

Table S3. GOTERM_MF analysis. Analysis of total DEGs and the subgroups of up- and down-regulated DEGs. Numbers in brackets indicate count of DEGs.

GO:0097367	Carbohydrate derivative binding	37	28	4.10E-06	1.40E-04	BLM, NEK2, DTYMK, TTK, CHEK1, AURKA, AURKB, HMMR, TK1, PAK6, KIF2C, TUBB, BUB1, POLQ, TOP2A, TUBA1C, TRIP13, CDK1, KIF11, MKI67, KIF15, TPX2, CENPE, MCM2, UBE2C, MCM5, SMC4, PLK4, ILF2, LAMC2, RUVBL1, CIT, UBE2S, MELK, UBE2T, KIF26B, KIF20A
GO:0035639	Purine ribonucleoside triphosphate binding	35	26.5	3.50E-07	3.40E-05	BLM, NEK2, DTYMK, TTK, CHEK1, AURKA, AURKB, TK1, PAK6, KIF2C, TUBB, BUB1, POLQ, TOP2A, TUBA1C, TRIP13, CDK1, KIF11, MKI67, KIF15, TPX2, CENPE, MCM2, UBE2C, MCM5, SMC4, PLK4, ILF2, RUVBL1, CIT, UBE2S, MELK, UBE2T, KIF26B, KIF20A
GO:0032550	Purine ribonucleoside binding	35	26.5	3.90E-07	3.20E-05	BLM, NEK2, DTYMK, TTK, CHEK1, AURKA, AURKB, TK1, PAK6, KIF2C, TUBB, BUB1, POLQ, TOP2A, TUBA1C, TRIP13, CDK1, KIF11, MKI67, KIF15, TPX2, CENPE, MCM2, UBE2C, MCM5, SMC4, PLK4, ILF2, RUVBL1, CIT, UBE2S, MELK, UBE2T, KIF26B, KIF20A
GO:0001883	Purine nucleoside binding	35	26.5	4.10E-07	2.80E-05	BLM, NEK2, DTYMK, TTK, CHEK1, AURKA, AURKB, TK1, PAK6, KIF2C, TUBB, BUB1, POLQ, TOP2A, TUBA1C, TRIP13, CDK1, KIF11, MKI67, KIF15, TPX2, CENPE, MCM2, UBE2C, MCM5, SMC4, PLK4, ILF2, RUVBL1, CIT, UBE2S, MELK, UBE2T, KIF26B, KIF20A
Analysis of Down-regulated DGEs						
GO:0043167	Ion binding	92	32.2	2.50E-03	1.10E-01	THRA, PTGS2, LMO3, SNCA, PTGS1, PDLIM3, SOBP, ADH1B, RORA, ATP2B4, PTGIS, CD93, ANG, NR2F1, SPON1, EGRI, KCNMA1, KCND3, CRYAB, ROCK2, SPARCL1, RUNXIT1, ACTN1, MGP, CPXM2, PCDH7, NRXN1, SLIT3, EYA4, PGM5, CHRM3, ZNF135, CD34, PRDM6, PDE5A, PYGO1, PLA2G2A, ZFPM2, DST, CASQ2, SGCA, ADAMTSL3, FHL1, PAMR1, NR3C2, C1S, ZBTB16, MYL9, P3H2, ANXA6, IRAK3, PRUNE2, FAT3, PDE1C, SORBS2, DMD, PKD2, GALNT15, PLCD4, ADAMTSL10, FYCO1, DTNA, BHMT2, ADARB1, SVEP1, LPP, SYT11, PDZRN4, ZNF25, CREB5, PDZRN3, CSRPI, ACACB, ATP1A2, SOD3, ITPR1, MSRB3, CSGALNACT1, ZFHX4, RNF150, PLSCR4, FBLN5, ITGA8, PRICKLE2, CDH19, AOX1, ZBTB4, ANTXR2, DPYD, MYLK, CDH11, PYGB
GO:0043169	Cation binding	90	31.5	1.60E-03	8.80E-02	THRA, PTGS2, LMO3, SNCA, PTGS1, PDLIM3, SOBP, ADH1B, RORA, ATP2B4, PTGIS, CD93, ANG, NR2F1, SPON1, EGRI, KCNMA1, KCND3, CRYAB, ROCK2, SPARCL1, RUNXIT1, ACTN1, MGP, CPXM2, PCDH7, NRXN1, SLIT3, EYA4, PGM5, CHRM3, ZNF135, PRDM6, PDE5A, PYGO1, PLA2G2A, ZFPM2, DST, CASQ2, SGCA, ADAMTSL3, FHL1, PAMR1, NR3C2, C1S, ZBTB16, MYL9, P3H2, ANXA6, IRAK3, PRUNE2, FAT3, PDE1C, SORBS2, DMD, PKD2, GALNT15, PLCD4, ADAMTSL10, FYCO1, DTNA, BHMT2, ADARB1, SVEP1, LPP, SYT11, PDZRN4, ZNF25, CREB5, PDZRN3, CSRPI, ACACB, ATP1A2, SOD3, ITPR1, MSRB3, CSGALNACT1, ZFHX4, RNF150, PLSCR4, FBLN5, ITGA8, PRICKLE2, CDH19, AOX1, ZBTB4, ANTXR2, DPYD, MYLK, CDH11
GO:0046872	Metal ion binding	89	31.1	1.70E-03	8.80E-02	THRA, PTGS2, LMO3, SNCA, PTGS1, PDLIM3, SOBP, ADH1B, RORA, ATP2B4, PTGIS, CD93, ANG, NR2F1, SPON1, EGRI, KCNMA1, KCND3, CRYAB, ROCK2, SPARCL1, RUNXIT1, ACTN1, MGP, CPXM2, PCDH7, NRXN1, SLIT3, EYA4, PGM5, ZNF135, PRDM6, PDE5A, PYGO1, PLA2G2A, ZFPM2, DST, CASQ2, SGCA, ADAMTSL3, FHL1, PAMR1, NR3C2, C1S, ZBTB16, MYL9, P3H2, ANXA6, IRAK3, PRUNE2, FAT3, PDE1C, SORBS2, DMD, PKD2, GALNT15, PLCD4, ADAMTSL10, FYCO1, DTNA, BHMT2, ADARB1, SVEP1, LPP, SYT11, PDZRN4, ZNF25, CREB5, PDZRN3, CSRPI, ACACB, ATP1A2, SOD3, ITPR1, MSRB3, CSGALNACT1, ZFHX4, RNF150, PLSCR4, FBLN5, ITGA8, PRICKLE2, CDH19, AOX1, ZBTB4, ANTXR2, DPYD, MYLK, CDH11
GO:0097367	Carbohydrate derivative binding	51	17.8	8.60E-03	2.40E-01	RHOJ, FGF9, FGF10, DDR2, VCL, CKB, KIF13A, ACTG2, ATP2B4, GPC3, ANG, ILK, RAB23, TUBB6, RHOB, TUBA1A, FGF2, SGK1, ROCK2, PKDCC, NDNF, FLNA, SLIT3, PRELP, PDE5A, CNTN1, ABCA8, FMOD, RERGL, CAMK2G, ABCA6, ANXA6, IRAK3, DMD, ACTC1, ACACB, AK4, ATP1A2, SOD3, EPHA3, NTRK3, ABCC9, HSPA12A, EPHA7, RAB30, MYH11, TGFBR3, ABCC4, HBEGF, PTCH1, MYLK
GO:0008092	Cytoskeletal protein binding	45	15.7	3.30E-12	2.30E-09	CALD1, SNCA, PDLIM3, CACNB2, TPM2, TPM1, DSTN, MYL9, VCL, KIF13A, DES, SORBS1, ANG, SORBS2, DMD, MAPT, PKD2, CNN1, LMOD1, RCSD1, KCNMA1, DIXDC1, ACTC1, CRYAB, SYT11, MAP1A, MAP1B, ACTN1, SYNPO2, REEP1, NEXN, PALLD, FLNC, FLNA, LSP1, SYNE1, TNS1, TAGLN, SVIL, MYH11, SYNLM, DST, MAP7D3, MYLK, TMOD1
GO:0044877	Macromolecular complex binding	33	11.5	1.00E-02	2.50E-01	THRA, CACNB2, TPM2, TPM1, MEIS1, DDR2, DSTN, FOS, SORBS1, MAPT, ILK, YAP1, RCSD1, EGRI, SVEP1, SPARCL1, CRTAP, ACTN1, FLNC, NEXN, FLNA, HHEX, SYNE1, FBLN5, SVIL, PYGO1, MYH11, TGFBR3, PTCH1, SYNLM, DST, JAM3, TMOD1
GO:0046983	Protein dimerization activity	32	11.2	3.40E-03	1.40E-01	RBPMS2, PTGS2, CAMK2G, ZBTB16, MEIS1, ANXA6, FOS, IRAK3, ANG, PKD2, ATOH8, MYOM1, LRRFIP1, STX2, CRYAB, SYT11, MAOB, ACTN1, FLNA, HHEX, RBPMS, SYNE1, HSPB6, PRDM6, FBLN5, HIF3A, ZBTB4, ID4, DPYD, DST, JAM3, CASQ2
GO:0042802	Identical protein binding	32	11.2	2.80E-02	4.60E-01	RBPMS2, PTGS2, CAMK2G, SNCA, ZBTB16, C1S, ANXA6, IRAK3, DES, ANG, PKD2, MYOM1, LRRFIP1, CRYAB, SYT11, MAOB, ACTN1, FLNA, HHEX, RBPMS, SYNE1, FNBPI, HSPB6, PRDM6, PLN, FBLN5, ZBTB4, DPYD, DST, JAM3, CASQ2, SH3GL2
GO:0003779	Actin binding	29	10.1	4.70E-11	1.60E-08	CALD1, CACNB2, TPM2, TPM1, DSTN, VCL, SORBS1, ANG, DMD, LMOD1, CNN1, RCSD1, KCNMA1, DIXDC1, ACTN1, SYNPO2, FLNC, PALLD, NEXN, FLNA, LSP1, SYNE1, TNS1, TAGLN, SVIL, MYH11, DST, MYLK, TMOD1
GO:0005509	Calcium ion binding	26	9.1	2.20E-04	2.20E-02	PAMR1, SNCA, C1S, MYL9, ANXA6, FAT3, CD93, PKD2, PLCD4, SVEP1, SPARCL1, SYT11, ACTN1, MGP, NRXN1, PCDH7, ITPR1, SLIT3, PLSCR4, FBLN5, CDH19, PLA2G2A, DST, CASQ2, SGCA, CDH11