

Supplementary Table 7.
DEGs across all cells in ScRNA-seq data

gene	<i>p</i>	logFC	FDR	dysregulated
AFP	0	4.292044	0	UP
APOE	0	1.791304	0	UP
COL1A1	0	3.233877	0	UP
COL1A2	0	2.835984	0	UP
COL3A1	0	4.895316	0	UP
COL5A1	0	1.886475	0	UP
COL5A2	0	1.708109	0	UP
COL6A2	0	1.668378	0	UP
DLK1	0	1.673893	0	UP
FN1	0	2.054434	0	UP
H19	0	2.56776	0	UP
KRT19	0	2.23541	0	UP
LINC0151	0	1.1463	0	UP
LUM	0	1.248495	0	UP
MGP	0	1.147485	0	UP
MT-CO1	0	1.84234	0	UP
MYADM	0	1.174221	0	UP
POSTN	0	1.529894	0	UP
PRKCG	0	1.183933	0	UP
RBMS3	0	4.225381	0	UP
ROR1	0	1.824285	0	UP
RPL10	0	3.973079	0	UP
RPL11	0	2.739141	0	UP
RPL12	0	2.257229	0	UP
RPL13	0	3.023097	0	UP
RPL32	0	2.680507	0	UP
RPL34	0	2.688286	0	UP
RPL36A	0	1.77243	0	UP
RPL39	0	3.313599	0	UP

RPS15A	0	2.794304	0	UP
RPS18	0	3.435877	0	UP
RPS2	0	3.401807	0	UP
RPS21	0	1.477527	0	UP
RPS23	0	3.237307	0	UP
RPS3	0	3.062002	0	UP
SLIT3	0	2.884309	0	UP
TPT1	0	3.145769	0	UP
UTY	0	4.149617	0	UP
RBMS1	0	1.787517	0	UP
MT-ND3	0	1.255695	0	UP
IGF2	0	1.023752	0	UP
RPS4X	0	2.689992	0	UP
EEF1A1	0	2.711375	1.4E-306	UP
PLCB1	5.3E-305	2.406406	1.3E-302	UP
SEC24D	1.5E-304	1.209294	3.4E-302	UP
FGF13	6.3E-302	1.8327	1.5E-299	UP
KRT8	1.3E-301	1.242338	3E-299	UP
RPL30	2.3E-301	2.44331	5.3E-299	UP
CLIC4	6.7E-301	1.602792	1.5E-298	UP
KIAA1217	7.6E-301	1.34987	1.7E-298	UP
RPL14	2.7E-300	2.389164	6E-298	UP
RPS28	2.4E-292	2.455189	5.2E-290	UP
RPL26	4.3E-290	2.223048	8.9E-288	UP
RPL28	7E-288	2.172781	1.4E-285	UP
RPL7A	1.3E-287	2.865287	2.6E-285	UP
FBLN1	6.5E-287	1.126129	1.3E-284	UP
CDKN1C	3.3E-283	1.155924	6.5E-281	UP
RPS8	4.3E-283	2.312575	8.5E-281	UP
IGFBP3	7.2E-281	1.045889	1.4E-278	UP
RPL10A	2.5E-277	1.822314	4.7E-275	UP
NPNT	8E-275	1.04762	1.5E-272	UP
RPL37	1E-274	1.920578	1.9E-272	UP
RPL18A	4.3E-273	2.176239	7.9E-271	UP

MDK	1.1E-272	1.623448	1.9E-270	UP
PABPC1	1.9E-269	1.245994	3.4E-267	UP
RPS27	1.3E-256	1.941382	2.3E-254	UP
RPL18	2.5E-255	2.538628	4.2E-253	UP
RPS24	4.9E-254	2.555156	8.3E-252	UP
SLC38A2	1.8E-253	1.720108	3E-251	UP
RPS12	4.1E-252	2.447567	6.8E-250	UP
COL11A1	1.7E-246	1.021887	2.7E-244	UP
LMNA	6.5E-246	1.225588	1E-243	UP
RPL17	5.9E-241	2.091554	9.1E-239	UP
TRERF1	3.6E-235	1.232496	5.4E-233	UP
FBN2	1.6E-233	1.00319	2.3E-231	UP
HAND2-A	3.1E-233	2.159273	4.7E-231	UP
DIAPH2	4.8E-233	1.168421	7E-231	UP
STAG1	2.1E-232	2.260983	3.1E-230	UP
RPL8	1.3E-230	2.240127	1.9E-228	UP
FOXN3	2.3E-230	1.979247	3.4E-228	UP
HMGA2	4.1E-228	1.066991	5.9E-226	UP
FUS	2.2E-227	1.285952	3.2E-225	UP
CDK6	1.5E-222	1.903357	2.1E-220	UP
COL25A1	4.8E-222	1.37807	6.5E-220	UP
RPL41	3.9E-221	2.459203	5.2E-219	UP
RPL29	3.1E-216	2.109707	4E-214	UP
ZNF804A	9E-215	2.225396	1.2E-212	UP
ROBO2	5E-213	1.413798	6.4E-211	UP
PPFIBP1	1.7E-212	1.195101	2.1E-210	UP
FOSB	1.9E-212	1.051773	2.4E-210	UP
RPS7	3.3E-211	2.078494	4.1E-209	UP
CASC15	6.1E-211	1.890372	7.7E-209	UP
RPLP0	2.5E-210	2.037848	3.1E-208	UP
GAS5	5.2E-208	1.249645	6.3E-206	UP
ASAP1	6.5E-208	1.321389	7.9E-206	UP
KCNQ1O	7E-206	1.972422	8.3E-204	UP
PTPRK	1.1E-204	1.750092	1.3E-202	UP

RPL35A	7.7E-202	1.823209	8.7E-200	UP
RPL23A	7.2E-197	1.484865	8E-195	UP
RPL5	1.1E-196	2.233814	1.2E-194	UP
RPS14	1.2E-196	2.215457	1.4E-194	UP
RPS13	3E-195	1.932466	3.3E-193	UP
SNHG29	1.5E-194	1.568089	1.7E-192	UP
RPL19	1.3E-193	1.861305	1.4E-191	UP
RACK1	1.3E-188	1.496403	1.3E-186	UP
MATN2	2.3E-188	1.066614	2.4E-186	UP
GNAS	3.5E-187	1.625268	3.5E-185	UP
RPS9	4.9E-187	1.462474	5E-185	UP
GAS7	6.9E-186	1.036045	7E-184	UP
SRSF7	2.2E-185	1.172749	2.2E-183	UP
RPS5	2.2E-184	1.552044	2.2E-182	UP
RPLP2	7E-184	1.611961	6.9E-182	UP
RPL24	1.2E-183	1.869348	1.2E-181	UP
RPS27A	3.7E-183	2.104806	3.6E-181	UP
SQSTM1	3.5E-182	1.359419	3.4E-180	UP
ZFAS1	3.7E-176	1.205731	3.4E-174	UP
IGF2BP2	1.5E-175	2.470872	1.4E-173	UP
NPM1	6.2E-175	1.530968	5.7E-173	UP
ARHGAP	5.6E-172	1.552427	5.1E-170	UP
MT-ND1	1.9E-170	1.735412	1.7E-168	UP
ALK	4.1E-166	1.308536	3.5E-164	UP
RPS3A	4.9E-166	2.257302	4.2E-164	UP
RUNX1T1	1.2E-164	1.582677	9.8E-163	UP
SOX4	1.3E-164	1.986675	1.1E-162	UP
NREP	2.7E-162	1.900826	2.2E-160	UP
EPB41	7.8E-162	1.348735	6.4E-160	UP
HAND2	3.1E-161	1.261013	2.6E-159	UP
STARD4	7.5E-159	1.51744	6E-157	UP
RPS6	1.3E-158	1.801269	1E-156	UP
RPL6	1.9E-158	1.93555	1.5E-156	UP
ADARB2	2.4E-158	1.158578	1.9E-156	UP

RPS25	7.6E-157	1.554822	5.9E-155	UP
TSHZ2	1.7E-156	1.58843	1.3E-154	UP
CALD1	1.5E-155	1.584813	1.1E-153	UP
RPS16	8.8E-151	1.678776	6.5E-149	UP
RPL15	4.1E-149	1.933977	2.9E-147	UP
RPL37A	1.3E-147	1.59341	9.5E-146	UP
RBMS3-A	6.5E-147	1.343878	4.6E-145	UP
RPL7	5E-145	1.450094	3.4E-143	UP
PTPRR	1.9E-144	1.487105	1.3E-142	UP
BTG1	2.3E-144	1.354828	1.6E-142	UP
IFRD1	4.6E-143	1.10251	3.1E-141	UP
DUOX1	3.8E-142	1.149533	2.5E-140	UP
SEC31A	4.8E-140	1.132592	3.1E-138	UP
RPL22	2.8E-139	1.397706	1.8E-137	UP
ASXL1	6.2E-139	1.001177	4E-137	UP
MIR4435-	8E-139	1.00544	5.1E-137	UP
RPS6KA5	2.7E-137	1.136804	1.7E-135	UP
PTMA	8.2E-137	2.167216	5.2E-135	UP
LARGE1	7.5E-132	1.349932	4.6E-130	UP
FMN1	6.1E-131	1.004677	3.7E-129	UP
LINC0068	6.5E-128	1.351639	3.7E-126	UP
PHOX2B-	2.7E-126	1.463182	1.5E-124	UP
PDZRN3	3.3E-125	1.181401	1.8E-123	UP
DLC1	1.1E-124	1.285809	5.9E-123	UP
RBFOX2	1.5E-124	1.542892	8.2E-123	UP
RPLP1	2.2E-124	1.807689	1.2E-122	UP
DLEU2	1.3E-120	1.178058	6.7E-119	UP
RPL9	3E-119	1.613135	1.5E-117	UP
GLCCI1	9.3E-118	1.141951	4.8E-116	UP
ATP11A	6.1E-117	1.125403	3.1E-115	UP
SREBF2	3.3E-113	1.317586	1.6E-111	UP
LINC0161	1.4E-111	1.824437	6.6E-110	UP
KLHL13	5E-111	1.011225	2.4E-109	UP
RPL13A	1.4E-110	1.442278	6.5E-109	UP

RPL36	1.8E-110	1.155851	8.6E-109	UP
AKAP12	1.5E-109	1.335829	7.2E-108	UP
RPL3	4.4E-109	1.724022	2E-107	UP
ATCAY	4.5E-109	1.137765	2.1E-107	UP
CCDC144	1.1E-104	1.473484	4.8E-103	UP
HSP90AB	9.5E-104	1.532961	4.1E-102	UP
FAM163A	2.9E-103	1.131305	1.3E-101	UP
EVL	2.6E-99	1.139783	1.05E-97	UP
MAPRE2	3E-99	1.070761	1.23E-97	UP
RPS10	1.27E-98	1.356035	5.12E-97	UP
NFE2L3	1.95E-98	1.119655	7.86E-97	UP
RPS19	1.08E-95	1.707743	4.22E-94	UP
RPS15	5.33E-95	1.345179	2.07E-93	UP
DPYD	4.07E-91	1.634849	1.5E-89	UP
ADAMTS	9.37E-91	1.04479	3.42E-89	UP
SRRM4	1.3E-88	1.212941	4.62E-87	UP
GAB2	5.85E-86	1.080193	2.01E-84	UP
CACNA2I	1.31E-83	1.273907	4.39E-82	UP
TFDP2	2.11E-83	1.212166	7.06E-82	UP
RPS11	1.31E-82	1.173363	4.32E-81	UP
PTPRD	5.38E-82	1.049827	1.77E-80	UP
ENSG000	1.68E-81	1.028476	5.45E-80	UP
EFNA5	2.9E-81	1.166339	9.39E-80	UP
NREP-AS	3.9E-81	1.086392	1.26E-79	UP
RPL21	7.23E-79	1.148639	2.27E-77	UP
SHISA9	6.92E-78	1.088637	2.13E-76	UP
RIMBP2	8.51E-74	1.009176	2.47E-72	UP
NACA	3.1E-72	1.414792	8.76E-71	UP
ZNF704	4.61E-72	1.233996	1.3E-70	UP
PRKG1	5.5E-72	1.061167	1.55E-70	UP
KCNQ5	8.27E-56	1.231743	1.77E-54	UP
HDAC9	5.36E-46	1.094148	9.51E-45	UP
EIF1	1.39E-35	1.006603	1.95E-34	UP
TMSB10	2.36E-35	1.005174	3.28E-34	UP

AUTS2	1.21E-28	1.663358	1.39E-27	UP
ACTG1	1.58E-19	1.083232	1.31E-18	UP
ADCY2	0	-2.35132	0	DOWN
ADGRV1	0	-2.78348	0	DOWN
ANKFN1	0	-1.21538	0	DOWN
ARMC3	0	-1.32827	0	DOWN
BMPR1B	0	-2.20674	0	DOWN
C8orf34	0	-2.07288	0	DOWN
CCDC30	0	-1.01258	0	DOWN
CDHR3	0	-1.1063	0	DOWN
CFAP43	0	-1.28881	0	DOWN
CFAP47	0	-1.09929	0	DOWN
CFAP54	0	-1.24817	0	DOWN
CHL1	0	-1.1067	0	DOWN
CKB	0	-2.13566	0	DOWN
CLU	0	-1.24908	0	DOWN
CSMD1	0	-1.25144	0	DOWN
CSRNP3	0	-1.46672	0	DOWN
DCDC1	0	-1.5464	0	DOWN
DNAH11	0	-1.08129	0	DOWN
DNAH7	0	-1.81079	0	DOWN
DOCK3	0	-1.60734	0	DOWN
DTNA	0	-2.31146	0	DOWN
EFNB3	0	-1.03206	0	DOWN
ENSG0000	0	-1.02534	0	DOWN
ENSG0000	0	-1.04059	0	DOWN
ENSG0000	0	-2.79722	0	DOWN
ENSG0000	0	-1.24586	0	DOWN
ENSG0000	0	-1.4022	0	DOWN
ENSG0000	0	-1.91538	0	DOWN
FAT3	0	-2.9993	0	DOWN
FMN2	0	-1.6432	0	DOWN
GLIS3	0	-2.19295	0	DOWN
GPM6B	0	-1.37344	0	DOWN

GRIN2A	0	-1.1217	0	DOWN
HECW2	0	-1.00016	0	DOWN
HOTAIRM	0	-1.00718	0	DOWN
HYDIN	0	-1.4999	0	DOWN
IGFBP5	0	-1.42533	0	DOWN
KCNMA1	0	-2.00724	0	DOWN
LIMCH1	0	-1.21477	0	DOWN
MAGI2	0	-3.38656	0	DOWN
MEIS2	0	-2.35938	0	DOWN
METRNL	0	-1.21771	0	DOWN
MIR99AH	0	-2.34618	0	DOWN
NAV2	0	-2.14052	0	DOWN
NEBL	0	-1.60781	0	DOWN
NFIA	0	-1.86551	0	DOWN
NOVA1	0	-2.01544	0	DOWN
NPAS3	0	-3.64056	0	DOWN
NTN1	0	-3.27831	0	DOWN
NTRK2	0	-1.82744	0	DOWN
PACRG	0	-1.23697	0	DOWN
PTPRZ1	0	-1.78066	0	DOWN
QKI	0	-2.14711	0	DOWN
RFX3	0	-2.0313	0	DOWN
RFX4	0	-3.53424	0	DOWN
RGMA	0	-1.01448	0	DOWN
RGS6	0	-1.43409	0	DOWN
RMST	0	-4.03422	0	DOWN
RNF220	0	-1.22372	0	DOWN
RTN1	0	-1.2827	0	DOWN
SHROOM	0	-1.60728	0	DOWN
SLC1A3	0	-1.50366	0	DOWN
SLIT1	0	-1.18106	0	DOWN
SPARCL1	0	-1.25083	0	DOWN
SPON1	0	-2.19118	0	DOWN
SRGAP3	0	-2.27555	0	DOWN

STK33	0	-1.49619	0	DOWN
TEX9	0	-1.06917	0	DOWN
TMEM163	0	-1.05804	0	DOWN
TMEM232	0	-1.56541	0	DOWN
TNIK	0	-1.74861	0	DOWN
TTC6	0	-2.24479	0	DOWN
TTTY14	0	-1.59831	0	DOWN
VIM	0	-1.38168	0	DOWN
ENSG000	0	-1.23682	0	DOWN
SULF1	0	-1.37342	7.9E-308	DOWN
ULK4	0	-1.06962	2.1E-306	DOWN
STX17-DT	1.8E-304	-1.13189	4.3E-302	DOWN
LRP1B	5.7E-296	-1.15812	1.2E-293	DOWN
TRIM2	1.3E-290	-1.49478	2.8E-288	DOWN
SNHG14	2.3E-289	-2.2522	4.8E-287	DOWN
FOXP2	2.7E-288	-1.4663	5.6E-286	DOWN
DST	3E-279	-2.89175	5.8E-277	DOWN
SORBS2	2.5E-274	-2.20007	4.6E-272	DOWN
AQP4-AS	4.3E-273	-1.02409	7.9E-271	DOWN
PITPNC1	4.9E-273	-1.15116	8.8E-271	DOWN
NRG3	3.8E-269	-1.0589	6.8E-267	DOWN
MSI2	1.4E-256	-1.18872	2.3E-254	DOWN
PLXDC2	6E-253	-1.55796	1E-250	DOWN
CDH2	8E-251	-1.63924	1.3E-248	DOWN
ALCAM	9.1E-251	-1.2467	1.5E-248	DOWN
TUBB2B	1.1E-249	-1.22852	1.8E-247	DOWN
ITGB8	1.3E-245	-1.21576	2.2E-243	DOWN
ADGRL3	5.8E-239	-2.54766	8.8E-237	DOWN
SEMA6D	3E-234	-1.57164	4.6E-232	DOWN
DMD	2E-223	-1.40769	2.8E-221	DOWN
PARD3B	2.2E-221	-1.45711	3E-219	DOWN
MARCHF	1.3E-219	-1.63702	1.7E-217	DOWN
PDLIM3	3.2E-218	-1.28129	4.2E-216	DOWN
TENM4	4.5E-184	-1.01375	4.5E-182	DOWN

NLGN1	3.8E-179	-1.67525	3.6E-177	DOWN
TNRC6A	1.8E-177	-1.55495	1.7E-175	DOWN
NEGR1	3.5E-170	-1.01378	3.1E-168	DOWN
FMNL2	7.7E-165	-1.28184	6.5E-163	DOWN
NCAM1	1.5E-163	-2.25793	1.2E-161	DOWN
PLEKHA5	5E-162	-1.55857	4.1E-160	DOWN
SOX2-OT	3.2E-159	-1.20388	2.5E-157	DOWN
NFIB	3.4E-158	-1.11694	2.7E-156	DOWN
C1QTNF7	3.3E-154	-1.09726	2.5E-152	DOWN
MAML2	4.8E-149	-1.87454	3.5E-147	DOWN
KIF26B	4.1E-142	-1.00981	2.7E-140	DOWN
MAPK10	1.3E-138	-2.09218	8.1E-137	DOWN
BASP1	7.7E-129	-1.03235	4.5E-127	DOWN
LINC0231	8.4E-123	-1.37588	4.6E-121	DOWN
MACF1	2.3E-121	-1.11404	1.2E-119	DOWN
TUBA1A	2.5E-115	-1.12424	1.3E-113	DOWN
KAZN	1.1E-110	-1.33109	5E-109	DOWN
DCLK1	1E-109	-1.69203	4.8E-108	DOWN
ADGRB3	2.8E-108	-1.70908	1.3E-106	DOWN
CNTN4	6.8E-107	-1.01213	3.1E-105	DOWN
TMSB4X	7.7E-106	-1.39322	3.4E-104	DOWN
SDK1	4.3E-104	-1.46505	1.9E-102	DOWN
GAPDH	4.6E-103	-1.10349	1.9E-101	DOWN
AKAP6	2.4E-102	-1.34991	1E-100	DOWN
KC6	2.5E-100	-1.01018	1.02E-98	DOWN
SLIT2	4.99E-90	-1.35918	1.8E-88	DOWN
PBX1	9.85E-88	-1.15918	3.45E-86	DOWN
ZBTB20	7.97E-81	-1.42919	2.57E-79	DOWN
FRMD5	8.62E-74	-1.07219	2.5E-72	DOWN
ERBB4	1.25E-67	-1.03328	3.29E-66	DOWN
ANK2	4.1E-40	-1.05046	6.38E-39	DOWN

Enrichment of Down-regulated genes across all cells in ScRNA-seq data

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> -value	gene ID	count
GO:0010975	regulation of neuron projection development	20/106	7.74E-13	1.4347E-09	1.17E-09	EFNB3/FAT3/HECW2/MAGI2/METRN/NTN1/NTRK2/RGMA/SLIT1/TNFRSF25/ULK4/CDH2/TUBB2B/SEMA6D/NLGN1/NEGR1/MACF1/ADGRB3/SLIT2	20
GO:0007409	axonogenesis	19/106	6.24E-12	5.783E-09	4.72E-09	BMPR1B/CHL1/EFNB3/METRN/NTN1/NTRK2/PTPRZ1/RGMA/SLIT1/CDH2/ALCAM/TUBB2B/SEMA6D/NCAM1/NFIB/MACF1/DCLK1/CNTN4/SLIT2	19
GO:0034329	cell junction assembly	18/106	5.38E-11	3.324E-08	2.71E-08	CDHR3/EFNB3/GPM6B/LIMCH1/NTN1/NTRK2/SLIT1/DST/NRG3/CDH2/ADGRL3/NLGN1/NEGR1/MACF1/ADGRB3/SDK1/ERBB4/ANK2	18
GO:0007416	synapse assembly	12/106	1.33E-09	6.1603E-07	5.03E-07	EFNB3/NTN1/NTRK2/SLIT1/NRG3/CDH2/ADGRL3/NLGN1/NEGR1/ADGRB3/SDK1/ERBB4	12
GO:0007411	axon guidance	12/106	7.49E-09	2.3126E-06	1.89E-06	BMPR1B/CHL1/EFNB3/NTN1/SLIT1/ALCAM/TUBB2B/SEMA6D/NCAM1/NFIB/CNTN4/SLIT2	12

GO:0097485	neuron projection guidance	12/106	7.49E-09	2.3126E-06	1.89E-06	BMPR1B/CHL1/EFNB3/NTN1/SLIT1/ALCAM/TUBB2B/SEMA6D/NCAM1/NFIB/CNTN4/SLIT2	12
GO:0050770	regulation of axonogenesis	10/106	1.91E-08	5.0687E-06	4.14E-06	EFNB3/METRN/NTN1/NTRK2/RGMA/SLIT1/CDH2/SEMA6D/MACF1/SLIT2	10
GO:0001764	neuron migration	10/106	5.99E-08	1.3865E-05	1.13E-05	CHL1/FAT3/NTN1/NTRK2/ULK4/NGR3/TUBB2B/ADGRL3/TUBA1A/DCLK1	10
GO:0050808	synapse organization	15/106	8.19E-08	1.6858E-05	1.38E-05	EFNB3/NFIA/NTN1/NTRK2/SLIT1/SPARCL1/NGR3/CDH2/ADGRL3/NLGN1/NEGR1/TUBA1A/ADGRB3/SDK1/ERBB4	15
GO:0010977	negative regulation of neuron projection development	9/106	9.39E-08	1.7392E-05	1.42E-05	EFNB3/FAT3/NTN1/RGMA/SLIT1/VIM/SEMA6D/NLGN1/SLIT2	9

GO:0010001	glial cell differentiation	11/106	1.76E-07	2.9669E-05	2.42E-05	CLU/GPM6B/METR/NFIA/NTRK2/PTPRZ1/VIM/CDH2/TENM4/NFIB/TUBA1A	11
GO:1901888	regulation of cell junction assembly	10/106	3.37E-07	5.2071E-05	4.25E-05	EFNB3/GPM6B/LIMCH1/NTN1/NTRK2/SLIT1/NLGN1/NEGR1/MACF1/ADGRB3	10
GO:0042063	gliogenesis	12/106	4.38E-07	6.2369E-05	5.09E-05	CLU/GPM6B/METR/NFIA/NTN1/NTRK2/PTPRZ1/VIM/CDH2/TENM4/NFIB/TUBA1A	12
GO:0048588	developmental cell growth	10/106	9.68E-07	0.00012813	0.000105	NTN1/RGMA/SLIT1/SORBS2/ALCAM/SEMA6D/MACF1/DCLK1/AKAP6/SLIT2	10
GO:0060560	developmental growth involved in morphogenesis	10/106	1.17E-06	0.00014429	0.000118	MAGI2/NTN1/RGMA/SLIT1/ALCAM/SEMA6D/KIF26B/MACF1/DCLK1/SLIT2	10

GO:0031345	negative regulation of cell projection organization	9/106	1.36E-06	0.00015754	0.000129	EFNB3/FAT3/NTN1/RGMA/SLIT1/VIM/SEMA6D/NLGN1/SLIT2	9
GO:0042552	myelination	8/106	1.6E-06	0.00017305	0.000141	CLU/GPM6B/NTRK2/PTPRZ1/QKI/TMEM163/TENM4/ANK2	8
GO:0007272	ensheathment of neurons	8/106	1.77E-06	0.00017305	0.000141	CLU/GPM6B/NTRK2/PTPRZ1/QKI/TMEM163/TENM4/ANK2	8
GO:0008366	axon ensheathment	8/106	1.77E-06	0.00017305	0.000141	CLU/GPM6B/NTRK2/PTPRZ1/QKI/TMEM163/TENM4/ANK2	8
GO:0051960	regulation of nervous system development	13/106	2.12E-06	0.00019643	0.00016	EFNB3/METRNL/NTN1/NTRK2/PTPRZ1/RGMA/SLIT1/SEMA6D/TENM4/NLGN1/MACF1/ADGRB3/SLIT2	13

GO:0030900	forebrain development	12/106	3.05E-06	0.00026941	0.00022	NTRK2/RFX4/SLIT1/FOXP2/NRG3/CDH2/TUBB2B/NFIB/TUBA1A/DCLK1/SLIT2/ERBB4	12
GO:0021537	telencephalon development	10/106	3.53E-06	0.00029261	0.000239	NTRK2/RFX4/FOXP2/NRG3/CDH2/TUBB2B/NFIB/TUBA1A/SLIT2/ERBB4	10
GO:0051963	regulation of synapse assembly	7/106	3.63E-06	0.00029261	0.000239	EFNB3/NTN1/NTRK2/SLIT1/NLG1/NEGR1/ADGRB3	7
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	10/106	3.88E-06	0.0002999	0.000245	CDHR3/FAT3/SPARCL1/CDH2/ALCAM/ADGRL3/TENM4/NLGN1/CNTN4/SDK1	10
GO:0048675	axon extension	7/106	5.4E-06	0.00040003	0.000327	NTN1/SLIT1/ALCAM/SEMA6D/MACF1/DCLK1/SLIT2	7

GO:0050919	negative chemotaxis	5/106	6.47E-06	0.00046092	0.000376	NTN1/SLIT1/NRG3/SEMA6D/SLIT2	5
GO:0031290	retinal ganglion cell axon guidance	4/106	7.67E-06	0.00052649	0.00043	BMPR1B/SLIT1/ALCAM/SLIT2	4
GO:0050807	regulation of synapse organization	9/106	9.63E-06	0.00063722	0.00052	EFNB3/NTN1/NTRK2/SLIT1/CDH2/NLGN1/NEGR1/TUBA1A/ADGRB3	9
GO:0050803	regulation of synapse structure or activity	9/106	1.17E-05	0.0007473	0.00061	EFNB3/NTN1/NTRK2/SLIT1/CDH2/NLGN1/NEGR1/TUBA1A/ADGRB3	9
GO:0050767	regulation of neurogenesis	11/106	1.22E-05	0.00075642	0.000617	EFNB3/METRN/NTN1/NTRK2/PTPRZ1/RGMA/SLIT1/SEMA6D/TENM4/MACF1/SLIT2	11

GO:1902430	negative regulation of amyloid-beta formation	4/106	2E-05	0.00119847	0.000978	CLU/NTRK2/RTN1/SPON1	4
GO:0016049	cell growth	12/106	2.28E-05	0.00131825	0.001076	IGFBP5/NTN1/RGMA/SLIT1/SORBS2/NRG3/ALCAM/SEMA6D/MACF1/DCLK1/AKAP6/SLIT2	12
GO:0007018	microtubule-based movement	11/106	2.43E-05	0.00136549	0.001115	CFAP43/CFAP47/CFAP54/DNAH11/DNAH7/FMN2/HYDIN/RFX3/DST/KIF26B/TUBA1A	11
GO:1902992	negative regulation of amyloid precursor protein catabolic process	4/106	3E-05	0.00163313	0.001333	CLU/NTRK2/RTN1/SPON1	4
GO:0031346	positive regulation of cell projection organization	10/106	3.14E-05	0.00166479	0.001359	MAGI2/METRNL/NTN1/NTRK2/RGMA/TUBB2B/NLGN1/NEGR1/MACF1/SLIT2	10

GO:0050771	negative regulation of axonogenesis	5/106	3.46E-05	0.00178215	0.001455	EFNB3/NTN1/RGMA/SLIT1/SEMA6D	5
GO:0051962	positive regulation of nervous system development	9/106	3.77E-05	0.00188856	0.001542	METRN/NTN1/NTRK2/PTPRZ1/TENM4/NLGN1/MACF1/ADGRB3/SLIT2	9
GO:0048846	axon extension involved in axon guidance	4/106	5.99E-05	0.00284783	0.002325	SLIT1/ALCAM/SEMA6D/SLIT2	4
GO:1902284	neuron projection extension involved in neuron projection guidance	4/106	5.99E-05	0.00284783	0.002325	SLIT1/ALCAM/SEMA6D/SLIT2	4
GO:0022612	gland morphogenesis	6/106	6.5E-05	0.00301087	0.002458	CSMD1/IGFBP5/NTN1/SULF1/NRG3/NFIB	6

GO:1990138	neuron projection extension	7/106	6.8E-05	0.00307246	0.002508	NTN1/SLIT1/ALCAM/SEMA6D/ MACF1/DCLK1/SLIT2	7
GO:0007389	pattern specification process	11/106	7.4E-05	0.00322983	0.002637	BMPR1B/DNAH11/MEIS2/RFX3/ RFX4/RNF220/SHROOM3/NRG3/ BASP1/PBX1/ERBB4	11
GO:0050890	cognition	9/106	7.5E-05	0.00322983	0.002637	CHL1/CSMD1/DNAH11/GRIN2A/ MEIS2/NTRK2/PTPRZ1/TUBA1A/ ADGRB3	9
GO:0050772	positive regulation of axonogenesis	5/106	7.75E-05	0.00326548	0.002666	METRNL/NTN1/NTRK2/MACF1/ SLIT2	5
GO:0021987	cerebral cortex development	6/106	8.13E-05	0.00334613	0.002731	NTRK2/FOXP2/CDH2/TUBB2B/ TUBA1A/SLIT2	6

GO:0003351	epithelial cilium movement involved in extracellular fluid movement	4/106	9.81E-05	0.00386653	0.003156	CFAP43/CFAP54/DNAH11/RFX3	4
GO:0060443	mammary gland morphogenesis	4/106	9.81E-05	0.00386653	0.003156	CSMD1/IGFBP5/NTN1/NRG3	4
GO:0006858	extracellular transport	4/106	0.000128	0.00494188	0.004034	CFAP43/CFAP54/DNAH11/RFX3	4
GO:0040013	negative regulation of locomotion	10/106	0.000135	0.00510754	0.004169	IGFBP5/LIMCH1/MAGI2/SLIT1/S RGAP3/SULF1/NRG3/SEMA6D/S LIT2/FRMD5	10
GO:0003341	cilium movement	7/106	0.000149	0.00549843	0.004488	CFAP43/CFAP47/CFAP54/DNAH1 1/DNAH7/HYDIN/RFX3	7

GO:1902003	regulation of amyloid-beta formation	4/106	0.000151	0.00549843	0.004488	CLU/NTRK2/RTN1/SPON1	4
GO:0007611	learning or memory	8/106	0.000158	0.00561423	0.004583	CSMD1/DNAH11/GRIN2A/MEIS2/NTRK2/PTPRZ1/TUBA1A/ADGRB3	8
GO:0007612	learning	6/106	0.000203	0.00708159	0.005781	CSMD1/GRIN2A/MEIS2/NTRK2/TUBA1A/ADGRB3	6
GO:0060419	heart growth	5/106	0.000218	0.00746558	0.006094	SORBS2/TENM4/BASP1/AKAP6/ERBB4	5
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	4/106	0.000223	0.0075094	0.00613	CDH2/ALCAM/TENM4/NLGN1	4

GO:0072006	nephron development	6/106	0.00025	0.00828631	0.006764	MAGI2/SULF1/KIF26B/BASP1/PBX1/ERBB4	6
GO:1902991	regulation of amyloid precursor protein catabolic process	4/106	0.000257	0.00836702	0.00683	CLU/NTRK2/RTN1/SPON1	4
GO:0010976	positive regulation of neuron projection development	6/106	0.000268	0.00856911	0.006995	MAGI2/NTRK2/RGMA/TUBB2B/NLGN1/NEGR1	6
GO:0060041	retina development in camera-type eye	6/106	0.000277	0.00856953	0.006995	BMPR1B/FAT3/NFIA/NTRK2/NFIB/SDK1	6
GO:0034205	amyloid-beta formation	4/106	0.000276	0.00856953	0.006995	CLU/NTRK2/RTN1/SPON1	4

GO:0001539	cilium or flagellum-dependent cell motility	6/106	0.000317	0.00947647	0.007736	CFAP43/CFAP47/CFAP54/DNAH11/DNAH7/RFX3	6
GO:0060285	cilium-dependent cell motility	6/106	0.000317	0.00947647	0.007736	CFAP43/CFAP47/CFAP54/DNAH11/DNAH7/RFX3	6
GO:0048709	oligodendrocyte differentiation	5/106	0.000329	0.00966893	0.007893	CLU/GPM6B/NTRK2/PTPRZ1/TE NM4	5
GO:2000146	negative regulation of cell motility	9/106	0.00034	0.00968577	0.007907	IGFBP5/LIMCH1/MAGI2/SRGAP3/SULF1/NRG3/SEMA6D/SLIT2/FR MD5	9
GO:0014009	glial cell proliferation	4/106	0.000338	0.00968577	0.007907	CLU/NFIA/NTN1/NFIB	4

GO:0016358	dendrite development	7/106	0.000346	0.0097072	0.007924	FAT3/HECW2/TNFRK1/ADGRB3/SDK1	7
GO:0001654	eye development	9/106	0.000359	0.00986897	0.008056	BMPR1B/FAT3/MEIS2/NFIA/NTRK2/VIM/NFIB/SDK1/PBX1	9
GO:0008045	motor neuron axon guidance	3/106	0.000362	0.00986897	0.008056	SLIT1/ALCAM/SLIT2	3
GO:0061387	regulation of extent of cell growth	5/106	0.000374	0.01004294	0.008198	NTN1/RGMA/SLIT1/SEMA6D/MACF1	5
GO:0150063	visual system development	9/106	0.000387	0.01024471	0.008363	BMPR1B/FAT3/MEIS2/NFIA/NTRK2/VIM/NFIB/SDK1/PBX1	9

GO:0048880	sensory system development	9/106	0.000432	0.01117272	0.00912	BMPR1B/FAT3/MEIS2/NFIA/NTRK2/VIM/NFIB/SDK1/PBX1	9
GO:0050769	positive regulation of neurogenesis	7/106	0.000434	0.01117272	0.00912	METRNL/NTN1/NTRK2/PTPRZ1/TENM4/MACF1/SLIT2	7
GO:0001964	startle response	3/106	0.000457	0.01128685	0.009214	CSMD1/GRIN2A/TUBA1A	3
GO:0022010	central nervous system myelination	3/106	0.000457	0.01128685	0.009214	CLU/GPM6B/TENM4	3
GO:0032291	axon ensheathment in central nervous system	3/106	0.000457	0.01128685	0.009214	CLU/GPM6B/TENM4	3

GO:0072001	renal system development	8/106	0.000486	0.01177794	0.009615	MAGI2/NFIA/SULF1/KIF26B/BASP1/SLIT2/PBX1/ERBB4	8
GO:0050435	amyloid-beta metabolic process	4/106	0.000489	0.01177794	0.009615	CLU/NTRK2/RTN1/SPON1	4
GO:0048638	regulation of developmental growth	8/106	0.000527	0.01252166	0.010222	NTN1/RGMA/SLIT1/SEMA6D/BASP1/MACF1/AKAP6/ERBB4	8
GO:0048857	neural nucleus development	4/106	0.000549	0.01288509	0.010518	CKB/FOXP2/NFIB/BASP1	4
GO:0001558	regulation of cell growth	9/106	0.000572	0.01308868	0.010684	IGFBP5/NTN1/RGMA/SLIT1/NG3/SEMA6D/MACF1/AKAP6/SLIT2	9

GO:0021952	central nervous system projection neuron axonogenesis	3/106	0.000566	0.01308868	0.010684	NFIB/DCLK1/SLIT2	3
GO:0042987	amyloid precursor protein catabolic process	4/106	0.000581	0.01313301	0.010721	CLU/NTRK2/RTN1/SPON1	4
GO:0042692	muscle cell differentiation	9/106	0.000592	0.01321812	0.01079	IGFBP5/NEBL/QKI/SORBS2/CDH 2/DMD/ADGRB3/AKAP6/ANK2	9
GO:0021782	glial cell development	5/106	0.000626	0.01381859	0.01128	CLU/GPM6B/NTRK2/VIM/TENM 4	5
GO:0008361	regulation of cell size	6/106	0.000657	0.01431452	0.011685	KCNMA1/NTN1/RGMA/SLIT1/SE MA6D/MACF1	6

GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	3/106	0.000691	0.01488178	0.012148	DMD/AKAP6/ANK2	3
GO:0034249	negative regulation of amide metabolic process	8/106	0.000733	0.01544475	0.012608	CLU/IGFBP5/NTRK2/RTN1/SPON1/TRIM2/TNRC6A/GAPDH	8
GO:0021543	pallium development	6/106	0.000733	0.01544475	0.012608	NTRK2/FOXP2/CDH2/TUBB2B/TUBA1A/SLIT2	6
GO:0140058	neuron projection arborization	3/106	0.000759	0.01580321	0.0129	NLGN1/MACF1/TUBA1A	3
GO:0060074	synapse maturation	3/106	0.000908	0.01870096	0.015266	NFIA/NLGN1/ADGRB3	3

GO:0030879	mammary gland development	5/106	0.000925	0.01883882	0.015378	CSMD1/IGFBP5/NTN1/NRG3/ERBB4	5
GO:0051402	neuron apoptotic process	7/106	0.000984	0.01981371	0.016174	CHL1/CLU/NTRK2/PTPRZ1/TRIM2/TUBA1A/GAPDH	7
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	3/106	0.001075	0.02141869	0.017484	DMD/AKAP6/ANK2	3
GO:0048813	dendrite morphogenesis	5/106	0.001127	0.02221842	0.018137	HECW2/TNIK/NLGN1/DCLK1/ADGRB3	5
GO:0032535	regulation of cellular component size	8/106	0.001151	0.02225662	0.018168	KCNMA1/NTN1/RGMA/SLIT1/SEMA6D/MACF1/TMSB4X/SLIT2	8

GO:0048854	brain morphogenesis	3/106	0.001165	0.02225662	0.018168	SLIT1/CDH2/TUBA1A	3
GO:1903514	release of sequestered calcium ion into cytosol by endoplasmic reticulum	3/106	0.001165	0.02225662	0.018168	DMD/AKAP6/ANK2	3
GO:0030336	negative regulation of cell migration	8/106	0.001211	0.02290457	0.018697	IGFBP5/LIMCH1/MAGI2/SRGAP3/SULF1/NRG3/SEMA6D/SLIT2	8
GO:0009612	response to mechanical stimulus	6/106	0.001288	0.02343511	0.01913	ADGRV1/MEIS2/SLC1A3/CDH2/DMD/TUBA1A	6
GO:0099111	microtubule-based transport	6/106	0.00132	0.02343511	0.01913	CFAP43/CFAP54/DNAH11/RFX3/DST/TUBA1A	6

GO:0008306	associative learning	4/106	0.001343	0.02343511	0.01913	CSMD1/GRIN2A/MEIS2/TUBA1A	4
GO:0032414	positive regulation of ion transmembrane transporter activity	4/106	0.001343	0.02343511	0.01913	DMD/TMSB4X/AKAP6/ANK2	4
GO:0014912	negative regulation of smooth muscle cell migration	3/106	0.00126	0.02343511	0.01913	IGFBP5/SEMA6D/SLIT2	3
GO:0021955	central nervous system neuron axonogenesis	3/106	0.001359	0.02343511	0.01913	NFIB/DCLK1/SLIT2	3
GO:0038179	neurotrophin signaling pathway	3/106	0.001359	0.02343511	0.01913	DOCK3/MAGI2/NTRK2	3

GO:0038130	ERBB4 signaling pathway	2/106	0.001366	0.02343511	0.01913	NRG3/ERBB4	2
GO:0097104	postsynaptic membrane assembly	2/106	0.001366	0.02343511	0.01913	CDH2/NLGN1	2
GO:0099550	trans-synaptic signaling, modulating synaptic transmission	2/106	0.001366	0.02343511	0.01913	EFNB3/NTRK2	2
GO:0060421	positive regulation of heart growth	3/106	0.001463	0.02487936	0.020309	BASP1/AKAP6/ERBB4	3
GO:0050768	negative regulation of neurogenesis	5/106	0.001534	0.02560635	0.020903	EFNB3/NTN1/RGMA/SLIT1/SEM A6D	5

GO:0048864	stem cell development	4/106	0.001527	0.02560635	0.020903	MSI2/CDH2/SEMA6D/ERBB4	4
GO:0072073	kidney epithelium development	5/106	0.00158	0.02565789	0.020945	MAGI2/KIF26B/BASP1/SLIT2/PBX1	5
GO:0021954	central nervous system neuron development	4/106	0.001592	0.02565789	0.020945	NTRK2/NFIB/DCLK1/SLIT2	4
GO:0055017	cardiac muscle tissue growth	4/106	0.001592	0.02565789	0.020945	SORBS2/TENM4/AKAP6/ERBB4	4
GO:0120316	sperm flagellum assembly	3/106	0.001573	0.02565789	0.020945	CFAP43/CFAP47/CFAP54	3

GO:0021889	olfactory bulb interneuron differentiation	2/106	0.001663	0.02656987	0.021689	SLIT2/ERBB4	2
GO:0050804	modulation of chemical synaptic transmission	9/106	0.001743	0.02759775	0.022528	EFNB3/GRIN2A/NTRK2/SLC1A3/ NRG3/CDH2/TUBB2B/NLGN1/C NTN4	9
GO:0099177	regulation of trans-synaptic signaling	9/106	0.001767	0.02774748	0.022651	EFNB3/GRIN2A/NTRK2/SLC1A3/ NRG3/CDH2/TUBB2B/NLGN1/C NTN4	9
GO:0030516	regulation of axon extension	4/106	0.001799	0.02788564	0.022763	NTN1/SLIT1/SEMA6D/MACF1	4
GO:0070296	sarcoplasmic reticulum calcium ion transport	3/106	0.001806	0.02788564	0.022763	DMD/AKAP6/ANK2	3

GO:0051961	negative regulation of nervous system development	5/106	0.001825	0.0279429	0.02281	EFNB3/NTN1/RGMA/SLIT1/SEMA6D	5
GO:0001822	kidney development	7/106	0.001976	0.02901565	0.023686	MAGI2/SULF1/KIF26B/BASP1/SLIT2/PBX1/ERBB4	7
GO:0032412	regulation of monoatomic ion transmembrane transporter activity	6/106	0.001944	0.02901565	0.023686	HECW2/DMD/NLGN1/TMSB4X/AKAP6/ANK2	6
GO:0060294	cilium movement involved in cell motility	5/106	0.001984	0.02901565	0.023686	CFAP43/CFAP47/CFAP54/DNAH11/DNAH7	5
GO:0032411	positive regulation of transporter activity	4/106	0.001947	0.02901565	0.023686	DMD/TMSB4X/AKAP6/ANK2	4

GO:0030501	positive regulation of bone mineralization	3/106	0.00193	0.02901565	0.023686	ADGRV1/BMPR1B/GPM6B	3
GO:0071679	commissural neuron axon guidance	2/106	0.001989	0.02901565	0.023686	NCAM1/NFIB	2
GO:0007044	cell-substrate junction assembly	4/106	0.002024	0.02929478	0.023914	GPM6B/LIMCH1/DST/MACF1	4
GO:0035082	axoneme assembly	4/106	0.002103	0.02996974	0.024465	CFAP43/CFAP47/DNAH7/HYDIN	4
GO:0042982	amyloid precursor protein metabolic process	4/106	0.002103	0.02996974	0.024465	CLU/NTRK2/RTN1/SPON1	4

GO:0022898	regulation of transmembrane transporter activity	6/106	0.002306	0.03048025	0.024881	HECW2/DMD/NLGN1/TMSB4X/AKAP6/ANK2	6
GO:0050905	neuromuscular process	5/106	0.002273	0.03048025	0.024881	CSMD1/GRIN2A/SLC1A3/DMD/TUBA1A	5
GO:0001657	ureteric bud development	4/106	0.002267	0.03048025	0.024881	KIF26B/BASP1/SLIT2/PBX1	4
GO:0060993	kidney morphogenesis	4/106	0.002267	0.03048025	0.024881	KIF26B/BASP1/PBX1/ERBB4	4
GO:0050773	regulation of dendrite development	4/106	0.002352	0.03048025	0.024881	FAT3/HECW2/TNFRSF25/ADGRB3	4

GO:0072163	mesonephric epithelium development	4/106	0.002352	0.03048025	0.024881	KIF26B/BASP1/SLIT2/PBX1	4
GO:0072164	mesonephric tubule development	4/106	0.002352	0.03048025	0.024881	KIF26B/BASP1/SLIT2/PBX1	4
GO:0030517	negative regulation of axon extension	3/106	0.002194	0.03048025	0.024881	NTN1/SLIT1/SEMA6D	3
GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	3/106	0.002335	0.03048025	0.024881	CDHR3/CDH2/NLGN1	3
GO:0021781	glial cell fate commitment	2/106	0.002342	0.03048025	0.024881	NFIA/NFIB	2

GO:0048853	forebrain morphogenesis	2/106	0.002342	0.03048025	0.024881	SLIT1/TUBA1A	2
GO:0060287	epithelial cilium movement involved in determination of left/right asymmetry	2/106	0.002342	0.03048025	0.024881	DNAH11/RFX3	2
GO:1902667	regulation of axon guidance	2/106	0.002342	0.03048025	0.024881	TUBB2B/SLIT2	2
GO:0008542	visual learning	3/106	0.00248	0.03169342	0.025872	GRIN2A/MEIS2/TUBA1A	3
GO:0014003	oligodendrocyte development	3/106	0.00248	0.03169342	0.025872	CLU/GPM6B/TENM4	3

GO:0048639	positive regulation of developmental growth	5/106	0.002525	0.03204188	0.026156	NTN1/BASP1/MACF1/AKAP6/ERBB4	5
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	5/106	0.002591	0.03265601	0.026658	CDHR3/FAT3/CDH2/CNTN4/SDK1	5
GO:0150115	cell-substrate junction organization	4/106	0.002622	0.03272099	0.026711	GPM6B/LIMCH1/DST/MACF1	4
GO:2001259	positive regulation of cation channel activity	3/106	0.002631	0.03272099	0.026711	TMSB4X/AKAP6/ANK2	3
GO:0045926	negative regulation of growth	6/106	0.002716	0.0331823	0.027087	IGFBP5/NTN1/RGMA/SLIT1/SEMA6D/SLIT2	6

GO:0001823	mesonephros development	4/106	0.002716	0.0331823	0.027087	KIF26B/BASP1/SLIT2/PBX1	4
GO:0060019	radial glial cell differentiation	2/106	0.002722	0.0331823	0.027087	METRN/CDH2	2
GO:0046622	positive regulation of organ growth	3/106	0.00295	0.03572715	0.029165	BASP1/AKAP6/ERBB4	3
GO:0050806	positive regulation of synaptic transmission	5/106	0.003013	0.03625756	0.029598	EFNB3/GRIN2A/NTRK2/SLC1A3/NLGN1	5
GO:0090660	cerebrospinal fluid circulation	2/106	0.003129	0.03740895	0.030537	CFAP43/CFAP54	2

GO:0035265	organ growth	5/106	0.003242	0.03851358	0.031439	SORBS2/TENM4/BASP1/AKAP6/ERBB4	5
GO:0043010	camera-type eye development	7/106	0.003284	0.03860322	0.031512	BMPR1B/FAT3/NFIA/NTRK2/VI M/NFIB/SDK1	7
GO:0045778	positive regulation of ossification	3/106	0.003292	0.03860322	0.031512	ADGRV1/BMPR1B/GPM6B	3
GO:0048732	gland development	8/106	0.00352	0.03959737	0.032324	CSMD1/IGFBP5/NTN1/SULF1/NR G3/NFIB/PBX1/ERBB4	8
GO:0010720	positive regulation of cell development	8/106	0.003569	0.03959737	0.032324	METR1/NTN1/NTRK2/PTPRZ1/R FX3/TENM4/MACF1/SLIT2	8

GO:0021953	central nervous system neuron differentiation	5/106	0.003567	0.03959737	0.032324	BMPR1B/NTRK2/NFIB/DCLK1/S LIT2	5
GO:0035249	synaptic transmission, glutamatergic	4/106	0.003555	0.03959737	0.032324	CDHR3/GRIN2A/CDH2/NLGN1	4
GO:0070169	positive regulation of biomineral tissue development	3/106	0.003471	0.03959737	0.032324	ADGRV1/BMPR1B/GPM6B	3
GO:0007158	neuron cell-cell adhesion	2/106	0.003563	0.03959737	0.032324	NLGN1/CNTN4	2
GO:0017014	protein nitrosylation	2/106	0.003563	0.03959737	0.032324	DMD/GAPDH	2

GO:0018119	peptidyl-cysteine S-nitrosylation	2/106	0.003563	0.03959737	0.032324	DMD/GAPDH	2
GO:0097091	synaptic vesicle clustering	2/106	0.003563	0.03959737	0.032324	CDH2/NLGN1	2
GO:0007632	visual behavior	3/106	0.003848	0.04244106	0.034645	GRIN2A/MEIS2/TUBA1A	3
GO:0003012	muscle system process	8/106	0.003973	0.043563	0.035561	DTNA/IGFBP5/KCNMA1/SULF1/ SORBS2/DMD/AKAP6/ANK2	8
GO:0048640	negative regulation of developmental growth	4/106	0.004035	0.04358018	0.035575	NTN1/RGMA/SLIT1/SEMA6D	4

GO:0043113	receptor clustering	3/106	0.004045	0.04358018	0.035575	MAGI2/CDH2/NLGN1	3
GO:0003356	regulation of cilium beat frequency	2/106	0.004023	0.04358018	0.035575	CFAP43/DNAH11	2
GO:0007281	germ cell development	7/106	0.004147	0.04442181	0.036262	BMPR1B/CFAP43/CFAP47/CFAP54/FMN2/PACRG/QKI	7
GO:0032409	regulation of transporter activity	6/106	0.004277	0.04537544	0.037041	HECW2/DMD/NLGN1/TMSB4X/AKAP6/ANK2	6
GO:0030308	negative regulation of cell growth	5/106	0.004285	0.04537544	0.037041	NTN1/RGMA/SLIT1/SEMA6D/SLIT2	5

GO:0090036	regulation of protein kinase C signaling	2/106	0.00451	0.04748198	0.03876	ADGRV1/ULK4	2
GO:0072009	nephron epithelium development	4/106	0.004693	0.04913101	0.040106	MAGI2/KIF26B/BASP1/PBX1	4

Enrichment of Up-regulated genes across all cells in ScRNA-seq data

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> -value	gene ID	count
GO:0002181	cytoplasmic translation	67/180	2.47E-97	6.5277E-94	5.9E-94	RPL10/RPL11/RPL12/RPL13/RPL32/RPL34/RPL36A/RPL39/RPS15A/RPS18/RPS2/RPS21/RPS23/RPS3/RPS4X/RPL30/RPL14/RPS28/RPL26/RPL28/RPL7A/RPS8/RPL10A/RPL37/RPL18A/PABPC1/RPS27/RPL18/RPS24/RPS12/RPL17/RPL8/RPL41/RPL29/RPS7/RPLP0/RPL35A/RPL23A/RPL5/RPS14/RPS13/RPL19/RACK1/RPS9/RPS5/RPLP2/RPL24/RPS27A/RPS3A/RPS6/RPL6/RPS25/RPS16/RPL15/RPL37A/RPL7/RPL22/RPLP1/RPL9/RPL13A/RPL36/RPL3/RPS10/RPS19/RPS15/RPS11/RPL21	67
GO:0042254	ribosome biogenesis	35/180	7.64E-27	1.011E-23	9.14E-24	RPL10/RPL11/RPS15A/RPS21/RPS23/RPS4X/RPL14/RPS28/RPL26/RPL7A/RPS8/RPL10A/RPS27/RPS24/RPS12/RPS7/RPLP0/RPL35A/RPL23A/RPL5/RPS14/RPS13/RPS9/RPS5/RPL24/NPM1/RPS3A/RPS6/RPL6/RPS25/RPS16/RPL7/RPS19/RPS15/RPS11	35
GO:0042274	ribosomal small subunit biogenesis	22/180	9.36E-24	8.2521E-21	7.46E-21	RPS15A/RPS21/RPS23/RPS4X/RPS28/RPS8/RPS27/RPS24/RPS12/RPS7/RPS14/RPS13/RPS9/RPS5/NPM1/RPS3A/RPS6/RPS25/RPS16/RPS19/RPS15/RPS11	22

GO:0042255	ribosome assembly	14/180	9.78E-16	6.4703E-13	5.85E-13	RPL10/RPL11/RPS28/RPS27/RPLP0/RPL23A/RPL5/RPS14/RPS5/RPL24/NPM1/RPL6/RPS19/RPS15	14
GO:0042273	ribosomal large subunit biogenesis	14/180	1.27E-14	6.7325E-12	6.09E-12	RPL10/RPL11/RPL14/RPL26/RPL7A/RPL10A/RPLP0/RPL35A/RPL23A/RPL5/RPL24/NPM1/RPL6/RPL7	14
GO:0006364	rRNA processing	20/180	4.71E-14	2.0773E-11	1.88E-11	RPL11/RPS21/RPL14/RPS28/RPL26/RPL7A/RPS8/RPL10A/RPS27/RPS24/RPS7/RPL35A/RPL5/RPS14/RPS6/RPS25/RPS16/RPL7/RPS19/RPS15	20
GO:0016072	rRNA metabolic process	20/180	9.56E-13	3.6126E-10	3.27E-10	RPL11/RPS21/RPL14/RPS28/RPL26/RPL7A/RPS8/RPL10A/RPS27/RPS24/RPS7/RPL35A/RPL5/RPS14/RPS6/RPS25/RPS16/RPL7/RPS19/RPS15	20

GO:0140694	non-membrane-bounded organelle assembly	21/180	3.7E-10	1.223E-07	1.11E-07	KRT19/RPL10/RPL11/RPS23/RPS3/KRT 8/RPS28/RPS27/STAG1/RPLP0/RPL23A/ RPL5/RPS14/RPS5/RPL24/NPM1/RPL6/ MAPRE2/RPS19/RPS15/ACTG1	21
GO:0034470	ncRNA processing	21/180	1.39E-09	4.0762E-07	3.69E-07	H19/RPL11/RPS21/RPL14/RPS28/RPL26 /RPL7A/RPS8/RPL10A/RPS27/RPS24/RP S7/RPL35A/RPL5/RPS14/RPS6/RPS25/R PS16/RPL7/RPS19/RPS15	21
GO:0000027	ribosomal large subunit assembly	7/180	3.61E-09	9.5451E-07	8.63E-07	RPL10/RPL11/RPLP0/RPL23A/RPL5/RP L24/RPL6	7
GO:0022618	protein-RNA complex assembly	15/180	7.9E-09	1.8989E-06	1.72E-06	RPL10/RPL11/RPS28/RPS27/RPLP0/RPL 23A/RPL5/RPS14/RPS5/RPL24/RPL6/RP L13A/HSP90AB1/RPS19/RPS15	15

GO:0071826	protein-RNA complex organization	15/180	1.24E-08	2.7337E-06	2.47E-06	RPL10/RPL11/RPS28/RPS27/RPLP0/RPL23A/RPL5/RPS14/RPS5/RPL24/RPL6/RPL13A/HSP90AB1/RPS19/RPS15	15
GO:0000028	ribosomal small subunit assembly	6/180	1.7E-08	3.4512E-06	3.12E-06	RPS28/RPS27/RPS14/RPS5/RPS19/RPS15	6
GO:0010810	regulation of cell-substrate adhesion	12/180	1.39E-06	0.0002628	0.000238	COL1A1/FN1/MYADM/POSTN/FBLN1/NPNT/MDK/CDK6/FMN1/DLC1/EFNA5/ACTG1	12
GO:0030199	collagen fibril organization	7/180	2.79E-06	0.00049238	0.000445	COL1A1/COL1A2/COL3A1/COL5A1/COL5A2/LUM/COL11A1	7

GO:0031589	cell-substrate adhesion	14/180	8.52E-06	0.00128918	0.001166	COL1A1/COL3A1/FN1/MYADM/POSTN/FBLN1/NPNT/MDK/CDK6/PTPRK/FMN1/DLC1/EFNA5/ACTG1	14
GO:1901796	regulation of signal transduction by p53 class mediator	8/180	8.56E-06	0.00128918	0.001166	RPL11/RPL26/RPL37/RPS7/RPL5/NPM1/SOX4/RPS15	8
GO:1901798	positive regulation of signal transduction by p53 class mediator	5/180	8.77E-06	0.00128918	0.001166	RPL11/RPL26/RPL37/RPS7/RPS15	5
GO:0031397	negative regulation of protein ubiquitination	7/180	9.55E-06	0.00132921	0.001202	PRKCG/RPL11/RPS3/RPS7/RPL5/SQSTM1/SOX4	7

GO:0030490	maturation of SSU-rRNA	6/180	1.1E-05	0.00145059	0.001312	RPS21/RPS28/RPS8/RPS14/RPS16/RPS19	6
GO:0060560	developmental growth involved in morphogenesis	11/180	2.33E-05	0.00280568	0.002537	APOE/FN1/POSTN/SLIT3/FGF13/IFRD1/FMN1/HSP90AB1/EFNA5/PRKG1/AUTS2	11
GO:0031396	regulation of protein ubiquitination	10/180	2.29E-05	0.00280568	0.002537	PRKCG/RPL11/RPS2/RPS3/RPS7/RPL5/SQSTM1/NPM1/SOX4/HSP90AB1	10
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	7/180	2.45E-05	0.00282098	0.002551	PRKCG/RPL11/RPS3/RPS7/RPL5/SQSTM1/SOX4	7

GO:1901874	negative regulation of post-translational protein modification	7/180	3.99E-05	0.0043953	0.003974	PRKCG/RPL11/RPS3/RPS7/RPL5/SQSTM1/SOX4	7
GO:0150115	cell-substrate junction organization	7/180	5.51E-05	0.00582814	0.00527	FN1/PTPRK/FMN1/DLC1/MAPRE2/EFNA5/ACTG1	7
GO:0030198	extracellular matrix organization	12/180	6.21E-05	0.00622666	0.00563	COL1A1/COL1A2/COL3A1/COL5A1/COL5A2/LUM/POSTN/FBLN1/NPNT/COL11A1/MATN2/LARGE1	12
GO:0043062	extracellular structure organization	12/180	6.4E-05	0.00622666	0.00563	COL1A1/COL1A2/COL3A1/COL5A1/COL5A2/LUM/POSTN/FBLN1/NPNT/COL11A1/MATN2/LARGE1	12

GO:0045229	external encapsulating structure organization	12/180	6.59E-05	0.00622666	0.00563	COL1A1/COL1A2/COL3A1/COL5A1/COL5A2/LUM/POSTN/FBLN1/NPNT/COL11A1/MATN2/LARGE1	12
GO:0031400	negative regulation of protein modification process	14/180	8.07E-05	0.0073641	0.006659	APOE/MYADM/PRKCG/RPL11/RPS3/FBLN1/CDKN1C/IGFBP3/RPS7/RPL5/RACK1/SQSTM1/NPM1/SOX4	14
GO:0001503	ossification	14/180	9.55E-05	0.00798179	0.007217	COL1A1/COL1A2/COL5A2/MGP/IGF2/IGFBP3/NPNT/MDK/COL11A1/FBN2/CDK6/KCNQ1OT1/HAND2/RPS15	14
GO:1901873	regulation of post-translational protein modification	11/180	9.22E-05	0.00798179	0.007217	PRKCG/RPL11/RPS2/RPS3/RPS7/RPL5/SQSTM1/NPM1/SOX4/HSP90AB1/AUTS2	11

GO:0007160	cell-matrix adhesion	10/180	0.000103	0.00798179	0.007217	COL3A1/FN1/POSTN/NPNT/CDK6/PTP RK/FMN1/DLC1/EFNA5/ACTG1	10
GO:0048588	developmental cell growth	10/180	0.000103	0.00798179	0.007217	APOE/FN1/POSTN/SLIT3/FGF13/IFRD1/ HSP90AB1/EFNA5/PRKG1/AUTS2	10
GO:0035987	endodermal cell differentiation	5/180	0.000101	0.00798179	0.007217	COL5A1/COL5A2/FN1/COL11A1/HMG A2	5
GO:1903320	regulation of protein modification by small protein conjugation or removal	10/180	0.000118	0.00888773	0.008036	PRKCG/RPL11/RPS2/RPS3/RPS7/RPL5/ SQSTM1/NPM1/SOX4/HSP90AB1	10

GO:0048668	collateral sprouting	4/180	0.000137	0.01007122	0.009106	FGF13/IFRD1/EFNA5/PRKG1	4
GO:0001706	endoderm formation	5/180	0.000227	0.01625266	0.014695	COL5A1/COL5A2/FN1/COL11A1/HMG A2	5
GO:0072331	signal transduction by p53 class mediator	8/180	0.000281	0.01907423	0.017247	RPL11/RPL26/RPL37/RPS7/RPL5/NPM1 /SOX4/RPS15	8
GO:1900024	regulation of substrate adhesion- dependent cell spreading	5/180	0.000288	0.01907423	0.017247	MYADM/POSTN/FBLN1/MDK/EFNA5	5

GO:1900025	negative regulation of substrate adhesion-dependent cell spreading	3/180	0.000288	0.01907423	0.017247	POSTN/FBLN1/EFNA5	3
GO:0007044	cell-substrate junction assembly	6/180	0.000298	0.01924991	0.017406	FN1/PTPRK/FMN1/DLC1/EFNA5/ACTG1	6
GO:0016049	cell growth	14/180	0.000306	0.0192537	0.017409	APOE/FN1/POSTN/SLIT3/FGF13/IGFBP3/RACK1/NPM1/BTG1/IFRD1/HSP90AB1/EFNA5/PRKG1/AUTS2	14
GO:0007409	axonogenesis	13/180	0.000379	0.02168533	0.019608	APOE/FN1/SLIT3/FGF13/ROBO2/RPL24/IFRD1/RPS6KA5/HSP90AB1/EFNA5/PRKG1/AUTS2/ACTG1	13

GO:0034446	substrate adhesion-dependent cell spreading	6/180	0.000394	0.02168533	0.019608	FN1/MYADM/POSTN/FBLN1/MDK/EFNA5	6
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	5/180	0.000361	0.02168533	0.019608	RPL11/RPS3/RPL26/RPS7/RACK1	5
GO:0010812	negative regulation of cell-substrate adhesion	5/180	0.000388	0.02168533	0.019608	COL1A1/POSTN/FBLN1/DLC1/EFNA5	5
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4/180	0.000372	0.02168533	0.019608	RPS21/RPS8/RPS16/RPS19	4

GO:0051444	negative regulation of ubiquitin-protein transferase activity	3/180	0.000357	0.02168533	0.019608	RPL11/RPS7/RPL5	3
GO:0071560	cellular response to transforming growth factor beta stimulus	10/180	0.000447	0.02410924	0.021799	COL1A1/COL1A2/COL3A1/POSTN/CDKN1C/NPNT/FBN2/PTPRK/NREP/HSP90AB1	10
GO:0150116	regulation of cell-substrate junction organization	5/180	0.000479	0.02484242	0.022462	FMN1/DLC1/MAPRE2/EFNA5/ACTG1	5
GO:1903051	negative regulation of proteolysis involved in protein catabolic process	5/180	0.000479	0.02484242	0.022462	PRKCG/RPL11/RPS7/RPL5/HSP90AB1	5

GO:0021543	pallium development	8/180	0.000505	0.02532374	0.022897	COL3A1/PLCB1/FGF13/MDK/SLC38A2/CDK6/ALK/LARGE1	8
GO:0051438	regulation of ubiquitin-protein transferase activity	4/180	0.000507	0.02532374	0.022897	RPL11/RPS2/RPS7/RPL5	4
GO:0071559	response to transforming growth factor beta	10/180	0.000525	0.02570638	0.023243	COL1A1/COL1A2/COL3A1/POSTN/CDKN1C/NPNT/FBN2/PTPRK/NREP/HSP90AB1	10
GO:0007369	gastrulation	8/180	0.000619	0.02960525	0.026769	COL5A1/COL5A2/FN1/MYADM/COL11A1/HMGA2/RACK1/RPS6	8

GO:1904666	regulation of ubiquitin protein ligase activity	3/180	0.000627	0.02960525	0.026769	RPL11/RPS7/RPL5	3
GO:0060840	artery development	6/180	0.000686	0.03182337	0.028774	APOE/COL3A1/MDK/ROBO2/SOX4/H ND2	6
GO:0045663	positive regulation of myoblast differentiation	4/180	0.000739	0.03370581	0.030476	PLCB1/IGFBP3/SOX4/BTG1	4
GO:0040013	negative regulation of locomotion	12/180	0.000775	0.03473234	0.031405	APOE/COL3A1/PLCB1/CLIC4/FBLN1/I GFBP3/ROBO2/PTPRK/PTPRR/DLC1/E VL/PRKG1	12

GO:0001649	osteoblast differentiation	9/180	0.000829	0.0365618	0.033059	COL1A1/IGF2/IGFBP3/NPNT/FBN2/CDK6/KCNQ1OT1/HAND2/RPS15	9
GO:0071604	transforming growth factor beta production	4/180	0.000879	0.03812324	0.034471	COL3A1/FN1/LUM/HSP90AB1	4
GO:0048844	artery morphogenesis	5/180	0.001008	0.04230642	0.038253	APOE/COL3A1/MDK/SOX4/HAND2	5
GO:0048670	regulation of collateral sprouting	3/180	0.001	0.04230642	0.038253	FGF13/IFRD1/EFNA5	3

GO:0048675	axon extension	6/180	0.001077	0.0444905	0.040228	APOE/FN1/SLIT3/IFRD1/HSP90AB1/AU TS2	6
GO:0006413	translational initiation	6/180	0.001172	0.04695564	0.042457	RPS3/RPS5/NPM1/RPS3A/RPL13A/EIF1	6
GO:0010811	positive regulation of cell- substrate adhesion	6/180	0.001172	0.04695564	0.042457	FN1/MYADM/NPNT/MDK/CDK6/FMN1	6
GO:0007492	endoderm development	5/180	0.001189	0.04695564	0.042457	COL5A1/COL5A2/FN1/COL11A1/HMG A2	5

GO:2000146	negative regulation of cell motility	11/180	0.001285	0.04861532	0.043957	APOE/COL3A1/PLCB1/CLIC4/FBLN1/IGFBP3/PTPRK/PTPRR/DLC1/EVL/PRKG1	11
GO:0001952	regulation of cell-matrix adhesion	6/180	0.001273	0.04861532	0.043957	POSTN/CDK6/FMN1/DLC1/EFNA5/ACTG1	6
GO:0048041	focal adhesion assembly	5/180	0.001323	0.04861532	0.043957	PTPRK/FMN1/DLC1/EFNA5/ACTG1	5
GO:0021542	dentate gyrus development	3/180	0.001314	0.04861532	0.043957	MDK/CDK6/LARGE1	3

GO:0031290	retinal ganglion cell axon guidance	3/180	0.001314	0.04861532	0.043957	ROBO2/RPL24/EFNA5	3
GO:0021537	telencephalon development	9/180	0.001365	0.04945706	0.044719	COL3A1/PLCB1/FGF13/MDK/SLC38A2/ CDK6/ROBO2/ALK/LARGE1	9