

chrM	pos	ref	alt	gene	afMean					p.clinality	GOterm
					p.At-Lb_div	.Founde r	afMean .NoAd	afMean .At	afMean .Lb		
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 follicle cell
2L	469463	C	A	(MED15)	7.30E-05	0.124	0.142	0.121	0.068	1.11E-01	development;positive regulation of autophagy
2L	1101026	C	G	CG4629	1.40E-05	0.442	0.416	0.285	0.471	6.94E-01	NA 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 store-operated calcium entry;sensory perception of chemical stimulus
2L	2087653	A	G	dpr3	6.96E-05	0.412	0.434	0.463	0.299	1.67E-01	
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	tutI	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; pristineregulation 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 calmodulin binding;cytoplasm;response to oxidative stress;inositol-1
2L	9783859	G	C	IP3K1	1.19E-04	0.173	0.139	0.118	0.185	3.62E-01	NA
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

											serine-type endopeptidase activity;proteolysis;carboxylic ester hydrolase activity;serine-type exopeptidase activity
2L	1E+07	G	A	CG5355	2.90E-06	0.041	0.035	0.029	0.070	7.65E-01	
2L	1.2E+07	A	T	(CG31706)	2.85E-05	0.099	0.122	0.144	0.077	NA	NA
											calcium- and calmodulin-regulated 3',5'-cyclic-AMP/GMP phosphodiesterase activity; calmodulin binding; male mating behavior; signal transduction
2L	1.2E+07	T	A	Pde1c	7.77E-05	0.242	0.206	0.237	0.176	8.84E-01	
											nucleotide binding;RNA binding;mRNA binding;negative regulation of translation
2L	1.2E+07	G	A	bru-2	1.25E-04	0.040	0.054	0.072	0.010	1.10E-01	
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
											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	A	rk	4.75E-05	0.634	0.705	0.599	0.757	9.03E-01	
											acetylcholine-gated cation-selective channel activity;transmembrane signaling receptor;cation transport;chemical synaptic transmission;ion transmembrane transport;nervous system process;regulation of membrane potential
2L	1.4E+07	G	T	αAcRalpha-34I	7.24E-05	0.040	0.037	0.012	0.054	4.39E-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
2L	1.5E+07	C	T	GABA-B-R1	1.39E-04	0.158	0.231	0.158	0.253	5.37E-01	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-la)	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
											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
2L	1.6E+07	C	T	Ca-alpha1D	5.70E-06	0.170	0.159	0.251	0.122	2.63E-01	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	
											cation channel activity;mechanosensitive ion channel activity;calcium channel activity;inositol 1,4,5 triphosphate binding;adult walking behavior;neuromuscular process controlling posture
2L	1.7E+07	G	A	trpgamma	4.10E-06	0.640	0.673	0.599	0.668	1.67E-03	
2L	1.8E+07	T	C	(CR43304)	1.45E-04	0.062	0.110	0.091	0.147	NA	NA

											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	A	C	CadN2	1.27E-07	0.279	0.321	0.370	0.199	6.71E-01	NA
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
											proteolysis;metalloexopeptidase activity;dipeptidyl-peptidase activity;dipeptidase activity
2L	1.8E+07	A	G	CG42750	4.44E-05	0.013	0.032	0.027	0.078	3.08E-01	NA
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	
											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	G	A	Ddc	6.03E-05	0.512	0.534	0.512	0.587	7.52E-02	

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;halter 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;halter 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
											DNA-binding transcription factor
2R	4237786	A	G	pdm3	1.49E-04	0.027	0.028	0.019	0.062	5.67E-01	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
											integral component of membrane;transmembrane
2R	5046734	G	C	CG8008	1.23E-04	0.554	0.473	0.440	0.570	2.02E-01	transport
											extracellular region;vitelline membrane formation
											involved in chorion-containing eggshell
											formation;terminal region determination;torso
2R	5486967	C	T	clos	4.55E-05	0.334	0.377	0.320	0.406	4.07E-03	signaling pathway
											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
2R	5941384	T	C	magu	1.13E-04	0.417	0.456	0.403	0.587	5.12E-04	size
											potassium channel activity;potassium ion
											transport;calcium-activated potassium channel
											activity;membrane;neurogenesis;neuron
2R	6289071	A	C	CG42732	1.10E-04	0.143	0.154	0.143	0.241	2.11E-01	projection morphogenesis
											cytoplasm;cytoskeleton organization;receptor
											signaling pathway via JAK-STAT;ovarian follicle
											cell-cell adhesion;Ran GTPase binding;larval
											feeding behavior;dorsal appendage
2R	6321928	C	T	RanBPM	1.13E-05	0.091	0.116	0.092	0.129	6.93E-02	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

											myosuppressin receptor activity;G protein-coupled receptor activity;neuropeptide receptor activity;adult locomotory behavior
3L	2327513	T	C	DmsR-1	7.35E-05	0.217	0.223	0.226	0.282	NA	NA
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
											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	4404707	A	G	Syx17	5.37E-05	0.589	0.581	0.667	0.500	1.52E-02	NA
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
											serine-type endopeptidase activity;extracellular region;proteolysis;eggshell chorion assembly;oocyte dorsal/ventral axis specification;maternal specification of dorsal/ventral axis
3L	6590431	A	G	ndl	1.23E-04	0.117	0.099	0.153	0.105	NA	integral component of membrane;transmembrane transport
3L	7335246	G	A	CG8596	3.16E-05	0.109	0.077	0.099	0.141	8.79E-05	NA
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	NA
3L	8318762	G	C	(CG34461)	4.52E-05	0.462	0.342	0.432	0.317	8.96E-01	NA
											cytoplasm;lipid metabolic process;integral component of membrane;oxidoreductase activity
3L	8606593	T	G	CG6282	7.18E-05	0.224	0.237	0.115	0.200	9.25E-01	NA
3L	8688265	G	A	(h)	1.04E-04	0.046	0.051	0.052	0.022	3.73E-01	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/M1 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	8843663	C	T	dally	1.05E-04	0.210	0.224	0.304	0.187	NA	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	
											inorganic anion exchanger activity;anion transport;anion:anion antiporter activity;integral component of membrane
3L	9769486	G	T	CG8177	1.49E-04	0.048	0.062	0.030	0.080	8.97E-01	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

											nucleotide binding;mRNA binding;nucleus;cytoplasm;nervous system development;imaginal disc-derived wing vein specification;transcription factor binding;transcription regulatory region DNA
3L	1E+07	C	T	A2bp1	1.33E-05	0.055	0.062	0.079	0.027	1.60E-01	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	
											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	GlcAT-P	1.09E-04	0.032	0.031	0.011	0.051	6.41E-01	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
											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	C	Mob2	9.70E-05	0.068	0.100	0.050	0.134	9.23E-01	junction;cell hair;cell periphery

											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	1.2E+07	T	G	Nrx-IV	1.34E-04	0.858	0.867	0.877	0.768	3.76E-05	
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
											DNA-binding transcription factor activity;nucleus;regulation of transcription nucleus;plasma membrane;border follicle cell migration;imaginal disc development
3L	1.4E+07	A	T	Sox21b	1.39E-04	0.101	0.154	0.201	0.108	8.62E-01	
3L	1.5E+07	C	A	bbg	1.27E-04	0.063	0.050	0.021	0.046	9.38E-01	
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
											protein serine/threonine kinase activity;ATP binding;protein phosphorylation;protein N-linked glycosylation;neuromuscular junction development
3L	1.6E+07	C	A	sff	8.40E-05	0.126	0.136	0.155	0.084	8.88E-01	
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 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	5950686	A	G	knk	1.22E-04	0.053	0.116	0.156	0.079	2.48E-04	NA
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	voltage-gated chloride channel activity;chloride channel activity;chloride transport;actin cytoskeleton;membrane;adenyl nucleotide binding;transmembrane transport
3R	7634750	G	A	ClC-a	2.83E-05	0.026	0.039	0.011	0.045	4.50E-01	NA
3R	7982089	G	C	dpr15	8.24E-05	0.097	0.175	0.192	0.140	1.28E-02	sensory perception of chemical stimulus

											calcium ion binding;nucleus;cytoplasm;mitochondrion;rough endoplasmic reticulum;rhabdomere;axon;rhabdomere
3R	7990369	G	C	Cpn	5.55E-05	0.041	0.056	0.055	0.013	1.65E-01	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	
											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 smoothed signaling pathway;positive regulation of JNK cascade;lateral inhibition;eye morphogenesis
3R	9820259	C	G	rdx	8.81E-05	0.261	0.267	0.263	0.189	6.85E-01	
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
											Golgi membrane;alpha-mannosidase activity;mannosyl-oligosaccharide 1
											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	1.2E+07	T	G	ss	7.25E-05	0.081	0.084	0.054	0.107	8.52E-05	
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 protein kinase activity;ATP binding;protein phosphorylation;phosphatidylinositol binding;neuron projection morphogenesis
3R	1.4E+07	G	T	CG7156	1.25E-04	0.085	0.150	0.130	0.189	1.57E-04	biological_process
3R	1.5E+07	T	A	CG42613	1.55E-05	0.193	0.248	0.300	0.245	NA	single strand break repair;mRNA splicing
3R	1.5E+07	A	G	CG5316	1.50E-04	0.169	0.137	0.210	0.148	8.88E-01	transcription regulatory region sequence-specific DNA binding;DNA-binding transcription factor activity;nucleus;regulation of transcription
3R	1.6E+07	C	T	mun	9.40E-05	0.389	0.394	0.300	0.412	1.39E-01	calcium ion binding;NA;signal transduction metalloendopeptidase activity;proteolysis;zinc ion binding;meprin A complex
3R	1.7E+07	T	G	lbl	3.71E-05	0.735	0.655	0.658	0.771	2.22E-01	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	1.9E+07	A	G	CG13830	1.22E-04	0.339	0.311	0.354	0.255	NA	NA
3R	1.9E+07	T	C	CG6763	8.94E-05	0.552	0.532	0.493	0.684	1.49E-02	NA
3R	2E+07	A	G	mbc	2.21E-05	0.795	0.713	0.741	0.645	NA	NA
3R	2E+07	T	A	(Esys2)	1.03E-04	0.323	0.320	0.315	0.219	7.54E-01	DNA-binding transcription factor activity;regulation of transcription
3R	2E+07	G	A	CG13624	1.00E-04	0.257	0.313	0.196	0.333	3.76E-02	transferase activity
3R	2.1E+07	T	A	CG31370	4.07E-05	0.090	0.065	0.109	0.052	7.04E-01	mitochondrial envelope;transmembrane transporter activity;transmembrane transport
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
											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	A	C	Gprk2	5.11E-05	0.753	0.786	0.799	0.720	3.86E-01	mitotic spindle elongation;structural constituent of ribosome;ribosome;translation;mitotic spindle organization;cytosolic large ribosomal subunit;NA;centrosome duplication
3R	2.7E+07	G	A	RpL6	4.20E-06	0.424	0.387	0.375	0.430	1.76E-02	
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 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	2381099	A	G	trol	4.18E-05	0.312	0.289	0.205	0.358	2.51E-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	2461125	A	G	Pdfr	3.54E-05	0.022	0.045	0.012	0.056	8.26E-01	ubiquitin-protein transferase activity;nucleus;ubiquitin-dependent protein catabolic process;multicellular organism development;zinc ion binding;protein ubiquitination
X	2602978	C	A	CG2681	8.94E-05	0.313	0.335	0.376	0.317	7.48E-02	
X	3326693	G	A	CG12535	2.43E-06	0.026	0.018	0.013	0.045	2.64E-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	5495935	G	T	Vsx1	1.43E-04	0.055	0.038	0.013	0.053	2.81E-01	
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

											L-ornithine transmembrane transporter activity;NA;amino acid transmembrane transport;mitochondrial envelope;mitochondrial inner membrane;amino acid transmembrane transporter activity;transmembrane transporter activity
X	1E+07	C	T	CG1628	1.46E-04	0.035	0.039	0.078	0.042	6.37E-01	
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	RNA: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
											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	A	G	CG15056	1.34E-04	0.026	0.021	0.012	0.043	NA	serine-type endopeptidase activity;proteolysis;regulation of melanization
X	1.8E+07	G	A	CG6361	8.68E-05	0.047	0.049	0.013	0.044	1.58E-01	defense response
X	1.8E+07	G	T	CG15042	2.20E-05	0.424	0.423	0.447	0.351	7.57E-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	1.9E+07	A	G	CCKLR-17D1	2.82E-05	0.078	0.061	0.050	0.016	1.49E-01	

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