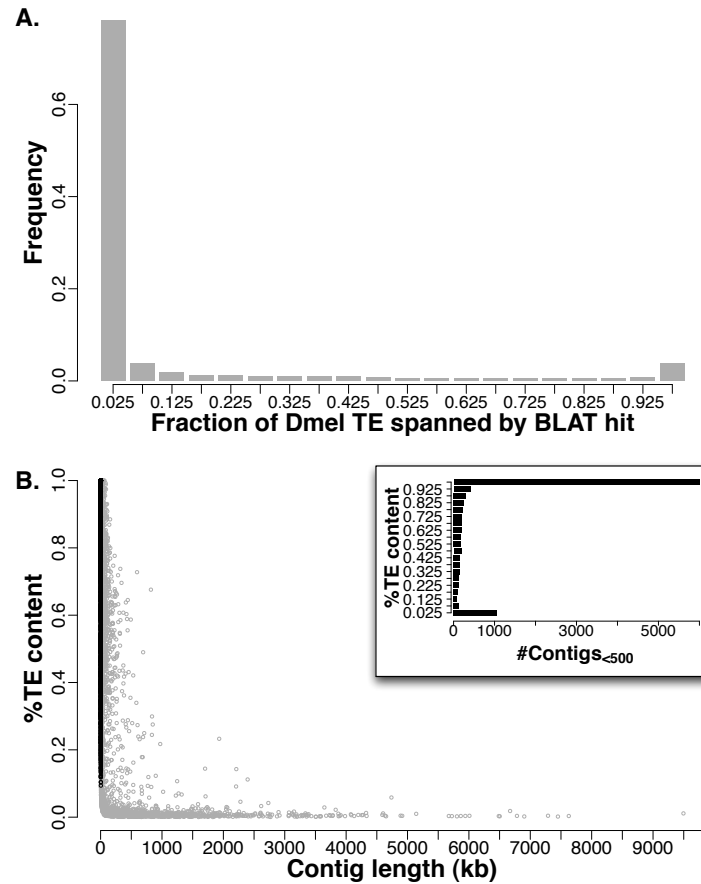
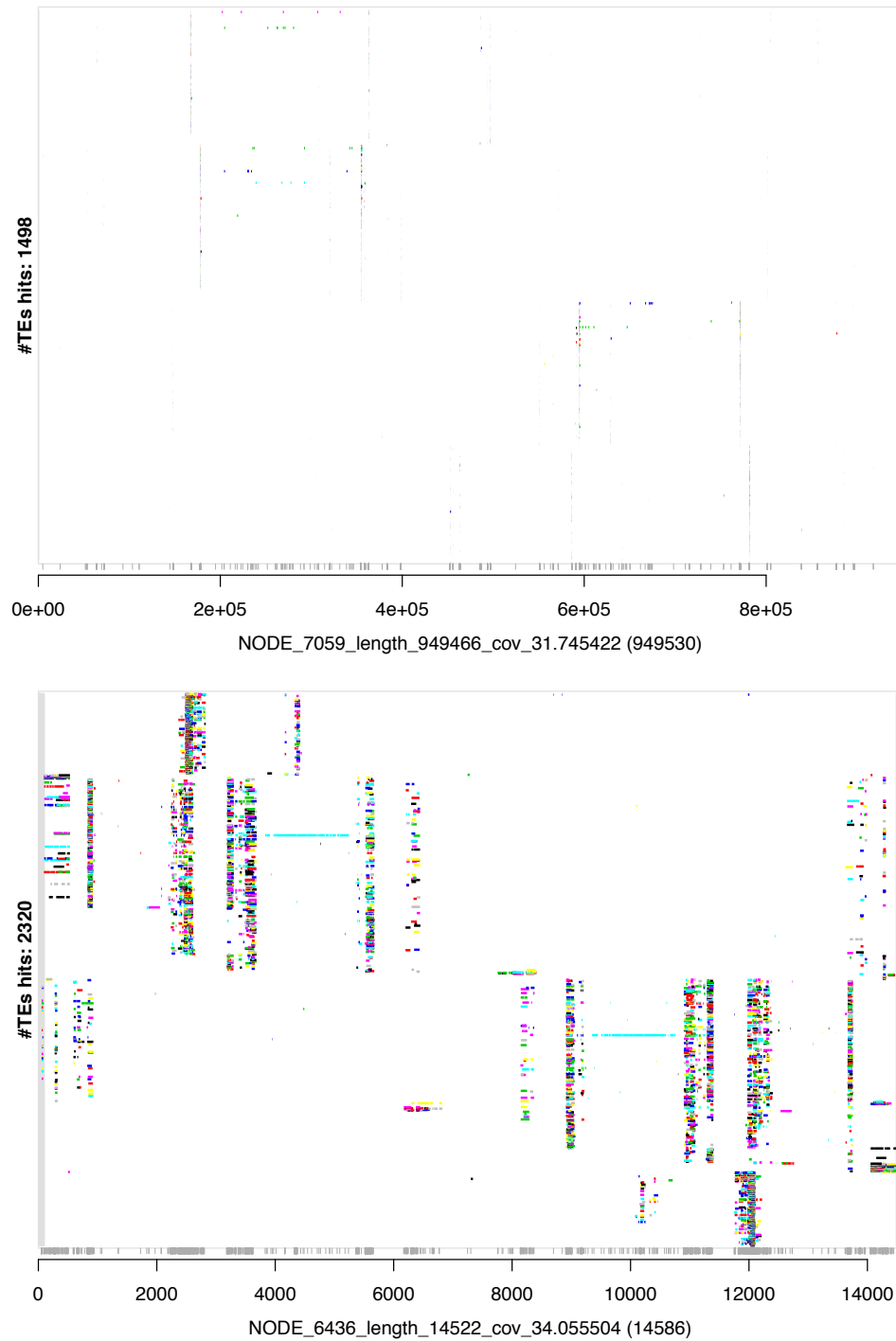


Supplementary Figures



Supplementary Figure 1. Presence of *D. melanogaster* transposons in Velvet contigs.

A, Histogram depicting the presence of *D. melanogaster* transposons to Velvet contigs with at least one BLAT hit to a *D. melanogaster* transposon. **B**, Relationship between the length of Velvet contigs with the total similarity to *D. melanogaster* transposons. The inset focuses in on the distribution of the amount matched to *D. melanogaster* transposons for contigs <500 bps (in black; total of 6,985).

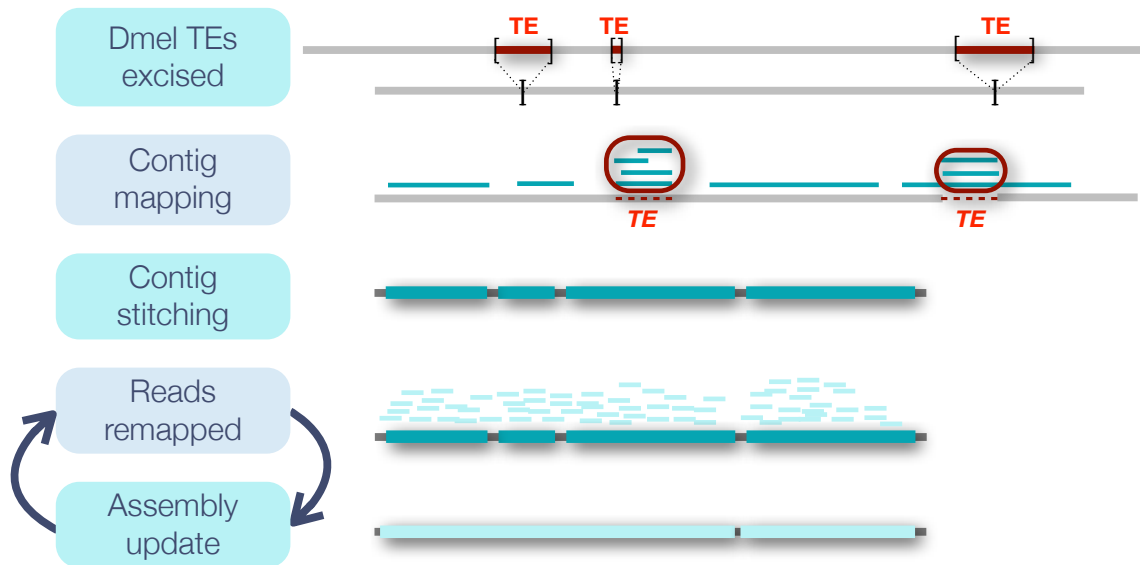


Supplementary Figure 2. Presence of *D. melanogaster* transposons in two contigs.

Each row and color represents the match to a *D. melanogaster* transposon. The vertical gray bars at both ends correspond to the first and last 500 bps of the contig. The gray ticks along the x-axis denote the position in the contig matching one or more *D. melanogaster* transposons.

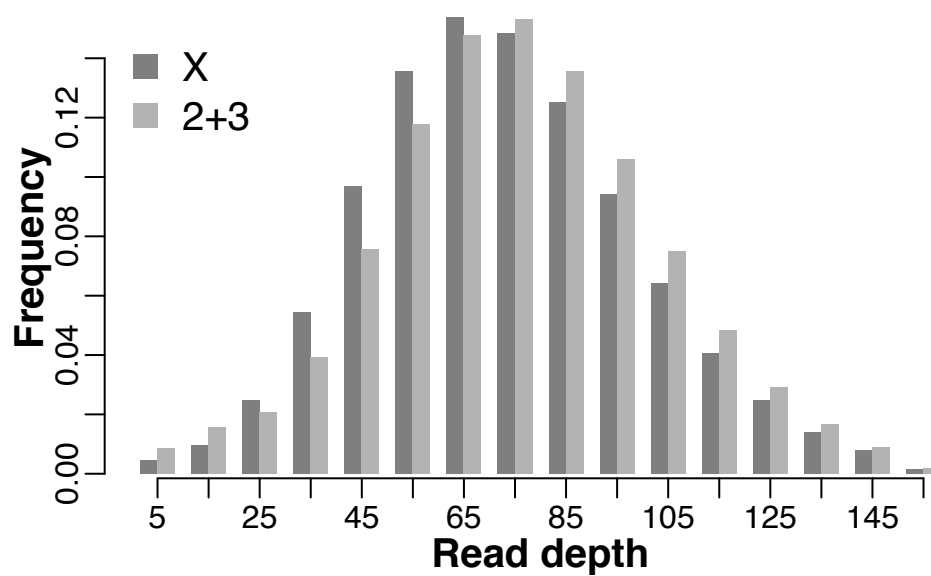
Assembly of contigs

Example of a representative region

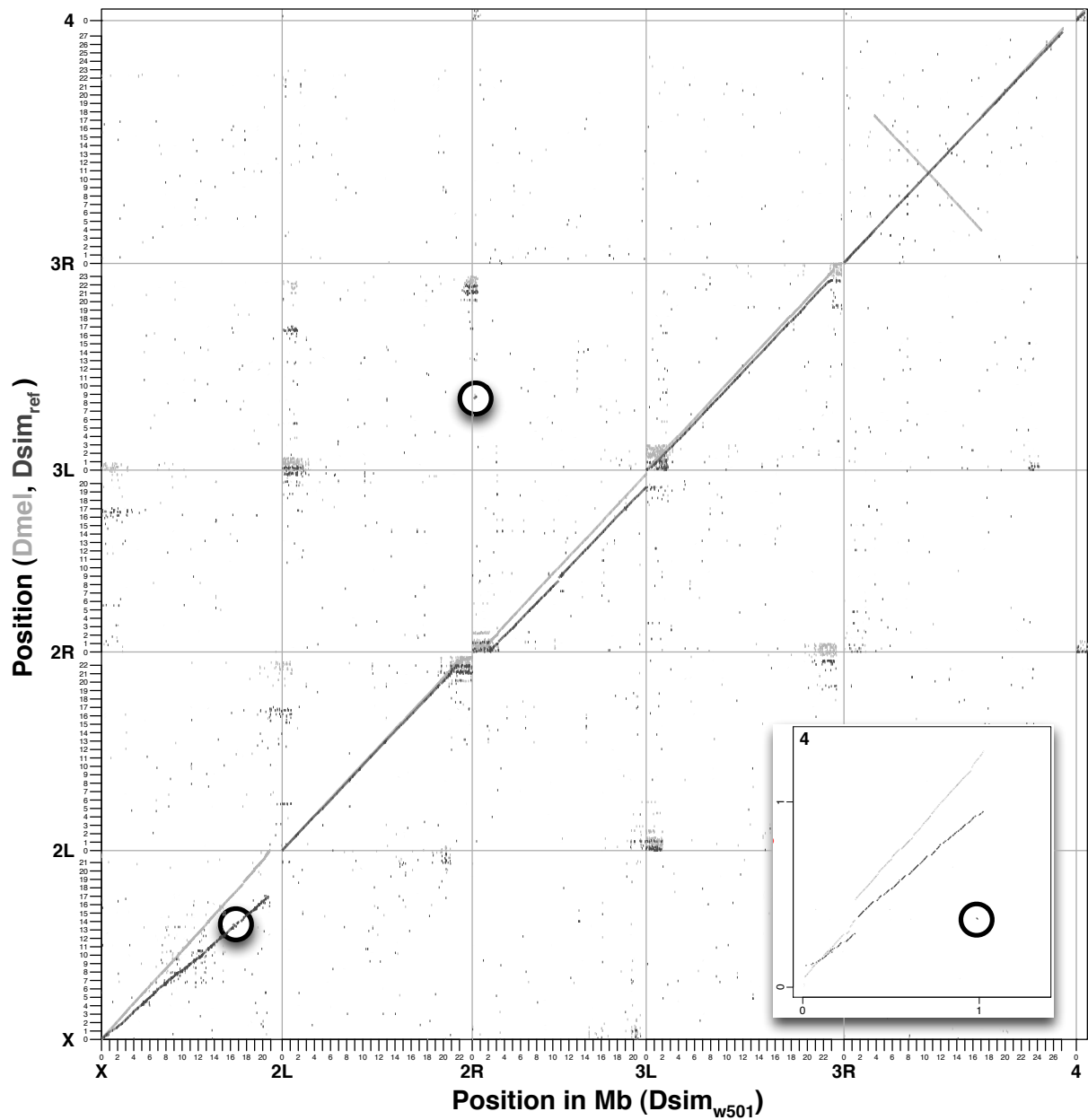


Supplementary Figure 3. Scaffolding of contigs using the *D. melanogaster* genome.

Prior to mapping, all annotated transposable elements (red) were first excised from the *D. melanogaster* genome (light gray). All Velvet contigs (turquoise) were then mapped to this reduced version of the *D. melanogaster* genome with BWA. Non-uniquely mapped contigs and those engulfed by larger contigs (circled in red) were set aside and likely represent repetitive elements in *D. simulans* (dashed red lines). The final set of uniquely mapped contigs (turquoise) were stitched together with a 100 bp buffering of Ns (dark gray). Finally, all reads (light sky blue) were re-mapped to this initial assembly and only homozygous SNV and indel differences to the assembly were incorporated. Three iterations of assembly updating by re-mapping of reads were performed resulting in minor improvements in the total number of paired-reads mapped.

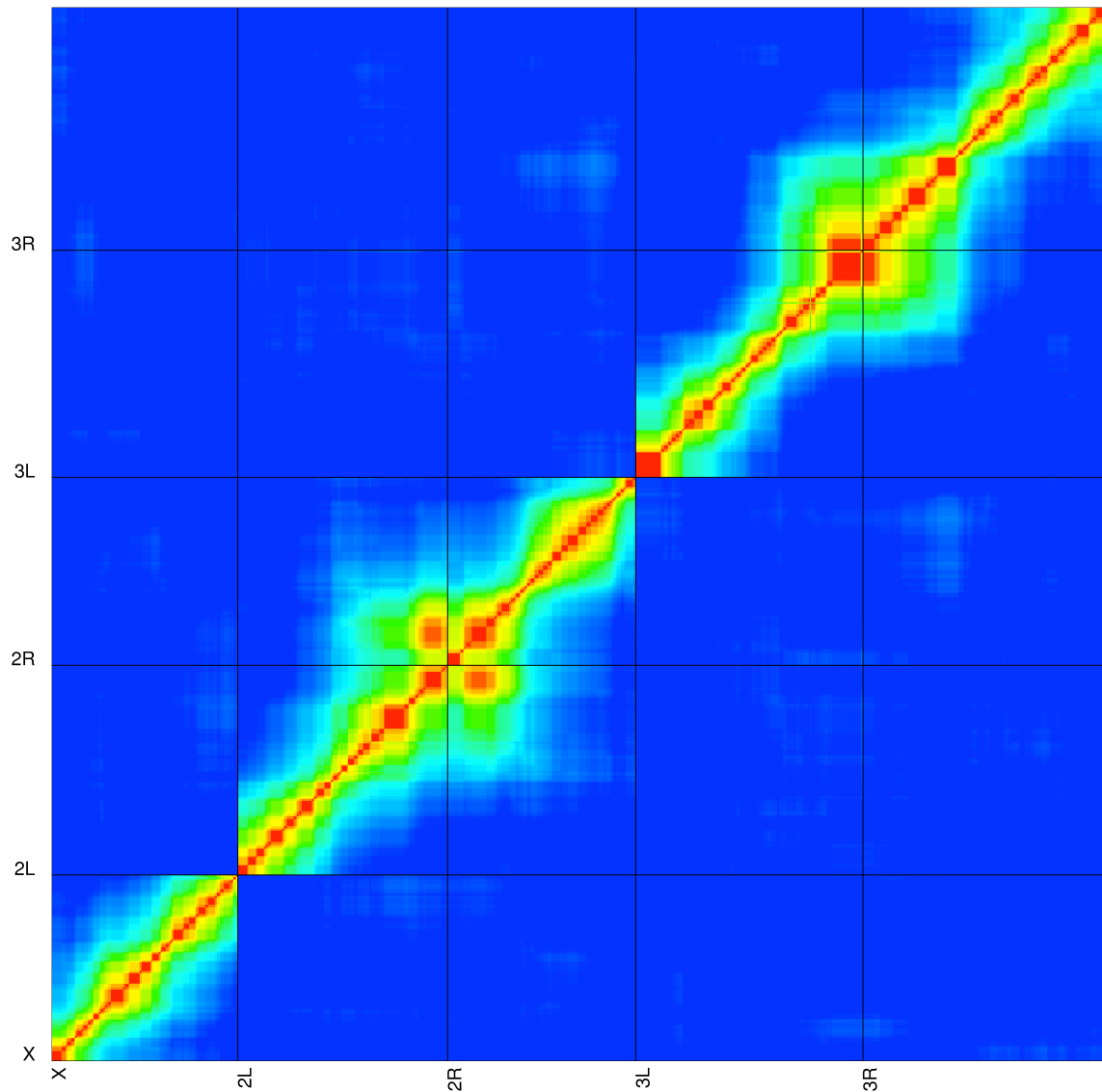


Supplementary Figure 4. Read coverage after BWA-mapping to the *Dsim_{w501}* assembly for the X chromosome and 2+3 autosomes. Positions in the genome with read depths greater than 160 were excluded. See Supplementary Table 3 for mean and median coverage.

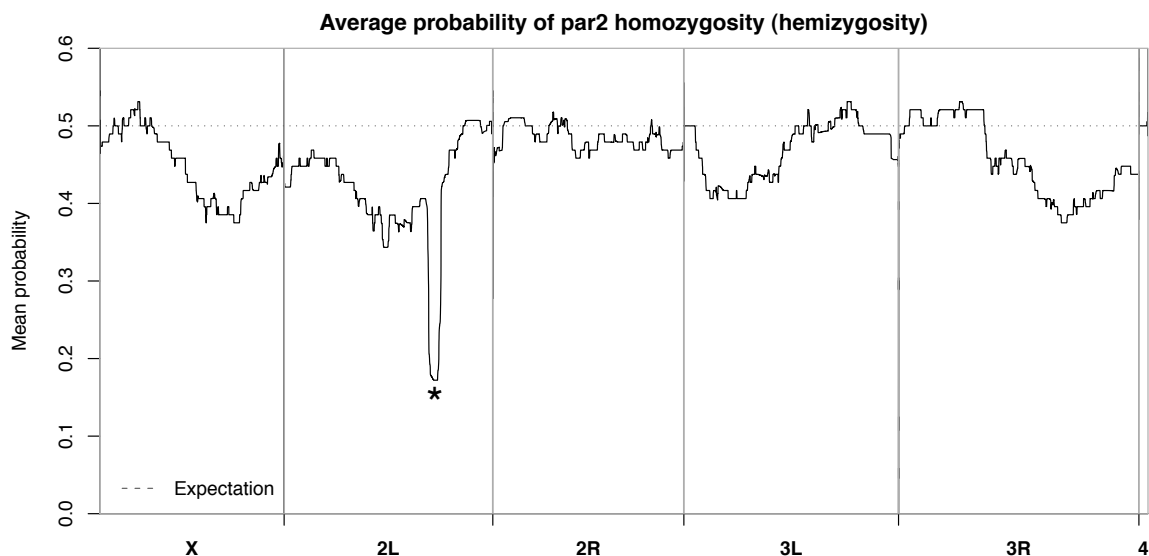


Supplementary Figure 5. Dotplot between this assembly to the *D. melanogaster* (light gray) and the *D. simulans* reference assembly (dark gray) (Begun et al. 2007).

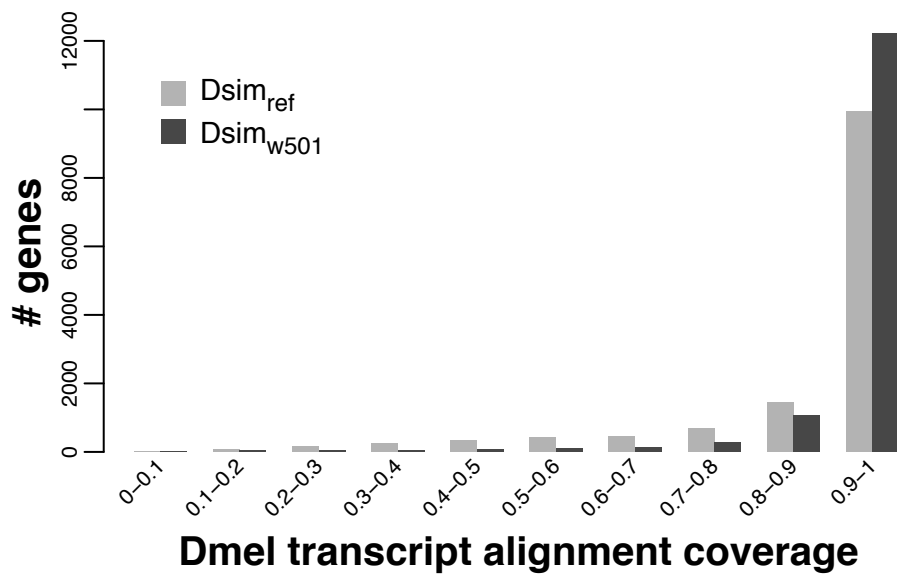
Misassembled regions in the *D. simulans* reference assembly highlighted in circles. Note that the inversion on 3R between *D. simulans* and *D. melanogaster* has been reported previously (Lemeunier and Ashburner 1976). Inset is a closeup of chromosome 4.



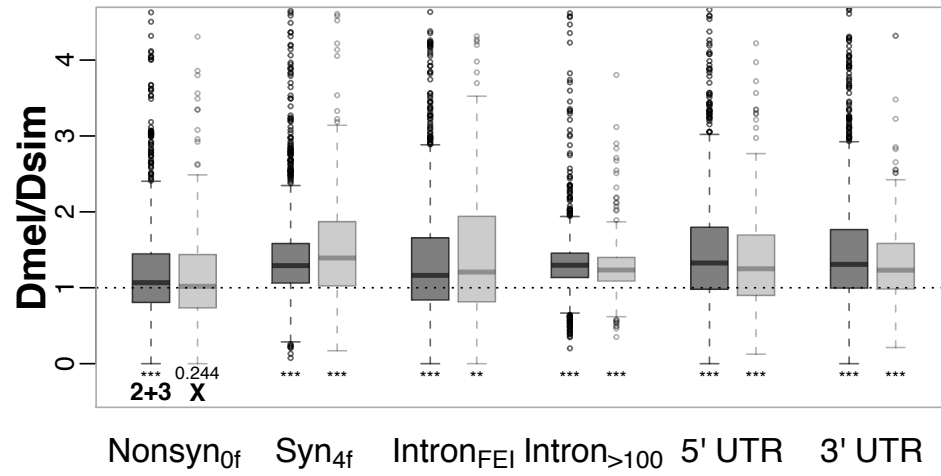
Supplementary Figure 6. Genetic correlation between all pairs of markers that differentiate *D. simulans* and *D. sechellia*. Unlike $Dsim_{ref}$, the $Dsim_{w501}$ assembly properly conforms with the inferred genetic ordering of markers using the previously published genetic cross genotyping data of Andolfatto et al. (2011a). The colors indicate the extent of genetic correlation between pairs of sites (blue is low, red is high). The width of the diagonal depends on the extent of linkage where regions of larger width correspond to regions of lower recombination (such as the centromeres, in fact). The previously reported region showing excessive heterozygosity (Supplementary Figure 7) was masked prior to BWA-mapping.



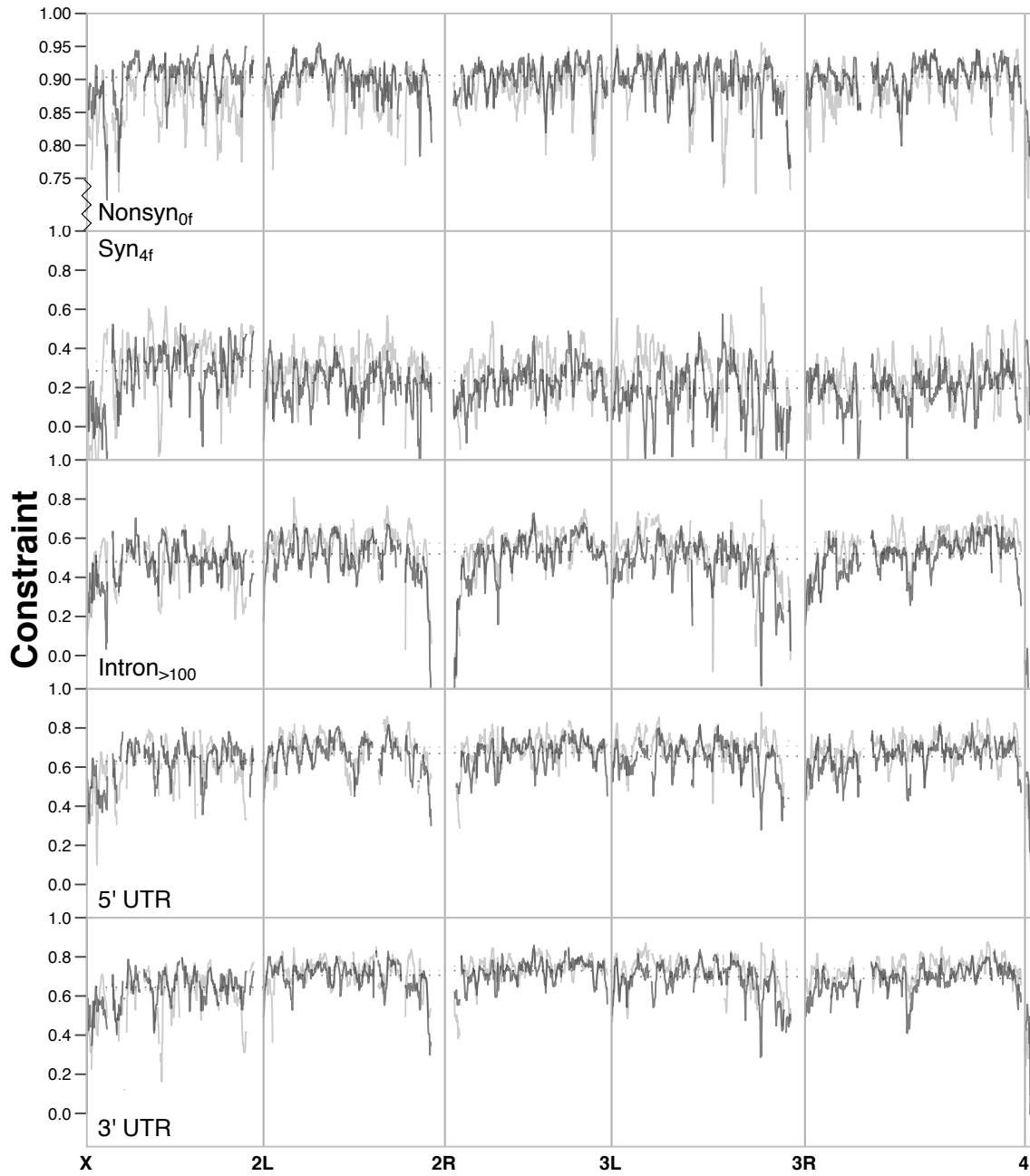
Supplementary Figure 7. Segregation plot. The expected probability of a heterozygous genotype in F1-backcross individuals is 0.5 (dotted line). The asterisk on chromosome 2 denotes the region with significant segregation distortion (excessive heterozygosity) also previously reported (Andolfatto et al. 2011a). This region spanning the centromere of chromosome 2 (2L:16114186-17755545) was masked in Supplementary Figure 6.



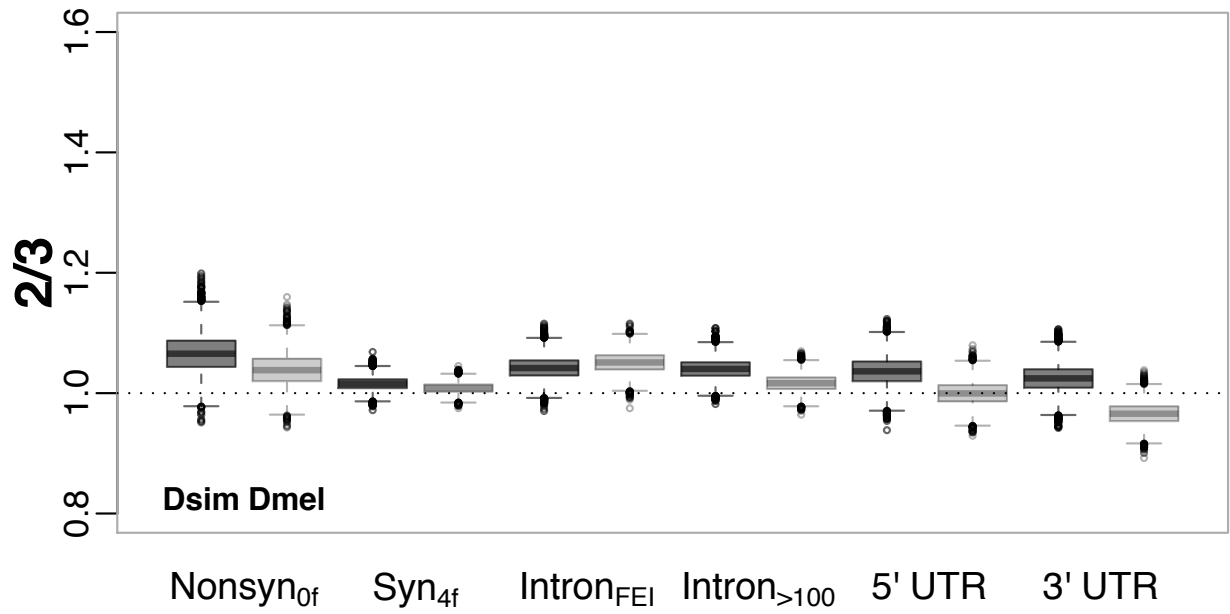
Supplementary Figure 8. Coverage comparison of *D. melanogaster* protein-coding transcripts based on BLAT between the different *D. simulans* assemblies.



Supplementary Figure 9. The distribution of $Dmel/Dsim$ divergence ratios among non-overlapping 50 kb windows of *D. melanogaster*/*D. simulans* for autosomal (left) and the X chromosome (right). Whether divergence along the *D. melanogaster* lineage is faster than that in *D. simulans* is indicated by the P-value beneath each boxplot (** $P < .00001$, ** $P < .001$, * $P < .01$, Two-tailed P-values are based on a Sign test).



Supplementary Figure 10. Constraint by site class across the genome in *D. simulans* and *D. melanogaster*. Constraint, measured as $1 - \frac{D_{annot}}{D_{intron_{FEI}}}$, is plotted in 500 kb windows with a 50 kb step with respect to *D. melanogaster* coordinates. Each window requires a minimum of 10 genes each with at least 10 non-N sites for intron_{FEI} sites and 100 non-N sites for all other site classes (*annot*). The dotted line denotes the chromosome arm average. In each panel, the darker line represents *D. simulans* and the lighter line for *D. melanogaster*.



Supplementary Figure 11. The chromosome 2 to chromosome 3 (2/3) divergence ratio in *D. simulans* and *D. melanogaster*. The distributions of 2/3 divergence ratios reflect 10,000 bootstrap samples with replacement by gene across the various site classes, separately for genes on chromosomes 2 and 3. Refer to Supplementary Table 8 for bootstrap P-values.

Supplementary Tables

Supplementary Table 1. Sequencing datasets

Dataset	Insert size	# reads
HiSeq Illumina PE (104 bp)	500 bps	93710318
GA II Illumina PE (101 bp)	500 bps	48162184
Sanger plasmid PE (Begun et al. 2007)	4 kb	546232
Sanger fosmid PE (Begun et al. 2007)	40 kb	125606

Note that PE denotes “paired-end” reads.

Supplementary Table 2. Summary of the Velvet assembly

Assembly size (bp)	124231044
#contigs	21613
#contigs ≥ 500 bp	4560
Largest contig (bp)	949466
N50 (contigs ≥ 500 bp)	149140
Reads used	107696845 (73.7%)

Note that prior to assembly with Velvet, reads were error-corrected using Quake (Kelley et al. 2010) with a k-mer of size 17. The N50 statistic is a weighted median statistic such that 50% of the entire assembly is contained in contigs or scaffolds equal to or larger than this value.

Supplementary Table 3. Read depth coverage across all datasets (Supplementary Table 1)

Chromosome	Mean	Median
X	75.6	72
2+3	77.7	76
4	71.0	68
mtDNA	612.9	196
Unassembled	158.0	61
Overall	82.4	75

Supplementary Table 4. Inter-chromosomal transpositions (ICT) and locally rearranged (LR; syntenic but not necessarily colinear) genes between *D. melanogaster* and *D. simulans* (w501)

Gene	Isoform	Dmel position	Dsim position	State	SYN.ARM ¹	GLEAN.ARM ²	Sheet ³
FBgn0000316	FBtr0070064	X:148943-152446 +	X:86491-89998 +	LR			
FBgn0259722	FBtr0299979	X:148943-152446 +	X:86479-89940 +	LR			
FBgn0052816	FBtr0070102	X:210609-228832 -	X:143361-286994 -	LR			
FBgn0024989	FBtr0070068	X:237078-244237 +	X:112778-172718 +	LR			
FBgn0052817	FBtr0300328	X:373479-374199 +	X:295458-296129 +	LR			
FBgn0029524	FBtr0070078	X:375895-376691 +	X:295423-296129 +	LR			
FBgn0014903	FBtr0070175	X:925538-927198 +	X:828810-830519 +	LR			
FBgn0003638	FBtr0070176	X:927349-940075 +	X:809472-835899 +	LR			
FBgn0010294	FBtr0070540	X:3134058-3134604 -	X:2891477-2891896 +	LR	AAAA	A—	lineage_supp_lo_conf
FBgn0010295	FBtr0070539	X:3135524-3136117 -	X:2890571-2891149 -	LR	AAAA	A-AA	single_species_low_conf
FBgn0021738	FBtr0070599	X:3688900-3691372 +	X:3395910-3397397 +	LR			
FBgn0260484	FBtr0070600	X:3693181-3695607 +	X:3391026-3393444 +	LR			
FBgn0029679	FBtr0070605	X:3722335-3724913 +	X:3420944-3423511 +	LR			
FBgn0000542	FBtr0112802	X:3740111-3751658 +	X:3403947-3449920 +	LR			
FBgn0029705	FBtr0070654	X:4221113-4223336 -	X:3914765-3917257 -	LR			
FBgn0262738	FBtr0100670	X:4241951-4258913 +	X:3910298-3952600 +	LR			
FBgn0052713	FBtr0071243	X:8350962-8351665 -	X:7930233-7930863 -	LR			
FBgn0030040	FBtr0302500	X:8352527-8354927 -	X:7923466-7925259 -	LR			
FBgn0014032	FBtr0071241	X:8357338-8359030 -	X:7927619-7929350 -	LR			
FBgn0053223	FBtr0071239	X:8359723-8377918 -	X:7922079-7948438 -	LR			
FBgn0030071	FBtr0071265	X:8817256-8817651 -	X:8377055-8377450 -	LR	AAAA	AAAA	lineage_supp_lo_conf
FBgn0261549	FBtr0302660	X:8819217-8918969 +	X:8361028-8468230 +	LR			
FBgn0030181	FBtr0112973	X:10047645-10049044 +	2L:11127716-11129027 -	ICT			
FBgn0040940	FBtr0071434	X:10052843-10053124 +	2L:11124213-11124493 -	ICT			
FBgn0040942	FBtr0071481	X:10158257-10159290 -	X:9649934-9651028 -	LR			
FBgn0259170	FBtr0299633	X:10170088-10203140 -	X:8657253-9701433 -	LR			
FBgn0030252	FBtr0273267	X:10832482-10858079 +	X:10290736-10315704 +	LR			
FBgn0052670	FBtr0073401	X:10845642-10846519 -	X:10019179-10303660 -	LR			
FBgn0259101	FBtr0299514	X:10990306-11002192 +	2L:21583246-22729194 -	ICT			
FBgn0030538	FBtr0089267	X:14065520-14066657 -	X:13486587-13487594 +	LR	AAAA	A—	lineage_supp_lo_conf
FBgn0030539	FBtr0073891	X:14068794-14069703 +	X:13207245-13208178 +	LR			
FBgn0030577	FBtr0073935	X:14669392-14670151 +	X:13865448-13865994 +	LR			
FBgn0030578	FBtr0073936	X:14670807-14672016 +	X:13864946-13865995 +	LR	AAQA	AA-A	lineage_supp_lo_conf
FBgn0030654	FBtr0074072	X:15464410-15466135 -	X:14633979-14635726 -	LR			
FBgn0030655	FBtr0074071	X:15466103-15468618 -	X:14614024-14616384 -	LR			
FBgn0030693	FBtr0074185	X:15687752-15690082 -	X:14864814-14867126 -	LR	AAAA	AAAA	single_species_low_conf
FBgn0052581	FBtr0074184	X:15690936-15693189 -	X:14864812-14867099 -	LR			
FBgn0030696	FBtr0074098	X:15703588-15704980 +	X:14877673-14879065 +	LR	AAQA	AA-A	lineage_supp_hi_conf_one_gene
FBgn0000345	FBtr0112825	X:15706362-15719755 +	X:14873953-14893851 +	LR	AAAA	AAAA	single_species_low_conf
FBgn0000319	FBtr0074182	X:15722019-15729507 -	X:14896149-14903622 -	LR	AAAA	AAAA	single_species_hi_conf_one_gene
FBgn0030697	FBtr0074103	X:15731863-15735093 +	X:14764380-14766745 +	LR			
FBgn0259700	FBtr0299951	X:15987103-15989945 -	X:15114708-15126301 -	LR			
FBgn0259699	FBtr0299953	X:15987103-15989945 -	X:15114721-15126301 -	LR			
FBgn0030834	FBtr0074446	X:17142405-17143575 -	X:16254134-16255365 -	LR			
FBgn0262111	FBtr0304061	X:17153508-17174997 +	X:16239258-16286652 +	LR			
FBgn0053497	FBtr0089610	X:20076060-20080509 -	X:18904089-18910426 -	LR			
FBgn0003654	FBtr0089406	X:20099187-20107456 -	X:18903622-18911752 -	LR			
FBgn0031100	FBtr0077338	X:20181336-20182700 -	2R:14186443-14187800 +	ICT	AAQA	AA-A	single_species_low_conf
FBgn0031101	FBtr0077297	X:20198521-20199708 +	2R:14169898-14171058 -	ICT			
FBgn0083956	FBtr0110827	X:20994980-21011281 +	X:19723518-19756730 +	LR			
FBgn0052511	FBtr0077258	X:21027391-21028092 -	X:18681415-18681565 -	LR			
FBgn0031208	FBtr0300690	2L:7529-9484 +	X:17996861-17999232 -	ICT	BAQQ	B—	single_species_low_conf
FBgn0041337	FBtr0077748	2L:2564882-2573047 -	2L:21006417-22219747 -	LR			
FBgn0031434	FBtr0077746	2L:2575276-2577006 -	2L:2463808-2465528 -	LR			
FBgn0051642	FBtr0079199	2L:6118512-6120522 +	2L:5913317-5915329 +	LR			
FBgn0051641	FBtr0304908	2L:6120674-6124412 +	2L:5895652-5919255 +	LR			
FBgn0051630	FBtr0079400	2L:7042467-7047267 +	2L:6803330-6807989 +	LR			
FBgn0022201	FBtr0079399	2L:7050226-7054854 +	2L:6798823-6816698 +	LR			
FBgn0053723	FBtr0091721	2L:9440011-9440740 -	2L:9130305-9131052 -	LR	BBBB	BBBB	lineage_supp_lo_conf
FBgn0002973	FBtr0079822	2L:9449830-9463293 +	2L:9127862-9153667 +	LR			
FBgn0051864	FBtr0080288	2L:11995792-11996471 +	2L:11667543-11667888 +	LR			
FBgn0051865	FBtr0080289	2L:11996811-11997960 +	2L:11664659-11665807 +	LR			
FBgn0051848	FBtr0303784	2L:13264996-13265876 -	2L:12883041-12883890 -	LR			

Gene	Isoform	Dmel position	Dsim position	State	SYN_ARM ¹	GLEAN_ARM ²	Sheet ³
FBgn0032497	Fbtr0305068	2L:13267492-13284043 +	2L:12879043-12902169 +	LR			single_species_hi_conf.one_gene
FBgn0002652	Fbtr0080887	2L:16680056-16681653 +	2L:16246560-16248232 +	LR	BBBC	BBBC	
FBgn0261278	Fbtr0080886	2L:16685177-16699926 +	2L:16246550-16266750 +	LR			
FBgn0051809	Fbtr0113414	2L:16853619-16858453 -	2L:22340701-23196133 +	LR			
FBgn0032615	Fbtr0080923	2L:16860073-16861419 -	2L:16418464-16419832 -	LR			
FBgn0051687	Fbtr0081361	2L:20450207-20452538 +	2L:19914496-19915700 +	LR			
FBgn0042175	Fbtr0081364	2L:20457057-20459082 -	2L:19912216-19914250 -	LR			
FBgn0032891	Fbtr0290042	2L:20832858-20835607 -	2L:20284932-20287674 -	LR			
FBgn0028986	Fbtr0081450	2L:20836621-20838179 -	2L:7968238-7969642 -	LR			
FBgn0032949	Fbtr0085896	2L:21573378-21577103 +	2R:1269942-1276717 +	ICT			
FBgn0022893	Fbtr0100293	2L:21626590-21629930 -	2L:20908388-20911646 -	LR			
FBgn0023416	Fbtr0085897	2L:21632599-21647967 +	2L:20905014-20924448 +	LR			
FBgn0032968	Fbtr0085930	2L:21916361-21917450 +	2L:21199522-21200615 +	LR			
FBgn0032969	Fbtr0300121	2L:21981572-21992933 -	2L:20840763-21267727 -	LR			
FBgn0040011	Fbtr0111252	2L:22471796-22478851 +	2L:21797977-21803417 +	LR			
FBgn0058006	Fbtr0111230	2L:22515149-22649081 -	2L:21734804-22268851 -	LR			
FBgn0058005	Fbtr0111235	2L:22842025-22843012 -	2L:23156791-23157782 +	LR			
FBgn0000384	Fbtr0111126	2L:22874534-22885080 +	2L:23115948-23158190 +	LR			
FBgn0262117	Fbtr0111268	2R:123268-130444 -	2R:510281-518043 -	LR			
FBgn0260798	Fbtr0111121	2R:209942-358573 -	2R:35712-2859196 -	LR			
FBgn0046692	Fbtr0111111	2R:434225-452786 +	2L:21662904-23561401 +	ICT			
FBgn0039979	Fbtr0111272	2R:618351-619068 -	X:15366344-15367965 +	ICT			
FBgn0040649	Fbtr0299925	2R:837172-909460 +	3L:22851312-24181455 -	ICT	CIIN	CIIN	
FBgn0026238	Fbtr0089754	2R:1004715-1009755 -	2R:2029591-2037739 -	LR	CHAC	CHAC	
FBgn0033010	Fbtr0086081	2R:1032202-1041693 +	2R:1559234-2063933 +	LR			
FBgn0053554	Fbtr0091528	2R:1065506-1138553 -	2R:2081409-2188671 -	LR			
FBgn0033015	Fbtr0086082	2R:1181588-1183475 +	2R:74004-2215512 +	LR			
FBgn0259247	Fbtr0299918	2R:1301241-1335479 +	2R:2286891-2317796 +	LR			
FBgn0050440	Fbtr0086076	2R:1355819-1383341 -	2R:1329897-2397190 -	LR			
FBgn0033027	Fbtr0086075	2R:1390942-1395371 -	2R:2405235-2411225 -	LR			
FBgn0050438	Fbtr0086069	2R:1406637-1437059 +	2R:2398055-2444428 +	LR	CCCC	CCCC	lineage_supp_hi_conf.one_gene
FBgn0050384	Fbtr0089048	2R:3070502-3072808 +	2R:3918626-3920944 +	LR	CCCB	CCCB	
FBgn0003090	Fbtr0089044	2R:3074767-3110885 +	2R:3886535-3946963 +	LR			lineage_supp_lo_conf
FBgn0085245	Fbtr0112409	2R:3591320-3592442 -	2R:4431187-4432308 -	LR			
FBgn0003733	Fbtr0112838	2R:3592678-3597042 -	2R:4430547-4436948 -	LR			
FBgn0042173	Fbtr0089426	2R:3716562-3717934 +	2R:4551851-4552640 +	LR			
FBgn0050382	Fbtr0088894	2R:3717918-3719274 -	2R:4550011-4551464 -	LR			
FBgn0053199	Fbtr0088688	2R:4835938-4838609 -	2R:5645353-5648001 -	LR			
FBgn0033356	Fbtr0290278	2R:4837014-4838609 -	2R:5645033-5648001 -	LR			
FBgn0050339	Fbtr0088534	2R:5488936-5490406 -	2R:6274371-6275841 -	LR			
FBgn0033434	Fbtr0088532	2R:5491228-5493129 +	2R:6267025-6278549 +	LR			
FBgn0028560	Fbtr0089674	2R:5972947-5974568 -	2R:6748331-6749936 -	LR			
FBgn0033484	Fbtr0088409	2R:5975079-5983921 +	2R:6748143-6759842 +	LR			
FBgn0033518	Fbtr0088259	2R:6306225-6307266 +	2R:7082807-7083697 -	LR			
FBgn0033519	Fbtr0088316	2R:6307919-6308572 -	2R:7076995-7077658 -	LR	CCCB	CCCB	
FBgn0033555	Fbtr0088226	2R:6709176-6709914 +	X:12575126-12575712 -	ICT			
FBgn0050489	Fbtr0089419	2R:7007610-7009353 -	2R:7724603-7726344 -	LR	CCCC	C—	
FBgn0053503	Fbtr0089418	2R:7011159-7013119 -	2R:7724467-7726344 -	LR	CCCC	C—	
FBgn0033651	Fbtr0088065	2R:7675313-7676998 -	2R:8380560-8382246 -	LR			
FBgn0033652	Fbtr0304623	2R:7677874-7701667 +	2R:8363300-8407165 +	LR			
FBgn0033748	Fbtr0087945	2R:8395396-8398311 -	2R:9107015-9110505 -	LR			
FBgn0033749	Fbtr0087942	2R:8399035-8402556 -	2R:9106673-9110916 -	LR			
FBgn0033836	Fbtr0087716	2R:9295547-9297458 -	2R:9963686-9965589 -	LR	CCCC	C—	lineage_supp_lo_conf
FBgn0053470	Fbtr0087656	2R:9299244-9300590 +	2R:9962667-9963983 +	LR			
FBgn0024556	Fbtr0301389	2R:9395081-9396837 +	2R:10058331-10060106 +	LR	CCCC	C-CC	single_species_hi_conf.one_gene
FBgn0033846	Fbtr0301388	2R:9397123-9400617 +	2R:10057214-10063850 +	LR			
FBgn0033848	Fbtr0087671	2R:9402764-9404951 +	2R:10065995-10068185 +	LR	CCCC	CCCC	single_species_hi_conf.one_gene
FBgn0260964	Fbtr0091492	2R:9405741-9417355 -	2R:10063864-10083488 -	LR	CCCC	CCCC	
FBgn0034062	Fbtr0087263	2R:11896906-11898850 -	2R:12562903-12564855 -	LR			single_species_low_conf
FBgn0034063	Fbtr0087205	2R:11899196-11901329 +	2R:12561887-12567337 +	LR			
FBgn0000079	Fbtr0087004	2R:13006211-13007808 -	2R:13681862-13683203 +	LR			
FBgn0034195	Fbtr0110777	2R:13010398-13011742 -	2R:13679949-13681677 -	LR			
FBgn0260764	Fbtr0301266	2R:13573348-13573915 +	2R:14265391-14265959 +	LR			
FBgn0034261	Fbtr0086840	2R:13574253-13578327 +	2R:14263153-14270442 +	LR			
FBgn0050323	Fbtr0273321	2R:13740846-13741766 +	2R:14430634-14431573 +	LR			
FBgn0041585	Fbtr0114614	2R:13743010-13748075 +	2R:14420856-14437910 +	LR			
FBgn0260401	Fbtr0300664	2R:14054782-14055885 +	2R:14735619-14736717 +	LR			
FBgn0260392	Fbtr0300662	2R:14054787-14055885 +	2R:14735569-14736717 +	LR			
FBgn0002716	Fbtr0086461	2R:15343700-15347029 +	2R:15995107-15998390 +	LR			

Gene	Isoform	Dmel position	Dsrm position	State	SYN_ARM ¹	GLEAN_ARM ²	Sheet ³
FBgn0260934	FBtr0301503	2R:15355019-15371978 +	2R:15995086-16024466 +	LR			
FBgn0011824	FBtr0071639	2R:16983447-16984808 -	2R:17541095-17542448 -	LR			
FBgn0085425	FBtr0112645	2R:16985617-16988961 +	2R:17537285-17546773 +	LR			
FBgn0034601	FBtr0071627	2R:17065259-17066141 -	2R:17620432-17621315 -	LR			
FBgn0003162	FBtr0071580	2R:17066624-17070121 +	2R:17618067-17625283 +	LR			
FBgn0260477	FBtr0300950	2R:17427089-17428078 -	2R:17980923-17981850 -	LR	CCCC	CCCC	single_species_low_conf
FBgn0003731	FBtr0071654	2R:17435074-17446932 +	2R:17964042-18001576 +	LR			
FBgn0034739	FBtr0071853	2R:18482193-18483858 +	2L:20501581-20503125 -	ICT			
FBgn0034782	FBtr0302717	2R:18722170-18724224 +	2R:19251217-19253322 +	LR			
FBgn0034783	FBtr0071893	2R:18724886-18726814 +	2R:19251191-19255909 +	LR			
FBgn0023000	FBtr0072571	3L:343378-346909 -	3L:314065-317239 -	LR	DDQD	D-D	single_species_low_conf
FBgn0261985	FBtr0301818	3L:347463-356046 +	3L:298654-326915 +	LR			
FBgn0085296	FBtr0112462	3L:500046-500446 -	3L:464575-464954 +	LR			
FBgn0085297	FBtr0112463	3L:500964-501371 +	3L:463687-464136 -	LR			
FBgn0004428	FBtr0072630	3L:1212827-1213406 +	3L:1149283-1149863 -	LR			
FBgn0004430	FBtr0072631	3L:1227747-1228238 +	3L:1142334-1142806 -	LR			
FBgn0035208	FBtr0072725	3L:1321782-1322802 -	3L:1245407-1246431 -	LR			
FBgn0010246	FBtr0072674	3L:1324563-1329623 +	3L:1242532-1253138 +	LR			
FBgn0011204	FBtr0072706	3L:1503226-1517238 -	3L:1420936-1427441 -	LR			
FBgn0261243	FBtr0072699	3L:1517586-1523380 +	3L:1420566-1433598 +	LR			
FBgn0035344	FBtr0072967	3L:2476259-2478493 -	3L:2363841-2366054 -	LR			
FBgn0035347	FBtr0072918	3L:2480742-2499228 +	3L:2354474-2386757 +	LR			
FBgn0024177	FBtr0076983	3L:6597455-6599129 -	3L:6471611-6473287 -	LR			
FBgn0035707	FBtr0076977	3L:6599299-6601860 +	3L:6471379-6475979 +	LR			
FBgn0035861	FBtr0076718	3L:8224914-8233701 -	2R:1928966-2498414 +	ICT			
FBgn0001223	FBtr0100558	3L:9366031-9368064 +	3L:9141030-9142968 +	LR			
FBgn0001228	FBtr0100655	3L:9366031-9368064 +	3L:9140825-9142968 +	LR			
FBgn0053272	FBtr0076159	3L:11503423-11503689 -	3L:11283089-11283358 -	LR	DDDD	D—	lineage_supp_lo_conf
FBgn0036168	FBtr0302797	3L:11506667-11512004 +	3L:11227387-11232768 +	LR			
FBgn0053270	FBtr0076149	3L:11571387-11571653 -	3L:11283088-11283358 -	LR	DDDD	D—	lineage_supp_lo_conf
FBgn0053269	FBtr0076148	3L:11574950-11575216 -	3L:11222818-11223086 +	LR	DDDD	D—	lineage_supp_lo_conf
FBgn0036199	FBtr0076115	3L:11714020-11721218 +	2R:1149289-1351494 +	ICT			
FBgn0036415	FBtr0075737	3L:14211325-14212074 +	3L:13883561-13884309 +	LR	DDND	DD-D	single_species_low_conf
FBgn0013718	FBtr0100043	3L:14212845-14226350 +	3L:13856626-13898203 +	LR			
FBgn0036441	FBtr0075687	3L:14698582-14699256 +	3L:14351435-14352110 +	LR			
FBgn0259175	FBtr0299651	3L:14699854-14740971 +	3L:14318655-14390006 +	LR			
FBgn0003515	FBtr0075391	3L:16490755-16493563 +	3L:16102198-16104944 +	LR			
FBgn0260387	FBtr0300653	3L:16495391-16516025 -	3L:16096821-16127205 -	LR			
FBgn0042178	FBtr0075312	3L:16588519-16593267 +	3L:16196642-16201483 +	LR	DDDD	D—	lineage_supp_lo_conf
FBgn0042177	FBtr0075313	3L:16596187-16601254 +	3L:16196633-16201784 +	LR	DDDD	D—	lineage_supp_lo_conf
FBgn0052170	FBtr0075258	3L:16870419-16872472 +	3L:16462337-16464498 +	LR			
FBgn0261565	FBtr0302786	3L:16892567-16900256 +	3L:16449339-16507212 +	LR			
FBgn0052188	FBtr0075164	3L:17826377-17826694 -	3L:17407287-17407617 -	LR	DDDD	D—	lineage_supp_lo_conf
FBgn0052189	FBtr0075163	3L:17827844-17828274 -	3L:17407207-17407650 -	LR	DDDD	D—	lineage_supp_lo_conf
FBgn0054002	FBtr0302155	3L:17851574-17853582 +	2R:1090934-1092523 +	ICT	DDDD	DD-D	lineage_supp_lo_conf
FBgn0053255	FBtr0303862	3L:19416858-19417246 +	3L:19115774-19116075 +	LR			
FBgn0053062	FBtr0302886	3L:19434818-19439483 +	3L:19090109-19094781 -	LR			
FBgn0052214	FBtr0273411	3L:19460449-19460969 +	3L:19115834-19116228 +	LR			
FBgn0052208	FBtr0273406	3L:19464756-19465328 -	3L:19115774-19118981 +	LR			
FBgn0036872	FBtr0074930	3L:19465593-19466152 +	3L:19130946-19131453 -	LR			
FBgn0036873	FBtr0074984	3L:19468117-19468674 -	3L:19115724-19116162 +	LR			
FBgn0262516	FBtr0074952	3L:19706960-19711450 -	3L:19352436-19356801 -	LR			
FBgn0261360	FBtr0302279	3L:19712627-19786663 -	3L:19351740-19395955 -	LR			
FBgn0083952	FBtr0110816	3L:19798341-19799136 -	3L:19407320-19408116 -	LR			
FBgn0036909	FBtr0074880	3L:19799214-19800032 +	3L:19407263-19409013 +	LR			
FBgn0013303	FBtr0302048	3L:19985023-19990798 +	3L:19577868-19583657 +	LR			
FBgn0036926	FBtr0074900	3L:19987413-19989012 +	3L:19577861-19581885 +	LR			
FBgn0036959	FBtr0074828	3L:20234371-20238412 +	3L:19818495-19822714 +	LR			
FBgn0024814	FBtr0301126	3L:20235590-20236835 +	3L:19818279-19821122 +	LR			
FBgn0037005	FBtr0078208	3L:20499132-20500475 +	3L:20060923-20062267 +	LR			
FBgn0052425	FBtr0078205	3L:20502787-20507212 +	3L:20052293-20068867 +	LR			
FBgn0041607	FBtr0089463	3L:21166218-21168073 +	3L:20715333-20717426 +	LR			
FBgn0021760	FBtr0089461	3L:21168900-21176378 +	3L:20714652-20725614 +	LR			
FBgn0250816	FBtr0299882	3L:23547715-23682722 +	2R:464201-2469541 +	ICT			
FBgn0039977	FBtr0299868	3L:23708125-23709789 +	3L:23702772-23704455 -	LR			
FBgn0058298	FBtr0111169	3L:23719967-23721046 +	3L:23113685-23114756 +	LR			
FBgn0040056	FBtr0111167	3L:23731058-23742158 +	3L:23117550-23128474 +	LR			
FBgn0058470	FBtr0111152	3L:23832959-23979490 -	2R:82737-3162001 +	ICT			
FBgn0058045	FBtr0111163	3L:24021615-24028959 +	2R:1011870-2151332 +	ICT			

Gene	Isoform	Dmel position	Dsim position	State	SYN_ARM ¹	GLEAN_ARM ²	Sheet ³
FBgn0011288	Fbtr0304625	3L:24067329-24292305 +	2R:5605-5073146 -	ICT			
FBgn0259697	Fbtr0113473	3L:24317967-24394755 +	3L:22875655-23532106 +	LR			
FBgn0040045	Fbtr0302384	3L:24527189-24528567 +	X:15366046-15368582 +	ICT			
FBgn0037294	Fbtr0078773	3R:985334-986627 +	3R:892181-893485 +	LR			
FBgn0037295	Fbtr0110950	3R:991029-995841 +	3R:883520-901808 +	LR			
FBgn0004781	Fbtr0081693	3R:2520870-2521993 -	3R:2420639-2421698 +	LR			
FBgn0004783	Fbtr0081691	3R:2529804-2530625 +	3R:2414711-2426221 +	LR			
FBgn0262362	Fbtr0304643	3R:3866970-3881259 +	3R:17075139-17081542 -	LR			
FBgn0037548	Fbtr0113204	3R:3919846-3930805 +	2L:19601482-19604199 -	ICT			
FBgn0003129	Fbtr0111026	3R:4143895-4159514 -	3R:16807368-16822885 +	LR			
FBgn0037576	Fbtr0081836	3R:4147469-4148776 +	3R:16818030-16819345 -	LR			
FBgn0262729	Fbtr0301971	3R:4204893-4303315 -	3R:16673359-16762357 +	LR			
FBgn0051462	Fbtr0081851	3R:4210766-4213924 -	3R:16753328-16756478 +	LR			
FBgn0037614	Fbtr0300543	3R:4541956-4547050 +	3R:16445317-16450340 -	LR			
FBgn0037615	Fbtr0081907	3R:4544920-4545867 +	3R:16446466-16447417 -	LR			
FBgn0037624	Fbtr0081915	3R:4573528-4579827 +	3R:16412179-16418886 -	LR			
FBgn0083971	Fbtr0110904	3R:4574928-4578463 -	3R:16413972-16417499 +	LR			
FBgn0046874	Fbtr0091716	3R:4600008-4618269 -	3R:16373829-16391843 +	LR			
FBgn0053191	Fbtr0081941	3R:4604099-4605645 -	3R:16386220-16387767 +	LR			
FBgn0261015	Fbtr0304160	3R:4606669-4625666 -	3R:16365345-16391843 +	LR			
FBgn0037630	Fbtr0081917	3R:4620406-4622367 +	3R:16369814-16371765 -	LR			
FBgn0037632	Fbtr0081918	3R:4627275-4631958 +	3R:16360130-16364921 -	LR			
FBgn0037633	Fbtr0081934	3R:4629193-4631352 -	3R:16360836-16362997 +	LR			
FBgn0051100	Fbtr0082011	3R:4820950-4827608 -	3R:16185531-16192225 +	LR			
FBgn0037650	Fbtr0300742	3R:4823419-4824400 +	3R:16188784-16189755 -	LR	EEEE	EEEE	single_species_low_conf
FBgn0010222	Fbtr0081996	3R:4868226-4876271 -	3R:16137065-16145103 +	LR			
FBgn0014018	Fbtr0089338	3R:4869900-4873699 -	3R:16139618-16143432 +	LR			
FBgn0003165	Fbtr0081992	3R:4895479-5062743 -	3R:15950420-16119872 +	LR			
FBgn0037662	Fbtr0081972	3R:5003239-5004627 +	3R:16009369-16010746 -	LR			
FBgn0037676	Fbtr0301210	3R:5120690-5154227 -	3R:15872003-15897818 +	LR			
FBgn0037675	Fbtr0082016	3R:5147492-5148083 +	3R:15878248-15878858 -	LR	EEEE	EEEE	lineage_supp_lo_conf
FBgn0037717	Fbtr0082073	3R:5407034-5412370 +	3R:15614428-15619717 -	LR			
FBgn0053654	Fbtr0091633	3R:5408237-5408944 -	3R:15617812-15618516 +	LR			
FBgn0012344	Fbtr0112870	3R:5466062-5475982 +	3R:15550684-15563032 -	LR			
FBgn0037724	Fbtr0082101	3R:5470851-5471874 -	3R:15554852-15556015 +	LR			
FBgn0085438	Fbtr0112676	3R:5568598-5571207 -	3R:15463262-15465892 +	LR			
FBgn0051415	Fbtr0082127	3R:5569239-5570386 +	3R:15464078-15465261 -	LR			
FBgn0250818	Fbtr0112576	3R:5700403-5814598 +	3R:15227904-15346541 -	LR			
FBgn0037769	Fbtr0082148	3R:5806775-5807898 +	3R:15241065-15242199 -	LR			
FBgn0053208	Fbtr0082209	3R:5828033-5868543 -	3R:15180751-15221089 +	LR			
FBgn0051407	Fbtr0082214	3R:5848568-5849330 -	3R:15200062-15200825 +	LR			
FBgn0037792	Fbtr0082185	3R:5966283-5969896 -	3R:15079063-15082494 +	LR			
FBgn0261817	Fbtr0303304	3R:5968809-5969111 +	3R:15079719-15080022 -	LR			
FBgn0004575	Fbtr0100471	3R:6016411-6047805 +	3R:15007904-15033399 -	LR			
FBgn0025879	Fbtr0082245	3R:6029597-6038726 -	3R:15016981-15026148 +	LR			
FBgn0037802	Fbtr0305358	3R:6081071-6087462 -	2L:20833905-21936137 +	ICT	EEEE	EEEE	single_species_hi_conf.one_gene
FBgn0020385	Fbtr0082264	3R:6522240-6529038 +	3R:14546381-14553077 -	LR			
FBgn0037822	Fbtr0082267	3R:6522369-6524698 +	3R:14550727-14553042 -	LR			
FBgn0037842	Fbtr0113217	3R:6676815-6680144 -	3R:14403089-14406363 +	LR			
FBgn0037841	Fbtr0113216	3R:6678446-6679366 +	3R:14403867-14404786 -	LR			
FBgn0037856	Fbtr0082325	3R:6711269-6722140 +	3R:14360693-14371717 -	LR			
FBgn0042094	Fbtr0082331	3R:6713288-6715310 -	3R:14367606-14369622 +	LR			
FBgn0051388	Fbtr0082356	3R:7063537-7065836 +	3R:14026904-14029245 -	LR			
FBgn0037889	Fbtr0082357	3R:7066905-7067842 +	3R:14040515-14041272 -	LR			
FBgn0046225	Fbtr0082392	3R:7263507-7291360 +	3R:13810172-13838399 -	LR			
FBgn0037906	Fbtr0082396	3R:7278563-7283742 -	3R:13817860-13822997 +	LR			
FBgn0037921	Fbtr0082451	3R:7447188-7451366 -	3R:13649708-13653837 +	LR			
FBgn0037922	Fbtr0082416	3R:7449096-7450670 +	3R:13650340-13651928 -	LR			
FBgn0051368	Fbtr0301042	3R:7708517-7718104 +	3R:13387457-13397103 -	LR			
FBgn0037960	Fbtr0082515	3R:7709660-7712887 -	3R:13392658-13395961 +	LR			
FBgn0037963	Fbtr0082513	3R:7719234-7727915 -	3R:13377747-13386323 +	LR			
FBgn0085336	Fbtr0301079	3R:7723304-7724141 +	3R:13381435-13382259 -	LR			
FBgn0013275	Fbtr0082512	3R:7779885-7782514 -	3R:13322786-13325419 +	LR			
FBgn0013276	Fbtr0082482	3R:7784275-7786673 +	3R:13323054-13325424 +	LR			
FBgn0037976	Fbtr0082488	3R:7819897-7831194 -	3R:13276510-13287688 +	LR			
FBgn0260746	Fbtr0082487	3R:7825029-7829239 +	3R:13278404-13282544 -	LR			
FBgn0085431	Fbtr0112654	3R:8211971-8228627 +	3R:12882971-12899722 -	LR			
FBgn0053098	Fbtr0082579	3R:8213287-8214519 +	3R:12897228-12898460 -	LR			
FBgn0038035	Fbtr0082600	3R:8224733-8227535 -	3R:12884065-12886851 +	LR			

Gene	Isoform	Dmel position	Dsim position	State	SYN_ARM ¹	GLEAN_ARM ²	Sheet ³
FBgn0038037	FTr0082598	3R:8229057-8231809 -	3R:12886781-12889544 +	LR			
FBgn0038058	FTr0082680	3R:8288284-8291020 -	3R:12823400-12826147 +	LR			
FBgn0013277	FTr0082679	3R:8291026-8293500 -	3R:13323052-13325414 +	LR			
FBgn0013279	FTr0082638	3R:8334798-8337183 +	3R:13323038-13325227 +	LR			
FBgn0250910	FTr0290334	3R:8337292-8373951 -	3R:12784508-12821286 +	LR			
FBgn0028374	FTr0082639	3R:8351910-8354798 +	3R:12803502-12806523 -	LR			
FBgn0040493	FTr0082730	3R:8775764-8787357 -	3R:12371570-12388757 +	LR			
FBgn0087021	FTr0082690	3R:8787474-8788975 +	3R:12376123-12377396 -	LR			
FBgn0051342	FTr01113403	3R:8811786-8817265 +	3R:12347781-12353257 -	LR			
FBgn0038102	FTr0082724	3R:8813098-8814233 -	3R:12350818-12351939 +	LR			
FBgn0038110	FTr0082719	3R:8834106-8837010 -	3R:12328100-12330971 +	LR			
FBgn0038109	FTr0082698	3R:8835617-8836808 +	3R:12328302-12329473 -	LR			
FBgn0038118	FTr0082712	3R:8914373-8989598 +	3R:12183140-12250757 -	LR			
FBgn0260793	FTr0301436	3R:8951833-8981386 -	3R:12191320-12213184 +	LR			
FBgn0085412	FTr01112621	3R:9540945-9587371 +	3R:11590179-11638274 -	LR			
FBgn0038175	FTr0082838	3R:9543176-9543898 -	3R:11635292-11636014 +	LR			
FBgn0086364	FTr0100361	3R:9793674-9809083 -	3R:11327288-11387406 +	LR			
FBgn0038194	FTr0089766	3R:9854952-9857206 +	3R:11327862-11330074 -	LR			
FBgn0024321	FTr0082942	3R:10155862-10195354 -	3R:11010331-11052807 +	LR			
FBgn0051320	FTr0082943	3R:10184078-10187461 -	3R:11021318-11024727 +	LR			
FBgn0086901	FTr01112630	3R:10217402-10307061 -	3R:10902168-10991610 +	LR			
FBgn0085417	FTr0301081	3R:10244315-10247577 +	3R:10961682-10964971 -	LR			
FBgn0038237	FTr0300330	3R:10339622-10355513 -	3R:10854345-10870320 +	LR			
FBgn0085302	FTr01112468	3R:10342764-10343209 +	3R:10866735-10867172 -	LR			
FBgn0038248	FTr0082976	3R:10452395-10468285 -	3R:10742044-10757923 +	LR			
FBgn0038247	FTr0082965	3R:10460475-10467334 +	3R:10742960-10749817 -	LR			
FBgn0262718	FTr0305692	3R:10567309-10621590 +	3R:10589055-10642845 -	LR			
FBgn0038257	FTr0083017	3R:10571623-10573043 -	3R:10637109-10638534 +	LR	EEEE	EEE-	lineage_supp.lo.conf
FBgn0053555	FTr0091513	3R:10632263-10646665 -	3R:10530500-10580693 +	LR			
FBgn0038266	FTr0082994	3R:10670765-10672459 +	3R:10537601-10539259 -	LR	EEEE	EEEE	lineage_supp.lo.conf
FBgn0038321	FTr0083119	3R:11163630-11168978 -	3R:10060120-10065434 +	LR			
FBgn0021750	FTr0083086	3R:11166407-11167939 +	3R:10061148-10062681 -	LR			
FBgn0262483	FTr0304826	3R:11200584-11225733 +	3R:10003137-10028471 -	LR			
FBgn0038334	FTr0083107	3R:11207129-11208673 -	3R:10020286-10021889 +	LR			
FBgn0003227	FTr0083193	3R:11648709-11658354 -	3R:9588212-9597826 +	LR			
FBgn0038366	FTr0083180	3R:11651471-11656044 +	3R:9590525-9595128 -	LR			
FBgn0003483	FTr0083183	3R:11663159-11670138 +	3R:9576281-9583168 -	LR			
FBgn0038371	FTr0083190	3R:11663868-11665193 -	3R:9581135-9582418 +	LR			
FBgn0051150	FTr0083189	3R:11670188-11679301 -	3R:9567182-9576230 +	LR			
FBgn0038373	FTr0083184	3R:11672230-11674158 +	3R:9572276-9574210 -	LR			
FBgn0051183	FTr0083187	3R:11683801-11695774 -	3R:9550901-9562691 +	LR			
FBgn0038377	FTr0083185	3R:11685918-11687200 +	3R:9559339-9560587 -	LR			
FBgn0051291	FTr0083244	3R:11736088-11743526 -	3R:9507508-9514919 +	LR			
FBgn0085304	FTr01112470	3R:11737987-11739653 -	3R:9511345-9512986 +	LR			
FBgn0038385	FTr0083201	3R:11746635-11758614 +	3R:9492316-9504407 -	LR			
FBgn0085305	FTr01112471	3R:11751827-11752321 +	3R:9498771-9499256 -	LR			
FBgn0013334	FTr0083204	3R:11760841-11787847 +	3R:9463134-9490114 -	LR			
FBgn0051088	FTr0083241	3R:11775923-11776665 -	3R:9474124-9474889 +	LR			
FBgn0026059	FTr0083231	3R:11894245-11924483 -	3R:9326757-9356604 +	LR			
FBgn0052855	FTr0083234	3R:11904702-11906720 -	3R:9344247-9346308 +	LR			
FBgn0040271	FTr0083273	3R:12136264-12164260 -	3R:9086139-9114652 +	LR			
FBgn0038414	FTr0083269	3R:12149185-12150775 +	3R:9099786-9101384 -	LR			
FBgn0004577	FTr0089287	3R:12840340-12853760 +	3R:8406790-8420479 -	LR			
FBgn0038467	FTr0083373	3R:12844502-12846810 -	3R:8413966-8416724 +	LR			
FBgn0038499	FTr0083452	3R:13200555-13217054 -	3R:8044657-8061035 +	LR			
FBgn0038500	FTr0083434	3R:13210374-13210682 +	3R:8051025-8051327 -	LR			
FBgn0038511	FTr0083442	3R:13251494-13272215 +	3R:7987618-8008440 -	LR			
FBgn0038510	FTr01113244	3R:13264690-13266450 -	3R:7993389-7995072 +	LR			
FBgn0085448	FTr0273220	3R:13384652-13394126 +	3R:7872532-7882111 -	LR			
FBgn0038522	FTr0083459	3R:13393676-13394026 +	3R:7872625-7872967 -	LR			
FBgn0053547	FTr0301555	3R:13700763-13734462 -	3R:7533319-7566706 +	LR			
FBgn0038558	FTr0083519	3R:13732167-13732880 +	3R:7534918-7535622 -	LR			
FBgn0026250	FTr0083573	3R:14100387-14108206 +	3R:7171061-7178812 -	LR			
FBgn0038595	FTr0083600	3R:14103903-14105252 -	3R:7173991-7175339 +	LR			
FBgn0051232	FTr0083625	3R:14222717-14230448 +	3R:7046299-7054377 -	LR	EEEE	EEEE	lineage_supp.hi.conf.one.gene
FBgn0038617	FTr0083655	3R:14226091-14228435 -	3R:7048325-7050655 +	LR			
FBgn0038629	FTr0083639	3R:14418740-14447049 -	3R:6810233-6848091 +	LR			
FBgn0038630	FTr0083636	3R:14424529-14425819 +	3R:6841060-6842386 -	LR			
FBgn0038638	FTr0083665	3R:14495114-14500401 +	3R:6756955-6762286 -	LR			

Gene	Isoform	Dmel position	Dsim position	State	SYN_ARM ¹	GLEAN_ARM ²	Sheet ³
FBgn0051230	FTr0083666	3R:14497401-14497816 +	3R:6759540-6759950 -	LR	EECE	EE-E	single_species_low_conf
FBgn0000303	FTr0089367	3R:14531245-14558068 +	3R:6699634-6725833 -	LR			
FBgn0038645	FTr0083686	3R:14551116-14552156 -	3R:6705622-6706726 +	LR			
FBgn0260779	FTr0083718	3R:14851896-14854558 -	3R:6403177-6405910 +	LR			
FBgn0027785	FTr0083712	3R:14853074-14853737 +	3R:6403998-6404662 -	LR			
FBgn0086613	FTr0083771	3R:15194717-15228870 -	3R:6030517-6068339 +	LR			
FBgn0038697	FTr0083775	3R:15199479-15200471 -	3R:6062864-6063858 +	LR			
FBgn0051221	FTr0083762	3R:15238416-15286033 +	3R:5981208-6019654 -	LR			
FBgn0038706	FTr0083770	3R:15249479-15250921 -	3R:6007261-6008707 +	LR			
FBgn0260003	FTr0110919	3R:15289255-15421117 +	3R:5845173-5980409 -	LR			
FBgn0038709	FTr0083768	3R:15315292-15316837 -	3R:5949541-5951089 +	LR			
FBgn0038721	FTr0302492	3R:15459140-15468460 -	3R:5798154-5807535 +	LR			
FBgn0083974	FTr0110954	3R:15460671-15461601 +	3R:5805039-5805979 -	LR			
FBgn0024963	FTr0100127	3R:15556681-15601162 +	3R:5679837-5718090 -	LR			
FBgn0038755	FTr0083846	3R:15755436-15834244 -	3R:5450632-5529293 +	LR			
FBgn0021776	FTr0083847	3R:15757521-15760842 -	3R:5523822-5527149 +	LR			
FBgn0038762	FTr0273259	3R:15839848-15843976 +	3R:5440924-5445299 -	LR			
FBgn0051210	FTr0083844	3R:15840511-15843034 -	3R:5441868-5444371 +	LR			
FBgn0038771	FTr0083836	3R:15882140-15885487 -	3R:5399043-5402374 +	LR			
FBgn0038772	FTr0083835	3R:15883472-15885013 +	3R:5399529-5401036 -	LR			
FBgn0083975	FTr0301680	3R:16030531-16071195 +	3R:5225327-5267838 -	LR	EEEE	EEEE	single_species_low_conf
FBgn0038775	FTr0083874	3R:16033923-16035513 -	3R:5262816-5264403 +	LR			
FBgn0261970	FTr0303770	3R:16225972-16275315 -	3R:4992662-5078162 +	LR			
FBgn0038795	FTr0083894	3R:16232337-16233568 -	3R:5070656-5071884 +	LR			
FBgn0067783	FTr0089480	3R:16378111-16383403 -	3R:4923501-4928792 +	LR			
FBgn0067782	FTr0090034	3R:16378356-16380131 -	3R:4926752-4928511 +	LR			
FBgn0038803	FTr0083905	3R:16386582-16398636 +	3R:4908376-4920342 -	LR			
FBgn0038804	FTr0083950	3R:16388208-16389789 -	3R:4917156-4918711 +	LR			
FBgn0259222	FTr0299771	3R:16565836-16582361 +	3R:4724183-4740531 -	LR			
FBgn0051199	FTr0083930	3R:16568522-16569591 -	3R:4736854-4737924 +	LR			
FBgn0038840	FTr0110956	3R:16727716-16733987 +	3R:4572633-4578839 -	LR			
FBgn0044810	FTr0083985	3R:16730638-16731240 -	3R:4575359-4575960 +	LR			
FBgn0051191	FTr0302412	3R:16734935-16757075 -	3R:4533416-4571753 +	LR			
FBgn0038842	FTr0113257	3R:16740023-16754935 +	3R:4551199-4566268 -	LR			
FBgn0013995	FTr0083998	3R:16803998-16840182 +	3R:4463079-4499971 -	LR			
FBgn0038845	FTr0084048	3R:16830882-16832709 -	3R:4470542-4472326 +	LR			
FBgn0025803	FTr0084020	3R:16982100-17038409 +	3R:4272486-4335440 -	LR			
FBgn0038865	FTr0084028	3R:16984960-16986815 -	3R:4323578-4325419 +	LR			
FBgn0038880	FTr0301815	3R:17102386-17119720 -	3R:4187924-4205276 +	LR			
FBgn0038879	FTr0084056	3R:17108919-17109772 +	3R:4197836-4198702 -	LR			
FBgn0002781	FTr0084064	3R:17188689-17203121 -	3R:4108531-4134555 +	LR			
FBgn0261842	FTr0303406	3R:17191351-17194002 +	3R:4117775-4120561 -	LR			
FBgn0051176	FTr0084114	3R:17498018-17545380 -	3R:3766267-3814662 +	LR			
FBgn0262541	FTr0304877	3R:18596991-18597492 -	3R:18121855-18122357 -	LR			
FBgn0039026	FTr0084312	3R:18610206-18619752 +	3R:18101598-18144460 +	LR			
FBgn0086610	FTr0113461	3R:20202587-20203427 +	3R:19735249-19736090 +	LR			
FBgn0039197	FTr0084621	3R:20208635-20210770 -	3R:19731834-19743069 -	LR			
FBgn0046685	FTr0084669	3R:20452796-20455810 -	3R:19981893-19984950 -	LR			
FBgn0039213	FTr0084657	3R:20456018-20460436 +	3R:19980592-19989582 +	LR			
FBgn0000139	FTr0114545	3R:20475769-20479099 +	X:5241677-5243688 -	ICT	FEEF	F—	lineage_supp_lo_conf
FBgn0051125	FTr0084665	3R:20479089-20480543 -	X:5240226-5241687 +	ICT			
FBgn0039215	FTr0089916	3R:20480884-20485101 +	X:5235710-5239886 -	ICT			
FBgn0051126	FTr0084663	3R:20485353-20485987 +	X:5234805-5235440 -	ICT			
FBgn0020018	FTr0084664	3R:20485919-20487573 -	X:5233219-5234874 +	ICT			
FBgn0045761	FTr0113352	3R:21149027-21155024 -	2R:1149383-1351495 +	ICT			
FBgn0010441	FTr0085179	3R:23076853-23078902 -	3R:22518533-22520577 -	LR			
FBgn0011289	FTr0085155	3R:23079152-23082186 +	3R:22518532-22523861 +	LR			
FBgn0039694	FTr0085538	3R:25604995-25606453 -	3R:24959858-24961282 -	LR			
FBgn0001297	FTr0290076	3R:25614658-25619838 +	3R:24947633-24974402 +	LR			
FBgn0261479	FTr0085863	3R:27572167-27573251 -	3R:26847746-26848830 -	LR			
FBgn0022349	FTr0085839	3R:27573367-27576745 +	3R:26847353-26852290 +	LR			
FBgn0040037	FTr0299529	4:24053-25621 +	3R:83867-85429 -	ICT			
FBgn0039900	FTr0089137	4:299303-326439 -	2L:20854374-23501000 -	ICT			
FBgn0039904	FTr0089126	4:380603-395610 +	3L:17868903-17882255 -	ICT			single_species_hi_conf_one_gene
FBgn0262636	FTr0089128	4:396260-414016 -	3L:17850352-17867863 +	ICT			
FBgn0039907	FTr0089111	4:457577-464533 -	3L:17802198-17809016 +	ICT			single_species_low_conf
FBgn0016126	FTr0089065	4:466207-474566 +	3L:17795054-17800292 -	ICT			
FBgn0024728	FTr0089090	4:684214-690510 +	4:496654-503317 +	LR			
FBgn0039920	FTr0089091	4:701245-706796 +	4:274007-508831 +	LR			

Gene	Isoform	Dmel position	Dsim position	State	SYN_ARM ¹	GLEAN_ARM ²	Sheet ³
FBgn0052021	FBtr0089244	4:927898-929810 -	2L:21860215-23129397 -	ICT			

Data, if available, for SYN_ARM, GLEAN_ARM, and Sheet are derived from Supplemental materials file "Supp all PRG data.xml" of Bhutkar et al. (2007). We find that six positionally relocated genes in *D. simulans* reported by Bhutkar et al. (2007) (FBgn0026238, FBgn0030578, FBgn0023000, FBgn0038645, FBgn0036415, FBgn0030696) are not confirmed in our assembly. Since these are not found in *D. sechellia* or *D. yakuba*, they are candidates for misassemblies in the original *D. simulans* reference genome. Our assembly contains four genes involved in ICT events that were not reported in Bhutkar et al. (2007). Two of these (FBgn0039904, FBgn0262636) reside on the same 474 kb velvet contig mapping to 3L in our assembly. Since these are located on chromosome 4 in *D. melanogaster* (as well as *D. sechellia* and *D. yakuba*), they are candidates for misassembly in our assembly. The remaining two (FBgn0054002, FBgn0037802) map to multiple locations in the *D. melanogaster* genome.

1, Gene location by *Drosophila* Muller element based on Synpipe for species order *D. melanogaster*, *D. sechellia*, *D. simulans* and *D. yakuba* (Bhutkar et al. 2007).

2, Gene location by *Drosophila* Muller element based on GLEANR for species order *D. melanogaster*, *D. sechellia*, *D. simulans* and *D. yakuba* (Bhutkar et al. 2007).

3, Corresponding sheet in file "Supp all PRG data.xml" of Bhutkar et al. (2007).

Supplementary Table 5. Number of *D. melanogaster*/*D. simulans*/*D. yakuba* orthologs established and analyzed

Chromosome	Dsim_{ref}	Dsim_{w501}
X	1808 (1795)	1538 (1530)
2L	2208 (2206)	2212 (2210)
2R	2457 (2456)	2405 (2404)
3L	2350 (2345)	2332 (2326)
3R	2995 (2989)	2934 (2929)
4	53 (53)	39 (39)

Full-length *D. simulans* ortholog counts ($\geq 90\%$ non-N codons) are reported in parentheses.

Supplementary Table 6. Previously reported discordantly mapped regions between *D. simulans* and *D. melanogaster*

Dsim _{ref}	Dmel	Dmel (BLAT)	Dsim _{w501} (BLAT)	Note
2L:10266499-10268452	X:14805876-14807830	X:14805876-14807830	X:13988797-13990750	4
2L:10270396-10275311	X:14810804-14812777	X:14810804-14814669	X:13992397-13996272	4
2L:10999214-10999699	3L:18245188-18245946	-	2L:10856105-10856590	1, 5
2L:20232720-20234353	2R:10657104-10658417	X:22112703-22113172	2L:20094185-20095818	2, 5
2L:20299846-20300157	X:10326498-10326845	X:10326498-10326803	X:9797778-9798089	4
2L:21630954-21632088	2R:2603847-2605312	2R:2604047-2605181	2R:3466507-3467641	4
2R:3882202-3883050	3L:13081679-13083069	3L:13081912-13082760	3L:12773645-12774493	4
2R:4621875-4622291	3R:9417998-9418336	3R:9417998-9418381	3R:11761478-11761894	4
2R:6779351-6781192	3R:8033879-8036079	-	2R:9013567-9015408	1, 5
2R:8471690-8473688	3L:247495-250314	3L:248001-249964	3L:218376-220374	3, 4
2R:8474216-8481704	3L:250229-257950	3L:250510-257625	3L:220902-228034	3, 4
2R:8482487-8483090	3L:258350-259097	3L:258392-258997	3L:228817-229420	3, 4
2R:8483614-8488356	3L:259286-264378	3L:259503-264210	3L:229944-234686	3, 4
2R:8488975-8489561	3L:264782-265599	3L:264852-265444	3L:235305-235891	3, 4
2R:8492270-8493159	3L:267764-270340	3L:268243-269119	3L:238600-239489	3, 4
2R:8496241-8497365	3L:272210-273370	3L:272241-273355	3L:242571-243695	3, 4
2R:8497561-8498894	3L:271640-275021	3L:273565-274889	3L:243891-245224	3, 4
2R:8499357-8500565	3L:275164-276661	3L:275338-276567	3L:245687-246895	3, 4
2R:8516564-8516848	3L:290727-305292	3L:292905-293189	3L:263394-263678	3, 4
2R:8521573-8527566	3L:290727-305292	3L:297898-303876	3L:268403-274396	3, 4
2R:8530054-8539812	3L:306207-319880	3L:306359-314027	3L:276884-284675	3, 4
2R:8547640-8550369	3L:321232-324717	3L:321929-324655	3L:292505-295234	3, 4
2R:8550894-8553274	3L:324985-327987	3L:325236-327628	3L:295759-298211	3, 4
2R:8555693-8557587	3L:329822-332306	3L:330040-331936	3L:300704-302598	3, 4
2R:8582318-8582686	3L:357981-358486	3L:358031-358399	3L:328920-329288	3, 4
2R:8582783-8585414	3L:357851-361383	3L:358497-361128	3L:329385-332016	3, 4
2R:8585932-8589521	3L:361478-365681	3L:361658-365246	3L:332534-336122	3, 4
2R:8590063-8590554	3L:365664-366437	3L:365831-366322	3L:336664-337155	3, 4
2R:8591818-8601097	3L:366524-377316	3L:367582-376663	3L:338419-347698	3, 4
2R:8615384-8616176	3L:390941-392824	3L:390941-391760	3L:362012-362804	3, 4
2R:8651806-8652279	3L:433230-433891	3L:433230-433701	3L:396994-397467	3, 4
2R:8653703-8727410	3L:434258-540589	3L:435118-508511	3L:398891-472038	3, 4
2R:8761911-8762932	3L:540851-542147	3L:541041-542062	3L:504313-505338	3, 4
2R:8763098-8763730	3L:542122-542916	3L:542230-542852	3L:505504-506136	3, 4
2R:8769495-8814396	3L:543070-576065	3L:547779-573322	3L:511086-537559	3, 4
3L:4426029-4434446	2L:17501467-17525517	3L:4886946-4895291	3L:4832150-4840591	2, 5
3L:6733464-6734340	X:17604819-17645728	X:17628903-17629773	X:16741681-16742557	4
3L:9523741-9524778	2R:20136578-20138826	2R:20136578-20137621	2R:20620491-20621528	4
3L:20381490-20382451	2L:5051193-5053209	2L:5051308-5052269	2L:4864727-4865687	4
3L:20384075-20386645	2L:5047818-5050877	2L:5048364-5050877	2L:4861724-4864294	4
3L:20523086-20524147	2L:5718121-5720896	2L:5718401-5719451	2L:5523304-5524365	4
3R:5290673-5293143	X:20894417-20896915	X:20894674-20896817	X:19623855-19625996	4
3R:5820760-5821392	X:8292973-8297975	X:8293428-8294023	X:7864173-7864771	4
3R:12095492-12096283	4:1144800-1145807	4:1144891-1145662	4:928454-929245	4
3R:14631731-14632538	X:19852422-19853421	X:19852791-19853400	X:18691844-18692601	4
X:3126370-3130982	2R:953796-957715	U:133149-377626	2R:2006091-2010703	3, 4
X:3156780-3159925	2R:978092-982595	2R:979419-982558	2R:2019954-2023099	3, 4
X:3171579-3175408	2R:1004715-1015817	2R:1005168-1009507	2R:2030046-2033196	3, 4
X:11941312-11941568	3L:19945280-19945890	3L:19945634-19945890	3L:19538623-19538878	4
X:11943043-11943608	3L:19942282-19944235	3L:19943615-19944172	3L:19536582-19537147	4
X:16222116-16223702	2R:18691027-18694490	2R:18691799-18694186	2R:19220975-19223243	3, 4
X:17019891-17022024	3R:5377765-5379469	X:22274852-22276978	X:20735097-20737229	2, 4

Derived from *D. simulans* release 1.3 (ftp://ftp.flybase.net/genomes/Drosophila_simulans/dsim_r1.3_FB2010.07/gff). Each putatively misassembled regions in Dsim_{ref} was BLAT-ed (default options with `-extendThroughN` enabled) against *D. melanogaster* and Dsim_{w501}, with the best hit (greatest number of matches) recorded.

- 1, Not detected with BLAT in *D. melanogaster*.
- 2, Different BLAT position reported for *D. melanogaster*.
- 3, Confirmed via genetic linkage analysis (please refer to Table S9.2 of Andolfatto et al. (2011a)).
- 4, Confirmed in Dsim_{w501}: Likely a misassembly in Dsim_{ref}.
- 5, Not confirmed in Dsim_{w501}: Potentially a real translocation in *D. simulans*.

Supplementary Table 7. Bootstrap P-values testing the null hypothesis that the X/A ratio is ≤ 1

Annotation	Dsim_{w501}	Dmel
Nonsyn _{0f}	0.00000	0.00970
Syn _{4f}	1.00000	0.99950
Intron _{FEI}	0.39610	0.00920
Intron _{>100}	0.00000	0.00000
5' UTR	0.00000	0.00000
3' UTR	0.00000	0.00000

Fraction of 10,000 bootstrap samplings with replacement where the X/A ratio is less than or equal to 1 (see Figure 6). For each sampling, the number of genes sampled corresponds to the total number of genes that reside on the X, and separately for the autosomes.

Supplementary Table 8. Bootstrap P-values testing the null hypothesis that the 2/3 ratio is ≤ 1

Annotation	Dsim_{w501}	Dmel
Nonsyn _{0f}	0.01950	0.08260
Syn _{4f}	0.07900	0.17300
Intron _{FEI}	0.01080	0.00160
Intron _{>100}	0.00710	0.12070
5' UTR	0.06660	0.51030
3' UTR	0.13630	0.96640

Fraction of 10,000 bootstrap samplings with replacement where the 2/3 ratio is less than or equal to 1 (see Supplementary Figure 11). For each sampling, the number of genes sampled corresponds to the total number of genes that reside on chromosome 2, and similarly for chromosome 3.

Supplementary Table 9. Breakdown of synonymous substitutions by codon change class

Codon change	Chromosome	Dsim_{w501}	Dmel
P->U	X	6589 (0.44177)	12196 (0.56890)
U->P	X	3705 (0.24841)	2653 (0.12375)
P->P	X	975 (0.06537)	1325 (0.06181)
U->U	X	3646 (0.24445)	5264 (0.24555)
P->U	2+3	39799 (0.43271)	63470 (0.52557)
U->P	2+3	22542 (0.24509)	19763 (0.16365)
P->P	2+3	5771 (0.06274)	63470 (0.06028)
U->U	2+3	23864 (0.25946)	19763 (0.25050)

The fraction of sites by codon change class is reported in parentheses.

Supplementary Table 10. ANOVA comparing the effects of gene ontology (GO) and X-linkage (X)

Species	Annotation	+GO ^a	+X ^b	#GO categories	GO ids ^c
Dsim	Nonsyn _{0f}	25.929***	1.213 (0.271)	8	1111100000110001
Dsim	Syn _{4f}	10.157***	12.280**	9	1111100100110010
Dsim	Intron _{FEI}	5.568***	1.759 (0.185)	6	0010111100000001
Dsim	Intron _{>100}	11.431***	9.587*	6	1100110001100000
Dsim	5' UTR	6.877***	22.407***	7	0101000110110001
Dsim	3' UTR	6.229***	88.991***	7	1011101001000001
Dmel	Nonsyn _{0f}	20.000***	0.962 (0.327)	9	0111110100110001
Dmel	Syn _{4f}	10.699***	4.193 (0.041)	8	1010110010110010
Dmel	Intron _{FEI}	4.940**	8.535*	5	0000101001000101
Dmel	Intron _{>100}	8.517***	5.564 (0.018)	9	1110111110100000
Dmel	5' UTR	4.180**	9.751*	5	1100000100001001
Dmel	3' UTR	5.900***	58.225***	6	0011100000111000

To test the effect of gene ontology and X-linkage on levels of lineage-specific divergence in *D. simulans* and *D. melanogaster*, we compare models controlling for X-linkage and adding in information regarding gene function^a and alternatively, controlling for gene function and adding in X-linkage information^b. Prior to testing for X-linkage, only significant GO terms (separately performed for each site class) were included using a stepwise regression based on Akaike's Information Criterion^c. The F-test statistic and P-value (*** P<.00001, ** P<.001, * P<.01, ANOVA) are reported for comparisons between models.

^a log(Dxy)~X vs. log(Dxy)~X + GO

^b log(Dxy)~GO vs. log(Dxy)~GO + X

^c Binary representation of GO categories included: GO:0001071, GO:0003824, GO:0005198, GO:0005215, GO:0005488, GO:0009055, GO:0016015, GO:0016209, GO:0016247, GO:0016530, GO:0030234, GO:0030528, GO:0031386, GO:0045182, GO:0045735, GO:0060089.

Supplementary Table 11. Comparing effects of sex-biased expression (SBE) and X linkage (X)

Species	Annotation	+SBE ^a	+X ^b
Dsim	Nonsyn _{0f}	442.589***	15.968**
Dsim	Syn _{4f}	12.711**	5.961 (0.015)
Dsim	Intron _{FEI}	31.121***	0.201 (0.654)
Dsim	Intron _{>100}	29.217***	5.816 (0.016)
Dsim	5' UTR	6.156 (0.013)	17.987**
Dsim	3' UTR	72.771***	85.244***
Dmel	Nonsyn _{0f}	299.613***	13.580**
Dmel	Syn _{4f}	65.946***	8.767*
Dmel	Intron _{FEI}	20.169***	0.888 (0.346)
Dmel	Intron _{>100}	26.848***	3.362 (0.067)
Dmel	5' UTR	0.085 (0.770)	4.838 (0.028)
Dmel	3' UTR	51.634***	63.195***

To test the effect of sex-biased expression and X-linkage on levels of lineage-specific divergence in *D. simulans* and *D. melanogaster*, we compare models controlling for X-linkage and adding in information regarding male-to-female expression bias^a and alternatively, controlling for male-to-female expression bias and adding in X-linkage information^b. The F-test statistic and P-value (***) $P < .00001$, ** $P < .001$, * $P < .01$, ANOVA) are reported for comparisons between models.

^a $\log(\text{Dxy}) \sim X$ vs. $\log(\text{Dxy}) \sim X + \log(\text{SBE})$

^b $\log(\text{Dxy}) \sim \log(\text{SBE})$ vs. $\log(\text{Dxy}) \sim \log(\text{SBE}) + X$

Supplementary Table 12. ANOVA comparing the effects of gene ontology (GO) and chromosome 2-linkage (chr2) for autosomal genes.

Species	Annotation	+GO ^a	+chr2 ^b	#GO categories	GO ids ^c
Dsim	Nonsyn _{0f}	21.441***	0.332 (0.564)	9	1101110000110011
Dsim	Syn _{4f}	8.033***	0.139 (0.710)	11	1110111110110010
Dsim	Intron _{FEI}	10.368***	4.315 (0.038)	3	0010100100000000
Dsim	Intron _{>100}	13.827***	0.878 (0.349)	4	1000110000100000
Dsim	5' UTR	7.160***	2.364 (0.124)	6	0101000100110001
Dsim	3' UTR	4.840**	0.375 (0.540)	6	0011100001010001
Dmel	Nonsyn _{0f}	18.274***	0.379 (0.538)	9	0111110100110001
Dmel	Syn _{4f}	9.286***	0.082 (0.774)	7	0110110000110001
Dmel	Intron _{FEI}	5.075**	4.224 (0.040)	5	0000101001000101
Dmel	Intron _{>100}	7.020***	0.653 (0.419)	9	1110111100100001
Dmel	5' UTR	3.573 (0.013)	0.169 (0.681)	3	1000000000001001
Dmel	3' UTR	5.662***	2.975 (0.085)	7	0010110110011000

To test the effect of gene ontology and chromosome 2-linkage vs. chromosome 3-linkage on levels of lineage-specific divergence in *D. simulans* and *D. melanogaster*, we compare models controlling for chromosome 2-linkage and adding in information regarding gene function^a and alternatively, controlling for gene function and adding in chromosome 2-linkage information^b. Prior to testing for chromosome 2-linkage, only significant GO terms (separately performed for each site class) were included using a stepwise regression based on Akaike's Information Criterion^c. All genes on the X and 4 were excluded from this analysis. The F-test statistic and P-value (***) $P < .00001$, ** $P < .001$, * $P < .01$, ANOVA) are reported for comparisons between models.

^a $\log(\text{Dxy}) \sim \text{chr2}$ vs. $\log(\text{Dxy}) \sim \text{chr2} + \text{GO}$

^b $\log(\text{Dxy}) \sim \text{GO}$ vs. $\log(\text{Dxy}) \sim \text{GO} + \text{chr2}$

^c Binary representation of GO categories included: GO:0001071, GO:0003824, GO:0005198, GO:0005215, GO:0005488, GO:0009055, GO:0016015, GO:0016209, GO:0016247, GO:0016530, GO:0030234, GO:0030528, GO:0031386, GO:0045182, GO:0045735, GO:0060089.

Supplementary Table 13. Comparing effects of sex-biased expression (SBE) and chromosome 2-linkage (chr2) for autosomes only.

Species	Annotation	+SBE ^a	+chr2 ^b
Dsim	Nonsyn _{0f}	373.598***	3.162 (0.075)
Dsim	Syn _{4f}	5.582 (0.018)	1.765 (0.184)
Dsim	Intron _{FEI}	27.042***	3.372 (0.066)
Dsim	Intron _{>100}	27.551***	1.420 (0.234)
Dsim	5' UTR	3.941 (0.047)	0.004 (0.949)
Dsim	3' UTR	73.539***	0.798 (0.372)
Dmel	Nonsyn _{0f}	241.557***	1.589 (0.207)
Dmel	Syn _{4f}	51.676***	1.237 (0.266)
Dmel	Intron _{FEI}	15.620**	3.540 (0.060)
Dmel	Intron _{>100}	18.755**	1.129 (0.288)
Dmel	5' UTR	1.073 (0.300)	4.067 (0.044)
Dmel	3' UTR	46.552***	2.919 (0.088)

To test the effect of sex-biased expression and chromosome 2-linkage vs. chromosome 3-linkage on levels of lineage-specific divergence in *D. simulans* and *D. melanogaster*, we compare models controlling for chromosome 2-linkage and adding in information regarding male-to-female expression bias^a and alternatively, controlling for male-to-female expression bias and adding in chromosome 2-linkage information^b. All genes on the X and 4 were excluded from this analysis. The F-test statistic and P-value (*** P<.00001, ** P<.001, * P<.01, ANOVA) are reported for comparisons between models.

^a log(Dxy)~chr2 vs. log(Dxy)~chr2 + log(SBE)

^b log(Dxy)~log(SBE) vs. log(Dxy)~log(SBE) + chr2

Supplementary Table 14. Substitution rates at intron_{FEI} sites

<i>D. simulans</i> X				
	G	A	T	C
G	-	0.02439	0.016466	0.03483
A	0.02813	-	0.019074	0.04168
T	0.01374	0.01917	-	0.03897
C	0.01261	0.01557	0.041895	-

<i>D. simulans</i> 2+3				
	G	A	T	C
G	-	0.02906	0.02199	0.04106
A	0.02363	-	0.01999	0.03472
T	0.01062	0.01984	-	0.03359
C	0.01317	0.02190	0.04254	-

<i>D. melanogaster</i> X				
	G	A	T	C
G	-	0.04511	0.02681	0.06131
A	0.02477	-	0.02090	0.03627
T	0.01148	0.02087	-	0.03382
C	0.01413	0.02513	0.06346	-

<i>D. melanogaster</i> 2+3				
	G	A	T	C
G	-	0.04705	0.02556	0.06113
A	0.02353	-	0.02165	0.03448
T	0.01072	0.02171	-	0.03389
C	0.01319	0.02577	0.06105	-

The tables represent the rate relative to the reconstructed ancestor for each of the 16 types of base substitution found at intron_{FEI} sites (see Materials and Methods).

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