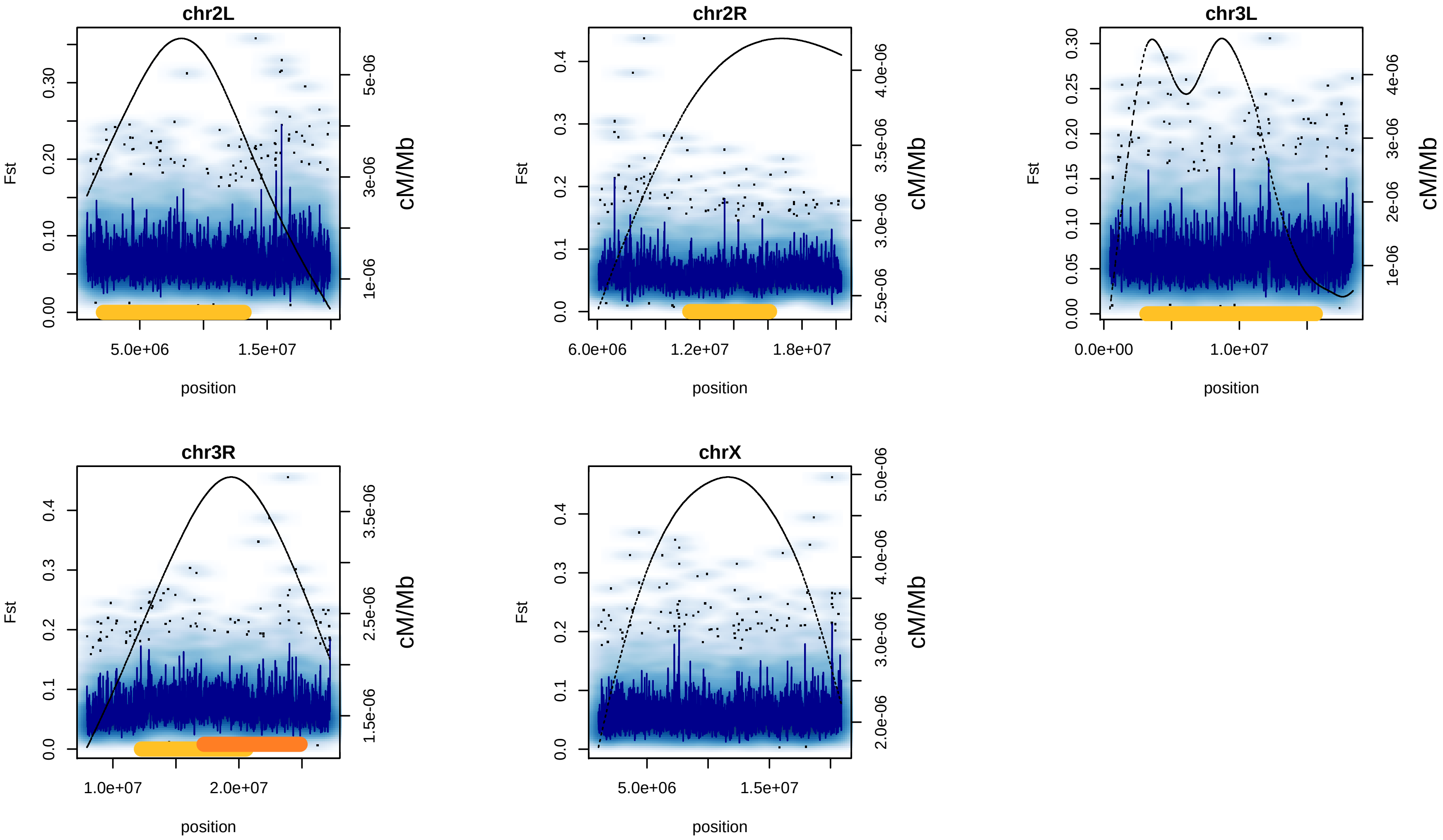

Figure S1 Australian cline Fst across chromosome arms

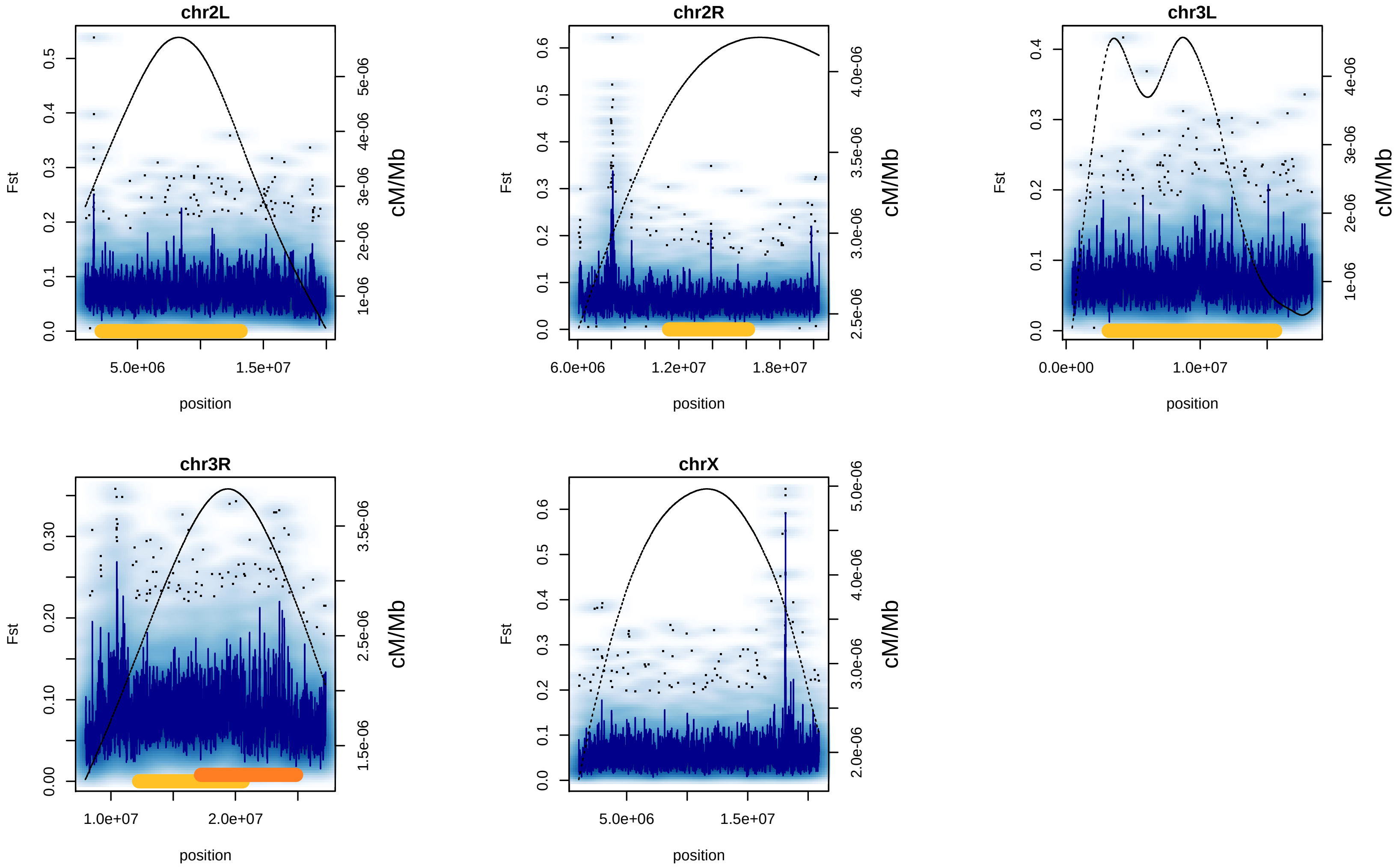

Figure S2 North American cline Fst across chromosome arms

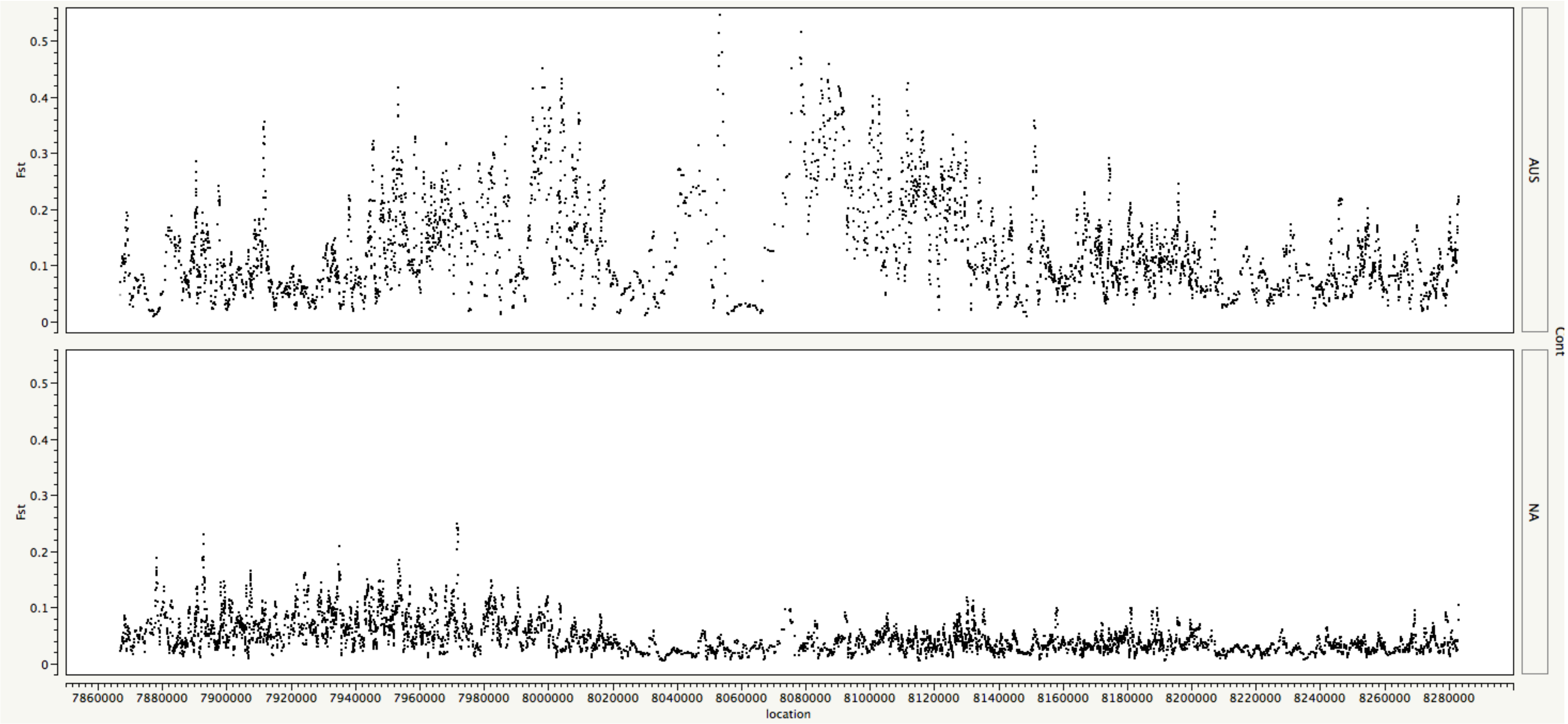

Figure S3 Comparison of Fst between continents in Cyp6G1 region

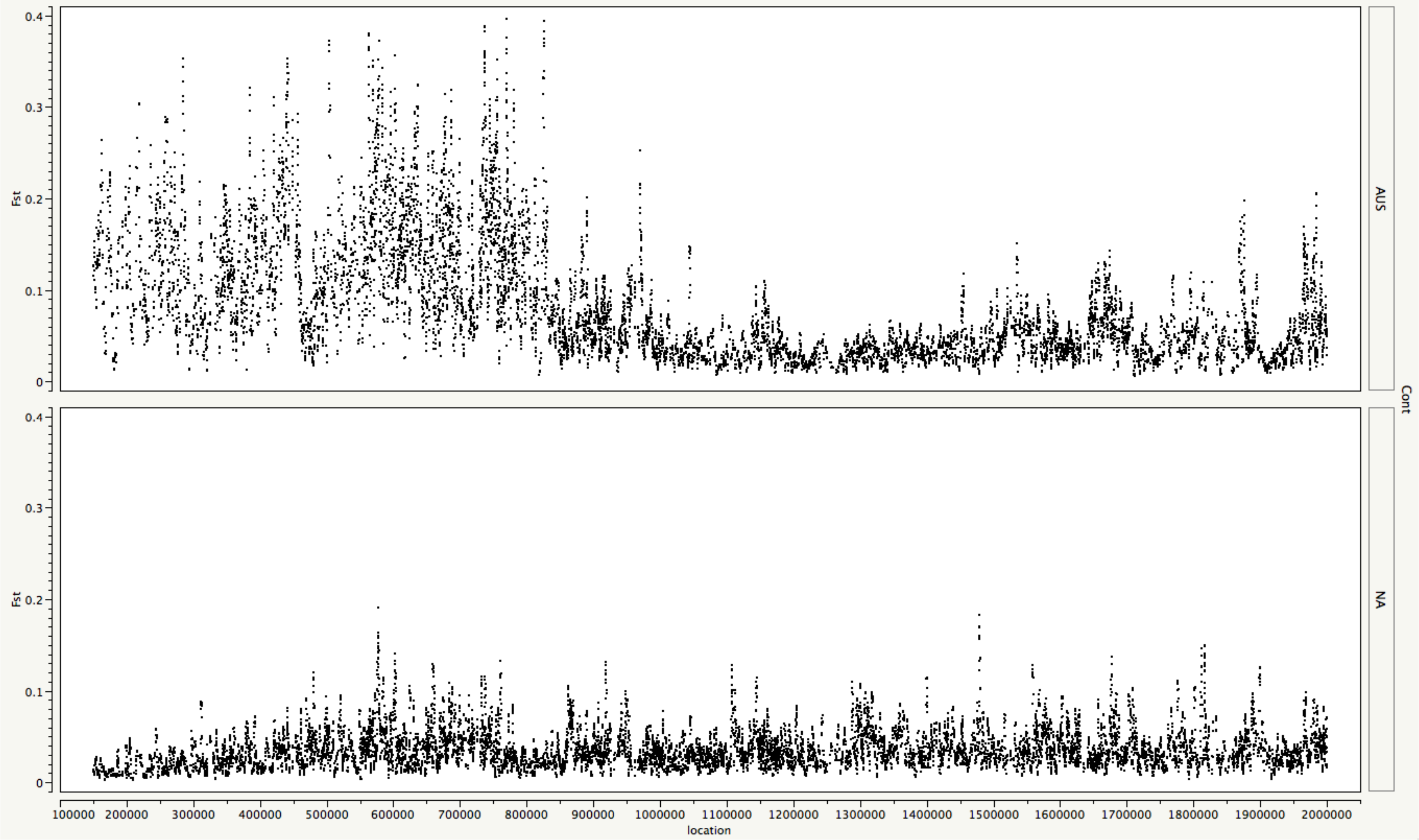

Figure S4 Comparison of Fst between continents at tip of chromosome X

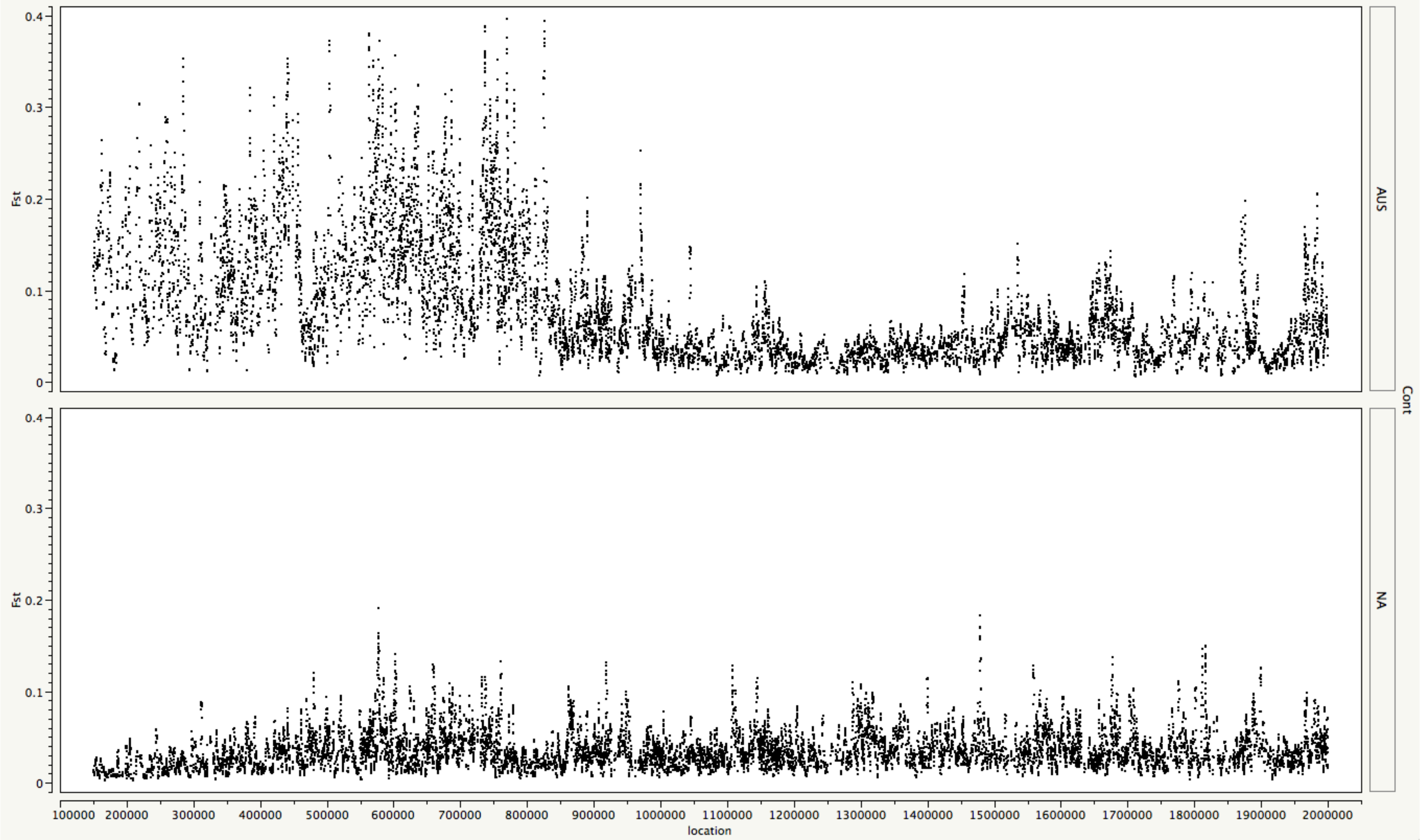

Figure S5 Comparison of Fst between continents in Upd2 region

Table S1 GO term enrichment for biological process in the Australian cline for genes that overlap windows in the top 1% tail of Fst.

	1 % Tail Biological Process	
GO term	q-value	description
GO:0008355	4.99E-06	olfactory learning
GO:0007611	9.11E-06	learning or memory
GO:0001738	9.68E-05	morphogenesis of a polarized epithelium
GO:0007156	9.68E-05	homophilic cell adhesion
GO:0008285	9.68E-05	negative regulation of cell proliferation
GO:0007165	9.68E-05	signal transduction
GO:0007306	1.74E-04	eggshell chorion assembly
GO:0007507	2.37E-04	heart development
GO:0007427	2.68E-04	epithelial cell migration, open tracheal system
GO:0051276	3.00E-04	chromosome organization
GO:0008104	3.08E-04	protein localization
GO:0017148	3.71E-04	negative regulation of translation
GO:0007623	4.62E-04	circadian rhythm
GO:0007155	6.08E-04	cell adhesion
GO:0006811	6.12E-04	ion transport
GO:0002009	7.72E-04	morphogenesis of an epithelium
GO:0007424	8.38E-04	open tracheal system development
GO:0048477	9.93E-04	oogenesis
GO:0007391	1.23E-03	dorsal closure
GO:0007435	1.23E-03	salivary gland morphogenesis
GO:0045475	1.36E-03	locomotor rhythm
GO:0006355	1.37E-03	regulation of transcription, DNA-dependent
GO:0007275	1.37E-03	multicellular organismal development
GO:0006468	1.73E-03	protein amino acid phosphorylation
GO:0007476	4.39E-03	imaginal disc-derived wing morphogenesis
GO:0002121	6.46E-03	inter-male aggressive behavior
GO:0006813	6.60E-03	potassium ion transport
GO:0048749	9.21E-03	compound eye development
GO:0045449	1.17E-02	regulation of transcription
GO:0007411	1.24E-02	axon guidance
GO:0016319	1.38E-02	mushroom body development
GO:0007298	1.40E-02	border follicle cell migration
GO:0001700	1.87E-02	embryonic development via the syncytial blastoderm
GO:0007015	2.28E-02	actin filament organization
GO:0001745	2.73E-02	compound eye morphogenesis
GO:0006814	2.94E-02	sodium ion transport
GO:0008360	4.19E-02	regulation of cell shape
GO:0055085	4.19E-02	transmembrane transport
GO:0007269	4.73E-02	neurotransmitter secretion
GO:0016192	4.95E-02	vesicle-mediated transport

Table S2 GO term enrichment for biological process in the Australian cline for genes that overlap windows in the top 2.5% tail of Fst.

	2.5 % Tail Biological Process	
GO term	q-value	description
GO:0006355	2.24E-07	regulation of transcription, DNA-dependent
GO:0007611	1.26E-06	learning or memory
GO:0006468	1.26E-06	protein amino acid phosphorylation
GO:0008543	3.05E-06	fibroblast growth factor receptor signaling pathway
GO:0007476	3.11E-06	imaginal disc-derived wing morphogenesis
GO:0008284	3.49E-06	positive regulation of cell proliferation
GO:0007424	5.44E-06	open tracheal system development
GO:0008355	1.11E-05	olfactory learning
GO:0007156	1.56E-05	homophilic cell adhesion
GO:0007435	1.87E-05	salivary gland morphogenesis
GO:0007155	1.87E-05	cell adhesion
GO:0007275	1.87E-05	multicellular organismal development
GO:0007507	1.87E-05	heart development
GO:0046331	1.87E-05	lateral inhibition
GO:0007280	4.39E-05	pole cell migration
GO:0007513	4.39E-05	pericardial cell differentiation
GO:0007427	4.39E-05	epithelial cell migration, open tracheal system
GO:0008406	4.76E-05	gonad development
GO:0048190	4.98E-05	wing disc dorsal/ventral pattern formation
GO:0007411	5.20E-05	axon guidance
GO:0048477	7.54E-05	oogenesis
GO:0007623	1.42E-04	circadian rhythm
GO:0048749	1.42E-04	compound eye development
GO:0008104	1.70E-04	protein localization
GO:0007391	2.08E-04	dorsal closure
GO:0007419	2.14E-04	ventral cord development
GO:0007398	3.20E-04	ectoderm development
GO:0045475	3.20E-04	locomotor rhythm
GO:0001751	3.20E-04	compound eye photoreceptor cell differentiation
GO:0001738	3.82E-04	morphogenesis of a polarized epithelium
GO:0008345	3.82E-04	larval locomotory behavior
GO:0007509	4.07E-04	mesoderm migration
GO:0007498	4.07E-04	mesoderm development
GO:0035225	4.07E-04	determination of genital disc primordium
GO:0008354	4.07E-04	germ cell migration
GO:0007617	4.07E-04	mating behavior
GO:0006811	4.92E-04	ion transport
GO:0007219	4.92E-04	Notch signaling pathway

GO:0007428	5.97E-04	primary branching, open tracheal system
GO:0007274	6.14E-04	neuromuscular synaptic transmission
GO:0008356	6.14E-04	asymmetric cell division
GO:0051225	6.14E-04	spindle assembly
GO:0045433	7.31E-04	male courtship behavior, veined wing generated song production
GO:0045187	7.31E-04	regulation of circadian sleep/wake cycle, sleep
GO:0010552	7.31E-04	positive regulation of gene-specific transcription from RNA polymerase II promoter
GO:0016477	8.59E-04	cell migration
GO:0008285	8.59E-04	negative regulation of cell proliferation
GO:0007480	8.59E-04	imaginal disc-derived leg morphogenesis
GO:0007165	8.59E-04	signal transduction
GO:0002121	8.89E-04	inter-male aggressive behavior
GO:0042127	1.20E-03	regulation of cell proliferation
GO:0048675	1.20E-03	axon extension
GO:0008407	1.20E-03	bristle morphogenesis
GO:0007622	1.20E-03	rhythmic behavior
GO:0016079	1.20E-03	synaptic vesicle exocytosis
GO:0008344	1.24E-03	adult locomotory behavior
GO:0001709	1.24E-03	cell fate determination
GO:0008347	1.24E-03	glial cell migration
GO:0007494	1.64E-03	midgut development
GO:0002009	1.64E-03	morphogenesis of an epithelium
GO:0035023	1.64E-03	regulation of Rho protein signal transduction
GO:0045449	1.71E-03	regulation of transcription
GO:0007268	1.77E-03	synaptic transmission
GO:0016360	1.77E-03	sensory organ precursor cell fate determination
GO:0007390	1.77E-03	germ-band shortening
GO:0007475	1.77E-03	apposition of dorsal and ventral imaginal disc-derived wing surfaces
GO:0000902	1.77E-03	cell morphogenesis
GO:0055085	1.77E-03	transmembrane transport
GO:0008049	2.57E-03	male courtship behavior
GO:0007431	2.57E-03	salivary gland development
GO:0030707	2.66E-03	ovarian follicle cell development
GO:0008340	3.61E-03	determination of adult lifespan
GO:0042052	3.61E-03	rhabdomere development
GO:0007314	3.61E-03	oocyte anterior/posterior axis specification
GO:0007298	3.68E-03	border follicle cell migration
GO:0007306	4.11E-03	eggshell chorion assembly
GO:0051017	4.11E-03	actin filament bundle formation
GO:0001745	4.11E-03	compound eye morphogenesis
GO:0008587	4.11E-03	imaginal disc-derived wing margin morphogenesis
GO:0016055	4.73E-03	Wnt receptor signaling pathway
GO:0030162	4.75E-03	regulation of proteolysis

GO:0030718	4.82E-03	germ-line stem cell maintenance
GO:0035277	5.70E-03	spiracle morphogenesis, open tracheal system
GO:0008103	5.70E-03	oocyte microtubule cytoskeleton polarization
GO:0006914	5.70E-03	autophagy
GO:0035147	5.70E-03	branch fusion, open tracheal system
GO:0007269	6.05E-03	neurotransmitter secretion
GO:0007367	6.05E-03	segment polarity determination
GO:0007619	6.05E-03	courtship behavior
GO:0008586	7.37E-03	imaginal disc-derived wing vein morphogenesis
GO:0051276	7.37E-03	chromosome organization
GO:0007616	7.37E-03	long-term memory
GO:0009408	7.37E-03	response to heat
GO:0006816	7.37E-03	calcium ion transport
GO:0019991	7.37E-03	septate junction assembly
GO:0007455	7.37E-03	eye-antennal disc morphogenesis
GO:0007552	7.37E-03	metamorphosis
GO:0045892	7.50E-03	negative regulation of transcription, DNA-dependent
GO:0006813	7.95E-03	potassium ion transport
GO:0016319	8.34E-03	mushroom body development
GO:0008293	9.71E-03	torso signaling pathway
GO:0017148	9.77E-03	negative regulation of translation
GO:0042078	9.77E-03	germ-line stem cell division
GO:0033227	1.23E-02	dsRNA transport
GO:0007426	1.31E-02	tracheal outgrowth, open tracheal system
GO:0046843	1.35E-02	dorsal appendage formation
GO:0007417	1.48E-02	central nervous system development
GO:0045893	1.51E-02	positive regulation of transcription, DNA-dependent
GO:0006897	1.51E-02	endocytosis
GO:0042067	1.67E-02	establishment of ommatidial polarity
GO:0007444	1.88E-02	imaginal disc development
GO:0007242	1.98E-02	intracellular signaling cascade
GO:0007399	2.06E-02	nervous system development
GO:0006325	2.10E-02	chromatin organization
GO:0007422	2.11E-02	peripheral nervous system development
GO:0008360	2.18E-02	regulation of cell shape
GO:0006357	2.48E-02	regulation of transcription from RNA polymerase II promoter
GO:0048666	2.70E-02	neuron development
GO:0006470	3.05E-02	protein amino acid dephosphorylation
GO:0007317	3.14E-02	regulation of pole plasm oskar mRNA localization
GO:0007224	3.14E-02	smoothened signaling pathway
GO:0008045	3.14E-02	motor axon guidance
GO:0042048	3.15E-02	olfactory behavior
GO:0001700	3.33E-02	embryonic development via the syncytial blastoderm
GO:0007423	3.49E-02	sensory organ development

GO:0007474	3.69E-02	imaginal disc-derived wing vein specification
GO:0007163	3.69E-02	establishment or maintenance of cell polarity
GO:0007349	3.69E-02	cellularization
GO:0007015	4.26E-02	actin filament organization
GO:0008595	4.39E-02	determination of anterior/posterior axis, embryo
GO:0008063	4.39E-02	Toll signaling pathway

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

Table S4 GO term enrichment for molecular function in the Australian cline for genes that overlap windows in the top 1% tail of Fst.

	1 % Tail Molecular Function	
GO term	q-value	description
GO:0005515	1.79E-06	protein binding
GO:0000166	9.09E-03	nucleotide binding
GO:0003700	1.17E-02	transcription factor activity
GO:0004674	1.17E-02	protein serine/threonine kinase activity
GO:0004672	1.17E-02	protein kinase activity
GO:0004871	1.26E-02	signal transducer activity
GO:0043565	1.50E-02	sequence-specific DNA binding
GO:0004930	1.81E-02	G-protein coupled receptor activity
GO:0005509	3.32E-02	calcium ion binding
GO:0003779	3.37E-02	actin binding
GO:0003729	3.60E-02	mRNA binding
GO:0042623	3.60E-02	ATPase activity, coupled
GO:0005524	4.08E-02	ATP binding

Table S5 GO term enrichment for molecular function in the Australian cline for genes that overlap windows in the top 2.5% tail of Fst.

	2.5 % Tail Molecular Function	
GO term	q-value	description
GO:0005515	5.44E-10	protein binding
GO:0003700	3.20E-09	transcription factor activity
GO:0004672	9.65E-06	protein kinase activity
GO:0004674	3.88E-05	protein serine/threonine kinase activity
GO:0043565	3.88E-05	sequence-specific DNA binding
GO:0005509	9.56E-05	calcium ion binding
GO:0008270	2.82E-04	zinc ion binding
GO:0004871	6.54E-04	signal transducer activity
GO:0004702	6.54E-04	receptor signaling protein serine/threonine kinase activity
GO:0004725	1.60E-03	protein tyrosine phosphatase activity
GO:0005524	1.60E-03	ATP binding
GO:0003702	1.98E-03	RNA polymerase II transcription factor activity
GO:0005089	2.78E-03	Rho guanyl-nucleotide exchange factor activity
GO:0004714	3.11E-03	transmembrane receptor protein tyrosine kinase activity
GO:0003676	4.02E-03	nucleic acid binding
GO:0008188	4.02E-03	neuropeptide receptor activity
GO:0005096	4.02E-03	GTPase activator activity
GO:0005102	4.13E-03	receptor binding
GO:0008026	5.10E-03	ATP-dependent helicase activity
GO:0003713	5.26E-03	transcription coactivator activity
GO:0005249	5.58E-03	voltage-gated potassium channel activity
GO:0004713	8.82E-03	protein tyrosine kinase activity
GO:0004930	8.82E-03	G-protein coupled receptor activity
GO:0003704	8.82E-03	specific RNA polymerase II transcription factor activity
GO:0016563	1.37E-02	transcription activator activity
GO:0004872	1.37E-02	receptor activity
GO:0003779	1.37E-02	actin binding
GO:0000166	1.39E-02	nucleotide binding
GO:0016566	1.42E-02	specific transcriptional repressor activity
GO:0008236	1.47E-02	serine-type peptidase activity
GO:0004222	1.60E-02	metalloendopeptidase activity
GO:0042803	1.68E-02	protein homodimerization activity
GO:0008083	1.81E-02	growth factor activity
GO:0019992	2.47E-02	diacylglycerol binding
GO:0004888	2.47E-02	transmembrane receptor activity
GO:0005516	3.85E-02	calmodulin binding
GO:0008017	4.56E-02	microtubule binding
GO:0046983	4.56E-02	protein dimerization activity
GO:0003729	4.85E-02	mRNA binding

Table S6 GO term enrichment for molecular function in the Australian cline for genes that overlap windows in the top 5% tail of Fst.

	5 % Tail Molecular Function	
GO term	q-value	description
GO:0003700	3.39E-14	transcription factor activity
GO:0005515	1.99E-13	protein binding
GO:0005524	8.48E-09	ATP binding
GO:0043565	3.00E-07	sequence-specific DNA binding
GO:0005509	3.00E-07	calcium ion binding
GO:0004672	1.97E-06	protein kinase activity
GO:0004674	2.91E-06	protein serine/threonine kinase activity
GO:0008188	7.43E-05	neuropeptide receptor activity
GO:0008270	1.12E-04	zinc ion binding
GO:0003702	2.61E-04	RNA polymerase II transcription factor activity
GO:0003779	6.72E-04	actin binding
GO:0004871	9.13E-04	signal transducer activity
GO:0005245	1.64E-03	voltage-gated calcium channel activity
GO:0005096	1.64E-03	GTPase activator activity
GO:0004702	1.67E-03	receptor signaling protein serine/threonine kinase activity
GO:0004725	2.56E-03	protein tyrosine phosphatase activity
GO:0004889	3.99E-03	nicotinic acetylcholine-activated cation-selective channel activity
GO:0032027	3.99E-03	myosin light chain binding
GO:0003774	4.34E-03	motor activity
GO:0003707	5.47E-03	steroid hormone receptor activity
GO:0005249	6.08E-03	voltage-gated potassium channel activity
GO:0004386	9.04E-03	helicase activity
GO:0004190	9.04E-03	aspartic-type endopeptidase activity
GO:0003777	9.04E-03	microtubule motor activity
GO:0008026	9.04E-03	ATP-dependent helicase activity
GO:0005102	1.01E-02	receptor binding
GO:0004222	1.01E-02	metalloendopeptidase activity
GO:0003676	1.16E-02	nucleic acid binding
GO:0004872	1.25E-02	receptor activity
GO:0003704	1.25E-02	specific RNA polymerase II transcription factor activity
GO:0003713	1.47E-02	transcription coactivator activity
GO:0005089	1.57E-02	Rho guanyl-nucleotide exchange factor activity
GO:0004888	1.57E-02	transmembrane receptor activity
GO:0019992	1.57E-02	diacylglycerol binding
GO:0000166	1.79E-02	nucleotide binding
GO:0008239	1.82E-02	dipeptidyl-peptidase activity
GO:0004879	1.82E-02	ligand-dependent nuclear receptor activity
GO:0042626	1.82E-02	ATPase activity, coupled to transmembrane movement of substances
GO:0003746	1.82E-02	translation elongation factor activity
GO:0016566	1.87E-02	specific transcriptional repressor activity

GO:0004930	2.17E-02	G-protein coupled receptor activity
GO:0005085	2.17E-02	guanyl-nucleotide exchange factor activity
GO:0017111	2.55E-02	nucleoside-triphosphatase activity
GO:0004714	2.55E-02	transmembrane receptor protein tyrosine kinase activity
GO:0005516	2.55E-02	calmodulin binding
GO:0003677	2.55E-02	DNA binding
GO:0005215	2.55E-02	transporter activity
GO:0008017	2.97E-02	microtubule binding
GO:0042623	3.27E-02	ATPase activity, coupled
GO:0016563	3.55E-02	transcription activator activity
GO:0050839	3.62E-02	cell adhesion molecule binding
GO:0035091	3.62E-02	phosphoinositide binding
GO:0008083	3.86E-02	growth factor activity
GO:0004713	4.10E-02	protein tyrosine kinase activity
GO:0003714	4.16E-02	transcription corepressor activity
GO:0032183	4.36E-02	SUMO binding

Table S7 GO term enrichment for cellular component in the Australian cline for genes that overlap windows in the top 1% tail of Fst.

	1 % Tail Cellular Component	
GO term	q-value	description
GO:0005886	1.97E-06	plasma membrane
GO:0045211	2.47E-04	postsynaptic membrane
GO:0042600	6.03E-04	chorion
GO:0005887	6.03E-04	integral to plasma membrane
GO:0005578	2.51E-03	proteinaceous extracellular matrix
GO:0043234	2.51E-03	protein complex
GO:0016020	2.51E-03	membrane
GO:0005622	1.45E-02	intracellular
GO:0005634	2.82E-02	nucleus
GO:0016021	3.70E-02	integral to membrane
GO:0005875	3.70E-02	microtubule associated complex

Table S8 GO term enrichment for cellular component in the Australian cline for genes that overlap windows in the top 2.5% tail of Fst.

2.5 % Tail Cellular Component		
GO term	q-value	description
GO:0005886	2.11E-13	plasma membrane
GO:0005634	1.38E-06	nucleus
GO:0005887	5.67E-05	integral to plasma membrane
GO:0005918	1.44E-04	septate junction
GO:0045211	9.38E-04	postsynaptic membrane
GO:0005912	1.42E-03	adherens junction
GO:0035003	1.42E-03	subapical complex
GO:0016327	1.42E-03	apicolateral plasma membrane
GO:0016324	1.42E-03	apical plasma membrane
GO:0045202	2.26E-03	synapse
GO:0016021	2.37E-03	integral to membrane
GO:0008076	3.27E-03	voltage-gated potassium channel complex
GO:0016459	5.74E-03	myosin complex
GO:0008021	6.02E-03	synaptic vesicle
GO:0045179	8.90E-03	apical cortex
GO:0043234	8.90E-03	protein complex
GO:0005667	1.15E-02	transcription factor complex
GO:0042600	1.48E-02	chorion
GO:0005622	1.68E-02	intracellular
GO:0016020	1.76E-02	membrane
GO:0005578	1.92E-02	proteinaceous extracellular matrix
GO:0005739	2.91E-02	mitochondrion
GO:0005875	3.68E-02	microtubule associated complex
GO:0005938	4.85E-02	cell cortex

Table S9 GO term enrichment for cellular component in the Australian cline for genes that overlap windows in the top 5% tail of Fst.

5 % Tail Cellular Component		
GO term	q-value	description
GO:0005886	1.98E-14	plasma membrane
GO:0005634	4.17E-11	nucleus
GO:0005887	2.97E-08	integral to plasma membrane
GO:0016021	2.72E-06	integral to membrane
GO:0016324	2.27E-04	apical plasma membrane
GO:0005913	3.46E-04	cell-cell adherens junction
GO:0045211	6.54E-04	postsynaptic membrane
GO:0035003	8.56E-04	subapical complex
GO:0005912	8.62E-04	adherens junction
GO:0005918	1.31E-03	septate junction
GO:0005737	1.76E-03	cytoplasm
GO:0045179	2.09E-03	apical cortex
GO:0005892	2.41E-03	nicotinic acetylcholine-gated receptor-channel complex
GO:0043195	2.41E-03	terminal button
GO:0016459	2.41E-03	myosin complex
GO:0005622	2.41E-03	intracellular
GO:0045202	2.41E-03	synapse
GO:0016323	2.41E-03	basolateral plasma membrane
GO:0008076	2.41E-03	voltage-gated potassium channel complex
GO:0016327	3.14E-03	apicolateral plasma membrane
GO:0005875	3.83E-03	microtubule associated complex
GO:0016020	4.18E-03	membrane
GO:0009986	4.52E-03	cell surface
GO:0008021	5.40E-03	synaptic vesicle
GO:0005578	6.13E-03	proteinaceous extracellular matrix
GO:0005604	8.43E-03	basement membrane
GO:0005938	8.74E-03	cell cortex
GO:0043190	1.26E-02	ATP-binding cassette (ABC) transporter complex
GO:0043025	1.36E-02	cell soma
GO:0005705	1.36E-02	polytene chromosome interband
GO:0030425	3.37E-02	dendrite
GO:0015629	3.37E-02	actin cytoskeleton
GO:0005667	3.98E-02	transcription factor complex

Table S10 GO term enrichment for biological process in the North American cline for genes that overlap windows in the top 1% tail of Fst.

	1 % Tail Biological Process	
GO term	q-value	description
GO:0007411	8.92E-06	axon guidance
GO:0006355	8.92E-06	regulation of transcription, DNA-dependent
GO:0007455	1.28E-04	eye-antennal disc morphogenesis
GO:0048749	1.30E-04	compound eye development
GO:0007165	1.54E-04	signal transduction
GO:0007155	2.44E-04	cell adhesion
GO:0007476	2.44E-04	imaginal disc-derived wing morphogenesis
GO:0007424	2.78E-04	open tracheal system development
GO:0007611	3.13E-04	learning or memory
GO:0030707	4.18E-04	ovarian follicle cell development
GO:0035317	4.18E-04	imaginal disc-derived wing hair organization
GO:0007530	4.18E-04	sex determination
GO:0007156	4.60E-04	homophilic cell adhesion
GO:0007422	5.26E-04	peripheral nervous system development
GO:0007350	7.08E-04	blastoderm segmentation
GO:0006811	1.16E-03	ion transport
GO:0006468	1.25E-03	protein amino acid phosphorylation
GO:0008355	1.77E-03	olfactory learning
GO:0006350	1.80E-03	transcription
GO:0016310	1.80E-03	phosphorylation
GO:0008104	1.82E-03	protein localization
GO:0006813	2.37E-03	potassium ion transport
GO:0007391	2.37E-03	dorsal closure
GO:0008407	2.75E-03	bristle morphogenesis
GO:0007623	2.85E-03	circadian rhythm
GO:0007420	2.85E-03	brain development
GO:0007186	3.70E-03	G-protein coupled receptor protein signaling pathway
GO:0007399	3.70E-03	nervous system development
GO:0045449	4.03E-03	regulation of transcription
GO:0048477	4.67E-03	oogenesis
GO:0048813	6.08E-03	dendrite morphogenesis
GO:0007242	8.01E-03	intracellular signaling cascade
GO:0008360	8.37E-03	regulation of cell shape
GO:0002121	8.37E-03	inter-male aggressive behavior
GO:0007417	9.30E-03	central nervous system development
GO:0007507	1.13E-02	heart development
GO:0007017	1.75E-02	microtubule-based process
GO:0006470	2.98E-02	protein amino acid dephosphorylation

Table S11 GO term enrichment for biological process in the North American cline for genes that overlap windows in the top 2.5% tail of Fst.

	2.5 % Tail Biological Process	
GO term	q-value	description
GO:0007476	1.63E-07	imaginal disc-derived wing morphogenesis
GO:0048749	1.63E-07	compound eye development
GO:0006355	1.63E-07	regulation of transcription, DNA-dependent
GO:0007411	3.96E-07	axon guidance
GO:0007350	1.62E-06	blastoderm segmentation
GO:0007155	4.43E-06	cell adhesion
GO:0007513	5.83E-06	pericardial cell differentiation
GO:0045449	8.22E-06	regulation of transcription
GO:0016203	1.10E-05	muscle attachment
GO:0007435	1.10E-05	salivary gland morphogenesis
GO:0007424	1.55E-05	open tracheal system development
GO:0006468	2.18E-05	protein amino acid phosphorylation
GO:0007156	2.62E-05	homophilic cell adhesion
GO:0007611	3.07E-05	learning or memory
GO:0035023	3.11E-05	regulation of Rho protein signal transduction
GO:0048477	8.61E-05	oogenesis
GO:0008355	8.63E-05	olfactory learning
GO:0007472	9.07E-05	wing disc morphogenesis
GO:0007399	9.14E-05	nervous system development
GO:0007242	1.17E-04	intracellular signaling cascade
GO:0007614	1.17E-04	short-term memory
GO:0007619	1.86E-04	courtship behavior
GO:0007165	2.23E-04	signal transduction
GO:0030097	2.46E-04	hemopoiesis
GO:0007268	2.87E-04	synaptic transmission
GO:0048800	3.69E-04	antennal morphogenesis
GO:0016318	4.06E-04	ommatidial rotation
GO:0008360	4.06E-04	regulation of cell shape
GO:0007417	4.06E-04	central nervous system development
GO:0016055	4.70E-04	Wnt receptor signaling pathway
GO:0007507	4.82E-04	heart development
GO:0035277	4.82E-04	spiracle morphogenesis, open tracheal system
GO:0007474	5.54E-04	imaginal disc-derived wing vein specification
GO:0007186	5.87E-04	G-protein coupled receptor protein signaling pathway
GO:0007617	6.47E-04	mating behavior
GO:0035172	6.47E-04	hemocyte proliferation
GO:0035225	6.47E-04	determination of genital disc primordium
GO:0007455	7.31E-04	eye-antennal disc morphogenesis
GO:0008407	7.66E-04	bristle morphogenesis
GO:0007428	1.01E-03	primary branching, open tracheal system

GO:0007420	1.03E-03	brain development
GO:0006811	1.05E-03	ion transport
GO:0008104	1.05E-03	protein localization
GO:0008356	1.07E-03	asymmetric cell division
GO:0007391	1.12E-03	dorsal closure
GO:0045433	1.15E-03	male courtship behavior, veined wing generated song production
GO:0007632	1.15E-03	visual behavior
GO:0001745	1.22E-03	compound eye morphogenesis
GO:0008586	1.25E-03	imaginal disc-derived wing vein morphogenesis
GO:0007400	1.43E-03	neuroblast fate determination
GO:0040014	1.43E-03	regulation of multicellular organism growth
GO:0016477	1.47E-03	cell migration
GO:0007422	1.57E-03	peripheral nervous system development
GO:0006813	1.80E-03	potassium ion transport
GO:0030707	1.83E-03	ovarian follicle cell development
GO:0045475	1.85E-03	locomotor rhythm
GO:0040018	1.85E-03	positive regulation of multicellular organism growth
GO:0048675	1.85E-03	axon extension
GO:0007173	1.99E-03	epidermal growth factor receptor signaling pathway
GO:0045165	1.99E-03	cell fate commitment
GO:0008286	1.99E-03	insulin receptor signaling pathway
GO:0030162	1.99E-03	regulation of proteolysis
GO:0007498	2.01E-03	mesoderm development
GO:0007017	2.07E-03	microtubule-based process
GO:0008105	2.68E-03	asymmetric protein localization
GO:0007442	2.68E-03	hindgut morphogenesis
GO:0007475	2.68E-03	apposition of dorsal and ventral imaginal disc-derived wing surfaces
GO:0006916	2.68E-03	anti-apoptosis
GO:0007443	2.68E-03	Malpighian tubule morphogenesis
GO:0030307	2.68E-03	positive regulation of cell growth
GO:0035317	2.68E-03	imaginal disc-derived wing hair organization
GO:0048149	2.68E-03	behavioral response to ethanol
GO:0006816	2.68E-03	calcium ion transport
GO:0008345	2.68E-03	larval locomotory behavior
GO:0007623	2.82E-03	circadian rhythm
GO:0001737	3.83E-03	establishment of imaginal disc-derived wing hair orientation
GO:0002168	3.83E-03	instar larval development
GO:0016199	3.83E-03	axon midline choice point recognition
GO:0030713	3.83E-03	ovarian follicle cell stalk formation
GO:0007369	3.83E-03	gastrulation
GO:0008049	3.83E-03	male courtship behavior
GO:0007431	3.83E-03	salivary gland development
GO:0042051	3.83E-03	compound eye photoreceptor development
GO:0007629	3.83E-03	flight behavior

GO:0007528	3.83E-03	neuromuscular junction development
GO:0008045	4.17E-03	motor axon guidance
GO:0007419	4.17E-03	ventral cord development
GO:0007427	4.17E-03	epithelial cell migration, open tracheal system
GO:0007269	5.13E-03	neurotransmitter secretion
GO:0007446	5.54E-03	imaginal disc growth
GO:0051017	5.54E-03	actin filament bundle formation
GO:0007416	5.54E-03	synapse assembly
GO:0001736	5.54E-03	establishment of planar polarity
GO:0007298	6.19E-03	border follicle cell migration
GO:0007140	6.53E-03	male meiosis
GO:0042067	6.53E-03	establishment of ommatidial polarity
GO:0030178	6.53E-03	negative regulation of Wnt receptor signaling pathway
GO:0007398	6.53E-03	ectoderm development
GO:0045893	6.86E-03	positive regulation of transcription, DNA-dependent
GO:0007349	6.86E-03	cellularization
GO:0001709	7.60E-03	cell fate determination
GO:0008344	7.60E-03	adult locomotory behavior
GO:0048190	7.89E-03	wing disc dorsal/ventral pattern formation
GO:0007494	8.46E-03	midgut development
GO:0007520	8.46E-03	myoblast fusion
GO:0001700	8.54E-03	embryonic development via the syncytial blastoderm
GO:0007530	9.93E-03	sex determination
GO:0001708	9.93E-03	cell fate specification
GO:0002121	9.93E-03	inter-male aggressive behavior
GO:0007390	9.93E-03	germ-band shortening
GO:0051276	9.93E-03	chromosome organization
GO:0000226	9.93E-03	microtubule cytoskeleton organization
GO:0019991	9.93E-03	septate junction assembly
GO:0055059	1.06E-02	asymmetric neuroblast division
GO:0007015	1.16E-02	actin filament organization
GO:0007517	1.19E-02	muscle organ development
GO:0007602	1.19E-02	phototransduction
GO:0045944	1.28E-02	positive regulation of transcription from RNA polymerase II promoter
GO:0007224	1.31E-02	smoothened signaling pathway
GO:0007317	1.31E-02	regulation of pole plasm oskar mRNA localization
GO:0016310	1.31E-02	phosphorylation
GO:0007274	1.31E-02	neuromuscular synaptic transmission
GO:0007163	1.68E-02	establishment or maintenance of cell polarity
GO:0007480	1.72E-02	imaginal disc-derived leg morphogenesis
GO:0006915	2.03E-02	apoptosis
GO:0030036	2.03E-02	actin cytoskeleton organization
GO:0006357	2.05E-02	regulation of transcription from RNA polymerase II promoter
GO:0030718	2.05E-02	germ-line stem cell maintenance

GO:0008595	2.05E-02	determination of anterior/posterior axis, embryo
GO:0001751	2.13E-02	compound eye photoreceptor cell differentiation
GO:0007346	2.13E-02	regulation of mitotic cell cycle
GO:0040007	2.13E-02	growth
GO:0006350	2.20E-02	transcription
GO:0006470	2.33E-02	protein amino acid dephosphorylation
GO:0007444	2.44E-02	imaginal disc development
GO:0008340	2.44E-02	determination of adult lifespan
GO:0002009	2.66E-02	morphogenesis of an epithelium
GO:0048813	3.11E-02	dendrite morphogenesis
GO:0006911	3.11E-02	phagocytosis, engulfment
GO:0006836	3.30E-02	neurotransmitter transport
GO:0008298	4.08E-02	intracellular mRNA localization
GO:0016321	4.24E-02	female meiosis chromosome segregation
GO:0016567	4.99E-02	protein ubiquitination
GO:0046843	4.99E-02	dorsal appendage formation

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

Table S13 GO term enrichment for molecular function in the North American cline for genes that overlap windows in the top 1% tail of Fst.

	1 % Tail Molecular Function	
GO term	q-value	description
GO:0003700	3.80E-07	transcription factor activity
GO:0043565	2.48E-05	sequence-specific DNA binding
GO:0003704	5.27E-05	specific RNA polymerase II transcription factor activity
GO:0004672	2.96E-04	protein kinase activity
GO:0005515	5.34E-04	protein binding
GO:0000166	5.34E-04	nucleotide binding
GO:0019992	2.01E-03	diacylglycerol binding
GO:0016563	3.32E-03	transcription activator activity
GO:0004674	7.09E-03	protein serine/threonine kinase activity
GO:0003702	7.18E-03	RNA polymerase II transcription factor activity
GO:0004725	7.68E-03	protein tyrosine phosphatase activity
GO:0008188	7.68E-03	neuropeptide receptor activity
GO:0008270	1.08E-02	zinc ion binding
GO:0005509	1.64E-02	calcium ion binding
GO:0042803	1.89E-02	protein homodimerization activity
GO:0003729	1.89E-02	mRNA binding
GO:0004713	2.04E-02	protein tyrosine kinase activity
GO:0003677	2.07E-02	DNA binding
GO:0003779	2.20E-02	actin binding
GO:0003774	2.55E-02	motor activity
GO:0008017	3.42E-02	microtubule binding
GO:0020037	3.96E-02	heme binding
GO:0003723	4.02E-02	RNA binding
GO:0042623	4.75E-02	ATPase activity, coupled
GO:0004930	4.94E-02	G-protein coupled receptor activity

Table S14 GO term enrichment for molecular function in the North American cline for genes that overlap windows in the top 2.5% tail of Fst.

	2.5% Tail Molecular Function	
GO term	q-value	description
GO:0003700	4.16E-10	transcription factor activity
GO:0043565	1.61E-08	sequence-specific DNA binding
GO:0005515	2.23E-05	protein binding
GO:0005089	4.38E-05	Rho guanyl-nucleotide exchange factor activity
GO:0003702	1.09E-04	RNA polymerase II transcription factor activity
GO:0004714	1.09E-04	transmembrane receptor protein tyrosine kinase activity
GO:0004871	1.62E-04	signal transducer activity
GO:0004672	1.87E-04	protein kinase activity
GO:0008270	2.93E-04	zinc ion binding
GO:0003707	3.28E-04	steroid hormone receptor activity
GO:0004879	3.28E-04	ligand-dependent nuclear receptor activity
GO:0008227	4.83E-04	amine receptor activity
GO:0003713	5.28E-04	transcription coactivator activity
GO:0008134	7.22E-04	transcription factor binding
GO:0000166	7.22E-04	nucleotide binding
GO:0003729	1.66E-03	mRNA binding
GO:0004713	1.68E-03	protein tyrosine kinase activity
GO:0003779	1.76E-03	actin binding
GO:0005509	1.89E-03	calcium ion binding
GO:0008188	1.89E-03	neuropeptide receptor activity
GO:0004674	1.90E-03	protein serine/threonine kinase activity
GO:0003704	2.08E-03	specific RNA polymerase II transcription factor activity
GO:0019992	2.68E-03	diacylglycerol binding
GO:0008092	2.68E-03	cytoskeletal protein binding
GO:0004888	2.68E-03	transmembrane receptor activity
GO:0005096	4.22E-03	GTPase activator activity
GO:0003714	4.22E-03	transcription corepressor activity
GO:0004725	5.05E-03	protein tyrosine phosphatase activity
GO:0005524	5.99E-03	ATP binding
GO:0016563	7.45E-03	transcription activator activity
GO:0005102	7.82E-03	receptor binding
GO:0003677	8.76E-03	DNA binding
GO:0042803	9.25E-03	protein homodimerization activity
GO:0005085	1.00E-02	guanyl-nucleotide exchange factor activity
GO:0008017	1.18E-02	microtubule binding
GO:0004930	1.23E-02	G-protein coupled receptor activity
GO:0003774	1.87E-02	motor activity
GO:0003723	1.95E-02	RNA binding
GO:0008083	2.42E-02	growth factor activity
GO:0032183	2.42E-02	SUMO binding

GO:0042623	2.42E-02	ATPase activity, coupled
GO:0003676	4.34E-02	nucleic acid binding
GO:0003777	4.95E-02	microtubule motor activity

Table S15 GO term enrichment for molecular function in the North American cline for genes that overlap windows in the top 5% tail of Fst.

	5% Tail Molecular Function	
GO term	q-value	description
GO:0019904	0.00E+00	protein domain specific binding
GO:0003700	9.43E-13	transcription factor activity
GO:0043565	5.69E-09	sequence-specific DNA binding
GO:0005515	6.05E-09	protein binding
GO:0005089	1.47E-07	Rho guanyl-nucleotide exchange factor activity
GO:0003704	1.19E-06	specific RNA polymerase II transcription factor activity
GO:0005509	6.53E-06	calcium ion binding
GO:0004871	1.82E-05	signal transducer activity
GO:0008270	4.25E-05	zinc ion binding
GO:0003702	5.31E-05	RNA polymerase II transcription factor activity
GO:0016563	6.32E-05	transcription activator activity
GO:0017147	7.70E-05	Wnt-protein binding
GO:0004674	2.20E-04	protein serine/threonine kinase activity
GO:0004714	3.05E-04	transmembrane receptor protein tyrosine kinase activity
GO:0005267	3.09E-04	potassium channel activity
GO:0008188	3.09E-04	neuropeptide receptor activity
GO:0003779	4.30E-04	actin binding
GO:0008017	5.96E-04	microtubule binding
GO:0004879	8.37E-04	ligand-dependent nuclear receptor activity
GO:0003707	8.37E-04	steroid hormone receptor activity
GO:0004672	8.90E-04	protein kinase activity
GO:0005041	1.27E-03	low-density lipoprotein receptor activity
GO:0004888	1.63E-03	transmembrane receptor activity
GO:0003713	1.63E-03	transcription coactivator activity
GO:0004713	1.88E-03	protein tyrosine kinase activity
GO:0008227	2.12E-03	amine receptor activity
GO:0008134	2.31E-03	transcription factor binding
GO:0005326	2.31E-03	neurotransmitter transporter activity
GO:0004889	3.22E-03	nicotinic acetylcholine-activated cation-selective channel activity
GO:0005524	3.50E-03	ATP binding
GO:0032183	4.08E-03	SUMO binding
GO:0003714	5.58E-03	transcription corepressor activity
GO:0005096	5.58E-03	GTPase activator activity
GO:0005102	7.22E-03	receptor binding
GO:0003677	7.22E-03	DNA binding
GO:0004725	1.73E-02	protein tyrosine phosphatase activity
GO:0008092	1.97E-02	cytoskeletal protein binding
GO:0005112	2.38E-02	Notch binding
GO:0042803	2.51E-02	protein homodimerization activity
GO:0042623	2.97E-02	ATPase activity, coupled

GO:0005085	3.07E-02	guanyl-nucleotide exchange factor activity
GO:0030528	3.28E-02	transcription regulator activity
GO:0004930	3.32E-02	G-protein coupled receptor activity
GO:0000166	4.61E-02	nucleotide binding
GO:0000287	4.61E-02	magnesium ion binding
GO:0004653	4.93E-02	polypeptide N-acetylgalactosaminyltransferase activity
GO:0050839	4.93E-02	cell adhesion molecule binding
GO:0003729	4.93E-02	mRNA binding
GO:0019992	4.98E-02	diacylglycerol binding

Table S16 GO term enrichment for cellular component in the North American cline for genes that overlap windows in the top 1% tail of Fst.

	1 % Tail Cellular Component	
GO term	q-value	description
GO:0005634	6.87E-09	nucleus
GO:0005622	4.74E-03	intracellular
GO:0005886	4.74E-03	plasma membrane
GO:0016021	2.47E-02	integral to membrane
GO:0005875	2.47E-02	microtubule associated complex
GO:0005938	2.47E-02	cell cortex
GO:0005887	2.47E-02	integral to plasma membrane
GO:0016020	2.93E-02	membrane
GO:0005737	4.09E-02	cytoplasm
GO:0005794	4.95E-02	Golgi apparatus

Table S17 GO term enrichment for cellular component in the North American cline for genes that overlap windows in the top 2.5% tail of Fst.

2.5% Tail Cellular Component		
GO term	q-value	description
GO:0005634	2.94E-12	nucleus
GO:0005886	8.90E-10	plasma membrane
GO:0005737	1.72E-04	cytoplasm
GO:0045211	8.60E-04	postsynaptic membrane
GO:0016021	8.60E-04	integral to membrane
GO:0005622	8.60E-04	intracellular
GO:0005578	8.60E-04	proteinaceous extracellular matrix
GO:0045179	8.60E-04	apical cortex
GO:0005887	1.11E-03	integral to plasma membrane
GO:0045202	2.75E-03	synapse
GO:0005918	3.83E-03	septate junction
GO:0005875	4.55E-03	microtubule associated complex
GO:0016459	6.83E-03	myosin complex
GO:0005794	1.15E-02	Golgi apparatus
GO:0005938	1.15E-02	cell cortex
GO:0005576	2.29E-02	extracellular region
GO:0005912	2.30E-02	adherens junction
GO:0005700	2.37E-02	polytene chromosome
GO:0016020	4.28E-02	membrane
GO:0008021	4.90E-02	synaptic vesicle

Table S18 GO term enrichment for cellular component in the North American cline for genes that overlap windows in the top 5% tail of Fst.

	5% Tail Cellular Component	
GO term	q-value	description
GO:0005634	6.54E-12	nucleus
GO:0005886	5.50E-10	plasma membrane
GO:0005622	5.70E-07	intracellular
GO:0005737	2.14E-04	cytoplasm
GO:0045179	2.14E-04	apical cortex
GO:0005578	4.05E-04	proteinaceous extracellular matrix
GO:0016021	4.33E-04	integral to membrane
GO:0005887	9.71E-04	integral to plasma membrane
GO:0035003	9.71E-04	subapical complex
GO:0005938	1.01E-03	cell cortex
GO:0009986	1.09E-03	cell surface
GO:0005918	1.47E-03	septate junction
GO:0045211	2.63E-03	postsynaptic membrane
GO:0005875	3.15E-03	microtubule associated complex
GO:0005892	3.25E-03	nicotinic acetylcholine-gated receptor-channel complex
GO:0016324	3.57E-03	apical plasma membrane
GO:0016459	1.42E-02	myosin complex
GO:0005768	1.42E-02	endosome
GO:0005794	1.64E-02	Golgi apparatus
GO:0005795	1.90E-02	Golgi stack
GO:0045172	2.14E-02	germline ring canal
GO:0030135	2.14E-02	coated vesicle
GO:0000775	2.40E-02	chromosome, centromeric region
GO:0005813	3.04E-02	centrosome
GO:0045177	3.04E-02	apical part of cell
GO:0005868	3.04E-02	cytoplasmic dynein complex
GO:0005912	3.39E-02	adherens junction
GO:0045202	3.69E-02	synapse
GO:0005874	3.69E-02	microtubule
GO:0043190	4.14E-02	ATP-binding cassette (ABC) transporter complex
GO:0005576	4.25E-02	extracellular region
GO:0016020	4.75E-02	membrane

Table S19 Annotations of single nucleotide polymorphisms present on both continents

	All shared SNPs	All convergent SNPs	Strongly convergent SNPs (top 10% FST on both continents)
All annotations	361171	229705	4038
Three Prime UTR	11399	6552	107
Five prime UTR	8684	5107	99
Nonsynonymous	13526	8811	147
Synonymous	45398	29450	499
Intronic	150302	97021	1754
Intergenic	131799	82754	1432

Table S20 Functional annotation of strongly convergent UTR and nonsynonymous SNPs

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.161463/-/DC1

Table S21 Functional annotation of extremely differentiated convergent SNPs

Chr	Position	SNP classification	Fbgn	Gene Name	Functional Summary	AUFST	NAFST	Codon change	AA change
3R	15229365	five prime UTR	FBgn0038704	Aprataxin-like protein	DNA repair, metal binding	5.24E-01	6.31E-01	NA	NA
3R	12842274	five prime UTR	FBgn0004577	Dmel_CG15337	Unknown	5.26E-01	5.22E-01	NA	NA
X	8054656	nonsynonymous	FBgn0030014	Dmel_CG31091	lipid and ester catabolism	5.12E-01	4.65E-01	ATG->TTG	M->L
2R	7013061	nonsynonymous	FBgn0053503	Dmel_CG4218	Unknown	8.23E-01	6.75E-01	TTA->TCA	L->S
2L	14547899	nonsynonymous	FBgn0250844	Dmel_CG6454	calcium channel membrane targeting	5.12E-01	4.65E-01	AAG->ATG	K->M
3R	20766471	nonsynonymous	FBgn0029157	Peroxidase	response to oxidative stress /peroxide metabolism	8.23E-01	5.46E-01	TTG->TTC	L->F
3R	20177828	nonsynonymous	FBgn0039187	Probable cytochrome P450 12d1	oxidation/reduction, metal binding	6.44E-01	6.45E-01	ACT->AGT	T->S
3R	21727544	nonsynonymous	FBgn0051091	slingshot	eye development/mushroom body development	7.39E-01	7.55E-01	TCC->GCC	S->A

Table S22 Candidate convergent nonsynonymous SNPs

Position	N1	N2	Fst	Codon		AA	mel and outgroup ref sequence state
hkl							
AUS 19,045,921	20	29	0.34	aac/gac	N/D	D= mel,sim, sech, yak, ere; Q = ana	
AUS 19,045,936	20	30	0.21	aaa/gaa	K/E	many changes from E to K and reverse	
NA 19,045,921	not segregating						
NA 19,045,936	not segregating						
NA 19,046,788	28	34	0.35	aca/cca	T/P	P = mel,sim, sech, yak, ere, ana; other species not T	
NA 19,046,828	29	27	0.48	aac/agc	N/S	S=mel,sim,sech,ana,pse,pers,vir,moj,grim; T = ere, L=will	
AUS 19,046,788	not segregating						
AUS 19,046,828	not segregating						
otk							
AUS 7,890,468	29	22	0.38	gtg/ctg	V/L	L = all species	
AUS 7, 890,646	18	26	0.33	gat/gag	D/E	D = mel; E = other species	
AUS 7,901,503	36	43	0.26	ttg/tcg		L/S	L = all species
NA 7,890,468		not segregating					
NA 7, 890,646	not segregating						
NA 7,901,503		not segregating					
NA 7,892,834				0.71	tct/gct		S/A
NA 7,892,839				0.70	agc/aac	S/N	
AUS 7,892,834	not segregating						
AUS 7,892,839	not segregating						
Position	N1	N2	Fst	Codon		AA	mel and outgroup ref sequence state
ana1							
AUS 20,359,353	31	37	0.36	gag/gcg	E/A	E=mel;A=sim,sech,yak,ere	
AUS 20,359,385	33	36	0.45	cga/gga	R/G	R=mel,sim,yak,ere,ana	
NA 20,359,353	15	49	0.007				
NA 20,359,385	not segregating						

NA 20,360,921	36	52	0.33	atg/ctg	M/L	L=all flies except virilis; virilis=M		
NA 20,361,171	36	39	0.38	cag/ctg	Q/L	Q= mel, si, sech,yak, pse, pers. will, moj; R=ere;H=ana;L=vir, gri		
AUS 20,360,921	43	28	0.007					
AUS 20,361,171	35	27	0.06					
Chm								
AUS 7,413,693	23	29	0.52	cag/gag	Q/E	Q= all species		
NA 7,413,693		not segregating						
NA 7,412,813		30	56	0.24	gat/tat		D/Y	Y=mel;D=si, sech, yak, ere, ana, wil, vir, moj, gri;E=pse,pers
NA 7,413,132		23	36	0.22	cca/cga	P/R	R=all species; no data for willistoni	
AUS 7,412,813	not segregating							
AUS 7,413,132	not segregating							
Trp								
AUS 25,740,476	20	24	0.35	ggc/agc	G/S	S=mel;G=sim,sech,yak,ere,ana,;A=pse;T=will, other no data		
AUS 25,741,376	36	27	0.22	tca/cca	S/P	P=mel,si,sech,ya,ere,ana,pse,pers,will;T=vir,gri;others ND		
NA 25,740,476	38	52	0.02					
NA 25,741,376	36	56	0.06					
NA 25,741,665	27	28	0.34	ttc/tcc		F/S	S=mel,sim,sech,yak,ere;A=ana,pse.pers.will.moj.gri	
NA 25,743,316	32	40	0.24	cac/aac	H/N	N=ana; H=all other species		
AUS 25,741,665	not segregating							
AUS 25,743,316	27	18	0.10					

CANDIDATE NORTH AMERICAN SPECIFIC DIFFERENTIATED NONSYNONYMOUS SNPS

Gene	Position	N1	N2	Fst	codon		residue	references sequence states	
Lsp2 (3L) 12,122,543		37	36	0.41	atg/gtg	M/V		V=mel,sim,sech,yak,ere,ana,pse,pers,grim;	
	Not segregating in AUS								L=wil,vi,moj
Oatp33Ea (2L) 12,442,835		31	65	0.50	tgt/ggt		C/G		L=all species
In AUS		29	37	0.08					

Table S23.

	Average coverage		Number of fixed or polymorphic bases		Number of singleton bases	
Seed length	30	45	30	45	30	45
k1n3	25.4	25.1	15801	15336	74753	72716
k2n5	30	29.9	19737	19522	149263	148169
k3n7	32	32	22457	22306	157904	157193
k4n9	32.4	32.4	23891	23744	160718	160294

s = seed length   k = number of errors allowed in the seed

n = number of errors allowed in the entire read

Table S24 Genome-wide average pairwise 1KB window Fst

	FLA	MAINE	QUE	TAZ
FLA	-	0.066	0.063	0.077
MAINE	-	-	0.066	0.067
QUE	-	-	-	0.072
TAZ	-	-	-	-

Table S25 ChrX average pairwise 1KB window Fst

	FLA	MAINE	QUE	TAZ
FLA	-	0.061	0.061	0.071
MAINE	-	-	0.058	0.069
QUE	-	-	-	0.06
TAZ	-	-	-	-

Table S26 Chr2L average pairwise 1KB window Fst

	FLA	MAINE	QUE	TAZ
FLA	-	0.069	0.063	0.083
MAINE	-	-	0.068	0.067
QUE	-	-	-	0.075
TAZ	-	-	-	-

Table S27 Chr2R average pairwise 1KB window Fst

	FLA	MAINE	QUE	TAZ
FLA	-	0.062	0.064	0.073
MAINE	-	-	0.062	0.067
QUE	-	-	-	0.067
TAZ	-	-	-	-

Table S28 Chr3L average pairwise 1KB window Fst

	FLA	MAINE	QUE	TAZ
FLA	-	0.065	0.064	0.077
MAINE	-	-	0.064	0.069
QUE	-	-	-	0.072
TAZ	-	-	-	-

Table S29 Chr3R average pairwise 1KB window Fst

	FLA	MAINE	QUE	TAZ
FLA	-	0.071	0.064	0.081
MAINE	-	-	0.076	0.06
QUE	-	-	-	0.083
TAZ	-	-	-	-