Supplementary Methods

Meiosis time courses

Meiotic time courses were performed as described by Berchowitz *et al* (Berchowitz et al. 2013). Briefly, SK1 yeast cells were grown to saturation in YPD, diluted in BYTA medium to an OD_{600} = 0.25, and grown for 20 hours to reach a G1 phase state. These cells were washed once with water, then resuspended in sporulation medium to an OD_{600} = 1.9. Cells were allowed to proceed through meiosis for 6 hours at 30°C. During this time, cells accumulated at a meiotic prophase arrest due to the *NDT80* transcription factor being under an inducible promoter (Benjamin et al. 2003). After harvesting samples for the 6-hour time point, cells were released from the prophase arrest by the induction of *NDT80* with 1uM β-estradiol, allowing synchronous progression through the meiotic divisions (Carlile and Amon 2008). RNA and immunofluorescence samples were harvested in parallel at the indicated time points. For the RNA samples, 2mL of cells were pelleted, flash frozen in liquid nitrogen, and stored at -80°C until further processing. Tubulin immunofluorescence was performed as described by Berchowitz *et al*. We also observe in the *dbr1Δ* strain, introns that are abundant in the rRNA subtraction are depleted in the poly(A) selection, explaining discrepancies between these samples in the clustering since reads inside the intron specifically identify the retained intron isoform instead of the spliced isoform.

RNA isolation

RNA isolation for Lariat-seq and Branch-seq was performed as follows. Yeast were grown to OD_{600} 0.94-0.98 and were collected by centrifugation at 7000 RPM for 5 min at 4°C. Media was poured off and yeast were washed twice in water and frozen at -80°C. Cells were thawed and transferred to tubes containing 2.8mm ceramic beads and 1mL Trizol (Life Technologies) was added to 1/10 cell pellet. An Omni Bead Ruptor was used to lyse the cells, twice for 20 seconds on ½ max speed and once for 10 seconds on max speed. Samples were incubated at room temp for 5 min, 1/5 volume of chloroform was added and mixed, samples incubated at room temp 2-3 min and were spun at max speed for 15 min at 4°C. The upper aqueous layer was transferred to a new tube and precipitated with ½ volume isopropanol. After 5min on ice, samples were spun at max speed, 4°C for 25 min. The RNA pellet was washed with 70% ethanol before storage at -80°C.

RNA isolation for RNA-seq was performed as follows. Overnight yeast cultures were grown in 5mL YPD media and were diluted in the morning into 50mL YPD and grown to log phase (OD_{600} 0.5 to 1), spun down, and the pellets were frozen in liquid nitrogen. RNA was isolated as in (Clarkson et al. 2010). Pellets were resuspended in 1mL Acid Phenol and an equal volume of AES buffer (50mM NaAcetate pH 5.2, 10mM EDTA, 1% SDS) was added. In 2mL Eppendorf tubes, samples were incubated at 65°C for 10 min with vortexing every minute. Samples were incubated on ice for 5 min and then transferred to a phaselock tube and one volume chloroform was added. After spinning, the top aqueous layer was transferred to a fresh phaselock tube and one volume of phenol:chloroform:isoamyl alcohol (25:24:1) was added, tubes were spun, one volume of chloroform was added, tubes were spun, and the aqueous layer was transferred to a fresh tube to be precipitated with 50uL 3M NaOAc (pH 5.5) and 550uL isopropanol. Samples were spun at max speed for 25 minutes at 4°C. The pellet was washed twice with 70% ethanol and resuspended in water.

Isolation of in vitro-spliced *Drosophila melanogaster* lariat RNA

Radio labeled *FTZ* lariat RNA was used to assess the fidelity of each step of the Branch-seq protocol during protocol development. The *FTZ* lariat RNA was included as a positive control spike-in during all subsequent Branch-seq experiments to ensure successful debranching. *FTZ* lariat RNA was generated using Hela nuclear extracts for in-vitro splicing. Hela nuclear extracts were a kind gift from the Reed Lab (Folco et al. 2012). Coupled in vitro transcription and splicing were performed similar to Folco and Reed (Folco and Reed 2014) except without addition of α-amanitin to obtain as many lariats as possible. Reactions were digested with RNase R (Epicenter) at 37°C for 1 hour to obtain radio labeled *FTZ* lariats.

Debranching enzyme purification

S. cer. DBR1 cDNA was generated from WT S288C yeast and cloned into the pET151 expression vector from Invitrogen. Protein was expressed in Rosetta 2(DE3)pLysS competent cells grown in YT media at 37°C until they were induced with IPTG and grown at 18°C. Bacteria were lysed using Native Lysis Buffer (Qiagen). Protein was purified with a Ni-NTA column (Qiagen) and subsequently over an S200 column (Buffer: 125 mM KCL, 20mM HEPES pH 7.3, 1mM DTT, 10% glycerol). Protein was concentrated (final 50% glycerol) and flash frozen. Protein was tested for RNase activity and debranching activity on linear RNA and an in vitro spliced lariat, respectively.

Reverse transcription

Reverse transcription was performed using primer /5Phos/AGATCGGAAGAGCGTCGTGTAGGGAAAG/iSp18/CACTCA/iSp18/GTGACTGGAGTTCCTTGGCACCCGAGAATTCCA/TTTTTTTTTTTTTTTTTTTTVN (designed in collaboration with Yarden Katz (Katz et al. 2014)) incubated with SuperScriptIII RT (Invitrogen) for 30 min at 48°C. Subsequently 2.1 uL of 1M NaOH was added and samples were incubated at 98°C for 15 min. The RT primer is a modified version if the ribosome footprint profiling RT primer where the 5' end of the RNA gets sequenced first and paired end, barcoded sequencing is possible (Ingolia et al. 2009).

The samples were then run on a 6% TBE-urea gels (Invitrogen) for 93 min at 200V to remove excess RT primer. Gels were stained with SYBR gold and gel slices were excised where product was observed to run above the RT primer for the top, middle, and bottom lariat samples. Gel slices were shredded and DNA was eluted in 400uL PAGE elution buffer overnight (see 2D gels Methods). Gel was removed before precipitation using a Nanosep column.

Circularization

Circligase (Epicentre) was used to circularize the gel isolated RT products for 1 hour at 60°C and the enzyme was inactivated by heating at 80°C for 10 minutes.

PCR

Phusion high-fidelity polymerase (NEB) was used to amplify the circularized products. Illumina PCR primer 1.0 AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT was paired with Illumnia barcode primers (RPI#s)

(RPI1) CAAGCAGAAGACGGCATACGAGATCGTGATGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA
(RPI2) CAAGCAGAAGACGGCATACGAGATACATCGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA
(RPI3) CAAGCAGAAGACGGCATACGAGATGCCTAAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA
(RPI4) CAAGCAGAAGACGGCATACGAGATTGGTCAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

Samples were removed after 6, 8, 10 and 12 PCR cycles and run on an 8% TBE gel (Invitrogen) for 40 min at 200V. PCR products were gel isolated by shredding the gel through a hole poked with a needle in the bottom of a 0.5 mL Eppendorf tube and eluted in 400uL PAGE elution puffer (see above) at 65°C , shaking at 1400RPM for one hour. Gel was removed with a Nanosep column and precipitated with isopropanol.

http://epigenome.usc.edu/docs/resources/core_protocols/Illumina%20Sequence%20Information%20for%20Customers%20DEC2008.pdf

Sequencing

For Branch-seq, one Illumina MiSeq flow cell was sequenced at the MIT Bio Micro Center (November 2011). 5' end reads were 50 bases and 3' end reads were 250 bases. 3' end reads were sequenced with custom sequencing primer GTGACTGGAGTTCCTTGGCACCCGAGAATTCCATTTTTTTTTTTTTTTTTTTT to avoid sequencing the untemplated As added by the poly(A) tailing reaction. The 3' end sequencing primer was gel purified prior to use in sequencing (primer design might need to be changed for sequencing on other Illumina machines).

Lariat-seq library prep

Reverse transcription was performed on 2D gel isolated lariat RNA using 1ul Random hexamer Primers (3ug/ul) (Invitrogen) and SuperScript III reverse transcriptase (Invitrogen). RNA and primer mix was heated at 70°C for 10 minutes and then put on ice.

12 uL of Mix A (mix A: 4uL 5x 1st strand buffer, 2uL 100mM DTT, 1uL dNTPs (10mM), 4uL Actinomycin D [1mg/1mL], 1uL SuperaseIn (20U/ul)) was added to the RNA and primer. Then 1 uL of SSIII was added and the RT program was run: 25^0C 10 minutes, 42^0C 50 minutes, 70^0C 15 minutes, 4^0C hold. Sample volume was brought up to 200uL with water and then samples were phenol choloroform extracted and ethanol precipitated. Second strand synthesis was performed with DNA pol I and dUTP to make strand specific libraries. Next the samples underwent SPRI-TE (end repair, adenlyation, adapter ligation, gel purification #1). Subsequently uracil digestion was performed with USER, samples underwent PCR and gel purification before sequencing (1/30 of a HiSeq2000 lane).

RNA-seq library prep

RNA was isolated using the hot acid phenol method (see RNA isolation above) to ensure isolation of high quality RNA. All 6 samples, 2 WT, 2 *dbr1Δ*, 2 *upf1Δ,* had RQN (quality) values of 8.8 or higher as measured on the Advanced Analytical machine. Strand specific libraries were prepared by the MIT Bio Micro Center using the TruSeq™ RNA Sample Prep Kit v2 (RS-122-2101 kit) through cDNA after which LM-PCR was preformed using the Beckman Coulter SPRIte system with a 200-400bp size cutoff. Samples were barcoded and all sequenced in one HiSeq2000 lane, 60 X 60 bp.

Ribosomal RNA subtraction for the rapamycin treatment, *dbr1 Δ* , and the meiosis time course samples was performed using the Illumina Ribo-Zero Gold rRNA Removal Kit (Yeast) followed by standard strand-specific library preparation. All 20 samples were sequenced in one NextSeq lane, 75 x 75 bp.

Branch-seq read mapping

Reads were trimmed to 30 by 30 nt and mapped with Bowtie1 (Langmead et al. 2009) (bowtie-1.0.0) using the following parameters: **bowtie -S -m 1 -1 end1reads.fastq -2 end2reads.fastq.** Branch-seq reads for each gel slice were mapped to the genome and then combined using **samtools merge** (samtools-0.1.7a) (Li et al. 2009). Reads were initially mapped to SacCer2 (S288C_reference_genome_R61-1-1_20080605) and subsequently to SacCer3 (S288C_reference_genome_R64-1-1_20110203) downloaded from SGD. Peak calling was performed using the SacCer2 genome and peak calls were converted to SacCer3 coordinates using liftOver tool (http://genome.ucsc.edu/) for some analyses. Peaks were called using the combined reads from the top, middle, and bottom sections of the arc. For Figure 1d if there were multiple peaks within 3 nt of the annotated BP, the annotated BP was only counted once.

winBP peak calling

A sliding window approach adapted from Arribere and Gilbert (Juneau et al. 2009; Arribere and Gilbert 2013) was used with some modifications in the winBP peak caller. A 200nt region was taken starting at the 5' end of each chromosome. Average read coverage per nucleotide, α, for this region was calculated using only BP end (second end) reads and was required to be at least 0.1. A sliding window of 5 nt (196 of these windows/200nt region) within each 200 nt region was used to reduce spurious calls in regions with uneven coverage. If coverage in the 5 nt sliding window was at least 12α a peak was called. At least 1nt was required between reported peaks. Peak calling was performed for each strand, always in the 5' to 3' direction. The 200nt regions were shifted 100 nt down the chromosome, and the steps outlined above were repeated until reaching the end of the chromosome. winBP recovered 58% (153/260) (Table 1) of annotated BPs in expressed genes. GEM-BP peak calling is described in Supplemental Methods.

GEM-BP peak calling

To discover BP events from the data, we extended the ChIP-seq and ChIP-exo peak caller GEM[4] that calls events with high spatial resolution. Unlike other peak callers, GEM does not assume any specific distribution of reads, and therefore is flexible to adapt to a new data type by learning a data-specific empirical spatial read distribution. We used a +/-10bp window around the confident set of annotated BPs to learn the empirical read distribution (Fig. 1c) and used it for peak calling by GEM. To avoid including noisy reads from the non-BP strand, we modified GEM to perform single-strand peak calling and used only the 3' end (BP end) reads as input. As part of the integrated event finding and motif discovery process, GEM discovered the consensus BP motif TACTAAC, some variants that are similar to the consensus motifs, and a poly A motif that represents technical artifacts resulting from anchored oligo(dT) RT step of the protocol. To distinguish events associated with different motifs, we modified GEM to use multiple position weight matrix (PWM) motifs as the positional priors for event discovery. If a base position is matched by multiple motifs, GEM chooses the PWM model that has a more significant p-value to set the positional prior. For each called event, GEM computes an event shape score that quantifies the similarity of the event read distribution to the empirical read distribution. The event shape score is defined as the Pearson correlation of read count values across the +/-10bp bases between the called event and the empirical read distribution. The new functionalities of the GEM software, which we called GEM-BP, were implemented in version 2.6. The following parameters were used to analyzed the Branch-seq data: --k 7 --a 2 --q 1 --bp --pp_pwm --not_update_model --nrf --nf.

We then post-processed the GEM-BP event calls to discover BP events using a Random Forest classifier (Breiman 2001) in the MATLAB software (MathWorks 2012). The features for the Random Forest include GEM-BP event read count, event shape score, and the binary motif categorical variables. We used the GEM-BP calls that overlap with the annotated BPs as the positive training set, and those that overlap with the tRNA genes as the negative training set. The trained Random Forest classifier was then applied to all of the GEM-BP event calls to make the final BP event calls.

In total, GEM-BP discovered 546 BPs (Table 1), including 75% of expressed BPs (196/260) (Table 1) within 3 nt of their annotated locations (Fig. 1d). Of 546 GEM-BP predicted BPs, 47 (8.6%) had more than one mismatch from the BP consensus motif TACTAAC, compared to 74 (21.5%) of the 344 peaks identified by the winBP approach. These numbers indicate that the GEM-BP predictions are more biased toward consensus BP, presumably because of its use of motif information and training on annotated BP, which match the consensus very closely, information which is not used by the winBP approach. Thus, we used the union of predictions made by both peak callers for subsequent analyses.

Typical 5'SS filter for putative novel BPs

GEM-BP and winBP together called numerous unannotated BPs in the yeast genome; the union of their peak calls yielded 430 putative novel BP peaks in all (Table 1). To define a high confidence subset of putative novel BPs, the paired-end sequencing information from Branch-seq was used as a built-in quality control for BP identification. Branch-seq data contains strand-specific read pairs connecting the BPs and 5'SS. Authentic putative novel BP resulting from splicing should be associated with a plausible 5'SS motif at the start of the associated 5' end reads, while any artefactual putative novel BP peaks would not be expected to have such a motif (or only at the background frequency of this motif in the genome).

For each BP, we took all BP end reads (3' end) within 5nt of the BP peak, accounting for strand. We obtained the paired 5'SS read for each BP read in this set and noted the location of the 5'SS read start. We calculated the mode position from all 5'SS read starts for that BP and looked at the 6mer motif at that position and one position 3'. We considered 6mers that matched the yeast 5'SS consensus GTATGT perfectly or with at most one mismatch as ‘typical 5'SS motifs’, and all others as ‘atypical 5'SS motifs’.

Almost all (97%) annotated yeast introns in nuclear genes have typical 5'SS motifs by this definition (Table S3). Of the Branch-seq 3' end peaks that were associated with annotated BP, 76% (149/196) and 90% (138/153) had 5' end peaks at the annotated 5'SS for GEM-BP and winBP, respectively (Table S1). This result indicates that our approach can reliably and comprehensively map both the BP and 5'SS of introns, as intended.

After applying the typical 5'SS filter to the 430 putative novel BP, 268 cnBP remained. This subset of 268 should be treated as highly confident and was used for all downstream analyses. We estimate the FDR for the set of 268 BP is 1.1%, which is the genomic background frequency of 6mers matching typical 5'SS motifs in the yeast nuclear genome (Table S3, see bellow). Note, if the GEM-BP and winBP peaks were very close together, only the GEM-BP peak was counted.

Nicked lariats are expected to be extremely unstable in vivo. However, the presence of such species in the 2D gel arc used in Branch-seq could result in read pairs that have 3' ends located at arbitrary positions in an intron paired with authentic 5'SS, potentially resulting in artefactual BP identification. The putative BP sequence identified from such read pairs should be sampled more or less randomly from intron locations, and therefore would show no bias for proximity to a BP sequence motif, allowing estimation of the frequency of such artifacts from the frequency of poor matches to the BP consensus motif. In our analysis, we used a window +/- 15 bp from the peak of Branch-seq reads to identify BP motifs (see "Novel and annotated BP motifs"). Noting that for 247/268 cnBP the best match to the yeast consensus TACTAAC was within 2 nt of the peak of Branch-seq reads (a window of 5 start positions), and most matched well to the consensus, we calculated the probability P3mm+ (= 45%) that the best matching 7mer to the yeast consensus within 15 bp of an arbitrary position in an annotated yeast intron was NOT within 2 bp of the center, AND was a poor match to the consensus (3 mismatches or more from TACTAAC). Thus, we expect 45% of artefactual cases to have these features. From the observed number of cnBPs that have these features (= 5), one can estimate the number of artefactual BPs within the cnBP set as 5/0.45 = ~11, or about 4% of the total. One might expect that the peak of Branch-seq reads should correspond very closely to the BP, as it did for annotated BPs (Fig. 2E), and we observed that the proportion of cnBPs with 3+ mismatches was much lower (7/247 = ~3%) when the best BP motif was within 2 bp of the Branch-seq peak, than when it was not (5/21 = 24%). These considerations motivate that cases where the best BP motif is within 2 bp of the peak be designated as "high confidence novel BPs" (hcnBPs) and cases where it is located further away – which likely have a much higher frequency of artifacts – be designated "low confidence novel BPs" (lcnBPs). Columns in Table S2 distinguish these two categories.

Another potential concern is that proteins bound to RNA may prevent exonucleolytic trimming causing identification of erroneous BP peaks downstream of annotated BPs. This is likely uncommon as 1) expanding the x-axis on Fig. 1C does not reveal strong peaks downstream of annotated BPs and 2) there are only 4 cases where a cnBP is located 3' of the annotated BP where the annotated and cnBP share the same 5'SS.

As a note, the overlap between the GEM-BP and winBP cnBP was only 80 BPs (Table 1), further suggesting that the two methods have different strengths and weaknesses in their ability to call novel BPs and there is benefit to using both methods.

One random position was selected in each of the 298 nuclear encoded intron containing genes in the SacCer3 genome annotation. The 6mer motif beginning at this location was score for number of mismatches from "GTATGT." This was done 10 times to obtain 2980 simulated 5'SS in introns. 10 motifs had 0 mismatches and 24 motifs had 1 mismatch for an estimated FDR of 1.1% ((10+24)/2980) (Table S3).

Lariat tails are largely absent in vivo

Lariat tails appear to be efficiently digested *in vivo,* as previously reported, evidenced by a dearth of Lariat-seq reads in the long lariat tail of *UBC13* (Fig. S1B). With Branch-seq we are able to see RT priming preferences based on the nucleotides left down stream of the BP nucleotide after digestion of the lariat tail. It appears 2 nt are generally left after the BP, resulting in RT priming peaks that begin at the +1 or +2 position relative to the BP (Fig S1C) depending on the genomic sequence at those positions (Fig. S1D-E). The peak at -2 relative to the BP is likely to miss-priming of RT (Fig. S1D). See Fig. S1 legend for more information. To our knowledge, this is the first report of the precise number of nucleotides downstream of the BP nucleotide left undigested in lariat tails from RNA isolated from *dbr1Δ* yeast.

Comparison of cnBP to Qin et al. novel BPs

All 268 cnBP were compared to the 41 novel BP identified by Qin et al. Qin et al coordinates were liftedover from SacCer3 to SacCer2 for this comparison. Overall, 22 of the 41 novel BP reported by Qin et al were located within 7nt of cnBP (Table S2). Of the remaining 19 Qin BP, only 9 which had a good BP motif had no support from Branch-seq data and 7 of those 9 came from lariat loops > 100nt in length. We observe that Branch-seq is better at recovering lariat loops <100nt in length (Fig S3), explaining some of these 9 BPs. The remaining 10 Qin et al BPs are explained by a combination of difference reference BP annotations used, 5’SS with more than one mismatch from “GTATGT”, and sequencing depth at those BP positions.

Mapping lariat junction reads

Lariat junction reads were identified and aligned in four main steps:

1. Reads were attempted to be aligned to the *S.cer.* genome using the Bowtie (version 1.0.0) read aligner and those aligning with fewer than 4 mismatches were omitted from further analysis.

2. Each unalignable read was split into two fragments such that each fragment was at least 12 bases long and the hexamer beginning the second fragment had maximum probability of being sampled from the *S.cer.* 5'ss position weight matrix. Reads for which this maximum probability was less than 0.01 were omitted from further analysis. The fragments will be referred to by their position at the 3' or 5' end of the original read moving forwards.

3. The fragment pairs were mapped to the *S.cer.* genome using the bowtie read aligner allowing no mismatches. The fragments were required to map in an inverted order (3' fragment upstream of 5' fragment). The final base of each 5' fragment, the putative BP nucleotide, was omitted from this alignment due to the prevalence of mismatches at this position.

4. For all fragment pairs with a valid alignment, the final base of each 5' fragment was re-added. The aligned position of the 3' end of the 5' fragment was called as a BP and the aligned position of the 5' end of the 3' fragment was called as the corresponding 5'ss.

Skipping across lariat 5'SS-BP junctions

We found that reverse transcriptase often introduces short insertions and deletions when crossing a lariat junction. This results in the 3' end of 5' fragment of lariat junction reads not always ending directly at the BP. The frequency of these events was determined by comparing the BP location called by each lariat junction read to a known BP location as annotated by Meyer et al. within 25 nts if one exists. Figure S2D reports the distribution when allowing no mismatches as used elsewhere in this paper. This criterion precluded observing insertion events as they were found to always have the sequence UACUACU at the 3' end of the 5' fragment, resulting in mismatches in the last two positions when aligned to the BP consensus motif.

BP calling from lariat junction reads

In order to make precise BP calls from the lariat junction reads, a probabilistic model based on the observed skipping rates in introns with annotated BP and a self-learned BP motif position weight matrix (PWM) was used.

Reads were separated into clusters based on proximity of their downstream ends. The i^{th}cluster of reads is denoted by R_i. The distribution $P(B_i = x \mid R_i)$, where B_i is a RV indicating the location of the BP generating R_i, was computed using the proportion $P(B_i = x \mid R_i) \propto P(R_i \mid B_i = x) * P(B_i = x)$. Assuming a uniform prior and that reads are independent given a BP, we rewrite this proportion as $P(B_i = x \mid R_i) \propto \prod_{r \in R_i} P(r \mid B_i = x)$. Note that $P(r \mid B_i = x)$ is simply the probability of observing a deletion of the size in read r given $B_i = x$.

An EM framework was used to learn a BP motif PWM, which was then used to improve precision. Beginning with an unbiased motif, the following protocol was repeated until the motif did not change between iterations:

1. Calculate $P(B_i = x \mid R_i, M)$, where M is the current motif, by multiplying $P(B_i = x \mid R_i)$ and the probability that the motif implied by $B_i = x$ would be sampled from $M$and then normalizing by the sum across each cluster.
2. Refine M based on the updated distribution. For each nucleotide in all positions in M, start with a pseudocount of 1. For all possible x, in all clusters i, add $P(B_i = x \mid R_i, M)$ to the count for the nucleotide in the respective position, for each position in the motif. Normalize by dividing all counts by the number of clusters plus 4.

Mapping RNA-seq reads for entropy calculations

60 X 60 bp reads (WT, upf1 null, and dbr1 null samples) were initially mapped with TopHat2 (Kim et al. 2013) (tophat-2.0.0.Linux_x86_64) giving TopHat no annotations and allowing it to discover novel splice junctions using the following parameters: **tophat -i 20 -I 10000 -a 10 --segment-length 15 --bowtie1 SacCer3 end1.fastq end2.fastq** Each barcoded sample was mapped on its own and additionally all samples were mapped together to find as many novel splice junctions as possible. A custom Bowite index was created for all splice junctions found by Tophat by concatenating the 50nt of sequence

immediately before and after the junction to ensure the reads had at least a 10nt overhang on each side of the junction. Bowtie1 was run with this custom index (genome + novel splice junctions) on each end of each sequencing library separately because parried end reads would be able to map to this custom index with many 100nt fragments. Bowtie was run as follows: **bowtie -S -m 1 -SacCer3_custom_index one_end_reads.fastq outfile.sam**. Bowtie read mapping to the custom splice index was used to calculate entropy of each splice junction (Graveley et al. 2011) using the formula below, as in Graveley et al., using the positions around the junction where read starts may fall.

pi = reads at offset i / total reads to junction window
Entopy = - sumi(pi * log(pi) / log2)

The entropy cutoff of 2 bits corresponds to uniform coverage of at least 4 distinct read start positions around each splice junction, or more variable coverage of a larger number of positions (Fig. S4A).

RPL30 AT-AC isoforms

These isoforms insert a stop codon early in the message, generating an upstream open reading frame (uORF). These isoforms might therefore be translated under specific conditions via uORF-medated translational regulation (Hinnebusch 1993), potentially producing a truncated protein comprising the C-terminal half of full length RPL30. RPL30 is known to regulate splicing and translation of transcripts from the *RPL30* locus by binding to RNA secondary structure at the 5' end of the pre-mRNA or mRNA.

Sequence conservation

PhastCons scores were downloaded from the UCSC genome browser (phastCons7way) for the novel BP and novel splice site analyses. For the novel splice site plots, the entire region surrounding the splice site in the figure had to fall into the region of question (i.e., intron or CDS). “Intergenic” refers to any region completely outside of a CDS or intron. For the BP conservation plot, only the location of the BP was considered for classifying the BP by location.

Protein length analysis

For all novel splice junctions with entropy at least 2 that overlap an annotated gene, the protein sequence of the resultant transcript was constructed. The length of each novel protein sequence was compared to the length of the annotated protein from the same gene and reported in Figure 4C. When constructing the novel protein sequences, the following assumptions were followed:

1. In cases where a gene has multiple novel splice junctions, only one is considered at a time (i.e. if there are 3 novel splice junctions in one gene, three protein sequences are created).
2. All annotated introns are spliced out, except if they overlap the novel splice junction being considered at the time.
3. If a novel splice junction removes the annotated translation start site, the next available AUG is used.

MISO analysis of splicing

In order to produce Figure 6A, retained intron annotations were created from all splice junctions with entropy >=2. Retained introns were splice junctions detected in the WT, upf1 null, or dbr1 null samples that did not overlap any other splice junctions detected, annotated or novel. To build the RI MISO annotations 200nt flanking the intron was used as exonic sequence. MISO (misopy/0.4.6) was run. For Waern et al data (downloaded from http://downloads.yeastgenome.org/published_datasets/Waern_2013_PMID_23390610/fastq/), --read-length = 76. For Brar et al. data (GEO accession number GSE34082), only reads of length 28-30 nt were used and --read-length was set to 29. Only footprints are shown for Brar et al. data because the total RNA libraries had few reads that fell into the 28-30 nt range. Prior to mapping Brar et al. data, poly(A) adaptor sequences were trimmed off of the reads using Cutadapt. Brar et al. and Waern et al. reads were mapped to the genome, defined splice junctions (UCSC, sacCer3), and novel splice junctions with entropy ≥ 2 in the WT, upf1 null, and dbr1 null RNA-seq (see above) using Tophat2. Summary tables from MISO output were generated for events with x=1, y=0, n=20, psi confidence = 0.5 (see

“Using the read class counts” https://miso.readthedocs.org/en/fastmiso/). These were considered “confident” psi values (see bellow).

In order to produce Figure 6B, annotations for all splice junctions detected in any sample with entropy ≥ 2 and all annotated introns were created. Splicing events that overlapped each other were grouped into one "gene" agnostic to known gene boundaries. The 200 nt flanking the furthest upstream 5'ss and the furthest downstream 3'ss for a given "gene" were used as exonic sequence. Miso (misopy/0.5.3) was run for all samples of both polyA and riboZero data. Events with a PSI confidence interval >= .5 or less than 20 reads uniquely assignable to either the given event isoform or the retained intron isoform were filtered out.

Clustering of PSI values

If an event had confident PSI values in at least half of the conditions, the missing psi values were replaced with the mean PSI from the confident samples. Clustering was done with heatmap.2 in R (Warnes et al. 2015).

Cufflinks (RNA-seq FPKMs)

Cufflinks(Trapnell et al. 2012) (version 2.2.1) was used to calculate FPKMs for the RNA-seq data using the command **cuffdiff -o . --library-type fr-firststrand -u -N -b SacCer3.fsa saccharomyces_cerevisiae_R64-1-1_20110208.gff wt1.bam,wt1.bam dbr1-1.bam,dbr1-2.bam upf1-1.bam,upf1-2.bam**

Branch-seq CPM calculations

Branch-seq CPMs were calculated using the formula CPM = F/((L)(M/1,000,000)) Where M is the total number of mapped reads. F is the number of strand-specific BP (3' end) reads within the L nucleotides centered on the BP peak. L=11 nt.

Genes with multiple BPs

5'SS-BP pairs from annotated introns with computationally predicted BPs (282)(Meyer et al. 2011) and all 268 cnBPs with typical 5'SS 5'SS-BP were considered in this analysis for a total of 550 5'SS-BP pairs. Any overlapping 5'SS-BP pairs on the same strand were grouped into one “intron island.” For islands that contain 2 or more BPs, it was required that there was a BP motif with 2 or fewer mismatches from “TACTAAC” within 3nt of the BP peak the keep the peak for downstream analyses. This yielded 11 intron islands that use 2 BPs and one intron island that uses 3 BPs. For the genes that use 2 BPs the distance from the 5'SS to the BP is the distance for each BP to its paired 5'SS. BP1 is the more 5'SS BP in the intron island. Sequence logos made with WebLogo (Crooks et al. 2004).

Novel and annotated BP motifs

Sequence 15nt up and downstream of the BP peaks were submitted to MEME (Bailey et al. 2009) (Version 4.10.0) to generate sequence logos. Only BP detected by Branch-seq are in the logos in Figure 2.

Human BP motif was generated using sequences 10 nt up and downstream of the BP nt from Mercer et al’s (Mercer et al. 2015) annotated BPs. 1000 sequences were submitted to MEME (maximum MEME accepts) to generate the motif.

Conditions in Figure 6A

Conditions in (A), from table 1 of (Waern and Snyder 2013) include Exponential growth: YPD medium, Salt: 1M NaCl for 45 min, DNA damage: 1mM MMS for 1 hr, Alpha factor: 2.5mM for 45 min and add additional 50 uL to 25 mL yeast for additional 30 min, Sorbitol: 1M for 45 min, Oxidative stress: 0.4M H_2O_2 for 45 min, Heat shock: 37 deg C for 1 hr, Stationary phase: 18 day at 30 deg C, SC glycerol media: 4% glycerol instead of glucose, High calcium = 10mM calcium chloride medium, Low nitrogen: 20% of normal amount of Yeast Nitrogen Base in YPAD, Calcoflour: 0.1% for 1 hr, Hydroxyurea: 0.075M for 1 hr, Grape juice: filtered Walgreen’s brand grape juice, Benomyl: 5 ug/mL for 1 hr, Congo red: 30 ug/mL for 1 hr.

LSM2 qPCR primer sequences

Actin primers:

ScerACT1_junct_F: ATGGATTCTGAGGTTGCTGCT

ScerACT1_mRNA_Rev: GGAGTCTTTTTGACCCATACCGA

LSM2 constitutive exon:

LSM2 qPCR Exon 2F constitutive: TAAAAAACGACATTGAAATAAAAGGTACA

LSM qPCR Exon 2R constitutive: TTCATCTGTGCATGATATGTTGTCTA

LSM2 novel 3'SS (PTC isoform):

LSM2 qPCR new 3’ss junction F: GTGGTCGTAGAGTCAAGTACTAAC

LSM qPCR Exon 2R constitutive: TTCATCTGTGCATGATATGTTGTCTA

LSM2 annotated 3'SS isoform:

LSM2 qPCR canonical (normal) 3’ss junction F: GTGGTCGTAGAGTTAAAAAACGAC

LSM qPCR Exon 2R constitutive: TTCATCTGTGCATGATATGTTGTCTA

RNA14 (NMD negative control):

GG10_for: ATGTCCAGCTCTACGACTCCTGAT

GG11_rev: GCGTATGACTCTTGAGTTTCCAAA (From Joshua Arribere(Arribere and Gilbert 2013))

TCA17 (NMD positive control):

GG8_for:GCCTTGCTTCGTATCATTGATAGA

GG9_rev:CATCATCAGCTCCACTTAGGCTTT (From Joshua Arribere(Arribere and Gilbert 2013))

***RPL30* primer sequences**

RT: SuperScript II protocol (Invitrogen)

GG13_YGL030W_rev: AAGCCAACTTTTGGTTGATAGA

PCR: Phusion (NEB)

GG14:YGL030W_5’end_for: agaccggagtgtttaagaacct

GG15:YGL030W_rev_ATACjunc: TAACTGGGGCctgttgaaat

***SED1* primers**

For Figure S4B:

RT: Random hexamers (Invitorgen), following SuperScript II protocol (Invitrogen).

PCR: Phusion (NEB)

GG17:SED1_for: TACATCTTTGCCACCAAGCA

GG18:SED1_rev: TTTGGTGGTAGTGCCCTTAGA

For Figure S5E - SED1 apparent RT artifact

Colony PCR was performed to put a T7 primer onto the start of the SED1 sequence. PCR product was gel extracted and used as a temple for T7 in vitro transcription (Epicentre AmpliScribe™ T7-Flash™ Transcription Kit), DNA was digested, and RNA product was cleaned via phenol chloroform extraction. RNA was gel extracted using UV shadowing visualization. RT and PCR were performed as in Figure S5B.

Scer_SED1_colony_Forward: TAATACGACTCACTATAGGGgacaagcaaaataaaatacgttcg
Scer_SED1_colony_Reverse: ttaaactacccctattgcttttaga

Plotting

Additional plots in this paper were made with ggplot2(Wickham 2009), IGV (Robinson et al. 2011), matplotlib, Pictogram, WebLobo, and MEME.

Legends to Supplemental Figures

Figure S1. Additional details pertaining to Branch-seq protocol.

(A) Left: 2D gel used to isolate lariats from top, middle, and bottom sections of arc. Right: Top and bottom splices excised. D1: 6% TBE-urea. D2: 20% TBE-urea. (B) Read coverage (green) in *UBC13* intron from Larita-seq. Depletion of reads between BP and 3'SS indicates lariat tails are digested when lariats accumulate in *dbr1*Δ yeast (Chapman and Boeke 1991). (C) Additional examples like inset in figure 1B of read start plots for BPs in 4 individual introns. The majority of reads are located at +1 or +2 position on an intron by intron basis. (D) Hypothesis for predominant +1 vs +2 read start position in individual introns. RNA sequence in black, question marks are unknown nucleotides after the BP. BP A in red. The RT primer, green, may prime at different locations, and produce sequencing products (blue arrow), starting at different positions relative to the BP nucleotide. +1 sequencing is expected if nucleotide after TACTAAC is an A because of anchored oligo(dT) priming step in RT. Similarly, +2 position is expected if nucleotide after TACTAAC is C, G, or T. Sequencing at -2 is due to mis-priming of anchored oligo(dT) primer over the terminal C of the BP motif. (E) Genomic sequence immediately downstream of annoated BPs (boxed) with maximum peak from (C) at +1, left, and +2, right, confirms hypothesis in (D). (F) Branch-seq reads in the *EFM5* intron are shifted 5 nt from the annotated BP location (blue underline) corresponding to a <u>A</u>ACTAAC BP (red underline).

Figure S2. Further characterization of novel BPs.

(A) Left: Novel BPs (blue) are not conserved compared to annotated BPs (red). Right: novel BPs from blue line in left plot broken down by genomic location. (B) 5'SS motif of 162 putative novel BP with atypical 5'SS. (C) Novel BP overlapping *YDL138W* ORF (plus strand) comes from the minus strand, potentially from a longer form of the annotated CUT/SUT on the minus strand. Novel BP is confirmed by one Branch-seq read pair and several Lariat-seq junction reads. (D) RT sometimes skips over the BP nucleotide in Lariat-seq junction reads (see methods).

Figure S3. Characteristics of lariats captured by Branch-seq.

(A) Comparison of expression levels of lariats recovered in Branch-seq (combined top, middle, and bottom slices of arc) to expression of their parent mRNA in poly(A) selected RNA-seq. Only annotated BPs are plotted. (B) Same as (A) but regression calculated for different lariat sizes, suggested that Branch-seq read counts are semi-quantitative for lariat loops smaller than 100 nt. (C) Expression level of annotated and novel BPs recovered by Branch-seq. (D) Lariat loop lengths recovered by Branch-seq and Lariat-seq LJ reads.

Figure S4. Novel introns confirmed by entropy resemble annotated introns but preferentially come from short transcripts.

(A) Entropy of annotated (green) and novel (pink) splice junctions, separated by splice site motif AT/AC, GC/AG, GT/AG. A cutoff of entropy of 2 was used to define novel splice junctions(Graveley et al. 2011). (B) 5'SS and 3'SS motifs for annotated (top) and novel (bottom) splice sites. (C) Gene lengths (TSS to poly(A) site) (Pelechano et al. 2013) for genes containing novel BPs identified in Branch-seq and genes containing novel introns with entropy ≥ 2 identified in RNA-seq data.

Figure S5. Experimental testing of AT-AC splice site introns.

RT-PCR on total RNA to verify (A) *RPL30* and (B) *SED1* AT-AC splice sites. *SED1* AT-AC splice site intron is located inside a long repeat (C) highlighted in green and (D) shown in a dot plot. (E) RT-PCR on in-vitro transcribed full length *SED1* RNA. The presence of a product here of the expected spliced size suggests the presence of some sort of RT artifact.

Figure S6. Conservation of novel intron splice sites from isoforms that show splicing patterns similar to annotated introns.

Arrows above each splice site indicate sequence direction. UCSC browser snapshots are shown for splice sites located outside of coding sequences.

Figure S7. Translation of YNL194-YNL195C fusion transcript changes throughout meiosis time course.

Sashimi plots depict reads in exons and reads spanning splice junction (numbered arcs) with PSI value shown to the right with confidence bounds (tie fighter plot). Plots are ordered by progression through meiosis time course from Brar et al. (Brar et al. 2012) for (A) ribosome footprint profiling data.

Table S1: Branch-seq BP peaks paired 5'SS motifs.

Table S2: SacCer2 coordinates of GEM-BP and winBP peaks.

Table S3: GTATGT motif frequency at 5'SS and generally in introns.

Table S4: Branch-seq CPMs.

Table S5: Saccer3 coordinates of lariat junction reads.

Table S6: Novel splice junctions with entropy ≥ 2bits.

Table S7: Figure 6A PSI values.

Table S8: Figure 6A event annotations.

Table S9: Figure 6B PSI values.

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Figure S1

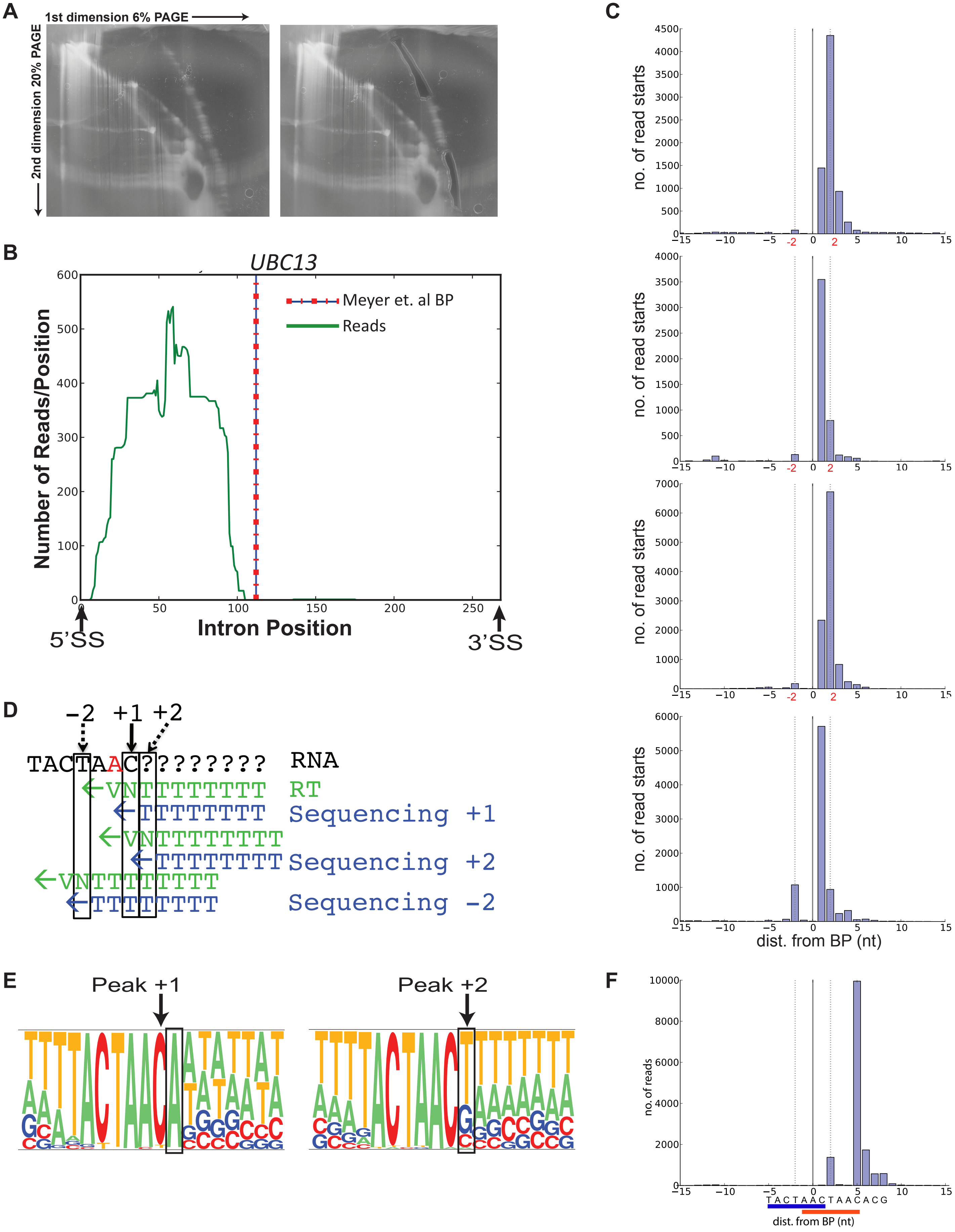

A
1st dimension 6% PAGE
2nd dimension 20% PAGE
B
UBC13
Meyer et. al BP
Reads
Number of Reads/Position
600
500
400
300
200
100
0
0
50
100
150
200
250
Intron Position
5'SS
3'SS
C
no. of read starts
4500
4000
3500
3000
2500
2000
1500
1000
500
0
−15
−10
−5
-2
0
2
5
10
15
no. of read starts
4000
3500
3000
2500
2000
1500
1000
500
0
no. of read starts
7000
6000
5000
4000
3000
2000
1000
0
no. of read starts
6000
5000
4000
3000
2000
1000
0
dist. from BP (nt)
D
−2
+1
+2
TACTAAC????????? RNA
←VNTTTTTTTT RT
←TTTTTTTT Sequencing +1
←VNTTTTTTTT
←TTTTTTTT Sequencing +2
←VNTTTTTTTT
←TTTTTTTT Sequencing −2
E
Peak +1
Peak +2
F
no. of reads
10000
8000
6000
4000
2000
0
−15
−10
−5
0
5
10
15
TACTAACTAACACG
dist. from BP (nt)

Figure S2

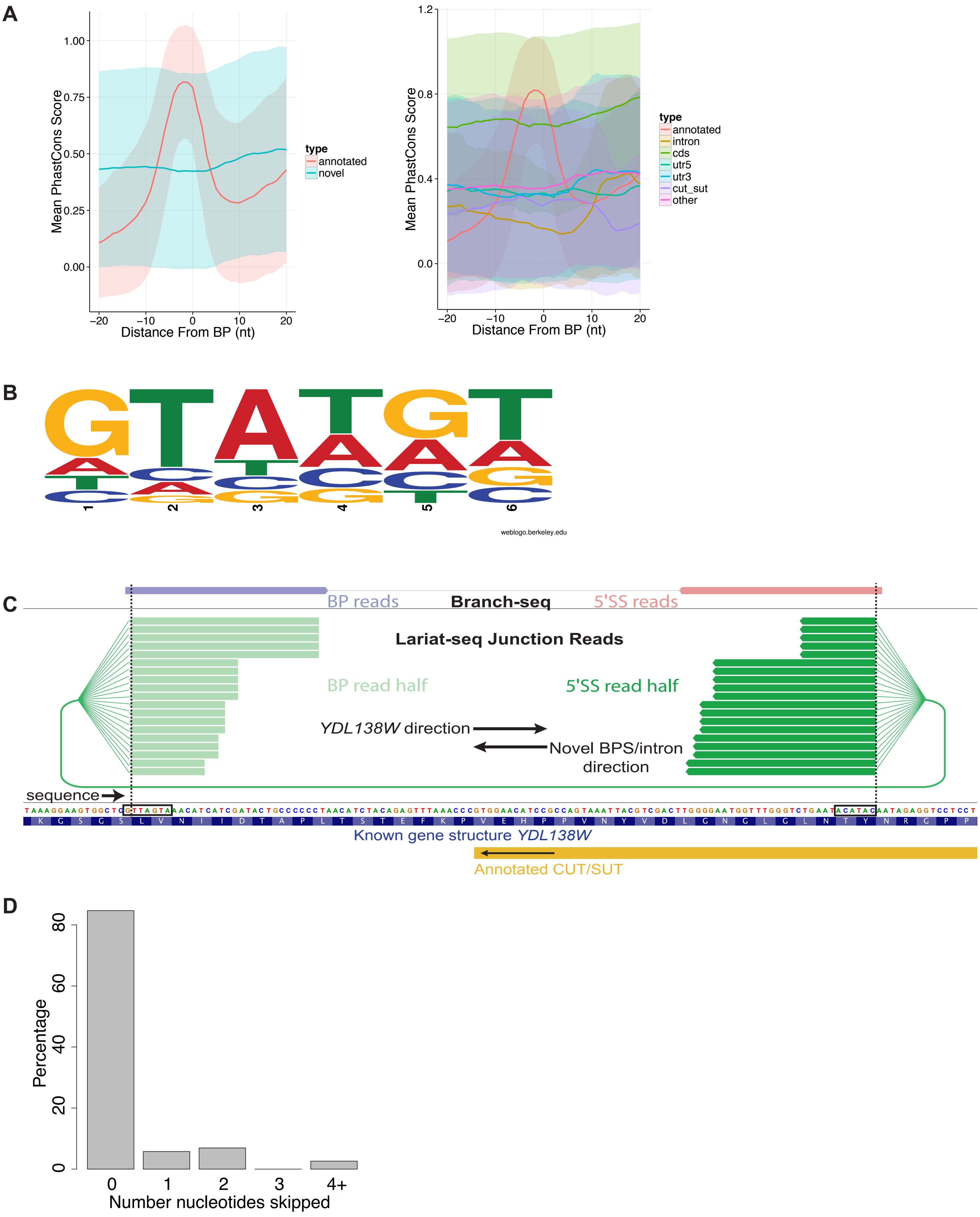

A
Mean PhastCons Score
1.00
0.75
0.50
0.25
0.00
−20
−10
0
10
20
Distance From BP (nt)
type
annotated
novel
Mean PhastCons Score
1.2
0.8
0.4
0.0
−20
−10
0
10
20
Distance From BP (nt)
type
annotated
intron
cds
utr5
utr3
cut_sut
other
B
1
2
3
4
5
6
weblogo.berkeley.edu
C
BP reads
Branch-seq
5'SS reads
Lariat-seq Junction Reads
BP read half
5'SS read half
YDL138W direction
Novel BPS/intron direction
sequence
TAAAGGAAGTGGCTCGTTAGTAAACATCATCGATACTGCCCCCCTAACATCTACAGAGTTTAAACCCGTGGAACATCCGCCAGTAAATTACGTCGACTTGGGGAATGGTTTGGGTCTGAATACATACAATAGAGGTCCTCCT
K G S G S L V N I I D T A P L T S T E F K P V E H P P V N Y V D L G N G L G L N T Y N R G P P
Known gene structure YDL138W
Annotated CUT/SUT
D
Percentage
0
20
40
60
80
0
1
2
3
4+
Number nucleotides skipped

Figure S3

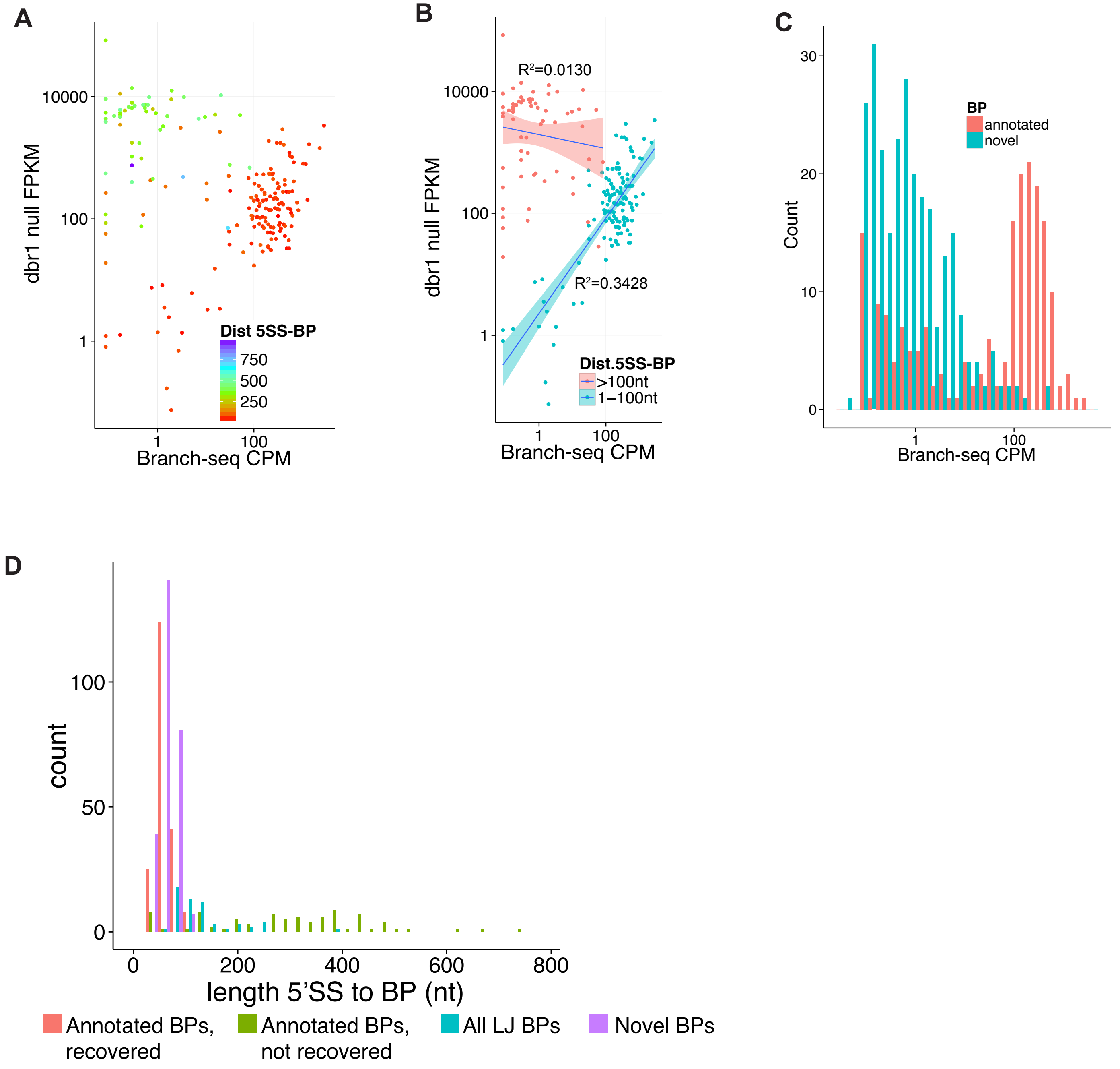

A
dbr1 null FPKM
10000
100
1
Branch-seq CPM
1
100
Dist 5SS-BP
750
500
250
B
R²=0.0130
R²=0.3428
10000
100
1
dbr1 null FPKM
Branch-seq CPM
1
100
Dist.5SS-BP
>100nt
1–100nt
C
Count
30
20
10
0
BP
annotated
novel
Branch-seq CPM
1
100
D
count
100
50
0
0
200
400
600
800
length 5'SS to BP (nt)
Annotated BPs, recovered
Annotated BPs, not recovered
All LJ BPs
Novel BPs

Figure S4

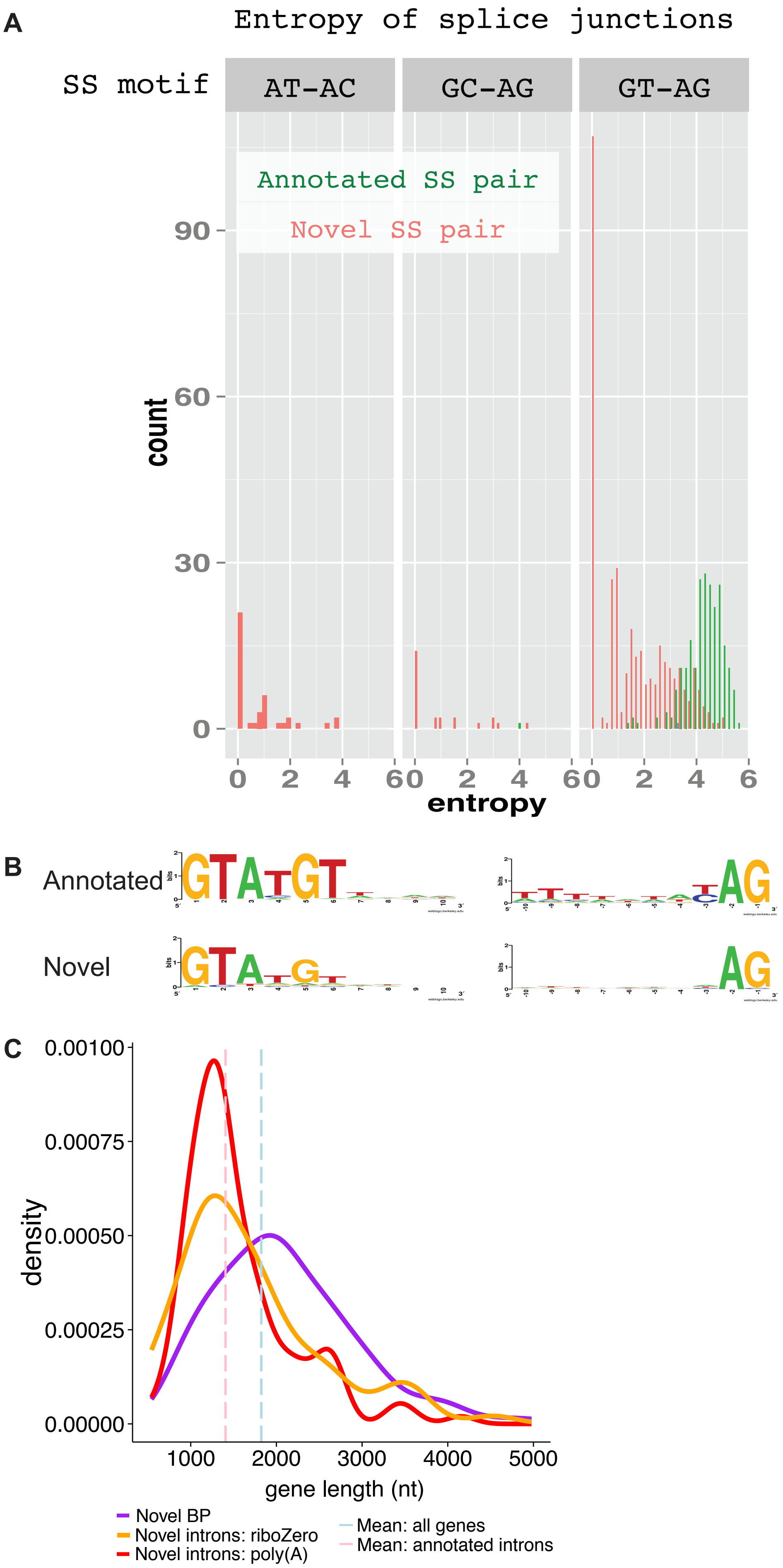
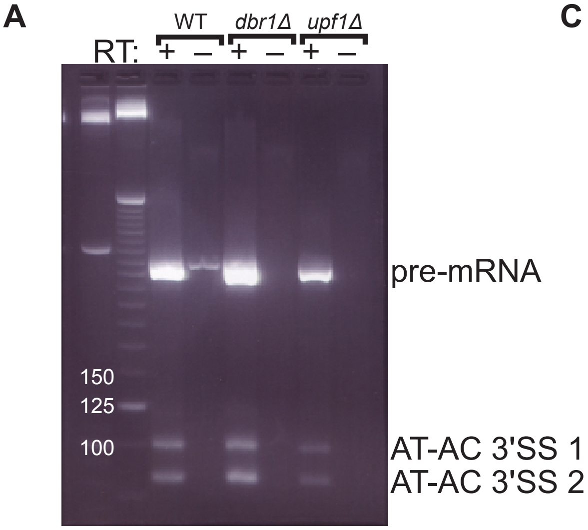
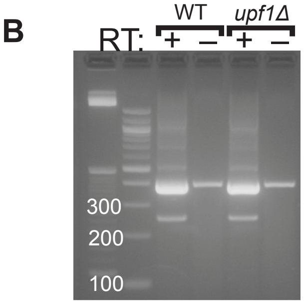

A
Entropy of splice junctions
SS motif
AT-AC
GC-AG
GT-AG
Annotated SS pair
Novel SS pair
count
90
60
30
0
0
2
4
6
entropy
B
Annotated
Novel
GTATGT
AG
GTAG
AG
C
0.00100
0.00075
0.00050
0.00025
0.00000
density
1000
2000
3000
4000
5000
gene length (nt)
Novel BP
Novel introns: riboZero
Novel introns: poly(A)
Mean: all genes
Mean: annotated introns

Figure S5



RPL30 PCR Expected Sizes
pre-mRNA = 297nt
AT-AC = 83nt



SED1 PCR Expected Sizes
No intron = 409nt
predicited (ent) AT-AC = 301nt
actual AT-AC = 256nt

C

```
CLUSTAL 2.1 multiple sequence alignment


SED1_Genomic      ATGAAATTATCAACTGTCCTATTATCTGCCGGTTTAGCCTCGACTACTTTGGCCCAATTT 60
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      TCCAACAGTACATCTGCTTCTTCCACCGATGTCACTTCCTCCTCTTCCATCTCCACTTCC 120
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      TCTGGCTCAGTAACTATCACATCTTCTGAAGCTCCAGAATCCGACAACGGTACCAGCACA 180
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      GCTGCACCAACTGAAACCTCAACAGAGGCTCCAACCACTGCTATCCCAACTAACGGTACC 240
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      TCTACTGAAGCTCCAACCACTGCTATCCCAACTAACGGTACCTCTACTGAAGCTCCAACT 300
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      GATACTACTACTGAAGCTCCAACCACCGCTCTTCCAACTAACGGTACTTCTACTGAAGCT 360
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      CCAACTGATACTACTACTGAAGCTCCAACCACCGGTCTTCCAACCAACGGTACCACTTCA 420
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      GCTTTCCCACCAACTACATCTTTGCCACCAAGCAACACTACCACCACTCCTCCTTACAAC 480
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      CCATCTACTGACTACACCACTGACTACACTGTAGTCACTGAATATACTACTTACTGTCCA 540
PCR-band-05       -CATCTACTGACTACACCACTGACTACACTGTAGTCACTGAATATACTACTTACTGTCCA 59
                   ***********************************************************

SED1_Genomic      GAACCAACCACTTTCACCACAAACGGTAAGACTTACACCGTCACTGAACCAACCACATTG 600
PCR-band-05       GAACCAACCACTTTCACCACAAACGGTAAGACTTACACCGTCACTGAACCAACCAC---- 115
                  ********************************************************

SED1_Genomic      ACTATCACTGACTGTCCATGCACCATTGAAAAGCCAACAACCACATCAACCACCGAATAC 660
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      ACTGTAGTCACTGAGTACACTACTTACTGTCCAGAACCAACCACTTTCACCACAAACGGT 720
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      AAGACTTACACCGTCACTGAACCAACCACTTTGACTATCACTGACTGTCCATGTACTATT 780
PCR-band-05       -----------------------------TTTGACTATCACTGACTGTCCATGTACTATT 146
                                               *******************************

SED1_Genomic      GAAAAGAGCGAAGCCCCTGAGTCTTCTGTCCCAGTTACCGAATCTAAGGGCACTACCACC 840
PCR-band-05       GAAAAGAGCGAAGCCCCTGAGTCTTCTGTCCCAGTTACCGAATCTAAGGGCACTACCACC 206
                  ************************************************************

SED1_Genomic      AAAGAAACAGGTGTTACTACCAAACAAACCACAGCCAACCCAAGTCTAACCGTCTCCACA 900
PCR-band-05       AAA--------------------------------------------------------- 209
                  ***

SED1_Genomic      GTCGTCCCAGTTTCATCCTCTGCTTCTTCTCATTCCGTTGTCATCAACAGTAACGGTGCT 960
PCR-band-05       ------------------------------------------------------------

SED1_Genomic      AACGTCGTCGTTCCAGGTGCTTTAGGTTTGGCTGGTGTTGCTATGTTATTCTTATAA 1017
PCR-band-05       ---------------------------------------------------------
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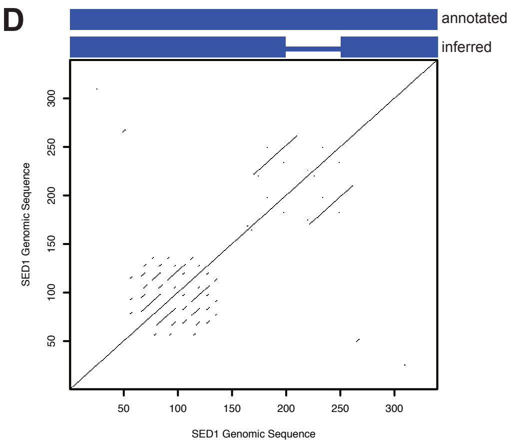


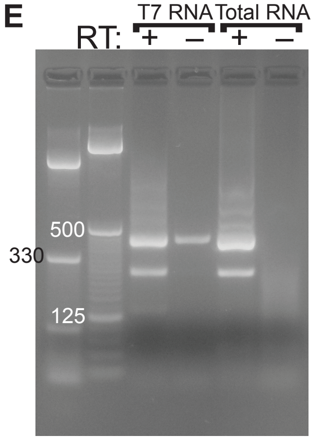
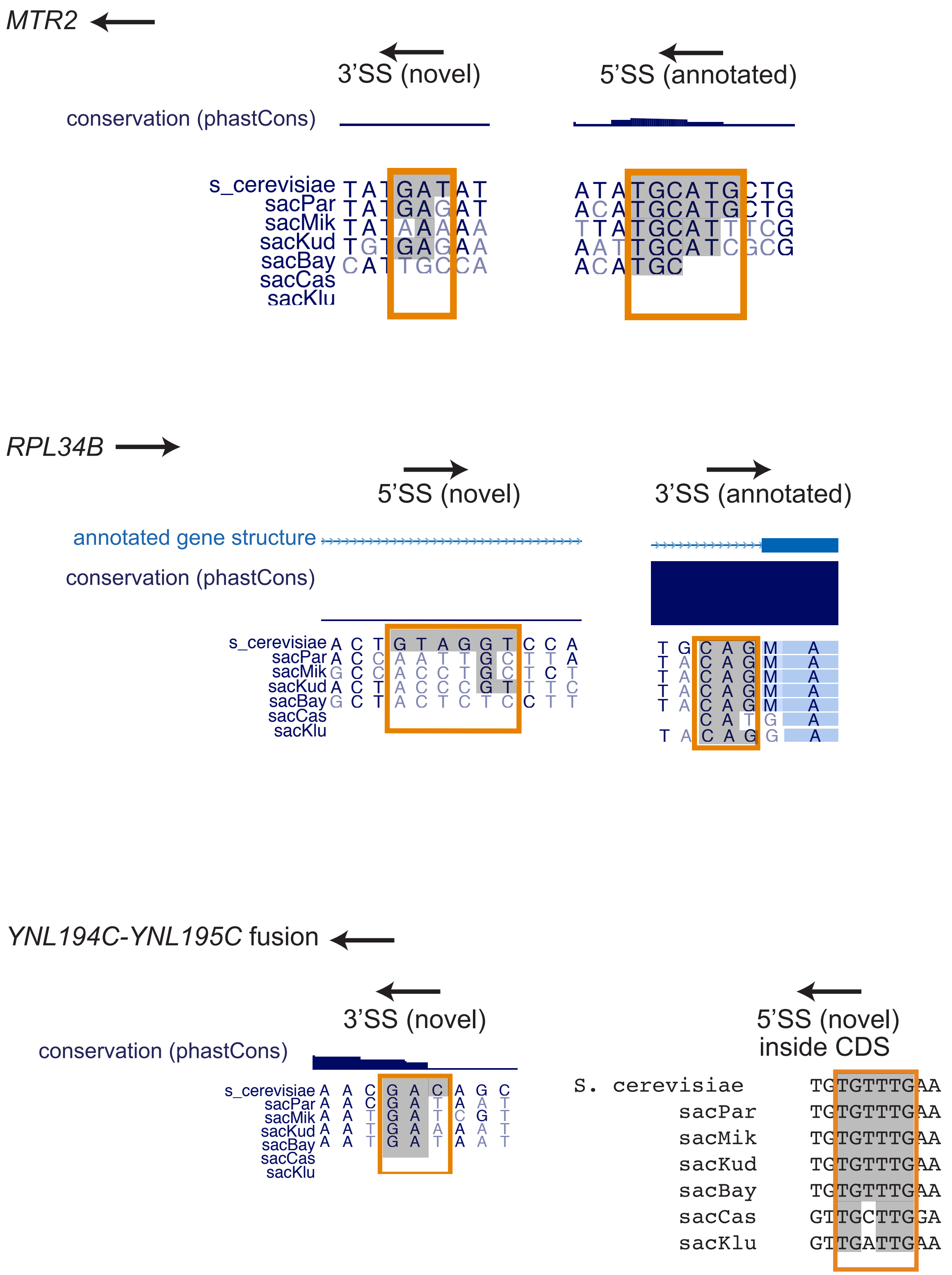
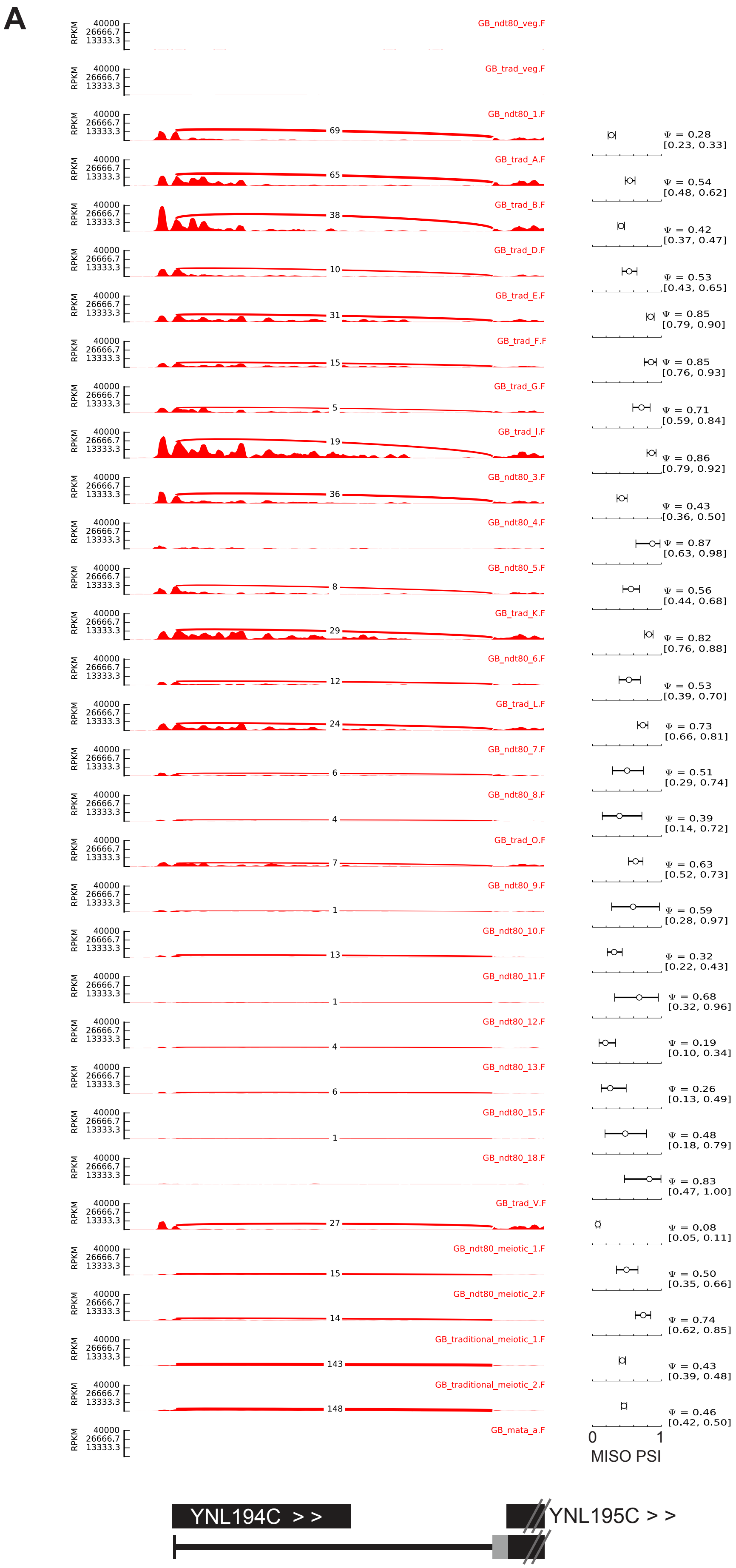


Figure S6



MTR2
3'SS (novel)
5'SS (annotated)
conservation (phastCons)
s_cerevisiae
sacPar
sacMik
sacKud
sacBay
sacCas
sacKlu
TATGATAT
TATGAGAT
TATAAAAA
TGTGAGAA
CATTGCCA
ATATGCATGCTG
ACATGCATGCTG
TTATGCATTTCG
AATTGCATCGCG
ACATGC
RPL34B
5'SS (novel)
3'SS (annotated)
annotated gene structure
conservation (phastCons)
s_cerevisiae
sacPar
sacMik
sacKud
sacBay
sacCas
sacKlu
A C T G T A G G T C C A
A C C A A T T G C T T A
G C C A C C T G C T C T
A C T A C C C G T T T C
G C T A C T C T C C T T
T G C A G M A
T A C A G M A
T A C A G M A
T A C A G M A
T A C A G M A
C A T G A
T A C A G G A
YNL194C-YNL195C fusion
3'SS (novel)
5'SS (novel)
inside CDS
conservation (phastCons)
s_cerevisiae
sacPar
sacMik
sacKud
sacBay
sacCas
sacKlu
A A C G A C A G C
A A C G A T A A T
A A T G A T C G T
A A T G A A A A T
A A T G A T A A T
S. cerevisiae
sacPar
sacMik
sacKud
sacBay
sacCas
sacKlu
TGTGTTTGAA
TGTGTTTGAA
TGTGTTTGAA
TGTGTTTGAA
TGTGTTTGAA
GTTGCTTGGA
GTTGATTGAA

Figure S7


A
RPKM
40000
26666.7
13333.3
GB_ndt80_veg.F
GB_trad_veg.F
GB_ndt80_1.F
69
Ψ = 0.28 [0.23, 0.33]
GB_trad_A.F
65
Ψ = 0.54 [0.48, 0.62]
GB_trad_B.F
38
Ψ = 0.42 [0.37, 0.47]
GB_trad_D.F
10
Ψ = 0.53 [0.43, 0.65]
GB_trad_E.F
31
Ψ = 0.85 [0.79, 0.90]
GB_trad_F.F
15
Ψ = 0.85 [0.76, 0.93]
GB_trad_G.F
5
Ψ = 0.71 [0.59, 0.84]
GB_trad_I.F
19
Ψ = 0.86 [0.79, 0.92]
GB_ndt80_3.F
36
Ψ = 0.43 [0.36, 0.50]
GB_ndt80_4.F
Ψ = 0.87 [0.63, 0.98]
GB_ndt80_5.F
8
Ψ = 0.56 [0.44, 0.68]
GB_trad_K.F
29
Ψ = 0.82 [0.76, 0.88]
GB_ndt80_6.F
12
Ψ = 0.53 [0.39, 0.70]
GB_trad_L.F
24
Ψ = 0.73 [0.66, 0.81]
GB_ndt80_7.F
6
Ψ = 0.51 [0.29, 0.74]
GB_ndt80_8.F
4
Ψ = 0.39 [0.14, 0.72]
GB_trad_O.F
7
Ψ = 0.63 [0.52, 0.73]
GB_ndt80_9.F
1
Ψ = 0.59 [0.28, 0.97]
GB_ndt80_10.F
13
Ψ = 0.32 [0.22, 0.43]
GB_ndt80_11.F
1
Ψ = 0.68 [0.32, 0.96]
GB_ndt80_12.F
4
Ψ = 0.19 [0.10, 0.34]
GB_ndt80_13.F
6
Ψ = 0.26 [0.13, 0.49]
GB_ndt80_15.F
1
Ψ = 0.48 [0.18, 0.79]
GB_ndt80_18.F
Ψ = 0.83 [0.47, 1.00]
GB_trad_V.F
27
Ψ = 0.08 [0.05, 0.11]
GB_ndt80_meiotic_1.F
15
Ψ = 0.50 [0.35, 0.66]
GB_ndt80_meiotic_2.F
14
Ψ = 0.74 [0.62, 0.85]
GB_traditional_meiotic_1.F
143
Ψ = 0.43 [0.39, 0.48]
GB_traditional_meiotic_2.F
148
Ψ = 0.46 [0.42, 0.50]
GB_mata_a.F
0
1
MISO PSI
YNL194C > >
YNL195C > >

Supplementary Tables

Table S1. Branch-seq BP peaks paired 5'SS motifs.

No. mismatches from /GTATGT	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**All**	0 or 1 mut	% 0 or 1 mut
153 annotated BPs: winBP	103	35	7	7	1	0	0	153	138	90.20
191 putative novel BPs: winBP	64	62	28	13	18	5	1	191	126	65.97
196 annotated BPs: GEM-BP	105	44	24	16	7	0	0	196	149	76.02
350 putative novel BPs: GEM-BP	61	161	78	34	12	3	1	350	222	63.43

Table S2: GEM-BP and winBP peaks

chr	bp_nt	strand	5ss_bp_pair	winBP	GEM-BP	bp_anno	5ss_anno	5ss_mm	5ss	u_a	u_n	cnBP	lcnBP	hcnBP	Qin_novel	best_bp_in15	best_bp_mm	best_bp_nt_in15
chrI	30553	-	chrI:30553:30626:-	0	1	0	0	3	AAGTGT	0	1	0	0	0	0	GATTAAC	2	30553
chrI	31426	-	chrI:31426:31464:-	0	1	0	0	3	ATAACT	0	1	0	0	0	0	CATTAAC	2	31426
chrI	78465	+	chrI:78419:78465:+	0	1	0	0	2	GTGTGG	0	1	0	0	0	0	TACTAAC	0	78465
chrI	87439	+	chrI:87389:87439:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	87439
chrI	126072	+	chrI:125985:126072:+	0	1	0	0	1	GTATGG	0	1	1	0	1	0	CATTAAC	2	126072
chrI	134872	-	chrI:134872:134944:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	CACTAAC	1	134872
chrI	142338	+	chrI:142256:142338:+	1	0	0	1	0	GTATGT	0	0	0	0	0	0	AACTAAT	2	142344
chrI	142344	+	chrI:142256:142344:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	AACTAAT	2	142344
chrI	151022	-	chrI:151022:151098:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	151022
chrI	152002	-	chrI:152002:152055:-	1	0	0	0	2	GTATAC	0	0	0	0	0	0	TACTAAT	1	152004
chrI	152004	-	chrI:152004:152055:-	0	1	0	0	2	GTATAC	0	1	0	0	0	0	TACTAAT	1	152004
chrI	157810	-	chrI:157810:157862:-	0	1	0	0	2	GTATAC	0	1	0	0	0	0	TACTAAT	1	157810
chrII	13950	-	chrII:13950:14027:-	1	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	13950
chrII	45936	+	chrII:45875:45936:+	0	1	0	0	2	GCATGC	0	1	0	0	0	0	TACTAAC	0	45936
chrII	47071	-	chrII:47071:47143:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAT	1	47071
chrII	49796	+	chrII:49765:49796:+	0	1	0	0	3	GAACGC	0	1	0	0	0	0	AACTAAT	2	49796
chrII	76232	+	chrII:76189:76232:+	0	1	0	0	1	GTCTGT	0	1	1	0	1	0	TACTAAC	0	76232
chrII	89158	-	chrII:89158:89219:-	0	1	0	0	4	CAAAGC	0	1	0	0	0	0	TACTAAC	0	89158
chrII	110451	-	chrII:110451:110507:-	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	110451
chrII	110932	+	chrII:110882:110932:+	1	1	1	1	1	GTATGC	1	0	0	0	0	0	TACTAAC	0	110932
chrII	115534	+	chrII:115478:115534:+	1	0	0	0	0	GTATGT	0	1	1	0	1	1	TACTTAC	1	115536
chrII	125234	+	chrII:125158:125234:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	125234
chrII	142787	-	chrII:142787:142849:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	142787
chrII	142813	-	chrII:142813:142850:-	1	0	0	0	3	CTAAGA	0	1	0	0	0	0	ATCGAAC	3	142801
chrII	167928	+	chrII:167855:167928:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAT	1	167928
chrII	168770	+	chrII:168696:168770:+	0	1	1	0	2	GTAATT	1	0	0	0	0	0	TACTAAC	0	168770
chrII	170731	+	chrII:170680:170731:+	1	0	0	1	0	GTATGT	0	1	1	0	1	1	AACTAAC	1	170730
chrII	170771	+	chrII:170680:170771:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	170771
chrII	186375	-	chrII:186375:186430:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	186375
chrII	206285	+	chrII:206192:206285:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	206285
chrII	221024	+	chrII:220982:221024:+	1	0	0	0	1	GTATGA	0	1	1	1	0	0	CTCTAAC	2	221027
chrII	290471	-	chrII:290471:290528:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	AACTGAC	2	290471
chrII	291715	-	chrII:291715:291771:-	1	0	0	0	1	GTAAGT	0	1	1	0	1	0	AACTATC	2	291713
chrII	306856	-	chrII:306856:306902:-	1	0	0	0	2	GTATCA	0	0	0	0	0	0	TACTGAC	1	306858
chrII	306858	-	chrII:306858:306902:-	0	1	0	0	2	GTATCA	0	1	0	0	0	0	TACTGAC	1	306858
chrII	331390	-	chrII:331390:331438:-	1	0	0	0	1	GTATGA	0	0	0	0	0	0	TACTAAT	1	331392
chrII	331392	-	chrII:331392:331438:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAT	1	331392
chrII	333365	+	chrII:333319:333365:+	1	1	1	0	2	GTAGGA	1	0	0	0	0	0	TACTAAC	0	333365
chrII	341037	-	chrII:341037:341094:-	1	0	0	0	0	GTATGT	0	0	0	0	0	0	GACTAAC	1	341039
chrII	341039	-	chrII:341039:341094:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	GACTAAC	1	341039
chrII	342755	+	chrII:342697:342755:+	1	0	0	0	1	GTGTGT	0	0	0	0	0	0	TATTAAC	1	342757
chrII	342757	+	chrII:342697:342757:+	0	1	0	0	1	GTGTGT	0	1	1	0	1	0	TATTAAC	1	342757
chrII	366534	-	chrII:366534:366582:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	AACTAAC	1	366534
chrII	372031	+	chrII:371971:372031:+	0	1	0	0	2	GAACGT	0	1	0	0	0	0	AACTAAC	1	372031
chrII	407047	-	chrII:407047:407116:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	407047
chrII	419960	+	chrII:419915:419960:+	0	1	0	0	2	TTATGG	0	1	0	0	0	0	GACTAAC	1	419960
chrII	425496	-	chrII:425496:425538:-	0	1	0	0	2	CTAAGT	0	1	0	0	0	0	CATTAAC	2	425496
chrII	426524	-	chrII:426524:426624:-	0	1	1	0	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	426524
chrII	431595	-	chrII:431595:431650:-	0	1	0	0	1	GTAGGT	0	1	1	0	1	0	TACTGAC	1	431595
chrII	443735	-	chrII:443735:443827:-	1	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	443735
chrII	462255	+	chrII:462204:462255:+	1	1	1	1	1	GTATGA	1	0	0	0	0	0	TACTGAC	1	462255
chrII	462472	+	chrII:462424:462472:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	462472
chrII	479389	+	chrII:479340:479389:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	479389
chrII	519068	-	chrII:519068:519131:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAC	0	519068
chrII	592709	-	chrII:592709:592763:-	1	0	0	1	0	GTATGT	0	1	1	1	0	0	CGCTAAC	2	592712
chrII	602175	+	chrII:602099:602175:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	CACTAAC	1	602175
chrII	606346	+	chrII:606276:606346:+	1	0	0	1	0	GTATGT	0	1	1	0	1	0	TCGTCAC	3	606344
chrII	606615	+	chrII:606567:606615:+	1	1	1	0	1	TTATGT	1	0	0	0	0	0	TACTAAC	0	606615
chrII	643000	-	chrII:643000:643073:-	1	0	0	0	3	GCTCGT	0	1	0	0	0	0	TGCGAGC	3	643004
chrII	653429	+	chrII:653364:653429:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	GATTAAC	2	653429
chrII	679973	-	chrII:679973:680034:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	GACTAAC	1	679973
chrII	726947	-	chrII:726947:727006:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	CGCTAAC	2	726947
chrII	756983	-	chrII:756983:757037:-	0	1	0	0	1	GTAGGT	0	1	1	0	1	0	AACTAAC	1	756983
chrII	792452	-	chrII:792452:792495:-	0	1	0	0	2	GTACTT	0	1	0	0	0	0	TATTAAC	1	792452
chrIII	17807	+	chrIII:17761:17807:+	0	1	0	0	2	GTAGGC	0	1	0	0	0	0	AACTAAC	1	17807
chrIII	27690	-	chrIII:27690:27745:-	0	1	0	0	3	GTAATG	0	1	0	0	0	0	TACTAAC	0	27690
chrIII	42034	+	chrIII:41999:42034:+	1	0	0	0	3	CTAATT	0	1	0	0	0	0	TATAAAA	3	42034
chrIII	84710	+	chrIII:84665:84710:+	0	1	0	0	1	GTCTGT	0	1	1	0	1	0	TTCTAAC	1	84710
chrIII	101646	-	chrIII:101646:101700:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	101646
chrIII	107089	+	chrIII:107034:107089:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	107089
chrIII	107255	+	chrIII:107192:107255:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	107255
chrIII	111588	-	chrIII:111588:111632:-	1	1	1	1	1	GTATGC	1	0	0	0	0	0	GACTAAC	1	111588
chrIII	119535	-	chrIII:119535:119586:-	0	1	0	0	3	GTACTG	0	1	0	0	0	0	TACTAAC	0	119535
chrIII	120380	+	chrIII:120290:120380:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAC	0	120380
chrIII	123571	-	chrIII:123571:123637:-	1	0	0	0	3	GTCTAG	0	1	0	0	0	0	TTTTTAC	3	123563
chrIII	169190	-	chrIII:169190:169268:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TTCTAAC	1	169190
chrIII	173137	-	chrIII:173137:173194:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	173137
chrIII	177952	-	chrIII:177952:178031:-	1	1	1	0	1	GTATAT	1	0	0	0	0	0	TACTAAC	0	177952
chrIII	221010	+	chrIII:220979:221010:+	0	1	0	0	4	TATTCT	0	1	0	0	0	0	TACTAAT	1	221010
chrIII	228654	+	chrIII:228610:228654:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	AACTAAC	1	228657

chrIII	228657	+	chrIII:228610:228657:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	AACTAAC	1	228657
chrIII	290581	+	chrIII:290522:290581:+	0	1	0	0	1	GTATTT	0	1	1	0	1	0	AACTAAC	1	290581
chrIV	22303	-	chrIV:22303:22355:-	1	0	0	0	1	GTAAGT	0	1	1	0	1	0	AGCTAAC	2	22305
chrIV	65358	+	chrIV:65308:65358:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	65358
chrIV	104616	+	chrIV:104542:104616:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TATTAAC	1	104616
chrIV	107156	+	chrIV:107107:107156:+	1	0	0	0	1	GTAGGT	0	1	1	1	0	0	TACTCAC	1	107159
chrIV	122157	+	chrIV:122079:122157:+	1	0	0	1	0	GTATGT	0	0	0	0	0	0	TACTAAC	0	122160
chrIV	122160	+	chrIV:122079:122160:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	122160
chrIV	130286	-	chrIV:130286:130359:-	0	1	0	0	2	GTATCG	0	1	0	0	0	0	TACTAAT	1	130286
chrIV	130329	+	chrIV:130289:130329:+	0	1	0	0	1	GTATGC	0	1	1	0	1	0	AACTAAC	1	130329
chrIV	188134	-	chrIV:188134:188194:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TATTAAC	1	188134
chrIV	217970	+	chrIV:217907:217970:+	0	1	1	0	2	GTATTA	1	0	0	0	0	0	TACTAAC	0	217970
chrIV	230262	+	chrIV:230202:230262:+	0	1	1	0	1	GTATTT	1	0	0	0	0	0	TACTAAC	0	230262
chrIV	232835	+	chrIV:232747:232835:+	1	0	0	0	1	GTATAT	0	0	0	0	0	0	CACTGAC	2	232838
chrIV	232838	+	chrIV:232747:232838:+	0	1	0	0	1	GTATAT	0	1	1	0	1	0	CACTGAC	2	232838
chrIV	235105	+	chrIV:235039:235105:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	TTCTAAC	1	235108
chrIV	235108	+	chrIV:235039:235108:+	0	1	0	0	1	GTATGA	0	1	1	0	1	1	TTCTAAC	1	235108
chrIV	239421	-	chrIV:239421:239509:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	239421
chrIV	247246	-	chrIV:247246:247300:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TACTAAC	0	247246
chrIV	248591	+	chrIV:248513:248591:+	0	1	0	0	2	GTCAGT	0	1	0	0	0	0	CACTAAC	1	248591
chrIV	254999	-	chrIV:254999:255044:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	GACTAAC	1	254999
chrIV	267780	+	chrIV:267726:267780:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	267780
chrIV	268934	-	chrIV:268934:269000:-	1	1	0	0	1	GTACGT	0	1	1	0	1	1	TACTGAC	1	268934
chrIV	273738	+	chrIV:273662:273738:+	0	1	0	0	2	GTCCGT	0	1	0	0	0	0	CACTAAC	1	273738
chrIV	299960	-	chrIV:299960:300001:-	0	1	0	0	2	GTTTGG	0	1	0	0	0	0	TACTAAC	0	299960
chrIV	307375	-	chrIV:307375:307457:-	0	1	1	0	2	GGAAGT	1	0	0	0	0	0	TACTAAC	0	307375
chrIV	331276	+	chrIV:331190:331276:+	1	0	0	0	1	GTAAGT	0	0	0	0	0	0	CACTAAC	1	331278
chrIV	331278	+	chrIV:331190:331278:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	CACTAAC	1	331278
chrIV	333710	+	chrIV:333639:333710:+	0	1	0	0	1	GTATGC	0	1	1	0	1	0	TACTAAT	1	333710
chrIV	337596	+	chrIV:337525:337596:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	337596
chrIV	381065	-	chrIV:381065:381143:-	0	1	0	0	1	GTATCT	0	1	1	0	1	0	CACTAAC	1	381065
chrIV	392638	+	chrIV:392591:392638:+	1	0	0	0	0	GTATGT	0	1	1	1	0	0	TACTAAA	1	392642
chrIV	392679	+	chrIV:392591:392679:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TATTAAC	1	392682
chrIV	392682	+	chrIV:392591:392682:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	392682
chrIV	399468	+	chrIV:399360:399468:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	399468
chrIV	431423	-	chrIV:431423:431470:-	1	1	1	1	1	GTACGT	1	0	0	0	0	0	TACTAAC	0	431423
chrIV	437849	+	chrIV:437796:437849:+	1	0	0	0	4	AAAGAT	0	1	0	0	0	0	TCGTCAT	4	437854
chrIV	438275	+	chrIV:438208:438275:+	1	0	0	0	1	GTAAGT	0	1	1	0	1	0	CTCTAAC	2	438277
chrIV	451430	-	chrIV:451430:451488:-	1	0	0	0	1	GTATGG	0	1	1	0	1	0	TGCTAAC	1	451431
chrIV	451996	-	chrIV:451996:452077:-	0	1	0	0	2	GTCGGT	0	1	0	0	0	0	AACTAAC	1	451996
chrIV	456687	-	chrIV:456687:456757:-	1	0	0	0	1	GTAAGT	0	0	0	0	0	0	TACTAAT	1	456689
chrIV	456689	-	chrIV:456689:456757:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAT	1	456689
chrIV	458048	-	chrIV:458048:458095:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	458048
chrIV	491873	+	chrIV:491792:491873:+	0	1	1	0	3	ATTTTT	1	0	0	0	0	0	TACTAAC	0	491873
chrIV	540580	+	chrIV:540538:540580:+	1	0	0	0	1	GTAAGT	0	0	0	0	0	0	TACTAAT	1	540586
chrIV	540586	+	chrIV:540538:540586:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAT	1	540586
chrIV	569665	-	chrIV:569665:569722:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	569665
chrIV	579963	+	chrIV:579894:579963:+	1	1	1	0	1	GTATGG	1	0	0	0	0	0	TACTAAC	0	579963
chrIV	630016	+	chrIV:629904:630016:+	0	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	630016
chrIV	653424	+	chrIV:653365:653424:+	0	1	0	0	3	TTACGA	0	1	0	0	0	0	TACTAAC	0	653424
chrIV	655244	+	chrIV:655202:655244:+	1	0	0	0	1	GTATGC	0	1	1	1	0	0	TACTAAG	1	655257
chrIV	657891	+	chrIV:657846:657891:+	0	1	0	0	2	GTATCA	0	1	0	0	0	0	AACTGAC	2	657891
chrIV	676355	+	chrIV:676270:676355:+	1	0	0	0	1	GTACGT	0	0	0	0	0	0	AACTAAC	1	676358
chrIV	676358	+	chrIV:676270:676358:+	0	1	0	0	1	GTACGT	0	1	1	0	1	0	AACTAAC	1	676358
chrIV	698042	-	chrIV:698042:698092:-	0	1	0	0	1	GTACGT	0	1	1	0	1	0	TATTAAC	1	698042
chrIV	715265	-	chrIV:715265:715356:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	715265
chrIV	715306	-	chrIV:715264:715306:-	1	0	0	0	2	GTTAGT	0	1	0	0	0	0	TTCTACC	2	715298
chrIV	721692	-	chrIV:721692:721739:-	0	1	0	0	1	GTTTGT	0	1	1	0	1	0	TTCTAAC	1	721692
chrIV	733713	-	chrIV:733713:733773:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	733713
chrIV	768399	-	chrIV:768399:768453:-	1	0	0	0	1	ATATGT	0	0	0	0	0	0	AACTAAC	1	768401
chrIV	768401	-	chrIV:768401:768453:-	0	1	0	0	1	ATATGT	0	1	1	0	1	0	AACTAAC	1	768401
chrIV	885149	+	chrIV:885101:885149:+	0	1	0	0	2	GTATCA	0	1	0	0	0	0	GACTAAC	1	885149
chrIV	929251	+	chrIV:929206:929251:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	AACTAAC	1	929254
chrIV	929254	+	chrIV:929206:929254:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	AACTAAC	1	929254
chrIV	992896	+	chrIV:992862:992896:+	1	0	0	0	4	CCATCG	0	1	0	0	0	0	TGCGCAC	3	992899
chrIV	1021387	+	chrIV:1021323:1021387:+	0	1	0	0	1	ATATGT	0	1	1	0	1	0	GACTAAC	1	1021387
chrIV	1073346	-	chrIV:1073346:1073398:-	1	1	1	1	1	GTATGC	1	0	0	0	0	0	TACTAAC	0	1073346
chrIV	1080239	-	chrIV:1080239:1080322:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	CACTAAC	1	1080239
chrIV	1081205	+	chrIV:1081142:1081205:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	AATTAAC	2	1081205
chrIV	1103871	+	chrIV:1103808:1103871:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	CACTAAC	1	1103871
chrIV	1111888	+	chrIV:1111836:1111888:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	CACTAAC	1	1111888
chrIV	1114332	+	chrIV:1114289:1114332:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TACTAAC	0	1114335
chrIV	1114335	+	chrIV:1114289:1114335:+	0	1	0	0	0	GTATGT	0	1	1	0	1	1	TACTAAC	0	1114335
chrIV	1145148	+	chrIV:1145107:1145148:+	1	0	0	0	1	GTACGT	0	1	1	1	0	0	TGCTAAC	1	1145151
chrIV	1181081	+	chrIV:1181036:1181081:+	0	1	0	0	3	AGATCT	0	1	0	0	0	0	CACTAAC	1	1181081
chrIV	1212941	+	chrIV:1212871:1212941:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	1212941
chrIV	1237581	+	chrIV:1237527:1237581:+	1	1	1	0	1	GTTTGT	1	0	0	0	0	0	GACTAAC	1	1237581
chrIV	1238769	-	chrIV:1238769:1238817:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	AACTAAC	1	1238769
chrIV	1256999	-	chrIV:1256999:1257056:-	1	0	0	0	4	GGTTAG	0	1	0	0	0	0	TCCGCAT	4	1257001
chrIV	1266790	-	chrIV:1266790:1266854:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	1266790
chrIV	1266846	+	chrIV:1266789:1266846:+	1	0	0	0	2	GTTAGT	0	0	0	0	0	0	AACTAAC	1	1266849
chrIV	1266849	+	chrIV:1266789:1266849:+	0	1	0	0	2	GTTAGT	0	1	0	0	0	0	AACTAAC	1	1266849

chrIV	1319627	-	chrIV:1319627:1319690:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	1319627
chrIV	1319751	-	chrIV:1319751:1319809:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	1319751
chrIV	1333317	-	chrIV:1333317:1333401:-	0	1	0	0	1	GTATGC	0	1	1	0	1	0	TACTAAT	1	1333317
chrIV	1355141	-	chrIV:1355141:1355228:-	0	1	0	0	3	GTAGAG	0	1	0	0	0	0	AACTAAC	1	1355141
chrIV	1407178	+	chrIV:1407133:1407178:+	0	1	0	0	2	GTATAC	0	1	0	0	0	0	TACTAAC	0	1407178
chrIV	1411915	-	chrIV:1411915:1411963:-	1	1	0	0	2	ACATGT	0	1	0	0	0	0	GACTAAC	1	1411915
chrIV	1450485	-	chrIV:1450485:1450533:-	1	1	1	0	3	GTTGTT	1	0	0	0	0	0	TACTAAC	0	1450485
chrIV	1453413	+	chrIV:1453370:1453413:+	0	1	0	0	2	GTTGGT	0	1	0	0	0	0	TACTAAC	0	1453413
chrIV	1490516	-	chrIV:1490516:1490571:-	1	0	0	0	0	GTATGT	0	0	0	0	0	0	GACTAAC	1	1490518
chrIV	1490518	-	chrIV:1490518:1490571:-	0	1	0	0	0	GTATGT	0	1	1	0	1	1	GACTAAC	1	1490518
chrIV	1519506	-	chrIV:1519506:1519576:-	0	1	0	0	1	GTATGC	0	1	1	0	1	1	GACTAAC	1	1519506
chrV	7558	-	chrV:7558:7625:-	0	1	0	0	2	GTATAA	0	1	0	0	0	0	TACTAAC	0	7558
chrV	61195	+	chrV:61112:61195:+	0	1	0	0	1	GTACGT	0	1	1	0	1	0	TACTAAT	1	61195
chrV	124639	-	chrV:124639:124687:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	AACTAAC	1	124639
chrV	131853	+	chrV:131777:131853:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	CACTAAC	1	131853
chrV	148254	+	chrV:148194:148254:+	1	1	1	1	1	GTATGC	1	0	0	0	0	0	TACTAAC	0	148254
chrV	151105	+	chrV:151038:151105:+	1	0	0	0	0	GTATGT	0	1	1	1	0	0	TACTTAC	1	151108
chrV	159013	-	chrV:159013:159086:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	AACTAAC	1	159013
chrV	160515	+	chrV:160465:160515:+	0	1	0	0	1	GTATAT	0	1	1	0	1	0	ATCTAAC	2	160515
chrV	166786	-	chrV:166786:166873:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	166786
chrV	166806	-	chrV:166806:166873:-	1	0	0	1	0	GTATGT	0	1	1	0	1	0	TTTTGAC	3	166805
chrV	201996	+	chrV:201953:201996:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TACTGAC	1	201998
chrV	201998	+	chrV:201953:201998:+	0	1	0	0	0	GTATGT	0	1	1	0	1	1	TACTGAC	1	201998
chrV	203929	+	chrV:203855:203929:+	0	1	0	0	1	GTATGG	0	1	1	0	1	0	TATTAAC	1	203929
chrV	239667	-	chrV:239667:239710:-	0	1	1	1	1	GTACGT	1	0	0	0	0	0	TACTAAC	0	239667
chrV	258656	+	chrV:258593:258656:+	1	0	0	0	2	GTAGGA	0	0	0	0	0	0	TACTAAC	0	258658
chrV	258658	+	chrV:258593:258658:+	0	1	0	0	2	GTAGGA	0	1	0	0	0	0	TACTAAC	0	258658
chrV	269803	-	chrV:269803:269865:-	0	1	1	0	3	GTGTTA	1	0	0	0	0	0	TACTAAC	0	269803
chrV	292572	-	chrV:292572:292618:-	1	1	0	0	2	GTACAT	0	1	0	0	0	0	TACTAAC	0	292572
chrV	305682	+	chrV:305624:305682:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	ATCTAAC	2	305685
chrV	305685	+	chrV:305624:305685:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	ATCTAAC	2	305685
chrV	307801	+	chrV:307743:307801:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	307801
chrV	308040	+	chrV:307953:308040:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	308040
chrV	336934	+	chrV:336866:336934:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	TACTAAC	0	336937
chrV	336937	+	chrV:336866:336937:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAC	0	336937
chrV	348217	-	chrV:348217:348272:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	348217
chrV	362828	+	chrV:362729:362828:+	1	0	0	1	0	GTATGT	0	0	0	0	0	0	TTCTAAC	1	362831
chrV	362831	+	chrV:362729:362831:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	362831
chrV	374670	-	chrV:374670:374721:-	1	0	0	0	1	GTTTGT	0	0	0	0	0	0	GACTGAC	2	374672
chrV	374672	-	chrV:374672:374721:-	0	1	0	0	1	GTTTGT	0	1	1	0	1	1	GACTGAC	2	374672
chrV	397225	+	chrV:397147:397225:+	0	1	1	0	3	TGTTGT	1	0	0	0	0	0	TACTAAC	0	397225
chrV	423912	+	chrV:423821:423912:+	1	0	0	0	3	GTAGAG	0	0	0	0	0	0	TACTAAC	0	423914
chrV	423914	+	chrV:423821:423914:+	0	1	0	0	3	GTAGAG	0	1	0	0	0	0	TACTAAC	0	423914
chrV	433162	+	chrV:433110:433162:+	0	1	1	0	3	TTCTCT	1	0	0	0	0	0	TACTAAC	0	433162
chrV	435438	-	chrV:435438:435498:-	0	1	0	0	2	GTAAAT	0	1	0	0	0	0	AACTAAC	1	435438
chrV	487860	+	chrV:487816:487860:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAC	0	487860
chrV	517899	+	chrV:517847:517899:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TACTAAC	0	517902
chrV	517902	+	chrV:517847:517902:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	517902
chrV	540383	-	chrV:540383:540436:-	1	0	0	0	0	GTATGT	0	1	1	0	1	0	TCCTAAC	1	540384
chrV	548611	+	chrV:548548:548611:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	548611
chrV	561246	+	chrV:561200:561246:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	CACTAAC	1	561246
chrVI	32029	-	chrVI:32029:32077:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	AACTAAC	1	32029
chrVI	63915	-	chrVI:63915:63972:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	63915
chrVI	64615	-	chrVI:64615:64682:-	0	1	1	0	4	GCAGTA	1	0	0	0	0	0	TACTAAC	0	64615
chrVI	96257	+	chrVI:96184:96257:+	1	0	0	0	1	GTATTT	0	0	0	0	0	0	TTCTAAC	1	96259
chrVI	96259	+	chrVI:96184:96259:+	0	1	0	0	1	GTATTT	0	1	1	0	1	0	TTCTAAC	1	96259
chrVI	103131	-	chrVI:103131:103173:-	0	1	0	0	2	TTTTGT	0	1	0	0	0	0	TACTAAC	0	103131
chrVI	109970	-	chrVI:109970:110026:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	GATTAAC	2	109970
chrVI	131143	-	chrVI:131143:131201:-	0	1	0	0	2	GTTAGT	0	1	0	0	0	0	GACTAAT	2	131143
chrVI	137939	+	chrVI:137848:137939:+	0	1	0	0	4	ATGGAT	0	1	0	0	0	0	TACTAAC	0	137939
chrVI	176326	-	chrVI:176326:176385:-	1	0	0	0	1	GTATGG	0	0	0	0	0	0	AACTAAC	1	176328
chrVI	176328	-	chrVI:176328:176385:-	0	1	0	0	1	GTATGG	0	1	1	0	1	1	AACTAAC	1	176328
chrVI	203304	-	chrVI:203304:203374:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	203304
chrVI	221291	-	chrVI:221291:221402:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	221291
chrVI	242044	+	chrVI:241997:242044:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TATTAAC	1	242044
chrVI	268723	+	chrVI:268674:268723:+	0	1	0	0	1	GTATGC	0	1	1	0	1	0	CACTAAC	1	268723
chrVII	16567	+	chrVII:16513:16567:+	0	1	0	0	4	ATTAAT	0	1	0	0	0	0	TACTGAC	1	16567
chrVII	34394	-	chrVII:34394:34444:-	0	1	0	0	4	ACCGGT	0	1	0	0	0	0	GACTAAC	1	34394
chrVII	35284	-	chrVII:35284:35351:-	1	0	0	0	2	GTAAGG	0	0	0	0	0	0	TACTAAC	0	35288
chrVII	35288	-	chrVII:35288:35351:-	0	1	0	0	2	GTAAGG	0	1	0	0	0	0	TACTAAC	0	35288
chrVII	51959	+	chrVII:51882:51959:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTGAC	2	51959
chrVII	59557	+	chrVII:59483:59557:+	0	1	0	0	1	GTATGG	0	1	1	0	1	0	AACTAAT	2	59557
chrVII	62173	+	chrVII:62132:62173:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	62173
chrVII	73034	-	chrVII:73034:73136:-	1	1	1	1	1	GTACGT	1	0	0	0	0	0	TACTAAC	0	73034
chrVII	77521	+	chrVII:77467:77521:+	0	1	0	0	2	GTATCA	0	1	0	0	0	0	AACTAAC	1	77521
chrVII	140634	+	chrVII:140554:140634:+	0	1	0	0	1	GTATCT	0	1	1	0	1	0	ATCTAAC	2	140634
chrVII	143935	-	chrVII:143935:143984:-	1	0	0	0	0	GTATGT	0	1	1	0	1	0	TACTTAC	1	143937
chrVII	148658	-	chrVII:148658:148721:-	1	0	0	0	2	TTACGT	0	0	0	0	0	0	TACTAAC	0	148660
chrVII	148660	-	chrVII:148660:148721:-	0	1	0	0	2	TTACGT	0	1	0	0	0	0	TACTAAC	0	148660
chrVII	157245	-	chrVII:157245:157288:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	CACTAAC	1	157245
chrVII	166587	+	chrVII:166543:166587:+	0	1	0	0	3	ATACGC	0	1	0	0	0	0	TACTGAC	1	166587
chrVII	167428	+	chrVII:167361:167428:+	1	0	0	1	0	GTATGT	0	0	0	0	0	0	TTCTAAC	1	167431

chrVII	167431	+	chrVII:167361:167431:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	167431
chrVII	188026	-	chrVII:188026:188070:-	0	1	0	0	3	GTACCG	0	1	0	0	0	0	TACTAAC	0	188026
chrVII	253204	-	chrVII:253204:253253:-	1	0	0	0	1	GTATGA	0	0	0	0	0	0	TACTAAT	1	253206
chrVII	253206	-	chrVII:253206:253253:-	0	1	0	0	1	GTATGA	0	1	1	0	1	1	TACTAAT	1	253206
chrVII	262617	-	chrVII:262617:262696:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	CACTAAC	1	262617
chrVII	293423	+	chrVII:293335:293423:+	0	1	0	0	1	GTATTT	0	1	1	0	1	0	GACTAAC	1	293423
chrVII	293818	+	chrVII:293737:293818:+	0	1	0	0	1	GTATGG	0	1	1	0	1	0	TACTAAC	0	293818
chrVII	311486	+	chrVII:311402:311486:+	0	1	1	0	2	GGTTGT	1	0	0	0	0	0	TACTAAC	0	311486
chrVII	314263	-	chrVII:314263:314298:-	0	1	0	0	2	ATATAT	0	1	0	0	0	0	TACTGAC	1	314263
chrVII	345544	-	chrVII:345544:345614:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAT	1	345544
chrVII	346854	-	chrVII:346854:346896:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	346854
chrVII	380661	-	chrVII:380661:380732:-	0	1	0	0	1	GTATTT	0	1	1	0	1	0	TATTGAC	2	380661
chrVII	383552	+	chrVII:383489:383552:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TATTAAC	1	383555
chrVII	383555	+	chrVII:383489:383555:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	383555
chrVII	414314	+	chrVII:414250:414314:+	0	1	0	0	1	GTATGG	0	1	1	0	1	0	AACTAAC	1	414314
chrVII	423868	-	chrVII:423868:423911:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	AACTAAC	1	423868
chrVII	427173	-	chrVII:427173:427221:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	427173
chrVII	435728	+	chrVII:435686:435728:+	0	1	1	0	2	TTAAGT	1	0	0	0	0	0	TACTAAC	0	435728
chrVII	436362	+	chrVII:436318:436362:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TACTAAC	0	436365
chrVII	436365	+	chrVII:436318:436365:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	436365
chrVII	439462	+	chrVII:439387:439462:+	1	0	0	0	1	GTAAGT	0	1	1	1	0	0	CGCTAAC	2	439465
chrVII	443013	-	chrVII:443013:443066:-	1	1	0	0	2	GTCAGT	0	1	0	0	0	0	TACTGAC	1	443013
chrVII	472352	-	chrVII:472352:472397:-	1	0	0	0	2	GTGAGT	0	1	0	0	0	0	TGCTAAC	1	472354
chrVII	497394	-	chrVII:497394:497462:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	497394
chrVII	497408	-	chrVII:497408:497462:-	1	0	0	1	0	GTATGT	0	1	1	1	0	0	TACTAAC	0	497394
chrVII	497961	-	chrVII:497961:498003:-	1	0	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	497961
chrVII	504218	-	chrVII:504218:504268:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TTCTAAC	1	504218
chrVII	543691	+	chrVII:543643:543691:+	1	0	0	1	0	GTATGT	0	1	1	1	0	0	TCCAATC	3	543686
chrVII	543708	+	chrVII:543643:543708:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TATTAAC	1	543708
chrVII	555885	+	chrVII:555835:555885:+	1	0	0	1	0	GTATGT	0	1	1	1	0	0	CACGAAA	3	555891
chrVII	556282	+	chrVII:556232:556282:+	1	1	1	0	3	GTGGAT	1	0	0	0	0	0	TACTAAC	0	556282
chrVII	561204	-	chrVII:561204:561267:-	1	0	0	0	2	GGTTGT	0	0	0	0	0	0	TACTAAC	0	561206
chrVII	561206	-	chrVII:561206:561267:-	0	1	0	0	2	GGTTGT	0	1	0	0	0	0	TACTAAC	0	561206
chrVII	574775	+	chrVII:574705:574775:+	1	0	0	0	1	GTATTT	0	0	0	0	0	0	TACTAAC	0	574778
chrVII	574778	+	chrVII:574705:574778:+	0	1	0	0	1	GTATTT	0	1	1	0	1	0	TACTAAC	0	574778
chrVII	593473	+	chrVII:593395:593473:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTGAC	1	593473
chrVII	594137	-	chrVII:594137:594202:-	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TACTAAC	0	594141
chrVII	594141	-	chrVII:594141:594202:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	594141
chrVII	607019	-	chrVII:607019:607091:-	0	1	0	0	1	GTATGG	0	1	1	0	1	0	AACTAAC	1	607019
chrVII	627186	-	chrVII:627186:627225:-	1	0	0	0	4	AACTGA	0	1	0	0	0	0	AAGAAAT	4	627187
chrVII	658297	+	chrVII:658204:658297:+	0	1	0	0	1	GTTTGT	0	1	1	0	1	0	TACTAAC	0	658297
chrVII	682970	-	chrVII:682970:683069:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	682970
chrVII	700757	+	chrVII:700717:700757:+	1	0	0	0	4	TCCTGA	0	1	0	0	0	0	TATCAAT	3	700761
chrVII	730064	+	chrVII:730017:730064:+	0	1	0	0	1	GTATGG	0	1	1	0	1	0	GACTAAT	2	730064
chrVII	772105	+	chrVII:772019:772105:+	0	1	0	0	0	GTATGT	0	1	1	0	1	1	TACTGAC	1	772105
chrVII	792328	-	chrVII:792328:792385:-	0	1	0	0	1	GTATCT	0	1	1	0	1	0	TACTAAC	0	792328
chrVII	859434	-	chrVII:859434:859478:-	1	0	0	1	0	GTATGT	0	1	1	0	1	0	TAAAAAT	3	859434
chrVII	875661	+	chrVII:875581:875661:+	0	1	0	0	1	GCATGT	0	1	1	0	1	0	ATCTAAC	2	875661
chrVII	878176	-	chrVII:878176:878242:-	0	1	0	0	3	TTAAGA	0	1	0	0	0	0	TACTAAC	0	878176
chrVII	914791	-	chrVII:914791:914879:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	AACTAAC	1	914791
chrVII	937275	+	chrVII:937216:937275:+	0	1	0	0	2	GTAAGA	0	1	0	0	0	0	CACTAAC	1	937275
chrVII	946407	+	chrVII:946331:946407:+	1	1	1	1	1	GTACGT	1	0	0	0	0	0	TACTAAC	0	946407
chrVII	951679	-	chrVII:951679:951729:-	0	1	0	0	2	GTATAC	0	1	0	0	0	0	TACTAAT	1	951679
chrVII	962304	+	chrVII:962229:962304:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	962304
chrVII	1002937	+	chrVII:1002886:1002937:+	0	1	0	0	1	GCATGT	0	1	1	0	1	0	TACTAAC	0	1002937
chrVII	1017561	-	chrVII:1017561:1017603:-	0	1	0	0	5	CCACCA	0	1	0	0	0	0	CACTAAC	1	1017561
chrVII	1052639	-	chrVII:1052639:1052724:-	0	1	0	0	1	GTATGG	0	1	1	0	1	0	TACTAAC	0	1052639
chrVII	1083748	-	chrVII:1083748:1083798:-	0	1	0	0	2	GTATAA	0	1	0	0	0	0	TACTAAC	0	1083748
chrVIII	97942	-	chrVIII:97942:98036:-	0	1	0	0	1	GTACGT	0	1	1	0	1	0	GACTAAT	2	97942
chrVIII	104751	+	chrVIII:104684:104751:+	0	1	1	0	2	ACATGT	1	0	0	0	0	0	TACTAAC	0	104751
chrVIII	107815	+	chrVIII:107766:107815:+	0	1	0	0	2	GCAAGT	0	1	0	0	0	0	AACTAAC	1	107815
chrVIII	107875	+	chrVIII:107827:107875:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	107875
chrVIII	115533	+	chrVIII:115489:115533:+	0	1	0	0	2	GTATAA	0	1	0	0	0	0	TACTAAT	1	115533
chrVIII	129590	+	chrVIII:129523:129590:+	1	0	0	1	0	GTATGT	0	1	1	1	0	0	AACTTCC	3	129593
chrVIII	129611	+	chrVIII:129523:129611:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	129611
chrVIII	138274	-	chrVIII:138274:138323:-	0	1	1	0	1	GTCTGT	1	0	0	0	0	0	TACTAAC	0	138274
chrVIII	148770	-	chrVIII:148770:148814:-	1	1	0	0	1	GTATGC	0	1	1	0	1	0	CATTAAC	2	148770
chrVIII	187613	-	chrVIII:187613:187669:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	187613
chrVIII	189778	-	chrVIII:189778:189843:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TGCTAAC	1	189778
chrVIII	189806	-	chrVIII:189806:189844:-	1	0	0	0	4	GCTGAT	0	1	0	0	0	0	TCGGAAT	4	189806
chrVIII	236985	+	chrVIII:236958:236985:+	1	0	0	0	4	TTAAAA	0	1	0	0	0	0	AAATAAA	3	236997
chrVIII	251233	+	chrVIII:251158:251233:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	GACTAAC	1	251233
chrVIII	255689	-	chrVIII:255689:255752:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	255689
chrVIII	255706	-	chrVIII:255706:255753:-	1	0	0	0	3	GTCCAT	0	1	0	0	0	0	TTCTAAG	2	255702
chrVIII	262372	-	chrVIII:262372:262442:-	0	1	1	1	0	GTATGT	1	0	0	0	0	0	TATTAAC	1	262372
chrVIII	298418	-	chrVIII:298418:298487:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	298418
chrVIII	315810	-	chrVIII:315810:315861:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	315810
chrVIII	335608	-	chrVIII:335608:335675:-	0	1	0	0	1	GTACGT	0	1	1	0	1	1	TACTGAC	1	335608
chrVIII	354926	+	chrVIII:354868:354926:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	354926
chrVIII	372284	+	chrVIII:372191:372284:+	0	1	0	0	1	GTTTGT	0	1	1	0	1	0	TACTAAC	0	372284
chrVIII	382356	-	chrVIII:382356:382410:-	0	1	1	0	4	ATACAA	1	0	0	0	0	0	TACTAAC	0	382356
chrVIII	400569	-	chrVIII:400569:400651:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTGAC	1	400569

chrVIII	406673	-	chrVIII:406673:406756:-	1	0	0	0	1	GCATGT	0	1	1	0	1	0	TACTAAC	0	406675
chrVIII	442923	+	chrVIII:442871:442923:+	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TATTAAC	1	442923
chrVIII	491867	-	chrVIII:491867:491919:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAT	1	491867
chrVIII	498731	-	chrVIII:498731:498786:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	498731
chrVIII	508825	+	chrVIII:508795:508825:+	1	0	0	0	6	CCGGCC	0	1	0	0	0	0	TTCTCAA	3	508835
chrIX	40246	+	chrIX:40178:40246:+	0	1	0	0	3	TCAAGT	0	1	0	0	0	0	TACTAAC	0	40246
chrIX	47743	+	chrIX:47699:47743:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	47743
chrIX	54025	+	chrIX:53941:54025:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TTCTAAC	1	54027
chrIX	54027	+	chrIX:53941:54027:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	54027
chrIX	127052	-	chrIX:127052:127135:-	1	0	0	0	1	GTATAT	0	0	0	0	0	0	TATTAAC	1	127054
chrIX	127054	-	chrIX:127054:127135:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TATTAAC	1	127054
chrIX	128117	+	chrIX:128061:128117:+	1	0	0	0	2	TTTTGT	0	0	0	0	0	0	TACTAAC	0	128119
chrIX	128119	+	chrIX:128061:128119:+	0	1	0	0	2	TTTTGT	0	1	0	0	0	0	TACTAAC	0	128119
chrIX	134038	+	chrIX:133971:134038:+	1	0	0	0	1	GTAAGT	0	0	0	0	0	0	CACTAAC	1	134041
chrIX	134041	+	chrIX:133971:134041:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	CACTAAC	1	134041
chrIX	155276	+	chrIX:155220:155276:+	1	1	1	1	1	GCATGT	1	0	0	0	0	0	TACTAAC	0	155276
chrIX	155301	+	chrIX:155220:155301:+	1	0	0	1	1	GCATGT	0	1	1	1	0	0	TACAAGC	2	155293
chrIX	166484	+	chrIX:166432:166484:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TATTAAC	1	166484
chrIX	166501	+	chrIX:166432:166501:+	1	0	0	1	0	GTATGT	0	1	1	0	1	0	GAGTTAC	3	166502
chrIX	183435	-	chrIX:183435:183500:-	1	0	0	0	4	CCCAGT	0	1	0	0	0	0	CACTTAT	3	183433
chrIX	225117	+	chrIX:225035:225117:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAC	0	225117
chrIX	225834	-	chrIX:225834:225896:-	0	1	1	1	1	GTATAT	1	0	0	0	0	0	AACTAAC	1	225834
chrIX	232012	-	chrIX:232012:232070:-	1	1	1	0	3	GTACTG	1	0	0	0	0	0	TACTAAC	0	232012
chrIX	261764	+	chrIX:261723:261764:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	TACTAAT	1	261767
chrIX	261767	+	chrIX:261723:261767:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAT	1	261767
chrIX	317136	+	chrIX:317062:317136:+	1	1	1	0	2	TTCTGT	1	0	0	0	0	0	TACTAAC	0	317136
chrIX	317159	+	chrIX:317107:317159:+	1	0	0	0	5	ATGAAA	0	1	0	0	0	0	TCCTCAT	3	317160
chrIX	334601	-	chrIX:334601:334643:-	0	1	0	0	1	GTTTGT	0	1	1	0	1	0	TACTAAT	1	334601
chrIX	348380	-	chrIX:348380:348491:-	0	1	1	1	1	GTATGA	1	0	0	0	0	0	TACTAAC	0	348380
chrIX	360695	-	chrIX:360695:360737:-	0	1	0	0	1	GCATGT	0	1	1	0	1	0	TACTAAC	0	360695
chrIX	363684	+	chrIX:363652:363684:+	0	1	0	0	4	TAACGC	0	1	0	0	0	0	TACTAAC	0	363684
chrIX	387166	+	chrIX:387136:387166:+	1	0	0	0	5	CCAACA	0	1	0	0	0	0	AAAAAAA	4	387166
chrX	31819	+	chrX:31768:31819:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TATTAAC	1	31821
chrX	31821	+	chrX:31768:31821:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	31821
chrX	50351	-	chrX:50351:50411:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	50351
chrX	71474	+	chrX:71426:71474:+	1	0	0	0	2	GTTGGT	0	0	0	0	0	0	TACTAAC	0	71476
chrX	71476	+	chrX:71426:71476:+	0	1	0	0	2	GTTGGT	0	1	0	0	0	0	TACTAAC	0	71476
chrX	74178	+	chrX:74112:74178:+	1	1	1	0	2	GGTTGT	1	0	0	0	0	0	TACTAAC	0	74178
chrX	76268	+	chrX:76213:76268:+	0	1	1	0	2	GTATTG	1	0	0	0	0	0	TACTAAC	0	76268
chrX	119610	-	chrX:119610:119650:-	0	1	0	0	3	GAGTTT	0	1	0	0	0	0	TACTAAC	0	119610
chrX	165023	+	chrX:164962:165023:+	0	1	0	0	2	GTGGGT	0	1	0	0	0	0	CACTAAC	1	165023
chrX	172451	-	chrX:172451:172499:-	1	1	0	0	4	AGTTCT	0	1	0	0	0	0	TACTAAC	0	172451
chrX	209416	+	chrX:209358:209416:+	0	1	0	0	1	GTATGG	0	1	1	0	1	0	TACTAAC	0	209416
chrX	234005	+	chrX:233962:234005:+	1	0	0	0	4	CTGGCT	0	1	0	0	0	0	TCCTGGC	3	233999
chrX	237006	+	chrX:236962:237006:+	0	1	0	0	1	GTATGC	0	1	1	0	1	1	CACTGAC	2	237006
chrX	264006	-	chrX:264006:264058:-	1	0	0	0	2	GTGCGT	0	0	0	0	0	0	TACTAAC	0	264008
chrX	264008	-	chrX:264008:264058:-	0	1	0	0	2	GTGCGT	0	1	0	0	0	0	TACTAAC	0	264008
chrX	328113	-	chrX:328113:328177:-	0	1	0	0	2	GTAAGC	0	1	0	0	0	0	TACTAAC	0	328113
chrX	345274	+	chrX:345230:345274:+	0	1	0	0	3	GTAGAG	0	1	0	0	0	0	TACTAAC	0	345274
chrX	349226	+	chrX:349181:349226:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	CATTAAC	2	349226
chrX	365853	+	chrX:365780:365853:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	365854
chrX	387380	-	chrX:387380:387430:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTGAC	1	387381
chrX	396512	-	chrX:396512:396565:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	396513
chrX	422629	+	chrX:422549:422629:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	TACTAAT	1	422632
chrX	422632	+	chrX:422549:422632:+	0	1	0	0	1	GTATGA	0	1	1	0	1	1	TACTAAT	1	422632
chrX	432390	-	chrX:432390:432464:-	1	0	0	0	2	GTATAC	0	0	0	0	0	0	TACTAAC	0	432392
chrX	432392	-	chrX:432392:432464:-	0	1	0	0	2	GTATAC	0	1	0	0	0	0	TACTAAC	0	432392
chrX	435281	+	chrX:435222:435281:+	1	0	0	1	0	GTATGT	0	1	1	0	1	0	AAGTAAA	3	435279
chrX	435302	+	chrX:435222:435302:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	435303
chrX	455749	+	chrX:455690:455749:+	0	1	0	0	1	GTACGT	0	1	1	0	1	0	TACTAAC	0	455749
chrX	469190	-	chrX:469190:469256:-	1	1	1	1	2	GTTCGT	1	0	0	0	0	0	TACTAAC	0	469191
chrX	506240	+	chrX:506193:506240:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TTCTAAC	1	506240
chrX	517546	-	chrX:517546:517607:-	1	1	0	0	2	GTACGC	0	1	0	0	0	0	AACTAAC	1	517546
chrX	526804	-	chrX:526804:526879:-	0	1	0	0	2	TAATGT	0	1	0	0	0	0	TACTAAC	0	526804
chrX	535287	-	chrX:535287:535343:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	CACTAAC	1	535287
chrX	538617	+	chrX:538579:538617:+	1	0	0	0	5	TCCTAA	0	1	0	0	0	0	TACGGAA	3	538616
chrX	570579	-	chrX:570579:570633:-	1	0	0	0	3	GTAGTC	0	0	0	0	0	0	TACTAAC	0	570581
chrX	570581	-	chrX:570581:570633:-	0	1	0	0	3	GTAGTC	0	1	0	0	0	0	TACTAAC	0	570581
chrX	608540	+	chrX:608476:608540:+	0	1	1	0	1	GTAGGT	1	0	0	0	0	0	TACTAAC	0	608541
chrX	632997	-	chrX:632997:633051:-	1	1	0	0	1	GTATGC	0	1	1	0	1	1	AACTAAC	1	632997
chrX	633065	-	chrX:633065:633144:-	0	1	0	0	2	GTAAGC	0	1	0	0	0	0	TACTAAT	1	633065
chrX	649522	-	chrX:649522:649569:-	0	1	0	0	1	GCATGT	0	1	1	0	1	0	TACTAAC	0	649522
chrX	702871	-	chrX:702871:702937:-	0	1	1	0	1	TTATGT	1	0	0	0	0	0	TACTAAC	0	702872
chrX	712054	-	chrX:712054:712106:-	0	1	0	0	1	GTTTGT	0	1	1	0	1	0	TATTAAC	1	712054
chrXI	38910	+	chrXI:38829:38910:+	0	1	0	0	4	AGATAG	0	1	0	0	0	0	TACTGAC	1	38910
chrXI	67767	-	chrXI:67767:67805:-	1	0	0	0	4	GACTAA	0	1	0	0	0	0	AAAAAAG	4	67768
chrXI	74700	+	chrXI:74657:74700:+	1	0	0	0	4	GCGACT	0	1	0	0	0	0	TTTTAAC	2	74713
chrXI	83061	+	chrXI:83004:83061:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	83061
chrXI	93382	-	chrXI:93382:93470:-	1	0	0	1	1	GTACGT	0	0	0	0	0	0	AACTAAC	1	93385
chrXI	93385	-	chrXI:93385:93470:-	0	1	0	1	1	GTACGT	0	1	1	0	1	0	AACTAAC	1	93385
chrXI	94082	-	chrXI:94082:94154:-	1	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	94082
chrXI	96757	+	chrXI:96692:96757:+	1	0	0	0	1	GTAGGT	0	1	1	0	1	0	AACTTAC	2	96759

chrXI	158627	-	chrXI:158627:158679:-	0	1	0	0	1	ATATGT	0	1	1	0	1	0	TACTAAC	0	158627
chrXI	166477	+	chrXI:166405:166477:+	1	0	0	1	1	GTACGT	0	0	0	0	0	0	TACTAAC	0	166479
chrXI	166479	+	chrXI:166405:166479:+	0	1	0	1	1	GTACGT	0	1	1	0	1	0	TACTAAC	0	166479
chrXI	166501	+	chrXI:166452:166501:+	0	1	0	0	3	GTACTC	0	1	0	0	0	0	AACTAAC	1	166501
chrXI	191090	-	chrXI:191090:191173:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	AATTAAC	2	191090
chrXI	193009	-	chrXI:193009:193071:-	1	0	0	0	0	GTATGT	0	0	0	0	0	0	CACTAAC	1	193011
chrXI	193011	-	chrXI:193011:193071:-	0	1	0	0	0	GTATGT	0	1	1	0	1	1	CACTAAC	1	193011
chrXI	225773	-	chrXI:225773:225852:-	1	0	0	0	1	GTAAGT	0	0	0	0	0	0	TATTAAC	1	225775
chrXI	225775	-	chrXI:225775:225852:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TATTAAC	1	225775
chrXI	231493	+	chrXI:231447:231493:+	1	1	0	0	1	GTATGA	0	1	1	0	1	0	TATTAAC	1	231493
chrXI	262173	+	chrXI:262138:262173:+	0	1	0	0	3	AGAAGT	0	1	0	0	0	0	GACTAAC	1	262173
chrXI	272946	-	chrXI:272946:272992:-	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TTCTAAC	1	272948
chrXI	272948	-	chrXI:272948:272992:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	272948
chrXI	283016	+	chrXI:282962:283016:+	0	1	1	0	2	GGAAGT	1	0	0	0	0	0	TACTAAC	0	283016
chrXI	285869	+	chrXI:285816:285869:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAC	0	285869
chrXI	290611	-	chrXI:290611:290705:-	1	1	0	0	1	GTAGGT	0	1	1	0	1	0	TACTAAC	0	290611
chrXI	302664	+	chrXI:302572:302664:+	1	0	0	0	4	CTCAAT	0	1	0	0	0	0	TCCTGTC	3	302659
chrXI	313868	+	chrXI:313796:313868:+	0	1	0	0	2	GTAGAT	0	1	0	0	0	0	TACTAAC	0	313868
chrXI	408145	+	chrXI:408101:408145:+	1	0	0	0	1	GTAAGT	0	0	0	0	0	0	AACTAAC	1	408147
chrXI	408147	+	chrXI:408101:408147:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	AACTAAC	1	408147
chrXI	430163	-	chrXI:430163:430239:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	430163
chrXI	437526	+	chrXI:437481:437526:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	437526
chrXI	446831	-	chrXI:446831:446885:-	0	1	0	0	1	GTATGC	0	1	1	0	1	0	GACTAAC	1	446831
chrXI	447376	-	chrXI:447376:447453:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	447376
chrXI	449611	-	chrXI:449611:449663:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTGAC	1	449611
chrXI	465718	-	chrXI:465718:465764:-	0	1	0	0	2	GTAGGA	0	1	0	0	0	0	TATTAAC	1	465718
chrXI	468921	-	chrXI:468921:468975:-	1	0	0	0	1	GTATGC	0	1	1	0	1	0	TGCTAAC	1	468923
chrXI	490069	+	chrXI:489994:490069:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TACTTAT	2	490067
chrXI	490072	+	chrXI:489994:490072:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	ATCTAAC	2	490072
chrXI	552232	+	chrXI:552176:552232:+	0	1	0	0	2	GTAAAT	0	1	0	0	0	0	TACTAAC	0	552232
chrXI	618096	-	chrXI:618096:618168:-	1	1	1	0	1	GTTTGT	1	0	0	0	0	0	TACTAAC	0	618096
chrXI	625594	+	chrXI:625544:625594:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	625594
chrXI	633805	-	chrXI:633805:633874:-	0	1	0	0	1	GTCTGT	0	1	1	0	1	0	TACTAAC	0	633805
chrXI	649450	+	chrXI:649382:649450:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAC	0	649450
chrXII	40353	-	chrXII:40353:40399:-	1	1	1	1	1	GTATGC	1	0	0	0	0	0	TACTAAC	0	40353
chrXII	50295	+	chrXII:50224:50295:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	CATTAAC	2	50298
chrXII	50298	+	chrXII:50224:50298:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	CATTAAC	2	50298
chrXII	75836	-	chrXII:75836:75882:-	0	1	0	0	3	GTAAAC	0	1	0	0	0	0	TACTAAC	0	75836
chrXII	83743	-	chrXII:83743:83803:-	1	1	0	0	3	GTTGTT	0	1	0	0	0	0	TACTAAC	0	83743
chrXII	90639	+	chrXII:90568:90639:+	0	1	0	0	1	GTATGC	0	1	1	0	1	0	AACTAAC	1	90639
chrXII	155740	-	chrXII:155740:155813:-	1	0	0	0	1	GTAAGT	0	0	0	0	0	0	CACTAAC	1	155742
chrXII	155742	-	chrXII:155742:155813:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	CACTAAC	1	155742
chrXII	232371	+	chrXII:232297:232371:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	AACTAAT	2	232371
chrXII	242652	+	chrXII:242595:242652:+	0	1	1	0	2	GTACTT	1	0	0	0	0	0	TACTAAC	0	242652
chrXII	250899	-	chrXII:250899:250948:-	1	1	1	1	1	GTATGG	1	0	0	0	0	0	TACTAAC	0	250899
chrXII	263540	+	chrXII:263478:263540:+	0	1	1	0	4	GCAGTA	1	0	0	0	0	0	TACTAAC	0	263540
chrXII	286498	-	chrXII:286498:286557:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	286498
chrXII	286519	-	chrXII:286519:286557:-	1	0	0	1	0	GTATGT	0	1	1	1	0	0	TGCTAAA	2	286516
chrXII	316898	+	chrXII:316853:316898:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	AACTAAT	2	316898
chrXII	327295	-	chrXII:327295:327400:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	GACTAAC	1	327295
chrXII	327338	-	chrXII:327338:327400:-	1	0	0	0	4	CCATTA	0	1	0	0	0	0	TGCTCAT	3	327339
chrXII	331860	-	chrXII:331860:331922:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTGAC	1	331860
chrXII	333653	+	chrXII:333603:333653:+	0	1	0	0	3	GTAAAG	0	1	0	0	0	0	TATTAAC	1	333653
chrXII	366444	+	chrXII:366367:366444:+	0	1	0	0	2	GTATCG	0	1	0	0	0	0	AACTAAC	1	366444
chrXII	380685	+	chrXII:380627:380685:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	380685
chrXII	382367	+	chrXII:382302:382367:+	0	1	0	0	0	GTATGT	0	1	1	0	1	1	TATTAAC	1	382367
chrXII	382387	+	chrXII:382302:382387:+	1	0	0	0	0	GTATGT	0	1	1	0	1	1	TACTTAC	1	382389
chrXII	398583	+	chrXII:398534:398583:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	398583
chrXII	491543	+	chrXII:491497:491543:+	1	0	0	0	1	GTATAT	0	0	0	0	0	0	TATTAAC	1	491546
chrXII	491546	+	chrXII:491497:491546:+	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TATTAAC	1	491546
chrXII	522714	+	chrXII:522672:522714:+	1	0	0	1	0	GTATGT	0	0	0	0	0	0	TATTGAC	2	522716
chrXII	522716	+	chrXII:522672:522716:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	TATTGAC	2	522716
chrXII	522984	+	chrXII:522893:522984:+	0	1	1	0	1	GTATGC	1	0	0	0	0	0	TACTAAC	0	522984
chrXII	548706	-	chrXII:548706:548765:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	GACTAAC	1	548706
chrXII	564467	-	chrXII:564467:564515:-	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	GACTAAC	1	564467
chrXII	605300	-	chrXII:605300:605434:-	1	0	0	0	3	GCTCGT	0	1	0	0	0	0	CACTTTC	3	605298
chrXII	609448	-	chrXII:609448:609498:-	1	1	0	0	1	GTATGA	0	1	1	0	1	0	ATCTAAC	2	609448
chrXII	694444	+	chrXII:694385:694444:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	694444
chrXII	744185	+	chrXII:744185:744221:+	1	0	0	0	4	ATAATC	0	1	0	0	0	0	TTCTCAT	3	744189
chrXII	744219	+	chrXII:744156:744219:+	1	1	1	1	1	GTACGT	1	0	0	0	0	0	TACTAAC	0	744219
chrXII	766086	-	chrXII:766086:766129:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	AACTAAC	1	766086
chrXII	766205	-	chrXII:766205:766249:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	AACTAAC	1	766205
chrXII	783406	-	chrXII:783406:783492:-	0	1	0	0	2	TAATGT	0	1	0	0	0	0	TTCTAAC	1	783406
chrXII	786667	+	chrXII:786616:786667:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	786667
chrXII	791912	-	chrXII:791912:791964:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAT	1	791912
chrXII	818678	+	chrXII:818645:818678:+	1	0	0	0	3	GTGGCT	0	1	0	0	0	0	TTTTAAT	3	818685
chrXII	823171	+	chrXII:823108:823171:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TATTAAC	1	823171
chrXII	827562	-	chrXII:827562:827606:-	0	1	0	0	4	CGACTT	0	1	0	0	0	0	GACTAAC	1	827562
chrXII	857038	+	chrXII:856988:857038:+	1	1	1	0	2	GTAAGC	1	0	0	0	0	0	TACTAAC	0	857038
chrXII	898621	+	chrXII:898549:898621:+	1	0	0	0	2	GTATAA	0	0	0	0	0	0	TACTAAC	0	898624
chrXII	898624	+	chrXII:898549:898624:+	0	1	0	0	2	GTATAA	0	1	0	0	0	0	TACTAAC	0	898624
chrXII	907076	+	chrXII:907032:907076:+	0	1	0	0	3	GTCAGG	0	1	0	0	0	0	AACTAAC	1	907076

chrXII	918955	-	chrXII:918955:919021:-	0	1	0	0	1	ATATGT	0	1	1	0	1	0	CACTAAC	1	918955
chrXII	928302	-	chrXII:928302:928370:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TACTAAC	0	928302
chrXII	965103	+	chrXII:965038:965103:+	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TACTAAC	0	965103
chrXII	982467	-	chrXII:982467:982535:-	1	0	0	0	0	GTATGT	0	0	0	0	0	0	GACTAAC	1	982470
chrXII	982470	-	chrXII:982470:982535:-	0	1	0	0	0	GTATGT	0	1	1	0	1	1	GACTAAC	1	982470
chrXII	987191	+	chrXII:987139:987191:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	987191
chrXII	987202	+	chrXII:987139:987202:+	1	0	0	1	0	GTATGT	0	0	0	0	0	0	AACTAAC	1	987204
chrXII	987204	+	chrXII:987139:987204:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	AACTAAC	1	987204
chrXII	987241	+	chrXII:987139:987241:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	GTCTAAC	2	987241
chrXII	988410	+	chrXII:988329:988410:+	0	1	0	0	2	GTAAGC	0	1	0	0	0	0	TACTAAT	1	988410
chrXII	1024631	+	chrXII:1024570:1024631:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAT	1	1024631
chrXIII	38610	-	chrXIII:38610:38680:-	0	1	0	0	2	GTATCG	0	1	0	0	0	0	TACTAAC	0	38610
chrXIII	56619	+	chrXIII:56557:56619:+	0	1	0	0	1	GTATTT	0	1	1	0	1	0	TATTAAC	1	56619
chrXIII	82343	+	chrXIII:82291:82343:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	82343
chrXIII	99301	-	chrXIII:99301:99375:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	99301
chrXIII	112661	-	chrXIII:112661:112715:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	GACTAAC	1	112661
chrXIII	114129	-	chrXIII:114129:114189:-	0	1	0	0	3	TTAAGA	0	1	0	0	0	0	TACTAAC	0	114129
chrXIII	123777	-	chrXIII:123777:123824:-	1	0	1	0	3	ATCTCT	1	0	0	0	0	0	TACTAAC	0	123777
chrXIII	140113	-	chrXIII:140113:140183:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	CACTAAC	1	140113
chrXIII	182669	+	chrXIII:182594:182669:+	1	0	0	0	0	GTATGT	0	1	1	1	0	0	TACTAAA	1	182675
chrXIII	204537	-	chrXIII:204537:204588:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAC	0	204537
chrXIII	206162	+	chrXIII:206098:206162:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	206162
chrXIII	211547	+	chrXIII:211502:211547:+	1	1	1	0	4	TTTTAA	1	0	0	0	0	0	TACTAAC	0	211547
chrXIII	223421	-	chrXIII:223421:223496:-	0	1	1	0	2	GTACGC	1	0	0	0	0	0	TACTAAC	0	223421
chrXIII	225264	-	chrXIII:225264:225338:-	1	1	1	1	1	GTACGT	1	0	0	0	0	0	TACTAAC	0	225264
chrXIII	242969	-	chrXIII:242969:243056:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTGAC	1	242969
chrXIII	273521	-	chrXIII:273521:273577:-	0	1	0	0	1	GTGTGT	0	1	1	0	1	0	CACTAAC	1	273521
chrXIII	290869	+	chrXIII:290835:290869:+	1	0	0	0	4	CACCGT	0	1	0	0	0	0	GACTCCC	3	290860
chrXIII	301517	-	chrXIII:301517:301586:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAC	0	301517
chrXIII	337886	+	chrXIII:337817:337886:+	1	1	1	1	1	GTACGT	1	0	0	0	0	0	TACTAAC	0	337886
chrXIII	425094	+	chrXIII:424997:425094:+	1	0	0	1	0	GTATGT	0	1	1	1	0	0	TATCAAT	3	425101
chrXIII	425113	+	chrXIII:425020:425113:+	0	1	1	0	3	TTTTCT	1	0	0	0	0	0	TACTAAC	0	425113
chrXIII	480618	-	chrXIII:480618:480665:-	1	0	0	0	4	ATGACT	0	1	0	0	0	0	TTCTTTT	4	480615
chrXIII	491154	+	chrXIII:491103:491154:+	0	1	0	0	3	GTACTG	0	1	0	0	0	0	TACTAAC	0	491154
chrXIII	493958	+	chrXIII:493909:493958:+	0	1	0	0	1	GTTTGT	0	1	1	0	1	0	TACTAAT	1	493958
chrXIII	499898	-	chrXIII:499898:499948:-	0	1	1	0	1	TTATGT	1	0	0	0	0	0	TACTAAC	0	499898
chrXIII	517842	+	chrXIII:517791:517842:+	0	1	1	0	3	GTTAGC	1	0	0	0	0	0	TACTAAC	0	517842
chrXIII	537527	+	chrXIII:537448:537527:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	537527
chrXIII	551141	-	chrXIII:551141:551202:-	1	0	0	1	0	GTATGT	0	0	0	0	0	0	AACTAAT	2	551143
chrXIII	551143	-	chrXIII:551143:551202:-	0	1	0	1	0	GTATGT	0	1	1	0	1	0	AACTAAT	2	551143
chrXIII	552477	+	chrXIII:552425:552477:+	0	1	0	0	3	ATTTTT	0	1	0	0	0	0	AACTAAT	2	552477
chrXIII	559828	+	chrXIII:559782:559828:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TACTAAC	0	559831
chrXIII	559831	+	chrXIII:559782:559831:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	559831
chrXIII	608719	+	chrXIII:608660:608719:+	1	0	0	0	2	GTATTA	0	1	0	0	0	0	TGCTAAC	1	608722
chrXIII	637454	+	chrXIII:637403:637454:+	0	1	0	0	1	GTGTGT	0	1	1	0	1	0	AACTAAC	1	637454
chrXIII	647110	+	chrXIII:647059:647110:+	1	0	0	0	1	GCATGT	0	0	0	0	0	0	CACTAAC	1	647113
chrXIII	647113	+	chrXIII:647059:647113:+	0	1	0	0	1	GCATGT	0	1	1	0	1	0	CACTAAC	1	647113
chrXIII	649542	-	chrXIII:649542:649630:-	0	1	0	0	1	GTATGG	0	1	1	0	1	0	TACTAAC	0	649542
chrXIII	651593	+	chrXIII:651524:651593:+	0	1	1	0	2	GTACAT	1	0	0	0	0	0	TACTAAC	0	651593
chrXIII	652797	-	chrXIII:652797:652846:-	1	1	1	1	1	GTTTGT	1	0	0	0	0	0	CACTAAC	1	652797
chrXIII	652808	-	chrXIII:652808:652846:-	1	0	0	1	1	GTTTGT	0	1	1	1	0	0	CACTAAC	1	652797
chrXIII	653957	-	chrXIII:653957:654018:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	653957
chrXIII	666961	-	chrXIII:666961:667016:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	666961
chrXIII	701814	+	chrXIII:701740:701814:+	0	1	0	0	1	GTAGGT	0	1	1	0	1	0	TTCTAAC	1	701814
chrXIII	721231	-	chrXIII:721231:721344:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	721231
chrXIII	727506	+	chrXIII:727436:727506:+	0	1	0	0	6	TCCCAA	0	1	0	0	0	0	TACTAAC	0	727506
chrXIII	732835	+	chrXIII:732773:732835:+	0	1	1	0	2	GTATTA	1	0	0	0	0	0	TACTAAC	0	732835
chrXIII	753788	-	chrXIII:753788:753832:-	0	1	1	0	4	ATAAAA	1	0	0	0	0	0	TACTAAC	0	753788
chrXIII	810475	-	chrXIII:810475:810549:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	GACTAAC	1	810475
chrXIII	822588	-	chrXIII:822588:822625:-	1	0	0	0	5	ATCAAA	0	1	0	0	0	0	AAAAAAG	4	822589
chrXIII	832410	+	chrXIII:832362:832410:+	1	0	0	0	2	GTAAAT	0	0	0	0	0	0	TACTGAC	1	832413
chrXIII	832413	+	chrXIII:832362:832413:+	0	1	0	0	2	GTAAAT	0	1	0	0	0	0	TACTGAC	1	832413
chrXIII	845439	-	chrXIII:845439:845541:-	0	1	0	0	1	TTATGT	0	1	1	0	1	0	TACTAAC	0	845439
chrXIII	854879	+	chrXIII:854816:854879:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	854879
chrXIII	887492	+	chrXIII:887427:887492:+	0	1	0	0	3	CGTTGT	0	1	0	0	0	0	TACTAAC	0	887492
chrXIII	894576	-	chrXIII:894576:894616:-	0	1	0	0	4	CAATCA	0	1	0	0	0	0	TATTAAC	1	894576
chrXIII	910099	-	chrXIII:910099:910130:-	0	1	0	0	2	CGATGT	0	1	0	0	0	0	TAGTAAC	1	910099
chrXIV	17325	-	chrXIV:17325:17361:-	0	1	0	0	3	CCAAGT	0	1	0	0	0	0	CATTAAC	2	17325
chrXIV	48377	+	chrXIV:48293:48377:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	48377
chrXIV	62407	-	chrXIV:62407:62472:-	0	1	1	0	3	AGTTGT	1	0	0	0	0	0	TACTAAC	0	62407
chrXIV	64389	-	chrXIV:64389:64425:-	0	1	0	0	3	TTTTCT	0	1	0	0	0	0	TATTAAC	1	64389
chrXIV	69245	+	chrXIV:69184:69245:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	CACTAAC	1	69245
chrXIV	145191	-	chrXIV:145191:145255:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	145191
chrXIV	174520	-	chrXIV:174520:174572:-	1	0	0	0	2	GTATCG	0	0	0	0	0	0	AACTAAC	1	174522
chrXIV	174522	-	chrXIV:174522:174572:-	0	1	0	0	2	GTATCG	0	1	0	0	0	0	AACTAAC	1	174522
chrXIV	185553	+	chrXIV:185493:185553:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	185553
chrXIV	217114	-	chrXIV:217114:217193:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	217114
chrXIV	224800	+	chrXIV:224764:224800:+	0	1	0	0	3	TTAAGA	0	1	0	0	0	0	TATTAAC	1	224800
chrXIV	227321	-	chrXIV:227321:227353:-	0	1	0	0	4	GTGATA	0	1	0	0	0	0	TACTAAC	0	227321
chrXIV	250195	-	chrXIV:250195:250238:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	CACTGAC	2	250195
chrXIV	273232	+	chrXIV:273189:273232:+	0	1	0	0	1	GTACGT	0	1	1	0	1	0	AACTAAC	1	273232
chrXIV	273585	-	chrXIV:273585:273650:-	0	1	0	0	2	GTATAA	0	1	0	0	0	0	TATTAAC	1	273585

chrXIV	324786	-	chrXIV:324786:324827:-	0	1	0	0	5	AGGTAG	0	1	0	0	0	0	CACTAAC	1	324786
chrXIV	331803	+	chrXIV:331744:331803:+	0	1	1	0	2	ATATGC	1	0	0	0	0	0	TACTAAC	0	331803
chrXIV	349281	-	chrXIV:349281:349355:-	0	1	0	0	1	GTATGG	0	1	1	0	1	0	GTCTAAC	2	349281
chrXIV	351021	+	chrXIV:350960:351021:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	351021
chrXIV	359078	-	chrXIV:359078:359147:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TACTAAC	0	359078
chrXIV	366096	+	chrXIV:366038:366096:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	366096
chrXIV	369426	-	chrXIV:369426:369506:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	369426
chrXIV	373657	+	chrXIV:373596:373657:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	TACTAAT	1	373659
chrXIV	373659	+	chrXIV:373596:373659:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAT	1	373659
chrXIV	380699	-	chrXIV:380699:380783:-	1	0	0	1	0	GTATGT	0	0	0	0	0	0	TACTAAT	1	380703
chrXIV	380703	-	chrXIV:380703:380783:-	0	1	0	1	0	GTATGT	0	1	1	0	1	0	TACTAAT	1	380703
chrXIV	380726	-	chrXIV:380726:380783:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	380726
chrXIV	394038	+	chrXIV:393996:394038:+	0	1	0	0	1	GTATGC	0	1	1	0	1	0	GACTAAC	1	394038
chrXIV	401582	+	chrXIV:401504:401582:+	0	1	0	0	2	GTATCG	0	1	0	0	0	0	TATTAAC	1	401582
chrXIV	413438	-	chrXIV:413438:413482:-	1	0	0	0	4	CGGCGT	0	1	0	0	0	0	TAAAAAA	3	413441
chrXIV	415872	+	chrXIV:415827:415872:+	0	1	1	0	2	GCATGA	1	0	0	0	0	0	TACTAAC	0	415872
chrXIV	427176	+	chrXIV:427106:427176:+	1	0	0	0	1	GTATGA	0	0	0	0	0	0	GACTAAC	1	427178
chrXIV	427178	+	chrXIV:427106:427178:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	GACTAAC	1	427178
chrXIV	429574	-	chrXIV:429574:429637:-	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TTCTAAC	1	429576
chrXIV	429576	-	chrXIV:429576:429637:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCTAAC	1	429576
chrXIV	429600	-	chrXIV:429600:429637:-	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TTCGGTC	4	429600
chrXIV	494551	-	chrXIV:494551:494633:-	1	1	1	0	3	GTAATG	1	0	0	0	0	0	TACTAAC	0	494551
chrXIV	534915	-	chrXIV:534915:534966:-	1	1	1	1	1	GTATGC	1	0	0	0	0	0	TACTAAC	0	534915
chrXIV	545341	+	chrXIV:545293:545341:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	TACTAAC	0	545341
chrXIV	545603	+	chrXIV:545556:545603:+	0	1	0	0	2	GTAACT	0	1	0	0	0	0	TATTAAC	1	545603
chrXIV	557672	+	chrXIV:557612:557672:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	557672
chrXIV	561151	-	chrXIV:561151:561218:-	0	1	0	0	3	AAATAT	0	1	0	0	0	0	CACTAAC	1	561151
chrXIV	573918	-	chrXIV:573918:573973:-	0	1	0	0	2	GTTTGA	0	1	0	0	0	0	TACTGAC	1	573918
chrXIV	583911	-	chrXIV:583911:583971:-	1	1	0	0	0	GTATGT	0	1	1	0	1	0	AACTAAC	1	583911
chrXIV	598313	+	chrXIV:598259:598313:+	0	1	0	0	2	GTTTGA	0	1	0	0	0	0	TACTGAC	1	598313
chrXIV	609837	+	chrXIV:609792:609837:+	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	AACTAAC	1	609837
chrXIV	611577	+	chrXIV:611503:611577:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TATTAAC	1	611580
chrXIV	611580	+	chrXIV:611503:611580:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	611580
chrXIV	623270	+	chrXIV:623196:623270:+	0	1	1	0	3	GTACAG	1	0	0	0	0	0	TACTAAT	1	623270
chrXIV	724879	+	chrXIV:724794:724879:+	0	1	0	0	3	GGTAGT	0	1	0	0	0	0	TACTAAC	0	724879
chrXIV	726915	-	chrXIV:726915:726978:-	0	1	0	0	1	GTCTGT	0	1	1	0	1	0	TACTAAC	0	726915
chrXIV	763544	+	chrXIV:763498:763544:+	1	0	0	0	3	GTACAG	0	0	0	0	0	0	TACTAAC	0	763547
chrXIV	763547	+	chrXIV:763498:763547:+	0	1	0	0	3	GTACAG	0	1	0	0	0	0	TACTAAC	0	763547
chrXIV	767745	-	chrXIV:767745:767788:-	0	1	0	0	2	GTACGC	0	1	0	0	0	0	AACTAAC	1	767745
chrXV	87615	+	chrXV:87554:87615:+	0	1	0	0	1	GTATCT	0	1	1	0	1	0	TTCTAAC	1	87615
chrXV	92476	-	chrXV:92476:92521:-	1	1	1	0	3	GTAATG	1	0	0	0	0	0	TACTAAC	0	92476
chrXV	93868	-	chrXV:93868:93914:-	0	1	1	0	2	GTACGG	1	0	0	0	0	0	TACTAAC	0	93868
chrXV	117635	-	chrXV:117635:117684:-	1	0	0	0	1	GTATGC	0	1	1	0	1	0	GACTAGC	2	117636
chrXV	139435	+	chrXV:139377:139435:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTGAC	1	139435
chrXV	240976	-	chrXV:240976:241024:-	1	1	1	1	1	GTAAGT	1	0	0	0	0	0	GACTAAC	1	240976
chrXV	242453	-	chrXV:242453:242503:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	242453
chrXV	249914	+	chrXV:249872:249914:+	0	1	0	0	3	ATCGGT	0	1	0	0	0	0	TATTAAC	1	249914
chrXV	325376	-	chrXV:325376:325450:-	1	1	0	0	2	GTATCG	0	1	0	0	0	0	TACTAAC	0	325376
chrXV	349520	-	chrXV:349520:349598:-	1	0	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAG	1	349522
chrXV	418634	+	chrXV:418565:418634:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TTCTAAC	1	418634
chrXV	423676	-	chrXV:423676:423735:-	1	1	0	0	1	GTATGG	0	1	1	0	1	0	TACTGAC	1	423676
chrXV	437797	-	chrXV:437797:437846:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TACTAAC	0	437797
chrXV	448694	+	chrXV:448667:448694:+	1	0	0	0	3	TAATAT	0	1	0	0	0	0	AAAAAAA	4	448694
chrXV	505980	+	chrXV:505939:505980:+	1	0	0	1	0	GTATGT	0	1	1	1	0	0	GAGTAAC	2	505983
chrXV	506800	-	chrXV:506800:506870:-	1	0	0	0	1	GTATTT	0	0	0	0	0	0	TACTAAC	0	506802
chrXV	506802	-	chrXV:506802:506870:-	0	1	0	0	1	GTATTT	0	1	1	0	1	0	TACTAAC	0	506802
chrXV	518763	-	chrXV:518763:518826:-	1	0	0	0	1	ATATGT	0	0	0	0	0	0	TACTAAC	0	518765
chrXV	518765	-	chrXV:518765:518826:-	0	1	0	0	1	ATATGT	0	1	1	0	1	0	TACTAAC	0	518765
chrXV	527238	+	chrXV:527186:527238:+	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAT	1	527238
chrXV	594353	-	chrXV:594353:594426:-	1	0	0	0	5	GCGCAA	0	1	0	0	0	0	TGCAAAA	3	594341
chrXV	605430	+	chrXV:605379:605430:+	0	1	0	0	1	GTACGT	0	1	1	0	1	0	AACTAAC	1	605430
chrXV	630886	-	chrXV:630886:630936:-	0	1	0	0	2	GTATAG	0	1	0	0	0	0	AACTAAC	1	630886
chrXV	674438	-	chrXV:674438:674504:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	GACTAAC	1	674438
chrXV	720497	+	chrXV:720444:720497:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	TATTAAC	1	720500
chrXV	720500	+	chrXV:720444:720500:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TATTAAC	1	720500
chrXV	733353	-	chrXV:733353:733417:-	1	0	0	0	1	GCATGT	0	0	0	0	0	0	AACTAAC	1	733356
chrXV	733356	-	chrXV:733356:733417:-	0	1	0	0	1	GCATGT	0	1	1	0	1	0	AACTAAC	1	733356
chrXV	754238	-	chrXV:754238:754290:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	AACTAAC	1	754238
chrXV	778910	-	chrXV:778910:778959:-	0	1	1	0	4	GTCGAA	1	0	0	0	0	0	TACTAAC	0	778910
chrXV	791704	-	chrXV:791704:791753:-	1	1	0	0	2	TTACGT	0	1	0	0	0	0	TACTAAC	0	791704
chrXV	819160	+	chrXV:819077:819160:+	0	1	0	0	1	GTCTGT	0	1	1	0	1	0	TACTGAC	1	819160
chrXV	836399	-	chrXV:836399:836448:-	0	1	0	0	2	ATATTT	0	1	0	0	0	0	ATCTAAC	2	836399
chrXV	845020	+	chrXV:844959:845020:+	1	0	0	0	0	GTATGT	0	0	0	0	0	0	ATCTAAC	2	845023
chrXV	845023	+	chrXV:844959:845023:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	ATCTAAC	2	845023
chrXV	867516	+	chrXV:867439:867516:+	0	1	1	0	3	GTAAAA	1	0	0	0	0	0	TACTAAC	0	867516
chrXV	900802	-	chrXV:900802:900850:-	1	1	1	0	2	GTAATT	1	0	0	0	0	0	TACTAAC	0	900802
chrXV	930113	+	chrXV:930063:930113:+	1	0	0	0	1	GTAAGT	0	1	1	1	0	1	CGCTAAC	2	930116
chrXV	1003995	-	chrXV:1003995:1004066:-	0	1	0	0	2	GTGAGT	0	1	0	0	0	0	TACTAAC	0	1003995
chrXV	1030464	-	chrXV:1030464:1030507:-	0	1	0	0	4	ATCTAA	0	1	0	0	0	0	AACTAAC	1	1030464
chrXV	1059710	-	chrXV:1059710:1059794:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTGAC	1	1059710
chrXV	1062513	-	chrXV:1062513:1062560:-	1	1	0	0	1	GTATGC	0	1	1	0	1	0	TACTAAC	0	1062513
chrXVI	76014	-	chrXVI:76014:76071:-	0	1	1	0	2	GTCTTT	1	0	0	0	0	0	TACTAAC	0	76014

chrXVI	76164	-	chrXVI:76164:76223:-	1	0	0	1	0	GTATGT	0	1	1	0	1	0	CACTAAG	2	76166
chrXVI	96189	-	chrXVI:96189:96233:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	AATTAAC	2	96189
chrXVI	101223	+	chrXVI:101139:101223:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TATTAAC	1	101223
chrXVI	115267	+	chrXVI:115219:115267:+	1	0	0	1	0	GTATGT	0	0	0	0	0	0	TACTAAC	0	115270
chrXVI	115270	+	chrXVI:115219:115270:+	0	1	0	1	0	GTATGT	0	1	1	0	1	0	TACTAAC	0	115270
chrXVI	146508	-	chrXVI:146508:146597:-	1	1	0	0	1	GTATGA	0	1	1	0	1	0	TACTAAC	0	146508
chrXVI	159663	+	chrXVI:159585:159663:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAC	0	159663
chrXVI	174036	+	chrXVI:173971:174036:+	1	1	1	0	3	GTTTTA	1	0	0	0	0	0	TACTAAC	0	174036
chrXVI	196571	-	chrXVI:196571:196616:-	0	1	0	0	1	GTATGG	0	1	1	0	1	0	ATCTAAC	2	196571
chrXVI	218695	+	chrXVI:218646:218695:+	1	0	0	1	0	GTATGT	0	1	1	1	0	0	GAAGATC	4	218690
chrXVI	218711	+	chrXVI:218646:218711:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	218711
chrXVI	231558	+	chrXVI:231499:231558:+	1	0	0	0	2	GTAAGA	0	0	0	0	0	0	TACTAAC	0	231561
chrXVI	231561	+	chrXVI:231499:231561:+	0	1	0	0	2	GTAAGA	0	1	0	0	0	0	TACTAAC	0	231561
chrXVI	281450	-	chrXVI:281450:281502:-	1	0	0	1	0	GTATGT	0	1	1	0	1	0	CAATAAT	3	281450
chrXVI	305374	+	chrXVI:305306:305374:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	305374
chrXVI	335968	+	chrXVI:335905:335968:+	1	0	0	0	0	GTATGT	0	1	1	0	1	0	TACTTAC	1	335970
chrXVI	339246	+	chrXVI:339174:339246:+	0	1	0	0	1	GTATAT	0	1	1	0	1	0	TATTAAC	1	339246
chrXVI	339306	+	chrXVI:339230:339306:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTGAC	1	339306
chrXVI	345483	-	chrXVI:345483:345574:-	0	1	1	0	4	TAACGG	1	0	0	0	0	0	TACTAAC	0	345483
chrXVI	405426	+	chrXVI:405372:405426:+	0	1	1	0	3	ATTTAT	1	0	0	0	0	0	CACTAAC	1	405426
chrXVI	407002	+	chrXVI:406952:407002:+	1	1	1	0	1	GTGTGT	1	0	0	0	0	0	TACTAAC	0	407002
chrXVI	412958	+	chrXVI:412887:412958:+	1	1	1	0	2	TAATGT	1	0	0	0	0	0	TACTAAC	0	412958
chrXVI	445520	-	chrXVI:445520:445573:-	1	1	0	0	1	GTGTGT	0	1	1	0	1	0	GACTAAC	1	445520
chrXVI	481182	-	chrXVI:481182:481238:-	1	0	0	0	1	GTACGT	0	0	0	0	0	0	CACTAAC	1	481184
chrXVI	481184	-	chrXVI:481184:481238:-	0	1	0	0	1	GTACGT	0	1	1	0	1	0	CACTAAC	1	481184
chrXVI	490810	-	chrXVI:490810:490857:-	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TATTAAC	1	490810
chrXVI	492958	-	chrXVI:492958:493018:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	492958
chrXVI	513416	-	chrXVI:513416:513466:-	0	1	0	0	1	GTATGG	0	1	1	1	0	0	TACTAAA	1	513407
chrXVI	560471	+	chrXVI:560413:560471:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TACTAAT	1	560471
chrXVI	579896	-	chrXVI:579896:579965:-	0	1	0	0	1	GTATGA	0	1	1	0	1	0	TATTAAC	1	579896
chrXVI	584022	-	chrXVI:584022:584078:-	1	0	0	0	2	GTATTG	0	0	0	0	0	0	TACTGAC	1	584024
chrXVI	584024	-	chrXVI:584024:584078:-	0	1	0	0	2	GTATTG	0	1	0	0	0	0	TACTGAC	1	584024
chrXVI	590145	-	chrXVI:590145:590200:-	0	1	0	0	1	ATATGT	0	1	1	0	1	0	TACTGAC	1	590145
chrXVI	593080	-	chrXVI:593080:593139:-	1	0	0	0	2	GTATAA	0	0	0	0	0	0	AACTAAC	1	593082
chrXVI	593082	-	chrXVI:593082:593139:-	0	1	0	0	2	GTATAA	0	1	0	0	0	0	AACTAAC	1	593082
chrXVI	602284	-	chrXVI:602284:602338:-	1	0	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAA	1	602282
chrXVI	616652	+	chrXVI:616593:616652:+	0	1	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAT	1	616652
chrXVI	617123	+	chrXVI:617066:617123:+	0	1	0	0	1	GTAAGT	0	1	1	0	1	0	TATTAAC	1	617123
chrXVI	623662	+	chrXVI:623575:623662:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	623662
chrXVI	654534	+	chrXVI:654471:654534:+	0	1	1	0	2	GTATAA	1	0	0	0	0	0	TACTAAC	0	654534
chrXVI	656521	-	chrXVI:656521:656572:-	1	1	0	0	2	GTAGTT	0	1	0	0	0	0	TACTAAC	0	656521
chrXVI	678219	-	chrXVI:678219:678276:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	678219
chrXVI	685776	+	chrXVI:685691:685776:+	0	1	0	0	1	GTAGGT	0	1	1	0	1	0	AACTAAT	2	685776
chrXVI	717058	-	chrXVI:717058:717144:-	0	1	0	0	1	GTATGC	0	1	1	0	1	1	TACTAAC	0	717058
chrXVI	729395	-	chrXVI:729395:729479:-	1	0	0	1	0	GTATGT	0	1	1	0	1	0	TACCAAC	1	729397
chrXVI	729414	-	chrXVI:729414:729479:-	1	1	1	1	0	GTATGT	1	0	0	0	0	0	GACTAAC	1	729414
chrXVI	739748	-	chrXVI:739748:739794:-	1	0	0	0	2	GTAAGC	0	0	0	0	0	0	TATTAAC	1	739750
chrXVI	739750	-	chrXVI:739750:739794:-	0	1	0	0	2	GTAAGC	0	1	0	0	0	0	TATTAAC	1	739750
chrXVI	745392	+	chrXVI:745342:745392:+	0	1	0	0	2	TAATGT	0	1	0	0	0	0	CACTAAC	1	745392
chrXVI	777582	-	chrXVI:777582:777639:-	1	0	0	0	1	GTAAGT	0	1	1	0	1	0	AACTAGC	2	777580
chrXVI	800194	+	chrXVI:800147:800194:+	0	1	0	0	5	AACTTC	0	1	0	0	0	0	TACTAAT	1	800194
chrXVI	824942	-	chrXVI:824942:825021:-	0	1	0	0	2	GTGCGT	0	1	0	0	0	0	CACTAAC	1	824942
chrXVI	833779	+	chrXVI:833690:833779:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	AACTAAC	1	833779
chrXVI	841160	+	chrXVI:841109:841160:+	0	1	0	0	2	GAAAGT	0	1	0	0	0	0	AACTAAC	1	841160
chrXVI	883453	+	chrXVI:883384:883453:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	883453
chrXVI	883586	-	chrXVI:883586:883649:-	1	0	0	0	1	GTATAT	0	0	0	0	0	0	GACTAAC	1	883588
chrXVI	883588	-	chrXVI:883588:883649:-	0	1	0	0	1	GTATAT	0	1	1	0	1	0	GACTAAC	1	883588
chrXVI	911328	+	chrXVI:911273:911328:+	1	1	1	1	0	GTATGT	1	0	0	0	0	0	TACTAAC	0	911328
chrXVI	937232	-	chrXVI:937232:937285:-	0	1	0	0	2	GTATAC	0	1	0	0	0	0	TACTAAT	1	937232
chrXVI	937537	-	chrXVI:937537:937617:-	1	0	0	0	0	GTATGT	0	1	1	0	1	0	TACTAAA	1	937535
chrXVI	939905	-	chrXVI:939905:939951:-	1	0	0	0	3	GTACCG	0	0	0	0	0	0	TACTAAC	0	939907
chrXVI	939907	-	chrXVI:939907:939951:-	0	1	0	0	3	GTACCG	0	1	0	0	0	0	TACTAAC	0	939907
totals										198	430	268	21	247	22			

5ss_bp_pair is in the format chr:nt1:nt2:strand
nt1 < nt2
On the plus strand, nt1 is the 5'ss and nt2 is the BP
On the reverse strand, nt1 is the BP and nt2 is the 5'SS

In general 1=true, 0=false, excepet for 5ss_mm, the number of mismatches at the 5'ss from GTATGT, and best_bp_mm from TACTAAC
u_a and u_n are the union of annotated and novel BP, respectively, of both peak callers

lcnBP= low confidence novel BP (see supplemental methods for details)
hcnBP = high confidence novel BP (see supplemental methods for details)

Table S3. GTATGT motif frequency at 5'SS and generally in introns.

No. mismatches from /GTATGT	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**total**	0 or 1 mut	% 0 or 1 mut
Annotated 5'SS	216	73	6	18	7	7	3	330	289	87.58
Annotated 5'SS, no chrM	216	73	6	1	2	0	0	298	289	96.98
Arbitrary intron positions	10	24	130	471	982	973	390	2980	34	1.1

Table S4. Branch-seq CPMs.

bp_id	branch_seq_cpm	gene_name	bp_type
chrVII:497961:-	476.7266362	YGR001C	annotated
chrXIII:123777:-	1.126520145	YML073C	annotated
chrV:433162:+	0.292060778	YER133W	annotated
chrV:308040:+	205.9028487	YER074W-A	annotated
chrV:307801:+	248.1264927	YER074W-A	annotated
chrV:269803:-	0.083445937	YER056C-A	annotated
chrV:348217:-	221.7575767	YER093C-A	annotated
chrV:148254:+	301.9908448	YEL003W	annotated
chrV:239667:-	0.75101343	YER044C-A	annotated
chrV:131853:+	160.3830903	YEL012W	annotated
chrV:159013:-	674.4517831	YER003C	annotated
chrV:548611:+	1.376857955	YER179W	annotated
chrV:166786:-	251.2557153	YER007C-A	annotated
chrV:397225:+	0.333783747	YER117W	annotated
chrII:462255:+	274.036456	YBR111W-A	annotated
chrII:479389:+	247.9596008	YBR119W	annotated
chrII:602175:+	2.711992942	YBR186W	annotated
chrII:606615:+	0.917905303	YBR191W	annotated
chrII:653429:+	196.306566	YBR215W	annotated
chrII:170771:+	29.95709126	YBL026W	annotated
chrII:110932:+	198.5178833	YBL059W	annotated
chrII:333365:+	7.092904617	YBR048W	annotated
chrII:110451:-	375.590161	YBL059C-A	annotated
chrII:186375:-	513.1507876	YBL018C	annotated
chrII:462472:+	79.1901939	YBR111W-A	annotated
chrII:142787:-	241.9932163	YBL040C	annotated
chrII:47071:-	44.47668425	YBL091C-A	annotated
chrII:168770:+	0.166891873	YBL027W	annotated
chrII:426524:-	0.458952652	YBR090C	annotated
chrII:125234:+	112.1930619	YBL050W	annotated
chrII:366534:-	129.0491411	YBR062C	annotated
chrII:726947:-	120.9966082	YBR255C-A	annotated
chrII:679973:-	102.6802251	YBR230C	annotated
chrII:407047:-	2316.334033	YBR082C	annotated
chrVI:64615:-	0.458952652	YFL034C-A	annotated
chrVI:221291:-	3.00405372	YFR031C-A	annotated
chrVI:242044:+	349.5967517	YFR045W	annotated
chrVI:63915:-	332.3651658	YFL034C-B	annotated
chrVI:203304:-	787.2289666	YFR024C-A	annotated
chrXIV:62407:-	0.166891873	YNL302C	annotated
chrXIV:534915:-	362.1970881	YNL050C	annotated
chrXIV:494551:-	3.50472934	YNL069C	annotated
chrXIV:623270:+	0.083445937	YNL004W	annotated
chrXIV:351021:+	438.2163364	YNL147W	annotated

chrXIV:545341:+	1186.726388	YNL044W	annotated
chrXIV:48377:+	87.78512538	YNL312W	annotated
chrXIV:331803:+	0.50067562	YNL162W	annotated
chrXIV:185553:+	134.3062351	YNL246W	annotated
chrXIV:145191:-	172.9417038	YNL265C	annotated
chrXIV:609837:+	1.25168905	YNL012W	annotated
chrXIV:366096:+	225.1371371	YNL138W-A	annotated
chrXIV:380726:-	537.4335551	YNL130C	annotated
chrXIV:415872:+	0.292060778	YNL112W	annotated
chrXIV:557672:+	334.659929	YNL038W	annotated
chrXVI:96189:-	218.8369689	YPL241C	annotated
chrXVI:492958:-	403.210766	YPL031C	annotated
chrXVI:623662:+	391.1528281	YPR028W	annotated
chrXVI:729414:-	126.3788711	YPR098C	annotated
chrXVI:407002:+	9.679728654	YPL079W	annotated
chrXVI:305374:+	165.9322451	YPL129W	annotated
chrXVI:883453:+	202.1477816	YPR170W-B	annotated
chrXVI:678219:-	565.4713899	YPR063C	annotated
chrXVI:345483:-	0.083445937	YPL109C	annotated
chrXVI:76014:-	0.166891873	YPL249C-A	annotated
chrXVI:218711:+	254.3849379	YPL175W	annotated
chrXVI:654534:+	0.292060778	YPR043W	annotated
chrXVI:405426:+	0.083445937	YPL081W	annotated
chrXVI:911328:+	1047.663735	YPR187W	annotated
chrXVI:833779:+	136.8930591	YPR153W	annotated
chrXVI:412958:+	28.87229409	YPL075W	annotated
chrXVI:174036:+	0.792736398	YPL198W	annotated
chrXI:625594:+	630.6009434	YKR095W-A	annotated
chrXI:447376:-	229.267711	YKR004C	annotated
chrXI:430163:-	132.1366407	YKL006C-A	annotated
chrXI:283016:+	0.292060778	YKL081W	annotated
chrXI:437526:+	592.6330422	YKL002W	annotated
chrXI:449611:-	5.131925105	YKR005C	annotated
chrXI:83061:+	319.4727685	YKL190W	annotated
chrXI:618096:-	15.64611313	YKR094C	annotated
chrVII:543708:+	129.6332626	YGR029W	annotated
chrVII:946407:+	1.00135124	YGR225W	annotated
chrVII:497394:-	401.9590769	YGR001C	annotated
chrVII:157245:-	3.212668562	YGL183C	annotated
chrVII:435728:+	0.166891873	YGL033W	annotated
chrVII:346854:-	32.08496265	YGL087C	annotated
chrVII:73034:-	19.65151809	YGL226C-A	annotated
chrVII:311486:+	0.667567493	YGL103W	annotated
chrVII:556282:+	0.625844525	YGR034W	annotated
chrVII:62173:+	317.0945594	YGL232W	annotated
chrX:702871:-	0.166891873	YJR145C	annotated
chrX:387380:-	414.5594134	YJL031C	annotated

chrX:435302:+	207.3214297	YJL001W	annotated
chrX:76268:+	0.083445937	YJL189W	annotated
chrX:74178:+	31.33394922	YJL191W	annotated
chrX:365853:+	441.0117753	YJL041W	annotated
chrX:608540:+	0.792736398	YJR094W-A	annotated
chrX:396512:-	329.3193891	YJL024C	annotated
chrX:469190:-	15.47922125	YJR021C	annotated
chrX:50351:-	77.02059955	YJL205C	annotated
chrXV:93868:-	0.083445937	YOL120C	annotated
chrXV:240976:-	344.9655022	YOL048C	annotated
chrXV:778910:-	0.083445937	YOR234C	annotated
chrXV:867516:+	0.542398588	YOR293W	annotated
chrXV:242453:-	19.60979512	YOL047C	annotated
chrXV:92476:-	51.44441996	YOL121C	annotated
chrXV:900802:-	1.585472797	YOR312C	annotated
chrIX:166484:+	603.3141221	YIL106W	annotated
chrIX:232012:-	1.293412018	YIL069C	annotated
chrIX:225834:-	0.083445937	YIL073C	annotated
chrIX:317136:+	0.542398588	YIL018W	annotated
chrIX:47743:+	547.1132838	YIL156W-B	annotated
chrIX:155276:+	275.329868	YIL111W	annotated
chrIX:348380:-	0.50067562	YIL004C	annotated
chrXII:522984:+	0.292060778	YLR185W	annotated
chrXII:766205:-	535.8063594	YLR316C	annotated
chrXII:564467:-	31.12533438	YLR211C	annotated
chrXII:548706:-	175.1530211	YLR199C	annotated
chrXII:1024631:+	1.919256543	YLR445W	annotated
chrXII:398583:+	89.28715224	YLR128W	annotated
chrXII:286498:-	113.0275212	YLR078C	annotated
chrXII:786667:+	10.84797177	YLR329W	annotated
chrXII:857038:+	81.40151122	YLR367W	annotated
chrXII:40353:-	2850.179413	YLL050C	annotated
chrXII:694444:+	310.5023304	YLR275W	annotated
chrXII:250899:-	1.710641702	YLR054C	annotated
chrXII:327295:-	10.51418802	YLR093C	annotated
chrXII:744219:+	171.6900147	YLR306W	annotated
chrXII:766086:-	482.1506221	YLR316C	annotated
chrXII:987191:+	193.8031879	YLR426W	annotated
chrXII:242652:+	0.584121557	YLR048W	annotated
chrXII:263540:+	0.166891873	YLR061W	annotated
chrXIII:337886:+	835.6276098	YMR033W	annotated
chrXIII:666961:-	225.4291979	YMR201C	annotated
chrXIII:223421:-	0.292060778	YML026C	annotated
chrXIII:499898:-	0.208614842	YMR116C	annotated
chrXIII:732835:+	0.083445937	YMR230W	annotated
chrXIII:651593:+	0.166891873	YMR194W	annotated
chrXIII:854879:+	223.6768332	YMR292W	annotated

chrXIII:425113:+	0.083445937	YMR079W	annotated
chrXIII:82343:+	217.2932191	YML094W	annotated
chrXIII:206162:+	118.4515071	YML036W	annotated
chrXIII:140113:-	99.59272542	YML067C	annotated
chrXIII:537527:+	1.543749828	YMR133W	annotated
chrXIII:517842:+	0.083445937	YMR125W	annotated
chrXIII:721231:-	1.460303892	YMR225C	annotated
chrXIII:753788:-	0.125168905	YMR242C	annotated
chrXIII:652797:-	114.9885007	YMR194C-B	annotated
chrXIII:211547:+	59.9559055	YML034W	annotated
chrXIII:99301:-	437.2984311	YML085C	annotated
chrXIII:225264:-	634.5646254	YML025C	annotated
chrIII:111588:-	118.2428923	YCL002C	annotated
chrIII:177952:-	1.919256543	YCR031C	annotated
chrIII:173137:-	618.2926678	YCR028C-A	annotated
chrIII:101646:-	93.66806391	YCL012C	annotated
chrIII:107089:+	297.6099331	YCL005W-A	annotated
chrIII:107255:+	352.4339135	YCL005W-A	annotated
chrIV:1212941:+	276.3312193	YDR367W	annotated
chrIV:1266790:-	144.945592	YDR397C	annotated
chrIV:1237581:+	3.379560435	YDR381W	annotated
chrIV:1103871:+	150.8285305	YDR318W	annotated
chrIV:1073346:-	150.9119765	YDR305C	annotated
chrIV:1450485:-	1.960979512	YDR500C	annotated
chrIV:491873:+	0.166891873	YDR025W	annotated
chrIV:65358:+	205.9862947	YDL219W	annotated
chrIV:1238769:-	150.7868076	YDR381C-A	annotated
chrIV:1319751:-	113.277859	YDR424C	annotated
chrIV:254999:-	439.1342417	YDL115C	annotated
chrIV:267780:+	101.5537049	YDL108W	annotated
chrIV:239421:-	415.2687038	YDL125C	annotated
chrIV:217970:+	0.417229683	YDL136W	annotated
chrIV:431423:-	1294.872322	YDL012C	annotated
chrIV:337596:+	331.6975983	YDL064W	annotated
chrIV:715265:-	166.4746437	YDR129C	annotated
chrIV:579963:+	20.65286933	YDR064W	annotated
chrIV:399468:+	10.38901912	YDL029W	annotated
chrIV:630016:+	0.709290462	YDR092W	annotated
chrIV:733713:-	307.7903374	YDR139C	annotated
chrIV:569665:-	153.7491383	YDR059C	annotated
chrIV:458048:-	576.6531454	YDR005C	annotated
chrIV:307375:-	0.25033781	YDL083C	annotated
chrIV:230262:+	0.083445937	YDL130W	annotated
chrIV:1319627:-	157.2538677	YDR424C	annotated
chrI:151022:-	100.4271848	YAL001C	annotated
chrI:87439:+	179.6173787	YAL030W	annotated
chrVIII:354926:+	255.67835	YHR123W	annotated

chrVIII:129611:+	89.12026036	YHR012W	annotated
chrVIII:187613:-	1389.917244	YHR039C-A	annotated
chrVIII:498731:-	30.45776688	YHR199C-A	annotated
chrVIII:382356:-	0.083445937	YHR141C	annotated
chrVIII:298418:-	198.976836	YHR097C	annotated
chrVIII:104751:+	0.292060778	YHL001W	annotated
chrVIII:255689:-	528.1293332	YHR077C	annotated
chrVIII:107875:+	674.0345535	YHR001W-A	annotated
chrVIII:315810:-	286.3864547	YHR101C	annotated
chrVIII:189778:-	151.7881588	YHR041C	annotated
chrVIII:251233:+	92.41637486	YHR076W	annotated
chrVIII:262372:-	0.083445937	YHR079C-A	annotated
chrVIII:138274:-	0.083445937	YHR016C	annotated
chrV:151105:+	0.625844525	not_in_intron_or_TIF	cnBP
chrV:166806:-	0.625844525	YER007C-A	cnBP
chrV:540383:-	1.084797177	YER175C	cnBP
chrII:115534:+	15.47922125	YBL056W	cnBP
chrII:170731:+	24.44965944	YBL026W	cnBP
chrII:221024:+	3.087499657	not_in_intron_or_TIF	cnBP
chrII:606346:+	0.709290462	YBR191W	cnBP
chrII:291715:-	1.00135124	YBR025C	cnBP
chrII:592709:-	6.425337124	YBR181C	cnBP
chrXVI:218695:+	0.876182335	YPL175W	cnBP
chrXVI:335968:+	1.335134987	YPL114W	cnBP
chrXVI:76164:-	0.667567493	YPL249C-A	cnBP
chrXVI:281450:-	0.667567493	snR17b	cnBP
chrXVI:602284:-	4.839864327	not_in_intron_or_TIF	cnBP
chrXVI:729395:-	1.460303892	YPR098C	cnBP
chrXVI:777582:-	0.834459367	not_in_intron_or_TIF	cnBP
chrXVI:937537:-	1.25168905	not_in_intron_or_TIF	cnBP
chrXI:96757:+	2.795438878	YKL184W	cnBP
chrXI:468921:-	0.917905303	YKR015C	cnBP
chrVII:439462:+	5.25709401	YGL030W	cnBP
chrVII:543691:+	2.419932163	YGR029W	cnBP
chrVII:555885:+	0.542398588	YGR034W	cnBP
chrVII:143935:-	6.174999314	not_in_intron_or_TIF	cnBP
chrVII:497408:-	1.543749828	YGR001C	cnBP
chrVII:859434:-	5.799492599	YGR183C	cnBP
chrXIII:182669:+	0.959628272	YML046W	cnBP
chrXIII:425094:+	0.375506715	YMR079W	cnBP
chrXIII:652808:-	3.50472934	YMR194C-B	cnBP
chrXV:505980:+	4.965033232	YOR096W	cnBP
chrXV:930113:+	2.086148417	YOR326W	cnBP
chrXV:117635:-	0.792736398	not_in_intron_or_TIF	cnBP
chrXV:349520:-	1.209966082	not_in_intron_or_TIF	cnBP
chrIX:155301:+	1.084797177	YIL111W	cnBP
chrIX:166501:+	0.709290462	YIL106W	cnBP

chrXII:382387:+	3.713344182	YLR116W	cnBP
chrXII:286519:-	3.212668562	YLR078C	cnBP
chrX:435281:+	1.376857955	YJL001W	cnBP
chrIV:107156:+	1.710641702	YDL195W	cnBP
chrIV:392638:+	0.50067562	not_in_intron_or_TIF	cnBP
chrIV:438275:+	1.75236467	YDL007W	cnBP
chrIV:655244:+	1.960979512	YDR100W	cnBP
chrIV:1145148:+	30.37432095	YDR336W	cnBP
chrIV:22303:-	3.75506715	not_in_intron_or_TIF	cnBP
chrIV:451430:-	4.130573865	YDR001C	cnBP
chrVIII:129590:+	0.75101343	YHR012W	cnBP
chrVIII:406673:-	0.959628272	not_in_intron_or_TIF	cnBP
chrV:61194:+	0.166891873	not_in_intron_or_TIF	cnBP
chrV:124638:-	0.667567493	YEL016C	cnBP
chrV:160514:+	0.375506715	YER004W, YER005W	cnBP
chrV:201997:+	46.43766376	YER023W	cnBP
chrV:203928:+	0.333783747	YER024W	cnBP
chrV:305684:+	9.26249897	YER073W	cnBP
chrV:336936:+	1.543749828	YER088W-B	cnBP
chrV:362830:+	1.75236467	YER102W	cnBP
chrV:374671:-	2.461655132	YER107C	cnBP
chrV:487859:+	0.625844525	not_in_intron_or_TIF	cnBP
chrV:517901:+	395.3668479	YER167W	cnBP
chrV:561245:+	0.083445937	not_in_intron_or_TIF	cnBP
chrII:13949:-	0.959628272	not_in_intron_or_TIF	cnBP
chrII:76231:+	0.75101343	not_in_intron_or_TIF	cnBP
chrII:167927:+	0.166891873	not_in_intron_or_TIF	cnBP
chrII:206284:+	0.125168905	not_in_intron_or_TIF	cnBP
chrII:290470:-	0.083445937	YBR025C	cnBP
chrII:331391:-	5.090202137	YBR046C	cnBP
chrII:341038:-	0.75101343	not_in_intron_or_TIF	cnBP
chrII:342756:+	5.50743182	not_in_intron_or_TIF	cnBP
chrII:431594:-	0.50067562	not_in_intron_or_TIF	cnBP
chrII:443734:-	32.29357749	YBR101C	cnBP
chrII:519067:-	0.292060778	not_in_intron_or_TIF	cnBP
chrII:756982:-	0.25033781	not_in_intron_or_TIF	cnBP
chrVI:32028:-	0.625844525	not_in_intron_or_TIF	cnBP
chrVI:96258:+	1.209966082	YFL021W	cnBP
chrVI:109969:-	0.292060778	not_in_intron_or_TIF	cnBP
chrVI:176327:-	3.75506715	YFR015C	cnBP
chrVI:268722:+	0.375506715	not_in_intron_or_TIF	cnBP
chrXIV:69244:+	0.834459367	YNL298W	cnBP
chrXIV:217113:-	0.542398588	YNL231C	cnBP
chrXIV:250194:-	0.083445937	YNL211C	cnBP
chrXIV:273231:+	0.125168905	not_in_intron_or_TIF	cnBP
chrXIV:349280:-	0.125168905	YNL149C	cnBP
chrXIV:359077:-	0.083445937	not_in_intron_or_TIF	cnBP

chrXIV:369425:-	0.125168905	YNL137C	cnBP
chrXIV:373658:+	2.086148417	not_in_intron_or_TIF	cnBP
chrXIV:380702:-	16.6057414	YNL130C	cnBP
chrXIV:394037:+	0.584121557	YNL124W	cnBP
chrXIV:427177:+	1.710641702	not_in_intron_or_TIF	cnBP
chrXIV:429575:-	8.886992255	not_in_intron_or_TIF	cnBP
chrXIV:429599:-	0.458952652	not_in_intron_or_TIF	cnBP
chrXIV:583910:-	3.546452309	YNL025C	cnBP
chrXIV:611579:+	4.464357612	YNL012W	cnBP
chrXIV:726914:-	0.125168905	not_in_intron_or_TIF	cnBP
chrXVI:101222:+	0.208614842	YPL237W	cnBP
chrXVI:115269:+	65.7553981	YPL230W	cnBP
chrXVI:146507:-	10.9314177	not_in_intron_or_TIF	cnBP
chrXVI:159662:+	0.208614842	YPL208W	cnBP
chrXVI:196570:-	0.125168905	YPL184C	cnBP
chrXVI:339245:+	0.083445937	not_in_intron_or_TIF	cnBP
chrXVI:339305:+	0.083445937	not_in_intron_or_TIF	cnBP
chrXVI:445519:-	3.629898245	not_in_intron_or_TIF	cnBP
chrXVI:481183:-	4.00540496	YPL037C	cnBP
chrXVI:490809:-	0.333783747	YPL032C	cnBP
chrXVI:513415:-	0.125168905	YPL020C	cnBP
chrXVI:560470:+	0.50067562	not_in_intron_or_TIF	cnBP
chrXVI:579895:-	0.333783747	YPR010C	cnBP
chrXVI:590144:-	0.125168905	YPR015C	cnBP
chrXVI:616651:+	0.125168905	not_in_intron_or_TIF	cnBP
chrXVI:617122:+	0.125168905	not_in_intron_or_TIF	cnBP
chrXVI:685775:+	0.083445937	YPR070W	cnBP
chrXVI:717057:-	0.417229683	YPR091C	cnBP
chrXVI:883587:-	2.044425448	not_in_intron_or_TIF	cnBP
chrXI:93384:-	13.39307284	YKL186C	cnBP
chrXI:94081:-	5.215371042	not_in_intron_or_TIF	cnBP
chrXI:158626:-	0.083445937	not_in_intron_or_TIF	cnBP
chrXI:166478:+	4.464357612	YKL150W	cnBP
chrXI:191089:-	0.083445937	YKL134C	cnBP
chrXI:193010:-	38.80236055	YKL133C	cnBP
chrXI:225774:-	3.671621214	not_in_intron_or_TIF	cnBP
chrXI:231492:+	0.458952652	YKL109W	cnBP
chrXI:272947:-	0.834459367	not_in_intron_or_TIF	cnBP
chrXI:285868:+	0.625844525	YKL080W	cnBP
chrXI:290610:-	0.959628272	not_in_intron_or_TIF	cnBP
chrXI:408146:+	25.74307146	YKL015W	cnBP
chrXI:446830:-	0.292060778	YKR004C	cnBP
chrXI:490071:+	6.717397902	not_in_intron_or_TIF	cnBP
chrXI:633804:-	0.208614842	YKR098C	cnBP
chrXI:649449:+	0.083445937	not_in_intron_or_TIF	cnBP
chrVII:51958:+	0.375506715	YGL238W	cnBP
chrVII:59556:+	0.125168905	YGL233W	cnBP

chrVII:140633:+	0.083445937	not_in_intron_or_TIF	cnBP
chrVII:167430:+	6.00810744	YGL178W	cnBP
chrVII:253205:-	95.17009077	YGL136C	cnBP
chrVII:262616:-	0.083445937	not_in_intron_or_TIF	cnBP
chrVII:293422:+	0.083445937	YGL114W	cnBP
chrVII:293817:+	0.75101343	YGL114W	cnBP
chrVII:345543:-	0.125168905	not_in_intron_or_TIF	cnBP
chrVII:380660:-	0.083445937	YGL065C	cnBP
chrVII:383554:+	94.46080031	YGL063W	cnBP
chrVII:414313:+	0.041722968	YGL045W	cnBP
chrVII:423867:-	0.333783747	not_in_intron_or_TIF	cnBP
chrVII:427172:-	0.375506715	YGL037C	cnBP
chrVII:436364:+	39.9288807	not_in_intron_or_TIF	cnBP
chrVII:504217:-	0.125168905	not_in_intron_or_TIF	cnBP
chrVII:574777:+	1.919256543	not_in_intron_or_TIF	cnBP
chrVII:593472:+	0.292060778	not_in_intron_or_TIF	cnBP
chrVII:594140:-	1.043074208	not_in_intron_or_TIF	cnBP
chrVII:607018:-	0.375506715	not_in_intron_or_TIF	cnBP
chrVII:658296:+	0.083445937	YGR089W	cnBP
chrVII:682969:-	0.083445937	not_in_intron_or_TIF	cnBP
chrVII:730063:+	0.083445937	not_in_intron_or_TIF	cnBP
chrVII:772104:+	0.417229683	YGR141W	cnBP
chrVII:792327:-	0.625844525	YGR150C	cnBP
chrVII:875660:+	0.125168905	not_in_intron_or_TIF	cnBP
chrVII:914790:-	0.667567493	YGR210C	cnBP
chrVII:962303:+	0.667567493	not_in_intron_or_TIF	cnBP
chrVII:1002936:+	0.166891873	not_in_intron_or_TIF	cnBP
chrVII:1052638:-	0.333783747	not_in_intron_or_TIF	cnBP
chrXIII:56618:+	0.25033781	YML106W	cnBP
chrXIII:112660:-	0.208614842	YML076C	cnBP
chrXIII:204536:-	0.584121557	not_in_intron_or_TIF	cnBP
chrXIII:242968:-	0.50067562	YML015C	cnBP
chrXIII:273520:-	0.458952652	not_in_intron_or_TIF	cnBP
chrXIII:301516:-	0.417229683	YMR015C	cnBP
chrXIII:493957:+	0.125168905	not_in_intron_or_TIF	cnBP
chrXIII:551142:-	6.049830409	YMR142C	cnBP
chrXIII:559830:+	128.5484654	not_in_intron_or_TIF	cnBP
chrXIII:637453:+	0.667567493	YMR189W	cnBP
chrXIII:647112:+	1.168243113	YMR192W	cnBP
chrXIII:649541:-	0.125168905	not_in_intron_or_TIF	cnBP
chrXIII:653956:-	0.166891873	not_in_intron_or_TIF	cnBP
chrXIII:701813:+	0.166891873	YMR217W	cnBP
chrXIII:810474:-	0.292060778	YMR272C	cnBP
chrXIII:845438:-	0.083445937	not_in_intron_or_TIF	cnBP
chrXV:87614:+	0.667567493	YOL123W	cnBP
chrXV:139434:+	0.208614842	not_in_intron_or_TIF	cnBP
chrXV:418633:+	0.125168905	not_in_intron_or_TIF	cnBP

chrXV:423675:-	1.293412018	YOR049C	cnBP
chrXV:437796:-	0.458952652	not_in_intron_or_TIF	cnBP
chrXV:506801:-	16.68918733	YOR097C	cnBP
chrXV:518764:-	2.711992942	not_in_intron_or_TIF	cnBP
chrXV:527237:+	0.417229683	YOR109W	cnBP
chrXV:605429:+	0.292060778	not_in_intron_or_TIF	cnBP
chrXV:674437:-	0.083445937	YOR180C	cnBP
chrXV:720499:+	2.75371591	not_in_intron_or_TIF	cnBP
chrXV:733355:-	7.76047211	YOR207C	cnBP
chrXV:754237:-	0.166891873	not_in_intron_or_TIF	cnBP
chrXV:819159:+	0.125168905	YOR264W	cnBP
chrXV:845022:+	13.05928909	not_in_intron_or_TIF	cnBP
chrXV:1059709:-	0.125168905	not_in_intron_or_TIF	cnBP
chrXV:1062512:-	1.877533575	not_in_intron_or_TIF	cnBP
chrIX:54026:+	0.834459367	YIL153W	cnBP
chrIX:127053:-	1.126520145	not_in_intron_or_TIF	cnBP
chrIX:134040:+	8.636654445	YIL121W	cnBP
chrIX:225116:+	0.166891873	not_in_intron_or_TIF	cnBP
chrIX:261766:+	1.710641702	not_in_intron_or_TIF	cnBP
chrIX:334600:-	0.208614842	not_in_intron_or_TIF	cnBP
chrIX:360694:-	0.166891873	not_in_intron_or_TIF	cnBP
chrXII:50297:+	1.877533575	YLL043W	cnBP
chrXII:90638:+	0.25033781	YLL026W	cnBP
chrXII:155741:-	0.792736398	YLR002C	cnBP
chrXII:232370:+	0.166891873	not_in_intron_or_TIF	cnBP
chrXII:316897:+	0.292060778	YLR088W	cnBP
chrXII:331859:-	0.584121557	YLR095C	cnBP
chrXII:380684:+	0.458952652	YLR115W	cnBP
chrXII:382366:+	1.418580923	YLR116W	cnBP
chrXII:491545:+	3.838513087	not_in_intron_or_TIF	cnBP
chrXII:522715:+	14.56131595	YLR185W	cnBP
chrXII:609447:-	7.885641015	YLR233C	cnBP
chrXII:791911:-	0.083445937	not_in_intron_or_TIF	cnBP
chrXII:823170:+	0.292060778	not_in_intron_or_TIF	cnBP
chrXII:918954:-	0.458952652	YLR398C	cnBP
chrXII:928301:-	0.667567493	not_in_intron_or_TIF	cnBP
chrXII:965102:+	0.083445937	not_in_intron_or_TIF	cnBP
chrXII:982469:-	71.84695147	not_in_intron_or_TIF	cnBP
chrXII:987203:+	7.969086952	YLR426W	cnBP
chrXII:987240:+	0.542398588	YLR426W	cnBP
chrIII:84709:+	0.083445937	not_in_intron_or_TIF	cnBP
chrIII:120379:+	0.125168905	not_in_intron_or_TIF	cnBP
chrIII:169189:-	0.208614842	not_in_intron_or_TIF	cnBP
chrIII:228656:+	0.834459367	YCR063W	cnBP
chrIII:290580:+	0.166891873	YCR095W-A	cnBP
chrX:31820:+	12.18310675	YJL213W	cnBP
chrX:209415:+	0.333783747	YJL111W	cnBP

chrX:237005:+	0.25033781	YJL100W	cnBP
chrX:349225:+	0.50067562	not_in_intron_or_TIF	cnBP
chrX:422631:+	4.631249485	not_in_intron_or_TIF	cnBP
chrX:455748:+	0.083445937	not_in_intron_or_TIF	cnBP
chrX:506239:+	0.125168905	not_in_intron_or_TIF	cnBP
chrX:535286:-	0.125168905	not_in_intron_or_TIF	cnBP
chrX:632996:-	59.1631691	YJR109C	cnBP
chrX:649521:-	0.125168905	not_in_intron_or_TIF	cnBP
chrX:712053:-	0.125168905	not_in_intron_or_TIF	cnBP
chrIV:104615:+	0.625844525	not_in_intron_or_TIF	cnBP
chrIV:122159:+	465.4614348	YDL189W	cnBP
chrIV:130328:+	0.208614842	YDL185W	cnBP
chrIV:188133:-	0.166891873	YDL148C	cnBP
chrIV:232837:+	1.00135124	YDL128W	cnBP
chrIV:235107:+	4.631249485	YDL127W	cnBP
chrIV:247245:-	0.125168905	YDL119C	cnBP
chrIV:268933:-	2.127871385	not_in_intron_or_TIF	cnBP
chrIV:331277:+	31.87634781	YDL070W	cnBP
chrIV:333709:+	0.25033781	not_in_intron_or_TIF	cnBP
chrIV:381064:-	0.166891873	YDL040C	cnBP
chrIV:392681:+	0.584121557	not_in_intron_or_TIF	cnBP
chrIV:456688:-	1.376857955	YDR005C	cnBP
chrIV:540585:+	1.293412018	YDR041W	cnBP
chrIV:676357:+	1.335134987	YDR110W	cnBP
chrIV:698041:-	0.125168905	YDR123C	cnBP
chrIV:721691:-	0.125168905	not_in_intron_or_TIF	cnBP
chrIV:768400:-	1.50202686	not_in_intron_or_TIF	cnBP
chrIV:929253:+	2.086148417	YDR232W	cnBP
chrIV:1021386:+	0.125168905	YDR280W	cnBP
chrIV:1080238:-	0.125168905	YDR309C	cnBP
chrIV:1081204:+	0.50067562	not_in_intron_or_TIF	cnBP
chrIV:1111887:+	0.458952652	not_in_intron_or_TIF	cnBP
chrIV:1114334:+	2.378209195	not_in_intron_or_TIF	cnBP
chrIV:1333316:-	0.125168905	YDR435C	cnBP
chrIV:1490517:-	1.084797177	not_in_intron_or_TIF	cnBP
chrIV:1519505:-	0.125168905	YDR541C	cnBP
chrI:126071:+	0.166891873	YAL016W	cnBP
chrI:134871:-	0.083445937	YAL010C	cnBP
chrI:142343:+	4.297465739	YAL003W	cnBP
chrVIII:97941:-	0.166891873	YHL007C	cnBP
chrVIII:148769:-	5.674323694	not_in_intron_or_TIF	cnBP
chrVIII:335607:-	0.75101343	YHR112C	cnBP
chrVIII:372283:+	0.292060778	YHR134W	cnBP
chrVIII:400568:-	0.25033781	YHR151C	cnBP
chrVIII:442922:+	0.083445937	YHR169W	cnBP
chrVIII:491866:-	0.083445937	not_in_intron_or_TIF	cnBP

The format of the bp_id is chromsome:bp_nucleotide:strand_of_bp

Branch_seq_cpm are the counts per million calculated from all data (top, middle, and bottom slices of gel arc combined).

If the gene_name is “not_in_intron_or_TIF” it did not fall inside a gene according to Pelechano et al. (2013).

Bp_type is “annotated” if the peak fell within 3nt of an annotated BP location according to Meyer et al. (2011).

Table S5. Saccer 3 coordinates of lariat junction reads*
*List of BPs detected through LJ reads from the Lariat-seq data. BP positions were determined from locations of the 3' most end of LJ reads and sequence information as described in the methods. The 'reads_at_dist_to_bp' field represents the number of LJ reads ending at various positions from the reported BP, the first in the list is zero away. The final two fields are marked 1, if the 5'SS or BP was previously annotated in the SGD annotations or by Meyer et al.[7] respectively, or 0 otherwise.

strand	chrom	5'ss	bp	reads_at_dist_to_bp	bp_seq	anno_5'ss	anno_bp
-	chrII	47146	47074	2,0,2	GTTACTAATATG	1	1
+	chrII	125155	125231	49	ATTACTAACATT	1	1
+	chrII	170677	170768	0,11	AGTACTAACGTT	1	1
-	chrIII	178213	177956	1,6	GATACTAACAAC	1	1
+	chrIV	122078	122159	19	CGTACTAACAAC	1	0
-	chrIV	215384	215274	19	TTTACTAACGAG	0	0
+	chrIV	230020	230262	122,12,5	TTTACTAACAAA	1	1
-	chrIV	239509	239421	4,9,353	AATACTAACAAT	1	1
+	chrIV	331189	331277	23	ATCACTAACCTG	0	0
+	chrIV	399362	399470	100,5,0,0,0,0,3	AATACTAACCAT	1	1
-	chrIV	715358	715267	109	TATACTAACAAA	1	1
-	chrIX	99385	99153	1,6,33	AATACTAACAAA	1	1
+	chrIX	225875	225994	2	TTTACTAATATT	0	0
+	chrIX	317018	317138	5	TTTACTAACAGG	0	1
-	chrIX	348494	348383	1,16	TTTACTAACTAT	1	1
-	chrV	166874	166787	4	ATTACTAACATC	1	1
-	chrV	248671	248563	2	CATTCTAACATT	0	0
+	chrV	362733	362835	2	AATTCTAACGCA	1	0
-	chrV	505180	505049	0,0,2	AGTACTAACCAG	0	0
-	chrVI	221414	221303	30,0,0,0,0,0,0,0,0,8	TATACTAACAGA	1	1
-	chrVII	73137	73035	10	ATTACTAACAAG	1	1
+	chrVII	249887	250015	35	GTTACTAACAGG	1	1
-	chrVII	497458	497390	0,0,5	CTTACTAACTGT	1	1
-	chrVII	1061028	1060825	10	GATACTAACTTT	0	0
+	chrVII	1084883	1085006	14	CTTACTAACTGA	1	1
+	chrVIII	129529	129617	2	AATACTAACATA	1	1
-	chrVIII	138408	138281	5,65	TGTACTAACAAC	1	1
+	chrVIII	251156	251231	0,1	GAGACTAACTTT	1	1
-	chrVIII	505516	505289	15	TTTACTAACAAG	1	1
+	chrX	73797	74179	2	TTTACTAACAAC	1	1
+	chrX	236903	237010	3	ATCACTGACATA	0	0
+	chrX	435228	435309	2	ATTACTAACTAA	1	1
+	chrX	608307	608548	32,3,3	TTTACTAACAAA	1	1

-	chrX	703054	702881	5	TTTACTAACGAG	1	1
-	chrXI	355283	355153	0,4	CATACTTACAGT	0	0
-	chrXI	430596	430520	3,5	GCTACTAACTAT	1	1
-	chrXII	327399	327294	5	TAGACTAACGTT	1	1
+	chrXII	382301	382388	6	TTTACTTACTAG	0	0
-	chrXII	707892	707769	0,0,2	CGTACTGACATT	0	0
-	chrXIII	23658	23500	3,30	TTTACTAACAGT	1	1
+	chrXIII	236592	236788	72,2,1	GCCACTAACAAT	1	1
-	chrXIII	243056	242969	0,0,4	AATACTGACAAT	0	0
+	chrXIII	424998	425114	255,10,6	TTTACTAACAAA	1	1
-	chrXIII	500151	499899	2,42	CTTACTAACAAA	1	1
-	chrXIII	721345	721232	313	AATACTAACAGC	1	1
+	chrXIV	48294	48378	10,0,3	ATTACTAACAAT	1	1
-	chrXIV	237531	237419	0,0,9	TTTACTGACCTA	0	0
-	chrXIV	380781	380701	11	ATTACTAATCTG	1	0
+	chrXIV	502164	502269	0,0,10	GATACTGACTAT	0	0
+	chrXIV	616067	616229	4,0,4	TCAACTTACTGT	0	0
-	chrXV	552874	552738	27,23,51	ATTACTAACTGG	1	1
+	chrXV	780121	780265	604,27,100	TTGACTAACACA	1	1
-	chrXVI	76223	76014	6	GTTACTAACATA	1	1
-	chrXVI	281503	281386	18	TTGACTAACACA	1	1
-	chrXVI	582701	582570	76,0,0,0,0,0,0,0,0,0,10,59	TATACTAACAAA	1	1
+	chrXVI	623578	623665	481,39,30	TATACTAACAAG	1	1
+	chrXVI	833694	833783	18	AAAACTAACAAT	1	1
+	chrXVI	943051	943174	6,0,1,0,5	CTTACTAACTGA	1	1

Table S6. Novel splice junctions with entropy ≥ 2bits.

Junction field is the chromosome, first splice site coordinate, second splice site coordinate, and strand joined by colons. The first splice site is always the one more 5' on the chromosome (lower number), so if the strand is "+" the first SS is the 5'SS and if the strand is "-" the first SS is the 3'SS. a_ss1 and a_ss2 are 0 for unannotated splice sites and 1 for annotated splice sites. a_ss_pair is 1 if this pair of splice sites is annotated as a splice junction in the existing SGD gff annotations. K_SS_1, K_SS_2 and K_SS_pair are set to: 0 if not annotated and not found by Kawashima et al., 1 if annotated by Kawashima et al., 2 if not annotated but occurring in a Kawashima et al. junction from WT or UPF1 null, and 3 if not annotated, but occurring in a Kawashima et al. junction not from WT or UPF1 null. intron_containing_gene is set to 0 if not from an intron containing gene and 1 if it is.

junction	a_SS1	a_SS2	a_SS_pair	strand	entropy	5ss_long	3ss_long	k_SS1	k_SS2	k_SS_pair	intron_containing_gene	lib_discovered
chrXVI:717048	0	0	0	-	2.61	GTATGCTTTT	CGCTATAAAG	0	0	0	0	polyA
chrVII:72983:	0	1	0	-	4.21	GTACGTTGC	CTTAAGAAAG	2	1	2	1	polyA
chrXIV:494321	0	1	0	-	3.24	GTACGTAAA	CTCCATCTAG	3	1	3	1	polyA
chrIV:1401795	0	1	0	+	3.66	GTTGGTACG	ATTATCGTAG	2	1	2	1	polyA
chrXVI:406645	1	0	0	+	3.54	GTATGTCCAT	AATTTAAAAG	1	2	0	1	polyA
chrXI:618373:	1	0	0	-	4.19	GTTTGTTTGT	TTTTGTACAG	1	2	0	1	polyA
chrV:131775:1	1	0	0	+	3.50	GTATGTTTG	AACTTCAAAG	1	2	0	1	polyA
chrXIV:443658	0	1	0	-	2.32	GTATGTTAA	AACCATCTAG	0	1	0	1	polyA
chrIV:601387:	0	0	0	+	3.73	ATTGACTAT	AACCAACCAC	0	0	0	0	polyA
chrII:110218:	0	1	0	-	2.86	GTAAGTATC	ATTGAGGAAG	3	1	3	1	polyA
chrXIV:557609	1	0	0	+	2.16	GTATGTATT	ATTTGCCCAG	1	2	0	1	polyA
chrII:426515:4	2	0	0	-	3.88	GTAAGTCAG	ATTAACTTAG	1	2	0	1	polyA
chrXII:242320	1	0	0	+	2.00	GTATGTACA	GTCCACCAAG	1	2	0	1	polyA
chrII:393179:	1	0	0	+	4.78	GTATGTACA	TTTATCTAAG	1	2	0	1	polyA
chrV:423823:4	0	1	0	+	2.85	GTAGAGGCA	TAATTTTTAG	0	1	0	0	polyA
chrX:608481:6	0	1	0	+	2.72	GTAGGTCCA	TTTTTTGCAG	0	1	0	1	polyA
chrXIV:331451	0	1	0	+	3.38	GTATAATCT	TTCTATTTAG	2	1	2	1	polyA
chrXVI:138724	1	0	0	+	4.10	GTATGTTAT	GTACAGTCAG	1	3	0	1	polyA
chrVII:436311	0	0	0	+	3.90	GTATGTATTT	ATCTTTACAG	0	0	0	1	polyA
chrXVI:412311	0	0	0	+	3.23	GTATGGAGT	ATTGGAACAG	2	2	2	1	polyA
chrIV:308521:	0	1	0	+	2.48	GCATGCATA	ATTATATCAG	0	1	0	1	polyA
chrIII:107032	1	0	0	+	2.25	GTATGTGTC	AGAAGTACAG	1	0	0	1	polyA
chrII:60188:6	0	1	0	-	2.12	GTATGTTAA	AACTAGTTAG	2	1	2	1	polyA
chrXVI:412255	0	0	0	+	2.95	GTATGGTAT	ATTGGAACAG	2	2	2	1	polyA
chrXIII:23359	1	0	0	-	3.03	GTATGCGTT	TTTACAACAG	1	2	0	1	polyA
chrXII:28461:	0	0	0	-	2.25	GTATGACAC	GGATATTAAG	0	0	0	0	polyA
chrIV:1359968	1	0	0	+	4.10	GTATGTTTAT	TATCAATAAG	1	2	0	1	polyA
chrXIII:55195	1	0	0	+	4.13	GTATGTTTT	TTTTGGTAAG	1	2	0	1	polyA
chrXIV:185490	1	0	0	+	3.78	GTATGTAGG	ATGCACTTAG	1	2	0	1	polyA
chrII:168647:	0	1	0	+	2.59	GTACGTGTC	TTTTTCACAG	0	1	0	1	polyA
chrXIII:91440	0	0	0	-	2.16	GTAAGTAAG	ATGTGGTCAG	0	0	0	0	polyA
chrXIII:42499	1	0	0	+	4.52	GTATGTTGT	CAAACACAAG	1	2	0	1	polyA
chrIV:216156:	1	0	0	+	2.92	GTATGTAAC	AGGAATTAAG	1	0	0	0	polyA
chrVII:311227	0	1	0	+	3.45	GTACTCTTC	TTTTGTACAG	3	1	3	1	polyA
chrXVI:271302	0	0	0	+	2.42	GTAAGTATG	GTTCATCAAG	0	0	0	0	polyA
chrVII:365508	0	1	0	-	3.19	GTATGTATA	TTGACCCCAG	3	1	3	1	polyA
chrXI:551679:	1	0	0	+	3.03	GTATGTTCG	CTACCAACAG	1	2	0	1	polyA
chrXII:242320	1	0	0	+	2.48	GTATGTACA	TGGTCGACAG	1	3	0	1	polyA
chrVII:555829	1	0	0	+	2.99	GTATGTTTG	CCGGCTTTAG	1	2	0	1	polyA
chrVII:497364	1	1	0	-	2.32	GTAAGTACA	TATAAAATAG	1	1	0	1	polyA
chrXI:155270:	1	0	0	+	4.46	GTATGTTTA	AAGTACGAAG	1	2	0	1	polyA
chrVIII:49870	0	1	0	-	3.90	GTATGTCAC	GAAACAACAG	2	1	2	1	polyA
chrVII:253184	0	0	0	-	4.80	GTATGAACC	CTTATTTTAG	0	0	0	0	polyA
chrIV:417220:	0	0	0	-	3.29	GTATGTATTT	ATTGTTATAG	0	0	0	0	polyA
chrIV:629904:	1	0	0	+	2.66	GTATGTTCA	TTTTGTCCAG	1	3	0	1	polyA
chrIV:601314:	0	0	0	+	3.43	ATACTACTTA	CACTGAGTAC	0	0	0	0	polyA
chrII:691965:	0	0	0	+	2.46	GTATGGAAA	AGTTTAGAAG	0	0	0	0	polyA
chrXII:233641	0	0	0	-	3.45	GTATGTCTT	ACCGCCCCAG	0	0	0	0	polyA
chrXI:437836:	1	0	0	+	2.90	GTATGTTGT	CTTTAGAAAG	1	2	0	1	polyA
chrXII:766185	0	1	0	-	3.20	GTATGTATCT	CATATATAAG	3	1	3	1	polyA
chrXIV:557573	0	1	0	+	2.75	GTACGTAAAT	AACAATGCAG	2	1	2	1	polyA
chrVII:534472	1	0	0	-	2.94	GTATCTATAA	TTTATCATAG	1	2	0	0	polyA

chrXII:242320	1	0	0	+	2.29	GTATGTACA	TCTCTTCCAG	1	2	0	1	polyA
chrII:393179:	1	0	0	+	2.52	GTATGTACA	AGTATCCAAG	1	0	0	1	polyA
chrII:691965:	0	0	0	+	3.87	GTATGGAAA	AGGTAAGCAG	0	0	0	0	polyA
chrX:74112:74	0	1	0	+	4.44	GTTGTTAGAT	TCATGTATAG	2	1	2	1	polyA
chrII:653367:	1	0	0	+	3.61	GTATGTTCT	ACGCAAACAG	1	3	0	1	polyA
chrIV:399360:	1	0	0	+	2.67	GTATGTTGT	CCTTGATCAG	1	2	0	1	polyA
chrI:128520:1	0	0	0	-	3.96	GTATGGATG	GCAACAGCAG	0	0	0	0	polyA
chrXIV:616065	0	0	0	+	2.97	GTATGTGCA	ACTATCAAAG	0	0	0	0	polyA
chrIV:733684:	0	1	0	-	2.97	GTATGTTCAT	AAATTAACAG	3	1	3	1	polyA
chrXII:281426	0	0	0	-	2.83	GTAGGTCAT	AACTATCTAG	0	0	0	0	polyA
chrII:142752:	0	1	0	-	4.03	GTATGTTACT	GACCATCAAG	2	1	2	1	polyA
chrXIV:185490	1	0	0	+	3.96	GTATGTAGG	AGTGCGGTAG	1	2	0	1	polyA
chrIV:306804:	0	0	0	-	3.46	GTACGTTGA	GTTAATTTAG	0	0	0	1	polyA
chrI:128523:1	0	0	0	-	3.11	GTATGGATG	CCAGCAACAG	0	0	0	0	polyA
chrXIII:55782	0	0	0	-	2.64	GTAAGATCA	AGTTCTTAAG	0	0	0	0	polyA
chrXVI:729352	0	1	0	-	2.72	GTATGTACA	TCCTATGTAG	2	1	2	1	polyA
chrVII:62130:	1	0	0	+	3.86	GTATGTCTG	TAGTTTAAAG	1	2	0	1	polyA
chrIV:307015:	0	1	0	-	2.62	GTATGTTAA	CTTACGACAG	0	1	0	1	polyA
chrIV:1406991	0	0	0	+	2.16	GTATGTTAC	ACTCACTTAG	0	0	0	0	polyA
chrX:649513:6	0	0	0	-	2.24	GTAAGTTAT	ATACAAAAAG	0	0	0	0	polyA
chrXII:982457	0	0	0	-	2.78	GTATGTATG	GTTTGAGTAG	0	0	0	0	polyA
chrXVI:673747	0	0	0	+	2.50	GTATGTCTG	TGAACAAAAG	0	0	0	0	polyA
chrXII:856568	0	1	0	+	3.18	GCATGGTAT	CCTTATTTAG	2	1	2	1	polyA
chrXV:867396	0	1	0	+	3.88	GTATGAAAT	TTTTATACAG	2	1	2	1	polyA
chrVI:223439:	1	0	0	-	3.05	GCAGGTAG	TCTTCTCCAG	1	3	0	0	polyA
chrVI:64352:6	0	1	0	-	3.28	GTACGTTAAT	TTTGAAGAAG	2	1	2	1	polyA
chrII:604513:	1	0	0	+	2.55	GTACGTATT	TTTTTAGGAG	1	0	0	1	polyA
chrVII:439096	0	1	0	+	4.16	GTATAACAT	ATTTCAACAG	2	1	2	1	polyA
chrVII:439098	0	0	0	+	3.80	ATAACATGAT	TATCGTTTAC	2	2	2	1	polyA
chrXIV:62360:	0	1	0	-	3.59	GTACGTATA	GACGTTGCAG	2	1	2	1	polyA
chrXV:505936	1	0	0	+	3.34	GTATGTTATT	AGGAAAAAAG	1	2	0	1	polyA
chrII:170619:	0	1	0	+	4.07	GTATGCTTTT	TTCCACTCAG	0	1	0	1	polyA
chrVIII:50524	0	1	0	-	3.08	GTATGTTGAT	ATATAGAAAG	2	1	2	1	polyA
chrII:342697:	0	0	0	+	3.63	GTGTGTTAG	TATAATCAAG	0	0	0	0	polyA
chrXIV:272386	0	0	0	-	2.28	GTTTGTGTA	ATTTCGACAG	0	0	0	0	polyA
chrII:170675:	1	0	0	+	3.87	GTATGTTCAT	TTGAAAAAAG	1	2	0	1	polyA
chrXIV:72855	0	0	0	+	3.35	GTAAGTATT	GCCAGCACAG	0	0	0	0	polyA
chrXIII:55978	0	0	0	+	5.14	GTATGTCTG	ATTTTTGAAG	0	0	0	0	polyA
chrII:565749:	0	0	0	+	2.25	ATGGATTTTT	CTGTACGGAC	0	0	0	0	polyA
chrXII:898547	0	1	0	+	3.51	GTATAAAAA	ATTATTGCAG	2	1	2	0	polyA
chrVII:439380	0	0	0	+	4.35	GTAAGTACA	TTTGAGAAAG	2	2	2	1	polyA
chrXII:457115	0	0	0	-	2.92	GTTAAAAAG	GTTGTTGCAG	0	0	0	0	polyA
chrIV:340809:	1	0	0	-	3.82	GTATGCAGA	TTGGTTATAG	1	0	0	0	polyA
chrII:60207:6	0	1	0	-	2.65	GTATGTTAA	CGATATTGAG	3	1	3	1	polyA
chrXI:109576:	1	0	0	+	2.82	GTATGTCAA	CAGGCTAAAG	1	2	0	1	polyA
chrXV:423656	0	0	0	-	2.85	GTATGGTAC	TGTCGTACAG	0	0	0	0	polyA
chrIX:317016:	0	1	0	+	4.39	GTATGAGAA	ATTTAAACAG	2	1	2	1	polyA
chrV:362911:3	0	1	0	+	2.37	GTACTGCAA	ATTAAAATAG	3	1	3	0	polyA
chrXIII:55195	1	0	0	+	2.16	GTATGTTTT	TGGTAAGAAG	1	0	0	1	polyA
chrIII:101604	0	1	0	-	2.59	GTATGTATAT	TGCGTTCAAG	3	1	3	1	polyA
chrII:168553:	0	1	0	+	3.45	GTTGGTAG	TTTTTCACAG	3	1	3	1	polyA
chrXI:93365:9	0	1	0	-	5.06	GTACGTATA	GTTTTTATAG	2	1	2	0	polyA
chrIV:216156:	1	0	0	+	3.08	GTATGTAAC	GATTTCATAG	1	0	0	0	polyA
chrXII:855876	1	0	0	+	4.37	GTATGTGGA	CAAAACATAG	1	0	0	0	polyA
chrXI:437836:	1	0	0	+	2.99	GTATGTTGT	AGAATCAAAG	1	2	0	1	polyA
chrXVI:795028	1	0	0	+	2.66	GTATGTACA	TTGTCAAAAG	1	2	0	1	polyA
chrXIV:49452	1	0	0	-	2.12	GTAATGGTA	TTTATTATAG	1	0	0	1	polyA
chrIV:491687:	0	1	0	+	4.33	GCATGTTTAT	CTTTTTTTAG	2	1	2	1	polyA
chrXV:778858	1	0	0	-	4.31	GTATGAATAT	ATTTTGATAG	1	3	0	1	polyA
chrX:469182:4	1	0	0	-	3.10	GCAGGTAAA	TGTAGTATAG	1	2	2	1	polyA
chrVIII:14811	1	0	0	-	4.02	GTATGCGTT	TTCATTACAG	1	2	0	1	polyA
chrVIII:10361	0	0	0	-	3.11	GTAAGGTGA	GTAACTTGAG	0	0	0	0	polyA
chrVII:383484	0	0	0	+	3.31	GTATGTATG	ATGGTAGTAG	0	0	0	0	polyA
chrXVI:79513	0	1	0	+	3.90	GTAAGGGA	TTTAAAACAG	2	1	2	1	polyA
chrXV:349496	0	0	0	-	2.73	GTATGTTTTT	TTACTTTTAG	0	0	0	0	polyA

chrXIV:144846	0	1	0	-	3.20	GTATGTTTAT	AAGCTATCAG	2	1	2	1	polyA
chrXII:242320	1	0	0	+	3.33	GTATGTACA	TGGCTGCTAG	1	0	0	1	polyA
chrXI:625900:	1	0	0	+	3.18	GTAAGTAGA	AGAACTAAAG	1	2	0	1	polyA
chrVII:62130:	1	0	0	+	3.91	GTATGTCTG	CGATCAAAAG	1	2	0	1	polyA
chrVII:920663	1	0	0	+	2.65	GTATGTTATA	GTTCACCAAG	1	2	0	1	polyA
chrXII:522889	0	1	0	+	3.42	GTATGCCTG	TTTTAAATAG	3	1	3	1	polyA
chrVII:365525	1	0	0	-	2.82	GTCTATTTTA	ATTATTACAG	1	2	0	1	polyA
chrXIV:62369:	0	1	0	-	2.50	GTACGTATA	TCAATTAGAG	0	1	0	1	polyA
chrIV:122076:	1	0	0	+	2.11	GTATGTTGA	AACAACTAAG	1	0	0	0	polyA
chrIV:306804:	0	1	0	-	3.76	GTATGTTAA	GTTAATTTAG	0	1	0	1	polyA
chrXVI:30356	0	0	0	+	2.00	ATTGGTTTG	TGCTTCTGAC	0	0	0	0	polyA
chrXV:505936	1	0	0	+	2.34	GTATGTTATT	CATTTACAAG	1	0	0	1	polyA
chrIV:655202:	0	0	0	+	3.06	GTATGCTTC	TGATAATCAG	0	0	0	0	polyA
chrXII:987140	1	0	0	+	3.45	GTATGTAAA	AATGGCATAG	1	2	0	1	polyA
chrIV:122076:	1	0	0	+	2.00	GTATGTTGA	AGTATATAAG	1	0	0	0	polyA
chrXVI:243488	0	0	0	-	3.55	GTATGTTTCT	TACTTAGAAG	0	0	0	0	polyA
chrII:168599:	0	1	0	+	2.69	GTACGAATT	TTTTTCACAG	0	1	0	1	polyA
chrXV:373898	0	0	0	+	2.48	GTAAGCATT	ATCCTATAAG	0	0	0	0	polyA
chrXIII:66692	0	1	0	-	2.04	GTATGTGTG	AGGCTAACAG	2	1	2	1	polyA
chrXII:453363	0	0	0	-	2	GTTTTCATG	GAAGGAATAG	0	0	0	0	riboZero
chrX:50320:50	0	1	0	-	3.835	GTATGTTCAT	TGTTTCGAAG	2	1	2	1	riboZero
chrXII:593144	0	0	0	+	2.1175	GTTGGAATA	CTCAGAATAG	0	0	0	0	riboZero
chrXI:447150:	0	0	0	-	2.5216	GTATGCCAG	ATAAATAAAG	0	3	0	1	riboZero
chrXIV:282743	0	0	0	-	4.0427	GTCTTGTTG	GGATTTGGAG	0	0	0	0	riboZero
chrXII:453697	0	0	0	-	2.2516	GTGGGGAAA	AAGACTGAAG	0	0	0	0	riboZero
chrIV:122076:	1	0	0	+	2.4056	GTATGTTGA	AAGGAGTTAG	1	0	0	0	riboZero
chrII:592415:	1	0	0	-	2.4508	GTATACCCA	TTTATAACAG	1	0	0	1	riboZero
chrVII:937211	0	0	0	+	3.1069	GTAAGATTT	TGTGATAAAG	0	0	0	0	riboZero
chrXV:29674:3	0	0	0	+	2.512	GTGGAACCG	AGAAAGAGAG	0	0	0	0	riboZero
chrIV:1329745	0	0	0	+	2.4508	GTGGTTACG	GGCTCCAGAG	0	0	0	0	riboZero
chrXV:296674	0	0	0	+	2.3219	GTAAGTATC	CAAAAATTAG	0	0	0	0	riboZero
chrX:50318:50	0	1	0	-	3.4399	GTATGTTCAT	TTTCGAAGAG	0	1	2	1	riboZero
chrX:400191:4	0	0	0	+	3.9917	GTGCTGAAG	AGTGCTGGAG	0	0	0	0	riboZero
chrI:128513:1	0	0	0	-	2	GTATGGATG	CAGTTGTTAG	0	0	0	0	riboZero
chrVII:62130:	1	0	0	+	2.6464	GTATGTCTG	GGATTCTTAG	1	0	0	1	riboZero
chrX:503769:5	0	0	0	+	4.1314	GTAAGTTGA	AACATTATAG	0	0	0	0	riboZero
chrXV:31111:3	0	0	0	+	3.1219	GTTGAACCG	AGTGGCGGAG	0	0	0	0	riboZero
chrXI:220776:	0	0	0	+	4.3865	GTGCTGGAG	ATGATGGGAG	0	0	0	0	riboZero
chrIV:1329769	0	0	0	+	3.6645	GTGGCTACG	TATTCCAGAG	0	0	0	0	riboZero
chrXII:789112	0	0	0	-	4.1486	GTTTGTTGG	TCCTCCACAG	0	0	0	0	riboZero
chrXIII:61080	0	0	0	+	4.1788	GTATGTAAA	GATGAATAAG	0	0	0	0	riboZero
chrIV:122076:	1	0	0	+	3.2729	GTATGTTGA	TCTCTTCAAG	1	0	0	0	riboZero
chrXII:458101	0	0	0	+	3.7363	GTTTGAATT	TTCCCCCAAG	0	0	0	0	riboZero
chrX:400245:4	0	0	0	+	2.6358	GTGCTGGAG	GGTACTGGAG	0	0	0	0	riboZero
chrI:12486:12	0	0	0	+	4.1491	GTGGTAATG	CTGGTAACAG	0	0	0	0	riboZero
chrXVI:656504	0	0	0	-	2.25	GTAGTTGAG	CGGAGGACAG	0	0	0	0	riboZero
chrXII:564435	0	1	0	-	3.7185	GTAAGTTTTT	TATTATTGAG	0	1	0	1	riboZero
chrXVI:29539:	0	0	0	+	2	GTATGAAAT	ATTTATCCAG	0	0	0	0	riboZero
chrXI:155412:	0	1	0	+	4.3201	GTGAGTTCT	AAATGACCAG	0	1	0	1	riboZero
chrXII:452056	0	0	0	-	2.2516	GTCAGAATC	CGCCTCTAAG	0	0	0	0	riboZero
chrIV:601072:	0	0	0	-	3.1972	GTACCGTTA	TTCAGTAGAG	0	0	0	0	riboZero
chrXII:789133	0	0	0	-	4.0525	GTTTGTTGG	TCCTTCACAG	0	0	0	0	riboZero
chrXI:155412:	0	0	0	+	4.5864	GTGAGTTCT	AAGTACGAAG	0	2	0	1	riboZero
chrIX:23755:2	0	0	0	-	2.666	GTTCCAAAG	ACCTCTGAAG	0	0	0	0	riboZero
chrIV:169349:	0	0	0	+	3.0221	GTAAGTTGA	GCTTCTTTAG	0	0	0	0	riboZero
chrXIV:282623	0	0	0	-	2.7255	GTCTTGGAT	AGACTTGGAG	0	0	0	0	riboZero
chrVII:946323	0	1	0	+	3.182	GTGGTACGT	TTTTCTACAG	0	1	0	1	riboZero
chrV:369419:3	0	0	0	-	2	GTATTTTTTT	TTAATAAAAG	0	0	0	0	riboZero
chrXVI:582557	1	0	0	-	2.2359	GTATGTGATT	AAAAAACTAG	1	0	0	1	riboZero
chrX:570566:5	0	0	0	-	2	GTAGTCCTT	CATTTCCAAG	0	0	0	0	riboZero
chrIV:427465:	0	0	0	+	2	GTGGCTTCG	GGCTCCAGAG	0	0	0	0	riboZero
chrXIV:282623	0	0	0	-	3.8299	GTCTTGTTG	AGACTTGGAG	0	0	0	0	riboZero
chrXIV:427102	0	0	0	+	2.6887	GTATGACAC	ACTGTCTCAG	0	0	0	0	riboZero
chrIV:601362:	0	0	0	-	2.585	GTCTTACCG	ACGGTGTAAG	0	0	0	0	riboZero
chrX:637808:6	1	0	0	+	3.027	GTATGTATAT	TATGCGCAAG	1	0	0	1	riboZero

chrVII:682947	0	0	0	-	2	GTATGTTCC	GTTTATATAG	0	0	0	0	riboZero
chrXVI:44550	0	0	0	-	3.4118	GTGTGTTCA	AGCTTCGCAG	0	0	0	0	riboZero
chrXII:987140	1	0	0	+	2.1281	GTATGTAAA	GGTCTCTAAG	1	2	2	1	riboZero
chrXII:456443	0	0	0	-	2.8464	GTTGGTGGA	CCGTTCTTAG	0	0	0	0	riboZero
chrVII:937211	0	0	0	+	3.2608	GTAAGATTT	GATGTTGTAG	0	0	0	0	riboZero
chrXII:454262	0	0	0	+	2.585	GTCTTTCGC	GTTCGATTAG	0	0	0	0	riboZero
chrXIV:28372	0	0	0	+	3.6959	GTATCTTCG	CAAGTAGTAG	0	0	0	0	riboZero
chrII:170619:	0	0	0	+	2.6464	GTATGCTTT	TTGAAAAAAG	0	2	0	1	riboZero
chrVII:946319	0	1	0	+	3.6057	GTCTGTGGT	TTTTCTACAG	0	1	0	1	riboZero
chrXII:452964	0	0	0	-	2.5216	GTGAAGAAA	AATGTCAAAG	0	0	0	0	riboZero
chrII:60148:6	0	1	0	-	2.75	GTATGTTAA	CTGACAACAG	2	1	2	1	riboZero
chrXVI:69796	0	0	0	-	2	GTAAGTATA	TTTCTGACAG	0	0	0	0	riboZero
chrIV:451410:	0	0	0	-	3.5944	GTATGGTGG	ATCTATGTAG	0	0	0	0	riboZero
chrXII:458296	0	0	0	-	2.2516	GTCTCTATA	ATCTGCCTAG	0	0	0	0	riboZero
chrXII:787693	0	0	0	+	2.585	GTAAGTTGG	GAAATTTCAG	0	0	0	0	riboZero
chrVI:109957:	0	0	0	-	2.281	GTAAGTAAA	AAATCGAAAG	0	0	0	0	riboZero
chrIV:601030:	0	0	0	-	3.295	GTACCGTTA	TTCAGTAGAG	0	0	0	0	riboZero
chrIX:23442:2	0	0	0	+	4.1452	GTGACAGTC	AGCTTCAGAG	0	0	0	0	riboZero
chrV:468240:4	0	0	0	+	2.75	GTAAGTATAT	TAACGCTAAG	0	0	0	0	riboZero
chrXIV:28262	0	0	0	-	3.3833	GTCTTGTTG	AGACTTGGAG	0	0	0	0	riboZero
chrII:115473:	0	0	0	+	2.2516	GTATGTATAT	GCACCAATAG	0	0	0	0	riboZero
chrXII:244384	0	0	0	-	3.0391	GTACGTACC	TTGTATCTAG	0	0	0	0	riboZero
chrV:348200:	1	0	0	-	2.5216	GTACGAAAA	CTGAAAGCAG	1	0	0	1	riboZero
chrXIV:28372	0	0	0	+	3.7835	GTATCTTCG	TATCAAGTAG	0	0	0	0	riboZero
chrVIII:52610	0	0	0	-	3.5766	GTATGTATT	GTACCATCAG	0	0	0	0	riboZero
chrVI:109947:	0	0	0	-	2.9183	GTAAGTAAA	CTAAATAAAG	0	0	0	0	riboZero
chrIX:47701:4	0	0	0	+	3.485	GTACCCAAA	GGTTAGGTAG	0	3	0	1	riboZero
chrIX:390678:	0	0	0	+	2.7093	GTAGTTTCA	GCATCCAGAG	0	0	0	0	riboZero
chrIV:132974	0	0	0	+	2.7948	GTGGTTACG	AGTCCTAGAG	0	0	0	0	riboZero
chrXII:457962	0	0	0	+	2.3219	GTTTCCTCT	ACTCTTTGAG	0	0	0	0	riboZero
chrIV:60477:6	0	0	0	-	4.9836	GTTCGTTAA	GTAACTGTAG	0	0	0	0	riboZero
chrIV:132972	0	0	0	+	2.585	GTGGATTTG	GGCTCCAGAG	0	0	0	0	riboZero

Table S7 : Figure 6A PSI values

exp1	exp3	alpha1	alpha2	sorbitol1	sorbitol2
chrI:142053:1	0.04	0.03	0.01	0.03	0.02
chrI:87187:87	0.14	0.05	0.03	0.06	0.08
chrII:124954:	0.31	0.25	-1	0.42	0.35
chrII:186428:	0.47	0.39	-1	-1	-1
chrII:332675:	0.14	0.21	0.14	0.11	0.2
chrII:342498:	-1	-1	0.85	-1	-1
chrII:407123:	0.14	0.11	0.09	0.13	0.15
chrII:415260:	0.06	0.07	0.03	0.04	0.06
chrII:45444:4	0.06	0.09	0.05	0.05	0.07
chrII:462009:	0.95	0.95	0.95	0.95	0.97
chrII:462229:	-1	-1	-1	-1	-1
chrII:47147:4	0.93	0.91	-1	0.78	0.57
chrII:479145:	-1	-1	-1	-1	-1
chrII:592769:	0.03	0.04	0.02	0.02	0.04
chrII:606080:	0.04	0.05	0.02	0.03	0.05
chrII:680040:	0.1	0.11	0.14	0.08	0.13
chrII:89441:8	0.01	0.02	0.01	0.01	0.02
chrIII:111634	0.96	0.94	0.96	0.92	0.97
chrIII:178214	0.01	0.01	0	0.01	0.01
chrIV:1103609	-1	-1	-1	-1	-1
chrIV:117466:	0.01	0.01	0	0.01	0.01
chrIV:1212677	-1	-1	-1	-1	-1
chrIV:1236642	0.16	0.17	0.15	0.18	0.2
chrIV:1266862	0.79	0.92	0.75	0.48	0.79
chrIV:1319698	0.08	0.07	-1	-1	-1
chrIV:1319817	-1	-1	-1	-1	-1
chrIV:1355551	0.06	0.11	0.04	0.03	0.09
chrIV:1406792	0.92	0.95	0.86	0.87	0.91
chrIV:1450847	0.05	0.07	0.04	0.04	0.08
chrIV:217402:	0.02	0.03	0.01	0.01	0.02
chrIV:229819:	0.08	0.09	0.05	0.08	0.05
chrIV:255045:	0.93	0.95	0.92	0.91	0.93
chrIV:267525:	-1	-1	-1	-1	-1
chrIV:308227:	0.03	0.02	0.01	0.01	0.02
chrIV:314337:	-1	-1	-1	-1	-1
chrIV:322082:	0.01	0.01	0.01	0.01	0.01
chrIV:337324:	-1	0.31	-1	-1	-1
chrIV:417627:	0.21	-1	-1	0.42	0.29
chrIV:431473:	0.3	0.29	0.23	0.19	0.2
chrIV:458098:	0.93	0.94	0.93	-1	0.92
chrIV:491359:	0.07	0.08	0.05	0.05	0.07
chrIV:569724:	-1	-1	-1	-1	-1
chrIV:579278:	0.42	0.52	0.24	0.26	0.56
chrIV:65106:6	-1	-1	-1	-1	-1
chrIV:655003:	0.97	0.99	0.99	0.99	0.99
chrIX:127461:	0.04	0.02	-1	0.04	0.02
chrIX:166234:	-1	-1	-1	-1	-1

chrIX:232367:	0.03	0.06	0.03	0.03	0.05
chrIX:257027:	0.03	0.03	0.02	0.02	0.03
chrIX:348495:	0.24	0.24	0.16	0.11	0.37
chrIX:47498:4	0.28	0.17	-1	0.26	-1
chrIX:68515:6	0.02	0.02	0.01	0.01	0.02
chrIX:99386:9	0.05	0.06	0.03	0.04	0.04
chrV:159088:1	0.65	0.47	-1	0.45	0.5
chrV:166875:1	-1	-1	-1	-1	-1
chrV:270149:2	0.02	0.02	0.01	0.02	0.02
chrV:306125:3	0.02	0.04	0.02	0.02	0.05
chrV:307546:3	0.17	-1	-1	-1	-1
chrV:307756:3	0.11	-1	-1	0.18	-1
chrV:348277:3	0.13	-1	-1	-1	0.18
chrV:396610:3	0.07	0.07	0.07	0.08	0.07
chrV:432471:4	0.03	0.03	0.02	0.03	0.02
chrVI:203387:	0.9	0.97	0.95	0.95	0.82
chrVI:221415:	0.39	0.33	0.27	0.48	0.23
chrVI:223772:	0.06	0.08	0.07	0.06	0.07
chrVI:241809:	0.89	-1	-1	-1	-1
chrVI:63974:6	-1	-1	-1	-1	-1
chrVI:64921:6	0.71	0.72	0.59	0.62	0.61
chrVII:148967	0.04	0.04	0.01	0.03	0.05
chrVII:150526	0.14	0.16	0.15	0.13	0.17
chrVII:249686	-1	-1	-1	-1	-1
chrVII:253249	0.92	0.94	0.93	0.9	0.91
chrVII:365433	0.03	0.04	0.03	0.03	0.03
chrVII:383285	-1	0.88	-1	-1	0.82
chrVII:436112	-1	-1	-1	0.52	-1
chrVII:438398	0.02	0.03	0.02	0.02	0.03
chrVII:439181	1	1	1	1	1
chrVII:543438	0.11	0.08	0.14	0.08	0.1
chrVII:726838	0.04	0.05	0.03	0.02	0.04
chrVII:859474	0.17	0.14	0.18	0.1	0.19
chrVIII:10385	0.99	0.99	0.99	0.99	0.99
chrVIII:10420	0.02	0.03	0.01	0.01	0.02
chrVIII:10763	-1	-1	-1	0.6	0.73
chrVIII:12635	0.08	0.11	0.09	0.08	0.08
chrVIII:12932	-1	-1	-1	-1	-1
chrVIII:13840	-1	-1	-1	-1	-1
chrVIII:18767	0.03	0.02	-1	-1	0.02
chrVIII:25095	0.95	0.91	0.91	0.91	0.93
chrVIII:25575	-1	-1	-1	-1	-1
chrVIII:29848	-1	-1	-1	-1	-1
chrVIII:35466	-1	-1	-1	-1	-1
chrVIII:38274	0.1	0.13	0.08	0.07	0.12
chrX:157250:1	0.02	0.02	0.01	0.01	0.03
chrX:172753:1	0.31	0.49	0.29	0.24	0.29
chrX:365584:3	0.56	0.5	-1	-1	0.51
chrX:387436:3	0.92	-1	-1	-1	-1

chrX:396571:	-1	-1	-1	-1	-1
chrX:435027:	0.08	0.09	0.06	0.05	0.08
chrX:469264:	0.83	-1	-1	-1	0.68
chrX:50412:5	0.27	0.3	0.26	0.31	0.17
chrX:608282:	0.06	0.07	0.04	0.04	0.07
chrX:649658:	-1	-1	-1	-1	-1
chrX:703055:	0.05	0.09	0.07	0.04	0.1
chrX:75738:7	0.01	0.01	0.01	0.01	0.01
chrX:90894:9	0.02	0.02	0.01	0.01	0.03
chrXI:166199:	-1	-1	-1	-1	0.37
chrXI:282895:	0.05	0.04	0.02	0.03	0.03
chrXI:430597:	0.38	0.32	0.4	0.31	0.3
chrXI:431834:	0.02	0.03	0.01	0.01	0.03
chrXI:93466:	0.16	0.1	0.27	0.28	0.25
chrXII:102866	0.06	0.07	0.04	0.04	0.07
chrXII:233886	1	1	1	1	1
chrXII:263005	0.15	0.14	0.14	0.14	0.16
chrXII:281629	0.98	0.97	0.96	0.98	0.96
chrXII:286557	-1	-1	-1	-1	-1
chrXII:28835:	0.9	0.96	0.85	0.94	0.92
chrXII:40401:	-1	0.02	-1	0.01	0.02
chrXII:466255	0.99	0.89	1	1	1
chrXII:564514	-1	-1	-1	-1	-1
chrXII:694182	-1	-1	-1	-1	-1
chrXII:713156	0.04	0.04	0.03	0.02	0.04
chrXII:766130	-1	-1	-1	-1	-1
chrXII:796336	0.05	0.08	0.04	0.03	0.06
chrXII:819130	0.06	0.08	0.04	0.03	0.08
chrXII:856374	0.13	0.13	0.08	0.09	0.11
chrXII:931699	0.02	0.03	0.01	0.01	0.03
chrXII:982539	0.96	0.95	0.97	0.95	0.94
chrXIII:12415	0.03	0.07	0.02	0.02	0.04
chrXIII:14018	-1	-1	-1	-1	-1
chrXIII:16371	0.26	0.28	0.15	0.2	0.15
chrXIII:20589	0.38	-1	-1	-1	0.42
chrXIII:22378	0.01	0.02	0.01	0.01	0.01
chrXIII:22569	0	0.01	0	0	0.01
chrXIII:23639	0.16	0.09	-1	0.2	0.09
chrXIII:33761	-1	-1	-1	-1	-1
chrXIII:50015	0.03	0.02	0.02	0.02	0.03
chrXIII:55800	0.99	0.99	0.99	0.99	0.99
chrXIII:55958	0.62	0.54	0.37	0.29	0.59
chrXIII:65096	0.14	0.15	0.07	0.08	0.12
chrXIII:65284	0.32	-1	-1	-1	0.32
chrXIII:72134	0.09	0.1	0.05	0.09	0.1
chrXIII:73226	0.02	0.03	0.02	0.02	0.02
chrXIII:75422	0.2	0.25	0.1	0.11	0.19
chrXIII:82090	-1	-1	-1	-1	-1
chrXIII:85461	0.81	0.57	0.8	-1	0.55

chrXIII:9146	0.99	0.99	0.99	0.98	0.94
chrXIII:99376	0.22	0.26	-1	-1	0.24
chrXIV:27360	0.89	0.85	0.88	0.86	0.83
chrXIV:35075	0.18	0.32	0.39	0.33	-1
chrXIV:41471	0.04	0.06	0.05	0.06	0.04
chrXIV:48093	-1	-1	-1	-1	-1
chrXIV:54509	0.28	-1	-1	-1	-1
chrXIV:61586	0.95	0.87	0.93	0.83	0.88
chrXIV:62274	0.34	0.24	0.15	0.26	0.23
chrXIV:64451	0.19	0.18	0.07	0.06	0.12
chrXIV:72230	0.05	0.06	0.05	0.06	0.02
chrXIV:72835	0.99	0.99	0.99	0.99	0.99
chrXV:241026	-1	-1	-1	-1	-1
chrXV:242505	-1	-1	-1	NA	-1
chrXV:349599	0.96	0.96	0.93	0.94	NA
chrXV:373699	0.93	0.82	0.83	0.89	0.93
chrXV:423735	0.97	0.96	0.94	0.96	0.95
chrXV:552875	0.06	0.06	0.05	0.05	0.05
chrXV:678791	0.01	0.01	0.01	0.01	0.01
chrXV:80160:	0.03	0.04	0.01	0.02	0.02
chrXV:901194	0.11	0.13	0.07	0.07	0.12
chrXV:92831:	0.1	0.09	0.06	0.1	0.07
chrXV:94291:	0.12	0.12	0.08	0.13	0.09
chrXVI:11501	-1	-1	-1	-1	-1
chrXVI:17296	0.31	0.19	0.07	0.17	0.21
chrXVI:17346	0.12	0.21	0.27	0.12	0.22
chrXVI:21844	-1	-1	-1	-1	-1
chrXVI:24402	0.98	0.97	0.97	0.96	0.98
chrXVI:27110	0.99	0.99	0.99	0.99	0.99
chrXVI:28194	0.03	0.03	0.02	0.02	0.03
chrXVI:30510	0.15	0.16	0.13	0.21	0.21
chrXVI:34559	-1	-1	-1	-1	0.25
chrXVI:37839	0.02	0.03	0.01	0.01	0.02
chrXVI:40475	0.18	0.16	0.1	0.12	0.17
chrXVI:58270	0.07	0.08	0.06	0.07	0.05
chrXVI:62337	0.95	0.97	0.91	0.87	0.71
chrXVI:65396	0.08	0.08	0.05	0.06	0.06
chrXVI:67354	0.99	1	0.99	0.99	0.99
chrXVI:67828	0.14	-1	-1	-1	0.13
chrXVI:71714	0.98	0.96	0.96	0.96	0.96
chrXVI:83349	-1	0.92	-1	-1	0.93
chrXVI:88318	0.06	0.08	0.08	0.1	0.08
chrXVI:91107	0.08	0.09	-1	-1	-1
chrXVI:96234	0.93	-1	-1	-1	-1

exp2	salt1	salt2	DNA1	DNA2	ox1
0.03	0.05	0.04	0.04	0.03	0.03
0.11	0.06	0.19	0.14	0.13	0.04
0.42	0.29	0.42	0.39	0.33	0.28
-1	-1	-1	-1	-1	-1
0.14	0.15	0.26	0.26	0.12	0.14
-1	0.9	-1	-1	-1	-1
0.1	0.12	0.09	0.08	0.1	0.09
0.05	0.06	0.11	0.12	0.05	0.05
0.06	0.06	0.08	0.11	0.05	0.05
0.92	0.95	-1	-1	-1	0.9
-1	-1	-1	-1	-1	-1
0.63	0.74	0.82	0.84	0.87	-1
-1	-1	-1	-1	-1	-1
0.03	0.03	0.05	0.05	0.02	0.03
0.04	0.05	0.11	0.09	0.03	0.03
0.11	0.14	0.14	0.16	0.08	-1
0.02	0.01	0.02	0.02	0.01	0.02
0.93	0.97	0.92	-1	0.93	0.94
0.01	0.01	0.02	0.02	-1	-1
0.89	-1	-1	-1	-1	-1
0.01	0.01	0.01	0.02	0.01	0.01
-1	-1	0.83	0.76	-1	-1
0.13	0.16	0.28	0.2	0.14	0.12
0.67	0.88	0.63	-1	0.66	0.87
-1	0.15	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.09	0.07	0.14	0.14	0.09	0.1
0.91	0.92	-1	-1	-1	-1
0.07	0.06	0.1	0.09	0.05	0.06
0.02	0.02	0.06	0.04	0.01	0.02
0.07	0.08	0.06	0.07	0.06	0.04
0.9	0.94	0.89	0.88	-1	-1
-1	-1	-1	-1	-1	-1
0.01	0.03	0.06	0.04	-1	0.02
-1	-1	-1	-1	-1	-1
0.01	0.01	0.02	0.02	0.01	0.01
-1	0.26	-1	-1	-1	-1
-1	0.21	0.17	0.19	-1	-1
0.2	0.24	0.48	0.3	0.23	0.28
0.88	0.92	-1	-1	-1	-1
0.05	0.06	0.12	0.1	0.05	0.05
-1	-1	-1	-1	-1	-1
0.49	0.43	0.6	0.87	0.37	0.39
-1	-1	-1	-1	-1	-1
0.98	0.99	0.94	0.96	0.99	0.97
0.03	0.03	-1	-1	0.05	0.03
-1	-1	-1	-1	-1	-1

0.04	0.04	0.08	0.1	0.04	0.04
0.02	0.02	0.05	0.05	0.02	0.02
0.13	0.22	0.36	-1	-1	0.23
-1	0.24	-1	-1	-1	-1
0.02	0.01	0.03	0.04	0.01	0.02
0.06	0.05	0.15	0.08	0.08	0.08
0.46	0.43	-1	-1	0.42	0.66
-1	-1	-1	-1	-1	-1
0.02	0.02	0.07	0.05	0.03	0.03
0.04	0.02	0.04	0.04	0.01	0.02
-1	-1	-1	-1	-1	-1
0.14	0.16	-1	-1	-1	-1
-1	0.1	-1	0.09	0.09	0.08
0.07	0.07	0.08	0.08	0.07	0.06
0.02	0.03	0.04	0.03	0.02	0.01
0.95	0.95	-1	0.92	0.88	0.91
0.29	0.37	0.28	0.25	0.27	0.24
0.08	0.07	0.07	0.1	0.06	0.07
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.78	0.68	0.9	0.9	0.88	0.63
0.04	0.04	0.08	0.1	0.03	0.03
0.16	0.14	0.43	0.31	0.15	-1
-1	-1	-1	-1	-1	-1
0.94	0.89	0.91	0.91	0.87	-1
0.04	0.03	0.04	0.04	0.02	0.03
0.94	0.91	0.91	0.87	-1	-1
-1	-1	-1	-1	-1	-1
0.03	0.02	0.05	0.03	0.03	0.02
1	1	1	1	1	1
0.11	0.1	0.61	0.25	0.12	0.12
0.03	0.04	0.05	0.06	0.03	0.03
0.17	0.14	0.18	0.23	-1	-1
0.99	0.99	0.99	0.98	0.98	0.98
0.02	0.02	0.04	0.04	0.02	0.03
0.44	-1	-1	-1	-1	-1
0.08	0.08	0.1	0.12	0.07	0.07
-1	-1	-1	-1	-1	-1
-1	-1	-1	0.62	-1	-1
-1	0.03	-1	-1	-1	-1
0.93	0.94	0.9	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.07	0.11	0.12	0.12	0.05	0.08
0.02	0.02	0.04	0.04	0.02	0.02
0.29	0.39	-1	-1	0.32	-1
0.34	0.54	-1	-1	-1	-1
0.87	0.79	-1	-1	-1	-1

-1	-1	-1	-1	-1	-1
0.09	0.06	0.12	0.1	0.07	0.06
0.69	-1	0.82	-1	-1	-1
0.18	0.26	-1	-1	0.25	-1
0.08	0.05	0.1	-1	0.06	-1
-1	-1	-1	-1	-1	-1
0.05	0.05	0.04	0.06	0.03	0.05
0.01	0.01	0.02	0.02	0.01	0.01
0.02	0.02	0.05	0.04	0.02	0.02
-1	-1	0.3	-1	-1	-1
0.02	0.03	0.05	-1	0.04	-1
0.37	0.36	0.51	0.44	0.39	0.27
0.02	0.03	0.04	0.05	0.02	0.02
0.14	0.23	-1	0.33	0.28	-1
0.06	0.07	0.1	0.1	0.05	0.05
1	1	1	1	1	1
0.15	0.16	0.22	0.25	0.19	0.19
0.98	0.98	0.89	-1	0.87	0.92
-1	-1	-1	-1	-1	-1
0.91	0.92	0.92	0.93	0.86	0.9
0.02	0.02	-1	-1	-1	-1
1	0.99	0.82	0.87	0.97	0.95
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.03	0.03	0.07	0.06	0.03	0.03
-1	-1	-1	-1	-1	-1
0.04	0.05	0.09	0.12	0.04	0.05
0.05	0.05	0.08	0.07	0.04	0.05
0.09	0.13	0.11	0.1	0.07	0.09
0.03	0.02	0.05	0.06	0.03	0.03
0.94	0.96	-1	-1	0.95	NA
0.04	0.04	0.09	0.09	0.03	0.04
-1	-1	-1	-1	-1	-1
0.14	0.24	0.17	0.13	0.18	0.22
-1	0.34	-1	-1	-1	-1
0.01	0.01	0.02	0.03	0.01	0.01
0.01	0.01	0.01	0.02	0.01	0.01
0.11	0.12	0.33	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.03	0.03	0.03	0.03	0.02	0.04
0.99	0.99	0.97	0.94	0.97	0.98
0.39	0.38	0.78	0.71	-1	-1
0.1	0.13	0.21	0.23	0.14	0.15
0.23	-1	0.53	0.35	-1	-1
0.11	0.07	0.32	0.21	0.11	0.09
0.03	0.02	0.05	0.05	0.02	0.02
0.18	0.2	0.29	0.54	0.18	0.15
-1	-1	-1	-1	-1	-1
0.86	0.72	-1	-1	-1	-1

0.96	0.99	0.97	0.96	0.97	0.97
0.23	0.31	-1	-1	0.18	0.13
0.65	0.9	0.92	0.94	0.72	0.84
0.23	0.17	-1	-1	-1	-1
0.04	0.04	0.07	-1	0.06	0.07
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.89	0.84	0.87	0.85	0.86	0.85
0.21	0.22	0.48	0.29	0.2	0.22
0.11	0.17	0.27	0.21	0.21	0.17
0.03	0.06	0.22	-1	-1	-1
0.99	0.99	0.98	0.98	0.97	0.97
-1	-1	-1	-1	-1	-1
-1	-1	0.92	0.94	-1	-1
-1	0.92	NA	NA	-1	-1
0.94	0.92	0.92	0.84	0.88	-1
0.97	0.98	0.96	0.96	0.94	0.9
0.05	0.05	0.1	0.09	0.05	0.06
0.01	0.01	0.02	0.02	0.01	0.01
0.02	0.03	0.04	0.04	0.01	0.01
0.08	0.1	0.08	0.14	0.05	0.05
0.1	0.1	0.14	0.14	0.11	0.09
0.1	0.12	0.1	0.12	0.1	0.1
-1	-1	-1	-1	-1	-1
0.19	0.33	-1	-1	0.34	0.31
0.16	0.13	0.06	0.08	0.1	0.1
-1	-1	-1	-1	-1	-1
0.98	0.98	0.97	0.94	0.96	0.94
0.99	0.99	0.98	0.98	0.99	0.99
0.03	0.03	0.04	0.05	0.02	0.03
0.06	0.19	0.3	0.39	0.15	0.11
-1	-1	-1	-1	-1	-1
0.02	0.02	0.04	0.06	0.02	0.02
0.18	0.17	0.21	0.15	0.27	0.26
0.06	0.06	0.15	-1	0.05	0.05
0.72	0.77	-1	-1	0.74	-1
0.06	0.07	0.11	0.11	0.06	0.06
0.99	0.99	0.96	0.97	0.99	0.98
0.21	0.18	-1	-1	-1	-1
0.96	0.97	0.97	0.92	0.92	0.94
-1	-1	0.94	-1	-1	NA
0.08	0.08	0.11	0.17	0.07	0.07
-1	0.07	-1	-1	-1	-1
0.92	0.88	-1	-1	-1	-1

ox2	heat1	heat2	stationary1	stationary2	sc1
0.01	0.01	0.03	0.03	0.15	0.15
0.08	0.09	0.09	0.1	0.48	0.44
0.41	-1	0.34	0.43	0.94	0.93
-1	-1	-1	-1	0.91	0.93
0.11	0.07	0.17	0.18	0.39	0.35
NA	NA	-1	-1	-1	-1
0.11	0.08	0.13	0.11	0.63	0.64
0.02	0.02	0.07	0.08	0.29	0.23
0.04	0.05	0.08	0.07	0.6	0.56
0.93	-1	0.95	0.94	0.99	0.93
-1	-1	-1	-1	0.56	0.47
-1	-1	-1	-1	0.93	0.95
-1	-1	-1	-1	-1	-1
0.02	0.02	0.07	0.06	0.36	0.37
0.02	0.01	0.06	0.05	0.41	0.35
-1	-1	0.1	0.07	0.32	0.32
0.01	0.01	0.04	0.04	0.17	0.14
0.91	-1	0.88	0.94	0.94	0.92
-1	0.01	0.02	0.02	0.15	0.13
-1	-1	-1	-1	-1	-1
0	0	0.02	0.02	0.2	0.17
-1	-1	-1	-1	-1	-1
0.03	0.02	0.14	0.12	0.37	0.47
-1	-1	0.64	0.62	0.9	0.94
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.04	0.05	0.14	0.15	0.76	0.84
-1	NA	-1	0.89	-1	-1
0.03	0.02	0.13	0.11	0.46	0.4
0.01	0.01	0.03	0.03	0.27	0.24
0.04	0.04	0.08	0.07	0.14	0.14
0.91	-1	-1	0.73	0.96	0.95
-1	-1	-1	-1	-1	-1
0.01	0.01	0.04	0.04	0.42	0.52
-1	NA	-1	-1	0.95	0.91
0.01	0.01	0.02	0.02	0.28	0.26
-1	-1	-1	-1	0.91	0.94
0.18	-1	-1	-1	0.45	-1
0.19	0.09	0.26	0.28	0.63	0.75
-1	-1	-1	-1	-1	0.83
0.04	0.03	0.09	0.1	0.77	0.7
-1	-1	-1	-1	0.32	0.4
0.19	0.11	0.31	0.28	0.32	0.27
-1	-1	-1	-1	-1	-1
0.98	0.97	0.98	0.98	0.95	0.92
0.04	-1	0.05	0.07	0.28	0.24
-1	-1	-1	-1	-1	-1

0.02	0.02	0.08	0.08	0.47	0.42
0.01	0.01	0.05	0.05	0.25	0.21
-1	-1	0.2	0.17	0.26	0.33
-1	-1	-1	0.22	0.85	0.61
0.01	0.01	0.02	0.02	0.2	0.16
0.03	0.03	0.09	0.07	0.49	0.53
0.63	0.73	0.53	0.4	-1	0.7
-1	-1	-1	-1	-1	-1
0.02	0.02	0.05	0.06	0.28	0.24
0.01	0.01	0.04	0.03	0.25	0.24
-1	-1	-1	-1	0.83	0.63
-1	-1	-1	-1	0.67	0.6
-1	-1	0.07	0.1	0.59	0.53
0.06	0.06	0.07	0.09	0.34	0.3
0.03	-1	0.02	0.02	0.18	0.16
-1	-1	0.87	0.88	0.9	0.84
0.22	0.24	0.31	0.29	0.59	0.46
0.07	0.06	0.12	0.12	0.47	0.53
NA	NA	0.83	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.52	0.56	0.93	0.96	0.93	0.95
0.02	0.02	0.07	0.06	0.31	0.29
-1	-1	0.19	0.16	0.41	0.35
-1	-1	-1	-1	-1	-1
0.94	-1	0.87	0.94	0.96	0.93
0.02	0.02	0.03	0.03	0.19	0.16
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.02	0.02	0.05	0.06	0.27	0.2
1	1	1	1	1	0.99
0.21	0.13	0.17	0.19	0.4	0.31
0.02	0.02	0.03	0.03	0.21	0.19
-1	-1	0.2	0.13	0.54	0.51
0.98	0.96	0.98	0.99	0.97	0.97
0.01	0.01	0.02	0.03	0.29	0.25
-1	-1	-1	0.61	0.99	0.99
0.05	0.05	0.07	0.09	0.51	0.42
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	0.79	0.81
-1	-1	0.04	-1	0.35	0.23
-1	-1	0.94	0.82	-1	-1
NA	NA	-1	-1	-1	-1
-1	-1	-1	-1	0.33	0.31
-1	-1	-1	-1	-1	NA
0.06	0.04	0.12	0.11	0.46	0.35
0.01	0.01	0.03	0.03	0.37	0.34
0.87	-1	0.18	0.2	1	1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

-1	-1	-1	-1	-1	-1
0.05	-1	0.06	0.08	0.15	0.2
-1	-1	-1	-1	0.9	0.94
0.32	-1	0.32	0.21	0.6	0.66
0.05	0.04	0.1	0.11	0.52	0.44
-1	-1	-1	-1	-1	-1
0.04	0.03	0.08	0.05	0.2	0.24
0.01	0.01	0.01	0.02	0.21	0.22
0.01	0.02	0.03	0.03	0.17	0.17
-1	-1	-1	-1	0.28	0.26
0.02	-1	0.05	0.06	0.39	-1
0.4	0.38	0.45	0.26	0.67	0.75
0.01	0.01	0.04	0.04	0.18	0.17
0.31	-1	-1	0.34	0.69	0.92
0.04	0.04	0.06	0.08	0.66	0.49
1	1	1	1	1	1
0.18	0.15	0.27	0.24	0.37	0.36
0.95	0.92	0.97	0.97	0.94	0.97
-1	-1	-1	-1	0.73	0.93
NA	NA	0.94	0.91	0.94	0.97
-1	-1	0.03	0.03	0.19	0.15
0.98	0.99	0.96	0.97	1	1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.01	0.01	0.06	0.07	0.42	0.31
-1	-1	-1	-1	-1	-1
0.03	0.02	0.1	0.09	0.48	0.5
0.03	0.03	0.06	0.06	0.53	0.45
0.08	0.09	0.09	0.09	0.23	0.22
0.01	0.01	0.05	0.04	0.33	0.31
-1	-1	-1	0.93	0.95	0.94
0.02	0.01	0.08	0.07	0.38	0.4
-1	-1	-1	-1	-1	-1
0.13	0.05	0.16	0.22	-1	-1
-1	-1	-1	-1	-1	-1
0.01	0	0.02	0.02	0.3	0.22
0	0	0.01	0.01	0.22	0.19
-1	-1	-1	-1	0.71	0.83
-1	-1	-1	-1	-1	-1
0.03	0.03	0.04	0.04	0.2	0.22
0.99	0.99	0.98	0.99	0.96	0.97
-1	-1	-1	0.22	0.33	0.72
0.07	0.04	0.24	0.22	0.74	0.63
-1	-1	-1	-1	0.4	0.35
0.08	0.09	0.13	0.12	0.42	0.47
0.02	0.02	0.05	0.05	0.49	0.36
0.06	0.04	0.43	0.42	0.84	0.83
-1	-1	-1	-1	-1	-1
0.77	-1	0.58	0.52	0.82	0.9

0.92	0.92	0.97	0.97	0.93	0.89
-1	-1	0.29	-1	-1	0.95
-1	-1	0.77	0.88	0.91	0.87
-1	-1	-1	0.35	0.92	0.89
0.03	0.02	0.16	0.19	0.57	0.71
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	0.86	0.94
0.85	0.9	0.83	0.93	0.94	0.95
-1	-1	0.23	0.24	0.36	0.5
0.13	0.13	0.08	0.1	-1	0.11
0.08	-1	0.06	0.1	0.39	0.89
0.99	0.98	0.98	0.98	0.91	0.96
-1	NA	-1	-1	0.8	0.81
NA	NA	0.79	-1	-1	-1
0.93	-1	-1	-1	0.94	0.98
0.86	-1	-1	0.94	0.79	0.92
-1	-1	0.94	0.94	0.96	0.95
0.03	0.02	0.08	0.08	0.36	0.32
0.01	0.01	0.02	0.02	0.46	0.45
0.01	0.01	0.04	0.03	0.54	0.52
0.04	0.03	0.12	0.11	0.66	0.55
0.1	0.12	0.13	0.15	0.56	0.51
0.09	0.09	0.1	0.13	0.26	0.19
NA	NA	-1	-1	0.91	0.92
0.11	0.15	0.15	0.24	0.92	0.87
0.09	0.06	0.15	0.12	0.13	0.14
-1	-1	-1	-1	-1	-1
0.96	0.9	0.96	0.97	0.97	0.97
0.97	0.97	0.98	0.99	0.98	0.99
0.01	0.01	0.04	0.04	0.25	0.23
0.11	0.17	0.22	0.21	0.53	0.6
-1	-1	-1	-1	-1	-1
0.01	0.01	0.03	0.03	0.23	0.22
0.09	0.08	0.14	0.13	0.73	0.59
0.09	-1	0.08	0.05	0.27	0.24
-1	-1	0.69	0.4	0.96	0.94
0.05	0.05	0.1	0.1	0.57	0.58
0.98	0.99	0.99	0.98	0.97	0.98
-1	-1	0.25	0.18	0.62	0.52
0.94	-1	0.96	0.97	-1	0.88
NA	NA	-1	NA	0.92	-1
0.04	0.06	0.05	0.07	0.29	0.23
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

sc2	gylcerol1	gylcerol2	calcium1	calcium2	lowN1
0.03	0.03	0.04	0.03	0.03	0.02
0.13	0.08	0.08	0.09	0.16	0.05
0.43	0.44	0.31	0.46	0.42	0.42
-1	-1	-1	-1	-1	-1
0.14	0.15	0.2	0.23	0.13	0.16
-1	-1	-1	-1	-1	-1
0.18	0.15	0.14	0.11	0.1	0.1
0.03	0.03	0.05	0.05	0.05	0.03
0.04	0.04	0.04	0.04	0.03	0.03
0.93	0.93	-1	-1	0.91	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.02	0.02	0.04	0.04	0.03	0.03
0.03	0.03	0.05	0.06	0.04	0.03
-1	0.17	-1	-1	-1	-1
0.02	0.01	0.02	0.02	0.02	0.02
-1	0.85	0.95	0.96	0.92	0.89
-1	-1	0.01	0.01	-1	-1
-1	-1	-1	-1	-1	-1
0.01	0.01	0.01	0.01	0.01	0.01
-1	-1	-1	-1	-1	-1
0.18	0.14	0.17	0.15	0.1	0.09
-1	0.79	0.9	0.84	0.77	0.81
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.04	0.05	0.1	0.09	0.09	0.11
-1	0.88	-1	0.89	-1	-1
0.06	0.08	0.08	0.08	0.08	0.06
0.01	0.01	0.02	0.01	0.01	0.01
0.05	0.05	0.06	0.06	0.05	0.05
-1	0.94	0.9	0.92	0.77	-1
-1	-1	-1	-1	-1	-1
-1	0.01	0.03	0.03	0.02	0.02
-1	-1	-1	-1	-1	NA
0.01	0.01	0.01	0.01	0.01	0.01
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.15	0.15	0.34	0.33	0.36	0.24
-1	0.86	-1	-1	-1	-1
0.05	0.06	0.07	0.08	0.06	0.06
-1	-1	-1	-1	-1	-1
0.26	0.34	0.51	0.52	0.44	0.46
-1	-1	-1	-1	-1	-1
0.97	0.98	0.97	0.96	0.96	0.93
0.03	0.02	0.03	0.02	-1	-1
-1	-1	-1	-1	-1	-1

0.03	0.03	0.04	0.05	0.03	0.03
0.02	0.02	0.02	0.02	0.02	0.02
-1	0.29	-1	0.23	-1	-1
-1	-1	-1	-1	-1	-1
0.01	0.01	0.02	0.02	0.01	0.01
0.03	0.05	0.05	0.07	0.04	0.05
-1	0.47	-1	0.49	-1	-1
-1	-1	-1	-1	-1	-1
0.02	0.02	0.02	0.02	0.02	0.01
0.02	0.02	0.03	0.03	0.02	0.02
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.06	0.05	0.06	0.06	0.05	0.05
0.02	0.02	0.02	0.03	0.02	0.01
-1	-1	-1	0.9	-1	-1
0.27	0.22	0.26	0.31	0.27	0.23
0.07	0.07	0.08	0.07	0.06	0.05
-1	-1	NA	NA	NA	NA
-1	-1	-1	-1	-1	-1
0.63	0.61	0.61	0.55	0.39	0.43
0.04	0.04	0.05	0.06	0.04	0.04
0.18	0.2	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.91	0.85	-1	0.91	-1	-1
0.03	0.04	0.03	0.03	0.02	0.02
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.02	0.02	0.03	0.02	0.02	0.02
1	1	1	1	1	1
0.16	0.15	-1	0.19	-1	-1
0.02	0.03	0.03	0.03	0.03	0.03
-1	-1	-1	-1	-1	-1
0.98	0.97	0.97	0.97	0.97	0.98
0.02	0.02	0.03	0.04	0.03	0.03
-1	-1	-1	-1	-1	-1
0.05	0.06	0.06	0.06	0.06	0.05
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	0.04	-1	-1	-1
-1	0.9	0.93	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.07	0.07	0.09	0.1	0.08	0.05
0.01	0.02	0.03	0.03	0.02	0.02
0.17	0.26	0.14	0.17	0.37	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

-1	-1	-1	-1	-1	-1
0.06	0.06	0.1	0.11	0.09	0.04
-1	-1	-1	-1	-1	-1
-1	-1	-1	0.36	-1	-1
0.05	0.08	0.05	0.07	0.07	0.08
-1	-1	-1	-1	-1	-1
0.05	0.06	0.09	0.11	0.08	0.13
0.01	0.01	0.01	0.01	0.01	0.01
0.02	0.01	0.03	0.02	0.03	0.02
-1	-1	-1	-1	-1	-1
0.03	-1	0.04	0.04	-1	-1
0.38	0.36	0.58	0.48	0.31	0.45
0.02	0.02	0.03	0.04	0.02	0.03
-1	0.22	-1	-1	-1	-1
0.05	0.06	0.09	0.08	0.06	0.09
1	1	1	1	1	1
0.18	0.13	0.18	0.19	0.18	0.13
0.85	0.93	0.95	0.94	0.92	0.93
-1	-1	-1	-1	-1	-1
-1	0.91	-1	0.92	NA	-1
-1	-1	-1	-1	-1	-1
1	1	0.95	0.87	0.96	0.97
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.02	0.02	0.03	0.03	0.03	0.02
-1	-1	-1	-1	-1	-1
0.05	0.05	0.06	0.05	0.05	0.06
0.01	0.03	0.06	0.07	0.05	0.04
0.09	0.1	0.11	0.1	0.1	0.07
0.02	0.02	0.02	0.02	0.02	0.02
-1	-1	-1	-1	-1	-1
0.03	0.04	0.07	0.06	0.04	0.06
-1	-1	-1	-1	-1	-1
0.11	0.1	0.24	0.39	0.21	0.19
-1	-1	-1	-1	-1	-1
0.01	0.01	0.01	0.01	0.01	0.01
0	0	0.01	0.01	0	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.03	0.03	0.03	0.04	0.03	0.03
0.98	0.99	0.98	0.96	0.97	0.97
-1	-1	0.74	0.83	-1	-1
0.13	0.11	0.18	0.17	0.22	0.2
-1	-1	-1	-1	-1	-1
0.06	0.1	0.12	0.12	0.1	0.11
0.03	0.02	0.02	0.02	0.01	0.01
0.16	0.21	0.18	0.19	0.18	0.24
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

0.95	0.97	0.98	0.97	0.96	0.97
-1	0.23	-1	-1	-1	-1
0.92	0.93	0.84	0.77	0.8	0.88
-1	-1	-1	-1	-1	-1
0.03	0.03	0.03	0.02	0.03	0.02
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.8	0.87	0.93	0.87	0.82	0.8
0.19	0.21	0.22	0.18	-1	0.18
0.1	0.11	0.15	0.14	0.11	0.09
-1	-1	-1	0.04	0.05	-1
0.98	0.98	0.98	0.98	0.98	0.98
-1	-1	-1	-1	-1	-1
-1	-1	NA	NA	NA	-1
NA	-1	-1	-1	-1	-1
-1	0.9	-1	0.89	-1	-1
0.94	0.95	0.92	-1	-1	0.93
0.09	0.07	0.08	0.05	0.07	0.08
0.01	0.01	0.01	0.01	0.01	0.01
0.01	0.02	0.03	0.03	0.02	0.01
0.03	0.06	0.11	0.11	0.09	0.1
0.11	0.1	0.1	0.12	0.1	0.09
0.1	0.09	0.1	0.11	0.08	0.08
-1	-1	NA	-1	NA	-1
0.13	0.08	0.32	0.24	0.15	0.1
0.09	0.12	0.14	0.15	0.1	0.14
-1	-1	-1	-1	-1	-1
0.93	0.96	0.95	0.96	0.94	0.96
0.97	0.98	0.98	0.97	0.98	0.98
0.02	0.02	0.03	0.03	0.02	0.02
0.11	0.15	0.28	0.18	0.19	0.1
-1	-1	-1	-1	NA	-1
0.01	0.01	0.03	0.03	0.02	0.02
0.12	0.07	0.17	0.19	0.13	0.08
-1	0.09	-1	-1	-1	-1
-1	0.85	0.92	0.91	0.94	0.87
0.06	0.07	0.08	0.09	0.08	0.07
0.98	0.99	0.99	0.99	0.98	0.98
-1	-1	-1	-1	-1	-1
0.97	0.93	0.91	0.92	-1	0.92
-1	-1	-1	-1	NA	NA
0.11	0.1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

lowN2	lowPhos1	lowPhos2	calcofluor1	calcofluor2	urea1
0.05	0.03	0.02	0.03	0.04	0.05
0.11	0.11	0.14	0.07	0.05	0.04
0.66	0.37	0.33	0.38	0.5	0.43
-1	-1	-1	-1	-1	-1
0.18	0.22	0.17	0.15	0.2	0.18
-1	-1	-1	-1	NA	NA
0.11	0.16	0.13	0.12	0.15	0.17
0.08	0.07	0.05	0.05	0.05	0.07
0.06	0.06	0.04	0.04	0.04	0.06
-1	-1	0.93	0.92	-1	0.92
-1	-1	-1	-1	-1	-1
-1	-1	-1	0.89	-1	-1
-1	-1	-1	-1	-1	-1
0.04	0.05	0.03	0.03	0.06	0.07
0.05	0.05	0.04	0.05	0.07	0.07
0.1	0.08	-1	-1	-1	-1
0.02	0.01	0.01	0.02	0.02	0.02
-1	-1	0.94	0.95	0.9	0.94
-1	-1	-1	-1	-1	0.01
-1	-1	-1	-1	-1	-1
0.01	0.01	-1	0.01	0.01	0.01
-1	-1	-1	-1	-1	-1
0.1	0.09	0.24	0.22	0.23	0.25
0.56	0.55	0.65	-1	0.81	0.93
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.12	0.12	0.09	0.08	0.13	0.12
-1	-1	-1	0.9	-1	-1
0.11	0.12	0.08	0.08	0.1	0.08
0.04	0.02	0.01	0.01	0.02	0.02
0.08	0.08	0.05	0.05	0.07	0.08
-1	-1	0.89	0.89	-1	0.92
-1	-1	-1	-1	-1	-1
0.06	0.05	-1	-1	0.04	0.04
-1	-1	-1	-1	NA	-1
0.02	0.02	0.01	0.01	0.01	0.01
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.24	0.13	0.29	0.38	0.23	0.39
-1	-1	-1	-1	-1	-1
0.11	0.09	0.05	0.07	0.08	0.09
-1	-1	-1	-1	-1	-1
0.59	0.62	0.35	0.33	0.59	0.56
-1	-1	-1	-1	-1	-1
0.97	0.95	0.96	0.97	0.95	0.95
0.04	-1	0.02	0.03	0.03	0.02
-1	-1	-1	-1	-1	-1

0.08	0.08	0.04	0.04	0.06	0.08
0.03	0.02	0.03	0.02	0.02	0.03
0.17	-1	0.17	-1	-1	0.21
-1	-1	-1	-1	-1	-1
0.02	0.02	0.02	0.02	0.02	0.02
0.08	0.05	0.04	0.04	0.08	0.07
0.39	-1	0.69	-1	0.5	0.42
-1	-1	-1	-1	-1	-1
0.03	0.02	0.02	0.01	0.02	0.03
0.03	0.03	0.02	0.02	0.03	0.04
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.12	0.04	-1	-1	0.08	-1
0.08	0.08	0.04	0.05	0.05	0.06
0.03	0.02	-1	0.01	0.01	0.02
-1	-1	-1	0.89	-1	0.89
0.28	0.33	0.31	0.29	0.26	0.3
0.07	0.08	0.07	0.07	0.06	0.08
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.79	0.58	0.52	0.41	0.59	0.49
0.04	0.04	0.04	0.05	0.07	0.07
0.05	0.06	-1	0.19	0.21	0.22
-1	-1	-1	-1	-1	-1
-1	-1	0.94	0.89	0.8	0.92
0.03	0.04	0.03	0.02	0.03	0.03
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.04	0.04	0.02	0.03	0.03	0.03
1	1	1	1	1	1
-1	0.05	0.12	0.17	0.16	0.11
0.03	0.03	0.04	0.03	0.03	0.04
0.07	0.11	-1	-1	-1	-1
0.96	0.98	0.99	0.98	0.98	0.98
0.05	0.06	0.03	0.03	0.04	0.05
0.38	0.36	-1	-1	-1	-1
0.06	0.09	0.06	0.06	0.06	0.07
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	0.04
-1	-1	-1	0.85	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.08	0.09	0.1	0.11	0.08	0.12
0.03	0.03	0.02	0.03	0.03	0.03
0.27	0.27	0.23	0.2	0.25	0.2
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

-1	-1	-1	-1	-1	-1
0.11	0.09	0.02	0.04	0.05	0.15
-1	0.84	-1	-1	-1	-1
-1	-1	-1	0.29	-1	0.47
0.1	0.09	0.09	0.08	0.08	0.09
-1	-1	-1	-1	-1	-1
0.05	0.08	0.12	0.1	0.11	0.13
0.02	0.01	0.01	0.01	0.01	0.01
0.02	0.02	0.02	0.02	0.04	0.04
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	0.05	0.04
0.26	0.22	0.24	0.28	0.46	0.34
0.04	0.04	0.02	0.03	0.03	0.04
-1	0.33	-1	0.27	0.29	0.42
0.04	0.05	0.11	0.11	0.11	0.11
1	1	1	1	1	1
0.23	0.22	0.13	0.14	0.21	0.22
0.97	0.95	0.94	0.91	0.98	0.97
-1	-1	-1	-1	-1	-1
0.84	0.83	0.88	0.9	0.88	-1
-1	-1	-1	-1	-1	-1
1	1	0.95	0.93	0.99	0.99
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.04	0.03	0.02	0.03	0.03	0.04
-1	-1	-1	-1	-1	-1
0.07	0.07	0.06	0.05	0.06	0.1
0.04	0.04	0.05	0.05	0.07	0.06
0.07	0.04	0.08	0.08	0.09	0.11
0.03	0.04	0.02	0.02	0.03	0.03
NA	-1	NA	0.93	NA	-1
0.07	0.1	0.03	0.04	0.06	0.09
-1	-1	-1	-1	-1	-1
-1	0.38	0.14	0.14	0.16	0.21
-1	-1	-1	-1	-1	-1
0.03	0.03	0.01	0.01	0.02	0.02
0.01	0.01	0.01	0.01	0.01	0.01
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.04	0.03	0.04	0.02	0.04	0.03
0.97	0.98	0.97	0.98	0.94	0.96
-1	-1	-1	-1	-1	-1
0.22	0.23	0.19	0.17	0.23	0.24
-1	0.09	-1	-1	-1	-1
0.11	0.09	0.05	0.08	0.13	0.1
0.05	0.04	0.02	0.02	0.03	0.04
0.24	0.28	0.28	0.25	0.26	0.26
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

0.93	0.94	0.99	0.99	0.97	0.98
-1	-1	0.51	-1	-1	-1
0.94	0.92	0.92	0.81	-1	0.76
-1	-1	-1	-1	-1	-1
0.09	0.05	0.03	0.03	0.04	0.04
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.77	0.84	0.85	0.94	0.72	0.92
0.19	0.19	0.15	0.14	0.2	0.32
0.15	0.1	0.12	0.11	0.09	0.12
-1	-1	-1	-1	0.04	-1
0.98	0.98	0.98	0.98	0.97	0.98
-1	-1	-1	-1	-1	-1
-1	NA	-1	-1	NA	NA
-1	-1	-1	-1	-1	-1
-1	0.89	-1	0.87	-1	0.89
0.94	0.95	0.93	0.94	0.92	-1
0.06	0.04	0.05	0.06	0.05	0.1
0.01	0.01	0.01	0.01	0.01	0.01
0.03	0.03	0.02	0.02	0.04	0.04
0.06	0.05	0.1	0.1	0.1	0.11
0.14	0.11	0.08	0.09	0.11	0.11
0.13	0.1	0.08	0.09	0.09	0.09
-1	-1	-1	-1	NA	NA
0.49	0.3	0.18	0.18	0.22	0.25
0.08	0.13	0.17	0.15	0.1	0.13
-1	-1	-1	-1	-1	-1
0.96	0.97	0.97	0.97	0.95	0.97
0.97	0.97	0.96	0.99	0.98	0.98
0.05	0.05	0.03	0.04	0.04	0.04
0.13	0.07	0.23	0.18	0.23	0.26
-1	0.23	-1	-1	-1	-1
0.02	0.03	-1	0.02	0.04	0.04
0.19	0.1	0.1	0.1	0.13	0.15
0.05	0.04	-1	-1	-1	-1
-1	-1	0.93	0.95	-1	0.9
0.09	0.08	0.09	0.08	0.09	0.1
0.99	0.99	0.99	0.99	0.99	0.99
-1	-1	-1	-1	-1	0.23
0.95	0.97	0.97	0.94	0.96	0.94
-1	-1	NA	-1	-1	-1
-1	-1	-1	-1	0.11	0.12
-1	-1	-1	-1	-1	-1
-1	-1	-1	0.92	-1	-1

urea2	juice1	juice2	benomyl1	benomyl2	cRed1
0.02	0.02	0.04	0.04	0.03	0.03
0.1	0.07	0.07	0.04	0.1	0.08
0.54	0.41	0.47	0.58	0.64	-1
-1	-1	-1	-1	-1	-1
0.1	0.09	0.09	0.08	0.17	0.16
-1	-1	-1	-1	-1	NA
0.08	0.1	0.12	0.14	0.15	0.08
0.03	0.04	0.05	0.04	0.07	0.07
0.03	0.03	0.05	0.05	0.04	0.04
-1	0.91	0.94	0.93	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	0.42	-1	-1
-1	-1	-1	-1	-1	-1
0.02	0.02	0.03	0.02	0.04	0.03
0.03	0.03	0.02	0.02	0.05	0.04
-1	-1	0.18	0.14	-1	-1
0.01	0.01	0.03	0.02	0.02	0.02
0.9	0.92	0.86	0.82	0.92	0.93
-1	0.01	-1	-1	0.01	-1
-1	-1	-1	-1	-1	-1
0.01	0.01	0	0.01	0.01	0.01
-1	-1	-1	-1	-1	-1
0.18	0.18	0.15	0.14	0.26	0.27
-1	0.52	0.64	0.62	0.93	0.85
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.08	0.05	0.07	0.04	0.13	0.12
-1	-1	-1	0.89	0.88	-1
0.06	0.07	0.05	0.03	0.07	0.07
0.02	0.01	0.02	0.02	0.02	0.02
0.04	0.06	0.05	0.06	0.07	0.05
-1	0.91	-1	0.57	0.91	-1
-1	-1	-1	-1	-1	-1
0.02	0.01	-1	0.02	0.03	0.02
NA	-1	NA	NA	-1	NA
0.01	0.01	0.01	0.01	0.01	0.01
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.2	0.26	0.14	0.16	0.25	0.33
-1	-1	-1	0.83	-1	-1
0.03	0.05	0.04	0.05	0.07	0.06
-1	-1	-1	-1	-1	-1
0.34	0.28	0.52	0.35	0.48	0.42
-1	-1	-1	-1	-1	-1
0.96	0.97	0.96	0.99	0.95	0.95
-1	0.02	0.04	0.05	0.03	0.03
-1	-1	-1	-1	-1	-1

0.03	0.02	0.03	0.03	0.05	0.06
0.03	0.02	0.03	0.02	0.03	0.02
-1	-1	0.11	0.08	0.15	-1
-1	-1	-1	0.2	-1	-1
0.01	0.01	0.01	0.01	0.02	0.02
0.04	0.04	0.07	0.03	0.05	0.05
-1	-1	0.44	0.51	0.52	-1
-1	-1	-1	-1	-1	-1
0.02	0.03	0.04	0.03	0.02	0.02
0.02	0.02	0.01	0.01	0.03	0.02
-1	-1	-1	-1	-1	-1
-1	-1	-1	0.14	-1	-1
-1	-1	-1	0.09	-1	-1
0.06	0.05	0.08	0.07	0.07	0.05
0.02	0.02	0.01	0.01	0.02	0.02
-1	-1	0.88	0.9	-1	-1
0.28	0.27	0.25	0.26	0.27	0.28
0.06	0.06	0.07	0.07	0.06	0.05
-1	-1	-1	0.68	-1	-1
-1	-1	-1	-1	-1	-1
0.51	0.5	0.98	0.97	0.57	0.53
0.04	0.04	0.04	0.04	0.05	0.04
-1	0.22	-1	0.06	0.16	0.21
-1	-1	-1	-1	-1	-1
-1	0.85	0.87	0.96	0.85	0.91
0.02	0.03	0.04	0.03	0.03	0.03
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.02	0.02	0.03	0.03	0.03	0.02
1	1	1	1	1	1
-1	0.14	0.07	0.14	0.07	-1
0.02	0.02	0.02	0.02	0.03	0.03
-1	-1	-1	0.08	-1	-1
0.97	0.99	0.99	0.99	0.99	0.95
0.02	0.02	0.02	0.01	0.03	0.03
-1	-1	0.31	0.27	-1	-1
0.05	0.05	0.06	0.05	0.07	0.06
-1	-1	-1	-1	-1	-1
-1	-1	-1	0.43	-1	-1
-1	-1	0.03	0.03	-1	-1
-1	0.86	-1	0.83	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.09	0.07	0.04	0.04	0.08	0.08
0.02	0.02	0.01	0.01	0.03	0.03
-1	0.23	0.58	0.5	0.28	0.17
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1

-1	-1	0.1	-1	-1	-1
-1	0.04	0.04	0.03	0.11	0.12
-1	-1	-1	0.82	-1	-1
-1	0.33	0.35	0.52	0.44	-1
0.05	0.05	0.06	0.03	0.08	0.09
-1	-1	-1	-1	-1	-1
0.07	0.07	0.03	0.02	0.08	0.07
0.01	0.01	0.01	0.01	0.01	0.01
0.02	0.02	0.02	0.01	0.03	0.03
-1	-1	-1	-1	-1	-1
0.02	-1	0.07	0.06	0.03	0.05
0.4	0.31	0.12	0.1	0.47	0.47
0.02	0.02	0.02	0.01	0.03	0.03
-1	0.26	0.32	0.37	0.24	-1
0.07	0.07	0.05	0.04	0.08	0.1
1	1	1	1	1	1
0.15	0.18	0.45	0.31	0.22	0.2
0.95	0.97	0.96	0.98	0.92	0.97
-1	-1	-1	-1	-1	-1
-1	0.94	0.92	0.95	0.76	-1
-1	-1	-1	0.01	-1	-1
0.94	0.94	0.97	1	1	1
-1	-1	-1	-1	-1	NA
-1	-1	-1	-1	-1	-1
0.03	0.03	0.03	0.02	0.04	0.03
-1	-1	-1	-1	-1	-1
0.04	0.05	0.03	0.02	0.05	0.05
0.03	0.04	0.03	0.03	0.05	0.04
0.08	0.1	0.1	0.12	0.09	0.09
0.02	0.02	-1	0.03	0.03	0.02
NA	-1	0.93	0.97	-1	-1
0.03	0.03	0.03	0.02	0.07	0.05
-1	-1	-1	-1	-1	-1
0.14	0.13	0.13	0.08	0.17	0.15
-1	-1	-1	-1	-1	-1
0.01	0	0.01	0.01	0.01	0.01
0.01	0.01	0.01	0	0.01	0.01
-1	-1	0.59	0.52	0.21	-1
-1	-1	-1	-1	-1	-1
0.03	0.03	0.04	0.04	0.04	0.03
0.97	0.94	0.98	0.99	0.97	0.96
-1	-1	-1	-1	0.68	-1
0.14	0.11	0.17	0.11	0.2	0.2
-1	-1	0.18	0.14	-1	-1
0.05	0.1	0.15	0.12	0.08	0.06
0.02	0.02	0.02	0.02	0.03	0.03
0.22	0.15	0.16	0.1	0.14	0.16
-1	-1	-1	-1	-1	-1
-1	-1	0.86	0.89	-1	-1

0.97	0.98	0.94	0.97	0.98	0.96
-1	-1	0.2	0.24	0.28	-1
0.85	0.64	0.93	0.92	0.85	0.76
-1	-1	-1	-1	-1	-1
0.05	0.02	0.08	0.06	0.02	0.02
-1	-1	-1	-1	-1	-1
-1	-1	-1	-1	-1	-1
0.86	0.85	0.88	0.93	0.93	0.89
0.16	0.18	0.23	0.35	0.19	0.19
0.07	0.09	0.13	0.12	0.09	0.09
-1	-1	0.08	0.07	0.04	0.05
0.97	0.98	0.99	0.99	0.98	0.98
-1	-1	-1	-1	-1	-1
NA	NA	0.94	-1	NA	NA
-1	-1	-1	-1	-1	-1
-1	0.9	0.92	0.88	-1	-1
0.92	-1	0.98	0.98	0.91	-1
0.05	0.05	0.03	0.02	0.06	0.06
0.01	0.01	0.02	0.01	0.01	0.01
0.02	0.02	0.02	0.01	0.03	0.03
0.1	0.07	0.05	0.03	0.08	0.08
0.09	0.11	0.13	0.13	0.12	0.1
0.09	0.09	0.11	0.09	0.11	0.1
NA	-1	-1	-1	-1	NA
0.11	0.13	0.93	0.95	0.26	0.33
0.11	0.08	0.05	0.04	0.08	0.07
-1	-1	-1	-1	-1	-1
0.95	0.96	0.98	0.98	0.96	0.94
0.97	0.98	0.99	0.99	0.99	0.98
0.03	0.02	0.02	0.01	0.02	0.02
0.21	0.27	0.38	0.55	0.3	0.32
-1	-1	-1	-1	-1	NA
0.02	0.01	0.01	0.01	0.03	0.02
0.09	0.11	0.16	0.19	0.16	0.14
-1	-1	0.04	0.08	-1	-1
-1	-1	-1	0.41	0.87	0.87
0.06	0.07	0.07	0.05	0.1	0.09
0.98	0.99	0.99	0.99	0.99	0.99
-1	-1	0.07	-1	-1	-1
0.93	0.95	0.95	0.96	0.95	-1
-1	-1	-1	-1	-1	NA
-1	0.07	0.09	0.1	0.09	-1
-1	-1	-1	-1	-1	-1
-1	-1	0.93	0.95	-1	-1

cRed2	
0.03	0.02
0.18	0.08
0.48	0.49
-1	-1
0.11	0.14
-1	NA
0.13	0.13
0.05	0.05
0.04	0.04
0.92	-1
-1	-1
-1	-1
-1	-1
0.03	0.03
0.03	0.03
-1	-1
0.02	0.02
0.89	0.94
0.01	0.01
-1	-1
0.01	0.01
-1	-1
0.21	0.22
0.79	0.77
-1	-1
-1	-1
0.1	0.1
-1	-1
0.06	0.07
0.01	0.02
0.05	0.06
0.88	-1
-1	-1
0.03	0.02
-1	-1
0.01	0.01
-1	-1
-1	-1
0.29	0.27
-1	-1
0.05	0.06
-1	-1
0.28	0.36
-1	-1
0.97	0.95
0.04	0.03
-1	-1

0.04	0.05
0.02	0.02
0.22	-1
-1	-1
0.02	0.01
0.05	0.05
0.75	0.49
-1	-1
0.02	0.02
0.03	0.02
-1	-1
0.22	-1
-1	-1
0.06	0.06
0.02	0.02
0.79	-1
0.24	0.22
0.07	0.06
-1	-1
-1	-1
0.68	0.66
0.04	0.04
0.14	-1
-1	-1
0.91	0.82
0.03	0.03
-1	-1
-1	-1
0.02	0.03
1	1
0.25	0.1
0.03	0.03
0.22	-1
0.98	0.98
0.02	0.03
-1	-1
0.06	0.06
-1	-1
-1	-1
0.03	-1
-1	-1
-1	-1
-1	-1
-1	-1
0.07	0.09
0.02	0.02
0.3	0.2
-1	-1
-1	-1

-1	-1
0.12	0.06
-1	-1
0.28	0.37
0.08	0.07
-1	-1
0.04	0.05
0.01	0.01
0.02	0.02
-1	-1
0.02	0.03
0.46	0.39
0.03	0.03
0.31	0.31
0.06	0.06
1	1
0.17	0.22
0.95	0.98
-1	-1
0.85	0.87
-1	-1
1	1
-1	-1
-1	-1
0.04	0.04
-1	-1
0.05	0.05
0.04	0.05
0.11	0.1
0.02	0.02
-1	-1
0.04	0.04
-1	-1
0.12	0.15
-1	-1
0.01	0.01
0.01	0.01
-1	-1
-1	-1
0.03	0.03
0.98	0.98
-1	-1
0.12	0.16
-1	-1
0.09	0.08
0.03	0.02
0.13	0.17
-1	-1
0.83	-1

0.97	0.97
0.17	-1
0.88	0.64
-1	-1
0.04	0.04
-1	-1
-1	-1
0.87	0.9
0.15	0.23
0.09	0.08
0.08	0.05
0.98	0.98
-1	-1
NA	NA
-1	-1
0.86	-1
0.92	-1
0.05	0.04
0.01	0.01
0.02	0.02
0.07	0.09
0.1	0.11
0.09	0.09
NA	NA
0.33	0.25
0.07	0.07
-1	-1
0.98	0.96
0.98	0.98
0.02	0.02
0.22	0.18
-1	-1
0.02	0.02
0.18	0.14
0.12	-1
0.89	0.88
0.07	0.08
0.99	0.99
-1	-1
0.92	0.93
-1	NA
0.05	-1
0.14	-1
-1	-1

Table S8. Figure 6A event annotations

Splicing events	Annotation (1=Yes,0=No)
chrXII:982539:982739:-@chrXII:982258:982458:-	0
chrXVI:717147:717347:-@chrXVI:716849:717049:-	0
chrXVI:883187:883387:+@chrXVI:883487:883687:+	1
chrXIV:414711:414911:+@chrXIV:415914:416114:+	1
chrVII:365433:365633:-@chrVII:364764:364964:-	1
chrX:387436:387636:-@chrX:387148:387348:-	1
chrIX:127461:127661:+@chrIX:128149:128349:+	1
chrII:45444:45644:+@chrII:45978:46178:+	1
chrVII:438398:438598:-@chrVII:437741:437941:-	1
chrIX:232367:232567:-@chrIX:231757:231957:-	1
chrXVI:623377:623577:+@chrXVI:623711:623911:+	1
chrXII:766130:766330:-@chrXII:765873:766073:-	1
chrIV:117466:117666:+@chrIV:118158:118358:+	1
chrIV:569724:569924:-@chrIV:569433:569633:-	1
chrV:306125:306325:+@chrV:306792:306992:+	1
chrXVI:218446:218646:+@chrXVI:218747:218947:+	1
chrXIV:350757:350957:+@chrXIV:351054:351254:+	1
chrVI:64921:65121:-@chrVI:64153:64353:-	0
chrIV:417627:417827:-@chrIV:417021:417221:-	0
chrXVI:345597:345797:-@chrXVI:345244:345444:-	1
chrXII:286557:286757:-@chrXII:286267:286467:-	1
chrXI:166199:166399:+@chrXI:166488:166688:+	1
chrXVI:833493:833693:+@chrXVI:833828:834028:+	1
chrII:407123:407323:-@chrII:406827:407027:-	1
chrXIII:236391:236591:+@chrXIII:236954:237154:+	1
chrVII:543438:543638:+@chrVII:543722:543922:+	1
chrXII:233886:234086:-@chrXII:233442:233642:-	0
chrVIII:382748:382948:-@chrVIII:382106:382306:-	1
chrXIII:223782:223982:-@chrXIII:223180:223380:-	1
chrIV:229819:230019:+@chrIV:230321:230521:+	1
chrXII:694182:694382:+@chrXII:694473:694673:+	1
chrIV:491359:491559:+@chrIV:491899:492099:+	1
chrII:680040:680240:-@chrII:679742:679942:-	1
chrXIII:225691:225891:+@chrXIII:226290:226490:+	1
chrXIII:721346:721546:-@chrXIII:720998:721198:-	1
chrXII:40401:40601:-@chrXII:40021:40221:-	1
chrXVI:911076:911276:+@chrXVI:911353:911553:+	1
chrX:172753:172953:-@chrX:172232:172432:-	1
chrIX:99386:99586:-@chrIX:98895:99095:-	1
chrIX:257027:257227:-@chrIX:256354:256554:-	1
chrII:462229:462429:+@chrII:462500:462700:+	1
chrX:157250:157450:-@chrX:156589:156789:-	1
chrX:608282:608482:+@chrX:608582:608782:+	0
chrXII:796336:796536:-@chrXII:795712:795912:-	1
chrVIII:107631:107831:+@chrVIII:107895:108095:+	1
chrX:396571:396771:-@chrX:396293:396493:-	1
chrXVI:653967:654167:+@chrXVI:654571:654771:+	1

chrXIV:545091:545291:+@chrXIV:545371:545571:+	1
chrV:432471:432671:+@chrV:433197:433397:+	1
chrII:342498:342698:+@chrII:342790:342990:+	0
chrVIII:354664:354864:+@chrVIII:354956:355156:+	1
chrVIII:103857:104057:-@chrVIII:103417:103617:-	0
chrVII:383285:383485:+@chrVII:383581:383781:+	0
chrXIV:273602:273802:-@chrXIV:272187:272387:-	0
chrXV:80160:80360:+@chrXV:80775:80975:+	1
chrI:87187:87387:+@chrI:87501:87701:+	1
chrIII:111634:111834:-@chrIII:111357:111557:-	1
chrXIV:728354:728554:+@chrXIV:728922:729122:+	0
chrIV:458098:458298:-@chrIV:457817:458017:-	1
chrVII:436112:436312:+@chrVII:436375:436575:+	0
chrXV:349599:349799:-@chrXV:349297:349497:-	0
chrXIII:559582:559782:+@chrXIII:560158:560358:+	0
chrXII:931699:931899:-@chrXII:931149:931349:-	1
chrVIII:250955:251155:+@chrVIII:251249:251449:+	1
chrIV:1103609:1103809:+@chrIV:1103893:1104093:+	1
chrXV:552875:553075:-@chrXV:552465:552665:-	1
chrVII:726838:727038:+@chrVII:727358:727558:+	1
chrXIII:754220:754420:-@chrXIII:753542:753742:-	1
chrXVI:582702:582902:-@chrXVI:582358:582558:-	1
chrV:396610:396810:+@chrV:397282:397482:+	1
chrIV:579278:579478:+@chrIV:580018:580218:+	1
chrIX:68515:68715:+@chrIX:69150:69350:+	1
chrV:307756:307956:+@chrV:308068:308268:+	1
chrXII:713156:713356:-@chrXII:712525:712725:-	1
chrVIII:129328:129528:+@chrVIII:129648:129848:+	1
chrVII:249686:249886:+@chrVII:250087:250287:+	1
chrVIII:104205:104405:+@chrVIII:104804:105004:+	1
chrVII:439181:439381:+@chrVII:439480:439680:+	0
chrVI:63974:64174:-@chrVI:63659:63859:-	1
chrXI:431834:432034:+@chrXI:432433:432633:+	1
chrXIII:124158:124358:-@chrXIII:123542:123742:-	1
chrXIII:140184:140384:-@chrXIII:139890:140090:-	1
chrIII:178214:178414:-@chrIII:177706:177906:-	1
chrXVI:115018:115218:+@chrXVI:115294:115494:+	1
chrIV:217402:217602:+@chrIV:218008:218208:+	1
chrIV:1319817:1320017:-@chrIV:1319520:1319720:-	1
chrIV:322082:322282:+@chrIV:322704:322904:+	1
chrVII:148967:149167:-@chrVII:148398:148598:-	1
chrXIII:163717:163917:-@chrXIII:163108:163308:-	1
chrVII:150526:150726:-@chrVII:149983:150183:-	1
chrIV:1236642:1236842:+@chrIV:1237609:1237809:+	1
chrIX:47498:47698:+@chrIX:47761:47961:+	1
chrXIII:854616:854816:+@chrXIII:854899:855099:+	1
chrXIII:500152:500352:-@chrXIII:499678:499878:-	1
chrXIV:615866:616066:+@chrXIV:616413:616613:+	0
chrV:348277:348477:-@chrV:348001:348201:-	1

chrXVI:404756:404956:+@chrXVI:405458:405658:+	1
chrXVI:378390:378590:-@chrXVI:377795:377995:-	1
chrXVI:305106:305306:+@chrXVI:305412:305612:+	1
chrXIV:48093:48293:+@chrXIV:48402:48602:+	1
chrXIII:650960:651160:+@chrXIII:651624:651824:+	1
chrV:166875:167075:-@chrV:166571:166771:-	1
chrII:89441:89641:-@chrII:88932:89132:-	1
chrXII:28835:29035:-@chrXII:28262:28462:-	0
chrXII:281629:281829:-@chrXII:281227:281427:-	0
chrII:124954:125154:+@chrII:125271:125471:+	1
chrXV:92831:93031:-@chrXV:92240:92440:-	1
chrIV:1212677:1212877:+@chrIV:1212979:1213179:+	1
chrXVI:96234:96434:-@chrXVI:95953:96153:-	1
chrXII:263005:263205:+@chrXII:263595:263795:+	1
chrXIV:722303:722503:-@chrXIV:721570:721770:-	1
chrII:592769:592969:-@chrII:592216:592416:-	1
chrVII:253249:253449:-@chrVII:252985:253185:-	0
chrX:90894:91094:+@chrX:91412:91612:+	1
chrXIII:558002:558202:-@chrXIII:557628:557828:-	0
chrVIII:126351:126551:+@chrVIII:127113:127313:+	1
chrXII:819130:819330:+@chrXII:819778:819978:+	1
chrXV:423735:423935:-@chrXV:423457:423657:-	0
chrIV:267525:267725:+@chrIV:267807:268007:+	1
chrXII:466255:466455:-@chrXII:456916:457116:-	0
chrIV:314337:314537:-@chrIV:313844:314044:-	1
chrX:365584:365784:+@chrX:365903:366103:+	1
chrXV:241026:241226:-@chrXV:240747:240947:-	1
chrIV:1319698:1319898:-@chrIV:1319417:1319617:-	1
chrI:142053:142253:+@chrI:142620:142820:+	1
chrIV:1450847:1451047:-@chrIV:1450257:1450457:-	1
chrII:332675:332875:+@chrII:333387:333587:+	1
chrVI:223772:223972:-@chrVI:223240:223440:-	1
chrVIII:187677:187877:-@chrVIII:187314:187514:-	1
chrX:703055:703255:-@chrX:702598:702798:-	1
chrIV:308227:308427:+@chrIV:308793:308993:+	1
chrIX:166234:166434:+@chrIX:166520:166720:+	1
chrIV:1355551:1355751:-@chrIV:1355036:1355236:-	1
chrX:75738:75938:+@chrX:76325:76525:+	1
chrII:606080:606280:+@chrII:606669:606869:+	1
chrXV:242505:242705:-@chrXV:242241:242441:-	1
chrXVI:281940:282140:+@chrXVI:282666:282866:+	1
chrX:435027:435227:+@chrX:435344:435544:+	1
chrXIII:337617:337817:+@chrXIII:337904:338104:+	1
chrXIII:732265:732465:+@chrXIII:732876:733076:+	1
chrX:50412:50612:-@chrX:50068:50268:-	1
chrXV:94291:94491:-@chrXV:93643:93843:-	1
chrXII:1028668:1028868:+@chrXII:1029253:1029453:+	1
chrIV:655003:655203:+@chrIV:655273:655473:+	0
chrXIV:64451:64651:-@chrXIV:63818:64018:-	1

chrXII:856374:856574:+@chrXII:857058:857258:+	1
chrXIII:205897:206097:+@chrXIII:206204:206404:+	1
chrVIII:255751:255951:-@chrVIII:255437:255637:-	1
chrVI:221415:221615:-@chrVI:221067:221267:-	1
chrXV:678791:678991:-@chrXV:678179:678379:-	1
chrXI:93466:93666:-@chrXI:93166:93366:-	0
chrIV:1406792:1406992:+@chrIV:1407232:1407432:+	0
chrXVI:172962:173162:+@chrXVI:173572:173772:+	1
chrV:270149:270349:-@chrV:269551:269751:-	1
chrIX:348495:348695:-@chrIX:348163:348363:-	1
chrV:159088:159288:-@chrV:158794:158994:-	1
chrIV:255045:255245:-@chrIV:254774:254974:-	1
chrVI:241809:242009:+@chrVI:242082:242282:+	1
chrXIII:652848:653048:-@chrXIII:652575:652775:-	1
chrII:462009:462209:+@chrII:462290:462490:+	1
chrXI:430597:430797:-@chrXI:430255:430455:-	1
chrII:479145:479345:+@chrII:479435:479635:+	1
chrIV:337324:337524:+@chrIV:337635:337835:+	1
chrXII:564514:564714:-@chrXII:564254:564454:-	1
chrVIII:298485:298685:-@chrVIII:298160:298360:-	1
chrXIII:99376:99576:-@chrXIII:99059:99259:-	1
chrXVI:271103:271303:+@chrXVI:271897:272097:+	0
chrII:415260:415460:-@chrII:414553:414753:-	1
chrII:47147:47347:-@chrII:46858:47058:-	1
chrXIV:622744:622944:+@chrXIV:623287:623487:+	1
chrIV:1266862:1267062:-@chrIV:1266569:1266769:-	1
chrX:649658:649858:-@chrX:649314:649514:-	0
chrII:186428:186628:-@chrII:186152:186352:-	1
chrVIII:138409:138609:-@chrVIII:138040:138240:-	1
chrIV:65106:65306:+@chrIV:65378:65578:+	1
chrXIII:82090:82290:+@chrXIII:82374:82574:+	1
chrXI:282895:283095:+@chrXI:283422:283622:+	1
chrXVI:173465:173665:+@chrXVI:174073:174273:+	1
chrXVI:673548:673748:+@chrXVI:674377:674577:+	0
chrXIII:914649:914849:-@chrXIII:914204:914404:-	0
chrX:469264:469464:-@chrX:468983:469183:-	1
chrV:307546:307746:+@chrV:307849:308049:+	1
chrIV:431473:431673:-@chrIV:431186:431386:-	1
chrXVI:678280:678480:-@chrXVI:677993:678193:-	1
chrXV:373699:373899:+@chrXV:374123:374323:+	0
chrXV:901194:901394:-@chrXV:900567:900767:-	1
chrXVI:244026:244226:-@chrXVI:243289:243489:-	0
chrVI:203387:203587:-@chrVI:203092:203292:-	1
chrVII:859474:859674:-@chrVII:859060:859260:-	1

Table S9. Figure 6B PSI values

event	WT_1_polyA	WT_2_polyA	DBR1_1_poly
chrII:168400:168600:+@chrII:168809:169009:	1	1	1
chrX:50119:50319:-@chrX:50412:50612:-@A3	0.99	0.99	0.99
chrV:396610:396810:+@chrV:397282:397482:	0.06	0.05	0.08
chrXVI:173465:173665:+@chrXVI:174073:174	0.03	0.03	0.06
chrIX:256354:256554:-@chrIX:257027:257227	0.06	0.05	0.08
chrII:691766:691966:+@chrII:692126:692334:	0.96	0.98	0.95
chrII:662381:662581:-@chrII:663003:663203:	0.99	0.98	0.98
chrI:12287:12487:+@chrI:12776:12976:+@no	0.97	0.98	0.98
chrXIII:23160:23360:-@chrXIII:23659:23859:-	0.05	0.12	0.06
chrXIV:5731:5931:-@chrXIV:6080:6280:-@ann	0.74	0.57	0.61
chrIV:1329546:1329746:+@chrIV:1329837:133	1	1	1
chrVI:109748:109948:-@chrVI:110033:110233	0.94	NA	0.92
chrIV:600831:601031:-@chrIV:601140:601340:	1	1	1
chrVII:383285:383485:+@chrVII:383581:3837	0.96	0.98	0.85
chrVII:310815:311015:+@chrVII:311527:3117	0.19	0.11	0.26
chrVIII:558415:558615:+@chrVIII:558715:558	0.99	0.99	0.99
chrIV:601115:601315:+@chrIV:601471:601697	1	1	1
chrXIII:223180:223380:-@chrXIII:223782:223	0.05	0.04	0.06
chrXV:778659:778859:-@chrXV:779387:77958	0.15	0.11	0.16
chrXIII:123542:123742:-@chrXIII:124158:1243	0.08	0.05	0.07
chrXII:457763:457963:+@chrXII:467102:4674	1	1	1
chrIV:229819:230019:+@chrIV:230321:230521	0.08	0.07	0.1
chrXV:80160:80360:+@chrXV:80775:80975:+	0.05	0.04	0.08
chrXVI:75785:75985:-@chrXVI:76224:76424:-	0.05	0.05	0.08
chrII:592216:592416:-@chrII:592769:592969:	0.08	0.05	0.09
chrIV:579278:579478:+@chrIV:580018:58021	0.18	0.1	0.23
chrIV:313844:314044:-@chrIV:314337:314537:	0.48	0.25	0.8
chrXIV:615866:616066:+@chrXIV:616413:616	0.98	0.96	0.99
chrII:604314:604514:+@chrII:604928:605131:	0.14	0.19	0.15
chrX:90894:91094:+@chrX:91412:91612:+@a	0.06	0.05	0.07
chrIV:121877:122077:+@chrIV:122168:122402	0.87	0.81	0.89
chrXIII:652575:652775:-@chrXIII:652848:653	0.63	0.61	0.57
chrVII:497165:497365:-@chrVII:498000:49820	1	1	1
chrXII:786415:786615:+@chrXII:786713:7869	0.83	0.96	0.85
chrX:608106:608306:+@chrX:608582:608782:	0.07	0.03	0.11
chrV:4122:4322:-@chrV:4602:4802:-@annotat	0.97	0.98	0.97
chrXIV:272187:272387:-@chrXIV:273602:2738	0.95	1	0.98
chrXV:30912:31112:+@chrXV:31215:31415:+	0.97	0.99	0.98
chrVII:346608:346808:-@chrVII:346894:34709	0.14	0.17	NA
chrXV:505737:505937:+@chrXV:506339:50653	0.04	0.03	0.05
chrVIII:126351:126551:+@chrVIII:127113:127	0.08	0.03	0.09
chrXII:456916:457116:-@chrXII:466255:46763	0.99	0.98	0.98
chrIV:569433:569633:-@chrIV:569724:569924:	0.47	0.48	0.39
chrIV:306605:306805:-@chrIV:307766:307966:	1	1	1
chrXI:449751:449951:-@chrXI:450021:450221	NA	NA	0.9
chrXV:900567:900767:-@chrXV:901194:90139	0.09	0.07	0.15
chrXI:155071:155271:+@chrXI:155655:15585	0.56	0.72	0.79

chrIV:60278:60478:-@chrIV:61788:61988:-@n	0.5	0.95	0.7
chrXII:454063:454263:+@chrXII:463402:4674	0.74	0.64	0.7
chrXVI:406446:406646:+@chrXVI:407068:407	0.07	0.07	0.08
chrIX:390479:390679:+@chrIX:390812:391012	0.97	0.94	0.93
chrIX:68515:68715:+@chrIX:69150:69350:+@	0.08	0.07	0.1
chrVII:946127:946327:+@chrVII:946421:9466	NA	NA	NA
chrVIII:315571:315771:-@chrVIII:315859:316	NA	0.18	0.21
chrII:479145:479345:+@chrII:479435:479635:	0.37	0.26	0.39
chrV:362712:362912:+@chrV:363093:363293:	0.14	0.12	0.18
chrIV:65106:65306:+@chrIV:65378:65578:+@	0.32	0.37	0.23
chrXVI:281940:282140:+@chrXVI:282666:282	0.03	0.02	0.03
chrV:147994:148194:+@chrV:148283:148483:	0.69	0.83	0.98
chrIV:1506858:1507058:-@chrIV:1507315:150	0.94	0.97	0.94
chrXV:242241:242441:-@chrXV:242505:242705	0.95	0.81	0.88
chrIV:1450257:1450457:-@chrIV:1450847:145	0.05	0.03	0.07
chrIV:337324:337524:+@chrIV:337635:337835	0.18	0.18	0.26
chrII:170420:170620:+@chrII:170805:171005:	1	0.99	1
chrXII:1066884:1067084:+@chrXII:1067364:1	0.78	0.81	0.86
chrI:128321:128521:-@chrI:129022:129222:-@	0.97	0.98	0.98
chrVIII:147916:148116:-@chrVIII:148667:148	0.55	0.42	0.63
chrXIV:494122:494322:-@chrXIV:494974:4951	1	1	1
chrVIII:505047:505247:-@chrVIII:505517:505	0.03	0.02	0.07
chrXVI:445302:445502:-@chrXVI:445577:4457	0.89	0.91	NA
chrX:387148:387348:-@chrX:387436:387636:-	0.7	0.72	0.61
chrX:468983:469183:-@chrX:469264:469606:-	0.92	0.99	0.99
chrII:168224:168424:+@chrII:168809:169009:	0.04	0.04	0.06
chrIV:121877:122077:+@chrIV:122195:122402	0.97	0.93	0.97
chrVIII:498519:498719:-@chrVIII:498787:498	0.51	0.58	0.54
chrXIV:331125:331325:+@chrXIV:331838:332	0.07	0.05	0.1
chrII:342498:342698:+@chrII:342790:342990:	0.9	0.9	0.94
chrII:59949:60149:-@chrII:60698:60898:-@A3	1	1	1
chrII:462009:462209:+@chrII:462290:462490:	0.81	0.89	0.71
chrVII:497165:497365:-@chrVII:497459:49820	0.89	0.67	0.67
chrXI:430255:430455:-@chrXI:430597:430797	0.5	0.38	0.57
chrXVI:138525:138725:+@chrXVI:138865:139	0.16	0.23	0.23
chrXII:788913:789113:-@chrXII:789219:78941	1	1	1
chrX:503570:503770:+@chrX:503982:504182:	0.83	0.97	0.8
chrIX:47498:47698:+@chrIX:47761:47965:+@	0.58	0.61	0.49
chrXIII:537248:537448:+@chrXIII:537565:537	NA	NA	NA
chrXIII:550601:550801:-@chrXIII:551204:551	0.12	0.1	0.15
chrXII:819130:819330:+@chrXII:819778:8199	0.08	0.06	0.1
chrVI:64399:64599:-@chrVI:64921:65121:-@a	0.96	0.57	0.99
chrIV:1319520:1319720:-@chrIV:1319817:132	0.3	0.43	0.63
chrIV:733502:733702:-@chrIV:733776:733976:	0.23	0.29	0.3
chrVII:61931:62131:+@chrVII:62184:62415:+	0.99	0.99	0.99
chrXIV:609590:609790:+@chrXIV:609875:610	0.93	0.94	0.95
chrVIII:255437:255637:-@chrVIII:255751:255	NA	NA	NA
chrIX:348163:348363:-@chrIX:348495:348695	0.21	0.19	0.23
chrVII:72788:72988:-@chrVII:73138:73338:-@	0.21	0.18	0.24

chrXIV:545091:545291:+@chrXIV:545371:5455	0.21	0.42	0.32
chrII:59989:60189:-@chrII:60698:60898:-@A3	1	1	1
chrIII:293739:293939:+@chrIII:293994:29419	NA	NA	NA
chrXIV:426903:427103:+@chrXIV:427193:4273	0.95	0.99	0.98
chrXII:242121:242321:+@chrXII:242681:2433	0.78	0.77	0.79
chrXI:282895:283095:+@chrXI:283422:283622	0.01	0.03	0.03
chrXIII:854616:854816:+@chrXIII:854899:855	0.15	0.18	0.22
chrII:110679:110879:+@chrII:110949:111149:	0.76	0.76	0.9
chrIV:1238430:1238630:-@chrIV:1238825:1239	0.99	1	0.98
chrII:142549:142749:-@chrII:142847:143047:-	0.16	0.14	0.2
chrIV:451211:451411:-@chrIV:451491:451691:	0.99	0.99	0.99
chrXI:155213:155413:+@chrXI:155637:155855	1	1	1
chrXIII:551751:551951:+@chrXIII:552496:552	0.84	0.82	0.85
chrXII:765981:766181:-@chrXII:766250:76645	0.83	0.63	0.92
chrIV:117466:117666:+@chrIV:118158:118358	0.02	0.01	0.04
chrXIV:494324:494524:-@chrXIV:494974:4951	0.14	0.07	0.11
chrXIII:205897:206097:+@chrXIII:206204:206	0.39	0.19	0.35
chrXIV:414711:414911:+@chrXIV:415914:4161	0.02	0.03	0.03
chrIV:254774:254974:-@chrIV:255045:255245:	0.95	0.94	0.89
chrXII:453498:453698:-@chrXII:462837:46763	0.94	0.96	0.95
chrXV:240747:240947:-@chrXV:241026:24122	NA	0.33	0.19
chrXI:220577:220777:+@chrXI:220832:221032	1	1	1
chrVIII:189549:189749:-@chrVIII:189851:190	0.65	0.51	0.59
chrVII:438893:439093:+@chrVII:439324:4395	0.55	0.46	0.54
chrVII:436112:436312:+@chrVII:436375:4365	NA	NA	NA
chrXI:82798:82998:+@chrXI:83075:83275:+@	0.16	0.25	0.19
chrXIV:622744:622944:+@chrXIV:623287:6234	0.19	0.21	0.39
chrXVI:794829:795029:+@chrXVI:795378:7955	0.9	0.9	0.93
chrXII:451857:452057:-@chrXII:461196:46763	0.98	0.89	0.94
chrXIII:650960:651160:+@chrXIII:651624:651	0.22	0.16	0.27
chrV:183969:184169:-@chrV:184678:184878:-	0.7	0.67	0.76
chrX:4381:4581:-@chrX:4970:5170:-@annotate	0.97	0.94	0.97
chrXIV:380489:380689:-@chrXIV:380782:3809	0.23	0.27	0.27
chrXVI:345244:345444:-@chrXVI:345597:3457	0.43	0.39	0.36
chrIV:239198:239398:-@chrIV:239510:239710:	0.15	0.35	0.16
chrXVI:697763:697963:-@chrXVI:698315:6985	0.94	0.96	0.95
chrIII:106833:107033:+@chrIII:107111:10750	0.97	0.97	0.97
chrXII:765873:766073:-@chrXII:766130:76633	0.72	0.71	0.8
chrXIV:185291:185491:+@chrXIV:185567:1857	0.93	0.99	0.99
chrXVI:653967:654167:+@chrXVI:654571:6547	0.07	0.04	0.09
chrIX:98895:99095:-@chrIX:99386:99586:-@a	0.09	0.05	0.1
chrVII:364764:364964:-@chrVII:365433:36563	0.03	0.03	0.05
chrIV:1073112:1073312:-@chrIV:1073402:107	0.56	0.36	0.67
chrX:580147:580347:+@chrX:581053:581253:	1	1	1
chrX:570367:570567:-@chrX:570641:570841:-	1	1	1
chrXV:29475:29675:+@chrXV:30636:30836:+@	0.99	1	0.99
chrX:649314:649514:-@chrX:649658:649858:-	0.74	0.48	0.39
chrII:653168:653368:+@chrII:653453:653725:	0.9	0.97	0.97
chrXIII:236391:236591:+@chrXIII:236954:237	0.18	0.55	0.49

chrII:462229:462429:+@chrII:462500:462700:	0.46	0.51	0.56
chrXVI:942850:943050:+@chrXVI:943199:943	0.98	0.91	0.91
chrXIII:211244:211444:+@chrXIII:211571:211	0.2	0.26	0.32
chrXII:522469:522669:+@chrXII:523029:5232	0.06	0.03	0.07
chrV:432471:432671:+@chrV:433197:433397:	0.05	0.1	0.07
chrXIV:350757:350957:+@chrXIV:351054:3512	0.23	0.23	0.36
chrXVI:656305:656505:-@chrXVI:656576:6567	0.98	0.98	0.98
chrII:332675:332875:+@chrII:333387:333587:	0.07	0.04	0.07
chrXIII:753542:753742:-@chrXIII:754220:7544	0.15	0.09	0.16
chrIV:340610:340810:-@chrIV:341184:341384:	0.06	0.05	0.09
chrXVI:172962:173162:+@chrXVI:173572:1737	0.39	0.89	0.89
chrIV:399161:399361:+@chrIV:399485:399696	0.58	0.56	0.55
chrXVI:677993:678193:-@chrXVI:678280:6784	0.22	0.21	0.25
chrXII:743953:744153:+@chrXII:744288:7444	0.29	0.5	0.78
chrVII:365309:365509:-@chrVII:365986:36618	1	1	1
chrIV:1266569:1266769:-@chrIV:1266862:126	0.54	0.34	0.48
chrVI:75639:75839:+@chrVI:76092:76292:+@	1	1	1
chrXVI:412056:412256:+@chrXVI:412996:413	0.99	1	0.99
chrIV:1236642:1236842:+@chrIV:1237609:123	0.35	0.43	0.41
chrVIII:250955:251155:+@chrVIII:251249:251	0.91	0.95	0.84
chrII:115274:115474:+@chrII:115570:115770:	0.98	0.99	0.99
chrVIII:187314:187514:-@chrVIII:187677:187	0.08	0.06	0.13
chrVIII:138040:138240:-@chrVIII:138409:138	0.16	0.25	0.2
chrX:50068:50268:-@chrX:50412:50612:-@an	0.31	0.36	0.42
chrXI:109377:109577:+@chrXI:109884:110091	0.32	0.3	0.28
chrVII:555630:555830:+@chrVII:556308:5565	0.07	0.05	0.99
chrXIV:365835:366035:+@chrXIV:366158:366	0.48	0.66	0.72
chrXII:453164:453364:-@chrXII:462503:46763	0.96	0.92	0.94
chrXI:158415:158615:+@chrXI:158967:159167	0.16	0.11	0.19
chrII:168354:168554:+@chrII:168809:169009:	1	1	1
chrVII:252985:253185:-@chrVII:253249:25344	0.93	0.96	0.97
chrXI:431834:432034:+@chrXI:432433:432633	0.05	0.03	0.06
chrXIII:610607:610807:+@chrXIII:611037:611	0.93	0.99	0.97
chrVIII:262154:262354:-@chrVIII:262441:262	NA	0.91	NA
chrII:46858:47058:-@chrII:47147:47347:-@an	0.88	0.82	0.96
chrV:306125:306325:+@chrV:306792:306992:	0.06	0.04	0.07
chrXVI:404756:404956:+@chrXVI:405458:405	0.12	0.42	0.51
chrXIII:99059:99259:-@chrXIII:99376:99576:-	0.11	0.11	0.11
chrXIII:914204:914404:-@chrXIII:914649:914	1	0.99	0.99
chrXIII:225691:225891:+@chrXIII:226290:226	0.04	0.04	0.06
chrXI:446951:447151:-@chrXI:447243:447443	0.99	0.99	0.96
chrXI:551480:551680:+@chrXI:552003:552244	0.63	0.59	0.67
chrIV:307133:307333:-@chrIV:307766:307966:	0.06	0.04	0.07
chrVII:920464:920664:+@chrVII:921120:9213	0.42	0.4	0.42
chrXVI:412061:412261:+@chrXVI:413013:413	0.99	1	0.99
chrV:158794:158994:-@chrV:159088:159288:-	0.16	0.15	0.19
chrII:170420:170620:+@chrII:170758:171005:	1	1	1
chrXII:855677:855877:+@chrXII:856428:8566	0.27	0.32	0.27
chrXII:242121:242321:+@chrXII:242691:2433	1	1	1

chrVII:438897:439097:+@chrVII:439324:4395	0.63	0.64	0.65
chrVIII:107631:107831:+@chrVIII:107895:108	0.26	0.36	0.26
chrXII:244185:244385:-@chrXII:245150:24535	1	1	1
chrVII:167154:167354:+@chrVII:167995:1681	0.63	0.58	0.5
chrIV:431186:431386:-@chrIV:431473:431673	0.31	0.39	0.34
chrXIV:728354:728554:+@chrXIV:728922:7291	1	0.99	0.99
chrVII:435479:435679:+@chrVII:435750:4359	NA	NA	NA
chrVII:543438:543638:+@chrVII:543722:5439	0.58	0.77	0.73
chrXII:250660:250860:-@chrXII:250948:25114	NA	NA	NA
chrII:366302:366502:-@chrII:366585:366785:-	0.68	0.71	0.91
chrV:269551:269751:-@chrV:270149:270349:-	0.07	0.05	0.09
chrII:606080:606280:+@chrII:606669:606869:	0.06	0.05	0.07
chrIII:106833:107033:+@chrIII:107305:10750	0.73	0.6	0.65
chrV:348001:348201:-@chrV:348277:348487:-	0.45	0.39	0.45
chrIV:629705:629905:+@chrIV:630174:630374	0.17	0.18	0.23
chrXV:911885:912085:-@chrXV:912433:91263	0.98	0.99	0.98
chrIV:1406792:1406992:+@chrIV:1407232:140	0.96	0.98	0.98
chrIV:1355036:1355236:-@chrIV:1355551:135	0.11	0.07	0.16
chrXVI:794829:795029:+@chrXVI:795395:795	0.13	0.12	0.11
chrXVI:29340:29540:+@chrXVI:29659:29859:+	0.96	0.98	0.97
chrII:170476:170676:+@chrII:170805:171005:	0.18	0.2	0.24
chrX:156589:156789:-@chrX:157250:157450:-	0.04	0.03	0.08
chrVII:439181:439381:+@chrVII:439480:4396	1	1	1
chrVII:726838:727038:+@chrVII:727358:7275	0.03	0.03	0.08
chrXII:281227:281427:-@chrXII:281629:28182	1	0.99	1
chrXV:505737:505937:+@chrXV:505996:50653	1	1	1
chrXVI:911076:911276:+@chrXVI:911353:911	0.14	0.12	0.18
chrVII:249686:249886:+@chrVII:250087:2502	0.09	0.18	0.17
chrXI:618174:618374:-@chrXI:618743:618943	0.37	0.36	0.73
chrII:679742:679942:-@chrII:680040:680240:-	0.22	0.34	0.22
chrVIII:129328:129528:+@chrVIII:129648:129	0.12	0.13	0.17
chrIV:601163:601363:-@chrIV:601518:601718:	1	1	1
chrVII:1084682:1084882:+@chrVII:1085031:1	0.72	0.58	0.6
chrXII:242121:242321:+@chrXII:242827:2433	0.98	0.98	0.99
chrXIV:62172:62372:-@chrXIV:62924:63124:-	0.11	0.08	0.13
chrV:468041:468241:+@chrV:468388:468588:	0.98	0.99	0.99
chrIV:457817:458017:-@chrIV:458098:458298:	0.4	0.32	0.26
chrXII:3715:3915:-@chrXII:4015:4215:-@anno	0.99	0.99	0.98
chrVII:365326:365526:-@chrVII:365986:36618	0.15	0.16	0.29
chrII:565550:565750:+@chrII:566936:567136:	0.99	0.98	0.99
chrXII:694182:694382:+@chrXII:694473:6946	0.28	NA	0.34
chrIX:23243:23443:+@chrIX:23765:23965:+@	0.99	1	0.99
chrXIII:337617:337817:+@chrXIII:337904:338	0.28	0.29	0.43
chrXV:92240:92440:-@chrXV:92831:93031:-@	0.08	0.05	0.09
chrIV:1401600:1401800:+@chrIV:1402185:140	0.16	0.1	0.16
chrIX:155022:155222:+@chrIX:155311:155511	0.46	0.23	0.53
chrXII:898348:898548:+@chrXII:898646:8988	0.2	0.16	0.31
chrII:186152:186352:-@chrII:186428:186628:-	0.39	0.4	0.34
chrVIII:298160:298360:-@chrVIII:298485:2986	0.11	0.12	NA

chrXII:327058:327258:-@chrXII:327400:32760	0.2	0.16	0.34
chrXIII:499678:499878:-@chrXIII:500152:5003	0.09	0.07	0.08
chrII:392980:393180:+@chrII:393511:393870:	0.66	0.61	0.62
chrIV:1359769:1359969:+@chrIV:1360405:136	0.06	0.07	0.08
chrXIV:282424:282624:-@chrXIV:282685:2830	1	1	1
chrXIII:3591:3791:-@chrXIII:3891:4091:-@an	0.99	0.98	0.96
chrIX:231757:231957:-@chrIX:232367:232567	0.06	0.04	0.09
chrVII:946120:946320:+@chrVII:946421:9466	NA	NA	NA
chrIV:1103609:1103809:+@chrIV:1103893:110	0.45	0.52	0.63
chrXIII:732265:732465:+@chrXIII:732876:733	0.05	0.04	0.1
chrXII:456244:456444:-@chrXII:465583:46763	1	0.96	1
chrXII:982258:982458:-@chrXII:982539:98273	0.68	0.77	0.34
chrIV:267525:267725:+@chrIV:267807:268007	0.38	0.23	0.39
chrII:414553:414753:-@chrII:415260:415460:-	0.07	0.08	0.11
chrVII:937012:937212:+@chrVII:937321:9375	0.99	0.99	0.99
chrV:548352:548552:+@chrV:548645:548845:-	0.95	0.98	0.96
chrXIII:517363:517563:+@chrXIII:517886:518	0.08	0.15	0.33
chrI:87187:87387:+@chrI:87501:87701:+@an	0.13	0.22	0.17
chrIV:417021:417221:-@chrIV:417627:417827:	0.32	0.29	0.53
chrXVI:716849:717049:-@chrXVI:717147:7173	0.99	1	0.99
chrIV:306605:306805:-@chrIV:307074:307274:	1	1	1
chrIV:121877:122077:+@chrIV:122187:122402	0.73	0.76	0.89
chrVII:156999:157199:-@chrVII:157283:15748	NA	NA	NA
chrXVI:377795:377995:-@chrXVI:378390:3785	0.03	0.03	0.05
chrXIV:185291:185491:+@chrXIV:185587:1857	0.42	0.27	0.38
chrX:399992:400192:+@chrX:400256:400510:-	0.98	0.98	0.98
chrXII:712525:712725:-@chrXII:713156:71335	0.08	0.08	0.2
chrXII:242121:242321:+@chrXII:242776:2433	1	1	1
chrVI:221067:221267:-@chrVI:221415:221615	0.1	0.08	0.13
chrXIV:283523:283723:+@chrXIV:283806:2840	NA	NA	NA
chrIV:217402:217602:+@chrIV:218008:218208	0.03	0.03	0.08
chrXVI:582358:582558:-@chrXVI:582702:5832	0.43	0.52	0.65
chrV:423624:423824:+@chrV:423952:424152:-	0.14	0.11	0.22
chrX:435027:435227:+@chrX:435344:435544:-	0.1	0.09	0.14
chrVI:241809:242009:+@chrVI:242082:242282	0.81	0.73	0.67
chrXII:550258:550458:-@chrXII:550575:55077	0.37	0.33	0.5
chrVIII:103417:103617:-@chrVIII:103857:1040	0.98	0.98	0.98
chrVIII:382106:382306:-@chrVIII:382748:382	0.06	0.07	0.14
chrI:150806:151006:-@chrI:151097:151297:-@	NA	NA	NA
chrIV:169150:169350:+@chrIV:169602:169802	1	1	1
chrXIII:559582:559782:+@chrXIII:560158:560	0.29	0.3	0.34
chrX:365584:365784:+@chrX:365903:366103:-	0.22	0.19	0.16
chrXIII:666733:666933:-@chrXIII:667018:6672	0.66	0.3	0.69
chrXVI:492718:492918:-@chrXVI:493021:4932	0.32	0.16	0.39
chrXV:296475:296675:+@chrXV:297193:29739	0.95	0.97	0.93
chrVII:61931:62131:+@chrVII:62197:62415:+	0.98	0.96	0.98
chrXII:787494:787694:+@chrXII:788229:7884	1	1	1
chrIX:4398:4598:-@chrIX:4987:5187:-@annota	0.98	0.94	0.98
chrIV:1329546:1329746:+@chrIV:1329816:133	1	1	1

chrIV:655003:655203:+@chrIV:655273:655473	1	1	1
chrXIII:720998:721198:-@chrXIII:721346:7215	0.32	0.33	0.34
chrXIV:557374:557574:+@chrXIV:557685:5578	0.99	0.99	0.99
chrV:307756:307956:+@chrV:308068:308268:	0.12	0.18	0.27
chrXVI:271103:271303:+@chrXVI:271897:2720	1	1	1
chrXIII:424797:424997:+@chrXIII:425154:425	0.12	0.12	0.14
chrXII:28262:28462:-@chrXII:28835:29035:-@	0.93	0.94	0.95
chrV:369220:369420:-@chrV:369489:369689:-	0.99	0.98	0.98
chrVII:61931:62131:+@chrVII:62190:62415:+	0.42	0.51	0.68
chrVIII:104205:104405:+@chrVIII:104804:105	0.08	0.07	0.09
chrII:110220:110420:-@chrII:110506:110706:	0.14	0.17	0.2
chrXVI:305106:305306:+@chrXVI:305412:3056	0.23	0.18	0.35
chrVI:203092:203292:-@chrVI:203387:203587	0.41	0.34	0.45
chrXIII:557628:557828:-@chrXIII:558002:5582	1	1	1
chrXIV:557410:557610:+@chrXIV:557685:5578	0.5	0.54	0.55
chrXII:931149:931349:-@chrXII:931699:93189	0.03	0.03	0.05
chrXII:398332:398532:+@chrXII:398627:3988	NA	0.31	NA
chrXII:9250:9450:-@chrXII:9550:9750:-@anno	0.99	0.99	0.98
chrV:131576:131776:+@chrV:131900:132100:	0.13	0.15	0.22
chrIV:491359:491559:+@chrIV:491899:492099	0.05	0.04	0.06
chrXVI:303361:303561:+@chrXVI:303625:3038	1	1	1
chrXVI:883187:883387:+@chrXVI:883487:8836	0.11	0.09	0.12
chrIV:1319417:1319617:-@chrIV:1319698:1319	0.37	0.45	0.78
chrXIV:443626:443826:-@chrXIV:444172:4443	0.08	0.09	0.1
chrVIII:525903:526103:-@chrVIII:526207:5264	0.93	0.96	0.98
chrI:128314:128514:-@chrI:129022:129222:-@	0.98	1	0.99
chrXV:678179:678379:-@chrXV:678791:678991	0.03	0.03	0.08
chrXVI:218446:218646:+@chrXVI:218747:2189	0.75	0.79	0.65
chrXIV:721570:721770:-@chrXIV:722303:7225	0.04	0.17	0.14
chrXII:1024372:1024572:+@chrXII:1024655:1	NA	NA	0.9
chrIX:23556:23756:-@chrIX:23865:24065:-@n	0.99	1	0.99
chrXV:349297:349497:-@chrXV:349599:349799	0.97	0.98	0.98
chrVI:63659:63859:-@chrVI:63974:64174:-@a	0.27	0.15	0.35
chrIII:101433:101633:-@chrIII:101701:101901	0.18	0.22	0.24
chrXVI:95953:96153:-@chrXVI:96234:96434:-	0.51	0.55	0.61
chrXII:986941:987141:+@chrXII:987222:98755	0.99	0.99	0.99
chrV:239423:239623:-@chrV:239712:239912:-	NA	NA	NA
chrIV:1212677:1212877:+@chrIV:1212979:121	0.28	0.28	0.25
chrI:142053:142253:+@chrI:142620:142820:+	0.06	0.08	0.08
chrII:59993:60193:-@chrII:60698:60898:-@an	0.05	0.04	0.05
chrVII:859060:859260:-@chrVII:859474:85967	0.26	0.37	0.33
chrXIII:139890:140090:-@chrXIII:140184:1403	0.14	0.22	0.25
chrXII:286267:286467:-@chrXII:286557:28675	0.34	0.27	0.33
chrII:601903:602103:+@chrII:602217:602417:	0.98	0.95	0.98
chrIV:215957:216157:+@chrIV:216513:216722	0.69	0.69	0.8
chrXIV:144949:145149:-@chrXIV:145255:14545	0.12	0.19	0.18
chrII:426316:426516:-@chrII:426874:427074:	0.71	0.76	0.75
chrVII:682748:682948:-@chrVII:683066:68326	0.98	0.98	0.98
chrIII:294039:294239:+@chrIII:294292:29449	NA	NA	NA

chrIV:427266:427466:+@chrIV:427575:427775	0.19	0.2	0.27
chrXIV:282424:282624:-@chrXIV:282760:2830	1	1	1
chrXI:625701:625901:+@chrXI:625977:626187	0.68	0.7	0.7
chrVIII:1697:1897:-@chrVIII:2671:2871:-@an	1	0.99	1
chrXVI:623377:623577:+@chrXVI:623711:6239	0.1	0.1	0.1
chrXI:437637:437837:+@chrXI:437914:438126	0.94	0.92	0.97
chrVI:54177:54377:-@chrVI:54687:54887:-@a	0.02	0.04	0.04
chrVI:223240:223440:-@chrVI:223728:223928	0.18	0.14	0.21
chrIX:316571:316771:+@chrIX:317172:317372	0.05	0.05	0.07
chrX:73596:73796:+@chrX:74205:74405:+@a	0.27	0.56	0.59
chrXII:1028668:1028868:+@chrXII:1029253:1	0.15	0.11	0.21
chrXIV:62161:62361:-@chrXIV:62924:63124:-@	0.99	1	1
chrXII:40021:40221:-@chrXII:40401:40601:-@	0.08	0.1	0.1
chrXIV:48093:48293:+@chrXIV:48402:48602:+	0.16	0.16	0.21
chrXII:452765:452965:-@chrXII:462104:46763	0.63	0.72	0.65
chrXIII:82090:82290:+@chrXIII:82374:82574:	0.25	0.2	0.31
chrVII:534273:534473:-@chrVII:534782:53498	0.09	0.08	0.12
chrIII:172915:173115:-@chrIII:173199:173399	0.2	0.23	0.26
chrXV:93643:93843:-@chrXV:94291:94491:-@a	0.02	0.02	0.03
chrXVI:243289:243489:-@chrXVI:244026:2442	0.99	0.99	1
chrXI:447506:447706:-@chrXI:447811:448011	0.32	0.21	0.43
chrXIII:163108:163308:-@chrXIII:163717:1639	0.05	0.07	0.09
chrXV:552465:552665:-@chrXV:552875:553075	0.1	0.13	0.13
chrII:3916:4116:-@chrII:4216:4416:-@annotat	0.99	0.99	0.99
chrII:124954:125154:+@chrII:125271:125471:	0.09	0.1	0.11
chrIV:1329525:1329725:+@chrIV:1329816:133	1	1	1
chrXII:548477:548677:-@chrXII:548764:54896	0.35	0.26	0.39
chrIV:715047:715247:-@chrIV:715359:715559:	0.25	0.39	0.29
chrXIII:225039:225239:-@chrXIII:225339:2255	0.36	0.26	0.45
chrX:702598:702798:-@chrX:703055:703255:-	0.04	0.04	0.09
chrIII:177706:177906:-@chrIII:178214:178414	0.03	0.03	0.06
chrII:392980:393180:+@chrII:393508:393870:	0.95	0.95	0.93
chrIX:225609:225809:-@chrIX:225900:226100	NA	NA	NA
chrXVI:673548:673748:+@chrXVI:674377:6745	1	1	1
chrIX:166234:166434:+@chrIX:166520:16672	0.43	0.33	0.29
chrXVI:729185:729385:-@chrXVI:729482:7296	0.06	0.19	0.18
chrXIII:551751:551951:+@chrXIII:552508:552	0.89	0.9	0.95
chrXII:263005:263205:+@chrXII:263595:26379	0.12	0.11	0.28
chrXIV:534674:534874:-@chrXIV:534966:5351	0.25	0.23	0.39
chrVIII:354664:354864:+@chrVIII:354956:355	0.28	0.34	0.38
chrII:406827:407027:-@chrII:407123:407323:	0.09	0.09	0.07
chrIII:111357:111557:-@chrIII:111634:111834	0.94	0.86	0.93
chrXII:856374:856574:+@chrXII:857058:85725	0.42	0.37	0.62
chrIV:308227:308427:+@chrIV:308793:308993	0.06	0.06	0.11
chrXIV:63818:64018:-@chrXIV:64451:64651:-@	0.16	0.19	0.35
chrXII:986941:987141:+@chrXII:987213:98755	0.94	0.92	0.93
chrX:75738:75938:+@chrX:76325:76525:+@a	0.04	0.02	0.09
chrXV:866949:867149:+@chrXV:867587:86778	0.08	0.06	0.07
chrXV:373699:373899:+@chrXV:374123:37432	0.98	0.99	0.98

chrV:307546:307746:+@chrV:307849:308049:-	0.15	0.18	0.18
chrXIV:282424:282624:-@chrXIV:282745:2830	1	1	1
chrXVI:833493:833693:+@chrXVI:833828:834	0.89	0.59	0.8
chrXV:423457:423657:-@chrXV:423735:42393	0.99	1	0.99
chrXII:233442:233642:-@chrXII:233886:23408	1	1	1
chrX:396293:396493:-@chrX:396571:396771:-	0.19	0.27	0.37
chrXVI:5640:5840:-@chrXVI:5989:6189:-@ann	0.73	0.58	0.61
chrIV:322082:322282:+@chrIV:322704:322904	0.01	0.01	0.03
chrVII:31226:31426:-@chrVII:31579:31779:-@	NA	NA	NA
chrXI:155071:155271:+@chrXI:155637:15585	0.69	0.66	0.6
chrV:166571:166771:-@chrV:166875:167075:-	0.16	0.19	0.18
chrXI:437637:437837:+@chrXI:437906:43812	0.67	0.79	0.71
chrII:726717:726917:-@chrII:727012:727212:-	0.7	0.4	0.59
chrXII:564254:564454:-@chrXII:564514:56471	0.68	0.62	NA
chrXI:93166:93366:-@chrXI:93466:93666:-@n	0.41	0.52	0.61

DBR1_2_poly	UPF1_2_polyA	UPF1_1_polyA	DBR1_1_riboZ	DBR1_2_riboZ	sk1_2_riboZer
1	1	1	1	1	1
0.99	0.99	0.99	0.97	0.97	0.89
0.07	0.09	0.08	0.97	0.97	0.03
0.07	0.04	0.03	0.32	0.42	0.04
0.06	0.07	0.08	1	1	0.03
0.98	0.97	0.84	0.98	0.99	0.96
0.97	0.99	0.99	0.87	0.97	0.88
0.97	0.99	0.99	0.96	0.99	0.73
0.11	0.1	0.08	0.86	0.93	0.09
0.69	0.47	0.54	0.82	0.92	0.42
1	1	1	0.99	0.99	0.99
NA	0.92	0.91	NA	NA	NA
1	1	1	1	1	0.96
0.88	0.95	0.94	0.96	0.89	0.94
0.22	0.76	0.67	0.88	0.91	0.1
0.98	0.99	1	0.99	0.99	0.77
1	1	1	1	1	1
0.06	0.07	0.06	1	1	0.05
0.15	0.18	0.14	0.98	0.98	0.24
0.08	0.12	0.1	0.95	0.94	0.04
0.99	1	1	1	0.89	1
0.09	0.15	0.13	0.89	0.85	0.03
0.1	0.07	0.07	0.95	0.96	0.07
0.11	0.09	0.08	0.97	0.98	0.09
0.08	0.11	0.11	0.93	0.93	0.04
0.17	0.5	0.46	1	1	0.06
0.69	0.45	0.48	0.98	0.98	0.33
0.99	0.99	0.99	0.98	0.98	0.94
0.26	0.19	0.17	0.94	0.96	0.24
0.08	0.08	0.07	0.96	0.95	0.05
0.97	0.94	0.89	0.8	0.69	0.88
0.62	0.79	0.63	0.5	0.51	0.59
1	1	1	1	1	1
0.92	0.95	0.97	NA	NA	NA
0.14	0.11	0.08	1	1	0.06
0.96	0.98	0.97	1	1	0.83
0.99	0.99	0.98	0.93	0.86	0.79
0.98	0.98	0.97	0.99	0.99	1
0.21	0.17	0.24	0.27	0.33	NA
0.04	0.05	0.05	0.99	0.99	0.05
0.06	0.1	0.08	0.93	0.94	0.03
0.99	1	1	1	0.83	1
0.52	0.6	0.63	0.36	0.33	NA
1	1	1	1	1	1
0.94	NA	0.94	0.91	NA	NA
0.24	0.14	0.13	1	1	0.06
0.48	0.5	0.46	1	1	0.53

0.5	0.43	0.51	0.78	0.92	0.69
0.82	0.71	0.73	1	0.77	1
0.1	0.09	0.08	0.95	0.95	0.08
0.94	0.97	0.98	NA	NA	0.98
0.1	0.1	0.09	1	1	0.06
NA	NA	0.95	NA	NA	NA
0.35	0.29	0.26	NA	NA	NA
0.36	0.29	0.43	NA	NA	NA
0.21	0.2	0.2	1	1	0.13
0.22	0.29	0.17	0.44	0.58	0.54
0.03	0.04	0.04	0.99	0.99	0.03
0.94	0.98	0.99	0.72	0.59	0.55
0.95	0.97	0.97	0.84	NA	0.73
0.93	0.91	0.96	NA	NA	NA
0.12	0.08	0.07	0.79	0.8	0.04
0.19	0.2	0.2	0.23	0.33	0.22
0.99	1	1	0.98	0.99	0.97
0.88	0.9	0.84	0.99	0.99	0.69
0.96	0.98	0.96	0.99	0.99	1
0.48	0.64	0.58	1	1	0.38
1	1	1	1	1	1
0.43	0.05	0.05	0.96	0.96	0.04
NA	0.87	0.89	NA	NA	NA
0.69	0.88	0.52	NA	NA	NA
0.99	0.99	0.99	0.96	0.98	0.78
0.06	0.07	0.07	0.98	0.98	0.02
0.9	0.9	0.9	0.95	0.85	0.76
0.68	0.3	0.26	0.86	0.9	NA
0.08	0.15	0.15	0.98	0.98	0.04
0.97	0.95	0.97	NA	NA	NA
1	1	1	1	1	1
0.96	0.96	0.95	0.73	0.72	0.61
0.71	0.64	0.68	0.99	0.99	0.98
0.51	0.59	0.63	0.7	0.7	0.44
0.24	0.26	0.25	0.2	0.16	0.19
1	1	1	0.98	0.97	0.47
0.91	0.73	0.94	0.94	0.92	NA
0.64	0.68	0.66	0.46	0.38	0.48
NA	NA	0.6	NA	NA	NA
0.17	0.22	0.19	1	1	0.07
0.08	0.1	0.09	1	1	0.08
0.96	1	1	1	1	0.66
0.54	0.55	0.32	0.41	0.6	NA
0.31	0.39	0.37	0.34	0.35	0.22
0.99	0.98	0.98	0.98	0.97	0.99
0.93	0.98	0.98	NA	NA	NA
0.42	NA	NA	0.88	0.84	0.9
0.24	0.3	0.35	0.28	0.24	0.33
0.24	0.19	0.22	0.43	0.42	0.28

0.4	0.42	0.42	0.33	0.42	0.21
1	1	1	1	1	1
NA	NA	NA	NA	NA	NA
0.99	0.97	0.97	0.99	0.99	0.98
0.79	0.77	0.78	0.92	0.91	0.79
0.05	0.02	0.02	0.98	0.98	0.05
0.21	0.23	0.2	0.27	0.28	0.15
0.84	0.97	0.96	0.82	0.66	0.83
0.99	0.99	0.99	0.87	0.91	0.8
0.23	0.26	0.27	0.42	0.41	0.62
0.99	0.99	1	0.99	0.99	0.98
0.99	0.99	1	1	1	1
0.84	0.86	0.85	1	1	0.83
0.89	0.77	0.69	0.88	NA	NA
0.04	0.06	0.05	0.98	0.99	0.02
0.11	0.16	0.17	0.97	0.97	0.2
0.3	0.21	0.25	0.59	0.68	0.47
0.03	0.03	0.05	0.55	0.69	0.15
0.98	0.99	0.98	0.95	0.96	0.94
0.98	0.99	0.99	1	0.98	1
0.31	0.42	0.31	NA	NA	NA
1	1	1	1	1	0.94
0.57	0.68	0.69	0.26	0.23	0.15
0.5	0.59	0.58	0.93	1	0.39
NA	NA	NA	NA	NA	NA
0.31	0.17	0.2	0.47	0.37	NA
0.3	0.63	0.54	0.98	0.98	0.22
0.93	0.93	0.92	1	1	0.95
0.87	1	1	1	0.87	1
0.24	0.37	0.38	0.99	0.99	0.12
0.72	0.97	0.97	0.62	0.81	0.56
0.95	0.99	0.98	0.99	0.99	0.84
0.29	0.23	0.3	0.33	0.3	0.3
0.58	0.59	0.52	0.5	0.38	0.38
0.33	0.28	0.24	0.19	0.17	0.16
0.97	0.98	0.97	0.89	0.88	NA
0.98	0.96	0.96	0.94	0.95	0.96
0.77	0.85	0.87	0.88	0.9	NA
0.97	0.97	1	0.95	0.92	0.99
0.07	0.11	0.1	0.98	0.98	0.03
0.16	0.14	0.13	1	1	0.08
0.06	0.05	0.04	1	1	0.04
0.3	0.67	0.55	0.83	0.72	0.67
1	1	1	0.99	0.99	0.99
1	1	1	0.99	0.99	0.99
1	0.99	1	0.99	0.99	0.99
0.56	0.95	0.79	NA	NA	0.66
0.97	0.97	0.97	0.97	0.97	0.93
0.86	0.29	0.29	0.59	0.68	0.25

0.52	0.32	0.35	0.52	0.45	NA
0.85	0.88	0.88	0.97	0.99	0.96
0.22	0.22	0.29	NA	NA	NA
0.13	0.09	0.07	0.92	0.94	0.04
0.14	0.05	0.05	1	1	0.19
0.35	0.31	0.25	0.29	0.38	0.2
0.98	0.98	0.99	0.98	0.99	0.92
0.06	0.11	0.1	1	1	0.05
0.11	0.2	0.18	1	1	0.05
0.09	0.15	0.14	1	1	0.04
0.98	0.95	0.95	1	1	0.98
0.51	0.6	0.56	0.43	0.37	0.56
0.26	0.28	0.27	0.29	0.27	0.26
0.76	0.49	0.56	0.9	0.73	NA
1	1	1	1	1	1
0.4	0.47	0.49	0.65	0.63	0.91
1	1	1	1	0.99	0.84
1	0.99	0.98	1	1	0.97
0.35	0.42	0.36	0.97	0.97	0.22
0.86	0.93	0.91	0.95	0.9	0.92
0.98	0.98	0.98	0.96	0.95	0.98
0.09	0.14	0.13	0.08	0.09	0.07
0.39	0.2	0.21	0.22	0.29	NA
0.62	0.44	0.49	0.39	0.29	0.27
0.33	0.28	0.27	0.97	0.97	0.25
0.99	0.1	0.09	1	1	0.06
0.91	0.72	0.89	0.7	0.79	0.43
0.97	0.98	0.99	1	0.98	1
0.48	0.24	0.2	1	1	0.15
1	1	1	1	1	1
0.96	0.96	0.89	0.91	0.83	0.91
0.05	0.1	0.08	0.98	0.98	0.02
0.98	0.99	0.99	0.86	0.93	0.89
NA	NA	NA	NA	NA	NA
0.93	0.97	0.97	0.54	0.84	0.51
0.06	0.13	0.1	0.94	0.94	0.02
1	0.37	0.35	1	1	0.24
0.13	0.15	0.12	0.16	0.21	0.16
0.99	0.99	1	0.99	0.99	0.98
0.06	0.07	0.06	0.86	0.89	0.04
0.98	0.99	1	0.92	0.96	0.95
0.63	0.67	0.66	1	1	0.47
0.08	0.09	0.08	0.97	0.98	0.04
0.4	0.38	0.41	0.79	0.79	0.53
1	0.99	1	1	1	0.97
0.22	0.19	0.21	0.19	0.18	0.24
1	0.99	0.99	0.99	0.99	0.97
0.24	0.48	0.45	0.37	0.34	0.47
1	1	1	1	1	1

0.62	0.71	0.72	0.99	1	0.76
0.44	0.37	0.34	NA	NA	0.1
1	1	1	0.98	0.99	0.97
0.58	0.59	0.62	1	1	0.71
0.51	0.5	0.52	0.22	0.18	0.21
0.99	0.99	0.98	0.99	0.99	1
NA	NA	NA	NA	NA	NA
0.7	0.94	0.91	0.22	0.21	0.34
NA	0.92	0.92	NA	NA	NA
0.77	0.89	0.71	0.72	0.56	0.82
0.08	0.1	0.11	1	1	0.04
0.08	0.1	0.1	0.92	0.91	0.06
0.62	0.71	0.61	0.73	0.79	0.75
0.48	0.54	0.27	0.38	0.37	0.39
0.24	0.27	0.24	0.37	0.35	0.44
0.98	1	1	0.98	0.98	NA
0.94	0.98	0.99	0.99	1	0.83
0.14	0.18	0.18	0.97	0.98	0.1
0.11	0.13	0.12	0.88	0.87	0.07
0.98	0.98	0.99	0.96	0.97	NA
0.21	0.23	0.23	0.49	0.44	0.41
0.13	0.08	0.07	1	1	0.02
1	1	1	1	1	1
0.07	0.06	0.05	0.98	0.98	0.04
0.99	1	1	0.99	0.99	0.99
1	1	1	0.93	0.9	1
0.18	0.21	0.18	0.21	0.29	0.27
0.2	0.16	0.21	0.39	0.52	0.24
0.7	0.54	0.51	1	1	0.54
0.33	0.22	0.3	0.22	0.18	0.15
0.23	0.14	0.14	NA	NA	NA
1	1	1	1	1	1
0.69	0.47	0.54	0.84	0.93	0.4
0.97	0.97	0.97	1	1	1
0.1	0.13	0.12	0.99	0.98	0.09
0.99	0.99	1	0.93	0.9	NA
0.5	0.22	0.21	0.68	0.72	0.89
0.98	0.99	0.99	0.99	1	0.91
0.46	0.2	0.17	0.99	0.99	0.2
0.98	0.99	0.99	0.96	0.97	0.97
0.35	0.23	0.32	NA	NA	NA
1	0.99	0.99	1	1	1
0.27	0.3	0.32	0.43	0.36	0.39
0.09	0.14	0.11	1	1	0.04
0.13	0.3	0.25	0.99	0.99	0.09
0.36	0.63	0.54	0.43	0.36	0.63
0.22	0.34	0.34	1	1	0.2
0.32	0.46	0.44	0.43	0.63	0.76
0.15	0.22	0.14	NA	0.28	NA

0.29	0.31	0.26	0.32	0.41	0.39
0.08	0.08	0.08	1	1	0.07
0.65	0.6	0.63	1	1	0.56
0.07	0.08	0.07	0.99	0.99	0.12
1	1	1	1	0.99	0.97
0.97	0.98	0.98	0.99	0.99	NA
0.07	0.12	0.1	0.96	0.96	0.03
NA	NA	0.93	NA	NA	NA
0.66	0.56	0.44	NA	NA	NA
0.1	0.09	0.08	1	1	0.07
0.98	1	1	1	0.96	1
0.62	0.7	0.87	NA	0.47	NA
0.34	0.48	0.49	0.41	NA	0.53
0.16	0.16	0.14	0.99	0.99	0.04
0.99	1	1	0.99	0.98	0.97
0.98	0.98	0.99	NA	NA	NA
0.97	0.16	0.08	1	1	0.34
0.29	0.21	0.17	0.19	0.19	0.23
0.47	0.38	0.47	0.87	0.72	0.19
0.99	0.99	0.99	0.96	0.98	0.98
1	1	1	1	1	1
0.95	0.87	0.93	0.84	0.94	0.94
NA	NA	NA	NA	NA	NA
0.05	0.05	0.04	0.92	0.9	0.03
0.37	0.37	0.26	0.78	0.66	0.48
0.96	0.97	0.98	0.95	0.98	0.83
0.24	0.16	0.15	0.91	0.95	0.03
1	1	1	1	1	1
0.11	0.23	0.19	0.09	0.07	0.06
NA	NA	NA	NA	NA	NA
0.13	0.09	0.09	1	1	0.02
0.57	0.56	0.66	0.92	0.84	0.43
0.18	0.28	0.25	1	0.99	0.1
0.16	0.32	0.28	0.16	0.14	0.12
0.87	0.71	0.69	0.63	0.69	NA
0.43	0.47	0.35	0.69	0.81	0.44
0.99	0.99	1	1	1	0.99
0.17	0.11	0.11	0.86	0.86	0.07
NA	NA	NA	0.66	NA	NA
1	1	1	0.99	0.99	0.98
0.34	0.41	0.39	0.72	0.58	0.39
0.22	0.19	0.13	0.11	0.17	0.13
0.75	0.47	0.65	0.63	0.73	NA
0.27	0.46	0.31	0.42	0.49	0.28
0.97	0.97	0.99	0.94	0.94	NA
0.98	0.88	0.95	0.92	0.96	0.97
1	1	1	1	0.99	0.99
0.95	0.99	0.98	0.99	0.99	0.84
1	1	0.99	0.99	0.99	0.99

1	1	1	0.99	0.97	0.98
0.47	0.57	0.55	0.32	0.31	0.31
0.99	0.99	0.99	0.96	0.98	0.97
0.35	0.13	0.14	0.17	0.2	NA
1	1	1	0.99	0.98	0.98
0.14	0.13	0.2	0.13	0.13	0.07
0.95	0.97	0.97	0.98	0.99	0.95
0.98	0.99	0.98	0.98	0.97	0.99
0.63	0.67	0.65	0.67	0.66	0.62
0.1	0.14	0.12	1	1	0.02
0.24	0.15	0.18	0.18	0.2	0.12
0.3	0.38	0.43	0.32	0.33	0.36
0.38	0.35	0.4	0.16	0.22	NA
1	1	1	1	0.99	1
0.52	0.48	0.46	0.81	0.68	0.52
0.05	0.06	0.06	1	1	0.05
0.5	0.56	NA	NA	NA	NA
0.98	0.98	0.99	1	0.99	0.92
0.27	0.22	0.18	NA	NA	NA
0.04	0.07	0.06	0.94	0.93	0.04
1	1	1	1	1	1
0.09	0.16	0.12	0.16	0.17	0.14
0.86	0.38	0.55	0.45	0.44	0.33
0.17	0.13	0.13	0.99	0.99	0.08
0.91	0.96	0.98	0.95	0.94	NA
1	1	1	1	1	1
0.07	0.09	0.08	0.95	0.95	0.02
0.64	0.83	0.9	0.86	0.68	0.64
0.7	0.06	0.06	1	1	0.99
NA	0.94	0.86	NA	NA	NA
0.99	0.99	0.99	1	0.99	NA
0.98	0.96	0.97	0.88	0.91	NA
0.28	0.4	0.2	0.92	0.69	0.95
0.2	0.23	0.14	0.18	0.3	0.33
0.72	0.87	0.81	0.45	0.4	0.64
0.99	0.99	1	0.98	0.96	0.98
NA	0.94	0.97	NA	NA	NA
0.27	0.34	0.34	0.17	0.13	0.13
0.32	0.07	0.05	0.97	0.97	0.1
0.05	0.07	0.06	0.62	0.68	0.07
0.46	0.45	0.4	1	1	0.34
0.31	0.44	0.28	NA	NA	0.18
0.38	0.46	0.34	0.44	0.37	0.39
0.98	0.99	0.99	0.94	0.89	NA
0.91	0.8	0.78	1	1	0.55
0.13	0.18	0.26	NA	NA	NA
0.76	0.86	0.87	1	1	0.98
0.96	0.98	0.98	0.97	0.97	0.98
NA	NA	NA	NA	NA	NA

0.26	0.23	0.26	0.99	1	1
1	1	1	1	1	1
0.68	0.67	0.68	0.82	0.53	0.51
0.99	1	1	0.99	0.99	1
0.1	0.08	0.09	0.25	0.27	0.23
0.97	0.92	0.93	0.97	0.97	0.96
0.08	0.04	0.03	0.7	0.98	0.05
0.16	0.22	0.2	0.99	0.97	0.17
0.08	0.13	0.1	1	1	0.04
0.75	0.61	0.54	0.97	0.98	0.2
0.61	0.21	0.15	0.96	0.95	0.05
1	1	1	1	1	0.98
0.15	0.19	0.17	0.15	0.14	0.15
0.18	0.27	0.23	0.17	0.26	0.37
0.68	0.76	0.66	1	0.98	1
0.21	0.3	0.37	0.36	0.36	0.29
0.16	0.12	0.11	1	1	0.08
0.24	0.23	0.23	0.21	0.21	0.24
0.02	0.04	0.03	0.07	0.07	0.03
0.99	1	0.99	0.99	0.99	0.99
0.46	0.37	0.31	NA	NA	NA
0.14	0.06	0.05	0.99	0.99	0.1
0.19	0.26	0.24	0.42	0.73	0.09
0.99	0.99	0.99	0.99	0.99	0.75
0.14	0.18	0.13	0.2	0.19	0.19
1	0.99	0.99	1	1	1
0.52	0.47	0.39	NA	NA	NA
0.37	0.21	0.18	0.17	0.17	0.24
0.23	0.52	0.35	0.39	0.72	0.39
0.49	0.08	0.06	0.98	1	0.04
0.06	0.07	0.07	1	1	0.02
0.94	0.95	0.92	1	1	0.96
NA	0.88	0.94	NA	NA	NA
1	0.99	0.99	1	0.99	1
0.55	0.61	0.43	NA	NA	NA
0.3	0.22	0.17	0.2	0.19	NA
0.91	0.9	0.93	1	1	0.69
0.28	0.58	0.44	1	1	0.05
NA	0.54	0.39	NA	NA	NA
0.38	0.53	0.39	NA	NA	0.34
0.09	0.08	0.07	0.21	0.22	0.19
0.89	0.91	0.89	0.88	0.9	0.73
0.99	0.36	0.47	1	1	0.83
0.13	0.12	0.12	1	1	0.06
0.52	0.21	0.22	1	1	0.2
0.95	0.94	0.97	0.91	0.86	0.95
0.11	0.08	0.08	1	1	0.02
0.06	0.07	0.06	1	1	0.08
0.9	0.96	0.99	0.97	0.96	0.94

0.18	0.17	0.17	0.4	0.47	0.3
1	1	1	1	1	1
0.71	0.67	0.57	0.86	0.97	0.87
0.99	1	0.99	0.98	0.98	0.99
1	1	1	1	1	1
0.23	0.35	0.34	NA	NA	NA
0.69	0.47	0.54	0.84	0.93	0.4
0.06	0.02	0.02	0.84	0.86	0.01
NA	NA	NA	NA	NA	NA
0.92	0.86	0.95	1	1	0.65
0.22	0.19	0.23	0.51	0.34	0.45
0.84	0.89	0.72	0.77	0.85	0.85
0.52	0.59	0.73	0.82	0.87	NA
NA	0.65	0.64	NA	NA	NA
0.62	0.7	0.53	0.58	0.59	0.28

RAPplus_1_rib	RAPminus_1_	t0_1_riboZero	t0_2_riboZero	t3_1_riboZero	t3_2_riboZero
0.99	1	1	1	1	1
0.95	0.95	0.95	0.88	0.96	0.97
0.16	0.05	0.16	0.28	0.04	0.13
0.08	0.04	0.07	0.1	0.04	0.09
0.22	0.05	0.13	0.18	0.06	0.18
0.94	0.96	0.98	0.98	0.99	0.98
0.75	0.8	0.88	0.79	0.87	0.9
0.99	0.98	0.23	0.17	0.28	0.25
0.1	0.08	0.22	0.15	0.08	0.08
0.4	0.7	NA	0.35	0.33	0.22
0.98	0.99	0.99	1	1	0.99
NA	NA	NA	NA	NA	NA
1	0.99	0.97	0.96	0.97	0.97
NA	0.94	0.92	0.94	0.85	0.94
0.2	0.12	0.34	0.44	0.11	0.2
0.99	0.99	0.85	0.55	0.48	0.57
1	1	1	1	1	1
0.21	0.07	0.12	0.17	0.04	0.09
0.6	0.37	0.67	0.85	0.26	0.36
0.24	0.08	0.31	0.38	0.06	0.35
1	1	0.93	0.58	0.77	0.64
0.08	0.04	0.14	0.21	0.04	0.22
0.27	0.09	0.14	0.23	0.05	0.12
0.21	0.09	0.15	0.24	0.06	0.09
0.16	0.07	0.14	0.2	0.04	0.13
0.37	0.1	0.31	0.32	0.05	0.08
NA	NA	0.24	0.23	0.17	0.19
0.97	0.94	0.78	0.67	0.86	0.86
0.35	0.21	0.29	0.46	0.14	0.33
0.12	0.05	0.08	0.14	0.05	0.11
0.68	0.88	NA	NA	0.76	NA
0.39	0.61	0.26	0.25	0.35	NA
1	1	0.99	0.99	1	0.99
NA	NA	NA	NA	0.28	0.24
0.25	0.09	0.27	0.32	0.11	0.47
0.97	0.93	0.73	0.64	0.81	0.86
0.98	0.88	0.87	0.7	0.88	0.9
1	1	1	1	1	1
0.24	NA	NA	NA	NA	NA
0.22	0.07	0.27	0.35	0.05	0.18
0.24	0.05	0.14	0.15	0.02	0.09
1	1	1	1	1	1
0.3	NA	0.21	0.14	0.16	0.13
1	1	1	1	1	0.99
NA	NA	NA	NA	0.17	0.13
0.24	0.09	0.24	0.34	0.05	0.23
0.63	0.51	0.58	0.52	0.67	0.84

0.96	0.8	0.94	0.92	0.48	0.35
1	1	1	1	1	1
0.1	0.08	0.13	0.22	0.06	0.18
NA	NA	1	1	1	1
0.12	0.08	0.1	0.1	0.06	0.12
NA	NA	NA	NA	0.32	0.27
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
0.37	0.14	0.19	0.27	0.11	0.3
0.34	0.74	NA	NA	0.61	0.4
0.13	0.04	0.17	0.25	0.03	0.12
0.68	0.55	0.5	0.44	0.47	0.6
0.92	NA	0.93	0.97	0.95	0.91
0.57	NA	NA	NA	0.65	NA
0.13	0.05	0.13	0.22	0.03	0.07
NA	0.25	NA	0.76	0.22	0.2
0.94	0.98	0.97	0.97	0.99	0.97
0.94	0.79	0.57	0.5	0.62	0.63
0.99	0.99	0.99	1	1	0.99
0.83	0.75	0.78	0.9	0.48	0.79
1	1	1	1	1	1
0.2	0.05	0.23	0.27	0.04	0.25
NA	NA	NA	0.18	NA	NA
NA	NA	NA	0.89	NA	NA
0.91	0.92	0.91	0.92	0.71	0.73
0.12	0.03	0.08	0.09	0.01	0.07
0.91	0.89	0.88	0.79	0.9	NA
0.56	NA	NA	NA	NA	NA
0.21	0.08	0.16	0.18	0.05	0.11
0.91	NA	0.48	0.66	NA	NA
0.99	1	0.99	0.99	0.99	0.97
0.58	NA	0.67	NA	0.76	NA
0.99	0.98	0.96	0.99	0.98	0.87
0.5	0.78	0.57	0.52	0.45	0.28
0.22	0.23	0.25	0.16	0.24	0.29
0.99	0.98	0.72	0.53	0.58	0.57
0.98	0.92	0.94	0.96	0.99	0.99
0.34	0.33	0.27	0.29	0.3	0.25
NA	NA	NA	NA	0.23	0.25
0.21	0.1	0.22	0.22	0.09	0.13
0.18	0.09	0.19	0.32	0.08	0.16
0.96	0.94	1	0.99	0.54	0.94
0.29	NA	NA	NA	0.22	NA
0.27	0.27	0.27	0.27	0.28	0.47
0.96	0.98	0.97	0.95	0.96	0.94
0.92	NA	0.92	0.93	0.39	0.38
NA	NA	0.49	0.96	NA	NA
0.3	0.4	0.29	0.35	0.4	0.46
0.2	0.23	0.22	0.22	0.29	NA

0.35	0.36	0.32	0.51	0.17	0.21
0.99	1	0.99	0.98	0.99	0.98
NA	NA	NA	NA	NA	NA
0.96	0.98	0.97	0.98	0.98	0.97
0.78	0.77	0.81	0.76	0.87	0.84
0.09	0.05	0.15	0.18	0.09	0.26
0.21	0.22	0.25	NA	0.25	0.04
NA	0.79	0.84	0.67	0.53	NA
0.8	0.96	0.92	0.88	0.8	0.92
0.29	0.48	0.41	0.37	0.31	0.18
0.99	0.99	1	0.98	1	1
1	1	1	1	1	1
0.95	0.93	0.98	0.98	0.92	0.95
NA	NA	NA	NA	NA	NA
0.06	0.03	0.05	0.05	0.01	0.05
0.61	0.27	0.71	0.84	0.25	0.62
0.53	0.46	NA	NA	NA	NA
0.49	0.16	0.35	0.33	0.07	0.19
0.84	0.91	0.69	0.81	0.7	0.58
1	1	1	1	1	1
NA	NA	NA	NA	0.08	0.07
1	1	0.92	0.88	0.96	0.89
0.35	0.16	0.19	0.27	0.22	0.19
NA	0.38	0.48	0.63	0.43	NA
NA	NA	NA	NA	0.09	0.15
0.2	0.24	NA	0.28	0.22	0.2
0.17	0.27	0.29	0.25	0.14	0.16
0.99	0.97	0.99	0.99	0.95	0.99
1	1	1	1	1	1
0.25	0.17	0.46	0.66	0.19	0.35
0.46	0.41	0.86	0.95	0.96	0.97
0.95	0.9	0.88	0.86	0.92	0.96
0.32	0.18	0.37	0.44	0.26	0.17
0.29	0.45	0.13	0.17	0.18	0.2
0.25	0.18	0.11	0.15	0.12	0.16
0.99	NA	NA	0.88	0.89	NA
0.97	0.97	0.96	0.94	0.96	0.96
0.9	NA	NA	NA	0.95	0.92
0.97	0.99	0.98	0.95	0.97	0.97
0.15	0.05	0.14	0.19	0.02	0.14
0.48	0.15	0.32	0.56	0.1	0.42
0.14	0.05	0.15	0.18	0.05	0.15
0.89	NA	NA	0.7	0.63	NA
0.99	0.99	1	0.99	0.99	0.99
0.93	0.98	0.99	0.97	0.95	NA
0.99	0.98	0.9	0.95	0.88	0.87
NA	0.75	NA	NA	NA	NA
0.97	0.91	0.88	0.75	0.8	0.86
0.17	0.14	0.15	0.14	0.07	0.12

0.47	0.6	NA	NA	NA	NA
0.95	0.97	0.73	0.97	0.99	0.97
NA	NA	NA	NA	NA	NA
0.26	0.07	0.27	0.4	0.05	0.35
0.1	0.14	0.09	0.11	0.06	0.06
NA	0.31	NA	NA	0.18	0.23
0.94	0.97	0.76	0.97	NA	0.9
0.21	0.09	0.28	0.37	0.04	0.1
0.3	0.08	0.37	0.71	0.11	0.46
0.14	0.07	0.15	0.16	0.04	0.17
0.98	0.99	0.99	0.99	0.49	0.32
0.51	0.48	0.37	0.55	0.45	0.52
0.22	0.22	0.32	0.26	0.22	0.31
0.67	NA	NA	NA	0.73	NA
0.98	1	0.99	0.99	0.99	0.97
0.68	0.71	0.54	0.81	0.39	0.28
1	0.99	0.89	0.62	0.84	0.91
0.98	0.99	0.97	0.94	0.95	0.95
0.47	0.21	0.33	0.33	0.14	0.18
0.48	0.93	0.86	0.84	0.88	0.92
0.96	0.96	0.98	0.99	0.96	0.94
0.06	0.05	0.1	0.13	0.1	0.11
0.09	NA	NA	0.22	0.2	0.17
0.53	0.41	0.42	0.42	0.29	0.32
0.37	0.27	0.36	0.29	0.49	NA
0.23	0.07	0.21	0.32	0.06	0.14
0.83	0.79	0.94	0.94	0.76	0.7
1	1	1	1	1	1
0.27	0.18	0.31	0.34	0.16	0.35
0.99	1	1	1	1	0.99
0.88	0.9	0.89	0.69	0.83	0.71
0.12	0.04	0.14	0.18	0.02	0.13
0.97	0.89	0.44	0.33	0.58	0.64
NA	NA	NA	NA	0.43	0.52
0.4	0.78	NA	0.41	0.48	0.81
0.13	0.04	0.12	0.19	0.03	0.1
0.96	0.27	0.93	0.95	0.74	0.9
0.13	0.16	0.17	0.11	0.13	0.17
0.98	0.99	1	1	0.99	0.97
0.1	0.05	0.11	0.14	0.05	0.07
0.95	0.95	0.95	0.9	0.98	0.97
0.51	0.43	0.47	0.34	0.5	0.41
0.3	0.07	0.15	0.25	0.04	0.22
0.5	0.44	0.54	0.52	0.46	0.55
0.98	0.99	0.98	0.96	0.96	0.94
0.19	0.21	0.14	0.19	0.16	0.23
0.99	0.99	0.99	0.99	0.99	0.97
0.74	0.46	0.75	0.98	0.16	0.29
0.99	1	1	1	1	0.99

0.71	0.83	0.79	0.81	0.85	0.81
0.17	NA	0.08	0.07	0.06	0.08
0.99	0.99	0.93	0.97	0.99	0.99
0.84	0.82	0.6	0.78	0.38	0.26
0.29	0.32	0.28	0.28	0.19	0.15
0.99	0.99	0.99	0.99	0.98	0.97
NA	NA	NA	NA	0.63	0.54
0.27	0.2	0.3	0.28	NA	0.39
NA	NA	NA	NA	NA	NA
0.65	NA	NA	0.32	0.23	0.36
0.23	0.05	0.22	0.24	0.08	0.29
0.32	0.07	0.24	0.37	0.05	0.24
0.71	0.8	0.73	0.74	0.62	0.7
NA	0.51	NA	0.29	0.19	0.36
0.25	0.31	0.32	0.33	0.29	0.35
0.88	0.88	NA	NA	NA	NA
0.68	0.91	0.9	0.8	0.8	0.93
0.58	0.19	0.31	0.54	0.12	0.29
0.15	0.08	0.11	0.14	0.07	0.1
0.96	0.92	NA	0.86	0.96	0.94
0.37	0.33	0.33	0.48	0.24	NA
0.1	0.03	0.12	0.14	0.04	0.11
1	1	1	1	1	0.99
0.09	0.07	0.12	0.21	0.02	0.13
0.98	0.99	0.98	0.99	0.9	NA
1	1	1	1	1	0.99
0.26	0.25	0.19	0.24	0.21	NA
0.1	0.16	0.14	0.14	0.22	0.17
0.76	0.76	0.81	0.88	0.51	0.89
0.17	0.14	0.07	0.08	0.08	0.09
NA	NA	NA	NA	NA	NA
1	1	1	1	1	1
0.4	0.68	NA	0.35	0.33	0.22
0.99	0.99	1	1	0.99	0.99
0.34	0.1	0.22	0.23	0.08	0.21
0.87	0.82	0.8	0.71	0.87	0.95
0.6	0.65	NA	NA	0.12	0.14
0.99	0.99	0.94	0.68	0.68	0.75
0.7	0.26	0.67	0.77	0.31	0.55
0.98	0.97	0.96	0.97	0.98	0.97
NA	NA	NA	NA	NA	NA
1	1	1	1	1	1
0.47	0.36	0.52	NA	0.39	NA
0.2	0.07	0.12	0.14	0.02	0.18
0.36	0.15	0.2	0.31	0.13	0.36
0.19	0.29	0.21	0.33	0.16	NA
0.59	0.21	0.36	0.42	0.26	0.36
0.85	0.86	NA	0.84	0.87	0.92
0.19	NA	0.12	0.12	0.17	0.18

0.15	0.41	0.16	0.13	0.1	0.16
0.11	0.07	0.12	0.2	0.08	0.24
0.57	0.55	0.62	0.76	0.57	0.71
0.18	0.13	0.19	0.26	0.14	0.22
1	0.99	0.97	0.97	0.98	0.97
0.98	0.98	NA	NA	0.29	0.35
0.19	0.07	0.19	0.21	0.03	0.21
NA	NA	NA	NA	0.92	0.96
NA	NA	NA	NA	NA	NA
0.15	0.08	0.16	0.16	0.06	0.12
1	1	0.79	0.46	0.57	0.5
NA	NA	NA	NA	NA	NA
0.38	0.33	NA	NA	NA	NA
0.33	0.07	0.17	0.24	0.03	0.09
0.99	0.98	0.99	0.98	0.99	0.99
0.91	NA	NA	NA	0.13	0.12
0.43	0.37	0.34	0.41	0.21	0.31
0.17	0.21	0.19	0.13	0.19	0.18
0.09	0.16	0.21	0.16	0.26	0.39
0.96	0.98	0.98	0.96	0.98	0.97
0.97	1	1	0.99	0.99	0.94
0.91	0.82	NA	NA	0.87	NA
NA	NA	NA	NA	0.47	0.4
0.15	0.04	0.14	0.15	0.04	0.1
0.66	0.51	0.45	0.51	NA	NA
0.99	0.94	0.92	0.93	0.95	0.92
0.07	0.06	0.04	0.05	0.02	0.05
0.99	1	1	1	1	0.99
0.18	0.06	0.2	0.26	NA	NA
NA	NA	NA	NA	NA	NA
0.06	0.03	0.1	0.11	0.02	0.07
0.81	0.88	0.07	0.08	0.16	0.08
0.47	0.14	0.24	0.31	NA	0.33
0.08	0.09	0.09	0.05	0.08	0.05
0.59	NA	NA	0.45	NA	NA
0.39	0.45	0.59	NA	0.57	0.38
1	0.99	0.99	0.99	1	0.99
0.12	0.08	0.14	0.23	0.08	0.11
0.41	NA	NA	NA	0.44	0.42
0.99	0.99	0.98	0.99	0.99	0.98
0.28	0.31	0.22	0.26	0.17	0.17
0.14	0.14	0.17	0.19	0.06	0.14
0.52	NA	NA	0.37	0.33	0.36
0.23	0.46	NA	NA	0.29	0.32
0.94	0.9	0.9	0.9	0.88	0.85
0.82	0.94	0.97	0.94	0.94	NA
1	0.99	1	0.99	1	1
0.96	0.92	0.88	0.87	0.92	0.95
0.99	0.99	0.99	0.99	1	0.99

0.99	0.99	0.98	0.98	0.99	0.99
0.34	0.25	0.18	0.23	0.22	0.22
0.96	0.98	0.96	0.94	0.97	0.97
0.13	0.15	NA	0.09	NA	0.08
0.99	0.99	0.99	0.99	1	0.99
NA	0.14	NA	NA	NA	NA
0.95	0.95	0.98	0.96	0.9	0.88
0.98	0.97	0.97	0.94	0.97	0.97
0.72	0.63	0.69	0.44	0.51	NA
0.11	0.06	0.12	0.17	0.03	0.08
0.08	0.19	0.12	0.11	0.12	0.14
0.49	0.37	NA	NA	NA	NA
0.12	NA	NA	0.3	NA	NA
0.99	1	0.99	0.98	0.99	0.96
0.71	0.6	0.56	0.54	0.76	0.63
0.46	0.09	0.16	0.33	0.03	0.19
NA	NA	NA	NA	NA	NA
0.99	0.99	0.94	0.65	0.71	0.75
0.19	NA	0.15	0.11	0.14	0.1
0.24	0.05	0.17	0.22	0.05	0.27
1	1	1	1	1	1
0.19	0.15	0.11	0.12	0.11	0.18
0.19	0.25	NA	NA	0.15	0.23
0.19	0.09	0.27	0.31	0.07	0.36
0.96	0.91	0.96	0.94	0.97	0.98
1	1	0.99	1	1	0.99
0.06	0.04	0.05	0.05	0.02	0.05
0.6	0.67	NA	NA	NA	NA
1	1	0.99	1	1	1
NA	NA	NA	NA	0.12	0.12
1	0.99	NA	NA	NA	NA
0.71	0.81	NA	NA	0.84	0.92
0.63	0.87	NA	NA	NA	NA
0.29	NA	0.21	0.2	0.26	0.25
0.5	0.44	NA	NA	0.32	0.35
0.97	0.99	0.96	0.97	0.98	0.96
0.92	NA	NA	NA	0.45	0.4
NA	0.14	NA	NA	NA	NA
0.11	0.08	0.13	0.22	0.09	0.16
0.14	0.05	0.15	0.21	0.14	0.25
0.28	0.47	0.2	0.19	0.2	0.23
NA	NA	NA	NA	NA	NA
0.32	0.43	0.3	0.2	0.3	NA
NA	0.92	NA	NA	0.21	0.2
0.67	0.57	0.72	0.44	0.81	0.8
NA	NA	NA	NA	NA	NA
0.97	0.98	0.97	0.96	0.98	0.97
0.98	0.98	0.95	0.96	0.99	0.99
NA	NA	NA	0.51	NA	NA

0.98	1	0.97	0.99	0.98	0.81
1	1	1	1	1	0.99
0.83	0.81	0.48	0.48	0.47	0.46
0.99	0.99	0.99	1	1	1
0.13	0.14	0.15	0.38	0.22	0.13
0.96	0.95	0.96	0.97	0.98	0.94
0.04	0.05	0.06	0.09	0.05	0.05
0.34	0.17	0.31	0.37	0.12	0.53
0.21	0.05	0.23	0.31	0.05	0.15
0.75	0.28	0.54	0.6	0.17	0.27
0.26	0.08	0.25	0.51	0.08	0.24
0.95	0.99	0.98	0.99	0.98	0.97
0.12	0.12	0.13	0.15	0.14	0.13
NA	NA	NA	NA	0.13	0.13
1	1	1	1	1	1
NA	0.33	NA	0.32	NA	NA
0.14	0.1	0.13	0.14	0.06	0.17
0.22	0.22	0.25	0.24	0.25	0.26
0.11	0.04	0.17	0.27	0.03	0.07
0.99	0.99	0.96	0.98	0.98	0.98
NA	NA	NA	NA	NA	NA
0.24	0.14	0.29	0.4	NA	0.8
0.08	0.08	0.08	0.1	0.08	0.1
0.99	0.99	0.82	0.53	0.48	0.57
0.13	0.11	0.13	0.13	0.14	0.07
1	1	1	1	1	1
NA	NA	NA	NA	NA	NA
0.08	0.12	0.16	0.14	0.17	0.21
0.45	0.79	NA	NA	NA	NA
0.17	0.06	0.09	0.14	0.03	0.11
0.07	0.03	0.09	0.15	0.02	0.15
0.97	0.97	0.98	0.94	0.98	0.97
NA	NA	NA	NA	0.36	0.33
1	1	0.99	0.99	1	0.99
NA	NA	NA	NA	NA	NA
0.08	NA	0.07	0.08	0.14	0.14
0.6	0.67	0.84	0.92	0.85	0.65
0.15	0.05	0.26	0.21	0.04	0.17
NA	NA	NA	NA	NA	NA
0.23	NA	NA	NA	0.52	0.86
0.21	0.21	0.25	0.34	0.18	0.22
0.85	0.88	0.72	0.91	0.71	0.91
1	0.97	1	1	1	1
0.31	0.09	0.21	0.37	0.11	0.63
0.53	0.17	0.93	0.63	0.19	0.48
0.88	0.95	0.95	0.97	0.93	0.9
0.19	0.04	0.13	0.11	0.01	0.08
0.43	0.11	0.16	0.26	0.06	0.15
0.97	0.95	0.97	0.96	0.94	0.97

0.28	0.33	0.15	0.19	0.12	0.18
1	1	1	1	1	0.99
0.89	0.9	NA	0.78	NA	NA
0.98	0.97	0.99	0.99	0.99	0.98
1	1	1	1	0.99	0.99
NA	NA	NA	NA	0.16	0.12
0.4	0.69	NA	0.35	0.33	0.22
0.07	0.02	0.05	0.06	0.01	0.04
NA	NA	NA	0.91	0.9	0.82
0.63	0.66	0.62	0.7	0.62	0.45
0.38	0.29	0.32	0.46	NA	NA
0.71	0.56	0.57	0.47	0.67	0.7
0.65	0.89	NA	NA	0.29	NA
NA	NA	NA	NA	0.6	0.59
0.79	0.51	0.72	0.57	0.79	0.88

t6_1_riboZero	t6_2_riboZero	t7.5_1_riboZe	t7.5_2_riboZe	t8.5_1_riboZe	t8.5_2_riboZe
1	1	NA	NA	NA	NA
0.94	0.97	0.9	0.89	0.94	0.94
0.09	0.09	0.1	0.09	0.12	0.23
0.14	0.11	NA	NA	NA	NA
0.16	0.16	0.21	0.31	0.4	0.68
0.98	0.99	0.98	0.98	0.99	0.99
0.84	0.92	NA	0.66	0.47	NA
0.35	0.28	0.25	0.28	0.27	0.21
0.08	0.06	0.27	0.23	0.37	0.38
0.32	0.22	0.27	0.31	0.29	0.16
0.99	1	0.99	1	0.99	0.99
NA	NA	0.98	0.99	0.96	0.98
0.97	0.97	0.98	0.95	0.96	0.98
0.91	0.97	NA	NA	NA	NA
0.22	0.2	0.08	0.06	0.17	0.12
0.57	0.62	0.92	0.7	0.79	0.92
1	1	1	1	1	1
0.07	0.05	NA	NA	NA	NA
0.35	0.37	0.19	0.21	0.17	0.46
0.2	0.16	NA	NA	NA	NA
0.73	0.93	1	1	1	1
0.07	0.05	0.07	0.05	NA	0.18
0.08	0.07	0.12	0.05	NA	NA
0.1	0.05	NA	NA	NA	NA
0.12	0.08	0.37	NA	NA	0.44
0.1	0.08	0.4	0.65	0.65	0.54
0.16	0.22	0.22	0.09	0.21	0.22
0.92	0.85	0.85	0.8	0.94	0.96
0.18	0.11	0.3	0.16	NA	0.32
0.07	0.05	0.06	0.05	NA	NA
0.93	0.94	NA	0.93	NA	NA
0.41	0.44	NA	NA	NA	0.49
0.99	0.99	0.99	0.99	0.99	0.99
0.19	0.28	0.84	0.83	0.77	0.92
0.18	0.18	0.39	NA	NA	NA
0.82	0.91	0.83	0.96	0.98	0.92
0.62	0.64	0.5	0.39	0.54	0.62
1	1	1	1	1	1
NA	NA	NA	NA	NA	NA
0.1	0.1	0.14	NA	NA	NA
0.05	0.07	0.12	0.08	NA	NA
1	1	1	1	1	1
0.17	0.19	0.19	0.15	0.2	0.19
0.99	1	0.99	0.98	0.97	0.98
0.11	0.15	0.17	0.15	0.28	0.26
0.14	0.22	0.17	0.32	0.22	NA
0.65	0.71	0.99	0.99	0.93	0.88

0.39	0.39	0.35	0.34	0.5	0.45
1	1	1	1	1	1
0.09	0.13	NA	0.15	NA	NA
1	0.99	0.96	0.99	0.98	0.97
0.07	0.07	0.08	0.12	0.11	0.09
0.19	0.3	0.36	0.34	0.37	0.37
NA	0.22	0.23	0.19	0.18	0.21
0.35	NA	NA	NA	NA	NA
0.1	0.13	NA	NA	NA	NA
0.57	0.33	NA	NA	NA	NA
0.17	0.12	0.19	0.11	0.11	0.3
0.44	0.53	0.91	0.88	0.73	0.87
0.92	0.95	0.9	0.91	0.96	0.96
0.23	0.2	0.22	0.19	0.31	0.32
0.08	0.05	0.05	0.11	0.02	0.05
0.37	0.27	0.15	0.17	0.09	0.1
0.97	0.99	0.98	0.99	0.99	0.99
0.57	0.65	0.66	0.91	0.8	0.67
0.98	0.99	0.98	1	0.99	0.99
0.59	0.49	NA	NA	NA	NA
1	1	0.99	0.99	NA	NA
0.1	0.13	0.18	0.17	NA	NA
0.12	0.06	NA	NA	NA	NA
0.38	0.26	NA	NA	NA	NA
0.71	0.78	0.76	0.74	0.64	0.57
0.04	0.03	NA	NA	NA	NA
NA	0.72	NA	NA	NA	NA
0.33	0.51	NA	NA	NA	NA
0.08	0.05	0.05	NA	NA	NA
0.91	0.96	0.96	0.71	0.89	0.96
0.98	0.99	0.96	0.97	0.95	0.92
NA	NA	NA	NA	NA	NA
0.96	0.97	0.9	0.96	0.81	0.66
0.35	0.33	0.62	NA	NA	NA
0.28	0.26	0.18	NA	0.34	NA
0.62	0.52	0.64	0.62	0.63	0.81
0.99	0.99	0.98	1	0.99	0.98
0.38	0.29	0.5	0.48	0.4	0.3
0.24	0.25	NA	NA	NA	NA
0.11	0.12	NA	NA	NA	NA
0.11	0.11	0.17	0.06	0.17	NA
0.96	0.98	0.86	0.94	0.87	0.9
0.33	0.34	NA	NA	NA	NA
0.61	0.51	0.57	0.57	0.48	0.38
0.93	0.97	NA	0.92	NA	NA
0.31	0.42	0.32	0.35	0.31	0.32
NA	0.3	NA	0.37	NA	NA
0.54	0.55	NA	NA	NA	NA
0.31	0.3	0.4	NA	NA	NA

0.34	0.3	0.29	0.22	0.2	0.2
0.97	0.98	0.95	0.95	0.93	0.92
NA	0.2	NA	NA	NA	NA
0.97	0.97	0.88	NA	0.94	NA
0.79	0.86	0.92	0.95	0.9	0.89
0.11	0.12	0.29	0.23	0.26	0.39
0.13	0.08	0.86	0.83	0.37	0.43
0.47	0.49	NA	0.46	NA	0.48
0.8	0.63	NA	0.8	0.82	0.57
0.32	0.39	NA	NA	NA	NA
0.99	1	0.99	0.99	0.99	0.99
1	1	0.99	0.99	0.99	0.99
0.86	0.92	0.72	0.92	NA	0.94
NA	NA	NA	NA	NA	NA
0.02	0.02	0.04	0.04	0.06	0.11
0.4	0.4	0.27	NA	NA	NA
NA	0.4	0.86	0.9	0.85	0.86
0.27	0.29	0.42	0.5	0.79	0.89
0.68	0.39	0.43	0.62	0.52	0.47
1	1	1	1	1	1
0.07	0.08	0.35	0.21	0.26	0.27
0.93	0.94	0.99	0.97	0.99	0.98
0.34	0.46	NA	NA	NA	NA
NA	NA	0.87	NA	NA	NA
0.19	0.19	NA	NA	NA	NA
0.34	0.55	0.49	0.62	0.36	0.41
0.27	0.18	NA	NA	NA	NA
0.96	0.97	0.98	0.98	0.98	0.96
1	1	1	1	1	1
0.27	0.3	0.5	0.81	NA	0.34
0.78	0.77	0.6	0.37	0.54	0.55
0.96	0.97	0.94	0.98	0.99	0.97
0.3	0.26	0.18	0.21	NA	NA
0.19	0.16	0.37	NA	0.77	0.63
0.11	0.09	0.1	0.06	0.21	0.17
0.96	0.95	1	0.86	1	1
0.95	0.96	0.99	1	1	1
0.96	0.98	NA	NA	NA	NA
0.99	0.99	0.95	NA	NA	NA
0.07	0.05	0.08	0.06	NA	NA
0.23	0.22	NA	NA	NA	NA
0.06	0.06	0.09	0.06	NA	NA
0.33	0.53	NA	0.35	NA	NA
0.99	1	0.95	0.96	0.57	0.59
0.97	0.97	NA	NA	NA	NA
0.74	0.86	0.96	0.78	0.94	0.95
NA	NA	NA	NA	NA	NA
0.95	0.92	0.91	0.88	NA	0.89
0.11	0.1	0.11	0.06	0.09	0.12

NA	NA	NA	NA	NA	NA
0.96	0.95	0.94	0.97	0.98	0.93
NA	NA	0.07	0.05	0.06	0.07
0.23	0.21	0.22	0.22	0.14	0.24
0.06	0.06	0.06	0.04	0.06	0.06
0.24	0.28	NA	NA	0.29	0.3
0.88	0.83	0.89	0.88	NA	NA
0.1	0.06	0.06	0.08	NA	NA
0.3	0.28	0.44	0.38	NA	NA
0.09	0.06	NA	NA	NA	NA
0.54	0.49	0.74	NA	NA	NA
0.52	0.37	NA	0.29	0.48	NA
0.23	0.23	0.24	0.26	0.24	0.44
0.85	0.78	NA	NA	NA	NA
0.99	0.99	0.95	0.98	0.95	NA
0.47	0.29	NA	NA	NA	NA
0.95	0.98	1	0.97	0.99	1
0.93	0.95	0.64	0.47	0.61	0.71
0.29	0.3	0.39	0.31	0.24	0.28
0.85	0.93	0.9	0.54	0.86	0.92
0.97	0.96	0.86	NA	NA	NA
0.15	0.1	NA	0.35	NA	NA
0.14	0.13	0.41	0.72	NA	0.46
0.3	0.25	0.52	0.57	0.53	0.73
0.48	0.5	0.4	0.55	NA	NA
0.11	0.12	0.19	0.21	0.33	0.32
0.63	0.88	NA	NA	NA	NA
1	1	1	1	1	1
0.42	0.43	0.53	0.51	NA	0.45
1	1	NA	NA	NA	NA
0.78	0.81	0.87	0.85	0.87	0.82
0.05	0.04	0.07	0.1	NA	NA
0.77	0.85	0.46	0.46	0.74	0.64
0.47	0.52	0.69	0.52	0.46	0.59
0.54	0.46	NA	NA	NA	NA
0.07	0.05	0.15	0.1	NA	NA
0.76	0.82	0.89	0.76	0.84	0.51
0.12	0.18	0.22	0.17	0.24	0.21
0.98	0.99	0.99	0.99	0.99	0.99
0.05	0.07	0.06	0.05	NA	NA
0.98	0.99	0.98	0.99	0.99	0.99
0.38	0.58	0.94	NA	0.88	NA
0.2	0.15	0.24	0.36	NA	NA
0.5	0.55	0.61	0.48	NA	NA
0.9	0.95	0.85	0.91	0.83	0.67
0.26	0.2	0.08	0.03	0.13	0.11
0.98	0.99	0.99	0.99	0.99	1
0.43	0.38	0.38	0.61	NA	NA
1	1	0.99	0.99	0.97	0.98

0.67	0.78	0.89	NA	NA	NA
0.07	0.1	NA	NA	NA	NA
1	1	1	1	1	1
0.25	0.25	0.39	0.37	0.47	0.49
0.07	0.17	0.1	0.05	0.05	0.05
0.99	0.99	0.98	0.96	0.99	0.99
0.87	0.62	0.74	0.37	NA	NA
NA	0.6	NA	NA	NA	NA
NA	NA	0.22	0.21	0.14	0.15
0.34	0.44	0.98	0.83	0.96	0.98
0.31	0.3	0.68	0.48	0.86	0.92
0.11	0.09	NA	0.2	NA	NA
0.69	0.7	0.41	0.38	0.42	0.4
0.15	0.18	NA	NA	NA	NA
0.25	0.26	0.43	0.4	0.58	0.36
NA	0.81	0.9	0.96	0.89	0.9
0.93	0.93	0.94	0.94	0.73	0.79
0.3	0.24	NA	NA	NA	NA
0.08	0.06	0.07	0.08	0.07	0.07
0.92	0.95	NA	NA	NA	NA
0.29	0.15	NA	0.12	0.12	0.1
0.19	0.22	0.16	0.23	NA	0.29
0.99	1	0.98	0.95	0.93	0.94
0.07	0.04	0.11	0.1	0.19	NA
0.93	0.9	NA	NA	NA	NA
0.99	1	0.98	0.99	0.98	0.97
0.24	0.37	NA	NA	NA	NA
0.21	0.23	NA	NA	NA	NA
0.79	0.75	NA	NA	NA	NA
0.09	0.09	0.11	0.08	0.06	0.1
NA	NA	NA	NA	NA	NA
1	1	1	1	1	1
0.32	0.22	0.27	0.32	0.29	0.16
0.99	0.99	0.97	0.99	0.97	0.97
0.14	0.18	NA	0.15	0.47	NA
0.88	0.96	0.82	0.77	0.83	0.73
0.2	0.2	NA	NA	NA	NA
0.79	0.87	0.88	0.77	0.88	0.95
0.41	0.23	0.51	0.46	NA	NA
0.97	0.96	0.99	0.99	0.99	0.99
NA	NA	NA	NA	NA	NA
1	1	1	1	1	1
0.32	0.47	NA	NA	NA	NA
0.07	0.07	NA	NA	NA	NA
0.25	0.23	0.32	0.29	NA	NA
0.18	0.13	0.17	0.14	0.12	0.14
0.44	0.42	NA	NA	NA	NA
0.89	0.77	NA	NA	NA	NA
NA	0.12	0.11	0.11	NA	0.11

NA	0.17	0.16	0.1	0.09	0.08
0.1	0.13	NA	0.1	NA	NA
0.68	0.66	0.77	0.88	0.84	0.7
0.22	0.15	0.15	0.21	NA	0.23
0.96	0.94	0.97	0.95	0.97	0.95
0.3	0.39	NA	NA	NA	NA
0.12	0.11	NA	NA	NA	NA
0.98	0.92	0.99	0.96	0.98	0.99
NA	NA	NA	NA	NA	NA
0.12	0.12	0.13	NA	NA	NA
0.55	0.75	1	1	1	1
0.77	NA	NA	NA	0.82	NA
0.29	0.67	0.25	0.55	0.22	0.2
0.07	0.06	0.06	0.04	0.13	NA
0.97	0.99	0.97	0.98	0.96	0.92
0.12	0.15	0.16	NA	NA	NA
0.27	0.24	0.24	0.18	0.15	0.19
0.14	0.19	0.12	0.14	0.12	0.11
0.48	0.46	0.66	0.65	0.42	0.31
0.99	0.98	0.92	0.9	0.92	0.96
0.97	0.97	0.9	0.85	0.91	0.73
0.91	0.79	NA	NA	NA	NA
0.52	0.45	NA	NA	NA	NA
0.08	0.07	0.17	0.33	0.12	0.23
NA	0.14	NA	NA	NA	NA
0.94	0.96	NA	0.92	0.94	0.97
0.05	0.05	0.02	0.03	0.02	0.02
0.99	0.99	0.98	0.88	0.98	0.97
0.22	0.34	NA	NA	NA	NA
NA	NA	0.86	NA	NA	NA
0.05	0.04	NA	NA	NA	NA
0.1	0.08	0.31	0.09	0.21	0.24
NA	NA	NA	NA	NA	NA
0.06	0.07	0.05	0.06	0.04	0.03
NA	NA	NA	NA	NA	NA
0.57	0.52	0.78	0.88	0.76	0.55
0.99	0.99	0.98	0.98	0.98	0.98
0.11	0.09	0.15	0.1	NA	0.22
NA	0.55	NA	NA	0.49	0.48
0.98	0.99	0.96	0.99	0.99	0.97
0.17	0.17	0.18	0.18	0.21	0.22
0.27	0.22	NA	NA	NA	NA
0.3	0.36	NA	NA	NA	NA
0.26	0.43	NA	NA	NA	NA
0.93	0.92	0.92	0.99	0.94	0.91
0.79	0.85	NA	0.95	NA	NA
0.99	1	1	1	0.99	0.99
0.95	0.97	0.92	0.98	0.99	0.97
0.99	1	0.99	0.99	1	0.99

1	0.99	0.98	0.99	0.99	0.98
0.28	0.18	NA	0.37	NA	NA
0.97	0.98	NA	NA	NA	0.9
0.07	0.07	NA	NA	NA	NA
0.99	0.99	0.99	0.99	1	1
NA	NA	0.03	0.05	0.03	0.04
0.9	0.95	0.87	0.9	0.9	0.76
0.98	0.99	0.99	1	1	0.99
0.55	0.51	NA	0.53	NA	NA
0.06	0.04	NA	NA	NA	NA
0.1	0.09	0.17	0.13	NA	0.19
0.21	NA	NA	0.23	0.19	0.12
0.29	0.19	NA	NA	NA	NA
0.98	0.98	0.99	0.98	0.98	0.98
0.59	0.77	NA	NA	NA	NA
0.08	0.04	0.09	0.09	NA	NA
NA	NA	0.72	0.53	0.6	0.74
0.8	0.86	0.91	0.78	0.9	0.94
0.13	0.17	NA	NA	0.23	0.19
0.1	0.11	0.14	NA	NA	NA
1	1	0.99	1	0.99	0.99
0.12	0.12	0.18	0.33	NA	NA
0.17	0.24	NA	0.16	NA	0.2
0.13	0.14	0.24	0.22	0.19	0.2
0.97	0.96	0.94	0.98	0.94	0.95
1	1	0.99	0.99	1	1
0.02	0.03	0.04	NA	NA	NA
NA	NA	0.36	0.32	0.45	0.32
1	1	1	1	1	1
0.13	0.11	0.07	0.06	0.17	NA
NA	NA	NA	NA	NA	NA
0.95	0.99	0.9	0.89	0.95	0.92
NA	0.86	NA	NA	NA	NA
0.23	0.19	NA	NA	NA	NA
0.65	0.34	0.5	0.21	0.39	0.15
0.98	0.98	0.97	0.97	0.97	0.97
0.45	0.47	NA	0.79	NA	NA
0.33	0.25	0.17	0.15	NA	0.2
0.15	0.17	0.11	0.1	0.08	0.13
0.25	0.23	0.27	0.58	0.29	0.5
0.18	0.19	0.26	0.28	0.31	0.3
NA	NA	NA	NA	NA	NA
0.27	0.34	NA	NA	NA	NA
0.22	0.22	NA	0.3	NA	NA
0.56	0.83	0.98	0.97	0.95	0.97
NA	NA	NA	NA	NA	NA
0.97	0.97	0.98	0.99	0.99	0.99
0.99	0.99	0.99	1	1	1
0.27	0.17	NA	NA	NA	NA

0.94	0.94	NA	0.92	NA	NA
0.99	0.99	0.99	0.99	1	0.99
0.45	0.56	NA	NA	0.65	0.6
1	1	1	1	1	1
NA	0.08	NA	NA	NA	NA
0.97	0.99	NA	0.93	0.92	0.95
0.07	0.07	0.06	0.07	0.06	0.08
0.22	0.27	0.31	0.51	0.16	0.24
0.18	0.09	NA	NA	NA	NA
0.22	0.21	0.33	0.14	0.38	0.28
0.11	0.12	NA	NA	NA	NA
0.97	0.95	0.89	0.98	0.89	NA
0.14	0.15	0.17	0.14	0.14	0.16
0.17	0.16	NA	0.32	NA	NA
1	1	1	1	1	1
NA	0.23	0.18	0.24	NA	NA
0.07	0.1	0.06	0.07	NA	NA
0.24	0.22	0.2	0.14	0.16	0.18
0.06	0.07	NA	NA	NA	NA
0.99	0.99	0.98	0.98	0.98	0.98
NA	NA	NA	NA	0.1	0.14
0.16	0.19	NA	NA	NA	NA
0.11	0.11	0.11	0.09	0.08	0.1
0.57	0.63	0.92	0.69	0.8	0.91
0.13	0.12	0.09	0.11	0.09	0.07
1	1	1	1	1	0.99
0.5	NA	NA	NA	NA	NA
0.16	0.18	NA	NA	NA	NA
NA	NA	0.14	0.18	0.12	0.12
NA	0.07	NA	NA	NA	NA
0.05	0.05	NA	NA	NA	NA
0.96	0.95	0.88	0.95	0.86	0.87
0.25	0.27	0.63	0.69	0.91	0.83
1	1	0.99	0.99	0.97	0.97
NA	NA	NA	0.34	0.18	0.23
0.09	0.13	NA	NA	NA	NA
0.84	0.71	0.89	NA	NA	0.91
0.14	0.18	0.23	NA	NA	NA
NA	NA	NA	NA	NA	NA
0.88	0.89	0.94	0.97	0.95	0.96
0.23	0.18	NA	0.34	NA	NA
0.74	0.84	NA	NA	NA	NA
1	1	0.97	0.91	0.99	0.98
0.17	0.22	NA	NA	NA	NA
0.38	0.3	0.57	0.48	0.69	0.73
0.89	0.89	0.66	0.97	0.92	0.81
0.04	0.04	0.06	0.17	NA	NA
0.13	0.09	0.12	NA	NA	NA
0.97	0.97	0.91	0.92	0.94	0.96

0.21	0.18	NA	0.12	NA	NA
0.98	0.99	0.99	0.99	0.99	0.99
NA	NA	0.43	0.83	0.47	0.67
0.99	0.99	0.94	0.94	0.96	0.96
0.99	0.98	0.99	1	0.98	0.98
0.11	0.11	NA	0.16	NA	NA
0.32	0.22	0.27	0.32	0.29	0.16
0.02	0.01	0.05	0.05	NA	NA
0.62	0.62	0.57	0.77	0.84	0.82
0.59	0.55	0.97	0.99	0.77	0.84
NA	NA	NA	NA	NA	NA
0.55	0.52	NA	0.67	0.64	0.62
0.15	0.16	0.48	0.46	0.3	0.25
0.51	0.58	NA	0.51	0.68	NA
0.66	0.57	NA	NA	0.62	NA

t12_1_riboZer	t12_2_riboZer	RAPplus_2_rib	RAPminus_2_	sk1_1_riboZero
0.98	NA	0.96	1	1
0.92	0.84	0.98	0.93	0.94
0.14	0.13	0.24	0.07	0.03
0.22	0.15	0.18	0.06	0.05
0.3	0.39	0.45	0.08	0.03
0.97	0.97	0.96	0.86	0.95
0.84	0.93	0.86	0.9	0.92
0.18	0.2	0.99	0.97	0.7
0.69	0.38	0.12	0.12	0.16
0.13	0.35	0.23	0.58	NA
0.99	0.99	0.99	0.98	0.98
0.87	0.91	NA	NA	NA
0.96	0.99	0.99	0.99	0.97
0.93	NA	NA	0.9	0.92
0.21	0.25	0.28	0.11	0.08
0.77	0.45	0.99	0.99	0.9
1	1	1	1	1
0.2	0.15	0.31	0.09	0.05
0.55	0.49	0.6	0.21	0.14
0.25	0.2	0.39	0.09	0.03
1	1	1	1	1
0.31	0.2	0.11	0.05	0.04
0.3	0.16	0.29	0.12	0.07
NA	0.2	0.28	0.1	0.08
NA	0.39	0.21	0.08	0.06
0.37	0.42	0.68	0.12	0.08
0.27	0.26	NA	NA	NA
0.86	0.8	0.97	0.96	0.96
0.32	0.25	0.39	0.09	0.07
0.08	0.07	0.15	0.06	0.04
0.94	0.92	0.9	0.93	0.95
0.55	0.47	0.59	0.57	0.42
0.99	0.99	1	1	1
0.93	NA	0.91	NA	NA
0.4	0.44	0.37	0.13	0.08
0.98	0.98	0.98	0.97	0.95
0.97	0.98	0.95	0.94	0.9
1	1	1	0.99	0.99
0.83	0.77	NA	NA	NA
0.27	0.19	0.3	0.07	0.05
0.24	0.17	0.58	0.09	0.03
1	1	1	1	1
0.21	0.2	0.3	0.39	NA
0.98	0.98	1	1	1
0.45	0.55	NA	NA	NA
0.16	0.24	0.36	0.13	0.07
0.86	0.84	0.59	0.52	0.59

0.96	0.97	0.73	0.65	0.69
1	1	1	1	1
0.34	NA	0.28	0.07	0.05
0.98	0.99	NA	NA	0.97
0.17	0.19	0.17	0.1	0.07
0.19	0.23	NA	NA	NA
NA	NA	NA	NA	NA
0.93	NA	NA	NA	NA
0.2	NA	0.62	0.19	0.14
0.97	0.95	NA	0.17	NA
0.24	0.28	0.25	0.05	0.03
0.88	0.46	0.83	0.81	0.74
0.99	0.99	NA	NA	0.83
0.69	0.75	0.81	NA	NA
0.35	0.29	0.18	0.06	0.04
0.36	0.29	0.35	0.22	0.27
0.99	0.98	0.98	0.97	0.97
0.81	0.89	0.96	0.97	0.65
1	1	0.98	0.97	0.99
NA	NA	0.96	0.84	0.43
0.99	0.98	1	1	1
0.36	0.33	0.36	0.07	0.05
0.33	0.22	NA	NA	NA
0.79	NA	NA	NA	NA
0.8	0.82	0.79	0.85	0.88
0.18	NA	0.29	0.04	0.03
0.89	NA	0.87	0.96	0.64
0.97	0.86	NA	NA	NA
0.3	0.2	0.22	0.09	0.04
NA	NA	NA	NA	NA
0.98	0.98	0.98	1	1
0.92	0.86	NA	0.83	NA
0.91	0.76	0.8	0.96	0.89
0.59	0.52	0.74	0.66	0.49
0.4	0.41	0.27	0.28	0.24
NA	NA	0.98	0.99	0.67
0.98	0.98	0.96	NA	NA
NA	0.39	0.33	0.36	0.59
0.75	0.77	NA	NA	NA
0.36	0.21	0.46	0.16	0.09
0.18	0.24	0.26	0.17	0.1
0.98	0.98	0.93	0.88	0.55
NA	NA	NA	NA	NA
0.73	0.54	0.27	0.32	0.25
0.92	0.96	0.89	0.97	0.96
0.89	0.92	0.9	NA	NA
0.47	0.34	NA	NA	0.89
0.74	0.81	0.35	0.37	0.37
0.83	NA	NA	NA	0.29

0.53	0.5	0.55	0.35	0.18
0.97	0.97	0.98	1	1
NA	NA	NA	NA	NA
0.97	0.99	0.93	0.92	0.98
0.96	0.93	0.89	0.82	0.82
0.3	0.19	0.14	0.05	0.06
0.56	0.37	0.17	0.16	0.14
0.98	0.96	NA	NA	0.89
0.96	0.91	0.55	0.78	0.5
0.51	0.36	0.27	0.24	0.38
0.99	0.97	1	0.99	0.98
1	1	1	1	0.99
0.9	0.88	0.83	0.88	0.78
NA	NA	NA	NA	NA
0.14	0.08	0.11	0.04	0.02
0.56	0.49	0.69	0.26	0.16
0.9	0.9	0.48	0.45	NA
0.26	0.3	0.68	0.18	0.13
0.94	0.81	NA	0.95	0.9
1	1	1	1	1
0.23	0.19	0.16	NA	NA
0.98	0.98	1	1	0.95
0.86	NA	0.57	0.24	0.28
NA	NA	NA	0.43	0.28
NA	NA	NA	NA	NA
0.86	0.77	0.26	0.28	0.35
0.19	0.22	0.2	0.21	0.34
0.98	0.97	0.99	0.95	0.94
1	1	1	1	1
0.76	0.76	0.37	0.23	0.12
0.77	0.79	0.68	0.57	0.47
0.99	0.99	0.97	0.94	0.95
0.87	0.37	0.23	0.29	0.28
0.43	0.3	0.31	0.35	0.55
0.71	0.67	0.25	0.15	0.12
1	1	0.99	0.92	NA
1	1	0.96	0.96	0.96
NA	NA	0.96	0.8	NA
0.98	0.98	0.95	0.99	0.99
0.24	0.1	0.3	0.07	0.03
0.5	0.28	0.47	0.16	0.08
0.14	0.07	0.21	0.07	0.04
0.97	0.86	0.94	0.9	0.85
0.99	0.99	0.99	0.99	0.99
0.98	0.98	0.89	0.98	0.99
0.84	0.74	0.99	0.97	0.99
0.85	0.56	NA	NA	NA
0.97	0.94	0.84	NA	0.88
NA	0.12	0.2	0.13	0.29

NA	NA	0.44	NA	NA
0.87	0.96	0.61	0.97	0.83
NA	NA	NA	NA	NA
0.22	0.17	0.29	0.08	0.04
0.08	0.07	0.1	0.13	0.15
0.49	0.42	0.4	NA	0.34
NA	NA	0.94	0.96	NA
0.25	0.16	0.34	0.09	0.04
0.31	0.4	0.39	0.1	0.05
0.14	NA	0.22	0.09	0.05
0.92	0.35	0.97	0.98	0.97
0.32	0.28	0.54	0.64	0.54
0.37	0.33	0.19	0.17	0.25
NA	NA	NA	NA	NA
NA	NA	0.97	1	1
0.95	0.97	0.7	0.72	0.73
0.99	0.96	1	1	1
0.7	NA	0.99	0.98	0.98
0.19	0.17	0.66	0.27	0.34
0.92	0.86	0.64	0.91	0.87
0.95	0.93	0.92	0.91	0.97
0.25	0.29	0.06	0.06	0.08
0.67	0.61	0.13	NA	NA
0.75	0.68	0.43	0.33	0.3
0.71	0.74	0.35	0.39	0.33
0.22	0.55	0.46	0.1	0.07
0.9	0.92	0.83	NA	NA
1	1	1	1	1
0.43	0.57	0.6	0.26	0.18
0.98	NA	0.98	1	1
0.89	0.96	0.9	0.87	0.9
0.17	0.23	0.27	0.04	0.02
0.23	0.21	0.97	0.93	NA
0.37	0.45	NA	NA	NA
0.86	0.57	0.43	0.38	NA
0.14	0.13	0.21	0.05	0.03
0.75	0.59	0.95	0.32	0.43
0.42	NA	0.21	0.14	0.16
0.98	0.98	0.99	0.99	0.97
0.13	0.1	0.14	0.06	0.05
0.98	0.98	0.95	0.96	0.94
0.88	0.79	0.75	0.68	0.63
0.33	0.35	0.47	0.09	0.05
0.34	0.74	0.33	0.52	0.59
NA	NA	0.98	0.98	0.98
0.26	0.17	0.17	0.22	0.25
0.99	0.99	0.98	0.98	0.98
0.59	0.94	0.94	0.79	0.61
0.99	0.99	0.99	1	1

0.76	0.76	0.78	0.67	0.82
0.2	0.15	0.22	NA	0.16
1	1	0.99	0.98	0.97
0.7	0.43	0.77	0.69	0.64
0.27	0.19	0.35	0.29	0.24
0.99	0.99	0.99	0.99	1
NA	NA	NA	NA	NA
0.94	NA	0.26	NA	NA
0.16	0.13	NA	NA	NA
0.99	0.98	0.74	NA	NA
0.47	0.41	0.51	0.08	0.05
0.33	0.19	0.33	0.07	0.05
0.5	0.52	0.81	0.63	0.6
0.66	0.73	NA	NA	NA
0.61	0.52	0.3	0.31	0.5
0.94	0.84	0.88	0.89	NA
0.91	0.87	0.79	0.85	NA
0.26	0.45	0.66	0.15	0.09
0.18	0.17	0.22	0.11	0.09
0.92	NA	0.89	0.89	NA
0.27	0.17	0.33	0.37	0.32
0.39	0.26	0.21	0.05	0.01
0.99	0.99	1	1	1
0.36	0.4	0.11	0.07	0.03
0.97	0.97	0.97	0.99	0.98
0.99	0.99	0.99	1	1
0.49	0.35	0.37	0.26	0.27
0.7	NA	0.11	0.14	0.13
0.64	0.85	0.88	0.77	0.43
0.19	0.23	0.14	0.15	0.19
NA	NA	NA	NA	NA
1	1	1	1	1
0.13	0.35	0.22	0.59	NA
0.98	0.98	0.99	1	1
0.37	0.54	0.52	0.15	0.08
0.91	0.85	0.89	0.92	NA
0.46	0.48	0.42	NA	NA
0.89	0.62	0.99	0.99	0.94
0.57	0.66	0.86	0.3	0.23
0.99	0.99	0.97	0.98	0.97
NA	NA	NA	NA	NA
1	1	1	0.99	1
0.63	NA	NA	0.47	0.29
0.3	NA	0.28	0.08	0.04
0.51	0.36	0.38	0.16	0.09
0.22	0.16	0.17	0.27	0.52
NA	NA	0.67	0.28	0.22
0.82	NA	0.62	0.75	0.82
0.26	0.29	0.25	NA	NA

0.1	0.07	0.27	0.24	0.45
0.25	0.33	0.16	0.07	0.07
0.74	0.83	0.59	0.6	0.57
0.23	NA	0.21	0.12	0.1
0.96	0.97	1	1	0.97
NA	NA	0.99	0.98	NA
0.28	0.25	0.24	0.08	0.03
0.99	0.96	NA	NA	NA
NA	NA	NA	NA	NA
0.13	0.1	0.15	0.09	0.07
1	1	1	1	1
NA	NA	NA	NA	NA
NA	0.74	0.57	0.43	NA
0.29	0.16	0.45	0.09	0.04
0.97	0.96	0.98	0.98	0.97
NA	NA	NA	NA	NA
0.24	0.2	0.29	0.19	0.3
0.12	0.22	0.21	0.2	0.18
0.39	0.35	0.16	0.23	0.27
0.98	0.97	0.97	0.98	0.97
0.86	0.87	0.98	1	1
0.95	0.91	0.87	0.95	0.88
0.96	0.95	NA	NA	NA
0.2	0.21	0.25	0.05	0.04
0.66	0.83	NA	0.59	0.43
0.91	0.93	0.97	0.97	0.88
0.02	0.01	0.12	0.07	0.03
0.98	0.96	0.99	1	1
0.72	0.54	0.47	0.13	0.08
0.91	NA	NA	NA	NA
0.19	0.1	0.14	0.05	0.02
0.26	0.25	0.74	0.94	0.49
0.85	NA	0.9	0.18	0.11
0.09	0.09	0.09	0.1	0.11
0.58	0.77	NA	NA	NA
0.96	0.96	0.67	0.51	0.47
0.97	0.99	0.98	0.99	0.98
0.18	0.15	0.23	0.07	0.06
0.91	0.69	NA	NA	NA
0.98	0.99	0.99	0.98	0.98
0.36	0.37	0.35	0.47	0.36
0.46	0.4	0.11	0.13	0.28
0.93	NA	NA	NA	NA
NA	NA	0.35	0.52	NA
0.98	0.99	0.84	0.94	0.92
NA	0.95	NA	0.89	0.93
0.99	1	0.99	0.99	0.99
0.99	0.99	0.96	0.93	0.95
1	0.99	0.99	0.98	0.98

0.99	0.99	1	0.99	0.98
0.4	NA	0.38	0.4	0.17
0.97	0.96	0.96	0.96	0.97
NA	0.16	NA	0.15	NA
1	1	0.99	0.98	0.98
0.1	0.06	0.12	0.07	NA
0.96	0.92	0.97	0.93	0.84
0.98	0.99	0.98	0.98	0.99
NA	0.86	NA	0.62	0.68
0.23	0.21	0.15	0.07	0.02
0.59	0.27	0.07	0.18	0.14
0.77	0.5	0.44	0.43	0.21
NA	NA	0.14	NA	NA
0.97	0.94	0.99	0.99	0.99
0.67	0.7	0.78	0.68	0.58
0.43	0.61	0.58	0.08	0.04
NA	0.81	NA	NA	NA
0.91	0.64	0.98	0.99	0.92
0.3	0.19	0.37	NA	NA
0.18	0.28	0.42	0.07	0.04
0.99	0.98	0.99	1	1
0.28	0.27	0.23	0.24	0.11
NA	NA	0.46	0.35	0.46
0.67	0.63	0.29	0.12	0.06
0.99	0.94	0.94	0.95	NA
1	1	0.99	0.99	0.99
0.05	NA	0.15	0.05	0.03
0.61	0.76	0.81	0.76	NA
1	1	1	1	1
0.94	0.92	NA	NA	NA
NA	NA	1	0.99	NA
0.92	0.92	0.88	0.89	NA
0.81	NA	0.89	0.85	0.84
0.23	0.23	0.43	0.32	0.13
0.91	0.81	0.64	NA	NA
0.92	0.96	0.98	0.98	0.97
NA	0.75	NA	NA	NA
NA	NA	NA	NA	0.22
0.09	0.07	0.17	0.06	0.12
0.46	0.41	0.26	0.08	0.07
0.3	0.34	0.32	0.44	0.31
0.3	NA	NA	NA	NA
0.9	0.68	0.54	0.28	NA
NA	0.87	NA	NA	NA
0.96	0.88	0.89	0.95	0.9
NA	NA	NA	NA	NA
1	0.99	0.99	0.94	0.94
0.98	0.99	0.97	0.98	0.98
NA	NA	NA	NA	NA

0.99	0.98	0.93	0.99	1
1	1	1	1	0.99
NA	NA	0.88	NA	0.63
1	1	0.99	0.99	1
0.12	0.16	0.08	0.1	0.18
0.97	0.96	0.97	0.96	0.94
0.08	0.11	0.05	0.04	0.05
0.43	0.43	0.45	0.24	0.17
0.18	0.27	0.37	0.08	0.05
0.59	0.46	0.91	0.5	0.3
0.61	0.45	0.48	0.12	0.06
0.88	NA	0.93	0.97	0.98
0.22	0.21	0.1	0.13	0.15
0.46	NA	NA	NA	NA
1	1	1	1	1
NA	NA	0.78	0.39	0.29
0.16	0.08	0.17	0.1	0.09
0.21	0.18	0.19	0.24	0.25
0.18	NA	0.2	0.04	0.03
0.96	0.97	0.97	0.99	0.99
NA	NA	NA	NA	NA
0.7	0.41	0.37	0.14	0.12
0.26	0.27	0.1	0.09	0.1
0.73	0.45	0.99	0.99	0.92
0.33	0.26	0.1	0.2	0.17
1	0.99	0.99	0.99	1
0.86	NA	NA	NA	NA
0.63	0.45	0.15	0.11	0.24
0.53	0.5	NA	0.7	NA
0.3	NA	0.35	0.09	0.04
0.11	0.06	0.14	0.04	0.02
0.88	0.87	0.99	0.95	0.96
0.97	0.95	NA	NA	NA
0.99	0.99	1	0.99	0.99
0.88	NA	NA	NA	NA
0.27	NA	0.18	NA	NA
0.9	0.91	0.79	0.7	0.78
0.2	NA	0.32	0.09	0.07
NA	NA	NA	NA	NA
0.88	0.87	0.31	0.37	0.56
NA	NA	0.22	0.21	0.19
0.75	0.72	0.81	0.92	0.75
0.73	0.88	1	0.7	0.74
0.62	0.43	0.51	0.11	0.08
0.75	0.58	0.9	0.27	0.27
0.92	0.97	0.94	0.96	0.96
0.22	0.17	0.26	0.09	0.03
0.23	0.3	0.48	0.1	0.07
0.97	0.96	0.96	0.94	0.96

0.25	NA	0.21	0.25	0.25
1	1	1	1	1
0.96	0.96	NA	0.81	0.93
0.97	0.96	0.97	0.97	0.99
0.98	0.97	1	1	1
NA	NA	NA	NA	NA
0.13	0.35	0.23	0.58	NA
0.07	0.06	0.14	0.03	0.01
0.97	0.99	NA	NA	NA
0.57	0.59	0.71	0.72	0.65
NA	NA	NA	NA	0.43
0.84	0.75	0.79	0.87	0.74
0.32	0.32	0.73	0.62	0.82
0.9	0.78	0.42	NA	NA
0.59	NA	0.86	NA	0.63