

Supplementary Material

Integrative evidence reveals adaptive divergence and speciation in gentoo penguins

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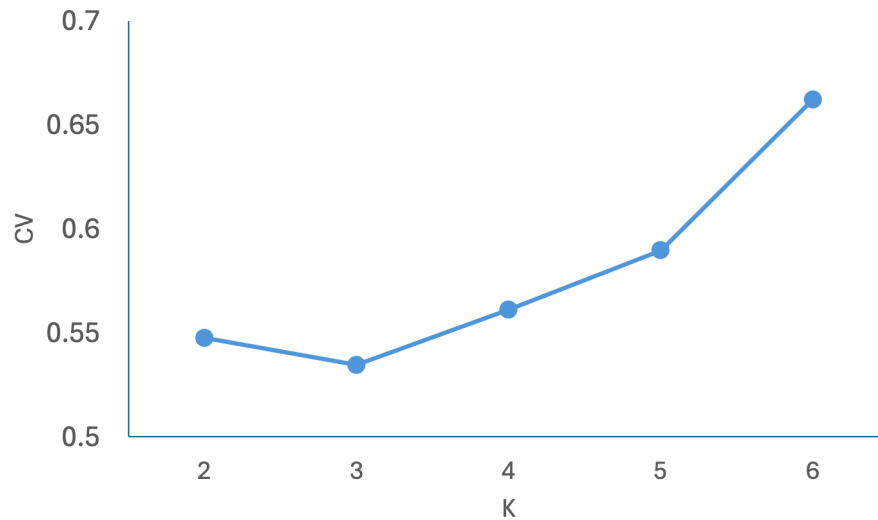


Fig. S1. Cross-validation error plot from ADMIXTURE analyses across $K = 1$ to $K = 6$. The model with $K = 3$ showed the lowest cross-validation error, suggesting potential genetic admixture in the Kerguelen population. However, $K = 4$ (highlighted in the main text) clearly reflects the genetic separation of the four lineages identified in this study.

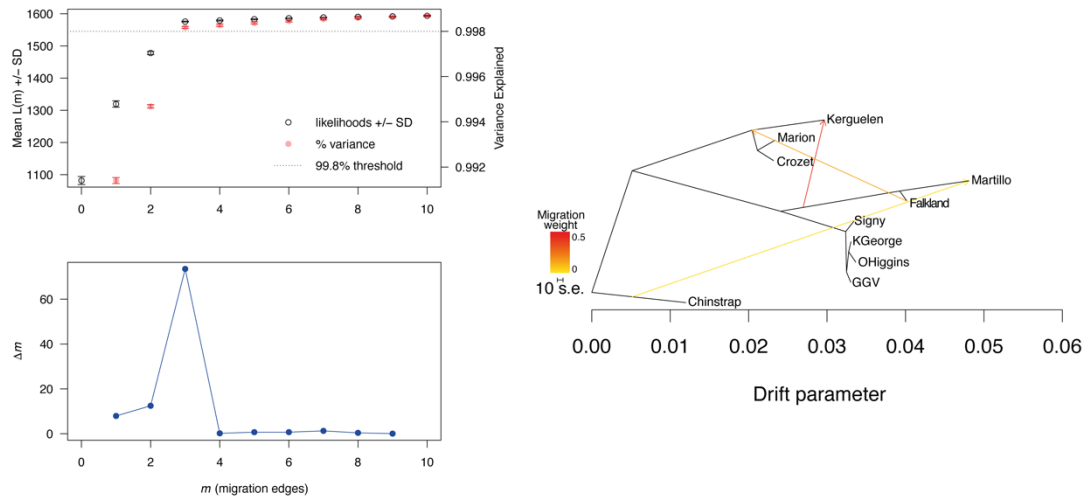


Fig. S2. Treemix results showing population splits and inferred migration events among *Pygoscelis* populations. Left panels: Model likelihood and variance explained across 0 to 10 migration edges (top), and Δm plot used to determine the optimal number of migration edges (bottom). A plateau in both variances explained, and likelihood is observed after $m = 3$, suggesting three significant migration events. Right panel: Maximum likelihood tree with three migration edges, where arrow color indicates migration weight (see legend). Notably, one inferred migration edge from chinstrap penguin, the outgroup, to the Martillo Island population is likely an artifact, as only one Chinstrap individual and five Martillo individuals were included in the analysis.

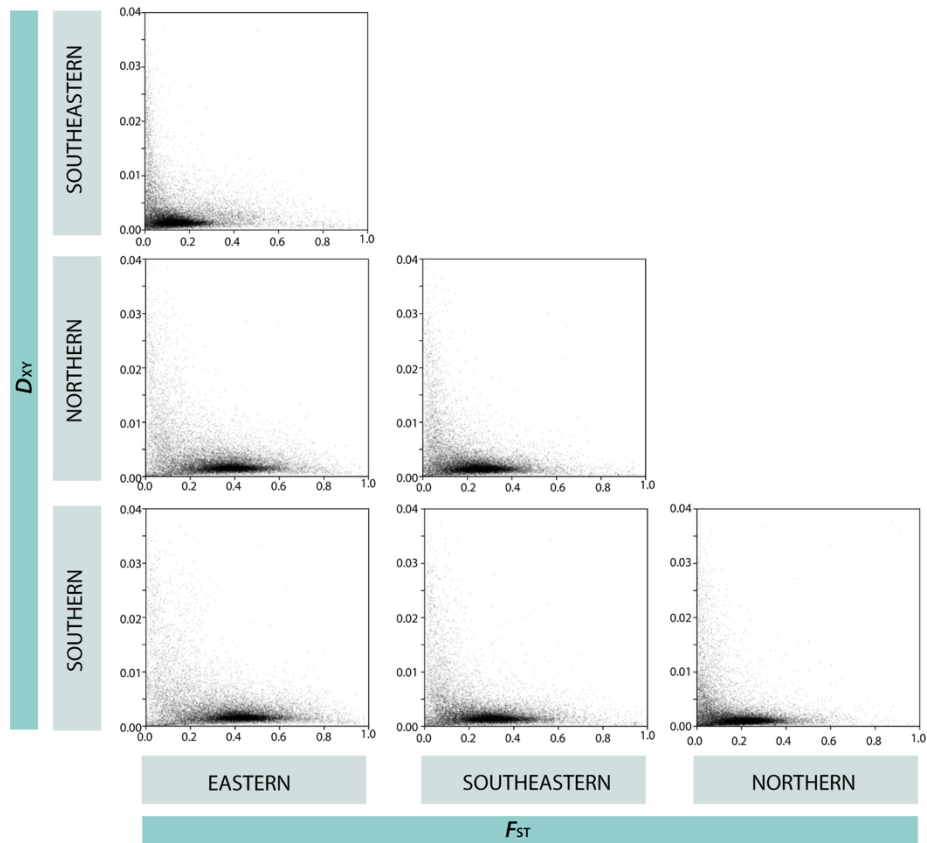


Fig. S3. Pairwise comparisons of relative genetic differentiation (F_{ST} , x-axis) and absolute divergence (D_{XY} , y-axis) among gentoo penguin lineages across 200 kb genomic windows, using both variant and invariant sites. Comparisons are shown for all pairs of lineages. Each panel represents a unique lineage pair. Elevated F_{ST} combined with reduced D_{XY} indicates localized genomic regions of differentiation potentially shaped by selection and/or reduced diversity.

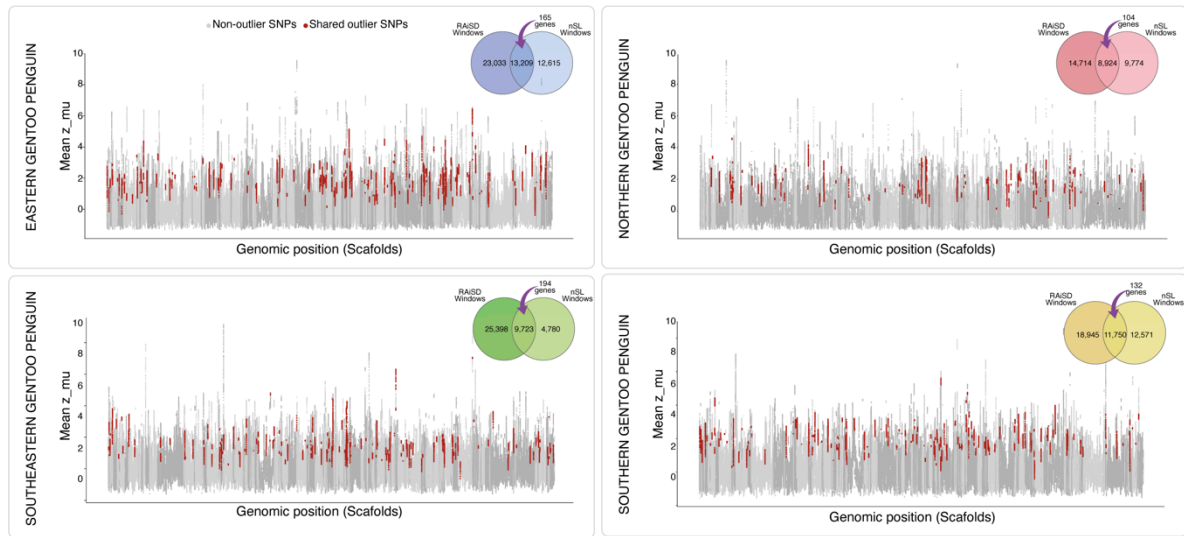


Fig. S4. Manhattan plot of outlier windows: Red point represent SNPs placed within the intersection of outlier windows.

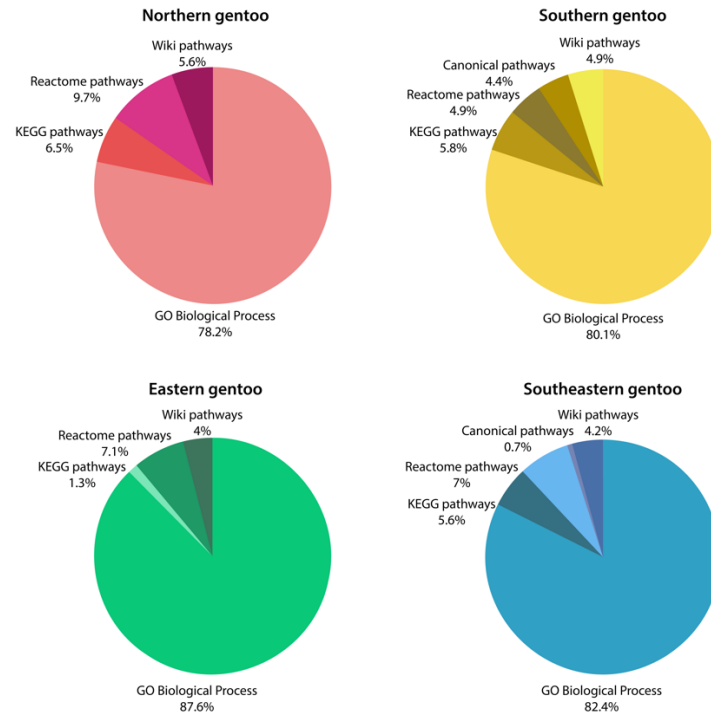


Fig. S5. Categories in enrichment analysis. The figure shows the proportion of functional categories assigned to the gene list of each lineage. The number of Entrez-mapped genes in METASCAPE was 103 out of 104 for the northern lineage, 130 out of 132 for the southern lineage, 191 out of 194 for the southeastern lineage, and 163 out of 165 for the eastern lineage.

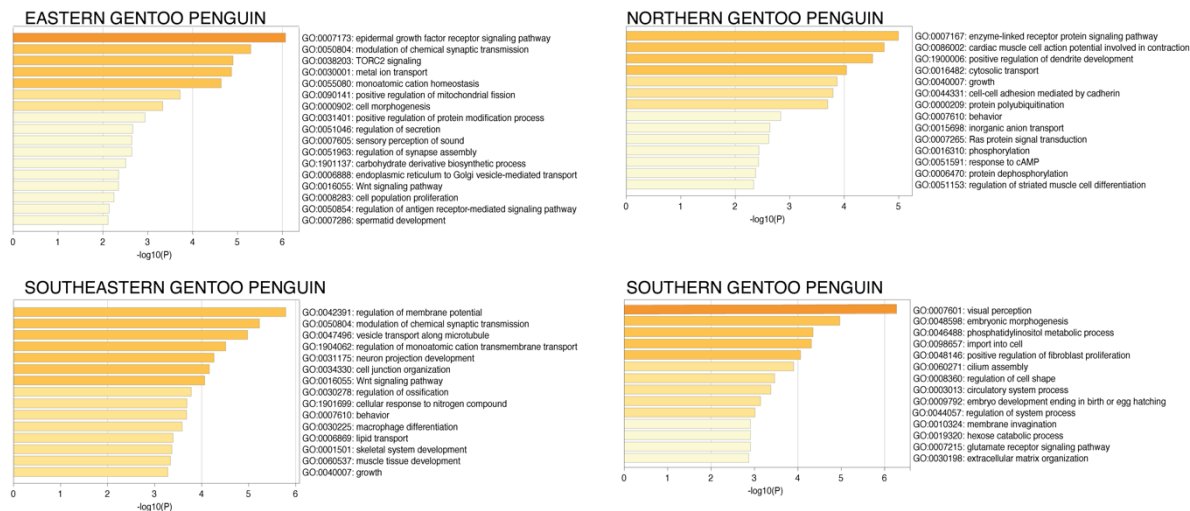


Fig. S6. Heatmaps of enriched functional categories across gentoo penguin lineages. Metascape-generated heatmaps showing significantly enriched biological pathways (GO Biological Process, Reactome, KEGG, and WikiPathways) for candidate genes located in outlier windows identified by both RAiSD and nSL. Each panel corresponds to a different gentoo penguin lineage, and enriched terms are displayed along the rows, with color intensity representing statistical significance (adjusted p-values). These visualizations allow comparison of functional enrichment patterns and highlight lineage-specific biological processes potentially associated with positive selection.

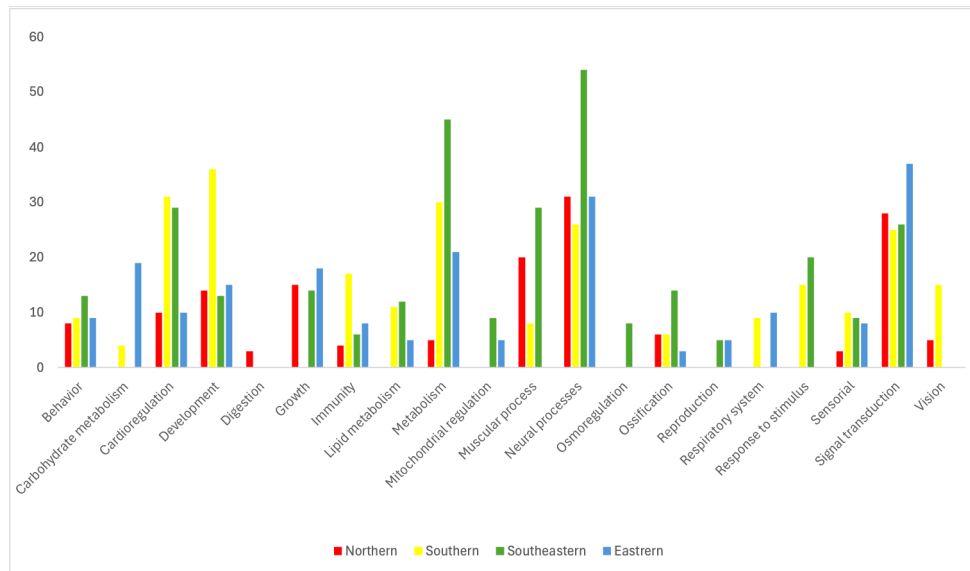


Fig. S7: Enrichment comparison. Bar plot showing the number of genes assigned to each enriched functional category per lineage, based on GO term enrichment analysis using Metascape. This plot was generated manually in Excel using data from Table S7, which includes genes located in outlier windows detected by both RAiSD and nSL. Only categories with significant enrichment (adjusted $p < 0.05$) were included. The figure illustrates the distribution and diversity of functional themes potentially involved in lineage-specific adaptive divergence.

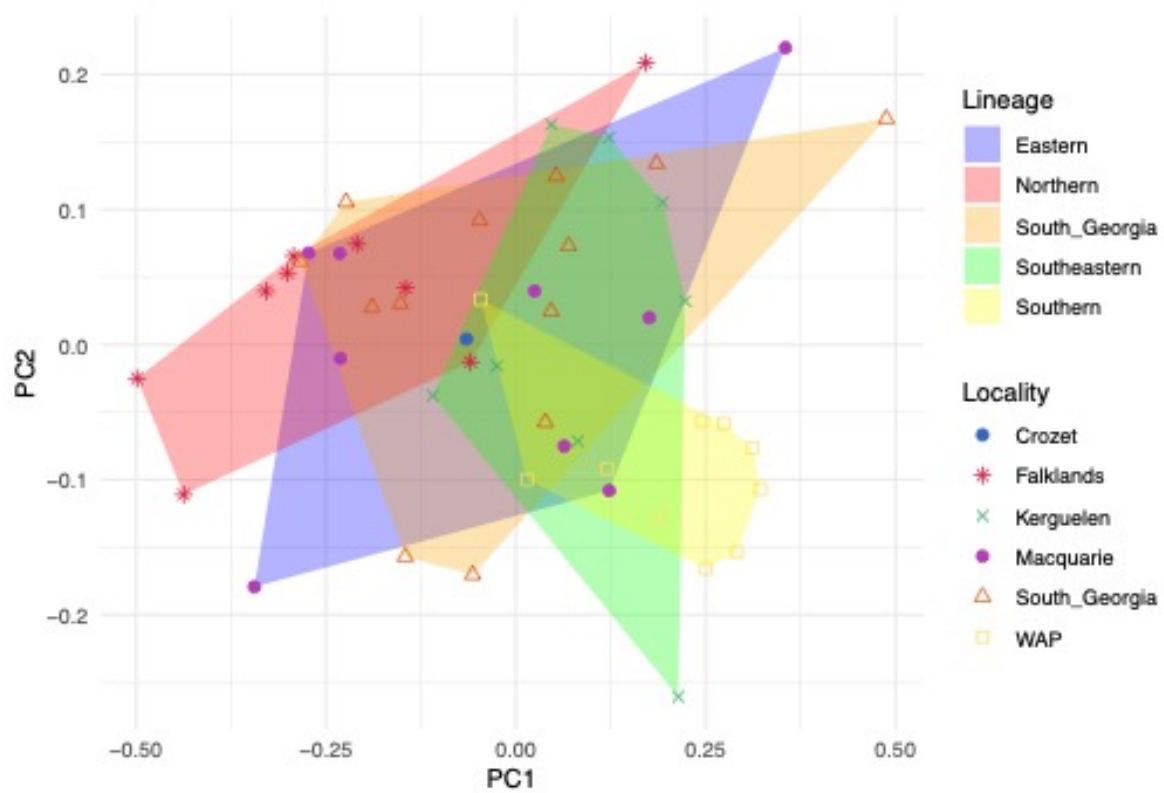


Fig. S8. **Morphological comparisons.** Principal component analysis of morphometric measures. Polygons indicate the six evolutionary units previously described.

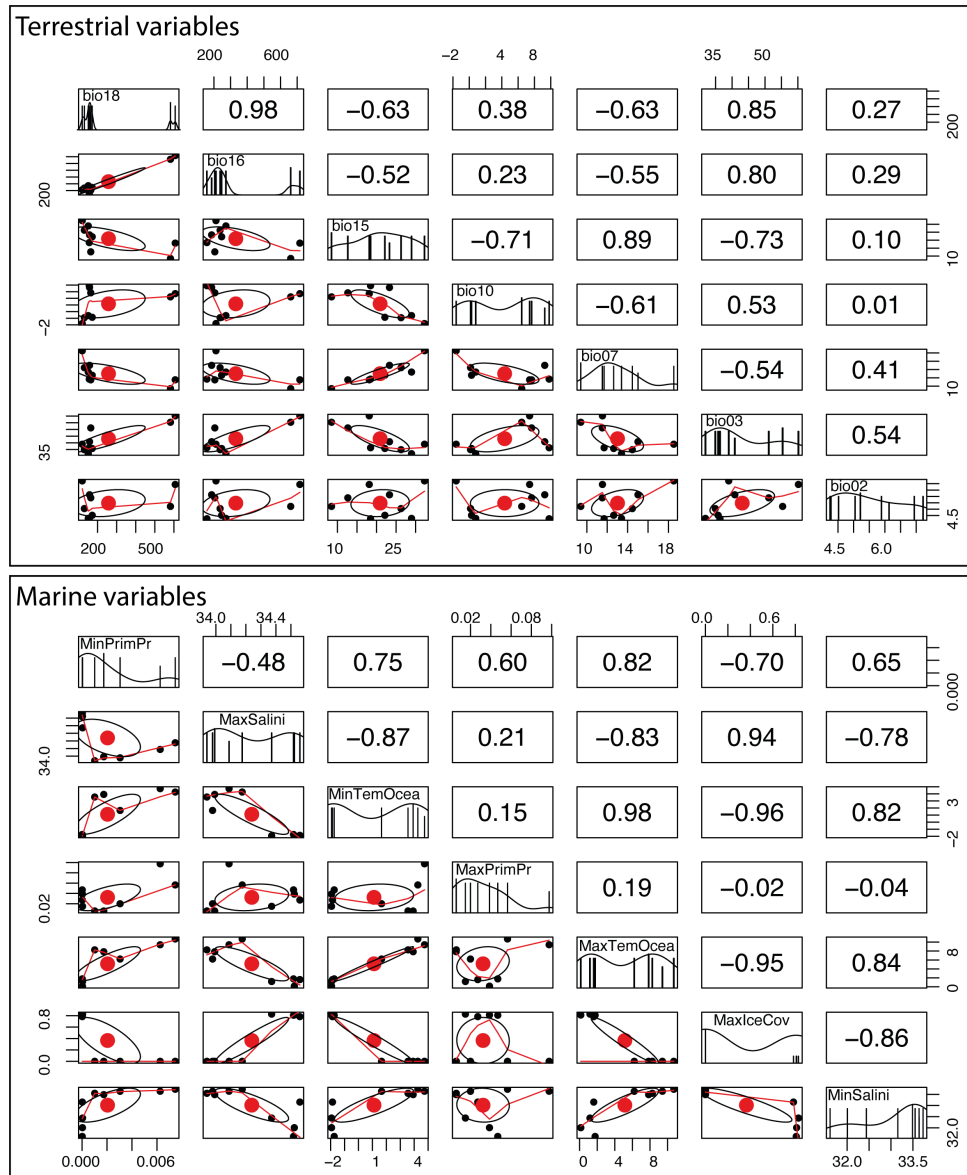


Fig. S9. Pairwise correlations among terrestrial (top panel) and marine (bottom panel) bioclimatic variables used in redundancy analysis (RDA). Scatterplots, histograms, and Pearson's correlation coefficients are shown for all variable pairs. Only variables with pairwise correlations below 0.95 were retained to reduce collinearity. The final selected variables included: Marine: Maximum Sea Ice Cover, Maximum and Minimum Primary Productivity, Maximum and Minimum Salinity, and Maximum and Minimum Ocean Temperature. Terrestrial: Mean Diurnal Range (Bio2), Isothermality (Bio3), Temperature Annual Range (Bio7), Mean Temperature of Warmest Quarter (Bio10), Precipitation Seasonality (Bio15), Precipitation of Wettest Quarter (Bio16), and Precipitation of Warmest Quarter (Bio18). These variables were later used to evaluate the association between environmental variation and putatively adaptive genetic variation (RDA based on outlier SNPs located within genes).

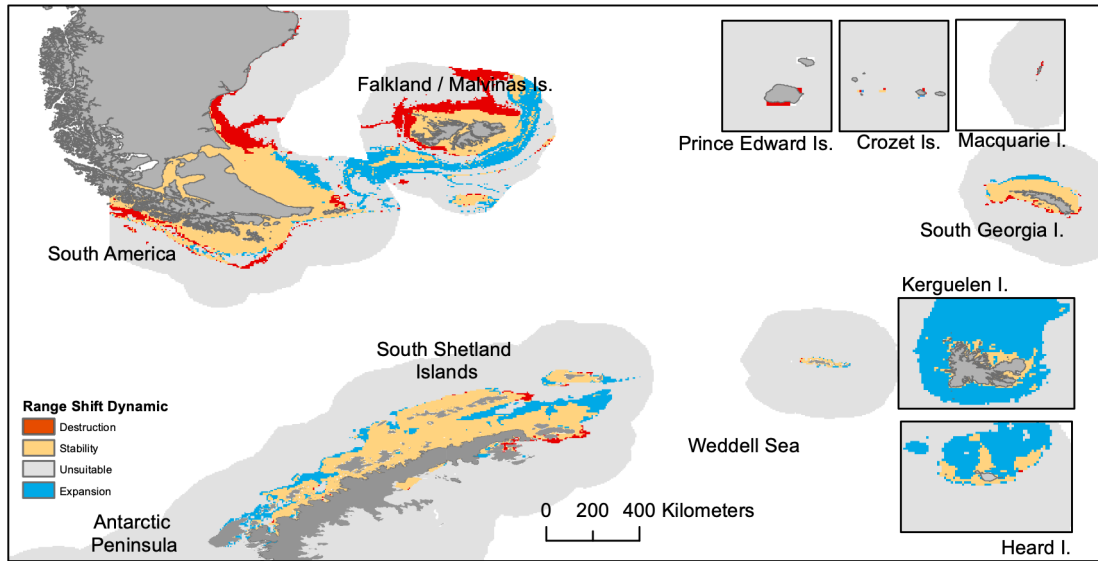


Fig. S10. Range shift projection for the four main gentoo penguin lineages under the RCP4.5 climate scenario for the year 2050 based on ecological niche modeling including bathymetry as variable. Colored areas indicate predicted range dynamics relative to the current conditions.

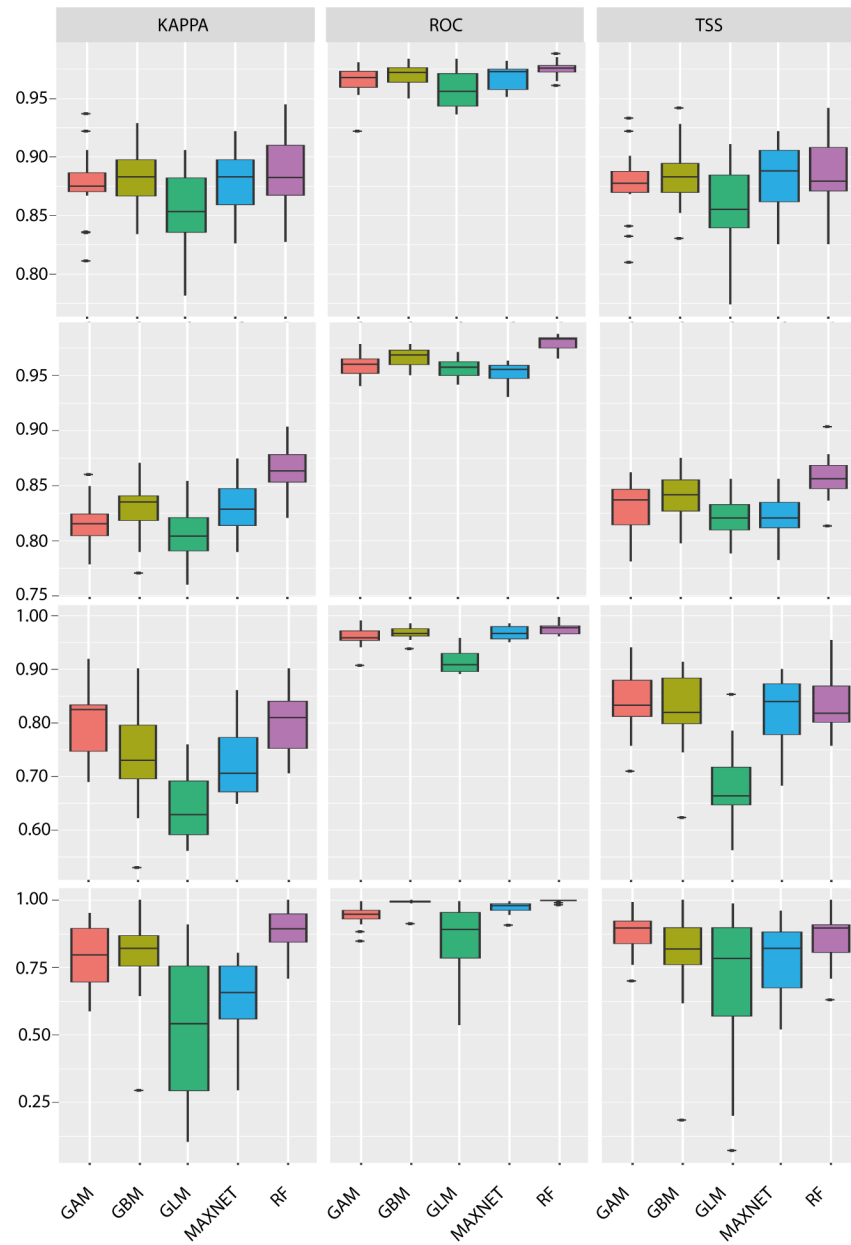


Fig. S11. Model performance evaluated under five modeling algorithms: Generalized Additive Models (GAM), Generalized Boosting Models (GBM), Generalized Linear Models (GLM), Maximum Entropy (MAXNET), and Random Forests (RF).



Fig. S12. Variable importance across species distribution models (SDMs) used for future projections. Relative contribution of environmental predictors to habitat suitability models for each gentoo penguin lineage (Northern, Southern, Southeastern, and Eastern) under five modeling algorithms: Generalized Additive Models (GAM), Generalized Boosting Models (GBM), Generalized Linear Models (GLM), Maximum Entropy (MAXNET), and Random Forests (RF). Variable importance was calculated based on each algorithm's internal method and expressed as the percentage contribution of each predictor to the final model. Environmental variables included bathymetry, surface chlorophyll concentration, pH, sea surface temperature, salinity (only in Northern and Southern models), and climate velocity. Boxplots represent variation across model replicates.

Table S1. Geographic distribution of the samples used for this study.

	Sampling Location	Num. genomes sequenced	Latitude	Longitude
Eastern gentoo	Crozet Is.	7	46°25'47.30"S	50°24'16.83"E
	Marion Is.	8	46°58'25.81"S	37°41 '54.43"E
Macquarie gentoo	Macquarie Is.	2	54°37'49.54"S	158°51'0.30"E
Southeastern gentoo	Kerguelen Is.	7	49°16'52.28"S	70°32'27.90"E
Northern gentoo	Falkland Is.	7	52°20'16.7"S	59°21'48.02"W
	Martillo Is.	5	54°54'1.79"S	67°23'45.35"W
Southern gentoo	Signy Is.	7	60°43'54.14"S	45°35'58.70"W
	B. O'Higgins Base	7	63°19'14.64"S	57°53'55.25"W
	King George (Stranger Point)	7	62°14'14.86"S	58°35'38.26"W
	G. G. Videla Base	7	64°49'26.12"S	62°51'29.04"W

[illegible]

Table S3. List of VCF files used in this study with their respective filters.

Number of sites	Description
31,860,273	Contain Adelie, chinstrap and 64 gentoo samples. Used to generate fasta files (bcftools consensus, BEDTOOLS genomcov - maskfasta)
30,130,090	Contain Adelie, chinstrap and 64 gentoo samples and exclude sex scaffolds
8,754,260	gentoo samples, file used for selection analysis (RAiSD - nSL)
4,674,861	file withouth outlier SNPs (placed within shared outlier windows)
138,248	Pruned dataset. Used for PCA, ADMIXTURE, treemix, Dsuite, Fst and Nm.
1,223,070,630	vcf file containig variant and invariant sites. Used to FST - DXY estimation using pixy

Table S4. List of the 126 scaffolds identified within sexual or linked to sex chromosomes from a total of 18,750 scaffolds.

Scaffolds linked to sexual chromosomes		
VUKY01000175.1	VUKY01005389.1	VUKY01011528.1
VUKY01000348.1	VUKY01005429.1	VUKY01011771.1
VUKY01000356.1	VUKY01005668.1	VUKY01011832.1
VUKY01000450.1	VUKY01005832.1	VUKY01012266.1
VUKY01000490.1	VUKY01006032.1	VUKY01012378.1
VUKY01000579.1	VUKY01006406.1	VUKY01012689.1
VUKY01000720.1	VUKY01006464.1	VUKY01012815.1
VUKY01000800.1	VUKY01006749.1	VUKY01013017.1
VUKY01000928.1	VUKY01007138.1	VUKY01013166.1
VUKY01000946.1	VUKY01007428.1	VUKY01013450.1
VUKY01000988.1	VUKY01007442.1	VUKY01013644.1
VUKY01001273.1	VUKY01007573.1	VUKY01013877.1
VUKY01001409.1	VUKY01007638.1	VUKY01014050.1
VUKY01001447.1	VUKY01007748.1	VUKY01014159.1
VUKY01001662.1	VUKY01007768.1	VUKY01014581.1
VUKY01001930.1	VUKY01007787.1	VUKY01014752.1
VUKY01002081.1	VUKY01008374.1	VUKY01014839.1
VUKY01002260.1	VUKY01008424.1	VUKY01015034.1
VUKY01002281.1	VUKY01008606.1	VUKY01015040.1
VUKY01002424.1	VUKY01008659.1	VUKY01015593.1
VUKY01002450.1	VUKY01008686.1	VUKY01015899.1
VUKY01002462.1	VUKY01008712.1	VUKY01016118.1
VUKY01002545.1	VUKY01008770.1	VUKY01016235.1
VUKY01002581.1	VUKY01008831.1	VUKY01016246.1
VUKY01002720.1	VUKY01009141.1	VUKY01016411.1
VUKY01002815.1	VUKY01009256.1	VUKY01016434.1
VUKY01003201.1	VUKY01009292.1	VUKY01016493.1
VUKY01003332.1	VUKY01009527.1	VUKY01016627.1
VUKY01003396.1	VUKY01009834.1	VUKY01016922.1
VUKY01003472.1	VUKY01009924.1	VUKY01016954.1
VUKY01003480.1	VUKY01010135.1	VUKY01016988.1
VUKY01003488.1	VUKY01010206.1	VUKY01017377.1
VUKY01003633.1	VUKY01010271.1	VUKY01017391.1
VUKY01003704.1	VUKY01010397.1	VUKY01017507.1
VUKY01003758.1	VUKY01010399.1	VUKY01017810.1
VUKY01004263.1	VUKY01010485.1	VUKY01017813.1
VUKY01004336.1	VUKY01010572.1	VUKY01017814.1
VUKY01004412.1	VUKY01010995.1	VUKY01017879.1
VUKY01004489.1	VUKY01011012.1	VUKY01018316.1
VUKY01004826.1	VUKY01011383.1	VUKY01018356.1
VUKY01005175.1	VUKY01011426.1	VUKY01018475.1
VUKY01005306.1	VUKY01011437.1	VUKY01018539.1

Table S5. Annotation of the biological function of the genes placed within of common outlier windows performed using METASCAPE.

Lineage	Gene name	Number of SNPs within gen	Description	Biological Process (GO)
Northern gentoo	KCNQ1	31	potassium voltage-gated channel subfamily Q member 1	GO:001698 gastrin-induced gastric acid secretion;GO:0035934 corticosterone secretion;GO:0035933 glucocorticoid secretion
Northern gentoo	POLA1	12	DNA polymerase alpha 1, catalytic subunit	GO:0006772 leading strand elongation;GO:0006773 lagging strand elongation;GO:1902292 cell cycle DNA replication initiation
Northern gentoo	CNKSR2	44	connector enhancer of kinase suppressor of Ras 2	GO:009084 postsynaptic specialization organization;GO:0099173 postsynapse organization;GO:0050808 synapse organization
Northern gentoo	cygb1	7	None	None
Northern gentoo	TCF20	28	transcription factor 20	GO:0045944 positive regulation of transcription by RNA polymerase II;GO:0045893 positive regulation of DNA-templated transcription;GO:1902680 positive regulation of RNA biosynthetic process
Northern gentoo	Ankfy1	20	ankyrin repeat and FYVE domain containing 1	GO:0048549 positive regulation of pinocytosis;GO:0090160 Golgi to lysosome transport;GO:0048548 regulation of pinocytosis
Northern gentoo	Ube2g1	10	ubiquitin conjugating enzyme E2 G1	GO:0070534 protein K63-linked ubiquitination;GO:0070936 protein K48-linked ubiquitination;GO:0000209 protein polyubiquitination
Northern gentoo	Etak1	76	ethanolamine kinase 1	GO:0006646 phosphatidylethanolamine biosynthetic process;GO:0046337 phosphatidylethanolamine metabolic process;GO:0046474 phosphatidylethanolamine biosynthetic process
Northern gentoo	EPSS8	6	EGFR pathway substrate 8, signaling adaptor	GO:0070538 actin polymerization-dependent cell motility;GO:0048149 behavioral response to ethanol;GO:0051764 actin crosslink formation
Northern gentoo	AKR1B10	8	aldo-keto reductase family 1 member B10	GO:0016107 sesquiterpene catabolic process;GO:0016487 farnesol metabolic process;GO:0016488 farnesol catabolic process
Northern gentoo	SOX5	11	SRY-box transcription factor 5	GO:2000741 positive regulation of mesenchymal stem cell differentiation;GO:0050539 asymmetric neuroblast division;GO:2000739 regulation of mesenchymal stem cell differentiation
Northern gentoo	AEBP2	15	AE binding protein 2	GO:0000122 negative regulation of transcription by RNA polymerase II;GO:0045892 negative regulation of DNA-templated transcription;GO:1902679 negative regulation of RNA biosynthetic process
Northern gentoo	STRAP	30	serine/threonine kinase receptor associated protein	GO:0030277 maintenance of gastrointestinal epithelium;GO:0000380 alternative mRNA splicing, via spliceosome;GO:0010669 epithelial structure maintenance
Northern gentoo	IGF1	23	insulin like growth factor 1	GO:0060283 negative regulation of oocyte development;GO:1904073 regulation of trophectodermal cell proliferation;GO:1904075 positive regulation of trophectodermal cell proliferation
Northern gentoo	PMCH	90	pro-melanin concentrating hormone	GO:0032227 negative regulation of synaptic transmission, dopaminergic;GO:0032225 regulation of synaptic transmission, dopaminergic;GO:0050805 negative regulation of synaptic transmission
Northern gentoo	PTPRT	3	protein tyrosine phosphatase receptor type T	GO:1990264 peptidyl-tyrosine phosphorylation involved in inactivation of protein kinase activity;GO:0035335 peptidyl-tyrosine dephosphorylation;GO:0071354 cellular response to interleukin-6
Northern gentoo	chr2	25	corticotropin releasing hormone receptor 2	GO:0043435 response to corticotropin-releasing hormone;GO:0071376 cellular response to corticotropin-releasing hormone stimulus;GO:0060291 long-term synaptic potentiation
Northern gentoo	ACVR2B	3	activin A receptor type 2B	GO:0032927 positive regulation of activin receptor signaling pathway;GO:0060836 lymphatic endothelial cell differentiation;GO:0048617 embryonic fascial morphogenesis
Northern gentoo	coc3	17	EBF transcription factor 3	GO:0045893 positive regulation of DNA-templated transcription;GO:1902680 positive regulation of RNA biosynthetic process;GO:0051254 positive regulation of RNA metabolic process
Northern gentoo	ARAP2	6	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	GO:0032956 regulation of actin cytoskeleton organization;GO:0032970 regulation of actin filament-based process;GO:0051493 regulation of cytoskeleton organization
Northern gentoo	EHD3	3	EH domain containing 3	GO:0006036 regulation of cardiac muscle cell membrane potential;GO:0090160 Golgi to lysosome transport;GO:0034498 early endosome to Golgi transport
Northern gentoo	RGS12	16	regulator of G protein signaling 12	GO:0008277 regulation of G protein-coupled receptor signaling pathway;GO:0007186 G protein-coupled receptor signaling pathway;GO:0009968 negative regulation of signal transduction
Northern gentoo	CDH18	1	cadherin 18	GO:0044331 cell-cell adhesion mediated by cadherin;GO:0016339 calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules;GO:0043332 adherens junction organization
Northern gentoo	Tiparp	16	TCDD inducible poly(ADP-ribose) polymerase	GO:1904612 response to 2,3,7,8-tetrachlorodibenzo-p-dioxine;GO:0048745 smooth muscle tissue development;GO:0008209 androgen metabolic process
Northern gentoo	PTPRM	9	protein tyrosine phosphatase receptor type M	GO:0031290 retinal ganglion cell axon guidance;GO:0010842 retina layer formation;GO:0060042 retina morphogenesis in camera-type eye
Northern gentoo	PIEZO2	3	piezo type mechanosensitive ion channel component 2	GO:0059974 detection of mechanical stimulus involved in sensory perception;GO:0059982 detection of mechanical stimulus;GO:0071260 cellular response to mechanical stimulus
Northern gentoo	CDH19	6	cadherin 19	GO:0044331 cell-cell adhesion mediated by cadherin;GO:0016339 calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules;GO:0043332 adherens junction organization
Northern gentoo	SCFD2	16	scf1 family domain containing 2	GO:0008886 intracellular protein transport;GO:0015031 protein transport;GO:0046907 intracellular transport
Northern gentoo	DLL1	9	delta like canonical Notch ligand 1	GO:0021688 cerebellar molecular layer formation;GO:0045610 regulation of hemocyte differentiation;GO:0045611 negative regulation of hemocyte differentiation
Northern gentoo	THBS2	86	thrombospondin 2	GO:0051965 positive regulation of synapse assembly;GO:1901890 positive regulation of cell junction assembly;GO:0016525 negative regulation of angiogenesis
Northern gentoo	Ptpk	14	protein tyrosine phosphatase receptor type K	GO:0010839 negative regulation of keratinocyte proliferation;GO:0048041 focal adhesion assembly;GO:0034394 protein localization to cell surface
Northern gentoo	Ra2	4	Ras like without CAAX 2	GO:0032489 regulation of Cdc42 protein signal transduction;GO:0032507 maintenance of protein location in cell;GO:0007265 Ras protein signal transduction
Northern gentoo	SETBP1	23	SET binding protein 1	GO:0006338 chromatin remodeling;GO:0006325 chromatin organization;GO:0006355 regulation of DNA-templated transcription
Northern gentoo	CACNA2D1	10	calcium voltage-gated channel auxiliary subunit alpha2delta 1	GO:0061577 calcium ion transmembrane transport via high voltage-gated calcium channel;GO:0086048 membrane depolarization during bundle of His cell action potential;GO:0070727 cellular micromolecular localization
Northern gentoo	FER	2	FER tyrosine kinase	GO:0120179 adherens junction disassembly;GO:0150147 cell-cell junction disassembly;GO:0033007 negative regulation of mast cell activation involved in immune response
Northern gentoo	FBXL17	5	F-box and leucine rich repeat protein 17	GO:0006515 protein quality control for misfolded or incompletely synthesized proteins;GO:0031146 SCF-dependent proteasomal ubiquitin-dependent protein catabolic process;GO:0008589 regulation of smoothness signaling pathway
Northern gentoo	NBEA	9	neurobeachin	GO:0001044 protein localization;GO:0006028 bundle of His cell action potential;GO:0033026 macromolecular localization
Northern gentoo	TOPI	2	DNA topoisomerase 1	GO:0040016 embryonic cleavage;GO:0006265 DNA topological change;GO:0032922 circadian regulation of gene expression
Northern gentoo	GLRA3	3	glycine receptor alpha 3	GO:0060079 excitatory postsynaptic potential;GO:0099565 chemical synaptic transmission, postsynaptic;GO:0060078 regulation of postsynaptic membrane potential
Northern gentoo	cep44	8	centrosomal protein 44	GO:0010457 centriole-centriole cohesion;GO:0007099 centriole replication;GO:0098534 centriole assembly
Northern gentoo	LUM	4	lumican	GO:0032914 positive regulation of transforming growth factor beta1 production;GO:0012908 regulation of transforming growth factor beta1 production;GO:0071636 positive regulation of transforming growth factor beta production
Northern gentoo	IQSEC1	24	IQ motif and Sec7 domain ArfGEF 1	GO:0120182 regulation of focal adhesion disassembly;GO:0120183 positive regulation of focal adhesion disassembly;GO:0051549 positive regulation of keratinocyte migration
Northern gentoo	DGKH	7	diacylglycerol kinase eta	GO:0141212 phospholipase C/protein kinase C signal transduction;GO:0046834 lipid phosphorylation;GO:0046339 diacylglycerol metabolic process
Northern gentoo	GTF2F2	2	general transcription factor IIF subunit 2	GO:0006368 transcription elongation by RNA polymerase II;GO:0006354 DNA-templated transcription elongation;GO:0032508 DNA duplex unwinding
Northern gentoo	PPP2R2B	1	protein phosphatase 2 regulatory subunit Bbeta	GO:0006915 apoptotic process;GO:0012501 programmed cell death;GO:0008219 cell death
Northern gentoo	ctbp2	12	C-terminal binding protein 2	GO:0048386 positive regulation of retinoic acid receptor signaling pathway;GO:0048385 regulation of retinoic acid receptor signaling pathway;GO:0050872 white fat cell differentiation
Northern gentoo	DST	235	dystronin	GO:0031581 hemidesmosome assembly;GO:0030011 maintenance of cell polarity;GO:0008090 retrograde axonal transport
Northern gentoo	HCRT2	44	hypocretin receptor 2	GO:0022014 circadian sleep/wake cycle process;GO:0010840 regulation of circadian sleep/wake cycle, wakefulness;GO:0042745 circadian sleep/wake cycle
Northern gentoo	TINAG	20	tubulointerstitial nephritis antigen	GO:0007155 cell adhesion;GO:0006508 proteolysis;GO:0019538 protein metabolic process
Northern gentoo	SMAP1	34	small ArfGAP 1	GO:2000349 regulation of clathrin-dependent endocytosis;GO:0045648 positive regulation of erythrocyte differentiation;GO:0045646 regulation of erythrocyte differentiation
Northern gentoo	B3GAT2	11	beta-1,3-glucosyltransferase 2	GO:0050650 chondroitin sulfate proteoglycan biosynthetic process;GO:0050654 chondroitin sulfate proteoglycan metabolic process
Northern gentoo	PTPNC1	3	phosphatidylinositol transfer protein cytoplasmic 1	GO:0030166 proteoglycan biosynthetic process
Northern gentoo	THSD4	3	thrombospondin type 1 domain containing 4	GO:0120009 intermembrane lipid transfer;GO:0015914 phospholipid transport;GO:0015748 organophosphate ester transport
Northern gentoo	Apha2	16	amyloid beta precursor protein binding family A member 2	GO:0146054 microfilament assembly;GO:0048351 elastic fiber assembly;GO:0083029 extracellular matrix assembly
Northern gentoo	WSCD1	3	WSC domain containing 1	GO:0099171 presynaptic modulation of chemical synaptic transmission;GO:0035264 multicellular organism growth;GO:0007626 locomotory behavior
Northern gentoo	KCNH5	1	potassium voltage-gated channel subfamily H member 5	GO:0010839 regulation of G2/M transition of mitotic cell cycle;GO:1902749 regulation of cell cycle G2/M phase transition;GO:0071805 potassium ion transmembrane transport
Northern gentoo	Slc4a10	4	solute carrier family 4 member 10	GO:0021860 pyramidal neuron development;GO:0021859 pyramidal neuron differentiation;GO:0048172 regulation of short-term neuronal synaptic plasticity
Northern gentoo	SCN2A	2	sodium voltage-gated channel alpha subunit 2	GO:0006627 intrinsic apoptotic signaling pathway in response to osmotic stress;GO:0021542 dentate gyrus development;GO:0019228 neuronal action potential
Northern gentoo	TLK1	8	tousled like kinase 1	GO:1902222 regulation of chromatin organization;GO:0097059 chromosome segregation;GO:0006468 protein phosphorylation
Northern gentoo	CTAP61	2	cilia and flagella associated protein 61	GO:0120316 sperm flagellum assembly;GO:0044458 motile cilium assembly;GO:0030317 flagellated sperm motility
Northern gentoo	nol6	29	nucleolar protein 6	GO:0006409 rRNA export from nucleus;GO:0051031 rRNA transport;GO:0006405 rRNA export from nucleus
Northern gentoo	ANTXR1	8	ANTXR cell adhesion molecule 1	GO:1901202 negative regulation of extracellular matrix assembly;GO:1903054 negative regulation of extracellular matrix organization;GO:1901201 regulation of extracellular matrix assembly
Northern gentoo	Ifitm10	1	interferon induced transmembrane protein 10	GO:0097237 cellular response to toxic substance;GO:0009636 response to toxic substance;GO:0070887 cellular response to chemical stimulus
Northern gentoo	ABTB2	1	ankyrin repeat and BTB domain containing 2	GO:0033539 fatty acid beta-oxidation using acyl-CoA dehydrogenase;GO:0006635 fatty acid beta-oxidation;GO:0019395 fatty acid oxidation
Northern gentoo	ETFDH	17	electron transfer flavoprotein dehydrogenase	GO:0004881 positive regulation of cAMP-dependent protein kinase activity;GO:2000670 positive regulation of dendritic cell apoptotic process;GO:0048022 negative regulation of melanin biosynthetic process
Northern gentoo	RAPGEF2	13	Rap guanine nucleotide exchange factor 2	GO:0042273 ribosomal large subunit biogenesis;GO:0042254 ribosome biogenesis;GO:0022613 ribonucleoprotein complex biogenesis
Northern gentoo	ANXA10	33	annexin A10	
Northern gentoo	MARCH1	2	membrane associated ring-CH-type finger 1	GO:0002495 antigen processing and presentation of peptide antigen via MHC class II;GO:0002504 antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;GO:0048002 antigen processing and presentation of peptide antigen
Northern gentoo	Bckdhh	8	branched chain keto acid dehydrogenase E1 subunit beta	GO:0009083 branched-chain amino acid catabolic process;GO:0009081 branched-chain amino acid metabolic process;GO:0051591 response to cAMP
Northern gentoo	ERC1	17	ELKS/RAB6-interacting/CAST family member 1	GO:0007252 1-azapB phosphorylation;GO:0048790 maintenance of presynaptic active zone structure;GO:1990709 presynaptic active zone organization
Northern gentoo	Cacna1c	4	calcium voltage-gated channel subunit alpha1 C	GO:0061577 calcium ion transmembrane transport via high voltage-gated calcium channel;GO:0098912 membrane depolarization during atrial cardiac muscle cell action potential;GO:0086045 membrane depolarization during AV node cell action potential
Northern gentoo	CTCF1	31	CCCTC-binding factor like	GO:0071169 establishment of protein localization to chromatin;GO:0070199 establishment of protein localization to chromosome;GO:0071514 genomic imprinting
Northern gentoo	Bmp7	15	bone morphogenetic protein 7	GO:1901145 mesenchymal cell apoptotic process involved in nephron morphogenesis;GO:0072134 nephrogenic mesenchyme morphogenesis;GO:0021502 neural fold elevation formation
Northern gentoo	NUAK1	61	NUAK family kinase 1	GO:2000772 regulation of cellular senescence;GO:1901796 regulation of signal transduction by p53 class mediator;GO:0006468 protein ribosylation
Northern gentoo	CHST11	10	carbohydrate sulfotransferase 11	GO:0030317 polysaccharide localization;GO:0048703 embryonic viscerocranium morphogenesis;GO:0030206 chondroitin sulfate biosynthetic process
Northern gentoo	PPM1L	18	protein phosphatase, Mg2+/Mn2+ dependent 1L	GO:0030148 sphingolipid biosynthetic process;GO:0046467 membrane lipid biosynthetic process;GO:0006665 sphingolipid metabolic process
Northern gentoo	snc4	13	structural maintenance of chromosomes 4	GO:0010032 meiotic chromosome condensation;GO:1905821 positive regulation of chromosome condensation;GO:0006023 regulation of chromosome condensation
Northern gentoo	RFXP1	1	relaxin family peptide receptor 1	GO:0006018 niple development;GO:0006058 niple morphogenesis;GO:0060427 lung connective tissue development

Northern gentoo	Stard13	1	STAR related lipid transfer domain containing 13	GO:0097498 endothelial tube lumen extension;GO:0003159 morphogenesis of an endothelium;GO:0061154 endothelial tube morphogenesis
Northern gentoo	PLCB4	3	phospholipase C beta 4	GO:0160135 phospholipase C-activating endothelin receptor signaling pathway;GO:0086100 endothelin receptor signaling pathway;GO:0048015 phosphatidylinositol-mediated signaling
Northern gentoo	AKR1D1	11	aldo-keto reductase family 1 member D1	GO:0030573 bile acid catabolic process;GO:0006707 cholesterol catabolic process;GO:0016127 steroid catabolic process
Northern gentoo	Ptn	11	plietrophin	GO:0031104 dendrite regeneration;GO:0043932 ossification involved in bone remodeling;GO:0007185 cell surface receptor protein tyrosine phosphatase signaling pathway
Northern gentoo	SLC13A4	87	solute carrier family 13 member 4	GO:1902358 sulfate transmembrane transport;GO:0072348 sulfur compound transport;GO:0098661 inorganic anion transmembrane transport
Northern gentoo	DENN2A	3	DENN domain containing 2A	GO:0042147 retrograde transport, endosome to Golgi;GO:0016482 cytosolic transport;GO:0016197 endosomal transport
Northern gentoo	ERCC4	30	ERCC excision repair 4, endonuclease catalytic subunit	GO:1901255 nucleotide-excision repair involved in interstrand cross-link repair;GO:0061819 telomeric DNA-containing double minutes formation;GO:1905764 regulation of protection from non-homologous end joining at telomere
Northern gentoo	ADSL	2	adenylsuccinate lyase	GO:0044209 AMP salvage;GO:0006189 'de novo' IMP biosynthetic process;GO:0097292 XMP metabolic process
Northern gentoo	HECTD2	6	HECT domain E3 ubiquitin protein ligase 2	GO:0002099 protein polyubiquitination;GO:0016567 protein ubiquitination;GO:0032446 protein modification by small protein conjugation
Northern gentoo	EMC2	1	ER membrane protein complex subunit 2	GO:0045050 protein insertion into ER membrane by stop-transfer membrane-anchor sequence;GO:0071816 tail-anchored membrane protein insertion into ER membrane;GO:0045048 protein insertion into ER membrane
Northern gentoo	Sybu	29	syntabulin	GO:0060025 regulation of synaptic activity;GO:1990048 anterograde neuronal dense core vesicle transport;GO:0099519 dense core granule cytoskeletal transport
Northern gentoo	FBXO22	1	F-box protein 22	GO:0048742 regulation of skeletal muscle fiber development;GO:0010830 regulation of myotube differentiation;GO:0032436 positive regulation of proteasomal ubiquitin-dependent protein catabolic process
Northern gentoo	UBE2Q2	6	ubiquitin conjugating enzyme E2 Q2	GO:0070936 protein K48-linked ubiquitination;GO:0000209 protein polyubiquitination;GO:0016567 protein ubiquitination
Northern gentoo	TTL12	7	tubulin tyrosine ligase like 12	GO:0060339 negative regulation of type I interferon-mediated signaling pathway;GO:0060338 regulation of type I interferon-mediated signaling pathway;GO:0045824 negative regulation of innate immune response
Northern gentoo	AK5	28	adenylate kinase 5	GO:0006173 dADP biosynthetic process;GO:0009183 purine deoxycarbonyl diphosphate biosynthetic process;GO:0046056 dADP metabolic process
Northern gentoo	ST3GAL3	24	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	GO:0010706 ganglioside biosynthetic process via lactosylceramide;GO:0018146 keratan sulfate biosynthetic process;GO:0001574 sialoside biosynthetic process
Northern gentoo	ZZZ3	7	zinc finger ZZ-type containing 3	GO:0090043 regulation of tubulin deacetylation;GO:0090311 regulation of protein deacetylation;GO:0045995 regulation of embryonic development
Northern gentoo	GRAMD1C	24	GRAM domain containing 1C	GO:0071397 cellular response to cholesterol;GO:0036215 cellular response to sterol;GO:0032366 intracellular sterol transport
Northern gentoo	F13A1	1	coagulation factor XIII A chain	GO:0072378 blood coagulation, fibrin clot formation;GO:0072376 protein activation cascade;GO:0018149 peptide cross-linking
Northern gentoo	PREP	8	prolyl endopeptidase	GO:0006508 proteolysis;GO:0019538 protein metabolic process;GO:0043170 macromolecule metabolic process
Northern gentoo	TRHR	8	thyrotropin releasing hormone receptor	GO:0007200 phosphatase C-activating G protein-coupled receptor signaling pathway;GO:0007186 G protein-coupled receptor signaling pathway;GO:0007165 signal transduction
Northern gentoo	CPED1	3	cadherin like and PC-esterase domain containing 1	
Northern gentoo	COBL	9	cordon-bleu WH2 repeat protein	GO:0048669 collateral sprouting in absence of injury;GO:0001757 somite specification;GO:0051639 actin filament network formation
Northern gentoo	Kat5a	4	lysine acetyltransferase 6A	GO:0009472 protein acetylation;GO:0034543 protein acylation;GO:0090398 cellular response
Northern gentoo	TACR3	19	tachykinin receptor 3	GO:0007217 tachykinin receptor signaling pathway;GO:0070474 positive regulation of uterine smooth muscle contraction;GO:0070472 regulation of uterine smooth muscle contraction
Northern gentoo	LIMD1	16	LIM domain containing 1	GO:0033962 P-body assembly;GO:0002076 osteoblast development;GO:0035331 negative regulation of hippo signaling
Northern gentoo	IMPG1	36	interphotoreceptor matrix proteoglycan 1	GO:0007601 visual perception;GO:005953 sensory perception of light stimulus;GO:00030198 extracellular matrix organization
Northern gentoo	kcnk9	5	potassium two pore domain channel subfamily K member 9	GO:2000856 negative regulation of mineralocorticoid secretion;GO:2000859 negative regulation of aldosterone secretion;GO:0099605 regulation of action potential firing rate
Northern gentoo	Ano2	206	anoctamin 2	GO:1902476 chloride transmembrane transport;GO:0006821 chloride transport;GO:0098661 inorganic anion transmembrane transport
Northern gentoo	VEGFD	7	vascular endothelial growth factor D	GO:0060754 positive regulation of mast cell chemotaxis;GO:0060753 regulation of mast cell chemotaxis;GO:0050930 induction of positive chemotaxis
Northern gentoo	ASB11	22	ankyrin repeat and SOCS box containing 11	GO:0070979 protein K11-linked ubiquitination;GO:0030968 endoplasmic reticulum unfolded protein response;GO:0034620 cellular response to unfolded protein
Northern gentoo	POLA1	1	DNA polymerase alpha 1, catalytic subunit	GO:0006272 leading strand elongation;GO:0006273 lagging strand elongation;GO:1902292 cell cycle DNA replication initiation
Northern gentoo	CKSR2	2	connector enhancer of kinase suppressor of Ras 2	GO:0099084 postsynaptic specialization organization;GO:0099173 postsynapse organization;GO:0050808 synapse organization
Northern gentoo	GLRA2	98	glycine receptor alpha 2	GO:0071361 cellular response to ethanol;GO:0071294 cellular response to zinc ion;GO:0010043 response to zinc ion
Northern gentoo	Angptl2	6	angiopoietin like 2	GO:0007596 blood coagulation;GO:0050817 coagulation;GO:0007599 hemostasis
Northern gentoo	Ralgs1	6	Ral GEF with PH domain and SH3 binding motif 1	GO:0032485 regulation of Ral protein signal transduction;GO:0007265 Ras protein signal transduction;GO:0007264 small GTPase-mediated signal transduction
Northern gentoo	Astx	8	ASXL transcriptional regulator 2	GO:0035360 positive regulation of peroxisome proliferator activated receptor signaling pathway;GO:0035358 regulation of peroxisome proliferator activated receptor signaling pathway;GO:0045600 positive regulation of fat cell differentiation
Northern gentoo	RP1	8	RP1 axonemal microtubule associated	GO:1902857 positive regulation of non-motile cilium assembly;GO:0046548 retinal rod cell development;GO:0046549 retinal cone cell development
Northern gentoo	CHD7	2	chromodomain helicase DNA binding protein 7	GO:0003226 right ventricular compact myocardium morphogenesis;GO:0003221 right ventricular cardiac muscle tissue morphogenesis;GO:0021553 olfactory nerve development
Northern gentoo	IGF1	2	insulin like growth factor 1	GO:0060283 negative regulation of oocyte development;GO:1904073 regulation of trophoblast cell proliferation;GO:1904075 positive regulation of trophoblast cell proliferation
Northern gentoo	PDE6C	82	phosphodiesterase 6C	GO:0046549 retinal cone cell development;GO:0007603 phototransduction, visible light;GO:0042670 retinal cone cell differentiation
Northern gentoo	TMT4	1	transmembrane O-nanomoyltransferase targeting cadherins 4	GO:0032470 positive regulation of endoplasmic reticulum calcium ion concentration;GO:1905584 outer hair cell apoptotic process;GO:0032609 protein O-linked monooxygenation
Northern gentoo	DPPE	32	dipeptidyl peptidase like 6	GO:1901379 regulation of potassium ion transmembrane transport;GO:0043266 regulation of potassium ion transport;GO:0072659 protein localization to plasma membrane
Northern gentoo	CNTNAP5	3	contactin associated protein family member 5	GO:0007155 cell adhesion;GO:0009987 cellular process;GO:0008150 biological process
Northern gentoo	Xrcc5	1	X-ray repair cross complementing 5	GO:0034462 small-subunit processome assembly;GO:0180025 cytosolic small ribosomal subunit assembly;GO:1904430 negative regulation of telomere formation
Northern gentoo	Eif5a	1	eukaryotic translation initiation factor 3 subunit A	GO:0002188 translation reinitiation;GO:0075525 viral translational termination-reinitiation;GO:0075522 IRES-dependent viral translational initiation
Northern gentoo	TBP2	3	C-terminal binding protein 2	GO:0048386 positive regulation of retinoic acid receptor signaling pathway;GO:0048385 regulation of retinoic acid receptor signaling pathway;GO:0050872 white fat cell differentiation
Northern gentoo	Tbc1d1	12	TBC1 domain family member 1	
Northern gentoo	TRANK1	10	tetratricopeptide repeat and ankyrin repeat containing 1	
Northern gentoo	GPATCH2	8	G-patch domain containing 2	
Northern gentoo	Auh	14	AU RNA binding methylglutaryl-CoA hydratase	GO:0006552 L-leucine catabolic process;GO:0006551 L-leucine metabolic process;GO:0009080 pyruvate family amino acid catabolic process
Northern gentoo	LNK1	32	ligand of numb-protein X 1	GO:0006074 synapse maturation;GO:0021700 developmental maturation;GO:0050808 synapse organization
Northern gentoo	ADAMTSL1	4	ADAMTSL like 1	GO:0030198 extracellular matrix organization;GO:0043062 extracellular structure organization;GO:0045229 external encapsulating structure organization
Northern gentoo	ARHGAP20	14	Rho GTPase activating protein 20	GO:0035023 regulation of Rho protein signal transduction;GO:0051056 regulation of small GTPase mediated signal transduction;GO:1902531 regulation of intracellular signal transduction
Northern gentoo	SLC2A13	19	solute carrier family 2 member 13	GO:0015798 myo-inositol regulation of amyloid-beta formation;GO:1902993 positive regulation of amyloid precursor protein catabolic process
Northern gentoo	KIF26B	89	kinesin family member 26B	GO:0072092 uterine bud invasion;GO:0072093 metanephric renal vesicle formation;GO:0060677 uterine bud elongation
Northern gentoo	RYR2	1	ryanodine receptor 2	GO:0097050 type B pancreatic cell apoptotic process;GO:0098907 regulation of SA node cell action potential;GO:0003220 left ventricular cardiac muscle tissue morphogenesis
Northern gentoo	SLC9A9	38	solute carrier family 9 member A9	GO:0098719 sodium ion import across plasma membrane;GO:0090382 phagosome maturation;GO:0051453 regulation of intracellular pH
Northern gentoo	FGFBP2	11	fibroblast growth factor binding protein 2	GO:0007267 cell-cell signaling;GO:0023052 signaling;GO:0007154 cell communication
Northern gentoo	LRP5	10	LDL receptor related protein 5	GO:0060764 cell-cell signaling involved in mammary gland development;GO:0110135 Notch signaling pathway;GO:1902262 apoptotic process involved in blood vessel morphogenesis
Northern gentoo	ZFX4	10	zinc finger homeobox 4	GO:0006357 regulation of transcription by RNA polymerase II;GO:0006355 regulation of DNA-templated transcription;GO:2001141 regulation of RNA biosynthetic process
Northern gentoo	IL22RA2	7	interleukin 22 receptor subunit alpha 2	GO:0140865 interleukin-22-mediated signaling pathway;GO:0042509 regulation of tyrosine phosphorylation of STAT protein;GO:0050730 regulation of peptide-tyrosine phosphorylation
Northern gentoo	Tbc1d32	5	TBC1 domain family member 32	GO:0060831 smoothened signaling pathway involved in dorsal/ventral neural tube patterning;GO:0003406 retinal pigment epithelium development;GO:0021904 dorsal/ventral neural tube patterning
Northern gentoo	MYB	115	MYB proto-oncogene, transcription factor	GO:1904897 regulation of hepatic stellate cell proliferation;GO:1904899 positive regulation of hepatic stellate cell proliferation;GO:2000843 regulation of testosterone secretion
Northern gentoo	LAMA2	22	laminin subunit alpha 2	GO:0032224 positive regulation of synaptic transmission, cholinergic;GO:0032222 regulation of synaptic transmission, cholinergic;GO:0110011 regulation of basement membrane organization
Northern gentoo	TENT2	32	terminal nucleotidyltransferase 2	GO:2006266 negative regulation of mRNA catabolic process;GO:0140958 target-directed mRNA degradation;GO:0071044 histone mRNA catabolic process
Northern gentoo	ESR1	51	estrogen receptor 1	GO:0060523 prostate epithelial cord elongation;GO:0060737 prostate gland morphogenesis;GO:0060750 epithelial cell proliferation involved in mammary gland duct elongation
Northern gentoo	GRM1	10	glutamate metabotropic receptor 1	GO:0007206 phospholipase C-activating G protein-coupled glutamate receptor signaling pathway;GO:0099538 synaptic signaling via neuropeptide;GO:0007196 adenylate cyclase-inhibiting G protein-coupled glutamate receptor signaling pathway
Northern gentoo	PLEKH01	1	pleckstrin homology domain containing O1	GO:002875 lamellipodium morphogenesis;GO:0051451 microblast migration;GO:1901739 regulation of microblast fusion
Northern gentoo	ZC3H12C	2	zinc finger CCH-type containing 12C	GO:0008150 biological process
Northern gentoo	ATP8A2	1	ATPase phospholipid transporting 8A2	GO:0003011 involuntary skeletal muscle contraction;GO:0061092 positive regulation of phospholipid translocation;GO:0061091 regulation of phospholipid translocation
Northern gentoo	GLI1	30	GLI1 family zinc finger 1	GO:0000122 negative regulation of transcription by RNA polymerase II;GO:0045944 positive regulation of transcription by RNA polymerase II;GO:0045892 negative regulation of DNA-templated transcription
Northern gentoo	LAMA4	27	laminin subunit alpha 4	GO:0120163 negative regulation of cold-induced thermogenesis;GO:0045995 regulation of embryonic development;GO:0120161 regulation of cold-induced thermogenesis
Northern gentoo	CDC40	121	cell division cycle 40	GO:1990403 embryonic brain development;GO:0000377 RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;GO:0000398 mRNA splicing, via spliceosome
Northern gentoo	FIG4	8	FIG4 phosphoinositide 5-phosphatase	GO:0031642 negative regulation of myelination;GO:0031645 negative regulation of nervous system process;GO:0036092 phosphatidylinositol-3-phosphate biosynthetic process
Northern gentoo	AFG1L	5	AFG1 like ATPase	GO:0035694 mitochondrial protein catabolic process;GO:0006123 mitochondrial electron transport, cytochrome c to oxygen;GO:0019646 aerobic electron transport chain
Northern gentoo	BEAN1	25	brain expressed associated with NEDD4 1	
Northern gentoo	Dync1i2	27	dyncin cytoplasmic 1 light intermediate chain 2	GO:0051642 centrosome localization;GO:0061842 microtubule organizing center localization;GO:1990090 cellular response to nerve growth factor stimulus
Northern gentoo	POLN	4	DNA polymerase nu	GO:0019985 translation synthesis;GO:0006301 postreplication repair;GO:0036297 interstrand cross-link repair
Northern gentoo	Ttn	10	titin	GO:0030241 skeletal muscle myosin thick filament assembly;GO:0071688 striated muscle myosin thick filament assembly;GO:0048769 sarcomere assembly
Northern gentoo	GULP1	4	GULP PTB domain containing engulfment adaptor 1	GO:0006911 phagocytosis, engulfment;GO:0090224 plasma membrane invagination;GO:0103234 membrane invagination
Northern gentoo	celf4	13	CUGBP Elav-like family member 4	GO:1902866 regulation of retina development in camera-type eye;GO:0090394 negative regulation of excitatory postsynaptic potential;GO:0048025 negative regulation of mRNA splicing, via spliceosome
Northern gentoo	Ash10	3	ankyrin repeat and SOCS box containing 10	GO:0016567 protein ubiquitination;GO:0032446 protein modification by small protein conjugation;GO:0070647 protein modification by small protein conjugation or removal
Northern gentoo	KITLG	1	KIT ligand	GO:0033026 negative regulation of mast cell apoptotic process;GO:0033024 mast cell apoptotic process;GO:0033023 mast cell homeostasis
Northern gentoo	ATP8A1	14	ATPase phospholipid transporting 8A1	GO:0061092 positive regulation of phospholipid translocation;GO:0061091 regulation of phospholipid translocation;GO:0140331 aminophospholipid translocation

Southern gentoo	NCAM2	10	neural cell adhesion molecule 2	GO:0007158 neuron cell-cell adhesion;GO:0007413 axonal fasciculation;GO:0106030 neuron projection fasciculation
Southern gentoo	SLC18A2	6	solute carrier family 18 member A2	GO:002552 serotonin secretion by mast cell;GO:0042137 sequestering of neurotransmitter;GO:0099123 somato-dendritic dopamine secretion
Southern gentoo	SLC22A2	5	solute carrier family 22 member 2	GO:0012842 norepinephrine transport;GO:0015870 acetylcholine transport;GO:0051615 histamine uptake
Southern gentoo	GAL5	36	phosphoglucomutase 1	GO:0034499 galactose catabolic process via UDP-galactose;GO:0019388 galactose catabolic process;GO:0006012 galactose metabolic process
Southern gentoo	AMP2	20	None	None
Southern gentoo	Brf1	7	BRF1 general transcription factor IIIB subunit	GO:0006384 transcription initiation at RNA polymerase III promoter;GO:0009304 rRNA transcription;GO:0045945 positive regulation of transcription by RNA polymerase III
Southern gentoo	FHIT	14	fragile histidine triad diadenosine triphosphatase	GO:0015962 diadenosine triphosphate metabolic process;GO:0015964 diadenosine triphosphate catabolic process;GO:0015961 diadenosine polyphosphate catabolic process
Southern gentoo	metnl	2	metornin like, glial cell differentiation regulator	GO:0090336 positive regulation of brown fat cell differentiation;GO:0090335 regulation of brown fat cell differentiation;GO:0014850 response to muscle activity
Southern gentoo	TSNARE1	2	t-SNARE domain containing 1	GO:0045278 vesicle docking;GO:0140056 organelle localization by membrane tethering;GO:0022406 membrane docking
Southern gentoo	MEGF11	9	multiple EGF like domains 11	GO:0010842 retina layer formation;GO:0034109 homotypic cell-cell adhesion;GO:0060042 retina morphogenesis in camera-type eye
Southern gentoo	Galnt16	4	polypeptide N-acetylgalactosaminyltransferase 16	GO:0018242 protein O-linked glycosylation via serine;GO:0018243 protein O-linked glycosylation via threonine;GO:0018210 peptidyl-threonine modification
Southern gentoo	CCDC66	2	coiled-coil domain containing 66	GO:1903564 regulation of protein localization to cilium;GO:0050908 detection of light stimulus involved in visual perception;GO:0050962 detection of light stimulus involved in sensory reception
Southern gentoo	ERC2	2	ELKS/RAB6-interacting/CAST family member 2	GO:0150037 regulation of calcium-dependent activation of synaptic vesicle fusion;GO:0048790 maintenance of presynaptic active zone structure;GO:1990709 presynaptic active zone organization
Southern gentoo	FAM208A	2	transcription activation suppressor	GO:0060809 mesodermal to mesenchymal transition involved in gastrulation;GO:0097355 protein localization to heterochromatin;GO:0007351 tripartite regional subdivision
Southern gentoo	VWA3B	3	von Willebrand factor A domain containing 3B	
Southern gentoo	DZIP1	8	DAZ interacting zinc finger protein 1	GO:0140706 protein-containing complex localization to centriolar satellite;GO:0032053 ciliary basal body organization;GO:1903566 positive regulation of protein localization to cilium
Southern gentoo	IFNLR1	45	interferon lambda receptor 1	GO:0038196 type III interferon-mediated signaling pathway;GO:0071358 cellular response to type III interferon;GO:0034342 response to type III interferon
Southern gentoo	EGFLAM	9	EGF like, fibronectin type III and laminin G domains	GO:0018814 positive regulation of cell-substrate adhesion;GO:0010810 regulation of cell-substrate adhesion;GO:0030198 extracellular matrix organization
Southern gentoo	HERC1	2	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1	GO:0021072 cerebellar Purkinje cell differentiation;GO:0021694 cerebellar Purkinje cell layer formation;GO:0021692 cerebellar Purkinje cell layer morphogenesis
Southern gentoo	SEMA3C	24	semaphorin 3C	GO:0140074 cardiac endothelial to mesenchymal transition;GO:0003350 pulmonary myocardium development;GO:1905310 regulation of cardiac neural crest cell migration involved in outflow tract morphogenesis
Southern gentoo	Pappa	2	pappalysin 1	GO:0032354 response to follicle-stimulating hormone;GO:0034698 response to gonadotropin;GO:0071548 response to dexamethasone
Southern gentoo	Acs3	15	acyl-CoA synthetase short chain family member 3	GO:0046951 ketone body biosynthetic process;GO:1902224 ketone body metabolic process;GO:1901570 fatty acid derivative biosynthetic process
Southern gentoo	NAV3	7	neuron navigator 3	GO:0022703 negative regulation of interleukin-2 production;GO:0007026 negative regulation of microtubule depolymerization;GO:0031116 positive regulation of microtubule polymerization
Southern gentoo	PIK3R1	30	phosphoinositide-3-kinase regulatory subunit 1	GO:0035655 interleukin-18-mediated signaling pathway;GO:0071351 cellular response to interleukin-18;GO:0120182 regulation of focal adhesion disassembly
Southern gentoo	LCP2	16	lymphocyte cytosolic protein 2	GO:0045576 mast cell activation;GO:0050852 T cell receptor signaling pathway;GO:0002274 myeloid leukocyte activation
Southern gentoo	KCNQ3	5	potassium voltage-gated channel subfamily Q member 3	GO:0097314 apoptosome assembly;GO:0099611 regulation of action potential firing threshold;GO:1905701 substantia propria of cornea development
Southern gentoo	POU6F2	2	POU class 6 homeobox 2	GO:0007601 visual perception;GO:0050953 sensory perception of light stimulus;GO:0007600 sensory perception
Southern gentoo	TAFl1	6	TATA-box binding protein associated factor 11	GO:0043923 positive regulation by host of viral transcription;GO:0042789 mRNA transcription by RNA polymerase II;GO:0009299 mRNA transcription
Southern gentoo	SUGCT1	1	succinyl-CoA:glutamate-CoA transferase	
Southern gentoo	BCL2A1	2	BCL2 related protein A1	GO:0008053 mitochondrial fusion;GO:0001836 release of cytochrome c from mitochondria;GO:0097192 extrinsic apoptotic signaling pathway in absence of ligand
Southern gentoo	ITGB2	24	integrin subunit beta 2	GO:2000361 regulation of prostaglandin-E synthase activity;GO:2000363 positive regulation of prostaglandin-E synthase activity;GO:0045914 negative regulation of catecholamine metabolic process
Southern gentoo	NCKAP5	39	NCK associated protein 5	GO:0007019 microtubule depolymerization;GO:0051261 protein depolymerization;GO:0031109 microtubule polymerization or depolymerization
Southern gentoo	UBR1	26	ubiquitin protein ligase E3 component N-recognin 1	GO:0071596 ubiquitin-dependent protein catabolic process via the N-end rule pathway;GO:0071233 cellular response to L-leucine;GO:0043201 response to L-leucine
Southern gentoo	Lrrc57	20	leucine rich repeat containing 57	
Southern gentoo	INO80	10	INO80 complex ATPase subunit	GO:0010571 positive regulation of nuclear cell cycle DNA replication;GO:0070914 UV-damage excision repair;GO:0032362 regulation of nuclear cell cycle DNA replication
Southern gentoo	CREB3L1	8	cAMP responsive element binding protein 3 like 1	GO:0070728 extracellular matrix constituent secretion;GO:1902236 negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway;GO:0040037 negative regulation of fibroblast growth factor receptor signaling pathway
Southern gentoo	FUT8	25	fucosyltransferase 8	GO:0034071 N-glycan fucosylation;GO:0046368 GDP-L-fucose metabolic process;GO:0019317 fucose catabolic process
Southern gentoo	TRAF6	4	TNF receptor associated factor 6	GO:0031173 interleukin-17A-mediated signaling pathway;GO:0038172 interleukin-33-mediated signaling pathway;GO:0097400 interleukin-17-mediated signaling pathway
Southern gentoo	CELF1	16	CUGBP Elav-like family member 1	GO:0006376 mRNA splice site recognition;GO:0000381 regulation of alternative mRNA splicing, via spliceosome;GO:0000245 spliceosomal complex assembly
Southern gentoo	ARHGAP15	11	Rho GTPase activating protein 15	GO:0008360 regulation of cell shape;GO:0022604 regulation of cell morphogenesis;GO:0007264 small GTPase-mediated signal transduction
Southern gentoo	TTC7B	1	tetratricopeptide repeat domain 7B	GO:0046854 phosphatidylinositol phosphate biosynthetic process;GO:0006661 phosphatidylinositol biosynthetic process;GO:0046488 phosphatidylinositol metabolic process
Southern gentoo	PARVA	4	parvin alpha	GO:0071670 smooth muscle cell chemotaxis;GO:0071963 establishment or maintenance of cell polarity regulating cell shape;GO:0014909 smooth muscle cell migration
Southern gentoo	KCNQ1	5	potassium voltage-gated channel subfamily Q member 1	GO:001698 actin-myosin-based matrix acid secretion;GO:0025924 corticotropinergic secretion;GO:0025923 glucocorticoid secretion
Southern gentoo	GPC5	9	glypican 5	GO:0090263 positive regulation of canonical Wnt signaling pathway;GO:0030177 positive regulation of Wnt signaling pathway;GO:1905475 regulation of protein localization to membrane
Southern gentoo	BBS9	28	Bardet-Biedl syndrome 9	GO:0061512 protein localization to cilium;GO:0045444 fat cell differentiation;GO:0007601 visual perception
Southern gentoo	ERC1	130	ELKS/RAB6-interacting/CAST family member 1	GO:0007252 L-kappaB phosphorylation;GO:0048790 maintenance of presynaptic active zone structure;GO:1990709 presynaptic active zone organization
Southern gentoo	PHF3	23	PHF finger protein 3	GO:0006351 DNA-templated transcription;GO:0032774 RNA biosynthetic process;GO:0141187 nucleic acid biosynthetic process
Southern gentoo	Dna1l	1	dynein axonemal intermediate chain 1	GO:0036158 outer dynein arm assembly;GO:0070286 axonemal dynein complex assembly;GO:0003351 epithelial cilium movement involved in extracellular fluid movement
Southern gentoo	WDR25	16	WD repeat domain 25	
Southern gentoo	GRIK2	10	glutamate ionotropic receptor kainate type subunit 2	GO:0062053 sensory perception of cold stimulus;GO:0120169 detection of cold stimulus involved in thermoreception;GO:0050960 detection of temperature stimulus involved in thermoreception
Southern gentoo	OR52R2	7	olfactory receptor family 52 subfamily B member 2	GO:0050911 detection of chemical stimulus involved in sensory perception of smell;GO:0007608 sensory perception of smell;GO:0050907 detection of chemical stimulus involved in sensory perception
Southern gentoo	DPH6	3	diphthamnine biosynthesis 6	GO:0017183 protein histidyl modification to diphthamide;GO:0018202 peptidyl-histidine modification;GO:0018193 peptidyl-amino acid modification
Southern gentoo	KIF16B	30	kinesin family member 16B	GO:0006895 Golgi to endosome transport;GO:0032801 receptor catabolic process;GO:0001919 regulation of receptor recycling
Southern gentoo	musch2b	4	ribonuclease H2 subunit B	GO:2000001 regulation of DNA damage checkpoint;GO:0006298 mismatch repair;GO:0048144 fibroblast proliferation
Southern gentoo	Ppp2r2a	12	protein phosphatase 2 regulatory subunit Balpha	GO:0043278 response to morphine;GO:0014072 response to isoquinoline alkaloid;GO:0006470 protein dephosphorylation
Southern gentoo	SMG1	498	SMG1 nonsense mediated mRNA decay associated PI3K related kinase	GO:0004814 nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;GO:0046854 phosphatidylinositol phosphate biosynthetic process;GO:0064616 mRNA export from nucleus
Southern gentoo	TBC1D14	8	TBC1 domain family member 14	GO:0071955 recycling endosome to Golgi transport;GO:2000785 regulation of autophagosome assembly;GO:0040408 regulation of vacuole organization
Southern gentoo	ST6GALNAC3	6	ST6 N-acetylglucosaminide alpha-2,6-sialyltransferase 3	GO:0006677 glycosylceramide metabolic process;GO:0001574 ganglioside biosynthetic process;GO:0001573 ganglioside metabolic process
Southern gentoo	MTMR12	4	myotubularin related protein 12	GO:0048856 phosphatidylinositol dephosphorylation;GO:0048329 phospholipid dephosphorylation;GO:0016311 dephosphorylation
Southern gentoo	PDZD2	48	PDZ domain containing 2	GO:0007155 cell adhesion;GO:0009987 cellular process;GO:0008150 biological process
Southern gentoo	CCBE1	16	collagen and calcium binding EGF domains 1	GO:1904977 lymphatic endothelial cell migration;GO:1901492 positive regulation of lymphangiogenesis;GO:1901490 regulation of lymphangiogenesis
Southern gentoo	Ntn4	37	netrin 4	GO:0060668 regulation of branching involved in salivary gland morphogenesis by extracellular matrix-epithelial cell signaling;GO:0070831 basement membrane assembly;GO:0035426 extracellular matrix cell signaling
Southern gentoo	MGLL	7	monoglyceride lipase	GO:2000124 regulation of endocannabinoid signaling pathway;GO:0052651 monoglycerol catabolic process;GO:0004642 monoglycerol metabolic process
Southern gentoo	INPP5A	5	inositol polyphosphate-5-phosphatase A	GO:1900737 negative regulation of phospholipase C-activating G protein-coupled receptor signaling pathway;GO:1900736 regulation of phospholipase C-activating G protein-coupled receptor signaling pathway;GO:0046856 phosphatidylinositol dephosphorylation
Southern gentoo	Fcho2	7	FCH and nu domain containing endocytic adaptor 2	GO:0045268 clathrin coat assembly;GO:0072583 clathrin-dependent endocytosis;GO:0010324 membrane invagination
Southern gentoo	AFAP1L2	20	actin filament associated protein 1 like 2	GO:0045742 positive regulation of epidermal growth factor receptor signaling pathway;GO:1901186 positive regulation of ERBB signaling pathway;GO:0032757 positive regulation of interleukin-8 production
Southern gentoo	GRM8	1	glutamate metabotropic receptor 8	GO:0007196 adenylate cyclase-inhibiting G protein-coupled glutamate receptor signaling pathway;GO:0007216 G protein-coupled glutamate receptor signaling pathway;GO:0007215 glutamate receptor signaling pathway
Southern gentoo	COBL	43	cordon-bleu WH2 repeat protein	GO:0048669 collateral sprouting in absence of injury;GO:0001757 somite specification;GO:0051639 actin filament network formation
Southern gentoo	ADRA1D	14	adrenoreceptor alpha 1D	GO:0150099 neuron-glia cell signaling;GO:0071880 adenylate cyclase-activating adrenergic receptor signaling pathway;GO:0071875 adrenergic receptor signaling pathway
Southern gentoo	MMP16	1	matrix metalloproteinase 16	GO:0035988 chondrocyte maturation;GO:0097094 craniofacial suture morphogenesis;GO:0001958 endochondral ossification
Southern gentoo	Kat5	38	lysine acetyltransferase 5A	GO:0006472 protein acetylation;GO:0043543 acetyl coenzyme A catabolic process;GO:0003038 cellular response
Southeastern gentoo	TRAK1	1	trafficking kinesin protein 1	GO:0099897 anterograde axonal transport of mitochondrion;GO:0019896 axonal transport of mitochondrion;GO:0048311 mitochondrion distribution
Southeastern gentoo	Ptpn21	84	protein tyrosine phosphatase non-receptor type 21	GO:0006470 protein dephosphorylation;GO:0016311 dephosphorylation;GO:0006338 chromatin remodeling
Southeastern gentoo	Slitr4	1	SLIT and NTRK like family member 4	GO:0051965 positive regulation of synapse assembly;GO:1901890 positive regulation of cell junction assembly;GO:0051963 regulation of synapse assembly
Southeastern gentoo	BMP4	3	bone morphogenetic protein 4	GO:0048390 intermediate mesoderm morphogenesis;GO:0048391 intermediate mesoderm formation;GO:0048392 intermediate mesodermal cell differentiation
Southeastern gentoo	TRIM6	1	tripartite motif containing 36	GO:0007340 acrosome reaction;GO:0000281 mitotic cytokinesis;GO:0061640 cytoskeleton-dependent cytokinesis
Southeastern gentoo	Kcnk2	8	potassium calcium-activated channel subfamily N member 2	GO:0098914 membrane repolarization during atrial cardiac muscle cell action potential;GO:0099624 atrial cardiac muscle cell membrane repolarization;GO:0086014 atrial cardiac muscle cell action potential
Southeastern gentoo	YTHDC2	23	YTH N6-methyladenosine RNA binding protein C2	GO:0051729 germline cell cycle switching, mitotic to meiotic cell cycle;GO:0051728 cell cycle switching, mitotic to meiotic cell cycle;GO:0060184 cell cycle switching
Southeastern gentoo	CAMSAP1	35	calmodulin regulated spectrin associated protein 1	GO:0031113 regulation of microtubule polymerization;GO:0031110 regulation of microtubule polymerization or depolymerization;GO:0070507 regulation of microtubule cytoskeleton organization
Southeastern gentoo	CBLN2	2	cerebellin 2 precursor	GO:0098814 spontaneous synaptic transmission;GO:0099550 trans-synaptic signaling, modulating synaptic transmission;GO:0099558 maintenance of synapse structure
Southeastern gentoo	ZADH2	20	prostaglandin reductase 3	GO:0045599 negative regulation of fat cell differentiation;GO:0045598 regulation of fat cell differentiation;GO:0045596 negative regulation of cell differentiation
Southeastern gentoo	LTBP2	2	latent transforming growth factor beta binding protein 2	GO:0007179 transforming growth factor beta receptor signaling pathway;GO:0009306 protein secretion;GO:0035592 establishment of protein localization to extracellular region
Southeastern gentoo	ADAMTS6	14	ADAM metalloproteinase with thrombospondin type 1 motif 6	GO:0009676 coronary vasculature development;GO:0035904 aorta development;GO:0060840 artery development
Southeastern gentoo	Trim23	4	tripartite motif containing 23	GO:0010508 positive regulation of autophagy;GO:0010506 regulation of autophagy;GO:0006886 intracellular protein transport
Southeastern gentoo	SH3BP1	20	SH3 domain containing kinase binding protein 1	GO:0050871 positive regulation of B cell activation;GO:0050864 regulation of B cell activation;GO:0008360 regulation of cell shape

Southeastern gentoo	BEND2	10	BEN domain containing 2	
Southeastern gentoo	WDTC1	26	WD and tetratricopeptide repeats 1	GO:0045717 negative regulation of fatty acid biosynthetic process;GO:0045922 negative regulation of fatty acid metabolic process;GO:0047004 regulation of fatty acid biosynthetic process
Southeastern gentoo	DSG2	125	desmoglein 2	GO:0003165 Parkinson's myocyte development;GO:0006073 bundle of His cell-Parkinson's myocyte adhesion involved in cell communication;GO:0003164 His-Parkinson's system development
Southeastern gentoo	XKR4	3	XK related 4	GO:0070782 phosphatidylserine exposure on apoptotic cell surface;GO:0043652 engulfment of apoptotic cell;GO:0017121 plasma membrane phospholipid scrambling
Southeastern gentoo	TMEM68	10	transmembrane protein 68	GO:0019432 triglyceride biosynthetic process;GO:0046460 neutral lipid biosynthetic process;GO:0046463 acylglycerol biosynthetic process
Southeastern gentoo	PSD3	20	pleckstrin and Sec7 domain containing 3	GO:0032012 regulation of ARF protein signal transduction;GO:0051056 regulation of small GTPase mediated signal transduction;GO:1902531 regulation of intracellular signal transduction
Southeastern gentoo	ECAP3	11	EcM29 proteasome adaptor and scaffold	GO:0043248 proteasome assembly;GO:0036503 ERAD pathway;GO:0034976 response to endoplasmic reticulum stress
Southeastern gentoo	KEL	15	Kell metallo-endopeptidase (Kell blood group)	GO:0010961 intracellular magnesium ion homeostasis;GO:0031133 regulation of axon diameter;GO:0010960 magnesium ion homeostasis
Southeastern gentoo	RELL1	1	RELT like 1	GO:1900745 positive regulation of p38MAPK cascade;GO:1900744 regulation of p38MAPK cascade;GO:0043410 positive regulation of MAPK cascade
Southeastern gentoo	Coo8a	4	coenzyme Q8A	GO:0006744 ubiquinone biosynthetic process;GO:1901663 ubiquinol biosynthetic process;GO:0006743 ubiquinol metabolic process
Southeastern gentoo	Auh	6	AU RNA binding methylglutacetyl-CoA hydratase	GO:0006552 L-leucine catabolic process;GO:0006551 L-leucine metabolic process;GO:0009080 pyruvate family amino acid catabolic process
Southeastern gentoo	EIF2A	36	eukaryotic translation initiation factor 2A	GO:0032933 SREBP signaling pathway;GO:0071501 cellular response to sterol depletion;GO:0006991 response to sterol depletion
Southeastern gentoo	Tiparp	2	TCDD inducible poly(ADP-ribose) polymerase	GO:1904612 response to 2,3,7,8-tetrachlorodibenzo-dioxin;GO:0048745 smooth muscle tissue development;GO:0008209 androgen metabolic process
Southeastern gentoo	AFG3L2	6	AFG3 like matrix AAA peptidase subunit 2	GO:0072753 cellular response to glutathione;GO:1901370 response to glutathione;GO:0141164 mitochondrial protein quality control
Southeastern gentoo	ACER2	11	alkaline ceramidase 2	GO:0009049 regulation of protein glycosylation;GO:0033629 negative regulation of cell adhesion mediated by integrin;GO:0046512 sphinganine biosynthetic process
Southeastern gentoo	DENN4C	28	DENN domain containing 4C	GO:0032483 regulation of Rab protein signal transduction;GO:0032869 cellular response to insulin stimulus;GO:0072659 protein localization to plasma membrane
Southeastern gentoo	ADAMTSL1	32	ADAMTSL like 1	GO:0030198 extracellular matrix organization;GO:0043062 extracellular structure organization;GO:0045229 external encapsulating structure organization
Southeastern gentoo	KIF26B	24	kinesin family member 26B	GO:0072092 ureteric bud invasion;GO:0072093 metanephric renal vesicle formation;GO:0060677 ureteric bud elongation
Southeastern gentoo	MTR	2	5-methyltetrahydrofolate-homocysteine methyltransferase	GO:0009235 cobalamin metabolic process;GO:0009086 methionine biosynthetic process;GO:0050667 homocysteine metabolic process
Southeastern gentoo	ACTN5	5	actinin alpha 2	GO:0051695 actin filament uncapping;GO:0006097 phospholipase C-activating angiotensin-activated signaling pathway;GO:0030035 microtubule assembly
Southeastern gentoo	PLSCR2	14	phospholipid scramblase 2	GO:0017121 plasma membrane phospholipid scrambling;GO:0045332 phospholipid translocation;GO:0034204 lipid translocation
Southeastern gentoo	PPP1R9A	10	protein phosphatase 1 regulatory subunit 9A	GO:0019722 calcium-mediated signaling;GO:0007015 actin filament organization;GO:0050804 modulation of chemical synaptic transmission
Southeastern gentoo	ZGRF1	4	zinc finger GRF-type containing 1	GO:0035408 DNA duplex unwinding;GO:0032292 DNA geometric change;GO:0071103 DNA conformation change
Southeastern gentoo	MFS3D	5	major facilitator superfamily domain containing 8	GO:1901424 fluoride transmembrane transporter;GO:0015705 iodide transport;GO:0070841 inclusion body assembly
Southeastern gentoo	CDC14A	35	cell division cycle 14A	GO:0007096 regulation of exit from mitosis;GO:0032467 positive regulation of cytokinesis;GO:0032465 regulation of cytokinesis
Southeastern gentoo	DPYD	7	dihydropyrimidine dehydrogenase	GO:0006214 thymidine catabolic process;GO:0046127 pyrimidine deoxyribonucleoside catabolic process;GO:0006212 uracil catabolic process
Southeastern gentoo	Abcd3	1	ATP binding cassette subfamily D member 3	GO:1903512 phytanic acid metabolic process;GO:0015910 long-chain fatty acid import into peroxisome;GO:0097089 methyl-branched fatty acid metabolic process
Southeastern gentoo	CHD6	2	chromodomain helicase DNA binding protein 6	GO:0045454 cell redox homeostasis;GO:0032508 DNA duplex unwinding;GO:0032392 DNA geometric change
Southeastern gentoo	USP28	4	ubiquitin specific peptidase 28	GO:0071947 protein deubiquitination involved in ubiquitin-dependent protein catabolic process;GO:0042771 intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator;GO:0072332 intrinsic apoptotic signaling pathway by p53 class mediator
Southeastern gentoo	L3MBTL3	1	L3MBTL histone methyl-lysine binding protein 3	GO:0160217 negative regulation of transcription initiation-coupled chromatin remodeling;GO:1905268 negative regulation of chromatin organization;GO:0043249 erythrocyte maturation
Southeastern gentoo	JMY	1	junction mediated and regulatory protein, p53 cofactor	GO:0070600 'de novo' actin filament nucleation;GO:0070358 actin polymerization-dependent cell motility;GO:0043144 Arp2/3 complex-mediated actin nucleation
Southeastern gentoo	OPRM1	5	opioid receptor mu 1	GO:0061358 negative regulation of Wnt protein secretion;GO:0071315 cellular response to morphine;GO:0071317 cellular response to norepinephrine alkaloid
Southeastern gentoo	MTHFD1L	3	methylentetrahydrofolate dehydrogenase (NADP+ dependent) 1 like	GO:0009257 10-formyltetrahydrofolate biosynthetic process;GO:0009256 10-formyltetrahydrofolate metabolic process;GO:0015942 formate metabolic process
Southeastern gentoo	CRYZ	3	crystallin zeta	GO:0042178 xenobiotic catabolic process;GO:0051289 protein homotetramerization;GO:0051262 protein tetramerization
Southeastern gentoo	CHD1	20	chromodomain helicase DNA binding protein 1	GO:0045923 positive regulation by host of viral transcription;GO:0032508 DNA duplex unwinding;GO:0051851 modulation by host of mitotic process
Southeastern gentoo	PATZ1	1	POZ/BTB and AT hook containing zinc finger 1	GO:0010596 negative regulation of endothelial cell migration;GO:0008584 male gonad development;GO:0046546 development of primary male sexual characteristics
Southeastern gentoo	Ap3a1	4	adaptor related protein complex 3 subunit sigma 1	GO:0016183 synaptic vesicle coating;GO:0035652 clathrin-coated vesicle cargo loading;GO:0035654 clathrin-coated vesicle cargo loading, AP-3-mediated
Southeastern gentoo	CDC40	1	cell division cycle 40	GO:1900403 embryonic brain development;GO:0000377 RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;GO:0000398 mRNA splicing, via spliceosome
Southeastern gentoo	CACNB2	20	calcium voltage-gated channel auxiliary subunit beta 2	GO:0098912 membrane depolarization during atrial cardiac muscle cell action potential;GO:1901843 positive regulation of high voltage-gated calcium channel activity;GO:1904879 positive regulation of calcium ion transmembrane transport via high voltage-gated calcium channel
Southeastern gentoo	CMT3	36	CKLF like MARVEL transmembrane domain containing 3	GO:0050861 positive regulation of B cell receptor signaling pathway;GO:0050855 regulation of B cell receptor signaling pathway;GO:0001835 blastocyst hatching
Southeastern gentoo	ORC6	43	origin recognition complex subunit 6	GO:0006270 DNA replication initiation;GO:0006261 DNA-templated DNA replication;GO:0002600 DNA replication
Southeastern gentoo	BRD7	9	bromodomain containing 7	GO:2000819 regulation of nucleotide-excision repair;GO:0070316 regulation of G0 to G1 transition;GO:0045663 positive regulation of myoblast differentiation
Southeastern gentoo	FKBP5	6	FKBP prolyl isomerase family member 15	GO:0004897 endocytosis;GO:0098657 import into cell;GO:0016192 vesicle-mediated transport
Southeastern gentoo	Ddr2	12	discoidin domain receptor tyrosine kinase 2	GO:1904897 regulation of hepatic stellate cell proliferation;GO:1904899 positive regulation of hepatic stellate cell proliferation;GO:2000491 positive regulation of hepatic stellate cell activation
Southeastern gentoo	GOLM1	2	golgi membrane protein 1	GO:0006997 nucleus organization;GO:0019216 regulation of lipid metabolic process;GO:0000996 organelle organization
Southeastern gentoo	NAA35	1	N-alpha-acetyltransferase 35, NatC auxiliary subunit	GO:0048659 smooth muscle cell proliferation;GO:0033002 muscle cell proliferation;GO:0008283 cell population proliferation
Southeastern gentoo	FRMD7	1	FERM domain containing 7	GO:0010592 positive regulation of lamellipodium assembly;GO:0051497 negative regulation of stress fiber assembly;GO:1902745 positive regulation of lamellipodium organization
Southeastern gentoo	STK26	14	serine/threonine kinase 26	GO:0030033 microvilli assembly;GO:0032528 microvilli organization;GO:0046777 protein autophosphorylation
Southeastern gentoo	Maml1	8	masternid like transcriptional coactivator 1	GO:0060928 atrioventricular node cell development;GO:0003292 cardiac septum cell differentiation;GO:0060922 atrioventricular node cell differentiation
Southeastern gentoo	NEK7	2	NIMA related 7	GO:0035865 cellular response to potassium ion;GO:0035864 response to potassium ion;GO:0032212 positive regulation of telomere maintenance via telomerase
Southeastern gentoo	RAB5A	1	RAB5A, member RAS oncogene family	GO:0150095 amyloid-beta clearance by transcytosis;GO:0051036 regulation of endosome size;GO:0097494 regulation of vesicle size
Southeastern gentoo	GADL1	8	glutamate decarboxylase like 1	GO:0019752 carboxylic acid metabolic process;GO:0043436 oxoacid metabolic process;GO:0006082 organic acid metabolic process
Southeastern gentoo	OSBP1.10	10	oxysterol binding protein like 10	GO:0036150 phosphatidylserine acyl-chain remodeling;GO:0006658 phosphatidylserine metabolic process;GO:0015914 phospholipid transport
Southeastern gentoo	A2ML1	5	alpha-2-macroglobulin like 1	GO:0052548 regulation of endopeptidase activity;GO:0052547 regulation of peptidase activity;GO:0051336 regulation of hydrolase activity
Southeastern gentoo	KSR2	1	kinase suppressor of ras 2	GO:007265 Ras protein signal transduction;GO:0120162 positive regulation of cold-induced thermogenesis;GO:0120161 regulation of cold-induced thermogenesis
Southeastern gentoo	EPB411A	12	erythrocyte membrane protein band 4.1 like 4A	GO:0031032 actomyosin structure organization;GO:0030036 actin cytoskeleton organization;GO:0030029 actin filament-based process
Southeastern gentoo	SATB2	8	SATB homeobox 2	GO:0002076 osteoblast development;GO:0009880 embryonic pattern specification;GO:0060021 roof of mouth development
Southeastern gentoo	CAVIN2	2	caveolae associated protein 2	GO:0097320 plasma membrane tubulation;GO:0007009 plasma membrane organization;GO:0010256 endomembrane system organization
Southeastern gentoo	Ap3d1	1	adaptor related protein complex 3 subunit delta 1	GO:0016182 synaptic vesicle budding from endosome;GO:0051138 positive regulation of NK T cell differentiation;GO:0140916 zinc ion import into lysosome
Southeastern gentoo	celf4	11	CUGBP Elav-like family member 4	GO:1902866 regulation of retina development in camera-type eye;GO:0090394 negative regulation of excitatory postsynaptic potential;GO:0048025 negative regulation of mRNA splicing, via spliceosome
Southeastern gentoo	RRM2B	6	ribonucleotide reductase regulatory TP53 inducible subunit M2B	GO:0070318 positive regulation of G0 to G1 transition;GO:0006264 mitochondrial DNA replication;GO:0009200 deoxyribonucleoside triphosphate metabolic process
Southeastern gentoo	FBXO43	3	F-box protein 43	GO:0045833 negative regulation of meiotic nuclear division;GO:0051447 negative regulation of meiotic cell cycle;GO:0040020 regulation of meiotic nuclear division
Southeastern gentoo	VPS13B	4	vacuolar protein sorting 13 homolog B	GO:0032458 slow endocytic recycling;GO:0090168 Golgi reassembly;GO:0036438 maintenance of lens transparency
Southeastern gentoo	CASP2	37	CASP2 and RIPK1 domain containing adaptor with death domain	GO:0006977 DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;GO:0031571 mitotic G1 DNA damage checkpoint signaling;GO:0048419 mitotic G1/S transition checkpoint signaling
Southeastern gentoo	CNOT4	7	CCR4-NOT transcription complex subunit 4	GO:0000289 nuclear-transcribed mRNA poly(A) tail shortening;GO:0000288 nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay;GO:0045652 regulation of mekarocyte differentiation
Southeastern gentoo	DCN	27	decorin	GO:0051901 positive regulation of mitochondrial depolarization;GO:1904181 positive regulation of membrane depolarization;GO:1900747 negative regulation of vascular endothelial growth factor signaling pathway
Southeastern gentoo	CNTNAP4	24	contactin associated protein family member 4	GO:2000821 regulation of grooming behavior;GO:0032225 regulation of synaptic transmission, dopaminergic;GO:0032228 regulation of synaptic transmission, GABAergic
Southeastern gentoo	IPO11	30	importin 11	GO:0006610 ribosomal protein import into nucleus;GO:0006606 protein import into nucleus;GO:0051170 import into nucleus
Southeastern gentoo	ZSWIM4	45	zinc finger SWIM-type containing 4	
Southeastern gentoo	ACTR8	7	actin related protein 8	GO:1904507 positive regulation of telomere maintenance in response to DNA damage;GO:0060382 regulation of DNA strand elongation;GO:1904505 regulation of telomere maintenance in response to DNA damage
Southeastern gentoo	CACNA2D3	2	calcium voltage-gated channel auxiliary subunit alpha2delta 3	GO:0099174 regulation of presynaptic organization;GO:0070588 calcium ion transmembrane transport;GO:0006816 calcium ion transport
Southeastern gentoo	TMEM64	3	transmembrane protein 64	GO:0045780 positive regulation of bone resorption;GO:0045672 positive regulation of osteoclast differentiation;GO:0045124 regulation of bone resorption
Southeastern gentoo	TBL3	2	transducin beta like 3	GO:0000472 endonucleolytic cleavage to generate mutant 5'-end of SSLI-RNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA);GO:0000967 rRNA 5'-end processing;GO:0000480 endonucleolytic cleavage in 5'-ETS of tritestic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
Southeastern gentoo	TALPID3	8	KIAA0586	GO:0007224 smoothened signaling pathway;GO:0060271 cilium assembly;GO:0044782 cilium organization
Southeastern gentoo	KHDRBS2	16	KH RNA binding domain containing, signal transduction associated 2	GO:0000381 regulation of alternative mRNA splicing, via spliceosome;GO:0048024 regulation of mRNA splicing, via spliceosome;GO:0050684 regulation of mRNA processing
Southeastern gentoo	COL21A1	1	collagen type XXI alpha 1 chain	
Southeastern gentoo	Prin2	8	DNA primase 2	GO:1903932 regulation of DNA primase activity;GO:1903934 positive regulation of DNA primase activity;GO:0006269 DNA replication, synthesis of primer
Southeastern gentoo	TRIO	1	trio Rho guanine nucleotide exchange factor	GO:0071875 cell surface receptor protein tyrosine phosphatase signaling pathway;GO:0099170 postsynaptic modulation of chemical synaptic transmission;GO:0045590 negative regulation of cell cycle differentiation
Southeastern gentoo	CTNND2	1	catenin delta 2	GO:0060997 dendritic spine morphogenesis;GO:0060996 dendritic spine development;GO:0097061 dendritic spine organization
Southeastern gentoo	Ctnd2	146	catenin delta 2	GO:0060997 dendritic spine morphogenesis;GO:0060996 dendritic spine development;GO:0097061 dendritic spine organization
Southeastern gentoo	MEF2C	5	myocyte enhancer factor 2C	GO:0003185 sinoatrial valve morphogenesis;GO:0003172 sinoatrial valve development;GO:0007521 muscle cell fate determination
Southeastern gentoo	GPR98	1	adhesion G protein-coupled receptor V1	GO:0010739 positive regulation of protein kinase A signaling;GO:0048496 maintenance of animal organ identity;GO:0010738 regulation of protein kinase A signaling
Southeastern gentoo	MOC52	1	molybdenum cofactor synthesis 2	GO:0006777 Mo-molybdopter cofactor biosynthetic process;GO:0019720 Mo-molybdopter cofactor metabolic process;GO:0032324 molybdopter cofactor biosynthetic process

Southeastern gentoo	CHRN3	2	cholinergic receptor nicotinic beta 3 subunit	GO:0007271 synaptic transmission, cholinergic;GO:0007274 neuromuscular synaptic transmission;GO:0099171 presynaptic modulation of chemical synaptic transmission
Southeastern gentoo	CHRN46	2	cholinergic receptor nicotinic alpha 6 subunit	GO:0014059 regulation of dopamine secretion;GO:0007271 synaptic transmission, cholinergic;GO:0007274 neuromuscular synaptic transmission
Southeastern gentoo	SPG11	18	SPG11 vesicle trafficking associated, spatacin	GO:0090386 phagosome maturation involved in apoptotic cell clearance;GO:0090387 phagolysosome assembly involved in apoptotic cell clearance;GO:0090389 phagosome-lysosome fusion involved in apoptotic cell clearance
Southeastern gentoo	ADAMTS17	3	ADAM metalloproteinase with thrombospondin type 1 motif 17	GO:0030198 extracellular matrix organization;GO:0043062 extracellular structure organization;GO:0045229 external encapsulating structure organization
Southeastern gentoo	PPP2R3B	2	protein phosphatase 2 regulatory subunit B-beta	GO:0004284 protein dephosphorylation;GO:0016311 dephosphorylation;GO:0051726 regulation of cell cycle
Southeastern gentoo	GABRA5	7	gamma-aminobutyric acid type A receptor subunit alpha5	GO:1904862 inhibitory synapse assembly;GO:0051932 synaptic transmission, GABAergic;GO:0060384 innervation
Southeastern gentoo	BRD1	12	bromodomain containing 1	GO:0043249 erythrocyte maturation;GO:0035902 response to immobilization stress;GO:0045648 positive regulation of erythrocyte differentiation
Southeastern gentoo	ATP13A3	72	ATPase 13A3	GO:0013847 putrescine transport;GO:1902047 polyamine transmembrane transport;GO:0015846 polyamine transport
Southeastern gentoo	UBAC2	5	UBA domain containing 2	GO:1904153 negative regulation of retrograde protein transport, ER to cytosol;GO:0070862 negative regulation of protein exit from endoplasmic reticulum;GO:1904152 regulation of retrograde protein transport, ER to cytosol
Southeastern gentoo	IL22RA1	60	interleukin 22 receptor subunit alpha 1	GO:0140865 interleukin-22-mediated signaling pathway;GO:0050829 defense response to Gram-negative bacterium;GO:0050728 negative regulation of inflammatory response
Southeastern gentoo	FABP1	13	fatty acid binding protein 1	GO:0035552 response to vitamin B3;GO:0032000 positive regulation of fatty acid beta-oxidation;GO:0046321 positive regulation of fatty acid oxidation
Southeastern gentoo	RICTOR	48	RPTOR independent companion of MTOR complex 2	GO:003203 TORC2 signaling;GO:2000114 regulation of establishment of cell polarity;GO:0032878 regulation of establishment or maintenance of cell polarity
Southeastern gentoo	mmt	24	MAX network transcriptional repressor	GO:0090398 cellular senescence;GO:2001234 negative regulation of apoptotic signaling pathway;GO:2001233 regulation of apoptotic signaling pathway
Southeastern gentoo	SH3PX2A	1	SH3 and PX domain 2A	GO:0027672 osteoclast fusion;GO:0072674 multicline osteoclast differentiation;GO:0042554 superoxide anion generation
Southeastern gentoo	GSTO1	10	glutathione S-transferase omega 1	GO:0014810 positive regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion;GO:0014809 regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion;GO:0014722 regulation of skeletal muscle contraction by calcium ion signaling
Southeastern gentoo	Ina	5	internexin neuronal intermediate filament protein alpha	GO:0099185 postsynaptic intermediate filament cytoskeleton organization;GO:0060052 neurofilament cytoskeleton organization;GO:0099188 postsynaptic cytoskeleton organization
Southeastern gentoo	CNOT10	12	CCR4-NOT transcription complex subunit 10	GO:0000289 nuclear-transcribed mRNA poly(A) tail shortening;GO:0000288 nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay;GO:0000956 nuclear-transcribed mRNA catabolic process
Southeastern gentoo	TOPAZ1	18	testis and ovary specific TOPAZ 1	GO:0048137 spermatocyte division;GO:0140742 lncRNA transcription;GO:0035234 ectopic germ cell programmed cell death
Southeastern gentoo	PEX1	2	peroxisomal biogenesis factor 1	GO:0060151 peroxisome localization;GO:0060152 microtubule-based peroxisome localization;GO:0043335 protein unfolding
Southeastern gentoo	PPP1R12A	1	protein phosphatase 1 regulatory subunit 12A	GO:000470 protein dephosphorylation;GO:0007098 catabolic cycle;GO:0011023 microtubule organizing center organization
Southeastern gentoo	FAM81A	3	family with sequence similarity 81 member A	
Southeastern gentoo	NXPH1	8	neurexophilin 1	GO:0050804 modulation of chemical synaptic transmission;GO:0099177 regulation of trans-synaptic signaling;GO:0020351 regulation of signaling
Southeastern gentoo	MED12	1	mediator complex subunit 12	GO:0090245 axis elongation involved in somitogenesis;GO:0048702 embryonic neurocranium morphogenesis;GO:1990403 embryonic brain development
Southeastern gentoo	PCSK5	5	proprotein convertase subtilisin/kexin type 5	GO:0001999 renal response to blood flow involved in circulatory renin-angiotensin regulation of systemic arterial blood pressure;GO:0002001 renin secretion into blood stream;GO:0140447 cytokine precursor processing
Southeastern gentoo	CEND3	6	cyclin D3	GO:0045737 positive regulation of cyclin-dependent protein serine/threonine kinase activity;GO:1904031 positive regulation of cyclin-dependent protein kinase activity;GO:1900087 positive regulation of G1/S transition of mitotic cell cycle
Southeastern gentoo	MPSF	79	None	None
Southeastern gentoo	Pts	5	6-pyruvyltetrahydropterin synthase	GO:0006729 tetrahydrobiopterin biosynthetic process;GO:0046146 tetrahydrobiopterin metabolic process;GO:0042559 pteridine-containing compound biosynthetic process
Southeastern gentoo	MKL1	4	maskelin 1	GO:0098968 neurotransmitter receptor transport postsynaptic membrane to endosome;GO:1902946 protein localization to early endosome;GO:0036010 protein localization to endosome
Southeastern gentoo	LRGUK	6	leucine rich repeats and glutylase kinase domain containing	GO:0045710 GDP metabolic process;GO:0046037 GMP metabolic process;GO:0009167 purine ribonucleoside monophosphate metabolic process
Southeastern gentoo	ERCC6L2	20	ERCC excision repair 6 like 2	GO:0036297 interstrand cross-link repair;GO:0034614 cellular response to reactive oxygen species;GO:0000302 response to reactive oxygen species
Southeastern gentoo	GTDCL1	1	glycosyltransferase like domain containing 1	
Southeastern gentoo	VWDE	5	von Willebrand factor D and EGF domain	GO:0006400 tRNA modification;GO:0008033 tRNA processing;GO:0009451 RNA modification
Southeastern gentoo	Dars	12	aspartyl-RNA synthetase 1	GO:0006422 aspartyl-RNA aminoacylation;GO:0006418 tRNA aminoacylation for protein translation;GO:0043039 tRNA aminoacylation
Southeastern gentoo	Ccn2	87	cyclin T2	GO:0019085 early viral transcription;GO:0019086 late viral transcription;GO:0019083 viral transcription
Southeastern gentoo	Cps1	68	carbamoyl-phosphate synthase 1	GO:0070408 carbamoyl phosphate metabolic process;GO:0070409 carbamoyl phosphate biosynthetic process;GO:0071400 cellular response to toxic acid
Southeastern gentoo	no6	8	nuclear protein 6	GO:0006409 tRNA export from nucleus;GO:0051031 tRNA transport;GO:0006405 tRNA export from nucleus
Southeastern gentoo	CALCA	3	calcitonin related polypeptide alpha	GO:0001984 artery vasodilation involved in baroreceptor response to increased systemic arterial blood pressure;GO:0001978 regulation of systemic arterial blood pressure by carotid sinus baroreceptor feedback
Southeastern gentoo	OTOG	2	etogelin	GO:019566 arabasic metabolic process;GO:0046373 L-arabasic metabolic process;GO:0019221 pentose metabolic process
Southeastern gentoo	PDE4B	9	phosphodiesterase 4B	GO:1901898 negative regulation of relaxation of cardiac muscle;GO:0071878 negative regulation of adenylate cyclase-activating adrenergic receptor signaling pathway;GO:1901897 regulation of relaxation of cardiac muscle
Southeastern gentoo	ROR1	4	receptor tyrosine kinase like orphan receptor 1	GO:0014002 astrocyte development;GO:0048708 astrocyte differentiation;GO:0051092 positive regulation of NF-kappaB transcription factor activity
Southeastern gentoo	GPC5	3	glypican 5	GO:0009263 positive regulation of canonical Wnt signaling pathway;GO:0030177 positive regulation of Wnt signaling pathway;GO:1905475 regulation of protein localization to membrane
Southeastern gentoo	TRIM2	1	tripartite motif containing 2	GO:0000209 protein polyubiquitination;GO:0043523 regulation of neuron apoptotic process;GO:0043161 proteasome-mediated ubiquitin-dependent protein catabolic process
Southeastern gentoo	TNKS	18	tanycase	GO:1904745 negative regulation of telomeric DNA binding;GO:1904742 regulation of telomeric DNA binding;GO:1904907 regulation of maintenance of mitotic sister chromatid cohesion, telomeric
Southeastern gentoo	KLHL1	4	kelch like family member 1	GO:0021680 cerebellar Purkinje cell layer development;GO:0007628 adult walking behavior;GO:0090659 walking behavior
Southeastern gentoo	KLFI2	2	KLF transcription factor 12	GO:0001222 negative regulation of transcription by RNA polymerase II;GO:0045944 positive regulation of transcription by RNA polymerase II;GO:0045892 negative regulation of DNA-templated transcription
Southeastern gentoo	ANKRD35	10	ankyrin repeat domain 55	
Southeastern gentoo	SLC39A9	18	solute carrier family 38 member 9	GO:0006867 asparagine transport;GO:0006868 glutamine transport;GO:0015801 branched-chain amino acid transport
Southeastern gentoo	CSP4	24	chondroitin sulfate proteoglycan 4	GO:0097178 ruffle assembly;GO:0006929 substrate-dependent cell migration;GO:0031529 ruffle organization
Southeastern gentoo	Ddx4	1	DEAD-box helicase 4	GO:0141006 transposable element silencing by piRNA-mediated heterochromatin formation;GO:0141176 gene silencing by piRNA-directed DNA methylation;GO:0141196 transposable element silencing by piRNA-mediated DNA methylation
Southeastern gentoo	Mrex	5	Mre4 exonome RNA helicase	GO:0016076 snRNA catabolic process;GO:0000460 maturation of 5.8S rRNA;GO:0016073 snRNA metabolic process
Southeastern gentoo	gpx-5	6	None	None
Southeastern gentoo	MPHOSPH9	2	M-phase phosphoprotein 9	GO:1902018 negative regulation of cilium assembly;GO:0120033 negative regulation of plasma membrane bounded cell projection assembly;GO:1902116 negative regulation of organelle assembly
Southeastern gentoo	RIMBP2	4	RIMS binding protein 2	GO:007274 neuromuscular synaptic transmission;GO:0007268 chemical synaptic transmission;GO:0098916 anterograde trans-synaptic signaling
Southeastern gentoo	KIF3A	4	kinesin family member 3A	GO:0072383 plus-end-directed vesicle transport along microtubule;GO:0072386 plus-end-directed organelle transport along microtubule;GO:0034454 microtubule anchoring at centrosome
Southeastern gentoo	VDAC1	7	voltage dependent anion channel 1	GO:0110099 negative regulation of calcium import into the mitochondrion;GO:0110097 regulation of calcium import into the mitochondrion;GO:0007270 neuron-neuron synaptic transmission
Southeastern gentoo	PCSK7	2	proprotein convertase subtilisin/kexin type 7	GO:0016486 peptide hormone processing;GO:0140448 signaling receptor ligand precursor processing;GO:0016485 protein processing
Southeastern gentoo	PPIP5K2	7	diphosphoinositol pentakisphosphate kinase 2	GO:0006020 inositol metabolic process;GO:0032958 inositol phosphate biosynthetic process;GO:0043647 inositol phosphate metabolic process
Southeastern gentoo	snc4	8	structural maintenance of chromosomes 4	GO:0010032 meiotic chromosome condensation;GO:1905821 positive regulation of chromosome condensation;GO:0060623 regulation of chromosome condensation
Southeastern gentoo	IL12A	7	interleukin 12A	GO:0028660 positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target;GO:0002857 positive regulation of natural killer cell mediated immune response to tumor cell;GO:0002858 regulation of natural killer cell mediated cytotoxicity directed against tumor cell target
Southeastern gentoo	MATN1	1	matrilin 1	GO:0003414 chondrocyte morphogenesis involved in endochondral bone morphogenesis;GO:0003429 growth plate cartilage chondrocyte morphogenesis;GO:0090171 chondrocyte morphogenesis
Southeastern gentoo	Il1rapl2	9	interleukin 1 receptor accessory protein like 2	GO:1905606 regulation of presynapse assembly;GO:0099174 regulation of presynapse organization;GO:0051963 regulation of synapse assembly
Southeastern gentoo	ECT2	7	epithelial cell transforming 2	GO:2000431 regulation of cytokinesis, actomyosin contractile ring assembly;GO:0032954 regulation of cytokinesis process;GO:1903436 regulation of mitotic cytokinesis process
Southeastern gentoo	FNDC3B	7	fibronectin type III domain containing 3B	
Southeastern gentoo	NHLRC3	9	NHL repeat containing 3	GO:0000209 protein polyubiquitination;GO:0043161 proteasome-mediated ubiquitin-dependent protein catabolic process;GO:0010498 proteasomal protein catabolic process
Southeastern gentoo	DOCK5	4	dedicator of cytokinesis 5	GO:1904694 negative regulation of vascular associated smooth muscle contraction;GO:0071800 podosome assembly;GO:0003056 regulation of vascular associated smooth muscle contraction
Southeastern gentoo	Grin2a	7	glutamate ionotropic receptor NMDA type subunit 2A	GO:0033058 directional locomotion;GO:0030431 sleep;GO:0042428 serotonin metabolic process
Southeastern gentoo	PEAK1	3	pseudopodium enriched atypical kinase 1	GO:0040441 focal adhesion assembly;GO:0070744 cell-substrate junction assembly;GO:0150115 cell-substrate junction organization
Southeastern gentoo	GDPP5	2	glycerophosphodiester phosphodiesterase domain containing 5	GO:0045666 positive regulation of neuron differentiation;GO:0045664 regulation of neuron differentiation;GO:0045597 positive regulation of cell differentiation
Southeastern gentoo	RAD1	6	RAD1 checkpoint DNA exonuclease	GO:0051598 meiotic recombination checkpoint signaling;GO:0033313 meiotic cell cycle checkpoint signaling;GO:0045835 negative regulation of meiotic nuclear division
Southeastern gentoo	Npr3	42	nutriuretic peptide receptor 3	GO:0002158 osesclast proliferation;GO:0035810 positive regulation of urine volume;GO:0051000 positive regulation of nitric-oxide synthase activity
Southeastern gentoo	Zf	79	zinc finger RNA binding protein	
Southeastern gentoo	PDZD2	44	PDZ domain containing 2	GO:0007155 cell adhesion;GO:0009987 cellular process;GO:0008150 biological process
Southeastern gentoo	RAI14	72	retinoic acid induced 14	GO:0007283 spermatogenesis;GO:0048232 male gamete generation;GO:0007276 aneuploidy generation
Southeastern gentoo	SUB1	6	SUB1 regulator of transcription	GO:1905462 regulation of DNA duplex unwinding;GO:1905463 negative regulation of DNA duplex unwinding;GO:0001109 promoter clearance during DNA-templated transcription
Southeastern gentoo	Slc22a23	13	solute carrier family 22 member 23	GO:0006811 monatomic ion transport;GO:0055085 transmembrane transport;GO:0006810 transport
Southeastern gentoo	CDH12	12	cadherin 12	GO:0044331 cell-cell adhesion mediated by cadherin;GO:0016339 calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules;GO:0044332 adherens junction organization
Southeastern gentoo	ZNRF3	6	zinc and ring finger 3	GO:0038018 Wnt receptor catabolic process;GO:2000051 negative regulation of non-canonical Wnt signaling pathway;GO:2000095 regulation of Wnt signaling pathway, planar cell polarity pathway
Southeastern gentoo	SLC4A11	8	solute carrier family 4 member 11	GO:0034445 borate transmembrane transport;GO:0046713 borate transport;GO:2000739 regulation of mesenchymal stem cell differentiation
Southeastern gentoo	Cadp2	3	calcium dependent secretion activator 2	GO:1999504 dense core granule exocytosis;GO:0032253 dense core granule localization;GO:0032252 secretory granule localization
Southeastern gentoo	GRAM3	3	glutamate metabotropic receptor 8	GO:0007196 adenylyl cyclase-inhibiting G protein-coupled glutamate receptor signaling pathway;GO:0007216 G protein-coupled glutamate receptor signaling pathway;GO:0007215 glutamate receptor signaling pathway
Southeastern gentoo	ELP1	6	elongator acetyltransferase complex subunit 1	GO:0002926 tRNA wobble base 5-methoxycarbonylmethyl-2-thiouridylation;GO:0002098 tRNA wobble uridine modification;GO:0002097 tRNA wobble base modification
Southeastern gentoo	Tsd2	1	thiosulfate sulfurtransferase like domain containing 2	
Southeastern gentoo	TBC1D2	12	TBC1 domain family member 2	GO:0043547 positive regulation of GTPase activity;GO:0043087 regulation of GTPase activity;GO:0051345 positive regulation of hydrolase activity
Southeastern gentoo	B4GALT1	6	beta-1,4-galactosyltransferase 1	GO:0061755 positive regulation of circulating fibrinogen levels;GO:0005989 lactose biosynthetic process;GO:0046351 disaccharide biosynthetic process

Southeastern gentoo	PSIP1	22	PC4 and SRSF1 interacting protein 1	GO:0000395 mRNA 5'-splice site recognition;GO:0045292 mRNA cis splicing, via spliceosome;GO:0006376 mRNA splice site recognition
Southeastern gentoo	BNC2	3	bismomelin zinc finger protein 2	GO:0045586 tongue development;GO:003416 endochondral bone growth;GO:0098868 bone growth
Southeastern gentoo	Nfsm	6	5,3'-nucleotidase, mitochondrial	GO:0040679 dUMP catabolic process;GO:0009131 pyrimidine nucleoside monophosphate catabolic process;GO:0009178 pyrimidine deoxyribonucleoside monophosphate catabolic process
Southeastern gentoo	CRK	1	CRK proto-oncogene, adaptor protein	GO:0035685 helper T cell diapedesis;GO:0061847 response to cholecystokinin;GO:1990859 cellular response to endothelin
Southeastern gentoo	HMBOX1	20	homobox containing 1	GO:1905324 telomere-terminase complex assembly;GO:0007004 telomere maintenance via telomerase;GO:0006278 RNA-templated DNA biosynthetic process
Southeastern gentoo	NDP	6	norrin cystine knot growth factor NDP	GO:0027501 actin blood vessel maintenance;GO:0000320 re-entry into mitotic cell cycle;GO:0110135 Norrin signaling pathway
Southeastern gentoo	MED14	3	mediator complex subunit 14	GO:0032968 positive regulation of transcription elongation by RNA polymerase II;GO:0035019 somatic stem cell population maintenance;GO:0032786 positive regulation of DNA-templated transcription, elongation
Southeastern gentoo	WDR4	6	WD repeat domain 4	GO:0106004 tRNA (guanine-N7)-methylation;GO:0036265 RNA (guanine-N7)-methylation;GO:0030488 tRNA methylation
Southeastern gentoo	LANCE1	2	Lanc1-like family member 3	GO:0031179 peptide modification;GO:0006138 peptide metabolic process;GO:0005975 carbohydrate metabolic process
Southeastern gentoo	UBA3	2	ubiquitin like modifier activating enzyme 3	GO:0007172 endomitotic cell cycle;GO:0005116 protein methylation;GO:0002738 mitotic cell cycle
Southeastern gentoo	ARL6IP5	15	ARF-like GTPase 6 interacting protein 5	GO:0000377 negative regulation of L-glutamate import across plasma membrane;GO:0002036 regulation of L-glutamate import across plasma membrane;GO:0098712 L-glutamate import across plasma membrane
Southeastern gentoo	Pla2g12a	1	phospholipase A2 group XIIA	GO:0050482 arachidonate secretion;GO:1903963 arachidonate transport;GO:0032309 isocannabinoid secretion
Southeastern gentoo	EIf4e	15	eukaryotic translation initiation factor 4E	GO:009578 regulation of translation at postsynapse, modulating synaptic transmission;GO:0099547 regulation of translation at synapse, modulating synaptic transmission;GO:0140245 regulation of translation at postsynapse
Eastern gentoo	MYRIP	28	myosin VIIA and Rab interacting protein	GO:0032024 positive regulation of insulin secretion;GO:0090277 positive regulation of peptide hormone secretion;GO:0002793 positive regulation of peptide secretion
Eastern gentoo	ALDH7A1	1	aldehyde dehydrogenase 7 family member A1	GO:019285 glycine betaine biosynthetic process from choline;GO:0031455 glycine betaine metabolic process;GO:0031456 glycine betaine biosynthetic process
Eastern gentoo	GUCY1A2	11	guanylate cyclase 1 soluble subunit alpha 2	GO:0010750 positive regulation of nitric oxide mediated signal transduction;GO:0010749 regulation of nitric oxide mediated signal transduction;GO:0006182 cGMP biosynthetic process
Eastern gentoo	AFF3	8	ALF transcription elongation factor 3	GO:0031166 embryonic hindlimb morphogenesis;GO:0031537 hindlimb morphogenesis;GO:0030326 embryonic limb morphogenesis
Eastern gentoo	Tmk1	21	TRAF2 and NCK interacting kinase	GO:0030033 microvillus assembly;GO:0032528 microvillus organization;GO:0048814 regulation of dendrite morphogenesis
Eastern gentoo	TRAPPC6B	10	trafficking protein particle complex subunit 6B	GO:0099022 vesicle tethering;GO:0006901 vesicle coating;GO:0006903 vesicle targeting
Eastern gentoo	PNN	10	pinin, desmosome associated protein	GO:0000377 RNA splicing, via transfection reactions
Eastern gentoo	TRAPPC13	8	trafficking protein particle complex subunit 13	GO:0099022 vesicle tethering;GO:0006901 vesicle coating;GO:0006903 vesicle targeting
Eastern gentoo	Akap10	1	A-kinase anchoring protein 10	GO:0008104 protein localization;GO:0070727 cellular macromolecule localization;GO:0033036 macromolecule localization
Eastern gentoo	CTPS2	5	CTP synthase 2	GO:0044210 de novo CTP biosynthetic process;GO:0019856 pyrimidine nucleobase biosynthetic process;GO:0006241 CTP biosynthetic process
Eastern gentoo	VEGFD	5	vascular endothelial growth factor D	GO:0060754 positive regulation of mast cell chemotaxis;GO:0060753 regulation of mast cell chemotaxis;GO:005930 induction of positive chemotaxis
Eastern gentoo	SYAP1	18	synapse associated protein 1	GO:0038203 TORC2 signaling;GO:1990314 cellular response to insulin-like growth factor stimulus;GO:0048172 regulation of short-term neuronal synaptic plasticity
Eastern gentoo	EPHA6	18	EPH receptor A6	GO:0038223 vascular endothelial growth factor receptor-1 signaling pathway;GO:0035790 platelet-derived growth factor receptor-alpha signaling pathway;GO:0036215 response to stem cell factor
Eastern gentoo	MAPKAP1	3	MAPK associated protein 1	GO:0038203 TORC2 signaling;GO:0046580 negative regulation of Ras protein signal transduction;GO:1900407 regulation of cellular response to oxidative stress
Eastern gentoo	LOXHD1	1	lipoxxygenase homology PLAT domains 1	GO:0007605 sensory perception of sound;GO:0050954 sensory perception of mechanical stimulus;GO:0007600 sensory perception
Eastern gentoo	TMEM47	80	transmembrane protein 47	GO:0096609 cell-cell adhesion;GO:0007155 cell adhesion;GO:0009987 cellular process
Eastern gentoo	CAMKK1	6	calcium/calmodulin dependent protein kinase kinase 1	GO:0035556 intracellular signal transduction;GO:0007165 signal transduction;GO:0023052 signaling
Eastern gentoo	STX8A1	38	STX8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	GO:0006491 N-glycan processing;GO:0006688 glycosphingolipid biosynthetic process;GO:0034605 cellular response to heat
Eastern gentoo	MICAL1	2	microtubule associated monooxygenase, calponin and LIM domain containing 1	GO:0194177 sulfur oxidation;GO:0030042 actin filament depolymerization;GO:0051261 protein depolymerization
Eastern gentoo	B3GALT2	8	beta-1,3-galactosyltransferase 2	GO:0006682 galactosylceramide biosynthetic process;GO:0019375 galactolipid biosynthetic process;GO:0046476 glycosylceramide biosynthetic process
Eastern gentoo	CDC73	17	cell division cycle 73	GO:0031442 positive regulation of mRNA 3'-end processing;GO:0031440 regulation of mRNA 3'-end processing;GO:0001711 endosomal cell fate commitment
Eastern gentoo	CNTN3	10	contactin 3	GO:0007155 cell adhesion;GO:0009987 cellular process;GO:0008150 biological process
Eastern gentoo	PLXND1	8	plexin D1	GO:0008039 synaptic target recognition;GO:0006666 dichotomous subdivision of terminal units involved in salivary gland branching;GO:0006600 dichotomous subdivision of an epithelial terminal unit
Eastern gentoo	Tmc1	72	transmembrane and coiled-coil domain family 1	GO:0097750 endosome membrane tubulation;GO:0140285 endosome fission;GO:0097749 membrane tubulation
Eastern gentoo	NALCN	1	sodium leak channel, non-selective	GO:0032224 positive regulation of synaptic transmission, cholinergic;GO:0032222 regulation of synaptic transmission, cholinergic;GO:0060075 regulation of resting membrane potential
Eastern gentoo	TMTc4	30	transmembrane O-mannosyltransferase targeting cadherins 4	GO:0032470 positive regulation of endoplasmic reticulum calcium ion concentration;GO:1905584 outer hair cell apoptotic process;GO:0035260 protein O-linked n-glycanation
Eastern gentoo	Dmbt1	14	deleted in malignant brain tumors 1	GO:0043152 induction of bacterial agglutination;GO:0019731 antibacterial humoral response;GO:0050829 defense response to Gram-negative bacterium
Eastern gentoo	FGFR2	10	fibroblast growth factor receptor 2	GO:0035602 fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptotic process in bone marrow cell;GO:0035603 fibroblast growth factor receptor signaling pathway involved in hemopoiesis;GO:0035604 fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow
Eastern gentoo	ADAM12	28	ADAM metalloproteinase domain 12	GO:0007520 myoblast fusion;GO:0000768 myoblast fusion formation by plasma membrane fusion;GO:0140253 cell-cell fusion
Eastern gentoo	LCLAT1	4	lysocardiolipin acyltransferase 1	GO:0035965 cardiolipin acyl-chain remodeling;GO:0036149 phosphatidylinositol acyl-chain remodeling;GO:0016024 CDP-diacylglycerol biosynthetic process
Eastern gentoo	TMEM63A	28	transmembrane protein 63A	GO:0160609 surfactant secretion;GO:0043129 surfactant homeostasis;GO:0140962 multicellular organismal-level chemical homeostasis
Eastern gentoo	Wd26	5	WD repeat domain 26	GO:0043161 proteasome-mediated ubiquitin-dependent protein catabolic process;GO:0010498 proteasomal protein catabolic process;GO:0006511 ubiquitin-dependent protein catabolic process
Eastern gentoo	Slc30a10	24	solute carrier family 30 member 10	GO:0140048 manganese ion export across plasma membrane;GO:0010312 detoxification of zinc ion;GO:1990359 stress response to zinc ion
Eastern gentoo	USH2A	16	usherin	GO:0048496 maintenance of animal organ identity;GO:0045494 photoreceptor cell maintenance;GO:0042941 inner ear auditory receptor cell differentiation
Eastern gentoo	SPATA17	2	spermatogenesis associated 17	GO:0000377 negative regulation of hematopoietic stem cell differentiation;GO:1902035 positive regulation of hematopoietic stem cell proliferation;GO:0015333 negative regulation of hematopoietic progenitor cell differentiation
Eastern gentoo	N4BP2L2	10	NEDD4 binding protein 2 like 2	GO:0034444 calcium import into the mitochondrion;GO:0001936 positive regulation of neurotransmitter secretion;GO:0006851 mitochondrial calcium ion transmembrane transport
Eastern gentoo	MICU3	3	mitochondrial calcium uptake family member 3	GO:1904881 cellular response to hydrogen sulfide;GO:0048597 post-embryonic camera-type eye morphogenesis;GO:1904880 response to hydrogen sulfide
Eastern gentoo	KDR	7	kinase insert domain receptor	GO:0006351 DNA-templated transcription;GO:0045944 positive regulation of transcription by RNA polymerase II;GO:0045893 positive regulation of DNA-templated transcription
Eastern gentoo	Gpbb1	3	GC-rich promoter binding protein 1	GO:0044331 cell-cell adhesion mediated by cadherin;GO:0016339 calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules;GO:0034332 adherens junction organization
Eastern gentoo	CDHR3	32	cadherin related family member 3	GO:0097050 type B pancreatic cell apoptotic process;GO:0098907 regulation of SA node cell action potential;GO:0003220 left ventricular cardiac muscle tissue morphogenesis
Eastern gentoo	RYR2	119	ryanodine receptor 2	GO:0032508 DNA duplex unwinding;GO:0032392 DNA isometric change;GO:0071103 DNA conformation change
Eastern gentoo	ZGRF1	5	zinc finger GRF-type containing 1	GO:0042761 very long-chain fatty acid biosynthetic process;GO:0000038 very long-chain fatty acid metabolic process;GO:0006633 fatty acid biosynthetic process
Eastern gentoo	TECRL	8	trans-2,3-enoyl-CoA reductase like	GO:0042761 very long-chain fatty acid biosynthetic process;GO:0030497 fatty acid elongation;GO:0035338 long-chain fatty-acyl-CoA biosynthetic process
Eastern gentoo	Tecr	30	trans-2,3-enoyl-CoA reductase	GO:0006352 DNA-templated transcription initiation;GO:0030099 myeloid cell differentiation;GO:0006351 DNA-templated transcription
Eastern gentoo	NCOA6	1	nuclear receptor coactivator 6	GO:0036148 phosphatidylglycerol acyl-chain remodeling;GO:0032367 intracellular cholesterol transport;GO:0032366 intracellular sterol transport
Eastern gentoo	SERAC1	48	serine active site containing 1	GO:0028059 BMP signaling pathway;GO:0071722 response to BMP;GO:0071723 cellular response to BMP stimulus
Eastern gentoo	BGMb	9	regulative guidance molecule BMP co-receptor b	GO:0003011 involuntary skeletal muscle contraction;GO:0061092 positive regulation of phospholipid translocation;GO:0061091 regulation of phospholipid translocation
Eastern gentoo	ATP8A2	1	ATPase phospholipid transporting 8A2	GO:0040019 positive regulation of embryonic development;GO:0045995 regulation of embryonic development;GO:0051094 positive regulation of developmental process
Eastern gentoo	RBM19	9	RNA binding motif protein 19	GO:0044672 positive regulation of collateral sprouting;GO:0071372 cellular response to follicle-stimulating hormone stimulus;GO:1900225 negative regulation of substrate adhesion-dependent cell spreading
Eastern gentoo	EFNA5	3	ephrin A5	GO:0150045 regulation of synaptic signaling by nitric oxide;GO:0045651 positive regulation of macrophage differentiation;GO:1905517 macrophage migration
Eastern gentoo	ROR2	4	receptor tyrosine kinase like orphan receptor 2	GO:0036415 regulation of tRNA stability;GO:0036416 tRNA stabilization;GO:1902370 regulation of tRNA catabolic process
Eastern gentoo	TRMT1	8	tRNA aspartic acid methyltransferase 1	GO:0008104 protein localization;GO:0070727 cellular macromolecule localization;GO:0033036 macromolecule localization
Eastern gentoo	NBEA	16	neurabin	GO:0033533 S-adenosylmethionine cycle;GO:0046500 S-adenosylmethionine metabolic process;GO:0006730 one-carbon metabolic process
Eastern gentoo	AHCYL2	2	adenosylhomocysteine like 2	
Eastern gentoo	RUND3B	2	RUN domain containing 3B	
Eastern gentoo	Lrrc38	2	leucine rich repeat containing 38	GO:1903818 positive regulation of voltage-gated potassium channel activity;GO:1901018 positive regulation of potassium ion transmembrane transporter activity;GO:1901381 positive regulation of potassium ion transmembrane transport
Eastern gentoo	AADACL2	25	arylsulfatase deacetylase like 4	GO:0030574 collagen catabolic process;GO:0001099 collagen fibril organization;GO:0032963 collagen metabolic process
Eastern gentoo	ADAM12	145	ADAM metalloproteinase with thrombospondin type 1 motif 2	GO:0002337 B-1a B cell differentiation;GO:0001923 B-1 B cell differentiation;GO:0002322 B cell proliferation involved in immune response
Eastern gentoo	PLCL2	5	phospholipase C like 2	GO:2000001 regulation of DNA damage checkpoint;GO:0070536 protein K63-linked deubiquitination;GO:0007095 mitotic G2 DNA damage checkpoint signaling
Eastern gentoo	BABAM2	3	BRISAC and BRCA1 A complex member 2	GO:0006911 phagocytosis, engulfment;GO:0099024 plasma membrane invagination;GO:0010324 membrane invagination
Eastern gentoo	GULP1	20	GULP PTB domain containing engulfment adaptor 1	GO:0006608 attachment of spindle microtubules to kinetochore;GO:0007095 mitotic G2 DNA damage checkpoint signaling;GO:0009307 mitotic spindle assembly
Eastern gentoo	ABRAXAS1	4	abraxas 1, BRCA1 A complex subunit	GO:010792 DNA double-strand break processing involved in repair via single-strand annealing;GO:0045002 double-strand break repair via single-strand annealing;GO:0045003 double-strand break repair via synthesis-dependent strand annealing
Eastern gentoo	HELQ	4	helicase, POLQ like	GO:0034497 protein localization to phagosome assembly site;GO:0000423 mitochondrion;GO:0000422 autophagy of double-strand break
Eastern gentoo	Lrra	4	LPS responsive beige-like anchor protein	GO:0032545 mitochondrial translation;GO:0140053 mitochondrial gene expression;GO:0006412 translation
Eastern gentoo	MRPS18C	4	mitochondrial ribosomal protein S18C	GO:0032458 slow endocytic recycling;GO:0090168 Golgi assembly;GO:0016438 maintenance of lens transparency
Eastern gentoo	VPS13B	20	vacuolar protein sorting 13 homolog B	GO:1904862 inhibitory synapse assembly;GO:0051932 synaptic transmission, GABAergic;GO:0007214 gamma-aminobutyric acid signaling pathway
Eastern gentoo	GABRA2	66	gamma-aminobutyric acid type A receptor subunit alpha2	GO:0071577 zinc ion transmembrane transport;GO:0006829 zinc ion transport;GO:0006882 zinc ion homeostasis
Eastern gentoo	slc30a9	2	solute carrier family 30 member 9	GO:0086046 membrane depolarization during SA node cell action potential;GO:0086015 SA node cell action potential;GO:0086018 SA node cell to atrial cardiac muscle cell signaling
Eastern gentoo	CACNA1D	27	calcium voltage-gated channel subunit alpha1 D	GO:1902383 negative regulation of primary amine oxidase activity;GO:1904049 negative regulation of spontaneous neurotransmitter secretion;GO:1902528 regulation of protein linear polyubiquitination
Eastern gentoo	PRKN	5	parkin RBR E3 ubiquitin protein ligase	GO:1904054 regulation of cholangiocyte proliferation;GO:0090175 regulation of establishment of planar polarity;GO:0051660 establishment of centrosome localization
Eastern gentoo	PKHD1	9	PKHD1 ciliary IPT domain containing fibrocystin/polyductin	GO:0050860 negative regulation of T cell receptor signaling pathway;GO:0050858 negative regulation of antigen receptor-mediated signaling pathway;GO:0050856 regulation of T cell receptor signaling pathway
Eastern gentoo	ELF1	2	E74 like E2F transcription factor 1	GO:0001817 regulation of cytokine production;GO:0000122 negative regulation of transcription by RNA polymerase II;GO:0045892 negative regulation of DNA-templated transcription
Eastern gentoo	ZBTB25	5	zinc finger and BTB domain containing 25	

Eastern gentoo	SLC9A3R2	5	NHERF family PDZ scaffold protein 2	GO:0072659 protein localization to plasma membrane;GO:1990778 protein localization to cell periphery;GO:0072657 protein localization to membrane
Eastern gentoo	FHIT	29	fragile histidine triad diadenosine triphosphatase	GO:0015962 diadenosine triphosphate metabolic process;GO:0015964 diadenosine triphosphate catabolic process;GO:0015961 diadenosine polyphosphate catabolic process
Eastern gentoo	UBTD2	1	ubiquitin domain containing 2	
Eastern gentoo	KHDRBS2	9	KH RNA binding domain containing, signal transduction associated 2	GO:0000381 regulation of alternative mRNA splicing, via spliceosome;GO:0048024 regulation of mRNA splicing, via spliceosome;GO:0050684 regulation of mRNA processing
Eastern gentoo	Cttnb2	38	catenin delta 2	GO:0060997 dendritic spine morphogenesis;GO:0060996 dendritic spine development;GO:0070761 dendritic spine organization
Eastern gentoo	Adgrb1	15	adhesion G protein-coupled receptor B1	GO:0043522 effluent of neuron;GO:0006010 abscission;GO:0006010 abscission;GO:1901741 positive regulation of myoblast fusion
Eastern gentoo	ABCA10	4	ATP binding cassette subfamily A member 10	GO:0006869 lipid transport;GO:0010876 lipid localization;GO:0055085 transmembrane transport
Eastern gentoo	RAB11FIP4	6	RAB11 family interacting protein 4	GO:1903452 positive regulation of G1 to G0 transition;GO:1903450 regulation of G1 to G0 transition;GO:0032456 endocytic recycling
Eastern gentoo	FSIP1	6	fibrous sheath interacting protein 1	
Eastern gentoo	DENNND6A	3	DENN domain containing 6A	GO:2000049 positive regulation of cell-cell adhesion mediated by cadherin;GO:2000047 regulation of cell-cell adhesion mediated by cadherin;GO:0022409 positive regulation of cell-cell adhesion
Eastern gentoo	OCA2	35	OCA2 melanosomal transmembrane protein	GO:0006582 melanin biosynthetic process from tyrosine;GO:0035752 lysosomal lumen pH elevation;GO:0051454 intracellular pH elevation
Eastern gentoo	chchd2-a	5	None	None
Eastern gentoo	BDH1	11	3-hydroxybutyrate dehydrogenase 1	GO:0008202 steroid metabolic process;GO:0006629 lipid metabolic process;GO:0044238 primary metabolic process
Eastern gentoo	UBAC2	6	UBA domain containing 2	GO:1904153 negative regulation of retrograde protein transport, ER to cytosol;GO:0070862 negative regulation of protein exit from endoplasmic reticulum;GO:1904152 regulation of retrograde protein transport, ER to cytosol
Eastern gentoo	WBP1L	5	WW domain binding protein 1 like	GO:0038160 CXCL12-activated CXCR4 signaling pathway;GO:0038159 C-X-C chemokine receptor CXCR4 signaling pathway;GO:0038146 chemokine (C-X-C motif) ligand 12 signaling pathway
Eastern gentoo	TOPAZ1	163	testis and ovary specific TOPAZ 1	GO:0048112 spermatocyte division;GO:0107472 mRNA transcription;GO:0035234 ectopic germ cell programming;cell death
Eastern gentoo	STS	196	steroid sulfatase	GO:0006706 steroid catabolic process;GO:0007565 female pregnancy;GO:0044703 multi-organism reproductive process
Eastern gentoo	RFX2	61	regulatory factor X2	GO:0001675 ascosome assembly;GO:0033363 secretory granule organization;GO:1990830 cellular response to leukemia inhibitory factor
Eastern gentoo	Tint2	14	transmembrane O-mannosyltransferase targeting cadherin 2	GO:0035269 protein O-linked mannosylation;GO:0035268 protein mannosylation;GO:0077502 mannosylation
Eastern gentoo	PCDH11X	1	protocadherin 11 X-linked	GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules;GO:0098742 cell-cell adhesion via plasma-membrane adhesion molecules;GO:0098609 cell-cell adhesion
Eastern gentoo	Aph2	2	amyloid beta precursor protein binding family A member 2	GO:0099171 presynaptic modulation of chemical synaptic transmission;GO:0035264 multicellular organism growth;GO:0007626 locomotory behavior
Eastern gentoo	TG	1	thyroglobulin	GO:0015705 iodide transport;GO:0006590 thyroid hormone generation;GO:0042403 thyroid hormone metabolic process
Eastern gentoo	SMG7	7	SMG7 nonsense mediated mRNA decay factor	GO:0035303 regulation of dephosphorylation;GO:0000184 nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;GO:0006406 mRNA export from nucleus
Eastern gentoo	RALA	1	RAS like proto-oncogene A	GO:0051665 membrane raft localization;GO:0090141 positive regulation of mitochondrial fusion;GO:0099149 regulation of postsynaptic neurotransmitter receptor internalization
Eastern gentoo	GUCY2C	23	guanylate cyclase 2C	GO:0006182 cGMP biosynthetic process;GO:0007168 receptor guanylyl cyclase signaling pathway;GO:0046068 cGMP metabolic process
Eastern gentoo	ATF7IP	2	activating transcription factor 7 interacting protein	GO:0006346 DNA methylation-dependent constitutive heterochromatin formation;GO:0140719 constitutive heterochromatin formation;GO:0031507 heterochromatin formation
Eastern gentoo	MED12	4	mediator complex subunit 12	GO:0090245 axis elongation involved in somitogenesis;GO:0048072 embryonic neurocranium morphogenesis;GO:1990403 embryonic brain development
Eastern gentoo	fastk1	2	FAST kinase domains 1	GO:004828 regulation of mitochondrial mRNA stability;GO:0000963 mitochondrial RNA processing;GO:0000959 mitochondrial RNA metabolic process
Eastern gentoo	TBC1D9	14	TBC1 domain family member 9	
Eastern gentoo	CDC93	19	coiled-coil domain containing 93	GO:0006893 Golgi to plasma membrane transport;GO:0032456 endocytic recycling;GO:0006892 post-Golgi vesicle-mediated transport
Eastern gentoo	COMM9	34	COMM domain containing 9	GO:0024632 cholesterol homeostasis;GO:0055992sterol homeostasis;GO:0055088 lipid homeostasis
Eastern gentoo	ZFYVE1	21	zinc finger FYVE-type containing 1	GO:004829 positive regulation by host of viral genome replication;GO:0140042 lipid droplet formation;GO:0044794 positive regulation by host of viral process
Eastern gentoo	PRRSL	19	proline rich S like	GO:0038203 TORC2 signaling;GO:0010762 regulation of fibroblast migration;GO:0031929 TOR signaling
Eastern gentoo	LDLRAD3	15	low density lipoprotein receptor class A domain containing 3	GO:0070613 regulation of protein processing;GO:1903317 regulation of protein maturation;GO:0006898 receptor-mediated endocytosis
Eastern gentoo	ARHGAP15	3	Rho GTPase activating protein 15	GO:0008360 regulation of cell shape;GO:0022604 regulation of cell morphogenesis;GO:0007264 small GTPase-mediated signal transduction
Eastern gentoo	NME7	9	NME/NM23 family member 7	GO:0006228 UTP biosynthetic process;GO:0006183 GTP biosynthetic process;GO:0046051 UTP metabolic process
Eastern gentoo	SENF7	12	SUMO specific peptidase 7	GO:0016926 protein deSUMoylation;GO:0140134 antiviral innate immune response;GO:0018205 peptidyl-histone modification
Eastern gentoo	ZBTB11	6	zinc finger and BTB domain containing 11	GO:0006357 regulation of transcription by RNA polymerase II;GO:0006355 regulation of DNA-templated transcription;GO:2001141 regulation of RNA biosynthetic process
Eastern gentoo	RASA3	3	RAS p21 protein activator 3	GO:0046580 negative regulation of Ras protein signal transduction;GO:0046578 regulation of Ras protein signal transduction;GO:0051058 negative regulation of small GTPase mediated signal transduction
Eastern gentoo	Slc5a7	15	solute carrier family 5 member 7	GO:0008292 acetylcholine biosynthetic process;GO:1900620 acetate ester biosynthetic process;GO:0008291 acetylcholine metabolic process
Eastern gentoo	CFAP61	35	cilia and flagella associated protein 61	GO:0120316 sperm flagellum assembly;GO:0044458 motile cilium assembly;GO:0030317 flagellated sperm motility
Eastern gentoo	HSFY1	37	heat shock transcription factor Y-linked 1	
Eastern gentoo	Dusp7	6	dual specificity phosphatase 7	GO:0035335 peptidyl-tyrosine dephosphorylation;GO:0043407 negative regulation of MAP kinase activity;GO:0070371 ERK1 and ERK2 cascade
Eastern gentoo	SEC16B	5	SEC16 homolog B, endoplasmic reticulum export factor	GO:0070973 protein localization to endoplasmic reticulum exit site;GO:0016559 peroxisome fusion;GO:0070863 positive regulation of protein exit from endoplasmic reticulum
Eastern gentoo	SCUBE2	3	signal peptide, CUB domain and EGF like domain containing 2	GO:0007165 signal transduction;GO:0023052 signaling;GO:0007154 cell communication
Eastern gentoo	LEPR	5	leptin receptor	GO:0033210 leptin-mediated signaling pathway;GO:0044520 cellular response to leptin stimulus;GO:0045721 negative regulation of rheumatogenesis
Eastern gentoo	CACHD1	32	cache domain containing 1	GO:0073588 calcium ion transmembrane transport;GO:0008816 calcium ion transport;GO:0030901 metal ion transport
Eastern gentoo	UBE3B	2	ubiquitin protein ligase E3B	GO:0150052 regulation of postsynapse assembly;GO:0099175 regulation of postsynapse organization;GO:0051963 regulation of synapse assembly
Eastern gentoo	INPP5D	4	inositol polyphosphate-5-phosphatase D	GO:0045659 negative regulation of neutrophil differentiation;GO:0045658 regulation of neutrophil differentiation;GO:0045656 negative regulation of monocyte differentiation
Eastern gentoo	NANOG	2	Nanog homeobox	GO:0001714 endodermal cell fate specification;GO:0001711 endodermal cell fate commitment;GO:0060795 cell fate commitment involved in formation of primary germ layer
Eastern gentoo	TRIM2	55	tripartite motif containing 2	GO:0000209 protein polyubiquitination;GO:0043523 regulation of neuron apoptotic process;GO:0043161 proteasome-mediated ubiquitin-dependent protein catabolic process
Eastern gentoo	KLHL1	48	kelch like family member 1	GO:0021680 cerebellar Purkinje cell layer development;GO:0007628 adult walking behavior;GO:0090659 walking behavior
Eastern gentoo	BMPER	68	BMP binding endothelial regulator	GO:0002042 blood vessel endothelial cell proliferation involved in sprouting angiogenesis;GO:0042118 endothelial cell activation;GO:0060395 SMAD protein signal transduction
Eastern gentoo	Agh5	16	AGBL carboxypeptidase 5	GO:0035611 protein branching point deglutamylation;GO:0035609 C-terminal protein deglutamylation;GO:0055610 protein side chain deglutamylation
Eastern gentoo	NPAS3	3	neuronal PAS domain protein 3	GO:0045895 positive regulation of DNA-templated transcription;GO:1902680 positive regulation of RNA biosynthetic process;GO:0051254 positive regulation of RNA metabolic process
Eastern gentoo	Prkg1	20	protein kinase cGMP-dependent 1	GO:0010920 negative regulation of inositol phosphate biosynthetic process;GO:0014050 negative regulation of glutamate secretion;GO:0060087 relaxation of vascular associated smooth muscle
Eastern gentoo	Iqcs3	10	IQ motif and Sec7 domain ARFGEF 3	GO:0032012 regulation of ARF protein signal transduction;GO:0051056 regulation of small GTPase mediated signal transduction;GO:0030036 actin cytoskeleton organization
Eastern gentoo	IGNS	66	longin, LGSN protein with glutamine synthetase domain	
Eastern gentoo	IL31RA	3	interleukin 31 receptor A	GO:0002438 acute inflammatory response to antigenic stimulus;GO:0030224 monocyte differentiation;GO:0043031 negative regulation of macrophage activation
Eastern gentoo	Ranbp1	1	RAN binding protein 1	GO:0046604 positive regulation of mitotic centrosome separation;GO:0046602 regulation of mitotic centrosome separation;GO:0006913 microtubule cytoskeleton transport
Eastern gentoo	GRIK2	2	glutamate ionotropic receptor kainate type subunit 2	GO:0002025 sensory perception of cold stimulus;GO:0120169 detection of cold stimulus involved in thermoreception;GO:0050960 detection of temperature stimulus involved in thermoreception
Eastern gentoo	HEBP2	52	heme binding protein 2	
Eastern gentoo	PPM1L	11	protein phosphatase, Mg2+/Mn2+ dependent 1L	GO:0030148 sphingolipid biosynthetic process;GO:0044667 membrane lipid biosynthetic process;GO:0006665 sphingolipid metabolic process
Eastern gentoo	PPIC	5	peptidylprolyl isomerase C	GO:0006457 protein folding;GO:0051604 protein maturation;GO:0006357 regulation of transcription by RNA polymerase II
Eastern gentoo	EMIL6	95	EMAP like 6	
Eastern gentoo	Codex5a	17	coiled-coil domain containing 85A	
Eastern gentoo	NAALADL2	62	N-acetylated alpha-linked acidic dipeptidase like 2	GO:0009671 response to bacterium;GO:0051707 response to other organism;GO:0043207 response to external biotic stimulus
Eastern gentoo	TNIP1	139	TNF AIP3 interacting protein 1	GO:0002042 blood vessel endothelial cell proliferation involved in sprouting angiogenesis;GO:0042118 endothelial cell activation;GO:0060395 SMAD protein signal transduction
Eastern gentoo	STC1	12	stanniocalcin 1	GO:0003421 growth plate cartilage axis specification;GO:1903403 negative regulation of renal phosphate excretion;GO:0003422 growth plate cartilage morphogenesis
Eastern gentoo	PRKAR1B	4	protein kinase cAMP-dependent type I regulatory subunit beta	GO:0141162 negative regulation of cAMP/PKA signal transduction;GO:1903367 positive regulation of fear response;GO:1903365 regulation of fear response
Eastern gentoo	CARD11	8	caspace recruitment domain family member 11	GO:0035739 CD4-positive, alpha-beta T cell proliferation;GO:2000563 positive regulation of CD4-positive, alpha-beta T cell proliferation;GO:0046710 GDP metabolic process
Eastern gentoo	ASIC1	5	acid sensing ion channel subunit 1	GO:0046929 negative regulation of neurotransmitter secretion;GO:0051589 negative regulation of neurotransmitter transport;GO:0050915 sensory perception of sour taste
Eastern gentoo	Sec11c	4	SEC11 homolog C, signal peptidase complex subunit	GO:0006465 signal peptide processing;GO:0016485 protein processing;GO:0051604 protein maturation
Eastern gentoo	CHIC1	2	cytosine rich hydrophobic domain 1	
Eastern gentoo	SKAP2	61	src kinase associated phosphoprotein 2	GO:0042113 B cell activation;GO:0046649 lymphocyte activation;GO:0043321 leukocyte activation
Eastern gentoo	GAB2	10	GRB2 associated binding protein 2	GO:0043306 positive regulation of mast cell degranulation;GO:0043302 positive regulation of leukocyte degranulation;GO:0043304 regulation of mast cell degranulation
Eastern gentoo	KCNIP4	9	potassium voltage-gated channel interacting protein 4	GO:1901379 regulation of potassium ion transmembrane transport;GO:0043266 regulation of potassium ion transport;GO:0071805 potassium ion transmembrane transport
Eastern gentoo	SUB1	21	SUB1 regulator of transcription	GO:1905462 regulation of DNA duplex unwinding;GO:1905463 negative regulation of DNA duplex unwinding;GO:0001109 promoter clearance during DNA-templated transcription
Eastern gentoo	chchd6	8	coiled-coil-helix-coiled-coil-helix domain containing 6	GO:0042407 cristae formation;GO:0007007 inner mitochondrial membrane organization;GO:0007006 mitochondrial membrane organization
Eastern gentoo	CDH10	11	cadherin 10	GO:0099560 synaptic membrane adhesion;GO:0044331 cell-cell adhesion mediated by cadherin;GO:0016339 calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules
Eastern gentoo	NRAP	3	nebulin related anchoring protein	GO:0071691 cardiac muscle thin filament assembly;GO:0055003 cardiac myofibril assembly;GO:0055013 cardiac muscle cell development
Eastern gentoo	SLC4A11	1	solute carrier family 4 member 11	GO:0035445 borate transmembrane transport;GO:0046713 borate transport;GO:2000739 regulation of mesenchymal stem cell differentiation
Eastern gentoo	FOX2	8	forkhead box P2	GO:0021757 candidate nucleus development;GO:0021758 putamen development;GO:0021756 striatum development
Eastern gentoo	GRM8	24	glutamate metabotropic receptor 8	GO:0007196 adenylyl cyclase-inhibiting G protein-coupled glutamate receptor signaling pathway;GO:0007216 G protein-coupled glutamate receptor signaling pathway;GO:0007215 glutamate receptor signaling pathway
Eastern gentoo	SEC24D	12	SEC24 homolog D, COPII coat complex component	GO:0099110 COPII-coated vesicle cargo loading;GO:0051549 vesicle cargo loading;GO:0090114 COPII-coated vesicle budding
Eastern gentoo	SHC3	99	SHC adaptor protein 3	GO:0007173 epidermal growth factor receptor signaling pathway;GO:0038127 ERBB signaling pathway;GO:0007169 cell surface receptor protein tyrosine kinase signaling pathway
Eastern gentoo	FLT4	3	fn3 related receptor tyrosine kinase 4	GO:0060312 regulation of blood vessel remodeling;GO:0001946 lymphangiogenesis;GO:0036303 lymph vessel morphogenesis

Eastern gentoo	MOCOS	33	molybdenum cofactor sulfirase	GO:0006777 Mo-molybdopterin cofactor biosynthetic process;GO:0019720 Mo-molybdopterin cofactor metabolic process;GO:0032324 molybdopterin cofactor biosynthetic process
Eastern gentoo	LRRTMI	44	leucine rich repeat transmembrane neuronal 1	GO:0002091 negative regulation of receptor internalization;GO:0099151 regulation of postsynaptic density assembly;GO:0099150 regulation of postsynaptic specialization assembly
Eastern gentoo	GULO	5	gulonolactone (L-) oxidase, pseudogene	

Table S6. Bioclimatic variables used in this study to perform RDA analysis obtained from Pertierra et al. 2020.

Sample	sites	lon	lat	o10_primpr	o11_salini	o14_temppi	o09_primpr	o13_temppa	o01_icecov	o12_salini	bio18	bio16	bio15	bio10	bio07	bio03	bio02
13A2	Kerguelen	70.533	-49.267	0.003048	33.9779015	1.65763	0.019921	6.2112999	0	33.6403999	164.6670074	205.3329926	12.6632996	7.6598301	11.5172997	51.1441994	5.8903999
15A2	Kerguelen	70.533	-49.267	0.003048	33.9779015	1.65763	0.019921	6.2112999	0	33.6403999	164.6670074	205.3329926	12.6632996	7.6598301	11.5172997	51.1441994	5.8903999
18A1	Kerguelen	70.533	-49.267	0.003048	33.9779015	1.65763	0.019921	6.2112999	0	33.6403999	164.6670074	205.3329926	12.6632996	7.6598301	11.5172997	51.1441994	5.8903999
19A1	Kerguelen	70.533	-49.267	0.003048	33.9779015	1.65763	0.019921	6.2112999	0	33.6403999	164.6670074	205.3329926	12.6632996	7.6598301	11.5172997	51.1441994	5.8903999
22A1	Kerguelen	70.533	-49.267	0.003048	33.9779015	1.65763	0.019921	6.2112999	0	33.6403999	164.6670074	205.3329926	12.6632996	7.6598301	11.5172997	51.1441994	5.8903999
24A1	Kerguelen	70.533	-49.267	0.003048	33.9779015	1.65763	0.019921	6.2112999	0	33.6403999	164.6670074	205.3329926	12.6632996	7.6598301	11.5172997	51.1441994	5.8903999
G6	Kerguelen	70.533	-49.267	0.003048	33.9779015	1.65763	0.019921	6.2112999	0	33.6403999	164.6670074	205.3329926	12.6632996	7.6598301	11.5172997	51.1441994	5.8903999
CRO05	Crozet	50.4	-46.417	0.001014	33.9401016	3.5575099	0.005987	8.2642298	0	33.5507011	607	716	18.1436005	7.4111099	11.5333004	60.1637993	6.93889
CRO07	Crozet	50.4	-46.417	0.001014	33.9401016	3.5575099	0.005987	8.2642298	0	33.5507011	607	716	18.1436005	7.4111099	11.5333004	60.1637993	6.93889
CRO08	Crozet	50.4	-46.417	0.001014	33.9401016	3.5575099	0.005987	8.2642298	0	33.5507011	607	716	18.1436005	7.4111099	11.5333004	60.1637993	6.93889
G7	Crozet	50.4	-46.417	0.001014	33.9401016	3.5575099	0.005987	8.2642298	0	33.5507011	607	716	18.1436005	7.4111099	11.5333004	60.1637993	6.93889
P2134	Crozet	50.4	-46.417	0.001014	33.9401016	3.5575099	0.005987	8.2642298	0	33.5507011	607	716	18.1436005	7.4111099	11.5333004	60.1637993	6.93889
P2136	Crozet	50.4	-46.417	0.001014	33.9401016	3.5575099	0.005987	8.2642298	0	33.5507011	607	716	18.1436005	7.4111099	11.5333004	60.1637993	6.93889
P2143	Crozet	50.4	-46.417	0.001014	33.9401016	3.5575099	0.005987	8.2642298	0	33.5507011	607	716	18.1436005	7.4111099	11.5333004	60.1637993	6.93889
GEN04	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GEN05	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GEN08	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GEN09	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GEN10	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GTP06	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GTP07	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GTP12	Marion	37.706	-46.967	0.00174	33.9920998	3.92435	0.005828	7.8485899	0	33.4903984	582	661	8.4925404	6.4398298	9.4098701	55.3672981	5.2161498
GSA10	Signy	-45.583	-60.65	0.000043	34.3714981	-1.9345	0.014932	1.17479	0.827842	32.4384995	120	212.25	32.269001	-1.60321	18.5240002	38.9822006	7.2182999
GSA12	Signy	-45.583	-60.65	0.000043	34.3714981	-1.9345	0.014932	1.17479	0.827842	32.4384995	120	212.25	32.269001	-1.60321	18.5240002	38.9822006	7.2182999
GSA14	Signy	-45.583	-60.65	0.000043	34.3714981	-1.9345	0.014932	1.17479	0.827842	32.4384995	120	212.25	32.269001	-1.60321	18.5240002	38.9822006	7.2182999
GSA15	Signy	-45.583	-60.65	0.000043	34.3714981	-1.9345	0.014932	1.17479	0.827842	32.4384995	120	212.25	32.269001	-1.60321	18.5240002	38.9822006	7.2182999
GSA7	Signy	-45.583	-60.65	0.000043	34.3714981	-1.9345	0.014932	1.17479	0.827842	32.4384995	120	212.25	32.269001	-1.60321	18.5240002	38.9822006	7.2182999
GSA8	Signy	-45.583	-60.65	0.000043	34.3714981	-1.9345	0.014932	1.17479	0.827842	32.4384995	120	212.25	32.269001	-1.60321	18.5240002	38.9822006	7.2182999
GSA9	Signy	-45.583	-60.65	0.000043	34.3714981	-1.9345	0.014932	1.17479	0.827842	32.4384995	120	212.25	32.269001	-1.60321	18.5240002	38.9822006	7.2182999
P0167	Ohiggins	-57.883	-63.317	0.000034	34.5225983	-1.93314	0.038683	0.134662	0.81191	32.0057983	131	237	26.2698002	0.163333	14.46	34.9015999	5.04667
P0169	Ohiggins	-57.883	-63.317	0.000034	34.5225983	-1.93314	0.038683	0.134662	0.81191	32.0057983	131	237	26.2698002	0.163333	14.46	34.9015999	5.04667
P0170	Ohiggins	-57.883	-63.317	0.000034	34.5225983	-1.93314	0.038683	0.134662	0.81191	32.0057983	131	237	26.2698002	0.163333	14.46	34.9015999	5.04667
P0173	Ohiggins	-57.883	-63.317	0.000034	34.5225983	-1.93314	0.038683	0.134662	0.81191	32.0057983	131	237	26.2698002	0.163333	14.46	34.9015999	5.04667
P0196	Ohiggins	-57.883	-63.317	0.000034	34.5225983	-1.93314	0.038683	0.134662	0.81191	32.0057983	131	237	26.2698002	0.163333	14.46	34.9015999	5.04667
P0198	Ohiggins	-57.883	-63.317	0.000034	34.5225983	-1.93314	0.038683	0.134662	0.81191	32.0057983	131	237	26.2698002	0.163333	14.46	34.9015999	5.04667
P0200	Ohiggins	-57.883	-63.317	0.000034	34.5225983	-1.93314	0.038683	0.134662	0.81191	32.0057983	131	237	26.2698002	0.163333	14.46	34.9015999	5.04667
P0402	Kgeorge	-58.583	-62.233	0.000021	34.5596008	-1.8650399	0.027137	1.6057	0.783842	33.1559982	172.25	246.25	22.1348	0.283258	12.6313	35.7792015	4.5197201
P0404	Kgeorge	-58.583	-62.233	0.000021	34.5596008	-1.8650399	0.027137	1.6057	0.783842	33.1559982	172.25	246.25	22.1348	0.283258	12.6313	35.7792015	4.5197201
P0405	Kgeorge	-58.583	-62.233	0.000021	34.5596008	-1.8650399	0.027137	1.6057	0.783842	33.1559982	172.25	246.25	22.1348	0.283258	12.6313	35.7792015	4.5197201
P0407	Kgeorge	-58.583	-62.233	0.000021	34.5596008	-1.8650399	0.027137	1.6057	0.783842	33.1559982	172.25	246.25	22.1348	0.283258	12.6313	35.7792015	4.5197201
P0408	Kgeorge	-58.583	-62.233	0.000021	34.5596008	-1.8650399	0.027137	1.6057	0.783842	33.1559982	172.25	246.25	22.1348	0.283258	12.6313	35.7792015	4.5197201
P0409	Kgeorge	-58.583	-62.233	0.000021	34.5596008	-1.8650399	0.027137	1.6057	0.783842	33.1559982	172.25	246.25	22.1348	0.283258	12.6313	35.7792015	4.5197201
P0412	Kgeorge	-58.583	-62.233	0.000021	34.5596008	-1.8650399	0.027137	1.6057	0.783842	33.1559982	172.25	246.25	22.1348	0.283258	12.6313	35.7792015	4.5197201
P0048	GGV	-62.85	-64.817	0.000017	34.5172997	-1.74269	0.046855	1.7645299	0.808374	31.6109009	151.5	272	28.9486008	0.798291	13.3973999	31.9101009	4.27564
P0051	GGV	-62.85	-64.817	0.000017	34.5172997	-1.74269	0.046855	1.7645299	0.808374	31.6109009	151.5	272	28.9486008	0.798291	13.3973999	31.9101009	4.27564
P0052	GGV	-62.85	-64.817	0.000017	34.5172997	-1.74269	0.046855	1.7645299	0.808374	31.6109009	151.5	272	28.9486008	0.798291	13.3973999	31.9101009	4.27564
P0056	GGV	-62.85	-64.817	0.000017	34.5172997	-1.74269	0.046855	1.7645299	0.808374	31.6109009	151.5	272	28.9486008	0.798291	13.3973999	31.9101009	4.27564
P0058	GGV	-62.85	-64.817	0.000017	34.5172997	-1.74269	0.046855	1.7645299	0.808374	31.6109009	151.5	272	28.9486008	0.798291	13.3973999	31.9101009	4.27564
P0065	GGV	-62.85	-64.817	0.000017	34.5172997	-1.74269	0.046855	1.7645299	0.808374	31.6109009	151.5	272	28.9486008	0.798291	13.3973999	31.9101009	4.27564
G4	GGV	-62.85	-64.817	0.000017	34.5172997	-1.74269	0.046855	1.7645299	0.808374	31.6109009	151.5	272	28.9486008	0.798291	13.3973999	31.9101009	4.27564
G5	Falkland	-59.35	-52.333	0.007465	34.175499	4.2620001	0.056462	10.7047997	0	33.7317009	156.75	157.75	18.4766006	9.8065701	11.6947002	36.3297005	4.2481098
P1884	Falkland	-59.35	-52.333	0.007465	34.175499	4.2620001	0.056462	10.7047997	0	33.7317009	156.75	157.75	18.4766006	9.8065701	11.6947002	36.3297005	4.2481098
P1885	Falkland	-59.35	-52.333	0.007465	34.175499	4.2620001	0.056462	10.7047997	0	33.7317009	156.75	157.75	18.4766006	9.8065701	11.6947002	36.3297005	4.2481098
P1887	Falkland	-59.35	-52.333	0.007465	34.175499	4.2620001	0.056462	10.7047997	0	33.7317009	156.75	157.75	18.4766006	9.8065701	11.6947002	36.3297005	4.2481098
P1889	Falkland	-59.35	-52.333	0.007465	34.175499	4.2620001	0.056462	10.7047997	0								

Table S7. Significance test for terrestrial and marine bioclimatic variables using ANOVA.

		Df	Variance	F	Pr(>F)	Signif
Marine environment: rda(formula = gen.imp ~ o10_primpr + o11_salini + o09_primpr + o13_tempma + o01_icecov + o12_salini, data = pred, scale = TRUE)	Model	6	6946.7	2.7206	0.001	***
	Residual	55	23405.3			
Terrestrial environment: rda(formula = gen.imp ~ bio18 + bio15 + bio10 + bio07 + bio03 + bio02, data = pred, scale = TRUE)	Model	6	7542.3	3.0311	0.001	***
	Residual	55	22809.7			

Table S8. Enrichment analysis containing all enriched terms and their cluster group ID founded within each gentoo penguin lineage. The analysis was performed using METASCAPE.

Lineage	Category	GO	Biological process	Description	PARENT_GO	LogP	Enrichment	Z-score	#Gene In GO And Hit List	%lnGO	STDP %lnGO	Hits	Log(q-value)
Northern	GO Biological Processes	GO:007167	Signal transduction	enzyme-linked receptor protein signaling pathway	19_GO:0050896 response to stimulus	-5	5.1	6.1	11	11	3	ACVR2B/BMP7/FGF1/PTN/PTPRK/RAPGEF2/PTPRIT/TIPARP/CHST11/PPM1L	-0.83
Northern	GO Biological Processes	GO:0086002	Cardioregulation	cardiac muscle cell action potential involved in contraction	19_GO:0032501 multicellular organismal process	-4.7	26	9.7	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.83
Northern	GO Biological Processes	GO:1900006	Neural processes	positive regulation of dendrite development	19_GO:0032502 developmental process	-4.5	49	12	3	2.9	1.7	BMP7/PTN/COBL	-0.83
Northern	GO Biological Processes	GO:0086003	Cardioregulation	cardiac muscle cell contraction	19_GO:0032501 multicellular organismal process	-4.5	23	9.1	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.83
Northern	GO Biological Processes	GO:0086001	Cardioregulation	cardiac muscle cell action potential	19_GO:0065007 biological regulation	-4.4	21	8.7	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.83
Northern	GO Biological Processes	GO:0030029	Muscular process	actin filament-based process	19_GO:0009987 cellular process	-4.3	4.8	5.5	10	9.7	2.9	CACNA1C/CACNA2D1/EPSS/FER/KCNQ1/SCN2A/IQSEC1/COBL/ANTXR1/STARD13	-0.83
Northern	Reactome Gene Sets	R-HSA-416476	Signal transduction	G alpha (q) signalling events		-4.2	9	6.5	6	5.8	2.3	HCTR2/PLCB4/PMCH/TACR3/TRHR/DGKH	-0.83
Northern	WikiPathways	WP474	Ossification	Endochondral ossification		-4.2	19	8.2	4	3.9	1.9	BMP7/IGF1/SOX5/CHST11	-0.83
Northern	WikiPathways	WP4808	Ossification	Endochondral ossification with skeletal dysplasias		-4.2	19	8.2	4	3.9	1.9	BMP7/IGF1/SOX5/CHST11	-0.83
Northern	GO Biological Processes	GO:0086019	Cardioregulation	cell-cell signaling involved in cardiac conduction	19_GO:0032501 multicellular organismal process	-4.1	37	10	3	2.9	1.7	CACNA1C/CACNA2D1/KCNQ1	-0.83
Northern	Reactome Gene Sets	R-HSA-372790	Cellular process	Signaling by GPCR		-4.1	4.5	5.3	10	9.7	2.9	CRHR2/CRTR2/PLCB4/PMCH/HRGS12/TACR3/TRHR/NBEARXFP1/DGKH	-0.83
Northern	GO Biological Processes	GO:0016482	Cellular process	cytosolic transport	19_GO:0051179 localization	-4	11	6.8	5	4.9	2.1	ERC1/DENND2A/EHD3/ANKFY1/SYBU	-0.78
Northern	GO Biological Processes	GO:0048589	Growth	developmental growth	19_GO:0040007 growth	-3.9	5.3	5.4	8	7.8	2.6	ACVR2B/APBA2/IGF1/PTN/COBL/DLL1/CHST11/SLC4A10	-0.71
Northern	GO Biological Processes	GO:0040007	Growth	growth	19_GO:0040007 growth	-3.9	5.3	5.4	8	7.8	2.6	ACVR2B/APBA2/IGF1/PTN/COBL/DLL1/CHST11/SLC4A10	-0.71
Northern	GO Biological Processes	GO:0070252	Muscular process	actin-mediated cell contraction	19_GO:0009987 cellular process	-3.8	15	7.3	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.71
Northern	Reactome Gene Sets	R-HSA-388396	Cellular process	GPCR downstream signalling		-3.8	4.6	5.1	9	8.7	2.8	HCTR2/PLCB4/PMCH/HRGS12/TACR3/TRHR/NBEARXFP1/DGKH	-0.71
Northern	WikiPathways	WP2857	Cellular process	Mesodermal commitment pathway		-3.8	9.9	6.4	5	4.9	2.1	ACVR2B/BMP7/CTBP2/DLL1/AEBP2	-0.71
Northern	GO Biological Processes	GO:0044331	Cellular process	cell-cell adhesion mediated by cadherin	19_GO:0009987 cellular process	-3.8	28	8.9	3	2.9	1.7	CDH11/EFER/CDH19	-0.71
Northern	KEGG Pathway	hsa04261	Cardioregulation	Adrenergic signaling in cardiomyocytes		-3.7	9.5	6.2	5	4.9	2.1	CACNA1C/CACNA2D1/KCNQ1/PLCB4/PPP2R2B	-0.7
Northern	GO Biological Processes	GO:0042391	Neural processes	regulation of membrane potential	19_GO:0065007 biological regulation	-3.7	5.1	5.2	8	7.8	2.6	CACNA1C/CACNA2D1/KCNQ1/SCN2A/SLC4A10/EPSS/CHST11	-0.7
Northern	GO Biological Processes	GO:0060048	Cardioregulation	cardiac muscle contraction	19_GO:0032501 multicellular organismal process	-3.7	14	7	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.7
Northern	GO Biological Processes	GO:0000209	Cellular process	protein polyubiquitination	19_GO:0009987 cellular process	-3.7	7.2	5.7	6	5.8	2.3	UBE2G1/FBXO2/MARCHF1/FBXL17/UBE2Q2/HECTD2	-0.7
Northern	GO Biological Processes	GO:0009791	Development	post-embryonic development	19_GO:0032502 developmental process	-3.6	13	6.7	4	3.9	1.9	ACVR2B/TIPARP/CHST11/SLC4A10	-0.63
Northern	GO Biological Processes	GO:0010976	Neural processes	positive regulation of neuron projection development	19_GO:0032502 developmental process	-3.6	8.9	6	5	4.9	2.1	BMP7/PTN/IRIT2/RAPGEF2/COBL	-0.63
Northern	KEGG Pathway	hsa04080	Neural processes	Neuroactive ligand-receptor interaction		-3.6	5.6	5.2	7	6.8	2.5	CRHR2/CRTR2/PMCH/TACR3/TRHR/GLR3A/RXFP1	-0.61
Northern	GO Biological Processes	GO:0042147	Cellular process	retrograde transport, endosome to Golgi	19_GO:0051179 localization	-3.5	12	6.4	4	3.9	1.9	ERC1/DENND2A/EHD3/ANKFY1	-0.55
Northern	GO Biological Processes	GO:0086091	Cardioregulation	regulation of heart rate by cardiac conduction	19_GO:0032501 multicellular organismal process	-3.5	22	7.8	3	2.9	1.7	CACNA1C/CACNA2D1/KCNQ1	-0.55
Northern	GO Biological Processes	GO:0086065	Cardioregulation	cell communication involved in cardiac conduction	19_GO:0032501 multicellular organismal process	-3.4	22	7.7	3	2.9	1.7	CACNA1C/CACNA2D1/KCNQ1	-0.55
Northern	GO Biological Processes	GO:0060047	Cardioregulation	heart contraction	19_GO:0032501 multicellular organismal process	-3.4	12	6.3	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.55
Northern	GO Biological Processes	GO:0030048	Muscular process	actin filament-based movement	19_GO:0009987 cellular process	-3.4	12	6.3	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.55
Northern	WikiPathways	WP2064	Neural processes	Neural crest differentiation		-3.4	12	6.3	4	3.9	1.9	BMP7/CTBP2/SOX5/DLL1	-0.55
Northern	GO Biological Processes	GO:0050773	Neural processes	regulation of dendrite development	19_GO:0032502 developmental process	-3.4	12	6.2	4	3.9	1.9	BMP7/PTN/RAPGEF2/COBL	-0.54
Northern	GO Biological Processes	GO:0030501	Ossification	positive regulation of bone mineralization	19_GO:0032502 developmental process	-3.3	20	7.4	3	2.9	1.7	ACVR2B/BMP7/PTN	-0.52
Northern	GO Biological Processes	GO:0003158	Development	endothelium development	19_GO:0032502 developmental process	-3.3	11	6.1	4	3.9	1.9	ACVR2B/RAPGEF2/DLL1/STARD13	-0.52
Northern	GO Biological Processes	GO:0002027	Cardioregulation	regulation of heart rate	19_GO:0032501 multicellular organismal process	-3.3	11	6.1	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/TACR3	-0.52
Northern	Reactome Gene Sets	R-HSA-375276	Cellular process	Peptide ligand-binding receptors		-3.3	7.7	5.4	5	4.9	2.1	HCTR2/PMCH/TACR3/TRHR/RXFP1	-0.52
Northern	GO Biological Processes	GO:0007178	Cellular process	cell surface receptor protein serine/threonine kinase signaling pathway	19_GO:0050896 response to stimulus	-3.3	7.7	5.4	5	4.9	2.1	ACVR2B/BMP7/PTPRK/CHST11/PPM1L	-0.52
Northern	GO Biological Processes	GO:0003015	Cardioregulation	heart process	19_GO:0032501 multicellular organismal process	-3.2	10	5.9	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.45
Northern	GO Biological Processes	GO:0098655	Cellular process	monatomic cation transmembrane transport	19_GO:0051179 localization	-3.2	3.8	4.3	9	8.7	2.8	CACNA1C/CACNA2D1/KCNQ1/PLCB4/SCN2A/SLC13A4/KCNH5/SLC4A10/PIEZO2	-0.43
Northern	GO Biological Processes	GO:0045933	Muscular process	positive regulation of muscle contraction	19_GO:0032501 multicellular organismal process	-3.2	17	6.8	3	2.9	1.7	CACNA1C/KCNQ1/TACR3	-0.43
Northern	Reactome Gene Sets	R-HSA-9006934	Signal transduction	Signaling by Receptor Tyrosine Kinases		-3.1	4.8	4.6	7	6.8	2.5	FER/GTF2F2/IGF1/PTN/PTPRK/IRIT2/THBS2	-0.43
Northern	GO Biological Processes	GO:0034330	Cellular process	cell junction organization	19_GO:0009987 cellular process	-3.1	4.2	4.4	8	7.8	2.6	DTSD/CDH11/EFER/PTPRK/CNKR2/ERC1/CDH19/SYBU	-0.43
Northern	GO Biological Processes	GO:0008016	Cardioregulation	regulation of heart contraction	19_GO:0032501 multicellular organismal process	-3.1	7	5.1	5	4.9	2.1	CACNA1C/CACNA2D1/KCNQ1/TACR3/EHD3	-0.4
Northern	GO Biological Processes	GO:0006941	Muscular process	striated muscle contraction	19_GO:0032501 multicellular organismal process	-3.1	9.7	5.6	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.4
Northern	GO Biological Processes	GO:0070169	Ossification	positive regulation of biomineral tissue development	19_GO:0032502 developmental process	-3.1	16	6.6	3	2.9	1.7	ACVR2B/BMP7/PTN	-0.4
Northern	GO Biological Processes	GO:0034332	Cellular process	adherens junction organization	19_GO:0009987 cellular process	-3.1	16	6.6	3	2.9	1.7	CDH11/EFER/CDH19	-0.4
Northern	Reactome Gene Sets	R-HSA-1630316	Metabolism	Glycosaminoglycan metabolism		-3.1	9.6	5.6	4	3.9	1.9	LUMST3/GAL3/CHST11/B3GAT2	-0.4
Northern	GO Biological Processes	GO:0045778	Ossification	positive regulation of ossification	19_GO:0032501 multicellular organismal process	-3.1	16	6.5	3	2.9	1.7	ACVR2B/BMP7/PTN	-0.39
Northern	GO Biological Processes	GO:0001508	Neural processes	action potential	19_GO:0065007 biological regulation	-3	9.1	5.4	4	3.9	1.9	CACNA1C/CACNA2D1/KCNQ1/SCN2A	-0.35
Northern	GO Biological Processes	GO:0007200	Signal transduction	phospholipase C-activating G protein-coupled receptor signaling pathway	19_GO:0050896 response to stimulus	-2.9	8.8	5.3	4	3.9	1.9	HCTR2/PLCB4/TRHR/DGKH	-0.32
Northern	GO Biological Processes	GO:0030166	Metabolism	proteoglycan biosynthetic process	19_GO:0009987 cellular process	-2.9	15	6.2	3	2.9	1.7	IGF1/CHST11/B3GAT2	-0.32
Northern	GO Biological Processes	GO:0048705	Muscular process	skeletal system morphogenesis	19_GO:0032502 developmental process	-2.9	6.4	4.8	5	4.9	2.1	ACVR2B/BMP7/SOX5/TIPARP/CHST11	-0.31
Northern	GO Biological Processes	GO:0098660	Cellular process	inorganic ion transmembrane transport	19_GO:0051179 localization	-2.9	3.4	4	9	8.7	2.8	CACNA1C/CACNA2D1/KCNQ1/PLCB4/SCN2A/SLC13A4/KCNH5/SLC4A10	-0.25
Northern	GO Biological Processes	GO:0007610	Behavior	behavior	19_GO:0032501 multicellular organismal process	-2.8	3.7	4	8	7.8	2.6	APBA2/EPSS/HCTR2/KCNQ1/PMCH/PTN/SCN2A/SLC4A10	-0.25
Northern	GO Biological Processes	GO:0031346	Cellular process	positive regulation of cell projection organization	19_GO:0048518 positive regulation of biological process	-2.8	4.9	4.3	6	5.8	2.3	BMP7/EPSS/PTN/IRIT2/RAPGEF2/COBL	-0.25
Northern	GO Biological Processes	GO:0061337	Cardioregulation	cardiac conduction	19_GO:0032501 multicellular organismal process	-2.8	13	5.9	3	2.9	1.7	CACNA1C/CACNA2D1/KCNQ1	-0.25
Northern	Reactome Gene Sets	R-HSA-112316	Neural processes	Neuronal System		-2.8	4.8	4.3	6	5.8	2.3	APBA2/CACNA2D1/KCNQ1/GLRA3/NBEA/KCNH5	-0.2
Northern	GO Biological Processes	GO:0030001	Cellular process	metal ion transport	19_GO:0051179 localization	-2.7	3.6	3.9	8	7.8	2.6	CACNA1C/CACNA2D1/KCNQ1/PLCB4/SCN2A/SLC13A4/KCNH5/SLC4A10	-0.17
Northern	GO Biological Processes	GO:0090257	Muscular process	regulation of muscle system process	19_GO:0032501 multicellular organismal process	-2.7	5.7	4.5	5	4.9	2.1	CACNA1C/IGF1/KCNQ1/TACR3/EHD3	-0.17

Northern	GO Biological Processes	GO:0050804	Neural processes	modulation of chemical synaptic transmission	19_GO:0050789 regulation of biological process	-2.7	4	4	7	6.8	2.5	APBA2 CRHR2 PMCH PTNRAPGEF2 SYB USL4A10	-0.15
Northern	GO Biological Processes	GO:0099177	Neural processes	regulation of trans-synaptic signaling	19_GO:0050789 regulation of biological process	-2.7	4	4	7	6.8	2.5	APBA2 CRHR2 PMCH PTNRAPGEF2 SYB USL4A10	-0.15
Northern	GO Biological Processes	GO:1903522	Cardioregulation	regulation of blood circulation	19_GO:0032501 multicellular organismal process	-2.7	5.5	4.3	5	4.9	2.1	CACNA1C CACNA2D1 KCQN1 TACR3 EH3	-0.14
Northern	WikiPathways	WP24	Cellular process	Peptide GPCRs		-2.7	12	5.5	3	2.9	1.7	HCRTR2 TACR3 TRHR	-0.14
Northern	GO Biological Processes	GO:0015698	Cellular process	inorganic anion transport	19_GO:0051179 localization	-2.6	7.3	4.7	4	3.9	1.9	KCNQ1 GLRA3 SLC13A4 SLC4A10	-0.12
Northern	GO Biological Processes	GO:0045669	Ossification	positive regulation of osteoblast differentiation	19_GO:0032502 developmental process	-2.6	11	5.4	3	2.9	1.7	ACVR2B BMP7 JGFI	-0.12
Northern	GO Biological Processes	GO:0009880	Development	embryonic pattern specification	19_GO:0032502 developmental process	-2.6	11	5.4	3	2.9	1.7	BMP7 COBL DLL1	-0.12
Northern	GO Biological Processes	GO:0098662	Cellular process	inorganic cation transmembrane transport	19_GO:0051179 localization	-2.6	3.4	3.8	8	7.8	2.6	CACNA1C CACNA2D1 KCQN1 PLCB4 SCN2A SLC13A4 KCNH5 SLC4A10	-0.12
Northern	GO Biological Processes	GO:0007265	Signal transduction	Ras protein signal transduction	19_GO:0050896 response to stimulus	-2.6	11	5.3	3	2.9	1.7	IGF1 RT2 RAPGEF2	-0.12
Northern	GO Biological Processes	GO:0055117	Cardioregulation	regulation of cardiac muscle contraction	19_GO:0032501 multicellular organismal process	-2.6	11	5.3	3	2.9	1.7	CACNA1C KCQN1 EHD3	-0.11
Northern	GO Biological Processes	GO:0007156	Cellular process	homophilic cell adhesion via plasma membrane adhesion molecules	19_GO:0009987 cellular process	-2.6	7	4.6	4	3.9	1.9	CDH18 PTPRMP TPR CDH19	-0.093
Northern	GO Biological Processes	GO:0030500	Ossification	regulation of bone mineralization	19_GO:0032502 developmental process	-2.6	11	5.2	3	2.9	1.7	ACVR2B BMP7 PTN	-0.075
Northern	GO Biological Processes	GO:0006937	Muscular process	regulation of muscle contraction	19_GO:0032501 multicellular organismal process	-2.5	6.7	4.4	4	3.9	1.9	CACNA1C KCQN1 TACR3 EHD3	-0.056
Northern	GO Biological Processes	GO:0006029	Metabolism	proteoglycan metabolic process	19_GO:0009987 cellular process	-2.5	10	5.1	3	2.9	1.7	IGF1 CHST11 B3GAT2	-0.056
Northern	GO Biological Processes	GO:0070848	Growth	response to growth factor	19_GO:0050896 response to stimulus	-2.5	3.7	3.7	7	6.8	2.5	ACVR2B BMP7 FER PTPRK SOX5 RAPGEF2 CHST11	-0.056
Northern	GO Biological Processes	GO:0031175	Neural processes	neuron projection development	19_GO:0032502 developmental process	-2.5	3.3	3.6	8	7.8	2.6	BMP7 PTN PTPRK PTPRMRAPGEF2 JQSE C1 PTPR COBL	-0.056
Northern	GO Biological Processes	GO:0035023	Signal transduction	regulation of Rho protein signal transduction	19_GO:0050896 response to stimulus	-2.5	10	5	3	2.9	1.7	EPSS8 RT2 STARD13	-0.056
Northern	KEGG Pathway	hsa04742	Sensorial	Taste transduction		-2.5	10	5	3	2.9	1.7	CACNA1C PLCB4 SCN2A	-0.056
Northern	GO Biological Processes	GO:0045446	Cellular process	endothelial cell differentiation	19_GO:0032502 developmental process	-2.5	10	5	3	2.9	1.7	ACVR2B RAPGEF2 DLL1	-0.056
Northern	GO Biological Processes	GO:0141091	Growth	transforming growth factor beta receptor superfamily signaling pathway	19_GO:0050896 response to stimulus	-2.5	6.6	4.4	4	3.9	1.9	ACVR2B BMP7 PTPRK CHST11	-0.045
Northern	GO Biological Processes	GO:0003012	Muscular process	muscle system process	19_GO:0032501 multicellular organismal process	-2.5	4.9	4	5	4.9	2.1	CACNA1C CACNA2D1 JGFI KCQN1 SCN2A	-0.03
Northern	GO Biological Processes	GO:0008015	Cardioregulation	blood circulation	19_GO:0032501 multicellular organismal process	-2.5	4.1	3.8	6	5.8	2.3	CACNA1C CACNA2D1 KCQN1 SCN2A TACR3 DLL1	-0.03
Northern	GO Biological Processes	GO:0016310	Cellular process	phosphorylation	19_GO:0009987 cellular process	-2.4	4.1	3.8	6	5.8	2.3	FER TOP1 TLK1 NUAK1 ERC1 DGKH	-0.015
Northern	GO Biological Processes	GO:0051591	Signal transduction	response to cAMP	19_GO:0050896 response to stimulus	-2.4	9.7	4.9	3	2.9	1.7	BCKD HIBK KCQN1 RAPGEF2	-0.014
Northern	GO Biological Processes	GO:0034329	Cellular process	cell junction assembly	19_GO:0009987 cellular process	-2.4	4.9	3.9	5	4.9	2.1	DS CDH118 FER PTPRK CDH19	-0.014
Northern	GO Biological Processes	GO:0051056	Signal transduction	regulation of small GTPase mediated signal transduction	19_GO:0050896 response to stimulus	-2.4	4.9	3.9	5	4.9	2.1	EPSS8 JGFI RT2 JQSE STARD13	-0.014
Northern	GO Biological Processes	GO:0006470	Cellular process	protein dephosphorylation	19_GO:0009987 cellular process	-2.4	9.3	4.7	3	2.9	1.7	PTPRK PTPRMP TPRT	0
Northern	GO Biological Processes	GO:0097553	Cellular process	calcium ion transmembrane import into cytosol	19_GO:0051179 localization	-2.4	9.3	4.7	3	2.9	1.7	CACNA1C CACNA2D1 PLCB4	0
Northern	Reactome Gene Sets	R-HSA-500792	Cellular process	GPCR ligand binding		-2.4	4	3.7	6	5.8	2.3	CRHR2 HCRTR2 PMCH TACR3 TRHR RXFP1	0
Northern	GO Biological Processes	GO:0048598	Development	embryonic morphogenesis	19_GO:0032502 developmental process	-2.4	3.4	3.5	7	6.8	2.5	ACVR2B BMP7 CACNA1C KCQN1 COBL DLL1 CHST11	0
Northern	Reactome Gene Sets	R-HSA-373076	Cellular process	Class A/1 (Rhodopsin-like receptors)		-2.3	4.7	3.8	5	4.9	2.1	HCRTR2 PMCH TACR3 TRHR RXFP1	0
Northern	GO Biological Processes	GO:0006814	Cellular process	sodium ion transport	19_GO:0051179 localization	-2.3	6	4.1	4	3.9	1.9	KCNQ1 SCN2A SLC13A4 SLC4A10	0
Northern	GO Biological Processes	GO:0051153	Muscular process	regulation of striated muscle cell differentiation	19_GO:0032502 developmental process	-2.3	9	4.6	3	2.9	1.7	IGF1 FBXO22 DLL1	0
Northern	WikiPathways	WP4540	Signal transduction	Hippo signaling regulation		-2.3	9	4.6	3	2.9	1.7	CDH18 PLCB4 CDH19	0
Northern	KEGG Pathway	hsa04510	Cardioregulation	Hypertrophic cardiomyopathy		-2.3	8.9	4.6	3	2.9	1.7	CACNA1C CACNA2D1 JGFI	0
Northern	GO Biological Processes	GO:0006942	Muscular process	regulation of striated muscle contraction	19_GO:0032501 multicellular organismal process	-2.3	8.7	4.5	3	2.9	1.7	CACNA1C KCQN1 EHD3	0
Northern	GO Biological Processes	GO:0070167	Ossification	regulation of biomineral tissue development	19_GO:0032502 developmental process	-2.3	8.6	4.5	3	2.9	1.7	ACVR2B BMP7 PTN	0
Northern	GO Biological Processes	GO:0098659	Cellular process	inorganic cation import across plasma membrane	19_GO:0051179 localization	-2.3	8.4	4.4	3	2.9	1.7	CACNA1C CACNA2D1 KCQN1	0
Northern	KEGG Pathway	hsa05414	Cardioregulation	Dilated cardiomyopathy		-2.3	8.4	4.4	3	2.9	1.7	CACNA1C CACNA2D1 JGFI	0
Northern	GO Biological Processes	GO:0099587	Cellular process	inorganic ion import across plasma membrane	19_GO:0051179 localization	-2.3	8.4	4.4	3	2.9	1.7	CACNA1C CACNA2D1 KCQN1	0
Northern	GO Biological Processes	GO:2000147	Cellular process	positive regulation of cell motility	19_GO:0040011 locomotion	-2.2	3.3	3.4	7	6.8	2.5	BMP7 FER JGFI PTN TACR3 RAPGEF2 JQSE EC1	0
Northern	Reactome Gene Sets	R-HSA-5173105	Cellular process	O-linked glycosylation		-2.2	8.2	4.4	3	2.9	1.7	ST3GAL3 THBS2 THSD4	0
Northern	KEGG Pathway	hsa04350	Signal transduction	TGF-beta signaling pathway		-2.2	8.2	4.4	3	2.9	1.7	ACVR2B BMP7 THSD4	0
Northern	GO Biological Processes	GO:0040017	Cellular process	positive regulation of locomotion	19_GO:0040011 locomotion	-2.2	3.2	3.3	7	6.8	2.5	BMP7 FER JGFI PTN TACR3 RAPGEF2 JQSE EC1	0
Northern	GO Biological Processes	GO:0007586	Digestion	digestion	19_GO:0032501 multicellular organismal process	-2.2	7.8	4.2	3	2.9	1.7	KCNQ1 AKR1D1 STRAP	0
Northern	GO Biological Processes	GO:0120035	Cellular process	regulation of plasma membrane bounded cell projection organization	19_GO:0050789 regulation of biological process	-2.2	3.2	3.3	7	6.8	2.5	BMP7 EPSS8 FER PTN RT2 RAPGEF2 COBL	0
Northern	GO Biological Processes	GO:0007218	Signal transduction	neuropeptide signaling pathway	19_GO:0050896 response to stimulus	-2.2	7.7	4.2	3	2.9	1.7	HCRTR2 PMCH RAPGEF2	0
Northern	GO Biological Processes	GO:0016358	Neural processes	dendrite development	19_GO:0032502 developmental process	-2.1	7.7	4.2	3	2.9	1.7	BMP7 PTN JQSE1	0
Northern	GO Biological Processes	GO:0048167	Neural processes	regulation of synaptic plasticity	19_GO:0050789 regulation of biological process	-2.1	5.3	3.7	4	3.9	1.9	CRHR2 PTN RAPGEF2 SLC4A10	0
Northern	KEGG Pathway	hsa04725	Neural processes	Cholinergic synapse		-2.1	7.6	4.2	3	2.9	1.7	CACNA1C KCQN1 PLCB4	0
Northern	GO Biological Processes	GO:0043010	Vision	camera-type eye development	19_GO:0032502 developmental process	-2.1	4.1	3.5	5	4.9	2.1	ACVR2B BMP7 CACNA1C PTPRM DLL1	0
Northern	Reactome Gene Sets	R-HSA-5576891	Cardioregulation	Cardiac conduction		-2.1	7.5	4.1	3	2.9	1.7	CACNA1C KCQN1 SCN2A	0
Northern	GO Biological Processes	GO:0031344	Cellular process	regulation of cell projection organization	19_GO:0050789 regulation of biological process	-2.1	3.1	3.2	7	6.8	2.5	BMP7 EPSS8 FER PTN RT2 RAPGEF2 COBL	0
Northern	GO Biological Processes	GO:0001501	Development	skeletal system development	19_GO:0032502 developmental process	-2.1	3.5	3.3	6	5.8	2.3	ACVR2B BMP7 JGFI SOX5 TIPARP CHST11	0
Northern	WikiPathways	WP4541	Signal transduction	Hippo Merfin signaling dysregulation		-2.1	7.3	4	3	2.9	1.7	CDH18 PLCB4 CDH19	0
Northern	KEGG Pathway	hsa04935	Growth	Growth hormone synthesis, secretion and action		-2.1	7.2	4	3	2.9	1.7	CACNA1C JGFI PLCB4	0
Northern	GO Biological Processes	GO:0061448	Development	connective tissue development	19_GO:0032502 developmental process	-2.1	5	3.6	4	3.9	1.9	BMP7 SOX5 CHST11 RXFP1	0
Northern	GO Biological Processes	GO:0016051	Metabolism	carbohydrate biosynthetic process	19_GO:0009987 cellular process	-2.1	7.2	4	3	2.9	1.7	ST3GAL3 CHST11 B3GAT2	0
Northern	GO Biological Processes	GO:0003013	Cardioregulation	circulatory system process	19_GO:0032501 multicellular organismal process	-2.1	3.4	3.2	6	5.8	2.3	CACNA1C CACNA2D1 KCQN1 SCN2A TACR3 DLL1	0
Northern	GO Biological Processes	GO:0030326	Development	embryonic limb morphogenesis	19_GO:0032502 developmental process	-2.1	7.1	4	3	2.9	1.7	BMP7 CACNA1C CHST11	0
Northern	GO Biological Processes	GO:0035113	Development	embryonic appendage morphogenesis	19_GO:0032502 developmental process	-2.1	7.1	4	3	2.9	1.7	BMP7 CACNA1C CHST11	0
Northern	GO Biological Processes	GO:0006936	Muscular process	muscle contraction	19_GO:0032501 multicellular organismal process	-2.1	5	3.6	4	3.9	1.9	CACNA1C CACNA2D1 KCQN1 SCN2A	0
Northern	GO Biological Processes	GO:0071363	Growth	cellular response to growth factor stimulus	19_GO:0050896 response to stimulus	-2	3.3	3.2	6	5.8	2.3	ACVR2B BMP7 PTPRK SOX5 RAPGEF2 CHST11	0
Northern	GO Biological Processes	GO:0030278	Ossification	regulation of ossification	19_GO:0032501 multicellular organismal process	-2	6.9	3.9	3	2.9	1.7	ACVR2B BMP7 PTN	0
Northern	Reactome Gene Sets	R-HSA-983168	Immunity	Antigen processing: Ubiquitination & Proteasome degradation		-2	4.8	3.5	4	3.9	1.9	UBE2G1 FBXO22 UBE2Q2 HECTD2	0
Southern	GO Biological Processes	GO:0007601	Vision	visual perception	19_GO:0032501 multicellular organismal process	-6.3	9.4	8.3	9	6.9	2.2	GRM8 IMP1 PDE6C RP1 POU6F2 BBS9K CNK9 ATP8A2 CCDC66	-2.2

Southern	GO Biological Processes	GO:0050953	Vision	sensory perception of light stimulus	19_GO:0032501 multicellular organismal process	-6.2	9.3	8.2	9	6.9	2.2	GRM8 IMP PDE6 CRP1 POU6F2 BBS9 CNK9 ATP8A2 CCDC66	-2.2
Southern	GO Biological Processes	GO:0005981	Response to stimulus	detection of external stimulus	19_GO:0050896 response to stimulus	-5.6	12	8.3	7	5.4	2	GRIK2 KCQN1 PDE6 CRP1 ITN ATP8A2 CCDC66	-1.8
Southern	GO Biological Processes	GO:0005982	Response to stimulus	detection of abiotic stimulus	19_GO:0050896 response to stimulus	-5.6	12	8.3	7	5.4	2	GRIK2 KCQN1 PDE6 CRP1 ITN ATP8A2 CCDC66	-1.8
Southern	WikiPathways	WP3932	Signal transduction	Focal adhesion PI3K Akt mTOR signaling		-5.2	6.9	6.8	9	6.9	2.2	VEGFD IGF1 ITGB2 LAMA2 LAMA4 KITLG PIK3R1 TBC1D1 CREB3L1	-1.5
Southern	GO Biological Processes	GO:0060041	Vision	retina development in camera-type eye	19_GO:0032502 developmental process	-5	9.6	7.4	7	5.4	2	LRP5 PDE6 CRP1 ATP8A2 CHD7 MEGF1 TBC1D32	-1.5
Southern	GO Biological Processes	GO:0060042	Vision	retina morphogenesis in camera-type eye	19_GO:0032502 developmental process	-5	17	8.8	5	3.8	1.7	LRP5 PDE6 CRP1 ATP8A2 MEGF1 TBC1D32	-1.5
Southern	GO Biological Processes	GO:0048598	Development	embryonic morphogenesis	19_GO:0032502 developmental process	-5	4.7	6	12	9.2	2.5	ITGB2 KCQN1 LRP5 MMP16 RVR2 TRAF6 COBL TASOR ATP8A2 KIF16 BCHD7 TBC1D32	-1.5
Southern	WikiPathways	WP4172	Signal transduction	PI3K Akt signaling		-4.8	6.2	6.3	9	6.9	2.2	VEGFD IGF1 LAMA2 LAMA4 KITLG MYB PIK3R1 PPP2R2A CREB3L1	-1.4
Southern	KEGG Pathway	hsa04151	Signal transduction	PI3K-Akt signaling pathway		-4.6	5.8	6	9	6.9	2.2	VEGFD IGF1 LAMA2 LAMA4 KITLG MYB PIK3R1 PPP2R2A CREB3L1	-1.2
Southern	GO Biological Processes	GO:0046488	Metabolism	phosphatidylinositol metabolic process	19_GO:0009987 cellular process	-4.4	9.4	6.8	6	4.6	1.8	INPP5A PIK3R1 FIG4 SMG1 MTMR12 TTC7B	-1.1
Southern	GO Biological Processes	GO:0098657	Cellular process	import into cell	19_GO:0051179 localization	-4.3	4	5.3	12	9.2	2.5	GRM1 ITGB2 KCQN1 KCQN3 LRP5 SLC18A2 SLC22A2 ATP8A1 CNK9 GULP1 FCHO2 SLC9A9	-1.1
Southern	GO Biological Processes	GO:0048146	Development	positive regulation of fibroblast proliferation	19_GO:0048518 positive regulation of biological process	-4.1	17	7.9	4	3.1	1.5	ESR1 IGF1 MYB RNASEH2B	-0.92
Southern	Canonical Pathways	M5885	Cellular process	NABA MATRISOME ASSOCIATED		-4	3.7	5	12	9.2	2.5	GPC5 VEGFD IGF1 KITLG MMP16 PAPPA SEMA3 ANGPTL2 FGFBP2 MEGF1 ADAMTS1 CCBE1	-0.91
Southern	GO Biological Processes	GO:0046854	Metabolism	phosphatidylinositol phosphate biosynthetic process	19_GO:0009987 cellular process	-4	17	7.7	4	3.1	1.5	PIK3R1 FIG4 SMG1 TTC7B	-0.91
Southern	WikiPathways	WP5087	Respiratory system	Pleural mesothelioma		-3.9	4.8	5.2	9	6.9	2.2	CTBP2 VEGFD IGF1 ITGB2 LAMA2 LAMA4 LRP5 KITLG LMD1	-0.88
Southern	GO Biological Processes	GO:0060271	Cellular process	cilium assembly	19_GO:0009987 cellular process	-3.9	5.4	5.4	8	6.2	2.1	KCNQ1 RP1D ZIP1 DNAI1 BBS9 PARVA TBC1D32 CCDC66	-0.88
Southern	GO Biological Processes	GO:0009583	Vision	detection of light stimulus	19_GO:0050896 response to stimulus	-3.8	15	7.3	4	3.1	1.5	PDE6 CRP1 ATP8A2 CCDC66	-0.83
Southern	KEGG Pathway	hsa04152	Signal transduction	AMPK signaling pathway		-3.7	9.5	6.2	5	3.8	1.7	IGF1 PIK3R1 PPP2R2A TBC1D1 CREB3L1	-0.75
Southern	Reactome Gene Sets	R-HSA-112316	Neural processes	Neuronal System		-3.7	5	5.1	8	6.2	2.1	GLRA2 GRIK2 GRM1 KCQN1 KCQN3 SLC18A2 SLC22A2 CNK9	-0.73
Southern	WikiPathways	WP306	Cellular process	Focal adhesion		-3.6	7	5.6	6	4.6	1.8	VEGFD IGF1 LAMA2 LAMA4 PIK3R1 PARVA	-0.71
Southern	GO Biological Processes	GO:0090596	Sensorial	sensory organ morphogenesis	19_GO:0032502 developmental process	-3.6	5.8	5.3	7	5.4	2	KCNQ1 LRP5 PDE6 CRP1 ATP8A2 CHD7 MEGF1	-0.71
Southern	GO Biological Processes	GO:0044782	Cellular process	cilium organization	19_GO:0009987 cellular process	-3.6	4.9	5	8	6.2	2.1	KCNQ1 RP1D ZIP1 DNAI1 BBS9 PARVA TBC1D32 CCDC66	-0.71
Southern	KEGG Pathway	hsa04510	Cellular process	Focal adhesion		-3.6	6.9	5.5	6	4.6	1.8	VEGFD IGF1 LAMA2 LAMA4 PIK3R1 PARVA	-0.7
Southern	GO Biological Processes	GO:0046856	Cellular process	phosphatidylinositol dephosphorylation	19_GO:0009987 cellular process	-3.6	24	8.2	3	2.3	1.3	INPP5A FIG4 MTMR12	-0.7
Southern	KEGG Pathway	hsa04015	Signal transduction	Rap1 signaling pathway		-3.5	6.6	5.4	6	4.6	1.8	VEGFD IGF1 ITGB2 LCP2 KITLG PIK3R1	-0.64
Southern	GO Biological Processes	GO:0048593	Vision	camera-type eye morphogenesis	19_GO:0032502 developmental process	-3.5	8.5	5.8	5	3.8	1.7	LRP5 PDE6 CRP1 ATP8A2 MEGF1 TBC1D32	-0.64
Southern	GO Biological Processes	GO:0008360	Cellular process	regulation of cell shape	19_GO:0032502 developmental process	-3.5	8.4	5.7	5	3.8	1.7	ITGB2 LMD1 PLEKH01 PARVA ARHGAP15	-0.63
Southern	GO Biological Processes	GO:0003013	Cardioregulation	circulatory system process	19_GO:0032501 multicellular organismal process	-3.4	4	4.6	9	6.9	2.2	ADRA1 DKCNQ1 LRP5 RVR2 SLC22A2 ITN ATP8A1 CHD7 SLC2A13	-0.58
Southern	Canonical Pathways	M110	Signal transduction	PID IL1 PATHWAY		-3.4	21	7.5	3	2.3	1.3	PIK3R1 TRAF6 ERC1	-0.58
Southern	Canonical Pathways	M143	Signal transduction	PID IL2 PI3K PATHWAY		-3.4	21	7.5	3	2.3	1.3	MYB PIK3R1 EIF3A	-0.58
Southern	GO Biological Processes	GO:0003407	Vision	neural retina development	19_GO:0032502 developmental process	-3.3	11	6.1	4	3.1	1.5	PDE6 CRP1 ATP8A2 MEGF1	-0.55
Southern	KEGG Pathway	hsa04261	Cardioregulation	Adrenergic signaling in cardiomyocytes		-3.3	7.6	5.4	5	3.8	1.7	ADRA1 DKCNQ1 PPP2R2A RVR2 CREB3L1	-0.49
Southern	GO Biological Processes	GO:0048145	Development	regulation of fibroblast proliferation	19_GO:0050789 regulation of biological process	-3.2	10	5.8	4	3.1	1.5	ESR1 IGF1 MYB RNASEH2B	-0.45
Southern	GO Biological Processes	GO:0120031	Cellular process	plasma membrane bounded cell projection assembly	19_GO:0009987 cellular process	-3.2	4.2	4.5	8	6.2	2.1	KCNQ1 RP1D ZIP1 DNAI1 BBS9 PARVA TBC1D32 CCDC66	-0.45
Southern	Canonical Pathways	M5887	Cellular process	NABA BASEMENT MEMBRANES		-3.2	17	6.8	3	2.3	1.3	LAMA2 LAMA4 NTN4	-0.45
Southern	GO Biological Processes	GO:0048144	Development	fibroblast proliferation	19_GO:0009987 cellular process	-3.2	17	6.8	3	2.3	1.3	ESR1 VEGFD RNASEH2B	-0.45
Southern	GO Biological Processes	GO:0014896	Muscular process	muscle hypertrophy	19_GO:0032501 multicellular organismal process	-3.2	17	6.8	3	2.3	1.3	IGF1 RVR2 ITN	-0.45
Southern	Canonical Pathways	M5883	Cellular process	NABA SECRETED FACTORS		-3.1	4.8	4.6	7	5.4	2	VEGFD IGF1 KITLG ANGPTL2 FGFBP2 MEGF1 CCBE1	-0.45
Southern	GO Biological Processes	GO:0009792	Development	embryo development ending in birth or egg hatching	19_GO:0032502 developmental process	-3.1	3.4	4.2	10	7.7	2.3	FUT8 MMP16 TRAF6 SEMA3 CELFL1 COBL CHD7 CELFA4 RNASEH2B TBC1D32	-0.45
Southern	GO Biological Processes	GO:0098739	Cellular process	import across plasma membrane	19_GO:0051179 localization	-3.1	7.1	5.1	5	3.8	1.7	GRM1 KCQN1 SLC22A2 KCQN9 SLC9A9	-0.45
Southern	GO Biological Processes	GO:0048592	Vision	eye morphogenesis	19_GO:0032502 developmental process	-3.1	7	5.1	5	3.8	1.7	LRP5 PDE6 CRP1 ATP8A2 MEGF1 TBC1D32	-0.45
Southern	GO Biological Processes	GO:0030031	Cellular process	cell projection assembly	19_GO:0009987 cellular process	-3.1	4.1	4.4	8	6.2	2.1	KCNQ1 RP1D ZIP1 DNAI1 BBS9 PARVA TBC1D32 CCDC66	-0.45
Southern	GO Biological Processes	GO:0046839	Cellular process	phospholipid dephosphorylation	19_GO:0009987 cellular process	-3.1	17	6.7	3	2.3	1.3	INPP5A FIG4 MTMR12	-0.45
Southern	GO Biological Processes	GO:0048568	Development	embryonic organ development	19_GO:0032502 developmental process	-3.1	4.1	4.4	8	6.2	2.1	KCNQ1 KITLG MMP16 RVR2 COBL CDC40 ATP8A2 CHD7	-0.45
Southern	GO Biological Processes	GO:0046486	Metabolism	glycerolipid metabolic process	19_GO:0009987 cellular process	-3.1	4.6	4.5	7	5.4	2	INPP5A PIK3R1 FIG4 MGLL SMG1 MTMR12 TTC7B	-0.45
Southern	GO Biological Processes	GO:0035239	Development	tube morphogenesis	19_GO:0032502 developmental process	-3.1	3.4	4.1	10	7.7	2.3	ESR1 VEGFD LRP5 RVR2 TRAF6 COBL KIF26B CHD7 PARVA CCBE1	-0.45
Southern	GO Biological Processes	GO:0043010	Vision	camera-type eye development	19_GO:0032502 developmental process	-3.1	4.6	4.5	7	5.4	2	LRP5 PDE6 CRP1 ATP8A2 CHD7 MEGF1 TBC1D32	-0.45
Southern	KEGG Pathway	hsa05410	Cardioregulation	Hypertrophic cardiomyopathy		-3.1	9.4	5.5	4	3.1	1.5	IGF1 LAMA2 RVR2 ITN	-0.45
Southern	GO Biological Processes	GO:0042391	Neural processes	regulation of membrane potential	19_GO:0065007 biological regulation	-3	4	4.3	8	6.2	2.1	GLRA2 GRIK2 GRM1 KCQN1 KCQN3 RVR2 CNK9 CELFA4	-0.45
Southern	GO Biological Processes	GO:0007507	Cardioregulation	heart development	19_GO:0032502 developmental process	-3	3.6	4.2	9	6.9	2.2	KCNQ1 RVR2 ITN SEMA3 CDZIP1 DNAI1 CHD7 PARVA TBC1D32	-0.45
Southern	GO Biological Processes	GO:0048729	Development	tissue morphogenesis	19_GO:0032502 developmental process	-3	3.6	4.2	9	6.9	2.2	ESR1 LRP5 RVR2 TRAF6 ITN SEMA3 CCOBL KIF26B CHD7	-0.45
Southern	GO Biological Processes	GO:0044057	Development	regulation of system process	19_GO:0032501 multicellular organismal process	-3	3.6	4.1	9	6.9	2.2	ADRA1 DGIRM1 IGF1 KCQN1 RVR2 FIG4 MGLL CNK9 CELFA4	-0.43
Southern	GO Biological Processes	GO:0034446	Cellular process	substrate adhesion-dependent cell spreading	19_GO:0009987 cellular process	-3	15	6.3	3	2.3	1.3	PIK3R1 PARVA NTN4	-0.42
Southern	Canonical Pathways	M239	Signal transduction	PID A6B1 A6B4 INTEGRIN PATHWAY		-3	15	6.3	3	2.3	1.3	LAMA2 LAMA4 PIK3R1	-0.42
Southern	KEGG Pathway	hsa05414	Cardioregulation	Dilated cardiomyopathy		-3	8.9	5.3	4	3.1	1.5	IGF1 LAMA2 RVR2 ITN	-0.4
Southern	GO Biological Processes	GO:0019320	Metabolism	hexose catabolic process	19_GO:0009987 cellular process	-2.9	14	6.1	3	2.3	1.3	FUT8 LRP5 GMI	-0.38
Southern	GO Biological Processes	GO:0007215	Signal transduction	glutamate receptor signaling pathway	19_GO:0050896 response to stimulus	-2.9	14	6.1	3	2.3	1.3	GRIK2 GRM1 GRM8	-0.38
Southern	GO Biological Processes	GO:0010324	Cellular process	membrane invagination	19_GO:0009987 cellular process	-2.9	14	6.1	3	2.3	1.3	ITGB2 GULP1 FCHO2	-0.38
Southern	Canonical Pathways	M5884	Cellular process	NABA CORE MATRISOME		-2.9	5.1	4.5	6	4.6	1.8	IMP LAMA2 LAMA4 NTN4 EGFLAMV W3B	-0.38
Southern	GO Biological Processes	GO:0060078	Neural processes	regulation of postsynaptic membrane potential	19_GO:0065007 biological regulation	-2.9	8.5	5.2	4	3.1	1.5	GLRA2 GRIK2 GRM1 CELFA4	-0.37
Southern	GO Biological Processes	GO:0030198	Cellular process	extracellular matrix organization	19_GO:0009987 cellular process	-2.9	5	4.4	6	4.6	1.8	IMP MMP16 NTN4 CREB3L1 ADAMTS1 EGFLAM	-0.36
Southern	GO Biological Processes	GO:0048771	Development	tissue remodeling	19_GO:0032501 multicellular organismal process	-2.9	8.4	5.1	4	3.1	1.5	LRP5 TRAF6 SEMA3 CHD7	-0.36

Southern	GO Biological Processes	GO:0043062	Cellular process	extracellular structure organization	19_GO:0009987 cellular process	-2.9	5	4.4	6	4.6	1.8	IMP1 MP16 NTN4 CREB3L1 ADAMTS1 EJGLAM	-0.36
Southern	GO Biological Processes	GO:0045229	Cellular process	external encapsulating structure organization	19_GO:0009987 cellular process	-2.9	5	4.4	6	4.6	1.8	IMP1 MP16 NTN4 CREB3L1 ADAMTS1 EJGLAM	-0.35
Southern	GO Biological Processes	GO:0120034	Cellular process	positive regulation of plasma membrane bounded cell projection assembly	19_GO:0048518 positive regulation of biological process	-2.8	8.2	5.1	4	3.1	1.5	PIK3R1 RP1 DZIP1 COBL	-0.35
Southern	GO Biological Processes	GO:0006650	Metabolism	glycerophospholipid metabolic process	19_GO:0009987 cellular process	-2.8	4.9	4.3	6	4.6	1.8	INPP5A PIK3R1 FIG4 SMG1 MTMR12 TTC7B	-0.34
Southern	GO Biological Processes	GO:0046365	Cellular process	monosaccharide catabolic process	19_GO:0009987 cellular process	-2.8	13	5.8	3	2.3	1.3	FUT8 LRP5 PGM1	-0.34
Southern	Reactome Gene Sets	R-HSA-1280218	Immunity	Adaptive Immune System		-2.8	3.3	3.9	9	6.9	2.2	DYNC1L2 TGB2LCP2 TRAF6 HERC1 LNK1 ASB10 ASB1 UBR1	-0.34
Southern	GO Biological Processes	GO:0006661	Metabolism	phosphatidylinositol biosynthetic process	19_GO:0009987 cellular process	-2.8	8	5	4	3.1	1.5	PIK3R1 FIG4 SMG1 TTC7B	-0.34
Southern	KEGG Pathway	hsa04725	Neural processes	Cholinergic synapse		-2.8	8	5	4	3.1	1.5	KCNQ1 KCNQ3 PIK3R1 CREB3L1	-0.34
Southern	Canonical Pathways	M3008	Cellular process	NABA ECM GLYCOPROTEINS		-2.8	5.9	4.6	5	3.8	1.7	LAMA2 LAMA4 NTN4 EGFLAM VWA3B	-0.34
Southern	GO Biological Processes	GO:0007610	Behavior	behavior	19_GO:0032501 multicellular organismal process	-2.8	3.3	3.9	9	6.9	2.2	GRIK2 GRM1 KCNQ1 KCNQ3 SLC18A2 F1G4 ATP8A1 ATP8A2 CHD7	-0.32
Southern	GO Biological Processes	GO:0001503	Ossification	ossification	19_GO:0032501 multicellular organismal process	-2.8	4.8	4.2	6	4.6	1.8	IGF1 LRP5 MMP16 TRAF6 LIMD1 CREB3L1	-0.32
Southern	GO Biological Processes	GO:0001654	Vision	eye development	19_GO:0032502 developmental process	-2.7	4	4	7	5.4	2	LRP5 PDE6C RP1 ATP8A2 CHD7 MEGF11 TBC1D32	-0.3
Southern	GO Biological Processes	GO:0006941	Muscular process	striated muscle contraction	19_GO:0032501 multicellular organismal process	-2.7	7.7	4.8	4	3.1	1.5	KCNQ1 RYR2 TTN ATP8A2	-0.29
Southern	GO Biological Processes	GO:0006874	Cellular process	intracellular calcium ion homeostasis	19_GO:0042592 homeostatic process	-2.7	5.7	4.4	5	3.8	1.7	GRIK2 GRM1 RYR2 ERC2 TMT4	-0.29
Southern	GO Biological Processes	GO:0150063	Vision	visual system development	19_GO:0032502 developmental process	-2.7	4	4	7	5.4	2	LRP5 PDE6C RP1 ATP8A2 CHD7 MEGF11 TBC1D32	-0.29
Southern	GO Biological Processes	GO:0031644	Neural processes	regulation of nervous system process	19_GO:0032501 multicellular organismal process	-2.7	7.5	4.8	4	3.1	1.5	GRM1 FIG4 MGLL CEL4	-0.28
Southern	GO Biological Processes	GO:0030099	Neural processes	myeloid cell differentiation	19_GO:0032502 developmental process	-2.7	4.6	4.1	6	4.6	1.8	KCNQ1 KITLG MYB PIK3R1 TRAF6 KAT6A	-0.28
Southern	GO Biological Processes	GO:0030968	Cellular process	endoplasmic reticulum unfolded protein response	19_GO:0050896 response to stimulus	-2.7	12	5.5	3	2.3	1.3	TMT4 CREB3L1 ASB1	-0.28
Southern	GO Biological Processes	GO:0048880	Sensorial	sensory system development	19_GO:0032502 developmental process	-2.7	3.9	4	7	5.4	2	LRP5 PDE6C RP1 ATP8A2 CHD7 MEGF11 TBC1D32	-0.28
Southern	GO Biological Processes	GO:0098916	Neural processes	anterograde trans-synaptic signaling	19_GO:0050789 regulation of biological process	-2.7	3.9	4	7	5.4	2	GLRA2 GRIK2 GRM1 KCNQ3 SLC18A2 ERC2 CEL4	-0.28
Southern	GO Biological Processes	GO:0007268	Neural processes	chemical synaptic transmission	19_GO:0050789 regulation of biological process	-2.7	3.9	4	7	5.4	2	GLRA2 GRIK2 GRM1 KCNQ3 SLC18A2 ERC2 CEL4	-0.28
Southern	GO Biological Processes	GO:0043009	Development	chordate embryonic development	19_GO:0032502 developmental process	-2.7	3.2	3.7	9	6.9	2.2	FUT8 MMP16 TRAF6 SEMA3C COBL CHD7 CEL4 RNASEH2B TBC1D32	-0.28
Southern	GO Biological Processes	GO:0055008	Cardioregulation	cardiac muscle tissue morphogenesis	19_GO:0032502 developmental process	-2.7	12	5.4	3	2.3	1.3	RYR2 TTN CHD7	-0.28
Southern	GO Biological Processes	GO:0051480	Cellular process	regulation of cytosolic calcium ion concentration	19_GO:0042592 homeostatic process	-2.7	12	5.4	3	2.3	1.3	GRM1 RYR2 ERC2	-0.28
Southern	Reactome Gene Sets	R-HSA-109582	Cardioregulation	Hemostasis		-2.7	3.5	3.8	8	6.2	2.1	VEGFD IGF1 TGB2LCP2 MYB TTN MGLL KIF26B	-0.28
Southern	Reactome Gene Sets	R-HSA-76002	Signal transduction	Platelet activation, signaling and aggregation		-2.6	5.5	4.3	5	3.8	1.7	VEGFD IGF1 LCP2 TTNMGLL	-0.27
Southern	WikiPathways	WP5072	Immunity	Modulators of TCR signaling and T cell activation		-2.6	11	5.4	3	2.3	1.3	LCP2 PIK3R1 TRAF6	-0.27
Southern	GO Biological Processes	GO:0003206	Cardioregulation	cardiac chamber morphogenesis	19_GO:0032502 developmental process	-2.6	7.2	4.7	4	3.1	1.5	RYR2 SEMA3C CHD7 PARVA	-0.27
Southern	GO Biological Processes	GO:0001508	Neural processes	action potential	19_GO:0065007 biological regulation	-2.6	7.2	4.7	4	3.1	1.5	GRIK2 KCNQ1 KCNQ3 RYR2	-0.27
Southern	GO Biological Processes	GO:0006562	Development	epithelial tube morphogenesis	19_GO:0032502 developmental process	-2.6	4.4	4	6	4.6	1.8	ESR1 LRP5 RYR2 TRAF6 COBL KIF26B	-0.26
Southern	GO Biological Processes	GO:0002040	Cardioregulation	sprouting angiogenesis	19_GO:0032502 developmental process	-2.6	11	5.3	3	2.3	1.3	VEGFD PARVA CCBE1	-0.26
Southern	Canonical Pathways	M10	Signal transduction	PID BCR SPATHWAY		-2.6	11	5.3	3	2.3	1.3	BCL2A1 PIK3R1 TRAF6	-0.26
Southern	GO Biological Processes	GO:0001667	Cellular process	ameboid-type cell migration	19_GO:0009987 cellular process	-2.6	7.1	4.6	4	3.1	1.5	FUT8 LRP5 KITLG SEMA3C	-0.26
Southern	GO Biological Processes	GO:0051606	Response to stimulus	detection of stimulus	19_GO:0050896 response to stimulus	-2.6	3.1	3.6	9	6.9	2.2	GRIK2 KCNQ1 PDE6C RP1 RYR2 TTN ATP8A2 OR52B2 CCDC66	-0.26
Southern	GO Biological Processes	GO:0009416	Vision	response to light stimulus	19_GO:0050896 response to stimulus	-2.6	4.4	4	6	4.6	1.8	PDE6C PIK3R1 RP1 ATP8A2 INO80 CCDC66	-0.25
Southern	GO Biological Processes	GO:0098900	Neural processes	regulation of action potential	19_GO:0050789 regulation of biological process	-2.6	11	5.2	3	2.3	1.3	KCNQ3 RYR2 KCN9	-0.25
Southern	GO Biological Processes	GO:0001578	Cellular process	microtubule bundle formation	19_GO:0009987 cellular process	-2.6	7	4.5	4	3.1	1.5	RP1 DNAI1 CCDC66 NCKAP5	-0.25
Southern	GO Biological Processes	GO:0099537	Neural processes	trans-synaptic signaling	19_GO:0050789 regulation of biological process	-2.6	3.8	3.8	7	5.4	2	GLRA2 GRIK2 GRM1 KCNQ3 SLC18A2 ERC2 CEL4	-0.25
Southern	GO Biological Processes	GO:0061512	Cellular process	protein localization to cilium	19_GO:0051179 localization	-2.6	11	5.2	3	2.3	1.3	DZIP1 BBS9 TBC1D32	-0.25
Southern	GO Biological Processes	GO:0009612	Response to stimulus	response to mechanical stimulus	19_GO:0050896 response to stimulus	-2.6	5.2	4.2	5	3.8	1.7	KCNQ1 KCNQ3 RYR2 TTN ATP8A2	-0.25
Southern	GO Biological Processes	GO:0009314	Response to stimulus	response to radiation	19_GO:0050896 response to stimulus	-2.5	3.7	3.8	7	5.4	2	PDE6C PIK3R1 RP1 XRC5 KCN9 INO80 CCDC66	-0.25
Southern	GO Biological Processes	GO:0104004	Response to stimulus	cellular response to environmental stimulus	19_GO:0050896 response to stimulus	-2.5	4.3	3.9	6	4.6	1.8	GRM1 PIK3R1 RP1 XRC5 KCN9 INO80	-0.23
Southern	GO Biological Processes	GO:0071214	Response to stimulus	cellular response to abiotic stimulus	19_GO:0050896 response to stimulus	-2.5	4.3	3.9	6	4.6	1.8	GRM1 PIK3R1 RP1 XRC5 KCN9 INO80	-0.23
Southern	GO Biological Processes	GO:0030097	Cardioregulation	hemopoiesis	19_GO:0032502 developmental process	-2.5	3	3.6	9	6.9	2.2	KCNQ1 KITLG MYB PIK3R1 TRAF6 XRCC5 KAT6 CHD7 TENT2	-0.23
Southern	GO Biological Processes	GO:0006873	Cellular process	intracellular monoatomic ion homeostasis	19_GO:0042592 homeostatic process	-2.5	3.7	3.7	7	5.4	2	GRIK2 GRM1 KCNQ1 RYR2 ERC2 TMT4 SLC9A9	-0.23
Southern	KEGG Pathway	hsa04915	Signal transduction	Estrogen signaling pathway		-2.5	6.7	4.4	4	3.1	1.5	ESR1 GRM1 PIK3R1 CREB3L1	-0.23
Southern	WikiPathways	WP5083	Signal transduction	Neuroinflammation and glutamatergic signaling		-2.5	6.7	4.4	4	3.1	1.5	GRIK2 GRM1 GRM8 IGF1	-0.22
Southern	GO Biological Processes	GO:0060079	Neural processes	excitatory postsynaptic potential	19_GO:0032501 multicellular organismal process	-2.5	10	5	3	2.3	1.3	GLRA2 GRIK2 CEL4	-0.21
Southern	GO Biological Processes	GO:0055074	Cellular process	calcium ion homeostasis	19_GO:0042592 homeostatic process	-2.5	5	4	5	3.8	1.7	GRIK2 GRM1 RYR2 ERC2 TMT4	-0.21
Southern	GO Biological Processes	GO:0003208	Cardioregulation	cardiac ventricle morphogenesis	19_GO:0032502 developmental process	-2.4	9.8	4.9	3	2.3	1.3	RYR2 SEMA3C CHD7	-0.18
Southern	GO Biological Processes	GO:0045600	Lipid metabolism	positive regulation of fat cell differentiation	19_GO:0032502 developmental process	-2.4	9.8	4.9	3	2.3	1.3	LRP5 ASXL2 METRNL	-0.18
Southern	GO Biological Processes	GO:0016311	Cellular process	dephosphorylation	19_GO:0009987 cellular process	-2.4	6.4	4.3	4	3.1	1.5	INPP5A APP2R2 AF1G4 MTMR12	-0.17
Southern	GO Biological Processes	GO:0019080	Immunity	viral gene expression	19_GO:0016032 viral process	-2.4	9.6	4.8	3	2.3	1.3	FUT8 EIF3A ST6GALNAC3	-0.17
Southern	GO Biological Processes	GO:0060415	Muscular process	muscle tissue morphogenesis	19_GO:0032502 developmental process	-2.4	9.6	4.8	3	2.3	1.3	RYR2 TTN CHD7	-0.17
Southern	GO Biological Processes	GO:0002009	Development	morphogenesis of an epithelium	19_GO:0032502 developmental process	-2.4	3.5	3.6	7	5.4	2	ESR1 LRP5 RYR2 TRAF6 SEMA3C COBL KIF26B	-0.17
Southern	GO Biological Processes	GO:0008283	Cellular process	cell population proliferation	19_GO:0009987 cellular process	-2.4	2.9	3.4	9	6.9	2.2	ESR1 VEGFD IGF1 LRP5 KITLG MMP16M YBX XRCC5 RNASEH2B	-0.17
Southern	KEGG Pathway	hsa04072	Signal transduction	Phospholipase D signaling pathway		-2.4	6.3	4.2	4	3.1	1.5	GRM1 GRM8 KITLG PIK3R1	-0.16
Southern	GO Biological Processes	GO:0060411	Cardioregulation	cardiac septum morphogenesis	19_GO:0032502 developmental process	-2.4	9.4	4.8	3	2.3	1.3	SEMA3C CHD7 PARVA	-0.16
Southern	Reactome Gene Sets	R-HSA-983168	Immunity	Antigen processing: Ubiquitination & Proteasome degradation		-2.4	4.8	3.9	5	3.8	1.7	HERC1 LNK1 ASB10 ASB11 UBR1	-0.16
Southern	GO Biological Processes	GO:0055082	Cellular process	intracellular chemical homeostasis	19_GO:0042592 homeostatic process	-2.4	3.1	3.5	8	6.2	2.1	GRIK2 GRM1 KCNQ1 PIK3R1 RYR2 ERC2 TMT4 SLC9A9	-0.16
Southern	GO Biological Processes	GO:0070897	Cellular process	transcription preinitiation complex assembly	19_GO:0009987 cellular process	-2.4	9.3	4.7	3	2.3	1.3	BRF1 ITAF11	-0.16
Southern	WikiPathways	WP69	Immunity	T cell receptor signaling		-2.4	9.3	4.7	3	2.3	1.3	LCP2 PIK3R1 TRAF6	-0.16
Southern	GO Biological Processes	GO:0099536	Neural processes	synaptic signaling	19_GO:0050789 regulation of biological process	-2.4	3.5	3.5	7	5.4	2	GLRA2 GRIK2 GRM1 KCNQ3 SLC18A2 ERC2 CEL4	-0.16
Southern	GO Biological Processes	GO:0035108	Development	limb morphogenesis	19_GO:0032502 developmental process	-2.4	6.1	4.2	4	3.1	1.5	LRP5 SEMA3C CHD7 TBC1D32	-0.16

Southern	GO Biological Processes	GO:0035107	Development	appendage morphogenesis	19_GO:0032502 developmental process	-2.4	6.1	4.2	4	3.1	1.5	LRP5[SEMA3C]CHD7[TBC1D32]	-0.16
Southern	GO Biological Processes	GO:0034620	Cellular process	cellular response to unfolded protein	19_GO:0050896 response to stimulus	-2.4	9.2	4.7	3	2.3	1.3	TMTc4[CREB3L1]ASB11	-0.16
Southern	Reactome Gene Sets	R-HSA-425366	Cellular process	Transport of bile salts and organic acids, metal ions and amine compounds		-2.4	9.2	4.7	3	2.3	1.3	SLC18A2[SLC22A2][SLC2A13]	-0.16
Southern	GO Biological Processes	GO:0099565	Neural processes	chemical synaptic transmission, postsynaptic	19_GO:0032501 multicellular organismal process	-2.4	9.2	4.7	3	2.3	1.3	GLRA2[GRK2][CELF4]	-0.16
Southern	GO Biological Processes	GO:0022604	Cellular process	regulation of cell morphogenesis	19_GO:0032502 developmental process	-2.4	4.7	3.8	5	3.8	1.7	ITGB2[LIMD1][PLEKHO1][PARVA][ARHGAP15]	-0.16
Southern	GO Biological Processes	GO:0051966	Neural processes	regulation of synaptic transmission, glutamatergic	19_GO:0050789 regulation of biological process	-2.3	9.1	4.7	3	2.3	1.3	GRK2[GRM1][GRM8]	-0.16
Southern	GO Biological Processes	GO:0002274	Immunity	myeloid leukocyte activation	19_GO:0002376 immune system process	-2.3	6	4.1	4	3.1	1.5	ITGB2[LP2][SLC18A2][TRAF6]	-0.16
Southern	GO Biological Processes	GO:0099504	Neural processes	synaptic vesicle cycle	19_GO:0051179 localization	-2.3	6	4.1	4	3.1	1.5	SLC18A2[ATP8A1][ERC2][FCHO2]	-0.16
Southern	GO Biological Processes	GO:0006644	Metabolism	phospholipid metabolic process	19_GO:0009987 cellular process	-2.3	3.9	3.6	6	4.6	1.8	INPP5A[PIK3R1][FIG4][SMG1][MTMR12][TTC7B]	-0.16
Southern	GO Biological Processes	GO:0070252	Muscular process	actin-mediated cell contraction	19_GO:0009987 cellular process	-2.3	9	4.6	3	2.3	1.3	KCNQ1[RYR2][PARVA]	-0.16
Southern	GO Biological Processes	GO:0007265	Signal transduction	Ras protein signal transduction	19_GO:0050896 response to stimulus	-2.3	9	4.6	3	2.3	1.3	IGF1[KITL][GRALGPS1]	-0.16
Southern	GO Biological Processes	GO:0050730	Cellular process	regulation of peptidyl-tyrosine phosphorylation	19_GO:0050789 regulation of biological process	-2.3	6	4.1	4	3.1	1.5	IGF1[ITGB2][KITL][GIL2][R2A2]	-0.16
Southern	GO Biological Processes	GO:0021915	Neural processes	neural tube development	19_GO:0032502 developmental process	-2.3	6	4.1	4	3.1	1.5	TRAF6[SEMA3C][COBL][TBC1D32]	-0.16
Southern	GO Biological Processes	GO:0031346	Cellular process	positive regulation of cell projection organization	19_GO:0048518 positive regulation of biological process	-2.3	3.9	3.6	6	4.6	1.8	PIK3R1[RP1][FIG4][DZIP1][COBLATP8A2]	-0.16
Southern	GO Biological Processes	GO:0032368	Lipid metabolism	regulation of lipid transport	19_GO:0051179 localization	-2.3	5.9	4.1	4	3.1	1.5	MYB[ATP8A1][KCNK9][ATP8A2]	-0.16
Southern	GO Biological Processes	GO:0007423	Sensorial	sensory organ development	19_GO:0032502 developmental process	-2.3	3.1	3.4	8	6.2	2.1	KCNQ1[LRP5][PDE6C][RP1][ATP8A2][CHD7][MEGF11][TBC1D32]	-0.15
Southern	WikiPathways	WP5205	Ossification	Clock controlled autophagy in bone metabolism		-2.3	8.7	4.5	3	2.3	1.3	IGF1[LRP5][TRAF6]	-0.14
Southern	GO Biological Processes	GO:0048644	Muscular process	muscle organ morphogenesis	19_GO:0032502 developmental process	-2.3	8.6	4.5	3	2.3	1.3	RYR2[TTN][CHD7]	-0.13
Southern	GO Biological Processes	GO:0019318	Metabolism	hexose metabolic process	19_GO:0009987 cellular process	-2.3	5.8	4	4	3.1	1.5	FUT8[KCNQ1][LRP5][PGM1]	-0.13
Southern	GO Biological Processes	GO:0001775	Cellular process	cell activation	19_GO:0032501 multicellular organismal process	-2.3	2.8	3.3	9	6.9	2.2	IGF1[ITGB2][LP2][KITL][MYB][PIK3R1][SLC18A2][TRAF6][CHD7]	-0.13
Southern	GO Biological Processes	GO:0060048	Cardioregulation	cardiac muscle contraction	19_GO:0032501 multicellular organismal process	-2.2	8.3	4.4	3	2.3	1.3	KCNQ1[RYR2][TTN]	-0.1
Southern	GO Biological Processes	GO:0051046	Cellular process	regulation of secretion	19_GO:0051179 localization	-2.2	3	3.3	8	6.2	2.1	IGF1[ITGB2][KCNQ1][LRP5][MYB][TTN][KCNK9][CHD7]	-0.1
Southern	GO Biological Processes	GO:0045321	Immunity	leukocyte activation	19_GO:0002376 immune system process	-2.2	3	3.3	8	6.2	2.1	ITGB2[LP2][KITL][MYB][PIK3R1][SLC18A2][TRAF6][CHD7]	-0.1
Southern	GO Biological Processes	GO:0003007	Cardioregulation	heart morphogenesis	19_GO:0032502 developmental process	-2.2	4.4	3.6	5	3.8	1.7	RYR2[TTN][SEMA3C][CHD7][PARVA]	-0.1
Southern	GO Biological Processes	GO:0045785	Cellular process	positive regulation of cell adhesion	19_GO:0048518 positive regulation of biological process	-2.2	3.3	3.4	7	5.4	2	IGF1[ITGB2][LAMA2][KITL][TRAF6][KIF26B][EGFLAM]	-0.1
Southern	WikiPathways	WP4298	Cardioregulation	Acute viral myocarditis		-2.2	8.2	4.4	3	2.3	1.3	ITGB2[LAMA2][PIK3R1]	-0.1
Southern	GO Biological Processes	GO:0030258	Lipid metabolism	lipid modification	19_GO:0009987 cellular process	-2.2	5.6	3.9	4	3.1	1.5	AUIH[INPP5A][FIG4][MTMR12]	-0.1
Southern	GO Biological Processes	GO:0071805	Cellular process	potassium ion transmembrane transport	19_GO:0051179 localization	-2.2	5.6	3.9	4	3.1	1.5	KCNQ1[KCNQ3][KCNK9][SLC9A9]	-0.1
Southern	Reactome Gene Sets	R-HSA-983712	Cellular process	Ion channel transport		-2.2	5.5	3.9	4	3.1	1.5	RYR2[ATP8A1][ATP8A2][ANO2]	-0.097
Southern	GO Biological Processes	GO:0007605	Sensorial	sensory perception of sound	19_GO:0032501 multicellular organismal process	-2.2	5.5	3.9	4	3.1	1.5	KCNQ1[KCNQ3][CHD7][TMTc4]	-0.09
Southern	GO Biological Processes	GO:0099003	Neural processes	vesicle-mediated transport in synapse	19_GO:0051179 localization	-2.2	5.5	3.8	4	3.1	1.5	SLC18A2[ATP8A1][ERC2][FCHO2]	-0.089
Southern	GO Biological Processes	GO:0010232	Cellular process	vascular transport	19_GO:0051179 localization	-2.2	8	4.3	3	2.3	1.3	SLC22A2[ATP8A1][SLC2A13]	-0.089
Southern	GO Biological Processes	GO:0150104	Cardioregulation	transport across blood-brain barrier	19_GO:0051179 localization	-2.2	8	4.3	3	2.3	1.3	SLC22A2[ATP8A1][SLC2A13]	-0.089
Southern	GO Biological Processes	GO:0048871	Metabolism	multicellular organismal-level homeostasis	19_GO:0042592 homeostatic process	-2.2	2.9	3.2	8	6.2	2.1	KCNQ1[LAMA2][KITL][GMYB][RP1][TRAF6][METRNL][CCDC66]	-0.085
Southern	GO Biological Processes	GO:0032370	Lipid metabolism	positive regulation of lipid transport	19_GO:0051179 localization	-2.2	7.9	4.3	3	2.3	1.3	MYB[ATP8A1][ATP8A2]	-0.08
Southern	GO Biological Processes	GO:0030205	Cardioregulation	cardiac chamber development	19_GO:0032502 developmental process	-2.2	5.4	3.8	4	3.1	1.5	RYR2[SEMA3C][CHD7][PARVA]	-0.08
Southern	GO Biological Processes	GO:0009101	Metabolism	glycoprotein biosynthetic process	19_GO:0009987 cellular process	-2.2	4.3	3.6	5	3.8	1.7	FUT8[GF1][GALNT1][TMTc4][ST6GALNAC3]	-0.08
Southern	GO Biological Processes	GO:0007369	Development	gastrulation	19_GO:0032502 developmental process	-2.2	5.4	3.8	4	3.1	1.5	ITGB2[LRP5][TASOR][KIF16B]	-0.077
Southern	GO Biological Processes	GO:0055080	Cellular process	monatomic cation homeostasis	19_GO:0042592 homeostatic process	-2.2	3.2	3.3	7	5.4	2	GRK2[GRM1][KCNQ1][RYR2][ERC2][TMTc4][SLC9A9]	-0.077
Southern	GO Biological Processes	GO:0001932	Cellular process	regulation of protein phosphorylation	19_GO:0050789 regulation of biological process	-2.2	2.9	3.2	8	6.2	2.1	IGF1[ITGB2][LP2][LRP5][KITL][TRAF6][XRC5][IL2][R2A2]	-0.077
Southern	GO Biological Processes	GO:0048660	Cardioregulation	regulation of smooth muscle cell proliferation	19_GO:0050789 regulation of biological process	-2.2	5.4	3.8	4	3.1	1.5	IGF1[MYB][PIK3R1][XRC5]	-0.077
Southern	GO Biological Processes	GO:0015850	Cellular process	organic hydroxy compound transport	19_GO:0051179 localization	-2.2	5.4	3.8	4	3.1	1.5	KCNQ1[SLC18A2][SLC22A2][SLC2A13]	-0.077
Southern	KEGG Pathway	hsa04211	Signal transduction	Longevity regulating pathway		-2.2	7.8	4.2	3	2.3	1.3	IGF1[PIK3R1][CREB3L1]	-0.073
Southern	GO Biological Processes	GO:0048762	Development	mesenchymal cell differentiation	19_GO:0032502 developmental process	-2.2	5.3	3.8	4	3.1	1.5	IGF1[KITL][SEMA3C][TASOR]	-0.073
Southern	GO Biological Processes	GO:0071478	Response to stimulus	cellular response to radiation	19_GO:0050896 response to stimulus	-2.1	5.3	3.8	4	3.1	1.5	PIK3R1[RP1][XRC5][JN080]	-0.067
Southern	GO Biological Processes	GO:0045995	Development	regulation of embryonic development	19_GO:0032502 developmental process	-2.1	7.7	4.2	3	2.3	1.3	LAMA2[LAMA4][JN080]	-0.067
Southern	GO Biological Processes	GO:0050804	Neural processes	modulation of chemical synaptic transmission	19_GO:0050789 regulation of biological process	-2.1	3.1	3.2	7	5.4	2	GLRA2[GRK2][GRM1][GRM8][KCNQ3][LAMA2][CELF4]	-0.067
Southern	GO Biological Processes	GO:0099177	Neural processes	regulation of trans-synaptic signaling	19_GO:0050789 regulation of biological process	-2.1	3.1	3.2	7	5.4	2	GLRA2[GRK2][GRM1][GRM8][KCNQ3][LAMA2][CELF4]	-0.065
Southern	GO Biological Processes	GO:0035967	Cellular process	cellular response to topologically incorrect protein	19_GO:0050896 response to stimulus	-2.1	7.6	4.2	3	2.3	1.3	TMTc4[CREB3L1]ASB11	-0.063
Southern	GO Biological Processes	GO:2000628	Metabolism	regulation of mRNA metabolic process	19_GO:0050789 regulation of biological process	-2.1	7.6	4.2	3	2.3	1.3	ESR1[MYB][TENT2]	-0.063
Southern	GO Biological Processes	GO:0033365	Cellular process	protein localization to organelle	19_GO:0051179 localization	-2.1	2.6	3.1	9	6.9	2.2	ESR1[KCNQ3][PIK3R1][RYR2][XRC5][DZIP1][TASOR][BBS9][TBC1D32]	-0.063
Southern	GO Biological Processes	GO:0050801	Cellular process	monatomic ion homeostasis	19_GO:0042592 homeostatic process	-2.1	3.1	3.2	7	5.4	2	GRK2[GRM1][KCNQ1][RYR2][ERC2][TMTc4][SLC9A9]	-0.062
Southern	GO Biological Processes	GO:0071897	Metabolism	DNA biosynthetic process	19_GO:0009987 cellular process	-2.1	7.4	4.1	3	2.3	1.3	POLA1[XRC5][POLN]	-0.046
Southern	Reactome Gene Sets	R-HSA-397014	Muscular process	Muscle contraction		-2.1	5.1	3.7	4	3.1	1.5	KCNQ1[RYR2][TTN][KCNK9]	-0.046
Southern	Reactome Gene Sets	R-HSA-382551	Cellular process	Transport of small molecules		-2.1	2.8	3.1	8	6.2	2.1	RYR2[SLC18A2][SLC22A2][ATP8A1][ATP8A2][ANO2][SLC2A13][SLC9A9]	-0.039
Southern	WikiPathways	WP117	Cellular process	GPCRs other		-2.1	7.3	4	3	2.3	1.3	ADRA1D[GRM1][GRM8]	-0.035
Southern	GO Biological Processes	GO:0006813	Cellular process	potassium ion transport	19_GO:0051179 localization	-2.1	5.1	3.6	4	3.1	1.5	KCNQ1[KCNQ3][KCNK9][SLC9A9]	-0.035
Southern	GO Biological Processes	GO:0005996	Carbohydrate metabolism	monosaccharide metabolic process	19_GO:0009987 cellular process	-2.1	5.1	3.6	4	3.1	1.5	FUT8[KCNQ1][LRP5][PGM1]	-0.035
Southern	GO Biological Processes	GO:0031589	Cellular process	cell-substrate adhesion	19_GO:0009987 cellular process	-2.1	5.1	3.6	4	3.1	1.5	ITGB2[PIK3R1][PARVA][NTN4]	-0.035
Southern	WikiPathways	WP4803	Cellular process	Ciliopathies		-2.1	5.1	3.6	4	3.1	1.5	RP1[DNAI1][BBS9][TBC1D32]	-0.035
Southern	GO Biological Processes	GO:0035282	Development	segmentation	19_GO:0032502 developmental process	-2.1	7.2	4	3	2.3	1.3	SEMA3C[COBL][TASOR]	-0.025
Southern	GO Biological Processes	GO:0003002	Development	regionalization	19_GO:0032502 developmental process	-2	3.4	3.2	6	4.6	1.8	LRP5[SEMA3C][COBL][TASOR][DNAI1][TBC1D32]	-0.0083
Southern	KEGG Pathway	hsa01522	Metabolism	Endocrine resistance		-2	7.1	4	3	2.3	1.3	ESR1[IGF1][PIK3R1]	-0.0083
Southern	GO Biological Processes	GO:0048863	Cellular process	stem cell differentiation	19_GO:0032502 developmental process	-2	4.9	3.6	4	3.1	1.5	ESR1[KITL][XRC5][SEMA3C]	-0.0083

Southern	GO Biological Processes	GO:1905952	Lipid metabolism	regulation of lipid localization	19_GO:0051179 localization	-2	4.9	3.6	4	3.1	1.5	MYB(ATP8A1 CKNK9 ATP8A2)	-0.0083
Southern	GO Biological Processes	GO:0002244	Cardioregulation	hematopoietic progenitor cell differentiation	19_GO:0032502 developmental process	-2	7	3.9	3	2.3	1.3	KITLG(XRCC5 TENT2)	-0.0083
Southern	GO Biological Processes	GO:0060047	Cardioregulation	heart contraction	19_GO:0032501 multicellular organismal process	-2	7	3.9	3	2.3	1.3	CKNQ1 RYR2 TTN	-0.0083
Southern	GO Biological Processes	GO:0060173	Development	limb development	19_GO:0032502 developmental process	-2	4.9	3.5	4	3.1	1.5	LRF5 SEMA3 CHD7 TBC1D32	-0.0083
Southern	GO Biological Processes	GO:0048736	Development	appendage development	19_GO:0032502 developmental process	-2	4.9	3.5	4	3.1	1.5	LRF5 SEMA3 CHD7 TBC1D32	-0.0083
Southern	GO Biological Processes	GO:0030312	Muscular process	muscle system process	19_GO:0032501 multicellular organismal process	-2	3.9	3.3	5	3.8	1.7	IGF1 CKNQ1 RYR2 TTN ATP8A2	-0.0079
Southern	GO Biological Processes	GO:0048661	Cardioregulation	positive regulation of smooth muscle cell proliferation	19_GO:0048518 positive regulation of biological process	-2	6.9	3.9	3	2.3	1.3	IGF1 MYB PIK3R1	-0.0049
Southern	GO Biological Processes	GO:0030048	Muscular process	actin filament-based movement	19_GO:0009987 cellular process	-2	6.9	3.9	3	2.3	1.3	CKNQ1 RYR2 PARVA	-0.0049
Southern	Reactome Gene Sets	R-HSA-1296071	Cellular process	Potassium Channels		-2	6.9	3.9	3	2.3	1.3	CKNQ1 CKNQ3 CKNK9	-0.0049
Southern	GO Biological Processes	GO:0010817	Metabolism	regulation of hormone levels	19_GO:0065007 biological regulation	-2	3	3.1	7	5.4	2	ESR1 CKNQ1 LRP5 MYBSL1 8A2 CKNK9 CHD7	-0.0023
Southern	GO Biological Processes	GO:0048562	Development	embryonic organ morphogenesis	19_GO:0032502 developmental process	-2	3.9	3.3	5	3.8	1.7	CKNQ1 JMP16 RYR2 ATP8A2 CHD7	-0.0015
Southern	GO Biological Processes	GO:0046474	Metabolism	glycerophospholipid biosynthetic process	19_GO:0009987 cellular process	-2	4.8	3.5	4	3.1	1.5	PIK3R1 FIG4 SMG1 TTC7B	-0.0015
Southern	WikiPathways	WP299	Signal transduction	Wnt signaling and pluripotency		-2	6.9	3.9	3	2.3	1.3	CTBP2 LRP5 PPP2R2A	-0.0015
Southern	GO Biological Processes	GO:0006351	Cellular process	DNA-templated transcription	19_GO:0009987 cellular process	-2	3	3	7	5.4	2	ESR1 BRF1 PIK3R1 TAF11 PHF3 NO80 CHD7	0
Southeastern	GO Biological Processes	GO:0042391	Neural processes	regulation of membrane potential	19_GO:0065007 biological regulation	-5.8	4.8	6.6	14	7.3	1.9	ACTN2 CACNB2 CHRN3 DCND2 GABR5 GRIN2A CKCN2 MEF2C NDP CHRNA6 ARL6 P5 CEL4 SLC4A11	-1.4
Southeastern	GO Biological Processes	GO:0050804	Neural processes	modulation of chemical synaptic transmission	19_GO:0050789 regulation of biological process	-5.2	4.3	6	14	7.3	1.9	CHRN3 EIF4E GRIN2A AGRM8 MEF2C JRA B5A TRIO CHRNA6 INAXPH1 PPP1R9A CEL4 CNTNAP4 CBLN2	-1.4
Southeastern	GO Biological Processes	GO:0099177	Neural processes	regulation of trans-synaptic signaling	19_GO:0050789 regulation of biological process	-5.2	4.3	6	14	7.3	1.9	CHRN3 EIF4E GRIN2A AGRM8 MEF2C JRA B5A TRIO CHRNA6 INAXPH1 PPP1R9A CEL4 CNTNAP4 CBLN2	-1.4
Southeastern	GO Biological Processes	GO:0099536	Neural processes	synaptic signaling	19_GO:0050789 regulation of biological process	-5	4.4	5.9	13	6.8	1.8	CACNB2 CHRN3 GABRA5 GRIN2A MEF2C COPR1 VDAC1 CHRNA6 RMBP2 CEL4 SPG11 CADPS2 CBLN2	-1.4
Southeastern	GO Biological Processes	GO:0047496	Cellular process	vesicle transport along microtubule	19_GO:0051179 localization	-5	17	8.8	5	2.6	1.2	AP3S1 AP3D1 KIF3A TRAK1 SPG11	-1.4
Southeastern	GO Biological Processes	GO:007268	Neural processes	chemical synaptic transmission	19_GO:0050789 regulation of biological process	-4.9	4.6	5.9	12	6.3	1.8	CACNB2 CHRN3 GABRA5 GRIN2A MEF2C VDAC1 CHRNA6 RMBP2 CEL4 SPG11 CADPS2 CBLN2	-1.4
Southeastern	GO Biological Processes	GO:0098916	Neural processes	anterograde trans-synaptic signaling	19_GO:0050789 regulation of biological process	-4.9	4.6	5.9	12	6.3	1.8	CACNB2 CHRN3 GABRA5 GRIN2A MEF2C VDAC1 CHRNA6 RMBP2 CEL4 SPG11 CADPS2 CBLN2	-1.4
Southeastern	GO Biological Processes	GO:0099537	Neural processes	trans-synaptic signaling	19_GO:0050789 regulation of biological process	-4.7	4.4	5.7	12	6.3	1.8	CACNB2 CHRN3 GABRA5 GRIN2A MEF2C VDAC1 CHRNA6 RMBP2 CEL4 SPG11 CADPS2 CBLN2	-1.3
Southeastern	Reactome Gene Sets	R-HSA-112316	Neural processes	Neuronal System		-4.6	4.7	5.7	11	5.8	1.7	ACTN2 CACNB2 CHRN3 GABRA5 GRIN2A CKCN2 CHRNA6 ARL6 P5 IL1RAPL2C ACNA23 SLITR4	-1.3
Southeastern	GO Biological Processes	GO:1904062	Cellular process	regulation of monoatomic cation transmembrane transport	19_GO:0051179 localization	-4.5	5.1	5.8	10	5.2	1.6	ACTN2 CACNB2 CALCAGRIN2A CKCN2 KELP DE4B VDAC1 GSTO1 AFG3L2	-1.3
Southeastern	GO Biological Processes	GO:0099518	Cellular process	vesicle cytoskeletal trafficking	19_GO:0051179 localization	-4.5	14	7.7	5	2.6	1.2	AP3S1 AP3D1 KIF3A TRAK1 SPG11	-1.3
Southeastern	GO Biological Processes	GO:0031175	Neural processes	neuron projection development	19_GO:0032502 developmental process	-4.3	3.3	5	15	7.9	1.9	CRK CTNND2 TRIP PP1R12 ANDP TRIO AFG3L2 TRAK1 PPP1R9A KHLH1 SPG11 ADGRV1 SLITR4 VPS13 BCAMSA1	-1.1
Southeastern	GO Biological Processes	GO:0034762	Cellular process	regulation of transmembrane transport	19_GO:0051179 localization	-4.2	4	5.2	12	6.3	1.8	ACTN2 CACNB2 CALCAGRIN2A CKCN2 KEL OPRM1 PDE4B VDAC1 GSTO1 ARL6 P5 AFG3L2	-1.1
Southeastern	GO Biological Processes	GO:0034330	Cellular process	cell junction organization	19_GO:0009987 cellular process	-4.2	3.6	5.1	13	6.8	1.8	ACTN2 CACNB2 CDH12 CRK CTNND2 DS G2 ECT2 GABRA5 NA AFG3L2 PEAK1 SPG11 CBLN2	-1.1
Southeastern	GO Biological Processes	GO:0060078	Neural processes	regulation of postsynaptic membrane potential	19_GO:0065007 biological regulation	-4.2	8.7	6.4	6	3.1	1.3	CHRN3 GABRA5 GRIN2A MEF2C CHRNA6 CEL4	-1.1
Southeastern	GO Biological Processes	GO:0034765	Cellular process	regulation of monoatomic ion transmembrane transport	19_GO:0051179 localization	-4.1	4.6	5.4	10	5.2	1.6	ACTN2 CACNB2 CALCAGRIN2A CKCN2 KEL PDE4B VDAC1 GSTO1 AFG3L2	-1.1
Southeastern	GO Biological Processes	GO:0060079	Neural processes	excitatory postsynaptic potential	19_GO:0032501 multicellular organismal process	-4.1	11	6.9	5	2.6	1.2	CHRN3 GRIN2A MEF2C CHRNA6 CEL4	-1.1
Southeastern	GO Biological Processes	GO:0016055	Signal transduction	Wnt signaling pathway	19_GO:0050896 response to stimulus	-4.1	5	5.4	9	4.7	1.5	CTNND2 NDP ROR1 RAB5A TNKS MED12 BRD7 ZNF3 UBAC2	-1
Southeastern	GO Biological Processes	GO:0099565	Neural processes	chemical synaptic transmission, postsynaptic	19_GO:0032501 multicellular organismal process	-3.9	10	6.6	5	2.6	1.2	CHRN3 GRIN2A MEF2C CHRNA6 CEL4	-0.91
Southeastern	GO Biological Processes	GO:0008088	Neural processes	axo-dendritic transport	19_GO:0051179 localization	-3.8	10	6.4	5	2.6	1.2	AP3S1 AP3D1 KIF3A TRAK1 SPG11	-0.87
Southeastern	Reactome Gene Sets	R-HSA-112315	Cellular process	Transmission across Chemical Synapses		-3.8	5.3	5.3	8	4.2	1.4	ACTN2 CACNB2 CHRN3 GABRA5 GRIN2A CHRNA6 ARL6 P5 CACNA2D3 BMP4 CALC MATN1 MEF2C DDR2 ADGRV1	-0.87
Southeastern	GO Biological Processes	GO:0030278	Ossification	regulation of ossification	19_GO:0032501 multicellular organismal process	-3.8	7.4	5.8	6	3.1	1.3	BMP4 CALC MATN1 MEF2C DDR2 ADGRV1	-0.86
Southeastern	GO Biological Processes	GO:0030500	Ossification	regulation of bone mineralization	19_GO:0032502 developmental process	-3.8	9.7	6.3	5	2.6	1.2	BMP4 MATN1 MEF2C DDR2 ADGRV1	-0.86
Southeastern	Reactome Gene Sets	R-HSA-196854	Metabolism	Metabolism of vitamins and cofactors		-3.7	5.9	5.4	7	3.7	1.4	GPC5 MOCS2 MTR PTS GSTO1 MTFHD1L COQ8A	-0.86
Southeastern	GO Biological Processes	GO:1901699	Cellular process	cellular response to nitrogen compound	19_GO:0050896 response to stimulus	-3.7	3.3	4.6	13	6.8	1.8	ACTN2 CHRN3 AP3S1 CPS1 CRK MEF2C MTR DDR2 OPRM1 CHRNA6 AFG3L2 WDTC1 DENND4C	-0.86
Southeastern	GO Biological Processes	GO:0007610	Behavior	behavior	19_GO:0032501 multicellular organismal process	-3.7	3.3	4.6	13	6.8	1.8	CALCA EIF4E GABRA5 GRIN2A MEF2C NDP OPRM1 VDAC1 ARL6 P5 KHLH1 SPG11 VPS13 BMFSD8	-0.86
Southeastern	GO Biological Processes	GO:0072384	Cellular process	organelle transport along microtubule	19_GO:0051179 localization	-3.7	9.2	6.1	5	2.6	1.2	AP3S1 AP3D1 KIF3A TRAK1 SPG11	-0.86
Southeastern	GO Biological Processes	GO:0043269	Cellular process	regulation of monoatomic ion transport	19_GO:0051179 localization	-3.7	3.7	4.7	11	5.8	1.7	ACTN2 CACNB2 CALCAGRIN2A CKCN2 KEL PDE4B VDAC1 GSTO1 AFG3L2 SPG11	-0.86
Southeastern	GO Biological Processes	GO:0008089	Neural processes	anterograde axonal transport	19_GO:0051179 localization	-3.7	13	6.8	4	2.1	1	AP3S1 AP3D1 KIF3A TRAK1	-0.86
Southeastern	GO Biological Processes	GO:0010959	Cellular process	regulation of metal ion transport	19_GO:0051179 localization	-3.6	3.9	4.7	10	5.2	1.6	ACTN2 CACNB2 CALCAGRIN2A CKCN2 KEL PDE4B VDAC1 GSTO1 AFG3L2 SPG11	-0.84
Southeastern	Reactome Gene Sets	R-HSA-113510	Cellular process	E2F mediated regulation of DNA replication		-3.6	24	8.1	3	1.6	0.9	PRIM2 ORC6 PPP2R3B	-0.84
Southeastern	GO Biological Processes	GO:0030225	Immunity	macrophage differentiation	19_GO:0032502 developmental process	-3.6	13	6.7	4	2.1	1	BMP4 NDP L3MBTL3 MFSD8	-0.84
Southeastern	GO Biological Processes	GO:1904063	Cellular process	negative regulation of cation transmembrane transport	19_GO:0051179 localization	-3.5	8.6	5.8	5	2.6	1.2	ACTN2 CALCA KEL VDAC1 GSTO1	-0.8
Southeastern	GO Biological Processes	GO:0034763	Cellular process	negative regulation of transmembrane transport	19_GO:0051179 localization	-3.5	6.7	5.4	6	3.1	1.3	ACTN2 CALCA KEL VDAC1 GSTO1 ARL6 P5	-0.8
Southeastern	GO Biological Processes	GO:0014910	Cardioregulation	regulation of smooth muscle cell migration	19_GO:0040011 locomotion	-3.5	8.4	5.8	5	2.6	1.2	BMP4 CRK MEF2C DDR2 DOCK5	-0.77
Southeastern	GO Biological Processes	GO:1904752	Cardioregulation	regulation of vascular associated smooth muscle cell migration	19_GO:0040011 locomotion	-3.4	12	6.3	4	2.1	1	BMP4 MEF2C DDR2 DOCK5	-0.72
Southeastern	GO Biological Processes	GO:0006869	Lipid metabolism	lipid transport	19_GO:0051179 localization	-3.4	4.1	4.6	9	4.7	1.5	FABP1 ABCD3 VDAC1 PLSCR2 SPG11 PLA2G12A XKR4 OSBP1 VPS13B	-0.7
Southeastern	GO Biological Processes	GO:0034766	Cellular process	negative regulation of monoatomic ion transmembrane transport	19_GO:0051179 localization	-3.4	8	5.6	5	2.6	1.2	ACTN2 CALCA KEL VDAC1 GSTO1	-0.7
Southeastern	GO Biological Processes	GO:0001501	Ossification	skeletal system development	19_GO:0032502 developmental process	-3.4	3.4	4.4	11	5.8	1.7	BMP4 MATN1 MEF2C NPR3 DDR2 PCKS5 MED12 SATB2 MTFHD1L TIPARP BNC2	-0.7
Southeastern	GO Biological Processes	GO:0060537	Muscular process	muscle tissue development	19_GO:0032502 developmental process	-3.3	4	4.5	9	4.7	1.5	ACTN2 BMP4 CNTN2 DSG2 KEL MEF2C MAHL1 TIPARP SPG11	-0.68

Southeastern	GO Biological Processes	GO:0070167	Ossification	regulation of biomineral tissue development	19_GO:0032502 developmental process	-3.3	7.7	5.4	5	2.6	1.2	BMP4MATN1MEF2CDDR2ADGRV1	-0.67
Southeastern	GO Biological Processes	GO:0042692	Muscular process	muscle cell differentiation	19_GO:0032502 developmental process	-3.3	4.4	4.6	8	4.2	1.4	ACTN2BMP4KELMEF2CMAML1AFG3L2DOCK5SPG11	-0.67
Southeastern	GO Biological Processes	GO:0048589	Growth	developmental growth	19_GO:0040007 growth	-3.3	3.6	4.4	10	5.2	1.6	BMP4MATN1DDR2MEDI2WDTC1BNC2KIF26BSPG11VPS13BMFSD8	-0.67
Southeastern	GO Biological Processes	GO:0040007	Growth	growth	19_GO:0040007 growth	-3.3	3.6	4.4	10	5.2	1.6	BMP4MATN1DDR2MEDI2WDTC1BNC2KIF26BSPG11VPS13BMFSD8	-0.67
Southeastern	Reactome Gene Sets	R-HSA-3700989	Cellular process	Transcriptional Regulation by TP53		-3.3	4.4	4.6	8	4.2	1.4	RAD1CRADDIBRD1BRD7RRM2BJMYISLC38A9R1CTOR	-0.67
Southeastern	GO Biological Processes	GO:0002573	Immunity	myeloid leukocyte differentiation	19_GO:0032502 developmental process	-3.2	5.9	5	6	3.1	1.3	BMP4NDP5H3PXD2AJL3MBTL3TMEM64MFS8	-0.65
Southeastern	GO Biological Processes	GO:0051146	Muscular process	striated muscle cell differentiation	19_GO:0032502 developmental process	-3.2	5	4.7	7	3.7	1.4	ACTN2BMP4KELMEF2CMAML1DOCK5SPG11	-0.65
Southeastern	GO Biological Processes	GO:0050808	Neural processes	synapse organization	19_GO:0009987 cellular process	-3.2	3.9	4.4	9	4.7	1.5	ACTN2CACNB2CRKCTNNND2GABRA5I1NA1AFG3L2SPG11CBLN2	-0.65
Southeastern	GO Biological Processes	GO:0073346	Cellular process	regulation of mitotic cell cycle	19_GO:0050789 regulation of biological process	-3.2	3.3	4.2	11	5.8	1.7	BMP4CCND3EIF4EDDR2CDC14ACRADDBRD7RRM2BYTHDC2NEK7FBXO43	-0.64
Southeastern	GO Biological Processes	GO:0006979	Mitochondrial regulation	response to oxidative stress	19_GO:0050896 response to stimulus	-3.2	3.8	4.4	9	4.7	1.5	CRKECT2FABP1ARL6IP5PSIP1RRM2B5TK26SLC4A11ERCC6L2	-0.62
Southeastern	GO Biological Processes	GO:0008283	Cellular process	cell population proliferation	19_GO:0009987 cellular process	-3.2	2.9	4	13	6.8	1.8	BMP4CALCACCN3CRKB4GALT1MEF2CNDPNR3ROR1DDR2USP28NAA35ZNR3	-0.62
Southeastern	GO Biological Processes	GO:0048705	Muscular process	skeletal system morphogenesis	19_GO:0032502 developmental process	-3.2	4.8	4.6	7	3.7	1.4	BMP4MATN1MEF2CMEDI2SATB2MTHFD1LTPARP	-0.62
Southeastern	GO Biological Processes	GO:0140588	Cellular process	chromatin looping	19_GO:0009987 cellular process	-3.2	5.7	4.8	6	3.1	1.3	CHD1AFG3L2MTRXDDX4YTHDC2CHD6	-0.62
Southeastern	GO Biological Processes	GO:0048771	Development	tissue remodeling	19_GO:0032501 multicellular organismal process	-3.2	7.1	5.2	5	2.6	1.2	CSPG4MEF2CNDPNR3DOCK5	-0.62
Southeastern	GO Biological Processes	GO:0007274	Neural processes	neuromuscular synaptic transmission	19_GO:0050789 regulation of biological process	-3.1	17	6.7	3	1.6	0.9	CHRN3CHRNA6RIMBP2	-0.62
Southeastern	GO Biological Processes	GO:0003416	Ossification	endochondral bone growth	19_GO:0040007 growth	-3.1	17	6.7	3	1.6	0.9	MATN1DDR2BNC2	-0.62
Southeastern	GO Biological Processes	GO:0030099	Neural processes	myeloid cell differentiation	19_GO:0032502 developmental process	-3.1	4.2	4.4	8	4.2	1.4	BMP4MEF2CNDP5H3PXD2ABRD1L3MBTL3TMEM64MFS8	-0.61
Southeastern	GO Biological Processes	GO:0008930	Neural processes	axonal transport	19_GO:0051179 localization	-3.1	9.8	5.6	4	2.1	1	AP3S1AP3D1KIF3ATRAK1	-0.6
Southeastern	GO Biological Processes	GO:0016358	Neural processes	dendrite development	19_GO:0032502 developmental process	-3.1	6.9	5	5	2.6	1.2	CRKCTNNND2NDPTRAK1KLHL1	-0.58
Southeastern	GO Biological Processes	GO:0010876	Lipid metabolism	lipid localization	19_GO:0051179 localization	-3.1	3.7	4.2	9	4.7	1.5	FABP1ABCD3VDAC1PLSCR2SPG11PLA2G12AXKR4OSBP10VPS13B	-0.58
Southeastern	GO Biological Processes	GO:0006575	Metabolism	modified amino acid metabolic process	19_GO:0009987 cellular process	-3.1	5.4	4.7	6	3.1	1.3	MTRNDPGSTO1ARL6IP5MTHFD1LOSBPL10	-0.57
Southeastern	GO Biological Processes	GO:1903169	Cellular process	regulation of calcium ion transmembrane transport	19_GO:0051179 localization	-3.1	5.4	4.7	6	3.1	1.3	CACNB2CALCAPDE4BVDAC1GSTO1AFG3L2	-0.57
Southeastern	GO Biological Processes	GO:0006937	Muscular process	regulation of muscle contraction	19_GO:0032501 multicellular organismal process	-3.1	5.4	4.7	6	3.1	1.3	CACNB2CALCADSG2PDE4BGSTO1DOCK5	-0.57
Southeastern	GO Biological Processes	GO:0051650	Cellular process	establishment of vesicle localization	19_GO:0051179 localization	-3	5.3	4.6	6	3.1	1.3	AP3S1AP3D1KIF3ATRAK1SPG11CADPS2	-0.54
Southeastern	GO Biological Processes	GO:0008868	Ossification	bone growth	19_GO:0040007 growth	-3	15	6.4	3	1.6	0.9	MATN1DDR2BNC2	-0.54
Southeastern	GO Biological Processes	GO:0051924	Cellular process	regulation of calcium ion transport	19_GO:0051179 localization	-2.9	4.4	4.3	7	3.7	1.4	CACNB2CALCAPDE4BVDAC1GSTO1AFG3L2SPG11	-0.48
Southeastern	GO Biological Processes	GO:0042558	Metabolism	pteridine-containing compound metabolic process	19_GO:0009987 cellular process	-2.9	14	6.1	3	1.6	0.9	MTRP1SMTHFD1L	-0.48
Southeastern	GO Biological Processes	GO:0009170	Neural processes	postsynaptic modulation of chemical synaptic transmission	19_GO:0050789 regulation of biological process	-2.9	14	6.1	3	1.6	0.9	EIF4ETRIOINA	-0.48
Southeastern	GO Biological Processes	GO:0001662	Behavior	behavioral fear response	19_GO:0032501 multicellular organismal process	-2.9	14	6	3	1.6	0.9	EIF4EGABRA5VDAC1	-0.45
Southeastern	Reactome Gene Sets	R-HSA-5633007	Cellular process	Regulation of TP53 Activity		-2.9	6.2	4.7	5	2.6	1.2	RAD1BRD1BRD7MYR1CTOR	-0.45
Southeastern	WikiPathways	WP2118	Cardioregulation	Arrhythmogenic right ventricular cardiomyopathy		-2.9	8.5	5.2	4	2.1	1	ACTN2CACNB2DSG2CACNA2D3	-0.45
Southeastern	GO Biological Processes	GO:0014706	Muscular process	striated muscle tissue development	19_GO:0032502 developmental process	-2.9	3.8	4.1	8	4.2	1.4	ACTN2BMP4CCNT2DSG2KELMEF2CMAML1SPG11	-0.45
Southeastern	GO Biological Processes	GO:0010564	Cellular process	regulation of cell cycle process	19_GO:0050789 regulation of biological process	-2.9	2.7	3.7	13	6.8	1.8	BMP4CCND3ECT2DDR2RAD1CDC14ATNKSICRADDSMC4BRD7RRM2B5USP28FBXO43	-0.45
Southeastern	GO Biological Processes	GO:0002209	Behavior	behavioral defense response	19_GO:0032501 multicellular organismal process	-2.9	14	5.9	3	1.6	0.9	EIF4EGABRA5VDAC1	-0.45
Southeastern	GO Biological Processes	GO:0043271	Cellular process	negative regulation of monatomic ion transport	19_GO:0051179 localization	-2.8	6.1	4.6	5	2.6	1.2	ACTN2CALCAKELVDAC1GSTO1	-0.44
Southeastern	GO Biological Processes	GO:0014902	Muscular process	myotube differentiation	19_GO:0032502 developmental process	-2.8	8.2	5.1	4	2.1	1	KELMEF2DOCK5SPG11	-0.44
Southeastern	GO Biological Processes	GO:0051648	Cellular process	vesicle localization	19_GO:0051179 localization	-2.8	4.9	4.4	6	3.1	1.3	AP3S1AP3D1KIF3ATRAK1SPG11CADPS2	-0.44
Southeastern	GO Biological Processes	GO:0045787	Cellular process	positive regulation of cell cycle	19_GO:0048518 positive regulation of biological process	-2.8	3.7	4	8	4.2	1.4	CCND3ECT2EIF4EDDR2CDC14ASMC4RRM2BYTHDC2	-0.41
Southeastern	GO Biological Processes	GO:0071466	Response to stimulus	cellular response to xenobiotic stimulus	19_GO:0050896 response to stimulus	-2.8	4.8	4.3	6	3.1	1.3	CRY2MEF2CPPP1R12APDE4BGSTO1ACER2	-0.41
Southeastern	GO Biological Processes	GO:0003161	Cardioregulation	cardiac conduction system development	19_GO:0032502 developmental process	-2.8	13	5.7	3	1.6	0.9	BMP4DSG2MAML1	-0.41
Southeastern	GO Biological Processes	GO:0048706	Development	embryonic skeletal system development	19_GO:0032502 developmental process	-2.8	5.9	4.5	5	2.6	1.2	BMP4PCSK5MEDI2SATB2MTHFD1L	-0.4
Southeastern	GO Biological Processes	GO:0016310	Cellular process	phosphorylation	19_GO:0009987 cellular process	-2.7	3.3	3.8	9	4.7	1.5	CALCADDR2TNKSMAML1STK26CO8APEAK1NEK7R1CTOR	-0.39
Southeastern	GO Biological Processes	GO:0006520	Metabolism	amino acid metabolic process	19_GO:0009987 cellular process	-2.7	4.1	4.1	7	3.7	1.4	AUIHCPS1DARS1DPYDMTRNDPPTS	-0.39
Southeastern	GO Biological Processes	GO:0000902	Cellular process	cell morphogenesis	19_GO:0032502 developmental process	-2.7	2.7	3.6	12	6.3	1.8	CDH12CTNNND2ECT2MATN1MEF2CPIP1R12ANDP1TRIOAFG3L2TRAK1SPG11SLTRK4	-0.38
Southeastern	GO Biological Processes	GO:0042596	Response to stimulus	fear response	19_GO:0032501 multicellular organismal process	-2.7	12	5.6	3	1.6	0.9	EIF4EGABRA5VDAC1	-0.38
Southeastern	GO Biological Processes	GO:0009410	Response to stimulus	response to xenobiotic stimulus	19_GO:0050896 response to stimulus	-2.7	3.3	3.8	9	4.7	1.5	CPS1CRYZGRIN2AMEF2CPPP1R12APDE4BACD3GSTO1ACER2	-0.38
Southeastern	GO Biological Processes	GO:0006874	Cellular process	intracellular calcium ion homeostasis	19_GO:0042592 homeostatic process	-2.7	4.7	4.2	6	3.1	1.3	CACNB2CALCAKELAFG3L2ATP13A3TMEM64	-0.38
Southeastern	GO Biological Processes	GO:0030029	Muscular process	actin filament-based process	19_GO:0009987 cellular process	-2.7	2.8	3.7	11	5.8	1.7	ACTN2CACNB2CRKCCNN2MKLN1SH3KBP1PPP1R19AKLHL1EPB41LAJMYR1CTOR	-0.38
Southeastern	WikiPathways	WP4022	Metabolism	Pyrimidine metabolism		-2.7	7.6	4.8	4	2.1	1	DPYDPRIM2RRM2BNT5M	-0.37
Southeastern	GO Biological Processes	GO:0061061	Muscular process	muscle structure development	19_GO:0032502 developmental process	-2.7	3	3.7	10	5.2	1.6	ACTN2BMP4CCNT2KELMEF2CMAML1AFG3L2DOCK5SPG11VPS13B	-0.37
Southeastern	GO Biological Processes	GO:0001974	Cardioregulation	blood vessel remodeling	19_GO:0032501 multicellular organismal process	-2.7	12	5.5	3	1.6	0.9	MEF2CNDPNR3	-0.37
Southeastern	GO Biological Processes	GO:0007611	Neural processes	learning or memory	19_GO:0032501 multicellular organismal process	-2.7	3.9	3.9	7	3.7	1.4	GABRA5GRIN2AMEF2CVDAC1ARL6IP5SPG11VPS13B	-0.35
Southeastern	KEGG Pathway	hsa05412	Cardioregulation	Arrhythmogenic right ventricular cardiomyopathy		-2.7	7.4	4.7	4	2.1	1	ACTN2CACNB2DSG2CACNA2D3	-0.35
Southeastern	GO Biological Processes	GO:0086065	Cardioregulation	cell communication involved in cardiac conduction	19_GO:0032501 multicellular organismal process	-2.7	12	5.4	3	1.6	0.9	CACNB2DSG2KCNN2	-0.35
Southeastern	GO Biological Processes	GO:0009394	Metabolism	2'-deoxyribonucleotide metabolic process	19_GO:0009987 cellular process	-2.6	11	5.3	3	1.6	0.9	DPYDRRM2BNT5M	-0.32
Southeastern	GO Biological Processes	GO:0033555	Response to stimulus	multicellular organismal response to stress	19_GO:0032501 multicellular organismal process	-2.6	7.1	4.6	4	2.1	1	CALCAEIF4EGABRA5VDAC1	-0.32
Southeastern	GO Biological Processes	GO:0019692	Metabolism	deoxyribose phosphate metabolic process	19_GO:0009987 cellular process	-2.6	11	5.3	3	1.6	0.9	DPYDRRM2BNT5M	-0.32
Southeastern	GO Biological Processes	GO:0007528	Neural processes	neuromuscular junction development	19_GO:0009987 cellular process	-2.6	11	5.3	3	1.6	0.9	CACNB2AFG3L2SPG11	-0.32

Southeastern	GO Biological Processes	GO:2001259	Cellular process	positive regulation of cation channel activity	19_GO:0051179 localization	-2.6	11	5.3	3	1.6	0.9	ACTN2 CACNB2 GSTO1	-0.32
Southeastern	GO Biological Processes	GO:0009262	Metabolism	deoxyribonucleotide metabolic process	19_GO:0009987 cellular process	-2.6	11	5.3	3	1.6	0.9	DPYD RRM2 BNT5M	-0.32
Southeastern	GO Biological Processes	GO:0048489	Neural processes	synaptic vesicle transport	19_GO:0051179 localization	-2.6	11	5.3	3	1.6	0.9	AP3S1 AP3D1 SPG11	-0.32
Southeastern	WikiPathways	WP4352	Cellular process	Ciliary landscape		-2.6	4.4	4	6	3.1	1.3	MKLN1 SMC4 AFG3L2 CNOT10 DOCK5 NEK7	-0.32
Southeastern	GO Biological Processes	GO:0051851	Response to stimulus	modulation by host of symbiont process	19_GO:0044419 biological process involved in interspecies interaction between organisms	-2.6	7	4.6	4	2.1	1	CNT2 CHD1 RAB5A YTHDC2	-0.32
Southeastern	GO Biological Processes	GO:0030501	Ossification	positive regulation of bone mineralization	19_GO:0032502 developmental process	-2.6	11	5.2	3	1.6	0.9	BMP4 MEF2C ADGRV1	-0.3
Southeastern	GO Biological Processes	GO:0043410	Signal transduction	positive regulation of MAPK cascade	19_GO:0048518 positive regulation of biological process	-2.5	3.1	3.6	9	4.7	1.5	BMP4 CRK CSPG4 MEF2C DDR2 OPRM1 ARL6IP5 KSR2 RELL1	-0.28
Southeastern	GO Biological Processes	GO:0070588	Cellular process	calcium ion transmembrane transport	19_GO:0051179 localization	-2.5	4.3	3.9	6	3.1	1.3	CACNB2 GRIN2A OPRM1 VDAC1 AFG3L2 CACNA2D3	-0.28
Southeastern	GO Biological Processes	GO:0048701	Ossification	embryonic cranial skeleton morphogenesis	19_GO:0032502 developmental process	-2.5	11	5.1	3	1.6	0.9	BMP4 MED12 MTFHD1L	-0.28
Southeastern	GO Biological Processes	GO:0044283	Metabolism	small molecule biosynthetic process	19_GO:0009987 cellular process	-2.5	3.1	3.6	9	4.7	1.5	CPS1 DPYD MTOR TRPT5 ABCD3 PP1P5K2 MT HFD1L LCOQ8A ACER2	-0.28
Southeastern	GO Biological Processes	GO:0051051	Cellular process	negative regulation of transport	19_GO:0051179 localization	-2.5	3.1	3.6	9	4.7	1.5	ACTN2 CALCA IL12A KELOPRM1 VDAC1 GSTO1 ARL6IP5 UBAC2	-0.28
Southeastern	GO Biological Processes	GO:0071375	Metabolism	cellular response to peptide hormone stimulus	19_GO:0050896 response to stimulus	-2.5	3.7	3.8	7	3.7	1.4	ACTN2 AP3S1 CPS1 CRK DDR2 WDC1 DENND4C	-0.28
Southeastern	GO Biological Processes	GO:0072331	Cellular process	signal transduction by p53 class mediator	19_GO:0050896 response to stimulus	-2.5	6.7	4.4	4	2.1	1	CRADD USP28 JMY ACER2	-0.28
Southeastern	GO Biological Processes	GO:0095500	Signal transduction	acetylcholine receptor signaling pathway	19_GO:0050896 response to stimulus	-2.5	10	5.1	3	1.6	0.9	CHRN3 OPRM1 CHRNA6	-0.27
Southeastern	GO Biological Processes	GO:0055007	Cardioregulation	cardiac muscle cell differentiation	19_GO:0032502 developmental process	-2.5	6.7	4.4	4	2.1	1	ACTN2 BMP4 MEF2C MAM1	-0.27
Southeastern	GO Biological Processes	GO:0010948	Cellular process	negative regulation of cell cycle process	19_GO:0048519 negative regulation of biological process	-2.5	3.7	3.7	7	3.7	1.4	BMP4 RAD1 TNKS CRADD BRD7 USP28 FBXO43	-0.27
Southeastern	GO Biological Processes	GO:0034329	Cellular process	cell junction assembly	19_GO:0009987 cellular process	-2.5	3.7	3.7	7	3.7	1.4	ACTN2 CHD1 2 CRK ECT2 GABRA5 PEAK1 CBLN2	-0.27
Southeastern	GO Biological Processes	GO:0048704	Muscular process	embryonic skeletal system morphogenesis	19_GO:0032502 developmental process	-2.5	6.6	4.4	4	2.1	1	BMP4 MED12 SATB2 MTFHD1L	-0.27
Southeastern	GO Biological Processes	GO:0045666	Neural processes	positive regulation of neuron differentiation	19_GO:0032502 developmental process	-2.5	6.6	4.4	4	2.1	1	BMP4 ECT2 MEF2C GDPD5	-0.27
Southeastern	GO Biological Processes	GO:0051784	Cellular process	negative regulation of nuclear division	19_GO:0048519 negative regulation of biological process	-2.5	10	5	3	1.6	0.9	BMP4 RAD1 FBXO43	-0.27
Southeastern	GO Biological Processes	GO:0034599	Mitochondrial regulation	cellular response to oxidative stress	19_GO:0050896 response to stimulus	-2.5	4.2	3.8	6	3.1	1.3	ECT2 FABP1 ARL6IP5 SLC4A11 ERCC6L2	-0.27
Southeastern	GO Biological Processes	GO:0006468	Cellular process	protein phosphorylation	19_GO:0009987 cellular process	-2.5	3.3	3.6	8	4.2	1.4	CALCA DDR2 TNKS MAM1 STK26 PEAK1 NEK7 RICTOR	-0.26
Southeastern	WikiPathways	WP437	Signal transduction	EGF EGFR signaling		-2.5	5	4	5	2.6	1.2	CRK MEF2C RAB5A SH3 KBP1 RICTOR	-0.26
Southeastern	GO Biological Processes	GO:0043065	Cellular process	positive regulation of apoptotic process	19_GO:0048518 positive regulation of biological process	-2.5	2.8	3.4	10	5.2	1.6	BMP4 ECT2 B4GALT1 GRIN2A IL12A MEF2C VDAC1 CRADD ARL6IP5 JMY	-0.26
Southeastern	Reactome Gene Sets	R-HSA-1793185	Metabolism	Chondroitin sulfate/dermatan sulfate metabolism		-2.5	9.9	4.9	3	1.6	0.9	CSPG4 DCN GPC5	-0.26
Southeastern	GO Biological Processes	GO:1905145	Cellular process	cellular response to acetylcholine	19_GO:0050896 response to stimulus	-2.5	9.9	4.9	3	1.6	0.9	CHRN3 OPRM1 CHRNA6	-0.26
Southeastern	GO Biological Processes	GO:0046173	Metabolism	polyol biosynthetic process	19_GO:0009987 cellular process	-2.5	9.9	4.9	3	1.6	0.9	PTSP PPP5K2 ACER2	-0.26
Southeastern	GO Biological Processes	GO:0001822	Osmoregulation	kidney development	19_GO:0032502 developmental process	-2.5	3.6	3.7	7	3.7	1.4	BMP4 MEF2C CPSK5 ADAMTS6 TIPARP RM2B KIF26B	-0.26
Southeastern	GO Biological Processes	GO:0032446	Cellular process	protein modification by small protein conjugation	19_GO:0009987 cellular process	-2.4	2.6	3.4	11	5.8	1.7	TRIM23 NDPC CNOT4 TNKS UBA3 MED12 WDC1 TRIM2 ZNF3 FBXO43 NHLRC3	-0.26
Southeastern	GO Biological Processes	GO:0045786	Cellular process	negative regulation of cell cycle	19_GO:0048519 negative regulation of biological process	-2.4	3.2	3.5	8	4.2	1.4	BMP4 RAD1 TNKS CRADD BRD7 USP28 YTHDC2 FBXO43	-0.26
Southeastern	GO Biological Processes	GO:0055074	Cellular process	calcium ion homeostasis	19_GO:0042592 homeostatic process	-2.4	4.1	3.8	6	3.1	1.3	CACNB2 CALCA CAKEL AFG3L2 ATP13A3 TMEM64	-0.26
Southeastern	GO Biological Processes	GO:1903170	Cellular process	negative regulation of calcium ion transmembrane transport	19_GO:0051179 localization	-2.4	9.7	4.9	3	1.6	0.9	CALCA VDAC1 GSTO1	-0.26
Southeastern	GO Biological Processes	GO:0007215	Signal transduction	glutamate receptor signaling pathway	19_GO:0050896 response to stimulus	-2.4	9.7	4.9	3	1.6	0.9	GRIN2A GRM8 MEF2C	-0.26
Southeastern	GO Biological Processes	GO:0071560	Growth	cellular response to transforming growth factor beta stimulus	19_GO:0050896 response to stimulus	-2.4	4.9	3.9	5	2.6	1.2	CRK LTBP2 MEF2C NDP DDR2	-0.24
Southeastern	GO Biological Processes	GO:0070647	Cellular process	protein modification by small protein conjugation or removal	19_GO:0009987 cellular process	-2.4	2.4	3.3	12	6.3	1.8	TRIM23 NDPC CNOT4 TNKS UBA3 MED12 WDC1 TRIM2 USP28 ZNF3 FBXO43 NHLRC3	-0.23
Southeastern	GO Biological Processes	GO:0098926	Neural processes	postsynaptic signal transduction	19_GO:0050896 response to stimulus	-2.4	9.3	4.7	3	1.6	0.9	CHRN3 OPRM1 CHRNA6	-0.22
Southeastern	GO Biological Processes	GO:0014911	Cardioregulation	positive regulation of smooth muscle cell migration	19_GO:0040011 locomotion	-2.4	9.3	4.7	3	1.6	0.9	CRK DDR2 DOCK5	-0.22
Southeastern	GO Biological Processes	GO:1905144	Cellular process	response to acetylcholine	19_GO:0050896 response to stimulus	-2.4	9.3	4.7	3	1.6	0.9	CHRN3 OPRM1 CHRNA6	-0.22
Southeastern	GO Biological Processes	GO:0098660	Cellular process	inorganic ion transmembrane transport	19_GO:0051179 localization	-2.4	2.4	3.2	12	6.3	1.8	CACNB2 GABRA5 GRIN2A C CN2 KELOPRM1 VDAC1 AP3D1 AFG3L2 CACNA2D3 SLC4A11 MFSD8	-0.22
Southeastern	GO Biological Processes	GO:0043085	Cellular process	positive regulation of catalytic activity	19_GO:0065007 biological regulation	-2.4	2.7	3.3	10	5.2	1.6	CALCA CCND3 ECT2 MEF2C NPR3 DDR2 PRIM2 CRADD ARL6IP5 TBC1D2	-0.22
Southeastern	GO Biological Processes	GO:0043068	Cellular process	positive regulation of programmed cell death	19_GO:0048518 positive regulation of biological process	-2.4	2.7	3.3	10	5.2	1.6	BMP4 ECT2 B4GALT1 GRIN2A IL12A MEF2C VDAC1 CRADD ARL6IP5 JMY	-0.22
Southeastern	GO Biological Processes	GO:0010562	Metabolism	positive regulation of phosphorus metabolic process	19_GO:0048518 positive regulation of biological process	-2.4	2.9	3.4	9	4.7	1.5	BMP4 CALCA CCND3 CSPG4 ECT2 IL12A MEF2C DDR2 RICTOR	-0.22
Southeastern	GO Biological Processes	GO:0045937	Metabolism	positive regulation of phosphate metabolic process	19_GO:0048518 positive regulation of biological process	-2.4	2.9	3.4	9	4.7	1.5	BMP4 CALCA CCND3 CSPG4 ECT2 IL12A MEF2C DDR2 RICTOR	-0.22
Southeastern	GO Biological Processes	GO:0072001	Osmoregulation	renal system development	19_GO:0032502 developmental process	-2.4	3.5	3.5	7	3.7	1.4	BMP4 MEF2C CPSK5 ADAMTS6 TIPARP RM2B KIF26B	-0.22
Southeastern	GO Biological Processes	GO:0051155	Muscular process	positive regulation of striated muscle cell differentiation	19_GO:0032502 developmental process	-2.4	9.1	4.7	3	1.6	0.9	BMP4 MEF2C MAM1	-0.22
Southeastern	GO Biological Processes	GO:0016567	Cellular process	protein ubiquitination	19_GO:0009987 cellular process	-2.4	2.7	3.3	10	5.2	1.6	TRIM23 NDPC CNOT4 TNKS MED12 WDC1 TRIM2 ZNF3 FBXO43 NHLRC3	-0.22
Southeastern	GO Biological Processes	GO:2001252	Cellular process	positive regulation of chromosome organization	19_GO:0048518 positive regulation of biological process	-2.4	6	4.1	4	2.1	1	TNKS SMC4 ACTR8 NEK7	-0.21
Southeastern	GO Biological Processes	GO:0071559	Growth	response to transforming growth factor beta	19_GO:0050896 response to stimulus	-2.3	4.7	3.8	5	2.6	1.2	CRK LTBP2 MEF2C NDP DDR2	-0.21
Southeastern	GO Biological Processes	GO:0099003	Neural processes	vesicle-mediated transport in synapse	19_GO:0051179 localization	-2.3	4.7	3.8	5	2.6	1.2	AP3S1 MKLN1 RAB5A AP3D1 CADPS2	-0.21
Southeastern	GO Biological Processes	GO:0014075	Cellular process	response to amine	19_GO:0050896 response to stimulus	-2.3	9	4.6	3	1.6	0.9	CPS1 GRIN2A ARRM2B	-0.21
Southeastern	GO Biological Processes	GO:0097479	Neural processes	synaptic vesicle localization	19_GO:0051179 localization	-2.3	9	4.6	3	1.6	0.9	AP3S1 AP3D1 SPG11	-0.21
Southeastern	GO Biological Processes	GO:0070169	Ossification	positive regulation of biomineral tissue development	19_GO:0032502 developmental process	-2.3	8.8	4.6	3	1.6	0.9	BMP4 MEF2C ADGRV1	-0.19
Southeastern	GO Biological Processes	GO:0033044	Cellular process	regulation of chromosome organization	19_GO:0050789 regulation of biological process	-2.3	3.9	3.6	6	3.1	1.3	TNKS SMC4 SUB1 BRD7 ACTR8 NEK7	-0.19
Southeastern	GO Biological Processes	GO:0055001	Muscular process	muscle cell development	19_GO:0032502 developmental process	-2.3	4.6	3.8	5	2.6	1.2	ACTN2 KEL MAM1 AFG3L2 SPG11	-0.19
Southeastern	GO Biological Processes	GO:0001934	Cellular process	positive regulation of protein phosphorylation	19_GO:0048518 positive regulation of biological process	-2.3	3.1	3.4	8	4.2	1.4	BMP4 CALCA CCND3 CSPG4 ECT2 IL12A DDR2 RICTOR	-0.19
Southeastern	GO Biological Processes	GO:0010970	Cellular process	transport along microtubule	19_GO:0051179 localization	-2.3	4.6	3.7	5	2.6	1.2	AP3S1 AP3D1 KIF3A TRAK1 SPG11	-0.19
Southeastern	GO Biological Processes	GO:0050890	Neural processes	cognition	19_GO:0032501 multicellular organismal process	-2.3	3.4	3.4	7	3.7	1.4	GABRA5 GRIN2A MEF2C VDAC1 ARL6IP5 SPG11 VPS13B	-0.19
Southeastern	GO Biological Processes	GO:0045778	Ossification	positive regulation of ossification	19_GO:0032501 multicellular organismal process	-2.3	8.6	4.5	3	1.6	0.9	BMP4 MEF2C ADGRV1	-0.19
Southeastern	GO Biological Processes	GO:0015909	Lipid metabolism	long-chain fatty acid transport	19_GO:0051179 localization	-2.3	8.6	4.5	3	1.6	0.9	FABP1 ABCD3 PLA2G12A	-0.19

Southeastern	GO Biological Processes	GO:0098655	Cellular process	monoatomic cation transmembrane transport	19_GO:0051179 localization	-2.3	2.5	3.2	11	5.8	1.7	CACNB2 GRIN2A KCNJ2 KEL OPRM1 VDAC1 AP3D1 AFG3L2 CACNA2D3 ATP13A3 SLC4A11	-0.19
Southeastern	GO Biological Processes	GO:0000278	Cellular process	mitotic cell cycle	19_GO:0009987 cellular process	-2.3	2.6	3.2	10	5.2	1.6	CNND3 ECT2 EIF4 PPP1R12A NDP TNKS CRADD UBA3 SMC4 TRIM36	-0.19
Southeastern	GO Biological Processes	GO:0006897	Cellular process	endocytosis	19_GO:0051179 localization	-2.3	2.8	3.3	9	4.7	1.5	CALCA AP3S1 NDPRAB5A AP3D1 FKBP1 SH3KBP1 SPG11 XKR4	-0.19
Southeastern	Reactome Gene Sets	R-HSA-1638091	Metabolism	Heparan sulfate/heparin (HS-GAG) metabolism		-2.3	8.5	4.5	3	1.6	0.9	CSPG4 DCN GPC5	-0.18
Southeastern	GO Biological Processes	GO:0006749	Metabolism	glutathione metabolic process	19_GO:0009987 cellular process	-2.3	8.5	4.5	3	1.6	0.9	NDPG GSTO1 ARL6IP5	-0.18
Southeastern	GO Biological Processes	GO:0034655	Cellular process	nucleobase-containing compound catabolic process	19_GO:0009987 cellular process	-2.3	3.3	3.4	7	3.7	1.4	DPYDC NCOT4 PDE4B MTREX CNOT10 NT5M MFSD8	-0.18
Southeastern	GO Biological Processes	GO:0051899	Neural processes	membrane depolarization	19_GO:0065007 biological regulation	-2.2	8.3	4.4	3	1.6	0.9	CACNB2 CHRN3 CHRNA6	-0.16
Southeastern	Reactome Gene Sets	R-HSA-112314	Neural processes	Neurotransmitter receptors and postsynaptic signal transmission		-2.2	4.4	3.7	5	2.6	1.2	ACTN2 CHRN3 GABRA5 GRIN2A CHRNA6	-0.16
Southeastern	GO Biological Processes	GO:0009166	Cellular process	nucleotide catabolic process	19_GO:0009987 cellular process	-2.2	5.6	3.9	4	2.1	1	DPYD PDE4B NT5M MFSD8	-0.15
Southeastern	GO Biological Processes	GO:0090257	Muscular process	regulation of muscle system process	19_GO:0032501 multicellular organismal process	-2.2	3.7	3.5	6	3.1	1.3	CACNB2 CALCAD DSG2 PDE4B GSTO1 DOCK5	-0.15
Southeastern	KEGG Pathway	hsa00240	Metabolism	Pyrimidine metabolism		-2.2	8.2	4.4	3	1.6	0.9	DPYD RRM2 NT5M	-0.15
Southeastern	GO Biological Processes	GO:0099173	Neural processes	postsynapse organization	19_GO:0009987 cellular process	-2.2	5.6	3.9	4	2.1	1	ACTN2 CRK CTNND2 JNA	-0.15
Southeastern	GO Biological Processes	GO:0008015	Cardioregulation	blood circulation	19_GO:0032501 multicellular organismal process	-2.2	3	3.3	8	4.2	1.4	CACNB2 CALCACP3 KCNJ2 KEL NPR3 PCSK5 DOCK5	-0.14
Southeastern	GO Biological Processes	GO:0051301	Cellular process	cell division	19_GO:0009987 cellular process	-2.2	2.7	3.2	9	4.7	1.5	CNND3 CNT2 ECT2 CDC14A TNKS SMC4 TRIM36 ACTR8 TOPAZ1	-0.14
Southeastern	GO Biological Processes	GO:0060350	Ossification	endochondral bone morphogenesis	19_GO:0032502 developmental process	-2.2	7.9	4.3	3	1.6	0.9	BMP4 MATN1 MEF2C	-0.12
Southeastern	GO Biological Processes	GO:0051480	Cellular process	regulation of cytosolic calcium ion concentration	19_GO:0042592 homeostatic process	-2.2	7.9	4.3	3	1.6	0.9	CACNB2 CALCAT MEM64	-0.12
Southeastern	GO Biological Processes	GO:1903706	Cardioregulation	regulation of hemopoiesis	19_GO:0002376 immune system process	-2.2	2.9	3.2	8	4.2	1.4	BMP4 CALCAMEF2C NCOT4 AP3D1 BRD1 BRD7 TMEM64	-0.11
Southeastern	GO Biological Processes	GO:0042327	Cellular process	positive regulation of phosphorylation	19_GO:0048518 positive regulation of biological process	-2.2	2.9	3.2	8	4.2	1.4	BMP4 CALC CCND3 CSPG4 ECT2 JL12A DDR2 RICTOR	-0.11
Southeastern	GO Biological Processes	GO:0010639	Cellular process	negative regulation of organelle organization	19_GO:0048519 negative regulation of biological process	-2.2	3.2	3.3	7	3.7	1.4	BMP4 RAD1 TNKS MPHOSPH9 SUB1 FRM7 FBXO43	-0.11
Southeastern	GO Biological Processes	GO:1903522	Cardioregulation	regulation of blood circulation	19_GO:0032501 multicellular organismal process	-2.2	3.6	3.4	6	3.1	1.3	CACNB2 DSG2 KCNJ2 PDE4B GSTO1 DOCK5	-0.11
Southeastern	GO Biological Processes	GO:0060261	Cellular process	positive regulation of transcription initiation by RNA polymerase II	19_GO:0048518 positive regulation of biological process	-2.1	7.7	4.2	3	1.6	0.9	MED14 MED12 SUB1	-0.098
Southeastern	GO Biological Processes	GO:0170041	Metabolism	non-proteinogenic amino acid metabolic process	19_GO:0009987 cellular process	-2.1	7.7	4.2	3	1.6	0.9	CPS1 DPYD MTFR	-0.098
Southeastern	Reactome Gene Sets	R-HSA-453279	Cellular process	Mitotic G1 phase and G1/S transition		-2.1	5.3	3.7	4	2.1	1	CNND3 PRIM2 ORC6 PPP2R3B	-0.098
Southeastern	WikiPathways	WP2005	Cellular process	miR targeted genes in muscle cell		-2.1	3.1	3.2	7	3.7	1.4	CHD1 DSG2 EIF4E AP3D1 RAI14 FNDCC3B DOCK5	-0.09
Southeastern	Reactome Gene Sets	R-HSA-196849	Metabolism	Metabolism of water-soluble vitamins and cofactors		-2.1	5.2	3.7	4	2.1	1	MCCS2 MTFR GSTO1 MTFHD1L	-0.09
Southeastern	WikiPathways	WP4808	Ossification	Endochondral ossification with skeletal dysplasias		-2.1	7.6	4.1	3	1.6	0.9	MEF2C DDR2 KIF3A	-0.089
Southeastern	WikiPathways	WP474	Ossification	Endochondral ossification		-2.1	7.6	4.1	3	1.6	0.9	MEF2C DDR2 KIF3A	-0.089
Southeastern	WikiPathways	WP45	Cellular process	G1 to S cell cycle control		-2.1	7.4	4.1	3	1.6	0.9	CNND3 PRIM2 ORC6	-0.077
Southeastern	Reactome Gene Sets	R-HSA-1630316	Metabolism	Glycosaminoglycan metabolism		-2.1	5.2	3.7	4	2.1	1	CSPG4 DCN GPC5 B4GALT1	-0.077
Southeastern	GO Biological Processes	GO:0006816	Cellular process	calcium ion transport	19_GO:0051179 localization	-2.1	3.5	3.3	6	3.1	1.3	CACNB2 GRIN2A OPRM1 VDAC1 AFG3L2 CACNA2D3	-0.077
Southeastern	GO Biological Processes	GO:0090068	Cellular process	positive regulation of cell cycle process	19_GO:0048518 positive regulation of biological process	-2.1	3.5	3.3	6	3.1	1.3	CNND3 ECT2 DDR2 CDC14A SMC4 RRM2B	-0.076
Southeastern	GO Biological Processes	GO:0048667	Neural processes	cell morphogenesis involved in neuron differentiation	19_GO:0032502 developmental process	-2.1	2.8	3.1	8	4.2	1.4	CTNND2 MEF2C NDP TRIO AFG3L2 TRAK1 SPG11 SLITRK4	-0.076
Southeastern	GO Biological Processes	GO:0051702	Response to stimulus	biological process involved in interaction with symbiont	19_GO:0044419 biological process involved in interspecies interaction between organisms	-2.1	5.1	3.7	4	2.1	1	CNT2 CHD1 RAB5A YTHDC2	-0.076
Southeastern	GO Biological Processes	GO:0045664	Neural processes	regulation of neuron differentiation	19_GO:0032502 developmental process	-2.1	4.1	3.4	5	2.6	1.2	BMP4 ECT2 EIF4E MEF2C GDPD5	-0.076
Southeastern	GO Biological Processes	GO:0036465	Neural processes	synaptic vesicle recycling	19_GO:0051179 localization	-2.1	7.3	4.1	3	1.6	0.9	AP3S1 RAB5A AP3D1	-0.076
Southeastern	GO Biological Processes	GO:0030036	Cellular process	actin cytoskeleton organization	19_GO:0009987 cellular process	-2.1	2.6	3	9	4.7	1.5	ACTN2 CRK MKLN1 SH3KBP1 PPP1R9A KLHL1 EBP41 LAJ MYR1CTOR	-0.076
Southeastern	GO Biological Processes	GO:0006259	Metabolism	DNA metabolic process	19_GO:0009987 cellular process	-2.1	2.3	2.9	11	5.8	1.7	PRIM2 RAD1 ORC6 RRM2B ZGF1 NT5M USP28 HMBXO1 ACTR8 JMY ERC6 CL2	-0.076
Southeastern	GO Biological Processes	GO:0048738	Cardioregulation	cardiac muscle tissue development	19_GO:0032502 developmental process	-2.1	4	3.4	5	2.6	1.2	ACTN2 BMP4 DSG2 MEF2C MAM1	-0.071
Southeastern	GO Biological Processes	GO:0061337	Cardioregulation	cardiac conduction	19_GO:0032501 multicellular organismal process	-2.1	7.2	4	3	1.6	0.9	CACNB2 DSG2 KCNJ2	-0.071
Southeastern	GO Biological Processes	GO:0019233	Sensorial	sensory perception of pain	19_GO:0032501 multicellular organismal process	-2.1	7.2	4	3	1.6	0.9	CALCA GRIN2A OPRM1	-0.071
Southeastern	GO Biological Processes	GO:0060113	Sensorial	inner ear receptor cell differentiation	19_GO:0032502 developmental process	-2.1	7.2	4	3	1.6	0.9	BMP4 GABRA5 ADGRV1	-0.071
Southeastern	GO Biological Processes	GO:0035051	Cardioregulation	cardiocyte differentiation	19_GO:0032502 developmental process	-2.1	5	3.6	4	2.1	1	ACTN2 BMP4 MEF2C MAM1	-0.071
Southeastern	GO Biological Processes	GO:0060828	Signal transduction	regulation of canonical Wnt signaling pathway	19_GO:0050896 response to stimulus	-2.1	3.4	3.2	6	3.1	1.3	CTNND2 GPC5 TNKS ZNF37 TMEM64 UBAC2	-0.071
Southeastern	GO Biological Processes	GO:0003014	Osmoregulation	renal system process	19_GO:0032501 multicellular organismal process	-2.1	5	3.6	4	2.1	1	BMP4 NPR3 PCSK5 RRM2B	-0.063
Southeastern	GO Biological Processes	GO:0060348	Ossification	bone development	19_GO:0032502 developmental process	-2.1	4	3.4	5	2.6	1.2	BMP4 MATN1 MEF2C DDR2 BNC2	-0.062
Southeastern	GO Biological Processes	GO:0051336	Cellular process	regulation of hydrolase activity	19_GO:0065007 biological regulation	-2.1	2.8	3	8	4.2	1.4	CRK ECT2 FABP1 MEF2C CRADD ARL6IP5 TBC1D2A2 ML1	-0.062
Southeastern	GO Biological Processes	GO:0051926	Cellular process	negative regulation of calcium ion transport	19_GO:0051179 localization	-2.1	7.1	4	3	1.6	0.9	CALCA VDAC1 GSTO1	-0.062
Southeastern	GO Biological Processes	GO:0030198	Cellular process	extracellular matrix organization	19_GO:0009987 cellular process	-2.1	3.4	3.2	6	3.1	1.3	B4GALT1 MATN1 DDR2 ADAMTS6 ADAMTS1 ADAMTS17	-0.061
Southeastern	GO Biological Processes	GO:0030705	Cellular process	cytoskeleton-dependent intracellular transport	19_GO:0051179 localization	-2	4	3.4	5	2.6	1.2	AP3S1 AP3D1 KIF3A TRAK1 SPG11	-0.061
Southeastern	Reactome Gene Sets	R-HSA-1474244	Cellular process	Extracellular matrix organization		-2	3.4	3.2	6	3.1	1.3	BMP4 DCN LTP2 MATN1 DDR2 COL21A1	-0.061
Southeastern	GO Biological Processes	GO:0043062	Cellular process	extracellular structure organization	19_GO:0009987 cellular process	-2	3.4	3.2	6	3.1	1.3	B4GALT1 MATN1 DDR2 ADAMTS6 ADAMTS1 ADAMTS17	-0.061
Southeastern	GO Biological Processes	GO:0001944	Cardioregulation	vasculature development	19_GO:0032502 developmental process	-2	2.6	3	9	4.7	1.5	BMP4 CALC CSPG4 B4GALT1 MEF2C NDP NPR3 ADAMTS6 TIPARP	-0.061
Southeastern	GO Biological Processes	GO:0030001	Cellular process	metal ion transport	19_GO:0051179 localization	-2	2.4	2.9	10	5.2	1.6	CACNB2 GRIN2A KCNJ2 KEL OPRM1 VDAC1 AP3D1 AFG3L2 CACNA2D3 SLC4A11	-0.061
Southeastern	GO Biological Processes	GO:0051445	Cellular process	regulation of meiotic cell cycle	19_GO:0022414 reproductive process	-2	7	3.9	3	1.6	0.9	RAD1 YTHDC2 FBXO43	-0.06
Southeastern	Reactome Gene Sets	R-HSA-9659379	Sensorial	Sensory processing of sound		-2	7	3.9	3	1.6	0.9	CACNB2 KCNJ2 OTOG	-0.06
Southeastern	GO Biological Processes	GO:0045229	Cellular process	external encapsulating structure organization	19_GO:0009987 cellular process	-2	3.4	3.2	6	3.1	1.3	B4GALT1 MATN1 DDR2 ADAMTS6 ADAMTS1 ADAMTS17	-0.06
Southeastern	KEGG Pathway	hsa04080	Neural processes	Neuroactive ligand-receptor interaction		-2	3	3.1	7	3.7	1.4	CALCA CHRN3 GABRA5 GRIN2A GRM8 OPRM1 CHRNA6	-0.055
Southeastern	GO Biological Processes	GO:0044706	Development	multi-multicellular organism process	19_GO:0032501 multicellular organismal process	-2	3.9	3.3	5	2.6	1.2	CALCA DSG2 B4GALT1 NDP PCSK5	-0.054
Southeastern	GO Biological Processes	GO:2000144	Cellular process	positive regulation of DNA-templated transcription initiation	19_GO:0048518 positive regulation of biological process	-2	6.9	3.9	3	1.6	0.9	MED14 MED12 SUB1	-0.054

Southeastern	GO Biological Processes	GO:0032414	Cellular process	positive regulation of ion transmembrane transporter activity	19_GO:0051179 localization	-2	6.9	3.9	3	1.6	0.9	ACTN2 CACNB2 GSTO1	-0.054
Southeastern	WikiPathways	WP707	Response to stimulus	DNA damage response		-2	6.9	3.9	3	1.6	0.9	CCND3 RAD1 RRM2B	-0.054
Southeastern	GO Biological Processes	GO:0051668	Cellular process	localization within membrane	19_GO:0051179 localization	-2	2.5	2.9	9	4.7	1.5	ACTN2 CACNB2 CRKGRIN2A AP3D1 ARL6P5 DENND4C SPG11 VPS13B	-0.054
Southeastern	GO Biological Processes	GO:0032870	Metabolism	cellular response to hormone stimulus	19_GO:0050896 response to stimulus	-2	2.5	2.9	9	4.7	1.5	ACTN2 AP3S1 CP51 CRKEIF4E MEF2C DR2 WDT1 DENND4C	-0.051
Southeastern	GO Biological Processes	GO:0002041	Reproduction	regulation of reproductive process	19_GO:0022414 reproductive process	-2	3.9	3.3	5	2.6	1.2	BMP4 B4GALT1 RAD1 YTHDC2 FBXO43	-0.049
Southeastern	Reactome Gene Sets	R-HSA-6794362	Neural processes	Protein-protein interactions at synapses		-2	6.8	3.9	3	1.6	0.9	GRIN2A IL1RAPL2 SLITRK4	-0.049
Southeastern	Reactome Gene Sets	R-HSA-381340	Lipid metabolism	Transcriptional regulation of white adipocyte differentiation		-2	6.8	3.9	3	1.6	0.9	CCND3 MED14 MED12	-0.049
Southeastern	GO Biological Processes	GO:0048662	Cardioregulation	negative regulation of smooth muscle cell proliferation	19_GO:0048519 negative regulation of biological process	-2	6.8	3.9	3	1.6	0.9	BMP4 IL12A MEF2C	-0.049
Southeastern	GO Biological Processes	GO:0008652	Metabolism	amino acid biosynthetic process	19_GO:0009987 cellular process	-2	6.8	3.9	3	1.6	0.9	CP51 DPYDMTR	-0.049
Southeastern	GO Biological Processes	GO:0062197	Cellular process	cellular response to chemical stress	19_GO:0050896 response to stimulus	-2	3.3	3.1	6	3.1	1.3	ECT2 FABP1 ARL6P5 STK26 SLC4A11 ERCC6L2	-0.048
Eastren	GO Biological Processes	GO:0007173	Growth	epidermal growth factor receptor signaling pathway	19_GO:0050896 response to stimulus	-6.1	14	9.1	7	4.3	1.6	FGFR2 FLT4 KDR ROR2 SHC3 SLC30A10 EPHA6	-2
Eastren	GO Biological Processes	GO:0038084	Cardioregulation	vascular endothelial growth factor signaling pathway	19_GO:0050896 response to stimulus	-5.9	17	9.6	6	3.7	1.5	FGFR2 VEGFD FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0007167	Signal transduction	enzyme-linked receptor protein signaling pathway	19_GO:0050896 response to stimulus	-5.8	4.4	6.4	15	9.2	2.3	EFNA5 GFR2 VEGFD FLT4 GUCY2C KDR ROR2 GAB2 SHC3 SLC30A10 JL1 RAPPAM1 BMPER EPHA6 RGMGB	-2
Eastren	GO Biological Processes	GO:0048010	Cardioregulation	vascular endothelial growth factor receptor signaling pathway	19_GO:0050896 response to stimulus	-5.3	14	8.5	6	3.7	1.5	FGFR2 VEGFD FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0050804	Neural processes	modulation of chemical synaptic transmission	19_GO:0050789 regulation of biological process	-5.3	4.7	6.2	13	8	2.1	ASIC1 APBA2 ADGRB1 GRIK2 GRM8 ROR2 PRKN PRKAR1B PLCL2 SYAP1 NALCN MICU3 LRRTM1	-2
Eastren	GO Biological Processes	GO:0099177	Neural processes	regulation of trans-synaptic signaling	19_GO:0050789 regulation of biological process	-5.3	4.7	6.2	13	8	2.1	ASIC1 APBA2 ADGRB1 GRIK2 GRM8 ROR2 PRKN PRKAR1B PLCL2 SYAP1 NALCN MICU3 LRRTM1	-2
Eastren	Reactome Gene Sets	R-HSA-194313	Cardioregulation	VEGF ligand-receptor interactions		-5.3	80	15	3	1.8	1.1	VEGFD FLT4 KDR	-2
Eastren	Reactome Gene Sets	R-HSA-195399	Cardioregulation	VEGF binds to VEGFR leading to receptor dimerization		-5.3	80	15	3	1.8	1.1	VEGFD FLT4 KDR	-2
Eastren	GO Biological Processes	GO:0048013	Signal transduction	ephrin receptor signaling pathway	19_GO:0050896 response to stimulus	-5.2	13	8.3	6	3.7	1.5	EFNA5 GFR2 FLT4 KDR ROR2 EPHA6	-2
Eastren	KEGG Pathway	hsa04014	Signal transduction	Ras signaling pathway		-5.2	7	6.9	9	5.5	1.8	EFNA5 GFR2 VEGFD FLT4 KDR RALA GAB2 RASA3 SHC3	-2
Eastren	GO Biological Processes	GO:0036323	Cardioregulation	vascular endothelial growth factor receptor-1 signaling pathway	19_GO:0050896 response to stimulus	-5.2	19	9.3	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0035790	Growth	platelet-derived growth factor receptor-alpha signaling pathway	19_GO:0050896 response to stimulus	-5.1	19	9.2	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0038145	Lipid metabolism	macrophage colony-stimulating factor signaling pathway	19_GO:0050896 response to stimulus	-5.1	18	9.1	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0038109	Signal transduction	Ki signaling pathway	19_GO:0050896 response to stimulus	-5.1	18	9.1	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0036216	Cellular process	cellular response to stem cell factor stimulus	19_GO:0050896 response to stimulus	-5.1	18	9.1	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0036215	Cellular process	response to stem cell factor	19_GO:0050896 response to stimulus	-5.1	18	9.1	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-2
Eastren	GO Biological Processes	GO:0031547	Neural processes	brain-derived neurotrophic factor receptor signaling pathway	19_GO:0050896 response to stimulus	-5	18	8.9	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.9
Eastren	GO Biological Processes	GO:0035924	Cardioregulation	cellular response to vascular endothelial growth factor stimulus	19_GO:0050896 response to stimulus	-4.9	12	7.8	6	3.7	1.5	FGFR2 VEGFD FLT4 KDR ROR2 EPHA6	-1.9
Eastren	GO Biological Processes	GO:0036006	Immunity	cellular response to macrophage colony-stimulating factor stimulus	19_GO:0050896 response to stimulus	-4.9	17	8.7	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.9
Eastren	GO Biological Processes	GO:0038203	Signal transduction	TORC2 signaling	19_GO:0050896 response to stimulus	-4.9	62	13	3	1.8	1.1	MAPKAP1 PRR5L SYAP1	-1.9
Eastren	GO Biological Processes	GO:0035791	Growth	platelet-derived growth factor receptor-beta signaling pathway	19_GO:0050896 response to stimulus	-4.9	17	8.6	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.9
Eastren	GO Biological Processes	GO:0048012	Signal transduction	hepatocyte growth factor receptor signaling pathway	19_GO:0050896 response to stimulus	-4.9	17	8.6	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.9
Eastren	GO Biological Processes	GO:0030001	Cellular process	metal ion transport	19_GO:0051179 localization	-4.9	4	5.6	14	8.6	2.2	ASIC1 CACNA1D RYR2 SLC30A9 PLCL2 COMMD9 SLC30A10 CACHD1 SLC5A7 KCNP4 SLC4A11 LRRC38 NALCN MICU3	-1.9
Eastren	GO Biological Processes	GO:0038063	Signal transduction	collagen-activated tyrosine kinase receptor signaling pathway	19_GO:0050896 response to stimulus	-4.8	16	8.4	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.9
Eastren	GO Biological Processes	GO:0036005	Immunity	response to macrophage colony-stimulating factor	19_GO:0050896 response to stimulus	-4.8	16	8.3	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.8
Eastren	GO Biological Processes	GO:0038065	Signal transduction	collagen-activated signaling pathway	19_GO:0050896 response to stimulus	-4.7	15	8.1	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.8
Eastren	GO Biological Processes	GO:0007169	Signal transduction	cell surface receptor protein tyrosine kinase signaling pathway	19_GO:0050896 response to stimulus	-4.6	4.8	5.8	11	6.7	2	EFNA5 GFR2 VEGFD FLT4 KDR ROR2 GAB2 SHC3 SLC30A10 JL1 RAE EPHA6	-1.8
Eastren	GO Biological Processes	GO:0055080	Cellular process	monatomic cation homeostasis	19_GO:0042592 homeostatic process	-4.6	4.4	5.6	12	7.4		GRIK2 KDR OCA2 PKHD1 RYR2 STC1 SLC23A9 SLC30A10 SLC4A11 TMTC4 TMTC2 MICU3	-1.8
Eastren	GO Biological Processes	GO:0050801	Cellular process	monatomic ion homeostasis	19_GO:0042592 homeostatic process	-4.6	4.3	5.5	12	7.4		GRIK2 KDR OCA2 PKHD1 RYR2 STC1 SLC23A9 SLC30A10 SLC4A11 TMTC4 TMTC2 MICU3	-1.7
Eastren	GO Biological Processes	GO:0055074	Cellular process	calcium ion homeostasis	19_GO:0042592 homeostatic process	-4.4	6.4	6.1	8	4.9	1.7	GRIK2 KDR PKHD1 RYR2 STC1 TMTC4 TMTC2 MICU3	-1.6
Eastren	WikiPathways	WP4223	Signal transduction	Ras signaling		-4.2	7.1	6.1	7	4.3	1.6	FGFR2 FLT4 KDR RALA GAB2 RASA3 SHC3	-1.4
Eastren	GO Biological Processes	GO:0048009	Growth	insulin-like growth factor receptor signaling pathway	19_GO:0050896 response to stimulus	-4.1	11	6.9	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.3
Eastren	GO Biological Processes	GO:0031929	Signal transduction	TOR signaling	19_GO:0050896 response to stimulus	-4.1	17	7.9	4	2.5	1.2	MAPKAP1 PRR5L CARD11 SYAP1	-1.3
Eastren	GO Biological Processes	GO:0098660	Cellular process	inorganic ion transmembrane transport	19_GO:0051179 localization	-4.1	3.3	4.9	14	8.6	2.2	ASIC1 CACNA1D GABRA2 OCA2 RYR2 SLC30A9 PLCL2 SLC30A10 CACHD1 KCNP4 SLC4A11 LRRC38 NALCN MICU3	-1.3
Eastren	GO Biological Processes	GO:0048008	Growth	platelet-derived growth factor receptor signaling pathway	19_GO:0050896 response to stimulus	-4	11	6.7	5	3.1	1.4	FGFR2 FLT4 KDR ROR2 EPHA6	-1.2
Eastren	GO Biological Processes	GO:0032869	Carbohydrate metabolism	cellular response to insulin stimulus	19_GO:0050896 response to stimulus	-4	6.6	5.8	7	4.3	1.6	FGFR2 FLT4 KDR ROR2 MAPKAP1 SYAP1 EPHA6	-1.2
Eastren	GO Biological Processes	GO:0098655	Cellular process	monatomic cation transmembrane transport	19_GO:0051179 localization	-3.9	3.4	4.8	13	8	2.1	ASIC1 CACNA1D RYR2 TMEM63A SLC30A9 PLCL2 SLC30A10 CACHD1 KCNP4 SLC4A11 LRRC38 NALCN MICU3	-1.2
Eastren	GO Biological Processes	GO:0030003	Cellular process	intracellular monatomic cation homeostasis	19_GO:0042592 homeostatic process	-3.9	4.3	5.1	10	6.1	1.9	GRIK2 OCA2 PKHD1 RYR2 STC1 SLC30A9 SLC30A10 SLC4A11 TMTC4 MICU3	-1.2
Eastren	GO Biological Processes	GO:0006873	Cellular process	intracellular monatomic ion homeostasis	19_GO:0042592 homeostatic process	-3.8	4.2	5	10	6.1	1.9	GRIK2 OCA2 PKHD1 RYR2 STC1 SLC30A9 SLC30A10 SLC4A11 TMTC4 MICU3	-1.1
Eastren	GO Biological Processes	GO:0098771	Cellular process	inorganic ion homeostasis	19_GO:0042592 homeostatic process	-3.8	4.2	5	10	6.1	1.9	GRIK2 KDR PKHD1 RYR2 STC1 SLC30A9 SLC30A10 TMTC4 TMTC2 MICU3	-1.1
Eastren	GO Biological Processes	GO:0090141	Mitochondrial regulation	positive regulation of mitochondrial fission	19_GO:0032502 developmental process	-3.7	27	8.6	3	1.8	1.1	KDR PRKN RALA	-1
Eastren	WikiPathways	WP4540	Signal transduction	Hippo signaling regulation		-3.7	9.5	6.2	5	3.1	1.4	CDH1 OFGFR2 FLT4 KDR PRKAR1B	-1
Eastren	GO Biological Processes	GO:0070588	Cellular process	calcium ion transmembrane transport	19_GO:0051179 localization	-3.7	5.9	5.4	7	4.3	1.6	ASIC1 CACNA1D RYR2 PLCL2 CACHD1 NALCN MICU3	-1
Eastren	GO Biological Processes	GO:0050806	Neural processes	positive regulation of synaptic transmission	19_GO:0048518 positive regulation of biological process	-3.7	7.1	5.7	6	3.7	1.5	GRIK2 ROR2 PRKAR1B NALCN MICU3 LRRTM1	-1
Eastren	GO Biological Processes	GO:0070372	Signal transduction	regulation of ERK1 and ERK2 cascade	19_GO:0050896 response to stimulus	-3.7	5	5.1	8	4.9	1.7	DUSP7 GFR2 FLT4 KDR PKHD1 TNIP1 SLC30A10 BMPER	-1
Eastren	GO Biological Processes	GO:0042391	Neural processes	regulation of membrane potential	19_GO:0065007 biological regulation	-3.7	4	4.8	10	6.1	1.9	ASIC1 CACNA1D GABRA2 GRIK2 KDR PRKN PRKAR1B RYR2 SLC4A11 NALCN	-1

Eastren	GO Biological Processes	GO:0071375	Metabolism	cellular response to peptide hormone stimulus	19_GO:0050896 response to stimulus	-3.6	5	5.1	8	4.9	1.7	FGFR2FLT4KDRROR2SLC30A10MAPKAP1SYAP1EPIHA6	-0.99
Eastren	GO Biological Processes	GO:0008543	Growth	fibroblast growth factor receptor signaling pathway	19_GO:0050896 response to stimulus	-3.6	9	6	5	3.1	1.4	FGFR2FLT4KDRROR2EPIHA6	-0.97
Eastren	GO Biological Processes	GO:0032870	Metabolism	cellular response to hormone stimulus	19_GO:0050896 response to stimulus	-3.6	3.6	4.6	11	6.7	2	EFNA5FGFR2FLT4KDRLEPRROR2STC1SLC30A10MAPKAP1SYAP1EPIHA6	-0.97
Eastren	GO Biological Processes	GO:0098662	Cellular process	inorganic cation transmembrane transport	19_GO:0051179 localization	-3.4	3.2	4.4	12	7.4		ASIC1CACNA1DVR2SLC30A9PLCL2S2LC30A10CACHD1KCNIP4SLC4A11LRC38NALCNMICU3	-0.83
Eastren	GO Biological Processes	GO:0002040	Cardioregulation	sprouting angiogenesis	19_GO:0032502 developmental process	-3.4	12	6.3	4	2.5	1.2	VEGFDFLT4KDRBMPER	-0.82
Eastren	GO Biological Processes	GO:0008286	Carbohydrate metabolism	insulin receptor signaling pathway	19_GO:0050896 response to stimulus	-3.4	8.1	5.6	5	3.1	1.4	FGFR2FLT4KDRROR2EPIHA6	-0.8
Eastren	GO Biological Processes	GO:0000902	Cellular process	cell morphogenesis	19_GO:0032502 developmental process	-3.3	3.2	4.3	12	7.4	2	ADGRB1CDH10CTNND2EFNA5FGFR2PKHD1PRKG1STC1TNIKATP8A2CDHR3EPIHA6	-0.75
Eastren	WikiPathways	WP4541	Signal transduction	Hippo Merlin signaling dysregulation		-3.3	7.7	5.4	5	3.1	1.4	CDH10FGFR2FLT4KDRPRKAR1B	-0.71
Eastren	GO Biological Processes	GO:009140	Mitochondrial regulation	regulation of mitochondrial fission	19_GO:0032502 developmental process	-3.3	19	7.1	3	1.8	1.1	KDRPRKNRRLA	-0.68
Eastren	GO Biological Processes	GO:0098868	Ossification	bone growth	19_GO:0040007 growth	-3.2	18	7	3	1.8	1.1	FGFR2LEPRSTC1	-0.65
Eastren	GO Biological Processes	GO:0032868	Carbohydrate metabolism	response to insulin	19_GO:0050896 response to stimulus	-3.2	4.9	4.7	7	4.3	1.6	FGFR2FLT4KDRROR2MAPKAP1SYAP1EPIHA6	-0.63
Eastren	GO Biological Processes	GO:1901699	Cellular process	cellular response to nitrogen compound	19_GO:0050896 response to stimulus	-3.2	3.2	4.2	11	6.7	2	FGFR2FLT4KDRROR2PRKNRYR2STC1SLC30A10MAPKAP1SYAP1EPIHA6	-0.62
Eastren	GO Biological Processes	GO:0006816	Cellular process	calcium ion transport	19_GO:0051179 localization	-3.2	4.8	4.6	7	4.3	1.6	ASIC1CACNA1DVR2PLCL2CACHD1NALCNMICU3	-0.61
Eastren	GO Biological Processes	GO:0044344	Growth	cellular response to fibroblast growth factor stimulus	19_GO:0050896 response to stimulus	-3.1	6.9	5.1	5	3.1	1.4	FGFR2FLT4KDRROR2EPIHA6	-0.55
Eastren	GO Biological Processes	GO:0006874	Cellular process	intracellular calcium ion homeostasis	19_GO:0042592 homeostatic process	-3.1	5.5	4.7	6	3.7	1.5	GRIK2PKHD1RYR2STC1TMTC4MICU3	-0.54
Eastren	Reactome Gene Sets	R-HSA-9860931	Cellular process	Response of endothelial cells to shear stress		-3.1	9.4	5.5	4	2.5	1.2	FLT4KDRPRKAR1BMAPKAP1	-0.53
Eastren	WikiPathways	WP2858	Development	Ectoderm differentiation		-3	6.6	4.9	5	3.1	1.4	CTNND2FGFR2ROR2STC1ARHGAP15	-0.47
Eastren	KEGG Pathway	hsa04015	Signal transduction	Rap1 signaling pathway		-3	5.3	4.6	6	3.7	1.5	EFNA5FGFR2VEGFDFLT4KDRRALA	-0.47
Eastren	GO Biological Processes	GO:0071774	Growth	response to fibroblast growth factor	19_GO:0050896 response to stimulus	-3	6.5	4.9	5	3.1	1.4	FGFR2FLT4KDRROR2EPIHA6	-0.47
Eastren	GO Biological Processes	GO:0031401	Cellular process	positive regulation of protein modification process	19_GO:0048518 positive regulation of biological process	-2.9	3.2	4	10	6.1	1.9	EFNA5FLT4KDRLEPRPRKNNTNIP1TNIBWP1LSYAP1IL31RA	-0.44
Eastren	Reactome Gene Sets	R-HSA-194138	Signal transduction	Signaling by VEGF		-2.9	8.6	5.2	4	2.5	1.2	VEGFDFLT4KDRMAPKAP1	-0.42
Eastren	KEGG Pathway	hsa04010	Signal transduction	MAPK signaling pathway		-2.9	4.3	4.3	7	4.3	1.6	CACNA1DUSP7EFNA5FGFR2VEGDFFLT4KDR	-0.42
Eastren	Reactome Gene Sets	R-HSA-9855142	Respiratory system	Cellular responses to mechanical stimuli		-2.9	8.4	5.1	4	2.5	1.2	FLT4KDRPRKAR1BMAPKAP1	-0.4
Eastren	GO Biological Processes	GO:0035239	Development	tube morphogenesis	19_GO:0032502 developmental process	-2.9	2.9	3.8	11	6.7	2	FGFR2VEGFDFLT4KDRLEPRPKHD1RALARYR2MED12PLXND1BMPER	-0.38
Eastren	GO Biological Processes	GO:0055082	Cellular process	intracellular chemical homeostasis	19_GO:0042592 homeostatic process	-2.8	3.1	3.9	10	6.1	1.9	GRIK2OCA2PKHD1RYR2STC1SLC30A9SLC30A10SLC4A11TMTC4MICU3	-0.37
Eastren	GO Biological Processes	GO:0019725	Cellular process	cellular homeostasis	19_GO:0042592 homeostatic process	-2.8	2.9	3.8	11	6.7	2	GRIK2OCA2PRKNPKHD1RYR2STC1SLC30A9SLC30A10SLC4A11TMTC4MICU3	-0.35
Eastren	GO Biological Processes	GO:0060562	Development	epithelial tube morphogenesis	19_GO:0032502 developmental process	-2.8	4.1	4.1	7	4.3	1.6	FGFR2KDRPKHD1RALARYR2MED12PLXND1	-0.32
Eastren	KEGG Pathway	hsa04713	Sensorial	Circadian entrainment		-2.7	7.7	4.8	4	2.5	1.2	CACNA1DGUCY1A2PRKG1RYR2	-0.28
Eastren	GO Biological Processes	GO:0051046	Cellular process	regulation of secretion	19_GO:0051179 localization	-2.7	3	3.7	10	6.1	1.9	ASIC1EFNA5PRKNPRKG1RALASTC1GAB2MYRIPMICAL1MICU3	-0.22
Eastren	GO Biological Processes	GO:0007605	Sensorial	sensory perception of sound	19_GO:0032501 multicellular organismal process	-2.6	5.5	4.3	5	3.1	1.4	ALDH7A1CACNA1DUSH2ATMT4LOXHD1	-0.22
Eastren	GO Biological Processes	GO:0051963	Neural processes	regulation of synapse assembly	19_GO:0032502 developmental process	-2.6	5.5	4.3	5	3.1	1.4	ASIC1ADGRB1EFNA5UBE3BLRRTM1	-0.22
Eastren	GO Biological Processes	GO:0071363	Growth	cellular response to growth factor stimulus	19_GO:0050896 response to stimulus	-2.6	3.2	3.7	9	5.5	1.8	FGFR2VEGFDFLT4KDRROR2SYAP1BMPEREPHA6RGMB	-0.2
Eastren	GO Biological Processes	GO:0043434	Metabolism	response to peptide hormone	19_GO:0050896 response to stimulus	-2.6	3.4	3.8	8	4.9	1.7	FGFR2FLT4KDRROR2SLC30A10MAPKAP1SYAP1EPIHA6	-0.2
Eastren	GO Biological Processes	GO:0019221	Signal transduction	cytokine-mediated signaling pathway	19_GO:0050896 response to stimulus	-2.6	3.4	3.8	8	4.9	1.7	FGFR2FLT4KDRLEPRROR2WBP1IL31RAEPIHA6	-0.2
Eastren	KEGG Pathway	hsa04020	Signal transduction	Calcium signaling pathway		-2.6	4.4	4	6	3.7	1.5	CACNA1DFGFR2VEGDFFLT4KDRRYR2	-0.18
Eastren	GO Biological Processes	GO:0001932	Cellular process	regulation of protein phosphorylation	19_GO:0050789 regulation of biological process	-2.6	2.9	3.6	10	6.1	1.9	DUSP7EFNA5FLT4KDRLEPRPRKNNTNIPKRR1LSYAP1IL31RA	-0.17
Eastren	WikiPathways	WP5087	Respiratory system	Pleural mesothelioma		-2.6	3.4	3.7	8	4.9	1.7	CDH10EFNA5FGFR2VEGFDFLT4KDRROR2TNIK	-0.17
Eastren	GO Biological Processes	GO:0035265	Growth	organ growth	19_GO:0040007 growth	-2.6	6.9	4.5	4	2.5	1.2	FGFR2LEPRPRKG1STC1	-0.17
Eastren	GO Biological Processes	GO:0048589	Growth	developmental growth	19_GO:0040007 growth	-2.6	3.4	3.7	8	4.9	1.7	APBA2EFNA5FGFR2LEPRPRKG1STC1MED12VPS13B	-0.17
Eastren	GO Biological Processes	GO:0040007	Growth	growth	19_GO:0040007 growth	-2.6	3.4	3.7	8	4.9	1.7	FGFR2VEGFDFLT4KDRLEPRPLXND1BMPER	-0.17
Eastren	GO Biological Processes	GO:0001525	Cardioregulation	angiogenesis	19_GO:0032502 developmental process	-2.5	3.7	3.8	7	4.3	1.6	FGFR2VEGFDFLT4KDRLEPRPLXND1BMPER	-0.17
Eastren	WikiPathways	WP2406	Cardioregulation	Cardiac progenitor differentiation		-2.5	11	5.1	3	1.8	1.1	KDRROR2NANOG	-0.16
Eastren	GO Biological Processes	GO:1901137	Carbohydrate metabolism	carbohydrate derivative biosynthetic process	19_GO:0009987 cellular process	-2.5	3	3.5	9	5.5	1.8	GUCY1A2GUCY2C2ST8SIA1B3GALT2TNIP1NME7CPS2TMTCTC2	-0.14
Eastren	GO Biological Processes	GO:0048286	Respiratory system	lung alveolus development	19_GO:0032502 developmental process	-2.5	10	5	3	1.8	1.1	FGFR2FLT4KDR	-0.14
Eastren	GO Biological Processes	GO:1901890	Cellular process	positive regulation of cell junction assembly	19_GO:0048518 positive regulation of biological process	-2.5	6.6	4.4	4	2.5	1.2	ADGRB1EFNA5KDRLRRTM1	-0.13
Eastren	GO Biological Processes	GO:0043408	Signal transduction	regulation of MAPK cascade	19_GO:0050896 response to stimulus	-2.5	2.8	3.5	10	6.1	1.9	DUSP7FGFR2FLT4KDRPRKNPKHD1TNIP1TNIKSLC30A10BMPER	-0.13
Eastren	Reactome Gene Sets	R-HSA-382551	Cellular process	Transport of small molecules		-2.5	2.8	3.5	10	6.1	1.9	ASIC1PRKAR1BRYR2ABCA10AHCYL2ATP8A2SLC30A10SLC5A7NALCNMICU3	-0.13
Eastren	GO Biological Processes	GO:2000648	Cellular process	positive regulation of stem cell proliferation	19_GO:0048518 positive regulation of biological process	-2.5	10	4.9	3	1.8	1.1	KDRN4BP2L2NANOG	-0.12
Eastren	GO Biological Processes	GO:1901888	Cellular process	regulation of cell junction assembly	19_GO:0050789 regulation of biological process	-2.5	4.1	3.8	6	3.7	1.5	ASIC1ADGRB1EFNA5KDRUBE3BLRRTM1	-0.11
Eastren	GO Biological Processes	GO:0070848	Growth	response to growth factor	19_GO:0050896 response to stimulus	-2.5	3	3.5	9	5.5	1.8	FGFR2VEGFDFLT4KDRROR2SYAP1BMPEREPHA6RGMB	-0.11
Eastren	GO Biological Processes	GO:0010821	Mitochondrial regulation	regulation of mitochondrion organization	19_GO:0050789 regulation of biological process	-2.4	6.4	4.3	4	2.5	1.2	KDRPRKNRRLASLC30A9	-0.092
Eastren	GO Biological Processes	GO:0018108	Cellular process	peptidyl-tyrosine phosphorylation	19_GO:0009987 cellular process	-2.4	9.6	4.8	3	1.8	1.1	FGFR2FLT4KDR	-0.092
Eastren	GO Biological Processes	GO:0090407	Metabolism	organophosphate biosynthetic process	19_GO:0009987 cellular process	-2.4	2.9	3.4	9	5.5	1.8	GUCY1A2GUCY2CINPP5DTECRNME7MOCOSCPS2SERAC1LCLAT1	-0.092
Eastren	GO Biological Processes	GO:1903530	Cellular process	regulation of secretion by cell	19_GO:0051179 localization	-2.4	2.9	3.4	9	5.5	1.8	ASIC1EFNA5PRKNPRKG1RALAGAB2MYRIPMICAL1MICU3	-0.086
Eastren	GO Biological Processes	GO:0018212	Cellular process	peptidyl-tyrosine modification	19_GO:0009987 cellular process	-2.4	9.4	4.8	3	1.8	1.1	FGFR2FLT4KDR	-0.081
Eastren	Reactome Gene Sets	R-HSA-112316	Neural processes	Neuronal System		-2.4	3.5	3.6	7	4.3	1.6	APBA2GABRA2GRIK2PRKAR1BNEASLCSA7LRRTM1	-0.081
Eastren	GO Biological Processes	GO:0006814	Cellular process	sodium ion transport	19_GO:0051179 localization	-2.4	4.7	3.9	5	3.1	1.4	ASIC1COMMD9SLC5A7SLC4A11NALCN	-0.064
Eastren	GO Biological Processes	GO:0050954	Sensorial	sensory perception of mechanical stimulus	19_GO:0032501 multicellular organismal process	-2.4	4.7	3.9	5	3.1	1.4	ALDH7A1CACNA1DUSH2ATMT4LOXHD1	-0.064
Eastren	GO Biological Processes	GO:0070374	Signal transduction	positive regulation of ERK1 and ERK2 cascade	19_GO:0048518 positive regulation of biological process	-2.4	4.7	3.8	5	3.1	1.4	FGFR2FLT4KDRSLC30A10BMPER	-0.057
Eastren	GO Biological Processes	GO:0006888	Cellular process	endoplasmic reticulum to Golgi vesicle-mediated transport	19_GO:0051179 localization	-2.3	6	4.1	4	2.5	1.2	SEC24DTRAPPC13SEC16BTRAPPC6B	-0.057
Eastren	GO Biological Processes	GO:0016055	Signal transduction	Wnt signaling pathway	19_GO:0050896 response to stimulus	-2.3	3.9	3.6	6	3.7	1.5	CTNND2ROR2MED12TNIKCDC73UBAC2	-0.057

Eastren	GO Biological Processes	GO:0042325	Cellular process	regulation of phosphorylation	19_GO:0050789 regulation of biological process	-2.3	2.7	3.3	10	6.1	1.9	DUSP7 EFNA5 FLT4 KDR LEPR PRKN TNIPRRS1 SYAP1 JL31 RA	-0.057
Eastren	KEGG Pathway	hsa00230	Metabolism	Purine metabolism	19_GO:0032502 developmental process	-2.3	5.8	4	4	2.5	1.2	FHIT GUCY1A2 GUCY2C NME7	-0.0021
Eastren	GO Biological Processes	GO:0051965	Neural processes	positive regulation of synapse assembly	19_GO:0032502 developmental process	-2.3	8.4	4.5	3	1.8	1.1	ADGRB1 EFNA5 LRRTM1	0
Eastren	GO Biological Processes	GO:0031175	Neural processes	neuron projection development	19_GO:0032502 developmental process	-2.2	2.6	3.2	10	6.1	1.9	ADGRB1 CTNND2 EFNA5 FGR2 PRKG1 TNK1 TP8A2 KLHL1 VPS13B EPHA6	0
Eastren	GO Biological Processes	GO:0008283	Cellular process	cell population proliferation	19_GO:0009987 cellular process	-2.2	2.6	3.2	10	6.1	1.9	FGFR2 VEGFD KDR LEPR OCA2 ST8SIA1 STC1 PLCL2 CARD11 BMPER	0
Eastren	GO Biological Processes	GO:0045912	Carbohydrate metabolism	negative regulation of carbohydrate metabolic process	19_GO:0048519 negative regulation of biological process	-2.2	8.3	4.4	3	1.8	1.1	LEPR PRKN PRKG1	0
Eastren	GO Biological Processes	GO:0048812	Neural processes	neuron projection morphogenesis	19_GO:0032502 developmental process	-2.2	3	3.3	8	4.9	1.7	ADGRB1 CTNND2 EFNA5 FGR2 PRKG1 TNK1 TP8A2 EPHA6	0
Eastren	GO Biological Processes	GO:0120039	Cellular process	plasma membrane bounded cell projection morphogenesis	19_GO:0032502 developmental process	-2.2	3	3.3	8	4.9	1.7	ADGRB1 CTNND2 EFNA5 FGR2 PRKG1 TNK1 TP8A2 EPHA6	0
Eastren	GO Biological Processes	GO:0048858	Cellular process	cell projection morphogenesis	19_GO:0032502 developmental process	-2.2	2.9	3.2	8	4.9	1.7	ADGRB1 CTNND2 EFNA5 FGR2 PRKG1 TNK1 TP8A2 EPHA6	0
Eastren	GO Biological Processes	GO:0050679	Cellular process	positive regulation of epithelial cell proliferation	19_GO:0048518 positive regulation of biological process	-2.2	4.3	3.6	5	3.1	1.4	FGFR2 FLT4 KDR PKHD1 ST8SIA1	0
Eastren	GO Biological Processes	GO:0048754	Development	branching morphogenesis of an epithelial tube	19_GO:0032502 developmental process	-2.2	5.3	3.8	4	2.5	1.2	FGFR2 KDR PKHD1 PLXND1	0
Eastren	GO Biological Processes	GO:0060560	Growth	developmental growth involved in morphogenesis	19_GO:0040007 growth	-2.1	5.3	3.7	4	2.5	1.2	EFNA5 FGR2 PRKG1 MEDI2	0
Eastren	GO Biological Processes	GO:0050854	Immunity	regulation of antigen receptor-mediated signaling pathway	19_GO:0002376 immune system process	-2.1	7.6	4.2	3	1.8	1.1	ELF1 PLCL2 CARD11	0
Eastren	GO Biological Processes	GO:0048167	Neural processes	regulation of synaptic plasticity	19_GO:0050789 regulation of biological process	-2.1	4.2	3.5	5	3.1	1.4	ADGRB1 GRIK2 PRKAR1B SYAP1 LRRTM1	0
Eastren	GO Biological Processes	GO:0001934	Cellular process	positive regulation of protein phosphorylation	19_GO:0048518 positive regulation of biological process	-2.1	3.1	3.2	7	4.3	1.6	EFNA5 FLT4 KDR LEPR TNK1 SYAP1 JL31 RA	0
Eastren	GO Biological Processes	GO:0050807	Neural processes	regulation of synapse organization	19_GO:0050789 regulation of biological process	-2.1	3.5	3.3	6	3.7	1.5	ASIC1 ADGRB1 EFNA5 ROR2 UBE3B LRRTM1	0
Eastren	GO Biological Processes	GO:0007610	Behavior	behavior	19_GO:0032501 multicellular organismal process	-2.1	2.6	3.1	9	5.5	1.8	ASIC1 APBA2 GRIK2 PRKN PRKAR1B ATP8A2 KLHL1 VPS13B LRRTM1	0
Eastren	GO Biological Processes	GO:0007286	Reproduction	spermatid development	19_GO:0022414 reproductive process	-2.1	4.1	3.5	5	3.1	1.4	OCA2 PRKG1 RFX2 CFAP61 VPS13B	0
Eastren	GO Biological Processes	GO:0051881	Mitochondrial regulation	regulation of mitochondrial membrane potential	19_GO:0065007 biological regulation	-2.1	7.4	4.1	3	1.8	1.1	KDR PRKN SLC4A11	0
Eastren	GO Biological Processes	GO:0046777	Cellular process	protein autophosphorylation	19_GO:0009987 cellular process	-2.1	5.1	3.7	4	2.5	1.2	FGFR2 FLT4 KDR TNK1	0
Eastren	GO Biological Processes	GO:0050803	Neural processes	regulation of synapse structure or activity	19_GO:0065007 biological regulation	-2.1	3.5	3.3	6	3.7	1.5	ASIC1 ADGRB1 EFNA5 ROR2 UBE3B LRRTM1	0
Eastren	GO Biological Processes	GO:0051966	Neural processes	regulation of synaptic transmission, glutamatergic	19_GO:0050789 regulation of biological process	-2.1	7.2	4	3	1.8	1.1	GRIK2 GRM8 ROR2	0
Eastren	GO Biological Processes	GO:0099175	Neural processes	regulation of postsynapse organization	19_GO:0050789 regulation of biological process	-2.1	5	3.6	4	2.5	1.2	ASIC1 ROR2 UBE3B LRRTM1	0
Eastren	GO Biological Processes	GO:0032456	Cellular process	endocytic recycling	19_GO:0051179 localization	-2.1	7.1	4	3	1.8	1.1	CCDC93 RAB11 FIP4 VPS13B	0
Eastren	KEGG Pathway	hsa04072	Signal transduction	Phospholipase D signaling pathway	19_GO:0022414 reproductive process	-2.1	5	3.6	4	2.5	1.2	GRM8 RALAGAB2 SHC3	0
Eastren	GO Biological Processes	GO:0048515	Reproduction	spermatid differentiation	19_GO:0051179 localization	-2.1	4	3.4	5	3.1	1.4	OCA2 PRKG1 RFX2 CFAP61 VPS13B	0
Eastren	GO Biological Processes	GO:0070972	Cellular process	protein localization to endoplasmic reticulum	19_GO:0051179 localization	-2	7.1	4	3	1.8	1.1	RYR2 SEC16B UBAC2	0
Eastren	GO Biological Processes	GO:0010594	Cellular process	regulation of endothelial cell migration	19_GO:0040011 locomotion	-2	3.9	3.3	5	3.1	1.4	ADGRB1 FLT4 KDR STC1 BMPER	0
Eastren	Reactome Gene Sets	R-HSA-9006934	Signal transduction	Signaling by Receptor Tyrosine Kinases		-2	3	3.1	7	4.3	1.6	DUSP7 VEGFD FLT4 KDR RALA SHC3 MAPKAP1	0
Eastren	KEGG Pathway	hsa01521	Cellular process	EGFR tyrosine kinase inhibitor resistance		-2	7	3.9	3	1.8	1.1	FGFR2 KDR SHC3	0
Eastren	Canonical Pathways	M223	Cellular process	PID BETA CATENIN NUC PATHWAY		-2	7	3.9	3	1.8	1.1	MED12 TNK1 KCNIP4	0
Eastren	Reactome Gene Sets	R-HSA-8876198	Cellular process	phosphorylation		-2	6.9	3.9	3	1.8	1.1	TRAPPC13 TRAPPC6B DENND6A	0
Eastren	Reactome Gene Sets	R-HSA-112315	Neural processes	Transmission across Chemical Synapses		-2	3.9	3.3	5	3.1	1.4	GABRA2 GRIK2 PRKAR1B NBEA SLC5A7	0
Eastren	GO Biological Processes	GO:0042327	Cellular process	positive regulation of phosphorylation	19_GO:0048518 positive regulation of biological process	-2	3	3.1	7	4.3	1.6	EFNA5 FLT4 KDR LEPR TNK1 SYAP1 JL31 RA	0
Eastren	GO Biological Processes	GO:0006900	Cellular process	vesicle budding from membrane	19_GO:0051179 localization	-2	6.8	3.9	3	1.8	1.1	SEC24D TRAPPC13 TRAPPC6B	0

Table S9. Linear morphological measurements for gentoo penguin study skins included in this study, from the Natural History Museum (NHM) and American Museum of Natural History (AMNH). The trait measurements are in millimeters and follow the trait descriptions in Baldwin et al. (1931): culmen length (CL; taken along the medial line), bill width at the base (BWB), bill height at gonys angle (BH), bill width at gonys angle (BWG), flipper width (FW; shortest distance from anterior surface of flipper above the radiale to the posterior side of the flipper), radius length (RL), manus length (ML; indent at radiale/radius/ulna to distal wing tip), tarsus length (TML; anterior surface), and middle toe length (MTL; digit 111 excluding nail).

Collection	Sex	Voucher	Locality	Lineage	CL	BWB	BH	BWG	FW	RL	ML	TML	MTL	Reference
AMNH	Male	445212	Falklands	Northern	60.33	20.87	15.74	9.167	52.83	58.31	138	37.14	77.83	Tyler et al 2020
AMNH	Unknown	525830	Falklands	Northern	55.8	13.56	14.89	6.72	51.14	52.97	124.5	34.39	70.61	Tyler et al 2020
AMNH	Male	445210	Falklands	Northern	60.16	18.47	15.91	9.25	53.37	58.07	136	33.21	75.77	Tyler et al 2020
AMNH	Unknown	525829	Falklands	Northern	51.21	17.27	16.38	10.23	53.36	58.72	130.9	33	74.19	Tyler et al 2020
AMNH	Male	445211	Falklands	Northern	60.92	23.42	19.08	10.23	55.37	63.79	136.3	36.35	78.81	Tyler et al 2020
AMNH	Male	445204	Falklands	Northern	62.25	19.87	17.46	9.46	54.5	59.35	135.3	35.24	76.63	Tyler et al 2020
AMNH	Male	445209	Falklands	Northern	58.61	19.47	17.34	9.033	51.63	58.32	135.7	38.12	77.39	Tyler et al 2020
NHM	Unknown	N/A (38, Tail 7/8)	Falklands	Northern	66.32	19.39	19.47	10.86	55.83	57.89	144.5	39.66	64.58	Tyler et al 2020
NHM	Unknown	N/A	Falklands	Northern	48.92	15.55	16.55	9.883	51.7	55.58	134.5	38.23	64.31	Tyler et al 2020
AMNH	Unknown	442462	Kerguelen	Southeastern	55.17	15.21	14.57	8.13	53.45	55.68	133.4	31.15	73.41	Tyler et al 2020
AMNH	Male	525824	Kerguelen	Southeastern	56.25	17.71	15.1	8.74	47.61	54.49	119.7	31.14	68.43	Tyler et al 2020
AMNH	Unknown	442459	Kerguelen	Southeastern	53.28	14.75	14.22	7.78	52.97	54.37	128.2	31.53	71.37	Tyler et al 2020
NHM	Unknown	80.11.18.772	Kerguelen	Southeastern	57.76	16.8	16.49	9.067	51.35	56.26	128.6	36.63	63.11	Tyler et al 2020
NHM	Unknown	41.7.8.2	Kerguelen	Southeastern	49.62	16.58	15.81	8.237	48.97	46.58	114.1	29.42	50.95	Tyler et al 2020
NHM	Unknown	80.11.18.773	Kerguelen	Southeastern	58.2	16.09	14.57	8.297	52.13	52.03	124.3	31.84	58.29	Tyler et al 2020
NHM	Unknown	90.5.3.4	Kerguelen	Southeastern	50.95	13.73	14.62	7.983	50.85	52.45	124.9	30.68	60.46	Tyler et al 2020
NHM	Unknown	80.11.18.771	24056	Southeastern	50.43	13.64	15.05	7.507	50.51	55.25	129	32.56	63.11	Tyler et al 2020
AMNH	Male	525820	Macquarie	Eastern	58.44	16.37	19.25	10.34	56.93	56.4	137.2	34.83	76.15	This study
AMNH	Male	525860	Macquarie	Eastern	45.49	12.12	13.66	7.097	51.09	53.43	120.7	32.49	68.87	This study
AMNH	Unknown	525821	Macquarie	Eastern	49.67	15.03	17.19	8.89	49.57	50.38	126.5	33.52	70.13	This study
AMNH	Unknown	525823	Macquarie	Eastern	57.42	16.79	18.99	9.577	53.2	55.26	137.2	34.52	75.66	This study
AMNH	Unknown	196415	Macquarie	Eastern	62.66	19.95	16.28	8.99	54.02	54.59	130.2	34.02	72.93	This study
NHM	Unknown	N/A	Macquarie	Eastern	50.44	14.62	13.51	8.377	51.2	52	125.8	34.57	61.65	This study
NHM	Unknown	1939.12.9.3615	Macquarie	Eastern	64.48	19.07	19.25	10.72	54.45	54.63	134.9	37.3	60.99	This study
NHM	Unknown	1905.21.2.37	Macquarie	Eastern	54.3	16.67	16.27	7.953	53.36	50.31	128.8	31.19	60.1	This study
NHM	Unknown	09.12.3.5	Macquarie	Eastern	50.88	15.88	15.62	8.797	51.29	51.53	125.7	28.93	57.93	This study
NHM	Female	1909.11.16.13	Crozet	Eastern	63.49	16.32	16.74	7.86	52.56	59.17	131.7	32.8	60.53	This study
AMNH	Unknown	525827	South Georgia	South Georgia	53.11	16.54	12.79	8.8	49.78	51.62	130.2	32.55	71.45	Tyler et al 2020
AMNH	Male	435822	South Georgia	South Georgia	53.75	16.97	16.45	10.22	57.65	56.12	130	34.04	73.4	Tyler et al 2021
AMNH	Unknown	525826	South Georgia	South Georgia	52.86	15.09	14.8	8.497	53.9	53.78	130.8	32.33	72.3	Tyler et al 2022
AMNH	Male	132463	South Georgia	South Georgia	62.14	16.6	17.24	9.32	54.94	56.85	134.8	35.73	75.8	Tyler et al 2023
AMNH	Female	439823	South Georgia	South Georgia	40.46	13.69	11.68	6.713	47.09	49.91	124.8	28.54	67.75	Tyler et al 2024
AMNH	Female	132465	South Georgia	South Georgia	57.2	18.07	16.32	9.527	54.15	56.05	129.1	35.65	73.59	Tyler et al 2025
AMNH	Female	269638	South Georgia	South Georgia	51.88	16.89	13.91	9.027	46.52	50.04	130.7	31.25	70.67	Tyler et al 2026
AMNH	Male	132462	South Georgia	South Georgia	59.85	18.27	17.07	9.88	54.53	55.48	139.5	36.75	77.24	Tyler et al 2027
AMNH	Male	132464	South Georgia	South Georgia	53.93	15.22	16.91	9.047	55.85	53.13	132.7	32.94	72.92	Tyler et al 2028
AMNH	Male	435821	South Georgia	South Georgia	48.92	14.71	13.95	7.777	53.92	50.91	130.7	31.39	71	Tyler et al 2029
NHM	Male	1914.3.8.8	South Georgia	South Georgia	53.04	17.71	15.25	7.887	52.36	50.05	126.9	34.68	63.06	Tyler et al 2030
NHM	Female	3.8.7	South Georgia	South Georgia	54.29	19.66	14.9	9.347	53.37	48.08	129.6	33.79	61.78	Tyler et al 2031
NHM	Male	1914.3.8.6	South Georgia	South Georgia	58.99	20.51	15.69	8.697	52.9	52.87	126.5	36.93	60.87	Tyler et al 2032
NHM	Male	1906.7.24.1	South Orkney	Southern	44.9	14.31	15.88	8.633	50.27	48.37	113.6	33.36	53.19	This study
AMNH	Male	196165	South Shetland	Southern	50	16.67	17.32	8.797	54.34	54.77	126.7	32.87	71.45	Tyler et al 2032
AMNH	Unknown	442416	South Shetland	Southern	42.02	17.29	12.89	7.777	46.93	46.27	110.1	30.2	62.18	Tyler et al 2033
AMNH	Unknown	442412	South Shetland	Southern	51.33	19.2	15.17	8.387	52.59	49.93	116.3	32.91	66.37	Tyler et al 2034
AMNH	Unknown	442414	South Shetland	Southern	44.85	14.79	14.06	8.627	46.48	46.52	111.7	30.89	63.02	Tyler et al 2035
AMNH	Unknown	442415	South Shetland	Southern	47.22	17.06	12.59	7.993	47.84	47.91	113.5	30.99	64.15	Tyler et al 2036
AMNH	Female	775712	Antarctic Peninsula	Southern	48.49	16.43	15.49	8.817	49.9	49.29	111.8	31.15	64.07	Tyler et al 2037
NHM	Female	1940.12.7.7	South Shetland	Southern	45.57	15.28	14.47	8.707	48.12	47.31	114.4	27.31	56.47	Tyler et al 2038
NHM	Male	1924.5.8.43	Antarctic Peninsula	Southern	48.47	15.5	15.38	8.353	51.06	49.18	116.9	31.84	56.64	Tyler et al 2039
NHM	Female	1924.5.8.44	Antarctic Peninsula	Southern	47.92	13.88	13.69	8.057	51.92	48.9	117.1	32.76	54.73	Tyler et al 2040

Table S10. Univariate comparisons of linear morphometric traits between all pairs of gentoo lineages (ANOVA p-values shown). Statistically significant differences ($p < 0.05$) are indicated in bold. Culmen length (CL; taken along the medial line), bill width at the base (BWB), bill height at gonys angle (BH), bill width at gonys angle (BWG), flipper width (FW; shortest distance from anterior surface of flipper above the radiale to the posterior side of the flipper), radius length (RL), manus length (ML; indent at radiale/radius/ulna to distal wing tip), tarsus length (TML; anterior surface), and middle toe length (MTL; digit I11 excluding nail).

Pair	CL	BWB	BH	BWG	RL	ML	TML	MTL
Eastern_vs_Macquarie	0.23	0.99	0.98	0.38	0.03	0.75	0.79	0.40
Eastern_vs_Northern	0.39	0.47	0.88	0.24	0.74	0.57	0.21	0.06
Eastern_vs_South_Georgia	0.11	0.77	0.39	0.34	0.05	0.76	0.76	0.10
Eastern_vs_Southeastern	0.03	0.64	0.07	0.52	0.12	0.35	0.69	0.70
Eastern_vs_Southern	0.00	0.87	0.21	0.18	0.00	0.01	0.48	0.91
Macquarie_vs_Northern	0.24	0.07	0.73	0.42	0.00	0.06	0.03	0.06
Macquarie_vs_South_Georgia	0.70	0.49	0.09	0.75	0.67	0.69	0.93	0.27
Macquarie_vs_Southeastern	0.72	0.47	0.07	0.10	0.87	0.15	0.16	0.33
Macquarie_vs_Southern	0.00	0.80	0.03	0.16	0.00	0.00	0.05	0.06
Northern_vs_South_Georgia	0.08	0.11	0.02	0.20	0.00	0.03	0.02	0.19
Northern_vs_Southeastern	0.07	0.02	0.01	0.02	0.01	0.00	0.00	0.01
Northern_vs_Southern	0.00	0.03	0.00	0.02	0.00	0.00	0.00	0.00
South_Georgia_vs_Southeastern	0.97	0.11	0.88	0.11	0.60	0.02	0.12	0.03
South_Georgia_vs_Southern	0.00	0.26	0.51	0.21	0.00	0.00	0.03	0.00
Southeastern_vs_Southern	0.00	0.53	0.53	0.35	0.00	0.00	0.64	0.45

Table S11. Pairwise MANOVA results among all gentoo penguin lineages for morphological traits. F-statistic is shown below diagonal with p values above; comparisons that are significant are indicated by red.

	Eastern	Northern	South_Georgia	Southeastern	Southern
Eastern	-	0.139	0.100	0.789	0.003
Northern	2.074	-	0.033	0.0445	0.001
South_Georgia	2.151	3.136	-	0.0009	0.000
Southeastern	0.556	3.594	7.943	-	0.020
Southern	6.446	10.430	10.131	4.439	-

Table S12. Pairwise MANOVA comparison of morphological traits north - south of the Antarctic Polar Fron including Kerguelen as part of the northern group (above) and separating Kerguelen because of the direct influence of the position of APF. P-values shown, bold indicates a significant difference.

	Df	Pillai	approx_F	num_Df	den_Df	Pr(>F)	
North_APF-South_APF	1	0.42912	2.9128	8	31	0.01518	*
Residuals	38						
North_APF-Kerguelen-South_APF	2	0.77082	2.43	16	62	0.006585	**
Residuals	37						

Table S13. Summary of diagnostic morphological traits of *P. kerguelensis*. The mean value (mm) for each taxon is given for Culmen length (CL), bill width at the base (BWB), bill height at gonys angle (BH), bill width at gonys angle (BWG), flipper width (FW), radius length (RL), manus length (ML), tarsus length (TML), and middle toe length (MTL). Statistically significant differences from *P. Kerguelensis* are indicated with bold (ANOVA $p < 0.05$; see Table S7 for all pairwise comparisons with p-values).

	CL	BWB	BH	BWG	FW	RL	ML	TML	MTL
<i>Papua ellsworthii ellsworthii</i>	47.08	16.04	14.69	8.41	49.95	48.84	115.2	31.43	61.23
<i>Papua ellsworthii poncetii</i>	53.88	16.92	15.15	8.83	52.84	52.68	130.49	33.58	70.14
<i>Papua taeniata</i>	55.73	16.28	16.68	8.86	52.77	53.77	129.86	33.42	66.49
<i>Papua papua</i>	58.28	18.65	16.98	9.43	53.3	58.11	135.08	36.15	73.35
<i>Papua kerguelensis</i>	53.96	15.56	15.05	8.22	50.98	53.39	125.27	31.87	63.64

Table S14. List of 100 selected UCE and the length of the alignment.

UCE_name	Alignment_length	UCE_name	Alignment_length
uce-1027	1437	uce-4828	1621
uce-1149	1620	uce-4855	1620
uce-1304	1607	uce-4856	1620
uce-1334	1620	uce-4940	1620
uce-1470	1680	uce-5085	1620
uce-1662	1621	uce-5269	1620
uce-175	1616	uce-5368	1622
uce-1843	1494	uce-53	1603
uce-1899	1620	uce-5440	1615
uce-2040	1620	uce-5481	1620
uce-2076	1626	uce-5494	1614
uce-2113	1620	uce-5573	1580
uce-211	1620	uce-5609	1618
uce-2261	1585	uce-5673	1621
uce-2274	1620	uce-5775	1613
uce-2284	1620	uce-5779	1599
uce-2349	1620	uce-5786	1620
uce-2513	1607	uce-5837	1620
uce-2598	1620	uce-5840	1616
uce-2609	1620	uce-5902	1620
uce-2619	1612	uce-5910	1620
uce-2687	1620	uce-6019	1620
uce-2843	1620	uce-603	1620
uce-2870	1620	uce-6050	1620
uce-3074	1620	uce-6218	1604
uce-3225	1621	uce-6226	1620
uce-3307	1620	uce-6252	1588
uce-3330	1620	uce-6568	1620
uce-3616	1621	uce-65	1598
uce-3632	1613	uce-6604	1619
uce-3662	1620	uce-6778	1621
uce-3734	1620	uce-6902	1620
uce-3767	1620	uce-6915	1586
uce-3789	1616	uce-6920	1620
uce-383	1611	uce-6934	1531
uce-3984	1620	uce-7095	1603
uce-398	1620	uce-7129	1261
uce-4005	1620	uce-7330	1620
uce-4014	1612	uce-7362	1620
uce-4027	1591	uce-7379	1620
uce-4116	1620	uce-7419	1620
uce-4180	1620	uce-7460	1620
uce-4181	1620	uce-7485	1618
uce-4327	1622	uce-7516	1616
uce-4414	1621	uce-7534	1620
uce-4538	1618	uce-7569	1620
uce-4592	1607	uce-7622	1616
uce-4660	1620	uce-7650	1620
uce-4725	1623	uce-7727	1604
uce-4823	1606	uce-913	1616

Table S15. Metrics of UCE alignments generated by the method of Koch et al (2021) indicating proprieties associated with their evolutionary signal and topological

Gene name	Position in dataset	Root-tip var.	Saturation	Missing data	Evolutionary rate	Tree length	Treeness	Av patristic dist.	Alignment length	Occupancy	Prop. variable sites	Av. bootstrap support	RF similarity
p2871 uce-6915	2871	6.07E-07	0.0037	0.0000	0.000159	0.00317	0.99811	0.00065	1586	0.8	0.00378	61.86	0.2941
p1711 uce-4660	1711	3.87E-07	0.0586	0.0000	0.000310	0.00682	0.72622	0.00135	1620	0.88	0.00556	63.89	0.2632
p3483 uce-913	3483	2.32E-07	0.0020	0.0000	0.000189	0.00435	0.99793	0.00115	1616	0.92	0.00495	69.33	0.2500
p1249 uce-3767	1249	4.62E-07	0.0022	0.0000	0.000129	0.00310	0.79896	0.00080	1620	0.96	0.00309	70.33	0.2381
p3178 uce-7534	3178	5.79E-07	0.0524	0.0000	0.000258	0.00619	0.50045	0.00129	1620	0.96	0.00556	61.33	0.2381
p2184 uce-5573	2184	9.66E-07	0.3652	0.0006	0.000318	0.00636	0.49994	0.00167	1580	0.8	0.00633	63.21	0.2353
p2713 uce-65	2713	1.82E-07	0.0110	0.0012	0.000299	0.00629	0.59997	0.00171	1598	0.84	0.00563	66.69	0.2222
p1365 uce-3984	1365	1.60E-06	0.1281	0.0000	0.000548	0.01151	0.50735	0.00212	1620	0.84	0.00864	65.00	0.2222
p2291 uce-5779	2291	2.58E-07	0.0028	0.0000	0.000143	0.00314	0.59983	0.00061	1599	0.88	0.00313	64.50	0.2105
p1819 uce-4855	1819	2.03E-07	0.2059	0.0000	0.000081	0.00186	0.99732	0.00051	1620	0.92	0.00123	63.00	0.2000
p2960 uce-7095	2960	1.50E-07	0.0030	0.0006	0.000109	0.00251	0.74864	0.00062	1603	0.92	0.00250	62.67	0.2000
p2977 uce-7129	2977	1.08E-06	0.0024	0.0000	0.000346	0.00795	0.59998	0.00195	1261	0.92	0.00793	63.11	0.2000
p1261 uce-3789	1261	2.95E-07	0.0152	0.0000	0.000297	0.00683	0.54575	0.00110	1616	0.92	0.00619	61.77	0.2000
p1186 uce-3662	1186	4.58E-07	0.2845	0.0000	0.000311	0.00746	0.74950	0.00215	1620	0.96	0.00556	72.10	0.1905
p2694 uce-6568	2694	3.41E-07	0.1887	0.0000	0.000155	0.00372	0.66652	0.00084	1620	0.96	0.00309	63.60	0.1905
p1394 uce-4027	1394	1.82E-06	0.2095	0.0000	0.000289	0.00694	0.63619	0.00174	1591	0.96	0.00629	62.07	0.1905
p2880 uce-6934	2880	1.68E-06	0.1973	0.0023	0.000361	0.00866	0.61679	0.00190	1531	0.96	0.00718	62.42	0.1905
p1386 uce-4014	1386	8.44E-08	0.0245	0.0095	0.000183	0.00440	0.57141	0.00097	1612	0.96	0.00434	66.27	0.1905
p1820 uce-4856	1820	1.59E-07	0.0524	0.0000	0.000232	0.00557	0.44495	0.00074	1620	0.96	0.00556	61.75	0.1905
p1231 uce-3734	1231	3.31E-07	0.0025	0.0000	0.000181	0.00434	0.42940	0.00085	1620	0.96	0.00432	61.13	0.1905
p1931 uce-5085	1931	7.79E-07	0.3512	0.0000	0.000276	0.00690	0.81832	0.00202	1620	1	0.00494	70.20	0.1818
p1749 uce-4725	1749	1.39E-07	0.0010	0.0018	0.000248	0.00496	0.37556	0.00076	1623	0.8	0.00678	60.58	0.1765
p415 uce-2113	415	5.92E-07	0.1839	0.0000	0.000223	0.00469	0.85947	0.00125	1620	0.84	0.00309	62.30	0.1667
p3120 uce-7419	3120	2.25E-07	0.0189	0.0000	0.000207	0.00434	0.71363	0.00089	1620	0.84	0.00370	69.00	0.1667
p2115 uce-5440	2115	1.37E-07	0.0033	0.0000	0.000089	0.00187	0.33476	0.00041	1615	0.84	0.00186	61.40	0.1667
p3091 uce-7362	3091	1.52E-07	0.0155	0.0025	0.000113	0.00248	0.99678	0.00052	1620	0.88	0.00247	63.00	0.1579
p162 uce-1470	162	8.51E-07	0.0015	0.0000	0.000217	0.00478	0.87378	0.00141	1680	0.88	0.00476	69.82	0.1579
p265 uce-175	265	1.54E-07	0.0000	0.0130	0.000229	0.00503	0.74803	0.00149	1616	0.88	0.00557	69.53	0.1579
p2418 uce-6019	2418	2.02E-06	0.5534	0.0000	0.000641	0.01410	0.72709	0.00334	1620	0.88	0.00926	60.85	0.1579
p1582 uce-4414	1582	8.48E-07	0.1804	0.0006	0.000313	0.00689	0.72687	0.00179	1621	0.88	0.00555	67.43	0.1579
p1542 uce-4327	1542	3.50E-07	0.0019	0.0012	0.000253	0.00557	0.66685	0.00150	1622	0.88	0.00555	62.00	0.1579
p535 uce-2349	535	1.07E-07	0.0042	0.0000	0.000085	0.00186	0.66630	0.00034	1620	0.88	0.00185	62.60	0.1579
p2426 uce-603	2426	2.08E-07	0.0031	0.0000	0.000113	0.00248	0.50039	0.00048	1620	0.88	0.00247	68.71	0.1579
p419 uce-211	419	3.13E-07	0.0536	0.0000	0.000225	0.00496	0.50010	0.00091	1620	0.88	0.00432	61.27	0.1579
p1020 uce-3330	1020	2.88E-07	0.0452	0.0000	0.000225	0.00496	0.37579	0.00095	1620	0.88	0.00432	61.55	0.1579
p787 uce-2843	787	9.04E-08	0.0030	0.0000	0.000135	0.00310	0.99806	0.00060	1620	0.92	0.00309	70.00	0.1500
p1167 uce-3632	1167	1.35E-07	0.0036	0.0018	0.000136	0.00312	0.99744	0.00060	1613	0.92	0.00310	61.20	0.1500
p2872 uce-6920	2872	1.80E-06	0.5123	0.0001	0.000246	0.00566	0.88699	0.00186	1620	0.92	0.00370	63.09	0.1500
p661 uce-2598	661	1.89E-07	0.1998	0.0000	0.000135	0.00310	0.79945	0.00102	1620	0.92	0.00247	66.25	0.1500
p2138 uce-5481	2138	3.03E-07	0.3087	0.0000	0.000135	0.00310	0.79934	0.00087	1620	0.92	0.00247	67.10	0.1500
p2433 uce-6050	2433	2.16E-07	0.2942	0.0000	0.000135	0.00310	0.79873	0.00077	1620	0.92	0.00247	68.80	0.1500
p2036 uce-5269	2036	1.47E-06	0.2580	0.0000	0.000379	0.00872	0.78502	0.00214	1620	0.92	0.00617	65.35	0.1500
p495 uce-2274	495	1.41E-06	0.2361	0.0000	0.000355	0.00816	0.76873	0.00252	1620	0.92	0.00679	66.13	0.1500
p2321 uce-5837	2321	8.41E-07	0.4001	0.0000	0.000189	0.00434	0.71378	0.00108	1620	0.92	0.00370	61.83	0.1500
p2142 uce-5494	2142	2.67E-06	0.4801	0.0000	0.000636	0.01463	0.69373	0.00320	1614	0.92	0.00805	63.30	0.1500
p667 uce-2609	667	8.39E-07	0.0895	0.0000	0.000431	0.00990	0.68702	0.00189	1620	0.92	0.00864	67.00	0.1500
p108 uce-1304	108	7.66E-07	0.3590	0.0001	0.000244	0.00562	0.66637	0.00132	1607	0.92	0.00498	63.50	0.1500
p706 uce-2687	706	4.19E-07	0.3158	0.0000	0.000166	0.00381	0.66579	0.00107	1620	0.92	0.00309	60.22	0.1500
p3287 uce-7727	3287	1.39E-07	0.0780	0.0000	0.000190	0.00438	0.57150	0.00100	1604	0.92	0.00374	63.11	0.1500
p54 uce-1149	54	3.46E-07	0.0079	0.0107	0.000300	0.00689	0.54521	0.00126	1620	0.92	0.00617	65.62	0.1500
p2237 uce-5673	2237	1.32E-07	0.0017	0.0006	0.000216	0.00496	0.50020	0.00106	1621	0.92	0.00555	61.50	0.1500
p3198 uce-7569	3198	1.64E-07	0.0032	0.0000	0.000189	0.00434	0.42910	0.00056	1620	0.92	0.00432	61.44	0.1500
p488 uce-2261	488	3.57E-07	0.0028	0.0000	0.000079	0.00190	0.99842	0.00060	1585	0.96	0.00189	70.20	0.1429
p3225 uce-7622	3225	1.33E-07	0.1022	0.0000	0.000156	0.00373	0.99786	0.00088	1616	0.96	0.00309	64.69	0.1429
p1473 uce-4180	1473	5.93E-07	0.5926	0.0000	0.000078	0.00186	0.99732	0.00079	1620	0.96	0.00123	65.57	0.1429
p1866 uce-4940	1866	3.97E-07	0.0819	0.0000	0.000155	0.00373	0.99732	0.00098	1620	0.96	0.00309	66.46	0.1429
p3168 uce-7516	3168	4.08E-07	0.2176	0.0000	0.000181	0.00435	0.85630	0.00129	1616	0.96	0.00371	65.45	0.1429
p2536 uce-6252	2536	3.53E-07	0.4349	0.0006	0.000185	0.00444	0.85524	0.00127	1588	0.96	0.00315	66.27	0.1429
p1798 uce-4823	1798	6.99E-07	0.4703	0.0060	0.000493	0.01183	0.83898	0.00285	1606	0.96	0.00685	67.81	0.1429
p2803 uce-6778	2803	2.75E-07	0.0108	0.0019	0.000155	0.00373	0.83199	0.00093	1621	0.96	0.00370	64.17	0.1429
p387 uce-2040	387	3.40E-06	0.4914	0.0000	0.000497	0.01193	0.78931	0.00345	1620	0.96	0.00679	63.32	0.1429
p1159 uce-3616	1159	1.26E-06	0.2741	0.0006	0.000341	0.00817	0.76917	0.00173	1621	0.96	0.00617	62.76	0.1429
p3243 uce-7650	3243	9.45E-06	0.4262	0.0000	0.000542	0.01301	0.76300	0.00440	1620	0.96	0.00926	66.56	0.1429
p1379 uce-4005	1379	7.62E-07	0.0179	0.0000	0.000439	0.01053	0.70579	0.00205	1620	0.96	0.00926	65.67	0.1429
p2517 uce-6218	2517	6.91E-07	0.1674	0.0006	0.000290	0.00695	0.63644	0.00183	1604	0.96	0.00499	60.00	0.1429
p1007 uce-3307	1007	1.99E-07	0.0422	0.0000	0.000207	0.00497	0.62557	0.00090	1620	0.96	0.00432	60.36	0.1429
p1369 uce-398	1369	5.01E-07	0.1268	0.0000	0.000209	0.00502	0.62425	0.00126	1620	0.96	0.00370	60.54	0.1429
p1670 uce-4592	1670	6.65E-07	0.0886	0.0000	0.000264	0.00633	0.60100	0.00143	1607	0.96	0.00498	61.58	0.1429
p804 uce-2870	804	4.80E-07	0.0011	0.0000	0.000258	0.00619	0.59968	0.00111	1620	0.96	0.00617	64.79	0.1429
p2206 uce-5609	2206	1.31E-06	0.0682	0.0000	0.000260	0.00623	0.59817	0.00175	1618	0.96	0.00556	65.50	0.1429
p2862 uce-6902	2862	8.25E-07	0.4625	0.0000	0.000310	0.00743	0.58384	0.00164	1620	0.96	0.00556	60.00	0.1429
p3077 uce-7330	3077	2.62E-06	0.2066	0.0000	0.000316	0.00758	0.58192	0.00184	1620	0.96	0.00617	61.62	0.1429
p618 uce-2513	618	3.36E-07	0.0012	0.0000	0.000183	0.00438	0.57123	0.00100	1607	0.96	0.00498	63.93	0.1429
p2289 uce-5775	2289	1.03E-06	0.3164	0.0000	0.000775	0.01860	0.56751	0.00424	1613	0.96	0.01178	61.14	0.1429
p502 uce-2284</													

p2716 uce-6604	2716	1.66E-07	0.0224	0.0000	0.000155	0.00372	0.50054	0.00068	1619	0.96	0.00309	63.00	0.1429
p673 uce-2619	673	1.04E-06	0.2961	0.0006	0.000285	0.00685	0.45506	0.00141	1612	0.96	0.00620	61.00	0.1429
p2095 uce-53	2095	1.78E-07	0.1864	0.0000	0.000183	0.00438	0.42916	0.00076	1603	0.96	0.00437	63.18	0.1429
p2294 uce-5786	2294	2.87E-07	0.0451	0.0000	0.000232	0.00557	0.33424	0.00109	1620	0.96	0.00494	60.09	0.1429
p1799 uce-4828	1799	1.73E-06	0.3389	0.0006	0.000404	0.01010	0.81061	0.00271	1621	1	0.00740	66.58	0.1364
p8 uce-1027	8	4.65E-07	0.0184	0.0000	0.000279	0.00699	0.69935	0.00142	1437	1	0.00626	61.81	0.1364
p1474 uce-4181	1474	3.83E-07	0.2810	0.0000	0.000198	0.00495	0.62455	0.00067	1620	1	0.00432	61.78	0.1364
p2523 uce-6226	2523	2.28E-07	0.0134	0.0000	0.000322	0.00805	0.61499	0.00181	1620	1	0.00741	68.44	0.1364
p117 uce-1334	117	9.47E-08	0.0208	0.0004	0.000149	0.00371	0.50012	0.00066	1620	1	0.00370	62.75	0.1364
p2361 uce-5910	2361	6.86E-06	0.0663	0.0000	0.000496	0.00991	0.75007	0.00246	1620	0.8	0.00864	65.29	0.1176
p1642 uce-4538	1642	4.35E-07	0.0015	0.0018	0.000252	0.00503	0.74951	0.00115	1597	0.8	0.00501	64.56	0.1176
p1440 uce-4116	1440	4.05E-07	0.4449	0.0000	0.000124	0.00248	0.74898	0.00066	1620	0.8	0.00185	62.57	0.1176
p898 uce-3074	898	8.98E-07	0.0851	0.0000	0.000279	0.00557	0.66631	0.00141	1620	0.8	0.00494	67.83	0.1176
p401 uce-2076	401	8.54E-07	0.2512	0.0037	0.000217	0.00434	0.57122	0.00108	1626	0.8	0.00308	66.56	0.1176
p2080 uce-5368	2080	5.17E-07	0.0437	0.0012	0.000402	0.00804	0.46173	0.00154	1622	0.8	0.00740	63.00	0.1176
p2355 uce-5902	2355	6.09E-06	0.2319	0.0000	0.000257	0.00540	0.99870	0.00265	1620	0.84	0.00432	69.44	0.1111
p233 uce-1662	233	3.95E-07	0.0010	0.0006	0.000177	0.00373	0.99678	0.00127	1621	0.84	0.00494	64.08	0.1111
p304 uce-1843	304	4.72E-07	0.3386	0.0124	0.000161	0.00337	0.99436	0.00114	1494	0.84	0.00335	63.26	0.1111
p1291 uce-383	1291	1.79E-07	0.0000	0.0032	0.000119	0.00251	0.74911	0.00054	1611	0.84	0.00248	64.09	0.1111
p965 uce-3225	965	1.28E-06	0.3069	0.0006	0.000236	0.00496	0.74887	0.00132	1621	0.84	0.00432	66.40	0.1111
p322 uce-1899	322	7.24E-08	0.0029	0.0000	0.000177	0.00372	0.66604	0.00090	1620	0.84	0.00370	61.30	0.1111
p3137 uce-7460	3137	1.79E-06	0.0000	0.0009	0.000324	0.00681	0.62928	0.00160	1620	0.84	0.00741	61.25	0.1111
p2324 uce-5840	2324	2.51E-07	0.0514	0.0000	0.000207	0.00435	0.57151	0.00068	1616	0.84	0.00371	61.67	0.1111

Table S16. Pairwise correlation values of terrestrial variables used to select those informative to perform RDA analysis.

	bio18	bio15	bio10	bio07	bio03	bio02
bio18	1	-0.6341656	0.38452482	-0.6262054	0.8528494	0.26909812
bio15	-0.6341656	1	-0.7076371	0.8874445	-0.7272719	0.10162702
bio10	0.3845248	-0.7076371	1	-0.6087511	0.5318022	0.01039951
bio07	-0.6262054	0.8874445	-0.6087511	1	-0.5417634	0.41326538
bio03	0.8528494	-0.7272719	0.53180218	-0.5417634	1	0.53707657
bio02	0.2690981	0.101627	0.01039951	0.4132654	0.5370766	1

Table S17. Pairwise correlation values of marine variables used to select those informative to perform RDA analysis.

	o10_primpr	o11_salini	o09_primpr	o13_tempma	o01_icecov	o12_salini
o10_primpr	1	-0.4815446	0.59520196	0.8175376	-0.6993561	0.65237001
o11_salini	-0.4815446	1	0.21455297	-0.8302807	0.9397682	-0.783103
o09_primpr	0.595202	0.214553	1	0.1872032	-0.0168878	-0.042142
o13_tempma	0.8175376	-0.8302807	0.18720315	1	-0.9493384	0.83587428
o01_icecov	-0.6993561	0.9397682	-0.0168878	-0.9493384	1	-0.8636195
o12_salini	0.65237	-0.783103	-0.042142	0.8358743	-0.8636195	1

Table S18. Occurrence data from breeding colony location data combined with GBIF information used as spatial occurrence data for future niche projection.

Gentoo lineage	x	y
Northern gentoo	-60.7	-51.35
Northern gentoo	-57.85	-51.7
Northern gentoo	-58.07	-51.76
Northern gentoo	-61.3	-51.71
Northern gentoo	-61.175002	-51.024997
Northern gentoo	-60.54	-51.29
Northern gentoo	-67.37	-54.91
Northern gentoo	-67.38	-54.91
Northern gentoo	-68.275002	-55.024997
Northern gentoo	-61.3	-51.73
Northern gentoo	-61.225002	-51.074997
Northern gentoo	-59.125002	-52.424997
Northern gentoo	-67.375002	-54.924997
Northern gentoo	-60.275002	-51.324997
Northern gentoo	-67.35	-54.88
Northern gentoo	-68.175002	-55.024997
Northern gentoo	-59.07	-52.45
Northern gentoo	-57.83	-51.48
Northern gentoo	-59.625002	-51.324997
Northern gentoo	-67.4	-54.9
Northern gentoo	-57.81	-51.68
Northern gentoo	-57.62	-51.69
Northern gentoo	-67.375002	-54.924997
Northern gentoo	-58.625002	-51.924997
Northern gentoo	-60.55	-51.29
Northern gentoo	-67.775002	-55.224997
Northern gentoo	-58.09	-51.75
Northern gentoo	-58.925002	-52.224997
Northern gentoo	-57.76	-51.69
Northern gentoo	-61.29	-51.75
Northern gentoo	-61.26	-51.69
Northern gentoo	-59.4	-51.71
Northern gentoo	-59.375002	-52.174997
Northern gentoo	-58.475002	-51.274997
Northern gentoo	-59.075002	-52.474997
Northern gentoo	-58.325002	-51.374997
Northern gentoo	-58.96	-51.25
Northern gentoo	-60.53	-51.25
Northern gentoo	-61.3	-51.72
Northern gentoo	-57.82	-51.69
Northern gentoo	-60.69	-51.35
Northern gentoo	-57.82	-51.67
Northern gentoo	-59.73	-51.16
Northern gentoo	-57.725002	-51.524997
Northern gentoo	-59.675002	-51.324997
Northern gentoo	-58.61	-52.28
Northern gentoo	-58.375002	-51.824997
Northern gentoo	-59.525002	-51.474997
Northern gentoo	-60.69	-51.36
Northern gentoo	-59.075002	-52.474997
Northern gentoo	-58.375002	-51.924997
Northern gentoo	-68.225002	-55.024997
Northern gentoo	-67.39	-54.91

Northern gentoo	-57.81	-51.65
Northern gentoo	-58.09	-51.76
Northern gentoo	-60.175002	-51.374997
Northern gentoo	-57.84	-51.48
Northern gentoo	-60.225002	-51.274997
Northern gentoo	-59.625002	-51.324997
Northern gentoo	-60.625002	-51.324997
Northern gentoo	-57.75	-51.62
Northern gentoo	-60.225002	-51.274997
Northern gentoo	-57.78	-51.68
Northern gentoo	-60.52	-51.31
Northern gentoo	-58.675002	-51.924997
Northern gentoo	-57.83	-51.47
Northern gentoo	-59.075002	-51.524997
Northern gentoo	-67.37	-54.9
Northern gentoo	-59.375002	-51.824997
Northern gentoo	-59.125002	-52.424997
Northern gentoo	-60.175002	-51.374997
Northern gentoo	-59.025002	-52.424997
Northern gentoo	-58.675002	-51.924997
Northern gentoo	-57.875002	-51.774997
Northern gentoo	-68.225002	-55.024997
Northern gentoo	-60.08	-51.36
Northern gentoo	-60.525002	-51.274997
Northern gentoo	-61.26	-51.7
Northern gentoo	-60.78	-51.42
Northern gentoo	-68.175002	-55.024997
Northern gentoo	-68.225002	-55.024997
Northern gentoo	-68.275002	-55.024997
Northern gentoo	-57.825002	-51.574997
Northern gentoo	-57.775002	-51.674997
Northern gentoo	-67.375002	-54.924997
Northern gentoo	-66.53	-55.06
Northern gentoo	-60.175002	-51.374997
Northern gentoo	-58.375002	-51.924997
Northern gentoo	-57.825002	-51.674997
Northern gentoo	-65.99	-54.9
Northern gentoo	-68.275002	-55.024997
Northern gentoo	-59.625002	-51.324997
Northern gentoo	-58.375002	-51.924997
Northern gentoo	-57.72	-51.68
Northern gentoo	-68.175002	-55.024997
Northern gentoo	-57.79	-51.69
Northern gentoo	-59.52	-51.62
Northern gentoo	-58.06	-51.76
Northern gentoo	-68.525002	-55.124997
Northern gentoo	-59.775002	-51.874997
Northern gentoo	-68.175002	-55.024997
Northern gentoo	-61.31	-51.72
Northern gentoo	-64.275002	-54.724997
Northern gentoo	-57.75	-51.64
Northern gentoo	-67.375002	-54.924997
Northern gentoo	-59.025002	-52.424997
Northern gentoo	-59.725002	-51.224997
Northern gentoo	-57.84	-51.47
Northern gentoo	-67.325002	-54.874997
Northern gentoo	-67.375002	-54.924997
Northern gentoo	-67.825002	-55.224997
Northern gentoo	-67.32	-54.88

Northern gentoo	-68.275002	-55.024997
Northern gentoo	-67.4	-54.91
Northern gentoo	-58.875002	-51.274997
Northern gentoo	-59.37	-51.28
Northern gentoo	-57.825002	-51.674997
Northern gentoo	-67.39	-54.91
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Northern gentoo	-68.275002	-55.024997
Northern gentoo	-60.225002	-51.274997
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Southern gentoo	-54.86	-61.15
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Southern gentoo	-36.775001	-54.474997
Southern gentoo	-35.775001	-54.774997
Southern gentoo	-62.61	-64.7
Southern gentoo	-62.425002	-64.874998
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Southern gentoo	-36.23	-54.3
Southern gentoo	-60.625002	-62.974998
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Southern gentoo	-36.175001	-54.424997
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Southern gentoo	-64.225002	-64.774998
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Southern gentoo	-58.475002	-62.274998
Southern gentoo	-58.67	-62.25
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Southern gentoo	-58.925002	-62.224998
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Southern gentoo	-55.2	-61.28
Southern gentoo	-63.975002	-65.124998
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Southern gentoo	-37.375001	-54.024997
Southern gentoo	-58.44	-62.18
Southern gentoo	-59.025002	-62.174998
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Southern gentoo	-62.15	-64.45
Southern gentoo	-26.58	-57.74
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Southern gentoo	-36.58	-54.2
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Southern gentoo	-62.72	-64.83
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Southern gentoo	-62.63	-64.84
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Southern gentoo	-62.725002	-64.674998
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Southern gentoo	-60.925002	-64.124998
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Southern gentoo	-59.975002	-62.624998
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Southern gentoo	-37.375001	-54.024997
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Southern gentoo	-56.57	-63.16
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Southern gentoo	-63.78	-64.81
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Southern gentoo	-58.425002	-62.174998
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Southern gentoo	-63.43	-64.78
Southern gentoo	-60.96	-64.16
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Southern gentoo	-64.25	-65.25
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Southern gentoo	-65.19	-65.58
Southern gentoo	-62.63	-64.69
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Southern gentoo	-62.525002	-64.874998
Southern gentoo	-62.525002	-64.874998
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Southern gentoo	-62.71	-64.8
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Southern gentoo	-37.85	-53.93
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Southern gentoo	-37.77	-53.89
Southern gentoo	-36.07	-54.43
Southern gentoo	-59.59	-62.55
Southern gentoo	-35.84	-54.67
Southern gentoo	-36	-54.46
Southern gentoo	-37.64	-53.91
Southern gentoo	-59.64	-62.39
Southern gentoo	-63.52	-64.88
Southern gentoo	-62.62	-64.73
Southern gentoo	-59.73	-62.4
Southern gentoo	-59.06	-62.92
Southern gentoo	-36.075001	-54.524997
Southern gentoo	-60.825002	-62.424998
Southern gentoo	-56	-63
Southern gentoo	-55	-61
Southern gentoo	-54	-61
Southern gentoo	-27.08	-59.43
Southern gentoo	-45.925002	-60.674997
Southern gentoo	-64.55	-65.28
Southern gentoo	-56.77	-64.45

Southern gentoo	-64	-64.79
Southern gentoo	-36.625001	-54.124997
Southern gentoo	-62.52	-64.85
Southern gentoo	-64.03	-65.1
Southern gentoo	-63.24	-64.87
Southern gentoo	-62.9	-64.78
Southern gentoo	-60.725002	-62.474998
Southern gentoo	-40.225001	-53.924997
Southern gentoo	-58.54	-63.28
Southern gentoo	-36.02	-54.54
Southern gentoo	-35.975001	-54.824997
Southern gentoo	-36.46	-54.18
Southern gentoo	-36.98	-54.08
Southern gentoo	-55.17	-61.07
Southern gentoo	-56.72	-63.38
Southern gentoo	-56.79	-63.39
Southern gentoo	-36.825001	-54.074997
Southern gentoo	-62.09	-64.66
Southern gentoo	-57	-63.38
Southern gentoo	-59.625002	-62.424998
Southern gentoo	-62.59	-64.6
Southern gentoo	-36.575001	-54.224997
Southern gentoo	-35.88	-54.91
Southern gentoo	-36.68	-54.19
Southern gentoo	-56.81	-63.45
Southern gentoo	-55.98	-63.61
Southern gentoo	-36.61	-54.15
Southern gentoo	-36.775001	-54.074997
Southern gentoo	-38.17	-53.85
Southern gentoo	-64.02	-65.07
Southern gentoo	-62.78	-64.62
Southern gentoo	-60.125002	-62.724998
Southern gentoo	-56.26	-63.46
Southern gentoo	-61.02	-63.87
Southern gentoo	-63.475002	-64.774998
Southern gentoo	-36.175001	-54.424997
Southern gentoo	-55.125002	-61.074997
Southern gentoo	-36.575001	-54.524997
Southern gentoo	-58.725002	-62.274998
Southern gentoo	-58.02	-62.06
Southern gentoo	-37.675001	-53.974997
Southern gentoo	-36.675001	-54.174997
Southern gentoo	-35.93	-54.62
Southern gentoo	-36.3	-54.29
Southern gentoo	-59.61	-62.35
Southern gentoo	-60.32	-62.46
Southern gentoo	-57.92	-62.1
Southern gentoo	-55.83	-63.61
Southern gentoo	-59.39	-62.22
Southern gentoo	-56.53	-63.48
Southern gentoo	-60.67	-62.97
Southern gentoo	-60.73	-63.92
Southern gentoo	-45.35	-60.75
Southern gentoo	-61.6	-64.11
Southern gentoo	-62	-64.55
Southern gentoo	-58.79	-62.78
Southern gentoo	-57.46	-63.91
Southern gentoo	-61.97	-64.43
Southern gentoo	-37.675001	-53.974997

Southern gentoo	-60.61	-62.97
Southern gentoo	-56.62	-63.51
Southern gentoo	-62.89	-64.22
Southern gentoo	-37.425001	-54.024997
Southern gentoo	-56.825002	-63.524998
Southern gentoo	-63.92	-65.04
Southern gentoo	-56.95	-63.34
Southern gentoo	-64.125002	-65.124998
Southern gentoo	-62.93	-64.9
Southern gentoo	-64.075002	-65.074998
Southern gentoo	-62.87	-64.82
Southern gentoo	-62.625002	-64.674998
Southern gentoo	-57.275002	-64.424998
Southern gentoo	-37.28	-54.03
Southeastern gentoo	70.22	-49.35
Southeastern gentoo	70.2750024	-49.424997
Southeastern gentoo	70.2750024	-49.674997
Southeastern gentoo	70.1750024	-49.624997
Southeastern gentoo	69.93	-49.47
Southeastern gentoo	70.0250024	-49.524997
Southeastern gentoo	69.95	-49.52
Southeastern gentoo	70.5750024	-49.224997
Southeastern gentoo	70.53	-49.3
Southeastern gentoo	70.5250024	-49.124997
Southeastern gentoo	70.4750024	-49.074997
Southeastern gentoo	70.3	-49.06
Southeastern gentoo	70.1750024	-49.124997
Southeastern gentoo	70.2	-49.35
Southeastern gentoo	70.08	-49.37
Southeastern gentoo	70.16	-49.35
Southeastern gentoo	70.07	-49.41
Southeastern gentoo	69.91	-49.52
Southeastern gentoo	69.9250024	-49.424997
Southeastern gentoo	70.4750024	-49.374997
Southeastern gentoo	70.02	-49.37
Southeastern gentoo	70.5750024	-49.174997
Southeastern gentoo	70.4750024	-49.374997
Southeastern gentoo	69.96	-49.44
Southeastern gentoo	70.4250024	-49.474997
Southeastern gentoo	70.23	-49.11
Southeastern gentoo	70.1250024	-49.124997
Southeastern gentoo	70.06	-49.52
Southeastern gentoo	70.0750024	-49.524997
Southeastern gentoo	69.61	-49.65
Southeastern gentoo	70.1250024	-49.124997
Southeastern gentoo	70.05	-49.48
Southeastern gentoo	70.11	-49.41
Southeastern gentoo	70.21	-49.35
Southeastern gentoo	70.09	-49.47
Southeastern gentoo	69.3750024	-49.124997
Southeastern gentoo	70.56	-49.21
Southeastern gentoo	70.0250024	-49.124997
Southeastern gentoo	70.1250024	-49.724997
Southeastern gentoo	69.6750024	-49.174997
Southeastern gentoo	70.04	-49.14
Southeastern gentoo	69.51	-49.16
Southeastern gentoo	73.3750025	-52.974997
Southeastern gentoo	73.7250025	-53.074997
Southeastern gentoo	73.6750025	-53.074997

Southeastern gentoo	69.4750024	-49.274997
Southeastern gentoo	73.21	-52.97
Southeastern gentoo	73.25	-53.26
Southeastern gentoo	72.58	-53.06
Southeastern gentoo	73.82	-53.18
Southeastern gentoo	73.38	-52.93
Southeastern gentoo	72.71	-53.05
Southeastern gentoo	72.61	-53.06
Southeastern gentoo	72.66	-53.02
Southeastern gentoo	73.26	-53.07
Southeastern gentoo	73.56	-52.99
Southeastern gentoo	72.66	-53.04
Southeastern gentoo	73.32	-52.93
Southeastern gentoo	73.46	-52.99
Southeastern gentoo	72.7	-53.08
Southeastern gentoo	72.63	-52.94
Southeastern gentoo	73.4250025	-53.024997
Southeastern gentoo	69.95	-49.46
Southeastern gentoo	69.99	-49.4
Southeastern gentoo	69.85	-49.49
Southeastern gentoo	70.01	-49.53
Southeastern gentoo	70.29	-49.48
Southeastern gentoo	70	-49.48
Southeastern gentoo	70.41	-49.64
Southeastern gentoo	70.47	-49.6
Southeastern gentoo	70.0250024	-49.374997
Southeastern gentoo	70.2750024	-49.674997
Southeastern gentoo	70.2250024	-49.374997
Southeastern gentoo	70.4250024	-49.474997
Southeastern gentoo	70.29	-49.06
Southeastern gentoo	70.24	-49.09
Southeastern gentoo	74.73	-52.47
Southeastern gentoo	74.24	-52.96
Southeastern gentoo	74.47	-52.93
Southeastern gentoo	74.22	-53.2
Southeastern gentoo	74.95	-52.43
Southeastern gentoo	74.92	-52.55
Southeastern gentoo	74.78	-52.47
Southeastern gentoo	73.41	-52.92
Southeastern gentoo	74.83	-52.48
Southeastern gentoo	74.03	-53.12
Southeastern gentoo	74.68	-52.45
Southeastern gentoo	73.41	-52.9
Southeastern gentoo	74.67	-52.43
Southeastern gentoo	74.3	-52.25
Southeastern gentoo	74.31	-52.93
Southeastern gentoo	74.26	-52.95
Southeastern gentoo	69.0750023	-48.674997
Southeastern gentoo	69.43	-48.9
Southeastern gentoo	69.81	-49.81
Southeastern gentoo	70.3750024	-49.024997
Southeastern gentoo	69.8750024	-49.374997
Southeastern gentoo	73.4250025	-53.024997
Southeastern gentoo	70.24	-49.51
Southeastern gentoo	70.07	-49.46
Southeastern gentoo	69.3750024	-49.624997
Southeastern gentoo	69.24	-49.61
Southeastern gentoo	69.07	-49.57
Southeastern gentoo	68.8750023	-49.424997

Southeastern gentoo	73.4250025	-53.024997
Southeastern gentoo	69.93	-49.54
Southeastern gentoo	69.51	-49.27
Southeastern gentoo	69.06	-48.78
Southeastern gentoo	69.1250023	-48.974997
Southeastern gentoo	69.93	-49.04
Southeastern gentoo	69.7250024	-49.524997
Southeastern gentoo	69.75	-49.26
Southeastern gentoo	70.04	-48.97
Southeastern gentoo	70.3750024	-49.024997
Southeastern gentoo	70.5750024	-49.224997
Southeastern gentoo	70.51	-49.32
Southeastern gentoo	73.66	-52.95
Southeastern gentoo	73.62	-53.2
Southeastern gentoo	73.6250025	-53.174997
Southeastern gentoo	73.35	-53.07
Southeastern gentoo	73.3	-52.95
Southeastern gentoo	73.4250025	-53.024997
Eastern gentoo	158.825005	-54.574997
Eastern gentoo	51.87	-46.43
Eastern gentoo	158.975005	-54.524997
Eastern gentoo	158.93	-54.49
Eastern gentoo	158.92	-54.56
Eastern gentoo	51.7250018	-46.474997
Eastern gentoo	158.825005	-54.574997
Eastern gentoo	158.925005	-54.474997
Eastern gentoo	37.7250013	-46.974997
Eastern gentoo	158.925005	-54.474997
Eastern gentoo	158.825005	-54.574997
Eastern gentoo	158.92	-54.57
Eastern gentoo	158.91	-54.55
Eastern gentoo	37.7250013	-46.974997
Eastern gentoo	37.9250013	-46.674997
Eastern gentoo	158.825005	-54.574997
Eastern gentoo	158.875005	-54.724997
Eastern gentoo	51.88	-46.43
Eastern gentoo	158.88	-54.7
Eastern gentoo	51.86	-46.43
Eastern gentoo	159.05	-54.43
Eastern gentoo	158.925005	-54.574997
Eastern gentoo	158.925005	-54.474997
Eastern gentoo	50.97	-46.3
Eastern gentoo	51.7250018	-46.324997
Eastern gentoo	158.825005	-54.674997
Eastern gentoo	158.83	-54.77
Eastern gentoo	158.85	-54.53
Eastern gentoo	158.94	-54.49
Eastern gentoo	51.82	-46.39
Eastern gentoo	37.7750013	-46.974997
Eastern gentoo	158.92	-54.67
Eastern gentoo	37.88	-46.89
Eastern gentoo	37.9	-46.78
Eastern gentoo	158.925005	-54.474997
Eastern gentoo	158.825005	-54.674997
Eastern gentoo	158.96	-54.51