Supplementary Table S6: GO terms and KEGG pathway analyses for the candidated low expressed DE-mRNAs in BC. Through GO terms analysis for the1708 candidate low expressed mRNAs targeted by the hub up-regulated solasonine-related DE-miRNAs in BC, 1311, 128, and 100 remarkably enriched biological process (BP), cellular component (CC) and molecular function (MF) terms were obtained respectively (adj.P-value ≤0.05); through KEGG pathway enrichment analysis, 78 remarkably enriched pathways was obtained (adj.P-value ≤0.05).

Group	ID	Description	GeneRatio	adj.p-value	geneID
BP	GO:0003012	muscle system process	131/1554	1.44E-33	ACTA2, ACTC1, ACTN2, ACTN3, ADRA1A, ADRA2A, ADRA2B, ADRB2, BIN1, ANK2, ANXA6, ARG2, ATP1A2, ATP2B4, BDKRB2, CACNA1C, CACNA2D1, CACNB2, CALD1, CASQ2, CAV1, CHRM2, CHRM3, CLIC2, CNN1, CCN2, DMD, DMPK, DTNA, EDNRA, EDNRB, FLNA, GATA6, GDNF, GNAO1, GPER1, GSN, HRC, IGF1, IGFBP5, IL6ST, ITGA1, KCNA1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNMA1, KIT, SMAD7, MEF2A, MEF2C, MYH2, MYH3, MYH11, MYL3, MYLK, PPP1R12B, P2RX1, P2RY1, PDE4B, PDE4D, PRKCA, PTGER3, PTGS2, RGS2, ROCK1, RYR2, SCN1B, SCN2B, SCN4B, SCN7A, SGCD, SMTN, SLC8A1, SLC8A3, SNTA1, SRF, STAC, STC1, TACR2, TACR1, TACR3, TLN1, TMOD1, TNNT2, TPM1, TPM2, TRPC3, UTRN, VCL, SLMAP, NR4A3, SSPN, DYSF, SORBS2, PDE5A, CACNA1H, MYOM2, KLF4, HAND2, AKAP6, ROCK2, HDAC4, GJC1, NMUR1, KLHL41, MYL9, SORBS1, PDLIM5, PPARGC1A, AKAP13, SYNM, KCNE4, LMOD1, KLF15, CTNNA3, LMCD1, TNNI3K, MYOZ2, ERRFI1, SCN3B, LMOD3, TBX20, TRIM63, MLIP, RCSD1, MYOCD, HSPB6, GATA5
BP	GO:0006936	muscle contraction	107/1554	2.22E-29	ACTA2, ACTC1, ACTN2, ACTN3, ADRA1A, ADRA2A, ADRA2B, ADRB2, BIN1, ANK2, ANXA6, ARG2, ATP1A2, ATP2B4, BDKRB2, CACNA1C, CACNA2D1, CACNB2, CALD1, CASQ2, CAV1, CHRM2, CHRM3, CLIC2, CNN1, CCN2, DMD, DMPK, DTNA, EDNRA, EDNRB, FLNA, GDNF, GNAO1, GPER1, HRC, ITGA1, KCNA1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNMA1, KIT, SMAD7, MYH2, MYH3, MYH11, MYL3, MYLK, PPP1R12B, P2RX1, PDE4B, PDE4D, PTGER3, PTGS2, RGS2, ROCK1, RYR2, SCN1B, SCN2B, SCN4B, SCN7A, SGCD, SMTN, SLC8A1, SLC8A3, SNTA1, SRF, STAC, STC1, TACR2, TACR1, TACR3, TLN1, TMOD1, TNNT2, TPM1, TPM2, UTRN, VCL, SLMAP, SSPN, DYSF, PDE5A, CACNA1H, MYOM2, ROCK2, HDAC4, GJC1, NMUR1, KLHL41, MYL9, SORBS1, SYNM, KCNE4, LMOD1, CTNNA3, TNNI3K, SCN3B, LMOD3, TBX20, TRIM63, RCSD1, MYOCD, HSPB6
BP	GO:0003015	heart process	79/1554	1.40E-18	ACTC1, ADRA1A, BIN1, ANK2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CHRM2, CLIC2, CCN2, DMD, DMPK, HBEGF, FLNA, FYN, GNAO1, HRC, IL2, ITPR1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK3, SMAD7, MEF2A, MYL3, NPR1, NPR2, PDE4B, PDE4D, RGS2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SGCD, SGCG, SLC8A2, SLC8A1, SLC8A3, SNTA1, STC1, TAC1, TACR3, THRA, TNNT2, TPM1, TRPC1, PDE5A, CACNA1H, HDAC4, GJC1, ABCC9, SEMA3A, CELF2, BVES, AKAP13, KCNE4, WWTR1, HSPB7, CTNNA3, KCNIP3, KCNIP1, TNNI3K, FXYD6, SCN3B, SPTBN4, KCNIP4, SGCZ
BP	GO:0060047	heart contraction	76/1554	8.12E-18	ACTC1, ADRA1A, BIN1, ANK2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CHRM2, CLIC2, CCN2, DMD, DMPK, HBEGF, FLNA, GNAO1, HRC, IL2, ITPR1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK3, SMAD7, MEF2A, MYL3, NPR1, NPR2, PDE4B, PDE4D, RGS2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SGCD, SGCG, SLC8A2, SLC8A1, SLC8A3, SNTA1, STC1, TAC1, TACR3, THRA, TNNT2, TPM1, TRPC1, PDE5A, CACNA1H, HDAC4, GJC1, ABCC9, SEMA3A, CELF2, BVES, KCNE4, HSPB7, CTNNA3, KCNIP3, KCNIP1, TNNI3K, FXYD6, SCN3B, SPTBN4, KCNIP4, SGCZ
BP	GO:0008016	regulation of heart contraction	71/1554	9.71E-18	ADRA1A, BIN1, ANK2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CHRM2, CLIC2, CCN2, DMD, DMPK, HBEGF, FLNA, GNAO1, HRC, IL2, ITPR1, KCND3, KCNH2, KCNJ3, KCNJ12, KCNK3, SMAD7, MEF2A, MYL3, NPR1, NPR2, PDE4B, PDE4D, RGS2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SLC8A2, SLC8A1, SLC8A3, SNTA1, STC1, TAC1, TACR3, THRA, TNNT2, TPM1, TRPC1, PDE5A, CACNA1H, HDAC4, GJC1, ABCC9, SEMA3A, CELF2, BVES, KCNE4, HSPB7, CTNNA3, KCNIP3, KCNIP1, TNNI3K, FXYD6, SCN3B, SPTBN4, KCNIP4
BP	GO:0060537	muscle tissue development	95/1554	9.71E-18	ACTC1, ACTN2, ACTN3, ADRA1A, ATF3, BCL2, BMP5, BMPR1A, CAV1, CFL2, COL19A1, DCN, S1PR1, EGR1, EGR2, ELN, EPHB1, EYA1, FGF2, FGF9, FGFR1, FOS, GATA6, HLF, ID2, IGF1, IGFBP5, KCNK2, SMAD7, MEF2A, MEF2C, MEF2D, MEIS1, MYH11, MYL3, MYLK, PDGFRA, PGM5, PIM1, PITX1, PKD2, PROX1, RBP4, RGS2, RYR2, SGCB, SGCD, SGCG, SHH, SLC8A1, SRF, SVIL, TBX5, TCF21, TGFBR2, TGFBR3, TNNT2, TPM1, BTG2, KCNAB1, FZD7, SORBS2, ITGA8, NEURL1, MYOM2, HAND1, AKAP6, HDAC4, GJC1, KLHL41, PDLIM5, PPARGC1A, BVES, AKAP13, DKK1, KDM6B, ZFPM2, MAFF, TIPARP, CDON, MYOZ2, SOX6, LMOD3, ADAMTS9, TBX20, JPH2, ALPK3, SOX17, MYOCD, FOXP2, OSR1, SGCZ, GATA5, SIK1, RBM24
BP	GO:1903522	regulation of blood circulation	78/1554	1.26E-17	ADRA1A, ADRA2A, ADRA2B, BIN1, ANK2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, BDKRB2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CHRM2, CHRM3, CLIC2, CCN2, DMD, DMPK, HBEGF,

					FLNA, GNAO1, HRC, IL2, ITPR1, KCND3, KCNH2, KCNJ3, KCNJ12, KCNK3, SMAD7, MEF2A, MYL3, NPR1, NPR2, P2RX1, PDE4B, PDE4D, PTGS2, RGS2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SLC8A2, SLC8A1, SLC8A3, SNTA1, STC1, TAC1, TACR3, THRA, TNNT2, TPM1, TRPC1, PDE5A, PER2, CACNA1H, HDAC4, GJC1, ABCC9, SEMA3A, CELF2, BVES, KCNE4, HSPB7, CTNNA3, KCNIP3, KCNIP1, TNNI3K, FXYD6, SCN3B, SPTBN4, KCNIP4
BP	GO:0007517	muscle organ development	94/1554	3.65E-17	ACTC1, ACTN3, ADARB1, ATF3, BCL2, BMPR1A, CAV1, CFL2, COL6A3, COL19A1, DCN, DMD, HBEGF, S1PR1, EGR1, EGR2, EGR3, ELN, EPHB1, EVC, FGF2, FGF9, FGFR1, FHL1, FOS, GATA6, HLF, IGF1, ITGA7, KCNK2, LIF, SMAD7, MEF2A, MEF2C, MEF2D, MEIS1, MSX1, MYH3, MYL3, MYLK, PIM1, PITX1, POU6F1, PROX1, RBP4, RGS2, RYR2, SGCB, SGCD, SGCG, SHH, SMTN, SVIL, TAGLN, TBX5, TCF21, TGFBR2, TGFBR3, TNNT2, TPM1, UTRN, BTG2, KCNAB1, FZD7, SGCE, CACNA1H, USP2, NEURL1, MYOM2, LARGE1, HAND1, AKAP6, HDAC4, KLHL41, BVES, MRAS, DKK1, SIRT1, ZFPM2, MAFF, CDON, MYOZ2, SOX6, LMOD3, TBX20, JPH2, SOX17, ARID5B, MYOCD, FOXP2, UNC45B, TCF23, RBM24, MKX
BP	GO:0090257	regulation of muscle system process	71/1554	3.90E-17	ACTN3, ADRA1A, ADRA2A, ADRA2B, ADRB2, BIN1, ANK2, ANXA6, ATP1A2, ATP2B4, CACNA1C, CASQ2, CAV1, CHRM2, CHRM3, CLIC2, CNN1, CCN2, DMD, DMPK, FLNA, GPER1, HRC, IGF1, IGFBP5, IL6ST, KCNA1, KCNMA1, KIT, SMAD7, MEF2A, MYL3, PPP1R12B, P2RX1, PDE4B, PDE4D, PRKCA, PTGS2, RGS2, ROCK1, RYR2, SLC8A1, SLC8A3, SRF, STC1, TACR2, TACR1, TACR3, TNNT2, TPM1, TRPC3, UTRN, NR4A3, PDE5A, KLF4, HAND2, AKAP6, ROCK2, HDAC4, MYL9, PPARGC1A, CTNNA3, LMCD1, TNNI3K, ERRFI1, TRIM63, MLIP, MYOCD, FBXO32, HSPB6, GATA5
BP	GO:0014706	striated muscle tissue development	88/1554	1.38E-15	ACTC1, ACTN2, ACTN3, ADRA1A, ATF3, BCL2, BMP5, BMPR1A, CAV1, CFL2, COL19A1, DCN, S1PR1, EGR1, EGR2, ELN, EPHB1, EYA1, FGF2, FGF9, FGFR1, FOS, GATA6, HLF, ID2, IGF1, KCNK2, SMAD7, MEF2A, MEF2C, MEF2D, MEIS1, MYH11, MYL3, PDGFRA, PGM5, PIM1, PITX1, PROX1, RBP4, RGS2, RYR2, SGCB, SGCD, SGCG, SHH, SLC8A1, SRF, SVIL, TBX5, TCF21, TGFBR2, TGFBR3, TNNT2, TPM1, BTG2, KCNAB1, FZD7, SORBS2, NEURL1, MYOM2, HAND1, AKAP6, HDAC4, GJC1, KLHL41, PDLIM5, BVES, AKAP13, DKK1, KDM6B, ZFPM2, MAFF, CDON, MYOZ2, SOX6, LMOD3, ADAMTS9, TBX20, JPH2, ALPK3, SOX17, MYOCD, FOXP2, SGCZ, GATA5, SIK1, RBM24
BP	GO:0006941	striated muscle contraction	52/1554	5.33E-14	ACTC1, ACTN3, ADRA1A, BIN1, ANK2, ARG2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CASQ2, CAV1, CLIC2, CCN2, DMD, DMPK, DTNA, FLNA, HRC, KCND3, KCNH2, KCNJ3, KCNJ8, SMAD7, MYH3, MYL3, PDE4B, PDE4D, RGS2, RYR2, SCN1B, SCN2B, SCN4B, SGCD, SLC8A1, SLC8A3, SNTA1, STAC, STC1, TNNT2, TPM1, PDE5A, HDAC4, GJC1, KLHL41, SYNM, KCNE4, CTNNA3, TNNI3K, SCN3B, LMOD3, RCSD1
BP	GO:0035637	multicellular organismal signaling	57/1554	5.33E-14	BIN1, ANK2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, DMPK, S1PR1, FLNA, GPER1, GRIK2, HRC, ITPR1, KCNA1, KCNA2, KCND3, KCNH2, KCNJ3, KCNJ12, KCNK3, MEF2A, NPR1, NPR2, NTRK3, P2RX1, PDE4D, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A2, SLC8A1, SLC8A3, TRPC1, CNTNAP1, CACNA1H, GJC1, ABCC9, NFASC, KCNE4, CTNNA3, KCNIP3, KCNIP1, TNNI3K, FXYD6, SCN3B, SPTBN4, KCNIP4, JAM3
BP	GO:0010959	regulation of metal ion transport	85/1554	7.29E-14	ABL1, ACTN2, ADCYAP1, ADCYAP1R1, ADRA2A, ADRB2, BIN1, ANK2, ATP1A2, ATP1B2, ATP2B4, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAMK2A, CASQ2, CAV1, CLIC2, CNTN1, DMD, DPP6, STOM, FHL1, FLNA, FYN, GEM, GNAO1, GPER1, HRC, HSPA2, IL16, KCNA1, KCNH2, KCNMB1, KCNS2, MYLK, P2RX1, PDE4B, PDE4D, PER1, PKD2, PTGS2, RCVRN, RYR2, SCN1B, SCN2B, SCN4B, CX3CL1, CXCL12, SLC8A1, SNCA, SNTA1, STAC, STC1, VAMP2, TRPC1, TRPC3, UTRN, VIP, WFS1, SLMAP, KCNAB1, DYSF, RGN, AKAP6, KCNE4, REM1, KCNIP3, KCNIP1, FXYD6, SCN3B, JPH2, SPTBN4, P2RY12, AHNAK, KCNIP4, JPH4, FCRL3, TMC2, OSR1, SIK1, CNKSR3, LRRC52
BP	GO:0072001	renal system development	70/1554	1.36E-13	ACTA2, ANGPT1, AQP2, ARG2, BCL2, CD34, COL4A3, COL4A4, DCN, EGR1, EPHA7, EYA1, FBN1, FGF2, FGF10, FGFR1, FOXF1, GDNF, GLI2, ID2, IL6R, CXCR2, ILK, LIF, SMAD7, MEF2C, MYC, NFIA, NID1, OVOL1, PBX1, PCSK5, PDGFRA, PECAM1, PKD1, PKD2, PROX1, PTCH1, RBP4, SALL1, SFRP1, SHH, TCF21, TEK, WFS1, WNT2B, ZBTB16, ITGA8, DCHS1, TBX18, RGN, GCNT3, SLIT2, ADIPOQ, ADAMTS1, MAGI2, SPRY1, WWTR1, KANK2, TIPARP, PYGO1, KLF15, SOX17, FAT4, PDGFD, ARID5B, MYOCD, LRRK2, OSR1, BMPER
BP	GO:0050804	modulation of chemical synaptic transmission	90/1554	1.41E-13	ABL1, ADCYAP1, ADRA1A, ADRB2, ATP1A2, BCHE, BDNF, CACNB2, CAMK2A, CBLN1, CHRM2, CHRNA7, CNR2, CX3CR1, DGKB, EGR2, EPHB1, FYN, GDNF, GPER1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, GRM7, KCNB1, KIT, MAP1A, MAP1B, MAPT, MEF2C, MPP2, NFATC4, NGF, NPTX1, ROR2, P2RX1, P2RY1, PRKN, PLCB4, PLCL1, PPP3CB, PRKAR2B, PRKCB, RELN, PTGS2, RAP1A, CX3CL1, SLC8A2, SLC8A3, SNCA, SRF, STXBP1, VAMP2, SYT4, TAC1, TACR2, CNTN2, PPFIA2, NEURL1, LGI1, ADIPOQ, NRXN1, STXBP5L, AKAP12, RIMS3, FAM107A, SYNPO, CPEB3, NTNG1, NLGN1, DKK1, SORCS3, IGSF9B, RIMS1, SYT11, NCS1, NLGN3, SYBU, SORCS2, CLSTN2, LRRC4, TMEM108, JPH4, PRRT2, LRRK2, CNTN4, LRRTM1, SHISA6
BP	GO:0042692	muscle cell differentiation	83/1554	1.41E-13	ABL1, ACTC1, ACTN2, ADRA1A, BIN1, ANK2, ADGRB3, BCL2, BDNF, CASQ2, CFL2, CTNNA2, DMD, DMPK, EDNRB, FGF9, FGF10, FOXF1, FLNC, GATA6, GPER1, IGF1, IGFBP5, KIT, MEF2A, MEF2C, MSX1, MYH3, MYH11, NFATC1, NFATC2, NFATC4, PDGFRA, PGM5, PROX1, RGS2, RORA, SGCB, SGCD, SHH, SLC8A1, SRF, TBX5, ZEB1, TMOD1, TNNT2, TPM1, DYSF, FZD7, SORBS2, ITGA8, BARX2, CACNA1H,

					MYOM2, AKAP6, HDAC4, KLHL41, PDLIM5, BVES, LDB3, AKAP13, DKK1, KDM6B, SYNE1, SIRT1, LMOD1, EHD2, CDON, PLEKHO1, FBXO40, MYOZ2, SOX6, LMOD3, ALPK3, PRDM6, MYOCD, WFIKKN2, SGCZ, SIK1, RBM24, SYPL2, TMEM119, RBPMS2
BP	GO:0099177	regulation of trans-synaptic signaling	90/1554	1.49E-13	ABL1, ADCYAP1, ADRA1A, ADRB2, ATP1A2, BCHE, BDNF, CACNB2, CAMK2A, CBLN1, CHRM2, CHRNA7, CNR2, CX3CR1, DGKB, EGR2, EPHB1, FYN, GDNF, GPER1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, GRM7, KCNB1, KIT, MAP1A, MAP1B, MAPT, MEF2C, MPP2, NFATC4, NGF, NPTX1, ROR2, P2RX1, P2RY1, PRKN, PLCB4, PLCL1, PPP3CB, PRKAR2B, PRKCB, RELN, PTGS2, RAP1A, CX3CL1, SLC8A2, SLC8A3, SNCA, SRF, STXBP1, VAMP2, SYT4, TAC1, TACR2, CNTN2, PPFIA2, NEURL1, LGI1, ADIPOQ, NRXN1, STXBP5L, AKAP12, RIMS3, FAM107A, SYNPO, CPEB3, NTNG1, NLGN1, DKK1, SORCS3, IGSF9B, RIMS1, SYT11, NCS1, NLGN3, SYBU, SORCS2, CLSTN2, LRRC4, TMEM108, JPH4, PRRT2, LRRK2, CNTN4, LRRTM1, SHISA6
BP	GO:0042391	regulation of membrane potential	89/1554	2.70E-13	ABL1, ACTN2, ADCYAP1, ADRA1A, ADRB2, BIN1, ANK2, ATP1A2, ATP1B2, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CBLN1, CHRNA7, CNR2, DCN, DMD, FHL1, FLNA, GABRA2, GABRA4, GABRG1, GNAQ, GPER1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, JUN, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNK2, KCNK3, KCNMA1, SMAD7, MAPT, MEF2C, MPP2, NTRK3, P2RX1, PRKN, RELN, RYR2, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A1, SNCA, SNTA1, TAC1, SLMAP, TCL1A, CNTNAP1, CACNA1H, NRXN1, AKAP6, RIMS3, GJC1, BVES, NLGN1, IGSF9B, RIMS1, SPART, KCNH4, KCNE4, CTNNA3, NLGN3, PID1, SCN3B, SLC17A7, PIEZO2, TMEM108, RNF122, LRRK2, NALCN, ABCB5, KCNT2, RGS7BP
BP	GO:0006937	regulation of muscle contraction	50/1554	3.42E-13	ACTN3, ADRA1A, ADRA2A, ADRA2B, ADRB2, BIN1, ANK2, ANXA6, ATP1A2, CACNA1C, CASQ2, CAV1, CHRM2, CHRM3, CLIC2, CNN1, CCN2, DMD, DMPK, FLNA, GPER1, HRC, KCNA1, KCNMA1, KIT, SMAD7, MYL3, PPP1R12B, P2RX1, PDE4B, PDE4D, PTGS2, RGS2, RYR2, SLC8A1, SLC8A3, SRF, STC1, TACR2, TACR1, TACR3, TNNT2, TPM1, PDE5A, HDAC4, MYL9, CTNNA3, TNNI3K, MYOCD, HSPB6
BP	GO:1904062	regulation of cation transmembrane transport	76/1554	3.61E-13	ABL1, ACTN2, ADRA2A, ADRB2, BIN1, ANK2, ATP1A2, ATP1B2, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CLIC2, CRHBP, DLG2, DMD, DPP6, STOM, FHL1, FLNA, FYN, GEM, GPER1, GRIA1, GRIN2A, HRC, HSPA2, KCNA1, KCNH2, KCNMB1, KCNS2, MEF2C, PDE4B, PDE4D, PKD2, RELN, RGS2, RYR2, SCN1B, SCN2B, SCN4B, CX3CL1, SLC8A1, SNCA, SNTA1, STAC, VAMP2, TRPC1, UTRN, SLMAP, KCNAB1, DYSF, RGN, AKAP6, PPARGC1A, NLGN1, KCNE4, REM1, KCNIP3, KCNIP1, FXYD6, NLGN3, SCN3B, JPH2, AHNAK, KCNIP4, JPH4, TMC2, OSR1, GSG1L, CNKSR3, SHISA6, LRRC52
BP	GO:0019932	second-messenger-mediated signaling	89/1554	4.70E-13	ACTN3, ADCY2, ADCY5, ADCY9, ADCYAP1, ADCYAP1R1, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ANK2, AQP1, ATP1A2, ATP2B4, ADGRB3, CXCR5, CACNA1C, CALCA, CASQ2, CD22, CLIC2, CCR6, CX3CR1, DMD, DMPK, RCAN1, LPAR1, EDNRB, EPHA5, GNAL, GNAQ, GPR3, GPR26, GPER1, GRIN2A, HRC, IGF1, CXCR2, INPP5A, ITPR1, LHCGR, MAPT, NFATC1, NFATC2, NFATC4, NPR1, NPR2, PDE2A, PDE3A, PDE3B, PDE4D, PKD2, PPP3CB, PRKAR2B, PRKCA, PTGER3, PTGER4, PTGFR, RGS2, RYR2, SELP, SGCD, SLC8A1, THBS1, VIP, PDE5A, RGN, AKAP6, HDAC4, RCAN2, NMUR1, AKAP13, RASD2, LMCD1, PDE11A, ACKR4, RASD1, MYOZ2, TMEM100, JPH2, ADGRL4, P2RY12, NDNF, NCALD, JPH4, C10orf71, LRRK2
BP	GO:0001655	urogenital system development	74/1554	4.70E-13	ACTA2, ANGPT1, ANXA1, AQP2, AR, ARG2, BCL2, CD34, COL4A3, COL4A4, DCN, EGR1, EPHA7, ESR1, EYA1, FBN1, FGF2, FGF10, FGFR1, FOXF1, GDNF, GLI2, ID2, ID4, IL6R, CXCR2, ILK, LIF, SMAD7, MEF2C, MYC, NFIA, NID1, OVOL1, PBX1, PCSK5, PDGFRA, PECAM1, PKD1, PKD2, PROX1, PTCH1, RBP4, SALL1, SFRP1, SHH, TCF21, TEK, WFS1, WNT2B, ZBTB16, ITGA8, DCHS1, TBX18, RGN, GCNT3, SLIT2, ADIPOQ, ADAMTS1, MAGI2, SPRY1, WWTR1, KANK2, TIPARP, PYGO1, KLF15, SOX17, FAT4, PDGFD, ARID5B, MYOCD, LRRK2, OSR1, BMPER
BP	GO:0031589	cell-substrate adhesion	77/1554	7.01E-13	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, ANGPT1, APOD, ARHGAP6, AXL, BCL2, CD34, COL13A1, CCN2, DUSP3, EDA, EPHA3, EPHB1, FER, FOXF1, FLNA, GPM6B, HSPG2, CCN1, ILK, ITGA1, ITGA5, ITGA7, ITGB3, LAMC1, LRP1, NID1, DDR2, PECAM1, PIK3R1, PKD1, ROCK1, CX3CL1, SFRP1, SRF, TEK, THBS1, UTRN, VCL, VWF, FZD7, PPFIA2, ITGA8, SGCE, ROCK2, LAMC3, DLC1, FBLN5, SORBS1, LYVE1, FERMT2, EMILIN1, BVES, FAM107A, MMRN1, CORO1C, ABI3BP, SNED1, TMEM8B, EPDR1, RADIL, PARVA, AJAP1, ADAMTS9, NDNF, PEAK1, JAM3, PHLDB2, EMILIN3, MYADM, CCDC80, FREM1, NEXMIF
BP	GO:0001503	ossification	83/1554	7.01E-13	ADRB2, BCL2, BMP5, BMPR1A, CEBPD, COL13A1, CCN2, S1PR1, EGR2, EPHA2, FGF9, GDF2, GDF10, GLI2, GPM6B, HGF, ID2, ID4, IGF1, IGFBP5, CCN1, IL6R, IL6ST, ILK, JUNB, JUND, MEF2C, MEF2D, MGP, MMP2, MMP16, MN1, NPR2, ROR2, DDR2, OMD, PBX1, ENPP1, PRKD1, PTCH1, PTGER4, PTGS2, RORB, SFRP1, SFRP2, SHH, SLC8A1, STC1, TAC1, TEK, TGFB3, THRA, KLF10, CLEC3B, ZBTB16, FGF23, DCHS1, CHRD, PDLIM7, HAND2, HDAC4, RASSF2, CLEC3A, DKK1, ZHX3, WWTR1, DHH, SBDS, CSGALNACT1, TP53INP2, FAT4, PKDCC, CHRDL1, TWIST2, OSR1, PPARGC1B, GLIS1, RANBP3L, IGSF10, TMEM119, RSPO2, OSTN, RFLNB
BP	GO:0006874	cellular calcium ion homeostasis	91/1554	7.01E-13	ABL1, ADCY5, ADCYAP1, ADCYAP1R1, ADRA1A, ANK2, ANXA6, ATP1A2, ATP2B3, ATP2B4, BCL2, BDKRB2, CXCR5, CACNA1C, CACNA2D1, CACNB2, CALCA, CASQ2, CAV1, MS4A1, CHRNA7, CLIC2, CCR6, CX3CR1, CD55, DMD, DMPK, S1PR1, LPAR1, S1PR3, EDNRA, EDNRB, EPHX2, ESR1, FGF2, FYN,

					GPR17, GPER1, GRIA1, GRIK2, GRIN2A, HRC, IL2, CXCR2, ITPR1, KCNK3, LRP1, P2RX1, P2RY1, PDE4D, PDGFRA, PKD1, PKD2, PRKCB, PTGER3, PTGER4, PTGFR, RYR2, RYR3, CX3CL1, CXCL12, SLC8A2, SLC8A1, SLC8A3, SNCA, STC1, TAC1, TACR1, TRPC1, TRPC3, TRPC4, WFS1, TRPA1, RGN, GPR55, AKAP6, CXCL13, SYNPO, RASA3, NCS1, P2RY10, ACKR4, JPH2, SLC24A3, SLC25A23, RIC3, JPH4, SLC24A4, SYPL2, P2RY8, FAM155A
BP	GO:0061337	cardiac conduction	45/1554	7.74E-13	BIN1, ANK2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, DMPK, FLNA, HRC, ITPR1, KCND3, KCNH2, KCNJ3, KCNJ12, KCNK3, MEF2A, NPR1, NPR2, PDE4D, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SLC8A2, SLC8A1, SLC8A3, TRPC1, GJC1, ABCC9, KCNE4, CTNNA3, KCNIP3, KCNIP1, TNNI3K, FXYD6, SCN3B, SPTBN4, KCNIP4
BP	GO:0055074	calcium ion homeostasis	92/1554	1.35E-12	ABL1, ADCY5, ADCYAP1, ADCYAP1R1, ADRA1A, ANK2, ANXA6, ATP1A2, ATP2B3, ATP2B4, BCL2, BDKRB2, CXCR5, CACNA1C, CACNA2D1, CACNB2, CALCA, CASQ2, CAV1, MS4A1, CHRNA7, CLIC2, CCR6, CX3CR1, CD55, DMD, DMPK, S1PR1, LPAR1, S1PR3, EDNRA, EDNRB, EPHX2, ESR1, FGF2, FYN, GPR17, GPER1, GRIA1, GRIK2, GRIN2A, HRC, IL2, CXCR2, ITPR1, KCNK3, LRP1, P2RX1, P2RY1, PDE4D, PDGFRA, PKD1, PKD2, PRKCB, PTGER3, PTGER4, PTGFR, RYR2, RYR3, CX3CL1, CXCL12, SGCD, SLC8A2, SLC8A1, SLC8A3, SNCA, STC1, TAC1, TACR1, TRPC1, TRPC3, TRPC4, WFS1, TRPA1, RGN, GPR55, AKAP6, CXCL13, SYNPO, RASA3, NCS1, P2RY10, ACKR4, JPH2, SLC24A3, SLC25A23, RIC3, JPH4, SLC24A4, SYPL2, P2RY8, FAM155A
BP	GO:0034765	regulation of ion transmembrane transport	93/1554	2.31E-12	ABL1, ACTN2, ADRA2A, ADRB2, BIN1, ANK2, ATP1A2, ATP1B2, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CLIC2, CRHBP, DLG2, DMD, DPP6, STOM, FHL1, FLNA, FYN, GEM, GPER1, GRIA1, GRIN2A, HRC, HSPA2, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNMA1, KCNMB1, KCNS2, MEF2C, PDE4B, PDE4D, ABCB1, PKD2, RELN, RGS2, RYR2, SCN1B, SCN2B, SCN4B, SCN7A, CX3CL1, SLC8A1, SNCA, SNTA1, STAC, VAMP2, THBS1, TRPC1, UTRN, SLMAP, KCNAB1, DYSF, PER2, CACNA1H, RGN, KCNQ4, AKAP6, PPARGC1A, NLGN1, KCNH4, KCNE4, CLIC4, REM1, KCNIP3, KCNIP1, FXYD6, NLGN3, SCN3B, KCNQ5, JPH2, AHNAK, KCNIP4, JPH4, TMC2, OSR1, GSG1L, CNKSR3, NALCN, SHISA6, LRRC52
BP	GO:0051480	regulation of cytosolic calcium ion concentration	76/1554	2.84E-12	ABL1, ADCY5, ADCYAP1, ADCYAP1R1, ADRA1A, ANK2, ATP1A2, ATP2B3, ATP2B4, BCL2, BDKRB2, CXCR5, CACNA1C, CACNA2D1, CACNB2, CALCA, CASQ2, CAV1, MS4A1, CLIC2, CCR6, CX3CR1, CD55, DMD, S1PR1, LPAR1, S1PR3, EDNRA, EDNRB, ESR1, FGF2, FYN, GPR17, GPER1, GRIA1, GRIN2A, HRC, IL2, CXCR2, ITPR1, KCNK3, LRP1, P2RX1, P2RY1, PDE4D, PDGFRA, PKD1, PKD2, PTGER3, PTGER4, PTGFR, RYR2, RYR3, CX3CL1, SLC8A1, SLC8A3, SNCA, TAC1, TACR1, TRPC1, TRPC3, TRPC4, TRPA1, GPR55, AKAP6, CXCL13, SYNPO, RASA3, NCS1, P2RY10, ACKR4, JPH2, RIC3, JPH4, P2RY8, FAM155A
BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	70/1554	6.33E-12	ABL1, ADCY5, ADCYAP1, ADCYAP1R1, ADRA1A, ANK2, ATP1A2, ATP2B4, BCL2, BDKRB2, CXCR5, CACNA1C, CACNA2D1, CACNB2, CALCA, CASQ2, CAV1, MS4A1, CLIC2, CCR6, CX3CR1, CD55, DMD, S1PR1, LPAR1, S1PR3, EDNRA, EDNRB, ESR1, FGF2, FYN, GPR17, GPER1, GRIN2A, HRC, IL2, CXCR2, ITPR1, LRP1, P2RY1, PDE4D, PDGFRA, PKD1, PKD2, PTGER3, PTGER4, PTGFR, RYR2, RYR3, CX3CL1, SLC8A1, SLC8A3, SNCA, TAC1, TACR1, TRPC1, TRPC3, TRPA1, GPR55, AKAP6, CXCL13, SYNPO, RASA3, P2RY10, ACKR4, JPH2, RIC3, JPH4, P2RY8, FAM155A
BP	GO:0001822	kidney development	64/1554	7.34E-12	ACTA2, ANGPT1, AQP2, ARG2, BCL2, CD34, COL4A3, COL4A4, DCN, EGR1, EPHA7, EYA1, FBN1, FGF2, FGF10, FGFR1, GDNF, GLI2, ID2, IL6R, CXCR2, ILK, LIF, SMAD7, MEF2C, MYC, NID1, OVOL1, PBX1, PCSK5, PDGFRA, PECAM1, PKD1, PKD2, PROX1, PTCH1, SALL1, SFRP1, SHH, TCF21, TEK, WFS1, WNT2B, ZBTB16, ITGA8, DCHS1, RGN, GCNT3, SLIT2, ADIPOQ, ADAMTS1, MAGI2, SPRY1, WWTR1, KANK2, TIPARP, PYGO1, KLF15, FAT4, PDGFD, ARID5B, LRRK2, OSR1, BMPER
BP	GO:0072503	cellular divalent inorganic cation homeostasis	93/1554	7.34E-12	ABL1, ADCY5, ADCYAP1, ADCYAP1R1, ADRA1A, ANK2, ANXA6, ATP1A2, ATP2B3, ATP2B4, BCL2, BDKRB2, CXCR5, CACNA1C, CACNA2D1, CACNB2, CALCA, CASQ2, CAV1, MS4A1, CHRNA7, CLIC2, CCR6, CX3CR1, CD55, DMD, DMPK, S1PR1, LPAR1, S1PR3, EDNRA, EDNRB, EPHX2, ESR1, FGF2, FYN, GPR17, GPER1, GRIA1, GRIK2, GRIN2A, HRC, IL2, CXCR2, ITPR1, KCNK3, LRP1, MT1A, P2RX1, P2RY1, PDE4D, PDGFRA, PKD1, PKD2, PRKCB, PTGER3, PTGER4, PTGFR, RYR2, RYR3, CX3CL1, CXCL12, SLC8A2, SLC8A1, SLC8A3, SNCA, STC1, TAC1, TACR1, TRPC1, TRPC3, TRPC4, WFS1, TRPA1, RGN, GPR55, AKAP6, CXCL13, SYNPO, RASA3, NCS1, SLC39A14, P2RY10, ACKR4, JPH2, SLC24A3, SLC25A23, RIC3, JPH4, SLC24A4, SYPL2, P2RY8, FAM155A
BP	GO:0070252	actin-mediated cell contraction	38/1554	9.64E-12	ACTC1, ACTN2, ACTN3, BIN1, ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CAV1, DMD, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, MYH2, MYH3, MYL3, PDE4B, PDE4D, ROCK1, RYR2, SCN1B, SCN2B, SCN4B, SGCD, SNTA1, STC1, TMOD1, TNNT2, TPM1, TPM2, GJC1, KCNE4, CTNNA3, PARVA, SCN3B
BP	GO:0006816	calcium ion transport	84/1554	2.83E-11	ABL1, ADCYAP1R1, ADRA1A, ADRA2A, BIN1, ANK2, ANXA6, ATP1A2, ATP2B3, ATP2B4, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAMK2A, CASQ2, CAV1, MS4A1, CHRNA7, CLIC2, CCN2, DMD, FGF2, FYN, GEM, GNAO1, GPM6A, GPER1, GRIN2A, HRC, HSPA2, IL16, ITPR1, MYLK, P2RX1, PDE2A, PDE4B, PDE4D, PKD1, PKD2, PRKCB, PTGS2, RCVRN, RYR2, RYR3, CX3CL1, CXCL12, SLC8A2, SLC8A1, SLC8A3, SNCA, STAC, STC1, TRPC1, TRPC3, TRPC4, WFS1, DYSF, CACNA1H, TRPA1, RGN, AKAP6,

					NMUR1, IL1RAPL1, RASA3, NCS1, REM1, JPH2, SLC24A3, CACHD1, P2RY12, AHNAK, SLC25A23, TRPM3, JPH4, SLC25A25, FCRL3, TMC2, SLC24A4, TRPM6, NALCN, MICU3, FAM155A
BP	GO:0060048	cardiac muscle contraction	41/1554	2.91E-11	ACTC1, ADRA1A, BIN1, ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CASQ2, CAV1, CLIC2, CCN2, DMD, FLNA, HRC, KCND3, KCNH2, KCNJ3, KCNJ8, SMAD7, MYL3, PDE4B, PDE4D, RGS2, RYR2, SCN1B, SCN2B, SCN4B, SGCD, SLC8A1, SNTA1, STC1, TNNT2, TPM1, PDE5A, HDAC4, GJC1, KCNE4, CTNNA3, TNNI3K, SCN3B
BP	GO:0007160	cell-matrix adhesion	55/1554	2.94E-11	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, APOD, ARHGAP6, BCL2, CD34, COL13A1, CCN2, DUSP3, EDA, EPHA3, GPM6B, ILK, ITGA1, ITGA7, ITGB3, LRP1, NID1, DDR2, PECAM1, PIK3R1, PKD1, ROCK1, CX3CL1, SFRP1, SRF, TEK, THBS1, UTRN, VCL, PPFIA2, ITGA8, SGCE, ROCK2, DLC1, FBLN5, SORBS1, LYVE1, FERMT2, EMILIN1, FAM107A, CORO1C, SNED1, TMEM8B, EPDR1, AJAP1, ADAMTS9, PEAK1, JAM3, PHLDB2, FREM1, NEXMIF
BP	GO:0061448	connective tissue development	62/1554	3.00E-11	ACTA2, ACVRL1, ANXA6, BMP5, BMPR1A, CD34, COL6A2, COL6A3, CCN2, EGR1, EVC, EFEMP1, FGF2, FGF9, FGFR1, GDF2, GLI2, HYAL1, ID2, ID4, CCN1, IL6R, MATN2, MEF2C, MEF2D, MGP, MSX1, NFIB, ROR2, PITX1, PKD1, SFRP2, SOX5, SRF, STC1, ZEB1, TGFBR2, THRA, TRPS1, WNT2B, WNT9A, ZBTB16, BARX2, HAND1, HAND2, ZNF516, PPARGC1A, SPART, SIRT1, SCARA3, SOX6, CSGALNACT1, EBF2, PDGFD, COL21A1, ARID5B, PKDCC, SLC25A25, OSR1, RSPO2, RFLNB, MUSTN1
BP	GO:0033002	muscle cell proliferation	57/1554	3.12E-11	ANGPT1, APOD, BMPR1A, CDKN1A, CNN1, HBEGF, S1PR1, ELN, EPHB1, FGF2, FGF9, FGFR1, GATA6, GPER1, ID2, IGF1, IGFBP5, IL6R, ILK, JUN, KCNK2, MEF2C, MEF2D, MEIS1, MMP2, NPR1, NPR3, OGN, PDE1A, PIM1, PTGS2, RBP4, CX3CL1, SHH, TBX5, TGFB3, TGFBR2, TGFBR3, THBS1, TNFAIP3, TPM1, VIP, VIPR2, NR4A3, KLF4, ADIPOQ, ADAMTS1, HDAC4, NAMPT, TRIB1, ABCC4, PPARGC1A, ZFPM2, TBX20, PDGFD, MYOCD, RBPMS2
BP	GO:0048738	cardiac muscle tissue development	56/1554	3.50E-11	ACTC1, ACTN2, ADRA1A, BMP5, BMPR1A, S1PR1, FGF2, FGF9, FGFR1, GATA6, ID2, IGF1, KCNK2, SMAD7, MEF2A, MEF2C, MEIS1, MYH11, MYL3, PDGFRA, PIM1, PROX1, RBP4, RGS2, RYR2, SGCB, SGCD, SGCG, SLC8A1, SRF, TBX5, TGFBR2, TGFBR3, TNNT2, TPM1, FZD7, SORBS2, MYOM2, HAND1, AKAP6, GJC1, PDLIM5, BVES, AKAP13, DKK1, KDM6B, ZFPM2, SOX6, ADAMTS9, TBX20, JPH2, ALPK3, MYOCD, SGCZ, GATA5, SIK1
BP	GO:0060485	mesenchyme development	62/1554	6.56E-11	ACTA2, ACTC1, ACVRL1, ANXA6, BCL2, BMP5, BMPR1A, ZFP36L1, LDLRAD4, EDNRA, EDNRB, EPHA3, FGF9, FGF10, FGFR1, FOXF1, GDNF, HGF, SMAD7, MEF2C, MEOX1, KITLG, MSX1, MYC, NRTN, PITX2, PKD2, SFRP1, SFRP2, SHH, TBX5, TCF21, TGFB1I1, TGFB3, TGFBR2, TGFBR3, DCHS1, NRP2, HAND1, HAND2, ZEB2, SPRY1, SEMA3A, OLFM1, ZFPM2, CORO1C, WWTR1, BNC2, TMEM100, SEMA3G, TBX20, FAM172A, KBTBD8, PHLDB2, VASN, OSR1, GATA5, DACT3, GLIPR2, RANBP3L, RBM24, RFLNB
BP	GO:0030048	actin filament-based movement	40/1554	1.54E-10	ACTC1, ACTN2, ACTN3, BIN1, ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CAV1, DMD, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, MYH2, MYH3, MYL3, PDE4B, PDE4D, ROCK1, RYR2, SCN1B, SCN2B, SCN4B, SGCD, SNTA1, STC1, TMOD1, TNNT2, TPM1, TPM2, WIPF1, GJC1, KCNE4, CTNNA3, PARVA, SCN3B, WIPF3
BP	GO:0032970	regulation of actin filament-based process	76/1554	1.78E-10	ABL1, ACTN2, BIN1, ANK2, RHOB, RND3, ARHGAP6, RHOH, ATP1A2, CACNA1C, CAV1, CFL2, CSF3, CCN2, CTNNA2, S1PR1, LPAR1, ELN, EPHA3, EPHA5, FER, FLNA, GPM6B, GSN, NCKAP1L, ILK, LRP1, MEF2C, NTRK3, PAM, PRKN, PDE4B, PDE4D, PDGFRA, PIK3R1, PROX1, PTGER4, ROCK1, RYR2, CX3CL1, CXCL12, SFRP1, STC1, TAC1, TEK, TGFB3, TMOD1, TPM1, SLIT2, ROCK2, ARHGEF10, DLC1, CDC42EP2, CDC42EP3, DSTN, FAM107A, FZD10, AKAP13, SYNPO, ARHGEF15, TMEFF2, LMOD1, RND1, CTNNA3, SNX9, LMOD3, RHOJ, SPTBN4, ARHGAP28, JAM3, DIXDC1, PHLDB2, MYADM, PLEKHH2, JMY, SYNPO2
BP	GO:0001508	action potential	39/1554	1.86E-10	ADRA1A, BIN1, ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CAV1, CNR2, DMD, FLNA, GNAQ, GPER1, GRIK2, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, NTRK3, P2RX1, RYR2, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A1, SNTA1, TAC1, SLMAP, CNTNAP1, CACNA1H, AKAP6, GJC1, KCNE4, CTNNA3, SCN3B
BP	GO:0006939	smooth muscle contraction	35/1554	1.86E-10	ACTA2, ADRA1A, ADRA2A, ADRA2B, ADRB2, ATP1A2, ATP2B4, BDKRB2, CAV1, CHRM2, CHRM3, CNN1, EDNRA, EDNRB, GDNF, GPER1, KCNMA1, KIT, MYH11, MYLK, P2RX1, PDE4D, PTGER3, PTGS2, RGS2, ROCK1, SMTN, SLC8A1, SRF, TACR2, TACR1, TACR3, ROCK2, NMUR1, MYOCD
BP	GO:0022898	regulation of transmembrane transporter activity	59/1554	3.82E-10	ACTN2, ADRA2A, ADRB2, ANK2, ATP1A2, ATP1B2, BCL2, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CLIC2, CRHBP, DLG2, DMD, STOM, FHL1, GEM, GRIA1, GRIN2A, HRC, HSPA2, KCNA1, KCNS2, MEF2C, PDE4B, PDE4D, ABCB1, PKD2, RELN, RYR2, SCN1B, SCN2B, SCN4B, SNCA, STAC, VAMP2, UTRN, SLMAP, KCNAB1, DYSF, RGN, AKAP6, PPARGC1A, NLGN1, KCNE4, REM1, FXYD6, NLGN3, SCN3B, JPH2, AHNAK, JPH4, OSR1, GSG1L, CNKSR3, SHISA6, LRRC52
BP	GO:0007611	learning or memory	57/1554	5.35E-10	ATP1A2, ADGRB3, BCHE, BDNF, CHRNA7, CRHBP, CX3CR1, BRINP1, EGR2, FOS, FYN, GRIA1, GRIN2A, ITGA5, JUN, KCNK2, KIT, LDLR, MAP1A, MAPT, MEF2C, MEIS2, NFATC4, NGF, PRKN, PPP3CB, PRKAR2B, RELN, PTGS2, ATXN1, SGK1, SLC8A2, SLC8A3, SRF, SYT4, TAC1, TACR2, CNTN2, THRA,

					CLDN5, VIP, VLDLR, BTG2, KCNAB1, FOSL1, ITGA8, NRXN1, NRXN2, PJA2, SYNPO, CPEB3, DKK1, SORCS3, NLGN3, SLC17A7, JPH4, FOXP2
BP	GO:0007409	axonogenesis	85/1554	5.35E-10	ABL1, ADARB1, APBB1, BCL2, BDNF, CDH4, CTNNA2, DPYSL2, EGR2, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, FYN, GDNF, GFRA1, GFRA2, GFRA3, GLI2, GRB10, ILK, LRP1, MAP1A, MAP1B, MAP6, MAPT, MATN2, NCAM1, NDN, NFIB, NGF, NGFR, NPTX1, NRTN, NTRK3, NR4A2, PIK3R1, PPP3CB, PRKCA, RELN, PTCH1, SCN1B, CXCL12, SHH, SLIT3, SRF, STXBP1, CNTN2, VCL, VLDLR, NR4A3, UNC5C, NRP2, DCLK1, LGI1, RPS6KA5, PDLIM7, SLIT2, NRXN1, NTN1, ZEB2, PLPPR4, UST, SEMA3A, OLFM1, NTNG1, PALLD, SPART, NFASC, FLRT2, ATL1, NLGN3, ENAH, SEMA3G, DSCAML1, ZSWIM5, ZSWIM6, SPTBN4, TRAK2, COL25A1, PLXNA4, CNTN4, DOK6, EPHA6
BP	GO:0048660	regulation of smooth muscle cell proliferation	44/1554	5.83E-10	APOD, BMPR1A, CDKN1A, CNN1, HBEGF, S1PR1, ELN, FGF2, FGF9, GPER1, ID2, IGF1, IGFBP5, IL6R, ILK, JUN, MEF2C, MEF2D, MMP2, NPR1, NPR3, OGN, PDE1A, PTGS2, CX3CL1, TGFB3, TGFBR2, THBS1, TNFAIP3, TPM1, VIP, VIPR2, NR4A3, KLF4, ADIPOQ, ADAMTS1, HDAC4, NAMPT, TRIB1, ABCC4, PPARGC1A, PDGFD, MYOCD, RBPMS2
BP	GO:0001763	morphogenesis of a branching structure	48/1554	6.91E-10	ABL1, AR, BCL2, PRDM1, COL13A1, EDNRA, EPHA2, EPHA7, ESR1, EYA1, FGF2, FGF7, FGF10, FGFR1, FOXF1, GDF2, GDNF, GLI2, HGF, ILK, MYC, NFATC4, PBX1, PGR, PKD1, PKD2, PROX1, PTCH1, SALL1, SFRP1, SFRP2, SHH, SRF, TCF21, TGFBR2, WNT2B, DCHS1, SOCS3, SLIT2, SPRY1, SPRY2, SEMA3A, TBX20, HHIP, FAT4, RSPO3, LRRK2, RSPO2
BP	GO:0007015	actin filament organization	76/1554	7.26E-10	ABL1, ACTC1, ACTN1, ACTN2, BIN1, RHOB, RND3, ARHGAP6, RHOH, BCL2, CFL2, CSF3, CCN2, CTNNA2, DPYSL3, S1PR1, LPAR1, ELN, FER, FLNA, GSN, NCKAP1L, PRKN, PIK3R1, PROX1, PTGER4, ROCK1, CX3CL1, CXCL12, SFRP1, SRF, TAC1, TGFB3, TMOD1, TPM1, TPM2, WIPF1, SORBS2, GAS7, MYOM2, SLIT2, ROCK2, ARHGEF10, DLC1, CDC42EP2, CAP2, SORBS1, CDC42EP3, WASF3, DSTN, FAM107A, SYNPO, ARHGEF15, CORO1C, TMEFF2, LMOD1, RND1, PDLIM3, SNX9, ENAH, LMOD3, RHOJ, MICAL3, SHROOM3, SPTBN4, ARHGAP28, CGNL1, PHLDB2, MYADM, PLEKHH2, PPARGC1B, JMY, XIRP1, SYNPO2, PHACTR1, RFLNB
BP	GO:0048659	smooth muscle cell proliferation	44/1554	8.45E-10	APOD, BMPR1A, CDKN1A, CNN1, HBEGF, S1PR1, ELN, FGF2, FGF9, GPER1, ID2, IGF1, IGFBP5, IL6R, ILK, JUN, MEF2C, MEF2D, MMP2, NPR1, NPR3, OGN, PDE1A, PTGS2, CX3CL1, TGFB3, TGFBR2, THBS1, TNFAIP3, TPM1, VIP, VIPR2, NR4A3, KLF4, ADIPOQ, ADAMTS1, HDAC4, NAMPT, TRIB1, ABCC4, PPARGC1A, PDGFD, MYOCD, RBPMS2
BP	GO:0050890	cognition	62/1554	9.05E-10	ATP1A2, ADGRB3, BCHE, BDNF, CHRNA7, CRHBP, CX3CR1, BRINP1, EGR2, FOS, FYN, GRIA1, GRIN2A, ITGA5, JUN, KCNK2, KIT, LDLR, LHCGR, MAP1A, MAPT, MEF2C, MEIS2, NFATC4, NGF, PRKN, PPP3CB, PRKAR2B, RELN, PTGS2, ATXN1, SGK1, SLC8A2, SLC8A3, SRF, SYT4, TAC1, TACR2, CNTN2, THRA, CLDN5, VIP, VLDLR, BTG2, KCNAB1, FOSL1, ITGA8, NRXN1, NRXN2, PJA2, FAM107A, SYNPO, CPEB3, DKK1, SORCS3, TMPRSS11E, NLGN3, SOBP, SLC17A7, JPH4, FOXP2, GPR155
BP	GO:0032412	regulation of ion transmembrane transporter activity	57/1554	9.07E-10	ACTN2, ADRA2A, ADRB2, ANK2, ATP1A2, ATP1B2, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CLIC2, CRHBP, DLG2, DMD, STOM, FHL1, GEM, GRIA1, GRIN2A, HRC, HSPA2, KCNA1, KCNS2, MEF2C, PDE4B, PDE4D, ABCB1, PKD2, RELN, RYR2, SCN1B, SCN2B, SCN4B, STAC, VAMP2, UTRN, SLMAP, KCNAB1, DYSF, RGN, AKAP6, PPARGC1A, NLGN1, KCNE4, REM1, FXYD6, NLGN3, SCN3B, JPH2, AHNAK, JPH4, OSR1, GSG1L, CNKSR3, SHISA6, LRRC52
BP	GO:0032409	regulation of transporter activity	60/1554	1.11E-09	ACTN2, ADRA2A, ADRB2, ANK2, ATP1A2, ATP1B2, BCL2, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CLIC2, CRHBP, DLG2, DMD, STOM, FHL1, GEM, GRIA1, GRIN2A, HRC, HSPA2, KCNA1, KCNS2, MEF2C, PDE4B, PDE4D, ABCB1, PKD2, RELN, RYR2, SCN1B, SCN2B, SCN4B, SGK1, SNCA, STAC, VAMP2, UTRN, SLMAP, KCNAB1, DYSF, RGN, AKAP6, PPARGC1A, NLGN1, KCNE4, REM1, FXYD6, NLGN3, SCN3B, JPH2, AHNAK, JPH4, OSR1, GSG1L, CNKSR3, SHISA6, LRRC52
BP	GO:0070588	calcium ion transmembrane transport	64/1554	1.60E-09	ABL1, ADRA2A, BIN1, ANK2, ANXA6, ATP1A2, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CHRNA7, CLIC2, DMD, FGF2, FYN, GEM, GPM6A, GPER1, GRIN2A, HRC, HSPA2, ITPR1, PDE2A, PDE4B, PDE4D, PKD1, PKD2, RYR2, RYR3, CX3CL1, SLC8A2, SLC8A1, SLC8A3, SNCA, STAC, TRPC1, TRPC3, TRPC4, DYSF, CACNA1H, TRPA1, RGN, AKAP6, IL1RAPL1, RASA3, NCS1, REM1, JPH2, SLC24A3, CACHD1, P2RY12, AHNAK, SLC25A23, TRPM3, JPH4, SLC25A25, TMC2, SLC24A4, TRPM6, NALCN, MICU3, FAM155A
BP	GO:0051146	striated muscle cell differentiation	61/1554	1.62E-09	ACTC1, ACTN2, ADRA1A, ADGRB3, BCL2, BDNF, CASQ2, CFL2, DMD, DMPK, FLNC, GATA6, IGF1, IGFBP5, MEF2A, MEF2C, MSX1, MYH3, MYH11, NFATC2, PDGFRA, PGM5, PROX1, RGS2, SGCB, SGCD, SHH, SLC8A1, SRF, TBX5, TMOD1, TNNT2, TPM1, DYSF, FZD7, SORBS2, BARX2, CACNA1H, MYOM2, AKAP6, HDAC4, KLHL41, PDLIM5, BVES, LDB3, AKAP13, DKK1, KDM6B, LMOD1, EHD2, CDON, PLEKHO1, MYOZ2, SOX6, LMOD3, ALPK3, MYOCD, WFIKKN2, SIK1, RBM24, TMEM119
BP	GO:0030278	regulation of ossification	48/1554	2.25E-09	ADRB2, BCL2, BMPR1A, CEBPD, S1PR1, EGR2, GDF10, GPM6B, HGF, ID2, IGF1, IGFBP5, CCN1, IL6R, IL6ST, ILK, JUND, MEF2C, MGP, DDR2, OMD, PBX1, ENPP1, PRKD1, PTCH1, PTGER4, RORB, SFRP1, SFRP2, SLC8A1, TAC1, TGFB3, ZBTB16, FGF23, CHRD, PDLIM7, HAND2, HDAC4, RASSF2, DKK1, ZHX3, PKDCC, TWIST2, OSR1, RANBP3L, TMEM119, OSTN, RFLNB

BP	GO:0003007	heart morphogenesis	56/1554	2.25E-09	ACTC1, ACVRL1, BMP5, BMPR1A, CPE, S1PR1, ELN, EYA1, FOXF1, GATA6, ID2, CCN1, ILK, JUN, SMAD7, MEF2C, MSX1, MYL3, PIM1, PITX2, PKD2, PROX1, PTCH1, RBP4, RYR2, SFRP2, SHH, SLIT3, SRF, TBX5, TEK, TGFBR2, TGFBR3, CLDN5, TNNT2, TPM1, DCHS1, NRP2, MYOM2, SLIT2, HAND1, HAND2, ADAMTS1, SPRY1, DLC1, OLFM1, DKK1, ZFPM2, FLRT2, TMEM100, PARVA, TBX20, SOX17, FAT4, GATA5, NOTO
BP	GO:0070838	divalent metal ion transport	85/1554	2.37E-09	ABL1, ADCYAP1R1, ADRA1A, ADRA2A, BIN1, ANK2, ANXA6, ATP1A2, ATP2B3, ATP2B4, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAMK2A, CASQ2, CAV1, MS4A1, CHRNA7, CLIC2, CCN2, DMD, FGF2, FYN, GEM, GNAO1, GPM6A, GPER1, GRIN2A, HRC, HSPA2, IL16, ITPR1, MYLK, P2RX1, PDE2A, PDE4B, PDE4D, PKD1, PKD2, PRKCB, PTGS2, RCVRN, RYR2, RYR3, CX3CL1, CXCL12, SLC8A2, SLC8A1, SLC8A3, SNCA, STAC, STC1, TRPC1, TRPC3, TRPC4, WFS1, DYSF, CACNA1H, TRPA1, RGN, AKAP6, NMUR1, IL1RAPL1, RASA3, NCS1, SLC39A14, REM1, JPH2, SLC24A3, CACHD1, P2RY12, AHNAK, SLC25A23, TRPM3, JPH4, SLC25A25, FCRL3, TMC2, SLC24A4, TRPM6, NALCN, MICU3, FAM155A
BP	GO:0032956	regulation of actin cytoskeleton organization	67/1554	3.07E-09	ABL1, ACTN2, BIN1, RHOB, RND3, ARHGAP6, RHOH, CFL2, CSF3, CCN2, CTNNA2, S1PR1, LPAR1, ELN, EPHA3, EPHA5, FER, FLNA, GPM6B, GSN, NCKAP1L, ILK, LRP1, MEF2C, NTRK3, PAM, PRKN, PDGFRA, PIK3R1, PROX1, PTGER4, ROCK1, CX3CL1, CXCL12, SFRP1, TAC1, TEK, TGFB3, TMOD1, TPM1, SLIT2, ROCK2, ARHGEF10, DLC1, CDC42EP2, CDC42EP3, DSTN, FAM107A, FZD10, AKAP13, SYNPO, ARHGEF15, TMEFF2, LMOD1, RND1, SNX9, LMOD3, RHOJ, SPTBN4, ARHGAP28, JAM3, DIXDC1, PHLDB2, MYADM, PLEKHH2, JMY, SYNPO2
BP	GO:0031032	actomyosin structure organization	47/1554	3.58E-09	ABL1, ACTC1, ACTN2, ARHGAP6, CASQ2, CFL2, CNN1, CCN2, S1PR1, LPAR1, ELN, MEF2A, MEF2C, MYH3, MYH11, PDGFRA, PGM5, PIK3R1, PROX1, PTGER4, ROCK1, SFRP1, SRF, TAC1, TGFB3, TMOD1, TNNT2, TPM1, CDC42BPA, MYOM2, ROCK2, ARHGEF10, KLHL41, DLC1, SORBS1, LDB3, AKAP13, ARHGEF15, TMEFF2, LMOD1, MYOZ2, LMOD3, ARHGAP28, PHLDB2, PHACTR1, FRMD3, LURAP1
BP	GO:0055001	muscle cell development	45/1554	3.87E-09	ACTC1, ACTN2, ADRA1A, BIN1, ANK2, BCL2, CASQ2, CFL2, DMD, FLNC, IGF1, MEF2A, MEF2C, MYH3, MYH11, NFATC2, NFATC4, PDGFRA, PGM5, PROX1, RGS2, SGCB, SGCD, SLC8A1, SRF, TMOD1, TNNT2, TPM1, DYSF, SORBS2, MYOM2, AKAP6, HDAC4, KLHL41, PDLIM5, BVES, LDB3, AKAP13, LMOD1, MYOZ2, LMOD3, ALPK3, WFIKKN2, SGCZ, SYPL2
BP	GO:0072511	divalent inorganic cation transport	85/1554	4.28E-09	ABL1, ADCYAP1R1, ADRA1A, ADRA2A, BIN1, ANK2, ANXA6, ATP1A2, ATP2B3, ATP2B4, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAMK2A, CASQ2, CAV1, MS4A1, CHRNA7, CLIC2, CCN2, DMD, FGF2, FYN, GEM, GNAO1, GPM6A, GPER1, GRIN2A, HRC, HSPA2, IL16, ITPR1, MYLK, P2RX1, PDE2A, PDE4B, PDE4D, PKD1, PKD2, PRKCB, PTGS2, RCVRN, RYR2, RYR3, CX3CL1, CXCL12, SLC8A2, SLC8A1, SLC8A3, SNCA, STAC, STC1, TRPC1, TRPC3, TRPC4, WFS1, DYSF, CACNA1H, TRPA1, RGN, AKAP6, NMUR1, IL1RAPL1, RASA3, NCS1, SLC39A14, REM1, JPH2, SLC24A3, CACHD1, P2RY12, AHNAK, SLC25A23, TRPM3, JPH4, SLC25A25, FCRL3, TMC2, SLC24A4, TRPM6, NALCN, MICU3, FAM155A
BP	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	50/1554	4.33E-09	ADCY2, ADCY5, ADCY9, ADCYAP1, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP2B4, ADGRB3, CALCA, CHRM2, CHRM3, S1PR1, LPAR1, S1PR3, EDNRA, FLNA, GNAL, GNAO1, GNAQ, GNAZ, GPR3, GPR26, GPER1, GRK5, GRIK3, GRM7, LHCGR, NPR3, P2RY1, PALM, PDE2A, PDE4D, PRKACB, PRKCA, PTGER3, PTGER4, PTGFR, RGS1, RGS2, VIP, GLP2R, AKAP12, GNA14, AKAP13, ADGRL4, P2RY12
BP	GO:0048167	regulation of synaptic plasticity	45/1554	4.47E-09	ABL1, CAMK2A, CBLN1, CHRNA7, CX3CR1, EGR2, GRIA1, GRID2, GRIK2, GRIN2A, KCNB1, KIT, MAP1A, MAP1B, MAPT, MEF2C, MPP2, NFATC4, PPP3CB, RELN, PTGS2, CX3CL1, SLC8A2, SLC8A3, SNCA, SRF, STXBP1, VAMP2, SYT4, CNTN2, NEURL1, RIMS3, FAM107A, SYNPO, CPEB3, NLGN1, SORCS3, RIMS1, NLGN3, SORCS2, JPH4, PRRT2, CNTN4, LRRTM1, SHISA6
BP	GO:0051216	cartilage development	48/1554	5.85E-09	ACVRL1, ANXA6, BMP5, BMPR1A, COL6A2, COL6A3, CCN2, EVC, EFEMP1, FGF2, FGF9, FGFR1, GDF2, GLI2, HYAL1, CCN1, MATN2, MEF2C, MEF2D, MGP, MSX1, NFIB, ROR2, PITX1, PKD1, SFRP2, SOX5, SRF, STC1, ZEB1, TGFBR2, THRA, TRPS1, WNT2B, WNT9A, ZBTB16, BARX2, HAND1, HAND2, SCARA3, SOX6, CSGALNACT1, COL21A1, PKDCC, OSR1, RSPO2, RFLNB, MUSTN1
BP	GO:0061138	morphogenesis of a branching epithelium	44/1554	6.03E-09	ABL1, AR, BCL2, EDNRA, EPHA2, ESR1, EYA1, FGF2, FGF7, FGF10, FGFR1, FOXF1, GDF2, GDNF, GLI2, HGF, ILK, MYC, NFATC4, PBX1, PGR, PKD1, PKD2, PROX1, PTCH1, SALL1, SFRP1, SFRP2, SHH, SRF, TCF21, TGFBR2, WNT2B, DCHS1, SOCS3, SLIT2, SPRY1, SPRY2, SEMA3A, TBX20, HHIP, FAT4, RSPO3, RSPO2
BP	GO:0086003	cardiac muscle cell contraction	25/1554	7.96E-09	BIN1, ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CAV1, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, PDE4B, PDE4D, RYR2, SCN1B, SCN2B, SCN4B, SGCD, SNTA1, STC1, GJC1, KCNE4, CTNNA3, SCN3B
BP	GO:0010517	regulation of phospholipase activity	25/1554	1.12E-08	ABL1, ADCYAP1R1, ADRA1A, ANXA1, ARHGAP6, BDNF, LPAR1, EDNRA, ESR1, FGF2, FGFR1, GNAQ, CCN1, ITK, KIT, LRP1, NTRK3, PDGFRA, PLA2G5, RGS2, SNCA, GPR55, NMUR1, P2RY12, RASGRP4
BP	GO:0007187	G protein-coupled receptor signaling pathway, coupled to	54/1554	1.13E-08	ADCY2, ADCY5, ADCY9, ADCYAP1, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ANXA1, ATP2B4, ADGRB3, CALCA, CHRM2, CHRM3, CNR2, S1PR1, LPAR1, S1PR3, EDNRA, FLNA, GNAL, GNAO1, GNAQ, GNAZ, GPR3, GPR26, GPER1, GRK5, GRIK3, GRM7, HTR4, LHCGR, NPR3, P2RY1, PALM,

		cyclic nucleotide second messenger			PDE2A, PDE4D, PRKACB, PRKCA, PTGER3, PTGER4, PTGFR, RGS1, RGS2, SSTR1, VIP, GLP2R, AKAP12, GNA14, AKAP13, ADGRL4, P2RY12
BP	GO:0035265	organ growth	46/1554	2.59E-08	ACACB, ADRA1A, ANXA6, AR, BCL2, BMPR1A, COL6A2, COL6A3, S1PR1, ESR1, EVC, FGF2, FGF7, FGF9, FGF10, FGFR1, GATA6, IGF1, KCNK2, LEPR, MATN2, MEF2C, MEIS1, DDR2, PIM1, PROX1, RBP4, RGS2, SHH, STC1, TBX5, TGFBR2, TGFBR3, SORBS2, AKAP6, SPRY2, PDLIM5, AKAP13, ZFPM2, LATS2, SCARA3, BNC2, TBX20, COL21A1, RSPO2, OSTN
BP	GO:0001505	regulation of neurotransmitter levels	66/1554	2.86E-08	ADRA1A, ARG2, ATP1A2, ATP2B4, BCHE, CACNB2, CAMK2A, CAV1, CD34, CHRM2, CLU, CX3CR1, CYP1B1, STX2, GABRA2, GDNF, GPM6B, GPER1, GRIN2A, HBB, ITGB3, MEF2C, P2RX1, P2RY1, PRKN, PKD2, PRKCB, PTGIS, PTGS2, PTPRN2, PTX3, RAP1A, RGS2, RORA, SLC18A2, SLC22A3, SNCA, STXBP1, VAMP2, SYT4, TACR2, TRH, PPFIA2, STX11, PER2, RGN, KLF4, NRXN1, NRXN2, ROCK2, STXBP5L, RIMS3, NAALAD2, KLF2, NLGN1, RIMS1, SYT11, NCS1, DMGDH, SLC17A7, SLC5A7, PRRT2, LRRK2, ENPP6, PRIMA1, RNF180
BP	GO:0002027	regulation of heart rate	30/1554	2.94E-08	ADRA1A, BIN1, ANK2, CACNA1C, CACNA2D1, CACNB2, CASQ2, CAV1, DMD, HRC, KCND3, KCNH2, KCNJ3, PDE4D, RYR2, SCN1B, SCN2B, SCN4B, SLC8A1, SNTA1, TAC1, TACR3, TPM1, SEMA3A, BVES, KCNE4, CTNNA3, TNNI3K, SCN3B, SPTBN4
BP	GO:2001257	regulation of cation channel activity	42/1554	3.30E-08	ACTN2, ADRB2, ANK2, CACNA2D1, CACNB2, CACNB4, CASQ2, CAV1, CLIC2, CRHBP, DLG2, DMD, STOM, GEM, GRIA1, GRIN2A, HRC, KCNA1, KCNS2, MEF2C, PDE4B, PDE4D, PKD2, RELN, SCN1B, STAC, VAMP2, SLMAP, KCNAB1, DYSF, AKAP6, PPARGC1A, NLGN1, KCNE4, REM1, NLGN3, JPH2, AHNAK, JPH4, GSG1L, SHISA6, LRRC52
BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	55/1554	4.36E-08	CBLN1, CDH4, CDH17, GRID2, IL1RN, ITGA5, MPZ, PCDHGC3, PCDH7, PCDH9, PECAM1, PKD1, PTPRD, CX3CL1, SELP, CNTN2, TGFBR2, CLDN5, SPARCL1, DCHS1, CLDN8, KLF4, ADIPOQ, NRXN1, IL1RAPL1, NTNG1, NLGN1, IGSF9B, PALLD, CRB1, PCDHGA12, PCDH11X, CDH19, PCDH18, DCHS2, PCDHGB7, PCDHGB3, PCDHGA9, PCDHGA5, PCDHGA3, PCDHGA2, PCDHB15, PCDHA3, DSCAML1, PCDH10, CADM3, CLSTN2, LRRC4, PCDH20, FAT4, PCDH11Y, MYADM, FAT3, GATA5, CNTN4
BP	GO:1900274	regulation of phospholipase C activity	19/1554	6.06E-08	ABL1, ADCYAP1R1, ADRA1A, ARHGAP6, BDNF, LPAR1, EDNRA, ESR1, FGF2, FGFR1, GNAQ, ITK, KIT, NTRK3, PDGFRA, GPR55, NMUR1, P2RY12, RASGRP4
BP	GO:0007411	axon guidance	55/1554	6.48E-08	BDNF, CDH4, DPYSL2, EGR2, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, FYN, GDNF, GFRA1, GFRA2, GFRA3, GLI2, GRB10, LRP1, MATN2, NCAM1, NFIB, NRTN, PIK3R1, PRKCA, RELN, PTCH1, SCN1B, CXCL12, SHH, SLIT3, CNTN2, VLDLR, NR4A3, UNC5C, NRP2, LGI1, RPS6KA5, PDLIM7, SLIT2, NRXN1, NTN1, SEMA3A, NTNG1, PALLD, NFASC, FLRT2, ENAH, SEMA3G, DSCAML1, ZSWIM5, ZSWIM6, SPTBN4, PLXNA4, CNTN4, DOK6, EPHA6
BP	GO:0097485	neuron projection guidance	55/1554	7.31E-08	BDNF, CDH4, DPYSL2, EGR2, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, FYN, GDNF, GFRA1, GFRA2, GFRA3, GLI2, GRB10, LRP1, MATN2, NCAM1, NFIB, NRTN, PIK3R1, PRKCA, RELN, PTCH1, SCN1B, CXCL12, SHH, SLIT3, CNTN2, VLDLR, NR4A3, UNC5C, NRP2, LGI1, RPS6KA5, PDLIM7, SLIT2, NRXN1, NTN1, SEMA3A, NTNG1, PALLD, NFASC, FLRT2, ENAH, SEMA3G, DSCAML1, ZSWIM5, ZSWIM6, SPTBN4, PLXNA4, CNTN4, DOK6, EPHA6
BP	GO:0019722	calcium-mediated signaling	47/1554	7.31E-08	ACTN3, ANK2, ATP1A2, ATP2B4, CXCR5, CACNA1C, CASQ2, CD22, CLIC2, CCR6, CX3CR1, DMD, DMPK, RCAN1, EDNRB, GRIN2A, HRC, IGF1, CXCR2, ITPR1, MAPT, NFATC1, NFATC2, NFATC4, PDE4D, PKD2, PPP3CB, PTGFR, RYR2, SELP, SGCD, SLC8A1, RGN, AKAP6, HDAC4, RCAN2, NMUR1, LMCD1, ACKR4, MYOZ2, TMEM100, JPH2, P2RY12, NCALD, JPH4, C10orf71, LRRK2
BP	GO:0048762	mesenchymal cell differentiation	47/1554	8.46E-08	ANXA6, BCL2, BMP5, BMPR1A, LDLRAD4, EDNRA, EDNRB, EPHA3, FGF10, FGFR1, GDNF, HGF, SMAD7, MEF2C, KITLG, MSX1, NRTN, PITX2, SFRP1, SFRP2, SHH, TBX5, TCF21, TGFB1I1, TGFB3, TGFBR2, TGFBR3, NRP2, HAND2, ZEB2, SPRY1, SEMA3A, OLFM1, CORO1C, WWTR1, TMEM100, SEMA3G, FAM172A, KBTBD8, PHLDB2, VASN, OSR1, GATA5, DACT3, GLIPR2, RANBP3L, RFLNB
BP	GO:0030336	negative regulation of cell migration	62/1554	1.04E-07	ACVRL1, ADARB1, APOD, RHOB, BCL2, BMP5, BMPR1A, LDLRAD4, CX3CR1, CYP1B1, DACH1, DCN, DPYSL3, DUSP1, DUSP3, FGF2, GDF2, HAS1, IGFBP5, ILK, LRP1, SMAD7, MEF2C, MITF, CD200, PTGER4, RRAS, CX3CL1, CXCL12, SFRP1, SFRP2, SHH, SRF, STC1, TBX5, THBS1, TPM1, VCL, RECK, CHRD, KLF4, SLIT2, ADIPOQ, MAGI2, TRIB1, SEMA3A, DLC1, CXCL13, PPARGC1A, EMILIN1, LRCH1, CORO1C, TMEFF2, CLIC4, ADAMTS9, NAV3, BMERB1, PHLDB2, STARD13, MYOCD, CYGB, NEXMIF
BP	GO:0030198	extracellular matrix organization	66/1554	1.33E-07	A2M, ABL1, COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, CCN2, CYP1B1, DCN, DPT, ELN, FBN1, FGF2, FOXF1, GPM6B, HAS1, HSPG2, CCN1, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, LAMA4, LAMC1, LRP1, MFAP4, MMP2, MMP16, MYH11, NID1, DDR2, PDGFRA, PECAM1, PTX3, SFRP2, THBS1, TIMP2, VWF, MFAP5, RECK, ITGA8, ADAMTS4, LAMC3, FBLN5, ADAMTS5, EMILIN1, FLRT2, ABI3BP, CSGALNACT1, ADAMTS9, JAM2, HPSE2, NDNF, THSD4, SCUBE1, JAM3, CRISPLD2, COL25A1, PHLDB2, CCDC80, SCUBE3
BP	GO:0055002	striated muscle cell development	40/1554	1.43E-07	ACTC1, ACTN2, ADRA1A, BCL2, CASQ2, CFL2, DMD, FLNC, IGF1, MEF2A, MEF2C, MYH3, MYH11, NFATC2, PDGFRA, PGM5, PROX1, RGS2, SGCB, SGCD, SLC8A1, SRF, TMOD1, TNNT2, TPM1, DYSF,

					SORBS2, MYOM2, AKAP6, HDAC4, KLHL41, PDLIM5, BVES, LDB3, AKAP13, LMOD1, MYOZ2, LMOD3, ALPK3, WFIKKN2
BP	GO:1904018	positive regulation of vasculature development	48/1554	1.43E-07	ABL1, ACVRL1, ANXA1, AQP1, RHOB, C3, C6, CD34, CHRNA7, CX3CR1, CYP1B1, EGR1, F3, FGF2, GATA6, GDF2, GPER1, HGF, HYAL1, IL6R, CXCR2, ITGA5, KIT, PRKCA, PRKCB, PRKD1, PTGIS, PTGS2, RAP1A, RRAS, CX3CL1, SFRP2, TEK, TGFBR2, THBS1, TNFSF12, KLF4, AKT3, SIRT1, PPP1R16B, ASB4, TMEM100, RHOJ, JCAD, PDGFD, MYOCD, HSPB6, BMPER
BP	GO:0042326	negative regulation of phosphorylation	78/1554	1.49E-07	ABL1, ACTN3, ADARB1, ANGPT1, RHOH, ATF3, BDKRB2, LDLRAD4, CAV1, CDKN1A, GADD45A, DMD, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, GFRA2, GNAQ, GPER1, HGF, IL2, ILK, JUN, LIF, SMAD7, MAPT, MYC, GADD45B, NTRK3, PRKN, PDE4D, ENPP1, PER1, PRKAR2B, RGS2, SFRP1, SFRP2, SNCA, TNFAIP3, PLPP3, SOCS3, GPRC5A, RGN, KLF4, SLIT2, ADIPOQ, HDAC4, RASSF2, HIPK3, TRIB1, SPRY1, SPRY2, PPARGC1A, EMILIN1, IRAK3, DKK1, SIRT1, CORO1C, WWTR1, LATS2, DACT1, PRKAG2, ERRFI1, PID1, DBNDD2, INKA2, DUSP26, ITPRIP, MIDN, MYADM, MYOCD, NIBAN1, LRRK2, DUSP19, CNKSR3, NLRP6
BP	GO:0060562	epithelial tube morphogenesis	60/1554	1.55E-07	ABL1, ACVRL1, AR, RHOB, BCL2, BMP5, EDNRA, EPHA2, EPHA7, ESR1, EYA1, FGF2, FGF10, FOXF1, GDF2, GDNF, GLI2, CXCR2, ILK, MEF2C, MYC, NFATC4, PBX1, PGR, PKD1, PKD2, PRKACB, PROX1, PTCH1, RYR2, SALL1, SFRP1, SFRP2, SHH, SRF, TCF21, TGFBR2, WNT2B, DCHS1, BCL10, SLIT2, HAND1, NTN1, HAND2, ZEB2, SPRY1, SPRY2, DLC1, SOSTDC1, TBX20, CC2D2A, SHROOM3, SOX17, HHIP, FAT4, STARD13, OSR1, PRICKLE1, RSPO2, NOTO
BP	GO:0072073	kidney epithelium development	35/1554	1.55E-07	ARG2, BCL2, CD34, EPHA7, EYA1, FGF2, FGFR1, GDNF, CXCR2, ILK, LIF, SMAD7, MEF2C, MYC, PBX1, PECAM1, PKD1, PKD2, PTCH1, SALL1, SFRP1, SHH, TCF21, WNT2B, DCHS1, SLIT2, ADIPOQ, MAGI2, SPRY1, WWTR1, KANK2, KLF15, FAT4, OSR1, BMPER
BP	GO:0001667	ameboidal-type cell migration	77/1554	1.65E-07	ABL1, ACVRL1, ANGPT1, ANXA1, ANXA6, RHOB, CCR6, CYP1B1, DCN, HBEGF, EDNRB, EGR3, EPHA2, FER, FGF2, FGF7, FGF10, FGFR1, GDF2, GDNF, HAS1, NR4A1, HYAL1, ILK, ITGB3, JUN, KIT, MEF2C, KITLG, NRTN, DDR2, PECAM1, PITX2, PRKCA, PRKD1, PROX1, PTGS2, SHH, SLC8A1, SRF, STC1, TAC1, TEK, TGFBR2, THBS1, TNS1, TNFSF12, NRP2, KLF4, SLIT2, HAND2, ROCK2, AKAP12, ZEB2, AKT3, SEMA3A, CXCL13, MAPRE2, SIRT1, CORO1C, KANK2, ADGRA2, AMOTL2, SEMA3G, ADAMTS9, RHOJ, JCAD, SOX17, P2RY12, ARID5B, ATOH8, STARD13, CYGB, GLIPR2, AMOTL1, CLEC14A, BMPER
BP	GO:0010863	positive regulation of phospholipase C activity	18/1554	1.71E-07	ADCYAP1R1, ADRA1A, ARHGAP6, BDNF, LPAR1, EDNRA, ESR1, FGF2, FGFR1, GNAQ, ITK, KIT, NTRK3, PDGFRA, GPR55, NMUR1, P2RY12, RASGRP4
BP	GO:0009612	response to mechanical stimulus	45/1554	1.77E-07	AQP1, ATP1A2, DCN, GADD45A, DMD, FOS, FOSB, FYN, IGFBP2, JUN, JUNB, JUND, KCNA1, KCNK2, KIT, MAP1B, MEIS2, P2RY1, PDE2A, PKD1, PKD2, PPL, PTCH1, PTGER4, PTGS2, RYR2, CXCL12, SLC8A1, TGFBR2, THBS1, BTG2, FOSL1, SCEL, BCL10, TRPA1, NRXN1, NRXN2, BAG3, HDAC4, TXNIP, HABP4, PIEZO2, FOXP2, TMC2, TMEM150C
BP	GO:0001933	negative regulation of protein phosphorylation	73/1554	1.83E-07	ABL1, ADARB1, ANGPT1, ATF3, BDKRB2, LDLRAD4, CAV1, CDKN1A, GADD45A, DMD, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, GFRA2, GNAQ, GPER1, HGF, IL2, ILK, JUN, LIF, SMAD7, MYC, GADD45B, NTRK3, PRKN, PDE4D, ENPP1, PER1, PRKAR2B, RGS2, SFRP1, SFRP2, SNCA, TNFAIP3, PLPP3, SOCS3, GPRC5A, RGN, KLF4, SLIT2, ADIPOQ, RASSF2, HIPK3, TRIB1, SPRY1, SPRY2, PPARGC1A, EMILIN1, IRAK3, DKK1, SIRT1, CORO1C, WWTR1, LATS2, DACT1, PRKAG2, ERRFI1, PID1, DBNDD2, INKA2, DUSP26, ITPRIP, MYADM, MYOCD, NIBAN1, LRRK2, DUSP19, CNKSR3, NLRP6
BP	GO:0007044	cell-substrate junction assembly	28/1554	1.83E-07	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, APOD, ARHGAP6, BCL2, DUSP3, EPHA3, GPM6B, ITGA5, LAMC1, LRP1, ROCK1, SFRP1, TEK, THBS1, TLN1, TNS1, ROCK2, DLC1, SORBS1, FERMT2, FAM107A, CORO1C, PEAK1, PHLDB2
BP	GO:0086001	cardiac muscle cell action potential	24/1554	1.84E-07	BIN1, ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CAV1, DMD, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, RYR2, SCN1B, SCN2B, SCN4B, SLC8A1, SNTA1, SLMAP, GJC1, KCNE4, CTNNA3, SCN3B
BP	GO:0045165	cell fate commitment	53/1554	1.87E-07	AR, BCL2, PRDM1, BMPR1A, ETS2, EYA1, FGF2, FGF10, FGFR1, GAS1, GATA6, GLI2, ID2, IRF4, LY9, MCL1, MEF2C, MITF, NTRK3, ROR2, PITX1, PROX1, PTCH1, RORA, SFRP1, SFRP2, SHH, SOX5, TAL1, TBX5, TGFB1I1, WNT2B, WNT9A, FZD7, TBX18, KLF4, TBX4, SPRY2, DKK1, MYT1L, KDM6B, ZNF521, SOSTDC1, CHD5, DHH, CDON, FEV, SOX6, TBX20, DSCAML1, SOX17, EBF2, GLIS1
BP	GO:1901342	regulation of vasculature development	72/1554	2.00E-07	ABL1, ACVRL1, ANXA1, AQP1, RHOB, ADGRB3, C3, C6, CD34, CHRNA7, COL4A3, CX3CR1, CYP1B1, DCN, EGR1, EPHA2, F3, FGF2, FGF9, GATA6, GDF2, GPER1, HGF, HSPG2, HYAL1, IL6R, CXCR2, ITGA5, KIT, NFATC1, NFATC2, NGFR, NPR1, PDE3B, PRKCA, PRKCB, PRKD1, PTGIS, PTGS2, RAP1A, ROCK1, RRAS, CX3CL1, SFRP1, SFRP2, TEK, TGFBR2, THBS1, TNFAIP3, RECK, TNFSF12, KLF4, ROCK2, AKT3, SPRY2, KLF2, CXCL13, EMILIN1, SIRT1, ADGRA2, PPP1R16B, ASB4, TMEM100, ADAMTS9, RHOJ, JCAD, PDGFD, PROK1, STARD13, MYOCD, HSPB6, BMPER
BP	GO:2000146	negative regulation of cell motility	63/1554	2.04E-07	ACVRL1, ADARB1, APOD, RHOB, BCL2, BMP5, BMPR1A, LDLRAD4, CX3CR1, CYP1B1, DACH1, DCN, DPYSL3, DUSP1, DUSP3, FGF2, GDF2, HAS1, IGFBP5, ILK, LRP1, SMAD7, MEF2C, MITF, CD200, PTGER4, RRAS, CX3CL1, CXCL12, SFRP1, SFRP2, SHH, SRF, STC1, TBX5, THBS1, TPM1, VCL, RECK, CHRD, RGN, KLF4, SLIT2, ADIPOQ, MAGI2, TRIB1, SEMA3A, DLC1, CXCL13, PPARGC1A, EMILIN1,

					LRCH1, CORO1C, TMEFF2, CLIC4, ADAMTS9, NAV3, BMERB1, PHLDB2, STARD13, MYOCD, CYGB, NEXMIF
BP	GO:0072006	nephron development	35/1554	2.07E-07	ACTA2, ANGPT1, BCL2, CD34, COL4A3, COL4A4, EGR1, EYA1, FGF2, GDNF, IL6R, ILK, LIF, MEF2C, MYC, NID1, PBX1, PDGFRA, PECAM1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, TEK, WNT2B, DCHS1, ADIPOQ, MAGI2, WWTR1, KLF15, FAT4, PDGFD, OSR1
BP	GO:0030323	respiratory tube development	40/1554	2.07E-07	BMPR1A, CCN2, FGF7, FGF9, FGF10, FGFR1, FOXF1, GATA6, GLI2, IGFBP5, LIF, NFIB, PCSK5, PDGFRA, PGR, PKD1, PROX1, RBP4, SHH, SRF, TBX5, TCF21, TGFB3, TGFBR2, THRA, WNT2B, TBX4, SPRY1, SPRY2, KLF2, ZFPM2, ERRFI1, HHIP, CRISPLD2, STK40, PKDCC, MYOCD, FOXP2, RSPO2, AARD
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	49/1554	2.07E-07	ABL1, ACVRL1, BMP5, BMPR1A, LDLRAD4, CAV1, CIDEA, FBN1, FGF9, FGF10, GDF2, GDF10, CCN1, ILK, INHBB, SMAD7, MSX1, SFRP1, SFRP2, SHH, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, LTBP4, CILP, ITGA8, CHRD, MAGI2, RBPMS, EMILIN1, FSTL1, DKK1, ZNF423, SPART, SIRT1, SOSTDC1, WWTR1, TBX20, PRDM16, GREM2, CHRDL1, MYOCD, VASN, WFIKKN2, BMPER, RBPMS2
BP	GO:0048754	branching morphogenesis of an epithelial tube	36/1554	2.61E-07	ABL1, AR, BCL2, EDNRA, EPHA2, ESR1, EYA1, FGF2, FGF10, FOXF1, GDF2, GDNF, GLI2, ILK, MYC, NFATC4, PBX1, PGR, PKD1, PKD2, PTCH1, SALL1, SFRP2, SHH, SRF, TCF21, TGFBR2, WNT2B, DCHS1, SLIT2, SPRY1, SPRY2, TBX20, HHIP, FAT4, RSPO2
BP	GO:0051271	negative regulation of cellular component movement	67/1554	2.61E-07	ACTN1, ACVRL1, ADARB1, BIN1, APOD, RHOB, BCL2, BMP5, BMPR1A, LDLRAD4, CX3CR1, CYP1B1, DACH1, DCN, DPYSL3, DUSP1, DUSP3, FGF2, GDF2, HAS1, IGFBP5, ILK, LRP1, SMAD7, MEF2C, MITF, CD200, PTGER4, RRAS, CX3CL1, CXCL12, SFRP1, SFRP2, SHH, SRF, STC1, TBX5, TGFBR3, THBS1, TPM1, VCL, RECK, CHRD, RGN, KLF4, SLIT2, ADIPOQ, MAGI2, TRIB1, SEMA3A, DLC1, CXCL13, PPARGC1A, EMILIN1, LRCH1, CORO1C, TMEFF2, CLIC4, SEMA3G, ADAMTS9, NAV3, BMERB1, PHLDB2, STARD13, MYOCD, CYGB, NEXMIF
BP	GO:0030324	lung development	39/1554	3.34E-07	BMPR1A, CCN2, FGF7, FGF9, FGF10, FGFR1, FOXF1, GATA6, GLI2, IGFBP5, LIF, NFIB, PDGFRA, PGR, PKD1, PROX1, RBP4, SHH, SRF, TBX5, TCF21, TGFB3, TGFBR2, THRA, WNT2B, TBX4, SPRY1, SPRY2, KLF2, ZFPM2, ERRFI1, HHIP, CRISPLD2, STK40, PKDCC, MYOCD, FOXP2, RSPO2, AARD
BP	GO:0045444	fat cell differentiation	46/1554	3.71E-07	ADRB2, ZFP36L1, RUNX1T1, CEBPD, EGR2, FGF10, GDF10, GPER1, GRK5, NR4A1, ID2, ID4, INHBB, NR4A2, ENPP1, PTGS2, RGS2, RORA, SFRP1, SFRP2, SLC2A4, TGFB1I1, ZFP36, ZBTB16, NR4A3, DYSF, PER2, KLF4, ADIPOQ, ZNF516, PPARGC1A, SIRT1, ZFPM2, WWTR1, CLIP3, PRDM16, EBF2, STEAP4, CCDC3, ARID5B, C1QTNF3, JDP2, GLIS1, VSTM2A, FNDC5, PTPRQ
BP	GO:0090287	regulation of cellular response to growth factor stimulus	55/1554	3.98E-07	ABL1, ACVRL1, LDLRAD4, CAV1, CIDEA, DCN, FBN1, FGF2, FGF9, FGF10, FGFR1, GDF2, GRB10, CCN1, ILK, ITGA5, ITGB3, SMAD7, MSX1, NTRK3, PRKCB, SFRP1, SFRP2, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, LTBP4, ITGA8, CHRD, SLIT2, SPRY1, SPRY2, CXCL13, EMILIN1, FSTL1, DKK1, ZNF423, SPART, SIRT1, SOSTDC1, ADGRA2, JCAD, PRDM16, GREM2, HHIP, TMEM108, CHRDL1, MYOCD, VASN, WFIKKN2, BMPER, RBPMS2
BP	GO:0051924	regulation of calcium ion transport	50/1554	4.20E-07	ABL1, ADCYAP1R1, ADRA2A, BIN1, ANK2, ATP1A2, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAMK2A, CASQ2, CAV1, CLIC2, DMD, FYN, GEM, GNAO1, GPER1, HRC, HSPA2, IL16, MYLK, P2RX1, PDE4B, PDE4D, PKD2, PTGS2, RCVRN, RYR2, CX3CL1, CXCL12, SLC8A1, SNCA, STAC, STC1, TRPC1, TRPC3, WFS1, DYSF, RGN, AKAP6, REM1, JPH2, P2RY12, AHNAK, JPH4, FCRL3, TMC2
BP	GO:0043062	extracellular structure organization	71/1554	4.20E-07	A2M, ABL1, CD34, COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, CCN2, CYP1B1, DCN, DPT, ELN, FBN1, FGF2, FOXF1, GPM6B, HAS1, HSPG2, HYAL1, CCN1, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, LAMA4, LAMC1, LRP1, MFAP4, MMP2, MMP16, MTTP, MYH11, NID1, DDR2, PDGFRA, PECAM1, PRKACB, PTX3, SFRP2, THBS1, TIMP2, VWF, MFAP5, RECK, SOAT2, ITGA8, ADAMTS4, LAMC3, FBLN5, ADAMTS5, EMILIN1, FLRT2, ABI3BP, CSGALNACT1, ADAMTS9, JAM2, HPSE2, NDNF, THSD4, SCUBE1, JAM3, CRISPLD2, COL25A1, PHLDB2, CCDC80, SCUBE3
BP	GO:0010975	regulation of neuron projection development	80/1554	4.52E-07	ABL1, ADCYAP1, APBB1, ADGRB3, BDNF, BMP5, CDH4, CNTN1, CTNNA2, DPYSL2, DPYSL3, LPAR1, EPHA3, EPHA7, FGFR1, FYN, GRID2, HGF, IL2, ILK, LRP1, MAP1B, MAP6, MAPT, MEF2C, NFATC4, NGF, NGFR, NTRK3, PRKN, PMP22, PRKD1, RELN, PTPRD, RAP1A, RGS2, SCN1B, CX3CL1, SDC2, CXCL12, SFRP1, SFRP2, SRF, SYT4, CNTN2, NR2F1, VLDLR, NEURL1, KLF4, SLIT2, CPNE6, NTN1, ZEB2, MAGI2, UST, SEMA3A, OLFM1, PDLIM5, IL1RAPL1, CPEB3, NLGN1, DKK1, RIMS1, TNIK, SPART, DENND5A, NCS1, NLGN3, SEMA3G, RGMA, ZSWIM5, ZSWIM6, TRAK2, NDNF, FBXO31, PLXNA4, LRRK2, NEGR1, ALKAL2, OSTN
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	62/1554	4.54E-07	ABL1, ACVRL1, BMP5, BMPR1A, LDLRAD4, CAV1, CIDEA, EGR1, FBN1, FGF9, FGF10, FOS, LRRC32, GDF2, GDF10, CCN1, ILK, INHBB, JUN, SMAD7, SMAD9, MSX1, ROR2, RYR2, SFRP1, SFRP2, SHH, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, CLDN5, LTBP4, CILP, ITGA8, CHRD, MAGI2, FERMT2, RBPMS, EMILIN1, FSTL1, DKK1, ZNF423, SPART, SIRT1, SOSTDC1, WWTR1, TMEM100, RGMA, TBX20, PRDM16, GREM2, ATOH8, CHRDL1, MYOCD, VASN, WFIKKN2, PPM1L, BMPER, RBPMS2

BP	GO:0086002	cardiac muscle cell action potential involved in contraction	20/1554	4.91E-07	BIN1, ANK2, CACNA1C, CACNA2D1, CACNB2, CAV1, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, RYR2, SCN1B, SCN2B, SCN4B, SNTA1, GJC1, KCNE4, CTNNA3, SCN3B
BP	GO:0086065	cell communication involved in cardiac conduction	20/1554	4.91E-07	ANK2, ATP1A2, ATP1B2, CACNA1C, CACNA2D1, CACNB2, CASQ2, CAV1, FLNA, HRC, KCNJ3, PDE4D, RYR2, SCN1B, SCN4B, SLC8A1, GJC1, CTNNA3, TNNI3K, SCN3B
BP	GO:0046683	response to organophosphorus	33/1554	5.17E-07	AQP1, ZFP36L1, CDO1, CNGA3, CRHBP, DUSP1, LPAR1, FOS, FOSB, IGFBP5, JUN, JUNB, JUND, P2RX1, P2RY1, PDE2A, PDE3A, PER1, PKD2, PLA2G5, PTGS2, RAP1A, RYR3, SLC8A1, SLC8A3, STC1, TEK, TRPC3, FOSL1, ADIPOQ, AKAP6, P2RY12, PPARGC1B
BP	GO:0034329	cell junction assembly	48/1554	5.30E-07	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, ANK2, APOD, ARHGAP6, BCL2, CAV1, CDH4, CDH17, DUSP3, EPHA2, EPHA3, FLNA, FLNC, GPM6B, ILK, ITGA5, LAMC1, LRP1, SMAD7, PECAM1, PRKCA, RAP1A, ROCK1, SFRP1, SRF, TEK, THBS1, TLN1, CLDN5, TNS1, VCL, CNTNAP1, ROCK2, GJC1, DLC1, SORBS1, FERMT2, FAM107A, NFASC, CORO1C, CDH19, PEAK1, PHLDB2, MPP7
BP	GO:0034333	adherens junction assembly	26/1554	5.33E-07	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, APOD, ARHGAP6, BCL2, DUSP3, EPHA3, GPM6B, LRP1, SMAD7, ROCK1, SFRP1, TEK, THBS1, VCL, ROCK2, DLC1, SORBS1, FERMT2, FAM107A, CORO1C, PEAK1, PHLDB2
BP	GO:0010927	cellular component assembly involved in morphogenesis	30/1554	5.60E-07	ACTC1, ACTN2, ANK2, CASQ2, CFL2, ILK, MEF2A, MEF2C, MYH3, MYH11, PDGFRA, PGM5, PMP22, PROX1, RFX2, SRF, TMOD1, TNNT2, TPM1, CNTNAP1, MYOM2, KLHL41, LDB3, AKAP13, NFASC, LMOD1, MYOZ2, LMOD3, CCDC136, PHLDB2
BP	GO:1903779	regulation of cardiac conduction	23/1554	5.93E-07	ANK2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CASQ2, CAV1, DMPK, FLNA, HRC, ITPR1, NPR1, NPR2, PDE4D, RYR2, RYR3, SLC8A2, SLC8A1, SLC8A3, TRPC1, ABCC9, TNNI3K, FXYD6
BP	GO:0060541	respiratory system development	42/1554	6.31E-07	ALDH1A3, BMPR1A, CCN2, EDA, FGF7, FGF9, FGF10, FGFR1, FOXF1, GATA6, GLI2, IGFBP5, LIF, NFIB, PDGFRA, PGR, PKD1, PROX1, RBP4, SHH, SRF, TBX5, TCF21, TGFB3, TGFBR2, THRA, WNT2B, KCNAB1, TBX4, SPRY1, SPRY2, KLF2, ZFPM2, ERRFI1, HHIP, CRISPLD2, STK40, PKDCC, MYOCD, FOXP2, RSPO2, AARD
BP	GO:0006942	regulation of striated muscle contraction	27/1554	6.52E-07	ACTN3, ADRA1A, BIN1, ANK2, ATP1A2, CACNA1C, CASQ2, CAV1, CLIC2, CCN2, DMD, DMPK, FLNA, HRC, SMAD7, MYL3, PDE4B, PDE4D, RGS2, RYR2, SLC8A1, SLC8A3, STC1, PDE5A, HDAC4, CTNNA3, TNNI3K
BP	GO:0014074	response to purine-containing compound	35/1554	6.56E-07	AQP1, ZFP36L1, CASQ2, CDO1, CNGA3, CRHBP, DUSP1, FOS, FOSB, IGFBP5, JUN, JUNB, JUND, P2RX1, P2RY1, PDE2A, PDE3A, PER1, PKD2, PLA2G5, PTGS2, RAP1A, RYR2, RYR3, SLC8A1, SLC8A3, STC1, TEK, TRPC3, FOSL1, ADIPOQ, AKAP6, PPARGC1A, P2RY12, PPARGC1B
BP	GO:0060401	cytosolic calcium ion transport	38/1554	8.01E-07	ABL1, ADCYAP1R1, ADRA1A, ANK2, ATP1A2, ATP2B4, BCL2, CACNA1C, CACNA2D1, CASQ2, CAV1, MS4A1, CLIC2, CCN2, DMD, FGF2, FYN, GPER1, GRIN2A, HRC, ITPR1, PDE4D, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SLC8A3, SNCA, TRPC1, TRPC3, TRPA1, AKAP6, RASA3, JPH2, SLC25A23, JPH4, FAM155A
BP	GO:0030900	forebrain development	65/1554	9.19E-07	ADCYAP1, ALDH1A3, AQP1, ATP2B4, AXL, BMPR1A, DCT, LPAR1, EPHA5, FGF10, FGFR1, FLNA, FYN, GLI2, GNAO1, ID2, ID4, KCNA1, LRP1, MSX1, NFIB, NR4A2, PITX1, PITX2, PROX1, RELN, SALL1, CXCL12, SHH, SLC8A1, SLC8A3, SRF, SSTR1, TACC1, CNTN2, WNT2B, BTG2, NR4A3, CHRD, NRP2, DCLK1, SLIT2, ZEB2, SEMA3A, DLC1, TACC2, PPARGC1A, DKK1, KDM6B, CHD5, SALL3, CDON, CRTAC1, GNG12, ZSWIM6, P2RY12, TMEM108, FAT4, DIXDC1, BMERB1, PLXNA4, FOXP2, LRRK2, DCLK2, PHACTR1
BP	GO:0060402	calcium ion transport into cytosol	36/1554	9.32E-07	ABL1, ADCYAP1R1, ADRA1A, ANK2, ATP1A2, ATP2B4, BCL2, CACNA1C, CACNA2D1, CASQ2, CAV1, MS4A1, CLIC2, DMD, FGF2, FYN, GPER1, GRIN2A, HRC, ITPR1, PDE4D, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SLC8A3, SNCA, TRPC1, TRPC3, TRPA1, AKAP6, RASA3, JPH2, JPH4, FAM155A
BP	GO:0050769	positive regulation of neurogenesis	76/1554	9.32E-07	ADCYAP1, ADRA2B, BIN1, APBB1, ASPA, BCL2, BDNF, BMP5, CDH4, CNTN1, CX3CR1, BRINP1, DCT, DPYSL3, LPAR1, EPHA3, FGFR1, FLNA, FYN, GLI2, GPER1, HGF, ID2, IL2, IL6ST, ILK, KIT, LIF, LRP1, MAP1B, MAP6, MAPT, MEF2C, NAP1L2, NGF, NGFR, NTRK3, PRKN, PRKD1, PROX1, RELN, PTPRD, RAP1A, RGS2, SCN1B, CX3CL1, CXCL12, SH3GL3, SHH, SRF, SYT4, TCF4, ZEB1, TIMP2, VLDLR, RNF112, SOCS2, NEURL1, SLIT2, CPNE6, NTN1, ZEB2, MAGI2, SEMA3A, IL1RAPL1, CPEB3, NLGN1, DKK1, RIMS1, CDON, P2RY12, NDNF, FBXO31, PLXNA4, NEGR1, ALKAL2
BP	GO:0007045	cell-substrate adherens junction assembly	24/1554	1.03E-06	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, APOD, ARHGAP6, BCL2, DUSP3, EPHA3, GPM6B, LRP1, ROCK1, SFRP1, TEK, THBS1, ROCK2, DLC1, SORBS1, FERMT2, FAM107A, CORO1C, PEAK1, PHLDB2
BP	GO:0048041	focal adhesion assembly	24/1554	1.03E-06	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, APOD, ARHGAP6, BCL2, DUSP3, EPHA3, GPM6B, LRP1, ROCK1, SFRP1, TEK, THBS1, ROCK2, DLC1, SORBS1, FERMT2, FAM107A, CORO1C, PEAK1, PHLDB2
BP	GO:0003018	vascular process in circulatory system	38/1554	1.06E-06	ACTA2, ADCYAP1, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ANGPT1, ATP1A2, BDKRB2, CAV1, CHRM3, EDNRA, EDNRB, EPHX2, GPER1, HBB, CXCR2, ITGA1, KCNMA1, KCNMB1, NPR1, P2RX1, P2RY1, PDE2A, PDE3A, PTGS2, RGS2, ROCK1, SLC8A1, TACR2, TEK, VIP, PER2, SLIT2, ROCK2, AKAP12, UTS2B

BP	GO:0071804	cellular potassium ion transport	44/1554	1.09E-06	ACTN2, BIN1, ANK2, AQP1, ATP1A2, ATP1B2, CASQ2, CAV1, DPP6, FHL1, FLNA, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, PKD2, VAMP2, KCNAB1, KCNQ4, AKAP6, ABCC9, KCNH4, KCNE4, KCNIP3, KCNIP1, KCNQ5, SLC24A3, P2RY12, KCNIP4, SLC24A4, NALCN, SLC9A9, KCNT2, LRRC52
BP	GO:0071805	potassium ion transmembrane transport	44/1554	1.09E-06	ACTN2, BIN1, ANK2, AQP1, ATP1A2, ATP1B2, CASQ2, CAV1, DPP6, FHL1, FLNA, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, PKD2, VAMP2, KCNAB1, KCNQ4, AKAP6, ABCC9, KCNH4, KCNE4, KCNIP3, KCNIP1, KCNQ5, SLC24A3, P2RY12, KCNIP4, SLC24A4, NALCN, SLC9A9, KCNT2, LRRC52
BP	GO:0006813	potassium ion transport	47/1554	1.14E-06	ACTN2, ADCYAP1, ADRA2A, BIN1, ANK2, AQP1, ATP1A2, ATP1B2, CASQ2, CAV1, DPP6, FHL1, FLNA, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, PKD2, VAMP2, VIP, KCNAB1, KCNQ4, AKAP6, ABCC9, KCNH4, KCNE4, KCNIP3, KCNIP1, KCNQ5, SLC24A3, P2RY12, KCNIP4, SLC24A4, NALCN, SLC9A9, KCNT2, LRRC52
BP	GO:0010518	positive regulation of phospholipase activity	20/1554	1.17E-06	ADCYAP1R1, ADRA1A, ARHGAP6, BDNF, LPAR1, EDNRA, ESR1, FGF2, FGFR1, GNAQ, CCN1, ITK, KIT, NTRK3, PDGFRA, PLA2G5, GPR55, NMUR1, P2RY12, RASGRP4
BP	GO:0010463	mesenchymal cell proliferation	17/1554	1.37E-06	BMPR1A, FGF7, FGF9, FGFR1, FOXF1, MSX1, MYC, NFIB, SHH, ZEB1, TGFBR2, DCHS1, CHRD, HAND2, FAT4, FOXP2, OSR1
BP	GO:0060560	developmental growth involved in morphogenesis	46/1554	1.59E-06	ABL1, BDNF, CDH4, DPYSL2, S1PR1, EPHA7, ESR1, FGF10, ILK, LRP1, MAP1B, MAPT, NDN, NGF, NTRK3, PRKN, PPP3CB, SALL1, CXCL12, SFRP1, SFRP2, SHH, SLIT3, SRF, SYT4, TGFBR2, VCL, NRP2, DCLK1, SLIT2, CPNE6, NTN1, ZEB2, MAGI2, SPRY1, SPRY2, SEMA3A, OLFM1, RIMS1, SPART, NLGN3, SEMA3G, TMEM108, NKD1, PLXNA4, OSTN
BP	GO:0045666	positive regulation of neuron differentiation	63/1554	1.65E-06	ADCYAP1, ADRA2B, APBB1, BCL2, BDNF, BMP5, CDH4, CNTN1, BRINP1, DPYSL3, LPAR1, EPHA3, FGFR1, FYN, GLI2, HGF, IL2, ILK, LRP1, MAP1B, MAP6, MAPT, MEF2C, NAP1L2, NGF, NGFR, NTRK3, PRKN, PRKD1, PROX1, RELN, PTPRD, RAP1A, RGS2, SCN1B, CX3CL1, CXCL12, SH3GL3, SRF, SYT4, TCF4, ZEB1, TIMP2, VLDLR, RNF112, SOCS2, NEURL1, SLIT2, CPNE6, NTN1, ZEB2, MAGI2, IL1RAPL1, CPEB3, NLGN1, DKK1, RIMS1, CDON, NDNF, FBXO31, PLXNA4, NEGR1, ALKAL2
BP	GO:0034330	cell junction organization	53/1554	1.67E-06	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, ANK2, APOD, ARHGAP6, BCL2, CAV1, CDH4, CDH17, DUSP3, EPHA2, EPHA3, FLNA, FLNC, GPM6B, ILK, ITGA5, LAMC1, LRP1, SMAD7, PECAM1, PRKCA, RAP1A, ROCK1, SFRP1, SRF, TEK, TGFB3, THBS1, TLN1, CLDN5, TNS1, VCL, CNTNAP1, ROCK2, GJC1, DLC1, SORBS1, FERMT2, MAPRE2, FAM107A, RASSF8, NFASC, CORO1C, CDH19, CADM3, PEAK1, PHLDB2, MPP7, CADM2
BP	GO:1901861	regulation of muscle tissue development	35/1554	1.69E-06	ACTN3, BCL2, BMPR1A, EPHB1, FGF2, FGF9, FGFR1, GATA6, IGF1, IGFBP5, KCNK2, MEF2C, MEIS1, PIM1, RBP4, RGS2, SHH, TBX5, TGFBR2, TGFBR3, FZD7, AKAP6, HDAC4, KLHL41, PPARGC1A, DKK1, ZFPM2, CDON, SOX6, LMOD3, TBX20, JPH2, SOX17, MYOCD, RBM24
BP	GO:0048638	regulation of developmental growth	60/1554	1.74E-06	ABL1, ACACB, ACTN3, ADRB2, AR, BCL2, BDNF, BMPR1A, CDH4, CDKN1A, DIO3, DPYSL2, EPHA7, FGF2, FGF9, FGFR1, GATA6, GHR, IGF1, ILK, KCNK2, LRP1, MAP1B, MAPT, MEF2C, MEIS1, NGF, NTRK3, PRKN, PIM1, PROX1, PTCH1, RBP4, RGS2, CXCL12, SFRP1, SFRP2, SRF, STAT5B, SYT4, TBX5, TGFBR2, TGFBR3, SOCS2, CPNE6, NTN1, AKAP6, SEMA3A, OLFM1, RIMS1, SPART, ZFPM2, LATS2, MBD5, SEMA3G, TBX20, SPTBN4, NKD1, PLXNA4, OSTN
BP	GO:0034332	adherens junction organization	33/1554	1.92E-06	ABL1, ACTN1, ACTN2, ACTN3, ACVRL1, APOD, ARHGAP6, BCL2, CDH4, CDH17, DUSP3, EPHA3, GPM6B, LRP1, SMAD7, ROCK1, SFRP1, TEK, THBS1, VCL, ROCK2, DLC1, SORBS1, FERMT2, MAPRE2, FAM107A, RASSF8, CORO1C, CDH19, CADM3, PEAK1, PHLDB2, CADM2
BP	GO:0050805	negative regulation of synaptic transmission	22/1554	1.92E-06	BCHE, CBLN1, CNR2, GRIA1, GRID2, GRIK2, GRIK3, KCNB1, MAPT, PRKN, PTGS2, RAP1A, SNCA, SRF, STXBP1, SYT4, ADIPOQ, SORCS3, SYT11, NLGN3, SORCS2, LRRK2
BP	GO:0001656	metanephros development	25/1554	1.97E-06	AQP2, BCL2, CD34, EGR1, EYA1, FBN1, FGF10, GDNF, ID2, CXCR2, LIF, MYC, PDGFRA, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, ITGA8, ADIPOQ, SPRY1, WWTR1, FAT4, OSR1
BP	GO:0014897	striated muscle hypertrophy	28/1554	2.01E-06	ADRA1A, ATP2B4, GATA6, IGF1, IGFBP5, IL6ST, MEF2A, MEF2C, PRKCA, RGS2, ROCK1, RYR2, TRPC3, NR4A3, SORBS2, PDE5A, HAND2, AKAP6, ROCK2, HDAC4, PDLIM5, AKAP13, KLF15, LMCD1, ERRFI1, TRIM63, MLIP, GATA5
BP	GO:0019935	cyclic-nucleotide-mediated signaling	43/1554	2.16E-06	ADCY2, ADCY5, ADCY9, ADCYAP1, ADCYAP1R1, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, AQP1, ATP2B4, ADGRB3, CALCA, LPAR1, EDNRB, EPHA5, GNAL, GNAQ, GPR3, GPR26, GPER1, LHCGR, NPR1, NPR2, PDE2A, PDE3A, PDE3B, PDE4D, PRKAR2B, PRKCA, PTGER3, PTGER4, PTGFR, RGS2, THBS1, VIP, AKAP6, AKAP13, RASD2, PDE11A, ADGRL4
BP	GO:0003205	cardiac chamber development	37/1554	2.18E-06	ANK2, PRDM1, BMP5, BMPR1A, CPE, FOXF1, GATA6, ID2, CCN1, KCNK2, SMAD7, MEF2C, MYL3, PCSK5, PDE2A, PROX1, RBP4, RYR2, SALL1, SFRP2, SLIT3, SRF, TBX5, TEK, TGFBR2, TGFBR3, TNNT2, TPM1, NRP2, SLIT2, HAND1, HAND2, ADAMTS1, ZFPM2, PARVA, TBX20, MYOCD
BP	GO:0061572	actin filament bundle organization	35/1554	2.24E-06	ABL1, ACTN1, RHOB, RND3, ARHGAP6, CCN2, DPYSL3, S1PR1, LPAR1, ELN, FLNA, PRKN, PIK3R1, PTGER4, ROCK1, CX3CL1, SFRP1, SRF, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, DLC1, SORBS1, FAM107A, SYNPO, ARHGEF15, TMEFF2, RND1, ARHGAP28, PHLDB2, SYNPO2, PHACTR1, RFLNB

BP	GO:0030239	myofibril assembly	22/1554	2.43E-06	ACTC1, ACTN2, CASQ2, CFL2, MEF2A, MEF2C, MYH3, MYH11, PDGFRA, PGM5, PROX1, SRF, TMOD1, TNNT2, TPM1, MYOM2, KLHL41, LDB3, AKAP13, LMOD1, MYOZ2, LMOD3
BP	GO:1903169	regulation of calcium ion transmembrane transport	34/1554	2.62E-06	ABL1, ADRA2A, BIN1, ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CLIC2, DMD, FYN, GEM, GPER1, HRC, HSPA2, PDE4B, PDE4D, PKD2, RYR2, CX3CL1, SLC8A1, SNCA, STAC, TRPC1, DYSF, RGN, AKAP6, REM1, JPH2, AHNAK, JPH4, TMC2
BP	GO:0007613	memory	29/1554	2.62E-06	BDNF, CHRNA7, CX3CR1, BRINP1, GRIA1, GRIN2A, ITGA5, KCNK2, LDLR, MAP1A, MAPT, NFATC4, NGF, PPP3CB, RELN, PTGS2, ATXN1, SGK1, SLC8A2, SLC8A3, SRF, SYT4, TAC1, VLDLR, ITGA8, PJA2, CPEB3, SORCS3, SLC17A7
BP	GO:0032835	glomerulus development	20/1554	2.66E-06	ACTA2, ANGPT1, BCL2, CD34, COL4A3, COL4A4, EGR1, IL6R, MEF2C, NID1, PDGFRA, PECAM1, TCF21, TEK, ADIPOQ, MAGI2, WWTR1, KLF15, PDGFD, OSR1
BP	GO:1902903	regulation of supramolecular fiber organization	60/1554	2.71E-06	ABL1, ACTN2, BIN1, ARHGAP6, CFL2, CHRNA7, CLU, CSF3, CCN2, CTNNA2, S1PR1, LPAR1, ELN, FER, FLNA, GSN, NCKAP1L, LDLR, MAP1A, MAP1B, MAPT, MEF2C, PRKN, PIK3R1, PROX1, PTGER4, ROCK1, CX3CL1, CXCL12, SFRP1, SNCA, TAC1, TGFB3, TMOD1, TPM1, SLIT2, ROCK2, ARHGEF10, DLC1, CDC42EP2, CDC42EP3, DSTN, EMILIN1, AKAP13, SYNPO, ARHGEF15, TMEFF2, LMOD1, CLIP3, SNX9, LMOD3, SPTBN4, ARHGAP28, NAV3, BMERB1, PHLDB2, MYADM, PLEKHH2, JMY, SYNPO2
BP	GO:0060191	regulation of lipase activity	26/1554	2.78E-06	ABL1, ADCYAP1R1, ADRA1A, ANXA1, ARHGAP6, BDNF, LPAR1, EDNRA, ESR1, FGF2, FGFR1, GNAQ, CCN1, ITK, KIT, LRP1, NTRK3, PCSK5, PDGFRA, PLA2G5, RGS2, SNCA, GPR55, NMUR1, P2RY12, RASGRP4
BP	GO:0014896	muscle hypertrophy	28/1554	2.86E-06	ADRA1A, ATP2B4, GATA6, IGF1, IGFBP5, IL6ST, MEF2A, MEF2C, PRKCA, RGS2, ROCK1, RYR2, TRPC3, NR4A3, SORBS2, PDE5A, HAND2, AKAP6, ROCK2, HDAC4, PDLIM5, AKAP13, KLF15, LMCD1, ERRFI1, TRIM63, MLIP, GATA5
BP	GO:0007612	learning	33/1554	2.99E-06	ATP1A2, ADGRB3, BCHE, FOS, FYN, GRIN2A, JUN, KIT, MAP1A, MEIS2, PRKN, PPP3CB, PRKAR2B, RELN, PTGS2, ATXN1, SLC8A2, SLC8A3, SRF, TAC1, TACR2, CNTN2, CLDN5, BTG2, FOSL1, NRXN1, NRXN2, SYNPO, DKK1, SORCS3, NLGN3, JPH4, FOXP2
BP	GO:0040013	negative regulation of locomotion	65/1554	3.28E-06	ACVRL1, ADARB1, APOD, RHOB, BCL2, BMP5, BMPR1A, LDLRAD4, CX3CR1, CYP1B1, DACH1, DCN, DPYSL3, DUSP1, DUSP3, FGF2, GDF2, HAS1, IGFBP5, ILK, LRP1, SMAD7, MEF2C, MITF, CD200, PTGER4, RRAS, CX3CL1, CXCL12, SFRP1, SFRP2, SHH, SRF, STC1, TBX5, THBS1, TPM1, VCL, RECK, CHRD, RGN, KLF4, SLIT2, ADIPOQ, MAGI2, TRIB1, SEMA3A, DLC1, CXCL13, PPARGC1A, MID2, EMILIN1, LRCH1, CORO1C, TMEFF2, CLIC4, SEMA3G, ADAMTS9, NAV3, BMERB1, PHLDB2, STARD13, MYOCD, CYGB, NEXMIF
BP	GO:0035051	cardiocyte differentiation	36/1554	3.36E-06	ACTC1, ACTN2, ADRA1A, GATA6, GPER1, IGF1, MEF2A, MEF2C, MYH11, PDGFRA, PITX2, PROX1, RGS2, SGCB, SGCD, SLC8A1, SRF, TBX5, TGFBR3, FZD7, SORBS2, MYOM2, HAND2, AKAP6, SPRY1, PDLIM5, BVES, AKAP13, DKK1, KDM6B, SOX6, ALPK3, SOX17, MYOCD, PRICKLE1, SIK1
BP	GO:0007519	skeletal muscle tissue development	35/1554	3.43E-06	ACTN3, ATF3, BCL2, CAV1, CFL2, COL19A1, DCN, EGR1, EGR2, ELN, EPHB1, FOS, HLF, MEF2C, MEF2D, PITX1, SHH, SVIL, TCF21, BTG2, KCNAB1, NEURL1, MYOM2, HDAC4, KLHL41, BVES, DKK1, MAFF, CDON, MYOZ2, LMOD3, SOX17, MYOCD, FOXP2, RBM24
BP	GO:0051017	actin filament bundle assembly	34/1554	3.45E-06	ABL1, ACTN1, RHOB, RND3, ARHGAP6, CCN2, DPYSL3, S1PR1, LPAR1, ELN, FLNA, PRKN, PIK3R1, PTGER4, ROCK1, CX3CL1, SFRP1, SRF, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, DLC1, SORBS1, FAM107A, SYNPO, ARHGEF15, TMEFF2, RND1, ARHGAP28, PHLDB2, SYNPO2, PHACTR1
BP	GO:0003300	cardiac muscle hypertrophy	27/1554	3.76E-06	ADRA1A, ATP2B4, GATA6, IGF1, IL6ST, MEF2A, MEF2C, PRKCA, RGS2, ROCK1, RYR2, TRPC3, NR4A3, SORBS2, PDE5A, HAND2, AKAP6, ROCK2, HDAC4, PDLIM5, AKAP13, KLF15, LMCD1, ERRFI1, TRIM63, MLIP, GATA5
BP	GO:0022604	regulation of cell morphogenesis	75/1554	3.81E-06	ABL1, ANXA1, RHOB, RND3, RHOH, ADGRB3, BDNF, CDH4, DPYSL2, LPAR1, EPHA7, FLNA, FYN, ILK, ITGA7, KIT, LRP1, MAP1B, MAP6, MAPT, MPL, NFATC4, NGF, NGFR, NTRK3, P2RY1, PALM, PRKN, RELN, PTPRD, SDC2, CXCL12, SRF, SYT4, CNTN2, TPM1, ZNF135, SLIT2, CPNE6, NTN1, ZEB2, UST, ENAM, SEMA3A, DLC1, CDC42EP2, OLFM1, CDC42EP3, PDLIM5, WASF3, FERMT2, IL1RAPL1, BVES, NLGN1, RIMS1, TNIK, SPART, CORO1C, RND1, PLEKHO1, NLGN3, PARVA, SEMA3G, RHOJ, SHROOM3, ZSWIM5, ZSWIM6, TRAK2, FBXO31, PLXNA4, MYADM, LRRK2, SH3D19, SYNE3, OSTN
BP	GO:0045667	regulation of osteoblast differentiation	30/1554	3.81E-06	BMPR1A, CEBPD, GDF10, HGF, ID2, IGF1, IGFBP5, CCN1, IL6R, IL6ST, ILK, JUND, MEF2C, DDR2, PRKD1, PTCH1, RORB, SFRP1, SFRP2, FGF23, CHRD, PDLIM7, HAND2, HDAC4, RASSF2, ZHX3, TWIST2, RANBP3L, TMEM119, OSTN
BP	GO:0043270	positive regulation of ion transport	50/1554	4.00E-06	ABL1, ACTN2, ADCYAP1R1, ADRA2A, ADRB2, ANK2, ATP1B2, CACNA2D1, CACNB2, CAMK2A, CAV1, CNTN1, DMD, FHL1, FLNA, GDNF, GPER1, HSPA2, KCNA1, KCNH2, KCNMB1, MYLK, P2RX1, P2RY1, ABCB1, PKD2, RELN, RYR2, SCN1B, SCN4B, CX3CL1, CXCL12, SNCA, STAC, STC1, STXBP1, SYT4, TACR2, TRH, TRPC1, TRPC3, WFS1, RGN, AKAP6, NLGN3, SCN3B, JPH2, P2RY12, CNKSR3, LRRC52
BP	GO:0050808	synapse organization	66/1554	4.35E-06	ABL1, ACTN1, ADGRB3, BDNF, C3, CACNB2, CACNB4, CBLN1, CHRNA7, CTNNA2, CX3CR1, DGKB, DLG2, EPHA7, EPHB1, FYN, GABRA2, GDNF, GPM6A, GRID2, MAP1B, MAPT, MEF2C, NFIA, NFATC4, NTRK3, PALM, PCDHGC3, RELN, PTPRD, CX3CL1, SNCA, CNTN2, UTRN, TUBA1A, SPARCL1, PPFIA2,

					NRP2, NEURL1, NRXN1, NRXN2, NTN1, MAGI2, PDLIM5, WASF3, IL1RAPL1, SYNPO, NTNG1, CNKSR2, NLGN1, ARHGEF15, DKK1, IGSF9B, PDZRN3, NFASC, FLRT2, NLGN3, SYBU, CLSTN2, LRRC4, TMEM108, CTTNBP2, LRRC4B, LRRK2, LRRTM1, SHISA6
BP	GO:0060538	skeletal muscle organ development	36/1554	4.38E-06	ACTN3, ATF3, BCL2, CAV1, CFL2, COL19A1, DCN, EGR1, EGR2, ELN, EPHB1, FOS, HLF, MEF2C, MEF2D, PITX1, SHH, SVIL, TCF21, BTG2, KCNAB1, NEURL1, MYOM2, LARGE1, HDAC4, KLHL41, BVES, DKK1, MAFF, CDON, MYOZ2, LMOD3, SOX17, MYOCD, FOXP2, RBM24
BP	GO:0018212	peptidyl-tyrosine modification	61/1554	4.40E-06	ABL1, ADRA1A, ADRA2A, ANGPT1, AXL, BDNF, BMX, CAV1, CNTN1, CSF3, CSPG4, HBEGF, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, EFEMP1, FER, FGF7, FGF10, FGFR1, FYN, GHR, HGF, IGF1, IL2, IL3, IL6R, IL6ST, ITGA5, ITGB3, ITK, KIT, LIF, KITLG, NTRK3, ROR1, ROR2, DDR2, PDGFRA, PECAM1, RELN, SFRP1, SFRP2, TAL1, TEK, WEE1, DYRK3, TPST1, SOCS3, GPRC5A, NEURL1, ADIPOQ, ERRFI1, PEAK1, PDGFD, TSLP, PKDCC, ALKAL2, EPHA6
BP	GO:0031960	response to corticosteroid	35/1554	4.47E-06	ADCYAP1, ANXA1, AQP1, BCHE, BCL2, ZFP36L1, KLF9, CDKN1A, CDO1, CNGA3, CPN1, CCN2, DUSP1, FOS, FOSB, GPER1, IGFBP2, IL1RN, NTRK3, PAM, PTGS2, SLIT3, STC1, TRH, ZFP36, FOSL1, SLIT2, ADIPOQ, FAM107A, AKAP13, ERRFI1, TRIM63, FBXO32, PPARGC1B, CREBRF
BP	GO:0048565	digestive tract development	31/1554	4.55E-06	BCL2, PRDM1, CDKN1A, EDNRB, FGF9, FGF10, FOXF1, GATA6, GLI2, ID2, KIT, OTC, PCSK5, PDGFRA, PKD1, SALL1, SFRP1, SFRP2, SHH, TCF21, TGFB3, TGFBR2, DCHS1, DACT1, SOX17, FAT4, CLMP, PKDCC, MYOCD, GATA5, RBPMS2
BP	GO:0055117	regulation of cardiac muscle contraction	23/1554	4.66E-06	ADRA1A, BIN1, ANK2, ATP1A2, CACNA1C, CASQ2, CAV1, CLIC2, CCN2, DMD, FLNA, HRC, SMAD7, PDE4B, PDE4D, RGS2, RYR2, SLC8A1, STC1, PDE5A, HDAC4, CTNNA3, TNNI3K
BP	GO:0086091	regulation of heart rate by cardiac conduction	15/1554	5.01E-06	BIN1, ANK2, CACNA1C, CACNA2D1, CACNB2, CAV1, KCND3, KCNH2, KCNJ3, SCN1B, SCN2B, SCN4B, KCNE4, CTNNA3, SCN3B
BP	GO:0048568	embryonic organ development	68/1554	5.42E-06	ALDH1A3, PRDM1, BMP5, BMPR1A, ZFP36L1, EPHA2, EYA1, FBN1, EFEMP1, FGF9, FGF10, FGFR1, FOXF1, GDNF, GLI2, HYAL1, ID2, CCN1, IL3, JUNB, KIT, LIF, MEF2C, KITLG, MMP16, MSX1, ROR2, PBX1, PCSK5, PDGFRA, PKD1, PKD2, PROX1, PTCH1, RBP4, RYR2, SALL1, SHH, SRF, TAL1, ZEB1, TCF21, TGFB3, TGFBR2, WNT9A, RNF112, NR4A3, ITGA8, SOCS3, KCNQ4, HAND1, NTN1, HAND2, TSHZ1, SPRY2, NES, ZFPM2, LRIG1, SOBP, TBX20, DSCAML1, CC2D2A, SOX17, RSPO3, PKDCC, OSR1, NOTO, RBPMS2
BP	GO:1901019	regulation of calcium ion transmembrane transporter activity	24/1554	5.57E-06	ADRA2A, ANK2, ATP1A2, CACNA2D1, CACNB2, CACNB4, CASQ2, CLIC2, DMD, GEM, HRC, HSPA2, PDE4B, PDE4D, PKD2, RYR2, STAC, DYSF, RGN, AKAP6, REM1, JPH2, AHNAK, JPH4
BP	GO:0006940	regulation of smooth muscle contraction	20/1554	5.59E-06	ADRA1A, ADRA2A, ADRA2B, ADRB2, ATP1A2, CAV1, CHRM2, CHRM3, CNN1, GPER1, KCNMA1, KIT, P2RX1, PTGS2, RGS2, SRF, TACR2, TACR1, TACR3, MYOCD
BP	GO:0001823	mesonephros development	26/1554	5.83E-06	ARG2, BCL2, EYA1, FGF2, FGF10, FGFR1, GDNF, ILK, SMAD7, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SFRP1, SHH, TCF21, WNT2B, ZBTB16, DCHS1, SLIT2, SPRY1, FAT4, OSR1, BMPER
BP	GO:0043500	muscle adaptation	29/1554	5.92E-06	ACTN3, ADRA1A, ATP2B4, GATA6, GSN, IGF1, IGFBP5, IL6ST, MEF2A, MEF2C, PRKCA, RGS2, ROCK1, TRPC3, NR4A3, PDE5A, KLF4, HAND2, AKAP6, ROCK2, HDAC4, PPARGC1A, KLF15, LMCD1, MYOZ2, ERRFI1, TRIM63, MLIP, GATA5
BP	GO:0003206	cardiac chamber morphogenesis	30/1554	6.09E-06	BMP5, BMPR1A, CPE, FOXF1, GATA6, ID2, CCN1, SMAD7, MEF2C, MYL3, PROX1, RBP4, RYR2, SFRP2, SLIT3, SRF, TBX5, TEK, TGFBR2, TGFBR3, TNNT2, TPM1, NRP2, SLIT2, HAND1, HAND2, ADAMTS1, ZFPM2, PARVA, TBX20
BP	GO:0001649	osteoblast differentiation	43/1554	6.74E-06	BMPR1A, CEBPD, EPHA2, FGF9, GDF2, GDF10, GLI2, HGF, ID2, ID4, IGF1, IGFBP5, CCN1, IL6R, IL6ST, ILK, JUNB, JUND, MEF2C, MEF2D, DDR2, PRKD1, PTCH1, RORB, SFRP1, SFRP2, SHH, FGF23, CHRD, PDLIM7, HAND2, HDAC4, RASSF2, ZHX3, WWTR1, DHH, TP53INP2, TWIST2, GLIS1, RANBP3L, TMEM119, RSPO2, OSTN
BP	GO:0045778	positive regulation of ossification	24/1554	6.76E-06	ADRB2, BMPR1A, CEBPD, GPM6B, HGF, IGF1, CCN1, IL6R, IL6ST, ILK, JUND, MEF2C, DDR2, PRKD1, SFRP2, SLC8A1, TAC1, TGFB3, ZBTB16, PDLIM7, ZHX3, PKDCC, OSR1, TMEM119
BP	GO:0018108	peptidyl-tyrosine phosphorylation	60/1554	6.94E-06	ABL1, ADRA1A, ADRA2A, ANGPT1, AXL, BDNF, BMX, CAV1, CNTN1, CSF3, CSPG4, HBEGF, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, EFEMP1, FER, FGF7, FGF10, FGFR1, FYN, GHR, HGF, IGF1, IL2, IL3, IL6R, IL6ST, ITGA5, ITGB3, ITK, KIT, LIF, KITLG, NTRK3, ROR1, ROR2, DDR2, PDGFRA, PECAM1, RELN, SFRP1, SFRP2, TAL1, TEK, WEE1, DYRK3, SOCS3, GPRC5A, NEURL1, ADIPOQ, ERRFI1, PEAK1, PDGFD, TSLP, PKDCC, ALKAL2, EPHA6
BP	GO:0010038	response to metal ion	60/1554	7.60E-06	APBB1, AQP1, AQP2, BCL2, CASQ2, CAV1, CNGA3, CRHBP, DLG2, DUSP1, FOS, FOSB, GSN, ID2, IGFBP2, ITPKB, JUN, JUNB, JUND, KCNA1, KCNK3, KCNMA1, KCNMB1, KIT, MAPT, MEF2A, MEF2C, MT1A, NFATC4, OTC, PAM, PRKN, PKD2, PRKAA2, PTGS2, RYR2, RYR3, SHH, SNCA, SOD3, SYT4, THBS1, TNNT2, TRPC1, TRPC3, FGF23, SLC25A12, CACNA1H, CPNE6, RASA4, TXNIP, PPARGC1A, NLGN1, SYT11, HAAO, CLIC4, SLC25A23, CYBRD1, SYT15, LRRK2
BP	GO:0051591	response to cAMP	25/1554	7.63E-06	AQP1, ZFP36L1, CDO1, CNGA3, CRHBP, DUSP1, FOS, FOSB, IGFBP5, JUN, JUNB, JUND, PDE2A, PER1, PKD2, PLA2G5, RAP1A, SLC8A1, SLC8A3, STC1, TEK, FOSL1, ADIPOQ, AKAP6, PPARGC1B

BP	GO:0042063	gliogenesis	51/1554	7.91E-06	ABL1, ADCYAP1, BIN1, ANXA1, ASPA, CLU, CSPG4, CX3CR1, GPR183, LPAR1, EGR2, FGF10, GPR17, GSN, ID2, ID4, IL6ST, ILK, LDLR, LEPR, LIF, LRP1, MAPT, MATN2, NDN, NFIB, NTRK3, ROR1, ROR2, P2RY1, PLP1, RELN, CX3CL1, SHH, SLC8A3, TAL1, CNTN2, TRPC4, RNF112, CNTNAP1, ARHGEF10, TSPAN2, LAMC3, WASF3, DAAM2, KLF15, NLGN3, SOX6, P2RY12, FA2H, BMERB1
BP	GO:0016202	regulation of striated muscle tissue development	33/1554	8.19E-06	ACTN3, BCL2, BMPR1A, EPHB1, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, RBP4, RGS2, SHH, TBX5, TGFBR2, TGFBR3, FZD7, AKAP6, HDAC4, KLHL41, DKK1, ZFPM2, CDON, SOX6, LMOD3, TBX20, JPH2, SOX17, MYOCD, RBM24
BP	GO:0003170	heart valve development	19/1554	8.54E-06	PRDM1, BMPR1A, ELN, CCN1, MEF2C, NFATC1, PDE2A, ROCK1, SLIT3, TBX5, TGFBR2, DCHS1, SLIT2, ROCK2, OLFM1, EMILIN1, ADAMTS9, TBX20, GATA5
BP	GO:0048645	animal organ formation	19/1554	8.54E-06	AR, BMPR1A, EYA1, FGF10, FGFR1, GATA6, GDNF, GLI2, MEF2C, PIM1, SHH, TBX5, TGFBR2, WNT2B, HAND2, SPRY1, DKK1, SOX17, GATA5
BP	GO:0048662	negative regulation of smooth muscle cell proliferation	20/1554	9.03E-06	APOD, CDKN1A, CNN1, GPER1, IGFBP5, ILK, MEF2C, NPR1, NPR3, OGN, TGFB3, TNFAIP3, TPM1, VIP, VIPR2, KLF4, ADIPOQ, TRIB1, PPARGC1A, MYOCD
BP	GO:0051384	response to glucocorticoid	32/1554	9.59E-06	ADCYAP1, ANXA1, AQP1, BCHE, BCL2, ZFP36L1, KLF9, CDKN1A, CDO1, CPN1, DUSP1, FOS, FOSB, IGFBP2, IL1RN, NTRK3, PAM, PTGS2, SLIT3, STC1, TRH, ZFP36, FOSL1, SLIT2, ADIPOQ, FAM107A, AKAP13, ERRFI1, TRIM63, FBXO32, PPARGC1B, CREBRF
BP	GO:0055123	digestive system development	32/1554	9.59E-06	BCL2, PRDM1, CDKN1A, EDNRB, FGF9, FGF10, FOXF1, GATA6, GLI2, ID2, KIT, OTC, PCSK5, PDGFRA, PKD1, SALL1, SFRP1, SFRP2, SHH, TCF21, TGFB3, TGFBR2, DCHS1, DACT1, SOX17, FAT4, CLMP, WLS, PKDCC, MYOCD, GATA5, RBPMS2
BP	GO:0070371	ERK1 and ERK2 cascade	54/1554	9.86E-06	ABL1, ADCYAP1, ADRA1A, ANGPT1, ATF3, ZFP36L1, CHRNA7, CCN2, DUSP1, DUSP3, DUSP4, GPR183, EPHA2, EPHA7, EPHB1, FGF2, FGF10, GPER1, IGF1, CCN1, JUN, KIT, LIF, LRP1, MYC, P2RY1, PDGFRA, PLA2G5, PRKCA, PTGER4, RAP1A, RRAS, CX3CL1, SLAMF1, TEK, FGF23, GPR55, KLF4, ADIPOQ, HAND2, AKAP12, SPRY1, SPRY2, EMILIN1, DNAJC27, ERRFI1, DUSP26, PDGFD, GLIPR2, CNKSR3, BMPER, NLRP6, ALKAL2, TNFAIP8L3
BP	GO:0050679	positive regulation of epithelial cell proliferation	40/1554	1.07E-05	ACVRL1, AR, BMP5, BMPR1A, EGR3, EYA1, F3, FGF2, FGF7, FGF9, FGF10, FGFR1, GDF2, NR4A1, HYAL1, IGF1, ITGB3, JUN, LAMC1, MYC, PRKCA, PRKD1, PROX1, CXCL12, SFRP1, SHH, TEK, TNFAIP3, VIP, NR4A3, DYSF, FZD7, TNFSF12, NRP2, AKT3, SIRT1, PPP1R16B, JCAD, FOXP2, OSR1
BP	GO:0090130	tissue migration	59/1554	1.10E-05	ABL1, ACTA2, ACTC1, ACVRL1, ANGPT1, ANXA1, RHOB, CCR6, CYP1B1, DCN, HBEGF, EGR3, EPHA2, FGF2, FGF7, FGF10, FGFR1, FOXF1, GDF2, NR4A1, HYAL1, ITGB3, JUN, KIT, MEF2C, PECAM1, PRKCA, PRKD1, PROX1, PTGS2, SRF, STC1, TAC1, TEK, TGFBR2, THBS1, TNFSF12, NRP2, KLF4, SLIT2, ROCK2, ZEB2, AKT3, SEMA3A, CXCL13, MAPRE2, SIRT1, CORO1C, KANK2, ADGRA2, ADAMTS9, RHOJ, JCAD, ATOH8, STARD13, GLIPR2, AMOTL1, CLEC14A, BMPER
BP	GO:0051592	response to calcium ion	32/1554	1.30E-05	CASQ2, CAV1, CRHBP, DUSP1, FOS, FOSB, ITPKB, JUN, JUNB, JUND, KCNMA1, KCNMB1, MEF2A, MEF2C, PKD2, PRKAA2, RYR2, RYR3, SYT4, THBS1, TNNT2, TRPC1, TRPC3, SLC25A12, CPNE6, RASA4, TXNIP, NLGN1, SYT11, CLIC4, SLC25A23, SYT15
BP	GO:0048705	skeletal system morphogenesis	44/1554	1.34E-05	ANXA6, FOXN3, COL6A2, COL6A3, COL13A1, CCN2, EYA1, FGFR1, HYAL1, MATN2, MEF2C, MEF2D, MGP, MMP2, MMP16, MSX1, ROR2, PDGFRA, PKD1, SFRP1, SFRP2, STC1, ZEB1, TEK, TGFB3, TGFBR2, THRA, WNT9A, BARX2, TBX4, TIPARP, SCARA3, RAB23, CSGALNACT1, DSCAML1, HHIP, CSRNP1, COL21A1, ARID5B, OSR1, PPARGC1B, FREM1, TMEM119, RFLNB
BP	GO:0043502	regulation of muscle adaptation	26/1554	1.44E-05	ACTN3, ADRA1A, ATP2B4, IGF1, IGFBP5, IL6ST, MEF2A, PRKCA, RGS2, ROCK1, TRPC3, UTRN, NR4A3, PDE5A, KLF4, HAND2, AKAP6, ROCK2, HDAC4, PPARGC1A, LMCD1, ERRFI1, TRIM63, MLIP, FBXO32, GATA5
BP	GO:0048634	regulation of muscle organ development	33/1554	1.44E-05	ACTN3, BCL2, BMPR1A, EPHB1, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, RBP4, RGS2, SHH, TBX5, TGFBR2, TGFBR3, FZD7, AKAP6, HDAC4, KLHL41, DKK1, ZFPM2, CDON, SOX6, LMOD3, TBX20, JPH2, SOX17, MYOCD, RBM24
BP	GO:0001704	formation of primary germ layer	28/1554	1.54E-05	BMPR1A, EPHA2, ETS2, EYA1, FGFR1, FOXF1, GATA6, ITGA5, ITGA7, ITGB3, MMP2, SFRP2, SRF, TAL1, TXNRD1, NR4A3, FZD7, ITGA8, CHRD, KLF4, HAND1, DKK1, KDM6B, TBX20, SOX17, WLS, SOX7, ATOH8
BP	GO:0003179	heart valve morphogenesis	17/1554	1.56E-05	BMPR1A, ELN, CCN1, MEF2C, NFATC1, ROCK1, SLIT3, TBX5, TGFBR2, DCHS1, SLIT2, ROCK2, OLFM1, EMILIN1, ADAMTS9, TBX20, GATA5
BP	GO:0061437	renal system vasculature development	12/1554	1.64E-05	ACTA2, ANGPT1, CD34, EGR1, IL6R, PDGFRA, PECAM1, PKD2, TCF21, TEK, PDGFD, OSR1
BP	GO:0061440	kidney vasculature development	12/1554	1.64E-05	ACTA2, ANGPT1, CD34, EGR1, IL6R, PDGFRA, PECAM1, PKD2, TCF21, TEK, PDGFD, OSR1
BP	GO:0019933	cAMP-mediated signaling	37/1554	1.70E-05	ADCY2, ADCY5, ADCY9, ADCYAP1, ADCYAP1R1, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP2B4, ADGRB3, CALCA, LPAR1, EPHA5, GNAL, GNAQ, GPR3, GPR26, GPER1, LHCGR, PDE2A,

					PDE3A, PDE3B, PDE4D, PRKCA, PTGER3, PTGER4, PTGFR, RGS2, VIP, AKAP6, AKAP13, RASD2, PDE11A, ADGRL4
BP	GO:0086012	membrane depolarization during cardiac muscle cell action potential	11/1554	1.93E-05	ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, SCN1B, SCN2B, SCN4B, SLC8A1, SLMAP, SCN3B
BP	GO:1901889	negative regulation of cell junction assembly	11/1554	1.93E-05	ACVRL1, APOD, ARHGAP6, LRP1, ROCK1, THBS1, ROCK2, DLC1, FAM107A, CORO1C, PHLDB2
BP	GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	23/1554	1.93E-05	ADCY2, ADCY5, ADCY9, ADRA2A, CHRM2, CHRM3, S1PR1, LPAR1, S1PR3, EDNRA, FLNA, GNAL, GNAZ, GRIK3, GRM7, NPR3, P2RY1, PALM, PDE2A, RGS1, RGS2, AKAP12, P2RY12
BP	GO:0086010	membrane depolarization during action potential	14/1554	2.00E-05	ANK2, ATP1A2, CACNA1C, CACNA2D1, CACNB2, KCNH2, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A1, SLMAP, CACNA1H, SCN3B
BP	GO:0045766	positive regulation of angiogenesis	39/1554	2.09E-05	ABL1, ACVRL1, ANXA1, AQP1, RHOB, C3, C6, CD34, CHRNA7, CX3CR1, CYP1B1, F3, FGF2, GATA6, GDF2, HGF, HYAL1, CXCR2, ITGA5, PRKCA, PRKCB, PRKD1, PTGIS, PTGS2, RRAS, CX3CL1, SFRP2, TEK, TGFBR2, THBS1, TNFSF12, KLF4, AKT3, SIRT1, PPP1R16B, RHOJ, JCAD, HSPB6, BMPER
BP	GO:0002062	chondrocyte differentiation	28/1554	2.09E-05	ACVRL1, ANXA6, BMPR1A, COL6A2, COL6A3, CCN2, EFEMP1, FGF9, FGFR1, GLI2, MATN2, MEF2C, MEF2D, NFIB, SFRP2, SOX5, TGFBR2, TRPS1, WNT2B, WNT9A, ZBTB16, SCARA3, SOX6, COL21A1, PKDCC, OSR1, RFLNB, MUSTN1
BP	GO:0048545	response to steroid hormone	61/1554	2.11E-05	ADCYAP1, ANXA1, AQP1, AR, ATP1A2, BCHE, BCL2, ZFP36L1, KLF9, CAV1, CDKN1A, CDO1, CNGA3, CPN1, CRY2, CCN2, DUSP1, ESR1, FOS, FOSB, GPER1, NR4A1, IGFBP2, IL1RN, NR3C2, NTRK3, NR4A2, PAM, PER1, PGR, PTGS2, RORA, RORB, SFRP1, SLIT3, STC1, TCF21, NR2F1, TGFB1I1, TGFB3, TGFBR2, THBS1, THRA, TRH, ZFP36, NR4A3, FOSL1, SLIT2, ADIPOQ, TXNIP, PPARGC1A, FAM107A, AKAP13, SIRT1, KANK2, ERRFI1, CALCOCO1, TRIM63, FBXO32, PPARGC1B, CREBRF
BP	GO:0042659	regulation of cell fate specification	8/1554	2.30E-05	AR, BMPR1A, FGF2, FGFR1, SFRP2, FZD7, DKK1, SOX17
BP	GO:0006836	neurotransmitter transport	47/1554	2.43E-05	ADCYAP1, ADRA1A, AQP1, ATP1A2, CACNB2, CAMK2A, CHRM2, STX2, GABRA2, GDNF, GPM6B, GPER1, HBB, ITGB3, MEF2C, P2RX1, P2RY1, PRKN, PRKCB, PTPRN2, RAP1A, RGS2, SLC18A2, SLC22A3, SNCA, STXBP1, VAMP2, SYT4, TACR2, TRH, TRPC4, PPFIA2, SLC25A12, STX11, PER2, NRXN1, NRXN2, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, SLC17A7, SLC5A7, PRRT2, LRRK2
BP	GO:0110053	regulation of actin filament organization	46/1554	2.45E-05	ABL1, ACTN2, BIN1, ARHGAP6, CFL2, CSF3, CCN2, CTNNA2, S1PR1, LPAR1, ELN, FER, FLNA, GSN, NCKAP1L, PRKN, PIK3R1, PTGER4, ROCK1, CX3CL1, CXCL12, SFRP1, TAC1, TGFB3, TMOD1, TPM1, SLIT2, ROCK2, ARHGEF10, DLC1, CDC42EP2, CDC42EP3, DSTN, SYNPO, ARHGEF15, TMEFF2, LMOD1, SNX9, LMOD3, SPTBN4, ARHGAP28, PHLDB2, MYADM, PLEKHH2, JMY, SYNPO2
BP	GO:0016049	cell growth	72/1554	2.52E-05	ABL1, ACVRL1, ADRA1A, APBB1, BCL2, BDNF, CDH4, CDKN1A, DPYSL2, HBEGF, EPHA7, FHL1, GDF2, HYAL1, IGF1, IGFBP5, IL2, ILK, LRP1, MAP1B, MAPT, MSX1, NDN, NGF, NPR1, NTRK3, PRKN, ENPP1, PPP3CB, RGS2, CXCL12, SFRP1, SFRP2, SGK1, SLIT3, SRF, SYT4, TGFBR2, VCL, LTBP4, SORBS2, NRP2, SOCS2, DCLK1, LGI1, SLIT2, CPNE6, NTN1, AKAP6, ZEB2, SEMA3A, OLFM1, FBLN5, PDLIM5, FAM107A, AKAP13, RIMS1, SPART, SIRT1, NLGN3, SEMA3G, PRDM11, TSPYL2, SOX17, TMEM108, JADE1, RERG, PLXNA4, MYOCD, DCUN1D3, DACT3, OSTN
BP	GO:0032231	regulation of actin filament bundle assembly	24/1554	2.52E-05	ABL1, ARHGAP6, CCN2, S1PR1, LPAR1, FLNA, PRKN, PIK3R1, PTGER4, ROCK1, CX3CL1, SFRP1, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, DLC1, SYNPO, ARHGEF15, TMEFF2, ARHGAP28, PHLDB2, SYNPO2
BP	GO:0021953	central nervous system neuron differentiation	36/1554	2.61E-05	ADARB1, CBLN1, EPHB1, GLI2, GRID2, ID4, MAPT, NFIB, NR4A2, PROX1, PTCH1, RORA, SALL1, SCN1B, SFRP1, SFRP2, SHH, TAL1, CNTN2, BTG2, NRP2, HERC1, DCLK1, SLIT2, ZEB2, SEMA3A, DKK1, FAIM2, CHD5, SALL3, CEND1, TBX20, ZSWIM6, SPTBN4, PLXNA4, DCLK2
BP	GO:0051588	regulation of neurotransmitter transport	30/1554	2.75E-05	ADRA1A, ATP1A2, CACNB2, CAMK2A, CHRM2, GDNF, GPM6B, GPER1, ITGB3, MEF2C, P2RX1, P2RY1, PRKN, PRKCB, RAP1A, RGS2, SNCA, STXBP1, SYT4, TACR2, TRH, PPFIA2, PER2, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, LRRK2
BP	GO:0051899	membrane depolarization	23/1554	2.75E-05	ABL1, ANK2, ATP1A2, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAV1, DCN, FHL1, JUN, KCNH2, SMAD7, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A1, SLMAP, CACNA1H, SCN3B, LRRK2
BP	GO:0051893	regulation of focal adhesion assembly	18/1554	2.75E-05	ABL1, ACVRL1, APOD, ARHGAP6, DUSP3, EPHA3, GPM6B, LRP1, ROCK1, SFRP1, TEK, THBS1, ROCK2, DLC1, FAM107A, CORO1C, PEAK1, PHLDB2
BP	GO:0090109	regulation of cell-substrate junction assembly	18/1554	2.75E-05	ABL1, ACVRL1, APOD, ARHGAP6, DUSP3, EPHA3, GPM6B, LRP1, ROCK1, SFRP1, TEK, THBS1, ROCK2, DLC1, FAM107A, CORO1C, PEAK1, PHLDB2

BP	GO:0060193	positive regulation of lipase activity	20/1554	2.75E-05	ADCYAP1R1, ADRA1A, ARHGAP6, BDNF, LPAR1, EDNRA, ESR1, FGF2, FGFR1, GNAQ, CCN1, ITK, KIT, NTRK3, PDGFRA, PLA2G5, GPR55, NMUR1, P2RY12, RASGRP4
BP	GO:0055007	cardiac muscle cell differentiation	29/1554	2.75E-05	ACTC1, ACTN2, ADRA1A, GATA6, IGF1, MEF2A, MEF2C, MYH11, PDGFRA, PROX1, RGS2, SGCB, SGCD, SLC8A1, SRF, TBX5, FZD7, SORBS2, MYOM2, AKAP6, PDLIM5, BVES, AKAP13, DKK1, KDM6B, SOX6, ALPK3, MYOCD, SIK1
BP	GO:0048639	positive regulation of developmental growth	36/1554	2.89E-05	ACACB, ACTN3, BCL2, BDNF, BMPR1A, CDH4, DIO3, FGF2, FGF9, FGFR1, GATA6, GHR, IGF1, ILK, LRP1, MAP1B, MAPT, MEF2C, NGF, NTRK3, PRKN, PIM1, PROX1, CXCL12, SRF, SYT4, TBX5, TGFBR2, TGFBR3, CPNE6, NTN1, AKAP6, RIMS1, ZFPM2, TBX20, SPTBN4
BP	GO:0072163	mesonephric epithelium development	24/1554	2.93E-05	ARG2, BCL2, EYA1, FGF2, FGFR1, GDNF, ILK, SMAD7, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SFRP1, SHH, TCF21, WNT2B, DCHS1, SLIT2, SPRY1, FAT4, OSR1, BMPER
BP	GO:0072164	mesonephric tubule development	24/1554	2.93E-05	ARG2, BCL2, EYA1, FGF2, FGFR1, GDNF, ILK, SMAD7, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SFRP1, SHH, TCF21, WNT2B, DCHS1, SLIT2, SPRY1, FAT4, OSR1, BMPER
BP	GO:0097553	calcium ion transmembrane import into cytosol	30/1554	3.09E-05	ABL1, ANK2, ATP1A2, ATP2B4, CACNA1C, CACNA2D1, CASQ2, CLIC2, DMD, FGF2, FYN, GPER1, GRIN2A, HRC, ITPR1, PDE4D, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SLC8A3, SNCA, TRPC1, TRPA1, AKAP6, RASA3, JPH2, JPH4, FAM155A
BP	GO:0050673	epithelial cell proliferation	66/1554	3.09E-05	ACVRL1, AR, BCL2L2, BMP5, BMPR1A, ZFP36L1, KLF9, CAV1, CD34, COL8A2, EDNRB, EGR3, EPHA2, ESR1, EYA1, F3, FGF2, FGF7, FGF9, FGF10, FGFR1, GDF2, HGF, NR4A1, HYAL1, ID2, IGF1, IGFBP5, ITGB3, JUN, KIT, LAMC1, MEF2C, MYC, NFIB, NGFR, PGR, PRKCA, PRKD1, PROX1, PTCH1, CXCL12, SFRP1, SFRP2, SHH, TEK, TGFBR3, THBS1, TNFAIP3, VIP, ZFP36, NR4A3, DYSF, FZD7, TNFSF12, NRP2, RGN, AKT3, SIRT1, PPP1R16B, ERRFI1, JCAD, ATOH8, FOXP2, OSR1, BMPER
BP	GO:0098693	regulation of synaptic vesicle cycle	26/1554	3.17E-05	ADRA1A, CACNB2, CAMK2A, CHRM2, P2RX1, P2RY1, PPP3CB, PRKCB, RAP1A, ROCK1, SLC2A4, SNCA, STXBP1, SYT4, PPFIA2, NRXN1, STXBP5L, RIMS3, MAGI2, NLGN1, RIMS1, SYT11, NCS1, NLGN3, SLC17A7, LRRK2
BP	GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	28/1554	3.19E-05	ABL1, LDLRAD4, CAV1, CIDEA, FBN1, SMAD7, SFRP1, SFRP2, TGFB1I1, TGFB3, TGFBR2, TGFBR3, CILP, CHRD, MAGI2, EMILIN1, DKK1, SPART, SIRT1, SOSTDC1, TBX20, PRDM16, GREM2, CHRDL1, VASN, WFIKKN2, BMPER, RBPMS2
BP	GO:0010976	positive regulation of neuron projection development	48/1554	3.35E-05	ADCYAP1, APBB1, BDNF, BMP5, CDH4, CNTN1, DPYSL3, LPAR1, EPHA3, FGFR1, FYN, HGF, IL2, ILK, LRP1, MAP1B, MAP6, MAPT, NGF, NGFR, NTRK3, PRKN, PRKD1, RELN, PTPRD, RAP1A, RGS2, SCN1B, CX3CL1, CXCL12, SRF, SYT4, VLDLR, NEURL1, SLIT2, CPNE6, NTN1, ZEB2, MAGI2, IL1RAPL1, CPEB3, NLGN1, RIMS1, NDNF, FBXO31, PLXNA4, NEGR1, ALKAL2
BP	GO:0035107	appendage morphogenesis	31/1554	3.37E-05	BMPR1A, CACNA1C, FGF9, FGF10, FGFR1, GLI2, AFF3, MBNL1, MSX1, MYH3, ROR2, PBX1, PCSK5, PITX1, PTCH1, SALL1, SFRP2, SHH, TBX5, WNT9A, ZBTB16, RECK, HAND2, TBX4, DKK1, SALL3, MAP3K20, PKDCC, OSR1, RSPO2, EVX2
BP	GO:0035108	limb morphogenesis	31/1554	3.37E-05	BMPR1A, CACNA1C, FGF9, FGF10, FGFR1, GLI2, AFF3, MBNL1, MSX1, MYH3, ROR2, PBX1, PCSK5, PITX1, PTCH1, SALL1, SFRP2, SHH, TBX5, WNT9A, ZBTB16, RECK, HAND2, TBX4, DKK1, SALL3, MAP3K20, PKDCC, OSR1, RSPO2, EVX2
BP	GO:0031346	positive regulation of cell projection organization	60/1554	3.40E-05	ADCYAP1, APBB1, BDNF, BMP5, CDH4, CNTN1, DPYSL3, LPAR1, EPHA3, FGFR1, FYN, GPM6A, HGF, IL2, ILK, KIT, LRP1, MAP1B, MAP6, MAPT, NGF, NGFR, NTRK3, PALM, PRKN, PRKD1, RELN, PTPRD, RAP1A, RGS2, SCN1B, CX3CL1, CXCL12, SRF, SYT4, TGFB3, VLDLR, NEURL1, SLIT2, CPNE6, NTN1, HDAC4, ZEB2, MAGI2, CDC42EP2, CDC42EP3, IL1RAPL1, CPEB3, NLGN1, DZIP1, RIMS1, CORO1C, P2RY12, NDNF, FBXO31, NAV3, PLXNA4, DOCK11, NEGR1, ALKAL2
BP	GO:0045765	regulation of angiogenesis	60/1554	3.40E-05	ABL1, ACVRL1, ANXA1, AQP1, RHOB, ADGRB3, C3, C6, CD34, CHRNA7, COL4A3, CX3CR1, CYP1B1, DCN, EPHA2, F3, FGF2, GATA6, GDF2, HGF, HSPG2, HYAL1, CXCR2, ITGA5, NGFR, NPR1, PDE3B, PRKCA, PRKCB, PRKD1, PTGIS, PTGS2, ROCK1, RRAS, CX3CL1, SFRP1, SFRP2, TEK, TGFBR2, THBS1, TNFAIP3, RECK, TNFSF12, KLF4, ROCK2, AKT3, SPRY2, KLF2, CXCL13, EMILIN1, SIRT1, ADGRA2, PPP1R16B, ADAMTS9, RHOJ, JCAD, PROK1, STARD13, HSPB6, BMPER
BP	GO:1903391	regulation of adherens junction organization	19/1554	3.40E-05	ABL1, ACVRL1, APOD, ARHGAP6, DUSP3, EPHA3, GPM6B, LRP1, ROCK1, SFRP1, TEK, THBS1, ROCK2, DLC1, MAPRE2, FAM107A, CORO1C, PEAK1, PHLDB2
BP	GO:0010171	body morphogenesis	16/1554	3.88E-05	MMP2, MSX1, MYH3, PDGFRA, RRAS, TGFB3, CLDN5, MAB21L2, DKK1, TIPARP, CDON, GREM2, CSRNP1, CRISPLD2, ARID5B, PHLDB2
BP	GO:0060425	lung morphogenesis	16/1554	3.88E-05	FGF7, FGF10, FOXF1, LIF, NFIB, SHH, SRF, TCF21, TGFBR2, WNT2B, SPRY1, SPRY2, HHIP, STK40, FOXP2, RSPO2
BP	GO:0086009	membrane repolarization	16/1554	3.88E-05	ANK2, ATP1A2, ATP1B2, CACNA2D1, CASQ2, CAV1, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, SCN1B, SCN4B, SNTA1, AKAP6, KCNE4

BP	GO:0048588	developmental cell growth	42/1554	3.93E-05	ABL1, ADRA1A, BDNF, CDH4, DPYSL2, EPHA7, IGF1, ILK, LRP1, MAP1B, MAPT, NDN, NGF, NTRK3, PRKN, PPP3CB, RGS2, CXCL12, SLIT3, SRF, SYT4, TGFBR2, VCL, SORBS2, NRP2, DCLK1, SLIT2, CPNE6, NTN1, AKAP6, ZEB2, SEMA3A, OLFM1, PDLIM5, AKAP13, RIMS1, SPART, NLGN3, SEMA3G, TMEM108, PLXNA4, OSTN
BP	GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	24/1554	4.05E-05	ACTN2, ADRA1A, ADRA2A, CALCA, CHRM2, CX3CR1, S1PR1, LPAR1, EDNRB, ESR1, GPR17, CXCR2, LHCGR, NPR3, P2RY1, PTGER3, TACR1, VIP, GPR55, GNA14, NMUR1, P2RY10, P2RY12, P2RY8
BP	GO:0051145	smooth muscle cell differentiation	20/1554	4.05E-05	EDNRB, FGF9, FGF10, FOXF1, GATA6, GPER1, KIT, MEF2C, NFATC1, NFATC2, NFATC4, SGCB, SHH, SRF, ZEB1, ITGA8, SIRT1, PRDM6, MYOCD, RBPMS2
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	50/1554	4.06E-05	ABL1, ADCYAP1, ADRA1A, ANGPT1, ATF3, CHRNA7, CCN2, DUSP1, DUSP3, DUSP4, GPR183, EPHA2, EPHA7, EPHB1, FGF2, FGF10, GPER1, CCN1, JUN, KIT, LIF, LRP1, P2RY1, PDGFRA, PLA2G5, PRKCA, RAP1A, RRAS, CX3CL1, SLAMF1, TEK, FGF23, GPR55, KLF4, ADIPOQ, HAND2, AKAP12, SPRY1, SPRY2, EMILIN1, DNAJC27, ERRFI1, DUSP26, PDGFD, GLIPR2, CNKSR3, BMPER, NLRP6, ALKAL2, TNFAIP8L3
BP	GO:0010631	epithelial cell migration	56/1554	4.09E-05	ABL1, ACVRL1, ANGPT1, ANXA1, RHOB, CCR6, CYP1B1, DCN, HBEGF, EGR3, EPHA2, FGF2, FGF7, FGF10, FGFR1, GDF2, NR4A1, HYAL1, ITGB3, JUN, KIT, MEF2C, PECAM1, PRKCA, PRKD1, PROX1, PTGS2, SRF, STC1, TAC1, TEK, TGFBR2, THBS1, TNFSF12, NRP2, KLF4, SLIT2, ROCK2, ZEB2, AKT3, SEMA3A, CXCL13, MAPRE2, SIRT1, CORO1C, KANK2, ADGRA2, ADAMTS9, RHOJ, JCAD, ATOH8, STARD13, GLIPR2, AMOTL1, CLEC14A, BMPER
BP	GO:0021537	telencephalon development	44/1554	4.24E-05	ALDH1A3, AQP1, ATP2B4, LPAR1, EPHA5, FLNA, ID2, ID4, KCNA1, LRP1, NFIB, PROX1, RELN, SALL1, CXCL12, SHH, SLC8A1, SLC8A3, SRF, TACC1, CNTN2, BTG2, NR4A3, NRP2, SLIT2, ZEB2, SEMA3A, TACC2, KDM6B, SALL3, CDON, CRTAC1, GNG12, ZSWIM6, P2RY12, TMEM108, FAT4, DIXDC1, BMERB1, PLXNA4, FOXP2, LRRK2, DCLK2, PHACTR1
BP	GO:0035296	regulation of tube diameter	30/1554	4.47E-05	ACTA2, ADCYAP1, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP1A2, BDKRB2, CAV1, CHRM3, EDNRA, EDNRB, EPHX2, GPER1, HBB, ITGA1, KCNMA1, KCNMB1, NPR1, P2RX1, P2RY1, PTGS2, RGS2, ROCK1, SLC8A1, VIP, PER2, ROCK2, UTS2B
BP	GO:0050880	regulation of blood vessel size	30/1554	4.47E-05	ACTA2, ADCYAP1, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP1A2, BDKRB2, CAV1, CHRM3, EDNRA, EDNRB, EPHX2, GPER1, HBB, ITGA1, KCNMA1, KCNMB1, NPR1, P2RX1, P2RY1, PTGS2, RGS2, ROCK1, SLC8A1, VIP, PER2, ROCK2, UTS2B
BP	GO:0097746	regulation of blood vessel diameter	30/1554	4.47E-05	ACTA2, ADCYAP1, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP1A2, BDKRB2, CAV1, CHRM3, EDNRA, EDNRB, EPHX2, GPER1, HBB, ITGA1, KCNMA1, KCNMB1, NPR1, P2RX1, P2RY1, PTGS2, RGS2, ROCK1, SLC8A1, VIP, PER2, ROCK2, UTS2B
BP	GO:0021952	central nervous system projection neuron axonogenesis	11/1554	4.47E-05	ADARB1, EPHB1, GLI2, NFIB, NR4A2, SCN1B, DCLK1, SLIT2, ZEB2, SPTBN4, PLXNA4
BP	GO:0072012	glomerulus vasculature development	11/1554	4.47E-05	ACTA2, ANGPT1, CD34, EGR1, IL6R, PDGFRA, PECAM1, TCF21, TEK, PDGFD, OSR1
BP	GO:0034764	positive regulation of transmembrane transport	38/1554	4.61E-05	ABL1, ACTN2, ADRB2, ANK2, ATP1B2, C3, CACNA2D1, CACNB2, DMD, FLNA, GPER1, HSPA2, IGF1, KCNA1, KCNH2, KCNMB1, MEF2A, ABCB1, PIK3R1, PKD2, RELN, RAP1A, RYR2, CX3CL1, SNCA, STAC, TRPC1, NR4A3, RGN, ADIPOQ, AKAP6, SORBS1, CLIP3, KLF15, NLGN3, JPH2, CNKSR3, LRRC52
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	24/1554	4.68E-05	BMPR1A, HBEGF, S1PR1, FGF2, FGF9, ID2, IGF1, IGFBP5, IL6R, JUN, MEF2D, MMP2, PTGS2, CX3CL1, TGFBR2, THBS1, NR4A3, ADAMTS1, HDAC4, NAMPT, ABCC4, PPARGC1A, PDGFD, RBPMS2
BP	GO:0051147	regulation of muscle cell differentiation	35/1554	4.74E-05	ABL1, BCL2, BDNF, CTNNA2, DMPK, FGF9, GPER1, IGF1, KIT, MEF2A, MEF2C, MSX1, NFATC1, NFATC2, PROX1, RGS2, SHH, SRF, ZEB1, FZD7, AKAP6, HDAC4, AKAP13, DKK1, SIRT1, EHD2, CDON, SOX6, LMOD3, PRDM6, MYOCD, SIK1, RBM24, TMEM119, RBPMS2
BP	GO:0001707	mesoderm formation	20/1554	4.84E-05	BMPR1A, EPHA2, EYA1, FGFR1, FOXF1, ITGB3, SFRP2, SRF, TAL1, TXNRD1, NR4A3, ITGA8, CHRD, KLF4, HAND1, DKK1, KDM6B, TBX20, SOX17, WLS
BP	GO:1901863	positive regulation of muscle tissue development	22/1554	4.93E-05	ACTN3, BCL2, BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, MEF2C, PIM1, SHH, TBX5, TGFBR3, AKAP6, PPARGC1A, ZFPM2, CDON, LMOD3, TBX20, SOX17, MYOCD, RBM24
BP	GO:1901888	regulation of cell junction assembly	22/1554	4.93E-05	ABL1, ACVRL1, APOD, ARHGAP6, CAV1, DUSP3, EPHA2, EPHA3, GPM6B, LRP1, RAP1A, ROCK1, SFRP1, TEK, THBS1, CLDN5, ROCK2, DLC1, FAM107A, CORO1C, PEAK1, PHLDB2
BP	GO:2000027	regulation of animal organ morphogenesis	44/1554	5.02E-05	ABL1, AR, BCL2, BMPR1A, CD34, DIO3, ESR1, EYA1, FGF7, FGF10, FGFR1, GDNF, HGF, LIF, MSX1, MYC, NFIB, ROR1, ROR2, PIM1, SFRP1, SFRP2, SHH, TBX5, TGFBR2, TNFAIP3, WNT2B, FZD7, HAND2, MAGI2, GPC6, ENAM, SPRY1, DKK1, DACT1, AJAP1, SOX17, RSPO3, NKD1, FOXP2, GATA5, PRICKLE1, PRICKLE2, RSPO2

BP	GO:0035150	regulation of tube size	30/1554	5.02E-05	ACTA2, ADCYAP1, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP1A2, BDKRB2, CAV1, CHRM3, EDNRA, EDNRB, EPHX2, GPER1, HBB, ITGA1, KCNMA1, KCNMB1, NPR1, P2RX1, P2RY1, PTGS2, RGS2, ROCK1, SLC8A1, VIP, PER2, ROCK2, UTS2B
BP	GO:0090132	epithelium migration	56/1554	5.04E-05	ABL1, ACVRL1, ANGPT1, ANXA1, RHOB, CCR6, CYP1B1, DCN, HBEGF, EGR3, EPHA2, FGF2, FGF7, FGF10, FGFR1, GDF2, NR4A1, HYAL1, ITGB3, JUN, KIT, MEF2C, PECAM1, PRKCA, PRKD1, PROX1, PTGS2, SRF, STC1, TAC1, TEK, TGFBR2, THBS1, TNFSF12, NRP2, KLF4, SLIT2, ROCK2, ZEB2, AKT3, SEMA3A, CXCL13, MAPRE2, SIRT1, CORO1C, KANK2, ADGRA2, ADAMTS9, RHOJ, JCAD, ATOH8, STARD13, GLIPR2, AMOTL1, CLEC14A, BMPER
BP	GO:0043405	regulation of MAP kinase activity	54/1554	5.11E-05	ADRA2A, ADRA2B, CAV1, CD40LG, CHRNA7, MAP3K8, CSPG4, GADD45A, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, LPAR1, FGF2, FGF10, FGFR1, GHR, HGF, IGF1, ILK, ITGA1, KIT, KITLG, GADD45B, NGF, NTRK3, ROR2, RGS2, SFRP1, SFRP2, TGFB3, THBS1, TPD52L1, PDE5A, ADIPOQ, ZEB2, HIPK3, TRIB1, SPRY1, SPRY2, FZD10, IRAK3, AKAP13, DKK1, TNIK, MAP3K20, AVPI1, PDGFD, PROK1, LRRK2, DUSP19, SAMD5
BP	GO:0048511	rhythmic process	49/1554	5.27E-05	AXL, KLF9, CREM, CRY2, EGR1, EGR2, EGR3, ESR1, GNAQ, HAS1, HLF, ID2, ID4, JUN, JUND, KCNA2, LHCGR, NFIL3, NGFR, NTRK3, PAM, PDGFRA, PER1, PGR, PPP1CB, PRKAA2, PROX1, PTX3, RORA, RORB, SLIT3, TEF, TGFB3, KLF10, PER3, PER2, USP2, SLIT2, ADIPOQ, ROCK2, ADAMTS1, NAMPT, PPARGC1A, NLGN1, SIRT1, PROK1, CIPC, OPN4, SIK1
BP	GO:0071248	cellular response to metal ion	36/1554	5.40E-05	AQP1, AQP2, CRHBP, DLG2, FOS, FOSB, GSN, ID2, ITPKB, JUN, JUNB, JUND, KCNA1, KCNK3, MEF2A, MEF2C, MT1A, NFATC4, PRKN, PKD2, PRKAA2, PTGS2, RYR3, SHH, SNCA, SYT4, CACNA1H, CPNE6, RASA4, PPARGC1A, NLGN1, SYT11, CLIC4, SLC25A23, SYT15, LRRK2
BP	GO:0010522	regulation of calcium ion transport into cytosol	24/1554	5.40E-05	ABL1, ADCYAP1R1, ANK2, ATP1A2, BCL2, CACNA1C, CASQ2, CAV1, CLIC2, DMD, FYN, GPER1, HRC, PDE4D, PKD2, RYR2, CX3CL1, SLC8A1, SNCA, TRPC1, TRPC3, AKAP6, JPH2, JPH4
BP	GO:0072009	nephron epithelium development	25/1554	5.50E-05	BCL2, CD34, EYA1, FGF2, GDNF, ILK, LIF, MEF2C, MYC, PBX1, PECAM1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, ADIPOQ, MAGI2, WWTR1, KLF15, FAT4, OSR1
BP	GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	33/1554	6.12E-05	CDH4, CDH17, PCDHGC3, PCDH7, PCDH9, PECAM1, PKD1, CNTN2, DCHS1, IGSF9B, PALLD, PCDHGA12, PCDH11X, CDH19, PCDH18, DCHS2, PCDHGB7, PCDHGB3, PCDHGA9, PCDHGA5, PCDHGA3, PCDHGA2, PCDHB15, PCDHA3, DSCAML1, PCDH10, CADM3, CLSTN2, PCDH20, FAT4, PCDH11Y, FAT3, CNTN4
BP	GO:0030168	platelet activation	31/1554	6.16E-05	ADRA2A, ADRA2B, AXL, CD40LG, DGKB, DGKG, F8, FLNA, FYN, GNAQ, HBB, ILK, ITGB3, ITPR1, MPL, P2RX1, P2RY1, PDGFRA, PIK3R1, PRKCA, PRKCB, SELP, SRF, STXBP1, TLN1, TRPC3, VCL, VWF, GNA14, MYL9, P2RY12
BP	GO:0010810	regulation of cell-substrate adhesion	39/1554	6.28E-05	ABL1, ACVRL1, APOD, ARHGAP6, BCL2, DUSP3, EPHA3, FOXF1, FLNA, GPM6B, CCN1, ILK, ITGA5, LRP1, NID1, DDR2, PIK3R1, ROCK1, CX3CL1, SFRP1, TEK, THBS1, UTRN, FZD7, ROCK2, DLC1, EMILIN1, FAM107A, MMRN1, CORO1C, ABI3BP, AJAP1, NDNF, PEAK1, PHLDB2, EMILIN3, MYADM, CCDC80, NEXMIF
BP	GO:0000302	response to reactive oxygen species	41/1554	6.97E-05	ABL1, ANXA1, APOD, AQP1, RHOB, AXL, BCL2, PLK3, CYP1B1, DUSP1, FER, FOS, FYN, GNAO1, HBB, HGF, HYAL1, JUN, MAPT, MMP2, PDGFRA, PKD2, SLC8A1, SOD3, TNFAIP3, TPM1, RNF112, NR4A3, FOSL1, TRPA1, RGN, KLF4, KLF2, FBLN5, TXNIP, PPARGC1A, KDM6B, SIRT1, PDGFD, LRRK2, PPARGC1B
BP	GO:0048332	mesoderm morphogenesis	20/1554	7.12E-05	BMPR1A, EPHA2, EYA1, FGFR1, FOXF1, ITGB3, SFRP2, SRF, TAL1, TXNRD1, NR4A3, ITGA8, CHRD, KLF4, HAND1, DKK1, KDM6B, TBX20, SOX17, WLS
BP	GO:0007202	activation of phospholipase C activity	12/1554	7.20E-05	ADCYAP1R1, ADRA1A, ARHGAP6, BDNF, LPAR1, EDNRA, GNAQ, ITK, GPR55, NMUR1, P2RY12, RASGRP4
BP	GO:0097106	postsynaptic density organization	12/1554	7.20E-05	CBLN1, DLG2, GRID2, NTRK3, RELN, PTPRD, NRXN1, NRXN2, NLGN1, LRRC4, TMEM108, LRRTM1
BP	GO:0033673	negative regulation of kinase activity	44/1554	7.25E-05	ABL1, ADARB1, RHOH, CAV1, CDKN1A, GADD45A, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, GNAQ, ILK, MAPT, GADD45B, PRKN, PRKAR2B, RGS2, SFRP1, SFRP2, TNFAIP3, SOCS3, GPRC5A, RGN, ADIPOQ, HIPK3, TRIB1, SPRY1, SPRY2, IRAK3, SIRT1, CORO1C, WWTR1, LATS2, PRKAG2, ERRFI1, DBNDD2, INKA2, DUSP26, ITPRIP, MIDN, MYOCD, DUSP19
BP	GO:0001657	ureteric bud development	23/1554	7.27E-05	ARG2, BCL2, EYA1, FGF2, FGFR1, GDNF, ILK, SMAD7, MYC, PBX1, PKD2, PTCH1, SALL1, SFRP1, SHH, TCF21, WNT2B, DCHS1, SLIT2, SPRY1, FAT4, OSR1, BMPER
BP	GO:0007369	gastrulation	35/1554	7.33E-05	BMPR1A, EPHA2, ETS2, EYA1, FGFR1, FOXF1, GATA6, IL1RN, ITGA5, ITGA7, ITGB3, MMP2, SFRP1, SFRP2, SRF, TAL1, TGFBR2, TXNRD1, NR4A3, FZD7, ITGA8, CHRD, KLF4, ADIPOQ, HAND1, DKK1, KDM6B, TBX20, SOX17, WLS, SOX7, ATOH8, PHLDB2, MYADM, OSR1
BP	GO:0014812	muscle cell migration	24/1554	7.43E-05	ANXA1, BCL2, BMPR1A, LPAR1, FGF9, IGF1, IGFBP5, ILK, ITGB3, LRP1, MEF2C, ROCK1, TPM1, NR4A3, SLIT2, ADIPOQ, ADAMTS1, HDAC4, TRIB1, PPARGC1A, PLEKHO1, PARVA, PDGFD, MYOCD

BP	GO:0045785	positive regulation of cell adhesion	61/1554	7.44E-05	ABL1, ANGPT1, ANXA1, CAV1, CD5, CD28, CD40LG, MAP3K8, CD55, EGR3, FOXF1, FLNA, FYN, GLI2, NCKAP1L, HYAL1, IGF1, IGFBP2, CCN1, IL2, IL6R, IL6ST, ILK, ITGA5, ITPKB, SMAD7, NID1, PIK3R1, PRKCA, ROCK1, CX3CL1, CXCL12, SFRP1, SFRP2, SHH, TEK, TGFBR2, TPM1, UTRN, ZBTB16, NR4A3, DYSF, PLPP3, CHRD, BCL10, GRAP2, TESPA1, CXCL13, EMILIN1, MMRN1, ABI3BP, VSIR, NFKBIZ, P2RY12, DUSP26, NDNF, EMILIN3, MYADM, TNFRSF13C, CCDC80, BTLA
BP	GO:0010001	glial cell differentiation	39/1554	8.50E-05	ABL1, BIN1, ASPA, CLU, LPAR1, EGR2, FGF10, GPR17, GSN, ID2, ID4, IL6ST, ILK, LDLR, LIF, LRP1, MAPT, NFIB, NTRK3, ROR1, ROR2, PLP1, RELN, SHH, SLC8A3, TAL1, CNTN2, TRPC4, RNF112, CNTNAP1, ARHGEF10, TSPAN2, LAMC3, WASF3, DAAM2, KLF15, NLGN3, SOX6, FA2H
BP	GO:0014743	regulation of muscle hypertrophy	20/1554	8.50E-05	ADRA1A, ATP2B4, IGF1, IGFBP5, IL6ST, MEF2A, PRKCA, RGS2, ROCK1, TRPC3, NR4A3, PDE5A, HAND2, AKAP6, ROCK2, LMCD1, ERRFI1, TRIM63, MLIP, GATA5
BP	GO:0030038	contractile actin filament bundle assembly	23/1554	8.50E-05	ABL1, ARHGAP6, CCN2, S1PR1, LPAR1, ELN, PIK3R1, PTGER4, ROCK1, SFRP1, SRF, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, DLC1, SORBS1, ARHGEF15, TMEFF2, ARHGAP28, PHLDB2, PHACTR1
BP	GO:0043149	stress fiber assembly	23/1554	8.50E-05	ABL1, ARHGAP6, CCN2, S1PR1, LPAR1, ELN, PIK3R1, PTGER4, ROCK1, SFRP1, SRF, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, DLC1, SORBS1, ARHGEF15, TMEFF2, ARHGAP28, PHLDB2, PHACTR1
BP	GO:0050848	regulation of calcium-mediated signaling	23/1554	8.50E-05	ACTN3, ATP2B4, CASQ2, CD22, CLIC2, DMD, RCAN1, HRC, IGF1, ITPR1, MAPT, PDE4D, PKD2, RGN, AKAP6, RCAN2, LMCD1, MYOZ2, TMEM100, JPH2, JPH4, C10orf71, LRRK2
BP	GO:0001952	regulation of cell-matrix adhesion	26/1554	8.53E-05	ABL1, ACVRL1, APOD, ARHGAP6, BCL2, DUSP3, EPHA3, GPM6B, ILK, LRP1, DDR2, PIK3R1, ROCK1, CX3CL1, SFRP1, TEK, THBS1, UTRN, ROCK2, DLC1, FAM107A, CORO1C, AJAP1, PEAK1, PHLDB2, NEXMIF
BP	GO:0010634	positive regulation of epithelial cell migration	33/1554	8.53E-05	ABL1, ANGPT1, ANXA1, RHOB, CCR6, HBEGF, FGF2, FGF7, FGF10, FGFR1, HYAL1, ITGB3, JUN, PRKCA, PRKD1, PROX1, PTGS2, TAC1, TEK, TGFBR2, THBS1, PLPP3, NRP2, ROCK2, AKT3, MAPRE2, SIRT1, ADGRA2, RHOJ, JCAD, ATOH8, GLIPR2, AMOTL1
BP	GO:0021700	developmental maturation	47/1554	8.53E-05	ACVRL1, AXL, ADGRB3, BCL2, C3, CDKN1A, CCR6, CX3CR1, S1PR1, EDNRB, FGFR1, ID2, IGF1, MAP1B, MMP2, NFIA, NFATC4, NPR2, NR4A2, PALM, PDE3A, PGR, POU2F2, RELN, CX3CL1, STXBP1, SYT4, TAL1, CNTN2, RECK, DCHS1, NEURL1, NRXN1, KLF2, ARHGEF15, NFASC, RND1, VSX1, CEND1, FEV, SYBU, SLC17A7, SPTBN4, FAT4, LRRK2, ZDHHC15, RFLNB
BP	GO:0043266	regulation of potassium ion transport	24/1554	8.53E-05	ACTN2, ADCYAP1, ADRA2A, BIN1, ANK2, ATP1B2, CASQ2, CAV1, DPP6, FHL1, FLNA, KCNA1, KCNH2, KCNMB1, KCNS2, VAMP2, VIP, KCNAB1, AKAP6, KCNE4, KCNIP3, KCNIP1, KCNIP4, LRRC52
BP	GO:0060419	heart growth	25/1554	8.53E-05	ACACB, ADRA1A, BMPR1A, S1PR1, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, PROX1, RBP4, RGS2, TBX5, TGFBR2, TGFBR3, SORBS2, AKAP6, PDLIM5, AKAP13, ZFPM2, TBX20
BP	GO:0030098	lymphocyte differentiation	55/1554	8.90E-05	ABL1, ANXA1, RHOH, AXL, BCL2, PRDM1, ZFP36L1, MS4A1, CD28, TNFSF8, CD40LG, CD79A, CD79B, CDH17, CCR6, KLF6, CR2, GPR183, EGR1, EGR3, GLI2, NCKAP1L, ID2, IL2, IRF4, ITK, ITPKB, KIT, LEPR, LY9, SMAD7, NFATC2, PIK3R1, POU2F2, PPP3CB, PTGER4, RORA, SATB1, SFRP1, SHH, SRF, ZEB1, TGFBR2, ZBTB16, FZD7, ITM2A, HDAC4, TESPA1, FGL2, PLA2G2D, AICDA, VSIR, NFKBIZ, FCRL3, DOCK11
BP	GO:0002028	regulation of sodium ion transport	21/1554	9.05E-05	ADRB2, ATP1A2, ATP1B2, ATP2B4, CNTN1, DMD, STOM, PER1, SCN1B, SCN2B, SCN4B, SLC8A1, SNTA1, UTRN, SLMAP, FXYD6, SCN3B, SPTBN4, OSR1, SIK1, CNKSR3
BP	GO:0051895	negative regulation of focal adhesion assembly	9/1554	9.15E-05	ACVRL1, APOD, ARHGAP6, LRP1, THBS1, DLC1, FAM107A, CORO1C, PHLDB2
BP	GO:1903531	negative regulation of secretion by cell	38/1554	9.15E-05	ADRA2A, ADRA2B, ANGPT1, ANXA1, ARG2, CD22, CD34, CIDEA, CRHBP, FOXF1, LRRC32, GRM7, INHBB, KCNB1, LIF, CD200, P2RY1, PRKN, PTGER4, RAP1A, CX3CL1, SFRP1, SNCA, SYT4, TACR2, TNFAIP3, TRH, FGF23, ADIPOQ, STXBP5L, IL1RAPL1, MAPKBP1, SYT11, STXBP6, P2RY12, MIDN, C1QTNF3, SSC5D
BP	GO:0051348	negative regulation of transferase activity	47/1554	9.15E-05	ABL1, ADARB1, RHOH, CAV1, CDKN1A, GADD45A, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, GNAQ, ILK, SMAD7, MAPT, GADD45B, PRKN, PRKAR2B, RGS2, SFRP1, SFRP2, TNFAIP3, ZFP36, SOCS3, GPRC5A, RGN, ADIPOQ, BAG2, HIPK3, TRIB1, SPRY1, SPRY2, IRAK3, SIRT1, CORO1C, WWTR1, LATS2, PRKAG2, ERRFI1, DBNDD2, INKA2, DUSP26, ITPRIP, MIDN, MYOCD, DUSP19
BP	GO:0048880	sensory system development	57/1554	9.15E-05	ACVRL1, ALDH1A3, ATP2B4, BCL2, PRDM1, C3, CACNA1C, COL8A2, CYP1B1, DCX, DIO3, EPHA2, EPHB1, FBN1, EFEMP1, FGF9, FGF10, GPM6A, JUN, MEIS1, MEIS2, MITF, NTRK3, PDGFRA, PITX2, PROX1, RBP4, RORB, SHH, SRF, ZEB1, TGFBR2, TMOD1, TUB, WNT2B, WNT9A, MYOM2, KLF4, ZEB2, LAMC3, SEMA3A, MAB21L2, NES, ARHGEF15, CRB1, VSX1, CDON, SLC17A7, RHOJ, CC2D2A, P2RY12, NKD1, CHRDL1, FOXP2, SLC25A25, UNC45B, ABCB5
BP	GO:0003156	regulation of animal organ formation	13/1554	9.25E-05	AR, EYA1, FGF10, FGFR1, GDNF, PIM1, SHH, TBX5, WNT2B, HAND2, SPRY1, DKK1, GATA5
BP	GO:0001764	neuron migration	31/1554	9.73E-05	AXL, CAMK2A, CTNNA2, DCX, FGFR1, FLNA, FYN, GFRA3, GPM6A, MAP1B, MATN2, MEF2C, NDN, NTRK3, NR4A2, RELN, CX3CL1, CXCL12, SRF, CNTN2, NRP2, DCLK1, NTN1, SEMA3A, FLRT2, TBX20, NDNF, FBXO31, PHACTR1, IGSF10, NEXMIF

BP	GO:0060325	face morphogenesis	12/1554	9.73E-05	MMP2, MSX1, MYH3, PDGFRA, RRAS, TGFB3, CLDN5, DKK1, TIPARP, CSRNP1, CRISPLD2, ARID5B
BP	GO:0086019	cell-cell signaling involved in cardiac conduction	12/1554	9.73E-05	ANK2, CACNA1C, CACNA2D1, CACNB2, CASQ2, FLNA, KCNJ3, RYR2, SCN1B, SCN4B, GJC1, SCN3B
BP	GO:0001570	vasculogenesis	20/1554	9.85E-05	ZFP36L1, CAV1, CD34, EPHA2, FOXF1, GDF2, JUNB, RAP1A, SHH, TBX5, TGFBR2, TGFBR3, GJC1, ZFPM2, TIPARP, ASB4, TMEM100, TBX20, SOX17, MYOCD
BP	GO:0001776	leukocyte homeostasis	21/1554	1.07E-04	ABL1, ANXA1, AXL, BCL2, GPR183, NCKAP1L, IL2, CXCR2, ITPKB, MEF2C, KITLG, MPL, PDE4B, PPP3CB, TNFAIP3, BCL10, TNFRSF13B, JAM3, TNFRSF13C, DOCK11, GAPT
BP	GO:0002576	platelet degranulation	27/1554	1.07E-04	A2M, ACTN1, ACTN2, CLU, CFD, F8, F13A1, FLNA, HGF, IGF1, ITGB3, P2RX1, PCDH7, PECAM1, SELP, SELENOP, STXBP1, TGFB3, THBS1, TLN1, CLEC3B, VCL, VWF, ABCC4, MMRN1, HABP4, CDC37L1
BP	GO:0007215	glutamate receptor signaling pathway	23/1554	1.14E-04	ACTN2, ADRB2, CRHBP, DLG2, FYN, GNAQ, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, GRM7, KCNB1, MEF2C, RELN, CX3CL1, SSTR1, PPARGC1A, NLGN1, NLGN3, CPEB4, GSG1L, SHISA6
BP	GO:0055024	regulation of cardiac muscle tissue development	23/1554	1.14E-04	BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, RBP4, RGS2, TBX5, TGFBR2, TGFBR3, FZD7, AKAP6, DKK1, ZFPM2, SOX6, TBX20, JPH2, MYOCD
BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	32/1554	1.14E-04	ABL1, LDLRAD4, CAV1, CIDEA, DCN, FBN1, SMAD7, SFRP1, SFRP2, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, CHRD, SLIT2, SPRY1, SPRY2, CXCL13, EMILIN1, DKK1, SPART, SIRT1, SOSTDC1, ADGRA2, PRDM16, GREM2, CHRDL1, VASN, WFIKKN2, BMPER, RBPMS2
BP	GO:0150063	visual system development	56/1554	1.21E-04	ACVRL1, ALDH1A3, ATP2B4, BCL2, PRDM1, C3, CACNA1C, COL8A2, CYP1B1, DCX, DIO3, EPHA2, EPHB1, FBN1, EFEMP1, FGF9, FGF10, GPM6A, JUN, MEIS1, MEIS2, MITF, NTRK3, PDGFRA, PITX2, PROX1, RBP4, RORB, SHH, SRF, ZEB1, TGFBR2, TMOD1, TUB, WNT2B, WNT9A, MYOM2, KLF4, ZEB2, LAMC3, MAB21L2, NES, ARHGEF15, CRB1, VSX1, CDON, SLC17A7, RHOJ, CC2D2A, P2RY12, NKD1, CHRDL1, FOXP2, SLC25A25, UNC45B, ABCB5
BP	GO:0048016	inositol phosphate-mediated signaling	16/1554	1.23E-04	ACTN3, ATP2B4, RCAN1, IGF1, INPP5A, ITPR1, NFATC1, NFATC2, NFATC4, PPP3CB, AKAP6, RCAN2, NMUR1, LMCD1, MYOZ2, C10orf71
BP	GO:0071559	response to transforming growth factor beta	43/1554	1.23E-04	ACVRL1, BMPR1A, ZFP36L1, LDLRAD4, CAV1, CIDEA, CX3CR1, FBN1, FOS, FYN, LRRC32, GDF10, JUN, SMAD7, SMAD9, MEF2C, PDE2A, PDE3A, ROCK1, SFRP1, SOX5, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, CLDN5, CLEC3B, LTBP4, CILP, ITGA8, ROCK2, PPARGC1A, FERMT2, EMILIN1, SIRT1, SOX6, PRDM16, PDGFD, MYOCD, VASN, WFIKKN2
BP	GO:0086005	ventricular cardiac muscle cell action potential	13/1554	1.24E-04	BIN1, ANK2, CACNA1C, CAV1, KCND3, KCNH2, KCNJ3, KCNJ8, RYR2, SNTA1, KCNE4, CTNNA3, SCN3B
BP	GO:0045844	positive regulation of striated muscle tissue development	21/1554	1.25E-04	ACTN3, BCL2, BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, MEF2C, PIM1, SHH, TBX5, TGFBR3, AKAP6, ZFPM2, CDON, LMOD3, TBX20, SOX17, MYOCD, RBM24
BP	GO:0048636	positive regulation of muscle organ development	21/1554	1.25E-04	ACTN3, BCL2, BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, MEF2C, PIM1, SHH, TBX5, TGFBR3, AKAP6, ZFPM2, CDON, LMOD3, TBX20, SOX17, MYOCD, RBM24
BP	GO:0060993	kidney morphogenesis	22/1554	1.30E-04	BCL2, EYA1, FGF2, FGF10, GDNF, ILK, LIF, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, GCNT3, WWTR1, FAT4, LRRK2, OSR1
BP	GO:0007265	Ras protein signal transduction	65/1554	1.34E-04	ABL1, ADRA1A, ADRA2A, RHOB, RND3, ARHGAP1, ARHGAP6, RHOH, CDKN1A, LPAR1, FGF2, FGF10, GPR17, IGF1, ITPKB, JUN, KITLG, NGF, NGFR, PECAM1, PRKD1, PSD, RAB27A, RAP1A, ROCK1, RRAS, TIMP2, GPR55, GRAP2, NTN1, ROCK2, ARHGEF10, ARHGEF17, RASA4, SPRY1, SPRY2, DLC1, CDC42EP2, CDC42EP3, MAPRE2, AKAP13, MRAS, RASA3, ARHGEF15, ARHGEF9, KANK2, ARHGEF26, TIAM2, RND1, RAB30, P2RY10, RAB9B, DNAJC27, RAB23, RHOJ, PREX2, KCTD10, RERG, ARHGEF25, RASGRP4, RAB3C, ABRA, P2RY8, RAB37, ARHGEF37
BP	GO:0099084	postsynaptic specialization organization	12/1554	1.34E-04	CBLN1, DLG2, GRID2, NTRK3, RELN, PTPRD, NRXN1, NRXN2, NLGN1, LRRC4, TMEM108, LRRTM1
BP	GO:0003231	cardiac ventricle development	27/1554	1.39E-04	PRDM1, BMPR1A, CPE, FOXF1, ID2, CCN1, KCNK2, SMAD7, MEF2C, MYL3, PDE2A, PROX1, RYR2, SALL1, SFRP2, SLIT3, TBX5, TGFBR2, TGFBR3, TNNT2, TPM1, SLIT2, HAND1, HAND2, ZFPM2, TBX20, MYOCD
BP	GO:0050806	positive regulation of synaptic transmission	32/1554	1.42E-04	ABL1, ADCYAP1, ADRA1A, ADRB2, CACNB2, CHRNA7, CX3CR1, GPER1, GRIK2, GRIN2A, MPP2, NFATC4, ROR2, RELN, PTGS2, SLC8A2, SLC8A3, SNCA, STXBP1, VAMP2, TAC1, TACR2, LGI1, NRXN1, RIMS3, FAM107A, NLGN1, IGSF9B, RIMS1, NLGN3, CLSTN2, LRRTM1
BP	GO:0010632	regulation of epithelial cell migration	47/1554	1.51E-04	ABL1, ACVRL1, ANGPT1, ANXA1, RHOB, CCR6, DCN, HBEGF, EPHA2, FGF2, FGF7, FGF10, FGFR1, GDF2, HYAL1, ITGB3, JUN, MEF2C, PRKCA, PRKD1, PROX1, PTGS2, STC1, TAC1, TEK, TGFBR2, THBS1,

					PLPP3, NRP2, KLF4, SLIT2, ROCK2, AKT3, SEMA3A, CXCL13, MAPRE2, SIRT1, CORO1C, ADGRA2, ADAMTS9, RHOJ, JCAD, ATOH8, STARD13, GLIPR2, AMOTL1, BMPER
BP	GO:0051952	regulation of amine transport	22/1554	1.52E-04	ADRA2A, ADRA2B, ATP1A2, GDNF, GRM7, KCNA2, KCNB1, P2RY1, PRKN, RGS2, CXCL12, SNCA, STXBP1, SYT4, TACR2, TRH, VIP, PER2, SYT11, P2RY12, SYT15, OSR1
BP	GO:0055006	cardiac cell development	22/1554	1.52E-04	ACTC1, ACTN2, ADRA1A, IGF1, MEF2A, MYH11, PDGFRA, PROX1, RGS2, SGCB, SGCD, SLC8A1, SRF, TGFBR3, SORBS2, MYOM2, AKAP6, SPRY1, PDLIM5, BVES, AKAP13, ALPK3
BP	GO:0110020	regulation of actomyosin structure organization	22/1554	1.52E-04	ABL1, ARHGAP6, CCN2, S1PR1, LPAR1, MEF2C, PIK3R1, PROX1, PTGER4, ROCK1, SFRP1, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, DLC1, AKAP13, ARHGEF15, TMEFF2, ARHGAP28, PHLDB2
BP	GO:0015837	amine transport	23/1554	1.53E-04	ADRA2A, ADRA2B, ATP1A2, GDNF, GRM7, KCNA2, KCNB1, P2RY1, PRKN, RGS2, CXCL12, SLC18A2, SNCA, STXBP1, SYT4, TACR2, TRH, VIP, PER2, SYT11, P2RY12, SYT15, OSR1
BP	GO:0010611	regulation of cardiac muscle hypertrophy	19/1554	1.55E-04	ADRA1A, ATP2B4, IGF1, IL6ST, MEF2A, PRKCA, RGS2, ROCK1, TRPC3, NR4A3, PDE5A, HAND2, AKAP6, ROCK2, LMCD1, ERRFI1, TRIM63, MLIP, GATA5
BP	GO:0007269	neurotransmitter secretion	32/1554	1.58E-04	ADRA1A, CACNB2, CAMK2A, CHRM2, STX2, GPER1, MEF2C, P2RX1, P2RY1, PRKN, PRKCB, PTPRN2, RAP1A, SLC18A2, SNCA, STXBP1, VAMP2, SYT4, TACR2, PPFIA2, STX11, NRXN1, NRXN2, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, SLC5A7, PRRT2, LRRK2
BP	GO:0036293	response to decreased oxygen levels	56/1554	1.58E-04	ACVRL1, AK4, AQP1, BCL2, ZFP36L1, CAV1, CD34, CHRNA7, PLK3, CCN2, EDNRA, EGR1, GATA6, ITPR1, KCNK2, KCNK3, KCNMA1, KCNMB1, MMP2, MPL, MYC, NR4A2, PAM, PTGIS, PTGS2, RORA, RYR2, CXCL12, SFRP1, SLC2A4, SLC8A1, SLC8A3, SOD3, SRF, STC1, TEK, TGFB3, TGFBR2, TGFBR3, THBS1, TRH, ADIPOQ, ROCK2, ARNT2, NAMPT, PPARGC1A, SIRT1, HIF3A, CPEB1, NDNF, CPEB4, APOLD1, MYOCD, CYGB, VASN, CPEB2
BP	GO:0060070	canonical Wnt signaling pathway	52/1554	1.59E-04	CAV1, EDA, EGR1, FGF9, FGF10, GPC5, GNAQ, IGFBP2, IGFBP6, ILK, MITF, ROR2, NR4A2, PRKN, RYR2, SFRP1, SFRP2, SHH, TBL1X, TLE4, WNT2B, WNT9A, FZD7, RECK, PLPP3, SCEL, TBX18, KLF4, FZD10, DKK1, DAAM2, SOSTDC1, WWTR1, ADGRA2, PYGO1, LATS2, RBMS3, DACT1, SOX17, JADE1, WLS, SOX7, RSPO3, NKD1, DIXDC1, TMEM88, LRRK2, CSNK1A1L, PRICKLE1, DACT3, RSPO2, SHISA6
BP	GO:0046677	response to antibiotic	51/1554	1.69E-04	ABL1, ACTC1, ADCY2, ADCY5, ADCYAP1, ADCYAP1R1, ANXA1, AQP1, RHOB, AXL, BCL2, CDO1, CLU, CRHBP, CSF3, CYP1B1, DUSP1, EGR1, FYN, GNAO1, GRIN2A, GSN, HBB, HGF, HYAL1, IL2, JUN, KCNMB1, MEF2C, NTRK3, PLA2G4A, RBP4, RGS2, SLC2A4, SLC8A1, TNFAIP3, TRH, RNF112, NR4A3, FOSL1, AOC3, TRPA1, KLF4, ADIPOQ, KLF2, TXNIP, KDM6B, SIRT1, PDGFD, SETD7, LRRK2
BP	GO:0007596	blood coagulation	52/1554	1.72E-04	A2M, ADRA2A, ADRA2B, AXL, CAV1, CD34, ENTPD1, CD40LG, DGKB, DGKG, F3, F8, F10, F13A1, FLNA, FYN, GATA6, GNAQ, HBB, ILK, ITGB3, ITPR1, MPL, P2RX1, P2RY1, SERPINB2, PDGFRA, PIK3R1, PRKACB, PRKAR2B, PRKCA, PRKCB, RAB27A, SELP, SHH, SRF, STXBP1, THBS1, TLN1, TRPC3, VCL, VWF, GNA14, MYL9, MMRN1, ZFPM2, MAFF, EHD2, P2RY12, SCUBE1, DOCK11, GATA5
BP	GO:0060021	roof of mouth development	21/1554	1.73E-04	BMPR1A, LRRC32, MEF2C, MSX1, PDGFRA, SHH, TCF21, TGFB3, TGFBR2, TGFBR3, CLDN5, HAND2, TSHZ1, TIPARP, BNC2, PRDM16, CSRNP1, ARID5B, PKDCC, WFIKKN2, OSR1
BP	GO:0071772	response to BMP	32/1554	1.75E-04	ABL1, ACVRL1, BMP5, BMPR1A, EGR1, FBN1, GATA6, GDF2, CCN1, ILK, SMAD7, SMAD9, MSX1, ROR2, RYR2, SFRP1, SFRP2, TGFBR3, CHRD, FSTL1, DKK1, ZNF423, SPART, SOSTDC1, TMEM100, RGMA, GREM2, CHRDL1, GATA5, BMPER, VSTM2A, RBPMS2
BP	GO:0071773	cellular response to BMP stimulus	32/1554	1.75E-04	ABL1, ACVRL1, BMP5, BMPR1A, EGR1, FBN1, GATA6, GDF2, CCN1, ILK, SMAD7, SMAD9, MSX1, ROR2, RYR2, SFRP1, SFRP2, TGFBR3, CHRD, FSTL1, DKK1, ZNF423, SPART, SOSTDC1, TMEM100, RGMA, GREM2, CHRDL1, GATA5, BMPER, VSTM2A, RBPMS2
BP	GO:0099643	signal release from synapse	32/1554	1.75E-04	ADRA1A, CACNB2, CAMK2A, CHRM2, STX2, GPER1, MEF2C, P2RX1, P2RY1, PRKN, PRKCB, PTPRN2, RAP1A, SLC18A2, SNCA, STXBP1, VAMP2, SYT4, TACR2, PPFIA2, STX11, NRXN1, NRXN2, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, SLC5A7, PRRT2, LRRK2
BP	GO:0043524	negative regulation of neuron apoptotic process	29/1554	1.76E-04	ANGPT1, AXL, BCL2, BDNF, CX3CR1, FYN, GDNF, GRIK2, ILK, JUN, LRP1, MEF2C, NFATC4, NGF, NR4A2, PRKN, ROCK1, CX3CL1, SNCA, STXBP1, TGFB3, WFS1, BTG2, NR4A3, NES, PPARGC1A, FAIM2, NDNF, CPEB4
BP	GO:0003158	endothelium development	27/1554	1.76E-04	ACVRL1, RHOB, CD34, COL4A4, S1PR1, S1PR3, GDF2, PDE2A, PDE4D, PECAM1, PROX1, RAP1A, ROCK1, STC1, ZEB1, CLDN5, ROCK2, KDM6B, PPP1R16B, ARHGEF26, TMEM100, SOX17, SCUBE1, APOLD1, ATOH8, STARD13, MYADM
BP	GO:0030111	regulation of Wnt signaling pathway	55/1554	1.78E-04	ABL1, CAV1, EDA, EGR1, ESR1, FGF9, FGF10, GPC5, GNAQ, GRB10, HIC1, IGFBP2, IGFBP6, ILK, LRP1, NFATC1, NFATC4, ROR2, PRKN, SALL1, SFRP1, SFRP2, SHH, TBL1X, TLE4, TNFAIP3, FZD7, RECK, PLPP3, SCEL, TBX18, ZEB2, DKK1, DAAM2, SOSTDC1, WWTR1, ADGRA2, LATS2, RBMS3, DACT1, SOX17, JADE1, WLS, SOX7, RSPO3, NKD1, DIXDC1, TMEM88, LRRK2, CSNK1A1L, PRICKLE1, DACT3, RSPO2, SHISA6, TRABD2B
BP	GO:0023061	signal release	66/1554	1.79E-04	ADCY5, ADCYAP1, ADRA1A, ADRA2A, ADRA2B, SLC25A4, ANXA1, CACNA1C, CACNB2, CAMK2A, CHRM2, CPE, CRHBP, EPHA5, STX2, FGFR1, GPER1, IL1RN, INHBB, ITPR1, KCNB1, LIF, LRP1, MEF2C, P2RX1, P2RY1, PRKN, PPP3CB, PRKCA, PRKCB, PTPRN2, RAP1A, RBP4, SFRP1, SLC18A2, SNCA,

					STXBP1, VAMP2, SYT4, TAC1, TACR2, TRH, VIP, FGF23, LTBP4, PPFIA2, STX11, PER2, ADIPOQ, NRXN1, NRXN2, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, MYRIP, SYBU, G6PC2, SLC5A7, WLS, MIDN, PRRT2, C1QTNF3, LRRK2
BP	GO:0048566	embryonic digestive tract development	12/1554	1.79E-04	FGF9, FGF10, FOXF1, GLI2, ID2, PCSK5, PDGFRA, SALL1, SHH, TCF21, PKDCC, RBPMS2
BP	GO:0030326	embryonic limb morphogenesis	26/1554	1.84E-04	BMPR1A, CACNA1C, FGF9, FGFR1, GLI2, AFF3, MBNL1, MSX1, MYH3, ROR2, PBX1, PITX1, PTCH1, SALL1, SFRP2, SHH, TBX5, WNT9A, ZBTB16, RECK, HAND2, TBX4, DKK1, MAP3K20, OSR1, RSPO2
BP	GO:0035113	embryonic appendage morphogenesis	26/1554	1.84E-04	BMPR1A, CACNA1C, FGF9, FGFR1, GLI2, AFF3, MBNL1, MSX1, MYH3, ROR2, PBX1, PITX1, PTCH1, SALL1, SFRP2, SHH, TBX5, WNT9A, ZBTB16, RECK, HAND2, TBX4, DKK1, MAP3K20, OSR1, RSPO2
BP	GO:0006469	negative regulation of protein kinase activity	40/1554	1.84E-04	ABL1, ADARB1, CAV1, CDKN1A, GADD45A, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, GNAQ, ILK, GADD45B, PRKAR2B, RGS2, SFRP1, SFRP2, TNFAIP3, SOCS3, GPRC5A, RGN, ADIPOQ, HIPK3, TRIB1, SPRY1, SPRY2, IRAK3, SIRT1, CORO1C, WWTR1, LATS2, PRKAG2, ERRFI1, DBNDD2, INKA2, DUSP26, ITPRIP, MYOCD, DUSP19
BP	GO:0010644	cell communication by electrical coupling	11/1554	1.86E-04	ATP1A2, ATP1B2, CACNA1C, CASQ2, CAV1, HRC, KCNA1, PDE4D, RYR2, SLC8A1, GJC1
BP	GO:0060536	cartilage morphogenesis	11/1554	1.86E-04	COL6A2, COL6A3, MATN2, MEF2C, MSX1, STC1, HAND1, HAND2, SCARA3, COL21A1, RSPO2
BP	GO:0071277	cellular response to calcium ion	20/1554	1.92E-04	CRHBP, FOS, FOSB, ITPKB, JUN, JUNB, JUND, MEF2A, MEF2C, PKD2, PRKAA2, RYR3, SYT4, CPNE6, RASA4, NLGN1, SYT11, CLIC4, SLC25A23, SYT15
BP	GO:0051056	regulation of small GTPase mediated signal transduction	52/1554	1.94E-04	A2M, ABL1, ADCYAP1R1, ADRA1A, RHOB, ARHGAP1, ARHGAP6, RHOH, LPAR1, FGF10, GPR17, IGF1, ITPKB, KITLG, NGF, RELN, PSD, TIMP2, GPR55, SLIT2, ARHGEF10, ARHGEF17, RASA4, SPRY1, SPRY2, DLC1, MAPRE2, AKAP13, RASA3, ARHGEF15, ARHGEF9, KANK2, ARHGEF26, TIAM2, P2RY10, CDON, FAM13B, RHOJ, ARHGAP20, ARHGAP28, PREX2, ARHGAP24, KCTD10, SYDE2, GARNL3, CGNL1, STARD13, ARHGEF25, RASGRP4, ABRA, P2RY8, ARHGEF37
BP	GO:0048736	appendage development	33/1554	1.94E-04	BMPR1A, CACNA1C, FGF9, FGF10, FGFR1, GLI2, AFF3, MBNL1, MSX1, MYH3, ROR2, PAM, PBX1, PCSK5, PITX1, PITX2, PTCH1, SALL1, SFRP2, SHH, TBX5, WNT9A, ZBTB16, RECK, HAND2, TBX4, DKK1, SALL3, MAP3K20, PKDCC, OSR1, RSPO2, EVX2
BP	GO:0060173	limb development	33/1554	1.94E-04	BMPR1A, CACNA1C, FGF9, FGF10, FGFR1, GLI2, AFF3, MBNL1, MSX1, MYH3, ROR2, PAM, PBX1, PCSK5, PITX1, PITX2, PTCH1, SALL1, SFRP2, SHH, TBX5, WNT9A, ZBTB16, RECK, HAND2, TBX4, DKK1, SALL3, MAP3K20, PKDCC, OSR1, RSPO2, EVX2
BP	GO:0007266	Rho protein signal transduction	36/1554	1.94E-04	ABL1, ADRA1A, ADRA2A, RHOB, RND3, ARHGAP1, ARHGAP6, RHOH, LPAR1, GPR17, NGFR, PECAM1, ROCK1, GPR55, NTN1, ROCK2, ARHGEF10, ARHGEF17, DLC1, CDC42EP2, CDC42EP3, AKAP13, ARHGEF15, ARHGEF9, KANK2, ARHGEF26, TIAM2, RND1, P2RY10, RHOJ, PREX2, KCTD10, ARHGEF25, ABRA, P2RY8, ARHGEF37
BP	GO:1901379	regulation of potassium ion transmembrane transport	21/1554	1.97E-04	ACTN2, BIN1, ANK2, ATP1B2, CASQ2, CAV1, DPP6, FHL1, FLNA, KCNA1, KCNH2, KCNMB1, KCNS2, VAMP2, KCNAB1, AKAP6, KCNE4, KCNIP3, KCNIP1, KCNIP4, LRRC52
BP	GO:0046928	regulation of neurotransmitter secretion	23/1554	1.98E-04	ADRA1A, CACNB2, CAMK2A, CHRM2, GPER1, MEF2C, P2RX1, P2RY1, PRKN, PRKCB, RAP1A, SNCA, STXBP1, SYT4, TACR2, PPFIA2, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, LRRK2
BP	GO:0009187	cyclic nucleotide metabolic process	13/1554	2.08E-04	ADCY2, ADCY5, ADCY9, EPHA2, NPR1, NPR2, PDE1A, PDE2A, PDE4B, PDE4D, RORA, PDE5A, PDE7B
BP	GO:1901214	regulation of neuron death	49/1554	2.10E-04	ABL1, ANGPT1, AXL, BCL2, BDNF, CD34, CHRNA7, CLU, CSF3, CX3CR1, EGR1, EPHA7, EPHB1, FOS, FYN, GDNF, GRID2, GRIK2, ILK, ITGA1, JUN, KCNB1, LRP1, MAPT, MCL1, MEF2C, CD200, NFATC4, NGF, NR4A2, PRKN, ROCK1, CX3CL1, SNCA, STXBP1, TGFB3, WFS1, BTG2, NR4A3, HDAC4, NES, PPARGC1A, DKK1, FAIM2, SIRT1, NDNF, CPEB4, LRRK2, NCOA7
BP	GO:0070997	neuron death	53/1554	2.10E-04	ABL1, ADARB1, ANGPT1, AXL, BCL2, BDNF, CD34, CHRNA7, CLU, CSF3, CX3CR1, DIO3, EGR1, EPHA7, EPHB1, FOS, FYN, GDNF, GRID2, GRIK2, ILK, ITGA1, JUN, KCNB1, LRP1, MAPT, MCL1, MEF2C, CD200, NFATC4, NGF, NGFR, NR4A2, PRKN, ROCK1, CX3CL1, SNCA, STXBP1, TGFB3, WFS1, BTG2, NR4A3, HDAC4, NAMPT, NES, PPARGC1A, DKK1, FAIM2, SIRT1, NDNF, CPEB4, LRRK2, NCOA7
BP	GO:0048745	smooth muscle tissue development	9/1554	2.24E-04	MYLK, PKD2, PROX1, SHH, SRF, ITGA8, TIPARP, FOXP2, OSR1
BP	GO:0060420	regulation of heart growth	20/1554	2.25E-04	ACACB, BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, PROX1, RBP4, RGS2, TBX5, TGFBR2, TGFBR3, AKAP6, ZFPM2, TBX20
BP	GO:0060421	positive regulation of heart growth	15/1554	2.28E-04	ACACB, BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, MEF2C, PIM1, PROX1, TBX5, TGFBR3, AKAP6, ZFPM2, TBX20
BP	GO:0072132	mesenchyme morphogenesis	15/1554	2.28E-04	ACTA2, ACTC1, ACVRL1, BMP5, BMPR1A, FGFR1, FOXF1, MSX1, MYC, TGFBR2, DCHS1, TMEM100, TBX20, OSR1, GATA5

BP	GO:0007009	plasma membrane organization	23/1554	2.28E-04	ABCD2, BIN1, ANK2, ANXA6, AR, CAV1, CLU, STX2, GSN, UGCG, DYSF, CAVIN2, SYT11, CRB1, TMEFF2, EHD2, SNX9, PLSCR4, FA2H, FAT4, XKR4, ANO4, SYPL2
BP	GO:0055017	cardiac muscle tissue growth	23/1554	2.28E-04	ADRA1A, BMPR1A, S1PR1, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, RBP4, RGS2, TBX5, TGFBR2, TGFBR3, SORBS2, AKAP6, PDLIM5, AKAP13, ZFPM2, TBX20
BP	GO:0014909	smooth muscle cell migration	21/1554	2.28E-04	BCL2, BMPR1A, LPAR1, FGF9, IGF1, IGFBP5, ILK, ITGB3, LRP1, MEF2C, TPM1, NR4A3, SLIT2, ADIPOQ, ADAMTS1, HDAC4, TRIB1, PPARGC1A, PARVA, PDGFD, MYOCD
BP	GO:1901653	cellular response to peptide	57/1554	2.31E-04	ACTN2, ADCY2, ADCY5, ADCY9, ADRB2, BCL2L2, ZFP36L1, CACNA2D1, CAMK2A, CAV1, CRHBP, FBN1, FER, FYN, GHR, GPER1, GRB10, NR4A1, IGF1, INHBB, LHCGR, LRP1, MAP1B, NGFR, NR4A2, PDE3B, PDK4, ENPP1, PIK3R1, PRKACB, PRKAR2B, PRKCB, ROCK1, SLC2A4, STAT5B, VAMP2, KLF10, NR4A3, KLF11, SOCS2, SOCS3, KLF4, GLP2R, ADIPOQ, ROCK2, NAMPT, KLF2, SORBS1, SIRT1, KLF15, ERRFI1, PID1, MBD5, ZNF106, CPEB1, GKAP1, CPEB2
BP	GO:0070482	response to oxygen levels	58/1554	2.31E-04	ACVRL1, AK4, AQP1, BCL2, ZFP36L1, CAV1, CD34, CDKN1A, CHRNA7, PLK3, CCN2, LPAR1, EDNRA, EGR1, GATA6, ITPR1, KCNK2, KCNK3, KCNMA1, KCNMB1, MMP2, MPL, MYC, NR4A2, PAM, PTGIS, PTGS2, RORA, RYR2, CXCL12, SFRP1, SLC2A4, SLC8A1, SLC8A3, SOD3, SRF, STC1, TEK, TGFB3, TGFBR2, TGFBR3, THBS1, TRH, ADIPOQ, ROCK2, ARNT2, NAMPT, PPARGC1A, SIRT1, HIF3A, CPEB1, NDNF, CPEB4, APOLD1, MYOCD, CYGB, VASN, CPEB2
BP	GO:0048333	mesodermal cell differentiation	12/1554	2.34E-04	BMPR1A, EYA1, FGFR1, FOXF1, ITGB3, SFRP2, TAL1, ITGA8, KLF4, DKK1, KDM6B, SOX17
BP	GO:0007599	hemostasis	52/1554	2.36E-04	A2M, ADRA2A, ADRA2B, AXL, CAV1, CD34, ENTPD1, CD40LG, DGKB, DGKG, F3, F8, F10, F13A1, FLNA, FYN, GATA6, GNAQ, HBB, ILK, ITGB3, ITPR1, MPL, P2RX1, P2RY1, SERPINB2, PDGFRA, PIK3R1, PRKACB, PRKAR2B, PRKCA, PRKCB, RAB27A, SELP, SHH, SRF, STXBP1, THBS1, TLN1, TRPC3, VCL, VWF, GNA14, MYL9, MMRN1, ZFPM2, MAFF, EHD2, P2RY12, SCUBE1, DOCK11, GATA5
BP	GO:0022612	gland morphogenesis	25/1554	2.43E-04	AR, BCL2, CAV1, EDA, EPHA2, ESR1, FGF7, FGF10, FGFR1, GLI2, HGF, ID4, IGFBP5, NFIB, PGR, PROX1, PTCH1, SFRP1, SHH, TGFB3, TGFBR2, TNFAIP3, NTN1, SEMA3A, SOSTDC1
BP	GO:0007498	mesoderm development	27/1554	2.47E-04	BMPR1A, BMX, ZFP36L1, EPHA2, ETS2, EYA1, FGFR1, FOXF1, ITGB3, OVOL1, SFRP2, SHH, SRF, TAL1, TXNRD1, NR4A3, ITGA8, CHRD, KLF4, HAND1, DKK1, KDM6B, ZFPM2, TBX20, SOX17, WLS, OSR1
BP	GO:0006688	glycosphingolipid biosynthetic process	10/1554	2.53E-04	ST8SIA1, UGCG, B3GALT2, B3GALT1, LARGE1, ST6GALNAC6, FA2H, ST6GALNAC5, ST6GALNAC3, ST8SIA6
BP	GO:0050817	coagulation	52/1554	2.54E-04	A2M, ADRA2A, ADRA2B, AXL, CAV1, CD34, ENTPD1, CD40LG, DGKB, DGKG, F3, F8, F10, F13A1, FLNA, FYN, GATA6, GNAQ, HBB, ILK, ITGB3, ITPR1, MPL, P2RX1, P2RY1, SERPINB2, PDGFRA, PIK3R1, PRKACB, PRKAR2B, PRKCA, PRKCB, RAB27A, SELP, SHH, SRF, STXBP1, THBS1, TLN1, TRPC3, VCL, VWF, GNA14, MYL9, MMRN1, ZFPM2, MAFF, EHD2, P2RY12, SCUBE1, DOCK11, GATA5
BP	GO:0051282	regulation of sequestering of calcium ion	26/1554	2.62E-04	ABL1, ANK2, ANXA6, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, FGF2, GPER1, HRC, ITPR1, PDE4D, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SNCA, TRPC1, TRPA1, AKAP6, RASA3, JPH2, SLC25A23, JPH4
BP	GO:0050678	regulation of epithelial cell proliferation	56/1554	2.62E-04	ACVRL1, AR, BMP5, BMPR1A, ZFP36L1, KLF9, CAV1, EDNRB, EGR3, EYA1, F3, FGF2, FGF7, FGF9, FGF10, FGFR1, GDF2, NR4A1, HYAL1, IGF1, ITGB3, JUN, LAMC1, MEF2C, MYC, NFIB, NGFR, PGR, PRKCA, PRKD1, PROX1, PTCH1, CXCL12, SFRP1, SFRP2, SHH, TEK, TGFBR3, THBS1, TNFAIP3, VIP, ZFP36, NR4A3, DYSF, FZD7, TNFSF12, NRP2, RGN, AKT3, SIRT1, PPP1R16B, ERRFI1, JCAD, ATOH8, FOXP2, OSR1
BP	GO:0001708	cell fate specification	22/1554	2.64E-04	AR, BMPR1A, EYA1, FGF2, FGFR1, GLI2, NTRK3, PTCH1, SFRP2, SHH, TBX5, FZD7, TBX18, TBX4, DKK1, MYT1L, DHH, CDON, FEV, SOX6, TBX20, SOX17
BP	GO:0048286	lung alveolus development	13/1554	2.65E-04	FGF10, FOXF1, GATA6, IGFBP5, LIF, PGR, TCF21, TGFB3, ERRFI1, STK40, PKDCC, MYOCD, FOXP2
BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	51/1554	2.67E-04	ADRA2A, ADRA2B, ADRB2, ATP2B4, CCND2, CD40LG, CHRNA7, MAP3K8, CSPG4, GADD45A, DUSP5, LPAR1, FGF2, FGF10, FGFR1, GHR, HGF, IGF1, ILK, ITGA1, KIT, KITLG, GADD45B, NGF, NTRK3, ROR2, PKD1, PKD2, PROX1, SNCA, TGFB3, THBS1, TPD52L1, TCL1A, PDE5A, ADIPOQ, ZEB2, SPRY2, FZD10, AKAP13, DKK1, TNIK, SIRT1, MAP3K20, TCIM, AVPI1, PDGFD, PROK1, LRRK2, DUSP19, SAMD5
BP	GO:0030282	bone mineralization	24/1554	2.89E-04	ADRB2, BMPR1A, S1PR1, GPM6B, IGF1, CCN1, MEF2C, MGP, ROR2, DDR2, OMD, ENPP1, PTGS2, SLC8A1, TGFB3, KLF10, CLEC3B, FGF23, SBDS, PKDCC, OSR1, TMEM119, RSPO2, RFLNB
BP	GO:0045446	endothelial cell differentiation	24/1554	2.89E-04	ACVRL1, COL4A4, S1PR1, S1PR3, GDF2, PDE2A, PDE4D, PECAM1, PROX1, RAP1A, ROCK1, STC1, ZEB1, CLDN5, ROCK2, KDM6B, PPP1R16B, ARHGEF26, TMEM100, SOX17, SCUBE1, APOLD1, ATOH8, MYADM
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	41/1554	2.94E-04	ACVRL1, BMPR1A, ZFP36L1, LDLRAD4, CAV1, CIDEA, CX3CR1, FBN1, FOS, FYN, LRRC32, GDF10, JUN, SMAD7, SMAD9, MEF2C, PDE2A, PDE3A, SFRP1, SOX5, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, CLDN5, CLEC3B, LTBP4, CILP, ITGA8, PPARGC1A, FERMT2, EMILIN1, SIRT1, SOX6, PRDM16, PDGFD, MYOCD, VASN, WFIKKN2

BP	GO:0001654	eye development	54/1554	2.97E-04	ACVRL1, ALDH1A3, ATP2B4, BCL2, PRDM1, CACNA1C, COL8A2, CYP1B1, DCX, DIO3, EPHA2, EPHB1, FBN1, EFEMP1, FGF9, FGF10, GPM6A, JUN, MEIS1, MEIS2, MITF, NTRK3, PDGFRA, PITX2, PROX1, RBP4, RORB, SHH, SRF, ZEB1, TGFBR2, TMOD1, TUB, WNT2B, WNT9A, MYOM2, KLF4, ZEB2, LAMC3, MAB21L2, NES, ARHGEF15, CRB1, VSX1, CDON, SLC17A7, RHOJ, CC2D2A, NKD1, CHRDL1, FOXP2, SLC25A25, UNC45B, ABCB5
BP	GO:0060348	bone development	37/1554	3.36E-04	ANXA6, FOXN3, COL6A2, COL6A3, COL13A1, FBN1, IGF1, KIT, MATN2, MEF2C, MEF2D, MEIS1, MMP16, MSX1, NPR2, PITX2, PTGER4, SFRP2, SRF, STC1, TAL1, TEK, TGFB3, TGFBR2, DCHS1, RGN, AKAP13, SBDS, SCARA3, RAB23, CSGALNACT1, FAT4, COL21A1, FREM1, RANBP3L, TMEM119, RFLNB
BP	GO:0003208	cardiac ventricle morphogenesis	18/1554	3.37E-04	BMPR1A, CPE, FOXF1, SMAD7, MEF2C, MYL3, PROX1, RYR2, SFRP2, TBX5, TGFBR2, TGFBR3, TNNT2, TPM1, HAND1, HAND2, ZFPM2, TBX20
BP	GO:1903392	negative regulation of adherens junction organization	9/1554	3.37E-04	ACVRL1, APOD, ARHGAP6, LRP1, THBS1, DLC1, FAM107A, CORO1C, PHLDB2
BP	GO:1990778	protein localization to cell periphery	48/1554	3.45E-04	ACTN2, ANK2, AR, CACNB2, CAV1, DLG2, DPP6, EPHA2, EPHA3, FLNA, GPER1, GRIN2A, KCNB1, LRP1, P2RY1, PALM, PIK3R1, PTCH1, RAP1A, ROCK1, STAC, STXBP1, VAMP2, TUB, SLMAP, DCHS1, LGI1, ADIPOQ, ROCK2, GPC6, SEC23A, SORBS1, EFR3B, TNIK, NFASC, CLIP3, KCNIP3, EHD2, PID1, SCN3B, SPTBN4, KIF13A, KCNIP4, PKDCC, MYADM, TMEM88, RAB3C, CNST
BP	GO:0061005	cell differentiation involved in kidney development	15/1554	3.51E-04	ACTA2, CD34, GDNF, LIF, MEF2C, PTCH1, SALL1, SHH, TCF21, ADIPOQ, MAGI2, WWTR1, KLF15, FAT4, OSR1
BP	GO:1903426	regulation of reactive oxygen species biosynthetic process	22/1554	3.56E-04	ABCD2, ARG2, ATP2B4, CAV1, CD34, CLU, CX3CR1, FYN, HBB, PKD2, PTGIS, PTGS2, PTX3, RAB27A, SLC18A2, SNCA, RGN, KLF4, ROCK2, HDAC4, KLF2, MPV17L
BP	GO:0060324	face development	14/1554	3.56E-04	ALDH1A3, MMP2, MSX1, MYH3, PDGFRA, RRAS, SRF, TGFB3, CLDN5, DKK1, TIPARP, CSRNP1, CRISPLD2, ARID5B
BP	GO:0030318	melanocyte differentiation	10/1554	3.62E-04	BCL2, EDNRB, KIT, MEF2C, KITLG, MITF, ENPP1, RAB27A, ZEB2, ADAMTS9
BP	GO:0072659	protein localization to plasma membrane	42/1554	3.65E-04	ACTN2, ANK2, AR, CACNB2, DPP6, EPHA2, EPHA3, FLNA, GPER1, KCNB1, LRP1, P2RY1, PALM, PIK3R1, PTCH1, RAP1A, ROCK1, STAC, STXBP1, VAMP2, SLMAP, DCHS1, ADIPOQ, ROCK2, SEC23A, SORBS1, EFR3B, TNIK, NFASC, CLIP3, KCNIP3, EHD2, PID1, SCN3B, SPTBN4, KIF13A, KCNIP4, PKDCC, MYADM, TMEM88, RAB3C, CNST
BP	GO:0051208	sequestering of calcium ion	26/1554	3.83E-04	ABL1, ANK2, ANXA6, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, FGF2, GPER1, HRC, ITPR1, PDE4D, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SNCA, TRPC1, TRPA1, AKAP6, RASA3, JPH2, SLC25A23, JPH4
BP	GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	27/1554	4.03E-04	ADCY2, ADCY5, ADCY9, ADCYAP1, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP2B4, ADGRB3, CALCA, GNAL, GNAQ, GPR3, GPR26, GPER1, LHCGR, PDE4D, PRKCA, PTGER3, PTGER4, PTGFR, VIP, AKAP13, ADGRL4
BP	GO:0060323	head morphogenesis	12/1554	4.12E-04	MMP2, MSX1, MYH3, PDGFRA, RRAS, TGFB3, CLDN5, DKK1, TIPARP, CSRNP1, CRISPLD2, ARID5B
BP	GO:0007548	sex differentiation	43/1554	4.12E-04	ADCYAP1, ADCYAP1R1, AR, AXL, BCL2, BCL2L2, BMP5, BMPR1A, DACH1, ESR1, FGF9, FGF10, FLNA, GATA6, INHBB, KIT, LHCGR, KITLG, ROR2, PBX1, PDGFRA, PGR, PKD1, PTX3, RBP4, SALL1, SFRP1, SFRP2, SHH, SLIT3, TCF21, WNT2B, SLIT2, ADAMTS1, SEMA3A, SIRT1, ZFPM2, TIPARP, DHH, ASB1, ARID5B, OSR1, RNF38
BP	GO:0045927	positive regulation of growth	43/1554	4.12E-04	ACACB, ACTN3, BCL2, BDNF, BMPR1A, CDH4, DIO3, HBEGF, FGF2, FGF9, FGFR1, GATA6, GHR, HYAL1, IGF1, IL2, ILK, LRP1, MAP1B, MAPT, MEF2C, NGF, NTRK3, PRKN, PIM1, PROX1, CXCL12, SFRP1, SFRP2, SRF, SYT4, TBX5, TGFBR2, TGFBR3, WFS1, LGI1, CPNE6, NTN1, AKAP6, RIMS1, ZFPM2, TBX20, SPTBN4
BP	GO:0048708	astrocyte differentiation	19/1554	4.15E-04	ABL1, BIN1, ID2, ID4, IL6ST, LDLR, LIF, LRP1, MAPT, NTRK3, ROR1, ROR2, PLP1, SHH, TAL1, CNTN2, TSPAN2, LAMC3, SOX6
BP	GO:0048562	embryonic organ morphogenesis	45/1554	4.37E-04	ALDH1A3, EPHA2, EYA1, FBN1, EFEMP1, FGF9, FGF10, FGFR1, FOXF1, GLI2, HYAL1, ID2, MEF2C, MMP16, MSX1, ROR2, PDGFRA, PKD2, PROX1, RBP4, RYR2, SALL1, SHH, SRF, ZEB1, TCF21, TGFB3, TGFBR2, WNT9A, NR4A3, ITGA8, KCNQ4, HAND1, NTN1, HAND2, TSHZ1, SPRY2, LRIG1, SOBP, TBX20, DSCAML1, SOX17, OSR1, NOTO, RBPMS2
BP	GO:0033173	calcineurin-NFAT signaling cascade	13/1554	4.42E-04	ACTN3, ATP2B4, RCAN1, IGF1, NFATC1, NFATC2, NFATC4, PPP3CB, AKAP6, RCAN2, LMCD1, MYOZ2, C10orf71
BP	GO:0001666	response to hypoxia	53/1554	4.50E-04	ACVRL1, AK4, AQP1, BCL2, ZFP36L1, CAV1, CD34, CHRNA7, PLK3, EDNRA, EGR1, GATA6, ITPR1, KCNK2, KCNK3, KCNMA1, KCNMB1, MMP2, MPL, MYC, NR4A2, PAM, PTGIS, PTGS2, RORA, RYR2, CXCL12, SFRP1, SLC2A4, SLC8A1, SLC8A3, SOD3, SRF, STC1, TEK, TGFB3, TGFBR2, TGFBR3, THBS1,

					TRH, ADIPOQ, ROCK2, ARNT2, PPARGC1A, SIRT1, HIF3A, CPEB1, NDNF, APOLD1, MYOCD, CYGB, VASN, CPEB2
BP	GO:0060078	regulation of postsynaptic membrane potential	27/1554	4.50E-04	ADCYAP1, ADRB2, CBLN1, CHRNA7, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, KCNA1, MEF2C, MPP2, P2RX1, RELN, SNCA, NRXN1, NLGN1, IGSF9B, RIMS1, NLGN3, SLC17A7, TMEM108, LRRK2, RGS7BP
BP	GO:0051090	regulation of DNA-binding transcription factor activity	61/1554	4.60E-04	AR, CAMK2A, CAV1, CD40LG, CLU, CSF3, CX3CR1, CYP1B1, EDA, EPHA5, ESR1, FER, FLNA, FOS, ID2, JUN, KIT, SMAD7, CD200, ROR1, DDR2, ENPP1, PIM1, PKD1, PKD2, PRKCB, PRKD1, PROX1, RELN, PTCH1, PTGIS, CX3CL1, SGK1, SHH, SRF, TNFAIP3, WFS1, FOSL1, PLPP3, BCL10, LRRFIP1, RPS6KA5, KLF4, HAND1, HAND2, HDAC4, TRIB1, PPARGC1A, MID2, TRIM31, IRAK3, ERC1, SIRT1, TCEAL7, ARID5B, MYOCD, PPARGC1B, JMY, ABRA, SIK1, NWD1
BP	GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	11/1554	4.70E-04	ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, HRC, PDE4D, RYR2, SLC8A1, AKAP6
BP	GO:0035690	cellular response to drug	54/1554	4.81E-04	ABL1, ADCY2, ADCY5, ANXA1, AQP1, RHOB, ATP2B4, AXL, KLF9, CASQ2, CD69, CHRM2, CHRM3, CHRNA7, CRHBP, CYP1B1, EGR1, FYN, GNAQ, HGF, KCNH2, KCNMB1, MEF2C, MSX1, MYC, PPP1R12A, P2RY1, PRKN, PDE2A, PDE4B, PPP3CB, PRKAA2, PTGS2, RAP1A, RYR2, RYR3, SFRP1, SLC8A1, TNFAIP3, RNF112, NR4A3, KLF4, SLIT2, ADIPOQ, ROCK2, KLF2, PPARGC1A, KDM6B, SIRT1, ERRFI1, P2RY12, PDGFD, FBXO32, LRRK2
BP	GO:1902105	regulation of leukocyte differentiation	43/1554	4.82E-04	ABL1, ANXA1, AXL, PRDM1, ZFP36L1, CD28, EGR3, FBN1, FOS, GLI2, NCKAP1L, ID2, IL2, IL17A, IRF4, ITPKB, JUN, LIF, SMAD7, KITLG, MITF, MYC, NFATC2, ROR2, PIK3R1, PRKCA, SFRP1, SHH, TAL1, ZEB1, TGFBR2, KLF10, ZBTB16, GPR55, ADIPOQ, RASSF2, TESPA1, TRIB1, FGL2, VSIR, NFKBIZ, FCRL3, PPARGC1B
BP	GO:0051048	negative regulation of secretion	39/1554	4.85E-04	ADRA2A, ADRA2B, ANGPT1, ANXA1, ARG2, CD22, CD34, CIDEA, CRHBP, FOXF1, LRRC32, GRM7, INHBB, KCNB1, LIF, CD200, P2RY1, PRKN, PTGER3, PTGER4, RAP1A, CX3CL1, SFRP1, SNCA, SYT4, TACR2, TNFAIP3, TRH, FGF23, ADIPOQ, STXBP5L, IL1RAPL1, MAPKBP1, SYT11, STXBP6, P2RY12, MIDN, C1QTNF3, SSC5D
BP	GO:0051279	regulation of release of sequestered calcium ion into cytosol	19/1554	4.85E-04	ABL1, ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, GPER1, HRC, PDE4D, PKD2, RYR2, CX3CL1, SLC8A1, SNCA, TRPC1, AKAP6, JPH2, JPH4
BP	GO:0055013	cardiac muscle cell development	20/1554	4.88E-04	ACTC1, ACTN2, ADRA1A, IGF1, MEF2A, MYH11, PDGFRA, PROX1, RGS2, SGCB, SGCD, SLC8A1, SRF, SORBS2, MYOM2, AKAP6, PDLIM5, BVES, AKAP13, ALPK3
BP	GO:0033622	integrin activation	9/1554	4.96E-04	CDH17, PTGER4, CX3CL1, CXCL12, SELP, TLN1, CXCL13, FERMT2, P2RY12
BP	GO:0051953	negative regulation of amine transport	10/1554	5.04E-04	ADRA2A, ADRA2B, GRM7, P2RY1, RGS2, SNCA, SYT4, TRH, P2RY12, OSR1
BP	GO:0018105	peptidyl-serine phosphorylation	46/1554	5.15E-04	ANGPT1, ATP2B4, BCL2, BDKRB2, CAMK2A, CAV1, CSF3, DMD, DMPK, HGF, HRC, ILK, LIF, SMAD7, NTRK3, PDE4D, PKD1, PLCL1, PRKAA2, PRKACB, PRKCA, PRKCB, PRKD1, PTGS2, ROCK1, SFRP2, SGK1, SNCA, TGFBR2, TCL1A, DYRK3, DCLK1, RPS6KA5, ROCK2, RASSF2, AKT3, HIPK3, SPRY2, DKK1, LATS2, STK32B, SPTBN4, LRRK2, CSNK1A1L, CNKSR3, DCLK2
BP	GO:0051283	negative regulation of sequestering of calcium ion	25/1554	5.19E-04	ABL1, ANK2, ANXA6, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, FGF2, GPER1, HRC, ITPR1, PDE4D, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SNCA, TRPC1, TRPA1, AKAP6, RASA3, JPH2, JPH4
BP	GO:0030509	BMP signaling pathway	29/1554	5.23E-04	ABL1, ACVRL1, BMP5, BMPR1A, EGR1, FBN1, GDF2, CCN1, ILK, SMAD7, SMAD9, MSX1, ROR2, RYR2, SFRP1, SFRP2, TGFBR3, CHRD, FSTL1, DKK1, ZNF423, SPART, SOSTDC1, TMEM100, RGMA, GREM2, CHRDL1, BMPER, RBPMS2
BP	GO:0001558	regulation of cell growth	59/1554	5.26E-04	ABL1, ACVRL1, APBB1, BCL2, BDNF, CDH4, CDKN1A, DPYSL2, HBEGF, EPHA7, FHL1, GDF2, HYAL1, IGF1, IGFBP5, IL2, ILK, LRP1, MAP1B, MAPT, MSX1, NGF, NPR1, NTRK3, PRKN, ENPP1, RGS2, CXCL12, SFRP1, SFRP2, SGK1, SLIT3, SRF, SYT4, LTBP4, SOCS2, LGI1, SLIT2, CPNE6, NTN1, AKAP6, SEMA3A, OLFM1, FBLN5, FAM107A, RIMS1, SPART, SIRT1, SEMA3G, PRDM11, TSPYL2, SOX17, JADE1, RERG, PLXNA4, MYOCD, DCUN1D3, DACT3, OSTN
BP	GO:0072088	nephron epithelium morphogenesis	18/1554	5.56E-04	BCL2, EYA1, FGF2, GDNF, ILK, LIF, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, FAT4, OSR1
BP	GO:0045926	negative regulation of growth	40/1554	6.01E-04	ACVRL1, ADRB2, APBB1, BCL2, CDKN1A, EPHA7, FHL1, GDF2, HYAL1, IGFBP5, KCNK2, MEIS1, MSX1, MT1A, NPR1, ENPP1, PTCH1, RBP4, RGS2, SFRP1, SFRP2, SLIT3, TBX5, TGFBR2, SOCS2, SLIT2, NTN1, SEMA3A, SPART, SIRT1, SEMA3G, PRDM11, TSPYL2, SOX17, JADE1, RERG, NKD1, DCUN1D3, DACT3, OSTN
BP	GO:0007389	pattern specification process	62/1554	6.13E-04	ACVRL1, AR, BMP5, BMPR1A, C3, EGR2, ETS2, EYA1, FGF10, FGFR1, FOXF1, GDNF, GLI2, MEF2C, MEOX1, MSX1, ROR2, PBX1, PBX3, PCSK5, PITX2, PKD2, PRKACB, RELN, PTCH1, SFRP1, SFRP2, SHH,

					SRF, STC1, TBX5, ZEB1, TGFBR2, WNT2B, ZBTB16, BTG2, DCHS1, CHRD, NRP2, TBX18, HAND1, HAND2, ZEB2, TSHZ1, SPRY1, SEMA3A, DKK1, DAAM2, SOSTDC1, CDON, TBX20, DSCAML1, CC2D2A, SHROOM3, SOX17, GREM2, HHIP, WLS, NKD1, OSR1, GATA5, NOTO
BP	GO:0010464	regulation of mesenchymal cell proliferation	11/1554	6.28E-04	BMPR1A, FGF9, FGFR1, FOXF1, MYC, NFIB, SHH, ZEB1, TGFBR2, CHRD, FOXP2
BP	GO:0048008	platelet-derived growth factor receptor signaling pathway	15/1554	6.48E-04	ABL1, APOD, F3, FER, LRP1, PDGFRA, SNCA, NR4A3, ADIPOQ, TXNIP, TIPARP, CSRNP1, PDGFD, ARID5B, MYOCD
BP	GO:0060043	regulation of cardiac muscle cell proliferation	15/1554	6.48E-04	BMPR1A, FGF2, FGF9, FGFR1, GATA6, KCNK2, MEF2C, MEIS1, PIM1, RBP4, TBX5, TGFBR2, TGFBR3, ZFPM2, TBX20
BP	GO:0030510	regulation of BMP signaling pathway	20/1554	6.62E-04	ABL1, ACVRL1, FBN1, GDF2, CCN1, ILK, SMAD7, MSX1, SFRP1, SFRP2, CHRD, FSTL1, DKK1, ZNF423, SPART, SOSTDC1, GREM2, CHRDL1, BMPER, RBPMS2
BP	GO:1901215	negative regulation of neuron death	35/1554	6.62E-04	ANGPT1, AXL, BCL2, BDNF, CD34, CSF3, CX3CR1, FYN, GDNF, GRIK2, ILK, JUN, LRP1, MEF2C, CD200, NFATC4, NGF, NR4A2, PRKN, ROCK1, CX3CL1, SNCA, STXBP1, TGFB3, WFS1, BTG2, NR4A3, NES, PPARGC1A, FAIM2, SIRT1, NDNF, CPEB4, LRRK2, NCOA7
BP	GO:0014910	regulation of smooth muscle cell migration	19/1554	6.62E-04	BCL2, BMPR1A, LPAR1, FGF9, IGF1, IGFBP5, ILK, LRP1, MEF2C, TPM1, NR4A3, SLIT2, ADIPOQ, ADAMTS1, HDAC4, TRIB1, PPARGC1A, PDGFD, MYOCD
BP	GO:0051492	regulation of stress fiber assembly	19/1554	6.62E-04	ABL1, ARHGAP6, CCN2, S1PR1, LPAR1, PIK3R1, PTGER4, ROCK1, SFRP1, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, DLC1, ARHGEF15, TMEFF2, ARHGAP28, PHLDB2
BP	GO:1902803	regulation of synaptic vesicle transport	19/1554	6.62E-04	ADRA1A, CACNB2, CAMK2A, CHRM2, P2RX1, P2RY1, PRKN, PRKCB, RAP1A, SLC2A4, STXBP1, SYT4, PPFIA2, STXBP5L, RIMS3, NLGN1, RIMS1, NCS1, LRRK2
BP	GO:0010761	fibroblast migration	12/1554	6.86E-04	FER, FGF2, HAS1, ILK, DDR2, SLC8A1, THBS1, TNS1, AKAP12, CORO1C, ARID5B, CYGB
BP	GO:0071241	cellular response to inorganic substance	36/1554	6.99E-04	AQP1, AQP2, CRHBP, DLG2, FOS, FOSB, GSN, ID2, ITPKB, JUN, JUNB, JUND, KCNA1, KCNK3, MEF2A, MEF2C, MT1A, NFATC4, PRKN, PKD2, PRKAA2, PTGS2, RYR3, SHH, SNCA, SYT4, CACNA1H, CPNE6, RASA4, PPARGC1A, NLGN1, SYT11, CLIC4, SLC25A23, SYT15, LRRK2
BP	GO:1904064	positive regulation of cation transmembrane transport	27/1554	7.04E-04	ABL1, ACTN2, ADRB2, ANK2, ATP1B2, CACNA2D1, CACNB2, DMD, FLNA, GPER1, HSPA2, KCNA1, KCNH2, KCNMB1, PKD2, RELN, RYR2, CX3CL1, SNCA, STAC, TRPC1, RGN, AKAP6, NLGN3, JPH2, CNKSR3, LRRC52
BP	GO:0045669	positive regulation of osteoblast differentiation	16/1554	7.07E-04	BMPR1A, CEBPD, HGF, IGF1, CCN1, IL6R, IL6ST, ILK, JUND, MEF2C, DDR2, PRKD1, SFRP2, PDLIM7, ZHX3, TMEM119
BP	GO:0051897	positive regulation of protein kinase B signaling	31/1554	7.13E-04	ANGPT1, AXL, CD28, CSF3, CX3CR1, HBEGF, ESR1, F3, F10, FGF2, FGF7, FGF9, FGF10, FGFR1, FYN, HGF, IGFBP5, ILK, KIT, KITLG, PDGFRA, PIK3R1, CX3CL1, TEK, THBS1, FGF23, NRG2, SPRY2, RASD2, P2RY12, TNFAIP8L3
BP	GO:0051057	positive regulation of small GTPase mediated signal transduction	17/1554	7.50E-04	ADCYAP1R1, LPAR1, FGF10, GPR17, IGF1, ITPKB, KITLG, NGF, RELN, GPR55, MAPRE2, AKAP13, P2RY10, CDON, RASGRP4, ABRA, P2RY8
BP	GO:0018209	peptidyl-serine modification	48/1554	7.55E-04	ANGPT1, ATP2B4, BCL2, BDKRB2, CAMK2A, CAV1, CSF3, DCN, DMD, DMPK, HGF, HRC, ILK, LIF, SMAD7, NTRK3, PDE4D, PKD1, PLCL1, PRKAA2, PRKACB, PRKCA, PRKCB, PRKD1, PTGS2, ROCK1, SFRP2, SGK1, SNCA, TGFBR2, TCL1A, DYRK3, DCLK1, RPS6KA5, ROCK2, RASSF2, AKT3, HIPK3, SPRY2, DKK1, LATS2, STK32B, SPTBN4, NDNF, LRRK2, CSNK1A1L, CNKSR3, DCLK2
BP	GO:0003214	cardiac left ventricle morphogenesis	7/1554	7.56E-04	CPE, FOXF1, RYR2, SFRP2, TBX5, TGFBR2, HAND1
BP	GO:0021954	central nervous system neuron development	18/1554	7.62E-04	ADARB1, EPHB1, GLI2, MAPT, NFIB, NR4A2, SCN1B, CNTN2, BTG2, NRP2, DCLK1, SLIT2, ZEB2, SEMA3A, SALL3, SPTBN4, PLXNA4, DCLK2
BP	GO:0055021	regulation of cardiac muscle tissue growth	18/1554	7.62E-04	BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, RBP4, RGS2, TBX5, TGFBR2, TGFBR3, AKAP6, ZFPM2, TBX20
BP	GO:0061333	renal tubule morphogenesis	18/1554	7.62E-04	BCL2, EYA1, FGF2, GDNF, ILK, MEF2C, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, FAT4, OSR1
BP	GO:0072028	nephron morphogenesis	18/1554	7.62E-04	BCL2, EYA1, FGF2, GDNF, ILK, LIF, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, FAT4, OSR1
BP	GO:0043523	regulation of neuron apoptotic process	35/1554	7.81E-04	ANGPT1, AXL, BCL2, BDNF, CX3CR1, EPHA7, FYN, GDNF, GRID2, GRIK2, ILK, ITGA1, JUN, KCNB1, LRP1, MCL1, MEF2C, NFATC4, NGF, NR4A2, PRKN, ROCK1, CX3CL1, SNCA, STXBP1, TGFB3, WFS1, BTG2, NR4A3, HDAC4, NES, PPARGC1A, FAIM2, NDNF, CPEB4
BP	GO:0050803	regulation of synapse structure or activity	37/1554	7.92E-04	ABL1, ADGRB3, BDNF, CBLN1, CTNNA2, DGKB, EPHA7, EPHB1, FYN, GPM6A, GRID2, MEF2C, NFATC4, NTRK3, RELN, PTPRD, SNCA, TUBA1A, NRP2, NEURL1, NRXN1, NTN1, PDLIM5, IL1RAPL1, NLGN1,

					ARHGEF15, DKK1, FLRT2, NLGN3, SYBU, SLC17A7, CLSTN2, CTTNBP2, LRRC4B, LRRK2, LRRTM1, SHISA6
BP	GO:1903409	reactive oxygen species biosynthetic process	24/1554	7.94E-04	ABCD2, ARG2, ATP2B4, CAV1, CD34, CLU, CX3CR1, CYP1B1, FYN, HBB, PKD2, PTGIS, PTGS2, PTX3, RAB27A, RORA, SLC18A2, SNCA, RGN, KLF4, ROCK2, HDAC4, KLF2, MPV17L
BP	GO:0071875	adrenergic receptor signaling pathway	11/1554	8.12E-04	ADCY9, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP2B4, PDE4D, RGS2, AKAP13
BP	GO:0046631	alpha-beta T cell activation	26/1554	8.56E-04	ABL1, ANXA1, ARG2, BCL2, PRDM1, CD28, TNFSF8, CD55, GPR183, NCKAP1L, IL2, IL6R, IRF4, ITK, ITPKB, LY9, SMAD7, PTGER4, RORA, SATB1, SHH, TGFBR2, ZBTB16, PLA2G2D, VSIR, NFKBIZ
BP	GO:0072080	nephron tubule development	20/1554	8.69E-04	BCL2, EYA1, FGF2, GDNF, ILK, LIF, MEF2C, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, WWTR1, FAT4, OSR1
BP	GO:0097720	calcineurin-mediated signaling	13/1554	8.69E-04	ACTN3, ATP2B4, RCAN1, IGF1, NFATC1, NFATC2, NFATC4, PPP3CB, AKAP6, RCAN2, LMCD1, MYOZ2, C10orf71
BP	GO:0017156	calcium ion regulated exocytosis	28/1554	8.75E-04	ADRA1A, ADRA2A, CACNB2, CAMK2A, CHRM2, STX2, KCNB1, P2RX1, P2RY1, PPP3CB, PRKCB, RAP1A, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, STX11, CACNA1H, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, SYT15, PRRT2, LRRK2
BP	GO:0003151	outflow tract morphogenesis	18/1554	8.92E-04	BMPR1A, ELN, EYA1, GATA6, ILK, JUN, MEF2C, PITX2, SFRP2, TGFBR2, TGFBR3, CLDN5, NRP2, HAND2, ZFPM2, PARVA, TBX20, SOX17
BP	GO:0070661	leukocyte proliferation	45/1554	9.00E-04	ABL1, ANXA1, ARG2, BCL2, MS4A1, CD22, CD28, TNFSF8, CD40LG, CD79A, CDKN1A, CLU, CR2, CD55, GPR183, FGF10, FYN, LRRC32, NCKAP1L, IGF1, IGFBP2, IL2, IL5RA, IL6R, IL6ST, KIT, MEF2C, KITLG, MPL, NFATC2, NPR3, PPP3CB, SATB1, CX3CL1, SHH, TAC1, TGFBR2, TNFAIP3, PDE5A, TNFRSF13B, PLA2G2D, VSIR, FCRL3, TNFRSF13C, GAPT
BP	GO:0001658	branching involved in ureteric bud morphogenesis	15/1554	9.33E-04	BCL2, EYA1, FGF2, GDNF, ILK, MYC, PBX1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, FAT4
BP	GO:0010882	regulation of cardiac muscle contraction by calcium ion signaling	10/1554	9.33E-04	ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, HRC, RYR2, SLC8A1, HDAC4
BP	GO:0002683	negative regulation of immune system process	63/1554	9.35E-04	A2M, ADCYAP1, ANGPT1, ANXA1, APOD, ARG2, AXL, BMP5, BPI, ZFP36L1, CD22, CNR2, CD55, DUSP1, DUSP3, FBN1, FER, FOXF1, LRRC32, GPR17, GPER1, ID2, IL2, CXCR2, IRF4, ITPKB, LDLR, SMAD7, MEIS1, MEIS2, KITLG, CD200, MYC, PIK3R1, PPP3CB, PTGER4, CX3CL1, CXCL12, SFRP1, SHH, TAL1, TGFB3, THBS1, TNFAIP3, ZFP36, ZBTB16, PDE5A, BCL10, IL1RL1, GPR55, SLIT2, ADIPOQ, TRIB1, FGL2, EMILIN1, IRAK3, LRCH1, TNFRSF13B, PLA2G2D, IL17D, VSIR, FCRL3, NLRP6
BP	GO:0048771	tissue remodeling	31/1554	9.43E-04	ACVRL1, ADRB2, ANXA1, AXL, CALCA, CAV1, CSPG4, S1PR1, EPHA2, FGF10, IGFBP5, IL2, ITGB3, LEPR, LIF, MEF2C, MITF, MMP2, PDK4, PRKCA, ROCK1, SFRP1, TGFB3, TNFAIP3, GPR55, HAND2, ROCK2, RASSF2, RSPO3, PPARGC1B, TMEM119
BP	GO:0046632	alpha-beta T cell differentiation	21/1554	9.52E-04	ABL1, ANXA1, BCL2, PRDM1, TNFSF8, GPR183, NCKAP1L, IL2, IRF4, ITK, ITPKB, LY9, SMAD7, PTGER4, RORA, SATB1, SHH, TGFBR2, ZBTB16, PLA2G2D, NFKBIZ
BP	GO:1902905	positive regulation of supramolecular fiber organization	34/1554	9.56E-04	ABL1, ACTN2, BIN1, CFL2, CLU, CSF3, CCN2, CTNNA2, LPAR1, FER, FLNA, GSN, NCKAP1L, MAP1B, MAPT, PROX1, CX3CL1, SFRP1, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, CDC42EP2, CDC42EP3, DSTN, SYNPO, ARHGEF15, LMOD1, SNX9, LMOD3, NAV3, JMY, SYNPO2
BP	GO:0010721	negative regulation of cell development	50/1554	9.79E-04	ADCYAP1, BCL2, BMPR1A, BRINP1, DIO3, DPYSL3, LPAR1, S1PR3, EDNRB, EPHA7, FBN1, ID2, ID4, IGF1, LDLR, LRP1, MEIS1, NFATC4, NGFR, NPR2, NTRK3, PBX1, PMP22, RGS2, CX3CL1, SHH, SYT4, CNTN2, NR2F1, SLIT2, NTN1, ZNF536, SEMA3A, NLGN1, DKK1, SPART, DENND5A, DAAM2, CORO1C, NLGN3, SEMA3G, RGMA, TRAK2, DIXDC1, BMERB1, LRRK2, CNTN4, NEXMIF, OSTN, RFLNB
BP	GO:0043434	response to peptide hormone	60/1554	9.89E-04	ACTN2, ADCY2, ADCY5, ADCY9, ANXA1, ZFP36L1, CAMK2A, CAV1, CDO1, CRHBP, CCN2, EDNRB, EGR1, EGR2, FBN1, FER, FYN, GHR, GPER1, GRB10, NR4A1, IGFBP5, INHBB, JUND, LHCGR, MAP1B, NR4A2, OTC, PDE3B, PDK4, ENPP1, PIK3R1, PRKACB, PRKAR2B, PRKCB, PTGS2, ROCK1, CXCL12, SLC2A4, STAT5B, VAMP2, TEK, TGFBR3, BTG2, NR4A3, SOCS2, SOCS3, GLP2R, ADIPOQ, ROCK2, SORBS1, SIRT1, KLF15, ERRFI1, PID1, MBD5, ZNF106, CPEB1, GKAP1, CPEB2
BP	GO:0070167	regulation of biomineral tissue development	20/1554	9.89E-04	ADRB2, BMPR1A, S1PR1, GPM6B, CCN1, MEF2C, MGP, DDR2, OMD, ENPP1, ROCK1, SLC8A1, TGFB3, FGF23, ROCK2, ENAM, PKDCC, OSR1, TMEM119, RFLNB
BP	GO:0072171	mesonephric tubule morphogenesis	16/1554	9.89E-04	BCL2, EYA1, FGF2, GDNF, ILK, MYC, PBX1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, FAT4, OSR1
BP	GO:0010881	regulation of cardiac muscle contraction by regulation of the release	9/1554	9.92E-04	ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, HRC, RYR2, SLC8A1

		of sequestered calcium ion			
BP	GO:0086064	cell communication by electrical coupling involved in cardiac conduction	9/1554	9.92E-04	ATP1A2, ATP1B2, CACNA1C, CAV1, HRC, PDE4D, RYR2, SLC8A1, GJC1
BP	GO:0051209	release of sequestered calcium ion into cytosol	24/1554	9.94E-04	ABL1, ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, FGF2, GPER1, HRC, ITPR1, PDE4D, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SNCA, TRPC1, TRPA1, AKAP6, RASA3, JPH2, JPH4
BP	GO:0045214	sarcomere organization	14/1554	1.00E-03	ACTN2, CASQ2, CFL2, MEF2C, MYH3, PROX1, SRF, TNNT2, TPM1, MYOM2, KLHL41, LDB3, AKAP13, MYOZ2
BP	GO:0051402	neuron apoptotic process	38/1554	1.04E-03	ADARB1, ANGPT1, AXL, BCL2, BDNF, CX3CR1, DIO3, EPHA7, FYN, GDNF, GRID2, GRIK2, ILK, ITGA1, JUN, KCNB1, LRP1, MCL1, MEF2C, NFATC4, NGF, NGFR, NR4A2, PRKN, ROCK1, CX3CL1, SNCA, STXBP1, TGFB3, WFS1, BTG2, NR4A3, HDAC4, NES, PPARGC1A, FAIM2, NDNF, CPEB4
BP	GO:0021955	central nervous system neuron axonogenesis	11/1554	1.04E-03	ADARB1, EPHB1, GLI2, NFIB, NR4A2, SCN1B, DCLK1, SLIT2, ZEB2, SPTBN4, PLXNA4
BP	GO:0034767	positive regulation of ion transmembrane transport	28/1554	1.06E-03	ABL1, ACTN2, ADRB2, ANK2, ATP1B2, CACNA2D1, CACNB2, DMD, FLNA, GPER1, HSPA2, KCNA1, KCNH2, KCNMB1, ABCB1, PKD2, RELN, RYR2, CX3CL1, SNCA, STAC, TRPC1, RGN, AKAP6, NLGN3, JPH2, CNKSR3, LRRC52
BP	GO:0042551	neuron maturation	13/1554	1.06E-03	ADGRB3, BCL2, C3, EDNRB, NR4A2, CX3CL1, CNTN2, NFASC, RND1, VSX1, FEV, SPTBN4, LRRK2
BP	GO:0098868	bone growth	13/1554	1.06E-03	ANXA6, COL6A2, COL6A3, EVC, LEPR, MATN2, DDR2, STC1, TGFBR2, SCARA3, BNC2, COL21A1, OSTN
BP	GO:0044091	membrane biogenesis	12/1554	1.07E-03	CAV1, STX2, PTPRD, UGCG, NRXN1, NRXN2, MAGI2, IL1RAPL1, NLGN1, CLIP3, NLGN3, SERINC1
BP	GO:0050873	brown fat cell differentiation	12/1554	1.07E-03	ADRB2, PTGS2, RGS2, SLC2A4, ADIPOQ, ZNF516, PPARGC1A, SIRT1, PRDM16, EBF2, VSTM2A, FNDC5
BP	GO:0048863	stem cell differentiation	40/1554	1.09E-03	A2M, ABL1, ANXA6, BCHE, BMPR1A, EDNRA, EDNRB, ESR1, GATA6, GDNF, GPM6A, KIT, LIF, MEF2C, MEOX1, KITLG, MSX1, NRTN, PDGFRA, PITX2, SFRP1, SHH, SOX5, SRF, TAL1, TBX5, NRP2, HAND2, ZEB2, SEMA3A, CORO1C, SOX6, SEMA3G, SOX17, FAM172A, KBTBD8, MYOCD, OSR1, PRICKLE1, RBM24
BP	GO:0030217	T cell differentiation	38/1554	1.12E-03	ABL1, ANXA1, RHOH, BCL2, PRDM1, ZFP36L1, CD28, TNFSF8, CCR6, GPR183, EGR1, EGR3, GLI2, NCKAP1L, IL2, IRF4, ITK, ITPKB, KIT, LEPR, LY9, SMAD7, NFATC2, PPP3CB, PTGER4, RORA, SATB1, SHH, SRF, ZEB1, TGFBR2, ZBTB16, FZD7, TESPA1, FGL2, PLA2G2D, VSIR, NFKBIZ
BP	GO:0061326	renal tubule development	20/1554	1.12E-03	BCL2, EYA1, FGF2, GDNF, ILK, LIF, MEF2C, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, WWTR1, FAT4, OSR1
BP	GO:0071695	anatomical structure maturation	29/1554	1.16E-03	ACVRL1, ADGRB3, BCL2, C3, CDKN1A, CX3CR1, S1PR1, EDNRB, IGF1, MMP2, NPR2, NR4A2, PDE3A, PGR, CX3CL1, TAL1, CNTN2, RECK, DCHS1, KLF2, NFASC, RND1, VSX1, CEND1, FEV, SPTBN4, FAT4, LRRK2, RFLNB
BP	GO:0014855	striated muscle cell proliferation	18/1554	1.18E-03	ANGPT1, BMPR1A, EPHB1, FGF2, FGF9, FGFR1, GATA6, KCNK2, MEF2C, MEIS1, PIM1, RBP4, SHH, TBX5, TGFBR2, TGFBR3, ZFPM2, TBX20
BP	GO:0110110	positive regulation of animal organ morphogenesis	18/1554	1.18E-03	AR, CD34, FGF7, FGF10, FGFR1, GDNF, LIF, MYC, PIM1, TGFBR2, TNFAIP3, WNT2B, HAND2, ENAM, SPRY1, DKK1, FOXP2, GATA5
BP	GO:0072078	nephron tubule morphogenesis	17/1554	1.18E-03	BCL2, EYA1, FGF2, GDNF, ILK, MYC, PBX1, PKD1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, FAT4, OSR1
BP	GO:2000095	regulation of Wnt signaling pathway, planar cell polarity pathway	7/1554	1.19E-03	ABL1, SFRP1, SFRP2, DKK1, DACT1, RSPO3, NKD1
BP	GO:0001782	B cell homeostasis	10/1554	1.21E-03	ABL1, BCL2, NCKAP1L, MEF2C, TNFAIP3, BCL10, TNFRSF13B, TNFRSF13C, DOCK11, GAPT
BP	GO:0099068	postsynapse assembly	10/1554	1.21E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, NRXN2, MAGI2, NLGN1, NLGN3, LRRTM1
BP	GO:0008217	regulation of blood pressure	31/1554	1.22E-03	ACTA2, ACVRL1, ADRA1A, ADRA2B, ADRB2, ADRB3, AR, ATP1A2, CD34, CES1, EDNRA, EDNRB, EPHX2, HBB, ID2, NPR1, NPR2, NPR3, P2RX1, PCSK5, PDE4D, PTGS1, PTGS2, SGK1, TAC1, TACR3, TPM1, ADIPOQ, NAMPT, NCALD, UTS2B
BP	GO:0048608	reproductive structure development	59/1554	1.24E-03	ADCYAP1, ANXA1, AR, AXL, BCL2, BCL2L2, PRDM1, BMP5, ZFP36L1, DCN, ESR1, FGF9, FGF10, FLNA, GATA6, GLI2, ID4, CCN1, INHBB, JUNB, KIT, LHCGR, LIF, KITLG, ROR2, PDGFRA, PGR, PKD1, PKD2, PTCH1, PTGIS, PTGS2, PTX3, RBP4, SALL1, SFRP1, SFRP2, SHH, SLIT3, STC1, TCF21, WNT2B, FOSL1, SOCS3, SLIT2, HAND1, ADAMTS1, SEMA3A, SIRT1, ZFPM2, TIPARP, DHH, ASB1, ARID5B, RSPO3, MYOCD, OSR1, TCF23, RNF38

BP	GO:0097305	response to alcohol	37/1554	1.26E-03	ACTC1, ADCY2, ADCY5, ADCYAP1, ADCYAP1R1, KLF9, CDKN1A, CDO1, CRHBP, CSF3, CYP7A1, FOS, FOSB, FYN, GRIN2A, GSN, IL2, KCNMB1, NTRK3, PRKAA2, PTCH1, PTGER4, PTGFR, RBP4, RGS2, SFRP1, SLC2A4, SLIT3, TGFBR2, TGFBR3, TRH, FOSL1, KLF4, SLIT2, ADIPOQ, KLF2, SETD7
BP	GO:0007272	ensheathment of neurons	25/1554	1.26E-03	ABCD2, ANK2, ASPA, CLU, LPAR1, EGR2, HGF, ID4, ILK, MPZ, NTRK3, PLP1, PMP22, SLC8A3, CNTN2, CNTNAP1, SLC25A12, ARHGEF10, TSPAN2, WASF3, NFASC, DHH, PRX, FA2H, JAM3
BP	GO:0008366	axon ensheathment	25/1554	1.26E-03	ABCD2, ANK2, ASPA, CLU, LPAR1, EGR2, HGF, ID4, ILK, MPZ, NTRK3, PLP1, PMP22, SLC8A3, CNTN2, CNTNAP1, SLC25A12, ARHGEF10, TSPAN2, WASF3, NFASC, DHH, PRX, FA2H, JAM3
BP	GO:0032355	response to estradiol	25/1554	1.26E-03	ADCYAP1R1, ANXA1, BCL2L2, CRHBP, CCN2, DUSP1, ESR1, FGF10, GPER1, IGFBP2, MAP1B, PAM, PTCH1, PTGFR, PTGS2, SFRP1, SSTR1, STAT5B, STXBP1, TACR3, SOCS2, ARNT2, TXNIP, PPARGC1A, DHH
BP	GO:0099151	regulation of postsynaptic density assembly	6/1554	1.28E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, LRRTM1
BP	GO:0055023	positive regulation of cardiac muscle tissue growth	13/1554	1.28E-03	BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, MEF2C, PIM1, TBX5, TGFBR3, AKAP6, ZFPM2, TBX20
BP	GO:0007623	circadian rhythm	34/1554	1.31E-03	KLF9, CREM, CRY2, EGR1, EGR3, GNAQ, ID2, ID4, JUN, JUND, KCNA2, NFIL3, NGFR, NTRK3, PER1, PPP1CB, PRKAA2, PROX1, RORA, RORB, KLF10, PER3, PER2, USP2, ADIPOQ, ROCK2, NAMPT, PPARGC1A, NLGN1, SIRT1, PROK1, CIPC, OPN4, SIK1
BP	GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	11/1554	1.31E-03	ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, HRC, PDE4D, RYR2, SLC8A1, AKAP6
BP	GO:0010470	regulation of gastrulation	12/1554	1.33E-03	BMPR1A, FGFR1, IL1RN, SFRP2, FZD7, KLF4, ADIPOQ, DKK1, SOX17, PHLDB2, MYADM, OSR1
BP	GO:0010613	positive regulation of cardiac muscle hypertrophy	12/1554	1.33E-03	ADRA1A, IGF1, IL6ST, MEF2A, PRKCA, ROCK1, TRPC3, NR4A3, PDE5A, HAND2, AKAP6, ROCK2
BP	GO:0016079	synaptic vesicle exocytosis	23/1554	1.33E-03	ADRA1A, CACNB2, CAMK2A, CHRM2, STX2, P2RX1, P2RY1, PRKCB, RAP1A, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, STX11, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, PRRT2, LRRK2
BP	GO:0002053	positive regulation of mesenchymal cell proliferation	9/1554	1.33E-03	BMPR1A, FGF9, FGFR1, FOXF1, MYC, SHH, TGFBR2, CHRD, FOXP2
BP	GO:0072202	cell differentiation involved in metanephros development	9/1554	1.33E-03	CD34, GDNF, LIF, SALL1, TCF21, ADIPOQ, WWTR1, FAT4, OSR1
BP	GO:1904861	excitatory synapse assembly	9/1554	1.33E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, NRXN2, NLGN1, LRRC4, LRRTM1
BP	GO:0030279	negative regulation of ossification	18/1554	1.34E-03	BCL2, GDF10, ID2, IGFBP5, MEF2C, ENPP1, PTCH1, RORB, SFRP1, FGF23, CHRD, HAND2, HDAC4, DKK1, TWIST2, RANBP3L, OSTN, RFLNB
BP	GO:0043491	protein kinase B signaling	41/1554	1.34E-03	ANGPT1, AXL, ZFP36L1, CD28, PLK3, CSF3, CX3CR1, HBEGF, EPHA2, ESR1, F3, F10, FGF2, FGF7, FGF9, FGF10, FGFR1, FYN, GPER1, HGF, IGF1, IGFBP5, ILK, KIT, KITLG, PDGFRA, PIK3R1, RRAS, CX3CL1, TEK, THBS1, FGF23, KLF4, NRG2, MAGI2, SPRY2, SIRT1, RASD2, TMEM100, P2RY12, TNFAIP8L3
BP	GO:0051580	regulation of neurotransmitter uptake	8/1554	1.34E-03	ATP1A2, GDNF, GPM6B, ITGB3, PRKN, RGS2, SNCA, PER2
BP	GO:0086014	atrial cardiac muscle cell action potential	8/1554	1.34E-03	ANK2, CACNA1C, CACNB2, FLNA, KCNJ3, RYR2, GJC1, SCN3B
BP	GO:0086026	atrial cardiac muscle cell to AV node cell signaling	8/1554	1.34E-03	ANK2, CACNA1C, CACNB2, FLNA, KCNJ3, RYR2, GJC1, SCN3B
BP	GO:0086066	atrial cardiac muscle cell to AV node cell communication	8/1554	1.34E-03	ANK2, CACNA1C, CACNB2, FLNA, KCNJ3, RYR2, GJC1, SCN3B
BP	GO:0098698	postsynaptic specialization assembly	8/1554	1.34E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, NRXN2, NLGN1, LRRTM1
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	32/1554	1.38E-03	ABL1, ADRA1A, ADRA2A, ANGPT1, BDNF, CNTN1, CSF3, CSPG4, HBEGF, FGF7, FGF10, FYN, GHR, HGF, IGF1, IL2, IL3, IL6R, IL6ST, ITGA5, ITGB3, KIT, LIF, KITLG, PECAM1, RELN, TAL1, SOCS3, NEURL1, ADIPOQ, TSLP, ALKAL2

BP	GO:0048813	dendrite morphogenesis	26/1554	1.38E-03	ADGRB3, CAMK2A, CHRNA7, CTNNA2, EPHB1, FYN, ILK, MAP6, MEF2A, NFATC4, RELN, PTPRD, SDC2, VLDLR, DCLK1, SEMA3A, PDLIM5, IL1RAPL1, NLGN1, TNIK, NLGN3, TRAK2, FBXO31, PREX2, LRRK2, PHACTR1
BP	GO:0043010	camera-type eye development	46/1554	1.38E-03	ACVRL1, ALDH1A3, ATP2B4, CACNA1C, COL8A2, CYP1B1, DCX, DIO3, EPHA2, EPHB1, FBN1, EFEMP1, FGF10, GPM6A, JUN, MEIS1, MITF, NTRK3, PDGFRA, PITX2, PROX1, RBP4, RORB, SHH, SRF, ZEB1, TGFBR2, TMOD1, TUB, WNT2B, WNT9A, MYOM2, KLF4, ZEB2, LAMC3, MAB21L2, NES, ARHGEF15, VSX1, CDON, SLC17A7, RHOJ, CC2D2A, FOXP2, SLC25A25, UNC45B
BP	GO:0051495	positive regulation of cytoskeleton organization	36/1554	1.38E-03	ABL1, ACTN2, BIN1, CFL2, CSF3, CCN2, CTNNA2, LPAR1, FER, FLNA, GSN, NCKAP1L, MAP1B, MAPT, NTRK3, PROX1, CX3CL1, SFRP1, TAC1, TEK, TGFB3, TPM1, ROCK2, ARHGEF10, CDC42EP2, CDC42EP3, NES, DSTN, SYNPO, ARHGEF15, LMOD1, SNX9, LMOD3, NAV3, JMY, SYNPO2
BP	GO:0071229	cellular response to acid chemical	34/1554	1.39E-03	AQP1, AQP2, BRINP1, EGR1, EPHA3, FYN, KCNMB1, LDLR, MMP2, NFATC4, NTRK3, PDGFRA, PDK4, PKD2, PRKAA2, PTGER4, PTGFR, RORB, SFRP1, ZEB1, WNT9A, FZD7, NEURL1, KLF4, KLF2, PPARGC1A, FZD10, CPEB3, PID1, RRAGD, CPEB1, PDGFD, CPEB4, OSR1
BP	GO:0001938	positive regulation of endothelial cell proliferation	22/1554	1.40E-03	ACVRL1, EGR3, F3, FGF2, FGFR1, GDF2, NR4A1, ITGB3, JUN, PRKCA, PRKD1, PROX1, CXCL12, TEK, VIP, DYSF, TNFSF12, NRP2, AKT3, SIRT1, PPP1R16B, JCAD
BP	GO:0003279	cardiac septum development	22/1554	1.40E-03	ANK2, PRDM1, BMP5, BMPR1A, GATA6, ID2, CCN1, SMAD7, PCSK5, PDE2A, PROX1, SALL1, SLIT3, TBX5, TGFBR2, TGFBR3, NRP2, SLIT2, HAND1, ZFPM2, PARVA, TBX20
BP	GO:0017158	regulation of calcium ion-dependent exocytosis	22/1554	1.40E-03	ADRA1A, ADRA2A, CACNB2, CAMK2A, CHRM2, KCNB1, P2RX1, P2RY1, PRKCB, RAP1A, STXBP1, SYT4, PPFIA2, CACNA1H, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, SYT15, LRRK2
BP	GO:0061458	reproductive system development	59/1554	1.41E-03	ADCYAP1, ANXA1, AR, AXL, BCL2, BCL2L2, PRDM1, BMP5, ZFP36L1, DCN, ESR1, FGF9, FGF10, FLNA, GATA6, GLI2, ID4, CCN1, INHBB, JUNB, KIT, LHCGR, LIF, KITLG, ROR2, PDGFRA, PGR, PKD1, PKD2, PTCH1, PTGIS, PTGS2, PTX3, RBP4, SALL1, SFRP1, SFRP2, SHH, SLIT3, STC1, TCF21, WNT2B, FOSL1, SOCS3, SLIT2, HAND1, ADAMTS1, SEMA3A, SIRT1, ZFPM2, TIPARP, DHH, ASB1, ARID5B, RSPO3, MYOCD, OSR1, TCF23, RNF38
BP	GO:0050807	regulation of synapse organization	35/1554	1.44E-03	ABL1, ADGRB3, BDNF, CBLN1, CTNNA2, DGKB, EPHA7, EPHB1, FYN, GPM6A, GRID2, MEF2C, NFATC4, NTRK3, RELN, PTPRD, SNCA, TUBA1A, NRP2, NEURL1, NRXN1, NTN1, PDLIM5, IL1RAPL1, NLGN1, ARHGEF15, DKK1, FLRT2, NLGN3, CLSTN2, CTTNBP2, LRRC4B, LRRK2, LRRTM1, SHISA6
BP	GO:0003014	renal system process	23/1554	1.45E-03	ADCY2, ADCY5, ADCY9, ADRA1A, AQP1, AQP2, BCL2, CD34, EDNRB, GSN, HBB, KCNMA1, MCAM, NPR1, NPR3, PCSK5, PRKACB, PRKAR2B, SGK1, STC1, TAC1, WFS1, ADIPOQ
BP	GO:0014033	neural crest cell differentiation	19/1554	1.46E-03	ANXA6, BMPR1A, EDNRA, EDNRB, GDNF, MEF2C, KITLG, NRTN, PITX2, SFRP1, SHH, NRP2, HAND2, ZEB2, SEMA3A, CORO1C, SEMA3G, FAM172A, KBTBD8
BP	GO:0015844	monoamine transport	19/1554	1.46E-03	ADRA2A, ADRA2B, GDNF, GPM6B, ITGB3, KCNA2, KCNB1, P2RX1, P2RY1, PRKN, CXCL12, SLC18A2, SLC22A3, SNCA, SYT4, VIP, SYT11, P2RY12, SYT15
BP	GO:0051961	negative regulation of nervous system development	46/1554	1.46E-03	ADCYAP1, BMPR1A, BRINP1, DIO3, DPYSL3, LPAR1, EDNRB, EPHA7, ID2, ID4, LDLR, LRP1, MEIS1, NFATC4, NGFR, NTRK3, PBX1, PMP22, PRKACB, CX3CL1, SHH, SYT4, CNTN2, NR2F1, CHRD, SLIT2, NTN1, ZNF536, SEMA3A, NLGN1, ARHGEF15, DKK1, SPART, DENND5A, DAAM2, CEND1, NLGN3, SEMA3G, RGMA, TRAK2, DIXDC1, BMERB1, LRRK2, CNTN4, NEXMIF, OSTN
BP	GO:1990138	neuron projection extension	29/1554	1.46E-03	ABL1, CDH4, DPYSL2, ILK, LRP1, MAP1B, MAPT, NDN, NTRK3, PRKN, PPP3CB, CXCL12, SLIT3, SRF, SYT4, VCL, NRP2, DCLK1, SLIT2, CPNE6, NTN1, SEMA3A, OLFM1, RIMS1, NLGN3, SEMA3G, TMEM108, PLXNA4, OSTN
BP	GO:1902305	regulation of sodium ion transmembrane transport	15/1554	1.48E-03	ATP1A2, ATP1B2, ATP2B4, DMD, STOM, SCN1B, SCN2B, SCN4B, SNTA1, UTRN, SLMAP, FXYD6, SCN3B, OSR1, CNKSR3
BP	GO:0048546	digestive tract morphogenesis	13/1554	1.51E-03	BCL2, FGF10, FOXF1, GLI2, ID2, PDGFRA, SFRP1, SFRP2, SHH, TCF21, DACT1, SOX17, RBPMS2
BP	GO:0071880	adenylate cyclase-activating adrenergic receptor signaling pathway	10/1554	1.52E-03	ADCY9, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, ATP2B4, PDE4D, AKAP13
BP	GO:0099174	regulation of presynapse organization	10/1554	1.52E-03	CBLN1, NTRK3, PTPRD, SNCA, NRXN1, IL1RAPL1, NLGN1, DKK1, NLGN3, LRRTM1
BP	GO:0099625	ventricular cardiac muscle cell membrane repolarization	10/1554	1.52E-03	ANK2, CACNA2D1, KCND3, KCNH2, KCNJ3, KCNJ8, SCN1B, SCN4B, SNTA1, KCNE4

BP	GO:0030500	regulation of bone mineralization	17/1554	1.52E-03	ADRB2, BMPR1A, S1PR1, GPM6B, CCN1, MEF2C, MGP, DDR2, OMD, ENPP1, SLC8A1, TGFB3, FGF23, PKDCC, OSR1, TMEM119, RFLNB
BP	GO:0060411	cardiac septum morphogenesis	17/1554	1.52E-03	BMP5, BMPR1A, GATA6, ID2, CCN1, SMAD7, PROX1, SLIT3, TBX5, TGFBR2, TGFBR3, NRP2, SLIT2, HAND1, ZFPM2, PARVA, TBX20
BP	GO:0001953	negative regulation of cell-matrix adhesion	12/1554	1.58E-03	ACVRL1, APOD, ARHGAP6, LRP1, PIK3R1, THBS1, DLC1, FAM107A, CORO1C, AJAP1, PHLDB2, NEXMIF
BP	GO:0014742	positive regulation of muscle hypertrophy	12/1554	1.58E-03	ADRA1A, IGF1, IL6ST, MEF2A, PRKCA, ROCK1, TRPC3, NR4A3, PDE5A, HAND2, AKAP6, ROCK2
BP	GO:0014912	negative regulation of smooth muscle cell migration	11/1554	1.60E-03	BMPR1A, IGFBP5, ILK, LRP1, MEF2C, TPM1, SLIT2, ADIPOQ, TRIB1, PPARGC1A, MYOCD
BP	GO:1903514	release of sequestered calcium ion into cytosol by endoplasmic reticulum	11/1554	1.60E-03	ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, HRC, PDE4D, RYR2, SLC8A1, AKAP6
BP	GO:0099504	synaptic vesicle cycle	32/1554	1.60E-03	ADRA1A, AMPH, CACNB2, CAMK2A, CHRM2, STX2, P2RX1, P2RY1, PPP3CB, PRKCB, RAP1A, ROCK1, SLC2A4, SLC18A2, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, STX11, NRXN1, STXBP5L, RIMS3, MAGI2, NLGN1, RIMS1, SYT11, NCS1, NLGN3, SLC17A7, PRRT2, LRRK2
BP	GO:0048675	axon extension	23/1554	1.60E-03	ABL1, CDH4, DPYSL2, ILK, LRP1, MAP1B, MAPT, NDN, NTRK3, PPP3CB, CXCL12, SLIT3, SRF, VCL, NRP2, DCLK1, SLIT2, NTN1, SEMA3A, OLFM1, NLGN3, SEMA3G, PLXNA4
BP	GO:0051963	regulation of synapse assembly	21/1554	1.67E-03	ADGRB3, BDNF, CBLN1, EPHA7, EPHB1, GRID2, MEF2C, NTRK3, PTPRD, SNCA, NRXN1, NTN1, PDLIM5, IL1RAPL1, NLGN1, DKK1, FLRT2, NLGN3, CLSTN2, LRRC4B, LRRTM1
BP	GO:0046622	positive regulation of organ growth	15/1554	1.73E-03	ACACB, BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, MEF2C, PIM1, PROX1, TBX5, TGFBR3, AKAP6, ZFPM2, TBX20
BP	GO:0060074	synapse maturation	9/1554	1.73E-03	CX3CR1, NFIA, NFATC4, PALM, RELN, NEURL1, NRXN1, ARHGEF15, SYBU
BP	GO:0060314	regulation of ryanodine-sensitive calcium-release channel activity	9/1554	1.73E-03	CASQ2, CLIC2, DMD, HRC, PDE4D, PKD2, AKAP6, JPH2, JPH4
BP	GO:0060914	heart formation	9/1554	1.73E-03	BMPR1A, EYA1, MEF2C, PIM1, TBX5, HAND2, DKK1, SOX17, GATA5
BP	GO:0043542	endothelial cell migration	41/1554	1.73E-03	ABL1, ACVRL1, ANGPT1, ANXA1, RHOB, CYP1B1, DCN, EGR3, EPHA2, FGF2, FGFR1, GDF2, NR4A1, ITGB3, MEF2C, PECAM1, PRKCA, PRKD1, PROX1, PTGS2, SRF, STC1, TEK, THBS1, TNFSF12, NRP2, KLF4, SLIT2, ROCK2, AKT3, CXCL13, SIRT1, ADGRA2, ADAMTS9, RHOJ, JCAD, ATOH8, STARD13, AMOTL1, CLEC14A, BMPER
BP	GO:2000377	regulation of reactive oxygen species metabolic process	32/1554	1.73E-03	ABCD2, ARG2, ATP2B4, BCL2, CAV1, CD34, CDKN1A, CLU, CX3CR1, CYP1B1, GADD45A, FYN, HBB, MAPT, PRKN, PKD2, PTGIS, PTGS2, PTX3, RAB27A, SLC18A2, SNCA, TGFBR2, THBS1, RGN, KLF4, ROCK2, HDAC4, KLF2, FBLN5, PID1, MPV17L
BP	GO:0001780	neutrophil homeostasis	7/1554	1.73E-03	ANXA1, AXL, CXCR2, ITPKB, MPL, PDE4B, JAM3
BP	GO:0055119	relaxation of cardiac muscle	7/1554	1.73E-03	ATP1A2, HRC, PDE4B, PDE4D, RGS2, SLC8A1, PDE5A
BP	GO:0071871	response to epinephrine	7/1554	1.73E-03	ATP2B4, PDE4B, PDE4D, RYR2, SNCA, ADIPOQ, PPARGC1A
BP	GO:1900242	regulation of synaptic vesicle endocytosis	7/1554	1.73E-03	PPP3CB, ROCK1, SLC2A4, NLGN1, SYT11, SLC17A7, LRRK2
BP	GO:0006809	nitric oxide biosynthetic process	17/1554	1.74E-03	ARG2, ATP2B4, CAV1, CD34, CLU, CX3CR1, CYP1B1, HBB, PKD2, PTGIS, PTGS2, PTX3, RORA, RGN, KLF4, ROCK2, KLF2
BP	GO:0002931	response to ischemia	13/1554	1.80E-03	BCL2, CAMK2A, CAV1, CX3CR1, EGR1, CX3CL1, PER2, ROCK2, PPARGC1A, BVES, FAIM2, NDNF, CPEB4
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	39/1554	1.81E-03	ABL1, ADRA1A, ADRA2A, ANGPT1, BDNF, CAV1, CNTN1, CSF3, CSPG4, HBEGF, EPHA7, FGF7, FGF10, FYN, GHR, HGF, IGF1, IL2, IL3, IL6R, IL6ST, ITGA5, ITGB3, KIT, LIF, KITLG, PECAM1, RELN, SFRP1, SFRP2, TAL1, SOCS3, GPRC5A, NEURL1, ADIPOQ, ERRFI1, PDGFD, TSLP, ALKAL2
BP	GO:0042542	response to hydrogen peroxide	26/1554	1.81E-03	ABL1, ANXA1, AQP1, RHOB, AXL, BCL2, CYP1B1, DUSP1, FYN, GNAO1, HBB, HGF, JUN, SLC8A1, TNFAIP3, RNF112, NR4A3, FOSL1, TRPA1, KLF4, KLF2, TXNIP, KDM6B, SIRT1, PDGFD, LRRK2
BP	GO:0043153	entrainment of circadian clock by photoperiod	8/1554	1.84E-03	CRY2, ID2, PER1, PPP1CB, PER3, PER2, USP2, SIK1
BP	GO:0010769	regulation of cell morphogenesis involved in differentiation	44/1554	1.86E-03	ABL1, ADGRB3, BDNF, CDH4, DPYSL2, EPHA7, FLNA, ILK, LRP1, MAP1B, MAP6, MAPT, MPL, NFATC4, NGF, NGFR, NTRK3, RELN, PTPRD, SDC2, CXCL12, SRF, CNTN2, SLIT2, NTN1, ZEB2, UST, SEMA3A, OLFM1, PDLIM5, IL1RAPL1, NLGN1, TNIK, SPART, CORO1C, NLGN3, SEMA3G, ZSWIM5, ZSWIM6, TRAK2, FBXO31, PLXNA4, MYADM, LRRK2

BP	GO:0003197	endocardial cushion development	12/1554	1.91E-03	ACVRL1, BMP5, BMPR1A, FOXF1, MSX1, TBX5, TGFBR2, DCHS1, TMEM100, TBX20, GATA5, RBM24
BP	GO:0003416	endochondral bone growth	12/1554	1.91E-03	ANXA6, COL6A2, COL6A3, EVC, MATN2, DDR2, STC1, TGFBR2, SCARA3, BNC2, COL21A1, OSTN
BP	GO:0014003	oligodendrocyte development	12/1554	1.91E-03	ASPA, CLU, LPAR1, GSN, ID2, ID4, PLP1, SHH, CNTN2, CNTNAP1, WASF3, FA2H
BP	GO:0035850	epithelial cell differentiation involved in kidney development	12/1554	1.91E-03	ACTA2, CD34, GDNF, LIF, MEF2C, SALL1, ADIPOQ, MAGI2, WWTR1, KLF15, FAT4, OSR1
BP	GO:0044706	multi-multicellular organism process	35/1554	1.91E-03	ADCYAP1, ADRA2B, AR, BCL2, PRDM1, CALCA, CRHBP, ESR1, FOS, FOSB, PRLHR, IGFBP2, IGFBP5, ITGA5, JUNB, LIF, MMP2, P2RX1, PAM, PCSK5, PGR, PTGFR, PTGIS, PTGS2, RGS2, STC1, TAC1, TGFB3, TGFBR2, FOSL1, RECK, PLA2G4C, NAMPT, MAFF, TCF23
BP	GO:0046660	female sex differentiation	22/1554	1.91E-03	ADCYAP1, ADCYAP1R1, AXL, BCL2, DACH1, ESR1, FGF10, INHBB, KIT, KITLG, PDGFRA, PGR, PTX3, RBP4, SFRP1, SLIT3, SLIT2, ADAMTS1, SIRT1, ZFPM2, TIPARP, ARID5B
BP	GO:0007616	long-term memory	10/1554	1.91E-03	GRIA1, LDLR, NFATC4, RELN, SGK1, SRF, TAC1, PJA2, CPEB3, SLC17A7
BP	GO:0045987	positive regulation of smooth muscle contraction	10/1554	1.91E-03	ADRA1A, ADRA2B, CHRM3, GPER1, KIT, PTGS2, SRF, TACR2, TACR3, MYOCD
BP	GO:0097479	synaptic vesicle localization	28/1554	1.91E-03	ADRA1A, CACNB2, CAMK2A, CHRM2, STX2, P2RX1, P2RY1, PRKN, PRKCB, RAB27A, RAP1A, SLC2A4, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, STX11, STXBP5L, RIMS3, MAGI2, NLGN1, RIMS1, SYT11, NCS1, NLGN3, PRRT2, LRRK2
BP	GO:0014888	striated muscle adaptation	14/1554	1.91E-03	ACTN3, ATP2B4, GATA6, GSN, IGFBP5, MEF2C, TRPC3, HDAC4, PPARGC1A, KLF15, MYOZ2, ERRFI1, TRIM63, MLIP
BP	GO:0014031	mesenchymal cell development	18/1554	1.91E-03	ANXA6, BCL2, BMPR1A, EDNRA, EDNRB, GDNF, KITLG, NRTN, PITX2, SHH, NRP2, HAND2, ZEB2, SEMA3A, CORO1C, SEMA3G, FAM172A, KBTBD8
BP	GO:1904705	regulation of vascular smooth muscle cell proliferation	18/1554	1.91E-03	BMPR1A, CDKN1A, CNN1, FGF2, FGF9, GPER1, IGF1, IGFBP5, JUN, MEF2C, MEF2D, MMP2, TGFB3, TPM1, NR4A3, ADIPOQ, ADAMTS1, MYOCD
BP	GO:1990874	vascular smooth muscle cell proliferation	18/1554	1.91E-03	BMPR1A, CDKN1A, CNN1, FGF2, FGF9, GPER1, IGF1, IGFBP5, JUN, MEF2C, MEF2D, MMP2, TGFB3, TPM1, NR4A3, ADIPOQ, ADAMTS1, MYOCD
BP	GO:0051928	positive regulation of calcium ion transport	23/1554	1.94E-03	ABL1, ADCYAP1R1, ANK2, CACNA2D1, CACNB2, CAMK2A, CAV1, GPER1, HSPA2, MYLK, PKD2, RYR2, CX3CL1, CXCL12, SNCA, STAC, STC1, TRPC1, TRPC3, WFS1, RGN, AKAP6, JPH2
BP	GO:0060045	positive regulation of cardiac muscle cell proliferation	11/1554	1.94E-03	BMPR1A, FGF2, FGF9, FGFR1, GATA6, MEF2C, PIM1, TBX5, TGFBR3, ZFPM2, TBX20
BP	GO:0071867	response to monoamine	11/1554	1.94E-03	ABL1, ATP2B4, PRKN, PDE4B, PDE4D, RYR2, SNCA, NR4A3, ADIPOQ, PPARGC1A, LRRK2
BP	GO:0071869	response to catecholamine	11/1554	1.94E-03	ABL1, ATP2B4, PRKN, PDE4B, PDE4D, RYR2, SNCA, NR4A3, ADIPOQ, PPARGC1A, LRRK2
BP	GO:0010827	regulation of glucose transmembrane transport	17/1554	1.96E-03	C3, EDNRA, GRB10, IGF1, MEF2A, ENPP1, PIK3R1, PRKCB, RAP1A, NR4A3, ADIPOQ, SORBS1, CLIP3, KLF15, PRKAG2, PID1, OSTN
BP	GO:2000300	regulation of synaptic vesicle exocytosis	17/1554	1.96E-03	ADRA1A, CACNB2, CAMK2A, CHRM2, P2RX1, P2RY1, PRKCB, RAP1A, STXBP1, SYT4, PPFIA2, STXBP5L, RIMS3, NLGN1, RIMS1, NCS1, LRRK2
BP	GO:1900449	regulation of glutamate receptor signaling pathway	15/1554	1.97E-03	ACTN2, ADRB2, CRHBP, DLG2, FYN, GRIA1, GRIN2A, MEF2C, RELN, CX3CL1, PPARGC1A, NLGN1, NLGN3, GSG1L, SHISA6
BP	GO:0006979	response to oxidative stress	60/1554	2.01E-03	ABL1, ANXA1, APOD, AQP1, RHOB, AXL, BCL2, PLK3, CYP1B1, DUSP1, STX2, FER, FOS, FYN, GNAO1, GPX3, HBB, HGF, HYAL1, JUN, MAPT, MCL1, MMP2, NR4A2, PRKN, PDGFRA, PKD2, PRKAA2, PRKD1, PTGS1, PTGS2, SELENOP, SLC8A1, SNCA, SOD3, TNFAIP3, TPM1, TXNRD1, RNF112, NR4A3, FOSL1, TRPA1, RGN, KLF4, ADIPOQ, KLF2, FBLN5, TXNIP, PPARGC1A, RBPMS, KDM6B, SIRT1, SCARA3, PDGFD, CYGB, LRRK2, CPEB2, PPARGC1B, NCOA7, MSRB3
BP	GO:0099150	regulation of postsynaptic specialization assembly	6/1554	2.01E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, LRRTM1
BP	GO:0150052	regulation of postsynapse assembly	6/1554	2.01E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, LRRTM1

BP	GO:0071496	cellular response to external stimulus	48/1554	2.01E-03	AQP1, AQP2, ATF3, ATP1A2, AXL, BCL2, CDKN1A, GADD45A, FOS, FYN, INHBB, JUN, KCNB1, NR4A2, P2RY1, PDE2A, PDK4, PIM1, PRKAA2, PRKD1, PTGER4, PTGS2, RYR3, SFRP1, SFRP2, SRF, KLF10, WNT2B, FOSL1, FGF23, BCL10, BAG3, HDAC4, NAMPT, FAM107A, HABP4, SIRT1, GABARAPL1, KANK2, RRAGD, PIEZO2, P2RY12, CPEB4, MYOCD, LRRK2, SIK1, TMEM150C, SIK1B
BP	GO:0043406	positive regulation of MAP kinase activity	39/1554	2.02E-03	ADRA2A, ADRA2B, CD40LG, CHRNA7, MAP3K8, CSPG4, GADD45A, DUSP5, LPAR1, FGF2, FGF10, FGFR1, GHR, HGF, IGF1, ILK, ITGA1, KIT, KITLG, GADD45B, NGF, NTRK3, ROR2, TGFB3, THBS1, TPD52L1, PDE5A, ZEB2, FZD10, AKAP13, DKK1, TNIK, MAP3K20, AVPI1, PDGFD, PROK1, LRRK2, DUSP19, SAMD5
BP	GO:0035249	synaptic transmission, glutamatergic	19/1554	2.06E-03	ADCYAP1, ATP1A2, GRID2, GRIK2, GRIK3, GRM7, MEF2C, ROR2, P2RX1, PRKN, RELN, PTGS2, STXBP1, NRXN1, NLGN1, DKK1, NLGN3, SLC17A7, LRRK2
BP	GO:0021782	glial cell development	22/1554	2.10E-03	ASPA, CLU, LPAR1, GSN, ID2, ID4, ILK, LDLR, LRP1, MAPT, NTRK3, ROR1, ROR2, PLP1, SHH, CNTN2, CNTNAP1, ARHGEF10, TSPAN2, LAMC3, WASF3, FA2H
BP	GO:0045668	negative regulation of osteoblast differentiation	13/1554	2.10E-03	GDF10, ID2, IGFBP5, PTCH1, RORB, SFRP1, FGF23, CHRD, HAND2, HDAC4, TWIST2, RANBP3L, OSTN
BP	GO:0048641	regulation of skeletal muscle tissue development	13/1554	2.10E-03	ACTN3, BCL2, EPHB1, MEF2C, SHH, HDAC4, KLHL41, DKK1, CDON, LMOD3, SOX17, MYOCD, RBM24
BP	GO:0035725	sodium ion transmembrane transport	25/1554	2.15E-03	ATP1A2, ATP1B2, ATP2B4, DMD, STOM, PKD2, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A2, SLC8A1, SLC8A3, SNTA1, UTRN, SLMAP, FXYD6, SCN3B, SLC17A7, SLC24A3, SLC24A4, OSR1, CNKSR3, NALCN, SLC9A9
BP	GO:0042552	myelination	24/1554	2.15E-03	ABCD2, ANK2, ASPA, CLU, LPAR1, EGR2, HGF, ID4, ILK, MPZ, NTRK3, PLP1, PMP22, SLC8A3, CNTN2, CNTNAP1, SLC25A12, ARHGEF10, TSPAN2, WASF3, NFASC, DHH, FA2H, JAM3
BP	GO:0001659	temperature homeostasis	29/1554	2.20E-03	ACTN3, ADCYAP1, ADRB2, ADRB3, CAV1, CIDEA, EDNRB, EGR1, GPR3, GRB10, IRF4, LAMA4, LEPR, NOVA1, NPR3, PLCL1, PTGER3, PTGS2, THRA, PER2, ADIPOQ, ZNF516, PPARGC1A, ADAMTS5, ZNF423, KDM6B, PRDM16, EBF2, PPARGC1B
BP	GO:0060326	cell chemotaxis	44/1554	2.20E-03	ANXA1, CXCR5, CALCA, CCR6, CNR2, CX3CR1, HBEGF, DUSP1, GPR183, S1PR1, LPAR1, EDNRB, EGR3, EPHA2, EPHB1, FGF2, FGFR1, CXCL2, NCKAP1L, HGF, NR4A1, IL1RN, IL6R, CXCR2, IL16, ITGA1, ITGA9, KIT, PDE4B, PDE4D, PDGFRA, PRKD1, CX3CL1, CXCL12, THBS1, DYSF, CH25H, SLIT2, CXCL13, SBDS, ACKR4, PARVA, PDGFD, JAM3
BP	GO:0060828	regulation of canonical Wnt signaling pathway	42/1554	2.20E-03	CAV1, EDA, EGR1, FGF9, FGF10, GPC5, GNAQ, IGFBP2, IGFBP6, ILK, ROR2, PRKN, SFRP1, SFRP2, SHH, TBL1X, TLE4, FZD7, RECK, SCEL, TBX18, DKK1, DAAM2, SOSTDC1, WWTR1, ADGRA2, LATS2, RBMS3, DACT1, SOX17, JADE1, WLS, SOX7, RSPO3, NKD1, TMEM88, LRRK2, CSNK1A1L, PRICKLE1, DACT3, RSPO2, SHISA6
BP	GO:0009649	entrainment of circadian clock	9/1554	2.21E-03	CRY2, GNAQ, ID2, PER1, PPP1CB, PER3, PER2, USP2, SIK1
BP	GO:0048732	gland development	58/1554	2.21E-03	ABL1, ADCYAP1, AK4, ALDH1A3, ANXA1, AR, BCL2, BMPR1A, CAV1, CDO1, EDA, EPHA2, ESR1, FGF7, FGF10, FGFR1, FOXF1, GATA6, GLI2, HGF, ID2, ID4, IGFBP5, JUN, MSX1, NFIB, OTC, PAM, PBX1, PDGFRA, PGR, PITX1, PITX2, PKD1, PKD2, PROX1, PTCH1, RAP1A, SALL1, SFRP1, SHH, SRF, TCF21, TGFB3, TGFBR2, TGFBR3, THRA, TNFAIP3, SOCS2, RGN, NEURL1, NTN1, HAND2, SEMA3A, SOSTDC1, FA2H, WLS, ARID5B
BP	GO:0099003	vesicle-mediated transport in synapse	33/1554	2.21E-03	ADRA1A, AMPH, CACNB2, CAMK2A, CHRM2, STX2, ITGB3, P2RX1, P2RY1, PRKN, PPP3CB, PRKCB, RAB27A, RAP1A, ROCK1, SLC2A4, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, STX11, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, NLGN3, SLC17A7, PRRT2, LRRK2, GSG1L
BP	GO:0016358	dendrite development	36/1554	2.21E-03	ADGRB3, BMP5, CAMK2A, CHRNA7, CTNNA2, LPAR1, EPHB1, FYN, IL2, ILK, MAP1A, MAP1B, MAP6, MATN2, MEF2A, MEF2C, NFATC4, RELN, PTPRD, SDC2, VLDLR, NEURL1, DCLK1, NTN1, SEMA3A, PDLIM5, IL1RAPL1, CPEB3, NLGN1, TNIK, NLGN3, TRAK2, FBXO31, PREX2, LRRK2, PHACTR1
BP	GO:0051148	negative regulation of muscle cell differentiation	15/1554	2.28E-03	BDNF, FGF9, MSX1, NFATC1, NFATC2, RGS2, SHH, FZD7, HDAC4, DKK1, SOX6, PRDM6, MYOCD, TMEM119, RBPMS2
BP	GO:0060389	pathway-restricted SMAD protein phosphorylation	15/1554	2.28E-03	ACVRL1, BMP5, BMPR1A, LDLRAD4, GDF2, GDF10, INHBB, SMAD7, TGFB3, TGFBR2, TGFBR3, RBPMS, EMILIN1, DKK1, BMPER
BP	GO:0060675	ureteric bud morphogenesis	15/1554	2.28E-03	BCL2, EYA1, FGF2, GDNF, ILK, MYC, PBX1, PKD2, PTCH1, SALL1, SHH, TCF21, WNT2B, DCHS1, FAT4
BP	GO:0043271	negative regulation of ion transport	27/1554	2.29E-03	ACTN2, ADCYAP1, ADRA2A, BIN1, ATP1A2, BCL2, CASQ2, CAV1, CLIC2, GEM, GNAO1, GPM6B, GRM7, KCNH2, PKD2, PTGS2, RGS2, SNCA, STC1, THBS1, TRH, VIP, KCNAB1, DYSF, KCNE4, REM1, OSR1

BP	GO:0051153	regulation of striated muscle cell differentiation	22/1554	2.32E-03	BCL2, BDNF, DMPK, IGF1, MEF2C, MSX1, NFATC2, PROX1, RGS2, SHH, FZD7, AKAP6, HDAC4, AKAP13, DKK1, EHD2, SOX6, LMOD3, MYOCD, SIK1, RBM24, TMEM119
BP	GO:0030049	muscle filament sliding	11/1554	2.38E-03	ACTC1, ACTN2, ACTN3, DMD, MYH2, MYH3, MYL3, TMOD1, TNNT2, TPM1, TPM2
BP	GO:0033275	actin-myosin filament sliding	11/1554	2.38E-03	ACTC1, ACTN2, ACTN3, DMD, MYH2, MYH3, MYL3, TMOD1, TNNT2, TPM1, TPM2
BP	GO:0060306	regulation of membrane repolarization	11/1554	2.38E-03	ANK2, CACNA2D1, CASQ2, CAV1, FLNA, KCNH2, SCN1B, SCN4B, SNTA1, AKAP6, KCNE4
BP	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	18/1554	2.45E-03	ANGPT1, CD28, CSF3, DCN, FGFR1, FYN, GPER1, HGF, IGF1, KIT, NTRK3, PDGFRA, PIK3R1, RELN, SELP, TEK, SIRT1, PDGFD
BP	GO:0001759	organ induction	8/1554	2.45E-03	AR, FGF10, FGFR1, GDNF, WNT2B, SPRY1, DKK1, GATA5
BP	GO:0097107	postsynaptic density assembly	7/1554	2.46E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, NRXN2, LRRTM1
BP	GO:0030514	negative regulation of BMP signaling pathway	13/1554	2.49E-03	ABL1, FBN1, SMAD7, SFRP1, SFRP2, CHRD, DKK1, SPART, SOSTDC1, GREM2, CHRDL1, BMPER, RBPMS2
BP	GO:0001101	response to acid chemical	48/1554	2.53E-03	AQP1, AQP2, ATP2B4, BCHE, CDO1, CCN2, BRINP1, DUSP1, EGR1, EPHA3, FYN, GSN, IGFBP2, KCNMB1, LDLR, MMP2, NFATC4, NTRK3, OTC, PDGFRA, PDK4, PKD2, PRKAA2, PTCH1, PTGER4, PTGFR, PTGS2, RBP4, RORB, SFRP1, ZEB1, TGFBR3, WNT9A, FZD7, NEURL1, KLF4, ADIPOQ, KLF2, PPARGC1A, FZD10, CPEB3, DKK1, PID1, RRAGD, CPEB1, PDGFD, CPEB4, OSR1
BP	GO:0070509	calcium ion import	17/1554	2.56E-03	ATP2B4, CACNA1C, CACNA2D1, CACNB2, MS4A1, FYN, PKD2, CXCL12, SLC8A1, SLC8A3, STC1, TRPC4, DYSF, CACNA1H, SLC25A23, FCRL3, FAM155A
BP	GO:0051896	regulation of protein kinase B signaling	37/1554	2.59E-03	ANGPT1, AXL, CD28, CSF3, CX3CR1, HBEGF, EPHA2, ESR1, F3, F10, FGF2, FGF7, FGF9, FGF10, FGFR1, FYN, GPER1, HGF, IGFBP5, ILK, KIT, KITLG, PDGFRA, PIK3R1, RRAS, CX3CL1, TEK, THBS1, FGF23, KLF4, NRG2, MAGI2, SPRY2, SIRT1, RASD2, P2RY12, TNFAIP8L3
BP	GO:0010675	regulation of cellular carbohydrate metabolic process	25/1554	2.59E-03	ACACB, ACTN3, ADCYAP1R1, GPER1, IGF1, LEPR, LHCGR, P2RY1, PRKN, PDK4, ENPP1, PPP1CB, RORA, SNCA, SLC25A12, RGN, ADIPOQ, HDAC4, SORBS1, PPARGC1A, SIRT1, PPP1R3B, MIDN, C1QTNF3, SIK1
BP	GO:0015850	organic hydroxy compound transport	39/1554	2.64E-03	ADRA2A, ADRA2B, AQP1, AQP2, CAV1, CES1, CLU, GDNF, GPM6B, ITGB3, KCNA2, KCNB1, LDLR, LRP1, P2RX1, P2RY1, PRKN, PTCH1, RBP4, CXCL12, SHH, SLC18A2, SLC22A3, SNCA, SYT4, TAC1, VIP, SOAT2, SLC16A7, ADIPOQ, SYT11, SIRT1, SLCO1C1, P2RY12, SYT15, SLC2A13, OSBPL1A, OSBPL5, OSBPL10
BP	GO:0043409	negative regulation of MAPK cascade	30/1554	2.72E-03	ABL1, ATF3, CAV1, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, GPER1, LIF, MYC, PRKN, PER1, RGS2, SFRP1, SFRP2, KLF4, ADIPOQ, HIPK3, SPRY1, SPRY2, EMILIN1, IRAK3, DACT1, ERRFI1, DUSP26, DUSP19, CNKSR3, NLRP6
BP	GO:0048017	inositol lipid-mediated signaling	30/1554	2.72E-03	ANGPT1, ZFP36L1, CD28, CSF3, DCN, FGFR1, FYN, GPER1, GSN, HGF, IGF1, KIT, NGF, NPR3, NTRK3, PDGFRA, PIK3R1, RELN, SELP, TEK, PIP5K1B, IER3, KLF4, SIRT1, NCS1, PPP1R16B, PITPNM2, PREX2, PDGFD, TNFAIP8L3
BP	GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	12/1554	2.75E-03	CBLN1, CDH4, GRID2, ITGA5, PTPRD, SELP, DCHS1, IL1RAPL1, NLGN1, CRB1, CADM3, FAT4
BP	GO:0060443	mammary gland morphogenesis	12/1554	2.75E-03	AR, CAV1, EPHA2, ESR1, FGF10, GLI2, IGFBP5, PGR, PTCH1, TGFBR2, NTN1, SOSTDC1
BP	GO:0009791	post-embryonic development	18/1554	2.77E-03	ABL1, BCL2, PRDM1, FBN1, EFEMP1, ITPR1, NDN, NR4A2, SELENOP, SLC18A2, KLF4, TIPARP, PYGO1, SOX6, CSRNP1, SCUBE1, ARID5B, FOXP2
BP	GO:0048644	muscle organ morphogenesis	18/1554	2.77E-03	ACTC1, ADARB1, BMPR1A, S1PR1, LIF, SMAD7, MYL3, MYLK, PROX1, RYR2, TGFBR3, TNNT2, TPM1, MYOM2, HAND1, ZFPM2, TBX20, ARID5B
BP	GO:0106106	cold-induced thermogenesis	25/1554	2.86E-03	ACTN3, ADCYAP1, ADRB2, ADRB3, CAV1, CIDEA, GPR3, GRB10, IRF4, LAMA4, LEPR, NOVA1, NPR3, PLCL1, THRA, PER2, ADIPOQ, ZNF516, PPARGC1A, ADAMTS5, ZNF423, KDM6B, PRDM16, EBF2, PPARGC1B
BP	GO:0120161	regulation of cold-induced thermogenesis	25/1554	2.86E-03	ACTN3, ADCYAP1, ADRB2, ADRB3, CAV1, CIDEA, GPR3, GRB10, IRF4, LAMA4, LEPR, NOVA1, NPR3, PLCL1, THRA, PER2, ADIPOQ, ZNF516, PPARGC1A, ADAMTS5, ZNF423, KDM6B, PRDM16, EBF2, PPARGC1B
BP	GO:0003180	aortic valve morphogenesis	9/1554	2.87E-03	ELN, NFATC1, ROCK1, SLIT3, SLIT2, ROCK2, EMILIN1, TBX20, GATA5

BP	GO:0033137	negative regulation of peptidyl-serine phosphorylation	9/1554	2.87E-03	BDKRB2, CAV1, DMD, HGF, SMAD7, PDE4D, RASSF2, DKK1, CNKSR3
BP	GO:0034614	cellular response to reactive oxygen species	28/1554	2.91E-03	ABL1, ANXA1, AQP1, RHOB, AXL, CYP1B1, FER, FOS, HGF, JUN, MAPT, MMP2, PDGFRA, PKD2, SOD3, TNFAIP3, TPM1, RNF112, NR4A3, RGN, KLF4, KLF2, FBLN5, KDM6B, SIRT1, PDGFD, LRRK2, PPARGC1B
BP	GO:0014032	neural crest cell development	17/1554	2.91E-03	ANXA6, BMPR1A, EDNRA, EDNRB, GDNF, KITLG, NRTN, PITX2, SHH, NRP2, HAND2, ZEB2, SEMA3A, CORO1C, SEMA3G, FAM172A, KBTBD8
BP	GO:0071470	cellular response to osmotic stress	11/1554	2.92E-03	AQP1, BDKRB2, ZFP36L1, MYLK, PKD2, PTGS2, SLC2A4, DYSF, ERRFI1, SLC25A23, RCSD1
BP	GO:0072210	metanephric nephron development	11/1554	2.92E-03	CD34, EGR1, GDNF, LIF, PDGFRA, PKD1, PKD2, SALL1, TCF21, ADIPOQ, OSR1
BP	GO:0030203	glycosaminoglycan metabolic process	27/1554	2.97E-03	ANGPT1, CSPG4, DCN, FGF2, GPC5, HAS1, HGF, HSPG2, HYAL1, OMD, OGN, PIM1, PRELP, SDC2, ST3GAL3, SDC3, HS3ST1, GPC6, UST, LYVE1, CSGALNACT1, HPSE2, NDNF, ITIH5, CHST9, DSEL, B3GAT2
BP	GO:0060795	cell fate commitment involved in formation of primary germ layer	10/1554	2.97E-03	BMPR1A, ETS2, EYA1, FGFR1, GATA6, SFRP2, FZD7, KLF4, DKK1, SOX17
BP	GO:0070050	neuron cellular homeostasis	10/1554	2.97E-03	ATP2B3, CACNB2, MAP1A, P2RX1, P2RY1, PRKN, CX3CL1, NCS1, HAAO, SLC17A7
BP	GO:0071868	cellular response to monoamine stimulus	10/1554	2.97E-03	ABL1, ATP2B4, PRKN, PDE4B, PDE4D, RYR2, SNCA, NR4A3, ADIPOQ, LRRK2
BP	GO:0071870	cellular response to catecholamine stimulus	10/1554	2.97E-03	ABL1, ATP2B4, PRKN, PDE4B, PDE4D, RYR2, SNCA, NR4A3, ADIPOQ, LRRK2
BP	GO:0070373	negative regulation of ERK1 and ERK2 cascade	16/1554	3.00E-03	ABL1, ATF3, DUSP1, DUSP3, DUSP4, GPER1, LIF, KLF4, ADIPOQ, SPRY1, SPRY2, EMILIN1, ERRFI1, DUSP26, CNKSR3, NLRP6
BP	GO:0032414	positive regulation of ion transmembrane transporter activity	20/1554	3.04E-03	ACTN2, ADRB2, ANK2, ATP1B2, CACNA2D1, CACNB2, DMD, HSPA2, KCNA1, ABCB1, PKD2, RELN, RYR2, STAC, RGN, AKAP6, NLGN3, JPH2, CNKSR3, LRRC52
BP	GO:0048489	synaptic vesicle transport	26/1554	3.04E-03	ADRA1A, CACNB2, CAMK2A, CHRM2, STX2, P2RX1, P2RY1, PRKN, PRKCB, RAB27A, RAP1A, SLC2A4, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, STX11, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, PRRT2, LRRK2
BP	GO:0097480	establishment of synaptic vesicle localization	26/1554	3.04E-03	ADRA1A, CACNB2, CAMK2A, CHRM2, STX2, P2RX1, P2RY1, PRKN, PRKCB, RAB27A, RAP1A, SLC2A4, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, STX11, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, PRRT2, LRRK2
BP	GO:0060038	cardiac muscle cell proliferation	15/1554	3.05E-03	BMPR1A, FGF2, FGF9, FGFR1, GATA6, KCNK2, MEF2C, MEIS1, PIM1, RBP4, TBX5, TGFBR2, TGFBR3, ZFPM2, TBX20
BP	GO:0010594	regulation of endothelial cell migration	35/1554	3.08E-03	ABL1, ACVRL1, ANGPT1, ANXA1, RHOB, DCN, EPHA2, FGF2, FGFR1, GDF2, ITGB3, MEF2C, PRKCA, PRKD1, PROX1, PTGS2, STC1, TEK, THBS1, PLPP3, NRP2, KLF4, SLIT2, ROCK2, AKT3, CXCL13, SIRT1, ADGRA2, ADAMTS9, RHOJ, JCAD, ATOH8, STARD13, AMOTL1, BMPER
BP	GO:1902107	positive regulation of leukocyte differentiation	25/1554	3.09E-03	ANXA1, AXL, ZFP36L1, EGR3, FOS, GLI2, NCKAP1L, ID2, IL2, IL17A, ITPKB, JUN, LIF, KITLG, ROR2, PRKCA, SHH, TGFBR2, KLF10, ZBTB16, TESPA1, TRIB1, VSIR, NFKBIZ, PPARGC1B
BP	GO:0032411	positive regulation of transporter activity	21/1554	3.10E-03	ACTN2, ADRB2, ANK2, ATP1B2, CACNA2D1, CACNB2, DMD, HSPA2, KCNA1, ABCB1, PKD2, RELN, RYR2, SGK1, STAC, RGN, AKAP6, NLGN3, JPH2, CNKSR3, LRRC52
BP	GO:0010454	negative regulation of cell fate commitment	6/1554	3.11E-03	SFRP2, FZD7, DKK1, SOSTDC1, SOX17, GLIS1
BP	GO:0031953	negative regulation of protein autophosphorylation	6/1554	3.11E-03	CAV1, GFRA2, JUN, ENPP1, ADIPOQ, ERRFI1
BP	GO:0071415	cellular response to purine-containing compound	6/1554	3.11E-03	CASQ2, P2RY1, RYR2, RYR3, SLC8A1, PPARGC1A
BP	GO:0071872	cellular response to epinephrine stimulus	6/1554	3.11E-03	ATP2B4, PDE4B, PDE4D, RYR2, SNCA, ADIPOQ
BP	GO:1902430	negative regulation of amyloid-beta formation	6/1554	3.11E-03	BIN1, CHRNA7, CLU, IGF1, ROCK1, SPON1

BP	GO:0072089	stem cell proliferation	22/1554	3.12E-03	ZFP36L1, CD34, CX3CR1, DCT, EML1, FGF2, FGFR1, ID4, KCNA1, KITLG, OVOL1, ABCB1, PIM1, CX3CL1, SFRP2, SHH, SOX5, WNT2B, NES, SOX17, HHIP, LRRK2
BP	GO:0010595	positive regulation of endothelial cell migration	23/1554	3.12E-03	ABL1, ANGPT1, ANXA1, RHOB, FGF2, FGFR1, ITGB3, PRKCA, PRKD1, PROX1, PTGS2, TEK, THBS1, PLPP3, NRP2, ROCK2, AKT3, SIRT1, ADGRA2, RHOJ, JCAD, ATOH8, AMOTL1
BP	GO:0090596	sensory organ morphogenesis	38/1554	3.14E-03	ALDH1A3, BCL2, PRDM1, COL8A2, DIO3, EPHA2, EPHB1, EYA1, FBN1, EFEMP1, FGF9, FGF10, FGFR1, GLI2, MEIS1, MSX1, ROR2, PITX2, PROX1, RBP4, RORB, SALL1, ZEB1, WNT2B, WNT9A, NR4A3, ITGA8, KCNQ4, NTN1, TSHZ1, SPRY2, CRB1, LRIG1, VSX1, CDON, SOBP, NKD1, OSR1
BP	GO:0048806	genitalia development	12/1554	3.23E-03	AR, AXL, BMP5, ESR1, FGF10, LHCGR, ROR2, PDGFRA, PKD1, RBP4, SHH, ASB1
BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	12/1554	3.23E-03	BMPR1A, FOS, JUN, NFATC4, NFIB, NGFR, SRF, TEAD1, FOSL1, KLF4, HDAC4, ATOH8
BP	GO:0030539	male genitalia development	8/1554	3.23E-03	AR, BMP5, FGF10, LHCGR, ROR2, PDGFRA, SHH, ASB1
BP	GO:2000050	regulation of non-canonical Wnt signaling pathway	8/1554	3.23E-03	ABL1, SFRP1, SFRP2, DKK1, DAAM2, DACT1, RSPO3, NKD1
BP	GO:0048709	oligodendrocyte differentiation	19/1554	3.23E-03	ASPA, CLU, LPAR1, GPR17, GSN, ID2, ID4, PLP1, SHH, SLC8A3, CNTN2, TRPC4, CNTNAP1, TSPAN2, WASF3, DAAM2, NLGN3, SOX6, FA2H
BP	GO:0046209	nitric oxide metabolic process	17/1554	3.24E-03	ARG2, ATP2B4, CAV1, CD34, CLU, CX3CR1, CYP1B1, HBB, PKD2, PTGIS, PTGS2, PTX3, RORA, RGN, KLF4, ROCK2, KLF2
BP	GO:0042133	neurotransmitter metabolic process	26/1554	3.27E-03	ARG2, ATP2B4, BCHE, CAV1, CD34, CLU, CX3CR1, CYP1B1, GRIN2A, HBB, PKD2, PTGIS, PTGS2, PTX3, RORA, TRH, RGN, KLF4, ROCK2, NAALAD2, KLF2, DMGDH, SLC5A7, ENPP6, PRIMA1, RNF180
BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	25/1554	3.36E-03	ABL1, CAV1, CDKN1A, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, PRKAR2B, RGS2, SFRP1, SFRP2, TNFAIP3, ADIPOQ, HIPK3, SPRY1, SPRY2, IRAK3, SIRT1, LATS2, PRKAG2, INKA2, MYOCD, DUSP19
BP	GO:0007422	peripheral nervous system development	16/1554	3.39E-03	BDNF, EDNRB, EGR2, EGR3, GDNF, GFRA3, ILK, NGF, NTRK3, PMP22, CNTNAP1, HAND2, ARHGEF10, NFASC, FA2H, PLXNA4
BP	GO:0051235	maintenance of location	46/1554	3.39E-03	ABL1, ACACB, ANK2, ANXA6, ATP1A2, C3, CACNA1C, CASQ2, CAV1, CIDEA, CLIC2, DMD, FBN1, FGF2, FLNA, GPER1, GSN, HRC, ITGB3, ITPR1, PDE4D, ENPP1, PKD1, PKD2, RYR2, RYR3, CX3CL1, SLC8A1, SLC18A2, SNCA, TLN1, TRPC1, DYSF, TRPA1, AKAP6, RASA3, DZIP1, SYNE1, SIRT1, SLC17A7, JPH2, SPTBN4, SLC25A23, JPH4, SYNE3, VSTM2A
BP	GO:0046620	regulation of organ growth	21/1554	3.41E-03	ACACB, BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, KCNK2, MEF2C, MEIS1, PIM1, PROX1, RBP4, RGS2, TBX5, TGFBR2, TGFBR3, AKAP6, ZFPM2, LATS2, TBX20
BP	GO:0044320	cellular response to leptin stimulus	7/1554	3.42E-03	INHBB, LEPR, UGCG, NR4A3, FGF23, SIRT1, PID1
BP	GO:0048557	embryonic digestive tract morphogenesis	7/1554	3.42E-03	FGF10, FOXF1, ID2, PDGFRA, SHH, TCF21, RBPMS2
BP	GO:0071375	cellular response to peptide hormone stimulus	45/1554	3.42E-03	ACTN2, ADCY2, ADCY5, ADCY9, ZFP36L1, CAMK2A, CAV1, CRHBP, FBN1, FER, FYN, GHR, GPER1, GRB10, NR4A1, INHBB, LHCGR, MAP1B, NR4A2, PDE3B, PDK4, ENPP1, PIK3R1, PRKACB, PRKAR2B, PRKCB, ROCK1, SLC2A4, STAT5B, VAMP2, NR4A3, SOCS2, SOCS3, GLP2R, ADIPOQ, ROCK2, SORBS1, SIRT1, ERRFI1, PID1, MBD5, ZNF106, CPEB1, GKAP1, CPEB2
BP	GO:0051965	positive regulation of synapse assembly	15/1554	3.46E-03	ADGRB3, BDNF, CBLN1, EPHB1, GRID2, NTRK3, PTPRD, NRXN1, IL1RAPL1, NLGN1, FLRT2, NLGN3, CLSTN2, LRRC4B, LRRTM1
BP	GO:0006027	glycosaminoglycan catabolic process	14/1554	3.48E-03	CSPG4, DCN, FGF2, GPC5, HSPG2, HYAL1, OMD, OGN, PRELP, SDC2, SDC3, GPC6, LYVE1, HPSE2
BP	GO:0032233	positive regulation of actin filament bundle assembly	14/1554	3.48E-03	ABL1, CCN2, LPAR1, FLNA, CX3CL1, SFRP1, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, SYNPO, ARHGEF15, SYNPO2
BP	GO:0033032	regulation of myeloid cell apoptotic process	9/1554	3.60E-03	ANXA1, BCL2, CXCR2, ITPKB, MEF2C, KITLG, THRA, ADIPOQ, SIRT1
BP	GO:1901385	regulation of voltage-gated calcium channel activity	10/1554	3.64E-03	CACNA2D1, CACNB2, CACNB4, DMD, GEM, PDE4B, STAC, DYSF, REM1, AHNAK
BP	GO:0016051	carbohydrate biosynthetic process	33/1554	3.64E-03	ADCYAP1R1, ATF3, GPER1, GYS2, HAS1, IGF1, IMPA2, LEPR, LHCGR, P2RY1, ENPP1, PPP1CB, RBP4, SNCA, SLC25A12, B3GALT2, B3GALT1, PER2, RGN, ADIPOQ, SORBS1, PPARGC1A, SIRT1, ST6GALNAC6, CSGALNACT1, G6PC2, PPP1R3B, ST6GALNAC5, CHST9, C1QTNF3, SIK1, PGM2L1, ST8SIA6

BP	GO:0042110	T cell activation	60/1554	3.69E-03	ABL1, ANXA1, ARG2, RHOH, BCL2, PRDM1, ZFP36L1, CAV1, CD1C, CD5, CD28, TNFSF8, CD40LG, CCR6, MAP3K8, CD55, DUSP3, GPR183, EGR1, EGR3, FYN, LRRC32, GLI2, GSN, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, IRF4, ITK, ITPKB, KIT, LEPR, LY9, SMAD7, NFATC2, PIK3R1, PPP3CB, PTGER4, RAB27A, RORA, SATB1, SHH, SRF, ZEB1, TGFBR2, ZBTB16, FZD7, PDE5A, BCL10, GRAP2, TESPA1, FGL2, PLA2G2D, VSIR, NFKBIZ, TNFRSF13C, BTLA
BP	GO:0050768	negative regulation of neurogenesis	42/1554	3.76E-03	ADCYAP1, BMPR1A, BRINP1, DIO3, DPYSL3, LPAR1, EDNRB, EPHA7, ID2, ID4, LDLR, LRP1, MEIS1, NFATC4, NGFR, NTRK3, PBX1, PMP22, CX3CL1, SHH, SYT4, CNTN2, NR2F1, SLIT2, NTN1, ZNF536, SEMA3A, NLGN1, DKK1, SPART, DENND5A, DAAM2, NLGN3, SEMA3G, RGMA, TRAK2, DIXDC1, BMERB1, LRRK2, CNTN4, NEXMIF, OSTN
BP	GO:0031214	biomineral tissue development	27/1554	3.77E-03	ADRB2, BMPR1A, S1PR1, GPM6B, IGF1, CCN1, MEF2C, MGP, ROR2, DDR2, OMD, ENPP1, PTGS2, ROCK1, SLC8A1, TGFB3, KLF10, CLEC3B, FGF23, ROCK2, ENAM, SBDS, PKDCC, OSR1, TMEM119, RSPO2, RFLNB
BP	GO:0099173	postsynapse organization	27/1554	3.77E-03	ACTN1, CBLN1, CHRNA7, DGKB, DLG2, EPHA7, EPHB1, FYN, GDNF, GRID2, NTRK3, RELN, PTPRD, NRP2, NRXN1, NRXN2, MAGI2, PDLIM5, IL1RAPL1, CNKSR2, NLGN1, NLGN3, LRRC4, TMEM108, LRRK2, LRRTM1, SHISA6
BP	GO:0042752	regulation of circadian rhythm	21/1554	3.77E-03	CREM, CRY2, GNAQ, ID2, KCNA2, PER1, PPP1CB, PRKAA2, PROX1, RORA, RORB, KLF10, PER3, PER2, USP2, ROCK2, PPARGC1A, NLGN1, CIPC, OPN4, SIK1
BP	GO:0060349	bone morphogenesis	21/1554	3.77E-03	ANXA6, FOXN3, COL6A2, COL6A3, COL13A1, MATN2, MEF2C, MEF2D, MMP16, MSX1, SFRP2, STC1, TEK, TGFB3, TGFBR2, SCARA3, RAB23, CSGALNACT1, COL21A1, FREM1, TMEM119
BP	GO:0045933	positive regulation of muscle contraction	12/1554	3.82E-03	ADRA1A, ADRA2B, CHRM3, CCN2, GPER1, KIT, PTGS2, RGS2, SRF, TACR2, TACR3, MYOCD
BP	GO:0051150	regulation of smooth muscle cell differentiation	12/1554	3.82E-03	FGF9, GPER1, KIT, NFATC1, NFATC2, SHH, SRF, ZEB1, SIRT1, PRDM6, MYOCD, RBPMS2
BP	GO:0048844	artery morphogenesis	16/1554	3.84E-03	ACVRL1, PRDM1, BMPR1A, EYA1, FOXF1, LDLR, LRP1, SMAD7, MYLK, PKD2, PROX1, SRF, HAND2, AKT3, ADAMTS9, MYOCD
BP	GO:0003002	regionalization	48/1554	3.85E-03	AR, BMPR1A, C3, EGR2, ETS2, FGF10, FGFR1, FOXF1, GDNF, GLI2, MEF2C, MEOX1, MSX1, ROR2, PBX1, PBX3, PCSK5, PITX2, PRKACB, RELN, PTCH1, SFRP1, SFRP2, SHH, SRF, WNT2B, ZBTB16, BTG2, CHRD, NRP2, TBX18, ZEB2, TSHZ1, SPRY1, SEMA3A, DKK1, SOSTDC1, CDON, TBX20, DSCAML1, SOX17, GREM2, HHIP, WLS, NKD1, OSR1, GATA5, NOTO
BP	GO:0021543	pallium development	28/1554	3.95E-03	ATP2B4, EPHA5, FLNA, ID4, KCNA1, LRP1, PROX1, RELN, SRF, TACC1, BTG2, NR4A3, NRP2, SLIT2, ZEB2, SEMA3A, TACC2, KDM6B, CDON, GNG12, P2RY12, TMEM108, FAT4, DIXDC1, BMERB1, FOXP2, DCLK2, PHACTR1
BP	GO:0001818	negative regulation of cytokine production	42/1554	3.97E-03	ABCD2, ANGPT1, ANXA1, APOD, ARG2, AXL, BPI, CD34, CHRNA7, CIDEA, CX3CR1, EPHA2, FGFR1, LRRC32, GATA6, NCKAP1L, HGF, IGF1, INHBB, SMAD7, CD200, PTGER4, CX3CL1, SLAMF1, TGFB3, THBS1, TNFAIP3, ZFP36, IL1RL1, RPS6KA5, KLF4, ADIPOQ, KLF2, IRAK3, MAPKBP1, SYT11, ASB1, ERRFI1, VSIR, NAV3, C1QTNF3, SSC5D
BP	GO:0048871	multicellular organismal homeostasis	62/1554	3.97E-03	ACACB, ACTN3, ADCY2, ADCY5, ADCY9, ADCYAP1, ADRB2, ADRB3, AQP1, AQP2, BCL2, CALCA, CAV1, CD34, CIDEA, CCN2, S1PR1, EDNRB, EGR1, GPR3, GRB10, IRF4, ITGB3, LAMA4, LEPR, NDN, NOVA1, NPR3, PDK4, PLCL1, PRKAA2, PRKACB, PRKAR2B, PRKCA, PTGER3, PTGS2, RBP4, SRF, THRA, TNFAIP3, TUB, UGCG, WFS1, NR4A3, PER2, LDB2, GPR55, ADIPOQ, ZNF516, AKT3, PPARGC1A, ADAMTS5, ZNF423, KDM6B, WWTR1, TP53INP2, PRDM16, EBF2, FA2H, PPARGC1B, LCA5, TMEM119
BP	GO:0061351	neural precursor cell proliferation	25/1554	3.98E-03	ADCYAP1, CX3CR1, DCT, EML1, EPHB1, FGFR1, FLNA, ID2, ID4, ILK, KCNA1, PROX1, RORA, CX3CL1, SHH, SOX5, BTG2, ZEB2, NES, CDON, CEND1, PTBP2, HHIP, DIXDC1, LRRK2
BP	GO:0003229	ventricular cardiac muscle tissue development	13/1554	3.98E-03	BMPR1A, ID2, SMAD7, MYL3, PROX1, RYR2, TBX5, TGFBR3, TNNT2, TPM1, HAND1, ZFPM2, ADAMTS9
BP	GO:0098900	regulation of action potential	13/1554	3.98E-03	ADRA1A, BIN1, ANK2, CACNA1C, CACNA2D1, CAV1, CNR2, FLNA, KCNB1, RYR2, TAC1, SLMAP, CTNNA3
BP	GO:0007626	locomotory behavior	31/1554	4.01E-03	ADCY5, ALDH1A3, ATP1A2, EGR1, GDNF, GNAO1, ID2, MEIS1, NOVA1, NR4A2, PRKN, PBX3, PPP3CB, CXCL12, SELENOP, SLC18A2, SNCA, TAL1, CNTN2, TMOD1, TRH, USP2, RASD2, HPGDS, CEND1, SOBP, SPTBN4, PREX2, LRRK2, NEGR1, LRRTM1
BP	GO:0050433	regulation of catecholamine secretion	14/1554	4.01E-03	ADRA2A, ADRA2B, GDNF, KCNA2, KCNB1, P2RY1, PRKN, CXCL12, SNCA, SYT4, VIP, SYT11, P2RY12, SYT15
BP	GO:0055025	positive regulation of cardiac muscle tissue development	14/1554	4.01E-03	BMPR1A, FGF2, FGF9, FGFR1, GATA6, IGF1, MEF2C, PIM1, TBX5, TGFBR3, AKAP6, ZFPM2, TBX20, MYOCD

BP	GO:0033135	regulation of peptidyl-serine phosphorylation	24/1554	4.05E-03	ANGPT1, ATP2B4, BCL2, BDKRB2, CAV1, CSF3, DMD, HGF, HRC, LIF, SMAD7, NTRK3, PDE4D, PLCL1, PRKD1, PTGS2, SFRP2, SNCA, TCL1A, RASSF2, SPRY2, DKK1, SPTBN4, CNKSR3
BP	GO:0070665	positive regulation of leukocyte proliferation	24/1554	4.05E-03	ANXA1, BCL2, CD28, CD40LG, CDKN1A, CD55, GPR183, FGF10, NCKAP1L, IGF1, IGFBP2, IL2, IL5RA, IL6R, IL6ST, MEF2C, KITLG, MPL, NFATC2, SHH, TAC1, TGFBR2, FCRL3, TNFRSF13C
BP	GO:0048015	phosphatidylinositol-mediated signaling	29/1554	4.06E-03	ANGPT1, ZFP36L1, CD28, CSF3, DCN, FGFR1, FYN, GPER1, GSN, HGF, IGF1, KIT, NGF, NPR3, NTRK3, PDGFRA, PIK3R1, RELN, SELP, TEK, PIP5K1B, IER3, KLF4, SIRT1, NCS1, PPP1R16B, PITPNM2, PREX2, PDGFD
BP	GO:0099622	cardiac muscle cell membrane repolarization	11/1554	4.17E-03	ANK2, CACNA2D1, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, SCN1B, SCN4B, SNTA1, KCNE4
BP	GO:2001222	regulation of neuron migration	11/1554	4.17E-03	CAMK2A, CTNNA2, FLNA, RELN, CX3CL1, SEMA3A, FLRT2, FBXO31, PHACTR1, IGSF10, NEXMIF
BP	GO:0060343	trabecula formation	8/1554	4.21E-03	MMP2, RBP4, SFRP1, SRF, TEK, TGFBR3, ADAMTS1, PPARGC1B
BP	GO:1903421	regulation of synaptic vesicle recycling	8/1554	4.21E-03	PPP3CB, ROCK1, SLC2A4, SNCA, NLGN1, SYT11, SLC17A7, LRRK2
BP	GO:0051937	catecholamine transport	16/1554	4.36E-03	ADRA2A, ADRA2B, GDNF, KCNA2, KCNB1, P2RY1, PRKN, CXCL12, SLC18A2, SLC22A3, SNCA, SYT4, VIP, SYT11, P2RY12, SYT15
BP	GO:0010453	regulation of cell fate commitment	10/1554	4.44E-03	AR, BMPR1A, FGF2, FGFR1, SFRP2, FZD7, DKK1, SOSTDC1, SOX17, GLIS1
BP	GO:0035137	hindlimb morphogenesis	10/1554	4.44E-03	BMPR1A, AFF3, MSX1, PITX1, PTCH1, SHH, ZBTB16, SALL3, OSR1, RSPO2
BP	GO:0050931	pigment cell differentiation	10/1554	4.44E-03	BCL2, EDNRB, KIT, MEF2C, KITLG, MITF, ENPP1, RAB27A, ZEB2, ADAMTS9
BP	GO:0060428	lung epithelium development	10/1554	4.44E-03	FGF7, FGF10, GATA6, NFIB, PKD1, SHH, THRA, KLF2, ERRFI1, FOXP2
BP	GO:0071709	membrane assembly	10/1554	4.44E-03	CAV1, STX2, PTPRD, UGCG, NRXN1, NRXN2, MAGI2, IL1RAPL1, NLGN1, NLGN3
BP	GO:2000310	regulation of NMDA receptor activity	10/1554	4.44E-03	ACTN2, CRHBP, DLG2, GRIA1, GRIN2A, MEF2C, RELN, PPARGC1A, NLGN1, NLGN3
BP	GO:0017157	regulation of exocytosis	33/1554	4.45E-03	ADRA1A, ADRA2A, ANXA1, CACNB2, CAMK2A, CHRM2, FER, FOXF1, KCNB1, P2RX1, P2RY1, PRKN, PRKCB, RAB27A, RAP1A, SNCA, STXBP1, VAMP2, SYT4, PPFIA2, CACNA1H, STXBP5L, RIMS3, IL1RAPL1, NLGN1, RIMS1, SYT11, NCS1, STXBP6, SYT15, RAB3C, LRRK2, LGI3
BP	GO:0034446	substrate adhesion-dependent cell spreading	19/1554	4.45E-03	ABL1, AXL, FER, FLNA, HSPG2, ILK, ITGB3, LAMC1, TEK, FZD7, ITGA8, LAMC3, FERMT2, BVES, CORO1C, RADIL, PARVA, PEAK1, MYADM
BP	GO:0060840	artery development	19/1554	4.45E-03	ACVRL1, PRDM1, BMPR1A, EYA1, FOXF1, LDLR, LRP1, SMAD7, MYLK, PDE2A, PKD2, PROX1, SHH, SRF, HAND2, AKT3, ADAMTS9, MYOCD, PRICKLE1
BP	GO:0034260	negative regulation of GTPase activity	12/1554	4.47E-03	ADCYAP1, RHOH, PTPRN2, RGN, SLIT2, RASA4, SPRY1, SPRY2, FZD10, LRCH1, LRRK2, CPEB2
BP	GO:1905606	regulation of presynapse assembly	9/1554	4.47E-03	CBLN1, NTRK3, PTPRD, SNCA, NRXN1, IL1RAPL1, NLGN1, DKK1, LRRTM1
BP	GO:0045598	regulation of fat cell differentiation	23/1554	4.47E-03	ZFP36L1, RUNX1T1, GPER1, ID2, ID4, ENPP1, PTGS2, RORA, SFRP1, SFRP2, TGFB1I1, ZFP36, ZBTB16, ADIPOQ, SIRT1, ZFPM2, WWTR1, PRDM16, CCDC3, JDP2, VSTM2A, FNDC5, PTPRQ
BP	GO:0001935	endothelial cell proliferation	30/1554	4.47E-03	ACVRL1, CAV1, CD34, EGR3, EPHA2, F3, FGF2, FGFR1, GDF2, NR4A1, ITGB3, JUN, MEF2C, NGFR, PRKCA, PRKD1, PROX1, CXCL12, TEK, THBS1, VIP, DYSF, TNFSF12, NRP2, AKT3, SIRT1, PPP1R16B, JCAD, ATOH8, BMPER
BP	GO:0032720	negative regulation of tumor necrosis factor production	15/1554	4.47E-03	ARG2, AXL, BPI, CD34, CHRNA7, CIDEA, IGF1, CX3CL1, SLAMF1, TNFAIP3, ADIPOQ, IRAK3, SYT11, ERRFI1, VSIR
BP	GO:0051966	regulation of synaptic transmission, glutamatergic	15/1554	4.47E-03	ADCYAP1, ATP1A2, GRIK2, GRIK3, GRM7, MEF2C, ROR2, RELN, PTGS2, STXBP1, NRXN1, NLGN1, DKK1, NLGN3, LRRK2
BP	GO:0060395	SMAD protein signal transduction	15/1554	4.47E-03	BMP5, BMPR1A, FOS, GDF2, GDF10, INHBB, JUN, SMAD9, ROR2, TGFB3, CILP, MAGI2, RBPMS, WWTR1, ATOH8
BP	GO:1904659	glucose transmembrane transport	20/1554	4.50E-03	C3, EDNRA, GRB10, IGF1, MEF2A, ENPP1, PIK3R1, PRKCB, RAP1A, SLC2A3, SLC2A4, NR4A3, ADIPOQ, SORBS1, CLIP3, KLF15, PRKAG2, PID1, SLC2A12, OSTN
BP	GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	22/1554	4.50E-03	ANGPT1, CD28, CSF3, DCN, FGFR1, FYN, GPER1, HGF, IGF1, KIT, NTRK3, PDGFRA, PIK3R1, RELN, SELP, TEK, PIP5K1B, IER3, KLF4, SIRT1, PPP1R16B, PDGFD

BP	GO:0007501	mesodermal cell fate specification	6/1554	4.53E-03	BMPR1A, EYA1, FGFR1, SFRP2, DKK1, SOX17
BP	GO:0009214	cyclic nucleotide catabolic process	6/1554	4.53E-03	PDE1A, PDE2A, PDE4B, PDE4D, PDE5A, PDE7B
BP	GO:1902656	calcium ion import into cytosol	6/1554	4.53E-03	ATP2B4, CACNA2D1, MS4A1, FYN, SLC8A3, FAM155A
BP	GO:1904889	regulation of excitatory synapse assembly	6/1554	4.53E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, LRRTM1
BP	GO:0048864	stem cell development	17/1554	4.55E-03	ANXA6, BMPR1A, EDNRA, EDNRB, GDNF, KITLG, NRTN, PITX2, SHH, NRP2, HAND2, ZEB2, SEMA3A, CORO1C, SEMA3G, FAM172A, KBTBD8
BP	GO:2001057	reactive nitrogen species metabolic process	17/1554	4.55E-03	ARG2, ATP2B4, CAV1, CD34, CLU, CX3CR1, CYP1B1, HBB, PKD2, PTGIS, PTGS2, PTX3, RORA, RGN, KLF4, ROCK2, KLF2
BP	GO:0001710	mesodermal cell fate commitment	7/1554	4.59E-03	BMPR1A, EYA1, FGFR1, SFRP2, KLF4, DKK1, SOX17
BP	GO:0021533	cell differentiation in hindbrain	7/1554	4.59E-03	CBLN1, GRID2, PROX1, RORA, HERC1, FAIM2, CEND1
BP	GO:0002040	sprouting angiogenesis	29/1554	4.66E-03	ABL1, ACVRL1, ANGPT1, ANXA1, EGR3, EPHA2, FGF2, NR4A1, ITGA5, NGFR, PTGS2, SRF, TEK, THBS1, RECK, KLF4, SLIT2, AKT3, KLF2, ADGRA2, PPP1R16B, PARVA, ADAMTS9, RHOJ, JCAD, RSPO3, STARD13, CLEC14A, BMPER
BP	GO:0007565	female pregnancy	30/1554	4.80E-03	ADCYAP1, ADRA2B, AR, BCL2, PRDM1, CALCA, CRHBP, ESR1, FOS, FOSB, PRLHR, IGFBP2, IGFBP5, ITGA5, JUNB, LIF, MMP2, PAM, PCSK5, PGR, PTGIS, PTGS2, RGS2, STC1, TGFB3, TGFBR2, FOSL1, RECK, NAMPT, TCF23
BP	GO:0008589	regulation of smoothened signaling pathway	16/1554	4.85E-03	EVC, FGF9, FGF10, GAS1, ENPP1, PRKACB, PTCH1, RORA, SFRP1, SHH, WNT9A, CHRD, SALL3, HHIP, SCUBE1, SCUBE3
BP	GO:0043407	negative regulation of MAP kinase activity	16/1554	4.85E-03	CAV1, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, RGS2, SFRP1, SFRP2, ADIPOQ, HIPK3, SPRY1, SPRY2, IRAK3, DUSP19
BP	GO:0007224	smoothened signaling pathway	23/1554	4.86E-03	EVC, FGF9, FGF10, FOXF1, GAS1, GLI2, ROR2, ENPP1, PRKACB, PTCH1, RORA, SFRP1, SHH, TGFBR2, WNT9A, DZIP1, SALL3, DHH, CDON, CC2D2A, HHIP, SCUBE1, SCUBE3
BP	GO:0031532	actin cytoskeleton reorganization	19/1554	4.89E-03	ABL1, ANXA1, CSF3, S1PR1, FER, FGF7, FGF10, FLNA, GSN, KIT, NTRK3, PDGFRA, TEK, CDC42BPA, PDLIM4, TNIK, PARVA, THSD7B, PHACTR1
BP	GO:0046545	development of primary female sexual characteristics	19/1554	4.89E-03	ADCYAP1, ADCYAP1R1, BCL2, DACH1, ESR1, INHBB, KIT, KITLG, PDGFRA, PGR, PTX3, SFRP1, SLIT3, SLIT2, ADAMTS1, SIRT1, ZFPM2, TIPARP, ARID5B
BP	GO:0070296	sarcoplasmic reticulum calcium ion transport	11/1554	4.91E-03	ANK2, ATP1A2, CACNA1C, CASQ2, CLIC2, DMD, HRC, PDE4D, RYR2, SLC8A1, AKAP6
BP	GO:0086004	regulation of cardiac muscle cell contraction	11/1554	4.91E-03	BIN1, ANK2, ATP1A2, CACNA1C, CAV1, FLNA, PDE4B, PDE4D, RYR2, STC1, CTNNA3
BP	GO:0002761	regulation of myeloid leukocyte differentiation	21/1554	4.95E-03	ZFP36L1, FBN1, FOS, ID2, IL17A, JUN, LIF, KITLG, MITF, MYC, ROR2, PIK3R1, PRKCA, SFRP1, TAL1, KLF10, GPR55, ADIPOQ, RASSF2, TRIB1, PPARGC1B
BP	GO:0007163	establishment or maintenance of cell polarity	32/1554	4.95E-03	AQP1, RHOB, RND3, RHOH, DLG2, EPHB1, FGF10, FOXF1, GSN, NCKAP1L, ILK, MAP1B, PKD1, ROCK1, SHH, TEK, WEE1, ROCK2, UST, SPRY1, SPRY2, CAP2, CRB1, CLIC4, RND1, AMOTL2, PARVA, RHOJ, JAM3, PARD3B, MPP7, AMOTL1
BP	GO:0030178	negative regulation of Wnt signaling pathway	32/1554	4.95E-03	CAV1, EGR1, FGF9, GRB10, HIC1, IGFBP2, IGFBP6, LRP1, NFATC1, NFATC4, ROR2, PRKN, SFRP1, SFRP2, SHH, TLE4, TBX18, DKK1, SOSTDC1, WWTR1, LATS2, RBMS3, DACT1, SOX17, JADE1, NKD1, TMEM88, CSNK1A1L, PRICKLE1, DACT3, SHISA6, TRABD2B
BP	GO:0043583	ear development	33/1554	5.01E-03	ALDH1A3, BCL2, BMP5, CEBPD, EYA1, FGF9, FGF10, FGFR1, GLI2, KCNK2, KCNK3, MSX1, NTRK3, ROR1, ROR2, PROX1, SALL1, SHH, ZEB1, TGFB3, NR4A3, ITGA8, DCHS1, KCNQ4, NTN1, PLPPR4, TSHZ1, SPRY2, LRIG1, SOBP, FAT4, OSR1, BMPER
BP	GO:1904427	positive regulation of calcium ion transmembrane transport	15/1554	5.06E-03	ABL1, ANK2, CACNA2D1, CACNB2, GPER1, HSPA2, PKD2, RYR2, CX3CL1, SNCA, STAC, TRPC1, RGN, AKAP6, JPH2
BP	GO:1901654	response to ketone	30/1554	5.14E-03	ADCY2, ADCY5, AQP1, AR, KLF9, CAV1, CDKN1A, DUSP1, FOS, FOSB, NTRK3, PRKAA2, PTGER4, PTGFR, SFRP1, SLIT3, TGFB3, TGFBR3, THBS1, TRH, FOSL1, KLF4, SLIT2, ROCK2, KLF2, TXNIP, SIRT1, ERRFI1, FOXP2, FBXO32

BP	GO:1902904	negative regulation of supramolecular fiber organization	24/1554	5.18E-03	ARHGAP6, CLU, CTNNA2, S1PR1, GSN, LDLR, MAP1B, PRKN, SNCA, TMOD1, SLIT2, DLC1, EMILIN1, TMEFF2, LMOD1, CLIP3, LMOD3, SPTBN4, ARHGAP28, NAV3, BMERB1, PHLDB2, MYADM, PLEKHH2
BP	GO:0046579	positive regulation of Ras protein signal transduction	14/1554	5.23E-03	LPAR1, FGF10, GPR17, IGF1, ITPKB, KITLG, NGF, GPR55, MAPRE2, AKAP13, P2RY10, RASGRP4, ABRA, P2RY8
BP	GO:0050432	catecholamine secretion	14/1554	5.23E-03	ADRA2A, ADRA2B, GDNF, KCNA2, KCNB1, P2RY1, PRKN, CXCL12, SNCA, SYT4, VIP, SYT11, P2RY12, SYT15
BP	GO:0009410	response to xenobiotic stimulus	41/1554	5.23E-03	AQP1, BCHE, CASQ2, CDO1, CES1, CNR2, CRHBP, CYP1B1, CYP2A7, EGR1, EPHX2, FMO2, FOSB, GHR, GNAO1, GRIN2A, GSTM5, NR4A2, PDE2A, PRKACB, PRKAR2B, PTGS1, RGS2, RORA, RYR2, RYR3, SLC8A1, SLC18A2, SNCA, STAT5B, TAC1, TACR3, AOC3, ARNT2, PPARGC1A, TIPARP, ERRFI1, AHRR, CYP2U1, FBXO32, APOBEC3A
BP	GO:0001755	neural crest cell migration	13/1554	5.29E-03	ANXA6, EDNRB, GDNF, KITLG, NRTN, PITX2, SHH, NRP2, HAND2, ZEB2, SEMA3A, CORO1C, SEMA3G
BP	GO:0043114	regulation of vascular permeability	10/1554	5.30E-03	ANGPT1, BDKRB2, CXCR2, NPR1, PDE2A, PDE3A, TACR2, TEK, SLIT2, AKAP12
BP	GO:1903427	negative regulation of reactive oxygen species biosynthetic process	10/1554	5.30E-03	ABCD2, ATP2B4, CAV1, CD34, FYN, PTGIS, SLC18A2, RGN, ROCK2, MPV17L
BP	GO:0009648	photoperiodism	8/1554	5.33E-03	CRY2, ID2, PER1, PPP1CB, PER3, PER2, USP2, SIK1
BP	GO:0043951	negative regulation of cAMP-mediated signaling	8/1554	5.33E-03	ATP2B4, LPAR1, PDE2A, PDE3A, PDE3B, PDE4D, RGS2, PDE11A
BP	GO:0046328	regulation of JNK cascade	29/1554	5.38E-03	CD40LG, CCN2, GADD45A, DUSP3, EPHB1, GRIK2, IL1RN, GADD45B, ROR2, PRKN, PER1, SFRP1, SFRP2, SLAMF1, TPD52L1, FZD7, RASSF2, ZEB2, PJA2, HIPK3, SEMA3A, FZD10, DKK1, TNIK, DACT1, MAP3K20, DUSP19, SH3RF3, SAMD5
BP	GO:1903708	positive regulation of hemopoiesis	29/1554	5.38E-03	ANXA1, AXL, ZFP36L1, CSF3, EGR3, FOS, GLI2, NCKAP1L, ID2, IL2, IL17A, ITPKB, JUN, LIF, KITLG, MPL, ROR2, PRKCA, SHH, STAT5B, TAL1, TGFBR2, KLF10, ZBTB16, TESPA1, TRIB1, VSIR, NFKBIZ, PPARGC1B
BP	GO:0030148	sphingolipid biosynthetic process	19/1554	5.39E-03	CCN1, P2RX1, PRKD1, ST8SIA1, UGCG, PLPP3, B3GALT2, B3GALT1, HACD1, LARGE1, ST6GALNAC6, ELOVL2, FA2H, CERS4, ST6GALNAC5, PPM1L, SGMS2, ST6GALNAC3, ST8SIA6
BP	GO:0021675	nerve development	16/1554	5.43E-03	ADARB1, BDNF, LPAR1, EGR2, EPHB1, ILK, KCNA2, NGF, NPTX1, NRTN, SALL1, NRP2, SEMA3A, LRIG1, COL25A1, PLXNA4
BP	GO:0034599	cellular response to oxidative stress	42/1554	5.43E-03	ABL1, ANXA1, AQP1, RHOB, AXL, BCL2, CYP1B1, FER, FOS, FYN, GPX3, HGF, JUN, MAPT, MCL1, MMP2, NR4A2, PRKN, PDGFRA, PKD2, PRKAA2, PRKD1, SNCA, SOD3, TNFAIP3, TPM1, TXNRD1, RNF112, NR4A3, RGN, KLF4, KLF2, FBLN5, PPARGC1A, KDM6B, SIRT1, PDGFD, LRRK2, CPEB2, PPARGC1B, NCOA7, MSRB3
BP	GO:0003401	axis elongation	9/1554	5.44E-03	ESR1, FGF10, SFRP1, SFRP2, SHH, MAGI2, SPRY1, SPRY2, NKD1
BP	GO:0010762	regulation of fibroblast migration	9/1554	5.44E-03	FER, FGF2, HAS1, DDR2, SLC8A1, THBS1, AKAP12, CORO1C, CYGB
BP	GO:0050849	negative regulation of calcium-mediated signaling	9/1554	5.44E-03	ACTN3, ATP2B4, CASQ2, CD22, CLIC2, RCAN1, ITPR1, PKD2, MYOZ2
BP	GO:0060292	long-term synaptic depression	9/1554	5.44E-03	CBLN1, GRIA1, GRID2, KCNB1, MAPT, SRF, STXBP1, SORCS3, SORCS2
BP	GO:0090075	relaxation of muscle	9/1554	5.44E-03	ATP1A2, HRC, KCNMA1, P2RY1, PDE4B, PDE4D, RGS2, SLC8A1, PDE5A
BP	GO:0070472	regulation of uterine smooth muscle contraction	5/1554	5.44E-03	ADRA2B, GPER1, TACR2, TACR1, TACR3
BP	GO:0071313	cellular response to caffeine	5/1554	5.44E-03	CASQ2, RYR2, RYR3, SLC8A1, PPARGC1A
BP	GO:0072203	cell proliferation involved in metanephros development	5/1554	5.44E-03	EGR1, MYC, PTCH1, SHH, OSR1
BP	GO:0072593	reactive oxygen species metabolic process	40/1554	5.53E-03	ABCD2, ARG2, ATP2B4, BCL2, CAV1, CD34, CDKN1A, CLU, CCN2, CX3CR1, CYP1B1, GADD45A, EPHX2, FYN, GPX3, HBB, CCN1, MAPT, PRKN, PDK4, PKD2, PTGIS, PTGS2, PTX3, RAB27A, RORA, SLC18A2, SNCA, SOD3, TGFBR2, THBS1, RGN, KLF4, ROCK2, HDAC4, KLF2, FBLN5, PID1, LRRK2, MPV17L

BP	GO:0046661	male sex differentiation	26/1554	5.66E-03	AR, BCL2, BCL2L2, BMP5, BMPR1A, ESR1, FGF9, FGF10, FLNA, GATA6, KIT, LHCGR, KITLG, ROR2, PDGFRA, SFRP1, SFRP2, SHH, TCF21, WNT2B, SEMA3A, ZFPM2, DHH, ASB1, ARID5B, RNF38
BP	GO:0006112	energy reserve metabolic process	17/1554	5.67E-03	ADRB3, GYS2, IGF1, IL6ST, LEPR, MYC, ENPP1, PPP1CB, PPP1R1A, PYGB, PER2, SORBS1, PRKAG2, PID1, PPP1R3B, STK40, PGM2L1
BP	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	15/1554	5.69E-03	ARG2, AXL, BPI, CD34, CHRNA7, CIDEA, IGF1, CX3CL1, SLAMF1, TNFAIP3, ADIPOQ, IRAK3, SYT11, ERRFI1, VSIR
BP	GO:0030308	negative regulation of cell growth	29/1554	5.75E-03	ACVRL1, APBB1, BCL2, CDKN1A, EPHA7, FHL1, GDF2, HYAL1, MSX1, NPR1, ENPP1, RGS2, SFRP1, SFRP2, SLIT3, SLIT2, NTN1, SEMA3A, SPART, SIRT1, SEMA3G, PRDM11, TSPYL2, SOX17, JADE1, RERG, DCUN1D3, DACT3, OSTN
BP	GO:0030902	hindbrain development	25/1554	5.89E-03	ABL1, BCL2, BMP5, CBLN1, CKB, CNTN1, CTNNA2, LPAR1, EGR2, FLNA, GLI2, GRID2, NFIB, PROX1, RORA, SHH, SSTR1, HERC1, DLC1, PPARGC1A, FAIM2, CEND1, PTBP2, WLS, FOXP2
BP	GO:0006026	aminoglycan catabolic process	14/1554	5.94E-03	CSPG4, DCN, FGF2, GPC5, HSPG2, HYAL1, OMD, OGN, PRELP, SDC2, SDC3, GPC6, LYVE1, HPSE2
BP	GO:0002573	myeloid leukocyte differentiation	31/1554	5.97E-03	ZFP36L1, CSF3, GPR183, EPHA2, FBN1, FOS, ID2, IL17A, IRF4, JUN, JUNB, KIT, LIF, MEF2C, KITLG, MITF, MYC, ROR2, PIK3R1, PRKCA, SFRP1, TAL1, TGFBR2, KLF10, GPR55, ADIPOQ, RASSF2, TSPAN2, TRIB1, SIRT1, PPARGC1B
BP	GO:0043949	regulation of cAMP-mediated signaling	12/1554	6.05E-03	ADCYAP1, ADCYAP1R1, ATP2B4, LPAR1, PDE2A, PDE3A, PDE3B, PDE4D, PRKCA, RGS2, RASD2, PDE11A
BP	GO:0070663	regulation of leukocyte proliferation	33/1554	6.09E-03	ANXA1, ARG2, BCL2, CD22, CD28, TNFSF8, CD40LG, CDKN1A, CD55, GPR183, FGF10, LRRC32, NCKAP1L, IGF1, IGFBP2, IL2, IL5RA, IL6R, IL6ST, MEF2C, KITLG, MPL, NFATC2, SHH, TAC1, TGFBR2, TNFAIP3, PDE5A, TNFRSF13B, PLA2G2D, VSIR, FCRL3, TNFRSF13C
BP	GO:0010738	regulation of protein kinase A signaling	7/1554	6.13E-03	ADRB2, ADIPOQ, AKAP6, AKAP12, PJA2, TCIM, LRRK2
BP	GO:0044262	cellular carbohydrate metabolic process	40/1554	6.26E-03	ACACB, ACTN3, ADCYAP1R1, GPER1, GYS2, HAS1, IGF1, IL6ST, IMPA2, INPP5A, LEPR, LHCGR, P2RY1, PRKN, PDK4, ENPP1, PPP1CB, PPP1R1A, PYGB, RORA, SNCA, DYSF, SLC25A12, PER2, RGN, ADIPOQ, HDAC4, SORBS1, PPARGC1A, TREH, SIRT1, PRKAG2, CSGALNACT1, RBKS, PPP1R3B, STK40, MIDN, C1QTNF3, SIK1, PGM2L1
BP	GO:0006022	aminoglycan metabolic process	27/1554	6.39E-03	ANGPT1, CSPG4, DCN, FGF2, GPC5, HAS1, HGF, HSPG2, HYAL1, OMD, OGN, PIM1, PRELP, SDC2, ST3GAL3, SDC3, HS3ST1, GPC6, UST, LYVE1, CSGALNACT1, HPSE2, NDNF, ITIH5, CHST9, DSEL, B3GAT2
BP	GO:0007190	activation of adenylate cyclase activity	10/1554	6.39E-03	ADCY2, ADCY5, ADCY9, ADCYAP1, ADRB2, ADRB3, EDNRA, LHCGR, VIPR2, CAP2
BP	GO:1901021	positive regulation of calcium ion transmembrane transporter activity	10/1554	6.39E-03	ANK2, CACNA2D1, CACNB2, HSPA2, PKD2, RYR2, STAC, RGN, AKAP6, JPH2
BP	GO:0034763	negative regulation of transmembrane transport	22/1554	6.44E-03	ACTN2, ADRA2A, BIN1, ATP1A2, CASQ2, CAV1, CLIC2, GEM, GRB10, KCNH2, ENPP1, PKD2, PRKCB, RGS2, THBS1, KCNAB1, DYSF, KCNE4, REM1, PID1, OSR1, OSTN
BP	GO:0014874	response to stimulus involved in regulation of muscle adaptation	6/1554	6.45E-03	ACTN3, UTRN, HDAC4, PPARGC1A, TRIM63, FBXO32
BP	GO:1901841	regulation of high voltage-gated calcium channel activity	6/1554	6.45E-03	CACNA2D1, CACNB2, GEM, PDE4B, DYSF, REM1
BP	GO:1905874	regulation of postsynaptic density organization	6/1554	6.45E-03	CBLN1, GRID2, NTRK3, PTPRD, NRXN1, LRRTM1
BP	GO:0060350	endochondral bone morphogenesis	15/1554	6.48E-03	ANXA6, COL6A2, COL6A3, COL13A1, MATN2, MEF2C, MEF2D, MMP16, STC1, TEK, TGFBR2, SCARA3, CSGALNACT1, COL21A1, TMEM119
BP	GO:0045137	development of primary sexual characteristics	33/1554	6.49E-03	ADCYAP1, ADCYAP1R1, AR, BCL2, BCL2L2, DACH1, ESR1, FGF9, FLNA, GATA6, INHBB, KIT, LHCGR, KITLG, PDGFRA, PGR, PTX3, SALL1, SFRP1, SFRP2, SLIT3, TCF21, WNT2B, SLIT2, ADAMTS1, SEMA3A, SIRT1, ZFPM2, TIPARP, DHH, ARID5B, OSR1, RNF38
BP	GO:0008645	hexose transmembrane transport	20/1554	6.59E-03	C3, EDNRA, GRB10, IGF1, MEF2A, ENPP1, PIK3R1, PRKCB, RAP1A, SLC2A3, SLC2A4, NR4A3, ADIPOQ, SORBS1, CLIP3, KLF15, PRKAG2, PID1, SLC2A12, OSTN

BP	GO:0014902	myotube differentiation	20/1554	6.59E-03	ADGRB3, BCL2, BDNF, DMPK, IGF1, MEF2C, NFATC2, SHH, BARX2, CACNA1H, HDAC4, KLHL41, EHD2, CDON, PLEKHO1, LMOD3, MYOCD, SIK1, RBM24, TMEM119
BP	GO:0019233	sensory perception of pain	19/1554	6.59E-03	ADCYAP1, CNR2, DLG2, EDNRB, EPHB1, FYN, GRIN2A, KCNA1, KCNA2, NDN, P2RY1, PTGS2, CXCL12, TAC1, VIP, TRPA1, MGLL, TMEM100, SCN3B
BP	GO:0001569	branching involved in blood vessel morphogenesis	9/1554	6.76E-03	ABL1, EDNRA, GDF2, NFATC4, SFRP2, SHH, SRF, TGFBR2, TBX20
BP	GO:0003176	aortic valve development	9/1554	6.76E-03	ELN, NFATC1, ROCK1, SLIT3, SLIT2, ROCK2, EMILIN1, TBX20, GATA5
BP	GO:0003171	atrioventricular valve development	8/1554	6.76E-03	BMPR1A, CCN1, SLIT3, TBX5, TGFBR2, DCHS1, OLFM1, TBX20
BP	GO:1904950	negative regulation of establishment of protein localization	30/1554	6.76E-03	ADRA2A, ANGPT1, ANXA1, APOD, ARG2, CD22, CD34, CIDEA, LRRC32, INHBB, KCNB1, MAPT, CD200, PRKN, PTGER4, CX3CL1, SFRP1, SYT4, TNFAIP3, ADIPOQ, STXBP5L, BAG3, MAPKBP1, SYT11, RAB23, MIDN, PKDCC, C1QTNF3, LRRK2, SSC5D
BP	GO:0045428	regulation of nitric oxide biosynthetic process	14/1554	6.77E-03	ATP2B4, CAV1, CD34, CLU, CX3CR1, HBB, PKD2, PTGIS, PTGS2, PTX3, RGN, KLF4, ROCK2, KLF2
BP	GO:0045637	regulation of myeloid cell differentiation	36/1554	6.88E-03	ZFP36L1, CSF3, FBN1, FOS, NCKAP1L, ID2, IL17A, ITPKB, JUN, LIF, MEF2C, MEIS1, MEIS2, KITLG, MITF, MPL, MYC, ROR2, PIK3R1, PRKCA, PRKCB, SFRP1, STAT5B, TAL1, THBS1, KLF10, ZFP36, ZBTB16, NR4A3, GPR55, ADIPOQ, RASSF2, TRIB1, MYL9, TNRC6C, PPARGC1B
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	32/1554	6.89E-03	ABL1, ADCYAP1, ADRA1A, ANGPT1, CHRNA7, CCN2, GPR183, FGF2, FGF10, GPER1, JUN, KIT, LRP1, P2RY1, PDGFRA, PLA2G5, PRKCA, RAP1A, CX3CL1, SLAMF1, TEK, FGF23, GPR55, HAND2, AKAP12, SPRY2, DNAJC27, PDGFD, GLIPR2, BMPER, ALKAL2, TNFAIP8L3
BP	GO:1990845	adaptive thermogenesis	25/1554	6.91E-03	ACTN3, ADCYAP1, ADRB2, ADRB3, CAV1, CIDEA, GPR3, GRB10, IRF4, LAMA4, LEPR, NOVA1, NPR3, PLCL1, THRA, PER2, ADIPOQ, ZNF516, PPARGC1A, ADAMTS5, ZNF423, KDM6B, PRDM16, EBF2, PPARGC1B
BP	GO:0001885	endothelial cell development	13/1554	6.99E-03	COL4A4, S1PR3, PDE2A, PDE4D, PECAM1, RAP1A, ROCK1, STC1, CLDN5, ROCK2, PPP1R16B, ARHGEF26, MYADM
BP	GO:0071466	cellular response to xenobiotic stimulus	28/1554	7.01E-03	AQP1, BCHE, CASQ2, CDO1, CES1, CRHBP, CYP1B1, CYP2A7, EGR1, EPHX2, FMO2, GHR, GSTM5, PDE2A, PTGS1, RORA, RYR2, RYR3, SLC8A1, STAT5B, AOC3, ARNT2, PPARGC1A, ERRFI1, AHRR, CYP2U1, FBXO32, APOBEC3A
BP	GO:2000649	regulation of sodium ion transmembrane transporter activity	12/1554	7.02E-03	ATP1A2, DMD, STOM, SCN1B, SCN2B, SCN4B, UTRN, SLMAP, FXYD6, SCN3B, OSR1, CNKSR3
BP	GO:0050900	leukocyte migration	62/1554	7.02E-03	ANGPT1, ANXA1, APOD, ATP1B2, CXCR5, BMP5, CALCA, CAV1, CD34, CD48, CCR6, CNR2, CX3CR1, DUSP1, GPR183, S1PR1, EDNRB, FER, FYN, GPR15, CXCL2, GYPC, NCKAP1L, IL1RN, IL6R, CXCR2, IL16, IL17A, ITGA1, ITGA5, ITGA9, ITGB3, KIT, KITLG, CD200, ROR2, PDE4B, PDE4D, PECAM1, PIK3R1, PTGER4, ROCK1, CX3CL1, SDC2, CXCL12, SELP, TEK, THBS1, DYSF, CH25H, SLIT2, SDC3, CXCL13, EMILIN1, LRCH1, SBDS, JAM2, P2RY12, PDGFD, CD99L2, JAM3, GCSAML
BP	GO:2000241	regulation of reproductive process	24/1554	7.18E-03	AR, DUSP1, EDNRB, ESR1, GPR3, IGF1, INHBB, LIF, MSX1, NPR2, OVOL1, P2RY1, PDE3A, PRKACB, SFRP1, SHH, STXBP1, VIP, PDE5A, CACNA1H, HDAC4, SEMA3A, ZFPM2, HPGDS
BP	GO:0051091	positive regulation of DNA-binding transcription factor activity	37/1554	7.25E-03	AR, CAMK2A, CAV1, CD40LG, CLU, CSF3, CX3CR1, EDA, EPHA5, ESR1, FER, KIT, CD200, ROR1, DDR2, PRKCB, PRKD1, RELN, CX3CL1, SHH, SRF, FOSL1, PLPP3, BCL10, LRRFIP1, RPS6KA5, HDAC4, PPARGC1A, MID2, TRIM31, IRAK3, ERC1, ARID5B, MYOCD, PPARGC1B, JMY, ABRA
BP	GO:0099601	regulation of neurotransmitter receptor activity	15/1554	7.32E-03	ACTN2, ADRB2, CRHBP, DLG2, GRIA1, GRIN2A, MEF2C, NPTX1, RELN, PPARGC1A, NLGN1, NLGN3, LYNX1, GSG1L, SHISA6
BP	GO:0030501	positive regulation of bone mineralization	10/1554	7.69E-03	ADRB2, BMPR1A, GPM6B, CCN1, MEF2C, SLC8A1, TGFB3, PKDCC, OSR1, TMEM119
BP	GO:0038179	neurotrophin signaling pathway	10/1554	7.69E-03	BDNF, NDN, NGF, NGFR, NTRK3, RAP1A, MAGI2, SPRY1, SPRY2, TMEM108
BP	GO:0050671	positive regulation of lymphocyte proliferation	22/1554	7.70E-03	ANXA1, BCL2, CD28, CD40LG, CDKN1A, CD55, GPR183, FGF10, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, MEF2C, MPL, NFATC2, SHH, TAC1, TGFBR2, FCRL3, TNFRSF13C
BP	GO:0060415	muscle tissue morphogenesis	16/1554	7.73E-03	ACTC1, ADARB1, BMPR1A, S1PR1, SMAD7, MYL3, MYLK, PROX1, RYR2, TGFBR3, TNNT2, TPM1, MYOM2, HAND1, ZFPM2, TBX20

BP	GO:0010469	regulation of signaling receptor activity	27/1554	8.03E-03	ACTN2, ADRA2A, ADRA2B, ADRB2, CRHBP, DLG2, GRIA1, GRIN2A, MEF2C, NPTX1, P2RY1, PDE4D, RELN, TAL1, GPRC5A, NEURL1, PPARGC1A, NLGN1, DKK1, CNRIP1, ERRFI1, NLGN3, GREM2, LYNX1, WFIKKN2, GSG1L, SHISA6
BP	GO:0015749	monosaccharide transmembrane transport	20/1554	8.05E-03	C3, EDNRA, GRB10, IGF1, MEF2A, ENPP1, PIK3R1, PRKCB, RAP1A, SLC2A3, SLC2A4, NR4A3, ADIPOQ, SORBS1, CLIP3, KLF15, PRKAG2, PID1, SLC2A12, OSTN
BP	GO:0046651	lymphocyte proliferation	38/1554	8.10E-03	ABL1, ANXA1, ARG2, BCL2, MS4A1, CD22, CD28, TNFSF8, CD40LG, CD79A, CDKN1A, CR2, CD55, GPR183, FGF10, FYN, LRRC32, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, MEF2C, MPL, NFATC2, PPP3CB, SATB1, SHH, TAC1, TGFBR2, PDE5A, TNFRSF13B, PLA2G2D, VSIR, FCRL3, TNFRSF13C, GAPT
BP	GO:0021697	cerebellar cortex formation	7/1554	8.10E-03	CBLN1, GRID2, PROX1, RORA, HERC1, FAIM2, CEND1
BP	GO:0030728	ovulation	7/1554	8.10E-03	INHBB, PGR, PTGS2, RGS2, TNFAIP6, ADAMTS1, SIRT1
BP	GO:0072111	cell proliferation involved in kidney development	7/1554	8.10E-03	EGR1, IL6R, MYC, PTCH1, SHH, PDGFD, OSR1
BP	GO:0098743	cell aggregation	7/1554	8.10E-03	CCN2, MGP, MPZ, ROR2, PKD1, THRA, BARX2
BP	GO:0022602	ovulation cycle process	11/1554	8.10E-03	ESR1, LHCGR, PAM, PDGFRA, PGR, PTX3, SLIT3, TGFB3, SLIT2, ADAMTS1, SIRT1
BP	GO:0050919	negative chemotaxis	11/1554	8.10E-03	EPHA7, ITGB3, SLIT3, UNC5C, NRP2, SLIT2, NTN1, SEMA3A, FLRT2, SEMA3G, PLXNA4
BP	GO:0099172	presynapse organization	11/1554	8.10E-03	CBLN1, NTRK3, PTPRD, SNCA, PPFIA2, NRXN1, IL1RAPL1, NLGN1, DKK1, NLGN3, LRRTM1
BP	GO:0071320	cellular response to cAMP	12/1554	8.20E-03	AQP1, ZFP36L1, CRHBP, IGFBP5, PDE2A, PKD2, RAP1A, SLC8A1, SLC8A3, STC1, ADIPOQ, AKAP6
BP	GO:0010092	specification of animal organ identity	9/1554	8.26E-03	AR, FGF10, FGFR1, GDNF, MEF2C, WNT2B, SPRY1, DKK1, GATA5
BP	GO:0019934	cGMP-mediated signaling	9/1554	8.26E-03	AQP1, EDNRB, NPR1, NPR2, PDE2A, PDE3A, PRKAR2B, THBS1, PDE11A
BP	GO:0033028	myeloid cell apoptotic process	9/1554	8.26E-03	ANXA1, BCL2, CXCR2, ITPKB, MEF2C, KITLG, THRA, ADIPOQ, SIRT1
BP	GO:0051955	regulation of amino acid transport	9/1554	8.26E-03	ATP1A2, GRM7, RGS2, SNCA, STXBP1, SYT4, TRH, PER2, OSR1
BP	GO:0060603	mammary gland duct morphogenesis	9/1554	8.26E-03	AR, EPHA2, ESR1, FGF10, GLI2, PGR, PTCH1, NTN1, SOSTDC1
BP	GO:0030183	B cell differentiation	22/1554	8.33E-03	ABL1, BCL2, ZFP36L1, MS4A1, CD40LG, CD79A, CD79B, CDH17, KLF6, CR2, GPR183, NCKAP1L, ID2, KIT, PIK3R1, POU2F2, SFRP1, ITM2A, HDAC4, AICDA, FCRL3, DOCK11
BP	GO:0032946	positive regulation of mononuclear cell proliferation	22/1554	8.33E-03	ANXA1, BCL2, CD28, CD40LG, CDKN1A, CD55, GPR183, FGF10, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, MEF2C, MPL, NFATC2, SHH, TAC1, TGFBR2, FCRL3, TNFRSF13C
BP	GO:0008154	actin polymerization or depolymerization	31/1554	8.35E-03	ACTN2, BIN1, ARHGAP6, CFL2, CSF3, CTNNA2, ELN, FER, GSN, NCKAP1L, CXCL12, TMOD1, WIPF1, GAS7, SLIT2, CDC42EP2, CAP2, CDC42EP3, WASF3, DSTN, FAM107A, LMOD1, SNX9, ENAH, LMOD3, MICAL3, SPTBN4, ARHGAP28, MYADM, PLEKHH2, JMY
BP	GO:0006814	sodium ion transport	32/1554	8.37E-03	ADRB2, ATP1A2, ATP1B2, ATP2B4, CNTN1, DMD, STOM, PER1, PKD2, SCN1B, SCN2B, SCN4B, SCN7A, SGK1, SLC8A2, SLC8A1, SLC8A3, SNTA1, UTRN, SLMAP, FXYD6, SCN3B, SLC17A7, SLC24A3, SPTBN4, SLC5A7, SLC24A4, OSR1, SIK1, CNKSR3, NALCN, SLC9A9
BP	GO:0002792	negative regulation of peptide secretion	24/1554	8.42E-03	ADRA2A, ANGPT1, ANXA1, ARG2, CD22, CD34, CIDEA, CRHBP, LRRC32, INHBB, KCNB1, CD200, PRKN, PTGER4, CX3CL1, SFRP1, SYT4, TNFAIP3, STXBP5L, MAPKBP1, SYT11, MIDN, C1QTNF3, SSC5D
BP	GO:0014065	phosphatidylinositol 3-kinase signaling	24/1554	8.42E-03	ANGPT1, ZFP36L1, CD28, CSF3, DCN, FGFR1, FYN, GPER1, HGF, IGF1, KIT, NTRK3, PDGFRA, PIK3R1, RELN, SELP, TEK, PIP5K1B, IER3, KLF4, SIRT1, PPP1R16B, PREX2, PDGFD
BP	GO:0048643	positive regulation of skeletal muscle tissue development	8/1554	8.43E-03	ACTN3, BCL2, MEF2C, SHH, CDON, LMOD3, SOX17, RBM24
BP	GO:0072207	metanephric epithelium development	8/1554	8.43E-03	CXCR2, LIF, PKD1, PKD2, ADIPOQ, WWTR1, FAT4, OSR1
BP	GO:0098810	neurotransmitter reuptake	8/1554	8.43E-03	ATP1A2, GDNF, GPM6B, ITGB3, PRKN, SLC18A2, SNCA, PER2
BP	GO:0021561	facial nerve development	5/1554	8.43E-03	ADARB1, EGR2, NRP2, SEMA3A, PLXNA4
BP	GO:0021604	cranial nerve structural organization	5/1554	8.43E-03	EGR2, KCNA2, NRP2, SEMA3A, PLXNA4

BP	GO:0021610	facial nerve morphogenesis	5/1554	8.43E-03	ADARB1, EGR2, NRP2, SEMA3A, PLXNA4
BP	GO:0032060	bleb assembly	5/1554	8.43E-03	LPAR1, EMP1, MYLK, PMP22, ROCK1
BP	GO:0070471	uterine smooth muscle contraction	5/1554	8.43E-03	ADRA2B, GPER1, TACR2, TACR1, TACR3
BP	GO:1905902	regulation of mesoderm formation	5/1554	8.43E-03	BMPR1A, FGFR1, SFRP2, DKK1, SOX17
BP	GO:0098659	inorganic cation import across plasma membrane	16/1554	8.49E-03	ATP1A2, ATP1B2, ATP2B4, CACNA2D1, CNGA3, FYN, KCNH2, KCNJ3, KCNJ8, KCNJ12, SLC8A1, SLC8A3, ABCC9, SLC39A14, SLC9A9, FAM155A
BP	GO:0099587	inorganic ion import across plasma membrane	16/1554	8.49E-03	ATP1A2, ATP1B2, ATP2B4, CACNA2D1, CNGA3, FYN, KCNH2, KCNJ3, KCNJ8, KCNJ12, SLC8A1, SLC8A3, ABCC9, SLC39A14, SLC9A9, FAM155A
BP	GO:0050770	regulation of axonogenesis	28/1554	8.60E-03	ABL1, BDNF, CDH4, DPYSL2, EPHA7, ILK, LRP1, MAP1B, MAP6, MAPT, NGF, NGFR, NTRK3, CXCL12, SRF, CNTN2, SLIT2, NTN1, ZEB2, UST, SEMA3A, OLFM1, SPART, SEMA3G, ZSWIM5, ZSWIM6, TRAK2, PLXNA4
BP	GO:0030099	myeloid cell differentiation	53/1554	8.64E-03	ACTN1, ZFP36L1, CSF3, GPR183, EPHA2, FBN1, FOS, NCKAP1L, ID2, IL17A, IRF4, ITPKB, JUN, JUNB, KIT, LIF, MEF2C, MEIS1, MEIS2, KITLG, MITF, MPL, MYC, ROR2, PIK3R1, PRKCA, PRKCB, SFRP1, SRF, STAT5B, TAL1, TGFBR2, TGFBR3, THBS1, THRA, KLF10, ZFP36, ZBTB16, NR4A3, DYRK3, GPR55, ADIPOQ, RASSF2, TSPAN2, TRIB1, KLF2, MYL9, SIRT1, SNRK, SOX6, TNRC6C, RASGRP4, PPARGC1B
BP	GO:0010812	negative regulation of cell-substrate adhesion	14/1554	8.64E-03	ACVRL1, APOD, ARHGAP6, LRP1, PIK3R1, CX3CL1, THBS1, FZD7, DLC1, FAM107A, CORO1C, AJAP1, PHLDB2, NEXMIF
BP	GO:0035914	skeletal muscle cell differentiation	14/1554	8.64E-03	ATF3, EGR1, EGR2, EPHB1, FOS, HLF, MEF2C, MEF2D, BTG2, KLHL41, MAFF, CDON, MYOCD, RBM24
BP	GO:0001837	epithelial to mesenchymal transition	23/1554	8.64E-03	BMP5, LDLRAD4, EPHA3, HGF, SMAD7, MSX1, SFRP1, SFRP2, TBX5, TGFB1I1, TGFB3, TGFBR2, TGFBR3, SPRY1, OLFM1, WWTR1, TMEM100, KBTBD8, PHLDB2, VASN, DACT3, GLIPR2, RFLNB
BP	GO:0045639	positive regulation of myeloid cell differentiation	17/1554	8.66E-03	ZFP36L1, CSF3, FOS, NCKAP1L, ID2, IL17A, JUN, LIF, KITLG, MPL, ROR2, PRKCA, STAT5B, TAL1, KLF10, TRIB1, PPARGC1B
BP	GO:0048872	homeostasis of number of cells	35/1554	8.66E-03	ABL1, ANXA1, AXL, BCL2, ZFP36L1, GPR183, NCKAP1L, ID2, IL2, CXCR2, ITPKB, KIT, MEF2C, KITLG, MPL, PDE4B, PPP3CB, SRF, STAT5B, TAL1, TGFBR3, THRA, TNFAIP3, ZFP36, DYRK3, BCL10, RASSF2, AKT3, KLF2, TNFRSF13B, SOX6, JAM3, TNFRSF13C, DOCK11, GAPT
BP	GO:0097529	myeloid leukocyte migration	31/1554	8.79E-03	ANXA1, CALCA, CX3CR1, DUSP1, EDNRB, CXCL2, NCKAP1L, IL1RN, IL6R, CXCR2, IL17A, ITGA1, ITGA9, KIT, CD200, ROR2, PDE4B, PDE4D, PECAM1, PTGER4, CX3CL1, CXCL12, THBS1, DYSF, SLIT2, CXCL13, EMILIN1, P2RY12, PDGFD, CD99L2, JAM3
BP	GO:0060572	morphogenesis of an epithelial bud	6/1554	8.79E-03	AR, FGF10, GLI2, SHH, WNT2B, SOSTDC1
BP	GO:0061684	chaperone-mediated autophagy	6/1554	8.79E-03	CLU, PLK3, EEF1A1, SNCA, BAG3, SYNPO2
BP	GO:0072224	metanephric glomerulus development	6/1554	8.79E-03	CD34, EGR1, PDGFRA, TCF21, ADIPOQ, OSR1
BP	GO:1902992	negative regulation of amyloid precursor protein catabolic process	6/1554	8.79E-03	BIN1, CHRNA7, CLU, IGF1, ROCK1, SPON1
BP	GO:0032943	mononuclear cell proliferation	38/1554	8.83E-03	ABL1, ANXA1, ARG2, BCL2, MS4A1, CD22, CD28, TNFSF8, CD40LG, CD79A, CDKN1A, CR2, CD55, GPR183, FGF10, FYN, LRRC32, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, MEF2C, MPL, NFATC2, PPP3CB, SATB1, SHH, TAC1, TGFBR2, PDE5A, TNFRSF13B, PLA2G2D, VSIR, FCRL3, TNFRSF13C, GAPT
BP	GO:0042476	odontogenesis	22/1554	8.89E-03	AQP1, BMPR1A, CD34, EDA, FGF10, GLI2, GNAO1, MSX1, NFIC, PAM, PDGFRA, PITX2, SHH, TGFB3, HAND1, HAND2, ENAM, ADAMTS5, SOSTDC1, SLC24A4, OSR1, RSPO2
BP	GO:0045995	regulation of embryonic development	22/1554	8.89E-03	AR, BMPR1A, FGFR1, GDNF, IGF1, IL1RN, LAMA4, PRKACB, SFRP1, SFRP2, SHH, WNT2B, FZD7, TBX18, KLF4, ADIPOQ, DKK1, SOX17, NKD1, PHLDB2, MYADM, OSR1
BP	GO:0071384	cellular response to corticosteroid stimulus	13/1554	9.00E-03	ADCYAP1, ANXA1, AQP1, ZFP36L1, KLF9, GPER1, STC1, ZFP36, FAM107A, AKAP13, ERRFI1, FBXO32, CREBRF
BP	GO:0046578	regulation of Ras protein signal transduction	34/1554	9.24E-03	ABL1, ADRA1A, LPAR1, FGF10, GPR17, IGF1, ITPKB, KITLG, NGF, PSD, TIMP2, GPR55, ARHGEF10, ARHGEF17, RASA4, SPRY1, SPRY2, DLC1, MAPRE2, AKAP13, RASA3, ARHGEF15, ARHGEF9, KANK2, ARHGEF26, TIAM2, P2RY10, PREX2, KCTD10, ARHGEF25, RASGRP4, ABRA, P2RY8, ARHGEF37

BP	GO:0051224	negative regulation of protein transport	29/1554	9.24E-03	ADRA2A, ANGPT1, ANXA1, APOD, ARG2, CD22, CD34, CIDEA, LRRC32, INHBB, KCNB1, CD200, PRKN, PTGER4, CX3CL1, SFRP1, SYT4, TNFAIP3, ADIPOQ, STXBP5L, BAG3, MAPKBP1, SYT11, RAB23, MIDN, PKDCC, C1QTNF3, LRRK2, SSC5D
BP	GO:0002763	positive regulation of myeloid leukocyte differentiation	12/1554	9.24E-03	ZFP36L1, FOS, ID2, IL17A, JUN, LIF, KITLG, ROR2, PRKCA, KLF10, TRIB1, PPARGC1B
BP	GO:0048066	developmental pigmentation	11/1554	9.24E-03	BCL2, DCT, EDNRB, KIT, MEF2C, KITLG, MITF, ENPP1, RAB27A, ZEB2, ADAMTS9
BP	GO:0061383	trabecula morphogenesis	11/1554	9.24E-03	BMP5, BMPR1A, S1PR1, MMP2, RBP4, SFRP1, SRF, TEK, TGFBR3, ADAMTS1, PPARGC1B
BP	GO:0070169	positive regulation of biomineral tissue development	11/1554	9.24E-03	ADRB2, BMPR1A, GPM6B, CCN1, MEF2C, SLC8A1, TGFB3, ENAM, PKDCC, OSR1, TMEM119
BP	GO:1903115	regulation of actin filament-based movement	11/1554	9.24E-03	BIN1, ANK2, ATP1A2, CACNA1C, CAV1, FLNA, PDE4B, PDE4D, RYR2, STC1, CTNNA3
BP	GO:0050709	negative regulation of protein secretion	23/1554	9.31E-03	ADRA2A, ANGPT1, ANXA1, ARG2, CD22, CD34, CIDEA, LRRC32, INHBB, KCNB1, CD200, PRKN, PTGER4, CX3CL1, SFRP1, SYT4, TNFAIP3, STXBP5L, MAPKBP1, SYT11, MIDN, C1QTNF3, SSC5D
BP	GO:0034219	carbohydrate transmembrane transport	20/1554	9.36E-03	C3, EDNRA, GRB10, IGF1, MEF2A, ENPP1, PIK3R1, PRKCB, RAP1A, SLC2A3, SLC2A4, NR4A3, ADIPOQ, SORBS1, CLIP3, KLF15, PRKAG2, PID1, SLC2A12, OSTN
BP	GO:0009914	hormone transport	43/1554	9.36E-03	ADCY5, ADCYAP1, ADRA2A, ADRA2B, SLC25A4, ANXA1, CACNA1C, CPE, CRHBP, CRYM, EPHA5, FGFR1, GPER1, IL1RN, INHBB, ITPR1, KCNB1, LIF, LRP1, P2RY1, PRKN, PPP3CB, PRKCA, PTPRN2, RAP1A, RBP4, SFRP1, SLC16A2, TAC1, TACR2, TRH, VIP, FGF23, LTBP4, PER2, ADIPOQ, STXBP5L, MYRIP, SLCO1C1, SYBU, G6PC2, MIDN, C1QTNF3
BP	GO:0045445	myoblast differentiation	16/1554	9.37E-03	ZFP36L1, IGF1, ILK, MBNL1, MEF2C, PITX1, SHH, SRF, KCNAB1, KLHL41, SOSTDC1, CDON, MYOCD, PRICKLE1, RANBP3L, RBM24
BP	GO:0099565	chemical synaptic transmission, postsynaptic	19/1554	9.51E-03	ADRB2, CBLN1, CHRNA7, GRID2, GRIK2, GRIN2A, MEF2C, MPP2, P2RX1, RELN, SNCA, NRXN1, NLGN1, IGSF9B, RIMS1, NLGN3, SLC17A7, TMEM108, LRRK2
BP	GO:0060079	excitatory postsynaptic potential	18/1554	9.58E-03	ADRB2, CBLN1, CHRNA7, GRID2, GRIK2, GRIN2A, MEF2C, MPP2, P2RX1, RELN, SNCA, NRXN1, NLGN1, RIMS1, NLGN3, SLC17A7, TMEM108, LRRK2
BP	GO:0001936	regulation of endothelial cell proliferation	27/1554	9.65E-03	ACVRL1, CAV1, EGR3, F3, FGF2, FGFR1, GDF2, NR4A1, ITGB3, JUN, MEF2C, NGFR, PRKCA, PRKD1, PROX1, CXCL12, TEK, THBS1, VIP, DYSF, TNFSF12, NRP2, AKT3, SIRT1, PPP1R16B, JCAD, ATOH8
BP	GO:0008360	regulation of cell shape	24/1554	9.66E-03	ANXA1, RHOB, RND3, RHOH, LPAR1, FYN, ITGA7, KIT, P2RY1, PALM, TPM1, DLC1, CDC42EP2, CDC42EP3, WASF3, FERMT2, BVES, RND1, PLEKHO1, PARVA, RHOJ, SHROOM3, PLXNA4, SYNE3
BP	GO:0042698	ovulation cycle	14/1554	9.66E-03	AXL, EGR1, ESR1, HAS1, LHCGR, PAM, PDGFRA, PGR, PTX3, SLIT3, TGFB3, SLIT2, ADAMTS1, SIRT1
BP	GO:0055008	cardiac muscle tissue morphogenesis	14/1554	9.66E-03	ACTC1, BMPR1A, S1PR1, SMAD7, MYL3, PROX1, RYR2, TGFBR3, TNNT2, TPM1, MYOM2, HAND1, ZFPM2, TBX20
BP	GO:2000243	positive regulation of reproductive process	14/1554	9.66E-03	AR, EDNRB, INHBB, MSX1, OVOL1, P2RY1, PDE3A, SHH, VIP, PDE5A, CACNA1H, HDAC4, SEMA3A, ZFPM2
BP	GO:0007435	salivary gland morphogenesis	9/1554	9.72E-03	EDA, FGF7, FGF10, FGFR1, HGF, NFIB, SHH, TGFB3, SEMA3A
BP	GO:0031128	developmental induction	9/1554	9.72E-03	AR, FGF10, FGFR1, GDNF, SALL1, WNT2B, SPRY1, DKK1, GATA5
BP	GO:0045920	negative regulation of exocytosis	9/1554	9.72E-03	ADRA2A, ANXA1, FOXF1, PRKN, RAP1A, SNCA, SYT4, IL1RAPL1, STXBP6
BP	GO:0070884	regulation of calcineurin-NFAT signaling cascade	9/1554	9.72E-03	ACTN3, ATP2B4, RCAN1, IGF1, AKAP6, RCAN2, LMCD1, MYOZ2, C10orf71
BP	GO:0106056	regulation of calcineurin-mediated signaling	9/1554	9.72E-03	ACTN3, ATP2B4, RCAN1, IGF1, AKAP6, RCAN2, LMCD1, MYOZ2, C10orf71
BP	GO:0009743	response to carbohydrate	33/1554	9.80E-03	ADCY5, ADRA2A, ZFP36L1, COL4A3, COL6A2, CCN2, CYP7A1, EGR1, EPHA5, GPER1, GYS2, KCNB1, LRP1, MAP1B, ME1, PPP3CB, PRKAA2, PRKCB, PTGS2, PTPRN2, RAP1A, SLC8A1, SRF, VAMP2, TGFBR2, THBS1, TRH, ADIPOQ, NAMPT, TXNIP, PPARGC1A, SYBU, COLEC12
BP	GO:0050863	regulation of T cell activation	42/1554	1.01E-02	ABL1, ANXA1, ARG2, PRDM1, CAV1, CD5, CD28, TNFSF8, CD40LG, MAP3K8, CD55, DUSP3, EGR3, FYN, LRRC32, GLI2, GSN, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, IRF4, ITPKB, SMAD7, NFATC2, PIK3R1, SHH, ZEB1, TGFBR2, ZBTB16, PDE5A, BCL10, GRAP2, TESPA1, FGL2, PLA2G2D, VSIR, NFKBIZ, TNFRSF13C, BTLA

BP	GO:0022010	central nervous system myelination	7/1554	1.01E-02	ASPA, CLU, ID4, PLP1, CNTN2, CNTNAP1, FA2H
BP	GO:0032291	axon ensheathment in central nervous system	7/1554	1.01E-02	ASPA, CLU, ID4, PLP1, CNTN2, CNTNAP1, FA2H
BP	GO:0044321	response to leptin	7/1554	1.01E-02	INHBB, LEPR, UGCG, NR4A3, FGF23, SIRT1, PID1
BP	GO:0046058	cAMP metabolic process	7/1554	1.01E-02	ADCY2, ADCY5, ADCY9, EPHA2, PDE4B, PDE4D, PDE7B
BP	GO:0032922	circadian regulation of gene expression	13/1554	1.01E-02	CRY2, EGR1, ID2, NGFR, PER1, PPP1CB, RORA, PER3, PER2, USP2, NAMPT, PPARGC1A, SIRT1
BP	GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	13/1554	1.01E-02	ACVRL1, BMP5, BMPR1A, LDLRAD4, GDF2, GDF10, INHBB, SMAD7, TGFB3, RBPMS, EMILIN1, DKK1, BMPER
BP	GO:1901862	negative regulation of muscle tissue development	13/1554	1.01E-02	EPHB1, IGFBP5, KCNK2, MEIS1, RBP4, RGS2, SHH, TBX5, TGFBR2, FZD7, DKK1, SOX6, MYOCD
BP	GO:0007416	synapse assembly	27/1554	1.03E-02	ADGRB3, BDNF, CBLN1, EPHA7, EPHB1, GABRA2, GPM6A, GRID2, MAP1B, MEF2C, NTRK3, PTPRD, SNCA, NRXN1, NRXN2, NTN1, MAGI2, PDLIM5, IL1RAPL1, NLGN1, DKK1, FLRT2, NLGN3, CLSTN2, LRRC4, LRRC4B, LRRTM1
BP	GO:0050772	positive regulation of axonogenesis	16/1554	1.04E-02	BDNF, CDH4, ILK, LRP1, MAP1B, MAP6, MAPT, NGF, NGFR, NTRK3, CXCL12, SRF, SLIT2, NTN1, ZEB2, PLXNA4
BP	GO:0021575	hindbrain morphogenesis	10/1554	1.04E-02	ABL1, CBLN1, GLI2, GRID2, PROX1, RORA, HERC1, DLC1, FAIM2, CEND1
BP	GO:0035136	forelimb morphogenesis	10/1554	1.04E-02	CACNA1C, MSX1, SHH, TBX5, WNT9A, ZBTB16, RECK, SALL3, OSR1, RSPO2
BP	GO:0098815	modulation of excitatory postsynaptic potential	10/1554	1.04E-02	ADRB2, CBLN1, CHRNA7, RELN, NRXN1, NLGN1, RIMS1, NLGN3, TMEM108, LRRK2
BP	GO:1902893	regulation of pri-miRNA transcription by RNA polymerase II	10/1554	1.04E-02	BMPR1A, FOS, JUN, NFATC4, NFIB, NGFR, SRF, TEAD1, HDAC4, ATOH8
BP	GO:0031668	cellular response to extracellular stimulus	37/1554	1.05E-02	AQP2, ATF3, AXL, BCL2, CDKN1A, FOS, FYN, INHBB, JUN, KCNB1, NR4A2, P2RY1, PDK4, PIM1, PRKAA2, PRKD1, PTGS2, RYR3, SFRP1, SFRP2, SRF, KLF10, WNT2B, FOSL1, FGF23, NAMPT, FAM107A, SIRT1, GABARAPL1, KANK2, RRAGD, P2RY12, CPEB4, MYOCD, LRRK2, SIK1, SIK1B
BP	GO:1903305	regulation of regulated secretory pathway	25/1554	1.06E-02	ADRA1A, ADRA2A, CACNB2, CAMK2A, CHRM2, FER, FOXF1, KCNB1, P2RX1, P2RY1, PRKCB, RAB27A, RAP1A, STXBP1, SYT4, PPFIA2, CACNA1H, STXBP5L, RIMS3, NLGN1, RIMS1, SYT11, NCS1, SYT15, LRRK2
BP	GO:0043268	positive regulation of potassium ion transport	11/1554	1.06E-02	ACTN2, ADRA2A, ANK2, ATP1B2, FHL1, FLNA, KCNA1, KCNH2, KCNMB1, AKAP6, LRRC52
BP	GO:0045912	negative regulation of carbohydrate metabolic process	11/1554	1.06E-02	ACTN3, LEPR, PRKN, ENPP1, SLC25A12, ADIPOQ, HDAC4, PPARGC1A, MIDN, C1QTNF3, SIK1
BP	GO:0071383	cellular response to steroid hormone stimulus	35/1554	1.08E-02	ADCYAP1, ANXA1, AQP1, AR, ATP1A2, ZFP36L1, KLF9, CRY2, ESR1, GPER1, NR4A1, NR3C2, NR4A2, PER1, PGR, RORA, RORB, SFRP1, STC1, TCF21, NR2F1, TGFB1I1, THRA, ZFP36, NR4A3, PPARGC1A, FAM107A, AKAP13, SIRT1, KANK2, ERRFI1, CALCOCO1, FBXO32, PPARGC1B, CREBRF
BP	GO:0042471	ear morphogenesis	20/1554	1.11E-02	ALDH1A3, EYA1, FGF9, FGF10, FGFR1, GLI2, MSX1, ROR2, PROX1, SALL1, ZEB1, NR4A3, ITGA8, KCNQ4, NTN1, TSHZ1, SPRY2, LRIG1, SOBP, OSR1
BP	GO:0007254	JNK cascade	31/1554	1.12E-02	CD40LG, CCN2, GADD45A, DUSP3, EPHB1, GRIK2, IL1RN, GADD45B, ROR2, PRKN, PER1, PTGER4, SFRP1, SFRP2, SLAMF1, TPD52L1, FZD7, RASSF2, ZEB2, PJA2, HIPK3, TRIB1, SEMA3A, FZD10, DKK1, TNIK, DACT1, MAP3K20, DUSP19, SH3RF3, SAMD5
BP	GO:0006024	glycosaminoglycan biosynthetic process	19/1554	1.14E-02	ANGPT1, CSPG4, DCN, GPC5, HAS1, HSPG2, HYAL1, OMD, OGN, PRELP, SDC2, ST3GAL3, SDC3, HS3ST1, GPC6, UST, CSGALNACT1, CHST9, DSEL
BP	GO:0061387	regulation of extent of cell growth	19/1554	1.14E-02	ABL1, BDNF, CDH4, DPYSL2, EPHA7, ILK, LRP1, MAP1B, MAPT, NGF, NTRK3, CXCL12, SRF, NTN1, SEMA3A, OLFM1, SPART, SEMA3G, PLXNA4
BP	GO:0003203	endocardial cushion morphogenesis	9/1554	1.18E-02	ACVRL1, BMP5, BMPR1A, MSX1, TGFBR2, DCHS1, TMEM100, TBX20, GATA5
BP	GO:0032102	negative regulation of response to external stimulus	47/1554	1.18E-02	ADCYAP1, ABCD2, APOD, ARG2, CD34, CDKN1A, CNR2, CTNNA2, DUSP1, DUSP3, FGF2, FOXF1, GPR17, GPER1, GRID2, HGF, IGF1, IL2, LDLR, CD200, SERPINB2, PDGFRA, PTGER4, PTGIS, RORA, CX3CL1, TEK, THBS1, TNFAIP3, TNFAIP6, SOCS3, KLF4, SLIT2, ADIPOQ, NRXN1, TRIB1, SEMA3A, CXCL13, FGL2, MAPKBP1, KANK2, AJAP1, SEMA3G, RGMA, PHLDB2, C1QTNF3, NLRP6

BP	GO:0046068	cGMP metabolic process	6/1554	1.18E-02	NPR1, NPR2, PDE1A, PDE2A, RORA, PDE5A
BP	GO:0048532	anatomical structure arrangement	6/1554	1.18E-02	BMPR1A, EGR2, KCNA2, NRP2, SEMA3A, PLXNA4
BP	GO:0030177	positive regulation of Wnt signaling pathway	27/1554	1.19E-02	ABL1, CAV1, EDA, FGF9, FGF10, GPC5, ILK, ROR2, SALL1, SFRP1, SFRP2, SHH, TBL1X, TNFAIP3, RECK, SCEL, ZEB2, DKK1, DAAM2, ADGRA2, DACT1, WLS, RSPO3, NKD1, DIXDC1, LRRK2, RSPO2
BP	GO:0097191	extrinsic apoptotic signaling pathway	32/1554	1.19E-02	AR, ATF3, BCL2, BCL2L2, BMP5, CAV1, EYA4, EYA1, FGF10, FGFR1, FYN, GDNF, GPER1, HGF, IGF1, IL2, IL6R, MCL1, KITLG, NGF, PIK3R1, CX3CL1, SFRP1, SFRP2, THBS1, TNFAIP3, TNFSF12, BCL10, BAG3, FAIM2, MOAP1, ITPRIP
BP	GO:0007162	negative regulation of cell adhesion	39/1554	1.19E-02	ABL1, ACVRL1, ANGPT1, ANXA1, APOD, ARG2, ARHGAP6, CYP1B1, DUSP1, DUSP3, LRRC32, IL1RN, IL2, LRP1, SMAD7, PDE3B, PIK3R1, CX3CL1, CXCL12, SHH, THBS1, FZD7, PDE5A, KLF4, ADIPOQ, DLC1, FGL2, FAM107A, CORO1C, PLA2G2D, RND1, AJAP1, JAM2, VSIR, PHLDB2, PLXNA4, MYADM, NEXMIF, MUC21
BP	GO:0060688	regulation of morphogenesis of a branching structure	12/1554	1.21E-02	ABL1, AR, ESR1, FGF7, FGF10, FGFR1, GDNF, HGF, SFRP1, SHH, WNT2B, LRRK2
BP	GO:0090183	regulation of kidney development	12/1554	1.21E-02	EGR1, GDNF, IL6R, LIF, MYC, SHH, WNT2B, ADIPOQ, WWTR1, FAT4, PDGFD, OSR1
BP	GO:0003207	cardiac chamber formation	5/1554	1.22E-02	MEF2C, TBX5, HAND1, HAND2, TBX20
BP	GO:0010649	regulation of cell communication by electrical coupling	5/1554	1.22E-02	CASQ2, CAV1, HRC, PDE4D, SLC8A1
BP	GO:0051481	negative regulation of cytosolic calcium ion concentration	5/1554	1.22E-02	ATP1A2, KCNK3, LRP1, RYR3, SLC8A1
BP	GO:0086067	AV node cell to bundle of His cell communication	5/1554	1.22E-02	CACNA1C, CACNB2, RYR2, SCN4B, GJC1
BP	GO:0097090	presynaptic membrane organization	5/1554	1.22E-02	PTPRD, CNTN2, IL1RAPL1, NLGN1, NLGN3
BP	GO:0097104	postsynaptic membrane assembly	5/1554	1.22E-02	NRXN1, NRXN2, MAGI2, NLGN1, NLGN3
BP	GO:0099566	regulation of postsynaptic cytosolic calcium ion concentration	5/1554	1.22E-02	GRIA1, ITPR1, SLC8A1, SLC8A3, SYNPO
BP	GO:0010677	negative regulation of cellular carbohydrate metabolic process	10/1554	1.23E-02	ACTN3, LEPR, PRKN, ENPP1, ADIPOQ, HDAC4, PPARGC1A, MIDN, C1QTNF3, SIK1
BP	GO:0017145	stem cell division	10/1554	1.23E-02	DCT, FGFR1, KIT, NAP1L2, SFRP2, SOX5, ZBTB16, FZD7, WWTR1, SOX17
BP	GO:0032958	inositol phosphate biosynthetic process	10/1554	1.23E-02	ADCYAP1R1, FGF2, GPER1, ITPKB, LHCGR, P2RY1, PLCB4, PLCL1, SNCA, PLCD4
BP	GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	11/1554	1.24E-02	ABL1, RHOH, ESR1, PER1, RORA, TNFAIP3, ADIPOQ, MAPKBP1, SIRT1, OTUD7A, NLRP6
BP	GO:0071453	cellular response to oxygen levels	33/1554	1.24E-02	AK4, AQP1, BCL2, ZFP36L1, CAV1, CD34, PLK3, LPAR1, EGR1, GATA6, KCNK2, KCNK3, KCNMB1, MPL, MYC, PTGIS, PTGS2, RORA, SFRP1, SLC2A4, SLC8A1, SLC8A3, STC1, ROCK2, NAMPT, PPARGC1A, SIRT1, HIF3A, CPEB1, NDNF, CPEB4, VASN, CPEB2
BP	GO:0045665	negative regulation of neuron differentiation	32/1554	1.25E-02	DIO3, DPYSL3, LPAR1, EDNRB, EPHA7, ID2, ID4, LRP1, MEIS1, NFATC4, NGFR, PBX1, PMP22, SHH, CNTN2, NR2F1, SLIT2, NTN1, ZNF536, SEMA3A, NLGN1, DKK1, SPART, DENND5A, NLGN3, SEMA3G, RGMA, TRAK2, DIXDC1, LRRK2, CNTN4, OSTN
BP	GO:0045822	negative regulation of heart contraction	8/1554	1.26E-02	ADRA1A, BIN1, ATP1A2, IL2, PDE4D, TAC1, PDE5A, SPTBN4
BP	GO:0048730	epidermis morphogenesis	8/1554	1.26E-02	BCL2, FGF7, FGF10, IGFBP5, SHH, TGM3, KLF4, SOSTDC1

BP	GO:0060441	epithelial tube branching involved in lung morphogenesis	8/1554	1.26E-02	FGF10, FOXF1, SHH, WNT2B, SPRY1, SPRY2, HHIP, RSPO2
BP	GO:0042100	B cell proliferation	17/1554	1.28E-02	ABL1, BCL2, MS4A1, CD22, CD40LG, CD79A, CDKN1A, CR2, GPR183, NCKAP1L, IL2, MEF2C, NFATC2, TNFRSF13B, FCRL3, TNFRSF13C, GAPT
BP	GO:0030100	regulation of endocytosis	38/1554	1.28E-02	ABL1, BIN1, ANGPT1, AXL, C3, C4A, C4B, CAV1, CD22, CLU, EPHA3, NCKAP1L, ITGB3, LRP1, PPP3CB, PRKD1, PTX3, RAB27A, RAP1A, ROCK1, SH3GL3, SLC2A4, SNCA, SYT4, TUB, DYSF, ADIPOQ, MAGI2, STON1, NLGN1, DKK1, SYT11, CLIP3, PIP4P2, SLC17A7, LRRK2, GSG1L, LRRTM1
BP	GO:0051589	negative regulation of neurotransmitter transport	7/1554	1.28E-02	GPM6B, PRKN, RAP1A, RGS2, SNCA, SYT4, SYT11
BP	GO:0060055	angiogenesis involved in wound healing	7/1554	1.28E-02	CD34, ITGB3, MCAM, CX3CL1, SRF, TNFAIP3, NDNF
BP	GO:0072170	metanephric tubule development	7/1554	1.28E-02	CXCR2, LIF, PKD1, PKD2, WWTR1, FAT4, OSR1
BP	GO:0072215	regulation of metanephros development	7/1554	1.28E-02	EGR1, GDNF, LIF, MYC, ADIPOQ, WWTR1, FAT4
BP	GO:0072243	metanephric nephron epithelium development	7/1554	1.28E-02	LIF, PKD1, PKD2, ADIPOQ, WWTR1, FAT4, OSR1
BP	GO:1903706	regulation of hemopoiesis	58/1554	1.28E-02	ABL1, ANXA1, AXL, PRDM1, ZFP36L1, CD28, CSF3, EGR3, FBN1, FOS, GLI2, NCKAP1L, ID2, IL2, IL17A, IRF4, ITPKB, JUN, LIF, SMAD7, MEF2C, MEIS1, MEIS2, KITLG, MITF, MPL, MYC, NFATC2, ROR2, PIM1, PIK3R1, PRKCA, PRKCB, SFRP1, SHH, STAT5B, TAL1, ZEB1, TGFBR2, THBS1, KLF10, ZFP36, ZBTB16, NR4A3, GPR55, ADIPOQ, RASSF2, TESPA1, TRIB1, MYL9, FGL2, IL17D, TCIM, TNRC6C, VSIR, NFKBIZ, FCRL3, PPARGC1B
BP	GO:0010770	positive regulation of cell morphogenesis involved in differentiation	24/1554	1.29E-02	ABL1, BDNF, CDH4, FLNA, ILK, LRP1, MAP1B, MAP6, MAPT, MPL, NGF, NGFR, NTRK3, RELN, PTPRD, CXCL12, SRF, SLIT2, NTN1, ZEB2, IL1RAPL1, FBXO31, PLXNA4, MYADM
BP	GO:0008406	gonad development	31/1554	1.34E-02	ADCYAP1, AR, BCL2, BCL2L2, ESR1, FGF9, FLNA, GATA6, INHBB, KIT, LHCGR, KITLG, PDGFRA, PGR, PTX3, SALL1, SFRP1, SFRP2, SLIT3, TCF21, WNT2B, SLIT2, ADAMTS1, SEMA3A, SIRT1, ZFPM2, TIPARP, DHH, ARID5B, OSR1, RNF38
BP	GO:0036294	cellular response to decreased oxygen levels	31/1554	1.34E-02	AK4, AQP1, BCL2, ZFP36L1, CD34, PLK3, EGR1, GATA6, KCNK2, KCNK3, KCNMB1, MPL, MYC, PTGIS, PTGS2, RORA, SFRP1, SLC2A4, SLC8A1, SLC8A3, STC1, ROCK2, NAMPT, PPARGC1A, SIRT1, HIF3A, CPEB1, NDNF, CPEB4, VASN, CPEB2
BP	GO:0050920	regulation of chemotaxis	31/1554	1.34E-02	CCR6, DUSP1, DUSP3, GPR183, S1PR1, LPAR1, F3, FGF2, FGF10, FGFR1, NCKAP1L, IL6R, CXCR2, IL16, NTRK3, PDGFRA, PRKD1, CXCL12, THBS1, DYSF, SLIT2, SEMA3A, CXCL13, ADGRA2, SEMA3G, ZSWIM5, ZSWIM6, P2RY12, PDGFD, JAM3, PLXNA4
BP	GO:0050670	regulation of lymphocyte proliferation	30/1554	1.35E-02	ANXA1, ARG2, BCL2, CD22, CD28, TNFSF8, CD40LG, CDKN1A, CD55, GPR183, FGF10, LRRC32, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, MEF2C, MPL, NFATC2, SHH, TAC1, TGFBR2, PDE5A, TNFRSF13B, PLA2G2D, VSIR, FCRL3, TNFRSF13C
BP	GO:1903510	mucopolysaccharide metabolic process	19/1554	1.35E-02	ANGPT1, CSPG4, DCN, FGF2, HAS1, HGF, HYAL1, OMD, OGN, PIM1, PRELP, ST3GAL3, UST, LYVE1, CSGALNACT1, NDNF, ITIH5, CHST9, DSEL
BP	GO:0019226	transmission of nerve impulse	14/1554	1.36E-02	S1PR1, GPER1, GRIK2, KCNA1, KCNA2, NTRK3, P2RX1, SCN1B, SCN7A, CNTNAP1, CACNA1H, NFASC, SPTBN4, JAM3
BP	GO:0038034	signal transduction in absence of ligand	14/1554	1.36E-02	BCL2, BCL2L2, EYA4, EYA1, FGF10, FGFR1, FYN, GDNF, IL2, MCL1, KITLG, CX3CL1, BAG3, MOAP1
BP	GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	14/1554	1.36E-02	BCL2, BCL2L2, EYA4, EYA1, FGF10, FGFR1, FYN, GDNF, IL2, MCL1, KITLG, CX3CL1, BAG3, MOAP1
BP	GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	18/1554	1.38E-02	ACVRL1, BMP5, BMPR1A, FGF9, GDF2, GDF10, CCN1, ILK, INHBB, MSX1, TGFB1I1, TGFB3, TGFBR3, THBS1, ITGA8, RBPMS, ZNF423, MYOCD
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	24/1554	1.39E-02	AR, ATF3, BCL2, BMP5, CAV1, EYA4, EYA1, FGF10, FGFR1, FYN, GDNF, GPER1, HGF, IGF1, MCL1, CX3CL1, SFRP1, SFRP2, THBS1, TNFAIP3, TNFSF12, BCL10, FAIM2, ITPRIP

BP	GO:0008585	female gonad development	17/1554	1.40E-02	ADCYAP1, BCL2, ESR1, INHBB, KIT, KITLG, PDGFRA, PGR, PTX3, SFRP1, SLIT3, SLIT2, ADAMTS1, SIRT1, ZFPM2, TIPARP, ARID5B
BP	GO:2000177	regulation of neural precursor cell proliferation	16/1554	1.41E-02	ADCYAP1, CX3CR1, DCT, FLNA, GLI2, ID2, ILK, PROX1, CX3CL1, SHH, BTG2, NES, CDON, CEND1, PTBP2, LRRK2
BP	GO:0060976	coronary vasculature development	11/1554	1.42E-02	PRDM1, GATA6, GPER1, PCSK5, SGCD, SRF, TBX5, TGFBR3, HAND2, MYOCD, PRICKLE1
BP	GO:0032944	regulation of mononuclear cell proliferation	30/1554	1.43E-02	ANXA1, ARG2, BCL2, CD22, CD28, TNFSF8, CD40LG, CDKN1A, CD55, GPR183, FGF10, LRRC32, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, MEF2C, MPL, NFATC2, SHH, TAC1, TGFBR2, PDE5A, TNFRSF13B, PLA2G2D, VSIR, FCRL3, TNFRSF13C
BP	GO:0099054	presynapse assembly	10/1554	1.43E-02	CBLN1, NTRK3, PTPRD, SNCA, NRXN1, IL1RAPL1, NLGN1, DKK1, NLGN3, LRRTM1
BP	GO:0016311	dephosphorylation	58/1554	1.45E-02	BCL2, CRY2, DLG2, DMPK, RCAN1, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, EPHX2, EYA4, EYA1, NCKAP1L, IMPA2, INPP5A, ITGA1, MEF2C, MYH3, PPP1R12A, PPP1CB, PPP1R1A, PPP2R2B, PPP3CB, PTPRD, PTPRN2, ROCK1, CILP, PLPP3, RGN, ROCK2, MAGI2, PLPPR4, RCAN2, DLC1, PTPN21, RIMBP2, PPP1R15A, PPP1R16B, PCDH11X, NT5DC3, PIP4P2, SLC7A14, G6PC2, DUSP26, PPP1R3B, CSRNP3, NT5C1A, PTPN5, FCRL3, PPARGC1B, DUSP19, PPM1L, PPM1K, CNST, PHACTR1, PTPRQ
BP	GO:0071236	cellular response to antibiotic	23/1554	1.47E-02	ABL1, ADCY2, ADCY5, ANXA1, AQP1, RHOB, AXL, CLU, CYP1B1, EGR1, HGF, KCNMB1, MEF2C, PLA2G4A, TNFAIP3, RNF112, NR4A3, KLF4, KLF2, KDM6B, SIRT1, PDGFD, LRRK2
BP	GO:1901016	regulation of potassium ion transmembrane transporter activity	13/1554	1.47E-02	ACTN2, ANK2, ATP1B2, CASQ2, CAV1, FHL1, KCNA1, KCNS2, VAMP2, KCNAB1, AKAP6, KCNE4, LRRC52
BP	GO:0032872	regulation of stress-activated MAPK cascade	33/1554	1.48E-02	CD40LG, CCN2, GADD45A, DUSP1, DUSP3, EPHB1, GRIK2, HGF, IL1RN, MYC, GADD45B, ROR2, PRKN, PER1, SFRP1, SFRP2, SLAMF1, TPD52L1, FZD7, HAND2, RASSF2, ZEB2, PJA2, HIPK3, SEMA3A, FZD10, DKK1, TNIK, DACT1, MAP3K20, DUSP19, SH3RF3, SAMD5
BP	GO:0048640	negative regulation of developmental growth	19/1554	1.48E-02	ADRB2, CDKN1A, EPHA7, KCNK2, MEIS1, PTCH1, RBP4, RGS2, SFRP1, SFRP2, TBX5, TGFBR2, SOCS2, NTN1, SEMA3A, SPART, SEMA3G, NKD1, OSTN
BP	GO:0030856	regulation of epithelial cell differentiation	24/1554	1.50E-02	ACVRL1, ZFP36L1, CAV1, S1PR3, GDF2, GDNF, LIF, PTCH1, ROCK1, ZEB1, CLDN5, ZFP36, ADIPOQ, ROCK2, ZEB2, MAFF, WWTR1, ERRFI1, TMEM100, AJAP1, FAT4, APOLD1, ATOH8, OSR1
BP	GO:0021696	cerebellar cortex morphogenesis	8/1554	1.53E-02	CBLN1, GLI2, GRID2, PROX1, RORA, HERC1, FAIM2, CEND1
BP	GO:0021772	olfactory bulb development	8/1554	1.53E-02	ID2, SALL1, SRF, SLIT2, SEMA3A, SALL3, CRTAC1, LRRK2
BP	GO:0051491	positive regulation of filopodium assembly	8/1554	1.53E-02	DPYSL3, GPM6A, PALM, SRF, TGFB3, NEURL1, NLGN1, DOCK11
BP	GO:0120162	positive regulation of cold-induced thermogenesis	17/1554	1.55E-02	ADCYAP1, ADRB2, ADRB3, CAV1, GPR3, GRB10, IRF4, LEPR, THRA, PER2, ADIPOQ, ZNF516, PPARGC1A, KDM6B, PRDM16, EBF2, PPARGC1B
BP	GO:0034109	homotypic cell-cell adhesion	15/1554	1.56E-02	FLNA, HBB, ILK, ITGB3, MPL, PDGFRA, PRKCA, STXBP1, TLN1, VCL, PLPP3, MYL9, CTNNA3, P2RY12, CD99L2
BP	GO:0046883	regulation of hormone secretion	36/1554	1.57E-02	ADCY5, ADCYAP1, ADRA2A, ADRA2B, SLC25A4, ANXA1, CACNA1C, CRHBP, EPHA5, FGFR1, GPER1, INHBB, ITPR1, KCNB1, LIF, LRP1, P2RY1, PRKN, PPP3CB, PRKCA, RAP1A, RBP4, SFRP1, TAC1, TACR2, TRH, VIP, FGF23, PER2, ADIPOQ, STXBP5L, MYRIP, SYBU, G6PC2, MIDN, C1QTNF3
BP	GO:0035904	aorta development	12/1554	1.57E-02	ACVRL1, PRDM1, BMPR1A, EYA1, LRP1, MYLK, PDE2A, PKD2, PROX1, SRF, ADAMTS9, PRICKLE1
BP	GO:0071385	cellular response to glucocorticoid stimulus	12/1554	1.57E-02	ADCYAP1, ANXA1, AQP1, ZFP36L1, KLF9, STC1, ZFP36, FAM107A, AKAP13, ERRFI1, FBXO32, CREBRF
BP	GO:0003181	atrioventricular valve morphogenesis	7/1554	1.61E-02	BMPR1A, CCN1, SLIT3, TBX5, TGFBR2, DCHS1, OLFM1
BP	GO:0003272	endocardial cushion formation	7/1554	1.61E-02	BMP5, BMPR1A, MSX1, TGFBR2, DCHS1, TMEM100, TBX20
BP	GO:0003418	growth plate cartilage chondrocyte differentiation	7/1554	1.61E-02	ANXA6, COL6A2, COL6A3, MATN2, TGFBR2, SCARA3, COL21A1
BP	GO:0035588	G protein-coupled purinergic receptor signaling pathway	7/1554	1.61E-02	ADCY5, P2RY1, CNTN2, P2RY14, P2RY10, P2RY12, P2RY8
BP	GO:0019369	arachidonic acid metabolic process	11/1554	1.64E-02	CYP1B1, CYP2A7, EPHX2, PLA2G4A, PTGIS, PTGS1, PTGS2, PLA2G4C, MGLL, HPGDS, CYP2U1

BP	GO:0045599	negative regulation of fat cell differentiation	11/1554	1.64E-02	RUNX1T1, GPER1, ID4, ENPP1, RORA, TGFB1I1, ADIPOQ, SIRT1, ZFPM2, WWTR1, JDP2
BP	GO:0010921	regulation of phosphatase activity	26/1554	1.64E-02	CRY2, DLG2, DMPK, RCAN1, NCKAP1L, ITGA1, MEF2C, PPP1R12A, PPP1R1A, PPP2R2B, ROCK1, RGN, ROCK2, MAGI2, RCAN2, RIMBP2, PPP1R15A, PPP1R16B, PCDH11X, SLC7A14, PPP1R3B, CSRNP3, FCRL3, PPARGC1B, CNST, PHACTR1
BP	GO:0007431	salivary gland development	9/1554	1.65E-02	EDA, FGF7, FGF10, FGFR1, HGF, NFIB, SHH, TGFB3, SEMA3A
BP	GO:0021587	cerebellum morphogenesis	9/1554	1.65E-02	ABL1, CBLN1, GLI2, GRID2, PROX1, RORA, HERC1, FAIM2, CEND1
BP	GO:1905314	semi-lunar valve development	9/1554	1.65E-02	ELN, NFATC1, ROCK1, SLIT3, SLIT2, ROCK2, EMILIN1, TBX20, GATA5
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	33/1554	1.65E-02	CD40LG, CCN2, GADD45A, DUSP1, DUSP3, EPHB1, GRIK2, HGF, IL1RN, MYC, GADD45B, ROR2, PRKN, PER1, SFRP1, SFRP2, SLAMF1, TPD52L1, FZD7, HAND2, RASSF2, ZEB2, PJA2, HIPK3, SEMA3A, FZD10, DKK1, TNIK, DACT1, MAP3K20, DUSP19, SH3RF3, SAMD5
BP	GO:0046888	negative regulation of hormone secretion	13/1554	1.65E-02	ADRA2A, ADRA2B, CRHBP, INHBB, KCNB1, LIF, PRKN, SFRP1, TACR2, FGF23, ADIPOQ, STXBP5L, MIDN
BP	GO:0051926	negative regulation of calcium ion transport	13/1554	1.65E-02	ADRA2A, BIN1, ATP1A2, BCL2, CASQ2, CLIC2, GEM, GNAO1, PKD2, PTGS2, STC1, DYSF, REM1
BP	GO:1905207	regulation of cardiocyte differentiation	13/1554	1.65E-02	GATA6, GPER1, IGF1, MEF2C, RGS2, TBX5, FZD7, AKAP6, DKK1, SOX6, SOX17, MYOCD, PRICKLE1
BP	GO:0051403	stress-activated MAPK cascade	38/1554	1.65E-02	ZFP36L1, CD40LG, MAP3K8, CCN2, GADD45A, DUSP1, DUSP3, EPHB1, GRIK2, HGF, IL1RN, MYC, GADD45B, ROR2, PRKN, PER1, PTGER4, SFRP1, SFRP2, SLAMF1, TPD52L1, ZFP36, FZD7, HAND2, RASSF2, ZEB2, PJA2, HIPK3, TRIB1, SEMA3A, FZD10, DKK1, TNIK, DACT1, MAP3K20, DUSP19, SH3RF3, SAMD5
BP	GO:0042136	neurotransmitter biosynthetic process	18/1554	1.65E-02	ARG2, ATP2B4, CAV1, CD34, CLU, CX3CR1, CYP1B1, HBB, PKD2, PTGIS, PTGS2, PTX3, RORA, RGN, KLF4, ROCK2, KLF2, SLC5A7
BP	GO:0010828	positive regulation of glucose transmembrane transport	10/1554	1.66E-02	C3, IGF1, MEF2A, PIK3R1, RAP1A, NR4A3, ADIPOQ, SORBS1, CLIP3, KLF15
BP	GO:0045601	regulation of endothelial cell differentiation	10/1554	1.66E-02	ACVRL1, S1PR3, GDF2, ROCK1, ZEB1, CLDN5, ROCK2, TMEM100, APOLD1, ATOH8
BP	GO:0001701	in utero embryonic development	47/1554	1.67E-02	ACVRL1, ADCY9, ANGPT1, AR, PRDM1, BMP5, BMPR1A, ZFP36L1, C6, EDNRA, FGFR1, FOXF1, GATA6, GLI2, IGF1, CCN1, JUNB, LIF, MBNL1, MSX1, PDGFRA, PKD1, PKD2, PTCH1, SRF, TGFB3, TGFBR2, TPM1, FOSL1, SOCS3, HAND1, HAND2, ARNT2, KLF2, ZFPM2, MAFF, FOXD3, SBDS, TENT5C, TMEM100, SOX6, SLC5A7, NECAB1, SOX17, RSPO3, SPIC, ST8SIA6
BP	GO:0051098	regulation of binding	47/1554	1.67E-02	ABL1, ADRB2, ANGPT1, BCL2, BDNF, CAV1, CLIC2, CSF3, ID2, ID4, IGF1, IRF4, JUN, LIF, LRP1, MEF2C, MSX1, NFATC4, NGF, P2RY1, PRKN, PKD1, PLCL1, ROCK1, TGFBR3, PER2, KLF4, ADIPOQ, HAND1, HAND2, BAG2, HDAC4, SPON1, NES, DZIP1, HABP4, DKK1, CDON, DACT1, CRTAC1, GREM2, EBF2, ARHGAP28, MYOCD, LRRK2, WFIKKN2, XIRP1
BP	GO:0099175	regulation of postsynapse organization	17/1554	1.69E-02	CBLN1, DGKB, EPHA7, FYN, GRID2, NTRK3, RELN, PTPRD, NRP2, NRXN1, PDLIM5, IL1RAPL1, NLGN1, NLGN3, LRRK2, LRRTM1, SHISA6
BP	GO:0005977	glycogen metabolic process	14/1554	1.70E-02	GYS2, IGF1, IL6ST, LEPR, ENPP1, PPP1CB, PPP1R1A, PYGB, PER2, SORBS1, PRKAG2, PPP1R3B, STK40, PGM2L1
BP	GO:0050710	negative regulation of cytokine secretion	14/1554	1.70E-02	ANGPT1, ANXA1, ARG2, CD34, CIDEA, LRRC32, CD200, PTGER4, CX3CL1, TNFAIP3, MAPKBP1, SYT11, C1QTNF3, SSC5D
BP	GO:0010717	regulation of epithelial to mesenchymal transition	16/1554	1.70E-02	BMP5, LDLRAD4, EPHA3, SMAD7, SFRP1, SFRP2, TBX5, TGFB1I1, TGFB3, TGFBR2, OLFM1, WWTR1, PHLDB2, VASN, DACT3, GLIPR2
BP	GO:0046849	bone remodeling	16/1554	1.70E-02	ADRB2, CALCA, S1PR1, EPHA2, ITGB3, LEPR, MITF, PDK4, PRKCA, SFRP1, TGFB3, TNFAIP3, GPR55, RASSF2, PPARGC1B, TMEM119
BP	GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	5/1554	1.70E-02	APOD, LRP1, SNCA, ADIPOQ, MYOCD
BP	GO:0014745	negative regulation of muscle adaptation	5/1554	1.70E-02	ATP2B4, IGFBP5, KLF4, ERRFI1, MLIP

BP	GO:0021681	cerebellar granular layer development	5/1554	1.70E-02	CBLN1, GRID2, PROX1, FAIM2, CEND1
BP	GO:0033623	regulation of integrin activation	5/1554	1.70E-02	CDH17, PTGER4, SELP, CXCL13, P2RY12
BP	GO:0035589	G protein-coupled purinergic nucleotide receptor signaling pathway	5/1554	1.70E-02	P2RY1, P2RY14, P2RY10, P2RY12, P2RY8
BP	GO:0043116	negative regulation of vascular permeability	5/1554	1.70E-02	ANGPT1, PDE2A, PDE3A, SLIT2, AKAP12
BP	GO:0060347	heart trabecula formation	5/1554	1.70E-02	RBP4, SRF, TEK, TGFBR3, ADAMTS1
BP	GO:0098703	calcium ion import across plasma membrane	5/1554	1.70E-02	ATP2B4, CACNA2D1, FYN, SLC8A3, FAM155A
BP	GO:2000052	positive regulation of non-canonical Wnt signaling pathway	5/1554	1.70E-02	ABL1, SFRP1, DKK1, RSPO3, NKD1
BP	GO:0006023	aminoglycan biosynthetic process	19/1554	1.73E-02	ANGPT1, CSPG4, DCN, GPC5, HAS1, HSPG2, HYAL1, OMD, OGN, PRELP, SDC2, ST3GAL3, SDC3, HS3ST1, GPC6, UST, CSGALNACT1, CHST9, DSEL
BP	GO:0021885	forebrain cell migration	12/1554	1.75E-02	AXL, RELN, CXCL12, SRF, CNTN2, NRP2, SLIT2, SEMA3A, P2RY12, DIXDC1, BMERB1, LRRK2
BP	GO:0070527	platelet aggregation	12/1554	1.75E-02	FLNA, HBB, ILK, ITGB3, MPL, PDGFRA, PRKCA, STXBP1, TLN1, VCL, MYL9, P2RY12
BP	GO:0097755	positive regulation of blood vessel diameter	12/1554	1.75E-02	ADCYAP1, ADRB2, ADRB3, BDKRB2, EDNRB, EPHX2, GPER1, ITGA1, KCNMA1, KCNMB1, RGS2, VIP
BP	GO:0016331	morphogenesis of embryonic epithelium	23/1554	1.81E-02	ABL1, ALDH1A3, AR, BMP5, FGF10, GDNF, GLI2, PRKACB, PTCH1, SFRP1, SFRP2, SHH, TGFB1I1, WNT2B, BCL10, TBX18, HAND1, ZEB2, DLC1, CC2D2A, SHROOM3, OSR1, PRICKLE1
BP	GO:0003299	muscle hypertrophy in response to stress	8/1554	1.82E-02	ATP2B4, GATA6, MEF2C, TRPC3, HDAC4, KLF15, ERRFI1, MLIP
BP	GO:0010719	negative regulation of epithelial to mesenchymal transition	8/1554	1.82E-02	BMP5, LDLRAD4, SMAD7, SFRP1, SFRP2, TBX5, VASN, DACT3
BP	GO:0014887	cardiac muscle adaptation	8/1554	1.82E-02	ATP2B4, GATA6, MEF2C, TRPC3, HDAC4, KLF15, ERRFI1, MLIP
BP	GO:0014898	cardiac muscle hypertrophy in response to stress	8/1554	1.82E-02	ATP2B4, GATA6, MEF2C, TRPC3, HDAC4, KLF15, ERRFI1, MLIP
BP	GO:0021988	olfactory lobe development	8/1554	1.82E-02	ID2, SALL1, SRF, SLIT2, SEMA3A, SALL3, CRTAC1, LRRK2
BP	GO:0048710	regulation of astrocyte differentiation	8/1554	1.82E-02	BIN1, ID2, ID4, IL6ST, LDLR, LIF, NTRK3, CNTN2
BP	GO:0086011	membrane repolarization during action potential	8/1554	1.82E-02	CACNA2D1, CAV1, FLNA, KCND3, KCNH2, KCNJ3, KCNJ8, KCNE4
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	25/1554	1.84E-02	ANGPT1, ARG2, AXL, BPI, CD34, CHRNA7, CIDEA, CLU, CX3CR1, IGF1, NFATC4, PIK3R1, CX3CL1, SLAMF1, THBS1, TNFAIP3, ZFP36, BCL10, ADIPOQ, AKAP12, IRAK3, SYT11, ERRFI1, VSIR, LRRK2
BP	GO:0032330	regulation of chondrocyte differentiation	11/1554	1.84E-02	ACVRL1, CCN2, EFEMP1, GLI2, SOX5, TRPS1, WNT9A, ZBTB16, SOX6, PKDCC, RFLNB
BP	GO:0048168	regulation of neuronal synaptic plasticity	11/1554	1.84E-02	CAMK2A, EGR2, GRIK2, KIT, SLC8A2, SNCA, SYT4, CNTN2, NEURL1, SYNPO, SHISA6
BP	GO:1904063	negative regulation of cation transmembrane transport	16/1554	1.87E-02	ACTN2, ADRA2A, BIN1, ATP1A2, CASQ2, CAV1, CLIC2, GEM, KCNH2, PKD2, RGS2, KCNAB1, DYSF, KCNE4, REM1, OSR1
BP	GO:0006073	cellular glucan metabolic process	14/1554	1.87E-02	GYS2, IGF1, IL6ST, LEPR, ENPP1, PPP1CB, PPP1R1A, PYGB, PER2, SORBS1, PRKAG2, PPP1R3B, STK40, PGM2L1

BP	GO:0044042	glucan metabolic process	14/1554	1.87E-02	GYS2, IGF1, IL6ST, LEPR, ENPP1, PPP1CB, PPP1R1A, PYGB, PER2, SORBS1, PRKAG2, PPP1R3B, STK40, PGM2L1
BP	GO:0006970	response to osmotic stress	15/1554	1.88E-02	AQP1, BDKRB2, ZFP36L1, PLK3, KCNMA1, MYLK, ABCB1, PKD2, PTGS2, SLC2A4, TACR3, DYSF, ERRFI1, SLC25A23, RCSD1
BP	GO:0007159	leukocyte cell-cell adhesion	43/1554	1.89E-02	ANXA1, ARG2, CAV1, CD5, CD28, CD40LG, MAP3K8, CX3CR1, CD55, DUSP3, EGR3, FYN, LRRC32, GLI2, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, ITGA5, ITPKB, SMAD7, PECAM1, PIK3R1, ROCK1, CXCL12, SELP, SHH, TGFBR2, ZBTB16, NR4A3, PDE5A, BCL10, KLF4, GRAP2, TESPA1, FGL2, PLA2G2D, VSIR, NFKBIZ, TNFRSF13C, BTLA
BP	GO:0048483	autonomic nervous system development	10/1554	1.91E-02	ADARB1, EDNRA, EDNRB, EGR2, GDNF, GFRA3, NRP2, HAND2, SEMA3A, PLXNA4
BP	GO:0048009	insulin-like growth factor receptor signaling pathway	9/1554	1.91E-02	AR, BMP5, GHR, IGF1, IGFBP2, IGFBP5, IGFBP6, PIK3R1, CILP
BP	GO:0051346	negative regulation of hydrolase activity	56/1554	1.95E-02	A2M, ABL1, ADCYAP1, BIN1, ANXA1, AQP1, RHOH, C3, C4A, C4B, COL4A3, COL6A3, CRY2, DLG2, NCKAP1L, HGF, LEPR, NGF, NGFR, SERPINB2, PPP1R1A, PTGS2, PTPRN2, PTX3, RGS2, ROCK1, SFRP2, SNCA, THBS1, TIMP2, TNNT2, WNT9A, RECK, RGN, KLF4, SLIT2, ROCK2, RASA4, SPRY1, SPRY2, FZD10, LRCH1, SIRT1, RIMBP2, PPP1R15A, PCDH11X, PI15, SLC7A14, CSRNP3, ITIH5, SERPINB11, LRRK2, WFIKKN2, CPEB2, CNST, PHACTR1
BP	GO:0032680	regulation of tumor necrosis factor production	24/1554	1.95E-02	ANGPT1, ARG2, AXL, BPI, CD34, CHRNA7, CIDEA, CLU, CX3CR1, IGF1, NFATC4, PIK3R1, CX3CL1, SLAMF1, THBS1, TNFAIP3, ZFP36, ADIPOQ, AKAP12, IRAK3, SYT11, ERRFI1, VSIR, LRRK2
BP	GO:0014829	vascular smooth muscle contraction	7/1554	1.95E-02	ACTA2, ADRA2B, CHRM3, EDNRA, EDNRB, P2RX1, SLC8A1
BP	GO:0031069	hair follicle morphogenesis	7/1554	1.95E-02	BCL2, FGF7, FGF10, IGFBP5, SHH, TGM3, SOSTDC1
BP	GO:0060571	morphogenesis of an epithelial fold	7/1554	1.95E-02	AR, BMP5, FGF10, GLI2, SHH, WNT2B, SOSTDC1
BP	GO:1905809	negative regulation of synapse organization	7/1554	1.95E-02	EPHA7, FYN, NFATC4, NLGN1, ARHGEF15, DKK1, NLGN3
BP	GO:2000311	regulation of AMPA receptor activity	7/1554	1.95E-02	ADRB2, MEF2C, RELN, NLGN1, NLGN3, GSG1L, SHISA6
BP	GO:0045619	regulation of lymphocyte differentiation	25/1554	1.95E-02	ABL1, ANXA1, AXL, PRDM1, ZFP36L1, CD28, EGR3, GLI2, NCKAP1L, ID2, IL2, IRF4, ITPKB, SMAD7, NFATC2, SFRP1, SHH, ZEB1, TGFBR2, ZBTB16, TESPA1, FGL2, VSIR, NFKBIZ, FCRL3
BP	GO:0050821	protein stabilization	26/1554	1.95E-02	ANK2, ATP1B2, CDKN1A, CLU, FLNA, GNAQ, IGF1, SMAD7, MSX1, PRKN, PIM1, PIK3R1, STXBP1, TBL1X, WFS1, PLPP3, PER3, USP2, BAG3, BAG2, RASSF2, CRTAP, PPARGC1A, CDC37L1, SOX17, TMEM88
BP	GO:0003422	growth plate cartilage morphogenesis	6/1554	1.95E-02	COL6A2, COL6A3, MATN2, STC1, SCARA3, COL21A1
BP	GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	6/1554	1.95E-02	FGF9, FGF10, GRB10, ITGA5, ITGB3, PRKCB
BP	GO:0032026	response to magnesium ion	6/1554	1.95E-02	CNGA3, KCNA1, RYR3, SNCA, THBS1, FGF23
BP	GO:0048486	parasympathetic nervous system development	6/1554	1.95E-02	ADARB1, EGR2, GDNF, NRP2, SEMA3A, PLXNA4
BP	GO:0060004	reflex	6/1554	1.95E-02	ADRA1A, ALDH1A3, SATB1, NR4A3, FOXP2, TMC2
BP	GO:0060438	trachea development	6/1554	1.95E-02	EDA, FOXF1, SHH, SRF, TGFBR2, RSPO2
BP	GO:2000696	regulation of epithelial cell differentiation involved in kidney development	6/1554	1.95E-02	GDNF, LIF, ADIPOQ, WWTR1, FAT4, OSR1
BP	GO:0046324	regulation of glucose import	12/1554	1.95E-02	GRB10, IGF1, MEF2A, ENPP1, PIK3R1, RAP1A, ADIPOQ, SORBS1, KLF15, PRKAG2, PID1, OSTN
BP	GO:2001023	regulation of response to drug	17/1554	1.99E-02	ATP1A2, GABRA4, GDNF, HGF, KCNA2, PRKN, RGS2, CXCL12, SNCA, SYT4, TACR2, NR4A3, PER2, SYT11, SYT15, LRRK2, OSR1

BP	GO:0010906	regulation of glucose metabolic process	19/1554	2.02E-02	ACACB, ACTN3, IGF1, LEPR, PRKN, PDK4, ENPP1, PPP1CB, RORA, SLC25A12, RGN, ADIPOQ, SORBS1, PPARGC1A, SIRT1, PPP1R3B, MIDN, C1QTNF3, SIK1
BP	GO:0046323	glucose import	13/1554	2.03E-02	GRB10, IGF1, MEF2A, ENPP1, PIK3R1, RAP1A, SLC2A4, ADIPOQ, SORBS1, KLF15, PRKAG2, PID1, OSTN
BP	GO:0050918	positive chemotaxis	13/1554	2.03E-02	ANGPT1, S1PR1, F3, FGF2, FGF7, FGF10, GDNF, HGF, IL16, LRP1, NTRK3, CX3CL1, CXCL12
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	16/1554	2.03E-02	ANXA1, ARG2, CD55, GPR183, NCKAP1L, IL2, IRF4, LY9, SMAD7, PTGER4, RORA, SATB1, TGFBR2, PLA2G2D, VSIR, NFKBIZ
BP	GO:0042310	vasoconstriction	14/1554	2.07E-02	ACTA2, ADRA1A, ADRA2A, ADRA2B, ATP1A2, BDKRB2, CAV1, CHRM3, EDNRA, EDNRB, P2RX1, PTGS2, SLC8A1, PER2
BP	GO:0032715	negative regulation of interleukin-6 production	11/1554	2.09E-02	BPI, NCKAP1L, HGF, CD200, CX3CL1, SLAMF1, TNFAIP3, KLF2, IRAK3, SYT11, C1QTNF3
BP	GO:0051149	positive regulation of muscle cell differentiation	18/1554	2.11E-02	ABL1, BCL2, CTNNA2, GPER1, IGF1, KIT, MEF2A, MEF2C, NFATC2, PROX1, SHH, AKAP6, SIRT1, EHD2, CDON, LMOD3, MYOCD, RBM24
BP	GO:0035587	purinergic receptor signaling pathway	8/1554	2.16E-02	ADCY5, P2RX1, P2RY1, CNTN2, P2RY14, P2RY10, P2RY12, P2RY8
BP	GO:0051385	response to mineralocorticoid	8/1554	2.16E-02	CDKN1A, CCN2, FOS, FOSB, GPER1, NTRK3, TRH, FOSL1
BP	GO:0051968	positive regulation of synaptic transmission, glutamatergic	8/1554	2.16E-02	ADCYAP1, ROR2, RELN, PTGS2, STXBP1, NRXN1, NLGN1, NLGN3
BP	GO:0061384	heart trabecula morphogenesis	8/1554	2.16E-02	BMP5, BMPR1A, S1PR1, RBP4, SRF, TEK, TGFBR3, ADAMTS1
BP	GO:0099623	regulation of cardiac muscle cell membrane repolarization	8/1554	2.16E-02	ANK2, CACNA2D1, FLNA, KCNH2, SCN1B, SCN4B, SNTA1, KCNE4
BP	GO:0002064	epithelial cell development	29/1554	2.16E-02	ACTA2, AR, PRDM1, BMP5, CDKN1A, COL4A4, S1PR3, EPHA2, ESR1, FGFR1, FLNA, PDE2A, PDE4D, PECAM1, PGR, PROX1, RAP1A, ROCK1, STC1, TMOD1, CLDN5, ADIPOQ, ROCK2, MAGI2, PALLD, PPP1R16B, ARHGEF26, SHROOM3, MYADM
BP	GO:0071456	cellular response to hypoxia	29/1554	2.16E-02	AK4, AQP1, BCL2, ZFP36L1, CD34, PLK3, EGR1, GATA6, KCNK2, KCNK3, KCNMB1, MPL, MYC, PTGIS, PTGS2, RORA, SFRP1, SLC2A4, SLC8A1, SLC8A3, STC1, ROCK2, PPARGC1A, SIRT1, HIF3A, CPEB1, NDNF, VASN, CPEB2
BP	GO:0043087	regulation of GTPase activity	57/1554	2.16E-02	ADCYAP1, ARHGAP1, ARHGAP6, RHOH, ADGRB3, S1PR1, EPHA2, EPHA3, EPHA5, GNAO1, GNAQ, NCKAP1L, JUN, NTRK3, PTPRN2, RAP1A, RGS1, RGS2, CX3CL1, SFRP1, RGS5, RGN, SLIT2, STXBP5L, ARHGEF10, RASA4, SPRY1, SPRY2, DLC1, CDC42EP2, SEC23A, CXCL13, MAPRE2, BVES, FZD10, RASA3, ARHGEF15, LRCH1, CORO1C, TIAM2, FAM13B, SNX9, ERRFI1, ARHGAP20, ARHGAP28, PREX2, ARHGAP24, SYDE2, GARNL3, STARD13, PLXNA4, LRRK2, CPEB2, DOCK11, RANBP3L, TBC1D10C, TBC1D3C
BP	GO:0001504	neurotransmitter uptake	10/1554	2.18E-02	ATP1A2, GDNF, GPM6B, ITGB3, PRKN, RGS2, SLC18A2, SLC22A3, SNCA, PER2
BP	GO:0031099	regeneration	28/1554	2.18E-02	ANXA1, APOD, AXL, BCL2, CDKN1A, FGF10, GSN, HGF, IGF1, JUN, LRP1, MAP1B, MATN2, NTRK3, PTCH1, RAP1A, CXCL12, TGFBR2, TGFBR3, NR4A3, DYSF, FZD7, RGN, LARGE1, KLF4, RGMA, JAM3, MUSTN1
BP	GO:0006470	protein dephosphorylation	41/1554	2.19E-02	BCL2, CRY2, DMPK, RCAN1, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, EYA4, EYA1, NCKAP1L, ITGA1, MYH3, PPP1R12A, PPP1CB, PPP1R1A, PPP2R2B, PPP3CB, PTPRD, PTPRN2, ROCK1, PLPP3, RGN, ROCK2, MAGI2, RCAN2, DLC1, PTPN21, PPP1R15A, PPP1R16B, DUSP26, PPP1R3B, PTPN5, FCRL3, DUSP19, PPM1L, PPM1K, PHACTR1, PTPRQ
BP	GO:0032535	regulation of cellular component size	46/1554	2.21E-02	ABL1, ACTN2, BIN1, AQP1, BDNF, CDH4, CFL2, CSF3, CTNNA2, DPYSL2, ELN, EPHA7, FER, GSN, NCKAP1L, ILK, KCNMA1, LRP1, MAP1B, MAPT, NGF, NTRK3, CXCL12, SRF, CNTN2, TMOD1, SLIT2, NTN1, AKT3, SEMA3A, CDC42EP2, OLFM1, CDC42EP3, DSTN, SPART, PPP1R15A, LMOD1, SNX9, LMOD3, SEMA3G, SPTBN4, ARHGAP28, PLXNA4, MYADM, PLEKHH2, JMY
BP	GO:0035886	vascular smooth muscle cell differentiation	9/1554	2.22E-02	FGF9, GATA6, GPER1, KIT, NFATC1, NFATC2, SGCB, SRF, MYOCD
BP	GO:1905330	regulation of morphogenesis of an epithelium	26/1554	2.22E-02	ABL1, AR, ESR1, FGF7, FGF10, FGFR1, GDNF, HGF, LIF, ROR1, ROR2, SFRP1, SFRP2, SHH, WNT2B, FZD7, MAGI2, GPC6, DKK1, DACT1, AJAP1, RSPO3, NKD1, PHLDB2, PRICKLE1, PRICKLE2
BP	GO:0046634	regulation of alpha-beta T cell activation	16/1554	2.23E-02	ANXA1, ARG2, PRDM1, CD28, CD55, NCKAP1L, IL2, IL6R, IRF4, ITPKB, SMAD7, SHH, TGFBR2, ZBTB16, VSIR, NFKBIZ

BP	GO:0019216	regulation of lipid metabolic process	50/1554	2.25E-02	ACACB, ADRA2A, ABCD2, ANXA1, APOD, BMP5, C3, CAV1, CIDEA, CYP7A1, EGR1, EPHX2, FGF2, GPER1, ID2, CCN1, KIT, LDLR, ME1, PDE3B, PDGFRA, PDK4, PIK3R1, PRKAA2, PRKD1, PROX1, PTGS2, RORA, SNCA, TBL1X, TEK, THRA, TXNRD1, NR4A3, SOCS2, SOCS3, RGN, KLF4, ADIPOQ, SORBS1, PPARGC1A, RGL1, SIRT1, TIAM2, DHH, PRKAG2, P2RY12, CCDC3, SIK1, TNFAIP8L3
BP	GO:0046879	hormone secretion	40/1554	2.26E-02	ADCY5, ADCYAP1, ADRA2A, ADRA2B, SLC25A4, ANXA1, CACNA1C, CPE, CRHBP, EPHA5, FGFR1, GPER1, IL1RN, INHBB, ITPR1, KCNB1, LIF, LRP1, P2RY1, PRKN, PPP3CB, PRKCA, PTPRN2, RAP1A, RBP4, SFRP1, TAC1, TACR2, TRH, VIP, FGF23, LTBP4, PER2, ADIPOQ, STXBP5L, MYRIP, SYBU, G6PC2, MIDN, C1QTNF3
BP	GO:0051260	protein homooligomerization	44/1554	2.26E-02	ACACB, ACTN2, ALDH1A3, ANXA6, AQP2, CAV1, CD79A, CD79B, CLU, DPYSL3, STOM, GPX3, KCNA1, KCNA2, KCNB1, KCND3, KCNJ12, KCNS2, MPP2, OTC, P2RX1, PAM, PKD2, RYR3, VWF, RNF112, TCL1A, BCL10, TRPA1, LGI1, ADIPOQ, EMILIN1, NLGN1, SYT11, ATL1, IKZF4, STEAP4, SCUBE1, COLEC12, KCTD10, KCTD12, NACC2, SCUBE3, SCARA5
BP	GO:0098739	import across plasma membrane	18/1554	2.28E-02	ATP1A2, ATP1B2, ATP2B4, CACNA2D1, CNGA3, FYN, KCNH2, KCNJ3, KCNJ8, KCNJ12, RGS2, SLC8A1, SLC8A3, PER2, ABCC9, SLC39A14, SLC9A9, FAM155A
BP	GO:0008344	adult locomotory behavior	14/1554	2.28E-02	ATP1A2, GDNF, ID2, NR4A2, PRKN, PBX3, CXCL12, SNCA, CNTN2, TMOD1, TRH, CEND1, SPTBN4, PREX2
BP	GO:0010752	regulation of cGMP-mediated signaling	5/1554	2.28E-02	NPR1, NPR2, PDE2A, THBS1, PDE11A
BP	GO:0038166	angiotensin-activated signaling pathway	5/1554	2.28E-02	ACTN2, CAMK2A, CAV1, ROCK1, ROCK2
BP	GO:0045651	positive regulation of macrophage differentiation	5/1554	2.28E-02	ID2, LIF, ROR2, PRKCA, TRIB1
BP	GO:0060732	positive regulation of inositol phosphate biosynthetic process	5/1554	2.28E-02	ADCYAP1R1, GPER1, LHCGR, P2RY1, SNCA
BP	GO:0072216	positive regulation of metanephros development	5/1554	2.28E-02	EGR1, GDNF, LIF, MYC, ADIPOQ
BP	GO:0090128	regulation of synapse maturation	5/1554	2.28E-02	NFATC4, RELN, NEURL1, NRXN1, ARHGEF15
BP	GO:1900452	regulation of long-term synaptic depression	5/1554	2.28E-02	CBLN1, GRID2, KCNB1, MAPT, SORCS3
BP	GO:1901213	regulation of transcription from RNA polymerase II promoter involved in heart development	5/1554	2.28E-02	BMPR1A, MSX1, SRF, MYOCD, GATA5
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	28/1554	2.30E-02	ACVRL1, BMPR1A, LDLRAD4, CAV1, CIDEA, FBN1, FOS, LRRC32, GDF10, JUN, SMAD7, SMAD9, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, CLDN5, LTBP4, ITGA8, FERMT2, EMILIN1, SIRT1, PRDM16, MYOCD, VASN, WFIKKN2
BP	GO:0010524	positive regulation of calcium ion transport into cytosol	11/1554	2.36E-02	ABL1, ADCYAP1R1, CAV1, GPER1, PKD2, CX3CL1, SNCA, TRPC1, TRPC3, AKAP6, JPH2
BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	17/1554	2.36E-02	CDKN1A, CLU, GADD45A, HBB, MAPT, PKD2, PTGS2, PTX3, RAB27A, SNCA, TGFBR2, THBS1, RGN, KLF4, HDAC4, KLF2, PID1
BP	GO:0032640	tumor necrosis factor production	24/1554	2.36E-02	ANGPT1, ARG2, AXL, BPI, CD34, CHRNA7, CIDEA, CLU, CX3CR1, IGF1, NFATC4, PIK3R1, CX3CL1, SLAMF1, THBS1, TNFAIP3, ZFP36, ADIPOQ, AKAP12, IRAK3, SYT11, ERRFI1, VSIR, LRRK2
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	24/1554	2.36E-02	ANGPT1, ARG2, AXL, BPI, CD34, CHRNA7, CIDEA, CLU, CX3CR1, IGF1, NFATC4, PIK3R1, CX3CL1, SLAMF1, THBS1, TNFAIP3, ZFP36, ADIPOQ, AKAP12, IRAK3, SYT11, ERRFI1, VSIR, LRRK2
BP	GO:0010460	positive regulation of heart rate	7/1554	2.36E-02	ADRA1A, HRC, PDE4D, RYR2, TACR3, TPM1, SCN3B
BP	GO:0032957	inositol trisphosphate metabolic process	7/1554	2.36E-02	GPER1, ITPKB, LHCGR, P2RY1, PLCB4, PLCL1, PLCD4

BP	GO:0043567	regulation of insulin-like growth factor receptor signaling pathway	7/1554	2.36E-02	AR, BMP5, IGF1, IGFBP2, IGFBP5, IGFBP6, CILP
BP	GO:0060740	prostate gland epithelium morphogenesis	7/1554	2.36E-02	AR, ESR1, FGF10, GLI2, ID4, SFRP1, SHH
BP	GO:0099560	synaptic membrane adhesion	7/1554	2.36E-02	PTPRD, SPARCL1, NRXN1, NTNG1, NLGN1, IGSF9B, LRRC4
BP	GO:0032103	positive regulation of response to external stimulus	41/1554	2.37E-02	C3, CD28, CCR6, S1PR1, LPAR1, F3, FGF2, FGF10, FGFR1, NCKAP1L, IL2, IL6R, IL6ST, CXCR2, IL16, IL17A, LDLR, LRP1, NTRK3, PDE2A, PRKCA, PRKD1, PTGER3, PTGER4, PTGS2, CX3CL1, CXCL12, SNCA, TAC1, THBS1, DYSF, IL1RL1, SLIT2, CXCL13, IL17D, NFKBIZ, P2RY12, PDGFD, TLR10, TSLP, LRRK2
BP	GO:0032147	activation of protein kinase activity	42/1554	2.41E-02	ABL1, ADCY2, ADCY5, ADCY9, ADRA2A, ADRA2B, ADRB2, ANGPT1, CALCA, CD40LG, CHRNA7, MAP3K8, CSPG4, GADD45A, DUSP5, LPAR1, FGF2, FGF10, GHR, NCKAP1L, HGF, IGF1, IL6R, ITGA1, ITGB3, KIT, GADD45B, NGF, NTRK3, PRKACB, PRKAR2B, TGFB3, TGFBR2, THBS1, GPRC5A, TNIK, PRKAG2, MAP3K20, AVPI1, PROK1, LRRK2, DUSP19
BP	GO:0002260	lymphocyte homeostasis	12/1554	2.45E-02	ABL1, BCL2, NCKAP1L, IL2, MEF2C, PPP3CB, TNFAIP3, BCL10, TNFRSF13B, TNFRSF13C, DOCK11, GAPT
BP	GO:0010676	positive regulation of cellular carbohydrate metabolic process	12/1554	2.45E-02	ACTN3, ADCYAP1R1, GPER1, IGF1, LHCGR, P2RY1, SNCA, SLC25A12, RGN, SORBS1, PPARGC1A, SIRT1
BP	GO:0001502	cartilage condensation	6/1554	2.45E-02	CCN2, MGP, ROR2, PKD1, THRA, BARX2
BP	GO:0006677	glycosylceramide metabolic process	6/1554	2.45E-02	UGCG, B3GALT2, B3GALT1, ST6GALNAC6, FA2H, ST6GALNAC3
BP	GO:0045019	negative regulation of nitric oxide biosynthetic process	6/1554	2.45E-02	ATP2B4, CAV1, CD34, PTGIS, RGN, ROCK2
BP	GO:0072234	metanephric nephron tubule development	6/1554	2.45E-02	LIF, PKD1, PKD2, WWTR1, FAT4, OSR1
BP	GO:0097503	sialylation	6/1554	2.45E-02	ST3GAL3, ST8SIA1, ST6GALNAC6, ST6GALNAC5, ST6GALNAC3, ST8SIA6
BP	GO:1904406	negative regulation of nitric oxide metabolic process	6/1554	2.45E-02	ATP2B4, CAV1, CD34, PTGIS, RGN, ROCK2
BP	GO:0031644	regulation of neurological system process	21/1554	2.45E-02	ADRB2, CBLN1, CHRNA7, EDNRB, HGF, NPTX1, RELN, VIP, SLC25A12, NRXN1, ROCK2, WASF3, MGLL, NLGN1, IGSF9B, RIMS1, NLGN3, TMEM100, TMEM108, LRRK2, SHISA6
BP	GO:0014911	positive regulation of smooth muscle cell migration	10/1554	2.47E-02	BCL2, LPAR1, FGF9, IGF1, IGFBP5, LRP1, NR4A3, ADAMTS1, HDAC4, PDGFD
BP	GO:0060291	long-term synaptic potentiation	15/1554	2.47E-02	ABL1, CHRNA7, CX3CR1, GRIN2A, MPP2, NFATC4, RELN, SLC8A2, SLC8A3, SNCA, VAMP2, FAM107A, NLGN1, NLGN3, LRRTM1
BP	GO:2001259	positive regulation of cation channel activity	13/1554	2.50E-02	ACTN2, ADRB2, ANK2, CACNA2D1, CACNB2, KCNA1, PKD2, RELN, STAC, AKAP6, NLGN3, JPH2, LRRC52
BP	GO:0022407	regulation of cell-cell adhesion	49/1554	2.50E-02	ABL1, ANXA1, ARG2, CAV1, CD5, CD28, CD40LG, MAP3K8, CD55, DUSP3, EGR3, EPHA7, FYN, LRRC32, GLI2, NCKAP1L, IGF1, IGFBP2, IL1RN, IL2, IL6R, IL6ST, ITPKB, SMAD7, PIK3R1, PRKCA, CX3CL1, CXCL12, SHH, TGFBR2, ZBTB16, NR4A3, PLPP3, PDE5A, BCL10, KLF4, ADIPOQ, GRAP2, TESPA1, CXCL13, FGL2, PLA2G2D, VSIR, NFKBIZ, MYADM, TNFRSF13C, BTLA, NEXMIF, MUC21
BP	GO:0010737	protein kinase A signaling	8/1554	2.52E-02	ADRB2, PRKACB, ADIPOQ, AKAP6, AKAP12, PJA2, TCIM, LRRK2
BP	GO:0035115	embryonic forelimb morphogenesis	8/1554	2.52E-02	CACNA1C, MSX1, SHH, TBX5, WNT9A, RECK, OSR1, RSPO2
BP	GO:0048011	neurotrophin TRK receptor signaling pathway	8/1554	2.52E-02	BDNF, NDN, NGF, NGFR, NTRK3, SPRY1, SPRY2, TMEM108
BP	GO:0017015	regulation of transforming growth	19/1554	2.53E-02	LDLRAD4, CAV1, CIDEA, FBN1, SMAD7, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, LTBP4, ITGA8, EMILIN1, SIRT1, PRDM16, MYOCD, VASN, WFIKKN2

		factor beta receptor signaling pathway			
BP	GO:0001709	cell fate determination	9/1554	2.53E-02	GATA6, MCL1, MEF2C, PROX1, PTCH1, KLF4, DSCAML1, SOX17, EBF2
BP	GO:0001941	postsynaptic membrane organization	9/1554	2.53E-02	GDNF, RELN, NRXN1, NRXN2, MAGI2, NLGN1, NLGN3, LRRC4, SHISA6
BP	GO:0045823	positive regulation of heart contraction	9/1554	2.53E-02	ADRA1A, CCN2, HRC, PDE4D, RGS2, RYR2, TACR3, TPM1, SCN3B
BP	GO:0090184	positive regulation of kidney development	9/1554	2.53E-02	EGR1, GDNF, IL6R, LIF, MYC, SHH, WNT2B, ADIPOQ, PDGFD
BP	GO:0034766	negative regulation of ion transmembrane transport	17/1554	2.54E-02	ACTN2, ADRA2A, BIN1, ATP1A2, CASQ2, CAV1, CLIC2, GEM, KCNH2, PKD2, RGS2, THBS1, KCNAB1, DYSF, KCNE4, REM1, OSR1
BP	GO:0048839	inner ear development	27/1554	2.61E-02	ALDH1A3, CEBPD, EYA1, FGF9, FGF10, FGFR1, GLI2, KCNK2, KCNK3, NTRK3, ROR1, ROR2, PROX1, SHH, ZEB1, TGFB3, NR4A3, ITGA8, DCHS1, KCNQ4, NTN1, PLPPR4, SPRY2, LRIG1, SOBP, FAT4, BMPER
BP	GO:0042116	macrophage activation	16/1554	2.64E-02	BPI, CLU, JUN, LDLR, MAPT, CD200, RORA, CX3CL1, SNCA, THBS1, DYSF, IL1RL1, PJA2, NAMPT, CD93, LRRK2
BP	GO:0043551	regulation of phosphatidylinositol 3-kinase activity	11/1554	2.64E-02	FGF2, KIT, PDGFRA, PIK3R1, PRKD1, TEK, SOCS2, SOCS3, KLF4, P2RY12, TNFAIP8L3
BP	GO:0051249	regulation of lymphocyte activation	57/1554	2.66E-02	ABL1, ANXA1, ARG2, AXL, BCL2, PRDM1, ZFP36L1, CAV1, CD5, CD22, CD28, TNFSF8, CD40LG, CDKN1A, MAP3K8, CD55, DUSP3, GPR183, EGR3, FGF10, FYN, LRRC32, GLI2, GSN, NCKAP1L, ID2, IGF1, IGFBP2, IL2, IL6R, IL6ST, IRF4, ITPKB, SMAD7, MEF2C, MPL, NFATC2, PIK3R1, SFRP1, SHH, TAC1, ZEB1, TGFBR2, TNFAIP3, ZBTB16, PDE5A, BCL10, GRAP2, TESPA1, FGL2, TNFRSF13B, PLA2G2D, VSIR, NFKBIZ, FCRL3, TNFRSF13C, BTLA
BP	GO:0009746	response to hexose	28/1554	2.73E-02	ADCY5, ADRA2A, COL4A3, COL6A2, CCN2, CYP7A1, EGR1, EPHA5, GPER1, GYS2, KCNB1, LRP1, PPP3CB, PRKAA2, PTGS2, PTPRN2, RAP1A, SLC8A1, SRF, VAMP2, TGFBR2, THBS1, TRH, ADIPOQ, NAMPT, TXNIP, PPARGC1A, SYBU
BP	GO:0050870	positive regulation of T cell activation	28/1554	2.73E-02	ANXA1, CAV1, CD5, CD28, CD40LG, MAP3K8, CD55, EGR3, FYN, GLI2, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, ITPKB, PIK3R1, SHH, TGFBR2, ZBTB16, BCL10, GRAP2, TESPA1, VSIR, NFKBIZ, TNFRSF13C, BTLA
BP	GO:0010811	positive regulation of cell-substrate adhesion	19/1554	2.74E-02	ABL1, FOXF1, FLNA, CCN1, ILK, ITGA5, NID1, ROCK1, CX3CL1, SFRP1, TEK, UTRN, EMILIN1, MMRN1, ABI3BP, NDNF, EMILIN3, MYADM, CCDC80
BP	GO:0034394	protein localization to cell surface	12/1554	2.74E-02	ACTN2, ANGPT1, ANK2, BDNF, FGF7, FGF10, FLNA, GPM6B, MAP1A, VCL, FBLN5, RIC3
BP	GO:0043536	positive regulation of blood vessel endothelial cell migration	14/1554	2.76E-02	ABL1, ANGPT1, ANXA1, FGF2, FGFR1, PRKCA, PRKD1, PTGS2, THBS1, AKT3, SIRT1, RHOJ, JCAD, AMOTL1
BP	GO:0043647	inositol phosphate metabolic process	13/1554	2.77E-02	ADCYAP1R1, FGF2, GPER1, IMPA2, INPP5A, ITPKB, LHCGR, P2RY1, PLCB4, PLCL1, SNCA, PLCD4, NUDT10
BP	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	17/1554	2.77E-02	ABL1, BCL2, BCL2L2, CDKN1A, CLU, EPHA2, HIC1, MCL1, NFATC4, PIK3R1, CXCL12, SFRP2, SIRT1, CIDEB, CDIP1, MOAP1, NACC2
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	17/1554	2.77E-02	AR, BCL2, BMP5, EYA4, EYA1, FGF10, FYN, GDNF, HGF, IGF1, MCL1, CX3CL1, SFRP2, THBS1, TNFAIP3, FAIM2, ITPRIP
BP	GO:0035272	exocrine system development	10/1554	2.82E-02	EDA, FGF7, FGF10, FGFR1, HGF, NFIB, SHH, TGFB3, SEMA3A, WLS
BP	GO:0046850	regulation of bone remodeling	10/1554	2.82E-02	CALCA, S1PR1, ITGB3, LEPR, PDK4, PRKCA, SFRP1, TNFAIP3, PPARGC1B, TMEM119
BP	GO:0055010	ventricular cardiac muscle tissue morphogenesis	10/1554	2.82E-02	BMPR1A, SMAD7, MYL3, PROX1, RYR2, TGFBR3, TNNT2, TPM1, HAND1, ZFPM2
BP	GO:0000188	inactivation of MAPK activity	7/1554	2.83E-02	CAV1, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8
BP	GO:0002026	regulation of the force of heart contraction	7/1554	2.83E-02	ADRA1A, ATP1A2, ATP2B4, CAV1, MYL3, RYR2, SLC8A1

BP	GO:0003148	outflow tract septum morphogenesis	7/1554	2.83E-02	BMPR1A, GATA6, TGFBR2, NRP2, ZFPM2, PARVA, TBX20
BP	GO:0045932	negative regulation of muscle contraction	7/1554	2.83E-02	ADRB2, BIN1, ATP1A2, KCNMA1, PTGS2, RGS2, PDE5A
BP	GO:0048668	collateral sprouting	7/1554	2.83E-02	ABL1, BDNF, EPHA7, LRP1, NGF, ZEB2, SPART
BP	GO:0060307	regulation of ventricular cardiac muscle cell membrane repolarization	7/1554	2.83E-02	ANK2, CACNA2D1, KCNH2, SCN1B, SCN4B, SNTA1, KCNE4
BP	GO:0008643	carbohydrate transport	22/1554	2.84E-02	AQP1, AQP2, C3, EDNRA, GRB10, IGF1, MEF2A, ENPP1, PIK3R1, PRKCB, RAP1A, SLC2A3, SLC2A4, NR4A3, ADIPOQ, SORBS1, CLIP3, KLF15, PRKAG2, PID1, SLC2A12, OSTN
BP	GO:1990823	response to leukemia inhibitory factor	16/1554	2.87E-02	SMAD7, MAT2A, RFX2, SSTR1, TLE4, NRP2, SOCS3, KLF4, SPRY2, PRDM5, MRAS, SIRT1, KAT6B, PCOLCE2, SOX17, ARID5B
BP	GO:1990830	cellular response to leukemia inhibitory factor	16/1554	2.87E-02	SMAD7, MAT2A, RFX2, SSTR1, TLE4, NRP2, SOCS3, KLF4, SPRY2, PRDM5, MRAS, SIRT1, KAT6B, PCOLCE2, SOX17, ARID5B
BP	GO:0030890	positive regulation of B cell proliferation	9/1554	2.93E-02	BCL2, CDKN1A, GPR183, NCKAP1L, IL2, MEF2C, NFATC2, FCRL3, TNFRSF13C
BP	GO:0043267	negative regulation of potassium ion transport	9/1554	2.93E-02	ACTN2, ADCYAP1, BIN1, CASQ2, CAV1, KCNH2, VIP, KCNAB1, KCNE4
BP	GO:0061028	establishment of endothelial barrier	9/1554	2.93E-02	S1PR3, PDE2A, PDE4D, RAP1A, ROCK1, CLDN5, ROCK2, PPP1R16B, MYADM
BP	GO:1901381	positive regulation of potassium ion transmembrane transport	9/1554	2.93E-02	ACTN2, ANK2, ATP1B2, FLNA, KCNA1, KCNH2, KCNMB1, AKAP6, LRRC52
BP	GO:1903170	negative regulation of calcium ion transmembrane transport	9/1554	2.93E-02	ADRA2A, BIN1, ATP1A2, CASQ2, CLIC2, GEM, PKD2, DYSF, REM1
BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	19/1554	2.94E-02	LDLRAD4, CAV1, CIDEA, FBN1, SMAD7, ZEB1, TGFB1I1, TGFB3, TGFBR2, TGFBR3, THBS1, LTBP4, ITGA8, EMILIN1, SIRT1, PRDM16, MYOCD, VASN, WFIKKN2
BP	GO:0010922	positive regulation of phosphatase activity	8/1554	2.96E-02	ITGA1, MEF2C, PPP1R12A, RGN, MAGI2, PPP1R15A, FCRL3, PPARGC1B
BP	GO:0098901	regulation of cardiac muscle cell action potential	8/1554	2.96E-02	BIN1, ANK2, CACNA1C, CAV1, FLNA, RYR2, SLMAP, CTNNA3
BP	GO:0022029	telencephalon cell migration	11/1554	2.96E-02	RELN, CXCL12, SRF, CNTN2, NRP2, SLIT2, SEMA3A, P2RY12, DIXDC1, BMERB1, LRRK2
BP	GO:0050879	multicellular organismal movement	11/1554	2.96E-02	ACTN3, DMD, DMPK, ITPR1, MAP1A, MYH3, SLC8A3, STAC, TNNT2, SYNM, RCSD1
BP	GO:0050881	musculoskeletal movement	11/1554	2.96E-02	ACTN3, DMD, DMPK, ITPR1, MAP1A, MYH3, SLC8A3, STAC, TNNT2, SYNM, RCSD1
BP	GO:0033604	negative regulation of catecholamine secretion	5/1554	2.97E-02	ADRA2A, ADRA2B, P2RY1, SYT4, P2RY12
BP	GO:0048368	lateral mesoderm development	5/1554	2.97E-02	BMPR1A, FGFR1, FOXF1, SHH, TBX20
BP	GO:0050651	dermatan sulfate proteoglycan biosynthetic process	5/1554	2.97E-02	CSPG4, DCN, UST, CSGALNACT1, DSEL
BP	GO:0072075	metanephric mesenchyme development	5/1554	2.97E-02	MYC, PKD2, SHH, TCF21, OSR1
BP	GO:0072160	nephron tubule epithelial cell differentiation	5/1554	2.97E-02	LIF, MEF2C, WWTR1, FAT4, OSR1

BP	GO:0090136	epithelial cell-cell adhesion	5/1554	2.97E-02	CYP1B1, KIT, SRF, VCL, BVES
BP	GO:0035023	regulation of Rho protein signal transduction	21/1554	3.00E-02	ABL1, ADRA1A, LPAR1, GPR17, GPR55, ARHGEF10, ARHGEF17, DLC1, AKAP13, ARHGEF15, ARHGEF9, KANK2, ARHGEF26, TIAM2, P2RY10, PREX2, KCTD10, ARHGEF25, ABRA, P2RY8, ARHGEF37
BP	GO:0060135	maternal process involved in female pregnancy	12/1554	3.01E-02	AR, PRDM1, ESR1, JUNB, LIF, PAM, PGR, PTGIS, PTGS2, RGS2, STC1, TCF23
BP	GO:2000378	negative regulation of reactive oxygen species metabolic process	12/1554	3.01E-02	ABCD2, ATP2B4, BCL2, CAV1, CD34, FYN, PRKN, PTGIS, SLC18A2, RGN, ROCK2, MPV17L
BP	GO:0001956	positive regulation of neurotransmitter secretion	6/1554	3.01E-02	CACNB2, GPER1, SNCA, STXBP1, TACR2, NLGN1
BP	GO:0015874	norepinephrine transport	6/1554	3.01E-02	ADRA2A, ADRA2B, KCNB1, P2RY1, SNCA, P2RY12
BP	GO:0035162	embryonic hemopoiesis	6/1554	3.01E-02	IL3, KIT, KITLG, PBX1, TAL1, TGFBR2
BP	GO:0035590	purinergic nucleotide receptor signaling pathway	6/1554	3.01E-02	P2RX1, P2RY1, P2RY14, P2RY10, P2RY12, P2RY8
BP	GO:0046716	muscle cell cellular homeostasis	6/1554	3.01E-02	CFL2, DMD, SRF, LARGE1, BAG3, SGCZ
BP	GO:0048485	sympathetic nervous system development	6/1554	3.01E-02	GDNF, GFRA3, NRP2, HAND2, SEMA3A, PLXNA4
BP	GO:0051412	response to corticosterone	6/1554	3.01E-02	CDKN1A, FOS, FOSB, NTRK3, TRH, FOSL1
BP	GO:0140058	neuron projection arborization	6/1554	3.01E-02	CHRNA7, ROCK1, SEMA3A, NLGN1, LRRK2, PHACTR1
BP	GO:2000380	regulation of mesoderm development	6/1554	3.01E-02	BMPR1A, FGFR1, SFRP2, SHH, DKK1, SOX17
BP	GO:0061035	regulation of cartilage development	13/1554	3.01E-02	ACVRL1, CCN2, EFEMP1, GDF2, GLI2, CCN1, SOX5, TRPS1, WNT9A, ZBTB16, SOX6, PKDCC, RFLNB
BP	GO:0043255	regulation of carbohydrate biosynthetic process	16/1554	3.09E-02	ADCYAP1R1, GPER1, IGF1, LEPR, LHCGR, P2RY1, ENPP1, PPP1CB, SNCA, ADIPOQ, SORBS1, PPARGC1A, SIRT1, PPP1R3B, C1QTNF3, SIK1
BP	GO:0008347	glial cell migration	10/1554	3.16E-02	CSPG4, CX3CR1, GPR183, LRP1, MATN2, NDN, P2RY1, RELN, P2RY12, BMERB1
BP	GO:1904707	positive regulation of vascular smooth muscle cell proliferation	10/1554	3.16E-02	BMPR1A, FGF2, FGF9, IGF1, IGFBP5, JUN, MEF2D, MMP2, NR4A3, ADAMTS1
BP	GO:0071774	response to fibroblast growth factor	22/1554	3.22E-02	ZFP36L1, CCN2, EGR3, FGF2, FGF7, FGF9, FGF10, FGFR1, NR4A1, HYAL1, SFRP1, SNCA, THBS1, ZFP36, FGF23, IER2, SPRY1, SPRY2, CXCL13, FLRT2, HHIP, FAT4
BP	GO:0021510	spinal cord development	17/1554	3.23E-02	ADARB1, GDNF, GLI2, PBX3, PKD1, PKD2, PROX1, RELN, PTCH1, SHH, TAL1, VLDLR, CHRD, BAG3, DAAM2, TBX20, PTBP2
BP	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	14/1554	3.27E-02	LDLRAD4, CAV1, CIDEA, FBN1, SMAD7, TGFB1I1, TGFB3, TGFBR2, TGFBR3, EMILIN1, SIRT1, PRDM16, VASN, WFIKKN2
BP	GO:0003211	cardiac ventricle formation	4/1554	3.27E-02	MEF2C, TBX5, HAND1, HAND2
BP	GO:0010739	positive regulation of protein kinase A signaling	4/1554	3.27E-02	ADRB2, ADIPOQ, AKAP12, TCIM
BP	GO:0014877	response to muscle inactivity involved in regulation of muscle adaptation	4/1554	3.27E-02	ACTN3, UTRN, HDAC4, FBXO32
BP	GO:0014894	response to denervation involved in regulation of muscle adaptation	4/1554	3.27E-02	ACTN3, UTRN, HDAC4, FBXO32

BP	GO:0021694	cerebellar Purkinje cell layer formation	4/1554	3.27E-02	RORA, HERC1, FAIM2, CEND1
BP	GO:0035865	cellular response to potassium ion	4/1554	3.27E-02	CRHBP, DLG2, CACNA1H, PPARGC1A
BP	GO:0060281	regulation of oocyte development	4/1554	3.27E-02	IGF1, NPR2, PDE3A, PDE5A
BP	GO:0060513	prostatic bud formation	4/1554	3.27E-02	AR, FGF10, GLI2, SHH
BP	GO:0070341	fat cell proliferation	4/1554	3.27E-02	FGF10, PER2, PID1, VSTM2A
BP	GO:0070344	regulation of fat cell proliferation	4/1554	3.27E-02	FGF10, PER2, PID1, VSTM2A
BP	GO:0071670	smooth muscle cell chemotaxis	4/1554	3.27E-02	LPAR1, SLIT2, PARVA, PDGFD
BP	GO:0086070	SA node cell to atrial cardiac muscle cell communication	4/1554	3.27E-02	ANK2, RYR2, GJC1, SCN3B
BP	GO:0090336	positive regulation of brown fat cell differentiation	4/1554	3.27E-02	PTGS2, PRDM16, VSTM2A, FNDC5
BP	GO:0097105	presynaptic membrane assembly	4/1554	3.27E-02	PTPRD, IL1RAPL1, NLGN1, NLGN3
BP	GO:0097278	complement-dependent cytotoxicity	4/1554	3.27E-02	C3, CD55, CFH, RAB27A
BP	GO:1903789	regulation of amino acid transmembrane transport	4/1554	3.27E-02	ATP1A2, RGS2, PER2, OSR1
BP	GO:1904338	regulation of dopaminergic neuron differentiation	4/1554	3.27E-02	SFRP1, SFRP2, SHH, DKK1
BP	GO:1905879	regulation of oogenesis	4/1554	3.27E-02	IGF1, NPR2, PDE3A, PDE5A
BP	GO:2001135	regulation of endocytic recycling	4/1554	3.27E-02	ACTN2, ARHGAP1, BVES, EHD2
BP	GO:2001214	positive regulation of vasculogenesis	4/1554	3.27E-02	CD34, RAP1A, ASB4, TMEM100
BP	GO:0051154	negative regulation of striated muscle cell differentiation	9/1554	3.30E-02	BDNF, MSX1, RGS2, FZD7, HDAC4, DKK1, SOX6, MYOCD, TMEM119
BP	GO:0033555	multicellular organismal response to stress	13/1554	3.30E-02	ADCYAP1, ADCYAP1R1, BCL2, BRINP1, EDNRB, GRIK2, MEF2C, NR4A2, RELN, TAC1, TACR1, THBS1, TRPA1
BP	GO:0090090	negative regulation of canonical Wnt signaling pathway	25/1554	3.30E-02	CAV1, EGR1, IGFBP2, IGFBP6, ROR2, PRKN, SFRP1, SFRP2, SHH, TLE4, TBX18, DKK1, SOSTDC1, WWTR1, LATS2, RBMS3, DACT1, SOX17, JADE1, NKD1, TMEM88, CSNK1A1L, PRICKLE1, DACT3, SHISA6
BP	GO:0001958	endochondral ossification	7/1554	3.30E-02	COL13A1, MEF2C, MEF2D, MMP16, TEK, CSGALNACT1, TMEM119
BP	GO:0035116	embryonic hindlimb morphogenesis	7/1554	3.30E-02	AFF3, MSX1, PITX1, SHH, ZBTB16, OSR1, RSPO2
BP	GO:0036075	replacement ossification	7/1554	3.30E-02	COL13A1, MEF2C, MEF2D, MMP16, TEK, CSGALNACT1, TMEM119
BP	GO:0060512	prostate gland morphogenesis	7/1554	3.30E-02	AR, ESR1, FGF10, GLI2, ID4, SFRP1, SHH
BP	GO:0085029	extracellular matrix assembly	7/1554	3.30E-02	GPM6B, HAS1, MFAP4, MYH11, FBLN5, EMILIN1, THSD4
BP	GO:1902003	regulation of amyloid-beta formation	7/1554	3.30E-02	BIN1, CHRNA7, CLU, IGF1, ROCK1, ROCK2, SPON1
BP	GO:2000463	positive regulation of excitatory postsynaptic potential	7/1554	3.30E-02	ADRB2, CHRNA7, RELN, NRXN1, NLGN1, RIMS1, NLGN3
BP	GO:0042472	inner ear morphogenesis	16/1554	3.31E-02	ALDH1A3, EYA1, FGF9, FGF10, FGFR1, GLI2, ROR2, PROX1, ZEB1, NR4A3, ITGA8, KCNQ4, NTN1, SPRY2, LRIG1, SOBP

BP	GO:0006109	regulation of carbohydrate metabolic process	28/1554	3.31E-02	ACACB, ACTN3, ADCYAP1R1, GPER1, IGF1, LEPR, LHCGR, P2RY1, PRKN, PDK4, ENPP1, PPP1CB, PRKAA2, RORA, SNCA, SLC25A12, RGN, ADIPOQ, HDAC4, SORBS1, PPARGC1A, MLXIP, SIRT1, PRKAG2, PPP1R3B, MIDN, C1QTNF3, SIK1
BP	GO:0030307	positive regulation of cell growth	24/1554	3.33E-02	BCL2, BDNF, CDH4, HBEGF, HYAL1, IGF1, IL2, ILK, LRP1, MAP1B, MAPT, NGF, NTRK3, PRKN, CXCL12, SFRP1, SFRP2, SRF, SYT4, LGI1, CPNE6, NTN1, AKAP6, RIMS1
BP	GO:0050728	negative regulation of inflammatory response	24/1554	3.33E-02	ADCYAP1, ABCD2, APOD, CNR2, FOXF1, GPR17, GPER1, HGF, IGF1, IL2, LDLR, CD200, PTGER4, PTGIS, RORA, CX3CL1, TEK, TNFAIP3, TNFAIP6, SOCS3, KLF4, ADIPOQ, C1QTNF3, NLRP6
BP	GO:0021915	neural tube development	23/1554	3.36E-02	ABL1, BMP5, ZFP36L1, EPHA2, GLI2, PKD1, PKD2, PRKACB, PROX1, PTCH1, SFRP1, SFRP2, SHH, DCHS1, CHRD, BCL10, ZEB2, DLC1, DACT1, CC2D2A, SHROOM3, SOX17, PRICKLE1
BP	GO:0035909	aorta morphogenesis	8/1554	3.36E-02	ACVRL1, BMPR1A, EYA1, LRP1, MYLK, PROX1, SRF, ADAMTS9
BP	GO:0051954	positive regulation of amine transport	8/1554	3.36E-02	GDNF, KCNB1, CXCL12, STXBP1, SYT4, TACR2, TRH, VIP
BP	GO:0050905	neuromuscular process	17/1554	3.43E-02	ABL1, ADARB1, ADCY5, ALDH1A3, CTNNA2, GRID2, GRIN2A, KCNA1, PRKN, NR4A3, CNTNAP1, HERC1, NRXN1, SPART, JPH4, PRRT2, TMEM150C
BP	GO:0042475	odontogenesis of dentin-containing tooth	15/1554	3.44E-02	BMPR1A, EDA, FGF10, GLI2, GNAO1, MSX1, NFIC, PDGFRA, SHH, HAND1, HAND2, ENAM, SOSTDC1, SLC24A4, RSPO2
BP	GO:0034284	response to monosaccharide	28/1554	3.51E-02	ADCY5, ADRA2A, COL4A3, COL6A2, CCN2, CYP7A1, EGR1, EPHA5, GPER1, GYS2, KCNB1, LRP1, PPP3CB, PRKAA2, PTGS2, PTPRN2, RAP1A, SLC8A1, SRF, VAMP2, TGFBR2, THBS1, TRH, ADIPOQ, NAMPT, TXNIP, PPARGC1A, SYBU
BP	GO:0032873	negative regulation of stress-activated MAPK cascade	10/1554	3.52E-02	DUSP1, DUSP3, MYC, PRKN, PER1, SFRP1, SFRP2, HIPK3, DACT1, DUSP19
BP	GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	10/1554	3.52E-02	DUSP1, DUSP3, MYC, PRKN, PER1, SFRP1, SFRP2, HIPK3, DACT1, DUSP19
BP	GO:0043433	negative regulation of DNA-binding transcription factor activity	24/1554	3.55E-02	CYP1B1, ESR1, FLNA, ID2, SMAD7, CD200, PIM1, PKD1, PKD2, PROX1, PTCH1, PTGIS, TNFAIP3, WFS1, KLF4, HAND1, HAND2, HDAC4, TRIB1, IRAK3, SIRT1, TCEAL7, SIK1, NWD1
BP	GO:0022409	positive regulation of cell-cell adhesion	33/1554	3.58E-02	ANXA1, CAV1, CD5, CD28, CD40LG, MAP3K8, CD55, EGR3, FYN, GLI2, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, ITPKB, SMAD7, PIK3R1, CX3CL1, SHH, TGFBR2, ZBTB16, NR4A3, PLPP3, BCL10, GRAP2, TESPA1, CXCL13, VSIR, NFKBIZ, TNFRSF13C, BTLA
BP	GO:0070301	cellular response to hydrogen peroxide	16/1554	3.61E-02	ABL1, ANXA1, AQP1, RHOB, AXL, CYP1B1, HGF, TNFAIP3, RNF112, NR4A3, KLF4, KLF2, KDM6B, SIRT1, PDGFD, LRRK2
BP	GO:0043393	regulation of protein binding	29/1554	3.62E-02	ABL1, ADRB2, ANGPT1, BCL2, BDNF, CAV1, CSF3, LRP1, MEF2C, NFATC4, PRKN, PKD1, PLCL1, ROCK1, TGFBR3, ADIPOQ, BAG2, HDAC4, SPON1, NES, DZIP1, DKK1, CDON, DACT1, CRTAC1, GREM2, LRRK2, WFIKKN2, XIRP1
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	21/1554	3.62E-02	ZFP36L1, CCN2, EGR3, FGF2, FGF7, FGF9, FGF10, FGFR1, NR4A1, HYAL1, SFRP1, SNCA, THBS1, ZFP36, FGF23, SPRY1, SPRY2, CXCL13, FLRT2, HHIP, FAT4
BP	GO:0035306	positive regulation of dephosphorylation	11/1554	3.64E-02	ITGA1, MEF2C, PPP1R12A, RGN, MAGI2, DLC1, PPP1R15A, PPP1R16B, DUSP26, FCRL3, PPARGC1B
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	38/1554	3.65E-02	ANXA1, ARG2, CAV1, CD5, CD28, CD40LG, MAP3K8, CD55, DUSP3, EGR3, FYN, LRRC32, GLI2, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, ITPKB, SMAD7, PIK3R1, CXCL12, SHH, TGFBR2, ZBTB16, NR4A3, PDE5A, BCL10, KLF4, GRAP2, TESPA1, FGL2, PLA2G2D, VSIR, NFKBIZ, TNFRSF13C, BTLA
BP	GO:0036119	response to platelet-derived growth factor	6/1554	3.66E-02	FER, FYN, HAS1, HYAL1, ERRFI1, PDGFD
BP	GO:0045649	regulation of macrophage differentiation	6/1554	3.66E-02	ID2, LIF, ROR2, PRKCA, ADIPOQ, TRIB1
BP	GO:0051195	negative regulation of cofactor metabolic process	6/1554	3.66E-02	ACTN3, FYN, SLC25A12, HDAC4, PPARGC1A, MPV17L
BP	GO:0006687	glycosphingolipid metabolic process	12/1554	3.66E-02	CREM, KIT, ST8SIA1, UGCG, B3GALT2, B3GALT1, LARGE1, ST6GALNAC6, FA2H, ST6GALNAC5, ST6GALNAC3, ST8SIA6

BP	GO:0015800	acidic amino acid transport	12/1554	3.66E-02	ATP1A2, GRM7, SNCA, STXBP1, VAMP2, SYT4, TRH, PPFIA2, SLC25A12, PER2, RIMS1, SLC17A7
BP	GO:0050727	regulation of inflammatory response	56/1554	3.69E-02	A2M, ADCYAP1, ABCD2, ANXA1, APOD, C1R, C1S, C3, C4A, C4B, C6, C7, CD28, CLU, CNR2, CPN1, CR2, CD55, EDNRB, ESR1, FOXF1, GPR17, GPER1, CFH, HGF, IGF1, IL2, IL6ST, IL17A, LDLR, CD200, PDE2A, PER1, PTGER3, PTGER4, PTGIS, PTGS2, RORA, CX3CL1, SNCA, TAC1, TEK, TNFAIP3, TNFAIP6, SOCS3, IL1RL1, KLF4, ADIPOQ, MGLL, IL17D, NFKBIZ, TLR10, TSLP, C1QTNF3, LRRK2, NLRP6
BP	GO:0043534	blood vessel endothelial cell migration	25/1554	3.70E-02	ABL1, ACVRL1, ANGPT1, ANXA1, EGR3, EPHA2, FGF2, FGFR1, GDF2, NR4A1, MEF2C, PRKCA, PRKD1, PTGS2, SRF, THBS1, KLF4, SLIT2, AKT3, SIRT1, RHOJ, JCAD, STARD13, AMOTL1, CLEC14A
BP	GO:0015696	ammonium transport	17/1554	3.70E-02	ADCYAP1, AQP1, GDNF, GPM6B, ITGB3, KCNA2, P2RX1, PRKN, CXCL12, SLC18A2, SLC22A3, SNCA, SYT4, TACR2, SYT11, SLC5A7, SYT15
BP	GO:0050867	positive regulation of cell activation	47/1554	3.72E-02	ANXA1, AXL, BCL2, CAV1, CD5, CD28, CD40LG, CDKN1A, MAP3K8, CCN2, CD55, GPR183, EGR3, FGF10, FYN, GLI2, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, ITPKB, MEF2C, MPL, NFATC2, PIK3R1, SELP, SHH, STXBP1, TAC1, TGFBR2, THBS1, ZBTB16, NR4A3, BCL10, IL1RL1, GRAP2, TESPA1, CRLF2, VSIR, NFKBIZ, TSLP, FCRL3, TNFRSF13C, LRRK2, BTLA
BP	GO:0003009	skeletal muscle contraction	9/1554	3.73E-02	ACTN3, DMD, DMPK, MYH3, SLC8A3, STAC, TNNT2, SYNM, RCSD1
BP	GO:0045773	positive regulation of axon extension	9/1554	3.73E-02	CDH4, ILK, LRP1, MAP1B, MAPT, NTRK3, CXCL12, SRF, NTN1
BP	GO:0055026	negative regulation of cardiac muscle tissue development	9/1554	3.73E-02	KCNK2, MEIS1, RBP4, RGS2, TBX5, TGFBR2, FZD7, DKK1, SOX6
BP	GO:0006837	serotonin transport	5/1554	3.73E-02	GPM6B, ITGB3, P2RX1, SLC18A2, SNCA
BP	GO:0007158	neuron cell-cell adhesion	5/1554	3.73E-02	NRXN1, NRXN2, NLGN1, NLGN3, CNTN4
BP	GO:0010919	regulation of inositol phosphate biosynthetic process	5/1554	3.73E-02	ADCYAP1R1, GPER1, LHCGR, P2RY1, SNCA
BP	GO:0014048	regulation of glutamate secretion	5/1554	3.73E-02	GRM7, SNCA, STXBP1, SYT4, TRH
BP	GO:0014061	regulation of norepinephrine secretion	5/1554	3.73E-02	ADRA2A, ADRA2B, KCNB1, P2RY1, P2RY12
BP	GO:0014866	skeletal myofibril assembly	5/1554	3.73E-02	ACTC1, MYH11, PROX1, MYOM2, LMOD3
BP	GO:0050655	dermatan sulfate proteoglycan metabolic process	5/1554	3.73E-02	CSPG4, DCN, UST, CSGALNACT1, DSEL
BP	GO:0051447	negative regulation of meiotic cell cycle	5/1554	3.73E-02	DUSP1, LIF, NPR2, OVOL1, PRKACB
BP	GO:0072109	glomerular mesangium development	5/1554	3.73E-02	ACTA2, CD34, EGR1, IL6R, PDGFD
BP	GO:0086103	G protein-coupled receptor signaling pathway involved in heart process	5/1554	3.73E-02	ATP2B4, CAV1, PDE4D, RGS2, AKAP13
BP	GO:0090335	regulation of brown fat cell differentiation	5/1554	3.73E-02	PTGS2, SIRT1, PRDM16, VSTM2A, FNDC5
BP	GO:1990000	amyloid fibril formation	5/1554	3.73E-02	CHRNA7, CLU, GSN, LDLR, MAPT
BP	GO:0050866	negative regulation of cell activation	27/1554	3.73E-02	ANXA1, ARG2, AXL, BPI, CNR2, DUSP3, FER, FOXF1, LRRC32, GPER1, ID2, IL2, LDLR, SMAD7, CD200, PDGFRA, CX3CL1, SFRP1, SHH, TNFAIP3, PDE5A, FGL2, EMILIN1, TNFRSF13B, PLA2G2D, VSIR, CYGB
BP	GO:0043666	regulation of phosphoprotein phosphatase activity	18/1554	3.74E-02	CRY2, DMPK, RCAN1, NCKAP1L, ITGA1, PPP1R12A, PPP1R1A, PPP2R2B, ROCK1, RGN, ROCK2, MAGI2, RCAN2, PPP1R15A, PPP1R16B, PPP1R3B, FCRL3, PHACTR1
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	29/1554	3.76E-02	ANXA1, CAV1, CD5, CD28, CD40LG, MAP3K8, CD55, EGR3, FYN, GLI2, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, ITPKB, PIK3R1, SHH, TGFBR2, ZBTB16, NR4A3, BCL10, GRAP2, TESPA1, VSIR, NFKBIZ, TNFRSF13C, BTLA

BP	GO:0050921	positive regulation of chemotaxis	20/1554	3.81E-02	CCR6, S1PR1, LPAR1, F3, FGF2, FGF10, FGFR1, NCKAP1L, IL6R, CXCR2, IL16, NTRK3, PRKD1, CXCL12, THBS1, DYSF, SLIT2, CXCL13, P2RY12, PDGFD
BP	GO:1901879	regulation of protein depolymerization	14/1554	3.84E-02	ACTN2, CFL2, GSN, MAP1A, MAP1B, TMOD1, NES, DSTN, LMOD1, LMOD3, SPTBN4, NAV3, BMERB1, PLEKHH2
BP	GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	14/1554	3.84E-02	LDLRAD4, CAV1, CIDEA, FBN1, SMAD7, TGFB1I1, TGFB3, TGFBR2, TGFBR3, EMILIN1, SIRT1, PRDM16, VASN, WFIKKN2
BP	GO:0035303	regulation of dephosphorylation	28/1554	3.85E-02	CRY2, DLG2, DMPK, RCAN1, NCKAP1L, ITGA1, MEF2C, PPP1R12A, PPP1R1A, PPP2R2B, ROCK1, RGN, ROCK2, MAGI2, RCAN2, DLC1, RIMBP2, PPP1R15A, PPP1R16B, PCDH11X, SLC7A14, DUSP26, PPP1R3B, CSRNP3, FCRL3, PPARGC1B, CNST, PHACTR1
BP	GO:0003091	renal water homeostasis	8/1554	3.85E-02	ADCY2, ADCY5, ADCY9, AQP1, AQP2, PRKACB, PRKAR2B, WFS1
BP	GO:0003417	growth plate cartilage development	8/1554	3.85E-02	ANXA6, COL6A2, COL6A3, MATN2, STC1, TGFBR2, SCARA3, COL21A1
BP	GO:1901020	negative regulation of calcium ion transmembrane transporter activity	8/1554	3.85E-02	ADRA2A, ATP1A2, CASQ2, CLIC2, GEM, PKD2, DYSF, REM1
BP	GO:1901099	negative regulation of signal transduction in absence of ligand	8/1554	3.85E-02	BCL2, EYA4, EYA1, FGF10, FYN, GDNF, MCL1, CX3CL1
BP	GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	8/1554	3.85E-02	BCL2, EYA4, EYA1, FGF10, FYN, GDNF, MCL1, CX3CL1
BP	GO:0007271	synaptic transmission, cholinergic	7/1554	3.85E-02	CHRM3, CHRNA7, TAC1, TACR2, SLC5A7, LYNX1, RIC3
BP	GO:0010954	positive regulation of protein processing	7/1554	3.85E-02	C3, C6, GSN, CNTN2, CLEC3B, BAG2, SPON1
BP	GO:0021602	cranial nerve morphogenesis	7/1554	3.85E-02	ADARB1, EGR2, EPHB1, KCNA2, NRP2, SEMA3A, PLXNA4
BP	GO:0032232	negative regulation of actin filament bundle assembly	7/1554	3.85E-02	ARHGAP6, S1PR1, PRKN, DLC1, TMEFF2, ARHGAP28, PHLDB2
BP	GO:0035025	positive regulation of Rho protein signal transduction	7/1554	3.85E-02	LPAR1, GPR17, GPR55, AKAP13, P2RY10, ABRA, P2RY8
BP	GO:0050974	detection of mechanical stimulus involved in sensory perception	7/1554	3.85E-02	FYN, KCNA1, KIT, CXCL12, TRPA1, PIEZO2, TMC2
BP	GO:0048146	positive regulation of fibroblast proliferation	10/1554	3.89E-02	AQP1, CDKN1A, ESR1, FGF10, IGF1, JUN, MYC, DDR2, PDGFRA, PDGFD
BP	GO:0051496	positive regulation of stress fiber assembly	10/1554	3.89E-02	ABL1, CCN2, LPAR1, SFRP1, TAC1, TGFB3, TPM1, ROCK2, ARHGEF10, ARHGEF15
BP	GO:0003281	ventricular septum development	13/1554	3.92E-02	PRDM1, ID2, CCN1, SMAD7, PDE2A, PROX1, SALL1, SLIT3, TBX5, TGFBR2, TGFBR3, SLIT2, ZFPM2
BP	GO:0021536	diencephalon development	13/1554	3.92E-02	ADCYAP1, BMPR1A, FGF10, GLI2, MSX1, NR4A2, PITX1, PITX2, SALL1, SHH, NRP2, ZEB2, SEMA3A
BP	GO:0021761	limbic system development	17/1554	3.93E-02	ALDH1A3, ATP2B4, EPHA5, FGFR1, ID4, KCNA1, PROX1, RELN, SRF, BTG2, NR4A3, NRP2, ZEB2, SEMA3A, KDM6B, TMEM108, DCLK2
BP	GO:0048747	muscle fiber development	12/1554	3.98E-02	BCL2, DMD, FLNC, MYH11, SGCB, SGCD, DYSF, MYOM2, HDAC4, KLHL41, LMOD3, WFIKKN2
BP	GO:0031102	neuron projection regeneration	11/1554	3.98E-02	APOD, BCL2, HGF, JUN, LRP1, MAP1B, MATN2, NTRK3, KLF4, RGMA, JAM3
BP	GO:0045843	negative regulation of striated muscle tissue development	11/1554	3.98E-02	EPHB1, KCNK2, MEIS1, RBP4, RGS2, TBX5, TGFBR2, FZD7, DKK1, SOX6, MYOCD

BP	GO:0097756	negative regulation of blood vessel diameter	14/1554	4.19E-02	ACTA2, ADRA1A, ADRA2A, ADRA2B, ATP1A2, BDKRB2, CAV1, CHRM3, EDNRA, EDNRB, P2RX1, PTGS2, SLC8A1, PER2
BP	GO:0014047	glutamate secretion	9/1554	4.22E-02	GRM7, SNCA, STXBP1, VAMP2, SYT4, TRH, PPFIA2, RIMS1, SLC17A7
BP	GO:0050982	detection of mechanical stimulus	9/1554	4.22E-02	FYN, KCNA1, KIT, PKD1, PKD2, CXCL12, TRPA1, PIEZO2, TMC2
BP	GO:0051489	regulation of filopodium assembly	9/1554	4.22E-02	DPYSL3, GPM6A, PALM, SRF, TGFB3, NEURL1, NLGN1, PPP1R16B, DOCK11
BP	GO:2001234	negative regulation of apoptotic signaling pathway	30/1554	4.26E-02	AR, BCL2, BCL2L2, BDKRB2, BDNF, BMP5, CLU, CX3CR1, EYA4, EYA1, FGF10, FYN, GDNF, HGF, IGF1, MCL1, NR4A2, PRKN, PTGS2, CX3CL1, CXCL12, SFRP2, THBS1, TNFAIP3, WFS1, FAIM2, SIRT1, ITPRIP, LRRK2, MPV17L
BP	GO:1901655	cellular response to ketone	15/1554	4.38E-02	ADCY2, ADCY5, AQP1, AR, KLF9, PRKAA2, PTGER4, PTGFR, SFRP1, KLF4, ROCK2, KLF2, SIRT1, ERRFI1, FBXO32
BP	GO:0007413	axonal fasciculation	6/1554	4.38E-02	EPHA3, NDN, CNTN2, SEMA3A, CRTAC1, CNTN4
BP	GO:0032959	inositol trisphosphate biosynthetic process	6/1554	4.38E-02	GPER1, LHCGR, P2RY1, PLCB4, PLCL1, PLCD4
BP	GO:0051151	negative regulation of smooth muscle cell differentiation	6/1554	4.38E-02	FGF9, NFATC1, NFATC2, SHH, PRDM6, RBPMS2
BP	GO:0060445	branching involved in salivary gland morphogenesis	6/1554	4.38E-02	FGF7, FGF10, FGFR1, HGF, SHH, SEMA3A
BP	GO:0070841	inclusion body assembly	6/1554	4.38E-02	CLU, HSPA2, MAPT, PRKN, BAG3, SACS
BP	GO:0106030	neuron projection fasciculation	6/1554	4.38E-02	EPHA3, NDN, CNTN2, SEMA3A, CRTAC1, CNTN4
BP	GO:0015872	dopamine transport	10/1554	4.38E-02	GDNF, KCNA2, PRKN, CXCL12, SLC18A2, SLC22A3, SNCA, SYT4, SYT11, SYT15
BP	GO:0030072	peptide hormone secretion	32/1554	4.38E-02	ADCY5, ADCYAP1, ADRA2A, SLC25A4, ANXA1, CACNA1C, CPE, CRHBP, EPHA5, GPER1, IL1RN, INHBB, ITPR1, KCNB1, LRP1, PRKN, PPP3CB, PRKCA, PTPRN2, RAP1A, RBP4, SFRP1, TACR2, TRH, VIP, LTBP4, PER2, STXBP5L, MYRIP, SYBU, G6PC2, MIDN
BP	GO:0003264	regulation of cardioblast proliferation	4/1554	4.38E-02	EYA1, PIM1, TBX5, HAND2
BP	GO:0010172	embryonic body morphogenesis	4/1554	4.38E-02	MAB21L2, CDON, GREM2, PHLDB2
BP	GO:0014870	response to muscle inactivity	4/1554	4.38E-02	ACTN3, UTRN, HDAC4, FBXO32
BP	GO:0019371	cyclooxygenase pathway	4/1554	4.38E-02	PTGIS, PTGS1, PTGS2, HPGDS
BP	GO:0033089	positive regulation of T cell differentiation in thymus	4/1554	4.38E-02	EGR3, GLI2, SHH, TESPA1
BP	GO:0034115	negative regulation of heterotypic cell-cell adhesion	4/1554	4.38E-02	IL1RN, KLF4, ADIPOQ, MYADM
BP	GO:0035739	CD4-positive, alpha-beta T cell proliferation	4/1554	4.38E-02	ARG2, CD55, TGFBR2, VSIR
BP	GO:0043117	positive regulation of vascular permeability	4/1554	4.38E-02	CXCR2, PDE2A, PDE3A, TACR2
BP	GO:0060947	cardiac vascular smooth muscle cell differentiation	4/1554	4.38E-02	GATA6, GPER1, SRF, MYOCD
BP	GO:0070587	regulation of cell-cell adhesion involved in gastrulation	4/1554	4.38E-02	IL1RN, KLF4, ADIPOQ, MYADM
BP	GO:0086016	AV node cell action potential	4/1554	4.38E-02	CACNA1C, CACNB2, RYR2, SCN4B
BP	GO:0086027	AV node cell to bundle of His cell signaling	4/1554	4.38E-02	CACNA1C, CACNB2, RYR2, SCN4B

BP	GO:0090193	positive regulation of glomerulus development	4/1554	4.38E-02	EGR1, IL6R, ADIPOQ, PDGFD
BP	GO:0098883	synapse pruning	4/1554	4.38E-02	C3, CX3CR1, CX3CL1, DKK1
BP	GO:1902093	positive regulation of flagellated sperm motility	4/1554	4.38E-02	CCR6, TACR2, TACR1, TACR3
BP	GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferation	4/1554	4.38E-02	ARG2, CD55, TGFBR2, VSIR
BP	GO:0048635	negative regulation of muscle organ development	11/1554	4.40E-02	EPHB1, KCNK2, MEIS1, RBP4, RGS2, TBX5, TGFBR2, FZD7, DKK1, SOX6, MYOCD
BP	GO:0034405	response to fluid shear stress	8/1554	4.40E-02	SMAD7, MEF2C, PKD1, PKD2, PTGS2, TGFB3, KLF4, KLF2
BP	GO:0050954	sensory perception of mechanical stimulus	23/1554	4.45E-02	COL4A3, CRYM, EYA4, EYA1, FGFR1, FYN, GRM7, KCNA1, KIT, ROR1, CXCL12, TBL1X, TUB, WFS1, TRPA1, KCNQ4, SPRY2, LRIG1, SOBP, SPTBN4, PIEZO2, TMC2, OTOGL
BP	GO:0021549	cerebellum development	16/1554	4.45E-02	ABL1, CBLN1, CKB, CNTN1, LPAR1, GLI2, GRID2, PROX1, RORA, SSTR1, HERC1, PPARGC1A, FAIM2, CEND1, PTBP2, FOXP2
BP	GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	7/1554	4.51E-02	ANXA6, COL6A2, COL6A3, MATN2, TGFBR2, SCARA3, COL21A1
BP	GO:0022037	metencephalon development	17/1554	4.55E-02	ABL1, BCL2, CBLN1, CKB, CNTN1, LPAR1, GLI2, GRID2, PROX1, RORA, SSTR1, HERC1, PPARGC1A, FAIM2, CEND1, PTBP2, FOXP2
BP	GO:0002262	myeloid cell homeostasis	21/1554	4.57E-02	ANXA1, AXL, ZFP36L1, NCKAP1L, ID2, CXCR2, ITPKB, KIT, KITLG, MPL, PDE4B, SRF, STAT5B, TAL1, TGFBR3, THRA, ZFP36, DYRK3, KLF2, SOX6, JAM3
BP	GO:0008584	male gonad development	20/1554	4.60E-02	AR, BCL2, BCL2L2, ESR1, FGF9, FLNA, GATA6, KIT, LHCGR, KITLG, PDGFRA, SFRP1, SFRP2, TCF21, WNT2B, SEMA3A, ZFPM2, DHH, ARID5B, RNF38
BP	GO:0002696	positive regulation of leukocyte activation	45/1554	4.60E-02	ANXA1, AXL, BCL2, CAV1, CD5, CD28, CD40LG, CDKN1A, MAP3K8, CD55, GPR183, EGR3, FGF10, FYN, GLI2, NCKAP1L, IGF1, IGFBP2, IL2, IL6R, IL6ST, ITPKB, MEF2C, MPL, NFATC2, PIK3R1, SHH, STXBP1, TAC1, TGFBR2, THBS1, ZBTB16, NR4A3, BCL10, IL1RL1, GRAP2, TESPA1, CRLF2, VSIR, NFKBIZ, TSLP, FCRL3, TNFRSF13C, LRRK2, BTLA
BP	GO:0002695	negative regulation of leukocyte activation	24/1554	4.62E-02	ANXA1, ARG2, AXL, BPI, CNR2, DUSP3, FER, FOXF1, LRRC32, GPER1, ID2, IL2, LDLR, SMAD7, CD200, CX3CL1, SFRP1, SHH, TNFAIP3, PDE5A, FGL2, TNFRSF13B, PLA2G2D, VSIR
BP	GO:0050708	regulation of protein secretion	54/1554	4.62E-02	ABL1, ADCY5, ADRA2A, ANGPT1, SLC25A4, ANXA1, APBB1, ARG2, CACNA1C, CD22, CD34, CD40LG, CIDEA, EPHA5, LRRC32, GPER1, IGF1, IL2, IL17A, INHBB, ITPR1, KCNB1, LRP1, CD200, PAM, PRKN, PPP3CB, PRKCA, PTGER4, RAP1A, RBP4, CX3CL1, SFRP1, SYT4, TGFB3, TNFAIP3, TRH, PER2, IL1RL1, STXBP5L, AKAP12, MAPKBP1, SYT11, MYRIP, SYBU, G6PC2, CRLF2, WLS, TLR10, TSLP, MIDN, C1QTNF3, LRRK2, SSC5D
BP	GO:0021783	preganglionic parasympathetic fiber development	5/1554	4.62E-02	ADARB1, EGR2, NRP2, SEMA3A, PLXNA4
BP	GO:0031000	response to caffeine	5/1554	4.62E-02	CASQ2, RYR2, RYR3, SLC8A1, PPARGC1A
BP	GO:0035988	chondrocyte proliferation	5/1554	4.62E-02	CCN2, MMP16, DDR2, STC1, MUSTN1
BP	GO:0036270	response to diuretic	5/1554	4.62E-02	CASQ2, RYR2, RYR3, SLC8A1, PPARGC1A
BP	GO:0048243	norepinephrine secretion	5/1554	4.62E-02	ADRA2A, ADRA2B, KCNB1, P2RY1, P2RY12
BP	GO:0061298	retina vasculature development in camera-type eye	5/1554	4.62E-02	ACVRL1, CYP1B1, PDGFRA, ARHGEF15, RHOJ
BP	GO:0061323	cell proliferation involved in heart morphogenesis	5/1554	4.62E-02	EYA1, PIM1, PITX2, TBX5, HAND2
BP	GO:0099509	regulation of presynaptic cytosolic calcium ion concentration	5/1554	4.62E-02	ATP2B3, CACNB2, P2RX1, P2RY1, NCS1
BP	GO:1901317	regulation of flagellated sperm motility	5/1554	4.62E-02	CCR6, TACR2, TACR1, TACR3, RGN

BP	GO:1903975	regulation of glial cell migration	5/1554	4.62E-02	CX3CR1, GPR183, LRP1, P2RY12, BMERB1
BP	GO:2000811	negative regulation of anoikis	5/1554	4.62E-02	BCL2, CAV1, ITGA5, MCL1, PDK4
BP	GO:0048678	response to axon injury	13/1554	4.66E-02	APOD, BCL2, DPYSL3, JUN, KCNK2, LRP1, MAP1B, MATN2, NTRK3, KLF4, RGMA, P2RY12, JAM3
BP	GO:0051932	synaptic transmission, GABAergic	9/1554	4.70E-02	ADRA1A, CNR2, GABRA2, GABRA4, GABRG1, PLCL1, STXBP1, TAC1, NLGN1
BP	GO:0007568	aging	39/1554	4.78E-02	ABL1, ADRA1A, APOD, ARG2, BCL2, BMPR1A, CDKN1A, CCN2, DCN, EDNRB, FOS, GNAO1, GSN, ID2, IGFBP2, IGFBP5, ILK, JUN, JUND, KCNMB1, LRP1, P2RY1, PDE4D, PRELP, PTGS2, CX3CL1, SNCA, SRF, TACR3, TGFB3, TGFBR2, TIMP2, RGN, AKT3, NAMPT, PPARGC1A, DKK1, SIRT1, LRRK2
BP	GO:0007229	integrin-mediated signaling pathway	16/1554	4.78E-02	ABL1, CDH17, CCN2, FLNA, ILK, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, PLP1, PRKD1, TLN1, ITGA8, ADAMTS1, FERMT2
BP	GO:0044264	cellular polysaccharide metabolic process	16/1554	4.78E-02	GYS2, HAS1, IGF1, IL6ST, LEPR, ENPP1, PPP1CB, PPP1R1A, PYGB, PER2, SORBS1, PRKAG2, CSGALNACT1, PPP1R3B, STK40, PGM2L1
BP	GO:0071214	cellular response to abiotic stimulus	40/1554	4.78E-02	AQP1, AQP2, RHOB, ATP1A2, OPN1SW, BDKRB2, ZFP36L1, CDKN1A, CRY2, GADD45A, EGR1, HYAL1, MFAP4, MYC, MYLK, NFATC4, PALM, PDE2A, PIK3R1, PKD2, PTGER4, PTGS2, RGR, SFRP1, SFRP2, SLC2A4, DYSF, BCL10, BAG3, HDAC4, NAMPT, HABP4, SIRT1, MAP3K20, ERRFI1, PIEZO2, SLC25A23, RCSD1, OPN4, TMEM150C
BP	GO:0104004	cellular response to environmental stimulus	40/1554	4.78E-02	AQP1, AQP2, RHOB, ATP1A2, OPN1SW, BDKRB2, ZFP36L1, CDKN1A, CRY2, GADD45A, EGR1, HYAL1, MFAP4, MYC, MYLK, NFATC4, PALM, PDE2A, PIK3R1, PKD2, PTGER4, PTGS2, RGR, SFRP1, SFRP2, SLC2A4, DYSF, BCL10, BAG3, HDAC4, NAMPT, HABP4, SIRT1, MAP3K20, ERRFI1, PIEZO2, SLC25A23, RCSD1, OPN4, TMEM150C
BP	GO:0035148	tube formation	21/1554	4.83E-02	ABL1, BMP5, EDA, FGF10, GDNF, NFIB, PRKACB, PROX1, PTCH1, SFRP1, SFRP2, SHH, BCL10, HAND1, ZEB2, DLC1, CC2D2A, SHROOM3, ATOH8, OSR1, PRICKLE1
BP	GO:0051494	negative regulation of cytoskeleton organization	21/1554	4.83E-02	ARHGAP6, CTNNA2, S1PR1, GSN, MAP1B, PRKN, SNCA, TMOD1, SLIT2, DLC1, TMEFF2, LMOD1, CLIP3, LMOD3, SPTBN4, ARHGAP28, NAV3, BMERB1, PHLDB2, MYADM, PLEKHH2
BP	GO:0045661	regulation of myoblast differentiation	10/1554	4.84E-02	ZFP36L1, ILK, MEF2C, KLHL41, SOSTDC1, CDON, MYOCD, PRICKLE1, RANBP3L, RBM24
BP	GO:0007405	neuroblast proliferation	11/1554	4.84E-02	CX3CR1, DCT, EML1, FGFR1, ID4, KCNA1, CX3CL1, SHH, SOX5, HHIP, LRRK2
BP	GO:0030888	regulation of B cell proliferation	11/1554	4.84E-02	BCL2, CD22, CDKN1A, GPR183, NCKAP1L, IL2, MEF2C, NFATC2, TNFRSF13B, FCRL3, TNFRSF13C
BP	GO:0034113	heterotypic cell-cell adhesion	11/1554	4.84E-02	IL1RN, ITGA5, ITGA7, ITGB3, CD200, KLF4, ADIPOQ, NFASC, CTNNA3, PARVA, MYADM
BP	GO:0042733	embryonic digit morphogenesis	11/1554	4.84E-02	BMPR1A, GLI2, MSX1, ROR2, SALL1, SFRP2, SHH, ZBTB16, HAND2, MAP3K20, OSR1
BP	GO:0045123	cellular extravasation	11/1554	4.84E-02	CX3CR1, FER, ITGA1, PECAM1, PTGER4, ROCK1, CX3CL1, CXCL12, SELP, PDGFD, CD99L2
BP	GO:0046513	ceramide biosynthetic process	11/1554	4.84E-02	CCN1, P2RX1, UGCG, B3GALT2, B3GALT1, ST6GALNAC6, FA2H, CERS4, SGMS2, ST6GALNAC3, ST8SIA6
BP	GO:0035304	regulation of protein dephosphorylation	20/1554	4.84E-02	CRY2, DMPK, RCAN1, NCKAP1L, ITGA1, PPP1R12A, PPP1R1A, PPP2R2B, ROCK1, RGN, ROCK2, MAGI2, RCAN2, DLC1, PPP1R15A, PPP1R16B, DUSP26, PPP1R3B, FCRL3, PHACTR1
BP	GO:0045580	regulation of T cell differentiation	20/1554	4.84E-02	ABL1, ANXA1, PRDM1, CD28, EGR3, GLI2, NCKAP1L, IL2, IRF4, ITPKB, SMAD7, NFATC2, SHH, ZEB1, TGFBR2, ZBTB16, TESPA1, FGL2, VSIR, NFKBIZ
BP	GO:0046546	development of primary male sexual characteristics	20/1554	4.84E-02	AR, BCL2, BCL2L2, ESR1, FGF9, FLNA, GATA6, KIT, LHCGR, KITLG, PDGFRA, SFRP1, SFRP2, TCF21, WNT2B, SEMA3A, ZFPM2, DHH, ARID5B, RNF38
BP	GO:0007260	tyrosine phosphorylation of STAT protein	14/1554	4.86E-02	CAV1, FER, FYN, GHR, IGF1, IL2, IL3, IL6R, IL6ST, KIT, LIF, PECAM1, SOCS3, TSLP
BP	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	14/1554	4.86E-02	ATF3, BCL2, BMP5, HGF, NGF, PIK3R1, SFRP1, SFRP2, THBS1, TNFAIP3, BAG3, FAIM2, MOAP1, ITPRIP
BP	GO:0009896	positive regulation of catabolic process	49/1554	4.96E-02	ACTN3, ADRA2A, ADRB2, ABCD2, ZFP36L1, CAV1, CLU, PLK3, DCN, IGF1, LDLR, LRP1, SMAD7, PRKN, PRKAA2, PRKD1, ROCK1, SNCA, TNFAIP3, VIP, ZFP36, BTG2, EPM2A, TNFSF12, RGN, ROCK2, BAG3, BAG2, TRIB1, MID2, CPEB3, SIRT1, TIPARP, HSPB8, DACT1, SNX9, TNRC6C, TP53INP2, VSIR, SOX17, FYCO1, NKD1, LRRK2, CSNK1A1L, ASB5, PRICKLE1, SH3D19, RBM24, RNF180

BP	GO:0030595	leukocyte chemotaxis	29/1554	4.98E-02	ANXA1, CXCR5, CALCA, CCR6, CNR2, DUSP1, GPR183, S1PR1, EDNRB, CXCL2, NCKAP1L, IL1RN, IL6R, CXCR2, IL16, ITGA1, ITGA9, KIT, PDE4B, PDE4D, CX3CL1, CXCL12, THBS1, DYSF, CH25H, SLIT2, CXCL13, SBDS, JAM3
BP	GO:0035329	hippo signaling	8/1554	4.99E-02	TEAD1, DCHS1, PJA2, WWTR1, LATS2, AMOTL2, FAT4, AMOTL1
BP	GO:0046329	negative regulation of JNK cascade	8/1554	4.99E-02	DUSP3, PRKN, PER1, SFRP1, SFRP2, HIPK3, DACT1, DUSP19
BP	GO:0051590	positive regulation of neurotransmitter transport	8/1554	4.99E-02	CACNB2, GPER1, PRKN, SNCA, STXBP1, TACR2, TRH, NLGN1
BP	GO:1903523	negative regulation of blood circulation	8/1554	4.99E-02	ADRA1A, BIN1, ATP1A2, IL2, PDE4D, TAC1, PDE5A, SPTBN4
BP	GO:1904706	negative regulation of vascular smooth muscle cell proliferation	8/1554	4.99E-02	CDKN1A, CNN1, GPER1, MEF2C, TGFB3, TPM1, ADIPOQ, MYOCD
CC	GO:0044449	contractile fiber part	76/1620	9.28E-26	ACTA2, ACTC1, ACTN1, ACTN2, ADRA1A, BIN1, ANK2, ATP2B4, CACNA1C, CASQ2, CFL2, DMD, FLNA, FLNC, HRC, ILK, MMP2, MYH2, MYH3, MYH11, MYL3, PPP1R12A, PPP1R12B, PDE4B, PECAM1, PGM5, PPP3CB, RYR2, RYR3, SLC8A1, SVIL, TMOD1, TNNT2, TPM1, TPM2, VCL, SORBS2, PDLIM4, MYOM2, PDLIM7, FHL5, BAG3, HDAC4, ABCC9, KLHL41, MYL9, PDLIM5, FERMT2, LDB3, SYNPO, HABP4, PALLD, SYNM, SYNE1, CORO1C, LMOD1, PDLIM3, MYOZ2, PARVA, SCN3B, LMOD3, JPH2, PDLIM2, AHNAK, SYNC, TRIM63, MYOZ3, AHNAK2, FBXO32, ARHGEF25, C10orf71, ABRA, SYNPO2, FBXL22, KY, MYZAP
CC	GO:0043292	contractile fiber	77/1620	5.54E-25	ACTA2, ACTC1, ACTN1, ACTN2, ADRA1A, BIN1, ANK2, ATP2B4, CACNA1C, CALD1, CASQ2, CFL2, DMD, FLNA, FLNC, HRC, ILK, MMP2, MYH2, MYH3, MYH11, MYL3, PPP1R12A, PPP1R12B, PDE4B, PECAM1, PGM5, PPP3CB, RYR2, RYR3, SLC8A1, SVIL, TMOD1, TNNT2, TPM1, TPM2, VCL, SORBS2, PDLIM4, MYOM2, PDLIM7, FHL5, BAG3, HDAC4, ABCC9, KLHL41, MYL9, PDLIM5, FERMT2, LDB3, SYNPO, HABP4, PALLD, SYNM, SYNE1, CORO1C, LMOD1, PDLIM3, MYOZ2, PARVA, SCN3B, LMOD3, JPH2, PDLIM2, AHNAK, SYNC, TRIM63, MYOZ3, AHNAK2, FBXO32, ARHGEF25, C10orf71, ABRA, SYNPO2, FBXL22, KY, MYZAP
CC	GO:0030016	myofibril	74/1620	2.94E-24	ACTC1, ACTN1, ACTN2, ADRA1A, BIN1, ANK2, ATP2B4, CACNA1C, CALD1, CASQ2, CFL2, DMD, FLNA, FLNC, HRC, ILK, MMP2, MYH2, MYH3, MYL3, PPP1R12A, PPP1R12B, PDE4B, PGM5, PPP3CB, RYR2, RYR3, SLC8A1, SVIL, TMOD1, TNNT2, TPM1, TPM2, VCL, SORBS2, PDLIM4, MYOM2, PDLIM7, FHL5, BAG3, HDAC4, ABCC9, KLHL41, MYL9, PDLIM5, FERMT2, LDB3, SYNPO, HABP4, PALLD, SYNM, SYNE1, CORO1C, LMOD1, PDLIM3, MYOZ2, PARVA, SCN3B, LMOD3, JPH2, PDLIM2, AHNAK, SYNC, TRIM63, MYOZ3, AHNAK2, FBXO32, ARHGEF25, C10orf71, ABRA, SYNPO2, FBXL22, KY, MYZAP
CC	GO:0030017	sarcomere	69/1620	2.33E-23	ACTC1, ACTN1, ACTN2, ADRA1A, BIN1, ANK2, ATP2B4, CACNA1C, CASQ2, CFL2, DMD, FLNA, FLNC, HRC, ILK, MMP2, MYH2, MYH3, MYL3, PPP1R12A, PPP1R12B, PDE4B, PGM5, PPP3CB, RYR2, RYR3, SLC8A1, TMOD1, TNNT2, TPM1, TPM2, SORBS2, PDLIM4, MYOM2, PDLIM7, FHL5, BAG3, HDAC4, ABCC9, KLHL41, MYL9, PDLIM5, FERMT2, LDB3, SYNPO, HABP4, PALLD, SYNE1, CORO1C, LMOD1, PDLIM3, MYOZ2, PARVA, SCN3B, LMOD3, JPH2, PDLIM2, SYNC, TRIM63, MYOZ3, AHNAK2, FBXO32, ARHGEF25, C10orf71, ABRA, SYNPO2, FBXL22, KY, MYZAP
CC	GO:0042383	sarcolemma	51/1620	1.94E-19	ADRA1A, BIN1, ANK2, ANXA1, AQP1, ATP1A2, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CAV1, COL6A2, COL6A3, DMD, DTNA, FLNC, KCNB1, KCND3, KCNJ3, PGM5, PPP3CB, RYR2, RYR3, SCN1B, SGCB, SGCD, SGCG, SLC2A4, SLC8A1, SLC8A3, SNTA1, STAC, TGFB3, UTRN, VCL, SLMAP, SSPN, DYSF, SGCE, AKAP6, ABCC9, BVES, SYNM, CORO1C, SNTG2, PRX, AHNAK, SYNC, MLIP, AHNAK2, SGCZ
CC	GO:0031674	I band	52/1620	3.34E-19	ACTC1, ACTN1, ACTN2, ADRA1A, BIN1, ANK2, ATP2B4, CACNA1C, CASQ2, CFL2, DMD, FLNA, FLNC, HRC, MYL3, PPP1R12A, PPP1R12B, PDE4B, PGM5, PPP3CB, RYR2, RYR3, SLC8A1, SORBS2, PDLIM4, MYOM2, PDLIM7, FHL5, BAG3, HDAC4, MYL9, PDLIM5, FERMT2, LDB3, SYNPO, PALLD, PDLIM3, MYOZ2, PARVA, SCN3B, JPH2, PDLIM2, SYNC, TRIM63, MYOZ3, AHNAK2, FBXO32, C10orf71, SYNPO2, FBXL22, KY, MYZAP
CC	GO:0030018	Z disc	49/1620	1.42E-18	ACTN1, ACTN2, ADRA1A, BIN1, ANK2, ATP2B4, CACNA1C, CASQ2, CFL2, DMD, FLNA, FLNC, HRC, PPP1R12A, PPP1R12B, PDE4B, PGM5, PPP3CB, RYR2, RYR3, SLC8A1, SORBS2, PDLIM4, MYOM2, PDLIM7, FHL5, BAG3, HDAC4, MYL9, PDLIM5, LDB3, SYNPO, PALLD, PDLIM3, MYOZ2, PARVA, SCN3B, JPH2, PDLIM2, SYNC, TRIM63, MYOZ3, AHNAK2, FBXO32, C10orf71, SYNPO2, FBXL22, KY, MYZAP
CC	GO:0097060	synaptic membrane	97/1620	1.84E-18	ACTN2, ADRA1A, ANK2, ANXA1, APBB1, ATP2B4, CACNA1C, CAMK2A, CBLN1, CHRM2, CHRM3, CHRNA7, CNTN1, COL13A1, CPE, CTNNA2, DLG2, DMD, EPHA7, STX2, GABRA2, GABRA4, GABRG1, GPM6A, GPER1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, GRM7, KCNA1, KCNA2, KCNB1, KCND3, KCNJ3, KCNMA1, MPP2, NTRK3, P2RX1, P2RY1, PALM, PDE2A, SLC8A1, SLC8A3, STXBP1, CNTN2, UTRN, RNF112, FOSL1, SSPN, CNTNAP1, ITGA8, PDLIM4, STX11, MPDZ, NRP2, NEURL1, DLGAP2, NRXN1, RIMS3, PJA2, PLPPR4, PDLIM5, IL1RAPL1, SYNPO, CPEB3, NTNG1, CNKSR2, NLGN1, SORCS3, IGSF9B,

					RIMS1, FAIM2, ERC1, SYT11, ARHGEF9, SYNE1, NCS1, FXYD6, NLGN3, ANKS1B, CADM3, CLSTN2, LRRC4, CPEB1, TMEM108, LRRTM4, CPEB4, LRRC4B, PRRT2, KCTD12, GSG1L, TMEM240, LRRTM1, SHISA6, RGS7BP
CC	GO:0062023	collagen-containing extracellular matrix	89/1620	3.17E-16	A2M, ANXA1, ANXA6, CBLN1, CLU, COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, CSPG4, CCN2, DCN, DPT, ELN, F3, F13A1, FBN1, EFEMP1, FGF9, FGF10, GPC5, GDF10, HSPG2, CCN1, LAMA4, LAMC1, MATN2, MFAP4, MGP, MMP2, NCAM1, NID1, OMD, OGN, PRELP, SDC2, CXCL12, SFRP1, SFRP2, SHH, SOD3, TGFB1I1, TGFB3, THBS1, TIMP2, CLEC3B, VWF, WNT2B, MFAP5, SPARCL1, LTBP4, CILP, ADIPOQ, NTN1, ADAMTS4, ADAMTS1, SDC3, GPC6, LAMC3, SPON1, FBLN5, FGL2, ADAMTS8, ADAMTS5, EMILIN1, MMRN1, ANGPTL2, ABI3BP, CDON, SCARA3, ADAMTS9, THSD4, ITIH5, COL21A1, COL25A1, EMILIN3, CBLN4, CCDC80, SBSPON, FREM1, CLEC14A, ADAMTS15, COL6A5, SSC5D, MXRA7
CC	GO:0045211	postsynaptic membrane	72/1620	1.81E-13	ACTN2, ADRA1A, ANK2, APBB1, CACNA1C, CAMK2A, CBLN1, CHRM2, CHRM3, CHRNA7, CNTN1, COL13A1, CTNNA2, DLG2, DMD, EPHA7, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, GRM7, KCNA1, KCNB1, KCND3, KCNMA1, NTRK3, P2RX1, P2RY1, SLC8A1, SLC8A3, CNTN2, UTRN, RNF112, SSPN, PDLIM4, MPDZ, NRP2, NEURL1, DLGAP2, PJA2, PLPPR4, PDLIM5, IL1RAPL1, SYNPO, CPEB3, CNKSR2, NLGN1, SORCS3, IGSF9B, FAIM2, ARHGEF9, SYNE1, NCS1, FXYD6, NLGN3, ANKS1B, CLSTN2, LRRC4, CPEB1, TMEM108, LRRTM4, CPEB4, PRRT2, KCTD12, GSG1L, LRRTM1, SHISA6, RGS7BP
CC	GO:0034703	cation channel complex	54/1620	7.95E-12	CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, DLG2, DPP6, GRIA1, GRIK2, GRIK3, GRIN2A, HSPA2, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNK2, KCNMA1, KCNMB1, KCNS2, PDE4B, PDE4D, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, VAMP2, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, KCNQ4, AKAP6, ABCC9, NLGN1, KCNH4, KCNE4, KCNIP3, KCNIP1, SCN3B, KCNQ5, CACHD1, KCNIP4, UNC80, SHISA6, LRRC52
CC	GO:0043025	neuronal cell body	88/1620	1.86E-10	ABL1, ACVRL1, ADCYAP1, APBB1, APOD, BMPR1A, C4A, CACNA1C, CD22, CHRM2, CKB, CNGA3, PLK3, CNR2, CPE, CRHBP, CX3CR1, BRINP1, LPAR1, EPHA5, EPHA7, FLNA, GPM6A, GRIA1, GRIK2, GRIK3, IL6ST, ILK, ITGA1, KCNA1, KCNA2, KCNB1, KCND3, KCNK2, KCNN3, LRP1, MAP1A, MAP1B, MAPT, CD200, MPL, NDN, ROR2, PAM, PCSK2, PDE1A, PDE1C, PRKAA2, PRKAR2B, SCN1B, CX3CL1, SLC2A3, SLC8A2, SLC8A3, SNCA, SYT4, TAC1, TACR3, CNTN2, TGFB3, TIMP2, VIP, KCNAB1, ITGA8, UNC5C, NEURL1, CPNE6, NRXN1, AKAP12, OLFM1, PPARGC1A, SYNPO, CNKSR2, IGSF9B, CBX6, CNNM1, TMEM100, KLHL14, SPTBN4, PTBP2, SLC5A7, TRAK2, RIC3, TTLL7, FBXO31, CYGB, LRRK2, RBFOX3
CC	GO:0034702	ion channel complex	61/1620	1.29E-09	CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CHRNA7, CLIC2, DLG2, DPP6, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, HSPA2, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNK2, KCNMA1, KCNMB1, KCNS2, PDE4B, PDE4D, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, VAMP2, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, KCNQ4, AKAP6, ABCC9, NLGN1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, CACHD1, KCNIP4, UNC80, SHISA6, LRRC52
CC	GO:1902495	transmembrane transporter complex	64/1620	1.29E-09	ATP1A2, ATP1B2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CHRNA7, CLIC2, CNGA3, DLG2, DPP6, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, HSPA2, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNK2, KCNMA1, KCNMB1, KCNS2, PDE4B, PDE4D, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, VAMP2, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, KCNQ4, AKAP6, ABCC9, NLGN1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, CACHD1, KCNIP4, UNC80, SHISA6, LRRC52
CC	GO:0042641	actomyosin	27/1620	2.25E-09	ACTC1, ACTN1, ILK, ABLIM1, LPP, MYLK, ROR1, PGM5, TEK, TPM1, CDC42BPA, PDLIM4, PDLIM7, BAG3, HDAC4, MYL9, SORBS1, PDLIM5, FERMT2, LDB3, FAM107A, SYNPO, PDLIM3, PDLIM2, XIRP1, SYNPO2, LURAP1
CC	GO:1990351	transporter complex	64/1620	3.33E-09	ATP1A2, ATP1B2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, CHRNA7, CLIC2, CNGA3, DLG2, DPP6, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, HSPA2, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNK2, KCNMA1, KCNMB1, KCNS2, PDE4B, PDE4D, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, VAMP2, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, KCNQ4, AKAP6, ABCC9, NLGN1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, CACHD1, KCNIP4, UNC80, SHISA6, LRRC52
CC	GO:0031252	cell leading edge	72/1620	8.00E-09	ABL1, ACTA2, ACTC1, ACTN1, AMPH, APBB1, BMX, CSPG4, CTNNA2, DPYSL3, EEF1A1, EPHA2, STX2, FER, GABRA2, GABRA4, GABRG1, GPER1, GRIA1, GSN, ILK, ITGA5, ITGB3, KCNA2, KCNB1, ABLIM1, MAPT, KITLG, MPP2, MYLK, PALM, PKD2, PSD, ROCK1, TACR3, TLN1, TPM1, WIPF1, DYSF, SORBS2, CDC42BPA, ITGA8, PDLIM4, UNC5C, SGCE, LDB2, PDLIM7, SPRY2, KLHL41, DLC1, WASF3, FERMT2, FAM107A, PALLD, SLC39A14, CORO1C, GABARAPL1, ARHGEF26, TIAM2, CTNNA3, PLEKHO1, SNX9, ENAH, PARVA, JCAD, WLS, PHLDB2, MYADM, PLEKHH2, JMY, AMOTL1, SHISA6

CC	GO:0001725	stress fiber	23/1620	4.19E-08	ACTN1, ILK, ABLIM1, LPP, MYLK, ROR1, PGM5, TEK, TPM1, PDLIM4, PDLIM7, BAG3, MYL9, SORBS1, PDLIM5, FERMT2, LDB3, FAM107A, SYNPO, PDLIM3, PDLIM2, XIRP1, SYNPO2
CC	GO:0097517	contractile actin filament bundle	23/1620	4.19E-08	ACTN1, ILK, ABLIM1, LPP, MYLK, ROR1, PGM5, TEK, TPM1, PDLIM4, PDLIM7, BAG3, MYL9, SORBS1, PDLIM5, FERMT2, LDB3, FAM107A, SYNPO, PDLIM3, PDLIM2, XIRP1, SYNPO2
CC	GO:0030315	T-tubule	20/1620	4.70E-08	ADRA1A, BIN1, ANK2, ATP1A2, ATP2B4, CACNA1C, CACNA2D1, CACNB2, KCNJ3, PPP3CB, SCN1B, SLC2A4, SLC8A1, STAC, TGFB3, DYSF, AKAP6, PRX, AHNAK, AHNAK2
CC	GO:0032432	actin filament bundle	24/1620	8.44E-08	ACTN1, ILK, ABLIM1, LPP, MYLK, ROR1, PGM5, TEK, TPM1, PDLIM4, PDLIM7, BAG3, MYL9, SORBS1, PDLIM5, FERMT2, LDB3, FAM107A, SYNPO, PDLIM3, PDLIM2, XIRP1, SYNPO2, RFLNB
CC	GO:0005884	actin filament	30/1620	8.62E-08	ACTC1, ACTN1, ACTN2, ACTN3, ANXA1, ARHGAP6, DPYSL3, FLNA, FYN, PKD2, SMTN, TEK, TMOD1, TPM1, TPM2, WIPF1, GAS7, PDLIM4, PDLIM7, PDLIM5, LDB3, AKAP13, PALLD, LMOD1, PDLIM3, GNG12, PDLIM2, RCSD1, SMTNL2, WIPF3
CC	GO:0099240	intrinsic component of synaptic membrane	37/1620	2.93E-07	ADRA1A, ATP2B4, CHRM2, CHRM3, CNTN1, EPHA7, GABRA4, GPM6A, GRIA1, GRID2, GRIN2A, KCNA1, KCNA2, KCND3, KCNJ3, NTRK3, P2RX1, P2RY1, SLC8A1, SLC8A3, CNTN2, NRP2, NRXN1, PLPPR4, NTNG1, NLGN1, SORCS3, SYT11, FXYD6, NLGN3, CADM3, CLSTN2, LRRC4, GSG1L, LRRTM1, SHISA6, RGS7BP
CC	GO:0098978	glutamatergic synapse	61/1620	3.12E-07	ACTC1, ACTN1, ACTN2, ADRA1A, ATP2B3, ATP2B4, CBLN1, CHRM2, CHRM3, DGKB, DLG2, EPHA7, EPHB1, FLNA, FYN, GPM6A, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITGB3, KCNA1, NPTX1, NTRK3, P2RX1, P2RY1, PLCB4, PPP3CB, PRKAR2B, PTPRD, RAP1A, SH3GL3, STXBP1, SYT4, SPARCL1, PPFIA2, NRP2, LGI1, NRXN1, PLPPR4, GPC6, WASF3, IL1RAPL1, SYNPO, NTNG1, CNKSR2, NLGN1, SORCS3, TNIK, NCS1, FXYD6, NLGN3, CLSTN2, LRRC4, CTTNBP2, LRRK2, GSG1L, LRRTM1, SHISA6, RGS7BP
CC	GO:0005911	cell-cell junction	74/1620	3.24E-07	ACTN1, ADCYAP1R1, ANK2, ANXA1, ATP1A2, CDH4, CDH17, COL13A1, CTNNA2, EPHA2, FLNA, ILK, ITGA5, ITK, KCNA2, KIT, SMAD7, PCDH9, PECAM1, PGM5, PIK3R1, PKD2, PMP22, PPL, SCN1B, SCN4B, SLC8A1, TEK, CLDN5, TRPC4, VCL, CDC42BPA, CNTNAP1, PDLIM4, MPDZ, CLDN8, PDLIM7, AKAP6, MAGI2, GJC1, SORBS1, PDLIM5, BVES, LDB3, SYNPO, NFASC, CRB1, FLRT2, CLIC4, PCDHGA12, PDLIM3, CDH19, STXBP6, CTNNA3, AMOTL2, AJAP1, KIAA1210, JCAD, SHROOM3, SPTBN4, CADM3, JAM2, PDLIM2, AHNAK, CLMP, TMEM47, CD99L2, JAM3, CGNL1, MYADM, PARD3B, MPP7, AMOTL1, HEPACAM
CC	GO:0032279	asymmetric synapse	58/1620	4.25E-07	ACTN2, CACNA1C, CAMK2A, CHRM2, CHRM3, CTNNA2, DLG2, EPHA7, FYN, GPER1, GRIA1, GRID2, GRIK2, GRIN2A, GRM7, ITPR1, MAP1B, MPP2, P2RY1, PALM, PDE4B, PLCB4, PSD, PTCH1, SH3GL3, RNF112, ITGA8, MPDZ, NEURL1, DCLK1, DLGAP2, MAGI2, PJA2, PLPPR4, CAP2, PDLIM5, SYNPO, CPEB3, CNKSR2, NLGN1, SORCS3, IGSF9B, TNIK, SYT11, ARHGEF9, NCS1, NLGN3, ANKS1B, SORCS2, CLSTN2, LRRC4, CPEB1, TMEM108, CPEB4, PRRT2, GSG1L, SHISA6, RGS7BP
CC	GO:0042734	presynaptic membrane	36/1620	5.00E-07	ADRA1A, APBB1, ATP2B4, CHRM2, CHRM3, CNTN1, CTNNA2, STX2, GPM6A, GPER1, GRIK2, GRIK3, GRIN2A, GRM7, KCNA1, KCNA2, KCNJ3, P2RX1, P2RY1, PDE2A, STXBP1, FOSL1, CNTNAP1, STX11, NRXN1, RIMS3, NTNG1, RIMS1, ERC1, SYT11, FXYD6, CADM3, LRRC4B, PRRT2, KCTD12, RGS7BP
CC	GO:0034705	potassium channel complex	26/1620	7.07E-07	DLG2, DPP6, GRIK2, GRIK3, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNK2, KCNMA1, KCNMB1, KCNS2, VAMP2, KCNAB1, KCNQ4, ABCC9, KCNH4, KCNE4, KCNIP3, KCNIP1, KCNQ5, KCNIP4, LRRC52
CC	GO:0016010	dystrophin-associated glycoprotein complex	11/1620	8.36E-07	DMD, PGM5, SGCB, SGCD, SGCG, SNTA1, UTRN, SSPN, SGCE, SNTG2, SGCZ
CC	GO:0090665	glycoprotein complex	11/1620	8.36E-07	DMD, PGM5, SGCB, SGCD, SGCG, SNTA1, UTRN, SSPN, SGCE, SNTG2, SGCZ
CC	GO:0043204	perikaryon	31/1620	1.77E-06	ADCYAP1, CACNA1C, CNGA3, CNR2, CRHBP, GRIK2, GRIK3, ITGA1, KCNA1, KCNA2, KCNB1, MAP1B, NDN, PAM, PCSK2, SCN1B, SLC2A3, SLC8A2, SLC8A3, VIP, KCNAB1, ITGA8, NEURL1, CPNE6, OLFM1, SYNPO, TMEM100, SLC5A7, TTLL7, LRRK2, RBFOX3
CC	GO:0098793	presynapse	75/1620	2.00E-06	ADCYAP1, ADRA1A, AMPH, BIN1, APBB1, ATP2B3, ATP2B4, BDNF, CACNB2, CHRM2, CHRM3, CNTN1, CRHBP, CTNNA2, STX2, GABRA2, GPM6A, GPER1, GRIA1, GRIK2, GRIK3, GRIN2A, GRM7, ILK, KCNA1, KCNA2, KCNJ3, KCNK2, NGF, ROR1, P2RX1, P2RY1, PRKN, PDE2A, PDE4B, PRKCB, PTPRN2, SH3GL3, SLC2A4, SLC18A2, SNCA, STXBP1, VAMP2, SYT4, WFS1, RNF112, FOSL1, PPFIA2, CNTNAP1, STX11, NRXN1, NRXN2, RIMS3, NTNG1, NLGN1, RIMS1, TNIK, ERC1, SYT11, NCS1, KCNIP3, FXYD6, NLGN3, SLC17A7, CADM3, SLC5A7, CTTNBP2, LRRC4B, PRRT2, KCTD12, RAB3C, LRRK2, LGI3, SYPL2, RGS7BP
CC	GO:0099572	postsynaptic specialization	58/1620	2.81E-06	ACTN2, CACNA1C, CAMK2A, CHRM3, CTNNA2, DLG2, EPHA7, FYN, GABRA4, GPER1, GRIA1, GRID2, GRIK2, GRIN2A, ITPR1, KCND3, MAP1B, MPP2, P2RY1, PALM, PDE4B, PLCB4, PSD, PTCH1, SH3GL3, RNF112, ITGA8, MPDZ, NEURL1, DCLK1, DLGAP2, MAGI2, PJA2, PLPPR4, CAP2, PDLIM5, SYNPO, CPEB3, CNKSR2, NLGN1, SORCS3, IGSF9B, TNIK, SYT11, ARHGEF9, NCS1, ANKS1B, SORCS2, CLSTN2, LRRC4, CPEB1, TMEM108, CPEB4, PRRT2, GSG1L, LRRTM1, SHISA6, RGS7BP
CC	GO:0014069	postsynaptic density	55/1620	3.05E-06	ACTN2, CACNA1C, CAMK2A, CHRM3, CTNNA2, DLG2, EPHA7, FYN, GPER1, GRIA1, GRID2, GRIK2, GRIN2A, ITPR1, MAP1B, MPP2, P2RY1, PALM, PDE4B, PLCB4, PSD, PTCH1, SH3GL3, RNF112, ITGA8, MPDZ, NEURL1, DCLK1, DLGAP2, MAGI2, PJA2, PLPPR4, CAP2, PDLIM5, SYNPO, CPEB3, CNKSR2,

					NLGN1, SORCS3, IGSF9B, TNIK, SYT11, ARHGEF9, NCS1, ANKS1B, SORCS2, CLSTN2, LRRC4, CPEB1, TMEM108, CPEB4, PRRT2, GSG1L, SHISA6, RGS7BP
CC	GO:0099699	integral component of synaptic membrane	33/1620	3.05E-06	ADRA1A, ATP2B4, CHRM2, CHRM3, EPHA7, GABRA4, GPM6A, GRIA1, GRID2, GRIN2A, KCNA1, KCNA2, KCND3, KCNJ3, NTRK3, P2RX1, P2RY1, SLC8A1, SLC8A3, NRP2, NRXN1, PLPPR4, NLGN1, SORCS3, SYT11, FXYD6, NLGN3, CADM3, CLSTN2, LRRC4, GSG1L, LRRTM1, SHISA6
CC	GO:0098984	neuron to neuron synapse	58/1620	3.15E-06	ACTN2, CACNA1C, CAMK2A, CHRM2, CHRM3, CTNNA2, DLG2, EPHA7, FYN, GPER1, GRIA1, GRID2, GRIK2, GRIN2A, GRM7, ITPR1, MAP1B, MPP2, P2RY1, PALM, PDE4B, PLCB4, PSD, PTCH1, SH3GL3, RNF112, ITGA8, MPDZ, NEURL1, DCLK1, DLGAP2, MAGI2, PJA2, PLPPR4, CAP2, PDLIM5, SYNPO, CPEB3, CNKSR2, NLGN1, SORCS3, IGSF9B, TNIK, SYT11, ARHGEF9, NCS1, NLGN3, ANKS1B, SORCS2, CLSTN2, LRRC4, CPEB1, TMEM108, CPEB4, PRRT2, GSG1L, SHISA6, RGS7BP
CC	GO:0008076	voltage-gated potassium channel complex	23/1620	5.22E-06	DLG2, DPP6, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNK2, KCNMA1, KCNMB1, KCNS2, VAMP2, KCNAB1, KCNQ4, KCNH4, KCNE4, KCNIP3, KCNIP1, KCNQ5, KCNIP4, LRRC52
CC	GO:0098857	membrane microdomain	53/1620	6.69E-06	ADCY2, ADCYAP1R1, ADRA1A, ANGPT1, ANK2, ATP1A2, ATP2B4, BMPR1A, CAV1, MS4A1, CD48, CD79A, CHRNA7, CNTN1, CD55, DMD, S1PR1, EDNRB, STOM, EPHB1, FYN, GPM6B, ITGA1, KCNMA1, MAPT, P2RX1, PECAM1, PRKAR2B, PTCH1, PTGIS, PTGS2, SHH, SLC2A4, TEK, TGFBR2, TRPC4, TUBA1A, DYSF, CAVIN2, BCL10, AKAP6, DLC1, SORBS1, BVES, FAIM2, CORO1C, CLIP3, EHD2, P2RY12, AHNAK, MYADM, LRRK2, CAVIN1
CC	GO:0005938	cell cortex	52/1620	6.69E-06	ACTN2, RHOB, RND3, RHOH, CALD1, CAV1, CCN2, CTNNA2, EEF1A1, FER, FLNA, GRM7, GSN, GYPC, GYS2, PKD2, SNCA, TMOD1, CLDN5, TRPC4, UTRN, WIPF1, PLA2G4C, AKAP12, RIMS3, CD302, FRY, DLC1, CAP2, FERMT2, DSTN, AKAP13, RIMS1, FNBP1, CORO1C, MYRIP, RND1, STXBP6, SNX9, RHOJ, MICAL3, PDZD4, SHROOM3, SPTBN4, CTTNBP2, PHLDB2, MYADM, PARD3B, PLEKHH2, SEPTIN10, WIPF3, MYZAP
CC	GO:0098936	intrinsic component of postsynaptic membrane	28/1620	6.69E-06	ADRA1A, CHRM2, CHRM3, CNTN1, EPHA7, GABRA4, GRIA1, GRID2, GRIN2A, KCNA1, KCND3, NTRK3, P2RX1, SLC8A1, SLC8A3, CNTN2, NRP2, PLPPR4, NLGN1, SORCS3, FXYD6, NLGN3, CLSTN2, LRRC4, GSG1L, LRRTM1, SHISA6, RGS7BP
CC	GO:0043034	costamere	10/1620	8.52E-06	ANK2, DMD, FLNC, ILK, PGM5, SVIL, VCL, SYNM, AHNAK, AHNAK2
CC	GO:0045121	membrane raft	52/1620	1.28E-05	ADCY2, ADCYAP1R1, ADRA1A, ANGPT1, ANK2, ATP1A2, ATP2B4, BMPR1A, CAV1, MS4A1, CD48, CD79A, CHRNA7, CNTN1, CD55, DMD, S1PR1, EDNRB, STOM, EPHB1, FYN, GPM6B, ITGA1, KCNMA1, MAPT, P2RX1, PECAM1, PRKAR2B, PTCH1, PTGIS, PTGS2, SHH, SLC2A4, TEK, TGFBR2, TRPC4, TUBA1A, CAVIN2, BCL10, AKAP6, DLC1, SORBS1, BVES, FAIM2, CORO1C, CLIP3, EHD2, P2RY12, AHNAK, MYADM, LRRK2, CAVIN1
CC	GO:0005901	caveola	21/1620	1.59E-05	ADCYAP1R1, ADRA1A, ATP1A2, ATP2B4, BMPR1A, CAV1, KCNMA1, PTCH1, PTGIS, PTGS2, TGFBR2, TRPC4, CAVIN2, AKAP6, DLC1, BVES, CORO1C, EHD2, P2RY12, LRRK2, CAVIN1
CC	GO:0016528	sarcoplasm	21/1620	1.59E-05	CACNA2D1, CASQ2, DMPK, FLNC, GSN, HRC, ITPR1, MEF2C, RYR2, RYR3, SRL, SGCD, SLC2A4, SLC8A3, THBS1, AKAP6, KLHL41, HABP4, RASD1, JPH2, JPH4
CC	GO:0098589	membrane region	53/1620	1.84E-05	ADCY2, ADCYAP1R1, ADRA1A, ANGPT1, ANK2, ATP1A2, ATP2B4, BMPR1A, CAV1, MS4A1, CD48, CD79A, CHRNA7, CNTN1, CD55, DMD, S1PR1, EDNRB, STOM, EPHB1, FYN, GPM6B, ITGA1, KCNMA1, MAPT, P2RX1, PECAM1, PRKAR2B, PTCH1, PTGIS, PTGS2, SHH, SLC2A4, TEK, TGFBR2, TRPC4, TUBA1A, DYSF, CAVIN2, BCL10, AKAP6, DLC1, SORBS1, BVES, FAIM2, CORO1C, CLIP3, EHD2, P2RY12, AHNAK, MYADM, LRRK2, CAVIN1
CC	GO:0032590	dendrite membrane	14/1620	2.18E-05	GABRA2, GABRA4, GABRG1, GPER1, GRIA1, KCNB1, MPP2, PALM, TACR3, ITGA8, SGCE, GABARAPL1, WLS, SHISA6
CC	GO:0030863	cortical cytoskeleton	26/1620	2.32E-05	ACTN2, CALD1, EEF1A1, FLNA, GSN, GYPC, GYS2, TMOD1, CLDN5, TRPC4, UTRN, WIPF1, RIMS3, DLC1, CAP2, DSTN, AKAP13, RIMS1, MYRIP, SNX9, SHROOM3, SPTBN4, MYADM, PLEKHH2, WIPF3, MYZAP
CC	GO:0030055	cell-substrate junction	62/1620	2.74E-05	ACTC1, ACTN1, ACTN2, ACTN3, ANXA1, ANXA6, RHOB, RND3, CAV1, CNN1, CSPG4, DMD, EPHA2, FHL1, FLNA, FLNC, GSN, HSPG2, ILK, ITGA1, ITGA5, ITGB3, LPP, LRP1, MCAM, PPP1R12A, DDR2, PGM5, PPP1CB, RRAS, SVIL, TEK, TGFB1I1, TLN1, TNS1, VCL, KLF11, SORBS2, ITGA8, PDLIM7, AKAP12, DLC1, SORBS1, FERMT2, MAPRE2, FAM107A, PALLD, NFASC, CORO1C, FLRT2, TES, ENAH, PARVA, AFAP1, AHNAK, PEAK1, ARHGAP24, CD99L2, DIXDC1, PHLDB2, XIRP1, SYNPO2
CC	GO:0031256	leading edge membrane	33/1620	3.07E-05	AMPH, BMX, CSPG4, EEF1A1, EPHA2, GABRA2, GABRA4, GABRG1, GPER1, GRIA1, ITGA5, ITGB3, KCNA2, KCNB1, MAPT, MPP2, PALM, PSD, TACR3, TLN1, TPM1, ITGA8, SGCE, SPRY2, DLC1, FERMT2, FAM107A, CORO1C, GABARAPL1, PLEKHO1, JCAD, WLS, SHISA6
CC	GO:0005925	focal adhesion	61/1620	3.07E-05	ACTC1, ACTN1, ACTN2, ACTN3, ANXA1, ANXA6, RHOB, RND3, CAV1, CNN1, CSPG4, EPHA2, FHL1, FLNA, FLNC, GSN, HSPG2, ILK, ITGA1, ITGA5, ITGB3, LPP, LRP1, MCAM, PPP1R12A, DDR2, PGM5, PPP1CB, RRAS, SVIL, TEK, TGFB1I1, TLN1, TNS1, VCL, KLF11, SORBS2, ITGA8, PDLIM7, AKAP12, DLC1, SORBS1, FERMT2, MAPRE2, FAM107A, PALLD, NFASC, CORO1C, FLRT2, TES, ENAH, PARVA, AFAP1, AHNAK, PEAK1, ARHGAP24, CD99L2, DIXDC1, PHLDB2, XIRP1, SYNPO2

CC	GO:0098562	cytoplasmic side of membrane	34/1620	3.11E-05	CACNB4, CNR2, DTNA, EEF1A1, FER, FYN, GEM, GNAL, GNAO1, GNAQ, GNAZ, GNG7, GNG11, KIT, PALM, PGM5, PKD2, RGS1, RGS2, STAC, TGM3, KCNAB1, GNA14, FERMT2, RASA3, CBX6, CDIP1, KCNIP1, SNX9, ERRFI1, AJAP1, GNG12, LRRK2, MYZAP
CC	GO:0005924	cell-substrate adherens junction	61/1620	3.76E-05	ACTC1, ACTN1, ACTN2, ACTN3, ANXA1, ANXA6, RHOB, RND3, CAV1, CNN1, CSPG4, EPHA2, FHL1, FLNA, FLNC, GSN, HSPG2, ILK, ITGA1, ITGA5, ITGB3, LPP, LRP1, MCAM, PPP1R12A, DDR2, PGM5, PPP1CB, RRAS, SVIL, TEK, TGFB1I1, TLN1, TNS1, VCL, KLF11, SORBS2, ITGA8, PDLIM7, AKAP12, DLC1, SORBS1, FERMT2, MAPRE2, FAM107A, PALLD, NFASC, CORO1C, FLRT2, TES, ENAH, PARVA, AFAP1, AHNAK, PEAK1, ARHGAP24, CD99L2, DIXDC1, PHLDB2, XIRP1, SYNPO2
CC	GO:0005581	collagen trimer	21/1620	5.68E-05	COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, DCN, EDA, FCN2, ADIPOQ, EMILIN1, SCARA3, COLEC12, COL21A1, COL25A1, C1QTNF3, C1QTNF7, COL6A5, C1QTNF9
CC	GO:0043197	dendritic spine	32/1620	6.89E-05	ACTN2, APBB1, ATP1A2, CAMK2A, LPAR1, GPM6A, GPER1, GRIA1, GRID2, GRIN2A, MAP1B, MAPT, MPP2, PALM, PDE4B, PRKAR2B, PSD, SLC8A2, SLC8A1, SLC8A3, ITGA8, PDLIM4, NEURL1, SYNPO, NLGN1, SYT11, ANKS1B, LRRC4, CPEB4, CTTNBP2, PRRT2, SHISA6
CC	GO:0009898	cytoplasmic side of plasma membrane	30/1620	7.22E-05	CACNB4, CNR2, DTNA, FER, FYN, GEM, GNAL, GNAO1, GNAQ, GNAZ, GNG7, GNG11, KIT, PALM, PGM5, RGS1, RGS2, STAC, TGM3, KCNAB1, GNA14, FERMT2, RASA3, CBX6, KCNIP1, SNX9, ERRFI1, AJAP1, GNG12, MYZAP
CC	GO:0099055	integral component of postsynaptic membrane	25/1620	7.53E-05	ADRA1A, CHRM2, CHRM3, EPHA7, GABRA4, GRIA1, GRID2, GRIN2A, KCNA1, KCND3, NTRK3, P2RX1, SLC8A1, SLC8A3, NRP2, PLPPR4, NLGN1, SORCS3, FXYD6, NLGN3, CLSTN2, LRRC4, GSG1L, LRRTM1, SHISA6
CC	GO:0044309	neuron spine	32/1620	8.42E-05	ACTN2, APBB1, ATP1A2, CAMK2A, LPAR1, GPM6A, GPER1, GRIA1, GRID2, GRIN2A, MAP1B, MAPT, MPP2, PALM, PDE4B, PRKAR2B, PSD, SLC8A2, SLC8A1, SLC8A3, ITGA8, PDLIM4, NEURL1, SYNPO, NLGN1, SYT11, ANKS1B, LRRC4, CPEB4, CTTNBP2, PRRT2, SHISA6
CC	GO:0009897	external side of plasma membrane	58/1620	8.68E-05	ANXA1, CXCR5, BMPR1A, CD1C, CD5, MS4A1, CD28, CD34, CD40LG, CD69, CD79A, CD79B, CCR6, CX3CR1, S1PR1, EPHA5, F3, F10, MS4A2, FCER2, GFRA1, GFRA2, GFRA3, GHR, IL5RA, IL6R, IL6ST, CXCR2, IL17A, ITGA1, ITGA5, KCNJ3, KIT, LDLR, LEPR, LIFR, MCAM, NCAM1, P2RX1, PDGFRA, PECAM1, CXCL12, SELP, SLC2A4, TGFBR2, TGFBR3, THBS1, IL1RL1, NLGN1, ACKR4, CRLF2, P2RY12, SCUBE1, TNFRSF13C, ANTXR2, RAET1E, CLEC14A, SSC5D
CC	GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	21/1620	1.08E-04	CNR2, DTNA, FER, FYN, GNAL, GNAO1, GNAQ, GNAZ, GNG7, GNG11, RGS1, STAC, TGM3, KCNAB1, GNA14, FERMT2, KCNIP1, SNX9, ERRFI1, GNG12, MYZAP
CC	GO:0048786	presynaptic active zone	18/1620	1.12E-04	ATP2B4, CTNNA2, STX2, GPM6A, GPER1, GRM7, P2RX1, P2RY1, STXBP1, PPFIA2, CNTNAP1, STX11, NRXN1, RIMS3, NTNG1, RIMS1, SYT11, SLC17A7
CC	GO:0048787	presynaptic active zone membrane	11/1620	1.27E-04	ATP2B4, STX2, GPM6A, P2RX1, P2RY1, STXBP1, CNTNAP1, STX11, NRXN1, NTNG1, SYT11
CC	GO:0033267	axon part	56/1620	1.40E-04	ADCYAP1, BIN1, ANK2, APBB1, CHRM2, CHRM3, CNGA3, CRHBP, DLG2, DPYSL3, GPM6A, GPER1, GRIA1, GRIK2, GRIK3, ILK, KCNA1, KCNA2, KCNK2, LRP1, MAP1A, MAP1B, MAPT, ROR1, PCDH9, PRKCB, PTCH1, PTPRN2, SCN1B, SLC18A2, SNCA, CNTN2, TIMP2, UTRN, KCNAB1, CNTNAP1, UNC5C, OLFM1, PALLD, NFASC, SYT11, NCS1, CBX6, TIAM2, KCNIP3, CRTAC1, SYBU, SPTBN4, PTBP2, TMEM108, TRAK2, CPEB4, STMN4, PRRT2, LRRK2, LRRTM1
CC	GO:0016323	basolateral plasma membrane	37/1620	1.44E-04	ADRA2A, ANK2, ANXA1, AQP1, AQP2, ATP2B4, CD34, CDH17, CHRM3, CTNNA2, DLG2, STX2, IL6R, ITGA9, LDLR, LEPR, LRP1, MPZ, MTTP, P2RY1, PALM, ENPP1, PKD1, PKD2, SLC8A2, TEK, TRPC4, CLDN8, KCNQ4, SLC22A8, HEPH, ABCC4, AJAP1, P2RY12, SLC26A10, CD300LG, PIANP
CC	GO:0030027	lamellipodium	34/1620	1.53E-04	ACTA2, ACTC1, APBB1, CSPG4, CTNNA2, DPYSL3, EPHA2, STX2, FER, GSN, ILK, ITGB3, KCNA2, ABLIM1, KITLG, MYLK, PKD2, ROCK1, DYSF, SORBS2, CDC42BPA, PDLIM4, UNC5C, WASF3, FERMT2, PALLD, SLC39A14, CORO1C, TIAM2, CTNNA3, ENAH, PARVA, PLEKHH2, AMOTL1
CC	GO:0044853	plasma membrane raft	23/1620	1.83E-04	ADCYAP1R1, ADRA1A, ATP1A2, ATP2B4, BMPR1A, CAV1, MS4A1, CHRNA7, KCNMA1, PTCH1, PTGIS, PTGS2, TGFBR2, TRPC4, CAVIN2, AKAP6, DLC1, BVES, CORO1C, EHD2, P2RY12, LRRK2, CAVIN1
CC	GO:0044304	main axon	17/1620	2.15E-04	BIN1, ANK2, APBB1, CNGA3, CRHBP, DLG2, KCNA1, KCNA2, MAP1A, MAP1B, MAPT, SCN1B, CNTN2, KCNAB1, CNTNAP1, NFASC, SPTBN4
CC	GO:0030864	cortical actin cytoskeleton	20/1620	2.73E-04	ACTN2, CALD1, EEF1A1, GSN, GYS2, CLDN5, UTRN, WIPF1, DLC1, CAP2, DSTN, AKAP13, MYRIP, SNX9, SHROOM3, SPTBN4, MYADM, PLEKHH2, WIPF3, MYZAP
CC	GO:0060076	excitatory synapse	14/1620	2.73E-04	CBLN1, CTNNA2, GRID2, KCNJ3, PDE4B, PLCB4, NLGN1, SYT11, NLGN3, SLC17A7, CADM3, LRRC4, LRRTM1, SHISA6
CC	GO:0032589	neuron projection membrane	15/1620	3.18E-04	GABRA2, GABRA4, GABRG1, GPER1, GRIA1, KCNB1, MAPT, MPP2, PALM, TACR3, ITGA8, SGCE, GABARAPL1, WLS, SHISA6
CC	GO:0044291	cell-cell contact zone	17/1620	3.69E-04	ACTN1, ANK2, ATP1A2, PCDH9, PECAM1, PGM5, SCN1B, SCN4B, SLC8A1, VCL, AKAP6, GJC1, CTNNA3, AJAP1, SPTBN4, AHNAK, JAM3

CC	GO:0005913	cell-cell adherens junction	23/1620	5.43E-04	ACTN1, ANXA1, CDH4, CDH17, CTNNA2, SMAD7, PGM5, VCL, PDLIM4, PDLIM7, SORBS1, PDLIM5, LDB3, CRB1, PDLIM3, CDH19, STXBP6, CTNNA3, AJAP1, KIAA1210, PDLIM2, CD99L2, PARD3B
CC	GO:0019897	extrinsic component of plasma membrane	29/1620	5.70E-04	ANXA1, CDH4, CDH17, CNR2, CTNNA2, DTNA, FER, FYN, GNAL, GNAO1, GNAQ, GNAZ, GNG7, GNG11, SMAD7, RGS1, STAC, TGM3, KCNAB1, GNA14, FERMT2, CNKSR2, CDH19, KCNIP1, SNX9, ERRFI1, GNG12, SCUBE1, MYZAP
CC	GO:0044448	cell cortex part	31/1620	7.27E-04	ACTN2, CALD1, CTNNA2, EEF1A1, FLNA, GSN, GYPC, GYS2, PKD2, TMOD1, CLDN5, TRPC4, UTRN, WIPF1, RIMS3, DLC1, CAP2, DSTN, AKAP13, RIMS1, MYRIP, STXBP6, SNX9, SHROOM3, SPTBN4, PHLDB2, MYADM, PLEKHH2, SEPTIN10, WIPF3, MYZAP
CC	GO:0043198	dendritic shaft	11/1620	7.27E-04	LPAR1, FLNA, GPER1, GRM7, ILK, MAP1A, MPP2, PRKAR2B, SLC8A1, NLGN1, JPH4
CC	GO:0031091	platelet alpha granule	19/1620	9.32E-04	A2M, ACTN1, ACTN2, CLU, CFD, F8, F13A1, HGF, IGF1, ITGB3, PCDH7, PECAM1, SELP, SNCA, STXBP1, TGFB3, THBS1, VWF, MMRN1
CC	GO:0044306	neuron projection terminus	25/1620	1.01E-03	ADCYAP1, CHRM2, CHRM3, CRHBP, DMD, GPER1, GRIK2, GRIK3, ILK, KCNA1, KCNA2, KCNK2, ROR1, PRKCB, PTPRN2, SLC18A2, SNCA, VAMP2, SYT4, SCRG1, SYT11, NCS1, KCNIP3, PRRT2, LRRK2
CC	GO:0150034	distal axon	42/1620	1.11E-03	ADCYAP1, APBB1, CHRM2, CHRM3, CRHBP, DPYSL3, GPM6A, GPER1, GRIK2, GRIK3, ILK, KCNA1, KCNA2, KCNK2, LRP1, MAP1B, MAPT, ROR1, PCDH9, PRKCB, PTCH1, PTPRN2, SLC18A2, SNCA, TIMP2, UTRN, UNC5C, OLFM1, PALLD, SYT11, NCS1, CBX6, TIAM2, KCNIP3, CRTAC1, PTBP2, TRAK2, CPEB4, STMN4, PRRT2, LRRK2, LRRTM1
CC	GO:0031941	filamentous actin	10/1620	1.16E-03	DPYSL3, PKD2, SMTN, PDLIM4, PDLIM7, PDLIM5, LDB3, PDLIM3, PDLIM2, SMTNL2
CC	GO:0016529	sarcoplasmic reticulum	16/1620	1.17E-03	CACNA2D1, CASQ2, DMPK, HRC, ITPR1, RYR2, RYR3, SRL, SGCD, SLC2A4, THBS1, AKAP6, KLHL41, RASD1, JPH2, JPH4
CC	GO:0031253	cell projection membrane	48/1620	1.54E-03	AQP1, OPN1SW, BMX, CSPG4, DMD, EEF1A1, EPHA2, EVC, GABRA2, GABRA4, GABRG1, GPER1, GRIA1, ITGA5, ITGB3, KCNA2, KCNB1, MAPT, MPP2, PALM, PKD1, PKD2, PSD, PTCH1, TACR3, TLN1, TPM1, UTRN, ITGA8, SGCE, SPRY2, DLC1, FERMT2, BVES, FAM107A, CORO1C, GABARAPL1, PLEKHO1, JCAD, HHIP, P2RY12, CYBRD1, WLS, OPN4, TRPM6, TBC1D10C, SHISA6, PRCD
CC	GO:0034704	calcium channel complex	15/1620	1.63E-03	CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, HSPA2, PDE4B, PDE4D, PKD1, RYR2, RYR3, TRPC4, CACNA1H, AKAP6, CACHD1
CC	GO:0098889	intrinsic component of presynaptic membrane	17/1620	2.07E-03	ADRA1A, ATP2B4, CHRM2, CHRM3, CNTN1, GPM6A, KCNA1, KCNA2, KCNJ3, P2RX1, P2RY1, NRXN1, NTNG1, SYT11, FXYD6, CADM3, RGS7BP
CC	GO:0032591	dendritic spine membrane	6/1620	2.10E-03	GPER1, GRIA1, MPP2, PALM, ITGA8, SHISA6
CC	GO:0098948	intrinsic component of postsynaptic specialization membrane	16/1620	2.93E-03	CHRM3, EPHA7, GABRA4, GRIA1, GRID2, GRIN2A, KCND3, PLPPR4, NLGN1, SORCS3, CLSTN2, LRRC4, GSG1L, LRRTM1, SHISA6, RGS7BP
CC	GO:0005788	endoplasmic reticulum lumen	43/1620	2.98E-03	BCHE, C3, C4A, CASQ2, CES1, CLU, COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, F8, F10, FBN1, HRC, IGFBP5, CCN1, LAMC1, MTTP, PTGS2, PTPRN2, SRL, SDC2, SHH, THBS1, WFS1, FGF23, SPARCL1, ENAM, SPON1, CRTAP, ADAMTS5, PRSS23, FSTL1, COLGALT2, PDGFD, COL21A1, COL25A1, CHRDL1, ADAMTSL1
CC	GO:0043209	myelin sheath	12/1620	3.07E-03	BCL2, GNAO1, GSN, MPZ, PLP1, PMP2, PMP22, CNTN2, TUBA1A, MPDZ, TSPAN2, JAM3
CC	GO:0099634	postsynaptic specialization membrane	19/1620	3.26E-03	ACTN2, CHRM3, DLG2, EPHA7, GABRA4, GRIA1, GRID2, GRIN2A, KCND3, PLPPR4, CNKSR2, NLGN1, SORCS3, CLSTN2, LRRC4, GSG1L, LRRTM1, SHISA6, RGS7BP
CC	GO:0098945	intrinsic component of presynaptic active zone membrane	7/1620	3.26E-03	ATP2B4, GPM6A, P2RX1, P2RY1, NRXN1, NTNG1, SYT11
CC	GO:0014704	intercalated disc	12/1620	3.61E-03	ACTN1, ANK2, ATP1A2, PGM5, SCN1B, SCN4B, SLC8A1, VCL, AKAP6, GJC1, CTNNA3, SPTBN4
CC	GO:0019898	extrinsic component of membrane	41/1620	3.86E-03	ANXA1, CDH4, CDH17, CNR2, CTNNA2, DTNA, FER, FYN, GFRA1, GFRA2, GFRA3, GNAL, GNAO1, GNAQ, GNAZ, GNG7, GNG11, SMAD7, PIK3R1, PSD, RGS1, STAC, TGM3, RNF112, KCNAB1, SOCS2, SOCS3, GNA14, SEC23A, FERMT2, MGLL, CNKSR2, CDH19, KCNIP1, EHD2, SNX9, ERRFI1, GNG12, SCUBE1, OSR1, MYZAP
CC	GO:0043679	axon terminus	21/1620	3.97E-03	ADCYAP1, CHRM2, CHRM3, CRHBP, GPER1, GRIK2, GRIK3, ILK, KCNA1, KCNA2, KCNK2, ROR1, PRKCB, PTPRN2, SLC18A2, SNCA, SYT11, NCS1, KCNIP3, PRRT2, LRRK2
CC	GO:0044224	juxtaparanode region of axon	5/1620	3.97E-03	DLG2, KCNA1, KCNA2, CNTN2, KCNAB1
CC	GO:0030175	filopodium	19/1620	4.47E-03	ACTA2, ACTC1, ACTN2, APBB1, DMD, EPHB1, GPM6A, ITGB3, KITLG, PALM, UTRN, UNC5C, CD302, NLGN1, CBX6, ADGRA2, TIAM2, ENAH, TBC1D10C

CC	GO:0099059	integral component of presynaptic active zone membrane	6/1620	4.69E-03	ATP2B4, GPM6A, P2RX1, P2RY1, NRXN1, SYT11
CC	GO:0098839	postsynaptic density membrane	15/1620	5.02E-03	ACTN2, CHRM3, DLG2, EPHA7, GRIA1, GRID2, GRIN2A, PLPPR4, CNKSR2, SORCS3, CLSTN2, LRRC4, GSG1L, SHISA6, RGS7BP
CC	GO:0099060	integral component of postsynaptic specialization membrane	15/1620	5.02E-03	CHRM3, EPHA7, GABRA4, GRIA1, GRID2, GRIN2A, KCND3, PLPPR4, NLGN1, SORCS3, CLSTN2, LRRC4, GSG1L, LRRTM1, SHISA6
CC	GO:0099146	intrinsic component of postsynaptic density membrane	12/1620	5.78E-03	CHRM3, EPHA7, GRIA1, GRID2, GRIN2A, PLPPR4, SORCS3, CLSTN2, LRRC4, GSG1L, SHISA6, RGS7BP
CC	GO:0098688	parallel fiber to Purkinje cell synapse	6/1620	6.69E-03	CBLN1, CTNNA2, GRID2, KCNJ3, PLCB4, CADM3
CC	GO:0005796	Golgi lumen	18/1620	8.63E-03	CSPG4, DCN, F10, GPC5, HSPG2, MMP16, NGF, OMD, OGN, PCSK5, PRELP, SDC2, SOD3, FGF23, SDC3, HS3ST1, GPC6, MUC21
CC	GO:0097440	apical dendrite	6/1620	9.44E-03	CLU, FLNA, MAP1B, NEURL1, PPARGC1A, CPEB3
CC	GO:0034706	sodium channel complex	7/1620	1.03E-02	GRIK2, GRIK3, SCN1B, SCN2B, SCN4B, SCN7A, SCN3B
CC	GO:0099061	integral component of postsynaptic density membrane	11/1620	1.13E-02	CHRM3, EPHA7, GRIA1, GRID2, GRIN2A, PLPPR4, SORCS3, CLSTN2, LRRC4, GSG1L, SHISA6
CC	GO:0099056	integral component of presynaptic membrane	14/1620	1.20E-02	ADRA1A, ATP2B4, CHRM2, CHRM3, GPM6A, KCNA1, KCNA2, KCNJ3, P2RX1, P2RY1, NRXN1, SYT11, FXYD6, CADM3
CC	GO:0005834	heterotrimeric G-protein complex	8/1620	1.22E-02	GNAL, GNAO1, GNAQ, GNAZ, GNG7, GNG11, GNA14, GNG12
CC	GO:1905360	GTPase complex	8/1620	1.22E-02	GNAL, GNAO1, GNAQ, GNAZ, GNG7, GNG11, GNA14, GNG12
CC	GO:0099092	postsynaptic density, intracellular component	6/1620	1.24E-02	ACTN2, CTNNA2, FYN, PSD, SH3GL3, TNIK
CC	GO:0044420	extracellular matrix component	11/1620	1.27E-02	COL4A3, COL4A4, COL4A6, ELN, FBN1, LAMC1, MFAP4, MFAP5, FBLN5, EMILIN1, THSD4
CC	GO:0097386	glial cell projection	7/1620	1.27E-02	CNGA3, FYN, KCNK2, MAPT, SCN7A, SYT4, NFASC
CC	GO:0031093	platelet alpha granule lumen	13/1620	1.44E-02	A2M, ACTN1, ACTN2, CLU, CFD, F8, F13A1, HGF, IGF1, TGFB3, THBS1, VWF, MMRN1
CC	GO:0031225	anchored component of membrane	25/1620	1.59E-02	CD48, CEACAM7, CNTN1, CD55, GPC5, GAS1, GFRA1, GFRA2, GFRA3, NCAM1, OPCML, CNTN3, CNTN2, XPNPEP2, RECK, GPC6, TREH, NTNG1, RGMA, LYNX1, RAB3C, ENPP6, CNTN4, NEGR1, RGS7BP
CC	GO:0070382	exocytic vesicle	29/1620	1.62E-02	AMPH, BIN1, BDNF, DPYSL3, STX2, GABRA2, GRIA1, GRIN2A, IGF1, NGF, PDE4B, PTPRN2, RAB27A, SLC18A2, SNCA, VAMP2, SYT4, WFS1, RNF112, STX11, SYT11, SLC17A7, SYT15, CTTNBP2, PRRT2, RAB3C, LRRK2, LGI3, SYPL2
CC	GO:0031672	A band	9/1620	1.82E-02	ANK2, MYL3, PPP1R12A, PPP1R12B, MYOM2, HDAC4, KLHL41, LMOD3, TRIM63
CC	GO:0001518	voltage-gated sodium channel complex	5/1620	1.94E-02	SCN1B, SCN2B, SCN4B, SCN7A, SCN3B
CC	GO:0043194	axon initial segment	6/1620	2.09E-02	BIN1, ANK2, CNGA3, MAP1A, NFASC, SPTBN4
CC	GO:0005604	basement membrane	16/1620	2.13E-02	COL4A3, COL4A4, COL4A6, COL8A2, FBN1, FGF9, HSPG2, LAMA4, LAMC1, MATN2, NID1, NTN1, ADAMTS1, LAMC3, CCDC80, FREM1
CC	GO:0098636	protein complex involved in cell adhesion	8/1620	2.55E-02	CD28, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, ITGA8, EMILIN1
CC	GO:0033268	node of Ranvier	5/1620	2.62E-02	BIN1, SCN1B, CNTN2, NFASC, SPTBN4
CC	GO:0042827	platelet dense granule	6/1620	2.62E-02	ITPR1, SELP, SELENOP, CLEC3B, ABCC4, CDC37L1
CC	GO:0099091	postsynaptic specialization, intracellular component	6/1620	2.62E-02	ACTN2, CTNNA2, FYN, PSD, SH3GL3, TNIK
CC	GO:0001527	microfibril	4/1620	2.93E-02	FBN1, MFAP4, MFAP5, THSD4
CC	GO:0098858	actin-based cell projection	28/1620	3.00E-02	ACTA2, ACTC1, ACTN2, ANGPT1, APBB1, DMD, EPHB1, GPM6A, ITGB3, KITLG, PALM, PDGFRA, TEK, UTRN, UNC5C, AOC3, CD302, NLGN1, NFASC, CRB1, CBX6, CLIC4, ADGRA2, TIAM2, ENAH, TMC2, LRRK2, TBC1D10C

CC	GO:0005891	voltage-gated calcium channel complex	9/1620	3.29E-02	CACNA1C, CACNA2D1, CACNB2, CACNB4, HSPA2, PDE4B, PDE4D, CACNA1H, CACHD1
CC	GO:0001726	ruffle	24/1620	3.29E-02	ACTN1, BMX, EEF1A1, EPHA2, GSN, ITGA5, ITGB3, PSD, ROCK1, TLN1, TPM1, WIPF1, PDLIM7, SPRY2, KLHL41, DLC1, FAM107A, PALLD, CORO1C, ARHGEF26, PLEKHO1, SNX9, JCAD, MYADM
CC	GO:0031463	Cul3-RING ubiquitin ligase complex	8/1620	4.08E-02	SPOP, KLHL21, KLHL41, KLHL42, KLHL15, KCTD10, KBTBD8, KLHL13
CC	GO:0031092	platelet alpha granule membrane	5/1620	4.37E-02	ITGB3, PCDH7, PECAM1, SELP, SNCA
CC	GO:0031143	pseudopodium	5/1620	4.37E-02	ACTN1, ACTN2, ACTN3, KLHL41, LDB3
CC	GO:0005865	striated muscle thin filament	7/1620	4.90E-02	TMOD1, TNNT2, TPM1, TPM2, MYOM2, LMOD1, LMOD3
CC	GO:0008305	integrin complex	7/1620	4.90E-02	ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, ITGA8, EMILIN1
MF	GO:0003779	actin binding	87/1535	4.84E-11	ABL1, ACTN1, ACTN2, ACTN3, BIN1, ANXA6, CACNB2, CALD1, CFL2, CNN1, CTNNA2, DMD, FLNA, FLNC, GSN, KCNMA1, ABLIM1, MAP1A, MAP1B, MAPT, MYH2, MYH3, MYH11, MYL3, MYLK, PRKN, SMTN, SNCA, SNTA1, SVIL, TAGLN, TLN1, TMOD1, TNNT2, TNS1, TPM1, TPM2, UTRN, VCL, WIPF1, GAS7, PDLIM4, MYOM2, PDLIM7, CAP2, SORBS1, PDLIM5, WASF3, FERMT2, DSTN, LDB3, FAM107A, SYNPO, PALLD, SYNE1, DAAM2, CORO1C, LMOD1, MYRIP, PDLIM3, CTNNA3, KLHL5, MYOZ2, SNTG2, ENAH, PARVA, KLHL4, LMOD3, MICAL3, SHROOM3, SPTBN4, AFAP1, PKNOX2, PDLIM2, NCALD, DIXDC1, MYOZ3, RCSD1, LRRK2, PLEKHH2, JMY, ABRA, SYNE3, XIRP1, SYNPO2, PHACTR1, WIPF3
MF	GO:0005261	cation channel activity	70/1535	1.17E-10	ANXA6, AQP1, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, CNGA3, GPM6A, GRIA1, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, P2RX1, PDE2A, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, TRPA1, KCNQ4, ABCC9, IL1RAPL1, RASA3, NCS1, KCNH4, KCNE4, KCNIP3, KCNIP1, SCN3B, KCNQ5, JPH2, SLC24A3, CACHD1, PIEZO2, TRPM3, KCNIP4, JPH4, TMC2, SLC24A4, TRPM6, NALCN, UNC80, KCNT2, LRRC52, FAM155A
MF	GO:0005216	ion channel activity	80/1535	2.36E-09	ANXA6, AQP1, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, CLIC2, CNGA3, GABRA2, GABRA4, GABRG1, GPM6A, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, P2RX1, PDE2A, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, TRPA1, KCNQ4, GJC1, ABCC9, IL1RAPL1, RASA3, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, JPH2, SLC24A3, CACHD1, PIEZO2, TRPM3, KCNIP4, JPH4, TMC2, ANO4, SLC24A4, TRPM6, ANO5, NALCN, UNC80, KCNT2, LRRC52, FAM155A
MF	GO:0022838	substrate-specific channel activity	81/1535	3.05E-09	ANXA6, AQP1, AQP2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, CLIC2, CNGA3, GABRA2, GABRA4, GABRG1, GPM6A, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, P2RX1, PDE2A, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, TRPA1, KCNQ4, GJC1, ABCC9, IL1RAPL1, RASA3, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, JPH2, SLC24A3, CACHD1, PIEZO2, TRPM3, KCNIP4, JPH4, TMC2, ANO4, SLC24A4, TRPM6, ANO5, NALCN, UNC80, KCNT2, LRRC52, FAM155A
MF	GO:0022836	gated channel activity	69/1535	4.91E-09	ANXA6, AQP1, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, CLIC2, CNGA3, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, P2RX1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, KCNAB1, CACNA1H, TRPA1, KCNQ4, IL1RAPL1, RASA3, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, JPH2, CACHD1, PIEZO2, TRPM3, KCNIP4, JPH4, TMC2, ANO4, ANO5, NALCN, KCNT2, LRRC52, TMEM150C, FAM155A
MF	GO:0015267	channel activity	83/1535	7.56E-09	ANXA6, AQP1, AQP2, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, CLIC2, CNGA3, GABRA2, GABRA4, GABRG1, GPM6A, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, P2RX1, PDE2A, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, TRPA1, KCNQ4, GJC1, ABCC9, IL1RAPL1, RASA3, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, JPH2, SLC24A3, CACHD1, PIEZO2, TRPM3, KCNIP4, JPH4, TMC2, ANO4, SLC24A4, TRPM6, ANO5, NALCN, UNC80, KCNT2, LRRC52, TMEM150C, FAM155A
MF	GO:0022839	ion gated channel activity	67/1535	7.56E-09	ANXA6, AQP1, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, CLIC2, CNGA3, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, P2RX1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, KCNAB1, CACNA1H, TRPA1, KCNQ4, IL1RAPL1, RASA3, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, JPH2, CACHD1, TRPM3, KCNIP4, JPH4, TMC2, ANO4, ANO5, NALCN, KCNT2, LRRC52, FAM155A

MF	GO:0022803	passive transmembrane transporter activity	83/1535	7.56E-09	ANXA6, AQP1, AQP2, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, CLIC2, CNGA3, GABRA2, GABRA4, GABRG1, GPM6A, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, P2RX1, PDE2A, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, TRPA1, KCNQ4, GJC1, ABCC9, IL1RAPL1, RASA3, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, JPH2, SLC24A3, CACHD1, PIEZO2, TRPM3, KCNIP4, JPH4, TMC2, ANO4, SLC24A4, TRPM6, ANO5, NALCN, UNC80, KCNT2, LRRC52, TMEM150C, FAM155A
MF	GO:0005201	extracellular matrix structural constituent	42/1535	8.43E-09	COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, DCN, DPT, ELN, FBN1, EFEMP1, HSPG2, CCN1, LAMA4, LAMC1, MATN2, MFAP4, MGP, NID1, OGN, PRELP, THBS1, VWF, MFAP5, LTBP4, CILP, ADIPOQ, ENAM, SPON1, FBLN5, FGL2, EMILIN1, MMRN1, ABI3BP, THSD4, COL21A1, COL25A1, EMILIN3, SBSPON, COL6A5
MF	GO:0046873	metal ion transmembrane transporter activity	78/1535	5.97E-08	ANXA6, AQP1, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, GPM6A, GRIK2, GRIK3, GRIN2A, ITPR1, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, PDE2A, PKD1, PKD2, RYR2, RYR3, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A2, SLC8A1, SLC8A3, SLC18A2, SLC22A3, TRPC1, TRPC3, TRPC4, KCNAB1, CACNA1H, TRPA1, KCNQ4, ABCC9, IL1RAPL1, RASA3, NCS1, KCNH4, SLC39A14, KCNE4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, JPH2, SLC24A3, CACHD1, SLC5A7, TRPM3, KCNIP4, JPH4, TMC2, SLC24A4, TRPM6, NALCN, SLC9A9, KCNT2, LRRC52, FAM155A
MF	GO:0015085	calcium ion transmembrane transporter activity	36/1535	1.32E-07	ANXA6, ATP2B3, ATP2B4, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, GPM6A, GRIN2A, ITPR1, PDE2A, PKD1, PKD2, RYR2, RYR3, SLC8A2, SLC8A1, SLC8A3, TRPC1, TRPC3, TRPC4, CACNA1H, TRPA1, IL1RAPL1, RASA3, NCS1, JPH2, SLC24A3, CACHD1, TRPM3, JPH4, TMC2, SLC24A4, TRPM6, FAM155A
MF	GO:0008201	heparin binding	40/1535	2.53E-07	COL13A1, CCN2, HBEGF, FBN1, FGF2, FGF7, FGF9, FGF10, FGFR1, CFH, CCN1, PLA2G5, PRELP, PTCH1, SELP, SFRP1, SLIT3, SOD3, TGFBR3, THBS1, CLEC3B, CHRD, NRP2, SLIT2, ADAMTS1, CXCL13, ADAMTS8, ADAMTS5, FSTL1, ABI3BP, PLA2G2D, PCOLCE2, GREM2, NDNF, CRISPLD2, COL25A1, RSPO3, CCDC80, ADAMTS15, RSPO2
MF	GO:0044325	ion channel binding	33/1535	2.53E-07	ACTN1, ACTN2, ACTN3, ANK2, CAV1, FHL1, FLNA, FYN, HRC, ID2, KCNB1, KCND3, PDE4B, PDE4D, PKD1, PKD2, RYR2, SCN1B, SCN4B, SLC8A1, SNTA1, STAC, KCNAB1, AKAP6, BAG2, RIMS3, ABCC9, RIMS1, KCNE4, KCNIP3, SCN3B, LRRK2, LRRC52
MF	GO:0005539	glycosaminoglycan binding	48/1535	4.72E-07	ANXA6, COL13A1, CCN2, DCN, DPYSL3, HBEGF, FBN1, FGF2, FGF7, FGF9, FGF10, FGFR1, CFH, CCN1, PLA2G5, PRELP, PTCH1, SELP, SFRP1, SHH, SLIT3, SOD3, TGFBR2, TGFBR3, THBS1, CLEC3B, TNFAIP6, LTBP4, CHRD, NRP2, SLIT2, ADAMTS1, CXCL13, LYVE1, ADAMTS8, ADAMTS5, FSTL1, ABI3BP, PLA2G2D, PCOLCE2, GREM2, NDNF, CRISPLD2, COL25A1, RSPO3, CCDC80, ADAMTS15, RSPO2
MF	GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	74/1535	1.25E-06	AR, ATF3, CEBPD, KLF6, EBF1, EGR1, EGR2, ERG, ESR1, FOXF1, FOS, FOSB, GLI2, HLF, NR4A1, IRF4, JUN, JUNB, JUND, MEF2A, MEF2C, MEF2D, MEIS1, MEIS2, MEOX1, MITF, MSX1, MYC, NDN, NFATC1, NFATC2, NFIA, NFIB, NFIC, NR4A2, OVOL1, PBX1, PBX3, PGR, PITX1, POU2F2, RORA, RORB, SRF, STAT5B, TBX5, TCF4, TCF21, KLF10, NR4A3, FOSL1, BARX2, TBX18, KLF4, HAND2, TBX4, IER2, ZEB2, ARNT2, MLXIP, MYT1L, SIRT1, MAFF, KLF15, TBX20, SOX17, EBF2, CSRNP1, CSRNP3, MYOCD, SPIC, GLIS1, CREBRF, EBF3
MF	GO:0005262	calcium channel activity	31/1535	2.43E-06	ANXA6, CACNA1C, CACNA2D1, CACNB2, CACNB4, CHRNA7, GPM6A, GRIN2A, ITPR1, PDE2A, PKD1, PKD2, RYR2, RYR3, TRPC1, TRPC3, TRPC4, CACNA1H, TRPA1, IL1RAPL1, RASA3, NCS1, JPH2, SLC24A3, CACHD1, TRPM3, JPH4, TMC2, SLC24A4, TRPM6, FAM155A
MF	GO:1901681	sulfur compound binding	49/1535	2.62E-06	ACACB, ANXA6, CD34, COL13A1, CCN2, DPYSL3, HBEGF, FBN1, FGF2, FGF7, FGF9, FGF10, FGFR1, CFH, CCN1, LRP1, ENPP1, PLA2G5, PRELP, PTCH1, RYR2, SELP, SFRP1, SLIT3, SOD3, TGFBR3, THBS1, CLEC3B, SOAT2, CHRD, NRP2, SLIT2, ADAMTS1, CXCL13, ADAMTS8, ADAMTS5, FSTL1, ABI3BP, PLA2G2D, PCOLCE2, HPSE2, GREM2, NDNF, CRISPLD2, COL25A1, RSPO3, CCDC80, ADAMTS15, RSPO2
MF	GO:0005244	voltage-gated ion channel activity	41/1535	5.21E-06	CACNA1C, CACNA2D1, CACNB2, CACNB4, CLIC2, GRIN2A, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNS2, PKD2, SCN1B, SCN2B, SCN4B, SCN7A, KCNAB1, CACNA1H, KCNQ4, IL1RAPL1, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, CACHD1, KCNIP4, TMC2, NALCN, KCNT2, LRRC52
MF	GO:0022832	voltage-gated channel activity	41/1535	5.21E-06	CACNA1C, CACNA2D1, CACNB2, CACNB4, CLIC2, GRIN2A, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNS2, PKD2, SCN1B, SCN2B, SCN4B, SCN7A, KCNAB1, CACNA1H, KCNQ4, IL1RAPL1, NCS1, KCNH4, KCNE4, CLIC4, KCNIP3, KCNIP1, SCN3B, KCNQ5, CACHD1, KCNIP4, TMC2, NALCN, KCNT2, LRRC52
MF	GO:0019955	cytokine binding	31/1535	5.21E-06	A2M, ACVRL1, CXCR5, CCR6, CX3CR1, LRRC32, GHR, IL1RN, IL5RA, IL6R, IL6ST, CXCR2, ITGB3, KIT, LEPR, LIFR, TGFB3, TGFBR2, TGFBR3, THBS1, ZFP36, LTBP4, CHRD, NRP2, IL1RL1, SOSTDC1, ACKR4, CRLF2, GREM2, VASN, WFIKKN2

MF	GO:0005267	potassium channel activity	29/1535	2.32E-05	AQP1, GRIK2, GRIK3, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, PKD2, KCNAB1, KCNQ4, ABCC9, KCNH4, KCNE4, KCNIP3, KCNIP1, KCNQ5, KCNIP4, KCNT2, LRRC52
MF	GO:0019838	growth factor binding	31/1535	2.39E-05	A2M, ACVRL1, BMPR1A, CCN2, DUSP1, FGFR1, LRRC32, GHR, IGFBP2, IGFBP5, IGFBP6, CCN1, IL1RN, IL6R, IL6ST, ITGB3, LIFR, NGFR, NTRK3, PDGFRA, TEK, TGFB3, TGFBR2, TGFBR3, THBS1, LTBP4, NRP2, CXCL13, FGFBP2, VASN, WFIKKN2
MF	GO:0019199	transmembrane receptor protein kinase activity	22/1535	2.45E-05	ACVRL1, AXL, BMPR1A, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, EFEMP1, FGFR1, KIT, NTRK3, ROR2, DDR2, PDGFRA, TEK, TGFBR2, TGFBR3, LTBP4, NRP2, SOSTDC1, EPHA6
MF	GO:0015079	potassium ion transmembrane transporter activity	34/1535	2.60E-05	AQP1, ATP1A2, ATP1B2, GRIK2, GRIK3, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, PKD2, KCNAB1, KCNQ4, ABCC9, KCNH4, KCNE4, KCNIP3, KCNIP1, KCNQ5, SLC24A3, KCNIP4, SLC24A4, SLC9A9, KCNT2, LRRC52
MF	GO:0005178	integrin binding	30/1535	2.89E-05	ACTN1, ACTN2, ACTN3, CDH17, COL4A3, CCN2, S1PR3, FBN1, FCER2, FGF2, IGF1, CCN1, ILK, ITGA5, ITGB3, PRKCA, CX3CL1, CXCL12, SFRP2, THBS1, TIMP2, TLN1, UTRN, VWF, LTBP4, FBLN5, ADAMTS8, ADAMTS5, EMILIN1, JAM3
MF	GO:0022843	voltage-gated cation channel activity	30/1535	1.39E-04	CACNA1C, CACNA2D1, CACNB2, CACNB4, GRIN2A, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNS2, PKD2, KCNAB1, CACNA1H, KCNQ4, IL1RAPL1, NCS1, KCNH4, KCNE4, KCNQ5, CACHD1, TMC2, KCNT2, LRRC52
MF	GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	43/1535	1.64E-04	ATF3, PRDM1, CREM, DACH1, ETS2, HIC1, MITF, MSX1, MYC, NFATC2, NFATC4, NFIL3, OVOL1, PRKN, POU6F1, PROX1, SALL1, SATB1, ZEB1, TCF21, NR2F1, TRPS1, ZBTB16, BTG2, TBX18, LRRFIP1, HAND1, ZNF536, ZEB2, PRDM5, KLF12, MYT1L, FOXD3, KCNIP3, PCBP3, SOX6, ZBTB4, ARID5B, FOXP2, JDP2, GLIS1, SNAI3, NOTO
MF	GO:0016247	channel regulator activity	30/1535	1.74E-04	ADRB2, ATP2B4, BCL2, CAV1, CHRNA7, DPP6, FLNA, GEM, GRM7, ITPR1, KCNMB1, PRKCB, SCN1B, SCN2B, SCN4B, SGK1, SNTA1, KCNAB1, NRXN1, NRXN2, ABCC9, KCNE4, REM1, KCNIP3, KCNIP1, FXYD6, SCN3B, LYNX1, KCNIP4, LRRC52
MF	GO:0097493	structural molecule activity conferring elasticity	7/1535	2.92E-04	ELN, FBN1, LAMC1, FBLN5, EMILIN1, AHNAK, EMILIN3
MF	GO:0051371	muscle alpha-actinin binding	10/1535	2.99E-04	PKD2, PDLIM4, MYOM2, PDLIM7, PDLIM5, LDB3, PALLD, PDLIM3, PDLIM2, SYNPO2
MF	GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	11/1535	3.35E-04	PDE1A, PDE1C, PDE2A, PDE3A, PDE3B, PDE4B, PDE4D, PRKAR2B, PDE5A, PDE7B, PDE11A
MF	GO:0004112	cyclic-nucleotide phosphodiesterase activity	11/1535	4.82E-04	PDE1A, PDE1C, PDE2A, PDE3A, PDE3B, PDE4B, PDE4D, PRKAR2B, PDE5A, PDE7B, PDE11A
MF	GO:0008083	growth factor activity	31/1535	7.12E-04	BDNF, BMP5, CSF3, CCN2, HBEGF, EFEMP1, FGF2, FGF7, FGF9, FGF10, GDF2, GDF10, GDNF, HGF, IGF1, IL2, IL3, IL6R, INHBB, LIF, KITLG, NGF, NRTN, OGN, CXCL12, TGFB3, FGF23, NRG2, DKK1, PDGFD, PROK1
MF	GO:0033613	activating transcription factor binding	20/1535	8.42E-04	EGR2, FOS, JUN, MEF2A, MEF2C, MEF2D, MYC, PITX2, TBX5, WFS1, LDB2, TBX18, HAND2, TBX4, ZNF516, HDAC4, TBX20, PRDM16, DUSP26, ATOH8
MF	GO:0030165	PDZ domain binding	20/1535	9.80E-04	ATP2B3, ATP2B4, DTNA, LPAR1, GRIA1, GRID2, GRIK2, PRKN, SDC2, SNTA1, TGFBR3, FZD7, NLGN1, ERC1, SNTG2, GNG12, USHBP1, NKD1, TMEM88, SHISA6
MF	GO:0051015	actin filament binding	35/1535	1.02E-03	ABL1, ACTN1, ACTN2, BIN1, ANXA6, CACNB2, CFL2, CTNNA2, FLNA, GSN, ABLIM1, MYH2, MYH3, MYH11, SVIL, TAGLN, TLN1, TMOD1, TPM1, TPM2, UTRN, WIPF1, GAS7, MYOM2, FERMT2, DSTN, SYNE1, CORO1C, CTNNA3, SHROOM3, PKNOX2, RCSD1, SYNE3, XIRP1, WIPF3
MF	GO:0008179	adenylate cyclase binding	7/1535	1.02E-03	ADCY2, ADCY5, ADCYAP1R1, ADRB2, AKAP6, AKAP12, CAP2
MF	GO:0005249	voltage-gated potassium channel activity	20/1535	1.08E-03	KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNS2, PKD2, KCNAB1, KCNQ4, KCNH4, KCNE4, KCNQ5, KCNT2, LRRC52
MF	GO:0050431	transforming growth factor beta binding	9/1535	1.17E-03	ACVRL1, LRRC32, TGFB3, TGFBR2, TGFBR3, THBS1, LTBP4, VASN, WFIKKN2
MF	GO:0004714	transmembrane receptor protein tyrosine kinase activity	16/1535	1.33E-03	AXL, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, EFEMP1, FGFR1, KIT, NTRK3, ROR2, DDR2, PDGFRA, TEK, NRP2, EPHA6
MF	GO:0099106	ion channel regulator activity	24/1535	1.52E-03	ADRB2, CAV1, DPP6, FLNA, GEM, GRM7, ITPR1, KCNMB1, PRKCB, SCN1B, SGK1, KCNAB1, NRXN1, NRXN2, ABCC9, KCNE4, REM1, KCNIP3, KCNIP1, FXYD6, SCN3B, LYNX1, KCNIP4, LRRC52

MF	GO:0004713	protein tyrosine kinase activity	26/1535	1.73E-03	ABL1, AXL, BMX, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, EFEMP1, FER, FGFR1, FYN, ITK, KIT, NTRK3, ROR2, DDR2, PDGFRA, TEK, WEE1, DYRK3, NRP2, HIPK3, PEAK1, PKDCC, EPHA6
MF	GO:0008307	structural constituent of muscle	13/1535	2.23E-03	ACTN2, ACTN3, DMD, MYH11, MYL3, SMTN, TPM1, TPM2, SORBS2, MYOM2, MYL9, SYNM, PDLIM3
MF	GO:0015276	ligand-gated ion channel activity	26/1535	2.69E-03	ANXA6, AQP1, CHRNA7, CNGA3, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNH2, KCNJ3, KCNJ8, KCNJ12, P2RX1, PKD2, RYR2, RYR3, TRPA1, RASA3, SLC17A7, JPH2, JPH4
MF	GO:0022834	ligand-gated channel activity	26/1535	2.69E-03	ANXA6, AQP1, CHRNA7, CNGA3, GABRA2, GABRA4, GABRG1, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, ITPR1, KCNH2, KCNJ3, KCNJ8, KCNJ12, P2RX1, PKD2, RYR2, RYR3, TRPA1, RASA3, SLC17A7, JPH2, JPH4
MF	GO:0008081	phosphoric diester hydrolase activity	20/1535	2.82E-03	BDKRB2, MPPED2, CHRM3, EDNRA, PDE1A, PDE1C, PDE2A, PDE3A, PDE3B, PDE4B, PDE4D, ENPP1, PLCB4, PLCL1, PRKAR2B, PDE5A, PDE7B, PDE11A, PLCD4, ENPP6
MF	GO:0008013	beta-catenin binding	18/1535	3.88E-03	AR, ESR1, SMAD7, NR4A2, PRKN, RORA, SALL1, TBL1X, TRPC4, VCL, KLF4, KDM6B, CTNNA3, DACT1, AJAP1, CALCOCO1, SOX17, DACT3
MF	GO:0051393	alpha-actinin binding	11/1535	4.15E-03	CACNA1C, PKD2, PDLIM4, MYOM2, PDLIM7, PDLIM5, LDB3, PALLD, PDLIM3, PDLIM2, SYNPO2
MF	GO:0015278	calcium-release channel activity	8/1535	4.47E-03	ITPR1, PKD2, RYR2, RYR3, TRPA1, RASA3, JPH2, JPH4
MF	GO:0048018	receptor ligand activity	65/1535	4.47E-03	ADCYAP1, BDNF, BMP5, CALCA, TNFSF8, CD40LG, CSF3, CCN2, HBEGF, EPHA7, FBN1, EFEMP1, FGF2, FGF7, FGF9, FGF10, GDF2, GDF10, GDNF, CXCL2, HGF, IGF1, IL1RN, IL2, IL3, IL6R, IL16, IL17A, INHBB, LIF, LTB, MAPT, KITLG, NGF, NRTN, OGN, CX3CL1, CXCL12, SFRP2, SHH, STC1, TGFB3, TRH, VIP, WNT9A, FGF23, TNFSF12, ADIPOQ, NRG2, NAMPT, SEMA3A, CDC42EP2, CXCL13, DKK1, FLRT2, IL17D, SEMA3G, GREM2, PDGFD, PROK1, TSLP, FNDC5, UTS2B, C1QTNF9, OSTN
MF	GO:0005516	calmodulin binding	33/1535	4.55E-03	ATP2B3, ATP2B4, CACNA1C, CALD1, CAMK2A, CNN1, EEF1A1, GEM, ITPKB, KCNN3, MAP6, MYH2, MYH3, MYH11, MYLK, NGFR, PDE1A, PDE1C, PPP3CB, RGS1, RGS2, RYR2, RYR3, SLC8A2, SLC8A1, SLC8A3, SNTA1, VAMP2, WFS1, KCNQ4, REM1, KCNQ5, CAMKK1
MF	GO:0004115	3',5'-cyclic-AMP phosphodiesterase activity	6/1535	4.55E-03	PDE2A, PDE3A, PDE3B, PDE4B, PDE4D, PDE7B
MF	GO:0051018	protein kinase A binding	13/1535	4.55E-03	PRKACB, PRKAR2B, RYR2, AKAP6, AKAP12, PJA2, AKAP13, MYRIP, DACT1, SPHKAP, C2orf88, LRRK2, DACT3
MF	GO:0001653	peptide receptor activity	27/1535	4.62E-03	ADCYAP1R1, BDKRB2, CXCR5, CCR6, CX3CR1, EDNRA, EDNRB, PRLHR, GPR17, CXCR2, LHCGR, NPR1, NPR2, NPR3, SSTR1, TACR2, TACR1, TACR3, VIPR2, GLP2R, NMUR1, SORCS3, ACKR4, SORCS2, NPFFR1, SORCS1, NLRP6
MF	GO:0050840	extracellular matrix binding	14/1535	4.91E-03	DCN, ELN, CCN1, ITGA9, ITGB3, NID1, SHH, THBS1, SPARCL1, SLIT2, ADAMTS5, CLEC14A, ADAMTS15, SSC5D
MF	GO:0099604	ligand-gated calcium channel activity	9/1535	5.17E-03	GRIN2A, ITPR1, PKD2, RYR2, RYR3, TRPA1, RASA3, JPH2, JPH4
MF	GO:0008528	G protein-coupled peptide receptor activity	26/1535	5.41E-03	ADCYAP1R1, BDKRB2, CXCR5, CCR6, CX3CR1, EDNRA, EDNRB, PRLHR, GPR17, CXCR2, LHCGR, NPR1, NPR3, SSTR1, TACR2, TACR1, TACR3, VIPR2, GLP2R, NMUR1, SORCS3, ACKR4, SORCS2, NPFFR1, SORCS1, NLRP6
MF	GO:0005217	intracellular ligand-gated ion channel activity	10/1535	5.60E-03	AQP1, CNGA3, ITPR1, PKD2, RYR2, RYR3, TRPA1, RASA3, JPH2, JPH4
MF	GO:0001085	RNA polymerase II transcription factor binding	27/1535	5.85E-03	AR, EGR2, ESR1, FOS, GATA6, ID2, ID4, JUN, MEF2A, NFATC1, PITX1, PITX2, SRF, TAL1, TBX5, TCF4, TEAD1, LDB2, TBX18, KLF4, TBX4, HDAC4, ZFPM2, DACT1, TBX20, DUSP26, MYOCD
MF	GO:0015459	potassium channel regulator activity	13/1535	6.11E-03	ADRB2, CAV1, DPP6, FLNA, KCNMB1, SGK1, KCNAB1, ABCC9, KCNE4, KCNIP3, KCNIP1, KCNIP4, LRRC52
MF	GO:0042562	hormone binding	20/1535	6.69E-03	ADCYAP1R1, ALDH1A3, AR, ATP1A2, CHRM3, CHRNA7, CRHBP, CRYM, EDNRB, GHR, GPER1, LEPR, LHCGR, NPR1, NPR2, NPR3, PIK3R1, THRA, VIPR2, GLP2R
MF	GO:0004896	cytokine receptor activity	19/1535	8.03E-03	CXCR5, CCR6, CX3CR1, F3, GFRA1, GFRA2, GHR, GPR17, IL5RA, IL6R, IL6ST, CXCR2, LEPR, LIFR, MPL, IL1RL1, ACKR4, IL17RD, CRLF2
MF	GO:0042578	phosphoric ester hydrolase activity	51/1535	8.03E-03	BDKRB2, MPPED2, CHRM3, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, EDNRA, EPHX2, EYA4, EYA1, IMPA2, INPP5A, MYH3, PDE1A, PDE1C, PDE2A, PDE3A, PDE3B, PDE4B, PDE4D, ENPP1, PLCB4, PLCL1, PPP1CB, PPP2R2B, PPP3CB, PRKAR2B, PTPRD, PTPRN2, PLPP3, PDE5A, PLPPR4, PTPN21, PDE7B, PDE11A, NT5DC3, PIP4P2, G6PC2, DUSP26, PPP1R3B, NT5C1A, PLCD4, PTPN5, ENPP6, DUSP19, PPM1L, PPM1K, PTPRQ

MF	GO:0030020	extracellular matrix structural constituent conferring tensile strength	11/1535	8.33E-03	COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, COL21A1, COL25A1, COL6A5
MF	GO:0099094	ligand-gated cation channel activity	20/1535	9.28E-03	AQP1, CHRNA7, CNGA3, GRIA1, GRIK2, GRIK3, GRIN2A, ITPR1, KCNH2, KCNJ3, KCNJ8, KCNJ12, P2RX1, PKD2, RYR2, RYR3, TRPA1, RASA3, JPH2, JPH4
MF	GO:0005003	ephrin receptor activity	7/1535	1.05E-02	EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, NTRK3, EPHA6
MF	GO:0017147	Wnt-protein binding	10/1535	1.32E-02	AXL, ROR1, ROR2, SFRP1, SFRP2, FZD7, RECK, FZD10, WLS, TRABD2B
MF	GO:0015026	coreceptor activity	11/1535	1.46E-02	CD28, GPR15, ITGB3, LRP1, NGFR, ROR1, ROR2, TGFBR3, RECK, GPC6, RGMA
MF	GO:0015271	outward rectifier potassium channel activity	6/1535	1.46E-02	KCNA2, KCND3, KCNK2, KCNMA1, PKD2, KCNT2
MF	GO:0033549	MAP kinase phosphatase activity	6/1535	1.46E-02	DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8
MF	GO:0001664	G protein-coupled receptor binding	40/1535	1.60E-02	ADCYAP1, ADRA2A, BDKRB2, C3, CALCA, S1PR1, EDNRB, FLNA, FYN, GNAL, GNAO1, GNAQ, GNAZ, CXCL2, IL2, ROR2, P2RY1, PALM, PRKN, PDE4D, PTCH1, CX3CL1, CXCL12, SFRP1, TAC1, TUB, WNT2B, WNT9A, FZD7, GNA14, MAGI2, CXCL13, CNRIP1, REEP2, REEP1, WLS, PROK1, RSPO3, UTS2B, RSPO2
MF	GO:0005496	steroid binding	18/1535	1.63E-02	ANXA6, APOD, AR, ATP1A2, CAV1, CYP21A2, GPR183, ESR1, GPER1, NR3C2, PGR, PMP2, PTCH1, RORA, SOAT2, OSBPL1A, OSBPL5, OSBPL10
MF	GO:0046332	SMAD binding	16/1535	1.63E-02	ACVRL1, BMPR1A, LDLRAD4, FLNA, FOS, JUN, SMAD7, MEF2A, TGFB1I1, TGFBR2, TGFBR3, ZEB2, MAGI2, PRDM16, MYOCD, RANBP3L
MF	GO:0015368	calcium:cation antiporter activity	5/1535	1.85E-02	SLC8A2, SLC8A1, SLC8A3, SLC24A3, SLC24A4
MF	GO:0017166	vinculin binding	5/1535	1.85E-02	ACTN1, DMD, TLN1, UTRN, SYNM
MF	GO:0001968	fibronectin binding	8/1535	1.94E-02	CCN2, IGFBP5, IGFBP6, ITGB3, SFRP2, THBS1, CCDC80, SSC5D
MF	GO:0042805	actinin binding	11/1535	1.94E-02	CACNA1C, PKD2, PDLIM4, MYOM2, PDLIM7, PDLIM5, LDB3, PALLD, PDLIM3, PDLIM2, SYNPO2
MF	GO:0035259	glucocorticoid receptor binding	6/1535	1.94E-02	ETS2, NR4A1, NR4A2, STAT5B, TACC1, NR4A3
MF	GO:0050839	cell adhesion molecule binding	63/1535	1.94E-02	ACTN1, ACTN2, ACTN3, ANXA1, ARHGAP1, CALD1, CDH4, CDH17, COL4A3, CPE, CCN2, CTNNA2, S1PR3, EPHA2, FBN1, FCER2, FGF2, FLNA, IGF1, CCN1, ILK, ITGA5, ITGB3, PPL, PRKCA, PTPRD, CX3CL1, CXCL12, SFRP2, THBS1, TIMP2, TLN1, TRPC4, UTRN, VCL, VWF, LTBP4, GPRC5A, LRRFIP1, NRXN1, NRXN2, BAG3, FBLN5, PDLIM5, ADAMTS8, ADAMTS5, EMILIN1, NTNG1, NLGN1, ERC1, TES, CDH19, STXBP6, CTNNA3, SNX9, NLGN3, DCHS2, PARVA, AHNAK, JAM3, PHLDB2, VASN, MPP7
MF	GO:0004675	transmembrane receptor protein serine/threonine kinase activity	6/1535	2.65E-02	ACVRL1, BMPR1A, TGFBR2, TGFBR3, LTBP4, SOSTDC1
MF	GO:0004935	adrenergic receptor activity	6/1535	2.65E-02	ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3
MF	GO:0005005	transmembrane-ephrin receptor activity	6/1535	2.65E-02	EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, EPHA6
MF	GO:1902282	voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization	5/1535	2.66E-02	KCND3, KCNH2, KCNJ3, KCNJ8, KCNE4
MF	GO:0019001	guanyl nucleotide binding	51/1535	2.86E-02	AK4, ANXA6, ARL4D, RHOB, RND3, RHOH, MPPED2, CNGA3, EEF1A1, GEM, GNAL, GNAO1, GNAQ, GNAZ, NPR1, NPR2, PDE2A, RAB27A, RAP1A, RRAS, SRL, RNF112, TUBA1A, PDE5A, GNA14, MRAS, RASD2, RND1, RAB30, REM1, EHD2, PDE11A, ATL1, RAB9B, DNAJC27, RASL12, RASD1, RAB23, ACSM5, GIMAP5, RHOJ, RRAGD, ARL14, TUBB6, RERG, RAB3C, LRRK2, DIRAS1, SEPTIN10, GIMAP1, RAB37
MF	GO:0032561	guanyl ribonucleotide binding	51/1535	2.86E-02	AK4, ANXA6, ARL4D, RHOB, RND3, RHOH, MPPED2, CNGA3, EEF1A1, GEM, GNAL, GNAO1, GNAQ, GNAZ, NPR1, NPR2, PDE2A, RAB27A, RAP1A, RRAS, SRL, RNF112, TUBA1A, PDE5A, GNA14, MRAS, RASD2, RND1, RAB30, REM1, EHD2, PDE11A, ATL1, RAB9B, DNAJC27, RASL12, RASD1, RAB23, ACSM5, GIMAP5, RHOJ, RRAGD, ARL14, TUBB6, RERG, RAB3C, LRRK2, DIRAS1, SEPTIN10, GIMAP1, RAB37
MF	GO:0001540	amyloid-beta binding	15/1535	2.90E-02	ADRB2, APBB1, BCHE, CHRNA7, CLU, GRIA1, GRIN2A, HSPG2, LDLR, LRP1, NGFR, ITM2A, NLGN1, COL25A1, GPRASP2
MF	GO:0070851	growth factor receptor binding	22/1535	2.90E-02	MS4A1, CSF3, HBEGF, EFEMP1, FER, FGF2, FGF7, FGF9, FGF10, FYN, IL1RN, IL2, IL3, IL6R, IL6ST, ITGA5, ITGB3, PDGFRA, FGF23, FLRT2, PDGFD, TSLP

MF	GO:0003707	steroid hormone receptor activity	12/1535	2.90E-02	AR, ESR1, GPER1, NR4A1, NR3C2, NR4A2, PGR, RORA, RORB, NR2F1, THRA, NR4A3
MF	GO:0017046	peptide hormone binding	11/1535	2.90E-02	ADCYAP1R1, CRHBP, EDNRB, GHR, LEPR, NPR1, NPR2, NPR3, PIK3R1, VIPR2, GLP2R
MF	GO:0043394	proteoglycan binding	9/1535	3.17E-02	FCN2, CFH, LRP1, NID1, THBS1, CHRD, SLIT2, PLA2G2D, HPSE2
MF	GO:0047555	3',5'-cyclic-GMP phosphodiesterase activity	6/1535	3.32E-02	PDE1A, PDE1C, PDE2A, PRKAR2B, PDE5A, PDE11A
MF	GO:0001608	G protein-coupled nucleotide receptor activity	5/1535	3.51E-02	P2RY1, P2RY14, P2RY10, P2RY12, P2RY8
MF	GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	5/1535	3.51E-02	DUSP1, DUSP2, DUSP4, DUSP5, DUSP8
MF	GO:0045028	G protein-coupled purinergic nucleotide receptor activity	5/1535	3.51E-02	P2RY1, P2RY14, P2RY10, P2RY12, P2RY8
MF	GO:0070679	inositol 1,4,5 trisphosphate binding	5/1535	3.51E-02	ITPR1, PLCL1, TRPC1, TRPC3, TRPC4
MF	GO:0001786	phosphatidylserine binding	12/1535	3.61E-02	ANXA6, AXL, SYT4, THBS1, TLN1, CAVIN2, CPNE6, SYT11, JPH2, SYT15, OSBPL5, OSBPL10
MF	GO:0015077	monovalent inorganic cation transmembrane transporter activity	49/1535	3.61E-02	AQP1, ATP1A2, ATP1B2, GRIK2, GRIK3, KCNA1, KCNA2, KCNB1, KCND3, KCNH2, KCNJ3, KCNJ8, KCNJ12, KCNK2, KCNK3, KCNMA1, KCNMB1, KCNN3, KCNS2, PKD2, SCN1B, SCN2B, SCN4B, SCN7A, SLC8A2, SLC8A1, SLC8A3, SLC18A2, SLC22A3, KCNAB1, KCNQ4, ABCC9, KCNH4, KCNE4, KCNIP3, KCNIP1, SCN3B, KCNQ5, SLC17A7, SLC24A3, SLC5A7, KCNIP4, SLC2A13, SLC24A4, SLC2A12, NALCN, SLC9A9, KCNT2, LRRC52
MF	GO:0098631	cell adhesion mediator activity	12/1535	4.11E-02	ANXA1, ITGA1, CD200, CNTN2, PDLIM5, EMILIN1, NTNG1, PALLD, NFASC, STXBP6, DSCAML1, CNTN4
MF	GO:0048156	tau protein binding	10/1535	4.34E-02	BIN1, APBB1, CLU, FYN, HSPA2, MAP1A, ROCK1, SNCA, ROCK2, BAG2
MF	GO:0019956	chemokine binding	8/1535	4.81E-02	A2M, CXCR5, CCR6, CX3CR1, CXCR2, ITGB3, ZFP36, ACKR4
KEGG	hsa04022	cGMP-PKG signaling pathway	50/730	1.83E-12	ADCY2, ADCY5, ADCY9, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, SLC25A4, ATP1A2, ATP1B2, ATP2B3, ATP2B4, BDKRB2, CACNA1C, EDNRA, EDNRB, GNAQ, ITPR1, KCNJ8, KCNMA1, KCNMB1, MEF2A, MEF2C, MEF2D, MYLK, PPP1R12A, NFATC1, NFATC2, NFATC4, NPR1, NPR2, PDE2A, PDE3A, PDE3B, PLCB4, PPP1CB, PPP3CB, RGS2, ROCK1, SLC8A2, SLC8A1, SLC8A3, SRF, PDE5A, ROCK2, CREB5, AKT3, MYL9
KEGG	hsa04921	Oxytocin signaling pathway	44/730	2.49E-10	ADCY2, ADCY5, ADCY9, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAMK2A, CDKN1A, RCAN1, FOS, GNAO1, GNAQ, ITPR1, JUN, KCNJ3, KCNJ12, MEF2C, MYLK, PPP1R12A, PPP1R12B, NFATC1, NFATC2, NFATC4, NPR1, NPR2, PLA2G4A, PLCB4, PPP1CB, PPP3CB, PRKAA2, PRKACB, PRKCA, PRKCB, PTGS2, RGS2, ROCK1, RYR2, RYR3, PLA2G4C, ROCK2, MYL9, PRKAG2, PPP1R12C
KEGG	hsa04020	Calcium signaling pathway	50/730	1.50E-09	ADCY2, ADCY9, ADRA1D, ADRA1A, ADRB2, ADRB3, SLC25A4, ATP2B3, ATP2B4, BDKRB2, CACNA1C, CAMK2A, CASQ2, CHRM2, CHRM3, CHRNA7, EDNRA, EDNRB, GNAL, GNAQ, GRIN2A, HRC, HTR4, ITPKB, ITPR1, LHCGR, MYLK, P2RX1, PDE1A, PDE1C, PDGFRA, PLCB4, PPP3CB, PRKACB, PRKCA, PRKCB, PTGER3, PTGFR, RYR2, RYR3, SLC8A2, SLC8A1, SLC8A3, TACR2, TACR1, TACR3, CACNA1H, GNA14, PDGFD, PLCD4
KEGG	hsa04010	MAPK signaling pathway	62/730	7.87E-09	ANGPT1, BDNF, CACNA1C, CACNA2D1, CACNB2, CACNB4, MAP3K8, GADD45A, DUSP1, DUSP2, DUSP3, DUSP4, DUSP5, DUSP8, EPHA2, FGF2, FGF7, FGF9, FGF10, FGFR1, FLNA, FLNC, FOS, HGF, NR4A1, HSPA2, IGF1, JUN, JUND, KIT, MAPT, MEF2C, KITLG, MYC, GADD45B, NFATC1, NGF, NGFR, PDGFRA, PLA2G4A, PPP3CB, PRKACB, PRKCA, PRKCB, RAP1A, RPS6KA2, RRAS, SRF, TEK, TGFB3, TGFBR2, FGF23, PLA2G4C, CACNA1H, RPS6KA5, AKT3, MRAS, MAP3K20, GNG12, PDGFD, PTPN5, RASGRP4
KEGG	hsa04510	Focal adhesion	48/730	1.08E-08	ACTN1, BCL2, CAV1, CCND2, COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, FLNA, FLNC, FYN, HGF, IGF1, ILK, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, JUN, LAMA4, LAMC1, MYLK, PPP1R12A, PPP1R12B, PDGFRA, PIK3R1, PPP1CB, PRKCA, PRKCB, RELN, RAP1A, ROCK1, THBS1, TLN1, VCL, VWF, PIP5K1B, ITGA8, ROCK2, AKT3, LAMC3, MYL9, PPP1R12C, PARVA, PDGFD, COL6A5
KEGG	hsa04261	Adrenergic signaling in cardiomyocytes	39/730	3.45E-08	ACTC1, ADCY2, ADCY5, ADCY9, ADRA1D, ADRA1A, ADRB2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, BCL2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CAMK2A, CREM, GNAQ, MYL3, PLCB4, PPP1CB, PPP1R1A, PPP2R2B, PRKACB, PRKCA, RYR2, SCN1B, SCN4B, SCN7A, SLC8A2, SLC8A1, SLC8A3, TNNT2, TPM1, TPM2, RPS6KA5, CREB5, AKT3

KEGG	hsa05414	Dilated cardiomyopathy	29/730	1.14E-07	ACTC1, ADCY2, ADCY5, ADCY9, CACNA1C, CACNA2D1, CACNB2, CACNB4, DMD, IGF1, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, MYL3, PRKACB, RYR2, SGCB, SGCD, SGCG, SLC8A2, SLC8A1, SLC8A3, TGFB3, TNNT2, TPM1, TPM2, ITGA8
KEGG	hsa04713	Circadian entrainment	29/730	1.30E-07	ADCY2, ADCY5, ADCY9, ADCYAP1, ADCYAP1R1, CACNA1C, CAMK2A, FOS, GNAO1, GNAQ, GNG7, GNG11, GRIA1, GRIN2A, ITPR1, KCNJ3, PER1, PLCB4, PRKACB, PRKCA, PRKCB, RYR2, RYR3, PER3, PER2, CACNA1H, RPS6KA5, RASD1, GNG12
KEGG	hsa04024	cAMP signaling pathway	47/730	2.44E-07	ADCY2, ADCY5, ADCY9, ADCYAP1, ADCYAP1R1, ADRB2, ATP1A2, ATP1B2, ATP2B3, ATP2B4, BDNF, CACNA1C, CAMK2A, CHRM2, CNGA3, EDNRA, FOS, GRIA1, GRIN2A, HTR4, JUN, LHCGR, PPP1R12A, NFATC1, NPR1, PDE3A, PDE3B, PDE4B, PDE4D, PIK3R1, PPP1CB, PRKACB, PTCH1, PTGER3, RAP1A, ROCK1, RRAS, RYR2, SSTR1, VIP, VIPR2, ROCK2, CREB5, AKT3, ABCC4, MYL9, HHIP
KEGG	hsa05410	Hypertrophic cardiomyopathy	27/730	3.33E-07	ACTC1, CACNA1C, CACNA2D1, CACNB2, CACNB4, DMD, IGF1, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, MYL3, PRKAA2, RYR2, SGCB, SGCD, SGCG, SLC8A2, SLC8A1, SLC8A3, TGFB3, TNNT2, TPM1, TPM2, ITGA8, PRKAG2
KEGG	hsa04371	Apelin signaling pathway	34/730	8.44E-07	ACTA2, ADCY2, ADCY5, ADCY9, CCN2, EGR1, GNAQ, GNG7, GNG11, ITPR1, MEF2A, MEF2C, MEF2D, MYL3, MYLK, PDE3B, PLCB4, PLIN1, PRKAA2, PRKACB, RRAS, RYR2, RYR3, SLC8A2, SLC8A1, SLC8A3, HDAC4, AKT3, KLF2, PPARGC1A, MRAS, GABARAPL1, PRKAG2, GNG12
KEGG	hsa04360	Axon guidance	40/730	1.57E-06	ABL1, CAMK2A, CFL2, DPYSL2, EPHA2, EPHA3, EPHA5, EPHA7, EPHB1, FYN, ILK, ABLIM1, NFATC2, NFATC4, PIK3R1, PPP3CB, PRKCA, PTCH1, ROCK1, RRAS, CXCL12, SHH, SLIT3, TRPC1, TRPC3, TRPC4, UNC5C, SLIT2, NTN1, ROCK2, SEMA3A, MYL9, NTNG1, RND1, ENAH, SEMA3G, RGMA, LRRC4, PLXNA4, EPHA6
KEGG	hsa04270	Vascular smooth muscle contraction	33/730	1.69E-06	ACTA2, ADCY2, ADCY5, ADCY9, ADRA1D, ADRA1A, CACNA1C, CALCA, CALD1, EDNRA, GNAQ, ITPR1, KCNMA1, KCNMB1, MYH11, MYLK, PPP1R12A, PPP1R12B, NPR1, NPR2, PLA2G4A, PLA2G5, PLCB4, PPP1CB, PRKACB, PRKCA, PRKCB, ROCK1, PLA2G4C, ROCK2, MYL9, PLA2G2D, PPP1R12C
KEGG	hsa04151	PI3K-Akt signaling pathway	63/730	1.77E-06	ANGPT1, BCL2, BDNF, CCND2, CDKN1A, CHRM2, COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, CSF3, LPAR1, EPHA2, FGF2, FGF7, FGF9, FGF10, FGFR1, GHR, GNG7, GNG11, GYS2, HGF, NR4A1, IGF1, IL2, IL3, IL6R, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, KIT, LAMA4, LAMC1, MCL1, KITLG, MYC, NGF, NGFR, PDGFRA, PIK3R1, PPP2R2B, PRKAA2, PRKCA, RELN, SGK1, TEK, THBS1, VWF, FGF23, TCL1A, ITGA8, CREB5, MAGI2, AKT3, LAMC3, GNG12, G6PC2, PDGFD, COL6A5
KEGG	hsa04725	Cholinergic synapse	29/730	2.95E-06	ADCY2, ADCY5, ADCY9, BCL2, CACNA1C, CAMK2A, CHRM2, CHRM3, CHRNA7, FOS, FYN, GNAO1, GNAQ, GNG7, GNG11, ITPR1, KCNJ3, KCNJ12, PIK3R1, PLCB4, PRKACB, PRKCA, PRKCB, KCNQ4, CREB5, AKT3, GNG12, KCNQ5, SLC5A7
KEGG	hsa05205	Proteoglycans in cancer	42/730	5.21E-06	ANK2, CAMK2A, CAV1, CDKN1A, DCN, HBEGF, ESR1, FGF2, FGFR1, FLNA, FLNC, HGF, HSPG2, IGF1, ITGA5, ITGB3, ITPR1, MMP2, MYC, PPP1R12A, PPP1R12B, PIK3R1, PPP1CB, PRKACB, PRKCA, PRKCB, PTCH1, ROCK1, RRAS, SDC2, SHH, THBS1, WNT2B, WNT9A, FZD7, ROCK2, AKT3, FZD10, MRAS, PPP1R12C, HPSE2, TWIST2
KEGG	hsa05412	Arrhythmogenic right ventricular cardiomyopathy	22/730	1.15E-05	ACTN2, ACTN3, CACNA1C, CACNA2D1, CACNB2, CACNB4, CTNNA2, DMD, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, RYR2, SGCB, SGCD, SGCG, SLC8A2, SLC8A1, SLC8A3, ITGA8, CTNNA3
KEGG	hsa05032	Morphine addiction	24/730	1.70E-05	ADCY2, ADCY5, ADCY9, GABRA2, GABRA4, GABRG1, GNAO1, GNG7, GNG11, GRK5, KCNJ3, PDE1A, PDE1C, PDE2A, PDE3A, PDE3B, PDE4B, PDE4D, PRKACB, PRKCA, PRKCB, PDE7B, PDE11A, GNG12
KEGG	hsa04925	Aldosterone synthesis and secretion	25/730	1.90E-05	ADCY2, ADCY5, ADCY9, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CACNA1C, CAMK2A, CYP21A2, GNAQ, NR4A1, ITPR1, KCNK3, LDLR, NPR1, NR4A2, PDE2A, PLCB4, PRKACB, PRKCA, PRKCB, PRKD1, CACNA1H, CREB5
KEGG	hsa04924	Renin secretion	20/730	2.37E-05	ADCY5, ADCYAP1, ADCYAP1R1, ADRB2, ADRB3, AQP1, CACNA1C, EDNRA, GNAQ, ITPR1, KCNMA1, NPR1, PDE1A, PDE1C, PDE3A, PDE3B, PLCB4, PPP3CB, PRKACB, PTGER4
KEGG	hsa04928	Parathyroid hormone synthesis, secretion and action	26/730	2.37E-05	ADCY2, ADCY5, ADCY9, BCL2, CDKN1A, HBEGF, EGR1, FGFR1, FOS, GNAQ, ITPR1, JUND, MEF2A, MEF2C, MEF2D, MMP16, NR4A2, PDE4B, PDE4D, PLCB4, PRKACB, PRKCA, PRKCB, FGF23, CREB5, AKAP13
KEGG	hsa04514	Cell adhesion molecules	32/730	3.48E-05	CD22, CD28, CD34, CD40LG, CDH4, CNTN1, ITGA9, MPZ, NCAM1, PECAM1, SDC2, SELP, CNTN2, CLDN5, CNTNAP1, ITGA8, CLDN8, NRXN1, NRXN2, SDC3, NTNG1, NLGN1, NFASC, NLGN3, CADM3, JAM2, LRRC4, VSIR, CD99L2, JAM3, LRRC4B, NEGR1
KEGG	hsa04080	Neuroactive ligand-receptor interaction	56/730	7.95E-05	ADCYAP1, ADCYAP1R1, ADRA1D, ADRA1A, ADRA2A, ADRA2B, ADRB2, ADRB3, BDKRB2, C3, CALCA, CHRM2, CHRM3, CHRNA7, CNR2, S1PR1, LPAR1, S1PR3, EDNRA, EDNRB, GABRA2, GABRA4, GABRG1, GHR, PRLHR, GRIA1, GRID2, GRIK2, GRIK3, GRIN2A, GRM7, HTR4, LEPR, LHCGR, P2RX1, P2RY1, PTGER3, PTGER4, PTGFR, SSTR1, TAC1, TACR2, TACR1, TACR3, THRA, TRH, VIP, VIPR2, GLP2R, P2RY14, NMUR1, P2RY10, NPFFR1, GPR156, UTS2B, P2RY8

KEGG	hsa04015	Rap1 signaling pathway	39/730	1.15E-04	ADCY2, ADCY5, ADCY9, ANGPT1, LPAR1, EPHA2, FGF2, FGF7, FGF9, FGF10, FGFR1, GNAO1, GNAQ, GRIN2A, HGF, IGF1, ITGB3, KIT, KITLG, NGF, NGFR, P2RY1, PDGFRA, PIK3R1, PLCB4, PRKCA, PRKCB, PRKD1, RAP1A, RRAS, TEK, THBS1, TLN1, FGF23, MAGI2, AKT3, MRAS, ENAH, PDGFD
KEGG	hsa04310	Wnt signaling pathway	32/730	1.48E-04	CAMK2A, CCND2, JUN, MYC, NFATC1, NFATC2, NFATC4, ROR1, ROR2, PLCB4, PPP3CB, PRKACB, PRKCA, PRKCB, SFRP1, SFRP2, TBL1X, WNT2B, WNT9A, FOSL1, FZD7, ROCK2, FZD10, DKK1, DAAM2, SOX17, RSPO3, NKD1, CSNK1A1L, PRICKLE1, PRICKLE2, RSPO2
KEGG	hsa04610	Complement and coagulation cascades	21/730	1.68E-04	A2M, BDKRB2, C1R, C1S, C3, C4A, C4B, C6, C7, CLU, CR2, CD55, CFD, F3, F8, F10, F13A1, CFH, SERPINB2, MASP1, VWF
KEGG	hsa04911	Insulin secretion	21/730	1.96E-04	ADCY2, ADCY5, ADCY9, ADCYAP1, ADCYAP1R1, ATP1A2, ATP1B2, CACNA1C, CAMK2A, CHRM3, GNAQ, KCNMA1, KCNMB1, KCNN3, PLCB4, PRKACB, PRKCA, PRKCB, RYR2, VAMP2, CREB5
KEGG	hsa04724	Glutamatergic synapse	25/730	2.32E-04	ADCY2, ADCY5, ADCY9, CACNA1C, GNAO1, GNAQ, GNG7, GNG11, GRIA1, GRIK2, GRIK3, GRIN2A, GRM7, ITPR1, KCNJ3, PLA2G4A, PLCB4, PPP3CB, PRKACB, PRKCA, PRKCB, TRPC1, PLA2G4C, GNG12, SLC17A7
KEGG	hsa04810	Regulation of actin cytoskeleton	39/730	2.35E-04	ACTN1, BDKRB2, CFL2, CHRM2, CHRM3, LPAR1, FGF2, FGF7, FGF9, FGF10, FGFR1, GSN, NCKAP1L, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, MYH11, MYLK, PPP1R12A, PPP1R12B, PDGFRA, PIK3R1, PPP1CB, ROCK1, RRAS, CXCL12, VCL, FGF23, PIP5K1B, ITGA8, ROCK2, MYL9, MRAS, PPP1R12C, ENAH, GNG12, PDGFD
KEGG	hsa04014	Ras signaling pathway	40/730	4.29E-04	ABL1, ANGPT1, BDNF, EPHA2, ETS2, FGF2, FGF7, FGF9, FGF10, FGFR1, GNG7, GNG11, GRIN2A, HGF, IGF1, KIT, KITLG, NGF, NGFR, PDGFRA, PIK3R1, PLA2G4A, PLA2G5, PRKACB, PRKCA, PRKCB, RAP1A, RRAS, TEK, FGF23, PLA2G4C, AKT3, RASA4, MRAS, RASA3, RGL1, PLA2G2D, GNG12, PDGFD, RASGRP4
KEGG	hsa04961	Endocrine and other factor-regulated calcium reabsorption	15/730	4.29E-04	ADCY9, ATP1A2, ATP1B2, ATP2B3, ATP2B4, BDKRB2, ESR1, GNAQ, PLCB4, PRKACB, PRKCA, PRKCB, SLC8A2, SLC8A1, SLC8A3
KEGG	hsa04970	Salivary secretion	21/730	5.79E-04	ADCY2, ADCY5, ADCY9, ADRA1D, ADRA1A, ADRB2, ADRB3, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CHRM3, GNAQ, ITPR1, KCNMA1, PLCB4, PRKACB, PRKCA, PRKCB, RYR3, VAMP2
KEGG	hsa04512	ECM-receptor interaction	20/730	7.58E-04	COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, HSPG2, ITGA1, ITGA5, ITGA7, ITGA9, ITGB3, LAMA4, LAMC1, RELN, THBS1, VWF, ITGA8, LAMC3, FREM1, COL6A5
KEGG	hsa04611	Platelet activation	25/730	8.36E-04	ADCY2, ADCY5, ADCY9, FYN, GNAQ, ITGB3, ITPR1, MYLK, PPP1R12A, P2RX1, P2RY1, PIK3R1, PLA2G4A, PLCB4, PPP1CB, PRKACB, PTGS1, RAP1A, ROCK1, TLN1, VWF, PLA2G4C, ROCK2, AKT3, P2RY12
KEGG	hsa04923	Regulation of lipolysis in adipocytes	15/730	9.53E-04	ADCY2, ADCY5, ADCY9, ADRB2, ADRB3, NPR1, PDE3B, PIK3R1, PLIN1, PRKACB, PTGER3, PTGS1, PTGS2, AKT3, MGLL
KEGG	hsa04927	Cortisol synthesis and secretion	16/730	1.30E-03	ADCY2, ADCY5, ADCY9, CACNA1C, CYP21A2, GNAQ, NR4A1, ITPR1, KCNK2, KCNK3, LDLR, PBX1, PLCB4, PRKACB, CACNA1H, CREB5
KEGG	hsa05031	Amphetamine addiction	16/730	2.66E-03	ADCY5, CACNA1C, CAMK2A, FOS, FOSB, GRIA1, GRIN2A, JUN, PPP1CB, PPP3CB, PRKACB, PRKCA, PRKCB, SLC18A2, CREB5, SIRT1
KEGG	hsa04340	Hedgehog signaling pathway	13/730	2.83E-03	BCL2, CCND2, EVC, GAS1, GLI2, PRKACB, PTCH1, SHH, SPOP, DHH, CDON, HHIP, CSNK1A1L
KEGG	hsa05218	Melanoma	16/730	4.19E-03	CDKN1A, GADD45A, FGF2, FGF7, FGF9, FGF10, FGFR1, HGF, IGF1, MITF, GADD45B, PDGFRA, PIK3R1, FGF23, AKT3, PDGFD
KEGG	hsa04060	Cytokine-cytokine receptor interaction	44/730	4.19E-03	ACVRL1, CXCR5, BMP5, BMPR1A, TNFSF8, CD40LG, CCR6, CSF3, CX3CR1, EDA, GDF2, GDF10, GHR, CXCL2, IL1RN, IL2, IL3, IL5RA, IL6R, IL6ST, CXCR2, IL16, IL17A, INHBB, LEPR, LIF, LIFR, LTB, MPL, NGF, NGFR, CX3CL1, CXCL12, TGFB3, TGFBR2, TNFSF12, IL1RL1, CXCL13, TNFRSF13B, ACKR4, IL17D, CRLF2, TSLP, TNFRSF13C
KEGG	hsa04350	TGF-beta signaling pathway	19/730	4.49E-03	BMP5, BMPR1A, DCN, FBN1, ID2, ID4, INHBB, SMAD7, SMAD9, MYC, PITX2, ROCK1, TGFB3, TGFBR2, THBS1, CHRD, RGMA, GREM2, THSD4
KEGG	hsa04728	Dopaminergic synapse	24/730	4.58E-03	ADCY5, CACNA1C, CAMK2A, FOS, GNAL, GNAO1, GNAQ, GNG7, GNG11, GRIA1, GRIN2A, ITPR1, KCNJ3, PLCB4, PPP1CB, PPP2R2B, PPP3CB, PRKACB, PRKCA, PRKCB, SLC18A2, CREB5, AKT3, GNG12
KEGG	hsa04972	Pancreatic secretion	20/730	4.58E-03	ADCY2, ADCY5, ADCY9, ATP1A2, ATP1B2, ATP2B3, ATP2B4, CHRM3, CPB1, GNAQ, ITPR1, KCNMA1, PLA2G5, PLCB4, PRKCA, PRKCB, RAP1A, RYR2, TRPC1, PLA2G2D
KEGG	hsa05146	Amoebiasis	20/730	4.58E-03	ACTN1, ARG2, CD1C, COL4A3, COL4A4, COL4A6, GNAL, GNAQ, CXCL2, LAMA4, LAMC1, PIK3R1, PLCB4, PRKACB, PRKCA, PRKCB, TGFB3, VCL, GNA14, LAMC3
KEGG	hsa04720	Long-term potentiation	15/730	4.94E-03	CACNA1C, CAMK2A, GNAQ, GRIA1, GRIN2A, ITPR1, PLCB4, PPP1CB, PPP1R1A, PPP3CB, PRKACB, PRKCA, PRKCB, RAP1A, RPS6KA2

KEGG	hsa04670	Leukocyte transendothelial migration	21/730	7.60E-03	ACTN1, RHOH, CTNNA2, ITK, MMP2, PECAM1, PIK3R1, PRKCA, PRKCB, RAP1A, ROCK1, CXCL12, CLDN5, VCL, CLDN8, ROCK2, MYL9, CTNNA3, JAM2, CD99L2, JAM3
KEGG	hsa04630	JAK-STAT signaling pathway	27/730	7.76E-03	BCL2, CCND2, CDKN1A, CSF3, FHL1, GHR, IL2, IL3, IL5RA, IL6R, IL6ST, LEPR, LIF, LIFR, MCL1, MPL, MYC, PDGFRA, PIM1, PIK3R1, STAT5B, SOCS2, SOCS3, AKT3, IL17D, CRLF2, TSLP
KEGG	hsa04922	Glucagon signaling pathway	20/730	7.76E-03	ACACB, ADCY2, CAMK2A, GNAQ, GYS2, ITPR1, PDE3B, PLCB4, PPP3CB, PRKAA2, PRKACB, PYGB, CREB5, AKT3, PPARGC1A, SIRT1, PRKAG2, G6PC2, SIK1, SIK1B
KEGG	hsa05144	Malaria	12/730	7.76E-03	CD40LG, CSF3, GYPC, HBB, HGF, KLRB1, LRP1, PECAM1, SDC2, SELP, TGFB3, THBS1
KEGG	hsa04726	Serotonergic synapse	21/730	7.76E-03	ADCY5, CACNA1C, DUSP1, GNAO1, GNAQ, GNG7, GNG11, HTR4, ITPR1, KCNJ3, PLA2G4A, PLCB4, PRKACB, PRKCA, PRKCB, PTGS1, PTGS2, SLC18A2, TRPC1, PLA2G4C, GNG12
KEGG	hsa04750	Inflammatory mediator regulation of TRP channels	19/730	7.76E-03	ADCY2, ADCY5, ADCY9, BDKRB2, CAMK2A, GNAQ, IGF1, ITPR1, NGF, PIK3R1, PLA2G4A, PLCB4, PPP1CB, PRKACB, PRKCA, PRKCB, PTGER4, PLA2G4C, TRPA1
KEGG	hsa04933	AGE-RAGE signaling pathway in diabetic complications	19/730	7.76E-03	BCL2, COL4A3, COL4A4, COL4A6, EGR1, F3, JUN, MMP2, NFATC1, PIM1, PIK3R1, PLCB4, PRKCA, PRKCB, STAT5B, TGFB3, TGFBR2, AKT3, PLCD4
KEGG	hsa04929	GnRH secretion	14/730	7.92E-03	CACNA1C, GNAQ, GPER1, ITPR1, KCNJ3, KCNN3, PIK3R1, PLCB4, PRKCA, PRKCB, TRPC1, TRPC4, CACNA1H, AKT3
KEGG	hsa04916	Melanogenesis	19/730	8.34E-03	ADCY2, ADCY5, ADCY9, CAMK2A, DCT, EDNRB, GNAO1, GNAQ, KIT, KITLG, MITF, PLCB4, PRKACB, PRKCA, PRKCB, WNT2B, WNT9A, FZD7, FZD10
KEGG	hsa04072	Phospholipase D signaling pathway	25/730	8.34E-03	ADCY2, ADCY5, ADCY9, DGKB, DGKG, LPAR1, MS4A2, FYN, GRM7, CXCR2, KIT, KITLG, PDGFRA, PIK3R1, PLA2G4A, PLCB4, PRKCA, PTGFR, RRAS, PIP5K1B, PLA2G4C, PLPP3, AKT3, MRAS, PDGFD
KEGG	hsa05226	Gastric cancer	25/730	9.03E-03	BCL2, CDH17, CDKN1A, CTNNA2, GADD45A, FGF2, FGF7, FGF9, FGF10, HGF, MYC, GADD45B, ABCB1, PIK3R1, SHH, TGFB3, TGFBR2, WNT2B, WNT9A, FGF23, FZD7, AKT3, FZD10, CTNNA3, CSNK1A1L
KEGG	hsa04260	Cardiac muscle contraction	17/730	9.05E-03	ACTC1, ATP1A2, ATP1B2, CACNA1C, CACNA2D1, CACNB2, CACNB4, CASQ2, HRC, MYL3, RYR2, SLC8A2, SLC8A1, SLC8A3, TNNT2, TPM1, TPM2
KEGG	hsa05163	Human cytomegalovirus infection	34/730	9.49E-03	ADCY2, ADCY5, ADCY9, CDKN1A, GNAO1, GNAQ, GNG7, GNG11, IL6R, CXCR2, ITGB3, ITPR1, MYC, NFATC1, NFATC2, NFATC4, PDGFRA, PIK3R1, PLCB4, PPP3CB, PRKACB, PRKCA, PRKCB, PTGER3, PTGER4, PTGS2, ROCK1, CX3CL1, CXCL12, ROCK2, CREB5, AKT3, AKAP13, GNG12
KEGG	hsa04974	Protein digestion and absorption	19/730	9.80E-03	ATP1A2, ATP1B2, COL4A3, COL4A4, COL4A6, COL6A2, COL6A3, COL8A2, COL13A1, COL19A1, CPB1, ELN, SLC8A2, SLC8A1, SLC8A3, XPNPEP2, COL21A1, COL25A1, COL6A5
KEGG	hsa04935	Growth hormone synthesis, secretion and action	21/730	1.02E-02	ADCY2, ADCY5, ADCY9, CACNA1C, FOS, GHR, GNAQ, IGF1, ITPR1, JUNB, PIK3R1, PLCB4, PRKACB, PRKCA, PRKCB, SSTR1, STAT5B, SOCS2, SOCS3, CREB5, AKT3
KEGG	hsa04727	GABAergic synapse	17/730	1.09E-02	ADCY2, ADCY5, ADCY9, CACNA1C, GABRA2, GABRA4, GABRG1, GNAO1, GNG7, GNG11, PLCL1, PRKACB, PRKCA, PRKCB, GABARAPL1, GNG12, TRAK2
KEGG	hsa04926	Relaxin signaling pathway	22/730	1.22E-02	ACTA2, ADCY2, ADCY5, ADCY9, COL4A3, COL4A4, COL4A6, EDNRB, FOS, GNAO1, GNG7, GNG11, JUN, MMP2, PIK3R1, PLCB4, PRKACB, PRKCA, TGFBR2, CREB5, AKT3, GNG12
KEGG	hsa04971	Gastric acid secretion	15/730	1.35E-02	ADCY2, ADCY5, ADCY9, ATP1A2, ATP1B2, CAMK2A, CHRM3, GNAQ, ITPR1, KCNK2, MYLK, PLCB4, PRKACB, PRKCA, PRKCB
KEGG	hsa04934	Cushing syndrome	25/730	1.38E-02	ADCY2, ADCY5, ADCY9, CACNA1C, CAMK2A, CDKN1A, CYP21A2, GNAQ, NR4A1, ITPR1, KCNK2, KCNK3, LDLR, PBX1, PLCB4, PRKACB, RAP1A, WNT2B, WNT9A, FZD7, CACNA1H, CREB5, FZD10, PDE11A, RASD1
KEGG	hsa04912	GnRH signaling pathway	17/730	1.66E-02	ADCY2, ADCY5, ADCY9, CACNA1C, CAMK2A, HBEGF, EGR1, GNAQ, ITPR1, JUN, MMP2, PLA2G4A, PLCB4, PRKACB, PRKCA, PRKCB, PLA2G4C
KEGG	hsa04913	Ovarian steroidogenesis	11/730	2.25E-02	ADCY2, ADCY5, ADCY9, CYP1B1, IGF1, LDLR, LHCGR, PLA2G4A, PRKACB, PTGS2, PLA2G4C
KEGG	hsa04710	Circadian rhythm	8/730	2.27E-02	CRY2, PER1, PRKAA2, RORA, RORB, PER3, PER2, PRKAG2
KEGG	hsa04915	Estrogen signaling pathway	22/730	2.58E-02	ADCY2, ADCY5, ADCY9, BCL2, HBEGF, ESR1, FKBP5, FOS, GNAO1, GNAQ, GPER1, HSPA2, ITPR1, JUN, KCNJ3, MMP2, PGR, PIK3R1, PLCB4, PRKACB, CREB5, AKT3
KEGG	hsa05224	Breast cancer	23/730	2.67E-02	CDKN1A, GADD45A, ESR1, FGF2, FGF7, FGF9, FGF10, FGFR1, FOS, IGF1, JUN, KIT, MYC, GADD45B, PGR, PIK3R1, WNT2B, WNT9A, FGF23, FZD7, AKT3, FZD10, CSNK1A1L
KEGG	hsa05231	Choline metabolism in cancer	17/730	2.67E-02	DGKB, DGKG, FOS, JUN, PDGFRA, PIK3R1, PLA2G4A, PRKCA, PRKCB, SLC22A3, PIP5K1B, PLA2G4C, PLPP3, AKT3, WASF3, SLC5A7, PDGFD
KEGG	hsa04730	Long-term depression	12/730	2.73E-02	GNAO1, GNAQ, GNAZ, GRIA1, GRID2, IGF1, ITPR1, PLA2G4A, PLCB4, PRKCA, PRKCB, PLA2G4C
KEGG	hsa04068	FoxO signaling pathway	21/730	2.73E-02	CCND2, CDKN1A, PLK3, GADD45A, S1PR1, IGF1, GADD45B, PIK3R1, PRKAA2, SGK1, SLC2A4, TGFB3, TGFBR2, AKT3, KLF2, SIRT1, GABARAPL1, PRKAG2, G6PC2, SETD7, FBXO32

KEGG	hsa04723	Retrograde endocannabinoid signaling	23/730	2.76E-02	ADCY2, ADCY5, ADCY9, CACNA1C, GABRA2, GABRA4, GABRG1, GNAO1, GNAQ, GNG7, GNG11, GRIA1, ITPR1, KCNJ3, PLCB4, PRKACB, PRKCA, PRKCB, PTGS2, MGLL, RIMS1, GNG12, SLC17A7
KEGG	hsa04640	Hematopoietic cell lineage	17/730	2.80E-02	CD1C, CD5, MS4A1, CD22, CD34, CR2, CSF3, CD55, FCER2, IL3, IL5RA, IL6R, ITGA1, ITGA5, ITGB3, KIT, KITLG
KEGG	hsa04390	Hippo signaling pathway	24/730	2.80E-02	BMP5, BMPR1A, CCND2, CCN2, CTNNA2, DLG2, GLI2, ID2, SMAD7, MYC, PPP1CB, PPP2R2B, TEAD1, TGFB3, TGFBR2, WNT2B, WNT9A, FZD7, FZD10, CRB1, WWTR1, LATS2, CTNNA3, NKD1
KEGG	hsa04931	Insulin resistance	18/730	3.00E-02	ACACB, GYS2, PIK3R1, PPP1CB, PRKAA2, PRKCB, PYGB, RPS6KA2, SLC2A4, SOCS3, CREB5, AKT3, PPARGC1A, MLXIP, PRKAG2, G6PC2, PPP1R3B, PPARGC1B
KEGG	hsa04625	C-type lectin receptor signaling pathway	17/730	4.38E-02	PLK3, EGR2, EGR3, IL2, ITPR1, JUN, NFATC1, NFATC2, NFATC4, PIK3R1, PPP3CB, PTGS2, RRAS, BCL10, AKT3, MRAS, IL17D
KEGG	hsa04392	Hippo signaling pathway - multiple species	7/730	4.82E-02	TEAD1, DCHS1, RASSF2, WWTR1, LATS2, DCHS2, FAT4

Note：GO,Gene Ontology; BC, Bladder Carcinoma; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; adj.P-value, adjusted p-value.