Supplementary Table 6. Biological process analysis of differentially downregulated genes.

GO.ID	Term	Ontology	Count	Pop.Hits	List.Total	Pop.Total	Fold.Enrichment	Pvalue	FDR	Enrichment.Score	GENES
GO:0044238	primary metabolic process	Biological process	75	7712	168	23448	1.3573466212211	0.000948705527999735	1	3.02286856882715	HHEX//SIX1//TCF25//FOXO6//PDE6H//TERF2//NKX3-1//HIST3H2A//C1RA//RNF220//MIB2//B4GALT2//CHST2//CHST1//GALK1//ACPP//NME5//RASL12//TUBG2//ATP7B//KATNAL2//MBD4//TTC5//A730011L01RIK//HMGA1//RUNX1T1//HOXB6//PIAS2//PITX1//RFX2//ZBTB17//ZFP2//ZFP62//HEYL//TCEAL8//SEC14L2//SMARCC2//CASZ1//ZFP618//MKL1//TCEAL5//LSM6//SREK1IP1//ESRP2//PCSK5//LATS1//LATS2//STK35//DYRK2//ACVR1C//IP6K3//PDP1//ADAM23//TRFR2//CAPN9//PRSS23//BC051665//PRSS48//TPH2//MGLL//SERINC5//LIPH//AGPAT1//ALOX8//GALR2//PRDX6//ABAT//CDA//CIRBP//CHDH//ITGB1BP3//SERPINB7//ADRA2C//CCL24//MAGI3
GO:0030521	androgen receptor signaling pathway	Biological process	3	35	168	23448	11.9632653061224	0.001998035880065	1	2.69939671712389	PIAS2//HEYL//NKX3-1
GO:0060766	negative regulation of androgen receptor signaling pathway	Biological process	2	10	168	23448	27.9142857142857	0.00221125885371372	1	2.65536041519638	PIAS2//HEYL
GO:0048518	positive regulation of biological process	Biological process	34	3029	168	23448	1.56666509456209	0.00495129307169558	1	2.30528136660868	SIX1//AGPAT1//NKX3-1//CCL24//ADORA3//C1RA//GALR2//MBD4//EMID2//ECM2//GRIN2B//STMN2//CIRBP//HMGA1//PIAS2//ZBTB17//SMARCC2//MKL1//HHEX//KCP//GOLPH3//TERF2//LATS1//ADRA2C//DYRK2//ACVR1C//MIB2//SEC14L2//HEYL//PDE6H//ISLR2//PITX1//FOXO6//UBASH3A
GO:0006825	copper ion transport	Biological process	2	16	168	23448	17.4464285714286	0.00573261788449944	1	2.24164700575438	ATP7B//HEPH
GO:0060765	regulation of androgen receptor signaling pathway	Biological process	2	16	168	23448	17.4464285714286	0.00573261788449944	1	2.24164700575438	PIAS2//HEYL
GO:0051145	smooth muscle cell differentiation	Biological process	3	53	168	23448	7.90026954177897	0.00650988712365872	1	2.18642654169251	FOXO6//SIX1//MKL1
GO:0034621	cellular macromolecular complex subunit organization	Biological process	9	466	168	23448	2.69558553034948	0.00659295791554832	1	2.18091969645461	HIST3H2A//SMARCC2//STMN2//ACVR1C//LATS1//LIMA1//CCL24//CIRBP//TUBG2
GO:0045736	negative regulation of cyclin-dependent protein kinase activity	Biological process	2	18	168	23448	15.5079365079365	0.00724081474869849	1	2.1402125635051	LATS1//LATS2
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	Biological process	2	18	168	23448	15.5079365079365	0.00724081474869849	1	2.1402125635051	ADRA2C//PDE6H
GO:0001964	startle response	Biological process	2	19	168	23448	14.6917293233083	0.00805482309558691	1	2.09394399335204	CTNNA2//GRIN2B
GO:0030878	thyroid gland development	Biological process	2	19	168	23448	14.6917293233083	0.00805482309558691	1	2.09394399335204	HHEX//SIX1
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	Biological process	2	19	168	23448	14.6917293233083	0.00805482309558691	1	2.09394399335204	PIAS2//HEYL
GO:0035329	hippo signaling cascade	Biological process	2	19	168	23448	14.6917293233083	0.00805482309558691	1	2.09394399335204	LATS1//LATS2
GO:0035094	response to nicotine	Biological process	2	20	168	23448	13.9571428571429	0.00890796627355639	1	2.05022143591686	CHRNB4//ABAT
GO:0009119	ribonucleoside metabolic process	Biological process	3	64	168	23448	6.54241071428571	0.0109349660656814	1	1.9611825603639	NME5//CDA//ACPP

GO:0046131	pyrimidine ribonucleoside metabolic process	Biological process	2	23	168	23448	12.1366459627329	0.0116962799805782	1	1.93195224430509	NME5//CDA
GO:0048522	positive regulation of cellular process	Biological process	30	2753	168	23448	1.52093819729127	0.0125323737851017	1	1.90196666051981	NKX3-1//CCL24//ADORA3//GALR2//MBD4//EMID2//ECM2//GRIN2B//STMN2//CIRBP//HMGA1//PIAS2//SIX1//ZBTB17//SMARCC2//MKL1//HHEX//KCP//GOLPH3//TERF2//LATS1//ADRA2C//DYRK2//ACVR1C//MIB2//HEYL//PDE6H//ISLR2//PITX1//FOXO6
GO:0008152	metabolic process	Biological process	81	9272	168	23448	1.21929310982374	0.0135170839666472	1	1.86911698840815	HHEX//SIX1//TCF25//FOXO6//PDE6H//TERF2//CHST2//CHST1//FAM109B//NKX3-1//HIST3H2A//C1RA//RNF220//MIB2//B4GALT2//GALK1//CHDH//ALOX8//PRDX6//HEPH//TPH2//ACPP//NME5//RASL12//TUBG2//ATP7B//KATNAL2//MBD4//TTC5//A730011L01RIK//HMGA1//RUNX1T1//HOXB6//PIAS2//PITX1//RFX2//ZBTB17//ZFP2//ZFP62//HEYL//TCEAL8//SEC14L2//SMARCC2//CASZ1//ZFP618//MKL1//TCEAL5//LSM6//SREK1IP1//ESRP2//PCSK5//LATS1//LATS2//STK35//DYRK2//ACVR1C//IP6K3//PDP1//ADAM23//TRFR2//CAPN9//PRSS23//BC051665//PRSS48//MGLL//SERINC5//LIPH//AGPAT1//GALR2//ABAT//CDA//SERPINB7//CIRBP//ITGB1BP3//MAGI3//ADRA2C//CCL24//SLC16A9//KIF9//NAGPA//NT5DC3
GO:0048854	brain morphogenesis	Biological process	2	25	168	23448	11.1657142857143	0.0137400793902946	1	1.86201075791204	HHEX//CTNNA2
GO:0006213	pyrimidine nucleoside metabolic process	Biological process	2	27	168	23448	10.3386243386243	0.0159265090579427	1	1.79787940706247	NME5//CDA
GO:0006284	base-excision repair	Biological process	2	27	168	23448	10.3386243386243	0.0159265090579427	1	1.79787940706247	HMGA1//MBD4
GO:0009755	hormone-mediated signaling pathway	Biological process	3	74	168	23448	5.65830115830116	0.0161552604266273	1	1.79168603665992	NKX3-1//LATS1//LATS2
GO:0030518	intracellular steroid hormone receptor signaling pathway	Biological process	3	74	168	23448	5.65830115830116	0.0161552604266273	1	1.79168603665992	PIAS2//NKX3-1//HEYL
GO:0051258	protein polymerization	Biological process	4	136	168	23448	4.10504201680672	0.016699833006755	1	1.77728787164328	LATS1//CCL24//STMN2//TUBG2
GO:0006974	response to DNA damage stimulus	Biological process	8	454	168	23448	2.45940843297671	0.0168938865089032	1	1.77227042768165	MBD4//TTC5//A730011L01RIK//HMGA1//TERF2//DYRK2//NKX3-1//FOXO6
GO:0071844	cellular component assembly at cellular level	Biological process	12	832	168	23448	2.01304945054945	0.0169282362870275	1	1.77138828765082	ZPBP2//HIST3H2A//LIMA1//ACVR1C//LATS1//CCL24//STMN2//PRDX6//CIRBP//HMGA1//BAIAP2L2//TUBG2
GO:0051148	negative regulation of muscle cell differentiation	Biological process	2	28	168	23448	9.96938775510204	0.0170718191011888	1	1.76772019982751	ITGB1BP3//FOXO6
GO:0009116	nucleoside metabolic process	Biological process	3	77	168	23448	5.4378478664193	0.0179500136710618	1	1.74593521631884	NME5//CDA//ACPP
GO:0006950	response to stress	Biological process	22	1913	168	23448	1.60510790829662	0.0184718239949093	1	1.73349021815952	PRDX6//NME5//GRIN2B//ABAT//ADORA3//IFNE//MBD4//TTC5//A730011L01RIK//HMGA1//CHST2//CCL24//CHST1//FOXO6//TERF2//ARPP21//DYRK2

											//MAGI3//C1RA//MGLL//NKX3-1//CIRBP
GO:0048856	anatomical structure development	Biological process	33	3218	168	23448	1.43127941045903	0.0203434678336706	1	1.69157501342629	PITX1//EGFL7//HHEX//NKX3-1//SIX1//ZPBP2//ZBTB17//PCSK5//ACVR1C//HEYL//NME5//FOXO6//SMARCC2//ISLR2//CTNNA2//GRIN2B//ATP7B//CCL24//PROM1//STMN2//LATS1//LATS2//HEPH//GALR2//EFHD1//SERINC5//ITGB1BP3//ADRA2C//BFSP1//HOXB6//PIAS2//MKL1//WHRN
GO:0001702	gastrulation with mouth forming second	Biological process	2	31	168	23448	9.00460829493088	0.0207095974606937	1	1.68382834255022	HHEX//ZBTB17
GO:0043647	inositol phosphate metabolic process	Biological process	2	31	168	23448	9.00460829493088	0.0207095974606937	1	1.68382834255022	IP6K3//GALR2
GO:0046486	glycerolipid metabolic process	Biological process	5	223	168	23448	3.12940422805894	0.0224640988724296	1	1.64851099806275	AGPAT1//SERINC5//MGLL//GALR2//IP6K3
GO:0006807	nitrogen compound metabolic process	Biological process	46	4850	168	23448	1.32377025036819	0.022516102689992	1	1.647506779305	HHEX//SIX1//TCF25//FOXO6//TERF2//HIST3H2A//ACPP//NME5//RASL12//TUBG2//ATP7B//KATNAL2//MBD4//TTC5//A730011L01RIK//HMGA1//RUNX1T1//HOXB6//PIAS2//NKX3-1//PITX1//RFX2//ZBTB17//ZFP2//ZFP62//HEYL//TCEAL8//SEC14L2//SMARCC2//CASZ1//ZFP618//MKL1//TCEAL5//LSM6//SREK1IP1//ESRP2//TPH2//GALR2//ABAT//CDA//CHDH//ITGB1BP3//CCL24//CHST1//SLC16A9//CIRBP
GO:0010646	regulation of cell communication	Biological process	16	1286	168	23448	1.73650299933348	0.0225490944961654	1	1.64687089339642	GRIN2B//ADORA3//NKX3-1//HHEX//KCP//GOLPH3//ADRA2C//MIB2//PDE6H//ACVR1C//UBASH3A//MGLL//PIAS2//HEYL//LATS1//LATS2
GO:0006644	phospholipid metabolic process	Biological process	5	226	168	23448	3.08786346396966	0.0236296747583149	1	1.62654225600797	AGPAT1//SERINC5//PRDX6//GALR2//IP6K3
GO:0006333	chromatin assembly or disassembly	Biological process	3	86	168	23448	4.8687707641196	0.0239749137447766	1	1.620242946628	HIST3H2A//SMARCC2//HMGA1
GO:0008064	regulation of actin polymerization or depolymerization	Biological process	3	86	168	23448	4.8687707641196	0.0239749137447766	1	1.620242946628	LATS1//LIMA1//CCL24
GO:0034622	cellular macromolecular complex assembly	Biological process	7	396	168	23448	2.46717171717172	0.0243559655530079	1	1.61339464884601	HIST3H2A//ACVR1C//LATS1//CCL24//STMN2//CIRBP//TUBG2
GO:0006650	glycerophospholipid metabolic process	Biological process	4	153	168	23448	3.64892623716153	0.024510143715298	1	1.61065414225352	AGPAT1//SERINC5//GALR2//IP6K3
GO:0030832	regulation of actin filament length	Biological process	3	87	168	23448	4.8128078817734	0.0247037847372153	1	1.60723650566458	LATS1//LIMA1//CCL24
GO:0034641	cellular nitrogen compound metabolic process	Biological process	45	4760	168	23448	1.31947779111645	0.025425088358688	1	1.59473752911814	HHEX//SIX1//TCF25//FOXO6//TERF2//HIST3H2A//ACPP//NME5//RASL12//TUBG2//ATP7B//KATNAL2//MBD4//TTC5//A730011L01RIK//HMGA1//RUNX1T1//HOXB6//PIAS2//NKX3-1//PITX1//RFX2//ZBTB17//ZFP2//ZFP62//HEYL//TCEAL8//SEC14L2//SMARCC2//CASZ1//ZFP618//MKL1//TCEAL5//LSM6//SREK1IP1//ESRP2//TPH2//GALR2//ABAT//CDA//CHDH//ITGB1BP3//CCL24//SLC16A9//CIRBP

GO:0044237	cellular metabolic process	Biological process	67	7615	168	23448	1.22800862958447	0.025549489760667	1	1.59261776857582	HHEX//SIX1//TCF25//FOXO6//PDE6H//TERF2//CHST2//CHST1//FAM109B//NKX3-1//HIST3H2A//RNF220//MIB2//GALK1//ACPP//NME5//RASL12//TUBG2//ATP7B//KATNAL2//MBD4//TTC5//A730011L01RIK//HMGA1//RUNX1T1//HOXB6//PIAS2//PITX1//RFX2//ZBTB17//ZFP2//ZFP62//HEYL//TCEAL8//SEC14L2//SMARCC2//CASZ1//ZFP618//MKL1//TCEAL5//LSM6//SREK1IP1//ESRP2//PCSK5//LATS1//LATS2//STK35//DYRK2//ACVR1C//IP6K3//PDP1//TPH2//MGLL//AGPAT1//SERINC5//ALOX8//GALR2//PRDX6//ABAT//CDA//CIRBP//ITGB1BP3//MAGI3//CHDH//ADRA2C//CCL24//SLC16A9
GO:0030182	neuron differentiation	Biological process	11	785	168	23448	1.9557779799818	0.0262032672202246	1	1.58164455420509	CTNNA2//STMN2//GALR2//EFHD1//SIX1//ADRA2C//HEYL//ISLR2//PIAS2//WHRN//PROM1
GO:0007267	cell-cell signaling	Biological process	10	687	168	23448	2.03160740278644	0.0265815108982639	1	1.57542033730864	SIX1//ADORA3//GALR2//GRIN2B//ABAT//ACVR1C//CTNNA2//CHRNB4//MGLL//NKX3-1
GO:0030154	cell differentiation	Biological process	25	2336	168	23448	1.49370107632094	0.0272166096799688	1	1.56516597498075	HHEX//ZPBP2//SIX1//HEYL//NME5//CTNNA2//STMN2//LATS1//LATS2//HEPH//GALR2//EFHD1//RUNX1T1//ITGB1BP3//ADRA2C//PIAS2//ISLR2//BFSP1//PITX1//MKL1//FOXO6//WHRN//PROM1//ACVR1C//EGFL7
GO:0014068	positive regulation of phosphatidylinositol 3-kinase cascade	Biological process	2	36	168	23448	7.75396825396825	0.0274136973027933	1	1.56203238693719	ADORA3//NKX3-1
GO:0034623	cellular macromolecular complex disassembly	Biological process	3	91	168	23448	4.60125588697017	0.0277379884371028	1	1.55692503721885	SMARCC2//STMN2//LIMA1
GO:0009891	positive regulation of biosynthetic process	Biological process	15	1217	168	23448	1.72027233243338	0.0288113956438605	1	1.54043570368603	GALR2//CIRBP//HMGA1//PIAS2//NKX3-1//SIX1//ZBTB17//SMARCC2//MKL1//SEC14L2//DYRK2//HHEX//PITX1//HEYL//FOXO6
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	Biological process	2	37	168	23448	7.54440154440154	0.0288460634080254	1	1.5399134461763	ADRA2C//PDE6H
GO:0045445	myoblast differentiation	Biological process	2	37	168	23448	7.54440154440154	0.0288460634080254	1	1.5399134461763	ITGB1BP3//PITX1
GO:0009966	regulation of signal transduction	Biological process	17	1443	168	23448	1.64429264429264	0.03007060545502	1	1.5218578275321	PDE6H//ADORA3//NKX3-1//HHEX//KCP//GOLPH3//CCL24//ADRA2C//MIB2//GRIN2B//MAGI3//UBASH3A//PIAS2//HEYL//LATS1//LATS2//MGLL
GO:0008630	DNA damage response, signal transduction resulting in induction of apoptosis	Biological process	2	38	168	23448	7.34586466165413	0.0303077788816352	1	1.51844588992056	DYRK2//MBD4
GO:0048869	cellular developmental process	Biological process	26	2484	168	23448	1.46089256958822	0.0311322810951932	1	1.5067890569352	HHEX//ZPBP2//SIX1//HEYL//NME5//CTNNA2//CCL24//STMN2//ACVR1C//EGFL7//LATS1//LATS2//HEPH//GALR2//EFHD1//RUNX1T1//ITGB1BP3//ADRA2C//PIAS2//ISLR2//BFSP1

											//PITX1//MKL1//FOXO6//WHRN//PROM1
GO:0032535	regulation of cellular component size	Biological process	4	165	168	23448	3.38354978354978	0.0311562062792084	1	1.50645542944333	LATS1//LIMA1//CCL24//ISLR2
GO:0032984	macromolecular complex disassembly	Biological process	3	96	168	23448	4.36160714285714	0.0317969323620039	1	1.49761477695008	SMARCC2//STMN2//LIMA1
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	Biological process	2	39	168	23448	7.15750915750916	0.0317983550385169	1	1.49759534593296	PIAS2//HEYL
GO:0023051	regulation of signaling	Biological process	19	1678	168	23448	1.5803677847778	0.0319345742040944	1	1.49573887008201	PDE6H//FAM109B//MGLL//GRIN2B//ADORA3//NKX3-1//HHEX//KCP//GOLPH3//CCL24//ADRA2C//MIB2//MAGI3//ACVR1C//UBASH3A//PIAS2//HEYL//LATS1//LATS2
GO:0048584	positive regulation of response to stimulus	Biological process	12	914	168	23448	1.83244763988746	0.0320225809667479	1	1.49454366759336	C1RA//ADORA3//NKX3-1//HHEX//KCP//GOLPH3//ADRA2C//MIB2//PDE6H//CCL24//UBASH3A//HMGA1
GO:0008154	actin polymerization or depolymerization	Biological process	3	97	168	23448	4.31664212076583	0.0326440405549091	1	1.48619609127554	LATS1//LIMA1//CCL24
GO:0030030	cell projection organization	Biological process	10	713	168	23448	1.95752354237628	0.0330590505518144	1	1.48070962342122	CTNNA2//STMN2//GALR2//EFHD1//LIMA1//PRDX6//ISLR2//BAIAP2L2//PIAS2//WHRN
GO:0016043	cellular component organization	Biological process	33	3345	168	23448	1.37693786034593	0.0333896991969784	1	1.47638749342484	TERF2//LATS1//ZPBP2//HEYL//HIST3H2A//LIMA1//CCL24//SMARCC2//SYNRG//TRFR2//SLC9A3//CSTAD//STMN2//FAM109B//LATS2//ACVR1C//CTNNA2//GOLPH3//BAIAP2L2//ECM2//CDA//GALR2//EFHD1//PRDX6//CIRBP//HMGA1//GRIN2B//PROM1//ISLR2//PIAS2//TUBG2//C1QTNF6//WHRN
GO:0032271	regulation of protein polymerization	Biological process	3	98	168	23448	4.27259475218659	0.0335028708560516	1	1.47491797673864	LATS1//CCL24//STMN2
GO:0071840	cellular component organization or biogenesis	Biological process	34	3470	168	23448	1.36755866611774	0.0336737995350366	1	1.47270787785003	TERF2//LATS1//ZPBP2//HEYL//HIST3H2A//LIMA1//CCL24//SMARCC2//LSM6//SYNRG//TRFR2//SLC9A3//CSTAD//STMN2//FAM109B//LATS2//ACVR1C//CTNNA2//GOLPH3//BAIAP2L2//ECM2//CDA//GALR2//EFHD1//PRDX6//CIRBP//HMGA1//GRIN2B//PROM1//ISLR2//PIAS2//TUBG2//C1QTNF6//WHRN
GO:0019637	organophosphate metabolic process	Biological process	5	251	168	23448	2.78030734206033	0.0348708154660457	1	1.45753789637903	AGPAT1//SERINC5//PRDX6//IP6K3//GALR2
GO:0048732	gland development	Biological process	5	253	168	23448	2.75832862789385	0.0358910919686751	1	1.4450133282715	NKX3-1//ATP7B//PITX1//HHEX//SIX1
GO:0042692	muscle cell differentiation	Biological process	5	255	168	23448	2.73669467787115	0.0369296595684235	1	1.43262469582144	ITGB1BP3//PITX1//MKL1//FOXO6//SIX1
GO:0045664	regulation of neuron differentiation	Biological process	6	343	168	23448	2.44148271553519	0.0374729282970648	1	1.4262823679266	STMN2//ADRA2C//HEYL//ISLR2//PIAS2//SIX1
GO:0035270	endocrine system development	Biological process	3	103	168	23448	4.06518723994452	0.0379719234449177	1	1.42053740337754	PITX1//HHEX//SIX1
GO:0072527	pyrimidine-containing compound metabolic process	Biological process	2	43	168	23448	6.49169435215947	0.0380396814861359	1	1.41976312815399	NME5//CDA
GO:0043623	cellular protein complex assembly	Biological process	5	258	168	23448	2.70487264673311	0.0385219375266144	1	1.41429187741574	ACVR1C//LATS1//CCL24//STMN2//TUBG2
GO:0032502	developmental process	Biological process	36	3757	168	23448	1.33738925434427	0.0387222237572227	1	1.41203970978929	PITX1//EGFL7//HHEX//NKX3-1//SIX1//ZPBP2//GRIN2B//TERF2//ZBTB17//PCSK5//ACVR1C

											//HEYL//CTNNA2//HOXB6//NME5//ISLR2//FOXO6//SMARCC2//ATP7B//CCL24//PROM1//STMN2//LATS1//LATS2//HEPH//GALR2//EFHD1//SERINC5//RUNX1T1//ITGB1BP3//ADRA2C//PIAS2//BFSP1//MKL1//WHRN//HMGA1
GO:0023057	negative regulation of signaling	Biological process	8	537	168	23448	2.07927640329875	0.0400641068096539	1	1.39724453498865	HHEX//NKX3-1//UBASH3A//MGLL//PIAS2//HEYL//LATS1//LATS2
GO:0010648	negative regulation of cell communication	Biological process	8	538	168	23448	2.07541157727031	0.0404308137430975	1	1.39328751761808	HHEX//NKX3-1//UBASH3A//MGLL//PIAS2//HEYL//LATS1//LATS2
GO:0065008	regulation of biological quality	Biological process	21	1957	168	23448	1.49770056208482	0.0406521786007356	1	1.39091617506562	TERF2//GRIN2B//CHRNB4//ADORA3//ATP7B//TRFR2//SLC9A3//GALR2//CCL24//PCSK5//HEPH//LATS1//LIMA1//HOXB6//ABAT//SERINC5//ISLR2//ACVR1C//CTNNA2//MGLL//NKX3-1
GO:0033554	cellular response to stress	Biological process	11	844	168	23448	1.81905890318213	0.040956822653398	1	1.38767374240381	MBD4//TTC5//A730011L01RIK//HMGA1//FOXO6//TERF2//ARPP21//PRDX6//DYRK2//MAGI3//NKX3-1
GO:0014066	regulation of phosphatidylinositol 3-kinase cascade	Biological process	2	45	168	23448	6.2031746031746	0.0413211966586014	1	1.3838271098363	ADORA3//NKX3-1
GO:0045471	response to ethanol	Biological process	2	45	168	23448	6.2031746031746	0.0413211966586014	1	1.3838271098363	GRIN2B//ABAT
GO:0065007	biological regulation	Biological process	75	8875	168	23448	1.179476861167	0.0417065906669785	1	1.37979531039476	HHEX//SIX1//TCF25//FOXO6//PDE6H//TERF2//GRIN2B//CHRNB4//UBASH3A//AGPAT1//FAM109B//NKX3-1//CCL24//ADORA3//ACVR1C//SLC9A3//C1RA//ADRA2C//GALR2//GPRC5C//RASL12//MIB2//ANK2//BAIAP2L2//MRGPRF//STMN2//ATP7B//MBD4//RUNX1T1//HOXB6//PIAS2//PITX1//RFX2//ZBTB17//ZFP2//ZFP62//HEYL//TCEAL8//SEC14L2//SMARCC2//CASZ1//ZFP618//MKL1//TCEAL5//TRFR2//NME5//OLFR301//DYRK2//ADAM23//LATS2//ALOX8//HMGA1//LATS1//MGLL//SERPINB7//EMID2//ECM2//GOLPH3//CIRBP//PCSK5//HEPH//CDA//EGFL7//KCP//LIMA1//CACNB1//CACNA2D4//ABAT//SERINC5//ESRP2//MAGI3//ITGB1BP3//ISLR2//CTNNA2//SLC15A1
GO:0048583	regulation of response to stimulus	Biological process	20	1853	168	23448	1.50643743736027	0.0430191771806162	1	1.36633790053469	PDE6H//C1RA//MGLL//ADORA3//NKX3-1//HHEX//KCP//GOLPH3//CCL24//ADRA2C//MIB2//GRIN2B//MAGI3//UBASH3A//CTNNA2//PIAS2//HEYL//LATS1//LATS2//HMGA1
GO:0006139	nucleobase-containing compound metabolic process	Biological process	41	4427	168	23448	1.29261996192197	0.0443606121141253	1	1.35300246982782	HHEX//SIX1//TCF25//FOXO6//TERF2//HIST3H2A//ACPP//NME5//RASL12//TUBG2//ATP7B//KATNAL2//MBD4//TTC5//A730011L01RIK//HMGA1//RUNX1T1//HOXB6//PIAS2//NKX3-1//PITX1//RFX2//ZBTB17//ZFP2

											//ZFP62//HEYL//TCEAL8//SEC14L2//SMARCC2//CASZ1//ZFP618//MKL1//TCEAL5//LSM6//SREK1IP1//ESRP2//GALR2//CDA//ITGB1BP3//CCL24//CIRBP
GO:0043242	negative regulation of protein complex disassembly	Biological process	2	47	168	23448	5.93920972644377	0.0447050722441681	1	1.34964319895575	STMN2//LIMA1
GO:0022607	cellular component assembly	Biological process	14	1183	168	23448	1.65173288250211	0.0453550495170607	1	1.34337435457267	ZPBP2//HIST3H2A//LIMA1//ACVR1C//LATS1//CCL24//STMN2//PRDX6//CIRBP//HMGA1//BAIAP2L2//TUBG2//C1QTNF6//CDA
GO:0048706	embryonic skeletal system development	Biological process	3	111	168	23448	3.77220077220077	0.0457209638685905	1	1.33988462258127	SIX1//HOXB6//PCSK5
GO:0043933	macromolecular complex subunit organization	Biological process	11	860	168	23448	1.78521594684385	0.0457937311600456	1	1.33919396978955	HIST3H2A//SMARCC2//STMN2//ACVR1C//LATS1//LIMA1//CCL24//CIRBP//TUBG2//C1QTNF6//CDA
GO:0031328	positive regulation of cellular biosynthetic process	Biological process	14	1194	168	23448	1.63651591289782	0.048318475986726	1	1.31588677225516	GALR2//CIRBP//HMGA1//PIAS2//NKX3-1//SIX1//ZBTB17//SMARCC2//MKL1//DYRK2//HHEX//PITX1//HEYL//FOXO6
GO:0048731	system development	Biological process	28	2835	168	23448	1.37848324514991	0.0484770918286577	1	1.31446344166045	PITX1//EGFL7//HHEX//NKX3-1//SIX1//PCSK5//HEYL//SMARCC2//ISLR2//CTNNA2//GRIN2B//ATP7B//PROM1//STMN2//FOXO6//LATS1//LATS2//HEPH//GALR2//EFHD1//SERINC5//ITGB1BP3//ADRA2C//CCL24//HOXB6//PIAS2//WHRN//BFSP1
GO:0010557	positive regulation of macromolecule biosynthetic process	Biological process	13	1087	168	23448	1.66920751741359	0.0492429812434556	1	1.30765566210976	CIRBP//HMGA1//PIAS2//NKX3-1//SIX1//ZBTB17//SMARCC2//MKL1//DYRK2//HHEX//PITX1//HEYL//FOXO6
GO:0048699	generation of neurons	Biological process	11	872	168	23448	1.76064875491481	0.0496698679622391	1	1.30390699449133	CTNNA2//STMN2//GALR2//EFHD1//SIX1//ADRA2C//HEYL//ISLR2//PIAS2//WHRN//PROM1
GO:0001508	regulation of action potential	Biological process	3	115	168	23448	3.64099378881988	0.0498665725226402	1	1.30219048110305	SERINC5//GRIN2B//CHRNB4
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	Biological process	2	50	168	23448	5.58285714285714	0.049965059054712	1	1.30133359495142	NME5//ATP7B