

Appendix A

Supplementary Data

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

| Entrez ID | Symbol | Entrez ID | Symbol | Entrez ID | Symbol | Entrez ID | Symbol |
|-----------|----------|-----------|----------|-----------|----------|-----------|----------|
| 11419 | Accn2 | 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 | Ctnn1 | 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 | Lanc1l |
| 14799 | Gria1 | 14800 | Gria2 | 14802 | Gria4 | 14810 | Grin1 |
| 14811 | Grin2a | 14812 | Grin2b | 15165 | Hcn1 | 15275 | Hk1 |
| 15441 | Hpl1bp3 | 15444 | Hpca | 15505 | Hsph1 | 15512 | Hspa2 |
| 15519 | Hsp90aa1 | 15568 | Elavl1 | 15571 | Elavl3 | 15572 | Elavl4 |
| 15898 | Icam5 | 16438 | Itpr1 | 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 | Klcl | 16594 | Klcl2 | 16646 | Kpna1 |
| 16653 | Kras | 16728 | L1cam | 16832 | Ldhh | 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 | Paln | 18488 | Cntn3 | 18526 | Pcdh10 |
| 18555 | Cdk16 | 18574 | Pdel1b | 18578 | Pde4b | 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 | Ptprs | 19281 | Ptprrt |
| 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

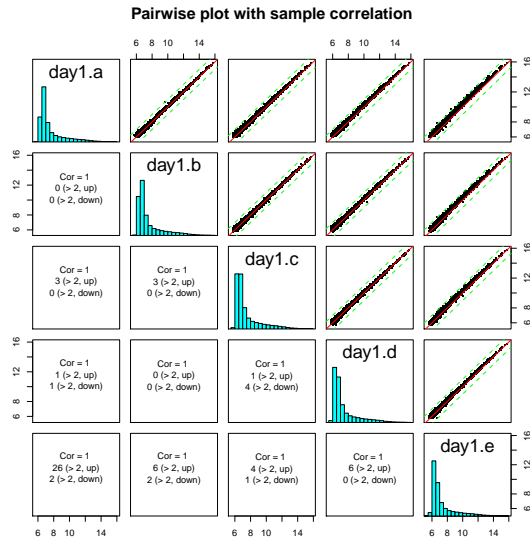
| Entrez ID | Symbol | Entrez ID | Symbol | Entrez ID | Symbol | Entrez ID | Symbol |
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| 23859 | Dlg2 | 23881 | G3bp2 | 23936 | Lynx1 | 23945 | Mgll |
| 23950 | Dnajb6 | 23966 | Odz4 | 23969 | Pacsin1 | 24012 | Rgs7 |
| 24050 | Sept3 | 26372 | Clcn6 | 26395 | Map2k1 | 26413 | Mapk1 |
| 26422 | Nbea | 26556 | Homer1 | 26557 | Homer2 | 26562 | Ncdn |
| 26757 | Dpysl4 | 26874 | Abcd2 | 26875 | Pclo | 26913 | Gprin1 |
| 26932 | Ppp2r5e | 26950 | Vsnl1 | 27062 | Cadps | 27204 | Syn3 |
| 27373 | Csnk1e | 27801 | Zdhhc8 | 27984 | Efhed2 | 28185 | Tomm70a |
| 29873 | Cspg5 | 30785 | Ctttnbp2 | 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 | Dynl1l | 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 | Plip | 67826 | Snap47 | 67834 | Idh3a | 67900 | 1700020C11Rik |
| 67972 | Atp2b1 | 68032 | Tmem85 | 68166 | Spire1 | 68203 | Diras2 |
| 68267 | Slc25a22 | 68404 | Nrn1 | 68507 | Ppfia4 | 68524 | Wipf2 |
| 68585 | Rtn4 | 68724 | Arl8a | 69219 | Ddah1 | 69399 | 1700025G04Rik |
| 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 | 2610110G12Rik | 73420 | 1700054N08Rik | 73442 | Hspa12a |
| 73710 | Tubb2b | 73728 | Psd | 73825 | Klraql | 73834 | Atp6v1d |
| 73991 | At1l | 74006 | Dnm1l | 74012 | Rap2b | 74053 | Grip1 |
| 74103 | Nebi | 74205 | Acs13 | 74256 | Cyld | 74342 | Lrrtm1 |
| 74998 | Rab11fp2 | 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 | Clasp2 | 76580 | Mib2 |
| 76686 | Clip3 | 76740 | Efr3a | 76742 | Snx27 | 76787 | Ppfia3 |
| 76809 | Bri3bp | 76820 | Fam49a | 76884 | Cyfp2 | 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 |
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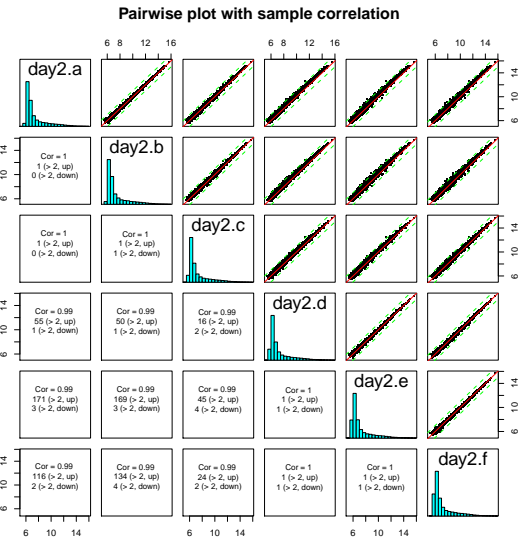
The list of putative neuron-specific genes

| Entrez ID | Symbol | Entrez ID | Symbol | Entrez ID | Symbol | 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 | Ppfia2 | 329152 | Hecw2 | 329165 | Abi2 | 330319 | Wipf3 |
| 330369 | Fbxo41 | 330790 | Hapln4 | 330814 | Lphn1 | 330908 | Opcml |
| 330914 | Grit | 331461 | Il1rapl1 | 347722 | Agap1 | 360213 | Trim46 |
| 380684 | Nefh | 380702 | Shisa6 | 380768 | Gm1568 | 381813 | Prmt8 |
| 381979 | Brsk1 | 382018 | Unc13a | 406218 | Panx2 | 433904 | Ociad2 |
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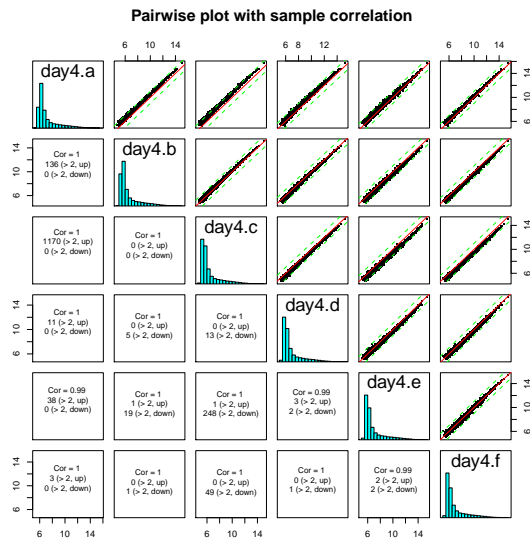
(a) 1DIV replicates



(b) 2DIV replicates



(c) 4DIV replicates



(d) 8DIV replicates

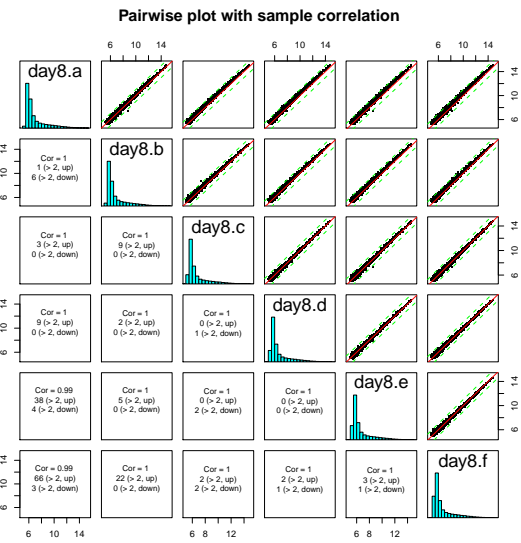
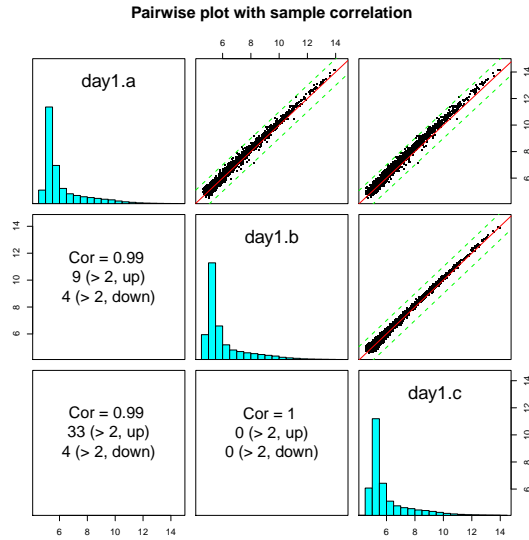


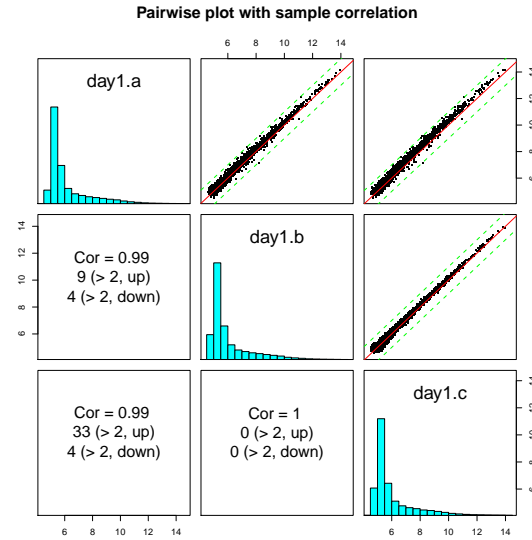
Figure A.1: Pairwise correlation of raw mRNA microarray probe intensities in profiles of hippocampal cultures.

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).

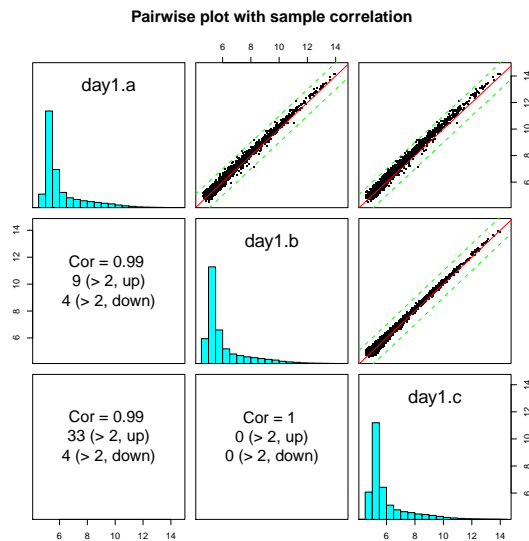
(a) 1DIV replicates



(b) 2DIV replicates



(c) 4DIV replicates



(d) 8DIV replicates

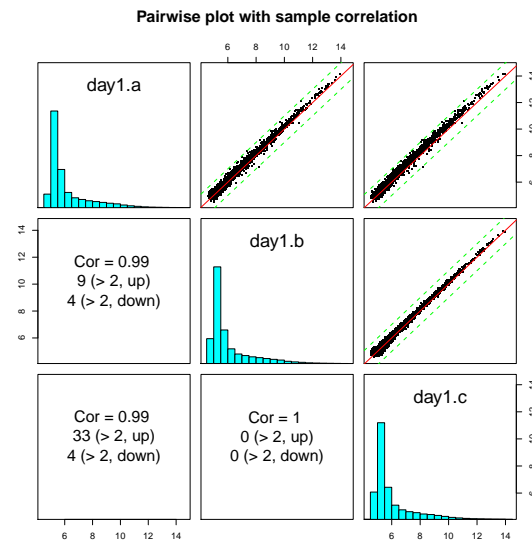
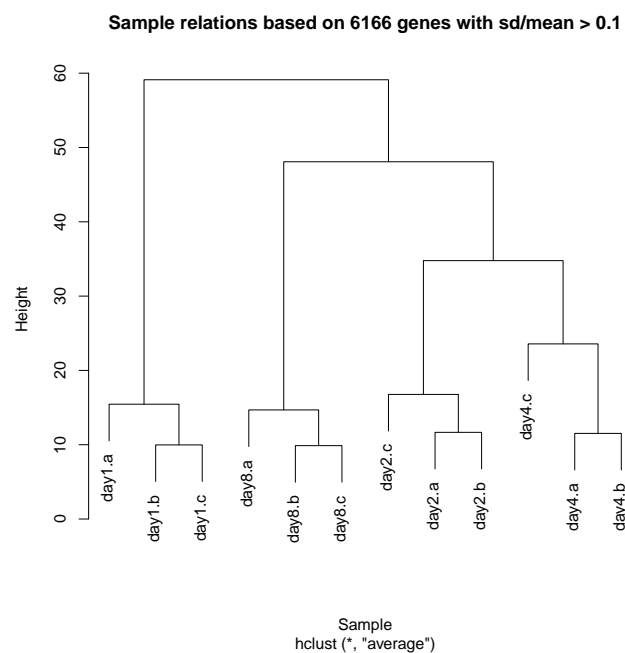


Figure A.2: Pairwise correlation of raw mRNA microarray probe intensities in profiles of hippocampal cultures.

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

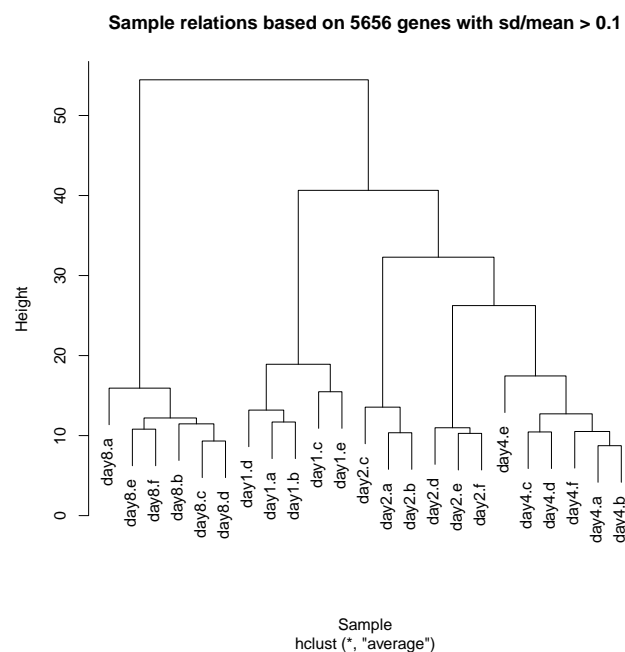
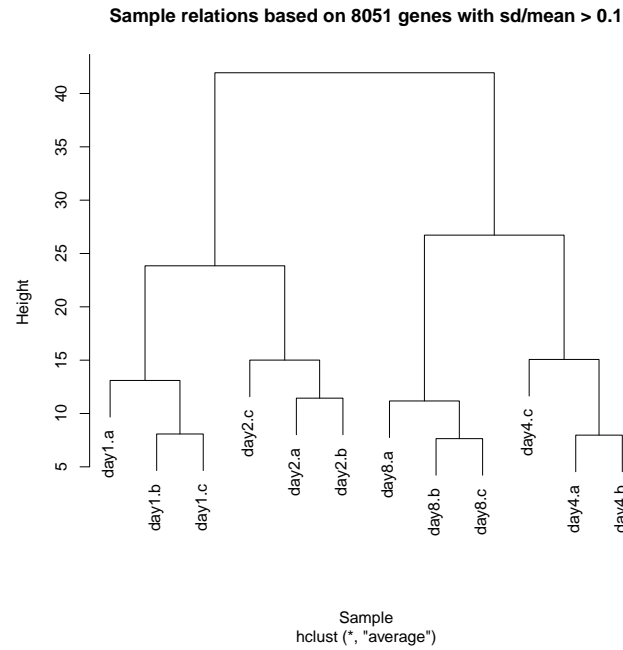


Figure A.3: Sample relation between raw mRNA microarray profiles between replicates of hippocampal and forebrain cultures.

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

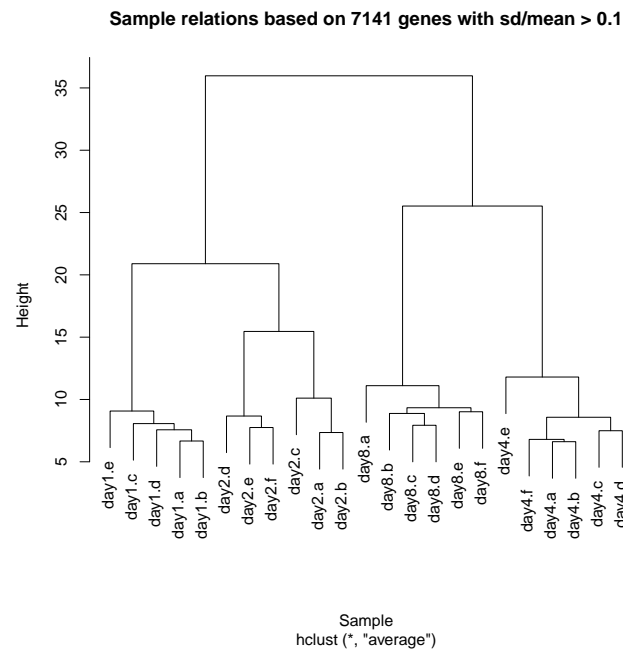


Figure A.4: Sample relation between normalised mRNA microarray profiles between replicates of hippocampal and forebrain cultures.

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 |

Continued on Next Page...

| 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 |

Continued on Next Page...

| 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 |

Continued on Next Page...

| 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 |

Continued on Next Page...

| 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.

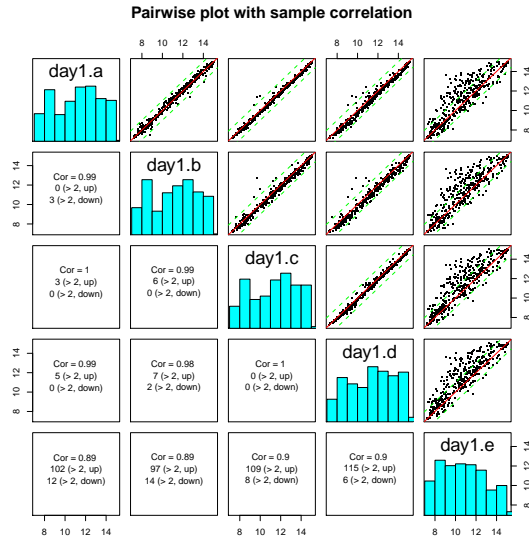
q - number of genes of a KEGG term that was among the upregulated genes, m - total number of genes of a KEGG term in the test universe, P - P-value of enrichment. See [Methods](#), section 2.10.

| 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 |

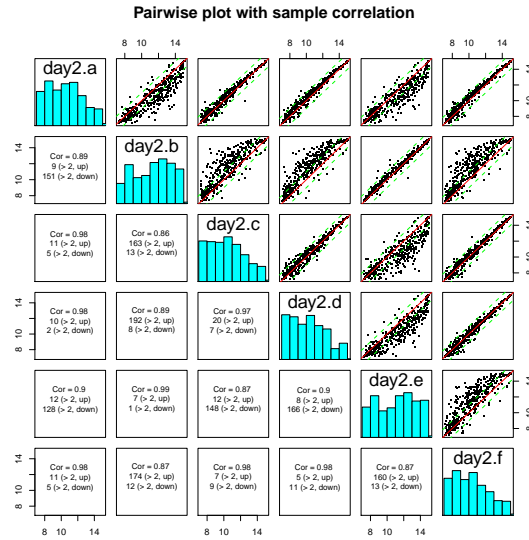
Continued on Next Page...

| ID | Term Description | q | m | P |
|-----------|-------------------------------------------------|----------|----------|----------|
| 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 |

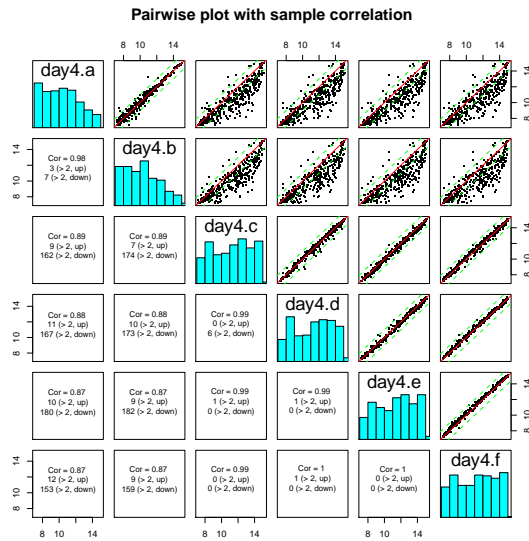
(a) 1DIV replicates



(b) 2DIV replicates



(c) 4DIV replicates



(d) 8DIV replicates

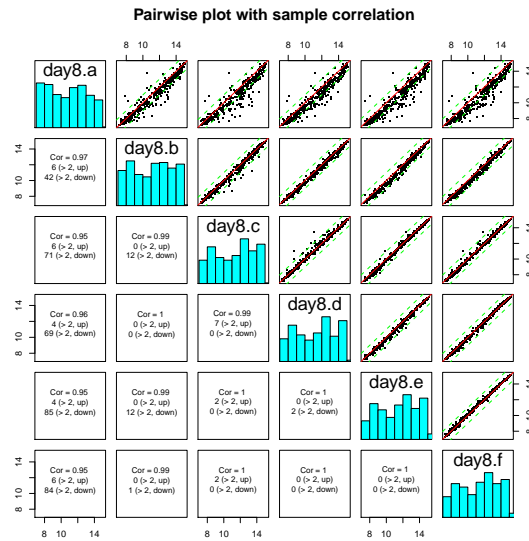
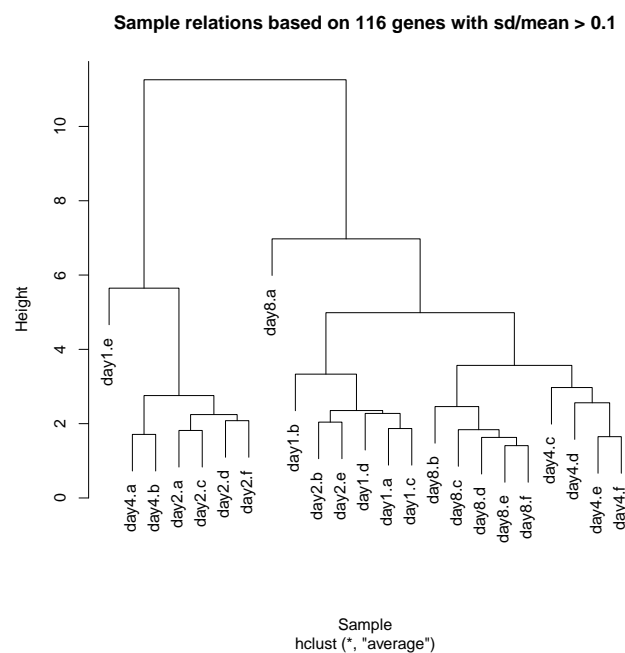


Figure A.5: Pairwise correlation of raw miRNA microarray probe intensities in profiles of forebrain cultures.

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)

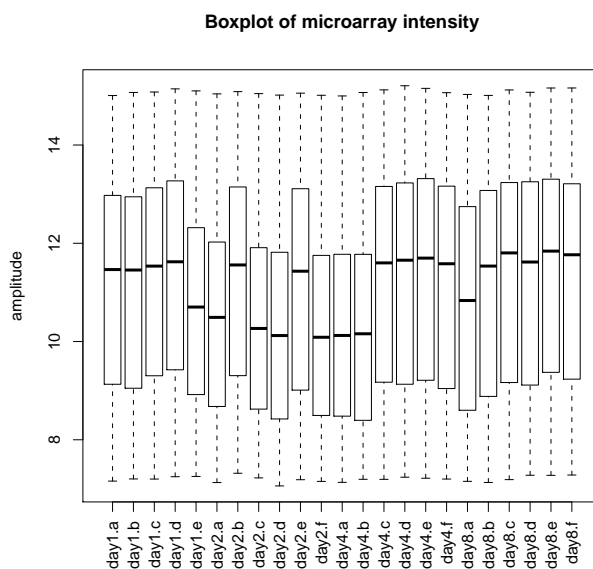


Figure A.6: Relationship between replicate raw miRNA microarray profiles.

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 |

Continued on Next Page...

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 | Entrez ID | Symbol | Entrez ID | Symbol | Entrez ID | Symbol |
|-----------|---------------|-----------|---------------|-----------|---------------|-----------|---------------|
| 11370 | Acadvl | 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 | Bckdha | 12042 | Bcl10 | 12161 | Bmp6 |
| 12192 | Zfp361l | 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 | Igf1p3 | 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 | Neddl | 18018 | Nfatc1 |
| 18028 | Nfib | 18029 | Nfic | 18032 | Nfix | 18073 | Nid1 |
| 18140 | Uhrf1 | 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 | Suclg2 | 20971 | Sdc4 | 21367 | Cntn2 |
| 21413 | Tcf4 | 21415 | Tcf7l1 | 21766 | Tex261 | 21859 | Timp3 |
| 21871 | Atp6v0a2 | 21873 | Tjp2 | 21915 | Dtymk | 22031 | Traf3 |
| 22092 | Rspbl | 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 | Rhpnl | 52538 | Acaa2 | 52585 | Dhrs1 |
| 52840 | Dbnnd2 | 53330 | Vamp4 | 53376 | Usp2 | 53378 | Sdcbp |
| 53415 | Htatip2 | 53599 | Cd164 | 53623 | Gria3 | 53860 | Sept9 |
| 54325 | Elovl1 | 54720 | Rcan1 | 56016 | Hebp2 | 56212 | Rhog |
| 56248 | Ak3 | 56309 | Mycbp | 56332 | Amotl2 | 56356 | Gltp |
| 56369 | Apip | 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 | Fmn12 | 71567 | Mcm9 |
| 71602 | Myo1e | 71712 | Dram1 | 71766 | Raver1 | 71801 | Plekhl2 |
| 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 | Pcdhl |
| 75646 | Rai14 | 75659 | Wdr54 | 75723 | Amotl1 | 76044 | Ncapg2 |
| 76178 | 6330578E17Rik | 76251 | 0610007P08Rik | 76263 | Gstk1 | 76491 | Abhd14b |
| 76566 | Fam101b | 76893 | Lass2 | 76895 | Bicd2 | 77034 | 2510039O18Rik |
| 77056 | Tmco4 | 77446 | Heg1 | 77559 | Agf | 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 | Fgfr1l |
| 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 | Wipf1 | 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 |
| 226519 | 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 | Klhl21 |
| 244152 | Tsku | 244631 | Psck1 | 246257 | Ovca2 | 246316 | Lgi2 |
| 259302 | Srgap3 | 268935 | Scube3 | 269593 | Luzp1 | 269941 | Chsy1 |
| 269999 | Orai3 | 286940 | Flnb | 319710 | Frmd6 | 319939 | Tns3 |
| 320184 | Lrrc58 | 320404 | Itpkb | 320736 | E130203B14Rik | 326618 | Tpm4 |
| 329274 | Fam163a | 330171 | Kctd10 | 330222 | Sdk1 | 330695 | Ctxn1 |
| 338365 | Slc41a2 | 382030 | Tmem188 | 382406 | Wdr51b | 414801 | Itprip |
| 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 | Gnb1l | 14043 | Ext2 | 14082 | Fadd |
| 14086 | Fscn1 | 14219 | Ctgf | 14230 | Fkbp10 | 14548 | Mrps33 |
| 14605 | Tsc22d3 | 14697 | Gnb5 | 14701 | Gng12 | 14726 | Pdpm |
| 14739 | Slpr2 | 14755 | Pigq | 14768 | Lanc1l | 14793 | Cdca3 |
| 15039 | H2-T22 | 15239 | Hgs | 15277 | Hk2 | 16011 | Igfbp5 |
| 16432 | Itm2b | 16594 | Klc2 | 16796 | Lasp1 | 16801 | Arhgef1 |
| 16885 | Limk1 | 17126 | Smad2 | 17132 | Maf | 17390 | Mmp2 |
| 17391 | Mmp24 | 17828 | Muted | 17865 | Mybl2 | 18011 | Neurl1a |
| 18018 | Nfatc1 | 18140 | Uhrf1 | 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 | Syngr3 | 21429 | Ubtg | 21766 | Tex261 |
| 21853 | Timeless | 22022 | Tpst2 | 22319 | Vamp3 | 22320 | Vamp8 |
| 22401 | Zmat3 | 22670 | Trim26 | 23936 | Lynx1 | 23969 | Pacs1l |
| 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 | Dnlz | 53598 | Dctn3 | 55963 | Slc1a4 |
| 56233 | Hdac7 | 56374 | Tmem59 | 56491 | Vapb | 56542 | Ick |
| 56722 | Litaf | 57028 | Pdcp | 57434 | Xrcc2 | 57436 | Gabaraapl1 |
| 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 | Entrez ID | Symbol | Entrez ID | Symbol | Entrez ID | Symbol |
|-----------|---------------|-----------|---------------|-----------|---------------|-----------|---------------|
| 66241 | Tmem9 | 66278 | 1810013D10Rik | 66314 | Tpd52l2 | 66442 | Sp25 |
| 66588 | Cmpk1 | 66840 | Wdr45l | 66855 | Tcf25 | 66962 | 2310047B19Rik |
| 67213 | Cmtm6 | 67513 | 2610002J02Rik | 67657 | Rabl3 | 67693 | 2310003F16Rik |
| 67695 | 2310016E02Rik | 67792 | Rgs8 | 67843 | Slc35a4 | 67861 | Akr1b10 |
| 67916 | Ppap2b | 68087 | Dcackd | 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 | Star5 | 170625 | Snx18 |
| 171508 | Creld1 | 192185 | Nadk | 192231 | Hexim1 | 207819 | 4930539E08Rik |
| 208501 | 1810043H04Rik | 209773 | Dnnd2a | 211286 | Cln5 | 211535 | Ccdc114 |
| 211798 | Mfsd9 | 212127 | 2810046L04Rik | 212508 | Mtg1 | 212996 | Wbscr17 |
| 213491 | D4Ert22e | 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 | Cycs | 13132 | Dab2 | 13204 | Dhx15 |
| 13837 | Epha3 | 13990 | Smnrcad1 | 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 | Uhmkl | 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 | Ica1 | 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 | Avl9 | 79464 | Lias | 80890 | Trim2 | 81840 | Sorcs2 |
| 81879 | Tcfcp211 | 83397 | Akap12 | 83671 | Sytl2 | 83675 | Bicc1 |
| 83997 | Slmap | 93871 | Brwd1 | 94040 | Clmn | 94190 | Ophn1 |
| 94282 | Sfxn5 | 98660 | Atp1a2 | 100317 | AU040320 | 100434 | Slc44a1 |
| 100710 | Pds5b | 100986 | Akap9 | 101565 | 6330503K22Rik | 102247 | Agpat6 |
| 103135 | Usp52 | 103537 | Mbt1 | 104625 | Cnot6 | 105638 | Dph3 |
| 106369 | Ypel1 | 106840 | Unc119b | 107029 | Me2 | 107568 | Wwp1 |
| 108071 | Grm5 | 108652 | Slc35b3 | 108653 | Rimklb | 108760 | Galnt1l |
| 108897 | Aif1l | 108912 | Cdca2 | 109079 | Sephs1 | 109232 | Sccpdh |
| 109552 | Sri | 109801 | Glo1 | 116914 | Slc19a2 | 117198 | Ivns1abp |
| 117600 | Srgap1 | 140740 | Sec63 | 170753 | Zfp704 | 170822 | Usp33 |
| 194401 | Mical3 | 207214 | Larp4 | 208659 | Fam20a | 208718 | Dis3l2 |
| 210004 | B3gnt1l | 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 | Dgap1 | 225283 | Rprd1a | 226144 | Erlin1 |
| 226151 | Fam178a | 226432 | Ipo9 | 226470 | Zbtb41 | 226562 | Bat2l2 |
| 226781 | Slc30a10 | 227682 | Trub2 | 228357 | Lrp4 | 228829 | Phf20 |
| 228876 | Zfp334 | 229709 | Ahcy1l | 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 | Plekhhm3 |
| 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 | Bcl11a | 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 | Serpinb6a |
| 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 | Clcn7 | 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 | Dcp1a |
| 76366 | Mtif3 | 76477 | Pcolce2 | 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 | Ppcs |
| 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 | Lhfpl2 |
| 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 | Nabp2 | 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 | Ddn | 13204 | Dhx15 | 13478 | Dpagt1 |
| 13483 | Dpp6 | 13527 | Dtna | 13690 | Elf4g2 | 13709 | Elf1 |
| 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 | Kif3c | 16589 | Uhmkl | 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 | Pou2f1 | 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 | Ragl1ap1 | 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 | Tpil | 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 | Pycl | 66246 | Osgp | 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 | Klhl5 | 71900 | Tmem106b | 71952 | 2410016O06Rik | 71963 | Cdca4 |
| 71978 | Ppp2r2a | 72075 | Ogfr | 72124 | Sehl1 | 72139 | 2610044O15Rik |
| 72170 | Chchd4 | 72193 | Sfrs2ip | 72195 | Supt7l | 72542 | Pgam5 |
| 72552 | Hsd1l | 72585 | Lypd1 | 72685 | Dnajc6 | 72792 | 2810459M11Rik |
| 72993 | Appl1 | 73137 | Prrc1 | 73713 | Rbm20 | 74022 | Glyr1 |
| 74030 | Rin2 | 74256 | Cyld | 74340 | Ahcyl2 | 74356 | 4931428F04Rik |
| 74450 | Pank2 | 74479 | Snx11 | 74493 | Tnks2 | 74763 | Nat15 |
| 74769 | Pik3cb | 75625 | Mageh1 | 75678 | Ippk | 75710 | Rbm12 |
| 75723 | Amotl1 | 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 | Glce | 93739 | Gabara1p2 |
| 97884 | B3galnt2 | 98741 | Kcnb2 | 99311 | Commd7 | 99887 | Tmem56 |
| 99889 | Arfp1 | 103266 | AI597468 | 103694 | Tmed4 | 104318 | Csnk1d |
| 104625 | Cnot6 | 104725 | 1110002B05Rik | 105000 | Dnalcl | 106298 | Rrn3 |
| 106522 | Pkdcc | 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 | Hmgal-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 | Ccnb1 | 269582 | Clspn | 269639 | Zfp512 |
| 272589 | Tbcel | 277414 | Trp53i11 | 319370 | Fam100b | 319468 | Ppmlh |
| 320184 | Lrrc58 | 320333 | D830030K20Rik | 320472 | Ppm1e | 320495 | Ipcefl |
| 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 | Tgfbli1 | 21813 | Tgfb2 |
| 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 | Tcfcp2l1 | 99237 | Tm9sf4 | 103266 | AI597468 |
| 103724 | Tbcl10a | 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 | Ccnb1 | 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

| ID | Term Description | q | m | P |
|-------|-----------------------------------------|----|-----|--------|
| 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.

| Term ID | Term Description | q | m | P |
|---------|-----------------------------------------------|----|-----|---------|
| 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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| ID | Term Description | q | m | P |
|------------|----------------------------------------------------------------------|----|------|---------|
| 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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| ID | Term Description | q | m | P |
|------------|---------------------------------|-----|------|----------|
| 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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| ID | Term Description | q | m | P |
|------------|------------------------------------------------|-----|------|----------|
| 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 |
|-------------------------------------------------------------|---------------------------------------------|
| miR-124 (Ranked 11, P \approx 0.0458) | |
| 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 |
| miR-145 (Ranked 97, P \approx 0.76) | |
| Col1a1 | collagen, type I, alpha 1 |
| miR-25 (Ranked 14, P \approx 0.0504) | |
| Dag1 | dystroglycan 1 |
| Sdc2 | syndecan 2 |
| Sdc3 | syndecan 3 |
| miR-434-3p (Ranked 2, P \approx 0.0149) | |
| 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 |
|---------------------------------------------------|------------------------------------------------------------|
| cel-miR-67 (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 |
| miR-124 (Ranked 100, $P \approx 0.735$) | |
| Nras | neuroblastoma ras oncogene |
| Tubb6 | tubulin, beta 6 |
| miR-143 (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 |
| miR-145 (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 |
| miR-25 (Ranked 95, $P \approx 0.728$) | |
| Adcy3 | adenylate cyclase 3 |
| miR-434-3p (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 |
|-------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|
| cel-miR-67 (Ranked 4, P \approx 0.0168) | |
| 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 |
| miR-124 (Ranked 76, P \approx 0.51) | |
| 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 |
| miR-143 (Ranked 58, P \approx 0.464) | |
| Egfr | epidermal growth factor receptor |
| Src | Rous sarcoma oncogene |
| miR-145 (Ranked 79, P \approx 0.607) | |
| Map2k4 | mitogen-activated protein kinase kinase 4 |
| Nras | neuroblastoma ras oncogene |
| miR-25 (Ranked 7, P \approx 0.0245) | |
| 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) |
| miR-434-3p (Ranked 24, P \approx 0.184) | |
| 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 |
|---------------------------------------------------|----------------------------------------------------------------------------------|
| cel-miR-67 (Ranked 68, $P \approx 0.527$) | |
| Amotl1 | angiomotin-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 |
| miR-124 (Ranked 3, $P \approx 0.00907$) | |
| Actn4 | actinin alpha 4 |
| Amotl1 | angiomotin-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 |
| miR-143 (Ranked 95, $P \approx 0.868$) | |
| Src | Rous sarcoma oncogene |
| miR-145 (Ranked 86, $P \approx 0.667$) | |
| Nras | neuroblastoma ras oncogene |
| Prkcz | protein kinase C, zeta |
| miR-25 (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 |
|---------------------------------------------------|------------------------------------------------|
| cel-miR-67 (Ranked 39, $P \approx 0.26$) | |
| Ccnb1 | cyclin B1 |
| Cycs | cytochrome c, somatic |
| Igfbp3 | insulin-like growth factor binding protein 3 |
| miR-124 (Ranked 23, $P \approx 0.111$) | |
| Ccnb1 | cyclin B1 |
| Cd82 | CD82 antigen |
| Igfbp3 | insulin-like growth factor binding protein 3 |
| Zmat3 | zinc finger matrin type 3 |
| miR-143 (Ranked 36, $P \approx 0.284$) | |
| Cd82 | CD82 antigen |
| Zmat3 | zinc finger matrin type 3 |
| miR-145 (Ranked 49, $P \approx 0.408$) | |
| Ccnb1 | cyclin B1 |
| Cycs | cytochrome c, somatic |
| miR-25 (Ranked 50, $P \approx 0.245$) | |
| Rrm2b | ribonucleotide reductase M2 B (TP53 inducible) |
| Zmat3 | zinc finger matrin type 3 |
| miR-434-3p (Ranked 3, $P \approx 0.0161$) | |
| Ccnb1 | cyclin B1 |
| Ccnb2 | cyclin B2 |
| Ccnb1 | cyclin B1 |

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 |
|---------------------------------------------------|-----------------------------------------------------------------------------|
| cel-miR-67 (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 |
| miR-124 (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 |
| miR-143 (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 |
| miR-145 (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 |
| miR-25 (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 |
| miR-434-3p (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 |
|---------------------------------------------------|---------------------------------------------------------------------------------------------|
| cel-miR-67 (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 |
| miR-124 (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 |
| miR-143 (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 |
| miR-145 (Ranked 94, $P \approx 0.738$) | |
| Col1a1 | collagen, type I, alpha 1 |
| Flnb | filamin, beta |
| Pdgfra | platelet derived growth factor receptor, alpha polypeptide |
| miR-25 (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 |
| miR-434-3p (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 |
|---------------------------------------------------|------------------------------------------------------------------------------------|
| cel-miR-67 (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) |
| miR-124 (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 |
| miR-143 (Ranked 1, $P \approx 0.0342$) | |
| Cacnb3 | 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 |
| miR-145 (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 |
| miR-25 (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 |
| miR-434-3p (Ranked 48, $P \approx 0.393$) | |
| Egfr | epidermal growth factor receptor |
| Fgf13 | fibroblast growth factor 13 |
| Tgfb2 | 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 |
|-------------------------------------------------------------|------------------------------------------------------------------------------------|
| cel-miR-67 (Ranked 9, P \approx 0.0272) | |
| 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) |
| miR-124 (Ranked 24, P \approx 0.111) | |
| 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 |
| miR-143 (Ranked 18, P \approx 0.125) | |
| Mapkapk3 | mitogen-activated protein kinase-activated protein kinase 3 |
| Nfatc1 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 |
| Src | Rous sarcoma oncogene |
| miR-145 (Ranked 50, P \approx 0.408) | |
| Nras | neuroblastoma ras oncogene |
| Ppp3ca | protein phosphatase 3, catalytic subunit, alpha isoform |
| miR-25 (Ranked 56, P \approx 0.27) | |
| Pik3cb | phosphatidylinositol 3-kinase, catalytic, beta polypeptide |
| Pik3r2 | phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta) |
| miR-434-3p (Ranked 49, P \approx 0.424) | |
| 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 |
|-------------------------------------------------------------|-----------------------------------------------------------------------------|
| cel-miR-67 (Ranked 19, P \approx 0.112) | |
| Map2k4 | mitogen-activated protein kinase kinase 4 |
| Mapk14 | mitogen-activated protein kinase 14 |
| Pik3cb | phosphatidylinositol 3-kinase, catalytic, beta polypeptide |
| Tollip | toll interacting protein |
| miR-124 (Ranked 44, P \approx 0.242) | |
| 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 |
| miR-143 (Ranked 89, P \approx 0.807) | |
| Fadd | Fas (TNFRSF6)-associated via death domain |
| miR-145 (Ranked 41, P \approx 0.329) | |
| Ikbkg | inhibitor of kappaB kinase gamma |
| Map2k4 | mitogen-activated protein kinase kinase 4 |
| Traf6 | TNF receptor-associated factor 6 |
| miR-25 (Ranked 13, P \approx 0.0453) | |
| 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.

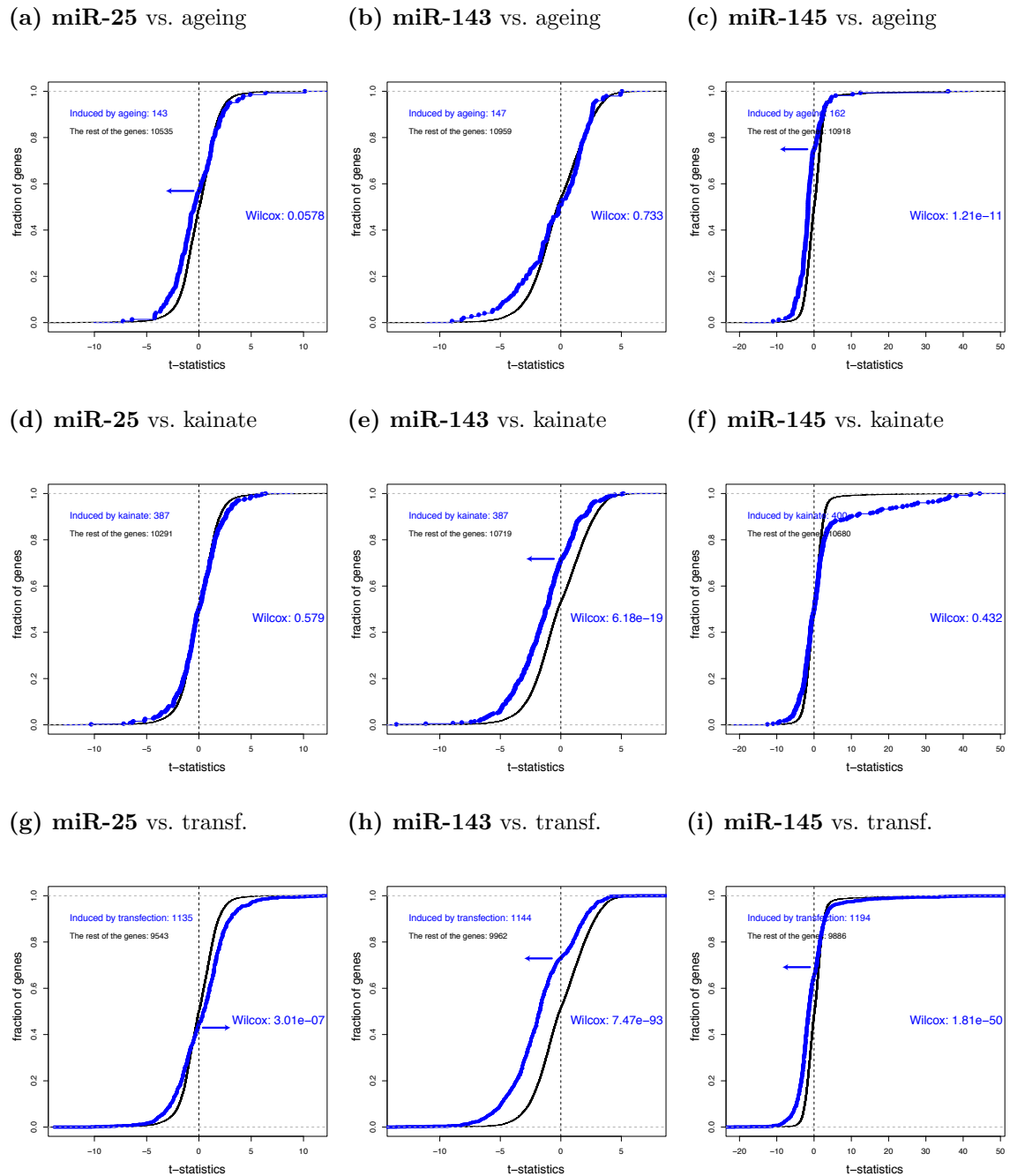
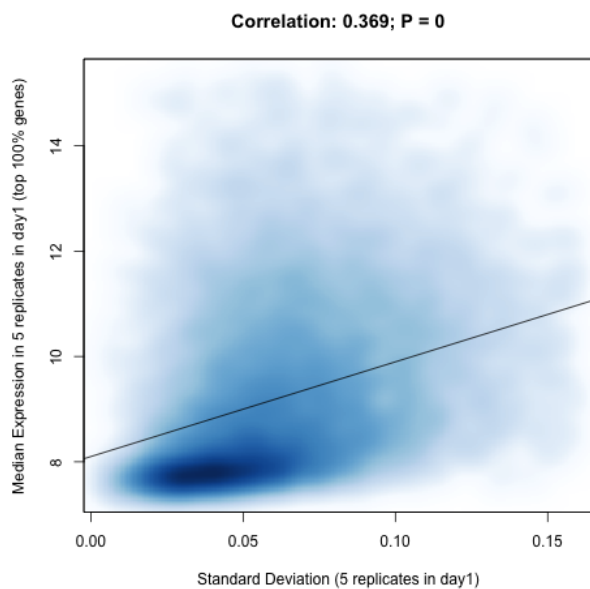


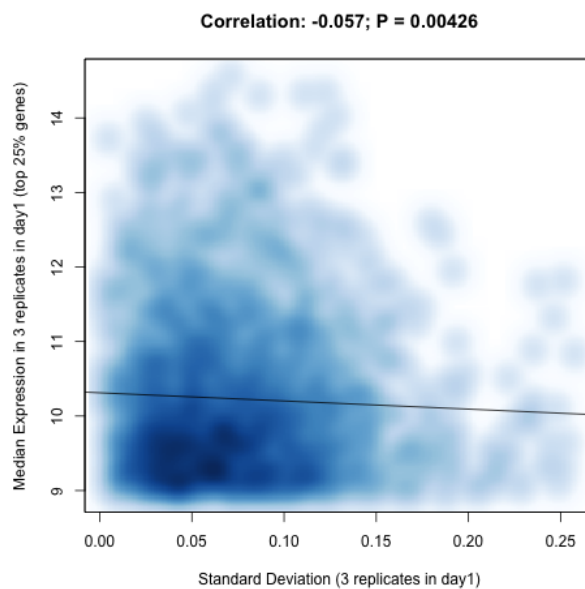
Figure A.7: Regulation of stress induced genes by miR-25, miR-143 and miR-145.

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.

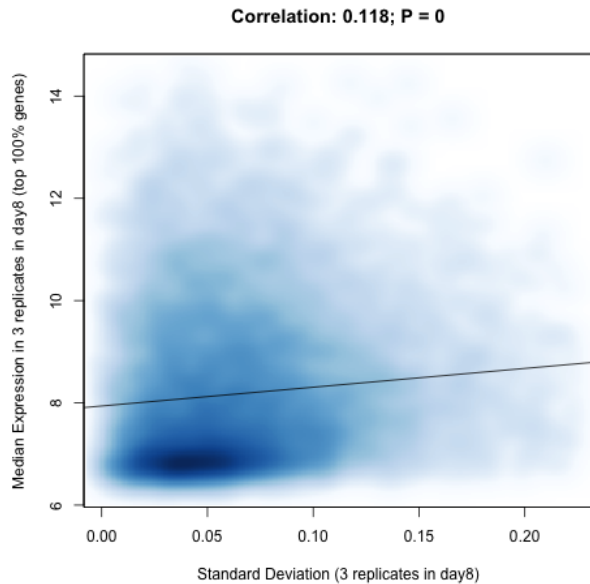
(a) HP cultures at 1DIV; 100% of genes



(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

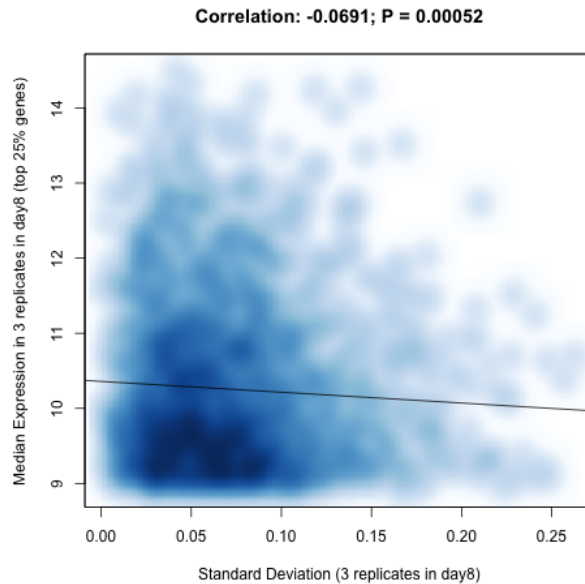
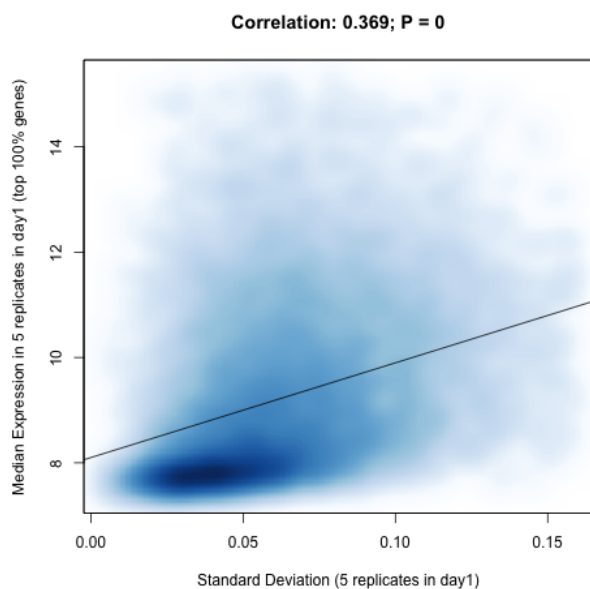
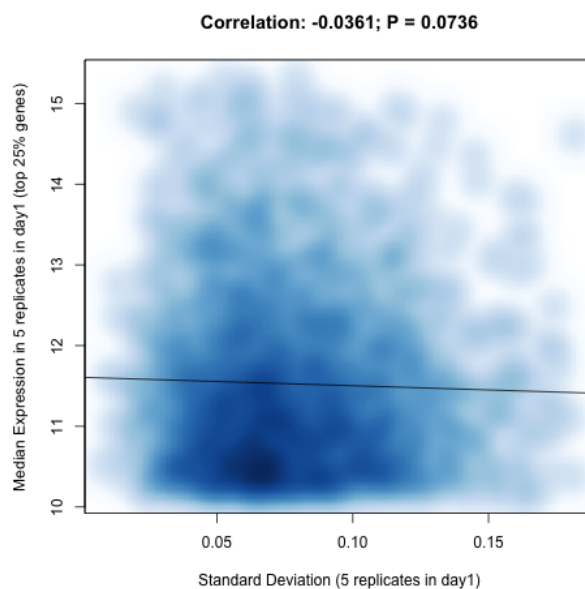


Figure A.8: Correlation of expression and standard deviation in hippocampal primary cultures.

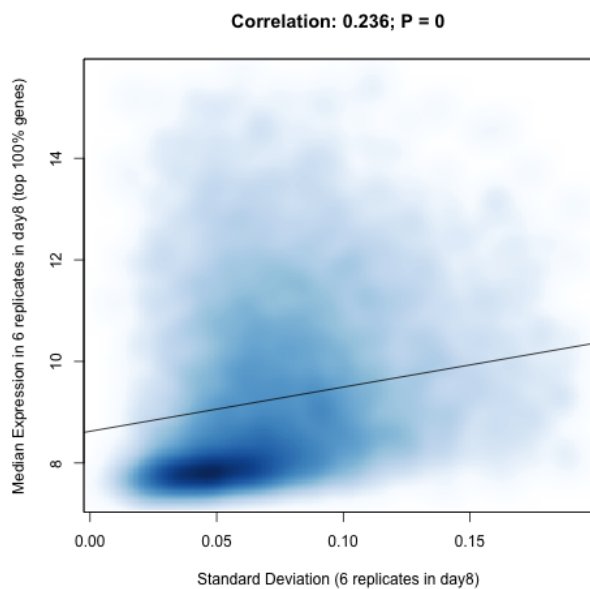
(a) FB cultures at 1DIV; 100% of genes



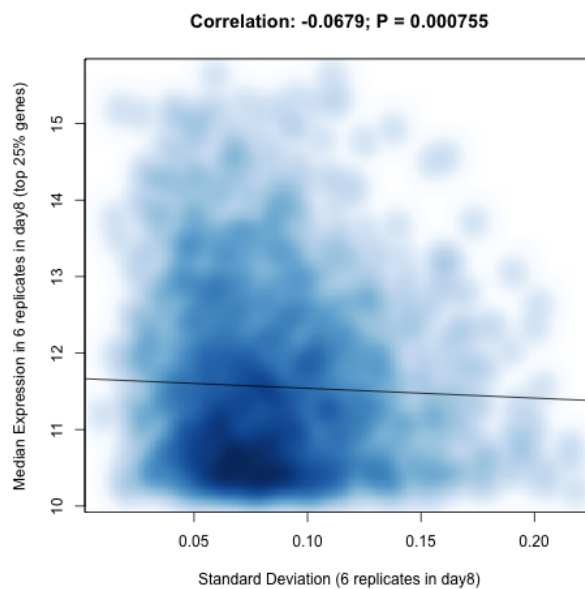
(b) FB cultures at 1DIV; top 25% of genes



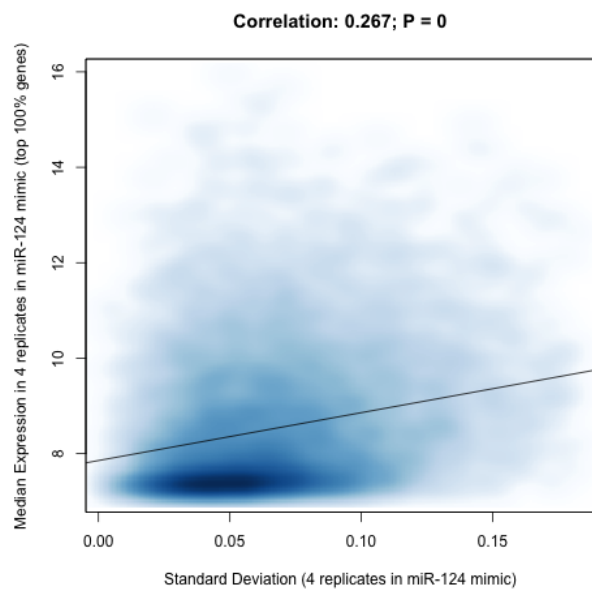
(c) FB cultures at 8DIV; 100% of genes



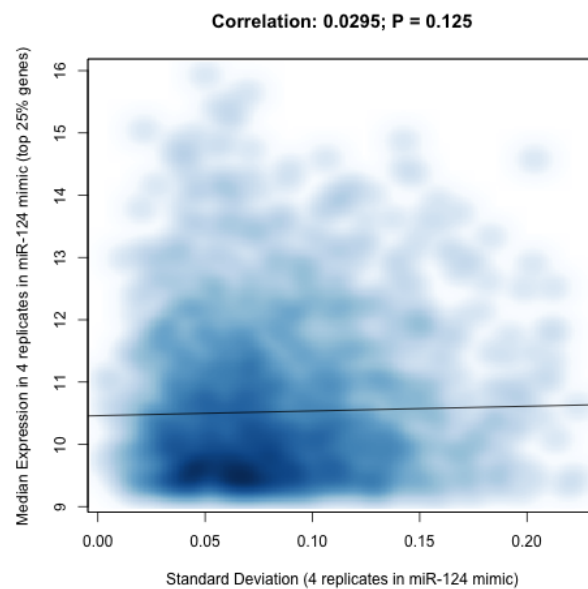
(d) FB cultures at 8DIV; top 25% of genes

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

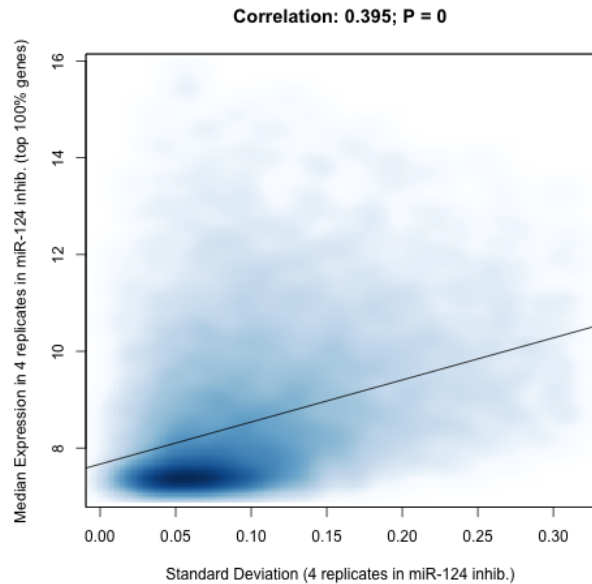
(a) Overexpression of miR-124; 100% of genes



(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

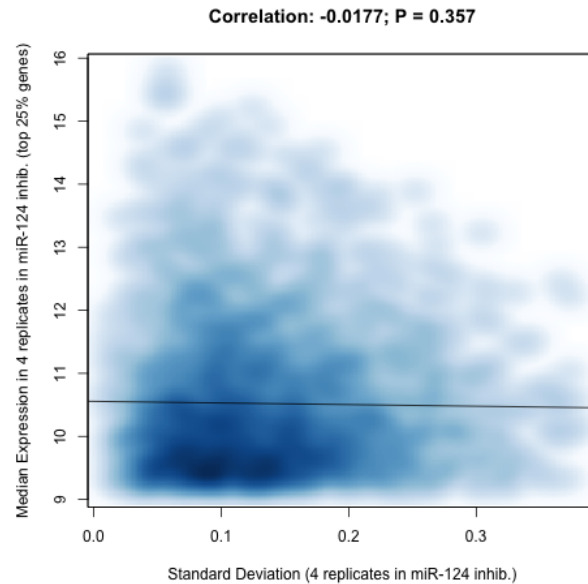
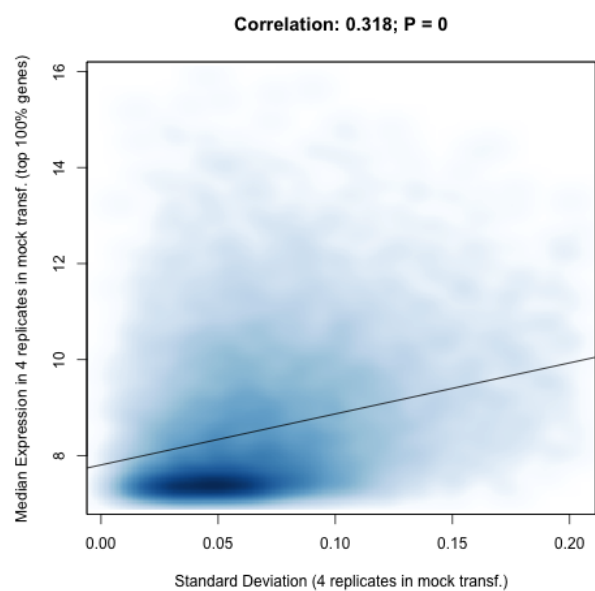
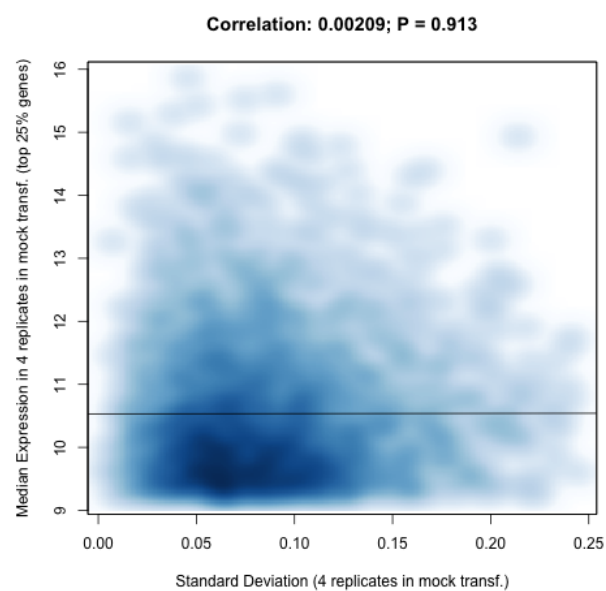


Figure A.10: Correlation of expression and standard deviation in miR-124 overexpression and inhibition.

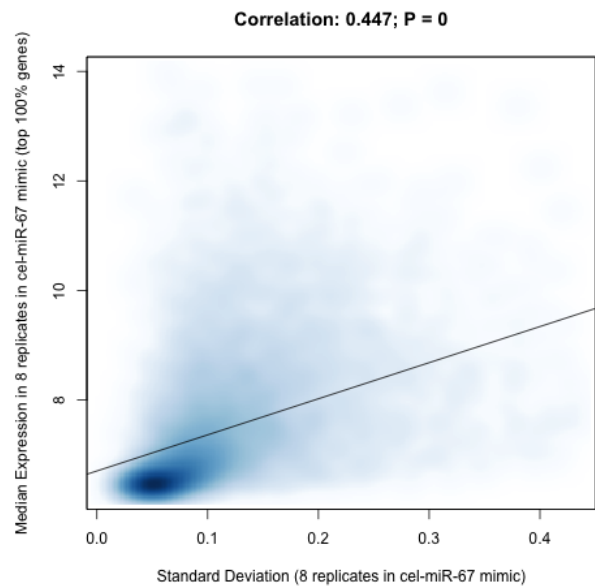
(a) mock transfection; 100% of genes



(b) mock transfection; top 25% of genes



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



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

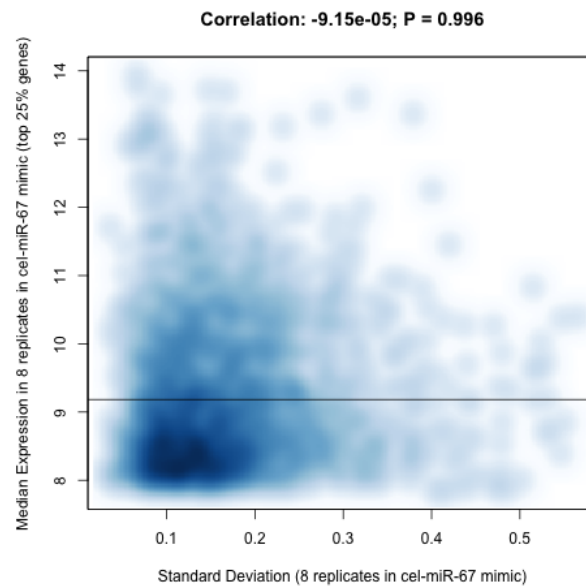


Figure A.11: Correlation of expression and standard deviation in mock transfection and cel-miR-67 overexpression.

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