

Supplementary Table 6.
DEGs in Astrocyte cluster

gene	<i>p</i>	logFC	FDR	dysregulation
UTY	1.1E-190	4.61721	4.1E-186	UP
COL3A1	1.48E-45	3.46272	1.43E-41	UP
H19	5.34E-34	3.48756	2.06E-30	UP
TLE4	1.75E-31	2.314622	4.83E-28	UP
COL1A1	1E-27	2.03704	1.94E-24	UP
MT-CO1	2.67E-26	2.140984	3.82E-23	UP
AFP	8.76E-26	4.289867	1.21E-22	UP
RPS18	6.3E-23	3.510903	6.4E-20	UP
HMGA2	1.59E-22	1.421194	1.54E-19	UP
ENSG00000289901	2.66E-22	1.678083	2.5E-19	UP
MT-CO2	4.97E-22	1.268229	4.57E-19	UP
HSP90AB1	3.09E-21	2.90887	2.59E-18	UP
HSPH1	6.43E-21	1.574993	5.17E-18	UP
CUX2	2.87E-19	1.754996	1.94E-16	UP
RPL10	2.97E-19	3.351807	1.98E-16	UP
MT-CYB	4.75E-19	1.937085	3.11E-16	UP
RPS3	1.25E-18	2.540618	7.79E-16	UP
KRT19	1.28E-18	1.33239	7.82E-16	UP
SDK1	1.74E-18	2.129498	1.02E-15	UP
ARID5B	2.52E-18	1.445777	1.4E-15	UP
CEMP2	2.54E-18	1.522441	1.4E-15	UP
SOX11	3.69E-17	1.067372	1.8E-14	UP
EPHA4	8.78E-17	1.172546	4.08E-14	UP
CASC15	1.08E-16	2.046174	4.97E-14	UP
RPL39	1.59E-16	2.668778	7.05E-14	UP
PDE1A	2.29E-16	1.46019	9.7E-14	UP
IGF2	2.35E-16	1.675649	9.85E-14	UP
MT-ATP6	1.06E-15	2.292742	4.11E-13	UP
AKAP12	1.22E-15	1.295895	4.65E-13	UP

RPL28	1.53E-15	2.10822	5.67E-13	UP
ENSG00000262198	3.85E-15	1.367385	1.34E-12	UP
ZDBF2	3.92E-15	1.260939	1.35E-12	UP
FN1	6.94E-15	1.383906	2.23E-12	UP
MAP1B	1.16E-14	1.986153	3.61E-12	UP
RPL37	1.69E-14	1.926318	5.01E-12	UP
SOX2-OT	1.68E-14	2.044892	5.01E-12	UP
RPL12	2.61E-14	1.836445	7.59E-12	UP
FGFR1	3.28E-14	1.304316	9.18E-12	UP
MT-ND4	6.42E-14	1.480934	1.75E-11	UP
RPL14	8.23E-14	2.210737	2.19E-11	UP
COL1A2	1.06E-13	1.436003	2.73E-11	UP
ENSG00000286850	1.05E-13	1.051343	2.73E-11	UP
RPL11	1.06E-13	1.655557	2.73E-11	UP
AUTS2	8.03E-13	2.53109	1.86E-10	UP
BCAT1	1.38E-12	1.052118	3.03E-10	UP
RPS15A	1.71E-12	1.669307	3.68E-10	UP
RPL32	1.82E-12	2.319995	3.87E-10	UP
RPS21	2.07E-12	1.19102	4.34E-10	UP
RPL34	2.42E-12	2.232682	4.92E-10	UP
ZSWIM6	8.35E-12	2.719836	1.53E-09	UP
KCNQ1OT1	8.52E-12	1.541809	1.55E-09	UP
NAP1L1	2.75E-11	1.335123	4.69E-09	UP
RPL18	2.81E-11	1.767844	4.78E-09	UP
TRIM24	3.87E-11	1.099972	6.47E-09	UP
RPS27	3.97E-11	1.891601	6.6E-09	UP
SLC35F1	5.97E-11	1.731199	9.64E-09	UP
SOX4	9.69E-11	1.750235	1.5E-08	UP
RPL18A	1.21E-10	1.768847	1.86E-08	UP
TNNT1	1.22E-10	1.078769	1.86E-08	UP
FXR1	3.17E-10	1.310304	4.5E-08	UP
SLC38A2	3.28E-10	1.024685	4.64E-08	UP
HSP90AA1	5.29E-10	1.032033	7.24E-08	UP
RPS3A	5.76E-10	2.791305	7.83E-08	UP

RPS7	6.58E-10	1.380528	8.79E-08	UP
MT-ND1	9.95E-10	1.159753	1.3E-07	UP
EXT1	1.03E-09	2.124214	1.33E-07	UP
RPS9	1.13E-09	1.59484	1.44E-07	UP
RPSA	1.26E-09	1.409156	1.59E-07	UP
RPS4X	1.5E-09	1.507634	1.86E-07	UP
RPL36A	3.96E-09	1.077449	4.58E-07	UP
RPS28	4.32E-09	2.072983	4.98E-07	UP
ENSG00000289474	4.37E-09	1.14799	5.03E-07	UP
IGF2BP2	8.57E-09	2.058848	9.38E-07	UP
RPL29	9.32E-09	1.774007	1.01E-06	UP
RPL5	1.03E-08	1.830686	1.09E-06	UP
RPS8	1.15E-08	1.390056	1.22E-06	UP
ASXL1	1.2E-08	1.087676	1.26E-06	UP
ATP1B3	1.3E-08	1.047117	1.35E-06	UP
RPL26	3.45E-08	1.161905	3.3E-06	UP
RPS12	4.09E-08	1.801878	3.87E-06	UP
TMEM161B-DT	4.62E-08	1.777554	4.29E-06	UP
PARD3B	1.06E-07	1.30085	9.29E-06	UP
RPL7A	1.07E-07	1.449693	9.39E-06	UP
PCCA	1.19E-07	1.684827	1.03E-05	UP
RPS2	1.34E-07	1.898947	1.14E-05	UP
MT-ND3	1.47E-07	1.248811	1.23E-05	UP
RPS23	1.9E-07	1.121752	1.53E-05	UP
TMSB10	2.12E-07	1.215044	1.67E-05	UP
RPLP2	2.56E-07	1.298685	1.95E-05	UP
RACK1	4.88E-07	1.156322	3.45E-05	UP
LARGE1	8.38E-07	1.122421	5.65E-05	UP
RTN4	9.52E-07	1.070781	6.35E-05	UP
NPM1	1.01E-06	1.304028	6.64E-05	UP
HDAC4	1.16E-06	1.034933	7.61E-05	UP
LINC03077	1.88E-06	1.139578	0.000116	UP
GNAS	2.22E-06	1.018631	0.000135	UP
RPL17	3.98E-06	1.330829	0.000227	UP

LRP2	5.84E-06	1.006677	0.000318	UP
RPLP0	6.21E-06	1.006759	0.000336	UP
CXCL14	6.33E-06	2.182289	0.00034	UP
RPL6	8.11E-06	1.251443	0.000426	UP
MT-ND2	8.85E-06	1.120484	0.000463	UP
NSD3	9.29E-06	1.039389	0.000481	UP
HMGB1	9.59E-06	1.251845	0.000492	UP
RPS14	1.33E-05	1.619809	0.00065	UP
RPL36	1.95E-05	1.032814	0.000913	UP
RPL8	2.4E-05	1.243145	0.001099	UP
STAG1	2.97E-05	1.203572	0.001312	UP
RPS15	4.18E-05	1.047067	0.001769	UP
SSBP2	7.07E-05	1.154715	0.002794	UP
TPT1	8.65E-05	1.140122	0.003281	UP
RPL41	0.000115	1.357752	0.004165	UP
EIF5	0.000121	1.032903	0.004344	UP
YWHAE	0.000124	1.068703	0.004423	UP
RPL13	0.000272	1.29251	0.008661	UP
MEIS1	0.000391	1.03458	0.011602	UP
MAP2	0.000461	1.333463	0.013248	UP
RPL35A	0.000475	1.047822	0.013593	UP
RASAL2	0.000551	1.175878	0.015318	UP
PTMA	0.000578	1.246667	0.015909	UP
HERC4	0.000613	1.039931	0.016698	UP
RPS10	0.000702	1.013896	0.018625	UP
PTK2	0.000746	1.929113	0.019461	UP
RNF130	0.000859	1.457775	0.021854	UP
EIF1	0.00092	1.550977	0.02312	UP
RPS6	0.001403	1.056587	0.032434	UP
CHST9	2.84E-64	-4.04618	5.47E-60	DOWN
AQP4-AS1	3.65E-46	-4.42949	4.7E-42	DOWN
PPP2R2B	3.55E-40	-4.19703	2.74E-36	DOWN
ADCY8	3.61E-39	-2.9875	2.33E-35	DOWN
AGT	2.8E-38	-1.25984	1.54E-34	DOWN

ENSG00000289084	3.28E-38	-3.22256	1.58E-34	DOWN
C8orf34	7.78E-38	-2.65344	3.34E-34	DOWN
DNAH7	1.52E-32	-3.09568	5.35E-29	DOWN
CNTN1	3.2E-32	-2.50009	1.03E-28	DOWN
ADCY2	1.54E-31	-2.38219	4.56E-28	DOWN
FRMD5	3.35E-31	-3.51694	8.08E-28	DOWN
KCNQ5	5.61E-30	-2.38561	1.2E-26	DOWN
LRP1B	9.34E-28	-3.70767	1.9E-24	DOWN
NRG3	1.3E-27	-3.42195	2.39E-24	DOWN
ENSG00000287704	6.7E-27	-1.72813	1.18E-23	DOWN
PAMR1	9.31E-27	-1.94667	1.56E-23	DOWN
WSB1	1E-26	-2.90174	1.61E-23	DOWN
ASTN2	1.44E-26	-1.97386	2.22E-23	DOWN
CHL1	1.54E-26	-1.66242	2.29E-23	DOWN
SPON1	1.02E-24	-2.07157	1.33E-21	DOWN
TMEM232	1.03E-24	-2.17426	1.33E-21	DOWN
FOXP2	1.77E-24	-2.12328	2.21E-21	DOWN
SEMA6D	2.47E-24	-1.87621	2.98E-21	DOWN
DNAH11	2.85E-24	-2.83374	3.33E-21	DOWN
IGFBP5	6.95E-24	-2.72673	7.66E-21	DOWN
IGFBP7	1.74E-23	-1.34239	1.86E-20	DOWN
EVA1C	1.21E-22	-1.52719	1.2E-19	DOWN
TNC	7.99E-22	-2.16771	7.17E-19	DOWN
MAGI2	1.48E-21	-3.8513	1.27E-18	DOWN
ALCAM	6.2E-21	-1.83365	5.09E-18	DOWN
ARMC3	9.55E-21	-1.51145	7.53E-18	DOWN
LUZP2	3.35E-20	-1.46972	2.59E-17	DOWN
ENSG00000257545	5.21E-20	-2.26595	3.95E-17	DOWN
FTH1	1E-19	-3.37969	7.28E-17	DOWN
CTNNA2	1.78E-19	-2.1923	1.28E-16	DOWN
GRIA4	9.81E-19	-2.01339	6.27E-16	DOWN
OBI1-AS1	1.73E-18	-1.70543	1.02E-15	DOWN
ANK2	2.28E-18	-1.85259	1.3E-15	DOWN
NEBL	2.61E-18	-2.69843	1.42E-15	DOWN

RSPH1	3.99E-18	-1.13052	2.11E-15	DOWN
MDGA2	4.1E-18	-2.70795	2.14E-15	DOWN
FREM1	6.17E-18	-1.51218	3.18E-15	DOWN
RFX4	1.47E-17	-1.55717	7.35E-15	DOWN
GLIS3	2.38E-17	-2.43502	1.18E-14	DOWN
AKAP6	4.34E-17	-2.7958	2.08E-14	DOWN
MFSD4B	1.1E-16	-2.88964	4.99E-14	DOWN
DYNC2H1	1.47E-16	-1.5337	6.58E-14	DOWN
CFAP43	1.65E-16	-1.56867	7.25E-14	DOWN
NOVA1	1.88E-16	-2.92942	8.07E-14	DOWN
EFNB3	2.45E-16	-1.38905	1E-13	DOWN
ENSG00000286924	2.91E-16	-1.2348	1.17E-13	DOWN
CCDC30	4.07E-16	-1.21203	1.62E-13	DOWN
ASTN1	5.17E-16	-1.23189	2.04E-13	DOWN
CSMD3	1.35E-15	-2.19523	5.11E-13	DOWN
DANT2	1.45E-15	-1.48244	5.45E-13	DOWN
CFAP54	1.87E-15	-1.55448	6.75E-13	DOWN
WWTR1	1.95E-15	-1.37734	6.98E-13	DOWN
STK33	3.58E-15	-1.50302	1.26E-12	DOWN
HELB	5.08E-15	-1.28851	1.73E-12	DOWN
NEGR1	5.57E-15	-2.31164	1.85E-12	DOWN
DCLK1	6.41E-15	-2.37002	2.11E-12	DOWN
ROBO2	6.49E-15	-2.36344	2.12E-12	DOWN
CLU	6.55E-15	-1.11603	2.12E-12	DOWN
CFAP299	7.46E-15	-1.39742	2.38E-12	DOWN
DTNA	1.17E-14	-2.69949	3.61E-12	DOWN
CSMD1	1.18E-14	-3.36556	3.61E-12	DOWN
CSGALNACT1	1.51E-14	-1.24915	4.59E-12	DOWN
TEKT1	1.55E-14	-1.03823	4.68E-12	DOWN
DGKB	2.05E-14	-1.98511	5.99E-12	DOWN
REV3L	2.67E-14	-3.09174	7.71E-12	DOWN
FAM13C	2.93E-14	-1.24352	8.37E-12	DOWN
SERINC5	2.99E-14	-1.22651	8.48E-12	DOWN
SLC44A1	4.64E-14	-1.06944	1.29E-11	DOWN

NFIB	5.13E-14	-2.35202	1.4E-11	DOWN
LINC02649	6.59E-14	-1.72624	1.78E-11	DOWN
LYPD6	1.03E-13	-1.05174	2.72E-11	DOWN
GPI	1.33E-13	-1.26802	3.4E-11	DOWN
FGF13	1.51E-13	-1.96205	3.8E-11	DOWN
CACNA1C	1.55E-13	-2.06543	3.9E-11	DOWN
FTX	1.72E-13	-1.76436	4.28E-11	DOWN
NBEA	1.73E-13	-2.90368	4.28E-11	DOWN
SOBP	3.29E-13	-1.33951	7.93E-11	DOWN
NFIA	6.61E-13	-2.19318	1.56E-10	DOWN
DNAI4	6.92E-13	-1.0669	1.63E-10	DOWN
VWA3A	9.67E-13	-1.38396	2.2E-10	DOWN
KALRN	1.06E-12	-1.61064	2.39E-10	DOWN
NCAM1	1.08E-12	-1.82021	2.42E-10	DOWN
SPARCL1	1.08E-12	-1.57116	2.42E-10	DOWN
LINGO2	1.17E-12	-1.86225	2.6E-10	DOWN
TNIK	1.34E-12	-1.46167	2.96E-10	DOWN
GULP1	1.61E-12	-1.43407	3.52E-10	DOWN
SPAG1	1.66E-12	-1.32872	3.61E-10	DOWN
GFAP	1.81E-12	-1.49731	3.87E-10	DOWN
NEK11	1.9E-12	-1.10026	4.01E-10	DOWN
GRIK1	2.13E-12	-1.24165	4.43E-10	DOWN
DELEC1	2.21E-12	-1.88738	4.57E-10	DOWN
EGR1	2.63E-12	-1.12375	5.31E-10	DOWN
MOB3B	2.9E-12	-1.17802	5.84E-10	DOWN
SPATA6	2.99E-12	-1.68306	5.97E-10	DOWN
DCDC1	3.06E-12	-1.23675	6.08E-10	DOWN
PKIB	3.68E-12	-1.0292	7.25E-10	DOWN
FUT9	3.82E-12	-1.37972	7.49E-10	DOWN
RGMA	4.5E-12	-1.6831	8.77E-10	DOWN
CFAP44	5.88E-12	-1.10208	1.11E-09	DOWN
C1QTNF7-AS1	6.41E-12	-1.7293	1.2E-09	DOWN
CADPS2	7.22E-12	-1.4829	1.33E-09	DOWN
SLC4A4	7.27E-12	-1.55947	1.34E-09	DOWN

LRRC9	8.93E-12	-1.12303	1.61E-09	DOWN
CNTN4	9.04E-12	-1.29606	1.62E-09	DOWN
ZBTB20	9.28E-12	-1.7107	1.66E-09	DOWN
ANKFN1	9.61E-12	-1.70798	1.71E-09	DOWN
RORA	2.24E-11	-2.64159	3.84E-09	DOWN
NLGN1	3.63E-11	-1.79857	6.09E-09	DOWN
PACRG	3.63E-11	-1.50493	6.09E-09	DOWN
HYDIN	3.98E-11	-1.27277	6.6E-09	DOWN
DCLK2	4.04E-11	-1.92413	6.66E-09	DOWN
CFAP47	4.68E-11	-1.11168	7.65E-09	DOWN
EPHA6	5.48E-11	-2.5827	8.9E-09	DOWN
CCDC91	1.36E-10	-1.1237	2.06E-08	DOWN
SHROOM3	1.36E-10	-1.43712	2.06E-08	DOWN
CEP126	1.49E-10	-1.12158	2.24E-08	DOWN
CLASP2	1.54E-10	-1.34311	2.3E-08	DOWN
PCDH7	1.72E-10	-1.45399	2.55E-08	DOWN
PLXDC2	2.46E-10	-1.16081	3.56E-08	DOWN
ANK2-AS1	4.01E-10	-1.58456	5.56E-08	DOWN
MAP3K19	6.01E-10	-1.05533	8.12E-08	DOWN
ANKS1B	6.34E-10	-1.12372	8.53E-08	DOWN
ADAM12	6.49E-10	-1.13371	8.7E-08	DOWN
HOTAIRM1	6.81E-10	-1.11502	9.06E-08	DOWN
SH3GL2	1.12E-09	-1.11432	1.44E-07	DOWN
TEX9	1.81E-09	-1.06822	2.22E-07	DOWN
ARFGEF3	2.14E-09	-1.08102	2.59E-07	DOWN
DYNC2I1	2.29E-09	-1.26952	2.75E-07	DOWN
CC2D2A	2.59E-09	-1.08648	3.08E-07	DOWN
TRPS1	3.1E-09	-1.38004	3.65E-07	DOWN
CSMD2	3.41E-09	-1.02792	4E-07	DOWN
STX17-DT	5.27E-09	-1.12311	5.99E-07	DOWN
CDH10	5.71E-09	-1.04715	6.43E-07	DOWN
PRKCQ	6.52E-09	-1.02912	7.26E-07	DOWN
LINC00486	8.24E-09	-1.74387	9.09E-07	DOWN
PBX1	9.74E-09	-1.57511	1.05E-06	DOWN

GNG12-AS1	9.86E-09	-1.17453	1.06E-06	DOWN
ATXN1	1.87E-08	-1.76817	1.88E-06	DOWN
METR1	2.2E-08	-1.12085	2.18E-06	DOWN
SORBS1	2.33E-08	-1.56422	2.29E-06	DOWN
NAV2	3.3E-08	-2.32417	3.19E-06	DOWN
CADM2	3.34E-08	-1.52462	3.22E-06	DOWN
IL1RAPL1	4.27E-08	-1.5747	3.99E-06	DOWN
SNHG14	4.26E-08	-4.11022	3.99E-06	DOWN
KCNMB2	4.39E-08	-1.06045	4.09E-06	DOWN
NTN1	5.27E-08	-2.39643	4.86E-06	DOWN
TGFB2	8.57E-08	-1.03963	7.66E-06	DOWN
OPHN1	8.85E-08	-1.0552	7.89E-06	DOWN
RFX3	9.62E-08	-1.6407	8.52E-06	DOWN
BMPR1B	1.19E-07	-1.07068	1.03E-05	DOWN
CALCRL-AS1	1.42E-07	-1.15658	1.2E-05	DOWN
FTL	1.6E-07	-2.94883	1.33E-05	DOWN
APC	1.66E-07	-1.011	1.36E-05	DOWN
FBXL7	2.41E-07	-1.40055	1.86E-05	DOWN
PCLO	2.52E-07	-1.02845	1.93E-05	DOWN
ENSG00000283674	2.86E-07	-1.48805	2.15E-05	DOWN
CLASP1-AS1	2.87E-07	-1.07999	2.16E-05	DOWN
DENND2A	3.72E-07	-1.21788	2.72E-05	DOWN
ENSG00000240499	4.06E-07	-1.25598	2.92E-05	DOWN
VIM	4.57E-07	-1.34447	3.25E-05	DOWN
AHI1	6.05E-07	-1.21619	4.2E-05	DOWN
PDE4D	7.68E-07	-1.67395	5.23E-05	DOWN
NCOA1	8.64E-07	-1.18983	5.8E-05	DOWN
ABCA1	1.19E-06	-1.15224	7.72E-05	DOWN
KANK1	1.2E-06	-1.29475	7.78E-05	DOWN
ITPR2	1.32E-06	-1.17547	8.45E-05	DOWN
SCN1A	1.43E-06	-1.20146	9.1E-05	DOWN
IMMP2L	1.67E-06	-1.02401	0.000105	DOWN
MAK	2.17E-06	-1.04107	0.000132	DOWN
LRRC4C	2.49E-06	-1.23456	0.000149	DOWN

CCNH	2.56E-06	-1.12507	0.000153	DOWN
FER	2.61E-06	-1.42456	0.000155	DOWN
ENSG00000251294	2.86E-06	-1.03515	0.000168	DOWN
DST	3.36E-06	-1.99045	0.000194	DOWN
DSCAM	3.37E-06	-1.1273	0.000194	DOWN
ESRRG	3.93E-06	-1.04553	0.000225	DOWN
EPN2	4.28E-06	-1.00896	0.00024	DOWN
CKB	4.36E-06	-1.63046	0.000243	DOWN
TEX14	5.2E-06	-1.49908	0.000288	DOWN
WDPCP	9.27E-06	-1.10104	0.000481	DOWN
MYCBP2-AS1	1.06E-05	-1.03258	0.000535	DOWN
A2ML1-AS1	1.09E-05	-1.15148	0.000549	DOWN
TMSB4X	1.64E-05	-1.30374	0.000784	DOWN
TUBB2B	2.31E-05	-1.09479	0.001063	DOWN
CRB1	3.56E-05	-1.11979	0.001546	DOWN
SCN1A-AS1	4.21E-05	-1.07561	0.001779	DOWN
MAML2	4.65E-05	-2.35998	0.001947	DOWN
SYNE1	5.19E-05	-1.28123	0.002142	DOWN
TUBA1A	5.26E-05	-1.51946	0.00216	DOWN
KCND2	7.71E-05	-1.11762	0.002975	DOWN
RMST	0.000298	-1.68313	0.009345	DOWN
ENSG00000285664	0.000306	-1.01489	0.009586	DOWN
NCKAP5	0.000464	-1.24728	0.013319	DOWN
FMN2	0.000587	-1.01118	0.016077	DOWN
GAPDH	0.000598	-1.12397	0.016338	DOWN
DLG2	0.00066	-1.20077	0.017751	DOWN
LINC01473	0.000773	-1.08403	0.020041	DOWN
MBD5	0.001137	-1.47709	0.027484	DOWN
ADGRL3	0.002245	-1.22031	0.047122	DOWN

Enrichment of Down-regulated genes in Astrocyte cluster

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> -value	gene ID	count
GO:0007409	axonogenesis	23/165	8.63E-12	1.23157E-08	1.03E-08	CNTN1/CHL1/SEMA6D/ALCAM/CTNNA2/EFNB3/DCLK1/ROBO2/NFIB/FGF13/KALRN/NCAM1/RGMA/CNTN4/EPHA6/PRKCQ/METRNTNTN1/OPHN1/BMPR1B/LRRC4C/DSCAM/TUBB2B	23
GO:0010975	regulation of neuron projection development	23/165	1.08E-11	1.23157E-08	1.03E-08	CNTN1/SEMA6D/MAGI2/CTNNA2/EFNB3/CSMD3/NEGR1/ROBO2/FGF13/TNIFK/GFAP/FUT9/RGMA/NLGN1/METRNTN1/IL1RAPL1/NTN1/VIM/KANK1/LRRC4C/DSCAM/TUBB2B/SYNE1	23
GO:0060271	cilium assembly	21/165	1.72E-11	1.23157E-08	1.03E-08	DNAH7/RSPH1/RFX4/DYNC2H1/CFAP43/CFAP54/WWTR1/TEKT1/DNAI4/SPAG1/SPATA6/CFAP44/HYDIN/CFAP47/CEP126/DYNC2H1/CC2D2A/RFX3/AHI1/MAK/WDRCP	21

GO:0007411	axon guidance	17/165	2.38E-11	1.23157E-08	1.03E-08	CNTN1/CHL1/SEMA6D/ALCAM/EFNB3/ROBO2/NFIB/KALRN/NCAM1/CNTN4/EPHA6/PRKCQ/NTN1/OPHN1/BMPRI1B/DSCAM/TUBB2B	17
GO:0097485	neuron projection guidance	17/165	2.38E-11	1.23157E-08	1.03E-08	CNTN1/CHL1/SEMA6D/ALCAM/EFNB3/ROBO2/NFIB/KALRN/NCAM1/CNTN4/EPHA6/PRKCQ/NTN1/OPHN1/BMPRI1B/DSCAM/TUBB2B	17
GO:0034329	cell junction assembly	22/165	5.51E-11	2.37984E-08	1.99E-08	AGT/NRG3/ANK2/EFNB3/NEGR1/ROBO2/FGF13/LINGO2/NLGN1/CLASP2/CDH10/SORBS1/IL1RAPL1/NTN1/OPHN1/APC/PCLO/FER/DST/DSCAM/WDPCP/ADGRL3	22
GO:0044782	cilium organization	21/165	6.82E-11	2.52402E-08	2.12E-08	DNAH7/RSPH1/RFX4/DYNC2H1/CFAP43/CFAP54/WWTR1/TEKT1/DNAI4/SPAG1/SPATA6/CFAP44/HYDIN/CFAP47/CEP126/DYNC2I1/CC2D2A/RFX3/AHI1/MAK/WDPCP	21

GO:0050808	synapse organization	20/165	8.87E-09	2.87126E-06	2.41E-06	NRG3/TNC/CTNNA2/EFNB3/NEGR1/ROBO2/FGF13/NFIA/SPARCL1/LINGO2/NLGN1/CDH10/IL1RAPL1/NTN1/OPHN1/PCLO/LRRC4C/DSCAM/TUBA1A/ADGRL3	20
GO:0007626	locomotory behavior	13/165	2.48E-08	7.14204E-06	5.99E-06	ADCY8/CNTN1/CHL1/EFNB3/ASTN1/NEGR1/SOBP/EGR1/NAV2/SCN1A/DSCAM/TUBA1A/KCND2	13
GO:0007018	microtubule-based movement	18/165	3.07E-08	7.94538E-06	6.66E-06	DNAH7/DNAH11/DYNC2H1/CFAP43/CFAP54/TEKT1/DNAI4/CFAP44/HYDIN/CFAP47/DYNC2I1/RFX3/MAK/DST/WDPCP/TUBA1A/FMN2/DLG2	18
GO:0001578	microtubule bundle formation	10/165	1.49E-07	3.37604E-05	2.83E-05	DNAH7/RSPH1/CFAP43/DNAI4/SPAG1/CFAP44/HYDIN/CFAP47/CC2D2A/NCKAP5	10

GO:0035082	axoneme assembly	9/165	1.62E-07	3.37604E-05	2.83E-05	DNAH7/RSPH1/CFAP43/DNAI4/SPAG1/CFAP44/HYDIN/CFAP47/CC2D2A	9
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	14/165	1.69E-07	3.37604E-05	2.83E-05	ALCAM/ROBO2/SPARCL1/CDNTN4/NLGN1/PCDH7/CDH10/CADM2/IL1RAPL1/TGFB2/LRRC4C/DSCAM/CRB1/ADGRL3	14
GO:0007416	synapse assembly	12/165	1.98E-07	3.66056E-05	3.07E-05	NRG3/EFNB3/NEGR1/ROBO2/FGF13/LINGO2/NLGN1/IL1RAPL1/NTN1/PCLO/DSCAM/ADGRL3	12
GO:0001764	neuron migration	11/165	4.57E-07	7.88945E-05	6.61E-05	NRG3/ASTN2/CHL1/CTNNA2/ASTN1/DCLK1/FGF13/NTN1/TUBB2B/TUBA1A/ADGRL3	11

GO:0044458	motile cilium assembly	7/165	1.74E-06	0.000269588	0.000226	CFAP43/CFAP54/SPATA6/CFAP44/CFAP47/CC2D2A/AHI1	7
GO:0003341	cilium movement	11/165	1.77E-06	0.000269588	0.000226	DNAH7/DNAH11/DYNC2H1/CFAP43/CFAP54/TEKT1/DNAI4/CFAP44/HYDIN/CFAP47/RFX3	11
GO:0099111	microtubule-based transport	11/165	2.95E-06	0.000425022	0.000356	DNAH11/DYNC2H1/CFAP43/CFAP54/DYNC2I1/RFX3/MAK/DST/WDPCP/TUBA1A/DLG2	11
GO:0010977	negative regulation of neuron projection development	9/165	3.95E-06	0.00053915	0.000452	SEMA6D/EFNB3/FGF13/GFAP/RGMA/NLGN1/NTN1/VIM/KANK1	9

GO:0031345	negative regulation of cell projection organization	10/165	7.51E-06	0.000962132	0.000806	SEMA6D/EFNB3/FGF13/GFAP/RGMA/NLGN1/NTN1/VIM/KANK1/MAK	10
GO:0016049	cell growth	16/165	7.8E-06	0.000962132	0.000806	AGT/NRG3/SEMA6D/IGFBP5/IGFBP7/TNC/ALCAM/AKAP6/DCLK1/FGF13/RGMA/SH3GL2/PRKCQ/NTN1/TGFB2/DSCAM	16
GO:0007158	neuron cell-cell adhesion	4/165	9.45E-06	0.001113124	0.000933	ASTN2/ASTN1/CNTN4/NLGN1	4
GO:0050770	regulation of axonogenesis	9/165	1.01E-05	0.001133342	0.00095	SEMA6D/EFNB3/ROBO2/FGF13/RGMA/METRNL/NTN1/LRRC4C/DSCAM	9

GO:0001539	cilium or flagellum-dependent cell motility	9/165	1.36E-05	0.001409862	0.001182	DNAH7/DNAH11/DYNC2H1/CFAP43/CFAP54/TEKT1/CFA P44/CFAP47/RFX3	9
GO:0060285	cilium-dependent cell motility	9/165	1.36E-05	0.001409862	0.001182	DNAH7/DNAH11/DYNC2H1/CFAP43/CFAP54/TEKT1/CFA P44/CFAP47/RFX3	9
GO:0031346	positive regulation of cell projection organization	13/165	1.51E-05	0.001503088	0.00126	CNTN1/MAGI2/NEGR1/ROBO2/FUT9/RGMA/NLGN1/ME TRN/IL1RAPL1/NTN1/APC/D SCAM/TUBB2B	13
GO:1901888	regulation of cell junction assembly	10/165	1.86E-05	0.001780444	0.001492	AGT/EFNB3/NEGR1/ROBO2/LINGO2/NLGN1/CLASP2/IL1 RAPL1/NTN1/WDPCP	10

GO:0072001	renal system development	12/165	2.9E-05	0.002683886	0.002249	AGT/MAGI2/DYNC2H1/WWTR1/ROBO2/NFIA/EGR1/CC2D2A/PBX1/TGFB2/AHI1/WDP CP	12
GO:0060560	developmental growth involved in morphogenesis	10/165	5.89E-05	0.005261926	0.00441	SEMA6D/TNC/MAGI2/ALCAM/DCLK1/FGF13/RGMA/SH3GL2/NTN1/DSCAM	10
GO:0030900	forebrain development	13/165	6.21E-05	0.005361206	0.004493	NRG3/FOXP2/RFX4/DYNC2H1/DCLK1/ROBO2/NFIB/FGF13/DCLK2/OPHN1/NCOA1/TUBB2B/TUBA1A	13
GO:0051963	regulation of synapse assembly	7/165	6.46E-05	0.005400689	0.004526	EFNB3/NEGR1/ROBO2/LINGO2/NLGN1/IL1RAPL1/NTN1	7

GO:0030902	hindbrain development	8/165	7.31E-05	0.005916822	0.004959	CNTN1/CTNNA2/NFIB/RORA/OPHN1/AHI1/NCOA1/TUBA1A	8
GO:0060294	cilium movement involved in cell motility	8/165	7.64E-05	0.005999184	0.005028	DNAH7/DNAH11/DYNC2H1/CFAP43/CFAP54/TEKT1/CFAP44/CFAP47	8
GO:0001558	regulation of cell growth	13/165	7.93E-05	0.006044204	0.005066	AGT/NRG3/SEMA6D/IGFBP5/IGFBP7/TNC/AKAP6/FGF13/RGMA/PRKCQ/NTN1/TGFB2/DSCAM	13
GO:0022612	gland morphogenesis	7/165	9.92E-05	0.007345888	0.006157	NRG3/IGFBP5/TNC/CSMD1/NFIB/NTN1/TGFB2	7

GO:0001822	kidney development	11/165	0.000103	0.007419191	0.006218	AGT/MAGI2/DYNC2H1/WWTR1/ROBO2/EGR1/CC2D2A/PBX1/TGFB2/AHI1/WDPCP	11
GO:0042391	regulation of membrane potential	13/165	0.000135	0.009484074	0.007949	KCNQ5/GRIA4/ANK2/AKAP6/FGF13/CACNA1C/GRIK1/SLC4A4/NLGN1/KCNMB2/SCN1A/SYNE1/KCND2	13
GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	4/165	0.000148	0.010058238	0.00843	ANK2/AKAP6/CACNA1C/PDE4D	4
GO:0021537	telencephalon development	10/165	0.000163	0.010654736	0.00893	NRG3/FOXP2/RFX4/ROBO2/NFIB/FGF13/DCLK2/NCOA1/TUBB2B/TUBA1A	10

GO:0014009	glial cell proliferation	5/165	0.000164	0.010654736	0.00893	CLU/NFIB/NFIA/GFAP/NTN1	5
GO:0001654	eye development	12/165	0.000173	0.010962628	0.009188	NFIB/CACNA1C/NFIA/CC2D2A/PBX1/TGFB2/BMPRI1B/VI M/AHI1/DSCAM/WDPCP/C RB1	12
GO:0007163	establishment or maintenance of cell polarity	9/165	0.000184	0.01129495	0.009467	FGF13/ANKFN1/CLASP2/OP HN1/KANK1/DST/WDPCP/C RB1/DLG2	9
GO:0150063	visual system development	12/165	0.000191	0.01129495	0.009467	NFIB/CACNA1C/NFIA/CC2D2A/PBX1/TGFB2/BMPRI1B/VI M/AHI1/DSCAM/WDPCP/C RB1	12

GO:0021953	central nervous system neuron differentiation	8/165	0.000196	0.01129495	0.009467	MDGA2/DYNC2H1/DCLK1/NFIB/RORA/DCLK2/OPHN1/BMPR1B	8
GO:0042063	gliogenesis	11/165	0.000196	0.01129495	0.009467	CNTN1/CLU/NFIB/NFIA/GFAP/METR/NTN1/TGFB2/VIM/CRB1/TUBA1A	11
GO:0048880	sensory system development	12/165	0.000219	0.012311024	0.010318	NFIB/CACNA1C/NFIA/CC2D2A/PBX1/TGFB2/BMPR1B/VIM/AHI1/DSCAM/WDPCP/CRB1	12
GO:0048813	dendrite morphogenesis	7/165	0.000223	0.012311024	0.010318	CTNNA2/DCLK1/TNFRK1/NLGN1/IL1RAPL1/DSCAM/SYNE1	7

GO:0043010	camera-type eye development	11/165	0.000228	0.012322439	0.010328	NFIB/CACNA1C/NFIA/CC2D2A/TGFB2/BMPRI1/DSCAM/WDPCP/CRB1	11
GO:0086004	regulation of cardiac muscle cell contraction	4/165	0.000239	0.012631808	0.010587	ANK2/FGF13/CACNA1C/PDE4D	4
GO:0051651	maintenance of location in cell	9/165	0.000245	0.012696307	0.010641	FTH1/ANK2/AKAP6/CACNA1C/FTL/PDE4D/ITPR2/TMSB4X/SYNE1	9
GO:0031503	protein-containing complex localization	8/165	0.000253	0.012878054	0.010793	DYNC2H1/NLGN1/DYNC2I1/OPHN1/MAK/WDPCP/SYNE1/DLG2	8

GO:0048588	developmental cell growth	9/165	0.000261	0.012990498	0.010888	SEMA6D/ALCAM/AKAP6/DCLK1/FGF13/RGMA/SH3GL2/NTN1/DSCAM	9
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	4/165	0.000267	0.01304927	0.010937	ANK2/AKAP6/CACNA1C/PDE4D	4
GO:0050771	negative regulation of axonogenesis	5/165	0.00028	0.013412719	0.011242	SEMA6D/EFNB3/FGF13/RGMA/NTN1	5
GO:1903514	release of sequestered calcium ion into cytosol by endoplasmic reticulum	4/165	0.000297	0.013803302	0.011569	ANK2/AKAP6/CACNA1C/PDE4D	4

GO:0001508	action potential	7/165	0.000302	0.013803302	0.011569	ANK2/AKAP6/FGF13/CACNA1C/KCNMB2/SCN1A/KCND2	7
GO:0050807	regulation of synapse organization	9/165	0.000304	0.013803302	0.011569	CTNNA2/EFNB3/NEGR1/ROBO2/LINGO2/NLGN1/IL1RAPL1/NTN1/TUBA1A	9
GO:0050803	regulation of synapse structure or activity	9/165	0.000363	0.016205999	0.013583	CTNNA2/EFNB3/NEGR1/ROBO2/LINGO2/NLGN1/IL1RAPL1/NTN1/TUBA1A	9
GO:0010001	glial cell differentiation	9/165	0.000384	0.016884154	0.014151	CNTN1/CLU/NFIB/NFIA/GFAP/METR/VIM/CRB1/TUBA1A	9

GO:0042698	ovulation cycle	5/165	0.000393	0.016980142	0.014231	ROBO2/EGR1/TGFB2/BMPRI B/NCOA1	5
GO:0052652	cyclic purine nucleotide metabolic process	4/165	0.000403	0.017118997	0.014348	ADCY8/ADCY2/RORA/PDE4 D	4
GO:0003015	heart process	9/165	0.000419	0.01751083	0.014676	AGT/ANK2/WWTR1/FGF13/C ACNA1C/TGFB2/PDE4D/SCN 1A/KCND2	9
GO:0009187	cyclic nucleotide metabolic process	4/165	0.000444	0.017681893	0.01482	ADCY8/ADCY2/RORA/PDE4 D	4

GO:0120316	sperm flagellum assembly	4/165	0.000444	0.017681893	0.01482	CFAP43/CFAP54/CFAP44/CFAP47	4
GO:1903115	regulation of actin filament-based movement	4/165	0.000444	0.017681893	0.01482	ANK2/FGF13/CACNA1C/PDE4D	4
GO:0010976	positive regulation of neuron projection development	7/165	0.000486	0.019076036	0.015988	CNTN1/MAGI2/NEGR1/FUT9/RGMA/NLGN1/TUBB2B	7
GO:0060041	retina development in camera-type eye	7/165	0.000505	0.019514473	0.016356	NFIB/NFIA/TGFB2/BMPRI1/AHI1/DSCAM/CRB1	7

GO:0003351	epithelial cilium movement involved in extracellular fluid movement	4/165	0.000533	0.019659985	0.016478	DNAH11/CFAP43/CFAP54/RFX3	4
GO:0060443	mammary gland morphogenesis	4/165	0.000533	0.019659985	0.016478	NRG3/IGFBP5/CSMD1/NTN1	4
GO:0070296	sarcoplasmic reticulum calcium ion transport	4/165	0.000533	0.019659985	0.016478	ANK2/AKAP6/CACNA1C/PDE4D	4
GO:0086003	cardiac muscle cell contraction	5/165	0.000539	0.019659985	0.016478	ANK2/FGF13/CACNA1C/PDE4D/SCN1A	5

GO:0007019	microtubule depolymerization	4/165	0.000635	0.0225437	0.018894	FGF13/CLASP2/APC/NCKAP5	4
GO:0008038	neuron recognition	4/165	0.000635	0.0225437	0.018894	EFNB3/ROBO2/CNTN4/DSCAM	4
GO:1902904	negative regulation of supramolecular fiber organization	7/165	0.000676	0.023661281	0.019831	CTNNA2/CLU/FGF13/CLASP2/APC/KANK1/TMSB4X	7
GO:0006858	extracellular transport	4/165	0.000691	0.023869925	0.020006	DNAH11/CFAP43/CFAP54/RFX3	4

GO:0050919	negative chemotaxis	4/165	0.00075	0.025241055	0.021155	NRG3/SEMA6D/ROBO2/NTN1	4
GO:0099054	presynapse assembly	4/165	0.00075	0.025241055	0.021155	EFNB3/NLGN1/IL1RAPL1/PCLO	4
GO:0010970	transport along microtubule	7/165	0.000832	0.027390007	0.022956	DYNC2H1/DYNC2I1/MAK/DST/WDPCP/TUBA1A/DLG2	7
GO:0051960	regulation of nervous system development	12/165	0.000835	0.027390007	0.022956	SEMA6D/EFNB3/ROBO2/FGF13/LINGO2/GFAP/RGMA/NLGN1/METRNL/IL1RAPL1/NTN1/DSCAM	12

GO:0042073	intraciliary transport	4/165	0.000879	0.028119054	0.023567	DYNC2H1/DYNC2I1/MAK/WPCP	4
GO:2001259	positive regulation of cation channel activity	4/165	0.000879	0.028119054	0.023567	ANK2/AKAP6/FGF13/TMSB4X	4
GO:0007389	pattern specification process	12/165	0.000985	0.031119528	0.026082	NRG3/DNAH11/RFX4/DYNC2H1/ROBO2/SHROOM3/CC2D2A/PBX1/RFX3/BMPR1B/ALDH1	12
GO:0031290	retinal ganglion cell axon guidance	3/165	0.001022	0.031122649	0.026085	ALCAM/ROBO2/BMPR1B	3

GO:0046058	cAMP metabolic process	3/165	0.001022	0.031122649	0.026085	ADCY8/ADCY2/PDE4D	3
GO:0048013	ephrin receptor signaling pathway	4/165	0.001023	0.031122649	0.026085	EFNB3/KALRN/EPHA6/ANK S1B	4
GO:0016358	dendrite development	8/165	0.001045	0.031122649	0.026085	CTNNA2/CSMD3/DCLK1/TNFI K/NLGN1/IL1RAPL1/DSCAM /SYNE1	8
GO:0051235	maintenance of location	10/165	0.001045	0.031122649	0.026085	FTH1/ANK2/AKAP6/CACNA 1C/FTL/PDE4D/ABCA1/ITPR 2/TMSB4X/SYNE1	10

GO:0099172	presynapse organization	4/165	0.001101	0.032406237	0.02716	EFNB3/NLGN1/IL1RAPL1/PCLO	4
GO:2000114	regulation of establishment of cell polarity	3/165	0.001161	0.033667503	0.028218	ANKFN1/KANK1/WDPCP	3
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	4/165	0.001182	0.033667503	0.028218	ALCAM/NLGN1/IL1RAPL1/CRB1	4
GO:0048260	positive regulation of receptor-mediated endocytosis	4/165	0.001182	0.033667503	0.028218	MAGI2/CLU/AHI1/SYNE1	4

GO:0050804	modulation of chemical synaptic transmission	12/165	0.001262	0.035391037	0.029662	ADCY8/NRG3/GRIA4/EFNB3 /GFAP/GRIK1/CNTN4/NLGN 1/OPHN1/LRRC4C/TUBB2B/S YNE1	12
GO:0001738	morphogenesis of a polarized epithelium	5/165	0.001282	0.035391037	0.029662	ASTN2/MAGI2/OPHN1/AHI1/ WDPCP	5
GO:0099177	regulation of trans-synaptic signaling	12/165	0.001284	0.035391037	0.029662	ADCY8/NRG3/GRIA4/EFNB3 /GFAP/GRIK1/CNTN4/NLGN 1/OPHN1/LRRC4C/TUBB2B/S YNE1	12
GO:0010842	retina layer formation	3/165	0.001311	0.035749409	0.029962	AHI1/DSCAM/CRB1	3

GO:0060047	heart contraction	8/165	0.001366	0.036861882	0.030895	AGT/ANK2/FGF13/CACNA1C /TGFB2/PDE4D/SCN1A/KCN D2	8
GO:0007026	negative regulation of microtubule depolymerization	3/165	0.001472	0.038925185	0.032624	FGF13/CLASP2/APC	3
GO:0099558	maintenance of synapse structure	3/165	0.001472	0.038925185	0.032624	NLGN1/OPHN1/PCLO	3
GO:0001964	startle response	3/165	0.001646	0.042218989	0.035385	CTNNA2/CSMD1/TUBA1A	3

GO:0032878	regulation of establishment or maintenance of cell polarity	3/165	0.001646	0.042218989	0.035385	ANKFN1/KANK1/WDPCP	3
GO:0099560	synaptic membrane adhesion	3/165	0.001646	0.042218989	0.035385	SPARCL1/CDH10/LRRC4C	3
GO:0035107	appendage morphogenesis	6/165	0.001807	0.045193814	0.037878	DYNC2H1/CACNA1C/NFIA/PBX1/TGFB2/WDPCP	6
GO:0035108	limb morphogenesis	6/165	0.001807	0.045193814	0.037878	DYNC2H1/CACNA1C/NFIA/PBX1/TGFB2/WDPCP	6

GO:0007288	sperm axoneme assembly	3/165	0.001831	0.045193814	0.037878	CFAP43/CFAP44/CFAP47	3
GO:0086010	membrane depolarization during action potential	3/165	0.001831	0.045193814	0.037878	ANK2/CACNA1C/SCN1A	3
GO:0050890	cognition	9/165	0.001934	0.046879203	0.039291	ADCY8/CHL1/DNAH11/CSMD1/GPI/FGF13/SOBP/ATXN1/TUBA1A	9
GO:0007224	smoothened signaling pathway	6/165	0.001936	0.046879203	0.039291	RFX4/DYNC2H1/RORA/CC2D2A/WDPCP/TUBA1A	6

GO:1903522	regulation of blood circulation	8/165	0.00199	0.047738364	0.040011	AGT/ANK2/FGF13/CACNA1C /KCNMB2/TGFB2/PDE4D/KC ND2	8
GO:0098901	regulation of cardiac muscle cell action potential	3/165	0.00203	0.04781041	0.040071	ANK2/FGF13/CACNA1C	3
GO:0099505	regulation of presynaptic membrane potential	3/165	0.00203	0.04781041	0.040071	KCNQ5/GRIA4/SCN1A	3
GO:0072073	kidney epithelium development	6/165	0.002072	0.048354072	0.040527	AGT/MAGI2/WWTR1/ROBO2 /PBX1/AHI1	6

GO:0097306	cellular response to alcohol	5/165	0.002114	0.048898384	0.040983	ADCY8/ADCY2/TNC/ABCA1 /ITPR2	5
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Enrichment of Up-regulated genes in Astrocyte cluster

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> -value	gene ID	count
GO:0002181	cytoplasmic translation	46/110	1.61E-68	3.559E-65	3.12E-65	RPS18/RPL10/RPS3/RPL39/RPL28/RPL37/RPL12/RPL14/RPL11/RPS15A/RPL32/RPS21/RPL34/RPL18/RPS27/RPL18A/RPS3A/RPS7/RPS9/RPSA/RPS4X/RPL36A/RPS28/RPL29/RPL5/RPS8/RPL26/RPS12/RPL7A/RPS2/RPS23/RPLP2/RACK1/RPL17/RPLP0/RPL6/RPS14/RPL36/RPL8/RPS15/RPL41/EIF5/RPL13/RPL35A/RPS10/RPS6	46
GO:0042254	ribosome biogenesis	26/110	1.63E-22	1.799E-19	1.58E-19	RPL10/RPL14/RPL11/RPS15A/RPS21/RPS27/RPS3A/RPS7/RPS9/RPSA/RPS4X/RPS28/RPL5/RPS8/RPL26/RPS12/RPL7A/RPS23/NPM1/RPLP0/RPL6/RPS14/RPS15/EIF5/RPL35A/RPS6	26
GO:0042274	ribosomal small subunit biogenesis	16/110	9.97E-19	7.327E-16	6.42E-16	RPS15A/RPS21/RPS27/RPS3A/RPS7/RPS9/RPSA/RPS4X/RPS28/RPS8/RPS12/RPS23/NPM1/RPS14/RPS15/RPS6	16
GO:0042255	ribosome assembly	12/110	2.12E-15	1.169E-12	1.02E-12	RPL10/RPL11/RPS27/RPSA/RPS28/RPL5/NPM1/RPLP0/RPL6/RPS14/RPS15/EIF5	12

GO:0042273	ribosomal large subunit biogenesis	10/110	2.07E-11	8.722E-09	7.64E-09	RPL10/RPL14/RPL11/RPL5/RPL26/RPL7A/NPM1/RPLP0/RPL6/RPL35A	10
GO:0140694	non-membrane-bounded organelle assembly	18/110	2.37E-11	8.722E-09	7.64E-09	RPL10/RPS3/KRT19/RPL11/RPS27/TNNT1/FXR1/RPSA/RPS28/RPL5/RPS23/NPM1/RPLP0/RPL6/RPS14/STAG1/RPS15/EIF5	18
GO:0006364	rRNA processing	14/110	5.24E-11	1.648E-08	1.44E-08	RPL14/RPL11/RPS21/RPS27/RPS7/RPS28/RPL5/RPS8/RPL26/RPL7A/RPS14/RPS15/RPL35A/RPS6	14
GO:0016072	rRNA metabolic process	14/110	4.33E-10	1.193E-07	1.05E-07	RPL14/RPL11/RPS21/RPS27/RPS7/RPS28/RPL5/RPS8/RPL26/RPL7A/RPS14/RPS15/RPL35A/RPS6	14
GO:0022618	protein-RNA complex assembly	13/110	1.13E-09	2.776E-07	2.43E-07	HSP90AB1/RPL10/RPL11/RPS27/HSP90AA1/RPSA/RPS28/RPL5/RPLP0/RPL6/RPS14/RPS15/EIF5	13
GO:0071826	protein-RNA complex organization	13/110	1.7E-09	3.758E-07	3.29E-07	HSP90AB1/RPL10/RPL11/RPS27/HSP90AA1/RPSA/RPS28/RPL5/RPLP0/RPL6/RPS14/RPS15/EIF5	13
GO:1901796	regulation of signal transduction by p53 class mediator	9/110	1.24E-08	2.49E-06	2.18E-06	RPL37/RPL11/TRIM24/SOX4/RPS7/RPL5/RPL26/NPM1/RPS15	9

GO:0034470	ncRNA processing	15/110	3.9E-08	7.157E-06	6.27E-06	H19/RPL14/RPL11/RPS21/RPS27/RPS7/RPS28/RPL5/RPS8/RPL26/RPL7A/RPS14/RPS15/RPL35A/RPS6	15
GO:0000028	ribosomal small subunit assembly	5/110	6.69E-08	1.135E-05	9.94E-06	RPS27/RPSA/RPS28/RPS14/RPS15	5
GO:0000027	ribosomal large subunit assembly	5/110	3.66E-07	5.769E-05	5.05E-05	RPL10/RPL11/RPL5/RPLP0/RPL6	5
GO:0050821	protein stabilization	10/110	5.66E-07	8.32E-05	7.29E-05	HSP90AB1/EPHA4/RPL11/SOX4/HSP90AA1/RPS7/RPL5/ATP1B3/RTN4/NPM1	10
GO:0051897	positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	9/110	7.08E-07	9.749E-05	8.54E-05	H19/HSP90AB1/IGF2/FN1/FGFR1/HSP90AA1/RTN4/LRP2/PTK2	9
GO:1901798	positive regulation of signal transduction by p53 class mediator	5/110	7.79E-07	9.965E-05	8.73E-05	RPL37/RPL11/RPS7/RPL26/RPS15	5
GO:1901873	regulation of post-translational protein modification	11/110	8.43E-07	9.965E-05	8.73E-05	HSP90AB1/RPS3/RPL11/AUTS2/SOX4/HSP90AA1/RPS7/RPL5/RPS2/NPM1/HDAC4	11

GO:0072331	signal transduction by p53 class mediator	9/110	8.59E-07	9.965E-05	8.73E-05	RPL37/RPL11/TRIM24/SOX4/RPS7/RPL5/RPL26/NPM1/RPS15	9
GO:1903320	regulation of protein modification by small protein conjugation or removal	10/110	1.58E-06	0.0001746	0.000153	HSP90AB1/RPS3/RPL11/SOX4/HSP90AA1/RPS7/RPL5/RPS2/NPM1/HDAC4	10
GO:0051896	regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	10/110	1.9E-06	0.0001997	0.000175	H19/HSP90AB1/IGF2/FN1/FGFR1/HSP90AA1/RACK1/RTN4/LRP2/PTK2	10
GO:0031396	regulation of protein ubiquitination	9/110	2.6E-06	0.0002605	0.000228	HSP90AB1/RPS3/RPL11/SOX4/HSP90AA1/RPS7/RPL5/RPS2/NPM1	9
GO:0031647	regulation of protein stability	11/110	3.13E-06	0.0002995	0.000262	HSP90AB1/EPHA4/RPL11/TRIM24/SOX4/HSP90AA1/RPS7/RPL5/ATP1B3/RTN4/NPM1	11
GO:0048675	axon extension	7/110	6.9E-06	0.0006337	0.000555	HSP90AB1/FN1/MAP1B/AUTS2/HSP90AA1/RTN4/MAP2	7
GO:0043491	phosphatidylinositol 3-kinase/protein kinase B signal transduction	10/110	7.63E-06	0.0006724	0.000589	H19/HSP90AB1/IGF2/FN1/FGFR1/HSP90AA1/RACK1/RTN4/LRP2/PTK2	10

GO:0048588	developmental cell growth	9/110	1.1E-05	0.0009354	0.000819	HSP90AB1/FN1/MAP1B/AUTS2/HSP90AA1/EXT1/RTN4/MEIS1/MAP2	9
GO:0060485	mesenchyme development	10/110	2.16E-05	0.0017394	0.001524	COL1A1/HMGA2/EPHA4/FN1/FGFR1/SOX4/RPS7/EXT1/RTN4/PTK2	10
GO:0032070	regulation of deoxyribonuclease activity	3/110	2.25E-05	0.0017394	0.001524	RPS3/NPM1/HMGB1	3
GO:0048762	mesenchymal cell differentiation	9/110	2.29E-05	0.0017394	0.001524	COL1A1/HMGA2/EPHA4/FN1/FGFR1/RPS7/EXT1/RTN4/PTK2	9
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	5/110	3.56E-05	0.002617	0.002292	RPS3/RPL11/RPS7/RPL26/RACK1	5
GO:1903051	negative regulation of proteolysis involved in protein catabolic process	5/110	4.78E-05	0.003399	0.002977	HSP90AB1/EPHA4/RPL11/RPS7/RPL5	5
GO:0034250	positive regulation of amide metabolic process	7/110	5.99E-05	0.0041243	0.003613	EPHA4/SOX4/FXR1/RPS4X/RPL5/RPL26/NPM1	7

GO:0051438	regulation of ubiquitin-protein transferase activity	4/110	7.68E-05	0.0051311	0.004494	RPL11/RPS7/RPL5/RPS2	4
GO:0001764	neuron migration	7/110	8.01E-05	0.0051951	0.00455	COL3A1/MAP1B/FGFR1/AUTS2/HSP90AA1/LARGE1/YWHAE	7
GO:0051444	negative regulation of ubiquitin-protein transferase activity	3/110	8.33E-05	0.0052477	0.004597	RPL11/RPS7/RPL5	3
GO:1990138	neuron projection extension	7/110	8.6E-05	0.0052648	0.004612	HSP90AB1/FN1/MAP1B/AUTS2/HSP90AA1/RTN4/MAP2	7
GO:0060560	developmental growth involved in morphogenesis	8/110	9.18E-05	0.0053554	0.004691	HSP90AB1/FN1/MAP1B/AUTS2/HSP90AA1/EXT1/RTN4/MAP2	8
GO:0031397	negative regulation of protein ubiquitination	5/110	9.25E-05	0.0053554	0.004691	RPS3/RPL11/SOX4/RPS7/RPL5	5
GO:0050767	regulation of neurogenesis	10/110	9.48E-05	0.0053554	0.004691	CUX2/SOX11/EPHA4/FN1/MAP1B/NAP1L1/FXR1/RTN4/LRP2/MAP2	10

GO:1904666	regulation of ubiquitin protein ligase activity	3/110	0.000148	0.0080649	0.007064	RPL11/RPS7/RPL5	3
GO:0051098	regulation of binding	8/110	0.00015	0.0080649	0.007064	HMGA2/SOX11/EPHA4/RPL11/RACK 1/HDAC4/HMGB1/MAP2	8
GO:0016049	cell growth	11/110	0.000154	0.0080973	0.007093	HSP90AB1/FN1/MAP1B/AUTS2/HSP9 0AA1/EXT1/RACK1/RTN4/NPM1/MEI S1/MAP2	11
GO:0045727	positive regulation of translation	6/110	0.000177	0.0090804	0.007954	SOX4/FXR1/RPS4X/RPL5/RPL26/NP M1	6
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	5/110	0.000182	0.0091214	0.00799	RPS3/RPL11/SOX4/RPS7/RPL5	5
GO:0021537	telencephalon development	8/110	0.000214	0.0104784	0.009178	COL3A1/ZSWIM6/FXR1/SLC38A2/EX T1/LARGE1/RTN4/YWHA	8
GO:0035264	multicellular organism growth	6/110	0.000222	0.0106439	0.009323	COL3A1/ARID5B/IGF2/EXT1/LARGE 1/RASAL2	6

GO:0030490	maturation of SSU-rRNA	4/110	0.000257	0.0116291	0.010186 RPS21/RPS28/RPS8/RPS14	4
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process	4/110	0.000257	0.0116291	0.010186 HSP90AB1/RPL11/RPS7/RPL5	4
GO:1901874	negative regulation of post-translational protein modification	5/110	0.000259	0.0116291	0.010186 RPS3/RPL11/SOX4/RPS7/RPL5	5
GO:0060348	bone development	7/110	0.000267	0.011754	0.010296 COL3A1/COL1A1/EXT1/ASXL1/LARGE1/GNAS/RPL13	7
GO:0032069	regulation of nuclease activity	3/110	0.000274	0.0118321	0.010364 RPS3/NPM1/HMGB1	3
GO:0007409	axonogenesis	10/110	0.000291	0.0123267	0.010797 HSP90AB1/EPHA4/FN1/MAP1B/AUTS2/HSP90AA1/EXT1/RTN4/MAP2/PTK2	10
GO:0030010	establishment of cell polarity	6/110	0.000306	0.0127261	0.011147 HSP90AB1/MAP1B/HSP90AA1/PARD3B/RACK1/PTK2	6

GO:0040029	epigenetic regulation of gene expression	7/110	0.00039	0.0159043	0.013931	HMGA2/IGF2/ZDBF2/KCNQ1OT1/HDAC4/HMGB1/EIF1	7
GO:0051960	regulation of nervous system development	10/110	0.000397	0.0159043	0.013931	CUX2/SOX11/EPHA4/FN1/MAP1B/NAP1L1/FXR1/RTN4/LRP2/MAP2	10
GO:1903050	regulation of proteolysis involved in protein catabolic process	7/110	0.000456	0.0179392	0.015713	HSP90AB1/EPHA4/RPL11/RPS7/RPL5/RACK1/PTK2	7
GO:0042104	positive regulation of activated T cell proliferation	3/110	0.000509	0.0193465	0.016946	RPS3/IGF2/HMGB1	3
GO:1905564	positive regulation of vascular endothelial cell proliferation	3/110	0.000509	0.0193465	0.016946	IGF2/FGFR1/HMGB1	3
GO:0050769	positive regulation of neurogenesis	7/110	0.000543	0.0202809	0.017764	CUX2/SOX11/EPHA4/FN1/MAP1B/NAP1L1/LRP2	7
GO:0030199	collagen fibril organization	4/110	0.000563	0.0206794	0.018114	COL3A1/COL1A1/COL1A2/EXT1	4

GO:0001837	epithelial to mesenchymal transition	6/110	0.000617	0.021919	0.019199	COL1A1/HMGA2/EPHA4/FGFR1/RTN4/PTK2	6
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	6/110	0.000617	0.021919	0.019199	HSP90AB1/RPL11/RPS7/RPL5/RACK1/PTK2	6
GO:0030900	forebrain development	9/110	0.00063	0.0220487	0.019313	COL3A1/ZSWIM6/FXR1/SLC38A2/EXT1/LARGE1/RTN4/LRP2/YWHAE	9
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	9/110	0.000664	0.02287	0.020032	COL3A1/AFP/HSP90AB1/SOX11/COL1A2/KCNQ1OT1/EXT1/LRP2/PTK2	9
GO:0051347	positive regulation of transferase activity	9/110	0.000712	0.0241268	0.021133	HMGA2/HSP90AB1/RPS3/EPHA4/IGF2/FGFR1/HSP90AA1/RPS2/PTK2	9
GO:0006413	translational initiation	5/110	0.000769	0.0256822	0.022496	RPS3/RPS3A/NPM1/EIF5/EIF1	5
GO:0008361	regulation of cell size	6/110	0.000798	0.0262515	0.022994	FN1/MAP1B/HSP90AA1/RTN4/NPM1/MAP2	6

GO:2001242	regulation of intrinsic apoptotic signaling pathway	6/110	0.000867	0.0280965	0.02461	RPS3/RPL11/RPS7/RPL26/RACK1/TP T1	6
GO:0021543	pallium development	6/110	0.000891	0.0284538	0.024923	COL3A1/FXR1/SLC38A2/LARGE1/RT N4/YWHAЕ	6
GO:0003007	heart morphogenesis	7/110	0.000906	0.028526	0.024987	SOX11/SOX4/EXT1/ASXL1/RTN4/LR P2/PTK2	7
GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	3/110	0.001101	0.0341859	0.029944	RPL11/RPS7/RPL26	3
GO:0010720	positive regulation of cell development	9/110	0.001163	0.0356015	0.031184	CUX2/SOX11/EPHA4/FN1/MAP1B/N AP1L1/SOX4/LRP2/HMGB1	9
GO:0071711	basement membrane organization	3/110	0.001196	0.0361189	0.031637	COL3A1/EXT1/LARGE1	3
GO:0045860	positive regulation of protein kinase activity	7/110	0.001327	0.0395211	0.034617	HMGA2/HSP90AB1/RPS3/EPHA4/FGF R1/HSP90AA1/PTK2	7

GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	3/110	0.001402	0.0398394	0.034896 SOX4/RPL26/NPM1	3
GO:0060563	neuroepithelial cell differentiation	3/110	0.001402	0.0398394	0.034896 SOX11/MAP1B/SOX4	3
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	3/110	0.001402	0.0398394	0.034896 RPS3/RPL26/TPT1	3
GO:0061448	connective tissue development	7/110	0.00141	0.0398394	0.034896 COL3A1/COL1A1/HMGA2/ARID5B/EXT1/LARGE1/RASAL2	7
GO:0051292	nuclear pore complex assembly	2/110	0.00147	0.0410046	0.035917 FXR1/RTN4	2
GO:0021955	central nervous system neuron axonogenesis	3/110	0.001512	0.0416544	0.036486 HSP90AB1/EPHA4/HSP90AA1	3
GO:0051962	positive regulation of nervous system development	7/110	0.001557	0.0423715	0.037114 CUX2/SOX11/EPHA4/FN1/MAP1B/NAP1L1/LRP2	7

GO:2001235	positive regulation of apoptotic signaling pathway	5/110	0.001603	0.0430822	0.037737 RPS3/RPL11/RPS7/RPL26/RACK1	5
GO:0003357	noradrenergic neuron differentiation	2/110	0.00179	0.0469544	0.041128 SOX11/SOX4	2
GO:0034163	regulation of toll-like receptor 9 signaling pathway	2/110	0.00179	0.0469544	0.041128 RTN4/HMGB1	2
GO:0021954	central nervous system neuron development	4/110	0.001824	0.0473041	0.041435 HSP90AB1/EPHA4/HSP90AA1/MAP2	4
GO:0001890	placenta development	5/110	0.001915	0.0490829	0.042993 HSP90AB1/KRT19/IGF2/PTK2/RPS6	5