Supplementary Information for:

Microbiome composition shapes rapid genomic adaptation of *Drosophila melanogaster*

Seth M. Rudman *, Sharon Greenblum, Rachel C. Hughes, Subhash Rajpurohit, Ozan Kiratli, Dallin B. Lowder, Skyler G. Lemmon , Dmitri A. Petrov, John M. Chaston, and Paul Schmidt

Corresponding author: Seth M Rudman
Email: srudman@sas.upenn.edu

This PDF includes:
Tables S1 to S5
Figures S1 to S9
SI references

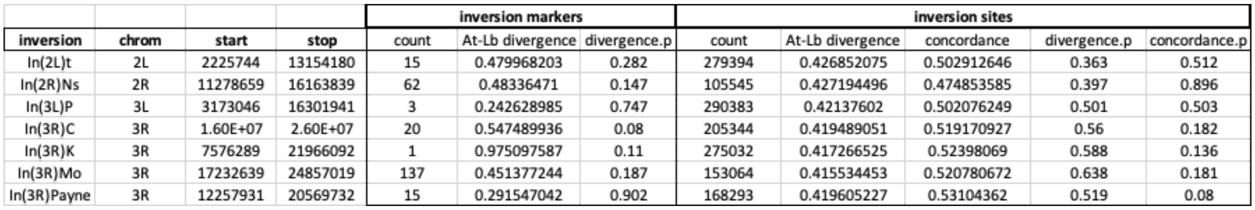
Other supplementary materials for this manuscript include the following:
Dataset S1

www.pnas.org/cgi/doi/10.1073/pnas.1907787 116

Table S1. List of sites that show significant divergence between *At* and *Lb* cages in the experiment (effect size >2% and FDR <.05). Table shows: the chromosome arm, position, reference allele, alternate allele, gene name, p-value for divergence between *At* and *Lb* treatments, average allele frequency in: founder, *No-Ad*, *At*, and *Lb* populations, p-value for divergence across clinal populations, and GO terms.

***Table is attached at the end of this document.**

Table S2. Enrichment of *At*-*Lb* divergence among sites strongly linked to large cosmopolitan inversions (inversion markers), and enrichment of *At*-*Lb* divergence and clinal concordance among sites within inversions. In each case, the number of sites tested, and their average *At*-*Lb* divergence score is indicated, as well as a non-parametric p-value indicating the percent of times (of 1,000 trials) that a random subset of sites of equivalent size had an equal or higher average divergence score (divergence.p). For sites within inversions, the concordance rate between the identity of the allele associated with experimentally-treated and natural clinal populations enriched for the same microbial taxa is also indicated, as well as a similar non-parametric p-value.



				inversion markers			inversion sites				
inversion	**chrom**	**start**	**stop**	count	At-Lb divergence	divergence.p	count	At-Lb divergence	concordance	divergence.p	concordance.p
In(2L)t	2L	2225744	13154180	15	0.479968203	0.282	279394	0.426852075	0.502912646	0.363	0.512
In(2R)Ns	2R	11278659	16163839	62	0.48336471	0.147	105545	0.427194496	0.474853585	0.397	0.896
In(3L)P	3L	3173046	16301941	3	0.242628985	0.747	290383	0.42137602	0.502076249	0.501	0.503
In(3R)C	3R	1.60E+07	2.60E+07	20	0.547489936	0.08	205344	0.419489051	0.519170927	0.56	0.182
In(3R)K	3R	7576289	21966092	1	0.975097587	0.11	275032	0.417266525	0.52398069	0.588	0.136
In(3R)Mo	3R	17232639	24857019	137	0.451377244	0.187	153064	0.415534453	0.520780672	0.638	0.181
In(3R)Payne	3R	12257931	20569732	15	0.291547042	0.902	168293	0.419605227	0.53104362	0.519	0.08

Table S3. List of sites that show divergence between *At* and *Lb* cages in the experiment (effect size >2% and p-value <.05) and that show the most pronounced variation along a cline in eastern North America (clinality FDR<10^{-8}). Of these 35 sites, 80% show concordance in the direction of allele change between experimental replicates enriched for AAB and populations that have a higher proportion of AAB in the microbiome.

Table shows: the chromosome arm, position, reference allele, alternate allele, gene name, p-value for divergence between *At* and *Lb* treatments, p-value for divergence across clinal populations, concordance between the allele associated with experimental populations and natural populations enriched for the same microbial taxa, average allele frequency in founder, *No-Ad*, *At*, and *Lb*, populations, and GO terms. Gene names for SNPs outside genic regions are in parenthesis and indicate the closest gene for gene-counting purposes.

***Table is attached at the end of this document.**

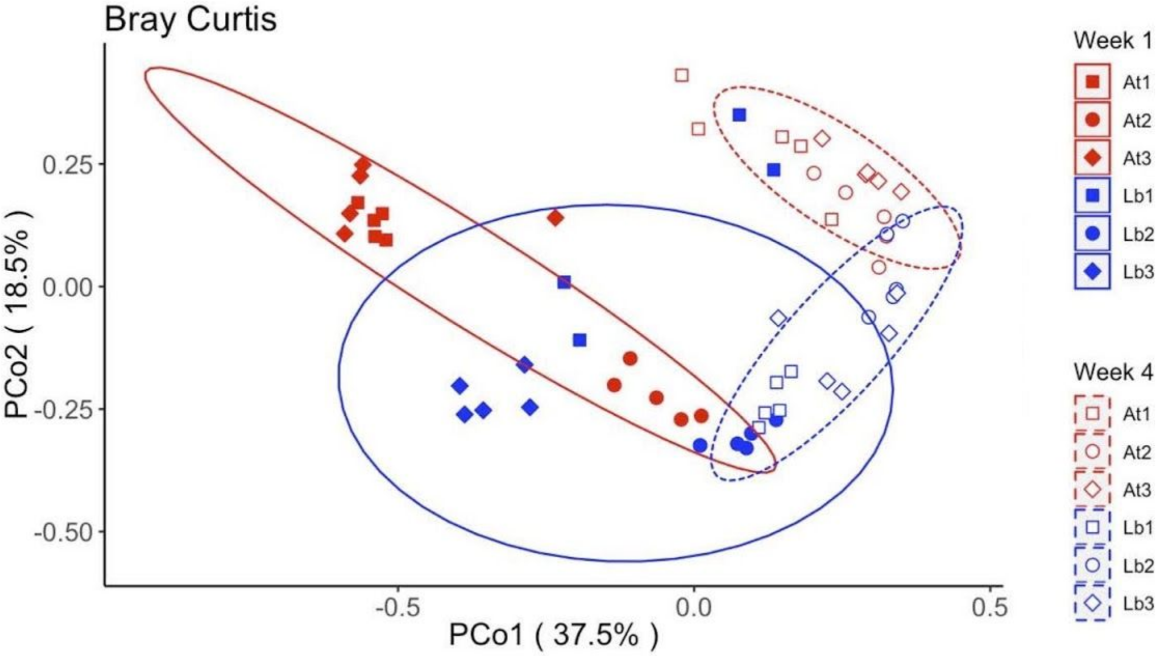
Table S4: Results of each filtering step for SNPs. All reads were first mapped to the *Drosophila melanogaster* reference genome (v5.39) using bwa (v0.7.9). To identify potential human contaminant reads (potentially due to index switching), all reads were also mapped to the human genome, using bbmap (1), with parameters suggested at https://jgi.doe.gov/data-and-tools/bbtools/bb-tools-user-guide/bbmap-guide/ for removing contaminant reads while minimizing false positives (minratio=0.9 maxindel=3 bwr=0.16 bw=12 fast minhits=2 qtrim=r trimq=10 untrim idtag printunmappedcount kfilter=25 maxsites=1 k=14) and a version of human reference genome hg19 masked for repeat short kmers, low entropy windows, and regions highly conserved across species (freely available at https://drive.google.com/file/d/0B3llHR93L14wd0pSSnFULUlhcUk/edit?usp=sharing). Reads that mapped to the human genome were marked as putative contaminants and were removed from the analysis, as well as any SNP sites in the *D. melanogaster* genome to which contaminant reads mapped (103 out of 3168422 sites; denoted in the 'HumanReads' column). As our samples were sequenced in two separate batches, we excluded any SNPs that showed distinct allele frequency ranges in the two batches ('BatchEffects'). We also excluded any sites with <1% minor allele frequency in either founder sample ('NoStandingVariation'), any SNPs within repeat regions as defined by UCSC RepeatMasker (2) ('RepeatRegions), SNPs with read depth <50x in any sample ('LowReadDepth'), and SNPs where neither the major nor minor allele matched the reference allele ('NoRef').

Chrom	Unfiltered	HumanReads	BatchEffects	NoStandingVariation	RepeatRegions	LowReadDepth	NoRef	RemainingSites
2L	720529	42	53	162636	45099	27127	57	485515
2R	620103	8	5	139941	72090	21976	53	386030
3L	722693	21	39	175514	70033	27070	49	449967
3R	670679	9	25	160405	21529	20390	46	468275
X	434418	23	53	118842	48200	68223	11	199066
all	3168422	103	175	757338	256951	164786	216	1988853

Table S5: Test for overlap between sets of SNPs found to be divergent between pairs of experimental treatments and SNPs that show significant seasonal changes in wild *D. melanogaster* populations (‘flipped model’ (3)). Tests for enrichment were conducted at a range of significance thresholds. Columns shown also list: the number of divergent sites between experimental treatments, the number of sites that vary significantly across season, the number of sites that show significant divergence between treatments and vary seasonally, the number of sites expected to show significant divergence between treatments and vary seasonally by chance alone, and the p-value from a hypergeometric test for the enrichment of *At*-*Lb* divergent sites among seasonally varying sites. Divergence was assessed between experimental populations and with respect to the founding population. *No*-*Ad* comparisons were done on randomly selected groups of 3 cages to match *At* and *Lb* replication.

treatments	enrichment of divergent sites among seasonal sites					
	threshold	divergedCt	seasonalCt	bothCt	bothCtExpected	p
Founder_NoAd	0.1	128455	212388	19867	19875	5.28E-01
	0.05	63683	123724	5765	5740	3.63E-01
	0.01	12462	35496	312	322	7.27E-01
	0.005	6182	20738	93	93	5.31E-01
	0.001	1268	6012	9	6	1.10E-01
Founder_Aceto	0.1	134090	212388	20600	20747	8.80E-01
	0.05	65094	123724	5920	5867	2.31E-01
	0.01	11749	35496	334	304	4.31E-02
	0.005	5688	20738	112	86	3.67E-03
	0.001	1042	6012	9	5	4.29E-02
Founder_Lacto	0.1	133352	212388	20934	20633	8.39E-03
	0.05	64208	123724	5823	5787	3.09E-01
	0.01	11646	35496	332	301	3.92E-02
	0.005	5639	20738	102	85	4.01E-02
	0.001	1041	6012	12	5	2.59E-03
NoAd_Aceto	0.1	129385	212388	19797	20019	9.64E-01
	0.05	64252	123724	5675	5791	9.51E-01
	0.01	12425	35496	313	321	6.89E-01
	0.005	6112	20738	80	92	9.14E-01
	0.001	1253	6012	6	5	4.69E-01
NoAd_Lacto	0.1	130203	212388	20249	20146	2.04E-01
	0.05	64375	123724	5838	5802	3.10E-01
	0.01	12449	35496	307	322	8.09E-01
	0.005	6197	20738	77	94	9.66E-01
	0.001	1216	6012	9	5	9.09E-02
Aceto_Lacto	0.1	124559	212388	19520	19272	2.13E-02
	0.05	60518	123724	5599	5455	1.87E-02
	0.01	11855	35496	345	307	1.49E-02
	0.005	5959	20738	108	90	3.43E-02
	0.001	1268	6012	6	6	4.80E-01
NoAd123_NoAd456	0.1	121309	212388	18911	18770	1.21E-01
	0.05	58250	123724	5378	5250	3.03E-02
	0.01	10870	35496	288	281	3.46E-01
	0.005	5384	20738	84	81	3.98E-01
	0.001	1028	6012	6	5	2.97E-01
NoAd136_NoAd278	0.1	126416	212388	19029	19560	1.00E+00
	0.05	61370	123724	5265	5531	1.00E+00
	0.01	11821	35496	298	306	6.80E-01
	0.005	5808	20738	78	88	8.66E-01
	0.001	1134	6012	4	5	7.31E-01
NoAd248_NoAd356	0.1	117051	212388	17883	18111	9.73E-01
	0.05	56312	123724	4964	5076	9.54E-01
	0.01	10491	35496	269	271	5.65E-01
	0.005	5129	20738	77	77	5.38E-01
	0.001	1022	6012	1	4	9.89E-01

Figure S1: Beta-diversity analysis of microbial communities based on 16S rRNA gene sequencing of whole-body flies collected at week 1 and week 4 of the experiment using Bray-Curtis, weighted Unifrac, and unweighted Unifrac distance metrics. At each time point, five replicate samples of five flies were collected from each cage, the flies were homogenized, and the homogenate was stored at -80°C until a 16S rRNA gene library was prepared. Libraries were sequenced paired-end with 250 bp reads on a Illumina HiSeq. Distance matrices were created using standard QIIME2 parameters. PERMANOVAs were calculated in R using the vegan package.



All data

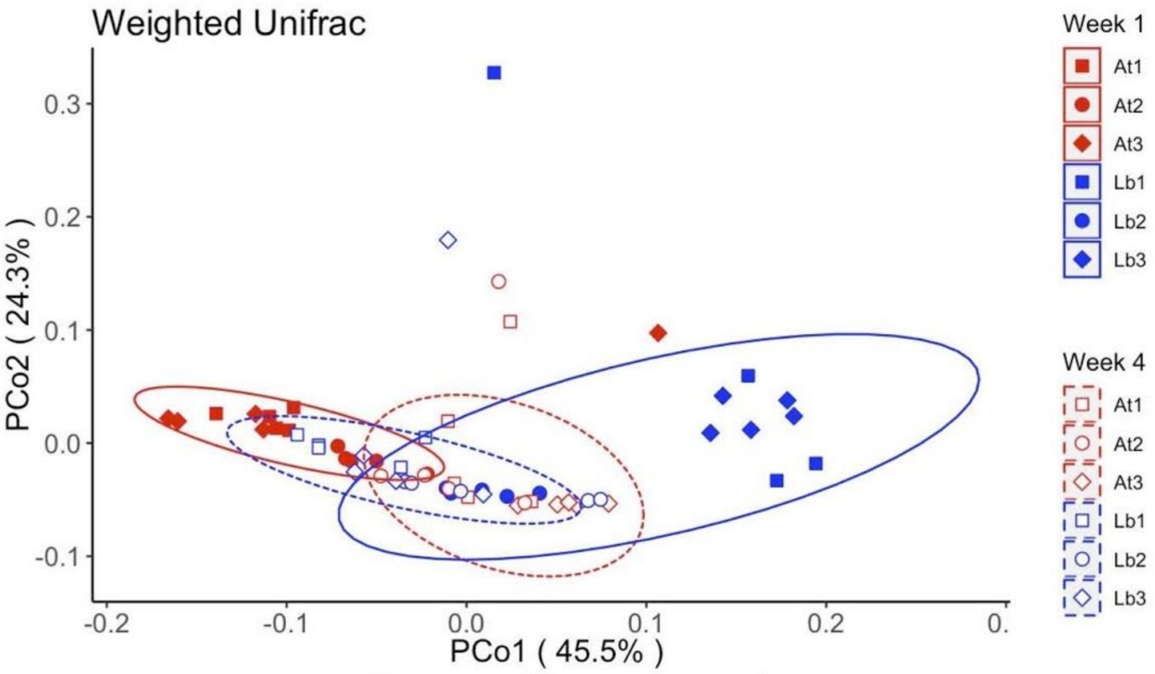
	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	1.73	1.73	25.3	0.13	0
date	1	3.68	3.68	53.72	0.27	0
treatment:cage	4	2.16	0.54	7.89	0.16	0
treatment:date	1	0.86	0.86	12.53	0.06	0
treatment:cage:date	4	2.1	0.52	7.65	0.15	0
Residuals	47	3.22	0.07	NA	0.23	NA
Total	58	13.76	NA	NA	1	NA

Week 1 only

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	1.57	1.57	16.38	0.21	0
treatment:cage	4	3.58	0.89	9.34	0.49	0
Residuals	23	2.2	0.1	NA	0.3	NA
Total	28	7.35	NA	NA	1	NA

Week 4 only

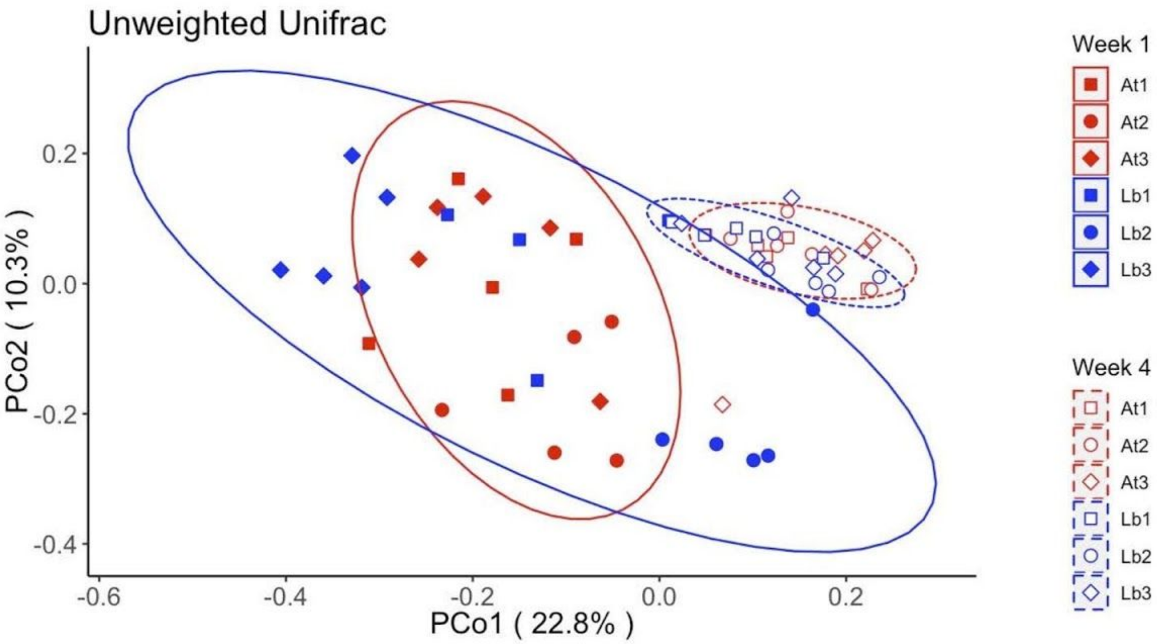
	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	0.99	0.99	22.96	0.36	0
treatment:cage	4	0.72	0.18	4.16	0.26	0
Residuals	24	1.04	0.04	NA	0.38	NA
Total	29	2.76	NA	NA	1	NA



	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	0.07	0.07	8.42	0.08	0
date	1	0.06	0.06	7.26	0.07	0
treatment:cage	4	0.08	0.02	2.33	0.08	0.01
treatment:date	1	0.21	0.21	24.33	0.22	0
treatment:cage:date	4	0.12	0.03	3.62	0.13	0
Residuals	47	0.4	0.01	NA	0.42	NA
Total	58	0.94	NA	NA	1	NA

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	0.25	0.25	21.21	0.37	0
treatment:cage	4	0.15	0.04	3.2	0.22	0
Residuals	23	0.27	0.01	NA	0.4	NA
Total	28	0.67	NA	NA	1	NA

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	0.03	0.03	4.87	0.12	0.01
treatment:cage	4	0.05	0.01	2.53	0.26	0.02
Residuals	24	0.12	0.01	NA	0.62	NA
Total	29	0.2	NA	NA	1	NA

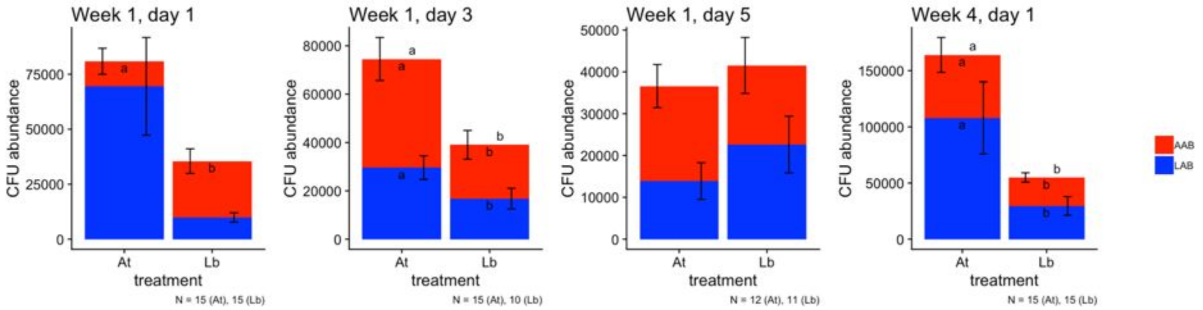


	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	0.18	0.18	1.94	0.02	0.03
date	1	1.3	1.3	13.8	0.16	0
treatment:cage	4	1.02	0.26	2.71	0.13	0
treatment:date	1	0.24	0.24	2.5	0.03	0.01
treatment:cage:date	4	0.82	0.2	2.16	0.1	0
Residuals	47	4.44	0.09	NA	0.55	NA
Total	58	8	NA	NA	1	NA

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	0.36	0.36	2.25	0.07	0
treatment:cage	4	1.21	0.3	1.87	0.23	0
Residuals	23	3.74	0.16	NA	0.7	NA
Total	28	5.31	NA	NA	1	NA

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
treatment	1	0.09	0.09	2.16	0.06	0.03
treatment:cage	4	0.38	0.09	2.23	0.25	0
Residuals	24	1.02	0.04	NA	0.68	NA
Total	29	1.49	NA	NA	1	NA

Figure S2: Absolute abundance of CFUs in *D. melanogaster* from outdoor enclosures. Pools of 5 male flies were collected from outdoor enclosures, homogenized in 125 ul phosphate-buffered saline (PBS), and dilution plated on modified de Man-Rogosa-Sharpe medium. Colony forming units (CFUs) were counted on plates after 1-3 days, and normalized to CFU per fly: AAB were copper or tan-colored, while LAB were yellow or white. Values are shown as a mean of all pools, which were collected from each of 3 separate experiments (usually 5 pools per cage per sampling time, exact N shown in caption). For each of three metrics - AAB abundance, LAB abundance, and AAB+LAB abundance - pairwise comparisons between absolute CFU abundances were determined by a Dunn test {dunn.test} and shown by compact letter displays over the bars {rcompanion}. LAB, AAB, and LAB+AAB abundances are shown within the blue bars, within the red bars, and outside of the bars, respectively. If no letters are shown there were no significant differences. The Kruskal-Wallis test statistic (KW), degrees of freedom (df), and p-values (p) for each comparison are reported. All statistics were calculated in R.



	KW	df	p
AABs+LABs	0.08	1	0.7715
AABs	9.05	1	0.0026
LABs	0.29	1	0.5896

	KW	df	p
AABs+LABs	4.93	1	0.0264
AABs	4.33	1	0.0374
LABs	3.88	1	0.0488

	KW	df	p
AABs+LABs	0.69	1	0.4054
AABs	1.37	1	0.2421
LABs	0.42	1	0.5177

	KW	df	p
AABs+LABs	7.74	1	0.0054
AABs	3.2	1	0.0735
LABs	8.2	1	0.0042

Figure S3: Microbiome composition of homogenized adult flies based on 16S sequence data. Individual bars represent cage-collected pools composed of 5 males with 5 replicate pools sequenced for each cage. Graphs show relative abundance of each microbiome group for each pool (5 from each cage) after 1 week of treatment and 4 weeks of treatment. Flies were sampled from throughout the experimental cages with care taken not to sample flies directly on media.

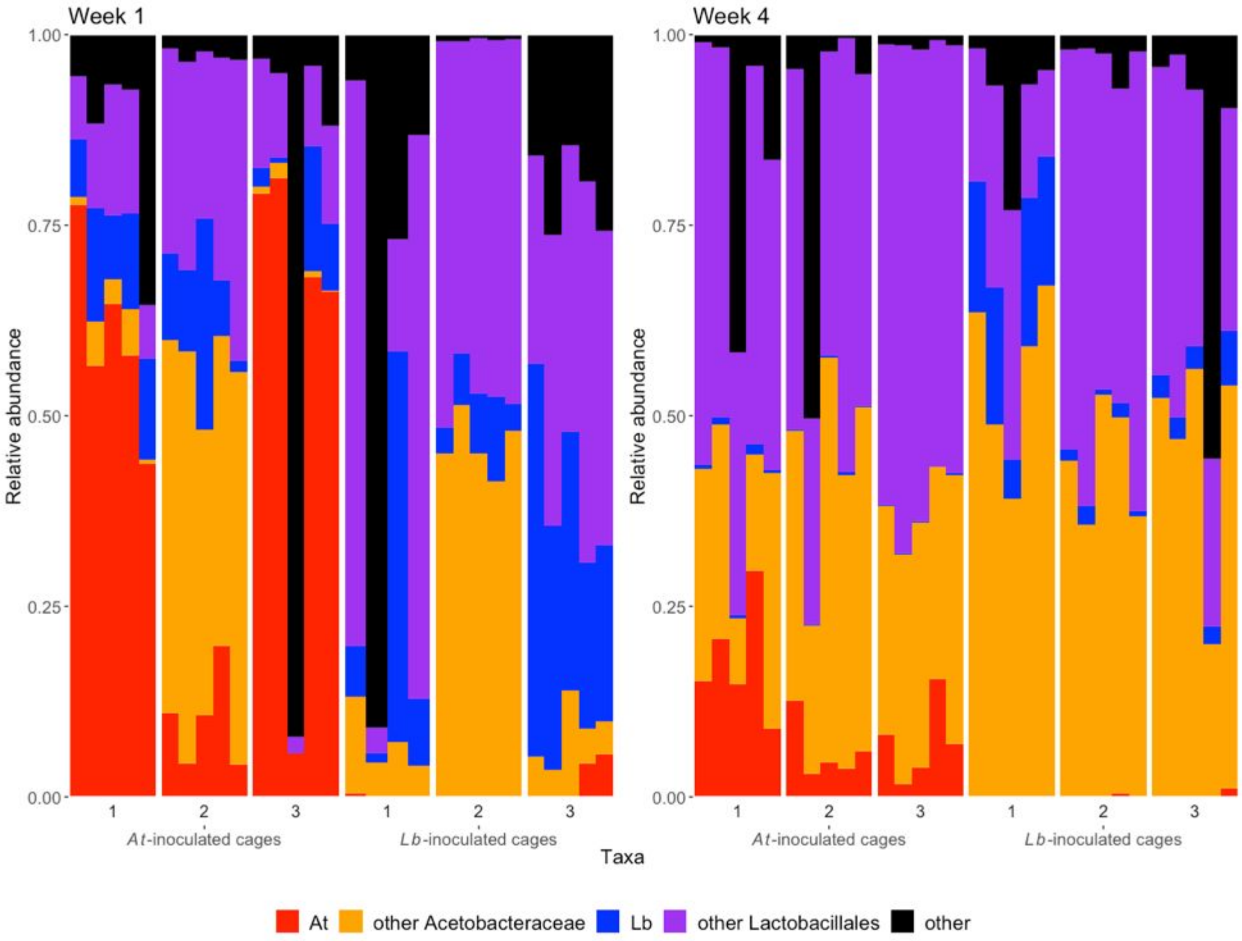


Figure S4: OTUs where we detected significant differences in abundance between microbiome treatments or within treatments over time as determined by ANCOM with the most stringent correction for multiple tests. Significant differences with treatment and/or time were subsequently confirmed by a mixed effects model with a binomial family and are shown as compact letter displays (different letters represent significant differences between conditions). Most OTUs could not be classified to the species level and are named according to the lowest taxonomic assignment.

Each panel shows the relative abundance of a specific OTU as a percentage of total the microbiome community in the *At* and *Lb* experimental treatments at week 1 and week 4 of the experiment. Bars are shaded based on taxonomic assignments and represent the mean +/- SE.

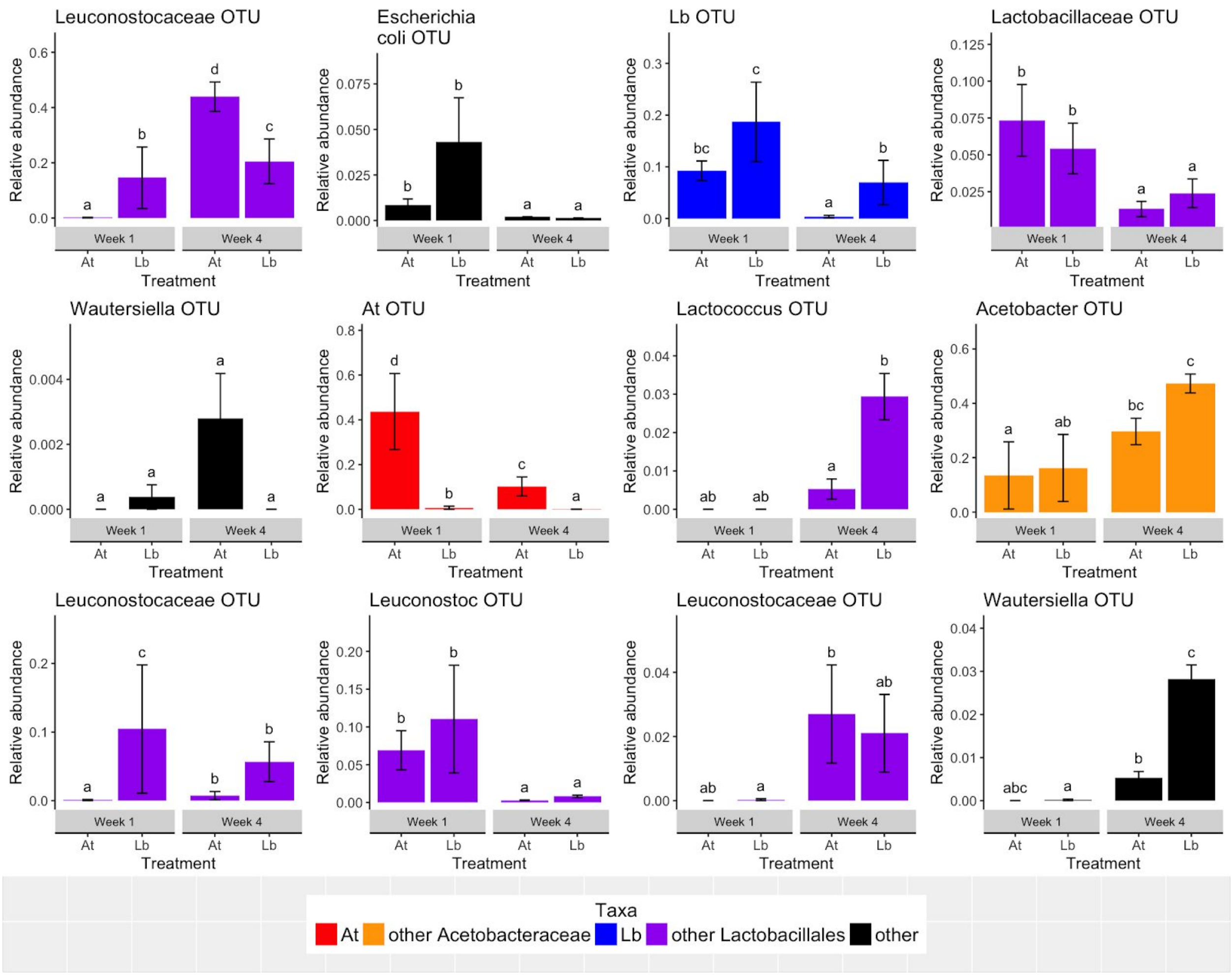


Figure S5. Taxonomic identity of randomly selected bacterial colonies isolated from whole body homogenates of caged *D. melanogaster.* For each of the *At* and *Lb* treatments, 10 AAB-like (copper-colored) and 10 LAB-like (white or yellow colored) colonies were randomly selected, streaked for isolation, and genome sequenced. Genomic libraries were prepared using 800μL of bacteria culture, which was centrifuged at 15,000 x g for 10 minutes. Pellets were resuspended in 600μL of lysis buffer, and the 600μL volume was extracted and quantified. In order to fragment the extracted DNA, 1.5μg of DNA was diluted in 2μL fragmentase buffer. 2μL NEB fragmentase was added and each sample was incubated at 37C to digest the fragments to approximately 500 bp (incubation times were optimized to the batch of fragmentase). Enzyme activity was halted after incubation using 10μL (0.25M) EDTA. DNA was cleaned using Zymo DNA Clean and Concentrator 25 columns. For end repair, 50μL fragmented DNA was mixed with 3μL NEB enzyme mix, 7μL NEB end prep reaction buffer, and placed in a thermocycler for 30 minutes each for 20C and 65 C. This reaction was combined with 30μL NEB ligation master mix, 1μL ligation enhancer, and 2.5μL of a unique illumina adapter and then ligated at 20C for 15 minutes. Fragment size selection was done using Ampure SPRI beads (SPB). The bead stock was diluted in a ratio of 109.25μL SPB to 74.75μL ddH2O. 160ul diluted SPB were added to 100 ul of end repaired sample, and incubated at 25°C for 5 minutes. The bead-separated supernatant was mixed with 30 ul of SPB stock and the supernatant was discarded. Samples were washed twice with 200ul 80% EtOH, resuspended in 22.5 ul RSB for 5 min, and 17.5 ul was transferred to an ALP plate. Barcode ligation was enriched with the KAPA Library Amplification kit according to manufacturer instructions, size selection was repeated, libraries normalized to 5ng/uL via Qubit, and sequenced by 2x125 bp sequencing on an Illumina HiSeq 2500 at the BYU DNA sequencing center.

Genome sequences were assembled using Velvet 1.2.10 as described previously (Newell, 2014). Briefly, the nucleotide coverage of each of the raw assemblies was determined based on the size of the expected genome (*A. tropicalis* DmCs_006 or *L. brevis* DmCs_002), assembled into contigs across a kmer range of 85-123, adjusted for expected coverage and coverage cutoff, and a single assembly that minimized node number while maximizing n50 value and total genome size was selected manually. When sequence reads provided greater than 200X nucleotide coverage, the raw reads were split evenly into subsets providing 101-200X coverage, and each subset was assembled as described above except that there were no adjustments for expected coverage and coverage cutoff. The contigs file from the multiple sub-assemblies for each genome were used to create a final assembly.

The similarity of each of these genomes was compared in an all against all mummer comparison that included the reference genomes for *A. tropicalis* DmCs_006 or *L. brevis* DmCs_002. Genomes were clustered according to a 99.9% or greater M-to-M score. Taxonomic identity of the representative sequence for each cluster, picked as the assembly with the fewest contigs, was assigned using JSpecies.

Taxonomic identities of bacterial isolates recovered from evolving flies. A pool of five male flies from a randomly-selected cage that had been inoculated with either *At* or *Lb* was collected, homogenized, and plated on mMRS. From each pool, ten AAB-like colonies and ten LAB-like colonies were cultured in isolation and subjected to whole genome sequencing. Whole genome nucleotide similarity of the strains was determined by ANIm, with different isolates assigned at ANIM>99.9%. The results show that strains identical to the inoculated *At* strain could be recovered from the treatment flies, confirming that the treatment bacteria were colonizing the flies.

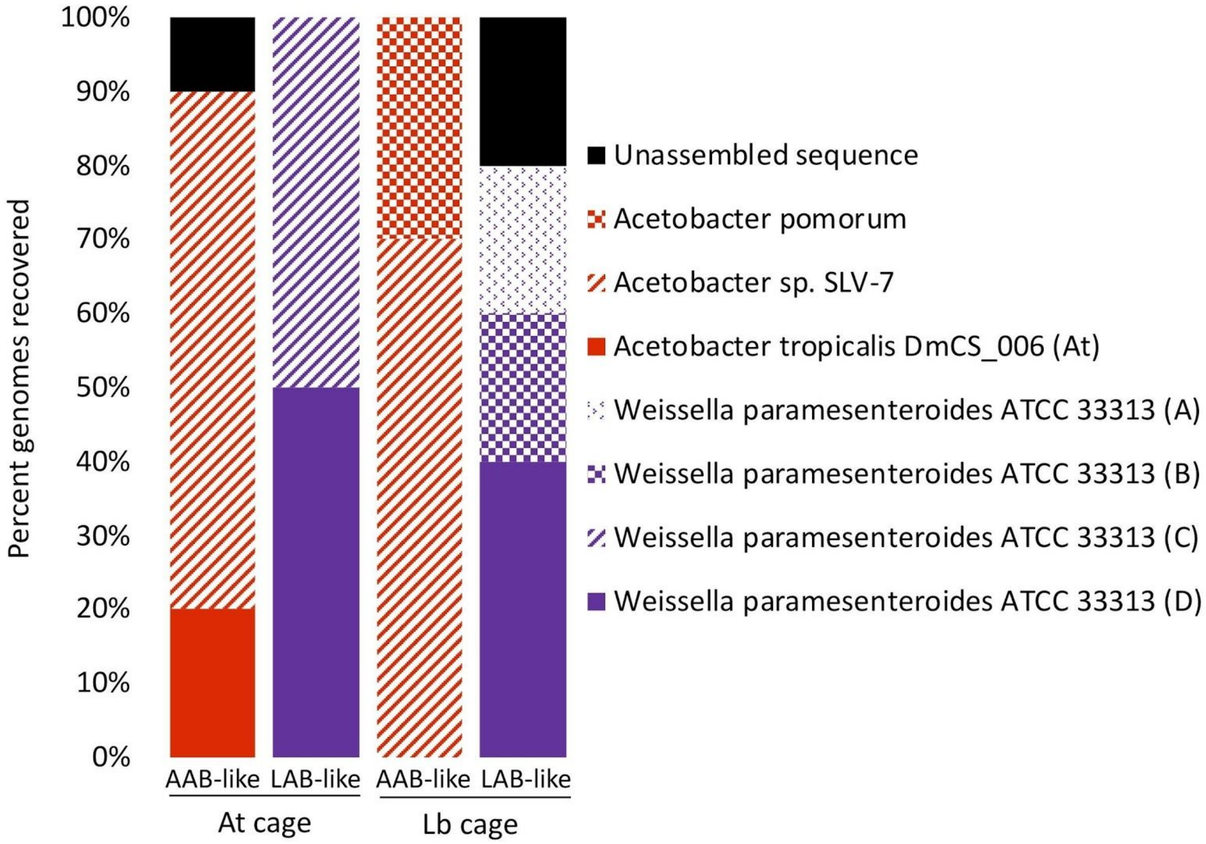


Figure S6. Influence of the microbiome treatments on *Wolbachia* abundance. For this figure *Wolbachia* reads in the 16S rRNA marker gene analysis were retained, the number of reads per sample was rarefied to 1250, and the correlation between AAB:LAB ratios in this dataset (panel A) and the CFU counts was defined as significant by a Spearman's rank test. Then, the absolute abundance of *Wolbachia* in the 16S dataset was estimated from the relative abundance of *Wolbachia* and AAB in the 16S and the absolute abundance of AAB from the CFU counts (panel B). Significant differences in the abundance of Wolbachia with treatment and date were defined by a Kruskal-Wallis test, with a Dunn test for post hoc multiple comparisons. Different letters over the groups of cages represent significant differences in the abundance of Wolbachia. R_S = Spearman's rank statistic, ρ = correlation coefficient, p = p-value, KW χ^2 = Kruskal-Wallis chi-square statistic.

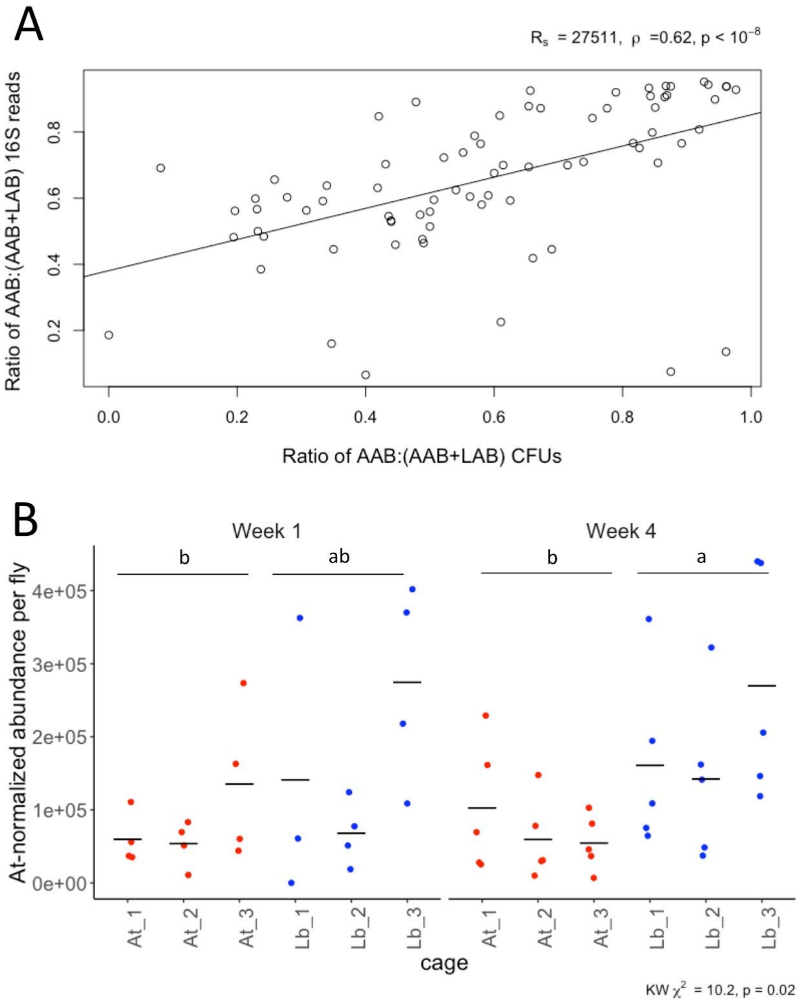


Fig S7: The influence of *At* and *Lb* on *D. melanogaster* larval development rate. This figure shows the difference in larval development rate of the outbred population of *D. melanogaster* used to found all experimental cages when mono-associated with *Lb* or *At* bacteria. Consistent with previous work, bacterial treatment significantly influenced larval development time; *At* led to ~10% higher development rate than *Lb* (Z=-15.9, P<0.001).

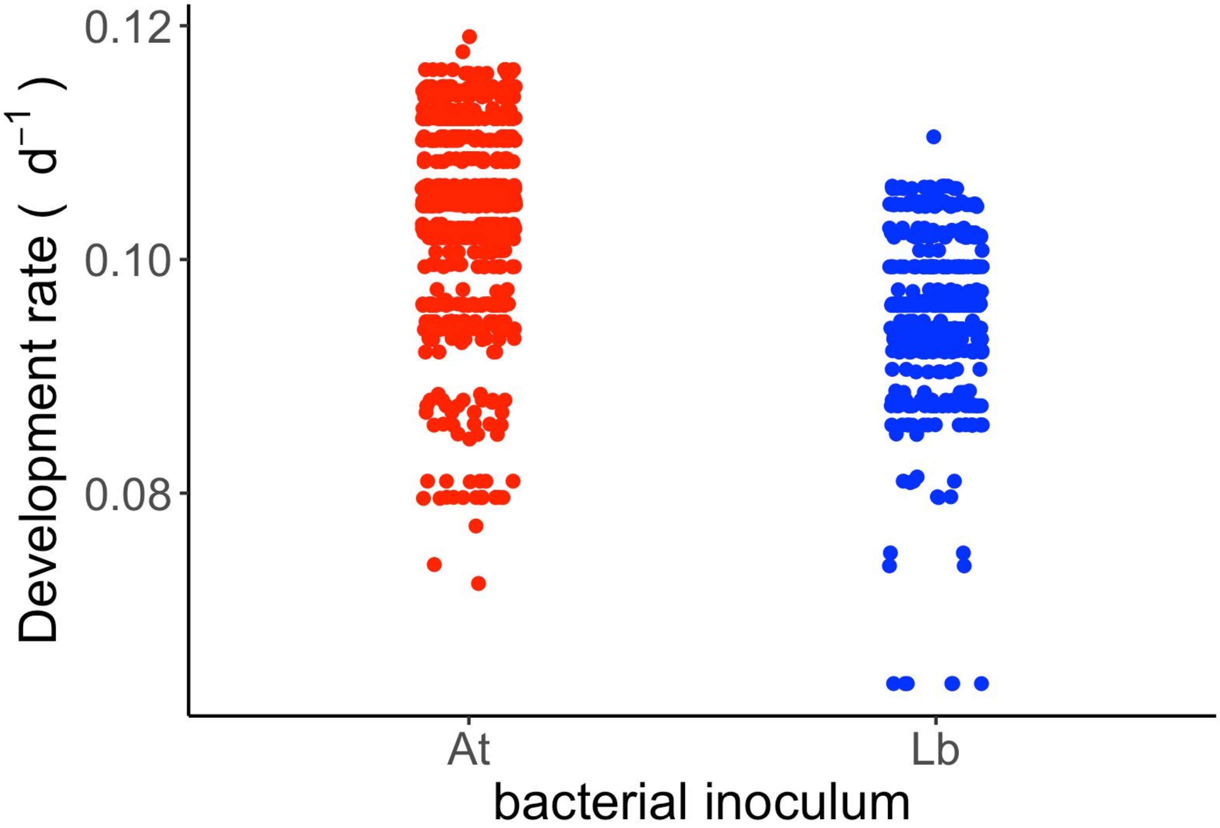


Fig S8: Average Fst between the founder population and each treatment for 1,000 subsets of 1,000 segregating sites. In each of the 1,000 rounds, 1,000 sites were randomly selected from across the genome and Fst was calculated at each site between the average allele frequency in the two founder samples and allele frequencies averaged within treatment groups. For the *No-Ad* treatment, a random sample of 3 replicate *No-Ad* populations was chosen for each site subset to match the number of *At* and *Lb* replicates.

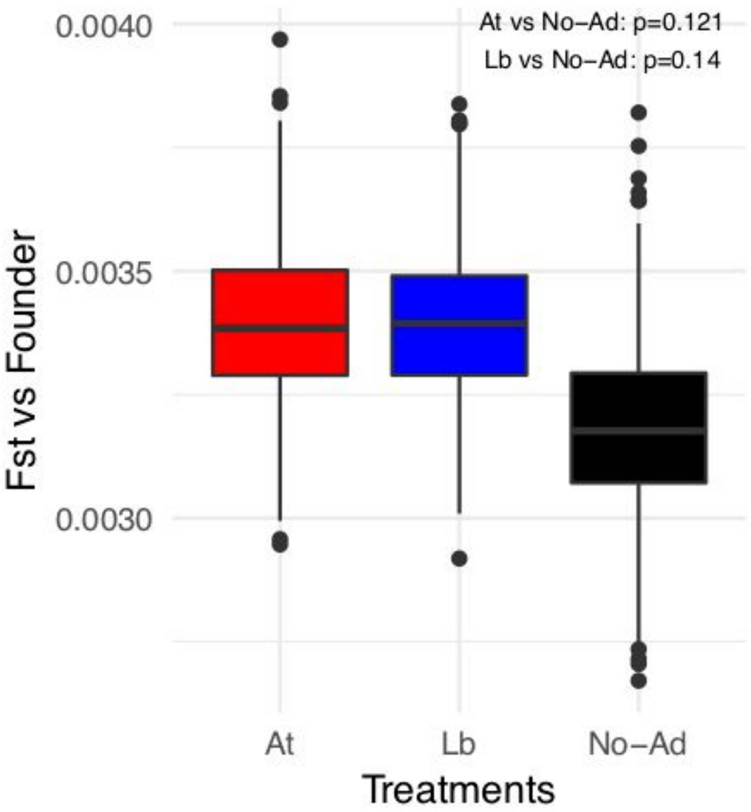
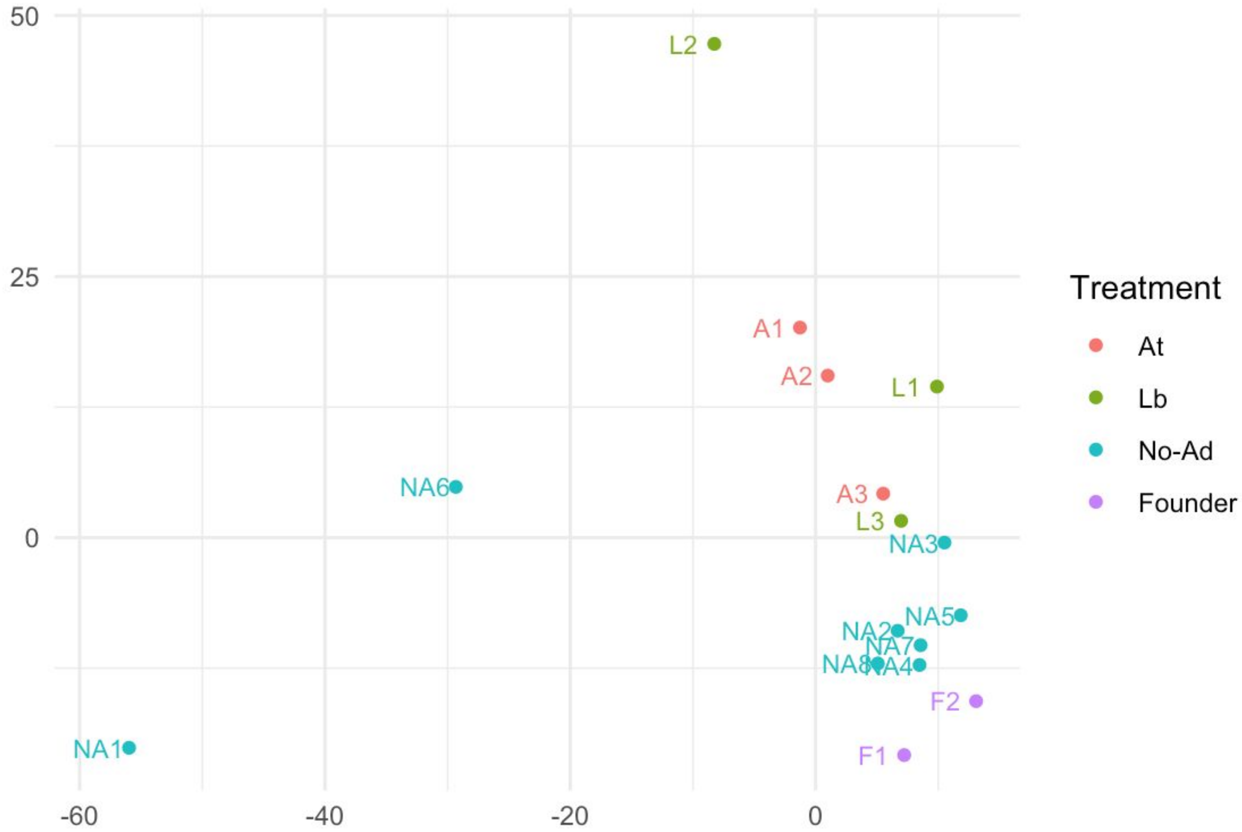


Figure S9: We used allele frequencies at each segregating site for each sample to conduct a principal component analysis using the R function *prcmp* with *scale=TRUE*, and the first two PCs were plotted to examine genome-wide divergence across samples visually. 'Founder' represent sub-samples of the initial population used to found each replicate and were sampled at Day 0. All outdoor treatment cages were sampled at Day 45. Experimental cages and founding populations are colored by treatment.



1. Bushnell B (2014) *BBMap: A Fast, Accurate, Splice-Aware Aligner* (Lawrence Berkeley National Lab. (LBNL), Berkeley, CA (United States)) Available at: https://www.osti.gov/biblio/1241166-bbmap-fast-accurate-splice-aware-aligner [Accessed July 10, 2019].

2. Kuhn RM, Haussler D, Kent WJ (2013) The UCSC genome browser and associated tools. *Brief Bioinform* 14(2):144–161.

3. Machado H, et al. (2018) Broad geographic sampling reveals predictable and pervasive seasonal adaptation in Drosophila. *bioRxiv*:337543.

chrm	pos	ref	alt	gene	p.At-Lb_div	afMean.Founder	afMean.NoAd	afMean.At	afMean.Lb	p.clinality	GOterm
2L	409409	A	G	alpha-Adaptin	4.65E-06	0.222	0.281	0.306	0.219	2.58E-01	protein transporter activity;clathrin adaptor activity;endocytosis;mitotic cleavage furrow ingression;ovarian follicale cell development;positive regulation of autophagy
2L	469463	C	A	(MED15)	7.30E-05	0.124	0.142	0.121	0.068	1.11E-01	NA
2L	1101026	C	G	CG4629	1.40E-05	0.442	0.416	0.285	0.471	6.94E-01	protein serine/threonine kinase activity;ATP binding;protein phosphorylation;cell adhesion;regulation of cell shape
2L	1674858	C	T	chinmo	5.48E-05	0.228	0.191	0.151	0.245	2.25E-01	DNA-binding transcription factor activity;imaginal disc-derived wing morphogenesis;mushroom body development;metal ion binding;dendrite morphogenesis
2L	1998051	T	A	CG33543	1.61E-05	0.248	0.233	0.257	0.220	8.28E-05	cell adhesion;membrane
2L	2087653	A	G	dpr3	6.96E-05	0.412	0.434	0.463	0.299	1.67E-01	store-operated calcium entry;sensory perception of chemical stimulus
2L	2334084	A	G	CG9967	2.69E-05	0.270	0.225	0.184	0.276	7.93E-01	
2L	2669544	T	A	(Gr23a)	4.15E-05	0.110	0.074	0.057	0.161	1.84E-01	NA
2L	3433591	T	G	(pgant2)	6.77E-05	0.088	0.100	0.076	0.136	5.67E-01	NA
2L	3852967	A	C	(slp2)	9.60E-05	0.563	0.543	0.632	0.478	6.96E-01	NA
2L	4132809	A	T	(Sr)	1.50E-04	0.043	0.063	0.034	0.091	9.99E-01	NA
2L	4313991	T	A	tutl	1.15E-04	0.020	0.057	0.025	0.046	6.49E-01	axon guidance;axonal defasciculation;peripheral nervous system development;flight behavior;mechanosensory behavior;synaptic target recognition;adult locomotory behavior;axon midline choice point recognition;larval behavior;lateral inhibition;regulation of dendrite morphogenesis;dendrite self-avoidance
2L	4814724	T	A	CG15629	8.35E-05	0.116	0.119	0.150	0.080	3.63E-01	metabolic process;oxidoreductase activity
2L	4867676	A	G	pog	4.54E-06	0.212	0.269	0.205	0.300	1.92E-01	regulation of antimicrobial peptide biosynthetic process;G protein-coupled receptor activity;G protein-coupled receptor signaling pathway;G protein-coupled glutamate receptor signaling pathway;germ-band extension;glutamate receptor activity;integral component of membrane

2L	5347750	G	C	nompC	1.24E-04	0.076	0.068	0.091	0.063	6.43E-01	startle response;ion channel activity;cation channel activity;calcium channel activity;cilium;cation transport;calcium ion transport;sensory perception of sound;mechanosensory behavior;cytoskeletal protein binding;mechanosensitive ion channel activity;response to auditory stimulus;dendrite;ankyrin binding;cation channel complex;locomotion;neuronal cell body;sensory perception of mechanical stimulus;detection of mechanical stimulus involved in sensory perception;sensory perception of touch;calcium ion transmembrane transport
2L	5870688	A	G	CG8965	2.21E-06	0.075	0.072	0.025	0.080	5.65E-02	protein homodimerization activity; Ras GTPase binding; glial cell development; prisitive regulation of epidermal growth factor receptor signaling pathway R7 cell development
2L	6256166	G	A	CG9486	1.49E-04	0.110	0.078	0.095	0.124	4.52E-01	N-acetyltransferase activity
2L	6499556	T	C	CG31637	8.75E-05	0.754	0.742	0.714	0.814	7.04E-04	sulfotransferase activity
2L	6603495	G	A	(CG11319)	9.78E-05	0.350	0.355	0.295	0.432	NA	NA
2L	7392478	T	C	CG5160	1.91E-05	0.063	0.106	0.056	0.106	2.62E-02	GTPase activity;GTP binding;obsolete GTP catabolic process;small GTPase mediated signal transduction;membrane;neurogenesis
2L	7417601	G	A	chm	1.40E-05	0.185	0.181	0.220	0.130	6.82E-01	DNA-binding transcription factor activity;transcription coactivator activity;histone acetyltransferase activity;nucleus;transcription factor binding;zinc ion binding;negative regulation of cell fate specification;H4 histone acetyltransferase activity;sensory organ precursor cell fate determination;gene silencing;chaeta development;negative regulation of transcription
2L	7435458	T	A	(CG5958)	1.26E-04	0.116	0.105	0.162	0.097	2.19E-01	NA
2L	7462699	G	A	(Gr28b)	1.05E-05	0.052	0.047	0.081	0.048	4.20E-01	NA
2L	7638255	G	T	(Slob)	1.14E-04	0.140	0.158	0.116	0.207	NA	NA
2L	8211227	A	T	(Ssb-c31a)	7.34E-06	0.035	0.016	0.016	0.042	NA	NA
2L	8304548	A	C	Scgalpha	7.24E-05	0.038	0.037	0.027	0.059	9.35E-01	calcium ion binding;structural constituent of muscle;sarcoglycan complex
2L	8784561	T	C	(CG9468)	3.68E-05	0.875	0.879	0.920	0.803	3.28E-01	NA
2L	9102902	G	A	(CG31609)	8.59E-05	0.196	0.209	0.156	0.271	6.33E-01	NA
2L	9185493	A	T	tai	1.10E-04	0.017	0.008	0.032	0.011	1.00E+00	transcription coactivator activity;obsolete signal transducer activity;nucleus;regulation of transcription

2L	9254319	A	G	lectin-30A	2.33E-05	0.333	0.250	0.357	0.195	4.60E-01	galactose binding;extracellular space;carbohydrate binding;multicellular organism reproduction
2L	9365904	C	T	(CG34181)	1.51E-04	0.056	0.095	0.043	0.132	5.87E-01	NA
2L	9447685	C	T	numb	1.21E-04	0.119	0.150	0.083	0.167	9.94E-01	cell fate determination;nucleic acid binding;Notch binding;protein binding;nucleus;cytoplasm;cell cortex;Notch signaling pathway;neuroblast fate determination;neuroblast proliferation;central nervous system development;ventral cord development;peripheral nervous system development;heart development;rhythmic behavior;protein localization;glial cell migration;asymmetric cell division;regulation of Notch signaling pathway;regulation of asymmetric cell division;sensory organ precursor cell fate determination;embryonic heart tube development;muscle cell fate specification;sensory organ precursor cell division;cell fate commitment;basal part of cell;basal cortex;negative regulation of Notch signaling pathway;positive regulation of endocytosis;regulation of neurogenesis;centrosome localization;regulation of nervous system development;asymmetric neuroblast division;pericardial nephrocyte differentiation;Malpighian tubule tip cell differentiation
2L	9772922	G	C	ppk16	7.39E-05	0.049	0.040	0.024	0.067	2.30E-01	sodium channel activity;sodium ion transport;integral component of membrane
2L	9783859	G	C	IP3K1	1.19E-04	0.173	0.139	0.118	0.185	3.62E-01	calmodulin binding;cytoplasm;response to oxidative stress;inositol-1
2L	9948936	G	T	(CG5853)	6.81E-05	0.105	0.139	0.095	0.223	3.47E-02	NA
2L	1E+07	A	G	CG42843	1.22E-04	0.143	0.169	0.100	0.227	4.17E-01	cell-cell adhesion mediator activity; G protein-coupled receptor activity; axon guidance; dendrite self-avoidance; homophilic cell adhesion
2L	1E+07	G	A	CG5355	2.90E-06	0.041	0.035	0.029	0.070	7.65E-01	serine-type endopeptidase activity;proteolysis;carboxylic ester hydrolase activity;serine-type exopeptidase activity
2L	1.2E+07	A	T	(CG31706)	2.85E-05	0.099	0.122	0.144	0.077	NA	NA
2L	1.2E+07	T	A	Pde1c	7.77E-05	0.242	0.206	0.237	0.176	8.84E-01	calcium- and calmodulin-regulated 3',5'-cyclic-AMP/GMP phosphodiesterase activity; calmodulin binding; male mating behavior; signal transduction
2L	1.2E+07	G	A	bru-2	1.25E-04	0.040	0.054	0.072	0.010	1.10E-01	nucleotide binding;RNA binding;mRNA binding;negative regulation of translation

2L	1.3E+07	A	T	(bun)	5.72E-05	0.284	0.285	0.182	0.242	2.34E-01	NA
2L	1.3E+07	C	A	CG15484	1.29E-04	0.013	0.031	0.049	0.012	4.73E-01	
2L	1.3E+07	A	T	(CG15483)	1.95E-05	0.058	0.086	0.093	0.048	4.35E-01	NA
2L	1.3E+07	C	A	(kek1)	6.80E-05	0.118	0.141	0.195	0.090	3.85E-01	NA
2L	1.3E+07	A	C	CG42784	3.30E-05	0.207	0.189	0.179	0.294	1.93E-01	
2L	1.4E+07	C	G	(nimB4)	1.54E-05	0.070	0.059	0.071	0.026	8.58E-01	NA
2L	1.4E+07	G	A	rk	4.75E-05	0.634	0.705	0.599	0.757	9.03E-01	epithelial to mesenchymal transition;G protein-coupled receptor activity;plasma membrane;integral component of plasma membrane;G protein-coupled receptor signaling pathway;neuropeptide signaling pathway;regulation of chitin-based cuticle tanning;neuropeptide receptor activity;integral component of membrane;protein-hormone receptor activity
2L	1.4E+07	G	T	nAcRalpha-34E	7.24E-05	0.040	0.037	0.012	0.054	4.39E-01	acethylcholine-gated cation-selective channel activity;transmembrane signaling receptor;cation transport;chemical synaptic transmission;ion transmembrane transport;nervous system process;regulation of membrane potential
2L	1.5E+07	C	T	GABA-B-R1	1.39E-04	0.158	0.231	0.158	0.253	5.37E-01	G protein-coupled GABA receptor activity;integral component of plasma membrane;G protein-coupled receptor signaling pathway;negative regulation of adenylate cyclase activity;gamma-aminobutyric acid signaling pathway;integral component of membrane;G protein-coupled receptor heterodimeric complex;protein heterodimerization activity
2L	1.6E+07	A	T	(l_2_35Di)	9.44E-05	0.153	0.178	0.214	0.128	2.75E-01	NA
2L	1.6E+07	G	A	(CG7653)	2.51E-05	0.147	0.159	0.178	0.107	1.66E-01	NA
2L	1.6E+07	G	A	(beat-Ia)	1.51E-04	0.028	0.053	0.022	0.050	7.62E-01	NA
2L	1.6E+07	G	C	(CG34168)	1.33E-04	0.141	0.145	0.187	0.093	6.22E-01	NA
2L	1.6E+07	C	T	Ca-alpha1D	5.70E-06	0.170	0.159	0.251	0.122	2.63E-01	voltage-gated calcium channel activity;voltage-gated calcium channel complex;calcium ion transport;muscle contraction;embryo development;basolateral plasma membrane;apical plasma membrane;epithelial fluid transport;calcium ion transmembrane transport
2L	1.6E+07	G	A	CG42818	6.96E-05	0.066	0.093	0.118	0.078	3.78E-02	
2L	1.7E+07	G	C	CG42389	7.61E-05	0.262	0.212	0.164	0.240	7.62E-01	

2L	1.7E+07	G	A	trpgamma	4.10E-06	0.640	0.673	0.599	0.668	1.67E-03	cation channel activity;mechanosensitive ion channel activity;calcium channel activity;inositol 1,4,5 triphosphate binding;adult walking behavior;neuromuscular process controlling posture
2L	1.8E+07	T	C	(CR43304)	1.45E-04	0.062	0.110	0.091	0.147	NA	NA
2L	1.8E+07	A	C	CadN2	1.27E-07	0.279	0.321	0.370	0.199	6.71E-01	NA;calcium ion binding;plasma membrane;integral component of plasma membrane;homophilic cell adhesion via plasma membrane adhesion molecules;ommatidial rotation;calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules;R8 cell development;R7 cell development;axon extension involved in axon guidance;cell adhesion molecule binding
2L	1.8E+07	C	T	(CadN2)	9.05E-05	0.114	0.070	0.042	0.107	4.11E-02	NA
2L	1.8E+07	T	C	rdo	1.09E-04	0.313	0.355	0.480	0.387	3.07E-01	ocellus development
2L	1.8E+07	A	G	CG42750	4.44E-05	0.013	0.032	0.027	0.078	3.08E-01	proteolysis;metalloexopeptidase activity;dipeptidyl-peptidase activity;dipeptidase activity
2L	1.8E+07	C	T	(CG31787)	7.40E-06	0.481	0.394	0.326	0.526	8.20E-04	NA
2L	1.8E+07	C	T	(CG31787)	6.37E-06	0.490	0.398	0.321	0.536	7.18E-04	NA
2L	1.8E+07	A	G	(CG31787)	1.33E-04	0.023	0.023	0.036	0.010	7.82E-01	NA
2L	1.9E+07	A	G	Pde11	8.90E-05	0.483	0.464	0.410	0.508	2.33E-01	3',5'-cyclic-AMP/GMP phosphodiesterase activity
2L	1.9E+07	T	C	(tup)	1.08E-04	0.855	0.860	0.898	0.820	3.48E-01	NA
2L	1.9E+07	T	A	CG10650	5.75E-05	0.039	0.038	0.029	0.066	1.00E+00	
2L	1.9E+07	G	A	Ddc	6.03E-05	0.512	0.534	0.512	0.587	7.52E-02	aromatic-L-amino-acid decarboxylase activity;catecholamine metabolic process;dopamine biosynthetic process from tyrosine;serotonin biosynthetic process from tryptophan;learning or memory;anesthesia-resistant memory;long-term memory;courtship behavior;eclosion rhythm;response to wounding;pyridoxal phosphate binding;wing disc development;growth;thermosensory behavior;thermotaxis;developmental pigmentation;regulation of adult chitin-containing cuticle pigmentation;adult chitin-containing cuticle pigmentation

2L	1.9E+07	T	C	drl	4.68E-06	0.066	0.067	0.094	0.028	3.62E-02	protein tyrosine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;plasma membrane;protein phosphorylation;signal transduction;axon guidance;salivary gland morphogenesis;haltere development;learning or memory;memory;olfactory learning;axon midline choice point recognition;muscle attachment;determination of muscle attachment site;Wnt-protein binding;axon
2L	1.9E+07	C	G	drl	4.45E-05	0.349	0.362	0.419	0.357	8.97E-01	protein tyrosine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;plasma membrane;protein phosphorylation;signal transduction;axon guidance;salivary gland morphogenesis;haltere development;learning or memory;memory;olfactory learning;axon midline choice point recognition;muscle attachment;determination of muscle attachment site;Wnt-protein binding;axon
2L	2E+07	C	T	bsh	1.04E-04	0.078	0.095	0.133	0.084	8.22E-04	transcription regulatory region sequence-specific DNA binding;DNA-binding transcription factor activity;nucleus;regulation of transcription
2L	2.1E+07	A	T	(Oseg5)	1.39E-04	0.248	0.255	0.360	0.246	8.32E-01	NA
2L	2.2E+07	C	A	(tsh)	4.04E-05	0.050	0.037	0.046	0.122	NA	NA
2R	1412432	A	G	CG30438	1.08E-04	0.017	0.063	0.053	0.033	5.97E-03	metabolic process;transferase activity
2R	2476210	T	C	jing	3.32E-05	0.095	0.085	0.068	0.147	3.73E-01	negative regulation of transcription by RNA polymerase II;nucleic acid binding;DNA-binding transcription factor activity;nucleus;regulation of transcription
2R	3527213	T	C	CG43340	2.11E-05	0.743	0.808	0.845	0.792	9.22E-01	intracellular protein transport;imaginal disc-derived wing morphogenesis;Rab GTPase binding
2R	4166659	T	C	(CG30371)	5.47E-05	0.094	0.063	0.095	0.049	1.10E-02	NA
2R	4180261	A	C	(CG30371)	7.55E-05	0.895	0.906	0.929	0.852	4.12E-01	NA
2R	4237786	A	G	pdm3	1.49E-04	0.027	0.028	0.019	0.062	5.67E-01	DNA-binding transcription factor activity;nucleus;regulation of transcription
2R	4684621	A	G	(sns)	3.90E-05	0.024	0.033	0.011	0.047	8.97E-02	NA
2R	5046734	G	C	CG8008	1.23E-04	0.554	0.473	0.440	0.570	2.02E-01	integral component of membrane;transmembrane transport
2R	5486967	C	T	clos	4.55E-05	0.334	0.377	0.320	0.406	4.07E-03	extracellular region;vitelline membrane formation involved in chorion-containing eggshell formation;terminal region determination;torso signaling pathway

2R	5941384	T	C	magu	1.13E-04	0.417	0.456	0.403	0.587	5.12E-04	calcium ion binding;extracellular region;NA;determination of adult lifespan;external side of plasma membrane;regulation of BMP signaling pathway;positive regulation of BMP signaling pathway;germ-line stem cell population maintenance;heparan sulfate proteoglycan binding;regulation of imaginal disc-derived wing size
2R	6289071	A	C	CG42732	1.10E-04	0.143	0.154	0.143	0.241	2.11E-01	potassium channel activity;potassium ion transport;calcium-activated potassium channel activity;membrane;neurogenesis;neuron projection morphogenesis
2R	6321928	C	T	RanBPM	1.13E-05	0.091	0.116	0.092	0.129	6.93E-02	cytoplasm;cytoskeleton organization;receptor signaling pathway via JAK-STAT;ovarian follicle cell-cell adhesion;Ran GTPase binding;larval feeding behavior;dorsal appendage formation;germ-line stem-cell niche homeostasis
2R	6322353	T	C	RanBPM	8.88E-05	0.131	0.138	0.144	0.113	8.76E-01	cytoplasm;cytoskeleton organization;receptor signaling pathway via JAK-STAT;ovarian follicle cell-cell adhesion;Ran GTPase binding;larval feeding behavior;dorsal appendage formation;germ-line stem-cell niche homeostasis
2R	6384019	T	G	lola	1.40E-04	0.807	0.737	0.770	0.650	6.70E-01	startle response;inter-male aggressive behavior;nucleic acid binding;DNA-binding transcription factor activity;protein binding;nucleus;regulation of transcription
2R	6679768	A	G	mthl13	1.21E-04	0.896	0.914	0.879	0.955	7.71E-02	G protein-coupled receptor activity;G protein-coupled receptor signaling pathway;integral component of membrane
2R	6746358	T	G	CG30015	1.41E-04	0.728	0.701	0.669	0.808	2.95E-01	
2R	7545689	A	G	Roc2	1.15E-05	0.195	0.200	0.241	0.155	7.51E-01	ubiquitin-protein transferase activity;zinc ion binding;protein ubiquitination
2R	7630421	T	C	(pyr)	1.43E-04	0.045	0.043	0.023	0.048	3.86E-01	NA
2R	7669315	G	A	ths	6.59E-05	0.091	0.115	0.153	0.095	4.22E-02	fibroblast growth factor receptor binding;hindgut morphogenesis;mesoderm development;heart development;larval visceral muscle development;larval somatic muscle development;growth factor activity;fibroblast growth factor receptor signaling pathway;glial cell differentiation;myoblast migration
2R	8090152	G	C	(CG8858)	1.07E-04	0.087	0.107	0.073	0.133	5.36E-01	NA
2R	8300037	T	C	(Cpr49Ah)	2.92E-05	0.606	0.638	0.702	0.617	6.15E-02	NA

2R	8669385	T	C	sca	1.12E-04	0.023	0.036	0.024	0.065	1.81E-01	obsolete signal transducer activity;extracellular region;fibrinogen complex;nervous system development;R8 cell fate commitment;chaeta morphogenesis;imaginal disc-derived wing margin morphogenesis;ommatidial rotation;female meiosis chromosome segregation;regulation of R8 cell spacing in compound eye;lateral inhibition;compound eye development;response to alcohol
2R	9412636	G	A	Vmat	2.69E-06	0.073	0.104	0.201	0.105	7.43E-01	obsolete synaptic vesicle amine transmembrane transporter activity;neurotransmitter transport;synaptic vesicle;monoamine transmembrane transporter activity;drug transmembrane transporter activity;aminergic neurotransmitter loading into synaptic vesicle;monoamine transport;dopamine transport;integral component of membrane;neuromuscular junction;histamine transport;transmembrane transport
2R	9609003	T	A	fas	1.49E-04	0.072	0.091	0.056	0.134	NA	morphogenesis of an epithelium;dorsal closure;salivary gland development;salivary gland morphogenesis;foregut morphogenesis;Malpighian tubule morphogenesis;cardioblast cell fate determination;head involution;maintenance of polarity of embryonic epithelium
2R	9821791	G	A	shot	1.22E-04	0.443	0.449	0.497	0.368	9.30E-01	microtubule cytoskeleton organization;astral microtubule;microtubule bundle formation;actin binding;calcium ion binding;protein binding;cytoskeleton;microtubule;adherens junction;microtubule-based process;negative regulation of microtubule depolymerization;cell cycle arrest;axonogenesis;sensory organ development;open tracheal system development;apposition of dorsal and ventral imaginal disc-derived wing surfaces;muscle organ development;microtubule binding;cytoskeletal protein binding;axon midline choice point recognition;muscle attachment;determination of muscle attachment site;mushroom body development;actin cytoskeleton organization;filopodium;growth cone;regulation of axon extension;oocyte fate determination;branch fusion
2R	9959741	A	G	Prosap	7.17E-05	0.616	0.621	0.598	0.694	2.63E-01	protein binding;postsynaptic density;GKAP/Homer scaffold activity;postsynaptic density assembly

2R	1.1E+07	T	C	CG30480	1.24E-04	0.270	0.316	0.248	0.391	9.02E-01	
2R	1.1E+07	T	A	mspo	8.89E-05	0.216	0.191	0.223	0.093	1.09E-01	regulation of myoblast fusion
2R	1.1E+07	A	C	igl	1.81E-05	0.517	0.485	0.504	0.440	5.71E-01	calmodulin binding;cell cortex;myosin light chain binding
2R	1.1E+07	A	T	trpm	9.55E-05	0.489	0.436	0.367	0.473	5.34E-01	zinc ion transmembrane transporter activity
2R	1.1E+07	C	T	(CG8157)	3.82E-05	0.192	0.202	0.160	0.225	1.48E-01	NA
2R	1.2E+07	C	T	shark	8.40E-05	0.431	0.306	0.353	0.266	6.88E-01	protein tyrosine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;cytoplasm;cell cortex;protein phosphorylation;JNK cascade;eggshell chorion assembly;dorsal closure;dorsal closure
2R	1.2E+07	T	C	(CG15711)	6.43E-05	0.027	0.045	0.055	0.029	5.45E-01	NA
2R	1.2E+07	A	T	CG8311	4.49E-05	0.043	0.070	0.031	0.077	4.92E-01	dolichol kinase activity;integral component of endoplasmic reticulum membrane;dolichyl monophosphate biosynthetic process
2R	1.3E+07	A	T	CG8910	8.57E-05	0.097	0.099	0.066	0.131	1.52E-03	zinc ion binding
2R	1.3E+07	G	A	CG6796	2.58E-05	0.060	0.070	0.030	0.074	5.01E-01	nucleic acid binding;asparagine-tRNA ligase activity;ATP binding;cytoplasm;asparaginyl-tRNA aminoacylation
2R	1.3E+07	G	C	CG30460	5.00E-05	0.867	0.838	0.871	0.798	NA	
2R	1.3E+07	T	C	CG30460	1.36E-04	0.868	0.836	0.871	0.791	NA	
2R	1.3E+07	A	G	(CG15611)	4.66E-05	0.031	0.063	0.080	0.026	5.00E-01	NA
2R	1.3E+07	C	T	mbl	6.98E-05	0.400	0.353	0.233	0.372	2.17E-01	regulation of alternative mRNA splicing
2R	1.4E+07	C	A	elk	6.46E-05	0.111	0.157	0.158	0.129	2.30E-01	
2R	1.4E+07	T	C	dpr13	6.36E-05	0.043	0.030	0.030	0.068	NA	sensory perception of chemical stimulus
2R	1.4E+07	G	A	(stau)	5.70E-05	0.055	0.050	0.074	0.031	8.07E-01	NA
2R	1.4E+07	G	A	CG18537	1.79E-05	0.180	0.156	0.128	0.186	8.63E-01	
2R	1.4E+07	A	C	Pepck	1.07E-04	0.385	0.436	0.341	0.498	3.57E-01	phosphoenolpyruvate carboxykinase (GTP) activity;GTP binding;mitochondrion;gluconeogenesis
2R	1.5E+07	C	A	Hs3st-A	7.68E-06	0.305	0.322	0.227	0.365	9.54E-01	[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity
2R	1.5E+07	A	C	(CG15115)	7.57E-05	0.068	0.050	0.081	0.029	6.80E-01	NA
2R	1.5E+07	A	T	CG10081	6.12E-05	0.082	0.066	0.046	0.078	9.57E-02	proteolysis;peptidase activity
2R	1.5E+07	G	C	(sm)	1.13E-04	0.116	0.089	0.088	0.052	NA	NA
2R	1.7E+07	G	C	(shg)	1.37E-04	0.160	0.190	0.180	0.274	4.96E-02	NA
2R	1.7E+07	A	T	king-tubby	1.35E-04	0.134	0.153	0.151	0.112	4.87E-01	phosphatidylinositol binding;deactivation of rhodopsin mediated signaling;protein localization to cilium;glucose homeostasis
2R	1.7E+07	C	A	Magi	5.31E-05	0.281	0.405	0.390	0.311	2.54E-01	guanylate kinase activity;membrane;Ral GTPase binding

2R	1.7E+07	C	T	(Rgk3)	1.45E-04	0.264	0.243	0.172	0.301	NA	NA
2R	1.7E+07	A	C	(Rgk3)	1.26E-04	0.251	0.239	0.158	0.292	NA	NA
2R	1.7E+07	C	T	Rgk3	1.02E-04	0.306	0.359	0.273	0.381	2.28E-02	GTP binding;obsolete GTP catabolic process;small GTPase mediated signal transduction;membrane
2R	1.7E+07	G	C	CG10505	1.30E-04	0.147	0.084	0.062	0.126	2.11E-01	transporter activity;ATP binding;response to zinc ion;ATPase activity
2R	1.7E+07	T	G	Sdc	1.34E-04	0.036	0.027	0.046	0.020	5.94E-01	transmembrane signaling receptor activity;extracellular region;plasma membrane;focal adhesion;axon guidance;epithelial cell migration
2R	1.8E+07	T	A	a	8.94E-06	0.656	0.573	0.571	0.658	NA	adherens junction;apical plasma membrane;compound eye development
2R	1.8E+07	C	T	dve	1.24E-04	0.288	0.249	0.305	0.178	NA	negative regulation of transcription by RNA polymerase II;AT DNA binding;DNA-binding transcription factor activity;nucleus;regulation of transcription
2R	1.8E+07	G	A	CG4554	1.10E-05	0.042	0.034	0.012	0.048	5.64E-01	neurogenesis
2R	1.9E+07	T	A	RpL23	3.26E-05	0.276	0.295	0.275	0.345	8.81E-01	mitotic spindle elongation;structural constituent of ribosome;ribosome;translation;mitotic spindle organization;myosin binding;neurogenesis;cytosolic large ribosomal subunit
2R	2E+07	C	T	CG9850	1.33E-04	0.084	0.052	0.095	0.029	1.71E-01	metalloendopeptidase activity;proteolysis;cell population proliferation
2R	2E+07	A	C	ytr	8.56E-05	0.185	0.215	0.224	0.134	2.02E-01	mRNA splicing
2R	2.1E+07	T	C	emp	2.18E-05	0.605	0.545	0.456	0.682	6.56E-01	scavenger receptor activity;lysosome;plasma membrane;integral component of plasma membrane;defense response;cell adhesion;salivary gland cell autophagic cell death;autophagic cell death
3L	331062	A	G	mthl9	8.76E-05	0.197	0.200	0.160	0.243	6.94E-01	G protein-coupled receptor activity;response to stress;G protein-coupled receptor signaling pathway;determination of adult lifespan;integral component of membrane
3L	1269786	C	G	CG9134	3.38E-05	0.068	0.055	0.073	0.026	4.91E-01	carbohydrate binding
3L	1658473	T	C	CG7971	5.94E-05	0.590	0.590	0.491	0.620	3.55E-01	mRNA splicing
3L	2198846	T	G	(CG8960)	9.58E-05	0.873	0.866	0.854	0.900	5.45E-02	NA
3L	2210365	C	G	(CG15878)	7.08E-05	0.634	0.607	0.738	0.538	2.26E-01	NA
3L	2327513	T	C	DmsR-1	7.35E-05	0.217	0.223	0.226	0.282	NA	myosuppressin receptor activity;G protein-coupled receptor activity;neuropeptide receptor activity;adult locomotory behavior

3L	2964616	C	A	(CG34025)	1.67E-05	0.115	0.131	0.083	0.146	NA	NA
3L	3476925	C	A	(CG32267)	2.14E-05	0.035	0.040	0.025	0.058	9.71E-01	NA
3L	3844675	A	G	(Awh)	7.39E-05	0.832	0.777	0.830	0.760	6.00E-01	NA
3L	4404707	A	G	Syx17	5.37E-05	0.589	0.581	0.667	0.500	1.52E-02	SNARE binding;autophagosome membrane;SNAP receptor activity;plasma membrane;endoplasmic reticulum to Golgi vesicle-mediated transport;neurotransmitter secretion;synaptic vesicle docking;vesicle-mediated transport;SNARE complex;neuron cellular homeostasis;endoplasmic reticulum-Golgi intermediate compartment organization;autophagosome maturation
3L	4842109	C	A	(CG13707)	2.50E-05	0.923	0.926	0.924	0.953	7.18E-01	NA
3L	5389566	G	C	(Ir64a)	9.40E-05	0.600	0.592	0.483	0.606	NA	NA
3L	6590431	A	G	ndl	1.23E-04	0.117	0.099	0.153	0.105	NA	serine-type endopeptidase activity;extracellular region;proteolysis;eggshell chorion assembly;oocyte dorsal/ventral axis specification;maternal specification of dorsal/ventral axis
3L	7335246	G	A	CG8596	3.16E-05	0.109	0.077	0.099	0.141	8.79E-05	integral component of membrane;transmembrane transport
3L	7454495	T	C	(CG42660)	1.33E-04	0.081	0.039	0.048	0.020	3.66E-01	NA
3L	7639899	A	T	(CG32373)	4.57E-05	0.331	0.283	0.212	0.358	1.14E-01	NA
3L	7951378	T	C	(exex)	1.02E-04	0.051	0.034	0.051	0.022	6.02E-01	NA
3L	8284093	G	A	CG7201	8.33E-05	0.074	0.071	0.088	0.033	4.19E-01	
3L	8318762	G	C	(CG34461)	4.52E-05	0.462	0.342	0.432	0.317	8.96E-01	NA
3L	8606593	T	G	CG6282	7.18E-05	0.224	0.237	0.115	0.200	9.25E-01	cytoplasm;lipid metabolic process;integral component of membrane;oxidoreductase activity
3L	8688265	G	A	(h)	1.04E-04	0.046	0.051	0.052	0.022	3.73E-01	NA

3L	8843663	C	T	dally	1.05E-04	0.210	0.224	0.304	0.187	NA	protein binding;extracellular region;NA;transforming growth factor beta receptor signaling pathway;nervous system development;axonogenesis;wing disc morphogenesis;imaginal disc-derived wing morphogenesis;imaginal disc-derived leg morphogenesis;motor neuron axon guidance;sensory organ boundary specification;decapentaplegic signaling pathway;G2/MI transition of meiotic cell cycle;chaeta morphogenesis;imaginal disc-derived wing vein morphogenesis;cell surface;membrane;Wnt signaling pathway;extrinsic component of plasma membrane;chaeta development;regulation of BMP signaling pathway;positive regulation of BMP signaling pathway;germ-line stem cell population maintenance;wing disc development;regulation of multicellular organism growth;heparan sulfate proteoglycan binding;regulation of imaginal disc growth;female germ-line stem cell asymmetric division;wing disc dorsal/ventral pattern formation;compound eye development;dendrite morphogenesis;regulation of cell cycle;negative regulation of semaphorin-plexin signaling pathway
3L	9368910	C	G	CG4461	5.90E-05	0.789	0.797	0.732	0.803	6.83E-01	response to heat
3L	9575690	C	T	CG42673	1.33E-05	0.403	0.453	0.504	0.426	1.93E-01	
3L	9593255	T	A	CG3222	1.36E-04	0.579	0.630	0.608	0.548	5.60E-01	
3L	9769486	G	T	CG8177	1.49E-04	0.048	0.062	0.030	0.080	8.97E-01	inorganic anion exchanger activity;anion transport;anion:anion antiporter activity;integral component of membrane
3L	1E+07	T	C	(dpr10)	5.84E-06	0.058	0.038	0.027	0.050	3.32E-03	NA
3L	1E+07	T	G	(dpr10)	3.31E-05	0.056	0.041	0.027	0.052	2.28E-03	NA
3L	1E+07	C	T	A2bp1	1.33E-05	0.055	0.062	0.079	0.027	1.60E-01	nucleotide binding;mRNA binding;nucleus;cytoplasm;nervous system development;imaginal disc-derived wing vein specification;transcription factor binding;transcription regulatory region DNA binding;positive regulation of transcription
3L	1.1E+07	G	A	(NijA)	1.28E-04	0.344	0.365	0.287	0.423	5.81E-02	NA
3L	1.1E+07	T	A	(Aps)	1.01E-04	0.404	0.472	0.459	0.532	6.64E-01	NA

3L	1.1E+07	G	A	(CG34050)	5.58E-05	0.419	0.455	0.351	0.485	NA	NA
3L	1.1E+07	T	G	CG7638	9.40E-05	0.086	0.088	0.151	0.096	9.05E-02	
3L	1.1E+07	G	A	GlcAT-P	1.09E-04	0.032	0.031	0.011	0.051	6.41E-01	glycosphingolipid biosynthetic process;peripheral nervous system development;glycoprotein biosynthetic process;galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity;glucuronosyltransferase activity;membrane;proteoglycan biosynthetic process;N-acetyllactosamine beta-1
3L	1.1E+07	G	A	(CG6168)	1.85E-05	0.115	0.131	0.256	0.107	7.66E-01	NA
3L	1.1E+07	C	A	(CG6163)	1.41E-04	0.171	0.185	0.147	0.195	4.91E-01	NA
3L	1.2E+07	T	C	Mob2	9.70E-05	0.068	0.100	0.050	0.134	9.23E-01	cell morphogenesis;protein binding;cytoplasm;plasma membrane;learning or memory;long-term memory;olfactory learning;rhabdomere;protein kinase binding;rhabdomere development;negative regulation of synaptic growth at neuromuscular junction;cell hair;cell periphery
3L	1.2E+07	T	G	Nrx-IV	1.34E-04	0.858	0.867	0.877	0.768	3.76E-05	heart process;transmembrane signaling receptor activity;plasma membrane;integral component of plasma membrane;septate junction;pleated septate junction;establishment or maintenance of cell polarity;dorsal closure;synaptic target recognition;establishment of blood-nerve barrier;protein localization;axon ensheathment;integral component of membrane;synaptic vesicle targeting;synaptic vesicle docking;septate junction assembly;nerve maturation;regulation of tube size
3L	1.3E+07	A	C	sowah	5.27E-05	0.461	0.459	0.529	0.419	9.54E-01	
3L	1.3E+07	G	C	CG32111	5.53E-05	0.076	0.032	0.052	0.026	6.34E-01	
3L	1.3E+07	C	G	(mirr)	8.82E-06	0.034	0.037	0.026	0.052	1.08E-01	NA
3L	1.3E+07	C	T	(mirr)	1.07E-04	0.177	0.168	0.108	0.189	2.98E-02	NA
3L	1.3E+07	G	A	(CG10943)	7.74E-05	0.027	0.025	0.044	0.096	6.44E-01	NA
3L	1.3E+07	C	T	(CG11262)	3.30E-05	0.557	0.539	0.443	0.588	NA	NA
3L	1.3E+07	T	A	CG17672	6.16E-05	0.066	0.058	0.010	0.064	6.54E-01	
3L	1.3E+07	G	A	(CR43913)	2.79E-05	0.215	0.249	0.142	0.272	4.10E-01	NA
3L	1.3E+07	G	T	(CR43912)	8.87E-05	0.042	0.031	0.072	0.026	3.17E-01	NA
3L	1.4E+07	A	T	Sox21b	1.39E-04	0.101	0.154	0.201	0.108	8.62E-01	DNA-binding transcription factor activity;nucleus;regulation of transcription

3L	1.5E+07	C	A	bbg	1.27E-04	0.063	0.050	0.021	0.046	9.38E-01	nucleus;plasma membrane;border follicle cell migration;imaginal disc development
3L	1.5E+07	C	A	(BobA)	1.35E-04	0.027	0.035	0.013	0.054	8.84E-01	NA
3L	1.5E+07	A	T	(Tollo)	1.04E-04	0.148	0.189	0.254	0.155	9.53E-01	NA
3L	1.5E+07	A	T	(Tollo)	4.77E-05	0.141	0.188	0.222	0.126	6.97E-01	NA
3L	1.5E+07	G	T	(CR43625)	1.33E-04	0.581	0.548	0.418	0.584	8.15E-01	NA
3L	1.6E+07	T	C	(CG34451)	1.12E-04	0.757	0.754	0.771	0.748	4.20E-01	NA
3L	1.6E+07	C	A	sff	8.40E-05	0.126	0.136	0.155	0.084	8.88E-01	protein serine/threonine kinase activity;ATP binding;protein phosphorylation;protein N-linked glycosylation;neuromuscular junction development
3L	1.6E+07	G	T	CG13070	9.09E-05	0.348	0.316	0.340	0.369	NA	
3L	1.6E+07	C	T	CG33158	3.73E-05	0.075	0.059	0.074	0.028	7.91E-02	translation elongation factor activity;GTPase activity;GTP binding;eukaryotic translation initiation factor 2 complex;translational elongation
3L	1.6E+07	T	C	CG33158	1.21E-05	0.077	0.061	0.077	0.029	7.77E-02	translation elongation factor activity;GTPase activity;GTP binding;eukaryotic translation initiation factor 2 complex;translational elongation
3L	1.8E+07	G	A	(CG5290)	2.51E-05	0.194	0.174	0.209	0.130	9.54E-04	NA
3L	1.8E+07	T	A	(grim)	4.02E-05	0.958	0.951	0.971	0.939	2.89E-01	NA
3L	1.9E+07	C	A	(CG32204)	1.09E-04	0.053	0.108	0.125	0.074	NA	NA
3L	1.9E+07	T	C	(Spn75F)	1.33E-04	0.039	0.047	0.071	0.023	6.55E-02	NA
3L	1.9E+07	C	T	CG32206	1.26E-04	0.077	0.082	0.056	0.029	3.16E-01	Wnt-protein binding;Wnt-activated receptor activity;Wnt signaling pathway involved in dorsal/ventral axis specification;lateral inhibition;canonical Wnt signaling pathway
3L	2E+07	A	G	CG42674	1.05E-04	0.229	0.196	0.179	0.228	4.95E-04	Rho guanyl-nucleotide exchange factor activity;cell adhesion;imaginal disc-derived leg morphogenesis;regulation of cell shape;positive regulation of Rho protein signal transduction
3L	2.1E+07	A	G	(CR43929)	1.52E-04	0.136	0.103	0.177	0.096	7.73E-01	NA
3L	2.2E+07	G	T	(mir-4942)	5.67E-05	0.063	0.217	0.173	0.273	2.19E-01	NA

3L	2.3E+07	G	A	alpha-Cat	1.33E-04	0.026	0.025	0.091	0.052	1.58E-01	actin binding;structural molecule activity;protein binding;plasma membrane;adherens junction;cell-cell adherens junction;spot adherens junction;zonula adherens;cytoskeletal anchoring at plasma membrane;cell adhesion;establishment or maintenance of cell polarity;cytoskeletal protein binding;actin cytoskeleton;catenin complex;cell-substrate junction;oocyte localization involved in germarium-derived egg chamber formation;adherens junction organization;cadherin binding;head morphogenesis
3R	1262668	C	A	CG14669	4.50E-05	0.281	0.233	0.278	0.214	1.15E-04	GTP binding;obsolete GTP catabolic process;small GTPase mediated signal transduction;membrane
3R	1892799	G	T	(CG15580)	8.55E-05	0.407	0.353	0.315	0.373	4.86E-01	NA
3R	2456272	T	C	sunz	1.51E-04	0.275	0.290	0.215	0.301	3.58E-01	calcium ion binding;male meiotic nuclear division
3R	5950686	A	G	knk	1.22E-04	0.053	0.116	0.156	0.079	2.48E-04	embryonic epithelial tube formation;chitin biosynthetic process;cuticle chitin biosynthetic process;terminal region determination;open tracheal system development;torso signaling pathway;chitin-based embryonic cuticle biosynthetic process;regulation of tube size
3R	6250938	C	A	(CG6345)	8.76E-06	0.582	0.562	0.518	0.608	2.02E-01	NA
3R	7105520	G	C	CG31386	1.37E-04	0.580	0.410	0.414	0.532	2.68E-01	
3R	7634750	G	A	ClC-a	2.83E-05	0.026	0.039	0.011	0.045	4.50E-01	voltage-gated chloride channel activity;chloride channel activity;chloride transport;actin cytoskeleton;membrane;adenyl nucleotide binding;transmembrane transport
3R	7982089	G	C	dpr15	8.24E-05	0.097	0.175	0.192	0.140	1.28E-02	sensory perception of chemical stimulus
3R	7990369	G	C	Cpn	5.55E-05	0.041	0.056	0.055	0.013	1.65E-01	calcium ion binding;nucleus;cytoplasm;mitochondrion;rough endoplasmic reticulum;rhabdomere;axon;rhabdomere development;cell body;sequestering of calcium ion
3R	8426065	G	A	(Octbeta2R)	5.94E-05	0.205	0.175	0.143	0.090	1.07E-02	NA
3R	9224993	T	C	CG9796	2.64E-05	0.138	0.109	0.046	0.078	7.87E-02	

3R	9820259	C	G	rdx	8.81E-05	0.261	0.267	0.263	0.189	6.85E-01	protein binding;nucleus;cellularization;protein ubiquitination;regulation of proteolysis;protein destabilization;establishment of ommatidial planar polarity;negative regulation of protein import into nucleus;protein homodimerization activity;positive regulation of apoptotic process;negative regulation of smoothened signaling pathway;positive regulation of JNK cascade;lateral inhibition;eye morphogenesis
3R	1E+07	T	C	(cv-c)	1.42E-04	0.227	0.240	0.200	0.293	9.87E-01	NA
3R	1.1E+07	A	T	Neu3	1.21E-04	0.035	0.023	0.011	0.033	2.02E-01	
3R	1.1E+07	T	C	(btsz)	1.37E-04	0.066	0.086	0.075	0.151	4.19E-01	NA
3R	1.1E+07	C	A	(CG3837)	3.19E-05	0.096	0.114	0.100	0.046	2.26E-01	NA
3R	1.1E+07	T	G	(CG43335)	5.07E-05	0.433	0.596	0.672	0.554	2.38E-02	NA
3R	1.1E+07	G	C	(pxb)	1.88E-05	0.017	0.026	0.041	0.010	6.69E-01	NA
3R	1.2E+07	C	T	alpha-Man-IIb	1.16E-04	0.078	0.093	0.132	0.089	5.63E-01	Golgi membrane;alpha-mannosidase activity;mannosyl-oligosaccharide 1
3R	1.2E+07	T	G	ss	7.25E-05	0.081	0.084	0.054	0.107	8.52E-05	negative regulation of transcription by RNA polymerase II;DNA binding;DNA-binding transcription factor activity;NA;obsolete signal transducer activity;nucleus;regulation of transcription
3R	1.3E+07	A	T	msa	5.21E-05	0.317	0.335	0.295	0.390	2.89E-02	
3R	1.3E+07	T	A	(Mur89F)	1.47E-04	0.030	0.066	0.097	0.027	NA	NA
3R	1.3E+07	C	A	(CG31262)	1.33E-04	0.298	0.230	0.175	0.293	4.45E-01	NA
3R	1.4E+07	C	T	CG18012	5.36E-06	0.270	0.296	0.311	0.225	4.68E-03	protein glycosylation;beta-1
3R	1.4E+07	T	C	(htl)	1.01E-05	0.876	0.884	0.947	0.855	4.11E-02	NA
3R	1.4E+07	G	A	CG14316	3.72E-05	0.191	0.159	0.137	0.079	7.39E-01	biological_process
3R	1.4E+07	G	T	CG7156	1.25E-04	0.085	0.150	0.130	0.189	1.57E-04	protein kinase activity;ATP binding;protein phosphorylation;phosphatidylinositol binding;neuron projection morphogenesis
3R	1.5E+07	T	A	CG42613	1.55E-05	0.193	0.248	0.300	0.245	NA	biological_process
3R	1.5E+07	A	G	CG5316	1.50E-04	0.169	0.137	0.210	0.148	8.88E-01	single strand break repair;mRNA splicing
3R	1.6E+07	C	T	mun	9.40E-05	0.389	0.394	0.300	0.412	1.39E-01	
3R	1.7E+07	T	G	lbl	3.71E-05	0.735	0.655	0.658	0.771	2.22E-01	transcription regulatory region sequence-specific DNA binding;DNA-binding transcription factor activity;nucleus;regulation of transcription

3R	1.9E+07	A	G	CG13830	1.22E-04	0.339	0.311	0.354	0.255	NA	calcium ion binding;NA;signal transduction
3R	1.9E+07	T	C	CG6763	8.94E-05	0.552	0.532	0.493	0.684	1.49E-02	metalloendopeptidase activity;proteolysis;zinc ion binding;meprin A complex
3R	2E+07	A	G	mbc	2.21E-05	0.795	0.713	0.741	0.645	NA	cell morphogenesis;ruffle;protein binding;cytoplasm;cytoskeleton organization;border follicle cell migration;dorsal closure;central nervous system development;skeletal muscle tissue development;myoblast fusion;larval visceral muscle development;muscle attachment;extrinsic component of plasma membrane;actin cytoskeleton organization;Rac guanyl-nucleotide exchange factor activity;NA;cell competition in a multicellular organism;anterior Malpighian tubule development
3R	2E+07	T	A	(Esyt2)	1.03E-04	0.323	0.320	0.315	0.219	7.54E-01	NA
3R	2E+07	G	A	CG13624	1.00E-04	0.257	0.313	0.196	0.333	3.76E-02	DNA-binding transcription factor activity;regulation of transcription
3R	2.1E+07	T	A	CG31370	4.07E-05	0.090	0.065	0.109	0.052	7.04E-01	transferase activity
3R	2.2E+07	T	A	CG4743	1.96E-05	0.024	0.038	0.050	0.013	2.04E-01	mitochondrial envelope;transmembrane transporter activity;transmembrane transport
3R	2.2E+07	T	C	malpha	8.38E-05	0.410	0.364	0.475	0.350	1.61E-03	
3R	2.2E+07	C	T	(CG6073)	1.15E-04	0.371	0.418	0.368	0.473	1.04E-01	NA
3R	2.2E+07	T	A	(CG6073)	7.44E-05	0.371	0.415	0.368	0.476	1.55E-01	NA
3R	2.3E+07	G	C	CG14253	7.63E-05	0.524	0.608	0.516	0.666	2.81E-01	
3R	2.3E+07	C	T	CG5611	1.09E-04	0.142	0.186	0.070	0.200	3.39E-01	metabolic process
3R	2.4E+07	A	T	CG34353	1.51E-04	0.086	0.095	0.180	0.091	1.99E-01	gravitaxis
3R	2.5E+07	G	A	CG10000	5.00E-05	0.074	0.091	0.127	0.065	5.20E-03	polypeptide N-acetylgalactosaminyltransferase activity;Golgi stack;oligosaccharide biosynthetic process;multicellular organism reproduction
3R	2.5E+07	C	A	CG10000	6.19E-05	0.037	0.020	0.056	0.010	1.01E-01	polypeptide N-acetylgalactosaminyltransferase activity;Golgi stack;oligosaccharide biosynthetic process;multicellular organism reproduction
3R	2.5E+07	G	C	(CG12558)	1.94E-05	0.526	0.408	0.401	0.522	2.20E-03	NA
3R	2.5E+07	G	A	CG14521	7.81E-05	0.052	0.033	0.012	0.049	9.35E-01	
3R	2.5E+07	A	C	CG11897	1.48E-04	0.469	0.474	0.421	0.526	3.50E-01	ATP binding;xenobiotic transmembrane transporting ATPase activity;drug transmembrane transporter activity;integral component of membrane;transmembrane transport
3R	2.5E+07	T	A	(Cnx99A)	8.52E-05	0.082	0.083	0.037	0.110	3.16E-01	NA

3R	2.5E+07	G	C	DopR2	1.43E-04	0.486	0.539	0.491	0.625	6.78E-01	
3R	2.6E+07	G	A	ncd	1.49E-04	0.148	0.145	0.093	0.208	3.16E-02	mitotic spindle elongation;meiotic spindle organization;microtubule bundle formation;microtubule motor activity;ATP binding;spindle;kinesin complex;minus-end kinesin complex;microtubule-based movement;spindle organization;mitotic spindle organization;spindle assembly involved in female meiosis;chromosome segregation;mitotic centrosome separation;microtubule binding;ATP-dependent microtubule motor activity
3R	2.6E+07	T	C	CG1983	1.19E-04	0.202	0.217	0.169	0.222	1.25E-01	pyridoxal phosphate binding
3R	2.6E+07	G	T	hdc	1.40E-04	0.236	0.243	0.340	0.206	NA	cytoplasm;open tracheal system development;terminal branching
3R	2.6E+07	T	A	PH4alphaEFB	2.92E-05	0.051	0.040	0.082	0.025	NA	procollagen-proline 4-dioxygenase activity;iron ion binding;endoplasmic reticulum;procollagen-proline 4-dioxygenase complex;oxidoreductase activity
3R	2.6E+07	C	T	(CG31013)	2.13E-05	0.050	0.094	0.073	0.151	1.69E-02	NA
3R	2.7E+07	C	T	(CG15545)	2.89E-05	0.238	0.261	0.168	0.288	1.27E-01	NA
3R	2.7E+07	G	A	(CG12071)	2.31E-05	0.447	0.444	0.387	0.520	6.72E-01	NA
3R	2.7E+07	C	T	(CG15550)	1.51E-04	0.075	0.088	0.050	0.081	3.48E-01	NA
3R	2.7E+07	G	A	CG12054	4.54E-05	0.061	0.046	0.028	0.060	3.03E-02	nucleic acid binding;metal ion binding
3R	2.7E+07	C	T	(CG1607)	2.29E-05	0.536	0.520	0.399	0.548	5.17E-04	NA
3R	2.7E+07	A	C	Gprk2	5.11E-05	0.753	0.786	0.799	0.720	3.86E-01	regulation of antimicrobial peptide biosynthetic process;apical constriction involved in gastrulation;protein serine/threonine kinase activity;G protein-coupled receptor kinase activity;ATP binding;cytoplasm;plasma membrane;protein phosphorylation;signal transduction;G protein-coupled receptor signaling pathway;smoothened signaling pathway;vitellogenesis;imaginal disc-derived wing vein specification;regulation of G protein-coupled receptor signaling pathway;regulation of smoothened signaling pathway;regulation of Toll signaling pathway;embryo development;termination of G protein-coupled receptor signaling pathway;positive regulation of cAMP-mediated signaling;negative regulation of smoothened signaling pathway;defense response to Gram-positive bacterium

3R	2.7E+07	G	A	RpL6	4.20E-06	0.424	0.387	0.375	0.430	1.76E-02	mitotic spindle elongation;structural constituent of ribosome;ribosome;translation;mitotic spindle organization;cytosolic large ribosomal subunit;NA;centrosome duplication
X	343943	C	A	CG32816	1.31E-04	0.300	0.225	0.195	0.318	9.93E-02	
X	1420447	T	C	Mur2B	5.20E-05	0.041	0.049	0.051	0.013	4.27E-01	extracellular matrix structural constituent;extracellular region;chitin metabolic process;chitin binding;extracellular matrix;chorion
X	2381099	A	G	trol	4.18E-05	0.312	0.289	0.205	0.358	2.51E-01	NA;basement membrane;lipid droplet;defasciculation of motor neuron axon;motor neuron axon guidance;maintenance of epithelial cell apical/basal polarity;asymmetric neuroblast division;response to anesthetic;positive regulation of semaphorin-plexin signaling pathway
X	2461125	A	G	Pdfr	3.54E-05	0.022	0.045	0.012	0.056	8.26E-01	G protein-coupled receptor activity;calcitonin receptor activity;integral component of plasma membrane;G protein-coupled receptor signaling pathway;neuropeptide signaling pathway;circadian rhythm;neuropeptide receptor activity;NA;integral component of membrane;gravitaxis;circadian sleep/wake cycle;regulation of circadian sleep/wake cycle;neuron projection;neuronal cell body;locomotor rhythm;circadian behavior
X	2602978	C	A	CG2681	8.94E-05	0.313	0.335	0.376	0.317	7.48E-02	ubiquitin-protein transferase activity;nucleus;ubiquitin-dependent protein catabolic process;multicellular organism development;zinc ion binding;protein ubiquitination
X	3326693	G	A	CG12535	2.43E-06	0.026	0.018	0.013	0.045	2.64E-01	
X	5495935	G	T	Vsx1	1.43E-04	0.055	0.038	0.013	0.053	2.81E-01	negative regulation of transcription by RNA polymerase II;optic lobe placode development;DNA-binding transcription factor activity;nucleus;phagocytosis;sequence-specific DNA binding;positive regulation of neural precursor cell proliferation
X	5891394	C	T	(CG5966)	9.11E-05	0.075	0.088	0.031	0.053	7.50E-01	NA
X	5929941	A	G	rux	9.56E-05	0.332	0.381	0.393	0.305	2.71E-01	mitotic cell cycle;nucleus;regulation of mitotic nuclear division;regulation of exit from mitosis;eye-antennal disc morphogenesis;regulation of meiotic nuclear division;compound eye development;regulation of cell cycle

X	6549545	G	A	l(1)G0148	1.02E-04	0.965	0.983	0.988	0.956	7.28E-02	protein serine/threonine kinase activity;obsolete signal transducer
X	6689046	T	C	C3G	6.98E-05	0.035	0.057	0.105	0.048	NA	Ras guanyl-nucleotide exchange factor activity;intracellular;Ras protein signal transduction;somatic muscle development;muscle attachment;Rap guanyl-nucleotide exchange factor activity;NA;sarcomere organization
X	8907108	A	G	rdgA	1.36E-04	0.077	0.052	0.092	0.023	4.05E-01	NAD+ kinase activity;diacylglycerol kinase activity;microtubule associated complex;phosphatidic acid biosynthetic process;phosphatidylinositol biosynthetic process;actin filament organization;protein kinase C-activating G protein-coupled receptor signaling pathway;visual perception;phototransduction;sensory perception of sound;sensory perception of smell;metabolic process;membrane;rhodopsin mediated signaling pathway;deactivation of rhodopsin mediated signaling;phosphorylation;diacylglycerol binding;intracellular signal transduction;thermotaxis;photoreceptor cell maintenance;lipid phosphorylation
X	8907110	T	C	rdgA	8.00E-05	0.062	0.053	0.092	0.023	3.89E-01	NAD+ kinase activity;diacylglycerol kinase activity;microtubule associated complex;phosphatidic acid biosynthetic process;phosphatidylinositol biosynthetic process;actin filament organization;protein kinase C-activating G protein-coupled receptor signaling pathway;visual perception;phototransduction;sensory perception of sound;sensory perception of smell;metabolic process;membrane;rhodopsin mediated signaling pathway;deactivation of rhodopsin mediated signaling;phosphorylation;diacylglycerol binding;intracellular signal transduction;thermotaxis;photoreceptor cell maintenance;lipid phosphorylation

X	8907115	G	A	rdgA	1.40E-04	0.083	0.052	0.093	0.023	5.38E-01	NAD+ kinase activity;diacylglycerol kinase activity;microtubule associated complex;phosphatidic acid biosynthetic process;phosphatidylinositol biosynthetic process;actin filament organization;protein kinase C-activating G protein-coupled receptor signaling pathway;visual perception;phototransduction;sensory perception of sound;sensory perception of smell;metabolic process;membrane;rhodopsin mediated signaling pathway;deactivation of rhodopsin mediated signaling;phosphorylation;diacylglycerol binding;intracellular signal transduction;thermotaxis;photoreceptor cell maintenance;lipid phosphorylation
X	9803147	C	G	(CG1986)	1.15E-04	0.143	0.128	0.057	0.105	3.70E-01	NA
X	1E+07	C	T	CG1628	1.46E-04	0.035	0.039	0.078	0.042	6.37E-01	L-ornithine transmembrane transporter activity;NA;amino acid transmembrane transport;mitochondrial envelope;mitochondrial inner membrane;amino acid transmembrane transporter activity;transmembrane transporter activity
X	1.2E+07	A	T	CR32661	7.83E-05	0.099	0.077	0.027	0.095	4.13E-01	
X	1.4E+07	T	A	tRNA:S474:12E	1.16E-04	0.115	0.114	0.142	0.087	4.31E-01	NA
X	1.5E+07	G	A	(Grip128)	7.12E-05	0.290	0.273	0.222	0.306	2.48E-01	NA
X	1.7E+07	C	A	(CG12998)	9.04E-05	0.019	0.014	0.014	0.052	4.44E-01	NA
X	1.7E+07	A	G	(B-H2-CR43491)	3.95E-05	0.513	0.530	0.589	0.500	8.13E-01	NA
X	1.8E+07	A	C	(RhoGAPp190)	1.20E-05	0.251	0.263	0.199	0.317	7.94E-01	NA
X	1.8E+07	A	G	CG15056	1.34E-04	0.026	0.021	0.012	0.043	NA	G2/M transition of mitotic cell cycle;ubiquitin-protein transferase activity;ubiquitin-dependent protein catabolic process;SCF ubiquitin ligase complex;positive regulation of BMP signaling pathway;SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
X	1.8E+07	G	A	CG6361	8.68E-05	0.047	0.049	0.013	0.044	1.58E-01	serine-type endopeptidase activity;proteolysis;regulation of melanization defense response
X	1.8E+07	G	T	CG15042	2.20E-05	0.424	0.423	0.447	0.351	7.57E-01	

X	1.9E+07	A	G	CCKLR-17D1	2.82E-05	0.078	0.061	0.050	0.016	1.49E-01	G protein-coupled receptor activity;cholecystokinin receptor activity;integral component of plasma membrane;response to stress;G protein-coupled receptor signaling pathway;positive regulation of cytosolic calcium ion concentration;neuropeptide signaling pathway;neuromuscular junction development;neuropeptide receptor activity;adult locomotory behavior;larval locomotory behavior;gastrin receptor activity;integral component of membrane;neuronal cell body;terminal bouton
X	2.1E+07	T	C	CG34120	1.88E-05	0.059	0.086	0.094	0.056	5.49E-02	transporter activity;ATP binding;transport;ATPase activity
X	2.1E+07	T	C	(CG32822)	2.36E-05	0.044	0.031	0.015	0.050	3.46E-01	NA
X	2.2E+07	C	T	(DIP1)	7.27E-05	0.314	0.290	0.231	0.341	NA	NA

chrm	pos	ref	alt	gene	p.At_Lb	p.cli	concord	afMean.Founder	afMean.No-Ad	afMean.At	afMean.Lb	GO terms
2L	9209955	G	C	tai	6.31E-03	9.50E-09	FALSE	0.033	0.034	0.021	0.052	nucleus;regulation of transcription; DNA-templated;border follicle cell migration;nuclear receptor binding;nuclear receptor transcription coactivator activity;cellular response to hormone stimulus;nuclear hormone receptor binding;steroid hormone receptor binding;positive regulation of growth;positive regulation of transcription by RNA polymerase II;protein dimerization activity;axon extension;germ-line stem-cell niche homeostasis;positive regulation of border follicle cell migration
2L	14353549	G	T	l(2)34Fd	7.46E-03	3.53E-09	TRUE	0.159	0.209	0.247	0.185	maturation of SSU-rRNA from tricistronic rRNA transcript;nucleolus;small-subunit processome
2R	738754	G	A	(CG14464)	6.47E-03	8.21E-12	FALSE	0.844	0.723	0.702	0.650	NA
3R	10964114	G	A	CG3984	2.28E-03	1.45E-09	TRUE	0.231	0.187	0.267	0.210	
3R	12086524	G	C	(tara)	7.86E-03	4.97E-10	FALSE	0.342	0.363	0.326	0.402	NA
3R	12254580	G	T	(tRNA:CR31497)	5.88E-03	1.21E-10	TRUE	0.073	0.115	0.121	0.047	NA

3R	12275145	A	T	Pak3	4.01E-03	7.48E-10	TRUE	0.044	0.053	0.065	0.021	activity;ATP binding;cytoplasm;protein phosphorylation;actin filament organization;myoblast fusion;cell migration;signal transduction by protein phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;protein homodimerization activity;regulation of MAPK cascade;protein autophosphorylation;Rac GTPase binding;regulation of axonogenesis;positive regulation of synapse assembly

3R	12787654	T	G	Abd-B	1.04E-03	7.47E-09	TRUE	0.168	0.152	0.166	0.081	transcription regulatory region sequence-specific DNA binding; RNA polymerase II distal enhancer sequence-specific DNA binding;pole cell migration;segment specification;specification of segmental identity; abdomen;open tracheal system development;salivary gland development;imaginal disc-derived genitalia development;midgut development;gonadal mesoderm development;heart development;sex differentiation;negative regulation of female receptivity;germ cell migration;male gonad development;negative regulation of cardioblast cell fate specification;male genitalia development;female genitalia development;genital disc development;genital disc anterior/posterior pattern formation;determination of genital disc primordium;external genitalia morphogenesis;genital disc sexually dimorphic development;spiracle morphogenesis; open tracheal system;negative regulation of salivary
3R	12811795	T	C	CG18622	1.52E-03	6.40E-09	TRUE	0.027	0.046	0.064	0.033	
3R	12835934	T	C	CG8907	6.88E-03	3.48E-09	TRUE	0.444	0.403	0.439	0.319	**actin binding**;plasma membrane;Rho protein signal transduction;Rac guanyl-nucleotide exchange factor activity;regulation of Rho protein signal transduction;olfactory behavior;synapse

3R	12900510	G	A	Keap1	9.85E-03	3.82E-13	TRUE	0.134	0.187	0.252	0.155	**actin binding**;nucleus;polytene chromosome puff;response to oxidative stress;protein homodimerization activity;protein autoubiquitination
3R	12900525	G	T	Keap1	2.81E-03	5.17E-13	TRUE	0.130	0.192	0.249	0.166	**actin binding**;nucleus;polytene chromosome puff;response to oxidative stress;protein homodimerization activity;protein autoubiquitination
3R	12922911	T	A	cher	5.58E-03	4.38E-09	TRUE	0.692	0.696	0.615	0.685	mitotic cell cycle;**actin binding**;actin filament;actin assembly;actin cytoskeleton;female germline ring canal formation;cytoplasmic transport;nurse cell to oocyte;long-term memory;motor neuron axon guidance;protein localization;determination of adult lifespan;Z disc;germarium-derived female germ-line cyst encapsulation;negative regulation of lamellocyte differentiation;apical cortex;sarcomere organization;behavioral response to ethanol;perinuclear region of cytoplasm;positive regulation of cytoskeleton organization;contractile ring
3R	12950403	T	C	(CG31269)	2.55E-03	1.50E-09	TRUE	0.030	0.055	0.072	0.024	NA
3R	13636748	A	G	CG18012	2.09E-03	1.70E-10	TRUE	0.074	0.065	0.094	0.046	
3R	14009775	C	T	CG7208	2.11E-04	5.70E-14	TRUE	0.064	0.068	0.073	0.026	
3R	14193535	C	T	Nup43	4.48E-03	4.42E-09	TRUE	0.074	0.086	0.111	0.035	mitotic cell cycle;nuclear pore outer ring

3R	14490730	C	A	Gos28	5.01E-03	2.66E-10	TRUE	0.066	0.069	0.124	0.085	Golgi trans cisterna;Golgi membrane;SNAP receptor activity;Golgi medial cisterna;cis-Golgi network;endoplasmic reticulum to Golgi vesicle-mediated transport;intra-Golgi vesicle-mediated transport;vesicle fusion;membrane;integral component of membrane;vesicle-mediated transport;SNARE complex;Golgi vesicle transport;regulation of vesicle targeting
3R	14647260	T	G	CG18208	4.06E-03	3.99E-10	TRUE	0.091	0.135	0.162	0.119	
3R	15874531	T	A	CG17193	1.24E-03	4.96E-09	TRUE	0.220	0.258	0.339	0.239	
3R	16514202	T	A	(Oamb)	3.77E-03	2.35E-09	TRUE	0.138	0.150	0.213	0.086	NA
3R	17066761	A	T	(e)	3.25E-03	3.04E-11	TRUE	0.197	0.222	0.237	0.131	NA
3R	17941912	T	A	Ir94b	6.93E-03	3.80E-09	TRUE	0.045	0.067	0.065	0.028	detection of chemical stimulus;ligand-gated ion channel activity;integral component of membrane

3R	19013520	T	A	cnc	8.34E-03	2.39E-09	TRUE	0.050	0.057	0.062	0.014	DNA binding;DNA-binding transcription factor activity;nucleus;polytene chromosome puff;response to oxidative stress;oocyte dorsal/ventral axis specification;regulation of pole plasm oskar mRNA localization;blastoderm segmentation;oocyte microtubule cytoskeleton polarization;determination of adult lifespan;regulation of bicoid mRNA localization;response to endoplasmic reticulum stress;intestinal stem cell homeostasis;bicoid mRNA localization;pole plasm oskar mRNA localization;positive regulation of transcription by RNA polymerase II;protein heterodimerization activity;dendrite morphogenesis;oocyte nucleus localization involved in oocyte dorsal/ventral axis specification;head development;pharynx development

3R	19696100	T	A	Pli	2.67E-03	7.07E-09	TRUE	0.059	0.078	0.111	0.046	protein polyubiquitination;positive regulation of antimicrobial peptide production;ubiquitin-protein transferase activity;protein binding;cytosol;Toll signaling pathway;cytoplasmic side of plasma membrane;kinase regulator activity;innate immune response;negative regulation of Toll signaling pathway;positive regulation of Toll signaling pathway;ubiquitin protein ligase activity;protein K48-linked ubiquitination;negative regulation of defense response to bacterium;negative regulation of antifungal innate immune response
3R	19965402	A	C	Npc2f	1.01E-03	1.15E-12	TRUE	0.028	0.030	0.055	0.025	sterol transport;intracellular cholesterol transport;sterol binding
3R	19979636	C	T	CG6178	2.40E-03	4.06E-12	TRUE	0.039	0.062	0.078	0.026	long-chain fatty acid metabolic process;fatty-acyl-CoA synthase activity;long-chain fatty acid-CoA ligase activity;peroxisome;fatty acid biosynthetic process;acyl-CoA metabolic process;fatty acid ligase activity;CoA-ligase activity;luciferin monooxygenase activity;fatty-acyl-CoA biosynthetic process
3R	19979912	G	A	CG6178	2.16E-03	9.63E-11	TRUE	0.044	0.065	0.073	0.029	long-chain fatty acid metabolic process;fatty-acyl-CoA synthase activity;long-chain fatty acid-CoA ligase activity;peroxisome;fatty acid biosynthetic process;acyl-CoA metabolic process;fatty acid ligase activity;CoA-ligase activity;luciferin monooxygenase activity;fatty-acyl-CoA biosynthetic process
3R	20077768	A	G	CG5706	8.69E-03	1.59E-12	TRUE	0.076	0.096	0.097	0.054	

3R	20165522	G	A	CG6432	6.77E-03	6.70E-11	FALSE	0.477	0.412	0.379	0.498	catalytic activity;fatty acid biosynthetic process;short-chain fatty acid-CoA ligase activity
3R	20165558	C	G	CG6432	2.18E-03	4.17E-11	FALSE	0.457	0.465	0.454	0.533	catalytic activity;fatty acid biosynthetic process;short-chain fatty acid-CoA ligase activity
3R	20341694	C	T	CG13617	6.59E-03	1.47E-09	TRUE	0.044	0.063	0.071	0.020	nucleic acid binding;cytoplasm;ciliary basal body;cilium assembly
3R	20570027	T	G	tok	4.36E-03	1.74E-11	TRUE	0.246	0.347	0.350	0.211	metalloendopeptidase activity;calcium ion binding;axon guidance;defasciculation of motor neuron axon;motor neuron axon guidance;zinc ion binding;imaginal disc-derived wing vein morphogenesis;negative regulation of gene expression;protein processing
3R	20653990	G	T	(niki)	5.51E-03	9.57E-11	FALSE	0.053	0.058	0.034	0.084	NA
3R	22886860	G	T	Nep5	3.52E-03	2.54E-09	FALSE	0.413	0.437	0.403	0.448	metalloendopeptidase activity;proteolysis;metallopeptidase activity;integral component of membrane