

Supplementary Table S1. DEGs at Day 14.

Gene	Chromosome	Description	Log2foldchange	Pvalue	Padj
RHOBTB2	Chromosome8	Rho related BTB domain containing 2	0.669612	9.83E-05	0.04719
POU2F2	Chromosome19	POU class 2 homeobox 2	1.155037	2.21E-05	0.01625
CDH1	Chromosome16	cadherin 1	3.513451	9.74E-09	1.74E-05
MAP3K13	Chromosome3	mitogen-activated protein kinase kinase kinase 13	-0.70969	2.88E-05	0.019962
RUNX1T1	Chromosome8	RUNX1 partner transcriptional co-repressor 1	1.025548	4.82E-05	0.027932
PCDHA6	Chromosome5	protocadherin alpha 6	1.279984	4.07E-10	1.02E-06
COCH	Chromosome14	cochlin	-0.96613	1.8E-05	0.014529
ESRP1	Chromosome8	epithelial splicing regulatory protein 1	3.205117	4.13E-05	0.026408
CDH6	Chromosome5	cadherin 6	-1.01866	0.000108	0.049112
EHHADH	Chromosome3	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase	-1.1781	2.84E-05	0.019962
ITGA4	Chromosome2	integrin subunit alpha 4	-1.20922	4.78E-05	0.027932
CCN2	Chromosome6	cellular communication network factor 2	-1.71999	8.53E-09	1.64E-05
ONECUT2	Chromosome18	one cut homeobox 2	0.717125	1.69E-05	0.014524
NEUROD4	Chromosome12	neuronal differentiation 4	1.181789	6.27E-05	0.03249
LRRC61	Chromosome7	leucine rich repeat containing 61	-5.62667	5.64E-05	0.030596
CCN1	Chromosome1	cellular communication network factor 1	-0.72065	1.48E-05	0.013234
LHX9	Chromosome1	LIM homeobox 9	1.20025	3.6E-06	0.004084
IGFBP3	Chromosome7	insulin like growth factor binding protein 3	-1.03333	3.92E-06	0.004255
HTR2C	ChromosomeX	5-hydroxytryptamine receptor 2C	-0.96333	0.000105	0.048926
INA	Chromosome10	internexin neuronal intermediate filament protein alpha	0.991458	4.99E-05	0.027932
RWDD2B	Chromosome21	RWD domain containing 2B	-1.14682	0.000106	0.048926
DMTN	Chromosome8	dematin actin binding protein	1.142605	6.28E-05	0.03249
CELF3	Chromosome1	CUGBP Elav-like family member 3	1.000989	9.04E-05	0.044241
FGF19	Chromosome11	fibroblast growth factor 19	0.976341	5.04E-05	0.027932
ANKRD30BL	Chromosome2	ankyrin repeat domain 30B like	-5.96489	1.92E-11	5.99E-08
ZNF283	Chromosome19	zinc finger protein 283	-0.87737	6.18E-06	0.006425
MMADHC	Chromosome2	metabolism of cobalamin associated D	-0.86747	2.33E-06	0.002912
INSM2	Chromosome14	INSM transcriptional repressor 2	1.211584	6.38E-05	0.03249
PCSK9	Chromosome1	proprotein convertase subtilisin/kexin type 9	-1.11235	7.03E-06	0.007017
ONECUT1	Chromosome15	one cut homeobox 1	1.516017	5.34E-07	0.000741
GAP43	Chromosome3	growth associated protein 43	1.213262	1.95E-05	0.015212
ALG10B	Chromosome12	ALG10 alpha-1,2-glucosyltransferase B	-4.29585	9.12E-41	2.28E-36
ZFP3	Chromosome17	ZFP3 zinc finger protein	1.120217	2.53E-06	0.003003
SRY	ChromosomeY	sex determining region Y	-6.22461	1.85E-09	3.86E-06
SLITRK2	ChromosomeX	SLIT and NTRK like family member 2	-6.35064	8.61E-08	0.000134
ZBED10P	Chromosome7	zinc finger BED-type containing 10, pseudogene	-5.6076	4.98E-05	0.027932
ELAVL3	Chromosome19	ELAV like RNA binding protein 3	0.793427	8.96E-05	0.044241
POTEF	Chromosome2	POTE ankyrin domain family member F	-3.68946	3E-05	0.020205
POU5F1	Chromosome6	POU class 5 homeobox 1	3.475177	4.08E-05	0.026408

ONECUT3	Chromosome19	one cut homeobox 3	1.989863	9.24E-06	0.008872
LINC01139	Chromosome1	long intergenic non-protein coding RNA 1139	4.400746	8.05E-21	5.02E-17
TTC34	Chromosome1	tetratricopeptide repeat domain 34	-9.11989	1.69E-17	7.04E-14
ZNF736	Chromosome7	zinc finger protein 736	-11.8101	6.25E-25	6.01E-21
PPIEL	Chromosome1	peptidylprolyl isomerase E like pseudogene	-2.09503	4.03E-20	2.01E-16
UNKNOWN	Chromosome15	novel transcript	1.138439	1.8E-05	0.014529
PCDHGA8	Chromosome5	protocadherin gamma subfamily A, 8	-1.66447	3.37E-07	0.000495
PCDHGB4	Chromosome5	protocadherin gamma subfamily B, 4	-2.41996	7.22E-25	6.01E-21
UNKNOWN	Chromosome8	novel transcript	3.890177	2.21E-05	0.01625
FPGT	Chromosome1	fucose-1-phosphate guanylyltransferase	-9.0428	3.81E-17	1.36E-13
LINC02301	Chromosome14	long intergenic non-protein coding RNA 2301	-5.96868	2.72E-10	7.55E-07
FPGT-TNNI3K	Chromosome1	FPGT-TNNI3K readthrough	-7.11343	1.10E-09	2.49E-06
LINC00664	Chromosome19	long intergenic non-protein coding RNA 664	-3.11982	4.42E-08	7.36E-05
UNKNOWN	Chromosome2	novel transcript	-1.53096	4.47E-05	0.027909
H3-7	Chromosome1	H3.7 histone (putative)	-6.27514	7.13E-07	0.000936
H4C6	Chromosome6	H4 clustered histone 6	-1.35358	1.22E-05	0.011257

Supplementary Table S2. DEGs at Day 63.

Gene	Chromosome	Description	Log2foldchange	Pvalue	Padj
PCDHA6	Chromosome5	protocadherin alpha 6	0.872531	6.41E-06	0.006875
HSD17B2	Chromosome16	hydroxysteroid 17-beta dehydrogenase 2	2.342497	1.39E-05	0.013431
PHACTR3	Chromosome20	phosphatase and actin regulator 3	-3.89591	4.05E-08	0.000106
PCDHB7	Chromosome5	protocadherin beta 7	1.038808	8.48E-07	0.001234
DUSP4	Chromosome8	dual specificity phosphatase 4	0.650908	5.28E-05	0.040641
VGF	Chromosome7	VGF nerve growth factor inducible	1.639064	8.36E-07	0.001234
SERPINF1	Chromosome17	serpin family F member 1	1.737584	6.36E-05	0.045024
ANKRD30BL	Chromosome2	ankyrin repeat domain 30B like	-6.66828	1.94E-11	6.33E-08
ZNF283	Chromosome19	zinc finger protein 283	-0.87006	1.47E-07	0.000349
MMADHC	Chromosome2	metabolism of cobalamin associated D	-0.87092	6.57E-06	0.006875
KCNK9	Chromosome8	potassium two pore domain channel subfamily K member 9	-1.5854	8.15E-06	0.008202
ALG10B	Chromosome12	ALG10 alpha-1,2-glucosyltransferase B	-4.57739	6.98E-26	9.13E-22
ETV4	Chromosome17	ETS variant transcription factor 4	1.039042	2.18E-05	0.018985
ZFP3	Chromosome17	ZFP3 zinc finger protein	1.245829	1.19E-06	0.001641
CSMD1	Chromosome8	CUB and Sushi multiple domains 1	2.122138	3.46E-06	0.004121
SLITRK2	ChromosomeX	SLIT and NTRK like family member 2	-10.4611	1.04E-15	6.78E-12
SPRY4	Chromosome5	sprouty RTK signaling antagonist 4	0.939426	6.72E-07	0.001173
LINC01139	Chromosome1	long intergenic non-protein coding RNA 1139	5.801755	2.93E-07	0.00064
TTC34	Chromosome1	tetratricopeptide repeat domain 34	-7.95605	2.19E-12	8.18E-09
ZNF736	Chromosome7	zinc finger protein 736	-8.6607	3.46E-15	1.81E-11
LURAP1L-AS1	Chromosome9	LURAP1L antisense RNA 1	1.872927	4.85E-06	0.005522
CECR7	Chromosome22	cat eye syndrome chromosome region, candidate 7	-3.05989	2.09E-06	0.00261
L1TD1	Chromosome1	LINE1 type transposase domain containing 1	-4.74316	4.77E-07	0.000891
PPIEL	Chromosome1	peptidylprolyl isomerase E like pseudogene	-1.60888	4.34E-19	3.78E-15
LINC02899	Chromosome5	long intergenic non-protein coding RNA 2899	-6.0976	2.48E-05	0.020682
PCDHGA8	Chromosome5	protocadherin gamma subfamily A, 8	-1.96081	5.30E-10	1.54E-06
PCDHGB4	Chromosome5	protocadherin gamma subfamily B, 4	-2.29778	6.18E-26	9.13E-22
FPGT	Chromosome1	fucose-1-phosphate guanylyltransferase	-8.73754	1.62E-14	7.09E-11
LINC01965	Chromosome2	long intergenic non-protein coding RNA 1965	-1.70088	2.53E-05	0.020682
ZNF578	Chromosome19	zinc finger protein 578	-1.74153	3.28E-05	0.02599
LINC02301	Chromosome14	long intergenic non-protein coding RNA 2301	-4.60798	7.23E-07	0.001183
FPGT-TNNI3K	Chromosome1	FPGT-TNNI3K readthrough	-3.93982	1.78E-05	0.016097
UNKNOWN	Chromosome2	novel transcript	-1.54812	1.36E-06	0.001783
H3-7	Chromosome1	H3.7 histone (putative)	-5.84017	1.62E-05	0.015106
ZNF229	Chromosome19	zinc finger protein 229	-5.2997	5.54E-05	0.041461
UNKNOWN	Chromosome19	novel transcript	-1.63122	5.79E-05	0.042081
UNKNOWN	Chromosome7	novel transcript	-6.78667	3.78E-07	0.00076

Supplementary Table S3. Common DEGs at day 14 & 63.

Gene	Chromosome	Function
PCDHA6	Chromosome5	Cell-cell connections in the brain
ANKRD30BL	Chromosome2	Unknown
ZNF283	Chromosome19	Transcriptional regulation
MMADHC	Chromosome2	Vitamin B12 metabolism
ALG10B	Chromosome12	Regulation of K ⁺ channel, protein glycosylation
ZFP3	Chromosome17	DNA binding activity
SLITRK2	Chromosomex	Synaptogenesis and excitatory synapse differentiation
LINC01139	Chromosome1	Unknown
TTC34	Chromosome1	Unknown
ZNF736	Chromosome7	Transcriptional regulation
PPIEL	Chromosome1	Unknown pseudogene
PCDHGA8	Chromosome5	Cell-cell connections in the brain
PCDHGB4	Chromosome5	Cell-cell connections in the brain
FPGT	Chromosome1	Cell-cell recognition
LINC02301	Chromosome14	Unknown
FPGT-TNNI3K	Chromosome1	Unknown
ENSG00000272054.1	Chromosome2	Unknown
H3-7	Chromosome1	Unknown pseudogene