

# Appendix A

## Supplementary Data

**Table A.1: The list of putative neuron-specific genes**

Entrez ID	Symbol						
11419	Acen2	11488	Adam11	11496	Adam22	11518	Add1
11519	Add2	11674	Aldoa	11676	Aldoc	11735	Ank3
11739	Slc25a4	11769	Ap1s1	11771	Ap2a1	11772	Ap2a2
11773	Ap2m1	11775	Ap3b2	11789	Apc	11829	Aqp4
11838	Arc	11842	Arf3	11899	Astn1	11931	Atp1b1
11932	Atp1b2	11938	Atp2a2	11941	Atp2b2	11964	Atp6v1a
11966	Atp6v1b2	11972	Atp6v0d1	11973	Atp6v1e1	11975	Atp6v0a1
11980	Atp8a1	11981	Atp9a	12032	Bcan	12217	Bsn
12286	Cacna1a	12287	Cacna1b	12293	Cacna2d1	12294	Cacna2d3
12295	Cacnb1	12297	Cacnb3	12298	Cacnb4	12300	Cacng2
12313	Calm1	12314	Calm2	12315	Calm3	12322	Camk2a
12323	Camk2b	12361	Cask	12386	Ctnna2	12554	Cdh13
12558	Cdh2	12561	Cdh4	12568	Cdk5	12569	Cdk5r1
12669	Chrm1	12704	Cit	12709	Ckb	12716	Ckmt1
12799	Cnp	12805	Cntn1	12933	Crmp1	12934	Dpysl2
12950	Hapln1	13004	Ncan	13116	Cyp46a1	13175	Dclk1
13191	Dctn1	13196	Asap1	13199	Ddn	13384	Mpp3
13385	Dlg4	13401	Dmwd	13426	Dync1i1	13429	Dnm1
13476	Reep5	13480	Dpm1	13483	Dpp6	13527	Dtna
13609	S1pr1	13628	Eef1a2	13806	Eno1	13807	Eno2
13821	Epb4.1l1	13823	Epb4.1l3	13829	Epb4.9	13838	Epha4
13855	Epn2	13858	Eps15	14007	Cugbp2	14073	Faah
14086	Fscn1	14226	Fkbp1b	14360	Fyn	14394	Gabra1
14395	Gabra2	14396	Gabra3	14397	Gabra4	14400	Gabrb1
14401	Gabrb2	14402	Gabrb3	14415	Gad1	14432	Gap43
14457	Gas7	14545	Gdap1	14567	Gdi1	14571	Gpd2
14580	Gfap	14586	Gfra2	14645	Glul	14660	Gls
14677	Gnail	14680	Gnal	14681	Gnao1	14682	Gnaq
14687	Gnaz	14688	Gnb1	14697	Gnb5	14702	Gng2
14704	Gng3	14708	Gng7	14758	Gpm6b	14768	Lancl1
14799	Gria1	14800	Gria2	14802	Gria4	14810	Grin1
14811	Grin2a	14812	Grin2b	15165	Hcn1	15275	Hkl1
15441	Hpl1bp3	15444	Hpsca	15505	Hsph1	15512	Hspa2
15519	Hsp90aa1	15568	Elavl1	15571	Elavl3	15572	Elavl4
15898	Icam5	16438	Itp1	16443	Itsn1	16485	Kcna1
16490	Kcna2	16497	Kcnab1	16498	Kcnab2	16499	Kcnab3
16500	Kcnb1	16508	Kcnd2	16531	Kcnma1	16536	Kcng2
16560	Kif1a	16563	Kif2a	16568	Kif3a	16572	Kif5a
16574	Kif5c	16593	Klcl1	16594	Klcl2	16646	Kpna1
16653	Kras	16728	L1cam	16832	Ldhd	17136	Mag
17196	Mbp	17441	Mog	17449	Mdh1	17754	Mtap1a
17755	Mtap1b	17756	Mtap2	17758	Mtap4	17760	Mtap6
17761	Mtap7	17762	Mapt	17876	Myef2	17918	Myo5a
17957	Napb	17967	Ncam1	17968	Ncam2	18039	Nefl
18040	Nefm	18082	Nipsnap1	18117	Cox4nb	18125	Nos1
18164	Nptx1	18189	Nrxn1	18190	Nrxn2	18191	Nrxn3
18195	Nsf	18223	Numbl	18377	Omg	18415	Hspa4l
18479	Pak1	18483	Palm	18488	Cntn3	18526	Pcdh10
18555	Cdk16	18574	Pdel1b	18578	Pdel4b	18641	Pfkl
18642	Pfkm	18648	Pgam1	18717	Pip5k1c	18739	Pitpnm1
18746	Pkm2	18749	Prkacb	18752	Prkcc	18754	Prkce
18795	Plcb1	18798	Plcb4	18807	Pld3	18823	Plp1
18845	Plxna2	18952	Sept4	19055	Ppp3ca	19056	Ppp3cb
19084	Prkar1a	19085	Prkar1b	19139	Prps1	19242	Ptn
19261	Sirpa	19266	Ptprd	19280	Ptp1b	19281	Ptp1c
19283	Ptprz1	19290	Pura	19291	Purb	19317	Qk
19339	Rab3a	19346	Rab6	19387	Rangap1	19418	Rasgrf2
19679	Pitpnm2	19878	Rock2	19894	Rph3a	20168	Rtn3
20191	Ryr2	20192	Ryr3	20320	Nptn	20361	Sema7a
20362	Sept8	20404	Sh3gl2	20511	Slc1a2	20512	Slc1a3
20604	Sst	20614	Snap25	20616	Snap91	20740	Spna2
20741	Spnb1	20743	Spnb3	20817	Srpk2	20907	Stx1a
20910	Stxbp1	20927	Abcc8	20964	Syn1	20965	Syn2
20974	Syng3	20977	Syp	20979	Syt1	20980	Syt2
21367	Cntn2	21402	Skp1a	21672	Prdx2	21838	Thy1
21960	Tnr	22031	Traf3	22142	Tuba1a	22143	Tuba1b
22151	Tubb2a	22152	Tubb3	22153	Tubb4	22223	Uchl1
22317	Vamp1	22318	Vamp2	22342	Lin7b	22393	Wfs1

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## The list of putative neuron-specific genes

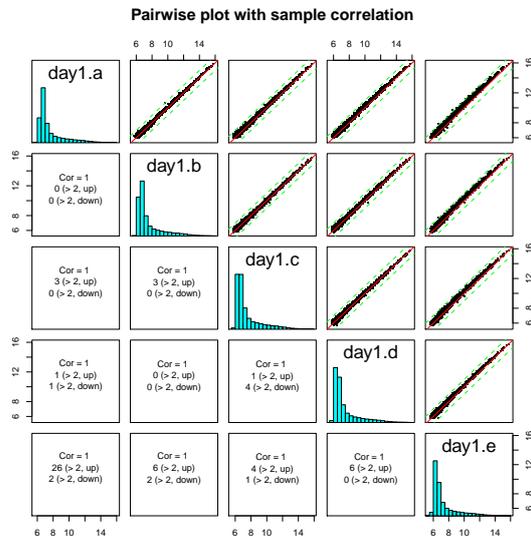
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23859	Dlg2	23881	G3bp2	23936	Lynx1	23945	Mgll
23950	Dnajb6	23966	Odz4	23969	Pacsin1	24012	Rgs7
24050	Sept3	26372	Cln6	26395	Map2k1	26413	Mapk1
26422	Nbea	26556	Homer1	26557	Homer2	26562	Ncdn
26757	Dpysl4	26874	Abcd2	26875	Pclo	26913	Gprin1
26932	Ppp2r5e	26950	Vsn1	27062	Cadps	27204	Syn3
27373	Csnk1e	27801	Zdhhc8	27984	Efh2	28185	Tomm70a
29873	Cspg5	30785	Cttnbp2	30948	Bin1	30957	Mapk8ip3
50791	Magi2	50876	Tmod2	50932	Mink1	50997	Mpp2
51792	Ppp2r1a	52389	Gpr123	52398	Sept11	52589	Ncald
52637	Cisd1	52822	Rufy3	52882	Rgs7bp	53310	Dlg3
53420	Syt5	53612	Vti1b	53623	Gria3	53870	Cntn6
53872	Caprin1	53972	Ngef	54161	Copg	54195	Gucy1b3
54216	Pcdh7	54376	Cacng3	54393	Gabbr1	54401	Ywhab
54403	Slc4a4	54411	Atp6ap1	54418	Fmn2	54525	Syt7
54637	Praf2	54712	Plxnc1	55992	Trim3	56013	Srcin1
56077	Dgke	56149	Grasp	56177	Olfm1	56320	Dbn1
56323	Dnajb5	56370	Tagln3	56421	Pfkp	56438	Rbx1
56455	Dynll1	56462	Mtch1	56491	Vapb	56508	Rapgef4
56526	Sept6	56541	Habp4	56637	Gsk3b	56695	Pnkd
56710	Dbc1	56737	Alg2	56808	Cacna2d2	56839	Lgi1
56876	Nelf	57138	Slc12a5	57340	Jph3	57440	Ehd3
57743	Sec61a2	57754	Cend1	57874	Ptplad1	58175	Rgs20
58234	Shank3	58244	Stx6	58994	Smpd3	64009	Syne1
64011	Nrgn	64051	Sv2a	64297	Gprc5b	64933	Ap3m2
65079	Rtn4r	65945	Clstn1	66049	Rogdi	66082	Abhd6
66098	Chchd6	66237	Atp6v1g2	66335	Atp6v1c1	66797	Cntnap2
66958	Tmx2	67166	Arl8b	67252	Cap2	67295	Rab3c
67306	Fam164a	67412	6330407J23Rik	67433	Ccdc127	67445	C1qtnf4
67453	Slc25a46	67564	Tmem35	67602	Necap1	67792	Rgs8
67801	Pllp	67826	Snap47	67834	Idh3a	67900	170020C11Rik
67972	Atp2b1	68032	Tmem85	68166	Spire1	68203	Diras2
68267	Slc25a22	68404	Nrn1	68507	Ppfa4	68524	Wipf2
68585	Rtn4	68724	Arl8a	69219	Ddah1	69399	170025G04Rik
69605	Lnp	69635	Dapk1	69642	2310046A06Rik	69683	2310044H10Rik
69807	Trim32	69894	2010107G23Rik	69908	Rab3b	69981	Tmem30a
70495	Atp6ap2	70549	Tln2	70620	Ube2v2	70762	Dclk2
71146	Golga7b	71302	Arhgap26	71435	Arhgap21	71764	C2cd2l
71770	Ap2b1	71803	Slc25a18	71835	Lanc12	71902	Cand1
72097	2010300C02Rik	72168	Aifm3	72325	1300018I17Rik	72685	Dnajc6
72727	B3gat3	72821	Scn2b	72832	Crtac1	72927	Hepacam
72948	Tppp	72961	Slc17a7	73072	BC068157	73094	Sgip1
73178	Wasl	73242	26101110G12Rik	73420	1700054N08Rik	73442	Hspa12a
73710	Tubb2b	73728	Psd	73825	Klra1	73834	Atp6v1d
73991	At1l	74006	Dnm1l	74012	Rap2b	74053	Grip1
74103	Neb1	74205	Acs13	74256	Cyld	74342	Lrrtm1
74998	Rab11fip2	75029	Purg	75607	Wnk2	75734	Mff
75770	Brsk2	75786	Ckap5	75914	Exoc6b	76089	Rapgef2
76108	Rap2a	76156	Fam131b	76179	Usp31	76192	Abhd12
76217	Jakmip2	76441	Daam2	76499	Clasp1	76580	Mib2
76686	Clip3	76740	Efr3a	76742	Snx27	76787	Ppfa3
76809	Bri3bp	76820	Fam49a	76884	Cyfip2	76960	Bcas1
77480	Kidins220	77531	Anks1b	77573	Vps33a	77579	Myh10
77629	Sphkap	78283	Mtap7d2	78506	Efha2	78779	Spata2L
78808	Stxbp5	78830	Slc25a12	80286	Tusc3	80297	Spnb4
80334	Kcnip4	80906	Kcnip2	80987	Nckipsd	81840	Sorcs2
83767	Wasf1	93739	Gabarapl2	93765	Ube2n	94040	Clmn
94047	Cecr6	94229	Slc4a10	94280	Sfxn3	94282	Sfxn5
97387	Strn4	98660	Atp1a2	98732	Rab3gap2	99010	Lpcat4
99512	Wdr47	100732	Mapre3	103466	Nt5dc3	103967	Dnm3
104001	Rtn1	104015	Synj1	104027	Synpo	104082	Wdr7
104418	Dgkz	104718	Ttc7b	104886	Rab15	105298	Epdr1
105445	Dock9	105689	Mycbp2	105853	Mal2	106042	Prickle1
107065	Lrrtm2	107831	Bail	108030	Lin7a	108068	Grm2
108069	Grm3	108071	Grm5	108083	Pip4k2b	108100	Baiap2
108123	Napg	108124	Napa	108664	Atp6v1h	108686	Ccdc88a
109676	Ank2	109934	Abr	110012	Gm16517	110279	Bcr
110391	Qdpr	110876	Scn2a1	110891	Slc8a2	116837	Rims1
116838	Rims2	117148	Necab2	118452	Baalc	140559	Igsf8

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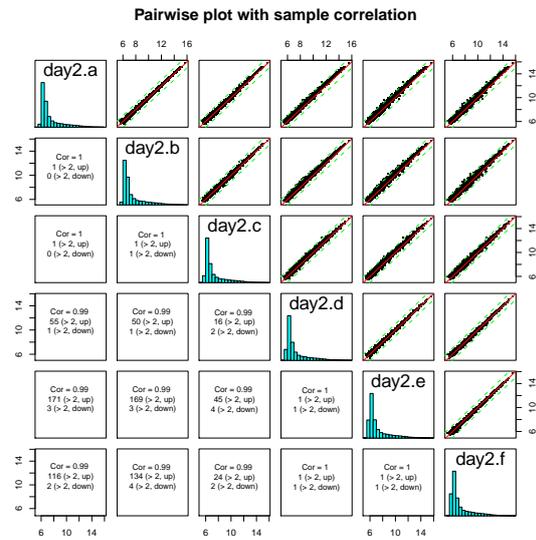
The list of putative neuron-specific genes

Entrez ID	Symbol						
140579	Elmo2	140580	Elmo1	170731	Mfn2	170790	Mlc1
192197	Bcas3	194590	Reps2	207393	Elfn2	207565	Camkk2
207615	Wdr37	207728	Pde2a	208158	Map6d1	208869	Dock3
208898	Unc13c	210274	Shank2	210933	Bai3	211446	Exoc3
212307	Mapre2	213056	Fam126b	213469	Lgi3	213582	Mtap9
213990	Agap3	214230	Pak6	215690	Nav1	215707	Ccdc92
216028	Lrrtm3	216049	Zfp365	216739	Acsl6	216810	Tom1l2
216831	AU040829	216856	Nlgn2	216963	Git1	216965	Taok1
217219	Fam171a2	217480	Dgkb	217692	Sipa1l1	217882	AW555464
218035	Vps41	218038	Amph	218194	Phactr1	218440	Ankrd34b
218461	Pde8b	223435	Trio	223601	Fam49b	224020	Pi4ka
224617	Tbcl1d24	224813	Gm88	224997	Dlgap1	225362	Reep2
225849	Ppp2r5b	226525	Rasal2	226751	Cdc42bpa	226778	Mark1
226977	Actr1b	227634	Camsap1	227937	Pkp4	228550	Itpka
228836	Dlgap4	228858	Gdap1l1	229521	Syt11	229709	Ahcy11
229759	Olfm3	229791	D3Bwg0562e	229877	Rap1gds1	230085	N28178
230235	6430704M03Rik	230868	Igsf21	230904	Fbxo2	231148	Ablim2
231570	A830010M20Rik	231760	Rimbp2	231876	Lmtk2	232227	Iqsec1
232232	Hdac11	232333	Slc6a1	232813	Shisa7	232975	Atp1a3
233071	Snx26	234267	Gpm6a	234353	Psd3	234663	Dync1li2
235044	BC018242	235072	Sept7	235106	Ntm	235339	Dlat
235380	Dmxl2	235402	Lingo1	235431	Coro2b	235604	Camkv
236915	Arhgef9	237459	Cdk17	238130	Dock4	238276	Akap5
238988	Erc2	240058	Cpne5	240121	Fsd1	240185	9430020K01Rik
241263	Gpr158	241520	Fam171b	241589	D430041D05Rik	241638	RP23-100C5.8
241656	Pak7	241688	6330439K17Rik	241727	Snph	241770	Rims4
242481	Palm2	242667	Dlgap3	243043	Kctd8	243300	6430598A04Rik
243312	Elfn1	243499	Lrrtm4	243548	Prickle2	243621	Iqsec3
243743	Plxna4	244310	Dlgap2	244723	Olfm2	245643	Frmpd3
245666	Iqsec2	245684	Cnksr2	245877	Mtap7d1	245880	Wasf3
259302	Srgap3	260297	Prrt1	267019	Rps15a	268566	Gphn
268709	Fam107a	268890	Lsamp	268932	Caskin1	269060	Dagla
269109	Dpp10	269116	Nfasc	269180	Inpp4a	269295	Rtn4rl2
269774	Aak1	269854	Nat14	270058	Mtap1s	270192	Rab6b
271564	Vps13a	319278	A230050P20Rik	319504	Nrcam	319613	5730410E15Rik
319807	3110047P20Rik	319984	Jph4	320271	Scai	320365	Fry
320707	Atp2b3	320772	Mdga2	320840	Negr1	320873	Cdh10
327814	Ppfa2	329152	Hecw2	329165	Abi2	330319	Wipf3
330369	Fbxo41	330790	Hapln4	330814	Lphn1	330908	Opcml
330914	Grit	331461	Il1rap1	347722	Agap1	360213	Trim46
380684	Nefh	380702	Shisa6	380768	Gm1568	381813	Prmt8
381979	Brsk1	382018	Unc13a	406218	Panx2	433904	Ociad2
545156	Kalrn	545389	Cep170	546071	Mast3	668212	Efr3b
100039795	Ildr2						

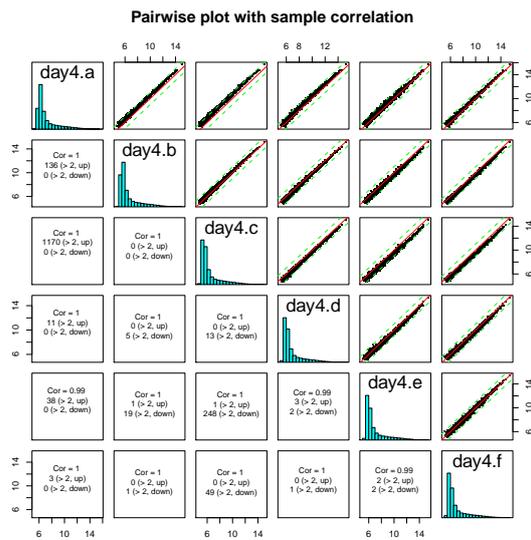
(a) 1DIV replicates



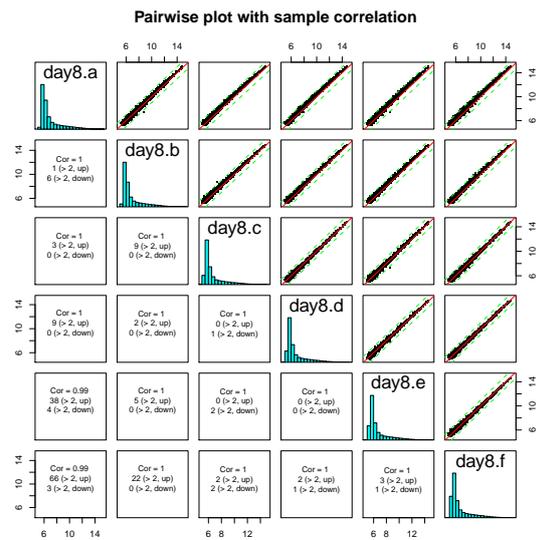
(b) 2DIV replicates



(c) 4DIV replicates



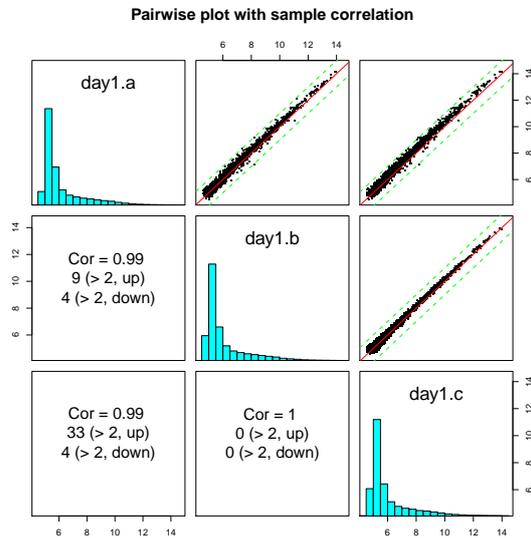
(d) 8DIV replicates



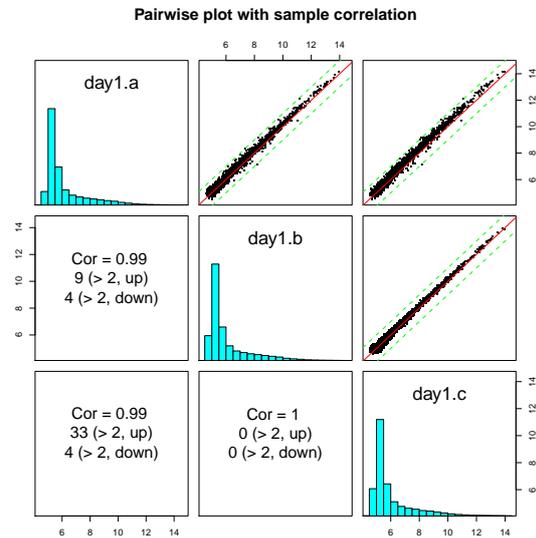
**Figure A.1: Pairwise correlation of raw mRNA microarray probe intensities in profiles of hippocampal cultures.**

Figure A.1a - correlation of replicates at 1 day of *in vitro* development (1DIV); Figure A.1b - at 2DIV; Figure A.1c - at 4DIV; Figure A.1d - at 8DIV. The plots were produced using *lumi* package (Du et al., 2008). The analysis of microarray data is described in Methods (section 2.7).

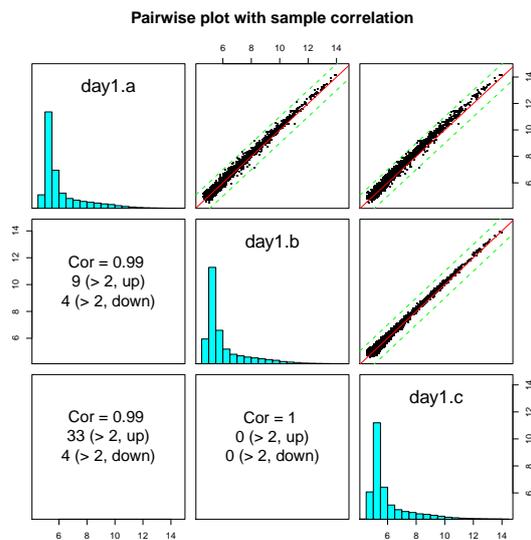
(a) 1DIV replicates



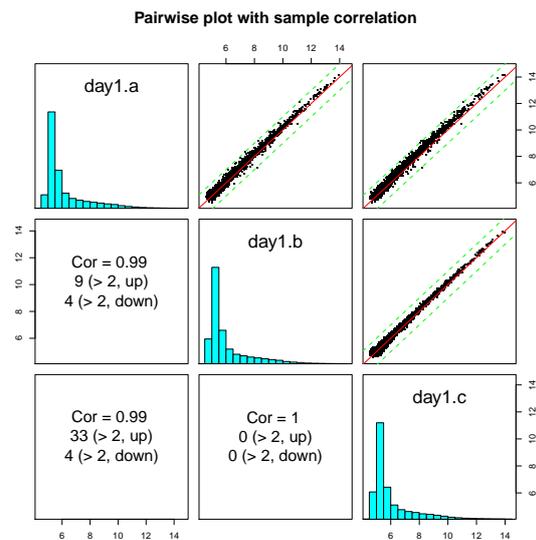
(b) 2DIV replicates



(c) 4DIV replicates



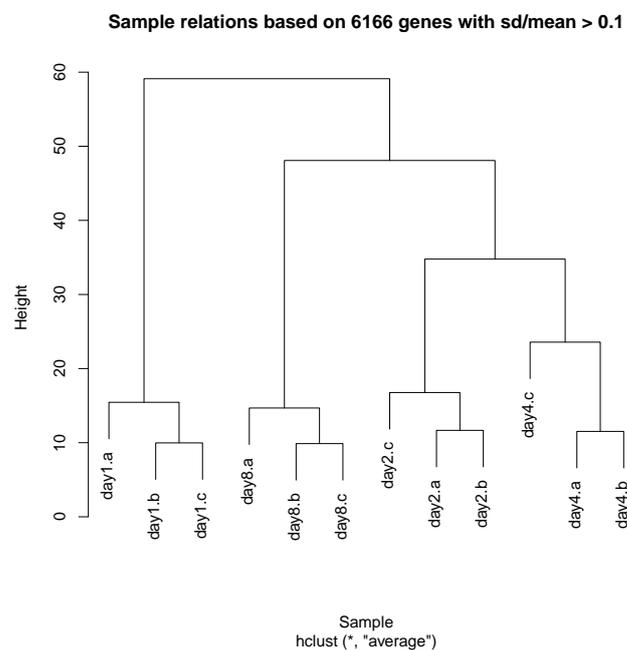
(d) 8DIV replicates



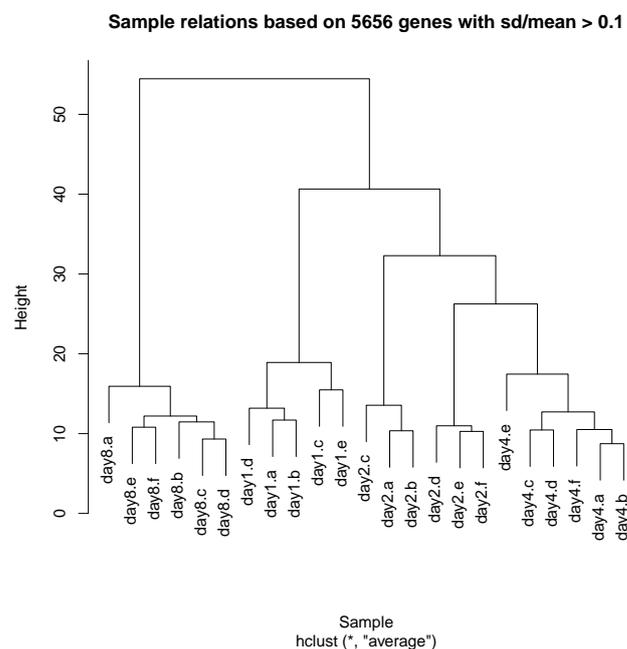
**Figure A.2: Pairwise correlation of raw mRNA microarray probe intensities in profiles of hippocampal cultures.**

Figure A.2a - correlation of replicates microarray profiling of RNA from replicates at 1 day of *in vitro* development (1DIV); Figure A.2b - at 2DIV; Figure A.2c - at 4DIV; Figure A.2d - at 8DIV. The plots were produced using *lumi* package (Du et al., 2008), see Methods, section 2.7. The analysis of microarray data is described in Methods (section 2.7).

## (a) Hippocampal cultures



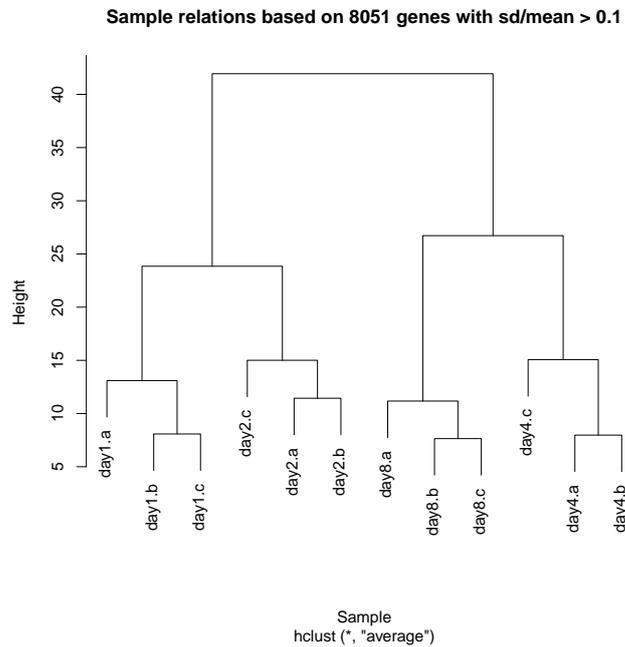
## (b) Forebrain cultures



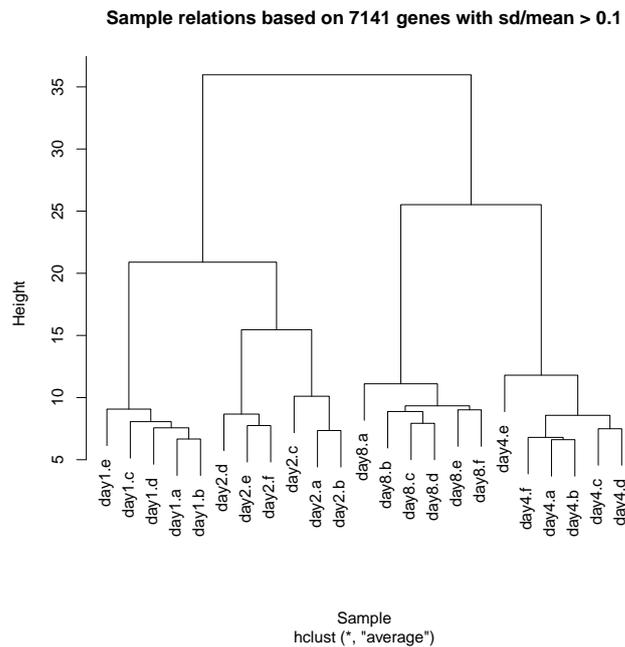
**Figure A.3: Sample relation between raw mRNA microarray profiles between replicates of hippocampal and forebrain cultures.**

Figure A.3a - replicates of hippocampal cultures; Figure A.3b - replicates of forebrain cultures. The plots were produced using *lumi* package (Du et al., 2008). The analysis of microarray data is described in Methods (section 2.7).

## (a) Hippocampal cultures



## (b) Forebrain cultures



**Figure A.4: Sample relation between normalised mRNA microarray profiles between replicates of hippocampal and forebrain cultures.**

Figure A.4a - hippocampal cultures experimental replicates; Figure A.4b - forebrain cultures replicates. The plots were produced using *lumi* package (Du et al., 2008), see Methods, section 2.7. The analysis of microarray data is described in Methods (section 2.7).

**Table A.2: Top 40 most enriched GO terms (“Biological process” type) in developmentally downregulated genes.**

$q$  - number of genes of a GO term that was among the downregulated genes,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1086	1651	1.05e-83
GO:0010467	gene expression	1012	1545	3.24e-75
GO:0044260	cellular macromolecule metabolic process	1507	2537	7.65e-73
GO:0006807	nitrogen compound metabolic process	1124	1793	5.86e-68
GO:0043170	macromolecule metabolic process	1560	2709	4.96e-62
GO:0009059	macromolecule biosynthetic process	888	1412	5.09e-52
GO:0034645	cellular macromolecule biosynthetic process	880	1401	4.01e-51
GO:0006350	transcription	680	1029	1.03e-49
GO:0010556	regulation of macromolecule biosynthetic process	659	1010	4.42e-45
GO:0010468	regulation of gene expression	672	1040	7.9e-44
GO:0045449	regulation of transcription	612	936	4.95e-42
GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	632	975	1.18e-41
GO:0009889	regulation of biosynthetic process	665	1037	1.19e-41
GO:0051171	regulation of nitrogen compound metabolic process	635	981	1.43e-41
GO:0031326	regulation of cellular biosynthetic process	664	1036	1.82e-41
GO:0016070	RNA metabolic process	547	821	7.25e-41
GO:0060255	regulation of macromolecule metabolic process	719	1156	1.96e-38
GO:0044237	cellular metabolic process	1700	3185	3.05e-37
GO:0031323	regulation of cellular metabolic process	719	1180	4.27e-34
GO:0080090	regulation of primary metabolic process	701	1148	1.4e-33
GO:0044249	cellular biosynthetic process	973	1695	1.44e-32
GO:0044238	primary metabolic process	1690	3206	2.04e-32
GO:0019222	regulation of metabolic process	746	1252	6.29e-31
GO:0009058	biosynthetic process	986	1741	6.5e-30
GO:0006396	RNA processing	211	274	1.21e-28
GO:0016071	mRNA metabolic process	160	201	9.84e-25
GO:0006259	DNA metabolic process	185	244	8.57e-24
GO:0051276	chromosome organization	179	235	1.87e-23
GO:0007049	cell cycle	257	376	2.01e-21
GO:0006325	chromatin organization	154	200	3.76e-21
GO:0006397	mRNA processing	141	179	4.04e-21
GO:0008152	metabolic process	1817	3604	5.23e-21
GO:0006996	organelle organization	380	604	5.39e-21
GO:0008380	RNA splicing	116	141	1.94e-20

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ID	Term Description	q	m	P
GO:0022403	cell cycle phase	142	184	9.44e-20
GO:0000279	M phase	125	157	1.41e-19
GO:0000278	mitotic cell cycle	126	160	5.6e-19
GO:0022402	cell cycle process	159	217	4.35e-18
GO:0000087	M phase of mitotic cell cycle	98	119	1.63e-17
GO:0000280	nuclear division	98	119	1.63e-17

**Table A.3: Top 40 most enriched GO terms (“Biological process” type) in developmentally upregulated genes.**

$q$  - number of genes of a GO term that was among the upregulated genes,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0006810	transport	652	1196	2.64e-21
GO:0051234	establishment of localization	655	1206	7.27e-21
GO:0051179	localization	718	1360	9.92e-19
GO:0006811	ion transport	192	293	1.22e-16
GO:0006629	lipid metabolic process	188	299	1.09e-13
GO:0006812	cation transport	145	223	1.86e-12
GO:0019226	transmission of nerve impulse	104	148	2.19e-12
GO:0044255	cellular lipid metabolic process	135	205	2.73e-12
GO:0044281	small molecule metabolic process	319	577	1.87e-11
GO:0023052	signaling	626	1244	7.91e-11
GO:0030001	metal ion transport	122	189	2.23e-10
GO:0007268	synaptic transmission	85	121	2.36e-10
GO:0006836	neurotransmitter transport	44	53	9.05e-10
GO:0007267	cell-cell signaling	109	168	1.33e-09
GO:0006066	alcohol metabolic process	108	167	2.08e-09
GO:0050877	neurological system process	166	280	2.39e-09
GO:0003008	system process	193	336	4.37e-09
GO:0005975	carbohydrate metabolic process	126	203	4.46e-09
GO:0007154	cell communication	262	480	7.24e-09
GO:0023060	signal transmission	495	985	1.57e-08
GO:0015672	monovalent inorganic cation transport	85	128	1.75e-08
GO:0023046	signaling process	495	986	1.87e-08
GO:0008610	lipid biosynthetic process	89	137	3.98e-08
GO:0032787	monocarboxylic acid metabolic process	73	111	3.2e-07
GO:0055114	oxidation reduction	165	295	6.49e-07
GO:0055085	transmembrane transport	129	223	9.96e-07
GO:0007610	behavior	97	162	2.82e-06

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ID	Term Description	q	m	P
GO:0006631	fatty acid metabolic process	53	78	3.01e-06
GO:0046483	heterocycle metabolic process	91	151	3.9e-06
GO:0065008	regulation of biological quality	255	493	4.56e-06
GO:0006814	sodium ion transport	35	47	6.09e-06
GO:0050801	ion homeostasis	74	119	6.31e-06
GO:0001505	regulation of neurotransmitter levels	32	42	6.73e-06
GO:0042180	cellular ketone metabolic process	127	225	6.86e-06
GO:0019637	organophosphate metabolic process	58	89	7.96e-06
GO:0006873	cellular ion homeostasis	69	110	8.37e-06
GO:0015837	amine transport	27	34	9.32e-06
GO:0015849	organic acid transport	30	39	9.42e-06
GO:0046942	carboxylic acid transport	30	39	9.42e-06
GO:0019725	cellular homeostasis	91	154	1.21e-05

**Table A.4: Top 40 most enriched GO terms (“Cellular compartment” type) in developmentally downregulated genes.**

$q$  - number of genes of a GO term that was among the downregulated genes,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0005634	nucleus	1502	2267	2.38e-133
GO:0044428	nuclear part	368	498	5.21e-43
GO:0043226	organelle	2207	4281	1.26e-41
GO:0043229	intracellular organelle	2205	4279	2.46e-41
GO:0044424	intracellular part	2521	5009	5.34e-41
GO:0005622	intracellular	2575	5141	2.23e-40
GO:0043227	membrane-bounded organelle	2015	3870	2.87e-39
GO:0043231	intracellular membrane-bounded organelle	2013	3867	4.21e-39
GO:0005694	chromosome	187	226	2.78e-33
GO:0044427	chromosomal part	164	194	1.53e-31
GO:0031981	nuclear lumen	204	278	2.49e-23
GO:0070013	intracellular organelle lumen	225	319	7.29e-22
GO:0043233	organelle lumen	225	320	1.4e-21
GO:0031974	membrane-enclosed lumen	233	335	2.54e-21
GO:0043228	non-membrane-bounded organelle	525	885	4.09e-21
GO:0043232	intracellular non-membrane-bounded organelle	525	885	4.09e-21
GO:0032991	macromolecular complex	680	1194	4.98e-21
GO:0030529	ribonucleoprotein complex	188	262	9.4e-20
GO:0044422	organelle part	734	1323	1.06e-18
GO:0044446	intracellular organelle part	728	1316	4.15e-18

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ID	Term Description	q	m	P
GO:0005681	spliceosomal complex	72	80	9.21e-18
GO:0000775	chromosome, centromeric region	69	77	7.87e-17
GO:0005654	nucleoplasm	146	201	2.38e-16
GO:0044451	nucleoplasm part	132	179	8.9e-16
GO:0000785	chromatin	78	95	3.52e-14
GO:0000776	kinetochore	41	45	5.03e-11
GO:0044454	nuclear chromosome part	47	58	1.09e-08
GO:0000502	proteasome complex	32	36	3.14e-08
GO:0000228	nuclear chromosome	49	63	6.37e-08
GO:0005667	transcription factor complex	66	92	9.2e-08
GO:0032993	protein-DNA complex	38	47	3.24e-07
GO:0000792	heterochromatin	28	32	5.06e-07
GO:0005730	nucleolus	57	79	5.08e-07
GO:0043234	protein complex	462	888	9.71e-07
GO:0005657	replication fork	16	16	2.28e-06
GO:0000790	nuclear chromatin	27	32	3.69e-06
GO:0000786	nucleosome	33	42	6.44e-06
GO:0034399	nuclear periphery	19	21	1.4e-05
GO:0005635	nuclear envelope	49	71	2.35e-05
GO:0005819	spindle	24	29	2.55e-05

**Table A.5: Top 40 most enriched GO terms (“Cellular compartment” type) in developmentally upregulated genes.**

$q$  - number of genes of a GO term that was among the upregulated genes,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0016020	membrane	1627	2810	4.21e-92
GO:0044425	membrane part	1337	2226	1.59e-85
GO:0031224	intrinsic to membrane	1167	1914	2.04e-77
GO:0016021	integral to membrane	1141	1877	4.62e-74
GO:0005886	plasma membrane	628	1023	8.58e-39
GO:0044459	plasma membrane part	303	486	7.99e-20
GO:0044444	cytoplasmic part	1053	2092	2.76e-17
GO:0005783	endoplasmic reticulum	256	423	1.34e-14
GO:0045202	synapse	123	175	5.21e-14
GO:0044456	synapse part	79	104	2.88e-12
GO:0005576	extracellular region	251	429	4.92e-12
GO:0031226	intrinsic to plasma membrane	105	153	3.87e-11
GO:0005887	integral to plasma membrane	101	148	1.52e-10

Continued on Next Page...

ID	Term Description	q	m	P
GO:0030054	cell junction	149	239	2.75e-10
GO:0005624	membrane fraction	136	219	2.42e-09
GO:0005626	insoluble fraction	139	225	2.66e-09
GO:0000267	cell fraction	153	253	3.66e-09
GO:0043005	neuron projection	77	113	2.59e-08
GO:0005773	vacuole	79	117	3.21e-08
GO:0030136	clathrin-coated vesicle	37	46	1.46e-07
GO:0031410	cytoplasmic vesicle	131	221	2.55e-07
GO:0031982	vesicle	133	225	2.58e-07
GO:0008021	synaptic vesicle	31	37	2.7e-07
GO:0000323	lytic vacuole	68	103	1.05e-06
GO:0005764	lysosome	68	103	1.05e-06
GO:0030135	coated vesicle	42	57	1.62e-06
GO:0045211	postsynaptic membrane	46	65	3.38e-06
GO:0030424	axon	44	62	4.9e-06
GO:0005794	Golgi apparatus	208	396	2.28e-05
GO:0016023	cytoplasmic membrane-bounded vesicle	74	121	2.33e-05
GO:0031988	membrane-bounded vesicle	76	125	2.44e-05
GO:0031225	anchored to membrane	32	44	4.46e-05
GO:0043025	neuronal cell body	34	48	6.3e-05
GO:0044297	cell body	34	48	6.3e-05
GO:0005737	cytoplasm	1568	3493	7.23e-05
GO:0019717	synaptosome	31	43	7.75e-05
GO:0044421	extracellular region part	115	208	0.00011
GO:0030665	clathrin coated vesicle membrane	15	17	0.000128
GO:0030425	dendrite	28	39	0.000194
GO:0042995	cell projection	152	289	0.000262

**Table A.6: Top 25 most enriched KEGG terms in developmentally downregulated genes.**  $q$  - number of genes of a KEGG term that was among the downregulated genes,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
03040	Spliceosome	73	81	3.04e-20
03030	DNA replication	27	28	8.61e-10
04110	Cell cycle	57	75	1.14e-09
03050	Proteasome	27	30	4.54e-08
03440	Homologous recombination	20	21	3.16e-07
03420	Nucleotide excision repair	29	36	2.08e-06
03018	RNA degradation	28	36	1.11e-05

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ID	Term Description	q	m	P
05322	Systemic lupus erythematosus	36	50	1.31e-05
03430	Mismatch repair	17	19	2.21e-05
00240	Pyrimidine metabolism	40	59	4.28e-05
03022	Basal transcription factors	17	20	8.97e-05
03410	Base excision repair	17	22	0.000772
03020	RNA polymerase	15	19	0.0011
05222	Small cell lung cancer	30	50	0.00695
04120	Ubiquitin mediated proteolysis	51	94	0.00922
04623	Cytosolic DNA-sensing pathway	15	22	0.0113
00310	Lysine degradation	15	24	0.0331
03010	Ribosome	20	34	0.0337
04115	p53 signaling pathway	20	34	0.0337
04670	Leukocyte transendothelial migration	28	51	0.04
04114	Oocyte meiosis	34	64	0.0437
04620	Toll-like receptor signaling pathway	24	43	0.0444
00230	Purine metabolism	46	91	0.0557
05200	Pathways in cancer	82	171	0.0568
04621	NOD-like receptor signaling pathway	13	22	0.078

**Table A.7: Top 25 most enriched KEGG terms in developmentally upregulated genes.**

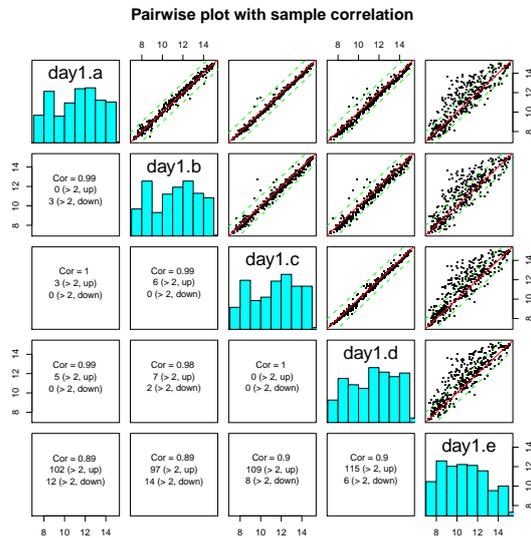
$q$  - number of genes of a KEGG term that was among the upregulated genes,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
01100	Metabolic pathways	303	564	1.46e-06
04142	Lysosome	53	80	8.44e-05
04020	Calcium signaling pathway	48	71	8.5e-05
04080	Neuroactive ligand-receptor interaction	44	64	9.14e-05
00600	Sphingolipid metabolism	21	26	0.000201
00640	Propanoate metabolism	15	17	0.00028
00010	Glycolysis / Gluconeogenesis	22	28	0.000293
04514	Cell adhesion molecules (CAMs)	29	42	0.00134
04720	Long-term potentiation	29	42	0.00134
00982	Drug metabolism - cytochrome P450	15	19	0.00272
00564	Glycerophospholipid metabolism	26	38	0.00292
00561	Glycerolipid metabolism	19	26	0.00345
00511	Other glycan degradation	7	7	0.00374
00603	Glycosphingolipid biosynthesis - globo series	7	7	0.00374
00980	Metabolism of xenobiotics by cytochrome P450	14	18	0.00485
00071	Fatty acid metabolism	15	20	0.00636

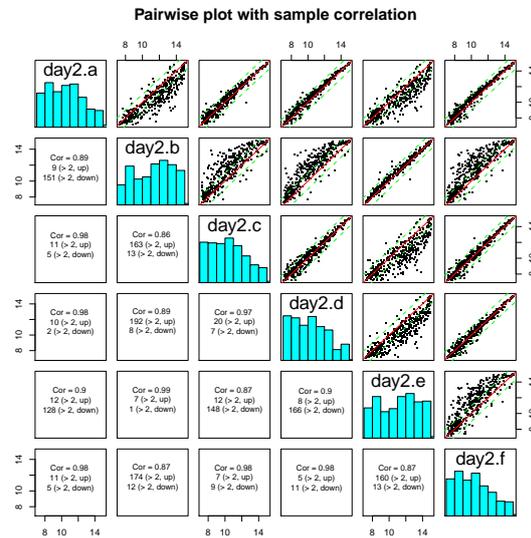
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<b>ID</b>	<b>Term Description</b>	<b>q</b>	<b>m</b>	<b>P</b>
04916	Melanogenesis	32	51	0.00778
03320	PPAR signaling pathway	20	29	0.0078
00062	Fatty acid elongation in mitochondria	6	6	0.00832
04540	Gap junction	34	55	0.00854
00280	Valine, leucine and isoleucine degradation	21	31	0.0088
00604	Glycosphingolipid biosynthesis - ganglio series	8	9	0.00908
00910	Nitrogen metabolism	8	9	0.00908
04260	Cardiac muscle contraction	28	44	0.00956
04730	Long-term depression	24	38	0.0182

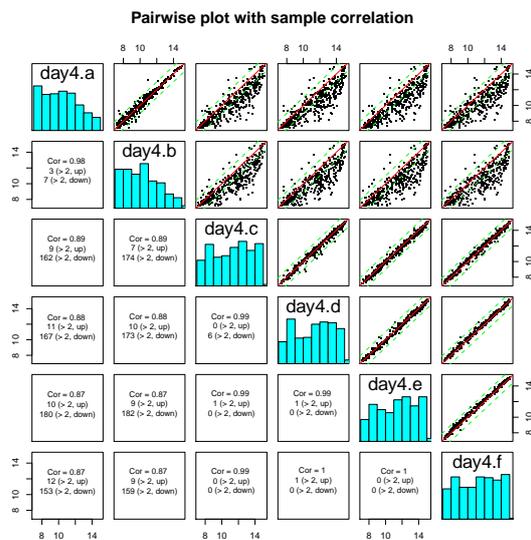
(a) 1DIV replicates



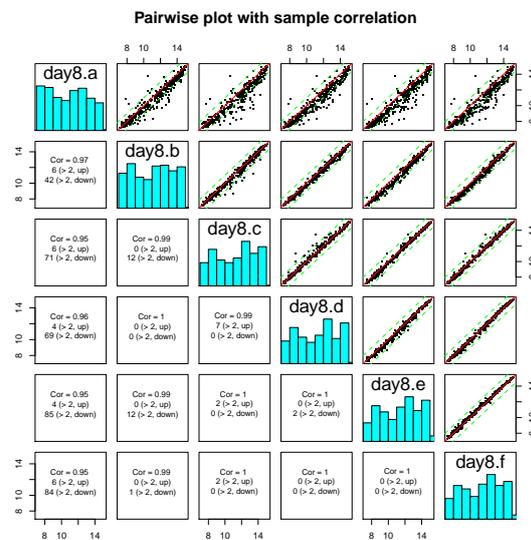
(b) 2DIV replicates



(c) 4DIV replicates



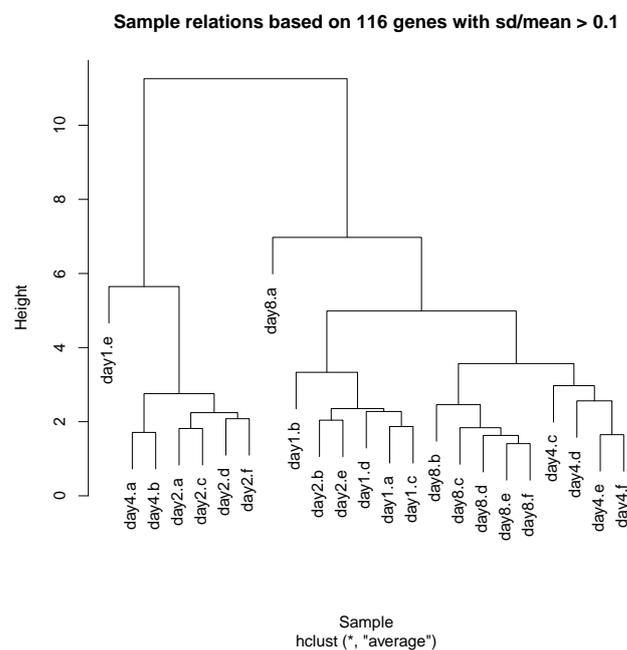
(d) 8DIV replicates



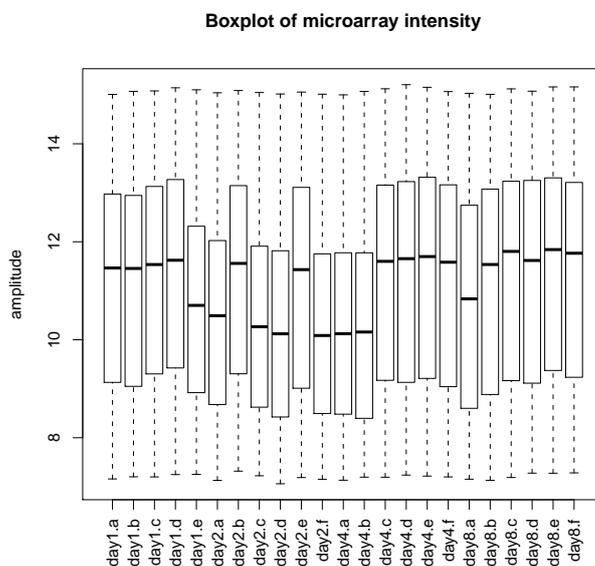
**Figure A.5: Pairwise correlation of raw miRNA microarray probe intensities in profiles of forebrain cultures.**

Figure A.1a - correlation of replicates at 1 day of *in vitro* development (1DIV); Figure A.1b - from 2DIV; Figure A.1c - from 4DIV; Figure A.1d - from 8DIV. The plots were produced using *lumi* package (Du et al., 2008). The analysis of microarray data is described in Methods (section 2.7).

(a)



(b)



**Figure A.6: Relationship between replicate raw miRNA microarray profiles.**

Figure A.6a - sample relation between raw miRNA microarray profiles between replicates of forebrain cultures; Figure A.6b - miRNA microarray intensities of replicates of forebrain cultures. The plots were produced using *lumi* package (Du et al., 2008). The analysis of microarray data is described in Methods (section 2.7).

**Table A.8: Three categories of miRNAs in development of primary forebrain cultures.**

miRNA identifiers, miRBase Release 13 (Griffiths-Jones, 2004; Griffiths-Jones et al., 2006, 2008), for each member of the three categories of miRNAs with distinct modes of expression are given together with the rank (“**Rank**”) of expression at the 8DIV timepoint in the development of cultures.

Steady state	Rank	Downregulated	Rank	Upregulated	Rank
mmu-miR-9	1	mmu-miR-15b	29	mmu-miR-690	17
mmu-miR-103	2	mmu-miR-99a	30	mmu-miR-24	24
mmu-let-7a	3	mmu-miR-21	39	mmu-miR-434-3p	31
mmu-miR-125b-5p	4	mmu-miR-135a	41	mmu-miR-376b	33
mmu-let-7b	5	mmu-miR-20a	43	mmu-miR-7a	34
mmu-miR-711	6	mmu-miR-135b	47	mmu-miR-218	35
mmu-miR-16	7	mmu-miR-93	52	mmu-miR-709	36
mmu-miR-26a	8	mmu-miR-106b	53	mmu-miR-22	38
mmu-miR-137	9	mmu-miR-149	56	mmu-miR-551b	40
mmu-miR-124	10	mmu-miR-99b	65	mmu-miR-410	44
mmu-let-7d	11	mmu-miR-706	66	mmu-miR-128	45
mmu-let-7g	12	mmu-miR-30e	68	mmu-miR-331-3p	46
mmu-miR-191	13	mmu-miR-335-5p	70	mmu-miR-342-3p	48
mmu-miR-9*	14	mmu-miR-25	72	mmu-miR-30d	50
mmu-let-7c	15	mmu-miR-20b	78	mmu-miR-487b	51
mmu-let-7f	16	mmu-miR-92a	81	mmu-miR-139-5p	54
mmu-miR-125a-5p	18	mmu-miR-15a	83	mmu-miR-127	55
mmu-miR-30c	19	mmu-miR-98	86	mmu-miR-129-3p	59
mmu-miR-17	20	mmu-miR-195	88	mmu-miR-379	60
mmu-let-7i	21	mmu-miR-350	89	mmu-miR-382	61
mmu-miR-181a	22	mmu-miR-18a	91	mmu-miR-138	62
mmu-let-7e	23	mmu-miR-27b	93	mmu-miR-154	63
mmu-miR-181b	25	mmu-miR-301a	94	mmu-miR-338-3p	67
mmu-miR-693-5p	26	mmu-miR-674	95	mmu-miR-132	69
mmu-miR-720	27	mmu-miR-101a	96	mmu-miR-298	74
mmu-miR-100	28	mmu-miR-744	100	mmu-miR-326	76
		mmu-miR-19b	102	mmu-miR-434-5p	80
		mmu-miR-27a	103	mmu-miR-323-3p	84
		mmu-miR-106a	106	mmu-miR-328	85
		mmu-miR-28	110	mmu-miR-495	90
		mmu-miR-181a-1*	116	mmu-miR-324-5p	92
		mmu-miR-374	117	mmu-miR-409-3p	97
		mmu-miR-672	122	mmu-miR-369-5p	99
		mmu-miR-19a	123	mmu-miR-369-3p	104
		mmu-miR-204	130	mmu-miR-668	105
		mmu-miR-322	132	mmu-miR-29c	111

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## Three types of miRNAs in development of primary forebrain cultures

Steady state	Rank	Downregulated	Rank	Upregulated	Rank
		mmu-miR-23a	135	mmu-miR-185	112
		mmu-miR-701	137	mmu-miR-376c	114
		mmu-miR-466a-3p	145	mmu-miR-676	115
		mmu-miR-210	149	mmu-miR-592	119
		mmu-miR-423-3p	150	mmu-miR-29a	120
		mmu-miR-126-3p	156	mmu-miR-541	121
		mmu-miR-130b	159	mmu-miR-134	125
		mmu-miR-30a*	160	mmu-miR-187	126
		mmu-miR-451	163	mmu-miR-376b*	127
		mmu-miR-219	167	mmu-miR-129-5p	128
		mmu-miR-351	169	mmu-miR-146b	129
		mmu-miR-297a	175	mmu-miR-673-5p	133
		mmu-miR-685	177	mmu-miR-136	134
		mmu-miR-615-3p	180	mmu-miR-329	136
		mmu-miR-339-5p	181	mmu-miR-376a*	139
		mmu-miR-126-5p	183	mmu-miR-29b	140
		mmu-miR-144	190	mmu-miR-337-3p	141
		mmu-miR-489	194	mmu-miR-7b	142
		mmu-miR-542-3p	195	mmu-miR-222	147
		mmu-miR-450a-5p	196	mmu-miR-370	148
		mmu-miR-192	197	mmu-miR-667	152
		mmu-miR-679	198	mmu-miR-378	154
		mmu-miR-203	202	mmu-miR-330*	162
		mmu-miR-503	203	mmu-miR-485	165
		mmu-miR-345-5p	204	mmu-miR-539	166
		mmu-miR-17*	205	mmu-miR-433	168
		mmu-miR-467a*	206	mmu-miR-433*	173
		mmu-miR-322*	214	mmu-miR-496	174
		mmu-miR-215	216	mmu-miR-485*	176
		mmu-miR-199a-5p	223	mmu-miR-365	184
		mmu-miR-146a	225	mmu-miR-383	191
		mmu-miR-761	226	mmu-miR-31	192
		mmu-miR-145	228	mmu-miR-543	200
		mmu-miR-155	232	mmu-miR-666-5p	207
		mmu-miR-450b-3p	238	mmu-miR-221	210
		mmu-miR-122	245	mmu-miR-700	211
		mmu-miR-142-3p	249	mmu-miR-770-3p	218
		mmu-miR-223	255	mmu-miR-377	224
		mmu-miR-301b	260	mmu-miR-501-3p	230

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## Three types of miRNAs in development of primary forebrain cultures

Steady state	Rank	Downregulated	Rank	Upregulated	Rank
		mmu-miR-703	264	mmu-miR-702	231
		mmu-miR-199a-3p	265	mmu-miR-296-5p	233
		mmu-miR-143	267	mmu-miR-182	235
		mmu-miR-325*	268	mmu-miR-183	239
		mmu-miR-142-5p	269	mmu-miR-715	242
		mmu-miR-302b	274	mmu-miR-689	247
		mmu-miR-214	275	mmu-miR-380-3p	248
		mmu-miR-697	276	mmu-miR-211	252
		mmu-miR-199b*	279	mmu-miR-378*	254
		mmu-miR-483*	283	mmu-miR-488*	256
		mmu-miR-450b-5p	288	mmu-miR-412	257
		mmu-miR-448	289	mmu-miR-380-5p	258
		mmu-miR-704	297	mmu-miR-431	259
		mmu-miR-224	298	mmu-miR-676*	272
		mmu-miR-217	312	mmu-miR-760	273
		mmu-miR-200a	329	mmu-miR-133a	277
		mmu-miR-452	336	mmu-miR-300	278
		mmu-miR-150	338	mmu-miR-24-1*	281
		mmu-miR-363	340	mmu-miR-206	292
		mmu-miR-216a	342	mmu-miR-208a	294
		mmu-miR-464	344	mmu-miR-686	296
		mmu-miR-698	347	mmu-miR-201	302
		mmu-miR-10a	349	mmu-miR-499	306
		mmu-miR-675-3p	358	mmu-miR-681	307
				mmu-miR-196b	315
				mmu-miR-705	321
				mmu-miR-692	322
				mmu-miR-196a	326
				mmu-miR-717	343
				mmu-miR-680	354

Table A.9: Putative direct targets of miR-124

Entrez ID	Symbol						
11370	Acadv1	11443	Chrnbl	11491	Adam17	11518	Add1
11600	Angpt1	11637	Ak2	11666	Abcd1	11736	Ankfy1
11744	Anxa11	11747	Anxa5	11867	Arpc1b	11928	Atp1a1
11974	Atp6v0e	12039	Bekdha	12042	Bcl10	12161	Bmp6
12192	Zfp3611	12321	Calu	12334	Capn2	12350	Car3
12389	Cav1	12443	Ccnd1	12476	Cd151	12499	Entpd5
12521	Cd82	12753	Clock	12826	Col4a1	12831	Col5a1
12837	Col8a1	12908	Crat	13559	E2f5	13610	S1pr3
13617	Ednra	13650	Rhbdf1	13731	Emp2	13846	Ephb4
13866	Erbp2	14020	Evi5	14082	Fadd	14085	Fah
14252	Flot2	14275	Folr1	14314	Fstl1	14375	Xrcc6
14420	Galc	14450	Gart	14595	B4galt1	14678	Gnai2
14726	Pdpm	14792	Lpcat3	15077	Hist2h3c1	15894	Icam1
16007	Cyr61	16009	Igfbp3	16206	Lrig1	16211	Kpnb1
16362	Irf1	16404	Itga7	16412	Itgb1	16561	Kif1b
16589	Uhmkl	16651	Sspn	16784	Lamp2	16848	Lfng
16854	Lgals3	16889	Lipa	16905	Lmna	17083	Tmed1
17127	Smad3	17129	Smad5	17150	Mfap2	17158	Man2a1
17196	Mbp	17216	Mcm2	17217	Mcm4	17242	Mdk
17865	Mybl2	17886	Myh9	17997	Nedd1	18018	Nfatc1
18028	Nfib	18029	Nfic	18032	Nfix	18073	Nid1
18140	Nhrf1	18176	Nras	18201	Nsmaf	18212	Ntrk2
18230	Nxn	18451	P4ha1	18553	Pcsk6	18810	Plec
18824	Plp2	18933	Prrx1	19027	Sypl	19193	Pipox
19205	Ptbp1	19247	Ptpn11	19248	Ptpn12	19250	Ptpn14
19294	Pvrl2	19334	Rab22a	19340	Rab3d	19356	Rad17
19376	Rab34	19697	Rela	19724	Rfx1	19729	Rag1ap1
20130	Rras	20187	Ryk	20249	Scd1	20397	Sgpl1
20416	Shc1	20481	Ski	20496	Slc12a2	20648	Snta1
20848	Stat3	20917	Sucg2	20971	Sdc4	21367	Cntn2
21413	Tcf4	21415	Tcf7l1	21766	Tex261	21859	Timp3
21871	Atp6v0a2	21873	Tjp2	21915	Dtymk	22031	Traf3
22092	Rsph1	22117	Tst	22158	Tulp3	22169	Cmpk2
22271	Upp1	22319	Vamp3	22352	Vim	22401	Zmat3
22403	Wisp2	22695	Zfp36	23885	Gmcl1	23959	Nt5e
23972	Papss2	24044	Scamp2	26416	Mapk14	26425	Nubp1
26433	Plod3	26457	Slc27a1	26564	Ror2	26754	Cops5
27041	G3bp1	27081	Zfp275	27401	Skp2	27410	Abca3
28146	Serp1	28193	Reep3	29875	Iqgap1	30934	Tor1b
30935	Tor3a	50496	E2f6	50918	Myadm	52009	Hn1l
52398	Sept11	52428	Rhpn2	52538	Acaa2	52585	Dhrs1
52840	Dbn2d2	53330	Vamp4	53376	Usp2	53378	Sdcbp
53415	Htatip2	53599	Cd164	53623	Gria3	53860	Sept9
54325	Elovl1	54720	Recan1	56016	Hebp2	56212	Rhog
56248	Ak3	56309	Mycbp	56332	Amotl2	56356	Gltp
56369	Ap1	56494	Gosr2	56517	Slc22a21	56520	Nme4
56709	Dnajb12	56722	Litaf	56741	Igdcc4	57267	Apba3
57315	Wdr46	58809	Rnase4	60595	Actn4	65960	Twsg1
66153	Fbxo36	66395	Ahnak	66500	Slc30a7	66523	2810004N23Rik
66616	Snx9	66659	Acp6	66717	Ccdc96	66853	Pnpla2
66859	Slc16a9	66913	Kdelr2	66990	Tmem134	67145	Tomm34
67213	Cmtm6	67374	Jam2	67603	Dusp6	67605	Akt1s1
67843	Slc35a4	67951	Tubb6	67980	Gnpda2	67991	Nacc2
68041	Mid1ip1	68066	Slc25a39	68226	Efcab2	68270	Lrrc50
68465	Adipor2	68520	Zfyve21	68539	Tmem109	68581	Tmed10
68606	Ppm1f	68682	Slc44a2	68738	Acss1	68794	Flnc
69274	Ctdspl	69683	2310044H10Rik	69737	Ttl	70024	Mcm10
70218	Kif18b	70417	Megf10	70435	Inf2	70461	Crtc3
70806	D19Ert652e	70984	4931406C07Rik	71409	Fmnl2	71567	Mcm9
71602	Myo1e	71712	Dram1	71766	Raver1	71801	Plekhh2
71918	Zcchc24	71943	Tom1l1	71946	Endod1	71956	Rnf135
72157	Pgm2	72287	Plekhl1	72792	2810459M11Rik	73284	Ddit4l
73827	1110012D08Rik	74098	0610037L13Rik	74105	Gga2	74533	Gzfl
75452	Ascc2	75556	1700026D08Rik	75563	Dnali1	75599	Pcdh1
75646	Rai14	75659	Wdr54	75723	Amotl1	76044	Ncapg2
76178	6330578E17Rik	76251	0610007P08Rik	76263	Gstk1	76491	Abhd14b
76566	Fam101b	76893	Lass2	76895	Bid2	77034	2510039O18Rik
77056	Tmco4	77446	Heg1	77559	Ag1	77569	Limch1

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Putative direct targets of miR-124							
Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
77579	Myh10	78388	Mvp	78619	Zfp449	78829	Tsc22d4
78926	Gas2l1	79202	Tnfrsf22	80290	Gpr146	80888	Hspb8
81840	Sorcs2	81879	Tcfcp2l1	81910	Rrbp1	83436	Plekha2
83675	Bicc1	99003	Qser1	99889	Arfp1	100072	Camta1
101543	Wtip	102462	Imp3	102626	Mapkapk3	102644	Oaf
102693	Phldb1	104027	Synpo	105501	Abhd4	106581	Itfg3
106639	Vmac	106840	Unc119b	107976	Bre	108657	Rnpepl1
108673	Ccdc86	108682	Gpt2	108705	Pttglip	108735	Sft2d2
109145	Gins4	109154	Mlec	109333	Pkn2	109672	Cyb5
110379	Sec13	110826	Etfb	114774	Pawr	116701	Fgfr11
116972	Fam57a	117150	Pip4k2c	140570	Plxnb2	140579	Elmo2
170625	Snx18	170748	BC017612	171212	Galnt10	171286	Slc12a8
207175	Cetn4	209195	Clic6	209378	Itih5	209601	4922501L14Rik
211945	Plekhh1	212647	Aldh4a1	214345	Lrrc1	214968	Sema6d
215280	Wipfl	215751	BC013529	217365	Nploc4	217430	Pqlc3
217684	4933426M11Rik	217718	Nek9	218503	Fcho2	218630	Ccno
218952	Fermt2	219148	Fam167a	219189	1300010F03Rik	223693	Tmem184b
224143	Ktelc1	225164	Mib1	226162	Dpcd	226265	Eno4
224519	Lamc1	227292	Ctdsp1	227737	Fam129b	228775	Trib3
228942	Cbln4	228966	Ppp1r3d	229096	Ythdf3	229285	Spg20
230709	Zmpste24	230751	Oscp1	230779	Serinc2	230789	Fam76a
230967	BC046331	231452	Sdad1	233033	Samd4b	233315	Mtmr10
234839	Fam38a	237806	Dnahc9	239273	Abcc4	240660	Tmem20
242553	Kank4	242585	Slc35d1	242687	Wasf2	242785	Kihl121
244152	Tsku	244631	Psck1	246257	Ovca2	246316	Lgi2
259302	Srgap3	268935	Scube3	269593	Luzp1	269941	Chsy1
269999	Orai3	286940	Flnb	319710	Frmf6	319939	Tns3
320184	Lrrc58	320404	Itpkb	320736	E130203B14Rik	326618	Tpm4
329274	Fam163a	330171	Ketd10	330222	Sdk1	330695	Ctxn1
338365	Slc41a2	382030	Tmem188	382406	Wdr51b	414801	Itpr1p
432572	Cytsb	544963	Iqgap2	100045343	LOC100045343	100046855	LOC100046855
100047738	LOC100047738	100047856	LOC100047856	100048877	LOC100048877		

Table A.10: Putative direct targets of miR-143

Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
11438	Chrna4	11652	Akt2	11676	Aldoc	11692	Gfer
11717	Ampd3	11745	Anxa3	11778	Ap3s2	11799	Birc5
11932	Atp1b2	12125	Bcl2l11	12192	Zfp361l	12297	Cacnb3
12366	Casp2	12400	Cbfb	12476	Cd151	12521	Cd82
12633	Cflar	12702	Socs3	12704	Cit	12751	Tpp1
12798	Cnn2	12856	Cox17	12908	Crat	12972	Cryz
13010	Cst3	13135	Dad1	13386	Dlk1	13445	Cdk2ap1
13481	Dpm2	13644	Efs	13649	Egfr	13728	Mark2
13870	Ercc1	13972	Gnb11	14043	Ext2	14082	Fadd
14086	Fscn1	14219	Ctgf	14230	Fkbp10	14548	Mrps33
14605	Tsc22d3	14697	Gnb5	14701	Gng12	14726	Pdpn
14739	S1pr2	14755	Pigq	14768	Lancl1	14793	Cdca3
15039	H2-T22	15239	Hgs	15277	Hk2	16011	Igfbp5
16432	Itm2b	16594	Klc2	16796	Laspl	16801	Arhgef1
16885	Limk1	17126	Smad2	17132	Maf	17390	Mmp2
17391	Mmp24	17828	Muted	17865	Mybl2	18011	Neurl1a
18018	Nfatc1	18140	Uhrfl	18174	Slc11a2	18563	Pcx
18591	Pdgfb	18595	Pdgfra	19039	Lgals3bp	19079	Prkab1
19192	Psme3	19725	Rfx2	19763	Ring1	20111	Rps6ka1
20446	St6galnac2	20511	Slc1a2	20681	Sox8	20779	Src
20922	Supt4h1	20974	Syng3	21429	Ubtf	21766	Tex261
21853	Timeless	22022	Tpst2	22319	Vamp3	22320	Vamp8
22401	Zmat3	22670	Trim26	23936	Lynx1	23969	Pacsin1
24068	Sra1	26362	Axl	26433	Plod3	26894	Cops7a
27081	Zfp275	27276	Plekhh1	27366	Txn14a	27965	Spg21
28000	Prpf19	28035	Usp39	50918	Myadm	51875	Tmem141
52004	Cdk2ap2	52064	Coq5	52276	Cdca8	52585	Dhrs1
52683	Ncaph2	52838	Nlz	53598	Dctn3	55963	Slc1a4
56233	Hdac7	56374	Tmem59	56491	Vapb	56542	Ick
56722	Litaf	57028	Ptxp	57434	Xrcc2	57436	Gabarapl1
57776	Ttyh1	58238	Fam181b	60441	Mrpl38	64075	Smoc1
66078	Tsen34	66179	1110031102Rik	66191	Ier3ip1	66236	1500011B03Rik

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Putative direct targets of miR-143

Entrez ID	Symbol						
66241	Tmem9	66278	1810013D10Rik	66314	Tpd5212	66442	Spc25
66588	Cmpk1	66840	Wdr451	66855	Tcf25	66962	2310047B19Rik
67213	Cmtm6	67513	2610002J02Rik	67657	Rabl3	67693	2310003F16Rik
67695	2310016E02Rik	67792	Rgs8	67843	Slc35a4	67861	Akr1b10
67916	Ppap2b	68087	Dcakd	68338	Golt1a	68505	1110014N23Rik
68597	1110021J02Rik	68666	Svop	68713	Ifitm1	68889	Ubac2
68910	Zfp467	69035	Zdhhc3	69195	Tmem121	69310	Pacrg
69549	2310009B15Rik	69928	Apitd1	69961	2810432D09Rik	70225	Ppil3
70296	Tbc1d13	70612	5730494N06Rik	70686	Dusp16	71448	Tmem80
71452	Ankrd40	71711	Mus81	71726	Smug1	71803	Slc25a18
71909	Haus5	71918	Zcchc24	72106	Jmjd8	72151	Rfc5
72500	Ier5l	72514	Fgfbp3	72775	Fance	72792	2810459M11Rik
73095	Slc25a42	74105	Gga2	74137	Nuak2	74244	Atg7
74342	Lrrtm1	74763	Nat15	75007	Fam63a	75104	Mmd2
75146	Tmem180	75210	Prr3	75495	Morn5	76156	Fam131b
76626	Msi2	76799	2510006D16Rik	76854	Gper	76877	Rab36
77031	Slc9a8	77254	Yif1b	78339	Ttyh3	78829	Tsc22d4
78935	Saal1	81489	Dnajb1	94044	Bcl2l13	94047	Cecr6
94282	Sfxn5	99237	Tm9sf4	99543	Olfml3	100169	Phactr4
101095	Zfp282	102626	Mapkapk3	102693	Phldb1	103743	Tmem98
104418	Dgkz	104479	Ccdc117	105245	Txndc5	105352	Dusp22
105675	Ppif	107522	Ece2	107976	Bre	108037	Shmt2
108912	Cdca2	109006	Ciapin1	109154	Mlec	109648	Npy
109674	Ampd2	111241	Hmgal-rs1	116972	Fam57a	117146	Ube3b
117592	B3galt6	140499	Ube2j2	170460	Stard5	170625	Snx18
171508	Creld1	192185	Nadk	192231	Hexim1	207819	4930539E08Rik
208501	1810043H04Rik	209773	Dennd2a	211286	Cln5	211535	Ccdc114
211798	Mfsd9	212127	2810046L04Rik	212508	Mtg1	212996	Wbscr17
213491	D4ErtD22e	214058	Megf11	214895	Lman2l	214932	Cecr5
217715	Eif2b2	219151	Scara3	223690	Ankrd54	224139	Golgb1
226970	Arhgef4	227619	Man1b1	229504	Isg20l2	230514	Leprot
231863	Fbxl18	235431	Coro2b	235584	Dusp7	237988	Cdr2l
243867	Fbxo46	244152	Tsku	245828	Trappc1	246104	Rhbdl3
246257	Ovca2	252864	Dusp15	268417	Zkscan17	268420	Alkbh5
319757	Smo	320394	Cenpt	330260	Pon2	378702	Serf2
381045	Ccdc58	381921	Taok2	384009	Glipr2	100113398	Adat3

Table A.11: Putative direct targets of miR-145

Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
11421	Ace	11492	Adam19	11676	Aldoc	11758	Prdx6
11765	Ap1g1	11799	Birc5	11932	Atp1b2	11988	Slc7a2
12014	Bach2	12153	Bmp1	12388	Ctnnd1	12400	Cbfb
12450	Ccng1	12545	Cdc7	12753	Clock	12842	Coll1a1
12848	Cops2	13063	Cyca	13132	Dab2	13204	Dhx15
13837	Epha3	13990	Smarcad1	14007	Cugbp2	14057	Sfxn1
14062	F2r	14086	Fscn1	14199	Fhl1	14402	Gabrb3
14571	Gpd2	14583	Gfpt1	14634	Gli3	14725	Lrp2
14772	Grk4	14783	Grb10	15077	Hist2h3c1	15270	H2afx
15530	Hspg2	16007	Cyr61	16011	Igfbp5	16151	Ikbkg
16526	Kcnk2	16561	Kif1b	16568	Kif3a	16574	Kif5c
16579	Kifap3	16589	Uhmk1	17129	Smad5	17196	Mbp
17294	Mest	17389	Mmp16	17920	Myo6	17967	Ncam1
17975	Ncl	17995	Ndufv1	18003	Nedd9	18027	Nfia
18028	Nfib	18176	Nras	18212	Ntrk2	18424	Otx2
18569	Pdcd4	18595	Pdgfra	18762	Prkcz	18823	Plp1
18858	Pmp22	19055	Ppp3ca	19108	Prkx	19206	Ptch1
19212	Pter	19244	Ptp4a2	19285	Ptrf	19290	Pura
19291	Purb	19302	Pxmp3	19655	Rbmx	19714	Rev3l
19731	Rgl1	19820	Rlim	20166	Rtkn	20174	Ruvbl2
20239	Atxn2	20249	Scd1	20356	Sema5a	20358	Sema6a
20397	Sgpl1	20463	Cox7a2l	20529	Slc31a1	20682	Sox9
20689	Sall3	20747	Spop	20913	Stxbp4	20947	Swap70
21346	Tagln2	21844	Tiam1	21981	Ppp1r13b	22034	Traf6
22042	Tfrc	22422	Wnt7b	22687	Zfp259	22718	Zfp60
23972	Papss2	26398	Map2k4	26401	Map3k1	26432	Plod2
26897	Acot1	26951	Zw10	27205	Podxl	27360	Add3
27406	Abcf3	27418	Mkl1	28075	Pppde2	28193	Reep3

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Putative direct targets of miR-145							
Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
29806	Limd1	30930	Vps26a	50755	Fbxo18	50789	Fbxl3
50793	Orc3l	50876	Tmod2	50912	Exosc10	52357	Wwc2
52398	Sept11	52874	D19Bwg1357e	53945	Slc40a1	54161	Copg
54403	Slc4a4	55946	Ap3m1	55989	Nop58	56150	Mad2l1
56426	Pdcd10	56430	Clip1	56496	Tspan6	56554	Raet1d
56709	Dnajb12	56771	Med20	56805	Zbtb33	57434	Xrcc2
57776	Ttyh1	58998	Pvrl3	59008	Anapc5	64297	Gprc5b
64602	Ireb2	66074	Tmem167	66084	Rmnd1	66101	Ppih
66161	Pop4	66420	Polr2e	66427	Cyb5b	66586	Crls1
66868	Mfsd1	66869	Zfp869	66882	Bzw1	66884	Appbp2
66953	Cdca7	67064	Chmp1b	67072	Cdc37l1	67073	Pi4k2b
67211	Armc10	67273	Ndufa10	67370	Zfp606	67414	Mfn1
67433	Ccdc127	67452	Pnpla8	67528	Nudt7	67544	Fam120b
67603	Dusp6	67629	Spc24	67784	Plxnd1	67920	Mak16
68038	Chid1	68145	Etaa1	68187	Fam135a	68268	Zdhhc21
68275	Rpal	68581	Tmed10	68659	Fam198b	68693	Hnrnpul2
68738	Acss1	69035	Zdhhc3	69207	Sfrs11	69692	Hddc2
69718	Ipmk	69727	Usp46	69821	Mterfd2	70052	Prpf4
70296	Tbcd13	70375	Ica11	70417	Megf10	70454	Cenpl
71435	Arhgap21	71436	Flrt3	71770	Ap2b1	71782	Ankle2
71914	Antxr2	72102	Dusp11	72141	Adpgk	72181	Nsun4
72238	Tbcd15	72349	Dusp3	72425	2410042D21Rik	72459	Htatsf1
72519	Tmem55a	72759	Tmem135	72792	2810459M11Rik	72823	Pard3b
72925	March1	73122	Tgfbra1	73230	Bmper	73284	Ddit4l
73296	Rhobtb3	74030	Rin2	74186	Ccdc3	74492	Kbtbd13
74498	Gorasp1	74868	Tmem65	75678	Ippk	75805	Nln
76178	6330578E17Rik	76267	Fads1	76376	Slc24a2	76574	Mfsd2a
76742	Snx27	77106	Tmem181a	77574	Fam115a	77976	Nuak1
78100	8430410K20Rik	78593	Nrip3	78655	Eif3j	78748	Rassf10
78937	Av19	79464	Lias	80890	Trim2	81840	Sorcs2
81879	Tcfcp211	83397	Akap12	83671	Sytl2	83675	Bicc1
83997	Slmap	93871	Brwd1	94040	Clmn	94190	Ophn1
94282	Sfn5	98660	Atpl2	100317	AU040320	100434	Slc44a1
100710	Pds5b	100986	Akap9	101565	6330503K22Rik	102247	Agpat6
103135	Usp52	103537	Mbtd1	104625	Cnot6	105638	Dph3
106369	Ypel1	106840	Unc119b	107029	Me2	107568	Wwp1
108071	Grm5	108652	Slc35b3	108653	Rimklb	108760	Galnt11
108897	Aif11	108912	Cdca2	109079	Sephs1	109232	Scepdh
109552	Sri	109801	Glo1	116914	Slc19a2	117198	Ivns1abp
117600	Srgap1	140740	Sec63	170753	Zfp704	170822	Usp33
194401	Mical3	207214	Lrp4	208659	Fam20a	208718	Dis3l2
210004	B3gnt11	211286	Cln5	211535	Ccdc114	211914	Asap2
211945	Plekhh1	211949	Spsb4	213056	Fam126b	213391	Rassf4
213582	Mtap9	214137	Arhgap29	214944	Mobkl2b	215008	Vezt
216440	Os9	216578	Papolg	216825	Usp22	216965	Taok1
217431	Nol10	217653	C79407	217864	Rcor1	217893	Pacs2
218397	Rasa1	218454	Lhfp12	219148	Fam167a	223739	5031439G07Rik
224836	Usp49	224997	Dlgap1	225283	Rprd1a	226144	Erlin1
226151	Fam178a	226432	Ipo9	226470	Zbtb41	226562	Bat2l2
226781	Slc30a10	227682	Trub2	228357	Lrp4	228829	Phf20
228876	Zfp334	229709	Ahcy11	230234	BC026590	230753	Thrap3
230857	Ece1	231238	Sel1l3	231834	Snx8	232164	Paip2b
232431	Gprc5a	233103	4931406P16Rik	233271	Luzp2	233315	Mtmr10
233532	Rsf1	234549	Heatr3	234734	Aars	235132	Zbtb44
235542	Ppp2r3a	236920	Stard8	237082	Nxt2	241075	Plekhh3
241589	D430041D05Rik	242362	Manea	242585	Slc35d1	242687	Wasf2
243725	Ppp1r9a	245446	Slitrk4	246154	Vasn	246196	Zfp277
259302	Srgap3	268882	Fbxo45	269003	Sap130	286940	Flnb
320508	Cachd1	320705	Bend6	320713	Mysm1	321022	Cdv3
326618	Tpm4	329641	6030405A18Rik	329828	AI464131	329941	Col8a2
330260	Pon2	407786	Taf9b	432572	Cytsb	100037258	Dnajc3
100039795	Ildr2	100043555	LOC100043555				

Table A.12: Putative direct targets of miR-25

Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
11302	Aatk	11886	Asah1	11906	Zfhx3	12036	Bcat2
12111	Bgn	12125	Bcl2l11	12577	Cdkn1c	13138	Dag1

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Putative direct targets of miR-25

Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
13356	Dgcr2	13640	Efna5	13654	Egr2	14020	Evi5
14025	Ecl11a	14057	Sfxn1	14165	Fgf10	14167	Fgf12
14584	Gfpt2	14675	Gna14	15166	Hcn2	15529	Sdc2
16001	Igflr	16011	Igfbp5	16579	Kifap3	16909	Lmo2
17158	Man2a1	17918	Myo5a	18027	Nfia	18029	Nfic
18032	Nfix	18046	Nfyc	18417	Cldn11	18549	Pcsk2
18555	Cdk16	18627	Per2	18640	Pfkfb2	18709	Pik3r2
18717	Pip5k1c	18738	Pitpna	19084	Prkar1a	19085	Prkar1b
19277	Ptpro	19326	Rab11b	19352	Rabggtb	19679	Pitpnm2
19822	Rnf4	20320	Nptn	20393	Sgk1	20544	Slc9a1
20595	Smn1	20621	Snn	20652	Soat1	20719	Serpnb6a
20965	Syn2	20970	Sdc3	21685	Tef	21841	Tia1
21858	Timp2	21885	Tle1	22348	Slc32a1	22401	Zmat3
22418	Wnt5a	22644	Rnf103	22781	Ikzf4	23792	Adam23
26373	Clen7	26398	Map2k4	26419	Mapk8	27362	Dnajb9
50781	Dkk3	51813	Cenc	52882	Rgs7bp	54418	Fmn2
56248	Ak3	56468	Socs5	56613	Rps6ka4	56747	Sez6l
56876	Nelf	57431	Dnajc4	59046	Arpp19	64378	Gpr88
64933	Ap3m2	65247	Asb1	65964	B230120H23Rik	66114	Dnajc30
66259	Camk2n1	66310	Dpy30	66686	Dcbld1	66701	Spryd4
66756	4933411K20Rik	66878	Riok3	66894	Wwp2	66902	Mtap
67117	Dynlt3	67398	Srpr	67602	Necap1	68202	Ndufa5
68365	Rab14	68514	Efha1	68520	Zfyve21	68659	Fam198b
69046	Isca1	70052	Prpf4	70465	Wdr77	70599	Ssfa2
71063	Zfp597	71722	Cic	71982	Snx10	72007	Fndc3b
72056	1810055G02Rik	72344	Usp36	72536	Tagap	73744	Man2c1
74106	Dcaf6	74158	Josd1	74197	Gtf2e1	74349	Fam160a2
74513	Neto2	74519	Cyp2j9	74769	Pik3cb	75901	Dcpl1a
76366	Mtif3	76477	Peolce2	76740	Efr3a	76788	Klhdc10
78937	Avl9	81535	Sgpp1	83922	Tsga14	94249	Slc24a3
94282	Sfxn5	98682	Mfsd6	98952	Fam102a	99738	Kcnc4
100383	Bsdc1	101476	Plekha1	102323	Dcun1d2	103768	Tubg2
103850	Nt5m	104111	Adcy3	105171	Arrdc3	106564	Ppes
107767	Scamp1	108652	Slc35b3	109205	Sobp	114896	Afg3l1
117197	Cno	140919	Slc17a6	170625	Snx18	195209	Gm22
209318	Gps1	210106	Papd7	211255	Kbtbd7	211499	Tmem87a
213056	Fam126b	216134	Pdxk	216558	Ugp2	216742	Fnip1
216965	Taok1	217119	Xylt2	217351	Tnrc6c	218454	Lhfp12
218503	Fcho2	223254	Farp1	223693	Tmem184b	225280	Ino80c
225642	Grp	226252	Fam160b1	226856	Lpgat1	227723	Bat2l
228942	Cbln4	228983	Osbp12	228998	Arfgap1	229541	Dennd4b
230514	Leprot	232947	Lrrc68	234734	Aars	235281	Scn3b
235283	Gramd1b	241494	Zfp385b	245944	Vps54	252966	Cables2
268860	Abat	269401	Znf512b	269593	Luzp1	270076	Gcdh
319642	Rab9b	319832	Tmem229a	319865	E130114P18Rik	320492	A830018L16Rik
328329	Mast4	333789	N4bp2	338467	Morc3	353047	Plekhn1
382985	Rrm2b	403187	Opa3	432450	Nkain2	433100	AA388235

Table A.13: Putative direct targets of cel-miR-67

Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
11566	Adss	11610	Agtrap	11736	Ankfy1	11765	Ap1g1
12043	Bcl2	12050	Bcl2l2	12055	Bcl7c	12166	Bmpr1a
12177	Bnip3l	12457	Cern4l	12555	Cdh15	12633	Cflar
12805	Cntn1	12807	Hps3	12915	Atf6b	12937	Pcdha6
12953	Cry2	13014	Cstb	13063	Cycs	13135	Dad1
13193	Dcx	13199	Pdxk	13204	Dhx15	13478	Dpagt1
13483	Dpp6	13527	Dtna	13690	Eif4g2	13709	Elfl
13844	Ephb2	13855	Epn2	14007	Cugbp2	14042	Ext1
14057	Sfxn1	14105	Sfrs13a	14230	Fkbp10	14365	Fzd3
14388	Gab1	14615	Gjcl	14674	Gna13	14696	Gnb4
14718	Got1	14897	Trip12	15200	Hbegf	15312	Hmgn1
15525	Hspa4	16009	Igfbp3	16210	Impact	16362	Irf1
16561	Kif1b	16570	Kif3b	16589	Uhmk1	16653	Kras
16889	Lipa	17535	Mrel1a	17918	Myo5a	18000	Sept2
18011	Neurl1a	18082	Nipsnap1	18140	Uhrf1	18167	Npy2r
18212	Ntrk2	18616	Peg3	18744	Pja1	18768	Pkib
18799	Plcd1	18986	Pou2fl	19043	Ppm1b	19046	Ppp1cb

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Putative direct targets of cel-miR-67							
Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
19055	Ppp3ca	19058	Ppp3r1	19070	Mobkl3	19072	Prep
19084	Prkar1a	19159	Cyth3	19245	Ptp4a3	19267	Ptpre
19288	Ptx3	19290	Pura	19349	Rab7	19384	Ran
19645	Rb1	19726	Rfx3	19729	Rag1ap1	19820	Rlim
19891	Rpa2	20168	Rtn3	20224	Sar1a	20250	Scd2
20382	Sfrs2	20399	Sh2b1	20587	Smarcb1	20617	Snca
20652	Soat1	20842	Stag1	20843	Stag2	20853	Stau1
20887	Sult1a1	20932	Surf4	20935	Surf6	20971	Sdc4
21912	Tspan7	21991	Tpi1	22129	Ttc3	22350	Ezr
22380	Wbp4	22764	Zfx	22793	Zyx	24017	Rnfl3
24030	Mrps12	24116	Whsc2	26398	Map2k4	26416	Mapk14
27041	G3bp1	27055	Fkbp9	27096	Trappc3	28028	Mrpl50
28146	Serp1	29806	Limd1	29820	Tnfrsf19	29861	Dpfl
29864	Rnfl1	30058	Timm8a1	50754	Fbxw7	50996	Pdcd7
52206	Anapc4	52468	Ctdsp2	52666	D10Ert610e	52850	Sgsm1
52882	Rgs7bp	53323	Ube2k	53380	Psm10	53619	Blcap
54151	Cyhr1	54473	Tollip	54484	Mkrn1	54613	St3gal6
56048	Lgals8	56248	Ak3	56309	Mycbp	56351	Ptges3
56367	Scoc	56386	B4galt6	56418	Ykt6	56433	Vps29
56459	Sae1	57743	Sec61a2	57912	Cdc42se1	58194	Sh3kbp1
58239	Dexi	58242	Nudt11	58243	Nap115	59069	Tpm3
64010	Sav1	64050	Yeats4	64143	Ralb	64297	Gprc5b
65973	Asph	66046	Ndufb5	66052	Sdhc	66140	Fam33a
66191	Ier3ip1	66194	Pycl1	66246	Osgep	66335	Atp6v1c1
66566	2310079N02Rik	66648	5730494M16Rik	66700	Vps24	66849	Ppp1r2
66884	Appbp2	66892	Eif4e3	66923	Pbrm1	66953	Cdca7
66966	Trit1	67027	Mkrn2	67070	Lsm14a	67130	Ndufa6
67181	Dullard	67238	2810453I06Rik	67245	Peli1	67326	1700037H04Rik
67388	1110008F13Rik	67414	Mfn1	67529	Fgfr1op2	67590	Tctn3
67738	Ppid	67808	Tprgl	67887	Tmem66	67889	Rbm18
67897	Rnmt	67933	Hcfc2	68050	Akirin1	68149	Otub2
68272	Rbm28	68364	0610030E20Rik	68477	Rmnd5a	68558	Ankra2
68861	1190002N15Rik	68874	Klhdc9	68969	Eif1b	69053	1810013L24Rik
69109	Fam58b	69136	Tusc1	69150	Snx4	69227	2810407C02Rik
69329	1700003M02Rik	69372	Mocs3	69538	Antxr1	70093	Ube2q1
70369	Bag5	70556	Slc25a33	70584	Pak4	70612	5730494N06Rik
71778	Klh15	71900	Tmem106b	71952	2410016O06Rik	71963	Cdca4
71978	Ppp2r2a	72075	Ogfr	72124	Seh1l	72139	2610044O15Rik
72170	Chchd4	72193	Sfrs2ip	72195	Supt7l	72542	Pgam5
72552	Hsd1l	72585	Lypd1	72685	Dnajc6	72792	2810459M11Rik
72993	App1l	73137	Prrc1	73713	Rbm20	74022	Glyr1
74030	Rin2	74256	Cyld	74340	Ahcy12	74356	4931428F04Rik
74450	Pank2	74479	Snx11	74493	Tnks2	74763	Nat15
74769	Pik3cb	75625	Mageh1	75678	Ippk	75710	Rbm12
75723	Amot1l	75769	4833424O15Rik	75778	Them4	75956	Srrm2
76007	Zmym2	76252	Atp6v0e2	76302	Pcnp	76308	Rab1b
76626	Msi2	76688	Arfrp1	76893	Lass2	76958	2210418O10Rik
77305	Wdr82	77781	Epm2aip1	78408	Fam131a	78757	Rictor
78808	Stxbp5	78938	Fbxo34	80509	Med8	80909	Gatsl2
80986	Ckap2	81879	Tcfcp2l1	93683	Gfce	93739	Gabarapl2
97884	B3galnt2	98741	Kcnb2	99311	Commd7	99887	Tmem56
99889	Arfp1	103266	AI597468	103694	Tmed4	104318	Csnk1d
104625	Cnot6	104725	1110002B05Rik	105000	Dnalc1	106298	Rrn3
106522	Pkdec	106840	Unc119b	106894	Hmgxb3	107566	Arl2bp
107581	Col16a1	107823	Whsc1	107885	Mthfs	108958	Fam73b
108960	Irak2	109006	Ciapi1	109689	Arrb1	109711	Actn1
110809	Sfrs1	110959	Nudt19	111241	Hmga1-rs1	116731	Pcdha1
116873	Stim2	117109	Pop5	140904	Caln1	170459	Stard4
193813	Mcf2	207806	Gm608	208292	Zfp871	209268	Igsf1
211286	Cln5	211739	Vstm2a	213056	Fam126b	213464	Rbbp5
213541	Ythdf2	214162	Mll1	214579	Aldh5a1	214952	Rhot2
216119	A130042E20Rik	216549	Aftph	216792	A230051G13Rik	216987	Utp6
217732	2310044G17Rik	217864	Rcor1	217893	Pacs2	218772	Rarb
218975	Mapk1ip1l	219022	Ttc5	219181	Akap11	223752	Gramd4
224105	Pak2	224129	Adcy5	224647	D17Wsu92e	225215	Rsl24d1
225280	Ino80c	225363	Etf1	226043	Cbwd1	226144	Erlin1
226744	Cnst	226844	Mfsd7b	227619	Man1b1	227682	Trub2
228071	Sestd1	228714	Csrp2bp	228812	Pigu	228880	Zmynd8
229517	Slc25a44	229593	Golph3l	229615	Pias3	230235	6430704M03Rik
230709	Zmpste24	230917	Tmem201	231070	Insig1	231724	Rad9b

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Putative direct targets of cel-miR-67

Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
231834	Snx8	231997	Fkbp14	232784	Zfp212	233271	Luzp2
234728	Ftsjd1	234736	Rfwd3	235574	Atp2c1	237859	Ccdc55
241263	Gpr158	242291	Impad1	242297	Fam110b	242384	Lingo2
242687	Wasf2	242800	Ttc34	242864	Napepld	244058	Rgma
244631	Pskh1	244810	AW551984	245468	Pnma3	245555	C77370
246316	Lgi2	268697	Cenb1	269582	Clspn	269639	Zfp512
272589	Tbcel	277414	Trp53i11	319370	Fam100b	319468	Ppmlh
320184	Lrrc58	320333	D830030K20Rik	320472	Ppml1e	320495	Ipcf1
329739	Fam102b	330050	Fam185a	380614	Intu	381038	Parl
381280	Hjurp	381511	Pdp1	384763	Zfp667	504193	Cbx6-Nptxr
545260	Arsi	668661	2410002F23Rik	100041567	Gm10060	100042480	Nhs12
100043555	LOC100043555	100047834	LOC100047834				

Table A.14: Putative direct targets of miR-434-3p

Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol	Entrez ID	Symbol
11745	Anxa3	11799	Birc5	12444	Ccnd2	12450	Ccng1
12476	Cd151	12505	Cd44	12527	Cd9	12661	Chl1
12830	Col4a5	12842	Col1a1	13356	Dgcr2	13617	Ednra
13618	Ednrb	13649	Egfr	14168	Fgf13	14282	Fosb
14609	Gja1	14613	Gja5	14735	Gpc4	15529	Sdc2
15568	Elavl1	16601	Klf9	17973	Nck1	18041	Nfs1
19038	Ppic	19303	Pxn	20377	Sfrp1	20512	Slc1a3
20621	Snn	20689	Sall3	20818	Srprb	20848	Stat3
20922	Supt4h1	21417	Zeb1	21804	Tgfb1l1	21813	Tgfb1r2
22042	Tfrc	22319	Vamp3	23827	Bpnt1	23873	Faim
23947	Mid2	26362	Axl	27058	Srp9	27273	Pdk4
27428	Shroom3	30057	Timm8b	52276	Cdca8	53374	Chst3
53901	Rcan2	56078	Car5b	56248	Ak3	56291	Styx
56397	Morf4l2	56516	Rbms2	60599	Trp53inp1	65960	Twsg1
66273	1810020D17Rik	66467	Gtf2h5	66471	Anp32e	66628	Thgl1
66870	Serbp1	66905	Plin3	67145	Tomm34	67468	Mmd
68420	Ankrd13a	68659	Fam198b	68801	Elov15	69241	Polr2d
73569	Vgll3	73828	Dcaf4	74148	1300001I01Rik	75616	2810008M24Rik
75646	Rai14	76626	Msi2	78232	Trappc6b	78808	Stxbp5
80860	Ghdc	81879	Tefcp2l1	99237	Tm9sf4	103266	AI597468
103724	Tbcl1d10a	105245	Txndc5	107272	Psat1	107566	Arl2bp
108735	Sft2d2	109801	Glo1	110460	Acat2	114774	Pawr
116914	Slc19a2	117149	Tirap	171567	Nme7	192216	Tmem47
208936	Adamts18	209357	Gtf2h3	213673	9530068E07Rik	214944	Mobkl2b
219140	Spata13	223453	Dap	225280	Ino80c	226562	Bat2l2
229534	Pbxip1	232157	Mobkl1b	232313	Gxylt2	233406	Prc1
240725	Sulf1	268697	Cenb1	319613	5730410E15Rik	330192	Vps37b
384009	Glipr2	432879	Gm5465	504193	Cbx6-Nptxr	100041103	LOC100041103

Table A.15: Top 25 most enriched KEGG terms in targets of cel-miR-67.

$q$  - number of genes of a KEGG term that was among the predicted targets,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
04210	Apoptosis	8	48	6e-04
05014	Amyotrophic lateral sclerosis (ALS)	5	33	0.0102
04722	Neurotrophin signaling pathway	8	76	0.0116
04012	ErbB signaling pathway	6	51	0.0168
05222	Small cell lung cancer	6	51	0.0168
04660	T cell receptor signaling pathway	6	52	0.0184
04914	Progesterone-mediated oocyte maturation	6	52	0.0184

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ID	Term Description	q	m	P
00562	Inositol phosphate metabolism	4	26	0.0202
04370	VEGF signaling pathway	5	42	0.0272
05210	Colorectal cancer	6	59	0.0323
04710	Circadian rhythm - mammal	2	8	0.04
05223	Non-small cell lung cancer	4	36	0.0581
00100	Steroid biosynthesis	2	11	0.0725
04664	Fc epsilon RI signaling pathway	4	40	0.0797
04912	GnRH signaling pathway	5	57	0.0828
04662	B cell receptor signaling pathway	4	43	0.0982
05200	Pathways in cancer	11	175	0.101
04120	Ubiquitin mediated proteolysis	7	97	0.101
04620	Toll-like receptor signaling pathway	4	45	0.112
05212	Pancreatic cancer	4	47	0.126
05211	Renal cell carcinoma	4	48	0.133
04114	Oocyte meiosis	5	66	0.133
00534	Heparan sulfate biosynthesis	2	16	0.139
04650	Natural killer cell mediated cytotoxicity	4	50	0.148
05216	Thyroid cancer	2	17	0.153

**Table A.16: Top 25 most enriched KEGG term in targets of miR-124.**  $q$  - number of genes of a KEGG term that was among predicted targets,  $m$  - total number of genes of a KEGG term in a test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
04510	Focal adhesion	13	121	0.00211
04520	Adherens junction	7	46	0.00347
04530	Tight junction	8	68	0.00907
05416	Viral myocarditis	5	31	0.0104
05222	Small cell lung cancer	7	56	0.0105
05220	Chronic myeloid leukemia	6	49	0.0192
04810	Regulation of actin cytoskeleton	11	127	0.0223
05221	Acute myeloid leukemia	5	38	0.024
05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	5	42	0.0354
05216	Thyroid cancer	3	18	0.0421
04512	ECM-receptor interaction	5	45	0.0458
04670	Leukocyte transendothelial migration	6	60	0.0465
05213	Endometrial cancer	4	33	0.0549
02010	ABC transporters	3	20	0.0552
00240	Pyrimidine metabolism	6	63	0.0568

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ID	Term Description	q	m	P
05212	Pancreatic cancer	5	49	0.0623
04650	Natural killer cell mediated cytotoxicity	5	51	0.0716
04622	RIG-I-like receptor signaling pathway	4	38	0.0839
04514	Cell adhesion molecules (CAMs)	5	54	0.087
04660	T cell receptor signaling pathway	5	55	0.0925
04130	SNARE interactions in vesicular transport	3	26	0.104
05200	Pathways in cancer	13	204	0.11
04115	p53 signaling pathway	4	42	0.111
04370	VEGF signaling pathway	4	42	0.111
04662	B cell receptor signaling pathway	4	42	0.111

**Table A.17: Top 25 most enriched KEGG terms in targets of miR-143.**

$q$  - number of genes of a KEGG term that was among the predicted targets,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
04010	MAPK signaling pathway	9	172	0.0342
04810	Regulation of actin cytoskeleton	7	124	0.0422
04142	Lysosome	5	82	0.0624
00510	N-Glycan biosynthesis	3	36	0.0671
00563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	2	17	0.0719
05210	Colorectal cancer	4	61	0.0746
03440	Homologous recombination	2	20	0.0956
04140	Regulation of autophagy	2	20	0.0956
05218	Melanoma	3	42	0.0966
04540	Gap junction	4	67	0.0976
00130	Ubiquinone and other terpenoid-quinone biosynthesis	1	4	0.101
00460	Cyanoamino acid metabolism	1	4	0.101
00680	Methane metabolism	1	4	0.101
00534	Heparan sulfate biosynthesis	2	21	0.104
04520	Adherens junction	3	45	0.113
05214	Glioma	3	46	0.119
00561	Glycerolipid metabolism	2	23	0.121
04370	VEGF signaling pathway	3	47	0.125
01100	Metabolic pathways	21	626	0.127
04920	Adipocytokine signaling pathway	3	48	0.131
00750	Vitamin B6 metabolism	1	6	0.148
00051	Fructose and mannose metabolism	2	26	0.148
05200	Pathways in cancer	8	203	0.161
04130	SNARE interactions in vesicular transport	2	28	0.167

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ID	Term Description	q	m	P
04930	Type II diabetes mellitus	2	31	0.195

**Table A.18: Top 25 most enriched KEGG terms in targets of miR-145.**

$q$  - number of genes of a KEGG term that was among the predicted targets,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
04010	MAPK signaling pathway	14	166	0.000891
04340	Hedgehog signaling pathway	5	31	0.00307
04360	Axon guidance	8	80	0.00435
04144	Endocytosis	10	117	0.00463
00450	Selenoamino acid metabolism	3	16	0.0144
01040	Biosynthesis of unsaturated fatty acids	3	18	0.02
04614	Renin-angiotensin system	2	7	0.0205
00620	Pyruvate metabolism	3	20	0.0267
05016	Huntington's disease	8	115	0.0345
04720	Long-term potentiation	4	44	0.0558
05217	Basal cell carcinoma	3	34	0.101
04210	Apoptosis	4	55	0.107
04062	Chemokine signaling pathway	6	99	0.107
03018	RNA degradation	3	38	0.129
04912	GnRH signaling pathway	4	62	0.148
04540	Gap junction	4	64	0.16
04520	Adherens junction	3	42	0.161
03440	Homologous recombination	2	22	0.164
04114	Oocyte meiosis	4	66	0.173
05020	Prion diseases	2	23	0.176
04662	B cell receptor signaling pathway	3	44	0.177
04020	Calcium signaling pathway	5	92	0.187
04622	RIG-I-like receptor signaling pathway	3	47	0.203
00920	Sulfur metabolism	1	7	0.21
04260	Cardiac muscle contraction	3	48	0.211

**Table A.19: Top 25 most enriched KEGG terms in targets of miR-25.**

$q$  - number of genes of a KEGG term that was among the predicted targets,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
05218	Melanoma	5	42	0.00181

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ID	Term Description	q	m	P
04914	Progesterone-mediated oocyte maturation	5	54	0.00553
00770	Pantothenate and CoA biosynthesis	2	8	0.0118
04664	Fc epsilon RI signaling pathway	4	45	0.0151
04960	Aldosterone-regulated sodium reabsorption	3	26	0.0174
04930	Type II diabetes mellitus	3	28	0.0213
04012	ErbB signaling pathway	4	52	0.0245
04210	Apoptosis	4	52	0.0245
04910	Insulin signaling pathway	5	83	0.0316
05210	Colorectal cancer	4	57	0.033
04810	Regulation of actin cytoskeleton	6	117	0.0381
04010	MAPK signaling pathway	7	151	0.0414
04620	Toll-like receptor signaling pathway	4	63	0.0453
04512	ECM-receptor interaction	3	39	0.0504
00250	Alanine, aspartate and glutamate metabolism	2	19	0.0619
04070	Phosphatidylinositol signaling system	3	45	0.0715
05214	Glioma	3	45	0.0715
05212	Pancreatic cancer	3	47	0.0793
04510	Focal adhesion	5	111	0.0888
04514	Cell adhesion molecules (CAMs)	3	50	0.0916
04722	Neurotrophin signaling pathway	4	82	0.0987
00600	Sphingolipid metabolism	2	25	0.1
04666	Fc gamma R-mediated phagocytosis	3	54	0.109
05200	Pathways in cancer	7	190	0.111
00040	Pentose and glucuronate interconversions	1	6	0.123

**Table A.20: Top 25 most enriched KEGG terms in targets of miR-434-3p.**

$q$  - number of genes of a KEGG term that was among the predicted targets,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
04640	Hematopoietic cell lineage	3	23	0.00456
04512	ECM-receptor interaction	3	35	0.0149
04115	p53 signaling pathway	3	36	0.0161
03060	Protein export	2	17	0.0262
00620	Pyruvate metabolism	2	19	0.0323
05212	Pancreatic cancer	3	47	0.0326
00240	Pyrimidine metabolism	3	53	0.0443
05210	Colorectal cancer	3	56	0.0508
04510	Focal adhesion	4	102	0.0652
00730	Thiamine metabolism	1	5	0.0733

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ID	Term Description	q	m	P
00750	Vitamin B6 metabolism	1	5	0.0733
04144	Endocytosis	4	107	0.0751
04020	Calcium signaling pathway	3	68	0.0813
03420	Nucleotide excision repair	2	32	0.083
00072	Synthesis and degradation of ketone bodies	1	6	0.0874
00920	Sulfur metabolism	1	6	0.0874
05218	Melanoma	2	38	0.111
00900	Terpenoid backbone biosynthesis	1	8	0.115
04520	Adherens junction	2	39	0.116
05200	Pathways in cancer	5	182	0.135
00910	Nitrogen metabolism	1	10	0.141
04630	Jak-STAT signaling pathway	2	45	0.147
00532	Chondroitin sulfate biosynthesis	1	12	0.167
04012	ErbB signaling pathway	2	52	0.184
03020	RNA polymerase	1	14	0.192

**Table A.21: Top 25 most enriched KEGG terms in the induced by transfection set.**

$q$  - number of genes of a KEGG term that was among the predicted targets,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
04115	p53 signaling pathway	21	38	3.88e-09
04512	ECM-receptor interaction	18	37	6.75e-07
04510	Focal adhesion	34	107	2.69e-06
04110	Cell cycle	26	79	2.12e-05
05200	Pathways in cancer	46	188	0.000115
05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	14	40	0.000898
05322	Systemic lupus erythematosus	19	66	0.00179
05222	Small cell lung cancer	14	48	0.00619
05215	Prostate cancer	16	58	0.00641
04060	Cytokine-cytokine receptor interaction	22	89	0.0065
05221	Acute myeloid leukemia	11	35	0.00806
00071	Fatty acid metabolism	8	23	0.012
00980	Metabolism of xenobiotics by cytochrome P450	9	28	0.0138
05210	Colorectal cancer	15	59	0.0177
05213	Endometrial cancer	10	34	0.0184
05220	Chronic myeloid leukemia	12	45	0.0226
05410	Hypertrophic cardiomyopathy (HCM)	12	45	0.0226
05217	Basal cell carcinoma	10	35	0.0226

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**KEGG terms enriched in targets of mockTr**

<b>ID</b>	<b>Term Description</b>	<b>q</b>	<b>m</b>	<b>P</b>
00531	Glycosaminoglycan degradation	5	13	0.0294
04010	MAPK signaling pathway	33	167	0.0331
04142	Lysosome	18	82	0.0418
05414	Dilated cardiomyopathy	12	49	0.0422
04640	Hematopoietic cell lineage	8	29	0.0482
04621	NOD-like receptor signaling pathway	8	30	0.0578
04080	Neuroactive ligand-receptor interaction	19	93	0.0701

**Table A.22: Top 25 most enriched KEGG terms in the Ago HITS-CLIP set.**

$q$  - number of genes of a KEGG term that was in the Ago HITS-CLIP set,  $m$  - total number of genes of a KEGG term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

<b>Term ID</b>	<b>Term Description</b>	<b>q</b>	<b>m</b>	<b>P</b>
05010	Alzheimer's disease	34	103	0.00011
04720	Long-term potentiation	16	42	0.00142
04810	Regulation of actin cytoskeleton	36	127	0.00186
04360	Axon guidance	24	78	0.00334
00100	Steroid biosynthesis	6	10	0.00343
00190	Oxidative phosphorylation	25	83	0.0038
04142	Lysosome	24	80	0.00481
04512	ECM-receptor interaction	15	45	0.00859
04510	Focal adhesion	32	121	0.0102
05016	Huntington's disease	30	113	0.012
00600	Sphingolipid metabolism	9	25	0.0233
05214	Glioma	13	42	0.0264
04350	TGF-beta signaling pathway	14	47	0.03
00603	Glycosphingolipid biosynthesis - globo series	4	8	0.0383
04070	Phosphatidylinositol signaling system	13	45	0.0453
04530	Tight junction	18	68	0.0473
00010	Glycolysis / Gluconeogenesis	9	28	0.048
04960	Aldosterone-regulated sodium reabsorption	8	25	0.0623
04666	Fc gamma R-mediated phagocytosis	14	52	0.0662
05211	Renal cell carcinoma	14	53	0.0759
05012	Parkinson's disease	19	79	0.0972
04730	Long-term depression	11	41	0.099
05215	Prostate cancer	16	65	0.103
04662	B cell receptor signaling pathway	11	42	0.114
04540	Gap junction	14	58	0.138

**Table A.23: Top 40 most enriched GO terms (“Biological process” type) in targets of cel-miR-67.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0009790	embryonic development	23	333	0.000734
GO:0031399	regulation of protein modification process	9	75	0.000819
GO:0019079	viral genome replication	2	2	0.00111
GO:0032268	regulation of cellular protein metabolic process	13	148	0.00131
GO:0051246	regulation of protein metabolic process	15	186	0.00137
GO:0048592	eye morphogenesis	6	41	0.00219
GO:0001932	regulation of protein amino acid phosphorylation	7	58	0.00298
GO:0010224	response to UV-B	2	3	0.00325
GO:0019058	viral infectious cycle	2	3	0.00325
GO:0043374	CD8-positive, alpha-beta T cell differentiation	2	3	0.00325
GO:0044267	cellular protein metabolic process	58	1257	0.00545
GO:0048872	homeostasis of number of cells	7	65	0.00567
GO:0006582	melanin metabolic process	2	4	0.00636
GO:0048169	regulation of long-term neuronal synaptic plasticity	3	13	0.00818
GO:0006464	protein modification process	36	724	0.0097
GO:0006413	translational initiation	4	26	0.0101
GO:0016032	viral reproduction	2	5	0.0104
GO:0022415	viral reproductive process	2	5	0.0104
GO:0030168	platelet activation	2	5	0.0104
GO:0035020	regulation of Rac protein signal transduction	2	5	0.0104
GO:0043412	macromolecule modification	37	754	0.0107
GO:0007398	ectoderm development	6	57	0.0114
GO:0006633	fatty acid biosynthetic process	5	42	0.0123
GO:0043687	post-translational protein modification	31	614	0.0131
GO:0019748	secondary metabolic process	4	28	0.0132
GO:0032270	positive regulation of cellular protein metabolic process	5	43	0.0136
GO:0000082	G1/S transition of mitotic cell cycle	3	16	0.0149
GO:0048168	regulation of neuronal synaptic plasticity	3	16	0.0149
GO:0051656	establishment of organelle localization	3	16	0.0149
GO:0009994	oocyte differentiation	2	6	0.0152
GO:0048599	oocyte development	2	6	0.0152
GO:0019941	modification-dependent protein catabolic process	18	310	0.0156
GO:0043632	modification-dependent macromolecule catabolic process	18	310	0.0156
GO:0048513	organ development	38	801	0.0162
GO:0030218	erythrocyte differentiation	4	30	0.0167
GO:0031401	positive regulation of protein modification process	4	31	0.0187

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ID	Term Description	q	m	P
GO:0009653	anatomical structure morphogenesis	29	585	0.0203
GO:0048598	embryonic morphogenesis	11	163	0.0203
GO:0007173	epidermal growth factor receptor signaling pathway	2	7	0.0208
GO:0014047	glutamate secretion	2	7	0.0208

**Table A.24: Top 40 most enriched GO terms (“Biological process” type) in targets of miR-124.**

$q$  - number of genes from a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0009653	anatomical structure morphogenesis	47	585	4.79e-07
GO:0007275	multicellular organismal development	80	1244	4.88e-07
GO:0048856	anatomical structure development	72	1077	4.99e-07
GO:0001944	vasculature development	21	160	5.19e-07
GO:0032502	developmental process	84	1360	1.29e-06
GO:0048731	system development	67	1003	1.42e-06
GO:0048513	organ development	57	801	1.43e-06
GO:0001568	blood vessel development	20	158	1.74e-06
GO:0048514	blood vessel morphogenesis	18	135	2.72e-06
GO:0023034	intracellular signaling pathway	33	412	2.98e-05
GO:0048869	cellular developmental process	55	844	3.05e-05
GO:0061061	muscle structure development	16	136	4.78e-05
GO:0032501	multicellular organismal process	88	1593	6.23e-05
GO:0030154	cell differentiation	51	791	8.16e-05
GO:0048646	anatomical structure formation involved in morphogenesis	21	222	8.9e-05
GO:0051146	striated muscle cell differentiation	10	63	0.000106
GO:0009888	tissue development	27	331	0.000119
GO:0048518	positive regulation of biological process	44	660	0.000125
GO:0048522	positive regulation of cellular process	40	589	0.000176
GO:0000082	G1/S transition of mitotic cell cycle	5	16	0.000225
GO:0014706	striated muscle tissue development	11	84	0.000285
GO:0055001	muscle cell development	8	47	0.000319
GO:0007517	muscle organ development	13	115	0.000362
GO:0030029	actin filament-based process	13	117	0.000429
GO:0060537	muscle tissue development	11	88	0.00043
GO:0042692	muscle cell differentiation	10	75	0.000463
GO:0001501	skeletal system development	15	150	5e-04
GO:0030048	actin filament-based movement	4	11	0.000524
GO:0032787	monocarboxylic acid metabolic process	14	137	0.000616

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ID	Term Description	q	m	P
GO:0007155	cell adhesion	22	277	0.00073
GO:0022610	biological adhesion	22	277	0.00073
GO:0055002	striated muscle cell development	7	42	0.000861
GO:0051234	establishment of localization	70	1309	0.0011
GO:0007519	skeletal muscle tissue development	7	44	0.00115
GO:0060538	skeletal muscle organ development	7	44	0.00115
GO:0001525	angiogenesis	11	99	0.00117
GO:0009987	cellular process	233	5490	0.00124
GO:0006631	fatty acid metabolic process	11	100	0.00127
GO:0044281	small molecule metabolic process	41	673	0.00134
GO:0048705	skeletal system morphogenesis	8	58	0.00136

**Table A.25: Top 40 most enriched GO terms (“Biological process” type) in targets of miR-143.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0010720	positive regulation of cell development	5	28	0.000571
GO:0045743	positive regulation of fibroblast growth factor receptor signaling pathway	2	3	0.00183
GO:0008219	cell death	21	428	0.00234
GO:0016265	death	21	433	0.00268
GO:0046546	development of primary male sexual characteristics	4	24	0.00272
GO:0050769	positive regulation of neurogenesis	4	25	0.00317
GO:0006497	protein amino acid lipidation	4	27	0.00423
GO:0046661	male sex differentiation	4	27	0.00423
GO:0001501	skeletal system development	10	150	0.00429
GO:0000087	M phase of mitotic cell cycle	9	128	0.00469
GO:0000280	nuclear division	9	128	0.00469
GO:0007067	mitosis	9	128	0.00469
GO:0043066	negative regulation of apoptosis	9	128	0.00469
GO:0045597	positive regulation of cell differentiation	7	84	0.0049
GO:0043069	negative regulation of programmed cell death	9	131	0.00545
GO:0048285	organelle fission	9	132	0.00573
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	2	5	0.00591
GO:0060548	negative regulation of cell death	9	133	0.00602
GO:0042158	lipoprotein biosynthetic process	4	31	0.00702
GO:0006915	apoptosis	19	411	0.00705

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ID	Term Description	q	m	P
GO:0012501	programmed cell death	19	415	0.00779
GO:0008584	male gonad development	3	17	0.00807
GO:0007271	synaptic transmission, cholinergic	2	6	0.00872
GO:0042157	lipoprotein metabolic process	4	34	0.00976
GO:0009791	post-embryonic development	5	53	0.0101
GO:0001503	ossification	6	74	0.0102
GO:0000278	mitotic cell cycle	10	171	0.0105
GO:0010165	response to X-ray	2	7	0.012
GO:0060325	face morphogenesis	2	7	0.012
GO:0042981	regulation of apoptosis	13	257	0.0122
GO:0001701	in utero embryonic development	9	150	0.0128
GO:0043067	regulation of programmed cell death	13	261	0.0138
GO:0010941	regulation of cell death	13	262	0.0142
GO:0001649	osteoblast differentiation	4	38	0.0144
GO:0008543	fibroblast growth factor receptor signaling pathway	3	21	0.0147
GO:0006970	response to osmotic stress	2	8	0.0157
GO:0060323	head morphogenesis	2	8	0.0157
GO:0060324	face development	2	8	0.0157
GO:0060348	bone development	6	82	0.0164
GO:0051094	positive regulation of developmental process	7	109	0.0192

**Table A.26: Top 40 most enriched GO terms (“Biological process” type) in targets of miR-145.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO category in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0048731	system development	48	1003	0.000418
GO:0016337	cell-cell adhesion	9	81	0.000592
GO:0051301	cell division	15	200	0.000812
GO:0000724	double-strand break repair via homologous recombination	3	8	0.00127
GO:0000725	recombinational repair	3	8	0.00127
GO:0000087	M phase of mitotic cell cycle	11	128	0.00135
GO:0000280	nuclear division	11	128	0.00135
GO:0007067	mitosis	11	128	0.00135
GO:0000279	M phase	13	169	0.00142
GO:0048285	organelle fission	11	132	0.00173
GO:0007275	multicellular organismal development	54	1244	0.0018
GO:0048856	anatomical structure development	48	1077	0.00197
GO:0022403	cell cycle phase	14	198	0.00211

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ID	Term Description	q	m	P
GO:0060710	chorio-allantoic fusion	2	3	0.00254
GO:0021904	dorsal/ventral neural tube patterning	3	10	0.00259
GO:0006310	DNA recombination	6	48	0.00267
GO:0032501	multicellular organismal process	65	1593	0.00275
GO:0060348	bone development	8	82	0.00275
GO:0048872	homeostasis of number of cells	7	65	0.00287
GO:0032502	developmental process	57	1360	0.00295
GO:0022402	cell cycle process	15	234	0.00381
GO:0000278	mitotic cell cycle	12	171	0.00457
GO:0007049	cell cycle	22	410	0.00467
GO:0001501	skeletal system development	11	150	0.00469
GO:0007399	nervous system development	23	439	0.00514
GO:0021532	neural tube patterning	3	13	0.00579
GO:0001503	ossification	7	74	0.00593
GO:0016043	cellular component organization	46	1085	0.0064
GO:0048592	eye morphogenesis	5	41	0.0067
GO:0048873	homeostasis of number of cells within a tissue	3	14	0.00721
GO:0050804	regulation of synaptic transmission	5	42	0.00743
GO:0042592	homeostatic process	17	301	0.00759
GO:0051969	regulation of transmission of nerve impulse	5	43	0.00821
GO:0006826	iron ion transport	3	15	0.00882
GO:0031644	regulation of neurological system process	5	44	0.00905
GO:0051216	cartilage development	5	46	0.0109
GO:0009953	dorsal/ventral pattern formation	4	30	0.011
GO:0023052	signaling	55	1399	0.013
GO:0019226	transmission of nerve impulse	10	150	0.013
GO:0048878	chemical homeostasis	11	174	0.0137

**Table A.27: Top 40 most enriched GO terms (“Biological process” type) in targets of miR-25.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0006814	sodium ion transport	6	57	0.000454
GO:0006366	transcription from RNA polymerase II promoter	13	323	0.00432
GO:0055085	transmembrane transport	11	259	0.00572
GO:0006357	regulation of transcription from RNA polymerase II promoter	12	302	0.00667
GO:0033059	cellular pigmentation	2	8	0.00796

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<b>ID</b>	<b>Term Description</b>	<b>q</b>	<b>m</b>	<b>P</b>
GO:0065007	biological regulation	63	2781	0.00906
GO:0007272	ensheathment of neurons	3	25	0.00912
GO:0008366	axon ensheathment	3	25	0.00912
GO:0048536	spleen development	2	9	0.0101
GO:0015672	monovalent inorganic cation transport	7	141	0.0118
GO:0050801	ion homeostasis	7	142	0.0122
GO:0065008	regulation of biological quality	18	579	0.0123
GO:0006013	mannose metabolic process	2	10	0.0125
GO:0060441	branching involved in lung morphogenesis	2	10	0.0125
GO:0019228	regulation of action potential in neuron	3	29	0.0138
GO:0030850	prostate gland development	3	29	0.0138
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	8	181	0.0141
GO:0030001	metal ion transport	9	219	0.0147
GO:0001655	urogenital system development	5	83	0.015
GO:0042476	odontogenesis	3	30	0.0151
GO:0042592	homeostatic process	11	301	0.0165
GO:0035272	exocrine system development	3	31	0.0165
GO:0006244	pyrimidine nucleotide catabolic process	1	1	0.0175
GO:0006668	sphinganine-1-phosphate metabolic process	1	1	0.0175
GO:0009131	pyrimidine nucleoside monophosphate catabolic process	1	1	0.0175
GO:0009159	deoxyribonucleoside monophosphate catabolic process	1	1	0.0175
GO:0009178	pyrimidine deoxyribonucleoside monophosphate catabolic process	1	1	0.0175
GO:0009223	pyrimidine deoxyribonucleotide catabolic process	1	1	0.0175
GO:0009448	gamma-aminobutyric acid metabolic process	1	1	0.0175
GO:0010447	response to acidity	1	1	0.0175
GO:0016540	protein autoprocessing	1	1	0.0175
GO:0021561	facial nerve development	1	1	0.0175
GO:0021569	rhombomere 3 development	1	1	0.0175
GO:0021571	rhombomere 5 development	1	1	0.0175
GO:0021593	rhombomere morphogenesis	1	1	0.0175
GO:0021594	rhombomere formation	1	1	0.0175
GO:0021604	cranial nerve structural organization	1	1	0.0175
GO:0021610	facial nerve morphogenesis	1	1	0.0175
GO:0021612	facial nerve structural organization	1	1	0.0175
GO:0021658	rhombomere 3 morphogenesis	1	1	0.0175

**Table A.28: Top 40 most enriched GO terms (“Biological process” type) in targets of miR-434-3p.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO category in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0009790	embryonic development	12	333	3.49e-05
GO:0060429	epithelium development	8	145	4.17e-05
GO:0035295	tube development	8	163	9.57e-05
GO:0030855	epithelial cell differentiation	5	56	0.000133
GO:0009888	tissue development	11	331	0.000157
GO:0022612	gland morphogenesis	5	58	0.000158
GO:0009653	anatomical structure morphogenesis	15	585	0.000173
GO:0009887	organ morphogenesis	10	294	0.000265
GO:0002064	epithelial cell development	3	15	0.000288
GO:0048732	gland development	6	103	3e-04
GO:0035239	tube morphogenesis	6	107	0.000368
GO:0002070	epithelial cell maturation	2	4	0.000466
GO:0043009	chordate embryonic development	8	217	0.00067
GO:0001763	morphogenesis of a branching structure	5	81	0.000751
GO:0009792	embryonic development ending in birth or egg hatching	8	221	0.000755
GO:0048729	tissue morphogenesis	6	137	0.00135
GO:0007431	salivary gland development	3	26	0.00153
GO:0048754	branching morphogenesis of a tube	4	59	0.00184
GO:0035050	embryonic heart tube development	2	8	0.00212
GO:0002009	morphogenesis of an epithelium	5	105	0.0024
GO:0035272	exocrine system development	3	31	0.00257
GO:0048598	embryonic morphogenesis	6	163	0.00326
GO:0060442	branching involved in prostate gland morphogenesis	2	10	0.00338
GO:0023034	intracellular signaling pathway	10	412	0.00347
GO:0048523	negative regulation of cellular process	12	559	0.00374
GO:0048513	organ development	15	801	0.00432
GO:0018108	peptidyl-tyrosine phosphorylation	3	39	0.00496
GO:0018212	peptidyl-tyrosine modification	3	39	0.00496
GO:0007399	nervous system development	10	439	0.00543
GO:0007275	multicellular organismal development	20	1244	0.00544
GO:0007154	cell communication	11	513	0.00557
GO:0009069	serine family amino acid metabolic process	2	13	0.00575
GO:0007167	enzyme linked receptor protein signaling pathway	6	185	0.00604
GO:0009968	negative regulation of signal transduction	4	83	0.00633
GO:0023057	negative regulation of signaling process	4	83	0.00633
GO:0034329	cell junction assembly	2	14	0.00667

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ID	Term Description	q	m	P
GO:0032502	developmental process	21	1360	0.0069
GO:0050863	regulation of T cell activation	3	44	0.00696
GO:0048869	cellular developmental process	15	844	0.007
GO:0009966	regulation of signal transduction	8	317	0.00708

**Table A.29: Top 40 most enriched GO terms (“Biological process” type) in the induced by transfection set.**

$q$  - number of genes of a GO term that was in the mock transfection set,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0048513	organ development	147	801	5.78e-11
GO:0016043	cellular component organization	182	1085	5.58e-10
GO:0048731	system development	171	1003	5.84e-10
GO:0001944	vasculature development	45	160	1.41e-09
GO:0001568	blood vessel development	44	158	3.01e-09
GO:0048518	positive regulation of biological process	121	660	3.97e-09
GO:0048856	anatomical structure development	177	1077	5.26e-09
GO:0007275	multicellular organismal development	198	1244	7.72e-09
GO:0007155	cell adhesion	63	277	9.95e-09
GO:0022610	biological adhesion	63	277	9.95e-09
GO:0032501	multicellular organismal process	240	1593	2.23e-08
GO:0048514	blood vessel morphogenesis	38	135	2.64e-08
GO:0048522	positive regulation of cellular process	108	589	2.98e-08
GO:0032502	developmental process	210	1360	3.18e-08
GO:0008283	cell proliferation	68	326	9.93e-08
GO:0009653	anatomical structure morphogenesis	104	585	2.75e-07
GO:0051301	cell division	47	200	2.79e-07
GO:0007049	cell cycle	79	410	3.11e-07
GO:0050896	response to stimulus	147	911	4.35e-07
GO:0009987	cellular process	673	5490	8.56e-07
GO:0016049	cell growth	20	57	1.26e-06
GO:0048519	negative regulation of biological process	107	626	1.33e-06
GO:0042127	regulation of cell proliferation	50	230	1.44e-06
GO:0001525	angiogenesis	28	99	1.61e-06
GO:0048523	negative regulation of cellular process	96	559	3.95e-06
GO:0065007	biological regulation	368	2781	4.86e-06
GO:0022402	cell cycle process	49	234	5.59e-06
GO:0048869	cellular developmental process	133	844	6.1e-06
GO:0008285	negative regulation of cell proliferation	26	96	9.01e-06

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ID	Term Description	q	m	P
GO:0042221	response to chemical stimulus	59	308	1.22e-05
GO:0008361	regulation of cell size	20	65	1.25e-05
GO:0006260	DNA replication	24	87	1.41e-05
GO:0001558	regulation of cell growth	16	46	1.65e-05
GO:0030154	cell differentiation	124	791	1.69e-05
GO:0050789	regulation of biological process	346	2625	1.73e-05
GO:0090066	regulation of anatomical structure size	29	118	2.17e-05
GO:0010033	response to organic substance	36	161	2.22e-05
GO:0050794	regulation of cellular process	328	2479	2.41e-05
GO:0009888	tissue development	61	331	2.99e-05
GO:0000087	M phase of mitotic cell cycle	30	128	4.17e-05

**Table A.30: Top 40 most enriched GO terms (“Biological process” type) in the Ago HITS-CLIP set.**

$q$  - number of genes of a GO term that was in the Ago HITS-CLIP set,  $m$  - total number of genes of a GO term in test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0051179	localization	348	1469	1.16e-20
GO:0006810	transport	307	1300	8.74e-18
GO:0051234	establishment of localization	307	1309	2.56e-17
GO:0009987	cellular process	946	5490	1.02e-10
GO:0006812	cation transport	73	257	4.13e-08
GO:0006811	ion transport	86	333	2.94e-07
GO:0023052	signaling	277	1399	5.1e-07
GO:0019725	cellular homeostasis	50	173	3.29e-06
GO:0007154	cell communication	116	513	4.52e-06
GO:0055085	transmembrane transport	66	259	1.15e-05
GO:0023060	signal transmission	219	1113	1.66e-05
GO:0023046	signaling process	219	1114	1.77e-05
GO:0007275	multicellular organismal development	241	1244	1.83e-05
GO:0015672	monovalent inorganic cation transport	41	141	2.11e-05
GO:0030001	metal ion transport	57	219	2.34e-05
GO:0065007	biological regulation	491	2781	2.6e-05
GO:0065008	regulation of biological quality	124	579	3.35e-05
GO:0046034	ATP metabolic process	18	44	3.69e-05
GO:0032502	developmental process	258	1360	4.27e-05
GO:0009199	ribonucleoside triphosphate metabolic process	19	49	5.47e-05
GO:0009205	purine ribonucleoside triphosphate metabolic process	19	49	5.47e-05
GO:0055082	cellular chemical homeostasis	37	128	6.03e-05

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ID	Term Description	q	m	P
GO:0007264	small GTPase mediated signal transduction	55	216	6.23e-05
GO:0033036	macromolecule localization	121	570	6.32e-05
GO:0008104	protein localization	108	499	7e-05
GO:0006754	ATP biosynthetic process	17	42	7.1e-05
GO:0032501	multicellular organismal process	295	1593	7.28e-05
GO:0048731	system development	196	1003	7.59e-05
GO:0015031	protein transport	97	440	7.95e-05
GO:0048856	anatomical structure development	208	1077	9.3e-05
GO:0006873	cellular ion homeostasis	36	126	9.83e-05
GO:0009201	ribonucleoside triphosphate biosynthetic process	18	47	0.000103
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	18	47	0.000103
GO:0050801	ion homeostasis	39	142	0.000131
GO:0045184	establishment of protein localization	97	446	0.000136
GO:0009144	purine nucleoside triphosphate metabolic process	19	52	0.00014
GO:0009142	nucleoside triphosphate biosynthetic process	18	48	0.000142
GO:0009145	purine nucleoside triphosphate biosynthetic process	18	48	0.000142
GO:0015985	energy coupled proton transport, down electrochemical gradient	11	22	0.000144
GO:0015986	ATP synthesis coupled proton transport	11	22	0.000144

**Table A.31: Top 40 most enriched GO terms (“Cellular compartment” type) in targets of cel-miR-67.**

$q$  - number of genes from a GO category that was among the predicted targets,  $m$  - total number of genes of a GO category in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0008287	protein serine/threonine phosphatase complex	6	21	4.17e-05
GO:0005783	endoplasmic reticulum	30	469	0.000318
GO:0005955	calcineurin complex	2	3	0.00313
GO:0032153	cell division site	2	4	0.00612
GO:0032155	cell division site part	2	4	0.00612
GO:0044424	intracellular part	196	5358	0.00765
GO:0005794	Golgi apparatus	23	414	0.009
GO:0043231	intracellular membrane-bounded organelle	155	4119	0.01
GO:0043227	membrane-bounded organelle	155	4123	0.0104
GO:0044444	cytoplasmic part	91	2259	0.0131
GO:0005622	intracellular	199	5506	0.0133
GO:0005737	cytoplasm	142	3789	0.0186
GO:0000172	ribonuclease MRP complex	1	1	0.0327
GO:0005655	nucleolar ribonuclease P complex	1	1	0.0327

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ID	Term Description	q	m	P
GO:0005775	vacuolar lumen	1	1	0.0327
GO:0005845	mRNA cap binding complex	1	1	0.0327
GO:0016014	dystrobrevin complex	1	1	0.0327
GO:0030677	ribonuclease P complex	1	1	0.0327
GO:0030681	multimeric ribonuclease P complex	1	1	0.0327
GO:0030685	nucleolar preribosome	1	1	0.0327
GO:0032154	cleavage furrow	1	1	0.0327
GO:0034518	RNA cap binding complex	1	1	0.0327
GO:0000159	protein phosphatase type 2A complex	2	9	0.033
GO:0044452	nucleolar part	2	10	0.0403
GO:0001726	ruffle	3	24	0.0422
GO:0033176	proton-transporting V-type ATPase complex	2	11	0.0483
GO:0043229	intracellular organelle	163	4555	0.0565
GO:0043226	organelle	163	4557	0.0573
GO:0005819	spindle	3	28	0.0621
GO:0002102	podosome	1	2	0.0643
GO:0034708	methyltransferase complex	2	13	0.0656
GO:0035097	histone methyltransferase complex	2	13	0.0656
GO:0032991	macromolecular complex	50	1249	0.0722
GO:0030529	ribonucleoprotein complex	13	256	0.0771
GO:0005624	membrane fraction	12	233	0.0804
GO:0031594	neuromuscular junction	2	15	0.0846
GO:0005662	DNA replication factor A complex	1	3	0.095
GO:0005732	small nucleolar ribonucleoprotein complex	1	3	0.095
GO:0005826	actomyosin contractile ring	1	3	0.095
GO:0031932	TORC2 complex	1	3	0.095

**Table A.32: Top 40 most enriched GO terms (“Cellular compartment” type) in targets of miR-124.**

$q$  - number of genes from a GO category that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0001725	stress fiber	6	10	5.53e-07
GO:0005886	plasma membrane	77	1179	1.03e-06
GO:0032432	actin filament bundle	6	11	1.18e-06
GO:0042641	actomyosin	6	13	4.1e-06
GO:0016020	membrane	157	3144	2.24e-05
GO:0005623	cell	295	6995	0.000183
GO:0044464	cell part	295	6995	0.000183

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<b>ID</b>	<b>Term Description</b>	<b>q</b>	<b>m</b>	<b>P</b>
GO:0001772	immunological synapse	3	4	0.000216
GO:0005856	cytoskeleton	38	553	0.000296
GO:0030141	secretory granule	7	36	0.000361
GO:0005737	cytoplasm	176	3789	0.000399
GO:0015629	actin cytoskeleton	12	104	0.00059
GO:0044463	cell projection part	9	66	0.000852
GO:0030667	secretory granule membrane	3	6	0.00102
GO:0031088	platelet dense granule membrane	2	2	0.00146
GO:0042827	platelet dense granule	2	2	0.00146
GO:0044459	plasma membrane part	36	567	0.00179
GO:0030054	cell junction	21	274	0.00188
GO:0044420	extracellular matrix part	7	50	0.00273
GO:0044430	cytoskeletal part	21	285	0.00302
GO:0042588	zymogen granule	2	3	0.00427
GO:0005604	basement membrane	6	42	0.00491
GO:0005911	cell-cell junction	9	87	0.00586
GO:0043296	apical junction complex	6	49	0.0105
GO:0044425	membrane part	115	2498	0.0112
GO:0042383	sarcolemma	4	24	0.0122
GO:0005667	transcription factor complex	9	98	0.0125
GO:0016327	apicolateral plasma membrane	6	51	0.0127
GO:0035085	cilium axoneme	2	5	0.0135
GO:0005938	cell cortex	6	54	0.0165
GO:0031594	neuromuscular junction	3	15	0.0179
GO:0043209	myelin sheath	2	6	0.0198
GO:0005819	spindle	4	28	0.0208
GO:0005923	tight junction	5	42	0.0212
GO:0070160	occluding junction	5	42	0.0212
GO:0005626	insoluble fraction	16	240	0.0218
GO:0005576	extracellular region	32	578	0.0218
GO:0044424	intracellular part	223	5358	0.0259
GO:0005887	integral to plasma membrane	12	167	0.0264
GO:0005814	centriole	2	7	0.027

**Table A.33: Top 40 most enriched GO terms (“Cellular compartment” type) in targets of miR-143.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0005794	Golgi apparatus	21	414	0.0012
GO:0044431	Golgi apparatus part	9	119	0.0025
GO:0044444	cytoplasmic part	74	2259	0.00265
GO:0005802	trans-Golgi network	4	28	0.00449
GO:0000775	chromosome, centromeric region	6	65	0.00496
GO:0005737	cytoplasm	112	3789	0.00507
GO:0030496	midbody	2	5	0.00567
GO:0005623	cell	186	6995	0.00929
GO:0044464	cell part	186	6995	0.00929
GO:0016020	membrane	94	3144	0.00966
GO:0016021	integral to membrane	67	2123	0.0111
GO:0031224	intrinsic to membrane	68	2165	0.0117
GO:0030175	filopodium	2	8	0.0151
GO:0043231	intracellular membrane-bounded organelle	116	4119	0.0225
GO:0043227	membrane-bounded organelle	116	4123	0.0233
GO:0005775	vacuolar lumen	1	1	0.0244
GO:0005797	Golgi medial cisterna	1	1	0.0244
GO:0005831	steroid hormone aporeceptor complex	1	1	0.0244
GO:0016942	insulin-like growth factor binding protein complex	1	1	0.0244
GO:0032433	filopodium tip	1	1	0.0244
GO:0045180	basal cortex	1	1	0.0244
GO:0043229	intracellular organelle	126	4555	0.0281
GO:0043226	organelle	126	4557	0.0285
GO:0044425	membrane part	73	2498	0.0432
GO:0000109	nucleotide-excision repair complex	1	2	0.0483
GO:0000214	tRNA-intron endonuclease complex	1	2	0.0483
GO:0005682	U5 snRNP	1	2	0.0483
GO:0031501	mannosyltransferase complex	1	2	0.0483
GO:0031527	filopodium membrane	1	2	0.0483
GO:0033185	dolichol-phosphate-mannose synthase complex	1	2	0.0483
GO:0005869	dynactin complex	1	3	0.0716
GO:0008537	proteasome activator complex	1	3	0.0716
GO:0055037	recycling endosome	1	3	0.0716
GO:0034702	ion channel complex	4	67	0.081
GO:0034707	chloride channel complex	2	20	0.0848
GO:0000776	kinetochore	3	43	0.0872

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ID	Term Description	q	m	P
GO:0022624	proteasome accessory complex	1	4	0.0943
GO:0044424	intracellular part	141	5358	0.0962
GO:0005769	early endosome	2	22	0.0999
GO:0005925	focal adhesion	2	23	0.108

**Table A.34: Top 40 most enriched GO terms (“Cellular compartment” type) in targets of miR-145.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0030175	filopodium	3	8	0.00127
GO:0012506	vesicle membrane	5	40	0.00604
GO:0005623	cell	223	6995	0.00715
GO:0044464	cell part	223	6995	0.00715
GO:0042995	cell projection	17	304	0.0084
GO:0005622	intracellular	181	5506	0.0099
GO:0000775	chromosome, centromeric region	6	65	0.0119
GO:0043209	myelin sheath	2	6	0.012
GO:0030424	axon	6	66	0.0128
GO:0001673	male germ cell nucleus	2	7	0.0165
GO:0030659	cytoplasmic vesicle membrane	4	35	0.0188
GO:0044448	cell cortex part	4	35	0.0188
GO:0005938	cell cortex	5	54	0.0208
GO:0044433	cytoplasmic vesicle part	4	37	0.0227
GO:0043005	neuron projection	8	119	0.0241
GO:0043073	germ cell nucleus	2	9	0.0271
GO:0043229	intracellular organelle	150	4555	0.029
GO:0043226	organelle	150	4557	0.0294
GO:0000176	nuclear exosome (RNase complex)	1	1	0.0294
GO:0005775	vacuolar lumen	1	1	0.0294
GO:0005816	spindle pole body	1	1	0.0294
GO:0005960	glycine cleavage complex	1	1	0.0294
GO:0016939	kinesin II complex	1	1	0.0294
GO:0016942	insulin-like growth factor binding protein complex	1	1	0.0294
GO:0031205	endoplasmic reticulum Sec complex	1	1	0.0294
GO:0032433	filopodium tip	1	1	0.0294
GO:0043231	intracellular membrane-bounded organelle	137	4119	0.0299
GO:0043227	membrane-bounded organelle	137	4123	0.0309
GO:0005871	kinesin complex	2	10	0.0333

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ID	Term Description	q	m	P
GO:0005634	nucleus	84	2403	0.0386
GO:0044463	cell projection part	5	66	0.0445
GO:0044427	chromosomal part	10	185	0.0467
GO:0005694	chromosome	11	213	0.0501
GO:0044424	intracellular part	171	5358	0.0552
GO:0002102	podosome	1	2	0.058
GO:0002139	stereocilia coupling link	1	2	0.058
GO:0002141	stereocilia ankle link	1	2	0.058
GO:0002142	stereocilia ankle link complex	1	2	0.058
GO:0009331	glycerol-3-phosphate dehydrogenase complex	1	2	0.058
GO:0031527	filopodium membrane	1	2	0.058

**Table A.35: Top 40 most enriched GO terms (“Cellular compartment” type) in targets of miR-25.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0005952	cAMP-dependent protein kinase complex	2	6	0.00441
GO:0005942	phosphoinositide 3-kinase complex	2	7	0.0061
GO:0016939	kinesin II complex	1	1	0.0176
GO:0016942	insulin-like growth factor binding protein complex	1	1	0.0176
GO:0060077	inhibitory synapse	1	1	0.0176
GO:0030665	clathrin coated vesicle membrane	2	17	0.0352
GO:0005739	mitochondrion	22	834	0.0353
GO:0005886	plasma membrane	29	1179	0.0375
GO:0000267	cell fraction	9	269	0.048
GO:0001533	cornified envelope	1	3	0.0519
GO:0030118	clathrin coat	2	21	0.052
GO:0005626	insoluble fraction	8	240	0.0614
GO:0016020	membrane	65	3144	0.0642
GO:0042383	sarcolemma	2	24	0.066
GO:0016011	dystroglycan complex	1	4	0.0686
GO:0046540	U4/U6 x U5 tri-snRNP complex	1	4	0.0686
GO:0030662	coated vesicle membrane	2	25	0.071
GO:0030136	clathrin-coated vesicle	3	55	0.0723
GO:0031410	cytoplasmic vesicle	8	249	0.0727
GO:0031982	vesicle	8	253	0.0782
GO:0044425	membrane part	52	2498	0.0913
GO:0000300	peripheral to membrane of membrane fraction	1	6	0.101

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ID	Term Description	q	m	P
GO:0016010	dystrophin-associated glycoprotein complex	1	6	0.101
GO:0030125	clathrin vesicle coat	1	6	0.101
GO:0044445	cytosolic part	2	31	0.103
GO:0045202	synapse	6	184	0.106
GO:0030135	coated vesicle	3	65	0.106
GO:0016023	cytoplasmic membrane-bounded vesicle	5	145	0.113
GO:0014069	postsynaptic density	1	7	0.117
GO:0042470	melanosome	1	7	0.117
GO:0048770	pigment granule	1	7	0.117
GO:0005624	membrane fraction	7	233	0.117
GO:0030117	membrane coat	2	34	0.12
GO:0048475	coated membrane	2	34	0.12
GO:0031988	membrane-bounded vesicle	5	149	0.122
GO:0044421	extracellular region part	8	282	0.124
GO:0016021	integral to membrane	44	2123	0.125
GO:0030659	cytoplasmic vesicle membrane	2	35	0.126
GO:0005615	extracellular space	5	151	0.128
GO:0001750	photoreceptor outer segment	1	8	0.132

**Table A.36: Top 40 most enriched GO terms (“Cellular compartment” type) in targets of miR-434-3p.**

$q$  - number of genes of a GO term that was among the predicted targets,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0016323	basolateral plasma membrane	4	53	0.00147
GO:0005922	connexon complex	2	9	0.00298
GO:0044459	plasma membrane part	12	567	0.00619
GO:0005912	adherens junction	3	44	0.00792
GO:0005921	gap junction	2	15	0.00837
GO:0070161	anchoring junction	3	46	0.00895
GO:0000439	core TFIIF complex	1	1	0.00934
GO:0000441	SSL2-core TFIIF complex	1	1	0.00934
GO:0032806	carboxy-terminal domain protein kinase complex	1	1	0.00934
GO:0005737	cytoplasm	46	3789	0.0137
GO:0030054	cell junction	7	274	0.014
GO:0005623	cell	74	6995	0.0156
GO:0044464	cell part	74	6995	0.0156
GO:0005925	focal adhesion	2	23	0.0192
GO:0005924	cell-substrate adherens junction	2	24	0.0209

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ID	Term Description	q	m	P
GO:0030055	cell-substrate junction	2	25	0.0225
GO:0005886	plasma membrane	18	1179	0.0229
GO:0043235	receptor complex	2	28	0.0279
GO:0005856	cytoskeleton	10	553	0.0328
GO:0009986	cell surface	3	75	0.0329
GO:0005587	collagen type IV	1	4	0.0369
GO:0005786	signal recognition particle, endoplasmic reticulum targeting	1	4	0.0369
GO:0030935	sheet-forming collagen	1	4	0.0369
GO:0042719	mitochondrial intermembrane space protein transporter complex	1	4	0.0369
GO:0048500	signal recognition particle	1	4	0.0369
GO:0005892	nicotinic acetylcholine-gated receptor-channel complex	1	5	0.0459
GO:0030496	midbody	1	5	0.0459
GO:0005911	cell-cell junction	3	87	0.0477
GO:0005625	soluble fraction	2	38	0.0488
GO:0016020	membrane	37	3144	0.0536
GO:0005844	polysome	1	7	0.0636
GO:0043231	intracellular membrane-bounded organelle	46	4119	0.0637
GO:0043227	membrane-bounded organelle	46	4123	0.0648
GO:0009897	external side of plasma membrane	2	45	0.066
GO:0043229	intracellular organelle	50	4555	0.0663
GO:0043226	organelle	50	4557	0.0668
GO:0016021	integral to membrane	26	2123	0.0757
GO:0005741	mitochondrial outer membrane	2	49	0.0765
GO:0031968	organelle outer membrane	2	50	0.0793
GO:0019867	outer membrane	2	52	0.0848

**Table A.37: Top 40 most enriched GO terms (“Cellular component” type) in the Ago HITS-CLIP set.**

$q$  - number of genes of a GO term that was in the Ago HITS-CLIP set,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0005623	cell	1229	6995	4.47e-26
GO:0044464	cell part	1229	6995	4.47e-26
GO:0016020	membrane	654	3144	5.98e-24
GO:0044425	membrane part	529	2498	1.05e-19
GO:0016021	integral to membrane	454	2123	3.91e-17
GO:0031224	intrinsic to membrane	461	2165	4.5e-17

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<b>ID</b>	<b>Term Description</b>	<b>q</b>	<b>m</b>	<b>P</b>
GO:0005737	cytoplasm	708	3789	5.88e-13
GO:0044444	cytoplasmic part	453	2259	6.25e-12
GO:0005783	endoplasmic reticulum	127	469	2.3e-11
GO:0005622	intracellular	950	5506	2.28e-09
GO:0044424	intracellular part	923	5358	1.25e-08
GO:0005624	membrane fraction	66	233	2.9e-07
GO:0005886	plasma membrane	241	1179	5.38e-07
GO:0043005	neuron projection	40	119	6.07e-07
GO:0005626	insoluble fraction	66	240	9.36e-07
GO:0031410	cytoplasmic vesicle	66	249	3.77e-06
GO:0000267	cell fraction	70	269	3.91e-06
GO:0043229	intracellular organelle	781	4555	4.81e-06
GO:0043226	organelle	781	4557	5.22e-06
GO:0031982	vesicle	66	253	6.73e-06
GO:0045202	synapse	49	184	5.76e-05
GO:0005794	Golgi apparatus	92	414	0.000124
GO:0043234	protein complex	185	940	0.000137
GO:0016469	proton-transporting two-sector ATPase complex	12	26	0.000206
GO:0016023	cytoplasmic membrane-bounded vesicle	39	145	0.000255
GO:0043227	membrane-bounded organelle	697	4123	0.00029
GO:0043231	intracellular membrane-bounded organelle	696	4119	0.000314
GO:0031090	organelle membrane	90	414	0.000326
GO:0005789	endoplasmic reticulum membrane	19	55	0.000364
GO:0042175	nuclear envelope-endoplasmic reticulum network	19	55	0.000364
GO:0031988	membrane-bounded vesicle	39	149	0.000463
GO:0005792	microsome	22	69	0.000471
GO:0033017	sarcoplasmic reticulum membrane	4	4	0.000568
GO:0042598	vesicular fraction	22	70	0.000589
GO:0044456	synapse part	30	107	6e-04
GO:0044432	endoplasmic reticulum part	21	66	0.000649
GO:0005829	cytosol	48	197	0.000652
GO:0005856	cytoskeleton	113	553	0.000741
GO:0030136	clathrin-coated vesicle	18	55	0.00107
GO:0071212	subs synaptic reticulum	24	83	0.00128

**Table A.38: Top 40 most enriched GO terms (“Cellular compartment” type) in the induced by transfection set.**

$q$  - number of genes of a GO term that was among in the mock transfection set,  $m$  - total number of genes of a GO term in the test universe,  $P$  - P-value of enrichment. See [Methods](#), section 2.10.

Term ID	Term Description	q	m	P
GO:0005578	proteinaceous extracellular matrix	42	135	1.69e-10
GO:0044421	extracellular region part	68	282	1.89e-10
GO:0031012	extracellular matrix	43	146	7.13e-10
GO:0005576	extracellular region	108	578	1.15e-08
GO:0044420	extracellular matrix part	19	50	5.76e-07
GO:0043228	non-membrane-bounded organelle	145	910	1.26e-06
GO:0043232	intracellular non-membrane-bounded organelle	145	910	1.26e-06
GO:0044427	chromosomal part	43	185	1.28e-06
GO:0005604	basement membrane	16	42	4.33e-06
GO:0005694	chromosome	46	213	4.75e-06
GO:0005856	cytoskeleton	94	553	8.36e-06
GO:0032993	protein-DNA complex	18	55	1.33e-05
GO:0015629	actin cytoskeleton	27	104	1.46e-05
GO:0000786	nucleosome	16	49	4.13e-05
GO:0005623	cell	817	6995	0.000137
GO:0044464	cell part	817	6995	0.000137
GO:0000323	lytic vacuole	25	105	0.000139
GO:0005764	lysosome	25	105	0.000139
GO:0005886	plasma membrane	166	1179	0.000283
GO:0005615	extracellular space	31	151	0.000424
GO:0032432	actin filament bundle	6	11	0.000499
GO:0005773	vacuole	26	120	0.000511
GO:0009986	cell surface	18	75	0.00105
GO:0000785	chromatin	21	95	0.00131
GO:0005826	actomyosin contractile ring	3	3	0.00133
GO:0043256	laminin complex	3	3	0.00133
GO:0070938	contractile ring	3	3	0.00133
GO:0016323	basolateral plasma membrane	14	53	0.00138
GO:0005605	basal lamina	4	6	0.00183
GO:0005912	adherens junction	12	44	0.00222
GO:0001725	stress fiber	5	10	0.00252
GO:0009897	external side of plasma membrane	12	45	0.00273
GO:0070161	anchoring junction	12	46	0.00333
GO:0044459	plasma membrane part	83	567	0.00367
GO:0005581	collagen	5	11	0.0042
GO:0005626	insoluble fraction	40	240	0.00477

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ID	Term Description	q	m	P
GO:0005587	collagen type IV	3	4	0.0049
GO:0030935	sheet-forming collagen	3	4	0.0049
GO:0032153	cell division site	3	4	0.0049
GO:0032155	cell division site part	3	4	0.0049

Symbol	Description
<b>miR-124 (Ranked 11, P <math>\approx</math> 0.0458)</b>	
Col4a1	collagen, type IV, alpha 1
Col5a1	collagen, type V, alpha 1
Itga7	integrin alpha 7
Itgb1	integrin beta 1 (fibronectin receptor beta)
Lamc1	laminin, gamma 1
<b>miR-145 (Ranked 97, P <math>\approx</math> 0.76)</b>	
Col1a1	collagen, type I, alpha 1
<b>miR-25 (Ranked 14, P <math>\approx</math> 0.0504)</b>	
Dag1	dystroglycan 1
Sdc2	syndecan 2
Sdc3	syndecan 3
<b>miR-434-3p (Ranked 2, P <math>\approx</math> 0.0149)</b>	
Cd44	CD44 antigen
Col1a1	collagen, type I, alpha 1
Sdc2	syndecan 2

**Table A.39: miRNA targets within “ECM-receptor interaction” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “ECM-receptor interaction” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67</b> (Ranked 55, $P \approx 0.42$ )	
Adcy5	adenylate cyclase 5
Csnk1d	casein kinase 1, delta
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
<b>miR-124</b> (Ranked 100, $P \approx 0.735$ )	
Nras	neuroblastoma ras oncogene
Tubb6	tubulin, beta 6
<b>miR-143</b> (Ranked 10, $P \approx 0.0976$ )	
Egfr	epidermal growth factor receptor
Pdgfb	platelet derived growth factor, B polypeptide
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
Src	Rous sarcoma oncogene
<b>miR-145</b> (Ranked 16, $P \approx 0.16$ )	
Grm5	glutamate receptor, metabotropic 5
Nras	neuroblastoma ras oncogene
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
Prkx	protein kinase, X-linked
<b>miR-25</b> (Ranked 95, $P \approx 0.728$ )	
Adcy3	adenylate cyclase 3
<b>miR-434-3p</b> (Ranked 28, $P \approx 0.207$ )	
Egfr	epidermal growth factor receptor
Gja1	gap junction protein, alpha 1

**Table A.40: miRNA targets within “Gap junction” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “Gap junction” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67 (Ranked 4, P <math>\approx</math> 0.0168)</b>	
Gab1	growth factor receptor bound protein 2-associated protein 1
Hbegf	heparin-binding EGF-like growth factor
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
Map2k4	mitogen-activated protein kinase kinase 4
Pak4	p21 protein (Cdc42/Rac)-activated kinase 4
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
<b>miR-124 (Ranked 76, P <math>\approx</math> 0.51)</b>	
ErbB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
Nras	neuroblastoma ras oncogene
Shc1	src homology 2 domain-containing transforming protein C1
<b>miR-143 (Ranked 58, P <math>\approx</math> 0.464)</b>	
Egfr	epidermal growth factor receptor
Src	Rous sarcoma oncogene
<b>miR-145 (Ranked 79, P <math>\approx</math> 0.607)</b>	
Map2k4	mitogen-activated protein kinase kinase 4
Nras	neuroblastoma ras oncogene
<b>miR-25 (Ranked 7, P <math>\approx</math> 0.0245)</b>	
Map2k4	mitogen-activated protein kinase kinase 4
Mapk8	mitogen-activated protein kinase 8
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
<b>miR-434-3p (Ranked 24, P <math>\approx</math> 0.184)</b>	
Egfr	epidermal growth factor receptor
Nck1	non-catalytic region of tyrosine kinase adaptor protein 1

**Table A.41: miRNA targets within “ErbB signaling pathway” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “ErbB signaling pathway” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67</b> (Ranked 68, $P \approx 0.527$ )	
Amot1l	angiomin-like 1
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
<b>miR-124</b> (Ranked 3, $P \approx 0.00907$ )	
Actn4	actinin alpha 4
Amot1l	angiomin-like 1
Jam2	junction adhesion molecule 2
Myh10	myosin, heavy polypeptide 10, non-muscle
Myh9	myosin, heavy polypeptide 9, non-muscle
Nras	neuroblastoma ras oncogene
Rras	Harvey rat sarcoma oncogene, subgroup R
Tjp2	tight junction protein 2
<b>miR-143</b> (Ranked 95, $P \approx 0.868$ )	
Src	Rous sarcoma oncogene
<b>miR-145</b> (Ranked 86, $P \approx 0.667$ )	
Nras	neuroblastoma ras oncogene
Prkcz	protein kinase C, zeta
<b>miR-25</b> (Ranked 76, $P \approx 0.412$ )	
B230120H23Rik	RIKEN cDNA B230120H23 gene
Cldn11	claudin 11

**Table A.42: miRNA targets within “Tight junction” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “Tight junction” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67</b> (Ranked 39, $P \approx 0.26$ )	
Ccnb1	cyclin B1
Cycs	cytochrome c, somatic
Igfbp3	insulin-like growth factor binding protein 3
<b>miR-124</b> (Ranked 23, $P \approx 0.111$ )	
Ccnb1	cyclin D1
Cd82	CD82 antigen
Igfbp3	insulin-like growth factor binding protein 3
Zmat3	zinc finger matrin type 3
<b>miR-143</b> (Ranked 36, $P \approx 0.284$ )	
Cd82	CD82 antigen
Zmat3	zinc finger matrin type 3
<b>miR-145</b> (Ranked 49, $P \approx 0.408$ )	
Ccnb1	cyclin G1
Cycs	cytochrome c, somatic
<b>miR-25</b> (Ranked 50, $P \approx 0.245$ )	
Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)
Zmat3	zinc finger matrin type 3
<b>miR-434-3p</b> (Ranked 3, $P \approx 0.0161$ )	
Ccnb1	cyclin B1
Ccnb2	cyclin D2
Ccnb1	cyclin G1

**Table A.43: miRNA targets within “p53 signaling pathway” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “p53 signaling pathway” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67</b> (Ranked 65, $P \approx 0.494$ )	
Gna13	guanine nucleotide binding protein, alpha 13
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
Pak4	p21 protein (Cdc42/Rac)-activated kinase 4
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Wasf2	WAS protein family, member 2
<b>miR-124</b> (Ranked 7, $P \approx 0.0223$ )	
Actn4	actinin alpha 4
Arpc1b	actin related protein 2/3 complex, subunit 1B
Iqgap1	IQ motif containing GTPase activating protein 1
Itga7	integrin alpha 7
Itgb1	integrin beta 1 (fibronectin receptor beta)
Myh10	myosin, heavy polypeptide 10, non-muscle
Myh9	myosin, heavy polypeptide 9, non-muscle
Nras	neuroblastoma ras oncogene
Pip4k2c	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma
Rras	Harvey rat sarcoma oncogene, subgroup R
Wasf2	WAS protein family, member 2
<b>miR-143</b> (Ranked 2, $P \approx 0.0422$ )	
Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1
Arhgef4	Rho guanine nucleotide exchange factor (GEF) 4
Egfr	epidermal growth factor receptor
Gng12	guanine nucleotide binding protein (G protein), gamma 12
Limk1	LIM-domain containing, protein kinase
Pdgfb	platelet derived growth factor, B polypeptide
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
<b>miR-145</b> (Ranked 52, $P \approx 0.413$ )	
F2r	coagulation factor II (thrombin) receptor
Nras	neuroblastoma ras oncogene
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
Tiam1	T-cell lymphoma invasion and metastasis 1
Wasf2	WAS protein family, member 2
<b>miR-25</b> (Ranked 11, $P \approx 0.0381$ )	
Fgf10	fibroblast growth factor 10
Fgf12	fibroblast growth factor 12
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma
Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1
<b>miR-434-3p</b> (Ranked 31, $P \approx 0.226$ )	
Egfr	epidermal growth factor receptor
Fgf13	fibroblast growth factor 13
Pxn	paxillin

**Table A.44: miRNA targets within “Regulation of actin cytoskeleton” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “Regulation of actin cytoskeleton” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67</b> (Ranked 76, $P \approx 0.622$ )	
Bcl2	B-cell leukemia/lymphoma 2
Pak4	p21 protein (Cdc42/Rac)-activated kinase 4
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Zyx	zyxin
<b>miR-124</b> (Ranked 1, $P \approx 0.00211$ )	
Actn4	actinin alpha 4
Capn2	calpain 2
Cav1	caveolin 1, caveolae protein
Ccnd1	cyclin D1
Col4a1	collagen, type IV, alpha 1
Col5a1	collagen, type V, alpha 1
ErbB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived [...]
Flnb	filamin, beta
Flnc	filamin C, gamma
Itga7	integrin alpha 7
Itgb1	integrin beta 1 (fibronectin receptor beta)
Lamc1	laminin, gamma 1
Shc1	src homology 2 domain-containing transforming protein C1
<b>miR-143</b> (Ranked 42, $P \approx 0.346$ )	
Egfr	epidermal growth factor receptor
Pdgfb	platelet derived growth factor, B polypeptide
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
Src	Rous sarcoma oncogene
<b>miR-145</b> (Ranked 94, $P \approx 0.738$ )	
Col1a1	collagen, type I, alpha 1
Flnb	filamin, beta
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
<b>miR-25</b> (Ranked 19, $P \approx 0.0888$ )	
Igflr	insulin-like growth factor I receptor
Mapk8	mitogen-activated protein kinase 8
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma
<b>miR-434-3p</b> (Ranked 9, $P \approx 0.0652$ )	
Ccnd2	cyclin D2
Col1a1	collagen, type I, alpha 1
Egfr	epidermal growth factor receptor
Pxn	paxillin

**Table A.45: miRNA targets within “Focal adhesion” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “Focal adhesion” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67</b> (Ranked 44, $P \approx 0.287$ )	
Arrb1	arrestin, beta 1
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
Map2k4	mitogen-activated protein kinase kinase 4
Mapk14	mitogen-activated protein kinase 14
Ntrk2	neurotrophic tyrosine kinase, receptor, type 2
Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)
<b>miR-124</b> (Ranked 55, $P \approx 0.315$ )	
Dusp6	dual specificity phosphatase 6
Flnb	filamin, beta
Flnc	filamin C, gamma
Mapk14	mitogen-activated protein kinase 14
Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3
Nras	neuroblastoma ras oncogene
Ntrk2	neurotrophic tyrosine kinase, receptor, type 2
Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
Rras	Harvey rat sarcoma oncogene, subgroup R
<b>miR-143</b> (Ranked 1, $P \approx 0.0342$ )	
Caacb3	calcium channel, voltage-dependent, beta 3 subunit
Dusp16	dual specificity phosphatase 16
Dusp7	dual specificity phosphatase 7
Egfr	epidermal growth factor receptor
Gng12	guanine nucleotide binding protein (G protein), gamma 12
Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3
Pdgfb	platelet derived growth factor, B polypeptide
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
Rps6ka1	ribosomal protein S6 kinase polypeptide 1
<b>miR-145</b> (Ranked 1, $P \approx 0.000891$ )	
Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)
Dusp6	dual specificity phosphatase 6
Flnb	filamin, beta
Ikbkg	inhibitor of kappaB kinase gamma
Map2k4	mitogen-activated protein kinase kinase 4
Map3k1	mitogen-activated protein kinase kinase kinase 1
Nras	neuroblastoma ras oncogene
Ntrk2	neurotrophic tyrosine kinase, receptor, type 2
Pdgfra	platelet derived growth factor receptor, alpha polypeptide
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform
Prkx	protein kinase, X-linked
Rasa1	RAS p21 protein activator 1
Taok1	TAO kinase 1
Traf6	TNF receptor-associated factor 6
<b>miR-25</b> (Ranked 12, $P \approx 0.0414$ )	
B230120H23Rik	RIKEN cDNA B230120H23 gene
Fgf10	fibroblast growth factor 10
Fgf12	fibroblast growth factor 12
Map2k4	mitogen-activated protein kinase kinase 4
Mapk8	mitogen-activated protein kinase 8
Rps6ka4	ribosomal protein S6 kinase, polypeptide 4
Taok1	TAO kinase 1
<b>miR-434-3p</b> (Ranked 48, $P \approx 0.393$ )	
Egfr	epidermal growth factor receptor
Fgf13	fibroblast growth factor 13
Tgfbr2	transforming growth factor, beta receptor II

**Table A.46: miRNA targets within “MAPK signaling pathway” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “MAPK signaling pathway” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67 (Ranked 9, P <math>\approx</math> 0.0272)</b>	
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
Mapk14	mitogen-activated protein kinase 14
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)
<b>miR-124 (Ranked 24, P <math>\approx</math> 0.111)</b>	
Mapk14	mitogen-activated protein kinase 14
Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3
Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
Nras	neuroblastoma ras oncogene
<b>miR-143 (Ranked 18, P <math>\approx</math> 0.125)</b>	
Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3
Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
Src	Rous sarcoma oncogene
<b>miR-145 (Ranked 50, P <math>\approx</math> 0.408)</b>	
Nras	neuroblastoma ras oncogene
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform
<b>miR-25 (Ranked 56, P <math>\approx</math> 0.27)</b>	
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
<b>miR-434-3p (Ranked 49, P <math>\approx</math> 0.424)</b>	
Pxn	paxillin

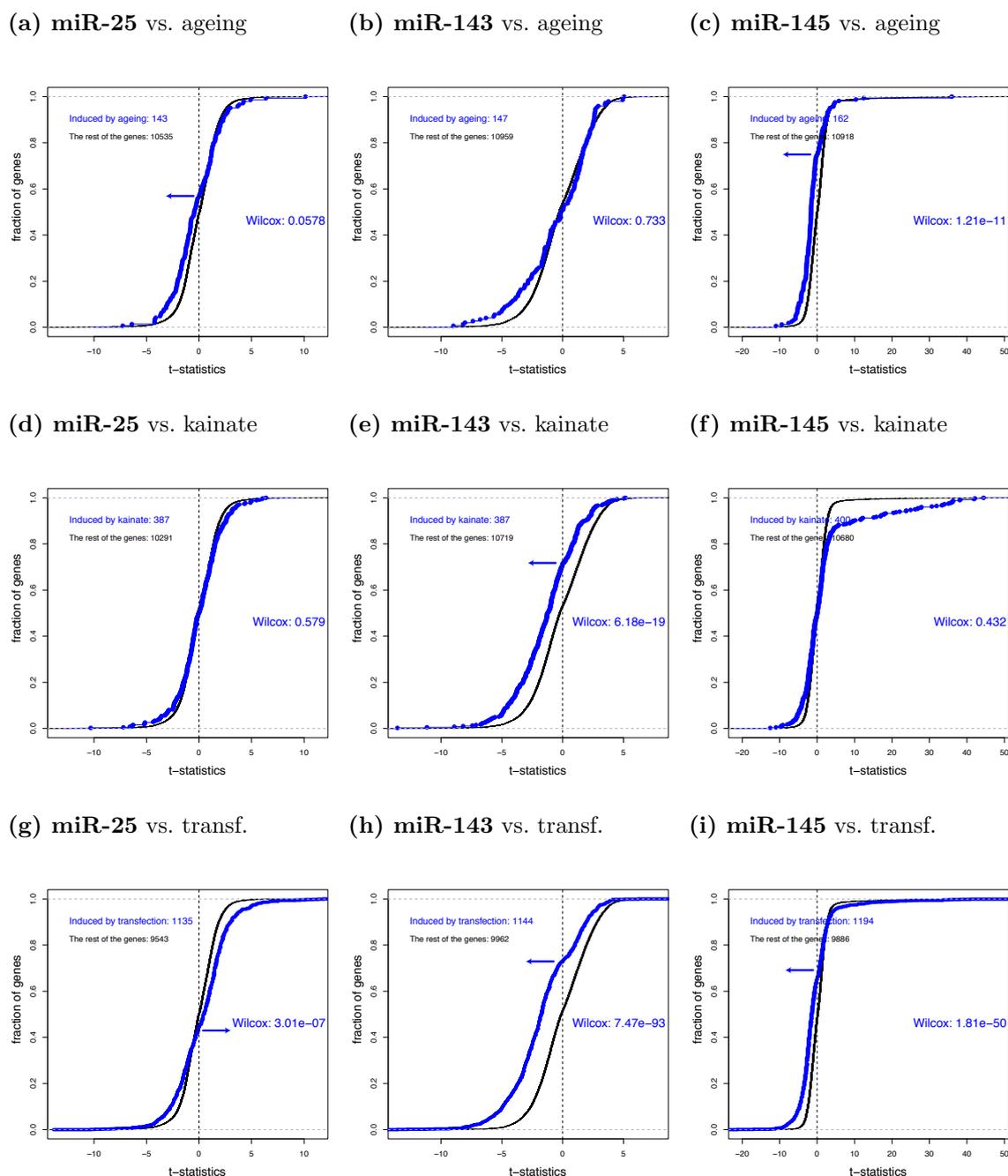
**Table A.47: miRNA targets within “VEGF signaling pathway” KEGG pathway.**

The text in parenthesis shows the rank of the enrichment of the “VEGF signaling pathway” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.

Symbol	Description
<b>cel-miR-67 (Ranked 19, P <math>\approx</math> 0.112)</b>	
Map2k4	mitogen-activated protein kinase kinase 4
Mapk14	mitogen-activated protein kinase 14
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Tollip	toll interacting protein
<b>miR-124 (Ranked 44, P <math>\approx</math> 0.242)</b>	
Fadd	Fas (TNFRSF6)-associated via death domain
Mapk14	mitogen-activated protein kinase 14
Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
Traf3	TNF receptor-associated factor 3
<b>miR-143 (Ranked 89, P <math>\approx</math> 0.807)</b>	
Fadd	Fas (TNFRSF6)-associated via death domain
<b>miR-145 (Ranked 41, P <math>\approx</math> 0.329)</b>	
Ikbkg	inhibitor of kappaB kinase gamma
Map2k4	mitogen-activated protein kinase kinase 4
Traf6	TNF receptor-associated factor 6
<b>miR-25 (Ranked 13, P <math>\approx</math> 0.0453)</b>	
Map2k4	mitogen-activated protein kinase kinase 4
Mapk8	mitogen-activated protein kinase 8
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)

**Table A.48: miRNA targets within “Toll-like receptor signaling pathway” KEGG pathway.**

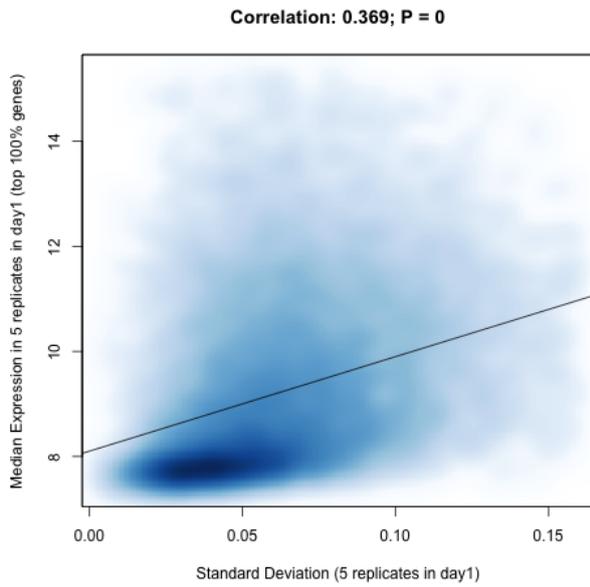
The text in parenthesis shows the rank of the enrichment of the “Toll-like receptor signaling pathway” among all the KEGG pathways and the P-value of that enrichment. The text is in bold if the enrichment was ranked within the top 25 most enriched pathways.



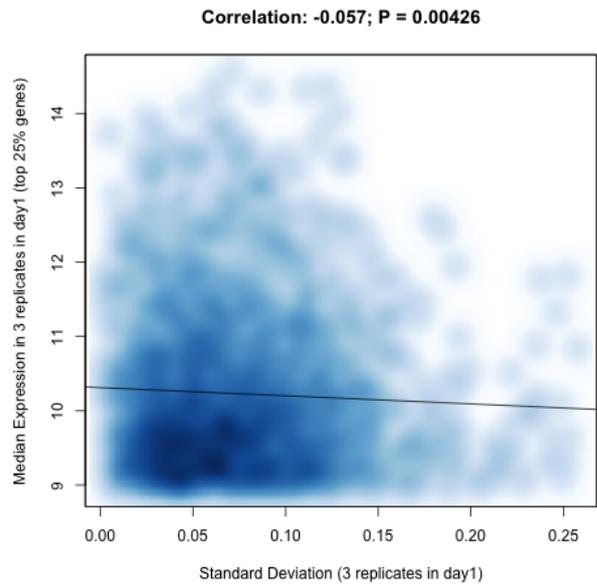
**Figure A.7: Regulation of stress induced genes by miR-25, miR-143 and miR-145.**

The y-axes show the cumulative fraction of genes, the x-axes show the fold change t-statistics (Methods, section 2.7). Genes significantly induced (differential expression  $P < 0.05$ ) by one of the three stresses (the ageing, kainate or transfection stresses) are shown as the blue line/points. The rest of the genes (except 0.01% most highly up- and downregulated genes, which were not plotted for the purpose of better scaling) is shown as the black lines. The text in the plot areas shows: 1) The number of genes *induced by* a stress that were expressed in the miRNA transfection experiments; 2) The number of other expressed genes (*The rest of the genes*); 3) The Wilcoxon test P-value for the difference in medians of the fold change t-statistics for the stress induced genes and the rest of the genes (*Wilcox*). The blue arrows show the direction of the shift in experiments where the Wilcoxon test P-value was significant ( $P < 0.05$ ). The titles of the subfigures show: The names of the perturbed miRNAs (in bold) and the name of the stress experiment where the stress induced genes were identified.

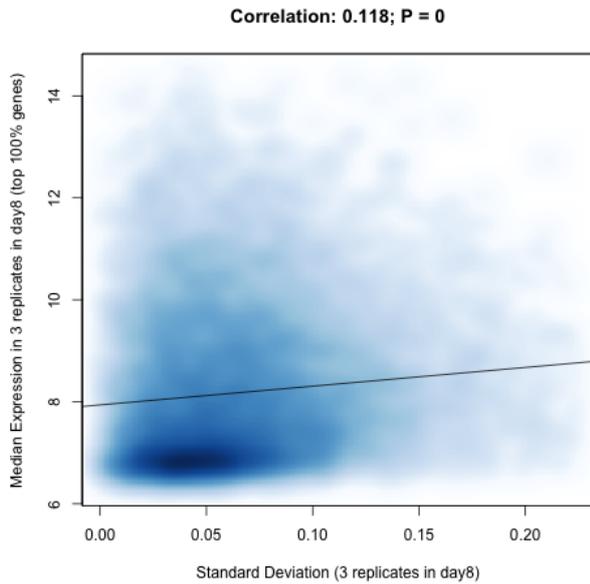
(a) HP cultures at 1DIV; 100% of genes



(b) HP cultures at 1DIV; top 25% of genes



(c) HP cultures at 8DIV; 100% of genes



(d) HP cultures at 8DIV; top 25% of genes

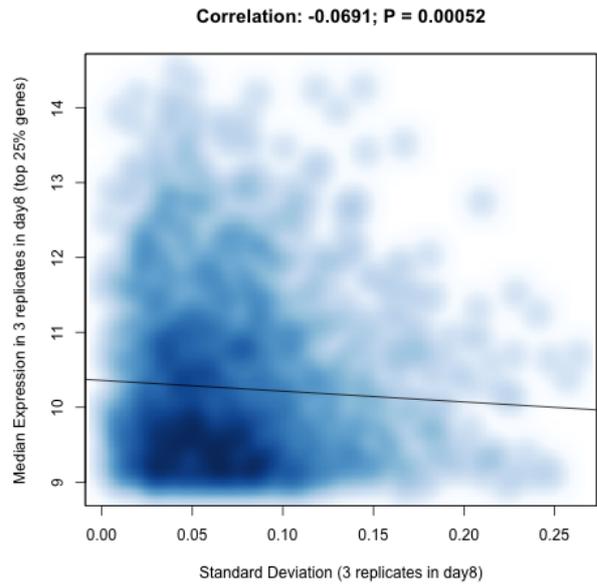
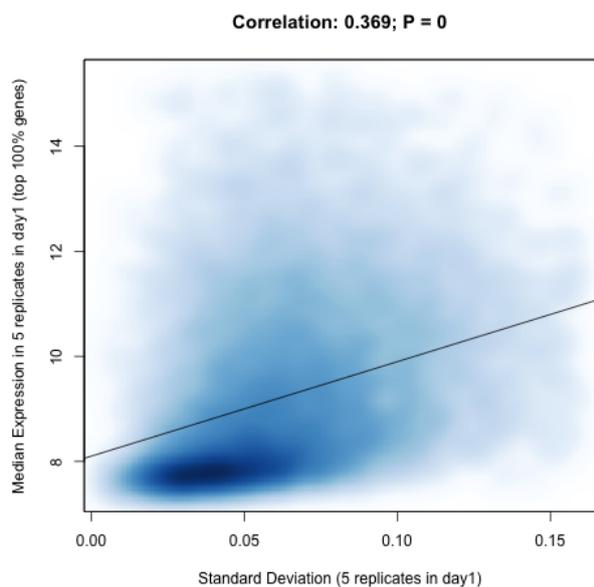
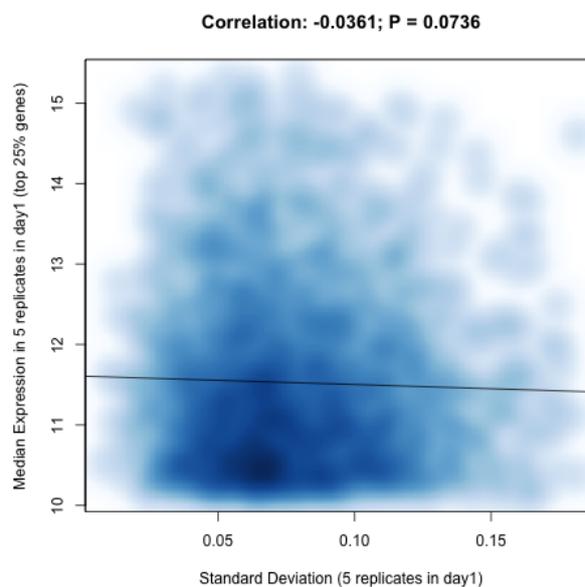


Figure A.8: Correlation of expression and standard deviation in hippocampal primary cultures.

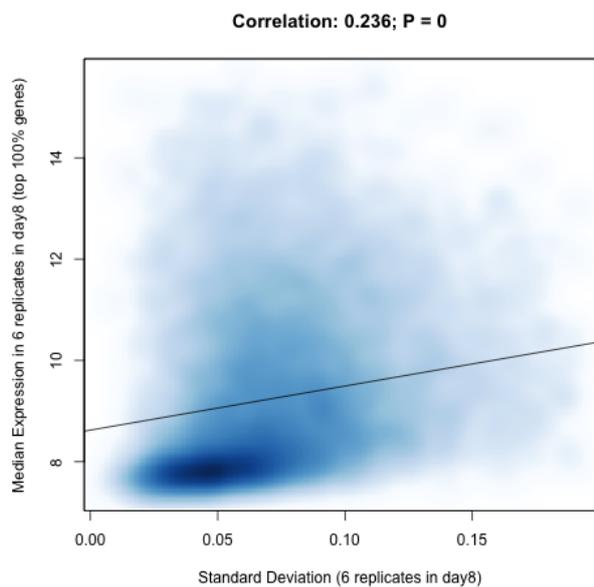
(a) FB cultures at 1DIV; 100% of genes



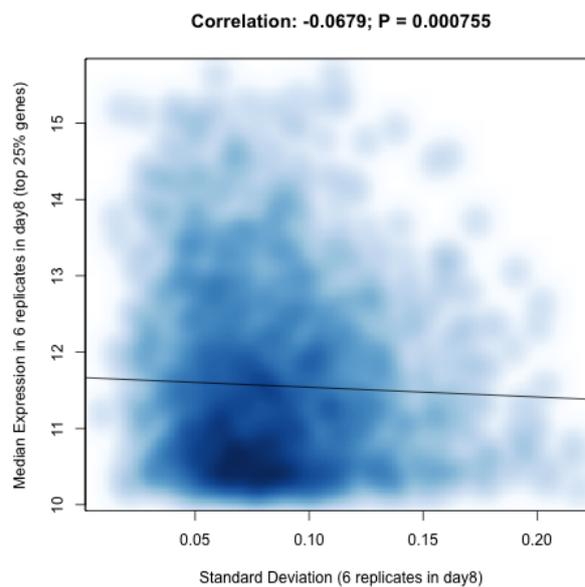
(b) FB cultures at 1DIV; top 25% of genes



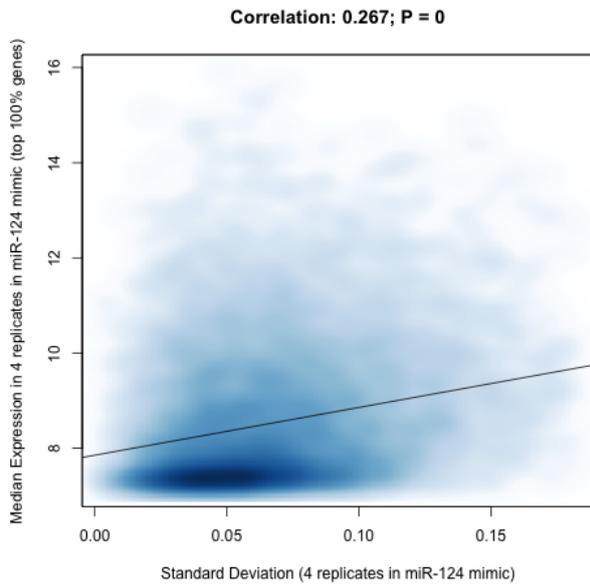
(c) FB cultures at 8DIV; 100% of genes



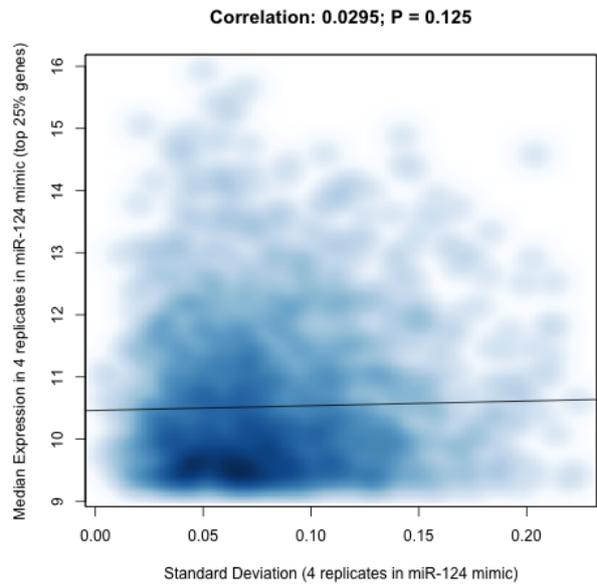
(d) FB cultures at 8DIV; top 25% of genes

**Figure A.9: Correlation of expression and standard deviation in forebrain primary cultures.**

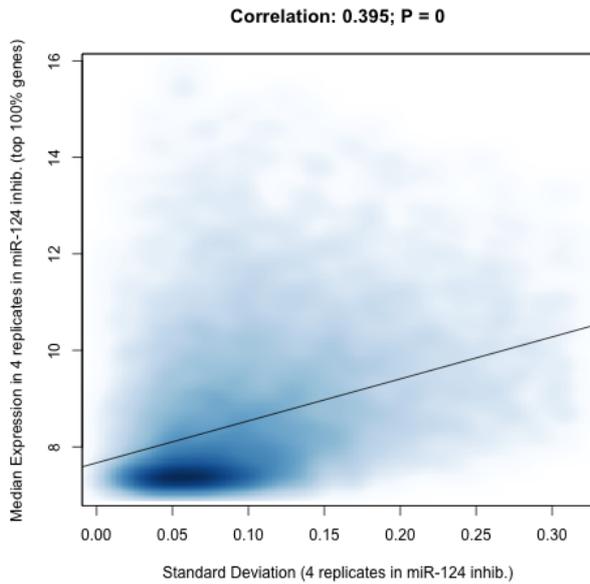
(a) Overexpression of miR-124; 100% of genes



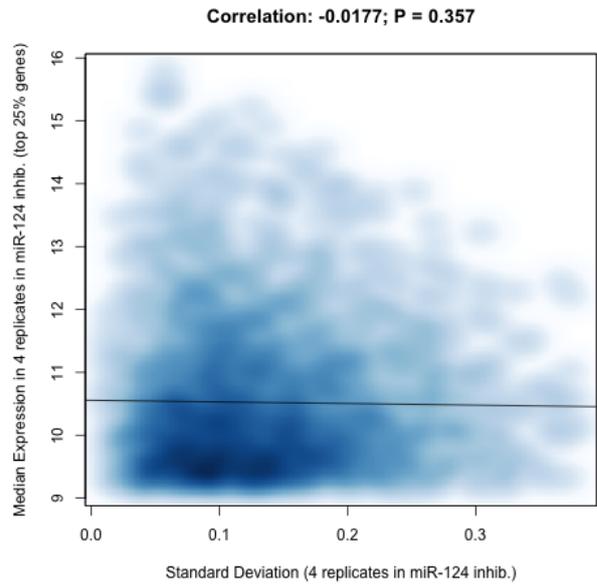
(b) Overexpression of miR-124; top 25% of genes



(c) Inhibition of miR-124; 100% of genes

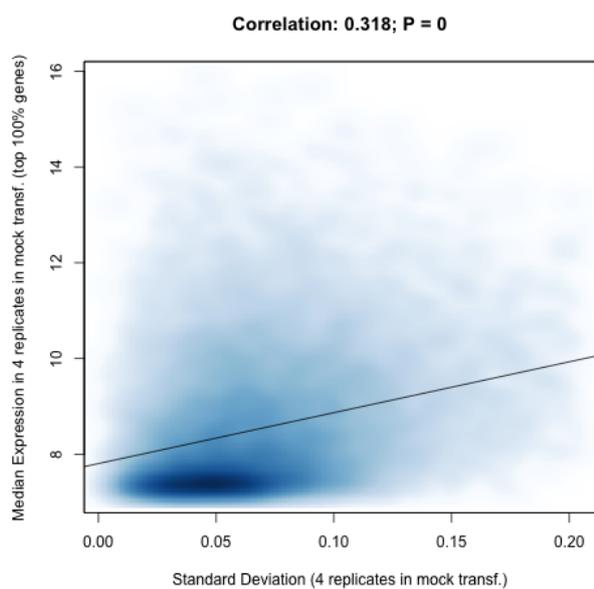


(d) Inhibition of miR-124; top 25% of genes

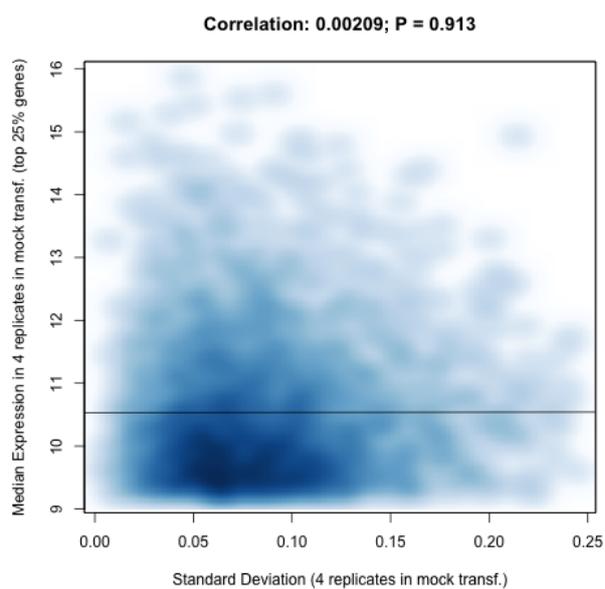


**Figure A.10: Correlation of expression and standard deviation in miR-124 overexpression and inhibition.**

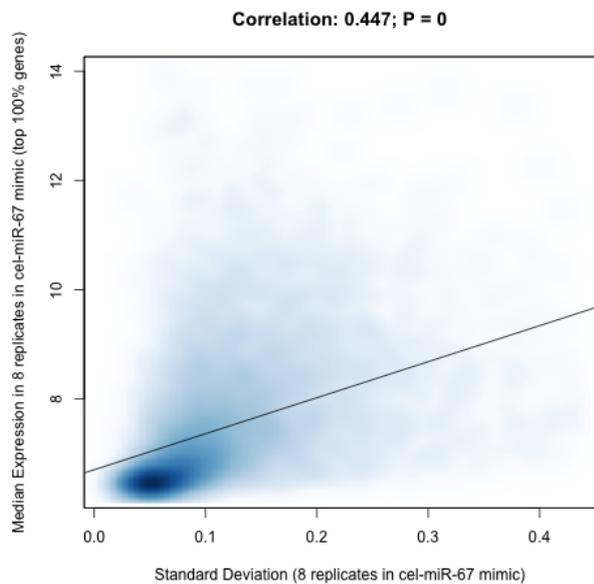
(a) mock transfection; 100% of genes



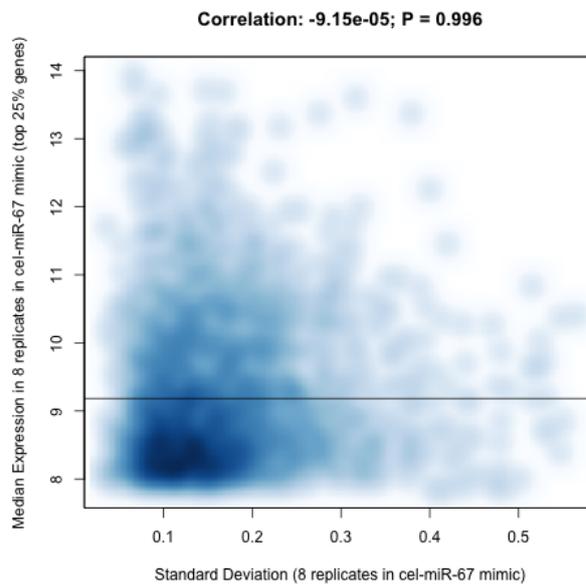
(b) mock transfection; top 25% of genes



(c) Overexpression cel-miR-67; 100% of genes



(d) Overexpression cel-miR-67; top 25% of genes



**Figure A.11: Correlation of expression and standard deviation in mock transfection and cel-miR-67 overexpression.**



# Appendix B

## Publications and presentations of this work

### Publications:

- **S.A Manakov**, A. Morton, S.G Grant, A.J Enright. A neuronal transcriptome response involving stress pathways is buffered by neuronal microRNAs. *In preparation*.
- **S.A Manakov**, S.G Grant, A.J Enright. Reciprocal regulation of microRNA and mRNA profiles in neuronal development and synapse formation. *BMC Genomics* (2009) vol. 10 (1) pp. 419
- *Methods of this work were used in the following:*  
D Santhakumar, T Forster, N.N Laqtom, R Fragkoudis, P Dickinson, C Abreu-Goodger, **S.A Manakov**, N.R Choudhury, S.J Griffiths, A Vermeulen, A.J Enright, B Dutiae, A Kohle, P Ghazalb, A.H. Buck. Combined agonist–antagonist genome-wide functional screening identifies broadly active antiviral microRNAs. *Proceedings of the National Academy of Sciences* (2010) vol. 107 (31) pp. 13830

### Presentations:

- **S.A Manakov**, A.J Enright, S.G Grant. Activity of evolutionary distinct classes of microRNAs in neuronal development. *The Society for Neuroscience annual meeting, San Diego, U.S.A.* (2010) Poster presentation
- **S.A Manakov**, S.G Grant, A.J Enright. Role of miRNAs in the genetic program of synaptogenesis. *The Society for Neuroscience annual meeting, Washington D.C., U.S.A.* (2008) Slide presentation