

TABLE S6

Significantly-enriched Gene Ontology categories in top 1% 1kb copy-number variable (CNV) regions.

Biological Process		
GO accession	P-value	Description
GO:0006355	3.58E-10	regulation of transcription, DNA-dependent
GO:0007417	1.10E-08	central nervous system development
GO:0045449	6.87E-08	regulation of transcription
GO:0007507	3.73E-06	heart development
GO:0007155	1.98E-05	cell adhesion
GO:0008585	3.54E-05	female gonad development
GO:0006813	3.81E-05	potassium ion transport
GO:0048477	1.20E-04	oogenesis
GO:0001700	1.55E-04	embryonic development via the syncytial blastoderm
GO:0007399	5.02E-04	nervous system development
GO:0007304	5.70E-04	chorion-containing eggshell formation
GO:0007619	5.97E-04	courtship behavior
GO:0008587	7.14E-04	imaginal disc-derived wing margin morphogenesis
GO:0007411	7.35E-04	axon guidance
GO:0007186	8.06E-04	G-protein coupled receptor protein signaling pathway
GO:0007494	8.06E-04	midgut development
GO:0007480	9.94E-04	imaginal disc-derived leg morphogenesis
GO:0007165	1.03E-03	signal transduction
GO:0007476	1.03E-03	imaginal disc-derived wing morphogenesis
GO:0008360	1.03E-03	regulation of cell shape
GO:0045475	1.33E-03	locomotor rhythm
GO:0007422	1.39E-03	peripheral nervous system development
GO:0007224	1.53E-03	smoothened signaling pathway
GO:0048190	1.72E-03	wing disc dorsal/ventral pattern formation
GO:0042048	1.80E-03	olfactory behavior
GO:0002121	1.86E-03	inter-male aggressive behavior
GO:0007623	1.95E-03	circadian rhythm
GO:0008354	1.95E-03	germ cell migration
GO:0008104	2.26E-03	protein localization
GO:0007455	2.51E-03	eye-antennal disc morphogenesis
GO:0035023	2.87E-03	regulation of Rho protein signal transduction
GO:0016318	2.87E-03	ommatidial rotation
GO:0007400	2.87E-03	neuroblast fate determination
GO:0007015	2.96E-03	actin filament organization
GO:0008285	3.38E-03	negative regulation of cell proliferation
GO:0009987	5.31E-03	cellular process
GO:0006911	5.79E-03	phagocytosis, engulfment

GO:0016321	8.07E-03	female meiosis chromosome segregation
GO:0009790	8.83E-03	embryonic development
GO:0007419	8.83E-03	ventral cord development
GO:0048749	8.83E-03	compound eye development
GO:0007268	9.23E-03	synaptic transmission
GO:0007517	9.23E-03	muscle organ development
GO:0007163	9.23E-03	establishment or maintenance of cell polarity
GO:0008407	9.23E-03	bristle morphogenesis
GO:0016567	9.23E-03	protein ubiquitination
GO:0007498	1.17E-02	mesoderm development
GO:0006508	1.17E-02	proteolysis
GO:0006366	1.32E-02	transcription from RNA polymerase II promoter
GO:0016481	1.32E-02	negative regulation of transcription
GO:0007423	1.34E-02	sensory organ development
GO:0006350	1.42E-02	transcription
GO:0007420	1.42E-02	brain development
GO:0030707	1.71E-02	ovarian follicle cell development
GO:0007611	1.96E-02	learning or memory
GO:0030036	1.96E-02	actin cytoskeleton organization
GO:0006357	1.97E-02	regulation of transcription from RNA polymerase II promoter
GO:0016055	1.97E-02	Wnt receptor signaling pathway
GO:0007269	2.02E-02	neurotransmitter secretion
GO:0006470	2.03E-02	protein amino acid dephosphorylation
GO:0006468	2.05E-02	protein amino acid phosphorylation
GO:0007242	2.12E-02	intracellular signaling cascade
GO:0007219	2.20E-02	Notch signaling pathway
GO:0035071	2.24E-02	salivary gland cell autophagic cell death
GO:0007409	2.34E-02	axonogenesis
GO:0019730	2.34E-02	antimicrobial humoral response
GO:0000381	2.49E-02	regulation of alternative nuclear mRNA splicing, via spliceosome
GO:0007298	2.68E-02	border follicle cell migration
GO:0008355	3.04E-02	olfactory learning
GO:0000122	3.30E-02	negative regulation of transcription from RNA polymerase II promoter
GO:0016319	3.57E-02	mushroom body development
GO:0007017	4.20E-02	microtubule-based process
GO:0008283	4.71E-02	cell proliferation
GO:0006811	4.82E-02	ion transport

Molecular Function

GO accession	P-value	Description
GO:0003700	1.71E-13	transcription factor activity
GO:0005515	4.61E-13	protein binding
GO:0008270	2.69E-11	zinc ion binding
GO:0043565	7.85E-08	sequence-specific DNA binding
GO:0004879	3.69E-06	ligand-dependent nuclear receptor activity
GO:0003704	5.63E-06	specific RNA polymerase II transcription factor activity
GO:0005041	6.03E-06	low-density lipoprotein receptor activity
GO:0030528	8.75E-06	transcription regulator activity
GO:0003702	1.03E-04	RNA polymerase II transcription factor activity
GO:0008239	1.91E-04	dipeptidyl-peptidase activity
GO:0003779	1.91E-04	actin binding

GO:0003707	3.69E-04	steroid hormone receptor activity
GO:0000166	4.35E-04	nucleotide binding
GO:0016566	5.63E-04	specific transcriptional repressor activity
GO:0005249	5.95E-04	voltage-gated potassium channel activity
GO:0003729	6.33E-04	mRNA binding
GO:0004930	9.72E-04	G-protein coupled receptor activity
GO:0005089	3.13E-03	Rho guanyl-nucleotide exchange factor activity
GO:0005509	3.30E-03	calcium ion binding
GO:0004872	5.40E-03	receptor activity
GO:0004871	6.59E-03	signal transducer activity
GO:0005200	6.59E-03	structural constituent of cytoskeleton
GO:0004674	7.26E-03	protein serine/threonine kinase activity
GO:0004222	8.70E-03	metalloendopeptidase activity
GO:0042803	8.70E-03	protein homodimerization activity
GO:0008188	9.50E-03	neuropeptide receptor activity
GO:0046982	1.52E-02	protein heterodimerization activity
GO:0004725	2.36E-02	protein tyrosine phosphatase activity
GO:0005198	3.55E-02	structural molecule activity
GO:0004842	3.66E-02	ubiquitin-protein ligase activity
GO:0051082	3.66E-02	unfolded protein binding
GO:0016564	3.66E-02	transcription repressor activity
GO:0003676	4.08E-02	nucleic acid binding

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