

chrM	pos	ref	alt	gene	p.At_Lb	p.cli	concord	afMean			GO terms	
								.Found	afMean	afMean		
								.No-Ad	.At	.Lb		
											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	
2L	9209955	G	C	tai	6.31E-03	9.50E-09	FALSE	0.033	0.034	0.021	0.052	border follicle cell migration
2L	14353549	G	T	l(2)34Fd (CG1446	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	4)	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:CR 31497)	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	ruffle;protein serine/threonine kinase 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
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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 gland boundary specification; negative
3R	12811795	T	C	CG18622	1.52E-03	6.40E-09	TRUE	0.027	0.046	0.064	0.033	<b>actin binding</b> ; plasma membrane; Rho protein signal transduction; Rac guanylnucleotide exchange factor activity; regulation of Rho protein signal transduction; olfactory behavior; synapse
3R	12835934	T	C	CG8907	6.88E-03	3.48E-09	TRUE	0.444	0.403	0.439	0.319	

3R	12900510	G	A	Keap1	9.85E-03	3.82E-13	TRUE	0.134	0.187	0.252	0.155	<b>actin binding</b> ;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	<b>actin binding</b> ;nucleus;polytene chromosome puff;response to oxidative stress;protein homodimerization activity;protein autoubiquitination mitotic cell cycle; <b>actin binding</b> ;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	12922911	T	A	cher (CG3126	5.58E-03	4.38E-09	TRUE	0.692	0.696	0.615	0.685	ring
3R	12950403	T	C	9)	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

												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	14490730	C	A	Gos28	5.01E-03	2.66E-10	TRUE	0.066	0.069	0.124	0.085	
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
												detection of chemical stimulus;ligand-gated ion channel activity;integral component of membrane
3R	17941912	T	A	Ir94b	6.93E-03	3.80E-09	TRUE	0.045	0.067	0.065	0.028	

3R	19013520	T	A	cnc	8.34E-03	2.39E-09	TRUE	0.050	0.057	0.062	0.014	<p>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</p> <p>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</p>
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												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 sterol transport;intracellular cholesterol transport;sterol binding
3R	19696100	T	A	Pli	2.67E-03	7.07E-09	TRUE	0.059	0.078	0.111	0.046	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	19965402	A	C	Npc2f	1.01E-03	1.15E-12	TRUE	0.028	0.030	0.055	0.025	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	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 metalloendopeptidase activity;calcium ion binding;axon guidance;defasciculation of motor neuron axon;motor neuron axon guidance;zinc ion binding;imaginal disc-derived wing vein
3R	20570027	T	G	tok	4.36E-03	1.74E-11	TRUE	0.246	0.347	0.350	0.211	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 metalloendopeptidase activity;proteolysis;metallopeptidase activity;integral component of membrane
3R	22886860	G	T	Nep5	3.52E-03	2.54E-09	FALSE	0.413	0.437	0.403	0.448	