

**Table S3**

## GENE ONTOLOGY ANALYSIS OF DOWN-REGULATED GENES IN THE PFC OF DA-D2RKO MICE

GO:0048167	regulation of synaptic plasticity (BP)	12	1.27E-09	9,74E-08 Sipa1l1,Htt,Atp2b2,Grin2b,Psen1,Syngap1,Mecp2,Psn2,Gipc1,Rapgef2,Grin1,Ctnnd2
GO:0007050	cell cycle arrest (BP)	20	1.68E-09	1,21E-07 Sesn2,Notch2,Tgbf2,Pkd1,Pcbp4,Stk11,Ilk,Smad3,Prml,Pkd2,Apb2,Dit3,Mll5,Wdr6,Ern1,Gas2l1,Macf1,Apc,Tcf7l2,Cdkn1b
GO:0030306	actin cytoskeleton organization (BP)	22	3.02E-09	2,13E-07 Ebp4,12l,Daam2,Olc1,Ab1,Diapl1,Sfrp1,Diap2,Fmn1,Sht1,Was2,Arhgef17,Csrp1,Epd4,15,Enah,Fgd1,Cttnbp2,Shz2b2,Srf,Taok2,Cdc42bpb,Fmn1,Parva
GO:0007389	pattern specification process (BP)	20	5.01E-09	3,31E-07 Alx4,Ptch1,Gl3,Foxo3,C2cd3,Hey2,Foxo1,Bmp7,Syngap1,Disp1,Smo,Eya1,2ic3,Fox2,Ascl1,Foxk1,Apc,Bmp1ia,Fox2,Foxn3
GO:0001666	response to hypoxia (BP)	20	1.67E-08	9,37E-07 Pygm,Tgbf2,Itpr2,Csp2,Plid2,Arrnt,Smad3,Igfb3,Prml,Ece1,Mecp2,Raf1,Egn1,Scap,Flt1,Ednra,Abat,Epas1,Nra2
GO:0016485	protein processing (BP)	13	6.44E-08	3,13E-06 Ptch1,Gl3,C2cd3,P22,Cdh1,Psen1,Aph1a,Ece1,Casp2,Ptsk6,Psen2,Furin,Adams3
GO:0001755	neural crest cell migration (BP)	11	1.52E-07	6,88E-06 Zeb2,Lef1,Mrp2,Efmb1,Sema3c,Klf1,Edn3,Sox10,Smo,Sema4f,Erb4
GO:0090090	negative regulation of canonical Wnt receptor signaling pathway (BP)	15	2,13E-07	9,52E-06 Dab2ip,Apc2,Il3,Sfrp1,Lef1,Mcc,Dab2,Wnt5a,Dit3,Sox10,Sox9,Notch1,Apc,Tcf7l2,Lrp4
GO:0043085	positive regulation of catalytic activity (BP)	11	2,18E-07	9,60E-06 P2rx7,Stk11,Atp7a,Psn1,Aph1a,Ppar,Psn2,Bgt,fzf2,Sod1,Nra42
GO:0043966	histone H3 acetylation (BP)	12	2,28E-07	9,91E-06 Myst4,Phf17,Tada3,efl1,Sap130,Map3k7,Kat2a,Brd1,Myst3,Smarda,Brfp3,Tcf3
GO:0006897	endocytosis (BP)	22	2,49E-07	1,07E-05 Rpn3,Trp53,Epn1,Syng,Ab1,Fkbp15,Snx18,Arrb2,Itsn1,Lrp10,Was2f,Lrp8,Lrp6,Usp20,Hip1,Dnm2,Ston2,Npc1,Lrp1,Ap2a1,1700021K19Rik,Lrp4
GO:0007411	organ guidance (BP)	19	2,52E-07	1,07E-05 Plxn3,Trp53,Itgb2,Robo2,Npr2,Ehfb1,Lbx2,Lmtk2,Bmp7,Wnt5a,Apbb2,L1cam,Pvr1,Sema4f,Enah,Sema6a,Dcc,Sema3f,Slt3
GO:0007612	insulin receptor signaling pathway (BP)	12	3,08E-07	1,27E-05 Foxo3,Atk1,Foxo1,Atk2,Sik2,Sorb1,Gsx3a,Zfp106,Socs7,Shz2b,Srebf1,Insr
GO:0031175	neuron projection development (BP)	16	5,16E-07	2,08E-05 Dock7,Diap1,Phghd,Lyn,Pld2,Nfg,Ptprm,Mecp2,L1cam,Ult1,Srf,Apc,Ncdn,Fgr1,Btg2,Lamb2
GO:0021915	neural tube development (BP)	10	5,43E-07	2,17E-05 Gl3,Sfrp1,Phghd,Lyn,Pld2,Nfg,Ptprm,Mecp2,L1cam,Ult1,Srf,Apc,Ncdn,Fgr1,Btg2,Lamb2
GO:0042593	glucose homeostasis (BP)	15	6,17E-07	2,40E-05 Cacna1c,Cacna1e,Ptch1,Foxo3,Akt1,Nco2,Stk11,Adra2a,Inpp5k,Crtc2,Igfbp5,Stat3,Sh2b2,Tcf7l2,Insr
GO:0035264	multicellular organism growth (BP)	14	7,02E-07	2,67E-05 Slc12a5,Ccm2,Wdtc1,Ankrd11,Bbs1,Arid5b,Frfr2,Kat2a,Smo,Apba1,Slc12a2,Tenc1,Ncoa3,Hepl
GO:0009887	organ morphogenesis (BP)	18	1,02E-06	3,63E-05 Rdh10,Notch2,Ptch1,Pdgrfa,Med1,Bmp7,Tgb3,Tbx3,gdf11,Wnt5a,Rela,Fgf2,Thra,Eya1,Slt3,Igf2,Insr
GO:0001764	neuron migration (BP)	17	1,16E-06	4,05E-05 Nrk2l,Doc,Fyn,Cels1,Psn1,Aphb1,Dab1,Frz2,Nav1,Cdc,Srf,Arx,Ascl1,A930038C07Rik,Mdg1a,Nra2a,Fktn
GO:0007626	locomotory behavior (BP)	15	2,31E-06	7,50E-05 Gng7,Cacna1c,Dlg4,Cels1,Itt,Apb7a,Atp2b2,Dscam,Nrg1,Adcy5,Astr1,Chd7,Apha1,Abat,Sod1
GO:0008360	regulation of cell shape (BP)	16	2,50E-06	7,94E-05 Epb4,1L2,Cdc42ep3,Dlc1,Ferm2,Diap1,Cyfip1,Fmn1,Fyn,Plxn1,Gna12,Palmd,Fgd1,Cdc42ep4,Gna13,Tao2,Limd1
GO:0006812	cation transport (BP)	18	2,47E-06	7,95E-05 Trpm3,Atp10a,Stm1,Grin2c,P2rx7,Atp11a,Arb1,Frz2,Nav1,Cdc,Srf,Arx,Ascl1,A930038C07Rik,Mdg1a,Nra2a,Atp2b2,Grin3a,Slc9a1,Atp13a2,Atp13a1,Grin1,Slc12a2,Grin2d
GO:0021987	cerbral cortex development (BP)	10	2,86E-06	8,67E-05 Mkks,Bbs1,Lrp6,Nr2e1,Cdn1,Ptrps,Grin1,Ascl1,Ern2
GO:0007611	learning or memory (BP)	10	2,86E-06	8,67E-05 Prkca,Grn2a,Ncam1,Htt,Shc3,Grin2b,Psn1,Psn2,Thra,Grin1
GO:0030308	negative regulation of cell growth (BP)	18	3,79E-06	0,00011185 Dab2ip,Tgb2,Sfrp1,Lef1,Adipor2,Smad3,Dab2,Fhl1,Pml,Apbb2,Gas2l1,Agt,Smarda,Adipor1,Foxk1,Slt3,Cdkn1b
GO:0043401	steroid hormone mediated signaling (BP)	12	3,96E-06	0,000117001 Lef1,Nr2f2,Rxa,Nr2c2,Nr3c2,Bmp7,Nr2e1,Ppar,Nr1d1,Rxfb,Thra,Nra42
GO:0035335	peptidyl-tyrosine dephosphorylation (BP)	16	4,01E-06	0,000117395 Shh,Dusp8,Ptprm,Cdc14a,Ptprm,Ptprn,Ptprn21,Ptnp13,Ptppg,Eya1,Dusp10,Ptprs,Ptprm,Mtrm3,Dusp22
GO:0001751	somitogenesis (BP)	11	5,30E-06	0,000149869 Zeb2,Sfrp1,Lef1,Prp6,Smad3,Psn1,Wnt5a,Psn2,Ip15,Kat2a,Bmp1a
GO:0006461	protein complex assembly (BP)	12	6,09E-06	0,000169306 Rims1,Dlg4,Llg1,Max,Pml,Mll1,Sox9,Snap23,Dlgap3,Apc,Zfp148,Tgfbr3
GO:0007268	synaptic transmission (BP)	18	6,37E-06	0,000175685 Slc12a5,Gmc4,Cacna1c,Grk2,Unc13c,Lrp6,Nrxn2,Grin2b,Stom2,Mcp2,Ip15,Grcn3,Grin5,Grin1,Apha1,Mink1,Grm2
GO:0007605	sensory perception of sound (BP)	17	6,92E-06	0,000187668 Tprn,Nipb1,Fzd4,Diap1,Gabrb3,Gi3,Cou34,Atp2b2,Sk1a3,Chd7,Otof,Gjb6,Slc12a5,Cdk1b,Grf1,Matp1a,Aqp4
GO:0000902	cell morphogenesis (BP)	12	1,12E-05	0,000279594 Shroom4,Idua,Tgbf2,Shroom1,Ssh1,P2rx7,Med1,Arhgef2,Atp2b2,Nrg1,Smarda4,Egfr
GO:0008104	protein localization (BP)	13	1,80E-05	0,000405984 Erc3,Grin2c,Tsc2,Pled3,Atk2,Meep2,Mac1,Ult1,Atk1,Atk10,Grp1,Lrb3,Doc2b,Lrp4
GO:0006874	cellular calcium ion homeostasis (BP)	13	2,13E-05	0,00048846 Cst1,Cacna1c,Prkca,Girk2,Igap2,Psen1,Krd2,Trdn,Grin1,Cherp,Grp12
GO:0042493	response to drug (BP)	18	2,39E-05	0,000520718 Slc12a5,Hda4,Sfrp1,P2rx7,Permt,Bche,Lyst,Prmr,Nraf2,Slc1a3,Npc1,Abat,Emx2,Igf2,Sod1,Tcf3,Dgr2,Alad
GO:0070588	calcium ion transmembrane transport (BP)	13	2,92E-05	0,000582578 Cacna1c,Cacna1e,Itp2,Cacng7,Atp2b2,Psn1,Cacng1,Cacnb1,Cacnb3,Ryr2,Cacna1,Grin1,Tpcn1
GO:0030336	negative regulation of cell migration (BP)	12	3,31E-05	0,000647304 Podn,Cx3cr1,Clc1,Sfrp1,Eglf7,Tiel1,Abhd2,Ptpru,Stk24,Clic1,jgfbp5,Tcf7l2,Insr
GO:0009579	embryo development (BP)	16	3,57E-05	0,000690647 Fzd2,Foxo3,Foxo1,Hit,Tgbf3,Grin2b,Psn1,Wnt5a,Notch1,Fox2,Foxk1,Foxn3,Tgfbr3
GO:0030182	neuron differentiation (BP)	13	3,97E-05	0,000746299 Brsk1,Hip2,Lhb1,Pigt,Atp2b2,Psn1,Mecp2,Edm3,Notch1,Ascl1,Emx2,Btg2,Nra42
GO:0030198	extracellular matrix organization (BP)	14	5,01E-05	0,000920981 Fn1,fbn5,Tgb2,Pdgfra,Npr1,Atp2a,Nr2e1,Abp2,Sox9,Arx,Grf2,Smarda4,A930038C07Rik,Fox2
GO:0007409	axonogenesis (BP)	14	6,52E-05	0,00114792 Brsk1,Dock7,Adcy1,Amigo1,Slc11,Kaln1,Nrng2,Ilk2,Fgr2,Sltr2,Notch1,Ult1,Apct,Ptpr1
GO:0016567	protein ubiquitination (BP)	19	6,85E-05	0,00119934 Trim23,Tnk2,cd34,Trim9,Ube2a,Akt1,Arr2,Tnfaj1,Rnf182,Rnf131,Urb4,Ube2q1,Wwp2,Smurf2,Klh13,Socs7,Mgrn1,Klh20,Herc2
GO:0006916	anti-apoptosis (BP)	18	7,60E-05	0,00129628 Vegfb,Fn1,Bag3,Dapk1,Foxo1,Hit,Tbx3,Psn1,Nrg1,Rela,Psn2,Tgfa,Axt,Ctf7l2,Tek,Sod1,Hipk3,Mkl1,Lcat,Seirin5
GO:0010976	positive regulation of neuron projection development (BP)	11	8,49E-05	0,00144025 Grn,Lyn,Cfbf2a2,Wnt5a,Ppp2rb,Sec16a,Occ,Epha3,A930038C07Rik,Ppp2rb5,Fgf1
GO:0008283	cell proliferation (BP)	20	8,73E-05	0,00147378 Crib3,Scrib,Cspg4,Crebbp,Purb,Enep,CSf1,Grm606,Pard,Nrg1,Stat3,lrp1,Kat2a,Pura,Entpd5,Furin,Tcf7l2,Egfr,Src,Mapk3k1
GO:0006629	lipid metabolic process (BP)	25	0,000102	0,00168612 Pldc3,Srebpf2,Acox3,Gm2,Plcg1,Cpt1c,Plcd4,Lrp10,Slc27a1,Adipor2,Fads1,Fads2,Plcd3,Mbtpls1,Plce1,Scap,Naa,Adipor1,Ptch2,Srebfp1,Acsf2b,Cpt1a
GO:0006914	autophagy (BP)	10	0,000157	0,00236813 Ab1,I5430411K18Rik,Stk11,Psn1,1Ulk1,Arb1,Arb2,1Ulk1,Arb3,1Ulk1,1700021K19Rik
GO:0006200	ATP catabolic process (BP)	26	0,000167	0,00245209 Errc3,Ddx17,Atp11a,1300001F03Rik,Dyn2ch1,Myo1c,Ddx21,Atp7a,Abcb1a,0610007P08Rik,Atp2b2,Upf1,Snnrp200,Smarcal1,Entpd1,Aba1,Atp1b2,Chd4,Aba2,Atp13a2,Atp13a1,Smarda4,Lonnf3,Abg1,Dync1h1
GO:0006974	response to DNA damage stimulus (BP)	30	0,000206	0,00292422 Brsk1,Erc3,Nipbl,Int3,Hubel1,Ab1,Hip2,Kat2a,Nrco4,lyn,Strai3,Foxo1,Stk11,Olcre1b,Urb5,0610007P08Rik,Obfc2b,lns80d,Psn1,Nfatc2,Hus1,Mcrs1,Alkbh3,Tao2,Apc,Gnl1,Rad9,Her2,2fye26,8tg2,H2afx
GO:0008203	cholesterol metabolic process (BP)	10	0,000398	0,0049909 Lrp5,Srebpf2,Cln6,Mbtp1s1,Abc1a,Abc2a,Scap,Abcg1,Srebfp1,Cat
GO:0007049	cell cycle (BP)	43	0,000682	0,00744729 Urgcp,Cd34,Brsk1,Nipbl,Usp2,Casp1,ck,PKmy1,Cd2ap,Stk13,Chmp1a,Pard3,Hcf1c,Anapc1,Nek6,Rassf2,Rab11b,Cdc26,Cdkn2a,2fye26,5rc,Ngc4p3,H2afx,Foxn3,Suv39h1,Klh13,Cdk16,Trp3bP2,Stard13,Chmp1a,Pard3,Hcf1c,Anapc1,Nek6,Rassf2,Rab11b,Cdc26,Cdkn2a,2fye26,5rc,Ngc4p3,H2afx,Foxn3
GO:0055114	oxidation-reduction process (BP)	48	0,000763	0,00820224 Rdh10,Mtrr,Dhhd,Kdm4a,Aldh18a1,Alkbh5,Hsd12,Sqrld,Acox3,Phgdh,Fmo1,Aldh11,1Tet1,Dhtkd1,Dio2,Moxd1,Txdncl2,Glud1,Ctbp2,Plod3,Phf2,Smox,Pcyox1,Cyp29,Cryz,Fads1,Vat1,Cy5b3r3,Fads2,Gpx8,Kdm4c,Ctbp1,Jhdm1d,Egl1,2fye26,5rc,Ncapd3,H2afx,Foxn3,Decr2,Ppox,Suxo,Cyp4f16,Kdm4b
GO:0006417	regulation of translation (BP)	12	0,000999	0,00998364 Tnrc6a,Eif2c2,Akt1,Eif4g3,Zfp361,Mknk2,Mif4gd,Pum1,Akt2,Tnrc6c,Eif2c1,Aco1

GO:0006887	exocytosis (BP)	10	0.002007	0,0161596 Rims1,Unc13a,Arfgef2,Sytl2,Unc13c,Ligl1,Scamp5,Snap23,Cadps,Srcin1
GO:0016042	lipid catabolic process (BP)	11	0.002223	0,0175101 Plcd3,Plcg1,Plcd4,Pla2g5,Pld2,Abhd4,Plcb3,Plce1,Pla2g16,Pla2g4e,Plch2
GO:0051291	protein heterooligomerization (BP)	10	0.002478	0,0179404 Casp8,Tsc2,Stk11,Ilk,Aka2,Kcnh6,Hr,Lims1,Med24,Parva
GO:0006508	proteolysis (BP)	42	0.002965	0,0206579 Sec11a,Josd1,Immp1l1,Bace1,Adamts1,Casp8,Usp2,Mmp14,Tingl1,Adam11,Dpp9,Enpep,Bmp1,Adam15,Pm20d1,Tpp1,Bap1,Adamts10,Usp20,Psen1,Usp32, Mbtsp1,Adamts9,Ece1,Casp2,3110056003Rk,Pcsk6,Mmp15,Psen2,Anpep,H13,Ctsa,Otud7a,Lmr3,Furin,Rhbd1,Capn2,Usp31,Senp1,Opcrt,Usp30,Adamts32, Kljdua,Pygm,Akt1,Bgalat2,Alh464131,Man2a2,Akt2,Gne,Gsk3a,Mlec,Gbe1,Chst1,Igf2,Phkb,Man2b2,Chi3l1
GO:0005975	carbohydrate metabolic process (BP)	17	0.004368	0,0276916 Klf1dua,Pygm,Akt1,Bgalat2,Alh464131,Man2a2,Akt2,Gne,Gsk3a,Mlec,Gbe1,Chst1,Igf2,Phkb,Man2b2,Chi3l1
GO:0007010	cytoskeleton organization (BP)	10	0.006865	0,0356599 Zmym3,Dlc1,Diap1,Svil,Raf1,Mast1,Fgd1,Limd1,Tnik,Pdzd8
GO:0032259	methylation (BP)	15	0.009204	0,0447889 Dnmt1,Aldh1l1,Prmt5,Setd2,Pemt,Ash1l,Tyms,Mll1,Mll5,Nsun3,Suv39h1,Setd1b,Nsd1,Mll2,Dnmt3a

**Table S3**

## KEGG PATHWAY ANALYSIS OF DOWN-REGULATED GENES IN THE PFC OF DA-D2RKO MICE

Kegg:02010 ABC transporters  
Kegg:04210 Apoptosis

6 0,0198174 0,0454351 Abcg4,Abca9,Abcb1a,Abca1,Abca2,Abcg1  
9 0,0205786 0,0466117 Rela,Casp8,Myd88,Ngf,Capn2,Irak2,Prkx,Akt2,Akt1