

**Supplementary Table 1. Genes implicated by IBDs SNPs-promoters interactions in hypothalamic-like neurons**

PROXY_SNP	SNP_LOC	SENTINEL_SNP	R2	GWAS_LOCUS	FRAG_RES	GENES
rs11230563	chr11:60776209	rs11230563		1 MS4A15		4
rs11230563	chr11:60776209	rs11230563		1 MS4A15		4 TCONS_00019908 TCONS_00019310
rs72743461	chr15:67441750	rs17293632		1 IQCH		4
rs72743461	chr15:67441750	rs17293632		1 IQCH		4
rs17293632	chr15:67442596	rs17293632		1 IQCH		4
rs17293632	chr15:67442596	rs17293632		1 IQCH		4
rs11742570	chr5:40410584	rs7711427		1 TTC33		4 TCONS_00009928
rs12761675	chr10:35438337	rs34779708	0.995697	CCNY		4
rs12761675	chr10:35438337	rs34779708	0.995697	CCNY		4 CREM
rs61889537	chr11:58395627	rs11229555	0.994726	OR5B3		4
rs61889537	chr11:58395627	rs11229555	0.994726	OR5B3		4 CNTF
rs61889537	chr11:58395627	rs11229555	0.994726		28	1 CNTF
rs61889537	chr11:58395627	rs11229555	0.994726	OR5B3		4 AP001258.4 FAM111A
rs230522	chr4:103462797	rs3774937	0.991167	TACR3		4 SLC9B2
rs118882	chr4:103463007	rs3774937	0.991167	TACR3		4 SLC9B2
rs76768758	chr8:49177322	rs7011507	0.990937	C8orf22		4 SNAI2
rs67111717	chr5:176790162	rs4976646	0.986912	UNC5A		4 LMAN2
rs67111717	chr5:176790162	rs4976646	0.986912		221	1
rs67111717	chr5:176790162	rs4976646	0.986912	UNC5A		4
rs67111717	chr5:176790162	rs4976646	0.986912	UNC5A		4 PRR7 PRR7-AS1
rs67111717	chr5:176790162	rs4976646	0.986912	UNC5A		4 PRR7 PRR7-AS1
rs62361398	chr5:72529325	rs10061469	0.986594	ZNF366		4 FOXD1
rs6568423	chr6:106442096	rs7746082	0.985597	CRYBG1		4 PRDM1
rs9557195	chr13:99956622	rs3742130	0.982945		180	1 UBAC2 GPR183
rs4626115	chr3:18772770	rs73178598	0.97426	KCNH8		4
rs4626115	chr3:18772770	rs73178598	0.97426		287	1
rs73069539	chr7:26903661	rs3801810	0.971376		186	1 SKAP2
rs73069539	chr7:26903661	rs3801810	0.971376		186	1
rs6062510	chr20:62372148	rs6062504	0.961669	LAMA5		4 TPD52L2
rs2857656	chr17:32582007	rs9889296	0.959529		331	1
rs4809221	chr20:62372706	rs6062504	0.956937	LAMA5		4 TPD52L2
rs11679791	chr2:234156536	rs6752107	0.949251		265	1 ATG16L1
rs5870	chr10:104239100	rs3740415	0.928603	CFAP43		4 NFKB2
rs202657	chr22:41844786	rs727563	0.917883	SREBF2		4 ACO2 PHF5A
rs16841912	chr1:197702476	rs2488389	0.912864	DENND1B		1 DENND1B
rs106860	chr22:41840407	rs727563	0.912708		282	1 ACO2 PHF5A
rs106860	chr22:41840407	rs727563	0.912708	SREBF2		4 ACO2 PHF5A
rs12654812	chr5:176794191	rs4976646	0.906051		221	1
rs12654812	chr5:176794191	rs4976646	0.906051	UNC5A		4 PRR7 PRR7-AS1
rs3811699	chr3:49396360	rs3197999	0.875274		166	1 TCTA RHOA
rs12337739	chr9:117670664	rs4979473	0.870424	TLR4		4
rs12337739	chr9:117670664	rs4979473	0.870424	TLR4		4 RP11-402G3.5 TCONS_00016858
rs12337739	chr9:117670664	rs4979473	0.870424		222	1 RP11-402G3.5 TCONS_00016858
rs12337739	chr9:117670664	rs4979473	0.870424	TLR4		4
rs12337739	chr9:117670664	rs4979473	0.870424	TLR4		4
rs2069776	chr4:123371976	rs7657746	0.835903		299	1
rs2941522	chr17:37910368	rs12946510	0.829413	TBC1D3K		4
rs2941522	chr17:37910368	rs12946510	0.829413	TBC1D3K		4 STARD3
rs212838	chr7:26698194	rs3801810	0.82282	SKAP2		4 CBX3 HNRNPA2B1
rs212838	chr7:26698194	rs3801810	0.82282	SKAP2		4
rs212838	chr7:26698194	rs3801810	0.82282	SKAP2		4
rs212838	chr7:26698194	rs3801810	0.82282	SKAP2		4 AC004540.5 TCONS_I2_00027077 TC
rs212838	chr7:26698194	rs3801810	0.82282	SKAP2		4 ONS_I2_00025728 TCONS_I2_00025
rs212838	chr7:26698194	rs3801810	0.82282	SKAP2		4
rs11564258	chr12:40792300	rs148319899	0.822739		80	1
rs7191618	chr16:28565667	rs26528	0.818268	IL27		4
rs10267797	chr7:107515300	rs4380874	0.805257	COG5		4 GPR22
rs10267797	chr7:107515300	rs4380874	0.805257		200	1 GPR22

**Supplementary table 2. GTEx average gene expression in transcript per million (TPM) for genes implicated in hypothalamic-like neurons**

<b>gene</b>	<b>hypothalamus</b>
CREM	9.82
ACO2	66.83
ATG16L1	10.57
CBX3	38.27
CNTF	1.028
DENND1B	1.4
FAM111A	3.52
FOXD1	1.37
GPR183	4.17
GPR22	1.44
HNRNPA2B1	230.4
LMAN2	34.01
NFKB2	3.65
PHF5A	21.12
PRDM1	1.12
PRR7	10.86
PRR7-AS1	0.48
RHOA	176.8
SKAP2	8.08
SLC9B2	9.84
SNAI2	0.6906
STARD3	24.23
TCTA	35.35
TPD52L2	73.08
UBAC2	11.29

**Supplementary Table 3. Genes implicated by IBDs SNPs-promoters interactions in colonoids.**

PROXY_SNP	SNP_LOC	SENTINEL_SNP	R2	GWAS_LOCUS	FRAG_RES	GENES
rs7554511	chr1:200877562	rs12132298		1 GPR25	4	C1orf106
rs7554511	chr1:200877562	rs12132298		1 GPR25	4	C1orf106
rs7554511	chr1:200877562	rs12132298		1 GPR25	4	
rs7554511	chr1:200877562	rs12132298		1 GPR25	4	
rs41299637	chr1:200877850	rs7554511		1 GPR25	4	C1orf106
rs41299637	chr1:200877850	rs7554511		1 GPR25	4	C1orf106
rs41299637	chr1:200877850	rs7554511		1 GPR25	4	
rs41299637	chr1:200877850	rs7554511		1 GPR25	4	
rs11230563	chr11:60776209	rs11230563		1 MS4A15	4	CD6
rs11230563	chr11:60776209	rs11230563		1 MS4A15	4	
rs2885363	chr16:86009261	rs2361755		1 IRF8	4	
rs2885363	chr16:86009261	rs2361755		1 IRF8	4	
rs744166	chr17:40514201	rs12942547		1 TNS4	4	
rs17694108	chr19:33731551	rs17694108		1 CHST8	4	CEBPG
rs17694108	chr19:33731551	rs17694108		1 CHST8	1	CEBPG
rs17694108	chr19:33731551	rs17694108		1 CHST8	4	CEBPG
rs17694108	chr19:33731551	rs17694108		1 CHST8	1	CEBPG
rs17229679	chr2:199560757	rs17229679		1 SATB2	4	
rs2930047	chr5:10695526	rs2930047		1 DAP	4	
rs10061469	chr5:72518148	rs10061469		1 ZNF366	4	
rs10061469	chr5:72518148	rs10061469		1 ZNF366	4	FOXD1
rs10061469	chr5:72518148	rs10061469		1 ZNF366	4	RP11-79P5.7 AC099522.1 FOXD1
rs249642	chr5:141524980	rs6863411		1 PCDHGA1	4	GNPDA1
rs249642	chr5:141524980	rs6863411		1 PCDHGA1	1	GNPDA1
rs13204048	chr6:3420406	rs13204048		1 SLC22A23	4	
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	SKAP2
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	
rs3801807	chr7:26897439	rs10486483		1 SKAP2	1	
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	
rs3801807	chr7:26897439	rs10486483		1 SKAP2	1	
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	HOXA-AS2
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	HOXA3 HOXA-AS3
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	HOXA5
rs3801807	chr7:26897439	rs10486483		1 SKAP2	1	HOXA5
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	HOXA9
rs3801807	chr7:26897439	rs10486483		1 SKAP2	1	HOXA9
rs3801807	chr7:26897439	rs10486483		1 SKAP2	4	
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	SKAP2
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	
rs3801805	chr7:26897640	rs3801810		1 SKAP2	1	
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	
rs3801805	chr7:26897640	rs3801810		1 SKAP2	1	HOXA-AS2
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	HOXA3 HOXA-AS3
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	HOXA5
rs3801805	chr7:26897640	rs3801810		1 SKAP2	1	HOXA5
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	HOXA9
rs3801805	chr7:26897640	rs3801810		1 SKAP2	1	HOXA9
rs3801805	chr7:26897640	rs3801810		1 SKAP2	4	
rs543104	chr11:96025709	rs483905	0.99522	MAML2	4	MAML2
rs579807	chr11:96026073	rs483905	0.99522	MAML2	4	MAML2
rs538636	chr11:96026190	rs483905	0.99522	MAML2	4	MAML2
rs11669923	chr19:33731379	rs17694108	0.995152	CHST8	4	CEBPG
rs11669923	chr19:33731379	rs17694108	0.995152	CHST8	1	CEBPG
rs11669923	chr19:33731379	rs17694108	0.995152	CHST8	4	CEBPG
rs11669923	chr19:33731379	rs17694108	0.995152	CHST8	1	CEBPG
rs9633740	chr10:82265271	rs7097656	0.993519	NRG3	1	FAM213A

rs9633740	chr10:82265271	rs7097656	0.993519	NRG3	1	TSPAN14
rs9633740	chr10:82265271	rs7097656	0.993519	NRG3	1	
rs2871960	chr3:141121814	rs724016	0.991895	SPSB4	4	
rs11666367	chr19:47120381	rs11083840	0.991673	SAE1	1	TCONS_00027384
rs12765038	chr10:35416513	rs34779708	0.991399	CCNY	1	CUL2
rs9568150	chr13:49672440	rs2026029	0.990616	RCBTB1	1	FNDC3A
rs4781128	chr16:11707571	rs11641184	0.988013	TXNDC11	4	
rs4934730	chr10:35415555	rs34779708	0.987124	CCNY	1	CUL2
rs67111717	chr5:176790162	rs4976646	0.986912	UNC5A	4	LMAN2
rs67111717	chr5:176790162	rs4976646	0.986912	UNC5A	4	
rs67111717	chr5:176790162	rs4976646	0.986912	UNC5A	4	PRR7 PRR7-AS1
rs12993075	chr2:65658144	rs11675538	0.986357	SPRED2	1	SPRED2
rs12993075	chr2:65658144	rs11675538	0.986357	SPRED2	1	
rs539598	chr11:96026074	rs483905	0.9857	MAML2	4	MAML2
rs2283044	chr7:107440553	rs7797798	0.983684	COG5	1	DLD
rs7783301	chr7:107491324	rs4380874	0.983605	COG5	4	COG5 DUS4L
rs7783301	chr7:107491324	rs4380874	0.983605	COG5	4	AC002467.7 CBLL1
rs16935880	chr10:35415468	rs34779708	0.982834	CCNY	1	CUL2
rs8014798	chr14:88456559	rs8005161	0.977916	PTPN21	1	SPATA7
rs8014798	chr14:88456559	rs8005161	0.977916	PTPN21	4	SPATA7
rs73178580	chr3:18799878	rs73178598	0.973947	KCNH8	4	SATB1
rs73178580	chr3:18799878	rs73178598	0.973947	KCNH8	4	SATB1
rs73178580	chr3:18799878	rs73178598	0.973947	KCNH8	4	SATB1 TBC1D5 TCONS_I2_0 0018461 AC144521.1 TCONS
rs73178580	chr3:18799878	rs73178598	0.973947	KCNH8	4	
rs73069539	chr7:26903661	rs10486483	0.971376	SKAP2	1	SKAP2
rs73069539	chr7:26903661	rs10486483	0.971376	SKAP2	1	
rs73069539	chr7:26903661	rs10486483	0.971376	SKAP2	1	
rs73069539	chr7:26903661	rs10486483	0.971376	SKAP2	1	
rs73069539	chr7:26903661	rs10486483	0.971376	SKAP2	1	HOXA5
rs9557205	chr13:100035272	rs3742130	0.971363	CLYBL	4	
rs72797306	chr5:131800750	rs2188962	0.970913	FNIP1	4	C5orf56
rs1182968	chr16:68573945	rs1728785	0.970097	ZFP90	1	ZFP90
rs1182968	chr16:68573945	rs1728785	0.970097	ZFP90	1	
rs1170442	chr16:68574064	rs1728785	0.970097	ZFP90	1	ZFP90
rs1170442	chr16:68574064	rs1728785	0.970097	ZFP90	1	
rs76447456	chr3:18809802	rs73178598	0.965202	KCNH8	4	SATB1
rs76447456	chr3:18809802	rs73178598	0.965202	KCNH8	4	SATB1 TBC1D5 TCONS_I2_0 0018461 AC144521.1 TCONS
rs76447456	chr3:18809802	rs73178598	0.965202	KCNH8	4	
rs76447456	chr3:18809802	rs73178598	0.965202	KCNH8	4	
rs76447456	chr3:18809802	rs73178598	0.965202	KCNH8	1	
rs76447456	chr3:18809802	rs73178598	0.965202	KCNH8	4	
rs76447456	chr3:18809802	rs73178598	0.965202	KCNH8	4	
rs4645854	chr14:75746144	rs1569328	0.962288	TTL5	1	TMED10
rs1991431	chr3:141133450	rs724016	0.951724	SPSB4	4	
rs11174697	chr12:40396449	rs12422544	0.943489	LRRK2	4	SLC2A13
rs798491	chr7:2800521	rs1182188	0.94336	GNA12	4	
rs798491	chr7:2800521	rs1182188	0.94336	GNA12	1	
rs798491	chr7:2800521	rs1182188	0.94336	GNA12	1	
rs4783653	chr16:68562815	rs1728785	0.941585	ZFP90	1	CDH3
rs202653	chr22:41840158	rs727563	0.939603	SREBF2	4	ACO2 PHF5A
rs10889356	chr1:63155349	rs1748195	0.926199	ATG4C	1	RP11-230B22.1 DOCK7
rs10186307	chr2:43839896	rs10495903	0.918085	DYNC2LI1	4	ACO11242.6
rs106860	chr22:41840407	rs727563	0.912708	SREBF2	4	ACO2 PHF5A
rs6914698	chr6:3428216	rs13204048	0.90192	SLC22A23	4	
rs6916403	chr6:3428489	rs13204048	0.90192	SLC22A23	4	
rs34363169	chr3:49537712	rs3197999	0.887194	GMPPB	1	DAG1
rs35261698	chr3:49537839	rs3197999	0.887194	GMPPB	1	DAG1
rs2412960	chr22:30363448	rs131294	0.875558	HORMAD2	4	ASCC2
rs12337739	chr9:117670664	rs4979473	0.870424	TLR4	4	TCONS_I2_00029570

rs12337739	chr9:117670664	rs4979473	0.870424	TLR4	4	
rs12337739	chr9:117670664	rs4979473	0.870424	TLR4	4	TNFSF15
rs12337739	chr9:117670664	rs4979473	0.870424	TLR4	1	TNFSF15
rs4959239	chr6:3418794	rs13204048	0.860597	SLC22A23	4	
rs4959239	chr6:3418794	rs13204048	0.860597	SLC22A23	4	
rs4959239	chr6:3418794	rs13204048	0.860597	SLC22A23	4	
rs9405639	chr6:3419149	rs13204048	0.860597	SLC22A23	4	
rs9405639	chr6:3419149	rs13204048	0.860597	SLC22A23	4	
rs9405639	chr6:3419149	rs13204048	0.860597	SLC22A23	4	
rs7049009	chr9:117647508	rs4979473	0.853959	TLR4	4	TNFSF15
rs11748193	chr5:131725329	rs2188962	0.85068	FNIP1	4	C5orf56
rs11748193	chr5:131725329	rs2188962	0.85068	FNIP1	4	GDF9 UQCRCQ
rs2235092	chr17:54911929	rs3853824	0.843057	TOM1L1	1	RP11-670E13.3
rs2235092	chr17:54911929	rs3853824	0.843057	TOM1L1	1	TRIM25
						TCONS_00025252 TCONS_00
rs61463201	chr17:70636951	rs17780256	0.837822	KCNJ2	1	025151 TCONS_00026155 T
						CONS_00025759 TCONS_000
						TCONS_00025252 TCONS_00
rs60947290	chr17:70636944	rs17780256	0.836162	KCNJ2	1	025151 TCONS_00026155 T
						CONS_00025759 TCONS_000
						TCONS_00025252 TCONS_00
rs58953467	chr17:70636980	rs17780256	0.836162	KCNJ2	1	025151 TCONS_00026155 T
						CONS_00025759 TCONS_000
rs2941522	chr17:37910368	rs12946510	0.829413	TBC1D3K	1	
rs2108228	chr7:107500913	rs4380874	0.827543	COG5	4	AC002467.7 CBLL1
rs59320291	chr19:1184155	rs74610550	0.819693	STK11	4	SBNO2
rs7191618	chr16:28565667	rs26528	0.818268	IL27	4	
rs9611577	chr22:41793090	rs727563	0.805445	SREBF2	4	TEF
rs9611577	chr22:41793090	rs727563	0.805445	SREBF2	1	ACO2 PHF5A
rs9611577	chr22:41793090	rs727563	0.805445	SREBF2	4	ACO2 PHF5A
rs10267797	chr7:107515300	rs4380874	0.805257	COG5	4	
rs10267797	chr7:107515300	rs4380874	0.805257	COG5	4	AC002467.7 CBLL1

**Supplementary Table4. Pathways enrichment in hypothalamic-like neurons and colonoids**

p-value	q-value	term_goid	term	term_name	members_input_overlap_geneids	size	effective_size	effective_size
1.70E-07	1.32E-05	GO:0002520	b	2 immune system development	TCTA; FAM213A; CEBPG; SBNO2; GPR183; PRR7; HOXA5; HOXA3; PRDM1; SATB1; RHOA; SLC9B2; NFKB2; HOXA9	928	925	925
7.99E-08	2.06E-05	GO:0048534	b	4 hematopoietic or lymphoid organ development	TCTA; FAM213A; CEBPG; SBNO2; GPR183; PRR7; HOXA5; HOXA3; PRDM1; SATB1; RHOA; SLC9B2; NFKB2; HOXA9	872	870	870
1.02E-06	9.74E-05	GO:0048522	b	4 positive regulation of cellular process	TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; CD6; CBL1; ZFP90; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CNTF; TRIM25; FOXD1; DAG1; LMAN2; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; CREM; PHF5A; SLC9B2; HOXA9	5324	5307	5307
1.13E-06	9.74E-05	GO:0002521	b	4 leukocyte differentiation	FAM213A; SBNO2; CEBPG; GPR183; PRR7; PRDM1; SATB1; RHOA; SLC9B2; TCTA; TNFSF15; DOCK7; ZFP90; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CNTF; FOXD1; DAG1; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; CREM; PHF5A; HOXA9	504	502	502
1.85E-06	0.000132214	GO:0031325	b	5 positive regulation of cellular metabolic process	TNFSF15; DOCK7; ZFP90; GDF9; CEBPG; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; FOXD1; DAG1; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; PHF5A; HOXA9	3251	3239	3239
2.04E-06	0.000132214	GO:0010604	b	5 positive regulation of macromolecule metabolic process	FAM213A; SBNO2; CEBPG; GPR183; PRR7; HOXA5; PRDM1; SATB1; RHOA; SLC9B2; TCTA; HOXA9	3268	3256	3256
2.39E-06	0.000132214	GO:0030097	b	5 hemopoiesis	FAM213A; DOCK7; UQCRCQ; TMED10; GDF9; CEBPG; HOXA9; GPR183; PRR7; FNDC3A; NFKB2; CNTF; FOXD1; DAG1; SATB1; SNAI2; RHOA; ACO2; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; SLC9B2; TCTA	830	828	828
1.42E-06	0.000137379	GO:0048513	b	3 animal organ development	TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; CD6; CBL1; ZFP90; DENND1B; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; TRIM25; FOXD1; DAG1; LMAN2; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; PHF5A; SLC9B2; HOXA9	3452	3442	3442
1.66E-06	0.000137379	GO:0048518	b	3 positive regulation of biological process	TNFSF15; DOCK7; ZFP90; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; FOXD1; DAG1; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; PHF5A; HOXA9	6051	6034	6034
2.23E-06	0.000144107	GO:0009893	b	4 positive regulation of metabolic process	CEBPG; TEF; FOXD1; HOXA5; HOXA3; PRDM1; SATB1; SNAI2; NFKB2; HOXA9; CREM	924	916	916
3.88E-05	0.000697877	GO:0044212	m	5 transcription regulatory region DNA binding	CEBPG; TEF; FOXD1; HOXA5; HOXA3; PRDM1; SATB1; SNAI2; NFKB2; HOXA9; CREM	945	936	936
4.72E-05	0.000173365	GO:0003690	m	5 double-stranded DNA binding	CEBPG; TEF; FOXD1; HOXA5; HOXA3; PRDM1; SATB1; SNAI2; NFKB2; HOXA9; PRDM1	1134	1125	1125
5.20E-05	0.000173365	GO:0043565	m	5 sequence-specific DNA binding	TNFSF15; DOCK7; SPRED2; UBAC2; ZFP90; CBX3; TMED10; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	6130	6106	6106
8.05E-06	0.000415309	GO:0031323	b	4 regulation of cellular metabolic process	TNFSF15; DOCK7; ZFP90; GDF9; CEBPG; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CNTF; FOXD1; DAG1; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; CREM; PHF5A; HOXA9	3128	3116	3116
1.43E-05	0.000593563	GO:0051173	b	5 positive regulation of nitrogen compound metabolic process	FAM213A; SBNO2; CEBPG; GPR183; HOXA5; HOXA9; SLC9B2; TCTA	408	406	406
1.62E-05	0.000697877	GO:0030099	b	4 myeloid cell differentiation	CEBPG; TEF; FOXD1; HOXA5; HOXA3; PRDM1; SATB1; SNAI2; NFKB2; HOXA9; CREM	926	918	918
3.96E-05	0.000870804	GO:0001067	m	4 regulatory region nucleic acid binding	TNFSF15; DOCK7; SPRED2; UBAC2; ZFP90; CBX3; TMED10; GDF9; CEBPG; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	6156	6133	6133
2.97E-05	0.001094414	GO:0060255	b	4 regulation of macromolecule metabolic process	TNFSF15; DOCK7; SPRED2; UBAC2; ZFP90; CBX3; TMED10; GDF9; CEBPG; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	5904	5881	5881
3.75E-05	0.001210573	GO:0051171	b	4 regulation of nitrogen compound metabolic process	FAM213A; DOCK7; SPRED2; UQCRCQ; CBL1; TMED10; GDF9; CEBPG; HOXA9; GPR183; PRR7; FNDC3A; NFKB2; CREM; CNTF; DLD; FOXD1; DAG1; SATB1; SNAI2; RHOA; ACO2; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; SLC9B2; TCTA	5289	5275	5275
3.88E-05	0.001513589	GO:0007275	b	2 multicellular organism development	TNFSF15; DOCK7; SPRED2; UBAC2; ZFP90; CBX3; TMED10; GDF9; CEBPG; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	6071	6047	6047
6.81E-05	0.001800506	GO:0080090	b	4 regulation of primary metabolic process	GNPDA1; ZFP90; CBX3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	4296	4278	4278
7.56E-05	0.001800506	GO:0019438	b	4 aromatic compound biosynthetic process	SBNO2; TCTA	5	5	5
7.68E-05	0.001800506	GO:0072675	b	4 osteoclast fusion	CNTF; CEBPG; SBNO2; SKAP2; GPR183; TSPAN14; PRR7; CD6; PRDM1; SATB1; RHOA; NFKB2; HOXA9	1435	1432	1432
0.000125071	0.002547778	GO:0001775	b	2 cell activation	FAM213A; TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; GPR22; CD6; UBAC2; CBL1; ZFP90; DENND1B; PHF5A; CBX3; TMED10; GDF9; CEBPG; HOXA9; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; LMAN2; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; SLC9B2; TCTA; FAM111A	11539	11499	11499
0.000169202	0.002547778	GO:0050789	b	2 regulation of biological process	FAM213A; DOCK7; UQCRCQ; GDF9; CEBPG; HOXA9; GPR183; PRR7; FNDC3A; NFKB2; CREM; CNTF; DLD; FOXD1; DAG1; SATB1; SNAI2; RHOA; CDH3; SBNO2; HOXA5; PRDM1; SLC9B2; TCTA	4275	4265	4265
0.000217733	0.002547778	GO:0048869	b	2 cellular developmental process	SNAI2; HOXA5; FOXD1; PRDM1; DAG1	196	196	196
0.000219004	0.002547778	GO:0001763	b	2 morphogenesis of a branching structure	FAM213A; DOCK7; SPRED2; UQCRCQ; CBL1; TMED10; GDF9; CEBPG; HOXA9; GPR183; PRR7; FNDC3A; NFKB2; CREM; CNTF; DLD; FOXD1; DAG1; SATB1; SNAI2; RHOA; ACO2; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; SLC9B2; TCTA	5790	5773	5773
0.000228647	0.002547778	GO:0048856	b	2 anatomical structure development	GNPDA1; ZFP90; CBX3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	4434	4416	4416
0.000130347	0.002802458	GO:1901362	b	4 organic cyclic compound biosynthetic process	TNFSF15; DOCK7; SPRED2; UBAC2; ZFP90; CBX3; TMED10; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	6671	6647	6647
5.81E-05	0.00290677	GO:0019222	b	3 regulation of metabolic process	FAM213A; TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; GPR22; CD6; UBAC2; CBL1; ZFP90; DENND1B; PHF5A; CBX3; TMED10; GDF9; CEBPG; HOXA9; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CREM; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; LMAN2; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; SLC9B2; TCTA	10850	10810	10810
7.87E-05	0.00290677	GO:0050794	b	3 regulation of cellular process	SKAP2; DOCK7; SPRED2; UBAC2; CBL1; ZFP90; CBX3; GDF9; CEBPG; HOXA9; PRR7; HNRNPA2B1; CDH3; CREM; CNTF; TRIM25; FOXD1; DAG1; SATB1; SNAI2; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; TCTA; FAM111A	5219	5201	5201
9.10E-05	0.00290677	GO:0048519	b	3 negative regulation of biological process	FAM213A; DOCK7; UQCRCQ; GDF9; CEBPG; HOXA9; GPR183; PRR7; FNDC3A; NFKB2; CREM; CNTF; DLD; FOXD1; DAG1; SATB1; SNAI2; RHOA; CDH3; SBNO2; HOXA5; PRDM1; SLC9B2; TCTA	4089	4079	4079
0.000105064	0.00290677	GO:0030154	b	3 cell differentiation	FAM213A; HOXA9; HOXA5; PRDM1; RHOA; SLC9B2; TCTA	420	418	418
0.000158626	0.003148109	GO:1903706	b	4 regulation of hemopoiesis	GNPDA1; ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	4222	4204	4204
0.000172419	0.00317743	GO:0034654	b	4 nucleobase-containing compound biosynthetic process	CEBPG; HOXA5; HOXA3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	437	437	437
0.000208333	0.003413383	GO:0048732	b	4 gland development	GNPDA1; ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	4285	4267	4267
0.000219385	0.003413383	GO:0018130	b	4 heterocycle biosynthetic process	TCTA; CNTF; GDF9; GPR183; DOCK7; FOXD1; HOXA5; PRDM1; FAM213A; SNAI2; RHOA; SLC9B2; CDH3; HOXA9; DAG1	1963	1957	1957
0.000224913	0.003413383	GO:2000026	b	4 regulation of multicellular organismal development	CEBPG; FOXD1	21	21	21
0.001566353	0.003915883	GO:0008301	m	5 DNA binding, bending	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	3645	3628	3628
0.000157113	0.005133266	GO:0006351	b	5 transcription, DNA-templated	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	3705	3688	3688
0.000201267	0.005133266	GO:0032774	b	5 RNA biosynthetic process	FAM213A; SBNO2; GPR183; SLC9B2; TCTA	203	201	201
0.000246104	0.005133266	GO:0002573	b	5 myeloid leukocyte differentiation	SBNO2; CEBPG; NFKB2; TEF; FOXD1; HOXA5; HOXA3; HNRNPA2B1; ZFP90; PHF5A; MAML2; RHOA; CDH3; HOXA9; CREM	1983	1974	1974
0.000247386	0.005133266	GO:0009891	b	5 positive regulation of biosynthetic process	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	3795	3778	3778
0.000288463	0.005320531	GO:0051252	b	5 regulation of RNA metabolic process	CNTF; GDF9; MAML2; TNFSF15; SKAP2; TRIM25; GPR183; TSPAN14; SPRED2; FOXD1; RHOA; PRR7; CDH3	1579	1576	1576
0.000323296	0.00536671	GO:0009967	b	5 positive regulation of signal transduction	CEBPG; GPR183; PRR7; PRDM1; SATB1; RHOA	342	342	342
0.000378267	0.005421832	GO:0030098	b	4 lymphocyte differentiation	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	4174	4158	4158
0.0004209	0.006351763	GO:0031326	b	5 regulation of cellular biosynthetic process				

0.000467238	0.006463457	GO:0010468	b	5	regulation of gene expression	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; CNTF; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9 TCTA; CNTF; GDF9; CEBPG; NFKB2; GPR183; HOXA5; FOXD1; DOCK7; CD6; PRDM1; FAM213A; TRIM25; SNAI2; RHOA; SLC9B2; CDH3; HOXA9; DAG1	4492	4475	4475
0.000294556	0.00698518	GO:0051239	b	3	regulation of multicellular organismal process	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	2989	2983	2983
0.000545157	0.007082244	GO:0009889	b	4	regulation of biosynthetic process	CNTF; GDF9; CEBPG; TNFSF15; SKAP2; TRIM25; GPR183; TSPAN14; SPRED2; FOXD1; CD6; DENND1B; MAML2; RHOA; PRR7; CDH3	4246	4230	4230
0.000549011	0.007082244	GO:0048584	b	4	positive regulation of response to stimulus	FAM213A; DOCK7; UQCRCQ; TMED10; GDF9; CEBPG; HOXA9; GPR183; PRR7; FNDC3A; NFKB2; CNTF; FOXD1; DAG1; SATB1; SNAI2; RHOA; ACO2; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; SLC9B2; TCTA	2371	2366	2366
0.000367738	0.007630567	GO:0048731	b	3	system development	FAM213A; HOXA5; SLC9B2; TCTA; HOXA9	4713	4699	4699
0.000631647	0.0080523	GO:0045637	b	5	regulation of myeloid cell differentiation	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	249	247	247
0.000699292	0.0080523	GO:0010556	b	5	regulation of macromolecule biosynthetic process	CBLL1; ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9	4031	4015	4015
0.000775396	0.0080523	GO:0016070	b	5	RNA metabolic process	ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9	4644	4624	4624
0.000799611	0.0080523	GO:0019219	b	5	regulation of nucleobase-containing compound metabolic	PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	4070	4053	4053
0.000824633	0.0080523	GO:0010647	b	5	positive regulation of cell communication	CNTF; GDF9; MAML2; TNFSF15; SKAP2; TRIM25; GPR183; TSPAN14; SPRED2; FOXD1; RHOA; PRR7; CDH3	1741	1738	1738
0.000881537	0.008129731	GO:1902105	b	5	regulation of leukocyte differentiation	FAM213A; RHOA; SLC9B2; PRDM1; TCTA	268	266	266
0.000456375	0.008417581	GO:0006725	b	3	cellular aromatic compound metabolic process	GNPDA1; UQCRCQ; CBLL1; ZFP90; CBX3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	6015	5989	5989
0.000896465	0.00986112	GO:0001227	m	4	DNA-binding transcription repressor activity, RNA polymer	SNAI2; ZFP90; PRDM1; SATB1; CREM	267	267	267
0.001039458	0.010134715	GO:0021700	b	2	developmental maturation	RHOA; DLD; HOXA5; CDH3; DAG1	277	276	276
0.000856309	0.010520372	GO:0023056	b	4	positive regulation of signaling	CNTF; GDF9; MAML2; TNFSF15; SKAP2; TRIM25; GPR183; TSPAN14; SPRED2; FOXD1; RHOA; PRR7; CDH3	1748	1745	1745
0.001218634	0.010561498	GO:0044237	b	2	cellular metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRCQ; UBAC2; CBLL1; ZFP90; CBX3; TMED10; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CUL2; CREM; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; ACO2; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	10637	10598	10598
0.000642256	0.010661454	GO:0006139	b	3	nucleobase-containing compound metabolic process	GNPDA1; UQCRCQ; CBLL1; ZFP90; CBX3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	5810	5784	5784
0.000961894	0.011280388	GO:0046649	b	4	lymphocyte activation	CEBPG; SKAP2; GPR183; PRR7; CD6; PRDM1; SATB1; RHOA	737	736	736
0.001172372	0.011723722	GO:0016604	c	5	nuclear body	MAML2; TRIM25; DENND1B; HNRNPA2B1; SATB1; PHF5A; ASCC2; CBLL1	760	759	759
0.000845038	0.011909637	GO:1901360	b	3	organic cyclic compound metabolic process	GNPDA1; UQCRCQ; CBLL1; ZFP90; CBX3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	6220	6194	6194
0.000860938	0.011909637	GO:0044260	b	3	cellular macromolecule metabolic process	TNFSF15; TSPAN14; DOCK7; SPRED2; UBAC2; CBLL1; ZFP90; CBX3; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CUL2; PRDM1; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; CREM; ASCC2; HOXA9; FAM111A	8256	8225	8225
0.001026152	0.012242655	GO:0046483	b	3	heterocycle metabolic process	GNPDA1; UQCRCQ; CBLL1; ZFP90; CBX3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	5967	5941	5941
0.001050726	0.012242655	GO:0071695	b	3	anatomical structure maturation	RHOA; HOXA5; CDH3; DAG1	161	160	160
0.001106264	0.012242655	GO:0043170	b	3	macromolecule metabolic process	TNFSF15; TSPAN14; DOCK7; SPRED2; UBAC2; CBLL1; ZFP90; CBX3; TMED10; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CUL2; CREM; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	9445	9411	9411
0.001274335	0.014294714	GO:0042127	b	4	regulation of cell proliferation	CNTF; GDF9; SKAP2; GPR183; HOXA5; CD6; HOXA3; PRDM1; SNAI2; RHOA; CDH3; CUL2	1601	1592	1592
0.001390292	0.014945642	GO:0010467	b	4	gene expression	TSPAN14; ZFP90; CBX3; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; CNTF; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9	5440	5417	5417
0.001441532	0.014955896	GO:0044403	b	3	symbiont process	TRIM25; DAG1; SATB1; ATG16L1; RHOA; FAM111A; CUL2; CBLL1	784	784	784
0.001588629	0.014974949	GO:0048468	b	3	cell development	CNTF; GDF9; DLD; UQCRCQ; GPR183; DOCK7; FOXD1; HOXA5; PRDM1; SNAI2; FNDC3A; RHOA; SLC9B2; DAG1	2110	2106	2106
0.001688804	0.014974949	GO:0061138	b	3	morphogenesis of a branching epithelium	SNAI2; HOXA5; DAG1; FOXD1	182	182	182
0.00175005	0.014974949	GO:0050886	b	3	endocrine process	RHOA; GDF9; FOXD1	85	85	85
0.001804211	0.014974949	GO:0034641	b	3	cellular nitrogen compound metabolic process	GNPDA1; UQCRCQ; CBLL1; ZFP90; CBX3; TMED10; GDF9; CEBPG; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	6494	6465	6465
0.001573298	0.01562432	GO:0034645	b	4	cellular macromolecule biosynthetic process	ZFP90; CBX3; GDF9; MAML2; ATG16L1; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9; FAM111A	4867	4847	4847
0.001574544	0.01562432	GO:0090304	b	4	nucleic acid metabolic process	CBLL1; ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	5174	5151	5151
0.001665993	0.01591949	GO:0042110	b	4	T cell activation	GPR183; PRR7; CD6; PRDM1; SATB1; RHOA	456	455	455
0.001764755	0.016260959	GO:0044271	b	4	cellular nitrogen compound biosynthetic process	GNPDA1; ZFP90; CBX3; GDF9; MAML2; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9	4906	4885	4885
0.00054143	0.016393542	GO:0034399	c	4	nuclear periphery	PHF5A; DAG1; SATB1; HNRNPA2B1	134	134	134
0.000819677	0.016393542	GO:0005654	c	4	nucleoplasm	MAML2; CEBPG; DLD; SKAP2; TRIM25; DENND1B; SPATA7; COG5; DAG1; CBLL1; HOXA3; HNRNPA2B1; SATB1; PHF5A; SNAI2; ASCC2; NFKB2; CBX3; CUL2; PRDM1	3520	3501	3501
0.002111519	0.016469847	GO:0044419	b	2	interspecies interaction between organisms	TRIM25; DAG1; SATB1; ATG16L1; RHOA; FAM111A; CUL2; CBLL1	833	833	833
0.000824633	0.016492662	GO:0003700	m	2	DNA-binding transcription factor activity	CEBPG; ZFP90; TEF; FOXD1; HOXA5; HOXA3; PRDM1; SATB1; SNAI2; PHF5A; NFKB2; HOXA9; CREM	1750	1738	1738
0.001880319	0.016728354	GO:0060445	b	4	branching involved in salivary gland morphogenesis	SNAI2; DAG1	23	23	23
0.002581321	0.016775023	GO:0006807	b	2	nitrogen compound metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRCQ; UBAC2; CBLL1; ZFP90; CBX3; TMED10; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CUL2; PRDM1; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; CREM; ASCC2; DUS4L; HOXA9; FAM111A	10174	10136	10136
0.002666417	0.016775023	GO:0045321	b	2	leukocyte activation	SBNO2; CEBPG; SKAP2; GPR183; TSPAN14; PRR7; CD6; PRDM1; SATB1; RHOA	1284	1281	1281
0.002795837	0.016775023	GO:0048646	b	2	anatomical structure formation involved in morphogenesis	SBNO2; FOXD1; HOXA5; HOXA3; DAG1; SNAI2; RHOA; NFKB2; TCTA	1078	1075	1075
0.003075416	0.017063797	GO:0071704	b	2	organic substance metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRCQ; UBAC2; CBLL1; ZFP90; CBX3; TMED10; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CUL2; CREM; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; ACO2; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	11025	10986	10986
0.003281499	0.017063797	GO:0044238	b	2	primary metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRCQ; UBAC2; CBLL1; ZFP90; CBX3; TMED10; GDF9; CEBPG; ATG16L1; GPR183; TEF; PRR7; HNRNPA2B1; NFKB2; CUL2; CREM; CNTF; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; ACO2; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; DUS4L; HOXA9; FAM111A	10663	10624	10624
0.003572521	0.017416039	GO:0009653	b	2	anatomical structure morphogenesis	TCTA; CNTF; SBNO2; DLD; NFKB2; DOCK7; FOXD1; HOXA5; HOXA3; PRDM1; SNAI2; RHOA; CDH3; HOXA9; DAG1	2560	2554	2554
0.003870321	0.017757941	GO:0001816	b	2	cytokine production	CEBPG; TRIM25; CD6; SNAI2; DENND1B; NFKB2; CDH3	723	722	722
0.002047578	0.017889369	GO:0030878	b	5	thyroid gland development	HOXA5; HOXA3	24	24	24
0.004444454	0.019259299	GO:0009058	b	2	biosynthetic process	GNPDA1; ZFP90; CBX3; GDF9; CEBPG; ATG16L1; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9; FAM111A	6185	6163	6163
0.002403768	0.020672408	GO:0009059	b	4	macromolecule biosynthetic process	ZFP90; CBX3; GDF9; MAML2; ATG16L1; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; CEBPG; RHOA; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9; FAM111A	5010	4990	4990

0.002867384	0.02134675	GO:0050793	b	3	regulation of developmental process	TCTA; CNTF; GDF9; GPR183; DOCK7; FOXD1; HOXA5; PRDM1; FAM213A; SNAI2; RHOA; SLC9B2; CDH3; HOXA9; DAG1	2503	2497	2497
0.00289906	0.02134675	GO:0044093	b	3	positive regulation of molecular function	CEBPg; TNFSF15; TRIM25; NFKB2; DOCK7; PRR7; HOXA3; HNRNPA2B1; DENND1B; RHOA; CDH3; DAG1	1755	1754	1754
0.002957682	0.02134675	GO:0044249	b	3	cellular biosynthetic process	GNPDA1; ZFP90; CBX3; GDF9; CEBPG; ATG16L1; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9; FAM111A	6026	6004	6004
0.002804365	0.023339557	GO:0045595	b	4	regulation of cell differentiation	FAM213A; CNTF; GPR183; DOCK7; HOXA5; PRDM1; SNAI2; RHOA; SLC9B2; TCTA; HOXA9; DAG1	1753	1747	1747
0.002985122	0.024067547	GO:0060536	b	4	cartilage morphogenesis	SNAI2; HOXA5	29	29	29
0.003494181	0.024168086	GO:0048583	b	3	regulation of response to stimulus	CNTF; GDF9; CEBPG; PRR7; TNFSF15; SBNO2; SKAP2; TRIM25; GPR183; TSPAN14; SPRED2; FOXD1; CD6; UBAC2; DAG1; DENND1B; SNAI2; MAML2; RHOA; SLC9B2; CDH3	4227	4219	4219
0.003123805	0.024422477	GO:0001501	b	4	skeletal system development	HOXA5; HOXA3; SNAI2; RHOA; SLC9B2; HOXA9	518	516	516
0.00369629	0.024543362	GO:1901576	b	3	organic substance biosynthetic process	GNPDA1; ZFP90; CBX3; GDF9; CEBPG; ATG16L1; TEF; HNRNPA2B1; NFKB2; CUL2; CREM; DLD; TRIM25; FOXD1; SATB1; PHF5A; SNAI2; MAML2; RHOA; CDH3; SBNO2; HOXA5; HOXA3; PRDM1; ASCC2; HOXA9; FAM111A	6112	6090	6090
0.002985122	0.024776514	GO:0060441	b	5	epithelial tube branching involved in lung morphogenesis	HOXA5; DAG1	29	29	29
0.002544011	0.027656031	GO:0031981	c	4	nuclear lumen	MAML2; CEBPG; DLD; SKAP2; TRIM25; DENND1B; SPATA7; COG5; DAG1; CBLL1; HOXA3; HNRNPA2B1; SATB1; PHF5A; SNAI2; ASCC2; NFKB2; FAM111A; CBX3; CUL2; PRDM1	4134	4115	4115
0.003448716	0.027656031	GO:0005634	c	4	nucleus	SKAP2; DOCK7; CBLL1; ZFP90; DENND1B; CBX3; CEBPG; TEF; PRR7; HNRNPA2B1; NFKB2; CUL2; PRDM1; DLD; TRIM25; COG5; FOXD1; DAG1; SATB1; PHF5A; SNAI2; MAML2; RHOA; SBNO2; HOXA5; HOXA3; CREM; ASCC2; SPATA7; HOXA9; FAM111A	7415	7386	7386
0.003457004	0.027656031	GO:0016363	c	4	nuclear matrix	PHF5A; HNRNPA2B1; SATB1	108	108	108
0.003841033	0.029146659	GO:0016032	b	4	viral process	TRIM25; DAG1; SATB1; ATG16L1; RHOA; CUL2; FAM111A	721	721	721
0.004087966	0.032314398	GO:0007435	b	5	salivary gland morphogenesis	SNAI2; DAG1	34	34	34
0.005623076	0.033520674	GO:0043616	b	3	keratinocyte proliferation	SNAI2; CDH3	40	40	40
0.005641526	0.033520674	GO:0009887	b	3	animal organ morphogenesis	CNTF; FOXD1; HOXA5; HOXA3; PRDM1; SNAI2; RHOA; DAG1	981	979	979
0.00565409	0.033520674	GO:0007281	b	3	germ cell development	FNDC3A; GDF9; PRDM1; DLD	255	255	255
0.004706273	0.033639401	GO:0051172	b	5	negative regulation of nitrogen compound metabolic process	SBNO2; PRDM1; ZFP90; SPRED2; FOXD1; CREM; UBAC2; HNRNPA2B1; SATB1; SNAI2; RHOA; PRR7; CBX3; DAG1	2369	2366	2366
0.00482709	0.033639401	GO:0007431	b	5	salivary gland development	SNAI2; DAG1	37	37	37
0.004863528	0.033639401	GO:0007043	b	5	cell-cell junction assembly	SNAI2; RHOA; CDH3	122	122	122
0.004574349	0.033719491	GO:0033280	b	4	response to vitamin D	SNAI2; TRIM25	36	36	36
0.008680719	0.034159838	GO:0051716	b	2	cellular response to stimulus	FAM213A; TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; GPR22; CD6; UBAC2; DENND1B; CBX3; GDF9; CEBPG; GPR183; PRR7; HNRNPA2B1; NFKB2; CUL2; CNTF; TRIM25; FOXD1; DAG1; SNAI2;	7471	7448	7448
0.008758933	0.034159838	GO:0019953	b	2	sexual reproduction	MAML2; RHOA; CDH3; SBNO2; CREM; ASCC2; SLC9B2	841	841	841
0.004863528	0.034330726	GO:0038061	b	4	NIK/NF-kappaB signaling	RHOA; NFKB2; TNFSF15	122	122	122
0.004923399	0.034330726	GO:0051241	b	4	negative regulation of multicellular organismal process	CNTF; TRIM25; DOCK7; HOXA5; TCTA; SNAI2; RHOA; CDH3; HOXA9	1174	1171	1171
0.005132004	0.034843607	GO:0048523	b	4	negative regulation of cellular process	SKAP2; SPRED2; UBAC2; CBLL1; ZFP90; CBX3; GDF9; HOXA9; PRR7; HNRNPA2B1; CUL2; PRDM1; CNTF; FOXD1; DAG1; SATB1; SNAI2; RHOA; SBNO2; HOXA5; CREM; TCTA	4670	4652	4652
0.001603153	0.03526936	GO:0000981	m	3	DNA-binding transcription factor activity, RNA polymerase	CEBPg; ZFP90; TEF; FOXD1; HOXA5; HOXA3; PRDM1; SATB1; SNAI2; NFKB2; HOXA9; CREM	1646	1635	1635
0.005320014	0.035324893	GO:0048706	b	5	embryonic skeletal system development	HOXA5; HOXA3; HOXA9	126	126	126
0.00555761	0.036765728	GO:0006119	b	4	oxidative phosphorylation	RHOA; UQCRCQ; DLD	128	128	128
0.0083447	0.039011189	GO:0001228	m	4	DNA-binding transcription activator activity, RNA polymerase	HOXA5; CEBPG; NFKB2; TEF; FOXD1	457	449	449
0.008620909	0.039011189	GO:0005126	m	4	cytokine receptor binding	CNTF; GDF9; SPRED2; TNFSF15	288	288	288
0.008866179	0.039011189	GO:0003677	m	4	DNA binding	CEBPg; ZFP90; TEF; FOXD1; HOXA5; CREM; HOXA3; HNRNPA2B1; SATB1; SNAI2; PHF5A; NFKB2; HOXA9; PRDM1	2557	2542	2542
0.006439074	0.039588379	GO:0044409	b	5	entry into host	HOXA9; PRDM1	135	135	135
0.006439074	0.039588379	GO:0051806	b	5	entry into cell of other organism involved in symbiotic interaction	TRIM25; DAG1; CBLL1	135	135	135
0.006724385	0.039865996	GO:0042063	b	5	gliogenesis	TRIM25; DAG1; CBLL1	135	135	135
0.007073447	0.040489385	GO:0031103	b	5	axon regeneration	CNTF; RHOA; GPR183; DAG1	268	268	268
0.006439074	0.040773993	GO:0051828	b	4	entry into other organism involved in symbiotic interaction	CNTF; DAG1	45	45	45
0.006551617	0.040773993	GO:0060485	b	4	mesenchyme development	TRIM25; DAG1; CBLL1	135	135	135
0.006637627	0.040773993	GO:0061448	b	4	connective tissue development	SNAI2; HOXA5; DAG1; FOXD1	266	266	266
0.011923184	0.042608835	GO:0140253	b	2	cell-cell fusion	SNAI2; HOXA5; HOXA3; FOXD1	267	267	267
0.012017876	0.042608835	GO:0065009	b	2	regulation of molecular function	SBNO2; TCTA	62	59	59
0.012707064	0.043093521	GO:0006949	b	2	syncytium formation	CNTF; GDF9; CEBPG; TNFSF15; TRIM25; NFKB2; DOCK7; SPRED2; PRR7; HOXA3; DAG1; ZFP90; DENND1B; RHOA; CDH3; HNRNPA2B1	3198	3193	3193
0.013437705	0.043672541	GO:0009566	b	2	fertilization	SBNO2; TCTA	64	61	61
0.008016351	0.044000932	GO:0060986	b	5	endocrine hormone secretion	FNDC3A; GNPDA1; HOXA9	177	177	177
0.008286827	0.044000932	GO:1903707	b	5	negative regulation of hemopoiesis	GDF9; FOXD1	48	48	48
0.008482107	0.044000932	GO:0031324	b	5	negative regulation of cellular metabolic process	HOXA5; TCTA; HOXA9	150	148	148
0.022975898	0.045951796	GO:0061630	m	5	ubiquitin protein ligase activity	SBNO2; PRDM1; ZFP90; SPRED2; FOXD1; CREM; UBAC2; HNRNPA2B1; SATB1; SNAI2; RHOA; PRR7; CBX3; DAG1	2532	2529	2529
0.009144496	0.045999586	GO:0019058	b	5	viral life cycle	TRIM25; CBLL1; CUL2	217	217	217
0.008342556	0.047753944	GO:0061383	b	3	trabecula morphogenesis	TRIM25; FAM111A; DAG1; ATG16L1	293	293	293
0.008016351	0.048098106	GO:0035272	b	4	exocrine system development	SBNO2; RHOA	49	49	49
0.010061316	0.049122895	GO:0002066	b	5	columnar/cuboidal epithelial cell development	SNAI2; DAG1	48	48	48
0.010422375	0.049431838	GO:0002011	b	5	morphogenesis of an epithelial sheet	HOXA5; PRDM1	54	54	54
0.008595928	0.049734697	GO:0048754	b	4	branching morphogenesis of an epithelial tube	RHOA; DAG1	55	55	55
0.008674656	0.049734697	GO:0060425	b	4	lung morphogenesis	HOXA5; DAG1; FOXD1	150	150	150
						HOXA5; DAG1	50	50	50

**Supplementary Table 5. Pathways enrichment in hypothalamic-like neurons**

p-value	q-value	term_goid	term_category	term_level	term_name	members_input_overlap_genes	size	effective_size
2.11E-05	0.002950745	GO:0002521	b	4	leukocyte differentiation	GPR183; PRR7; PRDM1; RHOA; SLC9B2; TCTA	504	502
4.87E-05	0.00340628	GO:0048534	b	4	hematopoietic or lymphoid organ development	GPR183; PRR7; PRDM1; NFKB2; SLC9B2; RHOA; TCTA	872	870
7.18E-05	0.003950183	GO:0002520	b	2	immune system development	GPR183; PRR7; PRDM1; NFKB2; SLC9B2; RHOA; TCTA	928	925
0.001675352	0.005790994	GO:0043565	m	5	sequence-specific DNA binding	FOXD1; CREM; HNRNPA2B1; SNAI2; NFKB2; PRDM1	1134	1125
0.00396008	0.005790994	GO:0044212	m	5	transcription regulatory region DNA binding	SNAI2; NFKB2; FOXD1; PRDM1; CREM	924	916
0.004343245	0.005790994	GO:0003690	m	5	double-stranded DNA binding	SNAI2; NFKB2; FOXD1; PRDM1; CREM	945	936
0.000251041	0.011715265	GO:0009893	b	4	positive regulation of metabolic process	CNTF; HNRNPA2B1; GPR183; FOXD1; PRDM1; ATG16L1; SNAI2; PHF5A; RHOA; PRR7; NFKB2; CREM	3537	3525
0.000256258	0.011959961	GO:1902105	b	5	regulation of leukocyte differentiation	RHOA; SLC9B2; PRDM1; TCTA	268	266
0.00033393	0.011959961	GO:0030097	b	5	hemopoiesis	GPR183; PRR7; PRDM1; RHOA; SLC9B2; TCTA	830	828
0.000556963	0.011959961	GO:0031325	b	5	positive regulation of cellular metabolic process	CNTF; ATG16L1; GPR183; FOXD1; HNRNPA2B1; SNAI2; PHF5A; RHOA; PRR7; NFKB2; CREM	3251	3239
0.000583413	0.011959961	GO:0010604	b	5	positive regulation of macromolecule metabolic process	CNTF; HNRNPA2B1; GPR183; FOXD1; PRDM1; SNAI2; PHF5A; RHOA; PRR7; NFKB2; CREM	3268	3256
0.001949859	0.013324162	GO:0032934	m	4	sterol binding	STARD3; GPR183	55	55
0.003801386	0.013324162	GO:0001227	m	4	DNA-binding transcription repressor activity, RNA polymerase II-specific	SNAI2; PRDM1; CREM	267	267
0.003997248	0.013324162	GO:0001067	m	4	regulatory region nucleic acid binding	SNAI2; NFKB2; FOXD1; PRDM1; CREM	926	918
0.001018014	0.015379065	GO:0051172	b	5	negative regulation of nitrogen compound metabolic process	FOXD1; CREM; UBAC2; HNRNPA2B1; SNAI2; RHOA; PRR7; CBX3; PRDM1	2369	2366
0.001649618	0.015379065	GO:0031324	b	5	negative regulation of cellular metabolic process	FOXD1; CREM; UBAC2; HNRNPA2B1; SNAI2; RHOA; PRR7; CBX3; PRDM1	2532	2529
0.001700818	0.015379065	GO:0002573	b	5	myeloid leukocyte differentiation	GPR183; SLC9B2; TCTA	203	201
0.001804674	0.015379065	GO:0051173	b	5	positive regulation of nitrogen compound metabolic process	CNTF; GPR183; FOXD1; HNRNPA2B1; SNAI2; PHF5A; RHOA; PRR7; NFKB2; CREM	3128	3116
0.001810343	0.015379065	GO:0009890	b	5	negative regulation of biosynthetic process	FOXD1; CREM; HNRNPA2B1; SNAI2; RHOA; CBX3; PRDM1	1571	1571
0.001875496	0.015379065	GO:2000027	b	5	regulation of animal organ morphogenesis	SNAI2; CNTF; RHOA	208	208
0.000184297	0.016771008	GO:0048518	b	3	positive regulation of biological process	CNTF; PRR7; SKAP2; HNRNPA2B1; GPR183; FOXD1; ATG16L1; DENND1B; PRDM1; LMAN2; SNAI2; PHF5A; RHOA; SLC9B2; NFKB2; CREM	6051	6034
0.00247038	0.018415558	GO:0046530	b	5	photoreceptor cell differentiation	CNTF; PRDM1	62	62
0.000662691	0.023194169	GO:0030098	b	4	lymphocyte differentiation	RHOA; GPR183; PRDM1; PRR7	342	342
0.000831279	0.02327582	GO:0048522	b	4	positive regulation of cellular process	CNTF; PRR7; SKAP2; ATG16L1; GPR183; FOXD1; CREM; LMAN2; SNAI2; PHF5A; RHOA; SLC9B2; NFKB2; HNRNPA2B1	5324	5307
0.003841435	0.026249807	GO:0042063	b	5	gliogenesis	CNTF; RHOA; GPR183	268	268
0.001356046	0.026694553	GO:2000026	b	4	regulation of multicellular organismal development	CNTF; GPR183; FOXD1; PRDM1; SNAI2; RHOA; SLC9B2; TCTA	1963	1957
0.001396861	0.026694553	GO:1903706	b	4	regulation of hemopoiesis	RHOA; SLC9B2; PRDM1; TCTA	420	418
0.001525403	0.026694553	GO:0046649	b	4	lymphocyte activation	SKAP2; PHF5A; RHOA; GPR183; PRDM1; PRR7	737	736
0.000900098	0.028829858	GO:0002250	b	3	adaptive immune response	DENND1B; NFKB2; GPR183; PRDM1; PRR7	657	654
0.000950435	0.028829858	GO:0048513	b	3	animal organ development	CNTF; SLC9B2; PRR7; GPR183; FOXD1; PRDM1; SNAI2; RHOA; ACO2; NFKB2; TCTA	3452	3442
0.001051301	0.028910768	GO:0001775	b	2	cell activation	CNTF; SKAP2; GPR183; PRR7; PRDM1; RHOA; NFKB2	1435	1432
0.001582558	0.029013556	GO:0001763	b	2	morphogenesis of a branching structure	SNAI2; PRDM1; FOXD1	196	196
0.001906631	0.029658706	GO:0042110	b	4	T cell activation	RHOA; GPR183; PRDM1; PRR7	456	455
0.002392424	0.033493938	GO:0072678	b	4	T cell migration	RHOA; GPR183	61	61
0.005695234	0.035923781	GO:0062014	b	5	negative regulation of small molecule metabolic process	SNAI2; RHOA	95	95
0.001730485	0.036775107	GO:0050794	b	3	regulation of cellular process	CNTF; PRR7; ATG16L1; SKAP2; HNRNPA2B1; GPR183; FOXD1; SNAI2; DENND1B; UBAC2; PRDM1; LMAN2; GPR22; PHF5A; RHOA; SLC9B2; CBX3; NFKB2; TCTA; CREM	10850	10810
0.00202061	0.036775107	GO:0003170	b	3	heart valve development	SNAI2; PRDM1	56	56
0.00332984	0.039797521	GO:0045595	b	4	regulation of cell differentiation	CNTF; GPR183; PRDM1; SNAI2; RHOA; SLC9B2; TCTA	1753	1747
0.003411216	0.039797521	GO:0048523	b	4	negative regulation of cellular process	CNTF; SKAP2; FOXD1; CREM; UBAC2; HNRNPA2B1; SNAI2; RHOA; PRR7; CBX3; TCTA; PRDM1	4670	4652
0.003703636	0.039885312	GO:0031323	b	4	regulation of cellular metabolic process	CNTF; HNRNPA2B1; GPR183; FOXD1; UBAC2; PRDM1; ATG16L1; SNAI2; PHF5A; RHOA; PRR7; CBX3; NFKB2; CREM	6130	6106
0.0041878	0.041878	GO:0009892	b	4	negative regulation of metabolic process	FOXD1; CREM; UBAC2; HNRNPA2B1; SNAI2; RHOA; PRR7; CBX3; PRDM1	2890	2887
0.008919222	0.044533794	GO:0009967	b	5	positive regulation of signal transduction	CNTF; SKAP2; GPR183; PRR7; RHOA; FOXD1	1579	1576
0.008966843	0.044533794	GO:0045596	b	5	negative regulation of cell differentiation	SNAI2; CNTF; RHOA; TCTA	706	703
0.009119744	0.044533794	GO:0010605	b	5	negative regulation of macromolecule metabolic process	FOXD1; CREM; UBAC2; HNRNPA2B1; SNAI2; PRR7; CBX3; PRDM1	2653	2650
0.009232616	0.044533794	GO:0007043	b	5	cell-cell junction assembly	SNAI2; RHOA	122	122
0.004907527	0.045803587	GO:1901888	b	4	regulation of cell junction assembly	SNAI2; RHOA	88	88
0.004000563	0.047837298	GO:0030154	b	3	cell differentiation	CNTF; PRR7; GPR183; FOXD1; PRDM1; SNAI2; RHOA; SLC9B2; NFKB2; TCTA; CREM	4089	4079
0.004586722	0.047837298	GO:0050886	b	3	endocrine process	RHOA; FOXD1	85	85
0.004881406	0.047837298	GO:0030522	b	3	intracellular receptor signaling pathway	SNAI2; RHOA; CREM	292	292
0.005239206	0.047837298	GO:0051239	b	3	regulation of multicellular organismal process	CNTF; GPR183; FOXD1; PRDM1; SNAI2; RHOA; SLC9B2; NFKB2; TCTA	2989	2983
0.005256846	0.047837298	GO:0009887	b	3	animal organ morphogenesis	SNAI2; CNTF; RHOA; PRDM1; FOXD1	981	979

Supplementary Table 6. Pathways enrichment in colonoids

p-value	q-value	term_goid	term_category	term_level	term_name	members_input_overlap_genes	size	effective_size
1.12E-05	0.002033455	GO:0048522	b	4	positive regulation of cellular process	TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; CD6; CBLL1; ZFP90; GDF9; CEBPG; TEF; PRR7; CDH3; TRIM25; FOXD1; DAG1; LMAN2; MAML2; SBNO2; HOXA5; HOXA3; PHF5A; HOXA9	5324	5307
0.00073718	0.004785161	GO:0008301	m	5	DNA binding, bending	CEBPG; FOXD1	21	21
0.001585377	0.004785161	GO:0044212	m	5	transcription regulatory region DNA binding	CEBPG; TEF; FOXD1; HOXA5; HOXA3; SATB1; HOXA9	924	916
0.001794435	0.004785161	GO:0003690	m	5	double-stranded DNA binding	CEBPG; TEF; FOXD1; HOXA5; HOXA3; SATB1; HOXA9	945	936
7.71E-05	0.006335136	GO:0048513	b	3	animal organ development	FAM213A; SBNO2; GDF9; CEBPG; PRR7; UQCRCQ; DOCK7; FOXD1; HOXA5; HOXA3; DAG1; SATB1; FNDC3A; CDH3; ACO2; HOXA9; TMED10	3452	3442
0.000107375	0.006335136	GO:0048518	b	3	positive regulation of biological process	TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; CD6; CBLL1; ZFP90; GDF9; CEBPG; TEF; PRR7; CDH3; TRIM25; FOXD1; DAG1; LMAN2; MAML2; SBNO2; HOXA5; HOXA3; PHF5A; HOXA9	6051	6034
0.000143396	0.007334844	GO:0031325	b	5	positive regulation of cellular metabolic process	SBNO2; GDF9; CEBPG; TNFSF15; DOCK7; TEF; FOXD1; HOXA5; HOXA3; DAG1; ZFP90; PHF5A; MAML2; CDH3; PRR7; HOXA9	3251	3239
0.000152809	0.007334844	GO:0010604	b	5	positive regulation of macromolecule metabolic process	SBNO2; GDF9; CEBPG; TNFSF15; DOCK7; TEF; FOXD1; HOXA5; HOXA3; DAG1; ZFP90; PHF5A; MAML2; CDH3; PRR7; HOXA9	3268	3256
0.005015961	0.010031923	GO:0043565	m	5	sequence-specific DNA binding	CEBPG; TEF; FOXD1; HOXA5; HOXA3; SATB1; HOXA9	1134	1125
0.000348845	0.011163036	GO:0051173	b	5	positive regulation of nitrogen compound metabolic process	SBNO2; GDF9; CEBPG; TNFSF15; DOCK7; TEF; FOXD1; HOXA5; HOXA3; DAG1; ZFP90; PHF5A; MAML2; PRR7; HOXA9	3128	3116
0.000168939	0.012131161	GO:0048732	b	4	gland development	CEBPG; HOXA5; HOXA3; DAG1; ACO2; HOXA9	437	437
0.000201762	0.012131161	GO:0048534	b	4	hematopoietic or lymphoid organ development	FAM213A; SBNO2; CEBPG; PRR7; HOXA5; HOXA3; SATB1; HOXA9	872	870
0.000353206	0.012131161	GO:0019438	b	4	aromatic compound biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; HOXA9	4296	4278
0.000394478	0.012131161	GO:0009893	b	4	positive regulation of metabolic process	SBNO2; GDF9; CEBPG; TNFSF15; DOCK7; TEF; FOXD1; HOXA5; HOXA3; DAG1; ZFP90; PHF5A; MAML2; CDH3; PRR7; HOXA9	3537	3525
0.000453476	0.012131161	GO:0031323	b	4	regulation of cellular metabolic process	TNFSF15; DOCK7; SPRED2; ZFP90; TMED10; GDF9; MAML2; TEF; PRR7; CDH3; CUL2; TRIM25; FOXD1; DAG1; SATB1; ASCC2; CEBPG; SBNO2; HOXA5; HOXA3; PHF5A; HOXA9	6130	6106
0.000485829	0.012131161	GO:0060255	b	4	regulation of macromolecule metabolic process	TNFSF15; DOCK7; SPRED2; ZFP90; TMED10; GDF9; MAML2; TEF; PRR7; CDH3; CUL2; TRIM25; FOXD1; DAG1; SATB1; ASCC2; CEBPG; SBNO2; HOXA5; HOXA3; PHF5A; HOXA9	6156	6133
0.000533238	0.012131161	GO:1901362	b	4	organic cyclic compound biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; HOXA9	4434	4416
0.008271009	0.013233615	GO:0061630	m	5	ubiquitin protein ligase activity	TRIM25; CBLL1; CUL2	217	217
0.000585493	0.013239158	GO:0009967	b	5	positive regulation of signal transduction	GDF9; MAML2; TNFSF15; SKAP2; TRIM25; TSPAN14; SPRED2; FOXD1; CDH3; PRR7	1579	1576
0.000875169	0.013239158	GO:0009891	b	5	positive regulation of biosynthetic process	SBNO2; CEBPG; TEF; FOXD1; HOXA5; HOXA3; ZFP90; PHF5A; MAML2; CDH3; HOXA9	1983	1974
0.000881297	0.013239158	GO:0030097	b	5	hemopoiesis	FAM213A; SBNO2; CEBPG; PRR7; HOXA5; SATB1; HOXA9	830	828
0.000965355	0.013239158	GO:0030878	b	5	thyroid gland development	HOXA5; HOXA3	24	24
0.003006081	0.015030406	GO:0016604	c	5	nuclear body	MAML2; TRIM25; CBLL1; SATB1; ASCC2; PHF5A	760	759
0.001254592	0.015055104	GO:0010647	b	5	positive regulation of cell communication	GDF9; MAML2; TNFSF15; SKAP2; TRIM25; TSPAN14; SPRED2; FOXD1; CDH3; PRR7	1741	1738
0.001411492	0.01505591	GO:0060441	b	5	epithelial tube branching involved in lung morphogenesis	HOXA5; DAG1	29	29
0.001806512	0.015080803	GO:0048706	b	5	embryonic skeletal system development	HOXA5; HOXA3; HOXA9	126	126
0.001808854	0.015080803	GO:0006351	b	5	transcription, DNA-templated	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; HOXA9	3645	3628
0.002144917	0.015080803	GO:0032774	b	5	RNA biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; HOXA9	3705	3688
0.002199284	0.015080803	GO:0044409	b	5	entry into host	TRIM25; DAG1; CBLL1	135	135
0.002199284	0.015080803	GO:0051806	b	5	entry into cell of other organism involved in symbiotic interaction	TRIM25; DAG1; CBLL1	135	135
0.000819781	0.015698692	GO:0051171	b	4	regulation of nitrogen compound metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TNFSF15; TRIM25; CUL2; DOCK7; TEF; FOXD1; HOXA5; HOXA3; DAG1; SATB1; PHF5A; ASCC2; SPRED2; PRR7; HOXA9; TMED10	5904	5881
0.000944599	0.015698692	GO:0034654	b	4	nucleobase-containing compound biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; HOXA9	4222	4204
0.001016347	0.015698692	GO:0030099	b	4	myeloid cell differentiation	FAM213A; SBNO2; HOXA5; CEBPG; HOXA9	408	406
0.001103753	0.015698692	GO:0048584	b	4	positive regulation of response to stimulus	GDF9; CEBPG; TNFSF15; SKAP2; TRIM25; TSPAN14; SPRED2; FOXD1; CD6; MAML2; CDH3; PRR7	2371	2366
0.001127729	0.015698692	GO:0018130	b	4	heterocycle biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; HOXA9	4285	4267
0.001226498	0.015698692	GO:0080090	b	4	regulation of primary metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TNFSF15; TRIM25; CUL2; DOCK7; TEF; FOXD1; HOXA5; HOXA3; DAG1; SATB1; PHF5A; ASCC2; SPRED2; PRR7; HOXA9; TMED10	6071	6047
0.001293848	0.015698692	GO:0023056	b	4	positive regulation of signaling	GDF9; MAML2; TNFSF15; SKAP2; TRIM25; TSPAN14; SPRED2; FOXD1; CDH3; PRR7	1748	1745
0.002551661	0.016176839	GO:0031326	b	5	regulation of cellular biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; HOXA9	4174	4158
0.002748029	0.016176839	GO:0051252	b	5	regulation of RNA metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; HOXA9	3795	3778
0.002864649	0.016176839	GO:0016070	b	5	RNA metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; DUS4; HOXA9; CBLL1	4644	4624
0.00030609	0.017987405	GO:0002520	b	2	immune system development	FAM213A; SBNO2; CEBPG; PRR7; HOXA5; HOXA3; SATB1; HOXA9	928	925

0.000545073	0.017987405	GO:0007275	b	2	multicellular organism development	FAM213A; SBNO2; GDF9; CEBPG; PRR7; DLD; CBLL1; UQCRQ; DOCK7; SPRED2; FOXD1; HOXA5; HOXA3; DAG1; SATB1; FNDC3A; CDH3; ACO2; HOXA9; TMED10	5289	5275
0.003832631	0.020440698	GO:0060986	b	5	endocrine hormone secretion	GDF9; FOXD1	48	48
0.002199284	0.025016854	GO:0051828	b	4	entry into other organism involved in symbiotic interaction	TRIM25; DAG1; CBLL1	135	135
0.00055935	0.025382923	GO:0010556	b	5	regulation of macromolecule biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; HOXA9	4031	4015
0.0005549711	0.025382923	GO:0019219	b	5	regulation of nucleobase-containing compound metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; HOXA9	4070	4053
0.0005552514	0.025382923	GO:0010468	b	5	regulation of gene expression	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; HOXA9	4492	4475
0.001605377	0.025686025	GO:0001067	m	4	regulatory region nucleic acid binding	CEBPG; TEF; FOXD1; HOXA5; HOXA3; SATB1; HOXA9	926	918
0.002583307	0.02765658	GO:0002521	b	4	leukocyte differentiation	FAM213A; SBNO2; CEBPG; SATB1; PRR7	504	502
0.002964535	0.029404686	GO:0048754	b	4	branching morphogenesis of an epithelial tube	HOXA5; DAG1; FOXD1	150	150
0.00306972	0.029404686	GO:0009889	b	4	regulation of biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; TRIM25; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; HOXA9	4246	4230
0.001879509	0.031223159	GO:0021700	b	2	developmental maturation	CDH3; HOXA5; DAG1; DLD	277	276
0.001892313	0.031223159	GO:0048856	b	2	anatomical structure development	FAM213A; SBNO2; GDF9; CEBPG; PRR7; DLD; CBLL1; UQCRQ; DOCK7; SPRED2; FOXD1; HOXA5; HOXA3; DAG1; SATB1; FNDC3A; CDH3; ACO2; HOXA9; TMED10	5790	5773
0.002777406	0.036661753	GO:0044237	b	2	cellular metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRQ; CBLL1; ZFP90; TMED10; GDF9; CEBPG; TEF; PRR7; CDH3; CUL2; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; MAML2; ACO2; SBNO2; HOXA5; HOXA3; ASCC2; DUS4L; HOXA9	10637	10598
0.00106765	0.037436961	GO:0006725	b	3	cellular aromatic compound metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; UQCRQ; DUS4L; HOXA9; CBLL1	6015	5989
0.001653661	0.037436961	GO:0019222	b	3	regulation of metabolic process	TNFSF15; DOCK7; SPRED2; ZFP90; TMED10; GDF9; MAML2; TEF; PRR7; CDH3; CUL2; TRIM25; FOXD1; DAG1; SATB1; ASCC2; CEBPG; SBNO2; HOXA5; HOXA3; PHF5A; HOXA9	6671	6647
0.001726458	0.037436961	GO:1901360	b	3	organic cyclic compound metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; CDH3; UQCRQ; DUS4L; HOXA9; CBLL1	6220	6194
0.001941221	0.037436961	GO:0006139	b	3	nucleobase-containing compound metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; UQCRQ; DUS4L; HOXA9; CBLL1	5810	5784
0.002769974	0.037436961	GO:0046483	b	3	heterocycle metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; UQCRQ; DUS4L; HOXA9; CBLL1	5967	5941
0.003132233	0.037436961	GO:0034641	b	3	cellular nitrogen compound metabolic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; CBLL1; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; UQCRQ; DUS4L; HOXA9; TMED10	6494	6465
0.003434225	0.037436961	GO:0048731	b	3	system development	FAM213A; SBNO2; GDF9; CEBPG; PRR7; UQCRQ; DOCK7; FOXD1; HOXA5; HOXA3; DAG1; SATB1; FNDC3A; CDH3; ACO2; HOXA9; TMED10	4713	4699
0.003555327	0.037436961	GO:0071695	b	3	anatomical structure maturation	CDH3; HOXA5; DAG1	161	160
0.003993068	0.037436961	GO:0048519	b	3	negative regulation of biological process	SBNO2; GDF9; CEBPG; ZFP90; SKAP2; TRIM25; CUL2; DOCK7; SPRED2; FOXD1; HOXA5; HOXA3; DAG1; SATB1; CDH3; PRR7; HOXA9; CBLL1	5219	5201
0.004066625	0.037436961	GO:0003002	b	3	regionalization	HOXA5; HOXA3; HOXA9; FOXD1	342	342
0.004124411	0.037436961	GO:0050794	b	3	regulation of cellular process	FAM213A; TNFSF15; SKAP2; TSPAN14; DOCK7; SPRED2; CD6; CBLL1; ZFP90; PHF5A; TMED10; GDF9; CEBPG; TEF; PRR7; CDH3; CUL2; DLD; TRIM25; FOXD1; DAG1; SATB1; LMAN2; MAML2; SBNO2; HOXA5; HOXA3; ASCC2; HOXA9	10850	10810
0.004152182	0.037784855	GO:0060425	b	4	lung morphogenesis	HOXA5; DAG1	50	50
0.00454742	0.038328257	GO:0048598	b	3	embryonic morphogenesis	HOXA5; HOXA3; DAG1; HOXA9; DLD	573	573
0.005095331	0.040083267	GO:0061138	b	3	morphogenesis of a branching epithelium	HOXA5; DAG1; FOXD1	182	182
0.008909262	0.041948808	GO:0061659	m	4	ubiquitin-like protein ligase activity	TRIM25; CBLL1; CUL2	223	223
0.010084844	0.041948808	GO:0050660	m	4	flavin adenine dinucleotide binding	DUS4L; DLD	79	79
0.010487202	0.041948808	GO:0001228	m	4	DNA-binding transcription activator activity, RNA polymerase II-specific	HOXA5; CEBPG; TEF; FOXD1	457	449
0.004865275	0.04216572	GO:0045333	b	4	cellular respiration	UQCRQ; ACO2; DLD	179	179
0.005907531	0.043568041	GO:0030154	b	3	cell differentiation	FAM213A; SBNO2; GDF9; CEBPG; DLD; UQCRQ; DOCK7; FOXD1; HOXA5; DAG1; SATB1; FNDC3A; CDH3; PRR7; HOXA9	4089	4079
0.005277872	0.0436624	GO:0044271	b	4	cellular nitrogen compound biosynthetic process	SBNO2; GDF9; MAML2; CEBPG; ZFP90; DLD; TRIM25; GNPDA1; TEF; FOXD1; HOXA5; HOXA3; CUL2; SATB1; PHF5A; ASCC2; HOXA9	4906	4885
0.004715482	0.045873485	GO:0009566	b	2	fertilization	FNDC3A; GNPDA1; HOXA9	177	177
0.005064104	0.045873485	GO:0001775	b	2	cell activation	SBNO2; CEBPG; SKAP2; TSPAN14; PRR7; CD6; SATB1; HOXA9	1435	1432
0.005661678	0.045873485	GO:0071704	b	2	organic substance metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRQ; CBLL1; ZFP90; TMED10; GDF9; CEBPG; TEF; PRR7; CDH3; CUL2; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; MAML2; ACO2; SBNO2; HOXA5; HOXA3; ASCC2; DUS4L; HOXA9	11025	10986
0.006255475	0.045873485	GO:0001763	b	2	morphogenesis of a branching structure	HOXA5; DAG1; FOXD1	196	196
0.008218434	0.04730617	GO:0044238	b	2	primary metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRQ; CBLL1; ZFP90; TMED10; GDF9; CEBPG; TEF; PRR7; CUL2; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; MAML2; ACO2; SBNO2; HOXA5; HOXA3; ASCC2; DUS4L; HOXA9	10663	10624
0.009067287	0.04730617	GO:0048869	b	2	cellular developmental process	FAM213A; SBNO2; GDF9; CEBPG; DLD; UQCRQ; DOCK7; FOXD1; HOXA5; DAG1; SATB1; FNDC3A; CDH3; PRR7; HOXA9	4275	4265
0.009312077	0.04730617	GO:0006807	b	2	nitrogen compound metabolic process	TNFSF15; GNPDA1; TSPAN14; DOCK7; SPRED2; UQCRQ; CBLL1; ZFP90; TMED10; GDF9; MAML2; TEF; PRR7; CUL2; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; CEBPG; SBNO2; HOXA5; HOXA3; ASCC2; DUS4L; HOXA9	10174	10136
0.009486926	0.04730617	GO:0007389	b	2	pattern specification process	HOXA5; HOXA3; HOXA9; FOXD1	436	436
0.010034642	0.04730617	GO:0045321	b	2	leukocyte activation	SBNO2; CEBPG; SKAP2; TSPAN14; PRR7; CD6; SATB1	1284	1281

0.00686863	0.047676371	GO:0043170	b	3	macromolecule metabolic process	TNFSF15; TSPAN14; DOCK7; SPRED2; CBLL1; ZFP90; TMED10; GDF9; MAML2; TEF; PRR7; CDH3; CUL2; DLD; TRIM25; FOXD1; DAG1; SATB1; PHF5A; CEBPG; SBNO2; HOXA5; HOXA3; ASCC2; DUS4L; HOXA9	9445	9411
0.011747399	0.049517199	GO:0045637	b	5	regulation of myeloid cell differentiation	FAM213A; HOXA5; HOXA9	249	247
0.011863495	0.049517199	GO:0042773	b	5	ATP synthesis coupled electron transport	UQCRQ; DLD	86	86
0.007561727	0.049571324	GO:0051701	b	3	interaction with host	TRIM25; DAG1; CBLL1	210	210
0.002153244	0.049786788	GO:0034399	c	4	nuclear periphery	PHF5A; DAG1; SATB1	134	134
0.003829753	0.049786788	GO:0005654	c	4	nucleoplasm	MAML2; CEBPG; DLD; SKAP2; TRIM25; COG5; HOXA3; DAG1; SATB1; PHF5A; ASCC2; SPATA7; CUL2; CBLL1	3520	3501