Table S3 GO term enrichment for biological process in the Australian cline for genes that overlap windows in the top 5% tail of Fst.

	5 % Tail Biological Process	
GO term	q-value	description
GO:0046331	0.00E+00	lateral inhibition
GO:0016198	0.00E+00	axon choice point recognition
GO:0006355	4.83E-10	regulation of transcription, DNA-dependent
GO:0007156	5.44E-08	homophilic cell adhesion
GO:0007411	5.39E-07	axon guidance
GO:0006468	5.53E-07	protein amino acid phosphorylation
GO:0048190	2.06E-06	wing disc dorsal/ventral pattern formation
GO:0007611	2.06E-06	learning or memory
GO:0007476	2.67E-06	imaginal disc-derived wing morphogenesis
GO:0008284	6.75E-06	positive regulation of cell proliferation
GO:0042051	8.05E-06	compound eye photoreceptor development
GO:0008543	9.53E-06	fibroblast growth factor receptor signaling pathway
GO:0007165	1.17E-05	signal transduction
GO:0048477	3.51E-05	oogenesis
GO:0008355	4.04E-05	olfactory learning
GO:0007398	4.34E-05	ectoderm development
GO:0007424	4.98E-05	open tracheal system development
GO:0007507	5.28E-05	heart development
GO:0007498	7.16E-05	mesoderm development
GO:0001709	7.16E-05	cell fate determination
GO:0048749	7.16E-05	compound eye development
GO:0002009	7.48E-05	morphogenesis of an epithelium
GO:0007415	8.57E-05	defasciculation of motor neuron axon
GO:0007513	1.10E-04	pericardial cell differentiation
GO:0045570	1.10E-04	regulation of imaginal disc growth
GO:0007552	1.54E-04	metamorphosis
GO:0008104	1.73E-04	protein localization
GO:0007155	2.35E-04	cell adhesion
GO:0007419	2.35E-04	ventral cord development
GO:0008045	2.35E-04	motor axon guidance
GO:0007427	2.35E-04	epithelial cell migration, open tracheal system
GO:0055085	2.42E-04	transmembrane transport
GO:0007623	2.42E-04	circadian rhythm
GO:0007391	2.42E-04	dorsal closure
GO:0008406	2.46E-04	gonad development
GO:0008356	2.62E-04	asymmetric cell division
GO:0048096	2.66E-04	chromatin-mediated maintenance of transcription
GO:0035286	2.66E-04	leg segmentation
GO:0046667	2.66E-04	compound eye retinal cell programmed cell death
GO:0048814	2.66E-04	regulation of dendrite morphogenesis

GO:0045433	2.80E-04	male courtship behavior, veined wing generated song production
GO:0007275	3.42E-04	multicellular organismal development
GO:0008586	3.43E-04	imaginal disc-derived wing vein morphogenesis
GO:0007314	4.38E-04	oocyte anterior/posterior axis specification
GO:0042052	4.38E-04	rhabdomere development
GO:0008285	4.38E-04	negative regulation of cell proliferation
GO:0007413	4.87E-04	axonal fasciculation
GO:0008407	4.87E-04	bristle morphogenesis
GO:0008354	5.13E-04	germ cell migration
GO:0007435	5.78E-04	salivary gland morphogenesis
GO:0006816	6.54E-04	calcium ion transport
GO:0046620	6.77E-04	regulation of organ growth
GO:0006811	6.97E-04	ion transport
GO:0001751	7.25E-04	compound eye photoreceptor cell differentiation
GO:0042127	7.25E-04	regulation of cell proliferation
GO:0007444	7.78E-04	imaginal disc development
GO:0048100	8.18E-04	wing disc anterior/posterior pattern formation
GO:0007617	8.18E-04	mating behavior
GO:0035225	8.18E-04	determination of genital disc primordium
GO:0015012	8.18E-04	heparan sulfate proteoglycan biosynthetic process
GO:0007509	8.18E-04	mesoderm migration
GO:0051017	8.81E-04	actin filament bundle formation
GO:0030206	9.69E-04	chondroitin sulfate biosynthetic process
GO:0010002	9.69E-04	cardioblast differentiation
GO:0009408	9.69E-04	response to heat
GO:0045449	9.76E-04	regulation of transcription
GO:0007274	1.01E-03	neuromuscular synaptic transmission
GO:0007619	1.08E-03	courtship behavior
GO:0045475	1.08E-03	locomotor rhythm
GO:0001738	1.23E-03	morphogenesis of a polarized epithelium
GO:0008345	1.23E-03	larval locomotory behavior
GO:0007298	1.23E-03	border follicle cell migration
GO:0007280	1.50E-03	pole cell migration
GO:0008347	1.50E-03	glial cell migration
GO:0008344	1.50E-03	adult locomotory behavior
GO:0035147	1.50E-03	branch fusion, open tracheal system
GO:0007480	1.64E-03	imaginal disc-derived leg morphogenesis
GO:0007219	1.77E-03	Notch signaling pathway
GO:0045187	1.77E-03	regulation of circadian sleep/wake cycle, sleep
GO:0001745	2.13E-03	compound eye morphogenesis
GO:0007428	2.37E-03	primary branching, open tracheal system
GO:0007268	2.43E-03	synaptic transmission
GO:0007390	2.45E-03	germ-band shortening
GO:0016331	2.45E-03	morphogenesis of embryonic epithelium

GO:0009649	2.45E-03	entrainment of circadian clock
GO:0048149	2.45E-03	behavioral response to ethanol
GO:0016332	2.45E-03	establishment or maintenance of polarity of embryonic epithelium
GO:0016360	2.45E-03	sensory organ precursor cell fate determination
GO:0002121	2.45E-03	inter-male aggressive behavior
GO:0030162	2.48E-03	regulation of proteolysis
GO:0007422	2.50E-03	peripheral nervous system development
GO:0048675	3.39E-03	axon extension
GO:0007297	3.39E-03	ovarian follicle cell migration
GO:0007622	3.39E-03	rhythmic behavior
GO:0007479	3.39E-03	leg disc proximal/distal pattern formation
GO:0008340	3.46E-03	determination of adult lifespan
GO:0007010	3.46E-03	cytoskeleton organization
GO:0007474	3.50E-03	imaginal disc-derived wing vein specification
GO:0008587	3.72E-03	imaginal disc-derived wing margin morphogenesis
GO:0007520	3.72E-03	myoblast fusion
GO:0016339	3.72E-03	calcium-dependent cell-cell adhesion
GO:0007242	3.86E-03	intracellular signaling cascade
GO:0048666	4.48E-03	neuron development
GO:0006357	4.91E-03	regulation of transcription from RNA polymerase II promoter
GO:0035172	5.04E-03	hemocyte proliferation
GO:0007549	5.04E-03	dosage compensation
GO:0008105	5.75E-03	asymmetric protein localization
GO:0007475	5.75E-03	apposition of dorsal and ventral imaginal disc-derived wing surfaces
GO:0007399	5.75E-03	nervous system development
GO:0000902	5.75E-03	cell morphogenesis
GO:0048066	5.75E-03	pigmentation during development
GO:0007525	5.75E-03	somatic muscle development
GO:0045197	5.75E-03	establishment or maintenance of epithelial cell apical/basal polarity
GO:0042048	5.87E-03	olfactory behavior
GO:0006914	5.87E-03	autophagy
GO:0035071	6.05E-03	salivary gland cell autophagic cell death
GO:0007269	6.60E-03	neurotransmitter secretion
GO:0006813	6.78E-03	potassium ion transport
GO:0008293	7.58E-03	torso signaling pathway
GO:0048813	7.58E-03	dendrite morphogenesis
GO:0007186	7.93E-03	G-protein coupled receptor protein signaling pathway
GO:0016055	8.13E-03	Wnt receptor signaling pathway
GO:0007455	8.84E-03	eye-antennal disc morphogenesis
GO:0045167	8.84E-03	asymmetric protein localization involved in cell fate determination
GO:0007632	8.84E-03	visual behavior
GO:0035215	8.84E-03	genital disc development
GO:0010552	8.84E-03	positive regulation of gene-specific transcription from RNA polymerase II promoter

GO:0045610	8.84E-03	regulation of hemocyte differentiation
GO:0007362	9.17E-03	terminal region determination
GO:0007494	1.20E-02	midgut development
GO:0035023	1.20E-02	regulation of Rho protein signal transduction
GO:0016319	1.21E-02	mushroom body development
GO:0002168	1.31E-02	instar larval development
GO:0008049	1.31E-02	male courtship behavior
GO:0051225	1.31E-02	spindle assembly
GO:0007431	1.31E-02	salivary gland development
GO:0042078	1.31E-02	germ-line stem cell division
GO:0006812	1.38E-02	cation transport
GO:0006897	1.38E-02	endocytosis
GO:0030718	1.38E-02	germ-line stem cell maintenance
GO:0007400	1.38E-02	neuroblast fate determination
GO:0048542	1.38E-02	lymph gland development
GO:0007446	1.38E-02	imaginal disc growth
GO:0007306	1.38E-02	eggshell chorion assembly
GO:0045186	1.40E-02	zonula adherens assembly
GO:0030536	1.40E-02	larval feeding behavior
GO:0048800	1.40E-02	antennal morphogenesis
GO:0007519	1.40E-02	skeletal muscle tissue development
GO:0016079	1.40E-02	synaptic vesicle exocytosis
GO:0007173	1.47E-02	epidermal growth factor receptor signaling pathway
GO:0007291	1.52E-02	sperm individualization
GO:0007602	1.59E-02	phototransduction
GO:0008360	1.70E-02	regulation of cell shape
GO:0007179	1.74E-02	transforming growth factor beta receptor signaling pathway
GO:0007426	1.74E-02	tracheal outgrowth, open tracheal system
GO:0016477	1.74E-02	cell migration
GO:0051726	1.89E-02	regulation of cell cycle
GO:0008103	1.96E-02	oocyte microtubule cytoskeleton polarization
GO:0035277	1.96E-02	spiracle morphogenesis, open tracheal system
GO:0008286	1.96E-02	insulin receptor signaling pathway
GO:0007224	2.01E-02	smoothened signaling pathway
GO:0016318	2.01E-02	ommatidial rotation
GO:0030707	2.02E-02	ovarian follicle cell development
GO:0007517	2.04E-02	muscle organ development
GO:0001700	2.04E-02	embryonic development via the syncytial blastoderm
GO:0048102	2.04E-02	autophagic cell death
GO:0007315	2.08E-02	pole plasm assembly
GO:0007613	2.08E-02	memory
GO:0007293	2.08E-02	germarium-derived egg chamber formation
GO:0030307	2.08E-02	positive regulation of cell growth
GO:0042067	2.30E-02	establishment of ommatidial polarity

GO:0007303	2.72E-02	cytoplasmic transport, nurse cell to oocyte
GO:0019991	2.72E-02	septate junction assembly
GO:0007015	2.98E-02	actin filament organization
GO:0007528	3.04E-02	neuromuscular junction development
GO:0007304	3.04E-02	chorion-containing eggshell formation
GO:0035099	3.04E-02	hemocyte migration
GO:0045941	3.04E-02	positive regulation of transcription
GO:0006325	3.04E-02	chromatin organization
GO:0007367	3.04E-02	segment polarity determination
GO:0007309	3.04E-02	oocyte axis specification
GO:0051056	3.04E-02	regulation of small GTPase mediated signal transduction
GO:0006366	3.28E-02	transcription from RNA polymerase II promoter
GO:0045893	3.28E-02	positive regulation of transcription, DNA-dependent
GO:0009790	3.42E-02	embryonic development
GO:0007409	3.50E-02	axonogenesis
GO:0030097	3.53E-02	hemopoiesis
GO:0017148	3.53E-02	negative regulation of translation
GO:0007286	3.53E-02	spermatid development
GO:0007254	3.53E-02	JNK cascade
GO:0007310	3.53E-02	oocyte dorsal/ventral axis specification
GO:0055059	3.90E-02	asymmetric neuroblast division
GO:0000381	3.99E-02	regulation of alternative nuclear mRNA splicing, via spliceosome
GO:0046843	4.17E-02	dorsal appendage formation
GO:0040014	4.18E-02	regulation of multicellular organism growth
GO:0006378	4.18E-02	mRNA polyadenylation
GO:0007417	4.31E-02	central nervous system development
GO:0006470	4.32E-02	protein amino acid dephosphorylation
GO:0007350	4.68E-02	blastoderm segmentation