Table S12 GO term enrichment for biological process in the North American cline for genes that overlap windows in the top 5% tail of Fst.

	5 % Tail Biological Process	
GO term	q-value	description
GO:0006355	1.48E-08	regulation of transcription, DNA-dependent
GO:0007411	2.10E-08	axon guidance
GO:0007476	1.13E-07	imaginal disc-derived wing morphogenesis
GO:0048477	1.13E-07	oogenesis
GO:0035023	4.71E-07	regulation of Rho protein signal transduction
GO:0048749	9.49E-07	compound eye development
GO:0007350	5.78E-06	blastoderm segmentation
GO:0007399	5.78E-06	nervous system development
GO:0007513	1.22E-05	pericardial cell differentiation
GO:0045449	1.99E-05	regulation of transcription
GO:0007156	4.21E-05	homophilic cell adhesion
GO:0006468	4.21E-05	protein amino acid phosphorylation
GO:0007474	4.21E-05	imaginal disc-derived wing vein specification
GO:0007482	4.21E-05	haltere development
GO:0007455	4.38E-05	eye-antennal disc morphogenesis
GO:0007435	4.75E-05	salivary gland morphogenesis
GO:0008586	4.75E-05	imaginal disc-derived wing vein morphogenesis
GO:0007472	5.30E-05	wing disc morphogenesis
GO:0007155	5.88E-05	cell adhesion
GO:0007398	6.34E-05	ectoderm development
GO:0042051	8.75E-05	compound eye photoreceptor development
GO:0007419	8.76E-05	ventral cord development
GO:0007391	9.25E-05	dorsal closure
GO:0001745	9.25E-05	compound eye morphogenesis
GO:0007424	9.42E-05	open tracheal system development
GO:0010002	1.14E-04	cardioblast differentiation
GO:0048800	1.46E-04	antennal morphogenesis
GO:0035225	1.46E-04	determination of genital disc primordium
GO:0016203	1.46E-04	muscle attachment
GO:0007480	1.46E-04	imaginal disc-derived leg morphogenesis
GO:0035172	1.46E-04	hemocyte proliferation
GO:0006813	1.85E-04	potassium ion transport
GO:0007417	1.96E-04	central nervous system development
GO:0051276	2.00E-04	chromosome organization
GO:0007507	2.44E-04	heart development
GO:0007400	2.66E-04	neuroblast fate determination
GO:0007416	2.66E-04	synapse assembly
GO:0046331	3.30E-04	lateral inhibition
GO:0035286	3.30E-04	leg segmentation
GO:0035224	3.30E-04	genital disc anterior/posterior pattern formation

GO:0008356	3.30E-04	asymmetric cell division
GO:0046667	3.30E-04	compound eye retinal cell programmed cell death
GO:0008406	3.30E-04	gonad development
GO:0007425	3.30E-04	epithelial cell fate determination, open tracheal system
GO:0035309	3.30E-04	wing and notum subfield formation
GO:0007628	3.30E-04	adult walking behavior
GO:0007473	3.30E-04	wing disc proximal/distal pattern formation
GO:0030097	3.30E-04	hemopoiesis
GO:0007440	3.53E-04	foregut morphogenesis
GO:0035215	3.53E-04	genital disc development
GO:0007422	3.73E-04	peripheral nervous system development
GO:0035088	3.79E-04	establishment or maintenance of apical/basal cell polarity
GO:0007165	5.86E-04	signal transduction
GO:0016477	6.23E-04	cell migration
GO:0007498	6.67E-04	mesoderm development
GO:0008104	6.73E-04	protein localization
GO:0008407	7.59E-04	bristle morphogenesis
GO:0045893	7.59E-04	positive regulation of transcription, DNA-dependent
GO:0007479	8.97E-04	leg disc proximal/distal pattern formation
GO:0007442	8.97E-04	hindgut morphogenesis
GO:0007298	9.07E-04	border follicle cell migration
GO:0016055	9.07E-04	Wnt receptor signaling pathway
GO:0030162	1.05E-03	regulation of proteolysis
GO:0048100	1.08E-03	wing disc anterior/posterior pattern formation
GO:0042048	1.08E-03	olfactory behavior
GO:0008284	1.08E-03	positive regulation of cell proliferation
GO:0048813	1.08E-03	dendrite morphogenesis
GO:0007268	1.08E-03	synaptic transmission
GO:0007420	1.08E-03	brain development
GO:0008045	1.08E-03	motor axon guidance
GO:0007076	1.20E-03	mitotic chromosome condensation
GO:0007415	1.23E-03	defasciculation of motor neuron axon
GO:0007614	1.23E-03	short-term memory
GO:0008355	1.24E-03	olfactory learning
GO:0048190	1.36E-03	wing disc dorsal/ventral pattern formation
GO:0007186	1.39E-03	G-protein coupled receptor protein signaling pathway
GO:0008049	1.39E-03	male courtship behavior
GO:0007431	1.39E-03	salivary gland development
GO:0007494	1.49E-03	midgut development
GO:0046843	1.49E-03	dorsal appendage formation
GO:0007619	1.49E-03	courtship behavior
GO:0050770	1.61E-03	regulation of axonogenesis
GO:0030307	1.61E-03	positive regulation of cell growth
GO:0008360	1.86E-03	regulation of cell shape

GO:0001709	2.03E-03	cell fate determination
GO:0035277	2.03E-03	spiracle morphogenesis, open tracheal system
GO:0045165	2.03E-03	cell fate commitment
GO:0042052	2.13E-03	rhabdomere development
GO:0048854	2.13E-03	brain morphogenesis
GO:0001964	2.13E-03	startle response
GO:0045494	2.13E-03	photoreceptor cell maintenance
GO:0045433	2.13E-03	male courtship behavior, veined wing generated song production
GO:0009952	2.13E-03	anterior/posterior pattern formation
GO:0010552	2.13E-03	positive regulation of gene-specific transcription from RNA polymerase II promoter
GO:0045167	2.13E-03	asymmetric protein localization involved in cell fate determination
GO:0031987	2.13E-03	locomotion involved in locomotory behavior
GO:0008354	2.14E-03	germ cell migration
GO:0055059	2.14E-03	asymmetric neuroblast division
GO:0030707	2.20E-03	ovarian follicle cell development
GO:0030713	2.86E-03	ovarian follicle cell stalk formation
GO:0016199	2.86E-03	axon midline choice point recognition
GO:0040001	2.88E-03	establishment of mitotic spindle localization
GO:0007051	2.88E-03	spindle organization
GO:0016331	2.88E-03	morphogenesis of embryonic epithelium
GO:0007242	2.97E-03	intracellular signaling cascade
GO:0006816	3.07E-03	calcium ion transport
GO:0048149	3.07E-03	behavioral response to ethanol
GO:0006916	3.07E-03	anti-apoptosis
GO:0007443	3.07E-03	Malpighian tubule morphogenesis
GO:0007140	3.17E-03	male meiosis
GO:0007346	3.17E-03	regulation of mitotic cell cycle
GO:0007611	3.17E-03	learning or memory
GO:0007517	3.22E-03	muscle organ development
GO:0002121	3.26E-03	inter-male aggressive behavior
GO:0040018	3.94E-03	positive regulation of multicellular organism growth
GO:0030261	3.94E-03	chromosome condensation
GO:0046620	3.94E-03	regulation of organ growth
GO:0048675	3.94E-03	axon extension
GO:0007297	3.94E-03	ovarian follicle cell migration
GO:0008587	4.51E-03	imaginal disc-derived wing margin morphogenesis
GO:0035220	4.51E-03	wing disc development
GO:0040014	4.51E-03	regulation of multicellular organism growth
GO:0048542	4.51E-03	lymph gland development
GO:0007446	4.51E-03	imaginal disc growth
GO:0002009	4.65E-03	morphogenesis of an epithelium
GO:0006811	5.37E-03	ion transport
GO:0006979	5.47E-03	response to oxidative stress

GO:0008361	5.61E-03	regulation of cell size
GO:0045570	5.61E-03	regulation of imaginal disc growth
GO:0045466	5.61E-03	R7 cell differentiation
GO:0007447	5.61E-03	imaginal disc pattern formation
GO:0046329	5.61E-03	negative regulation of JNK cascade
GO:0007301	5.61E-03	ovarian ring canal formation
GO:0007617	5.61E-03	mating behavior
GO:0001700	5.93E-03	embryonic development via the syncytial blastoderm
GO:0008105	6.60E-03	asymmetric protein localization
GO:0007304	6.60E-03	chorion-containing eggshell formation
GO:0045197	6.60E-03	establishment or maintenance of epithelial cell apical/basal polarity
GO:0008345	6.60E-03	larval locomotory behavior
GO:0006836	6.60E-03	neurotransmitter transport
GO:0007379	6.60E-03	segment specification
GO:0009880	6.60E-03	embryonic pattern specification
GO:0007017	6.61E-03	microtubule-based process
GO:0007280	6.88E-03	pole cell migration
GO:0007548	6.88E-03	sex differentiation
GO:0007173	7.43E-03	epidermal growth factor receptor signaling pathway
GO:0030036	7.58E-03	actin cytoskeleton organization
GO:0007444	8.37E-03	imaginal disc development
GO:0016318	9.32E-03	ommatidial rotation
GO:0007427	9.32E-03	epithelial cell migration, open tracheal system
GO:0007157	1.00E-02	heterophilic cell adhesion
GO:0001751	1.00E-02	compound eye photoreceptor cell differentiation
GO:0007349	1.00E-02	cellularization
GO:0045610	1.00E-02	regulation of hemocyte differentiation
GO:0007632	1.00E-02	visual behavior
GO:0022416	1.00E-02	bristle development
GO:0030178	1.00E-02	negative regulation of Wnt receptor signaling pathway
GO:0016458	1.00E-02	gene silencing
GO:0016360	1.00E-02	sensory organ precursor cell fate determination
GO:0007552	1.00E-02	metamorphosis
GO:0007528	1.00E-02	neuromuscular junction development
GO:0007428	1.00E-02	primary branching, open tracheal system
GO:0019991	1.00E-02	septate junction assembly
GO:0007390	1.00E-02	germ-band shortening
GO:0007369	1.00E-02	gastrulation
GO:0007307	1.00E-02	eggshell chorion gene amplification
GO:0001708	1.00E-02	cell fate specification
GO:0000226	1.00E-02	microtubule cytoskeleton organization
GO:0035050	1.00E-02	embryonic heart tube development
GO:0055085	1.07E-02	transmembrane transport
GO:0007423	1.12E-02	sensory organ development

GO:0007163	1.19E-02	establishment or maintenance of cell polarity
GO:0006357	1.26E-02	regulation of transcription from RNA polymerase II promoter
GO:0006325	1.34E-02	chromatin organization
GO:0045944	1.41E-02	positive regulation of transcription from RNA polymerase II promoter
GO:0048666	1.41E-02	neuron development
GO:0002168	1.46E-02	instar larval development
GO:0016319	1.46E-02	mushroom body development
GO:0006955	1.46E-02	immune response
GO:0018991	1.54E-02	oviposition
GO:0007067	1.54E-02	mitosis
GO:0030718	1.54E-02	germ-line stem cell maintenance
GO:0008595	1.54E-02	determination of anterior/posterior axis, embryo
GO:0051533	1.54E-02	positive regulation of NFAT protein import into nucleus
GO:0007259	1.54E-02	JAK-STAT cascade
GO:0030536	1.54E-02	larval feeding behavior
GO:0007519	1.54E-02	skeletal muscle tissue development
GO:0007501	1.54E-02	mesodermal cell fate specification
GO:0042059	1.54E-02	negative regulation of epidermal growth factor receptor signaling pathway
GO:0060857	1.54E-02	establishment of glial blood-brain barrier
GO:0006915	1.64E-02	apoptosis
GO:0007269	1.64E-02	neurotransmitter secretion
GO:0007015	1.83E-02	actin filament organization
GO:0007623	2.08E-02	circadian rhythm
GO:0007409	2.08E-02	axonogenesis
GO:0035147	2.20E-02	branch fusion, open tracheal system
GO:0008344	2.20E-02	adult locomotory behavior
GO:0006914	2.20E-02	autophagy
GO:0008286	2.20E-02	insulin receptor signaling pathway
GO:0008103	2.20E-02	oocyte microtubule cytoskeleton polarization
GO:0008347	2.20E-02	glial cell migration
GO:0016567	2.23E-02	protein ubiquitination
GO:0051726	2.23E-02	regulation of cell cycle
GO:0009987	2.24E-02	cellular process
GO:0007475	2.29E-02	apposition of dorsal and ventral imaginal disc-derived wing surfaces
GO:0007062	2.29E-02	sister chromatid cohesion
GO:0007525	2.29E-02	somatic muscle development
GO:0001738	2.29E-02	morphogenesis of a polarized epithelium
GO:0007613	2.29E-02	memory
GO:0045746	2.29E-02	negative regulation of Notch signaling pathway
GO:0009312	2.29E-02	oligosaccharide biosynthetic process
GO:0008293	2.29E-02	torso signaling pathway
GO:0007088	2.61E-02	regulation of mitosis
GO:0040007	2.61E-02	growth
GO:0042067	2.61E-02	establishment of ommatidial polarity

GO:0042127	2.61E-02	regulation of cell proliferation
GO:0035317	2.96E-02	imaginal disc-derived wing hair organization
GO:0007530	2.96E-02	sex determination
GO:0006917	2.96E-02	induction of apoptosis
GO:0045475	2.96E-02	locomotor rhythm
GO:0001736	2.96E-02	establishment of planar polarity
GO:0016311	2.96E-02	dephosphorylation
GO:0035071	3.01E-02	salivary gland cell autophagic cell death
GO:0007169	3.32E-02	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0007629	3.32E-02	flight behavior
GO:0001737	3.32E-02	establishment of imaginal disc-derived wing hair orientation
GO:0007362	3.32E-02	terminal region determination
GO:0051056	3.32E-02	regulation of small GTPase mediated signal transduction
GO:0006897	3.80E-02	endocytosis
GO:0006396	4.00E-02	RNA processing
GO:0016321	4.00E-02	female meiosis chromosome segregation
GO:0007274	4.00E-02	neuromuscular synaptic transmission
GO:0007310	4.00E-02	oocyte dorsal/ventral axis specification
GO:0017148	4.00E-02	negative regulation of translation
GO:0051017	4.73E-02	actin filament bundle formation
GO:0006865	4.80E-02	amino acid transport
GO:0016481	4.97E-02	negative regulation of transcription