

Supplemental Material

Table s1: SCGS genes in the DNA replication / cell cycle module. The FIR score, percentile, and Bonferroni-corrected p-value (see Methods) are reported for each gene in the set.

Gene Name	Gene ID	Score	Binomial p-value	Percentile
<i>DNMT3B</i>	1789	0.508379888	2.94E-61	0.00296267
<i>MCM6</i>	4175	0.51396648	1.62E-62	0.002666403
<i>CDC25A</i>	993	0.525139665	4.62E-65	0.002024491
<i>PFAS</i>	5198	0.525139665	4.62E-65	0.002024491
<i>MCM4</i>	4173	0.452513966	3.30E-49	0.008641122
<i>XRCC5</i>	7520	0.480446927	4.11E-55	0.005184673
<i>HAUS6</i>	54801	0.458100559	2.28E-50	0.007406676
<i>TET1</i>	80312	0.458100559	2.28E-50	0.007406676
<i>IGF2BP1</i>	10642	0.541899441	5.95E-69	0.001580091
<i>PLAA</i>	9373	0.469273743	1.01E-52	0.006270986
<i>DEPDC1B</i>	55789	0.458100559	2.28E-50	0.007406676
<i>TEX10</i>	54881	0.458100559	2.28E-50	0.007406676
<i>CCDC99</i>	54908	0.558659218	6.26E-73	0.001234446
<i>MSH2</i>	4436	0.480446927	4.11E-55	0.005184673
<i>BUB1B</i>	701	0.480446927	4.11E-55	0.005184673
<i>MSH6</i>	2956	0.463687151	1.53E-51	0.007011653
<i>DLGAP5</i>	9787	0.491620112	1.53E-57	0.004147738
<i>SKIV2L2</i>	23517	0.469273743	1.01E-52	0.006270986
<i>CENPE</i>	1062	0.474860335	6.52E-54	0.005629074
<i>CHEK2</i>	11200	0.525139665	4.62E-65	0.002024491
<i>SOHLH2</i>	54937	0.603351955	5.68E-84	0.000345645
<i>CCNB1</i>	891	0.458100559	2.28E-50	0.007406676
<i>RRAS2</i>	22800	0.581005587	2.26E-78	0.000641912
<i>PRIM1</i>	5557	0.474860335	6.52E-54	0.005629074
<i>PAICS</i>	10606	0.469273743	1.01E-52	0.006270986
<i>CCNA2</i>	890	0.497206704	9.02E-59	0.003703338
<i>CPSF3</i>	51692	0.474860335	6.52E-54	0.005629074
<i>NUSAP1</i>	51203	0.469273743	1.01E-52	0.006270986
<i>LIN28B</i>	389421	0.502793296	5.21E-60	0.00320956
<i>IPO5</i>	3843	0.525139665	4.62E-65	0.002024491
<i>KIF11</i>	3832	0.48603352	2.54E-56	0.004690895
<i>BMPR1A</i>	657	0.452513966	3.30E-49	0.008641122
<i>NDC80</i>	10403	0.491620112	1.53E-57	0.004147738
<i>BCAT1</i>	586	0.519553073	8.75E-64	0.002419514
<i>CCNG1</i>	900	0.508379888	2.94E-61	0.00296267
<i>ZNF788</i>	388507	0.469273743	1.01E-52	0.006270986

<i>ASCC3</i>	10973	0.452513966	3.30E-49	0.008641122
<i>FANCB</i>	2187	0.458100559	2.28E-50	0.007406676
<i>MCM10</i>	55388	0.525139665	4.62E-65	0.002024491
<i>HMGA2</i>	8091	0.469273743	1.01E-52	0.006270986
<i>SKP2</i>	6502	0.469273743	1.01E-52	0.006270986
<i>TRIM24</i>	8805	0.541899441	5.95E-69	0.001580091
<i>ORC1</i>	4998	0.480446927	4.11E-55	0.005184673
<i>HDAC2</i>	3066	0.458100559	2.28E-50	0.007406676
<i>HESX1</i>	8820	0.480446927	4.11E-55	0.005184673
<i>C1orf135</i>	79000	0.51396648	1.62E-62	0.002666403
<i>INHBE</i>	83729	0.497206704	9.02E-59	0.003703338
<i>MIS18A</i>	54069	0.463687151	1.53E-51	0.007011653
<i>DCUN1D5</i>	84259	0.463687151	1.53E-51	0.007011653
<i>POLE2</i>	5427	0.48603352	2.54E-56	0.004690895
<i>MRPL3</i>	11222	0.469273743	1.01E-52	0.006270986
<i>CENPH</i>	64946	0.463687151	1.53E-51	0.007011653
<i>MYCN</i>	4613	0.458100559	2.28E-50	0.007406676
<i>HAUS1</i>	115106	0.474860335	6.52E-54	0.005629074
<i>GDF3</i>	9573	0.458100559	2.28E-50	0.007406676

Table s2: SCGS genes in the RNA transcription / protein synthesis module. The FIR score, percentile, and Bonferroni-corrected p-value (see Methods) are reported for each gene in the set.

Gene Name	Gene ID	Score	Binomial p-value	Percentile
<i>TBCE</i>	6905	0.491620112	1.53E-57	0.004147738
<i>RIOK2</i>	55781	0.597765363	1.48E-82	0.000395023
<i>BCKDHB</i>	594	0.458100559	2.28E-50	0.007406676
<i>RAD1</i>	5810	0.458100559	2.28E-50	0.007406676
<i>NREP</i>	9315	0.458100559	2.28E-50	0.007406676
<i>ADH5</i>	128	0.648044693	1.16E-95	0.000197511
<i>PLRG1</i>	5356	0.519553073	8.75E-64	0.002419514
<i>ROR1</i>	4919	0.670391061	9.24E-102	4.94E-05
<i>RAB3B</i>	5865	0.553072626	1.36E-71	0.001431957
<i>LOC285431</i>	285431	0.491620112	1.53E-57	0.004147738
<i>DBC1</i>	1620	0.48603352	2.54E-56	0.004690895
<i>KIF23</i>	9493	0.452513966	3.30E-49	0.008641122
<i>DIAPH3</i>	81624	0.502793296	5.21E-60	0.00320956
<i>GNL2</i>	29889	0.491620112	1.53E-57	0.004147738
<i>FGF2</i>	2247	0.681564246	7.10E-105	0
<i>TARDBP</i>	23435	0.458100559	2.28E-50	0.007406676
<i>NMNAT2</i>	23057	0.452513966	3.30E-49	0.008641122
<i>ZNF167</i>	55888	0.491620112	1.53E-57	0.004147738

<i>KIF20A</i>	10112	0.463687151	1.53E-51	0.007011653
<i>CENPI</i>	2491	0.480446927	4.11E-55	0.005184673
<i>DDX1</i>	1653	0.469273743	1.01E-52	0.006270986
<i>XXYLT1</i>	152002	0.525139665	4.62E-65	0.002024491
<i>GPR176</i>	11245	0.664804469	3.21E-100	9.88E-05
<i>FBXO22</i>	26263	0.469273743	1.01E-52	0.006270986
<i>BBS9</i>	27241	0.51396648	1.62E-62	0.002666403
<i>C14orf166</i>	51637	0.541899441	5.95E-69	0.001580091
<i>BOD1</i>	91272	0.519553073	8.75E-64	0.002419514
<i>CDC123</i>	8872	0.469273743	1.01E-52	0.006270986
<i>SNRPD3</i>	6634	0.502793296	5.21E-60	0.00320956
<i>FAM118B</i>	79607	0.56424581	2.82E-74	0.000987557
<i>DPH3</i>	285381	0.474860335	6.52E-54	0.005629074
<i>EIF2B3</i>	8891	0.469273743	1.01E-52	0.006270986
<i>KDELC1</i>	79070	0.586592179	9.33E-80	0.000543156
<i>RPF2</i>	84154	0.458100559	2.28E-50	0.007406676
<i>APLP1</i>	333	0.474860335	6.52E-54	0.005629074
<i>DACT1</i>	51339	0.536312849	1.20E-67	0.001777602
<i>PDHB</i>	5162	0.586592179	9.33E-80	0.000543156
<i>C14orf119</i>	55017	0.575418994	5.37E-77	0.000790045
<i>DTD1</i>	92675	0.469273743	1.01E-52	0.006270986
<i>SAMM50</i>	25813	0.497206704	9.02E-59	0.003703338
<i>CCL26</i>	10344	0.491620112	1.53E-57	0.004147738
<i>C4orf52</i>	389203	0.458100559	2.28E-50	0.007406676
<i>CCDC90B</i>	60492	0.458100559	2.28E-50	0.007406676
<i>MED20</i>	9477	0.56424581	2.82E-74	0.000987557
<i>UTP6</i>	55813	0.469273743	1.01E-52	0.006270986
<i>RARS2</i>	57038	0.458100559	2.28E-50	0.007406676
<i>KIAA0020</i>	9933	0.474860335	6.52E-54	0.005629074
<i>ARMCX2</i>	9823	0.569832402	1.25E-75	0.000839423
<i>RARS</i>	5917	0.491620112	1.53E-57	0.004147738
<i>MTHFD2</i>	10797	0.469273743	1.01E-52	0.006270986
<i>DHX15</i>	1665	0.452513966	3.30E-49	0.008641122
<i>HTR7</i>	3363	0.558659218	6.26E-73	0.001234446
<i>HIST1H4C</i>	8364	0.48603352	2.54E-56	0.004690895

Table s3: SCGS genes in the metabolism / hormone signaling / protein synthesis module. The FIR score, percentile, and Bonferroni-corrected p-value (see Methods) are reported for each gene in the set.

Gene Name	Gene ID	Score	Binomial p-value	Percentile
<i>MTHFD1L</i>	25902	0.541899441	5.95E-69	0.001580091

<i>ARMC9</i>	80210	0.569832402	1.25E-75	0.000839423
<i>XPOT</i>	11260	0.51396648	1.62E-62	0.002666403
<i>IARS</i>	3376	0.497206704	9.02E-59	0.003703338
<i>HDX</i>	139324	0.56424581	2.82E-74	0.000987557
<i>ACTRT3</i>	84517	0.530726257	2.39E-66	0.001925736
<i>ERCC2</i>	2068	0.458100559	2.28E-50	0.007406676
<i>TBC1D16</i>	125058	0.452513966	3.30E-49	0.008641122
<i>GARS</i>	2617	0.497206704	9.02E-59	0.003703338
<i>KIF7</i>	374654	0.61452514	7.83E-87	0.000296267
<i>UBE2K</i>	3093	0.508379888	2.94E-61	0.00296267
<i>SLC25A3</i>	5250	0.48603352	2.54E-56	0.004690895
<i>ICMT</i>	23463	0.530726257	2.39E-66	0.001925736
<i>UGGT2</i>	55757	0.48603352	2.54E-56	0.004690895
<i>ATP11C</i>	286410	0.48603352	2.54E-56	0.004690895
<i>SLC24A1</i>	9187	0.497206704	9.02E-59	0.003703338
<i>EIF2AK4</i>	440275	0.474860335	6.52E-54	0.005629074
<i>GPX8</i>	493869	0.491620112	1.53E-57	0.004147738
<i>ALX1</i>	8092	0.51396648	1.62E-62	0.002666403
<i>OSTC</i>	58505	0.525139665	4.62E-65	0.002024491
<i>TRPC4</i>	7223	0.458100559	2.28E-50	0.007406676
<i>HAS2</i>	3037	0.51396648	1.62E-62	0.002666403
<i>FZD2</i>	2535	0.452513966	3.30E-49	0.008641122
<i>TRNT1</i>	51095	0.519553073	8.75E-64	0.002419514
<i>MMADHC</i>	27249	0.536312849	1.20E-67	0.001777602
<i>SNX8</i>	29886	0.502793296	5.21E-60	0.00320956
<i>CDH6</i>	1004	0.458100559	2.28E-50	0.007406676
<i>HAT1</i>	8520	0.458100559	2.28E-50	0.007406676
<i>SEC11A</i>	23478	0.519553073	8.75E-64	0.002419514
<i>DIMT1</i>	27292	0.452513966	3.30E-49	0.008641122
<i>TM2D2</i>	83877	0.452513966	3.30E-49	0.008641122
<i>FST</i>	10468	0.536312849	1.20E-67	0.001777602
<i>GBE1</i>	2632	0.480446927	4.11E-55	0.005184673

Table s4: SCGS genes in the multicellular signaling / immune signaling / cell identity module. The FIR score, percentile, and Bonferroni-corrected p-value (see Methods) are reported for each gene in the set.

Gene Name	Gene ID	Score	Binomial p-value	Percentile
<i>NA</i>	80047	0.452513966	3.30E-49	0.008641122
<i>MLL3</i>	58508	0.508379888	2.94E-61	0.00296267
<i>MXI1</i>	4601	0.480446927	4.11E-55	0.005184673
<i>FKSG49</i>	400949	0.569832402	1.25E-75	0.000839423

<i>FAM185BP</i>	641808	0.48603352	2.54E-56	0.004690895
<i>ARRB2</i>	409	0.56424581	2.82E-74	0.000987557
<i>SMARCC2</i>	6601	0.497206704	9.02E-59	0.003703338
<i>WASH3P</i>	374666	0.491620112	1.53E-57	0.004147738
<i>PILRB</i>	29990	0.463687151	1.53E-51	0.007011653
<i>CTSH</i>	1512	0.48603352	2.54E-56	0.004690895
<i>SAT1</i>	6303	0.553072626	1.36E-71	0.001431957
<i>JUNB</i>	3726	0.452513966	3.30E-49	0.008641122
<i>CD53</i>	963	0.508379888	2.94E-61	0.00296267
<i>PECAM1</i>	5175	0.597765363	1.48E-82	0.000395023
<i>IL10RA</i>	3587	0.502793296	5.21E-60	0.00320956
<i>RCSD1</i>	92241	0.452513966	3.30E-49	0.008641122
<i>ARHGDI1</i>	397	0.452513966	3.30E-49	0.008641122
<i>GIMAP5</i>	55340	0.581005587	2.26E-78	0.000641912
<i>GIMAP6</i>	474344	0.474860335	6.52E-54	0.005629074
<i>HLA-DMB</i>	3109	0.597765363	1.48E-82	0.000395023
<i>PTPRC</i>	5788	0.502793296	5.21E-60	0.00320956
<i>C10orf128</i>	170371	0.502793296	5.21E-60	0.00320956
<i>CMBL</i>	134147	0.474860335	6.52E-54	0.005629074
<i>HLA-DRB5</i>	3127	0.558659218	6.26E-73	0.001234446
<i>HLA-DPA1</i>	3113	0.558659218	6.26E-73	0.001234446
<i>ABCG1</i>	9619	0.642458101	3.65E-94	0.000246889
<i>GIMAP7</i>	168537	0.480446927	4.11E-55	0.005184673
<i>HLA-DQA1</i>	3117	0.502793296	5.21E-60	0.00320956
<i>TSHZ2</i>	128553	0.463687151	1.53E-51	0.007011653
<i>RGCC</i>	28984	0.502793296	5.21E-60	0.00320956
<i>CCR1</i>	1230	0.502793296	5.21E-60	0.00320956
<i>NPR3</i>	4883	0.458100559	2.28E-50	0.007406676
<i>RSAD2</i>	91543	0.491620112	1.53E-57	0.004147738
<i>GIMAP1</i>	170575	0.474860335	6.52E-54	0.005629074
<i>TNFSF10</i>	8743	0.497206704	9.02E-59	0.003703338
<i>AFTPH</i>	54812	0.581005587	2.26E-78	0.000641912
<i>NA</i>	643187	0.458100559	2.28E-50	0.007406676
<i>MALAT1</i>	378938	0.497206704	9.02E-59	0.003703338
<i>UBXN2A</i>	165324	0.463687151	1.53E-51	0.007011653
<i>PDE4C</i>	5143	0.56424581	2.82E-74	0.000987557
<i>GIMAP8</i>	155038	0.474860335	6.52E-54	0.005629074
<i>FYB</i>	2533	0.547486034	2.87E-70	0.001530713
<i>MS4A7</i>	58475	0.525139665	4.62E-65	0.002024491
<i>C5orf56</i>	441108	0.458100559	2.28E-50	0.007406676
<i>LOC400931</i>	400931	0.474860335	6.52E-54	0.005629074
<i>MLLT6</i>	4302	0.664804469	3.21E-100	9.88E-05
<i>CTSS</i>	1520	0.48603352	2.54E-56	0.004690895

ZBTB20

26137

0.458100559

2.28E-50

0.007406676

Table s5: GO terms associated with the DNA replication / cell cycle expression module.

GO ID	p-value	Term
GO:0000280	7.52E-14	nuclear division
GO:0007067	7.52E-14	mitosis
GO:0048285	1.22E-13	organelle fission
GO:0000087	1.28E-13	M phase of mitotic cell cycle
GO:0022403	3.70E-13	cell cycle phase
GO:0000279	1.26E-12	M phase
GO:0000278	1.92E-12	mitotic cell cycle
GO:0022402	2.78E-12	cell cycle process
GO:0051301	3.40E-12	cell division
GO:0007049	3.88E-12	cell cycle
GO:0000070	6.02E-09	mitotic sister chromatid segregation
GO:0000819	7.13E-09	sister chromatid segregation
GO:0000226	2.29E-08	microtubule cytoskeleton organization
GO:0006996	4.19E-08	organelle organization
GO:0007059	6.75E-08	chromosome segregation
GO:0007051	7.94E-08	spindle organization
GO:0051276	8.06E-08	chromosome organization
GO:0000075	1.92E-07	cell cycle checkpoint
GO:0051656	3.08E-07	establishment of organelle localization
GO:0050000	4.99E-07	chromosome localization
GO:0051303	4.99E-07	establishment of chromosome localization
GO:0051726	9.53E-07	regulation of cell cycle
GO:0007017	1.09E-06	microtubule-based process
GO:0007093	1.63E-06	mitotic cell cycle checkpoint
GO:0051640	1.78E-06	organelle localization
GO:0006259	1.81E-06	DNA metabolic process
GO:0008608	3.22E-06	attachment of spindle microtubules to kinetochore
GO:0051313	3.22E-06	attachment of spindle microtubules to chromosome
GO:0007346	4.21E-06	regulation of mitotic cell cycle
GO:0040001	4.82E-06	establishment of mitotic spindle localization
GO:0006261	9.11E-06	DNA-dependent DNA replication
GO:0007080	9.42E-06	mitotic metaphase plate congression
GO:0051293	9.42E-06	establishment of spindle localization
GO:0051653	9.42E-06	spindle localization
GO:0007079	1.53E-05	mitotic chromosome movement towards spindle pole
GO:0051984	1.53E-05	positive regulation of chromosome segregation

GO:0051987	1.53E-05	positive regulation of attachment of spindle microtubules to kinetochore
GO:0051329	1.58E-05	interphase of mitotic cell cycle
GO:0051310	1.62E-05	metaphase plate congression
GO:0051325	2.26E-05	interphase
GO:0034453	2.57E-05	microtubule anchoring
GO:0010564	3.29E-05	regulation of cell cycle process
GO:0010638	3.35E-05	positive regulation of organelle organization
GO:0006260	3.41E-05	DNA replication
GO:0006189	4.59E-05	'de novo' IMP biosynthetic process
GO:0045842	4.59E-05	positive regulation of mitotic metaphase/anaphase transition
GO:0051305	4.59E-05	chromosome movement towards spindle pole
GO:0051988	4.59E-05	regulation of attachment of spindle microtubules to kinetochore
GO:0042770	5.20E-05	DNA damage response, signal transduction
GO:0070925	6.40E-05	organelle assembly
GO:0007052	7.38E-05	mitotic spindle organization
GO:0000077	8.44E-05	DNA damage checkpoint
GO:0045840	8.53E-05	positive regulation of mitosis
GO:0051225	8.53E-05	spindle assembly
GO:0051785	8.53E-05	positive regulation of nuclear division
GO:0006188	9.16E-05	IMP biosynthetic process
GO:0046040	9.16E-05	IMP metabolic process
GO:0031570	0.000102493	DNA integrity checkpoint
GO:0006270	0.000126262	DNA-dependent DNA replication initiation
GO:0045787	0.000138788	positive regulation of cell cycle
GO:0007095	0.000152304	mitotic cell cycle G2/M transition DNA damage checkpoint
GO:0034501	0.000152304	protein localization to kinetochore
GO:0043570	0.000152304	maintenance of DNA repeat elements
GO:0051096	0.000152304	positive regulation of helicase activity
GO:0071780	0.000152304	mitotic cell cycle G2/M transition checkpoint
GO:0007010	0.000158535	cytoskeleton organization
GO:0006974	0.000162218	response to DNA damage stimulus
GO:0002566	0.000227877	somatic diversification of immune receptors via somatic mutation
GO:0016446	0.000227877	somatic hypermutation of immunoglobulin genes
GO:0051383	0.000227877	kinetochore organization
GO:0000086	0.000242661	G2/M transition of mitotic cell cycle
GO:0031123	0.000242661	RNA 3'-end processing
GO:0000132	0.00031822	establishment of mitotic spindle orientation
GO:0051095	0.00031822	regulation of helicase activity

GO:0051294	0.00031822	establishment of spindle orientation
GO:0051297	0.00052015	centrosome organization
GO:0008340	0.000542761	determination of adult lifespan
GO:0010389	0.000542761	regulation of G2/M transition of mitotic cell cycle
GO:0045910	0.000542761	negative regulation of DNA recombination
GO:0031023	0.000559652	microtubule organizing center organization
GO:0090068	0.000644305	positive regulation of cell cycle process
GO:0016043	0.000661968	cellular component organization
GO:0090304	0.000751504	nucleic acid metabolic process
GO:0051716	0.000765834	cellular response to stimulus
GO:0006268	0.000825026	DNA unwinding involved in replication
GO:0051983	0.000987526	regulation of chromosome segregation
GO:0010259	0.001164124	multicellular organismal aging
GO:0031058	0.001164124	positive regulation of histone modification
GO:0071174	0.001164124	mitotic cell cycle spindle checkpoint
GO:0006139	0.001184437	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0033554	0.001264272	cellular response to stress
GO:0071103	0.001274869	DNA conformation change
GO:0034641	0.001471331	cellular nitrogen compound metabolic process
GO:0007088	0.001545082	regulation of mitosis
GO:0051783	0.001545082	regulation of nuclear division
GO:0032507	0.001787196	maintenance of protein location in cell
GO:0009127	0.00200931	purine nucleoside monophosphate biosynthetic process
GO:0009168	0.00200931	purine ribonucleoside monophosphate biosynthetic process
GO:0031577	0.00200931	spindle checkpoint
GO:0000082	0.002145096	G1/S transition of mitotic cell cycle
GO:0051130	0.002169458	positive regulation of cellular component organization
GO:0045185	0.002241011	maintenance of protein location
GO:0032392	0.002254764	DNA geometric change
GO:0032508	0.002254764	DNA duplex unwinding
GO:0006807	0.002269381	nitrogen compound metabolic process
GO:0051651	0.002440746	maintenance of location in cell
GO:0033043	0.002513612	regulation of organelle organization
GO:0016458	0.002651184	gene silencing
GO:0006298	0.002785911	mismatch repair
GO:0031572	0.002785911	G2/M transition DNA damage checkpoint
GO:0009126	0.003071393	purine nucleoside monophosphate metabolic process
GO:0009167	0.003071393	purine ribonucleoside monophosphate metabolic

		process
GO:0031056	0.003071393	regulation of histone modification
GO:0031124	0.003071393	mRNA 3'-end processing
GO:0000710	0.003955576	meiotic mismatch repair
GO:0003272	0.003955576	endocardial cushion formation
GO:0007100	0.003955576	mitotic centrosome separation
GO:0010610	0.003955576	regulation of mRNA stability involved in response to stress
GO:0021998	0.003955576	neural plate mediolateral regionalization
GO:0033129	0.003955576	positive regulation of histone phosphorylation
GO:0043146	0.003955576	spindle stabilization
GO:0043148	0.003955576	mitotic spindle stabilization
GO:0046680	0.003955576	response to DDT
GO:0048338	0.003955576	mesoderm structural organization
GO:0048352	0.003955576	paraxial mesoderm structural organization
GO:0060623	0.003955576	regulation of chromosome condensation
GO:0071281	0.003955576	cellular response to iron ion
GO:0071283	0.003955576	cellular response to iron(III) ion
GO:0002204	0.004006215	somatic recombination of immunoglobulin genes involved in immune response
GO:0002208	0.004006215	somatic diversification of immunoglobulins involved in immune response
GO:0007091	0.004006215	mitotic metaphase/anaphase transition
GO:0009156	0.004006215	ribonucleoside monophosphate biosynthetic process
GO:0030010	0.004006215	establishment of cell polarity
GO:0030071	0.004006215	regulation of mitotic metaphase/anaphase transition
GO:0031576	0.004006215	G2/M transition checkpoint
GO:0045190	0.004006215	isotype switching
GO:0010605	0.004216709	negative regulation of macromolecule metabolic process
GO:0008283	0.004296653	cell proliferation
GO:0002381	0.004343602	immunoglobulin production involved in immunoglobulin mediated immune response
GO:0006342	0.004693708	chromatin silencing
GO:0030261	0.004693708	chromosome condensation
GO:0051129	0.004995788	negative regulation of cellular component organization
GO:0009161	0.005431668	ribonucleoside monophosphate metabolic process
GO:0016447	0.005431668	somatic recombination of immunoglobulin gene segments

GO:0000018	0.005819321	regulation of DNA recombination
GO:0045814	0.005819321	negative regulation of gene expression, epigenetic
GO:0040029	0.005896798	regulation of gene expression, epigenetic
GO:0006281	0.006387647	DNA repair
GO:0009892	0.006597795	negative regulation of metabolic process
GO:0010639	0.006626223	negative regulation of organelle organization
GO:0016445	0.006631468	somatic diversification of immunoglobulins
GO:0008630	0.007492078	DNA damage response, signal transduction resulting in induction of apoptosis
GO:0000236	0.007895805	mitotic prometaphase
GO:0003203	0.007895805	endocardial cushion morphogenesis
GO:0009082	0.007895805	branched chain family amino acid biosynthetic process
GO:0010041	0.007895805	response to iron(III) ion
GO:0010424	0.007895805	DNA methylation on cytosine within a CG sequence
GO:0032776	0.007895805	DNA methylation on cytosine
GO:0033127	0.007895805	regulation of histone phosphorylation
GO:0048369	0.007895805	lateral mesoderm morphogenesis
GO:0048370	0.007895805	lateral mesoderm formation
GO:0048371	0.007895805	lateral mesodermal cell differentiation
GO:0048372	0.007895805	lateral mesodermal cell fate commitment
GO:0048377	0.007895805	lateral mesodermal cell fate specification
GO:0048378	0.007895805	regulation of lateral mesodermal cell fate specification
GO:0048382	0.007895805	mesendoderm development
GO:0051571	0.007895805	positive regulation of histone H3-K4 methylation
GO:0060897	0.007895805	neural plate regionalization
GO:0070562	0.007895805	regulation of vitamin D receptor signaling pathway
GO:0090307	0.007895805	spindle assembly involved in mitosis
GO:0032269	0.008382756	negative regulation of cellular protein metabolic process
GO:0002562	0.008872146	somatic diversification of immune receptors via germline recombination within a single locus
GO:0016444	0.008872146	somatic cell DNA recombination
GO:0048477	0.008872146	oogenesis
GO:0051235	0.009127171	maintenance of location
GO:0050767	0.009727988	regulation of neurogenesis
GO:0002200	0.009850495	somatic diversification of immune receptors
GO:0048863	0.010356874	stem cell differentiation
GO:0051248	0.010368518	negative regulation of protein metabolic process

GO:0006344	0.011820745	maintenance of chromatin silencing
GO:0010586	0.011820745	miRNA metabolic process
GO:0010587	0.011820745	miRNA catabolic process
GO:0031442	0.011820745	positive regulation of mRNA 3'-end processing
GO:0046499	0.011820745	S-adenosylmethioninamine metabolic process
GO:0048368	0.011820745	lateral mesoderm development
GO:0050685	0.011820745	positive regulation of mRNA processing
GO:0051299	0.011820745	centrosome separation
GO:0051573	0.011820745	negative regulation of histone H3-K9 methylation
GO:0060896	0.011820745	neural plate pattern specification
GO:0060914	0.011820745	heart formation
GO:0070507	0.011943695	regulation of microtubule cytoskeleton organization
GO:0031324	0.012021243	negative regulation of cellular metabolic process
GO:0006310	0.012383973	DNA recombination
GO:0033044	0.012494885	regulation of chromosome organization
GO:0051960	0.013012966	regulation of nervous system development
GO:0051053	0.013630083	negative regulation of DNA metabolic process
GO:0002377	0.015413557	immunoglobulin production
GO:0000089	0.015730456	mitotic metaphase
GO:0000281	0.015730456	cytokinesis after mitosis
GO:0001880	0.015730456	Mullerian duct regression
GO:0006269	0.015730456	DNA replication, synthesis of RNA primer
GO:0006346	0.015730456	methylation-dependent chromatin silencing
GO:0031062	0.015730456	positive regulation of histone methylation
GO:0031440	0.015730456	regulation of mRNA 3'-end processing
GO:0042661	0.015730456	regulation of mesodermal cell fate specification
GO:0045347	0.015730456	negative regulation of MHC class II biosynthetic process
GO:0051570	0.015730456	regulation of histone H3-K9 methylation
GO:0060218	0.015730456	hemopoietic stem cell differentiation
GO:0060236	0.015730456	regulation of mitotic spindle organization
GO:0070561	0.015730456	vitamin D receptor signaling pathway
GO:0072132	0.015730456	mesenchyme morphogenesis
GO:0032886	0.016029199	regulation of microtubule-based process
GO:0051495	0.017291676	positive regulation of cytoskeleton organization
GO:0040007	0.017363157	growth
GO:0042493	0.017388016	response to drug
GO:0031400	0.01786688	negative regulation of protein modification process
GO:0008629	0.017938333	induction of apoptosis by intracellular signals
GO:0060284	0.019513871	regulation of cell development
GO:0009628	0.01952189	response to abiotic stimulus

GO:0003197	0.019624993	endocardial cushion development
GO:0007501	0.019624993	mesodermal cell fate specification
GO:0010870	0.019624993	positive regulation of receptor biosynthetic process
GO:0030916	0.019624993	otic vesicle formation
GO:0031061	0.019624993	negative regulation of histone methylation
GO:0031573	0.019624993	intra-S DNA damage checkpoint
GO:0051382	0.019624993	kinetochore assembly
GO:0051569	0.019624993	regulation of histone H3-K4 methylation
GO:0070934	0.019624993	CRD-mediated mRNA stabilization
GO:0071305	0.019624993	cellular response to vitamin D
GO:0071398	0.019624993	cellular response to fatty acid
GO:0071453	0.019624993	cellular response to oxygen levels
GO:0071456	0.019624993	cellular response to hypoxia
GO:0071599	0.019624993	otic vesicle development
GO:0071600	0.019624993	otic vesicle morphogenesis
GO:0090224	0.019624993	regulation of spindle organization
GO:0007163	0.019938926	establishment or maintenance of cell polarity
GO:0014070	0.021040728	response to organic cyclic substance
GO:0009987	0.022113253	cellular process
GO:0044260	0.022685343	cellular macromolecule metabolic process
GO:0032268	0.022850588	regulation of cellular protein metabolic process
GO:0006398	0.023504417	histone mRNA 3'-end processing
GO:0031054	0.023504417	pre-microRNA processing
GO:0033762	0.023504417	response to glucagon stimulus
GO:0046498	0.023504417	S-adenosylhomocysteine metabolic process
GO:0051567	0.023504417	histone H3-K9 methylation
GO:0060033	0.023504417	anatomical structure regression
GO:0000079	0.024205165	regulation of cyclin-dependent protein kinase activity
GO:0009411	0.024205165	response to UV
GO:0031323	0.024229028	regulation of cellular metabolic process
GO:0016570	0.025724865	histone modification
GO:0002440	0.026466249	production of molecular mediator of immune response
GO:0006302	0.026466249	double-strand break repair
GO:0031145	0.026466249	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:0016569	0.026555857	covalent chromatin modification
GO:0016310	0.026882049	phosphorylation
GO:0034661	0.027368783	ncRNA catabolic process
GO:0051323	0.027368783	metaphase

GO:0060391	0.027368783	positive regulation of SMAD protein nuclear translocation
GO:0071396	0.027368783	cellular response to lipid
GO:0007292	0.028019516	female gamete generation
GO:0032270	0.028347257	positive regulation of cellular protein metabolic process
GO:0030900	0.029134926	forebrain development
GO:0010212	0.029608727	response to ionizing radiation
GO:0051439	0.029608727	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0032880	0.030472794	regulation of protein localization
GO:0044237	0.03110202	cellular metabolic process
GO:0009113	0.031218149	purine base biosynthetic process
GO:0010224	0.031218149	response to UV-B
GO:0017085	0.031218149	response to insecticide
GO:0019047	0.031218149	provirus integration
GO:0030069	0.031218149	lysogeny
GO:0031060	0.031218149	regulation of histone methylation
GO:0034508	0.031218149	centromere complex assembly
GO:0048340	0.031218149	paraxial mesoderm morphogenesis
GO:0048532	0.031218149	anatomical structure arrangement
GO:0048853	0.031218149	forebrain morphogenesis
GO:0055015	0.031218149	ventricular cardiac muscle cell development
GO:0060045	0.031218149	positive regulation of cardiac muscle cell proliferation
GO:0060390	0.031218149	regulation of SMAD protein nuclear translocation
GO:0071407	0.031218149	cellular response to organic cyclic substance
GO:0016064	0.031233241	immunoglobulin mediated immune response
GO:0019724	0.032058539	B cell mediated immunity
GO:0007420	0.032187216	brain development
GO:0051247	0.033532315	positive regulation of protein metabolic process
GO:0009950	0.035052572	dorsal/ventral axis specification
GO:0010453	0.035052572	regulation of cell fate commitment
GO:0010470	0.035052572	regulation of gastrulation
GO:0016572	0.035052572	histone phosphorylation
GO:0031503	0.035052572	protein complex localization
GO:0033205	0.035052572	cell cycle cytokinesis
GO:0042659	0.035052572	regulation of cell fate specification
GO:0010243	0.036312306	response to organic nitrogen
GO:0051641	0.037096512	cellular localization
GO:0045786	0.037642407	negative regulation of cell cycle
GO:0051246	0.038616306	regulation of protein metabolic process
GO:0001710	0.03887211	mesodermal cell fate commitment

GO:0006301	0.03887211	postreplication repair
GO:0006303	0.03887211	double-strand break repair via nonhomologous end joining
GO:0006349	0.03887211	regulation of gene expression by genetic imprinting
GO:0006378	0.03887211	mRNA polyadenylation
GO:0010869	0.03887211	regulation of receptor biosynthetic process
GO:0031057	0.03887211	negative regulation of histone modification
GO:0043584	0.03887211	nose development
GO:0045346	0.03887211	regulation of MHC class II biosynthetic process
GO:0071241	0.03887211	cellular response to inorganic substance
GO:0071248	0.03887211	cellular response to metal ion
GO:0071514	0.03887211	genetic imprinting
GO:0046661	0.041686743	male sex differentiation
GO:0051438	0.041686743	regulation of ubiquitin-protein ligase activity
GO:0048015	0.042610059	phosphoinositide-mediated signaling
GO:0006379	0.042676819	mRNA cleavage
GO:0045342	0.042676819	MHC class II biosynthetic process
GO:0048333	0.042676819	mesodermal cell differentiation
GO:0055012	0.042676819	ventricular cardiac muscle cell differentiation
GO:0051128	0.043302372	regulation of cellular component organization
GO:0051340	0.044479666	regulation of ligase activity
GO:0048519	0.045547242	negative regulation of biological process
GO:0034645	0.045691844	cellular macromolecule biosynthetic process
GO:0007281	0.046379426	germ cell development
GO:0031099	0.046379426	regeneration
GO:0001556	0.046466754	oocyte maturation
GO:0002021	0.046466754	response to dietary excess
GO:0007076	0.046466754	mitotic chromosome condensation
GO:0007094	0.046466754	mitotic cell cycle spindle assembly checkpoint
GO:0009083	0.046466754	branched chain family amino acid catabolic process
GO:0010714	0.046466754	positive regulation of collagen metabolic process
GO:0032967	0.046466754	positive regulation of collagen biosynthetic process
GO:0046112	0.046466754	nucleobase biosynthetic process
GO:0051568	0.046466754	histone H3-K4 methylation
GO:0051094	0.046704657	positive regulation of developmental process
GO:0006950	0.047411532	response to stress

Table s6: GO terms associated with the RNA transcription / protein synthesis expression module.

GO ID	p-value	Term
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GO:0006420	2.84E-05	arginyl-tRNA aminoacylation
GO:0018198	0.000197338	peptidyl-cysteine modification
GO:0009108	0.001505193	coenzyme biosynthetic process
GO:0008380	0.002033993	RNA splicing
GO:0006397	0.002458656	mRNA processing
GO:0022613	0.002766281	ribonucleoprotein complex biogenesis
GO:0007192	0.003118819	activation of adenylate cyclase activity by serotonin receptor signaling pathway
GO:0017014	0.003118819	protein amino acid nitrosylation
GO:0018119	0.003118819	peptidyl-cysteine S-nitrosylation
GO:0042660	0.003118819	positive regulation of cell fate specification
GO:0046294	0.003118819	formaldehyde catabolic process
GO:0048936	0.003118819	peripheral nervous system neuron axonogenesis
GO:0044281	0.003169195	small molecule metabolic process
GO:0051188	0.004581947	cofactor biosynthetic process
GO:0006520	0.005315717	cellular amino acid metabolic process
GO:0016071	0.005476853	mRNA metabolic process
GO:0000022	0.006228148	mitotic spindle elongation
GO:0000189	0.006228148	nuclear translocation of MAPK
GO:0019478	0.006228148	D-amino acid catabolic process
GO:0042699	0.006228148	follicle-stimulating hormone signaling pathway
GO:0046185	0.006228148	aldehyde catabolic process
GO:0046292	0.006228148	formaldehyde metabolic process
GO:0051231	0.006228148	spindle elongation
GO:0060128	0.006228148	adrenocorticotropin hormone secreting cell differentiation
GO:0060591	0.006228148	chondroblast differentiation
GO:0009987	0.006259244	cellular process
GO:0006396	0.00728534	RNA processing
GO:0006446	0.007904176	regulation of translational initiation
GO:0017157	0.008264316	regulation of exocytosis
GO:0006418	0.008631734	tRNA aminoacylation for protein translation
GO:0043038	0.008631734	amino acid activation
GO:0043039	0.008631734	tRNA aminoacylation
GO:0019752	0.009318116	carboxylic acid metabolic process
GO:0043436	0.009318116	oxoacid metabolic process
GO:0014889	0.009328015	muscle atrophy
GO:0017182	0.009328015	peptidyl-diphthamide metabolic process
GO:0017183	0.009328015	peptidyl-diphthamide biosynthetic process from peptidyl-histidine
GO:0018125	0.009328015	peptidyl-cysteine methylation

GO:0046416	0.009328015	D-amino acid metabolic process
GO:0060129	0.009328015	thyroid-stimulating hormone-secreting cell differentiation
GO:0070935	0.009328015	3'-UTR-mediated mRNA stabilization
GO:0044282	0.009730879	small molecule catabolic process
GO:0006082	0.009845979	organic acid metabolic process
GO:0042180	0.010395066	cellular ketone metabolic process
GO:0006732	0.012350571	coenzyme metabolic process
GO:0048511	0.012350571	rhythmic process
GO:0007008	0.012418447	outer mitochondrial membrane organization
GO:0043922	0.012418447	negative regulation by host of viral transcription
GO:0048935	0.012418447	peripheral nervous system neuron development
GO:0051409	0.012418447	response to nitrosative stress
GO:0070096	0.012418447	mitochondrial outer membrane translocase complex assembly
GO:0006413	0.014514097	translational initiation
GO:0044106	0.014817902	cellular amine metabolic process
GO:0021534	0.015499473	cell proliferation in hindbrain
GO:0021924	0.015499473	cell proliferation in the external granule layer
GO:0021930	0.015499473	granule cell precursor proliferation
GO:0032057	0.015499473	negative regulation of translational initiation in response to stress
GO:0048934	0.015499473	peripheral nervous system neuron differentiation
GO:0006067	0.018571121	ethanol metabolic process
GO:0006069	0.018571121	ethanol oxidation
GO:0007210	0.018571121	serotonin receptor signaling pathway
GO:0032055	0.018571121	negative regulation of translation in response to stress
GO:0032897	0.018571121	negative regulation of viral transcription
GO:0034308	0.018571121	monohydric alcohol metabolic process
GO:0060644	0.018571121	mammary gland epithelial cell differentiation
GO:0009063	0.019515168	cellular amino acid catabolic process
GO:0043921	0.021633418	modulation by host of viral transcription
GO:0046668	0.021633418	regulation of retinal cell programmed cell death
GO:0051775	0.021633418	response to redox state
GO:0052312	0.021633418	modulation of transcription in other organism involved in symbiotic interaction
GO:0052472	0.021633418	modulation by host of symbiont

		transcription
GO:0022618	0.022249871	ribonucleoprotein complex assembly
GO:0010001	0.022814877	glial cell differentiation
GO:0051301	0.023268534	cell division
GO:0006519	0.02370024	cellular amino acid and derivative metabolic process
GO:0009396	0.024686392	folic acid and derivative biosynthetic process
GO:0009435	0.024686392	NAD biosynthetic process
GO:0018202	0.024686392	peptidyl-histidine modification
GO:0043558	0.024686392	regulation of translational initiation in response to stress
GO:0046653	0.024686392	tetrahydrofolate metabolic process
GO:0046666	0.024686392	retinal cell programmed cell death
GO:0060045	0.024686392	positive regulation of cardiac muscle cell proliferation
GO:0009310	0.025133766	amine catabolic process
GO:0042698	0.025728003	ovulation cycle
GO:0051186	0.026128322	cofactor metabolic process
GO:0034622	0.026162461	cellular macromolecular complex assembly
GO:0002042	0.027730071	cell migration involved in sprouting angiogenesis
GO:0010453	0.027730071	regulation of cell fate commitment
GO:0019359	0.027730071	nicotinamide nucleotide biosynthetic process
GO:0021936	0.027730071	regulation of granule cell precursor proliferation
GO:0021940	0.027730071	positive regulation of granule cell precursor proliferation
GO:0030815	0.027730071	negative regulation of cAMP metabolic process
GO:0030818	0.027730071	negative regulation of cAMP biosynthetic process
GO:0042659	0.027730071	regulation of cell fate specification
GO:0043555	0.027730071	regulation of translation in response to stress
GO:0007188	0.028161812	G-protein signaling, coupled to cAMP nucleotide second messenger
GO:0042063	0.03068472	gliogenesis
GO:0030800	0.030764483	negative regulation of cyclic nucleotide metabolic process
GO:0030803	0.030764483	negative regulation of cyclic nucleotide biosynthetic process
GO:0030809	0.030764483	negative regulation of nucleotide

		biosynthetic process
GO:0043537	0.030764483	negative regulation of blood vessel endothelial cell migration
GO:0006412	0.03284547	translation
GO:0007128	0.033789655	meiotic prophase I
GO:0021984	0.033789655	adenohypophysis development
GO:0032855	0.033789655	positive regulation of Rac GTPase activity
GO:0051324	0.033789655	prophase
GO:0051851	0.033789655	modification by host of symbiont morphology or physiology
GO:0034660	0.03423083	ncRNA metabolic process
GO:0045761	0.034630745	regulation of adenylate cyclase activity
GO:0009308	0.035832323	amine metabolic process
GO:0000377	0.035987987	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	0.035987987	nuclear mRNA splicing, via spliceosome
GO:0031279	0.035987987	regulation of cyclase activity
GO:0051339	0.036674296	regulation of lyase activity
GO:0006086	0.036805614	acetyl-CoA biosynthetic process from pyruvate
GO:0009083	0.036805614	branched chain family amino acid catabolic process
GO:0010510	0.036805614	regulation of acetyl-CoA biosynthetic process from pyruvate
GO:0045980	0.036805614	negative regulation of nucleotide metabolic process
GO:0051046	0.03692867	regulation of secretion
GO:0019933	0.038062107	cAMP-mediated signaling
GO:0010608	0.038117727	posttranscriptional regulation of gene expression
GO:0018193	0.038921335	peptidyl-amino acid modification
GO:0043536	0.039812388	positive regulation of blood vessel endothelial cell migration
GO:0045947	0.039812388	negative regulation of translational initiation
GO:0046782	0.039812388	regulation of viral transcription
GO:0055021	0.039812388	regulation of cardiac muscle tissue growth
GO:0055024	0.039812388	regulation of cardiac muscle tissue development
GO:0060043	0.039812388	regulation of cardiac muscle cell proliferation
GO:0044237	0.040070335	cellular metabolic process
GO:0000375	0.042344467	RNA splicing, via transesterification reactions

GO:0006085	0.042810004	acetyl-CoA biosynthetic process
GO:0006700	0.042810004	C21-steroid hormone biosynthetic process
GO:0006760	0.042810004	folic acid and derivative metabolic process
GO:0051193	0.042810004	regulation of cofactor metabolic process
GO:0051196	0.042810004	regulation of coenzyme metabolic process
GO:0034621	0.043195956	cellular macromolecular complex subunit organization
GO:0030817	0.045295615	regulation of cAMP biosynthetic process
GO:0014003	0.04579849	oligodendrocyte development
GO:0017158	0.04579849	regulation of calcium ion-dependent exocytosis
GO:0019080	0.04579849	viral genome expression
GO:0019083	0.04579849	viral transcription
GO:0019363	0.04579849	pyridine nucleotide biosynthetic process
GO:0060420	0.04579849	regulation of heart growth
GO:0006171	0.046799216	cAMP biosynthetic process
GO:0030814	0.046799216	regulation of cAMP metabolic process
GO:0051726	0.047999309	regulation of cell cycle
GO:0007018	0.048321133	microtubule-based movement
GO:0050709	0.048777871	negative regulation of protein secretion
GO:0051702	0.048777871	interaction with symbiont
GO:0006399	0.049088873	tRNA metabolic process
GO:0007187	0.04986109	G-protein signaling, coupled to cyclic nucleotide second messenger

Table s7: GO terms associated with the metabolism / hormone signaling expression module.

GO ID	p-value	Term
GO:0034660	0.001322169	ncRNA metabolic process
GO:0006399	0.001776558	tRNA metabolic process
GO:0042278	0.002085852	purine nucleoside metabolic process
GO:0046128	0.002085852	purine ribonucleoside metabolic process
GO:0006409	0.002129925	tRNA export from nucleus
GO:0009642	0.002129925	response to light intensity
GO:0015957	0.002129925	bis(5'-nucleosidyl) oligophosphate biosynthetic process
GO:0015960	0.002129925	diadenosine polyphosphate biosynthetic process
GO:0015965	0.002129925	diadenosine tetraphosphate metabolic process
GO:0015966	0.002129925	diadenosine tetraphosphate biosynthetic process
GO:0032289	0.002129925	myelin formation in the central nervous system
GO:0051031	0.002129925	tRNA transport
GO:0001942	0.003573516	hair follicle development
GO:0022404	0.003573516	molting cycle process

GO:0022405	0.003573516	hair cycle process
GO:0006418	0.00409276	tRNA aminoacylation for protein translation
GO:0042303	0.00409276	molting cycle
GO:0042633	0.00409276	hair cycle
GO:0043038	0.00409276	amino acid activation
GO:0043039	0.00409276	tRNA aminoacylation
GO:0006348	0.004255476	chromatin silencing at telomere
GO:0006426	0.004255476	glycyl-tRNA aminoacylation
GO:0006428	0.004255476	isoleucyl-tRNA aminoacylation
GO:0006481	0.004255476	C-terminal protein amino acid methylation
GO:0015942	0.004255476	formate metabolic process
GO:0018410	0.004255476	peptide or protein carboxyl-terminal blocking
GO:0042780	0.004255476	tRNA 3'-end processing
GO:0009119	0.004836233	ribonucleoside metabolic process
GO:0055086	0.005692612	nucleobase, nucleoside and nucleotide metabolic process
GO:0006475	0.00637666	internal protein amino acid acetylation
GO:0015956	0.00637666	bis(5'-nucleosidyl) oligophosphate metabolic process
GO:0015959	0.00637666	diadenosine polyphosphate metabolic process
GO:0022010	0.00637666	myelination in the central nervous system
GO:0032291	0.00637666	ensheathment of axons in the central nervous system
GO:0035315	0.00637666	hair cell differentiation
GO:0043628	0.00637666	ncRNA 3'-end processing
GO:0046499	0.00637666	S-adenosylmethioninamine metabolic process
GO:0051798	0.00637666	positive regulation of hair follicle development
GO:0009116	0.007645128	nucleoside metabolic process
GO:0007199	0.008493487	G-protein signaling, coupled to cGMP nucleotide second messenger
GO:0032276	0.008493487	regulation of gonadotropin secretion
GO:0032277	0.008493487	negative regulation of gonadotropin secretion
GO:0040016	0.008493487	embryonic cleavage
GO:0046880	0.008493487	regulation of follicle-stimulating hormone secretion
GO:0046882	0.008493487	negative regulation of follicle-stimulating hormone secretion
GO:0051797	0.008493487	regulation of hair follicle development
GO:0060218	0.008493487	hemopoietic stem cell differentiation
GO:0035264	0.009928836	multicellular organism growth
GO:0032288	0.010605965	myelin assembly
GO:0032926	0.010605965	negative regulation of activin receptor signaling pathway

GO:0042634	0.010605965	regulation of hair cycle
GO:0006283	0.012714102	transcription-coupled nucleotide-excision repair
GO:0032274	0.012714102	gonadotropin secretion
GO:0046498	0.012714102	S-adenosylhomocysteine metabolic process
GO:0046884	0.012714102	follicle-stimulating hormone secretion
GO:0070509	0.012714102	calcium ion import
GO:0070588	0.012714102	calcium ion transmembrane transport
GO:0000154	0.014817908	rRNA modification
GO:0030825	0.014817908	positive regulation of cGMP metabolic process
GO:0033683	0.014817908	nucleotide-excision repair, DNA incision
GO:0044237	0.016838242	cellular metabolic process
GO:0006465	0.01691739	signal peptide processing
GO:0009396	0.01691739	folic acid and derivative biosynthetic process
GO:0043249	0.01691739	erythrocyte maturation
GO:0043558	0.01691739	regulation of translational initiation in response to stress
GO:0045684	0.01691739	positive regulation of epidermis development
GO:0046653	0.01691739	tetrahydrofolate metabolic process
GO:0044281	0.017394375	small molecule metabolic process
GO:0009163	0.019012558	nucleoside biosynthetic process
GO:0019934	0.019012558	cGMP-mediated signaling
GO:0042451	0.019012558	purine nucleoside biosynthetic process
GO:0042455	0.019012558	ribonucleoside biosynthetic process
GO:0043555	0.019012558	regulation of translation in response to stress
GO:0044060	0.019012558	regulation of endocrine process
GO:0046129	0.019012558	purine ribonucleoside biosynthetic process
GO:0009650	0.021103419	UV protection
GO:0018196	0.021103419	peptidyl-asparagine modification
GO:0018279	0.021103419	protein amino acid N-linked glycosylation via asparagine
GO:0048820	0.021103419	hair follicle maturation
GO:0030823	0.023189983	regulation of cGMP metabolic process
GO:0060986	0.023189983	endocrine hormone secretion
GO:0007164	0.025272258	establishment of tissue polarity
GO:0006486	0.026347976	protein amino acid glycosylation
GO:0043413	0.026347976	macromolecule glycosylation
GO:0070085	0.026347976	glycosylation
GO:0032925	0.027350252	regulation of activin receptor signaling pathway
GO:0048821	0.027350252	erythrocyte development
GO:0044249	0.027781463	cellular biosynthetic process
GO:0044260	0.028257369	cellular macromolecule metabolic process
GO:0006760	0.029423975	folic acid and derivative metabolic process
GO:0034645	0.030926132	cellular macromolecule biosynthetic process

GO:0001502	0.031493433	cartilage condensation
GO:0014003	0.031493433	oligodendrocyte development
GO:0006730	0.032794344	one-carbon metabolic process
GO:0046483	0.032943656	heterocycle metabolic process
GO:0006725	0.033244252	cellular aromatic compound metabolic process
GO:0032924	0.033558636	activin receptor signaling pathway
GO:0009058	0.034305782	biosynthetic process
GO:0009416	0.03460864	response to light stimulus
GO:0002244	0.035619593	hemopoietic progenitor cell differentiation
GO:0043616	0.035619593	keratinocyte proliferation
GO:0071695	0.035619593	anatomical structure maturation
GO:0009059	0.035896956	macromolecule biosynthetic process
GO:0008152	0.036403368	metabolic process
GO:0010558	0.036475033	negative regulation of macromolecule biosynthetic process
GO:0031069	0.037676311	hair follicle morphogenesis
GO:0006519	0.038301916	cellular amino acid and derivative metabolic process
GO:0031327	0.040019133	negative regulation of cellular biosynthetic process
GO:0030968	0.041777065	endoplasmic reticulum unfolded protein response
GO:0034620	0.041777065	cellular response to unfolded protein
GO:0043009	0.041931225	chordate embryonic development
GO:0009890	0.042699542	negative regulation of biosynthetic process
GO:0009792	0.043082223	embryo development ending in birth or egg hatching
GO:0000718	0.043821118	nucleotide-excision repair, DNA damage removal
GO:0007223	0.043821118	Wnt receptor signaling pathway, calcium modulating pathway
GO:0045682	0.043821118	regulation of epidermis development
GO:0046068	0.043821118	cGMP metabolic process
GO:0009987	0.045108181	cellular process
GO:0009101	0.045768921	glycoprotein biosynthetic process
GO:0042558	0.045860967	pteridine and derivative metabolic process
GO:0006412	0.049386928	translation
GO:0045055	0.049928082	regulated secretory pathway
GO:0048730	0.049928082	epidermis morphogenesis

Table s8: GO terms associated with the signaling / cellular identity expression module.

GO ID	p-value	Term
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GO:0006955	1.69E-08	immune response
GO:0002376	2.37E-08	immune system process
GO:0002504	4.25E-06	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0001910	2.04E-05	regulation of leukocyte mediated cytotoxicity
GO:0001911	3.22E-05	negative regulation of leukocyte mediated cytotoxicity
GO:0031341	3.34E-05	regulation of cell killing
GO:0031342	5.36E-05	negative regulation of cell killing
GO:0042492	5.36E-05	gamma-delta T cell differentiation
GO:0045586	5.36E-05	regulation of gamma-delta T cell differentiation
GO:0045588	5.36E-05	positive regulation of gamma-delta T cell differentiation
GO:0046643	5.36E-05	regulation of gamma-delta T cell activation
GO:0046645	5.36E-05	positive regulation of gamma-delta T cell activation
GO:0001909	6.18E-05	leukocyte mediated cytotoxicity
GO:0002704	0.00011219	negative regulation of leukocyte mediated immunity
GO:0002707	0.00011219	negative regulation of lymphocyte mediated immunity
GO:0002925	0.00011219	positive regulation of humoral immune response mediated by circulating immunoglobulin
GO:0033687	0.00011219	osteoblast proliferation
GO:0046629	0.00011219	gamma-delta T cell activation
GO:0002922	0.000149366	positive regulation of humoral immune response
GO:0002923	0.000149366	regulation of humoral immune response mediated by circulating immunoglobulin
GO:0002706	0.000215899	regulation of lymphocyte mediated immunity
GO:0019882	0.000271484	antigen processing and presentation
GO:0002714	0.000292106	positive regulation of B cell mediated immunity
GO:0002891	0.000292106	positive regulation of immunoglobulin mediated immune response
GO:0001906	0.000302434	cell killing
GO:0002703	0.00035299	regulation of leukocyte mediated immunity
GO:0002920	0.000413044	regulation of humoral immune response
GO:0065007	0.000531015	biological regulation

GO:0050789	0.000672523	regulation of biological process
GO:0002715	0.000715957	regulation of natural killer cell mediated immunity
GO:0042269	0.000715957	regulation of natural killer cell mediated cytotoxicity
GO:0001912	0.00080427	positive regulation of leukocyte mediated cytotoxicity
GO:0002698	0.00080427	negative regulation of immune effector process
GO:0050794	0.000941615	regulation of cellular process
GO:0050896	0.001113031	response to stimulus
GO:0031343	0.001207177	positive regulation of cell killing
GO:0046635	0.001207177	positive regulation of alpha-beta T cell activation
GO:0002683	0.001214137	negative regulation of immune system process
GO:0002712	0.001438112	regulation of B cell mediated immunity
GO:0002889	0.001438112	regulation of immunoglobulin mediated immune response
GO:0002252	0.001521832	immune effector process
GO:0002228	0.001560873	natural killer cell mediated immunity
GO:0042267	0.001560873	natural killer cell mediated cytotoxicity
GO:0002697	0.001840539	regulation of immune effector process
GO:0002824	0.001958061	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0050777	0.001958061	negative regulation of immune response
GO:0002449	0.00205033	lymphocyte mediated immunity
GO:0002821	0.002100019	positive regulation of adaptive immune response
GO:0045582	0.002100019	positive regulation of T cell differentiation
GO:0002705	0.002246722	positive regulation of leukocyte mediated immunity
GO:0002708	0.002246722	positive regulation of lymphocyte mediated immunity
GO:0002158	0.002358132	osteoclast proliferation
GO:0002361	0.002358132	CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation
GO:0002370	0.002358132	natural killer cell cytokine production
GO:0002727	0.002358132	regulation of natural killer cell cytokine production
GO:0002729	0.002358132	positive regulation of natural killer cell cytokine production

GO:0009720	0.002358132	detection of hormone stimulus
GO:0009726	0.002358132	detection of endogenous stimulus
GO:0032829	0.002358132	regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation
GO:0032831	0.002358132	positive regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation
GO:0034436	0.002358132	glycoprotein transport
GO:0045838	0.002358132	positive regulation of membrane potential
GO:0050904	0.002358132	diapedesis
GO:0060448	0.002358132	dichotomous subdivision of terminal units involved in lung branching
GO:0045621	0.002398149	positive regulation of lymphocyte differentiation
GO:0046634	0.002398149	regulation of alpha-beta T cell activation
GO:0002455	0.003404688	humoral immune response mediated by circulating immunoglobulin
GO:0007204	0.003545142	elevation of cytosolic calcium ion concentration
GO:0002443	0.003699526	leukocyte mediated immunity
GO:0065008	0.004027722	regulation of biological quality
GO:0002700	0.004167465	regulation of production of molecular mediator of immune response
GO:0051480	0.004272108	cytosolic calcium ion homeostasis
GO:0001915	0.004710882	negative regulation of T cell mediated cytotoxicity
GO:0002716	0.004710882	negative regulation of natural killer cell mediated immunity
GO:0034314	0.004710882	Arp2/3 complex-mediated actin nucleation
GO:0045591	0.004710882	positive regulation of regulatory T cell differentiation
GO:0045953	0.004710882	negative regulation of natural killer cell mediated cytotoxicity
GO:0050855	0.004710882	regulation of B cell receptor signaling pathway
GO:0051607	0.004786756	defense response to virus
GO:0002699	0.005221786	positive regulation of immune effector process
GO:0060402	0.005221786	calcium ion transport into cytosol
GO:0046631	0.005445889	alpha-beta T cell activation
GO:0060401	0.005674356	cytosolic calcium ion transport
GO:0045580	0.005907169	regulation of T cell differentiation
GO:0002822	0.006385745	regulation of adaptive immune response based on somatic recombination of

GO:0032879	0.006415683	immune receptors built from immunoglobulin superfamily domains
GO:0002819	0.006631468	regulation of localization
GO:0002032	0.007058262	regulation of adaptive immune response
		desensitization of G-protein coupled receptor protein signaling pathway by arrestin
GO:0002378	0.007058262	immunoglobulin biosynthetic process
GO:0045542	0.007058262	positive regulation of cholesterol biosynthetic process
GO:0045589	0.007058262	regulation of regulatory T cell differentiation
GO:0045896	0.007058262	regulation of transcription, mitotic
GO:0045897	0.007058262	positive regulation of transcription, mitotic
GO:0046021	0.007058262	regulation of transcription from RNA polymerase II promoter, mitotic
GO:0046022	0.007058262	positive regulation of transcription from RNA polymerase II promoter, mitotic
GO:0006917	0.00726145	induction of apoptosis
GO:0012502	0.007337971	induction of programmed cell death
GO:0045619	0.007923631	regulation of lymphocyte differentiation
GO:0048878	0.008359535	chemical homeostasis
GO:0045088	0.009319878	regulation of innate immune response
GO:0002710	0.009400284	negative regulation of T cell mediated immunity
GO:0033688	0.009400284	regulation of osteoblast proliferation
GO:0034113	0.009400284	heterotypic cell-cell adhesion
GO:0090205	0.009400284	positive regulation of cholesterol metabolic process
GO:0002440	0.009906968	production of molecular mediator of immune response
GO:0002521	0.010351705	leukocyte differentiation
GO:0006874	0.010942755	cellular calcium ion homeostasis
GO:2000021	0.011129305	regulation of ion homeostasis
GO:0045010	0.011736959	actin nucleation
GO:0045019	0.011736959	negative regulation of nitric oxide biosynthetic process
GO:0045066	0.011736959	regulatory T cell differentiation
GO:0050857	0.011736959	positive regulation of antigen receptor-mediated signaling pathway
GO:0016064	0.011764243	immunoglobulin mediated immune response
GO:0055074	0.012023642	calcium ion homeostasis
GO:0019724	0.012087588	B cell mediated immunity

GO:0006875	0.012668084	cellular metal ion homeostasis
GO:0050870	0.013762313	positive regulation of T cell activation
GO:0001916	0.0140683	positive regulation of T cell mediated cytotoxicity
GO:0007171	0.0140683	activation of transmembrane receptor protein tyrosine kinase activity
GO:0010887	0.0140683	negative regulation of cholesterol storage
GO:0031953	0.0140683	negative regulation of protein amino acid autophosphorylation
GO:0032366	0.0140683	intracellular sterol transport
GO:0032367	0.0140683	intracellular cholesterol transport
GO:0045059	0.0140683	positive thymic T cell selection
GO:0048304	0.0140683	positive regulation of isotype switching to IgG isotypes
GO:0055091	0.0140683	phospholipid homeostasis
GO:0060136	0.0140683	embryonic process involved in female pregnancy
GO:0055065	0.014365205	metal ion homeostasis
GO:0002573	0.015170568	myeloid leukocyte differentiation
GO:0010740	0.015260172	positive regulation of intracellular protein kinase cascade
GO:0006959	0.015531987	humoral immune response
GO:0001914	0.016394319	regulation of T cell mediated cytotoxicity
GO:0002031	0.016394319	G-protein coupled receptor internalization
GO:0006198	0.016394319	cAMP catabolic process
GO:0032689	0.016394319	negative regulation of interferon-gamma production
GO:0045060	0.016394319	negative thymic T cell selection
GO:0045824	0.016394319	negative regulation of innate immune response
GO:0060600	0.016394319	dichotomous subdivision of an epithelial terminal unit
GO:0035556	0.01664198	intracellular signal transduction
GO:0019221	0.017777681	cytokine-mediated signaling pathway
GO:0023036	0.017777681	initiation of signal transduction
GO:0023038	0.017777681	signal initiation by diffusible mediator
GO:0023049	0.017777681	signal initiation by protein/peptide mediator
GO:0043410	0.017777681	positive regulation of MAPKKK cascade
GO:0010872	0.018715026	regulation of cholesterol esterification
GO:0032365	0.018715026	intracellular lipid transport
GO:0043011	0.018715026	myeloid dendritic cell differentiation
GO:0043368	0.018715026	positive T cell selection
GO:0043383	0.018715026	negative T cell selection

GO:0046641	0.018715026	positive regulation of alpha-beta T cell proliferation
GO:0048302	0.018715026	regulation of isotype switching to IgG isotypes
GO:0030005	0.018740757	cellular di-, tri-valent inorganic cation homeostasis
GO:0006952	0.019140405	defense response
GO:0050776	0.01936046	regulation of immune response
GO:0030217	0.020972695	T cell differentiation
GO:0002820	0.021030435	negative regulation of adaptive immune response
GO:0002823	0.021030435	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0009214	0.021030435	cyclic nucleotide catabolic process
GO:0010893	0.021030435	positive regulation of steroid biosynthetic process
GO:0042987	0.021030435	amyloid precursor protein catabolic process
GO:0043372	0.021030435	positive regulation of CD4-positive, alpha beta T cell differentiation
GO:0045540	0.021030435	regulation of cholesterol biosynthetic process
GO:0045830	0.021030435	positive regulation of isotype switching
GO:0046902	0.021030435	regulation of mitochondrial membrane permeability
GO:0048291	0.021030435	isotype switching to IgG isotypes
GO:0045597	0.021730044	positive regulation of cell differentiation
GO:0055066	0.021730044	di-, tri-valent inorganic cation homeostasis
GO:0043065	0.021732802	positive regulation of apoptosis
GO:0043068	0.022200664	positive regulation of programmed cell death
GO:0007165	0.022734777	signal transduction
GO:0010942	0.022994253	positive regulation of cell death
GO:0001913	0.023340555	T cell mediated cytotoxicity
GO:0030146	0.023340555	diuresis
GO:0033700	0.023340555	phospholipid efflux
GO:0034374	0.023340555	low-density lipoprotein particle remodeling
GO:0045911	0.023340555	positive regulation of DNA recombination
GO:0030003	0.024489935	cellular cation homeostasis
GO:0051251	0.024830961	positive regulation of lymphocyte activation
GO:0001773	0.0256454	myeloid dendritic cell activation
GO:0002029	0.0256454	desensitization of G-protein coupled

GO:0002720	0.0256454	receptor protein signaling pathway
		positive regulation of cytokine production
		involved in immune response
GO:0010634	0.0256454	positive regulation of epithelial cell migration
GO:0022401	0.0256454	negative adaptation of signaling pathway
GO:0023058	0.0256454	adaptation of signaling pathway
GO:0031648	0.0256454	protein destabilization
GO:0031952	0.0256454	regulation of protein amino acid autophosphorylation
GO:0034433	0.0256454	steroid esterification
GO:0034434	0.0256454	sterol esterification
GO:0034435	0.0256454	cholesterol esterification
GO:0045061	0.0256454	thymic T cell selection
GO:0045123	0.0256454	cellular extravasation
GO:0050732	0.0256454	negative regulation of peptidyl-tyrosine phosphorylation
GO:0050853	0.0256454	B cell receptor signaling pathway
GO:0046907	0.026085117	intracellular transport
GO:0009967	0.026679788	positive regulation of signal transduction
GO:0051235	0.027090738	maintenance of location
GO:0023056	0.027940783	positive regulation of signaling process
GO:0001960	0.027944981	negative regulation of cytokine-mediated signaling pathway
GO:0002711	0.027944981	positive regulation of T cell mediated immunity
GO:0003091	0.027944981	renal water homeostasis
GO:0009125	0.027944981	nucleoside monophosphate catabolic process
GO:0010885	0.027944981	regulation of cholesterol storage
GO:0046640	0.027944981	regulation of alpha-beta T cell proliferation
GO:0046697	0.027944981	decidualization
GO:0090181	0.027944981	regulation of cholesterol metabolic process
GO:0002460	0.02943091	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002696	0.02990841	positive regulation of leukocyte activation
GO:0007187	0.02990841	G-protein signaling, coupled to cyclic nucleotide second messenger
GO:0001829	0.030239309	trophectodermal cell differentiation
GO:0006607	0.030239309	NLS-bearing substrate import into nucleus
GO:0010745	0.030239309	negative regulation of macrophage derived foam cell differentiation

GO:0010878	0.030239309	cholesterol storage
GO:0043370	0.030239309	regulation of CD4-positive, alpha beta T cell differentiation
GO:0045191	0.030239309	regulation of isotype switching
GO:0045577	0.030239309	regulation of B cell differentiation
GO:0050891	0.030239309	multicellular organismal water homeostasis
GO:0002250	0.030389025	adaptive immune response
GO:0050863	0.030872742	regulation of T cell activation
GO:0048585	0.03234233	negative regulation of response to stimulus
GO:0050867	0.03234233	positive regulation of cell activation
GO:0002717	0.032528396	positive regulation of natural killer cell mediated immunity
GO:0010631	0.032528396	epithelial cell migration
GO:0010632	0.032528396	regulation of epithelial cell migration
GO:0010888	0.032528396	negative regulation of lipid storage
GO:0034375	0.032528396	high-density lipoprotein particle remodeling
GO:0042147	0.032528396	retrograde transport, endosome to Golgi
GO:0042994	0.032528396	cytoplasmic sequestering of transcription factor
GO:0045954	0.032528396	positive regulation of natural killer cell mediated cytotoxicity
GO:0050854	0.032528396	regulation of antigen receptor-mediated signaling pathway
GO:0050995	0.032528396	negative regulation of lipid catabolic process
GO:0060716	0.032528396	labyrinthine layer blood vessel development
GO:0090132	0.032528396	epithelium migration
GO:0055080	0.032742446	cation homeostasis
GO:0046058	0.032838285	cAMP metabolic process
GO:0001893	0.034812254	maternal placenta development
GO:0002702	0.034812254	positive regulation of production of molecular mediator of immune response
GO:0032091	0.034812254	negative regulation of protein binding
GO:0046633	0.034812254	alpha-beta T cell proliferation
GO:0070661	0.034852141	leukocyte proliferation
GO:0019216	0.036393627	regulation of lipid metabolic process
GO:0051649	0.036897528	establishment of localization in cell
GO:0002709	0.037090894	regulation of T cell mediated immunity
GO:0042982	0.037090894	amyloid precursor protein metabolic process
GO:0046676	0.037090894	negative regulation of insulin secretion

GO:0051208	0.037090894	sequestering of calcium ion
GO:0090130	0.037090894	tissue migration
GO:0030097	0.03765206	hemopoiesis
GO:0030098	0.03796129	lymphocyte differentiation
GO:0045595	0.038541331	regulation of cell differentiation
GO:0032844	0.039020736	regulation of homeostatic process
GO:0043691	0.039364327	reverse cholesterol transport
GO:0045058	0.039364327	T cell selection
GO:0045940	0.039364327	positive regulation of steroid metabolic process
GO:0090278	0.039364327	negative regulation of peptide hormone secretion
GO:0006606	0.039554713	protein import into nucleus
GO:0019935	0.0406311	cyclic-nucleotide-mediated signaling
GO:0042592	0.040906208	homeostatic process
GO:0010627	0.041021136	regulation of intracellular protein kinase cascade
GO:0051170	0.041173479	nuclear import
GO:0002792	0.041632566	negative regulation of peptide secretion
GO:0006516	0.041632566	glycoprotein catabolic process
GO:0030104	0.041632566	water homeostasis
GO:0030838	0.041632566	positive regulation of actin filament polymerization
GO:0046638	0.041632566	positive regulation of alpha-beta T cell differentiation
GO:0051220	0.041632566	cytoplasmic sequestering of protein
GO:0051412	0.041632566	response to corticosterone stimulus
GO:0060441	0.041632566	epithelial tube branching involved in lung morphogenesis
GO:0019222	0.042224827	regulation of metabolic process
GO:0031400	0.042817175	negative regulation of protein modification process
GO:0048534	0.043888965	hemopoietic or lymphoid organ development
GO:0001825	0.043895621	blastocyst formation
GO:0002718	0.043895621	regulation of cytokine production involved in immune response
GO:0042992	0.043895621	negative regulation of transcription factor import into nucleus
GO:0043029	0.043895621	T cell homeostasis
GO:0060674	0.043895621	placenta blood vessel development
GO:0009187	0.044485396	cyclic nucleotide metabolic process
GO:0043367	0.046153505	CD4-positive, alpha beta T cell differentiation

GO:0006810	0.04615684	transport
GO:0007243	0.046177765	intracellular protein kinase cascade
GO:0023014	0.046177765	signal transmission via phosphorylation event
GO:0051094	0.046521539	positive regulation of developmental process
GO:0042308	0.048406228	negative regulation of protein import into nucleus
GO:0045744	0.048406228	negative regulation of G-protein coupled receptor protein signaling pathway
GO:0015031	0.048818151	protein transport
GO:0034504	0.049050825	protein localization in nucleus
GO:0051707	0.049921612	response to other organism

GEO Samples Included in the Concordia Database

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