

TABLE S5**Significantly-enriched Gene Ontology categories in top 2.5% 1kb F_{ST} regions.**

Biological Process		
GO accession	P-value	Description
GO:0007424	2.49E-09	open tracheal system development
GO:0007428	1.56E-06	primary branching, open tracheal system
GO:0007165	1.56E-06	signal transduction
GO:0007427	1.56E-06	epithelial cell migration, open tracheal system
GO:0002121	2.21E-06	inter-male aggressive behavior
GO:0007509	2.62E-06	mesoderm migration
GO:0042051	2.62E-06	compound eye photoreceptor development
GO:0006355	3.91E-06	regulation of transcription, DNA-dependent
GO:0007156	1.37E-05	homophilic cell adhesion
GO:0048477	1.78E-05	oogenesis
GO:0007435	1.78E-05	salivary gland morphogenesis
GO:0007507	1.82E-05	heart development
GO:0008543	2.13E-05	fibroblast growth factor receptor signaling pathway
GO:0035152	4.50E-05	regulation of tube architecture, open tracheal system
GO:0007614	8.48E-05	short-term memory
GO:0006816	8.48E-05	calcium ion transport
GO:0007431	1.54E-04	salivary gland development
GO:0007155	1.70E-04	cell adhesion
GO:0016044	2.50E-04	membrane organization
GO:0007293	4.51E-04	germarium-derived egg chamber formation
GO:0007411	4.51E-04	axon guidance
GO:0042048	4.51E-04	olfactory behavior
GO:0030707	4.51E-04	ovarian follicle cell development
GO:0008101	4.87E-04	decapentaplegic receptor signaling pathway
GO:0045570	4.87E-04	regulation of imaginal disc growth
GO:0035172	4.87E-04	hemocyte proliferation
GO:0007443	4.88E-04	Malpighian tubule morphogenesis
GO:0048813	4.88E-04	dendrite morphogenesis
GO:0048190	5.67E-04	wing disc dorsal/ventral pattern formation
GO:0007422	7.20E-04	peripheral nervous system development
GO:0016055	7.20E-04	Wnt receptor signaling pathway
GO:0007611	7.20E-04	learning or memory
GO:0007426	1.12E-03	tracheal outgrowth, open tracheal system
GO:0006813	1.21E-03	potassium ion transport
GO:0007517	1.32E-03	muscle organ development
GO:0048066	1.52E-03	pigmentation during development
GO:0007297	1.52E-03	ovarian follicle cell migration
GO:0048675	1.52E-03	axon extension

GO:0006811	1.67E-03	ion transport
GO:0007476	1.68E-03	imaginal disc-derived wing morphogenesis
GO:0030718	1.72E-03	germ-line stem cell maintenance
GO:0007619	2.08E-03	courtship behavior
GO:0045449	2.19E-03	regulation of transcription
GO:0007379	2.38E-03	segment specification
GO:0007417	3.00E-03	central nervous system development
GO:0007399	3.00E-03	nervous system development
GO:0030097	3.15E-03	hemopoiesis
GO:0007274	3.15E-03	neuromuscular synaptic transmission
GO:0007265	3.15E-03	Ras protein signal transduction
GO:0042078	3.15E-03	germ-line stem cell division
GO:0016199	3.46E-03	axon midline choice point recognition
GO:0007602	3.46E-03	phototransduction
GO:0048666	3.54E-03	neuron development
GO:0008355	3.91E-03	olfactory learning
GO:0008407	4.18E-03	bristle morphogenesis
GO:0016477	4.18E-03	cell migration
GO:0016339	4.96E-03	calcium-dependent cell-cell adhesion
GO:0055085	5.47E-03	transmembrane transport
GO:0008063	5.77E-03	Toll signaling pathway
GO:0008354	5.77E-03	germ cell migration
GO:0006357	6.28E-03	regulation of transcription from RNA polymerase II promoter
GO:0035147	6.60E-03	branch fusion, open tracheal system
GO:0008344	6.60E-03	adult locomotory behavior
GO:0009953	6.60E-03	dorsal/ventral pattern formation
GO:0035277	6.60E-03	spiracle morphogenesis, open tracheal system
GO:0006325	6.93E-03	chromatin organization
GO:0007494	6.93E-03	midgut development
GO:0002009	6.93E-03	morphogenesis of an epithelium
GO:0006468	8.66E-03	protein amino acid phosphorylation
GO:0019991	8.81E-03	septate junction assembly
GO:0007442	8.81E-03	hindgut morphogenesis
GO:0007291	8.81E-03	sperm individualization
GO:0007294	8.81E-03	germarium-derived oocyte fate determination
GO:0035071	9.76E-03	salivary gland cell autophagic cell death
GO:0007298	9.76E-03	border follicle cell migration
GO:0008104	1.11E-02	protein localization
GO:0000381	1.11E-02	regulation of alternative nuclear mRNA splicing, via spliceosome
GO:0017148	1.11E-02	negative regulation of translation
GO:0051225	1.11E-02	spindle assembly

GO:0001745	1.11E-02	compound eye morphogenesis
GO:0008360	1.12E-02	regulation of cell shape
GO:0007391	1.18E-02	dorsal closure
GO:0007498	1.35E-02	mesoderm development
GO:0007179	1.42E-02	transforming growth factor beta receptor signaling pathway
GO:0007350	1.42E-02	blastoderm segmentation
GO:0016481	1.45E-02	negative regulation of transcription
GO:0001700	1.49E-02	embryonic development via the syncytial blastoderm
GO:0007409	1.79E-02	axonogenesis
GO:0030162	1.80E-02	regulation of proteolysis
GO:0048749	1.95E-02	compound eye development
GO:0007018	1.95E-02	microtubule-based movement
GO:0007268	1.98E-02	synaptic transmission
GO:0007275	2.04E-02	multicellular organismal development
GO:0035023	2.20E-02	regulation of Rho protein signal transduction
GO:0007367	2.20E-02	segment polarity determination
GO:0006911	2.50E-02	phagocytosis, engulfment
GO:0048102	2.57E-02	autophagic cell death
GO:0009987	2.72E-02	cellular process
GO:0006096	2.82E-02	glycolysis
GO:0016318	3.31E-02	ommatidial rotation
GO:0008045	3.31E-02	motor axon guidance
GO:0030036	3.80E-02	actin cytoskeleton organization
GO:0046843	3.82E-02	dorsal appendage formation
GO:0045475	3.82E-02	locomotor rhythm
GO:0006342	3.82E-02	chromatin silencing
GO:0051726	3.82E-02	regulation of cell cycle
GO:0007474	3.82E-02	imaginal disc-derived wing vein specification
GO:0006350	3.82E-02	transcription
GO:0007186	4.03E-02	G-protein coupled receptor protein signaling pathway
GO:0000122	4.78E-02	negative regulation of transcription from RNA polymerase II promoter

Molecular Function

GO accession	P-value	Description
GO:0005515	1.57E-08	protein binding
GO:0003700	8.12E-07	transcription factor activity
GO:0005509	1.93E-04	calcium ion binding
GO:0004889	3.64E-04	nicotinic acetylcholine-activated cation-selective channel activity
GO:0003729	3.64E-04	mRNA binding
GO:0003702	3.64E-04	RNA polymerase II transcription factor activity
GO:0004871	3.64E-04	signal transducer activity

GO:0043565	8.02E-04	sequence-specific DNA binding
GO:0008188	1.87E-03	neuropeptide receptor activity
GO:0003704	1.89E-03	specific RNA polymerase II transcription factor activity
GO:0003777	3.08E-03	microtubule motor activity
GO:0005096	5.38E-03	GTPase activator activity
GO:0016566	5.92E-03	specific transcriptional repressor activity
GO:0016563	6.18E-03	transcription activator activity
GO:0005249	7.73E-03	voltage-gated potassium channel activity
GO:0003723	8.11E-03	RNA binding
GO:0003779	9.12E-03	actin binding
GO:0004888	1.02E-02	transmembrane receptor activity
GO:0005085	1.02E-02	guanyl-nucleotide exchange factor activity
GO:0008270	1.20E-02	zinc ion binding
GO:0003676	1.27E-02	nucleic acid binding
GO:0003730	1.64E-02	mRNA 3'-UTR binding
GO:0000166	1.68E-02	nucleotide binding
GO:0016251	2.52E-02	general RNA polymerase II transcription factor activity
GO:0016887	2.52E-02	ATPase activity
GO:0004725	2.97E-02	protein tyrosine phosphatase activity
GO:0005089	3.17E-02	Rho guanyl-nucleotide exchange factor activity
GO:0005524	3.65E-02	ATP binding
GO:0004674	3.67E-02	protein serine/threonine kinase activity
GO:0042623	3.67E-02	ATPase activity, coupled
GO:0005102	3.67E-02	receptor binding
GO:0004930	4.02E-02	G-protein coupled receptor activity
GO:0005516	4.16E-02	calmodulin binding
GO:0003713	4.98E-02	transcription coactivator activity

Reported P-values are corrected for a false-discovery rate of 0.05.