

Supplementary table 12: GO results of N-scRNA (GO categories shown in Figure 2.4)

		nGenes	Pathway Genes	Fold Enrichment	Pathway	URL	Genes
BP: GO - correlated with both human and chimpanzee ZEB2 (n = 214)	1.6E-90	68	178	37.99	GO:0002181 cytoplasmic translation	http://amigo.geneontology.org/amigo/term/GO:0002181	RPL31,RPL6,RP
	8.9E-51	74	784	9.84	GO:0006412 translation	http://amigo.geneontology.org/amigo/term/GO:0006412	RPL31,RPS5,RP
	1.3E-49	74	814	9.44	GO:0043043 peptide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043043	RPL31,RPS5,RP
	2.1E-44	74	959	7.95	GO:0043604 amide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043604	RPL31,RPS5,RP
	1.5E-13	26	327	7.80	GO:0042254 ribosome biogenesis	http://amigo.geneontology.org/amigo/term/GO:0042254	RPS5,RPL6,RPL
	2.1E-44	75	999	7.78	GO:0006518 peptide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0006518	RPL31,RPS5,RP
	4.3E-36	75	1259	5.91	GO:0034645 cellular macromolecule biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0034645	RPL31,RPS5,RP
	4.3E-36	75	1301	5.91	GO:0043603 cellular amide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0043603	RPL31,RPS5,RP
	4.4E-12	29	509	5.87	GO:0022613 ribonucleoprotein complex biogenesis	http://amigo.geneontology.org/amigo/term/GO:0022613	CELF2,RPS5,RP
	1.4E-27	79	1888	4.15	GO:1901566 organonitrogen compound biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:1901566	RPL31,RPS5,RP
BP: GO - Human-specific correlation genes (n = 789)	4.4E-09	82	996	2.23	GO:0000278 mitotic cell cycle	http://amigo.geneontology.org/amigo/term/GO:0000278	ZNF207,NDC80,
	1.4E-13	126	1522	2.16	GO:0048699 generation of neurons	http://amigo.geneontology.org/amigo/term/GO:0048699	EPHA3,NEDD4L
	6.3E-12	117	1449	2.10	GO:0030182 neuron differentiation	http://amigo.geneontology.org/amigo/term/GO:0030182	EPHA3,NEDD4L
	1.4E-13	139	1757	2.07	GO:0022008 neurogenesis	http://amigo.geneontology.org/amigo/term/GO:0022008	EPHA3,NEDD4L
	2.7E-07	80	1001	2.04	GO:0031175 neuron projection development	http://amigo.geneontology.org/amigo/term/GO:0031175	EPHA3,NEDD4L
	1.6E-08	93	1269	2.04	GO:0033043 reg. of organelle organization	http://amigo.geneontology.org/amigo/term/GO:0033043	ZNF207,TMSB10
	3.1E-08	91	1169	2.03	GO:0048666 neuron development	http://amigo.geneontology.org/amigo/term/GO:0048666	EPHA3,NEDD4L
	3.6E-08	94	1321	1.99	GO:0022402 cell cycle proc.	http://amigo.geneontology.org/amigo/term/GO:0022402	ZNF207,SMC1A
	1.3E-08	125	1937	1.81	GO:0007049 cell cycle	http://amigo.geneontology.org/amigo/term/GO:0007049	ZNF207,SMC1A
	4.1E-13	179	2618	1.81	GO:0007399 nervous system development	http://amigo.geneontology.org/amigo/term/GO:0007399	ACTB,GLUD1,C
	6.6E-11	162	2509	1.77	GO:0051128 reg. of cellular component organization	http://amigo.geneontology.org/amigo/term/GO:0051128	ZNF207,TMSB10
	3.1E-07	135	2254	1.67	GO:0006928 movement of cell or subcellular component	http://amigo.geneontology.org/amigo/term/GO:0006928	CD99,TMSB10,E
	6.3E-12	260	4617	1.53	GO:0048731 system development	http://amigo.geneontology.org/amigo/term/GO:0048731	ACTB,GLUD1,C
	1.3E-08	234	4552	1.47	GO:0030154 cell differentiation	http://amigo.geneontology.org/amigo/term/GO:0030154	VCAN,RRAS2,H
	4.4E-07	200	3774	1.47	GO:0048513 animal organ development	http://amigo.geneontology.org/amigo/term/GO:0048513	ACTB,GLUD1,C
	1.9E-08	234	4576	1.46	GO:0048869 cellular developmental proc.	http://amigo.geneontology.org/amigo/term/GO:0048869	VCAN,RRAS2,H
	4.9E-07	214	4206	1.44	GO:0006996 organelle organization	http://amigo.geneontology.org/amigo/term/GO:0006996	ACTB,HDAC2,T
BP: GO - Specific correlation genes (n = 268)	3.6E-10	30	452	5.13	GO:0007409 axonogenesis	http://amigo.geneontology.org/amigo/term/GO:0007409	EFNB1,METRN,
	1.0E-09	30	501	4.62	GO:0061564 axon development	http://amigo.geneontology.org/amigo/term/GO:0061564	EFNB1,METRN,
	1.3E-09	32	585	4.27	GO:0048667 cell morphogenesis involved in neuron differentiation	http://amigo.geneontology.org/amigo/term/GO:0048667	EFNB1,METRN,
	5.1E-10	35	647	4.21	GO:0048812 neuron projection morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0048812	EFNB1,METRN,
	6.6E-10	35	662	4.10	GO:0120039 plasma membrane bounded cell projection morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0120039	EFNB1,METRN,
	6.6E-10	35	667	4.07	GO:0048858 cell projection morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0048858	EFNB1,METRN,
	1.0E-09	35	686	3.96	GO:0032990 cell part morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0032990	EFNB1,METRN,
	6.6E-10	38	789	3.79	GO:0032989 cellular component morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0032989	EFNB1,METRN,
	1.9E-09	42	1001	3.29	GO:0031175 neuron projection development	http://amigo.geneontology.org/amigo/term/GO:0031175	STMN4,GPM6B,

BP:GO - Chimpanzee-specific genes (n = 2)	2.7E-09	45	1169	3.08	GO:0048666 neuron development	http://amigo.geneontology.org/amigo/term/GO:0048666	STMN4,GPM6B,	
	6.6E-10	54	1522	2.84	GO:0048699 generation of neurons	http://amigo.geneontology.org/amigo/term/GO:0048699	STMN4,GPM6B,	
	7.9E-09	50	1449	2.76	GO:0030182 neuron differentiation	http://amigo.geneontology.org/amigo/term/GO:0030182	STMN4,GPM6B,	
	1.0E-09	58	1757	2.65	GO:0022008 neurogenesis	http://amigo.geneontology.org/amigo/term/GO:0022008	STMN4,GPM6B,	
	5.6E-07	48	1563	2.48	GO:0120036 plasma membrane bounded cell projection organization	http://amigo.geneontology.org/amigo/term/GO:0120036	STMN4,GPM6B,	
	4.7E-07	49	1606	2.47	GO:0030030 cell projection organization	http://amigo.geneontology.org/amigo/term/GO:0030030	STMN4,CAPG,G	
	1.4E-10	77	2618	2.39	GO:0007399 nervous system development	http://amigo.geneontology.org/amigo/term/GO:0007399	CNP,BASP1,CAL	
	1.9E-07	61	2239	2.23	GO:0048468 cell development	http://amigo.geneontology.org/amigo/term/GO:0048468	STMN4,GPM6B,	
	1.0E-08	74	2867	2.13	GO:0009653 anatomical structure morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0009653	CDH19,EFNB1,S	
	4.6E-10	105	4617	1.90	GO:0048731 system development	http://amigo.geneontology.org/amigo/term/GO:0048731	CNP,BASP1,CAL	
	Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	URL	Genes	Category
BP:GO - cortical neurons: shared correlation genes between humans and chimpanzees (n = 71)	2.5E-11	7	13	69.47	GO:0034470 negative reg. of ubiquitin protein ligase activity	http://amigo.geneontology.org/amigo/term/GO:0034470	RPL5,RPL23,RP	Cellular compon
	1.3E-12	8	29	64.96	GO:0000027 ribosomal large subunit assembly	http://amigo.geneontology.org/amigo/term/GO:0000027	RPL6,RPLP0,RP	Cellular compon
	5.6E-110	62	178	52.24	GO:0002181 cytoplasmic translation	http://amigo.geneontology.org/amigo/term/GO:0002181	RPL31,RPL6,RP	Gene expression
	7.0E-20	14	79	48.09	GO:0042273 ribosomal large subunit biogenesis	http://amigo.geneontology.org/amigo/term/GO:0042273	RPL6,RPLP0,RP	Cellular compon
	3.8E-18	13	63	46.45	GO:0042255 ribosome assembly	http://amigo.geneontology.org/amigo/term/GO:0042255	RPS5,RPL6,RPL	Cellular compon
	2.9E-81	63	784	20.92	GO:0006412 translation	http://amigo.geneontology.org/amigo/term/GO:0006412	RPL31,RPS5,RP	Gene expression
	3.2E-81	63	814	20.76	GO:0043043 peptide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043043	RPL31,RPS5,RP	Metabolism
	3.5E-25	25	327	19.76	GO:0042254 ribosome biogenesis	http://amigo.geneontology.org/amigo/term/GO:0042254	RPS5,RPL6,RPL	Cellular compon
	5.2E-77	63	999	18.04	GO:0006518 peptide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0006518	RPL31,RPS5,RP	Metabolism
	9.8E-17	18	248	17.67	GO:0006364 rRNA processing	http://amigo.geneontology.org/amigo/term/GO:0006364	RPS16,RPL35,R	Gene expression
	1.1E-75	63	959	17.21	GO:0043604 amide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043604	RPL31,RPS5,RP	Metabolism
	4.6E-16	18	288	16.24	GO:0016072 rRNA metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0016072	RPS16,RPL35,R	RNA biosynthesi
	2.5E-11	14	240	13.89	GO:0022618 ribonucleoprotein complex assembly	http://amigo.geneontology.org/amigo/term/GO:0022618	RPS5,RPL6,RPL	RNA biosynthesi
	3.4E-11	14	248	13.45	GO:0071826 ribonucleoprotein complex subunit organization	http://amigo.geneontology.org/amigo/term/GO:0071826	RPS5,RPL6,RPL	RNA biosynthesi
	7.2E-68	63	1301	13.21	GO:0043603 cellular amide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0043603	RPL31,RPS5,RP	Metabolism
	2.6E-21	26	509	12.97	GO:0022613 ribonucleoprotein complex biogenesis	http://amigo.geneontology.org/amigo/term/GO:0022613	RPS5,RPL6,RPL	RNA biosynthesi
	4.0E-67	63	1259	12.85	GO:0034645 cellular macromolecule biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0034645	RPL31,RPS5,RP	Cellular compon
	3.8E-12	16	417	12.21	GO:0140694 non-membrane-bounded organelle assembly	http://amigo.geneontology.org/amigo/term/GO:0140694	RPS5,RPL6,RPL	Cellular compon
	4.6E-59	63	1888	9.72	GO:1901566 organonitrogen compound biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:1901566	RPL31,RPS5,RP	Metabolism
	3.2E-11	18	483	8.64	GO:0034470 ncRNA processing	http://amigo.geneontology.org/amigo/term/GO:0034470	RPS16,RPL35,R	Gene expression
BP:GO - cortical neurons: human-specific correlation genes (n = 11)	1.6E-03	5	784	14.63	GO:0006412 translation	http://amigo.geneontology.org/amigo/term/GO:0006412	RPS6,RPL38,RP	Gene expression
	1.6E-03	5	814	14.03	GO:0043043 peptide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043043	RPS6,RPL38,RP	Metabolism
	2.8E-03	5	959	11.82	GO:0043604 amide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043604	RPS6,RPL38,RP	Metabolism
	2.8E-03	5	999	11.41	GO:0006518 peptide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0006518	RPS6,RPL38,RP	Metabolism
	3.7E-03	6	1888	6.94	GO:1901566 organonitrogen compound biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:1901566	RPS6,RPL38,RP	Metabolism
	6.4E-03	5	1259	8.67	GO:0034645 cellular macromolecule biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0034645	RPS6,RPL38,RP	Cellular compon
	6.4E-03	5	1301	8.67	GO:0043603 cellular amide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0043603	RPS6,RPL38,RP	Metabolism
	3.2E-02	6	2867	4.30	GO:0009653 anatomical structure morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0009653	ALDOA,BCL11A	Development

O - central progenitors and neurons: Positively correlated human-specific genes (n = 35)	7.0E-03	8	745	8.05	GO:0043269 reg. of ion transport	http://amigo.geneontology.org/amigo/term/GO:0043269	SYT17,FGF12,V	(Synaptic) signal
	1.3E-02	5	291	11.14	GO:0007611 learning or memory	http://amigo.geneontology.org/amigo/term/GO:0007611	VIP,CNR1,SORC	Cognition
	1.3E-02	7	764	6.88	GO:0007268 chemical synaptic transmission	http://amigo.geneontology.org/amigo/term/GO:0007268	DLG2,NRXN1,Fc	(Synaptic) signal
	1.3E-02	7	764	6.88	GO:0098916 anterograde trans-synaptic signaling	http://amigo.geneontology.org/amigo/term/GO:0098916	DLG2,NRXN1,Fc	(Synaptic) signal
	1.3E-02	7	773	6.72	GO:0099537 trans-synaptic signaling	http://amigo.geneontology.org/amigo/term/GO:0099537	DLG2,NRXN1,Fc	(Synaptic) signal
	1.3E-02	7	810	6.66	GO:0099536 synaptic signaling	http://amigo.geneontology.org/amigo/term/GO:0099536	DLG2,NRXN1,Fc	(Synaptic) signal
	1.8E-02	5	347	9.97	GO:0050890 cognition	http://amigo.geneontology.org/amigo/term/GO:0050890	VIP,CNR1,SORC	Cognition
	1.8E-02	15	3602	2.60	GO:0010646 reg. of cell communication	http://amigo.geneontology.org/amigo/term/GO:0010646	AKAP7,TXN,NR	(Synaptic) signal
	1.8E-02	15	3615	2.57	GO:0023051 reg. of signaling	http://amigo.geneontology.org/amigo/term/GO:0023051	AKAP7,TXN,NR	(Synaptic) signal
BP:GO - central progenitors and neurons: Negatively correlated human-specific genes (n = 27)	1.1E-17	15	178	32.33	GO:0002181 cytoplasmic translation	http://amigo.geneontology.org/amigo/term/GO:0002181	RPL6,RPL15,RP	Gene expression
	6.4E-04	5	140	16.99	GO:0006413 translational initiation	http://amigo.geneontology.org/amigo/term/GO:0006413	EIF3E,RPL13A,E	Gene expression
	1.0E-03	5	240	14.89	GO:0022618 ribonucleoprotein complex assembly	http://amigo.geneontology.org/amigo/term/GO:0022618	RPL6,RPL3,RPL	RNA biosynthesi
	5.8E-15	17	784	14.54	GO:0006412 translation	http://amigo.geneontology.org/amigo/term/GO:0006412	RPL6,EIF3E,RPL	Gene expression
	5.8E-15	17	814	14.26	GO:0043043 peptide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043043	RPL6,EIF3E,RPL	RNA biosynthesi
	1.3E-03	5	248	13.95	GO:0071826 ribonucleoprotein complex subunit organization	http://amigo.geneontology.org/amigo/term/GO:0071826	RPL6,RPL3,RPL	RNA biosynthesi
	4.6E-14	17	999	12.31	GO:0006518 peptide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0006518	RPL6,EIF3E,RPL	Metabolism
	4.6E-14	17	959	12.25	GO:0043604 amide biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0043604	RPL6,EIF3E,RPL	Metabolism
	3.7E-03	5	417	10.44	GO:0140694 non-membrane-bounded organelle assembly	http://amigo.geneontology.org/amigo/term/GO:0140694	RPL6,RPL3,RPL	Cellular compone
	2.3E-12	17	1259	9.59	GO:0034645 cellular macromolecule biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0034645	RPL6,EIF3E,RPL	Cellular compone
	2.5E-12	17	1301	9.47	GO:0043603 cellular amide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0043603	RPL6,EIF3E,RPL	Metabolism
	1.7E-03	6	449	9.19	GO:0006417 reg. of translation	http://amigo.geneontology.org/amigo/term/GO:0006417	RPL13A,RPL5,R	Gene expression
	6.4E-04	7	509	8.79	GO:0022613 ribonucleoprotein complex biogenesis	http://amigo.geneontology.org/amigo/term/GO:0022613	RPL6,RPL3,RPL	RNA biosynthesi
	9.0E-03	5	327	8.44	GO:0042254 ribosome biogenesis	http://amigo.geneontology.org/amigo/term/GO:0042254	RPL6,RPL3,RPL	Cellular compone
	2.7E-03	6	514	8.33	GO:0034248 reg. of cellular amide metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0034248	RPL13A,RPL5,R	Metabolism
	2.8E-03	6	533	8.16	GO:2000112 reg. of cellular macromolecule biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:2000112	RPL13A,RPL5,R	Cellular compone
	2.5E-10	17	1888	7.11	GO:1901566 organonitrogen compound biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:1901566	RPL6,EIF3E,RPL	Metabolism
	5.6E-03	6	601	7.07	GO:0010608 post-transcriptional reg. of gene expression	http://amigo.geneontology.org/amigo/term/GO:0010608	RPL13A,RPL5,R	Gene expression
O - GM/S dorsal progenitors/radial glia: Shared positively correlated gene (n = 49)	1.4E-04	7	180	14.94	GO:0021953 central nervous system neuron differentiation	http://amigo.geneontology.org/amigo/term/GO:0021953	DCX,DLX2,SOX4	Neurogenesis
	1.4E-04	9	386	9.17	GO:0050767 reg. of neurogenesis	http://amigo.geneontology.org/amigo/term/GO:0050767	ASCL1,HES6,PA	Neurogenesis
	1.4E-04	10	470	8.43	GO:0051960 reg. of nervous system development	http://amigo.geneontology.org/amigo/term/GO:0051960	ASCL1,HES6,PA	Neurogenesis
	2.7E-04	8	345	9.73	GO:0042063 gliogenesis	http://amigo.geneontology.org/amigo/term/GO:0042063	DCX,DLX2,SOX4	Neurogenesis
	4.0E-04	7	249	11.45	GO:0010001 glial cell differentiation	http://amigo.geneontology.org/amigo/term/GO:0010001	DLX2,SOX4,ASC	Neurogenesis
	4.1E-04	16	1757	3.64	GO:0022008 neurogenesis	http://amigo.geneontology.org/amigo/term/GO:0022008	PAK3,DCX,STM	Neurogenesis
	5.4E-04	7	276	10.48	GO:0021537 telencephalon development	http://amigo.geneontology.org/amigo/term/GO:0021537	DCX,DLX5,DLX2	(Fore)brain deve
	6.2E-04	6	196	13.12	GO:0007219 Notch signaling pathway	http://amigo.geneontology.org/amigo/term/GO:0007219	ASCL1,DLL3,CD	(Synaptic) signal
	6.2E-04	8	409	7.94	GO:0030900 forebrain development	http://amigo.geneontology.org/amigo/term/GO:0030900	DCX,DLX5,DLX2	(Fore)brain deve
	6.2E-04	9	530	6.73	GO:0060284 reg. of cell development	http://amigo.geneontology.org/amigo/term/GO:0060284	ASCL1,HES6,PA	Development
	1.2E-03	14	1522	3.66	GO:0048699 generation of neurons	http://amigo.geneontology.org/amigo/term/GO:0048699	PAK3,DCX,STM	Neurogenesis

BP:GO - GM/S dorsal progenitors/radial glia: 2	1.2E-03	18	2680	2.88	GO:0050793 reg. of developmental proc.	http://amigo.geneontology.org/amigo/term/GO:0050793	PAK3,RND3,ASCC2	Development
	1.6E-03	18	2618	2.78	GO:0007399 nervous system development	http://amigo.geneontology.org/amigo/term/GO:0007399	PAK3,DCX,STMN2	Neurogenesis
BP:GO - GM/S dorsal progenitors/radial glia: Shared negatively correlated gene (n = 29)	3.2E-07	5	25	140.21	GO:0021871 forebrain regionalization	http://amigo.geneontology.org/amigo/term/GO:0021871	LHX2,EMX1,DMRT	(Fore)brain development
	9.3E-04	5	192	19.40	GO:0021543 pallium development	http://amigo.geneontology.org/amigo/term/GO:0021543	LHX2,EMX1,DMRT	(Fore)brain development
	4.3E-04	6	276	15.55	GO:0021537 telencephalon development	http://amigo.geneontology.org/amigo/term/GO:0021537	LHX2,HES1,EMX1	(Fore)brain development
	3.5E-04	7	377	12.70	GO:0003002 regionalization	http://amigo.geneontology.org/amigo/term/GO:0003002	HES1,SFRP1,LHX2	Development
	4.1E-04	7	409	12.03	GO:0030900 forebrain development	http://amigo.geneontology.org/amigo/term/GO:0030900	LHX2,HES1,EMX1	(Fore)brain development
	9.3E-04	7	491	9.81	GO:0007389 pattern specification proc.	http://amigo.geneontology.org/amigo/term/GO:0007389	HES1,SFRP1,LHX2	Development
	1.6E-03	8	816	6.97	GO:0007420 brain development	http://amigo.geneontology.org/amigo/term/GO:0007420	EMX1,EMX2,SFRP1	(Fore)brain development
	2.2E-03	8	865	6.54	GO:0060322 head development	http://amigo.geneontology.org/amigo/term/GO:0060322	EMX1,EMX2,SFRP1	(Fore)brain development
	4.2E-04	10	1123	6.29	GO:0007417 central nervous system development	http://amigo.geneontology.org/amigo/term/GO:0007417	EMX1,EMX2,VIM	Neurogenesis
	1.9E-03	16	4309	2.83	GO:0010556 reg. of macromolecule biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0010556	MAGED2,LHX2,SLC1A1	Cellular component
	3.6E-03	15	4112	2.78	GO:0051252 reg. of RNA metabolic proc.	http://amigo.geneontology.org/amigo/term/GO:0051252	MAGED2,LHX2,SLC1A1	Metabolism
	2.5E-03	16	4503	2.74	GO:0018130 heterocycle biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0018130	MAGED2,LHX2,SLC1A1	Metabolism
	2.5E-03	16	4482	2.71	GO:0031326 reg. of cellular biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:0031326	MAGED2,LHX2,SLC1A1	Metabolism
	3.2E-03	16	4676	2.64	GO:1901362 organic cyclic compound biosynthetic proc.	http://amigo.geneontology.org/amigo/term/GO:1901362	MAGED2,LHX2,SLC1A1	Metabolism
BP:GO - GM/S dorsal progenitors/radial glia: Positively correlated human-specific genes (n = 293)	1.2E-12	42	781	4.12	GO:0010564 reg. of cell cycle proc.	http://amigo.geneontology.org/amigo/term/GO:0010564	CLSPN,RANBP1	Cell cycle
	1.3E-14	43	689	4.64	GO:0051301 cell division	http://amigo.geneontology.org/amigo/term/GO:0051301	DCTN3,NUSAP1	Cell cycle
	1.6E-17	57	996	4.25	GO:0000278 mitotic cell cycle	http://amigo.geneontology.org/amigo/term/GO:0000278	NDC80,TPX2,CLSPN	Cell cycle
	1.7E-14	33	395	6.22	GO:0007059 chromosome segregation	http://amigo.geneontology.org/amigo/term/GO:0007059	SMC1A,TPX2,CLSPN	Cell cycle
	1.9E-15	40	564	5.33	GO:0048285 organelle fission	http://amigo.geneontology.org/amigo/term/GO:0048285	TOP2B,NDC80,TPX2	Cellular component
	2.7E-11	52	1269	3.13	GO:0033043 reg. of organelle organization	http://amigo.geneontology.org/amigo/term/GO:0033043	TMSB10,CAPZB	Cellular component
	3.2E-11	50	1213	3.20	GO:0051726 reg. of cell cycle	http://amigo.geneontology.org/amigo/term/GO:0051726	BIRC5,CLSPN,RANBP1	Cell cycle
	3.2E-13	51	1173	3.57	GO:0051276 chromosome organization	http://amigo.geneontology.org/amigo/term/GO:0051276	ACTB,HDAC2,SLC1A1	Cell cycle
	4.0E-11	45	986	3.47	GO:0007017 microtubule-based proc.	http://amigo.geneontology.org/amigo/term/GO:0007017	CFAP20,DYNC1H1	Cellular component
	4.3E-14	31	346	6.47	GO:0140014 mitotic nuclear division	http://amigo.geneontology.org/amigo/term/GO:0140014	NDC80,TPX2,RANBP1	Cellular component
	6.2E-14	112	4206	2.07	GO:0006996 organelle organization	http://amigo.geneontology.org/amigo/term/GO:0006996	ACTB,HDAC2,TPX2	Cellular component
	6.9E-17	63	1321	3.66	GO:0022402 cell cycle proc.	http://amigo.geneontology.org/amigo/term/GO:0022402	SMC1A,TPX2,CLSPN	Cell cycle
	6.9E-17	77	1937	3.06	GO:0007049 cell cycle	http://amigo.geneontology.org/amigo/term/GO:0007049	SMC1A,TPX2,CLSPN	Cell cycle
	8.7E-16	39	514	5.68	GO:0000280 nuclear division	http://amigo.geneontology.org/amigo/term/GO:0000280	TOP2B,NDC80,TPX2	Cellular component
	9.8E-16	49	825	4.37	GO:1903047 mitotic cell cycle proc.	http://amigo.geneontology.org/amigo/term/GO:1903047	NDC80,TPX2,CLSPN	Cell cycle
BP:GO - GM/S dorsal progenitors/radial glia: Positively correlated specific genes (n = 488)	1.4E-08	83	1522	2.22	GO:0048699 generation of neurons	http://amigo.geneontology.org/amigo/term/GO:0048699	SEMA6A,TMEM43	Neurogenesis
	1.6E-08	90	1757	2.10	GO:0022008 neurogenesis	http://amigo.geneontology.org/amigo/term/GO:0022008	SEMA6A,TMEM43	Neurogenesis
	3.2E-08	171	4617	1.57	GO:0048731 system development	http://amigo.geneontology.org/amigo/term/GO:0048731	PLP1,GLUD1,VCAM1	Development
	5.5E-08	115	2618	1.82	GO:0007399 nervous system development	http://amigo.geneontology.org/amigo/term/GO:0007399	PLP1,GLUD1,VCAM1	Neurogenesis
	1.1E-06	74	1449	2.08	GO:0030182 neuron differentiation	http://amigo.geneontology.org/amigo/term/GO:0030182	SEMA6A,TMEM43	Neurogenesis
	3.1E-05	60	1169	2.09	GO:0048666 neuron development	http://amigo.geneontology.org/amigo/term/GO:0048666	SEMA6A,TMEM43	Neurogenesis
	5.0E-05	54	1001	2.16	GO:0031175 neuron projection development	http://amigo.geneontology.org/amigo/term/GO:0031175	SEMA6A,TMEM43	Neurogenesis

BP:GO - GM/S dorsal Negative human-specific (n = 13)	1.2E-04	148	4552	1.46	GO:0030154 cell differentiation	http://amigo.geneontology.org/amigo/term/GO:0030154	VCAN,RRAS2,C	Development
	1.6E-04	148	4576	1.45	GO:0048869 cellular developmental proc.	http://amigo.geneontology.org/amigo/term/GO:0048869	VCAN,RRAS2,C	Development
	1.9E-04	130	3774	1.50	GO:0048513 animal organ development	http://amigo.geneontology.org/amigo/term/GO:0048513	PLP1,GLUD1,NN	Development
	4.2E-04	106	2867	1.56	GO:0009653 anatomical structure morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0009653	SDK2,MYDGF,S	Development
	5.3E-04	68	1563	1.79	GO:0120036 plasma membrane bounded cell projection organization	http://amigo.geneontology.org/amigo/term/GO:0120036	SEMA6A,TMEM	Cell projection
	5.9E-04	69	1606	1.77	GO:0030030 cell projection organization	http://amigo.geneontology.org/amigo/term/GO:0030030	SEMA6A,TMEM	Cell projection
Mesenchymal- d correlation g (n = 13)	1.6E-04	5	355	23.21	GO:0030198 extracellular matrix organization	http://amigo.geneontology.org/amigo/term/GO:0030198	COL1A1,COL1A	Cellular compone
	1.6E-04	5	356	23.13	GO:0043062 extracellular structure organization	http://amigo.geneontology.org/amigo/term/GO:0043062	COL1A1,COL1A	Cellular compone
	1.6E-04	5	359	23.13	GO:0045229 external encapsulating structure organization	http://amigo.geneontology.org/amigo/term/GO:0045229	COL1A1,COL1A	Cellular compone
	4.1E-04	6	883	11.47	GO:0097435 supramolecular fiber organization	http://amigo.geneontology.org/amigo/term/GO:0097435	MFAP4,MARCKS	Cellular compone