

Figure 3 – figure supplement 4

Term		Count	Fold Enrichment	PValue	FDR	Genes
GO:0006464	protein modification process	79	2.19	2.03E-11	3.22E-08	HECW1, RPS6KB2, CASK, RPS6KB1, ALG9, PAK6, CTTNBP2, KDM1A, CSNK2A1, PAK3, AAK1, MAP3K9, CLK4, EEF2K, OGT, TLK2, USP16, CDK13, PTPRK, PAN3, PTPRF, ROCK1, MADD, PICK1, WNK1, CDK8, PTPRS, MINK1, WNK3, WNK2, UBE2H, CDKL3, GAK, MGAT1, MAP4K3, ACVR2A, SPAG9, MAP4K4, DDR1, UHRF2, HUWE1, MAPK9, MAPK7, EIF2AK4, EP400, KALRN, FGFR2, GANAB, ERBB4, NEK1, CAMK2G, BRSK2, MKNK1, ABI1, PXX, PTK2, PPP3CB, DCLK2, LMTK3, CAMK2B, NEDD4L, PPAP2A, TCF3, TRIP12, PTPRD, ST6GAL2, PTPRZ1, PTPN5, PTPRA, CREBBP, MAP2K4, SMAD2, ATR, EPHA5, EPHA7, SLC4A10, AKTIP, PHF16, CDC42BPA
GO:0016310	phosphorylation	52	2.53	1.18E-09	1.88E-06	RPS6KB2, CASK, RPS6KB1, PAK6, CTTNBP2, CSNK2A1, PAK3, AAK1, MAP3K9, CLK4, EEF2K, TLK2, CDK13, PAN3, ROCK1, MADD, PICK1, CDK8, WNK1, MINK1, WNK3, WNK2, CDKL3, GAK, MAP4K3, MAP4K4, DDR1, SPAG9, ACVR2A, MAPK9, MAPK7, EIF2AK4, KALRN, FGFR2, ERBB4, CAMK2G, NEK1, BRSK2, MKNK1, ABI1, PXX, PTK2, DCLK2, LMTK3, CAMK2B, MAP2K4, PTPRA, SMAD2, ATR, EPHA5, EPHA7, CDC42BPA
GO:0044267	cellular protein metabolic process	98	1.64	2.69E-07	4.26E-04	RPS6KB2, CASK, RPS6KB1, KDM1A, CTTNBP2, CSNK2A1, AAK1, MAP3K9, CLK4, RBCK1, OGT, TLK2, PTPRK, PAN3, ROCK1, PTPRF, MADD, PICK1, WNK1, PTPRS, WNK3, WNK2, CDKL3, NKTR, MAP4K3, MGAT1, MAP4K4, SPAG9, UHRF2, HUWE1, FBXL5, MAPK9, MAPK7, EP400, EIF2AK4, KALRN, FGFR2, ERBB4, NEK1, PXX, PTK2, ARIH2, LMTK3, TCF3, ST6GAL2, PTPN5, CREBBP, MAP2K4, SMAD2, ATR, EPHA5, TULP4, SLC4A10, EPHA7, AKTIP, CDC42BPA, DNAJB5, HECW1, ALG9, SENP7, PAK6, PAK3, SLMAP, EEF2K, USP16, CDK13, CDK8, MINK1, UBE2H, GAK, PJA2, DDR1, ACVR2A, ATG4A, DDB2, GANAB, XIAP, CAMK2G, BRSK2, MKNK1, ABI1, MYCBP2, CYLD, GPHN, PIKFYVE, PPP3CB, DCLK2, CAMK2B, NEDD4L, USP34, PPAP2A, TRIP12, UBL7, PTPRD, PTPRZ1, PTPRA, PHF16, RNF111
GO:0007268	synaptic transmission	20	3.93	7.64E-07	0.0012	KCNMA1, GRIK1, GRIK2, NRXN3, SYNJ1, CLSTN1, GRIN1, PICK1, NLGN1, GRIA4, NRXN1, CTNNA2, CTTNBP2, PTK2, KIF1B, DMD, AGRN, SNAP25, UNC13B, CACNA1B
GO:0000902	cell morphogenesis	27	3.06	8.08E-07	0.0013	ABLIM1, DCC, LIMS1, PARD3, BRSK2, CXCL12, MYCBP2, ALCAM, NRCAM, PTK2, MACF1, ANK3, DMD, FAT1, ROBO2, CLASP2, APC, PTPRZ1, PCDH15, SLIT2, CTNNA2, 4930506M07RIK, EPHA7, SYNE2, APBB2, CHL1, ADD1
GO:0016568	chromatin modification	22	3.26	3.95E-06	0.0063	KDM6A, NASP, A730008H23RIK, MORF4L2, CREBBP, WHSC1, KDM1A, SMARCE1, HUWE1, BPTF, 2210018M11RIK, HJURP, PHF16, SMARCC2, PBRM1, ACTL6B, TLK2, KDM3B, USP16, NCOR1, TCF3, EP400, RERE
GO:0048812	neuron projection morphogenesis	18	3.58	1.13E-05	0.018	DCC, ABLIM1, PTPRZ1, CXCL12, SLIT2, CTNNA2, MYCBP2, ALCAM, NRCAM, 4930506M07RIK, PTK2, EPHA7, ANK3, DMD, ROBO2, APBB2, CHL1, APC
GO:0007409	axonogenesis	17	3.65	1.68E-05	0.027	DCC, ABLIM1, PTPRZ1, CXCL12, SLIT2, CTNNA2, MYCBP2, ALCAM, NRCAM, 4930506M07RIK, PTK2, EPHA7, ANK3, ROBO2, APBB2, CHL1, APC
GO:0048667	cell morphogenesis involved in neuron differentiation	18	3.46	1.76E-05	0.027	DCC, ABLIM1, PTPRZ1, PCDH15, CXCL12, SLIT2, MYCBP2, CTNNA2, ALCAM, NRCAM, 4930506M07RIK, PTK2, EPHA7, ANK3, ROBO2, APBB2, CHL1, APC
GO:0048858	cell projection morphogenesis	19	3.29	1.90E-05	0.030	DCC, ABLIM1, PTPRZ1, PCDH15, CXCL12, SLIT2, MYCBP2, CTNNA2, ALCAM, NRCAM, 4930506M07RIK, PTK2, EPHA7, ANK3, DMD, ROBO2, APBB2, CHL1, APC