

Identification of neuron-related genes for cell therapy of neurological disorders by network analysis

Table S2 Gene ontology enrichment analysis of biological process

The enrichment score based on geometric mean (-log scale) of the P -values for the members in a corresponding annotation cluster was used to rank their biological significance. P -values were calculated using Fisher's test. FDR corrections were calculated using Benjamini-Hochberg procedure

GROUP A UP-PATTERN

Category	Term	Count	%	Genes	P-Value	FDR
GOTERM_BP_FAT	GO:0030182--neuron differentiation	112	10.4575163	GPRIN1, PLXNA3, EFNA2, RORB, L1CAM, CSPG5, KLHL1, NRCAM, ATP2B2, ANK3, UNC5A, ROBO1, SS18L1, DSCAM, STMN3, EMX1, EFNB3, MDGA1, MDGA2, KIF5C, DLL1, TBR1, CTNNA2, SLITRK2, ASCL1, SLITRK1, NCAM2, SLITRK3, FOXG1, RELN, MAPK8, STMN1, IGSF9, SLITRK5, CDK5R1, LPPR4, SOX2, SOX5, RGD1311558, EPHB1, EPHB2, ARX, CRMP1, LHX2, LHX6, OLFM3, BHLHE22, CELSR3, EVL, CELSR2, GAS7, DLX2, FEZF2, EPHA4, EPHA7, NREP, DLX1, SEMA6C, NTRK2, MAP2, CHRN2, SYNGAP1, ATL1, AGTPBP1, UCHL1, PAX6, VGF, GPC2, CASP3, DYNLL2, MAPT, DLG4, SEMA3A, DLG2, TUBB3, KCNMA1, SLIT1, PSD, SEMA4F, CNTN2, CNTN4, GAP43, DCC, RAB3A, CCK, NDN, NNAT, BRSK1, BCL11B, POU3F4, POU3F2, CD24, DCX, SNAP25, NEFL, DCLK1, DFNA5, GNAO1, PTPRZ1, CREB1, NFASC, DPYSL5, NLGN1, NTNG2, DPYSL4, ISL1, WNT7B, PPP1R9A, NEUROD2, WNT7A, APBB1, FEZ1	3.95E-41	6.99E-38
GOTERM_BP_FAT	GO:0048666--neuron development	88	8.21661998	GPRIN1, PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, RORB, CSPG5, KLHL1, NRCAM, ATP2B2, ANK3, UNC5A, DYNLL2, ROBO1, DLG4, SEMA3A, SS18L1, DLG2, DSCAM, STMN3, EFNB3, KIF5C, TBR1, SLIT1, CTNNA2, SLITRK2, NCAM2, ASCL1, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, CNTN4, MAPK8, RELN, STMN1, IGSF9, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, CRMP1, BCL11B, LHX2, LHX6, CD24, DCX, OLFM3, SNAP25, NEFL, DCLK1, GNAO1, PTPRZ1, CREB1, NFASC, NLGN1, NTNG2, CELSR3, DPYSL4, CELSR2, EVL, ISL1, GAS7, FEZF2, EPHA4, EPHA7, NREP, WNT7B, PPP1R9A, SEMA6C, NTRK2, MAP2, NEUROD2, CHRN2, SYNGAP1, APBB1, FEZ1	2.75E-33	4.85E-30
GOTERM_BP_FAT	GO:0019226--transmission of nerve impulse	78	7.28291317	SYT1, SCN3A, SYT4, CLSTN2, GABRB3, GRIK1, AGTPBP1, CLSTN3, GRIK2, GRIK3, SYT3, GRIK4, SNCA, GRIK5, NRCAM, ANK2, GRIN2B, TRIM9, CHRNA7, SHC3, DLG2, KCNMA1, GJD2, GABRG1, GABRG2, STX1A, NRXN2, NOS1AP, SCN2A1, CACNG4, PCDH8, CACNG2, PCLO, STX1B, CTNNA2, GRM5, GRM7, ABAT, ERC2, NCAN, UNC13B, RAB3A, KCNMB4, PPFIA3, CPLX1, RAB3C, CACNB4, GAD2, SYN1, SYN3, SYN2, APBA2, POU3F2, POU3F1, AGRN, CD24, SNAP25, GAD1, APBA1, GABRA3, GRIN1, GABRA5, SLC12A5, NLGN1, NLGN3, GRIA4, SLC17A7, SLC17A6, GRIA2, NPY, GRIA1, TMOD2, SPTBN2, CHRN2, SCN8A, SYNGAP1, WNT7A, CACNA1B	4.25E-32	7.51E-29
GOTERM_BP_FAT	GO:0007268--synaptic transmission	68	6.34920635	SYT1, CLSTN2, SYT4, GABRB3, GRIK1, AGTPBP1, CLSTN3, GRIK2, GRIK3, SYT3, GRIK4, SNCA, GRIK5, GRIN2B, TRIM9, CHRNA7, SHC3, DLG2, GJD2, KCNMA1, GABRG1, GABRG2, STX1A, NRXN2, NOS1AP, PCDH8, STX1B, PCLO, CTNNA2, GRM5, GRM7, ABAT, ERC2, NCAN, UNC13B, RAB3A, PPFIA3, CPLX1, RAB3C, CACNB4, GAD2, SYN1, SYN3, SYN2, APBA2, AGRN, CD24, SNAP25, GAD1, APBA1, GABRA3, GRIN1, SLC12A5, GABRA5, NLGN1, NLGN3, GRIA4, SLC17A7, SLC17A6, GRIA2, NPY, GRIA1, TMOD2, SPTBN2, CHRN2, SYNGAP1, WNT7A, CACNA1B	2.23E-31	3.94E-28
GOTERM_BP_FAT	GO:0031175--neuron projection development	75	7.00280112	GPRIN1, PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, KLHL1, NRCAM, ANK3, UNC5A, ROBO1, SEMA3A, SS18L1, DSCAM, STMN3, EFNB3, KIF5C, SLIT1, TBR1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, CNTN4, MAPK8, RELN, STMN1, IGSF9, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, BCL11B, LHX2, CD24, DCX, SNAP25, NEFL, DCLK1, GNAO1, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, CELSR2, ISL1, GAS7, FEZF2, EPHA4, EPHA7, PPP1R9A, WNT7B, NREP, SEMA6C, MAP2, CHRN2, SYNGAP1, APBB1, FEZ1	9.49E-31	1.68E-27
GOTERM_BP_FAT	GO:0030030--cell projection organization	85	7.93650794	GPRIN1, MTSS1, PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, KLHL1, NRCAM, ATP2B2, ANK3, UNC5A, ROBO1, SEMA3A, SS18L1, DSCAM, STMN3, EFNB3, KIF5C, SLIT1, VANGL2, KIF5C, TBR1, SLIT1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, CNTN4, MAPK8, RELN, STMN1, IGSF9, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, BCL11B, LHX2, TTYH1, CD24, DCX, SNAP25, NEFL, DCLK1, FGD4, DN33, VAV3, GNAO1, KIF3A, PTPRZ1, CREB1, NFASC, NTNG2, CELSR3, EVL, CELSR2, ISL1, GAS7, FEZF2, EPHA4, EPHA7, CORO1A, NREP, WNT7B, PPP1R9A, SEMA6C, MAP2, TSGA10, CHRN2, SYNGAP1, APBB1, FEZ1	1.23E-29	2.17E-26
GOTERM_BP_FAT	GO:0007409--axonogenesis	59	5.50887021	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ANK3, ROBO1, UNC5A, SEMA3A, EFNB3, KIF5C, SLIT1, TBR1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, LHX2, BCL11B, DCX, SNAP25, NEFL, DCLK1, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, ISL1, FEZF2, EPHA4, EPHA7, NREP, SEMA6C, CHRN2, APBB1, FEZ1	9.28E-28	1.64E-24
GOTERM_BP_FAT	GO:0048667--cell morphogenesis involved in neuron differentiation	62	5.78898226	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ATP2B2, ANK3, ROBO1, UNC5A, SEMA3A, DSCAM, EFNB3, KIF5C, SLIT1, TBR1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, LHX2, BCL11B, DCX, SNAP25, NEFL, DCLK1, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, CELSR2, ISL1, FEZF2, EPHA4, EPHA7, NREP, SEMA6C, CHRN2, APBB1, FEZ1	1.22E-27	2.15E-24
GOTERM_BP_FAT	GO:0048812--neuron projection morphogenesis	63	5.88235294	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ANK3, ROBO1, UNC5A, SEMA3A, DSCAM, EFNB3, KIF5C, SLIT1, TBR1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, BCL11B, LHX2, DCX, SNAP25, NEFL, DCLK1, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, CELSR2, ISL1, GAS7, FEZF2, EPHA4, EPHA7, WNT7B, NREP, SEMA6C, CHRN2, APBB1, FEZ1	1.67E-27	2.96E-24
GOTERM_BP_FAT	GO:0007267--cell-cell signaling	78	7.28291317	SYT1, CLSTN2, SYT4, GABRB3, GRIK1, AGTPBP1, CLSTN3, GRIK2, GRIK3, SYT3, GRIK4, SNCA, GRIK5, FGF12, VGF, GRIN2B, TRIM9, CHRNA7, SHC3, DLG2, KCNMA1, GJD2, GABRG1, GABRG2, STX1A, NRXN2, NOS1AP, PCDH8, PCLO, STX1B, CTNNA2, GRM5, GRM7, ABAT, ERC2, NCAN, UNC13B, RAB3A, PPFIA3, CPLX1, RAB3C, PANX1, SOX2, CACNB4, RIMS2, EPHB1, GAD2, SYN1, SYN3, SYN2, APBA2, AGRN, CD24, SNAP25, GAD1, APBA1, DLGAP1, GABRA3, GRIN1, GABRA5, SLC12A5, NLGN1, NLGN3, GRIA4, SLC17A7, SLC17A6, GRIA2, NPY, GRIA1, SALL1, NTRK2, TMOD2, SPTBN2, CHRN2, SYNGAP1, WNT7A, SMPD3, CACNA1B	2.74E-27	4.84E-24

GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	65	6.0690943	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ANK3, ROBO1, UNC5A, SEMA3A, DSCAM, EFN3, KIF5C, VANG2, SLIT1, TBR1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, BCL11B, LHX2, DCX, SNAP25, NEFL, DCLK1, KIF3A, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, CELSR2, ISL1, GAS7, FEZF2, EPHA4, EPHA7, WNT7B, NREP, SEMA6C, CHRN2, APBB1, FEZ1	1.79E-26	3.16E-23
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	65	6.0690943	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ANK3, ROBO1, UNC5A, SEMA3A, DSCAM, EFN3, KIF5C, VANG2, SLIT1, TBR1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, BCL11B, LHX2, DCX, SNAP25, NEFL, DCLK1, KIF3A, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, CELSR2, ISL1, GAS7, FEZF2, EPHA4, EPHA7, WNT7B, NREP, SEMA6C, CHRN2, APBB1, FEZ1	2.18E-25	3.85E-22
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	63	5.88235294	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ATP2B2, ANK3, ROBO1, UNC5A, SEMA3A, DSCAM, EFN3, KIF5C, SLIT1, PROX1, TBR1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, SEMA4F, FOXG1, CNTN2, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, CDK5R1, LPPR4, CCK, NDN, RGD1311558, EPHB1, EPHB2, ARX, BCL11B, LHX2, DCX, SNAP25, NEFL, DCLK1, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, CELSR2, ISL1, FEZF2, EPHA4, EPHA7, NREP, SEMA6C, CHRN2, APBB1, FEZ1	1.94E-24	3.43E-21
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	71	6.62931839	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ATP2B2, ANK3, ROBO1, UNC5A, SEMA3A, DSCAM, EFN3, VANG2, KIF5C, TBR1, SLIT1, PROX1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, HMGIL1, SEMA4F, LOC685520, FOXG1, CNTN2, RGD1563668, LOC680968, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, HMG1B, CDK5R1, LPPR4, CCK, NDN, RGD1311558, BRSK1, EPHB1, EPHB2, ARX, BCL11B, LHX2, CLASP2, DCX, SNAP25, NEFL, DCLK1, KIF3A, PTPRZ1, CREB1, NFASC, CELSR3, NTNG2, EVL, CELSR2, ISL1, GAS7, FEZF2, EPHA4, EPHA7, NREP, WNT7B, SYNE2, SEMA6C, CHRN2, APBB1, FEZ1, LOC690940	1.57E-21	2.78E-18
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	73	6.81605976	PLXNA3, ATL1, EFNA2, UCHL1, PAX6, L1CAM, CSPG5, NRCAM, ATP2B2, ANK2, ANK3, UNC5A, ROBO1, SEMA3A, DSCAM, EFN3, VANG2, KIF5C, TBR1, SLIT1, PROX1, CTNNA2, SLITRK2, NCAM2, SLITRK1, SLITRK3, HMGIL1, SEMA4F, LOC685520, FOXG1, CNTN2, RGD1563668, LOC680968, RELN, STMN1, SLITRK5, GAP43, DCC, RAB3A, HMG1B, CDK5R1, LPPR4, CCK, NDN, RGD1311558, BRSK1, EPHB1, EPHB2, ARX, BCL11B, LHX2, CLASP2, DCX, SNAP25, NEFL, DCLK1, KIF3A, PTPRZ1, CREB1, NFASC, NTNG2, CELSR3, EVL, CELSR2, ISL1, GAS7, FEZF2, EPHA4, EPHA7, NREP, WNT7B, SYNE2, SEMA6C, CHN2, CHRN2, APBB1, FEZ1, LOC690940	3.19E-20	5.64E-17
GOTERM_BP_FAT	GO:0006836~neurotransmitter transport	34	3.17460317	PPFIA3, SYT1, RAB3A, RAB3C, CPLX1, SYT4, SLC6A1, SYT3, RIMS2, RIMS1, SLC32A1, SLC1A2, SYN1, TRIM9, SYN3, SYN2, APBA2, SV2A, SNAP25, APBA1, STX1A, NOS1AP, NRXN2, SLC6A11, NLGN1, PCLO, STX1B, SLC17A7, SLC17A6, SPTBN2, ERC2, WNT7A, UNC13B, CACNA1B	3.87E-17	6.83E-14
GOTERM_BP_FAT	GO:0001505~regulation of neurotransmitter levels	30	2.80112045	SYT1, RAB3A, PPFIA3, CPLX1, RAB3C, SYT4, AGTPBP1, SYT3, GAD2, SYN1, TRIM9, SYN3, SYN2, APBA2, SNAP25, GAD1, APBA1, STX1A, NOS1AP, NRXN2, NLGN1, PCLO, SLC17A7, SLC17A6, SPTBN2, ABAT, ERC2, WNT7A, UNC13B, CACNA1B	9.23E-16	1.57E-12
GOTERM_BP_FAT	GO:0007269~neurotransmitter secretion	24	2.24089636	PPFIA3, RAB3A, SYT1, STX1A, CPLX1, RAB3C, NOS1AP, SYT4, NRXN2, SYT3, NLGN1, PCLO, SYN1, TRIM9, SYN3, SYN2, SPTBN2, APBA2, ERC2, SNAP25, WNT7A, UNC13B, APBA1, CACNA1B	1.54E-15	2.75E-12
GOTERM_BP_FAT	GO:0007610~behavior	70	6.53594771	PLXNA3, ADCY1, SLC6A1, GRIK1, ADCY8, HMGCR, GRIK2, UCHL1, SNCA, ZIC1, CALB1, KLHL1, PRKAR2B, ATP2B2, SLC1A2, CASP3, GRIN2B, CHST10, ROBO1, SLC24A2, CHRNA7, SEMA3A, SHC3, PLCB1, DSCAM, GNG7, KCNMA1, GABRG2, EFN3, PCDH8, NTSR1, GRM5, GRM7, ABAT, RELN, TSHR, PRKCZ, CCK, CTNND2, ASTN1, CACNA8, KIT, EPHB2, NPAS3, PTN, APBA2, STRBP, SNAP25, APBA1, SCG2, GNAO1, GRIN1, GABRA5, ATP1A3, NLGN3, NPY1R, FEZF2, EPHA4, CORO1A, NPY, GRIA1, PRKAR1B, NTRK2, TMOD2, NEUROD2, CHRN2, SCN8A, SYNGAP1, APBB1, CACNA1B	1.95E-15	3.53E-12
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	41	3.82819795	PPFIA3, PRKCZ, RAB3A, SNCAIP, GRIK1, ERBB4, SLC6A1, GNAI1, GRIK2, GRIK3, SNCA, CTNND2, GRIK5, BCAN, CSPG5, KIT, VGF, RIMS1, CALB1, EPHB2, SYP, ATP2B2, GRIN2B, SLC24A2, SYN2, DLG4, CHRNA7, STX1A, GRIN1, NLGN1, NLGN3, GRIA4, CACNA2D2, GRM5, GRM3, GRIA2, GRIA1, NTRK2, CHRN2, SYNGAP1, CACNA1B	3.24E-15	5.70E-12
GOTERM_BP_FAT	GO:0007411~axon guidance	32	2.98786181	DCC, CDK5R1, PLXNA3, EFNA2, PAX6, L1CAM, EPHB1, EPHB2, NRCAM, ARX, ANK3, UNC5A, ROBO1, LHX2, SEMA3A, EFN3, KIF5C, NFASC, EVL, ISL1, TBR1, SLIT1, EPHA4, FEZF2, EPHA7, SEMA6C, SEMA4F, FOXG1, RELN, APBB1, GAP43, FEZ1	1.32E-14	2.34E-11
GOTERM_BP_FAT	GO:0006811~ion transport	91	8.49673203	KCNK1, SCN3A, GABRB3, GRIK1, ATP1B2, GRIK2, SCN3B, GABRB2, GRIK3, GABRB1, GRIK4, GLRA2, GRIK5, KCNIP1, KCNK10, ATP2B2, SLC1A2, KCNQ3, KCNK9, GRIN2B, SLC24A2, CHRNA7, SLC25A1, KCNQ2, ATP5I, SLC1A1, GRID1, KCNMA1, GABRG1, TRPM3, GABRG2, SVOP, KCND2, SCN2B, CACNG7, SLC22A23, SCN2A1, CACNG5, CACNG4, CACNG3, CACNG2, PRKCB, RYR3, KCNH7, KCNH8, ADD2, KCNH5, KCNMB4, CLCN3, PANX1, KCNA6, ATP6V1G2, CACNB4, KCNJ2, KCNRG, KCNJ3, FXYPD6, TTYH1, SLC4A8, CAMK2B, HCN3, HCN1, TRPC4, GABRA2, GABRA1, GABRA4, TRPC5, GABRA3, KCNB1, GRIN1, GABRA5, SLC12A5, ATP1A3, SLC10A4, GRIA4, CACNA2D3, CACNA2D2, SLC17A7, CORO1A, SLC4A10, SLC17A6, KCNJ6, GRIA2, GRIA1, KCNN3, KCNN2, CACNA1H, CACNA1E, CHRN2, SCN8A, CACNA1B	1.32E-14	2.34E-11
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	43	4.01493931	PPFIA3, PRKCZ, RAB3A, SNCAIP, CCK, GRIK1, ERBB4, SLC6A1, GNAI1, GRIK2, GRIK3, SNCA, CTNND2, GRIK5, BCAN, CSPG5, KIT, VGF, RIMS1, CALB1, EPHB2, SYP, ATP2B2, GRIN2B, SLC24A2, SYN2, DLG4, CHRNA7, STX1A, NOS1, GRIN1, NLGN1, NLGN3, GRIA4, CACNA2D2, GRM5, GRM3, GRIA2, GRIA1, NTRK2, CHRN2, SYNGAP1, CACNA1B	1.43E-14	2.51E-11
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	41	3.82819795	PPFIA3, PRKCZ, RAB3A, SNCAIP, GRIK1, ERBB4, SLC6A1, GNAI1, GRIK2, GRIK3, SNCA, CTNND2, GRIK5, BCAN, CSPG5, KIT, VGF, RIMS1, CALB1, EPHB2, SYP, ATP2B2, GRIN2B, SLC24A2, SYN2, DLG4, CHRNA7, STX1A, GRIN1, NLGN1, NLGN3, GRIA4, CACNA2D2, GRM5, GRM3, GRIA2, GRIA1, NTRK2, CHRN2, SYNGAP1, CACNA1B	3.35E-14	5.93E-11
GOTERM_BP_FAT	GO:0006928~cell motion	66	6.16246499	PLXNA3, PLXNA2, EFNA2, SORL1, PAX6, L1CAM, NRCAM, DAB1, ANK3, ROBO1, UNC5A, CHRNA7, SEMA3A, LOC300308, NR2F1, SATB2, EFN3, MDGA1, KIF5C, SLIT1, TBR1, CTNNA2, ASCL1, RGD1564409, SEMA4F, FOXG1, CNTN2, RELN, GAP43, DCC, SHROOM2, CDK5R1, CCK, NDN, ASTN1, KITLG, KIT, EPHB1, EPHB2, ARX, VCAM1, LHX2, POU3F3, LHX6, POU3F2, RGD1566251, STRBP, CLASP2, CD24, DCX, DCLK1, SCG2, VAV3, PODXL, NFASC, EVL, ISL1, FEZF2, EPHA4, EPHA7, CORO1A, SEMA6C, SYNE2, RGD1565071, LRP8, APBB1, FEZ1	9.75E-14	1.72E-10

GOTERM_BP_FAT	GO:0007611~learning or memory	33	3.08123249	PRKCZ, ADCY1, SLC6A1, HMGCR, ADCY8, CTNND2, KIT, CALB1, EPHB2, PRKAR2B, CASP3, CHST10, GRIN2B, SLC24A2, PTN, CHRNA7, PLCB1, SHC3, SNAP25, GRIN1, GABRA5, ATP1A3, NLGN3, PCDH8, GRM5, GRIA1, PRKAR1B, GRM7, TMOD2, NEUROD2, CHRN2, SYNGAP1, APBB1	1.99E-12	3.53E-09
GOTERM_BP_FAT	GO:0003001~generation of a signal involved in cell-cell signal	29	2.70774977	SYT1, RAB3A, PPFIA3, CPLX1, RAB3C, SYT4, SYT3, CACNB4, RIMS2, VGF, SYN1, TRIM9, SYN3, SYN2, APBA2, SNAP25, APBA1, STX1A, NOS1AP, NRXN2, NLGN1, PCLO, NTRK2, SPTBN2, ERC2, WNT7A, UNC13B, SMPD3, CACNA1B	6.68E-12	1.18E-08
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	41	3.82819795	PLXNA3, SOX2, SOX5, BEX1, PAX6, LRRC4C, KIT, EPHB2, ROBO1, TIAM1, MAPT, POU3F2, SEMA3A, CD24, NEFL, ACSL6, NEFM, LIMK1, GRIN1, NLGN1, DLL3, DLL1, DPYSL2, ISL1, RUFY3, GRM5, ASCL1, DLX2, DLX1, NREP, SEMA4F, FOXG1, NTRK2, RGS6, NEUROD1, CHRN2, PBX1, CNTN4, SEMA4D, SYNGAP1, WNT7A	8.71E-12	1.54E-08
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	43	4.01493931	PLXNA3, SOX2, SOX5, BEX1, PAX6, LRRC4C, KIT, EPHB2, ROBO1, TIAM1, MAPT, POU3F2, SEMA3A, AGRN, CD24, SNAP25, NEFL, ACSL6, NEFM, LIMK1, GRIN1, NLGN1, DLL3, DLL1, DPYSL2, ISL1, RUFY3, GRM5, ASCL1, DLX2, DLX1, NREP, SEMA4F, FOXG1, NTRK2, RGS6, NEUROD1, CHRN2, PBX1, CNTN4, SEMA4D, SYNGAP1, WNT7A	1.33E-11	2.35E-08
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	36	3.36134454	PLXNA3, SOX2, SOX5, BEX1, PAX6, LRRC4C, EPHB2, ROBO1, TIAM1, MAPT, POU3F2, SEMA3A, CD24, NEFL, ACSL6, NEFM, LIMK1, GRIN1, NLGN1, DLL1, DPYSL2, ISL1, RUFY3, ASCL1, NREP, SEMA4F, FOXG1, NTRK2, RGS6, NEUROD1, CHRN2, PBX1, CNTN4, SEMA4D, SYNGAP1, WNT7A	1.64E-11	2.91E-08
GOTERM_BP_FAT	GO:0044057~regulation of system process	52	4.85527544	THRA, SNCAIP, SLC6A1, GRIK1, GRIK2, GRIK3, SNCA, GRIK5, BCAN, CSPG5, VGF, CALB1, SYP, ATP2B2, GRIN2B, SLC24A2, DLG4, GUCY1A3, CHRNA7, SEMA3A, KCNMA1, STX1A, GRM5, GRM3, SSTR2, PPFIA3, PRKCZ, RAB3A, CCK, ERBB4, GNAI1, CTNND2, KIT, RIMS1, EPHB2, ARG2, SYN2, NOS1, GNAO1, GRIN1, NLGN1, CTNNG3, GRIA4, NPY1R, CACNA2D2, GRIA2, GRIA1, SP4, NTRK2, CHRN2, SYNGAP1, CACNA1B	2.15E-11	3.81E-08
GOTERM_BP_FAT	GO:0060284~regulation of cell development	43	4.01493931	PLXNA3, SOX2, SOX5, BEX1, PAX6, LRRC4C, KIT, EPHB2, ROBO1, TIAM1, MAPT, POU3F2, SEMA3A, AGRN, CD24, NEFL, ACSL6, NEFM, LIMK1, GRIN1, NLGN1, DLL3, DLL1, DPYSL2, ISL1, PROX1, RUFY3, GRM5, ASCL1, DLX2, DLX1, NREP, SEMA4F, FOXG1, NTRK2, RGS6, NEUROD1, CHRN2, PBX1, CNTN4, SEMA4D, SYNGAP1, WNT7A	3.19E-11	5.63E-08
GOTERM_BP_FAT	GO:0030001~metal ion transport	58	5.41549953	KCNK1, SCN3A, SCN3B, ATP1B2, KCNIP1, KCNK10, ATP2B2, KCNK9, KCNQ3, GRIN2B, SLC24A2, CHRNA7, KCNQ2, KCNMA1, KCND2, SCN2B, CACNG7, SCN2A1, CACNG5, CACNG4, CACNG3, CACNG2, PRKCB, RYR3, KCNH7, KCNH8, KCNH5, KCNMB4, KCNA6, CACNB4, KCNJ2, KCNRG, KCNJ3, SLC4A8, CAMK2B, HCN3, HCN1, TRPC4, TRPC5, KCNB1, SLC12A5, GRIN1, ATP1A3, SLC10A4, CACNA2D3, CACNA2D2, SLC17A7, CORO1A, SLC4A10, KCNJ6, SLC17A6, KCNN3, KCNN2, CACNA1H, CHRN2, CACNA1E, SCN8A, CACNA1B	2.03E-10	3.60E-07
GOTERM_BP_FAT	GO:0007612~learning	22	2.054155	SLC6A1, HMGCR, GRIN1, GABRA5, ATP1A3, CTNND2, NLGN3, KIT, EPHB2, GRM5, PRKAR2B, CHST10, GRIN2B, SLC24A2, GRM7, NEUROD2, PTN, CHRNA7, CHRN2, SYNGAP1, PLCB1, APBB1	3.25E-10	5.75E-07
GOTERM_BP_FAT	GO:0048489~synaptic vesicle transport	16	1.49393091	RAB3A, SYT1, STX1A, CPLX1, SYT3, SNCA, NLGN1, PCLO, TRIM9, SPTBN2, DLG4, APBA2, CD24, UNC13B, SH3GL2, APBA1	3.39E-09	5.99E-06
GOTERM_BP_FAT	GO:0030900~forebrain development	32	2.98786181	PLXNA3, ERBB4, EFNA2, SOX2, PAX6, BCAN, ARX, CASP3, SLC1A2, DAB1, LHX2, POU3F4, POU3F3, LHX6, POU3F2, DCLK1, NR2F1, GNAO1, EMX1, CREB1, GRIN1, ISL1, FEZF2, DLX2, ASCL1, DLX1, FOXG1, RELN, CHRN2, LRP8, FABP7, NFIB	6.36E-09	1.12E-05
GOTERM_BP_FAT	GO:0006812~cation transport	62	5.78898226	KCNK1, SCN3A, SCN3B, ATP1B2, KCNIP1, KCNK10, ATP2B2, KCNK9, KCNQ3, GRIN2B, SLC24A2, CHRNA7, ATP5I, KCNQ2, KCNMA1, TRPM3, KCND2, SCN2B, CACNG7, SCN2A1, CACNG5, CACNG4, CACNG3, CACNG2, PRKCB, RYR3, KCNH7, KCNH8, KCNH5, KCNMB4, PANX1, KCNA6, ATP6V1G2, CACNB4, KCNJ2, KCNRG, KCNJ3, SLC4A8, CAMK2B, HCN3, HCN1, TRPC4, TRPC5, KCNB1, SLC12A5, GRIN1, ATP1A3, SLC10A4, CACNA2D3, CACNA2D2, SLC17A7, CORO1A, SLC4A10, KCNJ6, SLC17A6, KCNN3, KCNN2, CACNA1H, CHRN2, CACNA1E, SCN8A, CACNA1B	9.05E-09	1.60E-05
GOTERM_BP_FAT	GO:0021537~telencephalon development	21	1.96078431	PLXNA3, EMX1, ERBB4, EFNA2, GRIN1, SOX2, PAX6, BCAN, ARX, DLX2, ASCL1, CASP3, SLC1A2, DLX1, DAB1, LHX2, POU3F3, RELN, LHX6, LRP8, POU3F2	1.63E-08	2.88E-05
GOTERM_BP_FAT	GO:0051046~regulation of secretion	39	3.64145658	SYT1, RAB3A, RAB3B, SNCAIP, RAB3C, GRIK1, PANX1, GNAI1, PFKFB2, SNCA, NNAT, GRIK5, SYT7, RIMS1, GRIN2B, TRIM9, PDE1C, SYN2, CHRNA7, PDE8B, SCG5, SNAP25, STX1A, NOS1, CREB1, NPY1R, PFKM, ISL1, STX1B, PCLO, PRKCB, CADPS, GRM7, GIPR, NTRK2, SPTBN2, CHRN2, APBB1, CACNA1B	1.93E-08	3.42E-05
GOTERM_BP_FAT	GO:0007214~gamma-aminobutyric acid signaling pathway	11	1.0270775	GABRG1, GABRG2, GABRA2, GABRA1, GABRA4, GABRA3, GABRB2, GABRB1, GABRA5, GABBR2, CACNB4	2.15E-08	3.81E-05
GOTERM_BP_FAT	GO:0007155~cell adhesion	58	5.41549953	CADM3, THRA, CADM4, CLSTN2, OPCML, CLSTN3, NELL2, BCAN, L1CAM, CXADR, NRCAM, DAB1, ROBO1, NEGR1, LOC690826, NRXN2, CNTN5, NRXN3, PCDH11X, PCDH9, PTPRS, PCDH8, NRXN1, CTNNA2, NCAM2, GPR56, CNTN2, CNTN1, RELN, CNTN4, CNTN3, NCAN, CDK5R1, CTNND2, ASTN1, DSCAML1, KITLG, PCDHB12, CDH4, DCHS1, CDH8, VCAM1, CDH7, CDH9, TNR, TTYH1, CD24, FLRT3, PCDH10, NFASC, NLGN1, CELSR3, NLGN3, CELSR2, PCDH17, CORO1A, WNT7B, CDH10	3.64E-08	6.43E-05
GOTERM_BP_FAT	GO:0022610~biological adhesion	58	5.41549953	CADM3, THRA, CADM4, CLSTN2, OPCML, CLSTN3, NELL2, BCAN, L1CAM, CXADR, NRCAM, DAB1, ROBO1, NEGR1, LOC690826, NRXN2, CNTN5, NRXN3, PCDH11X, PCDH9, PTPRS, PCDH8, NRXN1, CTNNA2, NCAM2, GPR56, CNTN2, CNTN1, RELN, CNTN4, CNTN3, NCAN, CDK5R1, CTNND2, ASTN1, DSCAML1, KITLG, PCDHB12, CDH4, DCHS1, CDH8, VCAM1, CDH7, CDH9, TNR, TTYH1, CD24, FLRT3, PCDH10, NFASC, NLGN1, CELSR3, NLGN3, CELSR2, PCDH17, CORO1A, WNT7B, CDH10	3.64E-08	6.43E-05
GOTERM_BP_FAT	GO:0021543~pallium development	17	1.58730159	PLXNA3, EMX1, GRIN1, SOX2, PAX6, BCAN, ARX, DLX2, ASCL1, CASP3, DLX1, DAB1, POU3F3, RELN, LHX6, POU3F2, LRP8	4.41E-08	7.79E-05
GOTERM_BP_FAT	GO:0016079~synaptic vesicle exocytosis	12	1.12044818	SYT1, RAB3A, STX1A, CPLX1, TRIM9, SYT3, NLGN1, SPTBN2, APBA2, UNC13B, PCLO, APBA1	4.51E-08	7.97E-05
GOTERM_BP_FAT	GO:0008038~neuron recognition	10	0.93370682	FEZF2, NCAM2, CDK5R1, NDN, EFN3, DYNLL2, FOXG1, CELSR3, SEMA3A, GAP43	5.23E-08	9.25E-05
GOTERM_BP_FAT	GO:0050808~synapse organization	16	1.49393091	DNM3, NRXN2, ERBB4, GLRA2, NFASC, NLGN1, NLGN3, CACNG2, CACNB4, CACNA2D2, ATP2B2, WNT7B, ANK3, AGRN, ERC2, WNT7A	9.92E-08	1.75E-04
GOTERM_BP_FAT	GO:0048167~regulation of synaptic plasticity	20	1.86741363	PPFIA3, GRIK1, GRIK2, GRIN1, SNCA, CTNND2, BCAN, KIT, VGF, CALB1, RIMS1, EPHB2, SYP, GRM5, ATP2B2, GRIN2B, GRIA1, SLC24A2, DLG4, SYNGAP1	1.12E-07	1.99E-04
GOTERM_BP_FAT	GO:0050770~regulation of axonogenesis	18	1.68067227	PLXNA3, LIMK1, GRIN1, DPYSL2, LRRC4C, RUFY3, EPHB2, ROBO1, TIAM1, SEMA4F, MAPT, POU3F2, SEMA3A, SEMA4D, SYNGAP1, NEFL, WNT7A, NEFM	1.94E-07	3.44E-04

GOTERM_BP_FAT	GO:007242--intracellular signaling cascade	92	8.59010271	GNAZ, ADCY1, NRG3, ADCY8, FGF13, MCF2L, PRKAR2B, CASP3, DAB1, EIF4EBP2, TIAM1, PAK3, GUCY1A2, RAPGEF5, GUCY1A3, CHRNA7, GNG3, PLCB1, SHC3, AGAP2, MAP2K6, GNG7, BCR, MAGI2, CAMK1G, STMN3, STMN2, MADD, PIK3C2B, STMN4, RXRG, SOCS7, ARHGEF9, PRKCE, PCLO, MARK1, PRKCB, DAPK1, ARL3, GRM5, RND2, GNAL, MAST1, SSTR2, GRM7, GIPR, ASB1, PDE9A, MAPK8, STMN1, TSHR, UNC13B, RAB3A, PRKCZ, RALGPS2, RAB3B, RAB3C, GNAI1, ADCYAP1R1, BRSK2, BRSK1, KIT, RIMS2, NECAB2, ADAP1, PLCL2, PLCL1, DGKB, SAFB, DCLK2, DCX, SCG2, FGD4, VAV3, LRRN3, DGKI, MAPK10, RALGDS, SHANK3, WNT7B, CNIH2, NPY, PRKAR1B, RGS6, MAPK8IP2, CHN2, RGS7, NEUROD1, RIT2, MAPK8IP1, SYNGAP1, SMC1A	2.12E-07	3.75E-04
GOTERM_BP_FAT	GO:0010975--regulation of neuron projection development	21	1.96078431	PLXNA3, LIMK1, GRIN1, DPYSL2, LRRC4C, RUFY3, EPHB2, ROBO1, TIAM1, SEMA4F, MAPT, NTRK2, CHRN2, POU3F2, SEMA3A, SEMA4D, SYNGAP1, NEFL, WNT7A, ACSL6, NEFM	2.41E-07	4.27E-04
GOTERM_BP_FAT	GO:0007626--locomotory behavior	33	3.08123249	PLXNA3, UCHL1, SNCA, ASTN1, CACNB4, CALB1, KLHL1, ATP2B2, NPAS3, ROBO1, APBA2, SEMA3A, APBA1, GNG7, DSCAM, SCG2, KCNMA1, GNAO1, EFNB3, GRIN1, ATP1A3, NPY1R, NTSR1, GRM5, EPHA4, FEZF2, CORO1A, ABAT, RELN, CHRN2, SCN8A, TSHR, CACNA1B	3.11E-07	5.50E-04
GOTERM_BP_FAT	GO:0048168--regulation of neuronal synaptic plasticity	15	1.40056022	PPFIA3, GRIK1, GRIK2, GRIN1, SNCA, BCAN, KIT, VGF, RIMS1, EPHB2, SYP, GRM5, GRIN2B, DLG4, SYNGAP1	3.95E-07	6.99E-04
GOTERM_BP_FAT	GO:0006813--potassium ion transport	26	2.42763772	KCNMB4, KCNC1, ATP1B2, KCNA6, KCNRG, KCNJ2, KCNIP1, KCNJ3, KCNK10, KCNQ3, KCNK9, SLC24A2, KCNQ2, HCN3, KCNMA1, HCN1, KCND2, KCNB1, SLC12A5, ATP1A3, KCNJ6, KCNN3, KCNN2, KCNH7, KCNH8, KCNH5	4.75E-07	8.39E-04
GOTERM_BP_FAT	GO:0001764--neuron migration	16	1.49393091	DCC, CDK5R1, SATB2, CCK, NDN, MDGA1, PAX6, ARX, ASCL1, DAB1, CNTN2, RELN, DCX, APBB1, DCLK1, NR2F1	6.34E-07	0.001121
GOTERM_BP_FAT	GO:0016477--cell migration	37	3.45471522	DCC, CDK5R1, SHROOM2, CCK, NDN, PLXNA2, SORL1, ASTN1, PAX6, KITLG, KIT, ARX, VCAM1, DAB1, ROBO1, POU3F3, LHX6, POU3F2, CLASP2, CD24, DCX, DCLK1, SCG2, NR2F1, SATB2, VAV3, PODXL, MDGA1, ISL1, CTNNA2, ASCL1, CORO1A, SYNE2, CNTN2, RELN, LRP8, APBB1	7.41E-07	0.00131
GOTERM_BP_FAT	GO:0032940--secretion by cell	32	2.98786181	PPFIA3, SYT1, RAB3A, RAB3B, SNCAIP, RAB3C, CPLX1, SYT4, SYT5, SYT3, RIMS2, VGF, RIMS1, SYN1, TRIM9, SYN3, SYN2, APBA2, SNAP25, APBA1, STX1A, NOS1AP, NRXN2, NLGN1, PCLO, CADPS, TRIM36, NTRK2, SPTBN2, ERC2, WNT7A, UNC13B, SMPD3, CACNA1B	7.80E-07	0.001378
GOTERM_BP_FAT	GO:0006816--calcium ion transport	23	2.14752568	TRPC4, TRPC5, CACNG7, GRIN1, CACNG5, CACNG4, CACNG3, CACNG2, CACNB4, CACNA2D3, CACNA2D2, PRKCB, ATP2B2, CORO1A, GRIN2B, SLC24A2, RYR3, CACNA1H, CHRNA7, CACNA1E, CHRN2, CAMK2B, CACNA1B	8.42E-07	0.001488
GOTERM_BP_FAT	GO:0016337--cell-cell adhesion	33	3.08123249	CDK5R1, CADM3, THRA, CLSTN2, CLSTN3, ASTN1, DSCAML1, L1CAM, PCDHB12, CDH4, DCHS1, VCAM1, CDH8, NRCAM, CDH7, DAB1, CDH9, ROBO1, TTYH1, CD24, LOC690826, PCDH1X, PCDH10, NLGN1, PCDH9, CELSR3, CELSR2, PCDH8, PCDH17, WNT7B, CNTN3, NCAN, CDH10	1.01E-06	0.001786
GOTERM_BP_FAT	GO:0060341--regulation of cellular localization	38	3.5480859	SYT1, RAB3A, RAB3B, SNCAIP, RAB3C, PANX1, PFKFB2, SNCA, NNAT, GRIK5, SYT7, RIMS1, GRIN2B, TRIM9, PDE1C, SYN2, CHRNA7, PDE8B, SCG5, SNAP25, STX1A, NOS1, CREB1, NPY1R, PFKM, ISL1, STX1B, PCLO, PKIA, PRKCB, CADPS, GRM7, GIPR, NTRK2, SPTBN2, CHRN2, APBB1, CACNA1B	1.39E-06	0.002453
GOTERM_BP_FAT	GO:0021953--central nervous system neuron differentiation	13	1.21381886	DCC, PLXNA3, SOX5, EPHB1, EPHB2, ARX, ASCL1, BCL11B, FOXG1, CHRN2, LHX6, DCX, DCLK1	1.51E-06	0.002671
GOTERM_BP_FAT	GO:0030534--adult behavior	20	1.86741363	KCNMA1, GABRG2, GRIK1, EFNB3, GRIN1, UCHL1, SNCA, ATP1A3, CACNB4, NTSR1, KLHL1, EPHA4, SLC1A2, NPY, GRM7, ABAT, CHRNA7, CHRN2, SCN8A, TSHR	1.56E-06	0.002758
GOTERM_BP_FAT	GO:0031344--regulation of cell projection organization	22	2.054155	PLXNA3, LIMK1, GRIN1, LRRC4C, KIT, DPYSL2, RUFY3, EPHB2, ROBO1, TIAM1, SEMA4F, MAPT, NTRK2, CHRN2, POU3F2, SEMA3A, SEMA4D, SYNGAP1, NEFL, WNT7A, ACSL6, NEFM	1.57E-06	0.002783
GOTERM_BP_FAT	GO:0042391--regulation of membrane potential	26	2.42763772	KCNMB4, PRKCZ, CCK, SCN3A, GRIK1, GRIK2, GRIK3, SNCA, GRIK5, CACNB4, KCNIP1, GRIN2B, ANK2, POU3F2, CHRNA7, POU3F1, KCNMA1, GJD2, KCND2, GRIN1, SCN2A1, NLGN3, CACNG2, GRIA1, CHRN2, SCN8A	1.99E-06	0.003523
GOTERM_BP_FAT	GO:0007613--memory	15	1.40056022	PRKCZ, ADCY1, ADCY8, GRIN1, ATP1A3, PCDH8, CHST10, GRIN2B, GRIA1, SLC24A2, GRM7, CHRN2, CHRNA7, PLCB1, SNAP25	2.93E-06	0.005182
GOTERM_BP_FAT	GO:0007156--homophilic cell adhesion	21	1.96078431	LOC690826, CADM3, CLSTN2, CLSTN3, PCDH1X, PCDH10, DSCAML1, CELSR3, PCDH9, L1CAM, CELSR2, PCDH8, PCDHB12, PCDH17, CDH4, DCHS1, CDH8, CDH7, CDH9, ROBO1, CDH10	2.95E-06	0.005206
GOTERM_BP_FAT	GO:0022604--regulation of cell morphogenesis	23	2.14752568	PALM, PLXNA3, LIMK1, GRIN1, LRRC4C, DPYSL2, GAS7, RUFY3, EPHB2, CORO1A, ROBO1, TIAM1, SEMA4F, MAPT, CHRN2, POU3F2, SEMA3A, SEMA4D, SYNGAP1, NEFL, WNT7A, NEFM, FGD4	3.97E-06	0.007011
GOTERM_BP_FAT	GO:0015672--monovalent inorganic cation transport	38	3.5480859	KCNMB4, KCNC1, SCN3A, ATP1B2, SCN3B, KCNA6, ATP6V1G2, KCNJ2, KCNRG, KCNJ3, KCNIP1, KCNK10, KCNQ3, KCNK9, SLC24A2, SLC4A8, ATP5I, KCNQ2, HCN3, KCNMA1, HCN1, KCND2, SCN2B, KCNB1, SCN2A1, SLC12A5, ATP1A3, SLC10A4, SLC17A7, SLC4A10, KCNJ6, SLC17A6, KCNN3, KCNN2, KCNH7, KCNH8, SCN8A, KCNH5	4.15E-06	0.007334
GOTERM_BP_FAT	GO:0048870--cell motility	41	3.82819795	DCC, CDK5R1, SHROOM2, CCK, NDN, PLXNA2, SORL1, ASTN1, PAX6, KITLG, KIT, ARX, VCAM1, DAB1, ROBO1, POU3F3, CHRNA7, LHX6, POU3F2, RGD1566251, CLASP2, CD24, DCX, LOC300308, DCLK1, SCG2, NR2F1, SATB2, VAV3, MDGA1, PODXL, ISL1, CTNNA2, ASCL1, RGD1564409, CORO1A, SYNE2, RGD1565071, CNTN2, RELN, LRP8, APBB1	4.95E-06	0.008743
GOTERM_BP_FAT	GO:0051674--localization of cell	41	3.82819795	DCC, CDK5R1, SHROOM2, CCK, NDN, PLXNA2, SORL1, ASTN1, PAX6, KITLG, KIT, ARX, VCAM1, DAB1, ROBO1, POU3F3, CHRNA7, LHX6, POU3F2, RGD1566251, CLASP2, CD24, DCX, LOC300308, DCLK1, SCG2, NR2F1, SATB2, VAV3, MDGA1, PODXL, ISL1, CTNNA2, ASCL1, RGD1564409, CORO1A, SYNE2, RGD1565071, CNTN2, RELN, LRP8, APBB1	4.95E-06	0.008743
GOTERM_BP_FAT	GO:0010769--regulation of cell morphogenesis involved in differer	19	1.77404295	PLXNA3, LIMK1, GRIN1, DPYSL2, LRRC4C, RUFY3, EPHB2, ROBO1, TIAM1, SEMA4F, MAPT, CHRN2, POU3F2, SEMA3A, SEMA4D, SYNGAP1, NEFL, WNT7A, NEFM	6.55E-06	0.01158
GOTERM_BP_FAT	GO:0021954--central nervous system neuron development	11	1.0270775	ARX, DCC, ASCL1, PLXNA3, FOXG1, LHX6, CHRN2, DCX, DCLK1, EPHB1, EPHB2	1.03E-05	0.018256
GOTERM_BP_FAT	GO:0046903--secretion	35	3.26797386	PPFIA3, SYT1, RAB3A, RAB3C, CPLX1, SYT4, SYT5, SYT3, CACNB4, RIMS2, VGF, RIMS1, SYN1, TRIM9, SYN3, SYN2, APBA2, SNAP25, APBA1, KCNMA1, STX1A, NOS1AP, NRXN2, NLGN1, PCLO, CADPS, TRIM36, NTRK2, SPTBN2, CHRN2, ERC2, WNT7A, UNC13B, SMPD3, CACNA1B	1.07E-05	0.018846
GOTERM_BP_FAT	GO:0050806--positive regulation of synaptic transmission	11	1.0270775	PRKCZ, GRIA2, GRIK1, ERBB4, GRIA1, GRIK2, SLC24A2, NTRK2, SNCA, CHRN2, GRIA4	1.84E-05	0.0326
GOTERM_BP_FAT	GO:0048169--regulation of long-term neuronal synaptic plastic	10	0.93370682	GRM5, GRIN2B, GRIK2, GRIN1, SNCA, DLG4, KIT, SYNGAP1, RIMS1, EPHB2	2.32E-05	0.041091
GOTERM_BP_FAT	GO:0017157--regulation of exocytosis	13	1.21381886	CADPS, SYT1, RAB3A, STX1A, RAB3B, RAB3C, TRIM9, SPTBN2, GRIK5, SYT7, RIMS1, PCLO, STX1B	2.39E-05	0.042283
GOTERM_BP_FAT	GO:0021987--cerebral cortex development	11	1.0270775	ARX, ASCL1, DAB1, EMX1, GRIN1, SOX2, POU3F3, RELN, LHX6, LRP8, POU3F2	2.42E-05	0.042831

GROUP A DOWN-PATTERN

Category	Term	Count	%	Genes	P-value	FDR
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	118	10.2341717	DLC1, APOBEC1, THRB, PTGS2, IL6ST, OSMR, PGF, PDGFA, PTGS1, FGFR1, TGFEB3, FGF10, TLR4, JAG1, PMAIP1, IL15, CXCL12, TGFBI, TGFBI2, H19, PGR, MYD88, S1PR1, CDKN2B, SERPINE1, PDGFC, RARG, MFGF8, THY1, VEGFC, CD38, SERPINF1, PTPRV, F3, VEGFA, PDGFRA, WDC1, TGIF1, RIPK2, PDGFRB, PMP22, NGF, CAV2, CAV1, CCL2, IFTM3, IFI30, ITGB1, IRAK4, LIF, VDR, ITGAV, RUNX2, RUNX3, BMP4, B4GALT1, BMP2, SPHK1, TGFBR2, HGF, SHOX2, NOTCH2, PLA2G4A, CDKN1A, ATF3, CD274, AVPR1A, KCTD11, KLF4, PLAU, SAT1, PPARG, FGF7, ACVRL1, PPARG, PRRX1, GJA1, PAWR, PRRX2, TENC1, DDR2, WISP2, ANG, HMOX1, HEY2, SHC1, FGF1, IL13RA1, FGF2, FOSL1, LYN, CDK6, MBD2, MMP12, PURA, CTH, CCND1, ADAM17, TBX18, EIF5A2, CSF1, NR3C1, STAT6, CAMK2D, PLCD1, CD28, NOX4, PTPRC, IL6, TBX3, TBX2, ANXA1, SPARC, STAT1, CLEC11A, CYBA, NUPR1, ID3	6.02E-24	1.11E-20
GOTERM_BP_FAT	GO:0010033~response to organic substance	141	12.2289679	DLC1, ADCY4, APOBEC1, ADCY7, PTGS2, PDGFA, PGF, OSMR, IL6ST, PTGS1, TGFBI, TLR3, TLR4, PMAIP1, TLR6, AQP1, CXCL12, MMP2, TGFBI, H19, B2M, TGFBI2, CD48, GSTM2, EIF4EBP1, MYD88, CDKN2B, CD44, PAPP, CREB3L2, CREB3L1, FAS, LOX, DNAC3, GNG5, BCL10, PLD1, CRYAB, MGP, MFGF8, CD38, SERPINF1, ABCB1B, PDGFRA, WDC1, PDGFRB, RIPK2, NFE2L2, COL1A1, CROT, NGF, ME1, IL1R1, CAV1, CYP1B1, CCL2, ENPP1, HSPA1A, HSPA1B, TIMP3, TIMP1, IRAK3, ALB, BMP4, PLAT, CFB, SPHK1, TGFBR2, EPHX1, P2RX4, PLA2G4A, CDKN1A, CXCL16, AVPR1A, CLEC7A, ATP6V0E1, IGF1BP7, PPARG, RHOQ, GJA1, NFKB2, SDC2, ASAH1, LATS2, ASAH2, ANG, GSN, HMOX1, GPX3, CASP8, SHC1, RHOC, LBP, CASP1, FOSL1, GHR, CYR61, EGR1, ACADM, EGR2, SP100, LYN, MMP19, STXB4, MMP14, PRKCD, CCND1, TNFRSF10B, ADAM17, CTSK, STEAP2, PROS1, ALPL, COL3A1, FHL2, TRIM16, GNG11, GNG12, DCN, NR3C1, STAT6, TNFRSF1A, ANXA7, COL6A3, COL6A2, CD4, PLCD1, ACSL5, IL6, ANXA1, TRIM25, SPARC, PCK2, ANXA5, STAT1, STAT3, CASP12, ID3, TIP2, MGST1, CD14, MGST2	5.63E-22	1.03E-18
GOTERM_BP_FAT	GO:0042060~wound healing	50	4.33651344	PPARD, ACVRL1, FGF7, PDGFA, TGFBI, GJA1, FGF10, SDC2, TGFBI, TGFBI2, DYF, CD44, GSN, HMOX1, SERPINE1, LOX, FGF2, TFPI2, RAB27A, PLAU, F3, TFPI, PDGFRA, PDGFRB, ADAM17, PROS1, COL3A1, DCN, ELK3, TPM1, TIMP3, TIMP1, PROCR, IL10RB, ENTPD1, PAPSS2, FN1, TEC, B4GALT1, EFEMP2, TGFBR2, AXL, SPARC, MUSTN1, ANXA5, GAS6, COL5A1, NOTCH2, ITGA5, PLAU	5.26E-19	9.66E-16
GOTERM_BP_FAT	GO:0009611~response to wounding	82	7.11188205	PPARD, FGF7, ACVRL1, PTGS2, PDGFA, TGFBI, GJA1, FGF10, TLR4, IL15, MMP2, TGFBI, SDC2, TGFBI2, H19, S1PR3, CASP4, DYF, CD44, GSN, HMOX1, SERPINE1, CFH, LBP, LOX, TFPI2, FGF2, RAB27A, PTGER3, LYN, PLAU, F3, PDGFRA, TFPI, ADAM17, PDGFRB, PROS1, NGF, CCL2, COL3A1, ELK3, DCN, TIMP3, TPM1, TIMP1, TNFRSF1A, TNFRSF1B, LAMB2, PROCR, IL10RB, C2, ENTPD1, PAPSS2, TEC, FN1, B4GALT1, BMP2, IL6, LIPA, OLR1, CFB, EFEMP2, MAP2K3, TGFBR2, SPHK1, AXL, MUSTN1, SPARC, ANXA5, COL5A1, GAS6, STAT3, CYBA, NOTCH2, CYP4F5, NUPR1, SLC7A2, ITGA5, ID3, PLAU, CD14, MPHOSPH8	5.85E-19	1.07E-15
GOTERM_BP_FAT	GO:0001568~blood vessel development	57	4.94362533	ACVRL1, PGF, PDGFA, WASF2, PRRX1, CSPG4, GJA1, FGF10, ANPEP, PRRX2, IL15, MMP2, CXCL12, TGFBI2, BAK1, S1PR1, CD44, ANG, CTGF, HMOX1, CASP8, HEY2, SHC1, LOX, FGF1, FGF2, CYR61, MMP14, ARHGAP24, MYH9, THY1, VEGFC, BGN, VEGFA, COL1A2, COL1A1, CAV1, COL3A1, ELK3, ZFP36L1, ITGAV, ZC3H12A, PLCD1, C1GALT1, PLAT, B4GALT1, BMP4, MYO1E, SPHK1, TGFBR2, ITGA4, EPHA2, COL5A1, ANXA2, LAMA4, AMOT, PLAU	2.51E-18	4.62E-15
GOTERM_BP_FAT	GO:0001944~vasculature development	57	4.94362533	ACVRL1, PGF, PDGFA, WASF2, PRRX1, CSPG4, GJA1, FGF10, ANPEP, PRRX2, IL15, MMP2, CXCL12, TGFBI2, BAK1, S1PR1, CD44, ANG, CTGF, HMOX1, CASP8, HEY2, SHC1, LOX, FGF1, FGF2, CYR61, MMP14, ARHGAP24, MYH9, THY1, VEGFC, BGN, VEGFA, COL1A2, COL1A1, CAV1, COL3A1, ELK3, ZFP36L1, ITGAV, ZC3H12A, PLCD1, C1GALT1, PLAT, B4GALT1, BMP4, MYO1E, SPHK1, TGFBR2, ITGA4, EPHA2, COL5A1, ANXA2, LAMA4, AMOT, PLAU	1.09E-17	2.00E-14
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	49	4.24978317	CAV1, ACVRL1, PGF, PDGFA, WASF2, PRRX1, CSPG4, GJA1, FGF10, ANPEP, PRRX2, IL15, ELK3, MMP2, CXCL12, TGFBI2, ZFP36L1, BAK1, S1PR1, ANG, CTGF, ITGAV, HMOX1, CASP8, HEY2, ZC3H12A, SHC1, PLCD1, FGF1, FGF2, C1GALT1, CYR61, B4GALT1, BMP4, PLAT, MYO1E, TGFBR2, ITGA4, MMP14, ARHGAP24, MYH9, EPHA2, ANXA2, THY1, VEGFC, BGN, VEGFA, AMOT, PLAU	5.76E-17	2.00E-13
GOTERM_BP_FAT	GO:0030198~extracellular matrix organization	32	2.7753686	ADAMTSL4, COL3A1, POSTN, DCN, NFKB2, SERPINH1, TGFBI2, SMOC2, P4HA1, ACAN, LOX, COL11A1, FN1, CYR61, B4GALT1, LGALS3, EGFL6, OLFML2B, CCDC80, NID1, LOC313641, COL5A2, COL5A1, EMILIN1, ANXA2, ITGA8, KAZALD1, FBLN5, COL1A2, PDGFRA, LAMC1, COL1A1	1.94E-15	3.46E-12
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	71	6.15784909	PPARD, FGF7, PTGS2, THRB, IL6ST, PGF, OSMR, PDGFA, PRRX1, FGF10, TLR4, PRRX2, IL15, DDR2, CXCL12, TGFBI, TGFBI2, S1PR1, MYD88, ANG, HEY2, SHC1, PDGFC, IL13RA1, FGF1, FGF2, LYN, CDK6, MFGF8, MMP12, PURA, CD38, VEGFC, CCND1, F3, VEGFA, PDGFRA, TGIF1, ADAM17, RIPK2, PDGFRB, EIF5A2, TBX18, NGF, CCL2, CSF1, ITGB1, IRAK4, LIF, ITGAV, CAMK2D, RUNX2, CD28, B4GALT1, BMP4, PTPRC, IL6, TBX3, TBX2, TGFBR2, SPHK1, HGF, STAT1, CLEC11A, SHOX2, CYBA, PLA2G4A, CDKN1A, ATF3, AVPR1A, ID3	4.82E-15	8.77E-12
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	58	5.03035559	PPARD, ACVRL1, SLC20A1, IL6ST, PRRX1, GJA1, FGF10, TLR3, TLR4, PRRX2, LPAR1, JAG1, TLR6, TGFBI, TGFBI2, MYD88, CDKN2B, HMOX1, CASP8, RHOC, LBP, CASP1, GHR, BCL10, LTBR, LYN, MBD2, PRKCD, TNFRSF10B, F3, VEGFA, RIPK2, ADAM17, TGFBI, NEK6, CAV2, CAV1, LITAF, CSF1, TRIM16, ITGB1, LIF, TNFRSF1A, ITGAV, CD4, BMP4, PTPRC, CFLAR, IL6, BMP2, LGALS1, EDAR, TRADD, SHOX2, IKKBE, P2RX4, NOTCH2, ITGA8	1.96E-14	3.61E-11
GOTERM_BP_FAT	GO:0001501~skeletal system development	55	4.77016479	PTGS2, PDLIM7, HEXA, HEXB, PRRX1, TGFBI, PRRX2, MMP2, TGFBI, TGFBI2, HOXC6, HOXC9, CTGF, COL11A1, GHR, RARG, ARID5B, MGP, MMP14, FMN1, HOXC10, EYA1, CTSK, CHRD1, PDGFRA, COL1A2, ROR2, PDGFRB, COL1A1, CSF1, COL3A1, FHL2, TIMP1, VDR, HOXA5, HOXA6, ACAN, RUNX1, GPNMB, PAPSS2, RUNX2, FN1, BMP4, BMP2, TBX3, LGALS3, FBN1, TGFBR2, NPR2, LOC313641, SPARC, WWTR1, COL5A2, EPHA2, SHOX2, BMP5	3.71E-14	6.81E-11
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	82	7.11188205	DLC1, ADCY4, APOBEC1, PTGS2, ADCY7, PGF, PDGFA, IGF1BP7, PPARG, PTGS1, TGFBI, GJA1, RHOQ, TLR4, AQP1, MMP2, CXCL12, LATS2, TGFBI, TGFBI2, H19, EIF4EBP1, ANG, PAPP, HMOX1, GPX3, CASP8, SHC1, RHOC, FAS, LOX, GNG5, FOSL1, GHR, PLD1, ACADM, EGR2, LYN, CRYAB, MMP19, MGP, MFGF8, STXB4, MMP14, PRKCD, CD38, CCND1, SERPINF1, ABCB1B, PDGFRA, WDC1, PDGFRB, COL1A1, STEAP2, NGF, ME1, ALPL, CAV1, CCL2, ENPP1, FHL2, GNG11, TRIM16, GNG12, TIMP3, TIMP1, PLCD1, ACSL5, BMP4, PLAT, IL6, TGFBR2, SPHK1, ANXA1, TRIM25, SPARC, STAT1, PCK2, STAT3, PLA2G4A, CDKN1A, AVPR1A	5.16E-14	9.48E-11

GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	88	7.63226366	DLC1, ADCY4, ATP6V0E1, APOBEC1, PTGS2, ADCY7, PGF, PDGFA, IGFBP7, PTGS1, PPARG, TGFβ3, GJA1, RHOQ, TLR4, AQP1, MMP2, CXCL12, LATS2, TGFβ1, TGFβ2, H19, EIF4EBP1, ANG, PAPPA, HMOX1, GPX3, CASP8, SHC1, RHOC, FAS, LOX, GNG5, FOSL1, GHR, PLD1, ACADM, EGR2, LYN, CRYAB, MMP19, MGP, MFGE8, STXBP4, MMP14, PRKCD, CD38, CCND1, SERPINF1, ABCB1B, PDGFRA, WDFC1, ADAM17, PDGFRB, COL1A1, STEAP2, CROT, NGF, ME1, ALPL, CAV1, CCL2, ENPP1, FHL2, GNG11, TRIM16, GNG12, TIMP3, TIMP1, PLCD1, ACSL5, BMP4, PLAT, IL6, TGFβR2, SPHK1, ANXA1, TRIM25, SPARC, STAT1, PCK2, STAT3, PLA2G4A, CDKN1A, CASP12, AVPR1A, MGST1, MGST2	8.00E-14	1.47E-10
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	60	5.20381613	PPARD, ACVRL1, PTGS2, SLC20A1, IL6ST, PRRX1, GJA1, FGF10, TLR3, TLR4, PRRX2, LPAR1, JAG1, TLR6, TGFβ1, TGFβ2, MYD88, CDKN2B, HMOX1, CASP8, RHOC, LBP, CASP1, GHR, BCL10, LTBR, LYN, MBD2, PRKCD, TNFRSF10B, F3, VEGFA, RIPK2, ADAM17, TGFβ1I1, NEK6, CAV2, CAV1, CCL2, LITAF, CSF1, TRIM16, ITGB1, LIF, TNFRSF1A, ITGAV, CD4, BMP4, PTPRC, CFLAR, IL6, BMP2, LGALS1, EDAR, TRADD, SHOX2, IKKBE, P2RX4, NOTCH2, ITGA8	2.84E-13	5.22E-10
GOTERM_BP_FAT	GO:0001525~angiogenesis	35	3.03555941	ACVRL1, PGF, PDGFA, WASF2, CSPG4, FGF10, ANPEP, ELK3, IL15, MMP2, CXCL12, S1PR1, ANG, CTGF, HMOX1, ITGAV, CASP8, ZC3H12A, SHC1, PLCD1, FGF1, FGF2, C1GALT1, CYR61, BMP4, B4GALT1, TGFβR2, MMP14, ARHGAP24, MYH9, THY1, ANXA2, VEGFC, VEGFA, PLAU	2.92E-13	5.37E-10
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	53	4.59670425	PTGS2, PDGFA, IGFBP7, PTGS1, PPARG, TGFβ3, TLR4, AQP1, MMP2, TGFβ1, TGFβ2, H19, PAPPA, HMOX1, CASP8, GPX3, RHOC, SHC1, FAS, LOX, FOSL1, GHR, ACADM, CRYAB, MGP, MFGE8, MMP14, CD38, CCND1, SERPINF1, ABCB1B, PDGFRA, WDFC1, PDGFRB, COL1A1, NGF, ALPL, CAV1, CCL2, TIMP3, PLAT, BMP4, IL6, SPHK1, TGFβR2, ANXA1, TRIM25, SPARC, PCK2, STAT3, PLA2G4A, CDKN1A, AVPR1A	2.64E-11	4.84E-08
GOTERM_BP_FAT	GO:0043062~extracellular structure organization	34	2.94882914	ADAMTSL4, COL3A1, UTRN, POSTN, DCN, NFKB2, SERPINH1, TGFβ2, SMOCK, P4HA1, 4.95E-11	9.10E-08	
GOTERM_BP_FAT	GO:0001558~regulation of cell growth	38	3.29575022	ACVRL1, ENPP1, IL6ST, HSD3B7, TNFRSF12A, IGFBP7, PPARG, GREM1, CXCL12, TGFβ1, TGFβ2, NOV, WISP2, DAB2, WISP1, CD44, CTGF, HTRA1, RHOC, FGF2, CYR61, CGRRF1, CRYAB, SPHK1, S100A10, PRKCD, INHBA, CD38, CTH, CDKN1A, CXCL16, KAZALD1, FBLN5, AVPR1A, TGIF1, ADAM17, WDFC1, NGF	5.37E-11	9.86E-08
GOTERM_BP_FAT	GO:0007155~cell adhesion	70	6.07111882	DLC1, PVR, PPARD, AEBP1, TLN1, IGFBP7, LMO7, POSTN, SDC4, DDR2, CD2AP, TGFβ2, VCL, WISP2, WISP1, CD44, CTGF, COL12A1, SHC1, RHOC, MSN, COL11A1, CYR61, ICAM1, ACTN1, MFGE8, CD164, MYH9, CERCAM, THY1, CD34, ROR2, ADAM17, LAMC1, PARVA, LIMS1, EPDR1, TNFRSF12A, COL3A1, ITGB1, SCARF2, ITGBL1, LGALS3BP, LAMB2, FAT1, ITGAV, ACAN, CD4, TNN, EMB, LAMB1, GPNMB, FN1, B4GALT1, PTPRC, SVEP1, OLR1, LPP, COL15A1, ITGA1, NID1, ITGA4, NID2, COL5A1, COL14A1, ITGA5, ITGA8, FBLN5, ANTXR1, CLEC7A	8.55E-11	1.57E-07
GOTERM_BP_FAT	GO:0022610~biological adhesion	70	6.07111882	DLC1, PVR, PPARD, AEBP1, TLN1, IGFBP7, LMO7, POSTN, SDC4, DDR2, CD2AP, TGFβ2, VCL, WISP2, WISP1, CD44, CTGF, COL12A1, SHC1, RHOC, MSN, COL11A1, CYR61, ICAM1, ACTN1, MFGE8, CD164, MYH9, CERCAM, THY1, CD34, ROR2, ADAM17, LAMC1, PARVA, LIMS1, EPDR1, TNFRSF12A, COL3A1, ITGB1, SCARF2, ITGBL1, LGALS3BP, LAMB2, FAT1, ITGAV, ACAN, CD4, TNN, EMB, LAMB1, GPNMB, FN1, B4GALT1, PTPRC, SVEP1, OLR1, LPP, COL15A1, ITGA1, NID1, ITGA4, NID2, COL5A1, COL14A1, ITGA5, ITGA8, FBLN5, ANTXR1, CLEC7A	8.55E-11	1.57E-07
GOTERM_BP_FAT	GO:0016477~cell migration	48	4.16305291	PVR, PPARD, ACVRL1, CCL2, TNFRSF12A, WASF2, CSPG4, ITGA11, GJA1, FGF10, CXCL12, CD2AP, ITGB1, TGFβ1, TGFβ2, NDE1, DOCK1, CD44, ANG, CTGF, ITGAV, CKLF, FCER1G, TNN, LBP, MSN, FGF2, TWIST1, B4GALT1, PLAT, ICAM1, ARID5B, ITGA1, AXL, ITGA4, MMP14, MYH9, COL5A1, ABCC9, ITGA5, CD34, VEGFA, CX3CR1, PDGFRB, AMOT, ADAM17, LAMC1, PLAU	1.42E-10	2.60E-07
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	37	3.20901995	PPARD, LITAF, SLC20A1, IL6ST, GJA1, FGF10, TLR3, TLR4, LPAR1, TLR6, ITGB1, TGFβ1, TGFβ2, LIF, TNFRSF1A, MYD88, HMOX1, ITGAV, CASP8, RHOC, CASP1, GHR, CFLAR, BCL10, PTPRC, IL6, LTBR, LYN, LGALS1, EDAR, PRKCD, TRADD, IKKBE, TNFRSF10B, F3, RIPK2, NEK6	2.65E-10	4.86E-07
GOTERM_BP_FAT	GO:0070482~response to oxygen levels	41	3.55594102	CAV1, CCL2, PGF, PDGFA, ACOT2, TGFβ3, TLR4, PDLIM1, MMP2, CXCL12, SDC2, TGFβ1, TGFβ2, PLOD1, ANG, PLOD2, HMOX1, CAMK2D, SHC1, RHOC, PLCD1, FAS, CASP1, PLAT, NOL3, ACTN4, TGFβR2, MMP14, CAPN2, PRKCD, SOD3, ITPR1, CD38, ABCC9, CDKN1A, CASP12, VEGFA, PDGFRA, PDGFRB, ADAM17, PLAU	2.70E-10	4.96E-07
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	48	4.16305291	DLC1, CAV2, PPARD, CAV1, ACVRL1, PTGS2, IFTM3, FGFR1, PPARG, TGFβ3, GJA1, IFI30, FGF10, PAWR, PMAIP1, IL15, TENC1, TGFβ1, TGFβ2, H19, VDR, WISP2, CDKN2B, ANG, HMOX1, FGF2, FOSL1, RUNX3, NOX4, B4GALT1, BMP4, IL6, BMP2, RARG, TGFβR2, CDK6, THY1, NOTCH2, CTH, CDKN1A, SERPINF1, NUPR1, PTPRV, CD274, TGIF1, WDFC1, PMP22, KLF4	2.78E-10	5.11E-07
GOTERM_BP_FAT	GO:0048771~tissue remodeling	22	1.90806592	NOX4, IL6, CAV1, RAB9A, LIPA, ENPP1, AXL, CSPG4, TGFβ3, FGF10, ITGA4, MMP14, MMP2, TGFβ1, GAS6, TGFβ2, BAK1, CTSK, BGN, PTPRV, TPPI, VEGFA	3.19E-10	5.85E-07
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	52	4.50997398	PTGS2, NUAKE2, IL6ST, PDGFA, IGFBP7, PPARG, TGFβ1, TGFβ2, H19, CD44, CDKN2B, GSN, HMOX1, FOSL1, GHR, ACADM, RARG, LYN, MGP, PRKCD, CD38, CCND1, SERPINF1, PDGFRB, COL1A1, ALPL, CAV1, CCL2, GSDMD, SIPA1, TRIM16, TIMP3, VDR, ALB, C2, RUNX1, ACSL5, PLEC, BMP4, BMP2, IL6, SPHK1, TGFβR2, AXL, TRIM25, SPARC, STAT1, PLA2G4A, CYBB, CDKN1A, AVPR1A, KLF4	3.39E-10	6.23E-07
GOTERM_BP_FAT	GO:0010941~regulation of cell death	90	7.8057242	DLC1, HTATIP2, NUAKE2, PTGS2, WFS1, TGFβ3, TLR4, PMAIP1, MMP2, TGFβ1, TGFβ2, BAK1, MYD88, CASP4, CD44, BAG3, HMOX1, CASP8, RHOC, FAS, NQO1, CASP1, FGF2, FOSL1, GHR, RAB27A, BCL10, NOL3, RARG, ACTN4, CRYAB, GZMB, PRKCD, THY1, INHBA, SERPINB9, EYA1, TNFRSF10B, F3, CX3CR1, VEGFA, RIPK3, AVEN, ADAM17, HSPB1, RIPK2, LRRK2, NGF, CCL2, ADAMTSL4, STK17B, HSPA1A, HSPA1B, NR3C1, TIMP3, MST4, TIMP1, VDR, ALB, FCER1G, PCSK6, PHLDA3, RUNX3, TEX261, FN1, HIP1, CD28, BMP4, B4GALT1, PTPRC, CFLAR, IL6, TBX3, SMAD6, SPHK1, ITGA1, ANXA1, CIDEA, NR4A1, HGF, STAT1, TRADD, PLEKHF1, P2RX4, NOTCH2, PLA2G4A, CDKN1A, NUPR1, ETS1, CASP12, ID3	3.51E-10	6.44E-07

GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	89	7.71899393	DLC1, HTATIP2, NUA2, PTGS2, WFS1, TGFB3, TLR4, PMAIP1, MMP2, TGFB1, TGFB2, BAK1, MYD88, CASP4, CD44, BAG3, HMOX1, CASP8, RHOC, FAS, NQO1, CASP1, FGF2, FOSL1, GHR, RAB27A, BCL10, NOL3, RARG, ACTN4, CRYAB, GZMB, PRKCD, THY1, INHBA, SERPINB9, EYA1, TNFRSF10B, F3, CX3CR1, VEGFA, RIPK3, AVEN, ADAM17, HSPB1, RIPK2, LRRK2, NGF, CCL2, ADAMTSL4, STK17B, HSPA1A, HSPA1B, NR3C1, TIMP3, MST4, TIMP1, VDR, ALB, FCER1G, PCSK6, PHLDA3, RUNX3, TEX261, FN1, HIP1, CD28, B4GALT1, PTNRC, CFLAR, IL6, TBX3, SMAD6, SPHK1, ITGA1, ANXA1, CIDEA, NR4A1, HGF, STAT1, TRADD, PLEKHF1, P2RX4, NOTCH2, PLA2G4A, CDKN1A, NUPR1, ETS1, CASP12, ID3	6.37E-10	1.17E-06
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	87	7.54553339	DLC1, HTATIP2, NUA2, PTGS2, WFS1, TGFB3, TLR4, PMAIP1, MMP2, TGFB1, TGFB2, BAK1, MYD88, CASP4, CD44, BAG3, HMOX1, CASP8, RHOC, FAS, NQO1, CASP1, FOSL1, GHR, RAB27A, BCL10, NOL3, RARG, ACTN4, CRYAB, GZMB, PRKCD, THY1, INHBA, SERPINB9, EYA1, TNFRSF10B, F3, CX3CR1, VEGFA, RIPK3, AVEN, ADAM17, HSPB1, RIPK2, NGF, CCL2, ADAMTSL4, STK17B, HSPA1A, HSPA1B, NR3C1, TIMP3, MST4, TIMP1, VDR, ALB, FCER1G, PCSK6, PHLDA3, RUNX3, TEX261, FN1, HIP1, CD28, B4GALT1, PTNRC, CFLAR, IL6, TBX3, SMAD6, SPHK1, ITGA1, ANXA1, CIDEA, NR4A1, HGF, STAT1, TRADD, PLEKHF1, P2RX4, NOTCH2, PLA2G4A, CDKN1A, NUPR1, ETS1, CASP12, ID3	1.65E-09	3.03E-06
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	48	4.16305291	ACVRL1, CCL2, FGF7, PDGFA, IL6ST, COL3A1, CSPG4, TGFB3, FGF10, RHOQ, FSTL1, DDR2, TGFB1, TGFB2, LIF, EIF4EBP1, HMCN1, CTGF, ZFYVE16, SHC1, PDGFC, FGF1, FGF2, GHR, CSF1R, BMP4, PLAT, BMP2, ARID5B, MYO1E, TGFB2, AXL, STXB4, HGF, EPHA2, STAT3, DOK1, VEGFC, GRB10, VEGFA, COL1A2, PDGFRA, ROR2, PDGFRB, ADAM17, TGFB11, BAMB1, NGF	2.09E-09	3.84E-06
GOTERM_BP_FAT	GO:0034097~response to cytokine stimulus	28	2.42844753	IL1R1, PTGS2, IL6ST, OSMR, COL3A1, NFKB2, MMP2, TGFB2, TIMP1, STAT6, IRAK3, MYD88, CDKN2B, CASP8, FAS, FOSL1, GHR, IL6, SP100, SPHK1, ANXA1, SPARC, STAT1, STAT3, CD38, CXCL16, PDGFRA, RIPK2	2.36E-09	4.33E-06
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	51	4.42324371	PDLIM7, THRB, IL6ST, PPARG, TGFB3, GJA1, JAG1, CXCL12, TGFB1, TGFB2, CDKN2B, HEY2, ERAP1, RHOC, FGF2, FNDC3B, CYR61, GHR, BCL10, LYN, INHBA, VEGFC, SERPINF1, F3, RIPK2, TGIF1, TGFB11, NGF, TNFRSF12A, CSF1, TRIM16, LIF, TNFRSF1A, VDR, IL2RG, RUNX1, RUNX2, THBS2, CSF1R, B4GALT1, BMP4, PTNRC, LPL, IL6, BMP2, SPHK1, TGFB2, TRADD, PLA2G4A, ETS1, AMOT	2.89E-09	5.31E-06
GOTERM_BP_FAT	GO:0032535~regulation of cellular component size	42	3.64267129	LIMA1, ATP6V0E1, ACVRL1, ENPP1, TNFRSF12A, IL6ST, PPARG, TGFB3, GREM1, MMP2, TPM1, CXCL12, TGFB1, TGFB2, DAB2, LAMB2, GSN, TMEM123, TNN, RHOC, FGF2, CDC42EP5, CGRRF1, CRYAB, SPHK1, FMN1, INHBA, ARPC1B, CD38, NOTCH2, CTH, CDKN1A, LEPRE1, NUPR1, CXCL16, CAPG, AVPR1A, TGIF1, ADAM17, EMP3, EMP1, NGF	4.28E-09	7.86E-06
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	53	4.59670425	DLC1, PTGS2, TGFB3, TLR4, PMAIP1, MMP2, TGFB1, TGFB2, BAK1, CD44, HMOX1, CASP8, RHOC, FAS, NQO1, CASP1, FOSL1, RAB27A, BCL10, RARG, GZMB, PRKCD, INHBA, TNFRSF10B, RIPK3, RIPK2, LRRK2, NGF, ADAMTSL4, STK17B, NR3C1, TIMP3, VDR, PHLDA3, TEX261, RUNX3, CD28, HIP1, B4GALT1, BMP4, PTNRC, ANXA1, ITGA1, NR4A1, STAT1, TRADD, PLEKHF1, NOTCH2, PLA2G4A, CDKN1A, NUPR1, CASP12, ID3	4.83E-09	8.88E-06
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	30	2.60190807	ALPL, CAV1, CCL2, PTGS2, IGFBP7, PTGS1, TLR4, H19, PAPP, GPX3, RHOC, SHC1, FAS, FOSL1, GHR, PLAT, BMP4, IL6, ACADM, ANXA1, MGP, SPARC, PCK2, PLA2G4A, CCND1, CDKN1A, SERPINF1, AVPR1A, COL1A1, NGF	5.03E-09	9.23E-06
GOTERM_BP_FAT	GO:0060348~bone development	29	2.5151778	PDLIM7, PTGS2, CSF1, TGFB3, FHL2, MMP2, TGFB1, TGFB2, CTGF, GPNMB, COL11A1, RUNX2, PAPSS2, FN1, GHR, BMP4, BMP2, RARG, MGP, NPR2, SPARC, LOC313641, MMP14, WWTR1, COL5A2, SHOX2, CTSK, CHRDL1, COL1A1	5.79E-09	1.06E-05
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	29	2.5151778	ALPL, CAV1, CCL2, PTGS2, IGFBP7, PTGS1, TLR4, H19, PAPP, GPX3, RHOC, SHC1, FAS, FOSL1, GHR, PLAT, BMP4, IL6, ACADM, ANXA1, MGP, SPARC, PCK2, PLA2G4A, CDKN1A, CCND1, SERPINF1, AVPR1A, NGF	5.79E-09	1.06E-05
GOTERM_BP_FAT	GO:0006952~defense response	59	5.11708586	APOBEC1, PTGS2, TLR3, TLR4, IL15, TLR6, TGFB1, S1PR3, CASP4, MYD88, CD44, HMOX1, IL1RAP, CFH, LBP, RAB27A, BCL10, PLD1, SP100, PTGER3, LYN, IRGM, F3, RIPK2, NGF, IL1R1, CCL2, HSPA1A, HSPA1B, SP110, TNFRSF1A, TNFRSF1B, TAP1, FCER1G, C2, FN1, B4GALT1, PTNRC, LY2Z, IL6, BMP2, LIPA, OLR1, CFB, MAP2K3, IL1RL2, SPHK1, MYO1F, STAT3, LSP1, CYBA, ABCC9, CYBB, PENK, NUPR1, CYP4F5, SLC7A2, CXCL16, MPHOSPH8, CD14	7.50E-09	1.38E-05
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	52	4.50997398	DLC1, PTGS2, TGFB3, TLR4, PMAIP1, MMP2, TGFB1, TGFB2, BAK1, CD44, HMOX1, CASP8, RHOC, FAS, NQO1, CASP1, FOSL1, RAB27A, BCL10, RARG, GZMB, PRKCD, INHBA, TNFRSF10B, RIPK3, RIPK2, LRRK2, NGF, ADAMTSL4, STK17B, NR3C1, TIMP3, VDR, PHLDA3, TEX261, RUNX3, CD28, HIP1, B4GALT1, PTNRC, ANXA1, ITGA1, NR4A1, STAT1, TRADD, PLEKHF1, NOTCH2, PLA2G4A, CDKN1A, NUPR1, CASP12, ID3	9.78E-09	1.80E-05
GOTERM_BP_FAT	GO:0007584~response to nutrient	38	3.29575022	ALPL, CAV1, CCL2, PTGS2, IL6ST, PDGFA, IGFBP7, PPARG, TRIM16, TIMP3, TGFB1, TGFB2, VDR, CD44, CDKN2B, GSN, HMOX1, C2, RUNX1, PLEC, ACSL5, BMP4, BMP2, RARG, ACADM, TGFB2, MGP, TRIM25, SPARC, STAT1, CD38, PLA2G4A, CYBB, CCND1, SERPINF1, PDGFRB, COL1A1, KLF4	1.77E-08	3.25E-05
GOTERM_BP_FAT	GO:0001666~response to hypoxia	36	3.12228968	CAV1, CCL2, PGF, PDGFA, ACOT2, TGFB3, PDLIM1, TLR4, MMP2, CXCL12, SDC2, TGFB1, TGFB2, PLOD1, ANG, PLOD2, HMOX1, CAMK2D, SHC1, RHOC, FAS, CASP1, PLAT, NOL3, ACTN4, TGFB2, MMP14, CAPN2, PRKCD, SOD3, ITPR1, CD38, ABCC9, VEGFA, ADAM17, PLAU	2.54E-08	4.67E-05
GOTERM_BP_FAT	GO:0030199~collagen fibril organization	12	1.04076323	P4HA1, COL3A1, COL1A2, ACAN, COL1A1, LOX, COL11A1, COL5A2, SERPINH1, COL5A1, TGFB2, ANXA2	3.34E-08	6.14E-05
GOTERM_BP_FAT	GO:0035295~tube development	42	3.64267129	DLC1, FGF7, PGF, PDGFA, CSF1, TGFB3, GJA1, FGF10, NR3C1, SDC4, GREM1, CXCL12, ASAH1, TGFB1, TGFB2, PGR, VDR, CD44, CTGF, HOXA5, AARD, CASP8, LOX, FGF1, FGF2, TWIST1, CYR61, B4GALT1, BMP4, BCL10, BMP2, LIPA, TGFB2, MGP, SPARC, MMP14, MAN2A1, EYA1, VEGFA, HSD11B1, PDGFRA, TGIF1	3.52E-08	6.47E-05
GOTERM_BP_FAT	GO:0008361~regulation of cell size	35	3.03555941	ATP6V0E1, ACVRL1, ENPP1, IL6ST, TNFRSF12A, PPARG, TGFB3, GREM1, MMP2, CXCL12, TGFB1, TGFB2, DAB2, LAMB2, TMEM123, TNN, RHOC, FGF2, CGRRF1, CRYAB, SPHK1, INHBA, CD38, NOTCH2, CTH, CDKN1A, LEPRE1, NUPR1, CXCL16, AVPR1A, TGIF1, ADAM17, EMP3, EMP1, NGF	3.73E-08	6.86E-05
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	35	3.03555941	DLC1, ACVRL1, PDGFA, ACOT2, TGFB3, PDLIM1, TLR4, MMP2, CXCL12, TGFB1, TGFB2, VCL, S1PR1, RRAS, RHOC, LAMB1, FGF2, CYR61, B4GALT1, ICAM1, PLD1, SP100, ACTN4, SPHK1, MYO1F, ACTN1, CD63, THY1, VEGFC, ETS1, CXCL16, VEGFA, PDGFRA, PDGFRB, AMOT, ADAM17	4.29E-08	7.87E-05
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	23	1.99479618	BCL10, CFLAR, PPARG, LTBR, SLC20A1, LITAF, LGALS1, TLR3, GJA1, TLR4, LPAR1, TLR6, TRADD, IKKBE, TNFRSF1A, MYD88, TNFRSF10B, HMOX1, CASP8, RIPK2, RHOC, CASP1, NEK6	4.40E-08	8.08E-05
GOTERM_BP_FAT	GO:0040008~regulation of growth	47	4.07632264	ACVRL1, ENPP1, IL6ST, HSD3B7, TNFRSF12A, CSF1, IGFBP7, LGMN, PPARG, CD53, GREM1, CXCL12, TGFB1, TGFB2, NOV, WISP2, DAB2, WISP1, CD44, CTGF, HTRA1, HEY2, SHC1, RHOC, FGF2, GHR, CYR61, CGRRF1, CRYAB, SPHK1, TGFB2, S100A10, PRKDCBP, STAT3, GAS6, INHBA, CD38, CTH, CDKN1A, CXCL16, FBLN5, KAZALD1, AVPR1A, TGIF1, WFDC1, ADAM17, NGF	4.53E-08	8.32E-05

GOTERM_BP_FAT043123~positive regulation of I-kappaB kinase/NF-kappaB c	22	1.90806592	BCL10, CFLAR, LTBR, SLC20A1, LITAF, LGALS1, TLR3, GJA1, TLR4, LPAR1, TLR6, TRADD, IKKBE, TNFRSF1A, MYD88, TNFRSF10B, HMOX1, CASP8, RIPK2, RHOC, CASP1, NEK6	4.58E-08	8.41E-05
GOTERM_BP_FAT GO:0043065~positive regulation of apoptosis	50	4.33651344	DLC1, PTGS2, ADAMTSL4, TGFB3, STK17B, TLR4, NR3C1, PMAIP1, TIMP3, MMP2, TGFB1, TGFB2, BAK1, VDR, CD44, HMOX1, CASP8, RHOC, FAS, CASP1, NQO1, PHLDA3, FOSL1, RUNX3, TEX261, HIP1, RAB27A, CD28, B4GALT1, PTPRC, BCL10, RARG, ITGA1, ANXA1, NR4A1, GZMB, STAT1, PRKCD, TRADD, PLEKHF1, INHBA, NOTCH2, PLA2G4A, TNFRSF10B, NUPR1, CASP12, RIPK3, RIPK2, ID3, NGF	5.77E-08	1.06E-04
GOTERM_BP_FAT GO:0031667~response to nutrient levels	45	3.9028621	ALPL, CAV1, CCL2, NUAKE2, PTGS2, PDGFA, IL6ST, IGFBP7, PPARG, TRIM16, TIMP3, TGFB1, TGFB2, H19, VDR, CD44, CDKN2B, GSN, ALB, HMOX1, C2, RUNX1, GHR, PLEC, ACCL5, BMP4, IL6, BMP2, RARG, ACADM, SPHK1, TGFB2, MGP, TRIM25, SPARC, STAT1, PRKCD, CD38, PLA2G4A, CYBB, CCND1, SERPINF1, PDGFRB, COL1A1, KLF4	6.48E-08	1.19E-04
GOTERM_BP_FAT GO:0051272~positive regulation of cell motion	24	2.08152645	ICAM1, PLD1, ACTN4, IL6ST, PDGFA, CSF1, SPHK1, MYO1F, CXCL12, TGFB1, TGFB2, VEGFC, S1PR1, ETS1, CXCL16, VEGFA, PDGFRA, ADAM17, PDGFRB, AMOT, RHOC, LAMB1, FGF2, CYR61	9.22E-08	1.69E-04
GOTERM_BP_FAT GO:0051674~localization of cell	49	4.24978317	PVR, PPARD, CCL2, ACVRL1, TNFRSF12A, WASF2, ITGA11, CSPG4, GJA1, FGF10, ITGB1, CD2AP, CXCL12, TGFB1, TGFB2, NDE1, DOCK1, CD44, ANG, CTGF, ITGAV, CKLF, FCER1G, TNN, LBP, MSN, FGF2, TWIST1, PLAT, B4GALT1, ICAM1, ARID5B, AXL, ITGA1, ITGA4, MYH9, MMP14, COL5A1, ABCC9, ETS1, CD34, ITGA5, CX3CR1, VEGFA, ADAM17, AMOT, PDGFRB, LAMC1, PLA1	1.13E-07	2.08E-04
GOTERM_BP_FAT GO:0048870~cell motility	49	4.24978317	PVR, PPARD, CCL2, ACVRL1, TNFRSF12A, WASF2, ITGA11, CSPG4, GJA1, FGF10, ITGB1, CD2AP, CXCL12, TGFB1, TGFB2, NDE1, DOCK1, CD44, ANG, CTGF, ITGAV, CKLF, FCER1G, TNN, LBP, MSN, FGF2, TWIST1, PLAT, B4GALT1, ICAM1, ARID5B, AXL, ITGA1, ITGA4, MYH9, MMP14, COL5A1, ABCC9, ETS1, CD34, ITGA5, CX3CR1, VEGFA, ADAM17, AMOT, PDGFRB, LAMC1, PLA1	1.13E-07	2.08E-04
GOTERM_BP_FAT GO:0010035~response to inorganic substance	43	3.72940156	CAV1, APOBEC1, PTGS2, PDGFA, NR3C1, MMP2, B2M, GSS, ANXA7, GSN, ALB, HMOX1, GPX3, CASP8, SERPINE1, SHC1, PLCD1, FAS, SEPP1, FOSL1, IL6, S100A16, ACADM, OLR1, CRYAB, SPHK1, ANXA1, MGP, SPARC, STAT1, PRKCD, SOD3, PLA2G4A, CCND1, CDKN1A, ABCB1B, AS3MT, CASP12, AVPR1A, PDGFRA, CYBRD1, PDGFRB, COL1A1	1.14E-07	2.10E-04
GOTERM_BP_FAT GO:0009628~response to abiotic stimulus	56	4.85689506	PPARD, APOBEC1, LXN, IGFBP7, PPARG, GJA1, PMAIP1, MMP2, CXCL12, TGFB1, TGFB2, BAK1, PLCB3, CASP8, SERPINE1, SHC1, COL11A1, ACADM, LYN, CRYAB, MGP, MMP14, PRKCD, EYA1, CCND1, ABCB1B, HSPB1, COL1A1, TGFB1, HIF, CAV1, CCL2, SIPA1, COL3A1, HSPA1A, HSPA1B, DCN, TIMP3, ANXA7, NTEC, PKD2, TRIP10, MYOF, BMP4, PTPRC, IL6, BMP2, TGFB2, ANXA1, SPARC, STAT1, PLA2G4A, CDKN1A, CASP12, AVPR1A, CD14	1.17E-07	2.15E-04
GOTERM_BP_FAT GO:0006955~immune response	57	4.94362533	APOBEC1, TLR3, TLR4, NFKB2, IL15, TLR6, CXCL12, TGFB1, B2M, MYD88, OASL2, ILIRAP, CFH, ERAP1, LBP, FAS, RAB27A, ICAM1, BCL10, SP100, LYN, IRGM, COLEC12, PRKCD, VEGFA, CX3CR1, ADAM17, IL1R1, CCL2, ENPP3, FCGRT, SP110, LIF, TNFRSF1B, PROCR, TAP1, FCER1G, CD4, IL2RG, MR1, C2, CD28, PTPRC, IL6, OLR1, SWAP70, CFB, IL1RL2, SMAD6, MYO1F, PLSCR1, CYBA, ABCC9, CYBB, CXCL13, CXCL16, CD14	1.71E-07	3.14E-04
GOTERM_BP_FAT GO:0051781~positive regulation of cell division	13	1.1274935	VEGFC, S100A6, FGF7, PDGFA, PGF, VEGFA, TGFB3, PDGFC, PDGFD, FGF1, FGF2, TGFB1, TGFB2	1.72E-07	3.17E-04
GOTERM_BP_FAT GO:0010627~regulation of protein kinase cascade	40	3.46921075	PPARD, CAV1, LITAF, SLC20A1, IL6ST, GJA1, FGF10, TLR3, TLR4, LPAR1, TLR6, ITGB1, TGFB1, TGFB2, LIF, TNFRSF1A, MYD88, MDIC, HMOX1, ITGAV, CASP8, RHOC, CASP1, PHLDA3, GHR, CFLAR, BCL10, PTPRC, IL6, LTBR, LYN, LGALS1, EDA2R, PRKCD, TRADD, IKKBE, TNFRSF10B, F3, RIPK2, NEK6	1.91E-07	3.51E-04
GOTERM_BP_FAT GO:0033273~response to vitamin	25	2.16825672	ALPL, CCL2, PTGS2, PDGFA, IGFBP7, PPARG, TRIM16, TIMP3, TGFB1, TGFB2, VDR, CD44, GSN, RUNX1, BMP4, BMP2, RARG, TRIM25, SPARC, CD38, CCND1, PLA2G4A, SERPINF1, PDGFRB, KLF4	2.42E-07	4.44E-04
GOTERM_BP_FAT GO:0050678~regulation of epithelial cell proliferation	21	1.82133565	BMP4, B4GALT1, IL6, PPARD, FGF7, TGFB3, FGF10, CDK6, TGFB1, MMP12, TGFB2, PGR, VEGFC, CDKN2B, SERPINF1, VEGFA, WFDC1, FGF1, TBX18, FGF2, RUNX3	2.82E-07	5.19E-04
GOTERM_BP_FAT GO:0048705~skeletal system morphogenesis	25	2.16825672	PRRX1, TGFB3, PRRX2, MMP2, TGFB1, TGFB2, HOXC6, HOXC9, CTGF, HOXA5, HOXA6, ACAN, COL11A1, RUNX2, GHR, RARG, ARID5B, TGFB2, LOC13641, FMN1, SHOX2, EYA1, PDGFRA, PDGFRB, ROR2, COL1A1	3.41E-07	6.26E-04
GOTERM_BP_FAT GO:0008219~cell death	56	4.85689506	DLC1, PPARD, NUAKE2, GJA1, PMAIP1, PAWR, TGFB1, TGFB2, ASAH2, BAK1, CASP4, UNC5B, GSN, HMOX1, BAG3, BAG2, CASP8, FAS, DAP, CASP1, FGF2, TWIST1, CIB1, BCL10, PARM1, GZMB, STK3, AHR, TNFRSF10B, F3, RIPK3, NEK6, NGF, LITAF, TNFRSF12A, GULP1, ADAMTSL4, STK17B, SP110, GREM1, TNFRSF1A, TNFRSF1B, TMEM123, ZC3H12A, PHLDA3, SRGN, HIP1, CFLAR, LYZ2, IL6, OLR1, CIDEA, TRADD, PLEKHF1, CASP12, MPHOSPH8	3.69E-07	6.77E-04
GOTERM_BP_FAT GO:0009612~response to mechanical stimulus	20	1.73460538	BMP4, BMP2, CAV1, IL6, CCL2, TGFB2, MGP, DCN, MMP14, STAT1, MMP2, PRKCD, TIMP3, CXCL12, PKD2, RHOC, COL1A1, COL11A1, FOSL1, NGF	3.76E-07	6.90E-04
GOTERM_BP_FAT GO:0030335~positive regulation of cell migration	22	1.90806592	ICAM1, PLD1, IL6ST, PDGFA, CSF1, SPHK1, MYO1F, CXCL12, TGFB1, TGFB2, VEGFC, S1PR1, CXCL16, VEGFA, PDGFRA, ADAM17, PDGFRB, AMOT, RHOC, LAMB1, FGF2, CYR61	3.82E-07	7.01E-04
GOTERM_BP_FAT169~transmembrane receptor protein tyrosine kinase signalin	34	2.94882914	CCL2, FGF7, PDGFA, CSPG4, FGF10, RHOQ, DDR2, TGFB1, EIF4EBP1, HMCN1, CTGF, SHC1, PDGFC, FGF1, FGF2, GHR, CSF1R, PLAT, ARID5B, MYO1E, AXL, HGF, STXB4, EPHA2, STAT3, VEGFC, DOK1, GRB10, VEGFA, PDGFRA, PDGFRB, ROR2, ADAM17, NGF	3.91E-07	7.18E-04
GOTERM_BP_FAT GO:0040017~positive regulation of locomotion	23	1.99479618	ICAM1, PLD1, IL6ST, PDGFA, CSF1, SPHK1, FGF10, MYO1F, CXCL12, TGFB1, TGFB2, VEGFC, S1PR1, CXCL16, VEGFA, PDGFRA, ADAM17, PDGFRB, AMOT, RHOC, LAMB1, FGF2, CYR61	5.77E-07	0.001059
GOTERM_BP_FAT GO:0016265~death	56	4.85689506	DLC1, PPARD, NUAKE2, GJA1, PMAIP1, PAWR, TGFB1, TGFB2, ASAH2, BAK1, CASP4, UNC5B, GSN, HMOX1, BAG3, BAG2, CASP8, FAS, DAP, CASP1, FGF2, TWIST1, CIB1, BCL10, PARM1, GZMB, STK3, AHR, TNFRSF10B, F3, RIPK3, NEK6, NGF, LITAF, TNFRSF12A, GULP1, ADAMTSL4, STK17B, SP110, GREM1, TNFRSF1A, TNFRSF1B, TMEM123, ZC3H12A, PHLDA3, SRGN, HIP1, CFLAR, LYZ2, IL6, OLR1, CIDEA, TRADD, PLEKHF1, CASP12, MPHOSPH8	6.39E-07	0.001173
GOTERM_BP_FAT GO:0002237~response to molecule of bacterial origin	26	2.25498699	CCL2, PTGS2, TLR4, NFKB2, DCN, TLR6, B2M, TNFRSF1A, IRAK3, MYD88, CASP8, FAS, LBP, BCL10, IL6, CFB, SPARC, STAT1, PLA2G4A, RIPK2, ADAM17, PROS1, MGST1, CD14, MGST2, NGF	7.32E-07	0.001345
GOTERM_BP_FAT GO:0031589~cell-substrate adhesion	19	1.64787511	DLC1, LIMS1, PPARD, EPDR1, TNFRSF12A, COL3A1, ACTN1, NID1, NID2, ITGB1, ITGBL1, THY1, CTGF, TNN, RHOC, ANTXR1, LAMC1, LAMB1, FN1	7.69E-07	0.001412
GOTERM_BP_FAT GO:0030155~regulation of cell adhesion	25	2.16825672	ICAM1, ACVRL1, EGFL6, CSF1, CCDC80, MYO1F, NID1, CDK6, MMP14, SDC4, CD63, MMP2, TPM1, TGFB1, TGFB2, EMILIN1, SMOC2, S1PR1, GSN, FBLN2, RHOC, COL1A1, FGF1, COL8A1, CYR61	7.76E-07	0.001425
GOTERM_BP_FAT GO:0001503~ossification	24	2.08152645	BMP4, BMP2, PDLM7, PTGS2, CSF1, TGFB3, FHL2, MGP, SPARC, LOC13641, MMP14, WWTR1, MMP2, COL5A2, TGFB1, SHOX2, CTSK, CHRDL1, CTGF, COL1A1, GPNMB, COL11A1, RUNX2, FN1	8.07E-07	0.001481

GOTERM_BP_FAT	GO:0030334~regulation of cell migration	30	2.60190807	DLC1, ACVRL1, PDGFA, IL6ST, CSF1, GREM1, TPM1, CXCL12, TGFBI, TGFBI2, VCL, SIPR1, RRAS, RHOC, LAMB1, FGF2, CYR61, ICAM1, PLD1, SPHK1, MYO1F, CD63, THY1, VEGFC, CXCL16, VEGFA, PDGFRA, PDGFRB, AMOT, ADAM17	9.86E-07	0.00181
GOTERM_BP_FAT	GO:0006928~cell motion	55	4.77016479	PVR, PPARG, ACVRL1, WASF2, CSPG4, FGF10, GJA1, CXCL12, CD2AP, TGFBI, TGFBI2, NDE1, CD44, UNC5B, ANG, CTGF, LBP, MSN, FGF2, TWIST1, ICAM1, EGR2, ARID5B, MMP14, MYH9, SLIT3, CD34, VEGFA, CX3CR1, PDGFRB, ADAM17, LAMC1, CCL2, TNFRSF12A, ITGA11, ITGB1, DOCK1, ITGAV, CKLF, FCER1G, TNN, B3GNT2, RUNX3, PLAT, B4GALT1, ITGA1, AXL, HGF, ITGA4, COL5A1, ABCCC9, ITGA5, ETS1, AMOT, PLA2	1.07E-06	0.001972
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	53	4.59670425	ADCY4, ADCY7, IL6ST, PDGFA, CSPG4, TGFBI, TGFBI2, TLR4, LPAR1, SDC4, TLR6, LATS2, SPRY4, TGFBI, TGFBI2, BAK1, CDKN2B, ANG, MDIC, PDGFC, SHC1, FGF1, FAM129A, FGF2, GHR, BCL10, LYN, PRKCD, THY1, VEGFC, CCND1, PDGFRB, ADAM17, GADD45B, CAV1, ENPP1, CSF1, DGKA, LIF, IRAK3, C1QTNF2, CD4, BMP4, PTPRC, IL6, BMP2, MAP2K3, SMAD6, SPHK1, TGFBR2, ITGA1, HGF, AVPI1, CDKN1A	1.50E-06	0.002753
GOTERM_BP_FAT	GO:0010810~regulation of cell-substrate adhesion	14	1.21422376	SMOC2, ACVRL1, FBLN2, EGFL6, CSF1, CCDC80, CDK6, NID1, COL1A1, MMP14, SDC4, COL8A1, CYR61, EMILIN1	1.66E-06	0.003057
GOTERM_BP_FAT	GO:0060541~respiratory system development	24	2.08152645	BMP4, RARG, LIPA, FGF7, PDGFA, TGFBR2, TGFBI, TGFBI2, MGP, SPARC, MMP14, ASAH1, TGFBI, TGFBI2, MAN2A1, HOXA5, CTGF, VEGFA, AARD, PDGFRA, HSD11B1, LOX, FGF1, FGF2	1.80E-06	0.003302
GOTERM_BP_FAT	GO:0031099~regeneration	24	2.08152645	CCL2, TGFBR2, PPARG, AXL, GJA1, FGF10, MUSTN1, HGF, MMP2, TIMP3, CXCL12, TGFBI, GAS6, PLAUR, LIF, NOTCH2, CCND1, CDKN1A, LAMB2, GSN, SERPINE1, SHC1, PLA2, TEC	1.80E-06	0.003302
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	54	4.68343452	DLC1, ADCY4, ADCY7, IL6ST, PDGFA, CSPG4, TGFBI, TGFBI2, TLR4, LPAR1, TLR6, SDC4, LATS2, SPRY4, TGFBI, TGFBI2, BAK1, CDKN2B, ANG, MDIC, PDGFC, SHC1, FGF1, FAM129A, FGF2, GHR, BCL10, LYN, PRKCD, THY1, VEGFC, CCND1, PDGFRB, ADAM17, GADD45B, CAV1, ENPP1, CSF1, DGKA, LIF, IRAK3, C1QTNF2, CD4, BMP4, PTPRC, IL6, BMP2, MAP2K3, SMAD6, SPHK1, TGFBR2, ITGA1, HGF, AVPI1, CDKN1A	2.21E-06	0.004058
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	54	4.68343452	DLC1, ADCY4, ADCY7, IL6ST, PDGFA, CSPG4, TGFBI, TGFBI2, TLR4, LPAR1, TLR6, SDC4, LATS2, SPRY4, TGFBI, TGFBI2, BAK1, CDKN2B, ANG, MDIC, PDGFC, SHC1, FGF1, FAM129A, FGF2, GHR, BCL10, LYN, PRKCD, THY1, VEGFC, CCND1, PDGFRB, ADAM17, GADD45B, CAV1, ENPP1, CSF1, DGKA, LIF, IRAK3, C1QTNF2, CD4, BMP4, PTPRC, IL6, BMP2, MAP2K3, SMAD6, SPHK1, TGFBR2, ITGA1, HGF, AVPI1, CDKN1A	2.21E-06	0.004058
GOTERM_BP_FAT	GO:0030324~lung development	23	1.99479618	BMP4, LIPA, FGF7, PDGFA, TGFBR2, TGFBI, TGFBI2, MGP, SPARC, MMP14, ASAH1, TGFBI, TGFBI2, MAN2A1, HOXA5, CTGF, VEGFA, AARD, PDGFRA, HSD11B1, LOX, FGF1, FGF2	2.22E-06	0.004085
GOTERM_BP_FAT	GO:0030323~respiratory tube development	23	1.99479618	BMP4, LIPA, FGF7, PDGFA, TGFBR2, TGFBI, TGFBI2, MGP, SPARC, MMP14, ASAH1, TGFBI, TGFBI2, MAN2A1, HOXA5, CTGF, VEGFA, AARD, PDGFRA, HSD11B1, LOX, FGF1, FGF2	3.05E-06	0.005592
GOTERM_BP_FAT	GO:0051302~regulation of cell division	13	1.1274935	VEGFC, S100A6, FGF7, PDGFA, PGF, VEGFA, TGFBI, TGFBI2, PDGFC, PDGFD, FGF1, FGF2, TGFBI, TGFBI2	3.31E-06	0.006073
GOTERM_BP_FAT	GO:0051216~cartilage development	18	1.56114484	BMP4, BMP2, RARG, PRRX1, MGP, PRRX2, LOC133641, TGFBI, TIMP1, SHOX2, HOXA5, CTGF, ACAN, ROR2, COL1A1, COL1A1, RUNX2, GHR	3.64E-06	0.00668
GOTERM_BP_FAT	GO:0060429~epithelium development	37	3.20901995	DLC1, PGF, CSF1, PPARG, GJA1, FGF10, NR3C1, JAG1, GREM1, TGFBI, H19, PGR, VDR, SIPR1, CD44, HOXA5, CASP8, TWIST1, PLEC, BMP4, B4GALT1, BCL10, BMP2, RARG, COL4A1, ANXA1, CD63, VEGFC, NOTCH2, EYA1, ABCB1B, VEGFA, TGIF1, TGFBI, ID3, TBX18, EMP1	3.90E-06	0.007165
GOTERM_BP_FAT	GO:0010811~positive regulation of cell-substrate adhesion	11	0.95403296	SMOC2, FBLN2, EGFL6, CSF1, CCDC80, CDK6, NID1, COL8A1, SDC4, EMILIN1, CYR61	4.31E-06	0.007906
GOTERM_BP_FAT	GO:0007568~aging	27	2.34171726	PTGS1, TGFBI, NFKB2, DCN, IL15, TIMP3, MMP2, TGFBI, TGFBI2, TIMP1, GSTM2, GSN, SERPINE1, SHC1, FAS, NOX4, IL6, TBX3, CRYAB, TBX2, TGFBR2, PRKCD, PRELP, PLA2G4A, SERPINF1, CASP12, CTSC	4.64E-06	0.008513
GOTERM_BP_FAT	GO:0006954~inflammatory response	34	2.94882914	CCL2, PTGS2, TLR4, IL15, TGFBI, TNFRSF1A, SIPR3, TNFRSF1B, CASP4, CD44, HMOX1, CFH, LBP, C2, FN1, B4GALT1, BMP2, IL6, PTGER3, LIPA, OLR1, LYN, CFB, MAP2K3, SPHK1, STAT3, CYBA, NUPR1, CYP4F5, SLC7A2, F3, MPHOSPH8, CD14, NGF	5.08E-06	0.009332
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	39	3.38248049	CAV1, IL6ST, STK17B, TGFBI, CSPG4, TLR4, LPAR1, LATS2, IRAK4, LIF, MYD88, MDIC, CLCF1, C1QTNF2, PKD2, SHC1, TNIP2, FGF1, FGF2, GHR, CDC42EP5, ZFP36, BCL10, PTPRC, CRYAB, MAP2K3, ITGA1, HGF, STAT1, TANK, STAT3, AVPI1, STK3, DOK1, RIPK3, ROR2, PDGFRB, GADD45B, LRRK2	5.08E-06	0.009332
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	31	2.68863833	DLC1, ACVRL1, PDGFA, IL6ST, CSF1, FGF10, GREM1, TPM1, CXCL12, TGFBI, TGFBI2, VCL, SIPR1, RRAS, RHOC, LAMB1, FGF2, CYR61, ICAM1, PLD1, SPHK1, MYO1F, CD63, THY1, VEGFC, CXCL16, VEGFA, PDGFRA, PDGFRB, AMOT, ADAM17	5.08E-06	0.009336
GOTERM_BP_FAT	GO:0045765~regulation of angiogenesis	16	1.3876843	BCL10, HTATIP2, SPHK1, RNH1, TNFRSF1A, VEGFC, SERPINF1, F3, CX3CR1, SERPINE1, AMOT, ERAP1, RUNX1, FGF2, THBS2, CYR61	5.31E-06	0.009747
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic pr	88	7.63226366	DLC1, ELF1, ACVRL1, THRB, ELF4, WFS1, IL6ST, PDGFA, PPARG, TGFBI, TGFBI2, RHOQ, GJA1, TLR4, PAWR, TGFBI, TGFBI2, PGR, MYD88, SIPR1, MDIC, PSMD1, SHC1, PDGFC, RHOC, FAM129A, FGF1, FGF2, FOSL1, SAMD4A, GHR, ZFP36, EGR1, BCL10, MYO6, SP100, EGR2, RARG, LYN, PCB1, AHR, THY1, INHBA, VEGFC, CCND1, EYA1, VEGFA, PDGFRA, ADAM17, PDGFRB, NFE2L2, LRRK2, EIF5A2, CLN6, CAV1, CSF1, TRIM16, NR3C1, IRAK4, LIF, STAT6, TNFRSF1A, C1QTNF2, NFAT5, CD4, RUNX1, RUNX2, CD28, BMP4, ZBTB7B, SOAT1, PTPRC, BMP2, IL6, MAP2K3, MAML2, SPHK1, NR4A1, TEAD1, TEAD3, AFF1, WWTR1, STAT3, SHOX2, ETS1, AVPR1A, NFIC, KLF4	5.72E-06	0.010504
GOTERM_BP_FAT	GO:0045937~positive regulation of phosphate metabolic proce	22	1.90806592	DLC1, BMP4, BCL10, BMP2, CAV1, IL6, LYN, IL6ST, SPHK1, TLR4, TGFBI, THY1, LIF, VEGFC, CCND1, ANG, ADAM17, CD4, FAM129A, FGF1, FGF2, GHR	6.01E-06	0.011044
GOTERM_BP_FAT	GO:0010562~positive regulation of phosphorus metabolic proc	22	1.90806592	DLC1, BMP4, BCL10, BMP2, CAV1, IL6, LYN, IL6ST, SPHK1, TLR4, TGFBI, THY1, LIF, VEGFC, CCND1, ANG, ADAM17, CD4, FAM129A, FGF1, FGF2, GHR	6.01E-06	0.011044
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylatio	29	2.5151778	CAV1, ENPP1, IL6ST, PDGFA, TLR4, TLR6, TGFBI, LIF, BAK1, MDIC, CD4, PDGFC, FAM129A, FGF1, FGF2, GHR, BMP4, PTPRC, BMP2, IL6, LYN, SMAD6, SPHK1, PRKCD, THY1, VEGFC, CCND1, PDGFRB, ADAM17	6.30E-06	0.011577
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	23	1.99479618	IL6, CCL2, PTGS2, CFB, TLR4, DCN, SPARC, NFKB2, STAT1, IRAK3, TNFRSF1A, PLA2G4A, MYD88, CASP8, ADAM17, RIPK2, FAS, LBP, PROS1, MGST1, CD14, MGST2, NGF	6.44E-06	0.011817
GOTERM_BP_FAT	GO:0045785~positive regulation of cell adhesion	16	1.3876843	EGFL6, CSF1, CCDC80, NID1, CDK6, SDC4, CD63, TPM1, TGFBI, EMILIN1, SMOC2, FBLN2, RHOC, COL8A1, FGF1, CYR61	6.62E-06	0.01215
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	19	1.64787511	B4GALT1, BMP4, BMP2, PGF, CSF1, TGFBR2, MGP, FGF10, MMP14, GREM1, CXCL12, TGFBI, PGR, VDR, EYA1, CD44, HOXA5, VEGFA, CYR61	6.70E-06	0.012298
GOTERM_BP_FAT	GO:0001822~kidney development	23	1.99479618	BMP4, BMP2, WFS1, PGF, MYO1E, ARID5B, FBN1, NID1, DCN, SDC4, WWTR1, GREM1, TENC1, TGFBI, EYA1, CD44, SERPINF1, ITGA8, PKD2, PDGFRB, ADAMTS1, ALDH9A1, C1GALT1	7.43E-06	0.013642
GOTERM_BP_FAT	GO:0045087~innate immune response	19	1.64787511	BCL10, IL1R1, SP100, CFB, IRGM, IL1R1, TLR3, TLR4, SP110, TLR6, TGFBI, CYBA, CYBB, MYD88, CXCL16, IL1RAP, LBP, C2, RAB27A	7.98E-06	0.01466

GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	37	3.20901995	THRB, PDLIM7, TNFRSF12A, IL6ST, CSF1, PPARG, TGFβ3, TRIM16, JAG1, CXCL12, TGFβ1, TGFβ2, LIF, CDKN2B, IL2RG, RHOC, RUNX1, RUNX2, FGF2, FNDC3B, GHR, CSF1R, BMP4, LPL, PTPRC, IL6, BMP2, LYN, TGFβR2, INHBA, VEGFC, SERPINF1, ETS1, TGIF1, RIPK2, TGFβ11, NGF	8.22E-06	0.015102
GOTERM_BP_FAT	GO:0006915~apoptosis	48	4.16305291	DLC1, PPARG, NUA2, LITAF, GULP1, ADAMTSL4, STK17B, GJA1, SP110, PMAIP1, PAWR, GREM1, TGFβ2, ASAH2, BAK1, TNFRSF1A, CASP4, UNC5B, GSN, BAG3, BAG2, CASP8, ZC3H12A, FAS, DAP, CASP1, PHLDA3, FGF2, SRGN, TWIST1, HIP1, CIB1, CFLAR, BCL10, IL6, PARM1, CIDEA, GZMB, AHR, STK3, TRADD, PLEKHF1, TNFRSF10B, F3, CASP12, RIPK3, NEK6, NGF	8.31E-06	0.015251
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	35	3.03555941	PVR, IL6ST, UNC93B1, TLR3, HSPA1A, TLR4, HSPA1B, IL15, TLR6, TGFβ1, TGFβ2, TGFβ2, LAMB2, GSN, HOXA5, SERPINE1, TNN, SEPP1, TEC, BMP4, BMP2, ARID5B, ICAM1, BCL10, PTPRC, IL6, LYN, CFB, TGFβR2, THY1, CD38, CDKN1A, RIPK2, ADAM17, CLEC7A	8.37E-06	0.015367
GOTERM_BP_FAT	GO:0009266~response to temperature stimulus	21	1.82133565	PPARG, IL6, ACADM, CCL2, LYN, CRYAB, LXN, IGFβP7, PPARG, HSPA1A, HSPA1B, PRKCD, CXCL12, TGFβ2, PLA2G4A, TFEC, CASP8, CASP12, HSPB1, TGFβ11, MYOF, CD14	1.02E-05	0.018711
GOTERM_BP_FAT	GO:0040007~growth	33	2.86209887	ATP6V0E1, PPARG, PTGS2, CSF1, TGFβ3, FGF10, GJA1, MMP2, TENC1, TIMP3, TGFβ1, TGFβ2, LAMB2, GSN, HOXA5, SERPINE1, TNN, SEPP1, TEC, BMP4, BMP2, ARID5B, AXL, MUSTN1, GAS6, PLAUR, INHBA, NOTCH2, LEPRE1, NUPR1, EMP3, EMP1, PLAU	1.11E-05	0.020395
GOTERM_BP_FAT	GO:0043627~response to estrogen stimulus	26	2.25498699	BMP4, CAV1, PTGS2, PDGFA, CRYAB, PPARG, TGFβR2, ANXA1, TGFβ3, MFGE8, TRIM25, MMP14, AQP1, MMP2, TIMP3, STAT3, TGFβ1, TGFβ2, CD38, CCND1, HMOX1, CASP8, PDGFRA, PDGFRB, WDC1, FAS	1.12E-05	0.020636
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	34	2.94882914	DLC1, FGF7, PGF, CSF1, FGF10, NR3C1, JAG1, GREM1, TGFβ1, TGFβ2, PGR, VDR, CD44, HOXA5, CASP8, COL11A1, RUNX3, TWIST1, BMP4, BCL10, BMP2, RARG, TBX3, SNAI1, EPHA2, NOTCH2, VEGFC, EYA1, COL1A2, TGIF1, COL1A1, TGFβ11, TBX18, KLF4	1.35E-05	0.024701
GOTERM_BP_FAT	GO:0042327~positive regulation of phosphorylation	21	1.82133565	BMP4, BCL10, BMP2, CAV1, IL6, LYN, IL6ST, SPHK1, TLR4, TGFβ1, THY1, LIF, VEGFC, CCND1, ANG, ADAM17, CD4, FAM129A, FGF1, FGF2, GHR	1.38E-05	0.025255
GOTERM_BP_FAT	GO:0012501~programmed cell death	48	4.16305291	DLC1, PPARG, NUA2, LITAF, GULP1, ADAMTSL4, STK17B, GJA1, SP110, PMAIP1, PAWR, GREM1, TGFβ2, ASAH2, BAK1, TNFRSF1A, CASP4, UNC5B, GSN, BAG3, BAG2, CASP8, ZC3H12A, FAS, DAP, CASP1, PHLDA3, FGF2, SRGN, TWIST1, HIP1, CIB1, CFLAR, BCL10, IL6, PARM1, CIDEA, GZMB, AHR, STK3, TRADD, PLEKHF1, TNFRSF10B, F3, CASP12, RIPK3, NEK6, NGF	1.47E-05	0.027015
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal pro	36	3.12228968	CAV1, CCL2, PTGS2, CSF1, PTGS1, TGFβ3, TLR3, TRIM16, TLR4, TGFβ1, TGFβ2, VDR, MYD88, ALB, HEY2, FCER1G, RHOC, SHC1, LBP, CASP1, FGF2, AGPAT2, GHR, BMP4, B4GALT1, IL6, BMP2, SPHK1, TRADD, CD38, PLA2G4A, AVPR1A, PDGFRB, RIPK2, ADAM17, CLEC7A	1.57E-05	0.028745
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	38	3.29575022	ADCY4, CAV1, ADCY7, CSF1, TGFβ3, CSPG4, LPAR1, TLR6, SDC4, LATS2, SPRY4, TGFβ1, TGFβ2, DGKA, IRAK3, CDKN2B, ANG, MDIC, C1QTNF2, CD4, PDGFC, SHC1, FGF2, GHR, PTPRC, IL6, MAP2K3, SPHK1, TGFβR2, ITGA1, HGF, PRKCD, AVPI1, THY1, CCND1, CDKN1A, ADAM17, GADD45B	1.75E-05	0.032069
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	94	8.15264527	RHOJ, DLC1, ADCY4, RAB9A, ADCY7, IL6ST, WASF2, TGFβ3, CSPG4, RHOQ, TLR4, LPAR1, LATS2, IQGAP1, PGR, S1PR3, PLCB3, ARL11, MYD88, S1PR1, PLCB4, GSN, CLCF1, CTGF, MDIC, HMOX1, SHC1, RHOC, TNIP2, FGF1, GNG5, PGF2, RHOG, GHR, RAB27A, ZFP36, BCL10, RSU1, MYO6, PTGER3, SP100, RARG, LYN, CRYAB, ARHGEF6, ARHGEF5, PRKCD, STK3, TANK, DOK1, CCND1, TNS1, PTPRV, RIPK3, COL1A2, ROR2, PDGFRB, GADD45B, LRRK2, LRRK1, NGF, CAV1, MAPKAPK3, STK17B, GNG11, NR3C1, GNG12, IRAK4, LIF, DGKA, VDR, CDC42EP1, RASGRP3, C1QTNF2, PKD2, PLCD1, PHLDA3, TEC, TYROBP, CDC42EP5, PTPRC, KLF9, MAP2K3, SPHK1, ITGA1, NPR2, HGF, NPR3, STAT1, STAT3, AVPI1, NUPR1, RAB34, AVPR1A	1.90E-05	0.034909
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	30	2.60190807	ADCY4, ADCY7, CSF1, TGFβ3, CSPG4, LPAR1, SDC4, TLR6, TGFβ1, TGFβ2, DGKA, ANG, MDIC, C1QTNF2, CD4, PDGFC, SHC1, FGF2, GHR, PTPRC, MAP2K3, SPHK1, TGFβR2, ITGA1, HGF, PRKCD, AVPI1, CCND1, ADAM17, GADD45B	1.94E-05	0.035576
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	26	2.25498699	DLC1, B4GALT1, BMP4, BCL10, BMP2, PGF, CSF1, TGFβR2, GJA1, MGP, FGF10, NR3C1, MMP14, GREM1, CXCL12, TGFβ1, PGR, VDR, EYA1, CD44, HOXA5, CASP8, VEGFA, TGIF1, TWIST1, CYR61	2.55E-05	0.046761
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	73	6.33130963	ELF1, ACVRL1, THRB, ELF4, PDGFA, PPARG, TGFβ3, TLR3, RHOQ, TLR4, PAWR, TGFβ1, TGFβ2, PGR, MYD88, S1PR1, MDIC, SHC1, RHOC, PDGFC, FAM129A, FGF2, FOSL1, SAMD4A, ZFP36, EGR1, BCL10, ICAM1, MYO6, SP100, EGR2, RARG, PCBD1, AHR, INHBA, VEGFA, PDGFRA, PDGFRB, NFE2L2, EIF5A2, TRIM16, NR3C1, IRAK4, LIF, STAT6, TNFRSF1A, C1QTNF2, NFAT5, PLCD1, RUNX1, RUNX2, ACSL5, CD28, SOAT1, ZBTB7B, BMP4, BMP2, IL6, MAP2K3, MAML2, ANXA1, NR4A1, TEAD1, AFF1, TEAD3, WWTR1, STAT3, SHOX2, PLA2G4A, ETS1, AVPR1A, NFIC, KLF4	2.65E-05	0.048646
GOTERM_BP_FAT	GO:0007565~female pregnancy	20	1.73460538	KLF9, PTGS2, PGF, CALD1, IGFβP7, SPHK1, TGFβR2, TGFβ3, TGFβ1, TGFβ2, LIF, PGR, CD38, VDR, PLA2G4A, GPX3, LAMB1, FOSL1, PLAU, PLEC	2.70E-05	0.049499