

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0032532~regulation of microvillus length	4	1.5504	5.25E-05	VIL1, USH1C, CDHR5, PLS1	226	7	19349	48.92288243	0.078398016	0.081639694	0.081377356
GOTERM_BP_DIRECT	GO:0007416~synapse assembly	7	2.7132	1.17E-04	PCLO, ERBB4, FLRT3, SLITRK6, DRD2, IGFN1, SHANK2	226	66	19349	9.080383481	0.167017114	0.091365726	0.091072134
GOTERM_BP_DIRECT	GO:0048856~anatomical structure development	6	2.3256	2.81E-04	EYA1, PAX7, WIF1, HNF4A, HNF4G, TDGF1	226	50	19349	10.27380531	0.354650412	0.114073932	0.11370773
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	20	7.7519	2.93E-04	DLX2, SRMS, CDX2, EYA1, DLX6, HNF4G, C9ORF24, CPLX2, ETV4, IGSF10, HNF4A, PEG10, PRAME, CDHR5, ANKS4B, TRIM54, TDGF1, FOXA3, NGEF, FOXA2	226	664	19349	2.578766393	0.36641597	0.114073932	0.11370773
GOTERM_BP_DIRECT	GO:0009653~anatomical structure morphogenesis	8	3.1008	9.03E-04	FBN3, MLXIPL, EYA1, SIX4, PAX7, GPC3, FOXA3, FOXA2	226	132	19349	5.18879056	0.754827995	0.227437507	0.226706667
GOTERM_BP_DIRECT	GO:0030326~embryonic limb morphogenesis	5	1.938	9.64E-04	SHH, FRAS1, DLX6, SALL4, SP9	226	38	19349	11.2651374	0.776929147	0.227437507	0.226706667
GOTERM_BP_DIRECT	GO:0007548~sex differentiation	4	1.5504	0.00131019	DMRT1, DMRT2, HNF4A, DMRT3	226	19	19349	18.02421984	0.869970287	0.227437507	0.226706667
GOTERM_BP_DIRECT	GO:0046661~male sex differentiation	3	1.1628	0.001315513	DMRT1, SIX4, DMRT3	226	5	19349	51.36902655	0.871044144	0.227437507	0.226706667
GOTERM_BP_DIRECT	GO:0033085~negative regulation of T cell differentiation in thymus	3	1.1628	0.001315513	BMP4, IHH, FOXJ1	226	5	19349	51.36902655	0.871044144	0.227437507	0.226706667
GOTERM_BP_DIRECT	GO:0021978~telencephalon regionalization	3	1.1628	0.001958148	BMP4, SHH, SIX3	226	6	19349	42.80752212	0.952634709	0.304687856	0.303708782
GOTERM_BP_DIRECT	GO:0007605~sensory perception of sound	8	3.1008	0.002196854	GABRB2, EYA1, USH1C, SLITRK6, DCDC2, CACNA1D, CRYM, COCH	226	154	19349	4.447534766	0.967355056	0.310755002	0.309756432
GOTERM_BP_DIRECT	GO:0010842~retina layer formation	4	1.5504	0.003311171	FOXN4, TSPAN12, PROM1, IGFN1	226	26	19349	13.17154527	0.994262498	0.400266562	0.398980359
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	26	10.078	0.003344129	DLX2, IHH, HNF4G, SHH, SIX4, EPCAM, SALL4, HNF4A, SIX3, ALX1, DRD2, CDX2, EYA1, DMRT1, DMRT2, HMG2, FOXJ1, FOXN4, ESRG, ETV4, BMP4, MLXIPL, TOX3, BMPR1B, FOXA3, FOXA2	226	1198	19349	1.858089441	0.994550249	0.400266562	0.398980359
GOTERM_BP_DIRECT	GO:0042733~embryonic digit morphogenesis	5	1.938	0.003818302	BMP4, SHH, IHH, LRP4, FREM2	226	55	19349	7.783185841	0.997401054	0.424376962	0.423013283
GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	6	2.3256	0.00407583	VIL1, UPK1B, DLX6, GSTA1, MS11, KRT20	226	92	19349	5.583589842	0.998965004	0.457213298	0.455744104
GOTERM_BP_DIRECT	GO:0042475~odontogenesis of dentin-containing tooth	5	1.938	0.005219029	BMP4, DLX2, SHH, LRP4, SOSTDC1	226	60	19349	7.134587021	0.999708967	0.466542736	0.465043562
GOTERM_BP_DIRECT	GO:0040008~regulation of growth	5	1.938	0.005535274	IGSF11, IGFBP2, IHH, HMG2, PRAME	226	61	19349	7.017626578	0.999822548	0.466542736	0.465043562
GOTERM_BP_DIRECT	GO:0007399~nervous system development	12	4.6512	0.005674726	CHRM3, GJB1, ERBB4, GDA, DLX6, MS11, GFRA3, PPP1R9A, CPLX2, PCDHAC2, NGEF, PCDHAC1	226	386	19349	2.661607593	0.999857337	0.466542736	0.465043562
GOTERM_BP_DIRECT	GO:0072205~metanephric collecting duct development	3	1.1628	0.005696859	BMP4, SHH, AQP2	226	10	19349	25.68451327	0.999862193	0.466542736	0.465043562
GOTERM_BP_DIRECT	GO:0007389~pattern specification process	4	1.5504	0.006546132	SHH, EYA1, SOSTDC1, FOXJ1	226	33	19349	10.37758112	0.999963539	0.486074868	0.484512931
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	5	1.938	0.006560136	BMP4, SPINK1, EYA1, DLX6, IHH	226	64	19349	6.688675332	0.99996433	0.486074868	0.484512931
GOTERM_BP_DIRECT	GO:0045880~positive regulation of smoothened signaling pathway	4	1.5504	0.009011147	SHH, IHH, GPC3, DCDC2	226	37	19349	9.255680459	0.999999236	0.637333867	0.635285879
GOTERM_BP_DIRECT	GO:0048745~smooth muscle tissue development	3	1.1628	0.009650553	BMP4, SHH, IHH	226	13	19349	19.7573179	0.99999972	0.652880901	0.650782955
GOTERM_BP_DIRECT	GO:0001658~branching involved in ureteric bud morphogenesis	4	1.5504	0.011950877	BMP4, SHH, EYA1, GPC3	226	41	19349	8.352687244	0.999999992	0.765694442	0.763233984
GOTERM_BP_DIRECT	GO:0006790~sulfur compound metabolic process	3	1.1628	0.01279438	CHST9, CHST6, CHST4	226	15	19349	17.12300885	0.999999998	0.765694442	0.763233984
GOTERM_BP_DIRECT	GO:0048148~behavioral response to cocaine	3	1.1628	0.01279438	PPP1R1B, OPRK1, DRD2	226	15	19349	17.12300885	0.999999998	0.765694442	0.763233984
GOTERM_BP_DIRECT	GO:0003382~epithelial cell morphogenesis	3	1.1628	0.014511161	CLDN3, POF1B, IHH	226	16	19349	16.0528208	1	0.819222494	0.816590031
GOTERM_BP_DIRECT	GO:0001755~neural crest cell migration	4	1.5504	0.016314293	SHH, ERBB4, SEMA3E, ALX1	226	46	19349	7.444786456	1	0.819222494	0.816590031
GOTERM_BP_DIRECT	GO:0009790~embryo development	3	1.1628	0.016321271	DLX2, CDX2, DLX6	226	17	19349	15.10853722	1	0.819222494	0.816590031
GOTERM_BP_DIRECT	GO:0036159~inner dynein arm assembly	3	1.1628	0.016321271	DNAH2, TEK2, ZMYND10	226	17	19349	15.10853722	1	0.819222494	0.816590031
GOTERM_BP_DIRECT	GO:0098962~regulation of postsynaptic neurotransmitter receptor activity	3	1.1628	0.016321271	DLGAP1, SHISA9, CACNG4	226	17	19349	15.10853722	1	0.819222494	0.816590031
GOTERM_BP_DIRECT	GO:0009948~anterior/posterior axis specification	3	1.1628	0.020211991	BMP4, CDX2, GPC3	226	19	19349	13.51816488	1	0.982808051	0.979649927
GOTERM_BP_DIRECT	GO:0006833~water transport	3	1.1628	0.022287962	AQP6, AQP5, AQP2	226	20	19349	12.84225664	1	0.999400979	0.996189537
GOTERM_BP_DIRECT	GO:1904106~protein localization to microvillus	2	0.7752	0.023122388	USH1C, ANKS4B	226	2	19349	85.61504425	1	0.999400979	0.996189537
GOTERM_BP_DIRECT	GO:0016539~intein-mediated protein splicing	2	0.7752	0.023122388	SHH, IHH	226	2	19349	85.61504425	1	0.999400979	0.996189537
GOTERM_BP_DIRECT	GO:0015757~galactose transport	2	0.7752	0.023122388	SLC2A10, SLC5A1	226	2	19349	85.61504425	1	0.999400979	0.996189537
GOTERM_BP_DIRECT	GO:0048015~phosphatidylinositol-mediated signaling	4	1.5504	0.026139358	PLCB4, PLCE1, PLCH1, CA8	226	55	19349	6.226548673	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0098719~sodium ion import across plasma membrane	3	1.1628	0.02901135	SLC9A2, SLC9A4, SLC5A1	226	23	19349	11.16717968	1	1	0.997427653
GOTERM_BP_DIRECT	GO:2000311~regulation of AMPA receptor activity	3	1.1628	0.02901135	SHISA9, CACNG4, SHANK2	226	23	19349	11.16717968	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0042391~regulation of membrane potential	5	1.938	0.030315087	KCNH2, GABRB2, KCNH8, HTR3A, SLC4A4	226	101	19349	4.238368527	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0034622~cellular macromolecular complex assembly	3	1.1628	0.031410379	USH1C, C9ORF24, ANKS4B	226	24	19349	10.70188053	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	7	2.7132	0.033021327	PRKAA2, WIF1, LRP4, SOSTDC1, TSPAN12, DRD2, LGR6	226	205	19349	2.923440535	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0006805~xenobiotic metabolic process	5	1.938	0.033247417	CYP26A1, CYP2W1, CYP2B6, HNF4A, GSTA1	226	104	19349	4.116107897	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0045821~positive regulation of glycolytic process	3	1.1628	0.033884827	MLXIPL, PRKAA2, SLC4A4	226	25	19349	10.27380531	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0060438~trachea development	2	0.7752	0.034483191	BMP4, HYDIN	226	3	19349	57.07669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0046639~negative regulation of alpha-beta T cell differentiation	2	0.7752	0.034483191	SHH, IHH	226	3	19349	57.07669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:1902896~terminal web assembly	2	0.7752	0.034483191	VIL1, PLS1	226	3	19349	57.07669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0072138~mesenchymal cell proliferation involved in ureteric bud development	2	0.7752	0.034483191	BMP4, GPC3	226	3	19349	57.07669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0051586~positive regulation of dopamine uptake involved in synaptic transmission	2	0.7752	0.034483191	RAB3B, DRD2	226	3	19349	57.07669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0001951~intestinal D-glucose absorption	2	0.7752	0.034483191	VIL1, PLS1	226	3	19349	57.07669617	1	1	0.997427653

GOTERM_BP_DIRECT	GO:1904970`brush border assembly	2	0.7752	0.034483191	USH1C, ANKS4B	226	3	19349	57.07669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0031016`pancreas development	3	1.1628	0.039051769	SHH, HNF4A, IHH	226	27	19349	9.512782694	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0007507`heart development	7	2.7132	0.039411443	SHH, ERBB4, FLRT3, PLCE1, FOXJ1, TDGF1, FREM2	226	214	19349	2.800492102	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0035116`embryonic hindlimb morphogenesis	3	1.1628	0.044496128	BMP4, SHH, GPC3	226	29	19349	8.856728715	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0051453`regulation of intracellular pH	3	1.1628	0.044496128	SLC9A2, SLC9A4, SLC4A4	226	29	19349	8.856728715	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0014706`striated muscle tissue development	2	0.7752	0.045712452	SHH, EYA1	226	4	19349	42.80752212	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0006570`tyrosine metabolic process	2	0.7752	0.045712452	HGD, IYD	226	4	19349	42.80752212	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0009880`embryonic pattern specification	3	1.1628	0.047317483	SHH, ERBB4, IHH	226	30	19349	8.561504425	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0046676`negative regulation of insulin secretion	3	1.1628	0.047317483	CHGA, FAM3D, DRD2	226	30	19349	8.561504425	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0031069`hair follicle morphogenesis	3	1.1628	0.047317483	SHH, SOSTDC1, TGM3	226	30	19349	8.561504425	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0043066`negative regulation of apoptotic process	12	4.6512	0.047943442	BMP4, SHH, PRKAA2, SIX4, ERBB4, EPCAM, PAX7, IHH, HMG42, PRAME, VTCN1, TDGF1	226	533	19349	1.92754321	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0007156`homophilic cell adhesion via plasma membrane adhesion molecules	6	2.3256	0.048796024	IGSF11, CDHR5, CDH16, IGFN1, PCDHAC2, PCDHAC1	226	170	19349	3.021707444	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0001569`branching involved in blood vessel morphogenesis	3	1.1628	0.050202437	SHH, IHH, SEMA3E	226	31	19349	8.285326863	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0043278`response to morphine	3	1.1628	0.053149142	PPP1R1B, OPRK1, DRD2	226	32	19349	8.026410398	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0048701`embryonic cranial skeleton morphogenesis	3	1.1628	0.053149142	BMP4, DLX2, SIX4	226	32	19349	8.026410398	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0042476`odontogenesis	3	1.1628	0.056155788	BMP4, AQP6, AQP5	226	33	19349	7.783185841	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0040018`positive regulation of multicellular organism growth	3	1.1628	0.056155788	VIL1, DRD2, PLS1	226	33	19349	7.783185841	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0046541`saliva secretion	2	0.7752	0.056811687	CHRM3, AQP5	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0034653`retinoic acid catabolic process	2	0.7752	0.056811687	CYP26A1, CYP2W1	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0042758`long-chain fatty acid catabolic process	2	0.7752	0.056811687	GLYT1L2, ACADL	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:1990048`anterograde neuronal dense core vesicle transport	2	0.7752	0.056811687	KIF1A, SYBU	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0051124`synaptic growth at neuromuscular junction	2	0.7752	0.056811687	LRP4, SHANK2	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0048755`branching morphogenesis of a nerve	2	0.7752	0.056811687	DLX2, DRD2	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0098708`glucose import across plasma membrane	2	0.7752	0.056811687	SLC2A10, SLC5A1	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0033088`negative regulation of immature T cell proliferation in thymus	2	0.7752	0.056811687	BMP4, IHH	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0051823`regulation of synapse structural plasticity	2	0.7752	0.056811687	DRD2, PPP1R9A	226	5	19349	34.2460177	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0007411`axon guidance	7	2.7132	0.056906504	SHH, FLRT3, CNTN1, SEMA3E, GFRA3, LGR6, RAP1GAP	226	235	19349	2.550235361	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0060548`negative regulation of cell death	4	1.5504	0.056946526	BMP4, AGR2, AGR3, DRD2	226	75	19349	4.566135693	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0030509`BMP signaling pathway	4	1.5504	0.060677415	BMP4, LEFTY1, SOSTDC1, BMPRI1B	226	77	19349	4.447534766	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0034504`protein localization to nucleus	3	1.1628	0.062341819	BMP4, SHH, SIX4	226	35	19349	7.338432364	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0001708`cell fate specification	3	1.1628	0.062341819	SHH, IHH, FOXA2	226	35	19349	7.338432364	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0006357`regulation of transcription from RNA polymerase II promoter	28	10.853	0.064742754	DLX2, DLX6, HNF4G, DACH1, SIX4, SALL4, HNF4A, SIX3, ALX1, MNX1, HES6, CDX2, DMRT1, DMRT2, ZBTB10, FOXJ1, DMRT3, ESRG, ETV4, MLXIPL, TOX3, PAX7, ZNF711, SP9, RCOR2, ZBTB8B, FOXA3, FOXA2	226	1713	19349	1.399428628	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0007154`cell communication	3	1.1628	0.065517746	GJB1, FRAS1, FREM2	226	36	19349	7.134587021	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0017157`regulation of exocytosis	3	1.1628	0.065517746	RAB3B, PCLO, CPLX2	226	36	19349	7.134587021	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0009953`dorsal/ventral pattern formation	3	1.1628	0.065517746	SHH, LRP4, BMPRI1B	226	36	19349	7.134587021	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0014807`regulation of somitogenesis	2	0.7752	0.067782395	CDX2, DMRT2	226	6	19349	28.53834808	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0031223`auditory behavior	2	0.7752	0.067782395	SLITRK6, DRD2	226	6	19349	28.53834808	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0072498`embryonic skeletal joint development	2	0.7752	0.067782395	SLC2A10, IHH	226	6	19349	28.53834808	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0002320`lymphoid progenitor cell differentiation	2	0.7752	0.067782395	BMP4, SHH	226	6	19349	28.53834808	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0015670`carbon dioxide transport	2	0.7752	0.067782395	AQP6, AQP5	226	6	19349	28.53834808	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0006682`galactosylceramide biosynthetic process	2	0.7752	0.067782395	UGT8, GALST1	226	6	19349	28.53834808	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0034765`regulation of ion transmembrane transport	5	1.938	0.071372609	CLIC6, KCNH2, KCNH8, SCN9A, CACNA1D	226	134	19349	3.194591203	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0050919`negative chemotaxis	3	1.1628	0.072027015	FLRT3, SEMA3E, LGR6	226	38	19349	6.759082441	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0048813`dendrite morphogenesis	3	1.1628	0.072027015	MAP2, DCDC2, LRP4	226	38	19349	6.759082441	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0042220`response to cocaine	3	1.1628	0.072027015	HTR3A, DRD2, CACNG4	226	38	19349	6.759082441	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0045597`positive regulation of cell differentiation	3	1.1628	0.072027015	DLX2, CDX2, BMPRI1B	226	38	19349	6.759082441	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0007281`germ cell development	3	1.1628	0.073537089	BMP4, DMRT1, TDRD5	226	39	19349	6.585772634	1	1	0.997427653
GOTERM_BP_DIRECT	GO:1901642`nucleoside transmembrane transport	2	0.7752	0.078626057	SLC29A4, SLC28A2	226	7	19349	24.46144121	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0060428`lung epithelium development	2	0.7752	0.078626057	SHH, FOXJ1	226	7	19349	24.46144121	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0042487`regulation of odontogenesis of dentin-containing tooth	2	0.7752	0.078626057	BMP4, DMRT3	226	7	19349	24.46144121	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0097009`energy homeostasis	3	1.1628	0.078735326	MLXIPL, PRKAA2, MRAP2	226	40	19349	6.421128319	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0032467`positive regulation of cytokinesis	3	1.1628	0.078735326	CENPV, DRD2, SSTR5	226	40	19349	6.421128319	1	1	0.997427653

GOTERM_BP_DIRECT	GO:0019722^calcium-mediated signaling	4	1.5504	0.078817236	CHRM3, PLCE1, KSR2, PPP1R9A	226	86	19349	3.982095081	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0007626^locomotory behavior	4	1.5504	0.078817236	PPP1R1B, CNTN1, OPRK1, DRD2	226	86	19349	3.982095081	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0007018^microtubule-based movement	4	1.5504	0.080963869	DNAH2, DNAH6, KIF1A, DYNC111	226	87	19349	3.936323873	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0098656^anion transmembrane transport	3	1.1628	0.08216017	SLC9A2, SLC9A4, SLC4A4	226	41	19349	6.264515433	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0003341^cilium movement	3	1.1628	0.089143586	ZEBX, HYDIN, ZMYND10	226	43	19349	5.973142622	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0060840^artery development	2	0.7752	0.089344139	SHH, SLC2A10	226	8	19349	21.40376106	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0045893^positive regulation of transcription, DNA-templated	13	5.0388	0.090273327	KCNH2, CDX2, HMGA2, ESRRG, BMP4, MLXIPL, SHH, SIX4, ERBB4, HNF4A, ZNF711, ALX1, FOXA2	226	667	19349	1.668659033	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0001654^eye development	3	1.1628	0.09629545	SIX3, BMPR1B, FREM2	226	45	19349	5.707669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0030513^positive regulation of BMP signaling pathway	3	1.1628	0.09629545	BMP4, GPC3, BMPR1B	226	45	19349	5.707669617	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0042130^negative regulation of T cell proliferation	3	1.1628	0.099930957	SHH, FOXJ1, VTCN1	226	46	19349	5.583589842	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0048699^generation of neurons	2	0.7752	0.099938088	SIX4, LRP4	226	9	19349	19.02556539	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0042403^thyroid hormone metabolic process	2	0.7752	0.099938088	IYD, CRYM	226	9	19349	19.02556539	1	1	0.997427653
GOTERM_BP_DIRECT	GO:0048387^negative regulation of retinoic acid receptor signaling pathway	2	0.7752	0.099938088	CYP26A1, PRAME	226	9	19349	19.02556539	1	1	0.997427653