

Supplementary table 10: GO results of N-RNA (GO groups marked in yellow are shown in Figure 2.3)

	Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	URL	Genes
BP:GO - correlated with both human and gorilla ZEB2 in the same direction (n = 1,607)	2.5E-02	84	902	1.65	GO:0035239 tube morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0035239	TNMD,FLT1,RASGEF1B
	2.7E-02	31	244	2.31	GO:0046777 protein autophosphorylation	http://amigo.geneontology.org/amigo/term/GO:0046777	PIM2,TEC,PIM1,TEK
	2.7E-02	88	1038	1.54	GO:2000145 regulation of cell motility	http://amigo.geneontology.org/amigo/term/GO:2000145	FGF4,SEMA5B,VEGFA
	2.7E-02	93	1109	1.52	GO:0051270 regulation of cellular component movement	http://amigo.geneontology.org/amigo/term/GO:0051270	FGF4,SEMA5B,VEGFA
	2.7E-02	96	1123	1.51	GO:0035295 tube development	http://amigo.geneontology.org/amigo/term/GO:0035295	TNMD,GRHL2,FGF4
	2.7E-02	123	1602	1.43	GO:0016477 cell migration	http://amigo.geneontology.org/amigo/term/GO:0016477	LAMC3,CTNNA2,CDK5,PRKAR1A
	2.7E-02	209	2867	1.30	GO:0009653 anatomical structure morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0009653	TNMD,CDKL5,NEDD4L
	2.7E-02	296	4552	1.23	GO:0030154 cell differentiation	http://amigo.geneontology.org/amigo/term/GO:0030154	MRC2,CDKL5,MED12
	2.7E-02	296	4576	1.22	GO:0048869 cellular developmental process	http://amigo.geneontology.org/amigo/term/GO:0048869	MRC2,CDKL5,MED12
	3.9E-02	90	1085	1.50	GO:0040012 regulation of locomotion	http://amigo.geneontology.org/amigo/term/GO:0040012	FGF4,SEMA5B,VEGFA
	3.9E-02	188	2680	1.30	GO:0050793 regulation of developmental process	http://amigo.geneontology.org/amigo/term/GO:0050793	TNMD,CDKL5,NEDD4L
	4.1E-02	133	1806	1.37	GO:0048870 cell motility	http://amigo.geneontology.org/amigo/term/GO:0048870	LAMC3,CTNNA2,CDK5,PRKAR1A
	4.1E-02	133	1806	1.37	GO:0051674 localization of cell	http://amigo.geneontology.org/amigo/term/GO:0051674	LAMC3,CTNNA2,CDK5,PRKAR1A
	4.1E-02	162	2254	1.33	GO:0006928 movement of cell or subcellular component	http://amigo.geneontology.org/amigo/term/GO:0006928	LAMC3,CTNNA2,CDK5,PRKAR1A
	4.2E-02	82	977	1.52	GO:0030334 regulation of cell migration	http://amigo.geneontology.org/amigo/term/GO:0030334	FGF4,SEMA5B,VEGFA
	4.5E-02	91	1071	1.48	GO:0000902 cell morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0000902	CDKL5,NEDD4L,PRKAR1A
	4.7E-02	46	446	1.77	GO:0001667 ameboidal-type cell migration	http://amigo.geneontology.org/amigo/term/GO:0001667	SEMA5B,PXN,SERPINC1
	4.7E-03	52	324	1.88	GO:0002263 cell activation involved in immune response	http://amigo.geneontology.org/amigo/term/GO:0002263	IL23A,CRACR2A,CDK5,PRKAR1A
	4.7E-03	52	320	1.92	GO:0002366 leukocyte activation involved in immune response	http://amigo.geneontology.org/amigo/term/GO:0002366	IL23A,CRACR2A,CDK5,PRKAR1A
	4.7E-03	109	717	1.55	GO:0006873 cellular ion homeostasis	http://amigo.geneontology.org/amigo/term/GO:0006873	CALCR,TBXA2R,TRPV1
	4.7E-03	114	769	1.51	GO:0030036 actin cytoskeleton organization	http://amigo.geneontology.org/amigo/term/GO:0030036	ARHGAP44,CAPZB,ACTB
	4.7E-03	125	867	1.47	GO:0055082 cellular chemical homeostasis	http://amigo.geneontology.org/amigo/term/GO:0055082	CALCR,TBXA2R,TRPV1
	4.7E-03	134	1089	1.45	GO:0032101 regulation of response to external stimulus	http://amigo.geneontology.org/amigo/term/GO:0032101	GRN,RORA,TRPV1
	4.7E-03	196	2190	1.35	GO:0006955 immune response	http://amigo.geneontology.org/amigo/term/GO:0006955	LTF,TNK2,IL4R,IL2RA
	4.7E-03	378	3356	1.23	GO:0065009 regulation of molecular function	http://amigo.geneontology.org/amigo/term/GO:0065009	DBNDD1,CASP1,CDK5,PRKAR1A
	4.7E-03	468	4103	1.20	GO:0065008 regulation of biological quality	http://amigo.geneontology.org/amigo/term/GO:0065008	LTF,ACTB,VCL,NEDD4L
	5.2E-03	97	615	1.55	GO:0003013 circulatory system process	http://amigo.geneontology.org/amigo/term/GO:0003013	TBXA2R,UTS2,NEDD4L
	5.2E-03	115	1054	1.48	GO:0050776 regulation of immune response	http://amigo.geneontology.org/amigo/term/GO:0050776	TLR8,UNC93B1,CDK5,PRKAR1A
	5.2E-03	124	857	1.46	GO:0030029 actin filament-based process	http://amigo.geneontology.org/amigo/term/GO:0030029	ARHGAP44,CAPZB,ACTB
	5.2E-03	126	1032	1.45	GO:0034097 response to cytokine	http://amigo.geneontology.org/amigo/term/GO:0034097	IL20RA,IL4R,TRPV1
	5.2E-03	168	1274	1.37	GO:0006812 cation transport	http://amigo.geneontology.org/amigo/term/GO:0006812	SLC7A2,LTF,ATP11A
	5.4E-03	91	731	1.55	GO:0031347 regulation of defense response	http://amigo.geneontology.org/amigo/term/GO:0031347	GRN,RORA,TRPV1
	5.4E-03	94	625	1.54	GO:0006875 cellular metal ion homeostasis	http://amigo.geneontology.org/amigo/term/GO:0006875	CALCR,TBXA2R,TRPV1

5.4E-03	106	1102	1.50	GO:0045087 innate immune response	http://amigo.gene	TNK2,HCK,REL
5.4E-03	117	809	1.47	GO:0098771 inorganic ion homeostasis	http://amigo.gene	CALCR,TBXA2R
5.4E-03	118	819	1.46	GO:0050801 ion homeostasis	http://amigo.gene	CALCR,TBXA2R
5.4E-03	145	1280	1.40	GO:0001775 cell activation	http://amigo.gene	VCL,ACTB,MYL
6.1E-03	51	276	1.82	GO:0003018 vascular process in circulatory system	http://amigo.gene	TBXA2R,TJP3,T
6.1E-03	84	527	1.57	GO:0008015 blood circulation	http://amigo.gene	TBXA2R,UTS2,N
6.2E-03	103	700	1.49	GO:0030003 cellular cation homeostasis	http://amigo.gene	CALCR,TBXA2R
6.2E-03	129	1355	1.42	GO:0098542 defense response to other organism	http://amigo.gene	LTF,TNK2,HCK,T
8.0E-03	103	714	1.48	GO:0055065 metal ion homeostasis	http://amigo.gene	CALCR,TBXA2R
8.0E-03	195	2031	1.32	GO:0006952 defense response	http://amigo.gene	TBXA2R,LTF,CD
8.5E-03	92	596	1.51	GO:0034762 regulation of transmembrane transport	http://amigo.gene	CACNG7,HAMP,
8.5E-03	112	935	1.45	GO:0071345 cellular response to cytokine stimulus	http://amigo.gene	IL20RA,IL4R,TR
8.6E-03	42	284	1.89	GO:0002274 myeloid leukocyte activation	http://amigo.gene	TREM2,DYSF,S
8.6E-03	42	247	1.90	GO:0002573 myeloid leukocyte differentiation	http://amigo.gene	TNFRSF11A,SIG
8.6E-03	66	422	1.64	GO:0050878 regulation of body fluid levels	http://amigo.gene	VCL,ACTB,MYL
8.6E-03	76	670	1.58	GO:0050778 positive regulation of immune response	http://amigo.gene	IL23A,CR2,THE
8.6E-03	291	2582	1.24	GO:0050790 regulation of catalytic activity	http://amigo.gene	DBNDD1,CASP
9.5E-03	208	1677	1.29	GO:0006811 ion transport	http://amigo.gene	SLC7A2,LTF,ATP
1.1E-02	112	794	1.43	GO:0055080 cation homeostasis	http://amigo.gene	CALCR,TBXA2R
1.2E-02	57	447	1.68	GO:0002831 regulation of response to biotic stimulus	http://amigo.gene	PTPN22,PARP9
1.2E-02	62	469	1.64	GO:0032102 negative regulation of response to external stimulus	http://amigo.gene	RORA,SERPINE
1.3E-02	296	3183	1.22	GO:0002376 immune system process	http://amigo.gene	CD38,ITGA3,LTF
1.5E-02	83	762	1.51	GO:0002252 immune effector process	http://amigo.gene	IL4R,IL23A,CR2
1.7E-02	87	653	1.49	GO:0002521 leukocyte differentiation	http://amigo.gene	TPD52,IL23A,CR
1.7E-02	130	972	1.37	GO:0098655 cation transmembrane transport	http://amigo.gene	SLC7A2,ATP2C
1.7E-02	345	2945	1.20	GO:0032879 regulation of localization	http://amigo.gene	FZD5,LEPROT,I
1.7E-02	361	3210	1.19	GO:0009966 regulation of signal transduction	http://amigo.gene	ATP2C1,TRIM38
1.9E-02	65	533	1.59	GO:0002683 negative regulation of immune system process	http://amigo.gene	CR2,PTPN22,NU
2.0E-02	131	967	1.37	GO:0019725 cellular homeostasis	http://amigo.gene	CALCR,TBXA2R
2.0E-02	123	1122	1.38	GO:0045321 leukocyte activation	http://amigo.gene	CD38,TPD52,TR
2.0E-02	78	511	1.51	GO:0034765 regulation of ion transmembrane transport	http://amigo.gene	CACNG7,HAMP,
2.0E-02	55	403	1.65	GO:0050727 regulation of inflammatory response	http://amigo.gene	GRN,RORA,TRB
2.0E-02	77	531	1.51	GO:0072503 cellular divalent inorganic cation homeostasis	http://amigo.gene	CALCR,TBXA2R
2.0E-02	117	1119	1.39	GO:0002684 positive regulation of immune system process	http://amigo.gene	CD38,TREM2,M
2.4E-02	46	377	1.71	GO:0031349 positive regulation of defense response	http://amigo.gene	TREM2,PARP9,I
2.4E-02	60	375	1.59	GO:1904062 regulation of cation transmembrane transport	http://amigo.gene	CACNG7,HAMP,
2.4E-02	163	1731	1.30	GO:0043207 response to external biotic stimulus	http://amigo.gene	LTF,TNK2,NOS1

BP:GO - Negatively correlated
(n = 3,

2.4E-02	176	1735	1.29	GO:0002682 regulation of immune system process	http://amigo.geneontology.org/amigo/term/GO:0002682	CD38,CEACAM1
2.4E-02	228	1916	1.25	GO:0042592 homeostatic process	http://amigo.geneontology.org/amigo/term/GO:0042592	LTF,ACTB,CALCR
2.4E-02	325	2990	1.19	GO:0007166 cell surface receptor signaling pathway	http://amigo.geneontology.org/amigo/term/GO:0007166	ITGA3,IL20RA,TNFR
2.4E-02	360	3300	1.18	GO:0070887 cellular response to chemical stimulus	http://amigo.geneontology.org/amigo/term/GO:0070887	IL20RA,GNA15,CD
2.5E-02	50	303	1.66	GO:0072659 protein localization to plasma membrane	http://amigo.geneontology.org/amigo/term/GO:0072659	ARHGAP44,EHD2
2.5E-02	63	549	1.56	GO:0002764 immune response-regulating signaling pathway	http://amigo.geneontology.org/amigo/term/GO:0002764	TLR8,UNC93B1,IRAK
2.5E-02	71	481	1.52	GO:0007015 actin filament organization	http://amigo.geneontology.org/amigo/term/GO:0007015	CAPG,LIMA1,WIP
2.5E-02	157	1241	1.31	GO:0048878 chemical homeostasis	http://amigo.geneontology.org/amigo/term/GO:0048878	CALCR,TBXA2R
2.5E-02	227	1874	1.24	GO:0051049 regulation of transport	http://amigo.geneontology.org/amigo/term/GO:0051049	FZD5,LEPROT,IL
2.5E-02	42	252	1.75	GO:0007599 hemostasis	http://amigo.geneontology.org/amigo/term/GO:0007599	VCL,ACTB,MYL9
2.6E-02	162	1728	1.30	GO:0051707 response to other organism	http://amigo.geneontology.org/amigo/term/GO:0051707	LTF,TNK2,NOS1
2.6E-02	247	2507	1.23	GO:0003008 system process	http://amigo.geneontology.org/amigo/term/GO:0003008	USH1C,TBXA2R
2.7E-02	332	3024	1.19	GO:0051239 regulation of multicellular organismal process	http://amigo.geneontology.org/amigo/term/GO:0051239	TBXA2R,WWC3
2.8E-02	79	558	1.47	GO:0072507 divalent inorganic cation homeostasis	http://amigo.geneontology.org/amigo/term/GO:0072507	CALCR,TBXA2R
2.8E-02	104	835	1.39	GO:0043086 negative regulation of catalytic activity	http://amigo.geneontology.org/amigo/term/GO:0043086	DBNDD1,IRAK3
2.8E-02	38	219	1.78	GO:0045216 cell-cell junction organization	http://amigo.geneontology.org/amigo/term/GO:0045216	OCEL1,TJP3,LS
3.0E-02	452	4338	1.15	GO:0048583 regulation of response to stimulus	http://amigo.geneontology.org/amigo/term/GO:0048583	ATP2C1,TRIM38
3.1E-02	261	2427	1.21	GO:0048584 positive regulation of response to stimulus	http://amigo.geneontology.org/amigo/term/GO:0048584	ATP2C1,TRIM38
3.2E-02	39	298	1.75	GO:0034612 response to tumor necrosis factor	http://amigo.geneontology.org/amigo/term/GO:0034612	TRAF5,TNFRSF
3.2E-02	163	1318	1.29	GO:0042325 regulation of phosphorylation	http://amigo.geneontology.org/amigo/term/GO:0042325	DBNDD1,FGF22
3.5E-02	39	302	1.74	GO:0045088 regulation of innate immune response	http://amigo.geneontology.org/amigo/term/GO:0045088	PARP9,NLRCS
3.6E-02	41	251	1.71	GO:0050817 coagulation	http://amigo.geneontology.org/amigo/term/GO:0050817	VCL,ACTB,MYL9
3.6E-02	55	459	1.58	GO:0002697 regulation of immune effector process	http://amigo.geneontology.org/amigo/term/GO:0002697	IL23A,CR2,PTPN
3.7E-02	51	384	1.60	GO:0008544 epidermis development	http://amigo.geneontology.org/amigo/term/GO:0008544	USH1C,OVOL2,
3.7E-02	179	1478	1.27	GO:0019220 regulation of phosphate metabolic process	http://amigo.geneontology.org/amigo/term/GO:0019220	DBNDD1,PPP1F
3.7E-02	179	1479	1.27	GO:0051174 regulation of phosphorus metabolic process	http://amigo.geneontology.org/amigo/term/GO:0051174	DBNDD1,PPP1F
4.1E-02	489	4576	1.13	GO:0048869 cellular developmental process	http://amigo.geneontology.org/amigo/term/GO:0048869	RRBP1,MYBBP1
4.1E-02	70	489	1.48	GO:0006874 cellular calcium ion homeostasis	http://amigo.geneontology.org/amigo/term/GO:0006874	CALCR,TBXA2R
4.1E-02	40	246	1.70	GO:0007596 blood coagulation	http://amigo.geneontology.org/amigo/term/GO:0007596	VCL,ACTB,MYL9
4.1E-02	203	1777	1.24	GO:0048585 negative regulation of response to stimulus	http://amigo.geneontology.org/amigo/term/GO:0048585	ARHGAP44,TLE
4.1E-02	38	285	1.73	GO:0031348 negative regulation of defense response	http://amigo.geneontology.org/amigo/term/GO:0031348	RORA,NLRCS
4.1E-02	57	448	1.54	GO:0050900 leukocyte migration	http://amigo.geneontology.org/amigo/term/GO:0050900	ITGA3,ITGA6,MA
4.1E-02	152	1218	1.29	GO:0034220 ion transmembrane transport	http://amigo.geneontology.org/amigo/term/GO:0034220	SLC7A2,ATP2C1
4.1E-02	191	1602	1.25	GO:0016477 cell migration	http://amigo.geneontology.org/amigo/term/GO:0016477	ITGA3,WWC3,P
4.1E-02	193	1729	1.25	GO:0007155 cell adhesion	http://amigo.geneontology.org/amigo/term/GO:0007155	VCL,ACTB,MYL9
4.1E-02	53	341	1.57	GO:0070588 calcium ion transmembrane transport	http://amigo.geneontology.org/amigo/term/GO:0070588	ATP2C1,TRPC5
4.3E-02	63	450	1.50	GO:0030099 myeloid cell differentiation	http://amigo.geneontology.org/amigo/term/GO:0030099	TNFRSF11A,FL

4.3E-02	72	508	1.46	GO:0055074 calcium ion homeostasis	http://amigo.gene	CALCR,TBXA2R
4.3E-02	127	977	1.32	GO:0030334 regulation of cell migration	http://amigo.gene	FGF22,MADCAN
4.3E-02	178	1917	1.26	GO:0044419 biological process involved in interspecies interaction between organisms	http://amigo.gene	LTF,TNK2,NOS1
4.3E-02	215	1830	1.23	GO:0010647 positive regulation of cell communication	http://amigo.gene	ATP2C1,TRIM38
4.4E-02	208	1835	1.23	GO:0042127 regulation of cell population proliferation	http://amigo.gene	CD38,FGF22,TG
4.4E-02	121	949	1.33	GO:0030001 metal ion transport	http://amigo.gene	LTF,ATP2C1,CP,
4.4E-02	485	4552	1.13	GO:0030154 cell differentiation	http://amigo.gene	RRBP1,MYBBP1
4.5E-02	194	1645	1.24	GO:0009967 positive regulation of signal transduction	http://amigo.gene	ATP2C1,TRIM38
4.7E-02	58	645	1.52	GO:0002250 adaptive immune response	http://amigo.gene	IL4R,IL23A,CR2
4.7E-02	63	552	1.49	GO:0032103 positive regulation of response to external stimulus	http://amigo.gene	TREM2,PARP9,X
4.7E-02	133	1078	1.30	GO:1902533 positive regulation of intracellular signal transduction	http://amigo.gene	ATP2C1,TRIM38
4.7E-02	146	1312	1.28	GO:0010628 positive regulation of gene expression	http://amigo.gene	FGF22,TLR8,FG
4.7E-02	53	342	1.55	GO:0007204 positive regulation of cytosolic calcium ion concentration	http://amigo.gene	CALCR,TBXA2R
4.8E-02	37	305	1.71	GO:0002703 regulation of leukocyte mediated immunity	http://amigo.gene	CR2,SUSD4,SYN
4.9E-02	91	642	1.38	GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	http://amigo.gene	TNK2,FGF22,EP

human-specific genes 0)	7.0E-05	34	172	2.89	GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules	http://amigo.gene	HMCN1,PTPRM
	7.0E-05	238	2618	1.39	GO:0007399 nervous system development	http://amigo.gene	WNT7A,MAOB,PLP1,CA
	3.8E-04	44	293	2.30	GO:0098742 cell-cell adhesion via plasma-membrane adhesion molecules	http://amigo.gene	CDH10,CDH20,CD
	4.2E-04	63	491	1.95	GO:0007389 pattern specification process	http://amigo.gene	HES1,ACVR1,TG
	1.0E-03	51	377	2.05	GO:0003002 regionalization	http://amigo.gene	HES1,ACVR1,BMP
	3.2E-03	111	1123	1.53	GO:0007417 central nervous system development	http://amigo.gene	MAOB,PLP1,CA
	8.2E-03	159	1757	1.38	GO:0022008 neurogenesis	http://amigo.gene	ISL1,TNFRSF1B
	1.3E-02	28	180	2.31	GO:0021953 central nervous system neuron differentiation	http://amigo.gene	EPHB2,ARX,PAF
	1.3E-02	49	409	1.83	GO:0030900 forebrain development	http://amigo.gene	WNT7A,ARX,PA
	1.3E-02	63	562	1.68	GO:0001501 skeletal system development	http://amigo.gene	SOX6,ANXA6,SL
	1.3E-02	87	865	1.55	GO:0060322 head development	http://amigo.gene	MAOB,PLP1,CA
	1.3E-02	108	1105	1.48	GO:0009887 animal organ morphogenesis	http://amigo.gene	PAFAH1B1,TBX3
	1.3E-02	354	4617	1.20	GO:0048731 system development	http://amigo.gene	WNT7A,MAOB,PLP1,CA
	1.3E-02	67	614	1.65	GO:0007423 sensory organ development	http://amigo.gene	OTOP1,RP1L1,CD
	1.3E-02	139	1522	1.39	GO:0048699 generation of neurons	http://amigo.gene	ISL1,WNT8B,FR
	1.3E-02	93	1104	1.51	GO:0098609 cell-cell adhesion	http://amigo.gene	CD99,CDH10,CD
	1.4E-02	82	816	1.55	GO:0007420 brain development	http://amigo.gene	MAOB,PLP1,CA
	1.4E-02	171	2086	1.33	GO:0009888 tissue development	http://amigo.gene	SOX10,SOX6,SL

BP:GO - Positively correlated
(n = 2,05)

1.8E-02	140	1563	1.37	GO:0120036 plasma membrane bounded cell projection organization	http://amigo.geneontology.org/amigo/term/GO:0120036	MKS1,ISL1,FRY
2.2E-02	39	317	1.90	GO:0060070 canonical Wnt signaling pathway	http://amigo.geneontology.org/amigo/term/GO:0060070	ADGRA2,WNT8
2.2E-02	121	1431	1.40	GO:0045892 negative regulation of transcription DNA-templated	http://amigo.geneontology.org/amigo/term/GO:0045892	SCML1,TRO,ZN
2.2E-02	121	1433	1.40	GO:1903507 negative regulation of nucleic acid-templated transcription	http://amigo.geneontology.org/amigo/term/GO:1903507	SCML1,TRO,ZN
2.3E-02	121	1435	1.40	GO:1902679 negative regulation of RNA biosynthetic process	http://amigo.geneontology.org/amigo/term/GO:1902679	SCML1,TRO,ZN
2.4E-02	36	306	1.93	GO:0045165 cell fate commitment	http://amigo.geneontology.org/amigo/term/GO:0045165	ISL1,WNT8B,SC
2.4E-02	67	641	1.59	GO:0048598 embryonic morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0048598	TBX3,OTOP1,VT
2.6E-02	286	3774	1.21	GO:0048513 animal organ development	http://amigo.geneontology.org/amigo/term/GO:0048513	MAOB,PLP1,CA
3.0E-02	46	410	1.75	GO:0044782 cilium organization	http://amigo.geneontology.org/amigo/term/GO:0044782	MKS1,KCTD17,C
3.2E-02	133	1602	1.35	GO:0016477 cell migration	http://amigo.geneontology.org/amigo/term/GO:0016477	CD99,FSCN1,SC
3.6E-02	31	249	1.98	GO:0010001 glial cell differentiation	http://amigo.geneontology.org/amigo/term/GO:0010001	TNFRSF1B,MET
3.6E-02	140	1606	1.33	GO:0030030 cell projection organization	http://amigo.geneontology.org/amigo/term/GO:0030030	MKS1,ISL1,FRY
4.2E-02	127	1546	1.35	GO:0051253 negative regulation of RNA metabolic process	http://amigo.geneontology.org/amigo/term/GO:0051253	SCML1,TRO,ZN
4.3E-02	25	169	2.13	GO:0021915 neural tube development	http://amigo.geneontology.org/amigo/term/GO:0021915	MKS1,TULP3,CB
4.3E-02	69	681	1.53	GO:0061061 muscle structure development	http://amigo.geneontology.org/amigo/term/GO:0061061	PLEKHO1,SIX1,
4.5E-02	128	1449	1.34	GO:0030182 neuron differentiation	http://amigo.geneontology.org/amigo/term/GO:0030182	ISL1,WNT8B,FR
4.6E-02	49	446	1.65	GO:0001667 ameboidal-type cell migration	http://amigo.geneontology.org/amigo/term/GO:0001667	SOX10,LPXN,AN
4.6E-02	136	1674	1.32	GO:0045934 negative regulation of nucleobase-containing compound metabolic process	http://amigo.geneontology.org/amigo/term/GO:0045934	SCML1,TRO,ZN
4.6E-02	178	2254	1.27	GO:0006928 movement of cell or subcellular component	http://amigo.geneontology.org/amigo/term/GO:0006928	CD99,PAFAH1B
4.6E-02	65	663	1.53	GO:0048729 tissue morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0048729	SOX10,TBX3,VA