

GO results of ncc-RNA (GO categories shown in Figure 2.5)							
	Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	URL	Genes
BP:GO - positively correlated only in human,ZEB2 (n = 1210)	1.8E-04	73	1563	1.91	GO:0120036 plasma membrane bounded cell projection organization	<a href="http://amigo.geneontology.org/amigo/term/GO:0120036">http://amigo.geneontology.org/amigo/term/GO:0120036</a>	MKS1,FRYL,NRCAM,N
	1.8E-04	114	2867	1.63	GO:0009653 anatomical structure morphogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0009653">http://amigo.geneontology.org/amigo/term/GO:0009653</a>	FRYL,NRCAM,N
	1.8E-04	164	4617	1.45	GO:0048731 system development	<a href="http://amigo.geneontology.org/amigo/term/GO:0048731">http://amigo.geneontology.org/amigo/term/GO:0048731</a>	FLT4,FRYL,NRCAM,N
	2.0E-04	73	1606	1.86	GO:0030030 cell projection organization	<a href="http://amigo.geneontology.org/amigo/term/GO:0030030">http://amigo.geneontology.org/amigo/term/GO:0030030</a>	MKS1,FRYL,NRCAM,N
	1.7E-03	100	2618	1.56	GO:0007399 nervous system development	<a href="http://amigo.geneontology.org/amigo/term/GO:0007399">http://amigo.geneontology.org/amigo/term/GO:0007399</a>	FRYL,NRCAM,N
	4.7E-03	62	1449	1.75	GO:0030182 neuron differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0030182">http://amigo.geneontology.org/amigo/term/GO:0030182</a>	FRYL,NRCAM,N
	1.3E-02	62	1522	1.67	GO:0048699 generation of neurons	<a href="http://amigo.geneontology.org/amigo/term/GO:0048699">http://amigo.geneontology.org/amigo/term/GO:0048699</a>	FRYL,NRCAM,N
	1.3E-02	84	2254	1.53	GO:0006928 movement of cell or subcellular component	<a href="http://amigo.geneontology.org/amigo/term/GO:0006928">http://amigo.geneontology.org/amigo/term/GO:0006928</a>	NRCAM,ITGA6,ITGA1
	1.3E-02	69	1757	1.61	GO:0022008 neurogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0022008">http://amigo.geneontology.org/amigo/term/GO:0022008</a>	FRYL,NRCAM,N
	1.9E-02	126	3774	1.37	GO:0048513 animal organ development	<a href="http://amigo.geneontology.org/amigo/term/GO:0048513">http://amigo.geneontology.org/amigo/term/GO:0048513</a>	FLT4,NRCAM,AT
	2.0E-02	90	2509	1.47	GO:0051128 regulation of cellular component organization	<a href="http://amigo.geneontology.org/amigo/term/GO:0051128">http://amigo.geneontology.org/amigo/term/GO:0051128</a>	FZD5,CLEC16A,ITGA1
	4.5E-02	80	2239	1.46	GO:0048468 cell development	<a href="http://amigo.geneontology.org/amigo/term/GO:0048468">http://amigo.geneontology.org/amigo/term/GO:0048468</a>	FRYL,NRCAM,N
	4.5E-02	141	4433	1.30	GO:0019219 regulation of nucleobase-containing compound metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0019219">http://amigo.geneontology.org/amigo/term/GO:0019219</a>	ALX4,EYA2,ZFA
	4.8E-02	97	2847	1.39	GO:0035556 intracellular signal transduction	<a href="http://amigo.geneontology.org/amigo/term/GO:0035556">http://amigo.geneontology.org/amigo/term/GO:0035556</a>	GJA1,CANT1,MAPK1
	4.9E-02	75	2086	1.47	GO:0009888 tissue development	<a href="http://amigo.geneontology.org/amigo/term/GO:0009888">http://amigo.geneontology.org/amigo/term/GO:0009888</a>	SIPA1L3,ATRNL
	4.9E-02	91	2642	1.41	GO:0008104 protein localization	<a href="http://amigo.geneontology.org/amigo/term/GO:0008104">http://amigo.geneontology.org/amigo/term/GO:0008104</a>	NPEPPS,FZD5,ITGA1
	5.0E-02	97	2859	1.39	GO:0006366 transcription by RNA polymerase II	<a href="http://amigo.geneontology.org/amigo/term/GO:0006366">http://amigo.geneontology.org/amigo/term/GO:0006366</a>	ALX4,ZXDC,ATX
	9.8E-03	29	491	2.68	GO:0007389 pattern specification process	<a href="http://amigo.geneontology.org/amigo/term/GO:0007389">http://amigo.geneontology.org/amigo/term/GO:0007389</a>	NPHP3,NPHP3-AS1
	2.1E-02	11	102	4.89	GO:0043535 regulation of blood vessel endothelial cell migration	<a href="http://amigo.geneontology.org/amigo/term/GO:0043535">http://amigo.geneontology.org/amigo/term/GO:0043535</a>	PRCP,APOE,PT
	2.1E-02	18	262	3.11	GO:0060828 regulation of canonical Wnt signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0060828">http://amigo.geneontology.org/amigo/term/GO:0060828</a>	XIAP,PLEKHA4,ITGA1
	2.1E-02	47	1123	1.90	GO:0035295 tube development	<a href="http://amigo.geneontology.org/amigo/term/GO:0035295">http://amigo.geneontology.org/amigo/term/GO:0035295</a>	PRCP,JCAD,GD
	2.1E-02	89	2618	1.54	GO:0007399 nervous system development	<a href="http://amigo.geneontology.org/amigo/term/GO:0007399">http://amigo.geneontology.org/amigo/term/GO:0007399</a>	NDRG2,CKB,SEMA3F
	2.1E-02	94	2805	1.52	GO:0009056 catabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0009056">http://amigo.geneontology.org/amigo/term/GO:0009056</a>	GALC,MMP2,CC
	2.4E-02	12	130	4.18	GO:0043534 blood vessel endothelial cell migration	<a href="http://amigo.geneontology.org/amigo/term/GO:0043534">http://amigo.geneontology.org/amigo/term/GO:0043534</a>	PRCP,APOE,PT
	2.4E-02	65	1777	1.66	GO:0048585 negative regulation of response to stimulus	<a href="http://amigo.geneontology.org/amigo/term/GO:0048585">http://amigo.geneontology.org/amigo/term/GO:0048585</a>	SEMA3F,SEMA3
	2.4E-02	139	4617	1.36	GO:0048731 system development	<a href="http://amigo.geneontology.org/amigo/term/GO:0048731">http://amigo.geneontology.org/amigo/term/GO:0048731</a>	NDRG2,CKB,SEMA3F
	2.5E-02	103	3210	1.45	GO:0009966 regulation of signal transduction	<a href="http://amigo.geneontology.org/amigo/term/GO:0009966">http://amigo.geneontology.org/amigo/term/GO:0009966</a>	HMOX1,NDFIP1
	2.6E-02	9	84	4.85	GO:0014032 neural crest cell development	<a href="http://amigo.geneontology.org/amigo/term/GO:0014032">http://amigo.geneontology.org/amigo/term/GO:0014032</a>	SEMA3F,SEMA3
	2.6E-02	9	79	5.16	GO:0030330 DNA damage response signal transduction by p53 class mediator	<a href="http://amigo.geneontology.org/amigo/term/GO:0030330">http://amigo.geneontology.org/amigo/term/GO:0030330</a>	CDKN1A,RPS27
	2.6E-02	10	98	4.62	GO:0014033 neural crest cell differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0014033">http://amigo.geneontology.org/amigo/term/GO:0014033</a>	SEMA3F,SEMA3
	2.6E-02	12	148	3.67	GO:0009799 specification of symmetry	<a href="http://amigo.geneontology.org/amigo/term/GO:0009799">http://amigo.geneontology.org/amigo/term/GO:0009799</a>	NPHP3,NPHP3-AS1
	2.6E-02	12	147	3.70	GO:0009855 determination of bilateral symmetry	<a href="http://amigo.geneontology.org/amigo/term/GO:0009855">http://amigo.geneontology.org/amigo/term/GO:0009855</a>	NPHP3,NPHP3-AS1
	2.6E-02	17	257	3.00	GO:0048863 stem cell differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0048863">http://amigo.geneontology.org/amigo/term/GO:0048863</a>	SEMA3F,SEMA3

BP:GO - negatively correlated only in human, ZEB2  
(n = 957)

2.6E-02	19	317	2.72	GO:0060070 canonical Wnt signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0060070">http://amigo.geneontology.org/amigo/term/GO:0060070</a>	WNT11,XIAP,PL
2.6E-02	21	368	2.59	GO:0016042 lipid catabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0016042">http://amigo.geneontology.org/amigo/term/GO:0016042</a>	GALC,APOE,CP
2.6E-02	23	435	2.40	GO:0001503 ossification	<a href="http://amigo.geneontology.org/amigo/term/GO:0001503">http://amigo.geneontology.org/amigo/term/GO:0001503</a>	ITGA11,COL6A1
2.6E-02	27	550	2.22	GO:0002009 morphogenesis of an epithelium	<a href="http://amigo.geneontology.org/amigo/term/GO:0002009">http://amigo.geneontology.org/amigo/term/GO:0002009</a>	PLEKHA4,NPHF
2.6E-02	52	1354	1.74	GO:0009968 negative regulation of signal transduction	<a href="http://amigo.geneontology.org/amigo/term/GO:0009968">http://amigo.geneontology.org/amigo/term/GO:0009968</a>	PIK3IP1,EYA1,G
2.8E-02	9	89	4.58	GO:0014031 mesenchymal cell development	<a href="http://amigo.geneontology.org/amigo/term/GO:0014031">http://amigo.geneontology.org/amigo/term/GO:0014031</a>	SEMA3F,SEMA3
2.8E-02	16	249	2.91	GO:0048762 mesenchymal cell differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0048762">http://amigo.geneontology.org/amigo/term/GO:0048762</a>	SEMA3F,SEMA3
2.8E-02	16	250	2.90	GO:2001234 negative regulation of apoptotic signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:2001234">http://amigo.geneontology.org/amigo/term/GO:2001234</a>	EYA1,LGALS3,T
2.8E-02	23	446	2.34	GO:0001667 ameboidal-type cell migration	<a href="http://amigo.geneontology.org/amigo/term/GO:0001667">http://amigo.geneontology.org/amigo/term/GO:0001667</a>	SEMA3F,SEMA3
2.8E-02	45	1150	1.77	GO:0072359 circulatory system development	<a href="http://amigo.geneontology.org/amigo/term/GO:0072359">http://amigo.geneontology.org/amigo/term/GO:0072359</a>	MEF2C,PDLIM4
2.8E-02	46	1189	1.75	GO:0009790 embryo development	<a href="http://amigo.geneontology.org/amigo/term/GO:0009790">http://amigo.geneontology.org/amigo/term/GO:0009790</a>	WHRN,SOBP,NF
2.9E-02	9	91	4.48	GO:0048864 stem cell development	<a href="http://amigo.geneontology.org/amigo/term/GO:0048864">http://amigo.geneontology.org/amigo/term/GO:0048864</a>	SEMA3F,SEMA3
2.9E-02	30	663	2.05	GO:0048729 tissue morphogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0048729">http://amigo.geneontology.org/amigo/term/GO:0048729</a>	PLEKHA4,NPHF
3.0E-02	16	257	2.82	GO:0045926 negative regulation of growth	<a href="http://amigo.geneontology.org/amigo/term/GO:0045926">http://amigo.geneontology.org/amigo/term/GO:0045926</a>	SEMA3F,SEMA3
3.0E-02	19	337	2.55	GO:0030111 regulation of Wnt signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0030111">http://amigo.geneontology.org/amigo/term/GO:0030111</a>	XIAP,PLEKHA4,I
3.0E-02	54	1483	1.65	GO:0010648 negative regulation of cell communication	<a href="http://amigo.geneontology.org/amigo/term/GO:0010648">http://amigo.geneontology.org/amigo/term/GO:0010648</a>	PIK3IP1,EYA1,G
3.0E-02	110	3615	1.38	GO:0023051 regulation of signaling	<a href="http://amigo.geneontology.org/amigo/term/GO:0023051">http://amigo.geneontology.org/amigo/term/GO:0023051</a>	HMOX1,NDFIP1
3.1E-02	54	1488	1.64	GO:0023057 negative regulation of signaling	<a href="http://amigo.geneontology.org/amigo/term/GO:0023057">http://amigo.geneontology.org/amigo/term/GO:0023057</a>	PIK3IP1,EYA1,G
3.1E-02	27	580	2.11	GO:1905114 cell surface receptor signaling pathway involved in cell-cell signaling	<a href="http://amigo.geneontology.org/amigo/term/GO:1905114">http://amigo.geneontology.org/amigo/term/GO:1905114</a>	WNT11,XIAP,PL
3.1E-02	37	902	1.86	GO:0035239 tube morphogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0035239">http://amigo.geneontology.org/amigo/term/GO:0035239</a>	PRCP,JCAD,GD
3.2E-02	9	96	4.25	GO:0060021 roof of mouth development	<a href="http://amigo.geneontology.org/amigo/term/GO:0060021">http://amigo.geneontology.org/amigo/term/GO:0060021</a>	SNAI2,WNT11,L
3.2E-02	11	139	3.59	GO:2000027 regulation of animal organ morphogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:2000027">http://amigo.geneontology.org/amigo/term/GO:2000027</a>	PLEKHA4,GDNF
3.2E-02	109	3602	1.37	GO:0010646 regulation of cell communication	<a href="http://amigo.geneontology.org/amigo/term/GO:0010646">http://amigo.geneontology.org/amigo/term/GO:0010646</a>	HMOX1,NDFIP1
3.3E-02	20	377	2.40	GO:0003002 regionalization	<a href="http://amigo.geneontology.org/amigo/term/GO:0003002">http://amigo.geneontology.org/amigo/term/GO:0003002</a>	SOSTDC1,DDIT
3.5E-02	11	142	3.51	GO:0090090 negative regulation of canonical Wnt signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0090090">http://amigo.geneontology.org/amigo/term/GO:0090090</a>	ANKRD6,DRAXI
3.6E-02	93	2990	1.41	GO:0007166 cell surface receptor signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0007166">http://amigo.geneontology.org/amigo/term/GO:0007166</a>	SEMA3F,BTN3A
4.2E-02	27	600	2.04	GO:0051272 positive regulation of cellular component movement	<a href="http://amigo.geneontology.org/amigo/term/GO:0051272">http://amigo.geneontology.org/amigo/term/GO:0051272</a>	SEMA3F,CD99,S
4.3E-02	75	2312	1.47	GO:1901575 organic substance catabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:1901575">http://amigo.geneontology.org/amigo/term/GO:1901575</a>	GALC,COMT,RN
4.5E-02	126	4338	1.32	GO:0048583 regulation of response to stimulus	<a href="http://amigo.geneontology.org/amigo/term/GO:0048583">http://amigo.geneontology.org/amigo/term/GO:0048583</a>	HMOX1,NDFIP1
4.7E-02	13	199	2.96	GO:0030308 negative regulation of cell growth	<a href="http://amigo.geneontology.org/amigo/term/GO:0030308">http://amigo.geneontology.org/amigo/term/GO:0030308</a>	SEMA3F,SEMA3
4.7E-02	20	395	2.29	GO:2001233 regulation of apoptotic signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:2001233">http://amigo.geneontology.org/amigo/term/GO:2001233</a>	EYA1,LGALS3,T
4.7E-02	28	641	1.98	GO:0048598 embryonic morphogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0048598">http://amigo.geneontology.org/amigo/term/GO:0048598</a>	WHRN,SOBP,NF
4.7E-02	77	2402	1.45	GO:0044248 cellular catabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0044248">http://amigo.geneontology.org/amigo/term/GO:0044248</a>	GALC,COMT,RN
1.8E-04	169	2618	1.42	GO:0071702 organic substance transport	<a href="http://amigo.geneontology.org/amigo/term/GO:0071702">http://amigo.geneontology.org/amigo/term/GO:0071702</a>	USP36,PINK1,U
1.9E-04	163	2509	1.43	GO:0051128 regulation of cellular component organization	<a href="http://amigo.geneontology.org/amigo/term/GO:0051128">http://amigo.geneontology.org/amigo/term/GO:0051128</a>	USP36,CDKL3,F

BP:GO - positively correlated only in chimp,ZEB2  
(n = 1617)

2.3E-04	255	4309	1.31	GO:0010556 regulation of macromolecule biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0010556">http://amigo.geneontology.org/amigo/term/GO:0010556</a>	ZNF195,ETV1,TFAM
3.3E-04	260	4433	1.29	GO:0019219 regulation of nucleobase-containing compound metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0019219">http://amigo.geneontology.org/amigo/term/GO:0019219</a>	ZNF195,ETV1,TFAM
5.9E-04	242	4112	1.30	GO:0051252 regulation of RNA metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0051252">http://amigo.geneontology.org/amigo/term/GO:0051252</a>	ZNF195,ETV1,TFAM
6.1E-04	270	4676	1.27	GO:1901362 organic cyclic compound biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:1901362">http://amigo.geneontology.org/amigo/term/GO:1901362</a>	NCBP1,ZNF195,TFAM
6.9E-04	228	3847	1.31	GO:0010604 positive regulation of macromolecule metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0010604">http://amigo.geneontology.org/amigo/term/GO:0010604</a>	RNF14,BCLAF1,TFAM
7.4E-04	261	4513	1.28	GO:0019438 aromatic compound biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0019438">http://amigo.geneontology.org/amigo/term/GO:0019438</a>	NCBP1,ZNF195,TFAM
8.5E-04	244	4181	1.29	GO:0009893 positive regulation of metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0009893">http://amigo.geneontology.org/amigo/term/GO:0009893</a>	ABHD5,RNF14,TFAM
8.8E-04	256	4425	1.28	GO:0034654 nucleobase-containing compound biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0034654">http://amigo.geneontology.org/amigo/term/GO:0034654</a>	NCBP1,ZNF195,TFAM
1.1E-03	259	4503	1.27	GO:0018130 heterocycle biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0018130">http://amigo.geneontology.org/amigo/term/GO:0018130</a>	NCBP1,ZNF195,TFAM
1.3E-03	172	2795	1.36	GO:0051246 regulation of protein metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0051246">http://amigo.geneontology.org/amigo/term/GO:0051246</a>	DBNDD1,RNF14,TFAM
1.6E-03	214	3630	1.30	GO:0044085 cellular component biogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0044085">http://amigo.geneontology.org/amigo/term/GO:0044085</a>	SMARCA5,EHD2,TFAM
2.2E-03	228	3936	1.28	GO:0006351 transcription DNA-templated	<a href="http://amigo.geneontology.org/amigo/term/GO:0006351">http://amigo.geneontology.org/amigo/term/GO:0006351</a>	NCBP1,ZNF195,TFAM
2.2E-03	228	3937	1.28	GO:0097659 nucleic acid-templated transcription	<a href="http://amigo.geneontology.org/amigo/term/GO:0097659">http://amigo.geneontology.org/amigo/term/GO:0097659</a>	NCBP1,ZNF195,TFAM
2.8E-03	228	3957	1.27	GO:0032774 RNA biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0032774">http://amigo.geneontology.org/amigo/term/GO:0032774</a>	NCBP1,ZNF195,TFAM
3.6E-03	172	2867	1.32	GO:0009653 anatomical structure morphogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0009653">http://amigo.geneontology.org/amigo/term/GO:0009653</a>	CDKL3,NEDD4L,TFAM
3.6E-03	219	3797	1.27	GO:0006355 regulation of transcription DNA-templated	<a href="http://amigo.geneontology.org/amigo/term/GO:0006355">http://amigo.geneontology.org/amigo/term/GO:0006355</a>	ZNF195,ETV1,TFAM
3.6E-03	219	3798	1.27	GO:1903506 regulation of nucleic acid-templated transcription	<a href="http://amigo.geneontology.org/amigo/term/GO:1903506">http://amigo.geneontology.org/amigo/term/GO:1903506</a>	ZNF195,ETV1,TFAM
3.9E-03	162	2680	1.33	GO:0050793 regulation of developmental process	<a href="http://amigo.geneontology.org/amigo/term/GO:0050793">http://amigo.geneontology.org/amigo/term/GO:0050793</a>	CDKL3,WWC3,NF140
3.9E-03	219	3807	1.27	GO:2001141 regulation of RNA biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:2001141">http://amigo.geneontology.org/amigo/term/GO:2001141</a>	ZNF195,ETV1,TFAM
6.3E-03	191	3283	1.28	GO:0009892 negative regulation of metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0009892">http://amigo.geneontology.org/amigo/term/GO:0009892</a>	DBNDD1,TIMP2,TFAM
1.0E-02	265	4823	1.21	GO:0006810 transport	<a href="http://amigo.geneontology.org/amigo/term/GO:0006810">http://amigo.geneontology.org/amigo/term/GO:0006810</a>	VPS18,USP36,TFAM
1.1E-02	245	4424	1.22	GO:0006950 response to stress	<a href="http://amigo.geneontology.org/amigo/term/GO:0006950">http://amigo.geneontology.org/amigo/term/GO:0006950</a>	MYH9,RAD52,TFAM
1.2E-02	167	2859	1.29	GO:0006366 transcription by RNA polymerase II	<a href="http://amigo.geneontology.org/amigo/term/GO:0006366">http://amigo.geneontology.org/amigo/term/GO:0006366</a>	NCBP1,ETV1,TFAM
1.2E-02	272	4987	1.20	GO:0051234 establishment of localization	<a href="http://amigo.geneontology.org/amigo/term/GO:0051234">http://amigo.geneontology.org/amigo/term/GO:0051234</a>	VPS18,USP36,TFAM
1.2E-02	254	4617	1.21	GO:0048731 system development	<a href="http://amigo.geneontology.org/amigo/term/GO:0048731">http://amigo.geneontology.org/amigo/term/GO:0048731</a>	HSPA5,MAPKAPK1
1.3E-02	174	3005	1.28	GO:0006796 phosphate-containing compound metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0006796">http://amigo.geneontology.org/amigo/term/GO:0006796</a>	DBNDD1,CDKL3,TFAM
1.3E-02	161	2748	1.29	GO:0031324 negative regulation of cellular metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0031324">http://amigo.geneontology.org/amigo/term/GO:0031324</a>	DBNDD1,TIMP2,TFAM
1.4E-02	175	3030	1.27	GO:0006793 phosphorus metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0006793">http://amigo.geneontology.org/amigo/term/GO:0006793</a>	DBNDD1,CDKL3,TFAM
1.5E-02	176	3057	1.27	GO:0010605 negative regulation of macromolecule metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0010605">http://amigo.geneontology.org/amigo/term/GO:0010605</a>	DBNDD1,TIMP2,TFAM
1.5E-02	188	3300	1.26	GO:0070887 cellular response to chemical stimulus	<a href="http://amigo.geneontology.org/amigo/term/GO:0070887">http://amigo.geneontology.org/amigo/term/GO:0070887</a>	HSPA5,SYT1,TGFR
1.8E-02	190	3356	1.25	GO:0065009 regulation of molecular function	<a href="http://amigo.geneontology.org/amigo/term/GO:0065009">http://amigo.geneontology.org/amigo/term/GO:0065009</a>	DBNDD1,GCLM,TFAM
2.5E-02	184	3269	1.24	GO:0010033 response to organic substance	<a href="http://amigo.geneontology.org/amigo/term/GO:0010033">http://amigo.geneontology.org/amigo/term/GO:0010033</a>	TIMP2,HSPA5,TFAM
4.2E-02	222	4103	1.19	GO:0065008 regulation of biological quality	<a href="http://amigo.geneontology.org/amigo/term/GO:0065008">http://amigo.geneontology.org/amigo/term/GO:0065008</a>	VPS18,MYH9,CDK1
1.1E-05	266	4338	1.35	GO:0048583 regulation of response to stimulus	<a href="http://amigo.geneontology.org/amigo/term/GO:0048583">http://amigo.geneontology.org/amigo/term/GO:0048583</a>	ECT2,GPR89A,SHC1
1.1E-07	273	4206	1.43	GO:0006996 organelle organization	<a href="http://amigo.geneontology.org/amigo/term/GO:0006996">http://amigo.geneontology.org/amigo/term/GO:0006996</a>	SMARCA5,USP3,TFAM
1.3E-05	188	2847	1.46	GO:0035556 intracellular signal transduction	<a href="http://amigo.geneontology.org/amigo/term/GO:0035556">http://amigo.geneontology.org/amigo/term/GO:0035556</a>	ECT2,GPR89A,SHC1

	1.4E-05	217	3403	1.41	GO:0051173 positive regulation of nitrogen compound metabolic process	<a href="http://amigo.gene">http://amigo.gene</a>	RNF14,BCLAF1,
	1.6E-11	277	3952	1.55	GO:0036211 protein modification process	<a href="http://amigo.gene">http://amigo.gene</a>	DBNDD1,CDKL3
	1.6E-11	291	4206	1.53	GO:0043412 macromolecule modification	<a href="http://amigo.gene">http://amigo.gene</a>	DBNDD1,CDKL3
	1.9E-11	275	3932	1.54	GO:0006464 cellular protein modification process	<a href="http://amigo.gene">http://amigo.gene</a>	DBNDD1,CDKL3
	2.0E-06	182	2642	1.52	GO:0008104 protein localization	<a href="http://amigo.gene">http://amigo.gene</a>	USP36,CCT4,PI
	2.1E-06	233	3602	1.43	GO:0010646 regulation of cell communication	<a href="http://amigo.gene">http://amigo.gene</a>	VPS18,ECT2,GR
	3.0E-05	162	2402	1.49	GO:0044248 cellular catabolic process	<a href="http://amigo.gene">http://amigo.gene</a>	USP36,UBE3C,A
	5.6E-07	212	3133	1.49	GO:0033036 macromolecule localization	<a href="http://amigo.gene">http://amigo.gene</a>	USP36,CCT4,PI
	6.3E-05	224	3617	1.37	GO:0031325 positive regulation of cellular metabolic process	<a href="http://amigo.gene">http://amigo.gene</a>	ABHD5,RNF14,B
	6.3E-05	268	4482	1.32	GO:0031326 regulation of cellular biosynthetic process	<a href="http://amigo.gene">http://amigo.gene</a>	ZNF195,ETV1,T
	6.5E-05	271	4545	1.32	GO:0009889 regulation of biosynthetic process	<a href="http://amigo.gene">http://amigo.gene</a>	ZNF195,ETV1,T
	7.4E-06	204	3120	1.44	GO:0051641 cellular localization	<a href="http://amigo.gene">http://amigo.gene</a>	VPS18,USP36,C
	7.8E-05	181	2805	1.42	GO:0009056 catabolic process	<a href="http://amigo.gene">http://amigo.gene</a>	USP36,UBE3C,A
	8.8E-07	215	3210	1.48	GO:0009966 regulation of signal transduction	<a href="http://amigo.gene">http://amigo.gene</a>	ECT2,GPR89A,S
	8.8E-07	236	3615	1.44	GO:0023051 regulation of signaling	<a href="http://amigo.gene">http://amigo.gene</a>	VPS18,ECT2,GR
BP:GO - n	3.1E-03	203	4823	1.32	GO:0006810 transport	<a href="http://amigo.gene">http://amigo.gene</a>	ITGB3,HTRA2,C
	4.6E-03	193	4617	1.31	GO:0048731 system development	<a href="http://amigo.gene">http://amigo.gene</a>	TNMD,ITGA2B,C
	4.6E-03	206	4987	1.30	GO:0051234 establishment of localization	<a href="http://amigo.gene">http://amigo.gene</a>	ITGB3,HTRA2,C