



Supporting Online Material for

Gene Transposition as a Cause of Hybrid Sterility in *Drosophila*

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Supporting Online Material

Materials and Methods

4-*sim* introgression. Flies were reared on standard cornmeal-dextrose-yeast-agar medium and crosses were performed at 24°C. Species crosses were made by mass mating ten *D. simulans* females from the fertility rescue strain *C167.4* to 20-25 *D. melanogaster* males from the viability-rescuing strain *Zhr*. Because this cross yields few progeny, adults were transferred to fresh food every five days for two weeks to maximize the number of F₁ hybrid females obtained. Hybrid females were then backcrossed to a *D. melanogaster* recessively-marked fourth chromosome stock for several generations to ensure that the major chromosomes were of *D. melanogaster* origin. We confirmed the presence of the 4-*sim* chromosome by sequencing a region of the *cubitus interruptus* locus that shows fixed nucleotide differences between these two species.

Male fertility tests. Fertility was assayed as described in Orr (1992). Briefly, sperm motility was scored in males aged 5-7 days in isolation. Testes were dissected, examined under a compound microscope with dark-field optics, and classified into three sperm motility classes: “Many”: abundant motile sperm present; “Few”: a few localized motile sperm present; “None”: no motile sperm present. Offspring production tests were performed by placing a single male in a vial with three *D. melanogaster* virgin females. Flies were then transferred to a fresh vial every three days up to day nine. All offspring that emerged from a vial by day 18 were scored.

P-element excisions. $P\{y^{+mDint2} w^{BR.E.BR} SUPor-P\}CG17923 (P\{y^+,w^+\}JYAlpha)$ was obtained from the Bloomington *Drosophila* Stock Center (#16983). We determined genetically that $P\{y^+,w^+\}JYAlpha$ lies on the fourth chromosome and sequenced the flanking region to verify its insertion in exon 3 of $JYAlpha^{mel}$. *Delta2-3* (99B) (1) was used as a transposase source to mobilize the *P*-element. We crossed *D. melanogaster* $y,w; \Delta 2-3,Sb; P\{y^+,w^+\}JYAlpha/ci^D$ males to $w; ci^D/ey^D$ virgin females by mass matings. White-eyed male progeny were then selected and mated individually to $w; ci^D/ey^D$ females to establish independent candidate excision stocks. Precise and imprecise excisions were confirmed by DNA sequencing.

***JYAlpha*^{sim} segregation test.** Because chromosome 4 is often entangled in the chromocenter in polytene squashes, and *JYAlpha* is the proximal-most gene on 4, we tested *JYAlpha*'s location in *D. simulans* by segregation analysis, not by *in situ* hybridization. *D. simulans* C167.4 females were crossed to an inbred *D. simulans* stock bearing the recessive visible mutation *ebony* (*e*; 3-61.0) by mass mating. F₁ males (who experience no recombination) were then single pair-mated to stock *e/e* females. The resulting progeny were genotypically *e/e* or *e/C167.4* at the third chromosome. We molecularly genotyped 20 individual backcross flies using a strain-specific indel difference in intron 2 of *JYAlpha*. Phenotypically *e*⁺ flies were always heterozygous for the *JYAlpha* marker, whereas phenotypically *e* flies were always homozygous for the relevant marker, as expected if *JYAlpha* resides on chromosome 3 in *D. simulans*.

Southern blots. Genomic DNA was restriction digested with *Hind*III and separated on a 1.0% agarose gel. Digested DNA was transferred to nitrocellulose paper and hybridized in 2X SSC, 5X Denhardt's at 65°C for 14 hours. Sequences used for the hybridization probes were PCR amplified from a highly conserved, 1.2 kb region of exon 3 from *D. melanogaster*. PCR product was gel purified and random primer labeled with [α -³²P]dCTP using the Rediprime II Random Prime labeling system (Amersham Biosciences). Hybridized and washed filters were exposed to X-ray film at -80°C for 14 hours.

PCR and sequencing. Primers were designed using the mosaic *D. simulans* and the annotated *D. melanogaster* genome assemblies and were used for PCR amplification of genomic DNA. (*JYAlpha* is misannotated [truncated] in release 4.3 of the *D. melanogaster* genome. We always used *JYAlpha*-specific primers, which do not amplify product from *ATP α* , another Na⁺/K⁺ ATPase that resides in the cytological region 93A4 in *D. melanogaster* and *D. simulans*.) PCR was performed using a standard protocol with the Qiagen *Taq* PCR Master Mix Kit (Valencia, CA, USA). Direct sequencing was performed on both strands of PCR products using ABI Prism BigDye Chemistry version 3.0 (PE Applied Biosystems) on an automated ABI sequencer. All sequences were edited using Sequencher version 4.2. K_a and K_s calculations were performed using DnaSP version 4.0 (2).

Supplementary Text

JYAlpha's location in the *Drosophila sechellia* trace archive

Whole genome shotgun sequencing of the *Drosophila sechellia* genome is currently completed at 3-fold coverage with a projected 8-fold coverage (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list_uids=12711). The *D. sechellia* trace archive was constructed briefly as follows. The genome was sheared, cloned, and used to generate fragments of 4, 10, and 40 kb. Each fragment was sequenced at both ends, creating two non-complementary sequences roughly 500-1000 base pairs in length associated with the same genomic fragment (Figure S1). These two sequences were then paired as "matepairs." This feature facilitates BLASTing the *D. sechellia* trace archive with a "target" gene or sequence of interest, then identifying the homologies of sequences 4-40 kb away from the target's location (MegaBLAST; <http://www.ncbi.nlm.nih.gov/blast/mmtrace.shtml>).

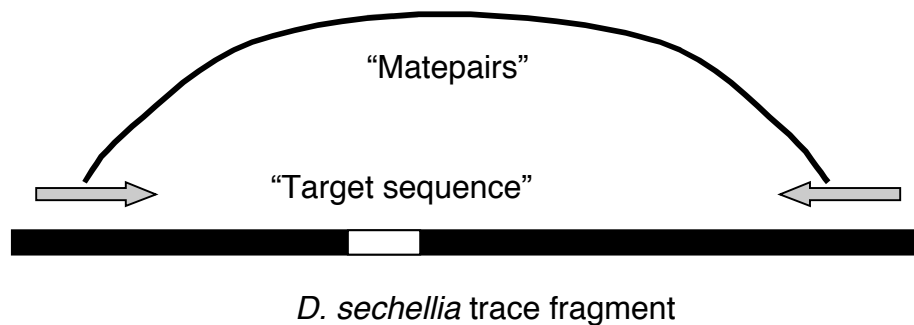


Figure S1. Trace archive matepair construction. Target sequences (white) that BLAST to fragments in the *D. sechellia* trace archive (black) are associated with matepairs (grey): sequences on the same genomic fragment that reside 4-40 kb away.

We performed a BLAST search of the *D. sechellia* trace archive using full length *JYAlpha* from *D. melanogaster*. Our search returned 26 hits (Table S2). Two of these (#25 and #26) were too weak to be reliable and were excluded from the analysis. We BLASTed the remaining 24 *D. sechellia* traces and their matepairs back to the *D. melanogaster* genome (FlyBase BLAST Service; <http://flybase.net/blast/>). If *JYAlpha* resides on chromosome 4 in *D. sechellia*, both the *JYAlpha*^{sech} target sequences and their respective matepairs should BLAST to chromosome 4 in *D. melanogaster*. If, however, *JYAlpha* resides on chromosome arm 3R in *D. sechellia*, as our breakpoint PCR results imply, only the *JYAlpha*^{sech} target sequences should BLAST to chromosome 4 in *D. melanogaster*: their matepairs should all BLAST to 3R. Table S3 shows that this is the pattern observed for most of the traces.

JYAlpha^{mel} corresponds to position 21555-25621 on chromosome 4 of the annotated *D. melanogaster* genome sequence (Build 4.3). Most of the *JYAlpha*^{sech} sequences obtained from the traces had BLAST hits to chromosome 4 of *D. melanogaster*, as expected, roughly corresponding to the region of *JYAlpha*^{mel} (Table S3). For *JYAlpha*^{sech} sequences that showed no clear BLAST hits to the *D. melanogaster* genome, we aligned *JYAlpha* from the *D. sechellia* trace with *JYAlpha* from *D. melanogaster*. In all cases, the two sequences closely matched. Most importantly, *JYAlpha*^{sech} trace matepairs never BLASTed to chromosome 4 of *D. melanogaster*; all those that localized to a chromosome, localized to chromosome 3. These results support our conclusion from our *D. sechellia* breakpoint PCR assay: *JYAlpha* resides on chromosome arm 3R in *D. sechellia*.

JYAlpha's location in Drosophila yakuba

The DNA sequence of *JYAlpha*^{mel} was compared to the April 2004 genome assembly of *D. yakuba* available from the Washington University Genome Sequencing Center (<http://genome.wustl.edu>). A custom BLAST database was built containing all *D. yakuba* contigs that could be assembled and assigned to chromosomes. We BLASTed this database using a sequence of 4,066 base pairs from chromosome 4 of *D. melanogaster* which included *JYAlpha*^{mel} and some of its flanking sequence. This chromosome 4 region from *D. melanogaster* closely matched chromosome 4 in *D. yakuba* (4,006 bases, 91% similarity, E-value=0.0).

We used coordinate information from our BLAST results to identify the contig carrying *JYAlpha*^{yak} (Contig66.19) in the assembly AGP files. Contig66.19 spans coordinates 1-126689 on the *D. yakuba* fourth chromosome, extending roughly from the centromere proximally, to *Ankyrin* (*Ank*) distally, and includes the sequence of *JYAlpha*^{yak} and its neighboring gene, *plexinB* (*plexB*). We then BLASTed Contig66.19 back to the *D. melanogaster* genome assembly. Most of the sequence from Contig66.19 matched chromosome 4 in *D. melanogaster*, as expected, although small regions had hits to other chromosomes. These are similar to heterochromatic sequences. Finally, we visually confirmed the *JYAlpha*^{yak} region using the UCSC BLAT genome browser (<http://genome.ucsc.edu/cgi-bin/hgBlat>) (3).

JYAlpha's location in Drosophila pseudoobscura and D. persimilis.

We performed a BLAST search (tblastn) of the *D. pseudoobscura* genome (Release 2.0) using the amino acid sequence from *JYAlpha*^{mel}. The best hit was to

chromosome arm *XL* (group 1a; E-value=0.0) which is the homologue of the *X* chromosome in *D. melanogaster*. This *XL*-linked locus shows ~71% amino acid identity to *JYAlpha^{mel}* and appears to be *JYAlpha*'s only location in *D. pseudoobscura*. (Similar results were obtained for *D. persimilis*.) Visual inspection of the sequence and its alignment with *JYAlpha^{mel}* confirms that this *XL*-linked locus is *JYAlpha*. We verified that the genome sequence in this region of *XL* was correct by performing PCR assays across both the proximal and distal "*JYAlpha-XL*" breakpoints. Reverse-transcription PCR shows that this gene produces a transcript in both *D. pseudoobscura* and *D. persimilis*. It appears, then, that *JYAlpha* has transposed more than once in the genus *Drosophila*.

Table S1. *JYAlpha*^{mel} BLAST hits to *D. sechellia* trace archive

<i>D. sechellia</i> trace fragment	(Bits)	e-value
1. gnltil831403209 G728P61071FC5.T0	1435	0.0
2. gnltil833115787 G728P65429FA9.T0	1360	0.0
3. gnltil832973287 G728P62735RG4.T0	1356	0.0
4. gnltil831882663 G728P6275FF11.T0	1342	0.0
5. gnltil834652536 G728P64815RF5.T0	1340	0.0
6. gnltil834537657 G728P63910FH4.T0	1275	0.0
7. gnltil833060564 G728P6590FB6.T0	1273	0.0
8. gnltil834541420 G728P62989RG9.T0	1120	0.0
9. gnltil833038441 G728P63415RG11.T0	1114	0.0
10. gnltil834733873 G728P61150FB5.T0	1114	0.0
11. gnltil838641402 G728P5834RF11.T0	1070	0.0
12. gnltil849173379 G728P64829FC1.T0	954	0.0
13. gnltil833088864 G728P63598RD6.T0	938	0.0
14. gnltil834532904 G728P62112FA3.T0	918	0.0
15. gnltil835675081 G728P64470FE12.T0	866	0.0
16. gnltil839073441 G728P5922FD4.T0	783	0.0
17. gnltil833042006 G728P6113FH12.T0	692	0.0
18. gnltil834356456 G728P6632RE9.T0	638	2e-180
19. gnltil831362150 G728P6907RG11.T0	630	5e-178
20. gnltil834712889 G728P6329FC11.T0	628	2e-177
21. gnltil839038841 G728P5486RH1.T0	605	3e-170
22. gnltil834515432 G728P62586FB5.T0	549	2e-153
23. gnltil835824696 G728P65063FC1.T0	525	2e-146
24. gnltil834729201 G728P6967FE9.T0	389	3e-105

25. gnltil838190041 G728P64983RH11.T0	250	2e-63
26. gnltil849947187 G728P64594FC4.T0	153	3e-34

Table S2. *D. sechellia* trace BLASTs back to *D. melanogaster*

<i>D. sechellia</i> trace	Fragment size	<i>JYAlpha</i> ^{sech} BLAST location in <i>D. melanogaster</i> Chromosome, position	Matepair BLAST location in <i>D. melanogaster</i> Chromosome, position
1.	4 kb	4, 24900	3R, ~95000
2.	4 kb	no hit, but matches <i>JYAlpha</i> ^{mel}	repetitive sequence, but best hit was chrU
3.	10 kb	4, 24900	3R, ~83000
4.	4 kb	4, 25000	3R, ~95000
5.	4 kb	weak hit to 4, but matches <i>JYAlpha</i> ^{mel}	3R, ~104000
6.	4 kb	4, 25000	3R, ~95000
7.	4 kb	no hit, but matches <i>JYAlpha</i> ^{mel}	3R, ~104000
8.	4 kb	no hit, but matches <i>JYAlpha</i> ^{mel}	3R, ~103000
9.	4 kb	4, 25000	3R, ~95000
10.	4 kb	4, 25000	3R, ~95000
11.	4 kb	4, 25000	no clear hit but best was to 3h
12.	10 kb	4, 25000	3R, ~109000
13.	4 kb	4, 24000	3R, ~103000
14.	4 kb	4, 24000	no clear hit but best was to 3h
15.	4 kb	4, 24000	no clear hit but best was to 3h
16.	4 kb	4, 24000	3R, ~103000
17.	4 kb	no hit, but matches <i>JYAlpha</i> ^{mel}	3R, ~103000

chrU = unplaced sequences; 3h = chromosome 3 heterochromatin

Table S2. con't

<i>D. sechellia</i> trace	Fragment size	<i>JYAlpha</i> ^{sech} BLAST location in <i>D. melanogaster</i> Chromosome, position	Matepair BLAST location in <i>D. melanogaster</i> Chromosome, position
18.	4 kb	many positions, but matches <i>JYAlpha</i> ^{mel}	3R, ~107000
19.	4 kb	many positions, but matches <i>JYAlpha</i> ^{mel}	3R, ~107000
20.	4 kb	no hit, but matches <i>JYAlpha</i> ^{mel}	no hit
21.	10 kb	weak hit to 2R but matches <i>JYAlpha</i> ^{mel}	repetitive sequence, best to 3L
22.	4 kb	weak hit to 2R but matches <i>JYAlpha</i> ^{mel}	3R, ~106000
23.	4 kb	weak hit to chr U but matches <i>JYAlpha</i> ^{mel} at beginning	3R, ~107000
24.	4 kb	no hit, but loosely matches <i>JYAlpha</i> ^{mel}	3R, ~107000

chrU = unplaced sequences; 3h = chromosome 3 heterochromatin; 2R = chromosome arm 2R; 3L = chromosome arm 3L

Figure S2. Alignment of a sub-section of cytological region 82A1 between *D. melanogaster*, *D. simulans* and *D. sechellia*

We obtained roughly 15,600 base pairs of contiguous sequence from cytological region 82A1 using the latest genome assemblies of *D. melanogaster*, *D. simulans*, and *D. sechellia* (available at UCSC Genome Browser; <http://genome.ucsc.edu>) (3). Sequences were aligned using CLUSTAL X (1.83.1) and manually adjusted. The aligned region includes part of *CG1092*, all of *CG9766*, all of *JYAlpha* (in *D. simulans* and *D. sechellia*), and part of *complexin* (*cpx*).

Genes in the region flanking *JYAlpha* in *D. simulans* and *D. sechellia* (*CG1092* and *CG9766* proximally, and *cpx* distally) show conserved gene order and strong sequence similarity between all three species. *JYAlpha*, however, is present and nearly identical in both *D. simulans* and *D. sechellia*, but absent from this region in *D. melanogaster*. Genes are shown from proximal to distal and color coded: *CG1092*, *CG9766*, *JYAlpha*, *cpx*. The respective starting and ending genome coordinates of the ~15.6 kb regions are given after the species names below.

```

sim_3R_168427-182237      ACTTCCATGCTAGAGACCTGAGCCGGGAGTACAAGGACCTGCGGATCTAC
sech_3R_113859-128167    ACTTCCATGCTAGAGACCTGAGCCGGGAGTACAAGGACCTGCGGATCTAC
mel_3R_93319-108570      ACTTCCATGCTAGAGACCTGAGCCGGGAGTACAAGGACCTGCGGATCTAC
*****

sim_3R_168427-182237      CGGGAGAGCTACGAACACAACGTGCGCAATCTGGAGCAGCACCGAAAAC
sech_3R_113859-128167    CGGGAGAGCTACGAACACAACGTGCGCAATCTGGAGCAGCACCGAAAAC
mel_3R_93319-108570      CGGGAGAGCTACGAACACAACGTTCGCAATCTGGAGCAGCACAGAAAAC
*****

sim_3R_168427-182237      GAATTCAACATACGAGCTGGGGGTTTCAGCGCACCATGCTGGATTGGAGCA
sech_3R_113859-128167    GAATTCAACATACGAGCTGGGTGTTTCAGCGCACCATGCTGGATTGGAGCA
mel_3R_93319-108570      GAATTCAACATACGAATTGGGGGTTTCAGCGCACCATGCTGGATTGGAGCA
*****

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sim_3R_168427-182237
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mel_3R_93319-108570
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TGTACCTCTATCAAAGCCGCAACAAGCCCATGTCCTACTTCTACTCCACG
TGTACCTCTTTTACAGAGCCGCAACAAGCCCATGTCCTACTTCTACTCCACG
***** **

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mel_3R_93319-108570
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TTTACGGTCCATTGTGACATGATGCTTTTTAATAGTCTGGAGCGTCAGCG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
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TGATTTACGCGGTTTCGCGAAGATGTGGAGTGTTTAAGGCTGCCGCAGT

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sech_3R_113859-128167
mel_3R_93319-108570
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TCGTTAATGTTCTGGATGAGGCCAGAATGCTGGCTGTGATCTACTTAAAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
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AGCTTCAGAGCCGCTGGATAGACTACAGCGCCTGGATCAACTCGCCCC
AGCTTCGAGCGCCTGGATAGACTACAGCGCCTGGATCAACTCGCCTCC
***** **

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mel_3R_93319-108570
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mel_3R_93319-108570
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***** **

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mel_3R_93319-108570
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***** **

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mel_3R_93319-108570
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GAACAAGGACTTTTACGACATATACTCTTGTGGTTTTCAAACGGAGAACC
GAACAAGGACTTTTACGACATATACTCTTGTGGATTCAAACGGAAAACC
***** **

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CTATGACTTGTGTTTAAATAGATCAAGTCAATTTCTATCATAACATATACTA
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CTATGACTTGTGTTTAAAGATCAAGACCATTCTACCATATAT-----
***** * **

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mel_3R_93319-108570
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--TTTAGCTTACGAGATATAATAAA-TCATTAACATCATCTTAACGCTGT
---TTAGTTTACGAGATACAATAAAAGCAATAACATTTCTATAAAGGTGT
*** **

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
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ACAAACCATTTGAAAAAATGGCTTTTCAGTAAAAACAAGCGA-AGTTAA
* **

sim_3R_168427-182237
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mel_3R_93319-108570
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* **

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mel_3R_93319-108570
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TATTGATCCTGATCAAGAATTAATATACTTTTATGGTCGGAAAAAATTT

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sech_3R_113859-128167
mel_3R_93319-108570

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sech_3R_113859-128167
mel_3R_93319-108570

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sech_3R_113859-128167
mel_3R_93319-108570

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sech_3R_113859-128167
mel_3R_93319-108570

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TATATTGCAATGAATCTAGTGTACACTTGTACTCTACGAGTAAATGGTAT

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sech_3R_113859-128167
mel_3R_93319-108570

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mel_3R_93319-108570

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sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CTAATTTGAATTCACAGTGATCTGCACGCTTCGTTATAGTATCTTTGGTAA
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sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
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TACCGTAGGCCATTGTTGGGTTTCAAACGAAATGCTCAATACACCTTGAG
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** *****

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mel_3R_93319-108570
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sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
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sech_3R_113859-128167
mel_3R_93319-108570
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TTTGGTGTCCCTCGTTATTGCAGTTGTGCCTTTGTCACTGCGTCTGCGGT
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sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CGCGACTGATTTCTGCAGCCTGAACTTTTGCACCTCGTCAAAGTAATCCT
CGCGACTGATTTCTGCAGCCTAAACTTTTGCACCTCGTCAAAGTAATCCT
CGCGACTGATTTCTCCAGCCTAAACTTTTGCACCTCGTCAAAGTAATCCT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
TTGCCTCCTGTCTGTGATAAAGTTTGGCCAAGTCGGCGCAAGTTTTGCCA
TTGCCTCCTGTCTGTGATAAAGTTTCGCCAAGTCGGCGCAAGTTTTGCCA
TTGCCTCCTGTCTGTGATAAAGTTTCGCCAAGTCAGTGAAGTTTTGCCA
***** * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
ACACCATCCACAGCCGCCAAGTCTGCGCCGTGCGTAACCAGGACTTTGAT
ACACCATCCACAGCCGCCAAGTCTGCGCCGTGCGTAACCAGGACTTTGAT
ACACCATCCAAAGCCGCCAAGTCTGCGCCGTGCGTAACAAGGACTTTGAT
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GAGCTCCATGCTAGCGTCCATAAACCCTGCAAGCAAAGAGCGAATTTAGA
GAGCTCCATGCTAGCGTCCATAAACCCTGCAAGCAAAGAGCGAATTTAAA
GAGCTCCATGCTAGCGTTCATAAACCCTGCAAGCAAAGGTGCGAATTTAAA
***** * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
TTCGATTAAAGCAGTTTCAGTCTTCTAGTCCCACCTGCGCGCATAAGAA
TTCGATTAAAGCAGTTTCAGTCTTCTAGTCCCACCTGCGCGCATAAGAA
TTCGATTAAAGCAGTTTCAGTCTTCTAGTCTACCTGCGCGCATAAGAA
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GGGTCCAGCCGCAGATGTCTCTGGCCTCCGCATTTCGCTCCCGCTTCGAGA
GGGTCCAGCCGCAGATGTCTCTGGCCTCCGCATTTCGCTCCCGCTTCGAGA
GGGTCCAGCCGCAGCGTCTCTGGCCTCAGCATTTCGCTCCCGCTTCGAGA
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CGGAACCTGACTATTTCCAGTTGATTGGCGTCAACGGCGCAGTGGGCGGG
CGGAACCTGACTATTTCCAGTTGATTGGCGTCAACGGCGCAGTGGGCGGG
CGGAACCTGACTATTTCCAGTTGATTGGCATCAACGGCGCAGTGGGCGGG
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
AGTCATGCCGTTACTGTCCGTCGCCTCCAGGCGGGCCTTCTTGTTCAGCA
AGTCATGCCGTTACTGTCCGTCGCCTCCAGGCGGGCCTTCTTGTTCAGCA
AGTCATGCCGTTACTGTCCGTCGCCTCCAGGCGGGCCTTCTTGTTCAGCA
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GAATGCGAGCGGACGGCAGGTGACCGTAGTAAAAAGCCAGCTGTGAGGTT
GAATGCGAGCGGACGGCAGGTGACCGTAGTAAAAAGCCAGCTGTGAGGTT
GAATGCGAGCGGACGGCAGGTGACCGTAGTAAAAAGCCAGCTGTGAGGTT
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
TAAAGCTCGTTAATAAAGTGGCAATTTAGACTAGGGCAGTCACCAACGTGC
TAAAGCTCGTTAATAAAGTGGCAATTTAGACTAGGGCAGTCACCAACGTGC
TAAAGCTCGTTAATAAAGTGGCAATTTAGACTAGTGCAGGTACCAACGTGC
*** ***** * ** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
AGCGGGGTCCGGCCGCTTCCCGGACTTCCAATGTGGACGTGCAACCGGC
AGCGGGGTCCGGCCGCTTCCCGGACTTCCAATGTGGACGTGCAACCGGC
AGCGGGGTCCGGCCGCTTCCCGGACTTCCAATGTGGACGTGCAACCGGC
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CGAGAGCAGCAAGTCAATGATGCACATCTCGCCCTGAATAATGGCATTTGG
CGAGAGCAGCAAGTCAATGATGCACATCTCGCCCTGAATAATGGCATTTGG
CGAGAGCAGCAAGTCAATGATGCACATCTCGCCCTGAATAATGGCATTTGG
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CAAGTGGCAGGAATCCGTTGGAAGCCGGATATTCATCAGACTCGGGCGGT
CAAGTGGCAGGAATCCGTTGGAAGCCGGATATTCATCAGACTCGGGCGGT
CAAGTGGCAGGAATCCGTTGGAAGCCGGATATTCATTAGGCTCGGGCGGA
***** ** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CGACGCAGCATTTCTTTAACCAGGAATTGCTGCCCTTTCTTATGGCTCG
CGACGCAGCATTTCTTTAACCAGGAATTGCTGCCCTTTCTTATGGCTCG
CGACGCAGCATTTCTTTAACAAGGAATTGCTGCCCTTTCTTATGGCTCG
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GCTTAGGCAGTGTGTAGATGGGAGTGCTGCAGCCGTGCAAGCCTAAGGTT
GCTTAGGCAGTGTGTAGATGGGAGTGCTGCAGCCGTGCAAGCCTAAGGTT
GCTTAAAGCAGTGTGTAGATGGGAGTGCTGCAGCCGTGCAAGCCTAATGTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
TTAGAAAGGGTAATTGTTATTGCGGACGATCCCATTTATACGAAACAAGA
TTAGAAAGGGTAATTGTTATTGCGGACGATCCCATTTATACGAAACAAGA
TTAGAAAGGGGAATTGTTATTGCGGACGATCCCATTGATATGAAACAAC-

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CAGAACGCAGCAGTCGACATCTTCGACTATCAGATACCCGTTACCTGGCT
CAGAACGCAGCAGTCGACTTCTTCGACTATCAGATACCCGTTACCTGGCT
CAGAACGTAACAGTCGACTTTTGGACTATCAGATAC-----ACCTAGCT
***** * ***** * * ***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
ATTAAAATGTAGCCTTATTAATTTAACATTTTGTGACTTGGCGATACAA
ATTAAAATGTAGCCTTATTAATTTAGCATTTTGTGACTTGGCGATACAA
AATAAAAATGTAGCCTTATTAATTTAACATTTTGTGACTTAGCGATACAA
* *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GTTAACAAAATAAGAAAATACAATATTATCATATATATCAAAATTTGTGGC
ATTAACAAAATAAGAAAATACAATATTATCATATATATCAAAATTTGTGGC
ATTAACAAAATACAAAATA-----TCTCATATATTTTAAAATTTTGGGA
***** ***** * ***** * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CGCGTCAGCTTTTGGAGTTTGGAGTTAAAGTGG-----
CGCGTCAGCTTTTGGAGTTTGGAGTTAAAGTGG-----
CGTGTTCAGCTTTTGGGAGCTGGGAGTTTGGGCGAGGTAGTTTGGGCGGC
** ***** * * ***** * *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
-----ACATGGGTCAACAACTTGC-----GCC
-----ACGTGGGTCAACAACTTGC-----GCC
CGTTGTGGCCGTTGCAACATGGGTGAACAAAATTGCTCTGCGTCTATGTC
** ***** ***** * *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
TACGAAACTGTATGCCTAATCTTAACCTGTAACCTTCT-----
TACGAAACTGTATGCCTAATCTTAAC-CTGTAACCTTGT-----
TTTAGAATCTGCATGGTGAATCTCAACATTCCTAGCTTCTTTATATATAC
* *** * * * * * * * * * * * * * * *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
-----ATAGTTCTCGACGTTTCATACGGACGGA-----
-----ATAGTTCTCGACGTTTCATACGGACGGA-----
AAGTTATATATAGTTCTCGACGTTTCATACGGACGGAACATGACAGAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGGACAAGGCTATTGAGCCTGATCCAGAATATATGTATAAATTATCATTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TAGTAGATTTTCCATATATTTATTAGCGTAAGTTTATTAATTACAATAGG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GCTTGCAGGCTGCACTTAATGAGACGAATAGTAAGTACGTGGCGATGA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCGACGCTTCTAATCTTCCAAAATCGACTGACTTAAGTATAGCAAGAGTT


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sim_3R_168427-182237      AATTTATCGCCAAGCTCATCTTCGCTTTGATTTGACTCCTTTTCCAAGGT
sech_3R_113859-128167    AATTTATCGCCAAGCTCATCTTCGCTTTGATTTGACTCCTTTTCCAAGGT
mel_3R_93319-108570      AATTTATCGTCAAGCTCATCTTCGCTTTGGTTTGAATTTTCCAAGT
*****

sim_3R_168427-182237      GCTGCACATCGGGCAACTTTGAGGTGTTTGAACAAAAAATTTCCGCTAAG
sech_3R_113859-128167    GCTGCACATCGGGCAACTTTGAGGTGTTTGAACAAAAAATTTCCGCT---
mel_3R_93319-108570      GCTGCACATCGGGCAACGTTGAGGT--TTAAACAAAAAATTTCCCTAAC
*****

sim_3R_168427-182237      CCTGGCGATAACAATTGACGAAGCAACGCCATGTTTACCAAAAAATCGAA
sech_3R_113859-128167    ---GGCGATAACAATTGACGAAGCAACGCCATGTTTACCAAAAAATCGAA
mel_3R_93319-108570      CTTAGCGATAATAATAAACGAAGCAACGCCATGTTTACCAAAAAATCGAA
*****

sim_3R_168427-182237      CTCTGTGCGCAACTCTCGAAAGCAATTGTTAAGCCAATATCAGC-----
sech_3R_113859-128167    CTCTGTGCGCAACTCTCGAAAGCAATTGTTAAGCCAATATCAGC-----
mel_3R_93319-108570      CTCAG-----AACTGTTAAGCCAATATCAGCTTGAAG
*** *

sim_3R_168427-182237      -----ATG
sech_3R_113859-128167    -----ATG
mel_3R_93319-108570      TCGATTATAAGGTTATCAATAGAAGTTTGCATGTTTGCCTTGCAAATG
***

sim_3R_168427-182237      TTGCCACGCCAC-----
sech_3R_113859-128167    TTGCTCCGCAAC-----
mel_3R_93319-108570      TTGCCACGCCACTGTAACTTCCACAAACCAGGCAAGGCTACCACTCCCA
****

sim_3R_168427-182237      -ACTTTTGAAAAATGTTTAGATATTTTTTTA-ATTTTTATTAG-TCTTGT
sech_3R_113859-128167    -ACTTTTGAAAAATGTTTAGATATTTCTTTTAATTTTTATTAG-TCTTGT
mel_3R_93319-108570      AACTTTTCCAAATGTTTAGAAATTTTTCATAGTTTTATAAGCTCTG--
*****

sim_3R_168427-182237      AAATTTCTATCGATTGCTAAAAATTTTTTTACCACGCCACTTTAAAGA
sech_3R_113859-128167    AAATTTCTATCGATTGCTAAAAATTTTTTTACCACGCCACTTTAAAGA
mel_3R_93319-108570      AAATTTCT-----TGTTACCACCCCATTTAAACGC
*****

sim_3R_168427-182237      CCACAAACGCCCA-AAAATCCCA---CGCCACAATTTGATTTTTAAT
sech_3R_113859-128167    CCAC---CGCCA-ATAATCCCA---CGCCACAATTTGATTTTTAAT
mel_3R_93319-108570      CCACAAACGCCCC-AACTACCATTTT-----AAAATTT--TGTTTAT
****

sim_3R_168427-182237      TTTTACTCGTTTTATTCCCAATATCTATCGATAAGCCAGAC-----AA
sech_3R_113859-128167    TTTTACTCGTTTTATTCCCAATATCTATCGATAAGCCAGAC-----AA
mel_3R_93319-108570      TTTTACTCGTTTTATTCCCAATATCTATCGAAAAGCCAGACCCAGACAA
*****

sim_3R_168427-182237      ATTATGAAATTTAGCGTTGGCGCTTACACAAGCTGAGTAATTGGTATCTG
sech_3R_113859-128167    ATTATGAAATTTAGCGTTGGCGCTTACACAAGCTGAGTAATTGGTATCTG
mel_3R_93319-108570      ATAATGTAATTTAGCGTTG-----
**

sim_3R_168427-182237      ATAGTCGGGGACTTCGACTATAGCATACTCTCTCGTTATATTACTTGTTC
sech_3R_113859-128167    ATAAFCGGGGACTTCGACTATAGCATACTCTCTCGTTATATTACTTGTTC
mel_3R_93319-108570      -----

sim_3R_168427-182237      AGTTTATTTGTTTCAGTTTATTAATAAACTTGACCACGCCGCTCAAAC
sech_3R_113859-128167    AGTTTATTTGTTTCAGTTTATTAATAAACTTGACCACGCCGCTCAAAC
mel_3R_93319-108570      -----

```

sim_3R_168427-182237 GCAACGCTATTATGAAAATTATTTTAAATGAATTTAATTTTATTATTTT
sech_3R_113859-128167 GCAACGCTATTATAGAAAATTATTTTAAATTAATTTAATTGTATTATTTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TCCTGCCTATTCCTATCGATATGCCAGCAAGAATTTTGATCTCTCTGGCT
sech_3R_113859-128167 TCCTGCCAATTCCTATCGATATGCCAGCAAGAATTTTGATCTCTCTGGTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TGCATTTTCTCTAGCTGAGTAACGGGTATCTTATAGCCGAGCGATGTGTC
sech_3R_113859-128167 AGCATTTTCTCTAGCTGAGTAACGGGTATCTTATAACCGAGCGATGTGTC
mel_3R_93319-108570 -----

sim_3R_168427-182237 CTGCTTATAATCAAGTTTCCTTGTTAAAATAGAGATACGCATTCGTTGA
sech_3R_113859-128167 TTGCTTATAATTAAGTTTCCTTGTTAAAATAGAGATACGCATTCGTTGA
mel_3R_93319-108570 -----

sim_3R_168427-182237 AATTGACTTTAATGGAGAGCACCCCTTTATAAATTCGCCAAAAAATAAA--
sech_3R_113859-128167 AATTGACTTTAATGGAGAGCACCCCTTTATAAATTCGTCAAAAAAAAAAAAA
mel_3R_93319-108570 -----

sim_3R_168427-182237 -TTAACGTTGTGTTTCAGAACTAATATAAATTTAAAAGTTTCCAGGCGACA
sech_3R_113859-128167 ATTAACGTTGTGTTTCAGAACTAATATAAATTTAAAAGTTTCCAGGCGACA
mel_3R_93319-108570 -----

sim_3R_168427-182237 TTTCAACTGTTGCCAGCACCCAACTC--TGCTGATA-TTACGTCTAGTAA
sech_3R_113859-128167 TTTCAACTGTTGCCAGCACCCAACTCCTCTGCTGATA-TTACGTCTAGTAA
mel_3R_93319-108570 -----
***** ** *****

sim_3R_168427-182237 GTGAGTGGATCGTTAAAAGTCGTTGTAACAAAAGAACTAGTGCTTCTT
sech_3R_113859-128167 GTGAGTGGATCGTTAAAAGGCGTTGTAACAAAAGAA-CTATTGCTTCTT
mel_3R_93319-108570 GT-----AAAAGTCCTTGTAAACAAAAGAACTATTCCGCCTT
** ***** * ***** ** * * **

sim_3R_168427-182237 GCAGGAGCATGTGTGCCAACCTAACGAGCCTTTGAGATACGTTTCCACGT
sech_3R_113859-128167 GCAGGAGCATGTGTGCCAACCTAACGAGCCTTTGAGATACGTTTCCACGT
mel_3R_93319-108570 GCAGAGGCGTGTGTGCCAACCTAACGACCCTTTGAGATACGTTTCTTGT
**** ** ***** ** * **

sim_3R_168427-182237 CGGCAATGATTCCGGAATTTTCAG----CCGACAGTTATCTCACCTGC
sech_3R_113859-128167 CGGCAATGATTTCGGAATTTTCAG----CCGACAGTTATCTCACCTGC
mel_3R_93319-108570 CGGCAATGATTCCGGAATTTTCGGAATTCGGACAGTTATCT-ACCCTGC
***** ***** * * * *****

sim_3R_168427-182237 ACAATGAGCCAATCATCGACCACCATGGAGGCATGGGCACCGGGCCACA
sech_3R_113859-128167 ACAATGAGCCAATCATCGACCACCATGGAGGCATGGGCACCGGGCCACA
mel_3R_93319-108570 ACAATGAGC-AATCATCGACCACCATGGAGGCATGGGCACCGGGCCACA
***** ***** *****

sim_3R_168427-182237 GAGATAGGAGTATCTCGTTTTTCAGCCGAGTCTCGGCTGACATGTCAAACA
sech_3R_113859-128167 GAGATAGGAGTATCTCGTTTTTCAGCCGAGTCTCGGCTGACATGTCAAACA
mel_3R_93319-108570 GAGATAGGAGTATCTCGATTTTCAGTCTCGGCTGACATATCAAACA
***** ***** *****

sim_3R_168427-182237 CAAAGACTGGCACAAGCACATGCGGAAAATATCATTGTCAAATCACA
sech_3R_113859-128167 CAAAGACTGGCACAAGCACATGCGGAAAATATCATTGTCAAATCACA
mel_3R_93319-108570 CAAAGACTGGCACAAGCACATGCGGAAAATATCATTGTCAAATCACA
***** *****

sim_3R_168427-182237 ACATGAAACCGTTTTAAATTTAGCCACTCTGCAGCCAGACGCCAAAGCCA
sech_3R_113859-128167 ACATGAAACCGTTTTAAATTTAGCCACTCTGCAGCCAGACGCCAAAGCCA
mel_3R_93319-108570 ACATGAAACCGTTTTAAATTTAGCCACTCTGCAGCTAGACGCTAAAGCCG

sim_3R_168427-182237 CCGCATCCCCAGCTTAAGCCCGCACGCCGCTCCTGCGGCAGCCTCACTGT
sech_3R_113859-128167 CCGCATCCCC----TTAAGCCCGCACGCCGCTCCTGCGGCAGCCTCACTGT
mel_3R_93319-108570 CCGCATCCCTCAGCTTAAGCCCGCACGCCGCTCCTGCGGCAGCCGCTTGT
***** * **

sim_3R_168427-182237 GCTTTTGCCGGCCCGAAATGACAATGTCTGCGGCTGAAGCT-----GGG
sech_3R_113859-128167 GCTTTTGCCGGCCCGAAATGACAATGTCTGCGGCTGAAGCT-----GGG
mel_3R_93319-108570 GCTTTTGCCAGGCCCGAAATGACAATGTCTGTGGCTGAAGCTGAAACTGGG
***** *****

sim_3R_168427-182237 AAAAGTTGAGTTGTCATCTTTGCGGCGGCTGCTCCTGAATTCATTGAT
sech_3R_113859-128167 AAAAGTTGAGTTGTCATCTTTGCGGCGGCTGCTCCTGAATTCATTGAT
mel_3R_93319-108570 AAAATTTGAGTTGTCATCTTTGCG-----AATTCATTGAT
**** *****

sim_3R_168427-182237 TGAAAAACGACCGTGCCAAGCGTCAAGGCGGCAGTTCTGGCTGCTTTGGAC
sech_3R_113859-128167 TGAAAAACGACCGTGCCAACCGTCAAGGCGGCAGTTCTGGCTGCTTTGGAC
mel_3R_93319-108570 TGAAAAACGACCGTACCAACCATCAAGGCGGCAGTTCTGGCTGCTTTGGAC
***** * *****

sim_3R_168427-182237 GGCGGGTTTTCAATATCATTATCTGTGACAGGGGACTTATAACTTCAAT
sech_3R_113859-128167 GGCGGGTTTTCAATATCATTATCTGTGAC-GGGGACTTATAACTTAAAT
mel_3R_93319-108570 GGCGGGTTTTCAATATCATTATTTGTGACGGGGGACTTATAACTTCAAT
***** *****

sim_3R_168427-182237 TACAAATGGCAATTGAAAATACCAAGAAGGAAAGCAATTGTATGCTTCGC
sech_3R_113859-128167 TACAAATGGCAATTGAAAATACCAAGAAGGAAAGCAATTGTATGTTTCGC
mel_3R_93319-108570 TACAAATGCCAATTGAAAATACCTAGAAGAAAAGCAATTGTAATTTTCGC
***** *****

sim_3R_168427-182237 GGCGGCGGGGACACGGACCCAGTGGCTTTTATAGTTTCATGGGATCTCGAC
sech_3R_113859-128167 GGCGGCGGGGACACGGACCCAGTGGCTTTTATAGTTTCATGGGATCTCGAC
mel_3R_93319-108570 GGCGGCGGGGACACGGCCTCAG-----
***** * **

sim_3R_168427-182237 GTTCATACGGATGGACATGGCCAGTTCGACTGGCCTATTGAGCCCTCTGC
sech_3R_113859-128167 GTTCATACGGATGGACATGGCCAGTTCGACTGGCCTATTGAGCCCTCTGC
mel_3R_93319-108570 -----

sim_3R_168427-182237 CTATCACATACTTTTCATGGCCAGTTCGACTGGCCTATTGAGCCCTCTGC
sech_3R_113859-128167 CTATCACATACTTATCAA---CAAATCTTTTGTACCCTTTTACTTTACGA
mel_3R_93319-108570 -----

sim_3R_168427-182237 CTATCACATACTTTTCA----AACAAGTACGGCGACGGAAATTTATTGGT
sech_3R_113859-128167 GCAAGGAGTATAATTAAGATTAACAAGTACGGCGACGGAAATTTATTGGT
mel_3R_93319-108570 -----

sim_3R_168427-182237 GTAACCTGGATACATAGCTGTAA**TTAATAATAAGTTTCTTGTTCACCCAG**
sech_3R_113859-128167 GTAACCTGGATACATAGCTGTAA**TTAATAATAAGTTTCTTGTTCACCCAG**
mel_3R_93319-108570 -----

sim_3R_168427-182237 **CCACCTGGATTTCTTCTTATTAGAAATCGACGACTTCTCATCAAAAAAGAA**
sech_3R_113859-128167 **CCACCTGGATTTCTTCTTATTAGAAATCGACGACTTCTCATCAAAAAAGAA**
mel_3R_93319-108570 -----

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AATTAACAGACCAAAGGGGAACGCATATATCCACCAAATAAATCTGGAAA
AATTAATAGACCAAAGGGGAACGCATATATCCACCAAATAAATCTGGAAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AACATTAGGTTTAAAGCCGTTTTTCATATTAGTTGTACTTACTTGATGGAA
AACATTAGGTTTAAACCCTTTT-CATATTAGTTGTACTTACTTGATGGAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TACATTCTCAATGTTTTTTCAAATACTGGAACATAGCAAAGTAGACAGGC
TACATTCTCAATGTTTTTTCAAATACTGGAACATAGCAAAGTAGACAGGC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AATGATGAATTCCAGAACCAAAGCGAAGTTAAGTACATGATTGCCCATAC
AATAATGAATTCCAGAACCAAAGCGAAGTTAAGTACATGATTGCCCATAC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CTTGTTGAAGTATTGAGTTTCGACGAGTTTTGCATATTTAAAGGTCGAAA
CTTGTTGAAGTATTGAGTTTCGACGAGTTTTGCATATTTAAAGGTCGAAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ACCTGTGTCACAACAATCGACACAAAAAACCCTGCTGCTGTATATTC
ACCTGTGTCACAACAATCGACACAAAAAACCCTGCTGCTGTATATTC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AAGAACTTTACGTTCCCTGTAGGTCTGCAAACATTTCAATAAATATAAAA
AAGAACTTTACGTTCCCTGTAGGTCTGGAACATTTCAAT-----

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TATAAATAAATTAATATAATAAGAGAAGACCAAATAGAACACAATACAG
-----TACGTTAAATATAATAAGAAAAGACCAAATAGAACACAACACAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTACCCATTCTTGTCCGTAGCCATCTTCAAGGTCTTCTACATTTTTTTGAG
TTACCCATTCTTGTCCGTAGCCATCTTCAAGGTCTTCTACATTTTTTTGAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCCCAGTCTTCTCGAATTCCTTAAAGTCTGGAGGGGGAAATCCATGTTC
TCCCAGTCTTCTCGAATTCCTTAAAGTCTGGAGGGGGAAATCCATGTTC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TGCCATTATAGCAAAAAAAGTAAAGAAACATGCAACCGTTTGTATAACTC
TGCCATTATAGCAAAAAAAGTAAAGAAACATGCAACCGTTTGTATAACTC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CAATTTGCAAGTAAGCCATTAGAATTAACCTAATGATTTAGAGATACCAA
CAATTTGCAAGTAAGCCATTAGAATTAACCTAATGATTTAGAGATACCAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ACATGTTAATCATAAATACTTCCAGGGGGTAAGTATCAATAAGCTTATTT
ACATGTTAATCATAAATACTTCCAGGGGGTAAGTATCAATAAGCTTATTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGGAAAAAAAAATATATTTGGTACAATATATATATATTTTACATTTTATATTTT
CGGAAAAAAAAATATATTTGGTACAATATATATATATTTTATATTTTATATTTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AAACAACATATAAACAAACTTCATATTTTTTAAACTCCTTTGGCAAAGCT
AAACAACATATAAACAAACTACATATTTTTTAAACTCCTTTGGCAAAGCT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CTATATGTTGATATGCGAAAAAAAAATTTAAAAATATGTATTACTTTTTGAGT
CTATATGTTGATATGCGAAAAAAAAATTTAAAAATTTATTACTTTTTGAGT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTTTGTGCGCGGGTGCATATCTAACGTTAAATGTCAAATTAAGCTGTGTG
TTTTGTGCGCGGGTGCATATGTAACTGTTAAATGTCAAATTAAGCTGCGTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GCTTTAGGCCAAATGATCTGGTAAAAATAAGTTTTTGGGAGTATATAGGG
GCTTTAGGCCAAATGATCTGGTAAAAATAAGTTTTTGGGAGTATATAGGG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GGATGCTGGGATGAAAGCAATTTTTAGGAGTATACTTTGCCTTAAAAGAA
GGATGCTGGGATGAAAGCAATTTTTAGGAGTATACTTTGCCTTAAAAGAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CTTATCTATATGAGTATATAAA-----TAATAATAATAAAA
CTTATCTATATGAGTATATAAACTCAGACTCTTACATCCTAATAATATA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ATATTTGTTAATAAATTTAAGAAAAATAGATATAGGACCCTCTTGATCT
ATATTTAATAAATAAATTTAAGAAAAATAGATATAGGACCCTCTTGATCT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ACGGAATAAGCTATACAAACTTACTTTTTATTACCAAACGGTCTTCAA
ACGGAATAAGCTATACAAACTTACTTTTTATTACCAAACGGTCTTCAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGGATCTCTTGGCATAACGCGCCATTATATCAGATTCAGCTTTTTCATAAG
CGGATCTCTTGGCATAACGCGCCATTATATCAGATTCAGCTTTTTCATAAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CTAGCGATATTGCCGGAAGCATGTCAGTGCCGATATCGATGCATAGGATT
CTAGCGATATTGCCGGAAGCATGTCAGTGCCGATATCGATGCATAGAATT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GCTATAGTGCCTAGAGCTAGAGGTATATCAAATATCACAAAAATAAAAA
GCAATAGTGCCAAGAGCTAAAGGTATATCAAATATCACAAAAATAAAAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGGCACTATTTTCAGGAAGATTTGAAGTCAGGGTATATGCGATGGACTTTT
CGGCACTATTTTCAGGAAGATTTGAAGTCAGGGTATATGCGATGGACTTTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TAAGATTATCGAAAATAATCCGCCCTCTTCAATGCCAACACAATGGAC
TAAGATTATCGAAAATAATCCGCCCTCTTCAATGCCAACACAATGGAC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GCAAAATTGTCATCCAATAGAATCATATCTGCCGCCTGCTTGAAACGTC
GCAAAATTGTCATCCAATAGAATCATATCTGCCGCCTGCTTGAAACGTC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AGATCCAGAAATACCCATTGCAACGCCAATATCGGCTCTTTTCAGTGCTG
AGATCCAGAAATACCCATTGCAACGCCAATATCGGCTCTTTTCAGTGCTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GAGAGTCATTACACCATCGCCAGTTACAGCAACGATTTACACAGTCTT
GAGAGTCATTACACCATCGCCAGTTACAGCAACAATTTACACAGTCTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TGGCAAGCTTCTACGATTATAAGCTTTTGCTGCGGAGAGGTTTCGGGCAA
TGGCAAGCTTCTACGATTATAAGCTTTTGCTGTTGGAGAGGTTTCGGGCAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AACGATTTTATTATGATAGTATATCACAGCGTCTAACTCTTCAGCTTTCA
AACGATTTTATTATGATAGTATATTACAGCGTCTAACTCTTCAGCTTTCA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCTCCCGAAGCTCACCCCGTGGACCACAATGGCAGTGGCTTGTTCGGGGA
TCTCTCGAAGCTCACCCCGTGGACCACAATAGCAGTGGCTTGTTCGGGGA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCGATGTCGAGAACTGTGACGCCACGTTGTTGGCAATGTCTCTGCAGT
TCGATGTCGAGAACTGTAACGCCACGTTGTTGGCAATGTCTCTGCAGT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AGGCGTTGTAATTATGCCACACTGCGGGCTATGGCTTTAGCTGTGATAG
AGGCGTTGTAATTATGCCACACTGCGGGCTATGGCTTTAGCTGTGATAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GGTGATCTCCAGTTACCATGATTACACGTACACCTGCTGAACGGCACTTT
GGTGATCTCCAGTTACCATGATTACACGTACACCTGCTGAACGGCACTTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GCAACTGCGTCTGGAACGGCTGCTCGTGGCGGGTCTATTAATGATATTA
GCAACTGCGTCTGGAACGGCTGCTCGTGGCGGGTCTATTAATGATATTA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCCAGAAAACGAAGATTTTCTAATGAAAAATTTGGAGGATCTGCGTTGA
TCCAGAAAACGAAGACTTTTCTAATGAAAAATTTGGAGGATCTGCGTTGA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ACTCGTAAGAAATTTGGGTATTTAGACATGGGAAGTATAAGGTCAGCAAAT
AGTCGTAAGAAATTTGGGTATTTAGACATGGGAAGTATAAGGTCAGCAAAT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCCAATACTCTTTGCCCCATACCGCCATTTCCAATAAGCTTCTTCGAA
CCCAATACTCTTTGCCCCATACCGCCATTTCCAATAAGCTTCTTCGAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTCCAATTTTAATGCAGGTGTAAGTTCTACAGACTGCCCTTGAATTAGTA
TTCCAATTTTAATGCAGGTGTAAGTTCTACAGACAGCCCTTGAATTATTA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCGTACTACAGCGATCCAATATTTCTCTCTGGTGCTCCTTTCATCTCAACT
TCGTACTACAGCGATCCAATATTTCTCTCTGGTGCTCCTTTCATCTCAACT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ATAAAGTATCCATCTCTGAATTAATTCGTGAACAGAACTTGATATTT
ATAAAGTATCCATCTCTGAATTAATTCGTGAACAGAACTTGATATTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTCCGTTGAATTAAGGGAATTTCCGGTCAATTTGATATGCTTTTGACGAA
TTCCGTTGAATTAAGGGAATTTCCGGTCAATTTGATATGTTTTGACGAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AAGCACTAATACCTCCAGAAATAGTTTCGGTGAACCTTTAAAAGAGCAGCC
AAGCACTAATACCTCCAGAAATAGTTTCGGTGAACCTTTAAAAGAGCAGCC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCTGATGCGTTGCCATTGACATCTTTTTTAAATACGGGTATATCATCTTG
TCTGATGCGTTGCCATTGACATCTTTTTTAAATACGGGTATATCATCTTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ACCACCTTTAAATTCAGCGGAATTGCAAAGTGCGGCACACATAAAAAGAG
ACCACCTTTAAATTCAGCGGAATTGCAAAGTGCGGCACACATAAAAAGAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CATTAAAAGATTTATCCTCAATTTTAAAATGGGATCCTCGAAAAGATTCA
CATTAAAAGATTTATCCTCAATTTTAAAATGGGATCCTCGAAAAGATTCA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GTAGTGTGAGATTCAACAATTTATTTGATCATAACCATAAGTGAGCAACAGT
GTAGTGTGAGATTCAACAATTTATTTGATCATAACCATAAGTGAGCAACAGT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CATTGATTTTGTAGTCAGGGTTCTGTTTTGTCTGAACAAATGTTGATG
CATTGATTTTGTAGTTAGGGTTCTGTTTTATCTGAACAAATGTTGATG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCGAACCAATGTCTCGACAGCTTCCAAGTTCTTAACCAACAATTTTTG
TCGAACCAATGTCTCGACAGCTTCCAAGTTCTTAACCAACAATTTTTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GATGCCATGCGCTTTGCAGTAAGGGTTAAACATACGGTAACAGTTACGAG
GATGCCATGCGCTTTGCAGTAAGGGTTAAACATACGGTAACAGTTACGAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TAAGCCCTCTGGTACGTTTGC GACTATAATGCCTATAAGAAACACAAC TG
TAAGCCCTCTGGTACGTTTGC GACTATAATGCCTATAAGAAACACAAC TG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CATCAATAAATTCATAACCTAATGTTAAACTTATCGCAAAAAAGATAGT
CATCAATAAATTCATAACCTAATGTTAAACTTATCGCAAAAAAGATAGT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCTAGTATTACTGCAAATATTGTAATAAACCGAATAAAAAGTTGAATTC
CCTAGTATTATTGCAAATATTGTAATAAACCGAATAAAAAGTTGTATTC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCGGGAAATGGGTGACTGAACATCGTCCAGTCCGCGCTAAGTTTGCTA
CCGGGAAATGGGTGACTGAACATCGTCCAGTCCGCGCTAAGTTTGCTA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TACGTCCCATTACTGTATTGTCCCAGTTGCAATGACAACACCTCGGCAG
TACGTCCCATTACTGTACTGTCCCAGTTGCAATGACAACACCTCGGCAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GTACCTTCGAGTACGTTTGTAGAGAAGAAAGCCAAGTTCTTTGTTTCCAA
GTACCTTCGAGTACGTTTGTAGAAAAAAAAGCCAAGTTCTTTGTTTCCAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AGGGTTTTTCATGTGTAAACTCTGTAGATCTCACTTGAGGCTCGGATTCTC
AGGGTTTTTCATGTGTAAACTCTGTAGATCTCACTTGAGGCTCGGATTCTC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CAGTCAAGGAAGAGTTATCCACTTTAAGTCCATGAGCTTCCAATATTCGA
CAGTCAAGGAAGAGTTATCCACTTTAAGTCCATGAGCTTCCAATATTCGA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ATGTCAGCGGGTACCCTATCACCAAAATTTAATTTCCACAATATCTCCTTT
ATGTCAGCGGGTACCCTATCACCAAAATTTAATTTCCACAATATCTCCTTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TACTAGTTCGTCTGAAGTTACTGTGTTTACTTCTCCTTCTCGTATAACTG
TACTAGTTCGTCTGAAGTTACTGTGTTTATTTCCCCTTCTCGTATAACTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TAGCGTATTGTGGAACAAGGTTTTTAAATGAATCCATTATAGAAGAGGAT
TAGCGTATTGTGGAACAAGGTTTTTAAATGAATCCATTATAGAAGAGGAT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTATGAACCTAATAAGTAAAAAATTTAAGACTATTATCCCAAAAATGT
TTATGAACCTAATAAGTAAAAAATTTAAGACTATTATCCCAAAAATGT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TAACAATTATTTGTATACTAAAAAATTTGTGTATTTAAACAAGAGAGAAT
TAACAATTATTTGTATACTAAAAAATTTGTGTATTTAAACAAGAGAGAAT

sim_3R_168427-182237 ACAACAGTCGAGTTCCTCCGACTATCAGATATCCATTAC--TCAGCGAGTG
sech_3R_113859-128167 ACAACAGTCGAGTTCCTCCGACTATCAGATATCCGTTAC--TCAGCTAGTG
mel_3R_93319-108570 -----

sim_3R_168427-182237 CGAATGCGAAATTTTCATAATTTTTCTTGGATTATCGATAGATACTAGTGA
sech_3R_113859-128167 CGAATGCGAAATTTTCATCATTTTTCTTGGATTATCGATAGATATTAGTGA
mel_3R_93319-108570 -----

sim_3R_168427-182237 ATTTAAATGAGAAA-ACATTTTAGAAAATGTTCAAAGTGTGGGCGTGACC
sech_3R_113859-128167 ATTTAAATGAGAAA-ACATTTTAGAAAATGTTCAAAGTGTGGGCGTGACC
mel_3R_93319-108570 -----

sim_3R_168427-182237 AGTTTGG-CGGCTTTAAG-GCGTTAAAGTGGTCGTGGCAAACAGTTTTTTT
sech_3R_113859-128167 AGTTTGG-CGGCTTTAAG-GCGTTAGAGTGGTCGTGACAAACAGTTTTTTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 GGCAAATCGATAGAAGTGTAAATACAAAAAGGAAAAAATATCAATACATTT
sech_3R_113859-128167 GGCAAATCGAAGGAACTGTAAATACAAAAAGGAAAAAATATCAATACATTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TTCAAGTGTGGTCGCAGCAGATTTCTGCGGCTTGTGGGTGTCGCAACATG
sech_3R_113859-128167 TTCAAGTGTGGTCGCAGCAGATTTCTGCGGCTTGTGGGTGTCGCAACATG
mel_3R_93319-108570 -----

sim_3R_168427-182237 AAAAGGCTGCATCTCAACACTTGAGCTTTTTATAGTTCCCTGGGATCGAGGC
sech_3R_113859-128167 AAAAAGCTGCATCTCAACACTTTAGCTTTTTATAGTTCCCTGGGATCGAGGC
mel_3R_93319-108570 -----

sim_3R_168427-182237 GTTCATGCGGACAGACGTACAGGGCCAGATCGACTCATCTATTGATCCAG
sech_3R_113859-128167 GTTCATGCGGACAGACGTACAGGGCCAGATCGACTCATCTTTTGATCCAG
mel_3R_93319-108570 -----

sim_3R_168427-182237 ATGAAGAATTTGTATACTTTATACGGTCGGAAACGCTTCCTTTCTGCCTG
sech_3R_113859-128167 ATAAAGAATTTGTATACTTTATACGGTCGGAAACGCTTCCTTTCTGCCTG
mel_3R_93319-108570 -----

sim_3R_168427-182237 TTACATAATTTTTCAACGAATCCAGTATAACCTTTTACTCTAAGAGAATAA
sech_3R_113859-128167 TTACATAATTTTTCAACGAATCCAGTATAACCTTTTACTCTAAGAGAATAA
mel_3R_93319-108570 -----

sim_3R_168427-182237 TAAGAGAAAGAGTTCCTAAATATCAAATAACCGCTATGGGGCAAACCAA
sech_3R_113859-128167 TATGAGAAACAGGTCCTAAATATCAAATAACCGCTAAGGGCAAACCAA
mel_3R_93319-108570 -----

sim_3R_168427-182237 ACTTAGACTTGACTTGTAAATAAGAGTAATTGTAATTTTTAGAAACATTTT
sech_3R_113859-128167 -CTTAGACTTGACTTGTAAATAAGAGTAATTGTAATTTTTAGAAACATTTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TAATATTTATTTATTTACCTGAAAATATGTAAATAACCTGTGACTATTA
sech_3R_113859-128167 TGATATGTATTTATTTACCTGAAAATATGTAAATAACCTGTGACTATTA
mel_3R_93319-108570 -----

sim_3R_168427-182237 CAAAAACAGTCAATGCAATGCCAAGATAGAGATTGTCATCTGGTGGTTCG
sech_3R_113859-128167 CAAAAACAGTCAATGCAATGCCAAGATAGAGATTGTCATCTGGTGGTTCG
mel_3R_93319-108570 -----

sim_3R_168427-182237 TGCTGGGTTTGTAAATGTATAAGATATCCGACAAAACAAAGAAAAGATCC
sech_3R_113859-128167 TGCTGGGTTTGTAAATGTATAAGATATCCGACAAAACAAAGAAAAGATCC
mel_3R_93319-108570 -----

sim_3R_168427-182237 TGCCCAAAGTAGTATTGCGAATCCACCAAACATGGTTTTTAAAGAAAACAA
sech_3R_113859-128167 TGCCCAAAGTAGTATTGCGAATCCACCAAACATGGTTTTTAAAGAAAACAA
mel_3R_93319-108570 -----

sim_3R_168427-182237 TCCATTTTGGTGTGGAGGCTGCGGCGTAAGTATGTTAGGGCCATTTATTT
sech_3R_113859-128167 TCCATTTTGGTGTGGAGGCTGCGGCGTAAGTATGTTAGGGCCATTTATTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TCCAATCTTAACCTGGCCTCAGCAAAAAGACAATCCCTATTAATAAATATAT
sech_3R_113859-128167 TCCAATCTTAACCTGGCCTCAGCAAAAAGACAATCCCTATTAATAAATATAT
mel_3R_93319-108570 -----

sim_3R_168427-182237 ATCACTTATAATCGTAGATCGTTGTAGATTCTCATACCCTGTTAGGATCT
sech_3R_113859-128167 ATCACTTATAATCGTAGATCGTTGTAGATTCTCATACCCTGTTAGGATCT
mel_3R_93319-108570 -----

sim_3R_168427-182237 GTCTTTAGGGCGCTCTAATAGTTCGCTACAGATATTTTATGATTGTCAGT
sech_3R_113859-128167 GTCTTTAGGGCGCTCTAATAGTTCGCTACAGATATTTTATGATTGTCAGT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TTCCACATCTTTTTTAAAGACTGAATGTCCTTTTTCTTTCTTTTCCAT
sech_3R_113859-128167 TTCCACATCTTTTTTAAAGACTGAATGTCCTTTTTCTTTCTTTTCCAT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TAATTTTGTGTTCTTTATTTTTTTTTTTTTTGTGATGGCATCCTCTAACGTTTT
sech_3R_113859-128167 TAATTTTGTGTTCTTTATTTTTTTTTTTTTTGTGATGGCATCCTCTAACGTTTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 GTAGTTTTTTTT-GATTAAGGGCTATGCTATATTGATACAATAAATAT
sech_3R_113859-128167 GTAGTTTTTTTTGATTAAGGGCTATGCTATATTGATACAATAAATAT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TTTTAAATATAACTTGTTAATGTAAATATAATATGTTAAACATAAATTT
sech_3R_113859-128167 TTTTAAATATAACTTGTTAATGTAAATATAATATGTTAAACATAAATTT
mel_3R_93319-108570 -----

sim_3R_168427-182237 TTTCAACATACATATAAACATATTTTTAAAAATTTAAACATAAACATAAA
sech_3R_113859-128167 TTTCAACATACATATAAACATATTTTTAAAAATTTAAACATAAACATAAA
mel_3R_93319-108570 -----

sim_3R_168427-182237 TATTCATTTTTGCAAGAAGCGAGTGTAGTGTATTATTAGAGATTCACTGAA
sech_3R_113859-128167 -GCTAGTGT-----AGTTTAGT-TTATTAGAGATTCACTGAA
mel_3R_93319-108570 -----

sim_3R_168427-182237 AATATTGGAAGTCCAATTAATACATAAGAATCTATTGCTCCCCAGCTATG
sech_3R_113859-128167 AATATTGGAAGTCCAATTAATACATAAGAATCTATTGCTCCCCAGCTATG
mel_3R_93319-108570 -----

sim_3R_168427-182237 AAGAGTAAAGTATGAAATCGTATAAGAGATTGTTTAACTCTTTAACAC
sech_3R_113859-128167 AAGAGTAAAGTATGAAATCGTATAAGAGATTGTTTAACTCTTTAACAC
mel_3R_93319-108570 -----

sim_3R_168427-182237 TGTGTGTTACTCAGTA-----CCAATTATAATCGCACACTATATAT
sech_3R_113859-128167 TGTGTGTTACTCAGTACCGGAAACCAATTATAATCGCACACTATATGT
mel_3R_93319-108570 -----

sim_3R_168427-182237 CGATGGGGATACATGCGCAGCTTATGCCAATTGGCAAGTAGAGGGAGTTA
sech_3R_113859-128167 CGATGGGGATACATGCGCAGCTTATGCCAATTGGCAAGTAGAGGGAGTTA
mel_3R_93319-108570 -----

sim_3R_168427-182237 ACAAAGTCGAAATACCTATGTTAGTTAAATTATTAGAGCCATTAGAGCGG
sech_3R_113859-128167 ACAAATTCGAAATACCTATTTTAGTTAAATTATTAGAGCCATTAGAGCAG
mel_3R_93319-108570 -----

sim_3R_168427-182237 AAAGATTGGTATAAGTTATTAATAAAGTAGAACTTCCATTAATAATCT
sech_3R_113859-128167 ATAGATTGGTATAAGTTATTAATAAAGTAGAACTTCCATTAATAATCT
mel_3R_93319-108570 -----

sim_3R_168427-182237 AGTAGTACTCAAGAATCACTTAGTATTCTATTATTTGGTGTAGTAAAA
sech_3R_113859-128167 AGTAGTACTCAAGAATCACTTAGTATTCTATTATTTGGTGTAGTAAAA
mel_3R_93319-108570 -----

sim_3R_168427-182237 GGGCCTTTATCTGATGAATTATAAGAATACATTGAGGACAAGTT--TAAT
sech_3R_113859-128167 GGGCCTTTATCTGATGAATTATAAGAATATATTGGGGACAAGTT--TAAT
mel_3R_93319-108570 -----CAATACCGTTAGTGTGGGCG--TGCG
**** * * * * *

sim_3R_168427-182237 AAAGAGCAATCTGTTCA---AATGCCAATAATATATACGTTAATATATA
sech_3R_113859-128167 AAAGATCAATCTGTTCA---AATGCTAATAATATATA-----
mel_3R_93319-108570 AAA----AAAATGTTA--GGATGC---CGATAGA-----AA
*** ** **** * **** ** *

sim_3R_168427-182237 TTATATAATGTATATAAATGCTGTTTATAATGCTAATAGTAATATCCAGT
sech_3R_113859-128167 -----TATAAATGCTGTTTATAATGCTAATAGTAATATCCAGT
mel_3R_93319-108570 T-----TAGAAAGACA--TTATAAATCAAAA--AATCTCTA--
** *** * * **** ** * *** ** *

sim_3R_168427-182237 CACAACATAAGAAAGAGTGAAGAAACATAAAGTCCGTTTGGAAATATAAAC
sech_3R_113859-128167 CACAACATAAGAAAGAGTGAAGAAACATAAAGCCTGTTTGGAAATATAAAC
mel_3R_93319-108570 CCCAACATTAAGAAAGTGCAGG-----TATGGC-AGTTTGG---GCGGAT
* ***** * **** * * ** * ***** *

sim_3R_168427-182237 TTTGAGATTTTGTAGCTATACGTAATATTGATACAACATCTAGACTTAAT
sech_3R_113859-128167 TTTGAGATTTTGTAGCTATACGTAATATTGATACAACATCTAGACTTAAT
mel_3R_93319-108570 TTTGTG-CATTAGAGCCG-GCGTGGT----AAAAAGTATTTCGGCA-AAT
**** * ** *** ** * * * * * * * *

sim_3R_168427-182237 TAAATAATAAATAATTCACACCTAAATAGTGCACCTTGCAAAA----ATA
sech_3R_113859-128167 TAAATAATAAATAATTCACACCTAAATATTGCGACCTTACAAAGTAAATA
mel_3R_93319-108570 CGATTGCAAAAAAGACTACAACAAAATTAATAAATAATGAAAA-----C
* * **** * * * **** * * ****

```

sim_3R_168427-182237      GAGTATTTGAAAATTACCG--CTATGAAATCTATGAA-ATCTATCAAATC
sech_3R_113859-128167    GAGTATTTGAAAATTACCG--CTATGAAATCTATGAA-ATCCTTCAAATC
mel_3R_93319-108570      ATTT--CCAAAAGTTGTGG--GCATGGCAGTTTTGGGTGGATGGTGAGCG
          *      *** * * * *      *      * * * *      *
sim_3R_168427-182237      TAG-T-----TGTGT
sech_3R_113859-128167    TAGTTAATGGAATAATGTCTCTACCACAAGAAGTGAATAGCGATGTGT
mel_3R_93319-108570      T-----TAGAT
          *                               * *
sim_3R_168427-182237      T-----
sech_3R_113859-128167    TCACAATGGGAATTTGAGAAAAACATTGATGAACAGTTACACGACATGT
mel_3R_93319-108570      TGGG-----
          *
sim_3R_168427-182237      -----
sech_3R_113859-128167    TTCATCAGCCGAATGCGTTCATTTGTTGAAACCCGTAAGTGAGTTTACAT
mel_3R_93319-108570      -----
sim_3R_168427-182237      -----
sech_3R_113859-128167    TTCCATTTGTTGAAATAAATAAATAAATAACACATTTATATGTACACATTT
mel_3R_93319-108570      -----
sim_3R_168427-182237      -----
sech_3R_113859-128167    TTA AAAAGGATACGTATGGCAGTTTTGTGTGGCTTGTGCGCATTAGAGTG
mel_3R_93319-108570      -----
sim_3R_168427-182237      -GCGCGATCACATTTAGAATCAATGGAATCTTCATGTCCAATCTCAATTC
sech_3R_113859-128167    GGCGTGATCACATTTAGAATCAATGGAATCTTCATGTCCAATCTCAATTC
mel_3R_93319-108570      --CGTGACCACATTTAGAATGAATGGAATTTTCATGTCCAATCTCAACTC
          ** * * ***** * * * * * * * * * * * * * * * * * *
sim_3R_168427-182237      TTTAGCTTTAATAGTTTCTGACTTTGTTGATCAGAAATATATATACTTCA
sech_3R_113859-128167    TTTAGCTTTAATAGTTTCTGACTTTGTAGATCAGAAATATATATACTTCA
mel_3R_93319-108570      TTTAACTTTAATAGTTTCTGACTTTGCTGATCAGAAATATATATACTTTA
          **** * * * * * * * * * * * * * * * * * * * * * *
sim_3R_168427-182237      TG-----TGGTCTGTTACATACTTTATAACGAGTCTAGTATACCATTT
sech_3R_113859-128167    TA-----TGGTCTGTTACATACTTTATAACGAATCTAGTATACCATTT
mel_3R_93319-108570      CGCTTCCCTTTTACCTGTTGCATACTTTTCAACGAAGATAGTACACCATTT
          *      * * * * * * * * * * * * * * * * * * * * * *
sim_3R_168427-182237      AACGGGTATAAAATGTTGTTA-----TTATTATATTGTGAGCA
sech_3R_113859-128167    AACGGGTATAAAATGTTGTTA-----TTATTATATTGTGAGCA
mel_3R_93319-108570      AACGAGTATAACAAGTTGTTAAATCATCCGCACTTATTA-ATTGTGAGCA
          **** * * * * * * * * * * * * * * * * * * * * * *
sim_3R_168427-182237      TATTTGTATAAAGCCTTTAATGGTATAGAC-----TTGTAATTGATAAAA
sech_3R_113859-128167    TATTTGAATAAAGCCTTTAATGGTATTGACATACTTTGTAATTGATAAAA
mel_3R_93319-108570      TATTTGTATAAATCCTATAATGGTATAGACATACTGTTGTAATTAATAAAA
          **** * * * * * * * * * * * * * * * * * * * * * *
sim_3R_168427-182237      CATCAGTCGAAGAACTCCACTAC-----ACCGTTCTGTAATGATGCTTT
sech_3R_113859-128167    CATCAGTCGTAGAACTCCACTAC-----ACCGTTCTGTAATGATGCTTT
mel_3R_93319-108570      CAACAGTCGAAGAACTCTACTACTAATCTAC-----TAATGATGCTTT
          ** * * * * * * * * * * * * * * * * * * * * * *
sim_3R_168427-182237      TAACCACC--ATCG---CAGTCTATGAAAAGAGGAATTGTTCCGAGAAGC
sech_3R_113859-128167    TAACAACC--ACCA---CAGTCTATAAAAAAAGGAATTGTTCCGAGAAGC
mel_3R_93319-108570      TAATCACCTAAACGTATCAGTCTATGAAAAAAG-----AAGC
          *** * * * * * * * * * * * * * * * * * * * * * *

```

sim_3R_168427-182237 CTTATAAATTATGCGGCTGTACTGAATGCTGCTAAAAATCTCCAGGCGA
sech_3R_113859-128167 CTTATAAATTATCACAGCTGTACTGAATGC-----
mel_3R_93319-108570 CATATAAATTATGCGGCTGAACTAAATGCTGCTAAAAATGTCCAGGCGA
* ***** * **** * * *****

sim_3R_168427-182237 ACGGGTCTCCTGCCTGTCTATTACCTCTTAAAGAAGCTGGAAACGACAGTG
sech_3R_113859-128167 -----ATTACCTCTTAAAGAAGCTGGAAACGACAGTG
mel_3R_93319-108570 ACGGGTCTCCTGGCTGTCTATTACCTCTTAAAAAAGCTGGAG----CAGTG
***** *****

sim_3R_168427-182237 AGCCAAATGTGGCCAATTAGCCTCCAGTCGTCTGATGATACGGAAGGCGA
sech_3R_113859-128167 AGCCAAATGTGGCCAATTAGCCTCCAGTCGTCTGATGATACGGAAGGCGA
mel_3R_93319-108570 AGCCAAATGTGGCCAATTTTCTCACGTCGTCTGATGATACGGGAGGCGA
*** *****

sim_3R_168427-182237 ATAA-CGAAATACGCTGAAAAAATAATCATAACTGGACAAATAGGCGA
sech_3R_113859-128167 ATAA-CGAAATACTCCTGAAAAACAAATCATAACTGGACAAATAAGCGA
mel_3R_93319-108570 ATGTGCGAAATACGCTGAAAAAATAATCATAACTGGGCAAATAGGCGA
** ***** * *****

sim_3R_168427-182237 TGAAGAAAGCCCAAGCAATTTCTTTGTATGATAATAGAAGTGGTAAGAA
sech_3R_113859-128167 TGAAGAAAGCCCAAGCAATTTCTTTGTATGATAATAGAAGTGGTAAGAA
mel_3R_93319-108570 TGAAGCAATCCCAC----TTTCC-----
***** ** **** *****

sim_3R_168427-182237 GGGAAATGGGCCGTGACGAGGCGGGATGCCACCTGTCTGGTGGCTTAAAGC
sech_3R_113859-128167 GGGAAATGGGCCGTGACGAGGCGGGATGCCACCTGTCTGGTGGCTTAAAGC
mel_3R_93319-108570 -----

sim_3R_168427-182237 GAAATGGGTTTGATTTTAATCAGAATAATGGGCTCTGACGCCGCATGATG
sech_3R_113859-128167 GAAATGGGTTTGATTTTAATCAGAATAATGGGCTTTGACGCCGCATGATG
mel_3R_93319-108570 -----CATTATG
*** **

sim_3R_168427-182237 ACGTGTGTGCTCTAATTAATAATTTATATAAATTGCCACCGCT-CTACC
sech_3R_113859-128167 ACGTGTGTGCTCTAATTAATAATTTATATAAATTGCCACCGCT-CTACC
mel_3R_93319-108570 ACGTGTATGCTCTAATTAATAATTTATATAAATTGCCACCGTTACTCCC
***** ***** * * *

sim_3R_168427-182237 ACGCGAAAACCCGCAGGAATTTCTGTTCGCCGCTCTCGAGCTTATCCT
sech_3R_113859-128167 ACGCGAAAACCCGCAGGAATTTCTGTTCGCCGCTCTCGAGCTTATCCT
mel_3R_93319-108570 ACGCAAAAACCCGCAGGAATTTCTGTTCGCCGCTCTCGAGCTTATCCT
*** *****

sim_3R_168427-182237 GCAGGAGCAGGCCAGGTTCGGAATCCCGGCGAATCGGCAAGCAATTCGGG
sech_3R_113859-128167 GCAGGAGCAGGCCAGGTTCGGAATCCCGGCGAATCGGCAAGCAATTCGGG
mel_3R_93319-108570 GCAGGAGCAGGCCCTGGTTCGGAATCCCGGCGTATCGACAACCAATTCGGG
***** *****

sim_3R_168427-182237 CATTAGCTGCTATCAATCCGCTTCCTCCGGCAGGTGTGTTAAAAAGCTTG
sech_3R_113859-128167 CATTAGCTGCTATCAATCCGCTTCCTCCGGCAGGTGTGTTAAAAAGCTAG
mel_3R_93319-108570 CATTAGCTGCTATCAATACGCTTCCTCCGGCGGGTGTGTTAAAAAGCAAG
***** *****

sim_3R_168427-182237 GCCCACAAGGAGATGGTGTCTACATGCTAAGAAATTAGCGGAGGATAAT
sech_3R_113859-128167 GCCCACAAGGAGATGGTGTCTACATGCTAAGAAATTAGCGGAGGATAAT
mel_3R_93319-108570 GCCCACAAGGATGTGGTGTCTACATGTTAAGAAATTAGCGGAGGATAAT
***** *****

sim_3R_168427-182237 CCGTCACCGGTTCCGCTTCCGAGCAATCTCTGCACGTACATGGTGCACCTT
sech_3R_113859-128167 CCGTCACCGGTTCCGCTTCCGAGCAATCTCTGCACGTACATGGTGCACCTT
mel_3R_93319-108570 CTGTACCGGTTCCGCTTCCGAGCAATCCCTGCCCGTACATGGTGCACCTT
* *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
TGTTTATCGCAACGCCAGACTACGAGGCTTATGTAAGCGTGCCAGTCAAT
TGTTTATCGCAACGCCAGACTACGAGGCTTATGTAAGCGTGCCAGTCAAT
TATTTATCGCAACGCCAGACTACGAGGCTTATGTAAGCGTGCCAGTCAAT
* *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
ACTGATGGGAAGTGGGAAAGGGGGCTCCTTGTCTATCAGGGCGTTCTGGG
ACTGATGGGAAGTGGGAAAGGGGGCTCCTTGTCTAGCAGGGCGTTCTAGG
ACTGATGAGGAATGGGAAAGGGGACTCCTTGTCTAGCAGGGCGTGAAGA
***** * * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
ACGGCGTCTCCGGCAGAAGGAAAGTTCGTTATTAGCCAACAATTCGGCTG
ACGGCGTCTCCGGCAGAAGGAAAGTTCGTTATTAGCCAACAATTCGGCTG
ACGGCGTCTCCGGCAGAAGGAAAGTTCGTTATTAGCCAACAATTCGGCTG
*** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
AAAGCTTTCGGCCAGCAAGCTTTCGTTTTGTTGGGGTCAACTGTCAAAA
AAAGCTTTCGGCCAGCAAGCTTTCGTTTTGTTGGGGTCAACTGTCAAAA
AAAGCTTTCGGCCAGCAAGCTTTCGTTTTGTTGGGGTCAACTGTCAAAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CTGACAGCAGTGTCTCTGCGTTGGGGACTCTCTCCTCGTTTCGGCGGT
CTGACAGCAGTGTCTCTGCGTTGGGGACTCTCTCCTCGTTTCGGCGGT
CTGACAGCAGTGTCTCTGCGTTGGGGACTCTCTCCTCGTTTCGGCGGT
***** * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GTTGTTACCACAAGAGCTGCTGGCTACCAGTATAACCGTTTCGGCAGTTA
GTTGTTACAACAAGAGCTGCTGGCTACCAGTATAACCGTTTCGGCAGTTA
GTTGTTACCACAAGAGCTGCTGGCTACCAGTATAACCGTTTCGGCAGTTA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
ATGTAGTTTCGGTACCAGGAGCAGCACCACCGCCCCAGAGCGAACTGTA
ATATAGTTTCGGGACCAGGAGCAGCACCACCGCCCCAGAGCGAACTTTA
ATGTAGTTTCGGTACCAGCAGCAGCACCACCGCCCCAGAGCGAACTTTT
** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CGGTTTGTATACGGGTCTCGTGCCGAGTGGCAATCAGTGGCAGATTGCGAG
CGGTTTGTATACGGGTCTCGTGCCGAGTGGCAATCAGTGGCAGATTGCGAG
CGGTTTGTATACGGGTCTCGTGACGAGTGGCAATCAGTGGCAGATTGCGAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
AGTGTAGCGTGCATTGGTGTGGGAAAAGTACCCAAGCCCTGTGCTTCTCC
AGTGTAGCGTGCATTGGTGTGGGAAAAGTACCCAAGCCCTGTGCTTCTCC
AGTGTAGCGTGCATTGGTGTGGGAAAAGTACCCAAGCCCTGTGCTTCTCC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GTGACCGACTGTTTAGGTAGAC-----TCCGCGGTCCGCGCTCCTTCC
GTGACCGACTGTTTAGGTAGAC-----TCCGCGGTCCGCGCTCCTTCC
GTGACCGACTGTTTAGGTAGACCCACGGTCCGCGGTCCGCGCTCCTTCC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GCGCAAGTCCCCACGCCAGCGGTCTAATGGCCAGTGGACTGTATCCCCA
GCGCAAGTCCCCACGCCAGCGGTCTAATGGCCAGTGGACTGTATCCCCA
GCGCAAGTCCCCACGCCAGCGGTCTAATGGCCAGTGGACTGTATCCCCA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
GGCTTCAATGCCCTAGTGGCCAGGTCGTGACTGTCTACTAAGCAAGGAG
GGCTTCAATGCCCTAGTGGCCAGGTCGTGACTGTCTACTAAGCAAGGAG
GCCTTTAATGCCCTAGTGGCCAGGTCGTGACTGTCTACTAAGCAAGGAG
* * * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570
CTTCGCTTTGTCGAGCCAGAAGTAATAAGCAATTTGTGGAGGAAAAATTA
CTTCGCTTTGTCGAGCCAGAAGTAATAAGCAATTTGTGGAGGAAAAATTA
CTTCGCTTTGTCGAGCCATAAGTAATAAGCAATTTGTGGAGGAAAAATTA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCTCACGCTGTGCAGCAGAGACTGGCTGGAGCGAGCTTGAGTGGTATTCA
TCTCACGCTGTGCAGCAGAGACTGGCTGGAGCGAGCTTGAGTGGTATTCA
TCTCACGCTGTGCAGCAAGGACTTGCTGGAGTGAAGTTCAGTTGTATAC-

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GGCCAGGCATGGAGTCGGGCGGGGACGGCAGCTAACCCATCC-ATACAGT
GGCCAGGAATGGAGTCGGGCGGGGACGGCAGCTAACCCATCC-ATGCAGT
-----GGGCGAGGAAGGCAGCTAACC--TCCCATTTCAGT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ACCAATCCACCAAGCTGTCTGGCAAACGATAAGAAATTATAATTGATTG
GCCAATCCACCAAGCTGTCTGGCAAACGCTAAGAAATTATAATTGATTG
GCCAATCCACCAAGCTGTCTGGCAAACGCTATGAAATTATAATTGATTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AGCGGAAAACAATGAAGCCAACTTAGTCGGCGATATTGGTATGGACTG
AGCGGAAAACAATGAAGCCAACTTAGTCGGCGATATTGGATCTG----TG
AGCGGAAAACAATGACGCCATCTTAGTCGGCCATATTGGTATGAACACTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCGGATCTGTGTGCGACTAATTAGAAGTCTGGAGGGTTCTCTGCGCCCT
TCGGATCTGTGTGCGACTAATTAGAAGTCTGGAGGATTCTCTGCGCCCT
TCGGATCTGTGTGCGACTAATTAGAAGTCTGGAGTATTCTCTGCGCCCT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GGGCAACCTCGGTTCGGAGCTCTTGGCACGGCATAGACTTCGAACCGACCA
GGGCAACCTCGGTTCGGAGCTCTTGGCACGACATAGACTTCGAACCGACCG
TGGCAACCTTGATAGGAGCTCTTGTACGACATAGACTTTGACCCGACCA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CTGTCCGATGGCGGACAGATGAGCGGATGTGGCCAGATCTTTGCAATTC
CTGTCCGATGGCGGACAGATGAGCGGATGTGGCCAGATCTTTGCAATTC
CTGTCCGATGGCGGACAGATGAGCGGATGTGGCCAGATCTTTGCAATTC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CTCCTT-AAAGCTCTGTGCTTCCGGTCCCGTCTTCTGCGCCTGGTTCAG
CTCCTTTAAAGCTCTGTGCTTCCGGTCCCGTCTTCTGCGCCTGGTTCAG-
CTCCTTTAAAGCTATGTGCTTCCGGTCCCGTCTTCTGCTGCCTGGTTCAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CACAGTCCGCCAGCATGTACACACGAATGTGTGCAAACAACTGGAGTG
--CAGTCCGCCAGCATGTACACACGAATGTGTGCAAACAACTGGAGTG
CACAGTCCGCCAGCATGTACACACGAATGTGTGCAAACAACTGGAGTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GCACTGACAAGCCAAACAAAGGCCGTTCCAGTGGGCTGAGGGCGCAGCCGG
GCTCTGACAAGCCAAACAAAGGCCGTTCCAGTGGGCTGAGGGCGCAGCCGG
GCACTGACAAGCCAAACAAAGGCCGTTCCAGTGGGTTGAGGGCGCAGCCGA
**

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GGGATGCGGTGCAGTTCGGCTGGCCCTCGCTCCGAGTGGTGATAATGGCT
GGGAAGCGGTGCAGTTCGGCTGGCTCTCGCTCCGAGTGGTGATAATGGCT
GGGATGCGGTGCAGTTCGGCTGGTTCGCTCCGAGTGGTGATAATGGCT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGTTGGCACAGCGAGCGTCTTATCAGTACGGCCTGGCCTGATGCCAAA-G
CGTTGGCACAGCGAGCGTTTTATCAGTACGGCCTGGCCTGATGCCAAA-G
CGTAGTACAGCGAGCGTCTTATCAGTACGGCATAGCCTGATGCTAAATG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTACAGGAACACTAACACGACCGCCACGAATCGATATCGCGTATACGCTA
TTACAGGAACACTAACACGACCGCCACGAATCGATATCGCGTATACGCTA
TTACAGGAACACTAACACGACCGCCACGAATCGATATCGCGTATACGCTA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CTCGGCGCAGGCGCCAGCTCCCAAATGTAGGCAGCGCTTTCGCTGCTGAT
CTCGGCGCAGGCGCCAGCTCCCAAATGTAGGCAGCGCTTTCGCTGCTGAT
TTCGGCGCAGGCGCCATCTCCCAAATGTAGGCAGCGCTTTCGCTGCTGAT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTCAAAGTCAAAAAGTCAAGAAATTGAGACCGAGAAAGAGAGCGAAGGAG
TTCAAAGTCAAAAAGTCAAGAAATTGAGACCGAGAAAGAGAGCGAAGGAG
TTCAAAGTCAAAAAGTCAAGAAATTGAGACCGAGAAAGAGAGCGAAGGAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GGAGAGAGTGAGAGCGAAAGACAGTCGGAA---AGACACGGAGGGGAAT
GGAGGGAGTGAGAGCGAAAGACAGTCGGAA---AGAGAGGGAGGGGAAT
GAAGAGAGTGAGAGCGAAAGACATTGAGAGGGATAGAGATAGAGGGGAAT
* * * ***** * * * * * * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGAATTATGTAACAGACAAAAAATAGCAG-CAGATAAATATATTAGAGAG
CGAATTATGTAACAGACAAAAAATAGCAG-CAGATAAATATATTAGAGAG
CGAATTATGTAACAGACAAAAAATAGCAGTCAGATAAATATATTAGAGAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AGAGAGCGAGAGAGAGAGAGGGCAGGGTAGGGTCTTTCAGTCC-G-CGG
AGAGAGCGAGAGACAGAGAGGGCAGGGTAGGGTCTTTCAGTCC-GCGCG
ACAGAGAGATAGAGAAAGGGGGCAGGGTAGGGTCTTTCAGTCCGCGCG
* *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCCTGCAATCCTCCCGTCAAACGAGTCCCACC-----GTTGTTGTCTTT
TCCTGCAATCCTCCCGTCAAACGAGTCCCACC-----GTTGTTGTCTTT
TCCTGCAATCCTCCCGTCAAACGAGTCCCACCCCACTGTTGCCCCTT
***** * **** ***** ***** *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ATCTATGTGAGTGC---CCGTGGAGCTCGTTTTCTCTCGGCAAGCCGAG
ATCTATGTGAGTGC---CTGTGGTGCCTCGTTTTCTCTCGGCAAGCCGAG
ATCTATGTGAGTGC---CTGTGGTGCCTCGTTTTCTCTCGGCAAGCCGAG
***** *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGGGAAAGCACTCAAACCCGAGCCGAGAATTTCCGGACGGCGCTAAAGC
CGGGAAAGCACTCAAACCCGAGCCGAGAATTTCCGGACGGCGCT-----
CGGGAAAGCACTCAAACCCGAGCCGAGAATTTCCGGACGGCGCTAAAGC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TCGGTCCCTCGAAGCCCGAAGCCCGAAGCCCGCTCTTACGGGATTTCCGG
-CGGTCCCTCGAAGCCCGAAGCCCGAAGCCCGCTCTTACGGGATTTCCGG
TCGGTCCCTCGAAGCCCG-----CTATTAAGTGGATTTCCGG
***** *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GGCCGAGCGGCGGGTCGGCTCCGACGCGCTGCCTCCGCCAGCGCTTT
GGTCGAGCGGCGGGTCGGCTCCGACGCGCTGCCTCCGCCAGCGCTTT
GGCCGAGCGGCGGGTCGGCTCCGACGCGCTGCCTCCGCCAGCGCTTT
* *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GTAAGGCGCTCGCATGCGGAACAGCGCAACGAGCCAAGTTTTCCGAGTT
GTAAGGCGCTCGCATGCGGAACAGCGCAACGAGCCAAGTTTTCCGAGTT
GTAAGGCGCTCGCATGCGGAACAGCGCAACGAGCCAGTTTACCAGGTT
***** *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TGCGAGTTTTCCGTGAGGTTACTCTGGCAGTGGCGTGACAGAGAGTGGC
TCCGAGTTTTCCGTGAGGTTACTCTGGCAGTGGCGTGACAGAAAGTGGC
T-----TTCGTGAGGTTACTCTGGCAGTGGCGTGACAGAGAGTGGC
* *

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AACATAGCATGAAGTAAGAAGCGCCGAGAAAACATAGCGACGGTCTAGTG
AACATAGCATGAAGTAAGAAGCGCCGAGAAAACATAGCGACGGTCTAGTG
AACATAGCATGAAGTAAGAAGCGCCGAGAAAACATAGCGACGGTCTAGTG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AAAAGTGGCAAGCAAAGCAAAGTATTAAGCACACACACTGCCAGTGC
AAAAGTGGCAAGCAAAGCAAAGTATTAAGCACACACACCGCCAGTGC
AAAAGTGGCAAGCAAAGCAAAGTATTAAGCACACACACTGCCAGTGC

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GCACGGACACACACAGCACACCAGCACACTCCAGCACCAACACACTAGAG
GCACGGACACACACAGCACACCAGCACACTCCAGCACCAACACACTAGAG
GCACGGACACACAC-----AGCACACTCCCGCACCAACACACTAGAG

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CAAGTGCCTGTACATAGAGGGTTTGTGCGGG-CACATATGTGCCACACAC
CAAGTGCCTGTACATAGAGGGTTTGTGCGGG-CACATATGTGCCACACAC
CAAGTGCCTGTACATAGAGGGTTTGTGTTGGGCACATATGTGCC-----

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ACACACACACTGGCAGTACGATGTCGATACTGGCTCACAGTGGTGGTAT
ACACACACATTGGCAGTACGATGTCGATACTGGCTCACAGTGGTGGTAT
-----CGCAGTATGTCGATACTGGCTCACATTGGTAGTAT
** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTAAAAATCGACGAACGGCCCGAGCTCGAA-GCACGACTGAAAACCTAAA
TTAAAAATCGACGAACGGCCCGAGCTCGAAAGCACACTGAAAACCTAAA
TTAAAAAGCGACGAACGGCCCGAGCTCGAAAGCACACTGAAAACCTAAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TTGATTAAGCGAATTTGTTCTATCAAGCTAATTCAATTGCTCGGCCAGTT
TTGATTAAGCGAATTTGTTCTATCAAGCTAATTCAATTGCTCGGCCAGTT
TTGATTAAGCGAATTTGTTCTATCAAGCTAATTCAATTGCTCGGCCAGTT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GACTGAGTGATCCACTGCGAGCGCAGCCTTATGTAATCGGAATCAGTGAA
GACTGAGTGATCCACTGCGAGCGCAGCCTTATGTAATCGGAATCAGTGAA
GACTGAGTGATCCACTGCAAGCGCAGCCTTATGTAATCGGAATCAGTGAA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

AAA-GCGAAACACGGCGCCGAGGAATACGACTCCAGGACCCAGGA
AAA-GCGATACACGGCGCCGAGGAATACGACTCCAGGACCCAGGA
AAAAGCGAAACACGGCGCCGAGGAATACGACTCCAGGACCCAGGT
*** **

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCCAGGACCCGAGTCCAATCGAATTTGTTTGTGCTGCGCGTATTACGTAAG
CCCGAGTCCC-----CAATCGAATTTGTTTGTGCTGCGCGTATTACGTAAG
CA-----AATCGAATTTGTTTGTGCTGCGCGTATTACGTAAG
* *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TAAAA-TCTTGTTTGCT-GTGGCACCCGCTCCTCGAACCCTCCCCACT
TAAAA-TCTTGTTTGCT-GTGGCACCCGCTCCTCGAACCCTCCCCACT
TAAAAATCTTGTTTGCTTGTGGCACCCGCTCCTCGAACCCTCCCCACT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGAAGAGGCACCTTACGTGCACGCTCCCATAAAAGAAACCTAATAAAGAA
CGAAAAGGCACCTTACGTGCACGCTCCCATAAAAGAAACCTAATAAAGAA
CAAAAAGGCACCTTACGTGCACGCTCCCATAAAAGAAACCTAATAAAGAA
* * *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

ATATCGATAAAAAGCAACAAAGCAAGTGGCACGCCAGCACATAACGACGA
ATATCGATAAAAAGCAACAAAGCAAGTGGCACGCCAGCACATAACGACGA
ATATCGATAAAAAGCAACAAAGCAAGTGGCACGCCAGCACATAACGACGA

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CGACAAGCGAAACATCGGTAACAATGCGACCCCTGGGGGTGTTGGTGTGT
CGACAAGCGAAACATCGGTAACAATGCGACCCCTGGGGGTGTTGGTGTGT
CGACAAGCGAAACATCGGTAACAATGCGACCCCTGGGGGTGTTGGTGTGT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

GTGTGTCTGCTATTTTTAAATTAGCGCCAGTCCTCTAGGTTCCGGCCCGAC
GTGTGTCTGCTATTTTTAAATTAGCGG-----GGCCCGAC
GTG--TCTGCTATTTTTAAATTAGCGCCAGTCCTCTAGGTTCCGGCTCGAC
*** ***** **

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCCGCCGAACCCTGAAACCTGCAACCCGGAAGCCACATAACCCTGGAAGC
CCCGCCGAACCCTGAAACCTGCAACCCGGGAGCCACATAACCCTGGAACC
CCCGCCGAACCCTGAAACCCGTAACCCGGGAGCCATATAACCCTGGAAGC
***** * ***** **

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCAGAACCCTGGACTGTGCACACCTAA-----CCCCTGTGTCTCTGTT
CCAGAACCCTGGACTGTGCACACCTAA-----CTCCTGTGTCTCTGTT
CCGAACCTGTGACTGTGAACACTAAACGACGCCTTCTGTGTCTCTGTT
***** ** ***** ** * ***** **

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TGTCTTTCAGGAAGCCTATCTGCCTAATGCACGCTCTTCACGGTGGATTT
TGTCTTTCAGGAAGCCTATCTGCCTAATGCACGCTCTTCACGGTGGATTT
TGTCTTTCAGGAAGCCTATCTGCCTAATGCACGCTCTTCACAGTGGATTT
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CCTTAGAACAAACACATTTTCGCGCAGACTAGTCGGAACCTTGCTCCTCAA
CCTTAGAACAAACACATTTTCGCGCAGACTAGTCGGAACCTTGCTCCTCAA
CCTTAGAACAAACACATTTTCGCGCAGACTAGTCGGAACCTTGCTCCTCAT

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

CAACCAAGTCCACGCACTCACAGGAATCTTCAAGGGAAATCTGAAAGGAA
CAACCAAGTCCACGCACTCACAGGAATCTTCAAGGGAAATCTGAAAGGAA
CAACCAAGTCCACGCACTCACAGGAATCTTCAAGCAAATCTGAAAGGAA
***** *****

sim_3R_168427-182237
sech_3R_113859-128167
mel_3R_93319-108570

TACTTGCTGAACTAAGGCCAGGTAAGTGGGTGGTC
TACTTGCTGAACTAAGGCCAGGTAAGTGGGTGGTC
TACTTGCTGAACTAAGGCCAGGTATGTGGGTGGTC
***** *****

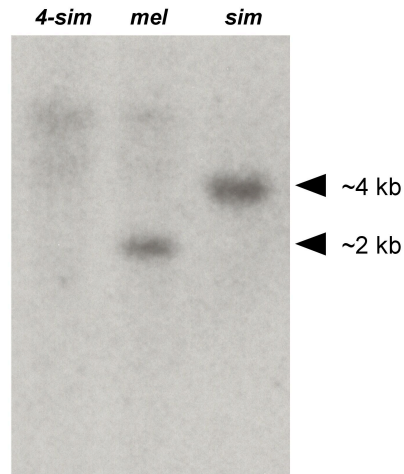


Figure S3. Southern blot analysis of *JYAlpha*. Genomic DNA was digested with *HindIII* and probed with a highly conserved 1.2 kb sequence from exon 3. Both *D. melanogaster* and *D. simulans* show single bands of the size expected from the genome assemblies and our own sequencing. As expected, neither of these species-specific bands is present in homozygous *4-sim* hybrids. Note that even if multiple copies of *JYAlpha* exist in *D. simulans*, no copies exist on the *D. simulans* fourth chromosome explaining the sterility of homozygous *4-sim* hybrids. We performed two replicates and both showed identical results. Abbreviations: *4-sim*=*4-sim* homozygotes; *mel*=*D. melanogaster*; *sim*=*D. simulans*.

Supplementary references and notes

1. H.M. Robertson *et al.*, *Genetics* **118**, 461 (1988).
2. J. Rozas, J.C. Sánchez-Delbarrio, X. Messeguer, R. Rozas, *Bioinformatics* **19**, 2496 (2003).
3. D. Karolchik *et al.*, *Nucl. Acids Res.* **31**, 51 (2003).