4:4ai
92	TRM2	TRM	9	89868	90720	95013	95341	2_nonsis	4294	4883	5472	3	31	1	0	1	4:4ai_5:3_4:4_6:2_5:3a_6:2_5:3a_4:4_5:3a
161	TRM2	TRM	15	700968	701028	701028	701208	2_nonsis	1	120	239	1	1	1	1	0	(5:3)_(4:4aCO)
172	TRM2	TRM	16	520684	520764	520832	521292	2_nonsis	69	338	607	1	1	1	1	0	(5:3)_(4:4aCO)
4	TRM2	TRM	2	99228	99630	99630	100295	2_nonsis	1	534	1066	1	1	1	1	0	(5:3)_(4:4aCO)
7	TRM2	TRM	2	184236	184932	184941	185478	2_nonsis	10	626	1241	1	1	1	1	0	(5:3)_(4:4aCO)
125	TRM2	TRM	12	520183	520774	521410	521614	2_nonsis	637	1034	1430	1	1	1	1	0	(5:3)_(4:4aCO)
89	TRM2	TRM	8	334431	334860	336133	336486	2_nonsis	1274	1664	2054	1	1	1	1	0	(5:3)_(4:4aCO)
35	TRM2	TRM	4	856201	856278	856278	856646	2_nonsis	1	223	444	1	2	1	1	0	(3:5)_(4:4aCO)
180	TRM2	TRM	16	841449	841490	842086	842864	2_nonsis	597	1006	1414	1	2	1	1	0	(3:5)_(4:4aCO)
60	TRM2	TRM	6	74035	74065	74254	74647	2_nonsis	190	401	611	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
53	TRM2	TRM	5	198962	199099	200070	200245	2_nonsis	972	1127	1282	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
136	TRM2	TRM	13	140137	140328	140970	141600	2_nonsis	643	1053	1462	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
24	TRM2	TRM	4	507130	507490	508845	509591	2_nonsis	1356	1908	2460	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
100	TRM2	TRM	10	143166	143550	144558	144785	2_nonsis	1009	1314	1618	1	11	1	1	0	(5:3)_(4:4ai)_(4:4bCO)
3	TRM2	TRM	2	83662	83698	86465	86473	2_nonsis	2768	2789	2810	1	11	1	1	0	(4:4ai)_(4:4bCO)_(3:5)_(4:4b)
176	TRM2	TRM	16	672209	672569	673223	673927	2_nonsis	655	1186	1717	1	11	1	1	0	(5:3)_(4:4ai)_(5:3)_(4:4ai)_(4:4bCO)
145	TRM2	TRM	14	133191	133521	135855	135913	2_nonsis	2335	2528	2721	1	11	1	1	0	(2:6)_(3:5)_(4:4ai)_(4:4bCO)_(3:5)_(4:4b)
5	TRM2	TRM	2	161757	161840	166703	167174	2_nonsis	4864	5140	5416	1	11	1	1	0	(4:4ai)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4bCO)
56	TRM2	TRM	5	376468	376801	377102	377190	2_nonsis	302	512	721	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
59	TRM2	TRM	6	46998	47804	48510	48613	2_nonsis	707	1161	1614	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
174	TRM2	TRM	16	611686	612509	613103	613637	2_nonsis	595	1273	1950	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
19	TRM2	TRM	3	251657	251939	252633	253903	2_nonsis	695	1470	2245	1	12	1	1	0	(5:3)_(6:2)_(4:4)_(4:4aCO)
64	TRM2	TRM	7	52694	53079	54306	54483	2_nonsis	1228	1508	1788	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)
163	TRM2	TRM	15	846027	846878	847716	848376	2_nonsis	839	1594	2348	1	12	1	1	0	(5:3)_(4:4aCO)_(5:3)_(4:4a)
178	TRM2	TRM	16	773283	774130	775174	775448	2_nonsis	1045	1605	2164	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)
39	TRM2	TRM	4	1044635	1044751	1049309	1050120	2_nonsis	4559	5022	5484	1	12	1	1	0	(5:3)_(6:2)_(5:3)_(4:4aCO)
106	TRM2	TRM	10	638018	638343	639618	639986	2_nonsis	1276	1622	1967	1	12	1	1	0	(6:2)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
134	TRM2	TRM	13	70356	71137	72351	73368	2_nonsis	1215	2113	3011	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
26	TRM2	TRM	4	596055	596902	597668	597800	2_nonsis	767	1256	1744	1	12	1	1	0	(2:6)_(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
127	TRM2	TRM	12	534194	534611	536245	536548	2_nonsis	1635	1994	2353	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4aCO)
173	TRM2	TRM	16	605225	605750	610303	610635	2_nonsis	4554	4982	5409	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
87	TRM2	TRM	8	229448	230585	236251	237146	2_nonsis	5667	6682	7697	1	12	1	1	0	(3:5)_(2:6)_(4:4)_(3:5)_(4:4)_(3:5)_(2:6)_(3:5)_(4:4)_(4:4aCO)
164	TRM2	TRM	15	860391	861174	861653	862224	2_nonsis	480	1156	1832	1	15	1	1	0	(6:2)_(4:4aCO)
115	TRM2	TRM	11	403011	403407	403561	404302	2_nonsis	155	723	1290	1	16	1	1	0	(2:6)_(4:4aCO)
18	TRM2	TRM	3	155243	155502	158956	159547	2_nonsis	3455	3879	4303	1	16	1	1	0	(2:6)_(4:4aCO)
123	TRM2	TRM	12	510745	510855	510745	510855	2_nonsis	0	55	109	1	100	1	1	0	(4:4aCO)
129	TRM2	TRM	12	660046	660371	660046	660371	2_nonsis	0	162	324	1	100	1	1	0	(4:4aCO)
55	TRM2	TRM	5	301990	302478	301990	302478	2_nonsis	0	244	487	1	100	1	1	0	(4:4aCO)
157	TRM2	TRM	15	606336	606849	606336	606849	2_nonsis	0	256	512	1	100	1	1	0	(4:4aCO)
147	TRM2	TRM	14	215285	216026	215285	216026	2_nonsis	0	370	740	1	100	1	1	0	(4:4aCO)
68	TRM2	TRM	7	244757	245112	245686	247666	2_nonsis	575	1742	2908	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
65	TRM2	TRM	7	81435	82858	84308	84678	2_nonsis	1451	2347	3242	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)

ID	Set		n	pos1	pos2	pos3	pos4	type	num	v1	v2	v3	a	b	c	d	e	descriptor
144	TRM2	TRM	14	92521	94896	96406	102722	2_nonsis		1511	5856	10200	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
49	TRM2	TRM	4	1474578	1475249	1476956	1477116	2_nonsis		1708	2123	2537	2	31	1	1	0	(3:5)_(3:5a)_(4:4aCO)
130	TRM2	TRM	12	748908	749136	751398	751824	2_nonsis		2263	2589	2915	2	32	1	1	0	(5:3)_(4:4aCO)_(3:5a)_(4:4a)
48	TRM2	TRM	4	1433731	1433930	1436744	1436939	2_nonsis		2815	3011	3207	2	32	1	1	0	(5:3)_(4:4ai)_(4:4)_(4:4ai)_(5:3a)_(6:2)_(5:3a)_(4:4ai)_(4:4bCO)
40	TRM2	TRM	4	1059127	1059179	1059396	1059445	2_nonsis		218	268	317	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
62	TRM2	TRM	6	166317	167037	167410	168102	2_nonsis		374	1079	1784	3	20	1	1	0	(5:3)_(2:6)_(4:4aCO)
90	TRM2	TRM	9	53832	54480	55461	56514	2_nonsis		982	1832	2681	3	20	1	1	0	(5:3)_(3:5)_(5:3a)_(4:4aCO)
104	TRM2	TRM	10	417590	417877	419940	420014	2_nonsis		2064	2244	2423	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(4:4aCO)
22	TRM2	TRM	4	391561	391712	394339	394723	2_nonsis		2628	2895	3161	3	20	1	1	0	(3:5)_(4:4)_(6:2)_(4:4aCO)
171	TRM2	TRM	16	479932	480004	482104	482155	2_nonsis		2101	2162	2222	3	20	1	1	0	(5:3)_(6:2)_(4:4aCO)_(2:6)_(4:4a)
28	TRM2	TRM	4	643256	643436	644629	652022	2_nonsis		1194	4980	8765	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(3:5)_(4:4a)
69	TRM2	TRM	7	325784	325875	327277	327346	2_nonsis		1403	1482	1561	3	20	1	1	0	(6:2)_(4:4)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
15	TRM2	TRM	2	735399	735582	737232	737329	2_nonsis		1651	1790	1929	3	20	1	1	0	(5:3)_(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
175	TRM2	TRM	16	615022	615128	616944	617005	2_nonsis		1817	1900	1982	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(4:4aCO)_(5:3a)_(4:4a)
167	TRM2	TRM	16	169623	169662	172925	173018	2_nonsis		3264	3329	3394	3	20	1	1	0	(6:2)_(5:3)_(6:2)_(3:5)_(4:4aCO)
149	TRM2	TRM	14	539186	539561	542443	543829	2_nonsis		2883	3763	4642	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(3:5)_(4:4aCO)
94	TRM2	TRM	9	202086	202303	205094	210741	2_nonsis		2792	5723	8654	3	20	1	1	0	(3:5)_(4:4)_(6:2)_(5:3)_(6:2)_(4:4aCO)
71	TRM2	TRM	7	370897	371116	373958	374507	2_nonsis		2843	3226	3609	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(3:5)_(2:6)_(3:5)_(4:4aCO)
61	TRM2	TRM	6	92224	92733	95746	95849	2_nonsis		3014	3319	3624	3	20	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(5:3)_(4:4aCO)_(2:6)_(4:4a)
63	TRM2	TRM	6	231775	232615	236256	236557	2_nonsis		3642	4212	4781	3	20	1	1	0	(3:5)_(5:3)_(2:6)_(4:4aCO)_(3:5)_(6:2)_(5:3)_(4:4a)
20	TRM2	TRM	3	275423	275765	280971	281752	2_nonsis		5207	5768	6328	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(3:5)_(5:3a)_(4:4aCO)
9	TRM2	TRM	2	320583	320632	325889	326118	2_nonsis		5258	5396	5534	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(3:5)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
154	TRM2	TRM	15	405136	405535	411283	411906	2_nonsis		5749	6259	6769	3	20	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(3:5)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)
155	TRM2	TRM	15	492036	492191	498928	499156	2_nonsis		6738	6929	7119	3	20	1	1	0	(3:5)_(2:6)_(5:3)_(2:6)_(5:3)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(4:4a)_(5:3)_(4:4a)
96	TRM2	TRM	9	265508	265732	268526	268579	2_nonsis		2795	2933	3070	3	21	1	1	0	(5:3)_(4:4ai)_(3:5)_(2:6)_(4:4bCO)
85	TRM2	TRM	7	970290	970527	973354	974385	2_nonsis		2828	3461	4094	3	21	1	1	0	(4:4ai)_(5:3)_(4:4ai)_(3:5)_(4:4bCO)
179	TRM2	TRM	16	779486	779914	786015	786161	2_nonsis		6102	6388	6674	3	21	1	1	0	(5:3)_(3:5)_(4:4ai)_(5:3a)_(4:4bCO)
50	TRM2	TRM	5	18839	18930	23151	23976	2_sis		4222	4679	5136	0	1	2	0	2	(2:6i)_(4:4)
97	TRM2	TRM	9	325450	325617	326724	327096	2_sis		1108	1377	1645	0	1	2	0	2	(5:3)_(4:4)_(6:2)_(4:4)
122	TRM2	TRM	12	506259	507492	507492	508649	2_sis		1	1195	2389	0	1	2	0	2	(2:6i)_(4:4)
153	TRM2	TRM	15	256412	256446	270164	270370	2_sis		13719	13838	13957	0	1	2	0	2	(2:6)_(3:5)_(1:7)_(0:8)_(1:7)_(0:8)_(1:7)_(0:8)_(1:7)_(0:8)_(1:7)_(2:6a)_(4:4)
6	TRM2	TRM	2	180607	181279	182901	183084		3	1623	2050	2476	0	2	2	1	1	(5:3)_(5:3a)_(6:2)_(5:3b)_(4:4aCO)
13	TRM2	TRM	2	638716	639238	654891	655336		4	15654	16137	16619	0	2	2	2	2	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4ai)_(4:4)_(3:5)_(4:4ai)_(2:6)_(3:5)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(3:5b)_(4:4bCO)
14	TRM2	TRM	2	695479	697455	710109	710907		4	12655	14041	15427	0	2	2	1	1	(3:5)_(2:6i)_(1:7)_(2:6i)_(1:7)_(2:6ai)_(2:6bi)_(4:4ai)_(5:3)_(6:2)_(4:4ai)_(3:5a)_(4:4bCO)_(3:5a)_(4:4b)
17	TRM2	TRM	3	72786	73095	74074	74394		3	980	1294	1607	0	2	2	1	1	(3:5)_(4:4aCO)_(2:6)_(4:4a)
31	TRM2	TRM	4	743850	744215	746186	746381		3	1972	2251	2530	0	2	2	1	1	(5:3)_(5:3a)_(6:2)_(4:4aCO)
33	TRM2	TRM	4	800984	801463	808940	810702		3	7478	8598	9717	0	2	2	1	1	(3:5)_(4:4)_(3:5)_(2:6)_(5:3)_(4:4aCO)_(5:3a)_(4:4a)_(5:3a)_(4:4a)_(6:2)_(5:3a)_(4:4a)_(5:3a)_(4:4a)_(5:3a)_(4:4a)
47	TRM2	TRM	4	1419516	1419978	1420608	1420714		3	631	914	1197	0	2	2	1	1	(6:2)_(4:4aCO)_(5:3)_(4:4a)
51	TRM2	TRM	5	54453	55841	77098	77310		3	21258	22057	22856	0	2	2	1	1	(3:5)_(2:6)_(3:5)_(2:6ai)_(2:6)_(2:6ai)_(3:5)_(4:4)_(2:6)_(1:7)_(2:6)_(1:7)_(2:6)_(0:8)_(2:6)_(1:7)_(2:6)_(1:7)_(3:5a)_(2:6b)_(1:7a)_(2:6b)_(3:5b)_(4:4aCO)_(3:5b)_(2:6c)_(3:5b)_(4:4a)
74	TRM2	TRM	7	472609	472656	475390	475467		3	2735	2796	2857	0	2	2	1	1	(2:6)_(5:3)_(4:4ai)_(3:5)_(2:6)_(3:5a)_(4:4bi)_(4:4cCO)
75	TRM2	TRM	7	609314	609405	611515	612267		4	2111	2532	2952	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(6:2)_(4:4ai)_(5:3a)_(4:4bCO)_(6:2ai)_(4:4b)
111	TRM2	TRM	11	190915	191290	192038	192111		3	749	972	1195	0	2	2	1	1	(6:2)_(2:6)_(4:4ai)_(3:5)_(4:4bCO)
116	TRM2	TRM	11	573116	573289	575843	576495		3	2555	2967	3378	0	2	2	1	1	(3:5)_(5:3a)_(5:3)_(6:2)_(5:3)_(4:4aCO)
151	TRM2	TRM	15	193911	194961	205904	205962		3	10944	11497	12050	0	2	2	1	1	(5:3)_(6:2)_(7:1)_(5:3a)_(4:4aCO)
162	TRM2	TRM	15	769620	770102	775426	775432		3	5325	5568	5811	0	2	2	1	1	(6:2)_(3:5)_(6:2)_(5:3)_(4:4)_(5:3a)_(2:6)_(4:4aCO)_(5:3b)_(4:4a)
8	TRM2	TRM	2	309822	310032	311676	312167	2_nonsis		1645	1995	2344	0	3	2	0	2	(2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4CO)
67	TRM2	TRM	7	177165	177524	183038	184145	2_nonsis		5515	6247	6979	0	3	2	0	2	(4:4ai)_(5:3)_(4:4bCO)_(5:3a)_(4:4CO)_(2:6)_(4:4)
76	TRM2	TRM	7	614580	615404	618272	618689	2_nonsis		2869	3489	4108	0	3	2	0	2	(5:3)_(4:4ai)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3a)_(4:4bCO)_(5:3)_(6:2)_(4:4CO)
80	TRM2	TRM	7	737189	737501	739321	739622	2_nonsis		1821	2127	2432	0	3	2	0	2	(4:4ai)_(5:3)_(4:4bCO)_(5:3)_(4:4b)_(5:3)_(4:4ai)_(4:4CO)
86	TRM2	TRM	8	69180	69741	74727	74846		3	4987	5326	5665	0	3	2	1	1	(3:5)_(4:4)_(3:5)_(3:5)_(5:3a)_(4:4aCO)_(3:5a)_(4:4bi)_(5:3)_(4:4cCO)_(5:3)_(4:4c)
108	TRM2	TRM	11	69153	69417	72681	73029	2_nonsis		3265	3570	3875	0	3	2	0	2	(3:5)_(4:4ai)_(4:4bCO)_(5:3)_(4:4CO)_(5:3a)_(4:4)_(3:5)_(4:4)
135	TRM2	TRM	13	97600	98070	101176	101469	2_nonsis		3107	3488	3868	0	3	2	0	2	(3:5)_(4:4)_(4:4aCO)_(5:3)_(6:2)_(4:4a)_(5:3a)_(3:5a)_(4:4CO)
138	TRM2	TRM	13	331787	332732	341111	341630		3	8380	9111	9842	0	3	2	1	1	(3:5)_(3:5a)_(4:4aCO)_(3:5a)_(2:6)_(4:4a)_(2:6a)_(4:4bCO)_(3:5b)_(4:4b)_(3:5b)_(4:4b)
143	TRM2	TRM	14	80433	81575	86054	86180		3	4480	5113	5746	0	3	2	1	1	(2:6)_(3:5)_(4:4)_(2:6)_(3:5a)_(3:5b)_(4:4aCO)_(5:3)_(4:4CO)
148	TRM2	TRM	14	279881	280112	282032	283073	2_nonsis		1921	2556	3191	0	3	2	0	2	(3:5)_(4:4aCO)_(3:5a)_(4:4a)_(2:6)_(4:4CO)
228	TRM3	TRM	16	560045	560053	560053	560087		1	1	21	41	1	1	1	0	1	05:03
54	TRM3	TRM	4	1201657	1201701	1201701	1201847		1	1	95	189	1	1	1	0	1	05:03
79	TRM3	TRM	7	17018	17097	17097	17234		1	1	108	215	1	1	1	0	1	05:03
53	TRM3	TRM	4	1149251	1149368	1149368	1149478		1	1	114	226	1	1	1	0	1	05:03
24	TRM3	TRM	3	233678	233870	233870	233910		1	1	116	231	1	1	1	0	1	05:03

220	TRM3	TRM	16	188788	188889	188889	189026	1	1	119	237	1	1	1	0	1	05:03
89	TRM3	TRM	7	754453	754648	754670	754678	1	23	124	224	1	1	1	0	1	05:03
45	TRM3	TRM	4	761375	761459	761459	761692	1	1	159	316	1	1	1	0	1	05:03
5	TRM3	TRM	2	96287	96328	96328	96610	1	1	162	322	1	1	1	0	1	05:03
36	TRM3	TRM	4	375374	375530	375542	375690	1	13	164	315	1	1	1	0	1	05:03
149	TRM3	TRM	13	91086	91149	91161	91448	1	13	187	361	1	1	1	0	1	05:03
103	TRM3	TRM	8	326640	326679	326679	327083	1	1	222	442	1	1	1	0	1	05:03
44	TRM3	TRM	4	671041	671079	671207	671379	1	129	233	337	1	1	1	0	1	05:03
182	TRM3	TRM	14	351650	351718	351888	352081	1	171	301	430	1	1	1	0	1	05:03
181	TRM3	TRM	14	324247	324447	324447	324866	1	1	310	618	1	1	1	0	1	05:03
55	TRM3	TRM	4	1229430	1229808	1229808	1230069	1	1	320	638	1	1	1	0	1	05:03
116	TRM3	TRM	10	104033	104395	104395	104685	1	1	326	651	1	1	1	0	1	05:03
91	TRM3	TRM	7	794244	794286	794323	794878	1	38	336	633	1	1	1	0	1	05:03
210	TRM3	TRM	15	667235	667477	667488	668097	1	12	437	861	1	1	1	0	1	05:03
159	TRM3	TRM	13	610928	611569	611569	611899	1	1	486	970	1	1	1	0	1	05:03
104	TRM3	TRM	8	346315	347026	347026	347311	1	1	498	995	1	1	1	0	1	05:03
145	TRM3	TRM	12	703971	704793	704829	704992	1	37	529	1020	1	1	1	0	1	05:03
41	TRM3	TRM	4	567805	567972	568131	568816	1	160	585	1010	1	1	1	0	1	05:03
69	TRM3	TRM	5	354038	355019	355038	355237	1	20	609	1198	1	1	1	0	1	05:03
27	TRM3	TRM	3	288246	288455	288455	289600	1	1	677	1353	1	1	1	0	1	05:03
14	TRM3	TRM	2	515316	515610	515996	516344	1	387	707	1027	1	1	1	0	1	05:03
119	TRM3	TRM	10	315327	315571	315888	316551	1	318	771	1223	1	1	1	0	1	05:03
142	TRM3	TRM	12	534194	534611	535113	535533	1	503	921	1338	1	1	1	0	1	05:03
209	TRM3	TRM	15	657269	657824	658496	658645	1	673	1024	1375	1	1	1	0	1	05:03
190	TRM3	TRM	14	589995	591830	591853	592102	1	24	1065	2106	1	1	1	0	1	05:03
217	TRM3	TRM	15	1048437	1048875	1049756	1049902	1	882	1173	1464	1	1	1	0	1	05:03
82	TRM3	TRM	7	113828	114793	114793	116310	1	1	1241	2481	1	1	1	0	1	05:03
137	TRM3	TRM	11	610232	610502	611219	612138	1	718	1312	1905	1	1	1	0	1	05:03
178	TRM3	TRM	14	162623	163370	163952	165064	1	583	1512	2440	1	1	1	0	1	05:03
187	TRM3	TRM	14	530418	530856	532165	532649	1	1310	1770	2230	1	1	1	0	1	05:03
169	TRM3	TRM	13	804869	804888	804888	804916	1	1	24	46	1	2	1	0	1	03:05
121	TRM3	TRM	10	459643	459751	459751	459766	1	1	62	122	1	2	1	0	1	03:05
110	TRM3	TRM	9	138346	138486	138486	138490	1	1	72	143	1	2	1	0	1	03:05
211	TRM3	TRM	15	752002	752064	752064	752146	1	1	72	143	1	2	1	0	1	03:05
203	TRM3	TRM	15	448955	448985	448985	449105	1	1	75	149	1	2	1	0	1	03:05
199	TRM3	TRM	15	260677	260759	260759	260837	1	1	80	159	1	2	1	0	1	03:05
63	TRM3	TRM	5	18839	18930	18949	19001	1	20	91	161	1	2	1	0	1	03:05
8	TRM3	TRM	2	288119	288197	288197	288303	1	1	92	183	1	2	1	0	1	03:05
168	TRM3	TRM	13	800816	800900	800900	801034	1	1	109	217	1	2	1	0	1	03:05
7	TRM3	TRM	2	132333	132460	132460	132576	1	1	122	242	1	2	1	0	1	03:05
47	TRM3	TRM	4	786128	786193	786207	786378	1	15	132	249	1	2	1	0	1	03:05
197	TRM3	TRM	15	207058	207203	207252	207320	1	50	156	261	1	2	1	0	1	03:05
164	TRM3	TRM	13	763221	763289	763289	763537	1	1	158	315	1	2	1	0	1	03:05
196	TRM3	TRM	15	205242	205541	205541	205574	1	1	166	331	1	2	1	0	1	03:05
131	TRM3	TRM	11	358089	358323	358323	358455	1	1	183	365	1	2	1	0	1	03:05
22	TRM3	TRM	3	114298	114644	114644	114698	1	1	200	399	1	2	1	0	1	03:05
11	TRM3	TRM	2	356648	356805	356805	357199	1	1	276	550	1	2	1	0	1	03:05
218	TRM3	TRM	16	29604	29674	29856	30029	1	183	304	424	1	2	1	0	1	03:05
165	TRM3	TRM	13	768344	768494	768514	768951	1	21	314	606	1	2	1	0	1	03:05
38	TRM3	TRM	4	396610	396700	396700	397411	1	1	401	800	1	2	1	0	1	03:05
112	TRM3	TRM	9	245693	245765	245832	246575	1	68	475	881	1	2	1	0	1	03:05
232	TRM3	TRM	16	704149	704396	704396	705129	1	1	490	979	1	2	1	0	1	03:05
234	TRM3	TRM	16	770699	770863	770864	771861	1	2	582	1161	1	2	1	0	1	03:05
146	TRM3	TRM	12	788350	788475	788874	789356	1	400	703	1005	1	2	1	0	1	03:05
101	TRM3	TRM	8	229448	230585	230585	230894	1	1	723	1445	1	2	1	0	1	03:05
94	TRM3	TRM	7	1022196	1022320	1022816	1023234	1	497	767	1037	1	2	1	0	1	03:05
99	TRM3	TRM	8	159962	160782	160782	161688	1	1	863	1725	1	2	1	0	1	03:05
74	TRM3	TRM	6	27763	27810	28662	28792	1	853	941	1028	1	2	1	0	1	03:05
93	TRM3	TRM	7	914816	915691	916059	916953	1	369	1253	2136	1	2	1	0	1	03:05
1	TRM3	TRM	1	60198	60267	61451	61708	1	1185	1347	1509	1	2	1	0	1	03:05

64	TRM3	TRM	5	19005	23151	23160	23192	1	10	2098	4186	1	2	1	0	1 03:05
72	TRM3	TRM	5	491556	491960	492329	498773	1	370	3793	7216	1	2	1	0	1 03:05
65	TRM3	TRM	5	67809	68268	68996	69083	1	729	1001	1273	1	3	1	0	1 5:3_6:2_5:3
171	TRM3	TRM	13	829176	829431	831156	831222	1	1726	1886	2045	1	3	1	0	1 5:3_4:4_5:3
67	TRM3	TRM	5	182381	182827	184363	184684	1	1537	1920	2302	1	3	1	0	1 5:3_4:4_5:3
172	TRM3	TRM	13	869428	870074	875718	876530	1	5645	6373	7101	1	3	1	0	1 5:3_6:2_5:3_4:4_5:3_4:4_5:3
177	TRM3	TRM	14	145206	145227	145376	145535	1	150	239	328	1	4	1	0	1 3:5_2:6_3:5
18	TRM3	TRM	2	717754	717945	718601	718700	1	657	801	945	1	4	1	0	1 3:5_4:4_3:5
158	TRM3	TRM	13	605013	605479	606387	606680	1	909	1288	1666	1	4	1	0	1 3:5_2:6_3:5
26	TRM3	TRM	3	252633	253903	254715	254941	1	813	1560	2307	1	4	1	0	1 3:5_4:4_3:5
130	TRM3	TRM	11	317104	317375	318939	319143	1	1565	1802	2038	1	4	1	0	1 3:5_4:4_3:5
128	TRM3	TRM	11	174833	175169	176780	177108	1	1612	1943	2274	1	4	1	0	1 3:5_4:4_3:5
42	TRM3	TRM	4	635526	635784	638098	638176	1	2315	2482	2649	1	4	1	0	1 3:5_4:4_3:5_4:4_3:5
126	TRM3	TRM	10	705639	705848	707333	707549	1	1486	1698	1909	1	4	1	0	1 3:5_4:4_3:5_2:6_3:5_4:4_3:5
229	TRM3	TRM	16	576041	576179	576287	576345	1	109	206	303	1	7	1	0	1 5:3_6:2
225	TRM3	TRM	16	366758	366909	367806	368095	1	898	1117	1336	1	7	1	0	1 6:2_5:3
135	TRM3	TRM	11	597543	597866	598922	599337	1	1057	1425	1793	1	7	1	0	1 5:3_6:2
147	TRM3	TRM	12	837543	837595	837962	840577	1	368	1701	3033	1	7	1	0	1 5:3_6:2
184	TRM3	TRM	14	399462	400449	400901	400998	1	453	994	1535	1	7	1	0	1 5:3_4:4_5:3_6:2
12	TRM3	TRM	2	493942	494538	496540	497133	1	2003	2597	3190	1	7	1	0	1 6:2_5:3_6:2_5:3
61	TRM3	TRM	4	1468724	1468738	1468802	1468862	1	65	101	137	1	8	1	0	1 2:6_3:5
90	TRM3	TRM	7	771558	771837	772172	772420	1	336	599	861	1	8	1	0	1 3:5_2:6
163	TRM3	TRM	13	751891	752227	752521	752958	1	295	681	1066	1	8	1	0	1 2:6_3:5
17	TRM3	TRM	2	706983	707207	707509	708202	1	303	761	1218	1	8	1	0	1 3:5_2:6
106	TRM3	TRM	8	379070	379353	379863	380348	1	511	894	1277	1	8	1	0	1 3:5_2:6
71	TRM3	TRM	5	415894	416514	416927	417310	1	414	915	1415	1	8	1	0	1 2:6_3:5
134	TRM3	TRM	11	581619	581803	583405	583946	1	1603	1965	2326	1	8	1	0	1 2:6_3:5
39	TRM3	TRM	4	408894	410728	411785	412382	1	1058	2273	3487	1	8	1	0	1 3:5_4:4_3:5_2:6
167	TRM3	TRM	13	789347	789974	791709	791894	1	1736	2141	2546	1	8	1	0	1 2:6_3:5_4:4_2:6_3:5
37	TRM3	TRM	4	386093	386162	386162	386167	1	1	37	73	1	10	1	0	1 06:02
28	TRM3	TRM	3	298120	298326	298597	298764	1	272	458	643	1	10	1	0	1 06:02
205	TRM3	TRM	15	490456	491189	491190	491476	1	2	511	1019	1	10	1	0	1 06:02
108	TRM3	TRM	9	49641	51046	53832	54480	1	2787	3813	4838	1	10	1	0	1 06:02
154	TRM3	TRM	13	432019	432230	432230	432244	1	1	113	224	1	10.1	1	0	1 02:06
189	TRM3	TRM	14	575525	576199	576199	576383	1	1	429	857	1	10.1	1	0	1 02:06
152	TRM3	TRM	13	420077	420098	420528	420568	1	431	461	490	1	10.1	1	0	1 02:06
215	TRM3	TRM	15	967253	967257	967611	967862	1	355	482	608	1	10.1	1	0	1 02:06
97	TRM3	TRM	8	70138	70273	70542	70883	1	270	507	744	1	10.1	1	0	1 02:06
109	TRM3	TRM	9	55837	56514	56514	57063	1	1	613	1225	1	10.1	1	0	1 02:06
96	TRM3	TRM	7	1050446	1051057	1051093	1051973	1	37	782	1526	1	10.1	1	0	1 02:06
75	TRM3	TRM	6	38974	39275	40232	40564	1	958	1274	1589	1	10.1	1	0	1 02:06
52	TRM3	TRM	4	1106617	1106884	1109358	1109568	1	2475	2713	2950	1	10.1	1	0	1 02:06
56	TRM3	TRM	4	1251240	1251845	1252149	1252244	2_nonsis	305	654	1003	3	30	1	0	1 3:5_6:2
170	TRM3	TRM	13	824885	825266	826921	827271	2_nonsis	1656	2021	2385	3	30	1	0	1 2:6_3:5
33	TRM3	TRM	4	181807	181859	184221	184727	2_nonsis	2363	2641	2919	3	30	1	0	1 3:5_3:5a_3:5
175	TRM3	TRM	14	42594	43912	45407	46489	2_nonsis	1496	2695	3894	3	30	1	0	1 5:3_5:3a_6:2
153	TRM3	TRM	13	424537	425033	429559	429941	2_nonsis	4527	4965	5403	3	30	1	0	1 6:2_5:3_4:4_2:6
32	TRM3	TRM	4	163327	163443	167826	169331	2_nonsis	4384	5194	6003	3	30	1	0	1 5:3_4:4_5:3_4:4_5:3_5:3a
216	TRM3	TRM	15	994385	995303	996329	996896	2_nonsis	1027	1769	2510	3	31	1	0	1 4:4ai_3:5_6:2_5:3
213	TRM3	TRM	15	780823	781222	783046	783669	2_nonsis	1825	2335	2845	3	31	1	0	1 3:5_2:6_3:5a_4:4ai_3:5a_4:4ai
57	TRM3	TRM	4	1300834	1301253	1303716	1304109	2_nonsis	2464	2869	3274	3	31	1	0	1 3:5_4:4_4:4ai_3:5_2:6_3:5_4:4ai
162	TRM3	TRM	13	716342	716494	724837	726144	2_nonsis	8344	9073	9801	3	31	1	0	1 4:4ai_6:2_3:5_2:6_3:5_2:6_4:4_3:5a
141	TRM3	TRM	12	532399	532555	532555	532747	2_nonsis	1	174	347	1	1	1	1	0 (5:3)_(4:4aCO)
173	TRM3	TRM	13	898277	898408	898692	898776	2_nonsis	285	392	498	1	1	1	1	0 (5:3)_(4:4aCO)
60	TRM3	TRM	4	1458432	1459261	1459261	1459669	2_nonsis	1	619	1236	1	1	1	1	0 (5:3)_(4:4aCO)
66	TRM3	TRM	5	85103	85578	85693	86770	2_nonsis	116	891	1666	1	1	1	1	0 (5:3)_(4:4aCO)
123	TRM3	TRM	10	524618	526730	526730	528639	2_nonsis	1	2011	4020	1	1	1	1	0 (5:3)_(4:4aCO)
204	TRM3	TRM	15	455342	456606	457679	458312	2_nonsis	1074	2022	2969	1	1	1	1	0 (5:3)_(4:4aCO)
176	TRM3	TRM	14	52324	52659	52925	53465	2_nonsis	267	704	1140	1	2	1	1	0 (3:5)_(4:4aCO)
43	TRM3	TRM	4	639649	640367	640565	640997	2_nonsis	199	773	1347	1	2	1	1	0 (3:5)_(4:4aCO)

30	TRM3	TRM	4	91959	93521	94379	95033	2_nonsis	859	1966	3073	1	2	1	1	0 (3:5)_(4:4aCO)
198	TRM3	TRM	15	208985	209157	209698	209867	2_nonsis	542	712	881	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
151	TRM3	TRM	13	322180	323059	323763	324584	2_nonsis	705	1554	2403	1	4	1	1	0 (4:4aCO)_(5:3)_(4:4a)
125	TRM3	TRM	10	632972	633146	633240	633350	2_nonsis	95	236	377	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
185	TRM3	TRM	14	480718	480827	480999	481081	2_nonsis	173	268	362	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
127	TRM3	TRM	11	88618	88890	89569	89674	2_nonsis	680	868	1055	1	7	1	1	0 (5:3)_(6:2)_(4:4aCO)
113	TRM3	TRM	9	279199	279316	279526	279602	2_nonsis	211	307	402	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
21	TRM3	TRM	3	70617	70770	71079	71223	2_nonsis	310	458	605	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
212	TRM3	TRM	15	769092	769431	769620	770027	2_nonsis	190	562	934	1	8	1	1	0 (6:2)_(5:3)_(4:4aCO)
13	TRM3	TRM	2	500498	500795	500915	501073	2_nonsis	121	348	574	1	9	1	1	0 (3:5)_(2:6)_(4:4aCO)
117	TRM3	TRM	10	106394	106893	107092	107239	2_nonsis	200	522	844	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
224	TRM3	TRM	16	346506	347009	347684	347716	2_nonsis	676	943	1209	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
6	TRM3	TRM	2	126921	128153	129488	130349	2_nonsis	1336	2382	3427	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
183	TRM3	TRM	14	389775	391590	392860	393703	2_nonsis	1271	2599	3927	1	10	1	1	0 (2:6)_(3:5)_(4:4aCO)
214	TRM3	TRM	15	944698	945099	945099	945153	2_nonsis	1	228	454	1	11	1	1	0 (4:4ai)_(4:4bCO)
157	TRM3	TRM	13	586528	586744	590250	590486	2_nonsis	3507	3732	3957	1	11	1	1	0 (4:4ai)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4bCO)
124	TRM3	TRM	10	581933	582214	582415	582424	2_nonsis	202	346	490	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
122	TRM3	TRM	10	461660	461801	462170	462595	2_nonsis	370	652	934	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
207	TRM3	TRM	15	592970	593587	594122	594439	2_nonsis	536	1002	1468	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
201	TRM3	TRM	15	377730	377924	378233	378285	2_nonsis	310	432	554	1	12	1	1	0 (6:2)_(5:3)_(6:2)_(4:4aCO)
143	TRM3	TRM	12	568114	568449	568917	569539	2_nonsis	469	947	1424	1	12	1	1	0 (6:2)_(4:4)_(5:3)_(4:4aCO)
92	TRM3	TRM	7	893319	893535	894550	894616	2_nonsis	1016	1156	1296	1	12	1	1	0 (2:6)_(4:4aCO)_(3:5)_(4:4a)
129	TRM3	TRM	11	307722	307923	309310	309621	2_nonsis	1388	1643	1898	1	12	1	1	0 (4:4aCO)_(6:2)_(5:3)_(4:4a)
87	TRM3	TRM	7	609760	609887	611515	612267	2_nonsis	1629	2068	2506	1	12	1	1	0 (5:3)_(4:4)_(5:3)_(4:4aCO)
50	TRM3	TRM	4	1000380	1001608	1003950	1004000	2_nonsis	2343	2981	3619	1	12	1	1	0 (3:5)_(4:4aCO)_(3:5)_(4:4a)
9	TRM3	TRM	2	291653	292193	293099	293297	2_nonsis	907	1275	1643	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(5:3)_(4:4a)
102	TRM3	TRM	8	237633	238630	239430	240144	2_nonsis	801	1656	2510	1	12	1	1	0 (5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)
186	TRM3	TRM	14	488598	488965	491114	491255	2_nonsis	2150	2403	2656	1	12	1	1	0 (3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
3	TRM3	TRM	1	187427	190025	191026	191704	2_nonsis	1002	2639	4276	1	12	1	1	0 (3:5)_(2:6)_(4:4)_(2:6)_(4:4aCO)
208	TRM3	TRM	15	639042	639159	642679	643115	2_nonsis	3521	3797	4072	1	12	1	1	0 (3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
70	TRM3	TRM	5	400915	401106	405271	406216	2_nonsis	4166	4733	5300	1	12	1	1	0 (2:6)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
77	TRM3	TRM	6	197486	197726	202500	202731	2_nonsis	4775	5010	5244	1	12	1	1	0 (2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
219	TRM3	TRM	16	155906	156745	158264	158999	2_nonsis	1520	2306	3092	1	12	1	1	0 (2:6)_(3:5)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
155	TRM3	TRM	13	452181	453503	456535	456718	2_nonsis	3033	3785	4536	1	12	1	1	0 (3:5)_(4:4)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4aCO)
85	TRM3	TRM	7	383665	383867	383908	384183	2_nonsis	42	280	517	1	15	1	1	0 (6:2)_(4:4aCO)
105	TRM3	TRM	8	375097	375221	375221	375658	2_nonsis	1	281	560	1	15	1	1	0 (6:2)_(4:4aCO)
202	TRM3	TRM	15	410471	410731	410754	411250	2_nonsis	24	401	778	1	15	1	1	0 (6:2)_(4:4aCO)
133	TRM3	TRM	11	488294	488405	488665	489458	2_nonsis	261	712	1163	1	15	1	1	0 (6:2)_(4:4aCO)
31	TRM3	TRM	4	114170	114468	114797	115526	2_nonsis	330	843	1355	1	15	1	1	0 (6:2)_(4:4aCO)
150	TRM3	TRM	13	256691	257090	257090	257217	2_nonsis	1	263	525	1	16	1	1	0 (2:6)_(4:4aCO)
16	TRM3	TRM	2	701871	702521	702600	702673	2_nonsis	80	441	801	1	16	1	1	0 (2:6)_(4:4aCO)
15	TRM3	TRM	2	641914	642355	642483	642776	2_nonsis	129	495	861	1	16	1	1	0 (2:6)_(4:4aCO)
62	TRM3	TRM	5	15966	16323	16323	17065	2_nonsis	1	550	1098	1	16	1	1	0 (2:6)_(4:4aCO)
230	TRM3	TRM	16	586309	586497	587432	587665	2_nonsis	936	1146	1355	1	16	1	1	0 (2:6)_(4:4aCO)
51	TRM3	TRM	4	1056242	1056383	1059534	1059598	2_nonsis	3152	3254	3355	1	16	1	1	0 (2:6)_(4:4aCO)
88	TRM3	TRM	7	748310	748532	748310	748532	2_nonsis	0	111	221	1	100	1	1	0 (4:4aCO)
120	TRM3	TRM	10	317491	317989	317491	317989	2_nonsis	0	249	497	1	100	1	1	0 (4:4aCO)
19	TRM3	TRM	2	738241	738886	738241	738886	2_nonsis	0	322	644	1	100	1	1	0 (4:4aCO)
95	TRM3	TRM	7	1024337	1024993	1024337	1024993	2_nonsis	0	328	655	1	100	1	1	0 (4:4aCO)
180	TRM3	TRM	14	295066	295803	295066	295803	2_nonsis	0	368	736	1	100	1	1	0 (4:4aCO)
10	TRM3	TRM	2	314330	315082	314330	315082	2_nonsis	0	376	751	1	100	1	1	0 (4:4aCO)
4	TRM3	TRM	2	72420	73226	72420	73226	2_nonsis	0	403	805	1	100	1	1	0 (4:4aCO)
195	TRM3	TRM	15	147007	150962	147007	150962	2_nonsis	0	1977	3954	1	100	1	1	0 (4:4aCO)
80	TRM3	TRM	7	80122	80305	81268	81306	2_nonsis	964	1074	1183	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)
111	TRM3	TRM	9	160585	160764	164332	164883	2_nonsis	3569	3933	4297	2	30	1	1	0 (5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
179	TRM3	TRM	14	195766	195994	200066	200248	2_nonsis	4073	4277	4481	2	30	1	1	0 (5:3)_(5:3a)_(4:4aCO)_(5:3a)_(6:2)_(4:4a)
223	TRM3	TRM	16	323207	323715	326546	326955	2_nonsis	2832	3290	3747	2	30	1	1	0 (5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(5:3a)_(6:2)_(4:4aCO)
81	TRM3	TRM	7	96869	96992	97411	97616	2_nonsis	420	583	746	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
2	TRM3	TRM	1	121235	128756	132066	135319	2_nonsis	3311	8697	14083	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)
115	TRM3	TRM	10	92203	92413	95205	96041	2_nonsis	2793	3315	3837	2	31	1	1	0 (3:5)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19
222	TRM3	TRM	16	308140	308234	309089	309787	2_nonsis		856	1251	1646	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
174	TRM3	TRM	14	37986	39122	40430	41146	2_nonsis		1309	2234	3159	2	32	1	1	0	(3:5)_(4:4aCO)_(3:5a)_(4:4a)
144	TRM3	TRM	12	678793	678817	682839	683018	2_nonsis		4023	4124	4224	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
76	TRM3	TRM	6	189847	190129	192732	192850	2_nonsis		2604	2803	3002	2	32	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
98	TRM3	TRM	8	72400	72478	75187	75639	2_nonsis		2710	2974	3238	2	32	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(2:6)_(4:4aCO)_(3:5a)_(4:4a)
160	TRM3	TRM	13	662059	662421	667065	667202	2_nonsis		4645	4894	5142	2	32	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(4:4aCO)
140	TRM3	TRM	12	286350	286840	288047	288269	2_nonsis		1208	1563	1918	2	20	1	1	0	(2:6)_(5:3)_(4:4aCO)
46	TRM3	TRM	4	765553	766047	766973	767007	2_nonsis		927	1190	1453	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
118	TRM3	TRM	10	152343	152475	154973	154996	2_nonsis		2499	2576	2652	3	20	1	1	0	(2:6)_(4:4aCO)_(5:3)_(4:4a)
25	TRM3	TRM	3	239515	240922	242917	243218	2_nonsis		1996	2849	3702	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
139	TRM3	TRM	12	254610	254773	255522	255647	2_nonsis		750	893	1036	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(4:4aCO)
40	TRM3	TRM	4	482050	482676	483837	484026	2_nonsis		1162	1569	1975	3	20	1	1	0	(6:2)_(5:3)_(4:4aCO)_(2:6)_(4:4a)
148	TRM3	TRM	13	79761	79783	82357	83128	2_nonsis		2575	2971	3366	3	20	1	1	0	(5:3)_(4:4)_(2:6)_(3:5)_(4:4aCO)
193	TRM3	TRM	14	743177	743251	744105	744202	2_nonsis		855	940	1024	3	20	1	1	0	(3:5)_(2:6)_(4:4aCO)_(5:3)_(6:2)_(4:4a)
29	TRM3	TRM	4	48046	48241	50436	50586	2_nonsis		2196	2368	2539	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(4:4aCO)_(3:5)_(4:4a)
132	TRM3	TRM	11	368145	368193	370652	370874	2_nonsis		2460	2594	2728	3	20	1	1	0	(3:5)_(4:4)_(2:6)_(4:4aCO)_(5:3)_(4:4a)
200	TRM3	TRM	15	300301	300580	303222	303785	2_nonsis		2643	3063	3483	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(4:4aCO)_(6:2)_(4:4a)
227	TRM3	TRM	16	525308	525445	526860	527307	2_nonsis		1416	1707	1998	3	20	1	1	0	(3:5)_(4:4)_(4:4aCO)_(5:3)_(4:4a)_(6:2)_(4:4a)
188	TRM3	TRM	14	554217	557562	559575	559694	2_nonsis		2014	3745	5476	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(5:3)_(4:4aCO)_(2:6)_(4:4a)
206	TRM3	TRM	15	543780	544647	548227	548302	2_nonsis		3581	4051	4521	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(2:6)_(3:5)_(4:4aCO)
58	TRM3	TRM	4	1315127	1315764	1318378	1318539	2_nonsis		2615	3013	3411	3	20	1	1	0	(3:5)_(6:2)_(4:4aCO)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4a)
231	TRM3	TRM	16	672902	672984	676743	677025	2_nonsis		3760	3941	4122	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(4:4aCO)_(2:6)_(3:5)_(4:4a)
49	TRM3	TRM	4	842636	842982	843857	843908		3	876	1074	1271	0	1	2	0	2	(2:6)_(3:5)_(6:2)_(4:4)_(5:3)_(6:2)_(4:4)
78	TRM3	TRM	7	10242	11635	11635	11737	2_sis		1	748	1494	0	1	2	0	2	(2:6i)_(4:4)
83	TRM3	TRM	7	140227	140416	140416	140631	2_sis		1	202	403	0	1	2	0	2	(2:6i)_(4:4)
114	TRM3	TRM	10	26958	26988	26988	28612	2_sis		1	827	1653	0	1	2	0	2	(6:2i)_(4:4)
156	TRM3	TRM	13	490393	490598	493334	493391	2_sis		2737	2867	2997	0	1	2	0	2	(6:2)_(7:1)_(6:2)_(8:0)_(4:4)_(5:3)_(4:4)_(6:2)_(4:4)
20	TRM3	TRM	2	750883	752417	756267	756533		3	3851	4750	5649	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
23	TRM3	TRM	3	222542	223339	224038	224261		3	700	1209	1718	0	2	2	1	1	(5:3)_(3:5)_(1:7)_(4:4aCO)
34	TRM3	TRM	4	209035	210091	214494	214858		3	4404	5113	5822	0	2	2	1	1	(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4)_(4:4aCO)_(5:3)_(4:4a)
35	TRM3	TRM	4	286258	287699	289475	290079		3	1777	2799	3820	0	2	2	1	1	(4:4aCO)_(3:5)_(4:4a)
59	TRM3	TRM	4	1410669	1411239	1420941	1421204		3	9703	10119	10534	0	2	2	1	1	(6:2)_(6:2a)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
84	TRM3	TRM	7	270688	270975	272144	272568		3	1170	1525	1879	0	2	2	1	1	(3:5)_(4:4ai)_(4:4bCO)
86	TRM3	TRM	7	444932	445067	454910	455013		4	9844	9962	10080	0	2	2	1	1	(5:3)_(4:4)_(5:3)_(4:4)_(2:6)_(3:5)_(2:6)_(4:4ai)_(3:5a)_(3:5b)_(5:3a)_(4:4bi)_(4:4cCO)
166	TRM3	TRM	13	770912	771046	774331	774570		3	3286	3472	3657	0	2	2	1	1	(6:2)_(7:1)_(8:0)_(6:2a)_(4:4aCO)
191	TRM3	TRM	14	640932	641101	641631	641859		3	531	729	926	0	2	2	1	1	(6:2)_(7:1)_(6:2)_(4:4aCO)
221	TRM3	TRM	16	254494	254696	260871	261137		3	6176	6409	6642	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(6:2)_(7:1)_(6:2)_(7:1)_(6:2)_(4:4aCO)
48	TRM3	TRM	4	805798	806142	808094	808170	2_nonsis		1953	2162	2371	0	3	2	0	2	(3:5)_(2:6)_(4:4aCO)_(6:2)_(5:3)_(4:4CO)
68	TRM3	TRM	5	211770	211989	213399	213423		3	1411	1532	1652	0	3	2	1	1	(2:6)_(4:4aCO)_(3:5)_(4:4bCO)
100	TRM3	TRM	8	187989	188673	192694	192776	2_nonsis		4022	4404	4786	0	3	2	0	2	(3:5)_(2:6)_(4:4aCO)_(4:4CO)
107	TRM3	TRM	8	488465	488588	491290	491435	2_nonsis		2703	2836	2969	0	3	2	0	2	(3:5)_(4:4aCO)_(3:5)_(4:4CO)_(2:6)_(4:4)
136	TRM3	TRM	11	606908	608039	608568	608639	2_nonsis		530	1130	1730	0	3	2	0	2	(3:5)_(4:4aCO)_(3:5)_(2:6)_(4:4CO)
138	TRM3	TRM	12	121057	121160	124986	126014		3	3827	4392	4956	0	3	2	1	1	(3:5)_(5:3)_(4:4aCO)_(5:3)_(6:2)_(5:3a)_(6:2)_(5:3a)_(6:2)_(4:4bCO)
161	TRM3	TRM	13	701024	701374	704739	704858	2_nonsis		3366	3600	3833	0	3	2	0	2	(3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(3:5)_(4:4CO)_(3:5)_(4:4)
192	TRM3	TRM	14	650921	650977	652419	652841	2_nonsis		1443	1681	1919	0	3	2	0	2	(3:5)_(4:4aCO)_(3:5)_(4:4CO)_(5:3)_(4:4)
194	TRM3	TRM	15	39607	39768	40593	40834	2_nonsis		826	1026	1226	0	3	2	0	2	(2:6)_(3:5)_(4:4aCO)_(4:4CO)
226	TRM3	TRM	16	461013	461079	464470	464526		3	3392	3452	3512	0	3	2	1	1	(3:5)_(6:2)_(5:3)_(4:4aCO)_(3:5a)_(2:6)_(4:4bCO)_(6:2)_(5:3)_(4:4aCO)
233	TRM3	TRM	16	715017	715923	717952	718160	2_nonsis		2030	2586	3142	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4CO)
235	TRM3	TRM	16	821491	821586	823454	824056	2_nonsis		1869	2217	2564	0	3	2	0	2	(5:3)_(2:6)_(4:4aCO)_(6:2)_(4:4CO)
236	TRM3	TRM	16	912387	912589	914775	915113		3	2187	2456	2725	0	3	2	1	1	(6:2)_(4:4aCO)_(3:5)_(5:3)_(6:2a)_(5:3)_(6:2a)_(4:4bCO)
161	TRM4	TRM	14	728185	728255	728255	728276		1	1	46	90	1	1	1	0	1	05:03
33	TRM4	TRM	4	565654	565705	565705	565786		1	1	66	131	1	1	1	0	1	05:03
56	TRM4	TRM	5	213244	213277	213277	213399		1	1	78	154	1	1	1	0	1	05:03
173	TRM4	TRM	15	670513	670593	670593	670904		1	1	196	390	1	1	1	0	1	05:03
59	TRM4	TRM	5	349434	349710	349715	350100		1	6	336	665	1	1	1	0	1	05:03
64	TRM4	TRM	5	468178	468234	468382	468715		1	149	343	536	1	1	1	0	1	05:03
171	TRM4	TRM	15	579517	580206	580206	580333		1	1	408	815	1	1	1	0	1	05:03
8	TRM4	TRM	2	314330	315082	315082	315271		1	1	471	940	1	1	1	0	1	05:03
34	TRM4	TRM	4	600978	601683	601683	602153		1	1	588	1174	1	1	1	0	1	05:03
84	TRM4	TRM	7	763747	765005	765005	765055		1	1	654	1307	1	1	1	0	1	05:03

182 TRM4	TRM	16	309089	309787	310045	310159	1	259	664	1069	1	1	1	0	1 05:03
98 TRM4	TRM	10	59496	59791	59791	60979	1	1	742	1482	1	1	1	0	1 05:03
190 TRM4	TRM	16	680837	681479	681836	682109	1	358	815	1271	1	1	1	0	1 05:03
96 TRM4	TRM	10	26958	26988	26988	28612	1	1	827	1653	1	1	1	0	1 05:03
113 TRM4	TRM	12	225226	225265	226242	226353	1	978	1052	1126	1	1	1	0	1 05:03
178 TRM4	TRM	15	835187	835656	836419	836747	1	764	1162	1559	1	1	1	0	1 05:03
15 TRM4	TRM	3	102360	102669	103955	104476	1	1287	1701	2115	1	1	1	0	1 05:03
188 TRM4	TRM	16	534581	534749	536429	536720	1	1681	1910	2138	1	1	1	0	1 05:03
175 TRM4	TRM	15	730821	731576	733608	733667	1	2033	2439	2845	1	1	1	0	1 05:03
10 TRM4	TRM	2	503196	503310	503310	503402	1	1	103	205	1	2	1	0	1 03:05
4 TRM4	TRM	2	28614	28912	28912	28960	1	1	173	345	1	2	1	0	1 03:05
86 TRM4	TRM	7	882241	882479	882479	882613	1	1	186	371	1	2	1	0	1 03:05
176 TRM4	TRM	15	745265	745547	745547	745659	1	1	197	393	1	2	1	0	1 03:05
158 TRM4	TRM	14	625573	625861	625861	626122	1	1	275	548	1	2	1	0	1 03:05
36 TRM4	TRM	4	656959	657366	657390	657549	1	25	307	589	1	2	1	0	1 03:05
83 TRM4	TRM	7	676218	676517	676517	676840	1	1	311	621	1	2	1	0	1 03:05
153 TRM4	TRM	14	365847	366158	366158	366581	1	1	367	733	1	2	1	0	1 03:05
44 TRM4	TRM	4	955755	955831	955831	956552	1	1	399	796	1	2	1	0	1 03:05
102 TRM4	TRM	11	21695	21787	21803	22806	1	17	564	1110	1	2	1	0	1 03:05
132 TRM4	TRM	13	245624	246258	246258	246803	1	1	590	1178	1	2	1	0	1 03:05
37 TRM4	TRM	4	801527	802100	802328	802553	1	229	627	1025	1	2	1	0	1 03:05
73 TRM4	TRM	7	10242	11635	11635	11737	1	1	748	1494	1	2	1	0	1 03:05
42 TRM4	TRM	4	929665	930059	930421	930813	1	363	755	1147	1	2	1	0	1 03:05
92 TRM4	TRM	9	53832	54480	55251	55362	1	772	1151	1529	1	2	1	0	1 03:05
160 TRM4	TRM	14	706575	707137	707187	708870	1	51	1173	2294	1	2	1	0	1 03:05
18 TRM4	TRM	3	174943	175328	175328	177291	1	1	1174	2347	1	2	1	0	1 03:05
186 TRM4	TRM	16	504597	505893	506604	507005	1	712	1560	2407	1	2	1	0	1 03:05
104 TRM4	TRM	11	282383	282489	283904	284248	1	1416	1640	1864	1	2	1	0	1 03:05
27 TRM4	TRM	4	103054	103456	105623	105784	1	2168	2449	2729	1	2	1	0	1 03:05
133 TRM4	TRM	13	372583	378680	378680	379214	1	1	3316	6630	1	2	1	0	1 03:05
43 TRM4	TRM	4	934184	934468	935575	935830	1	1108	1377	1645	1	3	1	0	1 5:3_6:2_5:3
156 TRM4	TRM	14	539950	542443	544998	545184	1	2556	3895	5233	1	3	1	0	1 5:3_4:4_5:3
125 TRM4	TRM	12	992002	992572	994078	994177	1	1507	1841	2174	1	3	1	0	1 5:3_4:4_5:3_4:4_5:3
129 TRM4	TRM	13	161385	161406	164021	164304	1	2616	2767	2918	1	3	1	0	1 5:3_6:2_5:3_6:2_5:3
16 TRM4	TRM	3	147587	147882	148481	148587	1	600	800	999	1	4	1	0	1 3:5_4:4_3:5
185 TRM4	TRM	16	423985	424087	424858	425006	1	772	896	1020	1	4	1	0	1 3:5_4:4_3:5
48 TRM4	TRM	4	1293998	1294207	1295100	1295582	1	894	1239	1583	1	4	1	0	1 3:5_4:4_3:5
151 TRM4	TRM	14	261812	262159	263848	263968	1	1690	1923	2155	1	4	1	0	1 3:5_4:4_3:5
193 TRM4	TRM	16	908942	909096	911014	911060	1	1919	2018	2117	1	4	1	0	1 3:5_4:4_3:5
170 TRM4	TRM	15	563779	564207	566373	566430	1	2167	2409	2650	1	4	1	0	1 3:5_4:4_3:5
52 TRM4	TRM	5	18839	18930	23160	23192	1	4231	4292	4352	1	4	1	0	1 3:5_2:6_3:5
110 TRM4	TRM	12	181616	181770	183574	183669	1	1805	1929	2052	1	4	1	0	1 3:5_4:4_3:5_4:4_3:5
24 TRM4	TRM	4	31776	31987	32114	32217	1	128	284	440	1	7	1	0	1 6:2_5:3
180 TRM4	TRM	16	173330	173535	173952	174782	1	418	935	1451	1	7	1	0	1 5:3_6:2
19 TRM4	TRM	3	177969	178367	178453	179122	1	87	620	1152	1	8	1	0	1 3:5_2:6
40 TRM4	TRM	4	860927	861257	861727	862580	1	471	1062	1652	1	8	1	0	1 3:5_2:6
138 TRM4	TRM	13	589690	590250	590865	591615	1	616	1270	1924	1	8	1	0	1 3:5_2:6
23 TRM4	TRM	3	248057	248367	249541	249898	1	1175	1508	1840	1	8	1	0	1 3:5_2:6
38 TRM4	TRM	4	806292	806407	806514	806992	1	108	404	699	1	8	1	0	1 2:6_4:4_2:6
146 TRM4	TRM	14	37986	39122	40430	41146	1	1309	2234	3159	1	8	1	0	1 2:6_3:5_2:6_3:5
111 TRM4	TRM	12	185198	185813	188905	189387	1	3093	3641	4188	1	8	1	0	1 3:5_2:6_3:5_2:6
74 TRM4	TRM	7	21868	21891	21891	21893	1	1	13	24	1	10	1	0	1 06:02
137 TRM4	TRM	13	557365	557409	557409	557425	1	1	30	59	1	10	1	0	1 06:02
148 TRM4	TRM	14	135441	135521	135521	135598	1	1	79	156	1	10	1	0	1 06:02
139 TRM4	TRM	13	610070	610099	610099	610293	1	1	112	222	1	10	1	0	1 06:02
29 TRM4	TRM	4	149839	150172	150172	150223	1	1	192	383	1	10	1	0	1 06:02
130 TRM4	TRM	13	178325	178570	178570	178780	1	1	228	454	1	10	1	0	1 06:02
120 TRM4	TRM	12	722745	722835	722982	723283	1	148	343	537	1	10	1	0	1 06:02
143 TRM4	TRM	13	810832	810963	810963	811653	1	1	411	820	1	10	1	0	1 06:02
53 TRM4	TRM	5	130380	130887	131075	131173	1	189	491	792	1	10	1	0	1 06:02

99	TRM4	TRM	10	159830	160511	160511	160930	1	1	550	1099	1	10	1	0	1	06:02
164	TRM4	TRM	15	252891	253882	253966	253991	1	85	592	1099	1	10	1	0	1	06:02
166	TRM4	TRM	15	285663	286242	286759	286903	1	518	879	1239	1	10	1	0	1	06:02
124	TRM4	TRM	12	952346	952469	953351	953629	1	883	1083	1282	1	10	1	0	1	06:02
135	TRM4	TRM	13	458051	458330	459995	460145	1	1666	1880	2093	1	10	1	0	1	06:02
46	TRM4	TRM	4	1163374	1163376	1163376	1163379	1	1	3	4	1	10.1	1	0	1	02:06
95	TRM4	TRM	9	350021	350025	350025	350044	1	1	12	22	1	10.1	1	0	1	02:06
63	TRM4	TRM	5	456116	456140	456140	456259	1	1	72	142	1	10.1	1	0	1	02:06
90	TRM4	TRM	8	122674	122848	122880	123006	1	33	182	331	1	10.1	1	0	1	02:06
141	TRM4	TRM	13	667202	667456	667511	667766	1	56	310	563	1	10.1	1	0	1	02:06
179	TRM4	TRM	15	943283	943688	943688	944039	1	1	378	755	1	10.1	1	0	1	02:06
183	TRM4	TRM	16	414884	415343	415490	415608	1	148	436	723	1	10.1	1	0	1	02:06
149	TRM4	TRM	14	210033	210155	210617	210679	1	463	554	645	1	10.1	1	0	1	02:06
69	TRM4	TRM	6	76491	76608	77256	77340	1	649	749	848	1	10.1	1	0	1	02:06
155	TRM4	TRM	14	531520	531611	532165	532649	1	555	842	1128	1	10.1	1	0	1	02:06
192	TRM4	TRM	16	833262	833341	834395	834534	1	1055	1163	1271	1	10.1	1	0	1	02:06
101	TRM4	TRM	10	568805	570822	570822	573135	2_nonsis	1	2165	4329	3	30	1	0	1	03:05
134	TRM4	TRM	13	445293	445712	447488	447619	2_nonsis	1777	2051	2325	3	30	1	0	1	3:5_4:4_6:2
50	TRM4	TRM	4	1422082	1422450	1424826	1424907	2_nonsis	2377	2601	2824	3	30	1	0	1	2:6_4:4_6:2
11	TRM4	TRM	2	530065	531256	533611	535193	2_nonsis	2356	3742	5127	3	30	1	0	1	3:5_4:4_6:2
2	TRM4	TRM	1	109735	110856	114824	115629	2_nonsis	3969	4931	5893	3	30	1	0	1	5:3_6:2_5:3
68	TRM4	TRM	6	41152	41461	43673	43907	2_nonsis	2213	2484	2754	3	30	1	0	1	3:5_3:5a_4:4_3:5
163	TRM4	TRM	15	183244	183991	187423	187590	2_nonsis	3433	3889	4345	3	30	1	0	1	3:5_5:3_6:2_5:3a
109	TRM4	TRM	11	641421	641652	643005	643139	2_nonsis	1354	1536	1717	3	30	1	0	1	3:5_3:5a_2:6_3:5a_2:6
172	TRM4	TRM	15	613660	614674	617280	617892	2_nonsis	2607	3419	4231	3	30	1	0	1	5:3_3:5_2:6_3:5a_4:4_2:6
107	TRM4	TRM	11	580815	581385	584769	584944	2_nonsis	3385	3757	4128	3	30	1	0	1	3:5_2:6_3:5_4:4_3:5_4:4_6:2_5:3
108	TRM4	TRM	11	586366	586587	586587	586747	2_nonsis	1	191	380	3	31	1	0	1	4:4ai
49	TRM4	TRM	4	1310837	1311566	1314589	1315113	2_nonsis	3024	3650	4275	3	31	1	0	1	5:3_6:2_5:3a_4:4ai_5:3
78	TRM4	TRM	7	428022	428152	428152	428325	2_nonsis	1	152	302	1	1	1	1	0	(5:3)_(4:4aCO)
80	TRM4	TRM	7	597592	598397	598397	598538	2_nonsis	1	473	945	1	1	1	1	0	(5:3)_(4:4aCO)
123	TRM4	TRM	12	873300	874112	875066	875233	2_nonsis	955	1444	1932	1	1	1	1	0	(5:3)_(4:4aCO)
114	TRM4	TRM	12	337082	338130	339496	340008	2_nonsis	1367	2146	2925	1	1	1	1	0	(5:3)_(4:4aCO)
79	TRM4	TRM	7	431867	432076	432076	432412	2_nonsis	1	273	544	1	2	1	1	0	(3:5)_(4:4aCO)
103	TRM4	TRM	11	243838	244481	244570	245116	2_nonsis	90	684	1277	1	2	1	1	0	(3:5)_(4:4aCO)
13	TRM4	TRM	2	662444	666708	666712	666849	2_nonsis	5	2205	4404	1	2	1	1	0	(3:5)_(4:4aCO)
162	TRM4	TRM	14	748773	748858	750473	750670	2_nonsis	1616	1756	1896	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
128	TRM4	TRM	13	82027	82207	85849	85889	2_nonsis	3643	3752	3861	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
7	TRM4	TRM	2	257565	258058	258153	258313	2_nonsis	96	422	747	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
117	TRM4	TRM	12	535963	536152	538497	539092	2_nonsis	2346	2737	3128	1	11	1	1	0	(4:4ai)_(2:6)_(3:5)_(2:6)_(4:4)_(2:6)_(3:5)_(2:6)_(4:4bCO)
12	TRM4	TRM	2	564041	564884	565133	565189	2_nonsis	250	699	1147	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
87	TRM4	TRM	7	902661	903030	904567	904780	2_nonsis	1538	1828	2118	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
76	TRM4	TRM	7	209130	209279	210194	210401	2_nonsis	916	1093	1270	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)
184	TRM4	TRM	16	417099	417454	418435	418963	2_nonsis	982	1423	1863	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
136	TRM4	TRM	13	493832	494083	495559	495665	2_nonsis	1477	1655	1832	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)
9	TRM4	TRM	2	447420	447949	449416	449588	2_nonsis	1468	1818	2167	1	12	1	1	0	(3:5)_(4:4aCO)_(2:6)_(4:4a)
3	TRM4	TRM	1	135325	136910	138499	138650	2_nonsis	1590	2457	3324	1	12	1	1	0	(5:3)_(4:4aCO)_(5:3)_(4:4a)
118	TRM4	TRM	12	555957	555993	557420	558341	2_nonsis	1428	1906	2383	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(4:4aCO)
152	TRM4	TRM	14	337051	337646	339555	340266	2_nonsis	1910	2562	3214	1	12	1	1	0	(2:6)_(4:4)_(3:5)_(2:6)_(4:4aCO)
142	TRM4	TRM	13	751553	751891	754263	754594	2_nonsis	2373	2707	3040	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)_(3:5)_(4:4a)
189	TRM4	TRM	16	599131	599378	602439	603262	2_nonsis	3062	3596	4130	1	12	1	1	0	(3:5)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
14	TRM4	TRM	2	736946	737232	740518	740972	2_nonsis	3287	3656	4025	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(4:4aCO)
105	TRM4	TRM	11	354308	355025	359854	360238	2_nonsis	4830	5380	5929	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)_(3:5)_(4:4a)
127	TRM4	TRM	13	26922	28623	31154	31858	2_nonsis	2532	3734	4935	1	12	1	1	0	(4:4aCO)_(5:3)_(4:4a)_(6:2)_(5:3)_(4:4a)
20	TRM4	TRM	3	184706	185221	190177	191932	2_nonsis	4957	6091	7225	1	12	1	1	0	(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
169	TRM4	TRM	15	493264	493331	496482	496659	2_nonsis	3152	3273	3394	1	12	1	1	0	(6:2)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)
91	TRM4	TRM	9	36872	36921	36921	36971	2_nonsis	1	50	98	1	15	1	1	0	(6:2)_(4:4aCO)
51	TRM4	TRM	4	1506604	1506887	1506887	1506970	2_nonsis	1	183	365	1	15	1	1	0	(6:2)_(4:4aCO)
26	TRM4	TRM	4	50767	51098	51199	51817	2_nonsis	102	576	1049	1	15	1	1	0	(6:2)_(4:4aCO)
22	TRM4	TRM	3	236387	236702	236946	238082	2_nonsis	245	970	1694	1	15	1	1	0	(6:2)_(4:4aCO)
194	TRM4	TRM	16	922942	923175	924130	924152	2_nonsis	956	1083	1209	1	15	1	1	0	(6:2)_(4:4aCO)

150	TRM4	TRM	14	216026	216647	216919	218712	2_nonsis		273	1479	2685	1	15	1	1	0	(6:2)_(4:4aCO)
167	TRM4	TRM	15	348389	348459	348459	348630	2_nonsis		1	121	240	1	16	1	1	0	(2:6)_(4:4aCO)
147	TRM4	TRM	14	109383	109413	109533	109626	2_nonsis		121	182	242	1	16	1	1	0	(2:6)_(4:4aCO)
77	TRM4	TRM	7	355193	355292	355292	356141	2_nonsis		1	474	947	1	16	1	1	0	(2:6)_(4:4aCO)
41	TRM4	TRM	4	926737	927283	927438	927608	2_nonsis		156	513	870	1	16	1	1	0	(2:6)_(4:4aCO)
60	TRM4	TRM	5	377471	377999	378297	378395	2_nonsis		299	611	923	1	16	1	1	0	(2:6)_(4:4aCO)
116	TRM4	TRM	12	512877	513766	513766	514165	2_nonsis		1	644	1287	1	16	1	1	0	(2:6)_(4:4aCO)
32	TRM4	TRM	4	547907	548255	548909	549184	2_nonsis		655	966	1276	1	16	1	1	0	(2:6)_(4:4aCO)
97	TRM4	TRM	10	36445	36722	36445	36722	2_nonsis		0	138	276	1	100	1	1	0	(4:4aCO)
126	TRM4	TRM	12	1015108	1015543	1015108	1015543	2_nonsis		0	217	434	1	100	1	1	0	(4:4aCO)
121	TRM4	TRM	12	724901	725366	724901	725366	2_nonsis		0	232	464	1	100	1	1	0	(4:4aCO)
54	TRM4	TRM	5	133686	134157	133686	134157	2_nonsis		0	235	470	1	100	1	1	0	(4:4aCO)
88	TRM4	TRM	7	1011510	1012069	1011510	1012069	2_nonsis		0	279	558	1	100	1	1	0	(4:4aCO)
55	TRM4	TRM	5	166218	166839	166218	166839	2_nonsis		0	310	620	1	100	1	1	0	(4:4aCO)
119	TRM4	TRM	12	627543	628215	627543	628215	2_nonsis		0	336	671	1	100	1	1	0	(4:4aCO)
61	TRM4	TRM	5	380871	381575	380871	381575	2_nonsis		0	352	703	1	100	1	1	0	(4:4aCO)
47	TRM4	TRM	4	1268647	1269918	1268647	1269918	2_nonsis		0	635	1270	1	100	1	1	0	(4:4aCO)
94	TRM4	TRM	9	320712	323343	320712	323343	2_nonsis		0	1315	2630	1	100	1	1	0	(4:4aCO)
25	TRM4	TRM	4	43482	46115	43482	46115	2_nonsis		0	1316	2632	1	100	1	1	0	(4:4aCO)
17	TRM4	TRM	3	171207	174943	171207	174943	2_nonsis		0	1868	3735	1	100	1	1	0	(4:4aCO)
159	TRM4	TRM	14	682580	686654	682580	686654	2_nonsis		0	2037	4073	1	100	1	1	0	(4:4aCO)
145	TRM4	TRM	14	23552	23618	26602	27918	2_nonsis		2985	3675	4365	2	30	1	1	0	(5:3)_(5:3a)_(4:4aCO)
82	TRM4	TRM	7	625479	625898	628498	628553	2_nonsis		2601	2837	3073	2	31	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(3:5)_(3:5a)_(4:4aCO)
106	TRM4	TRM	11	399930	399948	403407	403558	2_nonsis		3460	3544	3627	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4aCO)
191	TRM4	TRM	16	784177	784693	785910	786015	2_nonsis		1218	1528	1837	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(2:6)_(4:4aCO)
28	TRM4	TRM	4	119010	120812	123436	124765	2_nonsis		2625	4190	5754	2	32	1	1	0	(4:4ai)_(5:3)_(6:2)_(5:3a)_(5:3)_(4:4bCO)
181	TRM4	TRM	16	285465	286085	288762	289053	2_nonsis		2678	3133	3587	2	32	1	1	0	(5:3)_(6:2)_(4:4)_(5:3)_(4:4)_(5:3)_(6:2)_(5:3a)_(4:4aCO)
35	TRM4	TRM	4	604439	604670	608921	609170	2_nonsis		4252	4491	4730	2	32	1	1	0	(5:3)_(6:2)_(4:4aCO)_(5:3a)_(4:4a)_(5:3a)_(4:4a)_(5:3a)_(4:4a)
100	TRM4	TRM	10	411632	412419	414104	414830	2_nonsis		1686	2442	3197	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
144	TRM4	TRM	13	841022	841302	841704	841879	2_nonsis		403	630	856	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
140	TRM4	TRM	13	646440	646658	647871	648168	2_nonsis		1214	1471	1727	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(4:4aCO)
168	TRM4	TRM	15	459052	459568	463406	463444	2_nonsis		3839	4115	4391	3	20	1	1	0	(5:3)_(2:6)_(3:5)_(4:4aCO)
154	TRM4	TRM	14	517494	517634	518602	518686	2_nonsis		969	1080	1191	3	20	1	1	0	(3:5)_(2:6)_(6:2)_(4:4aCO)
45	TRM4	TRM	4	1126843	1126921	1128108	1128135	2_nonsis		1188	1240	1291	3	20	1	1	0	(5:3)_(6:2)_(2:6)_(4:4aCO)_(3:5)_(4:4a)
58	TRM4	TRM	5	248412	248522	251006	251267	2_nonsis		2485	2670	2854	3	20	1	1	0	(2:6)_(3:5)_(2:6)_(4:4aCO)_(6:2)_(4:4a)
1	TRM4	TRM	1	74786	75211	77737	78187	2_nonsis		2527	2964	3400	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(4:4)_(2:6)_(4:4aCO)
39	TRM4	TRM	4	847587	847735	851927	852118	2_nonsis		4193	4362	4530	3	20	1	1	0	(6:2)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(4:4a)
187	TRM4	TRM	16	520194	520400	524220	524743	2_nonsis		3821	4185	4548	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(4:4)_(5:3)_(4:4aCO)_(6:2)_(4:4a)
85	TRM4	TRM	7	796586	796791	801373	801844	2_nonsis		4583	4920	5257	3	20	1	1	0	(2:6)_(4:4)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(4:4aCO)
131	TRM4	TRM	13	196231	202482	210922	211049	2_nonsis		8441	11629	14817	3	20	1	1	0	(5:3)_(6:2)_(5:3)_(4:4)_(5:3)_(3:5)_(2:6)_(4:4aCO)_(3:5)_(4:4a)
93	TRM4	TRM	9	168511	169256	173732	174345	2_nonsis		4477	5155	5833	3	20	1	1	0	(3:5)_(2:6)_(4:4)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4)_(6:2)_(4:4aCO)_(5:3)_(4:4a)
174	TRM4	TRM	15	700551	700804	703419	710553	2_nonsis		2616	6309	10001	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(6:2)_(4:4a)
65	TRM4	TRM	5	473950	474031	475154	475295	2_nonsis		1124	1234	1344	3	21	1	1	0	(2:6)_(4:4ai)_(5:3)_(4:4bCO)
5	TRM4	TRM	2	72420	73226	79837	80052	2_nonsis		6612	7122	7631	3	21	1	1	0	(4:4aCO)_(3:5)_(3:5a)_(3:5)_(4:4bi)_(5:3)_(3:5a)_(4:4bi)_(3:5)_(4:4bi)_(6:2)_(4:4a)
21	TRM4	TRM	3	233678	233789	233870	233910	2_sis		1	116	231	0	1	2	0	2	(6:2i)_(4:4)
70	TRM4	TRM	6	203253	203623	204894	204909	2_sis		1272	1464	1655	0	1	2	0	2	(3:5)_(3:5a)_(2:6)_(3:5a)_(4:4)
75	TRM4	TRM	7	140227	140416	140416	140631	2_sis		1	202	403	0	1	2	0	2	(2:6i)_(4:4)
81	TRM4	TRM	7	611510	611515	611515	612267	2_sis		1	379	756	0	1	2	0	2	(6:2i)_(4:4)
115	TRM4	TRM	12	507075	507492	507531	508649		4	40	807	1573	0	1	2	0	2	(3:5)_(6:2i)_(4:4)
157	TRM4	TRM	14	552259	552403	554217	557562	2_sis		1815	3559	5302	0	1	2	0	2	(6:2)_(5:3)_(5:3a)_(4:4)
165	TRM4	TRM	15	260677	260759	260759	260837	2_sis		1	80	159	0	1	2	0	2	(2:6i)_(4:4)
6	TRM4	TRM	2	82087	82573	87833	88022		4	5261	5598	5934	0	2	2	2	0	(5:3)_(3:5)_(3:5a)_(4:4ai)_(3:5a)_(4:4bi)_(3:5b)_(4:4bi)_(5:3a)_(6:2)_(5:3a)_(4:4cCO)
30	TRM4	TRM	4	167048	167295	167826	169331	2_nonsis		532	1407	2282	0	3	2	0	2	(6:2)_(2:6)_(4:4aCO)_(4:CO)
31	TRM4	TRM	4	368620	368735	374909	375032		3	6175	6293	6411	0	3	2	1	1	(5:3)_(4:4aCO)_(2:6)_(3:5)_(5:3a)_(6:2)_(5:3a)_(4:4bCO)
57	TRM4	TRM	5	236202	236672	238122	238396		3	1451	1822	2193	0	3	2	1	1	(3:5)_(4:4aCO)_(2:6)_(3:5a)_(4:4bCO)
62	TRM4	TRM	5	406935	407141	410947	411277	2_nonsis		3807	4074	4341	0	3	2	0	2	(6:2)_(5:3)_(3:5)_(2:6)_(4:4aCO)_(4:CO)
66	TRM4	TRM	5	489897	490102	492329	492341		3	2228	2336	2443	0	3	2	1	1	(2:6)_(3:5)_(4:4aCO)_(2:6)_(3:5a)_(4:4bCO)_(3:5a)_(5:3)_(4:4b)
71	TRM4	TRM	6	211652	211974	214843	215586	2_nonsis		2870	3402	3933	0	3	2	0	2	(4:4aCO)_(3:5)_(4:4CO)_(3:5)_(5:3)_(3:5)_(4:4aCO)
72	TRM4	TRM	6	254081	254393	255483	255612	2_nonsis		1091	1311	1530	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2)_(4:CO)_(2:6)_(4:4)
89	TRM4	TRM	8	37944	38190	39721	39931	2_nonsis		1532	1759	1986	0	3	2	0	2	(5:3)_(4:4aCO)_(6:2)_(4:CO)_(5:3)_(4:4)

id	group		n	n1	n2	n3	n4	type	x	a	b	c	d	e	f	g	h	annotation
112	TRM4	TRM	12	190951	192023	194811	195201	2_nonsis		2789	3519	4249	0	3	2	0	2	(4:4aCO)_(6:2)_(5:3)_(4:4CO)_(5:3)_(4:4)
122	TRM4	TRM	12	837595	837962	840682	843387	2_nonsis		2721	4256	5791	0	3	2	0	2	(4:4aCO)_(5:3)_(4:4CO)
177	TRM4	TRM	15	802784	803471	805899	806960		3	2429	3302	4175	0	3	2	1	1	(4:4aCO)_(2:6)_(4:4bCO)
301	TRM4	TRM	10	724397	724519	726314	745751	NA		1796	11575	21353	0	4	1	NA	NA	2:6_4:4_3:5_1:7
126	TRM5	TRM	12	1042365	1042381	1042381	1042503	1		1	69	137	1	1	1	0	1	05:03
23	TRM5	TRM	3	233678	233870	233870	233910	1		1	116	231	1	1	1	0	1	05:03
40	TRM5	TRM	4	856001	856201	856201	856278	1		1	139	276	1	1	1	0	1	05:03
3	TRM5	TRM	1	101193	101198	101198	101547	1		1	177	353	1	1	1	0	1	05:03
68	TRM5	TRM	7	11635	11737	11737	12020	1		1	193	384	1	1	1	0	1	05:03
1	TRM5	TRM	1	60915	61084	61164	61414	1		81	290	498	1	1	1	0	1	05:03
180	TRM5	TRM	16	829386	829418	829418	830004	1		1	309	617	1	1	1	0	1	05:03
42	TRM5	TRM	4	928114	928279	928279	928753	1		1	320	638	1	1	1	0	1	05:03
32	TRM5	TRM	4	423912	424131	424226	424517	1		96	350	604	1	1	1	0	1	05:03
91	TRM5	TRM	10	315888	316551	316551	316590	1		1	351	701	1	1	1	0	1	05:03
98	TRM5	TRM	10	658094	658862	658862	658912	1		1	409	817	1	1	1	0	1	05:03
89	TRM5	TRM	10	278226	278337	278411	279038	1		75	443	811	1	1	1	0	1	05:03
43	TRM5	TRM	4	931013	931142	931376	931988	1		235	605	974	1	1	1	0	1	05:03
64	TRM5	TRM	6	44192	44668	45006	45201	1		339	674	1008	1	1	1	0	1	05:03
160	TRM5	TRM	15	427406	427719	427719	428753	1		1	674	1346	1	1	1	0	1	05:03
29	TRM5	TRM	4	264290	265338	265749	265807	1		412	964	1516	1	1	1	0	1	05:03
146	TRM5	TRM	14	477388	478186	478186	479345	1		1	979	1956	1	1	1	0	1	05:03
27	TRM5	TRM	4	127476	129270	129783	130517	1		514	1777	3040	1	1	1	0	1	05:03
70	TRM5	TRM	7	218950	218961	218961	219113	1		1	82	162	1	2	1	0	1	03:05
105	TRM5	TRM	11	464192	464453	464453	464456	1		1	132	263	1	2	1	0	1	03:05
111	TRM5	TRM	12	84153	84378	84378	84504	1		1	176	350	1	2	1	0	1	03:05
104	TRM5	TRM	11	358089	358323	358323	358455	1		1	183	365	1	2	1	0	1	03:05
149	TRM5	TRM	14	592518	592909	592909	593099	1		1	291	580	1	2	1	0	1	03:05
36	TRM5	TRM	4	653323	653336	653336	653906	1		1	292	582	1	2	1	0	1	03:05
51	TRM5	TRM	5	68798	68910	69083	69209	1		174	292	410	1	2	1	0	1	03:05
138	TRM5	TRM	14	86730	87215	87215	87864	1		1	567	1133	1	2	1	0	1	03:05
100	TRM5	TRM	11	261949	262136	262641	263151	1		506	854	1201	1	2	1	0	1	03:05
166	TRM5	TRM	15	690980	691843	692888	693526	1		1046	1796	2545	1	2	1	0	1	03:05
128	TRM5	TRM	13	103361	104510	105409	106249	1		900	1894	2887	1	2	1	0	1	03:05
102	TRM5	TRM	11	316845	317019	317375	317549	1		357	530	703	1	4	1	0	1	3:5_4:4_3:5
159	TRM5	TRM	15	422652	423321	423598	424102	1		278	864	1449	1	4	1	0	1	3:5_4:4_3:5
49	TRM5	TRM	4	1165728	1165878	1169278	1169426	1		3401	3549	3697	1	4	1	0	1	3:5_4:4_2:6_4:4_3:5_4:4_3:5_2:6_3:5_4:4_2:6_3:5_4:4_3:5
88	TRM5	TRM	10	176002	176039	180354	180756	1		4316	4535	4753	1	7	1	0	1	5:3_6:2
38	TRM5	TRM	4	795372	795537	800984	801463	1		5448	5769	6090	1	7	1	0	1	6:2_4:4_6:2_4:4_6:2
115	TRM5	TRM	12	401097	401327	402030	402353	1		704	980	1255	1	8	1	0	1	3:5_2:6
87	TRM5	TRM	10	108954	109360	109926	110584	1		567	1098	1629	1	8	1	0	1	3:5_2:6
123	TRM5	TRM	12	836343	837497	837595	840577	1		99	2166	4233	1	8	1	0	1	2:6_3:5
92	TRM5	TRM	10	360767	360976	361340	362386	1		365	992	1618	1	8	1	0	1	3:5_2:6_3:5_2:6
119	TRM5	TRM	12	514243	514581	519358	520183	1		4778	5359	5939	1	8	1	0	1	3:5_2:6_3:5_2:6
117	TRM5	TRM	12	407016	407206	408486	408647	1		1281	1456	1630	1	8	1	0	1	2:6_4:4_3:5_4:4_2:6_3:5
110	TRM5	TRM	11	623830	624124	627471	628158	1		3348	3838	4327	1	8	1	0	1	3:5_4:4_2:6_3:5_2:6_3:5_4:4_2:6
136	TRM5	TRM	13	759082	759285	759298	759350	1		14	141	267	1	10	1	0	1	06:02
173	TRM5	TRM	16	299735	299834	299834	300071	1		1	168	335	1	10	1	0	1	06:02
151	TRM5	TRM	14	646157	646249	646249	646547	1		1	195	389	1	10	1	0	1	06:02
165	TRM5	TRM	15	571945	572030	572030	572407	1		1	231	461	1	10	1	0	1	06:02
150	TRM5	TRM	14	640393	640431	640431	640932	1		1	270	538	1	10	1	0	1	06:02
8	TRM5	TRM	2	150200	150465	150492	151397	1		28	612	1196	1	10	1	0	1	06:02
45	TRM5	TRM	4	1061634	1061961	1062037	1062818	1		77	630	1183	1	10	1	0	1	06:02
157	TRM5	TRM	15	287386	288164	288307	288781	1		144	769	1394	1	10	1	0	1	06:02
11	TRM5	TRM	2	371139	371446	371746	372547	1		301	854	1407	1	10	1	0	1	06:02
82	TRM5	TRM	9	247495	247508	247508	247526	1		1	16	30	1	10.1	1	0	1	02:06
114	TRM5	TRM	12	252779	252873	252873	252898	1		1	60	118	1	10.1	1	0	1	02:06
21	TRM5	TRM	3	208072	208091	208091	208234	1		1	81	161	1	10.1	1	0	1	02:06
78	TRM5	TRM	8	66280	66557	66557	66569	1		1	145	288	1	10.1	1	0	1	02:06
16	TRM5	TRM	2	723102	723175	723232	723385	1		58	170	282	1	10.1	1	0	1	02:06
133	TRM5	TRM	13	510245	510365	510379	510599	1		15	184	353	1	10.1	1	0	1	02:06

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18
163	TRM5	TRM	15	511101	511376	511443	511466	1	68	216	364	1	10.1	1	0	1	02:06
52	TRM5	TRM	5	70531	70852	70852	70969	1	1	219	437	1	10.1	1	0	1	02:06
44	TRM5	TRM	4	1011430	1011449	1011449	1011936	1	1	253	505	1	10.1	1	0	1	02:06
135	TRM5	TRM	13	701024	701244	701374	701606	1	131	356	581	1	10.1	1	0	1	02:06
83	TRM5	TRM	9	273547	273624	273888	274009	1	265	363	461	1	10.1	1	0	1	02:06
24	TRM5	TRM	4	19746	19880	20223	20376	1	344	487	629	1	10.1	1	0	1	02:06
55	TRM5	TRM	5	123378	123491	123734	124202	1	244	534	823	1	10.1	1	0	1	02:06
152	TRM5	TRM	14	701567	701618	701618	702991	1	1	712	1423	1	10.1	1	0	1	02:06
108	TRM5	TRM	11	604059	604356	604404	605465	1	49	727	1405	1	10.1	1	0	1	02:06
35	TRM5	TRM	4	629725	630640	630640	631576	1	1	926	1850	1	10.1	1	0	1	02:06
20	TRM5	TRM	3	76973	77505	77900	78705	1	396	1064	1731	1	10.1	1	0	1	02:06
28	TRM5	TRM	4	261620	261828	262808	263012	2_nonsis	981	1186	1391	3	30	1	0	1	5:3_3:5
107	TRM5	TRM	11	597543	597866	600536	601065	2_nonsis	2671	3096	3521	3	30	1	0	1	3:5_2:6_5:3
69	TRM5	TRM	7	188960	189229	191348	192332	2_nonsis	2120	2746	3371	3	30	1	0	1	5:3_6:2_4:4_3:5
96	TRM5	TRM	10	587243	587401	590704	591944	2_nonsis	3304	4002	4700	3	30	1	0	1	3:5_3:5a_4:4_3:5
46	TRM5	TRM	4	1090817	1091087	1095230	1095364	2_nonsis	4144	4345	4546	3	30	1	0	1	3:5_4:4_5:3_6:2_5:3_4:4_5:3
112	TRM5	TRM	12	105323	106427	110610	110807	2_nonsis	4184	4834	5483	3	30	1	0	1	3:5_4:4_3:5_4:4_3:5_4:4_5:3_6:2_4:4_6:2
116	TRM5	TRM	12	403568	404007	404007	404478	2_nonsis	1	455	909	3	31	1	0	1	4:4ai
6	TRM5	TRM	2	77328	77577	77699	77714	2_nonsis	123	254	385	1	1	1	1	0	(5:3)_(4:4aCO)
53	TRM5	TRM	5	73006	73131	73131	74196	2_nonsis	1	595	1189	1	1	1	1	0	(5:3)_(4:4aCO)
56	TRM5	TRM	5	222592	222851	222851	222941	2_nonsis	1	175	348	1	2	1	1	0	(3:5)_(4:4aCO)
154	TRM5	TRM	15	198772	199130	199186	199433	2_nonsis	57	359	660	1	2	1	1	0	(3:5)_(4:4aCO)
15	TRM5	TRM	2	620443	620548	620548	621285	2_nonsis	1	421	841	1	2	1	1	0	(3:5)_(4:4aCO)
141	TRM5	TRM	14	171927	173272	173725	173830	2_nonsis	454	1178	1902	1	2	1	1	0	(3:5)_(4:4aCO)
85	TRM5	TRM	9	339115	339305	340858	341514	2_nonsis	1554	1976	2398	1	5	1	1	0	(3:5)_(4:4)_(4:4aCO)
18	TRM5	TRM	3	38318	38619	39706	39861	2_nonsis	1088	1315	1542	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
14	TRM5	TRM	2	501201	501490	501753	501897	2_nonsis	264	480	695	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
25	TRM5	TRM	4	28578	28798	30128	30404	2_nonsis	1331	1578	1825	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
145	TRM5	TRM	14	388136	388819	389671	391590	2_nonsis	853	2153	3453	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
57	TRM5	TRM	5	229778	230208	232802	232869	2_nonsis	2595	2843	3090	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
30	TRM5	TRM	4	311476	311602	311890	312042	2_nonsis	289	427	565	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
34	TRM5	TRM	4	616750	616883	617276	617367	2_nonsis	394	505	616	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
170	TRM5	TRM	15	929212	929593	930131	930244	2_nonsis	539	785	1031	1	9	1	1	0	(3:5)_(2:6)_(4:4aCO)
47	TRM5	TRM	4	1111885	1111980	1113224	1113566	2_nonsis	1245	1463	1680	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
169	TRM5	TRM	15	799553	800155	802489	802784	2_nonsis	2335	2783	3230	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
147	TRM5	TRM	14	516484	516536	519077	525141	2_nonsis	2542	5599	8656	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
158	TRM5	TRM	15	408436	408540	408540	410228	2_nonsis	1689	1764	1839	1	11	1	1	0	(6:2)_(4:4)_(5:3)_(4:4ai)_(4:4bCO)
12	TRM5	TRM	2	390744	391464	391731	392022	2_nonsis	268	773	1277	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
77	TRM5	TRM	7	914816	915939	916953	917004	2_nonsis	1015	1601	2187	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
172	TRM5	TRM	16	171729	171822	173054	173921	2_nonsis	1233	1712	2191	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
71	TRM5	TRM	7	351287	351684	352895	352964	2_nonsis	1212	1444	1676	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
59	TRM5	TRM	5	335687	335874	337830	337863	2_nonsis	1957	2066	2175	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
177	TRM5	TRM	16	669691	670096	672902	672984	2_nonsis	2807	3050	3292	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
129	TRM5	TRM	13	140757	140935	143613	144479	2_nonsis	2679	3200	3721	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4aCO)
66	TRM5	TRM	6	198468	199207	201959	202421	2_nonsis	2753	3353	3952	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
140	TRM5	TRM	14	116678	116796	121108	121220	2_nonsis	4313	4427	4541	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
139	TRM5	TRM	14	105047	105280	106177	106295	2_nonsis	898	1073	1247	1	12	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
171	TRM5	TRM	15	976799	976981	977995	978236	2_nonsis	1015	1226	1436	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
61	TRM5	TRM	5	465974	466823	468715	468771	2_nonsis	1893	2345	2796	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
39	TRM5	TRM	4	802711	805658	806992	807121	2_nonsis	1335	2872	4409	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
121	TRM5	TRM	12	747529	747710	751142	751398	2_nonsis	3433	3651	3868	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(3:5)_(4:4aCO)
80	TRM5	TRM	9	102480	102536	105213	105556	2_nonsis	2678	2877	3075	1	12	1	1	0	(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(4:4aCO)
132	TRM5	TRM	13	483557	485052	487393	487573	2_nonsis	2342	3179	4015	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)
10	TRM5	TRM	2	337090	337453	341451	341632	2_nonsis	3999	4270	4541	1	12	1	1	0	(3:5)_(4:4aCO)_(3:5)_(4:4a)_(2:6)_(4:4a)
75	TRM5	TRM	7	806907	807474	809973	810159	2_nonsis	2500	2876	3251	1	12	1	1	0	(6:2)_(4:4aCO)_(5:3)_(4:4a)_(5:3)_(6:2)_(4:4a)
76	TRM5	TRM	7	902661	903061	905084	905104	2_nonsis	2024	2233	2442	1	12	1	1	0	(3:5)_(2:6)_(4:4aCO)_(3:5)_(2:6)_(3:5)_(4:4a)_(3:5)_(2:6)_(5:3)_(4:4a)
63	TRM5	TRM	6	22425	22527	28662	28792	2_nonsis	6136	6251	6366	1	12	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(3:5)_(4:4)_(3:5)_(4:4)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4aCO)
37	TRM5	TRM	4	655090	655473	655473	655491	2_nonsis	1	201	400	1	15	1	1	0	(6:2)_(4:4aCO)
13	TRM5	TRM	2	436236	436888	436905	437154	2_nonsis	18	468	917	1	15	1	1	0	(6:2)_(4:4aCO)
155	TRM5	TRM	15	216499	217333	217521	218142	2_nonsis	189	916	1642	1	15	1	1	0	(6:2)_(4:4aCO)

33	TRM5	TRM	4	507535	507634	508191	508845	2_nonsis		558	934	1309	1	15	1	1	0	(6:2)_(4:4aCO)
99	TRM5	TRM	10	699696	699851	700864	701827	2_nonsis		1014	1572	2130	1	15	1	1	0	(6:2)_(4:4aCO)
103	TRM5	TRM	11	320103	320335	320400	320565	2_nonsis		66	264	461	1	16	1	1	0	(2:6)_(4:4aCO)
120	TRM5	TRM	12	568653	568917	568917	569539	2_nonsis		1	443	885	1	16	1	1	0	(2:6)_(4:4aCO)
9	TRM5	TRM	2	189223	190032	190032	190128	2_nonsis		1	453	904	1	16	1	1	0	(2:6)_(4:4aCO)
19	TRM5	TRM	3	74577	75202	75202	75484	2_nonsis		1	454	906	1	16	1	1	0	(2:6)_(4:4aCO)
72	TRM5	TRM	7	462199	462937	462984	463064	2_nonsis		48	456	864	1	16	1	1	0	(2:6)_(4:4aCO)
31	TRM5	TRM	4	370634	370756	371085	371249	2_nonsis		330	472	614	1	16	1	1	0	(2:6)_(4:4aCO)
144	TRM5	TRM	14	368045	368183	368391	368877	2_nonsis		209	520	831	1	16	1	1	0	(2:6)_(4:4aCO)
153	TRM5	TRM	15	181640	182622	182626	182727	2_nonsis		5	546	1086	1	16	1	1	0	(2:6)_(4:4aCO)
174	TRM5	TRM	16	374857	375235	375235	376113	2_nonsis		1	628	1255	1	16	1	1	0	(2:6)_(4:4aCO)
167	TRM5	TRM	15	716400	716849	717433	717703	2_nonsis		585	944	1302	1	16	1	1	0	(2:6)_(4:4aCO)
109	TRM5	TRM	11	618845	619007	620085	620113	2_nonsis		1079	1173	1267	1	16	1	1	0	(2:6)_(4:4aCO)
131	TRM5	TRM	13	234542	235023	235798	236240	2_nonsis		776	1237	1697	1	16	1	1	0	(2:6)_(4:4aCO)
73	TRM5	TRM	7	546929	547580	548503	549148	2_nonsis		924	1571	2218	1	16	1	1	0	(2:6)_(4:4aCO)
95	TRM5	TRM	10	504158	506424	507301	508327	2_nonsis		878	2523	4168	1	16	1	1	0	(2:6)_(4:4aCO)
65	TRM5	TRM	6	78202	78667	78202	78667	2_nonsis		0	232	464	1	100	1	1	0	(4:4aCO)
162	TRM5	TRM	15	507308	507811	507308	507811	2_nonsis		0	251	502	1	100	1	1	0	(4:4aCO)
93	TRM5	TRM	10	363087	363678	363087	363678	2_nonsis		0	295	590	1	100	1	1	0	(4:4aCO)
137	TRM5	TRM	13	862092	862695	862092	862695	2_nonsis		0	301	602	1	100	1	1	0	(4:4aCO)
164	TRM5	TRM	15	569110	569770	569110	569770	2_nonsis		0	330	659	1	100	1	1	0	(4:4aCO)
54	TRM5	TRM	5	121371	122148	121371	122148	2_nonsis		0	388	776	1	100	1	1	0	(4:4aCO)
130	TRM5	TRM	13	227027	227957	227027	227957	2_nonsis		0	465	929	1	100	1	1	0	(4:4aCO)
41	TRM5	TRM	4	894075	895202	894075	895202	2_nonsis		0	563	1126	1	100	1	1	0	(4:4aCO)
7	TRM5	TRM	2	90715	92062	90715	92062	2_nonsis		0	673	1346	1	100	1	1	0	(4:4aCO)
84	TRM5	TRM	9	299287	302738	299287	302738	2_nonsis		0	1725	3450	1	100	1	1	0	(4:4aCO)
79	TRM5	TRM	9	82237	82538	84138	85680	2_nonsis		1601	2522	3442	2	30	1	1	0	(5:3)_(5:3a)_(5:3)_(5:3a)_(4:4aCO)
125	TRM5	TRM	12	998854	999870	1002952	1003093	2_nonsis		3083	3661	4238	2	30	1	1	0	(5:3)_(4:4)_(5:3)_(5:3a)_(4:4aCO)
124	TRM5	TRM	12	849651	854846	857849	859351	2_nonsis		3004	6352	9699	2	32	1	1	0	(5:3)_(4:4)_(5:3a)_(4:4aCO)
179	TRM5	TRM	16	821711	822057	824738	824936	2_nonsis		2682	2953	3224	2	32	1	1	0	(2:6)_(3:5)_(2:6)_(3:5a)_(4:4aCO)
148	TRM5	TRM	14	529097	529112	531656	532165	2_nonsis		2545	2806	3067	2	32	1	1	0	(2:6)_(3:5)_(4:4)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)
122	TRM5	TRM	12	822252	822430	830741	830945	2_nonsis		8312	8502	8692	2	32	1	1	0	(6:2)_(5:3)_(6:2)_(5:3a)_(4:4aCO)_(5:3a)_(4:4a)
181	TRM5	TRM	16	921271	921352	921490	921713	2_nonsis		139	290	441	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)
142	TRM5	TRM	14	237838	238024	239023	239950	2_nonsis		1000	1556	2111	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
127	TRM5	TRM	13	75046	75133	75864	76140	2_nonsis		732	913	1093	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
74	TRM5	TRM	7	609044	609307	610218	610674	2_nonsis		912	1271	1629	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
161	TRM5	TRM	15	480673	480906	483971	484571	2_nonsis		3066	3482	3897	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
26	TRM5	TRM	4	53536	54185	57426	57781	2_nonsis		3242	3743	4244	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
86	TRM5	TRM	9	401375	402165	409125	409496	2_nonsis		6961	7541	8120	3	20	1	1	0	(5:3)_(6:2)_(5:3a)_(6:2)_(3:5)_(4:4aCO)
113	TRM5	TRM	12	192599	193426	196538	196849	2_nonsis		3113	3681	4249	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(4:4)_(6:2)_(2:6)_(4:4aCO)
178	TRM5	TRM	16	804145	810641	813879	814896	2_nonsis		3239	6995	10750	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(4:4)_(6:2)_(5:3)_(4:4aCO)
106	TRM5	TRM	11	569085	569468	573116	573289	2_nonsis		3649	3926	4203	3	20	1	1	0	(2:6)_(4:4)_(3:5)_(4:4)_(3:5)_(4:4)_(5:3)_(4:4aCO)
134	TRM5	TRM	13	526564	526779	529948	530525	2_nonsis		3170	3565	3960	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(4:4)_(3:5)_(5:3)_(3:5)_(5:3)_(4:4aCO)
67	TRM5	TRM	6	224275	224581	228349	228509	2_nonsis		3769	4001	4233	3	20	1	1	0	(5:3)_(4:4)_(5:3)_(6:2)_(4:4aCO)_(3:5)_(4:4a)_(3:5)_(4:4a)
101	TRM5	TRM	11	278179	278223	284656	284914	2_nonsis		6434	6584	6734	3	20	1	1	0	(3:5)_(3:5a)_(2:6)_(3:5a)_(2:6)_(4:4aCO)_(2:6)_(3:5a)_(2:6)_(4:4a)_(6:2)_(4:4a)
143	TRM5	TRM	14	310209	310493	315912	316244	2_nonsis		5420	5727	6034	3	21	1	1	0	(3:5)_(5:3)_(4:4ai)_(5:3)_(4:4ai)_(5:3)_(4:4bCO)
48	TRM5	TRM	4	1120367	1120689	1125071	1125228		3	4383	4622	4860	0	1	2	0	2	(3:5)_(5:3)_(3:5)_(2:6)_(3:5a)_(5:3a)_(4:4)
50	TRM5	TRM	5	18839	18930	23192	23309	2_sis		4263	4366	4469	0	1	2	0	2	(2:6i)_(4:4)
2	TRM5	TRM	1	66696	67715	69403	69677		3	1689	2335	2980	0	2	2	1	1	(3:5)_(3:5a)_(5:3)_(3:5a)_(4:4aCO)
4	TRM5	TRM	1	128756	129063	132066	135319		4	3004	4783	6562	0	2	2	2	2	(3:5)_(5:3)_(5:3a)_(4:4aCO)
5	TRM5	TRM	1	189825	189970	192196	192723		4	2227	2562	2897	0	2	2	1	1	(2:6)_(4:4ai)_(3:5)_(4:4ai)_(2:6)_(3:5)_(3:5a)_(1:7)_(3:5a)_(4:4bCO)
17	TRM5	TRM	2	786204	786307	787344	787463		3	1038	1148	1258	0	2	2	1	1	(2:6)_(4:4)_(3:5)_(4:4aCO)
58	TRM5	TRM	5	315416	315857	319404	319971		3	3548	4051	4554	0	2	2	1	1	(6:2)_(4:4)_(6:2a)_(4:4aCO)
90	TRM5	TRM	10	286743	287049	288267	288305		3	1219	1390	1561	0	2	2	1	1	(2:6)_(3:5)_(2:6ai)_(3:5)_(4:4aCO)_(3:5)_(4:4a)
94	TRM5	TRM	10	389963	390467	395307	395395		3	4841	5136	5431	0	2	2	1	1	(5:3)_(4:4)_(6:2)_(4:4)_(6:2)_(5:3a)_(4:4aCO)
97	TRM5	TRM	10	639041	639136	639519	639986		3	384	664	944	0	2	2	1	1	(3:5)_(4:4)_(4:4aCO)
156	TRM5	TRM	15	270656	270687	271168	271314		3	482	570	657	0	2	2	1	1	(6:2)_(6:2a)_(5:3)_(4:4aCO)
168	TRM5	TRM	15	777500	777648	781222	781811		3	3575	3943	4310	0	2	2	1	1	(6:2)_(5:3)_(5:3ai)_(4:4ai)_(5:3a)_(4:4bCO)
175	TRM5	TRM	16	461367	462319	466824	467922		4	4506	5530	6554	0	2	2	1	1	(6:2)_(4:4ai)_(3:5)_(3:5a)_(2:6i)_(4:4bCO)
176	TRM5	TRM	16	525636	525655	525874	526176		3	220	380	539	0	2	2	1	1	(6:2)_(2:6)_(3:5)_(4:4aCO)

22	TRM5	TRM	3	221877	222524	223339	223676	2_nonsis		816	1307	1798	0	3	2	0	2	(6:2)_(4:4aCO)_(4:4CO)
60	TRM5	TRM	5	372082	372263	373154	373393	2_nonsis		892	1101	1310	0	3	2	0	2	(4:4aCO)_(3:5)_(4:4CO)
81	TRM5	TRM	9	168511	169444	173732	174345		3	4289	5061	5833	0	3	2	1	1	(5:3)_(4:4aCO)_(5:3)_(6:2)_(4:4CO)_(6:2)_(5:3a)_(4:4bi)_(4:4aCO)_(2:6)_(4:4a)
118	TRM5	TRM	12	459475	490579	493890	494326	2_nonsis		3312	19081	34850	0	3	2	0	2	(3:5)_(2:6)_(4:4aCO)_(4:4CO)
251	TRM5	TRM	6	245875	246893	269707	270161		1	0	12143	24285	0	4	1	NA	NA		
358	TRM5	TRM	16	19545	19582	19545	19582		1	0	18	36	0	4	1	NA	NA		
124	TRM6	TRM	12	829398	829421	829421	829429		1	1	16	30	1	1	1	0	1	05:03
119	TRM6	TRM	12	617208	617274	617302	617371		1	29	96	162	1	1	1	0	1	05:03
43	TRM6	TRM	4	1462852	1462884	1462884	1463093		1	1	121	240	1	1	1	0	1	05:03
33	TRM6	TRM	4	923081	923093	923093	923384		1	1	152	302	1	1	1	0	1	05:03
116	TRM6	TRM	12	278823	278845	278861	279188		1	17	191	364	1	1	1	0	1	05:03
72	TRM6	TRM	7	547580	547656	547744	547892		1	89	200	311	1	1	1	0	1	05:03
120	TRM6	TRM	12	619230	619476	619476	619650		1	1	210	419	1	1	1	0	1	05:03
87	TRM6	TRM	8	261641	261724	261724	262100		1	1	230	458	1	1	1	0	1	05:03
157	TRM6	TRM	15	195170	195386	195386	195644		1	1	237	473	1	1	1	0	1	05:03
8	TRM6	TRM	2	307860	307919	308006	308284		1	88	256	423	1	1	1	0	1	05:03
76	TRM6	TRM	7	649342	649559	649559	649865		1	1	262	522	1	1	1	0	1	05:03
134	TRM6	TRM	13	511585	512090	512090	512189		1	1	302	603	1	1	1	0	1	05:03
142	TRM6	TRM	13	818603	818759	818970	819018		1	212	313	414	1	1	1	0	1	05:03
143	TRM6	TRM	13	831458	831576	831576	832164		1	1	353	705	1	1	1	0	1	05:03
91	TRM6	TRM	9	177082	177586	177586	177853		1	1	386	770	1	1	1	0	1	05:03
177	TRM6	TRM	16	785712	785737	786161	786518		1	425	615	805	1	1	1	0	1	05:03
24	TRM6	TRM	4	328835	328957	329319	329842		1	363	685	1006	1	1	1	0	1	05:03
74	TRM6	TRM	7	624636	625276	625479	625898		1	204	733	1261	1	1	1	0	1	05:03
51	TRM6	TRM	5	475014	475088	475676	475964		1	589	769	949	1	1	1	0	1	05:03
122	TRM6	TRM	12	789373	789615	789623	791142		1	9	889	1768	1	1	1	0	1	05:03
31	TRM6	TRM	4	834899	835164	836028	836051		1	865	1008	1151	1	1	1	0	1	05:03
113	TRM6	TRM	12	25985	27605	29131	29612		1	1527	2577	3626	1	1	1	0	1	05:03
26	TRM6	TRM	4	525590	525595	525595	525607		1	1	9	16	1	2	1	0	1	03:05
44	TRM6	TRM	5	18926	18930	18949	18964		1	20	29	37	1	2	1	0	1	03:05
4	TRM6	TRM	1	203038	203105	203111	203117		1	7	43	78	1	2	1	0	1	03:05
112	TRM6	TRM	11	578824	578904	578904	578942		1	1	59	117	1	2	1	0	1	03:05
151	TRM6	TRM	14	400797	400813	400849	400901		1	37	70	103	1	2	1	0	1	03:05
54	TRM6	TRM	6	28170	28318	28318	28390		1	1	110	219	1	2	1	0	1	03:05
68	TRM6	TRM	7	451921	452209	452209	452296		1	1	188	374	1	2	1	0	1	03:05
57	TRM6	TRM	6	95460	95585	95632	95849		1	48	218	388	1	2	1	0	1	03:05
35	TRM6	TRM	4	1079059	1079189	1079258	1079450		1	70	230	390	1	2	1	0	1	03:05
106	TRM6	TRM	11	195050	195153	195269	195507		1	117	287	456	1	2	1	0	1	03:05
1	TRM6	TRM	1	42484	42527	42684	43004		1	158	339	519	1	2	1	0	1	03:05
174	TRM6	TRM	16	664861	665235	665344	665441		1	110	345	579	1	2	1	0	1	03:05
80	TRM6	TRM	7	911599	911857	911857	912297		1	1	349	697	1	2	1	0	1	03:05
16	TRM6	TRM	2	575802	576303	576303	576535		1	1	367	732	1	2	1	0	1	03:05
131	TRM6	TRM	13	330241	330411	330584	330819		1	174	376	577	1	2	1	0	1	03:05
108	TRM6	TRM	11	231038	231246	231543	231603		1	298	431	564	1	2	1	0	1	03:05
67	TRM6	TRM	7	355166	355193	355292	356141		1	100	537	974	1	2	1	0	1	03:05
159	TRM6	TRM	15	246178	247071	247117	247341		1	47	605	1162	1	2	1	0	1	03:05
164	TRM6	TRM	15	627354	627543	627997	628281		1	455	691	926	1	2	1	0	1	03:05
6	TRM6	TRM	2	216631	216794	217109	218039		1	316	862	1407	1	2	1	0	1	03:05
71	TRM6	TRM	7	477384	478308	478509	478940		1	202	879	1555	1	2	1	0	1	03:05
101	TRM6	TRM	10	713591	714056	714056	715501		1	1	955	1909	1	2	1	0	1	03:05
84	TRM6	TRM	8	159962	160782	160782	161874		1	1	956	1911	1	2	1	0	1	03:05
20	TRM6	TRM	4	125573	126283	126408	127476		1	126	1014	1902	1	2	1	0	1	03:05
77	TRM6	TRM	7	677412	678405	678883	679675		1	479	1371	2262	1	2	1	0	1	03:05
38	TRM6	TRM	4	1242241	1242658	1242658	1246191		1	1	1975	3949	1	2	1	0	1	03:05
45	TRM6	TRM	5	19005	23151	23309	23976		1	159	2565	4970	1	2	1	0	1	03:05
14	TRM6	TRM	2	512888	513202	514671	514746		1	1470	1664	1857	1	3	1	0	1	5:3_6:2_5:3
150	TRM6	TRM	14	335395	335707	336952	336970		1	1246	1410	1574	1	3	1	0	1	5:3_6:2_5:3_4:4_5:3
133	TRM6	TRM	13	442504	442723	445293	445712		1	2571	2889	3207	1	3	1	0	1	5:3_6:2_5:3_4:4_5:3
32	TRM6	TRM	4	896324	896532	896774	897251		1	243	585	926	1	4	1	0	1	3:5_2:6_3:5
114	TRM6	TRM	12	53089	53554	54226	54244		1	673	914	1154	1	4	1	0	1	3:5_2:6_3:5

100	TRM6	TRM	10	709147	709369	710013	711083	1	645	1290	1935	1	4	1	0	1	3:5_2:6_3:5
96	TRM6	TRM	10	143550	143678	145040	145102	1	1363	1457	1551	1	4	1	0	1	3:5_4:4_3:5
13	TRM6	TRM	2	501490	501576	503196	503310	1	1621	1720	1819	1	4	1	0	1	3:5_2:6_3:5
55	TRM6	TRM	6	47804	48166	52738	52838	1	4573	4803	5033	1	4	1	0	1	3:5_2:6_3:5
161	TRM6	TRM	15	478915	480090	482126	483090	1	2037	3106	4174	1	4	1	0	1	3:5_2:6_3:5_4:4_3:5
22	TRM6	TRM	4	196851	198734	200994	201329	1	2261	3369	4477	1	4	1	0	1	3:5_4:4_3:5_2:6_3:5
170	TRM6	TRM	16	380368	380443	381362	381840	1	920	1196	1471	1	7	1	0	1	5:3_6:2
50	TRM6	TRM	5	375017	375200	376468	376801	1	1269	1526	1783	1	7	1	0	1	6:2_5:3
83	TRM6	TRM	8	145861	146232	147573	147641	1	1342	1561	1779	1	7	1	0	1	6:2_5:3
98	TRM6	TRM	10	460257	460723	467162	467199	1	6440	6691	6941	1	7	1	0	1	5:3_4:4_6:2
148	TRM6	TRM	14	186992	187730	187910	187964	1	181	576	971	1	8	1	0	1	2:6_3:5
79	TRM6	TRM	7	893550	893850	894515	894550	1	666	833	999	1	8	1	0	1	3:5_2:6
12	TRM6	TRM	2	463842	464330	465156	465417	1	827	1201	1574	1	8	1	0	1	2:6_3:5
140	TRM6	TRM	13	776333	776870	778144	778647	1	1275	1794	2313	1	8	1	0	1	2:6_3:5
146	TRM6	TRM	14	79050	79165	80433	81575	1	1269	1897	2524	1	8	1	0	1	3:5_2:6
58	TRM6	TRM	6	106583	106692	107042	107101	1	351	434	517	1	8	1	0	1	3:5_4:4_2:6
137	TRM6	TRM	13	645101	645268	646658	646699	1	1391	1494	1597	1	8	1	0	1	3:5_4:4_2:6
90	TRM6	TRM	9	165195	166074	166934	167635	1	861	1650	2439	1	8	1	0	1	3:5_4:4_2:6
105	TRM6	TRM	11	99224	99633	99646	100443	1	14	616	1218	1	10	1	0	1	06:02
160	TRM6	TRM	15	404582	405136	405487	405535	1	352	652	952	1	10	1	0	1	06:02
61	TRM6	TRM	6	224892	224997	226036	226238	1	1040	1193	1345	1	10	1	0	1	06:02
42	TRM6	TRM	4	1342837	1342926	1342926	1342986	1	1	75	148	1	10.1	1	0	1	02:06
118	TRM6	TRM	12	412590	412603	412603	412803	1	1	107	212	1	10.1	1	0	1	02:06
103	TRM6	TRM	11	37740	38242	38242	38739	1	1	500	998	1	10.1	1	0	1	02:06
125	TRM6	TRM	12	1002086	1002952	1003348	1004176	2_nonsis	397	1243	2089	3	30	1	0	1	3:5_3:5a
172	TRM6	TRM	16	640976	641225	642071	642462	2_nonsis	847	1166	1485	3	30	1	0	1	5:3_5:3a_5:3
60	TRM6	TRM	6	208668	209238	210590	210664	2_nonsis	1353	1674	1995	3	30	1	0	1	6:2_4:4_2:6
145	TRM6	TRM	14	51050	51868	54694	54722	2_nonsis	2827	3249	3671	3	30	1	0	1	2:6_3:5_3:5a
99	TRM6	TRM	10	568805	570822	576464	576551	2_nonsis	5643	6694	7745	3	30	1	0	1	6:2_2:6_3:5
37	TRM6	TRM	4	1167562	1167700	1169732	1170023	2_nonsis	2033	2247	2460	3	30	1	0	1	5:3_6:2_5:3a_6:2_5:3
65	TRM6	TRM	7	333791	334340	337618	338262	2_nonsis	3279	3875	4470	3	30	1	0	1	5:3_4:4_5:3_5:3a_6:2
109	TRM6	TRM	11	253028	253608	257258	257878	2_nonsis	3651	4250	4849	3	30	1	0	1	5:3_6:2_5:3_6:2_5:3_6:2_5:3a
46	TRM6	TRM	5	158705	158931	162567	163290	2_nonsis	3637	4111	4584	3	30	1	0	1	2:6_3:5_4:4_2:6_3:5_4:4_5:3_6:2
69	TRM6	TRM	7	455013	455625	459245	459317	2_nonsis	3621	3962	4303	3	30	1	0	1	3:5_2:6_3:5_2:6_3:5_3:5a_2:6_3:5a_2:6_3:5
9	TRM6	TRM	2	311099	311267	312473	313283	2_nonsis	1207	1695	2183	3	31	1	0	1	3:5_4:4ai_3:5
144	TRM6	TRM	14	18306	18562	19760	20559	2_nonsis	1199	1726	2252	3	31	1	0	1	5:3_6:2_5:3_4:4ai
171	TRM6	TRM	16	430826	431177	432506	432538	2_nonsis	1330	1521	1711	3	31	1	0	1	6:2_5:3_4:4ai_4:4_5:3a
62	TRM6	TRM	7	30150	30348	32037	32065	2_nonsis	1690	1802	1914	3	31	1	0	1	5:3_4:4ai_3:5_5:3_4:4ai_5:3a
73	TRM6	TRM	7	549178	549493	554163	554830	2_nonsis	4671	5161	5651	3	31	1	0	1	5:3_4:4_5:3_4:4ai_5:3_4:4ai
169	TRM6	TRM	16	359182	359890	361590	361807	2_nonsis	1701	2163	2624	3	31	1	0	1	3:5_4:4_3:5_4:4ai_4:4_3:5_4:4_3:5_2:6
141	TRM6	TRM	13	815081	815882	815882	815905	2_nonsis	1	412	823	1	1	1	1	0	(5:3)_(4:4aCO)
41	TRM6	TRM	4	1338120	1338269	1338669	1339080	2_nonsis	401	680	959	1	1	1	1	0	(5:3)_(4:4aCO)
111	TRM6	TRM	11	484474	484739	485195	485495	2_nonsis	457	739	1020	1	1	1	1	0	(5:3)_(4:4aCO)
135	TRM6	TRM	13	557425	557517	557517	558987	2_nonsis	1	781	1561	1	1	1	1	0	(5:3)_(4:4aCO)
17	TRM6	TRM	2	766200	766339	767430	768073	2_nonsis	1092	1482	1872	1	1	1	1	0	(5:3)_(4:4aCO)
93	TRM6	TRM	9	298626	299287	299287	302738	2_nonsis	1	2056	4111	1	1	1	1	0	(5:3)_(4:4aCO)
92	TRM6	TRM	9	289127	292353	292870	296453	2_nonsis	518	3922	7325	1	1	1	1	0	(5:3)_(4:4aCO)
7	TRM6	TRM	2	269210	269402	269402	269653	2_nonsis	1	222	442	1	2	1	1	0	(3:5)_(4:4aCO)
21	TRM6	TRM	4	161421	162357	162819	163031	2_nonsis	463	1036	1609	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
75	TRM6	TRM	7	636413	636660	637960	638253	2_nonsis	1301	1570	1839	1	4	1	1	0	(4:4aCO)_(5:3)_(4:4a)
132	TRM6	TRM	13	379442	379637	379984	380209	2_nonsis	348	557	766	1	6	1	1	0	(4:4aCO)_(3:5)_(4:4a)
175	TRM6	TRM	16	678652	678709	679119	679575	2_nonsis	411	667	922	1	7	1	1	0	(5:3)_(6:2)_(4:4aCO)
47	TRM6	TRM	5	222472	222545	222851	222941	2_nonsis	307	388	468	1	8	1	1	0	(6:2)_(5:3)_(4:4aCO)
127	TRM6	TRM	13	102320	102554	102686	103133	2_nonsis	133	473	812	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
86	TRM6	TRM	8	222295	222996	223791	223885	2_nonsis	796	1193	1589	1	10	1	1	0	(2:6)_(3:5)_(4:4aCO)
19	TRM6	TRM	3	214762	215005	218143	218372	2_nonsis	3139	3374	3609	1	11	1	1	0	(5:3)_(4:4ai)_(4:4bCO)_(6:2)_(4:4b)
138	TRM6	TRM	13	675083	675245	675387	675697	2_nonsis	143	378	613	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
49	TRM6	TRM	5	372836	373154	373442	373736	2_nonsis	289	594	899	1	12	1	1	0	(3:5)_(4:4aCO)_(3:5)_(4:4a)
139	TRM6	TRM	13	774012	774570	774827	774965	2_nonsis	258	605	952	1	12	1	1	0	(3:5)_(4:4aCO)_(3:5)_(4:4a)
163	TRM6	TRM	15	558128	558487	559768	560108	2_nonsis	1282	1631	1979	1	12	1	1	0	(2:6)_(4:4aCO)_(3:5)_(4:4a)

ID			n	V1	V2	V3	V4	Label	X	A	B	C						Formula
66	TRM6	TRM	7	350649	351015	352489	352538	2_nonsis		1475	1682	1888	1	12	1	1	0	(5:3)_(4:4)_(5:3)_(4:4aCO)
23	TRM6	TRM	4	312599	312701	314500	315175	2_nonsis		1800	2188	2575	1	12	1	1	0	(3:5)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4)_(4:4aCO)
89	TRM6	TRM	9	102742	103011	106806	106983	2_nonsis		3796	4018	4240	1	12	1	1	0	(6:2)_(5:3)_(4:4aCO)_(6:2)_(4:4a)_(5:3)_(4:4a)
34	TRM6	TRM	4	942264	942309	942309	942662	2_nonsis		1	199	397	1	15	1	1	0	(6:2)_(4:4aCO)
95	TRM6	TRM	10	29870	29930	30160	30194	2_nonsis		231	277	323	1	15	1	1	0	(6:2)_(4:4aCO)
11	TRM6	TRM	2	461887	462229	462229	462485	2_nonsis		1	299	597	1	15	1	1	0	(6:2)_(4:4aCO)
25	TRM6	TRM	4	394798	395086	395086	395767	2_nonsis		1	485	968	1	15	1	1	0	(6:2)_(4:4aCO)
126	TRM6	TRM	12	1042570	1042844	1043157	1043284	2_nonsis		314	514	713	1	15	1	1	0	(6:2)_(4:4aCO)
59	TRM6	TRM	6	109247	109334	109334	109402	2_nonsis		1	78	154	1	16	1	1	0	(2:6)_(4:4aCO)
167	TRM6	TRM	15	924485	924624	924624	924831	2_nonsis		1	173	345	1	16	1	1	0	(2:6)_(4:4aCO)
15	TRM6	TRM	2	574173	574257	574371	574533	2_nonsis		115	237	359	1	16	1	1	0	(2:6)_(4:4aCO)
129	TRM6	TRM	13	209285	209422	209542	209890	2_nonsis		121	363	604	1	16	1	1	0	(2:6)_(4:4aCO)
5	TRM6	TRM	2	23707	24209	24355	24379	2_nonsis		147	409	671	1	16	1	1	0	(2:6)_(4:4aCO)
70	TRM6	TRM	7	463348	463843	463843	464170	2_nonsis		1	411	821	1	16	1	1	0	(2:6)_(4:4aCO)
121	TRM6	TRM	12	703971	704793	704829	704992	2_nonsis		37	529	1020	1	16	1	1	0	(2:6)_(4:4aCO)
153	TRM6	TRM	14	480527	480558	481081	481350	2_nonsis		524	673	822	1	16	1	1	0	(2:6)_(4:4aCO)
102	TRM6	TRM	10	717626	718159	717626	718159	2_nonsis		0	266	532	1	100	1	1	0	(4:4aCO)
130	TRM6	TRM	13	326810	327622	326810	327622	2_nonsis		0	406	811	1	100	1	1	0	(4:4aCO)
107	TRM6	TRM	11	203378	204194	203378	204194	2_nonsis		0	408	815	1	100	1	1	0	(4:4aCO)
63	TRM6	TRM	7	81435	82858	81435	82858	2_nonsis		0	711	1422	1	100	1	1	0	(4:4aCO)
136	TRM6	TRM	13	637295	638784	637295	638784	2_nonsis		0	744	1488	1	100	1	1	0	(4:4aCO)
147	TRM6	TRM	14	182462	182621	184992	185309	2_nonsis		2372	2609	2846	2	30	1	1	0	(5:3)_(5:3a)_(6:2)_(4:4aCO)
158	TRM6	TRM	15	197183	197943	199433	201256	2_nonsis		1491	2782	4072	2	30	1	1	0	(6:2)_(5:3)_(5:3a)_(4:4aCO)
39	TRM6	TRM	4	1250194	1250522	1252379	1252668	2_nonsis		1858	2166	2473	2	30	1	1	0	(5:3)_(5:3a)_(5:3:4ai)_(4:4bCO)
2	TRM6	TRM	1	59659	60198	61999	62308	2_nonsis		1802	2225	2648	2	31	1	1	0	(3:5)_(3:5a)_(2:6)_(4:4aCO)
52	TRM6	TRM	5	490231	490291	491327	491424	2_nonsis		1037	1115	1192	2	32	1	1	0	(5:3)_(6:2)_(5:3a)_(4:4aCO)
110	TRM6	TRM	11	287808	288159	292695	293072	2_nonsis		4537	4900	5263	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(4:4aCO)
88	TRM6	TRM	8	327422	327845	329634	330227	2_nonsis		1790	2297	2804	2	32	1	1	0	(3:5)_(4:4)_(4:4ai)_(3:5a)_(4:4bCO)
10	TRM6	TRM	2	351083	351158	352358	352751	2_nonsis		1201	1434	1667	2	32	1	1	0	(5:3)_(4:4)_(6:2)_(4:4)_(5:3a)_(4:4aCO)
29	TRM6	TRM	4	715058	715352	716832	716915	2_nonsis		1481	1669	1856	2	32	1	1	0	(5:3)_(4:4aCO)_(5:3a)_(4:4a)_(5:3a)_(4:4a)
97	TRM6	TRM	10	254247	254489	257445	257831	2_nonsis		2957	3270	3583	2	32	1	1	0	(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(4:4aCO)
155	TRM6	TRM	15	43313	43318	44801	45210	2_nonsis		1484	1690	1896	2	32	1	1	0	(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4)_(4:4aCO)_(5:3a)_(4:4a)_(5:3a)_(4:4a)
117	TRM6	TRM	12	338685	339496	341507	341678	2_nonsis		2012	2502	2992	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
128	TRM6	TRM	13	145748	146198	149583	150480	2_nonsis		3386	4059	4731	3	20	1	1	0	(5:3)_(3:5)_(4:4aCO)
28	TRM6	TRM	4	682509	682954	683860	683890	2_nonsis		907	1144	1380	3	20	1	1	0	(3:5)_(4:4aCO)_(5:3)_(4:4a)
82	TRM6	TRM	8	68532	68854	69741	70108	2_nonsis		888	1232	1575	3	20	1	1	0	(2:6)_(3:5)_(5:3)_(4:4aCO)
78	TRM6	TRM	7	849524	849571	850323	850359	2_nonsis		753	794	834	3	20	1	1	0	(3:5)_(5:3)_(4:4aCO)_(3:5a)_(4:4a)
18	TRM6	TRM	3	95029	95071	96055	96799	2_nonsis		985	1377	1769	3	20	1	1	0	(3:5)_(6:2)_(5:3)_(3:5)_(4:4aCO)
30	TRM6	TRM	4	812212	812580	814490	814815	2_nonsis		1911	2257	2602	3	20	1	1	0	(3:5)_(4:4)_(5:3)_(4:4aCO)_(5:3)_(4:4a)
64	TRM6	TRM	7	268323	269104	272568	273422	2_nonsis		3465	4282	5098	3	20	1	1	0	(3:5)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
165	TRM6	TRM	15	831592	832096	834472	834731	2_nonsis		2377	2758	3138	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(5:3)_(6:2)_(5:3)_(4:4aCO)
176	TRM6	TRM	16	751172	751586	754351	754681	2_nonsis		2766	3137	3508	3	20	1	1	0	(3:5)_(2:6)_(3:5a)_(2:6)_(3:5a)_(6:2)_(4:4aCO)
27	TRM6	TRM	4	607973	608132	610717	610801	2_nonsis		2586	2707	2827	3	20	1	1	0	(3:5)_(4:4)_(3:5)_(2:6)_(3:5)_(6:2)_(5:3)_(6:2)_(5:3)_(4:4aCO)
56	TRM6	TRM	6	55021	55242	65094	65183	2_nonsis		9853	10007	10161	3	20	1	1	0	(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(5:3)_(4:4aCO)
149	TRM6	TRM	14	294681	294859	295990	296137	2_nonsis		1132	1294	1455	3	21	1	1	0	(5:3)_(6:2)_(4:4ai)_(3:5)_(4:4bCO)
48	TRM6	TRM	5	335812	335874	338773	339113	2_nonsis		2900	3100	3300	3	21	1	1	0	(5:3)_(4:4ai)_(3:5)_(4:4bCO)_(2:6)_(3:5)_(2:6)_(4:4b)
3	TRM6	TRM	1	101193	101198	101198	101547	2_sis		1	177	353	0	1	2	0	2	(6:2i)_(4:4)
40	TRM6	TRM	4	1266824	1266952	1270457	1270902	2_sis		3506	3792	4077	0	1	2	0	2	(5:3)_(4:4)_(5:3a)_(4:4)
104	TRM6	TRM	11	68369	68377	70841	71068		3	2465	2582	2698	0	1	2	0	2	(5:3)_(4:4)_(3:5)_(2:6)_(3:5)_(2:6)_(3:5)_(2:6)_(4:4)
166	TRM6	TRM	15	836747	837056	837630	838080	2_sis		575	954	1332	0	1	2	0	2	(5:3)_(5:3a)_(4:4)
81	TRM6	TRM	7	993849	994015	997972	998377		3	3958	4243	4527	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(4:4ai)_(5:3b)_(4:4bCO)_(5:3b)_(4:4b)_(5:3b)_(3:5)_(3:5a)_(4:4ai)_(4:4b)
123	TRM6	TRM	12	820606	821384	823256	827343			1873	4305	6736	0	2	2	1	1	(3:5)_(3:5a)_(4:4aCO)
152	TRM6	TRM	14	433271	434561	437581	439088			3021	4419	5816	0	2	2	1	1	(3:5)_(3:5a)_(4:4aCO)
162	TRM6	TRM	15	484571	485571	488732	488859		3	3162	3725	4287	0	2	2	1	1	(5:3)_(6:2)_(5:3)_(3:5)_(5:3)_(4:4)_(2:6)_(3:5a)_(4:4aCO)_(3:5a)_(4:4a)_(3:5a)_(2:6)_(3:5a)_(4:4a)
168	TRM6	TRM	15	1036160	1036163	1039824	1040442		4	3662	3972	4281	0	2	2	1	1	(5:3)_(4:4)_(5:3a)_(6:2i)_(5:3)_(4:4)_(5:3)_(1:7)_(3:5)_(2:6i)_(1:7a)_(2:6a)_(3:5a)_(4:4aCO)
173	TRM6	TRM	16	653303	653426	656784	656861		3	3359	3458	3557	0	2	2	1	1	(3:5)_(3:5a)_(2:6)_(3:5a)_(2:6)_(3:5a)_(2:6)_(4:4ai)_(5:3)_(4:4bCO)
36	TRM6	TRM	4	1145144	1145628	1147847	1147937	2_nonsis		2220	2506	2792	0	3	2	0	2	(2:6)_(4:4aCO)_(5:3)_(4:4a)_(3:5)_(4:4CO)
85	TRM6	TRM	8	182354	183701	190339	190671		3	6639	7478	8316	0	3	2	1	1	(5:3)_(6:2)_(5:3)_(4:4aCO)_(5:3)_(6:2)_(5:3)_(4:4a)_(6:2)_(5:3a)_(6:2a)_(5:3b)_(6:2a)_(5:3b)_(4:4CO)
94	TRM6	TRM	9	329125	332459	335079	336156	2_nonsis		2621	4826	7030	0	3	2	0	2	(3:5)_(2:6)_(3:5)_(4:4)_(6:2)_(4:4aCO)_(5:3)_(4:4CO)
115	TRM6	TRM	12	184390	184414	185813	186034	2_nonsis		1400	1522	1643	0	3	2	0	2	(2:6)_(4:4aCO)_(5:3)_(4:4CO)

154	TRM6	TRM	14	604250	605032	608001	610323	2_nonsis	2970	4521	6072	0	3	2	0	2	(3:5)_(4:4aCO)_(3:5)_(4:4CO)
156	TRM6	TRM	15	80664	80920	84226	84370	3	3307	3506	3705	0	3	2	0	2	(5:3)_(6:2)_(5:3a)_(5:3)_(6:2)_(4:4aCO)_(6:2)_(4:4CO)
242	TRM6	TRM	7	8977	9007	10242	11737	1	1236	1998	2759	0	4	1	NA	NA	6:2_5:3_6:2_5:3_4:4_5:3
80	TRMS1	TRMS	10	256690	256880	256992	257216	1	113	319	525	1	8	1	0	1	2:6_4:4_2:6
120	TRMS1	TRMS	14	135855	135879	135879	135908	1	1	27	52	1	10	1	0	1	06:02
153	TRMS1	TRMS	16	536711	536720	536720	536802	1	1	46	90	1	10	1	0	1	06:02
14	TRMS1	TRMS	2	742150	742220	742220	742472	1	1	161	321	1	10	1	0	1	06:02
93	TRMS1	TRMS	11	264063	264372	264372	264463	1	1	200	399	1	10	1	0	1	06:02
96	TRMS1	TRMS	11	362017	362101	362299	362315	1	199	248	297	1	10	1	0	1	06:02
43	TRMS1	TRMS	4	1279154	1279416	1279422	1279680	1	7	266	525	1	10	1	0	1	06:02
34	TRMS1	TRMS	4	851602	851855	851875	852118	1	21	268	515	1	10	1	0	1	06:02
23	TRMS1	TRMS	4	296244	296284	296339	296793	1	56	302	548	1	10	1	0	1	06:02
58	TRMS1	TRMS	7	276935	277086	277287	277346	1	202	306	410	1	10	1	0	1	06:02
35	TRMS1	TRMS	4	930077	930409	930421	930813	1	13	374	735	1	10	1	0	1	06:02
85	TRMS1	TRMS	10	462170	462595	462689	462896	1	95	410	725	1	10	1	0	1	06:02
40	TRMS1	TRMS	4	1152100	1152705	1152705	1153009	1	1	455	908	1	10	1	0	1	06:02
36	TRMS1	TRMS	4	954530	954939	955230	955309	1	292	535	778	1	10	1	0	1	06:02
37	TRMS1	TRMS	4	994719	995637	995637	995820	1	1	551	1100	1	10	1	0	1	06:02
53	TRMS1	TRMS	6	28062	28170	28662	28792	1	493	611	729	1	10	1	0	1	06:02
29	TRMS1	TRMS	4	750125	750698	750901	751203	1	204	641	1077	1	10	1	0	1	06:02
8	TRMS1	TRMS	2	289530	289601	289966	290536	1	366	686	1005	1	10	1	0	1	06:02
150	TRMS1	TRMS	16	121751	122624	122624	123134	1	1	692	1382	1	10	1	0	1	06:02
77	TRMS1	TRMS	9	386757	386765	387502	387531	1	738	756	773	1	10	1	0	1	06:02
122	TRMS1	TRMS	14	199873	200718	200718	201732	1	1	930	1858	1	10	1	0	1	06:02
159	TRMS1	TRMS	16	729729	730436	730436	731859	1	1	1065	2129	1	10	1	0	1	06:02
97	TRMS1	TRMS	11	381664	381721	382980	383052	1	1260	1324	1387	1	10	1	0	1	06:02
160	TRMS1	TRMS	16	783424	785712	786020	786518	1	309	1701	3093	1	10	1	0	1	06:02
3	TRMS1	TRMS	1	104068	107245	107245	107538	1	1	1735	3469	1	10	1	0	1	06:02
18	TRMS1	TRMS	4	119010	120812	121811	121990	1	1000	1990	2979	1	10	1	0	1	06:02
105	TRMS1	TRMS	12	320997	323570	324050	325206	1	481	2345	4208	1	10	1	0	1	06:02
76	TRMS1	TRMS	9	364755	366456	373063	375595	1	6608	8724	10839	1	10	1	0	1	06:02
25	TRMS1	TRMS	4	525607	525622	525629	525679	1	8	40	71	1	10.1	1	0	1	02:06
15	TRMS1	TRMS	3	212109	212264	212321	212415	1	58	182	305	1	10.1	1	0	1	02:06
144	TRMS1	TRMS	15	670593	670904	670904	670961	1	1	184	367	1	10.1	1	0	1	02:06
142	TRMS1	TRMS	15	609162	609382	609382	609537	1	1	188	374	1	10.1	1	0	1	02:06
24	TRMS1	TRMS	4	357201	357312	357312	357632	1	1	216	430	1	10.1	1	0	1	02:06
151	TRMS1	TRMS	16	127985	128230	128274	128399	1	45	229	413	1	10.1	1	0	1	02:06
111	TRMS1	TRMS	13	247126	247484	247502	247728	1	19	310	601	1	10.1	1	0	1	02:06
156	TRMS1	TRMS	16	622904	622932	623271	623671	1	340	553	766	1	10.1	1	0	1	02:06
16	TRMS1	TRMS	3	236772	236946	236961	238082	1	16	663	1309	1	10.1	1	0	1	02:06
63	TRMS1	TRMS	7	836443	837183	837489	837577	1	307	720	1133	1	10.1	1	0	1	02:06
116	TRMS1	TRMS	13	719868	720435	720681	721068	1	247	723	1199	1	10.1	1	0	1	02:06
128	TRMS1	TRMS	14	478186	479345	479395	479609	1	51	737	1422	1	10.1	1	0	1	02:06
98	TRMS1	TRMS	11	486393	486704	487567	487615	1	864	1043	1221	1	10.1	1	0	1	02:06
130	TRMS1	TRMS	14	651410	652054	652419	653557	1	366	1256	2146	1	10.1	1	0	1	02:06
124	TRMS1	TRMS	14	333286	335341	335341	336158	1	1	1436	2871	1	10.1	1	0	1	02:06
86	TRMS1	TRMS	10	467589	469453	469520	470533	1	68	1506	2943	1	10.1	1	0	1	02:06
88	TRMS1	TRMS	10	576551	576835	577732	578943	1	898	1645	2391	1	10.1	1	0	1	02:06
118	TRMS1	TRMS	13	859155	859920	861205	861520	1	1286	1825	2364	1	10.1	1	0	1	02:06
20	TRMS1	TRMS	4	195474	196150	198376	198685	1	2227	2719	3210	1	10.1	1	0	1	02:06
69	TRMS1	TRMS	8	76976	77201	79512	80825	1	2312	3080	3848	1	10.1	1	0	1	02:06
143	TRMS1	TRMS	15	638136	639159	639455	639510	2_nonsis	297	835	1373	3	30	1	0	1	2:6_6:2
89	TRMS1	TRMS	10	700864	701241	701478	701601	2_nonsis	238	487	736	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
106	TRMS1	TRMS	12	606562	606799	606928	607451	2_nonsis	130	509	888	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
95	TRMS1	TRMS	11	326807	327038	327707	327893	2_nonsis	670	878	1085	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
50	TRMS1	TRMS	5	465974	466823	466898	467945	2_nonsis	76	1023	1970	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
12	TRMS1	TRMS	2	640000	640627	641467	641914	2_nonsis	841	1377	1913	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
62	TRMS1	TRMS	7	785318	785828	786983	787089	2_nonsis	1156	1463	1770	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
107	TRMS1	TRMS	12	668550	669123	670460	670933	2_nonsis	1338	1860	2382	1	12	1	1	0	(6:2)_(4:4)_(4:4aCO)
81	TRMS1	TRMS	10	300402	300732	302943	303003	2_nonsis	2212	2406	2600	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)

46	TRMS1	TRMS	5	41711	41961	42708	43260	2_nonsis	748	1148	1548	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
146	TRMS1	TRMS	15	766612	766910	768090	768428	2_nonsis	1181	1498	1815	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
61	TRMS1	TRMS	7	670804	671038	672419	672632	2_nonsis	1382	1605	1827	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
101	TRMS1	TRMS	12	34343	35616	36792	36833	2_nonsis	1177	1833	2489	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
13	TRMS1	TRMS	2	678799	679276	680726	681166	2_nonsis	1451	1909	2366	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
39	TRMS1	TRMS	4	1139987	1140038	1140165	1143943	2_nonsis	128	2042	3955	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
113	TRMS1	TRMS	13	490598	490970	494666	495115	2_nonsis	3697	4107	4516	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
112	TRMS1	TRMS	13	344348	344475	344475	344829	2_nonsis	1	241	480	1	15	1	1	0	(6:2)_(4:4aCO)
51	TRMS1	TRMS	5	490952	491251	491327	491522	2_nonsis	77	323	569	1	15	1	1	0	(6:2)_(4:4aCO)
70	TRMS1	TRMS	8	121987	122169	122169	122633	2_nonsis	1	323	645	1	15	1	1	0	(6:2)_(4:4aCO)
103	TRMS1	TRMS	12	183745	184185	184185	184390	2_nonsis	1	323	644	1	15	1	1	0	(6:2)_(4:4aCO)
31	TRMS1	TRMS	4	811697	811787	811992	812212	2_nonsis	206	360	514	1	15	1	1	0	(6:2)_(4:4aCO)
21	TRMS1	TRMS	4	234211	234361	234547	234831	2_nonsis	187	403	619	1	15	1	1	0	(6:2)_(4:4aCO)
157	TRMS1	TRMS	16	659091	659254	659469	659868	2_nonsis	216	496	776	1	15	1	1	0	(6:2)_(4:4aCO)
28	TRMS1	TRMS	4	699436	699549	699549	700440	2_nonsis	1	502	1003	1	15	1	1	0	(6:2)_(4:4aCO)
147	TRMS1	TRMS	15	865407	866653	866689	866753	2_nonsis	37	691	1345	1	15	1	1	0	(6:2)_(4:4aCO)
72	TRMS1	TRMS	9	258253	259266	259266	259784	2_nonsis	1	766	1530	1	15	1	1	0	(6:2)_(4:4aCO)
54	TRMS1	TRMS	6	73933	74753	75101	75368	2_nonsis	349	892	1434	1	15	1	1	0	(6:2)_(4:4aCO)
71	TRMS1	TRMS	8	460801	462297	462825	463320	2_nonsis	529	1524	2518	1	15	1	1	0	(6:2)_(4:4aCO)
60	TRMS1	TRMS	7	584298	584414	585695	586087	2_nonsis	1282	1535	1788	1	15	1	1	0	(6:2)_(4:4aCO)
123	TRMS1	TRMS	14	272416	272546	273928	274328	2_nonsis	1383	1647	1911	1	15	1	1	0	(6:2)_(4:4aCO)
83	TRMS1	TRMS	10	452919	455260	455335	457950	2_nonsis	76	2553	5030	1	15	1	1	0	(6:2)_(4:4aCO)
131	TRMS1	TRMS	14	736660	736686	736686	736739	2_nonsis	1	40	78	1	16	1	1	0	(2:6)_(4:4aCO)
6	TRMS1	TRMS	2	216513	216541	216541	216631	2_nonsis	1	59	117	1	16	1	1	0	(2:6)_(4:4aCO)
49	TRMS1	TRMS	5	339113	339244	339325	339466	2_nonsis	82	217	352	1	16	1	1	0	(2:6)_(4:4aCO)
99	TRMS1	TRMS	11	619607	619794	619794	620047	2_nonsis	1	220	439	1	16	1	1	0	(2:6)_(4:4aCO)
91	TRMS1	TRMS	11	80854	81244	81244	81361	2_nonsis	1	254	506	1	16	1	1	0	(2:6)_(4:4aCO)
45	TRMS1	TRMS	4	1476514	1476956	1476956	1477116	2_nonsis	1	301	601	1	16	1	1	0	(2:6)_(4:4aCO)
30	TRMS1	TRMS	4	794075	794507	794603	794676	2_nonsis	97	349	600	1	16	1	1	0	(2:6)_(4:4aCO)
102	TRMS1	TRMS	12	147585	148018	148120	148252	2_nonsis	103	385	666	1	16	1	1	0	(2:6)_(4:4aCO)
110	TRMS1	TRMS	13	178203	178325	178570	178780	2_nonsis	246	411	576	1	16	1	1	0	(2:6)_(4:4aCO)
92	TRMS1	TRMS	11	217058	217298	217514	217814	2_nonsis	217	486	755	1	16	1	1	0	(2:6)_(4:4aCO)
17	TRMS1	TRMS	4	29701	30086	30545	30752	2_nonsis	460	755	1050	1	16	1	1	0	(2:6)_(4:4aCO)
44	TRMS1	TRMS	4	1361086	1361801	1362236	1362620	2_nonsis	436	985	1533	1	16	1	1	0	(2:6)_(4:4aCO)
125	TRMS1	TRMS	14	355289	355500	355500	357348	2_nonsis	1	1030	2058	1	16	1	1	0	(2:6)_(4:4aCO)
134	TRMS1	TRMS	15	296804	296918	297302	298844	2_nonsis	385	1212	2039	1	16	1	1	0	(2:6)_(4:4aCO)
94	TRMS1	TRMS	11	309310	309621	310861	310963	2_nonsis	1241	1447	1652	1	16	1	1	0	(2:6)_(4:4aCO)
117	TRMS1	TRMS	13	796648	796868	798261	798332	2_nonsis	1394	1539	1683	1	16	1	1	0	(2:6)_(4:4aCO)
139	TRMS1	TRMS	15	572419	572520	573534	574716	2_nonsis	1015	1656	2296	1	16	1	1	0	(2:6)_(4:4aCO)
56	TRMS1	TRMS	6	201959	202421	203799	204006	2_nonsis	1379	1713	2046	1	16	1	1	0	(2:6)_(4:4aCO)
11	TRMS1	TRMS	2	527703	528294	529552	530826	2_nonsis	1259	2191	3122	1	16	1	1	0	(2:6)_(4:4aCO)
133	TRMS1	TRMS	15	196803	197943	199433	200443	2_nonsis	1491	2565	3639	1	16	1	1	0	(2:6)_(4:4aCO)
5	TRMS1	TRMS	2	177287	177793	180379	181279	2_nonsis	2587	3289	3991	1	16	1	1	0	(2:6)_(4:4aCO)
38	TRMS1	TRMS	4	1034345	1034463	1034345	1034463	2_nonsis	0	59	117	1	100	1	1	0	(4:4aCO)
141	TRMS1	TRMS	15	586076	586304	586076	586304	2_nonsis	0	114	227	1	100	1	1	0	(4:4aCO)
79	TRMS1	TRMS	10	254247	254489	254247	254489	2_nonsis	0	121	241	1	100	1	1	0	(4:4aCO)
78	TRMS1	TRMS	10	71182	71728	71182	71728	2_nonsis	0	273	545	1	100	1	1	0	(4:4aCO)
149	TRMS1	TRMS	16	74327	74884	74327	74884	2_nonsis	0	278	556	1	100	1	1	0	(4:4aCO)
84	TRMS1	TRMS	10	459431	460257	459431	460257	2_nonsis	0	413	825	1	100	1	1	0	(4:4aCO)
55	TRMS1	TRMS	6	79488	80386	79488	80386	2_nonsis	0	449	897	1	100	1	1	0	(4:4aCO)
137	TRMS1	TRMS	15	493415	494313	493415	494313	2_nonsis	0	449	897	1	100	1	1	0	(4:4aCO)
135	TRMS1	TRMS	15	409351	410471	409351	410471	2_nonsis	0	560	1119	1	100	1	1	0	(4:4aCO)
2	TRMS1	TRMS	1	71616	72952	71616	72952	2_nonsis	0	668	1335	1	100	1	1	0	(4:4aCO)
129	TRMS1	TRMS	14	487250	488587	487250	488587	2_nonsis	0	668	1336	1	100	1	1	0	(4:4aCO)
158	TRMS1	TRMS	16	712507	713880	712507	713880	2_nonsis	0	686	1372	1	100	1	1	0	(4:4aCO)
87	TRMS1	TRMS	10	559033	560471	559033	560471	2_nonsis	0	719	1437	1	100	1	1	0	(4:4aCO)
136	TRMS1	TRMS	15	491483	493178	491483	493178	2_nonsis	0	847	1694	1	100	1	1	0	(4:4aCO)
127	TRMS1	TRMS	14	456437	458514	456437	458514	2_nonsis	0	1038	2076	1	100	1	1	0	(4:4aCO)
66	TRMS1	TRMS	7	956057	958235	956057	958235	2_nonsis	0	1089	2177	1	100	1	1	0	(4:4aCO)
57	TRMS1	TRMS	7	248225	250680	248225	250680	2_nonsis	0	1227	2454	1	100	1	1	0	(4:4aCO)

126	TRMS1	TRMS	14	453937	456437	453937	456437	2_nonsis		0	1250	2499	1	100	1	1	0 (4:4aCO)
7	TRMS1	TRMS	2	284108	286708	284108	286708	2_nonsis		0	1300	2599	1	100	1	1	0 (4:4aCO)
115	TRMS1	TRMS	13	692858	695679	692858	695679	2_nonsis		0	1410	2820	1	100	1	1	0 (4:4aCO)
27	TRMS1	TRMS	4	696499	699436	696499	699436	2_nonsis		0	1468	2936	1	100	1	1	0 (4:4aCO)
33	TRMS1	TRMS	4	848341	851311	848341	851311	2_nonsis		0	1485	2969	1	100	1	1	0 (4:4aCO)
73	TRMS1	TRMS	9	267668	270689	267668	270689	2_nonsis		0	1510	3020	1	100	1	1	0 (4:4aCO)
140	TRMS1	TRMS	15	574716	577827	574716	577827	2_nonsis		0	1555	3110	1	100	1	1	0 (4:4aCO)
74	TRMS1	TRMS	9	329125	332459	329125	332459	2_nonsis		0	1667	3333	1	100	1	1	0 (4:4aCO)
26	TRMS1	TRMS	4	586457	590328	586457	590328	2_nonsis		0	1935	3870	1	100	1	1	0 (4:4aCO)
108	TRMS1	TRMS	12	803833	808209	803833	808209	2_nonsis		0	2188	4375	1	100	1	1	0 (4:4aCO)
148	TRMS1	TRMS	15	1037505	1037595	1037757	1038438	2_nonsis		163	548	932	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
22	TRMS1	TRMS	4	284001	284171	284557	285372	2_nonsis		387	879	1370	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
1	TRMS1	TRMS	1	33077	33147	33358	33548	2_nonsis		212	341	470	3	20	1	1	0 (6:2)_(4:4aCO)_(2:6)_(4:4a)
19	TRMS1	TRMS	4	176519	176588	177780	177807	2_nonsis		1193	1240	1287	3	20	1	1	0 (2:6)_(4:4)_(6:2)_(4:4aCO)
155	TRMS1	TRMS	16	614501	614631	615882	616361	2_nonsis		1252	1556	1859	3	20	1	1	0 (2:6)_(4:4)_(6:2)_(4:4a)
114	TRMS1	TRMS	13	651148	651277	654624	654748	2_nonsis		3348	3474	3599	3	20	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)_(6:2)_(4:4a)
47	TRMS1	TRMS	5	115890	115997	116577	117072	2_sis		581	881	1181	0	1	2	0	2 (0:8)_(4:4)
109	TRMS1	TRMS	13	157807	159018	159018	160135	2_sis		1	1164	2327	0	1	2	0	2 (0:8)_(4:4)
145	TRMS1	TRMS	15	745114	745138	745929	746695	2_sis		792	1186	1580	0	1	2	0	2 (2:6)_(0:8)_(2:6a)_(4:4)
4	TRMS1	TRMS	1	112136	113132	129075	129476		3	15944	16642	17339	0	2	2	1	1 (6:2)_(6:2a)_(4:4aCO)
32	TRMS1	TRMS	4	843125	843494	847587	848341		3	4094	4655	5215	0	2	2	1	1 (6:2)_(6:2a)_(4:4aCO)
41	TRMS1	TRMS	4	1153966	1161539	1162787	1163371		3	1249	5327	9404	0	2	2	1	1 (6:2)_(2:6)_(6:2)_(4:4aCO)
68	TRMS1	TRMS	7	989982	990395	997225	997372		3	6831	7110	7389	0	2	2	1	1 (0:8)_(4:4)_(0:8)_(4:4)_(0:8)_(4:4)_(0:8)_(4:4)_(0:8)_(6:2)_(4:4aCO)_(0:8)_(4:4a)_(0:8)_(4:4a)_(0:8)_(4:4a)_(0:8)_(4:4a)_(0:8)_(4:4a)_(0:8)_(4:4a)_(0:8)_(4:4a)
75	TRMS1	TRMS	9	332503	333073	334775	334877		3	1703	2038	2373	0	2	2	1	1 (6:2)_(4:4)_(2:6)_(4:4aCO)
152	TRMS1	TRMS	16	383387	383599	383599	385830		3	1	1222	2442	0	2	2	1	1 (6:2)_(4:4aCO)
9	TRMS1	TRMS	2	432851	435650	435951	436119	2_nonsis		302	1785	3267	0	3	2	0	2 (2:6)_(4:4aCO)_(4:4CO)
48	TRMS1	TRMS	5	262042	262212	269239	269982	2_nonsis		7028	7484	7939	0	3	2	0	2 (2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)_(2:6)_(4:4CO)
64	TRMS1	TRMS	7	848688	849134	849134	849405		3	1	359	716	0	3	2	1	1 (4:4aCO)_(4:4bCO)
82	TRMS1	TRMS	10	332672	337220	341586	342031		4	4367	6863	9358	0	3	2	1	1 (6:2)_(4:4)_(6:2a)_(6:2b)_(4:4aCO)_(4:4CO)_(4:4bCO)
90	TRMS1	TRMS	11	68014	68298	71964	72168	2_nonsis		3667	3910	4153	0	3	2	0	2 (6:2)_(4:4aCO)_(2:6)_(4:4CO)
100	TRMS1	TRMS	12	17162	17865	18460	19080	2_nonsis		596	1257	1917	0	3	2	0	2 (2:6)_(4:4aCO)_(2:6)_(4:4CO)
138	TRMS1	TRMS	15	531055	531368	532110	538230	2_nonsis		743	3959	7174	0	3	2	0	2 (4:4aCO)_(6:2)_(4:4CO)
89	TRMS2	TRMS	16	187312	187323	187323	187324		1	1	6	11	1	10	1	0	1 06:02
72	TRMS2	TRMS	14	135855	135879	135879	135908		1	1	27	52	1	10	1	0	1 06:02
15	TRMS2	TRMS	4	1161819	1161892	1161892	1161927		1	1	54	107	1	10	1	0	1 06:02
23	TRMS2	TRMS	5	341688	342057	342057	342537		1	1	425	848	1	10	1	0	1 06:02
29	TRMS2	TRMS	7	49026	49323	49965	50143		1	643	880	1116	1	10	1	0	1 06:02
4	TRMS2	TRMS	2	451373	451982	452891	453417		1	910	1477	2043	1	10	1	0	1 06:02
75	TRMS2	TRMS	14	196345	196819	198236	198384		1	1418	1728	2038	1	10	1	0	1 06:02
48	TRMS2	TRMS	10	570822	573135	574412	576464		1	1278	3460	5641	1	10	1	0	1 06:02
52	TRMS2	TRMS	11	89262	89273	89285	89332		1	13	41	69	1	10.1	1	0	1 02:06
65	TRMS2	TRMS	13	209199	209233	209248	209422		1	16	119	222	1	10.1	1	0	1 02:06
58	TRMS2	TRMS	12	341507	341678	342190	342448		1	513	727	940	1	10.1	1	0	1 02:06
67	TRMS2	TRMS	13	453503	453738	454197	454515		1	460	736	1011	1	10.1	1	0	1 02:06
94	TRMS2	TRMS	16	842086	842864	843042	843391		1	179	742	1304	1	10.1	1	0	1 02:06
78	TRMS2	TRMS	14	433271	434561	434561	435509		1	1	1119	2237	1	10.1	1	0	1 02:06
45	TRMS2	TRMS	9	49641	51046	51375	53832		1	330	2260	4190	1	10.1	1	0	1 02:06
83	TRMS2	TRMS	15	295611	296401	296475	296786	2_nonsis		75	625	1174	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
34	TRMS2	TRMS	7	370360	370393	371116	372223	2_nonsis		724	1293	1862	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
16	TRMS2	TRMS	4	1168663	1168940	1170023	1170239	2_nonsis		1084	1330	1575	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
10	TRMS2	TRMS	4	521269	521409	521536	521623	2_nonsis		128	241	353	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
1	TRMS2	TRMS	1	51522	51774	52632	52846	2_nonsis		859	1091	1323	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
26	TRMS2	TRMS	6	63014	64252	65326	65504	2_nonsis		1075	1782	2489	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
60	TRMS2	TRMS	12	871504	872180	873300	874112	2_nonsis		1121	1864	2607	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
3	TRMS2	TRMS	2	99630	100295	101704	102053	2_nonsis		1410	1916	2422	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
36	TRMS2	TRMS	7	461146	461588	463348	463843	2_nonsis		1761	2229	2696	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
31	TRMS2	TRMS	7	74791	75209	80976	81268	2_nonsis		5768	6122	6476	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
77	TRMS2	TRMS	14	306527	307339	311556	311614	2_nonsis		4218	4652	5086	1	12	1	1	0 (6:2)_(4:4)_(4:4)_(4:4aCO)
21	TRMS2	TRMS	5	42280	42354	46756	46832	2_nonsis		4403	4477	4551	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)_(6:2)_(4:4a)
74	TRMS2	TRMS	14	186475	186921	186992	187434	2_nonsis		72	515	958	1	15	1	1	0 (6:2)_(4:4aCO)

88	TRMS2	TRMS	15	968360	968476	968991	969441	2_nonsis		516	798	1080	1	15	1	1	0	(6:2)_(4:4aCO)
81	TRMS2	TRMS	14	667685	668135	668135	669471	2_nonsis		1	893	1785	1	15	1	1	0	(6:2)_(4:4aCO)
17	TRMS2	TRMS	4	1268647	1269918	1269918	1270457	2_nonsis		1	905	1809	1	15	1	1	0	(6:2)_(4:4aCO)
61	TRMS2	TRMS	12	876120	877476	877699	878238	2_nonsis		224	1171	2117	1	15	1	1	0	(6:2)_(4:4aCO)
43	TRMS2	TRMS	7	1007272	1008949	1009315	1010365	2_nonsis		367	1730	3092	1	15	1	1	0	(6:2)_(4:4aCO)
46	TRMS2	TRMS	9	185865	188629	188919	189195	2_nonsis		291	1810	3329	1	15	1	1	0	(6:2)_(4:4aCO)
37	TRMS2	TRMS	7	701596	701914	702791	704403	2_nonsis		878	1842	2806	1	15	1	1	0	(6:2)_(4:4aCO)
55	TRMS2	TRMS	11	525514	525645	527630	527758	2_nonsis		1986	2115	2243	1	15	1	1	0	(6:2)_(4:4aCO)
11	TRMS2	TRMS	4	625839	629487	629532	631576	2_nonsis		46	2891	5736	1	15	1	1	0	(6:2)_(4:4aCO)
93	TRMS2	TRMS	16	736980	739339	741423	741972	2_nonsis		2085	3538	4991	1	15	1	1	0	(6:2)_(4:4aCO)
91	TRMS2	TRMS	16	348056	348373	356993	357487	2_nonsis		8621	9026	9430	1	15	1	1	0	(6:2)_(4:4aCO)
84	TRMS2	TRMS	15	384791	384919	384919	384942	2_nonsis		1	76	150	1	16	1	1	0	(2:6)_(4:4aCO)
80	TRMS2	TRMS	14	544744	545184	545184	545273	2_nonsis		1	265	528	1	16	1	1	0	(2:6)_(4:4aCO)
9	TRMS2	TRMS	4	263811	264106	264197	264290	2_nonsis		92	285	478	1	16	1	1	0	(2:6)_(4:4aCO)
30	TRMS2	TRMS	7	51531	51819	51819	52326	2_nonsis		1	398	794	1	16	1	1	0	(2:6)_(4:4aCO)
8	TRMS2	TRMS	4	171661	171817	172175	172830	2_nonsis		359	764	1168	1	16	1	1	0	(2:6)_(4:4aCO)
69	TRMS2	TRMS	13	759679	759844	760322	760768	2_nonsis		479	784	1088	1	16	1	1	0	(2:6)_(4:4aCO)
54	TRMS2	TRMS	11	309823	310035	310798	310828	2_nonsis		764	884	1004	1	16	1	1	0	(2:6)_(4:4aCO)
62	TRMS2	TRMS	13	25638	25829	26434	26922	2_nonsis		606	945	1283	1	16	1	1	0	(2:6)_(4:4aCO)
32	TRMS2	TRMS	7	253916	254088	254273	255756	2_nonsis		186	1013	1839	1	16	1	1	0	(2:6)_(4:4aCO)
38	TRMS2	TRMS	7	886106	886758	887281	887698	2_nonsis		524	1058	1591	1	16	1	1	0	(2:6)_(4:4aCO)
59	TRMS2	TRMS	12	776373	777814	778158	779222	2_nonsis		345	1597	2848	1	16	1	1	0	(2:6)_(4:4aCO)
56	TRMS2	TRMS	12	211226	212026	213226	213278	2_nonsis		1201	1626	2051	1	16	1	1	0	(2:6)_(4:4aCO)
87	TRMS2	TRMS	15	810765	811006	812380	812662	2_nonsis		1375	1636	1896	1	16	1	1	0	(2:6)_(4:4aCO)
50	TRMS2	TRMS	10	704426	705450	705450	707903	2_nonsis		1	1739	3476	1	16	1	1	0	(2:6)_(4:4aCO)
20	TRMS2	TRMS	5	24112	25325	26594	26638	2_nonsis		1270	1898	2525	1	16	1	1	0	(2:6)_(4:4aCO)
19	TRMS2	TRMS	4	1335831	1338084	1339443	1340160	2_nonsis		1360	2844	4328	1	16	1	1	0	(2:6)_(4:4aCO)
28	TRMS2	TRMS	6	205395	205576	209430	210003	2_nonsis		3855	4231	4607	1	16	1	1	0	(2:6)_(4:4aCO)
27	TRMS2	TRMS	6	196194	196491	196194	196491	2_nonsis		0	148	296	1	100	1	1	0	(4:4aCO)
51	TRMS2	TRMS	11	31754	32124	31754	32124	2_nonsis		0	185	369	1	100	1	1	0	(4:4aCO)
90	TRMS2	TRMS	16	217557	217929	217557	217929	2_nonsis		0	186	371	1	100	1	1	0	(4:4aCO)
66	TRMS2	TRMS	13	243623	244001	243623	244001	2_nonsis		0	189	377	1	100	1	1	0	(4:4aCO)
47	TRMS2	TRMS	9	267764	268176	267764	268176	2_nonsis		0	206	411	1	100	1	1	0	(4:4aCO)
2	TRMS2	TRMS	1	130362	130776	130362	130776	2_nonsis		0	207	413	1	100	1	1	0	(4:4aCO)
49	TRMS2	TRMS	10	641631	642317	641631	642317	2_nonsis		0	343	685	1	100	1	1	0	(4:4aCO)
14	TRMS2	TRMS	4	1008685	1009606	1008685	1009606	2_nonsis		0	460	920	1	100	1	1	0	(4:4aCO)
68	TRMS2	TRMS	13	556437	557365	556437	557365	2_nonsis		0	464	927	1	100	1	1	0	(4:4aCO)
64	TRMS2	TRMS	13	170002	170932	170002	170932	2_nonsis		0	465	929	1	100	1	1	0	(4:4aCO)
33	TRMS2	TRMS	7	329667	330839	329667	330839	2_nonsis		0	586	1171	1	100	1	1	0	(4:4aCO)
24	TRMS2	TRMS	5	450386	451710	450386	451710	2_nonsis		0	662	1323	1	100	1	1	0	(4:4aCO)
7	TRMS2	TRMS	4	133023	134651	133023	134651	2_nonsis		0	814	1627	1	100	1	1	0	(4:4aCO)
53	TRMS2	TRMS	11	299201	300874	299201	300874	2_nonsis		0	836	1672	1	100	1	1	0	(4:4aCO)
6	TRMS2	TRMS	2	695479	698250	695479	698250	2_nonsis		0	1385	2770	1	100	1	1	0	(4:4aCO)
85	TRMS2	TRMS	15	563779	566628	563779	566628	2_nonsis		0	1424	2848	1	100	1	1	0	(4:4aCO)
79	TRMS2	TRMS	14	539950	543829	539950	543829	2_nonsis		0	1939	3878	1	100	1	1	0	(4:4aCO)
70	TRMS2	TRMS	13	798063	798090	798261	798332	2_nonsis		172	220	268	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
13	TRMS2	TRMS	4	878186	884761	885455	885734	2_nonsis		695	4121	7547	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
40	TRMS2	TRMS	7	986604	986691	988528	988550	2_sis		1838	1892	1945	0	1	2	0	2	(0:8)_(4:4)_(0:8)_(4:4)_(0:8)_(4:4)_(0:8)_(4:4)_(0:8)_(4:4)_(0:8)_(4:4)
42	TRMS2	TRMS	7	1004566	1005019	1006156	1006862	2_sis		1138	1717	2295	0	1	2	0	2	(6:2)_(4:4)_(6:2a)_(4:4)
12	TRMS2	TRMS	4	699436	699549	703905	706032		3	4357	5476	6595	0	3	2	1	1	(6:2)_(4:4)_(6:2)_(4:4aCO)_(6:2)_(4:4a)_(4:4bCO)
39	TRMS2	TRMS	7	950639	951196	952040	952100		3	845	1153	1460	0	3	2	0	2	(4:4aCO)_(4:4CO)_(6:2)_(0:8)_(4:4)
76	TRMS2	TRMS	14	287504	287606	289345	289457	2_nonsis		1740	1846	1952	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2)_(4:4CO)
86	TRMS2	TRMS	15	771781	772232	774747	774866	2_nonsis		2516	2800	3084	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2)_(4:4CO)
208	TRN1	TRN	16	170258	170349	170759	170856		1	411	504	597	1	7	1	0	1	6:2_4:4_6:2
118	TRN1	TRN	10	194259	194790	196724	197018		1	1935	2347	2758	1	7	1	0	1	6:2_4:4_6:2
11	TRN1	TRN	2	175526	175964	179266	180070		1	3303	3923	4543	1	7	1	0	1	6:2_4:4_6:2
85	TRN1	TRN	7	613788	613946	620150	620222		1	6205	6319	6433	1	8	1	0	1	2:6_4:4_2:6
4	TRN1	TRN	1	102864	103068	103110	103141		1	43	160	276	1	10	1	0	1	06:02
67	TRN1	TRN	5	487274	487436	487470	487609		1	35	185	334	1	10	1	0	1	06:02
65	TRN1	TRN	5	370850	370893	370940	371210		1	48	204	359	1	10	1	0	1	06:02

115	TRN1	TRN	10	122256	122391	122391	122718	1	1	231	461	1	10	1	0	1 06:02
204	TRN1	TRN	16	21426	21432	21642	21690	1	211	237	263	1	10	1	0	1 06:02
2	TRN1	TRN	1	66148	66178	66178	66696	1	1	274	547	1	10	1	0	1 06:02
12	TRN1	TRN	2	181425	181705	181705	182128	1	1	352	702	1	10	1	0	1 06:02
114	TRN1	TRN	10	63405	63597	63597	64213	1	1	404	807	1	10	1	0	1 06:02
60	TRN1	TRN	5	180284	180460	180460	181108	1	1	412	823	1	10	1	0	1 06:02
132	TRN1	TRN	11	374056	374207	374411	375324	1	205	736	1267	1	10	1	0	1 06:02
109	TRN1	TRN	9	368159	368214	368868	369297	1	655	896	1137	1	10	1	0	1 06:02
73	TRN1	TRN	6	88777	89605	89980	90217	1	376	908	1439	1	10	1	0	1 06:02
202	TRN1	TRN	15	1038535	1038714	1039824	1040442	1	1111	1509	1906	1	10	1	0	1 06:02
209	TRN1	TRN	16	173330	173979	175137	175312	1	1159	1570	1981	1	10	1	0	1 06:02
3	TRN1	TRN	1	71616	73633	74190	74538	1	558	1740	2921	1	10	1	0	1 06:02
205	TRN1	TRN	16	31264	32078	33006	33858	1	929	1761	2593	1	10	1	0	1 06:02
174	TRN1	TRN	13	738608	739012	740606	741174	1	1595	2080	2565	1	10	1	0	1 06:02
162	TRN1	TRN	12	1034264	1035874	1036112	1038435	1	239	2205	4170	1	10	1	0	1 06:02
8	TRN1	TRN	1	137336	138499	139277	141984	1	779	2713	4647	1	10	1	0	1 06:02
169	TRN1	TRN	13	414719	415535	417524	418982	1	1990	3126	4262	1	10	1	0	1 06:02
123	TRN1	TRN	10	628891	629879	629879	635210	1	1	3160	6318	1	10	1	0	1 06:02
19	TRN1	TRN	2	695479	699461	700423	701135	1	963	3309	5655	1	10	1	0	1 06:02
5	TRN1	TRN	1	104068	108457	108928	110856	1	472	3630	6787	1	10	1	0	1 06:02
97	TRN1	TRN	8	203922	204071	209742	210057	1	5672	5903	6134	1	10	1	0	1 06:02
43	TRN1	TRN	4	462986	463089	469779	470731	1	6691	7218	7744	1	10	1	0	1 06:02
196	TRN1	TRN	15	698870	700016	703419	710179	1	3404	7356	11308	1	10	1	0	1 06:02
148	TRN1	TRN	12	409113	409269	416918	417083	1	7650	7810	7969	1	10	1	0	1 06:02
212	TRN1	TRN	16	444028	444118	444118	444202	1	1	87	173	1	10.1	1	0	1 02:06
20	TRN1	TRN	2	711439	711722	711722	711792	1	1	177	352	1	10.1	1	0	1 02:06
27	TRN1	TRN	3	70158	70491	70491	70617	1	1	230	458	1	10.1	1	0	1 02:06
92	TRN1	TRN	8	110129	110256	110256	110685	1	1	278	555	1	10.1	1	0	1 02:06
140	TRN1	TRN	12	29131	29612	29612	29773	1	1	321	641	1	10.1	1	0	1 02:06
203	TRN1	TRN	15	1043151	1043361	1043361	1043801	1	1	325	649	1	10.1	1	0	1 02:06
87	TRN1	TRN	7	970527	970797	970797	971296	1	1	385	768	1	10.1	1	0	1 02:06
25	TRN1	TRN	2	792247	792968	792968	793142	1	1	448	894	1	10.1	1	0	1 02:06
112	TRN1	TRN	9	427210	428011	428011	428213	1	1	502	1002	1	10.1	1	0	1 02:06
47	TRN1	TRN	4	931988	932298	932535	933005	1	238	627	1016	1	10.1	1	0	1 02:06
151	TRN1	TRN	12	566615	567266	567266	567957	1	1	671	1341	1	10.1	1	0	1 02:06
53	TRN1	TRN	4	1378471	1379733	1379733	1380091	1	1	810	1619	1	10.1	1	0	1 02:06
10	TRN1	TRN	2	73354	73472	73943	74853	1	472	985	1498	1	10.1	1	0	1 02:06
86	TRN1	TRN	7	678883	679675	679675	681013	1	1	1065	2129	1	10.1	1	0	1 02:06
16	TRN1	TRN	2	551109	551347	552407	552625	1	1061	1288	1515	1	10.1	1	0	1 02:06
94	TRN1	TRN	8	125140	125249	126397	126572	1	1149	1290	1431	1	10.1	1	0	1 02:06
54	TRN1	TRN	4	1382859	1383527	1384710	1384770	1	1184	1547	1910	1	10.1	1	0	1 02:06
90	TRN1	TRN	7	1046941	1050057	1050064	1050446	1	8	1756	3504	1	10.1	1	0	1 02:06
32	TRN1	TRN	4	51985	52534	53890	54185	1	1357	1778	2199	1	10.1	1	0	1 02:06
155	TRN1	TRN	12	623758	624838	627543	628215	1	2706	3581	4456	1	10.1	1	0	1 02:06
178	TRN1	TRN	14	95765	96083	96482	102681	1	400	3658	6915	1	10.1	1	0	1 02:06
211	TRN1	TRN	16	428065	428562	432538	433340	1	3977	4626	5274	1	10.1	1	0	1 02:06
141	TRN1	TRN	12	63859	65485	69317	69569	1	3833	4771	5709	1	10.1	1	0	1 02:06
34	TRN1	TRN	4	108917	109331	114468	115646	1	5138	5933	6728	1	10.1	1	0	1 02:06
38	TRN1	TRN	4	278692	280191	286258	287699	1	6068	7537	9006	1	10.1	1	0	1 02:06
158	TRN1	TRN	12	892436	930472	932256	932270	1	1785	20809	39833	1	10.1	1	0	1 02:06
102	TRN1	TRN	8	506475	506810	507567	508481 2_nonsis	758	1382	2005	3	30	1	0	1 2:6_6:2
44	TRN1	TRN	4	539680	540228	546573	547556 2_nonsis	6346	7111	7875	3	30	1	0	1 6:2_2:6
121	TRN1	TRN	10	618846	621779	624474	624648 2_nonsis	2696	4249	5801	3	30	1	0	1 6:2_4:4_2:6
84	TRN1	TRN	7	609887	609903	609958	610218 2_nonsis	56	193	330	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
173	TRN1	TRN	13	677544	678210	678756	680399 2_nonsis	547	1701	2854	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
128	TRN1	TRN	11	49756	52399	55280	56302 2_nonsis	2882	4714	6545	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
62	TRN1	TRN	5	228115	228711	229493	229569 2_nonsis	783	1118	1453	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
79	TRN1	TRN	7	73727	73810	74791	75209 2_nonsis	982	1232	1481	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
24	TRN1	TRN	2	783589	783778	785066	785146 2_nonsis	1289	1423	1556	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
154	TRN1	TRN	12	602685	602909	604223	604915 2_nonsis	1315	1772	2229	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)

64	TRN1	TRN	5	367125	367786	369120	369437	2_nonsis	1335	1823	2311	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
103	TRN1	TRN	9	93804	93903	96388	96801	2_nonsis	2486	2741	2996	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
41	TRN1	TRN	4	386506	386891	390027	390097	2_nonsis	3137	3364	3590	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
215	TRN1	TRN	16	529749	529944	533888	534359	2_nonsis	3945	4277	4609	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
186	TRN1	TRN	14	727862	728049	733411	733695	2_nonsis	5363	5598	5832	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
193	TRN1	TRN	15	476972	477610	487166	487809	2_nonsis	9557	10197	10836	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
160	TRN1	TRN	12	1006428	1006617	1006617	1006629	2_nonsis	1	101	200	1	15	1	1	0 (6:2)_(4:4aCO)
77	TRN1	TRN	6	246034	246259	246293	246533	2_nonsis	35	267	498	1	15	1	1	0 (6:2)_(4:4aCO)
142	TRN1	TRN	12	71722	72088	72088	72448	2_nonsis	1	363	725	1	15	1	1	0 (6:2)_(4:4aCO)
39	TRN1	TRN	4	292517	292751	292776	293276	2_nonsis	26	392	758	1	15	1	1	0 (6:2)_(4:4aCO)
147	TRN1	TRN	12	406709	406726	407016	407362	2_nonsis	291	472	652	1	15	1	1	0 (6:2)_(4:4aCO)
72	TRN1	TRN	6	41791	42233	42346	42743	2_nonsis	114	533	951	1	15	1	1	0 (6:2)_(4:4aCO)
119	TRN1	TRN	10	380706	380992	381120	381644	2_nonsis	129	533	937	1	15	1	1	0 (6:2)_(4:4aCO)
18	TRN1	TRN	2	590982	592600	592749	592905	2_nonsis	150	1036	1922	1	15	1	1	0 (6:2)_(4:4aCO)
52	TRN1	TRN	4	1355944	1357024	1357270	1357979	2_nonsis	247	1141	2034	1	15	1	1	0 (6:2)_(4:4aCO)
210	TRN1	TRN	16	177345	178167	179066	179451	2_nonsis	900	1503	2105	1	15	1	1	0 (6:2)_(4:4aCO)
200	TRN1	TRN	15	962816	965123	965240	966067	2_nonsis	118	1684	3250	1	15	1	1	0 (6:2)_(4:4aCO)
135	TRN1	TRN	11	540879	541329	542924	542955	2_nonsis	1596	1836	2075	1	15	1	1	0 (6:2)_(4:4aCO)
197	TRN1	TRN	15	717433	717703	718752	720202	2_nonsis	1050	1909	2768	1	15	1	1	0 (6:2)_(4:4aCO)
104	TRN1	TRN	9	133870	135647	136172	137266	2_nonsis	526	1961	3395	1	15	1	1	0 (6:2)_(4:4aCO)
176	TRN1	TRN	14	45407	46489	46932	49011	2_nonsis	444	2024	3603	1	15	1	1	0 (6:2)_(4:4aCO)
15	TRN1	TRN	2	451502	451982	454207	454272	2_nonsis	2226	2498	2769	1	15	1	1	0 (6:2)_(4:4aCO)
138	TRN1	TRN	11	638298	639711	642207	642394	2_nonsis	2497	3296	4095	1	15	1	1	0 (6:2)_(4:4aCO)
30	TRN1	TRN	3	236387	236702	239515	240922	2_nonsis	2814	3674	4534	1	15	1	1	0 (6:2)_(4:4aCO)
127	TRN1	TRN	10	717437	718433	720763	723650	2_nonsis	2331	4272	6212	1	15	1	1	0 (6:2)_(4:4aCO)
150	TRN1	TRN	12	511581	511773	516236	516783	2_nonsis	4464	4833	5201	1	15	1	1	0 (6:2)_(4:4aCO)
45	TRN1	TRN	4	714934	715058	719896	720645	2_nonsis	4839	5275	5710	1	15	1	1	0 (6:2)_(4:4aCO)
99	TRN1	TRN	8	311445	311928	317561	317992	2_nonsis	5634	6090	6546	1	15	1	1	0 (6:2)_(4:4aCO)
182	TRN1	TRN	14	284847	285069	291665	292265	2_nonsis	6597	7007	7417	1	15	1	1	0 (6:2)_(4:4aCO)
37	TRN1	TRN	4	172175	172830	183023	183468	2_nonsis	10194	10743	11292	1	15	1	1	0 (6:2)_(4:4aCO)
69	TRN1	TRN	5	539346	540205	551411	551635	2_nonsis	11207	11748	12288	1	15	1	1	0 (6:2)_(4:4aCO)
116	TRN1	TRN	10	127063	127567	146059	146367	2_nonsis	18493	18898	19303	1	15	1	1	0 (6:2)_(4:4aCO)
194	TRN1	TRN	15	564208	564299	564299	564575	2_nonsis	1	184	366	1	16	1	1	0 (2:6)_(4:4aCO)
76	TRN1	TRN	6	226238	226370	226370	226615	2_nonsis	1	189	376	1	16	1	1	0 (2:6)_(4:4aCO)
66	TRN1	TRN	5	476465	476681	476809	476888	2_nonsis	129	276	422	1	16	1	1	0 (2:6)_(4:4aCO)
63	TRN1	TRN	5	312176	312320	312496	312588	2_nonsis	177	294	411	1	16	1	1	0 (2:6)_(4:4aCO)
61	TRN1	TRN	5	182242	182338	182381	182827	2_nonsis	44	314	584	1	16	1	1	0 (2:6)_(4:4aCO)
48	TRN1	TRN	4	936290	936980	936980	937139	2_nonsis	1	425	848	1	16	1	1	0 (2:6)_(4:4aCO)
106	TRN1	TRN	9	229515	230147	230147	230680	2_nonsis	1	583	1164	1	16	1	1	0 (2:6)_(4:4aCO)
199	TRN1	TRN	15	905801	906405	906405	907000	2_nonsis	1	600	1198	1	16	1	1	0 (2:6)_(4:4aCO)
152	TRN1	TRN	12	569539	569709	569709	570914	2_nonsis	1	688	1374	1	16	1	1	0 (2:6)_(4:4aCO)
129	TRN1	TRN	11	89072	89262	89674	90100	2_nonsis	413	720	1027	1	16	1	1	0 (2:6)_(4:4aCO)
49	TRN1	TRN	4	1013843	1013924	1013983	1015229	2_nonsis	60	723	1385	1	16	1	1	0 (2:6)_(4:4aCO)
134	TRN1	TRN	11	533318	533844	534319	535346	2_nonsis	476	1252	2027	1	16	1	1	0 (2:6)_(4:4aCO)
36	TRN1	TRN	4	167826	169331	169331	170532	2_nonsis	1	1353	2705	1	16	1	1	0 (2:6)_(4:4aCO)
113	TRN1	TRN	10	44863	45922	46312	47473	2_nonsis	391	1500	2609	1	16	1	1	0 (2:6)_(4:4aCO)
13	TRN1	TRN	2	354720	355349	356462	356648	2_nonsis	1114	1521	1927	1	16	1	1	0 (2:6)_(4:4aCO)
145	TRN1	TRN	12	288686	288976	290359	290479	2_nonsis	1384	1588	1792	1	16	1	1	0 (2:6)_(4:4aCO)
201	TRN1	TRN	15	1010673	1011684	1011803	1013810	2_nonsis	120	1628	3136	1	16	1	1	0 (2:6)_(4:4aCO)
82	TRN1	TRN	7	375933	376066	377296	378026	2_nonsis	1231	1662	2092	1	16	1	1	0 (2:6)_(4:4aCO)
95	TRN1	TRN	8	139506	141400	141400	142863	2_nonsis	1	1679	3356	1	16	1	1	0 (2:6)_(4:4aCO)
110	TRN1	TRN	9	383441	383530	385232	385272	2_nonsis	1703	1767	1830	1	16	1	1	0 (2:6)_(4:4aCO)
181	TRN1	TRN	14	242111	242759	243530	245040	2_nonsis	772	1850	2928	1	16	1	1	0 (2:6)_(4:4aCO)
184	TRN1	TRN	14	538640	539186	539950	542443	2_nonsis	765	2284	3802	1	16	1	1	0 (2:6)_(4:4aCO)
126	TRN1	TRN	10	711083	711149	713591	715501	2_nonsis	2443	3430	4417	1	16	1	1	0 (2:6)_(4:4aCO)
21	TRN1	TRN	2	713781	714130	717754	717945	2_nonsis	3625	3894	4163	1	16	1	1	0 (2:6)_(4:4aCO)
26	TRN1	TRN	3	64304	64391	68233	68852	2_nonsis	3843	4195	4547	1	16	1	1	0 (2:6)_(4:4aCO)
107	TRN1	TRN	9	263911	267668	270599	270689	2_nonsis	2932	4855	6777	1	16	1	1	0 (2:6)_(4:4aCO)
29	TRN1	TRN	3	211504	211617	216424	216599	2_nonsis	4808	4951	5094	1	16	1	1	0 (2:6)_(4:4aCO)
111	TRN1	TRN	9	420788	420931	426032	426151	2_nonsis	5102	5232	5362	1	16	1	1	0 (2:6)_(4:4aCO)

35	TRN1	TRN	4	155836	156500	160479	162357	2_nonsis		3980	5250	6520	1	16	1	1	0	(2:6)_(4:4aCO)
190	TRN1	TRN	15	190009	191548	196465	196695	2_nonsis		4918	5802	6685	1	16	1	1	0	(2:6)_(4:4aCO)
108	TRN1	TRN	9	338670	339115	344826	344902	2_nonsis		5712	5972	6231	1	16	1	1	0	(2:6)_(4:4aCO)
146	TRN1	TRN	12	299315	299490	305929	308379	2_nonsis		6440	7752	9063	1	16	1	1	0	(2:6)_(4:4aCO)
56	TRN1	TRN	4	1473117	1473635	1482150	1483402	2_nonsis		8516	9400	10284	1	16	1	1	0	(2:6)_(4:4aCO)
59	TRN1	TRN	5	18839	23192	29923	31247	2_nonsis		6732	9570	12407	1	16	1	1	0	(2:6)_(4:4aCO)
139	TRN1	TRN	12	23826	23900	23826	23900	2_nonsis		0	37	73	1	100	1	1	0	(4:4aCO)
89	TRN1	TRN	7	1014216	1014432	1014216	1014432	2_nonsis		0	108	215	1	100	1	1	0	(4:4aCO)
68	TRN1	TRN	5	490952	491222	490952	491222	2_nonsis		0	135	269	1	100	1	1	0	(4:4aCO)
165	TRN1	TRN	13	75275	75558	75275	75558	2_nonsis		0	141	282	1	100	1	1	0	(4:4aCO)
191	TRN1	TRN	15	272726	273137	272726	273137	2_nonsis		0	205	410	1	100	1	1	0	(4:4aCO)
149	TRN1	TRN	12	507075	507492	507075	507492	2_nonsis		0	208	416	1	100	1	1	0	(4:4aCO)
156	TRN1	TRN	12	788874	789356	788874	789356	2_nonsis		0	241	481	1	100	1	1	0	(4:4aCO)
133	TRN1	TRN	11	406489	407067	406489	407067	2_nonsis		0	289	577	1	100	1	1	0	(4:4aCO)
216	TRN1	TRN	16	670672	671392	670672	671392	2_nonsis		0	360	719	1	100	1	1	0	(4:4aCO)
192	TRN1	TRN	15	283744	284515	283744	284515	2_nonsis		0	385	770	1	100	1	1	0	(4:4aCO)
96	TRN1	TRN	8	159962	160782	159962	160782	2_nonsis		0	410	819	1	100	1	1	0	(4:4aCO)
98	TRN1	TRN	8	309135	309963	309135	309963	2_nonsis		0	414	827	1	100	1	1	0	(4:4aCO)
122	TRN1	TRN	10	627141	627999	627141	627999	2_nonsis		0	429	857	1	100	1	1	0	(4:4aCO)
183	TRN1	TRN	14	293347	294319	293347	294319	2_nonsis		0	486	971	1	100	1	1	0	(4:4aCO)
136	TRN1	TRN	11	603048	604059	603048	604059	2_nonsis		0	505	1010	1	100	1	1	0	(4:4aCO)
57	TRN1	TRN	4	1485012	1486166	1485012	1486166	2_nonsis		0	577	1153	1	100	1	1	0	(4:4aCO)
143	TRN1	TRN	12	184588	185813	184588	185813	2_nonsis		0	612	1224	1	100	1	1	0	(4:4aCO)
7	TRN1	TRN	1	135325	136910	135325	136910	2_nonsis		0	792	1584	1	100	1	1	0	(4:4aCO)
167	TRN1	TRN	13	255052	256691	255052	256691	2_nonsis		0	819	1638	1	100	1	1	0	(4:4aCO)
198	TRN1	TRN	15	821660	823421	821660	823421	2_nonsis		0	880	1760	1	100	1	1	0	(4:4aCO)
22	TRN1	TRN	2	749103	750883	749103	750883	2_nonsis		0	890	1779	1	100	1	1	0	(4:4aCO)
180	TRN1	TRN	14	216919	218712	216919	218712	2_nonsis		0	896	1792	1	100	1	1	0	(4:4aCO)
9	TRN1	TRN	2	41298	43330	41298	43330	2_nonsis		0	1016	2031	1	100	1	1	0	(4:4aCO)
130	TRN1	TRN	11	148157	150866	148157	150866	2_nonsis		0	1354	2708	1	100	1	1	0	(4:4aCO)
6	TRN1	TRN	1	132066	135319	132066	135319	2_nonsis		0	1626	3252	1	100	1	1	0	(4:4aCO)
28	TRN1	TRN	3	79797	83502	79797	83502	2_nonsis		0	1852	3704	1	100	1	1	0	(4:4aCO)
124	TRN1	TRN	10	635321	640236	635321	640236	2_nonsis		0	2457	4914	1	100	1	1	0	(4:4aCO)
125	TRN1	TRN	10	697654	705639	697654	705639	2_nonsis		0	3992	7984	1	100	1	1	0	(4:4aCO)
93	TRN1	TRN	8	115113	115246	119053	119946	2_nonsis		3808	4320	4832	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
46	TRN1	TRN	4	825422	831279	837654	837953	2_nonsis		6376	9453	12530	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
179	TRN1	TRN	14	194143	194260	194860	195358	2_nonsis		601	908	1214	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
171	TRN1	TRN	13	504889	505551	507334	507502	2_nonsis		1784	2198	2612	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(4:4a)
33	TRN1	TRN	4	61275	62061	64539	64917	2_nonsis		2479	3060	3641	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
42	TRN1	TRN	4	433470	433591	439851	440205	2_nonsis		6261	6498	6734	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
188	TRN1	TRN	15	54339	55102	57166	57520	2_nonsis		2065	2623	3180	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)_(6:2)_(4:4a)
131	TRN1	TRN	11	345623	345918	348351	348497	2_nonsis		2434	2654	2873	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
58	TRN1	TRN	5	11381	11439	13009	13159	2_nonsis		1571	1674	1777	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)_(6:2)_(4:4a)
100	TRN1	TRN	8	481410	481494	485261	485522	2_nonsis		3768	3940	4111	3	20	1	1	0	(6:2)_(4:4)_(6:2)_(4:4)_(2:6)_(4:4aCO)
74	TRN1	TRN	6	93664	93934	102071	102489	2_nonsis		8138	8481	8824	3	20	1	1	0	(6:2)_(2:6)_(4:4)_(2:6)_(4:4aCO)_(4:4a)
78	TRN1	TRN	7	51330	51531	57855	58033		4	6325	6514	6702	0	1	2	0	2	(2:6)_(4:4)_(2:6)_(2:6a)_(0:8)_(8:0)_(2:6)_(4:4)
105	TRN1	TRN	9	138346	138429	145412	145517	2_sis		6984	7077	7170	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
153	TRN1	TRN	12	572294	572662	579316	581223	2_sis		6655	7792	8928	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
159	TRN1	TRN	12	936676	937242	939994	940048	2_sis		2753	3062	3371	0	1	2	0	2	(2:6)_(2:6a)_(4:4)
214	TRN1	TRN	16	520404	520684	521328	521940	2_sis		645	1090	1535	0	1	2	0	2	(6:2)_(8:0)_(4:4)
14	TRN1	TRN	2	427091	427568	436905	437703		3	9338	9975	10611	0	2	2	1	1	(2:6)_(0:8)_(2:6)_(4:4aCO)
17	TRN1	TRN	2	554757	555319	566265	566831		3	10947	11510	12073	0	2	2	1	1	(2:6)_(4:4)_(2:6)_(6:2)_(4:4aCO)
31	TRN1	TRN	3	249994	250855	266002	266699		3	15148	15926	16704	0	2	2	1	1	(2:6)_(4:4)_(2:6)_(0:8)_(2:6)_(0:8)_(2:6a)_(4:4)_(2:6a)_(4:4aCO)
40	TRN1	TRN	4	359534	360404	363511	363860		3	3108	3717	4325	0	2	2	1	1	(8:0)_(6:2)_(8:0)_(6:2a)_(4:4aCO)
55	TRN1	TRN	4	1415193	1416035	1417646	1417706		3	1612	2062	2512	0	2	2	1	1	(6:2)_(8:0)_(4:4aCO)
70	TRN1	TRN	6	26489	26713	29306	29691		3	2594	2898	3201	0	2	2	1	1	(2:6)_(6:2)_(4:4)_(4:4aCO)
71	TRN1	TRN	6	38359	38588	40232	40564		3	1645	1925	2204	0	2	2	1	1	(6:2)_(4:4aCO)_(6:2a)_(4:4a)_(6:2a)_(4:4a)
81	TRN1	TRN	7	222691	224665	226711	230011		3	2047	4683	7319	0	2	2	1	1	(6:2)_(6:2a)_(4:4aCO)
88	TRN1	TRN	7	1003534	1004173	1005941	1006143		3	1769	2189	2608	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
120	TRN1	TRN	10	385772	385990	387794	387923		3	1805	1978	2150	0	2	2	1	1	(2:6)_(0:8)_(4:4aCO)

137	TRN1	TRN	11	629639	631180	634635	635348	3	3456	4582	5708	0	2	2	1	1	(8:0)_(6:2)_(4:4aCO)
164	TRN1	TRN	13	15705	16287	21269	21523	3	4983	5400	5817	0	2	2	1	1	(2:6)_(6:2)_(2:6a)_(4:4aCO)
172	TRN1	TRN	13	581966	582869	587075	587600	3	4207	4920	5633	0	2	2	1	1	(2:6)_(0:8)_(4:4aCO)
177	TRN1	TRN	14	51868	52069	55899	57439	3	3831	4701	5570	0	2	2	1	1	(0:8)_(2:6)_(0:8)_(2:6a)_(4:4aCO)
185	TRN1	TRN	14	641892	642568	652841	655138	4	10274	11760	13245	0	2	2	2	0	(6:2)_(2:6)_(4:4aCO)
189	TRN1	TRN	15	79906	79930	92712	93135	3	12783	13006	13228	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
217	TRN1	TRN	16	840627	841238	844218	858788	3	2981	10571	18160	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
1	TRN1	TRN	1	61164	61414	62990	63992	2_nonsis	1577	2202	2827	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(4:4CO)
23	TRN1	TRN	2	764110	764239	775579	777303	4	11341	12267	13192	0	3	2	1	1	(2:6)_(4:4)_(2:6a)_(4:4aCO)_(4:4bCO)
50	TRN1	TRN	4	1115900	1116554	1117013	1117890	2_nonsis	460	1225	1989	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4CO)
51	TRN1	TRN	4	1248319	1248513	1259982	1260779	2_nonsis	11470	11965	12459	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)_(2:6)_(4:4CO)
80	TRN1	TRN	7	169612	170211	172407	172596	3	2197	2590	2983	0	3	2	1	1	(8:0)_(4:4aCO)_(2:6)_(4:4bCO)_(2:6)_(4:4b)
91	TRN1	TRN	8	23109	23521	27293	27988	4	3773	4326	4878	0	3	2	1	1	(4:4aCO)_(6:2)_(0:8)_(2:6)_(4:4bCO)
101	TRN1	TRN	8	490515	490863	493409	493855	3	2547	2943	3339	0	3	2	1	1	(4:4aCO)_(6:2)_(4:4bCO)
117	TRN1	TRN	10	161596	162223	163140	163580	3	918	1451	1983	0	3	2	1	1	(4:4aCO)_(4:4bCO)
144	TRN1	TRN	12	223946	224012	247140	247370	3	23129	23276	23423	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4bCO)_(2:6)_(4:4b)
157	TRN1	TRN	12	821384	822252	823256	826618	4	1005	3119	5233	0	3	2	1	1	(4:4aCO)_(4:4bCO)_(2:6)_(4:4aCO)
161	TRN1	TRN	12	1008837	1008873	1014017	1014198	3	5145	5253	5360	0	3	2	1	1	(6:2)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(6:2a)_(4:4bCO)
163	TRN1	TRN	12	1041901	1042079	1043638	1043701	3	1560	1680	1799	0	3	2	1	1	(6:2)_(4:4aCO)_(4:4bCO)_(2:6)_(4:4b)
166	TRN1	TRN	13	245624	247126	253309	253845	2_nonsis	6184	7202	8220	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4CO)
168	TRN1	TRN	13	335534	335853	354882	355271	4	19030	19383	19736	0	3	2	2	0	(2:6)_(4:4)_(6:2)_(4:4aCO)_(6:2)_(8:0)_(4:4a)_(8:0)_(6:2a)_(8:0)_(4:4bCO)
170	TRN1	TRN	13	487831	489569	496159	496520	3	6591	7640	8688	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)
175	TRN1	TRN	13	742337	744735	762006	762346	4	17272	18640	20008	0	3	2	2	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4bCO)
187	TRN1	TRN	15	42586	42784	45210	45897	2_nonsis	2427	2869	3310	0	3	2	0	2	(2:6)_(4:4)_(6:2)_(4:4aCO)_(4:4CO)
195	TRN1	TRN	15	642471	642646	648237	648434	2_nonsis	5592	5777	5962	0	3	2	1	1	(6:2)_(4:4)_(6:2)_(4:4aCO)_(2:6)_(4:4CO)
206	TRN1	TRN	16	34674	35338	77509	77995	4	42172	42746	43320	0	3	2	1	1	(6:2)_(6:2a)_(8:0)_(4:4)_(2:6)_(4:4aCO)_(2:6a)_(4:4a)_(6:2b)_(2:6b)_(4:4bCO)
207	TRN1	TRN	16	85729	86390	87536	88155	2_nonsis	1147	1786	2425	0	3	2	0	2	(2:6)_(4:4)_(2:6)_(4:4aCO)_(4:4CO)
213	TRN1	TRN	16	468648	469629	470217	470860	2_nonsis	589	1400	2211	0	3	2	0	2	(6:2)_(4:4aCO)_(4:4CO)
243	TRN1	TRN	2	800115	800195	801524	813184	3	1330	7199	13068	0	4	1	NA	NA	6:2_6:2
296	TRN1	TRN	7	24468	25442	24468	25442	1	0	487	973	0	4	1	NA	NA	
358	TRN1	TRN	11	656226	656592	658549	666816	1	0	5295	10589	0	4	1	NA	NA	
407	TRN1	TRN	14	778885	779009	781274	784333	1	2266	3857	5447	0	4	1	NA	NA	2:6_4:4_2:6_4:4_2:6_4:4_2:6
170	TRN10	TRN	12	876120	876459	881235	882746	1	4777	5701	6625	1	7	1	0	1	6:2_4:4_6:2
189	TRN10	TRN	13	765059	765109	765706	765773	1	598	656	713	1	8	1	0	1	2:6_4:4_2:6
26	TRN10	TRN	3	117992	118273	120719	121150	1	2447	2802	3157	1	8	1	0	1	2:6_4:4_2:6
137	TRN10	TRN	10	642375	642483	645565	646018	1	3083	3363	3642	1	8	1	0	1	2:6_4:4_2:6
224	TRN10	TRN	15	546393	546837	553518	554715	1	6682	7502	8321	1	8	1	0	1	2:6_4:4_2:6
198	TRN10	TRN	14	135855	135879	135879	135908	1	1	27	52	1	10	1	0	1	06:02
219	TRN10	TRN	15	221900	222314	222314	222653	1	1	377	752	1	10	1	0	1	06:02
77	TRN10	TRN	7	73286	73309	73727	73810	1	419	471	523	1	10	1	0	1	06:02
122	TRN10	TRN	10	125246	125687	125897	126262	1	211	613	1015	1	10	1	0	1	06:02
85	TRN10	TRN	7	372926	373531	373766	373940	1	236	625	1013	1	10	1	0	1	06:02
129	TRN10	TRN	10	388844	389073	389413	389929	1	341	713	1084	1	10	1	0	1	06:02
178	TRN10	TRN	13	308338	308762	309305	309395	1	544	800	1056	1	10	1	0	1	06:02
206	TRN10	TRN	14	425890	427278	427451	427715	1	174	999	1824	1	10	1	0	1	06:02
108	TRN10	TRN	8	396723	397520	398182	398452	1	663	1196	1728	1	10	1	0	1	06:02
192	TRN10	TRN	13	831576	832164	832607	833534	1	444	1201	1957	1	10	1	0	1	06:02
204	TRN10	TRN	14	396967	397399	398211	398753	1	813	1299	1785	1	10	1	0	1	06:02
110	TRN10	TRN	8	421840	422434	423045	423870	1	612	1321	2029	1	10	1	0	1	06:02
8	TRN10	TRN	2	100413	101103	102053	102116	1	951	1327	1702	1	10	1	0	1	06:02
163	TRN10	TRN	12	614751	616056	616330	617274	1	275	1399	2522	1	10	1	0	1	06:02
96	TRN10	TRN	7	985834	987315	987893	988358	1	579	1551	2523	1	10	1	0	1	06:02
233	TRN10	TRN	15	1004534	1007049	1007049	1007685	1	1	1576	3150	1	10	1	0	1	06:02
24	TRN10	TRN	2	797893	798747	799806	800055	1	1060	1611	2161	1	10	1	0	1	06:02
99	TRN10	TRN	8	56032	56225	57698	57905	1	1474	1673	1872	1	10	1	0	1	06:02
240	TRN10	TRN	16	529035	529207	529944	532161	1	738	1932	3125	1	10	1	0	1	06:02
197	TRN10	TRN	14	87215	87864	89494	89648	1	1631	2032	2432	1	10	1	0	1	06:02
20	TRN10	TRN	2	680726	681166	682449	683592	1	1284	2075	2865	1	10	1	0	1	06:02
203	TRN10	TRN	14	267621	268398	270133	270523	1	1736	2319	2901	1	10	1	0	1	06:02
62	TRN10	TRN	5	312348	312465	314632	315416	1	2168	2618	3067	1	10	1	0	1	06:02

64	TRN10	TRN	5	379092	379879	381978	382688	1	2100	2848	3595	1	10	1	0	1 06:02
229	TRN10	TRN	15	787105	787507	790680	790997	1	3174	3533	3891	1	10	1	0	1 06:02
42	TRN10	TRN	4	694587	694831	698508	698788	1	3678	3939	4200	1	10	1	0	1 06:02
231	TRN10	TRN	15	814826	815222	819348	819414	1	4127	4357	4587	1	10	1	0	1 06:02
13	TRN10	TRN	2	451124	451175	455916	456385	1	4742	5001	5260	1	10	1	0	1 06:02
190	TRN10	TRN	13	816350	816512	821494	822331	1	4983	5482	5980	1	10	1	0	1 06:02
68	TRN10	TRN	6	33008	33158	39488	39674	1	6331	6498	6665	1	10	1	0	1 06:02
216	TRN10	TRN	15	187590	188321	193685	196238	1	5365	7006	8647	1	10	1	0	1 06:02
103	TRN10	TRN	8	320071	320927	331868	334431	1	10942	12651	14359	1	10	1	0	1 06:02
109	TRN10	TRN	8	417913	418214	418214	418349	1	1	218	435	1	10.1	1	0	1 02:06
223	TRN10	TRN	15	467149	467407	467407	467641	1	1	246	491	1	10.1	1	0	1 02:06
165	TRN10	TRN	12	784218	784454	784477	784820	1	24	313	601	1	10.1	1	0	1 02:06
105	TRN10	TRN	8	341515	342157	342157	342405	1	1	445	889	1	10.1	1	0	1 02:06
5	TRN10	TRN	1	181119	181197	181491	181752	1	295	464	632	1	10.1	1	0	1 02:06
47	TRN10	TRN	4	931988	932298	932298	933005	1	1	509	1016	1	10.1	1	0	1 02:06
161	TRN10	TRN	12	576339	576702	576702	577535	1	1	598	1195	1	10.1	1	0	1 02:06
119	TRN10	TRN	9	407232	407953	408110	408521	1	158	723	1288	1	10.1	1	0	1 02:06
17	TRN10	TRN	2	633960	635127	635127	635445	1	1	743	1484	1	10.1	1	0	1 02:06
126	TRN10	TRN	10	279703	280016	280598	280699	1	583	789	995	1	10.1	1	0	1 02:06
155	TRN10	TRN	12	165496	165796	166515	166641	1	720	932	1144	1	10.1	1	0	1 02:06
74	TRN10	TRN	6	247354	247915	248365	248816	1	451	956	1461	1	10.1	1	0	1 02:06
154	TRN10	TRN	12	160756	161156	161416	162493	1	261	999	1736	1	10.1	1	0	1 02:06
131	TRN10	TRN	10	412419	412734	413049	414104	1	316	1000	1684	1	10.1	1	0	1 02:06
94	TRN10	TRN	7	806818	806907	807791	807996	1	885	1031	1177	1	10.1	1	0	1 02:06
200	TRN10	TRN	14	228789	229890	230322	230542	1	433	1093	1752	1	10.1	1	0	1 02:06
112	TRN10	TRN	8	483502	483796	484407	485261	1	612	1185	1758	1	10.1	1	0	1 02:06
4	TRN10	TRN	1	170945	172092	172585	172844	1	494	1196	1898	1	10.1	1	0	1 02:06
150	TRN10	TRN	11	590760	592478	592577	593181	1	100	1260	2420	1	10.1	1	0	1 02:06
160	TRN10	TRN	12	387156	387519	388456	388801	1	938	1291	1644	1	10.1	1	0	1 02:06
139	TRN10	TRN	10	713591	715501	715592	716361	1	92	1431	2769	1	10.1	1	0	1 02:06
55	TRN10	TRN	5	130380	130887	131558	132643	1	672	1467	2262	1	10.1	1	0	1 02:06
172	TRN10	TRN	12	1013592	1014017	1015108	1015543	1	1092	1521	1950	1	10.1	1	0	1 02:06
177	TRN10	TRN	13	237159	237882	238681	239557	1	800	1599	2397	1	10.1	1	0	1 02:06
106	TRN10	TRN	8	351610	352512	353343	354035	1	832	1628	2424	1	10.1	1	0	1 02:06
133	TRN10	TRN	10	467589	469453	469702	470610	1	250	1635	3020	1	10.1	1	0	1 02:06
174	TRN10	TRN	13	54586	54867	56369	56748	1	1503	1832	2161	1	10.1	1	0	1 02:06
118	TRN10	TRN	9	344556	344691	346155	346766	1	1465	1837	2209	1	10.1	1	0	1 02:06
124	TRN10	TRN	10	205252	205704	207452	207693	1	1749	2095	2440	1	10.1	1	0	1 02:06
75	TRN10	TRN	7	33274	33441	35451	35543	1	2011	2140	2268	1	10.1	1	0	1 02:06
142	TRN10	TRN	11	238513	239211	240992	241418	1	1782	2343	2904	1	10.1	1	0	1 02:06
135	TRN10	TRN	10	581933	582214	584209	584647	1	1996	2355	2713	1	10.1	1	0	1 02:06
51	TRN10	TRN	4	1106884	1107089	1109568	1109736	1	2480	2666	2851	1	10.1	1	0	1 02:06
167	TRN10	TRN	12	823256	826618	826618	829421	1	1	3083	6164	1	10.1	1	0	1 02:06
195	TRN10	TRN	14	52925	53465	56445	57439	1	2981	3747	4513	1	10.1	1	0	1 02:06
248	TRN10	TRN	16	754744	755194	758960	759209	1	3767	4116	4464	1	10.1	1	0	1 02:06
98	TRN10	TRN	7	997225	999165	1002898	1003128	1	3734	4818	5902	1	10.1	1	0	1 02:06
249	TRN10	TRN	16	844218	857345	857345	858788	1	1	7285	14569	1	10.1	1	0	1 02:06
152	TRN10	TRN	11	627471	628616	635970	636244	1	7355	8064	8772	1	10.1	1	0	1 02:06
184	TRN10	TRN	13	556437	557365	565610	565803	1	8246	8806	9365	1	10.1	1	0	1 02:06
3	TRN10	TRN	1	155505	158814	167179	170726	1	8366	11793	15220	1	10.1	1	0	1 02:06
57	TRN10	TRN	5	177603	177849	186890	187027	2_nonsis	9042	9233	9423	3	30	1	0	1 2:6_6:2
173	TRN10	TRN	13	44503	45656	51084	51141	2_nonsis	5429	6033	6637	3	30	1	0	1 6:2_2:6_4:4_2:6
66	TRN10	TRN	5	477110	477476	486863	486920	2_nonsis	9388	9599	9809	3	30	1	0	1 6:2_2:6_4:4_6:2
97	TRN10	TRN	7	989982	990718	991126	991917	2_nonsis	409	1172	1934	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
138	TRN10	TRN	10	706135	706547	707550	707655	2_nonsis	1004	1262	1519	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
157	TRN10	TRN	12	275125	276029	276866	277094	2_nonsis	838	1403	1968	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
215	TRN10	TRN	15	132713	135587	138847	139359	2_nonsis	3261	4953	6645	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
120	TRN10	TRN	10	30160	30194	31175	31246	2_nonsis	982	1034	1085	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
221	TRN10	TRN	15	408540	408953	410731	410742	2_nonsis	1779	1990	2201	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
185	TRN10	TRN	13	616649	617093	618959	619338	2_nonsis	1867	2278	2688	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)

7	TRN10	TRN	2	92818	93100	95376	96034	2_nonsis	2277	2746	3215	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
46	TRN10	TRN	4	842636	842982	846137	846996	2_nonsis	3156	3758	4359	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
11	TRN10	TRN	2	388386	388424	394430	394726	2_nonsis	6007	6173	6339	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
199	TRN10	TRN	14	192780	193276	200248	200718	2_nonsis	6973	7455	7937	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
162	TRN10	TRN	12	591568	591955	606238	606436	2_nonsis	14284	14576	14867	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
143	TRN10	TRN	11	288741	289501	295309	296531	2_nonsis	5809	6799	7789	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
63	TRN10	TRN	5	373736	374737	377471	377999	2_nonsis	2735	3499	4262	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
243	TRN10	TRN	16	650861	651044	660697	660982	2_nonsis	9654	9887	10120	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
37	TRN10	TRN	4	307671	307920	307920	307984	2_nonsis	1	157	312	1	15	1	1	0	(6:2)_(4:4aCO)
156	TRN10	TRN	12	229498	229597	229623	230005	2_nonsis	27	267	506	1	15	1	1	0	(6:2)_(4:4aCO)
41	TRN10	TRN	4	688689	688805	688841	689207	2_nonsis	37	277	517	1	15	1	1	0	(6:2)_(4:4aCO)
144	TRN10	TRN	11	308786	309009	309188	309294	2_nonsis	180	344	507	1	15	1	1	0	(6:2)_(4:4aCO)
179	TRN10	TRN	13	327938	328333	328409	328706	2_nonsis	77	422	767	1	15	1	1	0	(6:2)_(4:4aCO)
213	TRN10	TRN	14	764495	764938	765005	765537	2_nonsis	68	555	1041	1	15	1	1	0	(6:2)_(4:4aCO)
82	TRN10	TRN	7	284996	285065	285407	286154	2_nonsis	343	750	1157	1	15	1	1	0	(6:2)_(4:4aCO)
130	TRN10	TRN	10	395874	396515	396640	397262	2_nonsis	126	757	1387	1	15	1	1	0	(6:2)_(4:4aCO)
101	TRN10	TRN	8	73441	73687	74372	74397	2_nonsis	686	821	955	1	15	1	1	0	(6:2)_(4:4aCO)
81	TRN10	TRN	7	171278	171503	172231	172407	2_nonsis	729	929	1128	1	15	1	1	0	(6:2)_(4:4aCO)
38	TRN10	TRN	4	395767	396458	396700	397411	2_nonsis	243	943	1643	1	15	1	1	0	(6:2)_(4:4aCO)
69	TRN10	TRN	6	45217	45521	46302	46380	2_nonsis	782	972	1162	1	15	1	1	0	(6:2)_(4:4aCO)
91	TRN10	TRN	7	678883	679675	679675	681013	2_nonsis	1	1065	2129	1	15	1	1	0	(6:2)_(4:4aCO)
182	TRN10	TRN	13	384784	384946	385945	386028	2_nonsis	1000	1122	1243	1	15	1	1	0	(6:2)_(4:4aCO)
159	TRN10	TRN	12	372524	373651	373666	374858	2_nonsis	16	1175	2333	1	15	1	1	0	(6:2)_(4:4aCO)
61	TRN10	TRN	5	306189	308000	308152	308551	2_nonsis	153	1257	2361	1	15	1	1	0	(6:2)_(4:4aCO)
12	TRN10	TRN	2	442879	444175	444774	444887	2_nonsis	600	1304	2007	1	15	1	1	0	(6:2)_(4:4aCO)
23	TRN10	TRN	2	746171	748391	748391	748916	2_nonsis	1	1373	2744	1	15	1	1	0	(6:2)_(4:4aCO)
127	TRN10	TRN	10	349631	350244	351259	351479	2_nonsis	1016	1432	1847	1	15	1	1	0	(6:2)_(4:4aCO)
49	TRN10	TRN	4	1051761	1054524	1054662	1055183	2_nonsis	139	1780	3421	1	15	1	1	0	(6:2)_(4:4aCO)
147	TRN10	TRN	11	464192	464453	466102	466582	2_nonsis	1650	2020	2389	1	15	1	1	0	(6:2)_(4:4aCO)
209	TRN10	TRN	14	507599	508159	509646	510203	2_nonsis	1488	2046	2603	1	15	1	1	0	(6:2)_(4:4aCO)
169	TRN10	TRN	12	865078	867405	867405	869664	2_nonsis	1	2293	4585	1	15	1	1	0	(6:2)_(4:4aCO)
234	TRN10	TRN	16	21870	21970	22826	26114	2_nonsis	857	2550	4243	1	15	1	1	0	(6:2)_(4:4aCO)
36	TRN10	TRN	4	89925	90257	91959	93521	2_nonsis	1703	2649	3595	1	15	1	1	0	(6:2)_(4:4aCO)
168	TRN10	TRN	12	849651	854846	854846	855144	2_nonsis	1	2747	5492	1	15	1	1	0	(6:2)_(4:4aCO)
246	TRN10	TRN	16	710553	710988	713201	713880	2_nonsis	2214	2770	3326	1	15	1	1	0	(6:2)_(4:4aCO)
212	TRN10	TRN	14	682580	686654	686681	688572	2_nonsis	28	3010	5991	1	15	1	1	0	(6:2)_(4:4aCO)
60	TRN10	TRN	5	266722	268597	270473	271135	2_nonsis	1877	3145	4412	1	15	1	1	0	(6:2)_(4:4aCO)
6	TRN10	TRN	1	189825	190402	193260	193807	2_nonsis	2859	3420	3981	1	15	1	1	0	(6:2)_(4:4aCO)
148	TRN10	TRN	11	530688	531524	534319	535579	2_nonsis	2796	3843	4890	1	15	1	1	0	(6:2)_(4:4aCO)
102	TRN10	TRN	8	190671	191072	194830	195005	2_nonsis	3759	4046	4333	1	15	1	1	0	(6:2)_(4:4aCO)
117	TRN10	TRN	9	327096	333581	334383	334640	2_nonsis	803	4173	7543	1	15	1	1	0	(6:2)_(4:4aCO)
10	TRN10	TRN	2	342383	342611	347192	347803	2_nonsis	4582	5001	5419	1	15	1	1	0	(6:2)_(4:4aCO)
145	TRN10	TRN	11	378901	379079	384363	384792	2_nonsis	5285	5588	5890	1	15	1	1	0	(6:2)_(4:4aCO)
113	TRN10	TRN	8	513034	514468	520252	521047	2_nonsis	5785	6899	8012	1	15	1	1	0	(6:2)_(4:4aCO)
242	TRN10	TRN	16	641294	642071	648637	648799	2_nonsis	6567	7036	7504	1	15	1	1	0	(6:2)_(4:4aCO)
27	TRN10	TRN	3	123928	123999	131879	133715	2_nonsis	7881	8834	9786	1	15	1	1	0	(6:2)_(4:4aCO)
25	TRN10	TRN	3	83816	93455	105854	106362	2_nonsis	12400	17473	22545	1	15	1	1	0	(6:2)_(4:4aCO)
104	TRN10	TRN	8	339656	339696	339696	340031	2_nonsis	1	188	374	1	16	1	1	0	(2:6)_(4:4aCO)
247	TRN10	TRN	16	715923	716297	716297	716554	2_nonsis	1	316	630	1	16	1	1	0	(2:6)_(4:4aCO)
238	TRN10	TRN	16	424578	424841	425006	425302	2_nonsis	166	445	723	1	16	1	1	0	(2:6)_(4:4aCO)
202	TRN10	TRN	14	251477	251609	251874	252203	2_nonsis	266	496	725	1	16	1	1	0	(2:6)_(4:4aCO)
39	TRN10	TRN	4	399202	399570	399570	400197	2_nonsis	1	498	994	1	16	1	1	0	(2:6)_(4:4aCO)
235	TRN10	TRN	16	113385	114050	114102	114414	2_nonsis	53	541	1028	1	16	1	1	0	(2:6)_(4:4aCO)
134	TRN10	TRN	10	515737	516190	516436	516831	2_nonsis	247	670	1093	1	16	1	1	0	(2:6)_(4:4aCO)
87	TRN10	TRN	7	424261	424512	424942	425181	2_nonsis	431	675	919	1	16	1	1	0	(2:6)_(4:4aCO)
132	TRN10	TRN	10	464438	465282	465282	465795	2_nonsis	1	679	1356	1	16	1	1	0	(2:6)_(4:4aCO)
222	TRN10	TRN	15	455108	455286	455342	456606	2_nonsis	57	777	1497	1	16	1	1	0	(2:6)_(4:4aCO)
128	TRN10	TRN	10	367642	368828	368840	369255	2_nonsis	13	813	1612	1	16	1	1	0	(2:6)_(4:4aCO)
218	TRN10	TRN	15	218142	219124	219136	219822	2_nonsis	13	846	1679	1	16	1	1	0	(2:6)_(4:4aCO)
35	TRN10	TRN	4	24937	25195	25835	26111	2_nonsis	641	907	1173	1	16	1	1	0	(2:6)_(4:4aCO)

9	TRN10	TRN	2	250316	250789	251134	252027	2_nonsis	346	1028	1710	1	16	1	1	0	(2:6)_(4:4aCO)
50	TRN10	TRN	4	1079258	1079450	1079984	1080788	2_nonsis	535	1032	1529	1	16	1	1	0	(2:6)_(4:4aCO)
211	TRN10	TRN	14	678661	678891	679089	680556	2_nonsis	199	1047	1894	1	16	1	1	0	(2:6)_(4:4aCO)
245	TRN10	TRN	16	665970	666185	666924	667377	2_nonsis	740	1073	1406	1	16	1	1	0	(2:6)_(4:4aCO)
180	TRN10	TRN	13	339889	340680	341111	341630	2_nonsis	432	1086	1740	1	16	1	1	0	(2:6)_(4:4aCO)
141	TRN10	TRN	11	90751	91192	92069	92108	2_nonsis	878	1117	1356	1	16	1	1	0	(2:6)_(4:4aCO)
67	TRN10	TRN	6	26889	28318	28662	28792	2_nonsis	345	1124	1902	1	16	1	1	0	(2:6)_(4:4aCO)
239	TRN10	TRN	16	509084	509810	510291	510985	2_nonsis	482	1191	1900	1	16	1	1	0	(2:6)_(4:4aCO)
44	TRN10	TRN	4	777389	777638	779023	779427	2_nonsis	1386	1712	2037	1	16	1	1	0	(2:6)_(4:4aCO)
181	TRN10	TRN	13	379248	379442	380997	381204	2_nonsis	1556	1756	1955	1	16	1	1	0	(2:6)_(4:4aCO)
194	TRN10	TRN	14	46932	49011	49011	50444	2_nonsis	1	1756	3511	1	16	1	1	0	(2:6)_(4:4aCO)
40	TRN10	TRN	4	625839	628602	628602	629487	2_nonsis	1	1824	3647	1	16	1	1	0	(2:6)_(4:4aCO)
65	TRN10	TRN	5	451710	452483	453437	454403	2_nonsis	955	1824	2692	1	16	1	1	0	(2:6)_(4:4aCO)
31	TRN10	TRN	3	201258	202229	203463	204750	2_nonsis	1235	2363	3491	1	16	1	1	0	(2:6)_(4:4aCO)
29	TRN10	TRN	3	140025	140422	143843	144261	2_nonsis	3422	3829	4235	1	16	1	1	0	(2:6)_(4:4aCO)
52	TRN10	TRN	4	1366294	1366606	1370179	1370923	2_nonsis	3574	4101	4628	1	16	1	1	0	(2:6)_(4:4aCO)
220	TRN10	TRN	15	402509	402926	406895	406989	2_nonsis	3970	4225	4479	1	16	1	1	0	(2:6)_(4:4aCO)
43	TRN10	TRN	4	769508	769848	773893	774079	2_nonsis	4046	4308	4570	1	16	1	1	0	(2:6)_(4:4aCO)
45	TRN10	TRN	4	825422	831279	831279	837275	2_nonsis	1	5927	11852	1	16	1	1	0	(2:6)_(4:4aCO)
125	TRN10	TRN	10	264413	264641	270332	270695	2_nonsis	5692	5987	6281	1	16	1	1	0	(2:6)_(4:4aCO)
90	TRN10	TRN	7	589840	590641	596681	596824	2_nonsis	6041	6512	6983	1	16	1	1	0	(2:6)_(4:4aCO)
153	TRN10	TRN	12	150671	151170	159272	159591	2_nonsis	8103	8511	8919	1	16	1	1	0	(2:6)_(4:4aCO)
205	TRN10	TRN	14	409872	410941	419038	419074	2_nonsis	8098	8650	9201	1	16	1	1	0	(2:6)_(4:4aCO)
71	TRN10	TRN	6	90244	90659	98766	99605	2_nonsis	8108	8734	9360	1	16	1	1	0	(2:6)_(4:4aCO)
22	TRN10	TRN	2	731596	731934	743673	743899	2_nonsis	11740	12021	12302	1	16	1	1	0	(2:6)_(4:4aCO)
201	TRN10	TRN	14	235956	236810	248236	249065	2_nonsis	11427	12268	13108	1	16	1	1	0	(2:6)_(4:4aCO)
230	TRN10	TRN	15	810765	811006	810765	811006	2_nonsis	0	120	240	1	100	1	1	0	(4:4aCO)
58	TRN10	TRN	5	188873	189254	188873	189254	2_nonsis	0	190	380	1	100	1	1	0	(4:4aCO)
244	TRN10	TRN	16	662220	662624	662220	662624	2_nonsis	0	202	403	1	100	1	1	0	(4:4aCO)
84	TRN10	TRN	7	346294	346793	346294	346793	2_nonsis	0	249	498	1	100	1	1	0	(4:4aCO)
80	TRN10	TRN	7	112158	112793	112158	112793	2_nonsis	0	317	634	1	100	1	1	0	(4:4aCO)
164	TRN10	TRN	12	621288	621936	621288	621936	2_nonsis	0	324	647	1	100	1	1	0	(4:4aCO)
175	TRN10	TRN	13	96883	97548	96883	97548	2_nonsis	0	332	664	1	100	1	1	0	(4:4aCO)
28	TRN10	TRN	3	134648	135329	134648	135329	2_nonsis	0	340	680	1	100	1	1	0	(4:4aCO)
217	TRN10	TRN	15	197183	197943	197183	197943	2_nonsis	0	380	759	1	100	1	1	0	(4:4aCO)
88	TRN10	TRN	7	482421	483344	482421	483344	2_nonsis	0	461	922	1	100	1	1	0	(4:4aCO)
21	TRN10	TRN	2	686757	687872	686757	687872	2_nonsis	0	557	1114	1	100	1	1	0	(4:4aCO)
196	TRN10	TRN	14	80433	81575	80433	81575	2_nonsis	0	571	1141	1	100	1	1	0	(4:4aCO)
225	TRN10	TRN	15	554987	556316	554987	556316	2_nonsis	0	664	1328	1	100	1	1	0	(4:4aCO)
151	TRN10	TRN	11	603048	604404	603048	604404	2_nonsis	0	678	1355	1	100	1	1	0	(4:4aCO)
78	TRN10	TRN	7	94650	96070	94650	96070	2_nonsis	0	710	1419	1	100	1	1	0	(4:4aCO)
19	TRN10	TRN	2	676125	677644	676125	677644	2_nonsis	0	759	1518	1	100	1	1	0	(4:4aCO)
48	TRN10	TRN	4	1013983	1015515	1013983	1015515	2_nonsis	0	766	1531	1	100	1	1	0	(4:4aCO)
226	TRN10	TRN	15	556316	558487	556316	558487	2_nonsis	0	1085	2170	1	100	1	1	0	(4:4aCO)
176	TRN10	TRN	13	170002	172478	170002	172478	2_nonsis	0	1238	2475	1	100	1	1	0	(4:4aCO)
79	TRN10	TRN	7	97616	100362	97616	100362	2_nonsis	0	1373	2745	1	100	1	1	0	(4:4aCO)
166	TRN10	TRN	12	811301	815763	811301	815763	2_nonsis	0	2231	4461	1	100	1	1	0	(4:4aCO)
18	TRN10	TRN	2	662444	668076	662444	668076	2_nonsis	0	2816	5631	1	100	1	1	0	(4:4aCO)
171	TRN10	TRN	12	892436	930472	892436	930472	2_nonsis	0	19018	38035	1	100	1	1	0	(4:4aCO)
191	TRN10	TRN	13	824885	825266	826214	826499	2_nonsis	949	1281	1613	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
227	TRN10	TRN	15	624112	624475	625649	625813	2_nonsis	1175	1438	1700	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
59	TRN10	TRN	5	255702	256032	256810	258361	2_nonsis	779	1719	2658	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
214	TRN10	TRN	15	117525	123864	124780	124867	2_nonsis	917	4129	7341	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
15	TRN10	TRN	2	536450	536637	540838	541062	2_nonsis	4202	4407	4611	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
34	TRN10	TRN	3	242917	243218	247472	248057	2_nonsis	4255	4697	5139	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
16	TRN10	TRN	2	628807	629013	631768	632896	2_nonsis	2756	3422	4088	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
236	TRN10	TRN	16	150643	151045	154774	155088	2_nonsis	3730	4087	4444	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
89	TRN10	TRN	7	548503	549148	554163	554830	2_nonsis	5016	5671	6326	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
70	TRN10	TRN	6	51748	52738	62459	63014	2_nonsis	9722	10494	11265	3	20	1	1	0	(2:6)_(6:2)_(2:6)_(4:4aCO)
183	TRN10	TRN	13	504889	505362	520382	521041	2_nonsis	15021	15586	16151	3	20	1	1	0	(2:6)_(6:2)_(4:4)_(2:6)_(4:4aCO)

207	TRN10	TRN	14	480883	480999	486092	486859	2_nonsis		5094	5535	5975	3	20	1	1	0 (2:6)_(4:4)_(2:6)_(4:4)_(6:2)_(4:4aCO)
33	TRN10	TRN	3	221877	223339	238082	238725	4	14744	15796	16847	0	1	2	0	2	(0:8)_(8:0)_(6:2)_(4:4)
32	TRN10	TRN	3	204750	207459	216599	218143	4	9141	11267	13392	0	2	2	1	1	(8:0)_(4:4aCO)_(8:0)_(6:2)_(4:4a)
53	TRN10	TRN	4	1450144	1450588	1455942	1458372	3	5355	6791	8227	0	2	2	1	1	(6:2)_(4:4)_(6:2)_(8:0)_(6:2)_(4:4aCO)
83	TRN10	TRN	7	287343	287487	293303	294083	3	5817	6278	6739	0	2	2	1	1	(8:0)_(4:4aCO)
92	TRN10	TRN	7	783224	783677	785907	786618	3	2231	2812	3393	0	2	2	1	1	(6:2)_(4:4aCO)_(6:2a)_(4:4a)
93	TRN10	TRN	7	796858	798046	804084	804378	3	6039	6779	7519	0	2	2	1	1	(6:2)_(4:4)_(2:6)_(0:8)_(2:6)_(4:4aCO)_(2:6a)_(4:4a)
107	TRN10	TRN	8	359669	359915	377460	377707	3	17546	17792	18037	0	2	2	1	1	(2:6)_(0:8)_(2:6)_(0:8)_(2:6)_(4:4aCO)
111	TRN10	TRN	8	451172	452903	464743	465244	4	11841	12956	14071	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(0:8)_(2:6b)_(4:4aCO)
114	TRN10	TRN	9	93804	94143	103227	103838	3	9085	9559	10033	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)
115	TRN10	TRN	9	124830	125455	128732	129806	3	3278	4127	4975	0	2	2	1	1	(6:2)_(2:6)_(4:4aCO)
140	TRN10	TRN	11	44603	45993	48808	49402	3	2816	3807	4798	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)
149	TRN10	TRN	11	557299	558102	569085	569468	4	10984	11576	12168	0	2	2	1	1	(6:2)_(2:6)_(0:8)_(2:6)_(4:4aCO)
158	TRN10	TRN	12	281289	281896	301472	301852	3	19577	20070	20562	0	2	2	1	1	(2:6)_(0:8)_(2:6)_(2:6a)_(2:6b)_(2:6)_(0:8)_(2:6b)_(4:4aCO)
188	TRN10	TRN	13	755812	757200	763221	763537	3	6022	6873	7724	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)
228	TRN10	TRN	15	630587	632023	670328	670892	3	38306	39305	40304	0	2	2	1	1	(2:6)_(6:2)_(8:0)_(6:2a)_(8:0)_(6:2)_(4:4aCO)
232	TRN10	TRN	15	967611	967862	968504	968918	3	643	975	1306	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)
1	TRN10	TRN	1	71616	73633	80077	80554	3	6445	7691	8937	0	3	2	0	2	(2:6)_(4:4aCO)_(8:0)_(6:2)_(4:4CO)
2	TRN10	TRN	1	117940	118997	121235	128637	2_nonsis	2239	6468	10696	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4CO)_(6:2)_(4:4)
14	TRN10	TRN	2	463842	464330	469344	474261	3	5015	7717	10418	0	3	2	1	1	(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
54	TRN10	TRN	5	50279	50918	53537	53565	3	2620	2953	3285	0	3	2	0	2	(8:0)_(4:4aCO)_(2:6)_(4:4CO)
56	TRN10	TRN	5	134484	136262	136730	137133	2_nonsis	469	1559	2648	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4CO)
72	TRN10	TRN	6	110959	111466	114918	115088	2_nonsis	3453	3791	4128	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4CO)
73	TRN10	TRN	6	188428	188704	203172	204006	4	14469	15023	15577	0	3	2	2	0	(6:2)_(4:4aCO)_(4:4bCO)_(2:6)_(4:4cCO)
76	TRN10	TRN	7	65309	66501	69578	70474	2_nonsis	3078	4121	5164	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)
95	TRN10	TRN	7	935766	935861	936416	937376	2_nonsis	556	1083	1609	0	3	2	0	2	(4:4aCO)_(4:4CO)
100	TRN10	TRN	8	59498	59614	68905	69088	3	9292	9441	9589	0	3	2	0	2	(6:2)_(4:4)_(4:4aCO)_(6:2a)_(6:2)_(4:4CO)
116	TRN10	TRN	9	265508	265732	268278	269349	3	2547	3194	3840	0	3	2	1	1	(4:4aCO)_(6:2)_(4:4bCO)
121	TRN10	TRN	10	62076	62571	74077	74857	3	11507	12144	12780	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)_(2:6)_(4:4aCO)
123	TRN10	TRN	10	146059	146367	147445	147612	2_nonsis	1079	1316	1552	0	3	2	0	2	(6:2)_(4:4aCO)_(4:4CO)
136	TRN10	TRN	10	587861	589894	590704	601293	3	811	7121	13431	0	3	2	1	1	(4:4aCO)_(6:2)_(4:4bCO)
146	TRN10	TRN	11	446566	447357	454128	454594	4	6772	7400	8027	0	3	2	2	0	(6:2)_(4:4aCO)_(4:4bCO)
186	TRN10	TRN	13	620664	620984	627607	627725	3	6624	6842	7060	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)
187	TRN10	TRN	13	652808	652911	654160	654563	3	1250	1502	1754	0	3	2	1	1	(6:2)_(4:4)_(6:2a)_(4:4aCO)_(6:2b)_(4:4bCO)
193	TRN10	TRN	14	34917	37986	40430	41146	3	2445	4337	6228	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)
208	TRN10	TRN	14	495472	495918	504296	505410	2_nonsis	8379	9158	9937	0	3	2	0	2	(2:6)_(6:2)_(4:4aCO)_(4:4CO)
210	TRN10	TRN	14	537806	538122	539639	539821	2_nonsis	1518	1766	2014	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4a)_(2:6)_(4:4CO)
237	TRN10	TRN	16	254813	255611	258364	258671	2_nonsis	2754	3306	3857	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(4:4CO)
241	TRN10	TRN	16	610303	610743	617005	618453	3	6263	7206	8149	0	3	2	1	1	(6:2)_(4:4aCO)_(2:6)_(4:4bCO)
256	TRN10	TRN	2	36837	39234	45824	46603	NA	6591	8178	9765	0	4	1	NA	NA	2:6_0:8_2:6
370	TRN10	TRN	10	22158	22350	22158	22350	1	0	96	191	0	4	1	NA	NA	
391	TRN10	TRN	10	720763	723650	725123	745751	1	0	12494	24987	0	4	1	NA	NA	
78	TRN11	TRN	12	13986	14785	23981	25985	1	9197	10598	11998	1	8	1	0	1	2:6_4:4_2:6
1	TRN11	TRN	1	28975	29007	29007	29009	1	1	17	33	1	10	1	0	1	06:02
104	TRN11	TRN	14	21451	21949	21949	22021	1	1	285	569	1	10	1	0	1	06:02
94	TRN11	TRN	13	467817	467994	468051	469276	1	58	758	1458	1	10	1	0	1	06:02
101	TRN11	TRN	13	769971	770091	771058	771109	1	968	1053	1137	1	10	1	0	1	06:02
52	TRN11	TRN	7	1050064	1050785	1051093	1051973	1	309	1109	1908	1	10	1	0	1	06:02
53	TRN11	TRN	8	77625	78204	78270	79894	1	67	1168	2268	1	10	1	0	1	06:02
75	TRN11	TRN	11	256790	257878	258943	259176	1	1066	1726	2385	1	10	1	0	1	06:02
81	TRN11	TRN	12	320997	322903	324050	325937	1	1148	3044	4939	1	10	1	0	1	06:02
91	TRN11	TRN	13	10479	10737	13572	13768	1	2836	3062	3288	1	10	1	0	1	06:02
125	TRN11	TRN	16	832084	832297	834906	836893	1	2610	3709	4808	1	10	1	0	1	06:02
69	TRN11	TRN	11	13973	19020	21803	22806	1	2784	5808	8832	1	10	1	0	1	06:02
26	TRN11	TRN	4	928279	928753	938225	939572	1	9473	10383	11292	1	10	1	0	1	06:02
117	TRN11	TRN	15	474069	475032	487028	487166	1	11997	12547	13096	1	10	1	0	1	06:02
28	TRN11	TRN	4	1163374	1163376	1163376	1163436	1	1	31	61	1	10.1	1	0	1	02:06
100	TRN11	TRN	13	766972	767001	767001	767075	1	1	52	102	1	10.1	1	0	1	02:06
14	TRN11	TRN	3	208072	208091	208091	208234	1	1	81	161	1	10.1	1	0	1	02:06
82	TRN11	TRN	12	379334	379448	379448	379794	1	1	230	459	1	10.1	1	0	1	02:06

6	TRN11	TRN	2	190128	190246	190452	190583		1	207	331	454	1	10.1	1	0	1 02:06
32	TRN11	TRN	4	1380270	1381111	1381111	1381693		1	1	712	1422	1	10.1	1	0	1 02:06
15	TRN11	TRN	3	262264	262830	262830	264441		1	1	1089	2176	1	10.1	1	0	1 02:06
7	TRN11	TRN	2	524475	524659	525492	526248		1	834	1303	1772	1	10.1	1	0	1 02:06
49	TRN11	TRN	7	852125	852577	853758	854329		1	1182	1693	2203	1	10.1	1	0	1 02:06
36	TRN11	TRN	5	33706	34247	34985	36820		1	739	1926	3113	1	10.1	1	0	1 02:06
34	TRN11	TRN	4	1422969	1424231	1425814	1426000		1	1584	2307	3030	1	10.1	1	0	1 02:06
2	TRN11	TRN	1	137063	138499	139076	141984		1	578	2749	4920	1	10.1	1	0	1 02:06
74	TRN11	TRN	11	229929	230043	232839	234299		1	2797	3583	4369	1	10.1	1	0	1 02:06
120	TRN11	TRN	16	79797	82464	84812	84945		1	2349	3748	5147	1	10.1	1	0	1 02:06
99	TRN11	TRN	13	734873	734975	738421	739584		1	3447	4079	4710	1	10.1	1	0	1 02:06
21	TRN11	TRN	4	629487	629725	634632	635008		1	4908	5214	5520	1	10.1	1	0	1 02:06
29	TRN11	TRN	4	1193279	1193452	1200337	1201144		1	6886	7375	7864	1	10.1	1	0	1 02:06
87	TRN11	TRN	12	833667	834769	840682	843387		1	5914	7817	9719	1	10.1	1	0	1 02:06
124	TRN11	TRN	16	526860	527307	527574	528017	2_nonsis		268	712	1156	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
86	TRN11	TRN	12	727539	727901	728268	729242	2_nonsis		368	1035	1702	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
59	TRN11	TRN	9	405973	406436	411094	411481	2_nonsis		4659	5083	5507	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
73	TRN11	TRN	11	202339	203074	203124	203378	2_nonsis		51	545	1038	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
55	TRN11	TRN	8	516468	516908	519792	520081	2_nonsis		2885	3249	3612	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
60	TRN11	TRN	10	63405	63597	72040	72884	2_nonsis		8444	8961	9478	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
41	TRN11	TRN	5	509188	509437	509654	509797	2_nonsis		218	413	608	1	15	1	1	0 (6:2)_(4:4aCO)
51	TRN11	TRN	7	1044371	1045136	1045214	1045427	2_nonsis		79	567	1055	1	15	1	1	0 (6:2)_(4:4aCO)
23	TRN11	TRN	4	761151	762170	762170	762450	2_nonsis		1	650	1298	1	15	1	1	0 (6:2)_(4:4aCO)
106	TRN11	TRN	14	159822	160170	160170	161277	2_nonsis		1	728	1454	1	15	1	1	0 (6:2)_(4:4aCO)
62	TRN11	TRN	10	173515	173883	174303	175220	2_nonsis		421	1063	1704	1	15	1	1	0 (6:2)_(4:4aCO)
10	TRN11	TRN	2	778895	779836	780187	781183	2_nonsis		352	1320	2287	1	15	1	1	0 (6:2)_(4:4aCO)
111	TRN11	TRN	14	667685	669471	669471	670440	2_nonsis		1	1378	2754	1	15	1	1	0 (6:2)_(4:4aCO)
88	TRN11	TRN	12	866643	867405	867405	869664	2_nonsis		1	1511	3020	1	15	1	1	0 (6:2)_(4:4aCO)
37	TRN11	TRN	5	161191	161593	162567	163290	2_nonsis		975	1537	2098	1	15	1	1	0 (6:2)_(4:4aCO)
5	TRN11	TRN	2	186753	187142	188032	189113	2_nonsis		891	1625	2359	1	15	1	1	0 (6:2)_(4:4aCO)
22	TRN11	TRN	4	707555	707900	709241	709492	2_nonsis		1342	1639	1936	1	15	1	1	0 (6:2)_(4:4aCO)
85	TRN11	TRN	12	716177	716369	717529	718593	2_nonsis		1161	1788	2415	1	15	1	1	0 (6:2)_(4:4aCO)
8	TRN11	TRN	2	590982	592905	593500	594298	2_nonsis		596	1956	3315	1	15	1	1	0 (6:2)_(4:4aCO)
108	TRN11	TRN	14	408508	408778	410443	410941	2_nonsis		1666	2049	2432	1	15	1	1	0 (6:2)_(4:4aCO)
3	TRN11	TRN	1	189825	190402	191617	193131	2_nonsis		1216	2261	3305	1	15	1	1	0 (6:2)_(4:4aCO)
68	TRN11	TRN	10	629879	631130	631130	635210	2_nonsis		1	2666	5330	1	15	1	1	0 (6:2)_(4:4aCO)
83	TRN11	TRN	12	382702	382931	385961	386700	2_nonsis		3031	3514	3997	1	15	1	1	0 (6:2)_(4:4aCO)
47	TRN11	TRN	7	432934	433211	437195	438101	2_nonsis		3985	4576	5166	1	15	1	1	0 (6:2)_(4:4aCO)
66	TRN11	TRN	10	565667	566045	568805	572936	2_nonsis		2761	5015	7268	1	15	1	1	0 (6:2)_(4:4aCO)
109	TRN11	TRN	14	536139	536830	542443	543829	2_nonsis		5614	6652	7689	1	15	1	1	0 (6:2)_(4:4aCO)
9	TRN11	TRN	2	767430	769699	775579	777303	2_nonsis		5881	7877	9872	1	15	1	1	0 (6:2)_(4:4aCO)
19	TRN11	TRN	4	269406	269544	277276	278692	2_nonsis		7733	8509	9285	1	15	1	1	0 (6:2)_(4:4aCO)
44	TRN11	TRN	7	221407	221698	221698	221962	2_nonsis		1	278	554	1	16	1	1	0 (2:6)_(4:4aCO)
46	TRN11	TRN	7	395416	395553	395752	395815	2_nonsis		200	299	398	1	16	1	1	0 (2:6)_(4:4aCO)
77	TRN11	TRN	11	496962	497576	497576	497626	2_nonsis		1	332	663	1	16	1	1	0 (2:6)_(4:4aCO)
11	TRN11	TRN	2	782384	782557	782581	783142	2_nonsis		25	391	757	1	16	1	1	0 (2:6)_(4:4aCO)
103	TRN11	TRN	13	902696	902762	902762	903664	2_nonsis		1	484	967	1	16	1	1	0 (2:6)_(4:4aCO)
45	TRN11	TRN	7	378538	379046	379162	379420	2_nonsis		117	499	881	1	16	1	1	0 (2:6)_(4:4aCO)
64	TRN11	TRN	10	186025	186317	186317	187044	2_nonsis		1	510	1018	1	16	1	1	0 (2:6)_(4:4aCO)
76	TRN11	TRN	11	393718	394215	394215	394878	2_nonsis		1	580	1159	1	16	1	1	0 (2:6)_(4:4aCO)
115	TRN11	TRN	15	283315	283744	283744	284515	2_nonsis		1	600	1199	1	16	1	1	0 (2:6)_(4:4aCO)
112	TRN11	TRN	14	737192	737420	737900	737930	2_nonsis		481	609	737	1	16	1	1	0 (2:6)_(4:4aCO)
48	TRN11	TRN	7	604120	604147	604147	605491	2_nonsis		1	686	1370	1	16	1	1	0 (2:6)_(4:4aCO)
107	TRN11	TRN	14	190048	190426	190801	191177	2_nonsis		376	752	1128	1	16	1	1	0 (2:6)_(4:4aCO)
30	TRN11	TRN	4	1202939	1203967	1203967	1205010	2_nonsis		1	1036	2070	1	16	1	1	0 (2:6)_(4:4aCO)
122	TRN11	TRN	16	280470	281659	282326	282651	2_nonsis		668	1424	2180	1	16	1	1	0 (2:6)_(4:4aCO)
27	TRN11	TRN	4	1015515	1016426	1016597	1018516	2_nonsis		172	1586	3000	1	16	1	1	0 (2:6)_(4:4aCO)
90	TRN11	TRN	12	953059	953351	956047	956371	2_nonsis		2697	3004	3311	1	16	1	1	0 (2:6)_(4:4aCO)
119	TRN11	TRN	15	718180	719433	722071	722470	2_nonsis		2639	3464	4289	1	16	1	1	0 (2:6)_(4:4aCO)
43	TRN11	TRN	7	203693	205294	208986	209066	2_nonsis		3693	4533	5372	1	16	1	1	0 (2:6)_(4:4aCO)

95	TRN11	TRN	13	469552	473747	476241	476482	2_nonsis		2495	4712	6929	1	16	1	1	0	(2:6)_(4:4aCO)
71	TRN11	TRN	11	115995	116643	121247	122945	2_nonsis		4605	5777	6949	1	16	1	1	0	(2:6)_(4:4aCO)
20	TRN11	TRN	4	551991	552102	557899	558895	2_nonsis		5798	6351	6903	1	16	1	1	0	(2:6)_(4:4aCO)
84	TRN11	TRN	12	638087	638411	644551	645452	2_nonsis		6141	6753	7364	1	16	1	1	0	(2:6)_(4:4aCO)
18	TRN11	TRN	4	248008	249264	261167	261458	2_nonsis		11904	12677	13449	1	16	1	1	0	(2:6)_(4:4aCO)
80	TRN11	TRN	12	315642	316064	315642	316064	2_nonsis		0	211	421	1	100	1	1	0	(4:4aCO)
113	TRN11	TRN	15	172646	173080	172646	173080	2_nonsis		0	217	433	1	100	1	1	0	(4:4aCO)
33	TRN11	TRN	4	1382859	1383527	1382859	1383527	2_nonsis		0	334	667	1	100	1	1	0	(4:4aCO)
72	TRN11	TRN	11	131539	132251	131539	132251	2_nonsis		0	356	711	1	100	1	1	0	(4:4aCO)
89	TRN11	TRN	12	950047	950788	950047	950788	2_nonsis		0	370	740	1	100	1	1	0	(4:4aCO)
54	TRN11	TRN	8	325621	326461	325621	326461	2_nonsis		0	420	839	1	100	1	1	0	(4:4aCO)
50	TRN11	TRN	7	914816	915691	914816	915691	2_nonsis		0	437	874	1	100	1	1	0	(4:4aCO)
102	TRN11	TRN	13	881086	882052	881086	882052	2_nonsis		0	483	965	1	100	1	1	0	(4:4aCO)
96	TRN11	TRN	13	556209	557425	556209	557425	2_nonsis		0	608	1215	1	100	1	1	0	(4:4aCO)
116	TRN11	TRN	15	382531	383827	382531	383827	2_nonsis		0	648	1295	1	100	1	1	0	(4:4aCO)
35	TRN11	TRN	4	1488904	1490210	1488904	1490210	2_nonsis		0	653	1305	1	100	1	1	0	(4:4aCO)
67	TRN11	TRN	10	585466	586827	585466	586827	2_nonsis		0	680	1360	1	100	1	1	0	(4:4aCO)
24	TRN11	TRN	4	771211	772626	771211	772626	2_nonsis		0	707	1414	1	100	1	1	0	(4:4aCO)
61	TRN11	TRN	10	75279	76754	75279	76754	2_nonsis		0	737	1474	1	100	1	1	0	(4:4aCO)
16	TRN11	TRN	4	91959	93521	91959	93521	2_nonsis		0	781	1561	1	100	1	1	0	(4:4aCO)
57	TRN11	TRN	9	265732	267668	265732	267668	2_nonsis		0	968	1935	1	100	1	1	0	(4:4aCO)
13	TRN11	TRN	3	73479	75484	73479	75484	2_nonsis		0	1002	2004	1	100	1	1	0	(4:4aCO)
4	TRN11	TRN	2	66584	68817	66584	68817	2_nonsis		0	1116	2232	1	100	1	1	0	(4:4aCO)
97	TRN11	TRN	13	692123	694367	692123	694367	2_nonsis		0	1122	2243	1	100	1	1	0	(4:4aCO)
42	TRN11	TRN	7	82858	85120	82858	85120	2_nonsis		0	1131	2261	1	100	1	1	0	(4:4aCO)
31	TRN11	TRN	4	1254292	1256876	1254292	1256876	2_nonsis		0	1292	2583	1	100	1	1	0	(4:4aCO)
110	TRN11	TRN	14	662512	665097	662512	665097	2_nonsis		0	1292	2584	1	100	1	1	0	(4:4aCO)
79	TRN11	TRN	12	25985	28820	25985	28820	2_nonsis		0	1417	2834	1	100	1	1	0	(4:4aCO)
12	TRN11	TRN	3	65266	68233	65266	68233	2_nonsis		0	1483	2966	1	100	1	1	0	(4:4aCO)
70	TRN11	TRN	11	23532	27301	23532	27301	2_nonsis		0	1884	3768	1	100	1	1	0	(4:4aCO)
58	TRN11	TRN	9	329125	334329	329125	334329	2_nonsis		0	2602	5203	1	100	1	1	0	(4:4aCO)
39	TRN11	TRN	5	403078	403557	408144	408389	2_nonsis		4588	4949	5310	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
38	TRN11	TRN	5	292698	293301	296971	297515	2_nonsis		3671	4244	4816	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
40	TRN11	TRN	5	471885	472051	476912	477110	2_sis		4862	5043	5224	0	1	2	0	2	(0:8)_(2:6)_(4:4)
56	TRN11	TRN	9	125455	126162	142621	142688	2_sis		16460	16846	17232	0	1	2	0	2	(6:2)_(4:4)_(6:2)_(8:0)_(6:2a)_(4:4)
98	TRN11	TRN	13	695850	697269	709549	709740		3	12281	13085	13889	0	1	2	0	2	(0:8)_(2:6)_(6:2)_(4:4)
118	TRN11	TRN	15	656264	657201	662487	662592	2_sis		5287	5807	6327	0	1	2	0	2	(2:6)_(2:6a)_(4:4)_(2:6a)_(4:4)
17	TRN11	TRN	4	127476	130517	130537	130640		3	21	1592	3163	0	2	2	1	1	(6:2)_(4:4aCO)
25	TRN11	TRN	4	825422	831279	842636	842982		3	11358	14459	17559	0	2	2	1	1	(8:0)_(6:2)_(4:4aCO)
65	TRN11	TRN	10	323823	325190	334468	334858		3	9279	10157	11034	0	2	2	1	1	(6:2)_(4:4)_(6:2a)_(4:4)_(6:2a)_(4:4)_(6:2a)_(4:4aCO)
92	TRN11	TRN	13	55582	55751	57144	58688		4	1394	2250	3105	0	2	2	1	1	(2:6)_(6:2)_(4:4aCO)
93	TRN11	TRN	13	125006	125244	129456	129926		3	4213	4566	4919	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)
105	TRN11	TRN	14	78386	79032	86730	88013		3	7699	8663	9626	0	2	2	1	1	(8:0)_(6:2)_(8:0)_(4:4aCO)
114	TRN11	TRN	15	262203	262766	276153	277467		3	13388	14326	15263	0	2	2	1	1	(2:6)_(0:8)_(4:4aCO)
121	TRN11	TRN	16	155906	156308	156745	157225		3	438	878	1318	0	2	2	1	1	(6:2)_(4:4aCO)
63	TRN11	TRN	10	181820	182087	182825	183608	2_nonsis		739	1263	1787	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4aCO)
123	TRN11	TRN	16	420758	421124	433373	434613	2_nonsis		12250	13052	13854	0	3	2	0	2	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(4:4CO)
13	TRN2	TRN	2	514077	514468	515936	515987		1	1469	1689	1909	1	7	1	0	1	6:2_4:4_6:2
85	TRN2	TRN	9	136172	136619	146041	146193		1	9423	9722	10020	1	7	1	0	1	6:2_4:4_6:2
10	TRN2	TRN	2	392022	392314	399796	400827		1	7483	8144	8804	1	7	1	0	1	6:2_4:4_6:2_4:4_6:2
119	TRN2	TRN	12	107971	108813	109497	109602		1	685	1158	1630	1	8	1	0	1	2:6_4:4_2:6
149	TRN2	TRN	14	68923	69145	80433	81575		1	11289	11970	12651	1	8	1	0	1	2:6_4:4_2:6_4:4_2:6
151	TRN2	TRN	14	107060	107345	119414	119721		1	12070	12365	12660	1	8	1	0	1	2:6_4:4_2:6_4:4_2:6
3	TRN2	TRN	1	130362	130776	130776	130897		1	1	268	534	1	10	1	0	1	06:02
17	TRN2	TRN	2	700423	700950	701207	701303		1	258	569	879	1	10	1	0	1	06:02
128	TRN2	TRN	12	663368	663839	664157	664658		1	319	804	1289	1	10	1	0	1	06:02
58	TRN2	TRN	6	244444	245103	245922	246034		1	820	1205	1589	1	10	1	0	1	06:02
47	TRN2	TRN	5	80671	80717	81713	82641		1	997	1483	1969	1	10	1	0	1	06:02
148	TRN2	TRN	13	914143	916639	916816	917194		1	178	1614	3050	1	10	1	0	1	06:02
103	TRN2	TRN	11	19020	19563	21006	21221		1	1444	1822	2200	1	10	1	0	1	06:02

97	TRN2	TRN	10	414104	414830	416075	416512	1	1246	1827	2407	1	10	1	0	1 06:02
98	TRN2	TRN	10	464438	465282	467010	467107	1	1729	2199	2668	1	10	1	0	1 06:02
11	TRN2	TRN	2	402177	402843	404173	406111	1	1331	2632	3933	1	10	1	0	1 06:02
20	TRN2	TRN	2	773089	773889	775579	777303	1	1691	2952	4213	1	10	1	0	1 06:02
57	TRN2	TRN	6	199343	201607	203172	204006	1	1566	3114	4662	1	10	1	0	1 06:02
135	TRN2	TRN	13	28854	29616	31154	35547	1	1539	4116	6692	1	10	1	0	1 06:02
154	TRN2	TRN	14	368045	368391	373799	373925	1	5409	5644	5879	1	10	1	0	1 06:02
79	TRN2	TRN	8	384685	385098	392676	393017	1	7579	7955	8331	1	10	1	0	1 06:02
43	TRN2	TRN	4	1476956	1477116	1477174	1477237	1	59	170	280	1	10.1	1	0	1 02:06
63	TRN2	TRN	7	263382	263421	263851	263909	1	431	479	526	1	10.1	1	0	1 02:06
150	TRN2	TRN	14	95222	96083	96083	96181	1	1	480	958	1	10.1	1	0	1 02:06
109	TRN2	TRN	11	365453	365937	366213	366486	1	277	655	1032	1	10.1	1	0	1 02:06
134	TRN2	TRN	12	1011952	1012226	1012226	1013592	1	1	820	1639	1	10.1	1	0	1 02:06
177	TRN2	TRN	16	348815	349538	350221	350251	1	684	1060	1435	1	10.1	1	0	1 02:06
133	TRN2	TRN	12	997285	997480	998377	998806	1	898	1209	1520	1	10.1	1	0	1 02:06
116	TRN2	TRN	12	29131	29612	30558	30657	1	947	1236	1525	1	10.1	1	0	1 02:06
179	TRN2	TRN	16	498689	498848	500018	500240	1	1171	1361	1550	1	10.1	1	0	1 02:06
15	TRN2	TRN	2	662272	662444	662444	666708	1	1	2218	4435	1	10.1	1	0	1 02:06
23	TRN2	TRN	3	223339	224310	224793	228130	1	484	2637	4790	1	10.1	1	0	1 02:06
130	TRN2	TRN	12	802287	803833	803833	808209	1	1	2961	5921	1	10.1	1	0	1 02:06
112	TRN2	TRN	11	528277	528685	530688	532520	1	2004	3123	4242	1	10.1	1	0	1 02:06
102	TRN2	TRN	10	706608	707018	720763	723650	1	13746	15394	17041	1	10.1	1	0	1 02:06
82	TRN2	TRN	8	509758	509846	511654	511765	2_nonsis	1809	1908	2006	3	30	1	0	1 2:6_6:2
8	TRN2	TRN	2	176261	176636	183084	184932	2_nonsis	6449	7560	8670	3	30	1	0	1 2:6_6:2
170	TRN2	TRN	15	695231	696182	700856	700946	2_nonsis	4675	5195	5714	3	30	1	0	1 6:2_2:6_4:4_2:6
53	TRN2	TRN	5	545025	545863	546141	546545	2_nonsis	279	899	1519	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
182	TRN2	TRN	16	905582	905685	906627	907043	2_nonsis	943	1202	1460	1	12	1	1	0 (2:6)_(4:4)_(4:4aCO)
25	TRN2	TRN	4	32706	33135	35807	37096	2_nonsis	2673	3531	4389	1	12	1	1	0 (4:4aCO)_(2:6)_(4:4a)
108	TRN2	TRN	11	289859	292055	295309	296531	2_nonsis	3255	4963	6671	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
173	TRN2	TRN	15	1038438	1038535	1038960	1039487	2_nonsis	426	737	1048	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
142	TRN2	TRN	13	495773	496159	498745	499915	2_nonsis	2587	3364	4141	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
125	TRN2	TRN	12	541773	542794	545673	546249	2_nonsis	2880	3678	4475	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
136	TRN2	TRN	13	37125	38744	44157	44254	2_nonsis	5414	6271	7128	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)
48	TRN2	TRN	5	229778	230208	234579	234626	2_nonsis	4372	4610	4847	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
35	TRN2	TRN	4	1011299	1011430	1011430	1011449	2_nonsis	1	75	149	1	15	1	1	0 (6:2)_(4:4aCO)
46	TRN2	TRN	5	78895	79059	79059	79231	2_nonsis	1	168	335	1	15	1	1	0 (6:2)_(4:4aCO)
160	TRN2	TRN	15	90400	90802	90802	90886	2_nonsis	1	243	485	1	15	1	1	0 (6:2)_(4:4aCO)
80	TRN2	TRN	8	395744	396036	396060	396288	2_nonsis	25	284	543	1	15	1	1	0 (6:2)_(4:4aCO)
152	TRN2	TRN	14	124154	124235	124329	124691	2_nonsis	95	316	536	1	15	1	1	0 (6:2)_(4:4aCO)
88	TRN2	TRN	9	182483	182837	182939	183064	2_nonsis	103	342	580	1	15	1	1	0 (6:2)_(4:4aCO)
115	TRN2	TRN	11	656736	657110	657311	657441	2_nonsis	202	453	704	1	15	1	1	0 (6:2)_(4:4aCO)
42	TRN2	TRN	4	1474394	1474416	1474507	1475249	2_nonsis	92	473	854	1	15	1	1	0 (6:2)_(4:4aCO)
65	TRN2	TRN	7	392382	392993	393263	393326	2_nonsis	271	607	943	1	15	1	1	0 (6:2)_(4:4aCO)
40	TRN2	TRN	4	1461111	1461391	1461584	1462308	2_nonsis	194	695	1196	1	15	1	1	0 (6:2)_(4:4aCO)
44	TRN2	TRN	5	28312	28600	28694	29872	2_nonsis	95	827	1559	1	15	1	1	0 (6:2)_(4:4aCO)
178	TRN2	TRN	16	397049	397584	398024	398525	2_nonsis	441	958	1475	1	15	1	1	0 (6:2)_(4:4aCO)
118	TRN2	TRN	12	40119	41721	42243	42404	2_nonsis	523	1404	2284	1	15	1	1	0 (6:2)_(4:4aCO)
68	TRN2	TRN	7	702791	703857	703857	705631	2_nonsis	1	1420	2839	1	15	1	1	0 (6:2)_(4:4aCO)
180	TRN2	TRN	16	620016	620505	621480	622057	2_nonsis	976	1508	2040	1	15	1	1	0 (6:2)_(4:4aCO)
71	TRN2	TRN	7	911277	911494	913000	913222	2_nonsis	1507	1726	1944	1	15	1	1	0 (6:2)_(4:4aCO)
172	TRN2	TRN	15	952140	952654	953577	954766	2_nonsis	924	1775	2625	1	15	1	1	0 (6:2)_(4:4aCO)
36	TRN2	TRN	4	1102795	1102879	1104572	1105534	2_nonsis	1694	2216	2738	1	15	1	1	0 (6:2)_(4:4aCO)
111	TRN2	TRN	11	477203	477776	479521	480070	2_nonsis	1746	2306	2866	1	15	1	1	0 (6:2)_(4:4aCO)
121	TRN2	TRN	12	257813	258349	260323	260496	2_nonsis	1975	2329	2682	1	15	1	1	0 (6:2)_(4:4aCO)
94	TRN2	TRN	10	111408	111784	113443	115860	2_nonsis	1660	3056	4451	1	15	1	1	0 (6:2)_(4:4aCO)
54	TRN2	TRN	6	24251	24494	26889	28318	2_nonsis	2396	3231	4066	1	15	1	1	0 (6:2)_(4:4aCO)
164	TRN2	TRN	15	318818	319505	322341	322691	2_nonsis	2837	3355	3872	1	15	1	1	0 (6:2)_(4:4aCO)
19	TRN2	TRN	2	759221	759357	763528	763762	2_nonsis	4172	4356	4540	1	15	1	1	0 (6:2)_(4:4aCO)
161	TRN2	TRN	15	123921	124780	128730	129347	2_nonsis	3951	4688	5425	1	15	1	1	0 (6:2)_(4:4aCO)
78	TRN2	TRN	8	141400	142863	147763	148132	2_nonsis	4901	5816	6731	1	15	1	1	0 (6:2)_(4:4aCO)

61	TRN2	TRN	7	252806	253383	259594	260137	2_nonsis	6212	6771	7330	1	15	1	1	0 (6:2)_(4:4aCO)
126	TRN2	TRN	12	611203	611744	618297	618795	2_nonsis	6554	7073	7591	1	15	1	1	0 (6:2)_(4:4aCO)
24	TRN2	TRN	3	239515	242917	248853	249269	2_nonsis	5937	7845	9753	1	15	1	1	0 (6:2)_(4:4aCO)
41	TRN2	TRN	4	1463190	1463798	1471524	1471935	2_nonsis	7727	8236	8744	1	15	1	1	0 (6:2)_(4:4aCO)
45	TRN2	TRN	5	62117	62599	74196	75084	2_nonsis	11598	12282	12966	1	15	1	1	0 (6:2)_(4:4aCO)
72	TRN2	TRN	7	991938	991971	991971	992205	2_nonsis	1	134	266	1	16	1	1	0 (2:6)_(4:4aCO)
99	TRN2	TRN	10	471195	471532	471532	471814	2_nonsis	1	310	618	1	16	1	1	0 (2:6)_(4:4aCO)
21	TRN2	TRN	3	57568	58033	58033	59028	2_nonsis	1	730	1459	1	16	1	1	0 (2:6)_(4:4aCO)
123	TRN2	TRN	12	337082	338262	338295	338685	2_nonsis	34	818	1602	1	16	1	1	0 (2:6)_(4:4aCO)
84	TRN2	TRN	9	41664	41898	42679	42866	2_nonsis	782	992	1201	1	16	1	1	0 (2:6)_(4:4aCO)
56	TRN2	TRN	6	171501	172334	172612	173376	2_nonsis	279	1077	1874	1	16	1	1	0 (2:6)_(4:4aCO)
117	TRN2	TRN	12	36398	36458	37705	37937	2_nonsis	1248	1393	1538	1	16	1	1	0 (2:6)_(4:4aCO)
38	TRN2	TRN	4	1396824	1397034	1398006	1398785	2_nonsis	973	1467	1960	1	16	1	1	0 (2:6)_(4:4aCO)
141	TRN2	TRN	13	397289	397850	399189	399408	2_nonsis	1340	1729	2118	1	16	1	1	0 (2:6)_(4:4aCO)
158	TRN2	TRN	14	749652	749744	750744	752223	2_nonsis	1001	1786	2570	1	16	1	1	0 (2:6)_(4:4aCO)
127	TRN2	TRN	12	628424	629441	630568	630870	2_nonsis	1128	1787	2445	1	16	1	1	0 (2:6)_(4:4aCO)
100	TRN2	TRN	10	495458	496029	497589	497615	2_nonsis	1561	1859	2156	1	16	1	1	0 (2:6)_(4:4aCO)
29	TRN2	TRN	4	407403	408065	408894	410728	2_nonsis	830	2077	3324	1	16	1	1	0 (2:6)_(4:4aCO)
1	TRN2	TRN	1	67476	67715	68551	71312	2_nonsis	837	2336	3835	1	16	1	1	0 (2:6)_(4:4aCO)
163	TRN2	TRN	15	191548	193685	193685	196238	2_nonsis	1	2345	4689	1	16	1	1	0 (2:6)_(4:4aCO)
167	TRN2	TRN	15	472780	474069	475809	476517	2_nonsis	1741	2739	3736	1	16	1	1	0 (2:6)_(4:4aCO)
59	TRN2	TRN	7	20580	20692	23516	23602	2_nonsis	2825	2923	3021	1	16	1	1	0 (2:6)_(4:4aCO)
7	TRN2	TRN	2	110746	110917	113452	114676	2_nonsis	2536	3233	3929	1	16	1	1	0 (2:6)_(4:4aCO)
28	TRN2	TRN	4	333754	334214	336943	337582	2_nonsis	2730	3279	3827	1	16	1	1	0 (2:6)_(4:4aCO)
175	TRN2	TRN	16	72872	73929	77239	77440	2_nonsis	3311	3939	4567	1	16	1	1	0 (2:6)_(4:4aCO)
174	TRN2	TRN	16	22695	22824	26952	27014	2_nonsis	4129	4224	4318	1	16	1	1	0 (2:6)_(4:4aCO)
168	TRN2	TRN	15	580351	581450	586345	586852	2_nonsis	4896	5698	6500	1	16	1	1	0 (2:6)_(4:4aCO)
162	TRN2	TRN	15	183754	183991	190009	191548	2_nonsis	6019	6906	7793	1	16	1	1	0 (2:6)_(4:4aCO)
64	TRN2	TRN	7	267726	268323	274448	276180	2_nonsis	6126	7290	8453	1	16	1	1	0 (2:6)_(4:4aCO)
110	TRN2	TRN	11	368313	369378	376721	376929	2_nonsis	7344	7980	8615	1	16	1	1	0 (2:6)_(4:4aCO)
156	TRN2	TRN	14	671317	674407	680930	682206	2_nonsis	6524	8706	10888	1	16	1	1	0 (2:6)_(4:4aCO)
132	TRN2	TRN	12	982257	986295	994215	994222	2_nonsis	7921	9943	11964	1	16	1	1	0 (2:6)_(4:4aCO)
171	TRN2	TRN	15	740202	741051	751727	752002	2_nonsis	10677	11238	11799	1	16	1	1	0 (2:6)_(4:4aCO)
2	TRN2	TRN	1	71312	73633	85751	87490	2_nonsis	12119	14148	16177	1	16	1	1	0 (2:6)_(4:4aCO)
93	TRN2	TRN	9	387393	387502	387393	387502	2_nonsis	0	54	108	1	100	1	1	0 (4:4aCO)
9	TRN2	TRN	2	196417	196581	196417	196581	2_nonsis	0	82	163	1	100	1	1	0 (4:4aCO)
50	TRN2	TRN	5	311515	311716	311515	311716	2_nonsis	0	100	200	1	100	1	1	0 (4:4aCO)
31	TRN2	TRN	4	660197	660411	660197	660411	2_nonsis	0	107	213	1	100	1	1	0 (4:4aCO)
34	TRN2	TRN	4	1009654	1009957	1009654	1009957	2_nonsis	0	151	302	1	100	1	1	0 (4:4aCO)
49	TRN2	TRN	5	309648	309961	309648	309961	2_nonsis	0	156	312	1	100	1	1	0 (4:4aCO)
81	TRN2	TRN	8	410489	410833	410489	410833	2_nonsis	0	172	343	1	100	1	1	0 (4:4aCO)
114	TRN2	TRN	11	579153	579541	579153	579541	2_nonsis	0	194	387	1	100	1	1	0 (4:4aCO)
37	TRN2	TRN	4	1153303	1153699	1153303	1153699	2_nonsis	0	198	395	1	100	1	1	0 (4:4aCO)
12	TRN2	TRN	2	512167	512684	512167	512684	2_nonsis	0	258	516	1	100	1	1	0 (4:4aCO)
51	TRN2	TRN	5	407419	407957	407419	407957	2_nonsis	0	269	537	1	100	1	1	0 (4:4aCO)
70	TRN2	TRN	7	841068	841693	841068	841693	2_nonsis	0	312	624	1	100	1	1	0 (4:4aCO)
113	TRN2	TRN	11	575852	576492	575852	576492	2_nonsis	0	320	639	1	100	1	1	0 (4:4aCO)
30	TRN2	TRN	4	429969	430665	429969	430665	2_nonsis	0	348	695	1	100	1	1	0 (4:4aCO)
62	TRN2	TRN	7	261126	261844	261126	261844	2_nonsis	0	359	717	1	100	1	1	0 (4:4aCO)
14	TRN2	TRN	2	620443	621285	620443	621285	2_nonsis	0	421	841	1	100	1	1	0 (4:4aCO)
169	TRN2	TRN	15	690980	691843	690980	691843	2_nonsis	0	431	862	1	100	1	1	0 (4:4aCO)
73	TRN2	TRN	7	1011203	1012213	1011203	1012213	2_nonsis	0	505	1009	1	100	1	1	0 (4:4aCO)
87	TRN2	TRN	9	162266	163427	162266	163427	2_nonsis	0	580	1160	1	100	1	1	0 (4:4aCO)
165	TRN2	TRN	15	431558	433358	431558	433358	2_nonsis	0	900	1799	1	100	1	1	0 (4:4aCO)
67	TRN2	TRN	7	468105	469926	468105	469926	2_nonsis	0	910	1820	1	100	1	1	0 (4:4aCO)
77	TRN2	TRN	8	139506	141400	139506	141400	2_nonsis	0	947	1893	1	100	1	1	0 (4:4aCO)
106	TRN2	TRN	11	203378	205481	203378	205481	2_nonsis	0	1051	2102	1	100	1	1	0 (4:4aCO)
89	TRN2	TRN	9	240376	242535	240376	242535	2_nonsis	0	1079	2158	1	100	1	1	0 (4:4aCO)
181	TRN2	TRN	16	860540	863244	860540	863244	2_nonsis	0	1352	2703	1	100	1	1	0 (4:4aCO)
22	TRN2	TRN	3	204750	207459	204750	207459	2_nonsis	0	1354	2708	1	100	1	1	0 (4:4aCO)

90	TRN2	TRN	9	320712	323487	320712	323487	2_nonsis		0	1387	2774	1	100	1	1	0	(4:4aCO)
83	TRN2	TRN	8	512291	515162	512291	515162	2_nonsis		0	1435	2870	1	100	1	1	0	(4:4aCO)
18	TRN2	TRN	2	749103	752417	749103	752417	2_nonsis		0	1657	3313	1	100	1	1	0	(4:4aCO)
107	TRN2	TRN	11	235115	238513	235115	238513	2_nonsis		0	1699	3397	1	100	1	1	0	(4:4aCO)
52	TRN2	TRN	5	426333	429823	426333	429823	2_nonsis		0	1745	3489	1	100	1	1	0	(4:4aCO)
122	TRN2	TRN	12	262367	265975	262367	265975	2_nonsis		0	1804	3607	1	100	1	1	0	(4:4aCO)
96	TRN2	TRN	10	407535	411303	407535	411303	2_nonsis		0	1884	3767	1	100	1	1	0	(4:4aCO)
129	TRN2	TRN	12	798382	802287	798382	802287	2_nonsis		0	1952	3904	1	100	1	1	0	(4:4aCO)
16	TRN2	TRN	2	695479	699461	695479	699461	2_nonsis		0	1991	3981	1	100	1	1	0	(4:4aCO)
157	TRN2	TRN	14	682580	686654	682580	686654	2_nonsis		0	2037	4073	1	100	1	1	0	(4:4aCO)
104	TRN2	TRN	11	41369	45993	41369	45993	2_nonsis		0	2312	4623	1	100	1	1	0	(4:4aCO)
32	TRN2	TRN	4	825422	837275	825422	837275	2_nonsis		0	5926	11852	1	100	1	1	0	(4:4aCO)
92	TRN2	TRN	9	340507	340858	342462	342976	2_nonsis		1605	2037	2468	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
69	TRN2	TRN	7	798848	800148	801373	801946	2_nonsis		1226	2162	3097	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
26	TRN2	TRN	4	50767	51098	53077	53471	2_nonsis		1980	2342	2703	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
66	TRN2	TRN	7	463843	464170	466985	467277	2_nonsis		2816	3125	3433	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
27	TRN2	TRN	4	182019	182862	183901	183975	2_nonsis		1040	1498	1955	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
137	TRN2	TRN	13	98070	98310	101176	101469	2_nonsis		2867	3133	3398	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
176	TRN2	TRN	16	242227	242326	245496	246320	2_nonsis		3171	3632	4092	3	20	1	1	0	(6:2)_(4:4)_(2:6)_(4:4aCO)
74	TRN2	TRN	7	1023965	1024005	1025187	1025688	2_nonsis		1183	1453	1722	3	20	1	1	0	(2:6)_(4:4)_(4:4aCO)_(6:2)_(4:4a)
145	TRN2	TRN	13	821494	822331	825884	826148	2_nonsis		3554	4104	4653	3	20	1	1	0	(2:6)_(4:4)_(2:6)_(6:2)_(4:4aCO)
33	TRN2	TRN	4	959248	959287	963004	963556	2_nonsis		3718	4013	4307	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
60	TRN2	TRN	7	191252	192332	193477	193769	2_sis		1146	1831	2516	0	1	2	0	2	(2:6)_(2:6a)_(4:4)
124	TRN2	TRN	12	535113	535290	538633	539092	2_sis		3344	3661	3978	0	1	2	0	2	(2:6)_(2:6a)_(4:4)
153	TRN2	TRN	14	243530	244185	245680	246824	2_sis		1496	2395	3293	0	1	2	0	2	(6:2)_(4:4)_(6:2a)_(4:4)
4	TRN2	TRN	1	182210	182380	182447	183881		3	68	869	1670	0	2	2	1	1	(6:2)_(4:4aCO)
39	TRN2	TRN	4	1403147	1403669	1407535	1412849		3	3867	6784	9701	0	2	2	1	1	(6:2)_(4:4aCO)
76	TRN2	TRN	8	23964	24334	34071	34328		3	9738	10051	10363	0	2	2	1	1	(6:2)_(8:0)_(6:2)_(4:4aCO)
86	TRN2	TRN	9	148671	148730	158276	160453		3	9547	10664	11781	0	2	2	1	1	(6:2)_(4:4)_(6:2a)_(4:4)_(6:2a)_(4:4aCO)_(2:6)_(4:4a)
101	TRN2	TRN	10	658862	660402	672815	672937		3	12414	13244	14074	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4a)
131	TRN2	TRN	12	967302	969880	972928	974574		3	3049	5160	7271	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(4:4aCO)
138	TRN2	TRN	13	223609	224126	230470	230627		3	6345	6681	7017	0	2	2	1	1	(6:2)_(4:4)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
140	TRN2	TRN	13	383224	384682	395765	395969		4	11084	11914	12744	0	2	2	2	0	(2:6)_(0:8)_(2:6a)_(4:4aCO)
146	TRN2	TRN	13	856957	857240	864272	864551		3	7033	7313	7593	0	2	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(8:0)_(6:2)_(4:4a)
147	TRN2	TRN	13	908047	908906	912584	912804		3	3679	4218	4756	0	2	2	1	1	(6:2)_(8:0)_(4:4aCO)
155	TRN2	TRN	14	433271	435509	445056	446017		3	9548	11147	12745	0	2	2	1	1	(6:2)_(2:6)_(4:4aCO)
166	TRN2	TRN	15	437180	437266	442944	443071		3	5679	5785	5890	0	2	2	1	1	(6:2)_(6:2a)_(4:4aCO)
5	TRN2	TRN	2	36507	36690	36837	39234		3	148	1437	2726	0	3	2	1	1	(4:4aCO)_(4:4bCO)
6	TRN2	TRN	2	105973	106303	108452	108510		3	2150	2343	2536	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
55	TRN2	TRN	6	93664	93934	98152	98330		3	4219	4442	4665	0	3	2	1	1	(4:4aCO)_(6:2)_(4:4bCO)
75	TRN2	TRN	7	1042643	1043244	1051093	1051973		3	7850	8590	9329	0	3	2	0	2	(4:4aCO)_(4:4CO)_(2:6)_(4:4)_(2:6)_(4:4bCO)
91	TRN2	TRN	9	324424	325450	335079	336156		3	9630	10681	11731	0	3	3	3	0	(4:4aCO)_(2:6)_(2:6a)_(4:4bCO)
95	TRN2	TRN	10	270752	271477	284198	284309		4	12722	13139	13556	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(2:6)_(0:8)_(2:6a)_(4:4CO)_(2:6a)_(0:8)_(4:4)_(2:6a)_(4:4)_(6:2a)_(4:4bCO)
105	TRN2	TRN	11	77172	77759	80353	80724		4	2595	3073	3551	0	3	2	2	0	(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
120	TRN2	TRN	12	223258	223495	238547	238758	2_nonsis		15053	15276	15499	0	3	2	0	2	(2:6)_(4:4aCO)_(6:2)_(4:4CO)
139	TRN2	TRN	13	378772	378833	381609	382044	2_nonsis		2777	3024	3271	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)_(6:2)_(4:4)
143	TRN2	TRN	13	507334	508576	511632	512087		4	3057	3905	4752	0	3	2	2	0	(4:4aCO)_(6:2)_(4:4bCO)
144	TRN2	TRN	13	687199	687331	701668	702452		3	14338	14795	15252	0	3	2	0	2	(6:2)_(8:0)_(6:2)_(4:4aCO)_(6:2)_(4:4CO)
159	TRN2	TRN	15	78123	78272	87042	88455		3	8771	9551	10331	0	3	2	1	1	(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
203	TRN2	TRN	2	794651	794800	801524	813184		1	0	9266	18532	0	4	1	NA	NA	
259	TRN2	TRN	7	1063378	1063622	1064130	1090940		1	0	13781	27561	0	4	1	NA	NA	
129	TRN20	TRN	13	538839	539007	541435	541511		1	2429	2550	2671	1	7	1	0	1	6:2_4:4_6:2
25	TRN20	TRN	4	695576	695611	700250	700440		1	4640	4752	4863	1	7	1	0	1	6:2_4:4_6:2
173	TRN20	TRN	16	500339	500407	503192	503305		1	2786	2876	2965	1	7	1	0	1	6:2_4:4_6:2_4:4_6:2
76	TRN20	TRN	9	131891	132148	132756	133353		1	609	1035	1461	1	8	1	0	1	2:6_4:4_2:6
122	TRN20	TRN	13	24775	24787	26434	26922		1	1648	1897	2146	1	8	1	0	1	2:6_4:4_2:6
54	TRN20	TRN	7	171676	171763	173856	174098		1	2094	2258	2421	1	8	1	0	1	2:6_4:4_2:6
6	TRN20	TRN	2	110153	110550	116102	116107		1	5553	5753	5953	1	8	1	0	1	2:6_4:4_2:6
64	TRN20	TRN	7	970143	970290	970290	970357		1	1	107	213	1	10	1	0	1	06:02
4	TRN20	TRN	2	45269	45304	45304	45660		1	1	196	390	1	10	1	0	1	06:02

99	TRN20	TRN	11	208745	209107	209107	209296	1	1	276	550	1	10	1	0	1 06:02
59	TRN20	TRN	7	553132	553711	553711	553821	1	1	345	688	1	10	1	0	1 06:02
155	TRN20	TRN	15	486327	486494	486511	487028	1	18	359	700	1	10	1	0	1 06:02
87	TRN20	TRN	10	380706	380992	381120	381644	1	129	533	937	1	10	1	0	1 06:02
172	TRN20	TRN	16	298955	299549	299834	300071	1	286	701	1115	1	10	1	0	1 06:02
79	TRN20	TRN	9	262630	263455	263911	265508	1	457	1667	2877	1	10	1	0	1 06:02
69	TRN20	TRN	8	369898	370655	372114	372426	1	1460	1994	2527	1	10	1	0	1 06:02
17	TRN20	TRN	2	769903	770335	772342	772685	1	2008	2395	2781	1	10	1	0	1 06:02
43	TRN20	TRN	5	376275	376375	378586	379092	1	2212	2514	2816	1	10	1	0	1 06:02
125	TRN20	TRN	13	89876	90409	92531	93860	1	2123	3053	3983	1	10	1	0	1 06:02
55	TRN20	TRN	7	241708	244757	245686	247666	1	930	3444	5957	1	10	1	0	1 06:02
23	TRN20	TRN	4	196851	198376	202761	202877	1	4386	5206	6025	1	10	1	0	1 06:02
151	TRN20	TRN	15	318818	319505	325359	326413	1	5855	6725	7594	1	10	1	0	1 06:02
135	TRN20	TRN	14	80433	81575	88100	89169	1	6526	7631	8735	1	10	1	0	1 06:02
152	TRN20	TRN	15	346743	347366	354510	355477	1	7145	7939	8733	1	10	1	0	1 06:02
179	TRN20	TRN	16	694434	694716	704149	704396	1	9434	9698	9961	1	10	1	0	1 06:02
133	TRN20	TRN	13	751108	751553	761480	761798	1	9928	10309	10689	1	10	1	0	1 06:02
8	TRN20	TRN	2	191242	191470	191470	191528	1	1	143	285	1	10.1	1	0	1 02:06
103	TRN20	TRN	11	398924	399102	399102	399300	1	1	188	375	1	10.1	1	0	1 02:06
72	TRN20	TRN	8	482776	482818	482961	483130	1	144	249	353	1	10.1	1	0	1 02:06
94	TRN20	TRN	11	69153	69417	69425	69662	1	9	259	508	1	10.1	1	0	1 02:06
182	TRN20	TRN	16	826929	827031	827234	827379	1	204	327	449	1	10.1	1	0	1 02:06
95	TRN20	TRN	11	71211	71541	71541	71930	1	1	360	718	1	10.1	1	0	1 02:06
40	TRN20	TRN	5	219306	219359	219608	219959	1	250	451	652	1	10.1	1	0	1 02:06
75	TRN20	TRN	9	60434	60844	60879	61323	1	36	462	888	1	10.1	1	0	1 02:06
42	TRN20	TRN	5	360318	360499	360556	361242	1	58	491	923	1	10.1	1	0	1 02:06
148	TRN20	TRN	15	109424	109584	109584	110892	1	1	734	1467	1	10.1	1	0	1 02:06
176	TRN20	TRN	16	526860	527307	528017	528301	1	711	1076	1440	1	10.1	1	0	1 02:06
144	TRN20	TRN	14	486092	487177	487663	487830	1	487	1112	1737	1	10.1	1	0	1 02:06
105	TRN20	TRN	11	547337	547817	548704	548884	1	888	1217	1546	1	10.1	1	0	1 02:06
115	TRN20	TRN	12	516783	516845	517958	518152	1	1114	1241	1368	1	10.1	1	0	1 02:06
177	TRN20	TRN	16	686122	687687	687978	688591	1	292	1380	2468	1	10.1	1	0	1 02:06
149	TRN20	TRN	15	146419	147007	148159	148210	1	1153	1472	1790	1	10.1	1	0	1 02:06
86	TRN20	TRN	10	364028	364186	365022	366471	1	837	1640	2442	1	10.1	1	0	1 02:06
57	TRN20	TRN	7	414779	415307	416143	417265	1	837	1661	2485	1	10.1	1	0	1 02:06
161	TRN20	TRN	15	741453	741916	743338	743656	1	1423	1813	2202	1	10.1	1	0	1 02:06
78	TRN20	TRN	9	252174	252259	254108	254153	1	1850	1914	1978	1	10.1	1	0	1 02:06
45	TRN20	TRN	5	438946	439039	441415	441532	1	2377	2481	2585	1	10.1	1	0	1 02:06
186	TRN20	TRN	16	908156	908420	911060	911898	1	2641	3191	3741	1	10.1	1	0	1 02:06
127	TRN20	TRN	13	218051	218113	224985	225529	1	6873	7175	7477	1	10.1	1	0	1 02:06
171	TRN20	TRN	16	274818	275384	282651	283933	1	7268	8191	9114	1	10.1	1	0	1 02:06
90	TRN20	TRN	10	624648	627140	640236	640392	1	13097	14420	15743	1	10.1	1	0	1 02:06
12	TRN20	TRN	2	483944	484110	485003	485258	2_nonsis	894	1104	1313	3	30	1	0	1 6:2_2:6
49	TRN20	TRN	6	73471	73840	76126	76268	2_nonsis	2287	2542	2796	3	30	1	0	1 2:6_6:2
28	TRN20	TRN	4	888488	888611	895202	895289	2_nonsis	6592	6696	6800	3	30	1	0	1 6:2_2:6
114	TRN20	TRN	12	400601	400709	401664	402030	2_nonsis	956	1192	1428	3	30	1	0	1 6:2_4:4_2:6
50	TRN20	TRN	6	92224	92733	96853	96991	2_nonsis	4121	4444	4766	3	30	1	0	1 2:6_4:4_6:2
51	TRN20	TRN	6	110959	111466	112159	112326	2_nonsis	694	1030	1366	1	12	1	1	0 (4:4aCO)_(6:2)_(4:4a)
52	TRN20	TRN	6	171501	172334	172677	173376	2_nonsis	344	1109	1874	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
7	TRN20	TRN	2	119450	119490	120585	121110	2_nonsis	1096	1378	1659	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
163	TRN20	TRN	15	843892	843925	845840	846014	2_nonsis	1916	2019	2121	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
39	TRN20	TRN	5	182381	182827	190106	190541	2_nonsis	7280	7720	8159	1	12	1	1	0 (6:2)_(4:4)_(4:4aCO)
145	TRN20	TRN	14	510203	510728	511580	511838	2_nonsis	853	1244	1634	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
1	TRN20	TRN	1	44150	44384	46030	46375	2_nonsis	1647	1936	2224	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
100	TRN20	TRN	11	254358	254796	256637	256761	2_nonsis	1842	2122	2402	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
84	TRN20	TRN	10	318987	319218	321279	321299	2_nonsis	2062	2187	2311	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
178	TRN20	TRN	16	689677	691459	692547	693047	2_nonsis	1089	2229	3369	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
120	TRN20	TRN	12	1009697	1011169	1012226	1013592	2_nonsis	1058	2476	3894	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
110	TRN20	TRN	12	177778	178195	181616	182125	2_nonsis	3422	3884	4346	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
91	TRN20	TRN	10	648638	649035	653249	653590	2_nonsis	4215	4583	4951	1	12	1	1	0 (2:6)_(4:4)_(2:6)_(4:4aCO)

60	TRN20	TRN	7	661173	661245	665921	666261	2_nonsis	4677	4882	5087	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4aCO)
73	TRN20	TRN	9	36872	36921	42866	44800	2_nonsis	5946	6937	7927	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
29	TRN20	TRN	4	954530	954939	967966	968331	2_nonsis	13028	13414	13800	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
16	TRN20	TRN	2	741999	742150	745793	745895	2_nonsis	3644	3770	3895	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
180	TRN20	TRN	16	781741	783424	788617	788833	2_nonsis	5194	6143	7091	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
81	TRN20	TRN	10	127878	128296	140425	140646	2_nonsis	12130	12449	12767	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
143	TRN20	TRN	14	469170	470301	474965	475172	2_nonsis	4665	5333	6001	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
96	TRN20	TRN	11	93734	93852	93867	94121	2_nonsis	16	201	386	1	15	1	1	0	(6:2)_(4:4aCO)
119	TRN20	TRN	12	953629	953884	953884	954049	2_nonsis	1	210	419	1	15	1	1	0	(6:2)_(4:4aCO)
162	TRN20	TRN	15	836747	837056	837247	837673	2_nonsis	192	559	925	1	15	1	1	0	(6:2)_(4:4aCO)
139	TRN20	TRN	14	236860	237099	237838	238024	2_nonsis	740	952	1163	1	15	1	1	0	(6:2)_(4:4aCO)
153	TRN20	TRN	15	473069	474069	474069	475032	2_nonsis	1	982	1962	1	15	1	1	0	(6:2)_(4:4aCO)
68	TRN20	TRN	8	350845	351418	351889	352512	2_nonsis	472	1069	1666	1	15	1	1	0	(6:2)_(4:4aCO)
33	TRN20	TRN	4	1270902	1271755	1272147	1272726	2_nonsis	393	1108	1823	1	15	1	1	0	(6:2)_(4:4aCO)
142	TRN20	TRN	14	439088	440569	440622	441344	2_nonsis	54	1155	2255	1	15	1	1	0	(6:2)_(4:4aCO)
136	TRN20	TRN	14	122564	123158	123896	124154	2_nonsis	739	1164	1589	1	15	1	1	0	(6:2)_(4:4aCO)
154	TRN20	TRN	15	478915	479565	480144	480673	2_nonsis	580	1169	1757	1	15	1	1	0	(6:2)_(4:4aCO)
20	TRN20	TRN	3	273911	273985	275018	275423	2_nonsis	1034	1273	1511	1	15	1	1	0	(6:2)_(4:4aCO)
26	TRN20	TRN	4	703905	706032	706032	706601	2_nonsis	1	1348	2695	1	15	1	1	0	(6:2)_(4:4aCO)
184	TRN20	TRN	16	887070	887343	888536	888868	2_nonsis	1194	1496	1797	1	15	1	1	0	(6:2)_(4:4aCO)
109	TRN20	TRN	12	124986	126014	127219	127478	2_nonsis	1206	1849	2491	1	15	1	1	0	(6:2)_(4:4aCO)
117	TRN20	TRN	12	808279	809313	810333	811301	2_nonsis	1021	2021	3021	1	15	1	1	0	(6:2)_(4:4aCO)
21	TRN20	TRN	4	43482	46608	46818	47365	2_nonsis	211	2047	3882	1	15	1	1	0	(6:2)_(4:4aCO)
58	TRN20	TRN	7	430869	431116	432934	433211	2_nonsis	1819	2080	2341	1	15	1	1	0	(6:2)_(4:4aCO)
82	TRN20	TRN	10	223465	225236	226353	226665	2_nonsis	1118	2159	3199	1	15	1	1	0	(6:2)_(4:4aCO)
124	TRN20	TRN	13	56369	56748	59135	59485	2_nonsis	2388	2752	3115	1	15	1	1	0	(6:2)_(4:4aCO)
130	TRN20	TRN	13	543227	543392	545936	546319	2_nonsis	2545	2818	3091	1	15	1	1	0	(6:2)_(4:4aCO)
106	TRN20	TRN	11	588209	588593	590994	592478	2_nonsis	2402	3335	4268	1	15	1	1	0	(6:2)_(4:4aCO)
97	TRN20	TRN	11	165363	165754	169627	170362	2_nonsis	3874	4436	4998	1	15	1	1	0	(6:2)_(4:4aCO)
35	TRN20	TRN	4	1392322	1392396	1397878	1398006	2_nonsis	5483	5583	5683	1	15	1	1	0	(6:2)_(4:4aCO)
66	TRN20	TRN	8	14965	15038	24526	24674	2_nonsis	9489	9599	9708	1	15	1	1	0	(6:2)_(4:4aCO)
56	TRN20	TRN	7	247749	249983	259222	259380	2_nonsis	9240	10435	11630	1	15	1	1	0	(6:2)_(4:4aCO)
46	TRN20	TRN	5	479237	479528	480101	480122	2_nonsis	574	729	884	1	16	1	1	0	(2:6)_(4:4aCO)
92	TRN20	TRN	10	660402	660786	661171	661626	2_nonsis	386	805	1223	1	16	1	1	0	(2:6)_(4:4aCO)
128	TRN20	TRN	13	417524	418982	418982	419424	2_nonsis	1	950	1899	1	16	1	1	0	(2:6)_(4:4aCO)
37	TRN20	TRN	5	26413	26549	27272	27604	2_nonsis	724	957	1190	1	16	1	1	0	(2:6)_(4:4aCO)
167	TRN20	TRN	16	64540	66393	66527	66703	2_nonsis	135	1149	2162	1	16	1	1	0	(2:6)_(4:4aCO)
47	TRN20	TRN	5	482316	483903	483903	485006	2_nonsis	1	1345	2689	1	16	1	1	0	(2:6)_(4:4aCO)
146	TRN20	TRN	14	615762	617566	617566	618548	2_nonsis	1	1393	2785	1	16	1	1	0	(2:6)_(4:4aCO)
98	TRN20	TRN	11	204194	205481	205840	206732	2_nonsis	360	1449	2537	1	16	1	1	0	(2:6)_(4:4aCO)
77	TRN20	TRN	9	149978	150261	151918	152184	2_nonsis	1658	1932	2205	1	16	1	1	0	(2:6)_(4:4aCO)
101	TRN20	TRN	11	388737	389905	390798	391848	2_nonsis	894	2002	3110	1	16	1	1	0	(2:6)_(4:4aCO)
13	TRN20	TRN	2	486878	487183	489622	489703	2_nonsis	2440	2632	2824	1	16	1	1	0	(2:6)_(4:4aCO)
157	TRN20	TRN	15	623604	624112	627024	627279	2_nonsis	2913	3294	3674	1	16	1	1	0	(2:6)_(4:4aCO)
137	TRN20	TRN	14	156760	156907	161874	162100	2_nonsis	4968	5154	5339	1	16	1	1	0	(2:6)_(4:4aCO)
116	TRN20	TRN	12	564860	565172	570142	570914	2_nonsis	4971	5512	6053	1	16	1	1	0	(2:6)_(4:4aCO)
48	TRN20	TRN	6	53398	57870	61610	61904	2_nonsis	3741	6123	8505	1	16	1	1	0	(2:6)_(4:4aCO)
140	TRN20	TRN	14	245307	245680	252203	254039	2_nonsis	6524	7628	8731	1	16	1	1	0	(2:6)_(4:4aCO)
160	TRN20	TRN	15	728798	729380	739134	739347	2_nonsis	9755	10152	10548	1	16	1	1	0	(2:6)_(4:4aCO)
38	TRN20	TRN	5	63146	63176	75084	75225	2_nonsis	11909	11994	12078	1	16	1	1	0	(2:6)_(4:4aCO)
53	TRN20	TRN	7	113828	114793	128483	128648	2_nonsis	13691	14255	14819	1	16	1	1	0	(2:6)_(4:4aCO)
31	TRN20	TRN	4	1060416	1060655	1060416	1060655	2_nonsis	0	119	238	1	100	1	1	0	(4:4aCO)
15	TRN20	TRN	2	495218	495468	495218	495468	2_nonsis	0	125	249	1	100	1	1	0	(4:4aCO)
111	TRN20	TRN	12	222641	223058	222641	223058	2_nonsis	0	208	416	1	100	1	1	0	(4:4aCO)
11	TRN20	TRN	2	399052	399535	399052	399535	2_nonsis	0	241	482	1	100	1	1	0	(4:4aCO)
24	TRN20	TRN	4	314500	315119	314500	315119	2_nonsis	0	309	618	1	100	1	1	0	(4:4aCO)
181	TRN20	TRN	16	815485	816173	815485	816173	2_nonsis	0	344	687	1	100	1	1	0	(4:4aCO)
183	TRN20	TRN	16	880884	881834	880884	881834	2_nonsis	0	475	949	1	100	1	1	0	(4:4aCO)
30	TRN20	TRN	4	1057601	1058554	1057601	1058554	2_nonsis	0	476	952	1	100	1	1	0	(4:4aCO)
19	TRN20	TRN	3	160427	161541	160427	161541	2_nonsis	0	557	1113	1	100	1	1	0	(4:4aCO)

158	TRN20	TRN	15	630587	632023	630587	632023	2_nonsis		0	718	1435	1	100	1	1	0	(4:4aCO)
107	TRN20	TRN	12	40119	41721	40119	41721	2_nonsis		0	801	1601	1	100	1	1	0	(4:4aCO)
62	TRN20	TRN	7	900753	902391	900753	902391	2_nonsis		0	819	1637	1	100	1	1	0	(4:4aCO)
168	TRN20	TRN	16	79797	82464	79797	82464	2_nonsis		0	1333	2666	1	100	1	1	0	(4:4aCO)
85	TRN20	TRN	10	357628	361124	357628	361124	2_nonsis		0	1748	3495	1	100	1	1	0	(4:4aCO)
89	TRN20	TRN	10	568805	572936	568805	572936	2_nonsis		0	2065	4130	1	100	1	1	0	(4:4aCO)
27	TRN20	TRN	4	807222	816386	807222	816386	2_nonsis		0	4582	9163	1	100	1	1	0	(4:4aCO)
14	TRN20	TRN	2	491216	491476	492334	493122	2_nonsis		859	1382	1905	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
74	TRN20	TRN	9	55678	55716	58630	58961	2_nonsis		2915	3099	3282	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
185	TRN20	TRN	16	895917	896116	896854	897258	2_nonsis		739	1040	1340	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)
123	TRN20	TRN	13	46860	48814	54192	54469	2_nonsis		5379	6494	7608	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)_(2:6)_(4:4a)
147	TRN20	TRN	15	78272	78367	93175	94096	2_nonsis		14809	15316	15823	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(2:6)_(4:4a)
41	TRN20	TRN	5	344307	344574	348013	348215	2_sis		3440	3674	3907	0	1	2	0	2	(2:6)_(0:8)_(2:6)_(4:4)
44	TRN20	TRN	5	392326	392813	394357	394774	2_sis		1545	1996	2447	0	1	2	0	2	(2:6)_(0:8)_(2:6a)_(4:4)
112	TRN20	TRN	12	227856	228348	235940	236342		3	7593	8039	8485	0	1	2	0	2	(2:6)_(4:4)_(6:2)_(6:2a)_(4:4)
159	TRN20	TRN	15	652513	654602	656264	657201	2_sis		1663	3175	4687	0	1	2	0	2	(2:6)_(2:6a)_(4:4)
169	TRN20	TRN	16	83474	83873	86716	86878	2_sis		2844	3124	3403	0	1	2	0	2	(2:6)_(4:4)_(2:6)_(4:4)_(2:6a)_(4:4)
2	TRN20	TRN	1	79085	79449	80946	81253		3	1498	1833	2167	0	2	2	1	1	(6:2)_(4:4)_(6:2a)_(4:4aCO)
10	TRN20	TRN	2	390461	390744	394376	394430		3	3633	3801	3968	0	2	2	1	1	(2:6)_(2:6a)_(4:4aCO)
18	TRN20	TRN	3	72190	72786	77505	77826		3	4720	5178	5635	0	2	2	1	1	(6:2a)_(4:4aCO)
32	TRN20	TRN	4	1110571	1111002	1115198	1115651		3	4197	4638	5079	0	2	2	1	1	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
63	TRN20	TRN	7	942173	944010	947080	947885		3	3071	4391	5711	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4a)
65	TRN20	TRN	7	973354	975047	976713	976931		3	1667	2622	3576	0	2	2	1	1	(6:2)_(6:2a)_(4:4aCO)
83	TRN20	TRN	10	289772	289825	311129	311660		3	21305	21596	21887	0	2	2	1	1	(6:2)_(2:6)_(4:4aCO)_(2:6a)_(4:4a)
104	TRN20	TRN	11	523472	523649	524820	525008		3	1172	1354	1535	0	2	2	1	1	(6:2)_(4:4aCO)_(6:2a)_(4:4a)
113	TRN20	TRN	12	243937	244048	269839	270392		3	25792	26123	26454	0	2	2	1	1	(6:2)_(4:4aCO)_(6:2)_(8:0)_(6:2)_(4:4a)
118	TRN20	TRN	12	823256	830392	823256	830392		4	0	3568	7135	0	2	2	2	0	(4:4aCO)
126	TRN20	TRN	13	169522	170001	174577	174640		3	4577	4847	5117	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)
165	TRN20	TRN	15	989301	991111	993116	993617		3	2006	3161	4315	0	2	2	1	1	(6:2)_(4:4aCO)
170	TRN20	TRN	16	155661	155901	160237	160357		3	4337	4516	4695	0	2	2	1	1	(6:2)_(4:4)_(6:2)_(4:4)_(6:2a)_(4:4)_(6:2a)_(4:4aCO)
174	TRN20	TRN	16	506360	506595	510020	510985		3	3426	4025	4624	0	2	2	1	1	(6:2)_(8:0)_(4:4aCO)
3	TRN20	TRN	1	190429	190880	191617	193131		4	738	1720	2701	0	3	2	2	0	(6:2)_(4:4aCO)_(4:4bCO)
5	TRN20	TRN	2	90715	92062	97590	97676	2_nonsis		5529	6245	6960	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(4:4CO)
9	TRN20	TRN	2	284437	284893	291653	292254		3	6761	7289	7816	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)_(4:4CO)
22	TRN20	TRN	4	161421	162357	163031	163324	2_nonsis		675	1289	1902	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4CO)
34	TRN20	TRN	4	1345632	1346089	1347683	1349666	2_nonsis		1595	2814	4033	0	3	2	0	2	(6:2)_(4:4aCO)_(4:4CO)
36	TRN20	TRN	4	1418662	1418928	1424907	1424978		3	5980	6148	6315	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4bCO)_(2:6a)_(4:4b)
61	TRN20	TRN	7	728724	729111	729111	729333	2_nonsis		1	305	608	0	3	2	0	2	(4:4aCO)_(4:4CO)
67	TRN20	TRN	8	276840	277301	284440	285871	2_nonsis		7140	8085	9030	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)
70	TRN20	TRN	8	441044	441251	444619	444856		4	3369	3590	3811	0	3	2	2	0	(6:2)_(8:0)_(6:2)_(6:2a)_(4:4aCO)_(6:2a)_(4:4bCO)
71	TRN20	TRN	8	457249	457364	461762	463767	2_nonsis		4399	5458	6517	0	3	2	0	2	(2:6)_(4:4)_(2:6)_(4:4aCO)_(6:2)_(4:4CO)_(2:6)_(4:4)
80	TRN20	TRN	9	268278	269349	275507	275789		3	6159	6835	7510	0	3	2	1	1	(6:2)_(4:4aCO)_(4:4bCO)
88	TRN20	TRN	10	464438	465282	471532	471814		3	6251	6813	7375	0	3	2	0	2	(2:6)_(4:4)_(6:2)_(6:2a)_(4:4aCO)_(2:6)_(4:4CO)
93	TRN20	TRN	10	715592	716361	717437	718433	2_nonsis		1077	1959	2840	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)
102	TRN20	TRN	11	394215	394878	396831	397099	2_nonsis		1954	2419	2883	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)_(2:6)_(4:4CO)
108	TRN20	TRN	12	91515	91951	91992	92468	2_nonsis		42	497	952	0	3	2	0	2	(4:4aCO)_(4:4CO)
121	TRN20	TRN	12	1042570	1042844	1043701	1043895	2_nonsis		858	1091	1324	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)
131	TRN20	TRN	13	668902	669285	673975	674192	2_nonsis		4691	4990	5289	0	3	2	0	2	(2:6)_(4:4)_(2:6)_(4:4aCO)_(6:2)_(4:4a)_(4:4CO)
132	TRN20	TRN	13	699586	700248	703253	703444		3	3006	3432	3857	0	3	2	0	2	(2:6)_(0:8)_(2:6)_(4:4aCO)_(4:4CO)
134	TRN20	TRN	13	774012	774331	776909	777163		3	2579	2865	3150	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(2:6)_(4:4CO)
138	TRN20	TRN	14	196834	197191	202811	203039		3	5621	5913	6204	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)
141	TRN20	TRN	14	357524	357852	362994	363234		3	5143	5426	5709	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(4:4CO)_(2:6a)_(4:4)
150	TRN20	TRN	15	190009	192333	201256	202129		3	8924	10522	12119	0	3	2	1	1	(2:6)_(2:6a)_(4:4)_(2:6a)_(4:4)_(4:4aCO)_(4:4bCO)
156	TRN20	TRN	15	496163	496422	499909	499981	2_nonsis		3488	3653	3817	0	3	2	0	2	(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4CO)
164	TRN20	TRN	15	954766	955006	960152	960232	2_nonsis		5147	5306	5465	0	3	2	0	2	(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4CO)
166	TRN20	TRN	15	996896	997902	1006391	1007049		3	8490	9321	10152	0	3	2	1	1	(2:6)_(4:4)_(2:6)_(4:4)_(4:4aCO)_(4:4bCO)_(6:2)_(4:4aCO)
175	TRN20	TRN	16	512760	513619	520684	521328		3	7066	7817	8567	0	3	2	2	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2a)_(4:4CO)
187	TRN20	TRN	16	920048	920779	922477	922622		3	1699	2136	2573	0	3	2	1	1	(2:6)_(4:4aCO)_(6:2)_(4:4bCO)
53	TRN4	TRN	7	978531	978858	979683	979753		1	826	1024	1221	1	7	1	0	1	6:2_4:4_6:2
126	TRN4	TRN	15	162872	163253	164284	164383		1	1032	1271	1510	1	7	1	0	1	6:2_4:4_6:2

110	TRN4	TRN	13	856957	857240	860181	861184	1	2942	3584	4226	1	7	1	0	1	6:2_4:4_6:2
87	TRN4	TRN	12	530404	531361	534611	535533	1	3251	4190	5128	1	7	1	0	1	6:2_4:4_6:2
129	TRN4	TRN	15	316412	316429	316433	316591	1	5	92	178	1	10	1	0	1	06:02
47	TRN4	TRN	7	612267	612759	612759	612980	1	1	357	712	1	10	1	0	1	06:02
101	TRN4	TRN	13	340906	341020	341111	341630	1	92	408	723	1	10	1	0	1	06:02
22	TRN4	TRN	4	318659	319317	319317	319482	1	1	412	822	1	10	1	0	1	06:02
43	TRN4	TRN	7	327931	328052	328052	329109	1	1	589	1177	1	10	1	0	1	06:02
57	TRN4	TRN	8	375825	375930	376477	376578	1	548	650	752	1	10	1	0	1	06:02
10	TRN4	TRN	2	371139	371446	371746	372547	1	301	854	1407	1	10	1	0	1	06:02
112	TRN4	TRN	13	914143	916782	916782	916813	1	1	1335	2669	1	10	1	0	1	06:02
39	TRN4	TRN	5	516974	517321	518464	519506	1	1144	1838	2531	1	10	1	0	1	06:02
125	TRN4	TRN	15	152407	153180	154173	156059	1	994	2323	3651	1	10	1	0	1	06:02
103	TRN4	TRN	13	383224	384682	385945	387028	1	1264	2534	3803	1	10	1	0	1	06:02
66	TRN4	TRN	10	79553	79717	82809	82930	1	3093	3235	3376	1	10	1	0	1	06:02
44	TRN4	TRN	7	473951	474708	482421	483344	1	7714	8553	9392	1	10	1	0	1	06:02
130	TRN4	TRN	15	373492	374879	384491	384665	1	9613	10393	11172	1	10	1	0	1	06:02
25	TRN4	TRN	4	824244	831279	844304	848341	1	13026	18561	24096	1	10	1	0	1	06:02
45	TRN4	TRN	7	525956	526158	526158	526419	1	1	232	462	1	10.1	1	0	1	02:06
28	TRN4	TRN	4	1282347	1283112	1283387	1283592	1	276	760	1244	1	10.1	1	0	1	02:06
124	TRN4	TRN	15	39434	39886	40057	41027	1	172	882	1592	1	10.1	1	0	1	02:06
151	TRN4	TRN	16	842086	843391	843720	843861	1	330	1052	1774	1	10.1	1	0	1	02:06
12	TRN4	TRN	2	562773	564041	564041	565133	1	1	1180	2359	1	10.1	1	0	1	02:06
4	TRN4	TRN	2	41298	43330	43348	43654	1	19	1187	2355	1	10.1	1	0	1	02:06
92	TRN4	TRN	12	729962	731012	731012	732527	1	1	1283	2564	1	10.1	1	0	1	02:06
145	TRN4	TRN	16	659091	659254	660498	661094	1	1245	1624	2002	1	10.1	1	0	1	02:06
90	TRN4	TRN	12	674877	677323	677323	678512	1	1	1818	3634	1	10.1	1	0	1	02:06
61	TRN4	TRN	9	136172	138253	139068	139273	1	816	1958	3100	1	10.1	1	0	1	02:06
111	TRN4	TRN	13	889717	890524	890524	893651	1	1	1967	3933	1	10.1	1	0	1	02:06
35	TRN4	TRN	5	232874	233356	234931	235773	1	1576	2237	2898	1	10.1	1	0	1	02:06
68	TRN4	TRN	10	343574	344460	346113	346401	1	1654	2240	2826	1	10.1	1	0	1	02:06
137	TRN4	TRN	15	808677	808993	811067	811738	1	2075	2568	3060	1	10.1	1	0	1	02:06
62	TRN4	TRN	9	265508	265732	268278	269349	1	2547	3194	3840	1	10.1	1	0	1	02:06
96	TRN4	TRN	13	18729	20392	23353	23573	1	2962	3903	4843	1	10.1	1	0	1	02:06
71	TRN4	TRN	10	568805	572936	574799	577387	1	1864	5223	8581	1	10.1	1	0	1	02:06
139	TRN4	TRN	16	50951	51382	56290	63657	1	4909	8807	12705	1	10.1	1	0	1	02:06
94	TRN4	TRN	12	892436	930472	940926	947200	1	10455	32609	54763	1	10.1	1	0	1	02:06
81	TRN4	TRN	11	612809	613087	616059	616404	2_nonsis	2973	3284	3594	3	30	1	0	1	6:2_2:6
88	TRN4	TRN	12	576339	577535	585365	586124	2_nonsis	7831	8808	9784	3	30	1	0	1	6:2_2:6
132	TRN4	TRN	15	527323	529292	546837	547266	2_nonsis	17546	18744	19942	3	30	1	0	1	6:2_2:6
23	TRN4	TRN	4	419911	420270	422794	423046	2_nonsis	2525	2830	3134	3	30	1	0	1	2:6_4:4_6:2
42	TRN4	TRN	7	197225	197228	197230	197465	2_nonsis	3	121	239	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4a)
128	TRN4	TRN	15	311489	312220	313126	313924	2_nonsis	907	1671	2434	1	12	1	1	0	(4:4aCO)_(6:2)_(4:4a)
37	TRN4	TRN	5	348780	349106	350543	350741	2_nonsis	1438	1699	1960	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
13	TRN4	TRN	2	672354	672487	674481	675106	2_nonsis	1995	2373	2751	1	12	1	1	0	(2:6)_(4:4)_(4:4aCO)
1	TRN4	TRN	1	57739	59349	62990	63992	2_nonsis	3642	4947	6252	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
82	TRN4	TRN	11	631559	632039	634424	634635	2_nonsis	2386	2731	3075	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
97	TRN4	TRN	13	85411	86109	101176	101469	2_nonsis	15068	15563	16057	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
148	TRN4	TRN	16	723296	723524	726638	726715	2_nonsis	3115	3267	3418	1	12	1	1	0	(6:2)_(4:4)_(6:2)_(4:4)_(6:2)_(4:4aCO)
56	TRN4	TRN	8	199940	200213	203922	204071	2_nonsis	3710	3920	4130	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4)_(2:6)_(4:4aCO)
74	TRN4	TRN	10	671183	671903	675511	675536	2_nonsis	3609	3981	4352	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
48	TRN4	TRN	7	716908	716964	716964	717207	2_nonsis	1	150	298	1	15	1	1	0	(6:2)_(4:4aCO)
19	TRN4	TRN	4	28656	28798	29152	29441	2_nonsis	355	570	784	1	15	1	1	0	(6:2)_(4:4aCO)
21	TRN4	TRN	4	237971	238826	239002	239328	2_nonsis	177	767	1356	1	15	1	1	0	(6:2)_(4:4aCO)
7	TRN4	TRN	2	202227	202580	203030	203566	2_nonsis	451	895	1338	1	15	1	1	0	(6:2)_(4:4aCO)
24	TRN4	TRN	4	546573	547556	548255	548809	2_nonsis	700	1468	2235	1	15	1	1	0	(6:2)_(4:4aCO)
54	TRN4	TRN	8	49378	49451	50752	51058	2_nonsis	1302	1491	1679	1	15	1	1	0	(6:2)_(4:4aCO)
121	TRN4	TRN	14	679089	680930	680930	682206	2_nonsis	1	1559	3116	1	15	1	1	0	(6:2)_(4:4aCO)
108	TRN4	TRN	13	569867	571706	572735	573292	2_nonsis	1030	2227	3424	1	15	1	1	0	(6:2)_(4:4aCO)
114	TRN4	TRN	14	191916	192676	194860	195019	2_nonsis	2185	2644	3102	1	15	1	1	0	(6:2)_(4:4aCO)
30	TRN4	TRN	4	1361801	1362620	1364750	1365372	2_nonsis	2131	2851	3570	1	15	1	1	0	(6:2)_(4:4aCO)

147	TRN4	TRN	16	674900	676149	678266	678517	2_nonsis	2118	2867	3616	1	15	1	1	0	(6:2)_(4:4aCO)
64	TRN4	TRN	9	340356	340507	343174	343775	2_nonsis	2668	3043	3418	1	15	1	1	0	(6:2)_(4:4aCO)
113	TRN4	TRN	14	147866	148161	151307	151701	2_nonsis	3147	3491	3834	1	15	1	1	0	(6:2)_(4:4aCO)
50	TRN4	TRN	7	845918	851797	852125	852577	2_nonsis	329	3494	6658	1	15	1	1	0	(6:2)_(4:4aCO)
104	TRN4	TRN	13	395179	395296	399189	399471	2_nonsis	3894	4093	4291	1	15	1	1	0	(6:2)_(4:4aCO)
63	TRN4	TRN	9	311143	311461	315406	315641	2_nonsis	3946	4222	4497	1	15	1	1	0	(6:2)_(4:4aCO)
144	TRN4	TRN	16	504044	505893	509084	509810	2_nonsis	3192	4479	5765	1	15	1	1	0	(6:2)_(4:4aCO)
34	TRN4	TRN	5	107929	109005	113148	113457	2_nonsis	4144	4836	5527	1	15	1	1	0	(6:2)_(4:4aCO)
3	TRN4	TRN	1	121235	128637	129517	130254	2_nonsis	881	4950	9018	1	15	1	1	0	(6:2)_(4:4aCO)
138	TRN4	TRN	15	940429	940454	945784	946490	2_nonsis	5331	5696	6060	1	15	1	1	0	(6:2)_(4:4aCO)
86	TRN4	TRN	12	391460	391658	396641	398325	2_nonsis	4984	5924	6864	1	15	1	1	0	(6:2)_(4:4aCO)
98	TRN4	TRN	13	133437	133610	139664	140131	2_nonsis	6055	6374	6693	1	15	1	1	0	(6:2)_(4:4aCO)
2	TRN4	TRN	1	100840	101607	108928	110856	2_nonsis	7322	8669	10015	1	15	1	1	0	(6:2)_(4:4aCO)
55	TRN4	TRN	8	166655	167453	175480	176184	2_nonsis	8028	8778	9528	1	15	1	1	0	(6:2)_(4:4aCO)
152	TRN4	TRN	16	844011	858788	860540	861771	2_nonsis	1753	9756	17759	1	15	1	1	0	(6:2)_(4:4aCO)
134	TRN4	TRN	15	648434	649497	659154	660208	2_nonsis	9658	10716	11773	1	15	1	1	0	(6:2)_(4:4aCO)
142	TRN4	TRN	16	338953	339078	339098	339477	2_nonsis	21	272	523	1	16	1	1	0	(2:6)_(4:4aCO)
115	TRN4	TRN	14	196834	197191	197191	197707	2_nonsis	1	437	872	1	16	1	1	0	(2:6)_(4:4aCO)
60	TRN4	TRN	9	97151	97705	97705	98039	2_nonsis	1	444	887	1	16	1	1	0	(2:6)_(4:4aCO)
109	TRN4	TRN	13	594379	594694	594694	595371	2_nonsis	1	496	991	1	16	1	1	0	(2:6)_(4:4aCO)
89	TRN4	TRN	12	634219	634488	634488	635382	2_nonsis	1	582	1162	1	16	1	1	0	(2:6)_(4:4aCO)
58	TRN4	TRN	8	459885	460708	460801	461318	2_nonsis	94	763	1432	1	16	1	1	0	(2:6)_(4:4aCO)
150	TRN4	TRN	16	833734	834026	834629	834822	2_nonsis	604	846	1087	1	16	1	1	0	(2:6)_(4:4aCO)
131	TRN4	TRN	15	474069	475032	475032	475809	2_nonsis	1	870	1739	1	16	1	1	0	(2:6)_(4:4aCO)
118	TRN4	TRN	14	439088	440569	440622	441344	2_nonsis	54	1155	2255	1	16	1	1	0	(2:6)_(4:4aCO)
135	TRN4	TRN	15	740202	740490	741453	741916	2_nonsis	964	1339	1713	1	16	1	1	0	(2:6)_(4:4aCO)
15	TRN4	TRN	3	156289	156517	157807	157881	2_nonsis	1291	1441	1591	1	16	1	1	0	(2:6)_(4:4aCO)
29	TRN4	TRN	4	1354002	1355589	1355853	1357024	2_nonsis	265	1643	3021	1	16	1	1	0	(2:6)_(4:4aCO)
17	TRN4	TRN	3	220054	221651	221877	223339	2_nonsis	227	1756	3284	1	16	1	1	0	(2:6)_(4:4aCO)
33	TRN4	TRN	5	88547	88700	90218	91109	2_nonsis	1519	2040	2561	1	16	1	1	0	(2:6)_(4:4aCO)
27	TRN4	TRN	4	1276813	1277186	1279416	1279422	2_nonsis	2231	2420	2608	1	16	1	1	0	(2:6)_(4:4aCO)
32	TRN4	TRN	5	28312	28600	30664	31247	2_nonsis	2065	2500	2934	1	16	1	1	0	(2:6)_(4:4aCO)
116	TRN4	TRN	14	241440	242111	243530	245040	2_nonsis	1420	2510	3599	1	16	1	1	0	(2:6)_(4:4aCO)
100	TRN4	TRN	13	298131	301151	301274	303266	2_nonsis	124	2629	5134	1	16	1	1	0	(2:6)_(4:4aCO)
18	TRN4	TRN	3	243219	246581	247472	248367	2_nonsis	892	3020	5147	1	16	1	1	0	(2:6)_(4:4aCO)
102	TRN4	TRN	13	350372	351095	354466	354798	2_nonsis	3372	3899	4425	1	16	1	1	0	(2:6)_(4:4aCO)
31	TRN4	TRN	4	1421456	1421579	1426206	1427025	2_nonsis	4628	5098	5568	1	16	1	1	0	(2:6)_(4:4aCO)
20	TRN4	TRN	4	58356	58765	63704	63839	2_nonsis	4940	5211	5482	1	16	1	1	0	(2:6)_(4:4aCO)
59	TRN4	TRN	9	74541	74723	77594	82232	2_nonsis	2872	5281	7690	1	16	1	1	0	(2:6)_(4:4aCO)
14	TRN4	TRN	2	715932	716328	725754	726633	2_nonsis	9427	10064	10700	1	16	1	1	0	(2:6)_(4:4aCO)
146	TRN4	TRN	16	672569	672668	672569	672668	2_nonsis	0	49	98	1	100	1	1	0	(4:4aCO)
65	TRN4	TRN	9	345656	345871	345656	345871	2_nonsis	0	107	214	1	100	1	1	0	(4:4aCO)
140	TRN4	TRN	16	128692	128926	128692	128926	2_nonsis	0	117	233	1	100	1	1	0	(4:4aCO)
85	TRN4	TRN	12	274580	274968	274580	274968	2_nonsis	0	194	387	1	100	1	1	0	(4:4aCO)
73	TRN4	TRN	10	641631	642317	641631	642317	2_nonsis	0	343	685	1	100	1	1	0	(4:4aCO)
49	TRN4	TRN	7	782525	783224	782525	783224	2_nonsis	0	349	698	1	100	1	1	0	(4:4aCO)
77	TRN4	TRN	11	252204	252966	252204	252966	2_nonsis	0	381	761	1	100	1	1	0	(4:4aCO)
91	TRN4	TRN	12	728268	729242	728268	729242	2_nonsis	0	487	973	1	100	1	1	0	(4:4aCO)
78	TRN4	TRN	11	292055	293072	292055	293072	2_nonsis	0	508	1016	1	100	1	1	0	(4:4aCO)
11	TRN4	TRN	2	498923	499985	498923	499985	2_nonsis	0	531	1061	1	100	1	1	0	(4:4aCO)
117	TRN4	TRN	14	391752	392860	391752	392860	2_nonsis	0	554	1107	1	100	1	1	0	(4:4aCO)
105	TRN4	TRN	13	403536	404983	403536	404983	2_nonsis	0	723	1446	1	100	1	1	0	(4:4aCO)
143	TRN4	TRN	16	502052	503873	502052	503873	2_nonsis	0	910	1820	1	100	1	1	0	(4:4aCO)
70	TRN4	TRN	10	513875	515737	513875	515737	2_nonsis	0	931	1861	1	100	1	1	0	(4:4aCO)
69	TRN4	TRN	10	467589	469453	467589	469453	2_nonsis	0	932	1863	1	100	1	1	0	(4:4aCO)
95	TRN4	TRN	12	1009176	1011169	1009176	1011169	2_nonsis	0	996	1992	1	100	1	1	0	(4:4aCO)
93	TRN4	TRN	12	732527	736073	732527	736073	2_nonsis	0	1773	3545	1	100	1	1	0	(4:4aCO)
46	TRN4	TRN	7	533539	542099	533539	542099	2_nonsis	0	4280	8559	1	100	1	1	0	(4:4aCO)
72	TRN4	TRN	10	590704	601293	590704	601293	2_nonsis	0	5294	10588	1	100	1	1	0	(4:4aCO)
123	TRN4	TRN	15	22043	39402	22043	39402	2_nonsis	0	8679	17358	1	100	1	1	0	(4:4aCO)

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19
141	TRN4	TRN	16	169613	170076	171708	172192	2_nonsis		1633	2106	2578	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
16	TRN4	TRN	3	215020	215336	216257	216424	2_nonsis		922	1163	1403	3	20	1	1	0	(2:6)_(4:4)_(6:2)_(4:4aCO)
80	TRN4	TRN	11	524820	525008	531608	531920	2_nonsis		6601	6850	7099	3	20	1	1	0	(6:2)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
119	TRN4	TRN	14	492875	494368	496792	497090	2_sis		2425	3320	4214	0	1	2	0	2	(2:6)_(4:4)_(2:6a)_(4:4)
127	TRN4	TRN	15	185240	185951	192333	196238	2_sis		6383	8690	10997	0	1	2	0	2	(6:2)_(8:0)_(4:4)
6	TRN4	TRN	2	149400	149762	152171	152423		3	2410	2716	3022	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)
9	TRN4	TRN	2	253219	254436	258516	265770		4	4081	8316	12550	0	2	2	2	0	(2:6)_(0:8)_(2:6a)_(4:4aCO)
36	TRN4	TRN	5	236672	237191	242693	242801		3	5503	5816	6128	0	2	2	1	1	(2:6)_(4:4)_(6:2)_(2:6a)_(4:4aCO)
40	TRN4	TRN	5	519704	521844	521881	523683		4	38	2008	3978	0	2	2	2	0	(6:2)_(4:4aCO)
41	TRN4	TRN	7	165523	166667	181138	182388		3	14472	15668	16864	0	2	2	1	1	(2:6)_(2:6a)_(4:4aCO)
52	TRN4	TRN	7	959381	959587	976931	977277		3	17345	17620	17895	0	2	2	1	1	(6:2)_(8:0)_(6:2a)_(8:0)_(4:4aCO)_(6:2)_(8:0)_(6:2a)_(4:4a)_(6:2a)_(4:4a)
67	TRN4	TRN	10	325369	325803	342031	342558		4	16229	16709	17188	0	2	2	2	0	(2:6)_(0:8)_(4:4aCO)_(2:6a)_(4:4a)
76	TRN4	TRN	11	60173	65282	68377	68447		3	3096	5685	8273	0	2	2	1	1	(8:0)_(6:2)_(4:4aCO)
84	TRN4	TRN	12	259210	260086	271951	272455		4	11866	12555	13244	0	2	2	1	1	(8:0)_(6:2)_(6:2a)_(4:4aCO)
107	TRN4	TRN	13	555444	555852	565076	565610		3	9225	9695	10165	0	2	2	1	1	(2:6)_(2:6a)_(0:8)_(2:6)_(4:4aCO)
5	TRN4	TRN	2	56974	57115	73943	75564	2_nonsis		16829	17709	18589	0	3	2	0	2	(6:2)_(4:4)_(4:4aCO)_(6:2)_(4:4CO)
8	TRN4	TRN	2	204536	205151	207859	208543		3	2709	3358	4006	0	3	2	1	1	(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4bCO)
26	TRN4	TRN	4	939749	940069	951351	951669		3	11283	11601	11919	0	3	2	2	0	(6:2)_(6:2a)_(6:2)_(4:4aCO)_(6:2)_(4:4CO)
38	TRN4	TRN	5	407419	407957	412632	413862		3	4676	5559	6442	0	3	2	1	1	(4:4aCO)_(2:6)_(4:4bCO)
51	TRN4	TRN	7	902661	903030	907598	908105	2_nonsis		4569	5006	5443	0	3	2	0	2	(4:4aCO)_(4:4CO)
75	TRN4	TRN	10	697654	705639	707260	707549		3	1622	5758	9894	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4bCO)
79	TRN4	TRN	11	433660	433721	436087	436826	2_nonsis		2367	2766	3165	0	3	2	0	2	(2:6)_(4:4aCO)_(6:2)_(4:4CO)
83	TRN4	TRN	12	254321	254610	257504	258349		4	2895	3461	4027	0	3	2	2	0	(6:2)_(2:6)_(4:4aCO)_(4:4bCO)
99	TRN4	TRN	13	222095	224126	235798	237159		4	11673	13368	15063	0	3	2	2	0	(4:4aCO)_(6:2)_(2:6)_(4:4bCO)
106	TRN4	TRN	13	406917	410079	411264	411358	2_nonsis		1186	2813	4440	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(4:4CO)
120	TRN4	TRN	14	641101	641452	643956	644875	2_nonsis		2505	3139	3773	0	3	2	0	2	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4CO)
133	TRN4	TRN	15	582005	582404	585323	585644		3	2920	3279	3638	0	3	2	1	1	(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4bCO)_(6:2)_(4:4b)
136	TRN4	TRN	15	801285	801441	803637	804529		3	2197	2720	3243	0	3	2	1	1	(6:2)_(4:4aCO)_(6:2)_(4:4bCO)
149	TRN4	TRN	16	795316	796263	798282	798490	2_nonsis		2020	2597	3173	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2)_(4:4CO)
48	TRS10	TRS	16	520194	520400	520684	521940		1	285	1015	1745	1	10	1	0	1	06:02
17	TRS10	TRS	4	1455942	1458372	1459261	1459669		1	890	2308	3726	1	10	1	0	1	06:02
46	TRS10	TRS	16	345110	347009	347399	347684		1	391	1482	2573	1	10.1	1	0	1	02:06
8	TRS10	TRS	3	102669	103556	104476	105047		1	921	1649	2377	1	10.1	1	0	1	02:06
45	TRS10	TRS	16	226745	226835	228253	228815	2_nonsis		1419	1744	2069	3	30	1	0	1	6:2_2:6
1	TRS10	TRS	2	81826	81997	87294	87772	2_nonsis		5298	5622	5945	3	30	1	0	1	2:6_6:2_4:4_6:2
51	TRS10	TRS	16	781741	783796	788320	788362	2_nonsis		4525	5573	6620	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
44	TRS10	TRS	15	700551	700804	701028	701208	2_nonsis		225	441	656	1	15	1	1	0	(6:2)_(4:4aCO)
11	TRS10	TRS	4	833772	833834	834899	835164	2_nonsis		1066	1229	1391	1	15	1	1	0	(6:2)_(4:4aCO)
23	TRS10	TRS	6	199247	200563	200563	201948	2_nonsis		1	1351	2700	1	15	1	1	0	(6:2)_(4:4aCO)
35	TRS10	TRS	10	488230	488779	489013	490750	2_nonsis		235	1377	2519	1	15	1	1	0	(6:2)_(4:4aCO)
7	TRS10	TRS	2	540568	540838	547559	548176	2_nonsis		6722	7165	7607	1	15	1	1	0	(6:2)_(4:4aCO)
32	TRS10	TRS	10	273531	273972	281056	281289	2_nonsis		7085	7421	7757	1	15	1	1	0	(6:2)_(4:4aCO)
12	TRS10	TRS	4	960787	961189	962545	962923	2_nonsis		1357	1746	2135	1	16	1	1	0	(2:6)_(4:4aCO)
31	TRS10	TRS	10	189655	190275	191621	192156	2_nonsis		1347	1924	2500	1	16	1	1	0	(2:6)_(4:4aCO)
43	TRS10	TRS	15	534200	536230	536230	538230	2_nonsis		1	2015	4029	1	16	1	1	0	(2:6)_(4:4aCO)
2	TRS10	TRS	2	95376	96610	97884	98470	2_nonsis		1275	2184	3093	1	16	1	1	0	(2:6)_(4:4aCO)
5	TRS10	TRS	2	399796	400827	402177	404155	2_nonsis		1351	2855	4358	1	16	1	1	0	(2:6)_(4:4aCO)
13	TRS10	TRS	4	1111638	1112793	1115198	1115651	2_nonsis		2406	3209	4012	1	16	1	1	0	(2:6)_(4:4aCO)
30	TRS10	TRS	9	329125	332459	333581	334696	2_nonsis		1123	3347	5570	1	16	1	1	0	(2:6)_(4:4aCO)
25	TRS10	TRS	7	223151	224665	226711	229846	2_nonsis		2047	4371	6694	1	16	1	1	0	(2:6)_(4:4aCO)
18	TRS10	TRS	4	1465397	1465791	1470784	1470991	2_nonsis		4994	5294	5593	1	16	1	1	0	(2:6)_(4:4aCO)
33	TRS10	TRS	10	311915	312326	317491	317989	2_nonsis		5166	5620	6073	1	16	1	1	0	(2:6)_(4:4aCO)
36	TRS10	TRS	10	574412	574799	574412	574799	2_nonsis		0	193	386	1	100	1	1	0	(4:4aCO)
14	TRS10	TRS	4	1241519	1242241	1241519	1242241	2_nonsis		0	361	721	1	100	1	1	0	(4:4aCO)
40	TRS10	TRS	13	273267	274088	273267	274088	2_nonsis		0	410	820	1	100	1	1	0	(4:4aCO)
9	TRS10	TRS	3	115183	116011	115183	116011	2_nonsis		0	414	827	1	100	1	1	0	(4:4aCO)
4	TRS10	TRS	2	206083	207171	206083	207171	2_nonsis		0	544	1087	1	100	1	1	0	(4:4aCO)
24	TRS10	TRS	7	81435	82858	81435	82858	2_nonsis		0	711	1422	1	100	1	1	0	(4:4aCO)
37	TRS10	TRS	10	618846	621779	618846	621779	2_nonsis		0	1466	2932	1	100	1	1	0	(4:4aCO)
21	TRS10	TRS	6	76126	76268	80386	81527	2_nonsis		4119	4760	5400	3	20	1	1	0	(2:6)_(4:4aCO)_(6:2)_(2:6)_(4:4a)

34	TRS10	TRS	10	423063	423483	425486	426379	2_sis		2004	2660	3315	0	1	2	0	2	(2:6)_(0:8)_(4:4)
49	TRS10	TRS	16	525874	526176	531193	531957	2_sis		5018	5550	6082	0	1	2	0	2	(6:2)_(8:0)_(6:2)_(4:4)
3	TRS10	TRS	2	193122	193664	194226	195735		3	563	1588	2612	0	2	2	1	1	(8:0)_(6:2)_(4:4aCO)
10	TRS10	TRS	3	243219	246581	247158	247472		4	578	2415	4252	0	2	2	2	0	(8:0)_(4:4aCO)
15	TRS10	TRS	4	1274423	1274743	1280622	1281921		3	5880	6689	7497	0	2	2	1	1	(2:6)_(0:8)_(2:6)_(0:8)_(2:6)_(0:8)_(2:6)_(4:4aCO)
16	TRS10	TRS	4	1418937	1419231	1423497	1424231		3	4267	4780	5293	0	2	2	1	1	(2:6)_(0:8)_(2:6a)_(4:4aCO)
22	TRS10	TRS	6	97979	98011	100276	100356		3	2266	2321	2376	0	2	2	1	1	(2:6)_(2:6a)_(4:4aCO)
39	TRS10	TRS	13	157807	159018	160611	160665		3	1594	2226	2857	0	2	2	1	1	(0:8)_(2:6)_(4:4aCO)
47	TRS10	TRS	16	446142	446457	456724	458489		4	10268	11307	12346	0	2	2	2	0	(2:6)_(2:6a)_(0:8)_(2:6a)_(4:4aCO)
59	TRS10	TRS	3	59171	59465	60354	60633	NA		890	1176	1461	0	4	1	NA	NA	06:02
71	TRS10	TRS	5	96109	97220	96109	97220		1	0	555	1110	0	4	1	NA	NA	
105	TRS10	TRS	16	916537	916779	925093	948066		1	0	15764	31528	0	4	1	NA	NA	
43	TW1	TW	9	174391	174961	174961	175104		1	1	357	712	1	10	1	0	1	06:02
64	TW1	TW	12	88002	88069	88557	89489		1	489	988	1486	1	10	1	0	1	06:02
73	TW1	TW	13	301274	302548	302628	303266		1	81	1036	1991	1	10	1	0	1	06:02
79	TW1	TW	13	850650	851409	852118	852413		1	710	1236	1762	1	10	1	0	1	06:02
49	TW1	TW	10	303882	304262	305004	305635		1	743	1248	1752	1	10	1	0	1	06:02
19	TW1	TW	4	1086670	1087085	1087412	1088864		1	328	1261	2193	1	10	1	0	1	06:02
5	TW1	TW	2	705633	706449	707509	708202		1	1061	1815	2568	1	10	1	0	1	06:02
103	TW1	TW	16	840488	840627	842086	842864		1	1460	1918	2375	1	10	1	0	1	06:02
46	TW1	TW	9	329125	332459	332503	333073		1	45	1996	3947	1	10	1	0	1	06:02
58	TW1	TW	11	224634	225480	227482	227625		1	2003	2497	2990	1	10	1	0	1	06:02
21	TW1	TW	4	1333799	1333898	1335831	1337219		1	1934	2677	3419	1	10	1	0	1	06:02
27	TW1	TW	5	472756	473209	476048	476183		1	2840	3133	3426	1	10	1	0	1	06:02
84	TW1	TW	14	731562	732158	735174	735440		1	3017	3447	3877	1	10	1	0	1	06:02
51	TW1	TW	10	377543	378111	381650	381896		1	3540	3946	4352	1	10	1	0	1	06:02
17	TW1	TW	4	966497	966501	966501	966514		1	1	9	16	1	10.1	1	0	1	02:06
45	TW1	TW	9	247495	247522	247522	247526		1	1	16	30	1	10.1	1	0	1	02:06
87	TW1	TW	15	316361	316429	316429	316433		1	1	36	71	1	10.1	1	0	1	02:06
60	TW1	TW	11	364194	364367	364367	364384		1	1	95	189	1	10.1	1	0	1	02:06
94	TW1	TW	15	978995	979059	979155	979379		1	97	240	383	1	10.1	1	0	1	02:06
39	TW1	TW	8	233575	233885	234858	234994		1	974	1196	1418	1	10.1	1	0	1	02:06
6	TW1	TW	2	746171	747838	748391	748916		1	554	1649	2744	1	10.1	1	0	1	02:06
38	TW1	TW	8	136744	137997	139506	140123		1	1510	2444	3378	1	10.1	1	0	1	02:06
57	TW1	TW	11	51558	52399	53905	54957		1	1507	2453	3398	1	10.1	1	0	1	02:06
34	TW1	TW	7	800442	801373	803311	803587		1	1939	2542	3144	1	10.1	1	0	1	02:06
11	TW1	TW	4	238389	238635	241065	241166		1	2431	2604	2776	1	10.1	1	0	1	02:06
77	TW1	TW	13	673806	673846	676462	676599		1	2617	2705	2792	1	10.1	1	0	1	02:06
66	TW1	TW	12	200917	201288	204575	204907		1	3288	3639	3989	1	10.1	1	0	1	02:06
80	TW1	TW	14	74669	75232	78386	79032		1	3155	3759	4362	1	10.1	1	0	1	02:06
71	TW1	TW	12	867405	870134	872401	872807		1	2268	3835	5401	1	10.1	1	0	1	02:06
35	TW1	TW	7	973111	973354	979753	980911		1	6400	7100	7799	1	10.1	1	0	1	02:06
15	TW1	TW	4	833834	834320	837572	837654	2_nonsis		3253	3536	3819	3	30	1	0	1	6:2_4:4_2:6
89	TW1	TW	15	583999	584081	588933	589146	2_nonsis		4853	5000	5146	3	30	1	0	1	2:6_4:4_6:2
32	TW1	TW	7	558809	558946	559269	559414	2_nonsis		324	464	604	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
22	TW1	TW	4	1392696	1393214	1394881	1395687	2_nonsis		1668	2329	2990	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
69	TW1	TW	12	537242	538121	543116	543240	2_nonsis		4996	5497	5997	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
44	TW1	TW	9	185865	188629	189843	189896	2_nonsis		1215	2623	4030	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)_(2:6)_(4:4a)
25	TW1	TW	5	157999	158386	158386	158684	2_nonsis		1	343	684	1	15	1	1	0	(6:2)_(4:4aCO)
8	TW1	TW	3	136159	136789	136789	137021	2_nonsis		1	431	861	1	15	1	1	0	(6:2)_(4:4aCO)
100	TW1	TW	16	517881	518479	518518	518836	2_nonsis		40	497	954	1	15	1	1	0	(6:2)_(4:4aCO)
61	TW1	TW	11	401916	402660	402809	403011	2_nonsis		150	622	1094	1	15	1	1	0	(6:2)_(4:4aCO)
99	TW1	TW	16	371406	371706	371706	372742	2_nonsis		1	668	1335	1	15	1	1	0	(6:2)_(4:4aCO)
14	TW1	TW	4	699436	699549	700250	700440	2_nonsis		702	853	1003	1	15	1	1	0	(6:2)_(4:4aCO)
18	TW1	TW	4	1063173	1064173	1064285	1064864	2_nonsis		113	902	1690	1	15	1	1	0	(6:2)_(4:4aCO)
16	TW1	TW	4	938591	939572	940217	940688	2_nonsis		646	1371	2096	1	15	1	1	0	(6:2)_(4:4aCO)
1	TW1	TW	2	124959	125762	126565	126921	2_nonsis		804	1383	1961	1	15	1	1	0	(6:2)_(4:4aCO)
54	TW1	TW	10	629879	631130	631130	632972	2_nonsis		1	1547	3092	1	15	1	1	0	(6:2)_(4:4aCO)
90	TW1	TW	15	730821	731874	732609	733385	2_nonsis		736	1650	2563	1	15	1	1	0	(6:2)_(4:4aCO)
7	TW1	TW	3	45838	46119	47306	48335	2_nonsis		1188	1842	2496	1	15	1	1	0	(6:2)_(4:4aCO)

101	TW1	TW	16	697945	698725	700101	700285	2_nonsis		1377	1858	2339	1	15	1	1	0	(6:2)_(4:4aCO)
2	TW1	TW	2	314330	315271	316189	317232	2_nonsis		919	1910	2901	1	15	1	1	0	(6:2)_(4:4aCO)
40	TW1	TW	8	330660	331641	331868	334431	2_nonsis		228	1999	3770	1	15	1	1	0	(6:2)_(4:4aCO)
95	TW1	TW	15	1063186	1063200	1065166	1065443	2_nonsis		1967	2112	2256	1	15	1	1	0	(6:2)_(4:4aCO)
75	TW1	TW	13	470916	472484	473747	474399	2_nonsis		1264	2373	3482	1	15	1	1	0	(6:2)_(4:4aCO)
41	TW1	TW	8	515688	516015	518179	518458	2_nonsis		2165	2467	2769	1	15	1	1	0	(6:2)_(4:4aCO)
63	TW1	TW	11	624919	624949	627471	628397	2_nonsis		2523	3000	3477	1	15	1	1	0	(6:2)_(4:4aCO)
83	TW1	TW	14	659022	661270	662512	665017	2_nonsis		1243	3619	5994	1	15	1	1	0	(6:2)_(4:4aCO)
13	TW1	TW	4	590328	590885	594269	594975	2_nonsis		3385	4016	4646	1	15	1	1	0	(6:2)_(4:4aCO)
65	TW1	TW	12	105323	106427	109886	110400	2_nonsis		3460	4268	5076	1	15	1	1	0	(6:2)_(4:4aCO)
67	TW1	TW	12	233075	234128	234303	238370	2_nonsis		4176	4735	5294	1	15	1	1	0	(6:2)_(4:4aCO)
93	TW1	TW	15	843925	845688	849394	850123	2_nonsis		3707	4952	6197	1	15	1	1	0	(6:2)_(4:4aCO)
98	TW1	TW	16	171422	171708	171708	171729	2_nonsis		1	154	306	1	16	1	1	0	(2:6)_(4:4aCO)
20	TW1	TW	4	1275612	1275693	1276002	1276281	2_nonsis		310	489	668	1	16	1	1	0	(2:6)_(4:4aCO)
81	TW1	TW	14	366762	367502	367644	367843	2_nonsis		143	612	1080	1	16	1	1	0	(2:6)_(4:4aCO)
36	TW1	TW	7	1041874	1042463	1042643	1043244	2_nonsis		181	775	1369	1	16	1	1	0	(2:6)_(4:4aCO)
88	TW1	TW	15	477077	477610	477802	478649	2_nonsis		193	882	1571	1	16	1	1	0	(2:6)_(4:4aCO)
76	TW1	TW	13	645101	645268	646336	646440	2_nonsis		1069	1204	1338	1	16	1	1	0	(2:6)_(4:4aCO)
92	TW1	TW	15	831592	832096	833083	833356	2_nonsis		988	1376	1763	1	16	1	1	0	(2:6)_(4:4aCO)
48	TW1	TW	10	110584	110925	112239	112791	2_nonsis		1315	1761	2206	1	16	1	1	0	(2:6)_(4:4aCO)
26	TW1	TW	5	430620	430899	432416	432695	2_nonsis		1518	1796	2074	1	16	1	1	0	(2:6)_(4:4aCO)
91	TW1	TW	15	763262	763613	765140	765404	2_nonsis		1528	1835	2141	1	16	1	1	0	(2:6)_(4:4aCO)
3	TW1	TW	2	325371	325802	327003	327875	2_nonsis		1202	1853	2503	1	16	1	1	0	(2:6)_(4:4aCO)
23	TW1	TW	4	1416734	1416909	1418662	1418928	2_nonsis		1754	1974	2193	1	16	1	1	0	(2:6)_(4:4aCO)
29	TW1	TW	7	370897	371116	372926	373531	2_nonsis		1811	2222	2633	1	16	1	1	0	(2:6)_(4:4aCO)
86	TW1	TW	15	219136	219822	221862	221900	2_nonsis		2041	2402	2763	1	16	1	1	0	(2:6)_(4:4aCO)
30	TW1	TW	7	425497	426136	428152	428325	2_nonsis		2017	2422	2827	1	16	1	1	0	(2:6)_(4:4aCO)
28	TW1	TW	7	93397	94650	96337	96869	2_nonsis		1688	2580	3471	1	16	1	1	0	(2:6)_(4:4aCO)
68	TW1	TW	12	366239	366378	369062	369919	2_nonsis		2685	3182	3679	1	16	1	1	0	(2:6)_(4:4aCO)
24	TW1	TW	5	67809	68268	70969	71501	2_nonsis		2702	3197	3691	1	16	1	1	0	(2:6)_(4:4aCO)
50	TW1	TW	10	313986	314406	317491	317989	2_nonsis		3086	3544	4002	1	16	1	1	0	(2:6)_(4:4aCO)
85	TW1	TW	15	159369	159827	163253	163486	2_nonsis		3427	3772	4116	1	16	1	1	0	(2:6)_(4:4aCO)
82	TW1	TW	14	518162	518600	519077	525249	2_nonsis		478	3782	7086	1	16	1	1	0	(2:6)_(4:4aCO)
97	TW1	TW	16	66715	67491	70600	71375	2_nonsis		3110	3885	4659	1	16	1	1	0	(2:6)_(4:4aCO)
52	TW1	TW	10	384523	385172	388844	389073	2_nonsis		3673	4111	4549	1	16	1	1	0	(2:6)_(4:4aCO)
53	TW1	TW	10	463641	464252	467589	469453	2_nonsis		3338	4575	5811	1	16	1	1	0	(2:6)_(4:4aCO)
59	TW1	TW	11	307562	307722	307562	307722	2_nonsis		0	80	159	1	100	1	1	0	(4:4aCO)
74	TW1	TW	13	387576	387784	387576	387784	2_nonsis		0	104	207	1	100	1	1	0	(4:4aCO)
62	TW1	TW	11	572601	573116	572601	573116	2_nonsis		0	257	514	1	100	1	1	0	(4:4aCO)
55	TW1	TW	10	690126	690711	690126	690711	2_nonsis		0	292	584	1	100	1	1	0	(4:4aCO)
4	TW1	TW	2	505298	506138	505298	506138	2_nonsis		0	420	839	1	100	1	1	0	(4:4aCO)
31	TW1	TW	7	523740	524713	523740	524713	2_nonsis		0	486	972	1	100	1	1	0	(4:4aCO)
70	TW1	TW	12	836343	837497	836343	837497	2_nonsis		0	577	1153	1	100	1	1	0	(4:4aCO)
96	TW1	TW	16	49169	50572	49169	50572	2_nonsis		0	701	1402	1	100	1	1	0	(4:4aCO)
9	TW1	TW	3	228130	230267	228130	230267	2_nonsis		0	1068	2136	1	100	1	1	0	(4:4aCO)
78	TW1	TW	13	835125	837907	835125	837907	2_nonsis		0	1391	2781	1	100	1	1	0	(4:4aCO)
56	TW1	TW	11	23532	27301	23532	27301	2_nonsis		0	1884	3768	1	100	1	1	0	(4:4aCO)
47	TW1	TW	9	377556	378238	379276	379313	2_nonsis		1039	1398	1756	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
37	TW1	TW	8	45102	46055	50752	51058	2_nonsis		4698	5327	5955	3	20	1	1	0	(2:6)_(6:2)_(4:4aCO)
10	TW1	TW	4	126408	127476	129270	130517	2_sis		1795	2952	4108	0	1	2	0	2	(6:2)_(8:0)_(4:4)
12	TW1	TW	4	356226	356562	358348	358389		3	1787	1975	2162	0	2	2	1	1	(6:2)_(2:6)_(4:4aCO)
33	TW1	TW	7	737189	737501	743803	743974		3	6303	6544	6784	0	2	2	1	1	(2:6)_(4:4aCO)_(2:6a)_(4:4a)_(2:6a)_(4:4a)
72	TW1	TW	12	947218	947402	952886	953059		3	5485	5663	5840	0	2	2	1	1	(2:6)_(4:4)_(6:2)_(4:4aCO)
42	TW1	TW	9	87789	88444	89868	90521	2_nonsis		1425	2078	2731	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2)_(4:4aCO)
110	TW1	TW	2	800316	800859	801020	813184		1	0	6434	12867	0	4	1	NA	NA	
118	TW2	TW	16	694434	694716	697864	697918		1	3149	3316	3483	1	8	1	0	1	2:6_4:4_2:6
3	TW2	TW	1	198604	198630	198630	198642		1	1	19	37	1	10	1	0	1	06:02
87	TW2	TW	12	675042	675394	675407	675924		1	14	448	881	1	10	1	0	1	06:02
28	TW2	TW	4	1324886	1325344	1325346	1325849		1	3	483	962	1	10	1	0	1	06:02
73	TW2	TW	11	224634	225480	225480	225609		1	1	488	974	1	10	1	0	1	06:02

64	TW2	TW	10	255746	256123	256465	256690	1	343	643	943	1	10	1	0	1	06:02
1	TW2	TW	1	137336	138499	138650	139076	1	152	946	1739	1	10	1	0	1	06:02
10	TW2	TW	2	488899	489241	489580	490532	1	340	986	1632	1	10	1	0	1	06:02
111	TW2	TW	16	52231	52375	53348	53378	1	974	1060	1146	1	10	1	0	1	06:02
95	TW2	TW	13	713980	715257	715643	715773	1	387	1090	1792	1	10	1	0	1	06:02
83	TW2	TW	12	301472	301852	302944	303043	1	1093	1332	1570	1	10	1	0	1	06:02
37	TW2	TW	5	543192	543765	545109	545863	1	1345	2008	2670	1	10	1	0	1	06:02
78	TW2	TW	12	95236	97490	98655	99028	1	1166	2479	3791	1	10	1	0	1	06:02
114	TW2	TW	16	161120	161768	164063	164740	1	2296	2958	3619	1	10	1	0	1	06:02
121	TW2	TW	16	897661	898057	901144	901264	1	3088	3345	3602	1	10	1	0	1	06:02
82	TW2	TW	12	263151	263230	266628	266899	1	3399	3573	3747	1	10	1	0	1	06:02
74	TW2	TW	11	283495	283662	283662	283710	1	1	108	214	1	10.1	1	0	1	02:06
56	TW2	TW	8	421410	421507	421693	421840	1	187	308	429	1	10.1	1	0	1	02:06
85	TW2	TW	12	417974	418307	418481	418904	1	175	552	929	1	10.1	1	0	1	02:06
97	TW2	TW	14	78004	78115	78386	79032	1	272	650	1027	1	10.1	1	0	1	02:06
55	TW2	TW	8	334431	334860	335220	335465	1	361	697	1033	1	10.1	1	0	1	02:06
15	TW2	TW	3	38022	38178	38857	39123	1	680	890	1100	1	10.1	1	0	1	02:06
29	TW2	TW	4	1416431	1416617	1417706	1417872	1	1090	1265	1440	1	10.1	1	0	1	02:06
8	TW2	TW	2	324185	324220	325371	325802	1	1152	1384	1616	1	10.1	1	0	1	02:06
20	TW2	TW	4	105853	106143	106899	107966	1	757	1435	2112	1	10.1	1	0	1	02:06
35	TW2	TW	5	377471	377999	379092	379332	1	1094	1477	1860	1	10.1	1	0	1	02:06
48	TW2	TW	7	546929	547580	548503	549148	1	924	1571	2218	1	10.1	1	0	1	02:06
24	TW2	TW	4	698508	698668	700250	700440	1	1583	1757	1931	1	10.1	1	0	1	02:06
33	TW2	TW	5	140433	140700	142227	142565	1	1528	1830	2131	1	10.1	1	0	1	02:06
80	TW2	TW	12	233075	234128	235352	235684	1	1225	1917	2608	1	10.1	1	0	1	02:06
32	TW2	TW	5	18839	18972	18972	23192	1	1	2177	4352	1	10.1	1	0	1	02:06
59	TW2	TW	9	213470	213953	215186	216864	1	1234	2314	3393	1	10.1	1	0	1	02:06
30	TW2	TW	4	1464680	1465187	1467260	1467745	1	2074	2569	3064	1	10.1	1	0	1	02:06
13	TW2	TW	2	725754	726633	729547	730031	1	2915	3596	4276	1	10.1	1	0	1	02:06
62	TW2	TW	10	81409	81757	86001	86090	1	4245	4463	4680	1	10.1	1	0	1	02:06
54	TW2	TW	8	284440	285871	290985	291312	1	5115	5993	6871	1	10.1	1	0	1	02:06
2	TW2	TW	1	180982	181085	181957	182519	2_nonsis	873	1205	1536	3	30	1	0	1	2:6_4:4_6:2
25	TW2	TW	4	1052088	1052356	1053946	1054109	2_nonsis	1591	1806	2020	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
105	TW2	TW	15	420277	421530	423361	423370	2_nonsis	1832	2462	3092	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)
109	TW2	TW	15	942317	942594	945647	945784	2_nonsis	3054	3260	3466	1	12	1	1	0	(6:2)_(4:4aCO)_(6:2)_(4:4a)_(6:2)_(4:4a)
38	TW2	TW	6	95632	95746	95746	95849	2_nonsis	1	109	216	1	15	1	1	0	(6:2)_(4:4aCO)
86	TW2	TW	12	543240	543480	543544	543808	2_nonsis	65	316	567	1	15	1	1	0	(6:2)_(4:4aCO)
94	TW2	TW	13	496739	496955	496955	497568	2_nonsis	1	415	828	1	15	1	1	0	(6:2)_(4:4aCO)
22	TW2	TW	4	322680	323098	323200	323612	2_nonsis	103	517	931	1	15	1	1	0	(6:2)_(4:4aCO)
116	TW2	TW	16	466976	467922	467922	468494	2_nonsis	1	759	1517	1	15	1	1	0	(6:2)_(4:4aCO)
98	TW2	TW	14	239023	239950	240152	240414	2_nonsis	203	797	1390	1	15	1	1	0	(6:2)_(4:4aCO)
21	TW2	TW	4	302250	303051	303504	303806	2_nonsis	454	1005	1555	1	15	1	1	0	(6:2)_(4:4aCO)
75	TW2	TW	11	360940	361043	362017	362101	2_nonsis	975	1068	1160	1	15	1	1	0	(6:2)_(4:4aCO)
76	TW2	TW	11	499168	499999	500449	501047	2_nonsis	451	1165	1878	1	15	1	1	0	(6:2)_(4:4aCO)
17	TW2	TW	3	76009	76939	77505	77826	2_nonsis	567	1192	1816	1	15	1	1	0	(6:2)_(4:4aCO)
47	TW2	TW	7	457721	457920	459157	459245	2_nonsis	1238	1381	1523	1	15	1	1	0	(6:2)_(4:4aCO)
53	TW2	TW	8	271207	272321	273222	273580	2_nonsis	902	1637	2372	1	15	1	1	0	(6:2)_(4:4aCO)
117	TW2	TW	16	501709	502052	503314	503873	2_nonsis	1263	1713	2163	1	15	1	1	0	(6:2)_(4:4aCO)
45	TW2	TW	7	305233	305542	307066	307148	2_nonsis	1525	1720	1914	1	15	1	1	0	(6:2)_(4:4aCO)
96	TW2	TW	13	859174	859920	861205	861520	2_nonsis	1286	1816	2345	1	15	1	1	0	(6:2)_(4:4aCO)
34	TW2	TW	5	201006	201879	203277	203706	2_nonsis	1399	2049	2699	1	15	1	1	0	(6:2)_(4:4aCO)
39	TW2	TW	6	112435	112767	114707	114918	2_nonsis	1941	2212	2482	1	15	1	1	0	(6:2)_(4:4aCO)
44	TW2	TW	7	209279	209637	211975	212009	2_nonsis	2339	2534	2729	1	15	1	1	0	(6:2)_(4:4aCO)
71	TW2	TW	11	60173	62759	62759	65282	2_nonsis	1	2555	5108	1	15	1	1	0	(6:2)_(4:4aCO)
6	TW2	TW	2	194226	195735	196964	198241	2_nonsis	1230	2622	4014	1	15	1	1	0	(6:2)_(4:4aCO)
61	TW2	TW	9	336673	337083	339305	340356	2_nonsis	2223	2953	3682	1	15	1	1	0	(6:2)_(4:4aCO)
42	TW2	TW	7	85628	86297	88718	89311	2_nonsis	2422	3052	3682	1	15	1	1	0	(6:2)_(4:4aCO)
77	TW2	TW	11	629129	629639	633026	633545	2_nonsis	3388	3902	4415	1	15	1	1	0	(6:2)_(4:4aCO)
52	TW2	TW	8	155587	156307	159962	160782	2_nonsis	3656	4425	5194	1	15	1	1	0	(6:2)_(4:4aCO)
5	TW2	TW	2	121643	121908	126263	126565	2_nonsis	4356	4639	4921	1	15	1	1	0	(6:2)_(4:4aCO)

27	TW2	TW	4	1198548	1199289	1202939	1205010	2_nonsis		3651	5056	6461	1	15	1	1	0 (6:2)_(4:4aCO)
68	TW2	TW	10	543880	543944	543944	544103	2_nonsis		1	112	222	1	16	1	1	0 (2:6)_(4:4aCO)
81	TW2	TW	12	256727	257091	257091	257195	2_nonsis		1	234	467	1	16	1	1	0 (2:6)_(4:4aCO)
90	TW2	TW	12	1000048	1000203	1000203	1000542	2_nonsis		1	247	493	1	16	1	1	0 (2:6)_(4:4aCO)
12	TW2	TW	2	702673	703042	703042	703256	2_nonsis		1	292	582	1	16	1	1	0 (2:6)_(4:4aCO)
26	TW2	TW	4	1091826	1092239	1092239	1092561	2_nonsis		1	368	734	1	16	1	1	0 (2:6)_(4:4aCO)
99	TW2	TW	14	273490	273762	273928	274328	2_nonsis		167	502	837	1	16	1	1	0 (2:6)_(4:4aCO)
9	TW2	TW	2	481949	482720	482720	482984	2_nonsis		1	518	1034	1	16	1	1	0 (2:6)_(4:4aCO)
65	TW2	TW	10	280699	281003	281289	281583	2_nonsis		287	585	883	1	16	1	1	0 (2:6)_(4:4aCO)
115	TW2	TW	16	319694	320279	320399	320885	2_nonsis		121	656	1190	1	16	1	1	0 (2:6)_(4:4aCO)
108	TW2	TW	15	772232	773455	773455	773833	2_nonsis		1	801	1600	1	16	1	1	0 (2:6)_(4:4aCO)
101	TW2	TW	14	542443	543829	543829	544303	2_nonsis		1	930	1859	1	16	1	1	0 (2:6)_(4:4aCO)
50	TW2	TW	7	896389	896765	897531	897580	2_nonsis		767	979	1190	1	16	1	1	0 (2:6)_(4:4aCO)
84	TW2	TW	12	341070	341507	342190	342448	2_nonsis		684	1031	1377	1	16	1	1	0 (2:6)_(4:4aCO)
7	TW2	TW	2	290619	291653	292290	292401	2_nonsis		638	1210	1781	1	16	1	1	0 (2:6)_(4:4aCO)
43	TW2	TW	7	93397	95130	95130	96070	2_nonsis		1	1337	2672	1	16	1	1	0 (2:6)_(4:4aCO)
70	TW2	TW	10	662479	663134	664330	664516	2_nonsis		1197	1617	2036	1	16	1	1	0 (2:6)_(4:4aCO)
31	TW2	TW	5	14955	15170	16323	17065	2_nonsis		1154	1632	2109	1	16	1	1	0 (2:6)_(4:4aCO)
14	TW2	TW	2	772685	773889	774954	775070	2_nonsis		1066	1725	2384	1	16	1	1	0 (2:6)_(4:4aCO)
11	TW2	TW	2	586331	587309	588509	588671	2_nonsis		1201	1770	2339	1	16	1	1	0 (2:6)_(4:4aCO)
69	TW2	TW	10	545233	546078	547200	547730	2_nonsis		1123	1810	2496	1	16	1	1	0 (2:6)_(4:4aCO)
36	TW2	TW	5	522010	522421	523683	524394	2_nonsis		1263	1823	2383	1	16	1	1	0 (2:6)_(4:4aCO)
18	TW2	TW	3	228130	230267	230267	231791	2_nonsis		1	1831	3660	1	16	1	1	0 (2:6)_(4:4aCO)
41	TW2	TW	6	223659	224098	225457	226036	2_nonsis		1360	1868	2376	1	16	1	1	0 (2:6)_(4:4aCO)
102	TW2	TW	14	662512	665017	665502	665847	2_nonsis		486	1910	3334	1	16	1	1	0 (2:6)_(4:4aCO)
119	TW2	TW	16	832925	833262	834906	835242	2_nonsis		1645	1981	2316	1	16	1	1	0 (2:6)_(4:4aCO)
106	TW2	TW	15	556316	558487	559477	559768	2_nonsis		991	2221	3451	1	16	1	1	0 (2:6)_(4:4aCO)
104	TW2	TW	15	266279	266696	268456	269276	2_nonsis		1761	2379	2996	1	16	1	1	0 (2:6)_(4:4aCO)
23	TW2	TW	4	615641	615694	618471	618665	2_nonsis		2778	2901	3023	1	16	1	1	0 (2:6)_(4:4aCO)
110	TW2	TW	15	987247	987667	989690	991111	2_nonsis		2024	2944	3863	1	16	1	1	0 (2:6)_(4:4aCO)
63	TW2	TW	10	153254	154954	157189	157299	2_nonsis		2236	3140	4044	1	16	1	1	0 (2:6)_(4:4aCO)
120	TW2	TW	16	886776	886812	890080	890467	2_nonsis		3269	3480	3690	1	16	1	1	0 (2:6)_(4:4aCO)
46	TW2	TW	7	312031	312110	315611	315872	2_nonsis		3502	3671	3840	1	16	1	1	0 (2:6)_(4:4aCO)
103	TW2	TW	14	688572	689029	692612	692960	2_nonsis		3584	3986	4387	1	16	1	1	0 (2:6)_(4:4aCO)
92	TW2	TW	13	191452	191569	195572	195860	2_nonsis		4004	4206	4407	1	16	1	1	0 (2:6)_(4:4aCO)
79	TW2	TW	12	190522	190951	195645	196197	2_nonsis		4695	5185	5674	1	16	1	1	0 (2:6)_(4:4aCO)
40	TW2	TW	6	222196	222477	222196	222477	2_nonsis		0	140	280	1	100	1	1	0 (4:4aCO)
91	TW2	TW	13	95529	95911	95529	95911	2_nonsis		0	191	381	1	100	1	1	0 (4:4aCO)
72	TW2	TW	11	79874	80353	79874	80353	2_nonsis		0	239	478	1	100	1	1	0 (4:4aCO)
113	TW2	TW	16	153125	153659	153125	153659	2_nonsis		0	267	533	1	100	1	1	0 (4:4aCO)
51	TW2	TW	8	69180	69741	69180	69741	2_nonsis		0	280	560	1	100	1	1	0 (4:4aCO)
93	TW2	TW	13	479746	480327	479746	480327	2_nonsis		0	290	580	1	100	1	1	0 (4:4aCO)
100	TW2	TW	14	370839	371516	370839	371516	2_nonsis		0	338	676	1	100	1	1	0 (4:4aCO)
49	TW2	TW	7	825852	826536	825852	826536	2_nonsis		0	342	683	1	100	1	1	0 (4:4aCO)
4	TW2	TW	2	44210	44904	44210	44904	2_nonsis		0	347	693	1	100	1	1	0 (4:4aCO)
88	TW2	TW	12	729962	730685	729962	730685	2_nonsis		0	361	722	1	100	1	1	0 (4:4aCO)
112	TW2	TW	16	120748	121553	120748	121553	2_nonsis		0	402	804	1	100	1	1	0 (4:4aCO)
60	TW2	TW	9	237829	238849	237829	238849	2_nonsis		0	510	1019	1	100	1	1	0 (4:4aCO)
16	TW2	TW	3	47306	48335	47306	48335	2_nonsis		0	514	1028	1	100	1	1	0 (4:4aCO)
67	TW2	TW	10	524618	526176	524618	526176	2_nonsis		0	779	1557	1	100	1	1	0 (4:4aCO)
89	TW2	TW	12	837962	840577	837962	840577	2_nonsis		0	1307	2614	1	100	1	1	0 (4:4aCO)
66	TW2	TW	10	344939	345047	346529	346858	2_nonsis		1483	1701	1918	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
19	TW2	TW	4	60151	61039	62366	62726		3	1328	1951	2574	0	2	2	1	1 (6:2)_(6:2a)_(2:6)_(4:4aCO)
58	TW2	TW	9	87789	88444	89500	89756		3	1057	1512	1966	0	2	2	1	1 (6:2)_(4:4aCO)
107	TW2	TW	15	722071	722470	727650	727823		3	5181	5466	5751	0	2	2	1	1 (2:6)_(6:2)_(4:4aCO)
57	TW2	TW	8	511414	511546	514601	515162	2_nonsis	3056	3402	3747	0	3	2	0	2 (2:6)_(4:4)_(2:6)_(4:4aCO)_(4:CO)
30	TW3	TW	6	232697	233456	234160	234589		1	705	1298	1891	1	7	1	0	1 6:2_4:4_6:2
2	TW3	TW	1	113326	114283	116327	117399		1	2045	3059	4072	1	8	1	0	1 2:6_4:4_2:6
51	TW3	TW	10	236615	236674	236674	236901		1	1	143	285	1	10	1	0	1 06:02
85	TW3	TW	13	346842	346988	346988	347381		1	1	270	538	1	10	1	0	1 06:02

71	TW3	TW	12	246315	246534	246804	246946	1	271	451	630	1	10	1	0	1	06:02
32	TW3	TW	7	121932	122011	122622	123330	1	612	1005	1397	1	10	1	0	1	06:02
106	TW3	TW	16	130597	130644	131754	131951	1	1111	1232	1353	1	10	1	0	1	06:02
31	TW3	TW	7	22405	23215	23642	24468	1	428	1245	2062	1	10	1	0	1	06:02
99	TW3	TW	15	55233	55283	56472	56753	1	1190	1355	1519	1	10	1	0	1	06:02
58	TW3	TW	10	631130	632972	633743	634423	1	772	2032	3292	1	10	1	0	1	06:02
94	TW3	TW	14	252203	254039	255192	255432	1	1154	2191	3228	1	10	1	0	1	06:02
60	TW3	TW	11	223790	224066	226092	226549	1	2027	2393	2758	1	10	1	0	1	06:02
64	TW3	TW	11	588930	589078	590994	592478	1	1917	2732	3547	1	10	1	0	1	06:02
96	TW3	TW	14	518162	518600	519077	525141	1	478	3728	6978	1	10	1	0	1	06:02
28	TW3	TW	6	182500	182752	186589	186739	1	3838	4038	4238	1	10	1	0	1	06:02
53	TW3	TW	10	358569	358755	363087	363678	1	4333	4721	5108	1	10	1	0	1	06:02
88	TW3	TW	13	388681	388700	388700	388702	1	1	11	20	1	10.1	1	0	1	02:06
47	TW3	TW	9	350021	350025	350025	350044	1	1	12	22	1	10.1	1	0	1	02:06
45	TW3	TW	9	247495	247522	247522	247526	1	1	16	30	1	10.1	1	0	1	02:06
98	TW3	TW	14	763402	763447	763447	763497	1	1	48	94	1	10.1	1	0	1	02:06
49	TW3	TW	10	30793	30891	30927	31175	1	37	209	381	1	10.1	1	0	1	02:06
67	TW3	TW	12	29131	29612	29781	30008	1	170	523	876	1	10.1	1	0	1	02:06
39	TW3	TW	8	142863	143543	143727	143824	1	185	573	960	1	10.1	1	0	1	02:06
50	TW3	TW	10	80439	80673	81028	81358	1	356	637	918	1	10.1	1	0	1	02:06
93	TW3	TW	14	160630	161277	161474	161874	1	198	721	1243	1	10.1	1	0	1	02:06
12	TW3	TW	4	225248	226059	226209	227127	1	151	1015	1878	1	10.1	1	0	1	02:06
11	TW3	TW	4	104069	104854	105348	105623	1	495	1024	1553	1	10.1	1	0	1	02:06
55	TW3	TW	10	462170	462595	463641	464252	1	1047	1564	2081	1	10.1	1	0	1	02:06
80	TW3	TW	12	1027717	1028133	1028782	1030239	1	650	1586	2521	1	10.1	1	0	1	02:06
95	TW3	TW	14	300452	300720	303090	303243	1	2371	2581	2790	1	10.1	1	0	1	02:06
26	TW3	TW	5	525075	525798	527534	528932	1	1737	2797	3856	1	10.1	1	0	1	02:06
107	TW3	TW	16	255970	256183	257972	258230	2_nonsis	1790	2025	2259	3	30	1	0	1	6:2_4:4_6:2_2:6
42	TW3	TW	9	52260	53016	53103	53238	2_nonsis	88	533	977	1	12	1	1	0	(4:4aCO)_(2:6)_(4:4a)
87	TW3	TW	13	353814	354080	356625	356924	2_nonsis	2546	2828	3109	1	12	1	1	0	(2:6)_(4:4)_(2:6)_(4:4aCO)
1	TW3	TW	1	45030	45198	50024	50204	2_nonsis	4827	5000	5173	1	12	1	1	0	(2:6)_(4:4aCO)_(2:6)_(4:4a)
43	TW3	TW	9	58961	59552	59639	60280	2_nonsis	88	703	1318	1	15	1	1	0	(6:2)_(4:4aCO)
74	TW3	TW	12	559898	560519	560519	561781	2_nonsis	1	942	1882	1	15	1	1	0	(6:2)_(4:4aCO)
100	TW3	TW	15	212020	212816	213233	213488	2_nonsis	418	943	1467	1	15	1	1	0	(6:2)_(4:4aCO)
91	TW3	TW	13	858111	859063	859174	859920	2_nonsis	112	960	1808	1	15	1	1	0	(6:2)_(4:4aCO)
7	TW3	TW	2	569235	569496	570301	570754	2_nonsis	806	1162	1518	1	15	1	1	0	(6:2)_(4:4aCO)
24	TW3	TW	5	342057	342537	344171	344307	2_nonsis	1635	1942	2249	1	15	1	1	0	(6:2)_(4:4aCO)
92	TW3	TW	14	79032	79050	80433	81575	2_nonsis	1384	1963	2542	1	15	1	1	0	(6:2)_(4:4aCO)
44	TW3	TW	9	239431	239659	240939	242535	2_nonsis	1281	2192	3103	1	15	1	1	0	(6:2)_(4:4aCO)
34	TW3	TW	7	178509	179910	181138	181935	2_nonsis	1229	2327	3425	1	15	1	1	0	(6:2)_(4:4aCO)
59	TW3	TW	10	689090	689249	691434	691648	2_nonsis	2186	2372	2557	1	15	1	1	0	(6:2)_(4:4aCO)
5	TW3	TW	2	152894	153007	155354	155739	2_nonsis	2348	2596	2844	1	15	1	1	0	(6:2)_(4:4aCO)
37	TW3	TW	7	967106	967359	969826	969927	2_nonsis	2468	2644	2820	1	15	1	1	0	(6:2)_(4:4aCO)
6	TW3	TW	2	345288	346363	348664	348793	2_nonsis	2302	2903	3504	1	15	1	1	0	(6:2)_(4:4aCO)
22	TW3	TW	5	255503	255702	258489	258531	2_nonsis	2788	2908	3027	1	15	1	1	0	(6:2)_(4:4aCO)
72	TW3	TW	12	279533	280412	282626	283463	2_nonsis	2215	3072	3929	1	15	1	1	0	(6:2)_(4:4aCO)
46	TW3	TW	9	329125	332459	333581	334640	2_nonsis	1123	3319	5514	1	15	1	1	0	(6:2)_(4:4aCO)
68	TW3	TW	12	141390	141933	145067	145416	2_nonsis	3135	3580	4025	1	15	1	1	0	(6:2)_(4:4aCO)
70	TW3	TW	12	227490	227856	231430	231524	2_nonsis	3575	3804	4033	1	15	1	1	0	(6:2)_(4:4aCO)
10	TW3	TW	4	91959	93521	96538	96663	2_nonsis	3018	3861	4703	1	15	1	1	0	(6:2)_(4:4aCO)
65	TW3	TW	11	636244	637026	639711	641421	2_nonsis	2686	3931	5176	1	15	1	1	0	(6:2)_(4:4aCO)
108	TW3	TW	16	424230	424365	428065	428562	2_nonsis	3701	4016	4331	1	15	1	1	0	(6:2)_(4:4aCO)
27	TW3	TW	6	52838	53398	56854	58110	2_nonsis	3457	4364	5271	1	15	1	1	0	(6:2)_(4:4aCO)
4	TW3	TW	2	67361	68817	72420	73226	2_nonsis	3604	4734	5864	1	15	1	1	0	(6:2)_(4:4aCO)
66	TW3	TW	12	22201	22416	22509	22811	2_nonsis	94	352	609	1	16	1	1	0	(2:6)_(4:4aCO)
109	TW3	TW	16	865226	865451	865498	865918	2_nonsis	48	370	691	1	16	1	1	0	(2:6)_(4:4aCO)
48	TW3	TW	9	367929	368031	368217	368576	2_nonsis	187	417	646	1	16	1	1	0	(2:6)_(4:4aCO)
21	TW3	TW	5	70022	70335	70531	70852	2_nonsis	197	513	829	1	16	1	1	0	(2:6)_(4:4aCO)
61	TW3	TW	11	307266	307466	307855	307923	2_nonsis	390	523	656	1	16	1	1	0	(2:6)_(4:4aCO)
20	TW3	TW	5	43260	43494	43959	44019	2_nonsis	466	612	758	1	16	1	1	0	(2:6)_(4:4aCO)

#	Grp	TW	a	start1	start2	start3	end	type	b	v1	v2	v3	c	d	e	f	label
38	TW3	TW	7	1016640	1016792	1017034	1017661	2_nonsis		243	632	1020	1	16	1	1	0 (2:6)_(4:4aCO)
25	TW3	TW	5	409531	410181	410473	410947	2_nonsis		293	854	1415	1	16	1	1	0 (2:6)_(4:4aCO)
41	TW3	TW	8	487644	488458	488588	489445	2_nonsis		131	966	1800	1	16	1	1	0 (2:6)_(4:4aCO)
62	TW3	TW	11	451133	452823	452823	453079	2_nonsis		1	973	1945	1	16	1	1	0 (2:6)_(4:4aCO)
110	TW3	TW	16	866682	867792	867792	868671	2_nonsis		1	995	1988	1	16	1	1	0 (2:6)_(4:4aCO)
56	TW3	TW	10	495458	496029	496029	497589	2_nonsis		1	1066	2130	1	16	1	1	0 (2:6)_(4:4aCO)
76	TW3	TW	12	754651	754945	755890	755941	2_nonsis		946	1118	1289	1	16	1	1	0 (2:6)_(4:4aCO)
75	TW3	TW	12	656891	657792	658599	659350	2_nonsis		808	1633	2458	1	16	1	1	0 (2:6)_(4:4aCO)
29	TW3	TW	6	225130	225313	226825	226919	2_nonsis		1513	1651	1788	1	16	1	1	0 (2:6)_(4:4aCO)
69	TW3	TW	12	198146	198396	199541	200350	2_nonsis		1146	1675	2203	1	16	1	1	0 (2:6)_(4:4aCO)
79	TW3	TW	12	875259	876120	877476	877606	2_nonsis		1357	1852	2346	1	16	1	1	0 (2:6)_(4:4aCO)
104	TW3	TW	15	1038535	1038675	1040775	1041126	2_nonsis		2101	2346	2590	1	16	1	1	0 (2:6)_(4:4aCO)
84	TW3	TW	13	119630	120376	122362	122498	2_nonsis		1987	2427	2867	1	16	1	1	0 (2:6)_(4:4aCO)
18	TW3	TW	4	1249116	1249974	1252379	1252668	2_nonsis		2406	2979	3551	1	16	1	1	0 (2:6)_(4:4aCO)
83	TW3	TW	13	80821	80887	83964	84058	2_nonsis		3078	3157	3236	1	16	1	1	0 (2:6)_(4:4aCO)
102	TW3	TW	15	585323	585644	588536	588756	2_nonsis		2893	3163	3432	1	16	1	1	0 (2:6)_(4:4aCO)
54	TW3	TW	10	389929	389963	392871	393423	2_nonsis		2909	3201	3493	1	16	1	1	0 (2:6)_(4:4aCO)
52	TW3	TW	10	347951	348292	351479	351611	2_nonsis		3188	3424	3659	1	16	1	1	0 (2:6)_(4:4aCO)
89	TW3	TW	13	699056	699584	702605	703253	2_nonsis		3022	3609	4196	1	16	1	1	0 (2:6)_(4:4aCO)
77	TW3	TW	12	823256	826618	828844	829264	2_nonsis		2227	4117	6007	1	16	1	1	0 (2:6)_(4:4aCO)
3	TW3	TW	1	187427	189821	192723	193131	2_nonsis		2903	4303	5703	1	16	1	1	0 (2:6)_(4:4aCO)
35	TW3	TW	7	394219	394474	399537	399782	2_nonsis		5064	5313	5562	1	16	1	1	0 (2:6)_(4:4aCO)
23	TW3	TW	5	333688	334031	340292	340779	2_nonsis		6262	6676	7090	1	16	1	1	0 (2:6)_(4:4aCO)
78	TW3	TW	12	872180	872401	872180	872401	2_nonsis		0	110	220	1	100	1	1	0 (4:4aCO)
14	TW3	TW	4	598729	599029	598729	599029	2_nonsis		0	150	299	1	100	1	1	0 (4:4aCO)
103	TW3	TW	15	881577	882091	881577	882091	2_nonsis		0	257	513	1	100	1	1	0 (4:4aCO)
105	TW3	TW	16	41399	42125	41399	42125	2_nonsis		0	363	725	1	100	1	1	0 (4:4aCO)
90	TW3	TW	13	843360	844197	843360	844197	2_nonsis		0	418	836	1	100	1	1	0 (4:4aCO)
81	TW3	TW	12	1031842	1032807	1031842	1032807	2_nonsis		0	482	964	1	100	1	1	0 (4:4aCO)
13	TW3	TW	4	286258	287699	286258	287699	2_nonsis		0	720	1440	1	100	1	1	0 (4:4aCO)
33	TW3	TW	7	165523	167076	165523	167076	2_nonsis		0	776	1552	1	100	1	1	0 (4:4aCO)
86	TW3	TW	13	347796	349796	347796	349796	2_nonsis		0	1000	1999	1	100	1	1	0 (4:4aCO)
57	TW3	TW	10	568805	570822	568805	570822	2_nonsis		0	1008	2016	1	100	1	1	0 (4:4aCO)
15	TW3	TW	4	703905	706032	703905	706032	2_nonsis		0	1063	2126	1	100	1	1	0 (4:4aCO)
82	TW3	TW	13	31858	35547	31858	35547	2_nonsis		0	1844	3688	1	100	1	1	0 (4:4aCO)
8	TW3	TW	3	171207	174943	171207	174943	2_nonsis		0	1868	3735	1	100	1	1	0 (4:4aCO)
73	TW3	TW	12	285823	285976	288686	288976	2_nonsis		2711	2932	3152	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
9	TW3	TW	3	226498	228130	232833	233654	2_nonsis		4704	5930	7155	3	20	1	1	0 (2:6)_(6:2)_(4:4aCO)
101	TW3	TW	15	485588	485898	486511	487028	2_nonsis		614	1027	1439	3	20	1	1	0 (2:6)_(4:4aCO)_(6:2)_(4:4a)
63	TW3	TW	11	522153	522458	525645	526035	2_nonsis		3188	3535	3881	3	20	1	1	0 (2:6)_(4:4)_(2:6)_(6:2)_(4:4aCO)
16	TW3	TW	4	830066	830234	837275	837527		3	7042	7251	7460	0	2	2	1	1 (6:2)_(2:6)_(4:4aCO)
19	TW3	TW	4	1493732	1493869	1497031	1497133		3	3163	3282	3400	0	2	2	1	1 (2:6)_(4:4aCO)_(6:2)_(4:4a)
36	TW3	TW	7	956057	956978	962886	963014		3	5909	6433	6956	0	2	2	1	1 (6:2)_(4:4aCO)_(6:2)_(4:4a)_(8:0)_(6:2a)_(4:4a)
97	TW3	TW	14	604879	605032	606438	606872		3	1407	1700	1992	0	2	2	1	1 (2:6)_(4:4)_(6:2)_(4:4aCO)
17	TW3	TW	4	1108696	1109358	1113224	1113566	2_nonsis		3867	4368	4869	0	3	2	0	2 (6:2)_(4:4aCO)_(6:2)_(4:4CO)
40	TW3	TW	8	341249	341299	343561	344320	2_nonsis		2263	2667	3070	0	3	2	0	2 (2:6)_(4:4aCO)_(2:6)_(4:4CO)
62	TW4	TW	11	135691	136103	136103	136140		1	1	225	448	1	10	1	0	1 06:02
87	TW4	TW	14	646799	646869	647100	647124		1	232	278	324	1	10	1	0	1 06:02
66	TW4	TW	11	530289	530499	530688	531524		1	190	712	1234	1	10	1	0	1 06:02
27	TW4	TW	4	1453499	1453865	1455029	1455133		1	1165	1399	1633	1	10	1	0	1 06:02
79	TW4	TW	13	673147	673402	674283	675083		1	882	1409	1935	1	10	1	0	1 06:02
99	TW4	TW	16	339516	339687	341332	341647		1	1646	1888	2130	1	10	1	0	1 06:02
74	TW4	TW	13	40511	41051	42127	43336		1	1077	1951	2824	1	10	1	0	1 06:02
92	TW4	TW	15	587565	588022	590260	590710		1	2239	2692	3144	1	10	1	0	1 06:02
12	TW4	TW	2	765669	765957	768073	769699		1	2117	3073	4029	1	10	1	0	1 06:02
10	TW4	TW	2	660972	661314	662444	666708		1	1131	3433	5735	1	10	1	0	1 06:02
64	TW4	TW	11	467333	467504	471237	471301		1	3734	3851	3967	1	10	1	0	1 06:02
81	TW4	TW	13	719868	720435	723996	724346		1	3562	4020	4477	1	10	1	0	1 06:02
65	TW4	TW	11	519020	519160	523718	524191		1	4559	4865	5170	1	10	1	0	1 06:02
15	TW4	TW	3	224038	224261	228130	230267		1	3870	5049	6228	1	10	1	0	1 06:02

77	TW4	TW	13	331787	332507	337176	337732	1	4670	5307	5944	1	10	1	0	1 06:02
38	TW4	TW	7	900087	900140	900146	900198	1	7	59	110	1	10.1	1	0	1 02:06
40	TW4	TW	8	11695	12627	12627	12640	1	1	473	944	1	10.1	1	0	1 02:06
44	TW4	TW	8	340523	340650	341299	341482	1	650	804	958	1	10.1	1	0	1 02:06
102	TW4	TW	16	667536	667966	668032	669691	1	67	1111	2154	1	10.1	1	0	1 02:06
100	TW4	TW	16	481072	481542	482429	482737	1	888	1276	1664	1	10.1	1	0	1 02:06
93	TW4	TW	15	601325	601569	602638	603166	1	1070	1455	1840	1	10.1	1	0	1 02:06
82	TW4	TW	13	830235	830562	831576	832164	1	1015	1472	1928	1	10.1	1	0	1 02:06
49	TW4	TW	9	258908	259266	260488	260891	1	1223	1603	1982	1	10.1	1	0	1 02:06
4	TW4	TW	2	81136	81655	82573	83659	1	919	1721	2522	1	10.1	1	0	1 02:06
26	TW4	TW	4	1393304	1393417	1394881	1395687	1	1465	1924	2382	1	10.1	1	0	1 02:06
56	TW4	TW	10	517919	518880	519660	521093	1	781	1977	3173	1	10.1	1	0	1 02:06
101	TW4	TW	16	490554	490756	492354	493222	1	1599	2133	2667	1	10.1	1	0	1 02:06
96	TW4	TW	15	930310	930799	932673	933245	1	1875	2405	2934	1	10.1	1	0	1 02:06
19	TW4	TW	4	196851	198376	201393	201643	1	3018	3905	4791	1	10.1	1	0	1 02:06
86	TW4	TW	14	550773	551646	554217	557562	1	2572	4680	6788	1	10.1	1	0	1 02:06
67	TW4	TW	12	22811	22902	23475	23826	2_nonsis	574	794	1014	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
6	TW4	TW	2	116168	116257	117972	118304	2_nonsis	1716	1926	2135	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
76	TW4	TW	13	191318	191452	193159	194053	2_nonsis	1708	2221	2734	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4aCO)
37	TW4	TW	7	846529	846601	848688	849134	2_nonsis	2088	2346	2604	1	12	1	1	0 (2:6)_(4:4aCO)_(2:6)_(4:4a)
22	TW4	TW	4	698788	699229	702278	702480	2_nonsis	3050	3371	3691	1	12	1	1	0 (6:2)_(4:4aCO)_(6:2)_(4:4a)
23	TW4	TW	4	923102	923384	925318	925618	2_nonsis	1935	2225	2515	1	12	1	1	0 (6:2)_(4:4)_(6:2)_(4:4)_(4:4aCO)
52	TW4	TW	9	384418	384680	384922	385024	2_nonsis	243	424	605	1	15	1	1	0 (6:2)_(4:4aCO)
61	TW4	TW	11	96250	96552	96630	97113	2_nonsis	79	471	862	1	15	1	1	0 (6:2)_(4:4aCO)
70	TW4	TW	12	341974	342190	342533	342709	2_nonsis	344	539	734	1	15	1	1	0 (6:2)_(4:4aCO)
98	TW4	TW	16	280470	280994	280994	281659	2_nonsis	1	595	1188	1	15	1	1	0 (6:2)_(4:4aCO)
55	TW4	TW	10	361221	361485	361643	362386	2_nonsis	159	662	1164	1	15	1	1	0 (6:2)_(4:4aCO)
90	TW4	TW	15	240094	240194	240538	241147	2_nonsis	345	699	1052	1	15	1	1	0 (6:2)_(4:4aCO)
13	TW4	TW	3	40637	40987	41571	41852	2_nonsis	585	900	1214	1	15	1	1	0 (6:2)_(4:4aCO)
9	TW4	TW	2	487781	488751	489241	489580	2_nonsis	491	1145	1798	1	15	1	1	0 (6:2)_(4:4aCO)
103	TW4	TW	16	774844	774964	775873	776566	2_nonsis	910	1316	1721	1	15	1	1	0 (6:2)_(4:4aCO)
43	TW4	TW	8	187989	188673	189521	190024	2_nonsis	849	1442	2034	1	15	1	1	0 (6:2)_(4:4aCO)
58	TW4	TW	10	633425	633463	634739	635210	2_nonsis	1277	1531	1784	1	15	1	1	0 (6:2)_(4:4aCO)
51	TW4	TW	9	343174	343775	344902	345129	2_nonsis	1128	1541	1954	1	15	1	1	0 (6:2)_(4:4aCO)
28	TW4	TW	5	34247	34324	34985	36820	2_nonsis	662	1617	2572	1	15	1	1	0 (6:2)_(4:4aCO)
5	TW4	TW	2	106396	107123	108822	108951	2_nonsis	1700	2127	2554	1	15	1	1	0 (6:2)_(4:4aCO)
8	TW4	TW	2	451502	451813	453704	454122	2_nonsis	1892	2256	2619	1	15	1	1	0 (6:2)_(4:4aCO)
59	TW4	TW	10	695217	695391	697654	697926	2_nonsis	2264	2486	2708	1	15	1	1	0 (6:2)_(4:4aCO)
57	TW4	TW	10	543075	543177	545233	546078	2_nonsis	2057	2530	3002	1	15	1	1	0 (6:2)_(4:4aCO)
72	TW4	TW	12	731012	732527	732527	736073	2_nonsis	1	2531	5060	1	15	1	1	0 (6:2)_(4:4aCO)
97	TW4	TW	16	131951	132681	134518	135194	2_nonsis	1838	2540	3242	1	15	1	1	0 (6:2)_(4:4aCO)
41	TW4	TW	8	53097	53214	55477	56225	2_nonsis	2264	2696	3127	1	15	1	1	0 (6:2)_(4:4aCO)
48	TW4	TW	9	240939	242535	244304	244618	2_nonsis	1770	2724	3678	1	15	1	1	0 (6:2)_(4:4aCO)
78	TW4	TW	13	539282	539498	542119	542201	2_nonsis	2622	2770	2918	1	15	1	1	0 (6:2)_(4:4aCO)
33	TW4	TW	7	390274	390472	393326	393647	2_nonsis	2855	3114	3372	1	15	1	1	0 (6:2)_(4:4aCO)
45	TW4	TW	8	373101	373555	376829	377068	2_nonsis	3275	3621	3966	1	15	1	1	0 (6:2)_(4:4aCO)
83	TW4	TW	14	20018	20559	23618	24221	2_nonsis	3060	3631	4202	1	15	1	1	0 (6:2)_(4:4aCO)
63	TW4	TW	11	305056	306214	309310	309621	2_nonsis	3097	3831	4564	1	15	1	1	0 (6:2)_(4:4aCO)
31	TW4	TW	6	167037	167318	167410	168102	2_nonsis	93	579	1064	1	16	1	1	0 (2:6)_(4:4aCO)
21	TW4	TW	4	680128	680244	680813	681125	2_nonsis	570	783	996	1	16	1	1	0 (2:6)_(4:4aCO)
36	TW4	TW	7	659437	659791	660464	660488	2_nonsis	674	862	1050	1	16	1	1	0 (2:6)_(4:4aCO)
46	TW4	TW	9	46189	46556	47054	47493	2_nonsis	499	901	1303	1	16	1	1	0 (2:6)_(4:4aCO)
30	TW4	TW	6	129391	130480	130480	131200	2_nonsis	1	905	1808	1	16	1	1	0 (2:6)_(4:4aCO)
80	TW4	TW	13	709549	709740	710402	710752	2_nonsis	663	933	1202	1	16	1	1	0 (2:6)_(4:4aCO)
35	TW4	TW	7	584200	584249	585274	585476	2_nonsis	1026	1151	1275	1	16	1	1	0 (2:6)_(4:4aCO)
11	TW4	TW	2	674481	675106	675106	676899	2_nonsis	1	1209	2417	1	16	1	1	0 (2:6)_(4:4aCO)
88	TW4	TW	14	698189	698660	699152	700166	2_nonsis	493	1235	1976	1	16	1	1	0 (2:6)_(4:4aCO)
39	TW4	TW	7	1050064	1050446	1051093	1051973	2_nonsis	648	1278	1908	1	16	1	1	0 (2:6)_(4:4aCO)
29	TW4	TW	5	377471	377999	379092	379332	2_nonsis	1094	1477	1860	1	16	1	1	0 (2:6)_(4:4aCO)
7	TW4	TW	2	331827	332522	333382	334070	2_nonsis	861	1552	2242	1	16	1	1	0 (2:6)_(4:4aCO)

68	TW4	TW	12	35064	35190	36777	36792	2_nonsis		1588	1658	1727	1	16	1	1	0	(2:6)_(4:4aCO)
1	TW4	TW	1	91044	91629	92891	93563	2_nonsis		1263	1891	2518	1	16	1	1	0	(2:6)_(4:4aCO)
69	TW4	TW	12	122930	123453	124986	126014	2_nonsis		1534	2309	3083	1	16	1	1	0	(2:6)_(4:4aCO)
71	TW4	TW	12	498565	500275	501707	502161	2_nonsis		1433	2514	3595	1	16	1	1	0	(2:6)_(4:4aCO)
34	TW4	TW	7	578731	578856	581949	582077	2_nonsis		3094	3220	3345	1	16	1	1	0	(2:6)_(4:4aCO)
84	TW4	TW	14	77543	77941	80433	81575	2_nonsis		2493	3262	4031	1	16	1	1	0	(2:6)_(4:4aCO)
25	TW4	TW	4	1250091	1250153	1253598	1253640	2_nonsis		3446	3497	3548	1	16	1	1	0	(2:6)_(4:4aCO)
42	TW4	TW	8	68532	68854	72247	72400	2_nonsis		3394	3631	3867	1	16	1	1	0	(2:6)_(4:4aCO)
89	TW4	TW	15	106264	106384	109584	110892	2_nonsis		3201	3914	4627	1	16	1	1	0	(2:6)_(4:4aCO)
14	TW4	TW	3	208234	208480	212528	212637	2_nonsis		4049	4226	4402	1	16	1	1	0	(2:6)_(4:4aCO)
32	TW4	TW	7	223151	224665	226711	229846	2_nonsis		2047	4371	6694	1	16	1	1	0	(2:6)_(4:4aCO)
54	TW4	TW	10	238738	238867	238738	238867	2_nonsis		0	64	128	1	100	1	1	0	(4:4aCO)
17	TW4	TW	4	30545	30752	30545	30752	2_nonsis		0	103	206	1	100	1	1	0	(4:4aCO)
94	TW4	TW	15	702696	702920	702696	702920	2_nonsis		0	112	223	1	100	1	1	0	(4:4aCO)
16	TW4	TW	3	246853	247156	246853	247156	2_nonsis		0	151	302	1	100	1	1	0	(4:4aCO)
24	TW4	TW	4	993715	994135	993715	994135	2_nonsis		0	210	419	1	100	1	1	0	(4:4aCO)
53	TW4	TW	10	60064	60979	60064	60979	2_nonsis		0	457	914	1	100	1	1	0	(4:4aCO)
60	TW4	TW	11	21803	22806	21803	22806	2_nonsis		0	501	1002	1	100	1	1	0	(4:4aCO)
47	TW4	TW	9	84138	85680	84138	85680	2_nonsis		0	771	1541	1	100	1	1	0	(4:4aCO)
18	TW4	TW	4	133068	134651	133068	134651	2_nonsis		0	791	1582	1	100	1	1	0	(4:4aCO)
73	TW4	TW	12	837962	840577	837962	840577	2_nonsis		0	1307	2614	1	100	1	1	0	(4:4aCO)
50	TW4	TW	9	320712	323343	320712	323343	2_nonsis		0	1315	2630	1	100	1	1	0	(4:4aCO)
2	TW4	TW	1	121235	128637	121235	128637	2_nonsis		0	3701	7401	1	100	1	1	0	(4:4aCO)
3	TW4	TW	1	143085	143679	143852	144406	2_nonsis		174	747	1320	3	20	1	1	0	(6:2)_(2:6)_(4:4aCO)
85	TW4	TW	14	245680	246824	248236	249065		3	1413	2399	3384	0	2	2	1	1	(6:2)_(4:4)_(4:4aCO)
91	TW4	TW	15	456645	457110	457110	457531		3	1	443	885	0	2	2	1	1	(0:8)_(4:4aCO)
20	TW4	TW	4	366072	366513	369971	370499		3	3459	3943	4426	0	3	2	1	1	(2:6)_(4:4aCO)_(2:6)_(4:4bCO)
75	TW4	TW	13	55803	56231	57144	57911	2_nonsis		914	1511	2107	0	3	2	0	2	(2:6)_(4:4aCO)_(4:4CO)
95	TW4	TW	15	737331	737496	741072	741418	2_nonsis		3577	3832	4086	0	3	2	0	2	(6:2)_(4:4aCO)_(6:2)_(4:4CO)

```
###############################################################################
#

#SNP_indel_insolator

#Extraction of variant positions from the PySamStats output

#This is run twice for each spore, once for S288c, once for SK1.

#The example code here is for S288c, but the SK1 criteria are identical.

###############################################################################
#

SNP_indel_isolator_S288c <- function(df, filename, polys) {


  #Chromosome names must be converted to numbers in order to match those in the variant table.

  #(Chromosome names need to be roman numerals for PySamStats)

  df$chrom <- as.character(df$chrom)

  df$chrom[df$chrom == "XVI"] <- "16"

  df$chrom[df$chrom == "XV"] <- "15"

  df$chrom[df$chrom == "XIV"] <- "14"

  df$chrom[df$chrom == "XIII"] <- "13"

  df$chrom[df$chrom == "XII"] <- "12"

  df$chrom[df$chrom == "XI"] <- "11"

  df$chrom[df$chrom == "IX"] <- "9"

  df$chrom[df$chrom == "X"] <- "10"

  df$chrom[df$chrom == "VIII"] <- "8"

  df$chrom[df$chrom == "VII"] <- "7"

  df$chrom[df$chrom == "VI"] <- "6"

  df$chrom[df$chrom == "IV"] <- "4"

  df$chrom[df$chrom == "V"] <- "5"

  df$chrom[df$chrom == "III"] <- "3"

  df$chrom[df$chrom == "II"] <- "2"

  df$chrom[df$chrom == "I"] <- "1"


  #making a subtable from the coverage file containing only the important columns

  df<- subset(df, select = c(chrom, pos, reads_all, deletions, insertions, A, C, T, G))
```

```
df <-rename(df, c("pos"="pos_c"))


merged_data <- merge(polys, df, by=c("chrom", "pos_c"), all=FALSE, sort=FALSE)
```

#This merges the coverage dataset with the SNP table according to chromosome and position (this is why it's important to have the same chromosome names).

#all=FALSE means that any positions in the coverage file that are not in the SNP table are discarded.

```
merged_data<- subset(merged_data, select = c(uID, sID, chrom, pos_c, pos_k, seq_c, seq_k, type_c,
        type_k, Var_len, reads_all, deletions, insertions, A, C, T, G))


write.table(merged_data,file=sprintf("%sOut_S288c.txt",filename), row.names=F, quote=F,
sep='\t')
}
```


##
#

#SNP_indel_caller

#Genotype calling and production of statistics file

#This is run twice for each spore, once for S288c, once for SK1.

#The example code here is for the S288c call, but the SK1 call criteria are identical.

##
#

```
SNP_indel_caller_S288c <- function(df, filename, threshold_s, threshold_i, threshold_k){
```

#df - dataframe to use

#filename - name for files produced

#threshold_i -minimum number of reads for a SNP to be called (5)

#threshold_s -minimum number of reads for an indel to be called (5)

#threshold_k - additional threshold for indels (10) - if reads are above this limit, they have a more lenient calling threshold

#remove mitochondrial reads

```
df <- df[which(df$chrom!='mt'),]
```

#creates two new columns c and k containing the number of S288c and SK1 reads respectively for each position

#Because the reads were aligned to S288c, any indels will be relative to S288c.

#Thus for Sk1 reads I take insertions or deletions, but do not need to do the same for S288c.


```
df$k<-ifelse(df$type_k=='d', df$deletions,
        ifelse(df$type_k=='i', df$insertions,
            ifelse(df$type_k=='s' & df$seq_k == "T", df$T,
                ifelse(df$type_k=='s' & df$seq_k == "A", df$A,
                    ifelse(df$type_k=='s' & df$seq_k == "C", df$C,
                        ifelse(df$type_k=='s' & df$seq_k == "G", df$G,
                            0))))))


df$ctemp<-ifelse(df$seq_c == "T", df$T,
        ifelse(df$seq_c == "A", df$A,
            ifelse(df$seq_c == "C", df$C,
                ifelse(df$seq_c == "G", df$G,
                    0))))
```



```
df$c<-ifelse(df$type_k=='i', df$ctemp-df$k,
        df$ctemp)
df$c <- ifelse(df$c < 0, 0, df$c)
```


#Note: the first base of an in/del will always be called as reference now since it is the same in both backgrounds

#For insertions relative to the reference, insertion hits are subtracted from reference hits

#because the first base of an insertion is common to both parents, meaning it will always get 'reference' hits.


```
df$SNPreads <- (df$c+df$k) #total number of SNP (C and K) reads
```

```r
df$reads_all <-ifelse(df$type_k=='s', (df$reads_all+df$insertions), df$reads_all)
```

#insertions don't count seperately to 'reads_all'.

#When the type is S, we are expecting a SNP.

#if there are insertion or deletion reads, they should count against it being called as a SNP.

#deletion reads already count towards reads_all.

##Calling the genotypes##

#CP for S288C (higher confidence = > 5 reads)

#KP for SK1 (higher confidence = > 5 reads)

#CF for S288C with fewer than 5 reads

#KF for SK1 with fewer than 5 reads

#HP for het with = > 5 reads

#HF for het with < 5 reads

#NP for ambiguous with = >5 reads

#NF for ambiguous with <5 reads


```r
df$b <- ifelse(df$type_k=='i' & df$reads_all<threshold_i & (df$k/(df$reads_all))>=0.3, "KF",

        ifelse(df$type_k=='i' & df$reads_all>=threshold_i & (df$k/(df$reads_all))>=0.3, "KP",

            ifelse(df$type_k=='i' & df$reads_all>=threshold_i & df$k>=threshold_k &
(df$k/(df$reads_all))>=0.2, "KP",

                ifelse(df$type_k=='i' & df$reads_all>=threshold_i & df$Var_len>=20 &
(df$k/(df$reads_all))>=0.2, "KP",

                    #lower pass threshold for long insertions and positions with at least 10
insertion hits

                    ifelse(df$type_k=='i' & df$reads_all>=threshold_i & df$k<2 &
(df$c/(df$reads_all))>=0.95, "CP",

                        ifelse(df$type_k=='i' & df$reads_all<threshold_i & df$k<2 &
(df$c/(df$reads_all))>=0.95, "CF",

                            #if there aren't any insertion reads, it's probably S288c (unless read
depth is low).

                            #But need to check that the majority of reads match the reference as
well, else it might be a variant table error
```

```r
                                  ifelse(df$type_k=='d' & df$reads_all<threshold_i &
(df$k/(df$reads_all))>=0.3, "KF",

                                       ifelse(df$type_k=='d' & df$reads_all>=threshold_i &
(df$k/(df$reads_all))>=0.3, "KP",

                                         ifelse(df$type_k=='d' & df$reads_all>=threshold_i &
df$k>=threshold_k & (df$k/(df$reads_all))>=0.2, "KP",

                                           ifelse(df$type_k=='d' & df$reads_all>=threshold_i &
df$Var_len>=20 & (df$k/(df$reads_all))>=0.2, "KP",

                                             #as with insertions there is a reduced threshold for
positions with at least (threshold_k) deletion hits, and for longer deletions.

                                             #deletion thresholds are higher than insertion
thresholds because they aren't affected by the first base being the same,

                                             #but they still have a lower theshold than SNPs because
they don't align as well

                                             ifelse(df$type_k=='d' & df$reads_all<threshold_i &
df$k<2 &  (df$c/(df$reads_all))>=0.95, "CF",

                                               ifelse(df$type_k=='d' & df$reads_all>=threshold_i &
df$k<2 & (df$c/(df$reads_all))>=0.95, "CP",

                                             #if there aren't any deletion reads, it's probably
S288c (unless read depth is low).

                                             #But need to check that the majority of reads
match the reference as well, else it might be a variant table error

                                             #S288c hits are only evaluated if insertions =0 or
1

                                               ifelse(df$type_k=='s' &
df$reads_all<threshold_s & (df$k/(df$reads_all))>=0.75, "KF",

                                                 ifelse(df$type_k=='s' &
df$reads_all<threshold_s & (df$c/(df$reads_all))>=0.9, "CF",

                                                   ifelse(df$type_k=='s' &
df$reads_all>=threshold_s & (df$k/(df$reads_all))>=0.75, "KP",

                                                     ifelse(df$type_k=='s' &
df$reads_all>=threshold_s & (df$c/(df$reads_all))>=0.9, "CP",


                                                       ifelse((df$reads_all)<threshold_s
& ((df$SNPreads)/df$reads_all)>0.9 & (df$c/(df$SNPreads))<0.7 & (df$k/(df$SNPreads))<0.7, "HF",


ifelse((df$reads_all)>=threshold_s & ((df$SNPreads)/df$reads_all)>0.9 & (df$c/(df$SNPreads))<0.7 &
(df$k/(df$SNPreads))<0.7, "HP",
```

#heteroduplex calls for all variant types. Note, for indels, these should NOT be later converted - only used for statistical purposes.

#note, it is important to do the H calls before the N calls because the H calls also fit the criteria for N calls

#insertions never get called H with these criteria, (because insertions don't count seperately to 'reads_all'?)

ifelse(df$type_k=='i' & df$reads_all<threshold_i & (df$c/(df$reads_all))<0.95 & (df$k/(df$reads_all))<0.3, "NF",

ifelse(df$type_k=='i' & df$reads_all>=threshold_i & (df$c/(df$reads_all))<0.95 & (df$k/(df$reads_all))<0.3, "NP",

ifelse(df$type_k=='d' & df$reads_all<threshold_i & (df$c/(df$reads_all))<0.95 & (df$k/(df$reads_all))<0.3, "NF",

ifelse(df$type_k=='d' & df$reads_all>=threshold_i & (df$c/(df$reads_all))<0.95 & (df$k/(df$reads_all))<0.3, "NP",

ifelse(df$type_k=='s' & df$reads_all<threshold_s & (df$c/(df$reads_all))<0.9 & (df$k/(df$reads_all))<0.75, "NF",

ifelse(df$type_k=='s' & df$reads_all>=threshold_s & (df$c/(df$reads_all))<0.9 & (df$k/(df$reads_all))<0.75, "NP",

"U")))))))))))))))))))))))))))

###Collapsing deletions###
df_before_collapse <- df
dels <- df[which(df$type_k=='d'),]
delsFB <-dels[which(dels$seq_k!="-"),] #keep only the first base of each deletion
delsOB <-dels[which(dels$seq_k=="-"),] #the other bases of the deletions

#1bp = 100% (1 call)
#5bp = 40% (2 calls)
#10bp= 33% (3 calls)
#20bp= 25% (5 calls)

#50bp= 16% (8 calls)

#100bp=10% (10 calls)

#100+ =5%

Save delsFB to a new data frame so results can be compared afterward.

delsFB_new <- delsFB

Loop through the unique uID values in delsOB.

for (unique_id in unique(delsFB$uID)) {   #rarely, there may be occurences of uIDs in delsOB that are not in delsFB, which causes an error when combining the tables. So only run the loop for uIDs in delsFB.

   # Subset delsOB for the current unique uID.

   current_delsOB_subset <- delsOB[delsOB$uID == unique_id,]

   current_length <- current_delsOB_subset[1,10]-1 #store length of current indel for working out the average reads

   # Assign desired value to result based on the conditions.

   totalc = sum(current_delsOB_subset$c) #total c reads

   totalk = sum(current_delsOB_subset$k) #total k reads

   avgc <- totalc/current_length #average c reads

   avgk <- totalk/current_length #average k reads

   # Assign desired value to result based on the conditions.

   if ("KP" %in% current_delsOB_subset$b & "CP" %in% current_delsOB_subset$b) {

     result <- "HP"

   }

   else if ("KP" %in% current_delsOB_subset$b) {

     # Nested conditional logic to ensure a minimum proportion of "KP" values, according to the number of instances.

     #Only if the number of KPs or CPs >0, or it will give /0=infinite

     if (length(current_delsOB_subset$b) == 1 & length(current_delsOB_subset$b[current_delsOB_subset$b == "KP"]) == 1) {

       result <- "KP"

     }

```
    else if (length(current_delsOB_subset$b) > 1 & length(current_delsOB_subset$b) <= 5 &
length(current_delsOB_subset$b[current_delsOB_subset$b == "KP"]) >= 1 &
length(current_delsOB_subset$b[current_delsOB_subset$b ==
"KP"])/length(current_delsOB_subset$b) >= 0.4) {

    result <- "KP"

    }

    else if (length(current_delsOB_subset$b) > 5 & length(current_delsOB_subset$b) <= 10 &
length(current_delsOB_subset$b[current_delsOB_subset$b == "KP"]) >= 1 &
length(current_delsOB_subset$b[current_delsOB_subset$b ==
"KP"])/length(current_delsOB_subset$b) >= 0.33) {

    result <- "KP"

    }

    else if (length(current_delsOB_subset$b) > 10 & length(current_delsOB_subset$b) <= 20 &
length(current_delsOB_subset$b[current_delsOB_subset$b == "KP"]) >= 1 &
length(current_delsOB_subset$b[current_delsOB_subset$b ==
"KP"])/length(current_delsOB_subset$b) >= 0.25) {

    result <- "KP"

    }

    else if (length(current_delsOB_subset$b) > 20 & length(current_delsOB_subset$b) <= 50 &
length(current_delsOB_subset$b[current_delsOB_subset$b == "KP"]) >= 1 &
length(current_delsOB_subset$b[current_delsOB_subset$b ==
"KP"])/length(current_delsOB_subset$b) >= 0.16) {

    result <- "KP"

    }

    else if (length(current_delsOB_subset$b) > 50 & length(current_delsOB_subset$b) <= 100 &
length(current_delsOB_subset$b[current_delsOB_subset$b == "KP"]) >= 1 &
length(current_delsOB_subset$b[current_delsOB_subset$b ==
"KP"])/length(current_delsOB_subset$b) >= 0.1) {

    result <- "KP"

    }

    else if (length(current_delsOB_subset$b) > 100 &
length(current_delsOB_subset$b[current_delsOB_subset$b == "KP"]) >= 1 &
length(current_delsOB_subset$b[current_delsOB_subset$b ==
"KP"])/length(current_delsOB_subset$b) >= 0.05) {

    result <- "KP"

    }

    }
```

```r
else if ("CP" %in% current_delsOB_subset$b) {

  # Nested conditional logic to ensure a minimum proportion of "CP" values, according to the number of instances.

  #Only if the number of KPs or CPs >0, or it will give /0=infinite

  if (length(current_delsOB_subset$b) == 1 &
  length(current_delsOB_subset$b[current_delsOB_subset$b == "CP"]) == 1) {

    result <- "CP"

  }

  else if (length(current_delsOB_subset$b) > 1 & length(current_delsOB_subset$b) <= 5 &
  length(current_delsOB_subset$b[current_delsOB_subset$b == "CP"]) >= 1 &
  length(current_delsOB_subset$b[current_delsOB_subset$b ==
  "CP"])/length(current_delsOB_subset$b) >= 0.4) {

    result <- "CP"

  }

  else if (length(current_delsOB_subset$b) > 5 & length(current_delsOB_subset$b) <= 10 &
  length(current_delsOB_subset$b[current_delsOB_subset$b == "CP"]) >= 1 &
  length(current_delsOB_subset$b[current_delsOB_subset$b ==
  "CP"])/length(current_delsOB_subset$b) >= 0.33) {

    result <- "CP"

  }

  else if (length(current_delsOB_subset$b) > 10 & length(current_delsOB_subset$b) <= 20 &
  length(current_delsOB_subset$b[current_delsOB_subset$b == "CP"]) >= 1 &
  length(current_delsOB_subset$b[current_delsOB_subset$b ==
  "CP"])/length(current_delsOB_subset$b) >= 0.25) {

    result <- "CP"

  }

  else if (length(current_delsOB_subset$b) > 20 & length(current_delsOB_subset$b) <= 50 &
  length(current_delsOB_subset$b[current_delsOB_subset$b == "CP"]) >= 1 &
  length(current_delsOB_subset$b[current_delsOB_subset$b ==
  "CP"])/length(current_delsOB_subset$b) >= 0.16) {

    result <- "CP"

  }

  else if (length(current_delsOB_subset$b) > 50 & length(current_delsOB_subset$b) <= 100 &
  length(current_delsOB_subset$b[current_delsOB_subset$b == "CP"]) >= 1 &
  length(current_delsOB_subset$b[current_delsOB_subset$b ==
  "CP"])/length(current_delsOB_subset$b) >= 0.1) {

    result <- "CP"
```

```r
    }
    else if (length(current_delsOB_subset$b) > 100 &
length(current_delsOB_subset$b[current_delsOB_subset$b == "CP"]) >= 1 &
length(current_delsOB_subset$b[current_delsOB_subset$b ==
"CP"])/length(current_delsOB_subset$b) >= 0.05) {

      result <- "CP"

    }

  }

  else {

    result <- "U"

  }

  # Insert the result into delsFB$b.

  delsFB_new[delsFB_new$uID == unique_id, ]$b <- result

  delsFB_new[delsFB_new$uID == unique_id, ]$c <- avgc #replace the c reads for the first base with
the average c reads from the other bases

  delsFB_new[delsFB_new$uID == unique_id, ]$k <- avgk

}


#put delsFB rows back into dataframe#

df <- df[which(df$type_k!='d'),] #remove old del entries

df <- rbind(df, delsFB_new) #adding the converted dels back in

df <- df[order(df$chrom, df$pos_c),] #sort back into correct order


sub<- subset(df, select = c(uID, sID, chrom, pos_c, pos_k, type_c, type_k, Var_len, c, k, b))

write.table(sub,file=sprintf("%sCalled_S288c.txt",filename),row.names=F, quote=F, sep='\t')


##Make a dataframe to hold statistics##

S_reads<- df[which(df$type_k=='s'),]

I_reads<- df[which(df$type_k=='i'),]

D_reads_after <- df[which(df$type_k=='d'),]

D_reads_before <-df_before_collapse[which(df_before_collapse$type_k=='d'),]
```

```r
statistic <-
c('Median_SNP_reads','Mean_SNP_reads','Total_SNP_reads','Min_SNP_Reads','Max_SNP_reads',
'read_depth_threshold', 'Percent_failing_read_depth_threshold',
'Number_failing_read_depth_threshold', 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP',
'Number_NF', 'Number_NP', 'Number_HF', 'Number_HP', 'Percent_CF', 'Percent_CP', 'Percent_KF',
'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF', 'Percent_HP', 'Total_C', 'Total_K', 'Total_N',
'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H', 'Number_U', 'Percent_U')

value <- c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)


statstable <- data.frame(statistic, value)
```

#Stats about the number of reads - Median_SNP_reads,Mean_SNP_reads, Total_SNP_reads, Min_SNP_Reads,

#Max_SNP_reads, read_depth_threshold, Percent_failing_read_depth_threshold, Number_failing_read_depth_threshold

```r
statstable[1,2] <- median(S_reads$reads_all)

statstable[2,2] <- mean(S_reads$reads_all)

statstable[3,2] <- sum(S_reads$reads_all)

statstable[4,2] <- min(S_reads$reads_all)

statstable[5,2] <- max(S_reads$reads_all)

statstable[6,2] <- threshold_s

statstable[7,2] <- 100*(sum(S_reads$reads_all < threshold_s)/sum(S_reads$reads_all))

statstable[8,2] <- sum(S_reads$reads_all<threshold_s)
```

#More stats - 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP', 'Number_NF', 'Number_NP', 'Number_HF', 'Number_HP'

```r
statstable[9,2] <- sum(S_reads$b=='CF')

statstable[10,2] <- sum(S_reads$b=='CP')

statstable[11,2] <- sum(S_reads$b=='KF')

statstable[12,2] <- sum(S_reads$b=='KP')

statstable[13,2] <- sum(S_reads$b=='NF')

statstable[14,2] <- sum(S_reads$b=='NP')

statstable[15,2] <- sum(S_reads$b=='HF')

statstable[16,2] <- sum(S_reads$b=='HP')
```

```r
#'Percent_CF', 'Percent_CP', 'Percent_KF', 'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF', 'Percent_HP'

statstable[17,2] <-
100*(statstable[9,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))

statstable[18,2] <-
100*(statstable[10,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))

statstable[19,2] <-
100*(statstable[11,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))

statstable[20,2] <-
100*(statstable[12,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))

statstable[21,2] <-
100*(statstable[13,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))

statstable[22,2] <-
100*(statstable[14,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))

statstable[23,2] <-
100*(statstable[15,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))

statstable[24,2] <-
100*(statstable[16,2]/(statstable[9,2]+statstable[10,2]+statstable[11,2]+statstable[12,2]+statstable[13,2]+statstable[14,2]+statstable[15,2]+statstable[16,2]))


#'Total_C', 'Total_K', 'Total_N', 'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H'

statstable[25,2] <- (statstable[9,2] + statstable[10,2])

statstable[26,2] <- (statstable[11,2] + statstable[12,2])

statstable[27,2] <- (statstable[13,2] + statstable[14,2])

statstable[28,2] <- (statstable[15,2] + statstable[16,2])

statstable[33,2] <- sum(S_reads$b=='U')

statstable[29,2] <- 100*(statstable[25,2]/(statstable[25,2] + statstable[26,2]+ statstable[27,2]+ statstable[28,2]+statstable[33,2]))

statstable[30,2] <- 100*(statstable[26,2]/(statstable[25,2] + statstable[26,2]+ statstable[27,2]+ statstable[28,2]+statstable[33,2]))
```

```r
statstable[31,2] <- 100*(statstable[27,2]/(statstable[25,2] + statstable[26,2]+ statstable[27,2]+
statstable[28,2]+statstable[33,2]))

statstable[32,2] <- 100*(statstable[28,2]/(statstable[25,2] + statstable[26,2]+ statstable[27,2]+
statstable[28,2]+statstable[33,2]))

statstable[34,2] <- 100*(statstable[33,2]/(statstable[25,2] + statstable[26,2]+ statstable[27,2]+
statstable[28,2]+statstable[33,2]))


statstable$value <- round(statstable$value, digits = 3)


statstable <- rename(statstable, c("value"=paste(match.call()[3])))

write.table(statstable,file=sprintf("%sSNP_Stats_S288c.txt",filename),row.names=F, quote=F,
sep='\t')




#############################################################################
############

#Insertion stats#


statistic2 <-
c('Median_insertion_reads','Mean_insertion_reads','Total_insertion_reads','Min_insertion_Reads','
Max_insertion_reads', 'read_depth_threshold', 'Percent_failing_read_depth_threshold',
'Number_failing_read_depth_threshold', 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP',
'Number_NF', 'Number_NP', 'Number_HF', 'Number_HP', 'Percent_CF', 'Percent_CP', 'Percent_KF',
'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF', 'Percent_HP', 'Total_C', 'Total_K', 'Total_N',
'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H', 'Number_U', 'Percent_U')

value2 <- c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)


statstable2 <- data.frame(statistic2, value2)

#Stats about the number of reads - Median_SNP_reads,Mean_SNP_reads, Total_SNP_reads,
Min_SNP_Reads,

#Max_SNP_reads, read_depth_threshold, Percent_failing_read_depth_threshold,
Number_failing_read_depth_threshold

statstable2[1,2] <- median(I_reads$reads_all)

statstable2[2,2] <- mean(I_reads$reads_all)

statstable2[3,2] <- sum(I_reads$reads_all)

statstable2[4,2] <- min(I_reads$reads_all)
```

```r
statstable2[5,2] <- max(I_reads$reads_all)

statstable2[6,2] <- threshold_i

statstable2[7,2] <- 100*(sum(I_reads$reads_all < threshold_i)/sum(I_reads$reads_all))

statstable2[8,2] <- sum(I_reads$reads_all<threshold_i)


#More stats - 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP', 'Number_NF', 'Number_NP',
'Number_HF', 'Number_HP'

statstable2[9,2] <- sum(I_reads$b=='CF')

statstable2[10,2] <- sum(I_reads$b=='CP')

statstable2[11,2] <- sum(I_reads$b=='KF')

statstable2[12,2] <- sum(I_reads$b=='KP')

statstable2[13,2] <- sum(I_reads$b=='NF')

statstable2[14,2] <- sum(I_reads$b=='NP')

statstable2[15,2] <- sum(I_reads$b=='HF')

statstable2[16,2] <- sum(I_reads$b=='HP')


#'Percent_CF', 'Percent_CP', 'Percent_KF', 'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF',
'Percent_HP'

statstable2[17,2] <-
100*(statstable2[9,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+statst
able2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))

statstable2[18,2] <-
100*(statstable2[10,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+stats
table2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))

statstable2[19,2] <-
100*(statstable2[11,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+stats
table2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))

statstable2[20,2] <-
100*(statstable2[12,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+stats
table2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))

statstable2[21,2] <-
100*(statstable2[13,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+stats
table2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))

statstable2[22,2] <-
100*(statstable2[14,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+stats
table2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))
```

```
  statstable2[23,2] <-
100*(statstable2[15,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+stats
table2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))

  statstable2[24,2] <-
100*(statstable2[16,2]/(statstable2[9,2]+statstable2[10,2]+statstable2[11,2]+statstable2[12,2]+stats
table2[13,2]+statstable2[14,2]+statstable2[15,2]+statstable2[16,2]))


 #'Total_C', 'Total_K', 'Total_N', 'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H'

 statstable2[25,2] <- (statstable2[9,2] + statstable2[10,2])

 statstable2[26,2] <- (statstable2[11,2] + statstable2[12,2])

 statstable2[27,2] <- (statstable2[13,2] + statstable2[14,2])

 statstable2[28,2] <- (statstable2[15,2] + statstable2[16,2])

 statstable2[33,2] <- sum(I_reads$b=='U')

 statstable2[29,2] <- 100*(statstable2[25,2]/(statstable2[25,2] + statstable2[26,2]+
statstable2[27,2]+ statstable2[28,2]+statstable2[33,2]))

  statstable2[30,2] <- 100*(statstable2[26,2]/(statstable2[25,2] + statstable2[26,2]+
statstable2[27,2]+ statstable2[28,2]+statstable2[33,2]))

  statstable2[31,2] <- 100*(statstable2[27,2]/(statstable2[25,2] + statstable2[26,2]+
statstable2[27,2]+ statstable2[28,2]+statstable2[33,2]))

  statstable2[32,2] <- 100*(statstable2[28,2]/(statstable2[25,2] + statstable2[26,2]+
statstable2[27,2]+ statstable2[28,2]+statstable2[33,2]))

  statstable2[34,2] <- 100*(statstable2[33,2]/(statstable2[25,2] + statstable2[26,2]+
statstable2[27,2]+ statstable2[28,2]+statstable2[33,2]))


 statstable2$value2 <- round(statstable2$value2, digits = 3)


 statstable2 <- rename(statstable2, c("value2"=paste(match.call()[3])))

 #rename this column so it will have the sample name for merging

 write.table(statstable2,file=sprintf("%sinsertion_Stats_S288c.txt",filename),row.names=F, quote=F,
sep='\t')



###########################################################################
#############

 #Deletion stats - After#
```

```r
statistic3 <-
c('Median_deletion_reads','Mean_deletion_reads','Total_deletion_reads','Min_deletion_Reads','Ma
x_deletion_reads', 'read_depth_threshold', 'Percent_failing_read_depth_threshold',
'Number_failing_read_depth_threshold', 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP',
'Number_NF', 'Number_NP', 'Number_HF', 'Number_HP', 'Percent_CF', 'Percent_CP', 'Percent_KF',
'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF', 'Percent_HP', 'Total_C', 'Total_K', 'Total_N',
'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H', 'Number_U', 'Percent_U')

value3 <- c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)


statstable3 <- data.frame(statistic3, value3)

#Stats about the number of reads - Median_SNP_reads,Mean_SNP_reads, Total_SNP_reads,
Min_SNP_Reads,

#Max_SNP_reads, read_depth_threshold, Percent_failing_read_depth_threshold,
Number_failing_read_depth_threshold

statstable3[1,2] <- median(D_reads_after$reads_all)

statstable3[2,2] <- mean(D_reads_after$reads_all)

statstable3[3,2] <- sum(D_reads_after$reads_all)

statstable3[4,2] <- min(D_reads_after$reads_all)

statstable3[5,2] <- max(D_reads_after$reads_all)

statstable3[6,2] <- threshold_i

statstable3[7,2] <- 100*(sum(D_reads_after$reads_all <
threshold_i)/sum(D_reads_after$reads_all))

statstable3[8,2] <- sum(D_reads_after$reads_all<threshold_i)


#More stats - 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP', 'Number_NF', 'Number_NP',
'Number_HF', 'Number_HP'

statstable3[9,2] <- sum(D_reads_after$b=='CF')

statstable3[10,2] <- sum(D_reads_after$b=='CP')

statstable3[11,2] <- sum(D_reads_after$b=='KF')

statstable3[12,2] <- sum(D_reads_after$b=='KP')

statstable3[13,2] <- sum(D_reads_after$b=='NF')

statstable3[14,2] <- sum(D_reads_after$b=='NP')

statstable3[15,2] <- sum(D_reads_after$b=='HF')
```

```
  statstable3[16,2] <- sum(D_reads_after$b=='HP')


 #'Percent_CF', 'Percent_CP', 'Percent_KF', 'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF',
'Percent_HP'

  statstable3[17,2] <-
100*(statstable3[9,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+statst
able3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))

  statstable3[18,2] <-
100*(statstable3[10,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+stats
table3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))

  statstable3[19,2] <-
100*(statstable3[11,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+stats
table3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))

  statstable3[20,2] <-
100*(statstable3[12,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+stats
table3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))

  statstable3[21,2] <-
100*(statstable3[13,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+stats
table3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))

  statstable3[22,2] <-
100*(statstable3[14,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+stats
table3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))

  statstable3[23,2] <-
100*(statstable3[15,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+stats
table3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))

  statstable3[24,2] <-
100*(statstable3[16,2]/(statstable3[9,2]+statstable3[10,2]+statstable3[11,2]+statstable3[12,2]+stats
table3[13,2]+statstable3[14,2]+statstable3[15,2]+statstable3[16,2]))


 #'Total_C', 'Total_K', 'Total_N', 'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H'

 statstable3[25,2] <- (statstable3[9,2] + statstable3[10,2])

 statstable3[26,2] <- (statstable3[11,2] + statstable3[12,2])

 statstable3[27,2] <- (statstable3[13,2] + statstable3[14,2])

 statstable3[28,2] <- (statstable3[15,2] + statstable3[16,2])

 statstable[33,2] <- sum(D_reads_after$b=='U')

 statstable3[29,2] <- 100*(statstable3[25,2]/(statstable3[25,2] + statstable3[26,2]+
statstable3[27,2]+ statstable3[28,2]+statstable3[33,2]))
```

```r
statstable3[30,2] <- 100*(statstable3[26,2]/(statstable3[25,2] + statstable3[26,2]+
statstable3[27,2]+ statstable3[28,2]+statstable3[33,2]))

statstable3[31,2] <- 100*(statstable3[27,2]/(statstable3[25,2] + statstable3[26,2]+
statstable3[27,2]+ statstable3[28,2]+statstable3[33,2]))

statstable3[32,2] <- 100*(statstable3[28,2]/(statstable3[25,2] + statstable3[26,2]+
statstable3[27,2]+ statstable3[28,2]+statstable3[33,2]))

statstable3[34,2] <- 100*(statstable3[33,2]/(statstable3[25,2] + statstable3[26,2]+
statstable3[27,2]+ statstable3[28,2]+statstable3[33,2]))


statstable3$value3 <- round(statstable3$value3, digits = 3)


statstable3 <- rename(statstable3, c("value3"=paste(match.call()[3])))

#rename this column so it will have the sample name for merging

write.table(statstable3,file=sprintf("%sdeletion_Stats_after_S288c.txt",filename),row.names=F,
quote=F, sep='\t')



#################################################################################
############

#Deletion stats - Before#


statistic4 <-
c('Median_deletion_reads','Mean_deletion_reads','Total_deletion_reads','Min_deletion_Reads','Ma
x_deletion_reads', 'read_depth_threshold', 'Percent_failing_read_depth_threshold',
'Number_failing_read_depth_threshold', 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP',
'Number_NF', 'Number_NP', 'Number_HF', 'Number_HP', 'Percent_CF', 'Percent_CP', 'Percent_KF',
'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF', 'Percent_HP', 'Total_C', 'Total_K', 'Total_N',
'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H', 'Number_U', 'Percent_U')

value4 <- c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)


statstable4 <- data.frame(statistic4, value4)

#Stats about the number of reads - Median_SNP_reads,Mean_SNP_reads, Total_SNP_reads,
Min_SNP_Reads,

#Max_SNP_reads, read_depth_threshold, Percent_failing_read_depth_threshold,
Number_failing_read_depth_threshold

statstable4[1,2] <- median(D_reads_before$reads_all)
```

```
statstable4[2,2] <- mean(D_reads_before$reads_all)

statstable4[3,2] <- sum(D_reads_before$reads_all)

statstable4[4,2] <- min(D_reads_before$reads_all)

statstable4[5,2] <- max(D_reads_before$reads_all)

statstable4[6,2] <- threshold_i

statstable4[7,2] <- 100*(sum(D_reads_before$reads_all <
threshold_i)/sum(D_reads_before$reads_all))

statstable4[8,2] <- sum(D_reads_before$reads_all<threshold_i)


#More stats - 'Number_CF', 'Number_CP', 'Number_KF', 'Number_KP', 'Number_NF', 'Number_NP',
'Number_HF', 'Number_HP'

statstable4[9,2] <- sum(D_reads_before$b=='CF')

statstable4[10,2] <- sum(D_reads_before$b=='CP')

statstable4[11,2] <- sum(D_reads_before$b=='KF')

statstable4[12,2] <- sum(D_reads_before$b=='KP')

statstable4[13,2] <- sum(D_reads_before$b=='NF')

statstable4[14,2] <- sum(D_reads_before$b=='NP')

statstable4[15,2] <- sum(D_reads_before$b=='HF')

statstable4[16,2] <- sum(D_reads_before$b=='HP')


#'Percent_CF', 'Percent_CP', 'Percent_KF', 'Percent_KP', 'Percent_NF', 'Percent_NP', 'Percent_HF',
'Percent_HP'

statstable4[17,2] <-
100*(statstable4[9,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+statst
able4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))

statstable4[18,2] <-
100*(statstable4[10,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+stats
table4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))

statstable4[19,2] <-
100*(statstable4[11,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+stats
table4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))

statstable4[20,2] <-
100*(statstable4[12,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+stats
table4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))
```

```
  statstable4[21,2] <-
100*(statstable4[13,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+stats
table4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))

  statstable4[22,2] <-
100*(statstable4[14,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+stats
table4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))

  statstable4[23,2] <-
100*(statstable4[15,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+stats
table4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))

  statstable4[24,2] <-
100*(statstable4[16,2]/(statstable4[9,2]+statstable4[10,2]+statstable4[11,2]+statstable4[12,2]+stats
table4[13,2]+statstable4[14,2]+statstable4[15,2]+statstable4[16,2]))


  #'Total_C', 'Total_K', 'Total_N', 'Total_H', 'Percent_C', 'Percent_K', 'Percent_N', 'Percent_H'

  statstable4[25,2] <- (statstable4[9,2] + statstable4[10,2])

  statstable4[26,2] <- (statstable4[11,2] + statstable4[12,2])

  statstable4[27,2] <- (statstable4[13,2] + statstable4[14,2])

  statstable4[28,2] <- (statstable4[15,2] + statstable4[16,2])

  statstable4[33,2] <- sum(D_reads_before$b=='U')

  statstable4[29,2] <- 100*(statstable4[25,2]/(statstable4[25,2] + statstable4[26,2]+
statstable4[27,2]+ statstable4[28,2]+statstable4[33,2]))

  statstable4[30,2] <- 100*(statstable4[26,2]/(statstable4[25,2] + statstable4[26,2]+
statstable4[27,2]+ statstable4[28,2]+statstable4[33,2]))

  statstable4[31,2] <- 100*(statstable4[27,2]/(statstable4[25,2] + statstable4[26,2]+
statstable4[27,2]+ statstable4[28,2]+statstable4[33,2]))

  statstable4[32,2] <- 100*(statstable4[28,2]/(statstable4[25,2] + statstable4[26,2]+
statstable4[27,2]+ statstable4[28,2]+statstable4[33,2]))

  statstable4[34,2] <- 100*(statstable4[33,2]/(statstable4[25,2] + statstable4[26,2]+
statstable4[27,2]+ statstable4[28,2]+statstable4[33,2]))


  statstable4$value4 <- round(statstable4$value4, digits = 3)


  statstable4 <- rename(statstable4, c("value4"=paste(match.call()[3])))

  #rename this column so it will have the sample name for merging

  write.table(statstable4,file=sprintf("%sdeletion_Stats_before_S288c.txt",filename),row.names=F,
quote=F, sep='\t')
```

```
}


################################################################################
#

#Genotype calling is combined for each spore in a tetrad/octad

#Heteroduplex calling is performed on msh2 tetrads

#This is run twice for each spore, once for S288c, once for SK1.

#The example code here is for S288c, but the SK1 criteria are identical.

################################################################################
#

#Called SNPs Combiner

#Combines the 8 members of an octad into 1 file

table1 <- read.table("OM5ACalled_S288c.txt",header=T)

table2 <- read.table("OM5AlphaCalled_S288c.txt",header=T)

table3 <- read.table("OM5BCalled_S288c.txt",header=T)

table4 <- read.table("OM5BetaCalled_S288c.txt",header=T)

table5 <- read.table("OM5CCalled_S288c.txt",header=T)

table6 <- read.table("OM5GammaCalled_S288c.txt",header=T)

table7 <- read.table("OM5DCalled_S288c.txt",header=T)

table8 <- read.table("OM5DeltaCalled_S288c.txt",header=T)


library(plyr)

#plyr is needed for the renaming function so all the c, k and b columns don't have the same name


table1 <- rename(table1, c("c"="c1", "k"="k1", "b"="b1"))

table2 <- rename(table2, c("c"="c2", "k"="k2", "b"="b2"))

table3 <- rename(table3, c("c"="c3", "k"="k3", "b"="b3"))

table4 <- rename(table4, c("c"="c4", "k"="k4", "b"="b4"))

table5 <- rename(table5, c("c"="c5", "k"="k5", "b"="b5"))

table6 <- rename(table6, c("c"="c6", "k"="k6", "b"="b6"))

table7 <- rename(table7, c("c"="c7", "k"="k7", "b"="b7"))
```

```
table8 <- rename(table8, c("c"="c8", "k"="k8", "b"="b8"))
```

#merges the 8 dataframes into 1

```
merged <- merge(table1, table2, by=c("uID", "sID", "chrom", "pos_c", "pos_k", "type_k", "type_c", "Var_len"), all=FALSE, sort=FALSE)

merged <- merge(merged, table3, by=c("uID", "sID", "chrom", "pos_c", "pos_k", "type_k", "type_c", "Var_len"), all=FALSE, sort=FALSE)

merged <- merge(merged, table4, by=c("uID", "sID", "chrom", "pos_c", "pos_k", "type_k", "type_c", "Var_len"), all=FALSE, sort=FALSE)

merged <- merge(merged, table5, by=c("uID", "sID", "chrom", "pos_c", "pos_k", "type_k", "type_c", "Var_len"), all=FALSE, sort=FALSE)

merged <- merge(merged, table6, by=c("uID", "sID", "chrom", "pos_c", "pos_k", "type_k", "type_c", "Var_len"), all=FALSE, sort=FALSE)

merged <- merge(merged, table7, by=c("uID", "sID", "chrom", "pos_c", "pos_k", "type_k", "type_c", "Var_len"), all=FALSE, sort=FALSE)

merged <- merge(merged, table8, by=c("uID", "sID", "chrom", "pos_c", "pos_k", "type_k", "type_c", "Var_len"), all=FALSE, sort=FALSE)
```

#Puts the columns in the right order

```
merged <- merged[c("uID", "sID", "chrom", "pos_c", "pos_k", "type_c", "type_k", "Var_len", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "c8",

        "k1", "k2", "k3", "k4", "k5", "k6", "k7", "k8", "b1", "b2", "b3", "b4", "b5", "b6", "b7", "b8")]
```

#renames these two columns to match MC's specification

```
merged <- rename(merged, c("chrom" = "chr"))
```

```
write.table(merged,file="OM5_combined_S288c.txt", row.names=F, quote=F, sep='\t')
```

```
############################################################################
#
#call heteroduplex in tetrads
```

#Only for msh2 tetrads

#tetrad data is adapted to the octad pipeline by duplicating each spore.

#If a msh2 tetrad has a position called 'HP', one copy of the spore should have it converted to KP and the other to CP.

#Thus 'octadifying' the tetrad and making it a 7:1 event.

#Issue: Commonly, heteroduplex occurs near the end of chromosomes which is probably actually just from repetitive sequences.

#This creates small 'U' events entirely composed of hDNA. These can be removed from the event table.

df <- read.table("OM5_combined_S288c.txt", header=T)

#only if the type==S (indels seem to never be called HP anyway, and dels get converted to NP earlier - but may as well be on the safe side)

df$b1 <- as.character(df$b1)

df$b2 <- as.character(df$b2)

df$b3 <- as.character(df$b3)

df$b4 <- as.character(df$b4)

df$b5 <- as.character(df$b5)

df$b6 <- as.character(df$b6)

df$b7 <- as.character(df$b7)

df$b8 <- as.character(df$b8)

#ifelse statements don't work properly on factors - they return the factor level - so make sure these columns contain characters

df$b1 <- ifelse(df$type_k=='s' & df$b1 == 'HP', 'KP', df$b1)

df$b2 <- ifelse(df$type_k=='s' & df$b2 == 'HP', 'CP', df$b2)

df$b3 <- ifelse(df$type_k=='s' & df$b3 == 'HP', 'KP', df$b3)

df$b4 <- ifelse(df$type_k=='s' & df$b4 == 'HP', 'CP', df$b4)

df$b5 <- ifelse(df$type_k=='s' & df$b5 == 'HP', 'KP', df$b5)

df$b6 <- ifelse(df$type_k=='s' & df$b6 == 'HP', 'CP', df$b6)

df$b7 <- ifelse(df$type_k=='s' & df$b7 == 'HP', 'KP', df$b7)

df$b8 <- ifelse(df$type_k=='s' & df$b8 == 'HP', 'CP', df$b8)

write.table(df,file="OM5_combined_ConvertedHPs_S288c.txt", row.names=F, quote=F, sep='\t')

```
##############################################################################
###

###Make HPs File - table containing all positions called as HP in at least 1 spore###

###For analysis to make sure they don't occur in the same place in multiple samples##

df <- read.table("OM5_combined_S288c.txt", header=T)

HPs1 <-df[which(df$b1=='HP'),]

HPs2 <-df[which(df$b2=='HP'),]

HPs3 <-df[which(df$b3=='HP'),]

HPs4 <-df[which(df$b4=='HP'),]

HPs5 <-df[which(df$b5=='HP'),]

HPs6 <-df[which(df$b6=='HP'),]

HPs7 <-df[which(df$b7=='HP'),]

HPs8 <-df[which(df$b8=='HP'),]


total <- rbind(HPs1, HPs2, HPs3,HPs4, HPs5, HPs6, HPs7, HPs8)

total <- total[!duplicated(total), ]

write.table(total,file="HP-list_OM5_S288c.txt", row.names=F, quote=F, sep='\t')

####End###




##############################################################################
###############

#SK1_S288c_Combiner

#Reconcilation of genotype calls against SK1 and S288c.

#Produces a binary file compatible with the event caller script.

#Also creates a 'gr2' file containing raw reads and binary calls, for event imaging.

##############################################################################
###############

####IMPORTANT NOTE: Only use 'Converted HPs' version for msh2 tetrads.#########

dfc <- read.table("OM5_combined_S288c.txt", header=T)

#dfc <- read.table("OM5_combined_ConvertedHPs_S288c.txt", header=T)

dfk <- read.table("OM5_combined_SK1.txt", header=T)
```

```
#dfk <- read.table("OM5_combined_ConvertedHPs_SK1.txt", header=T)


dfkc <- merge(dfk, dfc, by=c("uID", "sID", "chr", "pos_c", "pos_k", "type_k", "type_c", "Var_len"),
sort=F, all=T)

dfkc <- dfkc[order(dfkc$chr, dfkc$pos_c),]

#it's important to sort after rather than during the merge, because otherwise it gets sorted on pos_k

#and messes up the order.


#there are rarely some rows in one set but not the other, they are kept if all=T but will contain NA

#turn NAs to 0

dfkc[is.na(dfkc)] <- 0

#this will give some warnings, because it doesn't want to convert the b columns to a number when
they previously contained a string.

#It's OK for them to remain NA, as long as the c and k columns are converted to 0.


dfkc$c1 <- (dfkc$c1.x+dfkc$c1.y)

dfkc$c2 <- (dfkc$c2.x+dfkc$c2.y)

dfkc$c3 <- (dfkc$c3.x+dfkc$c3.y)

dfkc$c4 <- (dfkc$c4.x+dfkc$c4.y)

dfkc$c5 <- (dfkc$c5.x+dfkc$c5.y)

dfkc$c6 <- (dfkc$c6.x+dfkc$c6.y)

dfkc$c7 <- (dfkc$c7.x+dfkc$c7.y)

dfkc$c8 <- (dfkc$c8.x+dfkc$c8.y)


dfkc$k1 <- (dfkc$k1.x+dfkc$k1.y)

dfkc$k2 <- (dfkc$k2.x+dfkc$k2.y)

dfkc$k3 <- (dfkc$k3.x+dfkc$k3.y)

dfkc$k4 <- (dfkc$k4.x+dfkc$k4.y)

dfkc$k5 <- (dfkc$k5.x+dfkc$k5.y)

dfkc$k6 <- (dfkc$k6.x+dfkc$k6.y)

dfkc$k7 <- (dfkc$k7.x+dfkc$k7.y)

dfkc$k8 <- (dfkc$k8.x+dfkc$k8.y)
```

#adding up k and c reads from the two alignments.

#These were previously divided by 2 to give the average, but that was removed to show the seperation better when plotting on a log scale.


```
dfkc$b1<- ifelse(dfkc$kb1 == "KP" & dfkc$b1=='CP', NA, ifelse(dfkc$kb1 == "CP" & dfkc$b1=='KP', NA,
ifelse(dfkc$kb1 == "KP", 0, ifelse(dfkc$kb1 == "CP", 1, ifelse(dfkc$b1 == "KP", 0, ifelse(dfkc$b1 ==
"CP", 1, NA))))))

dfkc$b2<- ifelse(dfkc$kb2 == "KP" & dfkc$b2=='CP', NA, ifelse(dfkc$kb2 == "CP" & dfkc$b2=='KP', NA,
ifelse(dfkc$kb2 == "KP", 0, ifelse(dfkc$kb2 == "CP", 1, ifelse(dfkc$b2 == "KP", 0, ifelse(dfkc$b2 ==
"CP", 1, NA))))))

dfkc$b3<- ifelse(dfkc$kb3 == "KP" & dfkc$b3=='CP', NA, ifelse(dfkc$kb3 == "CP" & dfkc$b3=='KP', NA,
ifelse(dfkc$kb3 == "KP", 0, ifelse(dfkc$kb3 == "CP", 1, ifelse(dfkc$b3 == "KP", 0, ifelse(dfkc$b3 ==
"CP", 1, NA))))))

dfkc$b4<- ifelse(dfkc$kb4 == "KP" & dfkc$b4=='CP', NA, ifelse(dfkc$kb4 == "CP" & dfkc$b4=='KP', NA,
ifelse(dfkc$kb4 == "KP", 0, ifelse(dfkc$kb4 == "CP", 1, ifelse(dfkc$b4 == "KP", 0, ifelse(dfkc$b4 ==
"CP", 1, NA))))))

dfkc$b5<- ifelse(dfkc$kb5 == "KP" & dfkc$b5=='CP', NA, ifelse(dfkc$kb5 == "CP" & dfkc$b5=='KP', NA,
ifelse(dfkc$kb5 == "KP", 0, ifelse(dfkc$kb5 == "CP", 1, ifelse(dfkc$b5 == "KP", 0, ifelse(dfkc$b5 ==
"CP", 1, NA))))))

dfkc$b6<- ifelse(dfkc$kb6 == "KP" & dfkc$b6=='CP', NA, ifelse(dfkc$kb6 == "CP" & dfkc$b6=='KP', NA,
ifelse(dfkc$kb6 == "KP", 0, ifelse(dfkc$kb6 == "CP", 1, ifelse(dfkc$b6 == "KP", 0, ifelse(dfkc$b6 ==
"CP", 1, NA))))))

dfkc$b7<- ifelse(dfkc$kb7 == "KP" & dfkc$b7=='CP', NA, ifelse(dfkc$kb7 == "CP" & dfkc$b7=='KP', NA,
ifelse(dfkc$kb7 == "KP", 0, ifelse(dfkc$kb7 == "CP", 1, ifelse(dfkc$b7 == "KP", 0, ifelse(dfkc$b7 ==
"CP", 1, NA))))))

dfkc$b8<- ifelse(dfkc$kb8 == "KP" & dfkc$b8=='CP', NA, ifelse(dfkc$kb8 == "CP" & dfkc$b8=='KP', NA,
ifelse(dfkc$kb8 == "KP", 0, ifelse(dfkc$kb8 == "CP", 1, ifelse(dfkc$b8 == "KP", 0, ifelse(dfkc$b8 ==
"CP", 1, NA))))))
```


#If the two files conflict, value is NA e.g. if kb1=="KP" & b1=="CP".

#value is also NA if neither call produced a KP or CP

#c=1 k=0


```
dfkc<- subset(dfkc, select = c(chr, pos_c,
c1,c2,c3,c4,c5,c6,c7,c8,k1,k2,k3,k4,k5,k6,k7,k8,b1,b2,b3,b4,b5,b6,b7,b8, type_k, Var_len))
```


##work out how many rows contain at least one NA, and so will be discarded later##

```r
statistic5 <- c('Total_Rows', 'Removed_Rows', 'Percent_Removed_Rows', 'S_total', 'I_total', 'D_total', 'Removed_S', 'Percent_Removed_S', 'Removed_I', 'Percent_Removed_I', 'Removed_D', 'Percent_Removed_D')

value5 <- c(0,0,0,0,0,0,0,0,0,0,0,0)

statstable5 <- data.frame(statistic5, value5)


#Work out some stats about the number of rows containing at least one NA (which will be discarded)

dfkc_noNA <- dfkc[complete.cases(dfkc),]

statstable5[1,2] <- nrow(dfkc)

statstable5[2,2] <- (nrow(dfkc) - nrow(dfkc_noNA))

statstable5[3,2] <- (statstable5[2,2]/statstable5[1,2])*100

s <- dfkc[which(dfkc$type_k=='s'),]

i <- dfkc[which(dfkc$type_k=='i'),]

d <- dfkc[which(dfkc$type_k=='d'),]

s_noNA <- dfkc_noNA[which(dfkc_noNA$type_k=='s'),]

i_noNA <- dfkc_noNA[which(dfkc_noNA$type_k=='i'),]

d_noNA <- dfkc_noNA[which(dfkc_noNA$type_k=='d'),]

statstable5[4,2]  <- nrow(s)

statstable5[5,2]  <- nrow(i)

statstable5[6,2]  <- nrow(d)

statstable5[7,2]  <- nrow(s)-nrow(s_noNA)

statstable5[8,2]  <- ((statstable5[7,2]/statstable5[4,2])*100)

statstable5[9,2]  <- nrow(i)-nrow(i_noNA)

statstable5[10,2]  <- ((statstable5[9,2]/statstable5[5,2])*100)

statstable5[11,2]  <- nrow(d)-nrow(d_noNA)

statstable5[12,2]  <- ((statstable5[11,2]/statstable5[6,2])*100)

statstable5$value5 <- round(statstable5$value5, digits = 2)


write.table(statstable5,file="OM5_additional_Stats_S288c_SK1.txt", row.names=F, quote=F, sep='\t')
```

```
#################################################

#makes the gr2 file which can be visualized in R


####Make gr2 with only INDEL 8-0 positions removed####

gr2 <- dfkc

gr2$temp <- (gr2$b1 + gr2$b2 + gr2$b3 + gr2$b4 + gr2$b5 + gr2$b6 + gr2$b7 + gr2$b8)


gr2i <- gr2[which(gr2$type_k=='i' & gr2$temp!=0 & gr2$temp!=8),] #This also removes ones where
the total is NA.

gr2d <- gr2[which(gr2$type_k=='d' & gr2$temp!=0 & gr2$temp!=8),]

gr2s <- gr2[which(gr2$type_k=='s'),]

gr2NA <- subset(gr2, is.na(gr2$temp)) #subset the ones where the total is NA

gr2 <- rbind(gr2i, gr2d, gr2s, gr2NA)

gr2 <- gr2[order(gr2$chr, gr2$pos_c),]

#remove the temp column

gr2<- subset(gr2, select = c(chr, pos_c,
c1,c2,c3,c4,c5,c6,c7,c8,k1,k2,k3,k4,k5,k6,k7,k8,b1,b2,b3,b4,b5,b6,b7,b8, type_k, Var_len))

gr2 <- unique(gr2) #remove any duplicates that may have been introduced from SNPs totalling NA


write.table(gr2,file="OM5_gr2_SNPEZ_CK.txt", row.names=F, quote=F, sep='\t')


####################################################


#This section makes the file compatible with the event caller

sub <- subset(dfkc, select = c(b1,b2,b3,b4,b5,b6,b7,b8))

#isolates the b columns


sub[!!rowSums(is.na(sub)),] <- NA

#if any column contains an NA, then all columns for that row are converted to NA


dfkc$b1 <- sub$b1

dfkc$b2 <- sub$b2
```

```r
dfkc$b3 <- sub$b3

dfkc$b4 <- sub$b4

dfkc$b5 <- sub$b5

dfkc$b6 <- sub$b6

dfkc$b7 <- sub$b7

dfkc$b8 <- sub$b8

#Puts the b columns back into the dataframe


write.table(dfkc,file="OM5_binarized_CK.txt", row.names=F, quote=F, sep='\t')

df <- read.table("OM5_binarized_CK.txt", header=T)


df$temp <- (df$b1 + df$b2 + df$b3 + df$b4 + df$b5 + df$b6 + df$b7 + df$b8)


#This outputs a table containing 8-0 positions for examination as they may not actually be SNPs

nonsnps8 <-df[which(df$temp==8),]

nonsnps0 <-df[which(df$temp==0),]

total <- rbind(nonsnps0, nonsnps8)


write.table(total,file="EZ-list_OM5_KC.txt", row.names=F, quote=F, sep='\t')


####Make binary with only INDEL 8-0 positions removed####


dfi <- df[which(df$type_k=='i' & df$temp!=0 & df$temp!=8),]

dfd <- df[which(df$type_k=='d' & df$temp!=0 & df$temp!=8),]

dfs <- df[which(df$type_k=='s'),]

df3 <- rbind(dfi, dfd, dfs)

df3 <- df3[order(df3$chr, df3$pos_c),]


statistic6 <- c('Total_Rows', 'Indel 8-0s Removed')

value6 <- c(0,0)

statstable6 <- data.frame(statistic6, value6)
```

```r
statstable6[1,2] <- nrow(df)

statstable6[2,2] <- (nrow(df) - nrow(df3))

write.table(statstable6,file="OM5_Indel_8-0s_Removed.txt", row.names=F, quote=F, sep='\t')


#remove the temp column and the c and k columns

df3<- subset(df3, select = c(chr, pos_c, b1,b2,b3,b4,b5,b6,b7,b8))

#To remove 'NA's, select only rows containing 0 or 1

df3 <- df3[df3$b1 %in% c(0, 1), ]


write.table(df3,file="OM5_binary_5.5.CK.HP.EZIn.txt", row.names=F, quote=F, sep='\t')

#This file is compatible with the event caller.


##seperate for statistical purposes###


dfk$b1<- ifelse(dfk$kb1 == "KP", 0, ifelse(dfk$kb1 == "CP", 1, NA))

dfk$b2<- ifelse(dfk$kb2 == "KP", 0, ifelse(dfk$kb2 == "CP", 1, NA))

dfk$b3<- ifelse(dfk$kb3 == "KP", 0, ifelse(dfk$kb3 == "CP", 1, NA))

dfk$b4<- ifelse(dfk$kb4 == "KP", 0, ifelse(dfk$kb4 == "CP", 1, NA))

dfk$b5<- ifelse(dfk$kb5 == "KP", 0, ifelse(dfk$kb5 == "CP", 1, NA))

dfk$b6<- ifelse(dfk$kb6 == "KP", 0, ifelse(dfk$kb6 == "CP", 1, NA))

dfk$b7<- ifelse(dfk$kb7 == "KP", 0, ifelse(dfk$kb7 == "CP", 1, NA))

dfk$b8<- ifelse(dfk$kb8 == "KP", 0, ifelse(dfk$kb8 == "CP", 1, NA))


dfk<- subset(dfk, select = c(chr, pos_c, type_k,
c1,c2,c3,c4,c5,c6,c7,c8,k1,k2,k3,k4,k5,k6,k7,k8,b1,b2,b3,b4,b5,b6,b7,b8))


##work out how many rows contain at least one NA, and so will be discarded later##

statistic5 <- c('Total_Rows', 'Removed_Rows', 'Percent_Removed_Rows', 'S_total', 'I_total', 'D_total',
'Removed_S', 'Percent_Removed_S', 'Removed_I', 'Percent_Removed_I', 'Removed_D',
'Percent_Removed_D')

value5 <- c(0,0,0,0,0,0,0,0,0,0,0,0)

statstable5 <- data.frame(statistic5, value5)
```

```r
#Work out some stats about the number of rows containing at least one NA (which will be
discarded)

df_noNA <- dfk[complete.cases(dfk),]

statstable5[1,2] <- nrow(dfk)

statstable5[2,2] <- (nrow(dfk) - nrow(df_noNA))

statstable5[3,2] <- (statstable5[2,2]/statstable5[1,2])*100

s <- dfk[which(dfk$type_k=='s'),]

i <- dfk[which(dfk$type_k=='i'),]

d <- dfk[which(dfk$type_k=='d'),]

s_noNA <- df_noNA[which(df_noNA$type_k=='s'),]

i_noNA <- df_noNA[which(df_noNA$type_k=='i'),]

d_noNA <- df_noNA[which(df_noNA$type_k=='d'),]

statstable5[4,2]  <- nrow(s)

statstable5[5,2]  <- nrow(i)

statstable5[6,2]  <- nrow(d)

statstable5[7,2]  <- nrow(s)-nrow(s_noNA)

statstable5[8,2]  <- ((statstable5[7,2]/statstable5[4,2])*100)

statstable5[9,2]  <- nrow(i)-nrow(i_noNA)

statstable5[10,2]  <- ((statstable5[9,2]/statstable5[5,2])*100)

statstable5[11,2]  <- nrow(d)-nrow(d_noNA)

statstable5[12,2]  <- ((statstable5[11,2]/statstable5[6,2])*100)

statstable5$value5 <- round(statstable5$value5, digits = 2)


write.table(statstable5,file="OM5_additional_Stats_SK1.txt", row.names=F, quote=F, sep='\t')


##seperate for statistical purposes###


dfc$b1<- ifelse(dfc$b1 == "KP", 0, ifelse(dfc$b1 == "CP", 1, NA))

dfc$b2<- ifelse(dfc$b2 == "KP", 0, ifelse(dfc$b2 == "CP", 1, NA))

dfc$b3<- ifelse(dfc$b3 == "KP", 0, ifelse(dfc$b3 == "CP", 1, NA))
```

```r
dfc$b4<- ifelse(dfc$b4 == "KP", 0, ifelse(dfc$b4 == "CP", 1, NA))

dfc$b5<- ifelse(dfc$b5 == "KP", 0, ifelse(dfc$b5 == "CP", 1, NA))

dfc$b6<- ifelse(dfc$b6 == "KP", 0, ifelse(dfc$b6 == "CP", 1, NA))

dfc$b7<- ifelse(dfc$b7 == "KP", 0, ifelse(dfc$b7 == "CP", 1, NA))

dfc$b8<- ifelse(dfc$b8 == "KP", 0, ifelse(dfc$b8 == "CP", 1, NA))


dfc<- subset(dfc, select = c(chr, pos_c, type_k,
c1,c2,c3,c4,c5,c6,c7,c8,k1,k2,k3,k4,k5,k6,k7,k8,b1,b2,b3,b4,b5,b6,b7,b8))


##work out how many rows contain at least one NA, and so will be discarded later##

statistic5 <- c('Total_Rows', 'Removed_Rows', 'Percent_Removed_Rows', 'S_total', 'I_total', 'D_total',
'Removed_S', 'Percent_Removed_S', 'Removed_I', 'Percent_Removed_I', 'Removed_D',
'Percent_Removed_D')

value5 <- c(0,0,0,0,0,0,0,0,0,0,0,0)

statstable5 <- data.frame(statistic5, value5)


#Work out some stats about the number of rows containing at least one NA (which will be
discarded)

df_noNA <- dfc[complete.cases(dfc),]

statstable5[1,2] <- nrow(dfc)

statstable5[2,2] <- (nrow(dfc) - nrow(df_noNA))

statstable5[3,2] <- (statstable5[2,2]/statstable5[1,2])*100

s <- dfc[which(dfc$type_k=='s'),]

i <- dfc[which(dfc$type_k=='i'),]

d <- dfc[which(dfc$type_k=='d'),]

s_noNA <- df_noNA[which(df_noNA$type_k=='s'),]

i_noNA <- df_noNA[which(df_noNA$type_k=='i'),]

d_noNA <- df_noNA[which(df_noNA$type_k=='d'),]

statstable5[4,2]  <- nrow(s)

statstable5[5,2]  <- nrow(i)

statstable5[6,2]  <- nrow(d)

statstable5[7,2]  <- nrow(s)-nrow(s_noNA)
```

```
statstable5[8,2]  <- ((statstable5[7,2]/statstable5[4,2])*100)

statstable5[9,2]  <- nrow(i)-nrow(i_noNA)

statstable5[10,2]  <- ((statstable5[9,2]/statstable5[5,2])*100)

statstable5[11,2]  <- nrow(d)-nrow(d_noNA)

statstable5[12,2]  <- ((statstable5[11,2]/statstable5[6,2])*100)

statstable5$value5 <- round(statstable5$value5, digits = 2)


write.table(statstable5,file="OM5_additional_Stats_S288c.txt", row.names=F, quote=F, sep='\t')
```

```
###############################################################################
##############
##Sorting events##
#This automatically categorizes events based on a few criteria.
#The categorized events can then be manually inspected to ensure consistency.
#It also calculates Spo11 hits per event.
#This script was adapted from scripts written by Marie-Claude Marsolier and Matt Neale.
###############################################################################
##############


event_sorter <- function(b, u, filename){
  #b: event table from event caller script
  #u: event table with U events (unclassified)


  b$nb_seg <- 0
  b$groupe <- 0


  #split file into three groups: sortable NCOs, sortable COs, anything else


  #COs to sort - consider only the CO events with 2 non-sister chromatids.
  b1<-b[which(b$CO==1 & b$chromatids=="2_nonsis"),]
```

#NCOs to sort - consider only the non-CO events with 1 chromatid or 2 non-sister chromatids

b2<-b[which(b$CO==0 & (b$chromatids=="1" | b$chromatids=="2_nonsis")),]

#remove sortable entries from original list

b3 <- b[which(b$CO>1),] #more than 1 CO

if(nrow(b3)>0){b3$classe <-3}

b4 <- b[which(b$CO==1 & b$chromatids!="2_nonsis"),]

if(nrow(b4)>0){b4$classe <-2}

b5 <- b[which(b$CO==0 & (b$chromatids=="2_sis" | b$chromatids=="3"| b$chromatids=="4")),]

if(nrow(b5)>0){b5$classe <-1}

b6 <- u[which(u$CO=="U"),]

if(nrow(b6)>0){

  b6$groupe <-0

  b6$seg_len <-0

  b6$seg_start <-0

  b6$seg_stop <-0

  b6$nb_seg <-0

  b6$classe <-4

  b6 <-b6[c("id","chr", "start5", "start3","stop5", "stop3", "type","CO", "chromatids", "len_min","len_mid", "len_max",

      "commande", "groupe", "seg_len","seg_start", "seg_stop", "nb_seg","classe", "nb_snp")]

  #To keep 'U' events from at the end of the chromosomes, use the information from the old event caller

  #and match the format of the file from the new event caller

 }

###(Run CO and NCO sorters)###

We call trans hDNA the segments 5:3 and 5:3a or the segments 3:5 and 3:5a belonging to a given event.

We call "incompatible events" the events containing both (5:3 or 6:2 segments) and (3:5 or 2:6 segments).

```
##CO Sorter##

# We make 3 groups :

# - group 1 = the events without trans hDNA nor incompatibility,

# - group 2 = the events with trans hDNA but without incompatibility,

# - group 3 = the incompatible events.


for (i in 1:length(b1$type)){
  s<-as.character(b1$type[i])
  b1$groupe[i]<-ifelse(length(grep("[5 6]:",s))*length(grep("[2 3]:",s)) > 0,3,
              ifelse(length(grep("[5:3 3:5]a",s))==1,2,1))
}


# Inside each group, we classify the events into different classes :
for (i in 1:length(b1$type)){
  s<-as.character(b1$type[i])
  len<-strsplit(s,"_")
  b1$nb_seg[i]<-length(len[[1]])


  if (b1$groupe[i]==1){
    b1$classe[i]<-ifelse(s=="(4:4aCO)",100,
              ifelse(s=="(5:3)_(4:4aCO)",1,
                ifelse(s=="(3:5)_(4:4aCO)",2,
                  ifelse(s=="(5:3)_(4:4)_(4:4aCO)",3,
                    ifelse(s=="(4:4aCO)_(5:3)_(4:4a)",4,
                      ifelse(s=="(3:5)_(4:4)_(4:4aCO)",5,
                        ifelse(s=="(4:4aCO)_(3:5)_(4:4a)",6,

                          ifelse(s=="(5:3)_(6:2)_(4:4aCO)",7,
                            ifelse(s=="(6:2)_(5:3)_(4:4aCO)",8,
                              ifelse(s=="(3:5)_(2:6)_(4:4aCO)",9,
```

```
                              ifelse(s=="(2:6)_(3:5)_(4:4aCO)",10,

                                      ifelse(length(grep("4:4.i",s))==1,11,


                                      ifelse(s=="(6:2)_(4:4aCO)",15,

ifelse(s=="(2:6)_(4:4aCO)",16,12)))))))))))))))}


  if (b1$groupe[i]==3){
    b1$classe[i]<-ifelse(length(grep("4:4.i",s))==1,21,20)}


  if (b1$groupe[i]==2){
    b1$classe[i]<-ifelse(length(grep("5:3\\)_\\(5:3a",s))==1,30,
                  ifelse(length(grep("3:5\\)_\\(3:5a",s))==1,31,32))}
}


# The b file is then ordered by 1) class, 2) nb of segments and 3) len_mid.


b1<-b1[order(b1$groupe, b1$classe,b1$nb_seg,b1$len_mid),]


####NCO sorter####
# We consider only the non-CO events with 1 chromatid or 2 non-sister chromatids
# Elimination of ( 4: 4) final and parentheses.


b2$type<-gsub("_\\(4:4\\)$","",b2$type)
b2$type<-gsub("\\(","",b2$type)
b2$type<-gsub("\\)","",b2$type)


 # We call trans hDNA the segments 5:3 and 5:3a or the segments 3:5 and 3:5a belonging to a given
event.


 # We make 3 groups :
 # - group 1 with chromatids=="1" but without TRANS hDNA,
```

```
# - group 2 with chromatids=="1" and with TRANS hDNA,

# - group 3 with chromatids = "2_nonsis".


for (i in 1:length(b2$type)){
 s<-as.character(b2$type[i])
 len<-strsplit(s,"_")
 b2$nb_seg[i]<-length(len[[1]])
 b2$groupe[i]<-ifelse(b2$chromatids[i]=="2_nonsis",3,
            ifelse(length(grep("[5:3 3:5]a",s))==1,2,1))}


# Inside each group, we classify the events into different classes :


for (i in 1:length(b2$type)){
 s<-as.character(b2$type[i])


 if (b2$groupe[i]==1){
  b2$classe[i]<-ifelse(s=="5:3",1,

             ifelse(s=="3:5",2,
                ifelse(length(grep("^5:3",s))*length(grep("5:3$",s))==1,3,
                   ifelse(length(grep("^3:5",s))*length(grep("3:5$",s))==1,4,
                      ifelse(s=="6:2",10,
                         ifelse(s=="2:6",10.1,
                            ifelse(length(grep("6:2",s))==1,7,
                               ifelse(length(grep("2:6",s))==1,8,9)))))))))}


 if (b2$groupe[i]==2) {
  b2$classe[i]<-ifelse(s=="5:3_5:3a",11,
             ifelse(s=="3:5_3:5a",12,
                ifelse(length(grep("5:3_5:3a",s))==1,13,
                   ifelse(length(grep("3:5_3:5a",s))==1,14,
```

```r
                              ifelse(s=="5:3_4:4_5:3a",15,

                                   ifelse(s=="3:5_4:4_3:5a",16,

                                        ifelse(length(grep("5:3_4:4_5:3a",s))==1,17,

                                             ifelse(length(grep("3:5_4:4_3:5a",s))==1,18,

                                                  ifelse(s=="5:3_6:2_5:3a",19,

                                                       ifelse(s=="3:5_2:6_3:5a",20,

                                                            ifelse(length(grep("5:3_6:2_5:3a",s))==1,21,

ifelse(length(grep("3:5_2:6_3:5a",s))==1,22,23)))))))))))}


  if (b2$groupe[i]==3) {

    b2$classe[i]<-ifelse(length(grep("4:4.i",s))==1,31,30)}


 }


# The b file is then ordered by 1) class, 2) nb of segments and 3) len_mid.


b2<-b2[order(b2$groupe, b2$classe,b2$nb_seg,b2$len_mid),]


####Continue####


b7 <- rbind(b2, b1, b5, b4, b3, b6) #adding the sets back together


#b2: sortable NCOs

#b5: unsortable NCOs (2_sis)

#b1: sortable COs

#b4: unsortable COs (3 and 4 chromatids)

#b3: Unsortable COs (multiple COs)

 #b6: Class U events - at end of chromosome, never return to 4:4 so impossible to know if they are
CO or NCO


    ##########################################################
```

```r
# Calculate Spo11 hits per event here and add column

#Loop through events and calculate Pan HpM for each event, then add to table b6$PanHpM.

Pan <- read.delim("FullMap.Cer3_Pan_HA_1_4h_c.txt")

TotalHits=sum(Pan$Watson+Pan$Crick)

Pan$TotalHpM=(Pan$Watson+Pan$Crick)/TotalHits*1000000 # Convert Pan data to Hits per million reads (HpM)


for (i in 1:nrow(b7)){

  Pan.1=subset(Pan, Chr==b7[i,"chr"] & Pos>=b7[i,"start5"] & Pos <=b7[i,"stop3"])

  b7[i,"PanHpM"]=sum(Pan.1$TotalHpM)

}


b7$PanHpM=round(b7$PanHpM,2) # Round PanHpM output to 2 decimals


# Now some extra bits:

b7$GenomeHpM=round(1/12.01*b7$len_max,2) # What is the expected HpM for an interval this size (assuming uniform Spo11-oligo hits across the 12.01 Mbp genome)?

b7$Obs_Exp_HpM=round(b7$PanHpM/b7$GenomeHpM,2) # What is the fold difference between observed and expected association with Spo11 hits for each event?

b7$GenomeHpM=round(1/12.01*b7$len_max,0) #round to nearest whole number before plotting

#############################################################


##Auto-classification##

##Suggested values only: Adjust manually during visual inspection##


b7$Notes <- "" #blank space to write in any notes during inspection


#min and max number of breaks necessary to explain the event. note: the breaks are not necessarily formed by Spo11.

b7$CutMin <-ifelse(b7$CO==1 & b7$groupe==3, 2, #COs with incompatible hDNA

        ifelse(b7$groupe==0 & (b7$classe==1 | b7$classe==2 | b7$classe==3), 2, #NCO 2sis, CO 3/4 chromatids, multiple COs

            1))
```

```r
b7$CutMax <-ifelse(b7$CO ==0 & b7$groupe==3,2, #NCOs with incompatible hDNA

          ifelse(b7$CO==1 & (b7$classe==15 | b7$classe==16 |b7$groupe==3), 2, #COs with gap
(could be double cut), and COs with incompatible hDNA

              ifelse(b7$groupe==0 & (b7$chromatids=="2_sis" | b7$chromatids==3)
&(b7$classe==1 | b7$classe==2), 2, #NCO 2_sis and CO with 3 chromatids

                  ifelse(b7$groupe==0 & b7$chromatids==4 & b7$classe==2, 3, #Co with 4
chromatids

                      ifelse(b7$groupe==0 & b7$classe==3, 2, #multiple COs on 2/3/4 chromatids

                          1)))))


  #Likely Spo11 Breaks: if there are multiple breaks, how many are likely to be caused by Spo11? i.e.
how many hit an additional chromo?

  b7$LSB <-ifelse(b7$groupe==0 & (b7$classe==1 | b7$classe==2), 2, #NCO 2_sis, CO with 3 or 4
chromatids, multiple COs

          ifelse(b7$groupe==0 & b7$classe==3 & b7$chromatids=="2_nonsis", 1,

              ifelse(b7$groupe==0 & b7$classe==3 & (b7$chromatids=="2_sis" | b7$chromatids==3
| b7$chromatids==4), 2, #multiple COs on 3 or 4 chromatids

                  1)))



  write.table(b7,file=sprintf("%s",filename), col.names =TRUE, row.names = FALSE, quote = FALSE,
sep="\t")



}


######################################################################
#Event Table and gr2 file Combiner
#Event and gr2 tables are combined into master tables for analysis and imaging
#This script is adapted from a script authored by Matt Neale.
######################################################################


# Create new empty master dataframe
```

```r
master=NULL

library(stringr)

# Sequentially imports each Event Table and combines into a Master Table
#with additional identified columns for Meiosis, Threshold, Genotype and GenotypeID (e.g. OM2,
1500, OM, 2)
files = list.files(pattern="SEvents_") # import files names with "SEvents_" string into variable "files"
files1 = length(files) # Count number of files
files2 = read.table(text = files, sep = "_", as.is = TRUE) #Split file names by "_" separator and create
table "files2"

for (j in 1:files1) {
 data=NULL
 data <- read.table(files[j], sep = "\t", header=TRUE) #Import datatable from files number 1 to j
 data["Meiosis"]=files2[j,2] # Insert Meiosis identifier from files2 into a new column
 data["threshold"]=files2[j,3] # Insert threshold value from files2 into a new column
 data["Genotype"]=gsub('([A-Z]+).*','\\1',files2[j,2]) # Extracts character portion of string
 data["GenotypeID"]=gsub('.*([0-9]+)','\\1',files2[j,2]) # Extracts digit portion of string
 data["midpoint"]=(data$start5+data$start3+data$stop5+data$stop3)/4 # Add midpoint column
 data["debut"]=(data$midpoint-(0.5*data$len_mid)) # Add event start column
 data["fin"]=(data$midpoint+(0.5*data$len_mid)) # Add event end column
 master <- rbind(master, data) # Combine data into master table

}

# Reorder columns
master=master[c("id","Meiosis","threshold","Genotype","GenotypeID","chr","start5",
        "start3","stop5","stop3","midpoint","debut","fin","type","CO",
        "chromatids","len_min","len_mid","len_max", "nb_seg", "seg_len",
        "seg_start",    "seg_stop", "PanHpM", "GenomeHpM","Obs_Exp_HpM",
        "nb_snp", "groupe", "classe", "Notes","CutMin", "CutMax", "LSB",  "commande")]
```

```
#Write out master files

wd = getwd()

out = paste(wd,"/","Output_Files","/","MasterEventTable_", Sys.time(),sep="")

write.table(master, out, col.names =TRUE, row.names = FALSE, quote = FALSE, sep="\t",
append=TRUE)


#####################


# Create new empty master dataframe

masterGR=NULL

require(stringr)


# Sequentially imports each gr2 Table and combines into a Master Table with additional identified
columns
#for Meiosis, Threshold, Genotype and GenotypeID (e.g. OM2, 1500, OM, 2)

filesGR = list.files(pattern="_gr2_") # import files names with "_gr2_" string into variable "files"

filesGR1 = length(filesGR) # Count number of files

filesGR2 = read.table(text = filesGR, sep = "_", as.is = TRUE) #Split file names by "_" separator and
create table "files2"


for (j in 1:filesGR1)


{data <- read.table(filesGR[j], sep = "\t", header=TRUE, stringsAsFactors=FALSE) #Import datatable
from files number 1 to j

data["Meiosis"]=filesGR2[j,1] # Insert Meiosis identifier from filesGR2 into a new column

data["Genotype"]=gsub('([A-Z]+).*','\\1',filesGR2[j,1]) # Extracts character portion of string

data["GenotypeID"]=gsub('.*([0-9]+)','\\1',filesGR2[j,1]) # Extracts digit portion of string

masterGR <- rbind(masterGR, data) # Combine data into masterGR table

}


############################
```

Create deriviative masterGR_noNA table that removes any line containing an NA call in the binary columns.

Removes positions with read depth that was too low to make a call.

This allows haplotype calls to be contiguous across such positions (rather than having gaps when drawn).


```
masterGR_noNA=na.omit(masterGR)

rownames(masterGR_noNA)=NULL
```


###############################

Add inter-SNP interval start and stop locations

```
masterGR_noNA[,"offset+1"]=masterGR_noNA[c(2:nrow(masterGR_noNA),NA),"pos_c"]

masterGR_noNA[,"offset-1"]=masterGR_noNA[c(NA,1:nrow(masterGR_noNA)-1),"pos_c"]


masterGR_noNA[,"startdif"]=(((masterGR_noNA[,"pos_c"]-masterGR_noNA[,"offset-1"])/2)+abs((masterGR_noNA[,"pos_c"]-masterGR_noNA[,"offset-1"])/2))/2 # Adding together real and absolute values and dividing by 2 creates zeros for negative values

masterGR_noNA[,"stopdif"]=(((masterGR_noNA[,"offset+1"]-masterGR_noNA[,"pos_c"])/2)+abs((masterGR_noNA[,"offset+1"]-masterGR_noNA[,"pos_c"])/2))/2 # Adding together real and absolute values and dividing by 2 creates zeros for negative values

masterGR_noNA[,"startdif"][masterGR_noNA[,"startdif"] == 0] <- NA # Syntax to convert all zeros to NA

masterGR_noNA[,"stopdif"][masterGR_noNA[,"stopdif"] == 0] <- NA # Syntax to convert all zeros to NA


masterGR_noNA[,"startSNP"]=masterGR_noNA[,"startdif"]+masterGR_noNA[,"offset-1"] # Calculate startSNP

masterGR_noNA[,"stopSNP"]=masterGR_noNA[,"stopdif"]+masterGR_noNA[,"pos_c"] # Calculate stopSNP
```


###############################

Add inter-SNP interval start and stop locations to masterGR table

```r
masterGR[,"offset+1"]=masterGR[c(2:nrow(masterGR),NA),"pos_c"]

masterGR[,"offset-1"]=masterGR[c(NA,1:nrow(masterGR)-1),"pos_c"]


masterGR[,"startdif"]=(((masterGR[,"pos_c"]-masterGR[,"offset-1"])/2)+abs((masterGR[,"pos_c"]-
masterGR[,"offset-1"])/2))/2 # Adding together real and absolute values and dividing by 2 creates
zeros for negative values

masterGR[,"stopdif"]=(((masterGR[,"offset+1"]-masterGR[,"pos_c"])/2)+abs((masterGR[,"offset+1"]-
masterGR[,"pos_c"])/2))/2 # Adding together real and absolute values and dividing by 2 creates
zeros for negative values

masterGR[,"startdif"][masterGR[,"startdif"] == 0] <- NA # Syntax to convert all zeros to NA

masterGR[,"stopdif"][masterGR[,"stopdif"] == 0] <- NA # Syntax to convert all zeros to NA


masterGR[,"startSNP"]=masterGR[,"startdif"]+masterGR[,"offset-1"] # Calculate startSNP

masterGR[,"stopSNP"]=masterGR[,"stopdif"]+masterGR[,"pos_c"] # Calculate stopSNP


#############################


#Write out masterGR and masterGR_noNA files


wd = getwd()

out = paste(wd,"/","Output_Files","/","MasterGRTable_", Sys.time(),sep="")

write.table(masterGR, out, col.names =TRUE, row.names = FALSE, quote = FALSE, sep="\t",
append=TRUE)


wd = getwd()

out = paste(wd,"/","Output_Files","/","MasterGRnoNATable_", Sys.time(),sep="")

write.table(masterGR_noNA, out, col.names =TRUE, row.names = FALSE, quote = FALSE, sep="\t",
append=TRUE)


#####################
```

```
############################################################################
##############
#Event_Imager
##Imaging events for manual inspection
#Plots variant positions above main graph
#plots indel locations and lengths. Triangle point down - deletion, triangle point up - insertion
(relative to S288c)
#Plots Spo11 profile, hotspot strength values, RMM profile, Rec8 peaks, genes.
#This script was adapted from scripts written by Marie-Claude Marsolier and Matt Neale.
############################################################################
##############


master$Meiosis <- as.character(master2$Meiosis)
masterGR$Var_len2 <- (masterGR$Var_len-1)
masterGR_noNA$Var_len2 <- (masterGR_noNA$Var_len-1)
#the variant lengths stored in this column are actually 1bp too long because they include the first
base upstream.
#Subtract 1 to make it more accurate.


#Opening files containing profiles for Spo11, hotspot, RMM, genes, Rec8
spo_file <- read.delim("FullMap.Cer3_Pan_HA_1_4h_c.txt")
smooth_spo_file <- read.delim("Spo11Cer3PanHA100bp.txt")
TotalHits=sum(spo_file$Watson+spo_file$Crick)
spo_file$TotalHits=(spo_file$Watson+spo_file$Crick)
spo_file$TotalHpM=(spo_file$Watson+spo_file$Crick)/TotalHits*1000000 # Convert Pan data to Hits
per million reads (HpM)
oldhotspots<- read.delim("Hotspot.Table.Cer3_Pan_HA_1_4h.txt")
hotspots<- read.delim("Pan.Hotspots.IGR.SacCer3_2016.08.10.txt")
rmm_file<-read.delim("RMMSubSamp_simple")
AllElementsDUB = read.table("AllElementsDUB.txt", sep = "\t", header=TRUE) #Import datatable
rec_file<-read.delim("Rec8Marg.txt")


hotspots$Total_HpM <-hotspots$HITS/TotalHits*1000000
```

```r
hotspots$Total_HpM=round(hotspots$Total_HpM,1)


# Subset the datatable

draw<-master2 # Temp holding table for events that will be drawn.


# Hash out and/or amend the following lines to subset the datatable as required

draw=subset(draw,threshold ==1500) # Threshold = 500,1500,5000 : Specifies which event calls to
view. Event painting is controlled by the next variable: "Mainoverlaythreshold"

mainoverlaythreshold=1500 # The variable that specifies the threshold to use for main event
painting/overlay

draw=subset(draw,Meiosis =="OM5" ) # Meiosis = OM2, OMT10, etc (refers to a specific meiosis)


######################


ordre=1:8 # Order of plotting spores

extend=5000 # How many bp to extend the plotting either side of the event


# Automated PDF generation

wd = getwd(); out = paste(wd,"/","Output_Files","/","Images_±",
extend,"bp_",Sys.time(),".pdf",sep=""); pdf(file=out, width=21,height=9);

# Replace funtion call with a loop that steps through the draw subtable


if(nrow(draw)==0){print("no lines in draw")}


if(nrow(draw)>0){
  for (j in 1: nrow(draw) ) {
    meiosis=draw[j,"Meiosis"]
    chromo=draw[j,"chr"]
    debut=draw[j,"debut"]
    fin=draw[j,"fin"]


    # How much to extend the plotting either side of the event
```

```
    debut=debut-extend

    fin=fin+extend


    # This sets up the graphing parameters: mfrow calculates number of rows of graphics to be drawn.
mar sets the margins of the graph

    layout(matrix(c(0,1,1,1,2:17,18,18,19,19,20,20,21,22,22,23,23,24,24,24,0),35, 1, byrow = T))

    par(mar=c(0,6,0,2),oma = c(4,0,0,0),las=1) # Sets margins per graph and outside margins per
grouped set


    # Subset the masterGR tables for the region of interest

    a<-subset(masterGR,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <= (fin))

    a1<-subset(masterGR_noNA,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <=
(fin))


    while (nrow(a1)<20){ # Check whether the region of interest contains sufficient SNPs to draw - this
is important to prevent an error when a/a1 contain no rows due to rare zero SNP events (i.e. COs)
that also lack SNPs in flanking thresholded region.

    debut=debut-1000

    fin=fin+1000

    a<-subset(masterGR,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <= (fin))

    a1<-subset(masterGR_noNA,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <=
(fin))

    }


  if(nrow(a)>0){


    # Subset master based on Meiosis and Chromosome being drawn

    e2=subset(master2, Meiosis==meiosis & chr == chromo)


    # Specify event colours based on type (CO or NCO) - fill in master table with this information

    for (i in 1:nrow(e2)){

      if(e2[i,"CO"]==1){e2[i,"eventcolour"]="wheat"}

      if(e2[i,"CO"]==0){e2[i,"eventcolour"]="thistle2"}
```

```r
    if(e2[i,"CO"]==2){e2[i,"eventcolour"]="wheat"}

    if(e2[i,"CO"]==3){e2[i,"eventcolour"]="wheat"}

    if(e2[i,"CO"]=="U"){e2[i,"eventcolour"]="powderblue"}

    }


    #Subset e2 based on threshold values so that each can be plotted

    e1000=subset(e2, Meiosis==meiosis & chr == chromo & threshold==1000)

    e1500=subset(e2, Meiosis==meiosis & chr == chromo & threshold==1500)

    e2000=subset(e2, Meiosis==meiosis & chr == chromo & threshold==2000)

    mainoverlay=subset(e2,Meiosis==meiosis & chr == chromo & threshold==mainoverlaythreshold)


    ######add SNP coordinates as text######

plot(a$pos_c,a[,1],type="n",ylim=c(0,300),ylab=paste("SNPs"),cex.lab=1,font=1,xlab="",xlim=c(debut
,fin), xaxt="n",yaxt="n", axes=FALSE, xaxs="i",yaxs="i")

    #type=n for no plotting. axes=FALSE gets rid of border.

    text(a$pos_c, y=100, labels = a$pos_c, srt=90, pos=3, cex=1)

    #cex=1 controls the size of the text; however, making it smaller doesn't really help with overlap

    arrows(a$pos_c,0,a$pos_c,50,col="black",length=0,lwd=1, code=3, lend=1)


    #####################################

    # Graphs of raw data

    for (i in (ordre+2)){

plot(a$pos_c,a[,i],type="l",lwd=2,col=2,cex.axis=0.8,ylim=c(0.6,300),yaxp=c(1,100,1),ylab=paste("S",i
-2,sep=""),cex.lab=1,font=1,xaxs="i",yaxs="i",xlab="",xlim=c(debut,fin), xaxt="n", log="y")

    points(a$pos_c,a[,i],pch=4,col=2,cex=2)

    points(a$pos_c,a[,(i+8)],pch=4,col=4,cex=2)

    lines(a$pos_c,a[,(i+8)],col=4,lwd=2)

    points(a$pos_c,rep(100,length(a$pos_c)),pch=-1*a[,(i+16)]+17,cex=1.5,col=-2*a[,(i+16)]+4)

    } #End of i first loop
```

```
# Graphs of binary data

position=c(85,95,85,95,85,95,85,95)

haut<-0

for (i in (ordre+2)){

    plot(a$pos_c,rep(100,length(a$pos_c)),xaxt="n",yaxt="n",type="n",ylab=paste("S",i-
2,sep=""),cex.lab=1,font=2,xaxs="i",yaxs="i",ylim=c(50,130),axes=FALSE,xlim=c(debut,fin))


    alt<-ifelse(haut==0,120,120)

    bas<-ifelse(haut==0,60,60)


arrows(mainoverlay$debut,90,mainoverlay$fin,90,col=mainoverlay$eventcolour,length=0,lwd=30,
lend=1) # Underlay a highlighting box across all event regions

    arrows(a$pos_c,position[i-2]-30,a$pos_c,position[i-2]+30,col=-2*a[,(i+16)]+4,length=0,lwd=1)

    arrows(a1$startSNP,position[i-2],a1$stopSNP,position[i-2],col=-
2*a1[,(i+16)]+4,length=0,lwd=15, lend=1) # Add SNP start/stop boundary overlays


    haut<-1-haut


    } #End of i second loop


    # Top <-1 Top toggles the lengths of the lines between top = 0 and top = 1


    # Addition of plots that indicate the events specified by 1000 and 2000bp event-calling
thresholds

plot(a$pos_c,rep(100,length(a$pos_c)),xaxt="n",yaxt="n",type="n",ylab=paste("Events"),cex.lab=1.2
5,font=2,xaxs="i",yaxs="i",ylim=c(0,165),axes=FALSE,xlim=c(debut,fin))

    arrows(e1000$debut,140,e1000$fin,140,col=e1000$eventcolour,length=0,lwd=12, code=3,
lend=1); text(debut,140, "1.0 kb merge",pos=4) # Underlay a highlighting box across all event regions

    arrows(e1500$debut,100,e1500$fin,100,col=e1500$eventcolour,length=0,lwd=12, code=3,
lend=1); text(debut,100, "1.5 kb merge",pos=4) # Underlay a highlighting box across all event regions

    arrows(e2000$debut,60,e2000$fin,60,col=e2000$eventcolour,length=0,lwd=12, code=3, lend=1);
text(debut,60, "2.0 kb merge",pos=4) # Underlay a highlighting box across all event regions
```

```
# Plot event midpoints

arrows(e1000$midpoint,130,e1000$midpoint,150,col="black",length=0,lwd=1, code=3, lend=1)

arrows(e1500$midpoint,90,e1500$midpoint,110,col="black",length=0,lwd=1, code=3, lend=1)

arrows(e2000$midpoint,50,e2000$midpoint,70,col="black",length=0,lwd=1, code=3, lend=1)


###################################################################

###plot indels as triangles with length underneath###

plot(a$pos_c,a[,1],type="n",ylim=c(0,300),ylab=paste("Indels"),cex.lab=1.25,font=2,xlab="",xlim=c(debut,fin), xaxt="n",yaxt="n", axes=FALSE, xaxs="i",yaxs="i")

#type=n for no plotting. axes=FALSE gets rid of border.

aDEL=subset(a, type_k=="d")

if(nrow(aDEL)>0){

  yDEL =rep(200, nrow(aDEL))

  points(aDEL$pos_c, yDEL, type = "p", pch=25, col="dimgrey", cex=2)

  text(aDEL$pos_c, (yDEL-145), labels = aDEL$Var_len2, pos=3, cex=1)

  }


aINS=subset(a, type_k=="i")

if(nrow(aINS)>0){

  yINS =rep(200, nrow(aINS))

  points(aINS$pos_c, yINS, type = "p", pch=24, col="dimgrey", cex=2)

  text(aINS$pos_c, (yINS-145), labels = aINS$Var_len2, pos=3, cex=1)

  }


###################################################################

rbPal <- colorRampPalette(c('black','blue','red','pink')) # Creates a colour palette if chosing to plot Spo11 as a coloured histogram "h"

spo_file$Col <- rbPal(10)[as.numeric(cut(spo_file$TotalHits,breaks = 10))]


map<-subset(spo_file,Chr == chromo & debut <= Pos & Pos <= fin)

map2<-subset(rmm_file,chr == chromo & debut <= pos & pos <= fin)
```

```r
    map5<-subset(hotspots,CHROM == chromo & debut <= HS_START & HS_END <= fin)

    map6<-subset(rec_file,Chr == chromo & debut <= Position & Position <= fin)

    map7<-subset(smooth_spo_file,chr == chromo & debut <= pos & pos <= fin)


plot(map7$pos,map7$spo,type="l",xlim=c(debut,fin),ylim=c(10,max(map7$spo)),yaxp=c(100,round(
max(map7$spo),-2),2),ylab="Spo11",bty="u",xaxs="i",lwd=2,xaxt="n",cex.axis=0.9,cex.lab=1.25)


plot(map5$midpoint,map5$Total_HpM,type="n",ylim=c(0,300),ylab="",cex.lab=1.25,font=2,xlab="",
xlim=c(debut,fin), xaxt="n",yaxt="n", axes=FALSE, xaxs="i",yaxs="i")

    #type=n for no plotting. axes=FALSE gets rid of border.

    if(nrow(map5)>0){

      arrows(map5$HS_START,140,map5$HS_END,140,col='lightsteelblue',length=0,lwd=12, code=3,
lend=1); text="" # Underlay a highlighting box across all event regions

      text(map5$midpoint, y=0, labels = map5$Total_HpM, pos=3, cex=1)

    }


#############################################################################
#########################################################################

    #Now plot the gene datatrack

    #First subset the relevant data

    genes=AllElementsDUB #First make a copy of the ALLElements table

    genes=subset(genes,chr==chromo & start>(debut-10000) & stop<(fin+10000)) #Make a sub-table
of ALLElements where chr = 1 and has limits just beyond plot range

    genes=subset(genes,type=="gene") #Make a sub-table of ALLElements

    #Now perform the plot

    plot(genes$start,genes$start, xaxt="n",yaxt="n",type="n",
ylab=paste("Genes"),cex.lab=1.5,font=2, xlim=c(debut,fin), ylim=c(0,120),axes=FALSE) #set up empty
plot

    # Following module draws arrows for each element

    xrange=fin-debut

    ahead=xrange/25 #make arrowhead length proportional to plot range
```

```r
ahead[(ahead>500)]=500 #limit max length to 500

av=75 #arrow vertical location relative to plot dimensions

ahw=15 #arrow/head width


genesW=subset(genes,genename !="Dubious_ORF" & orientation =="+") #Make a sub-table of ALLElements

if(nrow(genesW)>0){

  for (i in 1:nrow(genesW)){

    polygon(c(genesW[i,"start"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-ahead,genesW[i,"stop"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-ahead, genesW[i,"start"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw), col="palegreen", border="palegreen4")

    text((genesW[i,"start"]+genesW[i,"stop"])/2,av, font=3, genesW[i,"genename"], cex=0.9) }

  }


genesW=subset(genes,genename=="Dubious_ORF" & orientation =="+") #Make a sub-table of ALLElements

if(nrow(genesW)>0){

  for (i in 1:nrow(genesW)){

    polygon(c(genesW[i,"start"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-ahead,genesW[i,"stop"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-ahead, genesW[i,"start"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw), col="palegreen", border="palegreen4", lty=2)

    text((genesW[i,"start"]+genesW[i,"stop"])/2,av, font=3, genesW[i,"sysname"], cex=0.9) }

  }


av=25 #arrow vertical location for Crick genes relative to plot dimensions

genesC=subset(genes,genename !="Dubious_ORF" & orientation =="-") #Make a sub-table of ALLElements

if(nrow(genesC)>0){

  for (i in 1:nrow(genesC)){

    polygon(c(genesC[i,"stop"], genesC[i,"start"]+ahead, genesC[i,"start"]+ahead,genesC[i,"start"], genesC[i,"start"]+ahead, genesC[i,"start"]+ahead, genesC[i,"stop"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw), col="lightpink", border ="lightpink4")
```

```
      text((genesC[i,"start"]+genesC[i,"stop"])/2,av, font=3, genesC[i,"genename"], cex=0.9) }

    }


    genesC=subset(genes,genename=="Dubious_ORF" & orientation =="-") #Make a sub-table of
ALLElements

    if(nrow(genesC)>0){

     for (i in 1:nrow(genesC)){

       polygon(c(genesC[i,"stop"], genesC[i,"start"]+ahead, genesC[i,"start"]+ahead,genesC[i,"start"],
genesC[i,"start"]+ahead, genesC[i,"start"]+ahead,
genesC[i,"stop"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw), col="lightpink",
border ="lightpink4", lty=2)

       text((genesC[i,"start"]+genesC[i,"stop"])/2,av, font=3, genesC[i,"sysname"], cex=0.9) }

    }

    ####Plot RMM track###


plot(map2$pos,map2$rmm,type="l",xlim=c(debut,fin),ylim=c(1,max(map2$rmm)),yaxp=c(1,round(m
ax(map2$rmm),0),2),ylab="RMM",bty="u",xaxs="i",lwd=4,col='darkgoldenrod',

      xaxp=c((round(debut,-3)),(round(fin,-3)),(round(round(fin,-3)-round(debut,-3)) /
500)),cex.axis=0.9, cex.lab=1.25)

    if(nrow(map6)>0){

     arrows(map6$Position,0,map6$Position,50,col="black",length=0,lwd=1, code=3, lend=1)

    }

    ###Make figure legend###

    title(xlab = paste(sep="","Red=S288c, Blue=SK1",

            "\n",

            meiosis, "  Id=", draw[j,"id"],

            "  Chromosome=",chromo,

            "  Threshold=", draw[j,"threshold"], " bp",

            "  Mid Length=", draw[j,"len_mid"]," bp",

            "\n",

            "  Group=", draw[j,"groupe"],

            "  Class=", draw[j,"classe"],

            "  No. of COs=", draw[j,"CO"],
```

```
                    "   Variants=", draw[j,"nb_snp"],

                    "   Spo11 HpM=", draw[j,"PanHpM"],

                    "   Type=", draw[j,"type"]),


            outer = T, line = 2, cex.lab=1.4) # Cex.lab controls the labelling size

    }

  } #End of j loop

}

dev.off()
```

###
#####################

#After manual annotation, events identified as clusters can be split into the constituent events

#This script was adapted from a script written by Matt Neale.

###
#####################


```
# Create new empty master dataframe

masterA=NULL


library(stringr)

#library(data.table)


# Sequentially imports each Event Table and combines into a Master Table with additional identified
columns for Meiosis, Threshold, Genotype and GenotypeID (e.g. OM2, 1500, OM, 2)

files = list.files(pattern="Aevents_") # import files names with "AEvents_" string into variable "files"

files1 = length(files) # Count number of files

files2 = read.table(text = files, sep = "_", as.is = TRUE) #Split file names by "_" separator and create
table "files2"


for (j in 1:files1) {

  data=NULL
```

```r
  data <- read.table(files[j], sep = "\t", header=TRUE)

  #data <- fread(files[j],select = c(1:27), sep = "\t", header=TRUE) #Import datatable from files
  number 1 to j. Read only 27 columns

  data <- data[,c(1:27)]

  data["Meiosis"]=files2[j,2] # Insert Meiosis identifier from files2 into a new column

  data["threshold"]=str_extract(files2[j,3],"[[:digit:]]+") # Extracts digit portion of string

  #data["Genotype"]=str_extract(data[j,"Meiosis"],"[A-z]+") # Extracts character portion of string

  #data["GenotypeID"]=str_extract(data[j,"Meiosis"],"[[:digit:]]+") # Extracts digit portion of string

  data["Genotype"]=gsub('([A-Z]+).*','\\1',files2[j,2])

  data["GenotypeID"]=gsub('.*([0-9]+)','\\1',files2[j,2])

  data["midpoint"]=(data$start5+data$start3+data$stop5+data$stop3)/4 # Add midpoint column

  data["debut"]=(data$midpoint-(0.5*data$len_mid)) # Add event start column

  data["fin"]=(data$midpoint+(0.5*data$len_mid)) # Add event end column

  masterA <- rbind(masterA, data) # Combine data into master table


}


#Remove mitotic or false events
masterA <- masterA[which(masterA$LSB!=0),]
masterA <- masterA[which(masterA$threshold==1500),]


masterA$CO[masterA$CO == "U"] <- NA
masterA$CO <- as.numeric(as.character(masterA$CO))


masterA$LCO <- masterA$CO
masterA$LNCO <- (masterA$LSB-masterA$CO)
masterA$MaxNCO <- (masterA$CutMax-masterA$CO)
masterA$MinNCO <- (masterA$CutMin-masterA$CO)


masterA$midpoint1 <- 0
masterA$midpoint2 <- 0
```

```
masterA$midpoint3 <- 0


masterA$midpoint1 <-ifelse(masterA$LSB ==2, masterA$midpoint-(masterA$len_mid/4),

        ifelse(masterA$LSB ==3, masterA$midpoint-(masterA$len_mid/3),

            masterA$midpoint))


masterA$midpoint2 <-ifelse(masterA$LSB ==2, masterA$midpoint+(masterA$len_mid/4),

        ifelse(masterA$LSB ==3, masterA$midpoint,

            NA))


masterA$midpoint3 <-ifelse(masterA$LSB ==3, masterA$midpoint+(masterA$len_mid/3),

            NA)


# Reorder columns

masterA=masterA[c("id","Meiosis","threshold","Genotype","GenotypeID","chr","start5",

        "start3","stop5","stop3","debut","fin","type",

        "chromatids","len_min","len_mid","len_max", "nb_seg", "seg_len",

        "seg_start",   "seg_stop", "PanHpM", "GenomeHpM","Obs_Exp_HpM",

        "nb_snp", "groupe", "classe", "LSB", "LCO", "LNCO",

        "CutMin", "CutMax", "MaxNCO", "MinNCO", "midpoint", "midpoint1", "midpoint2",
"midpoint3",

        "commande", "Notes")]


#Write out master files

wd = getwd()

out = paste(wd,"/","Output_Files","/","MasterAEventTable_", Sys.time(),sep="")

write.table(masterA, out, col.names =TRUE, row.names = FALSE, quote = FALSE, sep="\t",
append=TRUE)


masterA$MId <-0 #set a master ID for each event

for(i in 1:nrow(masterA)){ masterA[i,41] <- i }
```

```r
masterB <- masterA

masterB <- masterB[rep(seq.int(1,nrow(masterB)), masterB$LSB),] #duplicate lines for cluster events


masterB$CO_NCO <- "U"

masterC <- NULL


for(i in 1:nrow(masterA)){
  subset <- masterB[which(masterB$MId==i),] #take all rows belonging to an event region i.e. if its a cluster of 3 events, take those 3 rows
  for(j in 1:nrow(subset)){ #for each row of the subset,
    subsubset <- subset[j,] #just look at that row,
    if(is.na(subsubset$LCO) ==FALSE){ #if there isn't an NA in LCO (which is the case for U events),
      if(j==1 && subsubset$LSB==1 && subsubset$LCO ==0){ #if there is likely 1 break and no COs, the type is NCO
        subsubset$CO_NCO ="NCO"
        subsubset$midpoint = subsubset$midpoint1
        masterC = rbind(masterC,subsubset)} #bind the line into masterC
      if(j==1 && subsubset$LSB==1 && subsubset$LCO ==1){ #if there is likely 1 break and 1 CO, the type is CO
        subsubset$CO_NCO ="CO"
        subsubset$midpoint = subsubset$midpoint1
        masterC = rbind(masterC,subsubset)}
      if(j==1 && subsubset$LSB==2 && subsubset$LCO ==0){ #if these are 2 breaks and no COs, type is NCO (first row)
        subsubset$CO_NCO ="NCO"
        subsubset$midpoint = subsubset$midpoint1
        masterC = rbind(masterC,subsubset)}
      if(j==2 && subsubset$LSB==2 && subsubset$LCO ==0){ #if these are 2 breaks and no COs, type is NCO (second row)
        subsubset$CO_NCO ="NCO"
        subsubset$midpoint = subsubset$midpoint2
        masterC = rbind(masterC,subsubset)}
```

```r
    if(j==1 && subsubset$LSB==2 && subsubset$LCO ==1){  #if these are 2 breaks and one CO, type is
CO (first row)

    subsubset$CO_NCO ="CO"

    subsubset$midpoint = subsubset$midpoint1

    masterC = rbind(masterC,subsubset)}

    if(j==2 && subsubset$LSB==2 && subsubset$LCO ==1){ #if these are 2 breaks and one NCO, type
is NCO (second row)

    subsubset$CO_NCO ="NCO"

    subsubset$midpoint = subsubset$midpoint2

    masterC = rbind(masterC,subsubset)}

    if(j==1 && subsubset$LSB==2 && subsubset$LCO ==2){#if these are 2 breaks and two COs, type is
CO (first row)

    subsubset$CO_NCO ="CO"

    subsubset$midpoint = subsubset$midpoint1

    masterC = rbind(masterC,subsubset)}

    if(j==2 && subsubset$LSB==2 && subsubset$LCO ==2){ #if these are 2 breaks and two COs, type
is CO (second row)

    subsubset$CO_NCO ="CO"

    subsubset$midpoint = subsubset$midpoint2

    masterC = rbind(masterC,subsubset)}

    if(j==1 && subsubset$LSB==3 && subsubset$LCO ==3){  #if these are 3 breaks and 3 COs, type is
CO (first row)

    subsubset$CO_NCO ="CO"

    subsubset$midpoint = subsubset$midpoint1

    masterC = rbind(masterC,subsubset)}

    if(j==2 && subsubset$LSB==3 && subsubset$LCO ==3){ #if these are 3 breaks and 3 COs, type is
CO (second row)

    subsubset$CO_NCO ="CO"

    subsubset$midpoint = subsubset$midpoint2

    masterC = rbind(masterC,subsubset)}

    if(j==3 && subsubset$LSB==3 && subsubset$LCO ==3){  #if these are 3 breaks and 3 COs, type is
CO (third row)

    subsubset$CO_NCO ="CO"
```

```
    subsubset$midpoint = subsubset$midpoint3
    masterC = rbind(masterC,subsubset)}
  }
  if(is.na(subsubset$LCO) ==TRUE) { #if the event is a U event
    subsubset$midpoint = subsubset$midpoint1
    masterC = rbind(masterC,subsubset)
  }


 }
}


# Reorder columns
masterC=masterC[c("id","Meiosis","threshold","Genotype","GenotypeID","chr","start5",
          "start3","stop5","stop3","debut","fin","type",
          "chromatids","len_min","len_mid","len_max", "nb_seg", "seg_len",
          "seg_start",   "seg_stop", "PanHpM", "GenomeHpM","Obs_Exp_HpM",
          "nb_snp", "groupe", "classe", "LSB", "midpoint", "MId", "CO_NCO",
          "commande", "Notes")]


#Write out master files
wd = getwd()
out = paste(wd,"/","Output_Files","/","SplitMasterAEventTable_", Sys.time(),sep="")
write.table(masterC, out, col.names =TRUE, row.names = FALSE, quote = FALSE, sep="\t",
append=TRUE)




#############################################################################
#########
#Detection and imaging of 'hDNA' tracts in octads and MSH2 tetrads
#Thought to actually represent novel duplications.
#Parts of this script were adapted from scripts written by Matt Neale and Marie-Claude Marsolier.
```

###

##PART 1. Remove common hDNA positions, which likely represent naturally duplicated regions of the genome##

###

#Make Master hDNA table#

Create new empty master dataframe

masterH=NULL

library(stringr)

Sequentially imports each and combines into a Master Table with additional identified oclumns for Meiosis, Threshold, Genotype and GenotypeID (e.g. OM2, 1500, OM, 2)

files = list.files(pattern="HP-list") # import files names with "HP-list" string into variable "files"

files1 = length(files) # Count number of files

files2 = read.table(text = files, sep = "_", as.is = TRUE) #Split file names by "_" separator and create table "files2"


```
for (j in 1:files1) {
  data=NULL
  data <- read.table(files[j], sep = "\t", header=TRUE) #Import datatable from files number 1 to j
  data["Meiosis"]=files2[j,2] # Insert Meiosis identifier from files2 into a new column
  data["Genotype"]=gsub('([A-Z]+).','\\1',files2[j,2]) # Extracts character portion of string
  data["GenotypeID"]=gsub('.*([0-9]+).*','\\1',files2[j,2]) # Extracts digit portion of string
  masterH <- rbind(masterH, data) # Combine data into master table
}
```


#Write out master files

wd = getwd()

```
out = paste(wd,"/","MasterHPTable_", Sys.time(),sep="")

write.table(masterH, out, col.names =TRUE, row.names = FALSE, quote = FALSE, sep="\t",
append=TRUE)


###########################

library(plyr)

hpdf<- subset(masterH, select = c(chr, pos_c))

hpdf <- hpdf[order(hpdf$chr, hpdf$pos_c),]

dfccounts <- ddply(hpdf,.(chr,pos_c),nrow)  #count up how many repeats

write.table(dfccounts,file="AllS288cHPs.txt", row.names=F, quote=F, sep='\t')

dfccounts <-dfccounts[which(dfccounts$V1>=2),]

write.table(dfccounts,file="commonS288cHPs.txt", row.names=F, quote=F, sep='\t')


################################################################

##PART 2. Examine Unique hDNA positions##

################################################################

##Remove Common HPs###

commonS288c <- read.table("commonS288cHPs.txt",header=T)

commonS288c$common <- "yes"


remove_common_HPs <- function(df){

  df <- merge(df, commonS288c, by=c("chr", "pos_c"), all=TRUE, sort=FALSE)

  df <- df[which(is.na(df$common)),]

  df <- subset(df, select=-c(V1,common))

}


##Work out whether HPs are consecutive- part of a hDNA tract, and also how long are the hDNA
tracts

##Output a list of positions of consecutive tracts (to match up w/events?)

library(stringr)

library(plyr)
```

```
tract_length <- function(df,filename){

 df <- df[order(df$sID),]

 df$tractno <- 0

 j<-1

 for(i in 1:nrow(df)){

   if(df[i,33]==0){df[i,33]=j} #if tract no. has not been assigned yet, assign a new number

   if(i!=nrow(df)){if(df[i,4] ==(df[i+1,4]-1)){ df[i+1,33]=df[i,33]}} #if the row is not the last one in the
dataframe, check if the next row has an sID one higher than the current row. If so, the next row
should have the same tract no. as the current row.

   if(i!=1){ if(df[i,4] ==(df[i-1,4]+1)){ df[i-1,33]=df[i,33]}} #if the row is not the first one in the
dataframe, check if the previous row has an sID one lower than the current row. If so, the previous
row should have the same tract no. as the current row.

   j<-j+1

 }

 tractlen <- table(df$tractno)

 tractlen <- data.frame(tractlen, stringsAsFactors=FALSE)

 tractlen <-rename(tractlen, c("Var1"="tractno", "Freq"="Tract_len_var"))

 df <- merge(df, tractlen, by=c("tractno"), all=TRUE, sort=TRUE)


 df_new <-df

 df_new$Tract_len_bp <-0

 for(k in 1:max(df_new$tractno)){

  current_subset <- df_new[df_new$tractno == k, ]

  if(nrow(current_subset)>0){

    result <- max(current_subset$pos_c) - min(current_subset$pos_c)

    df_new[df_new$tractno == k, ]$Tract_len_bp <- result}

 }


 df_new <-df_new[c("uID", "sID", "chr", "pos_c", "pos_k", "type_c", "type_k", "Var_len",
"tractno","Tract_len_var", "Tract_len_bp",
```

```r
"c1","c2","c3","c4","c5","c6","c7","c8","k1","k2","k3","k4","k5","k6","k7","k8","b1","b2","b3","b4","
b5","b6","b7","b8")]

  write.table(df_new,file=sprintf("%s_hDNA_tracts_S288c.txt",filename),row.names=F, quote=F,
sep='\t')


  newdf <- NULL
  for(i in 1:max(df_new$tractno)){
    df2 <- df_new[which(df_new$tractno == i),]
    if(nrow(df2)>0) {
      df2min <- min(df2$pos_c)
      df2max <- max(df2$pos_c)
      df2$length <- df2max-df2min
      df2$midpoint <- mean(df2$pos_c)
      newdf <- rbind(df2,newdf)
    }
  }


  newdf <-newdf[c("uID", "sID", "chr", "pos_c", "pos_k", "type_c", "type_k", "Var_len",
"tractno","Tract_len_var", "Tract_len_bp", "length", "midpoint",

"c1","c2","c3","c4","c5","c6","c7","c8","k1","k2","k3","k4","k5","k6","k7","k8","b1","b2","b3","b4","
b5","b6","b7","b8")]


  write.table(newdf,file=sprintf("%s_hDNA_tracts_S288c_imaging.txt",filename),row.names=F,
quote=F, sep='\t')

}


###Remove common HPS from pGAL-NDT80 strains###

files = list.files(pattern="HP-list") # import files names with "NF-list" string into variable "files"

files1 = length(files) # Count number of files

files2 = read.table(text = files, sep = "_", as.is = TRUE) #Split file names by "_" separator and create
table "files2"
```

```r
for (j in 1:files1) {

 data=NULL

 data <- read.table(files[j], sep = "\t", header=TRUE) #Import datatable from files number 1 to j

 name=files2[j,2]

 data <- remove_common_HPs(data)

 if(nrow(data)>1){tract_length(data, name)}


}


#Make Master hDNA table#


setwd("/mnt/nfs2/gdsc/mc482/hDNA_Tracts")


# Create new empty master dataframe

masterH=NULL


library(stringr)


# Sequentially imports each and combines into a Master Table with additional identified oclumns for
Meiosis, Threshold, Genotype and GenotypeID (e.g. OM2, 1500, OM, 2)

files = list.files(pattern="_hDNA_tracts_S288c_imaging") # import files names with "HP-list" string
into variable "files"

files1 = length(files) # Count number of files

files3 = read.table(text = files, sep = "_", as.is = TRUE) #Split file names by "_" separator and create
table "files2"


for (j in 1:files1) {

 data=NULL

 data <- read.table(files[j], sep = "\t", header=TRUE) #Import datatable from files number 1 to j

 data["Meiosis"]=files3[j,1] # Insert Meiosis identifier from files2 into a new column

 data["Genotype"]=gsub('([A-Z]+).','\\1',files3[j,1]) # Extracts character portion of string

 data["GenotypeID"]=gsub('.*([0-9]+).*','\\1',files3[j,1])  # Extracts digit portion of string
```

```r
  data["debut"]=(data$midpoint-(0.5*data$length)) # Add event start column

  data["fin"]=(data$midpoint+(0.5*data$length)) # Add event end column

  data <- subset(data, !duplicated(data$tractno))

  masterH <- rbind(masterH, data) # Combine data into master table



}




# Reorder columns

masterH=masterH[c("uID", "sID", "Meiosis","Genotype","GenotypeID","chr","pos_c",

         "pos_k","type_c","type_k","midpoint","debut","fin",

         "Var_len","tractno","Tract_len_var", "Tract_len_bp", "length")]



#Write out master files

wd = getwd()

out = paste(wd,"/","MasterhDNATable_", Sys.time(),sep="")

write.table(masterH, out, col.names =TRUE, row.names = FALSE, quote = FALSE, sep="\t",
append=TRUE)



##############################

##Count how Many HPs remain in TN and TRN##

TN <- masterH[which(masterH$Genotype == "TN"),]

TRN <- masterH[which(masterH$Genotype == "TRN"),]

TCMN <- masterH[which(masterH$Genotype == "TCMN"),]

OM <- masterH[which(masterH$Genotype == "OM"),]

OMT <- masterH[which(masterH$Genotype == "OMT"),]

TW <- masterH[which(masterH$Genotype == "TW"),]


avgOM <- nrow(OM)/9

avgOMT <- nrow(OMT)/10

avgWT <- nrow(WT)/4
```

```
avgTN <- nrow(TN)/4

avgTRN <- nrow(TRN)/6

avgTCMN <- nrow(TCMN)/6


TN <- TN[which(TN$Tract_len_var >1),]

TRN <- TRN[which(TRN$Tract_len_var >1),]

TCMN <- TCMN[which(TCMN$Tract_len_var >1),]

OM <- OM[which(OM$Tract_len_var >1),]

OMT <- OMT[which(OMT$Tract_len_var >1),]

TW <- TW[which(TW$Tract_len_var >1),]


# Automated PDF generation

wd = getwd()

out = paste(wd,"/","hDNA tract length in variants histograms.pdf", sep="")


pdf(file=out); par(mfrow=c(3,2));


hist(TN$Tract_len_var, breaks=(max(TN$Tract_len_var)-min(TN$Tract_len_var)+1),
xlim=c(min(TN$Tract_len_var),max(TN$Tract_len_var)),  xlab="Tract Length", main="hDNA tracts in
NDT80 arrest")

hist(TRN$Tract_len_var, breaks=(max(TRN$Tract_len_var)-min(TRN$Tract_len_var)+1),
xlim=c(min(TRN$Tract_len_var),max(TRN$Tract_len_var)),  xlab="Tract Length", main="hDNA tracts
in rad24 NDT80 arrest")

hist(TCMN$Tract_len_var, breaks=(max(TCMN$Tract_len_var)-min(TCMN$Tract_len_var)+1),
xlim=c(min(TCMN$Tract_len_var),max(TCMN$Tract_len_var)),  xlab="Tract Length", main="hDNA
tracts in pCLB2-MEC1 NDT80 arrest")


hist(TW$Tract_len_var,breaks=(max(TW$Tract_len_var)-min(TW$Tract_len_var)+1),
xlim=c(min(TW$Tract_len_var),max(TW$Tract_len_var)),   xlab="Tract Length", main="hDNA tracts
in WT")

hist(OM$Tract_len_var, breaks=(max(OM$Tract_len_var)-min(OM$Tract_len_var)+1),
xlim=c(min(OM$Tract_len_var),max(OM$Tract_len_var)),   xlab="Tract Length", main="hDNA tracts
in msh2")
```

```
hist(OMT$Tract_len_var, breaks=(max(OMT$Tract_len_var)-min(OMT$Tract_len_var)+1),
xlim=c(min(OMT$Tract_len_var),max(OMT$Tract_len_var)),  xlab="Tract Length", main="hDNA
tracts in tel1msh2")

dev.off()


wd = getwd()

out = paste(wd,"/","hDNA tract length in bp histograms.pdf", sep="")


pdf(file=out); par(mfrow=c(3,1));


hist(TN$Tract_len_bp, breaks=(max(TN$Tract_len_bp)-min(TN$Tract_len_bp)/100),
xlim=c(min(TN$Tract_len_bp),max(TN$Tract_len_bp)),  xlab="Tract Length", main="hDNA tracts in
NDT80 arrest")

hist(TRN$Tract_len_bp, breaks=(max(TRN$Tract_len_bp)-min(TRN$Tract_len_bp)/100),
xlim=c(min(TRN$Tract_len_bp),max(TRN$Tract_len_bp)),  xlab="Tract Length", main="hDNA tracts
in rad24 NDT80 arrest")

hist(TCMN$Tract_len_bp, breaks=(max(TCMN$Tract_len_bp)-min(TCMN$Tract_len_bp)/100),
xlim=c(min(TCMN$Tract_len_bp),max(TCMN$Tract_len_bp)),  xlab="Tract Length", main="hDNA
tracts in pCLB2-MEC1 NDT80 arrest")


hist(TW$Tract_len_bp,breaks=(max(TW$Tract_len_bp)-min(TW$Tract_len_bp)+1),
xlim=c(min(TW$Tract_len_bp),max(TW$Tract_len_bp)),   xlab="Tract Length", main="hDNA tracts in
WT")

hist(OM$Tract_len_bp, breaks=(max(OM$Tract_len_bp)-min(OM$Tract_len_bp)/100),
xlim=c(min(OM$Tract_len_bp),max(OM$Tract_len_bp)),   xlab="Tract Length", main="hDNA tracts in
msh2")

hist(OMT$Tract_len_bp, breaks=(max(OMT$Tract_len_bp)-min(OMT$Tract_len_bp)/100),
xlim=c(min(OMT$Tract_len_bp),max(OMT$Tract_len_bp)),  xlab="Tract Length", main="hDNA tracts
in tel1msh2")

dev.off()


##Plot Individual Tracts##


######################
setwd("/mnt/nfs2/gdsc/mc482/Event_Table_combining_and_imaging/Output_Files")
```

```r
masterGR_noNA <- read.delim("MasterGRnoNATable_2016-09-22")

masterGR <- read.delim("MasterGRTable_2016-09-22")

masterGR$Var_len2 <- (masterGR$Var_len-1)

masterGR_noNA$Var_len2 <- (masterGR_noNA$Var_len-1)
```

#the variant lengths stored in this column are actually 1bp too long because they include the first base upstream.

#Subtract 1 to make it more accurate.

```r
setwd("/mnt/nfs2/gdsc/mc482/Event_Table_combining_and_imaging")


spo_file <- read.delim("FullMap.Cer3_Pan_HA_1_4h_c.txt")

smooth_spo_file <- read.delim("Spo11Cer3PanHA100bp.txt")

TotalHits=sum(spo_file$Watson+spo_file$Crick)

spo_file$TotalHits=(spo_file$Watson+spo_file$Crick)

spo_file$TotalHpM=(spo_file$Watson+spo_file$Crick)/TotalHits*1000000 # Convert Pan data to Hits
per million reads (HpM)

oldhotspots<- read.delim("Hotspot.Table.Cer3_Pan_HA_1_4h.txt")

hotspots<- read.delim("Pan.Hotspots.IGR.SacCer3_2016.08.10.txt")

rmm_file<-read.delim("RMMSubSamp_simple")

AllElementsDUB = read.table("AllElementsDUB.txt", sep = "\t", header=TRUE) #Import datatable

rec_file<-read.delim("Rec8Marg.txt")


hotspots$Total_HpM <-hotspots$HITS/TotalHits*1000000

hotspots$Total_HpM=round(hotspots$Total_HpM,1)


setwd("/mnt/nfs2/gdsc/mc482/hDNA_Tracts")

#masterH <- read.delim("MasterhDNATable_2016-09-21")

masterH$Meiosis <- as.character(masterH$Meiosis)


# Subset the datatable

draw<-masterH # Temp holding table for events that will be drawn.
```

```r
# Hash out and/or amend the following lines to subset the datatable as required

#draw=subset(draw,Meiosis =="OMT7" ) # Meiosis = OM2, OMT10, etc (refers to a specific meiosis)

#draw <- draw[which(draw$Meiosis =="OMTNS1" | draw$Meiosis == "OMT1TN"),]

#draw=subset(draw,Genotype =="TN") # Genotype = OM, OMT, TN, TRN, TCMM, TRS, etc (refers to
a genotype containing multiple repeats)

draw <- draw[which(draw$Tract_len_var >1 & draw$Genotype == "TW"),]



#####################


ordre=1:8 # Order of plotting spores

extend=500 # How many bp to extend the plotting either side of the event


# Automated PDF generation

wd = getwd(); out = paste(wd,"/","Images_Â±", extend,"bp_",Sys.time(),".pdf",sep=""); pdf(file=out,
width=21,height=9);


for (j in 1: nrow(draw) ) {

  meiosis=draw[j,"Meiosis"]

  chromo=draw[j,"chr"]

  debut=draw[j,"debut"]

  fin=draw[j,"fin"]


  # How much to extend the plotting either side of the event

  debut=debut-extend

  fin=fin+extend


  # This sets up the graphing parameters: mfrow calculates number of rows of grpahics to be drawn.
mar sets the margins of the graph

  layout(matrix(c(0,1,1,1,2:17,18,18,19,19,20,20,21,22,22,23,23,24,24,24,0),35, 1, byrow = T))

  #layout.show(20)

  par(mar=c(0,6,0,2),oma = c(4,0,0,0),las=1) # Sets margins per graph and outside margins per
grouped set
```

```
  # Subset the masterGR tables for the region of interest

  a<-subset(masterGR,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <= (fin))

  a1<-subset(masterGR_noNA,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <=
(fin))


  while (nrow(a1)<20){ # Check whether the region of interest contains sufficient SNPs to draw - this
is important to prevent an error when a/a1 contain no rows due to rare zero SNP events (i.e. COs)
that also lack SNPs in flanking thresholded region.

    debut=debut-500

    fin=fin+500

    a<-subset(masterGR,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <= (fin))

    a1<-subset(masterGR_noNA,Meiosis==meiosis & chr == chromo & (debut) <= pos_c & pos_c <=
(fin))

  }


  if(nrow(a)>0){

    # Subset master based on Meiosis and Chromosome being drawn

    e2=subset(masterH, Meiosis==meiosis & chr == chromo)


    ######add SNP coordinates as text######

plot(a$pos_c,a[,1],type="n",ylim=c(0,300),ylab=paste("SNPs"),cex.lab=1,font=1,xlab="",xlim=c(debut
,fin), xaxt="n",yaxt="n", axes=FALSE, xaxs="i",yaxs="i")

    #type=n for no plotting. axes=FALSE gets rid of border.

    text(a$pos_c, y=100, labels = a$pos_c, srt=90, pos=3, cex=1)

    #cex=1 controls the size of the text; however, making it smaller doesn't really help with overlap

    arrows(a$pos_c,0,a$pos_c,50,col="black",length=0,lwd=1, code=3, lend=1)


    ####################################

    # Graphs of raw data

    for (i in (ordre+2)){
```

```r
plot(a$pos_c,a[,i],type="l",lwd=2,col=2,cex.axis=0.8,ylim=c(0.6,300),yaxp=c(1,100,1),ylab=paste("S",i
-2,sep=""),cex.lab=1,font=1,xaxs="i",yaxs="i",xlab="",xlim=c(debut,fin), xaxt="n", log="y")

    points(a$pos_c,a[,i],pch=4,col=2,cex=2)

    points(a$pos_c,a[,(i+8)],pch=4,col=4,cex=2)

    lines(a$pos_c,a[,(i+8)],col=4,lwd=2)

    points(a$pos_c,rep(100,length(a$pos_c)),pch=-1*a[,(i+16)]+17,cex=1.5,col=-2*a[,(i+16)]+4)

  } #End of i first loop


  # Graphs of binary data

  position=c(85,95,85,95,85,95,85,95)

  haut<-0

  for (i in (ordre+2)){

    plot(a$pos_c,rep(100,length(a$pos_c)),xaxt="n",yaxt="n",type="n",ylab=paste("S",i-
2,sep=""),cex.lab=1,font=2,xaxs="i",yaxs="i",ylim=c(50,130),axes=FALSE,xlim=c(debut,fin))


    alt<-ifelse(haut==0,120,120)

    bas<-ifelse(haut==0,60,60)

    arrows(e2$debut,90,e2$fin,90,col="mediumpurple",length=0,lwd=30, lend=1) # Underlay a
highlighting box across all event regions

    arrows(a$pos_c,position[i-2]-30,a$pos_c,position[i-2]+30,col=-2*a[,(i+16)]+4,length=0,lwd=1)


    arrows(a1$startSNP,position[i-2],a1$stopSNP,position[i-2],col=-2*a1[,(i+16)]+4,length=0,lwd=15,
lend=1) # Add SNP start/stop boundary overlays


    haut<-1-haut


  } #End of i second loop


  # Addition of plots that indicate the events specified by 1000 and 2000bp event-calling thresholds

plot(a$pos_c,rep(100,length(a$pos_c)),xaxt="n",yaxt="n",type="n",ylab=paste("Events"),cex.lab=1.2
5,font=2,xaxs="i",yaxs="i",ylim=c(0,165),axes=FALSE,xlim=c(debut,fin))
```

```
    arrows(e2$debut,140,e2$fin,140,col="mediumpurple",length=0,lwd=12, code=3, lend=1);
text(debut,140, "hDNA tract",pos=4) # Underlay a highlighting box across all event regions


    # Plot event midpoints

    arrows(e2$midpoint,130,e2$midpoint,150,col="black",length=0,lwd=1, code=3, lend=1)


    ####################################################################

    ###plot indels as triangles with length underneath###

plot(a$pos_c,a[,1],type="n",ylim=c(0,300),ylab=paste("Indels"),cex.lab=1.25,font=2,xlab="",xlim=c(d
ebut,fin), xaxt="n",yaxt="n", axes=FALSE, xaxs="i",yaxs="i")

    #type=n for no plotting. axes=FALSE gets rid of border.

    aDEL=subset(a, type_k=="d")

    if(nrow(aDEL)>0){

      yDEL =rep(200, nrow(aDEL))

      points(aDEL$pos_c, yDEL, type = "p", pch=25, col="dimgrey", cex=2)

      text(aDEL$pos_c, (yDEL-145), labels = aDEL$Var_len2, pos=3, cex=1)

    }


    aINS=subset(a, type_k=="i")

    if(nrow(aINS)>0){

      yINS =rep(200, nrow(aINS))

      points(aINS$pos_c, yINS, type = "p", pch=24, col="dimgrey", cex=2)

      text(aINS$pos_c, (yINS-145), labels = aINS$Var_len2, pos=3, cex=1)

    }


    ####################################################################

    rbPal <- colorRampPalette(c('black','blue','red','pink')) # Creates a colour palette if chosing to plot
Spo11 as a coloured histogram "h"

    spo_file$Col <- rbPal(10)[as.numeric(cut(spo_file$TotalHits,breaks = 10))]


    map<-subset(spo_file,Chr == chromo & debut <= Pos & Pos <= fin)
```

```r
    map2<-subset(rmm_file,chr == chromo & debut <= pos & pos <= fin)

    map5<-subset(hotspots,CHROM == chromo & debut <= HS_START & HS_END <= fin)

    map6<-subset(rec_file,Chr == chromo & debut <= Position & Position <= fin)

    map7<-subset(smooth_spo_file,chr == chromo & debut <= pos & pos <= fin)



plot(map7$pos,map7$spo,type="l",xlim=c(debut,fin),ylim=c(10,max(map7$spo)),yaxp=c(100,round(
max(map7$spo),-2),2),ylab="Spo11",bty="u",xaxs="i",lwd=2,xaxt="n",cex.axis=0.9,cex.lab=1.25)



plot(map5$midpoint,map5$Total_HpM,type="n",ylim=c(0,300),ylab="",cex.lab=1.25,font=2,xlab="",
xlim=c(debut,fin), xaxt="n",yaxt="n", axes=FALSE, xaxs="i",yaxs="i")

    #type=n for no plotting. axes=FALSE gets rid of border.

    if(nrow(map5)>0){

      arrows(map5$HS_START,140,map5$HS_END,140,col='lightsteelblue',length=0,lwd=12, code=3,
lend=1); text="" # Underlay a highlighting box across all event regions

      text(map5$midpoint, y=0, labels = map5$Total_HpM, pos=3, cex=1)

    }



#################################################################################
############################################################################

    #Now plot the gene datatrack

    #First subset the relevant data

    genes=AllElementsDUB #First make a copy of the ALLElements table

    genes=subset(genes,chr==chromo & start>(debut-10000) & stop<(fin+10000)) #Make a sub-table
of ALLElements where chr = 1 and has limits just beyond plot range

    genes=subset(genes,type=="gene") #Make a sub-table of ALLElements

    #Now perform the plot

    plot(genes$start,genes$start, xaxt="n",yaxt="n",type="n",
ylab=paste("Genes"),cex.lab=1.5,font=2, xlim=c(debut,fin), ylim=c(0,120),axes=FALSE) #set up empty
plot

    # Following module draws arrows for each element

    xrange=fin-debut
```

```
    ahead=xrange/25 #make arrowhead length proportional to plot range

    ahead[(ahead>500)]=500 #limit max length to 500

    av=75 #arrow vertical location relative to plot dimensions

    ahw=15 #arrow/head width


    genesW=subset(genes,genename !="Dubious_ORF" & orientation =="+") #Make a sub-table of
ALLElements

    if(nrow(genesW)>0){

     for (i in 1:nrow(genesW)){

        polygon(c(genesW[i,"start"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-
ahead,genesW[i,"stop"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-ahead,
genesW[i,"start"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw),
col="palegreen", border="palegreen4")

        text((genesW[i,"start"]+genesW[i,"stop"])/2,av, font=3, genesW[i,"genename"], cex=0.9) }

     }


    genesW=subset(genes,genename=="Dubious_ORF" & orientation =="+") #Make a sub-table of
ALLElements

    if(nrow(genesW)>0){

     for (i in 1:nrow(genesW)){

        polygon(c(genesW[i,"start"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-
ahead,genesW[i,"stop"], genesW[i,"stop"]-ahead, genesW[i,"stop"]-ahead,
genesW[i,"start"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw),
col="palegreen", border="palegreen4", lty=2)

        text((genesW[i,"start"]+genesW[i,"stop"])/2,av, font=3, genesW[i,"sysname"], cex=0.9) }

     }


    av=25 #arrow vertical location for Crick genes relative to plot dimensions

    genesC=subset(genes,genename !="Dubious_ORF" & orientation =="-") #Make a sub-table of
ALLElements

    if(nrow(genesC)>0){

     for (i in 1:nrow(genesC)){

        polygon(c(genesC[i,"stop"], genesC[i,"start"]+ahead, genesC[i,"start"]+ahead,genesC[i,"start"],
genesC[i,"start"]+ahead, genesC[i,"start"]+ahead,
```

```r
genesC[i,"stop"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw), col="lightpink",
border ="lightpink4")

    text((genesC[i,"start"]+genesC[i,"stop"])/2,av, font=3, genesC[i,"genename"], cex=0.9) }

  }


    genesC=subset(genes,genename=="Dubious_ORF" & orientation =="-") #Make a sub-table of
ALLElements

   if(nrow(genesC)>0){

    for (i in 1:nrow(genesC)){

      polygon(c(genesC[i,"stop"], genesC[i,"start"]+ahead, genesC[i,"start"]+ahead,genesC[i,"start"],
genesC[i,"start"]+ahead, genesC[i,"start"]+ahead,
genesC[i,"stop"]),c(av+ahw,av+ahw,av+ahw+ahw,av,av-ahw-ahw,av-ahw, av-ahw), col="lightpink",
border ="lightpink4", lty=2)

      text((genesC[i,"start"]+genesC[i,"stop"])/2,av, font=3, genesC[i,"sysname"], cex=0.9) }

   }

   ####Plot RMM track###


plot(map2$pos,map2$rmm,type="l",xlim=c(debut,fin),ylim=c(1,max(map2$rmm)),yaxp=c(1,round(m
ax(map2$rmm),0),2),ylab="RMM",bty="u",xaxs="i",lwd=4,col='darkgoldenrod',

      xaxp=c((round(debut,-3)),(round(fin,-3)),(round(round(fin,-3)-round(debut,-3)) /
1000)),cex.axis=0.9, cex.lab=1.25)

   if(nrow(map6)>0){

    arrows(map6$Position,0,map6$Position,50,col="black",length=0,lwd=1, code=3, lend=1)

   }

   ###Make figure legend###


   title(xlab = paste(sep="","Red=S288c, Blue=SK1",

             "  Id=", meiosis,

             "  Chromosome=",chromo,

             "  Tract Max Length=", draw[j,"length"], "bp",

             "  No. Variants=", draw[j,"Tract_len_var"]),

        outer = T, line = 2, cex.lab=1.4) # Cex.lab controls the labelling size

  }

} #End of j loop
```

```
dev.off()
```