Supplementary Table S4: GO terms and KEGG pathway analyses for up-regulated DE-miRNAs following solasonine-treated in BC. Through GO terms analysis of target genes for DE-miRNAs promoted by solasonine in BC, 1605, 171, and 149 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, 111 remarkably enriched pathways were obtained (adj.P-value ≤0.05).

Group	ID	Description	GeneRatio	adj.p-value	geneID
BP	GO:0009896	positive regulation of catabolic process	151/3408	3.64E-14	AKT2, APC, ATM, ZFP36L1, ZFP36L2, PTTG1IP, CAV1, CDKN1B, CPT1A, CSNK1D, CSNK1E, DAB2, DAPK1, DCN, FOXO1, FOXO3, FMR1, GJA1, GNAI3, GSK3B, HTT, HIF1A, HK2, HNRNPD, DNAJB2, INSR, LDLR, LRP1, SMAD7, ATXN3, NEDD4, NSF, OAZ2, FURIN, PAFAH1B2, PFKFB2, PFKFB3, PFKFB4, PHKG2, PIK3CB, PIP4K2A, PPARA, PRKAA1, PRKCE, MAPK3, MAPK9, PSMC2, PTEN, PTPN1, RALB, RDX, UPF1, SNCA, SNX1, SORL1, AURKA, TAF1, TNFRSF1B, TSC1, TWIST1, UVRAG, VCP, ZFP36, BTG2, ULK1, CUL4B, IRS2, ADAM9, USP13, CNOT8, ROCK2, SOCS5, EDEM1, PUM1, HERPUD1, RNF144A, AREL1, MFN2, BCL2L11, BCAP31, TOB1, TRIM13, TRIB1, TRIM22, NOD1, ARIH2, ATG7, SPTLC1, PLK2, SNF8, CPEB3, CNOT1, TNRC6B, LARP1, SIRT1, HSPBP1, RAB3GAP2, ARIH1, RNF19A, GIGYF2, FBXO22, HSPB8, PABPC1, TNRC6A, TRIB2, MYLIP, UBQLN2, UBQLN1, ABHD5, SH3GLB1, WAC, YTHDF2, DTL, TPCN1, ANKIB1, VPS13C, RBM23, VPS13D, FBXW7, VPS35, ZC3HAV1, SMURF1, HECW2, TNRC6C, METTL14, TP53INP2, DDA1, FYCO1, MUL1, LPCAT1, SESN2, ITCH, UQCC2, MTDH, TP53INP1, EGLN2, FAM122A, SOCS4, TRIM71, AMER1, SMCR8, SESN3, SH3D19, DAB2IP, RNF217, FLCN, TRIM65, RAB12, YTHDF3, RNF144B, RNF180
BP	GO:0007265	Ras protein signal transduction	156/3408	4.63E-14	ABL1, ABL2, ARF6, RHOA, RHOB, ARHGAP1, ARHGDIA, ARRB1, BCL6, CBL, CCNA2, CDC42, CDKN1A, CFL1, COL1A2, COL3A1, CRK, CRKL, MAPK14, CSF1, ECT2, EPHB2, EPS8, FGF2, FOXM1, GDI1, GNB1, GRB2, RAPGEF1, ARHGAP35, NRG1, ITGA3, ITGB1, ITPKB, JUN, KRAS, LIMK1, LYN, RAB8A, MET, KITLG, NOTCH2, NRAS, OPHN1, PLD1, RAB1A, RAB3B, RAB5A, RAB5B, RALB, RALGDS, RAP1B, RAP2A, RAP2B, RASA1, RB1, RDX, ROBO1, RREB1, SHC1, SOS1, TIAM1, TIMP2, TNFAIP1, TP53, TRIO, SHOC2, RND2, CUL3, MADD, IRS2, NRP1, SYNGAP1, KSR1, SQSTM1, WASF1, KALRN, F2RL3, ARHGEF2, RAB11B, CYTH3, CYTH1, RAB28, ARHGAP29, NTN1, MAP4K4, ROCK2, RAB36, RALGPS1, RAPGEF2, ARHGEF17, G3BP2, DENND4B, MFN2, G3BP1, ABI2, FARP1, WASF2, SPRY1, NET1, DLC1, RAPGEF3, CDC42EP2, VAV3, ARFGEF2, STAMBP, GNA13, PLK2, NCKAP1, RAB31, AKAP13, RASA3, RHOBTB3, RAB21, KANK1, ARHGEF9, PSD3, ARHGEF12, RHOQ, PLEKHG3, AUTS2, RAB30, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, RALGPS2, ARFGAP1, CDC42SE1, VANGL2, RAB22A, HEG1, USP28, RAB40C, RAP2C, RHOU, RAB17, PLEKHG2, MAPKAP1, SYNPO2L, PREX2, SPRY4, KCTD10, ARHGEF39, RAB39B, SSX2IP, FGD4, IQGAP3, DAB2IP, PLEKHG4B, FLCN, RAB12, SPATA13, RAB15, IQSEC3
BP	GO:0042326	negative regulation of phosphorylation	161/3408	4.63E-14	ABL1, ADAR, ADARB1, APC, RHOA, ARRB1, ARRB2, BAK1, BMP7, CALM1, CALM2, CALM3, CASP3, CAV1, CBL, CDKN1A, CDKN1B, CRKL, CSK, CYLD, DAG1, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EIF4G1, EPHB2, FOXM1, FOXO1, GBP1, GNAQ, RAPGEF1, HMGCR, HNRNPU, DNAJA1, IGF1R, ILK, JUN, IPO5, LRP6, LYN, SMAD4, SMAD6, SMAD7, MAPT, MEN1, MYC, NCK1, NF2, NTRK3, PAFAH1B1, PAK2, PAX6, PDE4D, ENPP1, PIN1, PPARA, PPP2CA, PPP2R1A, PPP2R5D, PKIA, PRKAR1A, PRKAR2A, PTEN, PTPN1, PTPRC, PTPRJ, PTPRR, RB1, RGS2, RGS4, SFRP1, SNCA, SORL1, STAT3, TESK1, NR2F2, TIMP3, TWIST1, YWHAG, NCK2, SOCS1, DYNLL1, IRS2, EIF3A, KAT2B, GPRC5A, LATS1, KLF4, NCOR1, SOCS5, RASSF2, SH2B3, CTDSP2, HIPK3, CTDSPL, TRIB1, SPRY1, TNIP1, BTN2A2, ZMYND11, PRDX3, DUSP14, PTPRT, DUSP10, STK38, ATG14, DKK1, ANKLE2, GPD1L, SIRT1, TARDBP, CORO1C, IBTK, LATS2, GREM1, PDCD4, TRIB2, DNAJC15, ERRFI1, DNAJC10, DDIT4, PARP14, LAX1, DUS2, CAMK2N1, PARD3, PMEPA1, NDRG2, HEG1, SEMA6A, CTDSP1, PRDM15, PBLD, CEP85, AIDA, WNK1, DUSP16, SH3BP5L, SPRY4, ITCH, AKT1S1, PPP1R15B, ITPRIP, MYADM, PIK3IP1, SOCS4, CD109, SMCR8, SIRPA, DUSP18, DAB2IP, CNKSR3, SPRED1, ZNF675, SPRED2, FLCN, PDE12, SPRED3
BP	GO:0031331	positive regulation of cellular catabolic process	133/3408	4.63E-14	AKT2, ATM, ZFP36L1, ZFP36L2, PTTG1IP, CAV1, CPT1A, CSNK1D, CSNK1E, DAB2, DAPK1, DCN, FOXO1, FOXO3, FMR1, GNAI3, GSK3B, HTT, HIF1A, HK2, HNRNPD, DNAJB2, INSR, LDLR, LRP1, SMAD7, ATXN3, FURIN, PAFAH1B2, PFKFB2, PFKFB3, PFKFB4, PHKG2, PIK3CB, PIP4K2A, PPARA, PRKAA1, MAPK3, MAPK9, PSMC2, PTEN, PTPN1, RALB, RDX, UPF1, SNCA, AURKA, TAF1, TNFRSF1B, TSC1, TWIST1, UVRAG, VCP, ZFP36, BTG2, ULK1, IRS2, ADAM9, USP13, CNOT8, ROCK2, SOCS5, EDEM1, PUM1, HERPUD1, RNF144A, MFN2, BCL2L11, BCAP31, TOB1, TRIM13, TRIB1, TRIM22, NOD1, ARIH2, SPTLC1, PLK2, CPEB3, CNOT1, TNRC6B, LARP1, SIRT1, HSPBP1, RAB3GAP2, ARIH1, RNF19A, GIGYF2, FBXO22, HSPB8, PABPC1, TNRC6A, TRIB2, UBQLN2, UBQLN1, ABHD5, SH3GLB1, WAC, YTHDF2, TPCN1, ANKIB1, VPS13C, RBM23, VPS13D, FBXW7, VPS35, ZC3HAV1, SMURF1, TNRC6C, METTL14, TP53INP2, DDA1, FYCO1, MUL1, SESN2, ITCH, UQCC2, MTDH, TP53INP1, FAM122A, SOCS4, TRIM71, AMER1, SMCR8, SESN3, SH3D19, DAB2IP, RNF217, FLCN, TRIM65, RAB12, YTHDF3, RNF144B, RNF180
BP	GO:0016358	dendrite development	97/3408	8.22E-14	ADAM10, ARF1, ARF6, RHOA, RERE, BMP7, CAMK2A, CDC42, CFL1, CRK, CRKL, CUX1, CELSR2, EPHA4, EPHB2, EPHB3, EZH2, ACSL4, FMR1, GSK3B, HDAC2, ILK, ITGB1, CAPRIN1, MAP1A, MAP1B, MARK1, MATN2, MECP2, MEF2A, MEF2C, NEDD4, SLC11A2, OPA1, PAFAH1B1, PAK2, PAK3, PPP3CA, MAPK6, PTEN, PTPRD, RAP2A, SDC2, STRN, VAMP7, TIAM1, VLDLR, NCK2, IQGAP1, NRP1, SYNGAP1, WASL, KALRN, DCLK1, DLG5, TAOK2, NTN1, RAPGEF2, ACTR2, ABI2, FARP1, SEMA3A, SLC9A6, PDLIM5, PLK2, CPEB3, NLGN1, BTBD3, TRAK1, SHANK2, RAB21, FSTL4, CAMSAP2, RBFOX2, NSMF, SIPA1L1, SS18L1, SLITRK5, MINK1, ASAP1, TRAPPC4, BCL11A, C21orf91, TMEM106B, UBA6, CAMK1D, SLC12A5, ARID1B, KIDINS220, HECW2, RAB17, GORASP1, TRAK2, PREX2, BHLHB9, DAB2IP, SDK1

BP	GO:0001933	negative regulation of protein phosphorylation	149/3408	1.62E-13	ABL1, ADAR, ADARB1, APC, ARRB1, ARRB2, BAK1, BMP7, CALM1, CALM2, CALM3, CASP3, CAV1, CBL, CDKN1A, CDKN1B, CRKL, CSK, CYLD, DAG1, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EIF4G1, EPHB2, FOXM1, FOXO1, GBP1, GNAQ, RAPGEF1, HMGCR, DNAJA1, IGF1R, ILK, JUN, IPO5, LRP6, LYN, SMAD4, SMAD6, SMAD7, MEN1, MYC, NCK1, NF2, NTRK3, PAFAH1B1, PAK2, PAX6, PDE4D, ENPP1, PIN1, PPP2CA, PPP2R1A, PPP2R5D, PKIA, PRKAR1A, PRKAR2A, PTEN, PTPN1, PTPRC, PTPRJ, PTPRR, RB1, RGS2, RGS4, SFRP1, SNCA, SORL1, TESK1, NR2F2, TIMP3, TWIST1, YWHAG, NCK2, SOCS1, EIF3A, KAT2B, GPRC5A, LATS1, KLF4, NCOR1, SOCS5, RASSF2, SH2B3, CTDSP2, HIPK3, CTDSPL, TRIB1, SPRY1, TNIP1, BTN2A2, ZMYND11, DUSP14, PTPRT, DUSP10, STK38, ATG14, DKK1, GPD1L, SIRT1, TARDBP, CORO1C, IBTK, LATS2, GREM1, PDCD4, TRIB2, ERRFI1, DNAJC10, DDIT4, PARP14, LAX1, DUS2, CAMK2N1, PARD3, PMEPA1, NDRG2, HEG1, SEMA6A, CTDSP1, PRDM15, PBLD, CEP85, AIDA, WNK1, DUSP16, SH3BP5L, SPRY4, ITCH, AKT1S1, PPP1R15B, ITPRIP, MYADM, SOCS4, CD109, SMCR8, SIRPA, DUSP18, DAB2IP, CNKSR3, SPRED1, ZNF675, SPRED2, FLCN, SPRED3
BP	GO:0016570	histone modification	154/3408	4.65E-13	ARRB1, ATM, ATRX, BCL6, BRCA1, CAMK2D, CCNA2, CHEK1, ATF2, CREBBP, CTNNB1, DNMT3B, DR1, ELK4, EP300, EYA4, EZH1, EZH2, FMR1, GATA2, GATA3, KAT2A, HCFC1, HDAC2, IGF2, IRF4, ISL1, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MTHFR, MYB, PRKAA1, PRKCA, MAPK3, MAPK8, RAG1, KDM5A, RNF2, SATB1, ATXN7, SET, SKI, SKP1, SNAI2, SNCA, AURKA, SUV39H1, TAF1, TBL1X, TP53, TWIST1, UBE2N, KDM6A, VEGFA, PRDM2, KAT6A, KMT2D, YEATS4, HMGA2, DPF3, DPF1, NCOA3, BAP1, CUL4B, KAT2B, LDB1, PER2, RPS6KA4, BAZ1B, MTA1, AURKB, RPS6KA5, TRIP12, GTF3C4, ATG5, CLOCK, MORF4L2, CTR9, KDM4A, HDAC9, SETD1A, KMT2B, PCGF3, CTCF, KDM5B, SRCAP, KAT7, MTF2, KDM2A, KDM1A, PHF8, KDM6B, RCOR1, SIRT1, SUZ12, WBP2, NIPBL, USP49, SIN3A, ZNF451, AUTS2, USP21, BRPF3, ING4, WAC, UBR5, TAF9B, ARID4B, RSF1, KDM3B, WDR5B, ING3, TET2, BCOR, KANSL2, MSL2, RIF1, SETD5, KMT2E, SMARCAD1, ATXN7L3, USP36, EP400, BEND3, MIER1, KMT2C, NSD1, MEAF6, BRCC3, CDC73, TBL1XR1, NAA40, NAA50, TET1, EPC1, SETD7, SETDB2, SETD3, BRMS1L, PCGF5, DPY30, TADA2B, MYSM1, NACC2, USP51, RNF168, TET3, FLCN, JMJD1C, KDM1B
BP	GO:0016569	covalent chromatin modification	158/3408	9.83E-13	ARRB1, ATM, ATRX, BCL6, BRCA1, CAMK2D, CCNA2, CHEK1, ATF2, CREBBP, CTNNB1, DNMT3A, DNMT3B, DR1, ELK4, EP300, EYA4, EZH1, EZH2, FMR1, GATA2, GATA3, KAT2A, HCFC1, HDAC2, IGF2, IRF4, ISL1, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MTHFR, MYB, PRKAA1, PRKCA, MAPK3, MAPK8, RAG1, KDM5A, RNF2, SATB1, ATXN7, SET, SKI, SKP1, SNAI2, SNCA, AURKA, SUV39H1, TAF1, TBL1X, TP53, TWIST1, UBE2N, KDM6A, VEGFA, PRDM2, KAT6A, KMT2D, YEATS4, HMGA2, DPF3, DPF1, NCOA3, BAP1, CUL4B, KAT2B, LDB1, PER2, MBD2, RPS6KA4, BAZ1B, MTA1, AURKB, RPS6KA5, TRIP12, GTF3C4, ATG5, CLOCK, MORF4L2, CTR9, KDM4A, HDAC9, SETD1A, KMT2B, PCGF3, CTCF, KDM5B, SRCAP, KAT7, MTF2, MORC2, KDM2A, KDM1A, PHF8, KDM6B, RCOR1, SIRT1, SUZ12, WBP2, NIPBL, USP49, SIN3A, ZNF451, AUTS2, USP21, BRPF3, ING4, WAC, UBR5, TAF9B, ARID4B, RSF1, KDM3B, WDR5B, ING3, TET2, BCOR, KANSL2, MSL2, RIF1, SETD5, ATF7IP, KMT2E, SMARCAD1, ATXN7L3, USP36, EP400, BEND3, MIER1, KMT2C, NSD1, MEAF6, BRCC3, CDC73, TBL1XR1, NAA40, NAA50, TET1, EPC1, SETD7, SETDB2, SETD3, BRMS1L, PCGF5, DPY30, TADA2B, MYSM1, NACC2, USP51, RNF168, TET3, FLCN, JMJD1C, KDM1B
BP	GO:0010498	proteasomal protein catabolic process	158/3408	1.64E-12	ALAD, AMFR, ARRB1, ARRB2, CAV1, CCNF, CDC34, CSNK1D, CSNK1E, CTNNB1, DAB2, FHIT, FMR1, GSK3B, UBE2K, DNAJB2, HSPA5, MAD2L1, SMAD7, MAP1A, DNAJB9, ATXN3, NEDD4, OPHN1, PKD1, PML, MAPK9, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAD23B, RNF4, SEL1L, SIAH1, SIAH2, SKP1, AURKA, STYX, TAF1, TBL1X, TMF1, TNFAIP1, UBE2D3, UBE2G1, UBE2G2, UBE2H, VCP, TRIM25, RNF103, CUL5, SPOP, CUL4B, CUL3, CUL2, ENC1, BTRC, USP13, MTA1, AURKB, SOCS6, UBE4A, PSMF1, CLOCK, SOCS5, EDEM1, HERPUD1, RNF144A, AREL1, BCAP31, PSME3, TRIM13, PSMD14, TRIB1, UBE4B, ARIH2, RBCK1, PLK2, TLK2, ATE1, ERLIN2, GABARAPL2, UBXN4, PSME4, TRIM2, UFL1, SIRT1, KCTD2, CD2AP, HSPBP1, ARIH1, ARMC8, RNF19A, LTN1, FBXL3, FBXO22, FBXO9, TRIB2, USP25, UBQLN2, UBQLN1, DERL2, BFAR, WAC, UCHL5, UBE2J1, GET4, DNAJC10, ANKIB1, FBXL19, DNAJB12, FBXL12, UBE2R2, UBE2W, FBXW7, YOD1, NPLOC4, NSFL1C, UGGT1, UBQLN4, CCDC47, PCNP, SMURF1, PELI1, HECW2, KLHL42, RMND5B, DDA1, GID4, TBL1XR1, KCTD17, SPSB1, EDEM3, KLHL15, TMUB1, ITCH, KCTD10, RHBDD1, DDI2, SYVN1, ZNRF1, FAM122A, RFFL, SOCS4, UBR3, TRIM71, UBXN2B, RNF187, DAB2IP, RNF217, UBR1, FBXO45, RNF144B, RNF180, SPOPL
BP	GO:0010975	regulation of neuron projection development	163/3408	2.15E-12	ABL1, ABL2, ADAM10, ADCY6, ARF1, ARF6, RHOA, ARHGDIA, BDNF, BMP7, BMPR2, SCARB2, CFL1, CNTN1, CRK, CRKL, CTSZ, CUX1, DVL3, EFNA5, EFNB2, MEGF8, MARK2, EP300, EPHA4, EPHA7, EPHB2, EPHB3, EZH2, FKBP4, FMR1, FN1, GATA3, GDI1, GOLGA4, RAPGEF1, ARHGAP35, GSK3B, HDAC2, HSPA5, ILK, ITGA6, ITGA3, L1CAM, LIMK1, LRP1, LYN, CAPRIN1, MAP1B, MAPT, MARK1, MDK, MEF2C, NCK1, NEDD4, NTRK3, OPA1, PAFAH1B1, PAK3, PRRX1, POU3F2, PPP3CA, MAPK6, PTEN, TWF1, PTPRD, PTPRF, PTPRG, RAP2A, RGS2, ROBO1, CX3CL1, SDC2, SFRP1, SKIL, SNAP25, SRF, VAMP7, SYT1, TIAM1, TSC1, VEGFA, VLDLR, RND2, SF3A2, FZD1, FZD4, STK24, SEMA7A, SNX3, IQGAP1, NRP1, SYNGAP1, KALRN, DLG5, KLF4, NTN1, MAP4K4, RAPGEF2, SEMA3E, LRIG2, UST, ACTR2, ABI2, SEMA3A, OLFM1, SEMA4B, PDLIM5, PLK2, CPEB3, NLGN1, TRAK1, SHANK2, DKK1, RAB21, KDM1A, MYCBP2, FSTL4, RAP1GAP2, PLXND1, KANK1, CAMSAP2, NCS1, SIN3A, NSMF, SIPA1L1, SS18L1, NPTN, MYLIP, ASAP1, NIN, SYT17, BCL11A, C21orf91, TMEM106B, RRN3, SEMA4C, YTHDF1, TENM3, RGMA, CAMK1D, SMURF1, KIDINS220, HECW2, SEMA6A, ZSWIM6, RAB17, GORASP1, CREB3L2, NDRG4, ZSWIM4, TRAK2, METRN, MUL1, BHLHB9, ITM2C, KREMEN1, PLXNA4, SYT2, WDR36, TTL, DAB2IP, SDK1
BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	142/3408	4.52E-12	AMFR, ARRB1, ARRB2, CAV1, CCNF, CDC34, CSNK1D, CSNK1E, CTNNB1, DAB2, FHIT, GSK3B, UBE2K, DNAJB2, HSPA5, MAD2L1, SMAD7, MAP1A, DNAJB9, ATXN3, NEDD4, PML, MAPK9, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAD23B, RNF4, SEL1L, SIAH1, SIAH2, SKP1, AURKA, STYX, TAF1, TBL1X, TNFAIP1, UBE2D3, UBE2G1, UBE2G2, UBE2H, VCP, TRIM25, RNF103, CUL5, SPOP, CUL4B, CUL3, CUL2, BTRC, MTA1, AURKB, UBE4A, PSMF1, CLOCK, SOCS5, EDEM1, HERPUD1, RNF144A, AREL1, BCAP31, PSME3, TRIM13, PSMD14, TRIB1, UBE4B, ARIH2, RBCK1, PLK2, TLK2, ERLIN2, UBXN4, PSME4, TRIM2, UFL1,

					SIRT1, KCTD2, CD2AP, HSPBP1, ARIH1, ARMC8, RNF19A, LTN1, FBXL3, FBXO22, FBXO9, TRIB2, UBQLN2, UBQLN1, DERL2, BFAR, WAC, UCHL5, UBE2J1, DNAJC10, ANKIB1, FBXL19, DNAJB12, FBXL12, UBE2R2, UBE2W, FBXW7, YOD1, NPLOC4, NSFL1C, UBQLN4, CCDC47, PCNP, SMURF1, PELI1, HECW2, KLHL42, RMND5B, DDA1, GID4, TBL1XR1, KCTD17, SPSB1, EDEM3, KLHL15, TMUB1, ITCH, KCTD10, SYVN1, ZNRF1, FAM122A, RFFL, SOCS4, UBR3, TRIM71, UBXN2B, RNF187, RNF217, UBR1, FBXO45, RNF144B, RNF180, SPOPL
BP	GO:0006470	protein dephosphorylation	114/3408	5.45E-11	ACP1, BCL2, CALM1, CALM2, CALM3, CDC25A, CRY2, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, ENSA, EYA4, FKBP1A, GNAI2, GSK3B, HTT, NCKAP1L, IKBKB, PPP1R12A, NCK1, PIN1, PPM1B, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PPP3R1, PPP6C, EIF2AK2, PTEN, PTPN1, PTPN4, PTPN11, PTPN12, PTPN14, PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRJ, PTPRK, PTPRN2, PTPRR, SET, STYX, TSC1, YWHAE, PTP4A1, SHOC2, PTP4A2, PPM1D, CDC14B, MTMR3, BTRC, MTMR7, MTMR4, ROCK2, PHACTR2, NUAK1, CTDSP2, CTDSPL, DLC1, TAB1, ARPP19, DUSP14, PTPN21, PTPRT, DUSP10, LMTK2, PPP6R1, PHLPP2, ANKLE2, PHLPP1, NSMF, PPP1R16B, PTPN18, DAPP1, PALD1, CYCS, SSH1, DUSP23, RPRD1A, PPP6R3, PPP2R2D, SLC39A10, PPM1H, PDP2, CTDSP1, DUSP16, FAM220A, PPP1R15B, SSH2, TIMM50, FAM122A, SPPL3, PPM1M, DUSP18, PPM1L, PPP4R2, PPTC7, CNEP1R1, BOD1L1, PPP1R37
BP	GO:0043405	regulation of MAP kinase activity	118/3408	5.77E-11	ADORA2B, ARRB1, BMP7, CAV1, CRK, CRKL, MAPK14, CSK, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, DVL3, EDN1, EGFR, EPHA4, EPHB2, ERBB2, ERCC6, EZH2, FGF1, FGF2, RAPGEF1, NRG1, HMGCR, DNAJA1, IGF1R, ILK, INSR, IRAK1, IRAK2, KIT, KRAS, LYN, MAP3K1, MAP3K3, MAP3K4, KITLG, MAP3K9, NTRK3, PAK3, PDGFA, PDGFB, PIK3CB, PPP2CA, PPP2R1A, PRKAA1, MAPK1, MAPK3, EIF2AK2, PTPN1, PTPN11, PTPRC, PTPRJ, RGS2, RGS4, ROBO1, RPS3, MAP2K4, SFRP1, SHC1, SORL1, SRC, SYK, TGFA, TGFBR1, THBS1, TIAM1, TPD52L1, UBE2N, UBE2V1, VEGFA, WNT7B, FZD5, FZD4, MADD, PEA15, ADAM9, IQGAP1, KSR1, SPAG9, TAOK2, SH2B3, HIPK3, TENM1, TRIB1, SPRY1, NOD1, TAB1, MAP3K2, FRS2, DUSP14, AKAP13, DUSP10, STK38, DKK1, TAB2, MAPK8IP3, PDCD4, TRIB2, LAX1, VANGL2, KIDINS220, TAOK1, AIDA, MUL1, DUSP16, SPRY4, IQGAP3, DUSP18, DAB2IP, SPRED1, ZNF675, SPRED2, EPGN, SPRED3
BP	GO:0051098	regulation of binding	127/3408	6.47E-11	ABL1, ACTB, ADD1, AMFR, ARF6, ARRB1, ARRB2, BAK1, BCL2, BDNF, CALM3, CAV1, CEBPG, CRK, CSNK1E, CTNNB1, CTSZ, CYLD, DAB2, EIF2S1, EIF4G1, MARK2, EP300, EPB41, EPHA4, ERCC2, FKBP1A, FOXC1, FMR1, GATA3, GSK3B, HDAC2, NRG1, HOXA3, HES1, DNAJB2, HSPA5, ID4, IFIT2, IRF4, ISL1, JUN, LRP1, LRPAP1, SMAD2, SMAD4, MEF2C, MEN1, MET, MSX1, NCBP1, NKX3-1, P2RY1, PAX6, PDGFB, PIN1, PKD1, PLCL1, POU4F1, PPARA, PPP1CA, PPP2CA, PPP3CA, MAPK3, MAPK8, PTPRF, RALB, RAN, RB1, SKI, SORL1, SOX11, SP100, SRC, STK4, AURKA, STYX, TAF1, TCF7L2, TMBIM6, TERT, TGFBR1, TGFBR3, TIAM1, TWIST1, TXN, HMGA2, TNKS, NRP1, PER2, MBD2, AURKB, KLF4, HAND1, TRAF4, RAPGEF2, PLK2, MAPRE3, DKK1, KDM1A, USP33, PLXND1, MAU2, NIPBL, SIN3A, LDLRAP1, HIPK2, CDON, NMD3, RSF1, GNL3L, PINX1, FBXW7, MEPCE, EPB41L5, ZNF462, NSD1, NUCKS1, AIDA, HMBOX1, ARHGAP28, SPPL3, WFIKKN2, TTBK2, DAB2IP, ZNF675, DPH3
BP	GO:0007409	axonogenesis	150/3408	1.04E-10	ABL1, ACTB, ADARB1, ADCY1, ALCAM, APBB2, RHOA, ARHGDIA, BCL2, BDNF, BMP7, BMPR2, CREB1, DAG1, EFNA3, EFNA5, EFNB1, EFNB2, CELSR3, MEGF8, MARK2, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, ETV1, FN1, GAB1, GATA3, GDI1, GOLGA4, GRB2, ARHGAP35, GSK3B, ILK, ISL1, ITGB1, L1CAM, LIMK1, LRP1, SMAD4, MAP1A, MAP1B, MAPT, MATN2, RAB8A, MYH10, NCAM1, NEFH, NEO1, NFIB, NPTX1, NTRK3, OPHN1, PAFAH1B1, PAK3, PAX2, PAX6, PIK3CB, PITPNA, POU3F2, POU4F1, PRKCA, MAPK1, MAPK3, PTCH1, PTEN, PTPN11, ROBO1, SHC1, SIAH1, SKIL, SOS1, SPTAN1, SPTBN1, SRC, SRF, TIAM1, TOP2B, TRIO, VCL, VEGFA, VLDLR, FZD3, NR4A3, RND2, USP9X, ULK1, SEMA7A, NUMB, IRS2, NRP1, SYNGAP1, DCLK1, RPS6KA5, PDLIM7, B4GALT6, TAOK2, NTN1, SEMA3E, UST, SEMA3A, OLFM1, SLC9A6, SEMA4B, FRS2, KIF3A, LYPLA2, TRAK1, RAB21, PALLD, USP33, MYCBP2, FSTL4, NFASC, PLXND1, SZT2, FLRT2, SIN3A, SIPA1L1, SLITRK5, AUTS2, CYFIP2, NPTN, NIN, SEMA4C, YTHDF1, PARD3, DPYSL5, VANGL2, SEMA6A, ZSWIM6, ISL2, BCL11B, RAPH1, ZSWIM4, TRAK2, METRN, PARD6B, PLXNA4, EMB, WDR36, SLITRK4, TTL, FBXO45, DOK6, AGRN, RNF165
BP	GO:0050769	positive regulation of neurogenesis	150/3408	3.01E-10	ABL2, ARF1, RHOA, ARHGDIA, BCL2, BCL6, BDNF, BMP7, BMPR2, SCARB2, CNTN1, CRKL, CSF1, CSNK1D, CSNK1E, CTNNB1, CUX1, DAG1, DLX2, DNMT3B, DVL3, ECT2, EFNA5, MEGF8, EIF4G1, MARK2, EP300, EPHA4, EPHB2, EZH2, FMR1, FN1, GATA2, GDI1, GOLGA4, RAPGEF1, ARHGAP35, HDAC2, HIF1A, FOXA1, HES1, HSPA5, IL6ST, ILK, ITGA6, ITGA3, KIT, L1CAM, LIG4, LIMK1, LRP1, LYN, CAPRIN1, MAN2A1, MAP1B, MAPT, MDK, MEF2C, MME, MYB, NAP1L1, NCK1, NTRK3, OPA1, PAFAH1B1, PAK3, PAX6, SERPINE2, PPP1CC, MAPK6, PROX1, PTEN, TWF1, PTPRD, RGS2, ROBO1, CX3CL1, SKIL, SOX11, SRF, VAMP7, SYT1, TCF4, TCF3, ZEB1, TIAM1, TIMP2, TNFRSF1B, VEGFA, VLDLR, XRCC5, FZD3, RND2, SF3A2, FZD1, FZD4, SEMA7A, NUMB, SNX3, IQGAP1, NRP1, SOCS2, KALRN, SPAG9, ARHGEF2, DLG5, NTN1, RAPGEF2, ACTR2, SEMA3A, CPEB3, NLGN1, TRAK1, SHANK2, DKK1, RAB21, SPEN, KDM1A, PLXND1, UFL1, DICER1, MMD, NIPBL, SIN3A, NSMF, SS18L1, HEYL, NPTN, SOX8, CDON, NIN, SYT17, C21orf91, TMEM106B, RRN3, TENM3, CAMK1D, SMURF1, KIDINS220, SEMA6A, TGIF2, CREB3L2, NDRG4, METRN, MUL1, BHLHB9, PLXNA4, SYT2, KCTD11, DAB2IP
BP	GO:0071383	cellular response to steroid hormone stimulus	93/3408	3.42E-10	AR, RHOA, ARRB2, ATP2B1, BMP7, BRCA1, ZFP36L1, ZFP36L2, KLF9, CALR, RUNX1, CBFB, CRY2, CTNNB1, DAB2, DDX5, DNMT3B, EDN1, EGFR, EIF4E, EP300, ESR2, ESRRA, ESRRG, FHL2, FKBP4, FOXO1, FOXO3, NR5A2, NR6A1, NR3C1, FOXA1, HNF4A, HNRNPU, DNAJA1, ISL1, NEDD4, NKX3-1, NPC1, PGR, PPARA, PPARD, RAN, RARG, RB1, RNF4, RORA, RORB, SFRP1, SRC, STC1, TAF1, NR2F2, TFPI, THRA, NR2C2, UBE2L3, NR1H2, VDR, ZFP36, NR4A3, KMT2D, NCOA3, NRIP1, ARID1A, TP63, AKR1C3, LATS1, CLOCK, NCOR1, NR1D2, BCL2L11, PGRMC2, DDX17, ABHD2, FAM107A, AKAP13, CNOT1, UFL1, SIRT1, RBFOX2, WBP2, HEYL, FOXP1, STRN3, UBR5, ERRFI1, DDIT4, PMEPA1, CALCOCO1, PAQR8, EGLN2, KCTD6

BP	GO:0016049	cell growth	152/3408	3.69E-10	ABL1, ACVR1B, ADAM10, ALCAM, APBB2, RHOA, BCL2, BCL6, BDNF, BMPR2, BTG1, OSGIN2, CAMK2D, CDC42, CDKN1A, CDKN1B, CRKL, CTNNB1, DDX3X, HBEGF, EDN1, EFNA5, MEGF8, EGFR, EIF4G1, EIF4G2, EPHA7, ERBB2, ESR2, EXTL3, FHL1, FN1, G6PD, GDI1, GJA1, GOLGA4, GSK3B, HNF4A, DNAJB2, IGFBP1, IGFBP5, ILK, ITGB1, L1CAM, LIMK1, LRP1, SMAD4, MAP1B, MAPT, MMP14, MSX1, NCBP1, NTRK3, PAFAH1B1, ENPP1, SERPINE2, PIN1, PML, PPARA, PPARD, PPP2CA, PPP2R1A, PTPRJ, RARG, RB1, RGS2, RGS4, RPS6KA3, MAP2K4, SFRP1, SH3GL2, SLC9A1, SMARCA2, SRF, AURKA, SYT1, ADAM17, TGFBR1, TIAM1, TP53, VCL, VEGFA, YY1, KMT2D, RND2, USP9X, BAP1, ULK1, SORBS2, SEMA7A, IQGAP1, NRP1, SOCS2, WASF1, DCLK1, TAOK2, NTN1, AKAP6, SEMA3E, SERTAD2, NET1, SEMA3A, ARIH2, OLFM1, SLC9A6, SEMA4B, PDLIM5, POSTN, FAM107A, AKAP13, RAB21, FSTL4, SIRT1, SGK3, SIN3A, AUTS2, CYFIP2, SERTAD3, DERL2, ADIPOR1, ZNF639, NIN, TAF9B, SYT17, BCL11A, INO80, SEMA4C, USP47, CHPT1, SMURF1, SEMA6A, EPB41L5, CXCL16, TSPYL2, RAPH1, CDC73, MUL1, ADIPOR2, SESN2, ITCH, KIAA1109, PLXNA4, EGLN2, FAM122A, DCUN1D3, SYT2, DCBLD2, WDR36, MTPN, TTL, FLCN, BRAT1
BP	GO:0048193	Golgi vesicle transport	123/3408	4.97E-10	AP1G1, ANK1, ARCN1, TRIM23, ARF1, ARL1, CAPZA2, CD59, COPB1, CSK, CSNK1D, CTSZ, CUX1, GOLGA3, GOLGA4, GOLGB1, HTT, INSIG1, KIF2A, RAB8A, MYO1B, MYO5A, NSF, PPP6C, RAB1A, RP2, SORT1, SNX1, SORL1, SPTAN1, SPTBN1, SURF4, VAMP2, VAMP7, TGFA, UVRAG, VCP, CUL3, USO1, DYNLL1, NAPA, AP3D1, RABEP1, VAPB, VAPA, CYTH3, KIF3B, KIF23, SCAMP1, GOSR1, GOSR2, PREPL, SEC24C, GOLGA5, SCAMP2, ATP9A, BCAP31, ARFRP1, CNIH1, LYPLA1, SEC23A, HYOU1, ARFGEF2, EXOC5, SEC24A, TMED10, KIF2C, RAB31, KIF3A, DCTN3, GABARAPL2, PPP6R1, VPS13A, EXOC6B, ANKRD28, BICD2, PITPNB, SEC31B, RAB30, TMED5, TMED7, DCTN4, ERGIC2, TRAPPC4, ANKFY1, VPS54, RAB14, RAB6B, TRAPPC2L, RAB8B, VPS13C, STX17, GOLPH3L, PPP6R3, ARFGAP1, BCAP29, SAR1A, ERGIC1, KIF13A, GORASP1, CREB3L2, KLC2, PGAP1, C16orf70, YIPF5, PITPNM3, COG3, SLC10A7, COG8, DCTN5, CEP19, YIF1B, PKDCC, TEX261, WHAMM, TBC1D20, EXOC8, RAB12, TMED4, STEAP2, ATP9B, MIA3, MYO18A
BP	GO:0034330	cell junction organization	103/3408	5.02E-10	ABL1, ACTB, ACTN4, ADD1, APC, ARF6, RHOA, BCL2, DST, CAV1, RUNX1, CBFB, CDC42, CDH6, CSK, CTNNA1, CTNNB1, CTNND1, CXADR, ECT2, EFNA5, FN1, GJA1, GJB1, RAPGEF1, IKBKB, ILK, ITGA6, ITGA5, JUP, LAMC1, LAMC2, LRP1, SMAD7, MMP14, MYO1C, NF2, OPHN1, PKP1, PLEC, PRKCA, PKN2, PTEN, PTPRJ, PTPRK, RAP1B, RDX, SDC4, SFRP1, SLC9A1, SNAI2, SNAI1, SRC, SRF, STRN, TGFBR1, THBS1, TLN1, TNS1, TSC1, VCL, VEGFA, FZD5, PKP4, NUMB, IQGAP1, NRP1, LDB1, DLG5, TAOK2, MAP4K4, ROCK2, RAPGEF2, SLK, PDCD6IP, GJC1, DLC1, FAM107A, RASSF8, LIMCH1, NFASC, CLASP1, PIP5K1C, CORO1C, CADM1, GRHL1, RAB8B, WNT4, FBLIM1, RCC2, PARD3, HEG1, NLGN2, EPB41L5, PEAK1, PARD6B, PHLDB2, MTDH, WHAMM, FLCN, HIPK1, SDK1, FMN1
BP	GO:0006914	autophagy	154/3408	5.87E-10	ABL1, ABL2, ANXA7, ATM, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, BCL2, CASP3, DAPK1, DCN, EEF1A1, EIF4G1, EIF4G2, MARK2, EP300, FOXO1, FOXO3, GAPDH, GNAI3, GSK3B, HTT, HIF1A, HK2, FOXK2, ITPR1, LAMP2, NBR1, MAPT, MCL1, RAB8A, MET, NEDD4, NPC1, TBC1D25, PAFAH1B2, PIK3CB, PIP4K2A, PRKAA1, PRKAB2, MAPK3, MAPK8, RAB1A, RAB5A, RALB, SNCA, SRC, SREBF2, STAT3, TMBIM6, TP53, TSC1, UVRAG, VCP, XBP1, FZD5, ULK1, DYNLL1, CD84, SQSTM1, MTMR3, USP13, ATP6V0D1, ATG5, VPS4B, KDM4A, ATG13, TOMM20, PLEKHM1, TECPR2, MFN2, BCL2L11, TRIM13, TRIM22, NOD1, ATG7, SPTLC1, PLK2, TLK2, SNF8, GABARAPL2, ATG14, USP33, TAB2, ATG2A, VPS13A, PACS2, LARP1, SIRT1, STX12, RAB3GAP2, KLHL3, HSPB8, HTRA2, UBQLN2, UBQLN1, VPS36, SH3GLB1, WAC, ATP6V1D, RAB23, ZFYVE1, TPCN1, VPS13C, FNBP1L, STX17, VPS37C, ATG16L1, ATG2B, VPS13D, FBXW7, DRAM1, YOD1, MFN1, VPS35, NSFL1C, UBQLN4, SMURF1, USP36, EPG5, TP53INP2, RRAGD, RRAGC, MLST8, MTMR9, ATG9A, FYCO1, MUL1, MAP1LC3B, C19orf12, SESN2, ATG10, BMF, MTDH, TP53INP1, RAB39B, WDR81, LIX1L, UBXN2B, SOGA1, SMCR8, SESN3, EXOC8, ATP6V0E2, VPS37D, TMEM74, FLCN, TRIM65, RAB12, TPCN2, FOXK1, ACER2, TMEM41B
BP	GO:0061919	process utilizing autophagic mechanism	154/3408	5.87E-10	ABL1, ABL2, ANXA7, ATM, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, BCL2, CASP3, DAPK1, DCN, EEF1A1, EIF4G1, EIF4G2, MARK2, EP300, FOXO1, FOXO3, GAPDH, GNAI3, GSK3B, HTT, HIF1A, HK2, FOXK2, ITPR1, LAMP2, NBR1, MAPT, MCL1, RAB8A, MET, NEDD4, NPC1, TBC1D25, PAFAH1B2, PIK3CB, PIP4K2A, PRKAA1, PRKAB2, MAPK3, MAPK8, RAB1A, RAB5A, RALB, SNCA, SRC, SREBF2, STAT3, TMBIM6, TP53, TSC1, UVRAG, VCP, XBP1, FZD5, ULK1, DYNLL1, CD84, SQSTM1, MTMR3, USP13, ATP6V0D1, ATG5, VPS4B, KDM4A, ATG13, TOMM20, PLEKHM1, TECPR2, MFN2, BCL2L11, TRIM13, TRIM22, NOD1, ATG7, SPTLC1, PLK2, TLK2, SNF8, GABARAPL2, ATG14, USP33, TAB2, ATG2A, VPS13A, PACS2, LARP1, SIRT1, STX12, RAB3GAP2, KLHL3, HSPB8, HTRA2, UBQLN2, UBQLN1, VPS36, SH3GLB1, WAC, ATP6V1D, RAB23, ZFYVE1, TPCN1, VPS13C, FNBP1L, STX17, VPS37C, ATG16L1, ATG2B, VPS13D, FBXW7, DRAM1, YOD1, MFN1, VPS35, NSFL1C, UBQLN4, SMURF1, USP36, EPG5, TP53INP2, RRAGD, RRAGC, MLST8, MTMR9, ATG9A, FYCO1, MUL1, MAP1LC3B, C19orf12, SESN2, ATG10, BMF, MTDH, TP53INP1, RAB39B, WDR81, LIX1L, UBXN2B, SOGA1, SMCR8, SESN3, EXOC8, ATP6V0E2, VPS37D, TMEM74, FLCN, TRIM65, RAB12, TPCN2, FOXK1, ACER2, TMEM41B
BP	GO:0022604	regulation of cell morphogenesis	151/3408	6.10E-10	ABL1, ACTN4, ADAM10, ANXA7, RHOA, RHOB, ARHGDIA, BDNF, BMPR2, FMNL1, CALR, CD44, CDC42, CFL1, CRK, CRKL, CUX1, DAG1, DIAPH1, DVL3, EFNA5, MEGF8, MARK2, EPB41, EPHA4, EPHA7, EPHB2, EPHB3, EPS8, FMR1, FN1, GBP1, GDI1, GOLGA4, ARHGAP35, GSK3B, ILK, KIT, L1CAM, LIMK1, LRP1, CAPRIN1, MAP1B, MAPT, MDK, MKLN1, MYH9, MYH10, MYO10, NEDD4, NEDD9, NTRK3, OPA1, P2RY1, PAFAH1B1, PAK3, POU3F2, PPP3CA, PTEN, PTPRD, RAP2A, RASA1, RDX, ROBO1, RREB1, CCL7, SDC2, SKIL, SPARC, SRC, SRF, VAMP7, SYT1, TIAM1, VEGFA, ZMYM2, RND2, FZD4, SEMA7A, NRP1, SYNGAP1, LIMD1, KALRN, ZMYM4, TAOK2, NTN1, RAPGEF2, SEMA3E, UST, ACTR2, ARPC2, ABI2, SEMA3A, DLC1, CDC42EP2, OLFM1, SEMA4B, PDLIM5, POSTN, GNA13, RHOBTB3, NLGN1, TRAK1, RAB21, MYCBP2, FSTL4, PLXND1, KANK1, RHOQ, CORO1C, SIN3A, NSMF, SIPA1L1, SS18L1, NIN, SYT17, BCL11A, BRWD1, FBLIM1, SEMA4C, YTHDF1, PHIP, PRPF40A, RCC2, CDC42SE1, SMURF1, HECW2, SEMA6A,

					SHROOM3, ZSWIM6, RHOU, GORASP1, ZSWIM4, TRAK2, METRN, MUL1, BHLHB9, FMNL3, PLXNA4, MYADM, ARHGAP18, LARP4, PDZD8, FGD4, SYT2, WDR36, TTL, SH3D19, CAMSAP1, AGO4, BRWD3
BP	GO:0051348	negative regulation of transferase activity	101/3408	8.02E-10	ABL1, ADAR, ADARB1, APC, BMP7, CASP3, CAV1, CBL, CDKN1A, CDKN1B, CSK, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EPHB2, GNAQ, GSK3B, HMGCR, HNRNPU, DNAJA1, IGF1R, ILK, IPO5, LIMK1, LRP6, LYN, MAD2L1, SMAD7, MAPT, MEN1, NCK1, NF2, PAK2, PPP2CA, PPP2R1A, PKIA, PRKAR1A, PRKAR2A, PTEN, PTPN1, PTPRC, PTPRJ, RB1, RGS2, RGS4, SFRP1, SORL1, SRC, TESK1, NR2F2, TP53, YWHAG, ZFP36, SOCS1, IRS2, KAT2B, GPRC5A, LATS1, SOCS5, SH2B3, HIPK3, TRIB1, SPRY1, CERS1, PRDX3, DUSP14, PTPRT, DUSP10, STK38, SIRT1, CORO1C, IBTK, LATS2, PDCD4, TRIB2, ERRFI1, LAX1, DUS2, PINX1, CAMK2N1, HEG1, CEP85, AIDA, WNK1, DUSP16, SH3BP5L, SPRY4, AKT1S1, ITPRIP, PIK3IP1, SOCS4, SMCR8, DUSP18, DAB2IP, SPRED1, ZNF675, SPRED2, SPRED3
BP	GO:0016311	dephosphorylation	149/3408	8.23E-10	ACP1, BCL2, CALM1, CALM2, CALM3, CDC25A, CRY2, DLG3, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, ENSA, EYA4, FKBP1A, GNAI2, GSK3B, HTT, NCKAP1L, IKBKB, IMPA2, MEF2C, MYO1D, PPP1R12A, NCK1, NT5E, PFKFB2, PFKFB3, PFKFB4, PIN1, PPM1B, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PPP3R1, PPP6C, EIF2AK2, PTEN, PTPN1, PTPN4, PTPN11, PTPN12, PTPN14, PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRJ, PTPRK, PTPRN2, PTPRR, SET, SRC, STYX, TSC1, YWHAE, PTP4A1, SHOC2, PTP4A2, PPM1D, CDC14B, INPP4B, IQGAP1, SYNJ1, SYNJ2, MTMR3, BTRC, MTMR7, MTMR4, ROCK2, BAG4, LPIN2, PHACTR2, SMG7, NUAK1, CTDSP2, FARP1, CTDSPL, DLC1, TAB1, ARPP19, DUSP14, PTPN21, PTPRT, DUSP10, LMTK2, PPP6R1, SACM1L, PHLPP2, RRP1B, ANKLE2, LPIN1, PHLPP1, SMG5, NSMF, PPP1R16B, PTPN18, DAPP1, PALD1, NT5DC3, ZFYVE1, CYCS, SSH1, SYTL2, DUSP23, RPRD1A, PPP6R3, PPP2R2D, INPP5E, SLC39A10, PPM1H, PDP2, SLC7A14, CTDSP1, ENOPH1, PCIF1, WNK1, MTMR9, DUSP16, SGPP1, ZCCHC9, FAM220A, PPP1R15B, SSH2, TIMM50, FAM122A, SPPL3, WDR81, PPM1M, NANP, DUSP18, PPM1L, PPP4R2, PPTC7, SPRED1, CNEP1R1, BOD1L1, PPP1R37
BP	GO:0032970	regulation of actin filament-based process	127/3408	8.23E-10	ABL1, ABL2, ADD1, ARF1, ARF6, RHOA, RHOB, ARHGDIA, ATP2A2, CACNA1C, CAMK2D, CAPZA2, CAV1, CD47, CDC42, CFL1, CFL2, CCR7, CNN2, CRK, DSC2, ECT2, S1PR1, EDN1, EFNA5, EPS8, FER, GRB2, ARHGAP35, NCKAP1L, ILK, JUP, KCNJ2, LIMK1, LRP1, SMAD4, MDK, MEF2C, MET, MYH9, MYO1C, NCK1, NF2, NOTCH2, NTRK3, PAK3, PDE4D, PDGFA, PDGFRA, PRKCE, PROX1, PTGER4, TWF1, PXN, RASA1, RDX, RGS4, CX3CL1, SDC4, SFRP1, SLC9A1, SPTAN1, SPTBN1, STC1, TESK1, TGFBR1, TRPM2, TSC1, RND2, NCK2, CDK10, NRP1, WASF1, WASL, LATS1, TAOK2, ROCK2, BAG4, NOS1AP, SEMA3E, FCHSD2, ARPC5, ACTR2, ARPC2, AKAP9, ABI2, WASF2, TENM1, DLC1, RAPGEF3, CDC42EP2, NCKAP1, IQGAP2, DSTN, CIT, FAM107A, AKAP13, RHOBTB3, LIMCH1, KANK1, CLASP1, COTL1, RHOQ, CD2AP, TMOD2, WNT4, ARHGAP17, FMN2, SPIRE1, VANGL2, TAOK1, RHOU, MLST8, PLEKHG2, ARHGAP28, SYNPO2L, DIXDC1, PHLDB2, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, SIGLEC15, SH3PXD2B, FMN1
BP	GO:0034329	cell junction assembly	89/3408	1.06E-09	ABL1, ACTB, ACTN4, APC, RHOA, BCL2, DST, CAV1, RUNX1, CBFB, CDC42, CDH6, CTNNA1, CTNNB1, CTNND1, ECT2, EFNA5, FN1, GJA1, GJB1, RAPGEF1, IKBKB, ILK, ITGA6, ITGA5, JUP, LAMC1, LAMC2, LRP1, SMAD7, MMP14, MYO1C, OPHN1, PKP1, PLEC, PRKCA, PKN2, PTEN, PTPRJ, PTPRK, RAP1B, SDC4, SFRP1, SLC9A1, SNAI2, SNAI1, SRC, SRF, STRN, THBS1, TLN1, TNS1, TSC1, VCL, VEGFA, FZD5, PKP4, IQGAP1, NRP1, LDB1, DLG5, TAOK2, MAP4K4, ROCK2, RAPGEF2, SLK, PDCD6IP, GJC1, DLC1, FAM107A, LIMCH1, NFASC, CLASP1, PIP5K1C, CORO1C, WNT4, FBLIM1, RCC2, PARD3, HEG1, EPB41L5, PEAK1, PARD6B, PHLDB2, MTDH, WHAMM, FLCN, HIPK1, FMN1
BP	GO:0048863	stem cell differentiation	93/3408	1.29E-09	ABL1, JAG1, BMP7, BMPR1A, ZFP36L2, RUNX2, RUNX1, CBFB, CDK6, CFL1, CHD2, EDN1, EFNB1, ERCC2, FOXC1, FN1, GATA2, GATA3, GATA6, NRG1, HIF1A, FOXA1, HNRNPU, HOXA7, HES1, RBPJ, ISL1, JARID2, KIT, LMO2, LRP6, SMAD4, MEF2C, KITLG, KMT2A, FOXO4, MSX1, MYB, PAX2, PDGFRA, MAPK1, MAPK3, EIF2AK2, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTPRC, SFRP1, SNAI2, SOX11, SRF, STAT3, TAL1, HNF1B, TCF3, TP53, TWIST1, XRCC5, HMGA2, FZD1, SEMA7A, TP63, NRP1, ALDH1A2, LDB1, PSMF1, PUM1, SEMA3E, SETD1A, FGF19, PSME3, PSMD14, SEMA3A, SEMA4B, SOX21, MTF2, PSME4, CORO1C, GREM1, SOX8, YTHDF2, PUS7, SEMA4C, SEMA6A, ITCH, FAM172A, KBTBD8, MSI2, RDH10
BP	GO:0031346	positive regulation of cell projection organization	125/3408	1.37E-09	ABL2, APC, ARF1, RHOA, ARHGDIA, ATP7A, BDNF, BMP7, BMPR2, SCARB2, CDC42, CCR7, CNTN1, CUX1, DVL3, EFNA5, MEGF8, MARK2, EP300, EPHA4, EPS8, EZH2, FMR1, FN1, KAT2A, GDI1, GOLGA4, RAPGEF1, ARHGAP35, HTT, HSPA5, ILK, ITGA6, ITGA3, KIT, L1CAM, LIMK1, LRP1, LYN, CAPRIN1, MAP1B, MAPT, MDK, NCK1, NTRK3, OPA1, PAFAH1B1, PAK3, MAPK6, TWF1, PTPRD, RGS2, ROBO1, RREB1, CX3CL1, SKIL, SRC, SRF, VAMP7, SYT1, TGFBR1, TIAM1, VEGFA, VLDLR, RND2, SF3A2, FZD1, FZD4, SEMA7A, DYNLL1, SNX3, IQGAP1, NRP1, WASL, KALRN, DLG5, NTN1, CEP135, RAPGEF2, PLEKHM1, ACTR2, ARPC2, WASF2, TENM1, CDC42EP2, NCKAP1, CPEB3, NLGN1, TRAK1, SHANK2, RAB21, KDM1A, PLXND1, ATMIN, RHOQ, CORO1C, FAM98A, SS18L1, AUTS2, NPTN, NIN, SYT17, RAB8B, C21orf91, ANLN, TMEM106B, RRN3, FNBP1L, TENM3, CAMK1D, SMURF1, KIDINS220, CREB3L2, NDRG4, METRN, MUL1, AKIRIN1, KCTD17, BHLHB9, NAV3, PLXNA4, SYT2, DAB2IP, CEP120, AGRN
BP	GO:0030099	myeloid cell differentiation	133/3408	1.45E-09	ACVR1B, ADAR, ADD1, JAG1, BCL6, ZFP36L1, CAMK4, CASP3, RUNX1, CBFB, CDC42, CDK6, CEBPB, CEBPG, CCR7, CREB1, CREBBP, MAPK14, CSF1, CTNNB1, EP300, EPAS1, ERCC2, ESRRA, FBN1, FOXO3, G6PD, GABPA, GATA2, GATA3, GNAS, NCKAP1L, HIF1A, HMGB3, HOXA5, HOXA7, HOXA9, HOXB8, RBPJ, IREB2, IRF4, ITPKB, JUN, KIT, LBR, LYN, MEF2C, MEIS2, KITLG, KMT2A, MYC, MYH9, CNOT4, NOTCH2, SLC11A2, PAFAH1B1, PDE1B, PIP4K2A, PKNOX1, PML, POU4F1, PRKCA, PTPN11, PURB, RARG, RB1, SFRP1, SP3, SRC, SRF, STAT1, STAT3, STAT5B, TAL1, TFRC, TGFBR3, THBS1, THRA, KLF10, VEGFA, ZFP36, KAT6A, NR4A3, KMT2D, PABPC4, FADD, KAT2B, LDB1, SH3PXD2A, CTR9, SETD1A, KMT2B, RASSF2, PTBP3, SH2B3, TSPAN2, WASF2, TRIB1, FSTL3, KLF2, PIAS3, TOB2, PRDX3, TNRC6B, SIRT1, RBFOX2, SIN3A, ZNF385A, AGO1, FOXP1, EIF2AK1, TNRC6A, HIPK2,

					TET2, SNRK, NCAPG2, SLC25A38, FBXW7, KMT2E, FAM20C, TNRC6C, KMT2C, CDC73, DPY30, SFXN1, BATF2, FAM210B, CD109, ZBTB46, ZNF675, AGO3, AGO4, SIGLEC15
BP	GO:1903706	regulation of hemopoiesis	147/3408	1.72E-09	ABL1, ACVR1B, ADA, JAG1, RHOA, AXL, BCL6, PRDM1, ZFP36L1, ZFP36L2, CAMK4, RUNX1, RUNX3, CBFB, CDK6, CEBPB, CLPTM1, CREB1, CREBBP, MAPK14, CSF1, CTNNB1, CYLD, EGR3, EP300, ERBB2, ESRRA, FBN1, FOXC1, FOXO3, GABPA, GATA2, GATA3, KAT2A, GNAS, NCKAP1L, HIF1A, HMGB3, HOXA5, HOXA7, HOXA9, HOXB8, HES1, IL7R, IL18, IRF1, IRF4, ITPKB, JUN, LMO2, LYN, SMAD7, MDK, MEF2C, MEIS2, KITLG, KMT2A, MMP14, MYB, MYC, CNOT4, NOTCH2, PIM1, POU4F1, PRKCA, EIF2AK2, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTPRC, PURB, RAG1, RARG, RB1, SFRP1, SOS1, STAT1, STAT3, STAT5B, SYK, TAL1, TCF3, ZEB1, THBS1, KLF10, XBP1, ZFP36, NR4A3, KMT2D, SOCS1, TNFSF9, FADD, KAT2B, LDB1, AP3D1, CD83, PSMF1, CTR9, SOCS5, SETD1A, KMT2B, RASSF2, PSME3, PSMD14, TRIB1, FSTL3, BTN2A2, PIAS3, TOB2, DUSP10, TNRC6B, PSME4, RBFOX2, SIN3A, AGO1, FOXP1, PRELID1, TNRC6A, YTHDF2, PUS7, NCAPG2, FBXW7, PCID2, KMT2E, CYP26B1, ZMIZ1, TNRC6C, KMT2C, CDC73, ITCH, DPY30, FNIP1, MYSM1, FAM210B, ZBTB46, ZNF675, AGO3, AGO4, FLCN, SIGLEC15, ATP11C, ATXN1L, NRARP
BP	GO:0001952	regulation of cell-matrix adhesion	54/3408	1.72E-09	ABL1, JAG1, RHOA, BCL2, BCL6, CDK6, CCR7, CSF1, DAG1, EFNA5, EMP2, GSK3B, HOXA7, ILK, JUP, LRP1, MMP14, NF2, SERPINE1, PIK3CB, PTEN, PTPRJ, RASA1, CX3CL1, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VEGFA, IQGAP1, NRP1, LDB1, MAP4K4, ROCK2, ONECUT2, SEMA3E, SLK, DLC1, POSTN, FAM107A, LIMCH1, CLASP1, CORO1C, MINK1, WNT4, FERMT1, RCC2, EPB41L5, PEAK1, PHLDB2, ACER2, FMN1
BP	GO:0048732	gland development	137/3408	1.78E-09	ABL1, ADA, AK4, AKT2, AR, ARF6, ATM, ATP7A, CCND1, BCL2, BMP7, BMPR1A, CAV1, CDKN1B, CEBPB, CEBPG, CREB1, CRKL, CSF1, CTNNB1, DAG1, EGFR, EPHB3, EZH2, FKBP4, FOXC1, GATA2, GATA3, GATA6, GJA1, GOT2, ARHGAP35, NRG1, HIF1A, HK2, FOXA1, HNF4A, HNRNPD, HOXA3, HOXA5, HOXA9, HOXB3, HOXD13, HES1, ID4, IGF2, IGF2R, IGFBP5, RBPJ, INSR, ISL1, JARID2, JUN, KRAS, LRP6, SMAD2, SMAD4, MAN2A1, MDK, MET, MSX1, NFIB, NKX3-1, OAS2, PAX6, PBX1, PDGFA, PDGFRA, PGR, SERPINE2, PKD1, PKM, PML, POU3F2, PPAT, MAPK1, MAPK3, PRLR, PROX1, PTCH1, PTEN, RAG1, RARG, ROBO1, RREB1, SFRP1, SNAI2, SP3, SRC, SRF, AURKA, TBX3, HNF1B, TGFBR1, TGFBR3, THRA, UMPS, USF2, VDR, VEGFA, WNT7B, XBP1, CUL3, TP63, IRS2, FADD, NRP1, SOCS2, ALDH1A2, BTRC, KALRN, LATS1, NTN1, ONECUT2, BCL2L11, FSTL3, CITED2, SEMA3A, KDM5B, FRS2, CIT, SEC63, PLXND1, UPF2, DKK3, SIX4, WNT4, FBXW7, SULF2, GNPNAT1, BCL11B, WDR77, PTCD2, ARID5B, IQGAP3, E2F7, ZDHHC21
BP	GO:0051056	regulation of small GTPase mediated signal transduction	113/3408	2.21E-09	ABL1, ABL2, ADCYAP1R1, ARF6, RHOA, RHOB, ARHGAP1, ARHGDIA, ARRB1, BCL6, CBL, CDC42, COL3A1, CRK, CRKL, CSF1, ECT2, EPHB2, EPS8, FOXM1, GDI1, GRB2, RAPGEF1, ARHGAP35, NRG1, ITGA3, ITGB1, ITPKB, KRAS, LYN, MET, KITLG, NOTCH2, OPHN1, RASA1, RDX, ROBO1, SHC1, SOS1, SRC, TIAM1, TIMP2, TNFAIP1, TRIO, SHOC2, CUL3, MADD, IRS2, NRP1, SYNGAP1, SQSTM1, KALRN, F2RL3, ARHGEF2, CYTH3, CYTH1, ARHGAP29, MAP4K4, RALGPS1, ARHGEF17, DENND4B, MFN2, FARP1, SPRY1, NET1, DLC1, VAV3, ARFGEF2, STAMBP, GNA13, AKAP13, RASA3, RAP1GAP2, KANK1, ARHGEF9, PSD3, ARHGEF12, RHOQ, CD2AP, PLEKHG3, SIPA1L1, AUTS2, CDON, RALGPS2, ARHGAP17, ARFGAP1, CDC42SE1, RALGAPA2, HEG1, SIPA1L2, RHOU, PLEKHG2, MAPKAP1, ARHGAP28, SYNPO2L, PREX2, ARHGAP39, SPRY4, KCTD10, SYDE2, ARHGEF39, CGNL1, ARHGAP18, ARHGAP12, ARAP2, SSX2IP, FGD4, DAB2IP, PLEKHG4B, AMOT, FLCN, SPATA13, IQSEC3
BP	GO:0032956	regulation of actin cytoskeleton organization	114/3408	2.54E-09	ABL1, ABL2, ADD1, ARF1, ARF6, RHOA, RHOB, ARHGDIA, CAPZA2, CD47, CDC42, CFL1, CFL2, CCR7, CRK, ECT2, S1PR1, EDN1, EFNA5, EPS8, FER, GRB2, ARHGAP35, NCKAP1L, ILK, LIMK1, LRP1, SMAD4, MDK, MEF2C, MET, MYO1C, NCK1, NF2, NOTCH2, NTRK3, PAK3, PDGFA, PDGFRA, PRKCE, PROX1, PTGER4, TWF1, PXN, RASA1, RDX, RGS4, CX3CL1, SDC4, SFRP1, SLC9A1, SPTAN1, SPTBN1, TESK1, TGFBR1, TRPM2, TSC1, RND2, NCK2, CDK10, NRP1, WASF1, WASL, LATS1, TAOK2, ROCK2, BAG4, SEMA3E, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, WASF2, TENM1, DLC1, RAPGEF3, CDC42EP2, NCKAP1, IQGAP2, DSTN, CIT, FAM107A, AKAP13, RHOBTB3, LIMCH1, KANK1, CLASP1, COTL1, RHOQ, CD2AP, TMOD2, WNT4, ARHGAP17, FMN2, SPIRE1, VANGL2, TAOK1, RHOU, MLST8, PLEKHG2, ARHGAP28, SYNPO2L, DIXDC1, PHLDB2, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, SIGLEC15, SH3PXD2B, FMN1
BP	GO:0046578	regulation of Ras protein signal transduction	87/3408	2.54E-09	ABL1, ABL2, ARF6, ARHGDIA, ARRB1, BCL6, CBL, COL3A1, CRK, CRKL, CSF1, ECT2, EPHB2, EPS8, FOXM1, GRB2, RAPGEF1, ARHGAP35, NRG1, ITGA3, ITGB1, ITPKB, KRAS, LYN, MET, KITLG, NOTCH2, OPHN1, RASA1, RDX, ROBO1, SHC1, SOS1, TIAM1, TIMP2, TNFAIP1, TRIO, SHOC2, CUL3, MADD, IRS2, NRP1, SYNGAP1, SQSTM1, KALRN, F2RL3, ARHGEF2, CYTH3, CYTH1, MAP4K4, RALGPS1, ARHGEF17, DENND4B, MFN2, FARP1, SPRY1, NET1, DLC1, VAV3, ARFGEF2, STAMBP, AKAP13, RASA3, KANK1, ARHGEF9, PSD3, ARHGEF12, PLEKHG3, AUTS2, RALGPS2, ARFGAP1, CDC42SE1, HEG1, PLEKHG2, MAPKAP1, SYNPO2L, PREX2, SPRY4, KCTD10, ARHGEF39, SSX2IP, FGD4, DAB2IP, PLEKHG4B, FLCN, SPATA13, IQSEC3
BP	GO:0033673	negative regulation of kinase activity	92/3408	2.54E-09	ABL1, ADAR, ADARB1, APC, BMP7, CASP3, CAV1, CBL, CDKN1A, CDKN1B, CSK, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EPHB2, GNAQ, HMGCR, HNRNPU, DNAJA1, IGF1R, ILK, IPO5, LRP6, LYN, MAPT, MEN1, NCK1, NF2, PAK2, PPP2CA, PPP2R1A, PKIA, PRKAR1A, PRKAR2A, PTEN, PTPN1, PTPRC, PTPRJ, RB1, RGS2, RGS4, SFRP1, SORL1, TESK1, NR2F2, YWHAG, SOCS1, IRS2, KAT2B, GPRC5A, LATS1, SOCS5, SH2B3, HIPK3, TRIB1, SPRY1, PRDX3, DUSP14, PTPRT, DUSP10, STK38, SIRT1, CORO1C, IBTK, LATS2, PDCD4, TRIB2, ERRFI1, LAX1, DUS2, CAMK2N1, HEG1, CEP85, AIDA, WNK1, DUSP16, SH3BP5L, SPRY4, AKT1S1, ITPRIP, PIK3IP1, SOCS4, SMCR8, DUSP18, DAB2IP, SPRED1, ZNF675, SPRED2, SPRED3
BP	GO:0006469	negative regulation of protein kinase activity	86/3408	3.00E-09	ABL1, ADAR, ADARB1, APC, BMP7, CASP3, CAV1, CBL, CDKN1A, CDKN1B, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EPHB2, GNAQ, HMGCR, DNAJA1, IGF1R, ILK, IPO5, LRP6, LYN, MEN1, NCK1, NF2, PAK2, PPP2CA, PPP2R1A, PKIA, PRKAR1A, PRKAR2A, PTEN, PTPN1, PTPRC, PTPRJ, RB1, RGS2, RGS4, SFRP1, SORL1, TESK1, NR2F2, YWHAG, SOCS1, KAT2B, GPRC5A,

					LATS1, SOCS5, SH2B3, HIPK3, TRIB1, SPRY1, DUSP14, PTPRT, DUSP10, STK38, SIRT1, CORO1C, IBTK, LATS2, PDCD4, TRIB2, ERRFI1, LAX1, DUS2, CAMK2N1, HEG1, CEP85, AIDA, WNK1, DUSP16, SH3BP5L, SPRY4, AKT1S1, ITPRIP, SOCS4, SMCR8, DUSP18, DAB2IP, SPRED1, ZNF675, SPRED2, SPRED3
BP	GO:0061458	reproductive system development	136/3408	3.19E-09	ADA, ADM, AR, ARRB1, ARRB2, ATM, ATRX, AXL, BAK1, CCND1, BCL2, BCL2L1, PRDM1, BMP7, BMPR2, ZFP36L1, CASP3, CBL, CCNF, CDKN1B, CEBPB, CRKL, MAPK14, CTNNA1, CTNNB1, CTSB, DCN, EGFR, EPAS1, BPTF, FKBP4, FOXC1, FOXO3, GATA2, GATA3, GATA6, GJA1, GJB1, GRB2, HIF1A, FOXA1, HOXA9, HOXD13, HES1, HSPA5, ID4, IGF2, RBPJ, INSR, ITGB8, KIT, LRP6, SMAD4, MAP3K4, MEN1, KITLG, MME, MMP14, NKX3-1, PDGFB, PDGFRA, PGR, SERPINE2, PKD1, PPARD, MAPK1, MAPK3, PTCH1, PTEN, PTGIS, PTPN11, RARG, KDM5A, SFRP1, SNAI1, SP3, SRC, STC1, STK4, TBX3, TCF7, NR2F2, TGFBR1, TMF1, TYRO3, VDR, VEGFA, WNT7B, WNT2B, SF1, CSDE1, FZD5, FOSL1, NRIP1, ARID1A, FZD4, STC2, TP63, AKR1C3, TNFSF10, SGPL1, HAND1, PCYT1B, ADAMTS1, KMT2B, BCL2L11, FSTL3, CITED2, SEMA3A, KDM5B, FRS2, PRDX3, RHOBTB3, VASH1, FNDC3A, SIRT1, NIPBL, DAZAP1, SOX8, ARID4B, SIX4, WNT4, LGR4, UBE2Q1, CHD7, BIRC6, PLEKHA1, WDR77, ARID5B, ZNF830, PLCD3, TBC1D20, E2F7, RNF38, RDH10, AGO4
BP	GO:0043401	steroid hormone mediated signaling pathway	72/3408	3.34E-09	AR, RHOA, ARRB2, BMP7, BRCA1, CALR, RUNX1, CBFB, CRY2, CTNNB1, DAB2, DDX5, EP300, ESR2, ESRRA, ESRRG, FHL2, FKBP4, NR5A2, NR6A1, NR3C1, FOXA1, HNF4A, DNAJA1, ISL1, NEDD4, NKX3-1, PGR, PPARA, PPARD, RAN, RARG, RB1, RNF4, RORA, RORB, SFRP1, SRC, TAF1, NR2F2, THRA, NR2C2, NR1H2, VDR, NR4A3, KMT2D, NCOA3, NRIP1, ARID1A, TP63, LATS1, CLOCK, NCOR1, NR1D2, PGRMC2, DDX17, ABHD2, AKAP13, CNOT1, UFL1, SIRT1, RBFOX2, WBP2, HEYL, FOXP1, STRN3, UBR5, PMEPA1, CALCOCO1, PAQR8, EGLN2, KCTD6
BP	GO:0043409	negative regulation of MAPK cascade	72/3408	3.34E-09	ABL1, ARRB1, BMP7, CAV1, CSK, CYLD, DAG1, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EPHB2, FOXM1, FOXO1, GBP1, RAPGEF1, HMGCR, DNAJA1, IGF1R, LYN, SMAD4, MEN1, MYC, NF2, PAFAH1B1, PIN1, PPP2CA, PPP2R1A, PTEN, PTPN1, PTPRC, PTPRJ, PTPRR, RGS2, RGS4, SFRP1, SORL1, TIMP3, EIF3A, KLF4, NCOR1, SH2B3, HIPK3, SPRY1, TNIP1, BTN2A2, ZMYND11, DUSP14, DUSP10, STK38, PDCD4, ERRFI1, LAX1, CAMK2N1, NDRG2, SEMA6A, PRDM15, AIDA, DUSP16, SPRY4, ITCH, SIRPA, DUSP18, DAB2IP, CNKSR3, SPRED1, ZNF675, SPRED2, FLCN, SPRED3
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	115/3408	3.34E-09	ABL1, ACVR1B, ACVR2B, RHOA, ARRB2, BMP3, BMP7, BMPR1A, BMPR2, CAV1, RUNX2, CBL, COL1A2, COL3A1, CREB1, CREBBP, MAPK14, DAB2, DDX5, MEGF8, EGR1, EP300, FBN1, FBN2, FKBP1A, FNTA, FUT8, GCNT2, HIVEP1, HNF4A, HES1, HSPA5, RBPJ, ILK, IRAK1, ITGA3, JUN, LNPEP, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEN1, MSX1, NEO1, FURIN, PCSK6, PIN1, PML, MAPK3, PTPRK, PXN, SFRP1, SKI, SKIL, SORL1, SOX11, SPTBN1, SRC, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, UBE2D3, ZNF8, USP9X, FZD1, ITGA8, CHRD, ADAM9, MTMR4, ONECUT2, ZFYVE16, TOB1, GDF11, FSTL3, CITED2, TAB1, FST, SUB1, FSTL1, DKK1, PEG10, ZC3H3, SIRT1, ZNF451, APPL1, GREM1, DKK3, PDCD4, HIPK2, TRIM33, NLK, RNF111, FERMT1, PARD3, PMEPA1, RGMA, SMURF1, TGIF2, PBLD, BTBD11, WFIKKN2, ACVR1C, CD109, PPM1L, BMPER, FLCN, CRB2, RBPMS2, BMP8A, RNF165
BP	GO:0048608	reproductive structure development	135/3408	3.55E-09	ADA, ADM, AR, ARRB1, ARRB2, ATM, ATRX, AXL, BAK1, CCND1, BCL2, BCL2L1, PRDM1, BMP7, BMPR2, ZFP36L1, CASP3, CBL, CCNF, CDKN1B, CEBPB, CRKL, MAPK14, CTNNA1, CTNNB1, CTSB, DCN, EGFR, EPAS1, BPTF, FKBP4, FOXC1, FOXO3, GATA2, GATA3, GATA6, GJA1, GJB1, GRB2, HIF1A, FOXA1, HOXA9, HOXD13, HES1, HSPA5, ID4, IGF2, RBPJ, INSR, ITGB8, KIT, LRP6, SMAD4, MAP3K4, MEN1, KITLG, MME, MMP14, NKX3-1, PDGFB, PDGFRA, PGR, SERPINE2, PKD1, PPARD, MAPK1, MAPK3, PTCH1, PTEN, PTGIS, PTPN11, RARG, KDM5A, SFRP1, SNAI1, SP3, SRC, STC1, STK4, TBX3, TCF7, NR2F2, TGFBR1, TMF1, TYRO3, VDR, VEGFA, WNT7B, WNT2B, SF1, CSDE1, FZD5, FOSL1, NRIP1, ARID1A, FZD4, STC2, TP63, AKR1C3, TNFSF10, SGPL1, HAND1, PCYT1B, ADAMTS1, KMT2B, BCL2L11, FSTL3, CITED2, SEMA3A, KDM5B, FRS2, PRDX3, RHOBTB3, VASH1, FNDC3A, SIRT1, NIPBL, DAZAP1, SOX8, ARID4B, SIX4, WNT4, LGR4, CHD7, BIRC6, PLEKHA1, WDR77, ARID5B, ZNF830, PLCD3, TBC1D20, E2F7, RNF38, RDH10, AGO4
BP	GO:0033044	regulation of chromosome organization	113/3408	3.93E-09	APC, ARRB1, ATM, ATR, ATRX, BCL6, BRCA1, CAMK2D, CCT6A, CHEK1, CTNNB1, DKC1, DNMT3B, DUSP1, FMR1, GATA2, GATA3, KAT2A, HMGA1, HNRNPC, HNRNPD, HNRNPU, IGF2, IK, ISL1, JARID2, LIG4, MAD2L1, SMAD4, MAPT, MECP2, MAP3K4, KMT2A, MLLT6, MTHFR, MYB, MYC, PARN, PML, MAPK1, MAPK3, MAPK8, RAD21, RB1, KDM5A, UPF1, RNF4, SET, SKI, SNAI2, SNCA, SRC, TAL1, TP53, TWIST1, UBE2N, VEGFA, XRCC5, CUL3, TNKS, RPS6KA4, AURKB, RPS6KA5, TRIP13, TRIP12, ATG5, CTR9, SETD1A, KMT2B, SMG7, CTCF, TLK2, KAT7, MTF2, MORC2, KDM1A, SMG1, PHF8, SMG5, SIRT1, WBP2, NIPBL, SIN3A, ZNF451, AUTS2, SENP6, UBR5, RTEL1, ATAD2B, XRN1, GNL3L, BCOR, PINX1, RIF1, SETD5, ATF7IP, RIOK2, PCID2, KMT2E, YLPM1, HECW2, MIER1, NSD1, NABP2, HMBOX1, NAA40, TET1, SETD7, SLX4, TADA2B, RMI2, SPTY2D1, FLCN
BP	GO:0045666	positive regulation of neuron differentiation	120/3408	4.48E-09	ABL2, ARF1, RHOA, ARHGDIA, BCL2, BCL6, BDNF, BMP7, BMPR2, SCARB2, CNTN1, CSNK1D, CSNK1E, CUX1, DLX2, DNMT3B, DVL3, ECT2, EFNA5, MEGF8, EIF4G1, MARK2, EP300, EPHA4, EZH2, FMR1, FN1, GATA2, GDI1, GOLGA4, RAPGEF1, ARHGAP35, FOXA1, HSPA5, ILK, ITGA6, ITGA3, L1CAM, LIMK1, LRP1, LYN, CAPRIN1, MAP1B, MAPT, MDK, MEF2C, NCK1, NTRK3, OPA1, PAFAH1B1, PAK3, MAPK6, PROX1, PTEN, TWF1, PTPRD, RGS2, ROBO1, CX3CL1, SKIL, SOX11, SRF, VAMP7, SYT1, TCF4, TCF3, ZEB1, TIAM1, TIMP2, VEGFA, VLDLR, RND2, SF3A2, FZD1, FZD4, SEMA7A, SNX3, IQGAP1, NRP1, SOCS2, KALRN, SPAG9, ARHGEF2, DLG5, NTN1, RAPGEF2, ACTR2, CPEB3, NLGN1, TRAK1, SHANK2, DKK1, RAB21, KDM1A, PLXND1, MMD, SIN3A, SS18L1, HEYL, NPTN, CDON, NIN, SYT17, C21orf91, TMEM106B, RRN3, TENM3, CAMK1D, SMURF1, KIDINS220, TGIF2, CREB3L2, NDRG4, METRN, MUL1, BHLHB9, PLXNA4, SYT2, KCTD11, DAB2IP
BP	GO:0010810	regulation of cell-substrate adhesion	80/3408	4.79E-09	ABL1, ACTN4, JAG1, RHOA, BCL2, BCL6, CALR, CDC42, CDK6, CCR7, COL1A1, CRK, CRKL, CSF1, DAG1, EFNA5, EMP2, FN1, GBP1, GCNT2, GSK3B, HOXA7, ILK, ITGA6, ITGA3, ITGA5, JUP, LRP1, MDK, MEN1, ATXN3, MMP14, NEDD9, NF2, NID1, SERPINE1, PIK3CB, PRKCE, PTEN, PTPRJ, RASA1, RREB1, CX3CL1, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VEGFA, FZD4, IQGAP1,

					NRP1, LDB1, MAP4K4, ROCK2, ONECUT2, SEMA3E, SLK, SPOCK2, ARPC2, DLC1, AGR2, POSTN, FAM107A, MMRN1, LIMCH1, KANK1, CLASP1, CORO1C, MINK1, WNT4, FERMT1, RCC2, EPB41L5, PEAK1, PHLDB2, MYADM, ACER2, FMN1
BP	GO:0048762	mesenchymal cell differentiation	81/3408	5.03E-09	JAG1, BCL2, BMP7, BMPR1A, CFL1, COL1A1, CTNNB1, DAB2, DAG1, DDX5, EDN1, EFNB1, EZH2, FOXC1, FN1, GCNT2, GSK3B, HDAC2, NRG1, HIF1A, FOXA1, HNRNPAB, HES1, RBPJ, ISL1, LOXL2, LRP6, SMAD2, SMAD4, SMAD7, MDK, MEF2C, KITLG, MSX1, PAX2, PPP2CA, MAPK1, MAPK3, PTEN, SFRP1, SNAI2, SNAI1, SOX11, STAT1, TGFBR1, TGFBR3, TIAM1, TWIST1, HMGA2, SEMA7A, NRP1, ALDH1A2, DLG5, SEMA3E, FGF19, SPRY1, SEMA3A, OLFM1, SEMA4B, DDX17, PHLDB1, CLASP1, CORO1C, HEYL, GREM1, PDCD4, SOX8, ADIPOR1, WNT4, SEMA4C, TRIM62, SEMA6A, EPB41L5, PBLD, FAM172A, KBTBD8, PHLDB2, AMER1, DAB2IP, RDH10, CRB2
BP	GO:1903311	regulation of mRNA metabolic process	108/3408	5.45E-09	ZFP36L1, ZFP36L2, CCNT1, MAPK14, DDX5, DYRK1A, EIF4G1, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPK, HNRNPU, TNPO1, MBNL1, HNRNPM, NCBP1, NUP98, PARN, PKP1, PRKCA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, UPF1, SET, SRSF1, SRSF2, SRSF4, SRSF7, TRA2B, SNRPA, SON, XPO1, ZFP36, BTG2, FXR1, PABPN1, ANP32A, PABPC4, CNOT8, ROCK2, PSMF1, CTR9, PUM1, RBM19, THRAP3, TOB1, MBNL2, PSME3, PSMD14, SYNCRIP, DDX17, PAIP1, IGF2BP1, IGF2BP3, CELF2, AHCYL1, SRSF10, PAPOLA, RNPS1, HNRNPA0, CPSF6, U2AF2, CPEB3, CNOT1, SAMD4A, TNRC6B, ZC3H3, PSME4, LARP1, TARDBP, RBFOX2, GIGYF2, SERBP1, DAZAP1, PABPC1, RBMX, TNRC6A, RBM15B, MYEF2, YTHDF2, XRN1, ALKBH5, SAMD4B, RBM23, SMU1, RBM38, PCID2, MBNL3, DCP1A, ZC3HAV1, TNRC6C, METTL14, RBM25, CDC73, PTCD2, CPSF7, FAM172A, TRIM71, SREK1, PDE12, YTHDF3, RBMXL1
BP	GO:0034976	response to endoplasmic reticulum stress	98/3408	5.95E-09	ADD1, AMFR, ATP2A2, BAK1, CCND1, BCL2, BCL2L1, CALR, CANX, CAV1, CEBPB, TPP1, ATF6B, EIF2S1, EP300, EXTL2, EXTL3, GFPT1, GRINA, GSK3B, HDGF, UBE2K, DNAJB2, HSPA5, IGFBP1, ITPR1, JUN, DNAJB9, ATXN3, NCK1, OPA1, PML, EIF2AK2, PTPN1, SEL1L, SHC1, SSR1, TMBIM6, THBS1, TLN1, TP53, UBE2G2, VCP, XBP1, TRIM25, RNF103, NCK2, STC2, USP13, ATP6V0D1, VAPB, UBE4A, GOSR2, EDEM1, HERPUD1, BCL2L11, CTDSP2, BCAP31, TRIM13, UBE4B, HYOU1, AGR2, SERINC3, ERLIN2, UBXN4, UFL1, SIRT1, TARDBP, BBC3, SERP1, USP25, UBQLN2, UBQLN1, DERL2, TXNDC12, BFAR, UBE2J1, GET4, DNAJC10, DNAJB12, FKBP14, TMEM33, YOD1, NPLOC4, ARFGAP1, UGGT1, CCDC47, TSPYL2, HERPUD2, CREB3L2, EDEM3, TMUB1, SESN2, ATG10, RHBDD1, SYVN1, PPP1R15B, DAB2IP
BP	GO:0046777	protein autophosphorylation	85/3408	6.01E-09	ABL1, ABL2, ACVR1B, ATM, ATR, CALM1, CALM2, CALM3, CAMK4, CAMK2A, CAMK2D, CAV1, CSK, DAPK1, DYRK1A, EGFR, EIF2S1, MARK2, EPHA4, EPHA7, EPHB3, EPHB4, ERBB2, FER, FGFR3, FLT4, MKNK2, GSK3B, IGF1R, INSR, IRAK1, JUN, KIT, LYN, MAP3K3, MAP3K9, PAK2, PDGFA, PDGFB, PDGFRA, ENPP1, PIM1, PPP2R5D, MAPK3, EIF2AK2, PTPRC, RAP2A, RAP2B, SRC, STK4, AURKA, STK10, SYK, TAF1, TESK1, TYRO3, VEGFA, ULK1, STK24, MKNK1, IQGAP1, DYRK1B, AURKB, STK17B, TAOK2, SLK, RASSF2, MELK, TNK2, GPNMB, AAK1, LMTK2, SMG1, PASK, GREM1, EIF2AK1, MINK1, NLK, ERRFI1, RIOK2, TAOK1, RAP2C, WNK1, PEAK1, SIK1
BP	GO:0009314	response to radiation	138/3408	6.67E-09	AKT2, ALAD, RHOB, ARRB1, ATM, ATR, BAK1, CCND1, BCL2, BCL2L1, BRCA1, CALM1, CASP3, CBL, CDC25A, CDKN1A, CDS1, CHEK1, COL3A1, CREB1, CREBBP, CRY2, MAPK14, CTNS, DNMT3A, DNMT3B, DUSP1, ECT2, EGFR, EGR1, EIF2S1, ELK1, EP300, ERCC2, ERCC6, FECH, FMR1, FNTA, GATA3, GNAQ, GNB1, GRB2, HIF1A, HMGCR, HSPA5, ITGB1, JUN, JUND, KCNC1, KIT, KRAS, LIG4, MECP2, MEIS2, MAP3K4, MEN1, MME, MYC, NEDD4, OGG1, PDE1B, PML, PPP1CA, PPP1CB, PPP1CC, PRKAA1, MAPK8, PTPRC, PTPRK, RAD1, RAD51, RAG1, RBL2, CCL7, SFRP1, SLC1A2, SNAI2, ELOVL4, TAF1, TP53, TXN, USP1, VCAM1, XRCC5, YY1, HMGA2, SMC1A, CUL4B, PPM1D, BHLHE40, B4GALT2, SYNGAP1, PER3, PER2, USP2, MTA1, AURKB, CLOCK, TRIM13, NET1, UBE4B, CERS1, METAP2, TLK2, CEP250, KDM1A, SIRT1, SPIDR, SLC7A11, NIPBL, FBXL3, NPTN, TRIAP1, DTL, INO80, USP47, USP28, PLEKHB1, INIP, RIC8A, NUCKS1, AEN, NABP1, NDRG4, INTS3, NABP2, BRCC3, CAMKMT, RHNO1, RHBDD1, LZIC, BMF, TP53INP1, DCUN1D3, SIK1, SDE2, RNF168, BRAT1
BP	GO:1901888	regulation of cell junction assembly	43/3408	7.06E-09	ABL1, RHOA, CAV1, RUNX1, CBFB, EFNA5, GJA1, RAPGEF1, IKBKB, LRP1, MMP14, MYO1C, PTEN, PTPRJ, RAP1B, SDC4, SFRP1, SLC9A1, SNAI2, SNAI1, SRC, THBS1, TSC1, VEGFA, FZD5, IQGAP1, NRP1, LDB1, MAP4K4, ROCK2, RAPGEF2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, FMN1
BP	GO:0043393	regulation of protein binding	80/3408	7.08E-09	ABL1, ACTB, ADD1, AMFR, ARF6, ARRB1, ARRB2, BAK1, BCL2, BDNF, CAV1, CRK, CSNK1E, CTSZ, CYLD, DAB2, EIF2S1, MARK2, EP300, EPB41, EPHA4, FKBP1A, GSK3B, NRG1, HOXA3, DNAJB2, HSPA5, IFIT2, ISL1, LRP1, LRPAP1, MEF2C, MEN1, MET, NKX3-1, PDGFB, PIN1, PKD1, PLCL1, PPARA, PPP1CA, PPP2CA, MAPK3, MAPK8, PTPRF, RALB, RAN, SORL1, SRC, STK4, AURKA, STYX, TAF1, TCF7L2, TMBIM6, TERT, TGFBR1, TGFBR3, TIAM1, NRP1, AURKB, TRAF4, RAPGEF2, PLK2, MAPRE3, DKK1, KDM1A, USP33, PLXND1, LDLRAP1, HIPK2, CDON, NMD3, GNL3L, EPB41L5, AIDA, SPPL3, WFIKKN2, TTBK2, DAB2IP
BP	GO:0031589	cell-substrate adhesion	115/3408	7.08E-09	ABL1, ACTN4, JAG1, RHOA, AXL, BCL2, BCL6, CALR, CD44, CDC42, CDK6, CCR7, COL1A1, COL3A1, CRK, CRKL, CSF1, CTNNB1, DAG1, EFNA5, MEGF9, EMP2, EPHB3, FER, FN1, GBP1, GCNT2, GSK3B, HOXA7, ILK, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, JUP, L1CAM, LAMC1, LAMC2, LRP1, SMAD6, MDK, MEN1, ATXN3, MKLN1, MMP14, NEDD9, NF2, NID1, SERPINE1, PIK3CB, PKD1, PPARD, PRKCE, PTEN, PTPRJ, PTPRK, PXN, RAB1A, RASA1, RREB1, CX3CL1, SDC4, SFRP1, SLC9A1, SRC, SRF, THBS1, THBS3, TIAM1, TSC1, TYRO3, VCAM1, VCL, VEGFA, FZD4, ITGA8, ADAM9, IQGAP1, NRP1, LDB1, TAOK2, MAP4K4, ROCK2, ONECUT2, SEMA3E, SLK, SPOCK2, BCL2L11, ARPC2, DLC1, AGR2, POSTN, HPSE, LYVE1, FAM107A, MMRN1, LIMCH1, KANK1, CLASP1, CORO1C, MINK1, COL5A3, WNT4, FERMT1, RCC2, ADAMTS9, EPB41L5, PEAK1, ANTXR1, PHLDB2, MYADM, WHAMM, ACER2, FMN1

BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	110/3408	7.08E-09	ADORA2B, RHOA, ARRB1, ATP2B4, CCND1, CALM1, CALM2, CALM3, CCND2, CCNT1, CCNT2, CDKN1B, CRK, CRKL, MAPK14, CSK, DDX3X, DUSP5, DUSP6, DUSP7, DUSP9, DVL3, EDN1, EGFR, EPHA4, ERBB2, ERCC6, EZH2, FGF1, FGF2, RAPGEF1, NRG1, IGF2, ILK, INSR, IRAK1, IRAK2, KIT, KRAS, MAP3K1, MAP3K3, MAP3K4, KITLG, MAP3K9, NTRK3, PAK3, PDGFA, PDGFB, PIK3CB, PKD1, PPP2CA, PRKAA1, MAPK1, MAPK3, EIF2AK2, PROX1, PTPN1, PTPN11, PTPRC, RALB, ROBO1, RPS3, MAP2K4, SHC1, SNCA, SRC, STK4, SYK, ADAM17, TGFA, TGFBR1, THBS1, TIAM1, TPD52L1, UBE2N, UBE2V1, VEGFA, WNT7B, FZD5, HMGA2, FZD4, MADD, PEA15, ADAM9, IQGAP1, SPAG9, TAOK2, RAPGEF2, DAZAP2, TENM1, NOD1, TAB1, MAP3K2, FRS2, AKAP13, MAPRE3, DKK1, TAB2, MAPK8IP3, SIRT1, ETAA1, VANGL2, KIDINS220, TAOK1, MLST8, MUL1, IQGAP3, DAB2IP, EPGN, SLC27A1
BP	GO:0060562	epithelial tube morphogenesis	107/3408	7.08E-09	ABL1, ADM, AR, RHOA, RHOB, BCL2, BMP7, CASP3, CFL1, COL4A1, CSF1, CTNNB1, CTSZ, DAG1, DVL3, EDN1, EFNB2, MEGF8, EPHA4, EPHA7, FGF1, FGF2, GATA3, KAT2A, GJA1, ARHGAP35, HIF1A, FOXA1, HOXA5, HES1, RBPJ, ILK, KRAS, LRP6, SMAD4, MDK, MEF2C, MET, MMP14, MTHFR, MYC, NKX3-1, PAX2, PBX1, PGR, PKD1, PML, PODXL, PPP1CA, PROX1, PTCH1, RARG, SDC4, SFRP1, SKI, SOX4, SOX11, SRC, SRF, STK4, TBX3, HNF1B, TSC1, TWIST1, KDM6A, VDR, VEGFA, WNT2B, LUZP1, FZD3, ARID1A, FZD1, FZD6, DCHS1, NRP1, BTRC, DLG5, HAND1, NTN1, SEMA3E, SPRY1, DLC1, GNA13, KDM5B, PLXND1, MTHFD1L, KLHL3, FOXP1, SOX8, SUFU, SIX4, WNT4, DLL4, AHI1, SEMA4C, IFT57, LGR4, VANGL2, MIB1, SHROOM3, NDRG4, SETDB2, LZTS2, TRIM71, RDH10, FMN1, NRARP
BP	GO:0018105	peptidyl-serine phosphorylation	101/3408	8.32E-09	AKT2, ARRB1, ARRB2, ATM, ATP2B4, ATR, BAK1, BCL2, CAMK4, CAMK2A, CAMK2D, CAV1, CD44, MAPK14, CSNK1D, CSNK1E, CSNK1G3, DYRK1A, EGFR, EIF4G1, MARK2, ERCC6, MKNK2, GSK3B, IKBKB, ILK, SMAD7, MARK1, NCK1, NTRK3, PAK2, PDE4D, PDGFB, PDK3, PKD1, PLCL1, PRKAA1, PRKCA, PRKCE, PKN2, MAPK1, MAPK3, MAPK8, MAPK9, RPS6KA3, RPS6KB1, SNCA, SRC, STK4, AURKA, SYK, TAF1, TGFBR1, TXN, VEGFA, HMGA2, ULK1, BCAR3, NCK2, DYRK2, MKNK1, TNKS, RPS6KA4, LATS1, DYRK1B, DCLK1, AURKB, RPS6KA5, ROCK2, BAG4, RASSF2, AKT3, HIPK3, AKAP9, TENM1, RAPGEF3, PLK2, IL24, TLK2, STK38, LMTK2, DKK1, STK38L, SMG1, GPD1L, MORC3, SGK3, LATS2, HIPK2, NLK, DDIT4, FNIP2, NSD1, WNK1, MAPKAP1, FNIP1, TTBK2, CNKSR3, HIPK1, RICTOR, MAST4
BP	GO:0010506	regulation of autophagy	108/3408	8.40E-09	ABL1, ABL2, ATM, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, BCL2, CASP3, DAPK1, DCN, EEF1A1, EIF4G1, EIF4G2, EP300, FOXO1, FOXO3, GAPDH, GNAI3, GSK3B, HTT, HIF1A, HK2, FOXK2, ITPR1, MAPT, MCL1, RAB8A, MET, NEDD4, NPC1, TBC1D25, PAFAH1B2, PIK3CB, PIP4K2A, PRKAA1, PRKAB2, MAPK3, MAPK8, RAB5A, RALB, SNCA, SREBF2, STAT3, TP53, TSC1, UVRAG, XBP1, FZD5, ULK1, MTMR3, USP13, ATP6V0D1, KDM4A, ATG13, MFN2, BCL2L11, TRIM13, TRIM22, NOD1, ATG7, SPTLC1, PLK2, TLK2, USP33, TAB2, LARP1, SIRT1, RAB3GAP2, HSPB8, HTRA2, UBQLN2, UBQLN1, SH3GLB1, WAC, ATP6V1D, TPCN1, VPS13C, VPS13D, FBXW7, DRAM1, VPS35, UBQLN4, SMURF1, USP36, TP53INP2, RRAGD, RRAGC, MLST8, MTMR9, FYCO1, MUL1, SESN2, BMF, MTDH, TP53INP1, RAB39B, SOGA1, SMCR8, SESN3, EXOC8, ATP6V0E2, FLCN, TRIM65, RAB12, TPCN2, FOXK1, ACER2
BP	GO:1902275	regulation of chromatin organization	71/3408	9.19E-09	ARRB1, ATM, ATRX, BCL6, BRCA1, CAMK2D, CHEK1, CTNNB1, DNMT3B, FMR1, GATA2, GATA3, KAT2A, HMGA1, HNRNPU, IGF2, ISL1, JARID2, SMAD4, MECP2, KMT2A, MLLT6, MTHFR, MYB, MAPK3, MAPK8, KDM5A, SET, SKI, SNAI2, SNCA, TAL1, TP53, TWIST1, UBE2N, VEGFA, RPS6KA4, RPS6KA5, TRIP12, ATG5, CTR9, SETD1A, KMT2B, CTCF, TLK2, KAT7, MTF2, MORC2, KDM1A, PHF8, SIRT1, WBP2, NIPBL, SIN3A, ZNF451, AUTS2, UBR5, ATAD2B, BCOR, RIF1, SETD5, ATF7IP, KMT2E, MIER1, NSD1, NAA40, TET1, SETD7, TADA2B, SPTY2D1, FLCN
BP	GO:0030522	intracellular receptor signaling pathway	96/3408	9.19E-09	ACTN4, AR, RHOA, ARRB2, BRCA1, CALR, RUNX1, CBFB, CRKL, CRY2, CTNNB1, CYLD, DAB2, DDX5, EP300, ESR2, ESRRA, ESRRG, EZH2, FHL2, FKBP4, NR5A2, NR6A1, NR3C1, FOXA1, DNAJA1, IRAK1, IRAK2, ISL1, NEDD4, NKX3-1, PDK3, PGR, PIM1, PML, PPARA, PPARD, PRCP, PTGIS, RAN, RARG, RB1, RNF4, RORA, RORB, SEC14L1, SFRP1, SNAI2, SRC, STAT3, TAF1, NR2F2, THRA, TSPAN6, TWIST1, UBE2N, UBE2V1, NR1H2, VDR, NR4A3, KMT2D, NCOA3, NRIP1, ARID1A, TP63, AKR1C3, ALDH1A2, LATS1, CLOCK, NCOR1, PUM1, NR1D2, CITED2, NOD1, TAB1, DDX17, CNOT1, TAB2, UFL1, SIRT1, RBFOX2, WBP2, LSM14A, HEYL, FOXP1, STRN3, UBR5, RNF125, NPLOC4, CYP26B1, PMEPA1, CALCOCO1, ITCH, EGLN2, DCBLD2, KCTD6
BP	GO:0001701	in utero embryonic development	119/3408	1.06E-08	ACVR1B, ADA, ADAM10, ADCY9, ADD1, ADM, AR, ATP7A, BCL2L1, PRDM1, BMP7, BMPR1A, ZFP36L1, CAPN2, CEBPB, CTNNB1, EDN1, EGFR, EPAS1, ERCC2, BPTF, FOXC1, FUT8, GABPA, GATA2, GATA3, GATA6, KAT2A, GJA1, GRB2, HCFC1, HIF1A, HES1, IGF2, RBPJ, ITGB1, JAG2, LIG4, SMAD2, SMAD4, MAFG, MAN2A1, MBNL1, MSX1, MYH9, MYH10, NDUFA2, NPAT, PDGFB, PDGFRA, PKD1, MAPK1, PTCH1, PTPRR, RBBP6, SKIL, SNAI1, SP3, SRF, STK4, TBX3, HNF1B, NR2F2, TGFBR1, TP53, TWIST1, KDM6A, VEGFA, WNT7B, FZD5, FOSL1, CUL3, LATS1, COPS2, HAND1, SH3PXD2A, CTR9, MFN2, BCL2L11, KLF2, TAB1, GNA13, VASH1, WDTC1, ATP11A, MAFF, C1orf43, SIN3A, HINFP, TANC2, PTPN18, SOX8, RRN3, BCOR, NCAPG2, CHD7, ASF1B, OTUD7B, ZMIZ1, BIRC6, HEG1, KIDINS220, MIB1, EPB41L5, DHX35, RIC8A, NXN, TBL1XR1, TET1, CMIP, UNK, ZNF830, PLCD3, UBR3, E2F7, AMOT, RDH10, FLCN, RPL7L1
BP	GO:0031056	regulation of histone modification	59/3408	1.19E-08	ARRB1, ATM, ATRX, BCL6, BRCA1, CAMK2D, CHEK1, CTNNB1, DNMT3B, FMR1, GATA2, GATA3, KAT2A, IGF2, ISL1, JARID2, SMAD4, MECP2, KMT2A, MLLT6, MTHFR, MYB, MAPK3, MAPK8, KDM5A, SET, SKI, SNAI2, SNCA, TP53, TWIST1, UBE2N, VEGFA, RPS6KA4, RPS6KA5, TRIP12, ATG5, CTR9, KMT2B, CTCF, KAT7, MTF2, KDM1A, SIRT1, WBP2, NIPBL, SIN3A, ZNF451, AUTS2, UBR5, BCOR, RIF1, SETD5, KMT2E, NSD1, TET1, SETD7, TADA2B, FLCN
BP	GO:0010212	response to ionizing radiation	60/3408	1.38E-08	ALAD, RHOB, ATM, ATR, BAK1, CCND1, BCL2, BCL2L1, BRCA1, CASP3, CBL, CDKN1A, MAPK14, DNMT3A, DNMT3B, ECT2, EGR1, ELK1, ERCC6, GATA3, GRB2, HSPA5, LIG4, MEN1, MYC, PML, PRKAA1, PTPRC, RAD1, RAD51, CCL7, SFRP1, SNAI2, TP53, VCAM1, XRCC5, HMGA2, MTA1, CLOCK, TRIM13, NET1, TLK2, KDM1A, SIRT1, SPIDR, NIPBL, INO80, USP28, INIP, NUCKS1, AEN, NABP1, INTS3, NABP2, BRCC3, RHNO1, LZIC, DCUN1D3, RNF168, BRAT1

BP	GO:0007160	cell-matrix adhesion	81/3408	1.74E-08	ABL1, JAG1, RHOA, BCL2, BCL6, CD44, CDK6, CCR7, COL3A1, CSF1, CTNNB1, DAG1, EFNA5, EMP2, FN1, GSK3B, HOXA7, ILK, ITGA6, ITGA3, ITGAV, ITGB1, JUP, L1CAM, LRP1, MKLN1, MMP14, NF2, NID1, SERPINE1, PIK3CB, PKD1, PTEN, PTPRJ, PTPRK, RASA1, CX3CL1, SDC4, SFRP1, SLC9A1, SRC, SRF, THBS1, THBS3, TIAM1, TSC1, VCAM1, VCL, VEGFA, ITGA8, ADAM9, IQGAP1, NRP1, LDB1, TAOK2, MAP4K4, ROCK2, ONECUT2, SEMA3E, SLK, BCL2L11, DLC1, POSTN, HPSE, LYVE1, FAM107A, LIMCH1, CLASP1, CORO1C, MINK1, COL5A3, WNT4, FERMT1, RCC2, ADAMTS9, EPB41L5, PEAK1, PHLDB2, WHAMM, ACER2, FMN1
BP	GO:0042176	regulation of protein catabolic process	120/3408	2.05E-08	ALAD, APC, PTTG1IP, CAV1, CDKN1B, CSNK1D, CSNK1E, DAB2, EEF1A1, EGFR, EPHA4, FHIT, FOXO1, FMR1, GJA1, GSK3B, NRG1, UBE2K, HMGCR, DNAJB2, LDLR, LRP1, MAD2L1, SMAD7, MAP1A, MDM4, ATXN3, NEDD4, NSF, OAZ2, OPHN1, FURIN, SERPINE2, PIN1, PKD1, PML, MAPK9, PSMC2, PSMD3, PTEN, RAD23B, RDX, SNCA, SNX1, SORL1, AURKA, STYX, TAF1, TIMP2, TIMP3, TMF1, TNFRSF1B, UBE2G2, VCP, XPO1, CUL4B, SNX3, ADAM9, BTRC, USP13, LATS1, PSMF1, SOCS5, EDEM1, HERPUD1, RNF144A, LRIG2, AREL1, BCAP31, PSME3, PSMD14, TRIB1, ARIH2, ATG7, PLK2, TLK2, SNF8, GABARAPL2, MYCBP2, UFL1, SF3B3, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, HIPK2, MYLIP, USP25, UBQLN2, UBQLN1, DERL2, WAC, UCHL5, UBE2J1, DTL, AZIN1, SUFU, ANKIB1, FBXW7, LAPTM4B, YOD1, VPS35, FMN2, UBQLN4, SMURF1, HECW2, DDA1, LPCAT1, ITCH, UQCC2, EGLN2, FAM122A, SOCS4, AMER1, SH3D19, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:0032535	regulation of cellular component size	117/3408	2.59E-08	ABL1, ADD1, ANXA7, ARF1, ARF6, RHOA, ATP7A, BDNF, BMPR2, CAPZA2, CFL1, CFL2, AP2M1, CLNS1A, CCR7, CREB1, EDN1, EFNA5, MEGF8, EPHA7, CLN8, EPS8, FER, FN1, GDI1, GOLGA4, GRB2, ARHGAP35, GSK3B, NCKAP1L, IL7R, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, MYO1C, NCK1, NTRK3, PAFAH1B1, PAK3, PPP1CA, PRKCE, PTEN, TWF1, RAB3B, RAB5A, RARG, RASA1, RDX, SLC12A4, SPTAN1, SPTBN1, SRF, TSC1, VEGFA, WNT7B, RND2, NCK2, SEMA7A, NRP1, WASF1, WASL, LATS1, NTN1, BAG4, SEMA3E, FCHSD2, SLC12A6, AKT3, ARPC5, ACTR2, ARPC2, ABI2, TENM1, SEMA3A, CDC42EP2, OLFM1, VAV3, SEMA4B, SLC12A7, NCKAP1, IQGAP2, DSTN, CIT, SNF8, RAB21, KDM1A, WDTC1, FSTL4, RAP1GAP2, KANK1, COTL1, SIN3A, TMOD2, HP1BP3, SEMA4C, FMN2, SPIRE1, RAB22A, SLC12A5, SEMA6A, PLEKHG2, ARHGAP28, AKT1S1, PLXNA4, MYADM, ARHGAP18, WHAMM, IQGAP3, JMY, WDR36, MTPN, TTL, RICTOR, FMN1
BP	GO:0043254	regulation of protein complex assembly	140/3408	2.94E-08	ABL1, ADD1, ARF1, ARF6, RHOA, ATM, ATR, CAPZA2, CDC42, CDKN1B, CCR7, CREB1, CTNNB1, DDX3X, DR1, DYRK1A, EIF4G1, EP300, EPS8, ERCC2, FER, FKBP4, GRB2, GSK3B, GTF2H3, HCFC1, NCKAP1L, INSIG1, JUN, SMAD6, MAP1B, MAPT, MECP2, MET, MYO1C, NCK1, PAK3, PRKAA1, PRKCE, MAPK9, EIF2AK2, PSMC2, PTGER4, TWF1, PTPN11, PEX5, RALB, RASA1, RB1, RDX, RNF4, RPS3, ATXN2, SNCA, SORL1, SPTAN1, SPTBN1, SRC, SRF, SYK, TAF1, TAL1, HNF1B, THRA, TP53, TWIST1, VCP, VDAC2, VEGFA, FOSL1, ULK1, NCK2, CUL4B, NAPA, WASF1, WASL, LATS1, ARHGEF2, BAG4, FCHSD2, G3BP2, BCL2L11, ARPC5, ACTR2, ARPC2, AKAP9, G3BP1, ABI2, TENM1, TUBB4A, CDC42EP2, UNC13B, NCKAP1, IQGAP2, SUB1, TPPP, ATXN2L, MAPRE3, DKK1, CNOT1, KANK1, CAMSAP2, CLASP1, COTL1, SPIDR, CLIP3, ZNF451, SENP6, DNAJC15, TMOD2, ASAP1, SH3GLB1, NIN, RRN3, FBLIM1, ATF7IP, VPS35, CAND1, SAR1A, FMN2, SPIRE1, PMEPA1, CNOT6, FNIP2, SLAIN2, PLEKHG2, ARHGAP28, NAV3, BMF, MYADM, ARHGAP18, FNIP1, WHAMM, MIEF2, JMY, MTPN, DAB2IP, CAMSAP1, RICTOR, FMN1
BP	GO:0001655	urogenital system development	107/3408	2.94E-08	ACVR2B, JAG1, AR, BCL2, BMP7, CDKN1B, COL4A1, CRKL, CTNNB1, DCN, EFNB2, EGR1, EPHA4, EPHA7, EPHB2, EPHB3, FBN1, FGF1, FGF2, FKBP4, FOXC1, GATA2, GATA3, FOXA1, HOXD13, HES1, ID4, IL6R, ILK, ITGA6, ITGA3, SMAD2, SMAD4, SMAD6, SMAD7, MEF2C, MME, MYC, NFIA, NID1, NKX3-1, PAX2, PBX1, PDGFA, PDGFB, PDGFRA, PKD1, PODXL, PPAT, PROX1, PTCH1, PTEN, RARG, SDC4, SFRP1, SOX4, SOX11, STAT1, HNF1B, TGFBR1, TSC1, VEGFA, WNT7B, WNT2B, ITGA8, TP63, DCHS1, FADD, IQGAP1, NRP1, ALDH1A2, SGPL1, DLG5, ADAMTS1, BCL2L11, GDF11, SPRY1, FSTL3, FRS2, TMED10, NIPBL, KLHL3, HEYL, SEC61A1, SOX8, RRM2B, APH1A, SIX4, WNT4, AHI1, CEP55, LGR4, NUP133, SULF2, CYP26B1, C1GALT1, VANGL2, WDR77, PTCD2, ARID5B, LZTS2, GLIS2, AMER1, RDH10, BMPER, FLCN, FMN1
BP	GO:0018209	peptidyl-serine modification	105/3408	2.95E-08	AKT2, ARRB1, ARRB2, ATM, ATP2B4, ATR, BAK1, BCL2, CAMK4, CAMK2A, CAMK2D, CAV1, CD44, MAPK14, CSNK1D, CSNK1E, CSNK1G3, DCN, DYRK1A, EGFR, EIF4G1, MARK2, ERCC6, GALNT1, GALNT2, MKNK2, GSK3B, IKBKB, ILK, SMAD7, MARK1, NCK1, NTRK3, PAK2, PDE4D, PDGFB, PDK3, PKD1, PLCL1, PRKAA1, PRKCA, PRKCE, PKN2, MAPK1, MAPK3, MAPK8, MAPK9, RPS6KA3, RPS6KB1, SNCA, SRC, STK4, AURKA, SYK, TAF1, TGFBR1, TXN, VEGFA, HMGA2, ULK1, BCAR3, NCK2, DYRK2, MKNK1, TNKS, RPS6KA4, LATS1, DYRK1B, DCLK1, AURKB, RPS6KA5, ROCK2, BAG4, RASSF2, SPOCK2, AKT3, HIPK3, AKAP9, TENM1, RAPGEF3, PLK2, IL24, TLK2, STK38, LMTK2, DKK1, STK38L, SMG1, GPD1L, MORC3, SGK3, LATS2, HIPK2, NLK, DDIT4, FNIP2, NSD1, WNK1, MAPKAP1, FNIP1, TTBK2, CNKSR3, HIPK1, RICTOR, MAST4
BP	GO:0044843	cell cycle G1/S phase transition	99/3408	2.96E-08	ACVR1B, ATM, ATP2B4, BCAT1, CCND1, BCL2, CAMK2A, CCNA2, CCND2, CDC25A, CDC34, CDK6, CDKN1A, CDKN1B, RCC1, DDX3X, E2F6, EGFR, EIF4E, EIF4G1, EP300, EZH2, FHL1, GSPT1, ID4, ITGB1, MAX, MCM3, MCM4, MCM7, MDM4, MEN1, MYC, CNOT4, NPAT, ORC5, PKD1, PML, POLA1, PPAT, PPP3CA, PPP6C, PTEN, RB1, RBL2, RDX, RPS6KB1, RRM2, SOX4, AURKA, ADAM17, TAF1, TERT, TFDP1, TFDP2, TP53, BTG2, CUL5, CUL4B, CUL3, CUL2, KLF11, CDK10, LATS1, CCNE2, KLF4, CNOT8, ADAMTS1, CTDSP2, PSME3, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, PHF8, ZNF385A, HINFP, GIGYF2, LATS2, TRIAP1, INO80, FBXW7, KMT2E, MEPCE, CNOT6, USP37, CTDSP1, RHOU, ZNF655, CDC73, SLFN11, DCUN1D3, IQGAP3, TRIM71, NACC2, CACUL1, E2F7
BP	GO:0051099	positive regulation of binding	68/3408	3.20E-08	ABL1, ADD1, AMFR, ARF6, ARRB1, BDNF, CALM3, CAV1, CEBPG, CTNNB1, EIF2S1, EIF4G1, EP300, EPB41, EPHA4, ERCC2, FKBP1A, FOXC1, FMR1, GATA3, GSK3B, HOXA3, HES1, IRF4, ISL1, LRP1, MEF2C, MEN1, MET, NCBP1, PAX6, PIN1, PKD1, PLCL1, POU4F1, PPP2CA, RALB, RAN, RB1, SKI, STK4, TAF1, TCF7L2, TERT, TIAM1, TWIST1, TXN, HMGA2, NRP1, MBD2, KLF4, TRAF4, RAPGEF2, PLK2, MAPRE3, KDM1A, USP33, PLXND1, MAU2, NIPBL, HIPK2, NMD3, GNL3L, PINX1, EPB41L5, HMBOX1, SPPL3, DPH3

BP	GO:0048813	dendrite morphogenesis	58/3408	3.26E-08	ADAM10, RERE, CAMK2A, CDC42, CFL1, CUX1, CELSR2, EPHA4, EPHB2, EPHB3, FMR1, GSK3B, ILK, ITGB1, CAPRIN1, MEF2A, NEDD4, SLC11A2, OPA1, PAFAH1B1, PAK3, PPP3CA, PTEN, PTPRD, RAP2A, SDC2, VAMP7, TIAM1, VLDLR, NRP1, WASL, KALRN, DCLK1, TAOK2, RAPGEF2, ACTR2, ABI2, FARP1, SEMA3A, PDLIM5, NLGN1, BTBD3, TRAK1, SHANK2, RAB21, RBFOX2, NSMF, SIPA1L1, SS18L1, SLITRK5, MINK1, TMEM106B, KIDINS220, HECW2, GORASP1, TRAK2, PREX2, BHLHB9
BP	GO:0000082	G1/S transition of mitotic cell cycle	94/3408	3.40E-08	ACVR1B, ATM, BCAT1, CCND1, BCL2, CAMK2A, CCND2, CDC25A, CDC34, CDK6, CDKN1A, CDKN1B, RCC1, DDX3X, E2F6, EGFR, EIF4E, EIF4G1, EP300, EZH2, FHL1, GSPT1, ID4, ITGB1, MAX, MCM3, MCM4, MCM7, MDM4, MYC, CNOT4, NPAT, ORC5, PKD1, PML, POLA1, PPAT, PPP3CA, PPP6C, PTEN, RB1, RBL2, RDX, RPS6KB1, RRM2, SOX4, AURKA, ADAM17, TERT, TFDP1, TFDP2, TP53, BTG2, CUL5, CUL4B, CUL3, CUL2, KLF11, CDK10, LATS1, CCNE2, KLF4, CNOT8, ADAMTS1, CTDSP2, PSME3, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, PHF8, ZNF385A, HINFP, GIGYF2, LATS2, TRIAP1, INO80, KMT2E, MEPCE, CNOT6, USP37, CTDSP1, RHOU, ZNF655, CDC73, SLFN11, DCUN1D3, IQGAP3, TRIM71, NACC2, CACUL1, E2F7
BP	GO:0016236	macroautophagy	98/3408	3.40E-08	ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, CASP3, DCN, GAPDH, GNAI3, HTT, HIF1A, LAMP2, NBR1, NEDD4, NPC1, TBC1D25, PAFAH1B2, PIP4K2A, PRKAA1, PRKAB2, MAPK3, MAPK8, RAB1A, RAB5A, RALB, SRC, TP53, TSC1, UVRAG, VCP, ULK1, DYNLL1, SQSTM1, MTMR3, ATP6V0D1, ATG5, VPS4B, ATG13, TOMM20, MFN2, TRIM13, NOD1, ATG7, SPTLC1, SNF8, GABARAPL2, ATG14, ATG2A, PACS2, LARP1, SIRT1, STX12, RAB3GAP2, KLHL3, HSPB8, HTRA2, UBQLN2, UBQLN1, VPS36, SH3GLB1, WAC, ATP6V1D, RAB23, ZFYVE1, VPS13C, STX17, VPS37C, ATG16L1, ATG2B, VPS13D, YOD1, MFN1, VPS35, NSFL1C, UBQLN4, SMURF1, USP36, EPG5, TP53INP2, RRAGD, RRAGC, MLST8, ATG9A, FYCO1, MAP1LC3B, SESN2, ATG10, TP53INP1, WDR81, LIX1L, UBXN2B, SMCR8, SESN3, EXOC8, ATP6V0E2, VPS37D, TMEM74, RAB12, TMEM41B
BP	GO:0048511	rhythmic process	98/3408	3.40E-08	ADA, ADCY1, ARRB1, ARRB2, ZFHX3, AXL, KLF9, CASP3, CPT1A, CREB1, CREBBP, CRY2, CSNK1D, CSNK1E, DDX5, DYRK1A, EGFR, EGR1, EGR3, EP300, EZH2, FOXO3, GFPT1, GNAQ, GSK3B, HDAC2, HNF4A, HNRNPD, HNRNPU, HSPA5, ID4, JUN, JUND, MDK, KMT2A, NFYA, NTRK3, SERPINE1, PDGFRA, PGR, PML, PPARA, PPP1CA, PPP1CB, PPP1CC, PRKAA1, MAPK8, MAPK9, PROX1, PTEN, KDM5A, RORA, RORB, SIAH2, SRC, SUV39H1, HNF1B, TEF, KLF10, TP53, TWIST1, TYRO3, NRIP1, USP9X, FZD4, BHLHE40, KAT2B, PER3, PER2, SGPL1, BTRC, USP2, MTA1, ROCK2, ADAMTS1, CLOCK, NCOR1, THRAP3, NR1D2, NCOA2, ATG7, KDM5B, CBX3, NLGN1, KDM2A, MYCBP2, PHLPP1, SIRT1, TARDBP, SIN3A, FBXL3, DTL, FBXW7, LGR4, PLEKHA1, ZNF830, BTBD9, SIK1
BP	GO:1901653	cellular response to peptide	120/3408	3.62E-08	ADCY1, ADCY6, ADCY9, AKT2, APC, ATP2B1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, ZFP36L1, CACNA2D1, CACNB1, CAMK2A, CAV1, CCNA2, CDC5L, CREB1, CRK, CSK, EDN1, EPHA4, ESRRA, FBN1, FER, FOXO1, FOXO3, GAB1, GNAI2, GRB2, GSK3B, IGF1R, IGF2, IGFBP1, INSR, LRP1, LYN, MAP1B, MAX, RAB8A, MEN1, FOXO4, MYO1C, MYO5A, NCK1, NFKB1, OPA1, PDK4, ENPP1, PIK3C2A, PKM, PPAT, PRKAA1, PRKAR1A, PRKAR2A, PRLR, PTEN, PTPN1, PTPN11, PXN, RAP1B, RPS6KB1, SHC1, SLC9A1, SORL1, SOS1, SRC, STAT1, STAT3, STAT5B, VAMP2, KLF10, TP53, TSC1, VCAM1, XBP1, YWHAG, NR4A3, KLF11, USO1, SOCS1, IRS2, SOCS2, KAT2B, ATP6V0D1, ARHGEF2, KLF4, ROCK2, LPIN2, HDAC9, C2CD5, TBC1D4, BCL2L11, KLF2, NOD1, AHCYL1, RAB31, WDTC1, LPIN1, KANK1, SIRT1, RHOQ, APPL1, SLC2A8, ADIPOR1, KLF3, ATP6V1D, CHMP5, RAB8B, ERRFI1, LEPROT, PHIP, ARID1B, NUCKS1, TRIM41, OSBPL8, CPEB2, SOGA1, SESN3, ATP6V0E2
BP	GO:0001503	ossification	123/3408	3.92E-08	ACVR2B, ADAR, JAG1, RHOA, ATP2B1, BCL2, BMP3, BMP7, BMPR1A, BMPR2, RUNX2, CBFB, CDK6, CEBPB, CEBPD, COL1A1, COL1A2, COL5A2, COL11A1, MAPK14, CSF1, CTNNB1, DDX5, S1PR1, EGFR, ERCC2, ESRRA, FBN2, FGFR3, FOXC1, GJA1, GNAS, HIF1A, HNRNPC, HNRNPU, ID4, IGF2, IGFBP5, RBPJ, IL6R, IL6ST, ILK, JUND, NBR1, SMAD6, MDK, MEF2C, MEF2D, MEN1, MMP14, MN1, NAB1, PBX1, ENPP1, MAPK1, MAPK3, PSMC2, PTCH1, PTGER4, RORB, RRBP1, SORT1, SFRP1, SKI, SLC8A1, SNAI2, SNAI1, SOX11, SP3, SPARC, STC1, THBS3, THRA, KLF10, TPM4, TWIST1, WNT7B, FZD1, SEMA7A, TP63, DCHS1, CHRD, LIMD1, DDX21, PDLIM7, RASSF2, MRC2, ZBTB40, TOB1, FSTL3, GPNMB, SYNCRIP, TOB2, DKK1, SNRNP200, SATB2, DNAJC13, UFL1, NIPBL, RSL1D1, OSTF1, GREM1, SND1, RBMX, SOX8, SUFU, WNT4, BCOR, LGR4, BMP2K, TXLNG, CSGALNACT1, BCAP29, ANKH, FAM20C, CCDC47, SMURF1, TP53INP2, SMOC1, KREMEN1, PKDCC, SH3PXD2B, BMP8A
BP	GO:0043434	response to peptide hormone	132/3408	4.05E-08	ADCY1, ADCY6, ADCY9, ADM, AKT2, APC, ATP2B1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, BMP7, ZFP36L1, BTG1, CAMK2A, CAV1, CCNA2, CDC5L, CDKN1B, COL1A1, CREB1, CRK, CSK, DAG1, EDN1, EGR1, ESRRA, FBN1, FER, FOXO1, FOXO3, GAB1, GJA1, GNAI2, GOT2, GRB2, GSK3B, HADHA, IGF1R, IGF2, IGFBP1, IGFBP5, INSR, JUND, LRP6, LYN, MAP1B, MAX, RAB8A, MEN1, FOXO4, MYO1C, MYO5A, NCK1, NFKB1, OPA1, PDK4, ENPP1, PIK3C2A, PKM, PPARA, PPAT, PRKAA1, PRKAR1A, PRKAR2A, PRLR, PTEN, PTPN1, PTPN11, PXN, RAP1B, RPS6KB1, SORT1, SRSF4, SHC1, SLC9A1, SORL1, SOS1, SPARC, SRC, STAT1, STAT2, STAT3, STAT5B, VAMP2, TGFBR3, TSC1, XBP1, YWHAG, BTG2, NR4A3, STC2, USO1, SOCS1, IRS2, TNFSF10, IQGAP1, SOCS2, KAT2B, ATP6V0D1, ROCK2, LPIN2, HDAC9, C2CD5, EPM2AIP1, TBC1D4, AHCYL1, RAB31, WDTC1, LPIN1, KANK1, SIRT1, RHOQ, APPL1, SLC2A8, ADIPOR1, INSIG2, ATP6V1D, RAB8B, ERRFI1, LEPROT, PHIP, ARID1B, NUCKS1, SESN2, OSBPL8, ACVR1C, CPEB2, SOGA1, SESN3, ATP6V0E2, SLC27A1
BP	GO:0071375	cellular response to peptide hormone stimulus	104/3408	4.70E-08	ADCY1, ADCY6, ADCY9, AKT2, APC, ATP2B1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, ZFP36L1, CAMK2A, CAV1, CCNA2, CDC5L, CREB1, CRK, CSK, EDN1, ESRRA, FBN1, FER, FOXO1, FOXO3, GAB1, GNAI2, GRB2, GSK3B, IGF1R, IGF2, IGFBP1, INSR, LYN, MAP1B, MAX, RAB8A, MEN1, FOXO4, MYO1C, MYO5A, NCK1, NFKB1, OPA1, PDK4, ENPP1, PIK3C2A, PKM, PPAT, PRKAA1, PRKAR1A, PRKAR2A, PRLR, PTEN, PTPN1, PTPN11, PXN, RAP1B, RPS6KB1, SHC1, SLC9A1, SORL1, SOS1, SRC, STAT1, STAT3, STAT5B, VAMP2, TSC1, XBP1, YWHAG, NR4A3, USO1, SOCS1, IRS2, SOCS2, KAT2B, ATP6V0D1, ROCK2, LPIN2, HDAC9, C2CD5, TBC1D4, AHCYL1, RAB31, WDTC1, LPIN1, KANK1, SIRT1, RHOQ, APPL1, SLC2A8, ADIPOR1, ATP6V1D, RAB8B, ERRFI1, LEPROT, PHIP, ARID1B, NUCKS1, OSBPL8, CPEB2, SOGA1, SESN3, ATP6V0E2

BP	GO:0010769	regulation of cell morphogenesis involved in differentiation	99/3408	4.80E-08	ABL1, ACTN4, ADAM10, RHOA, ARHGDIA, BDNF, BMPR2, CALR, CDC42, CFL1, CRK, CRKL, CUX1, EFNA5, MEGF8, MARK2, EPHA4, EPHA7, EPHB2, EPHB3, FMR1, FN1, GBP1, GDI1, GOLGA4, ARHGAP35, GSK3B, ILK, L1CAM, LIMK1, LRP1, CAPRIN1, MAP1B, MAPT, MDK, NEDD4, NEDD9, NTRK3, OPA1, PAFAH1B1, PAK3, POU3F2, PPP3CA, PTEN, PTPRD, RAP2A, ROBO1, RREB1, SDC2, SKIL, SRF, VAMP7, TIAM1, VEGFA, RND2, SEMA7A, NRP1, SYNGAP1, KALRN, NTN1, RAPGEF2, SEMA3E, UST, ACTR2, ARPC2, ABI2, SEMA3A, OLFM1, SEMA4B, PDLIM5, POSTN, NLGN1, TRAK1, RAB21, MYCBP2, FSTL4, PLXND1, KANK1, CORO1C, SIN3A, NSMF, SIPA1L1, SS18L1, NIN, SEMA4C, YTHDF1, RCC2, HECW2, SEMA6A, ZSWIM6, GORASP1, ZSWIM4, TRAK2, METRN, BHLHB9, PLXNA4, MYADM, WDR36, TTL
BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	58/3408	5.49E-08	ABL1, APC, BMP7, CASP3, CAV1, CDKN1A, CDKN1B, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, HMGCR, DNAJA1, IPO5, LRP6, LYN, MEN1, PPP2CA, PPP2R1A, PKIA, PRKAR1A, PRKAR2A, PTEN, PTPN1, PTPRJ, RB1, RGS2, RGS4, SFRP1, SORL1, TESK1, NR2F2, YWHAG, KAT2B, LATS1, SH2B3, HIPK3, SPRY1, DUSP14, DUSP10, STK38, SIRT1, LATS2, PDCD4, LAX1, HEG1, AIDA, WNK1, DUSP16, SPRY4, DUSP18, DAB2IP, SPRED1, ZNF675, SPRED2, SPRED3
BP	GO:0007044	cell-substrate junction assembly	44/3408	5.65E-08	ABL1, RHOA, BCL2, DST, EFNA5, FN1, ITGA6, ITGA5, LAMC1, LAMC2, LRP1, MMP14, PLEC, PTEN, PTPRJ, PTPRK, SDC4, SFRP1, SLC9A1, SRC, THBS1, TLN1, TNS1, TSC1, VEGFA, IQGAP1, NRP1, LDB1, TAOK2, MAP4K4, ROCK2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, WHAMM, FMN1
BP	GO:0060485	mesenchyme development	93/3408	5.67E-08	JAG1, BCL2, BMP7, BMPR1A, BMPR2, ZFP36L1, CFL1, COL1A1, CTNNB1, DAB2, DAG1, DDX5, EDN1, EFNB1, EZH2, FOXC1, FN1, GCNT2, GSK3B, HDAC2, NRG1, HIF1A, FOXA1, HNRNPAB, HOXA5, HES1, RBPJ, ISL1, LOXL2, LRP6, SMAD2, SMAD4, SMAD7, MDK, MDM4, MEF2C, KITLG, MSX1, MYC, PAX2, PPP2CA, MAPK1, MAPK3, PTEN, ROBO1, SFRP1, SNAI2, SNAI1, SOX11, STAT1, TGFBR1, TGFBR3, TIAM1, TWIST1, HMGA2, SEMA7A, DCHS1, NRP1, ALDH1A2, DLG5, HAND1, SEMA3E, FGF19, SPRY1, CITED2, SEMA3A, OLFM1, SEMA4B, DDX17, PHLDB1, CLASP1, CORO1C, HEYL, GREM1, PDCD4, SOX8, ADIPOR1, SIX4, WNT4, BNC2, SEMA4C, TRIM62, NUP133, SEMA6A, EPB41L5, PBLD, FAM172A, KBTBD8, PHLDB2, AMER1, DAB2IP, RDH10, CRB2
BP	GO:0050773	regulation of dendrite development	59/3408	6.04E-08	ADAM10, ARF1, ARF6, RHOA, BMP7, CFL1, CRK, CRKL, CUX1, EPHA4, EZH2, FMR1, GSK3B, HDAC2, ILK, CAPRIN1, MARK1, MEF2C, NEDD4, OPA1, PAFAH1B1, PAK3, PPP3CA, MAPK6, PTEN, PTPRD, RAP2A, SDC2, VAMP7, TIAM1, VLDLR, IQGAP1, KALRN, DLG5, RAPGEF2, ACTR2, ABI2, PDLIM5, PLK2, CPEB3, NLGN1, SHANK2, RAB21, FSTL4, CAMSAP2, NSMF, SIPA1L1, SS18L1, ASAP1, BCL11A, C21orf91, TMEM106B, CAMK1D, HECW2, RAB17, GORASP1, BHLHB9, DAB2IP, SDK1
BP	GO:0018205	peptidyl-lysine modification	122/3408	6.15E-08	ARRB1, ATP7A, ATRX, BRCA1, CHEK1, ATF2, CREBBP, CTNNB1, DNMT3B, DR1, EGR1, EP300, EZH1, EZH2, GATA2, GATA3, KAT2A, HCFC1, HDAC2, IRF4, ISL1, JARID2, LOXL2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MYB, NUP88, NUP98, PRKAA1, MAPK3, RANBP2, SET, SNAI2, SNCA, SOX4, SUV39H1, TAF1, TWIST1, KDM6A, PRDM2, KAT6A, KMT2D, YEATS4, DPF3, DPF1, NCOA3, CBX4, KAT2B, LDB1, RPS6KA4, RPS6KA5, GTF3C4, ATG5, CLOCK, MORF4L2, CTR9, HDAC9, SETD1A, KMT2B, POM121, PIAS3, CTCF, NUP50, SRCAP, KAT7, MTF2, KDM1A, SIRT1, SUZ12, WBP2, SIN3A, ZNF451, AUTS2, SENP6, BRPF3, ING4, PIAS4, TAF9B, ARID4B, RSF1, BCL11A, GNL3L, WDR5B, ING3, TET2, BCOR, KANSL2, MSL2, RIF1, SETD5, NDC1, NUP133, KMT2E, ZMIZ1, EP400, BEND3, KMT2C, NSD1, MEAF6, MUL1, VCPKMT, CAMKMT, NAA40, NAA50, EPC1, SETD7, SEH1L, ZMIZ2, SETDB2, SETD3, DPY30, TADA2B, ESCO1, METTL21A, TET3, FLCN, SENP5, NUP43, POM121C
BP	GO:0043543	protein acylation	85/3408	7.73E-08	ARRB1, BRCA1, CHEK1, ATF2, CREBBP, DR1, EP300, FOXO1, GATA2, GATA3, KAT2A, GSK3B, HCFC1, HDAC2, IRF4, ISL1, SMAD4, MAPT, MECP2, KMT2A, PPM1B, PRKAA1, MAPK3, SET, SNAI2, SNCA, SOX4, TAF1, TWIST1, KAT6A, YEATS4, DPF3, DPF1, NCOA3, KAT2B, LDB1, RPS6KA4, RPS6KA5, GTF3C4, ATG5, CLOCK, MORF4L2, RAPGEF3, CTCF, SRCAP, KAT7, ZDHHC17, SIRT1, WBP2, ZDHHC5, SIN3A, CLIP3, ZNF451, AUTS2, BRPF3, ZDHHC8, ABHD17B, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, SETD5, ZDHHC7, TAOK1, EP400, BEND3, ABHD17C, NAA35, ZDHHC6, MEAF6, NAA40, NAA25, NAA50, EPC1, ZDHHC18, TADA2B, ESCO1, NAA30, FLCN, ZDHHC20, ZDHHC23, ZDHHC22, ZDHHC21
BP	GO:0001558	regulation of cell growth	126/3408	8.72E-08	ABL1, ACVR1B, ADAM10, APBB2, RHOA, BCL2, BCL6, BDNF, BMPR2, BTG1, OSGIN2, CAMK2D, CDC42, CDKN1A, CDKN1B, CRKL, DDX3X, HBEGF, EDN1, EFNA5, MEGF8, EGFR, EIF4G1, EIF4G2, EPHA7, ERBB2, ESR2, EXTL3, FHL1, FN1, G6PD, GDI1, GJA1, GOLGA4, GSK3B, HNF4A, DNAJB2, IGFBP1, IGFBP5, ILK, L1CAM, LIMK1, LRP1, SMAD4, MAP1B, MAPT, MMP14, MSX1, NCBP1, NTRK3, PAFAH1B1, ENPP1, SERPINE2, PIN1, PML, PPARA, PPARD, PPP2CA, PPP2R1A, PTPRJ, RB1, RGS2, RGS4, RPS6KA3, SFRP1, SLC9A1, SMARCA2, SRF, SYT1, ADAM17, TGFBR1, TP53, VEGFA, YY1, RND2, BAP1, SEMA7A, NRP1, SOCS2, TAOK2, NTN1, AKAP6, SEMA3E, SERTAD2, NET1, SEMA3A, OLFM1, SEMA4B, FAM107A, RAB21, FSTL4, SIRT1, SGK3, SIN3A, SERTAD3, DERL2, ADIPOR1, ZNF639, TAF9B, SYT17, BCL11A, INO80, SEMA4C, USP47, CHPT1, SMURF1, SEMA6A, CXCL16, TSPYL2, CDC73, MUL1, ADIPOR2, SESN2, ITCH, KIAA1109, PLXNA4, EGLN2, FAM122A, DCUN1D3, SYT2, DCBLD2, WDR36, MTPN, TTL, FLCN, BRAT1
BP	GO:0042770	signal transduction in response to DNA damage	54/3408	1.02E-07	ABL1, ATM, ATR, ATRX, BRCA1, PTTG1IP, CD44, CDC5L, CDKN1A, CDKN1B, CHEK1, MAPK14, DDX5, DYRK1A, EP300, FOXM1, FOXO3, GRB2, MDM4, MSX1, MYO6, CNOT4, PML, RBL2, SNAI2, SNAI1, SOX4, SP100, AURKA, TFDP1, TFDP2, TP53, TWIST1, BTG2, PPM1D, CDC14B, CNOT8, PLK2, CNOT1, KDM1A, SIRT1, ZNF385A, HIPK2, ING4, TRIAP1, DTL, CNOT6, BRCC3, SESN2, E2F7, SPRED1, SPRED2, ACER2, SPRED3
BP	GO:0000209	protein polyubiquitination	100/3408	1.15E-07	AMFR, BCL2, BRCA1, CBFB, CBL, CCNF, CDC34, CTNNB1, UBE2K, LNPEP, NEDD4, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RBBP6, RNF4, SIAH1, SIAH2, SKP1, TAF1, TTC3, UBE2D2, UBE2D3, UBE2G1, UBE2G2, UBE2H, UBE2L3, UBE2N, UBE2V1, CUL3, TNKS, BTRC, TRIP12, UBE4A, PSMF1, RNF144A, AREL1, PSME3, PSMD14, UBE4B, ARIH2, UBE2E3, RBCK1, PSME4, MGRN1, TRIM2, MKRN1, ARIH1, HECTD1, RNF19A, FBXW2, FBXL3, KLHL3, FBXO22, FBXO9, MYLIP, RLIM, BFAR, UBR5,

					DTL, FBXO40, ANKIB1, FBXL19, RNF111, FBXL12, UBE2R2, RNF125, UBE2W, FBXW7, TRIM36, RNF114, SMURF1, PELI1, HECW2, KLHL42, RNF213, UNKL, SPSB1, ZFP91, TRIM56, ITCH, FBXO30, SYVN1, ZNRF1, LONRF1, RFFL, TRIM71, MIB2, RNF187, RNF217, RNF168, ZNRF2, RNF144B, SHPRH, RNF180, RNF165
BP	GO:1903391	regulation of adherens junction organization	34/3408	1.15E-07	ABL1, ADD1, ARF6, RHOA, EFNA5, LRP1, MMP14, PTEN, PTPRJ, RDX, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VEGFA, IQGAP1, NRP1, LDB1, MAP4K4, ROCK2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, FMN1
BP	GO:0001763	morphogenesis of a branching structure	71/3408	1.18E-07	ABL1, ADM, AR, RERE, BCL2, PRDM1, BMP7, COL4A1, CSF1, CTNNB1, CTSZ, DAG1, DLX2, EDN1, EPHA7, FGF1, FGF2, GRB2, FOXA1, HOXA5, HOXD13, ILK, KRAS, LRP6, SMAD4, MDK, MET, MMP14, MYC, NKX3-1, PAX2, PBX1, PDGFA, PGR, PKD1, PML, PPP1CA, PROX1, PTCH1, SFRP1, SNAI2, SRC, SRF, STK4, TBX3, HNF1B, VDR, VEGFA, WNT2B, FZD5, TP63, DCHS1, NRP1, BTRC, DLG5, SEMA3E, SPRY1, SEMA3A, GNA13, KDM5B, FRS2, PLXND1, SOX8, SIX4, BCL11A, WNT4, DLL4, LGR4, VANGL2, RDH10, NRARP
BP	GO:0009755	hormone-mediated signaling pathway	81/3408	1.31E-07	AR, RHOA, ARRB2, BMP7, BRCA1, CALR, RUNX1, CBFB, CRY2, CTNNB1, DAB2, DDX5, EP300, ESR2, ESRRA, ESRRG, FHL2, FKBP4, NR5A2, NR6A1, NR3C1, FOXA1, HNF4A, DNAJA1, ISL1, NEDD4, NKX3-1, PGR, PPARA, PPARD, PRCP, PRLR, PTPN11, RAN, RARG, RB1, RNF4, RORA, RORB, SFRP1, SRC, TAF1, NR2F2, THRA, NR2C2, NR1H2, VDR, NR4A3, KMT2D, NCOA3, NRIP1, ARID1A, TP63, LATS1, CLOCK, NCOR1, NR1D2, PGRMC2, DDX17, ABHD2, AKAP13, CNOT1, UFL1, SIRT1, RBFOX2, WBP2, APPL1, HEYL, LATS2, FOXP1, STRN3, ADIPOR1, UBR5, LGR4, PMEPA1, CALCOCO1, ADIPOR2, PAQR8, EGLN2, KCTD6, SLC27A1
BP	GO:0031098	stress-activated protein kinase signaling cascade	101/3408	1.32E-07	ADORA2B, FAS, RHOA, ZFP36L1, CCR7, CRKL, MAPK14, CYLD, DUSP1, DUSP9, DVL3, EDN1, EGFR, EPHA4, ERCC6, FOXM1, FOXO1, FLT4, RAPGEF1, HMGCR, DNAJA1, IGF1R, IKBKB, IRAK1, IRAK2, LYN, NBR1, MAP3K1, MAP3K3, MAP3K4, MEN1, MID1, MAP3K9, MYC, NFKB1, PAFAH1B1, PRDX1, PAK2, PAK3, MAPK1, MAPK3, MAPK8, MAPK9, EIF2AK2, PTGER4, PTPN1, RAP2A, RPS3, MAP2K4, SFRP1, SKP1, STK4, STK10, SYK, TIAM1, TPD52L1, UBE2N, UBE2V1, VEGFA, WNT7B, ZFP36, FZD5, FZD4, STK24, BTRC, SPAG9, TAOK2, MAP4K4, NCOR1, TRAF4, SLK, RASSF2, FGF19, HIPK3, TRIB1, SEMA3A, NOD1, TAB1, MAP3K2, ZMYND11, KAT7, DUSP10, DKK1, KLHDC10, TAB2, MAPK8IP3, PHLPP1, PDCD4, HIPK2, MINK1, SEMA4C, VANGL2, TAOK1, AIDA, MUL1, ITCH, SIRPA, DAB2IP, ZNF675, EMC10, SH3RF3
BP	GO:1902903	regulation of supramolecular fiber organization	110/3408	1.32E-07	ABL1, ADD1, APC, ARF1, ARF6, RHOA, CAPZA2, CD47, CDC42, CDKN1B, CFL1, CFL2, CCR7, DYRK1A, S1PR1, EDN1, EPS8, FER, FKBP4, GRB2, ARHGAP35, NCKAP1L, LDLR, LIMK1, SMAD4, MAP1A, MAP1B, MAPT, MECP2, MEF2C, MET, MID1, MYO1C, NCK1, NF2, PAK3, PRKCE, PROX1, PTGER4, TWF1, PXN, RASA1, RB1, RDX, RGS4, RPS3, CX3CL1, SDC4, SFRP1, SLC9A1, SNCA, SPTAN1, SPTBN1, TESK1, TGFBR1, TSC1, NCK2, NRP1, WASF1, WASL, LATS1, ARHGEF2, ROCK2, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, AKAP9, ABI2, WASF2, TENM1, TUBB4A, DLC1, RAPGEF3, CDC42EP2, NCKAP1, IQGAP2, DSTN, CIT, AKAP13, MAPRE3, LIMCH1, KANK1, CAMSAP2, CLASP1, COTL1, CLIP3, TMOD2, NIN, WNT4, FMN2, SPIRE1, TAOK1, SLAIN2, PLEKHG2, ARHGAP28, SYNPO2L, NAV3, PHLDB2, MYADM, ARHGAP18, WHAMM, JMY, MTPN, TTBK2, CAMSAP1, RICTOR, SH3PXD2B, FMN1
BP	GO:0071559	response to transforming growth factor beta	86/3408	1.36E-07	ACVR1B, ACVR2B, RHOA, ARRB2, ZFHX3, BMPR1A, BMPR2, ZFP36L1, ZFP36L2, CAV1, RUNX3, CBL, COL1A1, COL1A2, COL3A1, COL4A2, CREB1, CREBBP, CRK, CRKL, DAB2, EDN1, EP300, FBN1, FBN2, FNTA, FUT8, GCNT2, NR3C1, HDAC2, HSPA5, ITGA3, JUN, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEF2C, MEN1, FURIN, PDE3A, PIN1, PML, PTPRK, PXN, SFRP1, SKI, SKIL, SOX11, SRC, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, USP9X, ITGA8, ADAM9, MTMR4, ROCK2, ONECUT2, CITED2, TAB1, POSTN, PEG10, SIRT1, ZNF451, APPL1, DKK3, HIPK2, TRIM33, NLK, WNT4, RNF111, FERMT1, PARD3, PMEPA1, SMURF1, EPB41L5, PBLD, WFIKKN2, ACVR1C, CD109, FLCN
BP	GO:0070482	response to oxygen levels	120/3408	1.36E-07	ACTN4, ADA, ADM, AK4, ALAD, FAS, RHOA, ATM, ATP1B1, ATP6V1A, ATP7A, BCL2, BMP7, ZFP36L1, CAPN2, CASP3, CAV1, CBL, CCNA2, CDKN1A, CDKN1B, COL1A1, CREB1, CREBBP, DNMT3A, DNMT3B, EDN1, EGR1, EP300, EPAS1, ERCC2, FOXO1, FOXO3, GATA6, GNB1, HDAC2, HIF1A, HK2, RBPJ, IRAK1, ITPR1, ITPR2, KCNK3, LDHA, LOXL2, SMAD4, MDM4, MECP2, MMP14, MTHFR, MYB, MYC, NKX3-1, SLC11A2, OPA1, PDK3, PIN1, PKM, PML, PPARA, PPARD, PRKAA1, PRKCE, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, PTGIS, RORA, SFRP1, SLC8A1, SLC9A1, SRC, SRF, STC1, SUV39H1, ADAM17, TMBIM6, TERT, TGFBR3, THBS1, TP53, TSC1, TWIST1, VCAM1, VEGFA, VHL, CUL2, STC2, LIMD1, ATP6V0D1, ROCK2, PSMF1, PSME3, PSMD14, CITED2, HYOU1, ATG7, POSTN, PSME4, SIRT1, TXN2, HIPK2, UBQLN1, SLC2A8, HP1BP3, DDIT4, ALKBH5, HIF1AN, FMN2, CPEB4, APOLD1, EGLN2, EGLN3, CPEB2, TMEM199
BP	GO:0034333	adherens junction assembly	41/3408	1.54E-07	ABL1, RHOA, BCL2, CTNNB1, EFNA5, LRP1, SMAD7, MMP14, PTEN, PTPRJ, PTPRK, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VCL, VEGFA, IQGAP1, NRP1, LDB1, DLG5, TAOK2, MAP4K4, ROCK2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, PIP5K1C, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, WHAMM, HIPK1, FMN1
BP	GO:0070507	regulation of microtubule cytoskeleton organization	68/3408	1.54E-07	ABL1, APC, RHOA, BRCA1, CCNF, CDKN1B, CHEK1, CTNNB1, CYLD, DYRK1A, EFNA5, MARK2, FKBP4, KAT2A, GSK3B, HNRNPU, MAP1A, MAP1B, MAPT, MECP2, MET, MID1, PAFAH1B1, PKD1, PRKAA1, RNF4, RPS3, SNCA, AURKA, XPO1, SMC1A, KAT2B, ARHGEF2, ROCK2, VPS4B, PDCD6IP, AKAP9, TUBB4A, STAG2, PLK2, FAM107A, CEP250, MAPRE3, PHLDB1, CAMSAP2, BICD2, CLASP1, CLIP3, SENP6, NIN, CHMP5, TRIM36, NSFL1C, MDM1, CHMP1B, TAOK1, SLAIN2, CEP85, CEP97, DIXDC1, NAV3, PHLDB2, CCSAP, UBXN2B, TTBK2, CEP120, CAMSAP1, SKA2
BP	GO:0032868	response to insulin	90/3408	1.65E-07	ADM, AKT2, APC, ATP2B1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, ZFP36L1, EGR1, ESRRA, FER, FOXO1, FOXO3, GAB1, GNAI2, GOT2, GRB2, GSK3B, HADHA, IGF1R, IGF2, IGFBP1, INSR, LYN, MAX, RAB8A, FOXO4, MYO1C, MYO5A, NCK1, OPA1, PDK4, ENPP1, PIK3C2A, PKM, PPARA, PPAT, PRKAA1, PTEN, PTPN1, PTPN11, RPS6KB1, SORT1, SRSF4, SHC1, SLC9A1, SORL1, SOS1,

					SRC, STAT1, VAMP2, TSC1, XBP1, YWHAG, USO1, SOCS1, IRS2, TNFSF10, SOCS2, KAT2B, ATP6V0D1, LPIN2, HDAC9, C2CD5, EPM2AIP1, TBC1D4, RAB31, WDTC1, LPIN1, KANK1, SIRT1, RHOQ, APPL1, SLC2A8, ADIPOR1, INSIG2, ATP6V1D, RAB8B, ERRFI1, PHIP, NUCKS1, SESN2, OSBPL8, ACVR1C, CPEB2, SOGA1, SESN3, ATP6V0E2, SLC27A1
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	46/3408	1.65E-07	ATM, ATR, ATRX, BRCA1, PTTG1IP, CD44, CDKN1A, CDKN1B, DDX5, DYRK1A, EP300, FOXM1, FOXO3, MDM4, MSX1, MYO6, CNOT4, PML, RBL2, SNAI2, SNAI1, SOX4, SP100, AURKA, TFDP1, TFDP2, TP53, TWIST1, BTG2, PPM1D, CNOT8, PLK2, CNOT1, KDM1A, SIRT1, ZNF385A, HIPK2, ING4, TRIAP1, CNOT6, SESN2, E2F7, SPRED1, SPRED2, ACER2, SPRED3
BP	GO:2000027	regulation of animal organ morphogenesis	85/3408	1.96E-07	ABL1, JAG1, AR, RHOA, ARRB2, BCL2, BMP7, BMPR1A, BMPR2, RUNX2, CDC42, AP2M1, CSF1, CTNNB1, DAB2, DVL3, EDN1, CELSR3, CELSR2, FGF1, FOXC1, GATA3, HOXD13, HES1, RBPJ, ISL1, SMAD4, MDK, MLLT3, MSX1, MYC, NFIB, TNFRSF11B, PAX2, PAX9, PDGFA, PIM1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, ROBO1, SFRP1, SNAI2, STAT1, HNF1B, TGFBR1, TIAM1, TWIST1, VDR, VEGFA, WNT2B, XBP1, FZD5, FZD3, FZD1, FZD4, FZD6, PSMF1, GPC6, PSME3, PSMD14, SPRY1, CITED2, FRS2, DKK1, PSME4, GREM1, SOX8, SIX4, WNT4, AHI1, BCOR, FBXW7, LGR4, SULF2, SMURF1, VANGL2, PLEKHA4, VANGL1, ZNRF3, PRICKLE2
BP	GO:0010976	positive regulation of neuron projection development	92/3408	1.96E-07	ABL2, ARF1, RHOA, ARHGDIA, BDNF, BMP7, BMPR2, SCARB2, CNTN1, CUX1, DVL3, EFNA5, MEGF8, MARK2, EP300, EPHA4, EZH2, FMR1, FN1, GDI1, GOLGA4, RAPGEF1, ARHGAP35, HSPA5, ILK, ITGA6, ITGA3, L1CAM, LIMK1, LRP1, LYN, CAPRIN1, MAP1B, MAPT, MDK, NCK1, NTRK3, OPA1, PAFAH1B1, PAK3, MAPK6, TWF1, PTPRD, RGS2, ROBO1, CX3CL1, SKIL, SRF, VAMP7, SYT1, TIAM1, VEGFA, VLDLR, RND2, SF3A2, FZD1, FZD4, SEMA7A, SNX3, IQGAP1, NRP1, KALRN, DLG5, NTN1, RAPGEF2, ACTR2, CPEB3, NLGN1, TRAK1, SHANK2, RAB21, KDM1A, PLXND1, SS18L1, NPTN, NIN, SYT17, C21orf91, TMEM106B, RRN3, TENM3, CAMK1D, SMURF1, KIDINS220, CREB3L2, NDRG4, METRN, MUL1, BHLHB9, PLXNA4, SYT2, DAB2IP
BP	GO:2001233	regulation of apoptotic signaling pathway	122/3408	2.28E-07	FAS, AR, ARRB2, BAK1, BCL2, BCL2L1, BDNF, BRCA1, PTTG1IP, CAV1, CD44, CTNNA1, CTNNB1, CYLD, DDX3X, EYA4, GNAI2, GNAI3, GRINA, GSK3B, HTT, HIF1A, HNRNPK, DNAJA1, ITGA6, ITGAV, MAZ, MCL1, MNT, MSX1, NCK1, NKX3-1, OPA1, SERPINE1, PAK2, PLAGL2, PML, PPP1CA, PPP2R1A, PPP3R1, MAPK8, MAPK9, PTEN, PTPN1, PTPRC, RB1, RPS3, CX3CL1, SFRP1, SIAH1, SIAH2, SKIL, SNAI2, SNAI1, SOD2, SP100, SRC, STK4, TCF7L2, TMBIM6, TERT, TFDP1, TFDP2, TGFBR1, THBS1, TIMP3, TP53, TPD52L1, TPT1, TRAF1, VDAC2, XBP1, YWHAE, YWHAG, NCK2, MADD, TP63, PEA15, TNFSF10, FADD, NRP1, ARHGEF2, HERPUD1, BCL2L11, BCAP31, PSME3, HYOU1, RBCK1, ZMYND11, SERINC3, KDM1A, SIRT1, SGK3, ZNF385A, BBC3, PRELID1, HTRA2, UBQLN1, RRM2B, TXNDC12, TRIAP1, PIAS4, TAF9B, WNT4, RRN3, PHIP, USP47, FBXW7, MFF, BIRC6, MOAP1, TMBIM1, MUL1, ITM2C, SYVN1, ITPRIP, BMF, RFFL, NACC2, DAB2IP, FLCN, CHCHD10
BP	GO:0018394	peptidyl-lysine acetylation	63/3408	2.30E-07	ARRB1, BRCA1, CHEK1, ATF2, CREBBP, DR1, EP300, GATA2, GATA3, KAT2A, HCFC1, HDAC2, IRF4, ISL1, SMAD4, MECP2, KMT2A, PRKAA1, MAPK3, SET, SNAI2, SNCA, SOX4, TAF1, TWIST1, KAT6A, YEATS4, DPF3, DPF1, NCOA3, KAT2B, LDB1, RPS6KA4, RPS6KA5, GTF3C4, ATG5, CLOCK, MORF4L2, CTCF, SRCAP, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, SETD5, EP400, BEND3, MEAF6, NAA40, NAA50, EPC1, TADA2B, ESCO1, FLCN
BP	GO:0051893	regulation of focal adhesion assembly	31/3408	2.90E-07	ABL1, RHOA, EFNA5, LRP1, MMP14, PTEN, PTPRJ, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VEGFA, IQGAP1, NRP1, LDB1, MAP4K4, ROCK2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, FMN1
BP	GO:0090109	regulation of cell-substrate junction assembly	31/3408	2.90E-07	ABL1, RHOA, EFNA5, LRP1, MMP14, PTEN, PTPRJ, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VEGFA, IQGAP1, NRP1, LDB1, MAP4K4, ROCK2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, FMN1
BP	GO:0007623	circadian rhythm	73/3408	2.90E-07	ADA, ADCY1, ZFHX3, KLF9, CPT1A, CREB1, CRY2, CSNK1D, CSNK1E, DYRK1A, EGFR, EGR1, EGR3, EP300, EZH2, GFPT1, GNAQ, GSK3B, HDAC2, HNF4A, HNRNPD, HNRNPU, ID4, JUN, JUND, KMT2A, NTRK3, SERPINE1, PML, PPARA, PPP1CA, PPP1CB, PPP1CC, PRKAA1, MAPK8, MAPK9, PROX1, PTEN, KDM5A, RORA, RORB, SIAH2, SUV39H1, HNF1B, KLF10, TP53, NRIP1, USP9X, BHLHE40, PER3, PER2, BTRC, USP2, MTA1, ROCK2, CLOCK, NCOR1, THRAP3, NR1D2, NCOA2, ATG7, NLGN1, KDM2A, MYCBP2, PHLPP1, SIRT1, TARDBP, SIN3A, FBXL3, FBXW7, LGR4, BTBD9, SIK1
BP	GO:0098727	maintenance of cell number	60/3408	3.02E-07	JAG1, BCL9, BMP7, BMPR1A, ZFP36L2, CTNNB1, DDX6, EIF4E, ELAVL1, EZH2, FGF2, FOXO1, FOXO3, GATA2, HES1, RBPJ, KIT, LIG4, LOXL2, SMAD2, SMAD4, NOTCH2, PAX2, PBX1, PRRX1, POLR2D, POLR2K, PROX1, SFRP1, SKI, SOX4, SS18, STAT3, TAL1, TBX3, HNF1B, KLF10, HMGA2, NCOA3, SMC1A, ARID1A, TP63, LDB1, LDB2, KLF4, CTR9, IGF2BP1, MTF2, CNOT1, NIPBL, FOXP1, RIF1, VANGL2, METTL14, CDC73, MED28, TET1, MED10, HOOK3, FUT10
BP	GO:0032869	cellular response to insulin stimulus	75/3408	3.02E-07	AKT2, APC, ATP2B1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, ZFP36L1, ESRRA, FER, FOXO1, FOXO3, GAB1, GNAI2, GRB2, GSK3B, IGF1R, IGF2, IGFBP1, INSR, RAB8A, FOXO4, MYO1C, MYO5A, NCK1, OPA1, PDK4, ENPP1, PIK3C2A, PKM, PPAT, PRKAA1, PTEN, PTPN1, PTPN11, RPS6KB1, SHC1, SLC9A1, SORL1, SOS1, SRC, STAT1, VAMP2, TSC1, XBP1, YWHAG, USO1, SOCS1, IRS2, SOCS2, KAT2B, ATP6V0D1, LPIN2, HDAC9, C2CD5, TBC1D4, RAB31, WDTC1, LPIN1, KANK1, SIRT1, RHOQ, APPL1, SLC2A8, ADIPOR1, ATP6V1D, RAB8B, ERRFI1, PHIP, NUCKS1, OSBPL8, CPEB2, SOGA1, SESN3, ATP6V0E2
BP	GO:0007015	actin filament organization	120/3408	3.18E-07	ABL1, ACTN4, ADD1, ARF1, ARF6, RHOA, RHOB, ARRB1, BCL2, CAPZA2, CD47, CDC42, CFL1, CFL2, CCR7, DIAPH1, S1PR1, EMP2, EPS8, FAT1, FER, GRB2, ARHGAP35, NCKAP1L, HIP1, LIMK1, MARCKS, MET, MYO1B, MYO1C, NCK1, NEDD9, NF2, PAK3, PAWR, PLS3, PRKCE, PROX1, PTGER4, TWF1, PXN, RASA1, RDX, RGS4, CX3CL1, SDC4, SFRP1, SLC9A1, SPTAN1, SPTBN1, SRC, SRF, TESK1, TGFBR1, TNFAIP1, TPM3, TPM4, TSC1, RND2, NCK2, CUL3, SORBS2, NRP1, WASF1, WASL, LATS1, ARHGEF2, ROCK2,

					BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, WASF2, TENM1, DLC1, RAPGEF3, CDC42EP2, CAP2, CAP1, NEBL, NCKAP1, IQGAP2, DSTN, CIT, FAM107A, RHOBTB3, LIMCH1, KANK1, CLASP1, COTL1, RHOQ, CORO1C, CD2AP, PDLIM3, TMOD2, WNT4, ARHGAP17, TTC17, FMN2, SPIRE1, SHROOM3, RHOU, PLEKHG2, ARHGAP28, SYNPO2L, CGNL1, FHDC1, PHLDB2, MYADM, ARHGAP18, ARHGAP12, WHAMM, JMY, SHROOM1, MTPN, RICTOR, SH3PXD2B, FMN1
BP	GO:0016050	vesicle organization	102/3408	3.32E-07	AP1G1, AKT2, ARF1, BCL2, CALR, CAV1, SCARB2, CD59, LYST, AP2M1, CREB1, CSNK1D, CTSZ, GNAI3, HPS1, INSIG1, KIF5B, RAB8A, NSF, PAFAH1B1, SERPINE2, PPP6C, RAB1A, RAB5B, SORT1, SDC4, SNAP25, SNCA, STX3, VAMP1, VAMP7, SYT1, TGFA, TMF1, UVRAG, CUL3, USO1, SNX3, NAPA, SYNJ1, SQSTM1, AP3D1, WASL, F2RL3, SYT7, VAPB, VAPA, VPS4B, GOSR1, GOSR2, SEC24C, ZFYVE16, C2CD5, TBC1D4, PDCD6IP, CNIH1, VAV3, SEC23A, UNC13B, ARFGEF2, SEC24A, TMED10, SNF8, PPP6R1, TMCC1, ANKRD28, DNAJC13, VPS8, CORO1C, CD2AP, STX12, ZNF385A, SEC31B, VPS36, HOOK1, TRAPPC4, ANKFY1, CHMP5, RAB14, TRAPPC2L, RAB8B, FNBP1L, STX17, VPS37C, GOLPH3L, PPP6R3, PI4K2B, LAPTM4B, TMEM127, SAR1A, CHMP1B, RAB22A, KIF13A, GORASP1, HOOK3, CHMP7, TBC1D20, EXOC8, VPS37D, MIA3, MYO18A, SNX19
BP	GO:0061138	morphogenesis of a branching epithelium	66/3408	3.36E-07	ABL1, ADM, AR, BCL2, BMP7, COL4A1, CSF1, CTNNB1, CTSZ, DAG1, EDN1, FGF1, FGF2, GRB2, FOXA1, HOXA5, HOXD13, ILK, KRAS, LRP6, SMAD4, MDK, MET, MMP14, MYC, NKX3-1, PAX2, PBX1, PDGFA, PGR, PKD1, PML, PPP1CA, PROX1, PTCH1, SFRP1, SNAI2, SRC, SRF, STK4, TBX3, HNF1B, VDR, VEGFA, WNT2B, FZD5, TP63, DCHS1, NRP1, BTRC, DLG5, SEMA3E, SPRY1, SEMA3A, GNA13, KDM5B, FRS2, PLXND1, SOX8, SIX4, WNT4, DLL4, LGR4, VANGL2, RDH10, NRARP
BP	GO:0016573	histone acetylation	59/3408	3.50E-07	ARRB1, BRCA1, CHEK1, ATF2, CREBBP, DR1, EP300, GATA2, GATA3, KAT2A, HCFC1, IRF4, ISL1, SMAD4, MECP2, KMT2A, MAPK3, SET, SNAI2, SNCA, TAF1, TWIST1, KAT6A, YEATS4, DPF3, DPF1, NCOA3, KAT2B, LDB1, RPS6KA4, RPS6KA5, GTF3C4, ATG5, CLOCK, MORF4L2, CTCF, SRCAP, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, SETD5, EP400, BEND3, MEAF6, NAA40, NAA50, EPC1, TADA2B, FLCN
BP	GO:0000910	cytokinesis	63/3408	3.57E-07	APC, ARF1, RHOA, RHOB, BCL2L1, CALM1, CALM2, CALM3, CDC42, CENPA, CETN2, CFL1, ECT2, INCENP, MYH9, MYH10, PIN1, PRKCE, PKN2, RASA1, SON, SPTBN1, AURKA, UVRAG, CUL3, PKP4, CDC14B, PRC1, AURKB, KIF3B, ROCK2, KIF23, VPS4B, KLHL21, PDCD6IP, ACTR2, STAMBP, PLK2, JTB, CIT, DCTN3, ZFYVE26, CECR2, GIT1, SH3GLB1, CHMP5, ANLN, ALKBH4, CEP55, TRIM36, PRPF40A, FMN2, SPIRE1, CHMP1B, BIRC6, KIF13A, RAB11FIP4, LZTS2, KLHL13, CHMP7, E2F7, KLHDC8B, FLCN
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	83/3408	3.97E-07	ACVR1B, ACVR2B, RHOA, ARRB2, BMPR1A, BMPR2, ZFP36L1, ZFP36L2, CAV1, CBL, COL1A1, COL1A2, COL3A1, COL4A2, CREB1, CREBBP, CRK, CRKL, DAB2, EDN1, EP300, FBN1, FBN2, FNTA, FUT8, GCNT2, NR3C1, HDAC2, HSPA5, ITGA3, JUN, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEF2C, MEN1, FURIN, PDE3A, PIN1, PML, PTPRK, PXN, SFRP1, SKI, SKIL, SOX11, SRC, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, USP9X, ITGA8, ADAM9, MTMR4, ONECUT2, CITED2, TAB1, POSTN, PEG10, SIRT1, ZNF451, APPL1, DKK3, HIPK2, TRIM33, NLK, WNT4, RNF111, FERMT1, PARD3, PMEPA1, SMURF1, EPB41L5, PBLD, WFIKKN2, ACVR1C, CD109, FLCN
BP	GO:0045787	positive regulation of cell cycle	117/3408	3.97E-07	ABL1, RHOA, ATM, ATRX, CCND1, BRCA1, CALR, CCND2, CCNT1, CCNT2, CDC25A, CDC42, CDKN1A, CDKN1B, CHEK1, DDX3X, ECT2, EDN1, EGFR, EIF4E, EIF4G1, EP300, EZH2, GATA6, HCFC1, FOXA1, HNRNPU, HES1, HSPA2, IGF2, INSR, LRP6, MAD2L1, MDM4, MECP2, MEIS2, FOXO4, MSX1, NKX3-1, CNOT4, PAFAH1B1, PBX1, PDGFB, PKD1, PML, POU4F1, PRKCA, PRKCE, PKN2, PROX1, PTPN11, RAD21, RB1, RBL2, RDX, RPS6KB1, SOX4, SRC, AURKA, ADAM17, TAL1, TBX3, DYNLT3, TERT, TFDP1, TFDP2, TGFA, TP53, BTG2, NR4A3, FOSL1, HMGA2, CUL4B, CUL3, PKP4, CDC14B, CDK10, USP2, AURKB, CNOT8, KIF3B, ROCK2, KIF23, ADAMTS1, VPS4B, BCL2L11, CITED2, PLK2, ZNF268, CIT, MAPRE3, CNOT1, NIPBL, SIN3A, ZNF385A, SH2B1, TRIAP1, DTL, WNT4, INO80, PHIP, PCID2, KMT2E, RCC2, NSFL1C, MEPCE, CNOT6, WIZ, CDC73, RHNO1, RAB11FIP4, UBXN2B, E2F7, TTL, DAB2IP, CEP120, EPGN
BP	GO:0019827	stem cell population maintenance	59/3408	4.46E-07	JAG1, BCL9, BMP7, BMPR1A, ZFP36L2, CTNNB1, DDX6, EIF4E, ELAVL1, FGF2, FOXO1, FOXO3, GATA2, HES1, RBPJ, KIT, LIG4, LOXL2, SMAD2, SMAD4, NOTCH2, PAX2, PBX1, PRRX1, POLR2D, POLR2K, PROX1, SFRP1, SKI, SOX4, SS18, STAT3, TAL1, TBX3, HNF1B, KLF10, HMGA2, NCOA3, SMC1A, ARID1A, TP63, LDB1, LDB2, KLF4, CTR9, IGF2BP1, MTF2, CNOT1, NIPBL, FOXP1, RIF1, VANGL2, METTL14, CDC73, MED28, TET1, MED10, HOOK3, FUT10
BP	GO:0030324	lung development	63/3408	4.49E-07	ACVR2B, ADA, ATP7A, BMPR1A, BMPR2, CREB1, CTNNB1, CTSZ, DAG1, EGFR, EIF4E, EP300, EPAS1, FGF1, FLT4, GATA6, FOXA1, HOXA5, HES1, IGFBP5, RBPJ, ITGA3, KRAS, SMAD2, MAN2A1, MME, MMP14, NFIB, PDGFA, PDGFRA, PGR, PKD1, PPP1CA, MAPK1, MAPK3, PROX1, SIM2, SOX11, SP3, SPARC, SRF, THRA, VEGFA, WNT7B, WNT2B, ALDH1A2, DLG5, SPRY1, FSTL3, KLF2, TAB1, AGR2, MAN1A2, CIC, SLC7A11, ERRFI1, FBXW7, VANGL2, HEG1, STK40, PKDCC, RDH10, ATXN1L
BP	GO:0071453	cellular response to oxygen levels	79/3408	4.63E-07	AK4, FAS, ATP6V1A, ATP7A, BCL2, BMP7, ZFP36L1, CAV1, CBL, CCNA2, CREBBP, DNMT3A, DNMT3B, EDN1, EGR1, EP300, EPAS1, FOXO1, FOXO3, GATA6, GNB1, HIF1A, RBPJ, IRAK1, KCNK3, MDM4, MYC, NKX3-1, OPA1, PDK3, PPARD, PRKAA1, PRKCE, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, PTGIS, RORA, SFRP1, SLC8A1, SLC9A1, SRC, STC1, SUV39H1, TMBIM6, TERT, TP53, TSC1, TWIST1, VEGFA, VHL, CUL2, STC2, LIMD1, ATP6V0D1, ROCK2, PSMF1, PSME3, PSMD14, CITED2, HYOU1, ATG7, PSME4, SIRT1, HIPK2, UBQLN1, HP1BP3, HIF1AN, FMN2, CPEB4, EGLN2, EGLN3, CPEB2, TMEM199
BP	GO:0030323	respiratory tube development	64/3408	4.63E-07	ACVR2B, ADA, ATP7A, BMPR1A, BMPR2, CREB1, CTNNB1, CTSZ, DAG1, EGFR, EIF4E, EP300, EPAS1, FGF1, FLT4, GATA6, FOXA1, HOXA5, HES1, IGFBP5, RBPJ, ITGA3, KRAS, SMAD2, MAN2A1, MME, MMP14, NFIB, PDGFA, PDGFRA, PGR, PKD1, PPP1CA, MAPK1, MAPK3, PROX1, SIM2, SOX11, SP3, SPARC, SRF, THRA, VEGFA, WNT7B, WNT2B, ALDH1A2, DLG5, TRAF4, SPRY1, FSTL3, KLF2, TAB1, AGR2, MAN1A2, CIC, SLC7A11, ERRFI1, FBXW7, VANGL2, HEG1, STK40, PKDCC, RDH10, ATXN1L

BP	GO:0030968	endoplasmic reticulum unfolded protein response	49/3408	4.63E-07	ADD1, AMFR, BAK1, CCND1, CALR, CANX, TPP1, ATF6B, EIF2S1, EP300, EXTL2, EXTL3, GFPT1, HDGF, HSPA5, IGFBP1, DNAJB9, NCK1, EIF2AK2, PTPN1, SHC1, SSR1, TLN1, VCP, XBP1, NCK2, STC2, ATP6V0D1, VAPB, GOSR2, EDEM1, HERPUD1, BCL2L11, CTDSP2, HYOU1, AGR2, SERP1, DERL2, BFAR, FKBP14, TMEM33, YOD1, ARFGAP1, TSPYL2, HERPUD2, CREB3L2, SYVN1, PPP1R15B, DAB2IP
BP	GO:0045785	positive regulation of cell adhesion	120/3408	4.63E-07	ABL1, ADA, RHOA, ZFHX3, ATM, BCL6, BMP7, CALR, CAV1, RUNX1, RUNX3, CBFB, CD44, CD47, CDC42, CDK6, CCR7, CRK, CRKL, CSF1, CSK, CYLD, DAG1, EFNB1, EFNB2, EGR3, EMP2, ERBB2, FLOT2, FN1, GATA3, GCNT2, GRB2, GSK3B, NCKAP1L, FOXA1, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, ILK, IRAK1, ITGA6, ITGA3, ITGA5, ITGAV, ITPKB, JUP, LYN, SMAD7, MDK, MYB, MYO10, NCK1, NEDD9, NID1, PAK2, PAK3, PODXL, PPP3CA, PRKCA, PRKCE, PTAFR, PTPN11, PTPRC, PTPRJ, RAG1, RPS3, RREB1, CX3CL1, SDC4, SFRP1, SRC, STX3, SYK, TFRC, TSC1, VCAM1, VEGFA, XBP1, NR4A3, NCK2, CHRD, SOCS1, TNFSF9, ADAM9, FADD, IQGAP1, NRP1, LDB1, AP3D1, CYTH3, CD83, MAP4K4, BAG4, SOCS5, SPOCK2, ARPC2, FSTL3, CITED2, BTN2A2, VAV3, AGR2, NFAT5, DUSP10, MMRN1, ICOSLG, WNT4, EPB41L4B, FERMT1, ZMIZ1, EPB41L5, CD276, MYADM, SIRPA, FLCN, DENND6A, FMN1
BP	GO:0042752	regulation of circadian rhythm	47/3408	4.65E-07	ADA, ADCY1, ZFHX3, CREB1, CRY2, CSNK1D, CSNK1E, EZH2, GNAQ, GSK3B, HNF4A, HNRNPD, PML, PPARA, PPP1CA, PPP1CB, PPP1CC, PRKAA1, MAPK8, MAPK9, PROX1, RORA, RORB, SIAH2, SUV39H1, KLF10, TP53, USP9X, BHLHE40, PER3, PER2, BTRC, USP2, MTA1, ROCK2, CLOCK, THRAP3, NR1D2, ATG7, NLGN1, KDM2A, PHLPP1, TARDBP, SIN3A, FBXL3, FBXW7, SIK1
BP	GO:0051052	regulation of DNA metabolic process	126/3408	4.83E-07	ARRB2, ATM, ATR, ATRX, BCL6, BMPR2, BRCA1, CCNA2, CCT6A, CDKN1A, CEBPG, CHEK1, CTNNB1, DACH1, DKC1, DUSP1, EGFR, ERCC2, EYA4, ERCC6, FGF2, FOXM1, FUS, GATA3, GJA1, HNRNPC, HNRNPD, HNRNPU, IL7R, JUN, KPNA1, MECP2, MAP3K4, MEN1, MLH1, KMT2A, MYC, OGG1, PAK3, PARN, PDGFB, PML, PPP2CA, PPP2R1A, MAPK1, MAPK3, PTPRC, RAD51, RBBP6, UPF1, RPS3, MAP2K4, SRC, TFDP1, TFRC, TNFAIP1, TP53, TWIST1, UBE2N, UBE2V1, USP1, XRCC5, ZNF91, HMGA2, USP9X, SMC1A, TNKS, MBD2, AURKB, KLF4, TRIP12, SMG7, ACTR2, ATG7, CERS1, POLQ, STAG2, MORC2, KDM1A, SMG1, FAM168A, PDS5A, SMG5, SIRT1, SPIDR, PARM1, SH2B1, GREM1, UBR5, RTEL1, XRN1, GNL3L, INO80, OTUD4, CHTF8, PINX1, FIGN, RIF1, FBXW7, ATF7IP, YLPM1, FMN2, UBQLN4, SPIRE1, SMARCAD1, USP37, WIZ, TSPYL2, NUCKS1, NABP2, BRCC3, HMBOX1, KLHL15, TET1, SLX4, ZNF830, SLFN11, ESCO1, RMI2, E2F7, PPP4R2, USP51, RNF168, FLCN, KDM1B, ZBTB38
BP	GO:0060996	dendritic spine development	42/3408	4.97E-07	ADAM10, ARF1, ARF6, CAMK2A, CDC42, CFL1, EPHA4, EPHB2, EPHB3, ACSL4, FMR1, HDAC2, CAPRIN1, MEF2C, OPA1, PAFAH1B1, PAK2, PAK3, MAPK6, PTEN, TIAM1, NCK2, WASL, KALRN, DLG5, ACTR2, ABI2, SLC9A6, PDLIM5, PLK2, CPEB3, NLGN1, SHANK2, FSTL4, SIPA1L1, ASAP1, C21orf91, UBA6, SLC12A5, ARID1B, BHLHB9, SDK1
BP	GO:0060537	muscle tissue development	121/3408	5.04E-07	RHOA, ARRB2, BCL2, BCL9, BMP7, BMPR1A, CALR, CAV1, CCNT2, CFL2, COL3A1, COL11A1, COL19A1, CREB1, MAPK14, CSRP1, CTNNB1, CXADR, DCN, DDX5, S1PR1, EDN1, EFNB2, EGR1, EP300, FGF2, FKBP1A, FOXC1, FLNB, G6PD, GATA6, KAT2A, GJA1, NRG1, HMGCR, HNRNPU, FOXN2, IGFBP5, RBPJ, ISL1, ITGB1, JARID2, SMAD4, SMAD7, MEF2A, MEF2C, MEF2D, MYH10, PDGFRA, PIM1, PIN1, POU4F1, PPARA, PPP3CA, PRKAA1, PRKAR1A, MAPK1, PROX1, PTEN, RB1, RGS2, RGS4, MAP2K4, SGCD, SKI, SLC8A1, SLC9A1, SOX11, SRF, TBX3, NR2F2, TGFBR1, TGFBR3, TSC1, TWIST1, VEGFA, YY1, BTG2, ARID1A, SORBS2, ITGA8, ALDH1A2, COPS2, HAND1, AKAP6, ATG5, HDAC9, NR1D2, GJC1, UBE4B, ZBTB18, DDX17, NEBL, PDLIM5, FRS2, AKAP13, DKK1, KDM6B, MAFF, FBXO22, HEYL, GREM1, SOX8, CDON, SIX4, DLL4, CHD7, GPCPD1, CYP26B1, ADAMTS9, HEG1, ALPK3, NDRG4, AKIRIN1, PTCD2, UQCC2, ZNF689, MTPN, SIK1, ARID2, FLCN
BP	GO:0002262	myeloid cell homeostasis	56/3408	5.54E-07	ACVR1B, ADAR, ADD1, AXL, BAK1, BCL6, ZFP36L1, CASP3, CDK6, CEBPG, MAPK14, EPAS1, ERCC2, FOXO3, G6PD, GATA2, GATA3, NCKAP1L, HIF1A, HOXA5, IREB2, ITPKB, KIT, LYN, KITLG, SLC11A2, PRDX1, PIK3CB, PKNOX1, RB1, SP3, SRF, STAT1, STAT3, STAT5B, ADAM17, TAL1, TGFBR3, THRA, VEGFA, ZFP36, BAP1, LDB1, PTBP3, BCL2L11, SH2B3, KLF2, NCSTN, RBFOX2, SLC7A11, HIPK2, NCAPG2, SLC25A38, KMT2E, SFXN1, FAM210B
BP	GO:0006473	protein acetylation	71/3408	5.83E-07	ARRB1, BRCA1, CHEK1, ATF2, CREBBP, DR1, EP300, FOXO1, GATA2, GATA3, KAT2A, GSK3B, HCFC1, HDAC2, IRF4, ISL1, SMAD4, MAPT, MECP2, KMT2A, PRKAA1, MAPK3, SET, SNAI2, SNCA, SOX4, TAF1, TWIST1, KAT6A, YEATS4, DPF3, DPF1, NCOA3, KAT2B, LDB1, RPS6KA4, RPS6KA5, GTF3C4, ATG5, CLOCK, MORF4L2, RAPGEF3, CTCF, SRCAP, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, SETD5, TAOK1, EP400, BEND3, NAA35, MEAF6, NAA40, NAA25, NAA50, EPC1, TADA2B, ESCO1, NAA30, FLCN
BP	GO:2000756	regulation of peptidyl-lysine acetylation	30/3408	6.86E-07	ARRB1, BRCA1, CHEK1, GATA2, GATA3, KAT2A, HDAC2, ISL1, SMAD4, KMT2A, PRKAA1, MAPK3, SET, SNAI2, SNCA, SOX4, TWIST1, RPS6KA4, RPS6KA5, ATG5, CTCF, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, SETD5, TADA2B, FLCN
BP	GO:0043407	negative regulation of MAP kinase activity	36/3408	6.97E-07	BMP7, CAV1, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, HMGCR, DNAJA1, LYN, PPP2CA, PPP2R1A, PTPN1, PTPRJ, RGS2, RGS4, SFRP1, SORL1, SH2B3, HIPK3, SPRY1, DUSP14, DUSP10, STK38, PDCD4, LAX1, AIDA, DUSP16, SPRY4, DUSP18, DAB2IP, SPRED1, ZNF675, SPRED2, SPRED3
BP	GO:1903828	negative regulation of cellular protein localization	46/3408	7.12E-07	ARF6, BCL2L1, AP2M1, CSK, DAB2, GBP1, GDI1, GSK3B, DNAJA1, INSIG1, MAP1A, MAPT, PKIA, SP100, TXN, UBE2G2, NUMB, DCLK1, ROCK2, BAG4, LYPLA1, RHOQ, LEPROTL1, POLR1A, SIN3A, DERL2, ABHD17B, UBE2J1, SUFU, RAB23, LEPROT, YOD1, FERMT1, VPS35, NSFL1C, INPP5E, OTUD7B, TP53INP2, ABHD17C, TMBIM1, LZTS2, ANKRD13A, PKDCC, UBXN2B, TTBK2, FLCN
BP	GO:0097193	intrinsic apoptotic signaling pathway	92/3408	7.12E-07	ABL1, ATM, BAK1, BCL2, BCL2L1, BRCA1, PTTG1IP, CASP3, CAV1, CD44, CDKN1A, CEBPB, CYLD, DDX3X, DDX5, EP300, ERCC6, FHIT, GRINA, HIF1A, UBE2K, HNRNPK, DNAJA1, ITPR1, MCL1, MLH1, MSX1, NCK1, NKX3-1, OPA1, PLAGL2, PML, POU4F1, PTPN1, RPS3, SIAH1, SKIL, SNAI2, SNAI1, SOD2, SRC, TMBIM6, TNFRSF1B, TP53, TPT1, VDAC2, XBP1, CUL5, STK24, NCK2, DYRK2, CUL3,

					CUL2, TP63, ARHGEF2, HERPUD1, MELK, BCL2L11, BCAP31, HYOU1, SERINC3, KDM1A, SIRT1, PHLDA3, ZNF385A, BBC3, HTRA2, HIPK2, CDIP1, UBQLN1, RRM2B, TXNDC12, TRIAP1, PIAS4, TAF9B, DNAJC10, DDIT4, RRN3, USP47, FBXW7, FNIP2, USP28, MOAP1, AEN, SGPP1, SYVN1, BMF, JMY, NACC2, DAB2IP, FLCN, HIPK1
BP	GO:0048545	response to steroid hormone	115/3408	7.12E-07	ADM, ALAD, AR, RHOA, ARRB2, ATP2B1, CCND1, BCL2, BMP7, BRCA1, ZFP36L1, ZFP36L2, KLF9, CALM3, CALR, CASP3, CAV1, RUNX1, CBFB, CDKN1A, COL1A1, CRY2, CTNNB1, DAB2, DDX5, DNMT3B, DUSP1, EDN1, EGFR, EIF4E, EP300, ESR2, ESRRA, ESRRG, FHL2, FKBP4, FOXO1, FOXO3, FOSB, NR5A2, NR6A1, NR3C1, FOXA1, HNF4A, HNRNPU, DNAJA1, ISL1, KRAS, MDK, NEDD4, NKX3-1, NPC1, NTRK3, PAPPA, PGR, PPARA, PPARD, PTAFR, RAN, RARG, RB1, RNF4, RORA, RORB, SFRP1, SPARC, SRC, STC1, TAF1, NR2F2, TFPI, THBS1, THRA, NR2C2, UBE2L3, NR1H2, VDR, WNT7B, ZFP36, NR4A3, FOSL1, KMT2D, NCOA3, NRIP1, ARID1A, TP63, AKR1C3, ADAM9, LATS1, CLOCK, NCOR1, NR1D2, BCL2L11, PGRMC2, NCOA2, DDX17, ABHD2, FAM107A, AKAP13, CNOT1, UFL1, SIRT1, RBFOX2, WBP2, HEYL, FOXP1, STRN3, UBR5, ERRFI1, DDIT4, PMEPA1, CALCOCO1, PAQR8, EGLN2, KCTD6
BP	GO:0014706	striated muscle tissue development	116/3408	7.96E-07	RHOA, ARRB2, BCL2, BCL9, BMP7, BMPR1A, CALR, CAV1, CCNT2, CFL2, COL11A1, COL19A1, CREB1, MAPK14, CTNNB1, CXADR, DCN, DDX5, S1PR1, EDN1, EFNB2, EGR1, EP300, FGF2, FKBP1A, FOXC1, FLNB, G6PD, GATA6, KAT2A, GJA1, NRG1, HMGCR, HNRNPU, FOXN2, RBPJ, ISL1, ITGB1, JARID2, SMAD4, SMAD7, MEF2A, MEF2C, MEF2D, MYH10, PDGFRA, PIM1, PIN1, POU4F1, PPARA, PPP3CA, PRKAA1, PRKAR1A, MAPK1, PROX1, PTEN, RB1, RGS2, RGS4, MAP2K4, SGCD, SKI, SLC8A1, SLC9A1, SOX11, SRF, TBX3, NR2F2, TGFBR1, TGFBR3, TSC1, TWIST1, VEGFA, YY1, BTG2, ARID1A, SORBS2, ALDH1A2, COPS2, HAND1, AKAP6, ATG5, HDAC9, NR1D2, GJC1, UBE4B, ZBTB18, DDX17, NEBL, PDLIM5, FRS2, AKAP13, DKK1, KDM6B, MAFF, FBXO22, HEYL, GREM1, SOX8, CDON, SIX4, DLL4, CHD7, GPCPD1, CYP26B1, ADAMTS9, HEG1, ALPK3, NDRG4, AKIRIN1, PTCD2, UQCC2, ZNF689, MTPN, SIK1, ARID2
BP	GO:0051168	nuclear export	68/3408	8.08E-07	CALR, EIF4E, GSK3B, NCBP1, NUP88, NUP98, PKD1, POLR2D, PTPN11, PTPN14, RAN, RANBP2, UPF1, ABCE1, ATXN1, SRSF1, SRSF2, SRSF4, SRSF7, SP100, STYX, TCF7L2, TP53, TSC1, TXN, XPO1, YWHAE, PABPN1, POM121, SMG7, NUTF2, RAPGEF3, NXF1, ANP32B, NUP50, AHCYL1, RNPS1, CPSF6, AKAP13, XPOT, DDX19B, U2AF2, XPO7, SMG1, SMG5, UPF2, RBM15B, NMD3, DNAJC27, CDC40, CPSF2, RBM27, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, SMURF1, THOC2, XPO5, XPO4, DUSP16, SEH1L, LZTS2, NUP43, POM121C
BP	GO:0051403	stress-activated MAPK cascade	91/3408	8.53E-07	ADORA2B, FAS, ZFP36L1, CCR7, CRKL, MAPK14, CYLD, DUSP1, DUSP9, DVL3, EDN1, EGFR, EPHA4, ERCC6, FOXM1, FOXO1, FLT4, RAPGEF1, HMGCR, DNAJA1, IGF1R, IKBKB, IRAK1, IRAK2, NBR1, MAP3K3, MAP3K4, MEN1, MID1, MAP3K9, MYC, NFKB1, PAFAH1B1, PRDX1, MAPK1, MAPK3, MAPK8, MAPK9, EIF2AK2, PTGER4, PTPN1, RAP2A, RPS3, MAP2K4, SFRP1, SKP1, SYK, TIAM1, TPD52L1, UBE2N, UBE2V1, VEGFA, WNT7B, ZFP36, FZD5, FZD4, BTRC, SPAG9, TAOK2, MAP4K4, NCOR1, TRAF4, RASSF2, FGF19, HIPK3, TRIB1, SEMA3A, NOD1, TAB1, MAP3K2, ZMYND11, DUSP10, DKK1, KLHDC10, TAB2, MAPK8IP3, PHLPP1, PDCD4, HIPK2, MINK1, SEMA4C, VANGL2, TAOK1, AIDA, MUL1, ITCH, SIRPA, DAB2IP, ZNF675, EMC10, SH3RF3
BP	GO:0007163	establishment or maintenance of cell polarity	72/3408	8.80E-07	ANK1, ARF6, RHOA, RHOB, DST, CDC42, CENPA, CFL1, CCR7, CRK, CRKL, CTNNA1, DLG3, MARK2, FAT1, FLOT2, GATA3, ARHGAP35, GSK3B, HTT, NCKAP1L, HES1, ILK, MAD2L1, MAP1B, MAP4, MYH9, OPHN1, PAFAH1B1, PAX6, PKD1, RAP1B, SLC9A1, WNT7B, RND2, MAP7, ARHGEF2, DLG5, CYTH3, CYTH1, ROCK2, PDCD6IP, UST, ARPC5, ACTR2, SPRY1, CAP2, CAP1, KIF2C, RHOBTB3, RAB11FIP2, KANK1, WWC1, CLASP1, RHOQ, CLIC4, NDE1, FERMT1, FRMD4A, NSFL1C, PARD3, CYP26B1, VANGL2, RHOU, MAPKAP1, PARD6B, UBXN2B, AMOT, AMOTL1, RICTOR, CRB2, MYO18A
BP	GO:0036293	response to decreased oxygen levels	111/3408	9.40E-07	ACTN4, ADA, ADM, AK4, ALAD, RHOA, ATM, ATP1B1, ATP7A, BCL2, BMP7, ZFP36L1, CAPN2, CASP3, CAV1, CBL, CCNA2, CDKN1B, CREB1, CREBBP, DNMT3A, DNMT3B, EDN1, EGR1, EP300, EPAS1, ERCC2, FOXO3, GATA6, GNB1, HIF1A, HK2, RBPJ, IRAK1, ITPR1, ITPR2, KCNK3, LDHA, LOXL2, SMAD4, MDM4, MECP2, MMP14, MTHFR, MYB, MYC, NKX3-1, SLC11A2, OPA1, PDK3, PIN1, PKM, PML, PPARA, PPARD, PRKAA1, PRKCE, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, PTGIS, RORA, SFRP1, SLC8A1, SLC9A1, SRC, SRF, STC1, SUV39H1, ADAM17, TMBIM6, TERT, TGFBR3, THBS1, TP53, TSC1, TWIST1, VCAM1, VEGFA, VHL, CUL2, STC2, LIMD1, ROCK2, PSMF1, PSME3, PSMD14, CITED2, HYOU1, POSTN, PSME4, SIRT1, TXN2, HIPK2, UBQLN1, SLC2A8, HP1BP3, DDIT4, ALKBH5, HIF1AN, FMN2, CPEB4, APOLD1, EGLN2, EGLN3, CPEB2
BP	GO:0010822	positive regulation of mitochondrion organization	47/3408	1.08E-06	BAK1, BCL2, DCN, GSK3B, HTT, HIF1A, HK2, OPA1, PPP3R1, PRKAA1, MAPK8, SREBF2, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, BAP1, TP63, TNFSF10, ATG13, MFN2, BCL2L11, ARIH2, BBC3, HTRA2, SH3GLB1, MIEF1, LEPROT, VPS13C, VPS13D, FBXW7, VPS35, MFF, SMURF1, USP36, RHOU, MOAP1, MUL1, DDHD1, BMF, MIEF2, PLD6, CHCHD10
BP	GO:0018393	internal peptidyl-lysine acetylation	59/3408	1.08E-06	ARRB1, BRCA1, CHEK1, ATF2, CREBBP, DR1, EP300, GATA2, GATA3, KAT2A, HCFC1, IRF4, ISL1, SMAD4, MECP2, KMT2A, MAPK3, SET, SNAI2, SNCA, TAF1, TWIST1, KAT6A, YEATS4, DPF3, DPF1, NCOA3, KAT2B, LDB1, RPS6KA4, RPS6KA5, GTF3C4, ATG5, CLOCK, MORF4L2, CTCF, SRCAP, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, SETD5, EP400, BEND3, MEAF6, NAA40, NAA50, EPC1, TADA2B, FLCN
BP	GO:0035967	cellular response to topologically incorrect protein	59/3408	1.08E-06	ADD1, AMFR, BAK1, CCND1, CALR, CANX, TPP1, ATF6B, EIF2S1, EP300, EXTL2, EXTL3, GFPT1, HDGF, HSPA2, HSPA5, IGFBP1, DNAJB9, ATXN3, NCK1, EIF2AK2, PTPN1, SHC1, SSR1, TMBIM6, TLN1, VCP, XBP1, NCK2, CUL3, STC2, ATP6V0D1, VAPB, GOSR2, EDEM1, HERPUD1, BCL2L11, CTDSP2, HYOU1, AGR2, HSPB8, SERP1, DERL2, BFAR, DNAJB12, FKBP14, TMEM33, UBE2W, YOD1, ARFGAP1, UGGT1, TSPYL2, HERPUD2, CREB3L2, KLHL15, RHBDD1, SYVN1, PPP1R15B, DAB2IP

BP	GO:0045637	regulation of myeloid cell differentiation	82/3408	1.11E-06	ACVR1B, JAG1, ZFP36L1, CAMK4, RUNX1, CBFB, CDK6, CEBPB, CREB1, CREBBP, MAPK14, CSF1, CTNNB1, EP300, ESRRA, FBN1, FOXO3, GABPA, GATA2, GNAS, NCKAP1L, HIF1A, HMGB3, HOXA5, HOXA7, HOXA9, HOXB8, ITPKB, JUN, LYN, MEF2C, MEIS2, KITLG, KMT2A, MYC, CNOT4, NOTCH2, POU4F1, PRKCA, PURB, RARG, RB1, SFRP1, STAT1, STAT3, STAT5B, TAL1, THBS1, KLF10, ZFP36, NR4A3, KMT2D, FADD, KAT2B, LDB1, CTR9, SETD1A, KMT2B, RASSF2, TRIB1, FSTL3, PIAS3, TOB2, TNRC6B, RBFOX2, SIN3A, AGO1, FOXP1, TNRC6A, NCAPG2, FBXW7, KMT2E, TNRC6C, KMT2C, CDC73, DPY30, FAM210B, ZBTB46, ZNF675, AGO3, AGO4, SIGLEC15
BP	GO:0048013	ephrin receptor signaling pathway	38/3408	1.11E-06	ACTB, RHOA, CDC42, AP2M1, CRK, EFNA3, EFNA5, EFNB1, EFNB2, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, RBPJ, LYN, NCK1, NTRK3, PAK3, PTPN11, RASA1, SDC2, SRC, SS18, TIAM1, NCK2, WASL, KALRN, ROCK2, ARPC5, ACTR2, ARPC2, VAV3, NCSTN, SIPA1L1, GIT1, APH1A, APH1B
BP	GO:0090287	regulation of cellular response to growth factor stimulus	92/3408	1.14E-06	ABL1, BMPR2, CAV1, RUNX2, CREBBP, CTNNB1, DAB2, DCN, EP300, FBN1, FBN2, FGF1, FGF2, GATA3, HIF1A, HES1, HSPA5, RBPJ, ILK, ITGA3, ITGA5, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEN1, MSX1, MYO1C, NEDD4, NEO1, NTRK3, PCSK6, PIN1, PTPN1, ROBO1, SFRP1, SKI, SKIL, SORL1, SOX11, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, VEGFA, FZD1, FZD4, ITGA8, CHRD, WASF1, MTMR4, ONECUT2, TOB1, SPRY1, FSTL3, CITED2, FST, SLC9A6, FSTL1, DKK1, PEG10, SIRT1, DSTYK, ZNF451, MYOF, GREM1, CYFIP2, NPTN, DKK3, HIPK2, TRIM33, WNT4, RNF111, FERMT1, SULF2, PMEPA1, FAM20C, SMURF1, SEMA6A, PBLD, SPRY4, WFIKKN2, CD109, DAB2IP, BMPER, FLCN, CRB2, RBPMS2, RNF165
BP	GO:0019216	regulation of lipid metabolic process	120/3408	1.15E-06	ACACA, ACOX1, ADM, AKT2, ALAS1, ARF1, ASAH1, BRCA1, CAPN2, CAV1, CCR7, CPT1A, CREB1, CREBBP, EGR1, FGF1, FGF2, FGFR3, FHL2, HMGCR, HMGCS2, HNF4A, INSIG1, KIT, LDLR, FADS1, LSS, LYN, NFKB1, NFYA, NFYB, PDGFA, PDGFB, PDGFRA, PDK3, PDK4, PPARA, PPARD, PRKAA1, PRKAB2, PRKCE, PROX1, RAN, RB1, RBL2, RORA, SCD, SNAI2, SNAI1, SNCA, SORL1, SRC, SREBF2, TBL1X, THRA, TWIST1, NR1H2, VDR, SF1, NR4A3, NSMAF, AKR1C3, SOCS1, IRS2, SOCS2, MTMR3, MTMR4, SOCS6, KLF4, NCOR1, SOCS5, LPGAT1, FGF19, NR1D2, VAV3, NCOA2, GLIPR1, ERLIN2, ATG14, WDTC1, RGL1, SIRT1, SIN3A, LDLRAP1, DKK3, ORMDL2, DNAJC15, GRHL1, SOCS7, ADIPOR1, ABHD5, INSIG2, GOLM1, WNT4, PDPR, FBXW7, PDP2, ELOVL5, BCL11B, MTMR9, ELOVL6, ADIPOR2, TBL1XR1, LPCAT1, PANK2, CHD9, OPA3, LONP2, ORMDL1, ORMDL3, TGS1, PIK3IP1, WDR81, STARD4, SAMD8, SIK1, DAB2IP, RDH10, CNEP1R1, SLC27A1
BP	GO:0001666	response to hypoxia	108/3408	1.17E-06	ACTN4, ADA, ADM, AK4, ALAD, RHOA, ATM, ATP1B1, ATP7A, BCL2, BMP7, ZFP36L1, CAPN2, CASP3, CAV1, CCNA2, CDKN1B, CREB1, CREBBP, DNMT3A, DNMT3B, EDN1, EGR1, EP300, EPAS1, ERCC2, FOXO3, GATA6, GNB1, HIF1A, HK2, RBPJ, IRAK1, ITPR1, ITPR2, KCNK3, LDHA, LOXL2, SMAD4, MDM4, MECP2, MMP14, MTHFR, MYB, MYC, NKX3-1, SLC11A2, OPA1, PDK3, PIN1, PKM, PML, PPARA, PPARD, PRKAA1, PRKCE, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, PTGIS, RORA, SFRP1, SLC8A1, SLC9A1, SRC, SRF, STC1, SUV39H1, ADAM17, TMBIM6, TERT, TGFBR3, THBS1, TP53, TWIST1, VCAM1, VEGFA, VHL, CUL2, STC2, LIMD1, ROCK2, PSMF1, PSME3, PSMD14, CITED2, HYOU1, POSTN, PSME4, SIRT1, TXN2, HIPK2, UBQLN1, SLC2A8, HP1BP3, DDIT4, ALKBH5, HIF1AN, FMN2, APOLD1, EGLN2, EGLN3, CPEB2
BP	GO:0030900	forebrain development	113/3408	1.31E-06	RHOA, ATP2B4, ATP7A, ATRX, AXL, BMPR1A, CASP3, CDK6, COL3A1, CREB1, CRK, CRKL, CTNNB1, DLX2, EGFR, EPHB2, EPHB3, EZH1, EZH2, GATA2, KAT2A, ARHGAP35, GSK3B, NRG1, HIF1A, HES1, ID4, RBPJ, ISL1, KCNC1, KIF5B, KRAS, LRP1, LRP6, MDK, MSX1, MYH10, MYO1D, NF2, NFIB, OPHN1, OTX1, PAFAH1B1, PAX6, PEX13, POU3F2, POU4F1, PROX1, PTEN, ROBO1, TRA2B, SKI, SLC1A2, SLC8A1, SRC, SRF, TACC1, TBX3, NR2F2, TOP2B, TSC1, TYRO3, WNT7B, WNT2B, YWHAE, BTG2, NR4A3, ARID1A, SEMA7A, CHRD, NUMB, NRP1, ALDH1A2, DCLK1, RAPGEF2, ARPC5, SEMA3A, DLC1, IGF2BP1, FRS2, BTBD3, DKK1, KDM1A, PHLPP2, KDM6B, SATB2, SZT2, SLC7A11, SIN3A, CNTNAP2, SLITRK5, HTRA2, CDON, NIN, C21orf91, WNT4, SLC38A2, NDE1, UBA6, CHD7, ZSWIM6, METTL14, BCL11B, PGAP1, HOOK3, FUT10, DIXDC1, PLXNA4, PTCHD1, DAB2IP, CEP120, FBXO45, CCDC85C
BP	GO:0072001	renal system development	92/3408	1.34E-06	ACVR2B, JAG1, BCL2, BMP7, COL4A1, CTNNB1, DCN, EFNB2, EGR1, EPHA4, EPHA7, FBN1, FGF1, FGF2, FOXC1, GATA3, HES1, IL6R, ILK, ITGA6, ITGA3, SMAD2, SMAD4, SMAD6, SMAD7, MEF2C, MME, MYC, NFIA, NID1, NKX3-1, PAX2, PBX1, PDGFA, PDGFB, PDGFRA, PKD1, PODXL, PPAT, PROX1, PTCH1, SDC4, SFRP1, SOX4, SOX11, STAT1, HNF1B, TGFBR1, TSC1, VEGFA, WNT7B, WNT2B, ITGA8, DCHS1, FADD, IQGAP1, NRP1, ALDH1A2, SGPL1, DLG5, ADAMTS1, BCL2L11, GDF11, SPRY1, FSTL3, TMED10, NIPBL, KLHL3, HEYL, SEC61A1, SOX8, RRM2B, APH1A, SIX4, WNT4, AHI1, CEP55, LGR4, NUP133, SULF2, CYP26B1, C1GALT1, VANGL2, PTCD2, ARID5B, LZTS2, GLIS2, AMER1, RDH10, BMPER, FLCN, FMN1
BP	GO:0007369	gastrulation	65/3408	1.35E-06	ACVR2B, BMP7, BMPR1A, BMPR2, COL4A2, COL5A1, COL5A2, COL11A1, COL12A1, CTNNB1, DAG1, MEGF8, FOXC1, FN1, GATA6, HNF4A, HSBP1, ITGA3, ITGA5, ITGAV, ITGB1, LRP6, SMAD2, SMAD4, MBP, MMP14, NF2, PAX2, PRKAR1A, RNF2, SFRP1, SNAI1, SRF, TAL1, HNF1B, TP53, UGDH, KDM6A, NR4A3, HMGA2, ARID1A, CUL3, ITGA8, CHRD, LDB1, KLF4, HAND1, CTR9, ARFRP1, FRS2, DKK1, KDM6B, PHLDB1, CLASP1, VANGL2, EPB41L5, TGIF2, RIC8A, WNK1, CDC73, SOX7, PHLDB2, MYADM, AMOT, CRB2
BP	GO:0062012	regulation of small molecule metabolic process	131/3408	1.36E-06	ACACA, ADCYAP1R1, ADM, ADORA2B, AK4, AKT2, RHOA, ATP2B4, ATP7A, BRCA1, CAV1, COMT, CPT1A, EGR1, EP300, FGF1, FOXO1, KAT2A, GSK3B, HIF1A, HMGCR, IGF2, FOXK2, INSIG1, INSR, KIT, LDLR, LSS, ME2, NFKB1, NFYA, NFYB, NUP88, NUP98, OAZ2, P2RY1, PDGFB, PDK3, PDK4, ENPP1, PFKFB2, PFKFB3, PFKFB4, PGAM1, PHKG2, PPARA, PPP1CA, PPP1CB, PRKAA1, PRKAB2, PRKCE, PROX1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTAFR, RAN, RANBP2, RORA, SCD, SNAI2, SNAI1, SNCA, SRC, SREBF2, STAT3, TP53, TWIST1, NR1H2, VCP, VDR, NR4A3, DYRK2, AKR1C3, IRS2, KAT2B, PSMF1, NCOR1, EPM2AIP1, POM121, LPGAT1, FGF19, PSME3, PSMD14, NCOA2, NUP50, ARPP19, ERLIN2, SLC2A6, WDTC1, PASK, PSME4, SIRT1, ISCU, SLC7A11, LDLRAP1, DKK3, DNAJC15, ADIPOR1, INSIG2, AZIN1, WNT4, DDIT4, PDPR, NDC1, NUP133, PDP2, BEND3, ELOVL5,

					ELOVL6, ADIPOR2, PANK2, SEH1L, SESN2, LONP2, DNAJC30, UQCC2, STARD4, SOGA1, SIK1, RDH10, PPTC7, FLCN, PDE12, FOXK1, NUP43, POM121C
BP	GO:0006475	internal protein amino acid acetylation	60/3408	1.38E-06	ARRB1, BRCA1, CHEK1, ATF2, CREBBP, DR1, EP300, GATA2, GATA3, KAT2A, HCFC1, IRF4, ISL1, SMAD4, MAPT, MECP2, KMT2A, MAPK3, SET, SNAI2, SNCA, TAF1, TWIST1, KAT6A, YEATS4, DPF3, DPF1, NCOA3, KAT2B, LDB1, RPS6KA4, RPS6KA5, GTF3C4, ATG5, CLOCK, MORF4L2, CTCF, SRCAP, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, SETD5, EP400, BEND3, MEAF6, NAA40, NAA50, EPC1, TADA2B, FLCN
BP	GO:0034620	cellular response to unfolded protein	53/3408	1.45E-06	ADD1, AMFR, BAK1, CCND1, CALR, CANX, TPP1, ATF6B, EIF2S1, EP300, EXTL2, EXTL3, GFPT1, HDGF, HSPA2, HSPA5, IGFBP1, DNAJB9, NCK1, EIF2AK2, PTPN1, SHC1, SSR1, TMBIM6, TLN1, VCP, XBP1, NCK2, STC2, ATP6V0D1, VAPB, GOSR2, EDEM1, HERPUD1, BCL2L11, CTDSP2, HYOU1, AGR2, HSPB8, SERP1, DERL2, BFAR, FKBP14, TMEM33, YOD1, ARFGAP1, TSPYL2, HERPUD2, CREB3L2, RHBDD1, SYVN1, PPP1R15B, DAB2IP
BP	GO:0070997	neuron death	105/3408	1.47E-06	ABL1, ADARB1, AKT2, RHOA, ARRB1, ARRB2, ATM, AXL, BCL2, BCL2L1, BDNF, CAPN2, CASP3, CBL, CDC34, CEBPB, CREB1, ATF2, CSF1, CTNNB1, CTSZ, ATN1, EFNB2, EGR1, EIF2S1, EIF4G1, ELK1, EPHA7, FOXO3, G6PD, GAPDH, GATA3, GSK3B, HIF1A, HSPA5, ILK, ISL1, JUN, KRAS, LIG4, LRP1, MAPT, MAX, MCL1, MDK, MECP2, MEF2C, MYB, MYBL2, PAK3, PIN1, POU4F1, PPARA, RASA1, RB1, CX3CL1, MAP2K4, SET, SIAH1, SLC9A1, SNCA, SOD2, SORL1, STAT3, TERT, TNFRSF1B, TP53, TSC1, TYRO3, BTG2, NR4A3, FZD1, TP63, FADD, NRP1, SYNGAP1, BCL2L11, SIGMAR1, LANCL1, GPNMB, HYOU1, ATG7, STAMBP, CIT, DKK1, TRIM2, NCSTN, SIRT1, SLC7A11, NSMF, HTRA2, HIPK2, SIX4, SSH1, DDIT4, OXR1, FBXW7, VPS35, CPEB4, DNAJC5, BHLHB9, AKT1S1, EGLN2, EGLN3, RILPL1
BP	GO:0010256	endomembrane system organization	126/3408	1.47E-06	AKT2, AR, ARL1, ATP2A2, CAV1, SCARB2, CDC42, LYST, COL5A1, CREB1, CSNK1D, GOLGB1, HTT, MYH9, MYH10, PAFAH1B1, ATP8B1, SERPINE2, PPP2CA, PPP2R1A, PPP2R2A, PRKCA, MAPK1, MAPK3, PTEN, PTPRC, RAB1A, RAB5B, SH3GL2, SPTBN1, SURF4, TMF1, UGCG, USO1, SNX3, SYNJ1, SQSTM1, AP3D1, WASL, F2RL3, SYT7, SYNGR1, VAPB, TRIP11, VPS4B, TRAM2, USP6NL, GOLGA5, PDCD6IP, AKAP9, RTN3, ARFGEF2, TMED10, CIT, SNF8, GOLGA8A, TMCC1, ANKLE2, LPIN1, ARL6IP1, SYT11, CAMSAP2, DNAJC13, CLASP1, TARDBP, CORO1C, RAB3GAP2, ATL3, ZNF385A, SEC31B, MYOF, SERP1, RAB30, TOR1B, SEC61A1, ASAP1, TMED5, TMED7, VPS36, SH3GLB1, HOOK1, CHMP5, GET4, FNBP1L, STX17, VPS37C, TMEM33, GOLPH3L, PI4K2B, LAPTM4B, TMEM127, NPLOC4, NSFL1C, CCDC47, PLSCR4, CHMP1B, ATP8B2, RAB22A, ATL2, GORASP1, TMEM43, SH3TC2, VCPIP1, COG3, SGIP1, HOOK3, MICALL1, FHDC1, CHMP7, XKR4, FCHO2, WHAMM, TMEM170A, TBC1D20, TANGO2, UBXN2B, EXOC8, VPS37D, TOR1AIP2, REEP3, TMED4, CNEP1R1, MIA3, MYO18A, SNX19, GOLGA8B
BP	GO:0001649	osteoblast differentiation	75/3408	1.54E-06	ACVR2B, ADAR, JAG1, BMP3, BMP7, BMPR1A, BMPR2, RUNX2, CBFB, CDK6, CEBPB, CEBPD, COL1A1, CTNNB1, DDX5, ESRRA, FBN2, GJA1, GNAS, HNRNPC, HNRNPU, ID4, IGF2, IGFBP5, IL6R, IL6ST, ILK, JUND, NBR1, SMAD6, MEF2C, MEF2D, MEN1, PSMC2, PTCH1, RORB, RRBP1, SFRP1, SKI, SNAI2, SNAI1, SOX11, TPM4, TWIST1, WNT7B, FZD1, SEMA7A, TP63, CHRD, LIMD1, DDX21, PDLIM7, RASSF2, MRC2, TOB1, GPNMB, SYNCRIP, SNRNP200, SATB2, DNAJC13, UFL1, RSL1D1, GREM1, SND1, RBMX, SOX8, SUFU, WNT4, LGR4, BCAP29, FAM20C, CCDC47, TP53INP2, SMOC1, SH3PXD2B
BP	GO:0001822	kidney development	88/3408	1.66E-06	ACVR2B, JAG1, BCL2, BMP7, CTNNB1, DCN, EFNB2, EGR1, EPHA4, EPHA7, FBN1, FGF1, FGF2, FOXC1, GATA3, HES1, IL6R, ILK, ITGA3, SMAD2, SMAD4, SMAD6, SMAD7, MEF2C, MME, MYC, NID1, NKX3-1, PAX2, PBX1, PDGFA, PDGFB, PDGFRA, PKD1, PODXL, PPAT, PROX1, PTCH1, SDC4, SFRP1, SOX4, SOX11, STAT1, HNF1B, TGFBR1, TSC1, VEGFA, WNT7B, WNT2B, ITGA8, DCHS1, FADD, IQGAP1, NRP1, ALDH1A2, SGPL1, DLG5, ADAMTS1, BCL2L11, GDF11, SPRY1, FSTL3, TMED10, NIPBL, KLHL3, HEYL, SEC61A1, SOX8, RRM2B, APH1A, SIX4, WNT4, AHI1, LGR4, NUP133, SULF2, CYP26B1, C1GALT1, VANGL2, PTCD2, ARID5B, LZTS2, GLIS2, AMER1, RDH10, BMPER, FLCN, FMN1
BP	GO:0000188	inactivation of MAPK activity	18/3408	1.69E-06	CAV1, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, PPP2CA, PPP2R1A, RGS4, DUSP14, DUSP10, LAX1, DUSP16, DUSP18, SPRED1, SPRED2, SPRED3
BP	GO:0007548	sex differentiation	86/3408	1.70E-06	ACVR1B, ADCYAP1R1, AR, ARRB1, ARRB2, ATM, ATRX, AXL, BAK1, CCND1, BCL2, BCL2L1, BMPR1A, CASP3, CBL, CEBPB, CRKL, CTNNA1, CTNNB1, DACH1, FKBP4, FOXC1, FOXO3, GATA3, GATA6, GJA1, HNF4A, HOXA9, HOXD13, HSPA5, INSR, KIT, LRP6, SMAD4, KITLG, MMP14, NKX3-1, PBX1, PDGFRA, PGR, PKD1, PTPN11, KDM5A, SFRP1, SRC, TBX3, TCF7, TGFBR1, TMF1, TYRO3, VEGFA, WNT2B, SF1, CSDE1, NRIP1, FZD4, TP63, AKR1C3, TNFSF10, SGPL1, PCYT1B, ADAMTS1, KMT2B, BCL2L11, LHFPL2, FSTL3, CITED2, SEMA3A, RHOBTB3, FNDC3A, SIRT1, NIPBL, SOX8, ARID4B, SIX4, WNT4, LGR4, CHD7, PLEKHA1, ARID5B, CBX2, ZNF830, TBC1D20, RNF38, RDH10, AGO4
BP	GO:0060541	respiratory system development	68/3408	1.73E-06	ACVR2B, ADA, ATP7A, BMPR1A, BMPR2, CREB1, CTNNB1, CTSZ, DAG1, EGFR, EIF4E, EP300, EPAS1, FGF1, FLT4, GATA6, FOXA1, HOXA5, HES1, IGFBP5, RBPJ, ITGA3, KRAS, LRP6, SMAD2, MAN2A1, MME, MMP14, NFIB, PDGFA, PDGFRA, PGR, PKD1, PPP1CA, MAPK1, MAPK3, PROX1, RARG, SIM2, SKI, SOX11, SP3, SPARC, SRF, THRA, VEGFA, WNT7B, WNT2B, ALDH1A2, DLG5, SPRY1, FSTL3, KLF2, TAB1, AGR2, MAN1A2, CIC, SLC7A11, SIX4, ERRFI1, FBXW7, CHD7, VANGL2, HEG1, STK40, PKDCC, RDH10, ATXN1L
BP	GO:0043406	positive regulation of MAP kinase activity	83/3408	1.75E-06	ADORA2B, ARRB1, CRK, CRKL, MAPK14, CSK, DUSP5, DUSP6, DUSP7, DUSP9, DVL3, EDN1, EGFR, EPHA4, ERBB2, ERCC6, EZH2, FGF1, FGF2, RAPGEF1, NRG1, ILK, INSR, IRAK1, IRAK2, KIT, KRAS, MAP3K1, MAP3K3, MAP3K4, KITLG, MAP3K9, NTRK3, PAK3, PDGFA, PDGFB, PIK3CB, PRKAA1, MAPK1, MAPK3, EIF2AK2, PTPN1, PTPN11, PTPRC, ROBO1, RPS3, MAP2K4, SHC1, SRC, SYK, TGFA, TGFBR1, THBS1, TIAM1, TPD52L1, UBE2N, UBE2V1, VEGFA, WNT7B, FZD5, FZD4, MADD, PEA15, ADAM9, IQGAP1, SPAG9, TAOK2, TENM1, NOD1, TAB1, MAP3K2, FRS2, AKAP13, DKK1, TAB2, MAPK8IP3, VANGL2, KIDINS220, TAOK1, MUL1, IQGAP3, DAB2IP, EPGN

BP	GO:0006611	protein export from nucleus	63/3408	1.88E-06	CALR, EIF4E, GSK3B, NCBP1, NUP88, NUP98, PKD1, POLR2D, PTPN11, PTPN14, RAN, RANBP2, UPF1, ABCE1, SRSF1, SRSF2, SRSF4, SRSF7, SP100, STYX, TCF7L2, TP53, TSC1, TXN, XPO1, YWHAE, PABPN1, POM121, SMG7, NUTF2, RAPGEF3, NXF1, ANP32B, NUP50, AHCYL1, RNPS1, XPOT, DDX19B, U2AF2, XPO7, SMG1, SMG5, UPF2, RBM15B, NMD3, DNAJC27, CDC40, CPSF2, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, SMURF1, THOC2, XPO5, XPO4, DUSP16, SEH1L, NUP43, POM121C
BP	GO:0051169	nuclear transport	104/3408	1.99E-06	PTTG1IP, CALR, CDKN1A, MAPK14, ECT2, EIF4E, GSK3B, HMGA1, JUP, KPNA1, KPNA3, TNPO1, IPO5, PPP1R12A, NCBP1, NEDD4, NUP88, NUP98, PKD1, PML, POLR2D, PPP1CC, PPP3CA, PKIA, MAPK1, PTPN11, PTPN14, RAN, RANBP2, UPF1, ABCE1, ATXN1, SRSF1, SRSF2, SRSF4, SRSF7, SNRPF, SP100, STAT3, STYX, SYK, TCF7L2, TP53, TSC1, TXN, XPO1, YWHAE, PABPN1, ANP32A, POM121, SMG7, NUTF2, RAPGEF3, NXF1, ANP32B, NUP50, AHCYL1, RNPS1, CPSF6, AKAP13, XPOT, DDX19B, U2AF2, XPO7, SMG1, SMG5, TARDBP, KPNA6, UPF2, APPL1, FBXO22, RBM15B, GEMIN4, NMD3, DNAJC27, FAM53C, RSRC1, CDC40, UBR5, SUFU, RAB23, CPSF2, RBM27, ALKBH5, DDX19A, WDR33, FERMT1, IPO9, NDC1, NUP133, RIOK2, PCID2, SMURF1, THOC2, MAVS, XPO5, BACH2, XPO4, DUSP16, SEH1L, RPAIN, LZTS2, NUP43, POM121C
BP	GO:0030111	regulation of Wnt signaling pathway	108/3408	1.99E-06	ABL1, APC, CAV1, RUNX1, CBFB, COL1A1, MAPK14, CSNK1D, CSNK1E, CSNK1G3, CTNNB1, CTNND1, CYLD, DAB2, DDX3X, DVL3, EGFR, EGR1, FOXO1, FOXO3, GNAQ, RAPGEF1, GSK3B, IGFBP1, RBPJ, ILK, ISL1, ITGA3, JUP, LRP1, LRP6, MDK, MLLT3, NFKB1, PIN1, PPP1CA, PPP2CA, PPP2R1A, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, SIAH2, SKI, SNAI2, SOX4, SRC, STK4, TBL1X, HNF1B, TCF7L2, TERT, TIAM1, TLE1, TLE4, VCP, FZD1, FZD6, CUL3, TNKS, SNX3, MBD2, BTRC, LIMD1, LATS1, PSMF1, HMGXB4, G3BP1, ATP6AP2, PSME3, PSMD14, SPIN1, DKK1, KANK1, PSME4, LATS2, GREM1, DKK3, UBR5, NLK, GID8, USP47, LGR4, FERMT1, VPS35, SULF2, VANGL2, PLEKHA4, RNF213, PRDM15, NXN, TMEM237, WNK1, CDC73, TBL1XR1, SOX7, KREMEN1, ZNRF3, LZTS2, DIXDC1, AMER1, DAB2IP, NRARP, TMEM170B
BP	GO:0003007	heart morphogenesis	83/3408	2.06E-06	JAG1, BMP7, BMPR1A, BMPR2, COL5A1, COL11A1, ATF2, CRKL, CTNNB1, S1PR1, MEGF8, EPHB4, FKBP1A, FOXC1, GAA, GATA3, GATA6, GJA1, NRG1, HIF1A, HES1, RBPJ, ILK, INSR, ISL1, JUN, SMAD4, SMAD6, SMAD7, MDM4, MEF2C, MSX1, NOTCH2, PIM1, POU4F1, PROX1, PTCH1, ROBO1, SNAI2, SNAI1, SOS1, SOX4, SOX11, SRF, TBX3, TGFBR1, TGFBR3, TP53, TWIST1, KDM6A, VEGFA, FZD1, DCHS1, NRP1, ALDH1A2, HAND1, ADAMTS1, SPRY1, UBE4B, CITED2, DLC1, OLFM1, TAB1, DKK1, PLXND1, FLRT2, NIPBL, HEYL, PDCD4, SUFU, DLL4, AHI1, IFT57, CHD7, ZMIZ1, VANGL2, HEG1, MIB1, NDRG4, PTCD2, SYNPO2L, SETDB2, ARID2
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	68/3408	2.06E-06	ACVR1B, ACVR2B, RHOA, ARRB2, BMPR1A, BMPR2, CAV1, CBL, COL1A2, COL3A1, CREB1, CREBBP, DAB2, EP300, FBN1, FBN2, FNTA, FUT8, GCNT2, HSPA5, ITGA3, JUN, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEN1, FURIN, PIN1, PML, PTPRK, PXN, SKI, SKIL, SOX11, SRC, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, USP9X, ITGA8, ADAM9, MTMR4, ONECUT2, CITED2, TAB1, PEG10, SIRT1, ZNF451, APPL1, DKK3, HIPK2, TRIM33, NLK, RNF111, FERMT1, PARD3, PMEPA1, SMURF1, PBLD, WFIKKN2, ACVR1C, CD109, FLCN
BP	GO:0035966	response to topologically incorrect protein	68/3408	2.06E-06	ADD1, AMFR, BAK1, CCND1, CALR, CANX, TPP1, ATF6B, EIF2S1, EP300, EXTL2, EXTL3, GFPT1, HDGF, DNAJB2, DNAJA1, HSPA2, HSPA4, HSPA5, IGFBP1, DNAJB9, ATXN3, NCK1, EIF2AK2, PTPN1, SHC1, SSR1, TMBIM6, THBS1, TLN1, VCP, XBP1, NCK2, CUL3, STC2, ATP6V0D1, VAPB, GOSR2, EDEM1, HERPUD1, MFN2, BCL2L11, CTDSP2, HYOU1, AGR2, DNAJB4, UBXN4, HSPB8, SERP1, TOR1B, DERL2, BFAR, DNAJB12, FKBP14, TMEM33, UBE2W, YOD1, ARFGAP1, UGGT1, TSPYL2, HERPUD2, CREB3L2, EDEM3, KLHL15, RHBDD1, SYVN1, PPP1R15B, DAB2IP
BP	GO:0061013	regulation of mRNA catabolic process	68/3408	2.06E-06	ZFP36L1, ZFP36L2, MAPK14, EIF4G1, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPU, TNPO1, HNRNPM, PARN, PKP1, PRKCA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, UPF1, SET, XPO1, ZFP36, BTG2, FXR1, ANP32A, PABPC4, CNOT8, ROCK2, PSMF1, PUM1, THRAP3, TOB1, PSME3, PSMD14, SYNCRIP, PAIP1, IGF2BP1, IGF2BP3, HNRNPA0, CPEB3, CNOT1, SAMD4A, TNRC6B, PSME4, LARP1, TARDBP, GIGYF2, SERBP1, PABPC1, TNRC6A, MYEF2, YTHDF2, XRN1, ALKBH5, SAMD4B, RBM23, RBM38, PCID2, DCP1A, ZC3HAV1, TNRC6C, METTL14, TRIM71, PDE12, YTHDF3
BP	GO:1903362	regulation of cellular protein catabolic process	80/3408	2.10E-06	ALAD, PTTG1IP, CAV1, CSNK1D, CSNK1E, DAB2, EPHA4, FHIT, FMR1, GSK3B, UBE2K, DNAJB2, LDLR, LRP1, SMAD7, MAP1A, ATXN3, OPHN1, FURIN, PKD1, PML, MAPK9, PSMC2, PTEN, RAD23B, RDX, AURKA, STYX, TAF1, TMF1, UBE2G2, VCP, BTRC, USP13, LATS1, PSMF1, SOCS5, EDEM1, HERPUD1, RNF144A, BCAP31, PSME3, PSMD14, TRIB1, ARIH2, PLK2, TLK2, GABARAPL2, UFL1, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, HIPK2, MYLIP, USP25, UBQLN2, UBQLN1, DERL2, WAC, UCHL5, UBE2J1, SUFU, ANKIB1, FBXW7, LAPTM4B, YOD1, VPS35, UBQLN4, SMURF1, DDA1, UQCC2, FAM122A, SOCS4, AMER1, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:0060560	developmental growth involved in morphogenesis	77/3408	2.12E-06	ABL1, ALCAM, BDNF, BMPR2, CSF1, CTNNB1, S1PR1, EFNA5, MEGF8, EPHA7, FGF1, FN1, GDI1, GOLGA4, GSK3B, HOXD13, ILK, ITGB1, L1CAM, LIMK1, LRP1, LRP6, MAP1B, MAPT, NTRK3, PAFAH1B1, RARG, SFRP1, SH3GL2, SRF, AURKA, SYT1, HNF1B, TIAM1, VCL, VEGFA, WNT7B, RND2, USP9X, ULK1, SEMA7A, IQGAP1, NRP1, WASF1, DCLK1, NTN1, SEMA3E, SPRY1, SEMA3A, OLFM1, SLC9A6, SEMA4B, POSTN, KDM5B, RAB21, FSTL4, SIN3A, AUTS2, CYFIP2, NIN, SYT17, SIX4, BCL11A, SEMA4C, SMURF1, VANGL2, SEMA6A, EPB41L5, RAPH1, MUL1, LZTS2, PLXNA4, SYT2, WDR36, TTL, RDH10, FMN1
BP	GO:0035335	peptidyl-tyrosine dephosphorylation	42/3408	2.12E-06	ACP1, CDC25A, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EYA4, PTEN, PTPN1, PTPN4, PTPN11, PTPN12, PTPN14, PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRJ, PTPRK, PTPRN2, PTPRR, PTP4A1, PTP4A2, CDC14B, MTMR3, MTMR7, MTMR4, DUSP14, PTPN21, PTPRT, DUSP10, PTPN18, PALD1, SSH1, DUSP23, DUSP16, SSH2, TIMM50, DUSP18
BP	GO:0006986	response to unfolded protein	62/3408	2.17E-06	ADD1, AMFR, BAK1, CCND1, CALR, CANX, TPP1, ATF6B, EIF2S1, EP300, EXTL2, EXTL3, GFPT1, HDGF, DNAJB2, DNAJA1, HSPA2, HSPA4, HSPA5, IGFBP1, DNAJB9, NCK1, EIF2AK2, PTPN1, SHC1, SSR1, TMBIM6, THBS1, TLN1, VCP, XBP1, NCK2, STC2,

					ATP6V0D1, VAPB, GOSR2, EDEM1, HERPUD1, MFN2, BCL2L11, CTDSP2, HYOU1, AGR2, DNAJB4, UBXN4, HSPB8, SERP1, TOR1B, DERL2, BFAR, FKBP14, TMEM33, YOD1, ARFGAP1, TSPYL2, HERPUD2, CREB3L2, EDEM3, RHBDD1, SYVN1, PPP1R15B, DAB2IP
BP	GO:0034332	adherens junction organization	53/3408	2.22E-06	ABL1, ADD1, ARF6, RHOA, BCL2, CDH6, CSK, CTNNA1, CTNNB1, CTNND1, EFNA5, JUP, LRP1, SMAD7, MMP14, PTEN, PTPRJ, PTPRK, RDX, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VCL, VEGFA, NUMB, IQGAP1, NRP1, LDB1, DLG5, TAOK2, MAP4K4, ROCK2, SLK, DLC1, FAM107A, RASSF8, LIMCH1, CLASP1, PIP5K1C, CORO1C, CADM1, RAB8B, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, WHAMM, HIPK1, FMN1
BP	GO:0006913	nucleocytoplasmic transport	103/3408	2.28E-06	PTTG1IP, CALR, CDKN1A, MAPK14, ECT2, EIF4E, GSK3B, JUP, KPNA1, KPNA3, TNPO1, IPO5, PPP1R12A, NCBP1, NEDD4, NUP88, NUP98, PKD1, PML, POLR2D, PPP1CC, PPP3CA, PKIA, MAPK1, PTPN11, PTPN14, RAN, RANBP2, UPF1, ABCE1, ATXN1, SRSF1, SRSF2, SRSF4, SRSF7, SNRPF, SP100, STAT3, STYX, SYK, TCF7L2, TP53, TSC1, TXN, XPO1, YWHAE, PABPN1, ANP32A, POM121, SMG7, NUTF2, RAPGEF3, NXF1, ANP32B, NUP50, AHCYL1, RNPS1, CPSF6, AKAP13, XPOT, DDX19B, U2AF2, XPO7, SMG1, SMG5, TARDBP, KPNA6, UPF2, APPL1, FBXO22, RBM15B, GEMIN4, NMD3, DNAJC27, FAM53C, RSRC1, CDC40, UBR5, SUFU, RAB23, CPSF2, RBM27, ALKBH5, DDX19A, WDR33, FERMT1, IPO9, NDC1, NUP133, RIOK2, PCID2, SMURF1, THOC2, MAVS, XPO5, BACH2, XPO4, DUSP16, SEH1L, RPAIN, LZTS2, NUP43, POM121C
BP	GO:0035690	cellular response to drug	109/3408	2.44E-06	ABL1, ACTB, ADCY1, ADCY6, RHOB, ATP2B4, ATRX, AXL, BRCA1, KLF9, CCNA2, CD69, CRK, CRKL, CTNNA1, CTNNB1, DNMT3A, DNMT3B, ECT2, EDN1, EFNA5, EGFR, EGR1, EIF4E, EZH2, FOXO1, FOXO3, FMR1, GABPA, GNAI2, GNAQ, GNB1, NR3C1, HDAC2, HNRNPD, HSPA5, ITPR2, JUP, KCNC1, MEF2C, MET, KMT2A, MSX1, MTR, MYB, MYC, PPP1R12A, NFKB1, NKX3-1, OPA1, P2RY1, PAWR, PAX2, PDGFB, PPAT, PPP3CA, PRKAA1, PRKCE, MAPK1, MAPK3, PTAFR, PTEN, RAD51, RAP1B, RAP2A, RPS3, CCL7, SFRP1, SLC8A1, SRC, TAF1, TFRC, TP53, TRPM2, TXN, UMPS, NR4A3, HMGA2, ARHGEF2, KLF4, EFTUD2, ROCK2, NET1, SIGMAR1, KLF2, NOD1, ATG7, CERS1, ZNF277, KDM6B, LARP1, SIRT1, SPIDR, SIN3A, NDOR1, CHMP5, OSER1, BCL11A, ERRFI1, SSH1, XRN1, DDIT4, PLEKHA1, DDI2, TRIM41, TP53INP1, SIRPA, ACER2, AGRN
BP	GO:0048754	branching morphogenesis of an epithelial tube	55/3408	2.51E-06	ABL1, AR, BCL2, BMP7, COL4A1, CSF1, CTNNB1, CTSZ, DAG1, EDN1, FGF1, FGF2, FOXA1, HOXA5, ILK, KRAS, LRP6, SMAD4, MDK, MET, MMP14, MYC, NKX3-1, PAX2, PBX1, PGR, PKD1, PML, PPP1CA, PTCH1, SRC, SRF, STK4, TBX3, HNF1B, VDR, VEGFA, WNT2B, DCHS1, NRP1, BTRC, DLG5, SEMA3E, SPRY1, GNA13, KDM5B, PLXND1, SOX8, SIX4, WNT4, DLL4, LGR4, VANGL2, RDH10, NRARP
BP	GO:0035065	regulation of histone acetylation	27/3408	2.52E-06	ARRB1, BRCA1, CHEK1, GATA2, GATA3, KAT2A, ISL1, SMAD4, KMT2A, MAPK3, SET, SNAI2, SNCA, TWIST1, RPS6KA4, RPS6KA5, ATG5, CTCF, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, SETD5, TADA2B, FLCN
BP	GO:0010508	positive regulation of autophagy	46/3408	2.61E-06	DAPK1, DCN, FOXO1, FOXO3, GNAI3, GSK3B, HTT, HIF1A, HK2, PAFAH1B2, PIK3CB, PIP4K2A, PRKAA1, MAPK3, RALB, TSC1, UVRAG, ULK1, MFN2, BCL2L11, TRIM13, TRIM22, NOD1, SPTLC1, PLK2, LARP1, SIRT1, RAB3GAP2, HSPB8, SH3GLB1, WAC, TPCN1, VPS13C, VPS13D, SMURF1, TP53INP2, FYCO1, MUL1, SESN2, MTDH, TP53INP1, SMCR8, SESN3, FLCN, TRIM65, RAB12
BP	GO:0060021	roof of mouth development	38/3408	2.73E-06	ACVR2B, ASPH, BMPR1A, DLX6, EPHB2, EPHB3, INSIG1, JAG2, LRP6, SMAD2, SMAD4, MEF2C, MSX1, PDGFRA, PRRX1, SKI, SNAI2, SNAI1, SOS1, SOX11, TBX3, TGFBR1, TGFBR3, TWIST1, FZD1, SGPL1, GDF11, ANP32B, SATB2, INSIG2, BNC2, BCOR, PAK1IP1, CHD7, PLEKHA1, ARID5B, PKDCC, WFIKKN2
BP	GO:0018212	peptidyl-tyrosine modification	108/3408	2.89E-06	ABL1, ABL2, ARRB2, AXL, BDNF, CAV1, CBL, CD44, CNTN1, CSK, DLG3, DOCK3, HBEGF, DYRK1A, EFNA5, EGFR, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, ERCC6, FER, FGFR3, FLT4, HDAC2, NRG1, HES1, IGF1R, IGF2, IL6R, IL6ST, IL12RB2, IL18, INSR, ISL1, ITGA5, KIT, LYN, MET, KITLG, NEDD9, NF2, NTRK3, PAK2, PDGFA, PDGFB, PDGFRA, PPP2CA, PPP2R1A, PRKCE, MAPK3, EIF2AK2, PRLR, TWF1, PTPN1, PTPN11, PTPRC, PTPRJ, RAP2B, MAP2K4, SFRP1, SHC1, SRC, STAT3, SYK, ADAM17, TAL1, TESK1, TGFA, TP53, TYRO3, VEGFA, NCK2, DYRK2, SOCS1, IQGAP1, NRP1, BAZ1B, GPRC5A, DYRK1B, ARHGEF2, SOCS5, MELK, SH2B3, ABI2, TNK2, IL24, LMTK2, ARL2BP, DSTYK, IBTK, GREM1, EHD4, ERRFI1, PARP14, NCAPG2, FBXW7, RAP2C, PEAK1, SH3BP5L, AFAP1L2, PKDCC, SOCS4, TTL, RICTOR, EPGN
BP	GO:0030518	intracellular steroid hormone receptor signaling pathway	50/3408	2.89E-06	AR, RHOA, ARRB2, BRCA1, CALR, RUNX1, CBFB, CRY2, CTNNB1, DAB2, DDX5, EP300, ESR2, FHL2, FKBP4, NR3C1, FOXA1, DNAJA1, ISL1, NEDD4, NKX3-1, PGR, RAN, RB1, RNF4, SFRP1, SRC, TAF1, KMT2D, NCOA3, NRIP1, ARID1A, TP63, LATS1, CLOCK, NCOR1, DDX17, CNOT1, UFL1, SIRT1, RBFOX2, WBP2, HEYL, FOXP1, STRN3, UBR5, PMEPA1, CALCOCO1, EGLN2, KCTD6
BP	GO:0002244	hematopoietic progenitor cell differentiation	59/3408	2.97E-06	ABL1, ADAR, BCL2, RUNX1, CBFB, CDK6, CEBPD, CHD2, ERCC2, FOXC1, GATA2, GATA3, HOXB3, HES1, KIT, LIG4, LMO2, KITLG, KMT2A, MYB, PDGFRA, EIF2AK2, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTPRC, SFRP1, SOS1, SOX4, SRF, TAL1, TCF3, TP53, XRCC5, LDB1, PSMF1, SETD1A, PSME3, PSMD14, FSTL3, FST, PSME4, PRRC2C, TNFRSF13B, SIN3A, YTHDF2, ANLN, RBM47, PUS7, ITCH, STON2, C12orf29, FNIP1, ZNF784, FLCN
BP	GO:1903829	positive regulation of cellular protein localization	98/3408	3.06E-06	AKT2, APC, ARF6, BCL2, CCT6A, MAPK14, CYLD, DKC1, ECT2, EGFR, EPB41, STOM, EPHB2, ERBB2, GSK3B, ITGA3, ITGB1, JUP, KIF5B, IPO5, LRP1, MAP1A, MAPT, MYO1C, OAZ2, PPP3R1, PRKAA1, PRKCE, MAPK1, MAPK8, RAN, RDX, SORL1, SPTBN1, SRC, SREBF2, STX3, VAMP2, TCF7L2, TERT, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, BAP1, TP63, IQGAP1, SQSTM1, ROCK2, AKAP5, EDEM1, ATG13, C2CD5, LRIG2, BCAP31, TENM1, NUTF2, RAPGEF3, ARIH2, ANP32B, AGR2, KAT7, CEP250, RAB11FIP2, GPD1L, SYT11, TARDBP, CD2AP, NIPBL, CLIP3, NPTN, BBC3, HTRA2, NMD3, SH3GLB1, ABHD17B, UBR5, SSH1, MIEF1, GNL3L, LEPROT, PINX1, FBXW7, RIOK2, SAR1A, MFF, MAVS, USP36, RHOU, ABHD17C, XPO4, SESN2, GLIS2, MIEF2

BP	GO:0032092	positive regulation of protein binding	39/3408	3.24E-06	ABL1, ADD1, AMFR, ARF6, ARRB1, BDNF, CAV1, EP300, EPB41, EPHA4, FKBP1A, GSK3B, HOXA3, LRP1, MEF2C, MEN1, PIN1, PKD1, PLCL1, PPP2CA, RALB, RAN, STK4, TAF1, TCF7L2, TERT, TIAM1, NRP1, TRAF4, RAPGEF2, PLK2, MAPRE3, USP33, PLXND1, HIPK2, NMD3, GNL3L, EPB41L5, SPPL3
BP	GO:0001837	epithelial to mesenchymal transition	52/3408	3.31E-06	JAG1, BMP7, COL1A1, CTNNB1, DAB2, DAG1, DDX5, EZH2, FOXC1, GCNT2, GSK3B, HDAC2, HIF1A, FOXA1, HNRNPAB, RBPJ, ISL1, LOXL2, LRP6, SMAD2, SMAD4, SMAD7, MDK, MSX1, PPP2CA, PTEN, SFRP1, SNAI2, SNAI1, TGFBR1, TGFBR3, TIAM1, TWIST1, HMGA2, DLG5, SPRY1, OLFM1, DDX17, PHLDB1, CLASP1, HEYL, GREM1, PDCD4, ADIPOR1, WNT4, TRIM62, EPB41L5, PBLD, KBTBD8, PHLDB2, DAB2IP, CRB2
BP	GO:0018108	peptidyl-tyrosine phosphorylation	107/3408	3.41E-06	ABL1, ABL2, ARRB2, AXL, BDNF, CAV1, CBL, CD44, CNTN1, CSK, DLG3, DOCK3, HBEGF, DYRK1A, EFNA5, EGFR, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, ERCC6, FER, FGFR3, FLT4, HDAC2, NRG1, HES1, IGF1R, IGF2, IL6R, IL6ST, IL12RB2, IL18, INSR, ISL1, ITGA5, KIT, LYN, MET, KITLG, NEDD9, NF2, NTRK3, PAK2, PDGFA, PDGFB, PDGFRA, PPP2CA, PPP2R1A, PRKCE, MAPK3, EIF2AK2, PRLR, TWF1, PTPN1, PTPN11, PTPRC, PTPRJ, RAP2B, MAP2K4, SFRP1, SHC1, SRC, STAT3, SYK, ADAM17, TAL1, TESK1, TGFA, TP53, TYRO3, VEGFA, NCK2, DYRK2, SOCS1, IQGAP1, NRP1, BAZ1B, GPRC5A, DYRK1B, ARHGEF2, SOCS5, MELK, SH2B3, ABI2, TNK2, IL24, LMTK2, ARL2BP, DSTYK, IBTK, GREM1, EHD4, ERRFI1, PARP14, NCAPG2, FBXW7, RAP2C, PEAK1, SH3BP5L, AFAP1L2, PKDCC, SOCS4, RICTOR, EPGN
BP	GO:0048872	homeostasis of number of cells	79/3408	3.43E-06	ABL1, ACVR1B, ADA, ADAR, ADD1, AXL, BAK1, BCL2, BCL6, ZFP36L1, CASP3, CDK6, CEBPG, CCR7, MAPK14, CSF1, CYLD, EPAS1, ERCC2, EZH2, FOXO3, G6PD, GATA2, GATA3, NCKAP1L, HIF1A, HOXA5, IL7R, IREB2, ITPKB, KIT, KRAS, LYN, MEF2C, KITLG, SLC11A2, PRDX1, PIK3CB, PKNOX1, PTPN11, RAG1, RB1, SKIL, SOS1, SP3, SRF, STAT1, STAT3, STAT5B, ADAM17, TAL1, TGFBR3, THRA, VEGFA, ZFP36, BAP1, FADD, LDB1, RASSF2, UBAP2L, PTBP3, AKT3, BCL2L11, SH2B3, KLF2, NCSTN, TNFRSF13B, RBFOX2, SLC7A11, GIGYF2, HIPK2, VPS54, RRN3, NCAPG2, SLC25A38, LGR4, KMT2E, SFXN1, FAM210B
BP	GO:0048568	embryonic organ development	122/3408	3.47E-06	ADA, ADM, PRDM1, BMP7, BMPR1A, ZFP36L1, RUNX2, CEBPB, COL5A2, COL11A1, CTNNB1, DLX2, DLX6, EDN1, MEGF8, EGFR, EPAS1, EPHB2, ERCC2, BPTF, FBN1, FBN2, FOXC1, GATA2, GATA3, GJA1, GNAS, GRB2, HIF1A, HOXA3, HOXA5, HOXA7, HOXB3, HOXB5, HOXB8, HOXC4, HES1, IGF2, RBPJ, INSIG1, KIT, LRP6, SMAD2, MEF2C, KITLG, KMT2A, MMP14, MSX1, OTX1, PAX2, PAX6, PBX1, PDGFA, PDGFB, PDGFRA, PKD1, PRRX1, MAPK1, MAPK3, PROX1, PTCH1, RAD23B, RARG, RBBP6, TRA2B, SNAI1, SOX11, SP3, SRF, STK4, TAL1, TBX3, HNF1B, TCF7, ZEB1, NR2F2, TGFBR1, TP53, TWIST1, KDM6A, VEGFA, WNT7B, FZD5, FZD3, NR4A3, ARID1A, FZD6, ITGA8, ALDH1A2, MBD2, HAND1, NTN1, SH2B3, CITED2, FRS2, VASH1, SATB2, NIPBL, MTHFD1L, LRIG1, HIPK2, INSIG2, SUFU, SIX4, AHI1, IFT57, SOBP, CHD7, VANGL2, BIRC6, MIB1, NDRG4, SETDB2, PKDCC, PLCD3, TTC39C, E2F7, RDH10, ARID2, HIPK1, CRB2, RBPMS2
BP	GO:1901983	regulation of protein acetylation	33/3408	3.52E-06	ARRB1, BRCA1, CHEK1, GATA2, GATA3, KAT2A, GSK3B, HDAC2, ISL1, SMAD4, KMT2A, PRKAA1, MAPK3, SET, SNAI2, SNCA, SOX4, TWIST1, RPS6KA4, RPS6KA5, ATG5, RAPGEF3, CTCF, KAT7, SIRT1, WBP2, SIN3A, ZNF451, AUTS2, SETD5, TAOK1, TADA2B, FLCN
BP	GO:0045732	positive regulation of protein catabolic process	71/3408	3.52E-06	APC, PTTG1IP, CAV1, CDKN1B, CSNK1D, CSNK1E, DAB2, FOXO1, FMR1, GJA1, GSK3B, DNAJB2, LDLR, LRP1, SMAD7, ATXN3, NEDD4, NSF, OAZ2, FURIN, MAPK9, PSMC2, PTEN, RDX, SNX1, SORL1, AURKA, TAF1, TNFRSF1B, VCP, CUL4B, ADAM9, USP13, SOCS5, EDEM1, HERPUD1, RNF144A, AREL1, BCAP31, TRIB1, ARIH2, ATG7, PLK2, SNF8, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, MYLIP, UBQLN2, UBQLN1, DTL, ANKIB1, FBXW7, VPS35, SMURF1, HECW2, DDA1, LPCAT1, ITCH, UQCC2, EGLN2, FAM122A, SOCS4, AMER1, SH3D19, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:2001020	regulation of response to DNA damage stimulus	71/3408	3.52E-06	ABL1, ATM, ATR, BCL2, BCL2L1, BRCA1, PTTG1IP, CD44, CEBPG, CHEK1, DDX5, DYRK1A, EGFR, EYA4, ERCC6, FOXM1, FMR1, FUS, HNRNPK, MAPT, MCL1, MSX1, MYC, NKX3-1, OGG1, PML, RAD51, RPS3, SKIL, SNAI2, SNAI1, TP53, TPT1, TWIST1, UBE2N, UBE2V1, USP1, HMGA2, IER3, TRIP12, ACTR2, POLQ, KDM1A, SMG1, FAM168A, SIRT1, SPIDR, ZNF385A, UBR5, TRIAP1, PIAS4, TAF9B, RTEL1, ETAA1, USP47, FIGN, RIF1, FMN2, UBQLN4, SPIRE1, BRCC3, WDR76, KLHL15, RMI2, NACC2, PPP4R2, USP51, SPRED1, RNF168, SPRED2, SPRED3
BP	GO:0032886	regulation of microtubule-based process	72/3408	3.52E-06	ABL1, APC, RHOA, BRCA1, CCNF, CDKN1B, CHEK1, CTNNB1, CYLD, DIAPH1, DYRK1A, EFNA5, MARK2, ERBB2, FKBP4, KAT2A, GSK3B, HNRNPU, MAP1A, MAP1B, MAPT, MECP2, MET, MID1, NEFH, PAFAH1B1, PKD1, PRKAA1, RNF4, RPS3, SNCA, AURKA, XPO1, SMC1A, KAT2B, ARHGEF2, ROCK2, VPS4B, PDCD6IP, AKAP9, TUBB4A, STAG2, PLK2, FAM107A, CEP250, MAPRE3, PHLDB1, CAMSAP2, BICD2, CLASP1, CLIP3, SENP6, NIN, CHMP5, TRIM36, NSFL1C, MDM1, CHMP1B, KLHL42, TAOK1, SLAIN2, CEP85, CEP97, DIXDC1, NAV3, PHLDB2, CCSAP, UBXN2B, TTBK2, CEP120, CAMSAP1, SKA2
BP	GO:0034101	erythrocyte homeostasis	47/3408	3.60E-06	ACVR1B, ADAR, ADD1, AXL, BCL6, ZFP36L1, CASP3, CDK6, CEBPG, MAPK14, EPAS1, ERCC2, FOXO3, G6PD, GATA2, GATA3, NCKAP1L, HIF1A, HOXA5, IREB2, KIT, LYN, SLC11A2, PRDX1, PKNOX1, RB1, SP3, SRF, STAT1, STAT3, STAT5B, TAL1, TGFBR3, THRA, VEGFA, ZFP36, LDB1, PTBP3, SH2B3, KLF2, RBFOX2, HIPK2, NCAPG2, SLC25A38, KMT2E, SFXN1, FAM210B
BP	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	42/3408	3.60E-06	ABL1, ATM, BAK1, BCL2, BCL2L1, BRCA1, CD44, CDKN1A, EP300, ERCC6, HNRNPK, MCL1, MLH1, PML, RPS3, SKIL, SNAI2, SNAI1, TNFRSF1B, TP53, TPT1, DYRK2, TP63, BCL2L11, KDM1A, SIRT1, PHLDA3, ZNF385A, HTRA2, HIPK2, CDIP1, TRIAP1, PIAS4, TAF9B, DDIT4, USP47, FNIP2, USP28, MOAP1, AEN, NACC2, HIPK1

BP	GO:0072331	signal transduction by p53 class mediator	84/3408	3.63E-06	ATM, ATR, ATRX, BCL2, BRCA1, PTTG1IP, CD44, CDKN1A, CDKN1B, CHD3, CHD4, CHEK1, MAPK14, DDX5, DYRK1A, EP300, FHIT, FOXM1, FOXO3, HDAC2, HNRNPK, MDM4, MSX1, MYO6, CNOT4, PIN1, PML, POU4F1, PRKAA1, PRKAB2, RAD1, RBL2, SNAI2, SNAI1, SOX4, SP100, SSRP1, AURKA, TAF1, TAF4B, TFDP1, TFDP2, TP53, TWIST1, BTG2, KAT6A, DYRK2, PPM1D, TP63, AURKB, CNOT8, NUAK1, PLK2, SUPT16H, CNOT1, KDM1A, SIRT1, PHLDA3, ZNF385A, HIPK2, CDIP1, RRM2B, ING4, TRIAP1, TAF9B, DDIT4, RRN3, PAK1IP1, CNOT6, USP28, MEAF6, AEN, SESN2, RHNO1, TP53INP1, RMI2, RFFL, JMY, E2F7, SPRED1, SPRED2, HIPK1, ACER2, SPRED3
BP	GO:0061136	regulation of proteasomal protein catabolic process	63/3408	3.93E-06	ALAD, CAV1, CSNK1D, CSNK1E, DAB2, FHIT, FMR1, GSK3B, UBE2K, DNAJB2, SMAD7, MAP1A, ATXN3, OPHN1, PKD1, MAPK9, PSMC2, RAD23B, AURKA, STYX, TAF1, TMF1, UBE2G2, VCP, BTRC, USP13, PSMF1, SOCS5, EDEM1, HERPUD1, RNF144A, BCAP31, PSME3, PSMD14, TRIB1, ARIH2, PLK2, TLK2, GABARAPL2, UFL1, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, USP25, UBQLN2, UBQLN1, DERL2, WAC, UCHL5, UBE2J1, ANKIB1, FBXW7, YOD1, UBQLN4, DDA1, FAM122A, SOCS4, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:0007411	axon guidance	86/3408	4.10E-06	ALCAM, APBB2, BDNF, BMP7, BMPR2, DAG1, EFNA3, EFNA5, EFNB1, EFNB2, CELSR3, MEGF8, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, ETV1, GAB1, GATA3, GRB2, ARHGAP35, ISL1, L1CAM, LRP1, SMAD4, MATN2, MYH10, NCAM1, NEO1, NFIB, OPHN1, PAX6, PIK3CB, PRKCA, MAPK1, MAPK3, PTCH1, PTPN11, ROBO1, SHC1, SIAH1, SOS1, SPTAN1, SPTBN1, SRC, TRIO, VEGFA, VLDLR, FZD3, NR4A3, SEMA7A, IRS2, NRP1, RPS6KA5, PDLIM7, NTN1, SEMA3E, SEMA3A, SEMA4B, FRS2, KIF3A, LYPLA2, PALLD, USP33, MYCBP2, NFASC, PLXND1, FLRT2, CYFIP2, NPTN, SEMA4C, YTHDF1, DPYSL5, VANGL2, SEMA6A, ZSWIM6, ISL2, BCL11B, ZSWIM4, PLXNA4, EMB, DOK6, AGRN, RNF165
BP	GO:0071496	cellular response to external stimulus	101/3408	4.10E-06	ADORA2B, FAS, ASGR1, ATP2B1, AXL, BAK1, BCL2, BMPR2, CBL, CDKN1A, CHEK1, CNN2, COL1A1, COMT, DAG1, DSC2, EGFR, EIF2S1, EIF4G1, FOXO1, GJA1, ARHGAP35, HSPA5, ITGA6, IRF1, JUN, KCNJ2, LAMP2, FADS1, LYN, MAX, MAP3K1, NFKB1, OPA1, P2RY1, PDK4, PIM1, PRKAA1, MAPK1, MAPK3, MAPK8, EIF2AK2, PTGER4, PTPN11, PTPRC, RALB, MAP2K4, SFRP1, SLC1A2, SLC9A1, SNAI2, SREBF2, SRF, TAF1, KLF10, TP53, TSC1, USF2, VCAM1, VDR, WNT2B, XBP1, FOSL1, ULK1, STK24, PPM1D, AKR1C3, TNKS, FADD, MTMR3, ATG5, ATG7, POSTN, MAP3K2, FAM107A, GABARAPL2, ATG14, USP33, SZT2, SIRT1, TXN2, FBXO22, TNRC6A, DNAJC15, SH3GLB1, BCL11A, ZFYVE1, WNT4, SLC38A2, SSH1, RRAGD, RRAGC, CPEB4, MAP1LC3B, NUAK2, SEH1L, SESN2, FNIP1, MTPN, SESN3, SIK1
BP	GO:0060070	canonical Wnt signaling pathway	100/3408	4.24E-06	APC, BCL9, CAV1, COL1A1, MAPK14, CSNK1D, CSNK1E, CSNK1G3, CTNNB1, CTNND1, CYLD, DAB2, DDX3X, DVL3, EGFR, EGR1, FOXO1, FOXO3, GATA3, GNAQ, RAPGEF1, GSK3B, IGFBP1, RBPJ, ILK, ISL1, JUP, LRP6, MDK, MLLT3, NFKB1, PIN1, PPP1CA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAB5A, RARG, SFRP1, SIAH2, SNAI2, SOX4, SRC, STK4, TBL1X, TCF7, TCF7L2, TLE1, TLE4, KDM6A, VCP, WNT7B, WNT2B, FZD5, FZD3, FZD1, FZD4, FZD6, CUL3, TNKS, BTRC, LIMD1, LATS1, KLF4, PSMF1, G3BP1, PSME3, PSMD14, DKK1, KANK1, PSME4, LATS2, GREM1, DKK3, UBR5, WNT4, GID8, USP47, LGR4, FERMT1, VPS35, SULF2, PLEKHA4, PRDM15, WNK1, TBL1XR1, SOX7, KREMEN1, ZNRF3, LZTS2, DIXDC1, AMER1, DAB2IP, NRARP, TMEM170B
BP	GO:0031668	cellular response to extracellular stimulus	84/3408	4.24E-06	ADORA2B, FAS, ASGR1, ATP2B1, AXL, BCL2, BMPR2, CBL, CDKN1A, COL1A1, COMT, DSC2, EIF2S1, EIF4G1, FOXO1, ARHGAP35, HSPA5, ITGA6, JUN, LAMP2, FADS1, LYN, MAX, OPA1, P2RY1, PDK4, PIM1, PRKAA1, MAPK1, MAPK3, MAPK8, EIF2AK2, PTPRC, RALB, SFRP1, SLC1A2, SNAI2, SREBF2, SRF, TAF1, KLF10, TP53, TSC1, USF2, VCAM1, VDR, WNT2B, XBP1, FOSL1, ULK1, STK24, PPM1D, AKR1C3, TNKS, MTMR3, ATG5, ATG7, POSTN, FAM107A, GABARAPL2, ATG14, USP33, SZT2, SIRT1, TXN2, FBXO22, TNRC6A, DNAJC15, SH3GLB1, BCL11A, ZFYVE1, WNT4, SLC38A2, SSH1, RRAGD, RRAGC, CPEB4, MAP1LC3B, NUAK2, SEH1L, SESN2, FNIP1, SESN3, SIK1
BP	GO:0072659	protein localization to plasma membrane	82/3408	4.41E-06	ACTB, AKT2, ANK1, AR, ARF6, ATP1B1, BCL2L1, AP2M1, CSK, DAB2, EGFR, EMP2, EPHB2, FLOT2, GBP1, GOLGA4, IKBKB, ITGA3, ITGB1, JUP, KIF5B, LRP1, LRP6, RAB8A, MMP14, MYO5A, NSF, P2RY1, PRKCE, PTCH1, RAB3B, RAP2A, RDX, SPTBN1, STX3, VAMP2, VAMP7, DCHS1, NUMB, SQSTM1, MAP7, ROCK2, AKAP5, BAG4, PREPL, RAPGEF2, C2CD5, ARFRP1, LYPLA1, SEC23A, AGR2, EXOC5, RAB31, RAB11FIP2, NFASC, EFR3A, PACS2, RHOQ, CLIP3, APPL1, LDLRAP1, RAB8B, SYTL2, GOLPH3L, PACS1, VPS35, SMURF1, GPR158, KIF13A, TMBIM1, GORASP1, C16orf70, FAM126A, PKDCC, MYADM, FCHO2, TTC7B, ZDHHC23, ZDHHC22, FAM126B, RILPL1, RAB15
BP	GO:0001667	ameboidal-type cell migration	129/3408	4.44E-06	ABL1, ACVR1B, ARF6, RHOA, RHOB, BMP7, BMPR2, CALR, CFL1, DCN, HBEGF, EDN1, EFNB1, EFNB2, MEGF8, EGR3, EMP2, EPHB4, FER, FGF1, FGF2, FLT4, FN1, GATA2, GATA3, GPI, HIF1A, ILK, ISL1, ITGA3, ITGB1, JUN, JUP, KIT, LOXL2, MECP2, MEF2C, MAP3K3, MET, KITLG, MYH9, PAFAH1B1, PAK3, PDGFB, PIK3C2A, PML, PPARD, PRCP, PRKCA, PRKCE, PKN2, PROX1, PTEN, PTPN11, PTPRG, PTPRR, PXN, ROBO1, RREB1, SDC4, SLC8A1, SP100, SPARC, SRC, SRF, STC1, ADAM17, NR2F2, TGFBR1, THBS1, TNS1, TWIST1, VEGFA, SEMA7A, ADAM9, NRP1, SGPL1, KLF4, MAP4K4, ROCK2, BAG4, AKAP12, SEMA3E, HDAC9, FGF19, AKT3, WASF2, SEMA3A, CAP1, SEMA4B, PLK2, DUSP10, VASH1, PDXDC1, PLXND1, KANK1, CLASP1, SIRT1, CORO1C, APPL1, GREM1, FOXP1, SOX8, ADIPOR1, ANLN, EPB41L4B, DLL4, SEMA4C, FBXW7, FERMT1, RCC2, ADAMTS9, SEMA6A, EPB41L5, RIC8A, PBLD, ARID5B, NUS1, RFFL, ACVR1C, DAB2IP, AMOT, AMOTL1, SPRED1, BMPER, TMEM201, EMC10, CRB2, MIA3
BP	GO:0009267	cellular response to starvation	54/3408	4.44E-06	FAS, BCL2, BMPR2, CDKN1A, COMT, DSC2, EIF2S1, FOXO1, HSPA5, JUN, LAMP2, FADS1, MAX, PDK4, PRKAA1, MAPK1, MAPK3, MAPK8, EIF2AK2, RALB, SFRP1, SREBF2, KLF10, TP53, WNT2B, XBP1, STK24, PPM1D, AKR1C3, MTMR3, ATG5, ATG7, GABARAPL2, ATG14, USP33, SZT2, SIRT1, FBXO22, TNRC6A, DNAJC15, SH3GLB1, ZFYVE1, WNT4, SLC38A2, RRAGD, RRAGC, CPEB4, MAP1LC3B, NUAK2, SEH1L, SESN2, FNIP1, SESN3, SIK1

BP	GO:0010721	negative regulation of cell development	102/3408	4.47E-06	ACTN4, ADCY6, JAG1, ARF6, RHOA, ARHGDIA, BCL2, BMP7, BMPR1A, CALR, COL3A1, CTNNA1, CTNNB1, CTSZ, DDX6, DLX2, S1PR3, EFNA5, EFNB2, EIF4E, EPHA4, EPHA7, EPHB2, FBN1, FKBP4, FOXO3, G6PD, GBP1, GDI1, GSK3B, HDAC2, NRG1, HES1, ID4, IDH2, ISL1, LDLR, LRP1, SMAD4, NTRK3, PAFAH1B1, PAX6, PBX1, PPARA, PPP3CA, PTEN, PTPRG, RGS2, RGS4, CX3CL1, SKI, SORL1, SOX11, STAT3, TERT, TP53, TSC1, VEGFA, YY1, SEMA7A, NRP1, SYNGAP1, ARHGEF2, NTN1, MAP4K4, RAPGEF2, SEMA3E, LRIG2, RNF10, GDF11, SEMA3A, SEMA4B, POSTN, PLK2, DUSP10, NLGN1, DKK1, FSTL4, RAP1GAP2, KANK1, DICER1, CORO1C, MYLIP, SOX8, ASAP1, BCL11A, SEMA4C, FBXW7, RCC2, RGMA, MIB1, SEMA6A, CTDSP1, GORASP1, ISL2, TRAK2, ITM2C, KREMEN1, HOOK3, DIXDC1, KCTD11, PRTG
BP	GO:0036498	IRE1-mediated unfolded protein response	30/3408	4.56E-06	ADD1, BAK1, TPP1, EXTL2, EXTL3, GFPT1, HDGF, HSPA5, DNAJB9, PTPN1, SHC1, SSR1, TLN1, XBP1, ATP6V0D1, VAPB, GOSR2, EDEM1, BCL2L11, CTDSP2, HYOU1, AGR2, SERP1, BFAR, FKBP14, TMEM33, ARFGAP1, TSPYL2, SYVN1, DAB2IP
BP	GO:1905897	regulation of response to endoplasmic reticulum stress	36/3408	4.62E-06	BAK1, BCL2L1, CAV1, ATF6B, GRINA, HSPA5, DNAJB9, ATXN3, NCK1, OPA1, PTPN1, TMBIM6, UBE2G2, XBP1, NCK2, USP13, EDEM1, HERPUD1, BCL2L11, BCAP31, HYOU1, AGR2, SERINC3, SIRT1, USP25, UBQLN2, UBQLN1, DERL2, TXNDC12, BFAR, UBE2J1, TMEM33, YOD1, SYVN1, PPP1R15B, DAB2IP
BP	GO:0097485	neuron projection guidance	86/3408	4.66E-06	ALCAM, APBB2, BDNF, BMP7, BMPR2, DAG1, EFNA3, EFNA5, EFNB1, EFNB2, CELSR3, MEGF8, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, ETV1, GAB1, GATA3, GRB2, ARHGAP35, ISL1, L1CAM, LRP1, SMAD4, MATN2, MYH10, NCAM1, NEO1, NFIB, OPHN1, PAX6, PIK3CB, PRKCA, MAPK1, MAPK3, PTCH1, PTPN11, ROBO1, SHC1, SIAH1, SOS1, SPTAN1, SPTBN1, SRC, TRIO, VEGFA, VLDLR, FZD3, NR4A3, SEMA7A, IRS2, NRP1, RPS6KA5, PDLIM7, NTN1, SEMA3E, SEMA3A, SEMA4B, FRS2, KIF3A, LYPLA2, PALLD, USP33, MYCBP2, NFASC, PLXND1, FLRT2, CYFIP2, NPTN, SEMA4C, YTHDF1, DPYSL5, VANGL2, SEMA6A, ZSWIM6, ISL2, BCL11B, ZSWIM4, PLXNA4, EMB, DOK6, AGRN, RNF165
BP	GO:0051236	establishment of RNA localization	66/3408	4.83E-06	ATM, ATR, ZFP36L1, CETN2, EIF4E, FMR1, HNRNPU, MYO1C, NCBP1, NUP88, NUP98, POLR2D, PURA, RAN, RANBP2, UPF1, ABCE1, ATXN2, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, ZFP36, PABPN1, TNKS, QKI, TOMM20, POM121, SMG7, G3BP2, NUTF2, NXF1, IGF2BP1, IGF2BP3, NUP50, RNPS1, CPSF6, XPOT, DDX19B, U2AF2, XPO7, SMG1, ZC3H3, BICD2, SMG5, UPF2, RBM15B, NMD3, CDC40, CPSF2, RBM27, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, EIF5A2, THOC2, XPO5, SEH1L, NUP43, POM121C
BP	GO:0007034	vacuolar transport	52/3408	4.98E-06	AP1G1, ARF1, RHOB, TMEM50B, SCARB2, LYST, IGF2R, LAMP2, LRP1, M6PR, NEDD4, NPC1, SORT1, SORL1, VAMP7, VCP, AP3D1, ATP6V0D1, VPS4B, GOSR2, ZFYVE16, HMGXB4, SNF8, ATG14, DENND3, TRAK1, VPS13A, MGRN1, LEPROTL1, TMEM50A, AP3M1, VPS36, HOOK1, ANKFY1, CHMP5, VPS54, TMEM106B, LEPROT, VPS13C, VPS37C, VPS13D, VPS35, CHMP1B, SMURF1, EPG5, KIF13A, TRAK2, GNPTAB, HOOK3, CHMP7, VPS37D, RAB12
BP	GO:1990778	protein localization to cell periphery	94/3408	5.02E-06	ACTB, ADAM10, AKT2, ANK1, AR, ARF6, ATP1B1, BCL2L1, CAV1, AP2M1, CSK, DAB2, DAG1, EGFR, EMP2, EPB41, EPHB2, FLOT2, GBP1, GOLGA4, IKBKB, ITGA3, ITGB1, JUP, KIF5B, LRP1, LRP6, RAB8A, MMP14, MYO5A, NSF, P2RY1, PRKCE, PTCH1, RAB3B, RAP2A, RDX, SNAP25, SPTBN1, STX3, VAMP2, VAMP7, TUB, DCHS1, NUMB, SQSTM1, MAP7, RABEP1, ROCK2, AKAP5, BAG4, PREPL, RAPGEF2, C2CD5, GPC6, ARFRP1, LYPLA1, SEC23A, AGR2, EXOC5, RAB31, RAB11FIP2, KIF1B, NFASC, EFR3A, PACS2, RHOQ, CLIP3, APPL1, LDLRAP1, RAB8B, ADAM22, ANLN, SYTL2, GOLPH3L, PACS1, VPS35, SMURF1, GPR158, KIF13A, TMBIM1, GORASP1, C16orf70, FAM126A, PKDCC, MYADM, BBIP1, FCHO2, TTC7B, ZDHHC23, ZDHHC22, FAM126B, RILPL1, RAB15
BP	GO:0007045	cell-substrate adherens junction assembly	35/3408	5.22E-06	ABL1, RHOA, BCL2, EFNA5, LRP1, MMP14, PTEN, PTPRJ, PTPRK, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VEGFA, IQGAP1, NRP1, LDB1, TAOK2, MAP4K4, ROCK2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, WHAMM, FMN1
BP	GO:0048041	focal adhesion assembly	35/3408	5.22E-06	ABL1, RHOA, BCL2, EFNA5, LRP1, MMP14, PTEN, PTPRJ, PTPRK, SDC4, SFRP1, SLC9A1, SRC, THBS1, TSC1, VEGFA, IQGAP1, NRP1, LDB1, TAOK2, MAP4K4, ROCK2, SLK, DLC1, FAM107A, LIMCH1, CLASP1, CORO1C, WNT4, RCC2, EPB41L5, PEAK1, PHLDB2, WHAMM, FMN1
BP	GO:0051058	negative regulation of small GTPase mediated signal transduction	28/3408	5.23E-06	ABL2, BCL6, EPHB2, RAPGEF1, ARHGAP35, ITGA3, ITGB1, MET, RASA1, TIMP2, TNFAIP1, CUL3, SYNGAP1, MFN2, SPRY1, DLC1, STAMBP, RASA3, KANK1, CD2AP, HEG1, MAPKAP1, SPRY4, KCTD10, CGNL1, ARHGAP12, DAB2IP, FLCN
BP	GO:0035567	non-canonical Wnt signaling pathway	54/3408	5.42E-06	ABL1, RHOA, ARRB2, CALM1, CAMK2A, CDC42, AP2M1, CSNK1D, CSNK1E, CTNNB1, DAB2, DVL3, CELSR3, CELSR2, GNB1, MLLT3, PPP3CA, PPP3R1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, TCF7L2, TIAM1, FZD5, FZD3, FZD1, FZD4, FZD6, PSMF1, GPC6, PSME3, PSMD14, DKK1, TNRC6B, PSME4, AGO1, TNRC6A, NLK, WNT4, SMURF1, VANGL2, PLEKHA4, RNF213, TNRC6C, VANGL1, ZNRF3, PRICKLE2, AGO3, AGO4
BP	GO:0070646	protein modification by small protein removal	91/3408	5.44E-06	ACTB, APC, AR, RHOA, ARRB2, BRCA1, CCNA2, CDC25A, CYLD, EP300, GATA3, KAT2A, HCFC1, HIF1A, FOXK2, SMAD2, SMAD4, SMAD7, MDM4, ATXN3, FOXO4, MYC, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD23B, ATXN7, SIAH2, TGFBR1, TP53, TRAF3, USP1, VCP, YY1, USP9X, BAP1, SNX3, KAT2B, USP13, USP2, COPS2, PSMF1, TOMM20, SPATA2, JOSD1, RCE1, PSME3, PSMD14, TNIP1, TAB1, STAMBP, COPS8, USP33, PSME4, OTUD3, USP49, SENP6, USP21, USP25, DESI2, UCHL5,

					TAF9B, OTUD6B, INO80, OTUD4, INO80D, USP47, YOD1, OTUD7B, ATXN7L3, USP31, USP36, USP28, USP37, COPS7B, BRCC3, VCPIP1, ITCH, USP38, USP45, TADA2B, MYSM1, USP51, SENP5, KDM1B, FOXK1
BP	GO:0048738	cardiac muscle tissue development	75/3408	5.57E-06	ARRB2, BMP7, BMPR1A, CALR, COL11A1, CREB1, MAPK14, CXADR, S1PR1, EDN1, EFNB2, FGF2, FKBP1A, FOXC1, G6PD, GATA6, KAT2A, GJA1, NRG1, HNRNPU, RBPJ, ISL1, ITGB1, JARID2, SMAD4, SMAD7, MEF2A, MEF2C, MYH10, PDGFRA, PIM1, PIN1, POU4F1, PPARA, PRKAR1A, MAPK1, PROX1, PTEN, RGS2, RGS4, MAP2K4, SGCD, SLC8A1, SLC9A1, SRF, TBX3, TGFBR1, TGFBR3, TSC1, VEGFA, YY1, ARID1A, SORBS2, ALDH1A2, HAND1, AKAP6, ATG5, GJC1, UBE4B, NEBL, PDLIM5, FRS2, AKAP13, DKK1, KDM6B, GREM1, DLL4, CHD7, ADAMTS9, HEG1, ALPK3, NDRG4, PTCD2, SIK1, ARID2
BP	GO:0036294	cellular response to decreased oxygen levels	71/3408	5.74E-06	AK4, ATP7A, BCL2, BMP7, ZFP36L1, CBL, CCNA2, CREBBP, DNMT3A, EDN1, EGR1, EP300, EPAS1, FOXO3, GATA6, GNB1, HIF1A, RBPJ, IRAK1, KCNK3, MDM4, MYC, NKX3-1, OPA1, PDK3, PPARD, PRKAA1, PRKCE, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, PTGIS, RORA, SFRP1, SLC8A1, SLC9A1, SRC, STC1, SUV39H1, TMBIM6, TERT, TP53, TSC1, TWIST1, VEGFA, VHL, CUL2, STC2, LIMD1, ROCK2, PSMF1, PSME3, PSMD14, CITED2, HYOU1, PSME4, SIRT1, HIPK2, UBQLN1, HP1BP3, HIF1AN, FMN2, CPEB4, EGLN2, EGLN3, CPEB2
BP	GO:0042692	muscle cell differentiation	111/3408	5.93E-06	ABL1, ADM, ARRB2, ATP2A2, BCL2, BCL9, BDNF, BNIP2, CALR, CAPN2, CASP3, CDC42, CFL2, MAPK14, CSRP1, CTNNA1, CTNNB1, CXADR, EDN1, EFNB2, EZH2, G6PD, GATA6, KAT2A, NRG1, HNRNPU, HES1, IGF2, IGFBP5, RBPJ, ITGB1, KIT, KRAS, SMAD4, MECP2, MEF2A, MEF2C, FOXO4, MMP14, MSX1, MYH9, MYH10, PDGFB, PDGFRA, PIN1, PPARA, PPP3CA, PRKAR1A, PROX1, PTGFRN, RB1, RGS2, RGS4, RORA, SORT1, MAP2K4, SGCD, SKI, SLC8A1, SLC9A1, SOD2, SRF, TBX3, TCF3, ZEB1, TSC1, VEGFA, XBP1, YY1, ADAM12, ARID1A, SORBS2, ITGA8, SPAG9, DYRK1B, QKI, AKAP6, ATG5, MORF4L2, HDAC9, NEBL, PDLIM5, FRS2, AKAP13, DKK1, KDM1A, KDM6B, SIRT1, FBXO22, MYOF, GREM1, PDCD4, TMOD2, MYEF2, CDON, FBXO40, SIX4, WNT4, SEMA4C, RBM38, CYP26B1, ALPK3, PTCD2, SYNPO2L, MED28, EPC1, SETD3, WFIKKN2, MTPN, SIK1, RBPMS2
BP	GO:0007568	aging	96/3408	6.19E-06	ABL1, ADA, ADM, AMFR, ATM, ATP2B1, ATR, BAK1, BCL2, BCL6, BMPR1A, CALR, CANX, CDK6, CDKN1A, CHEK1, COL4A2, CREB1, MAPK14, CTNNA1, DAG1, DCN, DNMT3A, EDN1, EIF2S1, CLN8, ERCC2, FOXM1, FOXO3, GRB2, HMGCR, HMGA1, IGFBP1, IGFBP5, ILK, IRAK1, JUN, JUND, KRAS, LOXL2, LRP1, MAP3K3, FOXO4, MME, MNT, OGG1, OPA1, P2RY1, SERPINE1, PAWR, PAX2, PDE4D, PML, PPP3CA, PRELP, MAPK1, MAPK3, PTEN, CX3CL1, SLC1A2, SNCA, SOD2, SRF, STAT3, TBX3, TERT, TIMP2, TNFRSF1B, TP53, TWIST1, VCAM1, PRDM2, KAT6A, HMGA2, TP63, MBD2, KYNU, AURKB, NUAK1, AKT3, ATG7, PLK2, ZNF277, SEC63, VASH1, DKK1, SIRT1, MORC3, SIN3A, RSL1D1, SERP1, PDCD4, HTRA2, ZMIZ1, SMC6, RNF165
BP	GO:2001252	positive regulation of chromosome organization	60/3408	6.49E-06	ARRB1, ATM, ATR, ATRX, BCL6, BRCA1, CCT6A, CTNNB1, DKC1, DNMT3B, FMR1, GATA3, KAT2A, HNRNPD, HNRNPU, ISL1, JARID2, LIG4, SMAD4, MECP2, MAP3K4, KMT2A, MYB, PARN, PML, MAPK1, MAPK3, RAD21, RB1, SNAI2, TAL1, TP53, UBE2N, VEGFA, XRCC5, CUL3, TNKS, RPS6KA4, AURKB, RPS6KA5, CTR9, KAT7, MTF2, MORC2, KDM1A, SIRT1, WBP2, NIPBL, SIN3A, AUTS2, RTEL1, RIF1, ATF7IP, KMT2E, MIER1, NABP2, HMBOX1, TET1, SLX4, TADA2B
BP	GO:0048638	regulation of developmental growth	102/3408	6.56E-06	ABL1, ADRB1, AR, BCL2, BDNF, BMPR1A, BMPR2, CDKN1A, CDKN1B, CREB1, MAPK14, CSF1, DUSP6, EDN1, EFNA5, MEGF8, EPHA7, FGF2, FGFR3, FOXC1, FN1, G6PD, GATA6, GDI1, GJA1, GOLGA4, GSK3B, IGF2, RBPJ, ILK, INSR, JARID2, L1CAM, LIMK1, LRP1, MAP1B, MAPT, MEF2C, NTRK3, PAFAH1B1, PIM1, PIN1, POU3F2, PPARA, PPARD, MAPK1, PROX1, PTCH1, PTEN, RGS2, RGS4, SFRP1, SRF, STAT3, STAT5B, STK4, SYT1, HNF1B, TGFBR1, TGFBR3, VEGFA, YY1, RND2, SEMA7A, STC2, NRP1, SOCS2, SGPL1, LATS1, NTN1, AKAP6, SEMA3E, BCL2L11, SEMA3A, OLFM1, SEMA4B, AGR2, DUSP10, RAB21, FSTL4, WWC1, NIPBL, SIN3A, LATS2, SERP1, HTRA2, SYT17, SIX4, BCL11A, SEMA4C, CHD7, WWC3, SMURF1, SEMA6A, MUL1, WWC2, PLXNA4, SYT2, WDR36, TTL, SH3PXD2B, AGRN
BP	GO:0048588	developmental cell growth	75/3408	6.56E-06	ABL1, ALCAM, BDNF, BMPR2, CTNNB1, EDN1, EFNA5, MEGF8, EPHA7, FN1, G6PD, GDI1, GOLGA4, GSK3B, ILK, ITGB1, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, PIN1, PPARA, RARG, RGS2, RGS4, MAP2K4, SH3GL2, SRF, AURKA, SYT1, TIAM1, VCL, VEGFA, YY1, KMT2D, RND2, USP9X, ULK1, SORBS2, SEMA7A, IQGAP1, NRP1, WASF1, DCLK1, NTN1, AKAP6, SEMA3E, SEMA3A, ARIH2, OLFM1, SLC9A6, SEMA4B, PDLIM5, POSTN, AKAP13, RAB21, FSTL4, SIN3A, AUTS2, CYFIP2, NIN, SYT17, BCL11A, SEMA4C, SMURF1, SEMA6A, RAPH1, MUL1, PLXNA4, SYT2, WDR36, TTL
BP	GO:0006338	chromatin remodeling	62/3408	6.64E-06	ACTB, RERE, ATRX, CENPA, CHD3, CHD4, CHEK1, CTNNB1, DR1, EZH1, BPTF, GATA3, KAT2A, HDAC2, HMGB3, HMGA1, FOXA1, HNRNPC, JARID2, MYB, MYC, PTMA, RB1, KDM5A, SATB1, SMARCA2, SMARCC2, SMARCD2, SMARCE1, KDM6A, HMGA2, ARID1A, TP63, KAT2B, MBD2, BAZ1B, KDM4A, KMT2B, KDM5B, SRCAP, NUDT5, CBX3, MORC2, KDM6B, PSME4, SATB2, CECR2, BAZ2B, RSF1, INO80, CHD7, SMARCAD1, ZMIZ1, GATAD2B, ARID1B, ANP32E, ZMIZ2, ELOF1, CENPL, TADA2B, MYSM1, SPTY2D1
BP	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	70/3408	6.84E-06	ALAD, CAV1, CSNK1D, CSNK1E, DAB2, EPHA4, FHIT, FMR1, GSK3B, UBE2K, DNAJB2, SMAD7, MAP1A, ATXN3, OPHN1, PKD1, PML, MAPK9, PSMC2, PTEN, RAD23B, AURKA, STYX, TAF1, TMF1, UBE2G2, VCP, BTRC, USP13, LATS1, PSMF1, SOCS5, EDEM1, HERPUD1, RNF144A, BCAP31, PSME3, PSMD14, TRIB1, ARIH2, PLK2, TLK2, GABARAPL2, UFL1, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, HIPK2, USP25, UBQLN2, UBQLN1, DERL2, WAC, UCHL5, UBE2J1, SUFU, ANKIB1, FBXW7, YOD1, UBQLN4, SMURF1, DDA1, FAM122A, SOCS4, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:0031647	regulation of protein stability	87/3408	7.00E-06	ASPH, ATP1B1, BCL2, CALR, CASP3, CCT6A, CDKN1A, CREB1, CREBBP, DVL3, EP300, EPHA4, FLOT2, GAPDH, KAT2A, GNAQ, HCFC1, HTT, HIP1, KRAS, LAMP2, LSS, SMAD7, MDM4, MSX1, NF2, PIM1, PIN1, MAPK1, PTEN, SEL1L, SIAH1, SNCA, SOX4, SRC, STK4, AURKA, TAF1, TBL1X, TERT, TP53, TSC1, VHL, XBP1, USP9X, CUL3, PER3, BTRC, USP13, USP2, RASSF2, TSPAN1, CRTAP, FAM107A, AAK1, USP33, OTUD3, SIRT1, TARDBP, MORC3, STX12, HYPK, FBXL3, MYLIP, USP25, SH3GLB1, GET4, TAF9B, NLK,

					GNL3L, CMTM6, PINX1, USP47, QRSL1, FBXW7, ATF7IP, VPS35, USP36, USP28, WIZ, MTMR9, CDC73, MUL1, COG3, DDI2, SYVN1, WDR81
BP	GO:0032922	circadian regulation of gene expression	29/3408	7.05E-06	ZFHX3, CRY2, CSNK1D, CSNK1E, EGR1, GFPT1, HDAC2, HNRNPU, KMT2A, PML, PPARA, PPP1CA, PPP1CB, PPP1CC, KDM5A, RORA, HNF1B, NRIP1, BHLHE40, PER3, PER2, USP2, MTA1, CLOCK, NCOA2, KDM2A, MYCBP2, SIRT1, LGR4
BP	GO:0030218	erythrocyte differentiation	44/3408	7.26E-06	ACVR1B, ADAR, ADD1, BCL6, ZFP36L1, CASP3, CDK6, CEBPG, MAPK14, EPAS1, ERCC2, FOXO3, G6PD, GATA2, GATA3, NCKAP1L, HIF1A, HOXA5, KIT, LYN, SLC11A2, PKNOX1, RB1, SP3, SRF, STAT1, STAT3, STAT5B, TAL1, TGFBR3, THRA, VEGFA, ZFP36, LDB1, PTBP3, SH2B3, KLF2, RBFOX2, HIPK2, NCAPG2, SLC25A38, KMT2E, SFXN1, FAM210B
BP	GO:0010948	negative regulation of cell cycle process	105/3408	7.50E-06	APC, ATM, ATRX, CCND1, BCL2, BCL6, BMP7, BRCA1, ZFP36L1, ZFP36L2, CALR, CCNF, CDK6, CDKN1A, CDKN1B, CHEK1, FOXN3, DUSP1, E2F6, EP300, EZH2, FHL1, KAT2A, IK, MAD2L1, MAX, MDM4, MEN1, FOXO4, CNOT4, PML, PRKAR1A, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD1, RAD21, RAD51, RB1, RBL2, RNF2, RRM2, SKP1, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, HMGA2, SMC1A, CDC14B, TNKS, KAT2B, AURKB, KLF4, TRIP13, CNOT8, TAOK2, PSMF1, CTDSP2, YAF2, PSME3, PSMD14, CTDSPL, BTN2A2, GPNMB, STAG2, PLK2, ZNF268, FAM107A, CBX3, CNOT1, PSME4, MGA, CBX5, SUZ12, ZNF385A, GIGYF2, TRIAP1, DTL, PINX1, USP47, FBXW7, PCID2, MDM1, CNOT6, TAOK1, CTDSP1, ZNF655, BRCC3, CDC73, PHC3, EPC1, ZNF830, SLFN11, DCUN1D3, NACC2, E2F7, DAB2IP
BP	GO:0009416	response to light stimulus	94/3408	7.50E-06	AKT2, ARRB1, ATR, BAK1, CCND1, BCL2, CALM1, CASP3, CDC25A, CDKN1A, CDS1, CHEK1, CREB1, CREBBP, CRY2, CTNS, DUSP1, EGFR, EIF2S1, ELK1, EP300, ERCC2, ERCC6, FECH, FMR1, FNTA, GNAQ, GNB1, HIF1A, HMGCR, ITGB1, JUND, KCNC1, KIT, KRAS, MECP2, MEIS2, MAP3K4, MEN1, MME, MYC, NEDD4, OGG1, PDE1B, PML, PPP1CA, PPP1CB, PPP1CC, PRKAA1, MAPK8, PTPRK, RAG1, RBL2, SLC1A2, ELOVL4, TAF1, TP53, USP1, YY1, CUL4B, BHLHE40, B4GALT2, SYNGAP1, PER3, PER2, USP2, MTA1, AURKB, CLOCK, UBE4B, CERS1, METAP2, CEP250, KDM1A, SIRT1, SLC7A11, FBXL3, NPTN, TRIAP1, DTL, INO80, USP47, USP28, PLEKHB1, RIC8A, NDRG4, CAMKMT, RHNO1, RHBDD1, BMF, TP53INP1, DCUN1D3, SIK1, SDE2
BP	GO:0051402	neuron apoptotic process	76/3408	7.53E-06	ADARB1, AKT2, RHOA, ARRB1, ARRB2, ATM, AXL, BCL2, BCL2L1, BDNF, CASP3, CDC34, CEBPB, ATF2, CTNNB1, CTSZ, ATN1, EPHA7, FOXO3, G6PD, GAPDH, GATA3, HIF1A, HSPA5, ILK, ISL1, JUN, KRAS, LIG4, LRP1, MAX, MCL1, MDK, MECP2, MEF2C, MYB, MYBL2, PAK3, PIN1, POU4F1, RASA1, RB1, CX3CL1, MAP2K4, SET, SIAH1, SNCA, SOD2, TERT, TP53, TYRO3, BTG2, NR4A3, TP63, FADD, NRP1, SYNGAP1, BCL2L11, SIGMAR1, LANCL1, HYOU1, STAMBP, CIT, TRIM2, NCSTN, NSMF, HIPK2, SIX4, OXR1, FBXW7, CPEB4, DNAJC5, BHLHB9, AKT1S1, EGLN2, EGLN3
BP	GO:0008361	regulation of cell size	61/3408	7.88E-06	ABL1, ADD1, ANXA7, RHOA, ATP7A, BDNF, BMPR2, CLNS1A, CREB1, EDN1, EFNA5, MEGF8, EPHA7, CLN8, FN1, GDI1, GOLGA4, GSK3B, IL7R, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, PTEN, RARG, RDX, SLC12A4, SRF, TSC1, VEGFA, RND2, SEMA7A, NRP1, NTN1, SEMA3E, SLC12A6, AKT3, SEMA3A, OLFM1, VAV3, SEMA4B, SLC12A7, RAB21, KDM1A, WDTC1, FSTL4, RAP1GAP2, SIN3A, SEMA4C, SLC12A5, SEMA6A, AKT1S1, PLXNA4, IQGAP3, WDR36, MTPN, TTL
BP	GO:0042594	response to starvation	64/3408	8.09E-06	ADM, FAS, BCL2, BMPR2, CBL, CDKN1A, COMT, DSC2, EIF2S1, FOXO1, FOXO3, HSPA5, FOXK2, JUN, LAMP2, FADS1, MAX, PDK4, PRKAA1, MAPK1, MAPK3, MAPK8, EIF2AK2, RALB, SFRP1, SREBF2, KLF10, TP53, WNT2B, XBP1, ZFP36, ULK1, STK24, PPM1D, AKR1C3, MTMR3, ATG5, ATG7, FSTL1, GABARAPL2, ATG14, USP33, SZT2, LARP1, SIRT1, FBXO22, EIF2AK1, TNRC6A, DNAJC15, SH3GLB1, ZFYVE1, WNT4, SLC38A2, RRAGD, RRAGC, CPEB4, MAP1LC3B, NUAK2, SEH1L, SESN2, FNIP1, SESN3, SIK1, FOXK1
BP	GO:0071456	cellular response to hypoxia	68/3408	8.09E-06	AK4, ATP7A, BCL2, BMP7, ZFP36L1, CCNA2, CREBBP, DNMT3A, EDN1, EGR1, EP300, EPAS1, FOXO3, GATA6, GNB1, HIF1A, RBPJ, IRAK1, KCNK3, MDM4, MYC, NKX3-1, OPA1, PDK3, PPARD, PRKAA1, PRKCE, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, PTGIS, RORA, SFRP1, SLC8A1, SLC9A1, SRC, STC1, SUV39H1, TMBIM6, TERT, TP53, TWIST1, VEGFA, VHL, CUL2, STC2, LIMD1, ROCK2, PSMF1, PSME3, PSMD14, CITED2, HYOU1, PSME4, SIRT1, HIPK2, UBQLN1, HP1BP3, HIF1AN, FMN2, EGLN2, EGLN3, CPEB2
BP	GO:0030278	regulation of ossification	67/3408	8.09E-06	ACVR2B, JAG1, ATP2B1, BCL2, BMP7, BMPR1A, BMPR2, RUNX2, CDK6, CEBPB, CEBPD, MAPK14, CSF1, CTNNB1, DDX5, S1PR1, ESRRA, FBN2, GJA1, GNAS, HIF1A, IGFBP5, RBPJ, IL6R, IL6ST, ILK, JUND, NBR1, SMAD6, MDK, MEF2C, MEN1, PBX1, ENPP1, MAPK1, MAPK3, PTCH1, PTGER4, RORB, SFRP1, SKI, SLC8A1, SNAI2, SOX11, TWIST1, WNT7B, TP63, CHRD, LIMD1, PDLIM7, RASSF2, TOB1, TOB2, DKK1, NIPBL, GREM1, SUFU, WNT4, BCOR, BMP2K, TXLNG, ANKH, FAM20C, SMURF1, SMOC1, KREMEN1, PKDCC
BP	GO:0060218	hematopoietic stem cell differentiation	35/3408	9.67E-06	ABL1, RUNX1, CBFB, CDK6, CHD2, ERCC2, FOXC1, GATA2, GATA3, LMO2, KMT2A, MYB, EIF2AK2, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, SRF, TAL1, TCF3, TP53, XRCC5, LDB1, PSMF1, SETD1A, PSME3, PSMD14, PSME4, YTHDF2, PUS7, ITCH
BP	GO:0015931	nucleobase-containing compound transport	76/3408	1.06E-05	SLC25A6, ZFP36L1, CETN2, EIF4E, FMR1, GJA1, GJB1, HNRNPU, MYO1C, NCBP1, NUP88, NUP98, POLR2D, PURA, RAN, RANBP2, UPF1, ABCE1, ATXN2, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, ZFP36, PABPN1, TNKS, QKI, TOMM20, POM121, SMG7, G3BP2, NUTF2, SLC25A17, NXF1, SLC35A1, IGF2BP1, IGF2BP3, NUP50, RNPS1, CPSF6, XPOT, DDX19B, U2AF2, XPO7, SMG1, ZC3H3, BICD2, SMG5, UPF2, RBM15B, SLC25A24, SLC35B3, NMD3, CDC40, CPSF2, RBM27, ALKBH5, SLC25A36, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, EIF5A2, THOC2, XPO5, EPG5, SLC25A32, SEH1L, SLC35A4, NUP43, SLC35E2B, POM121C
BP	GO:0016579	protein deubiquitination	86/3408	1.14E-05	ACTB, APC, AR, RHOA, ARRB2, BRCA1, CCNA2, CDC25A, CYLD, EP300, GATA3, KAT2A, HCFC1, HIF1A, FOXK2, SMAD2, SMAD4, SMAD7, MDM4, ATXN3, FOXO4, MYC, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD23B, ATXN7, SIAH2, TGFBR1, TP53, TRAF3, USP1, VCP, YY1, USP9X, BAP1, SNX3, KAT2B, USP13, USP2, PSMF1, TOMM20, SPATA2, JOSD1, RCE1,

					PSME3, PSMD14, TNIP1, TAB1, STAMBP, USP33, PSME4, OTUD3, USP49, USP21, USP25, DESI2, UCHL5, TAF9B, OTUD6B, INO80, OTUD4, INO80D, USP47, YOD1, OTUD7B, ATXN7L3, USP31, USP36, USP28, USP37, BRCC3, VCPIP1, ITCH, USP38, USP45, TADA2B, MYSM1, USP51, KDM1B, FOXK1
BP	GO:0050657	nucleic acid transport	64/3408	1.20E-05	ZFP36L1, CETN2, EIF4E, FMR1, HNRNPU, MYO1C, NCBP1, NUP88, NUP98, POLR2D, PURA, RAN, RANBP2, UPF1, ABCE1, ATXN2, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, ZFP36, PABPN1, TNKS, QKI, TOMM20, POM121, SMG7, G3BP2, NUTF2, NXF1, IGF2BP1, IGF2BP3, NUP50, RNPS1, CPSF6, XPOT, DDX19B, U2AF2, XPO7, SMG1, ZC3H3, BICD2, SMG5, UPF2, RBM15B, NMD3, CDC40, CPSF2, RBM27, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, EIF5A2, THOC2, XPO5, SEH1L, NUP43, POM121C
BP	GO:0050658	RNA transport	64/3408	1.20E-05	ZFP36L1, CETN2, EIF4E, FMR1, HNRNPU, MYO1C, NCBP1, NUP88, NUP98, POLR2D, PURA, RAN, RANBP2, UPF1, ABCE1, ATXN2, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, ZFP36, PABPN1, TNKS, QKI, TOMM20, POM121, SMG7, G3BP2, NUTF2, NXF1, IGF2BP1, IGF2BP3, NUP50, RNPS1, CPSF6, XPOT, DDX19B, U2AF2, XPO7, SMG1, ZC3H3, BICD2, SMG5, UPF2, RBM15B, NMD3, CDC40, CPSF2, RBM27, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, EIF5A2, THOC2, XPO5, SEH1L, NUP43, POM121C
BP	GO:0043087	regulation of GTPase activity	131/3408	1.21E-05	ADRB1, AKT2, ARHGAP1, ARHGDIA, ARRB1, ARRB2, BCL6, BNIP2, CCR7, CRK, CRKL, DVL3, ECT2, S1PR1, EFNA5, EIF5, EPHA4, EPHB3, ERBB2, EZH2, GDI1, GNAQ, RAPGEF1, ARHGAP35, GSK3B, NCKAP1L, AGFG2, ITGA6, ITGB1, JUN, IPO5, NEDD9, NTRK3, TBC1D25, OPHN1, PAFAH1B1, PIN1, PTPRN2, RANBP2, RAP1GDS1, RASA1, RDX, RGS2, RGS4, RGS16, RP2, CCL7, CX3CL1, SFRP1, SOS1, TIAM1, TSC1, EVI5, RGS5, PKP4, IQGAP1, NRP1, SYNGAP1, KALRN, RABEP1, ARHGAP29, MAP4K4, RASAL2, RAPGEF2, USP6NL, GIT2, TBC1D4, RABGAP1L, TNK2, SPRY1, NET1, DLC1, RAPGEF3, CDC42EP2, VAV3, SEC23A, NUP50, IQGAP2, ADAP1, TBC1D8, RASA3, RAB11FIP2, TBC1D9B, RRP1B, TBC1D2B, RAP1GAP2, PLXND1, LRCH1, SNX13, DOCK9, ARHGEF12, ACAP2, CORO1C, RABGAP1, RAB3GAP2, TBC1D10B, SIPA1L1, GIT1, ASAP1, ERRFI1, WNT4, ARHGAP17, TBC1D22B, DEPDC1, ARFGAP1, RCC2, CDC42SE1, RALGAPA2, TBC1D24, SIPA1L2, RIC8A, WNK1, ARHGAP28, PREX2, ARHGAP39, SYDE2, PLXNA4, ARHGAP18, ARHGAP12, ARAP2, AGAP1, FGD4, IQGAP3, TBC1D20, CPEB2, STXBP5, DAB2IP, AMOT, FLCN, RICTOR, AGRN
BP	GO:0032386	regulation of intracellular transport	118/3408	1.49E-05	ADCY1, ADORA2B, AKT2, ARF1, ARHGAP1, ATP2A2, CALM3, CAMK2A, MAPK14, DAB2, ECT2, STOM, ERBB2, FER, FMR1, GATA2, GDI1, GSK3B, INSIG1, JUP, KIF5B, IPO5, LYN, MAP1B, MYO1C, PPP1R12A, NEDD4, NEFH, OAZ2, P2RY1, PPP1CC, PRKAA1, PKIA, MAPK1, MAPK3, PTPN1, PTPN11, PTPN14, RAB5A, RAN, RAP1B, RDX, SCP2, SORL1, SP100, SRC, SREBF2, VAMP1, VAMP2, VAMP7, SYK, SYT1, TCF7L2, TP53, TXN, UBE2D3, UBE2G2, UBE2L3, XPO1, YWHAE, FZD5, BAP1, SNX3, NAPA, CD84, RAB11B, BAG4, PREPL, EDEM1, ATG13, RIMS3, C2CD5, BCAP31, TENM1, NUTF2, RAPGEF3, ARIH2, UNC13B, ANP32B, CPSF6, NLGN1, RAB21, WWC1, DNAJC13, NCS1, TARDBP, LDLRAP1, HTRA2, GIT1, DERL2, SH3GLB1, DNAJC27, UBR5, UBE2J1, SUFU, RAB23, RBM27, MIEF1, LEPROT, FBXW7, YOD1, FERMT1, RIOK2, SAR1A, MFF, MAVS, XPO5, USP36, RHOU, XPO4, NDRG4, SH3TC2, YIPF5, DNAJC30, NUS1, MIEF2, TBC1D20, RIMS4
BP	GO:0070373	negative regulation of ERK1 and ERK2 cascade	32/3408	1.49E-05	ABL1, ARRB1, CSK, DUSP1, DUSP6, EPHB2, GBP1, RAPGEF1, LYN, SMAD4, PIN1, PTEN, PTPN1, PTPRC, PTPRR, TIMP3, EIF3A, KLF4, SPRY1, TNIP1, BTN2A2, DUSP10, ERRFI1, CAMK2N1, NDRG2, SEMA6A, SPRY4, SIRPA, DAB2IP, CNKSR3, SPRED1, FLCN
BP	GO:0031667	response to nutrient levels	135/3408	1.54E-05	ADA, ADM, ADRB1, ALAD, FAS, ATP2B1, BCKDHB, CCND1, BCL2, BMP7, BMPR2, CBL, CDKN1A, COL1A1, COMT, CREB1, DNMT3A, DNMT3B, DSC2, EGFR, EIF2S1, EIF4G1, ENSA, ACSL4, FOXO1, FOXO3, G6PD, KAT2A, GNAI2, HMGCR, HSPA5, FOXK2, JUN, LAMP2, LDHA, LDLR, FADS1, MAP1B, MAX, FOXO4, MTHFR, OGG1, OPA1, TNFRSF11B, P2RY1, PAX2, PDK4, PIM1, PKM, PPARA, PPARD, PRKAA1, MAPK1, MAPK3, MAPK8, EIF2AK2, PROX1, PTEN, RALB, RPS6KB1, SFRP1, SRSF2, SLC8A1, SLC16A1, SNAI2, SORL1, SPARC, SRC, SREBF2, SRF, STAT1, STC1, TAF1, TMBIM6, KLF10, TP53, TSC1, USF2, VCAM1, VDR, WNT2B, XBP1, ZFP36, TRIM25, ULK1, STK24, PPM1D, STC2, AKR1C3, TNKS, ALDH1A2, MTMR3, MBD2, KYNU, ATG5, ATG7, POSTN, FSTL1, FAM107A, GABARAPL2, ATG14, USP33, SZT2, LARP1, UFL1, SIRT1, TXN2, FBXO22, EIF2AK1, TNRC6A, DNAJC15, SH3GLB1, BCL11A, ZFYVE1, WNT4, SLC38A2, SSH1, CYP26B1, RRAGD, RRAGC, ATG9A, ADIPOR2, TBL1XR1, CPEB4, MAP1LC3B, NUAK2, SEH1L, SESN2, SGIP1, FNIP1, ACVR1C, SESN3, SIK1, FOXK1, BMP8A
BP	GO:0016241	regulation of macroautophagy	58/3408	1.73E-05	ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, CASP3, DCN, GAPDH, GNAI3, HTT, HIF1A, NEDD4, NPC1, TBC1D25, PAFAH1B2, PIP4K2A, PRKAA1, PRKAB2, MAPK3, MAPK8, RAB5A, RALB, TP53, TSC1, UVRAG, ULK1, MTMR3, ATP6V0D1, ATG13, MFN2, TRIM13, NOD1, SPTLC1, LARP1, SIRT1, RAB3GAP2, HSPB8, HTRA2, UBQLN2, UBQLN1, SH3GLB1, WAC, ATP6V1D, VPS13C, VPS13D, VPS35, UBQLN4, SMURF1, USP36, RRAGD, RRAGC, MLST8, FYCO1, SESN2, SMCR8, SESN3, EXOC8, ATP6V0E2, RAB12
BP	GO:0045862	positive regulation of proteolysis	104/3408	1.75E-05	FAS, RHOA, ARRB1, ASPH, BAK1, CASP10, CAV1, MAPK14, CSNK1D, CSNK1E, DAB2, DAPK1, DDX3X, EFNA3, EPHA4, FMR1, FN1, GSK3B, HDAC2, HIP1, DNAJB2, LYN, SMAD7, MAPT, MBP, ATXN3, MMP14, MYC, MYH9, NKX3-1, FURIN, PML, MAPK3, MAPK9, PSMC2, PTEN, ROBO1, RPS3, SNCA, SRC, STAT3, AURKA, SYK, TAF1, TNFRSF1B, VCP, TNFSF10, ADAM9, FADD, BTRC, USP13, ROCK2, SOCS5, EDEM1, HERPUD1, RNF144A, BCL2L11, BCAP31, PSME3, PSMD14, TRIB1, TNIP1, NOD1, DLC1, ARIH2, TIMM17A, ANP32B, PLK2, PSME4, SIRT1, HSPBP1, BCL2L13, MTCH1, ARIH1, RNF19A, FBXO22, CYFIP2, BBC3, PRELID1, HTRA2, TRIB2, UBQLN2, UBQLN1, CYCS, ANKIB1, IFT57, AKIRIN2, FBXW7, SMURF1, DDA1, MUL1, SOX7, ANTXR1, RHBDD1, EGLN3, FAM122A, SOCS4, ACVR1C, SH3D19, DAB2IP, RNF217, RNF144B, RNF180, ACER2

BP	GO:0043487	regulation of RNA stability	61/3408	1.75E-05	ZFP36L1, ZFP36L2, MAPK14, DKC1, EIF4G1, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPU, TNPO1, HNRNPM, PARN, PRKCA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, UPF1, SET, TNFRSF1B, XPO1, ZFP36, FXR1, ANP32A, PABPC4, ROCK2, PSMF1, PUM1, THRAP3, PSME3, PSMD14, SYNCRIP, PAIP1, IGF2BP1, IGF2BP3, HNRNPA0, CPEB3, SAMD4A, PSME4, LARP1, TARDBP, GIGYF2, SERBP1, PABPC1, MYEF2, YTHDF2, XRN1, ALKBH5, SAMD4B, RBM23, RBM38, PCID2, DCP1A, METTL14, TRIM71, PDE12, YTHDF3
BP	GO:0050770	regulation of axonogenesis	61/3408	1.75E-05	ABL1, RHOA, ARHGDIA, BDNF, BMPR2, EFNA5, MEGF8, MARK2, EPHA4, EPHA7, EPHB2, EPHB3, FN1, GDI1, GOLGA4, ARHGAP35, GSK3B, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, PAK3, POU3F2, PTEN, ROBO1, SKIL, SRF, TIAM1, VEGFA, RND2, SEMA7A, NRP1, SYNGAP1, NTN1, SEMA3E, UST, SEMA3A, OLFM1, SEMA4B, TRAK1, RAB21, MYCBP2, FSTL4, PLXND1, SIN3A, SIPA1L1, NIN, SEMA4C, YTHDF1, SEMA6A, ZSWIM6, ZSWIM4, TRAK2, METRN, PLXNA4, WDR36, TTL
BP	GO:0032147	activation of protein kinase activity	97/3408	1.80E-05	ABL1, ACVR2B, ADCY1, ADCY6, ADCY9, ADORA2B, ARRB1, CRK, CRKL, MAPK14, DUSP5, DUSP6, DUSP7, DUSP9, ECT2, EFNA5, EGFR, MARK2, EMP2, ERCC6, FGF1, FGF2, RAPGEF1, NCKAP1L, NRG1, IL6R, IL18, INSR, IRAK1, IRAK2, KIT, MAP3K1, MAP3K3, MAP3K4, MAP3K9, NTRK3, PAK2, PAK3, PDGFB, PIK3CB, PRKAA1, PRKAR1A, PRKAR2A, MAPK1, MAPK3, EIF2AK2, PRLR, PTPN1, PTPN11, PTPRC, MAP2K4, SHC1, SRC, STK4, STK10, SYK, TGFA, TGFBR1, THBS1, TXN, UBE2N, UBE2V1, VEGFA, WNT7B, STK24, MADD, SOCS1, PEA15, ADAM9, SPAG9, GPRC5A, TAOK2, MAP4K4, TRAF4, SLK, ATG13, NOD1, TAB1, MAP3K2, FRS2, COPS8, TAB2, MAPK8IP3, GREM1, MINK1, KIDINS220, TAOK1, MLST8, WNK1, MAPKAP1, MUL1, ZFP91, OSBPL8, IQGAP3, DAB2IP, RICTOR, EPGN
BP	GO:0110053	regulation of actin filament organization	80/3408	1.84E-05	ABL1, ADD1, ARF1, ARF6, RHOA, CAPZA2, CD47, CDC42, CFL1, CFL2, CCR7, S1PR1, EPS8, FER, GRB2, ARHGAP35, NCKAP1L, LIMK1, MET, MYO1C, NCK1, NF2, PAK3, PRKCE, PTGER4, TWF1, PXN, RASA1, RDX, RGS4, CX3CL1, SDC4, SFRP1, SLC9A1, SPTAN1, SPTBN1, TESK1, TGFBR1, TSC1, NCK2, NRP1, WASF1, WASL, LATS1, ROCK2, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, WASF2, TENM1, DLC1, RAPGEF3, CDC42EP2, NCKAP1, IQGAP2, DSTN, CIT, LIMCH1, KANK1, CLASP1, COTL1, TMOD2, WNT4, FMN2, SPIRE1, PLEKHG2, ARHGAP28, SYNPO2L, PHLDB2, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, SH3PXD2B, FMN1
BP	GO:0034248	regulation of cellular amide metabolic process	131/3408	1.89E-05	AKT2, RHOA, ZFP36L1, ZFP36L2, CALR, CASP3, DAPK1, DDX3X, DPH1, EEF1A1, EIF2S1, EIF2S3, EIF4B, EIF4E, EIF4G1, EIF4G2, EIF5, ELAVL1, EPHA4, ERBB2, ETF1, FOXO3, FMR1, GAPDH, MKNK2, HNRNPD, IGFBP5, IREB2, CAPRIN1, NCBP1, NCK1, PA2G4, PDK3, PDK4, PGAM1, PIN1, POLR2D, PPP1CA, PRKAA1, MAPK1, MAPK3, EIF2AK2, PTAFR, PURA, UPF1, RGS2, RPS3, RPS6KA3, RPS6KB1, ATXN2, SNCA, SORL1, SOX4, STAT3, THBS1, TSC1, ZFP36, CNBP, BTG2, FXR1, NSMAF, NCK2, ENC1, MKNK1, PER2, CNOT8, QKI, ROCK2, EIF5B, PUM1, SECISBP2L, TOB1, EIF1, SYNCRIP, PAIP1, IGF2BP1, IGF2BP3, TMED10, CPEB3, FASTKD2, CNOT1, SAMD4A, TNRC6B, PASK, LARP4B, LARP1, SLC7A11, ZNF385A, LTN1, GIGYF2, LSM14A, AGO1, PABPC1, EIF2AK1, SERP1, TNRC6A, ORMDL2, NGRN, YTHDF2, XRN1, PUS7, YTHDF1, PTCD3, PDPR, SAMD4B, RBM23, EIF5A2, CNOT6, PDP2, TNRC6C, METTL14, PCIF1, DNAJC1, CPEB4, SESN2, UQCC2, KBTBD8, PPP1R15B, UNK, ORMDL1, ORMDL3, LARP4, DNAJC24, TRIM71, CPEB2, MTPN, SAMD8, AGO3, AGO4, YTHDF3, DPH3
BP	GO:0010812	negative regulation of cell-substrate adhesion	30/3408	1.91E-05	ACTN4, JAG1, RHOA, BCL6, COL1A1, EFNA5, GBP1, GCNT2, HOXA7, LRP1, MEN1, MMP14, NF2, SERPINE1, PTEN, RASA1, CX3CL1, SRC, THBS1, FZD4, MAP4K4, SEMA3E, DLC1, POSTN, FAM107A, KANK1, CORO1C, RCC2, PHLDB2, ACER2
BP	GO:0097191	extrinsic apoptotic signaling pathway	71/3408	1.91E-05	ACVR1B, FAS, AR, BAK1, BCL2, BCL2L1, BRCA1, CASP3, CAV1, CTNNA1, CYLD, DAPK1, DDX3X, EYA4, FGFR3, FOXO3, MKNK2, GSK3B, HTT, IL6R, ITGA6, ITGAV, MCL1, KITLG, SERPINE1, PAK2, PML, PPP1CA, PPP2R1A, PTEN, PTPRC, SORT1, CX3CL1, SFRP1, SIAH2, SKIL, SNAI2, SP100, SRC, STK4, TCF7L2, TERT, TGFBR1, THBS1, TIMP3, TNFRSF1B, TRAF1, MADD, PEA15, TNFSF10, FADD, NRP1, ARHGEF2, DEDD, BCL2L11, PSME3, RBCK1, ZMYND11, SGK3, APPL1, HTRA2, PHIP, BIRC6, MOAP1, TMBIM1, SGPP1, ITM2C, ITPRIP, RFFL, DAB2IP, HIPK1
BP	GO:0006352	DNA-templated transcription, initiation	77/3408	1.98E-05	AR, CCND1, RUNX2, CBFB, CCNC, CDKN1A, CREB1, CREBBP, CTNNB1, DR1, E2F3, ERCC2, ESR2, ESRRA, ESRRG, NR5A2, NR6A1, NR3C1, GTF2A1, GTF2E1, GTF2H3, GTF2I, BRF1, GTF3C1, HNF4A, RBPJ, JUN, MAZ, MECP2, NOTCH2, PGR, POLR2D, POLR2K, PPARA, PPARD, MAPK3, PSMC2, PTEN, RARG, RORA, RORB, SRF, TAF1, TAF4B, TCF4, HNF1B, TEAD1, TEAD3, THRA, TP53, NR2C2, TWIST1, UBTF, NR1H2, VDR, NR4A3, FOSL1, PPM1D, KAT2B, GTF3C4, GTF3C3, MED24, THRAP3, MED13, NR1D2, SUB1, POLR1A, ZNF451, TAF9B, RSF1, RRN3, BRF2, ATF7IP, BDP1, CAND1, POLR1B, MED10
BP	GO:1905330	regulation of morphogenesis of an epithelium	60/3408	2.09E-05	ABL1, AR, RHOA, ARRB2, BMP7, CDC42, AP2M1, CTNNB1, DAB2, DVL3, CELSR3, CELSR2, FGF1, GATA3, HOXD13, MDK, MLLT3, PAX2, PDGFA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RREB1, SFRP1, SNAI2, STAT1, HNF1B, TIAM1, VEGFA, WNT2B, FZD5, FZD3, FZD1, FZD4, FZD6, PSMF1, GPC6, PSME3, PSMD14, DKK1, PSME4, CLASP1, FOXP1, SOX8, SIX4, WNT4, AHI1, LGR4, SMURF1, VANGL2, PLEKHA4, VANGL1, ZNRF3, PHLDB2, PRICKLE2
BP	GO:0031669	cellular response to nutrient levels	74/3408	2.13E-05	FAS, ATP2B1, BCL2, BMPR2, CBL, CDKN1A, COL1A1, COMT, DSC2, EIF2S1, EIF4G1, FOXO1, HSPA5, JUN, LAMP2, FADS1, MAX, OPA1, P2RY1, PDK4, PIM1, PRKAA1, MAPK1, MAPK3, MAPK8, EIF2AK2, RALB, SFRP1, SNAI2, SREBF2, SRF, TAF1, KLF10, TP53, TSC1, USF2, VDR, WNT2B, XBP1, ULK1, STK24, PPM1D, AKR1C3, TNKS, MTMR3, ATG5, ATG7, POSTN, FAM107A, GABARAPL2, ATG14, USP33, SZT2, SIRT1, TXN2, FBXO22, TNRC6A, DNAJC15, SH3GLB1, BCL11A, ZFYVE1, WNT4, SLC38A2, SSH1, RRAGD, RRAGC, CPEB4, MAP1LC3B, NUAK2, SEH1L, SESN2, FNIP1, SESN3, SIK1

BP	GO:0008286	insulin receptor signaling pathway	50/3408	2.14E-05	AKT2, APC, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, FER, FOXO1, FOXO3, GAB1, GNAI2, GRB2, GSK3B, IGF1R, IGF2, IGFBP1, INSR, FOXO4, NCK1, OPA1, PDK4, ENPP1, PIK3C2A, PRKAA1, PTPN1, PTPN11, RPS6KB1, SHC1, SORL1, SOS1, SRC, TSC1, SOCS1, IRS2, SOCS2, ATP6V0D1, C2CD5, KANK1, SIRT1, RHOQ, APPL1, SLC2A8, ADIPOR1, ATP6V1D, PHIP, NUCKS1, OSBPL8, SOGA1, SESN3, ATP6V0E2
BP	GO:0046580	negative regulation of Ras protein signal transduction	25/3408	2.16E-05	ABL2, BCL6, EPHB2, RAPGEF1, ARHGAP35, ITGA3, ITGB1, MET, RASA1, TIMP2, TNFAIP1, CUL3, SYNGAP1, MFN2, SPRY1, DLC1, STAMBP, RASA3, KANK1, HEG1, MAPKAP1, SPRY4, KCTD10, DAB2IP, FLCN
BP	GO:1901214	regulation of neuron death	92/3408	2.16E-05	ABL1, RHOA, ARRB1, ARRB2, ATM, AXL, BCL2, BCL2L1, BDNF, CAPN2, CASP3, CBL, CDC34, CEBPB, CREB1, ATF2, CSF1, CTNNB1, CTSZ, EFNB2, EGR1, EIF2S1, EIF4G1, ELK1, EPHA7, FOXO3, G6PD, GATA3, GSK3B, HIF1A, ILK, ISL1, JUN, KRAS, LIG4, LRP1, MAPT, MCL1, MDK, MECP2, MEF2C, MYB, MYBL2, PAK3, PIN1, POU4F1, PPARA, RASA1, CX3CL1, MAP2K4, SET, SNCA, SOD2, SORL1, STAT3, TERT, TNFRSF1B, TP53, TSC1, TYRO3, BTG2, NR4A3, FZD1, NRP1, SYNGAP1, BCL2L11, SIGMAR1, LANCL1, GPNMB, HYOU1, ATG7, STAMBP, DKK1, TRIM2, SIRT1, SLC7A11, NSMF, HTRA2, HIPK2, SIX4, SSH1, DDIT4, OXR1, FBXW7, VPS35, CPEB4, DNAJC5, BHLHB9, AKT1S1, EGLN2, EGLN3, RILPL1
BP	GO:0060840	artery development	39/3408	2.19E-05	ACVR2B, JAG1, PRDM1, BMPR1A, BMPR2, COL3A1, EFNB2, FOXC1, HES1, RBPJ, LDLR, LRP1, LTBP1, SMAD6, SMAD7, MDK, MYH10, NKX3-1, PRRX1, PROX1, ROBO1, SOX4, SRF, TGFBR1, VEGFA, LUZP1, NRP1, SNX17, AKT3, TAB1, PLXND1, HECTD1, SUFU, DLL4, CHD7, ADAMTS9, ZMIZ1, DCTN5, ARID2
BP	GO:0001764	neuron migration	54/3408	2.37E-05	APBB2, AXL, CAMK2A, COL3A1, CRK, CRKL, CTNNB1, CELSR3, MARK2, GATA2, GATA3, GJA1, NRG1, ITGA3, MAP1B, MARK1, MATN2, MDK, MEF2C, MYH10, NTRK3, PAFAH1B1, PAX6, PEX13, CX3CL1, SRF, STAT3, NR2F2, TOP2B, TWIST1, VEGFA, YWHAE, FZD3, USP9X, NRP1, ARHGEF2, DCLK1, NTN1, RAPGEF2, LRIG2, SEMA3A, SATB2, FLRT2, NIPBL, NSMF, AUTS2, DDIT4, NDE1, SEMA6A, POMGNT2, UNK, NAV1, DAB2IP, FBXO45
BP	GO:0006984	ER-nucleus signaling pathway	23/3408	2.43E-05	ATP2A2, CALR, ATF6B, EIF2S1, GSK3B, HSPA5, IGFBP1, INSIG1, NCK1, PTPN1, TP53, XBP1, NCK2, HERPUD1, BCL2L11, AGR2, ERLIN2, INSIG2, TMEM33, FBXW7, CCDC47, ATG10, PPP1R15B
BP	GO:0030307	positive regulation of cell growth	57/3408	2.46E-05	ADAM10, RHOA, BCL2, BDNF, BMPR2, CDC42, DDX3X, HBEGF, EDN1, EFNA5, MEGF8, EGFR, EIF4G1, EIF4G2, ERBB2, EXTL3, FN1, GDI1, GOLGA4, IGFBP1, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, MMP14, NCBP1, NTRK3, PAFAH1B1, PIN1, RPS6KA3, SFRP1, SLC9A1, SRF, SYT1, ADAM17, TGFBR1, VEGFA, RND2, SEMA7A, NRP1, NTN1, AKAP6, DERL2, ZNF639, TAF9B, SYT17, INO80, USP47, SMURF1, CXCL16, MUL1, FAM122A, SYT2, MTPN, BRAT1
BP	GO:0043488	regulation of mRNA stability	59/3408	2.48E-05	ZFP36L1, ZFP36L2, MAPK14, EIF4G1, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPU, TNPO1, HNRNPM, PARN, PRKCA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, UPF1, SET, XPO1, ZFP36, FXR1, ANP32A, PABPC4, ROCK2, PSMF1, PUM1, THRAP3, PSME3, PSMD14, SYNCRIP, PAIP1, IGF2BP1, IGF2BP3, HNRNPA0, CPEB3, SAMD4A, PSME4, LARP1, TARDBP, GIGYF2, SERBP1, PABPC1, MYEF2, YTHDF2, XRN1, ALKBH5, SAMD4B, RBM23, RBM38, PCID2, DCP1A, METTL14, TRIM71, PDE12, YTHDF3
BP	GO:0006403	RNA localization	72/3408	2.58E-05	ATM, ATR, ZFP36L1, CCT6A, CETN2, DKC1, EIF4E, FMR1, HNRNPU, MYO1C, NCBP1, NUP88, NUP98, PARN, POLR2D, PURA, RAN, RANBP2, UPF1, ABCE1, ATXN2, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, YY1, ZFP36, PABPN1, TNKS, QKI, TOMM20, POM121, SMG7, G3BP2, NUTF2, NXF1, IGF2BP1, IGF2BP3, NUP50, RNPS1, CPSF6, XPOT, DDX19B, U2AF2, XPO7, SMG1, ZC3H3, BICD2, SMG5, ZNF385A, UPF2, RBM15B, NMD3, CDC40, CPSF2, RBM27, ZNHIT6, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, EIF5A2, THOC2, XPO5, SEH1L, NUP43, POM121C
BP	GO:2000278	regulation of DNA biosynthetic process	41/3408	2.62E-05	ARRB2, ATM, ATR, BMPR2, CCT6A, CDKN1A, CTNNB1, DACH1, DKC1, DUSP1, FGF2, GJA1, HNRNPC, HNRNPD, HNRNPU, MAP3K4, MEN1, MYC, PAK3, PARN, PDGFB, MAPK1, MAPK3, SRC, TFDP1, TP53, XRCC5, TNKS, AURKB, KLF4, SMG7, CERS1, SMG5, PARM1, SH2B1, GREM1, XRN1, GNL3L, CHTF8, PINX1, HMBOX1
BP	GO:0007389	pattern specification process	122/3408	2.65E-05	ACVR1B, ACVR2B, APC, AR, ASPH, ATM, BMP7, BMPR1A, BMPR2, CRKL, CTNNB1, DLX2, EDN1, EFNB1, CELSR2, MEGF8, EP300, BPTF, FGF1, FOXC1, KAT2A, GJA1, HIF1A, FOXA1, HOXA3, HOXA5, HOXA7, HOXA9, HOXB3, HOXB5, HOXB8, HOXC4, HOXC8, HOXD13, HES1, RBPJ, ISL1, LRP6, SMAD2, SMAD4, SMAD6, MEF2C, MID1, MLLT3, MSX1, NKX3-1, OTX1, PCSK6, PAX2, PAX6, PBX1, PTCH1, RARG, RFX3, RNF2, ROBO1, SFRP1, TRA2B, SIM2, SKI, SNAI1, SRF, STC1, AURKA, TBX3, HNF1B, ZEB1, NR2F2, TGFBR1, TP53, KDM6A, WNT7B, WNT2B, YY1, BTG2, FZD5, BHLHE40, TP63, DCHS1, CHRD, NRP1, SYNGAP1, ALDH1A2, LDB1, KIF3B, HAND1, ATP6AP2, GDF11, SPRY1, CITED2, SEMA3A, FRS2, MTF2, DKK1, SATB2, POFUT1, HEYL, GREM1, HIPK2, CDON, DYNC2LI1, SUFU, DLL4, RNF111, AHI1, BCOR, IFT57, HES6, CYP26B1, VANGL2, MIB1, SHROOM3, EPB41L5, AIDA, NDRG4, PGAP1, SETDB2, ACVR1C, PLD6, HIPK1, CRB2, NRARP
BP	GO:0014033	neural crest cell differentiation	36/3408	2.71E-05	JAG1, BMP7, BMPR1A, CFL1, EDN1, EFNB1, FOXC1, FN1, NRG1, HIF1A, HES1, ISL1, LRP6, SMAD4, MEF2C, KITLG, MAPK1, MAPK3, SFRP1, SNAI2, SOX11, TWIST1, SEMA7A, NRP1, ALDH1A2, SEMA3E, FGF19, SEMA3A, SEMA4B, CORO1C, SOX8, SEMA4C, SEMA6A, FAM172A, KBTBD8, RDH10
BP	GO:0032271	regulation of protein polymerization	69/3408	2.71E-05	ABL1, ADD1, ARF1, ARF6, RHOA, CAPZA2, CDKN1B, CCR7, DYRK1A, EPS8, FER, FKBP4, GRB2, NCKAP1L, MAP1B, MAPT, MECP2, MET, MYO1C, NCK1, PAK3, PRKCE, TWF1, RASA1, RDX, RPS3, SNCA, SPTAN1, SPTBN1, VDAC2, NCK2, WASF1, WASL, LATS1, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, AKAP9, ABI2, TENM1, TUBB4A, CDC42EP2, NCKAP1, IQGAP2, TPPP, MAPRE3, KANK1, CAMSAP2, CLASP1, COTL1, CLIP3, TMOD2, NIN, FMN2, SPIRE1, SLAIN2, PLEKHG2, ARHGAP28, NAV3, MYADM, ARHGAP18, WHAMM, JMY, MTPN, CAMSAP1, RICTOR, FMN1

BP	GO:0016331	morphogenesis of embryonic epithelium	52/3408	2.75E-05	ABL1, ADM, AR, BMP7, CASP3, CFL1, CTNNB1, DVL3, GATA3, KAT2A, ARHGAP35, HIF1A, JAG2, LRP6, MTHFR, PAX2, PTCH1, RARG, SDC4, SFRP1, SKI, SOX4, SOX11, STK4, HNF1B, TSC1, TWIST1, KDM6A, WNT7B, WNT2B, LUZP1, FZD3, ARID1A, FZD1, FZD6, TP63, ALDH1A2, HAND1, DLC1, MTHFD1L, SOX8, SUFU, SIX4, WNT4, SEMA4C, IFT57, VANGL2, MIB1, SHROOM3, EPB41L5, TRIM71, RDH10
BP	GO:0003279	cardiac septum development	42/3408	2.79E-05	JAG1, PRDM1, BMP7, BMPR1A, BMPR2, GATA3, GATA6, HES1, RBPJ, ISL1, LTBP1, SMAD4, SMAD6, SMAD7, MDM4, MYH10, NOTCH2, PROX1, ROBO1, SOX4, SOX11, TBX3, TGFBR1, TGFBR3, TP53, LUZP1, FZD1, NRP1, TRIP11, HAND1, SNX17, CITED2, TAB1, FRS2, PLXND1, HECTD1, HEYL, SUFU, CHD7, VANGL2, HEG1, DCTN5
BP	GO:0010770	positive regulation of cell morphogenesis involved in differentiation	53/3408	2.79E-05	ABL1, RHOA, ARHGDIA, BDNF, BMPR2, CALR, CDC42, CRK, CRKL, CUX1, EFNA5, MEGF8, EPHA4, FN1, GDI1, GOLGA4, ILK, L1CAM, LIMK1, LRP1, CAPRIN1, MAP1B, MAPT, MDK, NEDD9, NTRK3, OPA1, PAFAH1B1, PAK3, PTPRD, ROBO1, RREB1, SKIL, SRF, VAMP7, TIAM1, VEGFA, RND2, SEMA7A, NRP1, KALRN, NTN1, ACTR2, ARPC2, TRAK1, RAB21, PLXND1, SS18L1, NIN, METRN, BHLHB9, PLXNA4, MYADM
BP	GO:0007569	cell aging	43/3408	2.98E-05	ABL1, ATM, ATR, BCL2, BCL6, BMPR1A, CALR, CDK6, CDKN1A, CHEK1, MAPK14, FOXM1, HMGA1, ILK, KRAS, MAP3K3, MME, MNT, OPA1, SERPINE1, PAWR, PML, PRELP, PTEN, SRF, TBX3, TERT, TP53, TWIST1, KAT6A, HMGA2, TP63, NUAK1, AKT3, PLK2, ZNF277, VASH1, SIRT1, MORC3, RSL1D1, PDCD4, ZMIZ1, SMC6
BP	GO:0060828	regulation of canonical Wnt signaling pathway	85/3408	3.19E-05	APC, CAV1, COL1A1, MAPK14, CSNK1D, CSNK1E, CSNK1G3, CTNNB1, CTNND1, CYLD, DAB2, DDX3X, DVL3, EGFR, EGR1, FOXO1, FOXO3, GNAQ, RAPGEF1, GSK3B, IGFBP1, RBPJ, ILK, ISL1, JUP, LRP6, MDK, MLLT3, NFKB1, PIN1, PPP1CA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, SIAH2, SNAI2, SOX4, SRC, STK4, TBL1X, TCF7L2, TLE1, TLE4, VCP, FZD1, FZD6, CUL3, TNKS, BTRC, LIMD1, LATS1, PSMF1, G3BP1, PSME3, PSMD14, DKK1, KANK1, PSME4, LATS2, GREM1, DKK3, UBR5, GID8, USP47, LGR4, FERMT1, VPS35, SULF2, PLEKHA4, PRDM15, WNK1, TBL1XR1, SOX7, KREMEN1, ZNRF3, LZTS2, AMER1, DAB2IP, NRARP, TMEM170B
BP	GO:0009952	anterior/posterior pattern specification	69/3408	3.19E-05	ACVR2B, ATM, BMPR1A, BMPR2, CRKL, CTNNB1, CELSR2, EP300, BPTF, FOXC1, KAT2A, HOXA3, HOXA5, HOXA7, HOXA9, HOXB3, HOXB5, HOXB8, HOXC4, HOXC8, HOXD13, HES1, RBPJ, LRP6, SMAD2, SMAD4, MLLT3, MSX1, NKX3-1, OTX1, PCSK6, PAX6, PBX1, RARG, RNF2, SFRP1, SKI, SRF, AURKA, TBX3, HNF1B, NR2F2, TGFBR1, TP53, KDM6A, WNT2B, YY1, BTG2, FZD5, BHLHE40, ALDH1A2, LDB1, ATP6AP2, GDF11, FRS2, DKK1, POFUT1, HEYL, HIPK2, CDON, HES6, VANGL2, MIB1, EPB41L5, PGAP1, PLD6, HIPK1, CRB2, NRARP
BP	GO:0035051	cardiocyte differentiation	56/3408	3.57E-05	JAG1, ARRB2, BMP7, CALR, CXADR, EDN1, EFNB2, EGFR, G6PD, GATA6, KAT2A, NRG1, HNRNPU, HES1, RBPJ, ISL1, ITGB1, SMAD4, MEF2A, MEF2C, MYH10, PDGFRA, PIN1, PPARA, MAPK1, MAPK3, PROX1, RGS2, RGS4, MAP2K4, SGCD, SLC8A1, SLC9A1, SRF, TBX3, TGFBR3, TSC1, TWIST1, VCAM1, VEGFA, YY1, ARID1A, SORBS2, AKAP6, ATG5, SPRY1, NEBL, PDLIM5, FRS2, AKAP13, DKK1, KDM6B, GREM1, PDCD4, ALPK3, SIK1
BP	GO:0003205	cardiac chamber development	57/3408	3.57E-05	JAG1, PRDM1, BMP7, BMPR1A, BMPR2, COL11A1, FKBP1A, FOXC1, GATA3, GATA6, NRG1, HIF1A, HES1, RBPJ, ISL1, LTBP1, SMAD4, SMAD6, SMAD7, MDM4, MEF2C, MYH10, NOTCH2, POU4F1, PROX1, ROBO1, SOS1, SOX4, SOX11, SRF, TBX3, TGFBR1, TGFBR3, TP53, LUZP1, ARID1A, FZD1, NRP1, TRIP11, HAND1, ADAMTS1, SNX17, UBE4B, CITED2, TAB1, FRS2, PLXND1, HECTD1, HEYL, SUFU, DLL4, CHD7, VANGL2, HEG1, PTCD2, DCTN5, TMEM65
BP	GO:0031952	regulation of protein autophosphorylation	23/3408	3.71E-05	CALM1, CALM2, CALM3, CAV1, EPHA7, JUN, PDGFA, PDGFB, ENPP1, PPP2R5D, PTPRC, RAP2A, RAP2B, SRC, TESK1, VEGFA, IQGAP1, TAOK2, RASSF2, GPNMB, GREM1, ERRFI1, RAP2C
BP	GO:1903573	negative regulation of response to endoplasmic reticulum stress	22/3408	3.92E-05	BCL2L1, ATF6B, GRINA, HSPA5, DNAJB9, NCK1, OPA1, PTPN1, TMBIM6, UBE2G2, XBP1, NCK2, HERPUD1, HYOU1, USP25, DERL2, TXNDC12, BFAR, UBE2J1, YOD1, SYVN1, PPP1R15B
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	74/3408	3.92E-05	ABL1, ACVR1B, ACVR2B, BMP3, BMP7, BMPR1A, BMPR2, CAV1, CREBBP, DAB2, EP300, FBN1, FBN2, FKBP1A, HES1, HSPA5, RBPJ, ILK, ITGA3, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEN1, MSX1, NEO1, PCSK6, PIN1, SFRP1, SKI, SKIL, SORL1, SOX11, SPTBN1, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, FZD1, ITGA8, CHRD, MTMR4, ONECUT2, TOB1, GDF11, FSTL3, CITED2, FST, FSTL1, DKK1, PEG10, ZC3H3, SIRT1, ZNF451, GREM1, DKK3, HIPK2, TRIM33, RNF111, FERMT1, PMEPA1, SMURF1, PBLD, WFIKKN2, CD109, BMPER, FLCN, CRB2, RBPMS2, BMP8A, RNF165
BP	GO:1902905	positive regulation of supramolecular fiber organization	65/3408	4.05E-05	ABL1, ARF1, ARF6, RHOA, CD47, CDC42, CDKN1B, CFL1, CFL2, CCR7, EDN1, FER, GRB2, NCKAP1L, LIMK1, MAP1B, MAPT, MECP2, MET, MYO1C, NCK1, NF2, PRKCE, PROX1, PXN, RB1, RPS3, CX3CL1, SDC4, SFRP1, TESK1, TGFBR1, TSC1, NCK2, NRP1, WASF1, WASL, ROCK2, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, AKAP9, ABI2, TENM1, RAPGEF3, CDC42EP2, NCKAP1, IQGAP2, DSTN, LIMCH1, CLASP1, NIN, WNT4, FMN2, SPIRE1, SLAIN2, SYNPO2L, NAV3, WHAMM, JMY, RICTOR, SH3PXD2B, FMN1
BP	GO:0035329	hippo signaling	20/3408	4.05E-05	CASP3, NF2, SOX11, STK4, TEAD1, TEAD3, YWHAE, DCHS1, LIMD1, LATS1, DLG5, TJP2, WWC1, LATS2, MOB1A, WWC3, MOB3B, WWC2, AMOT, AMOTL1
BP	GO:0035148	tube formation	51/3408	4.05E-05	ABL1, ADM, BMP7, CASP3, CFL1, CTNNB1, DVL3, GATA3, KAT2A, ARHGAP35, HIF1A, LRP6, MTHFR, NFIB, PAX2, PODXL, PROX1, PTCH1, RARG, SDC4, SFRP1, SKI, SOX4, SOX11, STK4, HNF1B, TSC1, TWIST1, KDM6A, VEGFA, LUZP1, FZD3, ARID1A, FZD1,

					FZD6, HAND1, BCL2L11, DLC1, DICER1, MTHFD1L, SOX8, SUFU, SIX4, WNT4, SEMA4C, IFT57, VANGL2, MIB1, SHROOM3, TRIM71, DAB2IP
BP	GO:0071214	cellular response to abiotic stimulus	95/3408	4.16E-05	AKT2, FAS, RHOB, ATM, ATR, BAK1, BCL2L1, ZFP36L1, CALM1, CASP3, CDC25A, CDKN1A, CHEK1, CNN2, COL1A1, CREBBP, CRY2, MAPK14, DAG1, DDX3X, ECT2, EGFR, EGR1, EIF2S1, ELK1, EP300, FMR1, FNTA, GATA3, GJA1, GNB1, GRB2, HSPA5, IRF1, KCNJ2, LETM1, LIG4, MAP3K1, MME, MYC, NEDD4, NFKB1, MAPK3, MAPK8, PTAFR, PTEN, PTGER4, PTPN11, PTPRK, RAD1, RAD51, RBL2, MAP2K4, SFRP1, SLC9A1, SNAI2, TAF1, TP53, XRCC5, YY1, HMGA2, CUL4B, FADD, ARHGEF2, AURKB, RAB11B, CLOCK, SLC12A6, NET1, MICU1, CERS1, MAP3K2, METAP2, TLK2, KDM1A, SIRT1, SPIDR, NIPBL, NSMF, TRIAP1, ERRFI1, SLC38A2, INO80, USP47, LRRC8D, USP28, NUCKS1, CAMKMT, RHNO1, RHBDD1, BMF, RCSD1, TP53INP1, MTPN, SDE2
BP	GO:0104004	cellular response to environmental stimulus	95/3408	4.16E-05	AKT2, FAS, RHOB, ATM, ATR, BAK1, BCL2L1, ZFP36L1, CALM1, CASP3, CDC25A, CDKN1A, CHEK1, CNN2, COL1A1, CREBBP, CRY2, MAPK14, DAG1, DDX3X, ECT2, EGFR, EGR1, EIF2S1, ELK1, EP300, FMR1, FNTA, GATA3, GJA1, GNB1, GRB2, HSPA5, IRF1, KCNJ2, LETM1, LIG4, MAP3K1, MME, MYC, NEDD4, NFKB1, MAPK3, MAPK8, PTAFR, PTEN, PTGER4, PTPN11, PTPRK, RAD1, RAD51, RBL2, MAP2K4, SFRP1, SLC9A1, SNAI2, TAF1, TP53, XRCC5, YY1, HMGA2, CUL4B, FADD, ARHGEF2, AURKB, RAB11B, CLOCK, SLC12A6, NET1, MICU1, CERS1, MAP3K2, METAP2, TLK2, KDM1A, SIRT1, SPIDR, NIPBL, NSMF, TRIAP1, ERRFI1, SLC38A2, INO80, USP47, LRRC8D, USP28, NUCKS1, CAMKMT, RHNO1, RHBDD1, BMF, RCSD1, TP53INP1, MTPN, SDE2
BP	GO:0006367	transcription initiation from RNA polymerase II promoter	61/3408	4.19E-05	AR, CCND1, RUNX2, CBFB, CCNC, CDKN1A, CREB1, CREBBP, DR1, E2F3, ERCC2, ESR2, ESRRA, ESRRG, NR5A2, NR6A1, NR3C1, GTF2A1, GTF2E1, GTF2H3, GTF2I, HNF4A, RBPJ, MAZ, MECP2, NOTCH2, PGR, POLR2D, POLR2K, PPARA, PPARD, PSMC2, PTEN, RARG, RORA, RORB, SRF, TAF1, TAF4B, TCF4, HNF1B, TEAD1, TEAD3, THRA, TP53, NR2C2, NR1H2, VDR, NR4A3, PPM1D, KAT2B, MED24, THRAP3, MED13, NR1D2, SUB1, ZNF451, TAF9B, ATF7IP, CAND1, MED10
BP	GO:0048008	platelet-derived growth factor receptor signaling pathway	26/3408	4.19E-05	ABL1, CBL, FER, RAPGEF1, HIP1, LRP1, PDGFA, PDGFB, PDGFRA, PIK3C2A, PTEN, PTPN1, PTPN11, PTPN12, PTPRJ, SNCA, SRC, VEGFA, NR4A3, IQGAP1, NRP1, SGPL1, LRIG2, PLEKHA1, NDRG4, ARID5B
BP	GO:0006979	response to oxidative stress	122/3408	4.52E-05	ABL1, ADA, ALAD, RHOB, ATP2A2, ATP7A, AXL, BAK1, BCL2, BMP7, BTG1, CAPN2, CASP3, CCNA2, CCR7, COL1A1, CRK, CTNNB1, DAPK1, DUSP1, ECT2, EDN1, EGFR, EIF2S1, EPAS1, CLN8, ERCC2, ERCC6, EZH2, FER, FOXO1, FOXO3, FUT8, G6PD, GPX3, HDAC2, HIF1A, HNRNPD, JUN, LDHA, MAPT, MCL1, MET, MMP14, MTF1, MTR, MYB, HNRNPM, NDUFA6, OGG1, PRDX1, PAWR, PAX2, PDGFRA, PML, PON2, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, PTPRK, PXN, RPS3, SLC8A1, SNCA, SOD2, SRC, STAT1, STAU1, TP53, TRPM2, TSC1, TXN, PXDN, NR4A3, FOSL1, FZD1, STK24, STC2, AKR1C3, ADAM9, KLF4, MELK, SLC23A2, NET1, SIGMAR1, LANCL1, KLF2, ATG7, PRDX3, ZNF277, KDM6B, SZT2, SIRT1, SLC7A11, PRDX5, TXN2, SIN3A, IPCEF1, HTRA2, SLC25A24, UBQLN1, RRM2B, MYEF2, OSER1, CYCS, OXR1, BRF2, FBXW7, PLEKHA1, MAPKAP1, C19orf12, SESN2, CHD6, PPP1R15B, TP53INP1, CPEB2, SIRPA, SESN3, VKORC1L1, MSRB3
BP	GO:1905269	positive regulation of chromatin organization	39/3408	4.70E-05	ARRB1, ATM, BCL6, BRCA1, CTNNB1, DNMT3B, FMR1, GATA3, KAT2A, ISL1, JARID2, SMAD4, MECP2, KMT2A, MYB, MAPK3, SNAI2, TAL1, TP53, UBE2N, VEGFA, RPS6KA4, RPS6KA5, CTR9, KAT7, MTF2, MORC2, KDM1A, SIRT1, WBP2, NIPBL, SIN3A, AUTS2, RIF1, ATF7IP, KMT2E, MIER1, TET1, TADA2B
BP	GO:0034599	cellular response to oxidative stress	88/3408	4.88E-05	ABL1, RHOB, ATP2A2, ATP7A, AXL, BCL2, BMP7, CCNA2, CRK, CTNNB1, DAPK1, ECT2, EGFR, EIF2S1, EPAS1, EZH2, FER, FOXO1, FOXO3, FUT8, G6PD, GPX3, HDAC2, HIF1A, HNRNPD, JUN, MAPT, MCL1, MET, MTR, MYB, PRDX1, PAWR, PAX2, PDGFRA, PML, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, PTPRK, PXN, RPS3, SNCA, SOD2, SRC, STAU1, TP53, TRPM2, TSC1, TXN, NR4A3, FZD1, STK24, AKR1C3, KLF4, MELK, NET1, SIGMAR1, LANCL1, KLF2, ATG7, PRDX3, ZNF277, KDM6B, SZT2, SIRT1, SLC7A11, PRDX5, SIN3A, HTRA2, SLC25A24, UBQLN1, OSER1, CYCS, OXR1, BRF2, FBXW7, PLEKHA1, MAPKAP1, SESN2, CHD6, TP53INP1, CPEB2, SIRPA, VKORC1L1, MSRB3
BP	GO:0014031	mesenchymal cell development	34/3408	4.88E-05	JAG1, BCL2, BMP7, BMPR1A, CFL1, EDN1, EFNB1, FOXC1, FN1, NRG1, HIF1A, HES1, ISL1, KITLG, MAPK1, MAPK3, SNAI2, SOX11, TWIST1, SEMA7A, NRP1, ALDH1A2, SEMA3E, FGF19, SEMA3A, SEMA4B, CORO1C, HEYL, SOX8, SEMA4C, SEMA6A, FAM172A, KBTBD8, RDH10
BP	GO:0048864	stem cell development	34/3408	4.88E-05	JAG1, BMP7, BMPR1A, CFL1, EDN1, EFNB1, FOXC1, FN1, NRG1, HIF1A, HES1, ISL1, KITLG, MAPK1, MAPK3, PTPRC, SNAI2, SOX11, TWIST1, SEMA7A, NRP1, ALDH1A2, SEMA3E, FGF19, SEMA3A, SEMA4B, CORO1C, SOX8, SEMA4C, SEMA6A, FAM172A, KBTBD8, MSI2, RDH10
BP	GO:1901532	regulation of hematopoietic progenitor cell differentiation	34/3408	4.88E-05	ABL1, RUNX1, CBFB, CDK6, FOXC1, GATA2, GATA3, HES1, LMO2, KITLG, KMT2A, MYB, EIF2AK2, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SOS1, TAL1, TCF3, LDB1, PSMF1, SETD1A, PSME3, PSMD14, PSME4, YTHDF2, PUS7, ITCH, FNIP1, FLCN
BP	GO:0071479	cellular response to ionizing radiation	30/3408	4.95E-05	RHOB, ATM, ATR, BCL2L1, CDKN1A, MAPK14, ECT2, EGR1, ELK1, GATA3, GRB2, HSPA5, LIG4, RAD1, RAD51, SFRP1, SNAI2, TP53, XRCC5, HMGA2, CLOCK, NET1, TLK2, KDM1A, SIRT1, SPIDR, NIPBL, INO80, NUCKS1, RHNO1
BP	GO:0090068	positive regulation of cell cycle process	87/3408	5.04E-05	RHOA, ATM, ATRX, CCND1, BRCA1, CCND2, CDC25A, CDC42, CDKN1A, CDKN1B, DDX3X, ECT2, EDN1, EGFR, EIF4G1, EP300, EZH2, GATA6, HNRNPU, HSPA2, IGF2, INSR, MAD2L1, MDM4, MECP2, FOXO4, MSX1, CNOT4, PBX1, PDGFB, PML, POU4F1, PRKCE, PKN2, RAD21, RB1, RBL2, RDX, SOX4, AURKA, ADAM17, TERT, TFDP1, TFDP2, TGFA, TP53, BTG2, HMGA2, CUL4B, CUL3,

					PKP4, CDC14B, CDK10, AURKB, CNOT8, KIF3B, ROCK2, KIF23, ADAMTS1, VPS4B, PLK2, CIT, CNOT1, NIPBL, SIN3A, ZNF385A, SH2B1, TRIAP1, DTL, WNT4, INO80, PHIP, PCID2, KMT2E, RCC2, NSFL1C, MEPCE, CNOT6, WIZ, CDC73, RHNO1, RAB11FIP4, UBXN2B, E2F7, DAB2IP, CEP120, EPGN
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	55/3408	5.06E-05	BCL2, BCL2L1, PTTG1IP, CAV1, CD44, CYLD, DDX3X, GRINA, HIF1A, HNRNPK, DNAJA1, MCL1, MSX1, NCK1, NKX3-1, OPA1, PLAGL2, PTPN1, RPS3, SIAH1, SKIL, SNAI2, SNAI1, SOD2, SRC, TMBIM6, TP53, TPT1, VDAC2, XBP1, NCK2, ARHGEF2, HERPUD1, BCL2L11, BCAP31, HYOU1, SERINC3, KDM1A, SIRT1, ZNF385A, BBC3, HTRA2, UBQLN1, RRM2B, TXNDC12, TRIAP1, PIAS4, TAF9B, RRN3, USP47, FBXW7, SYVN1, BMF, NACC2, FLCN
BP	GO:0007254	JNK cascade	67/3408	5.33E-05	ADORA2B, CCR7, CRKL, CYLD, DUSP9, DVL3, EDN1, EGFR, EPHA4, ERCC6, FLT4, RAPGEF1, DNAJA1, IGF1R, IRAK1, IRAK2, MAP3K4, MEN1, MAP3K9, PAFAH1B1, MAPK8, MAPK9, PTGER4, PTPN1, RAP2A, RPS3, MAP2K4, SFRP1, SYK, TIAM1, TPD52L1, UBE2N, UBE2V1, WNT7B, FZD5, FZD4, SPAG9, TAOK2, MAP4K4, NCOR1, TRAF4, RASSF2, FGF19, HIPK3, TRIB1, SEMA3A, NOD1, TAB1, MAP3K2, ZMYND11, DUSP10, DKK1, TAB2, MAPK8IP3, PHLPP1, PDCD4, HIPK2, MINK1, VANGL2, TAOK1, AIDA, MUL1, ITCH, SIRPA, DAB2IP, ZNF675, SH3RF3
BP	GO:0050808	synapse organization	112/3408	5.38E-05	ABL1, ACTB, ADAM10, ARF1, ARF6, RHOA, BDNF, CACNB1, CDC42, CFL1, COL4A1, COL4A5, CRKL, MAPK14, CTNNB1, DAG1, DLG3, EFNA5, EFNB2, EIF4G1, EPHA4, EPHA7, EPHB2, EPHB3, ERBB2, FMR1, FNTA, NRG1, IGF1R, IL1RAP, INSR, ITGA3, L1CAM, CAPRIN1, MAP1B, MAPT, MECP2, MEF2C, MYH10, MYO5A, NEDD4, NEFH, NFIA, NTRK3, OPA1, OPHN1, PAFAH1B1, PAK3, PCDHGC3, PIN1, POU4F1, PTEN, PTPRD, PTPRF, CX3CL1, SNCA, SPARC, STAU1, TIAM1, TSC1, VCP, WNT7B, FZD5, FZD1, NRP1, SYNGAP1, BSN, WASF1, WASL, KALRN, DLG5, NTN1, NOS1AP, SEMA3E, SPOCK2, ACTR2, ABI2, FARP1, WASF2, SLC9A6, UNC13B, PDLIM5, NLGN1, SHANK2, DKK1, PDZRN3, NFASC, PLXND1, SLC7A11, FLRT2, SIPA1L1, SLITRK5, NPTN, PCDH17, ABHD17B, SIX4, SSH1, VPS35, NLGN2, ABHD17C, DLGAP3, LRRC4, RAB17, ARHGAP39, BHLHB9, RAB39B, SLITRK4, DAB2IP, FBXO45, SDK1, AGRN, CHCHD10
BP	GO:0051650	establishment of vesicle localization	85/3408	5.43E-05	ACTN4, ADCY1, ADORA2B, ARF1, ATP2A2, CALM3, CAMK2A, CD59, CSNK1D, CTNNB1, CTSZ, FMR1, GSK3B, HTT, KIF5B, MYO1C, MYO5A, NSF, P2RY1, PAFAH1B1, PPP6C, RAB1A, RAB5A, RAP1B, SNAP25, SNCA, STX3, VAMP1, VAMP2, VAMP7, SYT1, TGFA, CUL3, USO1, NAPA, SYNJ1, AP3D1, WASL, SYT7, RAB11B, KIF3B, KIF23, GOSR1, GOSR2, PREPL, SEC24C, RIMS3, SV2A, CNIH1, AP3S2, SEC23A, UNC13B, SEC24A, TMED10, KIF3A, PPP6R1, NLGN1, TRAK1, KIF1B, SYT11, ANKRD28, CLASP1, PIP5K1C, NCS1, AP3M1, GIT1, TRAPPC4, TRAPPC2L, SYT17, NDE1, FNBP1L, PPP6R3, SAR1A, KIF13A, RAB17, GORASP1, TRAK2, MLPH, FYCO1, DNAJC5, CEP19, SYT2, TBC1D20, RIMS4, FAM91A1
BP	GO:0061014	positive regulation of mRNA catabolic process	23/3408	5.46E-05	ZFP36L1, ZFP36L2, HNRNPD, UPF1, ZFP36, BTG2, CNOT8, ROCK2, PUM1, TOB1, CPEB3, CNOT1, TNRC6B, GIGYF2, PABPC1, TNRC6A, YTHDF2, RBM23, ZC3HAV1, TNRC6C, METTL14, TRIM71, YTHDF3
BP	GO:0061448	connective tissue development	81/3408	5.47E-05	ATP7A, BMP3, BMP7, BMPR1A, BMPR2, RUNX2, RUNX3, CD44, COL1A1, COL5A1, COL6A2, COL11A1, COL12A1, ATF2, MAPK14, CSF1, CTNNB1, DLX2, EDN1, EGR1, ESRRA, FGF2, FGFR3, GNAS, HIF1A, FOXA1, HOXA3, HOXA5, HOXB3, HOXC4, ID4, IL6R, ITGB8, LOXL2, LRP6, MATN2, MDK, MEF2C, MEF2D, MSX1, NFIB, PDGFB, PKD1, PRRX1, PPARD, MAPK3, RARG, SNAI2, SNAI1, SORL1, SRF, STC1, ZEB1, TGFBR1, THBS3, THRA, TRPS1, WNT7B, WNT2B, XBP1, HMGA2, DYRK1B, TRIP11, HAND1, ZNF516, SATB2, SIRT1, GREM1, SOX8, CSGALNACT1, SULF2, ARRDC3, CREB3L2, TBL1XR1, ARID5B, COL27A1, PKDCC, AMER1, SH3PXD2B, BMP8A, SNX19
BP	GO:1901990	regulation of mitotic cell cycle phase transition	120/3408	5.47E-05	APC, ATM, CCND1, BCL2, BRCA1, ZFP36L1, ZFP36L2, CCND2, CDC25A, CDK6, CDKN1A, CDKN1B, CETN2, FOXN3, CSNK1D, CSNK1E, DDX3X, DUSP1, EGFR, EIF4G1, EP300, ERCC2, EZH2, FHL1, HSPA2, IK, MAD2L1, MDM4, MECP2, FOXO4, CNOT4, PAFAH1B1, PBX1, PKD1, PML, PPP2R1A, PKIA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD21, RB1, RBL2, RDX, SKP1, SOX4, AURKA, ADAM17, TERT, TFDP1, TFDP2, TP53, YWHAE, YWHAG, BTG2, HMGA2, CUL4B, CUL3, CDC14B, CDK10, DYNLL1, BTRC, AURKB, KLF4, TRIP13, CNOT8, TAOK2, PSMF1, ADAMTS1, VPS4B, CEP135, CTDSP2, AKAP9, PSME3, PSMD14, CTDSPL, TUBB4A, BTN2A2, GPNMB, PLK2, CNTRL, FAM107A, CEP250, DCTN3, CNOT1, PSME4, CLASP1, SIN3A, ZNF385A, GIGYF2, TRIAP1, DTL, ANLN, INO80, HAUS6, NDE1, PINX1, USP47, HAUS2, RIOK2, PCID2, KMT2E, RCC2, MEPCE, CNOT6, HECW2, TAOK1, CTDSP1, ZNF655, CDC73, ZNF830, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0046660	female sex differentiation	42/3408	5.56E-05	ACVR1B, ADCYAP1R1, ARRB1, ARRB2, ATM, AXL, BAK1, BCL2, BCL2L1, CASP3, CEBPB, CTNNA1, DACH1, FOXC1, FOXO3, HSPA5, INSR, KIT, SMAD4, KITLG, MMP14, PDGFRA, PGR, SFRP1, SRC, TBX3, TYRO3, VEGFA, NRIP1, FZD4, TP63, SGPL1, PCYT1B, ADAMTS1, KMT2B, LHFPL2, SIRT1, WNT4, CHD7, PLEKHA1, ARID5B, ZNF830
BP	GO:0003002	regionalization	99/3408	5.57E-05	ACVR2B, AR, ATM, BMPR1A, BMPR2, CRKL, CTNNB1, DLX2, EDN1, CELSR2, MEGF8, EP300, BPTF, FGF1, FOXC1, KAT2A, FOXA1, HOXA3, HOXA5, HOXA7, HOXA9, HOXB3, HOXB5, HOXB8, HOXC4, HOXC8, HOXD13, HES1, RBPJ, ISL1, LRP6, SMAD2, SMAD4, SMAD6, MEF2C, MLLT3, MSX1, NKX3-1, OTX1, PCSK6, PAX2, PAX6, PBX1, PTCH1, RARG, RNF2, ROBO1, SFRP1, TRA2B, SKI, SNAI1, SRF, AURKA, TBX3, HNF1B, NR2F2, TGFBR1, TP53, KDM6A, WNT7B, WNT2B, YY1, BTG2, FZD5, BHLHE40, TP63, CHRD, NRP1, ALDH1A2, LDB1, ATP6AP2, GDF11, SPRY1, CITED2, SEMA3A, FRS2, MTF2, DKK1, POFUT1, HEYL, GREM1, HIPK2, CDON, SUFU, DLL4, AHI1, IFT57, HES6, CYP26B1, VANGL2, MIB1, EPB41L5, AIDA, PGAP1, SETDB2, PLD6, HIPK1, CRB2, NRARP
BP	GO:0016239	positive regulation of macroautophagy	29/3408	5.59E-05	DCN, GNAI3, HTT, HIF1A, PAFAH1B2, PIP4K2A, MAPK3, RALB, TSC1, UVRAG, ULK1, MFN2, TRIM13, NOD1, SPTLC1, LARP1, SIRT1, RAB3GAP2, HSPB8, SH3GLB1, WAC, VPS13C, VPS13D, SMURF1, FYCO1, SESN2, SMCR8, SESN3, RAB12

BP	GO:1901800	positive regulation of proteasomal protein catabolic process	39/3408	5.85E-05	CAV1, CSNK1D, CSNK1E, DAB2, FMR1, GSK3B, DNAJB2, SMAD7, ATXN3, MAPK9, PSMC2, AURKA, TAF1, VCP, USP13, SOCS5, EDEM1, HERPUD1, RNF144A, BCAP31, TRIB1, ARIH2, PLK2, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, UBQLN2, UBQLN1, ANKIB1, FBXW7, DDA1, FAM122A, SOCS4, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:0071774	response to fibroblast growth factor	51/3408	5.85E-05	ZFP36L1, ZFP36L2, RUNX2, CBL, CD44, CDC5L, COL1A1, CRKL, CTNNB1, EGR3, ELK1, FGF1, FGF2, FGF5, FGFR3, GATA3, GRB2, KCNC1, HNRNPM, NCBP1, POLR2D, POLR2K, MAPK1, MAPK3, PTPN11, SFRP1, SNCA, THBS1, ZFP36, SHOC2, IQGAP1, FGF19, SPRY1, POSTN, KDM5B, FRS2, RBFOX2, FLRT2, DSTYK, NPTN, RAB14, WNT4, DLL4, ESRP1, SULF2, FAM20C, SHCBP1, SPRY4, TRIM71, SPRED1, SPRED2
BP	GO:0010821	regulation of mitochondrion organization	59/3408	5.88E-05	ARRB2, BAK1, BCL2, BCL2L1, DCN, GSK3B, HTT, HIF1A, HK2, MAPT, OPA1, PPP3R1, PRKAA1, MAPK8, SREBF2, STAT2, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, BAP1, TP63, TNFSF10, SQSTM1, BAG4, ATG13, MFN2, BCL2L11, ARIH2, ATG7, BBC3, PRELID1, HTRA2, SH3GLB1, TRIAP1, MIEF1, LEPROT, VPS13C, VPS13D, FBXW7, VPS35, MFF, SMURF1, FNIP2, USP36, RHOU, MOAP1, MUL1, DDHD1, BMF, FNIP1, MIEF2, FLCN, PLD6, CHCHD10
BP	GO:0030217	T cell differentiation	73/3408	6.10E-05	ABL1, ADA, RHOA, ATP7A, BCL2, BCL6, PRDM1, ZFP36L1, ZFP36L2, CAMK4, RUNX2, RUNX1, RUNX3, CBFB, CDK6, CLPTM1, CCR7, CTNNB1, CYLD, EGR1, EGR3, ERBB2, GATA3, KAT2A, NCKAP1L, IL7R, IL18, IRF1, IRF4, ITPKB, JAG2, KIT, LIG4, SMAD7, MDK, MYB, PKNOX1, PTGER4, PTPRC, RAG1, RORA, SATB1, SOS1, SOX4, SP3, SRF, STAT3, SYK, ADAM17, TCF7, ZEB1, TP53, TSC1, XBP1, FZD5, SOCS1, TNFSF9, FADD, AP3D1, CD83, ATG5, SOCS5, BTN2A2, DUSP10, FOXP1, PRELID1, WNT4, DLL4, CHD7, CYP26B1, ZMIZ1, BCL11B, NRARP
BP	GO:0031032	actomyosin structure organization	63/3408	6.68E-05	ABL1, RHOA, ARRB1, CD47, CDC42, CFL2, CNN2, CSRP1, ECT2, S1PR1, EDN1, EPB41, ITGB1, LIMK1, SMAD4, MEF2A, MEF2C, MET, MYH9, MYH10, NF2, PDGFRA, PRKAR1A, PROX1, PTGER4, PXN, SDC4, SFRP1, SLC9A1, SRC, SRF, TESK1, TGFBR1, TNFAIP1, TSC1, CUL3, NRP1, ROCK2, KIF23, BAG4, PDCD6IP, WASF2, DLC1, RAPGEF3, NEBL, CIT, AKAP13, LIMCH1, CLASP1, TMOD2, SIX4, WNT4, ANLN, EPB41L4B, ALKBH4, EPB41L5, ARHGAP28, SYNPO2L, FHDC1, PHLDB2, FRMD3, SH3PXD2B, MYO18A
BP	GO:0071478	cellular response to radiation	61/3408	6.89E-05	AKT2, RHOB, ATM, ATR, BAK1, BCL2L1, CALM1, CDC25A, CDKN1A, CHEK1, CREBBP, CRY2, MAPK14, ECT2, EGR1, EIF2S1, ELK1, EP300, FMR1, FNTA, GATA3, GNB1, GRB2, HSPA5, LIG4, MME, MYC, NEDD4, PTPRK, RAD1, RAD51, RBL2, SFRP1, SNAI2, TAF1, TP53, XRCC5, YY1, HMGA2, CUL4B, AURKB, CLOCK, NET1, CERS1, METAP2, TLK2, KDM1A, SIRT1, SPIDR, NIPBL, TRIAP1, INO80, USP47, USP28, NUCKS1, CAMKMT, RHNO1, RHBDD1, BMF, TP53INP1, SDE2
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	49/3408	6.96E-05	ZFP36L1, ZFP36L2, RUNX2, CBL, CD44, CDC5L, COL1A1, CRKL, CTNNB1, EGR3, FGF1, FGF2, FGF5, FGFR3, GATA3, GRB2, HNRNPM, NCBP1, POLR2D, POLR2K, MAPK1, MAPK3, PTPN11, SFRP1, SNCA, THBS1, ZFP36, SHOC2, IQGAP1, FGF19, SPRY1, POSTN, KDM5B, FRS2, RBFOX2, FLRT2, DSTYK, NPTN, RAB14, WNT4, DLL4, ESRP1, SULF2, FAM20C, SHCBP1, SPRY4, TRIM71, SPRED1, SPRED2
BP	GO:0010717	regulation of epithelial to mesenchymal transition	35/3408	7.00E-05	JAG1, BMP7, COL1A1, CTNNB1, DAB2, DAG1, EZH2, FOXC1, GCNT2, HDAC2, FOXA1, ISL1, LOXL2, SMAD2, SMAD4, SMAD7, MDK, PPP2CA, PTEN, SFRP1, SNAI1, TCF7L2, TGFBR1, TIAM1, TWIST1, OLFM1, PHLDB1, CLASP1, GREM1, ADIPOR1, TRIM62, PBLD, PHLDB2, DAB2IP, CRB2
BP	GO:2001235	positive regulation of apoptotic signaling pathway	58/3408	7.09E-05	FAS, BAK1, BCL2, BCL2L1, CAV1, CTNNA1, CYLD, GSK3B, MCL1, MSX1, NCK1, NKX3-1, PAK2, PLAGL2, PML, PPP1CA, PPP2R1A, PPP3R1, MAPK8, MAPK9, PTEN, PTPRC, RPS3, SFRP1, SIAH1, SKIL, STK4, TFDP1, TFDP2, TGFBR1, THBS1, TIMP3, TP53, TPD52L1, YWHAE, YWHAG, NCK2, TP63, PEA15, TNFSF10, FADD, BCL2L11, BCAP31, RBCK1, SERINC3, SIRT1, BBC3, HTRA2, PIAS4, FBXW7, MFF, MOAP1, ITM2C, BMF, NACC2, DAB2IP, FLCN, CHCHD10
BP	GO:0046677	response to antibiotic	93/3408	7.31E-05	ABL1, ADA, ADCY1, ADCY6, ADCYAP1R1, ALAD, RHOA, RHOB, ATP7A, AXL, BAK1, CCND1, BCL2, BCL2L1, CAPN2, CASP3, CBL, CDKN1B, COL1A1, CRK, DNMT3A, DUSP1, ECT2, EDN1, EFNA5, EGR1, EPS8, EZH2, FOXO1, FOXO3, G6PD, GATA3, GOT2, HDAC2, HMGCR, HNRNPD, HSPA5, ITPR2, JUN, LDHA, MEF2C, MET, MYB, NTRK3, OGG1, OPA1, PAWR, PAX2, PDGFB, PRKAA1, PRKCE, PTEN, RGS2, RGS4, RPS3, CCL7, SLC8A1, SLC9A1, SPARC, SRC, STAT1, STAT3, TP53, TRPM2, TXN, UROS, VCAM1, NR4A3, FOSL1, STK24, ADAM9, KLF4, ACTR2, PSMD14, NET1, SIGMAR1, KLF2, KDM5B, PRDX3, KAT7, ZNF277, KDM1A, KDM6B, LARP1, SIRT1, RSRC1, OSER1, XRN1, PLEKHA1, SETD7, PPP1R15B, TP53INP1, SIRPA
BP	GO:0006888	ER to Golgi vesicle-mediated transport	66/3408	7.34E-05	ANK1, ARCN1, ARF1, CAPZA2, CD59, COPB1, CSNK1D, CTSZ, GOLGB1, INSIG1, NSF, PPP6C, RAB1A, SORL1, SPTAN1, SPTBN1, VAMP7, TGFA, VCP, CUL3, USO1, DYNLL1, NAPA, VAPB, VAPA, GOSR1, GOSR2, SEC24C, BCAP31, CNIH1, SEC23A, HYOU1, SEC24A, TMED10, DCTN3, PPP6R1, ANKRD28, SEC31B, RAB30, TMED5, TMED7, DCTN4, ERGIC2, TRAPPC4, TRAPPC2L, STX17, PPP6R3, ARFGAP1, BCAP29, SAR1A, ERGIC1, GORASP1, CREB3L2, PGAP1, YIPF5, PITPNM3, COG3, COG8, DCTN5, YIF1B, TEX261, WHAMM, TBC1D20, RAB12, TMED4, MIA3
BP	GO:0001838	embryonic epithelial tube formation	44/3408	7.53E-05	ABL1, ADM, BMP7, CASP3, CFL1, CTNNB1, DVL3, GATA3, KAT2A, ARHGAP35, HIF1A, LRP6, MTHFR, PAX2, PTCH1, RARG, SDC4, SFRP1, SKI, SOX4, SOX11, STK4, HNF1B, TSC1, TWIST1, KDM6A, LUZP1, FZD3, ARID1A, FZD1, FZD6, HAND1, DLC1, MTHFD1L, SOX8, SUFU, SIX4, WNT4, SEMA4C, IFT57, VANGL2, MIB1, SHROOM3, TRIM71
BP	GO:0033157	regulation of intracellular protein transport	69/3408	7.99E-05	AKT2, MAPK14, ECT2, STOM, ERBB2, GDI1, GSK3B, INSIG1, JUP, KIF5B, IPO5, MYO1C, OAZ2, PRKAA1, PKIA, MAPK1, PTPN1, PTPN11, PTPN14, RAN, SORL1, SP100, SREBF2, VAMP2, VAMP7, TCF7L2, TP53, TXN, UBE2D3, UBE2G2, UBE2L3, XPO1, YWHAE, FZD5, BAP1, BAG4, EDEM1, ATG13, C2CD5, BCAP31, TENM1, NUTF2, RAPGEF3, ARIH2, ANP32B, TARDBP, HTRA2, DERL2,

					SH3GLB1, DNAJC27, UBR5, UBE2J1, SUFU, RAB23, MIEF1, LEPROT, FBXW7, YOD1, FERMT1, RIOK2, SAR1A, MFF, MAVS, XPO5, USP36, RHOU, XPO4, SH3TC2, MIEF2
BP	GO:0072175	epithelial tube formation	46/3408	7.99E-05	ABL1, ADM, BMP7, CASP3, CFL1, CTNNB1, DVL3, GATA3, KAT2A, ARHGAP35, HIF1A, LRP6, MTHFR, PAX2, PODXL, PROX1, PTCH1, RARG, SDC4, SFRP1, SKI, SOX4, SOX11, STK4, HNF1B, TSC1, TWIST1, KDM6A, LUZP1, FZD3, ARID1A, FZD1, FZD6, HAND1, DLC1, MTHFD1L, SOX8, SUFU, SIX4, WNT4, SEMA4C, IFT57, VANGL2, MIB1, SHROOM3, TRIM71
BP	GO:0051648	vesicle localization	88/3408	7.99E-05	ACTN4, ADCY1, ADORA2B, ARF1, ATP2A2, CALM3, CAMK2A, CD59, CSNK1D, CTNNB1, CTSZ, FMR1, GSK3B, HTT, KIF5B, MYO1C, MYO5A, NSF, P2RY1, PAFAH1B1, PPP6C, PTEN, RAB1A, RAB5A, RAP1B, SNAP25, SNCA, STX3, VAMP1, VAMP2, VAMP7, SYT1, TGFA, CUL3, USO1, NAPA, SYNJ1, AP3D1, WASL, SYT7, RAB11B, KIF3B, KIF23, GOSR1, GOSR2, PREPL, SEC24C, RIMS3, SV2A, CNIH1, AP3S2, SEC23A, UNC13B, SEC24A, TMED10, KIF3A, PPP6R1, NLGN1, TRAK1, KIF1B, SYT11, ANKRD28, CLASP1, PIP5K1C, NCS1, AP3M1, PCDH17, GIT1, TRAPPC4, TRAPPC2L, SYT17, NDE1, FNBP1L, PPP6R3, SAR1A, NLGN2, KIF13A, RAB17, GORASP1, TRAK2, MLPH, FYCO1, DNAJC5, CEP19, SYT2, TBC1D20, RIMS4, FAM91A1
BP	GO:0022407	regulation of cell-cell adhesion	110/3408	8.13E-05	ABL1, ADA, JAG1, RHOA, BCL6, BMP7, CASP3, CAV1, RUNX1, RUNX3, CBFB, CD44, CD47, CDC42, CEBPB, CCR7, MAPK14, CSK, CYLD, EFNA5, EFNB1, EFNB2, CELSR2, EGR3, EPHA7, EPHB3, ERBB2, FLOT2, GATA3, GCNT2, GRB2, NCKAP1L, FOXA1, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, IRAK1, ITGA6, IRF1, ITPKB, LYN, SMAD7, MBP, MDK, MYB, MYO10, NCK1, NF2, PAK2, PAK3, PAWR, SERPINE2, PODXL, PPARA, PRKAR1A, PRKCA, PTAFR, PTPN11, PTPRC, RAG1, RDX, RPS3, CX3CL1, SDC4, SNAI2, SRC, SYK, TFRC, VCAM1, VEGFA, XBP1, NR4A3, NCK2, SOCS1, TNFSF9, FADD, AP3D1, DLG5, SOCS6, CD83, KLF4, SOCS5, SH2B3, FSTL3, CITED2, BTN2A2, GPNMB, NFAT5, DUSP10, ICOSLG, MINK1, YTHDF2, WNT4, LAX1, TENM3, PAG1, PELI1, ZMIZ1, EPB41L5, WNK1, CD276, MYADM, SIRPA, ADAMTS18, DENND6A, MIA3, NRARP
BP	GO:1903364	positive regulation of cellular protein catabolic process	48/3408	8.29E-05	PTTG1IP, CAV1, CSNK1D, CSNK1E, DAB2, FMR1, GSK3B, DNAJB2, LDLR, LRP1, SMAD7, ATXN3, MAPK9, PSMC2, PTEN, RDX, AURKA, TAF1, VCP, USP13, SOCS5, EDEM1, HERPUD1, RNF144A, BCAP31, TRIB1, ARIH2, PLK2, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, UBQLN2, UBQLN1, ANKIB1, FBXW7, VPS35, SMURF1, DDA1, UQCC2, FAM122A, SOCS4, AMER1, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:1902105	regulation of leukocyte differentiation	80/3408	8.47E-05	ABL1, ADA, RHOA, AXL, BCL6, PRDM1, ZFP36L1, ZFP36L2, CAMK4, RUNX1, RUNX3, CBFB, CDK6, CEBPB, CLPTM1, CREB1, CSF1, CTNNB1, CYLD, EGR3, ERBB2, ESRRA, FBN1, GATA2, GATA3, KAT2A, GNAS, NCKAP1L, HMGB3, HOXA7, IL7R, IL18, IRF1, IRF4, ITPKB, JUN, LYN, SMAD7, MDK, KITLG, MMP14, MYB, MYC, NOTCH2, POU4F1, PRKCA, PTPRC, RAG1, RB1, SFRP1, SOS1, SYK, TAL1, ZEB1, KLF10, XBP1, SOCS1, TNFSF9, FADD, AP3D1, CD83, SOCS5, RASSF2, TRIB1, FSTL3, BTN2A2, PIAS3, TOB2, DUSP10, FOXP1, PRELID1, FBXW7, PCID2, CYP26B1, ZMIZ1, ZBTB46, ZNF675, SIGLEC15, ATP11C, NRARP
BP	GO:0051028	mRNA transport	51/3408	8.55E-05	ZFP36L1, CETN2, EIF4E, FMR1, MYO1C, NCBP1, NUP88, NUP98, POLR2D, RANBP2, UPF1, SRSF1, SRSF2, SRSF4, SRSF7, XPO1, ZFP36, PABPN1, TNKS, QKI, POM121, SMG7, G3BP2, NUTF2, NXF1, IGF2BP1, IGF2BP3, NUP50, RNPS1, DDX19B, U2AF2, XPO7, SMG1, ZC3H3, BICD2, SMG5, UPF2, RBM15B, CDC40, CPSF2, ALKBH5, DDX19A, WDR33, NDC1, NUP133, PCID2, EIF5A2, THOC2, SEH1L, NUP43, POM121C
BP	GO:0035303	regulation of dephosphorylation	65/3408	8.75E-05	CALM1, CALM2, CALM3, CRY2, DLG3, ENSA, FKBP1A, GNAI2, GSK3B, HTT, NCKAP1L, IKBKB, MEF2C, MYO1D, PPP1R12A, PIN1, PPP1R2, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, EIF2AK2, PTPRC, SET, SRC, TSC1, YWHAE, SHOC2, IQGAP1, MTMR3, MTMR4, ROCK2, BAG4, PHACTR2, SMG7, NUAK1, FARP1, DLC1, ARPP19, LMTK2, PPP6R1, RRP1B, ANKLE2, SMG5, NSMF, PPP1R16B, ZFYVE1, SYTL2, PPP6R3, PPP2R2D, SLC39A10, SLC7A14, PCIF1, WNK1, MTMR9, ZCCHC9, PPP1R15B, FAM122A, SPPL3, WDR81, PPP4R2, SPRED1, CNEP1R1, BOD1L1, PPP1R37
BP	GO:0031334	positive regulation of protein complex assembly	79/3408	8.76E-05	ARF1, ARF6, RHOA, ATM, ATR, CDKN1B, CCR7, CREB1, CTNNB1, EIF4G1, ERCC2, FER, GRB2, GSK3B, GTF2H3, NCKAP1L, JUN, MAP1B, MAPT, MECP2, MET, MYO1C, NCK1, PRKCE, MAPK9, PSMC2, RPS3, SRC, SRF, SYK, TAF1, TAL1, HNF1B, TP53, TWIST1, VCP, VEGFA, FOSL1, NCK2, CUL4B, WASF1, WASL, BAG4, FCHSD2, G3BP2, BCL2L11, ARPC5, ACTR2, ARPC2, AKAP9, G3BP1, ABI2, TENM1, CDC42EP2, UNC13B, NCKAP1, IQGAP2, SUB1, TPPP, CNOT1, CLASP1, SPIDR, ASAP1, SH3GLB1, NIN, CAND1, FMN2, SPIRE1, CNOT6, FNIP2, SLAIN2, NAV3, BMF, FNIP1, WHAMM, MIEF2, JMY, RICTOR, FMN1
BP	GO:2001234	negative regulation of apoptotic signaling pathway	70/3408	8.89E-05	FAS, AR, ARRB2, BCL2, BCL2L1, BDNF, BRCA1, PTTG1IP, CD44, CTNNA1, CTNNB1, DDX3X, EYA4, GNAI2, GNAI3, GRINA, HTT, HIF1A, DNAJA1, ITGA6, ITGAV, MAZ, MCL1, MNT, OPA1, SERPINE1, PTPN1, RB1, CX3CL1, SIAH2, SNAI2, SNAI1, SOD2, SRC, TCF7L2, TMBIM6, TERT, TGFBR1, THBS1, TPT1, VDAC2, XBP1, PEA15, TNFSF10, FADD, NRP1, ARHGEF2, HERPUD1, PSME3, HYOU1, ZMYND11, KDM1A, SIRT1, SGK3, ZNF385A, PRELID1, HTRA2, RRM2B, TXNDC12, TRIAP1, TAF9B, WNT4, RRN3, PHIP, USP47, BIRC6, TMBIM1, SYVN1, ITPRIP, RFFL
BP	GO:0030100	regulation of endocytosis	82/3408	8.89E-05	ABL1, ABL2, ACTN4, ARF1, ARF6, ARRB1, ARRB2, AXL, CALM3, CALR, CAV1, CBL, CD47, CSK, DAB2, EFNB2, FMR1, GATA2, RAPGEF1, NCKAP1L, HIP1, HNRNPK, IL15RA, ITGAV, LRP1, LRPAP1, MKLN1, OPHN1, SERPINE1, PIK3CB, PPP3CA, PTEN, PTPN1, PTPRC, PTPRJ, RAB5A, RAB5B, ATXN2, SH3GL2, SNCA, SRC, SYK, TFR2, TUB, NR1H2, VEGFA, NUMB, SNX3, WASL, SYT7, ATG5, ZFYVE16, SNX17, TSPAN1, TNK2, RAB31, AAK1, NLGN1, DKK1, RAB21, SYT11, CD2AP, CLIP3, APPL1, LDLRAP1, GREM1, UBQLN2, EHD4, ANKFY1, AHI1, RUFY2, ARFGAP1, CAMK1D, MIB1, RAB17, CBLL1, SGIP1, STON2, ANKRD13A, BTBD9, SIRPA, MYO18A
BP	GO:0051495	positive regulation of cytoskeleton organization	69/3408	9.15E-05	ABL1, ARF1, ARF6, RHOA, CD47, CDC42, CDKN1B, CFL1, CFL2, CCR7, EDN1, FER, GRB2, NCKAP1L, LIMK1, MAP1B, MAPT, MECP2, MET, MYO1C, NCK1, NF2, NTRK3, PRKCE, PROX1, PXN, RPS3, CX3CL1, SDC4, SFRP1, TESK1, TGFBR1, TSC1, NCK2, NRP1, WASF1, WASL, ROCK2, VPS4B, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, AKAP9, ABI2, TENM1, RAPGEF3, CDC42EP2,

					NCKAP1, IQGAP2, DSTN, LIMCH1, CLASP1, NIN, WNT4, NSFL1C, FMN2, SPIRE1, SLAIN2, SYNPO2L, NAV3, WHAMM, JMY, UBXN2B, CEP120, RICTOR, SH3PXD2B, FMN1
BP	GO:0010332	response to gamma radiation	25/3408	9.25E-05	ATM, ATR, BAK1, BCL2, BCL2L1, CBL, CDKN1A, EGR1, ELK1, ERCC6, GATA3, HSPA5, LIG4, MEN1, MYC, PML, PRKAA1, PTPRC, CCL7, TP53, XRCC5, TRIM13, TLK2, KDM1A, DCUN1D3
BP	GO:0032486	Rap protein signal transduction	11/3408	9.37E-05	CBL, RAPGEF1, RAP1B, RAP2A, RAP2B, RDX, TIMP2, RAPGEF2, RAPGEF3, PLK2, RAP2C
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	72/3408	9.67E-05	FAS, CCR7, CYLD, DUSP1, DVL3, EDN1, EGFR, EPHA4, ERCC6, FOXM1, FOXO1, FLT4, RAPGEF1, HMGCR, DNAJA1, IGF1R, LYN, NBR1, MAP3K3, MAP3K4, MEN1, MID1, MAP3K9, MYC, PAFAH1B1, PRDX1, MAPK1, MAPK3, EIF2AK2, PTPN1, RAP2A, RPS3, MAP2K4, SFRP1, SYK, TIAM1, TPD52L1, VEGFA, WNT7B, FZD5, FZD4, SPAG9, TAOK2, MAP4K4, NCOR1, TRAF4, RASSF2, FGF19, HIPK3, SEMA3A, NOD1, MAP3K2, ZMYND11, DUSP10, DKK1, KLHDC10, MAPK8IP3, PHLPP1, PDCD4, HIPK2, MINK1, SEMA4C, VANGL2, TAOK1, AIDA, MUL1, ITCH, SIRPA, DAB2IP, ZNF675, EMC10, SH3RF3
BP	GO:0070262	peptidyl-serine dephosphorylation	13/3408	9.98E-05	DUSP1, NCK1, PPP1CA, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP3CA, YWHAE, PPP1R16B, PPP2R2D, PPP1R15B, PPTC7
BP	GO:0051100	negative regulation of binding	55/3408	1.02E-04	ACTB, ARRB2, CAV1, CSNK1E, CTSZ, DAB2, EIF2S1, GSK3B, HDAC2, DNAJB2, HSPA5, ID4, IFIT2, ISL1, JUN, LRPAP1, MET, MSX1, NKX3-1, P2RY1, PDGFB, PIN1, PPARA, PPP1CA, PPP3CA, MAPK3, MAPK8, PTPRF, RALB, SORL1, SOX11, SP100, AURKA, STYX, TAF1, TMBIM6, HMGA2, TNKS, PER2, AURKB, HAND1, DKK1, KDM1A, USP33, SIN3A, RSF1, GNL3L, FBXW7, MEPCE, EPB41L5, ZNF462, ARHGAP28, WFIKKN2, TTBK2, ZNF675
BP	GO:0050768	negative regulation of neurogenesis	85/3408	1.02E-04	ADCY6, JAG1, ARF6, RHOA, ARHGDIA, BMP7, BMPR1A, CALR, COL3A1, CTNNA1, CTNNB1, CTSZ, DDX6, DLX2, EFNB2, EIF4E, EPHA4, EPHA7, EPHB2, FKBP4, FOXO3, GDI1, GSK3B, HDAC2, NRG1, HES1, ID4, IDH2, ISL1, LDLR, LRP1, NTRK3, PAFAH1B1, PAX6, PBX1, PPP3CA, PTEN, PTPRG, CX3CL1, SKI, SORL1, SOX11, STAT3, TERT, TP53, TSC1, SEMA7A, NRP1, SYNGAP1, ARHGEF2, NTN1, MAP4K4, RAPGEF2, SEMA3E, LRIG2, RNF10, GDF11, SEMA3A, SEMA4B, PLK2, DUSP10, NLGN1, DKK1, FSTL4, RAP1GAP2, KANK1, DICER1, MYLIP, SOX8, ASAP1, BCL11A, SEMA4C, RGMA, MIB1, SEMA6A, CTDSP1, GORASP1, ISL2, TRAK2, ITM2C, KREMEN1, HOOK3, DIXDC1, KCTD11, PRTG
BP	GO:0051017	actin filament bundle assembly	51/3408	1.02E-04	ABL1, ACTN4, ADD1, RHOA, RHOB, ARRB1, CD47, CDC42, S1PR1, EPS8, LIMK1, MARCKS, MET, MYO1B, NEDD9, NF2, PAWR, PLS3, PTGER4, PXN, RDX, CX3CL1, SDC4, SFRP1, SLC9A1, SRC, SRF, TESK1, TGFBR1, TNFAIP1, TSC1, RND2, CUL3, NRP1, ROCK2, BAG4, WASF2, DLC1, RAPGEF3, FAM107A, LIMCH1, CLASP1, WNT4, FMN2, SPIRE1, ARHGAP28, SYNPO2L, FHDC1, PHLDB2, SHROOM1, SH3PXD2B
BP	GO:0034968	histone lysine methylation	41/3408	1.02E-04	ATRX, BRCA1, CTNNB1, DNMT3B, EZH1, EZH2, GATA3, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MYB, SUV39H1, KDM6A, PRDM2, KMT2D, CTR9, SETD1A, KMT2B, MTF2, KDM1A, SIRT1, SUZ12, AUTS2, ARID4B, WDR5B, TET2, BCOR, RIF1, SETD5, KMT2E, BEND3, KMT2C, NSD1, SETD7, SETDB2, SETD3, DPY30, TET3
BP	GO:0007517	muscle organ development	111/3408	1.05E-04	ADARB1, RHOA, ARRB2, ZFHX3, BCL2, BCL9, BMPR1A, CAV1, CCNT2, CFL2, CHD2, COL3A1, COL11A1, COL19A1, CREB1, MAPK14, CTNNB1, DCN, DDX5, HBEGF, S1PR1, EDN1, EFNB2, EGR1, EGR3, EP300, ETV1, FGF2, FHL1, FKBP1A, FOXC1, FLNB, G6PD, GATA6, KAT2A, GJA1, NRG1, HMGCR, FOXN2, RBPJ, ISL1, JARID2, SMAD4, SMAD7, MEF2A, MEF2C, MEF2D, FOXO4, MSX1, PAX3, PIM1, PIN1, POU4F1, PPARA, PPP3CA, PRKAA1, MAPK1, PROX1, PTEN, RB1, RGS2, RGS4, SGCD, SKI, SOX11, TAGLN, NR2F2, TGFBR1, TGFBR3, TWIST1, XBP1, YY1, BTG2, FXR1, FZD1, CD164, USP2, COPS2, HAND1, AKAP6, HDAC9, NR1D2, UBE4B, ZBTB18, DDX17, FRS2, DKK1, SIRT1, MAFF, FBXO22, HEYL, GREM1, SERP1, SOX8, CDON, SFMBT1, SIX4, DLL4, CHD7, GPCPD1, CYP26B1, VANGL2, HEG1, AKIRIN1, PTCD2, ARID5B, UQCC2, ZNF689, EID2B, MTPN, FOXK1
BP	GO:0009791	post-embryonic development	34/3408	1.05E-04	ABL1, ACVR2B, ATM, ATRX, BAK1, BCL2, PRDM1, ERCC2, FBN1, GATA3, GNAS, IGF2R, IREB2, ITPR1, SMAD2, MECP2, PLAGL2, TGFBR1, VEGFA, FZD5, ALDH5A1, SGPL1, KLF4, BCL2L11, KDM5B, SZT2, MORC3, GIGYF2, SERP1, CCDC47, HEG1, PLEKHA1, BCL11B, ARID5B
BP	GO:0045137	development of primary sexual characteristics	68/3408	1.08E-04	ACVR1B, ADCYAP1R1, AR, ARRB1, ARRB2, ATM, ATRX, CCND1, BCL2, BCL2L1, CASP3, CBL, CEBPB, CRKL, CTNNA1, DACH1, FOXC1, FOXO3, GATA3, GATA6, GJA1, HOXA9, HSPA5, INSR, KIT, SMAD4, KITLG, MMP14, NKX3-1, PDGFRA, PGR, KDM5A, SFRP1, SRC, TGFBR1, TMF1, VEGFA, WNT2B, SF1, CSDE1, NRIP1, FZD4, AKR1C3, TNFSF10, SGPL1, PCYT1B, ADAMTS1, KMT2B, BCL2L11, LHFPL2, FSTL3, CITED2, SEMA3A, RHOBTB3, FNDC3A, SIRT1, SOX8, ARID4B, SIX4, WNT4, PLEKHA1, ARID5B, CBX2, ZNF830, TBC1D20, RNF38, RDH10, AGO4
BP	GO:0014032	neural crest cell development	32/3408	1.12E-04	JAG1, BMP7, BMPR1A, CFL1, EDN1, EFNB1, FOXC1, FN1, NRG1, HIF1A, HES1, ISL1, KITLG, MAPK1, MAPK3, SNAI2, SOX11, TWIST1, SEMA7A, NRP1, ALDH1A2, SEMA3E, FGF19, SEMA3A, SEMA4B, CORO1C, SOX8, SEMA4C, SEMA6A, FAM172A, KBTBD8, RDH10
BP	GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	32/3408	1.12E-04	CAV1, CSNK1D, CSNK1E, DAB2, GSK3B, DNAJB2, SMAD7, MAPK9, AURKA, TAF1, VCP, SOCS5, HERPUD1, RNF144A, BCAP31, TRIB1, ARIH2, PLK2, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, UBQLN2, UBQLN1, ANKIB1, DDA1, FAM122A, SOCS4, RNF217, RNF144B, RNF180

BP	GO:0045927	positive regulation of growth	79/3408	1.13E-04	ADAM10, RHOA, BCL2, BDNF, BMPR1A, BMPR2, CDC42, CREB1, MAPK14, CSF1, DDX3X, HBEGF, EDN1, EFNA5, MEGF8, EGFR, EIF4G1, EIF4G2, ERBB2, EXTL3, FGF2, FN1, GATA6, GDI1, GOLGA4, IGF2, IGFBP1, RBPJ, ILK, INSR, L1CAM, LIMK1, LRP1, MAP1B, MAPT, MEF2C, MMP14, NCBP1, NTRK3, PAFAH1B1, PIM1, PIN1, POU3F2, PPARD, MAPK1, PROX1, RPS6KA3, SFRP1, SLC9A1, SRF, SYT1, ADAM17, TGFBR1, TGFBR3, VEGFA, RND2, SEMA7A, NRP1, NTN1, AKAP6, AGR2, NIPBL, SERP1, DERL2, ZNF639, TAF9B, SYT17, INO80, USP47, CHD7, SMURF1, CXCL16, MUL1, FAM122A, SYT2, MTPN, BRAT1, SH3PXD2B, AGRN
BP	GO:0030098	lymphocyte differentiation	98/3408	1.15E-04	ABL1, ADA, RHOA, ATM, ATP7A, AXL, BAK1, BCL2, BCL6, PRDM1, ZFP36L1, ZFP36L2, CAMK4, RUNX2, RUNX1, RUNX3, CBFB, CDK6, CEBPG, CLPTM1, CCR7, KLF6, CTNNB1, CYLD, EGR1, EGR3, EP300, ERBB2, GATA3, KAT2A, NCKAP1L, HMGB3, RBPJ, IL7R, IL18, IRF1, IRF4, ITGB1, ITPKB, JAG2, KIT, LIG4, SMAD7, DNAJB9, MDK, MMP14, MYB, NOTCH2, PKNOX1, POU2F2, PTGER4, PTPRC, PTPRJ, RAG1, RORA, SATB1, SFRP1, SOS1, SOX4, SP3, SRF, STAT3, SYK, ADAM17, TCF3, TCF7, ZEB1, TP53, TPD52, TSC1, TYRO3, VCAM1, XBP1, FZD5, SOCS1, TNFSF9, FADD, AP3D1, CD83, ATG5, SOCS5, HDAC9, BTN2A2, DUSP10, TUSC2, FOXP1, PRELID1, WNT4, DLL4, CHD7, PCID2, CYP26B1, ZMIZ1, BCL11B, FNIP1, ATP11C, IRF2BP2, NRARP
BP	GO:0060998	regulation of dendritic spine development	30/3408	1.17E-04	ADAM10, ARF1, ARF6, CFL1, EPHA4, FMR1, HDAC2, CAPRIN1, MEF2C, OPA1, PAFAH1B1, PAK3, MAPK6, PTEN, TIAM1, KALRN, DLG5, ACTR2, ABI2, PDLIM5, PLK2, CPEB3, NLGN1, SHANK2, FSTL4, SIPA1L1, ASAP1, C21orf91, BHLHB9, SDK1
BP	GO:0000302	response to reactive oxygen species	70/3408	1.17E-04	ABL1, ADA, RHOB, ATP7A, AXL, BAK1, BCL2, BMP7, CAPN2, CASP3, CCNA2, CCR7, COL1A1, CRK, DUSP1, ECT2, EDN1, EGFR, ERCC6, EZH2, FER, FOXO1, FOXO3, HDAC2, HNRNPD, JUN, LDHA, MAPT, MET, MTR, MYB, PRDX1, PAWR, PAX2, PDGFRA, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, PTPRK, PXN, RPS3, SLC8A1, SOD2, SRC, STAT1, TRPM2, TXN, NR4A3, FOSL1, STK24, AKR1C3, ADAM9, KLF4, NET1, SIGMAR1, KLF2, PRDX3, ZNF277, KDM6B, SZT2, SIRT1, PRDX5, OSER1, PLEKHA1, SESN2, PPP1R15B, SIRPA, SESN3
BP	GO:1901987	regulation of cell cycle phase transition	126/3408	1.31E-04	APC, ATM, ATP2B4, CCND1, BCL2, BRCA1, ZFP36L1, ZFP36L2, CCND2, CDC25A, CDK6, CDKN1A, CDKN1B, CETN2, CHEK1, FOXN3, CSNK1D, CSNK1E, DDX3X, DUSP1, EGFR, EIF4G1, EP300, ERCC2, EZH2, FHL1, HSPA2, IK, MAD2L1, MDM4, MECP2, MEN1, FOXO4, CNOT4, PAFAH1B1, PBX1, PKD1, PML, PPP2R1A, PKIA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD21, RB1, RBL2, RDX, SKP1, SOX4, AURKA, ADAM17, TAF1, TERT, TFDP1, TFDP2, TP53, YWHAE, YWHAG, BTG2, HMGA2, CUL4B, CUL3, CDC14B, CDK10, DYNLL1, BTRC, AURKB, KLF4, TRIP13, CNOT8, TAOK2, PSMF1, ADAMTS1, VPS4B, CEP135, CTDSP2, AKAP9, PSME3, PSMD14, CTDSPL, TUBB4A, BTN2A2, GPNMB, PLK2, CNTRL, FAM107A, CEP250, DCTN3, CNOT1, PSME4, CLASP1, SIN3A, ZNF385A, GIGYF2, TRIAP1, DTL, ANLN, INO80, HAUS6, NDE1, PINX1, USP47, HAUS2, FBXW7, RIOK2, PCID2, KMT2E, RCC2, MEPCE, CNOT6, HECW2, TAOK1, CTDSP1, ZNF655, BRCC3, CDC73, ZNF830, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0032872	regulation of stress-activated MAPK cascade	71/3408	1.32E-04	FAS, CCR7, CYLD, DUSP1, DVL3, EDN1, EGFR, EPHA4, ERCC6, FOXM1, FOXO1, FLT4, RAPGEF1, HMGCR, DNAJA1, IGF1R, NBR1, MAP3K3, MAP3K4, MEN1, MID1, MAP3K9, MYC, PAFAH1B1, PRDX1, MAPK1, MAPK3, EIF2AK2, PTPN1, RAP2A, RPS3, MAP2K4, SFRP1, SYK, TIAM1, TPD52L1, VEGFA, WNT7B, FZD5, FZD4, SPAG9, TAOK2, MAP4K4, NCOR1, TRAF4, RASSF2, FGF19, HIPK3, SEMA3A, NOD1, MAP3K2, ZMYND11, DUSP10, DKK1, KLHDC10, MAPK8IP3, PHLPP1, PDCD4, HIPK2, MINK1, SEMA4C, VANGL2, TAOK1, AIDA, MUL1, ITCH, SIRPA, DAB2IP, ZNF675, EMC10, SH3RF3
BP	GO:1903313	positive regulation of mRNA metabolic process	31/3408	1.32E-04	ZFP36L1, ZFP36L2, HNRNPD, NCBP1, NUP98, UPF1, TRA2B, ZFP36, BTG2, CNOT8, ROCK2, PUM1, THRAP3, TOB1, CPEB3, CNOT1, TNRC6B, GIGYF2, DAZAP1, PABPC1, RBMX, TNRC6A, YTHDF2, RBM23, ZC3HAV1, TNRC6C, METTL14, CDC73, TRIM71, YTHDF3, RBMXL1
BP	GO:0032465	regulation of cytokinesis	34/3408	1.36E-04	RHOA, BCL2L1, CALM1, CALM2, CALM3, CDC42, CETN2, ECT2, INCENP, PIN1, PRKCE, PKN2, AURKA, UVRAG, CUL3, PKP4, CDC14B, PRC1, AURKB, KIF3B, KIF23, KLHL21, PLK2, CIT, ZFYVE26, GIT1, SH3GLB1, PRPF40A, BIRC6, KIF13A, RAB11FIP4, KLHL13, E2F7, FLCN
BP	GO:0007033	vacuole organization	53/3408	1.46E-04	ARF1, SCARB2, LYST, TPP1, CLN8, GAA, HPS1, MAN2A1, PIP4K2A, RAB1A, RAB5A, RALB, ULK1, MTMR3, SYT7, ATG5, VPS4B, ATG13, MFN2, ATG7, GABARAPL2, ATG14, ATG2A, PACS2, STX12, RAB3GAP2, UBQLN2, UBQLN1, SH3GLB1, HOOK1, CHMP5, RAB14, RAB23, TMEM106B, STX17, ATG16L1, ATG2B, LAPTM4B, VPS35, TMEM165, NSFL1C, SMURF1, TP53INP2, ATG9A, GNPTAB, MAP1LC3B, HOOK3, TP53INP1, UBXN2B, SMCR8, TMEM199, TPCN2, TMEM41B
BP	GO:0045931	positive regulation of mitotic cell cycle	53/3408	1.46E-04	ABL1, CCND1, CCND2, CDC25A, DDX3X, EDN1, EGFR, EIF4E, EIF4G1, FOXA1, HNRNPU, HES1, HSPA2, IGF2, INSR, MAD2L1, MECP2, MEIS2, NKX3-1, PAFAH1B1, PBX1, PDGFB, PRKCA, PKN2, PTPN11, RB1, RDX, RPS6KB1, AURKA, ADAM17, TAL1, DYNLT3, TERT, TGFA, CUL4B, CUL3, CDK10, USP2, ADAMTS1, VPS4B, NIPBL, SIN3A, SH2B1, DTL, PHIP, PCID2, KMT2E, RCC2, NSFL1C, MEPCE, UBXN2B, TTL, EPGN
BP	GO:0031954	positive regulation of protein autophosphorylation	15/3408	1.46E-04	CALM1, CALM2, CALM3, PDGFA, PDGFB, RAP2A, RAP2B, SRC, VEGFA, IQGAP1, TAOK2, RASSF2, GPNMB, GREM1, RAP2C
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	51/3408	1.47E-04	FAS, AR, BCL2, BCL2L1, BRCA1, CAV1, CTNNA1, CYLD, EYA4, HTT, ITGA6, ITGAV, MCL1, SERPINE1, PAK2, PML, PPP1CA, PPP2R1A, PTEN, PTPRC, CX3CL1, SFRP1, SIAH2, SKIL, SNAI2, SP100, SRC, STK4, TCF7L2, TERT, TGFBR1, THBS1, TIMP3, TRAF1, MADD, PEA15, TNFSF10, FADD, NRP1, ARHGEF2, PSME3, RBCK1, ZMYND11, SGK3, HTRA2, PHIP, BIRC6, TMBIM1, ITM2C, ITPRIP, RFFL

BP	GO:0006402	mRNA catabolic process	100/3408	1.47E-04	ATM, ZFP36L1, ZFP36L2, MAPK14, DDX5, DDX6, EIF4G1, ELAVL1, ETF1, FMR1, GSPT1, HNRNPC, HNRNPD, HNRNPU, TNPO1, MLH1, HNRNPM, NCBP1, CNOT4, PARN, PKP1, POLR2D, PPP2CA, PPP2R1A, PPP2R2A, PRKCA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, UPF1, RPL15, RPL28, RPL34, RPL37, RPS3, RPS23, SET, XPO1, ZFP36, CSDE1, BTG2, FXR1, ANP32A, PABPC4, CNOT8, ROCK2, PSMF1, PUM1, SMG7, THRAP3, TOB1, PSME3, PSMD14, SYNCRIP, PAIP1, IGF2BP1, IGF2BP3, HBS1L, RNPS1, HNRNPA0, CPEB3, CNOT1, SAMD4A, SMG1, TNRC6B, PSME4, LARP1, SMG5, TARDBP, LSM4, UPF2, GIGYF2, SERBP1, AGO1, PABPC1, TNRC6A, MYEF2, YTHDF2, XRN1, ALKBH5, SAMD4B, RBM23, RBM38, PCID2, DCP1A, ZC3HAV1, CNOT6, TNRC6C, METTL14, EDC3, TRIM71, AGO3, AGO4, PDE12, PATL1, YTHDF3
BP	GO:0043112	receptor metabolic process	60/3408	1.55E-04	ADM, ARF1, ARRB1, ARRB2, CAV1, AP2M1, EDN1, EFNB2, FMR1, FNTA, FUT8, GRB2, HDAC2, NRG1, HIF1A, HNRNPK, HOXA5, ITGAV, ITGB1, LRP1, LRPAP1, MKLN1, NEDD4, NSF, OPHN1, FURIN, PPARA, PTPN1, RAB5A, ATXN2, SH3GL2, SNAP25, SNCA, SNX1, SORL1, SYK, TFRC, UVRAG, VEGFA, VLDLR, NUMB, RAB11B, CALCRL, ARFGEF2, SEC24A, RAB31, LMTK2, DKK1, LDLRAP1, GREM1, MYLIP, UBQLN2, SH3GLB1, CHMP5, AHI1, SMURF1, ANKRD13C, ITCH, ZNRF3, ANKRD13A
BP	GO:0007223	Wnt signaling pathway, calcium modulating pathway	19/3408	1.55E-04	CALM1, CAMK2A, CTNNB1, GNB1, PPP3CA, PPP3R1, TCF7L2, FZD5, FZD3, FZD4, FZD6, DKK1, TNRC6B, AGO1, TNRC6A, NLK, TNRC6C, AGO3, AGO4
BP	GO:1905898	positive regulation of response to endoplasmic reticulum stress	19/3408	1.55E-04	BAK1, CAV1, ATXN3, NCK1, PTPN1, XBP1, NCK2, USP13, EDEM1, HERPUD1, BCL2L11, BCAP31, AGR2, SERINC3, SIRT1, UBQLN2, UBQLN1, TMEM33, DAB2IP
BP	GO:0030521	androgen receptor signaling pathway	26/3408	1.56E-04	AR, RHOA, ARRB2, BRCA1, CTNNB1, DAB2, DDX5, EP300, FHL2, FKBP4, DNAJA1, NKX3-1, RAN, RB1, RNF4, SFRP1, TAF1, NCOA3, NRIP1, ARID1A, NCOR1, DDX17, SIRT1, HEYL, FOXP1, PMEPA1
BP	GO:0051090	regulation of DNA-binding transcription factor activity	115/3408	1.57E-04	ADCY1, AR, ARRB1, ARRB2, BMP7, CAMK2A, CAV1, CEBPG, ATF2, MAPK14, CTNNB1, CYLD, EDN1, EP300, ESR2, EZH2, FER, FLOT2, HDAC2, FOXA1, IKBKB, IL1RAP, IL18, IRAK1, IRAK2, JUN, JUP, KIT, KRAS, LRP6, SMAD7, MEN1, MXI1, NFKB1, NKX3-1, ENPP1, PIM1, PKD1, POU4F1, PPP3CA, MAPK1, MAPK3, MAPK8, MAPK9, EIF2AK2, PROX1, PTCH1, PTEN, PTGIS, RB1, KDM5A, RNF2, RPS3, CX3CL1, SP100, SRF, STAT3, SYK, TAF1, TCF3, TCF7L2, TRAF1, TRAF3, TWIST1, UBE2N, UBE2V1, VEGFA, TRIM25, FOSL1, FZD1, FZD4, FZD6, BHLHE40, BTRC, RPS6KA4, ARHGEF2, RPS6KA5, KLF4, HAND1, CLOCK, G3BP2, MED13, TRIM13, TRIB1, TRIM22, NOD1, TAB1, RBCK1, PRDX3, KDM1A, ERC1, TAB2, UFL1, SIRT1, SGK3, HEYL, HIPK2, RLIM, PIAS4, SUFU, TRIM62, CAMK1D, PELI1, MAVS, CREBZF, ITCH, ARID5B, GLIS2, MTDH, JMY, MTPN, SIK1, DAB2IP, ZNF431, ZNF675
BP	GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	42/3408	1.61E-04	CAV1, CREBBP, DAB2, EP300, FBN1, FBN2, HSPA5, ITGA3, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEN1, PIN1, SKI, SKIL, SOX11, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, ITGA8, MTMR4, ONECUT2, CITED2, PEG10, SIRT1, ZNF451, DKK3, HIPK2, TRIM33, RNF111, FERMT1, PMEPA1, SMURF1, PBLD, WFIKKN2, CD109, FLCN
BP	GO:0071229	cellular response to acid chemical	64/3408	1.62E-04	ABL2, ACACA, ADCY6, ATM, ATP7A, BCL2L1, CAPN2, CEBPB, COL1A1, COL1A2, COL3A1, COL4A1, COL5A2, CPT1A, CREB1, AKR1C2, DNMT3A, EDN1, EGFR, EGR1, GNB1, HDAC2, HNRNPD, IPO5, LDLR, LYN, MYB, NTRK3, OPA1, PAX2, PDGFB, PDGFRA, PDK3, PDK4, PRKAA1, PRKCE, PTAFR, PTGER4, RARG, RORB, SFRP1, SRC, ZEB1, VEGFA, WNT7B, XBP1, XRCC5, FZD4, AKR1C3, SOCS1, ALDH1A2, KLF4, KLF2, CPEB3, NSMF, HTRA2, BCL11A, CYP26B1, RRAGD, RRAGC, CPEB4, SESN2, SESN3, UBR1
BP	GO:0044262	cellular carbohydrate metabolic process	82/3408	1.67E-04	ADCYAP1R1, AKT2, CALM1, SCARB2, EP300, EXTL2, EXTL3, FOXO1, GAA, KAT2A, GSK3B, GYS1, HAS3, HK1, HK2, NDST1, IDH2, IGF2, IL6ST, FOXK2, IMPA2, INSR, ITPK1, MECP2, P2RY1, PDK3, PDK4, ENPP1, PFKFB2, PFKFB3, PFKFB4, PGAM1, PHKA1, PHKG2, PPARA, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PRKCE, PTAFR, PTEN, PYGB, RANBP2, RORA, SLC5A3, SNCA, SRC, STAT3, TP53, UGP2, DYRK2, IRS2, KAT2B, PER2, SYNJ1, SYNJ2, MTMR7, NDST3, HS2ST1, EPM2AIP1, GNE, NCOA2, ARPP19, PASK, PPIP5K2, SIRT1, MYOF, ADIPOR1, DDIT4, CSGALNACT2, CSGALNACT1, INPP5E, GNPTAB, SESN2, STK40, B3GNT5, SOGA1, SIK1, FOXK1, GK5
BP	GO:1990138	neuron projection extension	54/3408	1.70E-04	ABL1, ALCAM, BMPR2, CTNNB1, MEGF8, FN1, GDI1, GOLGA4, GSK3B, ILK, ITGB1, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, SH3GL2, SRF, AURKA, SYT1, TIAM1, VCL, VEGFA, USP9X, ULK1, SEMA7A, IQGAP1, NRP1, WASF1, DCLK1, NTN1, SEMA3E, SEMA3A, OLFM1, SLC9A6, SEMA4B, POSTN, RAB21, SIN3A, AUTS2, CYFIP2, SYT17, BCL11A, SEMA4C, SMURF1, SEMA6A, RAPH1, MUL1, PLXNA4, SYT2, WDR36, TTL
BP	GO:0007611	learning or memory	75/3408	1.71E-04	ADCY1, AMFR, BDNF, CAMK4, CASP3, CEBPB, COMT, CREB1, CTNS, EGFR, EP300, EPHB2, CLN8, GATM, KAT2A, GM2A, HTT, HIF1A, HMGCR, INSR, ITGA3, ITGA5, ITGB1, JUN, KIT, KRAS, LDLR, MAP1A, MAPT, MDK, MECP2, MEF2C, MEIS2, MME, SLC11A2, PAFAH1B1, PDE1B, MAPK1, PTEN, RAG1, ATXN1, SNAP25, SRF, THRA, VLDLR, BTG2, FOSL1, ITGA8, B4GALT2, SYNGAP1, SYNJ1, KALRN, KMT2B, ACTR2, ATP8A1, PLK2, CPEB3, SHANK2, DKK1, CIC, NCSTN, SLC7A11, SLC24A2, ZNF385A, CNTNAP2, NPTN, TMOD2, YTHDF1, UBA6, SLC12A5, RIC8A, NDRG4, BHLHB9, BTBD9, ATXN1L
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	75/3408	1.71E-04	ABL1, ARRB2, BDNF, CAV1, CBL, CD44, CNTN1, DLG3, DOCK3, HBEGF, EFNA5, EGFR, EPHA4, EPHA7, ERCC6, FGFR3, HDAC2, NRG1, HES1, IGF2, IL6R, IL6ST, IL18, ISL1, ITGA5, KIT, LYN, KITLG, NEDD9, NF2, PAK2, PDGFA, PDGFB, PPP2CA, PPP2R1A, PRKCE, PTPN1, PTPN11, PTPRC, PTPRJ, RAP2B, SFRP1, SHC1, SRC, STAT3, SYK, ADAM17, TAL1, TGFA, TP53, VEGFA, NCK2,

					SOCS1, IQGAP1, NRP1, GPRC5A, ARHGEF2, SOCS5, SH2B3, TNK2, IL24, ARL2BP, IBTK, GREM1, EHD4, ERRFI1, PARP14, NCAPG2, FBXW7, RAP2C, SH3BP5L, AFAP1L2, SOCS4, RICTOR, EPGN
BP	GO:0030901	midbrain development	34/3408	1.72E-04	ACTB, RHOA, CALM1, CALM2, CALM3, CDC42, CSNK1D, CSNK1E, CTNNB1, G6PD, KAT2A, HES1, HSPA5, LRP6, MBP, MSX1, OTX1, RAD1, SFRP1, SOS1, TAF1, YWHAE, ZNF148, FZD3, FZD1, FZD6, DYNLL1, SYNGR3, DLG5, DKK1, NDRG2, GNB4, MAPKAP1, ZNF430
BP	GO:0031058	positive regulation of histone modification	34/3408	1.72E-04	ARRB1, ATM, BCL6, BRCA1, CTNNB1, DNMT3B, FMR1, GATA3, KAT2A, ISL1, JARID2, SMAD4, MECP2, KMT2A, MYB, MAPK3, SNAI2, TP53, UBE2N, VEGFA, RPS6KA4, RPS6KA5, CTR9, KAT7, MTF2, KDM1A, SIRT1, WBP2, NIPBL, AUTS2, RIF1, KMT2E, TET1, TADA2B
BP	GO:0001890	placenta development	50/3408	1.73E-04	ADA, ADM, PRDM1, BMP7, BMPR2, ZFP36L1, CCNF, CDKN1B, CEBPB, MAPK14, CTSB, DCN, EGFR, EPAS1, BPTF, GATA2, GJA1, GRB2, HIF1A, HES1, IGF2, RBPJ, ITGB8, MAP3K4, MEN1, MME, PDGFB, PKD1, PPARD, MAPK1, MAPK3, PTGIS, SNAI1, SP3, STC1, STK4, NR2F2, VDR, WNT7B, FZD5, FOSL1, ARID1A, STC2, HAND1, PRDX3, VASH1, DAZAP1, BIRC6, PLCD3, E2F7
BP	GO:0035904	aorta development	25/3408	1.77E-04	JAG1, PRDM1, BMPR1A, COL3A1, EFNB2, HES1, RBPJ, LRP1, LTBP1, SMAD6, MYH10, NKX3-1, PROX1, ROBO1, SOX4, SRF, SNX17, TAB1, PLXND1, HECTD1, SUFU, DLL4, CHD7, ADAMTS9, DCTN5
BP	GO:0007219	Notch signaling pathway	60/3408	1.78E-04	ADAM10, JAG1, ARRB1, BCL6, BMP7, CDH6, CDK6, CDKN1B, CNTN1, CREBBP, DLX2, S1PR3, EGFR, EP300, FOXC1, GATA2, FOXA1, HES1, RBPJ, IL6ST, JAG2, KIT, MDK, MMP14, MYC, NOTCH2, PBX1, ROBO1, SEL1L, SNAI2, SNAI1, STAT1, STAT3, ADAM17, HNF1B, SORBS2, TP63, KAT2B, POSTN, AAK1, SPEN, PLXND1, WWC1, NCSTN, POFUT1, HEYL, APH1A, EGFL7, YTHDF2, NEURL1B, DLL4, FBXW7, HIF1AN, ZMIZ1, MIB1, APH1B, ITCH, DTX2, MIB2, NRARP
BP	GO:0090114	COPII-coated vesicle budding	29/3408	1.78E-04	CD59, CSNK1D, CTSZ, INSIG1, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, NAPA, VAPB, VAPA, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, ANKRD28, SEC31B, TRAPPC4, TRAPPC2L, PPP6R3, SAR1A, GORASP1, TBC1D20, MIA3
BP	GO:1902036	regulation of hematopoietic stem cell differentiation	29/3408	1.78E-04	ABL1, RUNX1, CBFB, CDK6, FOXC1, GATA2, GATA3, LMO2, KMT2A, MYB, EIF2AK2, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, TAL1, TCF3, LDB1, PSMF1, SETD1A, PSME3, PSMD14, PSME4, YTHDF2, PUS7, ITCH
BP	GO:0043200	response to amino acid	40/3408	1.84E-04	ALAD, RHOA, ATP7A, BCL2L1, CAPN2, CASP3, CDKN1B, CEBPB, CFL1, COL1A1, COL1A2, COL3A1, COL4A1, COL5A2, CREB1, DNMT3A, EDN1, EGFR, HNRNPD, IPO5, LYN, MTHFR, OPA1, PDGFRA, SLC1A2, ZEB1, TMBIM6, XBP1, SOCS1, TOMM20, CPEB3, UFL1, NSMF, BCL11A, RRAGD, RRAGC, CPEB4, SESN2, SESN3, UBR1
BP	GO:1903708	positive regulation of hemopoiesis	58/3408	1.85E-04	ACVR1B, ADA, JAG1, RHOA, AXL, BCL6, ZFP36L1, RUNX1, RUNX3, CBFB, CREB1, MAPK14, CSF1, CYLD, EGR3, FOXC1, FOXO3, GATA2, GATA3, GNAS, NCKAP1L, HIF1A, HOXA5, IL7R, IL18, ITPKB, JUN, MDK, KITLG, MMP14, MYB, POU4F1, PRKCA, PTPRC, RAG1, RB1, STAT1, STAT3, STAT5B, SYK, TAL1, KLF10, XBP1, SOCS1, TNFSF9, FADD, AP3D1, CD83, SOCS5, TRIB1, BTN2A2, DUSP10, PCID2, ZMIZ1, FAM210B, ZBTB46, ATP11C, ATXN1L
BP	GO:0043523	regulation of neuron apoptotic process	64/3408	1.85E-04	RHOA, ARRB1, ARRB2, ATM, AXL, BCL2, BCL2L1, BDNF, CASP3, CDC34, CEBPB, ATF2, CTNNB1, CTSZ, EPHA7, FOXO3, G6PD, GATA3, HIF1A, ILK, ISL1, JUN, KRAS, LIG4, LRP1, MCL1, MDK, MECP2, MEF2C, MYB, MYBL2, PAK3, PIN1, POU4F1, RASA1, CX3CL1, MAP2K4, SET, SNCA, SOD2, TERT, TP53, TYRO3, BTG2, NR4A3, NRP1, SYNGAP1, BCL2L11, SIGMAR1, LANCL1, HYOU1, STAMBP, TRIM2, NSMF, HIPK2, SIX4, OXR1, FBXW7, CPEB4, DNAJC5, BHLHB9, AKT1S1, EGLN2, EGLN3
BP	GO:0050673	epithelial cell proliferation	115/3408	1.89E-04	AR, ATP7A, CCND1, BMPR1A, BMPR2, ZFP36L1, KLF9, CAV1, RUNX3, CDK6, CDKN1B, CEBPB, ATF2, CTNNB1, DLX6, EFNB2, EGFR, EGR3, ERBB2, FGF1, FGF2, FLT4, GATA2, GATA3, GJA1, HIF1A, HOXA5, HES1, IGFBP5, ISL1, JUN, KIT, LAMC1, LOXL2, MDK, MEF2C, MEN1, MMP14, MYC, NFIB, NKX3-1, NOTCH2, NRAS, PAX2, PAX6, PDGFB, PGR, PIK3CB, PPARD, PRKCA, MAPK1, PROX1, PTCH1, PTEN, PTPRK, PURA, RB1, ROBO1, RREB1, SFRP1, SNAI2, SOX11, SPARC, STAT1, STAT3, ADAM17, HNF1B, TCF7L2, NR2F2, TGFA, TGFBR1, TGFBR3, THBS1, TWIST1, VDR, VEGFA, XBP1, ZFP36, NR4A3, TP63, NRP1, ALDH1A2, BTRC, AIMP1, AKT3, KDM5B, FRS2, DUSP10, VASH1, NCSTN, SIRT1, PPP1R16B, EHF, EGFL7, SIX4, ERRFI1, DLL4, IFT57, AGGF1, FBXW7, LGR4, FERMT1, SULF2, PBLD, BCL11B, WDR77, CDC73, IQGAP3, CD109, DAB2IP, BMPER, RICTOR, EPGN, EMC10, NRARP
BP	GO:0048880	sensory system development	101/3408	1.89E-04	ACVR2B, JAG1, ATP2B1, ATP2B4, BAK1, BCL2, PRDM1, BMP7, BMPR2, CACNA1C, CDKN1B, COL4A1, COL5A1, COL5A2, CTNS, CTNNB1, DLX2, EGFR, EPHB2, CLN8, FAT1, FBN1, FBN2, FOXC1, GATA3, GJA1, GNB1, ARHGAP35, HDAC2, HIF1A, ISL1, JUN, LRP6, MAN2A1, MAX, MEIS2, MYH10, NF2, NHS, NTRK3, OPA1, PAX2, PAX6, PDGFRA, PKNOX1, POU4F1, PROX1, RARG, RORB, SALL2, SKI, SKIL, SOS1, SOX11, SP3, SRF, STAT3, ZEB1, TGFBR1, TUB, TWIST1, VEGFA, WNT7B, WNT2B, YY1, FZD5, ARID1A, FZD4, BCAR3, NRP1, ALDH1A2, KLF4, MFN2, ABI2, GDF11, SEMA3A, KDM5B, FRS2, PDS5B, SLC7A11, NIPBL, HIPK2, SOX8, CDON, DLL4, AHI1, CHD7, TENM3, MDM1, TGIF2, SMOC1, BCL11B, LPCAT1, RAB11FIP4, TBC1D20, RDH10, ADAMTS18, HIPK1, SDK1, SH3PXD2B, FREM2
BP	GO:0060491	regulation of cell projection assembly	56/3408	1.91E-04	APC, ARF6, ATP7A, CAV1, CDC42, CCR7, CYLD, EPS8, FER, FMR1, ARHGAP35, HTT, KIT, MAP4, MYO10, ATP8B1, PLD1, PODXL, TWF1, RAB5A, RDX, SRC, SRF, TGFBR1, TRPM2, CDK10, DYNLL1, NRP1, WASL, ATG5, CEP135, PLEKHM1, ARPC2, WASF2, TENM1, CDC42EP2, NCKAP1, NLGN1, KANK1, ATMIN, RHOQ, CORO1C, FAM98A, PPP1R16B, AUTS2, DYNC2LI1, ANLN, FNBP1L, RCC2, RAB17, CEP97, AKIRIN1, KCTD17, CEP120, AGRN, FAM110C
BP	GO:0043153	entrainment of circadian clock by photoperiod	13/3408	1.91E-04	CRY2, PML, PPP1CA, PPP1CB, PPP1CC, TP53, BHLHE40, PER3, PER2, USP2, MTA1, FBXL3, SIK1

BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	42/3408	1.93E-04	CEBPB, CHEK1, CREBBP, ATF6B, EGR1, EP300, EPAS1, HIF1A, HSPA5, RBPJ, JUN, NCK1, NEDD4, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RBL2, TAF1, TMBIM6, TP53, VEGFA, VHL, NCK2, CUL2, LIMD1, PSMF1, PSME3, PSMD14, KLF2, CITED2, PSME4, SIN3A, INO80, HIF1AN, SESN2, CHD6, EGLN2, EGLN3
BP	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	21/3408	1.95E-04	BCL2, CD44, CDKN1A, EP300, HNRNPK, PML, TP53, DYRK2, TP63, KDM1A, SIRT1, PHLDA3, ZNF385A, HIPK2, CDIP1, TRIAP1, TAF9B, DDIT4, USP28, AEN, HIPK1
BP	GO:0018022	peptidyl-lysine methylation	44/3408	2.00E-04	ATRX, BRCA1, CTNNB1, DNMT3B, EZH1, EZH2, GATA3, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MYB, SUV39H1, KDM6A, PRDM2, KMT2D, CTR9, SETD1A, KMT2B, MTF2, KDM1A, SIRT1, SUZ12, AUTS2, ARID4B, WDR5B, TET2, BCOR, RIF1, SETD5, KMT2E, BEND3, KMT2C, NSD1, VCPKMT, CAMKMT, SETD7, SETDB2, SETD3, DPY30, METTL21A, TET3
BP	GO:0006900	vesicle budding from membrane	37/3408	2.01E-04	ARF1, CD59, AP2M1, CSNK1D, CTSZ, INSIG1, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, SNX3, NAPA, AP3D1, WASL, VAPB, VAPA, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, ANKRD28, SEC31B, TRAPPC4, TRAPPC2L, FNBP1L, GOLPH3L, PPP6R3, SAR1A, GORASP1, TBC1D20, MIA3, MYO18A
BP	GO:0030509	BMP signaling pathway	51/3408	2.01E-04	ABL1, ACVR2B, BMP7, BMPR1A, BMPR2, RUNX2, DDX5, MEGF8, EGR1, FBN1, HIVEP1, HES1, RBPJ, ILK, ITGA3, SMAD2, SMAD4, SMAD6, SMAD7, MSX1, NEO1, PCSK6, MAPK3, SFRP1, SKI, SKIL, SORL1, SOX11, TGFBR3, UBE2D3, ZNF8, USP9X, FZD1, CHRD, ZFYVE16, TOB1, FSTL3, FST, FSTL1, DKK1, GREM1, PDCD4, HIPK2, TRIM33, RGMA, SMURF1, BMPER, CRB2, RBPMS2, BMP8A, RNF165
BP	GO:0061572	actin filament bundle organization	51/3408	2.01E-04	ABL1, ACTN4, ADD1, RHOA, RHOB, ARRB1, CD47, CDC42, S1PR1, EPS8, LIMK1, MARCKS, MET, MYO1B, NEDD9, NF2, PAWR, PLS3, PTGER4, PXN, RDX, CX3CL1, SDC4, SFRP1, SLC9A1, SRC, SRF, TESK1, TGFBR1, TNFAIP1, TSC1, RND2, CUL3, NRP1, ROCK2, BAG4, WASF2, DLC1, RAPGEF3, FAM107A, LIMCH1, CLASP1, WNT4, FMN2, SPIRE1, ARHGAP28, SYNPO2L, FHDC1, PHLDB2, SHROOM1, SH3PXD2B
BP	GO:2000058	regulation of ubiquitin-dependent protein catabolic process	49/3408	2.03E-04	CAV1, CSNK1D, CSNK1E, DAB2, FHIT, GSK3B, UBE2K, DNAJB2, SMAD7, MAP1A, PML, MAPK9, PTEN, RAD23B, AURKA, STYX, TAF1, VCP, LATS1, SOCS5, HERPUD1, RNF144A, BCAP31, TRIB1, ARIH2, PLK2, TLK2, UFL1, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, HIPK2, UBQLN2, UBQLN1, WAC, UCHL5, SUFU, ANKIB1, FBXW7, UBQLN4, SMURF1, DDA1, FAM122A, SOCS4, RNF217, RNF144B, RNF180
BP	GO:0000077	DNA damage checkpoint	48/3408	2.03E-04	ATM, ATR, CCND1, BRCA1, CDC5L, CDKN1A, CDKN1B, CHEK1, FOXN3, ATF2, MAPK14, EP300, MDM4, FOXO4, CNOT4, PML, PTPN11, RAD1, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, HMGA2, CDC14B, PEA15, CNOT8, TAOK2, CLOCK, PLK2, CNOT1, ZNF385A, HINFP, GIGYF2, WAC, TRIAP1, DTL, ETAA1, CNOT6, TAOK1, USP28, BRCC3, WDR76, RHNO1, ZNF830, E2F7
BP	GO:0032388	positive regulation of intracellular transport	65/3408	2.05E-04	ADORA2B, AKT2, ARF1, MAPK14, DAB2, ECT2, STOM, ERBB2, GATA2, GSK3B, JUP, KIF5B, IPO5, MYO1C, NEDD4, OAZ2, PRKAA1, MAPK1, RAN, RDX, SCP2, SORL1, SREBF2, VAMP2, VAMP7, SYK, SYT1, TCF7L2, TP53, UBE2D3, UBE2L3, YWHAE, FZD5, BAP1, EDEM1, ATG13, C2CD5, BCAP31, TENM1, NUTF2, RAPGEF3, ARIH2, UNC13B, ANP32B, CPSF6, NLGN1, RAB21, TARDBP, LDLRAP1, HTRA2, SH3GLB1, UBR5, RBM27, MIEF1, LEPROT, FBXW7, RIOK2, SAR1A, MFF, MAVS, USP36, RHOU, XPO4, MIEF2, TBC1D20
BP	GO:0030510	regulation of BMP signaling pathway	34/3408	2.13E-04	ABL1, BMPR2, FBN1, HES1, RBPJ, ILK, ITGA3, SMAD2, SMAD4, SMAD6, SMAD7, MSX1, NEO1, PCSK6, SFRP1, SKI, SKIL, SORL1, SOX11, FZD1, CHRD, TOB1, FSTL3, FST, FSTL1, DKK1, GREM1, HIPK2, TRIM33, SMURF1, BMPER, CRB2, RBPMS2, RNF165
BP	GO:0048194	Golgi vesicle budding	31/3408	2.16E-04	CD59, CSNK1D, CTSZ, INSIG1, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, NAPA, VAPB, VAPA, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, ANKRD28, SEC31B, TRAPPC4, TRAPPC2L, GOLPH3L, PPP6R3, SAR1A, GORASP1, TBC1D20, MIA3, MYO18A
BP	GO:0002064	epithelial cell development	63/3408	2.17E-04	ADD1, JAG1, AR, ATRX, PRDM1, CDK6, CDKN1A, CTNNB1, S1PR3, FAT1, FLNB, FOSL2, GJA1, RAPGEF1, GSK3B, GSTM3, HIF1A, FOXA1, HNF4A, HOXA5, IKBKB, MET, PAFAH1B1, PAX6, PDE4D, PDGFB, PGR, PODXL, PROX1, RAP1B, RARG, RDX, RFX3, STC1, VEGFA, WNT7B, XBP1, VEZF1, TP63, IQGAP1, TJP2, ROCK2, ONECUT2, SLC4A7, CLOCK, RAPGEF2, ABI2, RAPGEF3, FRS2, FNDC3A, PALLD, PPP1R16B, SOX8, ARID4B, C1GALT1, HEG1, SHROOM3, EPB41L5, RAP2C, BCL11B, MYADM, TBC1D20, RILPL1
BP	GO:1990089	response to nerve growth factor	23/3408	2.23E-04	ARF6, BDNF, CBL, CDC5L, CREB1, CRK, FOXO3, KAT2A, RAPGEF1, HSPA5, KCNC1, MAPT, NTRK3, PTEN, RPS3, SORT1, SH3GL2, WASF1, RAPGEF2, KIF1B, ACAP2, KIDINS220, MICALL1
BP	GO:0051146	striated muscle cell differentiation	83/3408	2.23E-04	ARRB2, BCL2, BCL9, BDNF, CALR, CAPN2, CASP3, CFL2, MAPK14, CSRP1, CXADR, EDN1, EFNB2, EZH2, G6PD, GATA6, KAT2A, NRG1, HNRNPU, IGF2, IGFBP5, RBPJ, ITGB1, KRAS, SMAD4, MEF2A, MEF2C, MMP14, MSX1, MYH9, MYH10, PDGFRA, PIN1, PPARA, PPP3CA, PRKAR1A, PROX1, PTGFRN, RB1, RGS2, RGS4, SORT1, MAP2K4, SGCD, SKI, SLC8A1, SLC9A1, SRF, TBX3, TSC1, VEGFA, XBP1, YY1, ADAM12, ARID1A, SORBS2, SPAG9, DYRK1B, AKAP6, ATG5, MORF4L2, HDAC9, NEBL, PDLIM5, FRS2, AKAP13, DKK1, KDM6B, FBXO22, MYOF, GREM1, TMOD2, MYEF2, CDON, SIX4, RBM38, CYP26B1, ALPK3, PTCD2, SYNPO2L, WFIKKN2, MTPN, SIK1

BP	GO:1901988	negative regulation of cell cycle phase transition	77/3408	2.25E-04	APC, ATM, CCND1, BCL2, BRCA1, ZFP36L1, ZFP36L2, CDK6, CDKN1A, CDKN1B, CHEK1, FOXN3, DUSP1, EP300, EZH2, FHL1, IK, MAD2L1, MDM4, MEN1, FOXO4, CNOT4, PML, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD21, RB1, RBL2, SKP1, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, HMGA2, CDC14B, AURKB, KLF4, TRIP13, CNOT8, TAOK2, PSMF1, CTDSP2, PSME3, PSMD14, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, PSME4, ZNF385A, GIGYF2, TRIAP1, DTL, PINX1, USP47, PCID2, CNOT6, TAOK1, CTDSP1, ZNF655, BRCC3, CDC73, ZNF830, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0110020	regulation of actomyosin structure organization	35/3408	2.25E-04	ABL1, RHOA, CD47, CDC42, ECT2, S1PR1, EDN1, LIMK1, SMAD4, MEF2C, MET, NF2, PROX1, PTGER4, PXN, SDC4, SFRP1, SLC9A1, TESK1, TGFBR1, TSC1, NRP1, ROCK2, BAG4, WASF2, DLC1, RAPGEF3, AKAP13, LIMCH1, CLASP1, WNT4, ARHGAP28, SYNPO2L, PHLDB2, SH3PXD2B
BP	GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	35/3408	2.25E-04	CAV1, CSNK1D, CSNK1E, DAB2, GSK3B, DNAJB2, SMAD7, MAPK9, PTEN, AURKA, TAF1, VCP, SOCS5, HERPUD1, RNF144A, BCAP31, TRIB1, ARIH2, PLK2, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, UBQLN2, UBQLN1, ANKIB1, FBXW7, SMURF1, DDA1, FAM122A, SOCS4, RNF217, RNF144B, RNF180
BP	GO:0010761	fibroblast migration	19/3408	2.25E-04	FER, FGF2, ILK, PAK3, PML, PRKCE, SDC4, SLC8A1, THBS1, TNS1, SGPL1, BAG4, AKAP12, CORO1C, APPL1, RCC2, ARID5B, RFFL, TMEM201
BP	GO:0071772	response to BMP	54/3408	2.26E-04	ABL1, ACVR2B, BMP7, BMPR1A, BMPR2, RUNX2, DDX5, MEGF8, EGR1, FBN1, GATA3, GATA6, HIVEP1, HES1, RBPJ, ILK, ITGA3, SMAD2, SMAD4, SMAD6, SMAD7, MSX1, NEO1, PCSK6, MAPK3, SFRP1, SKI, SKIL, SORL1, SOX11, TGFBR3, UBE2D3, ZNF8, USP9X, FZD1, CHRD, ZFYVE16, TOB1, FSTL3, FST, FSTL1, DKK1, HEYL, GREM1, PDCD4, HIPK2, TRIM33, RGMA, SMURF1, BMPER, CRB2, RBPMS2, BMP8A, RNF165
BP	GO:0071773	cellular response to BMP stimulus	54/3408	2.26E-04	ABL1, ACVR2B, BMP7, BMPR1A, BMPR2, RUNX2, DDX5, MEGF8, EGR1, FBN1, GATA3, GATA6, HIVEP1, HES1, RBPJ, ILK, ITGA3, SMAD2, SMAD4, SMAD6, SMAD7, MSX1, NEO1, PCSK6, MAPK3, SFRP1, SKI, SKIL, SORL1, SOX11, TGFBR3, UBE2D3, ZNF8, USP9X, FZD1, CHRD, ZFYVE16, TOB1, FSTL3, FST, FSTL1, DKK1, HEYL, GREM1, PDCD4, HIPK2, TRIM33, RGMA, SMURF1, BMPER, CRB2, RBPMS2, BMP8A, RNF165
BP	GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	42/3408	2.30E-04	CAV1, CSNK1D, CSNK1E, DAB2, FHIT, GSK3B, UBE2K, DNAJB2, SMAD7, MAP1A, MAPK9, RAD23B, AURKA, STYX, TAF1, VCP, SOCS5, HERPUD1, RNF144A, BCAP31, TRIB1, ARIH2, PLK2, TLK2, UFL1, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, UBQLN2, UBQLN1, WAC, UCHL5, ANKIB1, UBQLN4, DDA1, FAM122A, SOCS4, RNF217, RNF144B, RNF180
BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	42/3408	2.30E-04	CAV1, CREBBP, DAB2, EP300, FBN1, FBN2, HSPA5, ITGA3, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MEN1, PIN1, SKI, SKIL, SOX11, ADAM17, ZEB1, TGFBR1, TGFBR3, THBS1, TP53, ITGA8, MTMR4, ONECUT2, CITED2, PEG10, SIRT1, ZNF451, DKK3, HIPK2, TRIM33, RNF111, FERMT1, PMEPA1, SMURF1, PBLD, WFIKKN2, CD109, FLCN
BP	GO:0018107	peptidyl-threonine phosphorylation	43/3408	2.33E-04	ACVR1B, BCL2, BMP7, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, CHEK1, CSNK1D, CSNK1E, CSNK1G3, DYRK1A, EIF4G1, MARK2, GSK3B, UBE2K, SMAD7, PPP2R5D, PRKCA, MAPK1, MAPK8, TAF1, TGFBR1, ULK1, DYRK2, CDK10, TNKS, DYRK1B, ROCK2, HIPK3, CIT, LMTK2, HIPK2, NLK, DDIT4, PARD3, WNK1, TTBK2, SPRED1, SPRED2, HIPK1, SPRED3
BP	GO:0003231	cardiac ventricle development	44/3408	2.36E-04	JAG1, PRDM1, BMPR1A, BMPR2, COL11A1, FKBP1A, FOXC1, GATA3, NRG1, HIF1A, HES1, RBPJ, ISL1, LTBP1, SMAD4, SMAD6, SMAD7, MDM4, MEF2C, POU4F1, PROX1, ROBO1, SOX4, SOX11, TBX3, TGFBR1, TGFBR3, LUZP1, FZD1, TRIP11, HAND1, UBE4B, CITED2, FRS2, HECTD1, HEYL, SUFU, DLL4, CHD7, VANGL2, HEG1, PTCD2, DCTN5, TMEM65
BP	GO:0018210	peptidyl-threonine modification	45/3408	2.36E-04	ACVR1B, BCL2, BMP7, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, CHEK1, CSNK1D, CSNK1E, CSNK1G3, DYRK1A, EIF4G1, MARK2, GALNT1, GALNT2, GSK3B, UBE2K, SMAD7, PPP2R5D, PRKCA, MAPK1, MAPK8, TAF1, TGFBR1, ULK1, DYRK2, CDK10, TNKS, DYRK1B, ROCK2, HIPK3, CIT, LMTK2, HIPK2, NLK, DDIT4, PARD3, WNK1, TTBK2, SPRED1, SPRED2, HIPK1, SPRED3
BP	GO:0009649	entrainment of circadian clock	15/3408	2.36E-04	CRY2, GNAQ, PML, PPP1CA, PPP1CB, PPP1CC, TP53, BHLHE40, PER3, PER2, USP2, MTA1, PHLPP1, FBXL3, SIK1
BP	GO:0060384	innervation	15/3408	2.36E-04	ADARB1, ISL1, NPTX1, SERPINE2, POU4F1, VCAM1, NRP1, LRIG2, SEMA3A, UNC13B, LRIG1, CHD7, SULF2, FBXO45, RNF165
BP	GO:0043547	positive regulation of GTPase activity	108/3408	2.37E-04	ADRB1, AKT2, ARHGAP1, ARHGDIA, ARRB1, BNIP2, CCR7, CRK, CRKL, DVL3, ECT2, S1PR1, EIF5, ERBB2, EZH2, GDI1, GNAQ, RAPGEF1, ARHGAP35, GSK3B, NCKAP1L, AGFG2, ITGA6, ITGB1, JUN, NEDD9, NTRK3, TBC1D25, OPHN1, PIN1, RANBP2, RAP1GDS1, RASA1, RGS2, RGS4, RGS16, RP2, CCL7, CX3CL1, SFRP1, SOS1, TIAM1, TSC1, EVI5, RGS5, PKP4, IQGAP1, NRP1, SYNGAP1, KALRN, RABEP1, ARHGAP29, MAP4K4, RASAL2, RAPGEF2, USP6NL, GIT2, TBC1D4, RABGAP1L, NET1, DLC1, RAPGEF3, CDC42EP2, VAV3, SEC23A, NUP50, ADAP1, TBC1D8, RASA3, RAB11FIP2, TBC1D9B, TBC1D2B, RAP1GAP2, SNX13, DOCK9, ARHGEF12, ACAP2, CORO1C, RABGAP1, RAB3GAP2, TBC1D10B, SIPA1L1, GIT1, ASAP1, ERRFI1, WNT4, ARHGAP17, TBC1D22B, DEPDC1, ARFGAP1, RCC2, RALGAPA2, TBC1D24, SIPA1L2, RIC8A, ARHGAP28, PREX2, ARHGAP39, SYDE2, ARHGAP18, ARHGAP12, ARAP2, AGAP1, TBC1D20, STXBP5, DAB2IP, FLCN, AGRN

BP	GO:0045930	negative regulation of mitotic cell cycle	93/3408	2.43E-04	ABL1, APC, ATM, ATRX, CCND1, BCL2, BCL2L1, BCL6, BMP7, BRCA1, ZFP36L1, ZFP36L2, BTG1, CDK6, CDKN1A, CDKN1B, CHEK1, FOXN3, ATF2, CTNNB1, DUSP1, EGFR, EP300, EZH2, FHL1, FOXC1, IK, MAD2L1, MDM4, FOXO4, NKX3-1, CNOT4, PML, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD21, RB1, RBL2, SKP1, SOX4, AURKA, TFDP1, TFDP2, TIMP2, TOP2B, TP53, BTG2, FZD3, HMGA2, CDC14B, TNKS, AURKB, KLF4, TRIP13, CNOT8, TAOK2, PSMF1, CTDSP2, PSME3, PSMD14, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, PSME4, ZNF385A, GIGYF2, TRIAP1, PINX1, USP47, PCID2, CNOT6, TAOK1, CTDSP1, DCLRE1B, NABP1, INTS3, ZNF655, NABP2, CDC73, ZNF830, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0035601	protein deacylation	37/3408	2.43E-04	BCL6, CAMK2D, DYRK1A, ELK4, EP300, FNTA, HDAC2, MAPT, PRKAA1, MAPK8, KDM5A, SKI, TBL1X, TP53, VEGFA, PER2, MTA1, MORF4L2, HDAC9, FRY, LYPLA1, LYPLA2, RCOR1, SIRT1, NIPBL, SIN3A, ABHD17B, SMARCAD1, MIER1, ABHD17C, TBL1XR1, BRMS1L, LYPLAL1, NACC2, SPRED1, SPRED2, SPRED3
BP	GO:1990090	cellular response to nerve growth factor stimulus	22/3408	2.44E-04	ARF6, BDNF, CBL, CDC5L, CREB1, CRK, FOXO3, KAT2A, RAPGEF1, HSPA5, MAPT, NTRK3, PTEN, RPS3, SORT1, SH3GL2, WASF1, RAPGEF2, KIF1B, ACAP2, KIDINS220, MICALL1
BP	GO:0009100	glycoprotein metabolic process	111/3408	2.46E-04	AMFR, ASGR1, ATP7A, BCL2, BMPR2, CCR7, COL11A1, NCAN, CTNNB1, DCN, HBEGF, EXTL2, EXTL3, FUT8, GALNT1, GALNT2, GCNT2, GFPT1, HIF1A, NDST1, IDS, MAN2A1, MPI, NPC1, PCSK6, PAWR, PGM3, PMM2, PPARD, PRKCSH, RAB1A, SEL1L, ST3GAL1, SOAT1, TCF7L2, UBE2G2, UGDH, VCP, RNF103, ST8SIA4, B4GALT2, TRIP11, B4GALT6, NDST3, ITM2B, HS2ST1, EDEM1, SPOCK2, FAM20B, GFPT2, HS3ST3A1, HS3ST1, UST, TRIM13, TNIP1, ST3GAL6, HPSE, MAN1A2, GALNT6, PHLDA1, TRAK1, GANAB, NCSTN, POFUT1, BACE2, GLCE, SERP1, ST6GALNAC6, DERL2, ST8SIA3, CHST15, UBE2J1, GALNT7, TET2, CSGALNACT2, GALNT10, POMGNT1, CSGALNACT1, TMEM165, SULF2, ALG1, CHST7, UGGT1, C1GALT1, ADAMTS9, VANGL2, XYLT2, GORASP1, TRAK2, FKRP, GNPTAB, SRD5A3, EDEM3, TET1, ITM2C, CHST9, COG3, B3GNT5, SYVN1, ST6GAL2, FUT10, POMGNT2, HS6ST2, NUS1, CANT1, TET3, HS6ST3, GXYLT1, EOGT, DPY19L4, ACER2
BP	GO:0006479	protein methylation	56/3408	2.52E-04	ATRX, BRCA1, BTG1, CTNNB1, DNMT3B, ETF1, EZH1, EZH2, GATA3, GSPT1, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MTHFR, MYB, RAB3B, SATB1, SUV39H1, KDM6A, PRDM2, BTG2, KMT2D, CTR9, SETD1A, KMT2B, CTCF, MTF2, KDM1A, SIRT1, SUZ12, FAM98A, AUTS2, ARID4B, WDR5B, TET2, BCOR, RIF1, SETD5, KMT2E, BEND3, KMT2C, NSD1, VCPKMT, CAMKMT, TET1, SETD7, SETDB2, SETD3, DPY30, PCMTD1, METTL21A, TET3, FAM98B
BP	GO:0008213	protein alkylation	56/3408	2.52E-04	ATRX, BRCA1, BTG1, CTNNB1, DNMT3B, ETF1, EZH1, EZH2, GATA3, GSPT1, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MTHFR, MYB, RAB3B, SATB1, SUV39H1, KDM6A, PRDM2, BTG2, KMT2D, CTR9, SETD1A, KMT2B, CTCF, MTF2, KDM1A, SIRT1, SUZ12, FAM98A, AUTS2, ARID4B, WDR5B, TET2, BCOR, RIF1, SETD5, KMT2E, BEND3, KMT2C, NSD1, VCPKMT, CAMKMT, TET1, SETD7, SETDB2, SETD3, DPY30, PCMTD1, METTL21A, TET3, FAM98B
BP	GO:0006417	regulation of translation	112/3408	2.57E-04	AKT2, RHOA, ZFP36L1, ZFP36L2, CALR, DAPK1, DDX3X, DPH1, EIF2S1, EIF2S3, EIF4B, EIF4E, EIF4G1, EIF4G2, EIF5, ELAVL1, ERBB2, ETF1, FOXO3, FMR1, GAPDH, MKNK2, HNRNPD, IGFBP5, IREB2, CAPRIN1, NCBP1, NCK1, PA2G4, POLR2D, PPP1CA, MAPK1, MAPK3, EIF2AK2, PTAFR, PURA, UPF1, RGS2, RPS3, RPS6KA3, RPS6KB1, ATXN2, SOX4, STAT3, THBS1, TSC1, ZFP36, CNBP, BTG2, FXR1, NCK2, ENC1, MKNK1, PER2, CNOT8, QKI, ROCK2, EIF5B, PUM1, SECISBP2L, TOB1, EIF1, SYNCRIP, PAIP1, IGF2BP1, IGF2BP3, CPEB3, FASTKD2, CNOT1, SAMD4A, TNRC6B, PASK, LARP4B, LARP1, ZNF385A, LTN1, GIGYF2, LSM14A, AGO1, PABPC1, EIF2AK1, SERP1, TNRC6A, NGRN, YTHDF2, XRN1, PUS7, YTHDF1, PTCD3, SAMD4B, RBM23, EIF5A2, CNOT6, TNRC6C, METTL14, PCIF1, DNAJC1, CPEB4, SESN2, UQCC2, KBTBD8, PPP1R15B, UNK, LARP4, DNAJC24, TRIM71, CPEB2, MTPN, AGO3, AGO4, YTHDF3, DPH3
BP	GO:0043687	post-translational protein modification	98/3408	2.61E-04	ADAM10, CALU, CCNF, CSF1, EPAS1, FBN1, FN1, SERPIND1, HIF1A, IGFBP1, IGFBP5, LAMC1, LTBP1, RAB8A, MEN1, PRKCSH, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAB1A, RAB5A, RABGGTB, RCN1, SDC2, SKP1, VHL, CUL5, PTP4A2, GAN, CUL4B, CUL3, CUL2, STC2, SOCS2, BTRC, RAB11B, SOCS6, COPS2, ATG5, PSMF1, SOCS5, KLHL21, PSME3, PSMD14, DCAF7, FSTL3, CRTAP, ATG7, TGOLN2, COPS8, FSTL1, WDTC1, PSME4, UBXN7, FBXW2, FBXL3, KLHL3, FBXO22, FBXO9, KLHL5, GOLM1, DTL, FBXO40, DCUN1D1, FBXL19, FBXL12, TMEM132A, KLHL11, FBXW7, DCAF6, CAND1, FEM1C, FAM20C, TULP4, KLHL42, ANO8, COPS7B, DDA1, DCAF10, SPSB1, FBXO30, RHBDD1, KBTBD8, KBTBD6, KLHL13, ESCO1, DCUN1D3, ASB6, ASB7, TTL, KCTD7, KCTD6, FLCN, MIA3
BP	GO:0033077	T cell differentiation in thymus	28/3408	2.62E-04	ADA, BCL2, ZFP36L1, ZFP36L2, CAMK4, CDK6, CLPTM1, CCR7, CTNNB1, EGR3, ERBB2, GATA3, IL7R, ITPKB, JAG2, LIG4, PTPRC, RAG1, SOS1, SRF, ADAM17, ZEB1, TP53, FZD5, FADD, ATG5, WNT4, BCL11B
BP	GO:0000086	G2/M transition of mitotic cell cycle	72/3408	2.69E-04	ATM, CCND1, BRCA1, CALM3, CCNA2, CDC25A, CDKN1A, CETN2, FOXN3, CSNK1D, CSNK1E, ENSA, FHL1, FOXM1, HSPA2, MECP2, FOXO4, PPP1R12A, PPP1R12B, PAFAH1B1, PBX1, PPP1CB, PPP2R1A, PPP2R2A, PKIA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAD21, SKP1, AURKA, TPD52L1, YWHAE, YWHAG, HMGA2, PPM1D, DYNLL1, BTRC, LATS1, AURKB, TAOK2, PSMF1, VPS4B, CEP135, MELK, AKAP9, PSME3, PSMD14, TUBB4A, ARPP19, CNTRL, CIT, CEP250, DCTN3, PHLDA1, PSME4, CLASP1, SIN3A, DTL, HAUS6, NDE1, FBXL12, PINX1, USP47, HAUS2, RCC2, TAOK1, ZNF830
BP	GO:0032204	regulation of telomere maintenance	31/3408	2.70E-04	ATM, ATR, ATRX, CCT6A, CTNNB1, DKC1, HNRNPC, HNRNPD, HNRNPU, MAP3K4, MYC, PARN, PML, MAPK1, MAPK3, UPF1, SRC, XRCC5, TNKS, AURKB, SMG7, SMG1, SMG5, RTEL1, XRN1, GNL3L, PINX1, YLPM1, NABP2, HMBOX1, SLX4

BP	GO:1990823	response to leukemia inhibitory factor	35/3408	2.75E-04	BCAT2, CREB1, EPS8, NR5A2, HK2, HNRNPU, JARID2, SMAD7, MAT2A, MYBL2, NEFH, NFYB, PAX6, PIGA, PML, RARG, SRSF7, SRM, TFRC, TLE4, XBP1, XRCC5, TRIM25, FZD4, SYNGR1, KLF4, SPOCK2, GFPT2, KDM5B, MTF2, SIRT1, RIF1, MYNN, GNPNAT1, ARID5B
BP	GO:1990830	cellular response to leukemia inhibitory factor	35/3408	2.75E-04	BCAT2, CREB1, EPS8, NR5A2, HK2, HNRNPU, JARID2, SMAD7, MAT2A, MYBL2, NEFH, NFYB, PAX6, PIGA, PML, RARG, SRSF7, SRM, TFRC, TLE4, XBP1, XRCC5, TRIM25, FZD4, SYNGR1, KLF4, SPOCK2, GFPT2, KDM5B, MTF2, SIRT1, RIF1, MYNN, GNPNAT1, ARID5B
BP	GO:0043620	regulation of DNA-templated transcription in response to stress	43/3408	2.78E-04	CEBPB, CHEK1, CREBBP, ATF6B, EGR1, EP300, EPAS1, HIF1A, HSPA5, RBPJ, JUN, NCK1, NEDD4, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RBL2, RPS6KA3, TAF1, TMBIM6, TP53, VEGFA, VHL, NCK2, CUL2, LIMD1, PSMF1, PSME3, PSMD14, KLF2, CITED2, PSME4, SIN3A, INO80, HIF1AN, SESN2, CHD6, EGLN2, EGLN3
BP	GO:0071236	cellular response to antibiotic	48/3408	2.80E-04	ABL1, ADCY1, ADCY6, RHOB, ATP7A, AXL, CDKN1B, DNMT3A, ECT2, EFNA5, EGR1, EZH2, FOXO1, FOXO3, HDAC2, HSPA5, ITPR2, MEF2C, MET, MYB, PAWR, PAX2, PDGFB, PRKAA1, PRKCE, PTEN, RPS3, CCL7, SLC9A1, SRC, TP53, TRPM2, TXN, NR4A3, KLF4, ACTR2, NET1, SIGMAR1, KLF2, ZNF277, KDM6B, LARP1, SIRT1, OSER1, XRN1, PLEKHA1, TP53INP1, SIRPA
BP	GO:0030879	mammary gland development	47/3408	2.80E-04	AKT2, AR, ATP7A, CCND1, CAV1, CEBPB, CREB1, CSF1, GATA3, GJA1, GOT2, ARHGAP35, NRG1, HIF1A, HK2, HOXA5, HOXA9, IGFBP5, LRP6, MSX1, OAS2, PGR, PML, PPAT, MAPK1, PRLR, PTCH1, ROBO1, RREB1, SRC, TBX3, UMPS, USF2, VDR, VEGFA, WNT7B, XBP1, IRS2, SOCS2, BTRC, KALRN, LATS1, NTN1, BCL2L11, KDM5B, WNT4, IQGAP3
BP	GO:0006405	RNA export from nucleus	45/3408	2.80E-04	EIF4E, NCBP1, NUP88, NUP98, POLR2D, RAN, RANBP2, UPF1, ABCE1, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, PABPN1, POM121, SMG7, NXF1, NUP50, RNPS1, CPSF6, XPOT, DDX19B, U2AF2, SMG1, SMG5, UPF2, RBM15B, NMD3, CDC40, CPSF2, RBM27, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, THOC2, XPO5, SEH1L, NUP43, POM121C
BP	GO:0036503	ERAD pathway	36/3408	2.87E-04	AMFR, CAV1, DNAJB2, HSPA5, DNAJB9, ATXN3, SEL1L, UBE2G2, VCP, TRIM25, RNF103, USP13, UBE4A, EDEM1, HERPUD1, BCAP31, TRIM13, UBE4B, ERLIN2, UBXN4, USP25, UBQLN2, UBQLN1, DERL2, UBE2J1, GET4, DNAJC10, DNAJB12, YOD1, NPLOC4, UGGT1, CCDC47, EDEM3, TMUB1, RHBDD1, SYVN1
BP	GO:0001654	eye development	98/3408	2.87E-04	ACVR2B, JAG1, ATP2B1, ATP2B4, BAK1, BCL2, PRDM1, BMP7, BMPR2, CACNA1C, CDKN1B, COL4A1, COL5A1, COL5A2, CTNS, CTNNB1, DLX2, EGFR, EPHB2, CLN8, FAT1, FBN1, FBN2, FOXC1, GATA3, GJA1, GNB1, ARHGAP35, HDAC2, HIF1A, JUN, LRP6, MAN2A1, MAX, MEIS2, MYH10, NF2, NHS, NTRK3, OPA1, PAX2, PAX6, PDGFRA, PKNOX1, PROX1, RARG, RORB, SALL2, SKI, SKIL, SOS1, SOX11, SP3, SRF, STAT3, ZEB1, TGFBR1, TUB, TWIST1, VEGFA, WNT7B, WNT2B, YY1, FZD5, ARID1A, FZD4, BCAR3, NRP1, ALDH1A2, KLF4, MFN2, ABI2, GDF11, KDM5B, FRS2, PDS5B, SLC7A11, NIPBL, HIPK2, SOX8, CDON, DLL4, AHI1, CHD7, TENM3, MDM1, TGIF2, SMOC1, BCL11B, LPCAT1, RAB11FIP4, TBC1D20, RDH10, ADAMTS18, HIPK1, SDK1, SH3PXD2B, FREM2
BP	GO:1900006	positive regulation of dendrite development	29/3408	2.89E-04	ARF1, BMP7, CUX1, EPHA4, EZH2, FMR1, ILK, CAPRIN1, OPA1, PAFAH1B1, PAK3, MAPK6, PTPRD, VAMP7, TIAM1, VLDLR, IQGAP1, KALRN, DLG5, ACTR2, CPEB3, NLGN1, SHANK2, RAB21, SS18L1, C21orf91, TMEM106B, BHLHB9, DAB2IP
BP	GO:1901796	regulation of signal transduction by p53 class mediator	56/3408	2.91E-04	ATM, ATR, BCL2, BRCA1, PTTG1IP, CD44, CHD3, CHD4, CHEK1, MAPK14, DDX5, DYRK1A, EP300, HDAC2, HNRNPK, MDM4, MSX1, PIN1, PML, POU4F1, PRKAA1, PRKAB2, RAD1, SNAI2, SNAI1, SSRP1, AURKA, TAF1, TAF4B, TP53, TWIST1, KAT6A, DYRK2, TP63, AURKB, NUAK1, SUPT16H, KDM1A, SIRT1, ZNF385A, HIPK2, RRM2B, TRIAP1, TAF9B, RRN3, PAK1IP1, MEAF6, RHNO1, TP53INP1, RMI2, RFFL, JMY, SPRED1, SPRED2, HIPK1, SPRED3
BP	GO:0006892	post-Golgi vesicle-mediated transport	37/3408	2.96E-04	AP1G1, TRIM23, ARF1, CSK, GOLGA4, MYO1B, MYO5A, NSF, RP2, SORT1, SORL1, SPTBN1, VAMP2, VAMP7, AP3D1, RABEP1, SCAMP1, GOSR2, PREPL, SCAMP2, ARFRP1, LYPLA1, ARFGEF2, EXOC5, RAB31, VPS13A, EXOC6B, ANKFY1, VPS54, RAB14, VPS13C, GOLPH3L, KIF13A, C16orf70, PKDCC, EXOC8, STEAP2
BP	GO:0098732	macromolecule deacylation	37/3408	2.96E-04	BCL6, CAMK2D, DYRK1A, ELK4, EP300, FNTA, HDAC2, MAPT, PRKAA1, MAPK8, KDM5A, SKI, TBL1X, TP53, VEGFA, PER2, MTA1, MORF4L2, HDAC9, FRY, LYPLA1, LYPLA2, RCOR1, SIRT1, NIPBL, SIN3A, ABHD17B, SMARCAD1, MIER1, ABHD17C, TBL1XR1, BRMS1L, LYPLAL1, NACC2, SPRED1, SPRED2, SPRED3
BP	GO:0001953	negative regulation of cell-matrix adhesion	20/3408	2.96E-04	JAG1, BCL6, HOXA7, LRP1, MMP14, NF2, SERPINE1, PTEN, RASA1, SRC, THBS1, MAP4K4, SEMA3E, DLC1, POSTN, FAM107A, CORO1C, RCC2, PHLDB2, ACER2
BP	GO:1901991	negative regulation of mitotic cell cycle phase transition	72/3408	3.01E-04	APC, ATM, CCND1, BCL2, BRCA1, ZFP36L1, ZFP36L2, CDK6, CDKN1A, CDKN1B, FOXN3, DUSP1, EP300, EZH2, FHL1, IK, MAD2L1, MDM4, FOXO4, CNOT4, PML, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTEN, RAD21, RB1, RBL2, SKP1, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, HMGA2, AURKB, KLF4, TRIP13, CNOT8, TAOK2, PSMF1, CTDSP2, PSME3, PSMD14, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, PSME4, ZNF385A, GIGYF2, TRIAP1, PINX1, USP47, PCID2, CNOT6, TAOK1, CTDSP1, ZNF655, CDC73, ZNF830, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0097306	cellular response to alcohol	33/3408	3.07E-04	ACACA, ADCY1, ADCY6, ATP2B1, BRCA1, KLF9, CTNNA1, CTNNB1, DAG1, AKR1C2, DNMT3A, EFNA5, FOXO3, GNB1, ITPR2, JUP, LRP6, PRKAA1, PRKCE, PTCH1, PTEN, PTGER4, RAD51, CCL7, SFRP1, AKR1C3, KLF4, KLF2, LARP1, SPIDR, XRN1, GRAMD1B, TP53INP1

BP	GO:0051302	regulation of cell division	53/3408	3.08E-04	RHOA, BCL2L1, CALM1, CALM2, CALM3, CDC42, CETN2, ECT2, FGF1, FGF2, FGF5, IGF2, INCENP, MDK, MYC, NKX3-1, PAX6, PDGFA, PDGFB, PIN1, PRKCE, PKN2, PTCH1, RBL2, AURKA, TAL1, TGFA, UVRAG, VEGFA, NCOA3, CUL3, PKP4, CDC14B, TP63, PRC1, AURKB, KIF3B, KIF23, KLHL21, PLK2, CIT, ZFYVE26, GIT1, SH3GLB1, PRPF40A, BIRC6, KIF13A, PRDM15, RAB11FIP4, KLHL13, E2F7, FLCN, MACC1
BP	GO:0045165	cell fate commitment	77/3408	3.14E-04	JAG1, APC, AR, RHOA, BCL2, PRDM1, BMPR1A, CASP3, RUNX2, CEBPB, CTNNB1, CYLD, DLX2, EPAS1, FGF2, GATA2, GATA3, GATA6, NRG1, FOXA1, HES1, RBPJ, IRF4, ISL1, ITGB1, JAG2, SMAD2, SMAD4, MCL1, MEF2C, NOTCH2, NTRK3, PAX2, PAX6, PML, PRRX1, POU3F2, POU4F1, PROX1, PTCH1, RORA, SFRP1, SOX12, STAT3, TAL1, TBX3, HNF1B, TCF3, TCF7L2, TEAD3, NR2F2, TGFBR1, TP53, WNT7B, WNT2B, NRP1, LATS1, ARHGEF2, KLF4, ONECUT2, CTR9, DKK1, KDM6B, MGA, SATB2, ZNF521, SOX8, CDON, SUFU, WNT4, DLL4, ESRP1, CYP26B1, ISL2, BCL11B, CDC73, SH3PXD2B
BP	GO:0030433	ubiquitin-dependent ERAD pathway	30/3408	3.14E-04	AMFR, CAV1, DNAJB2, HSPA5, DNAJB9, SEL1L, UBE2G2, VCP, TRIM25, RNF103, UBE4A, EDEM1, HERPUD1, BCAP31, TRIM13, UBE4B, ERLIN2, UBXN4, UBQLN2, UBQLN1, DERL2, UBE2J1, DNAJC10, DNAJB12, YOD1, NPLOC4, CCDC47, EDEM3, TMUB1, SYVN1
BP	GO:0021915	neural tube development	51/3408	3.16E-04	ABL1, ADM, BMP7, ZFP36L1, CASP3, CFL1, DVL3, KAT2A, ARHGAP35, HIF1A, FOXA1, HES1, ITPK1, LRP6, MTHFR, PAX2, PAX6, PKD1, PROX1, PTCH1, RARG, SALL2, SDC4, SFRP1, SKI, SOX4, SOX11, STK4, TCF7, TSC1, TWIST1, KDM6A, LUZP1, FZD3, ARID1A, FZD1, FZD6, DCHS1, CHRD, ALDH1A2, ATP6AP2, DLC1, MTHFD1L, SUFU, SEMA4C, IFT57, NUP133, VANGL2, MIB1, SHROOM3, TRIM71
BP	GO:0046661	male sex differentiation	51/3408	3.16E-04	AR, ATRX, CCND1, BCL2, BCL2L1, BMPR1A, CBL, CRKL, CTNNA1, CTNNB1, FKBP4, GATA3, GATA6, GJA1, HOXA9, HOXD13, INSR, KIT, SMAD4, KITLG, MMP14, NKX3-1, PDGFRA, KDM5A, SFRP1, TBX3, TGFBR1, TMF1, WNT2B, SF1, CSDE1, AKR1C3, TNFSF10, SGPL1, BCL2L11, LHFPL2, FSTL3, CITED2, SEMA3A, RHOBTB3, FNDC3A, SOX8, ARID4B, SIX4, WNT4, LGR4, PLEKHA1, ARID5B, TBC1D20, RNF38, AGO4
BP	GO:0022612	gland morphogenesis	41/3408	3.23E-04	AR, BCL2, BMP7, CAV1, CEBPB, CSF1, DAG1, EGFR, FOXA1, HOXD13, ID4, IGFBP5, LRP6, MDK, NFIB, NKX3-1, PAX6, PDGFA, PGR, PML, PROX1, PTCH1, RARG, SFRP1, SNAI2, SRC, TBX3, VDR, XBP1, CUL3, TP63, NRP1, BTRC, NTN1, SEMA3A, KDM5B, FRS2, PLXND1, WNT4, FBXW7, SULF2
BP	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	41/3408	3.23E-04	CAV1, CSNK1D, CSNK1E, DAB2, FMR1, GSK3B, DNAJB2, SMAD7, ATXN3, MAPK9, PSMC2, PTEN, AURKA, TAF1, VCP, USP13, SOCS5, EDEM1, HERPUD1, RNF144A, BCAP31, TRIB1, ARIH2, PLK2, HSPBP1, ARIH1, RNF19A, FBXO22, TRIB2, UBQLN2, UBQLN1, ANKIB1, FBXW7, SMURF1, DDA1, FAM122A, SOCS4, DAB2IP, RNF217, RNF144B, RNF180
BP	GO:0000187	activation of MAPK activity	49/3408	3.23E-04	ADORA2B, ARRB1, CRKL, MAPK14, DUSP5, DUSP6, DUSP7, DUSP9, ERCC6, FGF1, FGF2, NRG1, INSR, IRAK1, IRAK2, KIT, MAP3K9, NTRK3, PAK3, PIK3CB, PRKAA1, MAPK1, MAPK3, PTPN1, PTPN11, PTPRC, MAP2K4, SHC1, SYK, TGFA, THBS1, UBE2N, UBE2V1, WNT7B, MADD, PEA15, SPAG9, TAOK2, NOD1, TAB1, MAP3K2, FRS2, TAB2, MAPK8IP3, TAOK1, MUL1, IQGAP3, DAB2IP, EPGN
BP	GO:0044839	cell cycle G2/M phase transition	76/3408	3.25E-04	ATM, CCND1, BRCA1, CALM3, CCNA2, CDC25A, CDKN1A, CETN2, CHEK1, FOXN3, CSNK1D, CSNK1E, ENSA, FHL1, FOXM1, HSPA2, MECP2, FOXO4, PPP1R12A, PPP1R12B, PAFAH1B1, PBX1, PPP1CB, PPP2R1A, PPP2R2A, PKIA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAD21, SKP1, AURKA, TP53, TPD52L1, YWHAE, YWHAG, HMGA2, PPM1D, CDC14B, DYNLL1, BTRC, LATS1, AURKB, TAOK2, PSMF1, VPS4B, CEP135, MELK, AKAP9, PSME3, PSMD14, TUBB4A, ARPP19, CNTRL, CIT, CEP250, DCTN3, PHLDA1, PSME4, CLASP1, SIN3A, DTL, HAUS6, NDE1, FBXL12, PINX1, USP47, HAUS2, RCC2, TAOK1, BRCC3, ZNF830
BP	GO:0051592	response to calcium ion	48/3408	3.25E-04	ADCY1, ADD1, ANXA7, CCND1, CALM1, CALM2, CALM3, CAMK2D, CAV1, DUSP1, ECT2, EDN1, EGFR, FOSB, FUS, GDI1, HNRNPD, HSPA5, ITPKB, JUN, JUND, MEF2A, MEF2C, NEDD4, PPP3CA, PRKAA1, SPARC, STIM1, SYT1, THBS1, TRPM2, AKR1C3, ADAM9, IQGAP1, CPNE3, SYT7, AHCYL1, NLGN1, SYT11, NCSTN, CLIC4, KCNMB4, SLC25A24, SYT17, WNK1, SYT2, CPNE8, CPNE2
BP	GO:0003158	endothelium development	44/3408	3.29E-04	ACVR2B, ADD1, JAG1, RHOA, RHOB, BMPR2, BTG1, CTNNB1, S1PR1, S1PR3, FGF1, GJA1, RAPGEF1, GSTM3, NRG1, HOXB5, RBPJ, IKBKB, SMAD4, MET, PDE4D, PROX1, RAP1B, RDX, STC1, ZEB1, NR2F2, VEGFA, WNT7B, VEZF1, NRP1, TJP2, ROCK2, RAPGEF2, RAPGEF3, KDM6B, PPP1R16B, FOXP1, DLL4, FOXJ2, HEG1, RAP2C, APOLD1, MYADM
BP	GO:0055007	cardiac muscle cell differentiation	44/3408	3.29E-04	ARRB2, CALR, CXADR, EDN1, EFNB2, G6PD, GATA6, KAT2A, NRG1, HNRNPU, RBPJ, ITGB1, SMAD4, MEF2A, MEF2C, MYH10, PDGFRA, PIN1, PPARA, PROX1, RGS2, RGS4, MAP2K4, SGCD, SLC8A1, SLC9A1, SRF, TBX3, TSC1, VEGFA, YY1, ARID1A, SORBS2, AKAP6, ATG5, NEBL, PDLIM5, FRS2, AKAP13, DKK1, KDM6B, GREM1, ALPK3, SIK1
BP	GO:0035024	negative regulation of Rho protein signal transduction	13/3408	3.30E-04	ABL2, BCL6, ARHGAP35, ITGA3, ITGB1, MET, TNFAIP1, CUL3, DLC1, KANK1, HEG1, KCTD10, FLCN
BP	GO:0051147	regulation of muscle cell differentiation	56/3408	3.32E-04	ABL1, ARRB2, BCL2, BDNF, BNIP2, CAPN2, CDC42, MAPK14, CTNNA1, CTNNB1, EDN1, EFNB2, EZH2, G6PD, KAT2A, NRG1, IGF2, RBPJ, KIT, SMAD4, MECP2, MEF2A, MEF2C, FOXO4, MMP14, MSX1, PDGFB, PIN1, PPARA, PROX1, RGS2, RGS4, SOD2, SRF, TCF3, ZEB1, XBP1, YY1, SPAG9, AKAP6, MORF4L2, HDAC9, FRS2, AKAP13, DKK1, SIRT1, FBXO22, GREM1, PDCD4, CDON, RBM38, CYP26B1, MED28, SETD3, SIK1, RBPMS2

BP	GO:0034644	cellular response to UV	31/3408	3.35E-04	ATR, BAK1, CDC25A, CDKN1A, CHEK1, CREBBP, EIF2S1, EP300, FMR1, MME, MYC, NEDD4, PTPRK, RBL2, TAF1, TP53, YY1, CUL4B, AURKB, CERS1, KDM1A, SIRT1, TRIAP1, INO80, USP47, USP28, RHNO1, RHBDD1, BMF, TP53INP1, SDE2
BP	GO:0030201	heparan sulfate proteoglycan metabolic process	18/3408	3.43E-04	CTNNB1, EXTL2, EXTL3, NDST1, TCF7L2, UGDH, NDST3, HS2ST1, HS3ST3A1, HS3ST1, HPSE, GLCE, CSGALNACT1, SULF2, VANGL2, XYLT2, HS6ST2, HS6ST3
BP	GO:0046545	development of primary female sexual characteristics	36/3408	3.48E-04	ACVR1B, ADCYAP1R1, ARRB1, ARRB2, ATM, BCL2, BCL2L1, CASP3, CEBPB, CTNNA1, DACH1, FOXC1, FOXO3, HSPA5, INSR, KIT, SMAD4, KITLG, MMP14, PDGFRA, PGR, SFRP1, SRC, VEGFA, NRIP1, FZD4, SGPL1, PCYT1B, ADAMTS1, KMT2B, LHFPL2, SIRT1, WNT4, PLEKHA1, ARID5B, ZNF830
BP	GO:0051055	negative regulation of lipid biosynthetic process	24/3408	3.48E-04	BRCA1, INSIG1, NFKB1, PDGFA, PDGFB, PRKAA1, PROX1, SNAI2, SNAI1, AKR1C3, FGF19, ERLIN2, WDTC1, SIRT1, DKK3, ORMDL2, INSIG2, WNT4, FBXW7, LPCAT1, ORMDL1, ORMDL3, SIK1, SLC27A1
BP	GO:0051961	negative regulation of nervous system development	87/3408	3.49E-04	ADCY6, JAG1, ARF6, RHOA, ARHGDIA, BMP7, BMPR1A, CALR, COL3A1, CTNNA1, CTNNB1, CTSZ, DDX6, DLX2, EFNB2, EIF4E, EPHA4, EPHA7, EPHB2, FKBP4, FOXO3, GDI1, GSK3B, HDAC2, NRG1, HES1, ID4, IDH2, ISL1, LDLR, LRP1, NTRK3, PAFAH1B1, PAX6, PBX1, PPP3CA, PTEN, PTPRG, CX3CL1, SKI, SORL1, SOX11, STAT3, TERT, TP53, TSC1, SEMA7A, CHRD, NRP1, SYNGAP1, ARHGEF2, NTN1, MAP4K4, RAPGEF2, SEMA3E, LRIG2, RNF10, GDF11, SEMA3A, SEMA4B, PLK2, DUSP10, NLGN1, DKK1, FSTL4, RAP1GAP2, KANK1, DICER1, MYLIP, SOX8, ASAP1, SUFU, BCL11A, SEMA4C, RGMA, MIB1, SEMA6A, CTDSP1, GORASP1, ISL2, TRAK2, ITM2C, KREMEN1, HOOK3, DIXDC1, KCTD11, PRTG
BP	GO:1902115	regulation of organelle assembly	59/3408	3.55E-04	RHOA, BRCA1, CYLD, EDN1, KAT2A, ARHGAP35, HTT, HNRNPU, IL1RAP, SMAD4, MAP4, MEF2C, NTRK3, PIP4K2A, PRKAA1, MAPK9, PROX1, PTPRD, RAB5A, RALB, RDX, RNF4, ATXN2, SDC4, SRC, SMC1A, ULK1, CDK10, DYNLL1, KAT2B, MTMR3, ARHGEF2, ATG5, VPS4B, CEP135, G3BP2, PDCD6IP, G3BP1, STAG2, PLK2, AKAP13, ATXN2L, CNOT1, ATMIN, RAB3GAP2, SENP6, UBQLN2, ASAP1, SH3GLB1, CHMP5, DYNC2LI1, MDM1, CHMP1B, CNOT6, CEP97, KCTD17, CCSAP, SMCR8, CEP120
BP	GO:0001841	neural tube formation	37/3408	3.58E-04	ABL1, ADM, BMP7, CASP3, CFL1, DVL3, KAT2A, ARHGAP35, HIF1A, LRP6, MTHFR, PAX2, PTCH1, RARG, SDC4, SFRP1, SKI, SOX4, SOX11, STK4, TSC1, TWIST1, KDM6A, LUZP1, FZD3, ARID1A, FZD1, FZD6, DLC1, MTHFD1L, SUFU, SEMA4C, IFT57, VANGL2, MIB1, SHROOM3, TRIM71
BP	GO:0009648	photoperiodism	14/3408	3.58E-04	CRY2, PML, PPP1CA, PPP1CB, PPP1CC, TP53, BHLHE40, PER3, PER2, USP2, MTA1, CLOCK, FBXL3, SIK1
BP	GO:0032509	endosome transport via multivesicular body sorting pathway	14/3408	3.58E-04	TMEM50B, LYST, SORT1, VCP, VPS4B, SNF8, LEPROTL1, TMEM50A, VPS36, LEPROT, VPS37C, LAPTM4B, CHMP1B, VPS37D
BP	GO:1900101	regulation of endoplasmic reticulum unfolded protein response	14/3408	3.58E-04	BAK1, ATF6B, HSPA5, DNAJB9, NCK1, PTPN1, XBP1, NCK2, BCL2L11, AGR2, BFAR, TMEM33, PPP1R15B, DAB2IP
BP	GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	17/3408	3.58E-04	ATM, ATR, PTTG1IP, CD44, DDX5, DYRK1A, MSX1, SNAI2, SNAI1, TP53, TWIST1, KDM1A, SIRT1, ZNF385A, SPRED1, SPRED2, SPRED3
BP	GO:0048048	embryonic eye morphogenesis	17/3408	3.58E-04	BMP7, FBN1, FBN2, LRP6, PAX2, PAX6, PROX1, RARG, SOX11, SP3, ZEB1, TWIST1, FZD5, ARID1A, FRS2, HIPK2, HIPK1
BP	GO:0007422	peripheral nervous system development	29/3408	3.61E-04	AKT2, BDNF, RUNX1, RUNX3, DAG1, EGR3, ERBB2, ETV1, GSTM3, NRG1, ILK, ISL1, NAB1, NEFH, NTRK3, POU3F2, POU4F1, SCN8A, SKI, SLC5A3, ONECUT2, NFASC, DICER1, SOX8, ADAM22, PARD3, ISL2, SH3TC2, PLXNA4
BP	GO:0045023	G0 to G1 transition	21/3408	3.67E-04	BRCA1, CHEK1, E2F6, EZH2, MAX, MDM4, FOXO4, RAD51, RNF2, RRM2, TFDP1, TFDP2, YAF2, CBX3, MGA, CBX5, SUZ12, PHC3, EPC1, RHNO1, DAB2IP
BP	GO:0061383	trabecula morphogenesis	21/3408	3.67E-04	RHOA, BMP7, BMPR1A, COL1A1, S1PR1, FBN2, FKBP1A, NRG1, RBPJ, SFRP1, SOS1, SRF, TGFBR1, TGFBR3, THBS3, ADAMTS1, UBE4B, GREM1, DLL4, CHD7, HEG1
BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	21/3408	3.67E-04	BMPR1A, DDX5, GATA2, NR3C1, HIF1A, JUN, SMAD4, SMAD6, NFIB, PDGFB, PPARA, PPARD, SREBF2, SRF, STAT3, TEAD1, TERT, TP53, YY1, FOSL1, KLF4

BP	GO:0070849	response to epidermal growth factor	21/3408	3.67E-04	ZFP36L1, ZFP36L2, CBL, COL1A1, EEF1A1, EGFR, ERBB2, FOXC1, MCM7, PAX2, MAPK1, MAPK3, PTPN11, PTPN12, SNAI2, STAT5B, ZFP36, IQGAP1, BAG4, ERRFI1, DAB2IP
BP	GO:0007266	Rho protein signal transduction	61/3408	3.80E-04	ABL1, ABL2, RHOA, RHOB, ARHGAP1, ARHGDIA, ARRB1, BCL6, CDC42, CFL1, COL1A2, COL3A1, ECT2, EPS8, ARHGAP35, ITGA3, ITGB1, LIMK1, MET, OPHN1, ROBO1, SOS1, TIAM1, TNFAIP1, TRIO, RND2, CUL3, NRP1, KALRN, F2RL3, ARHGEF2, ARHGAP29, NTN1, ROCK2, ARHGEF17, FARP1, NET1, DLC1, CDC42EP2, VAV3, GNA13, AKAP13, RHOBTB3, KANK1, ARHGEF9, ARHGEF12, RHOQ, PLEKHG3, CDC42SE1, VANGL2, HEG1, RHOU, PLEKHG2, SYNPO2L, PREX2, KCTD10, ARHGEF39, FGD4, PLEKHG4B, FLCN, SPATA13
BP	GO:0001704	formation of primary germ layer	41/3408	3.81E-04	BMP7, BMPR1A, BMPR2, COL4A2, COL5A1, COL5A2, COL11A1, COL12A1, CTNNB1, FOXC1, FN1, GATA6, HSBP1, ITGA3, ITGA5, ITGAV, ITGB1, SMAD2, MMP14, NF2, PAX2, PRKAR1A, SNAI1, SRF, TAL1, HNF1B, KDM6A, NR4A3, HMGA2, ARID1A, ITGA8, CHRD, KLF4, HAND1, CTR9, DKK1, KDM6B, EPB41L5, CDC73, SOX7, CRB2
BP	GO:0009411	response to UV	46/3408	3.83E-04	ATR, BAK1, CCND1, BCL2, CASP3, CDC25A, CDKN1A, CHEK1, CREBBP, EGFR, EIF2S1, EP300, ERCC2, ERCC6, FMR1, MAP3K4, MEN1, MME, MYC, NEDD4, PML, PRKAA1, MAPK8, PTPRK, RBL2, TAF1, TP53, USP1, YY1, CUL4B, AURKB, UBE4B, CERS1, KDM1A, SIRT1, TRIAP1, DTL, INO80, USP47, USP28, RHNO1, RHBDD1, BMF, TP53INP1, DCUN1D3, SDE2
BP	GO:0071230	cellular response to amino acid stimulus	27/3408	3.83E-04	ATP7A, BCL2L1, CAPN2, CEBPB, COL1A1, COL1A2, COL3A1, COL4A1, COL5A2, DNMT3A, EGFR, HNRNPD, IPO5, OPA1, PDGFRA, ZEB1, XBP1, SOCS1, CPEB3, NSMF, BCL11A, RRAGD, RRAGC, CPEB4, SESN2, SESN3, UBR1
BP	GO:0050684	regulation of mRNA processing	45/3408	3.84E-04	ZFP36L1, CCNT1, DDX5, DYRK1A, FMR1, HNRNPK, HNRNPU, MBNL1, NCBP1, NUP98, SRSF1, SRSF2, SRSF4, SRSF7, TRA2B, SNRPA, SON, PABPN1, CTR9, RBM19, THRAP3, MBNL2, DDX17, CELF2, AHCYL1, SRSF10, PAPOLA, RNPS1, CPSF6, U2AF2, CPEB3, ZC3H3, RBFOX2, DAZAP1, RBMX, RBM15B, SMU1, MBNL3, RBM25, CDC73, PTCD2, CPSF7, FAM172A, SREK1, RBMXL1
BP	GO:0060213	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	9/3408	3.85E-04	ZFP36, BTG2, TOB1, CPEB3, CNOT1, TNRC6B, PABPC1, TNRC6A, TNRC6C
BP	GO:1900402	regulation of carbohydrate metabolic process by regulation of transcription from RNA polymerase II promoter	9/3408	3.85E-04	FOXO1, KAT2A, FOXK2, PPARA, TP53, KAT2B, NCOR1, MLXIP, FOXK1
BP	GO:1903894	regulation of IRE1-mediated unfolded protein response	9/3408	3.85E-04	BAK1, HSPA5, DNAJB9, PTPN1, BCL2L11, AGR2, BFAR, TMEM33, DAB2IP
BP	GO:0006401	RNA catabolic process	105/3408	3.85E-04	ATM, ZFP36L1, ZFP36L2, MAPK14, DDX5, DDX6, DKC1, EIF4G1, ELAVL1, ETF1, FMR1, GSPT1, HNRNPC, HNRNPD, HNRNPU, TNPO1, MLH1, HNRNPM, NCBP1, CNOT4, OAS2, PARN, PKP1, POLR2D, PPP2CA, PPP2R1A, PPP2R2A, PRKCA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, UPF1, RPL15, RPL28, RPL34, RPL37, RPS3, RPS23, SET, TNFRSF1B, XPO1, ZFP36, CSDE1, BTG2, FXR1, ANP32A, PABPC4, CNOT8, ROCK2, PSMF1, PUM1, SMG7, THRAP3, TOB1, PSME3, PSMD14, SYNCRIP, PAIP1, IGF2BP1, IGF2BP3, HBS1L, RNPS1, POP1, HNRNPA0, CPEB3, CNOT1, SAMD4A, SMG1, TNRC6B, PSME4, LARP1, SMG5, TARDBP, LSM4, UPF2, GIGYF2, SERBP1, AGO1, PABPC1, SND1, TNRC6A, MYEF2, YTHDF2, XRN1, ALKBH5, SAMD4B, RBM23, RBM38, PCID2, DCP1A, ZC3HAV1, CNOT6, TNRC6C, METTL14, EDC3, TRIM71, AGO3, AGO4, PDE12, PATL1, YTHDF3
BP	GO:0003151	outflow tract morphogenesis	30/3408	3.86E-04	JAG1, BMP7, BMPR1A, BMPR2, ATF2, CRKL, CTNNB1, FOXC1, GATA6, HIF1A, HES1, RBPJ, ILK, ISL1, JUN, SMAD4, SMAD6, MEF2C, ROBO1, SOX11, TBX3, TGFBR3, TWIST1, VEGFA, FZD1, NRP1, CITED2, PLXND1, NIPBL, HEYL
BP	GO:0000075	cell cycle checkpoint	64/3408	3.89E-04	APC, ATM, ATR, CCND1, BCL2L1, BRCA1, CDC5L, CDKN1A, CDKN1B, CHEK1, FOXN3, ATF2, MAPK14, DUSP1, EP300, IK, MAD2L1, MDM4, FOXO4, CNOT4, PML, PROX1, PTPN11, RAD1, RB1, RBL2, SOX4, SOX11, AURKA, TFDP1, TFDP2, TOP2B, TP53, BTG2, HMGA2, CDC14B, PEA15, AURKB, TRIP13, CNOT8, TAOK2, CLOCK, PLK2, CNOT1, ZNF385A, HINFP, GIGYF2, WAC, TRIAP1, DTL, ETAA1, PCID2, CNOT6, TAOK1, USP28, DCLRE1B, NABP1, INTS3, NABP2, BRCC3, WDR76, RHNO1, ZNF830, E2F7
BP	GO:0003170	heart valve development	25/3408	3.91E-04	JAG1, PRDM1, BMPR1A, BMPR2, GATA3, RBPJ, SMAD4, SMAD6, MDM4, MEF2C, NOTCH2, RB1, ROBO1, SNAI2, SNAI1, SOX4, TNFRSF1B, TWIST1, DCHS1, ROCK2, OLFM1, HECTD1, HEYL, DLL4, ADAMTS9
BP	GO:0031503	protein-containing complex localization	79/3408	3.91E-04	ADAM10, ATM, ATR, DAG1, DLG3, EFNB2, EIF4E, FKBP4, HIP1, HNRNPU, TNPO1, SMAD7, RAB8A, NCBP1, NUP88, NUP98, OPHN1, POLR2D, PURA, RALB, RAN, RANBP2, UPF1, ABCE1, SRSF1, SRSF2, SRSF4, SRSF7, SGCD, SNAP25, STX3, TSC1, TUB, XPO1, PABPN1, NUMB, DYNLL1, AP3D1, WASL, TRIP11, KIF3B, POM121, SMG7, KLHL21, GPC6, NXF1, NUP50, RNPS1, KIF3A, XPOT, DDX19B, U2AF2, NLGN1, SMG1, SMG5, UPF2, NPTN, RBM15B, NMD3, CDC40, DYNC2LI1, ADAM22, CPSF2, ALKBH5, IFT57, DDX19A, WDR33, NDC1, VPS35, NUP133, RIOK2, PCID2, RCC2, THOC2, SEH1L, SSX2IP, NACC2, NUP43, POM121C

BP	GO:0030038	contractile actin filament bundle assembly	35/3408	4.01E-04	ABL1, RHOA, ARRB1, CD47, CDC42, S1PR1, LIMK1, MET, NF2, PTGER4, PXN, SDC4, SFRP1, SLC9A1, SRC, SRF, TESK1, TGFBR1, TNFAIP1, TSC1, CUL3, NRP1, ROCK2, BAG4, WASF2, DLC1, RAPGEF3, LIMCH1, CLASP1, WNT4, ARHGAP28, SYNPO2L, FHDC1, PHLDB2, SH3PXD2B
BP	GO:0043149	stress fiber assembly	35/3408	4.01E-04	ABL1, RHOA, ARRB1, CD47, CDC42, S1PR1, LIMK1, MET, NF2, PTGER4, PXN, SDC4, SFRP1, SLC9A1, SRC, SRF, TESK1, TGFBR1, TNFAIP1, TSC1, CUL3, NRP1, ROCK2, BAG4, WASF2, DLC1, RAPGEF3, LIMCH1, CLASP1, WNT4, ARHGAP28, SYNPO2L, FHDC1, PHLDB2, SH3PXD2B
BP	GO:0150063	visual system development	98/3408	4.10E-04	ACVR2B, JAG1, ATP2B1, ATP2B4, BAK1, BCL2, PRDM1, BMP7, BMPR2, CACNA1C, CDKN1B, COL4A1, COL5A1, COL5A2, CTNS, CTNNB1, DLX2, EGFR, EPHB2, CLN8, FAT1, FBN1, FBN2, FOXC1, GATA3, GJA1, GNB1, ARHGAP35, HDAC2, HIF1A, JUN, LRP6, MAN2A1, MAX, MEIS2, MYH10, NF2, NHS, NTRK3, OPA1, PAX2, PAX6, PDGFRA, PKNOX1, PROX1, RARG, RORB, SALL2, SKI, SKIL, SOS1, SOX11, SP3, SRF, STAT3, ZEB1, TGFBR1, TUB, TWIST1, VEGFA, WNT7B, WNT2B, YY1, FZD5, ARID1A, FZD4, BCAR3, NRP1, ALDH1A2, KLF4, MFN2, ABI2, GDF11, KDM5B, FRS2, PDS5B, SLC7A11, NIPBL, HIPK2, SOX8, CDON, DLL4, AHI1, CHD7, TENM3, MDM1, TGIF2, SMOC1, BCL11B, LPCAT1, RAB11FIP4, TBC1D20, RDH10, ADAMTS18, HIPK1, SDK1, SH3PXD2B, FREM2
BP	GO:0009895	negative regulation of catabolic process	85/3408	4.16E-04	ALAD, ATP2B4, BCL2, MAPK14, DKC1, EGFR, EIF4G1, EIF4G2, ELAVL1, EPHA4, FHIT, FMR1, NRG1, HMGCR, HNRNPC, HNRNPD, HNRNPU, FOXK2, MAD2L1, MAP1A, MCL1, MDM4, MET, NPC1, OPHN1, FURIN, PARN, SERPINE2, PIN1, PKP1, PML, PPARA, PRKAA1, SNCA, SORL1, STAT3, STYX, TAF1, TIMP2, TIMP3, TP53, TSC1, UBE2G2, ZFP36, SNX3, PSMF1, KDM4A, LRIG2, THRAP3, TOB1, SYNCRIP, ATG7, PAIP1, IGF2BP1, HNRNPA0, TLK2, GABARAPL2, MYCBP2, TAB2, LARP1, TARDBP, SF3B3, PABPC1, HTRA2, HIPK2, USP25, DERL2, WAC, UCHL5, UBE2J1, AZIN1, SUFU, DDIT4, LAPTM4B, YOD1, RBM38, VPS35, FMN2, UBQLN4, USP36, MTMR9, BMF, SMCR8, DAB2IP, FOXK1
BP	GO:0021537	telencephalon development	72/3408	4.18E-04	RHOA, ATP2B4, CASP3, CDK6, COL3A1, CRK, CRKL, CTNNB1, DLX2, EGFR, EPHB2, EPHB3, EZH1, EZH2, KAT2A, GSK3B, NRG1, HIF1A, HES1, ID4, KIF5B, LRP1, LRP6, MDK, MYH10, NF2, NFIB, PAFAH1B1, PAX6, PEX13, POU3F2, PROX1, PTEN, ROBO1, TRA2B, SKI, SLC1A2, SLC8A1, SRF, TACC1, TSC1, YWHAE, BTG2, NR4A3, SEMA7A, NUMB, NRP1, SEMA3A, IGF2BP1, BTBD3, KDM1A, PHLPP2, KDM6B, SZT2, SLC7A11, CNTNAP2, SLITRK5, CDON, NIN, SLC38A2, NDE1, UBA6, CHD7, ZSWIM6, BCL11B, FUT10, DIXDC1, PLXNA4, DAB2IP, CEP120, FBXO45, CCDC85C
BP	GO:0070371	ERK1 and ERK2 cascade	87/3408	4.21E-04	ABL1, ARRB1, ARRB2, ZFP36L1, ZFP36L2, CD44, CCR7, CRKL, CSK, DUSP1, DUSP6, EGFR, EPHA7, EPHB2, ERBB2, FGF2, FGFR3, FLT4, FN1, GBP1, GCNT2, GNAI2, RAPGEF1, HMGCR, ITGAV, JUN, KIT, LRP1, LYN, SMAD4, MYC, NOTCH2, P2RY1, PDGFA, PDGFB, PDGFRA, PIN1, PRKCA, MAPK1, MAPK3, PTEN, PTGER4, PTPN1, PTPN11, PTPRC, PTPRR, RAP1B, CCL7, CX3CL1, SHC1, SRC, STYX, SYK, TIAM1, TIMP3, SEMA7A, EIF3A, NRP1, KLF4, AKAP12, RAPGEF2, FGF19, SPRY1, TNIP1, BTN2A2, NOD1, GPNMB, FRS2, DUSP10, DSTYK, NPTN, DNAJC27, ERRFI1, FBXW7, CAMK2N1, NDRG2, SEMA6A, NDRG4, SPRY4, IQGAP3, SIRPA, DAB2IP, CNKSR3, SPRED1, BMPER, FLCN, SCIMP
BP	GO:0021953	central nervous system neuron differentiation	56/3408	4.34E-04	ADARB1, ATP7A, CRK, CRKL, CSNK1D, CSNK1E, CTNNB1, DLX2, EPHA4, EPHB2, EPHB3, CLN8, GATA2, ARHGAP35, HES1, ID4, ISL1, LRP6, MAPT, NFIB, OPHN1, PAFAH1B1, PAX6, POU4F1, PROX1, PTCH1, PTEN, ROBO1, RORA, SFRP1, SOX4, TAL1, BTG2, FZD1, NRP1, LDB1, DCLK1, B4GALT6, RAPGEF2, SEMA3A, DKK1, MYCBP2, SATB2, SZT2, SIN3A, GIGYF2, NIN, SUFU, C21orf91, DLL4, ZSWIM6, ISL2, BCL11B, PLXNA4, MTPN, FBXO45
BP	GO:0001954	positive regulation of cell-matrix adhesion	22/3408	4.44E-04	ABL1, CDK6, CCR7, CSF1, DAG1, EMP2, GSK3B, ILK, JUP, PTPRJ, CX3CL1, SDC4, SFRP1, TSC1, VEGFA, IQGAP1, NRP1, MAP4K4, WNT4, FERMT1, EPB41L5, FMN1
BP	GO:0048286	lung alveolus development	19/3408	4.48E-04	ADA, ATP7A, BMPR2, CREB1, FLT4, GATA6, FOXA1, HOXA5, IGFBP5, MAN2A1, PDGFA, PGR, MAN1A2, CIC, SLC7A11, ERRFI1, STK40, PKDCC, ATXN1L
BP	GO:0070317	negative regulation of G0 to G1 transition	19/3408	4.48E-04	BRCA1, CHEK1, E2F6, EZH2, MAX, FOXO4, RAD51, RNF2, RRM2, TFDP1, TFDP2, YAF2, CBX3, MGA, CBX5, SUZ12, PHC3, EPC1, DAB2IP
BP	GO:1903749	positive regulation of establishment of protein localization to mitochondrion	24/3408	4.53E-04	BCL2, PPP3R1, PRKAA1, MAPK8, SREBF2, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, BAP1, TP63, ATG13, ARIH2, BBC3, HTRA2, SH3GLB1, LEPROT, FBXW7, USP36, RHOU
BP	GO:0045667	regulation of osteoblast differentiation	42/3408	4.53E-04	ACVR2B, JAG1, BMP7, BMPR1A, BMPR2, RUNX2, CDK6, CEBPB, CEBPD, CTNNB1, DDX5, ESRRA, FBN2, GNAS, IGFBP5, IL6R, IL6ST, ILK, JUND, NBR1, SMAD6, MEF2C, MEN1, PTCH1, RORB, SFRP1, SKI, SNAI2, SOX11, TWIST1, WNT7B, TP63, CHRD, LIMD1, PDLIM7, RASSF2, TOB1, GREM1, SUFU, WNT4, FAM20C, SMOC1
BP	GO:0120032	regulation of plasma membrane bounded cell projection assembly	54/3408	4.56E-04	APC, ARF6, ATP7A, CAV1, CDC42, CCR7, CYLD, EPS8, FER, FMR1, ARHGAP35, HTT, KIT, MAP4, MYO10, ATP8B1, PLD1, PODXL, TWF1, RAB5A, RDX, SRF, TGFBR1, TRPM2, CDK10, DYNLL1, NRP1, WASL, ATG5, CEP135, PLEKHM1, ARPC2, WASF2, TENM1, CDC42EP2, NCKAP1, NLGN1, KANK1, ATMIN, RHOQ, CORO1C, FAM98A, PPP1R16B, AUTS2, DYNC2LI1, ANLN, FNBP1L, RCC2, RAB17, CEP97, AKIRIN1, KCTD17, CEP120, AGRN
BP	GO:0043010	camera-type eye development	86/3408	4.97E-04	ACVR2B, JAG1, ATP2B1, ATP2B4, BAK1, BMP7, BMPR2, CACNA1C, CDKN1B, COL4A1, CTNS, CTNNB1, DLX2, EGFR, EPHB2, CLN8, FAT1, FBN1, FBN2, FOXC1, GATA3, GJA1, GNB1, ARHGAP35, HDAC2, HIF1A, JUN, LRP6, MAN2A1, MAX, MYH10, NF2, NHS, NTRK3,

					OPA1, PAX2, PAX6, PDGFRA, PKNOX1, PROX1, RARG, RORB, SKI, SKIL, SOS1, SOX11, SP3, SRF, ZEB1, TGFBR1, TUB, TWIST1, VEGFA, WNT7B, WNT2B, YY1, FZD5, ARID1A, FZD4, BCAR3, NRP1, ALDH1A2, KLF4, MFN2, ABI2, GDF11, KDM5B, FRS2, PDS5B, SLC7A11, HIPK2, SOX8, CDON, DLL4, AHI1, CHD7, TENM3, MDM1, TGIF2, BCL11B, LPCAT1, RAB11FIP4, TBC1D20, RDH10, HIPK1, SDK1
BP	GO:0042110	T cell activation	119/3408	5.04E-04	ABL1, ADA, RHOA, ATP7A, BCL2, BCL6, PRDM1, ZFP36L1, ZFP36L2, CAMK4, CASP3, CAV1, RUNX2, RUNX1, RUNX3, CBFB, CD44, CD47, CDC42, CDK6, CEBPB, CLPTM1, CCR7, CSK, CTNNB1, CXADR, CYLD, EFNB1, EFNB2, EGR1, EGR3, ELF4, ERBB2, FKBP1A, FLOT2, GATA3, KAT2A, GJA1, GRB2, NCKAP1L, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, IRF1, IRF4, ITPKB, JAG2, KIT, LIG4, LYN, SMAD7, MDK, MYB, MYH9, NCK1, PAK2, PAK3, PAWR, PKNOX1, PPP3CA, PRKAR1A, PRLR, PTGER4, PTPN11, PTPRC, RAG1, RORA, RPS3, SATB1, SDC4, SOS1, SOX4, SP3, SRC, SRF, STAT3, SYK, ADAM17, TCF7, ZEB1, TFRC, TNFRSF1B, TP53, TSC1, VCAM1, XBP1, FZD5, NCK2, SOCS1, TNFSF9, FADD, AP3D1, DLG5, SOCS6, CD83, ATG5, SOCS5, BTN2A2, GPNMB, DUSP10, ICOSLG, NCSTN, FOXP1, PRELID1, WNT4, DLL4, LAX1, CHD7, PAG1, CYP26B1, PELI1, ZMIZ1, BCL11B, CD276, SIRPA, NRARP
BP	GO:2000045	regulation of G1/S transition of mitotic cell cycle	56/3408	5.05E-04	ATM, CCND1, BCL2, CCND2, CDK6, CDKN1A, CDKN1B, DDX3X, EGFR, EIF4G1, EP300, EZH2, FHL1, MDM4, CNOT4, PKD1, PML, PTEN, RB1, RBL2, RDX, SOX4, AURKA, ADAM17, TERT, TFDP1, TFDP2, TP53, BTG2, CUL4B, CDK10, KLF4, CNOT8, ADAMTS1, CTDSP2, PSME3, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, ZNF385A, GIGYF2, TRIAP1, INO80, KMT2E, MEPCE, CNOT6, CTDSP1, ZNF655, CDC73, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0060324	face development	21/3408	5.06E-04	ASPH, COL1A1, EP300, HOXB3, LRP6, MSX1, PAX9, PDGFRA, MAPK1, MAPK3, PTPN11, RARG, SKI, SRF, ALDH1A2, SGPL1, DKK1, NIPBL, CHD7, PLEKHA1, ARID5B
BP	GO:0061647	histone H3-K9 modification	21/3408	5.06E-04	ATRX, BRCA1, CHEK1, DNMT3B, GATA3, JARID2, SMAD4, MECP2, KMT2A, MYB, SUV39H1, KAT2B, KDM1A, SIRT1, ZNF451, ARID4B, RIF1, SETD5, BEND3, SETD7, SETDB2
BP	GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	25/3408	5.21E-04	BAK1, BCL2, BCL2L1, CEBPB, GRINA, UBE2K, ITPR1, NCK1, OPA1, PML, PTPN1, TMBIM6, TP53, XBP1, NCK2, HERPUD1, BCL2L11, HYOU1, SERINC3, SIRT1, BBC3, TXNDC12, DNAJC10, SYVN1, DAB2IP
BP	GO:0098751	bone cell development	17/3408	5.33E-04	EP300, FBN1, KIT, NOTCH2, PAFAH1B1, PIP4K2A, PTPN11, SRC, SRF, TAL1, SH2B3, WASF2, ZNF385A, FOXP1, FBXW7, FAM20C, SIGLEC15
BP	GO:0051897	positive regulation of protein kinase B signaling	54/3408	5.33E-04	ARRB2, AXL, CCR7, AKR1C2, HBEGF, EGFR, ERBB2, FGF1, FGF2, FGF5, FGFR3, GAB1, GATA3, GCNT2, GRB2, NRG1, HIP1, IGF1R, IGF2, IGFBP5, IL18, ILK, INSR, ITGB1, KIT, MAZ, MET, KITLG, PDGFA, PDGFB, PDGFRA, PIK3CB, PTPN11, PTPRJ, CX3CL1, SRC, TCF7L2, TGFA, TGFBR1, THBS1, TXN, AKR1C3, IRS2, BAG4, FGF19, FRS2, HPSE, MTDH, OSBPL8, PIK3AP1, NRG4, RICTOR, EPGN, FAM110C
BP	GO:0016571	histone methylation	45/3408	5.38E-04	ATRX, BRCA1, CTNNB1, DNMT3B, EZH1, EZH2, GATA3, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MTHFR, MYB, SATB1, SUV39H1, KDM6A, PRDM2, KMT2D, CTR9, SETD1A, KMT2B, CTCF, MTF2, KDM1A, SIRT1, SUZ12, AUTS2, ARID4B, WDR5B, TET2, BCOR, RIF1, SETD5, KMT2E, BEND3, KMT2C, NSD1, TET1, SETD7, SETDB2, SETD3, DPY30, TET3
BP	GO:0046546	development of primary male sexual characteristics	45/3408	5.38E-04	AR, ATRX, CCND1, BCL2, BCL2L1, CBL, CRKL, CTNNA1, GATA3, GATA6, GJA1, HOXA9, INSR, KIT, SMAD4, KITLG, MMP14, NKX3-1, PDGFRA, KDM5A, SFRP1, TGFBR1, TMF1, WNT2B, SF1, CSDE1, AKR1C3, TNFSF10, SGPL1, BCL2L11, LHFPL2, FSTL3, CITED2, SEMA3A, RHOBTB3, FNDC3A, SOX8, ARID4B, SIX4, WNT4, PLEKHA1, ARID5B, TBC1D20, RNF38, AGO4
BP	GO:0000281	mitotic cytokinesis	28/3408	5.39E-04	APC, ARF1, RHOA, RHOB, CENPA, CFL1, ECT2, INCENP, MYH10, RASA1, SON, SPTBN1, ROCK2, KIF23, VPS4B, PDCD6IP, STAMBP, JTB, CIT, ZFYVE26, CHMP5, ANLN, CEP55, TRIM36, CHMP1B, LZTS2, CHMP7, KLHDC8B
BP	GO:0030010	establishment of cell polarity	44/3408	5.40E-04	ARF6, RHOA, CDC42, CENPA, CFL1, CCR7, CRK, CRKL, MARK2, FLOT2, GATA3, GSK3B, HTT, HES1, MAD2L1, MAP1B, MAP4, MYH9, OPHN1, PAFAH1B1, PAX6, PKD1, RAP1B, ARHGEF2, CYTH3, CYTH1, ROCK2, UST, SPRY1, RAB11FIP2, KANK1, WWC1, CLASP1, NDE1, FERMT1, FRMD4A, NSFL1C, PARD3, CYP26B1, UBXN2B, AMOT, AMOTL1, RICTOR, MYO18A
BP	GO:0035270	endocrine system development	42/3408	5.43E-04	BAK1, BMPR1A, CDK6, CREB1, CRKL, FOXO1, GATA2, GATA3, GATA6, GSK3B, HNF4A, HOXA3, HOXA5, HOXB3, HES1, RBPJ, IL6R, INSR, ISL1, SMAD2, MDK, MEN1, MSX1, PAX6, PBX1, PDGFRA, POU3F2, MAPK1, MAPK3, RFX3, SOX4, SRF, TGFBR1, THRA, ALDH1A2, ONECUT2, CLOCK, FSTL3, CITED2, DKK3, WNT4, ARID5B
BP	GO:0071426	ribonucleoprotein complex export from nucleus	42/3408	5.43E-04	EIF4E, NCBP1, NUP88, NUP98, POLR2D, RAN, RANBP2, UPF1, ABCE1, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, PABPN1, POM121, SMG7, NXF1, NUP50, RNPS1, XPOT, DDX19B, U2AF2, SMG1, SMG5, UPF2, RBM15B, NMD3, CDC40, CPSF2, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, THOC2, SEH1L, NUP43, POM121C
BP	GO:0050678	regulation of epithelial cell proliferation	100/3408	5.47E-04	AR, ATP7A, CCND1, BMPR1A, BMPR2, ZFP36L1, KLF9, CAV1, RUNX3, CDK6, CDKN1B, ATF2, CTNNB1, DLX6, EFNB2, EGFR, EGR3, ERBB2, FGF1, FGF2, FLT4, GATA2, GATA3, GJA1, HIF1A, HOXA5, HES1, ISL1, JUN, LAMC1, MDK, MEF2C, MEN1, MYC, NFIB, NKX3-1, NOTCH2, NRAS, PAX2, PAX6, PDGFB, PGR, PPARD, PRKCA, PROX1, PTCH1, PTEN, PTPRK, RB1, ROBO1, RREB1, SFRP1, SNAI2, SOX11, SPARC, STAT1, STAT3, ADAM17, TCF7L2, NR2F2, TGFA, TGFBR1, TGFBR3, THBS1, TWIST1, VDR, VEGFA, XBP1, ZFP36, NR4A3, TP63, NRP1, ALDH1A2, AIMP1, AKT3, KDM5B, FRS2, DUSP10, VASH1, SIRT1, PPP1R16B, EGFL7, SIX4, ERRFI1, DLL4, IFT57, AGGF1, FBXW7, SULF2, PBLD, BCL11B, WDR77, CDC73, IQGAP3, CD109, DAB2IP, RICTOR, EPGN, EMC10, NRARP

BP	GO:0045926	negative regulation of growth	71/3408	5.57E-04	ACVR1B, ADRB1, APBB2, BCL2, BCL6, BMPR2, BTG1, OSGIN2, CDKN1A, CDKN1B, DDX3X, EPHA7, ESR2, FGFR3, FHL1, G6PD, GJA1, HIF1A, HNF4A, DNAJB2, IGFBP5, JARID2, SMAD4, MSX1, MT1M, NOTCH2, ENPP1, SERPINE2, PML, PPARA, PPARD, PPP2CA, PPP2R1A, PTCH1, PTEN, PTPRJ, RGS2, RGS4, SFRP1, SMARCA2, STK4, TP53, YY1, SEMA7A, STC2, NRP1, SOCS2, NTN1, SEMA3E, SERTAD2, SEMA3A, SEMA4B, DUSP10, FSTL4, WWC1, SIRT1, SERTAD3, ADIPOR1, ING4, BCL11A, SEMA4C, WWC3, SEMA6A, TSPYL2, MUL1, ADIPOR2, WWC2, SESN2, DCUN1D3, DCBLD2, FLCN
BP	GO:0015012	heparan sulfate proteoglycan biosynthetic process	16/3408	5.59E-04	CTNNB1, EXTL2, EXTL3, NDST1, TCF7L2, UGDH, NDST3, HS2ST1, HS3ST3A1, HS3ST1, GLCE, CSGALNACT1, VANGL2, XYLT2, HS6ST2, HS6ST3
BP	GO:0038128	ERBB2 signaling pathway	16/3408	5.59E-04	HBEGF, EGFR, ERBB2, GAB1, GRB2, NRG1, PRKCA, PTPN12, PTPRR, SHC1, SOS1, SRC, CUL5, CPNE3, PTPN18, NRG4
BP	GO:0048538	thymus development	20/3408	5.67E-04	ABL1, ATM, BCL2, CRKL, CTNNB1, EPHB3, GATA3, HOXA3, HES1, JARID2, PBX1, MAPK1, MAPK3, RAG1, SRF, TGFBR1, FADD, BCL2L11, SIX4, BCL11B
BP	GO:0070316	regulation of G0 to G1 transition	20/3408	5.67E-04	BRCA1, CHEK1, E2F6, EZH2, MAX, FOXO4, RAD51, RNF2, RRM2, TFDP1, TFDP2, YAF2, CBX3, MGA, CBX5, SUZ12, PHC3, EPC1, RHNO1, DAB2IP
BP	GO:0048596	embryonic camera-type eye morphogenesis	14/3408	5.80E-04	BMP7, LRP6, PAX2, PAX6, PROX1, SOX11, SP3, ZEB1, TWIST1, FZD5, ARID1A, FRS2, HIPK2, HIPK1
BP	GO:1902806	regulation of cell cycle G1/S phase transition	60/3408	5.82E-04	ATM, ATP2B4, CCND1, BCL2, CCND2, CDK6, CDKN1A, CDKN1B, DDX3X, EGFR, EIF4G1, EP300, EZH2, FHL1, MDM4, MEN1, CNOT4, PKD1, PML, PTEN, RB1, RBL2, RDX, SOX4, AURKA, ADAM17, TAF1, TERT, TFDP1, TFDP2, TP53, BTG2, CUL4B, CDK10, KLF4, CNOT8, ADAMTS1, CTDSP2, PSME3, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, ZNF385A, GIGYF2, TRIAP1, INO80, FBXW7, KMT2E, MEPCE, CNOT6, CTDSP1, ZNF655, CDC73, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0007162	negative regulation of cell adhesion	80/3408	5.86E-04	ABL1, ACTN4, ADAM10, JAG1, RHOA, ARHGDIA, BCL6, CASP3, RUNX1, RUNX3, CBFB, CEBPB, COL1A1, DUSP1, EFNA5, ERBB2, GBP1, GCNT2, HOXA7, IRF1, LRP1, SMAD7, MBP, MDK, MEN1, MMP14, NF2, SERPINE1, PAWR, SERPINE2, PODXL, PPARA, PRKAR1A, PTEN, PTPN11, PTPRC, RASA1, RDX, CX3CL1, SDC4, SNAI2, SRC, THBS1, VEGFA, FZD4, SOCS1, CD164, DLG5, SOCS6, KLF4, MAP4K4, SOCS5, SEMA3E, SH2B3, BTN2A2, DLC1, GPNMB, POSTN, FAM107A, PLXND1, KANK1, CORO1C, YTHDF2, ADAM22, LAX1, PAG1, RCC2, PELI1, SEMA6A, EPB41L5, JAM2, WNK1, CBLL1, PHLDB2, PLXNA4, MYADM, ADAMTS18, ACER2, MIA3, NRARP
BP	GO:0099518	vesicle cytoskeletal trafficking	22/3408	6.02E-04	ACTN4, HTT, KIF5B, MYO1C, MYO5A, PAFAH1B1, RAB1A, VAMP7, AP3D1, WASL, KIF3B, KIF23, AP3S2, KIF3A, TRAK1, KIF1B, AP3M1, NDE1, FNBP1L, KIF13A, TRAK2, FYCO1
BP	GO:0034446	substrate adhesion-dependent cell spreading	35/3408	6.05E-04	ABL1, ACTN4, AXL, CALR, CDC42, CRK, CRKL, EFNA5, MEGF9, EPHB3, FER, FN1, GBP1, ILK, ITGAV, LAMC1, LAMC2, MDK, NEDD9, PXN, RAB1A, RREB1, SRC, TYRO3, FZD4, ITGA8, NRP1, ARPC2, POSTN, KANK1, CORO1C, RCC2, PEAK1, ANTXR1, MYADM
BP	GO:0061640	cytoskeleton-dependent cytokinesis	35/3408	6.05E-04	APC, ARF1, RHOA, RHOB, CENPA, CFL1, ECT2, INCENP, MYH10, RASA1, SON, SPTBN1, AURKB, ROCK2, KIF23, VPS4B, PDCD6IP, ACTR2, STAMBP, JTB, CIT, DCTN3, ZFYVE26, CECR2, CHMP5, ANLN, ALKBH4, CEP55, TRIM36, FMN2, SPIRE1, CHMP1B, LZTS2, CHMP7, KLHDC8B
BP	GO:0001101	response to acid chemical	92/3408	6.11E-04	ABL2, ACACA, ADCY6, ALAD, RHOA, ATM, ATP2B4, ATP7A, BCL2L1, CAPN2, CASP3, CDKN1B, CEBPB, CFL1, CCR7, COL1A1, COL1A2, COL3A1, COL4A1, COL5A2, CPT1A, CREB1, ATF2, AKR1C2, DNMT3A, DUSP1, EDN1, EGFR, EGR1, FOXO1, GJA1, GNB1, HDAC2, HNRNPD, IGF2R, IPO5, LDLR, LYN, MTHFR, MYB, NTRK3, OGG1, OPA1, PAX2, PDGFB, PDGFRA, PDK3, PDK4, PRKAA1, PRKCE, PTAFR, PTCH1, PTGER4, RARG, RORB, SCD, SFRP1, SLC1A2, SPARC, SRC, ZEB1, TMBIM6, TGFBR3, VEGFA, WNT7B, XBP1, XRCC5, YY1, FZD4, AKR1C3, SOCS1, ALDH1A2, KLF4, TOMM20, KLF2, ATG7, CPEB3, DKK1, UFL1, NSMF, HTRA2, INSIG2, BCL11A, GDAP2, CYP26B1, RRAGD, RRAGC, CPEB4, SESN2, SESN3, UBR1, ACER2
BP	GO:0072073	kidney epithelium development	45/3408	6.31E-04	JAG1, BCL2, BMP7, CTNNB1, EFNB2, EPHA4, EPHA7, FGF1, FGF2, FOXC1, GATA3, HES1, ILK, SMAD2, SMAD4, SMAD6, SMAD7, MEF2C, MYC, PAX2, PBX1, PKD1, PODXL, PTCH1, SDC4, SFRP1, STAT1, HNF1B, VEGFA, WNT7B, WNT2B, DCHS1, IQGAP1, GDF11, SPRY1, KLHL3, HEYL, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, BMPER, FMN1
BP	GO:0061515	myeloid cell development	27/3408	6.32E-04	BCL6, EP300, ERCC2, FBN1, G6PD, NCKAP1L, KIT, NOTCH2, SLC11A2, PAFAH1B1, PIP4K2A, PTPN11, SRC, SRF, TAL1, PABPC4, PTBP3, SH2B3, TSPAN2, WASF2, KLF2, ZNF385A, FOXP1, FBXW7, FAM20C, FAM210B, SIGLEC15
BP	GO:0045995	regulation of embryonic development	43/3408	6.42E-04	AR, BMP7, BMPR1A, COL5A1, COL5A2, CTNNB1, DAG1, DVL3, GATA2, GATA3, HNF4A, HES1, INSR, LAMA4, MBP, PAFAH1B1, SFRP1, SNAI1, STK4, NR2C2, WNT2B, FZD3, FZD1, KLF4, TRIP12, RBM19, DKK1, PHLDB1, CLASP1, NIPBL, RAB14, SUFU, SIX4, WNT4, VANGL2, TGIF2, WNK1, PHLDB2, MYADM, CCSAP, AMOT, CRB2, NRARP
BP	GO:0071166	ribonucleoprotein complex localization	42/3408	6.44E-04	EIF4E, NCBP1, NUP88, NUP98, POLR2D, RAN, RANBP2, UPF1, ABCE1, SRSF1, SRSF2, SRSF4, SRSF7, TSC1, XPO1, PABPN1, POM121, SMG7, NXF1, NUP50, RNPS1, XPOT, DDX19B, U2AF2, SMG1, SMG5, UPF2, RBM15B, NMD3, CDC40, CPSF2, ALKBH5, DDX19A, WDR33, NDC1, NUP133, RIOK2, PCID2, THOC2, SEH1L, NUP43, POM121C

BP	GO:0072089	stem cell proliferation	40/3408	6.44E-04	ZFP36L1, RUNX1, CTNNA1, CTNNB1, FGF2, HIF1A, HNRNPU, ID4, KITLG, NF2, PAFAH1B1, PAX6, PIM1, EIF2AK2, PTPRC, CX3CL1, SNAI2, SOX11, TBX3, TEAD3, TERT, TP53, VEGFA, WNT7B, WNT2B, FZD3, HMGA2, NUMB, ARHGEF2, ARIH2, FRS2, KDM1A, YTHDF2, NDE1, FERMT1, ZNRF3, TRIM71, KCTD11, AGO3, ATXN1L
BP	GO:0051101	regulation of DNA binding	41/3408	6.44E-04	CALM3, CEBPG, CTNNB1, EP300, ERCC2, FOXC1, GATA3, HDAC2, HES1, ID4, IRF4, ISL1, JUN, MSX1, PAX6, POU4F1, MAPK8, RB1, SKI, SOX11, SP100, TAF1, TWIST1, TXN, HMGA2, TNKS, PER2, KLF4, HAND1, KDM1A, MAU2, NIPBL, SIN3A, HIPK2, RSF1, PINX1, FBXW7, ZNF462, NSD1, WFIKKN2, ZNF675
BP	GO:0050772	positive regulation of axonogenesis	31/3408	6.45E-04	RHOA, ARHGDIA, BDNF, BMPR2, EFNA5, MEGF8, FN1, GDI1, GOLGA4, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, ROBO1, SKIL, SRF, TIAM1, VEGFA, RND2, SEMA7A, NRP1, NTN1, TRAK1, PLXND1, NIN, METRN, PLXNA4
BP	GO:0072395	signal transduction involved in cell cycle checkpoint	28/3408	6.85E-04	ATM, BRCA1, CDC5L, CDKN1A, CDKN1B, CHEK1, EP300, MDM4, CNOT4, PML, RBL2, SOX4, SOX11, AURKA, TFDP1, TFDP2, TP53, BTG2, CDC14B, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, DTL, CNOT6, BRCC3, E2F7
BP	GO:0031570	DNA integrity checkpoint	49/3408	6.93E-04	ATM, ATR, CCND1, BRCA1, CDC5L, CDKN1A, CDKN1B, CHEK1, FOXN3, ATF2, MAPK14, EP300, MDM4, FOXO4, CNOT4, PML, PTPN11, RAD1, RBL2, SOX4, AURKA, TFDP1, TFDP2, TOP2B, TP53, BTG2, HMGA2, CDC14B, PEA15, CNOT8, TAOK2, CLOCK, PLK2, CNOT1, ZNF385A, HINFP, GIGYF2, WAC, TRIAP1, DTL, ETAA1, CNOT6, TAOK1, USP28, BRCC3, WDR76, RHNO1, ZNF830, E2F7
BP	GO:0051568	histone H3-K4 methylation	23/3408	7.00E-04	BRCA1, CTNNB1, DNMT3B, GATA3, SMAD4, KMT2A, MYB, KDM6A, KMT2D, CTR9, SETD1A, KMT2B, KDM1A, AUTS2, WDR5B, TET2, BCOR, KMT2E, BEND3, KMT2C, SETD3, DPY30, TET3
BP	GO:0090316	positive regulation of intracellular protein transport	48/3408	7.07E-04	AKT2, MAPK14, ECT2, STOM, ERBB2, GSK3B, JUP, KIF5B, IPO5, MYO1C, OAZ2, PRKAA1, MAPK1, RAN, SORL1, SREBF2, VAMP2, TCF7L2, TP53, UBE2D3, UBE2L3, YWHAE, FZD5, BAP1, EDEM1, ATG13, C2CD5, BCAP31, TENM1, NUTF2, RAPGEF3, ARIH2, ANP32B, TARDBP, HTRA2, SH3GLB1, UBR5, MIEF1, LEPROT, FBXW7, RIOK2, SAR1A, MFF, MAVS, USP36, RHOU, XPO4, MIEF2
BP	GO:0038179	neurotrophin signaling pathway	18/3408	7.07E-04	BDNF, CASP3, GRB2, RAPGEF1, NTRK3, PTPN11, SORT1, SOS1, SRC, WASF1, RAPGEF2, SPRY1, SLC9A6, FRS2, CYFIP2, DDIT4, KIDINS220, AKT1S1
BP	GO:0031016	pancreas development	29/3408	7.30E-04	ACVR2B, BAK1, CDK6, CTNNB1, FOXO1, NR5A2, GATA6, GSK3B, HNF4A, HES1, IGF2, IL6R, INSR, ISL1, SMAD2, MEIS2, MEN1, MET, PAX6, PROX1, RFX3, SOX4, HNF1B, TCF7L2, XBP1, ALDH1A2, ONECUT2, CLOCK, GDF11
BP	GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	29/3408	7.30E-04	AR, RHOA, ARRB2, BRCA1, CALR, RUNX1, CBFB, CRY2, DAB2, DDX5, EP300, FOXA1, ISL1, SFRP1, SRC, TAF1, KMT2D, TP63, LATS1, CLOCK, NCOR1, CNOT1, UFL1, SIRT1, WBP2, HEYL, FOXP1, STRN3, KCTD6
BP	GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	29/3408	7.30E-04	BCL2, PTTG1IP, CD44, CDKN1A, DDX5, EP300, FHIT, HNRNPK, MSX1, PML, POU4F1, TP53, DYRK2, TP63, KDM1A, SIRT1, PHLDA3, ZNF385A, HIPK2, CDIP1, RRM2B, TRIAP1, TAF9B, DDIT4, RRN3, USP28, AEN, JMY, HIPK1
BP	GO:0034605	cellular response to heat	44/3408	7.55E-04	ATM, ATP2A2, ATR, BAG1, CAMK2A, CAMK2D, CDKN1A, CREBBP, EIF2S1, EP300, FGF1, FKBP4, GSK3B, HDAC2, HSBP1, HSPA2, HSPA5, IRAK1, LYN, MAPT, ATXN3, NUP88, NUP98, POLR2D, MAPK1, MAPK3, RANBP2, THBS1, VCP, YWHAE, BAG4, POM121, NUP50, SIRT1, HSPB8, MYOF, HTRA2, NDC1, NUP133, MLST8, SEH1L, AKT1S1, NUP43, POM121C
BP	GO:1905475	regulation of protein localization to membrane	56/3408	7.66E-04	ACTB, ADAM10, AKT2, AR, ARF6, BCL2, BCL2L1, AP2M1, CRKL, CSK, DAB2, DAG1, EGFR, STOM, EPHB2, ERBB2, GBP1, GDI1, ITGA3, ITGB1, KIF5B, LRP1, MMP14, MYO1C, PPP3R1, PRKCE, MAPK8, SPTBN1, STX3, VAMP7, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, NUMB, SQSTM1, AKAP5, C2CD5, GPC6, LYPLA1, AGR2, RAB11FIP2, RHOQ, SLC7A11, CLIP3, APPL1, LDLRAP1, BBC3, SSH1, MIEF1, MFF, TMBIM1, PKDCC, MIEF2
BP	GO:0003206	cardiac chamber morphogenesis	42/3408	7.69E-04	JAG1, BMP7, BMPR1A, BMPR2, COL11A1, FKBP1A, FOXC1, GATA3, GATA6, NRG1, HIF1A, HES1, RBPJ, ISL1, SMAD4, SMAD6, SMAD7, MEF2C, NOTCH2, POU4F1, PROX1, ROBO1, SOS1, SOX4, SOX11, SRF, TBX3, TGFBR1, TGFBR3, TP53, FZD1, NRP1, HAND1, ADAMTS1, UBE4B, CITED2, HEYL, DLL4, CHD7, VANGL2, HEG1, PTCD2
BP	GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	41/3408	7.69E-04	ATM, CCND1, BCL2, CDK6, CDKN1A, CDKN1B, EP300, EZH2, FHL1, MDM4, CNOT4, PML, PTEN, RB1, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, KLF4, CNOT8, CTDSP2, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, ZNF385A, GIGYF2, TRIAP1, CNOT6, CTDSP1, ZNF655, CDC73, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0008406	gonad development	63/3408	7.69E-04	AR, ARRB1, ARRB2, ATM, ATRX, CCND1, BCL2, BCL2L1, CASP3, CBL, CEBPB, CRKL, CTNNA1, FOXC1, FOXO3, GATA3, GATA6, GJA1, HOXA9, HSPA5, INSR, KIT, SMAD4, KITLG, MMP14, NKX3-1, PDGFRA, PGR, KDM5A, SFRP1, SRC, TGFBR1, TMF1, VEGFA, WNT2B, SF1, CSDE1, NRIP1, FZD4, AKR1C3, TNFSF10, SGPL1, PCYT1B, ADAMTS1, KMT2B, BCL2L11, FSTL3, CITED2, SEMA3A, RHOBTB3, FNDC3A, SIRT1, SOX8, ARID4B, SIX4, WNT4, PLEKHA1, ARID5B, ZNF830, TBC1D20, RNF38, RDH10, AGO4
BP	GO:0060348	bone development	63/3408	7.69E-04	RHOA, BMPR2, RUNX2, FOXN3, COL1A1, COL6A2, COL12A1, MEGF8, EP300, FBN1, FGFR3, FOXC1, GJA1, GNAS, INSIG1, KIT, LRP6, MATN2, MEF2C, MEF2D, MMP14, MSX1, NAB1, NOTCH2, PAFAH1B1, PIP4K2A, PLS3, PRPSAP2, PTGER4, PTPN11, PTPRC, RARG, SKI, SPARC, SRC, SRF, STC1, TAL1, THBS3, TP53, TWIST1, DCHS1, PAPSS2, TRIP11, SH2B3, WASF2, AKAP13, TTC9,

					ZNF385A, GREM1, FOXP1, INSIG2, RAB23, FBXW7, CSGALNACT1, SULF2, CYP26B1, FAM20C, BBX, COL27A1, AMER1, SIGLEC15, SH3PXD2B
BP	GO:0010811	positive regulation of cell-substrate adhesion	40/3408	7.69E-04	ABL1, CALR, CDC42, CDK6, CCR7, CRK, CRKL, CSF1, DAG1, EMP2, FN1, GSK3B, ILK, ITGA6, ITGA3, ITGA5, JUP, MDK, NEDD9, NID1, PRKCE, PTPRJ, RREB1, CX3CL1, SDC4, SFRP1, TSC1, VEGFA, IQGAP1, NRP1, MAP4K4, SPOCK2, ARPC2, AGR2, MMRN1, WNT4, FERMT1, EPB41L5, MYADM, FMN1
BP	GO:0048675	axon extension	40/3408	7.69E-04	ABL1, ALCAM, BMPR2, MEGF8, FN1, GDI1, GOLGA4, GSK3B, ILK, ITGB1, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, SRF, VCL, VEGFA, USP9X, ULK1, SEMA7A, NRP1, DCLK1, NTN1, SEMA3E, SEMA3A, OLFM1, SLC9A6, SEMA4B, RAB21, SIN3A, AUTS2, SEMA4C, SEMA6A, RAPH1, PLXNA4, WDR36, TTL
BP	GO:0050890	cognition	81/3408	7.70E-04	ADCY1, AMFR, BDNF, CAMK4, CASP3, CEBPB, COMT, CREB1, CTNS, EGFR, EP300, EPHB2, CLN8, GATM, KAT2A, GM2A, HTT, HIF1A, HMGCR, INSR, ITGA3, ITGA5, ITGB1, JUN, KIT, KRAS, LDLR, MAP1A, MAPT, MDK, MECP2, MEF2C, MEIS2, MME, SLC11A2, PAFAH1B1, PDE1B, MAPK1, PTEN, RAG1, ATXN1, SLC1A4, SNAP25, SRF, THRA, VLDLR, BTG2, FOSL1, ITGA8, B4GALT2, SYNGAP1, SYNJ1, KALRN, KMT2B, ACTR2, ATP8A1, PLK2, FAM107A, CPEB3, SHANK2, DKK1, CIC, NCSTN, SLC7A11, SLC24A2, NIPBL, ZNF385A, CNTNAP2, NPTN, TMOD2, YTHDF1, SOBP, UBA6, CHD7, SLC12A5, RIC8A, NDRG4, BHLHB9, BTBD9, PTCHD1, ATXN1L
BP	GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	11/3408	7.71E-04	ZFP36L1, ZFP36L2, ZFP36, BTG2, TOB1, CPEB3, CNOT1, TNRC6B, PABPC1, TNRC6A, TNRC6C
BP	GO:0048736	appendage development	54/3408	8.10E-04	ASPH, ATRX, BAK1, BMP7, BMPR1A, BMPR2, CACNA1C, RUNX2, CREBBP, CTNNB1, DLX6, MEGF8, FBN2, KAT2A, GJA1, GNAS, HDAC2, HOXA9, HOXD13, ITGA6, LRP6, SMAD4, MBNL1, MSX1, PBX1, PRRX1, PTCH1, RARG, SKI, SOX4, SOX11, TBX3, NR2F2, TWIST1, FZD6, TP63, KAT2B, ALDH1A2, BCL2L11, DKK1, IQCE, SLC7A11, NIPBL, GREM1, CHD7, CYP26B1, SMOC1, KREMEN1, ZNRF3, PKDCC, RDH10, FREM2, FMN1, RNF165
BP	GO:0060173	limb development	54/3408	8.10E-04	ASPH, ATRX, BAK1, BMP7, BMPR1A, BMPR2, CACNA1C, RUNX2, CREBBP, CTNNB1, DLX6, MEGF8, FBN2, KAT2A, GJA1, GNAS, HDAC2, HOXA9, HOXD13, ITGA6, LRP6, SMAD4, MBNL1, MSX1, PBX1, PRRX1, PTCH1, RARG, SKI, SOX4, SOX11, TBX3, NR2F2, TWIST1, FZD6, TP63, KAT2B, ALDH1A2, BCL2L11, DKK1, IQCE, SLC7A11, NIPBL, GREM1, CHD7, CYP26B1, SMOC1, KREMEN1, ZNRF3, PKDCC, RDH10, FREM2, FMN1, RNF165
BP	GO:0051216	cartilage development	61/3408	8.33E-04	ATP7A, BMP3, BMP7, BMPR1A, BMPR2, RUNX2, RUNX3, CD44, COL1A1, COL6A2, COL11A1, COL12A1, MAPK14, CTNNB1, DLX2, EDN1, ESRRA, FGF2, FGFR3, GNAS, HIF1A, HOXA3, HOXA5, HOXB3, HOXC4, ITGB8, LOXL2, LRP6, MATN2, MDK, MEF2C, MEF2D, MSX1, NFIB, PKD1, PRRX1, MAPK3, RARG, SNAI2, SNAI1, SRF, STC1, ZEB1, TGFBR1, THBS3, THRA, TRPS1, WNT7B, WNT2B, HMGA2, TRIP11, HAND1, SATB2, GREM1, CSGALNACT1, SULF2, CREB3L2, COL27A1, PKDCC, BMP8A, SNX19
BP	GO:0010921	regulation of phosphatase activity	53/3408	8.36E-04	CALM1, CALM2, CALM3, CRY2, DLG3, ENSA, FKBP1A, GNAI2, GSK3B, HTT, NCKAP1L, IKBKB, MEF2C, MYO1D, PPP1R12A, PPP1R2, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, EIF2AK2, PTPRC, SET, TSC1, SHOC2, ROCK2, BAG4, PHACTR2, NUAK1, FARP1, ARPP19, LMTK2, PPP6R1, RRP1B, ANKLE2, PPP1R16B, ZFYVE1, SYTL2, PPP6R3, PPP2R2D, SLC39A10, SLC7A14, PCIF1, WNK1, MTMR9, ZCCHC9, PPP1R15B, FAM122A, WDR81, PPP4R2, SPRED1, BOD1L1, PPP1R37
BP	GO:0071985	multivesicular body sorting pathway	16/3408	8.36E-04	TMEM50B, LYST, SORT1, UVRAG, VCP, VPS4B, SNF8, LEPROTL1, TMEM50A, VPS36, CHMP5, LEPROT, VPS37C, LAPTM4B, CHMP1B, VPS37D
BP	GO:2000758	positive regulation of peptidyl-lysine acetylation	16/3408	8.36E-04	ARRB1, BRCA1, GATA3, KAT2A, ISL1, SMAD4, PRKAA1, MAPK3, SNAI2, SOX4, RPS6KA4, RPS6KA5, KAT7, WBP2, AUTS2, TADA2B
BP	GO:0048562	embryonic organ morphogenesis	79/3408	8.50E-04	BMP7, RUNX2, COL11A1, CTNNB1, DLX2, DLX6, EDN1, MEGF8, EPHB2, FBN1, FBN2, GATA2, GATA3, GJA1, GNAS, HIF1A, HOXA3, HOXA5, HOXA7, HOXB3, HOXB5, HOXB8, HOXC4, HES1, INSIG1, LRP6, SMAD2, MEF2C, MMP14, MSX1, OTX1, PAX2, PAX6, PDGFRA, PRRX1, MAPK1, MAPK3, PROX1, RARG, SOX11, SP3, SRF, TBX3, HNF1B, TCF7, ZEB1, TGFBR1, TWIST1, KDM6A, FZD5, FZD3, NR4A3, ARID1A, FZD6, ITGA8, HAND1, NTN1, FRS2, SATB2, NIPBL, MTHFD1L, LRIG1, HIPK2, INSIG2, SUFU, SIX4, AHI1, IFT57, SOBP, CHD7, VANGL2, MIB1, NDRG4, SETDB2, TTC39C, RDH10, HIPK1, CRB2, RBPMS2
BP	GO:0035264	multicellular organism growth	46/3408	8.53E-04	ADARB1, ADD1, ADRB1, AR, ATM, ATRX, BCL2, ZFP36L1, CREB1, CSF1, EP300, ERCC2, ERCC6, KAT2A, GNAS, HOXA5, IGF2, PDE4D, POU3F2, PTCH1, PTPN11, RARG, RBBP6, SLC1A2, SOS1, STAT3, STAT5B, TP53, KDM6A, STC2, SOCS2, SGPL1, KLF2, WDTC1, NIPBL, GIGYF2, HTRA2, CHD7, SLC12A5, HEG1, PLEKHA1, TBL1XR1, STK40, ARID5B, PKDCC, SH3PXD2B
BP	GO:0051896	regulation of protein kinase B signaling	69/3408	8.59E-04	ARRB2, AXL, CCR7, DAG1, AKR1C2, HBEGF, EGFR, ERBB2, FGF1, FGF2, FGF5, FGFR3, GAB1, GATA3, GCNT2, GRB2, RAPGEF1, NRG1, HIP1, IGF1R, IGF2, IGFBP5, IL18, ILK, INSR, ITGB1, KIT, MAZ, MET, KITLG, PDGFA, PDGFB, PDGFRA, PIK3CB, PTEN, PTPN11, PTPRJ, CX3CL1, SRC, TCF7L2, TGFA, TGFBR1, THBS1, TXN, AKR1C3, IRS2, KLF4, BAG4, FGF19, SH2B3, BTN2A2, FRS2,

					HPSE, PHLPP2, PHLPP1, OTUD3, SIRT1, PHLDA3, PLEKHA1, MUL1, MTDH, OSBPL8, PIK3AP1, SESN3, NRG4, FLCN, RICTOR, EPGN, FAM110C
BP	GO:0003281	ventricular septum development	28/3408	8.59E-04	PRDM1, BMPR2, GATA3, HES1, RBPJ, LTBP1, SMAD4, SMAD6, SMAD7, MDM4, PROX1, ROBO1, SOX4, SOX11, TBX3, TGFBR1, TGFBR3, LUZP1, FZD1, TRIP11, CITED2, FRS2, HECTD1, HEYL, SUFU, VANGL2, HEG1, DCTN5
BP	GO:0038127	ERBB signaling pathway	45/3408	8.66E-04	ABL1, CBL, CDC42, HBEGF, EGFR, ERBB2, FER, GAB1, GRB2, NRG1, HIP1, RBPJ, PIK3C2A, PRKCA, MAPK1, PTPN11, PTPN12, PTPRJ, PTPRR, SH3GL2, SHC1, SOS1, SRC, ADAM17, TGFA, CUL5, NCK2, DGKD, IQGAP1, CPNE3, GPRC5A, RPS6KA5, SOCS5, RASSF2, SPRY1, AGR2, PTPN18, ERRFI1, FBXW7, SH3TC2, AFAP1L2, SOCS4, NRG4, DAB2IP, EPGN
BP	GO:1903392	negative regulation of adherens junction organization	12/3408	8.72E-04	LRP1, MMP14, PTEN, RDX, SRC, THBS1, VEGFA, DLC1, FAM107A, CORO1C, RCC2, PHLDB2
BP	GO:0008584	male gonad development	44/3408	8.77E-04	AR, ATRX, CCND1, BCL2, BCL2L1, CBL, CRKL, CTNNA1, GATA3, GATA6, GJA1, HOXA9, INSR, KIT, SMAD4, KITLG, MMP14, NKX3-1, PDGFRA, KDM5A, SFRP1, TGFBR1, TMF1, WNT2B, SF1, CSDE1, AKR1C3, TNFSF10, SGPL1, BCL2L11, FSTL3, CITED2, SEMA3A, RHOBTB3, FNDC3A, SOX8, ARID4B, SIX4, WNT4, PLEKHA1, ARID5B, TBC1D20, RNF38, AGO4
BP	GO:0061008	hepaticobiliary system development	44/3408	8.77E-04	ADA, AK4, ARF6, ATP7A, CCND1, CEBPB, CEBPG, EGFR, EZH2, GATA6, HNF4A, HNRNPD, HES1, IGF2R, JARID2, JUN, KRAS, MAN2A1, MDK, MET, PKD1, PKM, PROX1, PTCH1, SP3, AURKA, HNF1B, TGFBR3, XBP1, CUL3, ALDH1A2, ONECUT2, CITED2, CIT, SEC63, NIPBL, UPF2, WNT4, FBXW7, SULF2, GNPNAT1, PTCD2, ARID5B, E2F7
BP	GO:0071364	cellular response to epidermal growth factor stimulus	19/3408	8.83E-04	ZFP36L1, ZFP36L2, CBL, COL1A1, EEF1A1, EGFR, ERBB2, FOXC1, MCM7, PAX2, PTPN11, PTPN12, SNAI2, STAT5B, ZFP36, IQGAP1, BAG4, ERRFI1, DAB2IP
BP	GO:0007041	lysosomal transport	36/3408	9.03E-04	AP1G1, ARF1, RHOB, SCARB2, LYST, IGF2R, LAMP2, LRP1, M6PR, NEDD4, NPC1, SORT1, SORL1, VAMP7, VCP, AP3D1, VPS4B, ZFYVE16, HMGXB4, ATG14, DENND3, TRAK1, MGRN1, AP3M1, HOOK1, ANKFY1, CHMP5, VPS54, TMEM106B, VPS35, EPG5, KIF13A, TRAK2, GNPTAB, HOOK3, RAB12
BP	GO:0021675	nerve development	29/3408	9.06E-04	ADARB1, BDNF, CTNNB1, DAG1, EPHB2, HOXA3, HOXB3, HES1, ILK, ISL1, NPTX1, PAX2, ATP8B1, SERPINE2, POU4F1, VCAM1, NRP1, LRIG2, SEMA3A, UNC13B, DICER1, LRIG1, SIX4, CHD7, SULF2, NAV2, PLXNA4, FBXO45, RNF165
BP	GO:1900034	regulation of cellular response to heat	29/3408	9.06E-04	ATM, ATR, BAG1, CAMK2A, CAMK2D, CREBBP, EP300, FKBP4, GSK3B, HSBP1, MAPT, NUP88, NUP98, MAPK1, MAPK3, RANBP2, YWHAE, BAG4, POM121, NUP50, SIRT1, HSPB8, NDC1, NUP133, MLST8, SEH1L, AKT1S1, NUP43, POM121C
BP	GO:0045446	endothelial cell differentiation	38/3408	9.11E-04	ACVR2B, ADD1, JAG1, BMPR2, BTG1, CTNNB1, S1PR1, S1PR3, RAPGEF1, GSTM3, NRG1, HOXB5, RBPJ, IKBKB, SMAD4, MET, PDE4D, PROX1, RAP1B, RDX, STC1, ZEB1, NR2F2, VEGFA, WNT7B, VEZF1, NRP1, TJP2, ROCK2, RAPGEF2, RAPGEF3, KDM6B, PPP1R16B, FOXJ2, HEG1, RAP2C, APOLD1, MYADM
BP	GO:0060148	positive regulation of posttranscriptional gene silencing	13/3408	9.11E-04	DDX5, EGFR, EIF4G1, FMR1, MYCN, STAT3, TP53, ZFP36, FXR1, LIMD1, PUM1, XPO5, TRIM71
BP	GO:0010171	body morphogenesis	21/3408	9.21E-04	ASPH, COL1A1, DAG1, EP300, GNAS, LRP6, MSX1, PAX9, PDGFRA, PTPN11, SKI, SGPL1, ATP6AP2, DKK1, PHLDB1, CLASP1, NIPBL, CDON, PLEKHA1, ARID5B, PHLDB2
BP	GO:0010718	positive regulation of epithelial to mesenchymal transition	21/3408	9.21E-04	JAG1, BMP7, COL1A1, CTNNB1, DAB2, EZH2, FOXC1, GCNT2, HDAC2, ISL1, LOXL2, SMAD2, SMAD4, MDK, SNAI1, TCF7L2, TGFBR1, TIAM1, TWIST1, OLFM1, CRB2
BP	GO:1901861	regulation of muscle tissue development	48/3408	9.47E-04	ARRB2, BCL2, BMPR1A, CREB1, MAPK14, CTNNB1, DDX5, EDN1, EFNB2, FGF2, G6PD, GATA6, KAT2A, GJA1, NRG1, HMGCR, IGFBP5, RBPJ, JARID2, SMAD4, MEF2C, PIM1, PIN1, PPARA, PRKAA1, MAPK1, PTEN, RGS2, RGS4, TGFBR1, TGFBR3, TWIST1, YY1, AKAP6, HDAC9, NR1D2, DDX17, FRS2, DKK1, FBXO22, GREM1, CDON, SIX4, CYP26B1, AKIRIN1, UQCC2, MTPN, FLCN
BP	GO:0071277	cellular response to calcium ion	30/3408	9.47E-04	ADCY1, ADD1, CAMK2D, ECT2, EDN1, FOSB, FUS, HSPA5, ITPKB, JUN, JUND, MEF2A, MEF2C, PRKAA1, SYT1, TRPM2, AKR1C3, IQGAP1, CPNE3, SYT7, NLGN1, SYT11, NCSTN, CLIC4, SLC25A24, SYT17, WNK1, SYT2, CPNE8, CPNE2
BP	GO:1901654	response to ketone	57/3408	9.53E-04	ACACA, ADCY1, ADCY6, AR, ATP2B1, CCND1, BCL2L1, KLF9, CALM3, CALR, CAV1, CBL, CDC5L, CDKN1A, CCR7, AKR1C2, DNMT3B, DUSP1, EDN1, EFNA5, EGFR, EIF4E, ELK1, FOXO1, FOXO3, FOSB, GNB1, NR3C1, HNRNPD, HOXD13, NKX3-1, NTRK3, OPA1, PRKAA1, PRKCE, PTAFR, PTGER4, SFRP1, SRC, TGFBR3, THBS1, FOSL1, AKR1C3, KLF4, ROCK2, KLF2, NCOA2, ABHD2, KIF1B, LARP1, SIRT1, WBP2, SIN3A, NDOR1, ERRFI1, XRN1, DDIT4
BP	GO:0006109	regulation of carbohydrate metabolic process	60/3408	9.72E-04	ADCYAP1R1, AKT2, SCARB2, EP300, FOXO1, KAT2A, GSK3B, HIF1A, IGF2, FOXK2, INSR, NFKB1, NUP88, NUP98, P2RY1, PDGFB, PDK3, PDK4, ENPP1, PFKFB2, PFKFB3, PFKFB4, PGAM1, PHKG2, PPARA, PPP1CA, PPP1CB, PRKAA1, PRKCE, PTAFR, RANBP2, RORA, SNCA, SRC, STAT3, TP53, DYRK2, IRS2, KAT2B, NCOR1, EPM2AIP1, POM121, NCOA2, NUP50, ARPP19, SLC2A6, MLXIP, PASK, SIRT1, ADIPOR1, DDIT4, NDC1, NUP133, SEH1L, SESN2, SOGA1, SIK1, FOXK1, NUP43, POM121C

BP	GO:0021543	pallium development	52/3408	9.82E-04	RHOA, ATP2B4, CASP3, CDK6, COL3A1, CRK, CRKL, CTNNB1, DLX2, EGFR, EZH1, EZH2, GSK3B, HIF1A, ID4, KIF5B, LRP1, LRP6, MDK, NF2, PAFAH1B1, PAX6, PEX13, POU3F2, PROX1, PTEN, ROBO1, TRA2B, SRF, TACC1, TSC1, YWHAE, BTG2, NR4A3, NRP1, SEMA3A, IGF2BP1, BTBD3, KDM1A, PHLPP2, KDM6B, CNTNAP2, CDON, SLC38A2, NDE1, UBA6, FUT10, DIXDC1, DAB2IP, CEP120, FBXO45, CCDC85C
BP	GO:0009101	glycoprotein biosynthetic process	92/3408	9.85E-04	ASGR1, ATP7A, BCL2, BMPR2, CCR7, NCAN, CTNNB1, DCN, HBEGF, EXTL2, EXTL3, FUT8, GALNT1, GALNT2, GCNT2, GFPT1, NDST1, MAN2A1, MPI, NPC1, PAWR, PGM3, PMM2, ST3GAL1, SOAT1, TCF7L2, UBE2G2, UGDH, VCP, ST8SIA4, B4GALT2, TRIP11, B4GALT6, NDST3, ITM2B, HS2ST1, FAM20B, GFPT2, HS3ST3A1, HS3ST1, UST, TNIP1, ST3GAL6, MAN1A2, GALNT6, PHLDA1, TRAK1, NCSTN, POFUT1, BACE2, GLCE, SERP1, ST6GALNAC6, ST8SIA3, CHST15, UBE2J1, GALNT7, TET2, CSGALNACT2, GALNT10, POMGNT1, CSGALNACT1, TMEM165, ALG1, CHST7, UGGT1, C1GALT1, VANGL2, XYLT2, GORASP1, TRAK2, FKRP, SRD5A3, EDEM3, TET1, ITM2C, CHST9, COG3, B3GNT5, SYVN1, ST6GAL2, FUT10, POMGNT2, HS6ST2, NUS1, CANT1, TET3, HS6ST3, GXYLT1, EOGT, DPY19L4, ACER2
BP	GO:0061351	neural precursor cell proliferation	46/3408	9.87E-04	RHOA, RERE, CTNNA1, CTNNB1, CTSZ, FOXO1, FOXO3, GATA2, GNAI2, RAPGEF1, HIF1A, ID4, ILK, LYN, MDK, NAP1L1, NF2, PAFAH1B1, PAX6, POU3F2, PROX1, RORA, CX3CL1, TEAD3, TP53, VEGFA, BTG2, FZD3, FZD6, PSMG1, NUMB, ARHGEF2, MELK, IGF2BP1, FRS2, KDM1A, CDON, DLL4, NDE1, SHCBP1, HOOK3, ZNF503, DIXDC1, TRIM71, KCTD11, CEP120
BP	GO:0034614	cellular response to reactive oxygen species	51/3408	1.01E-03	ABL1, RHOB, ATP7A, AXL, BMP7, CCNA2, CRK, ECT2, EGFR, EZH2, FER, FOXO1, FOXO3, HDAC2, HNRNPD, JUN, MAPT, MET, MTR, MYB, PRDX1, PAWR, PAX2, PDGFRA, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, PTPRK, PXN, RPS3, SOD2, SRC, TRPM2, TXN, NR4A3, AKR1C3, KLF4, NET1, SIGMAR1, KLF2, PRDX3, ZNF277, KDM6B, SZT2, SIRT1, PRDX5, OSER1, PLEKHA1, SIRPA
BP	GO:0035019	somatic stem cell population maintenance	27/3408	1.01E-03	BCL9, BMP7, ZFP36L2, FGF2, GATA2, HES1, RBPJ, KIT, LIG4, SMAD2, SMAD4, PAX2, PBX1, POLR2D, POLR2K, SFRP1, SKI, SOX4, STAT3, HNF1B, KLF10, TP63, LDB1, LDB2, KLF4, FOXP1, VANGL2
BP	GO:1903747	regulation of establishment of protein localization to mitochondrion	27/3408	1.01E-03	BCL2, DNAJA1, MAPT, PPP3R1, PRKAA1, MAPK8, SREBF2, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, BAP1, TP63, BAG4, ATG13, ARIH2, BBC3, HTRA2, SH3GLB1, LEPROT, FBXW7, USP36, RHOU
BP	GO:0048814	regulation of dendrite morphogenesis	32/3408	1.01E-03	ADAM10, CFL1, CUX1, EPHA4, FMR1, GSK3B, ILK, CAPRIN1, NEDD4, OPA1, PAFAH1B1, PAK3, PPP3CA, PTEN, PTPRD, RAP2A, SDC2, VAMP7, TIAM1, KALRN, RAPGEF2, ACTR2, ABI2, PDLIM5, NLGN1, RAB21, NSMF, SIPA1L1, SS18L1, HECW2, GORASP1, BHLHB9
BP	GO:0035304	regulation of protein dephosphorylation	44/3408	1.02E-03	CALM1, CALM2, CALM3, CRY2, ENSA, FKBP1A, GNAI2, GSK3B, HTT, NCKAP1L, IKBKB, PPP1R12A, PIN1, PPP1R2, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, EIF2AK2, PTPRC, SET, TSC1, YWHAE, SHOC2, ROCK2, PHACTR2, NUAK1, DLC1, ARPP19, LMTK2, PPP6R1, ANKLE2, NSMF, PPP1R16B, PPP6R3, PPP2R2D, SLC39A10, PPP1R15B, FAM122A, SPPL3, PPP4R2, CNEP1R1, BOD1L1, PPP1R37
BP	GO:0001889	liver development	43/3408	1.04E-03	ADA, AK4, ARF6, ATP7A, CCND1, CEBPB, CEBPG, EGFR, EZH2, GATA6, HNF4A, HNRNPD, HES1, IGF2R, JARID2, JUN, KRAS, MAN2A1, MDK, MET, PKD1, PKM, PROX1, PTCH1, SP3, AURKA, HNF1B, TGFBR3, XBP1, CUL3, ALDH1A2, ONECUT2, CITED2, CIT, SEC63, UPF2, WNT4, FBXW7, SULF2, GNPNAT1, PTCD2, ARID5B, E2F7
BP	GO:1902807	negative regulation of cell cycle G1/S phase transition	42/3408	1.05E-03	ATM, CCND1, BCL2, CDK6, CDKN1A, CDKN1B, EP300, EZH2, FHL1, MDM4, MEN1, CNOT4, PML, PTEN, RB1, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, KLF4, CNOT8, CTDSP2, CTDSPL, BTN2A2, GPNMB, PLK2, FAM107A, CNOT1, ZNF385A, GIGYF2, TRIAP1, CNOT6, CTDSP1, ZNF655, CDC73, SLFN11, DCUN1D3, NACC2, E2F7
BP	GO:0032091	negative regulation of protein binding	35/3408	1.07E-03	ACTB, ARRB2, CAV1, CSNK1E, CTSZ, DAB2, EIF2S1, GSK3B, DNAJB2, HSPA5, IFIT2, ISL1, LRPAP1, MET, NKX3-1, PDGFB, PIN1, PPARA, PPP1CA, MAPK3, MAPK8, PTPRF, RALB, SORL1, AURKA, STYX, TMBIM6, AURKB, DKK1, KDM1A, USP33, GNL3L, EPB41L5, WFIKKN2, TTBK2
BP	GO:0000380	alternative mRNA splicing, via spliceosome	28/3408	1.07E-03	DDX5, DYRK1A, FMR1, HNRNPU, MBNL1, HNRNPM, SRSF1, SRSF2, SRSF4, SRSF7, TRA2B, RBM19, THRAP3, MBNL2, DDX17, CELF2, SRSF10, RNPS1, KDM1A, RBFOX2, RBMX, RBM15B, RSRC1, SMU1, MBNL3, RBM25, FAM172A, SREK1
BP	GO:0006623	protein targeting to vacuole	17/3408	1.10E-03	SCARB2, LAMP2, M6PR, NEDD4, SORL1, VAMP7, AP3D1, GOSR2, ZFYVE16, VPS13A, AP3M1, VPS13C, VPS37C, VPS13D, SMURF1, GNPTAB, VPS37D
BP	GO:0031076	embryonic camera-type eye development	17/3408	1.10E-03	BMP7, LRP6, PAX2, PAX6, PROX1, RARG, SOX11, SP3, ZEB1, TWIST1, FZD5, ARID1A, ALDH1A2, FRS2, HIPK2, RDH10, HIPK1
BP	GO:2000142	regulation of DNA-templated transcription, initiation	17/3408	1.10E-03	CREB1, CTNNB1, DR1, JUN, PSMC2, SRF, TAF1, HNF1B, THRA, TP53, TWIST1, FOSL1, SUB1, ZNF451, RRN3, ATF7IP, CAND1

BP	GO:0000381	regulation of alternative mRNA splicing, via spliceosome	25/3408	1.11E-03	DDX5, DYRK1A, FMR1, HNRNPU, MBNL1, SRSF1, SRSF2, SRSF4, SRSF7, TRA2B, RBM19, THRAP3, MBNL2, DDX17, CELF2, SRSF10, RNPS1, RBFOX2, RBMX, RBM15B, SMU1, MBNL3, RBM25, FAM172A, SREK1
BP	GO:0031060	regulation of histone methylation	25/3408	1.11E-03	ATRX, BRCA1, CTNNB1, DNMT3B, GATA3, JARID2, SMAD4, MECP2, KMT2A, MLLT6, MTHFR, MYB, CTR9, KMT2B, CTCF, MTF2, KDM1A, SIRT1, AUTS2, BCOR, RIF1, KMT2E, NSD1, TET1, SETD7
BP	GO:0014065	phosphatidylinositol 3-kinase signaling	46/3408	1.15E-03	ZFP36L1, CBL, DCN, EDN1, EGFR, ERBB2, FLT4, GAB1, GATA3, IGF1R, IL18, INSR, KIT, LYN, MAZ, NEDD4, NKX3-1, NTRK3, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3C2A, PIK3CB, PIP4K2A, PPARD, MAPK1, MAPK3, PTEN, SRC, TWIST1, TYRO3, IRS2, IER3, KLF4, BTN2A2, STAMBP, PIP5K1C, SIRT1, PPP1R16B, CEP55, PLEKHA1, PREX2, PIK3IP1, PIK3AP1, DAB2IP
BP	GO:0045445	myoblast differentiation	30/3408	1.18E-03	JAG1, ZFP36L1, BTG1, MAPK14, DDX5, EPAS1, FLOT2, NRG1, HMGCR, RBPJ, IL18, ILK, ISL1, MBNL1, MEF2C, PPARD, RB1, SRF, TBX3, TCF7L2, DDX17, HINFP, GREM1, SOX8, CDON, HIF1AN, MBNL3, AKIRIN1, EID2B, PLEKHM3
BP	GO:0043491	protein kinase B signaling	74/3408	1.19E-03	ARRB2, AXL, ZFP36L1, CCR7, DAG1, AKR1C2, HBEGF, EGFR, ERBB2, FGF1, FGF2, FGF5, FGFR3, GAB1, GATA3, GCNT2, GRB2, RAPGEF1, NRG1, HIP1, IGF1R, IGF2, IGFBP5, IL18, ILK, INSR, ITGB1, KIT, MAZ, MET, KITLG, NKX3-1, PAX2, PDGFA, PDGFB, PDGFRA, PIK3CB, PTEN, PTPN11, PTPRJ, CX3CL1, SRC, TCF7L2, TGFA, TGFBR1, THBS1, TXN, TYRO3, AKR1C3, IRS2, KLF4, BAG4, FGF19, SH2B3, BTN2A2, FRS2, HPSE, PHLPP2, PHLPP1, OTUD3, SIRT1, PHLDA3, PLEKHA1, MUL1, SESN2, MTDH, OSBPL8, PIK3AP1, SESN3, NRG4, FLCN, RICTOR, EPGN, FAM110C
BP	GO:0030166	proteoglycan biosynthetic process	26/3408	1.20E-03	BMPR2, NCAN, CTNNB1, DCN, EXTL2, EXTL3, NDST1, TCF7L2, UGDH, NDST3, HS2ST1, FAM20B, HS3ST3A1, HS3ST1, UST, GLCE, CHST15, CSGALNACT2, CSGALNACT1, CHST7, VANGL2, XYLT2, CHST9, HS6ST2, CANT1, HS6ST3
BP	GO:0035023	regulation of Rho protein signal transduction	44/3408	1.20E-03	ABL1, ABL2, ARHGDIA, ARRB1, BCL6, COL3A1, ECT2, EPS8, ARHGAP35, ITGA3, ITGB1, MET, OPHN1, ROBO1, SOS1, TIAM1, TNFAIP1, TRIO, CUL3, NRP1, KALRN, F2RL3, ARHGEF2, ARHGEF17, FARP1, NET1, DLC1, VAV3, AKAP13, KANK1, ARHGEF9, ARHGEF12, PLEKHG3, CDC42SE1, HEG1, PLEKHG2, SYNPO2L, PREX2, KCTD10, ARHGEF39, FGD4, PLEKHG4B, FLCN, SPATA13
BP	GO:0061097	regulation of protein tyrosine kinase activity	31/3408	1.21E-03	BDNF, CAV1, CBL, DLG3, DOCK3, EPHA4, ERCC6, NRG1, NEDD9, PAK2, PDGFB, PTPN1, PTPRC, RAP2B, SHC1, SRC, ADAM17, TAL1, TGFA, NCK2, GPRC5A, SOCS5, IBTK, ERRFI1, NCAPG2, FBXW7, RAP2C, SH3BP5L, AFAP1L2, SOCS4, EPGN
BP	GO:0030219	megakaryocyte differentiation	33/3408	1.27E-03	RUNX1, CBFB, EP300, GABPA, GATA2, KIT, MEF2C, KMT2A, CNOT4, PIP4K2A, PTPN11, SP3, SRF, TAL1, THBS1, NR4A3, KMT2D, KAT2B, SETD1A, KMT2B, SH2B3, WASF2, TNRC6B, SIN3A, ZNF385A, AGO1, TNRC6A, KMT2E, TNRC6C, KMT2C, DPY30, AGO3, AGO4
BP	GO:0048096	chromatin-mediated maintenance of transcription	8/3408	1.27E-03	CHEK1, CTNNB1, ARID1A, KMT2B, ZMIZ1, ARID1B, ZMIZ2, ELOF1
BP	GO:1900102	negative regulation of endoplasmic reticulum unfolded protein response	8/3408	1.27E-03	ATF6B, HSPA5, DNAJB9, NCK1, PTPN1, NCK2, BFAR, PPP1R15B
BP	GO:0001736	establishment of planar polarity	40/3408	1.27E-03	ABL1, RHOA, ARRB2, CDC42, AP2M1, DAB2, DLG3, DVL3, CELSR3, CELSR2, MLLT3, PAFAH1B1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, TIAM1, FZD5, FZD3, FZD1, FZD4, FZD6, TP63, PSMF1, GPC6, PSME3, PSMD14, EXOC5, DKK1, PSME4, SMURF1, VANGL2, PLEKHA4, VANGL1, ZNRF3, PRICKLE2
BP	GO:0007164	establishment of tissue polarity	40/3408	1.27E-03	ABL1, RHOA, ARRB2, CDC42, AP2M1, DAB2, DLG3, DVL3, CELSR3, CELSR2, MLLT3, PAFAH1B1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, TIAM1, FZD5, FZD3, FZD1, FZD4, FZD6, TP63, PSMF1, GPC6, PSME3, PSMD14, EXOC5, DKK1, PSME4, SMURF1, VANGL2, PLEKHA4, VANGL1, ZNRF3, PRICKLE2
BP	GO:0072401	signal transduction involved in DNA integrity checkpoint	27/3408	1.27E-03	ATM, BRCA1, CDC5L, CDKN1A, CDKN1B, CHEK1, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CDC14B, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, DTL, CNOT6, BRCC3, E2F7
BP	GO:0072422	signal transduction involved in DNA damage checkpoint	27/3408	1.27E-03	ATM, BRCA1, CDC5L, CDKN1A, CDKN1B, CHEK1, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CDC14B, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, DTL, CNOT6, BRCC3, E2F7
BP	GO:0060071	Wnt signaling pathway, planar cell polarity pathway	36/3408	1.30E-03	ABL1, RHOA, ARRB2, CDC42, AP2M1, DAB2, DVL3, CELSR3, CELSR2, MLLT3, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, TIAM1, FZD5, FZD3, FZD1, FZD4, FZD6, PSMF1, GPC6, PSME3, PSMD14, DKK1, PSME4, SMURF1, VANGL2, PLEKHA4, VANGL1, ZNRF3, PRICKLE2
BP	GO:0002573	myeloid leukocyte differentiation	59/3408	1.30E-03	ZFP36L1, CAMK4, RUNX1, CDC42, CDK6, CEBPB, CCR7, CREB1, MAPK14, CSF1, CTNNB1, ESRRA, FBN1, GATA2, GATA3, GNAS, HOXA7, RBPJ, IREB2, IRF4, JUN, KIT, LBR, LYN, MEF2C, KITLG, MYC, MYH9, NOTCH2, PAFAH1B1, PDE1B, POU4F1, PRKCA, RB1,

					SFRP1, SP3, SRC, TAL1, TFRC, KLF10, VEGFA, FADD, SH3PXD2A, RASSF2, TSPAN2, TRIB1, FSTL3, PIAS3, TOB2, SIRT1, FOXP1, EIF2AK1, FBXW7, FAM20C, BATF2, CD109, ZBTB46, ZNF675, SIGLEC15
BP	GO:0023061	signal release	116/3408	1.33E-03	ACVR2B, ADCY1, ADM, ADORA2B, SLC25A6, ARRB1, ATP2A2, CACNA1B, CACNA1C, CACNA1E, CALM3, CAMK2A, CPT1A, CREB1, EDN1, EFNA5, EGFR, ENSA, FMR1, GATA3, GJA1, GNAS, GSK3B, HIF1A, HMGCR, HNF4A, ISL1, ITPR1, ITPR2, KCNC4, KIF5B, LRP1, LYN, SMAD2, SMAD4, MEF2C, MYB, MYO5A, NKX3-1, P2RY1, CDK16, PFKFB2, PPARD, PPP3CA, PRKCA, PRKCE, PTPN11, PTPRN2, RAB1A, RAB5A, RAP1B, RFX3, SFRP1, SCG5, SLC6A9, SLC16A1, SNAP25, SNCA, SOX4, SOX11, STX3, VAMP1, VAMP2, VAMP7, SYT1, TBX3, HNF1B, TCF7L2, TFR2, TIAM1, TMF1, FZD4, DYNLL1, IRS2, NAPA, PER2, SYNJ1, KALRN, SYT7, RAB11B, AIMP1, MAP4K4, CLOCK, PREPL, SNCAIP, RIMS3, SV2A, RAPGEF3, UNC13B, KDM5B, RAB11FIP2, NLGN1, PASK, SYT11, PIP5K1C, NCS1, TARDBP, ARL2BP, SERP1, KCNMB4, GIT1, SYT17, RAB8B, UBE2Q1, CHD7, VPS35, NLGN2, RAB11FIP1, DNAJC5, UQCC2, RASL10B, SYT2, ACVR1C, RIMS4, BMP8A, SNX19
BP	GO:0002011	morphogenesis of an epithelial sheet	22/3408	1.41E-03	JAG1, RHOA, BMP7, CD44, COL5A1, DAG1, HBEGF, MEGF8, ARHGAP35, ITGA5, LRP6, PTEN, RREB1, SOS1, SOX11, SRF, ADAM17, CLASP1, DLL4, VANGL2, PHLDB2, ARHGAP12
BP	GO:0070585	protein localization to mitochondrion	44/3408	1.41E-03	SLC25A6, BCL2, CALM3, HK1, HK2, DNAJA1, HSPA4, MAPT, PPP3R1, PRKAA1, MAPK8, SREBF2, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, BAP1, TP63, BAG4, ATG13, TOMM20, MFN2, BCL2L11, ARIH2, TIMM17A, MTCH2, BBC3, HTRA2, DNAJC15, SH3GLB1, LEPROT, FBXW7, MFF, USP36, RHOU, MOAP1, GRPEL1, BMF, TIMM50, GRPEL2
BP	GO:0032984	protein-containing complex disassembly	87/3408	1.41E-03	ADD1, APC, ASPH, CAPZA2, CAV1, CFL1, CFL2, CTNNB1, DVL3, EPS8, ETF1, GSK3B, GSPT1, HMGA1, IGF1R, INSR, KIF2A, KIF5B, LAMP2, LRP6, MAP1A, MAP1B, MID1, MYC, NSF, TBC1D25, PPP1CA, TWF1, RDX, UPF1, ABCE1, SET, SH3GL2, SMARCC2, SMARCD2, SMARCE1, SPTAN1, SPTBN1, UVRAG, VCP, FZD5, ARID1A, FZD1, DENR, NAPA, SYNJ1, ARHGEF2, VPS4B, MRPL19, KIF2C, DSTN, SUPT16H, MRPL3, GABARAPL2, ATG14, CAMSAP2, CLASP1, MCTS1, TMOD2, UBQLN1, MRPL37, CHMP5, MRPS21, MTRF1L, DDIT4, STX17, PTCD3, EIF5A2, UBQLN4, CHMP1B, SCAF4, TAOK1, EPG5, FYCO1, MAP1LC3B, NAV3, CHMP7, CCSAP, LIX1L, MTPN, AMER1, SMCR8, TTBK2, CAMSAP1, ARID2, KIF24, CHCHD10
BP	GO:0030865	cortical cytoskeleton organization	20/3408	1.44E-03	ARF6, FMNL1, CALR, ECT2, EPB41, NCKAP1L, IKBKB, PAFAH1B1, TLN1, WASL, ROCK2, KIF23, PDCD6IP, NCKAP1, CIT, NLGN1, RHOQ, ANLN, FMNL3, WIPF2
BP	GO:0051972	regulation of telomerase activity	20/3408	1.44E-03	CTNNB1, DKC1, HNRNPD, MAP3K4, MEN1, MYC, PARN, MAPK1, MAPK3, SRC, TP53, XRCC5, TNKS, AURKB, KLF4, CERS1, PARM1, GREM1, PINX1, HMBOX1
BP	GO:0072655	establishment of protein localization to mitochondrion	43/3408	1.44E-03	SLC25A6, BCL2, CALM3, HK1, HK2, DNAJA1, HSPA4, MAPT, PPP3R1, PRKAA1, MAPK8, SREBF2, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, BAP1, TP63, BAG4, ATG13, TOMM20, MFN2, BCL2L11, ARIH2, TIMM17A, BBC3, HTRA2, DNAJC15, SH3GLB1, LEPROT, FBXW7, MFF, USP36, RHOU, MOAP1, GRPEL1, BMF, TIMM50, GRPEL2
BP	GO:0030177	positive regulation of Wnt signaling pathway	53/3408	1.44E-03	ABL1, CAV1, COL1A1, CSNK1D, CSNK1E, CSNK1G3, DAB2, DDX3X, EGFR, RBPJ, ILK, JUP, MLLT3, NFKB1, PIN1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, SKI, SOX4, SRC, TBL1X, TERT, VCP, TNKS, MBD2, PSMF1, ATP6AP2, PSME3, PSMD14, SPIN1, DKK1, KANK1, PSME4, UBR5, GID8, USP47, LGR4, VPS35, SULF2, PLEKHA4, PRDM15, WNK1, CDC73, TBL1XR1, DIXDC1, AMER1, NRARP
BP	GO:1903320	regulation of protein modification by small protein conjugation or removal	65/3408	1.45E-03	ABL1, ARRB1, ARRB2, BRCA1, PTTG1IP, CAV1, CTNNB1, EGR1, FKBP1A, DNAJB2, DNAJA1, HSPA5, LIMK1, MAD2L1, SMAD7, PIN1, PRKCE, MAPK9, PTEN, RAB1A, RPS3, SIAH2, SOX4, TAF1, TGFBR1, UBE2L3, UBE2N, VCP, CUL3, CDC14B, PER2, MTA1, TRIP12, ATG5, CTR9, HERPUD1, TNIP1, PIAS3, FAM107A, U2AF2, KDM1A, MYCBP2, UFL1, HSPBP1, UBQLN1, UBR5, PIAS4, DCUN1D1, GNL3L, OTUD4, RNF111, PINX1, FANCI, FBXW7, PELI1, ARRDC3, NXN, GORASP1, MUL1, ITCH, ARRDC4, DCUN1D3, AMER1, RNF180, SPOPL
BP	GO:0032469	endoplasmic reticulum calcium ion homeostasis	12/3408	1.45E-03	ATP2A2, BAK1, BCL2, CAMK2D, GRINA, ITPR1, PML, RAP1GDS1, TMBIM6, HERPUD1, BCAP31, KCTD17
BP	GO:0001945	lymph vessel development	13/3408	1.45E-03	ACVR2B, BMPR2, EFNB2, FOXC1, FLT4, PKD1, PROX1, PTPN14, SYK, NR2F2, VEGFA, VASH1, HEG1
BP	GO:0034504	protein localization to nucleus	72/3408	1.46E-03	BMP7, PTTG1IP, CALR, CCT6A, CDKN1A, COL1A1, MAPK14, DKC1, ECT2, GSK3B, HNRNPU, JUP, KPNA1, KPNA3, TNPO1, IPO5, MSX1, NF2, NUP88, NUP98, PIN1, PML, PPP3CA, PKIA, MAPK1, RAN, RANBP2, SKP1, SP100, SRC, STAT3, SYK, TERT, TP53, TXN, XPO1, YWHAE, DCLK1, POM121, NUTF2, NUP50, KAT7, TARDBP, MORC3, ARL2BP, CD2AP, KPNA6, POLR1A, SIN3A, APPL1, NMD3, FAM53C, UBR5, SUFU, RAB23, SIX4, PINX1, FERMT1, IPO9, NUP133, OTUD7B, MAVS, SESN2, RPAIN, LZTS2, GLIS2, OSBPL8, TOR1AIP2, FLCN, CNEP1R1, CHCHD10, POM121C
BP	GO:0043467	regulation of generation of precursor metabolites and energy	48/3408	1.47E-03	AK4, AKT2, RHOA, ATP7A, GSK3B, HIF1A, IGF2, INSR, NUP88, NUP98, ENPP1, PFKFB2, PFKFB3, PFKFB4, PGAM1, PHKG2, PPARA, PPP1CA, PPP1CB, PRKAA1, RANBP2, SNCA, STAT3, TP53, VCP, DYRK2, IRS2, NCOR1, EPM2AIP1, POM121, NUP50, SLC2A6, PASK, ISCU, PRELID1, DNAJC15, DDIT4, NDC1, NUP133, CISD1, SEH1L, DNAJC30, UQCC2, FLCN, PDE12, NUP43, CHCHD10, POM121C

BP	GO:0000045	autophagosome assembly	32/3408	1.51E-03	PIP4K2A, RAB1A, RAB5A, RALB, ULK1, MTMR3, ATG5, ATG13, MFN2, ATG7, GABARAPL2, ATG14, ATG2A, PACS2, STX12, RAB3GAP2, UBQLN2, UBQLN1, SH3GLB1, RAB23, STX17, ATG16L1, ATG2B, NSFL1C, SMURF1, TP53INP2, ATG9A, MAP1LC3B, TP53INP1, UBXN2B, SMCR8, TMEM41B
BP	GO:0006476	protein deacetylation	32/3408	1.51E-03	BCL6, CAMK2D, DYRK1A, ELK4, EP300, FNTA, HDAC2, MAPT, PRKAA1, MAPK8, KDM5A, SKI, TBL1X, TP53, VEGFA, PER2, MTA1, MORF4L2, HDAC9, FRY, RCOR1, SIRT1, NIPBL, SIN3A, SMARCAD1, MIER1, TBL1XR1, BRMS1L, NACC2, SPRED1, SPRED2, SPRED3
BP	GO:1901655	cellular response to ketone	32/3408	1.51E-03	ACACA, ADCY1, ADCY6, AR, ATP2B1, KLF9, CDC5L, AKR1C2, DNMT3B, EFNA5, EGFR, EIF4E, ELK1, FOXO1, FOXO3, GNB1, NR3C1, PRKAA1, PRKCE, PTGER4, SFRP1, SRC, AKR1C3, KLF4, ROCK2, KLF2, LARP1, SIRT1, NDOR1, ERRFI1, XRN1, DDIT4
BP	GO:0014020	primary neural tube formation	33/3408	1.53E-03	ABL1, ADM, BMP7, CASP3, CFL1, DVL3, KAT2A, ARHGAP35, HIF1A, LRP6, MTHFR, PAX2, PTCH1, RARG, SDC4, SFRP1, SKI, TSC1, TWIST1, KDM6A, LUZP1, FZD3, ARID1A, FZD1, FZD6, DLC1, MTHFD1L, SUFU, SEMA4C, IFT57, VANGL2, SHROOM3, TRIM71
BP	GO:2001022	positive regulation of response to DNA damage stimulus	33/3408	1.53E-03	ATM, ATR, BRCA1, CEBPG, DDX5, EGFR, EYA4, ERCC6, FOXM1, FMR1, FUS, MSX1, MYC, NKX3-1, RPS3, SKIL, UBE2N, HMGA2, ACTR2, FAM168A, SIRT1, SPIDR, ZNF385A, PIAS4, RIF1, FMN2, SPIRE1, BRCC3, NACC2, SPRED1, RNF168, SPRED2, SPRED3
BP	GO:0043666	regulation of phosphoprotein phosphatase activity	38/3408	1.53E-03	CALM1, CALM2, CALM3, CRY2, ENSA, FKBP1A, GNAI2, GSK3B, HTT, NCKAP1L, IKBKB, PPP1R12A, PPP1R2, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, EIF2AK2, PTPRC, SET, TSC1, SHOC2, ROCK2, PHACTR2, NUAK1, ARPP19, LMTK2, PPP6R1, ANKLE2, PPP1R16B, PPP6R3, PPP2R2D, SLC39A10, PPP1R15B, FAM122A, PPP4R2, BOD1L1, PPP1R37
BP	GO:0031102	neuron projection regeneration	23/3408	1.54E-03	ADM, BCL2, CTNNA1, DAG1, EPHA4, ISL1, JUN, LRP1, MAP1B, MATN2, MTR, NTRK3, PRRX1, PTEN, PTPRF, ULK1, STK24, KLF4, MAP4K4, LRIG2, MAPK8IP3, RGMA, KREMEN1
BP	GO:0014897	striated muscle hypertrophy	36/3408	1.54E-03	ATP2A2, ATP2B4, CAMK2D, EDN1, EZH2, FOXO1, G6PD, GATA6, HDAC2, IGFBP5, IL6ST, JARID2, SMAD4, MEF2A, MEF2C, PIN1, PPARA, PPP3CA, PRKCA, TWF1, RGS2, RGS4, MAP2K4, SLC9A1, TIAM1, TNFRSF1B, YY1, NR4A3, SORBS2, AKAP6, ROCK2, PDLIM5, AKAP13, LMCD1, ERRFI1, MTPN
BP	GO:0042542	response to hydrogen peroxide	45/3408	1.59E-03	ABL1, ADA, RHOB, AXL, BAK1, BCL2, CAPN2, CASP3, COL1A1, CRK, DUSP1, ECT2, EZH2, FOXO1, FOXO3, HDAC2, JUN, LDHA, MET, MYB, PAWR, PAX2, PRKAA1, RPS3, SLC8A1, SRC, STAT1, TRPM2, TXN, NR4A3, FOSL1, STK24, ADAM9, KLF4, NET1, SIGMAR1, KLF2, PRDX3, ZNF277, KDM6B, SIRT1, OSER1, PLEKHA1, PPP1R15B, SIRPA
BP	GO:0072006	nephron development	44/3408	1.63E-03	JAG1, BCL2, BMP7, CTNNB1, EGR1, FGF1, FGF2, FOXC1, GATA3, HES1, IL6R, ILK, ITGA3, SMAD4, MEF2C, MYC, NID1, PAX2, PBX1, PDGFB, PDGFRA, PKD1, PODXL, PTCH1, STAT1, HNF1B, VEGFA, WNT7B, WNT2B, DCHS1, IQGAP1, KLHL3, HEYL, SEC61A1, SOX8, SIX4, WNT4, AHI1, LGR4, NUP133, SULF2, VANGL2, LZTS2, FMN1
BP	GO:0003179	heart valve morphogenesis	21/3408	1.63E-03	JAG1, BMPR1A, BMPR2, GATA3, SMAD4, SMAD6, MDM4, MEF2C, NOTCH2, RB1, ROBO1, SNAI2, SNAI1, SOX4, TWIST1, DCHS1, ROCK2, OLFM1, HEYL, DLL4, ADAMTS9
BP	GO:0099173	postsynapse organization	49/3408	1.64E-03	ACTB, ADAM10, ARF1, ARF6, CDC42, CFL1, CRKL, DLG3, EPHA4, EPHA7, EPHB2, EPHB3, FNTA, IGF1R, IL1RAP, INSR, ITGA3, CAPRIN1, MYH10, NEFH, NTRK3, OPA1, OPHN1, PAFAH1B1, PAK3, PTEN, PTPRD, TIAM1, NRP1, SYNGAP1, WASL, KALRN, NOS1AP, ACTR2, ABI2, WASF2, PDLIM5, NLGN1, SHANK2, SLC7A11, SIPA1L1, ABHD17B, SSH1, VPS35, NLGN2, ABHD17C, LRRC4, ARHGAP39, BHLHB9
BP	GO:0010639	negative regulation of organelle organization	101/3408	1.66E-03	ADD1, APC, ARRB2, ATM, ATRX, BCL2L1, BMP7, BRCA1, CAPZA2, CCNF, CHEK1, DNMT3B, DUSP1, DYRK1A, S1PR1, EPS8, FKBP4, KAT2A, HMGA1, HNRNPC, HNRNPU, IK, INSIG1, JARID2, MAD2L1, SMAD4, MAP1B, MAP4, MAPT, MET, MID1, MLLT6, OPA1, PRKAR1A, TWF1, RAD1, RAD21, KDM5A, RDX, SET, SKI, SNCA, SPTAN1, SPTBN1, SRC, TP53, TWIST1, XRCC5, CDK10, TNKS, KAT2B, ARHGEF2, AURKB, TRIP13, TRIP12, ATG5, BAG4, TBC1D4, WASF2, TUBB4A, DLC1, ATG7, MTF2, KDM1A, PHF8, KANK1, CAMSAP2, CLASP1, SIRT1, SIN3A, CLIP3, ZNF451, PRELID1, HTRA2, TMOD2, UBR5, TRIAP1, RTEL1, ATAD2B, XRN1, GNL3L, BCOR, PINX1, PCID2, MDM1, TAOK1, FNIP2, MUL1, CEP97, ARHGAP28, TET1, SLX4, NAV3, PHLDB2, MYADM, FNIP1, MTPN, SMCR8, TTBK2, CAMSAP1, FLCN
BP	GO:0090398	cellular senescence	28/3408	1.66E-03	ABL1, BCL6, BMPR1A, CALR, CDK6, CDKN1A, MAPK14, HMGA1, KRAS, MAP3K3, OPA1, PAWR, PML, SRF, TBX3, TERT, TP53, TWIST1, KAT6A, HMGA2, NUAK1, AKT3, PLK2, ZNF277, VASH1, SIRT1, RSL1D1, SMC6
BP	GO:0045815	positive regulation of gene expression, epigenetic	24/3408	1.68E-03	ACTB, CHEK1, CTNNB1, EP300, ERCC6, KAT2A, HMGA1, MYO1C, POLR2K, ARID1A, KAT2B, BAZ1B, DDX21, KMT2B, PHF8, WBP2, POLR1A, ATAD2B, ZMIZ1, ARID1B, TET1, ZMIZ2, POLR1B, ELOF1
BP	GO:0097581	lamellipodium organization	29/3408	1.73E-03	ATP7A, CD44, CDC42, S1PR1, FER, ITGB1, KIT, ABLIM1, NCK1, TWF1, RREB1, SNX1, SRC, VCL, NCK2, WASF1, ARPC5, ARPC2, WASF2, VAV3, NCKAP1, KANK1, CORO1C, ARFIP2, SH2B1, AUTS2, AKIRIN1, WHAMM, SPATA13
BP	GO:0007050	cell cycle arrest	66/3408	1.74E-03	ABL1, AKT2, APBB2, APC, ZFHX3, ATM, CCND1, BRCA1, CALR, CDK6, CDKN1A, CDKN1B, DUSP1, EIF4G2, EP300, FOXM1, GATA6, ILK, IRF1, MDM4, FOXO4, MYC, NKX3-1, CNOT4, NOTCH2, PKD1, PML, POU4F1, PRKAA1, PRKAB2, RB1, RBL2, SKIL, SOX4, AURKA, TCF7L2, TFDP1, TFDP2, TGFBR1, THBS1, TP53, BTG2, HMGA2, CDC14B, KAT2B, CNOT8, PLK2, ZNF268, VASH1, CNOT1, ZNF385A, ING4, TRIAP1, PRR11, KMT2E, RPRM, CNOT6, RRAGD, RRAGC, MLST8, TP53INP1, WHAMM, JMY, E2F7, DAB2IP, SDE2

BP	GO:0022409	positive regulation of cell-cell adhesion	70/3408	1.80E-03	ADA, RHOA, BCL6, BMP7, CAV1, RUNX1, RUNX3, CBFB, CD44, CD47, CDC42, CCR7, CSK, CYLD, EFNB1, EFNB2, EGR3, FLOT2, GATA3, GCNT2, GRB2, NCKAP1L, FOXA1, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, IRAK1, ITGA6, ITPKB, LYN, SMAD7, MDK, MYB, MYO10, NCK1, PAK2, PAK3, PODXL, PTAFR, PTPN11, PTPRC, RAG1, RPS3, CX3CL1, SRC, SYK, TFRC, VCAM1, XBP1, NR4A3, NCK2, SOCS1, TNFSF9, FADD, AP3D1, CD83, SOCS5, FSTL3, CITED2, BTN2A2, NFAT5, DUSP10, ICOSLG, ZMIZ1, CD276, SIRPA, DENND6A
BP	GO:0046328	regulation of JNK cascade	54/3408	1.80E-03	CCR7, CYLD, DVL3, EDN1, EGFR, EPHA4, ERCC6, FLT4, RAPGEF1, DNAJA1, IGF1R, MAP3K4, MEN1, MAP3K9, PAFAH1B1, PTPN1, RAP2A, RPS3, MAP2K4, SFRP1, SYK, TIAM1, TPD52L1, WNT7B, FZD5, FZD4, SPAG9, TAOK2, MAP4K4, NCOR1, TRAF4, RASSF2, FGF19, HIPK3, SEMA3A, NOD1, MAP3K2, ZMYND11, DUSP10, DKK1, MAPK8IP3, PHLPP1, PDCD4, HIPK2, MINK1, VANGL2, TAOK1, AIDA, MUL1, ITCH, SIRPA, DAB2IP, ZNF675, SH3RF3
BP	GO:0001656	metanephros development	31/3408	1.81E-03	BCL2, BMP7, CTNNB1, EGR1, FBN1, GATA3, HES1, SMAD4, MYC, NKX3-1, PAX2, PDGFA, PDGFB, PDGFRA, PKD1, PTCH1, STAT1, HNF1B, WNT7B, ITGA8, DLG5, GDF11, SPRY1, NIPBL, SOX8, APH1A, SIX4, WNT4, LGR4, RDH10, FMN1
BP	GO:0031330	negative regulation of cellular catabolic process	72/3408	1.81E-03	ALAD, ATP2B4, BCL2, MAPK14, DKC1, EIF4G1, EIF4G2, ELAVL1, EPHA4, FHIT, FMR1, HNRNPC, HNRNPD, HNRNPU, FOXK2, MAP1A, MCL1, MET, NPC1, OPHN1, FURIN, PARN, PKP1, PML, PPARA, SNCA, SORL1, STAT3, STYX, TAF1, TIMP2, TIMP3, TP53, TSC1, UBE2G2, ZFP36, PSMF1, KDM4A, LRIG2, THRAP3, TOB1, SYNCRIP, ATG7, PAIP1, IGF2BP1, HNRNPA0, TLK2, GABARAPL2, TAB2, LARP1, TARDBP, PABPC1, HTRA2, HIPK2, USP25, DERL2, WAC, UCHL5, UBE2J1, SUFU, DDIT4, LAPTM4B, YOD1, RBM38, VPS35, UBQLN4, USP36, MTMR9, BMF, SMCR8, DAB2IP, FOXK1
BP	GO:0097305	response to alcohol	65/3408	1.82E-03	ACACA, ADCY1, ADCY6, ADCYAP1R1, ALAD, RHOA, ATP2B1, BAK1, CCND1, BCL2L1, BRCA1, KLF9, CALM3, CBL, CDKN1A, CCR7, CTNNA1, CTNNB1, DAG1, AKR1C2, DNMT3A, EFNA5, EPS8, FOXO3, FOSB, G6PD, GATA3, GNB1, GOT2, HDAC2, HMGCR, HNRNPD, ITPR2, JUP, LRP6, SMAD2, NTRK3, OGG1, PRKAA1, PRKCE, PTCH1, PTEN, PTGER4, RAD51, RGS2, RGS4, CCL7, SFRP1, SPARC, STAT3, TGFBR1, TGFBR3, VCAM1, FOSL1, AKR1C3, KLF4, ACTR2, PSMD14, KLF2, LARP1, SPIDR, XRN1, GRAMD1B, SETD7, TP53INP1
BP	GO:0070936	protein K48-linked ubiquitination	22/3408	1.82E-03	AMFR, CDC34, UBE2K, RNF4, TTC3, UBE2D2, UBE2D3, UBE2G1, UBE2G2, UBE2H, ARIH2, UBE2E3, KLHL3, BFAR, UBR5, UBE2R2, PELI1, ITCH, SYVN1, ZNRF1, RFFL, RNF187
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	80/3408	1.82E-03	ABL1, ARRB1, ARRB2, CD44, CCR7, CRKL, CSK, DUSP1, DUSP6, EGFR, EPHA7, EPHB2, ERBB2, FGF2, FGFR3, FLT4, FN1, GBP1, GCNT2, GNAI2, RAPGEF1, HMGCR, JUN, KIT, LRP1, LYN, SMAD4, NOTCH2, P2RY1, PDGFA, PDGFB, PDGFRA, PIN1, PRKCA, MAPK3, PTEN, PTPN1, PTPN11, PTPRC, PTPRR, RAP1B, CCL7, CX3CL1, SHC1, SRC, STYX, SYK, TIAM1, TIMP3, SEMA7A, EIF3A, NRP1, KLF4, AKAP12, RAPGEF2, FGF19, SPRY1, TNIP1, BTN2A2, NOD1, GPNMB, FRS2, DUSP10, DSTYK, NPTN, DNAJC27, ERRFI1, FBXW7, CAMK2N1, NDRG2, SEMA6A, NDRG4, SPRY4, SIRPA, DAB2IP, CNKSR3, SPRED1, BMPER, FLCN, SCIMP
BP	GO:0060211	regulation of nuclear-transcribed mRNA poly(A) tail shortening	9/3408	1.82E-03	ZFP36, BTG2, TOB1, CPEB3, CNOT1, TNRC6B, PABPC1, TNRC6A, TNRC6C
BP	GO:0090110	cargo loading into COPII-coated vesicle	9/3408	1.82E-03	INSIG1, RAB1A, SEC24C, SEC23A, SEC24A, SEC31B, SAR1A, TBC1D20, MIA3
BP	GO:0006029	proteoglycan metabolic process	32/3408	1.82E-03	BMPR2, COL11A1, NCAN, CTNNB1, DCN, EXTL2, EXTL3, NDST1, IDS, PPARD, TCF7L2, UGDH, NDST3, HS2ST1, SPOCK2, FAM20B, HS3ST3A1, HS3ST1, UST, HPSE, GLCE, CHST15, CSGALNACT2, CSGALNACT1, SULF2, CHST7, VANGL2, XYLT2, CHST9, HS6ST2, CANT1, HS6ST3
BP	GO:0005976	polysaccharide metabolic process	37/3408	1.82E-03	AKT2, CALM1, EXTL2, EXTL3, GAA, GSK3B, GYS1, HAS3, NDST1, IGF2, IL6ST, INSR, NFKB1, PDGFB, ENPP1, PHKA1, PHKG2, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PYGB, UGP2, DYRK2, CHST1, IRS2, PER2, NDST3, HS2ST1, EPM2AIP1, PASK, CSGALNACT2, CSGALNACT1, CHST7, STK40, B3GNT5
BP	GO:0008543	fibroblast growth factor receptor signaling pathway	37/3408	1.82E-03	RUNX2, CBL, CRKL, CTNNB1, FGF1, FGF2, FGF5, FGFR3, GATA3, GRB2, HNRNPM, NCBP1, POLR2D, POLR2K, MAPK1, MAPK3, PTPN11, THBS1, SHOC2, IQGAP1, FGF19, SPRY1, FRS2, RBFOX2, FLRT2, DSTYK, NPTN, RAB14, WNT4, ESRP1, SULF2, FAM20C, SHCBP1, SPRY4, TRIM71, SPRED1, SPRED2
BP	GO:0072163	mesonephric epithelium development	33/3408	1.82E-03	BCL2, BMP7, CTNNB1, FGF1, FGF2, FOXC1, GATA3, HES1, ILK, SMAD2, SMAD4, SMAD6, SMAD7, MYC, PAX2, PBX1, PKD1, PTCH1, SDC4, SFRP1, HNF1B, VEGFA, WNT2B, DCHS1, GDF11, SPRY1, SOX8, SIX4, WNT4, LGR4, LZTS2, BMPER, FMN1
BP	GO:0072164	mesonephric tubule development	33/3408	1.82E-03	BCL2, BMP7, CTNNB1, FGF1, FGF2, FOXC1, GATA3, HES1, ILK, SMAD2, SMAD4, SMAD6, SMAD7, MYC, PAX2, PBX1, PKD1, PTCH1, SDC4, SFRP1, HNF1B, VEGFA, WNT2B, DCHS1, GDF11, SPRY1, SOX8, SIX4, WNT4, LGR4, LZTS2, BMPER, FMN1
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	33/3408	1.82E-03	BCL2, BCL2L1, PTTG1IP, CD44, DDX3X, GRINA, HIF1A, DNAJA1, MCL1, OPA1, PTPN1, SNAI2, SNAI1, SOD2, SRC, TMBIM6, TPT1, VDAC2, XBP1, ARHGEF2, HERPUD1, HYOU1, KDM1A, SIRT1, ZNF385A, HTRA2, RRM2B, TXNDC12, TRIAP1, TAF9B, RRN3, USP47, SYVN1

BP	GO:0061387	regulation of extent of cell growth	36/3408	1.82E-03	ABL1, BDNF, BMPR2, EFNA5, MEGF8, EPHA7, FN1, GDI1, GOLGA4, GSK3B, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, SRF, VEGFA, RND2, SEMA7A, NRP1, NTN1, SEMA3E, SEMA3A, OLFM1, SEMA4B, RAB21, FSTL4, SIN3A, SEMA4C, SEMA6A, PLXNA4, WDR36, TTL
BP	GO:0090175	regulation of establishment of planar polarity	36/3408	1.82E-03	ABL1, RHOA, ARRB2, CDC42, AP2M1, DAB2, DVL3, CELSR3, CELSR2, MLLT3, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, TIAM1, FZD5, FZD3, FZD1, FZD4, FZD6, PSMF1, GPC6, PSME3, PSMD14, DKK1, PSME4, SMURF1, VANGL2, PLEKHA4, VANGL1, ZNRF3, PRICKLE2
BP	GO:0003300	cardiac muscle hypertrophy	35/3408	1.83E-03	ATP2A2, ATP2B4, CAMK2D, EDN1, EZH2, FOXO1, G6PD, GATA6, HDAC2, IL6ST, JARID2, SMAD4, MEF2A, MEF2C, PIN1, PPARA, PPP3CA, PRKCA, TWF1, RGS2, RGS4, MAP2K4, SLC9A1, TIAM1, TNFRSF1B, YY1, NR4A3, SORBS2, AKAP6, ROCK2, PDLIM5, AKAP13, LMCD1, ERRFI1, MTPN
BP	GO:0010565	regulation of cellular ketone metabolic process	53/3408	1.84E-03	ADM, AKT2, ATP2B4, BRCA1, CAV1, COMT, CPT1A, EGR1, INSIG1, OAZ2, PDK3, PDK4, PPARA, PRKAB2, PRKCE, PROX1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SNCA, TWIST1, NR1H2, NR4A3, AKR1C3, IRS2, PSMF1, LPGAT1, FGF19, PSME3, PSMD14, ERLIN2, WDTC1, PSME4, SIRT1, SLC7A11, DKK3, ADIPOR1, INSIG2, AZIN1, WNT4, PDPR, PDP2, ELOVL5, ADIPOR2, PANK2, LONP2, STARD4, RDH10, PPTC7
BP	GO:0031057	negative regulation of histone modification	18/3408	1.87E-03	BRCA1, DNMT3B, JARID2, MLLT6, KDM5A, SET, SKI, SNCA, TWIST1, TRIP12, ATG5, MTF2, KDM1A, SIRT1, SIN3A, ZNF451, UBR5, BCOR
BP	GO:0048546	digestive tract morphogenesis	20/3408	1.87E-03	ACVR2B, BCL2, CTNNB1, EGFR, EPHB3, HIF1A, HOXD13, SMAD2, PDGFRA, SFRP1, SOX11, HNF1B, TCF7, TP63, AGR2, NIPBL, AHI1, VANGL2, EPB41L5, RBPMS2
BP	GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	20/3408	1.87E-03	CAV1, CTNNA1, CYLD, PAK2, PML, PPP1CA, PPP2R1A, PTEN, PTPRC, SFRP1, SKIL, STK4, THBS1, TIMP3, PEA15, TNFSF10, FADD, RBCK1, HTRA2, ITM2C
BP	GO:0050779	RNA destabilization	15/3408	1.89E-03	ZFP36L1, ZFP36L2, HNRNPD, UPF1, TNFRSF1B, ZFP36, ROCK2, PUM1, CPEB3, GIGYF2, YTHDF2, RBM23, METTL14, TRIM71, YTHDF3
BP	GO:0061384	heart trabecula morphogenesis	15/3408	1.89E-03	BMP7, BMPR1A, S1PR1, FKBP1A, NRG1, RBPJ, SOS1, SRF, TGFBR1, TGFBR3, ADAMTS1, UBE4B, DLL4, CHD7, HEG1
BP	GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	15/3408	1.89E-03	BCL2L1, GRINA, NCK1, OPA1, PTPN1, TMBIM6, XBP1, NCK2, HERPUD1, BCL2L11, HYOU1, SERINC3, SIRT1, TXNDC12, SYVN1
BP	GO:0019058	viral life cycle	86/3408	1.93E-03	ADAR, ADARB1, AXL, BCL2, CAV1, SCARB2, CDC42, CTSB, CXADR, DAG1, DDX3X, DDX5, DDX6, EFNB2, EGFR, STOM, FMR1, NR5A2, ITGA5, ITGAV, ITGB1, KPNA1, KPNA3, LDLR, NCAM1, NFIA, NPC1, NUP88, NUP98, FURIN, PML, PKN2, EIF2AK2, PROX1, RAB1A, RAB5A, RAN, RANBP2, SLC1A5, SLC20A2, STAU1, TFRC, TOP2B, TYRO3, UVRAG, VCP, XPO1, TRIM25, HMGA2, SNX3, VAPB, VAPA, ATG5, ROCK2, VPS4B, USP6NL, POM121, PDCD6IP, TRIM13, TNIP1, NUP50, SNF8, MORC2, LARP1, KPNA6, PABPC1, ZNF639, UBAP1, CHMP5, VPS37C, ATG16L1, TRIM62, NDC1, NUP133, ZC3HAV1, CHMP1B, MAVS, NUCKS1, SEH1L, ITCH, CHMP7, TBC1D20, VPS37D, PDE12, NUP43, POM121C
BP	GO:0010631	epithelial cell migration	91/3408	1.95E-03	ABL1, ARF6, RHOA, RHOB, BMPR2, CALR, DCN, HBEGF, EDN1, EFNB2, EGR3, EMP2, EPHB4, FGF1, FGF2, FLT4, GATA2, GATA3, GPI, HIF1A, ITGA3, ITGB1, JUN, JUP, KIT, LOXL2, MECP2, MEF2C, MAP3K3, MET, MYH9, PDGFB, PIK3C2A, PPARD, PRCP, PRKCA, PRKCE, PKN2, PROX1, PTEN, PTPN11, PTPRG, PTPRR, PXN, ROBO1, RREB1, SP100, SPARC, SRC, SRF, STC1, ADAM17, NR2F2, TGFBR1, THBS1, VEGFA, ADAM9, NRP1, KLF4, MAP4K4, ROCK2, HDAC9, AKT3, SEMA3A, PLK2, DUSP10, VASH1, PLXND1, KANK1, CLASP1, SIRT1, CORO1C, GREM1, FOXP1, ADIPOR1, ANLN, EPB41L4B, DLL4, FBXW7, FERMT1, ADAMTS9, EPB41L5, PBLD, NUS1, DAB2IP, AMOT, AMOTL1, SPRED1, BMPER, EMC10, MIA3
BP	GO:0045665	negative regulation of neuron differentiation	63/3408	1.95E-03	ADCY6, JAG1, ARF6, RHOA, ARHGDIA, BMP7, CALR, CTSZ, DDX6, DLX2, EFNB2, EIF4E, EPHA4, EPHA7, EPHB2, FKBP4, FOXO3, GDI1, GSK3B, HDAC2, HES1, ID4, ISL1, LRP1, PAFAH1B1, PAX6, PBX1, PPP3CA, PTEN, PTPRG, TSC1, SEMA7A, NRP1, SYNGAP1, NTN1, MAP4K4, RAPGEF2, SEMA3E, LRIG2, GDF11, SEMA3A, SEMA4B, PLK2, NLGN1, DKK1, FSTL4, RAP1GAP2, KANK1, MYLIP, SOX8, ASAP1, BCL11A, SEMA4C, RGMA, MIB1, SEMA6A, CTDSP1, GORASP1, ISL2, TRAK2, ITM2C, KREMEN1, DIXDC1
BP	GO:0090596	sensory organ morphogenesis	70/3408	1.95E-03	JAG1, BAK1, BCL2, PRDM1, BMP7, COL5A1, COL5A2, COL11A1, CTNNB1, DLX6, EDN1, EPHB2, FAT1, FBN1, FBN2, GATA2, GATA3, HDAC2, HIF1A, INSIG1, LRP6, MAN2A1, MSX1, OTX1, PAX2, PAX6, PRRX1, MAPK1, MAPK3, PROX1, RARG, RORB, SKI, SOX11, SP3, STAT3, ZEB1, TWIST1, VEGFA, WNT2B, YY1, FZD5, FZD3, NR4A3, ARID1A, FZD6, BCAR3, ITGA8, NTN1, MFN2, ABI2, GDF11, FRS2, NIPBL, LRIG1, HIPK2, SOX8, CDON, INSIG2, SIX4, AHI1, SOBP, CHD7, TENM3, CYP26B1, VANGL2, TTC39C, TBC1D20, HIPK1, SDK1

BP	GO:0048634	regulation of muscle organ development	47/3408	1.97E-03	ARRB2, BCL2, BMPR1A, CREB1, MAPK14, CTNNB1, DDX5, EDN1, EFNB2, FGF2, G6PD, GATA6, KAT2A, GJA1, NRG1, HMGCR, RBPJ, JARID2, SMAD4, MEF2C, PIM1, PIN1, PPARA, PRKAA1, MAPK1, PTEN, RGS2, RGS4, TGFBR1, TGFBR3, TWIST1, YY1, AKAP6, HDAC9, NR1D2, DDX17, FRS2, DKK1, FBXO22, GREM1, CDON, SFMBT1, SIX4, CYP26B1, AKIRIN1, UQCC2, MTPN
BP	GO:0051258	protein polymerization	76/3408	1.98E-03	ABL1, ADD1, ARF1, ARF6, RHOA, CAPZA2, CDKN1B, CCR7, CSNK1D, DIAPH1, DYRK1A, EPS8, FER, FKBP4, GRB2, NCKAP1L, UBE2K, MAP1B, MAPT, MECP2, MET, MYO1C, NCK1, OPA1, PAK3, PRKCE, TWF1, RASA1, RDX, RPS3, SNCA, SPTAN1, SPTBN1, VDAC2, NCK2, WASF1, WASL, LATS1, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, AKAP9, ABI2, TENM1, TUBB4A, CDC42EP2, NCKAP1, IQGAP2, TPPP, FAM107A, MAPRE3, KANK1, CAMSAP2, CLASP1, COTL1, CLIP3, TMOD2, NIN, NDE1, TTC17, FMN2, SPIRE1, SLAIN2, PLEKHG2, ARHGAP28, NAV3, MYADM, ARHGAP18, WHAMM, JMY, MTPN, CAMSAP1, RICTOR, FMN1
BP	GO:0030308	negative regulation of cell growth	54/3408	2.00E-03	ACVR1B, APBB2, BCL2, BCL6, BMPR2, BTG1, OSGIN2, CDKN1A, CDKN1B, DDX3X, EPHA7, ESR2, FHL1, G6PD, GJA1, HNF4A, DNAJB2, SMAD4, MSX1, ENPP1, SERPINE2, PML, PPARA, PPARD, PPP2CA, PPP2R1A, PTPRJ, RGS2, RGS4, SFRP1, SMARCA2, TP53, YY1, SEMA7A, NRP1, NTN1, SEMA3E, SERTAD2, SEMA3A, SEMA4B, FSTL4, SIRT1, SERTAD3, ADIPOR1, BCL11A, SEMA4C, SEMA6A, TSPYL2, MUL1, ADIPOR2, SESN2, DCUN1D3, DCBLD2, FLCN
BP	GO:1903312	negative regulation of mRNA metabolic process	28/3408	2.02E-03	CCNT1, MAPK14, DYRK1A, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPK, HNRNPU, PKP1, SRSF4, SRSF7, ZFP36, CTR9, THRAP3, TOB1, SYNCRIP, PAIP1, IGF2BP1, SRSF10, RNPS1, HNRNPA0, U2AF2, LARP1, TARDBP, PABPC1, RBMX, RBM38
BP	GO:0016202	regulation of striated muscle tissue development	46/3408	2.03E-03	ARRB2, BCL2, BMPR1A, CREB1, MAPK14, CTNNB1, DDX5, EDN1, EFNB2, FGF2, G6PD, GATA6, KAT2A, GJA1, NRG1, HMGCR, RBPJ, JARID2, SMAD4, MEF2C, PIM1, PIN1, PPARA, PRKAA1, MAPK1, PTEN, RGS2, RGS4, TGFBR1, TGFBR3, TWIST1, YY1, AKAP6, HDAC9, NR1D2, DDX17, FRS2, DKK1, FBXO22, GREM1, CDON, SIX4, CYP26B1, AKIRIN1, UQCC2, MTPN
BP	GO:0030902	hindbrain development	46/3408	2.03E-03	ABL1, ARCN1, RERE, ATP7A, BCL2, BMP7, CNTN1, CRK, CRKL, CTNNB1, EZH2, FOXC1, GATA2, KAT2A, HNRNPD, HOXB3, HES1, HSPA5, ITGB1, KCNC1, LRP6, MDK, MECP2, MYH10, NFIB, OPHN1, OTX1, SERPINE2, POU4F1, PROX1, PTPN11, RORA, HNF1B, TP53, FZD4, PSMG1, B4GALT2, ALDH1A2, LDB1, DLC1, NCSTN, RBFOX2, AHI1, SEMA4C, MTPN, TTBK2
BP	GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	14/3408	2.06E-03	CREBBP, DAB2, EP300, SMAD4, MEN1, ADAM17, TGFBR3, THBS1, ITGA8, CITED2, HIPK2, RNF111, FERMT1, FLCN
BP	GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	14/3408	2.06E-03	CREBBP, DAB2, EP300, SMAD4, MEN1, ADAM17, TGFBR3, THBS1, ITGA8, CITED2, HIPK2, RNF111, FERMT1, FLCN
BP	GO:0044783	G1 DNA damage checkpoint	24/3408	2.09E-03	ATM, CCND1, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, GIGYF2, WAC, TRIAP1, CNOT6, E2F7
BP	GO:0071695	anatomical structure maturation	49/3408	2.11E-03	ARCN1, RHOA, RERE, BCL2, CDKN1A, CTNNB1, DAG1, S1PR1, ERCC2, FGFR3, FOXO3, G6PD, GATA3, GJA1, HIF1A, FOXA1, HOXA5, RBPJ, MECP2, MYO5A, OPA1, PAX2, PDE3A, PGR, PPP2R1A, RB1, RFX3, CX3CL1, AURKA, TAL1, THBS3, XBP1, DCHS1, ALDH1A2, TRIP13, B4GALT6, PTBP3, KLF2, KDM1A, NFASC, MTCH1, CNTNAP2, GREM1, YTHDF2, BCL11A, FERMT1, FAM20C, FAM210B, AGRN
BP	GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	17/3408	2.12E-03	BCL2, BCL2L1, CD44, HNRNPK, RPS3, SKIL, SNAI2, SNAI1, TPT1, KDM1A, SIRT1, ZNF385A, TRIAP1, PIAS4, TAF9B, USP47, NACC2
BP	GO:0014896	muscle hypertrophy	36/3408	2.15E-03	ATP2A2, ATP2B4, CAMK2D, EDN1, EZH2, FOXO1, G6PD, GATA6, HDAC2, IGFBP5, IL6ST, JARID2, SMAD4, MEF2A, MEF2C, PIN1, PPARA, PPP3CA, PRKCA, TWF1, RGS2, RGS4, MAP2K4, SLC9A1, TIAM1, TNFRSF1B, YY1, NR4A3, SORBS2, AKAP6, ROCK2, PDLIM5, AKAP13, LMCD1, ERRFI1, MTPN
BP	GO:1902107	positive regulation of leukocyte differentiation	44/3408	2.15E-03	ADA, RHOA, AXL, BCL6, ZFP36L1, RUNX1, RUNX3, CBFB, CREB1, CSF1, CYLD, EGR3, GATA3, GNAS, NCKAP1L, IL7R, IL18, ITPKB, JUN, MDK, KITLG, MMP14, MYB, POU4F1, PRKCA, PTPRC, RAG1, RB1, SYK, KLF10, XBP1, SOCS1, TNFSF9, FADD, AP3D1, CD83, SOCS5, TRIB1, BTN2A2, DUSP10, PCID2, ZMIZ1, ZBTB46, ATP11C
BP	GO:0050821	protein stabilization	52/3408	2.15E-03	ATP1B1, CALR, CCT6A, CDKN1A, CREB1, DVL3, EP300, EPHA4, FLOT2, GAPDH, GNAQ, HCFC1, HIP1, LAMP2, SMAD7, MDM4, MSX1, PIM1, PIN1, PTEN, SEL1L, SOX4, STK4, TAF1, TBL1X, TP53, TSC1, VHL, USP9X, PER3, USP13, USP2, RASSF2, TSPAN1, CRTAP, AAK1, USP33, OTUD3, MORC3, STX12, HYPK, TAF9B, NLK, FBXW7, ATF7IP, USP36, WIZ, MTMR9, MUL1, COG3, SYVN1, WDR81
BP	GO:0090090	negative regulation of canonical Wnt signaling pathway	52/3408	2.15E-03	APC, CAV1, MAPK14, CTNND1, CYLD, DAB2, DVL3, EGR1, FOXO1, FOXO3, RAPGEF1, GSK3B, IGFBP1, ISL1, LRP6, MDK, MLLT3, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, SIAH2, SNAI2, STK4, TCF7L2, TLE1, TLE4, FZD1, FZD6, CUL3, LIMD1, LATS1, PSMF1, G3BP1, PSME3, PSMD14, DKK1, PSME4, LATS2, GREM1, DKK3, FERMT1, KREMEN1, ZNRF3, LZTS2, AMER1, DAB2IP, TMEM170B

BP	GO:0043090	amino acid import	13/3408	2.19E-03	CLN8, KCNJ10, RGS2, RGS4, SLC1A2, SLC1A5, SLC7A1, SLC7A2, PER2, ARL6IP1, SLC7A11, SLC25A38, SLC36A4
BP	GO:0048167	regulation of synaptic plasticity	54/3408	2.27E-03	ABL1, ADCY1, ARF1, CAMK2A, CREB1, EPHA4, EPHB2, FMR1, KAT2A, GSK3B, KCNJ10, KIT, KRAS, MAP1A, MAP1B, MAPT, MECP2, MEF2C, RAB8A, MME, MPP2, SERPINE2, MAPK1, PTEN, RAB5A, CX3CL1, SNAP25, SNCA, SRF, STAU1, STX3, VAMP2, YWHAG, SYNGAP1, SQSTM1, SYT7, SYNGR1, RAPGEF2, RIMS3, UNC13B, PLK2, FAM107A, CPEB3, NLGN1, SHANK2, NCDN, NCSTN, SLC24A2, NSMF, SIPA1L1, NPTN, SSH1, YTHDF1, RIMS4
BP	GO:0060216	definitive hemopoiesis	11/3408	2.27E-03	ADAR, ZFP36L2, CBFB, GATA2, HOXA9, HOXB3, SP3, TAL1, TGFBR3, RBFOX2, HIPK1
BP	GO:1900151	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	11/3408	2.27E-03	ZFP36L1, ZFP36L2, ZFP36, BTG2, TOB1, CPEB3, CNOT1, TNRC6B, PABPC1, TNRC6A, TNRC6C
BP	GO:0089718	amino acid import across plasma membrane	12/3408	2.27E-03	CLN8, KCNJ10, RGS2, RGS4, SLC1A2, SLC1A5, SLC7A1, SLC7A2, PER2, ARL6IP1, SLC7A11, SLC36A4
BP	GO:1901889	negative regulation of cell junction assembly	12/3408	2.27E-03	IKBKB, LRP1, MMP14, PTEN, SRC, THBS1, ROCK2, DLC1, FAM107A, CORO1C, RCC2, PHLDB2
BP	GO:2000637	positive regulation of gene silencing by miRNA	12/3408	2.27E-03	DDX5, EGFR, EIF4G1, FMR1, MYCN, STAT3, TP53, ZFP36, FXR1, LIMD1, PUM1, TRIM71
BP	GO:0051235	maintenance of location	86/3408	2.30E-03	ABL1, CACNA1C, CALM1, CALM2, CALM3, CALR, CAMK2D, CAV1, CCR7, DAG1, DIAPH1, FBN1, FBN2, FGF2, FKBP1A, FLNB, GAA, GM2A, HTT, HK1, HK2, HNRNPU, HSPA5, INSIG1, ITGAV, ITPR1, ITPR2, JUP, LETM1, LTBP1, LYN, MXI1, MYO5A, NFKB1, PAFAH1B1, PDE4D, ENPP1, PKD1, PML, PPARA, PPARD, PRKCE, TWF1, PTPRC, CX3CL1, SKP1, SLC8A1, SNCA, SOAT1, SORL1, SP100, SREBF2, TLN1, TRPM2, TXN, NR1H2, UVRAG, NRIP1, AP3D1, F2RL3, LATS1, AKAP6, ATG5, G3BP2, AKAP9, RASA3, VPS13A, SIRT1, MORC3, ARL2BP, IBTK, ABHD5, GET4, SUFU, TPCN1, VPS13C, VPS13D, FBXW7, CHD7, ANKRD13C, OSBPL8, ACVR1C, STARD4, SLC30A7, TPCN2, MCOLN2
BP	GO:0061180	mammary gland epithelium development	26/3408	2.31E-03	AKT2, AR, CCND1, CEBPB, CSF1, GATA3, HIF1A, HOXA5, LRP6, MSX1, PGR, PML, MAPK1, PTCH1, ROBO1, RREB1, SRC, TBX3, VDR, WNT7B, BTRC, LATS1, NTN1, KDM5B, WNT4, IQGAP3
BP	GO:0007492	endoderm development	27/3408	2.41E-03	BMPR1A, ZFP36L1, COL4A2, COL5A1, COL5A2, COL11A1, COL12A1, CTNNB1, BPTF, FN1, GATA6, HSBP1, ITGA5, ITGAV, LAMC1, SMAD2, SMAD4, MMP14, PAX9, HNF1B, HMGA2, LDB1, CTR9, DKK1, EPB41L5, CDC73, SOX7
BP	GO:0060411	cardiac septum morphogenesis	27/3408	2.41E-03	JAG1, BMP7, BMPR1A, BMPR2, GATA6, HES1, RBPJ, ISL1, SMAD4, SMAD6, SMAD7, NOTCH2, PROX1, ROBO1, SOX4, SOX11, TBX3, TGFBR1, TGFBR3, TP53, FZD1, NRP1, HAND1, CITED2, HEYL, CHD7, VANGL2
BP	GO:0048592	eye morphogenesis	45/3408	2.41E-03	JAG1, BAK1, BCL2, PRDM1, BMP7, COL5A1, COL5A2, CTNNB1, EPHB2, FAT1, FBN1, FBN2, HIF1A, LRP6, MAN2A1, PAX2, PAX6, PROX1, RARG, RORB, SKI, SOX11, SP3, STAT3, ZEB1, TWIST1, VEGFA, WNT2B, YY1, FZD5, ARID1A, BCAR3, MFN2, ABI2, GDF11, FRS2, NIPBL, HIPK2, SOX8, CDON, AHI1, TENM3, TBC1D20, HIPK1, SDK1
BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	49/3408	2.41E-03	ABL1, CAV1, DCN, FBN1, FBN2, GATA3, HSPA5, LTBP1, SMAD2, SMAD6, SMAD7, NEDD4, PIN1, PTPN1, SFRP1, SKI, SKIL, SORL1, ADAM17, TGFBR1, TGFBR3, THBS1, TP53, FZD1, CHRD, MTMR4, ONECUT2, TOB1, SPRY1, FSTL3, DKK1, PEG10, SIRT1, ZNF451, GREM1, HIPK2, TRIM33, WNT4, SULF2, PMEPA1, SMURF1, SEMA6A, PBLD, SPRY4, WFIKKN2, CD109, DAB2IP, BMPER, RBPMS2
BP	GO:0008064	regulation of actin polymerization or depolymerization	52/3408	2.45E-03	ADD1, ARF1, ARF6, RHOA, CAPZA2, CFL1, CFL2, CCR7, EPS8, FER, GRB2, ARHGAP35, NCKAP1L, MYO1C, NCK1, PAK3, PRKCE, TWF1, RASA1, RDX, SPTAN1, SPTBN1, NCK2, WASF1, WASL, LATS1, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, TENM1, CDC42EP2, NCKAP1, IQGAP2, DSTN, CIT, KANK1, COTL1, TMOD2, FMN2, SPIRE1, PLEKHG2, ARHGAP28, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, FMN1
BP	GO:0071347	cellular response to interleukin-1	52/3408	2.45E-03	CD47, CEBPB, EDN1, EGR1, GBP1, HIF1A, IKBKB, IL1R1, IL1RAP, IRAK1, IRAK2, MAP3K3, NFKB1, NKX3-1, MAPK3, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTGIS, UPF1, RORA, CCL7, CX3CL1, SFRP1, SKP1, TFPI, UBE2N, UBE2V1, YY1, SQSTM1, BTRC, RPS6KA4, RPS6KA5, PSMF1, AKAP12, PSME3, PSMD14, KLF2, NOD1, TAB1, TAB2, PSME4, RBMX, OTUD4, PELI1, SIRPA, DAB2IP, ZNF675

BP	GO:0031113	regulation of microtubule polymerization	20/3408	2.45E-03	ABL1, CDKN1B, DYRK1A, FKBP4, MAP1B, MAPT, MECP2, MET, RPS3, SNCA, AKAP9, TUBB4A, MAPRE3, CAMSAP2, CLASP1, CLIP3, NIN, SLAIN2, NAV3, CAMSAP1
BP	GO:0048645	animal organ formation	23/3408	2.47E-03	AR, BMP7, BMPR1A, CTNNB1, FGF1, GATA6, HOXA3, HES1, RBPJ, ISL1, MEF2C, PAX2, PIM1, MAPK1, MAPK3, ROBO1, WNT2B, TP63, SPRY1, CITED2, FRS2, DKK1, RDH10
BP	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	23/3408	2.47E-03	BCL2, BCL2L1, CAV1, MCL1, MSX1, NCK1, NKX3-1, PLAGL2, RPS3, SIAH1, SKIL, TP53, NCK2, BCL2L11, BCAP31, SERINC3, SIRT1, BBC3, PIAS4, FBXW7, BMF, NACC2, FLCN
BP	GO:2000736	regulation of stem cell differentiation	37/3408	2.49E-03	ABL1, JAG1, BMP7, ZFP36L2, RUNX1, CBFB, CDK6, FOXC1, GATA2, GATA3, GATA6, HNRNPU, HES1, LMO2, KMT2A, MYB, PDGFRA, EIF2AK2, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, STAT3, TAL1, TCF3, LDB1, PSMF1, SETD1A, PSME3, PSMD14, PSME4, YTHDF2, PUS7, ITCH
BP	GO:0021762	substantia nigra development	18/3408	2.49E-03	ACTB, RHOA, CALM1, CALM2, CALM3, CDC42, G6PD, HSPA5, MBP, RAD1, YWHAE, ZNF148, DYNLL1, SYNGR3, NDRG2, GNB4, MAPKAP1, ZNF430
BP	GO:0030866	cortical actin cytoskeleton organization	18/3408	2.49E-03	ARF6, FMNL1, CALR, ECT2, EPB41, NCKAP1L, IKBKB, TLN1, WASL, ROCK2, KIF23, PDCD6IP, NCKAP1, CIT, RHOQ, ANLN, FMNL3, WIPF2
BP	GO:0045773	positive regulation of axon extension	18/3408	2.49E-03	BMPR2, MEGF8, FN1, GDI1, GOLGA4, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, SRF, VEGFA, SEMA7A, NRP1, NTN1
BP	GO:1901985	positive regulation of protein acetylation	18/3408	2.49E-03	ARRB1, BRCA1, GATA3, KAT2A, ISL1, SMAD4, PRKAA1, MAPK3, SNAI2, SOX4, RPS6KA4, RPS6KA5, RAPGEF3, KAT7, WBP2, AUTS2, TAOK1, TADA2B
BP	GO:0051492	regulation of stress fiber assembly	29/3408	2.50E-03	ABL1, RHOA, CD47, CDC42, S1PR1, LIMK1, MET, NF2, PTGER4, PXN, SDC4, SFRP1, SLC9A1, TESK1, TGFBR1, TSC1, NRP1, ROCK2, BAG4, WASF2, DLC1, RAPGEF3, LIMCH1, CLASP1, WNT4, ARHGAP28, SYNPO2L, PHLDB2, SH3PXD2B
BP	GO:0090132	epithelium migration	91/3408	2.51E-03	ABL1, ARF6, RHOA, RHOB, BMPR2, CALR, DCN, HBEGF, EDN1, EFNB2, EGR3, EMP2, EPHB4, FGF1, FGF2, FLT4, GATA2, GATA3, GPI, HIF1A, ITGA3, ITGB1, JUN, JUP, KIT, LOXL2, MECP2, MEF2C, MAP3K3, MET, MYH9, PDGFB, PIK3C2A, PPARD, PRCP, PRKCA, PRKCE, PKN2, PROX1, PTEN, PTPN11, PTPRG, PTPRR, PXN, ROBO1, RREB1, SP100, SPARC, SRC, SRF, STC1, ADAM17, NR2F2, TGFBR1, THBS1, VEGFA, ADAM9, NRP1, KLF4, MAP4K4, ROCK2, HDAC9, AKT3, SEMA3A, PLK2, DUSP10, VASH1, PLXND1, KANK1, CLASP1, SIRT1, CORO1C, GREM1, FOXP1, ADIPOR1, ANLN, EPB41L4B, DLL4, FBXW7, FERMT1, ADAMTS9, EPB41L5, PBLD, NUS1, DAB2IP, AMOT, AMOTL1, SPRED1, BMPER, EMC10, MIA3
BP	GO:0048593	camera-type eye morphogenesis	36/3408	2.51E-03	JAG1, BAK1, BMP7, CTNNB1, EPHB2, FAT1, HIF1A, LRP6, MAN2A1, PAX2, PAX6, PROX1, RORB, SKI, SOX11, SP3, ZEB1, TWIST1, VEGFA, WNT2B, YY1, FZD5, ARID1A, BCAR3, MFN2, ABI2, GDF11, FRS2, HIPK2, SOX8, CDON, AHI1, TENM3, TBC1D20, HIPK1, SDK1
BP	GO:0001738	morphogenesis of a polarized epithelium	43/3408	2.52E-03	ABL1, RHOA, ARRB2, CDC42, AP2M1, DAB2, DLG3, DVL3, CELSR3, CELSR2, MLLT3, OPHN1, PAFAH1B1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, TIAM1, FZD5, FZD3, FZD1, FZD4, FZD6, TP63, DLG5, PSMF1, GPC6, PSME3, PSMD14, EXOC5, DKK1, PSME4, AHI1, SMURF1, VANGL2, PLEKHA4, VANGL1, ZNRF3, PRICKLE2
BP	GO:0022404	molting cycle process	30/3408	2.53E-03	ACVR1B, ATP7A, BCL2, CTNNB1, EGFR, ERCC2, HDAC2, IGFBP5, RBPJ, SMAD4, MYO5A, PDGFA, SNAI1, SOS1, FZD3, FZD6, TP63, LDB1, LDB2, FST, HPSE, SOX21, DKK1, LRIG1, LGR4, FERMT1, VANGL2, MYSM1, CD109, ZDHHC21
BP	GO:0022405	hair cycle process	30/3408	2.53E-03	ACVR1B, ATP7A, BCL2, CTNNB1, EGFR, ERCC2, HDAC2, IGFBP5, RBPJ, SMAD4, MYO5A, PDGFA, SNAI1, SOS1, FZD3, FZD6, TP63, LDB1, LDB2, FST, HPSE, SOX21, DKK1, LRIG1, LGR4, FERMT1, VANGL2, MYSM1, CD109, ZDHHC21
BP	GO:0046822	regulation of nucleocytoplasmic transport	34/3408	2.55E-03	MAPK14, ECT2, GSK3B, JUP, IPO5, PPP1R12A, NEDD4, PPP1CC, PKIA, MAPK1, PTPN11, PTPN14, RAN, SP100, TCF7L2, TP53, TXN, XPO1, YWHAE, NUTF2, RAPGEF3, ANP32B, CPSF6, TARDBP, DNAJC27, UBR5, SUFU, RAB23, RBM27, FERMT1, RIOK2, MAVS, XPO5, XPO4
BP	GO:0070498	interleukin-1-mediated signaling pathway	33/3408	2.55E-03	EGR1, IKBKB, IL1R1, IL1RAP, IRAK1, IRAK2, MAP3K3, NFKB1, MAPK3, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SKP1, UBE2N, UBE2V1, SQSTM1, BTRC, RPS6KA4, RPS6KA5, PSMF1, PSME3, PSMD14, NOD1, TAB1, TAB2, PSME4, OTUD4, PELI1, ZNF675
BP	GO:0008585	female gonad development	32/3408	2.55E-03	ARRB1, ARRB2, ATM, BCL2, BCL2L1, CASP3, CEBPB, CTNNA1, FOXC1, FOXO3, HSPA5, INSR, KIT, SMAD4, KITLG, MMP14, PDGFRA, PGR, SFRP1, SRC, VEGFA, NRIP1, FZD4, SGPL1, PCYT1B, ADAMTS1, KMT2B, SIRT1, WNT4, PLEKHA1, ARID5B, ZNF830
BP	GO:1905037	autophagosome organization	32/3408	2.55E-03	PIP4K2A, RAB1A, RAB5A, RALB, ULK1, MTMR3, ATG5, ATG13, MFN2, ATG7, GABARAPL2, ATG14, ATG2A, PACS2, STX12, RAB3GAP2, UBQLN2, UBQLN1, SH3GLB1, RAB23, STX17, ATG16L1, ATG2B, NSFL1C, SMURF1, TP53INP2, ATG9A, MAP1LC3B, TP53INP1, UBXN2B, SMCR8, TMEM41B

BP	GO:0048011	neurotrophin TRK receptor signaling pathway	15/3408	2.66E-03	BDNF, CASP3, GRB2, NTRK3, PTPN11, SORT1, SOS1, SRC, WASF1, SPRY1, SLC9A6, FRS2, CYFIP2, DDIT4, AKT1S1
BP	GO:1901797	negative regulation of signal transduction by p53 class mediator	15/3408	2.66E-03	BCL2, PTTG1IP, CD44, DYRK1A, SNAI2, SNAI1, TWIST1, KDM1A, SIRT1, ZNF385A, RRM2B, TRIAP1, TAF9B, RRN3, RFFL
BP	GO:0035330	regulation of hippo signaling	8/3408	2.66E-03	NF2, SOX11, LIMD1, DLG5, WWC1, WWC3, MOB3B, WWC2
BP	GO:0048934	peripheral nervous system neuron differentiation	8/3408	2.66E-03	RUNX1, RUNX3, ETV1, ISL1, NEFH, POU4F1, ONECUT2, ISL2
BP	GO:0048935	peripheral nervous system neuron development	8/3408	2.66E-03	RUNX1, RUNX3, ETV1, ISL1, NEFH, POU4F1, ONECUT2, ISL2
BP	GO:0071679	commissural neuron axon guidance	8/3408	2.66E-03	DAG1, EPHB2, NCAM1, NFIB, PTCH1, VEGFA, FZD3, NRP1
BP	GO:0032210	regulation of telomere maintenance via telomerase	21/3408	2.66E-03	ATM, ATR, CCT6A, CTNNB1, DKC1, HNRNPC, HNRNPU, MAP3K4, PARN, MAPK1, MAPK3, SRC, XRCC5, TNKS, AURKB, SMG7, SMG5, XRN1, GNL3L, PINX1, HMBOX1
BP	GO:0051054	positive regulation of DNA metabolic process	63/3408	2.68E-03	ARRB2, ATM, ATR, ATRX, BRCA1, CCT6A, CEBPG, CTNNB1, DKC1, EGFR, ERCC2, EYA4, ERCC6, FGF2, FOXM1, FUS, HNRNPD, JUN, MECP2, MAP3K4, MLH1, MYC, PAK3, PARN, PDGFB, PML, MAPK1, MAPK3, PTPRC, RAD51, RPS3, MAP2K4, SRC, TFRC, TNFAIP1, UBE2N, XRCC5, USP9X, TNKS, AURKB, KLF4, ACTR2, MORC2, FAM168A, SIRT1, SPIDR, PARM1, GREM1, RTEL1, INO80, OTUD4, CHTF8, RIF1, ATF7IP, FMN2, SPIRE1, WIZ, NABP2, BRCC3, HMBOX1, SLX4, E2F7, RNF168
BP	GO:0008360	regulation of cell shape	45/3408	2.72E-03	ANXA7, RHOA, RHOB, FMNL1, CDC42, CRK, DAG1, DIAPH1, MARK2, EPB41, EPS8, FN1, ARHGAP35, KIT, MKLN1, MYH9, MYH10, MYO10, P2RY1, RASA1, RDX, CCL7, VEGFA, RND2, LIMD1, TAOK2, SEMA3E, DLC1, CDC42EP2, GNA13, RHOBTB3, PLXND1, RHOQ, BRWD1, FBLIM1, PHIP, PRPF40A, CDC42SE1, SHROOM3, RHOU, FMNL3, PLXNA4, ARHGAP18, FGD4, BRWD3
BP	GO:0030832	regulation of actin filament length	52/3408	2.73E-03	ADD1, ARF1, ARF6, RHOA, CAPZA2, CFL1, CFL2, CCR7, EPS8, FER, GRB2, ARHGAP35, NCKAP1L, MYO1C, NCK1, PAK3, PRKCE, TWF1, RASA1, RDX, SPTAN1, SPTBN1, NCK2, WASF1, WASL, LATS1, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, TENM1, CDC42EP2, NCKAP1, IQGAP2, DSTN, CIT, KANK1, COTL1, TMOD2, FMN2, SPIRE1, PLEKHG2, ARHGAP28, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, FMN1
BP	GO:0003208	cardiac ventricle morphogenesis	26/3408	2.83E-03	JAG1, BMPR1A, COL11A1, FKBP1A, FOXC1, GATA3, NRG1, HIF1A, RBPJ, ISL1, SMAD4, SMAD7, MEF2C, POU4F1, PROX1, SOX4, SOX11, TGFBR1, TGFBR3, HAND1, UBE4B, HEYL, DLL4, CHD7, HEG1, PTCD2
BP	GO:0045646	regulation of erythrocyte differentiation	19/3408	2.83E-03	ACVR1B, ZFP36L1, CDK6, MAPK14, FOXO3, GATA2, NCKAP1L, HIF1A, HOXA5, LYN, STAT1, STAT3, STAT5B, TAL1, ZFP36, LDB1, RBFOX2, NCAPG2, FAM210B
BP	GO:0001709	cell fate determination	17/3408	2.85E-03	JAG1, CTNNB1, GATA2, GATA3, GATA6, HES1, ISL1, MCL1, MEF2C, NOTCH2, PAX2, PAX6, PRRX1, PROX1, PTCH1, KLF4, CYP26B1
BP	GO:0072583	clathrin-dependent endocytosis	17/3408	2.85E-03	CANX, AP2M1, DAB2, HIP1, PIK3CB, SH3GL2, WASL, FCHSD2, TNK2, AAK1, SYT11, PIP5K1C, UBQLN2, FNBP1L, GPR107, SGIP1, FCHO2
BP	GO:0035066	positive regulation of histone acetylation	14/3408	2.96E-03	ARRB1, BRCA1, GATA3, KAT2A, ISL1, SMAD4, MAPK3, SNAI2, RPS6KA4, RPS6KA5, KAT7, WBP2, AUTS2, TADA2B
BP	GO:0061157	mRNA destabilization	14/3408	2.96E-03	ZFP36L1, ZFP36L2, HNRNPD, UPF1, ZFP36, ROCK2, PUM1, CPEB3, GIGYF2, YTHDF2, RBM23, METTL14, TRIM71, YTHDF3
BP	GO:0110110	positive regulation of animal organ morphogenesis	28/3408	2.98E-03	JAG1, AR, BMP7, CSF1, CTNNB1, EDN1, FGF1, GATA3, RBPJ, SMAD4, MDK, MYC, PAX2, PIM1, ROBO1, TGFBR1, TWIST1, VDR, VEGFA, WNT2B, XBP1, SPRY1, FRS2, DKK1, SOX8, SIX4, WNT4, LGR4
BP	GO:0034249	negative regulation of cellular amide metabolic process	63/3408	3.00E-03	ZFP36L1, ZFP36L2, CALR, DAPK1, DDX3X, EIF2S1, EIF4E, EIF4G1, FMR1, GAPDH, HNRNPD, IGFBP5, IREB2, CAPRIN1, PIN1, PRKAA1, EIF2AK2, PURA, UPF1, RGS2, RPS3, SNCA, SORL1, STAT3, TSC1, ZFP36, BTG2, FXR1, ENC1, CNOT8, ROCK2, PUM1, TOB1, SYNCRIP, IGF2BP1, IGF2BP3, CPEB3, CNOT1, SAMD4A, TNRC6B, LARP1, GIGYF2, AGO1, EIF2AK1, TNRC6A, ORMDL2,

					YTHDF2, XRN1, PUS7, SAMD4B, RBM23, TNRC6C, METTL14, CPEB4, SESN2, UNK, ORMDL1, ORMDL3, TRIM71, CPEB2, AGO3, AGO4, YTHDF3
BP	GO:0051271	negative regulation of cellular component movement	97/3408	3.01E-03	ACTN4, ADA, ADARB1, JAG1, RHOA, RHOB, BCL2, BMPR1A, CALR, CDKN1B, COL3A1, CRK, CTNNA1, DACH1, DAG1, DCN, DUSP1, FGF2, FOXO3, GATA3, NRG1, HOXA7, IDH2, IGFBP5, ILK, JUP, LRP1, SMAD7, MECP2, MEF2C, NF2, SERPINE1, PIN1, PPARD, PTEN, PTGER4, PTPRG, PTPRJ, PTPRK, PTPRR, RAP2A, RAP2B, ROBO1, CX3CL1, SFRP1, SP100, SRF, STAT3, STC1, NR2F2, TGFBR3, THBS1, VCL, STK24, SEMA7A, CHRD, NRP1, WASL, DLG5, KLF4, SEMA3E, TRIB1, CITED2, SEMA3A, DLC1, SEMA4B, IL24, ABHD2, PTPRT, DUSP10, VASH1, LIMCH1, LRCH1, KANK1, CLASP1, CORO1C, CLIC4, GREM1, ADIPOR1, WNT4, DLL4, SEMA4C, ADAMTS9, SEMA6A, RAP2C, PBLD, NDRG4, NAV3, PHLDB2, TP53INP1, OSBPL8, ACVR1C, DAB2IP, SPRED1, ARID2, FLCN, MIA3
BP	GO:0031532	actin cytoskeleton reorganization	33/3408	3.05E-03	ABL1, ABL2, RHOA, ARHGDIA, CDC42, CXADR, S1PR1, EPS8, FER, GAB1, KIT, MDK, MKLN1, MYH9, NEDD9, NOTCH2, NTRK3, PDGFRA, PTPN1, RAP2A, SHC1, TRPM2, PDLIM4, NRP1, SEMA3E, RAPGEF3, CD2AP, SIPA1L1, AUTS2, MINK1, ANTXR1, WHAMM, RICTOR
BP	GO:0006260	DNA replication	73/3408	3.05E-03	ATM, ATR, ATRX, BCL6, BRCA1, CCNA2, CDC34, CHEK1, DACH1, EGFR, HMGA1, JUN, LIG4, MCM3, MCM4, MCM7, NAP1L1, NFIA, NFIB, NFIC, NFIX, NUP98, ORC5, POLA1, PPP2CA, PPP2R1A, RAD1, PURA, RAD51, RBBP6, UPF1, REV3L, RFC1, RRM2, MAP2K4, SET, SSRP1, TNFAIP1, TP53, SMC1A, CCNE2, CHAF1A, ATG7, POLQ, STAG2, KAT7, SUPT16H, PDS5A, SIN3A, POLL, RRM2B, ING4, DTL, RTEL1, ETAA1, INO80, CHTF8, FBXW7, USP37, WIZ, TSPYL2, NUCKS1, RHNO1, RPAIN, SLX4, ZNF830, SLFN11, ESCO1, RMI2, E2F7, SDE2, ZBTB38, BOD1L1
BP	GO:0001657	ureteric bud development	32/3408	3.05E-03	BCL2, BMP7, CTNNB1, FGF1, FGF2, FOXC1, GATA3, HES1, ILK, SMAD2, SMAD4, SMAD6, SMAD7, MYC, PAX2, PBX1, PTCH1, SDC4, SFRP1, HNF1B, VEGFA, WNT2B, DCHS1, GDF11, SPRY1, SOX8, SIX4, WNT4, LGR4, LZTS2, BMPER, FMN1
BP	GO:0032273	positive regulation of protein polymerization	41/3408	3.07E-03	ARF1, ARF6, RHOA, CDKN1B, CCR7, FER, GRB2, NCKAP1L, MAP1B, MAPT, MECP2, MET, MYO1C, NCK1, PRKCE, RPS3, NCK2, WASF1, WASL, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, AKAP9, ABI2, TENM1, CDC42EP2, NCKAP1, IQGAP2, TPPP, CLASP1, NIN, FMN2, SPIRE1, SLAIN2, NAV3, WHAMM, JMY, RICTOR, FMN1
BP	GO:1904356	regulation of telomere maintenance via telomere lengthening	23/3408	3.08E-03	ATM, ATR, CCT6A, CTNNB1, DKC1, HNRNPC, HNRNPU, MAP3K4, PARN, MAPK1, MAPK3, SRC, XRCC5, TNKS, AURKB, SMG7, SMG5, RTEL1, XRN1, GNL3L, PINX1, HMBOX1, SLX4
BP	GO:0051496	positive regulation of stress fiber assembly	20/3408	3.15E-03	ABL1, RHOA, CD47, CDC42, LIMK1, NF2, PXN, SDC4, SFRP1, TESK1, TGFBR1, TSC1, NRP1, ROCK2, BAG4, RAPGEF3, LIMCH1, WNT4, SYNPO2L, SH3PXD2B
BP	GO:0051569	regulation of histone H3-K4 methylation	13/3408	3.24E-03	BRCA1, CTNNB1, DNMT3B, GATA3, SMAD4, KMT2A, MYB, CTR9, KMT2B, KDM1A, AUTS2, BCOR, KMT2E
BP	GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	39/3408	3.24E-03	ABL1, CAV1, FBN1, FBN2, HSPA5, LTBP1, SMAD2, SMAD6, SMAD7, PIN1, SFRP1, SKI, SKIL, SORL1, ADAM17, TGFBR1, TGFBR3, TP53, FZD1, CHRD, MTMR4, ONECUT2, TOB1, FSTL3, FST, DKK1, PEG10, SIRT1, ZNF451, GREM1, HIPK2, TRIM33, PMEPA1, SMURF1, PBLD, WFIKKN2, CD109, BMPER, RBPMS2
BP	GO:0048207	vesicle targeting, rough ER to cis-Golgi	24/3408	3.24E-03	CD59, CSNK1D, CTSZ, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, NAPA, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, ANKRD28, TRAPPC4, TRAPPC2L, PPP6R3, SAR1A, GORASP1, TBC1D20
BP	GO:0048208	COPII vesicle coating	24/3408	3.24E-03	CD59, CSNK1D, CTSZ, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, NAPA, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, ANKRD28, TRAPPC4, TRAPPC2L, PPP6R3, SAR1A, GORASP1, TBC1D20
BP	GO:1904888	cranial skeletal system development	24/3408	3.24E-03	RUNX2, FOXN3, CRKL, CTNNB1, DLX2, MEGF8, GNAS, INSIG1, SMAD2, MEF2C, MMP14, PDGFRA, PRRX1, TGFBR1, TWIST1, TP63, NIPBL, MTHFD1L, INSIG2, RAB23, SIX4, CEP55, RDH10, SH3PXD2B
BP	GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	16/3408	3.27E-03	MLH1, CNOT4, PARN, ZFP36, BTG2, CNOT8, TOB1, CPEB3, CNOT1, SAMD4A, TNRC6B, PABPC1, TNRC6A, SAMD4B, CNOT6, TNRC6C
BP	GO:0035635	entry of bacterium into host cell	9/3408	3.29E-03	CAV1, CBL, CTNNB1, CTNND1, GRB2, ITGAV, MET, SRC, CBLL1
BP	GO:0051489	regulation of filopodium assembly	18/3408	3.30E-03	ARF6, CDC42, CCR7, FMR1, MYO10, RAB5A, SRF, TGFBR1, TRPM2, NRP1, WASL, TENM1, NLGN1, RHOQ, PPP1R16B, FNBP1L, RAB17, AGRN

BP	GO:0072091	regulation of stem cell proliferation	25/3408	3.38E-03	ZFP36L1, CTNNA1, CTNNB1, HIF1A, HNRNPU, KITLG, NF2, PAX6, PIM1, EIF2AK2, PTPRC, CX3CL1, SNAI2, SOX11, TBX3, TERT, TP53, VEGFA, FZD3, HMGA2, KDM1A, FERMT1, KCTD11, AGO3, ATXN1L
BP	GO:1901215	negative regulation of neuron death	58/3408	3.40E-03	RHOA, ARRB1, ARRB2, AXL, BCL2, BCL2L1, BDNF, CBL, CEBPB, CREB1, CSF1, CTNNB1, EIF4G1, GSK3B, HIF1A, ILK, ISL1, JUN, KRAS, LIG4, LRP1, MDK, MECP2, MEF2C, PIN1, POU4F1, PPARA, RASA1, CX3CL1, MAP2K4, SET, SNCA, SOD2, SORL1, STAT3, TERT, TNFRSF1B, TSC1, TYRO3, BTG2, NR4A3, FZD1, NRP1, SYNGAP1, GPNMB, HYOU1, ATG7, STAMBP, SIRT1, SLC7A11, HTRA2, HIPK2, SIX4, OXR1, VPS35, CPEB4, DNAJC5, BHLHB9
BP	GO:0003229	ventricular cardiac muscle tissue development	21/3408	3.43E-03	BMPR1A, COL11A1, FKBP1A, FOXC1, NRG1, RBPJ, ISL1, SMAD4, SMAD7, POU4F1, PROX1, TBX3, TGFBR1, TGFBR3, HAND1, UBE4B, DLL4, CHD7, ADAMTS9, HEG1, PTCD2
BP	GO:0030856	regulation of epithelial cell differentiation	46/3408	3.46E-03	ADD1, JAG1, CCND1, ZFP36L1, BTG1, CAV1, RUNX1, CBFB, CDKN1B, CEBPB, CTNNB1, S1PR3, EZH2, FOXC1, GATA3, GSK3B, HOXA7, HES1, IKBKB, MAFG, SERPINE1, PAX2, PAX6, PTCH1, RFX3, STAT1, TBX3, ZEB1, VDR, VEGFA, ZFP36, VEZF1, NCOA3, TP63, ROCK2, CLOCK, MAFF, GRHL1, ERRFI1, AHI1, ESRP1, FOXJ2, SGPP1, APOLD1, KIAA1109, CD109
BP	GO:0001783	B cell apoptotic process	12/3408	3.46E-03	ADA, BAK1, BCL6, CRKL, LYN, PTEN, IRS2, AURKB, BCL2L11, FOXP1, SLC39A10, FNIP1
BP	GO:1900078	positive regulation of cellular response to insulin stimulus	12/3408	3.46E-03	ESRRA, GNAI2, IGF2, MYO1C, OPA1, PTPN11, SORL1, SRC, SIRT1, ADIPOR1, NUCKS1, OSBPL8
BP	GO:0048199	vesicle targeting, to, from or within Golgi	26/3408	3.47E-03	CD59, CSNK1D, CTSZ, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, NAPA, GOSR1, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, ANKRD28, TRAPPC4, TRAPPC2L, PPP6R3, SAR1A, GORASP1, CEP19, TBC1D20
BP	GO:0045619	regulation of lymphocyte differentiation	49/3408	3.50E-03	ABL1, ADA, RHOA, AXL, BCL6, PRDM1, ZFP36L1, ZFP36L2, CAMK4, RUNX1, RUNX3, CBFB, CLPTM1, CYLD, EGR3, ERBB2, GATA3, KAT2A, NCKAP1L, HMGB3, IL7R, IL18, IRF1, IRF4, ITPKB, SMAD7, MDK, MMP14, MYB, PTPRC, RAG1, SFRP1, SOS1, SYK, ZEB1, XBP1, SOCS1, TNFSF9, AP3D1, CD83, SOCS5, BTN2A2, DUSP10, PRELID1, PCID2, CYP26B1, ZMIZ1, ATP11C, NRARP
BP	GO:0006024	glycosaminoglycan biosynthetic process	35/3408	3.51E-03	NCAN, DCN, EXTL2, EXTL3, GCNT2, HAS3, NDST1, CHST6, NFKB1, PDGFB, PRELP, SDC2, SDC4, ST3GAL1, UGDH, CHST1, B4GALT2, B4GALT6, NDST3, HS2ST1, HS3ST3A1, HS3ST1, ABCC5, GPC6, UST, ST3GAL6, GLCE, CHST15, CSGALNACT2, CSGALNACT1, CHST7, XYLT2, CHST9, HS6ST2, AGRN
BP	GO:0000271	polysaccharide biosynthetic process	27/3408	3.54E-03	AKT2, EXTL2, EXTL3, GSK3B, GYS1, HAS3, NDST1, IGF2, INSR, NFKB1, PDGFB, ENPP1, PHKG2, PPP1CA, PPP1CB, PPP1R3C, UGP2, DYRK2, IRS2, PER2, NDST3, HS2ST1, EPM2AIP1, PASK, CSGALNACT2, CSGALNACT1, B3GNT5
BP	GO:0061333	renal tubule morphogenesis	27/3408	3.54E-03	BCL2, COL4A1, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MEF2C, MYC, PAX2, PBX1, PKD1, PTCH1, HNF1B, VEGFA, WNT2B, DCHS1, KLHL3, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, FMN1
BP	GO:0072028	nephron morphogenesis	27/3408	3.54E-03	BCL2, BMP7, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MYC, PAX2, PBX1, PKD1, PTCH1, STAT1, HNF1B, VEGFA, WNT2B, DCHS1, KLHL3, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, FMN1
BP	GO:0043484	regulation of RNA splicing	41/3408	3.54E-03	DDX5, DYRK1A, FMR1, FUS, HNRNPK, HNRNPU, MBNL1, NCBP1, NUP98, SRSF1, SRSF2, SRSF4, SRSF7, TRA2B, SON, TMBIM6, AKAP17A, RBM19, THRAP3, PTBP3, MBNL2, DDX17, CELF2, SRSF10, RNPS1, U2AF2, RRP1B, RBFOX2, DAZAP1, RBMX, RBM15B, ESRP1, SMU1, RBM38, MBNL3, PRX, RBM25, AHNAK, FAM172A, SREK1, RBMXL1
BP	GO:0045056	transcytosis	10/3408	3.54E-03	LRP1, LRPAP1, PTAFR, RAB5A, SRC, USO1, RAB11B, VPS35, RAB17, MAL2
BP	GO:0051895	negative regulation of focal adhesion assembly	10/3408	3.54E-03	LRP1, MMP14, PTEN, SRC, THBS1, DLC1, FAM107A, CORO1C, RCC2, PHLDB2
BP	GO:0010801	negative regulation of peptidyl-threonine phosphorylation	11/3408	3.56E-03	CALM1, CALM2, CALM3, EIF4G1, SMAD7, PPP2R5D, DDIT4, PARD3, SPRED1, SPRED2, SPRED3
BP	GO:0035162	embryonic hemopoiesis	11/3408	3.56E-03	GATA2, GATA3, HIF1A, KIT, KITLG, KMT2A, PBX1, STK4, TAL1, VEGFA, SH2B3
BP	GO:0001823	mesonephros development	33/3408	3.57E-03	BCL2, BMP7, CTNNB1, FGF1, FGF2, FOXC1, GATA3, HES1, ILK, SMAD2, SMAD4, SMAD6, SMAD7, MYC, PAX2, PBX1, PKD1, PTCH1, SDC4, SFRP1, HNF1B, VEGFA, WNT2B, DCHS1, GDF11, SPRY1, SOX8, SIX4, WNT4, LGR4, LZTS2, BMPER, FMN1
BP	GO:0048024	regulation of mRNA splicing, via spliceosome	32/3408	3.60E-03	DDX5, DYRK1A, FMR1, HNRNPK, HNRNPU, MBNL1, NCBP1, NUP98, SRSF1, SRSF2, SRSF4, SRSF7, TRA2B, SON, RBM19, THRAP3, MBNL2, DDX17, CELF2, SRSF10, RNPS1, U2AF2, RBFOX2, DAZAP1, RBMX, RBM15B, SMU1, MBNL3, RBM25, FAM172A, SREK1, RBMXL1
BP	GO:0001942	hair follicle development	29/3408	3.60E-03	ACVR1B, ATP7A, BCL2, CTNNB1, EGFR, ERCC2, HDAC2, IGFBP5, RBPJ, SMAD4, MYO5A, PDGFA, SNAI1, SOS1, FZD3, FZD6, TP63, LDB1, LDB2, FST, HPSE, SOX21, DKK1, LGR4, FERMT1, VANGL2, MYSM1, CD109, ZDHHC21

BP	GO:0045621	positive regulation of lymphocyte differentiation	31/3408	3.61E-03	ADA, RHOA, AXL, BCL6, RUNX1, RUNX3, CBFB, CYLD, EGR3, GATA3, NCKAP1L, IL7R, IL18, ITPKB, MDK, MMP14, MYB, PTPRC, RAG1, SYK, XBP1, SOCS1, TNFSF9, AP3D1, CD83, SOCS5, BTN2A2, DUSP10, PCID2, ZMIZ1, ATP11C
BP	GO:1901216	positive regulation of neuron death	31/3408	3.61E-03	ABL1, RHOA, ATM, CAPN2, CASP3, CDC34, ATF2, CTNNB1, CTSZ, EFNB2, EGR1, EIF2S1, ELK1, EPHA7, FOXO3, GSK3B, JUN, MAPT, MCL1, MYB, MYBL2, PAK3, PIN1, MAP2K4, SNCA, TP53, BCL2L11, DKK1, SSH1, DDIT4, FBXW7
BP	GO:0042475	odontogenesis of dentin-containing tooth	30/3408	3.61E-03	ACVR2B, ADM, BMP7, BMPR1A, RUNX2, ATF2, CSF1, CTNNA1, CTNNB1, DLX2, FOXC1, FOXO1, HDAC2, ITGA6, JAG2, LRP6, MSX1, NF2, NFIC, TNFRSF11B, SERPINE1, PDGFRA, PPARA, STIM1, TP63, HAND1, BCL2L11, CNNM4, FAM20C, BCL11B
BP	GO:0001885	endothelial cell development	22/3408	3.61E-03	ADD1, CTNNB1, S1PR3, RAPGEF1, GSTM3, IKBKB, MET, PDE4D, RAP1B, RDX, STC1, VEGFA, WNT7B, VEZF1, TJP2, ROCK2, RAPGEF2, RAPGEF3, PPP1R16B, HEG1, RAP2C, MYADM
BP	GO:0043388	positive regulation of DNA binding	22/3408	3.61E-03	CALM3, CEBPG, CTNNB1, EP300, ERCC2, FOXC1, GATA3, HES1, IRF4, ISL1, PAX6, POU4F1, RB1, SKI, TWIST1, TXN, HMGA2, KLF4, MAU2, NIPBL, HIPK2, PINX1
BP	GO:0055010	ventricular cardiac muscle tissue morphogenesis	19/3408	3.64E-03	BMPR1A, COL11A1, FKBP1A, FOXC1, NRG1, RBPJ, ISL1, SMAD4, SMAD7, POU4F1, PROX1, TGFBR1, TGFBR3, HAND1, UBE4B, DLL4, CHD7, HEG1, PTCD2
BP	GO:0072666	establishment of protein localization to vacuole	19/3408	3.64E-03	SCARB2, LAMP2, M6PR, NEDD4, SORL1, VAMP7, AP3D1, GOSR2, ZFYVE16, SNF8, VPS13A, AP3M1, VPS36, VPS13C, VPS37C, VPS13D, SMURF1, GNPTAB, VPS37D
BP	GO:0035107	appendage morphogenesis	44/3408	3.64E-03	ASPH, ATRX, BAK1, BMP7, BMPR1A, CACNA1C, RUNX2, CREBBP, CTNNB1, DLX6, MEGF8, FBN2, GJA1, GNAS, HDAC2, HOXA9, HOXD13, LRP6, SMAD4, MBNL1, MSX1, PBX1, PRRX1, PTCH1, RARG, SKI, SOX4, SOX11, TBX3, TWIST1, FZD6, TP63, ALDH1A2, BCL2L11, DKK1, IQCE, NIPBL, CHD7, CYP26B1, PKDCC, RDH10, FREM2, FMN1, RNF165
BP	GO:0035108	limb morphogenesis	44/3408	3.64E-03	ASPH, ATRX, BAK1, BMP7, BMPR1A, CACNA1C, RUNX2, CREBBP, CTNNB1, DLX6, MEGF8, FBN2, GJA1, GNAS, HDAC2, HOXA9, HOXD13, LRP6, SMAD4, MBNL1, MSX1, PBX1, PRRX1, PTCH1, RARG, SKI, SOX4, SOX11, TBX3, TWIST1, FZD6, TP63, ALDH1A2, BCL2L11, DKK1, IQCE, NIPBL, CHD7, CYP26B1, PKDCC, RDH10, FREM2, FMN1, RNF165
BP	GO:0061028	establishment of endothelial barrier	17/3408	3.78E-03	ADD1, CTNNB1, S1PR3, RAPGEF1, IKBKB, PDE4D, RAP1B, RDX, VEGFA, WNT7B, TJP2, ROCK2, RAPGEF2, RAPGEF3, PPP1R16B, RAP2C, MYADM
BP	GO:0098927	vesicle-mediated transport between endosomal compartments	17/3408	3.78E-03	DAB2, EMP2, MYO1D, MAPK1, MAPK3, RAB5A, RDX, SORL1, SRC, SNX3, SNF8, LMTK2, RAB21, DNAJC13, HOOK1, HOOK3, WDR81
BP	GO:1902893	regulation of pri-miRNA transcription by RNA polymerase II	17/3408	3.78E-03	BMPR1A, GATA2, NR3C1, HIF1A, JUN, SMAD6, NFIB, PDGFB, PPARA, PPARD, SREBF2, SRF, STAT3, TEAD1, TERT, TP53, YY1
BP	GO:0031571	mitotic G1 DNA damage checkpoint	23/3408	3.80E-03	ATM, CCND1, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, GIGYF2, TRIAP1, CNOT6, E2F7
BP	GO:0044819	mitotic G1/S transition checkpoint	23/3408	3.80E-03	ATM, CCND1, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, GIGYF2, TRIAP1, CNOT6, E2F7
BP	GO:1903897	regulation of PERK-mediated unfolded protein response	7/3408	3.92E-03	HSPA5, NCK1, PTPN1, NCK2, AGR2, TMEM33, PPP1R15B
BP	GO:0007599	hemostasis	87/3408	3.94E-03	ACTB, ANXA7, ARRB1, ARRB2, AXL, CAPZA2, CAV1, ENTPD1, CD59, CDC42, COL1A1, COL1A2, COL3A1, CSRP1, EDN1, GATA2, GATA3, GATA6, GNAQ, GNAS, GNB1, GPI, SERPIND1, HDAC2, HNF4A, ILK, IRF1, ITPK1, ITPR1, ITPR2, LYN, MAFG, MYH9, P2RY1, SERPINE1, SERPINB2, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3CB, PRCP, PRKAR1A, PRKAR2A, PRKCA, PRKCE, MAPK1, MAPK3, PTPN11, RAB5A, RAP2B, SRC, SRF, SYK, TFPI, THBS1, TLN1, TYRO3, VCL, MAFK, FZD6, DGKE, DGKD, PABPC4, F2RL3, PAPSS2, MFN2, SH2B3, VAV3, MYL12A, GNA13, HPSE, AKAP10, MMRN1, KDM1A, RCOR1, DOCK9, CBX5, SLC7A11, MAFF, ZNF385A, SH2B1, AK3, HPS6, DGKH, ADAMTS18, JMJD1C
BP	GO:0043967	histone H4 acetylation	24/3408	3.97E-03	ARRB1, BRCA1, EP300, KAT2A, HCFC1, IRF4, KMT2A, KAT6A, YEATS4, ATG5, MORF4L2, KAT7, SIRT1, AUTS2, ING4, ING3, KANSL2, MSL2, EP400, BEND3, MEAF6, NAA40, NAA50, EPC1

BP	GO:2000573	positive regulation of DNA biosynthetic process	24/3408	3.97E-03	ARRB2, ATM, ATR, CCT6A, CTNNB1, DKC1, FGF2, HNRNPD, MAP3K4, MYC, PAK3, PARN, PDGFB, MAPK1, MAPK3, SRC, XRCC5, TNKS, AURKB, KLF4, PARM1, GREM1, CHTF8, HMBOX1
BP	GO:0006023	aminoglycan biosynthetic process	36/3408	3.98E-03	NCAN, DCN, EXTL2, EXTL3, GCNT2, HAS3, NDST1, CHST6, NFKB1, PDGFB, PRELP, SDC2, SDC4, ST3GAL1, UGDH, CHST1, B4GALT2, B4GALT6, NDST3, HS2ST1, HS3ST3A1, HS3ST1, ABCC5, GPC6, UST, ST3GAL6, GLCE, CHST15, CSGALNACT2, CSGALNACT1, CHST7, XYLT2, CHST9, B3GNT5, HS6ST2, AGRN
BP	GO:0043414	macromolecule methylation	80/3408	4.02E-03	ATRX, BRCA1, BTG1, CTNNB1, DNMT3A, DNMT3B, ETF1, EZH1, EZH2, GATA3, GNAS, GSPT1, JARID2, SMAD4, MECP2, MEN1, KMT2A, MLLT6, MTHFR, MYB, MYC, RAB3B, SATB1, SUV39H1, KDM6A, PRDM2, BTG2, KMT2D, PPM1D, MBD2, CTR9, SETD1A, KMT2B, CTCF, MTF2, KDM1A, CMTR1, SIRT1, SUZ12, FAM98A, AUTS2, RBM15B, TRMT6, ARID4B, WDR5B, TET2, GATAD2A, BCOR, RIF1, SETD5, NSUN5, ATF7IP, KMT2E, MEPCE, BEND3, METTL14, KMT2C, PCIF1, NSD1, METTL4, VCPKMT, CAMKMT, METTL8, CBLL1, TET1, SETD7, SETDB2, SETD3, DPY30, TGS1, PCMTD1, TRMT61A, TYW3, METTL21A, TRMT10B, TET3, PLD6, KDM1B, FAM98B, METTL2A
BP	GO:0030168	platelet activation	45/3408	4.02E-03	ACTB, ARRB1, ARRB2, AXL, COL1A1, COL1A2, COL3A1, CSRP1, GNAQ, GNAS, GNB1, ILK, ITPR1, ITPR2, LYN, MYH9, P2RY1, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3CB, PRKCA, PRKCE, MAPK1, MAPK3, PTPN11, RAP2B, SRC, SRF, SYK, TLN1, TYRO3, VCL, FZD6, DGKE, DGKD, F2RL3, SH2B3, VAV3, MYL12A, GNA13, SLC7A11, DGKH, ADAMTS18
BP	GO:0006406	mRNA export from nucleus	35/3408	4.05E-03	EIF4E, NCBP1, NUP88, NUP98, POLR2D, RANBP2, UPF1, SRSF1, SRSF2, SRSF4, SRSF7, PABPN1, POM121, SMG7, NXF1, NUP50, RNPS1, DDX19B, U2AF2, SMG1, SMG5, UPF2, RBM15B, CDC40, CPSF2, ALKBH5, DDX19A, WDR33, NDC1, NUP133, PCID2, THOC2, SEH1L, NUP43, POM121C
BP	GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	35/3408	4.05E-03	EIF4E, NCBP1, NUP88, NUP98, POLR2D, RANBP2, UPF1, SRSF1, SRSF2, SRSF4, SRSF7, PABPN1, POM121, SMG7, NXF1, NUP50, RNPS1, DDX19B, U2AF2, SMG1, SMG5, UPF2, RBM15B, CDC40, CPSF2, ALKBH5, DDX19A, WDR33, NDC1, NUP133, PCID2, THOC2, SEH1L, NUP43, POM121C
BP	GO:0090130	tissue migration	91/3408	4.07E-03	ABL1, ARF6, RHOA, RHOB, BMPR2, CALR, DCN, HBEGF, EDN1, EFNB2, EGR3, EMP2, EPHB4, FGF1, FGF2, FLT4, GATA2, GATA3, GPI, HIF1A, ITGA3, ITGB1, JUN, JUP, KIT, LOXL2, MECP2, MEF2C, MAP3K3, MET, MYH9, PDGFB, PIK3C2A, PPARD, PRCP, PRKCA, PRKCE, PKN2, PROX1, PTEN, PTPN11, PTPRG, PTPRR, PXN, ROBO1, RREB1, SP100, SPARC, SRC, SRF, STC1, ADAM17, NR2F2, TGFBR1, THBS1, VEGFA, ADAM9, NRP1, KLF4, MAP4K4, ROCK2, HDAC9, AKT3, SEMA3A, PLK2, DUSP10, VASH1, PLXND1, KANK1, CLASP1, SIRT1, CORO1C, GREM1, FOXP1, ADIPOR1, ANLN, EPB41L4B, DLL4, FBXW7, FERMT1, ADAMTS9, EPB41L5, PBLD, NUS1, DAB2IP, AMOT, AMOTL1, SPRED1, BMPER, EMC10, MIA3
BP	GO:0033692	cellular polysaccharide biosynthetic process	25/3408	4.07E-03	AKT2, EXTL2, EXTL3, GSK3B, GYS1, HAS3, NDST1, IGF2, INSR, ENPP1, PHKG2, PPP1CA, PPP1CB, PPP1R3C, UGP2, DYRK2, IRS2, PER2, NDST3, HS2ST1, EPM2AIP1, PASK, CSGALNACT2, CSGALNACT1, B3GNT5
BP	GO:0051057	positive regulation of small GTPase mediated signal transduction	25/3408	4.07E-03	ADCYAP1R1, ARRB1, COL3A1, CRKL, CSF1, GRB2, RAPGEF1, NRG1, ITPKB, KRAS, LYN, KITLG, NOTCH2, ROBO1, SHC1, SOS1, SRC, SHOC2, IRS2, F2RL3, MAP4K4, AKAP13, AUTS2, CDON, SYNPO2L
BP	GO:0010165	response to X-ray	14/3408	4.13E-03	ATM, CCND1, CASP3, CDKN1A, ERCC6, GATA3, LIG4, SFRP1, TP53, XRCC5, HMGA2, NIPBL, NUCKS1, BRCC3
BP	GO:1903393	positive regulation of adherens junction organization	14/3408	4.13E-03	ABL1, ADD1, ARF6, PTPRJ, SDC4, SFRP1, TSC1, VEGFA, IQGAP1, NRP1, MAP4K4, WNT4, EPB41L5, FMN1
BP	GO:0042177	negative regulation of protein catabolic process	40/3408	4.13E-03	ALAD, EGFR, EPHA4, FHIT, NRG1, HMGCR, MAD2L1, MAP1A, MDM4, OPHN1, FURIN, SERPINE2, PIN1, PML, SNCA, STYX, TAF1, TIMP2, TIMP3, UBE2G2, SNX3, PSMF1, LRIG2, TLK2, GABARAPL2, MYCBP2, SF3B3, HIPK2, USP25, DERL2, WAC, UCHL5, UBE2J1, AZIN1, SUFU, LAPTM4B, YOD1, VPS35, FMN2, DAB2IP
BP	GO:0042476	odontogenesis	40/3408	4.13E-03	ACVR2B, ADM, RHOA, BMP7, BMPR1A, RUNX2, COL1A1, COL1A2, ATF2, CSF1, CTNNA1, CTNNB1, DLX2, EDN1, FOXC1, FOXO1, HDAC2, ITGA6, JAG2, LRP6, MSX1, MYO5A, NF2, NFIC, TNFRSF11B, SERPINE1, PAX9, PDGFRA, PPARA, SRC, STIM1, TWIST1, TP63, HAND1, BCL2L11, ADAMTS5, CNNM4, BCOR, FAM20C, BCL11B
BP	GO:0050863	regulation of T cell activation	81/3408	4.14E-03	ABL1, ADA, RHOA, BCL6, PRDM1, CAMK4, CASP3, CAV1, RUNX1, RUNX3, CBFB, CD47, CDC42, CEBPB, CLPTM1, CCR7, CSK, CTNNB1, CYLD, EFNB1, EFNB2, EGR3, ERBB2, FLOT2, GATA3, KAT2A, GRB2, NCKAP1L, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, IRF1, IRF4, ITPKB, LYN, SMAD7, MDK, MYB, NCK1, PAK2, PAK3, PAWR, PRKAR1A, PTPN11, PTPRC, RAG1, RPS3, SDC4, SOS1, SRC, SYK, ZEB1, TFRC, TNFRSF1B, VCAM1, XBP1, NCK2, SOCS1, TNFSF9, FADD, AP3D1, DLG5, SOCS6, CD83, SOCS5, BTN2A2, GPNMB, DUSP10, ICOSLG, PRELID1, LAX1, PAG1, CYP26B1, PELI1, ZMIZ1, CD276, SIRPA, NRARP
BP	GO:0044264	cellular polysaccharide metabolic process	33/3408	4.16E-03	AKT2, CALM1, EXTL2, EXTL3, GAA, GSK3B, GYS1, HAS3, NDST1, IGF2, IL6ST, INSR, ENPP1, PHKA1, PHKG2, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PYGB, UGP2, DYRK2, IRS2, PER2, NDST3, HS2ST1, EPM2AIP1, PASK, CSGALNACT2, CSGALNACT1, STK40, B3GNT5

BP	GO:0048259	regulation of receptor-mediated endocytosis	33/3408	4.16E-03	ARF1, ARF6, ARRB1, ARRB2, CBL, DAB2, EFNB2, FMR1, HIP1, HNRNPK, LRPAP1, MKLN1, OPHN1, SERPINE1, PIK3CB, ATXN2, SH3GL2, SYK, VEGFA, NUMB, WASL, TNK2, AAK1, DKK1, RAB21, SYT11, CD2AP, LDLRAP1, GREM1, UBQLN2, AHI1, SGIP1, ANKRD13A
BP	GO:0030833	regulation of actin filament polymerization	47/3408	4.21E-03	ADD1, ARF1, ARF6, RHOA, CAPZA2, CCR7, EPS8, FER, GRB2, NCKAP1L, MYO1C, NCK1, PAK3, PRKCE, TWF1, RASA1, RDX, SPTAN1, SPTBN1, NCK2, WASF1, WASL, LATS1, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, TENM1, CDC42EP2, NCKAP1, IQGAP2, KANK1, COTL1, TMOD2, FMN2, SPIRE1, PLEKHG2, ARHGAP28, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, FMN1
BP	GO:0031110	regulation of microtubule polymerization or depolymerization	27/3408	4.21E-03	ABL1, APC, CDKN1B, DYRK1A, FKBP4, MAP1A, MAP1B, MAPT, MECP2, MET, MID1, RPS3, SNCA, ARHGEF2, AKAP9, TUBB4A, MAPRE3, CAMSAP2, CLASP1, CLIP3, NIN, TAOK1, SLAIN2, NAV3, TTBK2, CAMSAP1, SKA2
BP	GO:0140014	mitotic nuclear division	70/3408	4.22E-03	APC, RHOA, ATM, ATRX, BMP7, CDKN1B, RCC1, CHEK1, DUSP1, EDN1, EPS8, HNRNPU, IGF2, IK, INCENP, INSR, KIF2A, MAD2L1, MYBL2, PDGFB, PIN1, PPP2R1A, RAD21, RAN, RB1, AURKA, TGFA, SMC1A, CUL3, CDC14B, TNKS, PRC1, AURKB, TRIP13, KIF3B, KIF23, VPS4B, STAG2, KIF2C, PDS5B, POGZ, PDS5A, CLASP1, MAU2, NIPBL, SH2B1, CHMP5, ANLN, INO80, NDE1, CHTF8, PINX1, PHIP, CDCA8, RIOK2, PCID2, PPP2R2D, NSFL1C, CHMP1B, HECW2, CEP85, CEP97, NAA50, SEH1L, CHMP7, CCSAP, UBXN2B, PHF13, KLHDC8B, EPGN
BP	GO:0055006	cardiac cell development	31/3408	4.23E-03	JAG1, CXADR, EDN1, G6PD, HNRNPU, SMAD4, MEF2A, MYH10, PDGFRA, PIN1, PPARA, PROX1, RGS2, RGS4, MAP2K4, SGCD, SLC8A1, SRF, TBX3, TGFBR3, VEGFA, YY1, SORBS2, AKAP6, ATG5, SPRY1, NEBL, PDLIM5, AKAP13, PDCD4, ALPK3
BP	GO:0061326	renal tubule development	31/3408	4.23E-03	JAG1, BCL2, COL4A1, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MEF2C, MYC, PAX2, PBX1, PKD1, PTCH1, STAT1, HNF1B, VEGFA, WNT7B, WNT2B, DCHS1, KLHL3, HEYL, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, FMN1
BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	21/3408	4.23E-03	ATM, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7
BP	GO:0048017	inositol lipid-mediated signaling	52/3408	4.34E-03	RHOA, ZFP36L1, CBL, DCN, EDN1, EGFR, ERBB2, FLT4, GAB1, GATA3, IGF1R, IL18, INSR, KIT, LYN, MAZ, NEDD4, NKX3-1, NTRK3, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3C2A, PIK3CB, PIP4K2A, PLD1, PPARD, MAPK1, MAPK3, PTAFR, PTEN, RPS6KB1, SRC, TWIST1, TYRO3, IRS2, IER3, KLF4, BTN2A2, STAMBP, PIP5K1C, SIRT1, NCS1, PPP1R16B, CEP55, PITPNM2, PLEKHA1, PREX2, PIK3IP1, PIK3AP1, DAB2IP
BP	GO:0048639	positive regulation of developmental growth	52/3408	4.34E-03	BCL2, BDNF, BMPR1A, BMPR2, CREB1, MAPK14, CSF1, EDN1, EFNA5, MEGF8, FGF2, FN1, GATA6, GDI1, GOLGA4, IGF2, RBPJ, ILK, INSR, L1CAM, LIMK1, LRP1, MAP1B, MAPT, MEF2C, NTRK3, PAFAH1B1, PIM1, PIN1, POU3F2, PPARD, MAPK1, PROX1, SRF, SYT1, TGFBR3, VEGFA, RND2, SEMA7A, NRP1, NTN1, AKAP6, AGR2, NIPBL, SERP1, SYT17, CHD7, SMURF1, MUL1, SYT2, SH3PXD2B, AGRN
BP	GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	38/3408	4.36E-03	CBL, DCN, EGFR, FLT4, GAB1, IGF1R, IL18, INSR, KIT, LYN, MAZ, NEDD4, NKX3-1, NTRK3, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3CB, PIP4K2A, PPARD, MAPK1, MAPK3, PTEN, SRC, TWIST1, IRS2, IER3, KLF4, BTN2A2, STAMBP, PIP5K1C, SIRT1, PPP1R16B, CEP55, PIK3IP1, PIK3AP1, DAB2IP
BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	59/3408	4.39E-03	FAS, RHOA, ARRB1, ARRB2, BAK1, CASP10, CD44, DAPK1, DDX3X, EPHA7, HIP1, MAPT, MYC, NKX3-1, PAK2, PAX2, SERPINB9, PML, RAG1, ROBO1, RPS3, RPS6KA3, SIAH2, SNCA, SRC, SYK, THBS1, VCP, VEGFA, YWHAE, TP63, TNFSF10, FADD, KLF4, HERPUD1, BCL2L11, BCAP31, NOD1, DLC1, ANP32B, PRDX3, ARL6IP1, SIRT1, BCL2L13, MTCH1, PRDX5, BBC3, HTRA2, TRIAP1, CYCS, USP47, IFT57, MUL1, SOX7, FNIP1, EGLN3, RFFL, ACVR1C, ACER2
BP	GO:0001702	gastrulation with mouth forming second	13/3408	4.61E-03	ACVR2B, CTNNB1, MEGF8, LRP6, SMAD4, RNF2, SRF, UGDH, CHRD, LDB1, FRS2, AMOT, CRB2
BP	GO:0061912	selective autophagy	19/3408	4.71E-03	HTT, MAPK3, TP53, SQSTM1, ATG5, ATG13, MFN2, NOD1, SPTLC1, ATG14, KLHL3, HSPB8, HTRA2, UBQLN1, VPS13C, VPS13D, SMURF1, SESN2, WDR81
BP	GO:0043297	apical junction assembly	23/3408	4.72E-03	ACTN4, APC, RHOA, RUNX1, CBFB, CTNNA1, ECT2, GJA1, IKBKB, MYO1C, PKN2, SNAI2, SNAI1, SRF, STRN, VCL, FZD5, DLG5, ROCK2, PDCD6IP, PARD3, PARD6B, MTDH
BP	GO:0051817	modification of morphology or physiology of other	35/3408	4.73E-03	BCL2L1, CALM1, CALM2, CALM3, CCNT1, CFL1, DAG1, EP300, STOM, FMR1, GAPDH, IGF2R, INSR, ITGAV, JUN, KPNA1, KPNA3, NTRK3, SERPINB9, EIF2AK2, HMGA2, PABPN1, VAPB, VAPA, BCL2L11, TNIP1, ATG7, TUSC2, RRP1B, TARDBP, KPNA6, HIPK2, ZNF639, NUCKS1, TBC1D20

		organism involved in symbiotic interaction			
BP	GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	33/3408	4.94E-03	ACVR1B, ACVR2B, BMP3, BMP7, BMPR1A, BMPR2, CREBBP, DAB2, EP300, HES1, RBPJ, ILK, SMAD2, SMAD4, MEN1, MSX1, NEO1, SOX11, ADAM17, TGFBR1, TGFBR3, THBS1, ITGA8, GDF11, CITED2, ZC3H3, HIPK2, RNF111, FERMT1, FLCN, CRB2, BMP8A, RNF165
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	33/3408	4.94E-03	FAS, AR, BCL2, BCL2L1, BRCA1, CTNNA1, EYA4, HTT, ITGA6, ITGAV, MCL1, SERPINE1, CX3CL1, SIAH2, SNAI2, SRC, TCF7L2, TERT, TGFBR1, THBS1, PEA15, TNFSF10, FADD, NRP1, ARHGEF2, PSME3, ZMYND11, SGK3, PHIP, BIRC6, TMBIM1, ITPRIP, RFFL
BP	GO:0055123	digestive system development	43/3408	4.95E-03	ACVR2B, ADA, BCL2, PRDM1, CDKN1A, COL3A1, CRKL, CTNNB1, MEGF8, EGFR, EPHB3, GATA6, HIF1A, HOXA5, HOXD13, HES1, IGF2, INSR, ITGA6, KIT, SMAD2, PDGFRA, PKD1, RB1, SFRP1, SLC4A2, SOX11, HNF1B, TCF7, XBP1, TP63, DCHS1, ALDH1A2, AGR2, NIPBL, AHI1, LGR4, C1GALT1, VANGL2, EPB41L5, CLMP, PKDCC, RBPMS2
BP	GO:0120034	positive regulation of plasma membrane bounded cell projection assembly	32/3408	5.01E-03	APC, ATP7A, CDC42, CCR7, EPS8, FMR1, ARHGAP35, HTT, KIT, SRF, TGFBR1, DYNLL1, NRP1, WASL, CEP135, PLEKHM1, ARPC2, WASF2, TENM1, CDC42EP2, NCKAP1, NLGN1, ATMIN, RHOQ, FAM98A, AUTS2, ANLN, FNBP1L, AKIRIN1, KCTD17, CEP120, AGRN
BP	GO:0006509	membrane protein ectodomain proteolysis	17/3408	5.02E-03	ADAM10, DAG1, MYH9, FURIN, ADAM17, TIMP2, TIMP3, TNFRSF1B, ADAM9, LRIG2, NCSTN, BACE2, RBMX, APH1A, ERAP1, SPPL2A, SH3D19
BP	GO:0001893	maternal placenta development	15/3408	5.02E-03	PRDM1, BMPR2, CTSB, GJA1, MEN1, PPARD, MAPK1, MAPK3, PTGIS, STC1, NR2F2, VDR, STC2, PRDX3, DAZAP1
BP	GO:0021955	central nervous system neuron axonogenesis	15/3408	5.02E-03	ADARB1, EPHA4, EPHB2, EPHB3, ARHGAP35, NFIB, PAFAH1B1, PTEN, DCLK1, B4GALT6, MYCBP2, SZT2, NIN, PLXNA4, FBXO45
BP	GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	15/3408	5.02E-03	RHOA, BRCA1, CALR, CRY2, DAB2, ISL1, SFRP1, TP63, CLOCK, NCOR1, CNOT1, SIRT1, HEYL, FOXP1, STRN3
BP	GO:0045070	positive regulation of viral genome replication	15/3408	5.02E-03	ADAR, ADARB1, DDX3X, STOM, NR5A2, PKN2, STAU1, TOP2B, VAPB, VAPA, LARP1, PABPC1, NUCKS1, TBC1D20, PDE12
BP	GO:0030516	regulation of axon extension	31/3408	5.02E-03	ABL1, BMPR2, MEGF8, FN1, GDI1, GOLGA4, GSK3B, ILK, L1CAM, LIMK1, LRP1, MAP1B, MAPT, NTRK3, PAFAH1B1, SRF, VEGFA, SEMA7A, NRP1, NTN1, SEMA3E, SEMA3A, OLFM1, SEMA4B, RAB21, SIN3A, SEMA4C, SEMA6A, PLXNA4, WDR36, TTL
BP	GO:0097327	response to antineoplastic agent	31/3408	5.02E-03	ADAM10, ATRX, BRCA1, CTNNA1, CTNNB1, DNMT3B, EDN1, EGFR, EGR1, EIF4E, FOXO1, FOXO3, FMR1, NR3C1, HNRNPD, JUP, OPA1, PDGFB, PRKAA1, PTAFR, RAD51, ADAM9, KAT7, KIF1B, LARP1, SPIDR, KDM3B, ERRFI1, XRN1, DDIT4, DDI2
BP	GO:0021952	central nervous system projection neuron axonogenesis	12/3408	5.02E-03	ADARB1, EPHA4, EPHB2, EPHB3, NFIB, PAFAH1B1, DCLK1, MYCBP2, SZT2, NIN, PLXNA4, FBXO45
BP	GO:0051894	positive regulation of focal adhesion assembly	12/3408	5.02E-03	ABL1, PTPRJ, SDC4, SFRP1, TSC1, VEGFA, IQGAP1, NRP1, MAP4K4, WNT4, EPB41L5, FMN1
BP	GO:0048844	artery morphogenesis	26/3408	5.02E-03	JAG1, PRDM1, BMPR1A, BMPR2, COL3A1, EFNB2, FOXC1, HES1, RBPJ, LDLR, LRP1, SMAD7, MDK, PRRX1, PROX1, SOX4, SRF, TGFBR1, VEGFA, NRP1, AKT3, DLL4, CHD7, ADAMTS9, ZMIZ1, ARID2
BP	GO:0072088	nephron epithelium morphogenesis	26/3408	5.02E-03	BCL2, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MYC, PAX2, PBX1, PKD1, PTCH1, STAT1, HNF1B, VEGFA, WNT2B, DCHS1, KLHL3, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, FMN1
BP	GO:0046349	amino sugar biosynthetic process	8/3408	5.02E-03	GFPT1, PGM3, GFPT2, GNPDA1, GNE, GNPNAT1, UAP1L1, NANP

BP	GO:0090399	replicative senescence	8/3408	5.02E-03	ATM, ATR, CDKN1A, CHEK1, MME, SERPINE1, TERT, TP53
BP	GO:2000052	positive regulation of non-canonical Wnt signaling pathway	8/3408	5.02E-03	ABL1, CSNK1D, CSNK1E, DAB2, MLLT3, SFRP1, DKK1, PLEKHA4
BP	GO:0007030	Golgi organization	42/3408	5.05E-03	ARL1, CDC42, CSNK1D, GOLGB1, HTT, ATP8B1, MAPK1, MAPK3, RAB1A, SURF4, USO1, TRIP11, USP6NL, GOLGA5, AKAP9, TMED10, CIT, GOLGA8A, CAMSAP2, CLASP1, ATL3, RAB30, TMED5, TMED7, HOOK1, STX17, GOLPH3L, PI4K2B, NPLOC4, NSFL1C, ATP8B2, ATL2, GORASP1, VCPIP1, COG3, FHDC1, TBC1D20, TANGO2, UBXN2B, TMED4, MYO18A, GOLGA8B
BP	GO:0010675	regulation of cellular carbohydrate metabolic process	42/3408	5.05E-03	ADCYAP1R1, AKT2, SCARB2, EP300, FOXO1, KAT2A, GSK3B, IGF2, FOXK2, INSR, P2RY1, PDK3, PDK4, ENPP1, PFKFB2, PGAM1, PHKG2, PPARA, PPP1CA, PPP1CB, PRKCE, PTAFR, RANBP2, RORA, SNCA, SRC, STAT3, TP53, DYRK2, IRS2, KAT2B, EPM2AIP1, NCOA2, ARPP19, PASK, SIRT1, ADIPOR1, DDIT4, SESN2, SOGA1, SIK1, FOXK1
BP	GO:0097061	dendritic spine organization	27/3408	5.05E-03	ADAM10, ARF1, CDC42, CFL1, EPHA4, EPHB2, EPHB3, IGF1R, INSR, ITGA3, CAPRIN1, OPA1, PAFAH1B1, PAK3, PTEN, TIAM1, WASL, KALRN, ACTR2, ABI2, PDLIM5, NLGN1, SHANK2, SIPA1L1, ABHD17B, VPS35, BHLHB9
BP	GO:0043506	regulation of JUN kinase activity	29/3408	5.05E-03	DVL3, EDN1, EPHA4, ERCC6, DNAJA1, MAP3K4, MAP3K9, PTPN1, RPS3, MAP2K4, SFRP1, SYK, TIAM1, WNT7B, FZD5, FZD4, SPAG9, HIPK3, MAP3K2, DUSP10, DKK1, MAPK8IP3, PDCD4, VANGL2, TAOK1, AIDA, MUL1, DAB2IP, ZNF675
BP	GO:0098773	skin epidermis development	29/3408	5.05E-03	ACVR1B, ATP7A, BCL2, CTNNB1, EGFR, ERCC2, HDAC2, IGFBP5, RBPJ, SMAD4, MYO5A, PDGFA, SNAI1, SOS1, FZD3, FZD6, TP63, LDB1, LDB2, FST, HPSE, SOX21, DKK1, LGR4, FERMT1, VANGL2, MYSM1, CD109, ZDHHC21
BP	GO:0106027	neuron projection organization	29/3408	5.05E-03	ADAM10, ARF1, CDC42, CFL1, EPHA4, EPHB2, EPHB3, GSK3B, IGF1R, INSR, ITGA3, CAPRIN1, MAP1A, OPA1, PAFAH1B1, PAK3, PTEN, TIAM1, WASL, KALRN, ACTR2, ABI2, PDLIM5, NLGN1, SHANK2, SIPA1L1, ABHD17B, VPS35, BHLHB9
BP	GO:0048015	phosphatidylinositol-mediated signaling	51/3408	5.06E-03	RHOA, ZFP36L1, CBL, DCN, EDN1, EGFR, ERBB2, FLT4, GAB1, GATA3, IGF1R, IL18, INSR, KIT, LYN, MAZ, NEDD4, NKX3-1, NTRK3, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3C2A, PIK3CB, PIP4K2A, PPARD, MAPK1, MAPK3, PTAFR, PTEN, RPS6KB1, SRC, TWIST1, TYRO3, IRS2, IER3, KLF4, BTN2A2, STAMBP, PIP5K1C, SIRT1, NCS1, PPP1R16B, CEP55, PITPNM2, PLEKHA1, PREX2, PIK3IP1, PIK3AP1, DAB2IP
BP	GO:2000146	negative regulation of cell motility	88/3408	5.10E-03	ADA, ADARB1, JAG1, RHOA, RHOB, BCL2, BMPR1A, CALR, COL3A1, CRK, CTNNA1, DACH1, DAG1, DCN, DUSP1, FGF2, FOXO3, GATA3, NRG1, HOXA7, IDH2, IGFBP5, ILK, JUP, LRP1, SMAD7, MECP2, MEF2C, NF2, SERPINE1, PIN1, PPARD, PTEN, PTGER4, PTPRG, PTPRJ, PTPRK, PTPRR, RAP2A, RAP2B, ROBO1, CX3CL1, SFRP1, SP100, SRF, STAT3, STC1, NR2F2, THBS1, VCL, STK24, CHRD, WASL, DLG5, KLF4, TRIB1, CITED2, SEMA3A, DLC1, IL24, ABHD2, PTPRT, DUSP10, VASH1, LIMCH1, LRCH1, KANK1, CLASP1, CORO1C, CLIC4, GREM1, ADIPOR1, WNT4, DLL4, ADAMTS9, RAP2C, PBLD, NDRG4, NAV3, PHLDB2, TP53INP1, OSBPL8, ACVR1C, DAB2IP, SPRED1, ARID2, FLCN, MIA3
BP	GO:0010977	negative regulation of neuron projection development	45/3408	5.12E-03	ADCY6, ARF6, RHOA, ARHGDIA, CTSZ, EFNB2, EPHA4, EPHA7, EPHB2, FKBP4, GDI1, GSK3B, HDAC2, LRP1, PAFAH1B1, PPP3CA, PTEN, PTPRG, TSC1, SEMA7A, NRP1, SYNGAP1, NTN1, MAP4K4, RAPGEF2, SEMA3E, LRIG2, SEMA3A, SEMA4B, PLK2, NLGN1, DKK1, FSTL4, RAP1GAP2, KANK1, MYLIP, ASAP1, BCL11A, SEMA4C, RGMA, SEMA6A, GORASP1, TRAK2, ITM2C, KREMEN1
BP	GO:0046879	hormone secretion	80/3408	5.14E-03	ACVR2B, ADM, SLC25A6, ARRB1, CACNA1C, CACNA1E, CPT1A, CREB1, EDN1, EFNA5, EGFR, ENSA, GATA3, GJA1, GNAS, HIF1A, HMGCR, HNF4A, ISL1, ITPR1, ITPR2, KIF5B, LRP1, LYN, SMAD2, SMAD4, MYB, MYO5A, NKX3-1, P2RY1, CDK16, PFKFB2, PPARD, PPP3CA, PRKCA, PRKCE, PTPN11, PTPRN2, RAB1A, RFX3, SFRP1, SCG5, SLC16A1, SNAP25, SOX4, SOX11, VAMP7, TBX3, HNF1B, TCF7L2, TFR2, TIAM1, TMF1, FZD4, DYNLL1, IRS2, PER2, KALRN, SYT7, RAB11B, AIMP1, MAP4K4, CLOCK, RAPGEF3, KDM5B, RAB11FIP2, PASK, TARDBP, ARL2BP, SERP1, RAB8B, UBE2Q1, CHD7, NLGN2, RAB11FIP1, UQCC2, RASL10B, ACVR1C, BMP8A, SNX19
BP	GO:0048705	skeletal system morphogenesis	64/3408	5.14E-03	ACVR2B, BMP7, BMPR2, RUNX2, FOXN3, COL1A1, COL6A2, COL11A1, COL12A1, MAPK14, CTNNB1, DLX2, MEGF8, FBN2, FGFR3, FOXC1, GNAS, HOXA3, HOXA5, HOXA7, HOXB3, HOXB5, HOXB8, HOXC4, HOXC8, INSIG1, LRP6, SMAD2, MATN2, MEF2C, MEF2D, MMP14, MSX1, NAB1, PDGFRA, PKD1, PRRX1, RARG, SFRP1, SKI, SOX11, STC1, ZEB1, TGFBR1, THBS3, THRA, TWIST1, SGPL1, TRIP11, SATB2, NIPBL, MTHFD1L, GREM1, INSIG2, RAB23, SIX4, CSGALNACT1, CYP26B1, PLEKHA1, ARID5B, COL27A1, RDH10, SH3PXD2B, FMN1
BP	GO:0040013	negative regulation of locomotion	98/3408	5.17E-03	ADA, ADARB1, JAG1, RHOA, RHOB, BCL2, BMPR1A, CALR, COL3A1, CRK, CTNNA1, DACH1, DAG1, DCN, DUSP1, FGF2, FOXO3, GATA3, NRG1, HOXA7, IDH2, IGFBP5, ILK, JUP, LRP1, SMAD7, MECP2, MEF2C, NF2, SERPINE1, PIN1, PML, PPARD, PTEN, PTGER4, PTPRG, PTPRJ, PTPRK, PTPRR, RAP2A, RAP2B, ROBO1, CX3CL1, SFRP1, SP100, SRF, STAT3, STC1, NR2F2, THBS1, VCL, TRIM25, STK24, SEMA7A, CHRD, NRP1, WASL, DLG5, KLF4, SEMA3E, TRIM13, TRIB1, CITED2, SEMA3A, DLC1, SEMA4B, IL24, ABHD2, PTPRT, DUSP10, VASH1, LIMCH1, LRCH1, KANK1, CLASP1, CORO1C, CLIC4, GREM1, ADIPOR1, WNT4, DLL4, SEMA4C, ADAMTS9, SEMA6A, ARRDC3, RAP2C, PBLD, NDRG4, NAV3, PHLDB2, TP53INP1, OSBPL8, ACVR1C, DAB2IP, SPRED1, ARID2, FLCN, MIA3
BP	GO:0072431	signal transduction involved in mitotic	21/3408	5.30E-03	ATM, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7

		G1 DNA damage checkpoint			
BP	GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	21/3408	5.30E-03	ATM, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7
BP	GO:0007272	ensheathment of neurons	40/3408	5.40E-03	AKT2, CTNNB1, DAG1, ERBB2, ERCC2, GALC, NRG1, ID4, ILK, KCNJ10, MBP, MYO5A, NAB1, NTRK3, POU3F2, PPARD, PTEN, RARG, SCN8A, SKI, TNFRSF1B, TSC1, ZNF24, MALL, B4GALT6, QKI, RNF10, TSPAN2, NFASC, NCSTN, DICER1, ADAM22, ACER3, PARD3, PRX, SH3TC2, MARVELD1, FAM126A, MAL2, SERINC5
BP	GO:0008366	axon ensheathment	40/3408	5.40E-03	AKT2, CTNNB1, DAG1, ERBB2, ERCC2, GALC, NRG1, ID4, ILK, KCNJ10, MBP, MYO5A, NAB1, NTRK3, POU3F2, PPARD, PTEN, RARG, SCN8A, SKI, TNFRSF1B, TSC1, ZNF24, MALL, B4GALT6, QKI, RNF10, TSPAN2, NFASC, NCSTN, DICER1, ADAM22, ACER3, PARD3, PRX, SH3TC2, MARVELD1, FAM126A, MAL2, SERINC5
BP	GO:0048565	digestive tract development	40/3408	5.40E-03	ACVR2B, ADA, BCL2, PRDM1, CDKN1A, COL3A1, CRKL, CTNNB1, MEGF8, EGFR, EPHB3, GATA6, HIF1A, HOXA5, HOXD13, HES1, ITGA6, KIT, SMAD2, PDGFRA, PKD1, RB1, SFRP1, SLC4A2, SOX11, HNF1B, TCF7, TP63, DCHS1, ALDH1A2, AGR2, NIPBL, AHI1, LGR4, C1GALT1, VANGL2, EPB41L5, CLMP, PKDCC, RBPMS2
BP	GO:0043244	regulation of protein complex disassembly	35/3408	5.42E-03	ADD1, APC, ASPH, CAPZA2, CFL1, CFL2, EPS8, ETF1, IGF1R, INSR, MAP1A, MAP1B, MID1, TBC1D25, TWF1, RDX, UPF1, SPTAN1, SPTBN1, UVRAG, ARHGEF2, DSTN, CAMSAP2, CLASP1, TMOD2, EIF5A2, UBQLN4, SCAF4, TAOK1, FYCO1, NAV3, MTPN, SMCR8, TTBK2, CAMSAP1
BP	GO:0044003	modification by symbiont of host morphology or physiology	18/3408	5.46E-03	BCL2L1, DAG1, GAPDH, INSR, ITGAV, KPNA1, KPNA3, NTRK3, SERPINB9, EIF2AK2, PABPN1, VAPB, VAPA, BCL2L11, TNIP1, ATG7, KPNA6, HIPK2
BP	GO:0009914	hormone transport	82/3408	5.48E-03	ACVR2B, ADM, SLC25A6, ARRB1, CACNA1C, CACNA1E, CPT1A, CREB1, EDN1, EFNA5, EGFR, ENSA, GATA3, GJA1, GNAS, HIF1A, HMGCR, HNF4A, ISL1, ITPR1, ITPR2, KIF5B, LRP1, LYN, SMAD2, SMAD4, MYB, MYO5A, NKX3-1, P2RY1, CDK16, PFKFB2, PPARD, PPP3CA, PRKCA, PRKCE, PTPN11, PTPRN2, RAB1A, RFX3, SFRP1, SCG5, SLC16A1, SNAP25, SOX4, SOX11, VAMP7, TBX3, HNF1B, TCF7L2, TFR2, TIAM1, TMF1, FZD4, DYNLL1, IRS2, PER2, KALRN, SYT7, RAB11B, AIMP1, MAP4K4, CLOCK, RAPGEF3, KDM5B, RAB11FIP2, PASK, TARDBP, ARL2BP, SERP1, SLCO4A1, RAB8B, UBE2Q1, CHD7, NLGN2, RAB11FIP1, UQCC2, RASL10B, SLC16A10, ACVR1C, BMP8A, SNX19
BP	GO:0051571	positive regulation of histone H3-K4 methylation	9/3408	5.50E-03	BRCA1, CTNNB1, DNMT3B, SMAD4, KMT2A, MYB, CTR9, AUTS2, KMT2E
BP	GO:0071384	cellular response to corticosteroid stimulus	22/3408	5.54E-03	ATP2B1, ZFP36L1, ZFP36L2, KLF9, DNMT3B, EDN1, EGFR, EIF4E, FOXO1, FOXO3, NR3C1, HNRNPU, ISL1, STC1, UBE2L3, ZFP36, AKR1C3, BCL2L11, FAM107A, AKAP13, ERRFI1, DDIT4
BP	GO:0006644	phospholipid metabolic process	105/3408	5.55E-03	ARF1, ATM, CAPN2, CDS1, CHKA, CCR7, CLN8, FGF2, FGFR3, GATA6, HADHA, HMGCS2, IMPA2, KIT, LDLR, FADS1, LYN, MECP2, PAFAH1B1, PDGFA, PDGFB, PDGFRA, PIGA, PIK3C2A, PIK3CB, PIP4K2A, PLD1, PPARD, PTEN, RAB5A, SNCA, SRC, ALDH5A1, DGKE, SOCS1, INPP4B, SOCS2, SYNJ1, SYNJ2, CPNE3, MTMR3, MTMR7, MTMR4, SOCS6, KLF4, PCYT1B, SOCS5, LPIN2, IP6K1, LPGAT1, LPCAT3, CEPT1, VAV3, SPTLC1, SERINC3, ATG14, SACM1L, SMG1, EFR3A, GPD1L, LPIN1, PIP5K1C, SLC44A1, PISD, SOCS7, ABHD5, RAB14, PI4K2B, ETNK1, GPCPD1, INPP5E, AGPAT3, CHPT1, SERINC1, PITPNM2, PLEKHA4, PLEKHA1, MTMR9, SRD5A3, LPCAT1, PGAP1, DDHD1, PTDSS2, SGPP1, PITPNM3, FAR1, FAM126A, PLEKHA8, PGAP3, PIK3IP1, OSBPL8, NUS1, WDR81, MBOAT2, SAMD8, TTC7B, DAB2IP, DGKH, SGMS2, PLD6, LCLAT1, TMEM86B, SERINC5, FAM126B, SLC27A1
BP	GO:0034063	stress granule assembly	10/3408	5.56E-03	DDX3X, DDX6, EIF2S1, MAPT, PRKAA1, RPS23, ATXN2, G3BP2, G3BP1, ATXN2L
BP	GO:0031396	regulation of protein ubiquitination	56/3408	5.60E-03	ABL1, ARRB1, ARRB2, BRCA1, PTTG1IP, CAV1, FKBP1A, DNAJB2, DNAJA1, HSPA5, LIMK1, MAD2L1, SMAD7, PIN1, PRKCE, MAPK9, PTEN, RAB1A, RPS3, SIAH2, SOX4, TAF1, TGFBR1, UBE2L3, UBE2N, CUL3, CDC14B, PER2, MTA1, TRIP12, ATG5, CTR9, HERPUD1, FAM107A, U2AF2, KDM1A, MYCBP2, UFL1, HSPBP1, UBQLN1, UBR5, DCUN1D1, GNL3L, RNF111, PINX1, FANCI, FBXW7, PELI1, ARRDC3, NXN, GORASP1, ARRDC4, DCUN1D3, AMER1, RNF180, SPOPL
BP	GO:1902749	regulation of cell cycle G2/M phase transition	58/3408	5.64E-03	ATM, CCND1, BRCA1, CDC25A, CETN2, CHEK1, FOXN3, CSNK1D, CSNK1E, FHL1, HSPA2, MECP2, FOXO4, PAFAH1B1, PBX1, PPP2R1A, PKIA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAD21, SKP1, AURKA, TP53, YWHAE, YWHAG, HMGA2, CDC14B, DYNLL1, AURKB, TAOK2, PSMF1, VPS4B, CEP135, AKAP9, PSME3, PSMD14, TUBB4A, CNTRL, CEP250, DCTN3, PSME4, CLASP1, SIN3A, DTL, HAUS6, NDE1, PINX1, USP47, HAUS2, RCC2, TAOK1, BRCC3, ZNF830

BP	GO:0001569	branching involved in blood vessel morphogenesis	14/3408	5.64E-03	ABL1, COL4A1, CTNNB1, EDN1, MDK, SRF, STK4, VEGFA, NRP1, SEMA3E, GNA13, PLXND1, DLL4, NRARP
BP	GO:0003176	aortic valve development	14/3408	5.64E-03	JAG1, BMPR2, GATA3, RBPJ, SMAD6, RB1, ROBO1, SNAI2, SNAI1, TNFRSF1B, TWIST1, ROCK2, HEYL, DLL4
BP	GO:0060325	face morphogenesis	14/3408	5.64E-03	ASPH, COL1A1, EP300, LRP6, MSX1, PAX9, PDGFRA, PTPN11, SKI, SGPL1, DKK1, NIPBL, PLEKHA1, ARID5B
BP	GO:1903955	positive regulation of protein targeting to mitochondrion	14/3408	5.64E-03	PRKAA1, SREBF2, UBE2D3, UBE2L3, FZD5, BAP1, ATG13, ARIH2, HTRA2, SH3GLB1, LEPROT, FBXW7, USP36, RHOU
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	78/3408	5.68E-03	ADA, RHOA, BCL6, CASP3, CAV1, RUNX1, RUNX3, CBFB, CD44, CD47, CDC42, CEBPB, CCR7, CSK, CYLD, EFNB1, EFNB2, EGR3, ERBB2, FLOT2, GATA3, GRB2, NCKAP1L, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, IRAK1, IRF1, ITPKB, LYN, SMAD7, MDK, MYB, NCK1, PAK2, PAK3, PAWR, PPARA, PRKAR1A, PTAFR, PTPN11, PTPRC, RAG1, RPS3, SDC4, SRC, SYK, TFRC, VCAM1, XBP1, NR4A3, NCK2, SOCS1, TNFSF9, FADD, AP3D1, DLG5, SOCS6, CD83, KLF4, SOCS5, BTN2A2, GPNMB, NFAT5, DUSP10, ICOSLG, LAX1, PAG1, PELI1, ZMIZ1, WNK1, CD276, SIRPA, MIA3, NRARP
BP	GO:0072665	protein localization to vacuole	23/3408	5.70E-03	SCARB2, GBP1, LAMP2, M6PR, NEDD4, SORL1, VAMP7, AP3D1, ROCK2, GOSR2, ZFYVE16, SNF8, VPS13A, SZT2, AP3M1, VPS36, SH3GLB1, VPS13C, VPS37C, VPS13D, SMURF1, GNPTAB, VPS37D
BP	GO:0032506	cytokinetic process	16/3408	5.71E-03	ARF1, RHOA, ECT2, MYH9, AURKB, KIF23, VPS4B, PDCD6IP, CHMP5, ANLN, ALKBH4, CEP55, SPIRE1, CHMP1B, CHMP7, KLHDC8B
BP	GO:0051053	negative regulation of DNA metabolic process	45/3408	5.77E-03	ATM, ATR, BCL6, BMPR2, DACH1, DUSP1, GATA3, GJA1, HNRNPC, HNRNPU, MEN1, MLH1, KMT2A, OGG1, RPS3, SRC, TP53, TWIST1, XRCC5, ZNF91, HMGA2, SMC1A, TNKS, TRIP12, ATG7, CERS1, POLQ, STAG2, PDS5A, UBR5, RTEL1, XRN1, GNL3L, PINX1, RIF1, FBXW7, UBQLN4, TSPYL2, KLHL15, TET1, SLX4, ZNF830, SLFN11, RMI2, FLCN
BP	GO:0032231	regulation of actin filament bundle assembly	31/3408	5.84E-03	ABL1, RHOA, CD47, CDC42, S1PR1, LIMK1, MET, NF2, PTGER4, PXN, RDX, CX3CL1, SDC4, SFRP1, SLC9A1, TESK1, TGFBR1, TSC1, NRP1, ROCK2, BAG4, WASF2, DLC1, RAPGEF3, LIMCH1, CLASP1, WNT4, ARHGAP28, SYNPO2L, PHLDB2, SH3PXD2B
BP	GO:0001706	endoderm formation	19/3408	5.89E-03	COL4A2, COL5A1, COL5A2, COL11A1, COL12A1, CTNNB1, FN1, GATA6, HSBP1, ITGA5, ITGAV, SMAD2, MMP14, HNF1B, HMGA2, CTR9, DKK1, CDC73, SOX7
BP	GO:0060976	coronary vasculature development	19/3408	5.89E-03	PRDM1, MEGF8, GATA6, LTBP1, SMAD6, MYH10, SGCD, SRF, TGFBR1, TGFBR3, VEGFA, NRP1, SNX17, TAB1, PLXND1, SUFU, DCTN5, SPRED1, ARID2
BP	GO:0008154	actin polymerization or depolymerization	57/3408	5.90E-03	ADD1, ARF1, ARF6, RHOA, CAPZA2, CFL1, CFL2, CCR7, DIAPH1, EPS8, FER, GRB2, ARHGAP35, NCKAP1L, MYO1C, NCK1, PAK3, PRKCE, TWF1, RASA1, RDX, SPTAN1, SPTBN1, NCK2, WASF1, WASL, LATS1, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, TENM1, CDC42EP2, CAP2, CAP1, NCKAP1, IQGAP2, DSTN, CIT, FAM107A, KANK1, COTL1, TMOD2, TTC17, FMN2, SPIRE1, PLEKHG2, ARHGAP28, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, FMN1
BP	GO:0006282	regulation of DNA repair	37/3408	5.90E-03	BRCA1, CEBPG, CHEK1, EGFR, EYA4, ERCC6, FOXM1, FUS, OGG1, PML, RAD51, RPS3, TWIST1, UBE2N, UBE2V1, USP1, HMGA2, TRIP12, ACTR2, POLQ, KDM1A, FAM168A, SIRT1, SPIDR, UBR5, RTEL1, FIGN, RIF1, FMN2, UBQLN4, SPIRE1, BRCC3, KLHL15, RMI2, PPP4R2, USP51, RNF168
BP	GO:0072080	nephron tubule development	30/3408	5.90E-03	JAG1, BCL2, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MEF2C, MYC, PAX2, PBX1, PKD1, PTCH1, STAT1, HNF1B, VEGFA, WNT7B, WNT2B, DCHS1, KLHL3, HEYL, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, FMN1
BP	GO:0045580	regulation of T cell differentiation	41/3408	5.91E-03	ABL1, ADA, RHOA, BCL6, PRDM1, CAMK4, RUNX1, RUNX3, CBFB, CLPTM1, CYLD, EGR3, ERBB2, GATA3, KAT2A, NCKAP1L, IL7R, IL18, IRF1, IRF4, ITPKB, SMAD7, MDK, MYB, PTPRC, RAG1, SOS1, SYK, ZEB1, XBP1, SOCS1, TNFSF9, AP3D1, CD83, SOCS5, BTN2A2, DUSP10, PRELID1, CYP26B1, ZMIZ1, NRARP
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	59/3408	5.92E-03	ADA, RHOA, BCL6, CAV1, RUNX1, RUNX3, CBFB, CD44, CD47, CDC42, CCR7, CSK, CYLD, EFNB1, EFNB2, EGR3, FLOT2, GATA3, GRB2, NCKAP1L, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, IRAK1, ITPKB, LYN, MDK, MYB, NCK1, PAK2, PAK3, PTAFR, PTPN11, PTPRC, RAG1, RPS3, SRC, SYK, TFRC, VCAM1, XBP1, NR4A3, NCK2, SOCS1, TNFSF9, FADD, AP3D1, CD83, SOCS5, BTN2A2, NFAT5, DUSP10, ICOSLG, ZMIZ1, CD276, SIRPA
BP	GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	26/3408	5.96E-03	ZFP36L1, ZFP36L2, DDX6, MLH1, CNOT4, PARN, POLR2D, ZFP36, BTG2, CNOT8, TOB1, HBS1L, CPEB3, CNOT1, SAMD4A, TNRC6B, LSM4, PABPC1, TNRC6A, SAMD4B, DCP1A, CNOT6, TNRC6C, EDC3, PDE12, PATL1
BP	GO:0061418	regulation of transcription from	26/3408	5.96E-03	CREBBP, EGR1, EP300, EPAS1, HIF1A, RBPJ, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, TP53, VEGFA, VHL, CUL2, LIMD1, PSMF1, PSME3, PSMD14, CITED2, PSME4, HIF1AN, EGLN2, EGLN3

		RNA polymerase II promoter in response to hypoxia			
BP	GO:0009798	axis specification	28/3408	5.96E-03	BMPR1A, CTNNB1, LRP6, SMAD2, SMAD4, SMAD6, PCSK6, PAX6, PTCH1, RNF2, SFRP1, SKI, SRF, STC1, AURKA, TBX3, KDM6A, FZD5, LDB1, CITED2, FRS2, AHI1, BCOR, EPB41L5, PGAP1, SETDB2, PLD6, NRARP
BP	GO:0045682	regulation of epidermis development	28/3408	5.96E-03	ZFP36L1, RUNX1, CBFB, CTNNB1, EZH2, FOXC1, HOXA7, HES1, SMAD4, MAFG, NAB1, PPARD, PTCH1, VDR, ZFP36, NCOA3, TP63, ROCK2, FST, HPSE, MAFF, GRHL1, ERRFI1, ESRP1, FERMT1, SGPP1, MYSM1, CD109
BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	54/3408	6.11E-03	ATM, CCND1, BRCA1, CDC25A, CETN2, FOXN3, CSNK1D, CSNK1E, FHL1, HSPA2, MECP2, FOXO4, PAFAH1B1, PBX1, PPP2R1A, PKIA, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAD21, SKP1, AURKA, YWHAE, YWHAG, HMGA2, DYNLL1, AURKB, TAOK2, PSMF1, VPS4B, CEP135, AKAP9, PSME3, PSMD14, TUBB4A, CNTRL, CEP250, DCTN3, PSME4, CLASP1, SIN3A, DTL, HAUS6, NDE1, PINX1, USP47, HAUS2, RCC2, TAOK1, ZNF830
BP	GO:0006929	substrate-dependent cell migration	13/3408	6.42E-03	FMNL1, FN1, MYH10, NCK1, OPHN1, PTPRC, ROBO1, SNAI2, NRP1, NTN1, SEMA3A, CD2AP, EPB41L5
BP	GO:0032259	methylation	91/3408	6.44E-03	AMT, ATRX, PRDM1, BRCA1, BTG1, COMT, CTNNB1, DNMT3A, DNMT3B, ETF1, EZH1, EZH2, GATA3, GNAS, GSPT1, JARID2, SMAD4, MAT2A, MECP2, MEN1, KMT2A, MLLT6, MTHFR, MTR, MYB, MYC, RAB3B, SATB1, SUV39H1, TPMT, KDM6A, PRDM2, BTG2, KMT2D, PPM1D, MBD2, CTR9, SETD1A, KMT2B, CTCF, MTF2, KDM1A, CMTR1, SIRT1, SUZ12, FAM98A, AUTS2, MAT2B, RBM15B, TRMT6, ARID4B, WDR5B, TET2, GATAD2A, BCOR, RIF1, SETD5, NSUN5, ATF7IP, KMT2E, MEPCE, PRDM8, PRDM10, BEND3, METTL14, KMT2C, PCIF1, PRDM15, NSD1, METTL4, VCPKMT, CAMKMT, METTL8, CBLL1, TET1, SETD7, SETDB2, SETD3, DPY30, TGS1, SMYD4, PCMTD1, TRMT61A, TYW3, METTL21A, TRMT10B, TET3, PLD6, KDM1B, FAM98B, METTL2A
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	53/3408	6.45E-03	ABL1, ARRB2, BDNF, CD44, CNTN1, DLG3, DOCK3, HBEGF, EFNA5, EPHA4, ERCC6, FGFR3, HDAC2, NRG1, HES1, IGF2, IL6R, IL6ST, IL18, ISL1, ITGA5, KIT, LYN, KITLG, NEDD9, PAK2, PDGFB, PTPN1, PTPN11, PTPRC, PTPRJ, SRC, STAT3, SYK, ADAM17, TAL1, TGFA, TP53, VEGFA, IQGAP1, NRP1, ARHGEF2, TNK2, IL24, ARL2BP, GREM1, EHD4, PARP14, NCAPG2, FBXW7, AFAP1L2, RICTOR, EPGN
BP	GO:0002446	neutrophil mediated immunity	119/3408	6.45E-03	ACLY, ADAM10, ALAD, RHOA, ASAH1, CD44, CD47, CD59, CNN2, COPB1, MAPK14, CTSB, CTSS, CTSZ, DDX3X, CYB5R3, DIAPH1, DNASE1L1, EEF1A1, STOM, GAA, GM2A, GPI, NCKAP1L, IGF2R, IMPDH1, ITGAV, JUP, LAMP2, LTA4H, MME, NFKB1, NRAS, OLR1, PA2G4, PAFAH1B2, PGAM1, PKM, PKP1, PLD1, PRCP, MAPK1, PSMA2, PSMC2, PSMD3, PSMD13, PTAFR, PTPRB, PTPRC, PTPRJ, PTPRN2, PYGB, RAB5B, RAP1B, RAP2B, SNAP25, SPTAN1, STK10, SURF4, VAMP7, SYK, ADAM17, TIMP2, TNFAIP6, TNFRSF1B, TRPM2, VCL, VCP, XRCC5, PDXK, DYNLL1, IQGAP1, CPNE3, SYNGR1, VAPA, SCAMP1, MLEC, ARPC5, ACTR2, ATP6AP2, PSMD14, ATP8A1, CAP1, ATG7, IQGAP2, HPSE, PGRMC1, GLIPR1, RAB31, PDAP1, TUSC2, NFASC, ATP11B, ATP11A, DNAJC13, NCSTN, COTL1, ARMC8, OSTF1, ATP6V1D, RAB14, YPEL5, CMTM6, CAND1, KMT2E, KCMF1, RAP2C, TMBIM1, LPCAT1, PTGES2, PLEKHO2, DNAJC5, TXNDC5, FRMPD3, ORMDL3, CANT1, ARL8A, SIRPA, C6orf120
BP	GO:0030178	negative regulation of Wnt signaling pathway	57/3408	6.57E-03	APC, CAV1, MAPK14, CTNND1, CYLD, DAB2, DVL3, EGR1, FOXO1, FOXO3, RAPGEF1, GSK3B, IGFBP1, ISL1, LRP1, LRP6, MDK, MLLT3, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, SIAH2, SNAI2, STK4, TCF7L2, TLE1, TLE4, FZD1, FZD6, CUL3, LIMD1, LATS1, PSMF1, HMGXB4, G3BP1, PSME3, PSMD14, DKK1, PSME4, LATS2, GREM1, DKK3, NLK, FERMT1, RNF213, NXN, KREMEN1, ZNRF3, LZTS2, AMER1, DAB2IP, TMEM170B
BP	GO:0030520	intracellular estrogen receptor signaling pathway	21/3408	6.57E-03	AR, BRCA1, RUNX1, CBFB, DDX5, ESR2, FOXA1, ISL1, SRC, KMT2D, ARID1A, TP63, LATS1, DDX17, CNOT1, UFL1, RBFOX2, WBP2, STRN3, EGLN2, KCTD6
BP	GO:0060997	dendritic spine morphogenesis	21/3408	6.57E-03	ADAM10, CDC42, CFL1, EPHA4, EPHB2, EPHB3, CAPRIN1, OPA1, PAFAH1B1, PAK3, PTEN, TIAM1, WASL, KALRN, ACTR2, ABI2, PDLIM5, NLGN1, SHANK2, SIPA1L1, BHLHB9
BP	GO:0071385	cellular response to glucocorticoid stimulus	21/3408	6.57E-03	ATP2B1, ZFP36L1, ZFP36L2, KLF9, DNMT3B, EDN1, EGFR, EIF4E, FOXO1, FOXO3, NR3C1, HNRNPU, ISL1, STC1, UBE2L3, ZFP36, BCL2L11, FAM107A, AKAP13, ERRFI1, DDIT4
BP	GO:0043312	neutrophil degranulation	116/3408	6.61E-03	ACLY, ADAM10, ALAD, RHOA, ASAH1, CD44, CD47, CD59, CNN2, COPB1, MAPK14, CTSB, CTSS, CTSZ, DDX3X, CYB5R3, DIAPH1, DNASE1L1, EEF1A1, STOM, GAA, GM2A, GPI, NCKAP1L, IGF2R, IMPDH1, ITGAV, JUP, LAMP2, LTA4H, MME, NFKB1, NRAS, OLR1, PA2G4, PAFAH1B2, PGAM1, PKM, PKP1, PLD1, PRCP, MAPK1, PSMA2, PSMC2, PSMD3, PSMD13, PTAFR, PTPRB, PTPRC, PTPRJ, PTPRN2, PYGB, RAB5B, RAP1B, RAP2B, SNAP25, SPTAN1, STK10, SURF4, VAMP7, SYK, TIMP2, TNFAIP6, TNFRSF1B, TRPM2, VCL, VCP, XRCC5, PDXK, DYNLL1, IQGAP1, CPNE3, SYNGR1, VAPA, SCAMP1, MLEC, ARPC5, ACTR2, ATP6AP2, PSMD14, ATP8A1, CAP1, ATG7, IQGAP2, HPSE, PGRMC1, GLIPR1, RAB31, PDAP1, NFASC, ATP11B, ATP11A, DNAJC13, NCSTN, COTL1, ARMC8, OSTF1, ATP6V1D, RAB14, YPEL5, CMTM6, CAND1, KCMF1, RAP2C, TMBIM1, LPCAT1, PTGES2, PLEKHO2, DNAJC5, TXNDC5, FRMPD3, ORMDL3, CANT1, ARL8A, SIRPA, C6orf120

BP	GO:0048771	tissue remodeling	50/3408	6.62E-03	ACVR2B, JAG1, ATP7A, AXL, BAK1, BMPR2, CAV1, TPP1, CSK, CTNNB1, S1PR1, EGFR, EPAS1, FOXC1, FLT4, GJA1, HIF1A, HOXA3, IGFBP5, RBPJ, IL18, LRP6, MDK, MEF2C, MMP14, NOTCH2, TNFRSF11B, PDK4, PPP3CA, PRKCA, SFRP1, SRC, SYK, TFRC, TP53, VDR, SYT7, ATG5, ROCK2, RASSF2, PLEKHM1, GPNMB, NCDN, GREM1, DLL4, LGR4, CHD7, TMBIM1, ZNF675, SIGLEC15
BP	GO:0051973	positive regulation of telomerase activity	15/3408	6.63E-03	CTNNB1, DKC1, HNRNPD, MAP3K4, MYC, PARN, MAPK1, MAPK3, XRCC5, TNKS, AURKB, KLF4, PARM1, GREM1, HMBOX1
BP	GO:0071634	regulation of transforming growth factor beta production	15/3408	6.63E-03	CREB1, ATF2, GATA6, HIF1A, ITGAV, ITGB8, LTBP1, SMAD4, MYB, FURIN, CX3CL1, THBS1, ATP6AP2, CD2AP, LAPTM4B
BP	GO:0045807	positive regulation of endocytosis	44/3408	6.79E-03	ACTN4, ARF1, ARRB1, ARRB2, AXL, CALR, CBL, CD47, DAB2, FMR1, GATA2, RAPGEF1, NCKAP1L, HIP1, HNRNPK, IL15RA, ITGAV, LRP1, SERPINE1, PPP3CA, PTPRC, PTPRJ, SNCA, SYK, TFR2, TUB, VEGFA, WASL, TSPAN1, RAB31, NLGN1, RAB21, CLIP3, APPL1, LDLRAP1, GREM1, ANKFY1, AHI1, CAMK1D, MIB1, CBLL1, SGIP1, SIRPA, MYO18A
BP	GO:0062013	positive regulation of small molecule metabolic process	44/3408	6.79E-03	ADCYAP1R1, ADM, ADORA2B, AKT2, COMT, CPT1A, FGF1, FOXO1, KAT2A, HIF1A, IGF2, INSR, NFKB1, P2RY1, PDGFB, PFKFB2, PFKFB3, PFKFB4, PHKG2, PPARA, PRKAA1, PRKCE, PTAFR, SNCA, SRC, STAT3, TWIST1, NR1H2, VCP, NR4A3, DYRK2, IRS2, KAT2B, EPM2AIP1, LPGAT1, ARPP19, SIRT1, ISCU, LDLRAP1, WNT4, BEND3, ELOVL5, STARD4, RDH10
BP	GO:1905268	negative regulation of chromatin organization	22/3408	6.79E-03	BRCA1, DNMT3B, HMGA1, JARID2, MLLT6, KDM5A, SET, SKI, SNCA, TWIST1, TRIP12, ATG5, MTF2, KDM1A, PHF8, SIRT1, SIN3A, ZNF451, UBR5, ATAD2B, BCOR, TET1
BP	GO:0030336	negative regulation of cell migration	84/3408	6.79E-03	ADA, ADARB1, JAG1, RHOA, RHOB, BCL2, BMPR1A, CALR, COL3A1, DACH1, DAG1, DCN, DUSP1, FGF2, FOXO3, NRG1, HOXA7, IDH2, IGFBP5, ILK, JUP, LRP1, SMAD7, MECP2, MEF2C, NF2, SERPINE1, PPARD, PTEN, PTGER4, PTPRG, PTPRJ, PTPRK, PTPRR, RAP2A, RAP2B, ROBO1, CX3CL1, SFRP1, SP100, SRF, STAT3, STC1, NR2F2, THBS1, VCL, STK24, CHRD, WASL, DLG5, KLF4, TRIB1, CITED2, SEMA3A, DLC1, IL24, ABHD2, PTPRT, DUSP10, VASH1, LIMCH1, LRCH1, KANK1, CLASP1, CORO1C, CLIC4, GREM1, ADIPOR1, WNT4, DLL4, ADAMTS9, RAP2C, PBLD, NDRG4, NAV3, PHLDB2, TP53INP1, OSBPL8, ACVR1C, DAB2IP, SPRED1, ARID2, FLCN, MIA3
BP	GO:0046486	glycerolipid metabolic process	101/3408	6.81E-03	ARF1, ATM, CAPN2, CAV1, CDS1, CHKA, CPT1A, ACSL4, FGF2, HADHA, IMPA2, INSIG1, LDLR, MECP2, PAFAH1B1, PDGFA, PDGFB, PIGA, PIK3C2A, PIK3CB, PIP4K2A, PLD1, PTEN, PTPN11, RAB5A, SEL1L, SORL1, NR1H2, ALDH5A1, DGKE, DGKD, SOCS1, INPP4B, SOCS2, SYNJ1, SYNJ2, CPNE3, MTMR3, MTMR7, MTMR4, SOCS6, PCYT1B, SOCS5, LPIN2, IP6K1, LPGAT1, LPCAT3, CEPT1, SERINC3, ABHD2, MGLL, ATG14, SACM1L, SMG1, EFR3A, GPD1L, LPIN1, PIP5K1C, SIRT1, SLC44A1, PISD, SOCS7, ABHD5, INSIG2, RAB14, FBXW7, PI4K2B, ETNK1, GPCPD1, INPP5E, AGPAT3, CHPT1, SERINC1, PITPNM2, PLEKHA4, PLEKHA1, MTMR9, TBL1XR1, LPCAT1, PANK2, PGAP1, DDHD1, PTDSS2, PITPNM3, FAR1, FAM126A, PLEKHA8, PGAP3, OSBPL8, MBOAT2, TTC7B, SIK1, DGKH, PLD6, LCLAT1, TMEM86B, CNEP1R1, GK5, SERINC5, FAM126B, SLC27A1
BP	GO:0010952	positive regulation of peptidase activity	54/3408	6.81E-03	FAS, RHOA, ARRB1, ASPH, BAK1, CASP10, CAV1, MAPK14, DAPK1, DDX3X, EFNA3, EPHA4, FN1, HIP1, LYN, MAPT, MBP, MYC, NKX3-1, PML, MAPK3, ROBO1, RPS3, SNCA, STAT3, SYK, VCP, TNFSF10, FADD, ROCK2, BCL2L11, BCAP31, PSME3, PSMD14, NOD1, DLC1, ANP32B, PSME4, SIRT1, BCL2L13, MTCH1, CYFIP2, BBC3, PRELID1, HTRA2, CYCS, IFT57, AKIRIN2, MUL1, SOX7, ANTXR1, EGLN3, ACVR1C, ACER2
BP	GO:0060993	kidney morphogenesis	30/3408	6.96E-03	BCL2, BMP7, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MYC, PAX2, PBX1, PKD1, PTCH1, SOX4, STAT1, HNF1B, VEGFA, WNT7B, WNT2B, DCHS1, KLHL3, SOX8, SIX4, WNT4, AHI1, LGR4, VANGL2, LZTS2, FMN1
BP	GO:0001843	neural tube closure	29/3408	7.07E-03	ABL1, ADM, CASP3, DVL3, KAT2A, ARHGAP35, LRP6, MTHFR, PAX2, PTCH1, RARG, SDC4, SFRP1, SKI, TSC1, TWIST1, KDM6A, FZD3, ARID1A, FZD1, FZD6, DLC1, MTHFD1L, SUFU, SEMA4C, IFT57, VANGL2, SHROOM3, TRIM71
BP	GO:0006901	vesicle coating	24/3408	7.10E-03	CD59, CSNK1D, CTSZ, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, NAPA, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, ANKRD28, TRAPPC4, TRAPPC2L, PPP6R3, SAR1A, GORASP1, TBC1D20
BP	GO:0072078	nephron tubule morphogenesis	25/3408	7.16E-03	BCL2, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MYC, PAX2, PBX1, PKD1, PTCH1, HNF1B, VEGFA, WNT2B, DCHS1, KLHL3, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, FMN1
BP	GO:0071711	basement membrane organization	12/3408	7.16E-03	COL4A1, CTSS, DAG1, ITGB1, NID1, PXDN, PHLDB1, CLASP1, FLRT2, FERMT1, RIC8A, PHLDB2
BP	GO:0010833	telomere maintenance via telomere lengthening	27/3408	7.16E-03	ATM, ATR, CCT6A, CTNNB1, DKC1, HNRNPC, HNRNPU, MAP3K4, PARN, MAPK1, MAPK3, RAD51, RFC1, SRC, TERT, XRCC5, TNKS, AURKB, SMG7, SMG5, RTEL1, XRN1, GNL3L, PINX1, DCLRE1B, HMBOX1, SLX4
BP	GO:0071158	positive regulation of cell cycle arrest	27/3408	7.16E-03	ATM, BRCA1, CDKN1A, CDKN1B, EP300, GATA6, MDM4, FOXO4, CNOT4, PML, POU4F1, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, HMGA2, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7, DAB2IP

BP	GO:0014743	regulation of muscle hypertrophy	26/3408	7.17E-03	ATP2B4, CAMK2D, EDN1, FOXO1, G6PD, IGFBP5, IL6ST, JARID2, SMAD4, MEF2A, PIN1, PPARA, PPP3CA, PRKCA, TWF1, RGS2, RGS4, SLC9A1, TNFRSF1B, YY1, NR4A3, AKAP6, ROCK2, LMCD1, ERRFI1, MTPN
BP	GO:0048659	smooth muscle cell proliferation	48/3408	7.24E-03	BMPR1A, CDKN1A, CDKN1B, COMT, CTNNB1, HBEGF, S1PR1, EDN1, EGFR, FGF2, GNAI2, GNAI3, HMGCR, IGFBP5, IL6R, IL18, ILK, IRAK1, JUN, MEF2C, MEF2D, MYB, PDGFB, PPARD, PTAFR, PTEN, CX3CL1, SOD2, STAT1, TCF7L2, TERT, THBS1, XRCC5, SF1, NR4A3, KLF4, ADAMTS1, MFN2, CALCRL, TRIB1, LDLRAP1, FOXP1, PDCD4, FOXJ2, NDRG2, NAA35, NDRG4, RBPMS2
BP	GO:0016482	cytosolic transport	45/3408	7.36E-03	AP1G1, ARL1, AP1S1, DAB2, EMP2, KIF5B, MYO1D, MAPK1, MAPK3, RAB5A, RDX, SORT1, SNX1, SORL1, SRC, EVI5, SNX3, SPAG9, SYT7, GOSR1, GOSR2, PREPL, ACTR2, ARFRP1, SRSF10, SNF8, RHOBTB3, LMTK2, RAB21, ERC1, KIF1B, VPS13A, DNAJC13, TMEM87A, TBC1D10B, HOOK1, ANKFY1, VPS54, RAB14, RAB6B, HEATR5B, VPS13C, VPS35, HOOK3, WDR81
BP	GO:0007612	learning	42/3408	7.38E-03	COMT, CREB1, CTNS, EPHB2, CLN8, HTT, HIF1A, HMGCR, INSR, ITGB1, JUN, KIT, KRAS, MAP1A, MECP2, MEIS2, PDE1B, RAG1, ATXN1, SNAP25, SRF, BTG2, FOSL1, B4GALT2, SYNGAP1, SYNJ1, KALRN, ACTR2, ATP8A1, SHANK2, DKK1, CIC, SLC7A11, SLC24A2, CNTNAP2, NPTN, YTHDF1, UBA6, SLC12A5, RIC8A, NDRG4, ATXN1L
BP	GO:0030705	cytoskeleton-dependent intracellular transport	50/3408	7.40E-03	ACTN4, DST, CDC42, FLOT2, FMR1, HTT, HIF1A, HNRNPU, KIF5B, TNPO1, MAP1A, MAP1B, MAPT, MYO1C, MYO5A, MYO10, NEFH, OPA1, PAFAH1B1, PURA, RAB1A, VAMP7, TUB, DYNLL1, WASF1, AP3D1, WASL, TRIP11, KIF3B, KIF23, AP3S2, KIF3A, TRAK1, RAB21, KIF1B, MAPK8IP3, BICD2, AP3M1, HOOK1, DYNC2LI1, NDE1, FNBP1L, IFT57, KIF13A, TRAK2, FYCO1, HOOK3, SSX2IP, ARL8A, TMEM201
BP	GO:0032206	positive regulation of telomere maintenance	19/3408	7.44E-03	ATM, ATR, ATRX, CCT6A, CTNNB1, DKC1, HNRNPD, MAP3K4, PARN, PML, MAPK1, MAPK3, XRCC5, TNKS, AURKB, RTEL1, NABP2, HMBOX1, SLX4
BP	GO:0007626	locomotory behavior	54/3408	7.59E-03	ARCN1, ARRB2, ZFHX3, ATP7A, CACNA1B, CTNS, EGR1, EPHA4, CLN8, EPS8, GAA, NRG1, HOXB8, KCNJ10, MECP2, MYO5A, NPC1, PAFAH1B1, PDE1B, PEX13, PRKCE, PTEN, SNAP25, SNCA, STRN, TAL1, TSC1, FZD4, B4GALT2, KALRN, USP2, MTA1, NCOR1, PUM1, NCOA2, VPS13A, ZNF385A, GIGYF2, HTRA2, HIPK2, ZDHHC8, ADAM22, OXR1, SOBP, UBA6, CHD7, VPS35, ANKH, NLGN2, ARRDC3, PREX2, APH1B, NAV2, BTBD9
BP	GO:0031099	regeneration	54/3408	7.59E-03	ADM, AXL, BAK1, CCND1, BCL2, BCL9, CCNA2, CDKN1A, CDKN1B, CEBPB, CTNNA1, DAG1, EGFR, EPHA4, EZH2, GJA1, IGF2R, IGFBP1, ISL1, JUN, LRP1, MAP1B, MATN2, MDK, MTR, NTRK3, PKM, PRRX1, PPARD, PPAT, PPP3CA, PTCH1, PTEN, PTGFRN, PTPN12, PTPRF, AURKA, TGFBR3, NR4A3, ULK1, STK24, KLF4, MAP4K4, LRIG2, POSTN, DUSP10, MAPK8IP3, LPIN1, UPF2, SULF2, RGMA, AKIRIN1, KREMEN1, MTPN
BP	GO:0046890	regulation of lipid biosynthetic process	54/3408	7.59E-03	ACACA, ADM, ASAH1, BRCA1, CAPN2, CREB1, EGR1, FGF1, HMGCR, INSIG1, LDLR, LSS, NFKB1, NFYA, NFYB, PDGFA, PDGFB, PDK4, PRKAA1, PRKAB2, PROX1, RAN, SCD, SNAI2, SNAI1, SREBF2, NR1H2, VDR, SF1, NSMAF, AKR1C3, LPGAT1, FGF19, ERLIN2, WDTC1, SIRT1, DKK3, ORMDL2, ADIPOR1, INSIG2, WNT4, FBXW7, ELOVL5, ELOVL6, ADIPOR2, LPCAT1, ORMDL1, ORMDL3, STARD4, SAMD8, SIK1, RDH10, CNEP1R1, SLC27A1
BP	GO:0070555	response to interleukin-1	56/3408	7.64E-03	CD47, CEBPB, EDN1, EGR1, GBP1, HIF1A, IKBKB, IL1R1, IL1RAP, IRAK1, IRAK2, MAP3K3, MTHFR, NFKB1, NKX3-1, PRKCA, MAPK3, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTGIS, UPF1, RORA, CCL7, CX3CL1, SFRP1, SKP1, SNCA, SRC, TFPI, UBE2N, UBE2V1, YY1, SQSTM1, BTRC, RPS6KA4, RPS6KA5, PSMF1, AKAP12, PSME3, PSMD14, KLF2, NOD1, TAB1, TAB2, PSME4, RBMX, OTUD4, PELI1, SIRPA, DAB2IP, ZNF675
BP	GO:0070536	protein K63-linked deubiquitination	14/3408	7.68E-03	CYLD, ATXN3, VCP, USP13, SPATA2, PSMD14, STAMBP, USP33, USP25, DESI2, OTUD4, YOD1, OTUD7B, BRCC3
BP	GO:0032908	regulation of transforming growth factor beta1 production	7/3408	7.71E-03	GATA6, FURIN, CX3CL1, THBS1, ATP6AP2, CD2AP, LAPTM4B
BP	GO:0033327	Leydig cell differentiation	7/3408	7.71E-03	AR, CCND1, PDGFRA, TMF1, SF1, SGPL1, PLEKHA1
BP	GO:0060992	response to fungicide	7/3408	7.71E-03	BCL2L1, KLF4, KLF2, KDM5B, KDM1A, KDM6B, XRN1
BP	GO:0061314	Notch signaling involved in heart development	7/3408	7.71E-03	JAG1, RBPJ, NOTCH2, SNAI2, SNAI1, HEYL, DLL4
BP	GO:0007064	mitotic sister chromatid cohesion	11/3408	7.90E-03	ATRX, RB1, SMC1A, TNKS, PDS5B, POGZ, PDS5A, MAU2, NIPBL, CHTF8, NAA50
BP	GO:2000050	regulation of non-canonical Wnt signaling pathway	11/3408	7.90E-03	ABL1, CSNK1D, CSNK1E, DAB2, MLLT3, SFRP1, TIAM1, DKK1, PLEKHA4, RNF213, ZNRF3

BP	GO:0007596	blood coagulation	84/3408	7.97E-03	ACTB, ARRB1, ARRB2, AXL, CAPZA2, CAV1, ENTPD1, CD59, CDC42, COL1A1, COL1A2, COL3A1, CSRP1, EDN1, GATA2, GATA3, GATA6, GNAQ, GNAS, GNB1, SERPIND1, HDAC2, HNF4A, ILK, IRF1, ITPK1, ITPR1, ITPR2, LYN, MAFG, MYH9, P2RY1, SERPINE1, SERPINB2, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3CB, PRCP, PRKAR1A, PRKAR2A, PRKCA, PRKCE, MAPK1, MAPK3, PTPN11, RAB5A, RAP2B, SRC, SRF, SYK, TFPI, THBS1, TLN1, TYRO3, VCL, MAFK, FZD6, DGKE, DGKD, PABPC4, F2RL3, PAPSS2, MFN2, SH2B3, VAV3, MYL12A, GNA13, HPSE, AKAP10, MMRN1, KDM1A, RCOR1, DOCK9, CBX5, SLC7A11, MAFF, SH2B1, AK3, HPS6, DGKH, ADAMTS18, JMJD1C
BP	GO:0002283	neutrophil activation involved in immune response	116/3408	8.03E-03	ACLY, ADAM10, ALAD, RHOA, ASAH1, CD44, CD47, CD59, CNN2, COPB1, MAPK14, CTSB, CTSS, CTSZ, DDX3X, CYB5R3, DIAPH1, DNASE1L1, EEF1A1, STOM, GAA, GM2A, GPI, NCKAP1L, IGF2R, IMPDH1, ITGAV, JUP, LAMP2, LTA4H, MME, NFKB1, NRAS, OLR1, PA2G4, PAFAH1B2, PGAM1, PKM, PKP1, PLD1, PRCP, MAPK1, PSMA2, PSMC2, PSMD3, PSMD13, PTAFR, PTPRB, PTPRC, PTPRJ, PTPRN2, PYGB, RAB5B, RAP1B, RAP2B, SNAP25, SPTAN1, STK10, SURF4, VAMP7, SYK, TIMP2, TNFAIP6, TNFRSF1B, TRPM2, VCL, VCP, XRCC5, PDXK, DYNLL1, IQGAP1, CPNE3, SYNGR1, VAPA, SCAMP1, MLEC, ARPC5, ACTR2, ATP6AP2, PSMD14, ATP8A1, CAP1, ATG7, IQGAP2, HPSE, PGRMC1, GLIPR1, RAB31, PDAP1, NFASC, ATP11B, ATP11A, DNAJC13, NCSTN, COTL1, ARMC8, OSTF1, ATP6V1D, RAB14, YPEL5, CMTM6, CAND1, KCMF1, RAP2C, TMBIM1, LPCAT1, PTGES2, PLEKHO2, DNAJC5, TXNDC5, FRMPD3, ORMDL3, CANT1, ARL8A, SIRPA, C6orf120
BP	GO:0033619	membrane protein proteolysis	21/3408	8.09E-03	ADAM10, DAG1, MYH9, NFKB1, FURIN, ADAM17, TIMP2, TIMP3, TNFRSF1B, ADAM9, LRIG2, NCSTN, BACE2, RBMX, APH1A, ERAP1, APH1B, RHBDD1, SPPL2A, SPPL3, SH3D19
BP	GO:0046847	filopodium assembly	21/3408	8.09E-03	ARF6, CDC42, CCR7, FMR1, ITGA6, MYO10, RAB5A, SRF, TGFBR1, TRPM2, NRP1, WASL, TENM1, NLGN1, RHOQ, PPP1R16B, FNBP1L, RAB17, FGD4, SPATA13, AGRN
BP	GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	21/3408	8.09E-03	ATM, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7
BP	GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	21/3408	8.09E-03	ATM, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7
BP	GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	21/3408	8.09E-03	ATM, CDKN1A, CDKN1B, EP300, MDM4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, CNOT8, PLK2, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7
BP	GO:0051196	regulation of coenzyme metabolic process	30/3408	8.13E-03	HIF1A, INSR, ME2, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, SNCA, STAT3, TP53, NCOR1, POM121, NUP50, SLC2A6, DDIT4, PDPR, NDC1, NUP133, PDP2, SEH1L, PPTC7, NUP43, POM121C
BP	GO:1903076	regulation of protein localization to plasma membrane	30/3408	8.13E-03	ACTB, AR, ARF6, BCL2L1, AP2M1, CSK, DAB2, EGFR, EPHB2, GBP1, ITGA3, ITGB1, KIF5B, LRP1, MMP14, PRKCE, SPTBN1, STX3, NUMB, SQSTM1, AKAP5, LYPLA1, AGR2, RAB11FIP2, RHOQ, CLIP3, APPL1, LDLRAP1, TMBIM1, PKDCC
BP	GO:0042119	neutrophil activation	118/3408	8.19E-03	ACLY, ADAM10, ALAD, RHOA, ASAH1, CD44, CD47, CD59, CNN2, COPB1, MAPK14, CTSB, CTSS, CTSZ, DDX3X, CYB5R3, DIAPH1, DNASE1L1, EEF1A1, STOM, GAA, GM2A, GPI, NCKAP1L, IGF2R, IL18, IMPDH1, ITGAV, JUP, LAMP2, LTA4H, MME, NFKB1, NRAS, OLR1, PA2G4, PAFAH1B2, PGAM1, PKM, PKP1, PLD1, PRCP, MAPK1, PSMA2, PSMC2, PSMD3, PSMD13, PTAFR, PTPRB, PTPRC, PTPRJ, PTPRN2, PYGB, RAB5B, RAP1B, RAP2B, SNAP25, SPTAN1, STK10, SURF4, VAMP7, SYK, TIMP2, TNFAIP6, TNFRSF1B, TRPM2, VCL, VCP, XRCC5, PDXK, DYNLL1, IQGAP1, CPNE3, SYNGR1, VAPA, SCAMP1, MLEC, ARPC5, ACTR2, ATP6AP2, PSMD14, ATP8A1, CAP1, ATG7, IQGAP2, HPSE, PGRMC1, GLIPR1, RAB31, PDAP1, NFASC, ATP11B, ATP11A, DNAJC13, NCSTN, COTL1, ARMC8, OSTF1, ATP6V1D, RAB14, YPEL5, CMTM6, CAND1, KMT2E, KCMF1, RAP2C, TMBIM1, LPCAT1, PTGES2, PLEKHO2, DNAJC5, TXNDC5, FRMPD3, ORMDL3, CANT1, ARL8A, SIRPA, C6orf120
BP	GO:0010828	positive regulation of glucose transmembrane transport	17/3408	8.20E-03	AKT2, MAPK14, INSR, MEF2A, PTPN11, SLC1A2, TERT, NR4A3, IRS2, C2CD5, FGF19, ARPP19, RHOQ, CLIP3, APPL1, ADIPOR2, OSBPL8
BP	GO:0090311	regulation of protein deacetylation	17/3408	8.20E-03	BCL6, CAMK2D, DYRK1A, EP300, FNTA, MAPT, PRKAA1, MAPK8, KDM5A, SKI, TP53, VEGFA, FRY, NIPBL, SPRED1, SPRED2, SPRED3
BP	GO:0045638	negative regulation of myeloid cell differentiation	29/3408	8.26E-03	ZFP36L1, CDK6, CTNNB1, FBN1, GABPA, GATA2, HMGB3, HOXA5, HOXA7, HOXA9, HOXB8, ITPKB, LYN, MEIS2, MYC, SFRP1, TAL1, ZFP36, LDB1, CTR9, TRIB1, FSTL3, PIAS3, TOB2, NCAPG2, FBXW7, CDC73, ZBTB46, ZNF675

BP	GO:0060606	tube closure	29/3408	8.26E-03	ABL1, ADM, CASP3, DVL3, KAT2A, ARHGAP35, LRP6, MTHFR, PAX2, PTCH1, RARG, SDC4, SFRP1, SKI, TSC1, TWIST1, KDM6A, FZD3, ARID1A, FZD1, FZD6, DLC1, MTHFD1L, SUFU, SEMA4C, IFT57, VANGL2, SHROOM3, TRIM71
BP	GO:0042063	gliogenesis	74/3408	8.26E-03	ABL1, AKT2, RHOA, CDK6, CREB1, CRKL, CSF1, CSK, CTNNB1, DAG1, DLX2, EGFR, EPHA4, ERBB2, ERCC2, EZH2, FGF5, HDAC2, NRG1, HES1, ID4, IDH2, IL6ST, ILK, KCNJ10, KRAS, LDLR, LRP1, LYN, MAPT, MATN2, MDK, MMP14, MYB, NAB1, NF2, NFIB, NTRK3, P2RY1, PAFAH1B1, PAX2, PAX6, SERPINE2, POU3F2, PPP1CC, MAPK1, MAPK3, PTEN, PTPN11, CX3CL1, SKI, SOX4, SOX11, STAT3, TAL1, TERT, TIAM1, TNFRSF1B, B4GALT6, RNF10, TSPAN2, DUSP10, UFL1, NCSTN, DICER1, BACE2, SOX8, ADAM22, PARD3, PRDM8, METTL14, METRN, SH3TC2, DAB2IP
BP	GO:0006893	Golgi to plasma membrane transport	22/3408	8.27E-03	TRIM23, ARF1, CSK, GOLGA4, NSF, SPTBN1, VAMP2, VAMP7, RABEP1, PREPL, ARFRP1, LYPLA1, ARFGEF2, EXOC5, RAB31, EXOC6B, GOLPH3L, KIF13A, C16orf70, PKDCC, EXOC8, STEAP2
BP	GO:2001251	negative regulation of chromosome organization	42/3408	8.28E-03	APC, ATM, ATRX, BRCA1, DNMT3B, DUSP1, HMGA1, HNRNPC, HNRNPU, IK, JARID2, MAD2L1, MLLT6, RAD21, KDM5A, SET, SKI, SNCA, SRC, TWIST1, XRCC5, TNKS, AURKB, TRIP13, TRIP12, ATG5, MTF2, KDM1A, PHF8, SIRT1, SIN3A, ZNF451, UBR5, RTEL1, ATAD2B, XRN1, GNL3L, BCOR, PINX1, PCID2, TET1, SLX4
BP	GO:0001892	embryonic placenta development	28/3408	8.35E-03	ADM, PRDM1, BMP7, ZFP36L1, CEBPB, EGFR, EPAS1, BPTF, GATA2, GRB2, HIF1A, HES1, IGF2, RBPJ, PDGFB, PKD1, MAPK1, SNAI1, SP3, STK4, NR2F2, WNT7B, FZD5, HAND1, VASH1, BIRC6, PLCD3, E2F7
BP	GO:0006112	energy reserve metabolic process	28/3408	8.35E-03	AKT2, CALM1, GAA, GFPT1, GNAS, GSK3B, GYS1, IGF2, IL6ST, INSR, MYC, ENPP1, PHKA1, PHKG2, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PYGB, UGP2, DYRK2, IRS2, PER2, EPM2AIP1, GFPT2, PASK, STK40
BP	GO:0015807	L-amino acid transport	23/3408	8.41E-03	CTNS, CLN8, KCNJ10, RGS2, RGS4, SLC1A2, SLC1A4, SLC1A5, SLC6A9, SLC7A1, SLC7A2, SLC7A5, PER2, SLC7A6, SLC25A15, ARL6IP1, SLC7A11, SLC25A38, SLC38A1, SFXN1, SLC36A4, SLC43A2, SLC36A1
BP	GO:0045582	positive regulation of T cell differentiation	27/3408	8.43E-03	ADA, RHOA, BCL6, RUNX1, RUNX3, CBFB, CYLD, EGR3, GATA3, NCKAP1L, IL7R, IL18, ITPKB, MDK, MYB, PTPRC, RAG1, SYK, XBP1, SOCS1, TNFSF9, AP3D1, CD83, SOCS5, BTN2A2, DUSP10, ZMIZ1
BP	GO:0045913	positive regulation of carbohydrate metabolic process	27/3408	8.43E-03	ADCYAP1R1, AKT2, FOXO1, KAT2A, HIF1A, IGF2, INSR, NFKB1, P2RY1, PDGFB, PFKFB2, PFKFB3, PFKFB4, PHKG2, PPARA, PRKAA1, PRKCE, PTAFR, RANBP2, SNCA, SRC, DYRK2, IRS2, KAT2B, EPM2AIP1, ARPP19, SIRT1
BP	GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	10/3408	8.43E-03	BCL2L1, GRINA, OPA1, PTPN1, TMBIM6, XBP1, HERPUD1, HYOU1, TXNDC12, SYVN1
BP	GO:0031109	microtubule polymerization or depolymerization	34/3408	8.47E-03	ABL1, APC, CDKN1B, CSNK1D, DYRK1A, FKBP4, KIF2A, MAP1A, MAP1B, MAPT, MECP2, MET, MID1, RPS3, SNCA, ARHGEF2, AKAP9, TUBB4A, KIF2C, TPPP, MAPRE3, CAMSAP2, CLASP1, CLIP3, NIN, NDE1, TAOK1, SLAIN2, NAV3, CCSAP, TTBK2, CAMSAP1, KIF24, SKA2
BP	GO:0010611	regulation of cardiac muscle hypertrophy	25/3408	8.47E-03	ATP2B4, CAMK2D, EDN1, FOXO1, G6PD, IL6ST, JARID2, SMAD4, MEF2A, PIN1, PPARA, PPP3CA, PRKCA, TWF1, RGS2, RGS4, SLC9A1, TNFRSF1B, YY1, NR4A3, AKAP6, ROCK2, LMCD1, ERRFI1, MTPN
BP	GO:0032482	Rab protein signal transduction	25/3408	8.47E-03	GDI1, RAB8A, RAB1A, RAB3B, RAB5A, RAB5B, MADD, RAB11B, RAB28, RAB36, DENND4B, RAB31, RAB21, RAB30, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, RAB22A, RAB40C, RAB17, RAB39B, RAB12, RAB15
BP	GO:1902117	positive regulation of organelle assembly	25/3408	8.47E-03	RHOA, EDN1, ARHGAP35, HTT, PIP4K2A, MAPK9, PROX1, RALB, SDC4, SRC, ULK1, DYNLL1, VPS4B, CEP135, G3BP2, PDCD6IP, G3BP1, CNOT1, ATMIN, RAB3GAP2, ASAP1, SH3GLB1, CNOT6, KCTD17, CEP120
BP	GO:0071482	cellular response to light stimulus	38/3408	8.48E-03	AKT2, ATR, BAK1, CALM1, CDC25A, CDKN1A, CHEK1, CREBBP, CRY2, EIF2S1, EP300, FMR1, FNTA, GNB1, MME, MYC, NEDD4, PTPRK, RBL2, TAF1, TP53, YY1, CUL4B, AURKB, CERS1, METAP2, KDM1A, SIRT1, TRIAP1, INO80, USP47, USP28, CAMKMT, RHNO1, RHBDD1, BMF, TP53INP1, SDE2
BP	GO:0007159	leukocyte cell-cell adhesion	84/3408	8.49E-03	ADA, RHOA, BCL6, BMP7, CASP3, CAV1, RUNX1, RUNX3, CBFB, CD44, CD47, CDC42, CEBPB, CCR7, CSK, CYLD, EFNB1, EFNB2, EGR3, ERBB2, FLOT2, GATA3, GRB2, NCKAP1L, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, IRAK1, IRF1, ITGA5, ITGB1, ITPKB, LYN, SMAD7, MDK, MYB, NCK1, NT5E, PAK2, PAK3, PAWR, PPARA, PRKAR1A, PTAFR, PTPN11, PTPRC, RAG1, RPS3, SDC4, SRC, STK10, SYK, TFRC, VCAM1, XBP1, NR4A3, NCK2, SOCS1, TNFSF9, FADD, AP3D1, DLG5, SOCS6, CD83, KLF4, SOCS5, TNIP1, BTN2A2, GPNMB, NFAT5, DUSP10, ICOSLG, LAX1, PAG1, PELI1, ZMIZ1, WNK1, CD276, SIRPA, MIA3, NRARP
BP	GO:0048469	cell maturation	49/3408	8.54E-03	AXL, BCL2, RUNX2, CBFB, CDKN1A, CTNNB1, EPAS1, ERCC2, FOXO3, G6PD, GATA2, GATA3, GJA1, HIF1A, FOXA1, HOXA5, HES1, MECP2, OPA1, PDE3A, PGR, POU2F2, PPP2R1A, RB1, RFX3, CX3CL1, AURKA, TAL1, VEGFA, XBP1, FZD5, TRIP13, B4GALT6, PTBP3, GDF11, KLF2, ABHD2, TUSC2, KDM1A, NFASC, MTCH1, CNTNAP2, SOX8, YTHDF2, BCL11A, FAM20C, FAM210B, PLD6, AGRN

BP	GO:0035791	platelet-derived growth factor receptor-beta signaling pathway	8/3408	8.58E-03	ABL1, HIP1, LRP1, PDGFA, PDGFB, PTPN1, PTPN12, SRC
BP	GO:0036295	cellular response to increased oxygen levels	8/3408	8.58E-03	FAS, ATP6V1A, CAV1, DNMT3B, FOXO1, ATP6V0D1, ATG7, TMEM199
BP	GO:0043374	CD8-positive, alpha-beta T cell differentiation	8/3408	8.58E-03	BCL2, RUNX1, RUNX3, CBFB, NCKAP1L, IRF1, SATB1, SOCS1
BP	GO:0031111	negative regulation of microtubule polymerization or depolymerization	15/3408	8.63E-03	APC, DYRK1A, FKBP4, MAP1B, MID1, SNCA, ARHGEF2, TUBB4A, CAMSAP2, CLASP1, CLIP3, TAOK1, NAV3, TTBK2, CAMSAP1
BP	GO:0051567	histone H3-K9 methylation	15/3408	8.63E-03	ATRX, BRCA1, DNMT3B, JARID2, MECP2, MYB, SUV39H1, KDM1A, SIRT1, ARID4B, RIF1, SETD5, BEND3, SETD7, SETDB2
BP	GO:0060323	head morphogenesis	15/3408	8.63E-03	ASPH, COL1A1, EP300, LRP6, MSX1, PAX9, PDGFRA, PTPN11, SKI, SGPL1, ATP6AP2, DKK1, NIPBL, PLEKHA1, ARID5B
BP	GO:1905314	semi-lunar valve development	15/3408	8.63E-03	JAG1, BMPR2, GATA3, RBPJ, SMAD6, NOTCH2, RB1, ROBO1, SNAI2, SNAI1, TNFRSF1B, TWIST1, ROCK2, HEYL, DLL4
BP	GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	13/3408	8.63E-03	BCL2, PPP3R1, MAPK8, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, BCL2L11, BBC3, MOAP1, BMF
BP	GO:1904292	regulation of ERAD pathway	13/3408	8.63E-03	CAV1, ATXN3, UBE2G2, USP13, EDEM1, HERPUD1, BCAP31, USP25, UBQLN2, UBQLN1, DERL2, UBE2J1, YOD1
BP	GO:1904837	beta-catenin-TCF complex assembly	13/3408	8.63E-03	BCL9, CREBBP, CTNNB1, EP300, MEN1, MYC, TCF7, TCF7L2, TERT, TLE1, TLE4, KMT2D, CDC73
BP	GO:0071156	regulation of cell cycle arrest	33/3408	8.63E-03	AKT2, ATM, CCND1, BRCA1, CALR, CDKN1A, CDKN1B, EP300, FOXM1, GATA6, MDM4, FOXO4, CNOT4, PML, POU4F1, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, HMGA2, CNOT8, PLK2, ZNF268, CNOT1, ZNF385A, TRIAP1, CNOT6, E2F7, DAB2IP, SDE2
BP	GO:0007595	lactation	18/3408	8.63E-03	ATP7A, CCND1, CAV1, CREB1, GJA1, GOT2, HIF1A, HK2, OAS2, PPAT, PRLR, UMPS, USF2, VDR, VEGFA, XBP1, SOCS2, KALRN
BP	GO:0006474	N-terminal protein amino acid acetylation	9/3408	8.63E-03	CREBBP, EP300, SOX4, KAT2B, NAA35, NAA40, NAA25, NAA50, NAA30
BP	GO:0030011	maintenance of cell polarity	9/3408	8.63E-03	ANK1, DST, GSK3B, NCKAP1L, SLC9A1, DLG5, PDCD6IP, ARPC5, CRB2
BP	GO:0035855	megakaryocyte development	9/3408	8.63E-03	EP300, KIT, PIP4K2A, PTPN11, SRF, TAL1, SH2B3, WASF2, ZNF385A
BP	GO:2000811	negative regulation of anoikis	9/3408	8.63E-03	BCL2, CAV1, ITGA5, ITGB1, MCL1, PDK4, SNAI2, SRC, TLE1
BP	GO:0035265	organ growth	55/3408	8.64E-03	ACVR2B, AR, BCL2, BMPR1A, COL6A2, COL12A1, MAPK14, DUSP6, S1PR1, EDN1, FGF2, FGFR3, FOXC1, G6PD, GATA6, GJA1, RBPJ, JARID2, SMAD2, MATN2, MEF2C, PIM1, PIN1, PPARA, PRKAR1A, MAPK1, PROX1, PTEN, PTPN11, RARG, RGS2, RGS4, MAP2K4, STC1, STK4, TGFBR1, TGFBR3, THBS3, YY1, SORBS2, LATS1, AKAP6, BCL2L11, PDLIM5, AKAP13, WWC1, LATS2, SERP1, BNC2, WWC3, HEG1, NDRG4, WWC2, COL27A1, ARID2
BP	GO:0006650	glycerophospholipid metabolic process	80/3408	8.90E-03	ARF1, ATM, CAPN2, CDS1, CHKA, FGF2, HADHA, IMPA2, LDLR, MECP2, PAFAH1B1, PDGFA, PDGFB, PIGA, PIK3C2A, PIK3CB, PIP4K2A, PLD1, PTEN, RAB5A, ALDH5A1, SOCS1, INPP4B, SOCS2, SYNJ1, SYNJ2, CPNE3, MTMR3, MTMR7, MTMR4, SOCS6, PCYT1B, SOCS5, LPIN2, IP6K1, LPGAT1, LPCAT3, CEPT1, SERINC3, SACM1L, SMG1, EFR3A, GPD1L, LPIN1, PIP5K1C, SLC44A1, PISD, SOCS7, ABHD5, RAB14, PI4K2B, ETNK1, GPCPD1, INPP5E, AGPAT3, CHPT1, SERINC1, PITPNM2, PLEKHA4, PLEKHA1, MTMR9, LPCAT1, PGAP1, DDHD1, PTDSS2, PITPNM3, FAR1, FAM126A, PLEKHA8, PGAP3, OSBPL8, MBOAT2, TTC7B, DGKH, PLD6, LCLAT1, TMEM86B, SERINC5, FAM126B, SLC27A1

BP	GO:0030041	actin filament polymerization	50/3408	9.00E-03	ADD1, ARF1, ARF6, RHOA, CAPZA2, CCR7, DIAPH1, EPS8, FER, GRB2, NCKAP1L, MYO1C, NCK1, PAK3, PRKCE, TWF1, RASA1, RDX, SPTAN1, SPTBN1, NCK2, WASF1, WASL, LATS1, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, TENM1, CDC42EP2, NCKAP1, IQGAP2, FAM107A, KANK1, COTL1, TMOD2, TTC17, FMN2, SPIRE1, PLEKHG2, ARHGAP28, MYADM, ARHGAP18, WHAMM, JMY, MTPN, RICTOR, FMN1
BP	GO:0030203	glycosaminoglycan metabolic process	45/3408	9.10E-03	CD44, NCAN, DCN, EXTL2, EXTL3, FGF2, FOXC1, GCNT2, HAS3, NDST1, IDS, CHST6, NFKB1, PDGFB, PIM1, PRELP, SDC2, SDC4, ST3GAL1, SLC9A1, UGDH, CHST1, B4GALT2, B4GALT6, NDST3, HS2ST1, SPOCK2, HS3ST3A1, HS3ST1, ABCC5, GPC6, UST, ST3GAL6, HPSE, LYVE1, GLCE, CHST15, CSGALNACT2, CSGALNACT1, CHST7, XYLT2, ITIH5, CHST9, HS6ST2, AGRN
BP	GO:0030514	negative regulation of BMP signaling pathway	19/3408	9.10E-03	ABL1, FBN1, SMAD6, SMAD7, SFRP1, SKI, SKIL, SORL1, FZD1, CHRD, TOB1, FSTL3, DKK1, GREM1, HIPK2, TRIM33, SMURF1, BMPER, RBPMS2
BP	GO:2000677	regulation of transcription regulatory region DNA binding	19/3408	9.10E-03	CTNNB1, EP300, FOXC1, GATA3, MSX1, PAX6, POU4F1, RB1, SOX11, TAF1, TWIST1, HMGA2, PER2, KLF4, HAND1, SIN3A, FBXW7, NSD1, ZNF675
BP	GO:2000772	regulation of cellular senescence	19/3408	9.10E-03	ABL1, BCL6, BMPR1A, CDK6, HMGA1, KRAS, MAP3K3, PAWR, TERT, TP53, TWIST1, HMGA2, NUAK1, AKT3, PLK2, ZNF277, VASH1, SIRT1, RSL1D1
BP	GO:0017148	negative regulation of translation	56/3408	9.11E-03	ZFP36L1, ZFP36L2, CALR, DAPK1, DDX3X, EIF2S1, EIF4E, EIF4G1, FMR1, GAPDH, HNRNPD, IGFBP5, IREB2, CAPRIN1, EIF2AK2, PURA, UPF1, RGS2, RPS3, STAT3, TSC1, ZFP36, BTG2, FXR1, ENC1, CNOT8, ROCK2, PUM1, TOB1, SYNCRIP, IGF2BP1, IGF2BP3, CPEB3, CNOT1, SAMD4A, TNRC6B, LARP1, GIGYF2, AGO1, EIF2AK1, TNRC6A, YTHDF2, XRN1, PUS7, SAMD4B, RBM23, TNRC6C, METTL14, CPEB4, SESN2, UNK, TRIM71, CPEB2, AGO3, AGO4, YTHDF3
BP	GO:0090263	positive regulation of canonical Wnt signaling pathway	42/3408	9.21E-03	CAV1, COL1A1, CSNK1D, CSNK1E, CSNK1G3, DDX3X, EGFR, RBPJ, ILK, JUP, NFKB1, PIN1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SFRP1, SOX4, SRC, TBL1X, VCP, TNKS, PSMF1, PSME3, PSMD14, KANK1, PSME4, UBR5, GID8, USP47, LGR4, VPS35, SULF2, PLEKHA4, PRDM15, WNK1, TBL1XR1, AMER1, NRARP
BP	GO:0048660	regulation of smooth muscle cell proliferation	47/3408	9.29E-03	BMPR1A, CDKN1A, CDKN1B, COMT, CTNNB1, HBEGF, S1PR1, EDN1, EGFR, FGF2, GNAI2, GNAI3, HMGCR, IGFBP5, IL6R, IL18, ILK, IRAK1, JUN, MEF2C, MEF2D, MYB, PDGFB, PPARD, PTAFR, PTEN, CX3CL1, SOD2, STAT1, TCF7L2, TERT, THBS1, XRCC5, SF1, NR4A3, KLF4, ADAMTS1, MFN2, CALCRL, TRIB1, LDLRAP1, FOXP1, PDCD4, FOXJ2, NDRG2, NDRG4, RBPMS2
BP	GO:0002761	regulation of myeloid leukocyte differentiation	35/3408	9.34E-03	ZFP36L1, CAMK4, RUNX1, CDK6, CEBPB, CREB1, CSF1, CTNNB1, ESRRA, FBN1, GATA2, GNAS, HOXA7, JUN, LYN, KITLG, MYC, NOTCH2, POU4F1, PRKCA, RB1, SFRP1, TAL1, KLF10, FADD, RASSF2, TRIB1, FSTL3, PIAS3, TOB2, FOXP1, FBXW7, ZBTB46, ZNF675, SIGLEC15
BP	GO:0046394	carboxylic acid biosynthetic process	110/3408	9.41E-03	ACACA, ACLY, ATP2B4, BCAT1, BCAT2, BRCA1, CBR1, NCAN, DCN, EDN1, GAPDH, GATM, GLS, GOT2, GPI, HAS3, HIF1A, HK1, HK2, FOXK2, INSIG1, INSR, LDHA, FADS1, LTA4H, MTAP, MTHFR, MTR, MYO5A, NFKB1, NUP88, NUP98, PDGFB, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PRKAA1, PRKAB2, PROX1, PTGIS, RANBP2, ACSM3, SCD, SCP2, STAT3, ELOVL4, SYK, TP53, UGDH, UGP2, NR1H2, UROS, XBP1, AKR1C3, ALDH1A2, PER2, KYNU, FADS2, QKI, NCOR1, POM121, LPGAT1, FGF19, ABCC5, UST, AASS, NUP50, SERINC3, ABHD2, ERLIN2, SLC2A6, MGLL, SEPHS2, SEPHS1, WDTC1, SIRT1, AMACR, MTHFD1L, ADIPOR1, INSIG2, DDIT4, ADI1, NDC1, NUP133, RIMKLB, ENOPH1, ELOVL5, ELOVL6, ADIPOR2, SCD5, PTGES2, SEH1L, MRI1, ACSS1, GPT2, CBR4, STARD4, NANP, RDH10, ACSF3, FOXK1, SERINC5, RIMKLA, NAT8L, NUP43, POM121C
BP	GO:0071897	DNA biosynthetic process	53/3408	9.61E-03	ARRB2, ATM, ATR, BMPR2, CCT6A, CDKN1A, CTNNB1, DACH1, DKC1, DUSP1, FGF2, GJA1, HNRNPC, HNRNPD, HNRNPU, LIG4, MAP3K4, MEN1, MYC, PAK3, PARN, PDGFB, POLA1, MAPK1, MAPK3, REV3L, RFC1, SRC, TERT, TFDP1, TP53, VCP, XRCC5, TRIM25, TNKS, AURKB, KLF4, SMG7, CERS1, POLQ, SMG5, SIRT1, PARM1, SH2B1, GREM1, POLL, DTL, XRN1, GNL3L, CHTF8, PINX1, NPLOC4, HMBOX1
BP	GO:1903725	regulation of phospholipid metabolic process	28/3408	9.71E-03	ARF1, CAPN2, CCR7, FGF2, FGFR3, KIT, LDLR, LYN, PDGFA, PDGFB, PDGFRA, SRC, SOCS1, SOCS2, MTMR3, MTMR4, SOCS6, KLF4, SOCS5, VAV3, ATG14, SOCS7, MTMR9, LPCAT1, PIK3IP1, WDR81, DAB2IP, SLC27A1
BP	GO:2000177	regulation of neural precursor cell proliferation	28/3408	9.71E-03	RHOA, CTNNA1, CTNNB1, CTSZ, FOXO1, FOXO3, GATA2, GNAI2, RAPGEF1, HIF1A, ILK, LYN, MDK, NAP1L1, NF2, PAX6, PROX1, CX3CL1, TP53, VEGFA, BTG2, FZD3, KDM1A, CDON, DLL4, SHCBP1, TRIM71, KCTD11
BP	GO:0090342	regulation of cell aging	21/3408	9.76E-03	ABL1, BCL6, BMPR1A, CDK6, FOXM1, HMGA1, KRAS, MAP3K3, PAWR, PTEN, TERT, TP53, TWIST1, HMGA2, NUAK1, AKT3, PLK2, ZNF277, VASH1, SIRT1, RSL1D1
BP	GO:0048144	fibroblast proliferation	27/3408	9.87E-03	CCNA2, CDK6, CDKN1A, CREB1, CTNNB1, DACH1, EGFR, FN1, FOSL2, JUN, LIG4, MYB, MYC, PAWR, PDGFA, PDGFB, PDGFRA, PML, SFRP1, SKI, TP53, WNT7B, MORC3, ZMIZ1, CDC73, TP53INP1, DAB2IP
BP	GO:2000144	positive regulation of DNA-templated	12/3408	9.87E-03	CREB1, CTNNB1, JUN, PSMC2, SRF, TAF1, HNF1B, TP53, TWIST1, FOSL1, SUB1, CAND1

		transcription, initiation			
BP	GO:0045669	positive regulation of osteoblast differentiation	22/3408	9.92E-03	ACVR2B, JAG1, BMP7, BMPR1A, BMPR2, RUNX2, CEBPB, CEBPD, CTNNB1, FBN2, GNAS, IL6R, IL6ST, ILK, JUND, MEF2C, SOX11, WNT7B, TP63, PDLIM7, WNT4, FAM20C
BP	GO:0060135	maternal process involved in female pregnancy	22/3408	9.92E-03	AR, PRDM1, BMPR2, CTSB, GJA1, ITGA3, MEN1, PGR, PPARD, PPAT, MAPK1, MAPK3, PTGIS, RGS2, STC1, NR2F2, VDR, STC2, PRDX3, KPNA6, DAZAP1, WNT4
BP	GO:0008654	phospholipid biosynthetic process	67/3408	9.92E-03	ARF1, ATM, CAPN2, CDS1, CHKA, FGF2, HMGCS2, FADS1, PDGFA, PDGFB, PIGA, PIK3C2A, PIK3CB, PIP4K2A, PLD1, PPARD, PTEN, RAB5A, DGKE, INPP4B, SYNJ1, SYNJ2, CPNE3, MTMR3, MTMR7, MTMR4, PCYT1B, LPIN2, LPGAT1, LPCAT3, CEPT1, SPTLC1, SACM1L, GPD1L, LPIN1, PIP5K1C, SLC44A1, PISD, ABHD5, RAB14, PI4K2B, ETNK1, INPP5E, AGPAT3, CHPT1, SERINC1, PITPNM2, PLEKHA4, PLEKHA1, MTMR9, SRD5A3, LPCAT1, PGAP1, DDHD1, PTDSS2, PITPNM3, FAR1, PLEKHA8, PGAP3, NUS1, MBOAT2, SAMD8, SGMS2, PLD6, LCLAT1, SERINC5, SLC27A1
BP	GO:0002088	lens development in camera-type eye	26/3408	9.95E-03	CDKN1B, CTNS, CTNNB1, GATA3, GJA1, NF2, NHS, NTRK3, PAX6, PROX1, SKI, SKIL, SOX11, TGFBR1, WNT7B, WNT2B, BCAR3, ABI2, KDM5B, FRS2, PDS5B, SLC7A11, HIPK2, CDON, TBC1D20, HIPK1
BP	GO:0072009	nephron epithelium development	33/3408	9.97E-03	JAG1, BCL2, CTNNB1, FGF1, FGF2, FOXC1, GATA3, HES1, ILK, SMAD4, MEF2C, MYC, PAX2, PBX1, PKD1, PODXL, PTCH1, STAT1, HNF1B, VEGFA, WNT7B, WNT2B, DCHS1, IQGAP1, KLHL3, HEYL, SOX8, SIX4, WNT4, AHI1, LGR4, LZTS2, FMN1
BP	GO:0033866	nucleoside bisphosphate biosynthetic process	23/3408	9.97E-03	ACACA, ACLY, ACSL4, PDK3, PDK4, SCD, SNCA, ELOVL4, PAPSS2, ACSL6, SLC35B3, PANK1, PDPR, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, ACSS1, CBR4, ACSF3
BP	GO:0034030	ribonucleoside bisphosphate biosynthetic process	23/3408	9.97E-03	ACACA, ACLY, ACSL4, PDK3, PDK4, SCD, SNCA, ELOVL4, PAPSS2, ACSL6, SLC35B3, PANK1, PDPR, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, ACSS1, CBR4, ACSF3
BP	GO:0034033	purine nucleoside bisphosphate biosynthetic process	23/3408	9.97E-03	ACACA, ACLY, ACSL4, PDK3, PDK4, SCD, SNCA, ELOVL4, PAPSS2, ACSL6, SLC35B3, PANK1, PDPR, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, ACSS1, CBR4, ACSF3
BP	GO:0000422	autophagy of mitochondrion	25/3408	9.97E-03	MARK2, HTT, HIF1A, HK2, SREBF2, TP53, FZD5, SQSTM1, ATG5, ATG13, MFN2, ATG7, GABARAPL2, ATG14, ATG2A, HTRA2, VPS13C, ATG2B, VPS13D, FBXW7, SMURF1, USP36, ATG9A, MUL1, MAP1LC3B
BP	GO:0061726	mitochondrion disassembly	25/3408	9.97E-03	MARK2, HTT, HIF1A, HK2, SREBF2, TP53, FZD5, SQSTM1, ATG5, ATG13, MFN2, ATG7, GABARAPL2, ATG14, ATG2A, HTRA2, VPS13C, ATG2B, VPS13D, FBXW7, SMURF1, USP36, ATG9A, MUL1, MAP1LC3B
BP	GO:0043583	ear development	58/3408	9.98E-03	ADAM10, JAG1, BCL2, CCNA2, CDKN1B, CEBPD, COL11A1, DLX6, EDN1, EPHA4, EPHB2, GATA2, GATA3, HES1, RBPJ, INSIG1, JAG2, KCNK3, MSX1, NTRK3, OPA1, OTX1, PAFAH1B1, PAX2, ATP8B1, PRRX1, MAPK1, MAPK3, PROX1, PTPN11, SDC4, SPARC, ZEB1, TWIST1, FZD3, NR4A3, FZD6, ITGA8, DCHS1, TRIP11, NTN1, ATG5, SLC4A7, BCL2L11, ANP32B, NIPBL, LRIG1, INSIG2, SIX4, AHI1, ESRP1, SOBP, CHD7, VANGL2, TTC39C, RDH10, BMPER, FREM2
BP	GO:0016053	organic acid biosynthetic process	110/3408	9.99E-03	ACACA, ACLY, ATP2B4, BCAT1, BCAT2, BRCA1, CBR1, NCAN, DCN, EDN1, GAPDH, GATM, GLS, GOT2, GPI, HAS3, HIF1A, HK1, HK2, FOXK2, INSIG1, INSR, LDHA, FADS1, LTA4H, MTAP, MTHFR, MTR, MYO5A, NFKB1, NUP88, NUP98, PDGFB, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PRKAA1, PRKAB2, PROX1, PTGIS, RANBP2, ACSM3, SCD, SCP2, STAT3, ELOVL4, SYK, TP53, UGDH, UGP2, NR1H2, UROS, XBP1, AKR1C3, ALDH1A2, PER2, KYNU, FADS2, QKI, NCOR1, POM121, LPGAT1, FGF19, ABCC5, UST, AASS, NUP50, SERINC3, ABHD2, ERLIN2, SLC2A6, MGLL, SEPHS2, SEPHS1, WDTC1, SIRT1, AMACR, MTHFD1L, ADIPOR1, INSIG2, DDIT4, ADI1, NDC1, NUP133, RIMKLB, ENOPH1, ELOVL5, ELOVL6, ADIPOR2, SCD5, PTGES2, SEH1L, MRI1, ACSS1, GPT2, CBR4, STARD4, NANP, RDH10, ACSF3, FOXK1, SERINC5, RIMKLA, NAT8L, NUP43, POM121C
BP	GO:0016574	histone ubiquitination	17/3408	1.02E-02	RAG1, RNF2, SKP1, UBE2N, CUL4B, TRIP12, CTR9, PCGF3, KDM1A, SUZ12, WAC, UBR5, BCOR, ATXN7L3, CDC73, PCGF5, RNF168
BP	GO:0035987	endodermal cell differentiation	17/3408	1.02E-02	COL4A2, COL5A1, COL5A2, COL11A1, COL12A1, CTNNB1, FN1, GATA6, HSBP1, ITGA5, ITGAV, MMP14, HNF1B, HMGA2, CTR9, DKK1, CDC73
BP	GO:0043433	negative regulation of DNA-binding transcription factor activity	47/3408	1.04E-02	ARRB1, ARRB2, BMP7, CEBPG, CYLD, EZH2, HDAC2, IRAK1, IRAK2, SMAD7, MEN1, MXI1, PIM1, PKD1, PROX1, PTCH1, PTGIS, RB1, RNF2, SP100, TAF1, TCF7L2, TRAF3, TWIST1, FZD6, BHLHE40, BTRC, KLF4, HAND1, G3BP2, MED13, TRIB1, RBCK1, KDM1A, UFL1, SIRT1, HEYL, RLIM, PIAS4, SUFU, PELI1, ITCH, GLIS2, SIK1, DAB2IP, ZNF431, ZNF675
BP	GO:1903322	positive regulation of protein modification by small protein	39/3408	1.04E-02	ARRB1, ARRB2, BRCA1, PTTG1IP, CAV1, FKBP1A, HSPA5, SMAD7, PIN1, MAPK9, PTEN, RAB1A, UBE2L3, UBE2N, VCP, CUL3, CDC14B, MTA1, CTR9, TNIP1, PIAS3, FAM107A, KDM1A, MYCBP2, HSPBP1, UBQLN1, PIAS4, DCUN1D1, RNF111, FANCI, FBXW7, PELI1, ARRDC3, GORASP1, MUL1, ARRDC4, DCUN1D3, AMER1, RNF180

		conjugation or removal			
BP	GO:0016197	endosomal transport	59/3408	1.04E-02	ARF6, ARHGAP1, ARL1, TMEM50B, LYST, AP1S1, RAB8A, SORT1, SNX1, SORL1, VCP, EVI5, SQSTM1, AP3D1, SPAG9, DCLK1, RAB11B, VPS4B, GOSR1, GOSR2, PREPL, ZFYVE16, SNX17, AP5Z1, ARFRP1, SNF8, RHOBTB3, LMTK2, TMCC1, ERC1, LEPROTL1, ACAP2, TMEM50A, CORO1C, TMEM87A, TBC1D10B, EHD4, VPS36, UBAP1, ANKFY1, CHMP5, VPS54, RAB14, RAB6B, HEATR5B, LEPROT, CMTM6, VPS37C, LAPTM4B, VPS35, CHMP1B, EPG5, RAB17, NDRG4, RAB11FIP4, DPY30, MICALL1, CHMP7, VPS37D
BP	GO:0043255	regulation of carbohydrate biosynthetic process	30/3408	1.09E-02	ADCYAP1R1, AKT2, EP300, FOXO1, KAT2A, GSK3B, IGF2, FOXK2, INSR, NFKB1, P2RY1, PDGFB, ENPP1, PPARA, PPP1CA, PPP1CB, PTAFR, RANBP2, SNCA, DYRK2, IRS2, KAT2B, EPM2AIP1, ARPP19, PASK, SIRT1, SESN2, SOGA1, SIK1, FOXK1
BP	GO:0044773	mitotic DNA damage checkpoint	30/3408	1.09E-02	ATM, CCND1, CDKN1A, CDKN1B, FOXN3, ATF2, EP300, MDM4, FOXO4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TP53, BTG2, HMGA2, CNOT8, TAOK2, PLK2, CNOT1, ZNF385A, GIGYF2, TRIAP1, CNOT6, TAOK1, ZNF830, E2F7
BP	GO:0034260	negative regulation of GTPase activity	18/3408	1.09E-02	ARRB1, ARRB2, IPO5, PTPRN2, RDX, TSC1, IQGAP1, TNK2, SPRY1, IQGAP2, RRP1B, LRCH1, RCC2, CDC42SE1, WNK1, CPEB2, DAB2IP, AMOT
BP	GO:0030183	B cell differentiation	38/3408	1.09E-02	ABL1, ADA, ATM, BAK1, BCL2, BCL6, ZFP36L1, ZFP36L2, CEBPG, KLF6, CYLD, EP300, NCKAP1L, HMGB3, RBPJ, ITGB1, KIT, DNAJB9, MMP14, NOTCH2, POU2F2, PTPRC, PTPRJ, RAG1, SFRP1, SP3, SYK, ADAM17, TCF3, TP53, TPD52, VCAM1, XBP1, HDAC9, PCID2, FNIP1, ATP11C, IRF2BP2
BP	GO:0003272	endocardial cushion formation	11/3408	1.11E-02	BMP7, BMPR1A, RBPJ, SMAD4, MSX1, ROBO1, SNAI2, SNAI1, TGFBR1, DCHS1, HEYL
BP	GO:0046426	negative regulation of JAK-STAT cascade	11/3408	1.11E-02	CAV1, NF2, PPP2CA, PPP2R1A, VHL, SOCS1, SOCS2, SH2B3, ADIPOR1, PARP14, LEPROT
BP	GO:0086064	cell communication by electrical coupling involved in cardiac conduction	11/3408	1.11E-02	ATP1B1, CACNA1C, CALM1, CALM2, CALM3, CAMK2D, CAV1, GJA1, PDE4D, SLC8A1, GJC1
BP	GO:2000209	regulation of anoikis	11/3408	1.11E-02	BCL2, CAV1, ITGA5, ITGB1, MCL1, PDK4, SNAI2, SRC, TLE1, ANKRD13C, SIK1
BP	GO:0006903	vesicle targeting	29/3408	1.11E-02	CD59, CSNK1D, CTSZ, NSF, PPP6C, RAB1A, TGFA, CUL3, USO1, NAPA, GOSR1, GOSR2, SEC24C, CNIH1, SEC23A, SEC24A, TMED10, PPP6R1, NLGN1, ANKRD28, CLASP1, TRAPPC4, TRAPPC2L, PPP6R3, SAR1A, GORASP1, CEP19, TBC1D20, FAM91A1
BP	GO:1901184	regulation of ERBB signaling pathway	29/3408	1.11E-02	CBL, CDC42, HBEGF, EGFR, ERBB2, FER, GRB2, HIP1, RBPJ, PTPN12, PTPRJ, SH3GL2, SHC1, SOS1, ADAM17, TGFA, NCK2, GPRC5A, SOCS5, SPRY1, AGR2, PTPN18, ERRFI1, FBXW7, SH3TC2, AFAP1L2, SOCS4, DAB2IP, EPGN
BP	GO:0050870	positive regulation of T cell activation	54/3408	1.11E-02	ADA, RHOA, BCL6, CAV1, RUNX1, RUNX3, CBFB, CD47, CDC42, CCR7, CSK, CYLD, EFNB1, EFNB2, EGR3, FLOT2, GATA3, GRB2, NCKAP1L, HES1, IGF2, IL6R, IL6ST, IL7R, IL18, ITPKB, LYN, MDK, MYB, NCK1, PAK2, PAK3, PTPN11, PTPRC, RAG1, RPS3, SRC, SYK, TFRC, VCAM1, XBP1, NCK2, SOCS1, TNFSF9, FADD, AP3D1, CD83, SOCS5, BTN2A2, DUSP10, ICOSLG, ZMIZ1, CD276, SIRPA
BP	GO:0009225	nucleotide-sugar metabolic process	15/3408	1.12E-02	EXTL2, FUT8, GFPT1, MPI, PGM3, PMM2, UGDH, UGP2, GFPT2, GNPDA1, GNE, CSGALNACT1, UGGT1, GNPNAT1, UAP1L1
BP	GO:0045022	early endosome to late endosome transport	15/3408	1.12E-02	DAB2, EMP2, MAPK1, MAPK3, RAB5A, RDX, SRC, SNX3, SNF8, LMTK2, RAB21, DNAJC13, HOOK1, HOOK3, WDR81
BP	GO:0046326	positive regulation of glucose import	15/3408	1.12E-02	AKT2, MAPK14, INSR, MEF2A, PTPN11, SLC1A2, TERT, IRS2, C2CD5, FGF19, ARPP19, RHOQ, APPL1, ADIPOR2, OSBPL8
BP	GO:0046825	regulation of protein export from nucleus	15/3408	1.12E-02	GSK3B, PTPN11, PTPN14, SP100, TCF7L2, TP53, TXN, XPO1, YWHAE, RAPGEF3, ANP32B, DNAJC27, RIOK2, XPO5, XPO4
BP	GO:0071604	transforming growth factor beta production	15/3408	1.12E-02	CREB1, ATF2, GATA6, HIF1A, ITGAV, ITGB8, LTBP1, SMAD4, MYB, FURIN, CX3CL1, THBS1, ATP6AP2, CD2AP, LAPTM4B
BP	GO:0000186	activation of MAPKK activity	19/3408	1.13E-02	CRK, CRKL, EGFR, ERCC6, RAPGEF1, MAP3K1, MAP3K3, MAP3K4, MAP3K9, MAPK1, MAPK3, EIF2AK2, TGFBR1, ADAM9, TAOK2, MAP3K2, FRS2, KIDINS220, TAOK1
BP	GO:0006482	protein demethylation	13/3408	1.16E-02	JARID2, KDM5A, KDM6A, KDM4A, KDM5B, KDM2A, KDM1A, PHF8, KDM6B, KDM3B, ALKBH4, JMJD1C, KDM1B
BP	GO:0008214	protein dealkylation	13/3408	1.16E-02	JARID2, KDM5A, KDM6A, KDM4A, KDM5B, KDM2A, KDM1A, PHF8, KDM6B, KDM3B, ALKBH4, JMJD1C, KDM1B

BP	GO:0010762	regulation of fibroblast migration	13/3408	1.16E-02	FER, FGF2, PAK3, PRKCE, SDC4, SLC8A1, THBS1, BAG4, AKAP12, CORO1C, APPL1, RCC2, RFFL
BP	GO:0034694	response to prostaglandin	13/3408	1.16E-02	ACACA, ADCY6, CCR7, AKR1C2, EDN1, GNB1, PRKAA1, PRKCE, PTGER4, SFRP1, TGFBR3, YY1, AKR1C3
BP	GO:0045879	negative regulation of smoothened signaling pathway	13/3408	1.16E-02	RUNX2, MEGF8, ENPP1, SERPINE2, PTCH1, RB1, CHRD, BTRC, MGRN1, SUFU, GLIS2, KCTD11, KCTD6
BP	GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	13/3408	1.16E-02	BCL2, PTTG1IP, CD44, HNRNPK, MSX1, TP53, KDM1A, SIRT1, ZNF385A, RRM2B, TRIAP1, TAF9B, RRN3
BP	GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	13/3408	1.16E-02	BMPR1A, GATA2, NR3C1, HIF1A, JUN, SMAD6, PDGFB, SREBF2, SRF, STAT3, TEAD1, TERT, TP53
BP	GO:2001021	negative regulation of response to DNA damage stimulus	26/3408	1.17E-02	BCL2, BCL2L1, PTTG1IP, CD44, DYRK1A, OGG1, RPS3, SNAI2, SNAI1, TPT1, TWIST1, HMGA2, TRIP12, POLQ, KDM1A, SIRT1, ZNF385A, UBR5, TRIAP1, TAF9B, RTEL1, USP47, RIF1, UBQLN4, KLHL15, RMI2
BP	GO:0033002	muscle cell proliferation	62/3408	1.17E-02	BMPR1A, CDKN1A, CDKN1B, COMT, MAPK14, CTNNB1, HBEGF, S1PR1, EDN1, EGFR, FGF2, FOXC1, GATA6, GJA1, GNAI2, GNAI3, HMGCR, IGFBP5, RBPJ, IL6R, IL18, ILK, IRAK1, JARID2, JUN, MEF2C, MEF2D, MYB, PDGFB, PIM1, PPARD, PRKAR1A, MAPK1, PTAFR, PTEN, CX3CL1, SOD2, STAT1, STAT3, TCF7L2, TERT, TGFBR1, TGFBR3, THBS1, XRCC5, SF1, NR4A3, KLF4, ADAMTS1, MFN2, CALCRL, TRIB1, LDLRAP1, FOXP1, PDCD4, FOXJ2, NDRG2, NAA35, NDRG4, AKIRIN1, ARID2, RBPMS2
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	62/3408	1.17E-02	FAS, RHOA, ARRB1, ARRB2, ASPH, BAK1, CASP10, CD44, DAPK1, DDX3X, EPHA7, HIP1, MAPT, MYC, NKX3-1, PAK2, PAX2, SERPINB9, PML, RAG1, ROBO1, RPS3, RPS6KA3, SIAH2, SNCA, SRC, SYK, THBS1, VCP, VEGFA, YWHAE, TP63, TNFSF10, FADD, KLF4, HERPUD1, BCL2L11, BCAP31, NOD1, DLC1, ANP32B, PRDX3, ARL6IP1, SIRT1, BCL2L13, MTCH1, PRDX5, CYFIP2, BBC3, HTRA2, TRIAP1, CYCS, USP47, IFT57, PCID2, MUL1, SOX7, FNIP1, EGLN3, RFFL, ACVR1C, ACER2
BP	GO:1904029	regulation of cyclin-dependent protein kinase activity	32/3408	1.18E-02	ACTB, APC, CCND1, CASP3, CCNA2, CCNC, CCND2, CCNF, CCNG2, CCNT1, CCNT2, CDC25A, CDKN1A, CDKN1B, EGFR, IPO5, MEN1, PDGFB, PKD1, PROX1, PTEN, SRC, ADAM17, NR2F2, KAT2B, LATS1, CCNE2, MAPRE3, LATS2, CNPPD1, CCNJ, CAMK2N1
BP	GO:0032233	positive regulation of actin filament bundle assembly	21/3408	1.18E-02	ABL1, RHOA, CD47, CDC42, LIMK1, NF2, PXN, CX3CL1, SDC4, SFRP1, TESK1, TGFBR1, TSC1, NRP1, ROCK2, BAG4, RAPGEF3, LIMCH1, WNT4, SYNPO2L, SH3PXD2B
BP	GO:0048332	mesoderm morphogenesis	25/3408	1.18E-02	BMP7, BMPR1A, BMPR2, FOXC1, ITGA3, ITGB1, SMAD2, NF2, PAX2, PRKAR1A, SNAI1, SRF, TAL1, TBX3, KDM6A, NR4A3, HMGA2, ITGA8, CHRD, KLF4, HAND1, DKK1, KDM6B, EPB41L5, CRB2
BP	GO:0009743	response to carbohydrate	60/3408	1.19E-02	ACVR2B, RHOA, ARRB1, ZFP36L1, CASP3, CDKN1B, COL6A2, EFNA5, EGR1, ENSA, FOXO3, GJA1, HIF1A, HMGCR, HNF4A, IGF1R, KIF5B, LDHA, LRP1, LYN, SMAD2, MAP1B, MEN1, OPA1, PAX2, CDK16, PDK3, PFKFB2, PPARD, PPP3CA, PRKAA1, PRKCE, PTEN, PTPRN2, RAP1B, MAP2K4, TRA2B, SLC8A1, SOX4, SPARC, SRF, VAMP2, HNF1B, TCF7L2, THBS1, TIAM1, XBP1, DYNLL1, IRS2, RAB11B, MAP4K4, CALCRL, UNC13B, ATG7, KAT7, RAB11FIP2, TXN2, SIN3A, SESN2, ACVR1C
BP	GO:0060675	ureteric bud morphogenesis	22/3408	1.19E-02	BCL2, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MYC, PAX2, PBX1, PTCH1, HNF1B, VEGFA, WNT2B, DCHS1, SOX8, SIX4, WNT4, LGR4, LZTS2, FMN1
BP	GO:0008088	axo-dendritic transport	23/3408	1.19E-02	DST, FLOT2, FMR1, HIF1A, HNRNPU, KIF5B, MAP1A, MAPT, OPA1, PAFAH1B1, PURA, WASF1, AP3D1, KIF3B, AP3S2, KIF3A, TRAK1, RAB21, KIF1B, MAPK8IP3, AP3M1, TRAK2, ARL8A
BP	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	31/3408	1.21E-02	ACTB, APC, CCND1, CASP3, CCNA2, CCNC, CCND2, CCNF, CCNG2, CCNT1, CCNT2, CDC25A, CDKN1A, CDKN1B, EGFR, IPO5, MEN1, PDGFB, PKD1, PROX1, PTEN, SRC, ADAM17, NR2F2, KAT2B, LATS1, CCNE2, MAPRE3, LATS2, CNPPD1, CCNJ
BP	GO:0009408	response to heat	48/3408	1.22E-02	ATM, ATP2A2, ATR, BAG1, CAMK2A, CAMK2D, CDKN1A, CREBBP, EIF2S1, EP300, FGF1, FKBP4, GSK3B, HDAC2, HSBP1, DNAJA1, HSPA2, HSPA5, IRAK1, LYN, MAPT, ATXN3, NUP88, NUP98, POLR2D, MAPK1, MAPK3, RANBP2, THBS1, VCP, YWHAE, BAG4, POM121, DNAJA2, NUP50, DNAJB4, SIRT1, HSPB8, MYOF, HTRA2, NDC1, NUP133, MLST8, SEH1L, AKT1S1, TP53INP1, NUP43, POM121C
BP	GO:0050817	coagulation	84/3408	1.22E-02	ACTB, ARRB1, ARRB2, AXL, CAPZA2, CAV1, ENTPD1, CD59, CDC42, COL1A1, COL1A2, COL3A1, CSRP1, EDN1, GATA2, GATA3, GATA6, GNAQ, GNAS, GNB1, SERPIND1, HDAC2, HNF4A, ILK, IRF1, ITPK1, ITPR1, ITPR2, LYN, MAFG, MYH9, P2RY1, SERPINE1,

					SERPINB2, PDGFA, PDGFB, PDGFRA, SERPINE2, PIK3CB, PRCP, PRKAR1A, PRKAR2A, PRKCA, PRKCE, MAPK1, MAPK3, PTPN11, RAB5A, RAP2B, SRC, SRF, SYK, TFPI, THBS1, TLN1, TYRO3, VCL, MAFK, FZD6, DGKE, DGKD, PABPC4, F2RL3, PAPSS2, MFN2, SH2B3, VAV3, MYL12A, GNA13, HPSE, AKAP10, MMRN1, KDM1A, RCOR1, DOCK9, CBX5, SLC7A11, MAFF, SH2B1, AK3, HPS6, DGKH, ADAMTS18, JMJD1C
BP	GO:0033962	cytoplasmic mRNA processing body assembly	10/3408	1.22E-02	DDX6, ATXN2, LIMD1, ATXN2L, CNOT1, LSM4, LSM14A, CNOT6, EDC3, PATL1
BP	GO:0036499	PERK-mediated unfolded protein response	10/3408	1.22E-02	EIF2S1, HSPA5, IGFBP1, NCK1, PTPN1, NCK2, HERPUD1, AGR2, TMEM33, PPP1R15B
BP	GO:0036507	protein demannosylation	10/3408	1.22E-02	AMFR, SEL1L, RNF103, EDEM1, TRIM13, MAN1A2, DERL2, UGGT1, EDEM3, SYVN1
BP	GO:0036508	protein alpha-1,2-demannosylation	10/3408	1.22E-02	AMFR, SEL1L, RNF103, EDEM1, TRIM13, MAN1A2, DERL2, UGGT1, EDEM3, SYVN1
BP	GO:1904886	beta-catenin destruction complex disassembly	10/3408	1.22E-02	APC, CAV1, CTNNB1, DVL3, GSK3B, LRP6, PPP1CA, FZD5, FZD1, AMER1
BP	GO:0042552	myelination	38/3408	1.22E-02	AKT2, CTNNB1, DAG1, ERBB2, ERCC2, GALC, NRG1, ID4, ILK, KCNJ10, MBP, MYO5A, NAB1, NTRK3, POU3F2, PTEN, RARG, SCN8A, SKI, TNFRSF1B, TSC1, ZNF24, MALL, B4GALT6, QKI, RNF10, TSPAN2, NFASC, NCSTN, DICER1, ADAM22, ACER3, PARD3, SH3TC2, MARVELD1, FAM126A, MAL2, SERINC5
BP	GO:1990845	adaptive thermogenesis	43/3408	1.24E-02	ACVR2B, ADRB1, APC, CAV1, CEBPB, EPAS1, ESRRG, GATM, GJA1, GNAS, HNRNPU, IGF1R, RBPJ, IL18, IRF4, LAMA4, LNPEP, PLCL1, PRKAB2, PRLR, RB1, SCD, SORL1, SYK, ADAM17, THRA, NR1H2, VEGFA, PER2, ZNF516, IP6K1, MFN2, ADAMTS5, KDM1A, KDM6B, LPIN1, ADIPOR1, LGR4, ARRDC3, ELOVL6, ADIPOR2, FLCN, BMP8A
BP	GO:0046390	ribose phosphate biosynthetic process	75/3408	1.25E-02	ACACA, ACLY, ADCY1, ADCY6, ADCY9, AK2, AK4, ACSL4, G6PD, GAPDH, GPI, GUCY1A2, HIF1A, HK1, HK2, FOXK2, IMPDH1, INSR, LDHA, NME4, NUP88, NUP98, PDK3, PDK4, PFAS, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PPAT, PRKAA1, PRPSAP2, RANBP2, SCD, SNCA, STAT3, ELOVL4, TP53, UCK2, UMPS, VCP, PAPSS2, NCOR1, POM121, PAICS, NUP50, SLC2A6, ACSL6, AK3, SLC35B3, PANK1, DDIT4, PDPR, RFK, NDC1, NUP133, CTPS2, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, DNAJC30, ACSS1, CBR4, ACSF3, FLCN, FOXK1, NUP43, POM121C
BP	GO:1904375	regulation of protein localization to cell periphery	34/3408	1.26E-02	ACTB, ADAM10, AR, ARF6, BCL2L1, AP2M1, CSK, DAB2, DAG1, EGFR, EPB41, EPHB2, GBP1, ITGA3, ITGB1, KIF5B, LRP1, MMP14, PRKCE, SPTBN1, STX3, NUMB, SQSTM1, AKAP5, GPC6, LYPLA1, AGR2, RAB11FIP2, RHOQ, CLIP3, APPL1, LDLRAP1, TMBIM1, PKDCC
BP	GO:0071241	cellular response to inorganic substance	57/3408	1.27E-02	ADCY1, ADD1, ALAD, ATP7A, ATRX, CALR, CAMK2D, CCNA2, CDKN1B, CREB1, CRK, ECT2, EDN1, EGFR, EIF2S1, FOXO1, FMR1, FOSB, FUS, HNRNPD, HSPA5, ITPKB, JUN, JUND, KCNK3, LIG4, MEF2A, MEF2C, MT1M, MTR, OGG1, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, SNCA, SYT1, TFR2, TRPM2, AKR1C3, IQGAP1, CPNE3, SYT7, FSTL3, NLGN1, SYT11, NCSTN, SPIDR, CLIC4, SLC25A24, SYT17, WNK1, DDI2, SYT2, CPNE8, CPNE2
BP	GO:0002067	glandular epithelial cell differentiation	17/3408	1.29E-02	CDK6, GATA6, GSK3B, FOXA1, HNF4A, HOXA5, HES1, MEN1, PAX6, PROX1, RARG, RFX3, TP63, CLOCK, AGR2, WNT4, WDR77
BP	GO:0031623	receptor internalization	33/3408	1.31E-02	ADM, ARF1, ARRB1, ARRB2, CAV1, AP2M1, EFNB2, FMR1, GRB2, ITGB1, LRP1, LRPAP1, MKLN1, NEDD4, OPHN1, RAB5A, ATXN2, SH3GL2, SNAP25, SNCA, SNX1, SYK, TFRC, VEGFA, NUMB, CALCRL, RAB31, DKK1, LDLRAP1, GREM1, UBQLN2, AHI1, ANKRD13A
BP	GO:0003203	endocardial cushion morphogenesis	14/3408	1.31E-02	BMP7, BMPR1A, RBPJ, ISL1, SMAD4, MDM4, MSX1, ROBO1, SNAI2, SNAI1, TGFBR1, TWIST1, DCHS1, HEYL
BP	GO:0071108	protein K48-linked deubiquitination	14/3408	1.31E-02	CYLD, ATXN3, USP9X, BAP1, USP13, USP33, OTUD3, USP25, DESI2, OTUD4, YOD1, OTUD7B, USP37, VCPIP1
BP	GO:0110111	negative regulation of animal organ morphogenesis	14/3408	1.31E-02	BCL2, BMP7, BMPR2, CTNNB1, FOXC1, GATA3, NFIB, TNFRSF11B, PAX2, STAT1, HNF1B, GREM1, BCOR, FBXW7
BP	GO:1905332	positive regulation of morphogenesis of an epithelium	14/3408	1.31E-02	ABL1, AR, CTNNB1, GATA3, MDK, PAX2, RREB1, VEGFA, WNT2B, SOX8, SIX4, WNT4, AHI1, LGR4

BP	GO:1903035	negative regulation of response to wounding	28/3408	1.31E-02	CDKN1A, CDKN1B, CRK, EDN1, EPHA4, FGF2, GJA1, HMGCR, MDK, SERPINE1, SERPINB2, PDGFA, PDGFB, PDGFRA, SERPINE2, PTEN, TFPI, THBS1, LRIG2, SH2B3, DUSP10, CLASP1, WNT4, RGMA, KREMEN1, PHLDB2, CD109, ADAMTS18
BP	GO:0002902	regulation of B cell apoptotic process	9/3408	1.32E-02	ADA, BCL6, LYN, PTEN, IRS2, AURKB, FOXP1, SLC39A10, FNIP1
BP	GO:0006349	regulation of gene expression by genetic imprinting	9/3408	1.32E-02	BRCA1, DNMT3A, IGF2, MECP2, PCGF3, CTCF, ARID4B, PCGF5, KDM1B
BP	GO:0007221	positive regulation of transcription of Notch receptor target	9/3408	1.32E-02	CREBBP, EP300, RBPJ, PBX1, STAT1, KAT2B, PLXND1, WWC1, HEYL
BP	GO:0043555	regulation of translation in response to stress	9/3408	1.32E-02	EIF2S1, NCK1, PPP1CA, EIF2AK2, RPS6KA3, NCK2, EIF2AK1, SESN2, PPP1R15B
BP	GO:2000757	negative regulation of peptidyl-lysine acetylation	9/3408	1.32E-02	BRCA1, HDAC2, SET, SNCA, TWIST1, ATG5, SIRT1, SIN3A, ZNF451
BP	GO:0006665	sphingolipid metabolic process	44/3408	1.32E-02	ASAH1, CLN8, KDSR, GALC, GM2A, ITGB8, KIT, NAGA, PPP2CA, PPP2R1A, PRKAA1, ELOVL4, UGCG, ST8SIA4, ALDH5A1, NSMAF, SGPL1, VAPB, VAPA, B4GALT6, SPTLC1, CERS1, SERINC3, PDXDC1, HTRA2, ORMDL2, ST6GALNAC6, ST8SIA3, GLTP, SPTLC3, ACER3, ESYT2, SERINC1, ELOVL5, ELOVL6, SGPP1, ORMDL1, ORMDL3, SAMD8, PPM1L, SGMS2, CERS6, SERINC5, ACER2
BP	GO:0007043	cell-cell junction assembly	36/3408	1.32E-02	ACTN4, APC, RHOA, CAV1, RUNX1, CBFB, CDH6, CTNNA1, CTNND1, ECT2, GJA1, GJB1, IKBKB, JUP, MYO1C, PKP1, PRKCA, PKN2, SNAI2, SNAI1, SRF, STRN, TLN1, VCL, FZD5, PKP4, DLG5, ROCK2, PDCD6IP, GJC1, NFASC, PARD3, HEG1, PARD6B, MTDH, FLCN
BP	GO:0031440	regulation of mRNA 3'-end processing	12/3408	1.33E-02	ZFP36L1, CCNT1, NCBP1, SNRPA, CTR9, AHCYL1, PAPOLA, CPSF6, CPEB3, ZC3H3, CDC73, CPSF7
BP	GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	12/3408	1.33E-02	CREB1, DR1, PSMC2, SRF, TAF1, HNF1B, THRA, TP53, SUB1, ZNF451, ATF7IP, CAND1
BP	GO:0070076	histone lysine demethylation	12/3408	1.33E-02	JARID2, KDM5A, KDM6A, KDM4A, KDM5B, KDM2A, KDM1A, PHF8, KDM6B, KDM3B, JMJD1C, KDM1B
BP	GO:0090344	negative regulation of cell aging	12/3408	1.33E-02	ABL1, BCL6, CDK6, FOXM1, MAP3K3, PTEN, TERT, TWIST1, HMGA2, AKT3, PLK2, SIRT1
BP	GO:0032873	negative regulation of stress-activated MAPK cascade	18/3408	1.33E-02	CYLD, DUSP1, FOXM1, FOXO1, DNAJA1, MEN1, MYC, PAFAH1B1, SFRP1, NCOR1, HIPK3, ZMYND11, DUSP10, PDCD4, AIDA, ITCH, SIRPA, ZNF675
BP	GO:0060425	lung morphogenesis	18/3408	1.33E-02	CTNNB1, CTSZ, DAG1, FOXA1, HOXA5, KRAS, NFIB, MAPK1, MAPK3, SOX11, SRF, WNT7B, WNT2B, DLG5, SPRY1, VANGL2, STK40, RDH10
BP	GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	18/3408	1.33E-02	CYLD, DUSP1, FOXM1, FOXO1, DNAJA1, MEN1, MYC, PAFAH1B1, SFRP1, NCOR1, HIPK3, ZMYND11, DUSP10, PDCD4, AIDA, ITCH, SIRPA, ZNF675
BP	GO:2000725	regulation of cardiac muscle cell differentiation	18/3408	1.33E-02	ARRB2, EDN1, EFNB2, G6PD, KAT2A, NRG1, RBPJ, SMAD4, MEF2C, PIN1, PPARA, RGS2, RGS4, YY1, AKAP6, FRS2, DKK1, GREM1
BP	GO:0090559	regulation of membrane permeability	27/3408	1.33E-02	BAK1, BCL2, BCL2L1, CAMK2A, ATF2, GSK3B, HK2, PPP3R1, MAPK8, SLC9A1, STAT3, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, TJP2, PDCD6IP, BCL2L11, BBC3, LAPTM4B, HEG1, MOAP1, MUL1, BMF, CHCHD10
BP	GO:0006983	ER overload response	7/3408	1.33E-02	GSK3B, HSPA5, TP53, BCL2L11, CCDC47, ATG10, PPP1R15B

BP	GO:0010649	regulation of cell communication by electrical coupling	7/3408	1.33E-02	CALM1, CALM2, CALM3, CAMK2D, CAV1, PDE4D, SLC8A1
BP	GO:0032905	transforming growth factor beta1 production	7/3408	1.33E-02	GATA6, FURIN, CX3CL1, THBS1, ATP6AP2, CD2AP, LAPTM4B
BP	GO:0060368	regulation of Fc receptor mediated stimulatory signaling pathway	7/3408	1.33E-02	CD47, CSK, RAPGEF1, LYN, PTPRC, PTPRJ, APPL1
BP	GO:0071481	cellular response to X-ray	7/3408	1.33E-02	ATM, GATA3, SFRP1, XRCC5, HMGA2, NIPBL, NUCKS1
BP	GO:0072178	nephric duct morphogenesis	7/3408	1.33E-02	EFNB2, EPHA4, EPHA7, GATA3, PAX2, HNF1B, AHI1
BP	GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	7/3408	1.33E-02	JUN, NCK1, TMBIM6, VHL, NCK2, CITED2, HIF1AN
BP	GO:0006140	regulation of nucleotide metabolic process	41/3408	1.34E-02	ADORA2B, AK4, RHOA, ATP7A, HIF1A, INSR, ME2, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, SNCA, STAT3, TP53, VCP, NCOR1, POM121, NUP50, SLC2A6, ISCU, DNAJC15, DDIT4, PDPR, NDC1, NUP133, PDP2, BEND3, SEH1L, DNAJC30, UQCC2, FLCN, PDE12, NUP43, POM121C
BP	GO:0006491	N-glycan processing	8/3408	1.36E-02	FUT8, MAN2A1, PRKCSH, ST8SIA4, MAN1A2, GANAB, ST8SIA3, GNPTAB
BP	GO:0035067	negative regulation of histone acetylation	8/3408	1.36E-02	BRCA1, SET, SNCA, TWIST1, ATG5, SIRT1, SIN3A, ZNF451
BP	GO:0043517	positive regulation of DNA damage response, signal transduction by p53 class mediator	8/3408	1.36E-02	ATM, ATR, DDX5, MSX1, ZNF385A, SPRED1, SPRED2, SPRED3
BP	GO:0043518	negative regulation of DNA damage response, signal transduction by p53 class mediator	8/3408	1.36E-02	PTTG1IP, CD44, DYRK1A, SNAI2, SNAI1, TWIST1, KDM1A, SIRT1
BP	GO:0048569	post-embryonic animal organ development	8/3408	1.36E-02	BAK1, FBN1, LDHA, VEGFA, FZD5, KLF4, BCL2L11, BCL11B
BP	GO:0051127	positive regulation of actin nucleation	8/3408	1.36E-02	WASF1, WASL, FCHSD2, ABI2, NCKAP1, FMN2, WHAMM, FMN1
BP	GO:0021954	central nervous system neuron development	25/3408	1.37E-02	ADARB1, ATP7A, CRK, CRKL, EPHA4, EPHB2, EPHB3, GATA2, ARHGAP35, MAPT, NFIB, PAFAH1B1, PTEN, ROBO1, BTG2, NRP1, DCLK1, B4GALT6, RAPGEF2, SEMA3A, MYCBP2, SZT2, NIN, PLXNA4, FBXO45
BP	GO:0007229	integrin-mediated signaling pathway	31/3408	1.37E-02	ABL1, ADAM10, DST, CD47, CDC42, COL3A1, CTNNA1, EMP2, FUT8, ILK, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, MYH9, NEDD9, PTPN11, SRC, SYK, TLN1, CUL3, SEMA7A, ITGA8, ADAM9, NRP1, ADAMTS1, VAV3, FERMT1, RCC2
BP	GO:0038093	Fc receptor signaling pathway	62/3408	1.37E-02	ABL1, ACTB, CALM1, CD47, CDC42, CRK, FER, GRB2, RAPGEF1, NCKAP1L, IKBKB, JUN, KIT, LIMK1, LYN, MAP3K1, MYO1C, MYO10, NCK1, NFKB1, PAK2, PIK3CB, PPP3CA, PPP3R1, PRKCE, MAPK1, MAPK3, MAPK8, MAPK9, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, PTPRC, PTPRJ, MAP2K4, SHC1, SKP1, SOS1, SRC, SYK, NR4A3, BTRC, WASL, PSMF1, ARPC5, ACTR2, ARPC2, WASF2, PSME3, PSMD14, VAV3, TAB1, NCKAP1, TAB2, PSME4, APPL1, CYFIP2, WIPF2
BP	GO:0046605	regulation of centrosome cycle	20/3408	1.38E-02	BRCA1, CCNF, CHEK1, CTNNB1, KAT2A, AURKA, XPO1, KAT2B, ROCK2, VPS4B, PDCD6IP, PLK2, CEP250, CHMP5, NSFL1C, MDM1, CHMP1B, CEP85, UBXN2B, CEP120

BP	GO:0005977	glycogen metabolic process	24/3408	1.38E-02	AKT2, CALM1, GAA, GSK3B, GYS1, IGF2, IL6ST, INSR, ENPP1, PHKA1, PHKG2, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PYGB, UGP2, DYRK2, IRS2, PER2, EPM2AIP1, PASK, STK40
BP	GO:1900076	regulation of cellular response to insulin stimulus	24/3408	1.38E-02	ATP2B1, ESRRA, GNAI2, IGF2, MYO1C, NCK1, OPA1, ENPP1, PRKAA1, PTPN1, PTPN11, RPS6KB1, SORL1, SRC, TSC1, USO1, SOCS1, SOCS2, KANK1, SIRT1, ADIPOR1, NUCKS1, OSBPL8, SESN3
BP	GO:0007004	telomere maintenance via telomerase	23/3408	1.39E-02	ATM, ATR, CCT6A, CTNNB1, DKC1, HNRNPC, HNRNPU, MAP3K4, PARN, MAPK1, MAPK3, RFC1, SRC, TERT, XRCC5, TNKS, AURKB, SMG7, SMG5, XRN1, GNL3L, PINX1, HMBOX1
BP	GO:0009880	embryonic pattern specification	21/3408	1.39E-02	BMP7, CTNNB1, EFNB1, LRP6, SMAD2, SMAD4, SMAD6, PCSK6, PTCH1, SIM2, TBX3, KDM6A, FZD5, NRP1, SEMA3A, FRS2, SATB2, EPB41L5, PGAP1, PLD6, NRARP
BP	GO:0010676	positive regulation of cellular carbohydrate metabolic process	21/3408	1.39E-02	ADCYAP1R1, AKT2, FOXO1, KAT2A, IGF2, INSR, P2RY1, PFKFB2, PHKG2, PPARA, PRKCE, PTAFR, RANBP2, SNCA, SRC, DYRK2, IRS2, KAT2B, EPM2AIP1, ARPP19, SIRT1
BP	GO:0046824	positive regulation of nucleocytoplasmic transport	21/3408	1.39E-02	MAPK14, ECT2, GSK3B, JUP, IPO5, NEDD4, MAPK1, RAN, TCF7L2, TP53, YWHAE, NUTF2, RAPGEF3, ANP32B, CPSF6, TARDBP, UBR5, RBM27, RIOK2, MAVS, XPO4
BP	GO:0048857	neural nucleus development	21/3408	1.39E-02	ACTB, RHOA, BCL2, CALM1, CALM2, CALM3, CDC42, G6PD, HSPA5, KCNC1, MBP, NFIB, RAD1, YWHAE, ZNF148, DYNLL1, SYNGR3, NDRG2, GNB4, MAPKAP1, ZNF430
BP	GO:1900542	regulation of purine nucleotide metabolic process	40/3408	1.39E-02	ADORA2B, AK4, RHOA, ATP7A, HIF1A, INSR, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, SNCA, STAT3, TP53, VCP, NCOR1, POM121, NUP50, SLC2A6, ISCU, DNAJC15, DDIT4, PDPR, NDC1, NUP133, PDP2, BEND3, SEH1L, DNAJC30, UQCC2, FLCN, PDE12, NUP43, POM121C
BP	GO:0006513	protein monoubiquitination	22/3408	1.39E-02	CBL, RAG1, RNF2, SKP1, UBE2D3, TRIM25, CUL4B, CUL3, CTR9, UBE4B, PCGF3, MGRN1, WAC, DTL, BCOR, UBE2R2, UBE2W, ATXN7L3, CDC73, PCGF5, KBTBD8, RNF168
BP	GO:0072171	mesonephric tubule morphogenesis	22/3408	1.39E-02	BCL2, CTNNB1, FGF1, FGF2, GATA3, HES1, ILK, SMAD4, MYC, PAX2, PBX1, PTCH1, HNF1B, VEGFA, WNT2B, DCHS1, SOX8, SIX4, WNT4, LGR4, LZTS2, FMN1
BP	GO:0031062	positive regulation of histone methylation	15/3408	1.40E-02	BRCA1, CTNNB1, DNMT3B, JARID2, SMAD4, MECP2, KMT2A, MYB, CTR9, MTF2, SIRT1, AUTS2, RIF1, KMT2E, TET1
BP	GO:0033146	regulation of intracellular estrogen receptor signaling pathway	15/3408	1.40E-02	AR, BRCA1, RUNX1, CBFB, FOXA1, ISL1, SRC, KMT2D, TP63, LATS1, CNOT1, UFL1, WBP2, STRN3, KCTD6
BP	GO:0050775	positive regulation of dendrite morphogenesis	15/3408	1.40E-02	CUX1, EPHA4, ILK, CAPRIN1, OPA1, PAFAH1B1, PAK3, PTPRD, VAMP7, TIAM1, KALRN, ACTR2, RAB21, SS18L1, BHLHB9
BP	GO:2000648	positive regulation of stem cell proliferation	15/3408	1.40E-02	CTNNB1, HIF1A, HNRNPU, KITLG, PAX6, PTPRC, CX3CL1, SOX11, TBX3, TERT, VEGFA, FZD3, HMGA2, KDM1A, ATXN1L
BP	GO:0021987	cerebral cortex development	34/3408	1.40E-02	RHOA, COL3A1, CRK, CRKL, CTNNB1, EGFR, GSK3B, HIF1A, LRP1, LRP6, MDK, PAFAH1B1, PAX6, PEX13, POU3F2, ROBO1, TRA2B, TACC1, TSC1, YWHAE, NRP1, SEMA3A, BTBD3, KDM1A, CNTNAP2, CDON, SLC38A2, NDE1, FUT10, DIXDC1, DAB2IP, CEP120, FBXO45, CCDC85C
BP	GO:0050810	regulation of steroid biosynthetic process	29/3408	1.45E-02	ACACA, ADM, ASAH1, EGR1, FGF1, HMGCR, INSIG1, LSS, NFKB1, NFYA, NFYB, PRKAA1, PROX1, RAN, SCD, SNAI2, SNAI1, SREBF2, VDR, SF1, AKR1C3, FGF19, ERLIN2, SIRT1, DKK3, INSIG2, WNT4, ELOVL6, STARD4
BP	GO:0002065	columnar/cuboidal epithelial cell differentiation	33/3408	1.45E-02	ABL1, JAG1, PRDM1, CDK6, CDKN1A, CEBPB, GATA6, GSK3B, HIF1A, FOXA1, HNF4A, HOXA5, HES1, RBPJ, JAG2, MEN1, PAFAH1B1, SERPINE1, PAX6, PROX1, RARG, RFX3, SOX4, SOX11, TP63, SLC4A7, CLOCK, AGR2, WNT4, ESRP1, C1GALT1, FAM20C, WDR77
BP	GO:0042303	molting cycle	33/3408	1.45E-02	ACVR1B, ATP7A, BCL2, CTNNB1, EGFR, ERCC2, HDAC2, IGFBP5, RBPJ, SMAD4, MYO5A, PDGFA, SNAI1, SOS1, TERT, FZD3, FZD6, TP63, LDB1, LDB2, CLOCK, FST, HPSE, SOX21, DKK1, NIPBL, LRIG1, LGR4, FERMT1, VANGL2, MYSM1, CD109, ZDHHC21
BP	GO:0042633	hair cycle	33/3408	1.45E-02	ACVR1B, ATP7A, BCL2, CTNNB1, EGFR, ERCC2, HDAC2, IGFBP5, RBPJ, SMAD4, MYO5A, PDGFA, SNAI1, SOS1, TERT, FZD3, FZD6, TP63, LDB1, LDB2, CLOCK, FST, HPSE, SOX21, DKK1, NIPBL, LRIG1, LGR4, FERMT1, VANGL2, MYSM1, CD109, ZDHHC21

BP	GO:0060419	heart growth	33/3408	1.45E-02	BMPR1A, MAPK14, DUSP6, S1PR1, EDN1, FGF2, FOXC1, G6PD, GATA6, GJA1, RBPJ, JARID2, MEF2C, PIM1, PIN1, PPARA, PRKAR1A, MAPK1, PROX1, PTEN, RGS2, RGS4, MAP2K4, TGFBR1, TGFBR3, YY1, SORBS2, AKAP6, PDLIM5, AKAP13, HEG1, NDRG4, ARID2
BP	GO:0010950	positive regulation of endopeptidase activity	48/3408	1.46E-02	FAS, RHOA, ARRB1, ASPH, BAK1, CASP10, DAPK1, DDX3X, EFNA3, EPHA4, HIP1, LYN, MAPT, MBP, MYC, NKX3-1, PML, ROBO1, RPS3, SNCA, STAT3, SYK, VCP, TNFSF10, FADD, ROCK2, BCL2L11, BCAP31, PSME3, PSMD14, NOD1, DLC1, ANP32B, SIRT1, BCL2L13, MTCH1, CYFIP2, BBC3, PRELID1, HTRA2, CYCS, IFT57, AKIRIN2, MUL1, SOX7, EGLN3, ACVR1C, ACER2
BP	GO:0009260	ribonucleotide biosynthetic process	73/3408	1.46E-02	ACACA, ACLY, ADCY1, ADCY6, ADCY9, AK2, AK4, ACSL4, GAPDH, GPI, GUCY1A2, HIF1A, HK1, HK2, FOXK2, IMPDH1, INSR, LDHA, NME4, NUP88, NUP98, PDK3, PDK4, PFAS, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PPAT, PRKAA1, RANBP2, SCD, SNCA, STAT3, ELOVL4, TP53, UCK2, UMPS, VCP, PAPSS2, NCOR1, POM121, PAICS, NUP50, SLC2A6, ACSL6, AK3, SLC35B3, PANK1, DDIT4, PDPR, RFK, NDC1, NUP133, CTPS2, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, DNAJC30, ACSS1, CBR4, ACSF3, FLCN, FOXK1, NUP43, POM121C
BP	GO:0035459	cargo loading into vesicle	11/3408	1.50E-02	INSIG1, RAB1A, SEC24C, SEC23A, SEC24A, TMED10, SEC31B, SAR1A, KIF13A, TBC1D20, MIA3
BP	GO:0060444	branching involved in mammary gland duct morphogenesis	11/3408	1.50E-02	AR, CSF1, LRP6, PGR, PML, SRC, TBX3, VDR, BTRC, KDM5B, WNT4
BP	GO:0060571	morphogenesis of an epithelial fold	11/3408	1.50E-02	AR, BMP7, CFL1, CTNNB1, EGFR, HIF1A, HOXD13, WNT2B, LUZP1, TP63, RDH10
BP	GO:0060317	cardiac epithelial to mesenchymal transition	13/3408	1.50E-02	JAG1, RBPJ, SMAD4, MSX1, SNAI2, SNAI1, TGFBR1, TGFBR3, TWIST1, SPRY1, OLFM1, HEYL, PDCD4
BP	GO:0009612	response to mechanical stimulus	55/3408	1.51E-02	FAS, RHOA, BAK1, CHEK1, CNN2, COL1A1, COL3A1, COL11A1, MAPK14, DAG1, DCN, EDN1, EGFR, ETV1, FOSB, GJA1, HTT, IRF1, JUN, JUND, JUP, KCNC1, KCNJ2, KIT, MAP1B, MDK, MEIS2, MAP3K1, MMP14, NFKB1, P2RY1, SERPINE2, PKD1, MAPK3, MAPK8, MAPK9, PTCH1, PTGER4, PTPN11, MAP2K4, SLC8A1, SLC9A1, SRC, STAT1, THBS1, BTG2, FOSL1, FADD, MBD2, POSTN, MAP3K2, CNTNAP2, SLC38A2, STRBP, MTPN
BP	GO:0021700	developmental maturation	71/3408	1.51E-02	AP1G1, ARCN1, RHOA, RERE, AXL, BCL2, RUNX2, CBFB, CDKN1A, CTNNB1, DAG1, S1PR1, EPAS1, ERCC2, FGFR3, FOXO3, G6PD, GATA2, GATA3, GJA1, HIF1A, FOXA1, HOXA5, HES1, RBPJ, MAP1B, MECP2, MYO5A, NFIA, OPA1, PAX2, PDE3A, PGR, POU2F2, PPP2R1A, PTEN, RB1, RFX3, CX3CL1, AURKA, TAL1, THBS3, VEGFA, XBP1, FZD5, DCHS1, ALDH1A2, AP3D1, TRIP13, B4GALT6, PTBP3, GDF11, KLF2, UNC13B, ABHD2, TUSC2, KDM1A, NFASC, MTCH1, CNTNAP2, GREM1, SOX8, YTHDF2, BCL11A, FERMT1, FAM20C, FAM210B, DAB2IP, PLD6, AGRN, SNX19
BP	GO:0007093	mitotic cell cycle checkpoint	45/3408	1.53E-02	APC, ATM, CCND1, BCL2L1, BRCA1, CDKN1A, CDKN1B, FOXN3, ATF2, DUSP1, EP300, IK, MAD2L1, MDM4, FOXO4, CNOT4, PML, RB1, RBL2, SOX4, AURKA, TFDP1, TFDP2, TOP2B, TP53, BTG2, HMGA2, AURKB, TRIP13, CNOT8, TAOK2, PLK2, CNOT1, ZNF385A, GIGYF2, TRIAP1, PCID2, CNOT6, TAOK1, DCLRE1B, NABP1, INTS3, NABP2, ZNF830, E2F7
BP	GO:0044272	sulfur compound biosynthetic process	51/3408	1.53E-02	ACACA, ACLY, NCAN, DCN, ESD, ACSL4, GSTM3, NDST1, MAT2A, CHST6, MTAP, MTHFR, MTR, PDK3, PDK4, PRELP, SCD, ST3GAL1, SNCA, ELOVL4, UGDH, CHST1, B4GALT2, PAPSS2, B4GALT6, NDST3, UST, ST3GAL6, ACSL6, SLC7A11, GLCE, MAT2B, SLC35B3, CHST15, PDPR, ADI1, CSGALNACT2, CSGALNACT1, CHST7, PDP2, ENOPH1, ELOVL5, XYLT2, ELOVL6, PPCS, SCD5, CHST9, MRI1, ACSS1, CBR4, ACSF3
BP	GO:0106106	cold-induced thermogenesis	40/3408	1.56E-02	ACVR2B, ADRB1, APC, CAV1, CEBPB, EPAS1, ESRRG, GATM, GJA1, GNAS, IGF1R, RBPJ, IL18, IRF4, LAMA4, LNPEP, PLCL1, PRKAB2, PRLR, RB1, SCD, SYK, ADAM17, THRA, NR1H2, VEGFA, PER2, ZNF516, IP6K1, MFN2, ADAMTS5, KDM1A, KDM6B, LPIN1, ADIPOR1, LGR4, ARRDC3, ELOVL6, ADIPOR2, FLCN
BP	GO:0120161	regulation of cold-induced thermogenesis	40/3408	1.56E-02	ACVR2B, ADRB1, APC, CAV1, CEBPB, EPAS1, ESRRG, GATM, GJA1, GNAS, IGF1R, RBPJ, IL18, IRF4, LAMA4, LNPEP, PLCL1, PRKAB2, PRLR, RB1, SCD, SYK, ADAM17, THRA, NR1H2, VEGFA, PER2, ZNF516, IP6K1, MFN2, ADAMTS5, KDM1A, KDM6B, LPIN1, ADIPOR1, LGR4, ARRDC3, ELOVL6, ADIPOR2, FLCN
BP	GO:0047496	vesicle transport along microtubule	17/3408	1.57E-02	HTT, KIF5B, PAFAH1B1, RAB1A, VAMP7, AP3D1, KIF3B, KIF23, AP3S2, KIF3A, TRAK1, KIF1B, AP3M1, NDE1, KIF13A, TRAK2, FYCO1
BP	GO:0048145	regulation of fibroblast proliferation	26/3408	1.57E-02	CCNA2, CDK6, CDKN1A, CREB1, CTNNB1, DACH1, EGFR, FN1, FOSL2, JUN, LIG4, MYB, MYC, PAWR, PDGFA, PDGFB, PDGFRA, PML, SFRP1, SKI, TP53, MORC3, ZMIZ1, CDC73, TP53INP1, DAB2IP
BP	GO:2000106	regulation of leukocyte apoptotic process	26/3408	1.57E-02	ADA, AXL, BCL6, CCR7, HIF1A, IL7R, ITPKB, LYN, MEF2C, KITLG, PIK3CB, PTEN, RAG1, ADAM17, TP53, NR4A3, IRS2, FADD, AURKB, RAPGEF2, SIRT1, SLC7A11, FOXP1, PRELID1, SLC39A10, FNIP1

BP	GO:0006605	protein targeting	102/3408	1.57E-02	ACOX1, AKT2, SLC25A6, SCARB2, STOM, ERBB2, GDI1, HSPA4, HSPA5, LAMP2, M6PR, MYO1C, NEDD4, PEX13, PMM2, PRKAA1, PEX5, RPL15, RPL28, RPL34, RPL37, RPS3, RPS23, SCP2, SORL1, SREBF2, SSR1, SSR3, VAMP7, UBE2D2, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, USP9X, ACOX3, BAP1, AGPS, AP3D1, SYNGR1, TAOK2, AKAP6, AKAP5, BAG4, GOSR2, AKAP12, TRAM2, ZFYVE16, ATG13, TOMM20, C2CD5, MFN2, ARIH2, TIMM17A, SEC63, NLGN1, TRAK1, ARL6IP1, VPS13A, AP4E1, TRAM1, AMACR, AP3M1, HTRA2, SPCS1, DNAJC15, SEC61A1, SH3GLB1, PEX5L, RAB8B, MIEF1, LEPROT, VPS13C, VPS37C, VPS13D, FBXW7, ZDHHC7, PEX26, PARD3, MFF, SMURF1, USP36, RHOU, ZDHHC6, TRAK2, GNPTAB, GRPEL1, LONP2, ZDHHC18, FUT10, MICALL1, TIMM50, RAB3IP, MIEF2, AP1S3, GRPEL2, VPS37D, ZDHHC20, ZDHHC23, ZDHHC22, ZDHHC21
BP	GO:0031398	positive regulation of protein ubiquitination	34/3408	1.59E-02	ARRB1, ARRB2, BRCA1, PTTG1IP, CAV1, FKBP1A, HSPA5, SMAD7, PIN1, MAPK9, PTEN, RAB1A, UBE2L3, UBE2N, CUL3, CDC14B, MTA1, CTR9, FAM107A, KDM1A, MYCBP2, HSPBP1, UBQLN1, DCUN1D1, RNF111, FANCI, FBXW7, PELI1, ARRDC3, GORASP1, ARRDC4, DCUN1D3, AMER1, RNF180
BP	GO:0051153	regulation of striated muscle cell differentiation	34/3408	1.59E-02	ARRB2, BCL2, BDNF, CAPN2, MAPK14, EDN1, EFNB2, EZH2, G6PD, KAT2A, NRG1, RBPJ, SMAD4, MEF2C, MMP14, MSX1, PIN1, PPARA, PROX1, RGS2, RGS4, XBP1, YY1, AKAP6, MORF4L2, HDAC9, FRS2, AKAP13, DKK1, FBXO22, GREM1, RBM38, CYP26B1, SIK1
BP	GO:0007032	endosome organization	25/3408	1.60E-02	SCARB2, RAB5B, SNX3, SYNJ1, SQSTM1, VPS4B, PDCD6IP, ARFGEF2, SNF8, TMCC1, DNAJC13, CORO1C, VPS36, HOOK1, CHMP5, VPS37C, PI4K2B, LAPTM4B, TMEM127, CHMP1B, RAB22A, HOOK3, CHMP7, EXOC8, VPS37D
BP	GO:0009749	response to glucose	52/3408	1.60E-02	ACVR2B, RHOA, ARRB1, CASP3, CDKN1B, COL6A2, EFNA5, EGR1, ENSA, FOXO3, GJA1, HIF1A, HMGCR, HNF4A, IGF1R, KIF5B, LDHA, LRP1, SMAD2, MEN1, OPA1, PAX2, CDK16, PDK3, PFKFB2, PPARD, PPP3CA, PRKAA1, PRKCE, PTEN, PTPRN2, TRA2B, SLC8A1, SOX4, SRF, VAMP2, HNF1B, TCF7L2, THBS1, TIAM1, XBP1, DYNLL1, IRS2, RAB11B, MAP4K4, UNC13B, ATG7, RAB11FIP2, TXN2, SIN3A, SESN2, ACVR1C
BP	GO:0031103	axon regeneration	18/3408	1.62E-02	BCL2, CTNNA1, DAG1, EPHA4, ISL1, JUN, LRP1, MAP1B, MTR, NTRK3, PTEN, PTPRF, STK24, KLF4, LRIG2, MAPK8IP3, RGMA, KREMEN1
BP	GO:0006022	aminoglycan metabolic process	46/3408	1.62E-02	CD44, NCAN, DCN, EXTL2, EXTL3, FGF2, FOXC1, GCNT2, HAS3, NDST1, IDS, CHST6, NFKB1, PDGFB, PIM1, PRELP, SDC2, SDC4, ST3GAL1, SLC9A1, UGDH, CHST1, B4GALT2, B4GALT6, NDST3, HS2ST1, SPOCK2, HS3ST3A1, HS3ST1, ABCC5, GPC6, UST, ST3GAL6, HPSE, LYVE1, GLCE, CHST15, CSGALNACT2, CSGALNACT1, CHST7, XYLT2, ITIH5, CHST9, B3GNT5, HS6ST2, AGRN
BP	GO:0055024	regulation of cardiac muscle tissue development	30/3408	1.62E-02	ARRB2, BMPR1A, CREB1, MAPK14, EDN1, EFNB2, FGF2, G6PD, GATA6, KAT2A, GJA1, NRG1, RBPJ, JARID2, SMAD4, MEF2C, PIM1, PIN1, PPARA, MAPK1, PTEN, RGS2, RGS4, TGFBR1, TGFBR3, YY1, AKAP6, FRS2, DKK1, GREM1
BP	GO:0001707	mesoderm formation	24/3408	1.62E-02	BMP7, BMPR1A, BMPR2, FOXC1, ITGA3, ITGB1, SMAD2, NF2, PAX2, PRKAR1A, SNAI1, SRF, TAL1, KDM6A, NR4A3, HMGA2, ITGA8, CHRD, KLF4, HAND1, DKK1, KDM6B, EPB41L5, CRB2
BP	GO:0006073	cellular glucan metabolic process	24/3408	1.62E-02	AKT2, CALM1, GAA, GSK3B, GYS1, IGF2, IL6ST, INSR, ENPP1, PHKA1, PHKG2, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PYGB, UGP2, DYRK2, IRS2, PER2, EPM2AIP1, PASK, STK40
BP	GO:0044042	glucan metabolic process	24/3408	1.62E-02	AKT2, CALM1, GAA, GSK3B, GYS1, IGF2, IL6ST, INSR, ENPP1, PHKA1, PHKG2, PPP1CA, PPP1CB, PPP1CC, PPP1R2, PPP1R3C, PYGB, UGP2, DYRK2, IRS2, PER2, EPM2AIP1, PASK, STK40
BP	GO:0043551	regulation of phosphatidylinositol 3-kinase activity	19/3408	1.64E-02	CCR7, FGF2, FGFR3, KIT, LYN, PDGFB, PDGFRA, SRC, SOCS1, SOCS2, SOCS6, KLF4, SOCS5, VAV3, ATG14, SOCS7, PIK3IP1, WDR81, DAB2IP
BP	GO:0044380	protein localization to cytoskeleton	19/3408	1.64E-02	APC, CSNK1D, DIAPH1, GOLGB1, GSK3B, HNRNPU, MAP1A, MID1, AURKA, KLHL21, CEP250, MAPRE3, ABHD17B, ANLN, NSFL1C, ABHD17C, HOOK3, UBXN2B, TTBK2
BP	GO:0008333	endosome to lysosome transport	20/3408	1.66E-02	RHOB, LYST, M6PR, SORT1, VAMP7, VCP, AP3D1, VPS4B, HMGXB4, ATG14, DENND3, TRAK1, MGRN1, HOOK1, CHMP5, EPG5, KIF13A, TRAK2, HOOK3, RAB12
BP	GO:1902369	negative regulation of RNA catabolic process	20/3408	1.66E-02	MAPK14, DKC1, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPU, PARN, PKP1, ZFP36, THRAP3, TOB1, SYNCRIP, PAIP1, IGF2BP1, HNRNPA0, LARP1, TARDBP, PABPC1, RBM38
BP	GO:0048010	vascular endothelial growth factor receptor signaling pathway	29/3408	1.67E-02	RHOA, AXL, CDC42, CRK, MAPK14, FOXC1, FLT4, NCKAP1L, HIF1A, ITGA5, ITGAV, NCK1, NEDD4, PAK2, PIK3CB, PTPN1, PXN, SRC, VEGFA, FZD4, NCK2, NRP1, ROCK2, WASF2, VAV3, NCKAP1, MYOF, CYFIP2, DAB2IP
BP	GO:0098876	vesicle-mediated transport to the plasma membrane	29/3408	1.67E-02	TRIM23, ARF1, CSK, GOLGA4, RAB8A, NSF, SNAP25, SPTBN1, STX3, VAMP2, VAMP7, RABEP1, RAB11B, PREPL, SNX17, ARFRP1, LYPLA1, ARFGEF2, EXOC5, RAB31, EXOC6B, GOLPH3L, VPS35, KIF13A, C16orf70, MICALL1, PKDCC, EXOC8, STEAP2

BP	GO:0010869	regulation of receptor biosynthetic process	10/3408	1.70E-02	EDN1, HDAC2, HIF1A, HNRNPK, HOXA5, ITGAV, FURIN, PPARA, SEC24A, ANKRD13C
BP	GO:0043496	regulation of protein homodimerization activity	10/3408	1.70E-02	ARF6, BAK1, BCL2, NRG1, HSPA5, ISL1, MEF2C, TRAF4, GNL3L, AIDA
BP	GO:0046628	positive regulation of insulin receptor signaling pathway	10/3408	1.70E-02	GNAI2, IGF2, OPA1, PTPN11, SORL1, SRC, SIRT1, ADIPOR1, NUCKS1, OSBPL8
BP	GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	10/3408	1.70E-02	RUNX2, EP300, HIF1A, RBPJ, SMAD4, TP53, VEGFA, XBP1, SESN2, CHD6
BP	GO:1901984	negative regulation of protein acetylation	10/3408	1.70E-02	BRCA1, GSK3B, HDAC2, SET, SNCA, TWIST1, ATG5, SIRT1, SIN3A, ZNF451
BP	GO:1903077	negative regulation of protein localization to plasma membrane	10/3408	1.70E-02	BCL2L1, AP2M1, CSK, DAB2, GBP1, NUMB, LYPLA1, RHOQ, TMBIM1, PKDCC
BP	GO:2000773	negative regulation of cellular senescence	10/3408	1.70E-02	ABL1, BCL6, CDK6, MAP3K3, TERT, TWIST1, HMGA2, AKT3, PLK2, SIRT1
BP	GO:1903825	organic acid transmembrane transport	38/3408	1.70E-02	ACACA, AKT2, CPT1A, CLN8, KCNJ10, PRKAB2, RGS2, RGS4, SLC1A2, SLC1A4, SLC1A5, SLC6A8, SLC6A9, SLC7A1, SLC7A2, SLC16A1, THBS1, SLC7A5, IRS2, PER2, SLC5A6, SLC7A6, SLC16A7, SLC23A2, SLC25A15, ARL6IP1, SLC7A11, SLC38A2, SLC25A38, LRRC8D, SLC25A32, SLC38A1, SLC46A1, SLC16A10, SLC36A4, SLC43A2, EMB, SLC36A1
BP	GO:1905039	carboxylic acid transmembrane transport	38/3408	1.70E-02	ACACA, AKT2, CPT1A, CLN8, KCNJ10, PRKAB2, RGS2, RGS4, SLC1A2, SLC1A4, SLC1A5, SLC6A8, SLC6A9, SLC7A1, SLC7A2, SLC16A1, THBS1, SLC7A5, IRS2, PER2, SLC5A6, SLC7A6, SLC16A7, SLC23A2, SLC25A15, ARL6IP1, SLC7A11, SLC38A2, SLC25A38, LRRC8D, SLC25A32, SLC38A1, SLC46A1, SLC16A10, SLC36A4, SLC43A2, EMB, SLC36A1
BP	GO:0006672	ceramide metabolic process	28/3408	1.72E-02	ASAH1, CLN8, GALC, GM2A, ITGB8, NAGA, PPP2CA, PPP2R1A, PRKAA1, UGCG, ST8SIA4, ALDH5A1, NSMAF, SGPL1, B4GALT6, SPTLC1, CERS1, HTRA2, ORMDL2, ST6GALNAC6, ST8SIA3, ACER3, ORMDL1, ORMDL3, SAMD8, SGMS2, CERS6, ACER2
BP	GO:1903578	regulation of ATP metabolic process	35/3408	1.72E-02	AK4, RHOA, ATP7A, HIF1A, INSR, NUP88, NUP98, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, SNCA, STAT3, TP53, VCP, NCOR1, POM121, NUP50, SLC2A6, ISCU, DNAJC15, DDIT4, NDC1, NUP133, BEND3, SEH1L, DNAJC30, UQCC2, FLCN, PDE12, NUP43, POM121C
BP	GO:1904018	positive regulation of vasculature development	59/3408	1.74E-02	ABL1, ADM, RHOB, BRCA1, BTG1, RUNX1, EFNB2, EGR1, FGF1, FGF2, GAB1, GATA2, GATA6, HIF1A, HK2, IL6R, ISL1, ITGA5, ITGB1, ITGB8, JUP, KIT, MDK, MAP3K3, SERPINE1, PDGFB, PIK3C2A, PKM, PRKCA, PTGIS, CX3CL1, SOD2, STAT3, STIM1, TERT, THBS1, TWIST1, VEGFA, XBP1, ADAM12, HMGA2, NRP1, KLF4, RAPGEF2, HDAC9, AKT3, RAPGEF3, PLK2, SIRT1, PPP1R16B, HIPK2, ERAP1, AGGF1, HIF1AN, ADM2, MTDH, BMPER, HIPK1, EMC10
BP	GO:0010390	histone monoubiquitination	12/3408	1.74E-02	RAG1, RNF2, SKP1, CUL4B, CTR9, PCGF3, WAC, BCOR, ATXN7L3, CDC73, PCGF5, RNF168
BP	GO:0016577	histone demethylation	12/3408	1.74E-02	JARID2, KDM5A, KDM6A, KDM4A, KDM5B, KDM2A, KDM1A, PHF8, KDM6B, KDM3B, JMJD1C, KDM1B
BP	GO:0030970	retrograde protein transport, ER to cytosol	12/3408	1.74E-02	SEL1L, UBE2G2, VCP, EDEM1, HERPUD1, BCAP31, DERL2, UBE2J1, YOD1, NPLOC4, RHBDD1, SYVN1
BP	GO:0031365	N-terminal protein amino acid modification	12/3408	1.74E-02	CREBBP, EP300, PPM1B, SOX4, KAT2B, METAP2, NAA35, PDF, NAA40, NAA25, NAA50, NAA30

BP	GO:0044068	modulation by symbiont of host cellular process	12/3408	1.74E-02	BCL2L1, GAPDH, ITGAV, KPNA1, KPNA3, NTRK3, SERPINB9, PABPN1, VAPA, BCL2L11, TNIP1, ATG7
BP	GO:0060536	cartilage morphogenesis	12/3408	1.74E-02	COL6A2, COL12A1, HOXA5, LRP6, MATN2, MEF2C, MSX1, SNAI2, SNAI1, STC1, WNT7B, HAND1
BP	GO:0090162	establishment of epithelial cell polarity	12/3408	1.74E-02	ARF6, RHOA, CDC42, HES1, OPHN1, CYTH3, CYTH1, CLASP1, FERMT1, FRMD4A, PARD3, MYO18A
BP	GO:1903513	endoplasmic reticulum to cytosol transport	12/3408	1.74E-02	SEL1L, UBE2G2, VCP, EDEM1, HERPUD1, BCAP31, DERL2, UBE2J1, YOD1, NPLOC4, RHBDD1, SYVN1
BP	GO:2000171	negative regulation of dendrite development	12/3408	1.74E-02	ARF6, GSK3B, HDAC2, PPP3CA, PTEN, RAPGEF2, PLK2, NLGN1, FSTL4, ASAP1, BCL11A, GORASP1
BP	GO:2000765	regulation of cytoplasmic translation	12/3408	1.74E-02	DPH1, FMR1, NCK1, CNBP, CPEB3, ZNF385A, YTHDF2, CPEB4, UNK, DNAJC24, CPEB2, DPH3
BP	GO:0043470	regulation of carbohydrate catabolic process	27/3408	1.76E-02	SCARB2, HIF1A, INSR, NUP88, NUP98, PFKFB2, PFKFB3, PFKFB4, PGAM1, PHKG2, PPARA, PPP1CA, PPP1CB, PRKAA1, RANBP2, STAT3, TP53, NCOR1, POM121, NUP50, SLC2A6, DDIT4, NDC1, NUP133, SEH1L, NUP43, POM121C
BP	GO:0045185	maintenance of protein location	31/3408	1.77E-02	CAV1, DAG1, FBN1, FBN2, FLNB, HK1, HK2, HNRNPU, HSPA5, INSIG1, JUP, LTBP1, MXI1, PKD1, PML, TWF1, SKP1, SORL1, SP100, TLN1, TXN, LATS1, G3BP2, VPS13A, MORC3, ARL2BP, GET4, SUFU, VPS13C, VPS13D, ANKRD13C
BP	GO:0055017	cardiac muscle tissue growth	31/3408	1.77E-02	BMPR1A, MAPK14, S1PR1, EDN1, FGF2, FOXC1, G6PD, GATA6, GJA1, RBPJ, JARID2, MEF2C, PIM1, PIN1, PPARA, PRKAR1A, MAPK1, PTEN, RGS2, RGS4, MAP2K4, TGFBR1, TGFBR3, YY1, SORBS2, AKAP6, PDLIM5, AKAP13, HEG1, NDRG4, ARID2
BP	GO:0019318	hexose metabolic process	63/3408	1.80E-02	AKT2, CPT1A, MAPK14, EP300, FOXO1, FUT8, G6PD, GAA, GAPDH, KAT2A, GOT2, GPI, GSK3B, HK1, HK2, IGF2, FOXK2, INSR, MAN2A1, MPI, PDK3, PDK4, ENPP1, PFKFB2, PFKFB3, PFKFB4, PGAM1, PHKG2, PKM, PMM2, PPARA, PPARD, PPP1CA, PPP1CB, PRKAA1, RANBP2, RORA, SRC, TP53, ALDH5A1, DYRK2, CHST1, IRS2, KAT2B, PER2, H6PD, EPM2AIP1, NCOA2, ARPP19, WDTC1, PASK, SIRT1, POFUT1, SERP1, ADIPOR1, CHST15, SESN2, FUT10, GLYCTK, SOGA1, SIK1, BRAT1, FOXK1
BP	GO:0046632	alpha-beta T cell differentiation	30/3408	1.85E-02	ABL1, ADA, RHOA, ATP7A, BCL2, BCL6, PRDM1, RUNX1, RUNX3, CBFB, GATA3, NCKAP1L, IL18, IRF1, IRF4, ITPKB, SMAD7, MYB, PTGER4, RORA, SATB1, STAT3, SYK, TCF7, SOCS1, AP3D1, CD83, SOCS5, FOXP1, BCL11B
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	30/3408	1.85E-02	BMPR1A, HBEGF, S1PR1, EDN1, EGFR, FGF2, GNAI2, GNAI3, HMGCR, IGFBP5, IL6R, IL18, IRAK1, JUN, MEF2D, MYB, PDGFB, PTAFR, CX3CL1, STAT1, TERT, THBS1, NR4A3, ADAMTS1, MFN2, CALCRL, LDLRAP1, FOXP1, FOXJ2, RBPMS2
BP	GO:0003197	endocardial cushion development	16/3408	1.86E-02	JAG1, BMP7, BMPR1A, BMPR2, RBPJ, ISL1, SMAD4, MDM4, MSX1, ROBO1, SNAI2, SNAI1, TGFBR1, TWIST1, DCHS1, HEYL
BP	GO:0060412	ventricular septum morphogenesis	16/3408	1.86E-02	BMPR2, HES1, RBPJ, SMAD4, SMAD7, PROX1, ROBO1, SOX4, SOX11, TBX3, TGFBR1, TGFBR3, FZD1, CITED2, HEYL, VANGL2
BP	GO:0060999	positive regulation of dendritic spine development	16/3408	1.86E-02	ARF1, FMR1, CAPRIN1, OPA1, PAFAH1B1, PAK3, MAPK6, TIAM1, KALRN, DLG5, ACTR2, CPEB3, NLGN1, SHANK2, C21orf91, BHLHB9
BP	GO:0061001	regulation of dendritic spine morphogenesis	16/3408	1.86E-02	ADAM10, CFL1, EPHA4, CAPRIN1, OPA1, PAFAH1B1, PAK3, PTEN, TIAM1, KALRN, ACTR2, ABI2, PDLIM5, NLGN1, SIPA1L1, BHLHB9
BP	GO:0036303	lymph vessel morphogenesis	9/3408	1.90E-02	ACVR2B, BMPR2, FOXC1, FLT4, PKD1, PROX1, PTPN14, VEGFA, VASH1
BP	GO:0008542	visual learning	17/3408	1.93E-02	CREB1, CTNS, HIF1A, HMGCR, ITGB1, KIT, KRAS, MECP2, MEIS2, PDE1B, RAG1, B4GALT2, SYNGAP1, SLC7A11, NPTN, RIC8A, NDRG4
BP	GO:0051653	spindle localization	17/3408	1.93E-02	CENPA, HTT, MAD2L1, MAP4, MYH9, PAFAH1B1, PAX6, WASL, ARHGEF2, ACTR2, SPRY1, CLASP1, NDE1, NSFL1C, FMN2, SPIRE1, UBXN2B

BP	GO:0030198	extracellular matrix organization	88/3408	1.93E-02	ABL1, ADAM10, APBB2, ATP7A, CAPN2, CD44, CD47, COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL4A5, COL4A6, COL5A1, COL5A2, COL6A2, COL11A1, COL12A1, COL19A1, HAPLN1, NCAN, CTSS, DAG1, DCN, ERCC2, FBN1, FBN2, FGF2, FOXC1, FN1, HAS3, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, LAMA4, LAMC1, LAMC2, LOXL2, LRP1, MMP10, MMP14, NID1, TNFRSF11B, P4HA1, FURIN, SERPINE1, PDGFA, PDGFB, PDGFRA, RB1, SPARC, TGFBR1, THBS1, TIMP2, TLL1, TNFRSF1B, VCAM1, PXDN, ADAM12, ITGA8, SH3PXD2A, SPOCK2, POSTN, ADAMTS5, PHLDB1, CLASP1, FLRT2, GREM1, COL5A3, FERMT1, CSGALNACT1, SULF2, ADAMTS9, JAM2, RIC8A, THSD4, ANTXR1, COL27A1, PHLDB2, EXOC8, OLFML2A, SH3PXD2B, ATXN1L, AGRN
BP	GO:0038034	signal transduction in absence of ligand	23/3408	1.94E-02	BAK1, BCL2, BCL2L1, CASP3, CTNNA1, EYA4, FOXO3, MKNK2, GSK3B, ITGAV, MCL1, KITLG, PPP1CA, PPP2R1A, CX3CL1, SNAI2, TERT, FADD, BCL2L11, SGK3, APPL1, HTRA2, MOAP1
BP	GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	23/3408	1.94E-02	BAK1, BCL2, BCL2L1, CASP3, CTNNA1, EYA4, FOXO3, MKNK2, GSK3B, ITGAV, MCL1, KITLG, PPP1CA, PPP2R1A, CX3CL1, SNAI2, TERT, FADD, BCL2L11, SGK3, APPL1, HTRA2, MOAP1
BP	GO:0098739	import across plasma membrane	32/3408	1.95E-02	ATP1B1, ATP2B4, HCN2, CACNA2D1, CLN8, KCNJ2, KCNJ3, KCNJ10, RGS2, RGS4, SLC1A2, SLC1A5, SLC7A1, SLC7A2, SLC8A1, SLC9A1, SLC12A4, TRPM2, PER2, SLC12A6, SLC9A6, SLC12A7, ARL6IP1, ISCU, SLC7A11, SLC39A6, SLC39A10, SLC12A5, SLC39A8, SLC9A7, SLC46A1, SLC36A4
BP	GO:0051204	protein insertion into mitochondrial membrane	13/3408	1.95E-02	BCL2, PPP3R1, MAPK8, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, BCL2L11, BBC3, MOAP1, BMF
BP	GO:0060603	mammary gland duct morphogenesis	13/3408	1.95E-02	AR, CSF1, LRP6, PGR, PML, PTCH1, SRC, TBX3, VDR, BTRC, NTN1, KDM5B, WNT4
BP	GO:1901890	positive regulation of cell junction assembly	13/3408	1.95E-02	ABL1, CAV1, PTPRJ, SDC4, SFRP1, TSC1, VEGFA, IQGAP1, NRP1, MAP4K4, WNT4, EPB41L5, FMN1
BP	GO:0030072	peptide hormone secretion	63/3408	1.96E-02	ACVR2B, SLC25A6, ARRB1, CACNA1C, CACNA1E, CPT1A, EDN1, EFNA5, EGFR, ENSA, GJA1, HIF1A, HMGCR, HNF4A, ISL1, ITPR1, ITPR2, KIF5B, LRP1, SMAD2, MYO5A, CDK16, PFKFB2, PPARD, PPP3CA, PRKCA, PRKCE, PTPN11, PTPRN2, RAB1A, RFX3, SFRP1, SLC16A1, SNAP25, SOX4, HNF1B, TCF7L2, TFR2, TIAM1, DYNLL1, IRS2, PER2, KALRN, SYT7, RAB11B, AIMP1, MAP4K4, CLOCK, RAPGEF3, RAB11FIP2, PASK, TARDBP, ARL2BP, SERP1, RAB8B, UBE2Q1, CHD7, NLGN2, UQCC2, RASL10B, ACVR1C, BMP8A, SNX19
BP	GO:1900024	regulation of substrate adhesion-dependent cell spreading	18/3408	1.96E-02	ABL1, ACTN4, CALR, CDC42, CRK, CRKL, EFNA5, GBP1, MDK, NEDD9, RREB1, NRP1, ARPC2, POSTN, KANK1, CORO1C, RCC2, MYADM
BP	GO:1902373	negative regulation of mRNA catabolic process	18/3408	1.96E-02	MAPK14, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPU, PKP1, ZFP36, THRAP3, TOB1, SYNCRIP, PAIP1, IGF2BP1, HNRNPA0, LARP1, TARDBP, PABPC1, RBM38
BP	GO:0048704	embryonic skeletal system morphogenesis	28/3408	1.97E-02	BMP7, RUNX2, COL11A1, CTNNB1, DLX2, MEGF8, GNAS, HOXA3, HOXA5, HOXA7, HOXB3, HOXB5, HOXB8, HOXC4, SMAD2, MEF2C, MMP14, PDGFRA, PRRX1, SOX11, ZEB1, TGFBR1, TWIST1, SATB2, NIPBL, MTHFD1L, SIX4, RDH10
BP	GO:0030032	lamellipodium assembly	21/3408	1.97E-02	ATP7A, CDC42, S1PR1, FER, ITGB1, KIT, ABLIM1, NCK1, TWF1, VCL, NCK2, ARPC2, WASF2, VAV3, NCKAP1, ARFIP2, SH2B1, AUTS2, AKIRIN1, WHAMM, SPATA13
BP	GO:0043550	regulation of lipid kinase activity	21/3408	1.97E-02	CCR7, FGF2, FGFR3, KIT, LYN, PDGFB, PDGFRA, RB1, RBL2, SRC, SOCS1, SOCS2, SOCS6, KLF4, SOCS5, VAV3, ATG14, SOCS7, PIK3IP1, WDR81, DAB2IP
BP	GO:0046579	positive regulation of Ras protein signal transduction	21/3408	1.97E-02	ARRB1, COL3A1, CRKL, CSF1, GRB2, RAPGEF1, NRG1, ITPKB, KRAS, LYN, KITLG, NOTCH2, ROBO1, SHC1, SHOC2, IRS2, F2RL3, MAP4K4, AKAP13, AUTS2, SYNPO2L
BP	GO:0048488	synaptic vesicle endocytosis	19/3408	1.97E-02	ACTB, ARF6, CALM3, CANX, OPHN1, SH3GL2, SNCA, SYT1, SYNJ1, NLGN1, SYT11, PIP5K1C, SYT17, NLGN2, KIAA1109, STON2, BTBD9, FCHO2, SYT2
BP	GO:0140238	presynaptic endocytosis	19/3408	1.97E-02	ACTB, ARF6, CALM3, CANX, OPHN1, SH3GL2, SNCA, SYT1, SYNJ1, NLGN1, SYT11, PIP5K1C, SYT17, NLGN2, KIAA1109, STON2, BTBD9, FCHO2, SYT2
BP	GO:0043966	histone H3 acetylation	20/3408	1.98E-02	BRCA1, CHEK1, DR1, GATA3, KAT2A, IRF4, SMAD4, KMT2A, KAT6A, KAT2B, LDB1, KAT7, SIRT1, WBP2, SIN3A, ZNF451, BRPF3, ING4, TAF9B, MEAF6

BP	GO:0046794	transport of virus	20/3408	1.98E-02	CAV1, FMR1, KPNA1, KPNA3, NUP88, NUP98, RAN, RANBP2, XPO1, POM121, NUP50, KPNA6, UBAP1, VPS37C, NDC1, NUP133, SEH1L, VPS37D, NUP43, POM121C
BP	GO:0007059	chromosome segregation	78/3408	2.02E-02	APC, ATM, ATRX, BRCA1, CDC42, RCC1, CTNNB1, DDX3X, DUSP1, ECT2, ERCC2, NR3C1, HNRNPU, IK, INCENP, MAD2L1, MLH1, PPP2R1A, RAD21, RAN, RB1, RPS3, TOP2B, UVRAG, USP9X, SMC1A, CUL3, TNKS, PRC1, LATS1, CCNE2, AURKB, TRIP13, CIAO1, KIF23, VPS4B, PUM1, ACTR2, CTCF, STAG2, KIF2C, TLK2, PDS5B, POGZ, PDS5A, MAU2, NIPBL, CHMP5, INO80, NDE1, CHTF8, PINX1, CDCA8, FBXW7, NDC1, RIOK2, PCID2, RCC2, FMN2, SMARCAD1, CHMP1B, HECW2, CEP85, SMC6, NAA50, SEH1L, SETDB2, SLX4, CHMP7, ESCO1, RMI2, ARL8A, PHF13, TTL, AGO4, KLHDC8B, SKA2, NUP43
BP	GO:0044774	mitotic DNA integrity checkpoint	31/3408	2.02E-02	ATM, CCND1, CDKN1A, CDKN1B, FOXN3, ATF2, EP300, MDM4, FOXO4, CNOT4, PML, RBL2, SOX4, AURKA, TFDP1, TFDP2, TOP2B, TP53, BTG2, HMGA2, CNOT8, TAOK2, PLK2, CNOT1, ZNF385A, GIGYF2, TRIAP1, CNOT6, TAOK1, ZNF830, E2F7
BP	GO:0007173	epidermal growth factor receptor signaling pathway	34/3408	2.02E-02	ABL1, CBL, CDC42, HBEGF, EGFR, FER, GAB1, GRB2, HIP1, PIK3C2A, PTPN11, PTPN12, PTPRJ, SH3GL2, SHC1, SOS1, SRC, ADAM17, TGFA, NCK2, DGKD, IQGAP1, GPRC5A, RPS6KA5, SOCS5, RASSF2, SPRY1, AGR2, ERRFI1, FBXW7, AFAP1L2, SOCS4, DAB2IP, EPGN
BP	GO:0010001	glial cell differentiation	56/3408	2.02E-02	ABL1, AKT2, RHOA, CDK6, CSK, CTNNB1, DAG1, DLX2, EGFR, EPHA4, ERBB2, ERCC2, FGF5, HDAC2, NRG1, HES1, ID4, IL6ST, ILK, KCNJ10, KRAS, LDLR, LRP1, LYN, MAPT, MDK, NAB1, NFIB, NTRK3, PAX2, PAX6, SERPINE2, POU3F2, MAPK1, MAPK3, PTEN, PTPN11, SKI, SOX4, SOX11, STAT3, TAL1, TNFRSF1B, B4GALT6, TSPAN2, DUSP10, NCSTN, DICER1, BACE2, SOX8, ADAM22, PARD3, PRDM8, METTL14, METRN, SH3TC2
BP	GO:0022011	myelination in peripheral nervous system	11/3408	2.02E-02	AKT2, DAG1, NRG1, ILK, NTRK3, POU3F2, SKI, DICER1, ADAM22, PARD3, SH3TC2
BP	GO:0032292	peripheral nervous system axon ensheathment	11/3408	2.02E-02	AKT2, DAG1, NRG1, ILK, NTRK3, POU3F2, SKI, DICER1, ADAM22, PARD3, SH3TC2
BP	GO:1903203	regulation of oxidative stress-induced neuron death	11/3408	2.02E-02	CTNNB1, HIF1A, MCL1, TSC1, NR4A3, FZD1, LANCL1, ATG7, SLC7A11, OXR1, FBXW7
BP	GO:0055013	cardiac muscle cell development	27/3408	2.03E-02	CXADR, EDN1, G6PD, HNRNPU, SMAD4, MEF2A, MYH10, PDGFRA, PIN1, PPARA, PROX1, RGS2, RGS4, MAP2K4, SGCD, SLC8A1, SRF, TBX3, VEGFA, YY1, SORBS2, AKAP6, ATG5, NEBL, PDLIM5, AKAP13, ALPK3
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	47/3408	2.04E-02	ADAR, AXL, CAV1, RUNX1, CBFB, CSF1, CYLD, EDN1, HIF1A, UBE2K, IFNAR2, IKBKB, IL1R1, IRAK1, IRAK2, LIFR, PAFAH1B1, PTPN1, PTPN11, PTPRC, ABCE1, ROBO1, STAT1, SYK, ADAM17, TRAF1, NR1H2, PXDN, MADD, SOCS1, FADD, SPATA2, SH2B3, RBCK1, CLIP3, LSM14A, YTHDF2, PIAS4, PARP14, OTUD4, MAVS, MUL1, SPPL2A, RFFL, ZNF675, HIPK1, YTHDF3
BP	GO:1904951	positive regulation of establishment of protein localization	106/3408	2.04E-02	ABL1, AKT2, ARF1, ARF6, ARRB1, BCL2, CCT6A, MAPK14, DKC1, ECT2, EGFR, STOM, ERBB2, GAPDH, GATA3, GJA1, GPI, GSK3B, HIF1A, HK1, IL1RAP, ISL1, JUP, KIF5B, IPO5, LRP1, MBP, MDK, MYH10, MYO1C, OAZ2, PFKFB2, PPARD, PPP3R1, PRKAA1, PRKCE, MAPK1, MAPK3, MAPK8, PTGER4, RAN, SORL1, SOX4, SPTBN1, SRC, SREBF2, VAMP2, SYK, TCF7L2, TFDP1, TFDP2, TP53, TWIST1, UBE2D3, UBE2L3, XBP1, YWHAE, YWHAG, FZD5, BAP1, TP63, DYNLL1, IRS2, ADAM9, AKAP12, CEP135, EDEM1, ATG13, C2CD5, BCAP31, TENM1, NUTF2, RAPGEF3, ARIH2, UNC13B, ANP32B, POSTN, SEC24A, TARDBP, CD2AP, CADM1, IL17RA, BBC3, SERP1, HTRA2, SH3GLB1, UBR5, MIEF1, LEPROT, GOLPH3L, FBXW7, FERMT1, FRMD4A, VPS35, RIOK2, PANX2, SAR1A, MFF, MAVS, NLGN2, USP36, RHOU, XPO4, MIEF2, CEP120, MYO18A
BP	GO:0002070	epithelial cell maturation	8/3408	2.04E-02	CDKN1A, GJA1, HIF1A, FOXA1, HOXA5, PGR, RFX3, XBP1
BP	GO:0003222	ventricular trabecula myocardium morphogenesis	8/3408	2.04E-02	BMPR1A, NRG1, RBPJ, TGFBR1, UBE4B, DLL4, CHD7, HEG1
BP	GO:0014067	negative regulation of phosphatidylinositol 3-kinase signaling	8/3408	2.04E-02	SERPINE2, PTEN, TWIST1, KLF4, BTN2A2, STAMBP, PIK3IP1, DAB2IP
BP	GO:0035372	protein localization to microtubule	8/3408	2.04E-02	DIAPH1, HNRNPU, MAP1A, MID1, MAPRE3, ABHD17B, ABHD17C, TTBK2
BP	GO:0035970	peptidyl-threonine dephosphorylation	8/3408	2.04E-02	DUSP1, DUSP5, PPM1B, PPP1CA, PPP2CA, PPM1D, DUSP10, DUSP18

BP	GO:0048791	calcium ion-regulated exocytosis of neurotransmitter	8/3408	2.04E-02	ATP2A2, SYT1, SYT7, RIMS3, SYT11, SYT17, SYT2, RIMS4
BP	GO:0061158	3'-UTR-mediated mRNA destabilization	8/3408	2.04E-02	ZFP36L1, ZFP36L2, HNRNPD, UPF1, ZFP36, CPEB3, RBM23, TRIM71
BP	GO:0072176	nephric duct development	8/3408	2.04E-02	EFNB2, EPHA4, EPHA7, GATA3, PAX2, PKD1, HNF1B, AHI1
BP	GO:1904294	positive regulation of ERAD pathway	8/3408	2.04E-02	CAV1, ATXN3, USP13, EDEM1, HERPUD1, BCAP31, UBQLN2, UBQLN1
BP	GO:2000369	regulation of clathrin-dependent endocytosis	8/3408	2.04E-02	DAB2, PIK3CB, SH3GL2, WASL, TNK2, AAK1, SYT11, UBQLN2
BP	GO:2001224	positive regulation of neuron migration	8/3408	2.04E-02	MDK, ARHGEF2, RAPGEF2, SEMA3A, NIPBL, NSMF, SEMA6A, DAB2IP
BP	GO:0003183	mitral valve morphogenesis	6/3408	2.05E-02	BMPR1A, BMPR2, SMAD6, SOX4, TWIST1, DCHS1
BP	GO:0006930	substrate-dependent cell migration, cell extension	6/3408	2.05E-02	MYH10, NCK1, OPHN1, NRP1, NTN1, CD2AP
BP	GO:0007028	cytoplasm organization	6/3408	2.05E-02	KIF5B, SOS1, FOSL1, RRN3, ZMIZ1, PLD6
BP	GO:0010749	regulation of nitric oxide mediated signal transduction	6/3408	2.05E-02	ATP2B4, EGFR, GUCY1A2, THBS1, VEGFA, NOS1AP
BP	GO:0038063	collagen-activated tyrosine kinase receptor signaling pathway	6/3408	2.05E-02	COL1A1, COL4A1, COL4A2, COL4A5, COL4A6, SYK
BP	GO:0071609	chemokine (C-C motif) ligand 5 production	6/3408	2.05E-02	DDX3X, TUSC2, MAVS, MUL1, SIRPA, MCOLN2
BP	GO:1904338	regulation of dopaminergic neuron differentiation	6/3408	2.05E-02	CSNK1D, CSNK1E, GSK3B, SFRP1, TIAM1, DKK1
BP	GO:2000271	positive regulation of fibroblast apoptotic process	6/3408	2.05E-02	BTG1, SFRP1, TP63, STK17B, STK17A, BCL2L11
BP	GO:0072384	organelle transport along microtubule	26/3408	2.06E-02	CDC42, HTT, HIF1A, KIF5B, MAP1B, MAPT, NEFH, OPA1, PAFAH1B1, RAB1A, VAMP7, WASF1, AP3D1, KIF3B, KIF23, AP3S2, KIF3A, TRAK1, KIF1B, BICD2, AP3M1, NDE1, KIF13A, TRAK2, FYCO1, TMEM201
BP	GO:0045444	fat cell differentiation	57/3408	2.06E-02	ADRB1, JAG1, AKT2, CCND1, ZFP36L1, ZFP36L2, RUNX1T1, CEBPB, CEBPD, CREB1, ATF2, MAPK14, EP300, FOXO1, GATA2, GATA3, HNRNPU, HES1, ID4, INSIG1, ITGA6, SMAD6, ALDH6A1, ENPP1, PPARD, RGS2, RORA, SORT1, SFRP1, SNAI2, STK4, TCF7L2, TRIO, XBP1, ZFP36, NR4A3, HMGA2, SOCS1, PER2, KLF4, ZNF516, DUSP10, SIRT1, NIPBL, ZNF385A, CLIP3, FBXO9, TRIB2, SOX8, ERAP1, TBL1XR1, ARID5B, OSBPL8, TMEM120B, CCDC71L, ZADH2, SH3PXD2B
BP	GO:0038083	peptidyl-tyrosine autophosphorylation	14/3408	2.06E-02	ABL1, ABL2, CAV1, DYRK1A, EGFR, IGF1R, INSR, LYN, MAPK3, SRC, VEGFA, IQGAP1, TNK2, GREM1
BP	GO:1904358	positive regulation of telomere maintenance via	14/3408	2.06E-02	ATM, ATR, CCT6A, CTNNB1, DKC1, MAP3K4, PARN, MAPK1, MAPK3, XRCC5, TNKS, AURKB, RTEL1, HMBOX1

		telomere lengthening			
BP	GO:0016051	carbohydrate biosynthetic process	55/3408	2.11E-02	ADCYAP1R1, AKT2, EP300, EXTL2, EXTL3, FOXO1, FUT8, G6PD, GAPDH, KAT2A, GOT2, GPI, GSK3B, GYS1, HAS3, NDST1, IGF2, FOXK2, IMPA2, INSR, NFKB1, P2RY1, PDGFB, ENPP1, PGAM1, PHKG2, PPARA, PPP1CA, PPP1CB, PPP1R3C, PTAFR, RANBP2, SNCA, TKT, UGP2, DYRK2, IRS2, KAT2B, PER2, NDST3, HS2ST1, EPM2AIP1, ARPP19, PASK, SIRT1, ST6GALNAC6, CHST15, CSGALNACT2, CSGALNACT1, CHST9, SESN2, B3GNT5, SOGA1, SIK1, FOXK1
BP	GO:0001967	suckling behavior	7/3408	2.11E-02	DACH1, GLS, PEX13, POU4F1, DERL2, UBE2Q1, UBR3
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STAT protein	7/3408	2.11E-02	CAV1, NF2, PPP2CA, PPP2R1A, SOCS1, SH2B3, PARP14
BP	GO:0043970	histone H3-K9 acetylation	7/3408	2.11E-02	BRCA1, CHEK1, GATA3, SMAD4, KMT2A, KAT2B, ZNF451
BP	GO:0061029	eyelid development in camera-type eye	7/3408	2.11E-02	EGFR, HDAC2, JUN, SOS1, SOX11, SRF, TWIST1
BP	GO:0071696	ectodermal placode development	7/3408	2.11E-02	CTNNB1, HDAC2, PROX1, TBX3, NRP1, FRS2, SIX4
BP	GO:1900025	negative regulation of substrate adhesion-dependent cell spreading	7/3408	2.11E-02	ACTN4, EFNA5, GBP1, POSTN, KANK1, CORO1C, RCC2
BP	GO:1900103	positive regulation of endoplasmic reticulum unfolded protein response	7/3408	2.11E-02	BAK1, PTPN1, XBP1, BCL2L11, AGR2, TMEM33, DAB2IP
BP	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	25/3408	2.11E-02	CAV1, FBN1, FBN2, HSPA5, LTBP1, SMAD2, SMAD6, SMAD7, PIN1, SKI, SKIL, ADAM17, TGFBR1, TGFBR3, TP53, MTMR4, ONECUT2, PEG10, SIRT1, ZNF451, PMEPA1, SMURF1, PBLD, WFIKKN2, CD109
BP	GO:1903533	regulation of protein targeting	25/3408	2.11E-02	AKT2, STOM, ERBB2, GDI1, MYO1C, PRKAA1, SREBF2, VAMP7, UBE2D3, UBE2L3, FZD5, BAP1, BAG4, ATG13, C2CD5, ARIH2, HTRA2, SH3GLB1, MIEF1, LEPROT, FBXW7, MFF, USP36, RHOU, MIEF2
BP	GO:0051384	response to glucocorticoid	40/3408	2.11E-02	ADM, ALAD, RHOA, ATP2B1, CCND1, BCL2, ZFP36L1, ZFP36L2, KLF9, CALM3, CASP3, CDKN1A, DNMT3B, DUSP1, EDN1, EGFR, EIF4E, FOXO1, FOXO3, FOSB, NR3C1, HNRNPU, ISL1, KRAS, MDK, NTRK3, PAPPA, PTAFR, SPARC, STC1, UBE2L3, WNT7B, ZFP36, FOSL1, ADAM9, BCL2L11, FAM107A, AKAP13, ERRFI1, DDIT4
BP	GO:0060968	regulation of gene silencing	42/3408	2.12E-02	ADAR, DDX5, EGFR, EIF4G1, ELAVL1, FMR1, HMGA1, MYCN, NUP88, NUP98, POLR2D, POLR2K, PPP3CA, RANBP2, STAT3, TERT, TP53, ZFP36, FXR1, LIMD1, NCOR1, PUM1, POM121, NUP50, MORC2, PHF8, SIRT1, SIN3A, AGO1, TNRC6A, ATAD2B, NDC1, ATF7IP, NUP133, XPO5, MIER1, NAA40, TET1, SEH1L, TRIM71, NUP43, POM121C
BP	GO:0031124	mRNA 3'-end processing	29/3408	2.14E-02	ZFP36L1, CCNT1, NCBP1, POLR2D, SRSF1, SRSF2, SRSF4, SRSF7, SNRPA, PABPN1, CTR9, AHCYL1, PAPOLA, RNPS1, CPSF6, U2AF2, CPEB3, ZC3H3, RPRD2, CSTF2T, ZNF473, PABPC1, CDC40, CPSF2, RPRD1A, WDR33, THOC2, CDC73, CPSF7
BP	GO:0007098	centrosome cycle	35/3408	2.14E-02	BRCA1, CCNF, CETN2, CHD3, CHEK1, CTNNB1, KAT2A, PPP1R12A, SLC16A1, AURKA, UVRAG, XPO1, KAT2B, KIF3B, ROCK2, VPS4B, CEP135, PDCD6IP, PLK2, KIF3A, CEP250, USP33, NIN, CHMP5, HAUS6, NDE1, HAUS2, NSFL1C, MDM1, CHMP1B, CEP85, PARD6B, SSX2IP, UBXN2B, CEP120
BP	GO:0022037	metencephalon development	32/3408	2.16E-02	ABL1, ARCN1, RERE, ATP7A, BCL2, CNTN1, CRK, CRKL, EZH2, FOXC1, KAT2A, HNRNPD, HSPA5, KCNC1, LRP6, MDK, MECP2, MYH10, OPHN1, OTX1, SERPINE2, PROX1, PTPN11, RORA, TP53, FZD4, B4GALT2, LDB1, NCSTN, SEMA4C, MTPN, TTBK2
BP	GO:0035305	negative regulation of dephosphorylation	32/3408	2.16E-02	CRY2, DLG3, ENSA, FKBP1A, GNAI2, GSK3B, NCKAP1L, IKBKB, MYO1D, PPP1R2, SET, YWHAE, IQGAP1, ROCK2, BAG4, PHACTR2, FARP1, ARPP19, LMTK2, RRP1B, PPP1R16B, ZFYVE1, SYTL2, SLC7A14, PCIF1, WNK1, ZCCHC9, FAM122A, WDR81, SPRED1, BOD1L1, PPP1R37
BP	GO:2000779	regulation of double-strand break repair	24/3408	2.16E-02	CHEK1, FOXM1, FUS, OGG1, PML, RAD51, TWIST1, HMGA2, TRIP12, ACTR2, POLQ, KDM1A, SPIDR, UBR5, RTEL1, FIGN, RIF1, FMN2, UBQLN4, SPIRE1, KLHL15, RMI2, PPP4R2, USP51

BP	GO:0040019	positive regulation of embryonic development	15/3408	2.17E-02	AR, CTNNB1, DAG1, GATA3, HES1, PAFAH1B1, NR2C2, WNT2B, RBM19, PHLDB1, CLASP1, SIX4, WNT4, PHLDB2, AMOT
BP	GO:0009108	coenzyme biosynthetic process	65/3408	2.18E-02	ACACA, ACLY, ACSL4, GAPDH, GPI, HIF1A, HK1, HK2, IDH2, FOXK2, INSR, LDHA, MAT2A, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PRKAA1, PTGIS, PTS, RANBP2, SCD, SNCA, STAT3, ELOVL4, TP53, SLC25A16, PDXK, KYNU, NCOR1, POM121, NUP50, SLC2A6, NMNAT2, ACSL6, QPRT, MTHFD1L, MAT2B, PANK1, DDIT4, PDPR, RFK, NDC1, NUP133, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, ACSS1, CBR4, PPTC7, ACSF3, FOXK1, NUP43, POM121C
BP	GO:0031023	microtubule organizing center organization	37/3408	2.18E-02	BRCA1, CCNF, CETN2, CHD3, CHEK1, CTNNB1, KAT2A, PPP1R12A, PAFAH1B1, SLC16A1, AURKA, UVRAG, XPO1, KAT2B, KIF3B, ROCK2, VPS4B, CEP135, PDCD6IP, PLK2, KIF3A, CEP250, USP33, CLASP1, NIN, CHMP5, HAUS6, NDE1, HAUS2, NSFL1C, MDM1, CHMP1B, CEP85, PARD6B, SSX2IP, UBXN2B, CEP120
BP	GO:0090150	establishment of protein localization to membrane	80/3408	2.19E-02	AKT2, ATP1B1, BCL2, CALM3, CSK, EGFR, STOM, ERBB2, GDI1, GOLGA4, HSPA4, HSPA5, RAB8A, MYO1C, NPC1, NSF, PPP3R1, MAPK8, PEX5, RPL15, RPL28, RPL34, RPL37, RPS3, RPS23, SNAP25, SPTBN1, SSR1, SSR3, STX3, VAMP2, VAMP7, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, RAB11B, TAOK2, PREPL, TRAM2, C2CD5, BCL2L11, ARFRP1, LYPLA1, RAB31, SEC63, ARL6IP1, TRAM1, RAB3GAP2, BBC3, SEC61A1, GET4, RAB8B, MIEF1, VPS37C, GOLPH3L, ZDHHC7, PEX26, VPS35, PARD3, MFF, KIF13A, MOAP1, ZDHHC6, GORASP1, C16orf70, ZDHHC18, MICALL1, BMF, PKDCC, RAB3IP, MIEF2, VPS37D, ZDHHC20, ZDHHC23, ZDHHC22, ZDHHC21, RILPL1
BP	GO:0072522	purine-containing compound biosynthetic process	76/3408	2.19E-02	ACACA, ACLY, ADA, ADCY1, ADCY6, ADCY9, ADORA2B, AK2, AK4, DCK, ACSL4, GAPDH, GPI, GUCY1A2, HIF1A, HK1, HK2, FOXK2, IMPDH1, INSR, LDHA, MTAP, NME4, NT5E, NUP88, NUP98, PDK3, PDK4, PFAS, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PPAT, PRKAA1, PRPSAP2, RANBP2, SCD, SNCA, STAT3, ELOVL4, TP53, VCP, PAPSS2, NCOR1, POM121, PAICS, NUP50, SLC2A6, ACSL6, MTHFD1L, AK3, SLC35B3, PANK1, DDIT4, PDPR, NDC1, NUP133, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, DNAJC30, ACSS1, CBR4, ACSF3, FLCN, FOXK1, NUP43, POM121C
BP	GO:0009152	purine ribonucleotide biosynthetic process	69/3408	2.21E-02	ACACA, ACLY, ADCY1, ADCY6, ADCY9, AK2, AK4, ACSL4, GAPDH, GPI, GUCY1A2, HIF1A, HK1, HK2, FOXK2, IMPDH1, INSR, LDHA, NME4, NUP88, NUP98, PDK3, PDK4, PFAS, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PPAT, PRKAA1, RANBP2, SCD, SNCA, STAT3, ELOVL4, TP53, VCP, PAPSS2, NCOR1, POM121, PAICS, NUP50, SLC2A6, ACSL6, AK3, SLC35B3, PANK1, DDIT4, PDPR, NDC1, NUP133, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, DNAJC30, ACSS1, CBR4, ACSF3, FLCN, FOXK1, NUP43, POM121C
BP	GO:0022406	membrane docking	47/3408	2.22E-02	CAMK2A, CETN2, CSNK1D, CSNK1E, RAB8A, NSF, PAFAH1B1, PPP2R1A, RAB3B, RALB, SNAP25, STX3, SYT1, VCAM1, YWHAE, YWHAG, USO1, DYNLL1, SNX3, VAPB, CEP135, AKAP9, TUBB4A, UNC13B, EXOC5, CNTRL, CEP250, DCTN3, ATG14, EXOC6B, CLASP1, STX12, RAB8B, HAUS6, AHI1, NDE1, SYTL2, STX17, HAUS2, ESYT2, NDRG4, CEP97, RAB3IP, PDZD8, TTBK2, KIF24, RAB15
BP	GO:0140056	organelle localization by membrane tethering	45/3408	2.23E-02	CAMK2A, CETN2, CSNK1D, CSNK1E, RAB8A, NSF, PAFAH1B1, PPP2R1A, RAB3B, RALB, SNAP25, STX3, SYT1, YWHAE, YWHAG, USO1, DYNLL1, VAPB, CEP135, AKAP9, TUBB4A, UNC13B, EXOC5, CNTRL, CEP250, DCTN3, ATG14, EXOC6B, CLASP1, STX12, RAB8B, HAUS6, AHI1, NDE1, SYTL2, STX17, HAUS2, ESYT2, NDRG4, CEP97, RAB3IP, PDZD8, TTBK2, KIF24, RAB15
BP	GO:0007519	skeletal muscle tissue development	43/3408	2.24E-02	RHOA, BCL2, BCL9, CAV1, CCNT2, CFL2, COL19A1, MAPK14, CTNNB1, DCN, DDX5, EGR1, EP300, FLNB, HMGCR, FOXN2, MEF2C, MEF2D, PPP3CA, PRKAA1, RB1, SKI, SOX11, NR2F2, TWIST1, BTG2, COPS2, HDAC9, NR1D2, ZBTB18, DDX17, DKK1, MAFF, FBXO22, HEYL, SOX8, CDON, SIX4, GPCPD1, CYP26B1, AKIRIN1, UQCC2, ZNF689
BP	GO:0001974	blood vessel remodeling	16/3408	2.24E-02	ACVR2B, JAG1, ATP7A, AXL, BAK1, BMPR2, EPAS1, FOXC1, FLT4, HOXA3, RBPJ, MEF2C, ATG5, DLL4, CHD7, TMBIM1
BP	GO:0032456	endocytic recycling	16/3408	2.24E-02	ARF6, ARHGAP1, SORL1, RAB11B, SNX17, SNF8, LMTK2, ACAP2, EHD4, RAB14, CMTM6, EPG5, RAB17, NDRG4, RAB11FIP4, MICALL1
BP	GO:0001782	B cell homeostasis	12/3408	2.24E-02	ABL1, ADA, BAK1, BCL2, CASP3, NCKAP1L, HIF1A, LYN, MEF2C, SOS1, BCL2L11, TNFRSF13B
BP	GO:0051491	positive regulation of filopodium assembly	12/3408	2.24E-02	CDC42, CCR7, FMR1, SRF, TGFBR1, NRP1, WASL, TENM1, NLGN1, RHOQ, FNBP1L, AGRN
BP	GO:1904893	negative regulation of STAT cascade	12/3408	2.24E-02	CAV1, NF2, PPP2CA, PPP2R1A, VHL, SOCS1, SOCS2, SH2B3, PTPRT, ADIPOR1, PARP14, LEPROT
BP	GO:0043502	regulation of muscle adaptation	31/3408	2.24E-02	ATP2A2, ATP2B4, CAMK2D, DAG1, EDN1, FOXO1, FOXO3, G6PD, IGFBP5, IL6ST, JARID2, SMAD4, MEF2A, PIN1, PPARA, PPP3CA, PRKCA, TWF1, RGS2, RGS4, SLC9A1, TNFRSF1B, YY1, NR4A3, MTMR4, KLF4, AKAP6, ROCK2, LMCD1, ERRFI1, MTPN
BP	GO:0036465	synaptic vesicle recycling	22/3408	2.24E-02	ACTB, ARF6, CALM3, CANX, OPHN1, RAB5A, SH3GL2, SNCA, SYT1, SYNJ1, AP3D1, SYT7, NLGN1, SYT11, PIP5K1C, SYT17, NLGN2, KIAA1109, STON2, BTBD9, FCHO2, SYT2
BP	GO:0051865	protein autoubiquitination	22/3408	2.24E-02	AMFR, BRCA1, CNOT4, RAG1, RNF4, TAF1, UBE2D2, UBE2D3, MTA1, RNF10, TRIM13, UBE4B, LTN1, RNF11, RNF141, BFAR, KLHL24, RNF213, ITCH, TRIM71, RNF187, SH3RF3

BP	GO:0048663	neuron fate commitment	21/3408	2.28E-02	DLX2, GATA2, NRG1, FOXA1, RBPJ, ISL1, JAG2, SMAD4, NTRK3, PAX6, PRRX1, POU3F2, POU4F1, TGFBR1, SATB2, ZNF521, SUFU, DLL4, ESRP1, ISL2, BCL11B
BP	GO:0045778	positive regulation of ossification	27/3408	2.28E-02	ACVR2B, JAG1, ATP2B1, BMP7, BMPR1A, BMPR2, RUNX2, CEBPB, CEBPD, CTNNB1, FBN2, GNAS, IL6R, IL6ST, ILK, JUND, MEF2C, SLC8A1, SOX11, WNT7B, TP63, PDLIM7, TOB2, NIPBL, WNT4, FAM20C, PKDCC
BP	GO:0009226	nucleotide-sugar biosynthetic process	10/3408	2.28E-02	GFPT1, MPI, PGM3, PMM2, UGDH, UGP2, GFPT2, GNPDA1, GNPNAT1, UAP1L1
BP	GO:0016578	histone deubiquitination	10/3408	2.28E-02	KAT2A, ATXN7, BAP1, USP49, USP21, ATXN7L3, USP36, BRCC3, MYSM1, USP51
BP	GO:0051570	regulation of histone H3-K9 methylation	10/3408	2.28E-02	ATRX, BRCA1, DNMT3B, JARID2, MECP2, MYB, KDM1A, SIRT1, RIF1, SETD7
BP	GO:0060479	lung cell differentiation	10/3408	2.28E-02	CREB1, CTNNB1, GATA6, FOXA1, HOXA5, RBPJ, NFIB, THRA, KLF2, AGR2
BP	GO:0097150	neuronal stem cell population maintenance	10/3408	2.28E-02	JAG1, FOXO1, FOXO3, HES1, PRRX1, PROX1, SS18, IGF2BP1, HOOK3, FUT10
BP	GO:1902254	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	10/3408	2.28E-02	BCL2, PTTG1IP, CD44, KDM1A, SIRT1, ZNF385A, RRM2B, TRIAP1, TAF9B, RRN3
BP	GO:0045604	regulation of epidermal cell differentiation	20/3408	2.30E-02	ZFP36L1, RUNX1, CBFB, EZH2, FOXC1, HOXA7, HES1, MAFG, PTCH1, VDR, ZFP36, NCOA3, TP63, ROCK2, MAFF, GRHL1, ERRFI1, ESRP1, SGPP1, CD109
BP	GO:0007632	visual behavior	18/3408	2.30E-02	CREB1, CTNS, HIF1A, HMGCR, ITGB1, KIT, KRAS, MECP2, MEIS2, PDE1B, RAG1, SLC1A2, B4GALT2, SYNGAP1, SLC7A11, NPTN, RIC8A, NDRG4
BP	GO:1901185	negative regulation of ERBB signaling pathway	18/3408	2.30E-02	CBL, CDC42, HBEGF, EGFR, ERBB2, GRB2, PTPN12, PTPRJ, SH3GL2, TGFA, GPRC5A, SOCS5, SPRY1, PTPN18, ERRFI1, SOCS4, DAB2IP, EPGN
BP	GO:1902475	L-alpha-amino acid transmembrane transport	18/3408	2.30E-02	CLN8, KCNJ10, RGS2, RGS4, SLC1A2, SLC1A5, SLC7A1, SLC7A2, SLC7A5, PER2, SLC7A6, SLC25A15, ARL6IP1, SLC7A11, SLC25A38, SLC38A1, SLC36A4, SLC43A2
BP	GO:0043525	positive regulation of neuron apoptotic process	19/3408	2.30E-02	RHOA, ATM, CASP3, CDC34, ATF2, CTNNB1, CTSZ, EPHA7, FOXO3, JUN, MCL1, MYB, MYBL2, PAK3, PIN1, MAP2K4, TP53, BCL2L11, FBXW7
BP	GO:0075733	intracellular transport of virus	19/3408	2.30E-02	FMR1, KPNA1, KPNA3, NUP88, NUP98, RAN, RANBP2, XPO1, POM121, NUP50, KPNA6, UBAP1, VPS37C, NDC1, NUP133, SEH1L, VPS37D, NUP43, POM121C
BP	GO:1900180	regulation of protein localization to nucleus	33/3408	2.31E-02	CCT6A, MAPK14, DKC1, ECT2, GSK3B, JUP, IPO5, NF2, PIN1, PKIA, MAPK1, RAN, SRC, TERT, DCLK1, NUTF2, KAT7, TARDBP, CD2AP, POLR1A, SIN3A, NMD3, UBR5, SUFU, RAB23, PINX1, FERMT1, OTUD7B, MAVS, SESN2, LZTS2, GLIS2, FLCN
BP	GO:0043524	negative regulation of neuron apoptotic process	40/3408	2.32E-02	RHOA, ARRB1, ARRB2, AXL, BCL2, BCL2L1, BDNF, CEBPB, HIF1A, ILK, ISL1, JUN, KRAS, LIG4, LRP1, MDK, MECP2, MEF2C, PIN1, POU4F1, RASA1, CX3CL1, MAP2K4, SET, SNCA, SOD2, TERT, TYRO3, BTG2, NR4A3, NRP1, SYNGAP1, HYOU1, STAMBP, HIPK2, SIX4, OXR1, CPEB4, DNAJC5, BHLHB9
BP	GO:0045216	cell-cell junction organization	42/3408	2.33E-02	ACTN4, APC, RHOA, CAV1, RUNX1, CBFB, CDH6, CTNNA1, CTNND1, CXADR, ECT2, GJA1, GJB1, IKBKB, JUP, MYO1C, NF2, PKP1, PRKCA, PKN2, SNAI2, SNAI1, SRF, STRN, TGFBR1, TLN1, VCL, FZD5, PKP4, DLG5, ROCK2, PDCD6IP, GJC1, NFASC, GRHL1, PARD3, HEG1, NLGN2, PARD6B, MTDH, FLCN, SDK1
BP	GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	26/3408	2.34E-02	ARCN1, COPB1, HTT, KIF2A, NSF, RAB1A, SURF4, UVRAG, NAPA, KIF3B, KIF23, ATP9A, TMED10, KIF2C, KIF3A, BICD2, PITPNB, TMED7, ERGIC2, RAB6B, GOLPH3L, ARFGAP1, ERGIC1, KLC2, COG3, ATP9B
BP	GO:0008625	extrinsic apoptotic signaling pathway	26/3408	2.34E-02	FAS, BCL2, BCL2L1, BRCA1, DAPK1, DDX3X, SERPINE1, PTEN, SORT1, SFRP1, SKIL, SP100, STK4, THBS1, TIMP3, MADD, PEA15, TNFSF10, FADD, ARHGEF2, DEDD, MOAP1, TMBIM1, ITPRIP, RFFL, DAB2IP

		via death domain receptors			
BP	GO:0034637	cellular carbohydrate biosynthetic process	26/3408	2.34E-02	AKT2, EXTL2, EXTL3, GSK3B, GYS1, HAS3, NDST1, IGF2, IMPA2, INSR, ENPP1, PHKG2, PPP1CA, PPP1CB, PPP1R3C, UGP2, DYRK2, IRS2, PER2, NDST3, HS2ST1, EPM2AIP1, PASK, CSGALNACT2, CSGALNACT1, B3GNT5
BP	GO:0060291	long-term synaptic potentiation	26/3408	2.34E-02	ABL1, ADCY1, CREB1, EPHA4, EPHB2, GSK3B, MECP2, MME, MPP2, SERPINE2, MAPK1, PTEN, SNAP25, SNCA, STAU1, STX3, VAMP2, SQSTM1, PLK2, FAM107A, NLGN1, SHANK2, NCSTN, SLC24A2, NPTN, YTHDF1
BP	GO:0030326	embryonic limb morphogenesis	35/3408	2.37E-02	BMP7, BMPR1A, CACNA1C, RUNX2, CREBBP, CTNNB1, DLX6, MEGF8, FBN2, GJA1, GNAS, HDAC2, HOXA9, HOXD13, LRP6, SMAD4, MBNL1, MSX1, PBX1, PRRX1, PTCH1, RARG, SKI, TBX3, TWIST1, FZD6, TP63, ALDH1A2, BCL2L11, DKK1, NIPBL, CHD7, CYP26B1, RDH10, FREM2
BP	GO:0035113	embryonic appendage morphogenesis	35/3408	2.37E-02	BMP7, BMPR1A, CACNA1C, RUNX2, CREBBP, CTNNB1, DLX6, MEGF8, FBN2, GJA1, GNAS, HDAC2, HOXA9, HOXD13, LRP6, SMAD4, MBNL1, MSX1, PBX1, PRRX1, PTCH1, RARG, SKI, TBX3, TWIST1, FZD6, TP63, ALDH1A2, BCL2L11, DKK1, NIPBL, CHD7, CYP26B1, RDH10, FREM2
BP	GO:0031345	negative regulation of cell projection organization	49/3408	2.38E-02	ADCY6, ARF6, RHOA, ARHGDIA, CTSZ, EFNB2, EPHA4, EPHA7, EPHB2, FKBP4, GDI1, GSK3B, HDAC2, ITGA3, LRP1, MAP4, PAFAH1B1, PPP3CA, PTEN, PTPRG, TSC1, SEMA7A, CDK10, NRP1, SYNGAP1, NTN1, MAP4K4, RAPGEF2, SEMA3E, LRIG2, SEMA3A, SEMA4B, PLK2, NLGN1, DKK1, FSTL4, RAP1GAP2, KANK1, MYLIP, ASAP1, BCL11A, SEMA4C, RGMA, SEMA6A, GORASP1, TRAK2, CEP97, ITM2C, KREMEN1
BP	GO:0051783	regulation of nuclear division	49/3408	2.38E-02	APC, ATM, ATRX, BMP7, CALR, CDKN1B, RCC1, CHEK1, DUSP1, EDN1, HNRNPU, IGF2, IK, INSR, MAD2L1, MSX1, PDE3A, PDGFB, PIN1, PRKAR1A, RAD1, RAD21, RB1, AURKA, TGFA, SMC1A, CUL3, CDC14B, TNKS, AURKB, TRIP13, VPS4B, STAG2, NIPBL, SH2B1, CHMP5, WNT4, ANLN, PHIP, RIOK2, PCID2, NSFL1C, CHMP1B, HECW2, CEP85, CEP97, CCSAP, UBXN2B, EPGN
BP	GO:0030838	positive regulation of actin filament polymerization	29/3408	2.41E-02	ARF1, ARF6, RHOA, CCR7, FER, GRB2, NCKAP1L, MYO1C, NCK1, PRKCE, NCK2, WASF1, WASL, BAG4, FCHSD2, ARPC5, ACTR2, ARPC2, ABI2, TENM1, CDC42EP2, NCKAP1, IQGAP2, FMN2, SPIRE1, WHAMM, JMY, RICTOR, FMN1
BP	GO:1903510	mucopolysaccharide metabolic process	32/3408	2.41E-02	CD44, NCAN, DCN, FGF2, HAS3, NDST1, IDS, CHST6, NFKB1, PDGFB, PIM1, PRELP, ST3GAL1, SLC9A1, UGDH, CHST1, B4GALT2, B4GALT6, NDST3, SPOCK2, ABCC5, UST, ST3GAL6, LYVE1, GLCE, CHST15, CSGALNACT2, CSGALNACT1, CHST7, XYLT2, ITIH5, CHST9
BP	GO:0032355	response to estradiol	37/3408	2.41E-02	ADCYAP1R1, CCND1, BMP7, CALR, CASP3, CCNA2, CDKN1B, COL1A1, CTNNB1, DNMT3A, DNMT3B, DUSP1, EGFR, ESRRA, EZH2, GJA1, FOXA1, HNRNPD, MAP1B, OGG1, POU4F1, PTCH1, PTEN, SFRP1, STAT3, STAT5B, NR2F2, TFPI, NCOA3, NRIP1, SOCS2, ALDH1A2, MBD2, BCL2L11, POSTN, STRN3, FAM210B
BP	GO:0030279	negative regulation of ossification	25/3408	2.41E-02	BCL2, CDK6, HIF1A, IGFBP5, RBPJ, NBR1, SMAD6, MDK, MEF2C, MEN1, ENPP1, PTCH1, RORB, SFRP1, SKI, TWIST1, CHRD, LIMD1, TOB1, DKK1, GREM1, SUFU, BCOR, SMURF1, KREMEN1
BP	GO:0018345	protein palmitoylation	13/3408	2.41E-02	ZDHHC17, ZDHHC5, CLIP3, ZDHHC8, ABHD17B, ZDHHC7, ABHD17C, ZDHHC6, ZDHHC18, ZDHHC20, ZDHHC23, ZDHHC22, ZDHHC21
BP	GO:0031128	developmental induction	13/3408	2.41E-02	AR, CTNNB1, FGF1, ROBO1, WNT2B, FZD5, SPRY1, FRS2, DKK1, HIPK2, SOX8, WNT4, HIPK1
BP	GO:0032212	positive regulation of telomere maintenance via telomerase	13/3408	2.41E-02	ATM, ATR, CCT6A, CTNNB1, DKC1, MAP3K4, PARN, MAPK1, MAPK3, XRCC5, TNKS, AURKB, HMBOX1
BP	GO:0043276	anoikis	13/3408	2.41E-02	BCL2, CAV1, ITGA5, ITGB1, MCL1, PDK4, SNAI2, SRC, TFDP1, TLE1, ANKRD13C, BMF, SIK1
BP	GO:0071868	cellular response to monoamine stimulus	13/3408	2.41E-02	ABL1, ADCY6, ATP2B4, GABPA, GNB1, HDAC2, PDE4D, MAPK1, MAPK3, SLC9A1, SNCA, NR4A3, SIN3A
BP	GO:0071870	cellular response to catecholamine stimulus	13/3408	2.41E-02	ABL1, ADCY6, ATP2B4, GABPA, GNB1, HDAC2, PDE4D, MAPK1, MAPK3, SLC9A1, SNCA, NR4A3, SIN3A
BP	GO:0009746	response to hexose	52/3408	2.42E-02	ACVR2B, RHOA, ARRB1, CASP3, CDKN1B, COL6A2, EFNA5, EGR1, ENSA, FOXO3, GJA1, HIF1A, HMGCR, HNF4A, IGF1R, KIF5B, LDHA, LRP1, SMAD2, MEN1, OPA1, PAX2, CDK16, PDK3, PFKFB2, PPARD, PPP3CA, PRKAA1, PRKCE, PTEN, PTPRN2, TRA2B, SLC8A1, SOX4, SRF, VAMP2, HNF1B, TCF7L2, THBS1, TIAM1, XBP1, DYNLL1, IRS2, RAB11B, MAP4K4, UNC13B, ATG7, RAB11FIP2, TXN2, SIN3A, SESN2, ACVR1C
BP	GO:0034284	response to monosaccharide	53/3408	2.52E-02	ACVR2B, RHOA, ARRB1, CASP3, CDKN1B, COL6A2, EFNA5, EGR1, ENSA, FOXO3, GJA1, HIF1A, HMGCR, HNF4A, IGF1R, KIF5B, LDHA, LRP1, SMAD2, MEN1, OPA1, PAX2, CDK16, PDK3, PFKFB2, PPARD, PPP3CA, PRKAA1, PRKCE, PTEN, PTPRN2, TRA2B,

					SLC8A1, SOX4, SPARC, SRF, VAMP2, HNF1B, TCF7L2, THBS1, TIAM1, XBP1, DYNLL1, IRS2, RAB11B, MAP4K4, UNC13B, ATG7, RAB11FIP2, TXN2, SIN3A, SESN2, ACVR1C
BP	GO:0006997	nucleus organization	36/3408	2.54E-02	NUP98, PAFAH1B1, PML, PPP2CA, PPP2R1A, PPP2R2A, PRKCA, ATXN7, TMF1, SF1, VPS4B, ANKLE2, LPIN1, PSME4, TARDBP, PITPNB, SERBP1, TOR1B, HIPK2, GOLM1, CHMP5, RRN3, NDC1, NUP133, NSFL1C, CHMP1B, USP36, TMEM43, SEH1L, POLR1B, WDR73, CHMP7, TMEM170A, UBXN2B, REEP3, CNEP1R1
BP	GO:0001825	blastocyst formation	14/3408	2.56E-02	ADA, GABPA, SKIL, SP3, SRF, HNF1B, CUL3, LATS1, HAND1, CTR9, MFN2, PTPN18, TET1, RPL7L1
BP	GO:0006040	amino sugar metabolic process	14/3408	2.56E-02	EXTL2, GFPT1, CHST6, PGM3, ST3GAL1, CHST1, GFPT2, GNPDA1, GNE, CSGALNACT1, CHST7, GNPNAT1, UAP1L1, NANP
BP	GO:0015682	ferric iron transport	14/3408	2.56E-02	ARHGAP1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, TFR2, TFRC, ATP6V0D1, RAB11B, LMTK2, ATP6V1D, STEAP3, ATP6V0E2, STEAP2
BP	GO:0015804	neutral amino acid transport	14/3408	2.56E-02	CTNS, RGS2, RGS4, SLC1A4, SLC1A5, SLC6A9, SLC7A5, SLC38A2, SLC25A38, SLC38A1, SFXN1, SLC36A4, SLC43A2, SLC36A1
BP	GO:0016572	histone phosphorylation	14/3408	2.56E-02	ATM, CCNA2, CHEK1, FMR1, PRKAA1, PRKCA, MAPK3, AURKA, TWIST1, HMGA2, RPS6KA4, BAZ1B, AURKB, RPS6KA5
BP	GO:0046329	negative regulation of JNK cascade	14/3408	2.56E-02	CYLD, DNAJA1, MEN1, PAFAH1B1, SFRP1, NCOR1, HIPK3, ZMYND11, DUSP10, PDCD4, AIDA, ITCH, SIRPA, ZNF675
BP	GO:0072512	trivalent inorganic cation transport	14/3408	2.56E-02	ARHGAP1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, TFR2, TFRC, ATP6V0D1, RAB11B, LMTK2, ATP6V1D, STEAP3, ATP6V0E2, STEAP2
BP	GO:0097352	autophagosome maturation	14/3408	2.56E-02	LAMP2, TBC1D25, UVRAG, VCP, GABARAPL2, ATG14, UBQLN1, STX17, UBQLN4, EPG5, FYCO1, MAP1LC3B, LIX1L, SMCR8
BP	GO:0002320	lymphoid progenitor cell differentiation	9/3408	2.60E-02	BCL2, GATA3, HES1, KIT, LIG4, SOS1, SOX4, FNIP1, FLCN
BP	GO:0098780	response to mitochondrial depolarisation	9/3408	2.60E-02	HK2, SQSTM1, ATG13, MFN2, ATG14, HTRA2, VPS13C, SMURF1, MUL1
BP	GO:0010906	regulation of glucose metabolic process	33/3408	2.60E-02	AKT2, EP300, FOXO1, KAT2A, GSK3B, IGF2, FOXK2, INSR, PDK3, PDK4, ENPP1, PFKFB2, PHKG2, PPARA, PPP1CA, PPP1CB, RANBP2, RORA, SRC, TP53, DYRK2, IRS2, KAT2B, EPM2AIP1, NCOA2, ARPP19, PASK, SIRT1, ADIPOR1, SESN2, SOGA1, SIK1, FOXK1
BP	GO:1900371	regulation of purine nucleotide biosynthetic process	33/3408	2.60E-02	ADORA2B, AK4, HIF1A, INSR, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, SNCA, STAT3, TP53, VCP, NCOR1, POM121, NUP50, SLC2A6, DDIT4, PDPR, NDC1, NUP133, PDP2, SEH1L, DNAJC30, FLCN, NUP43, POM121C
BP	GO:0007176	regulation of epidermal growth factor-activated receptor activity	11/3408	2.61E-02	CBL, SHC1, ADAM17, TGFA, NCK2, GPRC5A, SOCS5, ERRFI1, FBXW7, SOCS4, EPGN
BP	GO:0036475	neuron death in response to oxidative stress	11/3408	2.61E-02	CTNNB1, HIF1A, MCL1, TSC1, NR4A3, FZD1, LANCL1, ATG7, SLC7A11, OXR1, FBXW7
BP	GO:0071514	genetic imprinting	11/3408	2.61E-02	BRCA1, DNMT3A, GNAS, IGF2, MECP2, CTR9, PCGF3, CTCF, ARID4B, PCGF5, KDM1B
BP	GO:0071887	leukocyte apoptotic process	30/3408	2.62E-02	ADA, AXL, BAK1, BCL6, CASP3, CCR7, CRKL, HIF1A, IL7R, ITPKB, LYN, MEF2C, KITLG, PIK3CB, PTEN, RAG1, ADAM17, TP53, NR4A3, IRS2, FADD, AURKB, RAPGEF2, BCL2L11, SIRT1, SLC7A11, FOXP1, PRELID1, SLC39A10, FNIP1
BP	GO:0048706	embryonic skeletal system development	35/3408	2.65E-02	BMP7, RUNX2, COL1A1, COL11A1, CTNNB1, DLX2, MEGF8, GNAS, HOXA3, HOXA5, HOXA7, HOXA9, HOXB3, HOXB5, HOXB8, HOXC4, SMAD2, MEF2C, MMP14, PBX1, PDGFRA, PRRX1, SOX11, SP3, ZEB1, TGFBR1, TWIST1, SATB2, NIPBL, MTHFD1L, SIX4, MBTD1, SULF2, KIAA1217, RDH10
BP	GO:0010470	regulation of gastrulation	15/3408	2.65E-02	BMPR1A, COL5A1, COL5A2, DAG1, HNF4A, MBP, KLF4, DKK1, PHLDB1, CLASP1, TGIF2, WNK1, PHLDB2, MYADM, CRB2
BP	GO:2001222	regulation of neuron migration	15/3408	2.65E-02	CAMK2A, COL3A1, NRG1, MDK, CX3CL1, STAT3, ARHGEF2, RAPGEF2, LRIG2, SEMA3A, FLRT2, NIPBL, NSMF, SEMA6A, DAB2IP

BP	GO:1905207	regulation of cardiocyte differentiation	21/3408	2.66E-02	ARRB2, BMP7, EDN1, EFNB2, EGFR, G6PD, GATA6, KAT2A, NRG1, RBPJ, SMAD4, MEF2C, PIN1, PPARA, RGS2, RGS4, YY1, AKAP6, FRS2, DKK1, GREM1
BP	GO:0006898	receptor-mediated endocytosis	76/3408	2.66E-02	ADM, ARF1, ARF6, ARRB1, ARRB2, ASGR1, CALR, CANX, CAV1, CBL, SCARB2, AP2M1, AP1S1, DAB2, EFNB2, FMR1, GRB2, HIP1, HNRNPK, IGF2R, INSR, ITGB1, LDLR, LRP1, LRP3, LRP6, LRPAP1, M6PR, MKLN1, NEDD4, OPHN1, SERPINE1, PIK3CB, RAB5A, ATXN2, SH3GL2, SNAP25, SNCA, SNX1, SORL1, SPARC, SYK, TFR2, TFRC, VEGFA, VLDLR, NUMB, WASF1, WASL, PDLIM7, SNX17, FCHSD2, TNK2, CALCRL, CAP1, HYOU1, RAB31, AAK1, DKK1, RAB21, SYT11, DNAJC13, PIP5K1C, CD2AP, LDLRAP1, GREM1, UBQLN2, AHI1, FNBP1L, LMBR1L, GPR107, CXCL16, SGIP1, MICALL1, ANKRD13A, FCHO2
BP	GO:0007498	mesoderm development	37/3408	2.69E-02	ACVR2B, BMP7, BMPR1A, BMPR2, ZFP36L1, FOXC1, ITGA3, ITGB1, SMAD2, SMAD4, NF2, PAX2, POU4F1, PPP2CA, PRKAR1A, SNAI1, SRF, TAL1, TBX3, KDM6A, VEGFA, NR4A3, HMGA2, ITGA8, TP63, CHRD, LDB1, KLF4, HAND1, GDF11, CITED2, DKK1, KDM6B, PUS7, NUP133, EPB41L5, CRB2
BP	GO:0031960	response to corticosteroid	43/3408	2.69E-02	ADM, ALAD, RHOA, ATP2B1, CCND1, BCL2, ZFP36L1, ZFP36L2, KLF9, CALM3, CASP3, CDKN1A, COL1A1, DNMT3B, DUSP1, EDN1, EGFR, EIF4E, FOXO1, FOXO3, FOSB, NR3C1, HNRNPU, ISL1, KRAS, MDK, NTRK3, PAPPA, PTAFR, SPARC, SRC, STC1, UBE2L3, WNT7B, ZFP36, FOSL1, AKR1C3, ADAM9, BCL2L11, FAM107A, AKAP13, ERRFI1, DDIT4
BP	GO:0099504	synaptic vesicle cycle	50/3408	2.70E-02	ACTB, ADCY1, ADORA2B, ARF6, ATP2A2, CALM3, CAMK2A, CANX, CTNNB1, FMR1, GSK3B, OPHN1, P2RY1, PLD1, PTEN, RAB3B, RAB5A, RAP1B, SH3GL2, SNAP25, SNCA, STX3, VAMP1, VAMP2, SYT1, NAPA, SYNJ1, BSN, AP3D1, SYT7, PREPL, RIMS3, SV2A, UNC13B, NLGN1, SYT11, PIP5K1C, NCS1, PCDH17, GIT1, SYT17, NLGN2, DNAJC5, KIAA1109, STON2, BTBD9, FCHO2, SYT2, STXBP5, RIMS4
BP	GO:0046620	regulation of organ growth	32/3408	2.70E-02	BMPR1A, MAPK14, DUSP6, EDN1, FGF2, FOXC1, G6PD, GATA6, GJA1, RBPJ, JARID2, MEF2C, PIM1, PIN1, PPARA, MAPK1, PROX1, PTEN, RGS2, RGS4, STK4, TGFBR1, TGFBR3, YY1, LATS1, AKAP6, BCL2L11, WWC1, LATS2, SERP1, WWC3, WWC2
BP	GO:0048640	negative regulation of developmental growth	32/3408	2.70E-02	ADRB1, CDKN1A, CDKN1B, EPHA7, FGFR3, G6PD, GJA1, JARID2, PPARA, PTCH1, PTEN, RGS2, RGS4, SFRP1, STK4, YY1, SEMA7A, STC2, NRP1, SOCS2, NTN1, SEMA3E, SEMA3A, SEMA4B, DUSP10, FSTL4, WWC1, BCL11A, SEMA4C, WWC3, SEMA6A, WWC2
BP	GO:0005978	glycogen biosynthetic process	16/3408	2.70E-02	AKT2, GSK3B, GYS1, IGF2, INSR, ENPP1, PHKG2, PPP1CA, PPP1CB, PPP1R3C, UGP2, DYRK2, IRS2, PER2, EPM2AIP1, PASK
BP	GO:0009250	glucan biosynthetic process	16/3408	2.70E-02	AKT2, GSK3B, GYS1, IGF2, INSR, ENPP1, PHKG2, PPP1CA, PPP1CB, PPP1R3C, UGP2, DYRK2, IRS2, PER2, EPM2AIP1, PASK
BP	GO:0031648	protein destabilization	16/3408	2.70E-02	CREBBP, EP300, HTT, SIAH1, SNCA, SRC, XBP1, CUL3, BTRC, SIRT1, FBXL3, MYLIP, FBXW7, VPS35, CDC73, MUL1
BP	GO:0050919	negative chemotaxis	16/3408	2.70E-02	RHOA, EFNA5, EPHA7, NRG1, ITGAV, PDGFA, ROBO1, SEMA7A, NTN1, SEMA3E, SEMA3A, SEMA4B, FLRT2, SEMA4C, SEMA6A, PLXNA4
BP	GO:0051646	mitochondrion localization	16/3408	2.70E-02	MARK2, KAT2A, HIF1A, MAP1B, MAPT, MARK1, MEF2A, OPA1, WASF1, MFN2, TRAK1, KIF1B, MFN1, TRAK2, MUL1, BRAT1
BP	GO:1990928	response to amino acid starvation	16/3408	2.70E-02	FAS, CDKN1A, EIF2S1, MAPK1, MAPK3, MAPK8, EIF2AK2, SZT2, LARP1, SH3GLB1, SLC38A2, RRAGD, RRAGC, SEH1L, SESN2, SESN3
BP	GO:0098930	axonal transport	19/3408	2.72E-02	DST, FMR1, HIF1A, KIF5B, MAP1A, MAPT, OPA1, PAFAH1B1, AP3D1, KIF3B, AP3S2, KIF3A, TRAK1, RAB21, KIF1B, MAPK8IP3, AP3M1, TRAK2, ARL8A
BP	GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	19/3408	2.72E-02	FAS, BCL2L1, BRCA1, SERPINE1, PTEN, SFRP1, SKIL, SP100, STK4, THBS1, TIMP3, MADD, PEA15, TNFSF10, FADD, ARHGEF2, TMBIM1, ITPRIP, RFFL
BP	GO:0009948	anterior/posterior axis specification	17/3408	2.72E-02	CTNNB1, LRP6, SMAD4, PCSK6, RNF2, SKI, SRF, AURKA, TBX3, KDM6A, FZD5, LDB1, FRS2, EPB41L5, PGAP1, PLD6, NRARP
BP	GO:0043489	RNA stabilization	17/3408	2.72E-02	MAPK14, DKC1, ELAVL1, HNRNPC, HNRNPD, HNRNPU, PARN, ZFP36, THRAP3, SYNCRIP, PAIP1, IGF2BP1, HNRNPA0, LARP1, TARDBP, PABPC1, RBM38
BP	GO:0046854	phosphatidylinositol phosphorylation	17/3408	2.72E-02	IMPA2, PIK3C2A, PIK3CB, PIP4K2A, SOCS1, SOCS2, SOCS6, SOCS5, IP6K1, SMG1, EFR3A, PIP5K1C, SOCS7, PI4K2B, FAM126A, TTC7B, FAM126B
BP	GO:0072698	protein localization to microtubule cytoskeleton	17/3408	2.72E-02	APC, CSNK1D, DIAPH1, GOLGB1, GSK3B, HNRNPU, MAP1A, MID1, AURKA, CEP250, MAPRE3, ABHD17B, NSFL1C, ABHD17C, HOOK3, UBXN2B, TTBK2

BP	GO:0035384	thioester biosynthetic process	18/3408	2.72E-02	ACACA, ACLY, ACSL4, PDK3, PDK4, SCD, SNCA, ELOVL4, ACSL6, PDPR, PDP2, ELOVL5, ELOVL6, PPCS, SCD5, ACSS1, CBR4, ACSF3
BP	GO:0043392	negative regulation of DNA binding	18/3408	2.72E-02	HDAC2, ID4, JUN, MSX1, SOX11, SP100, TAF1, HMGA2, TNKS, PER2, HAND1, KDM1A, SIN3A, RSF1, FBXW7, ZNF462, WFIKKN2, ZNF675
BP	GO:0051353	positive regulation of oxidoreductase activity	18/3408	2.72E-02	ABL1, ABL2, ATP7A, CALM3, EDN1, GNAI2, GNAI3, HIF1A, KRAS, SNCA, TERT, VDR, NOS1AP, NOD1, RFK, PDP2, NUS1, CHCHD10
BP	GO:0071616	acyl-CoA biosynthetic process	18/3408	2.72E-02	ACACA, ACLY, ACSL4, PDK3, PDK4, SCD, SNCA, ELOVL4, ACSL6, PDPR, PDP2, ELOVL5, ELOVL6, PPCS, SCD5, ACSS1, CBR4, ACSF3
BP	GO:1905477	positive regulation of protein localization to membrane	34/3408	2.76E-02	AKT2, ARF6, BCL2, EGFR, STOM, EPHB2, ERBB2, ITGA3, ITGB1, KIF5B, LRP1, MYO1C, PPP3R1, PRKCE, MAPK8, SPTBN1, STX3, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, SQSTM1, AKAP5, C2CD5, AGR2, RAB11FIP2, CLIP3, BBC3, SSH1, MIEF1, MFF, MIEF2
BP	GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	25/3408	2.76E-02	CAV1, FBN1, FBN2, HSPA5, LTBP1, SMAD2, SMAD6, SMAD7, PIN1, SKI, SKIL, ADAM17, TGFBR1, TGFBR3, TP53, MTMR4, ONECUT2, PEG10, SIRT1, ZNF451, PMEPA1, SMURF1, PBLD, WFIKKN2, CD109
BP	GO:1902850	microtubule cytoskeleton organization involved in mitosis	36/3408	2.80E-02	RHOA, CENPA, RCC1, HTT, HNRNPU, KIF2A, MAD2L1, MAP4, MECP2, MYBL2, PAFAH1B1, PAX6, PKD1, RAN, AURKA, TACC1, VCP, SMC1A, TNKS, PRC1, ARHGEF2, AURKB, KIF3B, KIF23, VPS4B, SPRY1, STAG2, PLK2, CLASP1, CHMP5, NDE1, NSFL1C, CHMP1B, CEP97, CCSAP, UBXN2B
BP	GO:0051261	protein depolymerization	31/3408	2.82E-02	ADD1, APC, ASPH, CAPZA2, CFL1, CFL2, EPS8, KIF2A, MAP1A, MAP1B, MID1, TWF1, RDX, SH3GL2, SPTAN1, SPTBN1, SYNJ1, ARHGEF2, VPS4B, KIF2C, DSTN, CAMSAP2, CLASP1, TMOD2, TAOK1, NAV3, CCSAP, MTPN, TTBK2, CAMSAP1, KIF24
BP	GO:0009185	ribonucleoside diphosphate metabolic process	38/3408	2.82E-02	AK2, AK4, GAPDH, GPI, HIF1A, HK1, HK2, FOXK2, INSR, LDHA, MPP1, NUP88, NUP98, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PRKAA1, RANBP2, STAT3, TP53, TJP2, ENTPD4, NCOR1, POM121, NUP50, NUDT5, SLC2A6, AK3, DDIT4, NDC1, NUP133, SEH1L, FOXK1, NUP43, POM121C
BP	GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	12/3408	2.85E-02	CCND1, CCND2, CCNT1, CCNT2, CDKN1B, EGFR, PDGFB, PKD1, PROX1, SRC, ADAM17, MAPRE3
BP	GO:0097106	postsynaptic density organization	12/3408	2.85E-02	ARF6, DLG3, IL1RAP, NTRK3, OPHN1, PTEN, PTPRD, SYNGAP1, NLGN1, SHANK2, NLGN2, LRRC4
BP	GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	12/3408	2.85E-02	BCL2, BCL2L1, CD44, SNAI2, SNAI1, TPT1, KDM1A, SIRT1, ZNF385A, TRIAP1, TAF9B, USP47
BP	GO:0001570	vasculogenesis	24/3408	2.85E-02	ADM, ZFP36L1, CAV1, CTNNB1, EMP2, ITGAV, ITGB8, RASA1, TGFBR3, VEGFA, WNT7B, FZD4, SGPL1, QKI, RAPGEF2, GJC1, EGFL7, AGGF1, FBXW7, HIF1AN, ZMIZ1, HEG1, AMOT, SPRED1
BP	GO:0045652	regulation of megakaryocyte differentiation	24/3408	2.85E-02	RUNX1, CBFB, EP300, GABPA, GATA2, MEF2C, KMT2A, CNOT4, THBS1, NR4A3, KMT2D, KAT2B, SETD1A, KMT2B, TNRC6B, SIN3A, AGO1, TNRC6A, KMT2E, TNRC6C, KMT2C, DPY30, AGO3, AGO4
BP	GO:0030808	regulation of nucleotide biosynthetic process	33/3408	2.89E-02	ADORA2B, AK4, HIF1A, INSR, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, SNCA, STAT3, TP53, VCP, NCOR1, POM121, NUP50, SLC2A6, DDIT4, PDPR, NDC1, NUP133, PDP2, SEH1L, DNAJC30, FLCN, NUP43, POM121C
BP	GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in	8/3408	2.89E-02	BRCA1, CDKN1A, FOXM1, SP100, TP53, ZNF385A, HIPK2, ING4

		transcription of p21 class mediator			
BP	GO:0015693	magnesium ion transport	8/3408	2.89E-02	KCNJ2, ZDHHC17, CNNM4, MRS2, NIPA2, MMGT1, NIPA1, NIPAL1
BP	GO:0035313	wound healing, spreading of epidermal cells	8/3408	2.89E-02	COL5A1, HBEGF, ITGA5, PTEN, RREB1, ADAM17, CLASP1, PHLDB2
BP	GO:0045324	late endosome to vacuole transport	8/3408	2.89E-02	TMEM50B, SNF8, LEPROTL1, TMEM50A, VPS36, LEPROT, CHMP1B, CHMP7
BP	GO:0072673	lamellipodium morphogenesis	8/3408	2.89E-02	CD44, RREB1, SNX1, SRC, WASF1, WASF2, KANK1, CORO1C
BP	GO:1904355	positive regulation of telomere capping	8/3408	2.89E-02	HNRNPD, MAP3K4, MAPK1, MAPK3, TNKS, AURKB, RTEL1, NABP2
BP	GO:1904380	endoplasmic reticulum mannose trimming	8/3408	2.89E-02	AMFR, SEL1L, RNF103, EDEM1, TRIM13, DERL2, UGGT1, SYVN1
BP	GO:2000641	regulation of early endosome to late endosome transport	8/3408	2.89E-02	DAB2, MAPK1, MAPK3, RDX, SRC, SNX3, RAB21, DNAJC13
BP	GO:0045727	positive regulation of translation	35/3408	2.93E-02	RHOA, DDX3X, EIF2S3, ELAVL1, ERBB2, FMR1, HNRNPD, NCK1, POLR2D, MAPK1, MAPK3, PTAFR, RPS6KB1, SOX4, THBS1, CNBP, FXR1, NCK2, PAIP1, CPEB3, FASTKD2, SAMD4A, PASK, LARP4B, LARP1, PABPC1, SERP1, NGRN, YTHDF2, YTHDF1, EIF5A2, PCIF1, UQCC2, LARP4, YTHDF3
BP	GO:0045833	negative regulation of lipid metabolic process	27/3408	2.93E-02	BRCA1, INSIG1, NFKB1, PDGFA, PDGFB, PRKAA1, PROX1, SNAI2, SNAI1, SORL1, AKR1C3, FGF19, ERLIN2, WDTC1, SIRT1, DKK3, ORMDL2, INSIG2, WNT4, FBXW7, LPCAT1, ORMDL1, ORMDL3, PIK3IP1, SIK1, DAB2IP, SLC27A1
BP	GO:0008593	regulation of Notch signaling pathway	30/3408	2.93E-02	ADAM10, JAG1, ARRB1, BCL6, BMP7, CREBBP, DLX2, EGFR, EP300, GATA2, HES1, RBPJ, IL6ST, JAG2, KIT, MMP14, ROBO1, STAT3, TP63, KAT2B, POSTN, AAK1, POFUT1, EGFL7, YTHDF2, DLL4, FBXW7, HIF1AN, ZMIZ1, NRARP
BP	GO:0015748	organophosphate ester transport	30/3408	2.93E-02	SLC25A6, SCARB2, GJA1, GJB1, LDLR, ATP8B1, PITPNA, SCP2, ATP9A, ATP8A1, SLC25A17, ATP11B, ATP11A, PITPNB, PITPNC1, PRELID1, SLC25A24, SLC35B3, GLTP, TRIAP1, SLC25A36, ATP8B2, ATP10D, PITPNM2, EPG5, SLC25A32, PLEKHA8, OSBPL8, ATP11C, ATP9B
BP	GO:1902750	negative regulation of cell cycle G2/M phase transition	30/3408	2.93E-02	ATM, BRCA1, CHEK1, FOXN3, FHL1, FOXO4, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, RAD21, SKP1, AURKA, HMGA2, CDC14B, AURKB, TAOK2, PSMF1, PSME3, PSMD14, PSME4, DTL, PINX1, USP47, TAOK1, BRCC3, ZNF830
BP	GO:0051701	interaction with host	53/3408	2.93E-02	AXL, BCL2L1, CAV1, CBL, SCARB2, CTNNB1, CTNND1, CTSB, CXADR, DAG1, EFNB2, EGFR, GAPDH, GRB2, INSR, ITGA5, ITGAV, ITGB1, KPNA1, KPNA3, LDLR, MET, NCAM1, NEDD4, NPC1, NTRK3, SERPINB9, PML, EIF2AK2, SLC1A5, SLC20A2, SRC, TFRC, TYRO3, UVRAG, TRIM25, PABPN1, SNX3, VAPB, VAPA, VPS4B, BCL2L11, TRIM13, TNIP1, ATG7, TUSC2, KPNA6, HIPK2, ZNF639, TRIM62, THOC2, CBLL1, ITCH
BP	GO:0006839	mitochondrial transport	63/3408	2.98E-02	ACACA, SLC25A6, BAK1, BCL2, BCL2L1, CAMK2A, CPT1A, ATF2, GSK3B, HK2, HSPA4, LETM1, OPA1, PPP3R1, PRKAA1, PRKAB2, MAPK8, SLC9A1, SREBF2, STAT3, TFDP1, TFDP2, TP53, UBE2D3, UBE2L3, YWHAE, YWHAG, FZD5, SLC25A16, BAP1, TP63, BAG4, ATG13, TOMM20, MFN2, BCL2L11, SLC25A15, MICU1, ARIH2, TIMM17A, BBC3, HTRA2, DNAJC15, SLC25A24, SH3GLB1, LEPROT, SLC25A38, SLC25A36, FBXW7, VPS35, MFF, MRS2, USP36, RHOU, MOAP1, MUL1, GRPEL1, SLC25A32, DNAJC30, BMF, TIMM50, GRPEL2, CHCHD10
BP	GO:0035909	aorta morphogenesis	13/3408	3.01E-02	JAG1, BMPR1A, COL3A1, EFNB2, HES1, RBPJ, LRP1, PROX1, SOX4, SRF, DLL4, CHD7, ADAMTS9
BP	GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	13/3408	3.01E-02	BAK1, BCL2, GSK3B, PPP3R1, MAPK8, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, BBC3, CHCHD10
BP	GO:1904031	positive regulation of cyclin-dependent	13/3408	3.01E-02	CCND1, CCND2, CCNT1, CCNT2, CDKN1A, CDKN1B, EGFR, PDGFB, PKD1, PROX1, SRC, ADAM17, MAPRE3

		protein kinase activity			
BP	GO:0003181	atrioventricular valve morphogenesis	10/3408	3.01E-02	BMPR1A, BMPR2, SMAD4, SMAD6, MDM4, SOX4, TWIST1, DCHS1, OLFM1, HEYL
BP	GO:0032925	regulation of activin receptor signaling pathway	10/3408	3.01E-02	ACVR1B, ACVR2B, FKBP1A, SMAD2, SMAD7, MEN1, SKI, FSTL3, FST, ZC3H3
BP	GO:0033119	negative regulation of RNA splicing	10/3408	3.01E-02	DYRK1A, HNRNPK, SRSF4, SRSF7, TMBIM6, PTBP3, SRSF10, RNPS1, U2AF2, RBMX
BP	GO:0034629	cellular protein-containing complex localization	10/3408	3.01E-02	SMAD7, RALB, SGCD, WASL, KLHL21, NDC1, NUP133, RCC2, SEH1L, NACC2
BP	GO:0036010	protein localization to endosome	10/3408	3.01E-02	ARF6, RDX, SORL1, NRP1, ROCK2, ABHD17B, VPS35, ABHD17C, MICALL1, ANKRD13A
BP	GO:0044346	fibroblast apoptotic process	10/3408	3.01E-02	BAK1, BTG1, MYC, SFRP1, TP53, CUL3, TP63, STK17B, STK17A, BCL2L11
BP	GO:0046697	decidualization	10/3408	3.01E-02	CTSB, GJA1, MEN1, PPARD, MAPK1, MAPK3, PTGIS, STC1, VDR, STC2
BP	GO:0099563	modification of synaptic structure	10/3408	3.01E-02	ABL1, RHOA, CDC42, EPHA4, FMR1, MYH10, STAU1, TIAM1, WASF1, DLGAP3
BP	GO:1904376	negative regulation of protein localization to cell periphery	10/3408	3.01E-02	BCL2L1, AP2M1, CSK, DAB2, GBP1, NUMB, LYPLA1, RHOQ, TMBIM1, PKDCC
BP	GO:0048644	muscle organ morphogenesis	26/3408	3.03E-02	ADARB1, BMPR1A, COL3A1, COL11A1, S1PR1, FKBP1A, FOXC1, NRG1, RBPJ, ISL1, SMAD4, SMAD7, POU4F1, PROX1, TGFBR1, TGFBR3, FZD1, HAND1, UBE4B, SERP1, DLL4, CHD7, VANGL2, HEG1, PTCD2, ARID5B
BP	GO:1903008	organelle disassembly	29/3408	3.05E-02	MARK2, HTT, HIF1A, HK2, KIF5B, SREBF2, TP53, VCP, FZD5, DENR, SQSTM1, ATG5, ATG13, MFN2, ATG7, GABARAPL2, ATG14, ATG2A, HTRA2, MCTS1, VPS13C, ATG2B, VPS13D, FBXW7, SMURF1, USP36, ATG9A, MUL1, MAP1LC3B
BP	GO:0046883	regulation of hormone secretion	65/3408	3.10E-02	SLC25A6, ARRB1, CACNA1C, CACNA1E, CPT1A, CREB1, EDN1, EFNA5, EGFR, ENSA, GJA1, GNAS, HIF1A, HMGCR, HNF4A, ISL1, ITPR1, ITPR2, KIF5B, LRP1, SMAD4, MYB, NKX3-1, P2RY1, CDK16, PFKFB2, PPARD, PPP3CA, PRKCA, PRKCE, PTPN11, RFX3, SFRP1, SCG5, SLC16A1, SNAP25, SOX4, SOX11, VAMP7, TCF7L2, TFR2, TIAM1, TMF1, DYNLL1, IRS2, PER2, KALRN, SYT7, AIMP1, MAP4K4, CLOCK, RAPGEF3, KDM5B, PASK, TARDBP, ARL2BP, SERP1, RAB8B, CHD7, NLGN2, RAB11FIP1, UQCC2, RASL10B, ACVR1C, BMP8A
BP	GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	36/3408	3.10E-02	FAS, RHOA, ARRB1, BAK1, CASP10, DAPK1, DDX3X, HIP1, MAPT, MYC, NKX3-1, PML, ROBO1, RPS3, SNCA, SYK, VCP, TNFSF10, FADD, BCL2L11, BCAP31, NOD1, DLC1, ANP32B, SIRT1, BCL2L13, MTCH1, BBC3, HTRA2, CYCS, IFT57, MUL1, SOX7, EGLN3, ACVR1C, ACER2
BP	GO:0019048	modulation by virus of host morphology or physiology	14/3408	3.14E-02	BCL2L1, DAG1, INSR, KPNA1, KPNA3, NTRK3, EIF2AK2, PABPN1, VAPB, VAPA, BCL2L11, ATG7, KPNA6, HIPK2
BP	GO:0043001	Golgi to plasma membrane protein transport	14/3408	3.14E-02	CSK, GOLGA4, NSF, SPTBN1, VAMP2, VAMP7, PREPL, ARFRP1, LYPLA1, RAB31, GOLPH3L, KIF13A, C16orf70, PKDCC
BP	GO:2000826	regulation of heart morphogenesis	14/3408	3.14E-02	JAG1, BMP7, BMPR2, CTNNB1, FOXC1, HES1, RBPJ, ISL1, SMAD4, PIM1, ROBO1, TGFBR1, TWIST1, DKK1
BP	GO:0042982	amyloid precursor protein metabolic process	20/3408	3.15E-02	ADAM10, CASP3, DYRK1A, EFNA3, EPHA4, FKBP1A, FLOT2, LYN, PAWR, PIN1, SOAT1, SORL1, ITM2B, ROCK2, TMED10, NCSTN, BACE2, LDLRAP1, APH1A, ITM2C
BP	GO:0014910	regulation of smooth muscle cell migration	25/3408	3.15E-02	ATP7A, BCL2, BMPR1A, CRK, IGFBP5, ILK, LRP1, MDK, MEF2C, FOXO4, SERPINE1, PDGFA, PDGFB, PPARD, SORL1, SRC, TERT, NR4A3, IQGAP1, NRP1, ADAMTS1, TRIB1, POSTN, SSH1, NDRG4

BP	GO:0007100	mitotic centrosome separation	7/3408	3.16E-02	CHEK1, AURKA, KIF3B, NDE1, NSFL1C, CEP85, UBXN2B
BP	GO:0043558	regulation of translational initiation in response to stress	7/3408	3.16E-02	EIF2S1, NCK1, PPP1CA, EIF2AK2, NCK2, EIF2AK1, PPP1R15B
BP	GO:0071361	cellular response to ethanol	7/3408	3.16E-02	DNMT3A, ITPR2, PRKAA1, PRKCE, PTEN, CCL7, TP53INP1
BP	GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	7/3408	3.16E-02	NUP88, RAN, ABCE1, TSC1, XPO1, NMD3, RIOK2
BP	GO:1901722	regulation of cell proliferation involved in kidney development	7/3408	3.16E-02	BMP7, EGR1, GATA3, IL6R, MYC, PDGFB, FLCN
BP	GO:1902043	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	7/3408	3.16E-02	PTEN, SFRP1, SKIL, STK4, THBS1, TIMP3, PEA15
BP	GO:0001659	temperature homeostasis	45/3408	3.16E-02	ACVR2B, ADRB1, APC, CAV1, CEBPB, EGR1, EPAS1, ESRRG, FOXO1, GATM, GJA1, GNAS, IGF1R, RBPJ, IL18, IRF4, LAMA4, LNPEP, PLCL1, PRKAB2, PRLR, RB1, SCD, STAT3, SYK, ADAM17, THRA, TRPM2, NR1H2, VEGFA, PER2, ZNF516, IP6K1, MFN2, ADAMTS5, KDM1A, KDM6B, LPIN1, ADIPOR1, LGR4, ARRDC3, ELOVL6, ADIPOR2, FLCN, SLC27A1
BP	GO:0010469	regulation of signaling receptor activity	45/3408	3.16E-02	CBL, DAPK1, DLG3, EPHB2, ESR2, FNTA, GRIA4, ITGB1, LRPAP1, MEF2C, NPTX1, P2RY1, SERPINE1, PDE4D, PTEN, SHC1, SRC, ADAM17, TAF1, TAL1, TGFA, NCOA3, NCK2, NRP1, GPRC5A, SOCS5, IL18BP, AKAP9, NLGN1, SHANK2, DKK1, NPTXR, CNRIP1, GREM1, DKK3, MINK1, ERRFI1, KLHL24, NCAPG2, FBXW7, NLGN2, NETO2, SOCS4, WFIKKN2, EPGN
BP	GO:0010771	negative regulation of cell morphogenesis involved in differentiation	28/3408	3.18E-02	ACTN4, RHOA, ARHGDIA, EFNA5, EPHA7, EPHB2, GBP1, GDI1, PPP3CA, PTEN, SEMA7A, NRP1, SYNGAP1, NTN1, RAPGEF2, SEMA3E, SEMA3A, SEMA4B, POSTN, NLGN1, FSTL4, KANK1, CORO1C, SEMA4C, RCC2, SEMA6A, GORASP1, TRAK2
BP	GO:0030316	osteoclast differentiation	28/3408	3.18E-02	CAMK4, CEBPB, CREB1, MAPK14, CSF1, CTNNB1, ESRRA, FBN1, GNAS, IREB2, NOTCH2, PAFAH1B1, POU4F1, SFRP1, SRC, TFRC, KLF10, SH3PXD2A, RASSF2, FSTL3, PIAS3, TOB2, FOXP1, FBXW7, FAM20C, CD109, ZNF675, SIGLEC15
BP	GO:0070527	platelet aggregation	19/3408	3.18E-02	ACTB, CSRP1, GNAS, ILK, LYN, MYH9, PDGFRA, SERPINE2, PIK3CB, PRKCA, RAP2B, SYK, TLN1, TYRO3, VCL, SH2B3, MYL12A, SLC7A11, ADAMTS18
BP	GO:0032924	activin receptor signaling pathway	15/3408	3.19E-02	ACVR1B, ACVR2B, BMPR2, FKBP1A, SMAD2, SMAD7, MEN1, SKI, TGFBR1, FSTL3, CITED2, FST, ZC3H3, TGIF2, ACVR1C
BP	GO:0034198	cellular response to amino acid starvation	15/3408	3.19E-02	FAS, CDKN1A, EIF2S1, MAPK1, MAPK3, MAPK8, EIF2AK2, SZT2, SH3GLB1, SLC38A2, RRAGD, RRAGC, SEH1L, SESN2, SESN3
BP	GO:0043616	keratinocyte proliferation	15/3408	3.19E-02	ZFP36L1, KLF9, EFNB2, MDK, NOTCH2, PPARD, PTCH1, PTPRK, SNAI2, VDR, ZFP36, TP63, FERMT1, BCL11B, CD109
BP	GO:0045746	negative regulation of Notch signaling pathway	15/3408	3.19E-02	JAG1, ARRB1, BCL6, BMP7, DLX2, EGFR, GATA2, JAG2, MMP14, EGFL7, YTHDF2, DLL4, FBXW7, HIF1AN, NRARP
BP	GO:0051293	establishment of spindle localization	15/3408	3.19E-02	CENPA, HTT, MAD2L1, MAP4, MYH9, PAFAH1B1, PAX6, ARHGEF2, SPRY1, CLASP1, NDE1, NSFL1C, FMN2, SPIRE1, UBXN2B
BP	GO:0007088	regulation of mitotic nuclear division	43/3408	3.19E-02	APC, ATM, ATRX, BMP7, CDKN1B, RCC1, CHEK1, DUSP1, EDN1, HNRNPU, IGF2, IK, INSR, MAD2L1, PDGFB, PIN1, RAD21, RB1, AURKA, TGFA, SMC1A, CUL3, CDC14B, TNKS, AURKB, TRIP13, VPS4B, STAG2, NIPBL, SH2B1, CHMP5, ANLN, PHIP, RIOK2, PCID2, NSFL1C, CHMP1B, HECW2, CEP85, CEP97, CCSAP, UBXN2B, EPGN

BP	GO:0001541	ovarian follicle development	18/3408	3.21E-02	ARRB1, ARRB2, ATM, BCL2, BCL2L1, CEBPB, CTNNA1, FOXC1, FOXO3, KIT, SMAD4, KITLG, MMP14, SRC, VEGFA, PCYT1B, KMT2B, ZNF830
BP	GO:0002090	regulation of receptor internalization	18/3408	3.21E-02	ARF1, ARRB1, ARRB2, EFNB2, FMR1, LRPAP1, MKLN1, OPHN1, ATXN2, SH3GL2, SYK, VEGFA, NUMB, DKK1, GREM1, UBQLN2, AHI1, ANKRD13A
BP	GO:0061098	positive regulation of protein tyrosine kinase activity	18/3408	3.21E-02	BDNF, DLG3, DOCK3, EPHA4, ERCC6, NRG1, NEDD9, PAK2, PDGFB, PTPN1, SRC, ADAM17, TAL1, TGFA, NCAPG2, FBXW7, AFAP1L2, EPGN
BP	GO:0070830	bicellular tight junction assembly	18/3408	3.21E-02	ACTN4, APC, RUNX1, CBFB, ECT2, GJA1, IKBKB, MYO1C, SNAI2, SNAI1, SRF, STRN, FZD5, ROCK2, PDCD6IP, PARD3, PARD6B, MTDH
BP	GO:0009266	response to temperature stimulus	60/3408	3.21E-02	ADM, ADRB1, ARRB2, ATM, ATP2A2, ATP2B1, ATR, BAG1, CAMK2A, CAMK2D, CDKN1A, CREBBP, EIF2S1, EP300, FGF1, FKBP4, FOXO1, GSK3B, HDAC2, HSBP1, DNAJA1, HSPA2, HSPA5, IRAK1, LYN, MAPT, ATXN3, NUP88, NUP98, POLR2D, PRKAA1, MAPK1, MAPK3, RANBP2, SLC9A1, THBS1, THRA, TRPM2, VCP, YWHAE, BAG4, ZNF516, POM121, DNAJA2, NUP50, DNAJB4, SIRT1, HSPB8, MYOF, HTRA2, NDC1, NUP133, SLC12A5, MLST8, SEH1L, AKT1S1, TP53INP1, NUP43, SLC27A1, POM121C
BP	GO:1903707	negative regulation of hemopoiesis	41/3408	3.21E-02	BCL6, ZFP36L1, RUNX1, RUNX3, CBFB, CDK6, CTNNB1, ERBB2, FBN1, GABPA, GATA2, HMGB3, HOXA5, HOXA7, HOXA9, HOXB8, HES1, IRF1, ITPKB, LYN, SMAD7, MDK, MEIS2, MYC, SFRP1, TAL1, ZFP36, SOCS1, LDB1, CTR9, SOCS5, TRIB1, FSTL3, PIAS3, TOB2, NCAPG2, FBXW7, CDC73, ZBTB46, ZNF675, NRARP
BP	GO:0006164	purine nucleotide biosynthetic process	72/3408	3.21E-02	ACACA, ACLY, ADA, ADCY1, ADCY6, ADCY9, ADORA2B, AK2, AK4, ACSL4, GAPDH, GPI, GUCY1A2, HIF1A, HK1, HK2, FOXK2, IMPDH1, INSR, LDHA, NME4, NUP88, NUP98, PDK3, PDK4, PFAS, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PPAT, PRKAA1, PRPSAP2, RANBP2, SCD, SNCA, STAT3, ELOVL4, TP53, VCP, PAPSS2, NCOR1, POM121, PAICS, NUP50, SLC2A6, ACSL6, AK3, SLC35B3, PANK1, DDIT4, PDPR, NDC1, NUP133, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, DNAJC30, ACSS1, CBR4, ACSF3, FLCN, FOXK1, NUP43, POM121C
BP	GO:0014911	positive regulation of smooth muscle cell migration	16/3408	3.21E-02	ATP7A, BCL2, CRK, IGFBP5, LRP1, MDK, FOXO4, PDGFB, SRC, TERT, NR4A3, IQGAP1, NRP1, ADAMTS1, POSTN, SSH1
BP	GO:0021695	cerebellar cortex development	16/3408	3.21E-02	ARCN1, RERE, ATP7A, EZH2, HSPA5, MDK, MYH10, OPHN1, SERPINE2, PROX1, PTPN11, RORA, B4GALT2, LDB1, MTPN, TTBK2
BP	GO:0048806	genitalia development	16/3408	3.21E-02	AR, AXL, BAK1, CTNNB1, HOXD13, LRP6, PDGFRA, PKD1, PTPN11, TBX3, TCF7, TYRO3, TP63, NIPBL, LGR4, CHD7
BP	GO:0032007	negative regulation of TOR signaling	17/3408	3.21E-02	ATM, HIF1A, PRKAA1, TSC1, SZT2, SIRT1, DDIT4, TMEM127, FNIP2, SESN2, AKT1S1, FNIP1, TNFAIP8L1, SESN3, SIK1, UBR1, FLCN
BP	GO:0048641	regulation of skeletal muscle tissue development	17/3408	3.21E-02	BCL2, CTNNB1, DDX5, HMGCR, MEF2C, PRKAA1, TWIST1, HDAC9, NR1D2, DDX17, DKK1, FBXO22, CDON, SIX4, CYP26B1, AKIRIN1, UQCC2
BP	GO:0002328	pro-B cell differentiation	6/3408	3.26E-02	HES1, LIG4, SOS1, SOX4, FNIP1, FLCN
BP	GO:0003174	mitral valve development	6/3408	3.26E-02	BMPR1A, BMPR2, SMAD6, SOX4, TWIST1, DCHS1
BP	GO:0006048	UDP-N-acetylglucosamine biosynthetic process	6/3408	3.26E-02	GFPT1, PGM3, GFPT2, GNPDA1, GNPNAT1, UAP1L1
BP	GO:0009950	dorsal/ventral axis specification	6/3408	3.26E-02	BMPR1A, CTNNB1, SMAD2, SMAD6, PAX6, SFRP1
BP	GO:0015014	heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process	6/3408	3.26E-02	EXTL2, EXTL3, NDST1, NDST3, HS2ST1, CSGALNACT1

BP	GO:0035404	histone-serine phosphorylation	6/3408	3.26E-02	PRKAA1, AURKA, HMGA2, RPS6KA4, AURKB, RPS6KA5
BP	GO:0046501	protoporphyrinogen IX metabolic process	6/3408	3.26E-02	ALAD, ALAS1, FECH, IREB2, UROS, EIF2AK1
BP	GO:0048548	regulation of pinocytosis	6/3408	3.26E-02	ACTN4, AXL, CAV1, NR1H2, APPL1, ANKFY1
BP	GO:0051574	positive regulation of histone H3-K9 methylation	6/3408	3.26E-02	BRCA1, JARID2, MECP2, MYB, SIRT1, RIF1
BP	GO:0060439	trachea morphogenesis	6/3408	3.26E-02	CTNNB1, HOXA5, LRP6, MAPK1, MAPK3, WNT7B
BP	GO:0060525	prostate glandular acinus development	6/3408	3.26E-02	FOXA1, HOXD13, SFRP1, TP63, FRS2, WDR77
BP	GO:0061307	cardiac neural crest cell differentiation involved in heart development	6/3408	3.26E-02	JAG1, BMP7, HES1, MAPK1, MAPK3, TWIST1
BP	GO:0061308	cardiac neural crest cell development involved in heart development	6/3408	3.26E-02	JAG1, BMP7, HES1, MAPK1, MAPK3, TWIST1
BP	GO:0072173	metanephric tubule morphogenesis	6/3408	3.26E-02	HES1, PAX2, PKD1, SOX8, WNT4, LGR4
BP	GO:1905146	lysosomal protein catabolic process	6/3408	3.26E-02	LAMP2, LDLR, LRP1, LAPTM4B, VPS35, TMEM199
BP	GO:2000615	regulation of histone H3-K9 acetylation	6/3408	3.26E-02	BRCA1, CHEK1, GATA3, SMAD4, KMT2A, ZNF451
BP	GO:0007565	female pregnancy	49/3408	3.27E-02	ACVR1B, ADM, AR, BCL2, PRDM1, BMPR2, CALR, CAPN2, COMT, CTSB, EMP2, ACSL4, FKBP4, FOSB, GJA1, GOT2, IGFBP5, ITGA3, ITGA5, KRAS, LNPEP, MEN1, PAPPA, PGR, PPARD, PPAT, MAPK1, MAPK3, PRLR, PTGIS, RGS2, SP3, STC1, TEAD3, NR2F2, UMPS, VDR, FOSL1, ARID1A, STC2, PRDX3, KPNA6, DAZAP1, WNT4, SLC38A2, UBE2Q1, ADIPOR2, POLR1B, ACVR1C
BP	GO:0048839	inner ear development	49/3408	3.27E-02	ADAM10, JAG1, CCNA2, CDKN1B, CEBPD, COL11A1, DLX6, EPHA4, EPHB2, GATA2, GATA3, HES1, RBPJ, INSIG1, JAG2, KCNK3, NTRK3, OPA1, OTX1, PAFAH1B1, PAX2, ATP8B1, PRRX1, PROX1, PTPN11, SDC4, SPARC, ZEB1, FZD3, NR4A3, FZD6, ITGA8, DCHS1, TRIP11, NTN1, ATG5, SLC4A7, ANP32B, LRIG1, INSIG2, SIX4, AHI1, ESRP1, SOBP, CHD7, VANGL2, TTC39C, BMPER, FREM2
BP	GO:0003180	aortic valve morphogenesis	11/3408	3.29E-02	JAG1, GATA3, SMAD6, RB1, ROBO1, SNAI2, SNAI1, TWIST1, ROCK2, HEYL, DLL4
BP	GO:0033137	negative regulation of peptidyl-serine phosphorylation	11/3408	3.29E-02	BAK1, CAV1, SMAD7, NCK1, PDE4D, NCK2, RASSF2, DKK1, GPD1L, DDIT4, CNKSR3
BP	GO:0036296	response to increased oxygen levels	11/3408	3.29E-02	FAS, ATP6V1A, CAV1, CDKN1A, COL1A1, DNMT3B, FOXO1, HDAC2, ATP6V0D1, ATG7, TMEM199
BP	GO:0045577	regulation of B cell differentiation	11/3408	3.29E-02	ZFP36L1, ZFP36L2, CYLD, NCKAP1L, HMGB3, MMP14, SFRP1, SYK, XBP1, PCID2, ATP11C
BP	GO:0010632	regulation of epithelial cell migration	70/3408	3.29E-02	ABL1, ARF6, RHOA, RHOB, BMPR2, CALR, DCN, HBEGF, EDN1, EMP2, FGF1, FGF2, FLT4, GATA2, GATA3, GPI, HIF1A, ITGA3, JUN, JUP, MECP2, MEF2C, MAP3K3, MET, PDGFB, PIK3C2A, PRCP, PRKCA, PRKCE, PROX1, PTEN, PTPRG, PTPRR, RREB1, SP100, SPARC, SRC, STC1, ADAM17, NR2F2, THBS1, VEGFA, ADAM9, NRP1, KLF4, MAP4K4, ROCK2, HDAC9, AKT3, SEMA3A, PLK2, DUSP10, VASH1, CLASP1, SIRT1, CORO1C, FOXP1, ADIPOR1, EPB41L4B, DLL4, FBXW7, ADAMTS9, EPB41L5, PBLD, NUS1, DAB2IP, AMOTL1, SPRED1, BMPER, EMC10

BP	GO:0046785	microtubule polymerization	23/3408	3.29E-02	ABL1, CDKN1B, CSNK1D, DYRK1A, FKBP4, MAP1B, MAPT, MECP2, MET, RPS3, SNCA, AKAP9, TUBB4A, TPPP, MAPRE3, CAMSAP2, CLASP1, CLIP3, NIN, NDE1, SLAIN2, NAV3, CAMSAP1
BP	GO:0046902	regulation of mitochondrial membrane permeability	23/3408	3.29E-02	BAK1, BCL2, BCL2L1, CAMK2A, ATF2, GSK3B, HK2, PPP3R1, MAPK8, SLC9A1, STAT3, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, BCL2L11, BBC3, MOAP1, MUL1, BMF, CHCHD10
BP	GO:0061045	negative regulation of wound healing	23/3408	3.29E-02	CDKN1A, CDKN1B, CRK, EDN1, FGF2, GJA1, HMGCR, SERPINE1, SERPINB2, PDGFA, PDGFB, PDGFRA, SERPINE2, PTEN, TFPI, THBS1, SH2B3, DUSP10, CLASP1, WNT4, PHLDB2, CD109, ADAMTS18
BP	GO:0019218	regulation of steroid metabolic process	34/3408	3.35E-02	ACACA, ADM, ASAH1, EGR1, FGF1, HMGCR, INSIG1, KIT, LDLR, LSS, NFKB1, NFYA, NFYB, PRKAA1, PROX1, RAN, RORA, SCD, SNAI2, SNAI1, SREBF2, VDR, SF1, AKR1C3, FGF19, ERLIN2, SIRT1, LDLRAP1, DKK3, INSIG2, WNT4, ELOVL6, PANK2, STARD4
BP	GO:0021549	cerebellum development	29/3408	3.38E-02	ABL1, ARCN1, RERE, ATP7A, CNTN1, CRK, CRKL, EZH2, FOXC1, HNRNPD, HSPA5, KCNC1, LRP6, MDK, MECP2, MYH10, OPHN1, SERPINE2, PROX1, PTPN11, RORA, TP53, FZD4, B4GALT2, LDB1, NCSTN, SEMA4C, MTPN, TTBK2
BP	GO:0030148	sphingolipid biosynthetic process	29/3408	3.38E-02	ASAH1, CLN8, KDSR, PRKAA1, ELOVL4, UGCG, ST8SIA4, NSMAF, SGPL1, VAPB, VAPA, B4GALT6, SPTLC1, CERS1, ORMDL2, ST6GALNAC6, ST8SIA3, SPTLC3, ACER3, ELOVL5, ELOVL6, SGPP1, ORMDL1, ORMDL3, SAMD8, PPM1L, SGMS2, CERS6, ACER2
BP	GO:0046488	phosphatidylinositol metabolic process	45/3408	3.40E-02	ARF1, ATM, CDS1, FGF2, IMPA2, PDGFA, PDGFB, PIGA, PIK3C2A, PIK3CB, PIP4K2A, PTEN, RAB5A, SOCS1, INPP4B, SOCS2, SYNJ1, SYNJ2, MTMR3, MTMR7, MTMR4, SOCS6, SOCS5, IP6K1, SACM1L, SMG1, EFR3A, PIP5K1C, SOCS7, RAB14, PI4K2B, INPP5E, PITPNM2, PLEKHA4, PLEKHA1, MTMR9, PGAP1, PITPNM3, FAM126A, PLEKHA8, PGAP3, TTC7B, LCLAT1, FAM126B, SLC27A1
BP	GO:0031290	retinal ganglion cell axon guidance	9/3408	3.44E-02	ALCAM, EFNA5, EPHA7, EPHB2, EPHB3, ISL1, VEGFA, NRP1, ISL2
BP	GO:0032986	protein-DNA complex disassembly	9/3408	3.44E-02	HMGA1, MYC, SET, SMARCC2, SMARCD2, SMARCE1, ARID1A, SUPT16H, ARID2
BP	GO:0048485	sympathetic nervous system development	9/3408	3.44E-02	CTNNB1, GATA3, SOX4, SOX11, FZD3, TP63, NRP1, SEMA3A, PLXNA4
BP	GO:0072111	cell proliferation involved in kidney development	9/3408	3.44E-02	BMP7, EGR1, GATA3, IL6R, MYC, PDGFB, PTCH1, STAT1, FLCN
BP	GO:2000810	regulation of bicellular tight junction assembly	9/3408	3.44E-02	RUNX1, CBFB, GJA1, IKBKB, MYO1C, SNAI2, SNAI1, FZD5, ROCK2
BP	GO:0010038	response to metal ion	85/3408	3.48E-02	ADCY1, ADD1, ALAD, ANXA7, ATP7A, CCND1, BCL2, CALM1, CALM2, CALM3, CALR, CAMK2D, CASP3, CAV1, CDKN1B, CREB1, DNMT3A, DUSP1, ECT2, EDN1, EGFR, EIF2S1, FOSB, FUS, G6PD, GDI1, HIF1A, HNRNPD, HSPA5, ITPKB, JUN, JUND, KCNC1, KCNK3, KIT, LIG4, LOXL2, MAPT, MEF2A, MEF2C, MT1M, MTF1, NEDD4, NPC1, SLC11A2, OGG1, TNFRSF11B, PPP1CA, PPP2CA, PPP3CA, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, PTEN, SNCA, SPARC, STIM1, SYT1, TERT, TFR2, THBS1, TRPM2, UROS, VCAM1, AKR1C3, ADAM9, IQGAP1, CPNE3, SYT7, FSTL3, AHCYL1, NLGN1, SYT11, NCSTN, CLIC4, KCNMB4, SLC25A24, SYT17, WNK1, CYBRD1, SYT2, CPNE8, CPNE2
BP	GO:0035914	skeletal muscle cell differentiation	21/3408	3.52E-02	BCL9, DDX5, EGR1, FOXN2, MEF2C, MEF2D, RB1, SOX11, BTG2, COPS2, NR1D2, DDX17, MAFF, HEYL, SOX8, CDON, SIX4, CYP26B1, AKIRIN1, UQCC2, ZNF689
BP	GO:0046323	glucose import	21/3408	3.52E-02	AKT2, MAPK14, HK2, INSR, MEF2A, ENPP1, PTPN11, SORT1, SLC1A2, TERT, TSC1, IRS2, PEA15, C2CD5, FGF19, ARPP19, RHOQ, APPL1, ADIPOR2, SESN2, OSBPL8
BP	GO:1903034	regulation of response to wounding	46/3408	3.53E-02	ATP7A, CAV1, CDKN1A, CDKN1B, CRK, HBEGF, EDN1, EPHA4, FGF2, GJA1, HMGCR, LRP1, LYN, MDK, MYH9, NTRK3, SERPINE1, SERPINB2, PDGFA, PDGFB, PDGFRA, SERPINE2, PPARD, PRKCA, PRKCE, PTEN, PTPRF, RREB1, SYK, TFPI, THBS1, XBP1, STK24, KLF4, LRIG2, SH2B3, HPSE, DUSP10, KANK1, CLASP1, WNT4, RGMA, KREMEN1, PHLDB2, CD109, ADAMTS18
BP	GO:0061311	cell surface receptor signaling pathway involved in heart development	12/3408	3.53E-02	JAG1, BMPR1A, CTNNB1, RBPJ, MSX1, NOTCH2, SNAI2, SNAI1, DKK1, HEYL, DLL4, VANGL2
BP	GO:0070570	regulation of neuron projection regeneration	12/3408	3.53E-02	EPHA4, LRP1, NTRK3, PRRX1, PTEN, PTPRF, STK24, KLF4, MAP4K4, LRIG2, RGMA, KREMEN1

BP	GO:0090504	epiboly	12/3408	3.53E-02	RHOA, CD44, COL5A1, HBEGF, MEGF8, ARHGAP35, ITGA5, PTEN, RREB1, ADAM17, CLASP1, PHLDB2
BP	GO:0043473	pigmentation	28/3408	3.53E-02	AP1G1, ARCN1, ATP7A, BCL2, LYST, HPS1, KIT, MEF2C, KITLG, MYO5A, ENPP1, RAB1A, SNAI2, SPARC, AP3D1, USP13, RAB11B, BCL2L11, ATP6AP2, SZT2, ADAMTS9, SHROOM3, KIF13A, RAB17, MLPH, HPS6, VANGL1, MYSM1
BP	GO:0000956	nuclear-transcribed mRNA catabolic process	52/3408	3.57E-02	ATM, ZFP36L1, ZFP36L2, DDX5, DDX6, EIF4G1, ETF1, GSPT1, MLH1, NCBP1, CNOT4, PARN, POLR2D, PPP2CA, PPP2R1A, PPP2R2A, UPF1, RPL15, RPL28, RPL34, RPL37, RPS3, RPS23, ZFP36, CSDE1, BTG2, CNOT8, SMG7, THRAP3, TOB1, HBS1L, RNPS1, CPEB3, CNOT1, SAMD4A, SMG1, TNRC6B, SMG5, LSM4, UPF2, AGO1, PABPC1, TNRC6A, XRN1, SAMD4B, PCID2, DCP1A, CNOT6, TNRC6C, EDC3, PDE12, PATL1
BP	GO:0030073	insulin secretion	52/3408	3.57E-02	ACVR2B, SLC25A6, ARRB1, CACNA1C, CACNA1E, CPT1A, EFNA5, ENSA, GJA1, HIF1A, HMGCR, HNF4A, ISL1, ITPR1, ITPR2, KIF5B, LRP1, SMAD2, MYO5A, CDK16, PFKFB2, PPARD, PPP3CA, PRKCA, PRKCE, PTPN11, PTPRN2, RFX3, SFRP1, SLC16A1, SNAP25, SOX4, HNF1B, TCF7L2, TIAM1, DYNLL1, IRS2, PER2, SYT7, RAB11B, MAP4K4, CLOCK, RAPGEF3, RAB11FIP2, TARDBP, ARL2BP, SERP1, NLGN2, UQCC2, ACVR1C, BMP8A, SNX19
BP	GO:0007051	spindle organization	44/3408	3.59E-02	RHOA, ATRX, RCC1, CHD3, CSNK1D, HNRNPU, KIF2A, MAP4, MECP2, MLH1, MYBL2, MYH9, PKD1, PPP2R1A, RAN, RNF4, RPS3, AURKA, TACC1, UVRAG, VCP, SMC1A, TNKS, PRC1, AURKB, KIF3B, KIF23, VPS4B, NCOR1, STAG2, PLK2, MAPRE3, CLASP1, SENP6, CHMP5, INO80, HAUS6, HAUS2, TRIM36, CHMP1B, CEP97, LZTS2, CCSAP, CEP120
BP	GO:0046834	lipid phosphorylation	20/3408	3.61E-02	IMPA2, PIK3C2A, PIK3CB, PIP4K2A, DGKE, DGKD, SOCS1, SOCS2, SOCS6, SOCS5, IP6K1, SMG1, EFR3A, PIP5K1C, SOCS7, PI4K2B, FAM126A, TTC7B, DGKH, FAM126B
BP	GO:0010970	transport along microtubule	42/3408	3.65E-02	DST, CDC42, FLOT2, FMR1, HTT, HIF1A, HNRNPU, KIF5B, TNPO1, MAP1A, MAP1B, MAPT, NEFH, OPA1, PAFAH1B1, PURA, RAB1A, VAMP7, TUB, DYNLL1, WASF1, AP3D1, TRIP11, KIF3B, KIF23, AP3S2, KIF3A, TRAK1, RAB21, KIF1B, MAPK8IP3, BICD2, AP3M1, DYNC2LI1, NDE1, IFT57, KIF13A, TRAK2, FYCO1, SSX2IP, ARL8A, TMEM201
BP	GO:0099111	microtubule-based transport	42/3408	3.65E-02	DST, CDC42, FLOT2, FMR1, HTT, HIF1A, HNRNPU, KIF5B, TNPO1, MAP1A, MAP1B, MAPT, NEFH, OPA1, PAFAH1B1, PURA, RAB1A, VAMP7, TUB, DYNLL1, WASF1, AP3D1, TRIP11, KIF3B, KIF23, AP3S2, KIF3A, TRAK1, RAB21, KIF1B, MAPK8IP3, BICD2, AP3M1, DYNC2LI1, NDE1, IFT57, KIF13A, TRAK2, FYCO1, SSX2IP, ARL8A, TMEM201
BP	GO:0021766	hippocampus development	24/3408	3.67E-02	ATP2B4, CASP3, CDK6, CRK, CRKL, DLX2, EZH1, EZH2, GSK3B, ID4, KIF5B, MDK, NF2, PAFAH1B1, PROX1, PTEN, SRF, TSC1, YWHAE, BTG2, NR4A3, PHLPP2, KDM6B, UBA6
BP	GO:0000578	embryonic axis specification	13/3408	3.68E-02	CTNNB1, SMAD2, SMAD4, SMAD6, PCSK6, PTCH1, TBX3, KDM6A, FZD5, FRS2, EPB41L5, PLD6, NRARP
BP	GO:0030224	monocyte differentiation	13/3408	3.68E-02	ZFP36L1, CDK6, CSF1, HOXA7, JUN, MEF2C, MYC, MYH9, PDE1B, SP3, VEGFA, FOXP1, ZBTB46
BP	GO:0033572	transferrin transport	13/3408	3.68E-02	ARHGAP1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, TFR2, TFRC, ATP6V0D1, RAB11B, LMTK2, ATP6V1D, STEAP3, ATP6V0E2
BP	GO:0051031	tRNA transport	13/3408	3.68E-02	NUP88, NUP98, RAN, RANBP2, TOMM20, POM121, NUP50, XPOT, NDC1, NUP133, SEH1L, NUP43, POM121C
BP	GO:1903131	mononuclear cell differentiation	13/3408	3.68E-02	ZFP36L1, CDK6, CSF1, HOXA7, JUN, MEF2C, MYC, MYH9, PDE1B, SP3, VEGFA, FOXP1, ZBTB46
BP	GO:0120193	tight junction organization	19/3408	3.68E-02	ACTN4, APC, RUNX1, CBFB, ECT2, GJA1, IKBKB, MYO1C, SNAI2, SNAI1, SRF, STRN, TGFBR1, FZD5, ROCK2, PDCD6IP, PARD3, PARD6B, MTDH
BP	GO:0006661	phosphatidylinositol biosynthetic process	32/3408	3.69E-02	ARF1, ATM, CDS1, FGF2, PDGFA, PDGFB, PIGA, PIK3C2A, PIK3CB, PIP4K2A, PTEN, RAB5A, INPP4B, SYNJ1, SYNJ2, MTMR3, MTMR7, MTMR4, SACM1L, PIP5K1C, RAB14, PI4K2B, INPP5E, PITPNM2, PLEKHA4, PLEKHA1, MTMR9, PGAP1, PITPNM3, PLEKHA8, PGAP3, SLC27A1
BP	GO:0034219	carbohydrate transmembrane transport	32/3408	3.69E-02	AKT2, MAPK14, EDN1, HK2, INSR, MEF2A, ENPP1, PPARD, PTPN11, SORT1, SLC1A2, SLC5A3, TERT, TSC1, NR4A3, IRS2, PEA15, C2CD5, SLC23A2, FGF19, ARPP19, SLC2A6, RHOQ, CLIP3, APPL1, SLC17A5, SLC2A8, TMEM144, ADIPOR2, SLC2A10, SESN2, OSBPL8
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	65/3408	3.75E-02	ABL1, RHOA, CASP10, CCR7, CTNNB1, ECT2, FKBP1A, GJA1, IKBKB, IRAK1, IRAK2, MAP3K3, PPM1B, PRKCE, RORA, CX3CL1, SLC20A1, STAT1, TLE1, TSPAN6, UBE2N, UBE2V1, TRIM25, TNFSF10, FADD, SQSTM1, BTRC, DDX21, VAPA, ROCK2, TRIM13, TNIP1, TRIM22, NOD1, TAB1, RBCK1, PLK2, ZMYND11, AKAP13, MAPKBP1, ERC1, TAB2, ZDHHC17, SIRT1, NKIRAS2, NKIRAS1, GOLT1B, CC2D1A, TRIM62, TMEM9B, OTUD7B, PELI1, MAVS, MIER1, MUL1, SNIP1, TMEM101, MTDH, CANT1, SIRPA, MIB2, DAB2IP, ZNF675, TMED4, C18orf32
BP	GO:0065002	intracellular protein transmembrane transport	18/3408	3.75E-02	AKT2, HSPA5, PEX13, PEX5, TRAM2, TOMM20, C2CD5, TIMM17A, SEC63, TRAM1, DNAJC15, SEC61A1, PEX5L, PEX26, GRPEL1, LONP2, TIMM50, GRPEL2
BP	GO:0090183	regulation of kidney development	18/3408	3.75E-02	BMP7, CTNNB1, EGR1, GATA3, IL6R, MYC, PAX2, PDGFA, PDGFB, STAT1, HNF1B, VEGFA, WNT2B, SOX8, SIX4, WNT4, LGR4, FLCN

BP	GO:0120192	tight junction assembly	18/3408	3.75E-02	ACTN4, APC, RUNX1, CBFB, ECT2, GJA1, IKBKB, MYO1C, SNAI2, SNAI1, SRF, STRN, FZD5, ROCK2, PDCD6IP, PARD3, PARD6B, MTDH
BP	GO:0006278	RNA-dependent DNA biosynthetic process	23/3408	3.80E-02	ATM, ATR, CCT6A, CTNNB1, DKC1, HNRNPC, HNRNPU, MAP3K4, PARN, MAPK1, MAPK3, RFC1, SRC, TERT, XRCC5, TNKS, AURKB, SMG7, SMG5, XRN1, GNL3L, PINX1, HMBOX1
BP	GO:0008344	adult locomotory behavior	23/3408	3.80E-02	ARCN1, ARRB2, CTNS, EPHA4, CLN8, EPS8, HOXB8, KCNJ10, MECP2, NPC1, PAFAH1B1, SNCA, TSC1, KALRN, PUM1, GIGYF2, HTRA2, HIPK2, ADAM22, OXR1, CHD7, PREX2, BTBD9
BP	GO:0016575	histone deacetylation	23/3408	3.80E-02	BCL6, CAMK2D, ELK4, HDAC2, MAPK8, KDM5A, SKI, TBL1X, TP53, VEGFA, PER2, MTA1, MORF4L2, HDAC9, RCOR1, SIRT1, NIPBL, SIN3A, SMARCAD1, MIER1, TBL1XR1, BRMS1L, NACC2
BP	GO:0072132	mesenchyme morphogenesis	17/3408	3.80E-02	BMP7, BMPR1A, FOXC1, RBPJ, ISL1, SMAD2, SMAD4, MDM4, MSX1, MYC, ROBO1, SNAI2, SNAI1, TGFBR1, TWIST1, DCHS1, HEYL
BP	GO:0007019	microtubule depolymerization	15/3408	3.81E-02	APC, KIF2A, MAP1A, MAP1B, MID1, ARHGEF2, KIF2C, CAMSAP2, CLASP1, TAOK1, NAV3, CCSAP, TTBK2, CAMSAP1, KIF24
BP	GO:0035307	positive regulation of protein dephosphorylation	15/3408	3.81E-02	CALM1, CALM2, CALM3, PPP1R12A, PIN1, PPP2R5D, PTPRC, DLC1, ANKLE2, NSMF, PPP1R16B, SLC39A10, PPP1R15B, SPPL3, CNEP1R1
BP	GO:1902667	regulation of axon guidance	15/3408	3.81E-02	BMPR2, MEGF8, VEGFA, SEMA7A, NRP1, SEMA3E, SEMA3A, SEMA4B, MYCBP2, SEMA4C, YTHDF1, SEMA6A, ZSWIM6, ZSWIM4, PLXNA4
BP	GO:1903214	regulation of protein targeting to mitochondrion	15/3408	3.81E-02	PRKAA1, SREBF2, UBE2D3, UBE2L3, FZD5, BAP1, BAG4, ATG13, ARIH2, HTRA2, SH3GLB1, LEPROT, FBXW7, USP36, RHOU
BP	GO:0030850	prostate gland development	16/3408	3.82E-02	AR, BMP7, CDKN1B, CTNNB1, FKBP4, FOXA1, HOXD13, ID4, NKX3-1, PTCH1, PTEN, RARG, SFRP1, TP63, FRS2, WDR77
BP	GO:0046850	regulation of bone remodeling	16/3408	3.82E-02	CSK, S1PR1, EGFR, GJA1, MDK, TNFRSF11B, PDK4, PRKCA, SFRP1, SRC, SYK, TFRC, SYT7, PLEKHM1, GREM1, SIGLEC15
BP	GO:0044706	multi-multicellular organism process	55/3408	3.83E-02	ACVR1B, ADM, AR, BCL2, PRDM1, BMPR2, CALR, CAPN2, COMT, CTSB, EDN1, EMP2, ACSL4, FKBP4, FOSB, GJA1, GOT2, IGFBP5, ITGA3, ITGA5, KRAS, LNPEP, MEN1, PAPPA, PGR, SERPINE2, PPARD, PPAT, MAPK1, MAPK3, PRLR, PTAFR, PTGIS, RGS2, SP3, STC1, TEAD3, NR2F2, UMPS, VDR, FOSL1, ARID1A, STC2, KALRN, PRDX3, KPNA6, MAFF, DAZAP1, WNT4, SLC38A2, UBE2Q1, ADIPOR2, POLR1B, ACVR1C, SH3PXD2B
BP	GO:0090276	regulation of peptide hormone secretion	52/3408	3.86E-02	SLC25A6, ARRB1, CACNA1C, CACNA1E, CPT1A, EFNA5, EGFR, ENSA, GJA1, HIF1A, HMGCR, HNF4A, ISL1, ITPR1, ITPR2, KIF5B, LRP1, CDK16, PFKFB2, PPARD, PPP3CA, PRKCA, PRKCE, PTPN11, RFX3, SFRP1, SLC16A1, SNAP25, SOX4, TCF7L2, TFR2, TIAM1, DYNLL1, IRS2, PER2, KALRN, SYT7, AIMP1, MAP4K4, CLOCK, RAPGEF3, PASK, TARDBP, ARL2BP, SERP1, RAB8B, CHD7, NLGN2, UQCC2, RASL10B, ACVR1C, BMP8A
BP	GO:0007026	negative regulation of microtubule depolymerization	10/3408	3.88E-02	APC, MAP1B, MID1, ARHGEF2, CAMSAP2, CLASP1, TAOK1, NAV3, TTBK2, CAMSAP1
BP	GO:0030325	adrenal gland development	10/3408	3.88E-02	INSR, SMAD2, MDK, PBX1, PDGFRA, FSTL3, CITED2, DKK3, WNT4, ARID5B
BP	GO:0060561	apoptotic process involved in morphogenesis	10/3408	3.88E-02	BAK1, BMP7, FOXC1, JAG2, PAX2, HNF1B, TNFRSF1B, VDR, FZD5, BCL2L11
BP	GO:2000679	positive regulation of transcription regulatory region DNA binding	10/3408	3.88E-02	CTNNB1, EP300, FOXC1, GATA3, PAX6, POU4F1, RB1, TWIST1, HMGA2, KLF4
BP	GO:0033135	regulation of peptidyl-serine phosphorylation	37/3408	3.90E-02	ARRB1, ARRB2, ATP2B4, BAK1, BCL2, CAV1, CD44, EGFR, EIF4G1, ERCC6, SMAD7, NCK1, NTRK3, PDE4D, PLCL1, PRKAA1, SNCA, STK4, TXN, VEGFA, BCAR3, NCK2, LATS1, BAG4, RASSF2, AKAP9, TENM1, RAPGEF3, DKK1, GPD1L, DDIT4, FNIP2, NSD1, MAPKAP1, FNIP1, CNKSR3, RICTOR
BP	GO:0010634	positive regulation of epithelial cell migration	44/3408	3.91E-02	ABL1, ARF6, RHOB, BMPR2, CALR, HBEGF, EDN1, FGF1, FGF2, FLT4, GATA2, GATA3, GPI, HIF1A, ITGA3, JUN, MAP3K3, MET, PDGFB, PIK3C2A, PRKCA, PRKCE, PROX1, RREB1, SPARC, SRC, ADAM17, THBS1, VEGFA, ADAM9, NRP1, MAP4K4, ROCK2, HDAC9, AKT3, PLK2, CLASP1, SIRT1, FOXP1, EPB41L4B, EPB41L5, NUS1, AMOTL1, EMC10

BP	GO:0017038	protein import	50/3408	3.95E-02	PTTG1IP, CDKN1A, MAPK14, ECT2, HSPA4, JUP, KPNA1, KPNA3, TNPO1, IPO5, LAMP2, NUP88, NUP98, PEX13, PML, PPP3CA, PKIA, MAPK1, PEX5, RAN, RANBP2, STAT3, SYK, TP53, TOMM20, POM121, NUTF2, TIMM17A, NUP50, TARDBP, KPNA6, APPL1, DNAJC15, FAM53C, UBR5, PEX5L, SUFU, RAB23, RAB8B, FERMT1, PEX26, IPO9, NUP133, MAVS, GRPEL1, LONP2, RPAIN, TIMM50, GRPEL2, POM121C
BP	GO:0009048	dosage compensation by inactivation of X chromosome	8/3408	3.95E-02	BRCA1, HNRNPU, UPF1, EIF1, PCGF3, RBM15B, RLIM, PCGF5
BP	GO:0031293	membrane protein intracellular domain proteolysis	8/3408	3.95E-02	ADAM10, NFKB1, ADAM17, NCSTN, APH1A, APH1B, RHBDD1, SPPL2A
BP	GO:0031468	nuclear envelope reassembly	8/3408	3.95E-02	PPP2CA, PPP2R1A, PPP2R2A, ANKLE2, NSFL1C, CHMP7, UBXN2B, REEP3
BP	GO:0036035	osteoclast development	8/3408	3.95E-02	FBN1, NOTCH2, PAFAH1B1, SRC, FOXP1, FBXW7, FAM20C, SIGLEC15
BP	GO:0042772	DNA damage response, signal transduction resulting in transcription	8/3408	3.95E-02	BRCA1, CDKN1A, FOXM1, SP100, TP53, ZNF385A, HIPK2, ING4
BP	GO:1902165	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	8/3408	3.95E-02	BCL2, CD44, HNRNPK, KDM1A, SIRT1, ZNF385A, TRIAP1, TAF9B
BP	GO:2000479	regulation of cAMP-dependent protein kinase activity	8/3408	3.95E-02	ATP2B4, HTT, PKIA, PRKAR1A, PRKAR2A, RAPGEF2, SIRT1, SESN2
BP	GO:0070301	cellular response to hydrogen peroxide	28/3408	3.96E-02	ABL1, RHOB, AXL, ECT2, EZH2, FOXO1, FOXO3, HDAC2, MET, MYB, PAWR, PAX2, PRKAA1, RPS3, SRC, TRPM2, TXN, NR4A3, KLF4, NET1, SIGMAR1, KLF2, ZNF277, KDM6B, SIRT1, OSER1, PLEKHA1, SIRPA
BP	GO:0003333	amino acid transmembrane transport	25/3408	3.99E-02	CLN8, KCNJ10, RGS2, RGS4, SLC1A2, SLC1A4, SLC1A5, SLC6A8, SLC6A9, SLC7A1, SLC7A2, SLC7A5, PER2, SLC7A6, SLC25A15, ARL6IP1, SLC7A11, SLC38A2, SLC25A38, LRRC8D, SLC38A1, SLC16A10, SLC36A4, SLC43A2, SLC36A1
BP	GO:0042058	regulation of epidermal growth factor receptor signaling pathway	25/3408	3.99E-02	CBL, CDC42, HBEGF, EGFR, FER, GRB2, HIP1, PTPN12, PTPRJ, SH3GL2, SHC1, SOS1, ADAM17, TGFA, NCK2, GPRC5A, SOCS5, SPRY1, AGR2, ERRFI1, FBXW7, AFAP1L2, SOCS4, DAB2IP, EPGN
BP	GO:0009165	nucleotide biosynthetic process	89/3408	4.01E-02	ACACA, ACLY, ADA, ADCY1, ADCY6, ADCY9, ADORA2B, AK2, AK4, CDS1, DCK, ACSL4, GAPDH, GPI, GUCY1A2, HIF1A, HK1, HK2, IDH2, FOXK2, IMPDH1, INSR, LDHA, NME4, NUP88, NUP98, PDK3, PDK4, PFAS, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PPAT, PRKAA1, MAPK1, PRPSAP2, PTGIS, RANBP2, RRM2, SCD, SNCA, STAT3, ELOVL4, TP53, UCK2, UMPS, VCP, KYNU, PAPSS2, NCOR1, POM121, PAICS, NUP50, SLC2A6, NMNAT2, ACSL6, QPRT, RRM2B, AK3, SLC35B3, PANK1, DDIT4, PDPR, RFK, NDC1, NUP133, CTPS2, AGPAT3, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, DNAJC30, ACSS1, CBR4, CMPK2, ACSF3, FLCN, FOXK1, LCLAT1, NUP43, POM121C
BP	GO:0050807	regulation of synapse organization	54/3408	4.04E-02	ABL1, ADAM10, ARF6, RHOA, BDNF, CFL1, CRKL, MAPK14, DAG1, EFNA5, EIF4G1, EPHA4, EPHA7, EPHB2, EPHB3, FMR1, IL1RAP, CAPRIN1, MEF2C, NEDD4, NTRK3, OPA1, PAFAH1B1, PAK3, PTEN, PTPRD, SNCA, SPARC, TIAM1, VCP, FZD1, KALRN, DLG5, NTN1, ACTR2, ABI2, PDLIM5, NLGN1, DKK1, SLC7A11, FLRT2, SIPA1L1, SLITRK5, ABHD17B, SIX4, SSH1, VPS35, NLGN2, ABHD17C, RAB17, BHLHB9, SLITRK4, DAB2IP, AGRN
BP	GO:0045766	positive regulation of angiogenesis	51/3408	4.06E-02	ABL1, ADM, RHOB, BRCA1, BTG1, RUNX1, FGF1, FGF2, GAB1, GATA2, GATA6, HIF1A, HK2, ISL1, ITGA5, ITGB1, ITGB8, JUP, MDK, MAP3K3, SERPINE1, PIK3C2A, PKM, PRKCA, PTGIS, CX3CL1, STAT3, STIM1, TERT, THBS1, TWIST1, VEGFA, XBP1, ADAM12, HMGA2, NRP1, KLF4, HDAC9, AKT3, RAPGEF3, PLK2, SIRT1, PPP1R16B, HIPK2, ERAP1, AGGF1, ADM2, MTDH, BMPER, HIPK1, EMC10

BP	GO:0060759	regulation of response to cytokine stimulus	48/3408	4.06E-02	ADAR, AXL, CAV1, RUNX1, CBFB, CSF1, CYLD, EDN1, HIF1A, UBE2K, IFNAR2, IKBKB, IL1R1, IRAK1, IRAK2, LIFR, PAFAH1B1, PTPN1, PTPN11, PTPRC, ABCE1, ROBO1, STAT1, SYK, ADAM17, TRAF1, NR1H2, PXDN, MADD, SOCS1, FADD, KLF4, SPATA2, SH2B3, RBCK1, CLIP3, LSM14A, YTHDF2, PIAS4, PARP14, OTUD4, MAVS, MUL1, SPPL2A, RFFL, ZNF675, HIPK1, YTHDF3
BP	GO:0071248	cellular response to metal ion	48/3408	4.06E-02	ADCY1, ADD1, ALAD, ATP7A, CALR, CAMK2D, CDKN1B, CREB1, ECT2, EDN1, EGFR, EIF2S1, FOSB, FUS, HSPA5, ITPKB, JUN, JUND, KCNK3, LIG4, MEF2A, MEF2C, MT1M, OGG1, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, SNCA, SYT1, TFR2, TRPM2, AKR1C3, IQGAP1, CPNE3, SYT7, FSTL3, NLGN1, SYT11, NCSTN, CLIC4, SLC25A24, SYT17, WNK1, SYT2, CPNE8, CPNE2
BP	GO:0030534	adult behavior	38/3408	4.07E-02	ARCN1, ARRB2, CTNS, EPHA4, CLN8, EPS8, HDAC2, HOXB8, KCNJ10, MAFG, MECP2, NPC1, PAFAH1B1, PPARA, PTEN, SLC1A2, SNCA, TSC1, NR4A3, FADD, KALRN, PUM1, SHANK2, NCSTN, SLC7A11, CNTNAP2, SLITRK5, GIGYF2, PCDH17, HTRA2, HIPK2, ADAM22, OXR1, CHD7, PREX2, BTBD9, SDK1, RNF180
BP	GO:0060147	regulation of posttranscriptional gene silencing	32/3408	4.09E-02	ADAR, DDX5, EGFR, EIF4G1, ELAVL1, FMR1, MYCN, NUP88, NUP98, POLR2D, POLR2K, PPP3CA, RANBP2, STAT3, TERT, TP53, ZFP36, FXR1, LIMD1, NCOR1, PUM1, POM121, NUP50, AGO1, TNRC6A, NDC1, NUP133, XPO5, SEH1L, TRIM71, NUP43, POM121C
BP	GO:0060966	regulation of gene silencing by RNA	32/3408	4.09E-02	ADAR, DDX5, EGFR, EIF4G1, ELAVL1, FMR1, MYCN, NUP88, NUP98, POLR2D, POLR2K, PPP3CA, RANBP2, STAT3, TERT, TP53, ZFP36, FXR1, LIMD1, NCOR1, PUM1, POM121, NUP50, AGO1, TNRC6A, NDC1, NUP133, XPO5, SEH1L, TRIM71, NUP43, POM121C
BP	GO:0046031	ADP metabolic process	34/3408	4.11E-02	AK2, AK4, GAPDH, GPI, HIF1A, HK1, HK2, FOXK2, INSR, LDHA, NUP88, NUP98, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PRKAA1, RANBP2, STAT3, TP53, NCOR1, POM121, NUP50, SLC2A6, AK3, DDIT4, NDC1, NUP133, SEH1L, FOXK1, NUP43, POM121C
BP	GO:0006006	glucose metabolic process	52/3408	4.17E-02	AKT2, CPT1A, MAPK14, EP300, FOXO1, G6PD, GAA, GAPDH, KAT2A, GOT2, GPI, GSK3B, HK1, HK2, IGF2, FOXK2, INSR, PDK3, PDK4, ENPP1, PFKFB2, PGAM1, PHKG2, PKM, PPARA, PPARD, PPP1CA, PPP1CB, PRKAA1, RANBP2, RORA, SRC, TP53, ALDH5A1, DYRK2, IRS2, KAT2B, PER2, H6PD, EPM2AIP1, NCOA2, ARPP19, WDTC1, PASK, SIRT1, SERP1, ADIPOR1, SESN2, SOGA1, SIK1, BRAT1, FOXK1
BP	GO:0060415	muscle tissue morphogenesis	24/3408	4.17E-02	ADARB1, BMPR1A, COL3A1, COL11A1, S1PR1, FKBP1A, FOXC1, NRG1, RBPJ, ISL1, SMAD4, SMAD7, POU4F1, PROX1, TGFBR1, TGFBR3, FZD1, HAND1, UBE4B, DLL4, CHD7, VANGL2, HEG1, PTCD2
BP	GO:0005979	regulation of glycogen biosynthetic process	11/3408	4.18E-02	AKT2, GSK3B, IGF2, INSR, ENPP1, PPP1CA, PPP1CB, DYRK2, IRS2, EPM2AIP1, PASK
BP	GO:0010644	cell communication by electrical coupling	11/3408	4.18E-02	ATP1B1, CACNA1C, CALM1, CALM2, CALM3, CAMK2D, CAV1, GJA1, PDE4D, SLC8A1, GJC1
BP	GO:0010962	regulation of glucan biosynthetic process	11/3408	4.18E-02	AKT2, GSK3B, IGF2, INSR, ENPP1, PPP1CA, PPP1CB, DYRK2, IRS2, EPM2AIP1, PASK
BP	GO:0014044	Schwann cell development	11/3408	4.18E-02	AKT2, DAG1, NRG1, ILK, NTRK3, POU3F2, SKI, DICER1, ADAM22, PARD3, SH3TC2
BP	GO:0031114	regulation of microtubule depolymerization	11/3408	4.18E-02	APC, MAP1A, MAP1B, MID1, ARHGEF2, CAMSAP2, CLASP1, TAOK1, NAV3, TTBK2, CAMSAP1
BP	GO:0031116	positive regulation of microtubule polymerization	11/3408	4.18E-02	CDKN1B, MAP1B, MAPT, MECP2, MET, RPS3, AKAP9, CLASP1, NIN, SLAIN2, NAV3
BP	GO:0060441	epithelial tube branching involved in lung morphogenesis	11/3408	4.18E-02	CTNNB1, CTSZ, DAG1, FOXA1, HOXA5, KRAS, WNT2B, DLG5, SPRY1, VANGL2, RDH10
BP	GO:1900181	negative regulation of protein localization to nucleus	11/3408	4.18E-02	GSK3B, PKIA, DCLK1, POLR1A, SIN3A, SUFU, RAB23, FERMT1, OTUD7B, LZTS2, FLCN
BP	GO:0050804	modulation of chemical synaptic transmission	99/3408	4.23E-02	ABL1, ADCY1, ADORA2B, ARF1, ARRB2, ATP2A2, BDNF, CACNA1B, CALM3, CAMK2A, CREB1, EDN1, EGFR, EIF4E, EPHA4, EPHB2, FMR1, KAT2A, GNAI2, GSK3B, ITGB1, KCNC4, KCNJ10, KIF5B, KIT, KRAS, MAP1A, MAP1B, MAPT, MECP2, MEF2C, RAB8A, MME, MPP2, NPTX1, OPHN1, P2RY1, SERPINE2, PLCL1, PPP3CA, PRKCE, MAPK1, PTEN, RAB3B, RAB5A, RAP1B, RGS4, CX3CL1, SLC6A9, SNAP25, SNCA, SRC, SRF, STAT3, STAU1, STX3, VAMP1, VAMP2, SYT1, YWHAG, DGKE, NAPA, SYNGAP1, SQSTM1, SYT7, SYNGR1, PREPL, AKAP12, SNCAIP, RAPGEF2, RIMS3, AKAP9, UNC13B, PLK2, FAM107A, CPEB3, NLGN1, SHANK2, DKK1,

					NCDN, SYT11, NCSTN, NCS1, NPTXR, SLC7A11, SLC24A2, RNF19A, NSMF, SIPA1L1, NPTN, PCDH17, KCNMB4, GIT1, SSH1, YTHDF1, NLGN2, LRRC4, TPRG1L, RIMS4
BP	GO:0010923	negative regulation of phosphatase activity	29/3408	4.24E-02	CRY2, DLG3, ENSA, FKBP1A, GNAI2, GSK3B, NCKAP1L, IKBKB, MYO1D, PPP1R2, SET, ROCK2, BAG4, PHACTR2, FARP1, ARPP19, LMTK2, RRP1B, ZFYVE1, SYTL2, SLC7A14, PCIF1, WNK1, ZCCHC9, FAM122A, WDR81, SPRED1, BOD1L1, PPP1R37
BP	GO:0014812	muscle cell migration	29/3408	4.24E-02	ATP7A, BCL2, BMPR1A, CRK, IGFBP5, ILK, LRP1, MDK, MEF2C, FOXO4, SERPINE1, PDGFA, PDGFB, PPARD, SORL1, SRC, TERT, NR4A3, IQGAP1, NRP1, ADAMTS1, ARPC5, TRIB1, NET1, POSTN, SIX4, SSH1, NDRG4, AKIRIN1
BP	GO:0055001	muscle cell development	47/3408	4.28E-02	ADM, ATP2A2, BCL2, CFL2, CSRP1, CXADR, EDN1, G6PD, HNRNPU, HES1, ITGB1, SMAD4, MEF2A, MEF2C, MYH10, PDGFRA, PIN1, PPARA, PPP3CA, PRKAR1A, PROX1, RGS2, RGS4, MAP2K4, SGCD, SKI, SLC8A1, SRF, TBX3, VEGFA, YY1, SORBS2, AKAP6, ATG5, HDAC9, NEBL, PDLIM5, AKAP13, KDM1A, FBXO22, MYOF, TMOD2, SIX4, ALPK3, PTCD2, SYNPO2L, WFIKKN2
BP	GO:0007040	lysosome organization	19/3408	4.28E-02	ARF1, SCARB2, LYST, TPP1, CLN8, GAA, HPS1, SYT7, HOOK1, CHMP5, RAB14, TMEM106B, LAPTM4B, VPS35, TMEM165, GNPTAB, HOOK3, TMEM199, TPCN2
BP	GO:0080171	lytic vacuole organization	19/3408	4.28E-02	ARF1, SCARB2, LYST, TPP1, CLN8, GAA, HPS1, SYT7, HOOK1, CHMP5, RAB14, TMEM106B, LAPTM4B, VPS35, TMEM165, GNPTAB, HOOK3, TMEM199, TPCN2
BP	GO:0043500	muscle adaptation	33/3408	4.32E-02	ATP2A2, ATP2B4, CAMK2D, EDN1, EZH2, FOXO1, FOXO3, G6PD, GATA6, GATM, IGFBP5, IL6ST, JARID2, SMAD4, MEF2A, MEF2C, PIN1, PPARA, PPP3CA, PRKCA, TWF1, RGS2, RGS4, SLC9A1, TNFRSF1B, YY1, NR4A3, KLF4, AKAP6, ROCK2, LMCD1, ERRFI1, MTPN
BP	GO:0008306	associative learning	23/3408	4.32E-02	CREB1, CTNS, CLN8, HIF1A, HMGCR, ITGB1, KIT, KRAS, MAP1A, MECP2, MEIS2, PDE1B, RAG1, SNAP25, SRF, BTG2, B4GALT2, SYNGAP1, ACTR2, SLC7A11, NPTN, RIC8A, NDRG4
BP	GO:0014909	smooth muscle cell migration	26/3408	4.33E-02	ATP7A, BCL2, BMPR1A, CRK, IGFBP5, ILK, LRP1, MDK, MEF2C, FOXO4, SERPINE1, PDGFA, PDGFB, PPARD, SORL1, SRC, TERT, NR4A3, IQGAP1, NRP1, ADAMTS1, ARPC5, TRIB1, POSTN, SSH1, NDRG4
BP	GO:0045639	positive regulation of myeloid cell differentiation	26/3408	4.33E-02	ACVR1B, JAG1, ZFP36L1, RUNX1, CREB1, MAPK14, CSF1, FOXO3, GATA2, GNAS, NCKAP1L, HIF1A, HOXA5, JUN, KITLG, POU4F1, PRKCA, RB1, STAT1, STAT3, STAT5B, TAL1, KLF10, FADD, TRIB1, FAM210B
BP	GO:0001755	neural crest cell migration	18/3408	4.38E-02	BMP7, CFL1, EFNB1, FN1, HIF1A, ISL1, KITLG, TWIST1, SEMA7A, NRP1, SEMA3E, FGF19, SEMA3A, SEMA4B, CORO1C, SOX8, SEMA4C, SEMA6A
BP	GO:0071398	cellular response to fatty acid	18/3408	4.38E-02	ACACA, ADCY6, CPT1A, CREB1, AKR1C2, EDN1, GNB1, LDLR, PDK3, PDK4, PRKAA1, PRKCE, PTAFR, PTGER4, SFRP1, SRC, XRCC5, AKR1C3
BP	GO:0007416	synapse assembly	45/3408	4.38E-02	ARF6, BDNF, CRKL, EFNA5, EFNB2, EIF4G1, EPHA7, EPHB2, EPHB3, NRG1, IL1RAP, MAP1B, MECP2, MEF2C, NTRK3, POU4F1, PTEN, PTPRD, SNCA, FZD5, FZD1, BSN, DLG5, NTN1, SPOCK2, FARP1, PDLIM5, NLGN1, SHANK2, DKK1, PLXND1, FLRT2, SLITRK5, NPTN, PCDH17, SIX4, VPS35, NLGN2, LRRC4, RAB17, BHLHB9, SLITRK4, FBXO45, SDK1, AGRN
BP	GO:0010092	specification of animal organ identity	12/3408	4.38E-02	AR, CTNNB1, FGF1, RBPJ, ISL1, MEF2C, PAX2, ROBO1, WNT2B, SPRY1, FRS2, DKK1
BP	GO:0010837	regulation of keratinocyte proliferation	12/3408	4.38E-02	ZFP36L1, KLF9, EFNB2, MDK, NOTCH2, PTPRK, SNAI2, VDR, ZFP36, TP63, BCL11B, CD109
BP	GO:0051443	positive regulation of ubiquitin-protein transferase activity	12/3408	4.38E-02	PIN1, PTEN, RAB1A, UBE2L3, UBE2N, CDC14B, DCUN1D1, FBXW7, ARRDC3, GORASP1, ARRDC4, DCUN1D3
BP	GO:0099084	postsynaptic specialization organization	12/3408	4.38E-02	ARF6, DLG3, IL1RAP, NTRK3, OPHN1, PTEN, PTPRD, SYNGAP1, NLGN1, SHANK2, NLGN2, LRRC4
BP	GO:1901342	regulation of vasculature development	96/3408	4.39E-02	ABL1, ADAM10, ADM, RHOA, RHOB, BMP7, BRCA1, BTG1, RUNX1, COL4A2, ATF2, CTNNB1, DCN, EFNA3, EFNB2, EGR1, EMP2, ERBB2, FGF1, FGF2, FOXC1, GAB1, GATA2, GATA6, GTF2I, HIF1A, HK2, HOXA5, IL6R, ISL1, ITGA5, ITGB1, ITGB8, JUP, KIT, MDK, MECP2, MAP3K3, FOXO4, SERPINE1, PDGFB, PIK3C2A, PKM, PML, PRKCA, PTGIS, CX3CL1, SFRP1, SOD2, SP100, SPARC, STAT1, STAT3, STIM1, TERT, THBS1, TWIST1, VEGFA, XBP1, ADAM12, HMGA2, NRP1, KLF4, ROCK2, RAPGEF2, SEMA3E, HDAC9, AKT3, KLF2, RAPGEF3, GPNMB, PLK2, VASH1, PLXND1, SIRT1, PPP1R16B, AGO1, PDCD4, HIPK2, ERAP1, WNT4, DLL4, AGGF1, FBXW7, HIF1AN, FOXJ2, ADAMTS9, SEMA6A, ADM2, MTDH, DAB2IP, AMOT, SPRED1, BMPER, HIPK1, EMC10
BP	GO:0035282	segmentation	28/3408	4.45E-02	ATM, BMPR1A, EP300, FOXC1, KAT2A, RBPJ, LRP6, SMAD4, MLLT3, NKX3-1, PCSK6, SFRP1, TBX3, TP53, KDM6A, FZD5, NRP1, ALDH1A2, SEMA3A, FRS2, MTF2, DKK1, POFUT1, MIB1, EPB41L5, PLD6, CRB2, NRARP

BP	GO:0099177	regulation of trans-synaptic signaling	99/3408	4.45E-02	ABL1, ADCY1, ADORA2B, ARF1, ARRB2, ATP2A2, BDNF, CACNA1B, CALM3, CAMK2A, CREB1, EDN1, EGFR, EIF4E, EPHA4, EPHB2, FMR1, KAT2A, GNAI2, GSK3B, ITGB1, KCNC4, KCNJ10, KIF5B, KIT, KRAS, MAP1A, MAP1B, MAPT, MECP2, MEF2C, RAB8A, MME, MPP2, NPTX1, OPHN1, P2RY1, SERPINE2, PLCL1, PPP3CA, PRKCE, MAPK1, PTEN, RAB3B, RAB5A, RAP1B, RGS4, CX3CL1, SLC6A9, SNAP25, SNCA, SRC, SRF, STAT3, STAU1, STX3, VAMP1, VAMP2, SYT1, YWHAG, DGKE, NAPA, SYNGAP1, SQSTM1, SYT7, SYNGR1, PREPL, AKAP12, SNCAIP, RAPGEF2, RIMS3, AKAP9, UNC13B, PLK2, FAM107A, CPEB3, NLGN1, SHANK2, DKK1, NCDN, SYT11, NCSTN, NCS1, NPTXR, SLC7A11, SLC24A2, RNF19A, NSMF, SIPA1L1, NPTN, PCDH17, KCNMB4, GIT1, SSH1, YTHDF1, NLGN2, LRRC4, TPRG1L, RIMS4
BP	GO:0032507	maintenance of protein location in cell	22/3408	4.46E-02	CAV1, DAG1, FLNB, HK1, HK2, HNRNPU, HSPA5, INSIG1, JUP, PML, TWF1, SKP1, SORL1, SP100, TLN1, TXN, VPS13A, MORC3, ARL2BP, VPS13C, VPS13D, ANKRD13C
BP	GO:0043507	positive regulation of JUN kinase activity	22/3408	4.46E-02	DVL3, EDN1, EPHA4, ERCC6, MAP3K4, MAP3K9, PTPN1, RPS3, MAP2K4, SYK, TIAM1, WNT7B, FZD5, FZD4, SPAG9, MAP3K2, DKK1, MAPK8IP3, VANGL2, TAOK1, MUL1, DAB2IP
BP	GO:0006646	phosphatidylethanolamine biosynthetic process	7/3408	4.46E-02	CHKA, LPIN2, CEPT1, LPIN1, PISD, ETNK1, SLC27A1
BP	GO:0042159	lipoprotein catabolic process	7/3408	4.46E-02	ATM, LDLR, LYPLA1, LYPLA2, ABHD17B, ABHD17C, LYPLAL1
BP	GO:0042762	regulation of sulfur metabolic process	7/3408	4.46E-02	COMT, PDK3, PDK4, SNCA, SLC7A11, PDPR, PDP2
BP	GO:0043508	negative regulation of JUN kinase activity	7/3408	4.46E-02	DNAJA1, SFRP1, HIPK3, DUSP10, PDCD4, AIDA, ZNF675
BP	GO:0045475	locomotor rhythm	7/3408	4.46E-02	ZFHX3, EGR1, PTEN, USP2, MTA1, NCOR1, NCOA2
BP	GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	7/3408	4.46E-02	CREB1, DR1, PSMC2, THRA, TP53, ATF7IP, CAND1
BP	GO:0051299	centrosome separation	7/3408	4.46E-02	CHEK1, AURKA, KIF3B, NDE1, NSFL1C, CEP85, UBXN2B
BP	GO:0060253	negative regulation of glial cell proliferation	7/3408	4.46E-02	HES1, IDH2, SKI, SOX11, TERT, RNF10, DICER1
BP	GO:0072075	metanephric mesenchyme development	7/3408	4.46E-02	BMP7, SMAD4, MYC, PAX2, STAT1, SIX4, WNT4
BP	GO:0090141	positive regulation of mitochondrial fission	7/3408	4.46E-02	DCN, MIEF1, VPS35, MFF, MUL1, DDHD1, MIEF2
BP	GO:2000095	regulation of Wnt signaling pathway, planar cell polarity pathway	7/3408	4.46E-02	ABL1, DAB2, MLLT3, SFRP1, DKK1, PLEKHA4, ZNRF3
BP	GO:0003156	regulation of animal organ formation	13/3408	4.47E-02	AR, BMP7, CTNNB1, FGF1, HES1, ISL1, PIM1, ROBO1, WNT2B, SPRY1, CITED2, FRS2, DKK1
BP	GO:0032885	regulation of polysaccharide biosynthetic process	13/3408	4.47E-02	AKT2, GSK3B, IGF2, INSR, NFKB1, PDGFB, ENPP1, PPP1CA, PPP1CB, DYRK2, IRS2, EPM2AIP1, PASK
BP	GO:2000249	regulation of actin cytoskeleton reorganization	13/3408	4.47E-02	ABL1, ABL2, ARHGDIA, CDC42, MDK, NOTCH2, NTRK3, PDGFRA, TRPM2, NRP1, SEMA3E, RAPGEF3, CD2AP

BP	GO:0021761	limbic system development	30/3408	4.47E-02	ATP2B4, CASP3, CDK6, CRK, CRKL, DLX2, EZH1, EZH2, GSK3B, ID4, KIF5B, MDK, NF2, PAFAH1B1, POU3F2, PROX1, PTEN, SRF, TBX3, TSC1, YWHAE, BTG2, NR4A3, NRP1, ARPC5, SEMA3A, PHLPP2, KDM6B, CNTNAP2, UBA6
BP	GO:0051149	positive regulation of muscle cell differentiation	30/3408	4.47E-02	ABL1, ARRB2, BCL2, BNIP2, CAPN2, CDC42, MAPK14, CTNNA1, CTNNB1, EDN1, EFNB2, KAT2A, NRG1, RBPJ, KIT, MEF2A, MEF2C, MMP14, PIN1, PROX1, SOD2, TCF3, SPAG9, AKAP6, MORF4L2, SIRT1, GREM1, CDON, CYP26B1, SETD3
BP	GO:0045844	positive regulation of striated muscle tissue development	25/3408	4.48E-02	ARRB2, BCL2, BMPR1A, CREB1, MAPK14, CTNNB1, EDN1, EFNB2, FGF2, GATA6, KAT2A, GJA1, NRG1, HMGCR, RBPJ, MEF2C, PIM1, PIN1, PRKAA1, MAPK1, TGFBR3, AKAP6, GREM1, CDON, CYP26B1
BP	GO:0048636	positive regulation of muscle organ development	25/3408	4.48E-02	ARRB2, BCL2, BMPR1A, CREB1, MAPK14, CTNNB1, EDN1, EFNB2, FGF2, GATA6, KAT2A, GJA1, NRG1, HMGCR, RBPJ, MEF2C, PIM1, PIN1, PRKAA1, MAPK1, TGFBR3, AKAP6, GREM1, CDON, CYP26B1
BP	GO:0042180	cellular ketone metabolic process	60/3408	4.48E-02	ADM, AKT2, ATP2B4, BRCA1, CAV1, COMT, CPT1A, AKR1C2, EGR1, KDSR, GOT2, HMGCR, INSIG1, OAZ2, PDK3, PDK4, PPARA, PRKAB2, PRKCE, PROX1, PSMA1, PSMA2, PSMB2, PSMC2, PSMD3, PSMD5, PSMD13, SNCA, TWIST1, NR1H2, NR4A3, AKR7A2, AKR1C3, IRS2, KYNU, PSMF1, LPGAT1, FGF19, PSME3, PSMD14, ERLIN2, WDTC1, PSME4, SIRT1, SLC7A11, DKK3, ADIPOR1, INSIG2, AZIN1, WNT4, PDPR, PDP2, ELOVL5, ADIPOR2, PANK2, LONP2, CBR4, STARD4, RDH10, PPTC7
BP	GO:0051205	protein insertion into membrane	16/3408	4.48E-02	BCL2, EGFR, PPP3R1, MAPK8, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, TRAM2, BCL2L11, BBC3, GET4, MOAP1, BMF
BP	GO:0035136	forelimb morphogenesis	14/3408	4.50E-02	ATRX, CACNA1C, RUNX2, CTNNB1, HOXA9, MSX1, TBX3, TWIST1, TP63, ALDH1A2, NIPBL, RDH10, FMN1, RNF165
BP	GO:0045616	regulation of keratinocyte differentiation	14/3408	4.50E-02	ZFP36L1, RUNX1, CBFB, FOXC1, HOXA7, VDR, ZFP36, NCOA3, TP63, ROCK2, GRHL1, ERRFI1, SGPP1, CD109
BP	GO:0010569	regulation of double-strand break repair via homologous recombination	15/3408	4.50E-02	CHEK1, FUS, RAD51, ACTR2, POLQ, KDM1A, SPIDR, RTEL1, FIGN, RIF1, UBQLN4, KLHL15, RMI2, PPP4R2, USP51
BP	GO:0048255	mRNA stabilization	15/3408	4.50E-02	MAPK14, ELAVL1, HNRNPC, HNRNPD, HNRNPU, ZFP36, THRAP3, SYNCRIP, PAIP1, IGF2BP1, HNRNPA0, LARP1, TARDBP, PABPC1, RBM38
BP	GO:0048483	autonomic nervous system development	15/3408	4.50E-02	ADARB1, CTNNB1, FN1, GATA3, HES1, SOX4, SOX11, VCAM1, FZD3, TP63, NRP1, SEMA3A, SOX8, NAV2, PLXNA4
BP	GO:0000423	mitophagy	9/3408	4.50E-02	TP53, SQSTM1, ATG13, MFN2, ATG14, HTRA2, VPS13C, VPS13D, SMURF1
BP	GO:0002089	lens morphogenesis in camera-type eye	9/3408	4.50E-02	CTNNB1, PROX1, SKI, SOX11, BCAR3, ABI2, HIPK2, TBC1D20, HIPK1
BP	GO:0036119	response to platelet-derived growth factor	9/3408	4.50E-02	ATP7A, CBL, CCNA2, CREB1, FER, RDX, SRC, IQGAP1, ERRFI1
BP	GO:0044321	response to leptin	9/3408	4.50E-02	CCND1, CCNA2, EDN1, PTEN, STAT3, UGCG, NR4A3, SIRT1, ADIPOR1
BP	GO:0060487	lung epithelial cell differentiation	9/3408	4.50E-02	CREB1, GATA6, FOXA1, HOXA5, RBPJ, NFIB, THRA, KLF2, AGR2
BP	GO:0071379	cellular response to prostaglandin stimulus	9/3408	4.50E-02	ACACA, ADCY6, AKR1C2, GNB1, PRKAA1, PRKCE, PTGER4, SFRP1, AKR1C3
BP	GO:0097320	plasma membrane tubulation	9/3408	4.50E-02	SH3GL2, WASL, ASAP1, SH3GLB1, FNBP1L, SGIP1, MICALL1, FCHO2, WHAMM
BP	GO:2001169	regulation of ATP biosynthetic process	27/3408	4.60E-02	AK4, HIF1A, INSR, NUP88, NUP98, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, STAT3, TP53, VCP, NCOR1, POM121, NUP50, SLC2A6, DDIT4, NDC1, NUP133, SEH1L, DNAJC30, FLCN, NUP43, POM121C
BP	GO:1901879	regulation of protein depolymerization	24/3408	4.67E-02	ADD1, APC, ASPH, CAPZA2, CFL1, CFL2, EPS8, MAP1A, MAP1B, MID1, TWF1, RDX, SPTAN1, SPTBN1, ARHGEF2, DSTN, CAMSAP2, CLASP1, TMOD2, TAOK1, NAV3, MTPN, TTBK2, CAMSAP1

BP	GO:0002683	negative regulation of immune system process	104/3408	4.72E-02	ADA, ADAR, ARRB2, ATM, AXL, BCL6, ZFP36L1, CASP3, RUNX1, RUNX3, CBFB, CD47, CD59, CDK6, CEBPB, COL3A1, CRK, CTNNB1, DUSP1, ERBB2, FBN1, FER, GABPA, GATA2, GBP1, HMGB3, HOXA5, HOXA7, HOXA9, HOXB8, HES1, IL7R, IRF1, IRF4, ITPKB, LDLR, LYN, SMAD7, MDK, MEIS2, KITLG, MYC, PAWR, SERPINB9, PPM1B, PRKAR1A, PSMA1, PTGER4, PTPRC, PTPRJ, CX3CL1, SDC4, SEC14L1, SFRP1, SOX11, TAL1, TMBIM6, THBS1, TSPAN6, TYRO3, NR1H2, ZFP36, SOCS1, FADD, CD84, LDB1, WASL, DLG5, SOCS6, CTR9, SOCS5, TRIB1, FSTL3, BTN2A2, PIAS3, GPNMB, TOB2, DUSP10, LRCH1, TNFRSF13B, APPL1, GREM1, UBQLN1, YTHDF2, PARP14, OTUD4, NCAPG2, LAX1, RNF125, FBXW7, LGR4, NPLOC4, PAG1, PELI1, PVRIG, CDC73, MUL1, ITCH, ZBTB46, DAB2IP, ZNF675, YTHDF3, MIA3, NRARP
BP	GO:0046626	regulation of insulin receptor signaling pathway	20/3408	4.78E-02	GNAI2, IGF2, NCK1, OPA1, ENPP1, PRKAA1, PTPN1, PTPN11, RPS6KB1, SORL1, SRC, TSC1, SOCS1, SOCS2, KANK1, SIRT1, ADIPOR1, NUCKS1, OSBPL8, SESN3
BP	GO:0051188	cofactor biosynthetic process	76/3408	4.81E-02	ACACA, ACLY, ALAD, ALAS1, CTNS, ACSL4, FECH, GAPDH, GPI, HIF1A, HK1, HK2, IDH2, FOXK2, INSR, IREB2, LDHA, MAT2A, SLC11A2, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PRKAA1, PTGIS, PTS, RANBP2, SCD, SNCA, STAT3, ELOVL4, TP53, UROS, SLC25A16, PDXK, KYNU, NCOR1, POM121, NUP50, SLC2A6, NMNAT2, ACSL6, QPRT, SLC7A11, MTHFD1L, MAT2B, PANK1, DDIT4, SLC25A38, PDPR, RFK, NDC1, NUP133, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, ACSS1, CBR4, PPTC7, ACSF3, IBA57, FOXK1, MMAB, NUP43, POM121C
BP	GO:0043542	endothelial cell migration	65/3408	4.85E-02	ABL1, RHOA, RHOB, BMPR2, CALR, DCN, EDN1, EFNB2, EGR3, EMP2, EPHB4, FGF1, FGF2, FLT4, GATA2, GATA3, GPI, HIF1A, ITGB1, JUP, LOXL2, MECP2, MEF2C, MAP3K3, MET, MYH9, PDGFB, PIK3C2A, PRCP, PRKCA, PROX1, PTEN, PXN, ROBO1, SP100, SPARC, SRF, STC1, ADAM17, NR2F2, TGFBR1, THBS1, VEGFA, NRP1, KLF4, ROCK2, HDAC9, AKT3, PLK2, VASH1, PLXND1, SIRT1, GREM1, FOXP1, DLL4, FBXW7, ADAMTS9, NUS1, DAB2IP, AMOT, AMOTL1, SPRED1, BMPER, EMC10, MIA3
BP	GO:0060538	skeletal muscle organ development	43/3408	4.85E-02	RHOA, BCL2, BCL9, CAV1, CCNT2, CFL2, COL19A1, MAPK14, CTNNB1, DCN, DDX5, EGR1, EP300, FLNB, HMGCR, FOXN2, MEF2C, MEF2D, PPP3CA, PRKAA1, RB1, SKI, SOX11, NR2F2, TWIST1, BTG2, COPS2, HDAC9, NR1D2, ZBTB18, DDX17, DKK1, MAFF, FBXO22, HEYL, SOX8, CDON, SIX4, GPCPD1, CYP26B1, AKIRIN1, UQCC2, ZNF689
BP	GO:0006110	regulation of glycolytic process	23/3408	4.90E-02	HIF1A, INSR, NUP88, NUP98, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, STAT3, TP53, NCOR1, POM121, NUP50, SLC2A6, DDIT4, NDC1, NUP133, SEH1L, NUP43, POM121C
BP	GO:0006446	regulation of translational initiation	23/3408	4.90E-02	DDX3X, EIF2S1, EIF4B, EIF4G1, EIF4G2, EIF5, FMR1, NCBP1, NCK1, POLR2D, PPP1CA, EIF2AK2, RPS6KB1, NCK2, EIF5B, EIF1, PAIP1, LARP1, EIF2AK1, YTHDF2, YTHDF1, PPP1R15B, YTHDF3
BP	GO:0048285	organelle fission	101/3408	4.92E-02	APC, RHOA, ATM, ATRX, BMP7, CALR, CDKN1B, RCC1, CHEK1, DCN, DUSP1, EDN1, EPS8, HNRNPU, HSPA2, IGF2, IK, INCENP, INSR, KIF2A, MAD2L1, MAPT, MLH1, MSX1, MYBL2, OPA1, PDE3A, PDGFB, PIN1, PPP2R1A, PRKAR1A, PSMD13, RAD1, RAD21, RAD51, RAN, RB1, STAT2, AURKA, TGFA, TOP2B, SMC1A, CUL3, CDC14B, TNKS, PRC1, CCNE2, AURKB, TRIP13, KIF3B, KIF23, VPS4B, ACTR2, STAG2, KIF2C, PDS5B, POGZ, PDS5A, CLASP1, MAU2, NIPBL, SH2B1, SLC2A8, CHMP5, WNT4, ANLN, MIEF1, INO80, NDE1, CHTF8, PINX1, PHIP, CDCA8, NDC1, VPS35, RIOK2, PCID2, PPP2R2D, NSFL1C, CYP26B1, FMN2, SPIRE1, MFF, CHMP1B, HECW2, CEP85, MUL1, CEP97, NAA50, DDHD1, SEH1L, MND1, SLX4, CHMP7, MIEF2, CCSAP, UBXN2B, PHF13, AGO4, KLHDC8B, EPGN
BP	GO:0002903	negative regulation of B cell apoptotic process	6/3408	4.92E-02	ADA, BCL6, IRS2, AURKB, FOXP1, SLC39A10
BP	GO:0009086	methionine biosynthetic process	6/3408	4.92E-02	MTAP, MTHFR, MTR, ADI1, ENOPH1, MRI1
BP	GO:0030950	establishment or maintenance of actin cytoskeleton polarity	6/3408	4.92E-02	RHOA, RHOB, ARHGAP35, RND2, MAPKAP1, RICTOR
BP	GO:0042118	endothelial cell activation	6/3408	4.92E-02	HOXA9, SMAD4, TGFBR1, FOXP1, APOLD1, BMPER
BP	GO:0045579	positive regulation of B cell differentiation	6/3408	4.92E-02	NCKAP1L, MMP14, SYK, XBP1, PCID2, ATP11C
BP	GO:0060394	negative regulation of pathway-restricted SMAD protein phosphorylation	6/3408	4.92E-02	SMAD6, SMAD7, DKK1, GREM1, PMEPA1, PBLD

BP	GO:0060788	ectodermal placode formation	6/3408	4.92E-02	CTNNB1, HDAC2, PROX1, TBX3, FRS2, SIX4
BP	GO:0060900	embryonic camera-type eye formation	6/3408	4.92E-02	PAX2, PROX1, SOX11, TWIST1, ARID1A, FRS2
BP	GO:0071697	ectodermal placode morphogenesis	6/3408	4.92E-02	CTNNB1, HDAC2, PROX1, TBX3, FRS2, SIX4
BP	GO:1902337	regulation of apoptotic process involved in morphogenesis	6/3408	4.92E-02	BMP7, FOXC1, PAX2, HNF1B, TNFRSF1B, VDR
BP	GO:1905666	regulation of protein localization to endosome	6/3408	4.92E-02	RDX, SORL1, ROCK2, ABHD17B, ABHD17C, ANKRD13A
BP	GO:0003171	atrioventricular valve development	10/3408	4.92E-02	BMPR1A, BMPR2, SMAD4, SMAD6, MDM4, SOX4, TWIST1, DCHS1, OLFM1, HEYL
BP	GO:0032800	receptor biosynthetic process	10/3408	4.92E-02	EDN1, HDAC2, HIF1A, HNRNPK, HOXA5, ITGAV, FURIN, PPARA, SEC24A, ANKRD13C
BP	GO:0045992	negative regulation of embryonic development	10/3408	4.92E-02	BMP7, COL5A1, COL5A2, CTNNB1, GATA3, SNAI1, FZD3, DKK1, SUFU, NRARP
BP	GO:0048169	regulation of long-term neuronal synaptic plasticity	10/3408	4.92E-02	EPHB2, KCNJ10, KIT, KRAS, RAB8A, RAB5A, SNCA, SYNGAP1, SYNGR1, NPTN
BP	GO:0060037	pharyngeal system development	10/3408	4.92E-02	BMP7, BMPR1A, BMPR2, GATA3, HES1, ISL1, NKX3-1, PTCH1, TGFBR1, SIX4
BP	GO:0060740	prostate gland epithelium morphogenesis	10/3408	4.92E-02	AR, BMP7, FOXA1, HOXD13, ID4, NKX3-1, RARG, SFRP1, TP63, FRS2
BP	GO:1900739	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	10/3408	4.92E-02	BCL2, PPP3R1, MAPK8, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, BBC3
BP	GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	10/3408	4.92E-02	BCL2, PPP3R1, MAPK8, TFDP1, TFDP2, TP53, YWHAE, YWHAG, TP63, BBC3
BP	GO:1901293	nucleoside phosphate biosynthetic process	89/3408	4.92E-02	ACACA, ACLY, ADA, ADCY1, ADCY6, ADCY9, ADORA2B, AK2, AK4, CDS1, DCK, ACSL4, GAPDH, GPI, GUCY1A2, HIF1A, HK1, HK2, IDH2, FOXK2, IMPDH1, INSR, LDHA, NME4, NUP88, NUP98, PDK3, PDK4, PFAS, PFKFB2, PFKFB3, PFKFB4, PGAM1, PKM, PPARA, PPAT, PRKAA1, MAPK1, PRPSAP2, PTGIS, RANBP2, RRM2, SCD, SNCA, STAT3, ELOVL4, TP53, UCK2, UMPS, VCP, KYNU, PAPSS2, NCOR1, POM121, PAICS, NUP50, SLC2A6, NMNAT2, ACSL6, QPRT, RRM2B, AK3, SLC35B3, PANK1, DDIT4, PDPR, RFK, NDC1, NUP133, CTPS2, AGPAT3, PDP2, ELOVL5, ELOVL6, PANK3, PPCS, SCD5, PANK2, SEH1L, DNAJC30, ACSS1, CBR4, CMPK2, ACSF3, FLCN, FOXK1, LCLAT1, NUP43, POM121C
BP	GO:0016079	synaptic vesicle exocytosis	32/3408	4.96E-02	ADCY1, ADORA2B, ATP2A2, CALM3, CAMK2A, FMR1, GSK3B, P2RY1, RAB5A, RAP1B, SNAP25, SNCA, STX3, VAMP1, VAMP2, SYT1, NAPA, SYNJ1, SYT7, PREPL, RIMS3, SV2A, UNC13B, NLGN1, SYT11, PIP5K1C, NCS1, GIT1, SYT17, DNAJC5, SYT2, RIMS4
BP	GO:0051193	regulation of cofactor metabolic process	32/3408	4.96E-02	CTNS, HIF1A, INSR, ME2, NUP88, NUP98, PDK3, PDK4, PFKFB2, PFKFB3, PFKFB4, PGAM1, PPARA, PRKAA1, RANBP2, SNCA, STAT3, TP53, NCOR1, POM121, NUP50, SLC2A6, SLC7A11, DDIT4, PDPR, NDC1, NUP133, PDP2, SEH1L, PPTC7, NUP43, POM121C

CC	GO:0005925	focal adhesion	142/3499	2.17E-14	ACTB, ACTN4, ADAM10, ADD1, ALCAM, ARF1, ARF6, RHOA, RHOB, DST, CALR, CAPN2, CAV1, CBL, SCARB2, CD44, CD59, CDC42, CFL1, CNN2, CSRP1, CTNNA1, CTNNB1, DAB2, DAG1, EFNB2, EGFR, FAT1, FGFR3, FHL1, FHL2, FLNB, FLOT2, GJA1, HMGA1, HNRNPK, HSPA5, IGF2R, ILK, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, JUP, KRAS, L1CAM, LASP1, LIMK1, LPP, LRP1, MARCKS, MME, MMP14, MYH9, PPP1R12A, NEDD9, NHS, PLEC, PPP1CB, PPP1CC, PRKAR2A, MAPK1, MAPK3, TWF1, PTPN12, PTPRC, PXN, RDX, RPS3, SDC4, SLC4A2, SLC9A1, SNTB1, SNTB2, ADAM17, TLN1, TNS1, TPM4, VCL, YWHAE, YWHAG, ZNF185, FZD1, KLF11, SORBS2, PPFIBP1, ITGA8, NUMB, ADAM9, IQGAP1, NRP1, CPNE3, WASF1, LIMD1, MPZL1, ARHGEF2, PDLIM7, MAP4K4, KIF23, AKAP12, GIT2, MRC2, PDCD6IP, ARPC5, ACTR2, ARPC2, G3BP1, DLC1, CAP1, HYOU1, GNA13, NCKAP1, FAM107A, MTF2, RAB21, PALLD, USP33, NFASC, MPRIP, CLASP1, NCSTN, PIP5K1C, CORO1C, FLRT2, TES, PABPC1, GIT1, DCTN4, FBLIM1, FERMT1, DCAF6, EPB41L5, RHOU, AFAP1, AHNAK, ZFYVE21, PEAK1, SPRY4, DIXDC1, PHLDB2
CC	GO:0005924	cell-substrate adherens junction	142/3499	2.23E-14	ACTB, ACTN4, ADAM10, ADD1, ALCAM, ARF1, ARF6, RHOA, RHOB, DST, CALR, CAPN2, CAV1, CBL, SCARB2, CD44, CD59, CDC42, CFL1, CNN2, CSRP1, CTNNA1, CTNNB1, DAB2, DAG1, EFNB2, EGFR, FAT1, FGFR3, FHL1, FHL2, FLNB, FLOT2, GJA1, HMGA1, HNRNPK, HSPA5, IGF2R, ILK, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, JUP, KRAS, L1CAM, LASP1, LIMK1, LPP, LRP1, MARCKS, MME, MMP14, MYH9, PPP1R12A, NEDD9, NHS, PLEC, PPP1CB, PPP1CC, PRKAR2A, MAPK1, MAPK3, TWF1, PTPN12, PTPRC, PXN, RDX, RPS3, SDC4, SLC4A2, SLC9A1, SNTB1, SNTB2, ADAM17, TLN1, TNS1, TPM4, VCL, YWHAE, YWHAG, ZNF185, FZD1, KLF11, SORBS2, PPFIBP1, ITGA8, NUMB, ADAM9, IQGAP1, NRP1, CPNE3, WASF1, LIMD1, MPZL1, ARHGEF2, PDLIM7, MAP4K4, KIF23, AKAP12, GIT2, MRC2, PDCD6IP, ARPC5, ACTR2, ARPC2, G3BP1, DLC1, CAP1, HYOU1, GNA13, NCKAP1, FAM107A, MTF2, RAB21, PALLD, USP33, NFASC, MPRIP, CLASP1, NCSTN, PIP5K1C, CORO1C, FLRT2, TES, PABPC1, GIT1, DCTN4, FBLIM1, FERMT1, DCAF6, EPB41L5, RHOU, AFAP1, AHNAK, ZFYVE21, PEAK1, SPRY4, DIXDC1, PHLDB2
CC	GO:0030055	cell-substrate junction	142/3499	3.82E-14	ACTB, ACTN4, ADAM10, ADD1, ALCAM, ARF1, ARF6, RHOA, RHOB, DST, CALR, CAPN2, CAV1, CBL, SCARB2, CD44, CD59, CDC42, CFL1, CNN2, CSRP1, CTNNA1, CTNNB1, DAB2, DAG1, EFNB2, EGFR, FAT1, FGFR3, FHL1, FHL2, FLNB, FLOT2, GJA1, HMGA1, HNRNPK, HSPA5, IGF2R, ILK, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, JUP, KRAS, L1CAM, LASP1, LIMK1, LPP, LRP1, MARCKS, MME, MMP14, MYH9, PPP1R12A, NEDD9, NHS, PLEC, PPP1CB, PPP1CC, PRKAR2A, MAPK1, MAPK3, TWF1, PTPN12, PTPRC, PXN, RDX, RPS3, SDC4, SLC4A2, SLC9A1, SNTB1, SNTB2, ADAM17, TLN1, TNS1, TPM4, VCL, YWHAE, YWHAG, ZNF185, FZD1, KLF11, SORBS2, PPFIBP1, ITGA8, NUMB, ADAM9, IQGAP1, NRP1, CPNE3, WASF1, LIMD1, MPZL1, ARHGEF2, PDLIM7, MAP4K4, KIF23, AKAP12, GIT2, MRC2, PDCD6IP, ARPC5, ACTR2, ARPC2, G3BP1, DLC1, CAP1, HYOU1, GNA13, NCKAP1, FAM107A, MTF2, RAB21, PALLD, USP33, NFASC, MPRIP, CLASP1, NCSTN, PIP5K1C, CORO1C, FLRT2, TES, PABPC1, GIT1, DCTN4, FBLIM1, FERMT1, DCAF6, EPB41L5, RHOU, AFAP1, AHNAK, ZFYVE21, PEAK1, SPRY4, DIXDC1, PHLDB2
CC	GO:0000790	nuclear chromatin	127/3499	8.04E-12	ACTB, AR, ATRX, RUNX2, RUNX3, CEBPB, CENPA, RCC1, CHD3, CHD4, CREB1, CREBBP, CTNNB1, DFFB, DNMT3A, DVL3, ETV3, EZH2, BPTF, FER, FOXC1, GABPA, GATA3, KAT2A, HDAC2, HIF1A, HMGB3, HNRNPC, HNRNPK, IRF1, IRF4, JUN, JUND, MXD1, SMAD2, SMAD4, MAX, MEF2A, MEF2C, MEF2D, MEN1, MYC, PAWR, PAX6, POU4F1, PPARD, RAD51, RARG, RB1, RFX3, RNF2, SATB1, SNAI2, SMARCA2, SMARCC2, SMARCD2, SMARCE1, SRF, SSRP1, SS18, STAT1, STAT3, TAF1, TAL1, TCF4, TCF3, TCF7, TCF7L2, TP53, TRPS1, YY1, KAT6A, DPF3, DPF1, NCOA3, NRIP1, ARID1A, TP63, LDB1, MBD2, MTA1, KLF4, NCOR1, SETD1A, CHAF1A, HMGXB4, KLF2, CITED2, POLR3G, SRCAP, CPSF6, KAT7, CBX3, KDM1A, POGZ, SIRT1, TARDBP, CBX5, CBX7, SUZ12, WBP2, NIPBL, SIN3A, ZNF385A, NSMF, SS18L1, RBMX, CECR2, UCHL5, RSF1, ING3, INO80, GATAD2A, RIF1, ASF1B, GATAD2B, ARID1B, EP400, CALCOCO1, BEND3, NUCKS1, SAP130, ANP32E, SETD3, BRMS1L, SLX4, NACC2
CC	GO:0031252	cell leading edge	131/3499	5.13E-11	ABL1, AKT2, ANK1, APBB2, APC, ARF1, ARF6, RHOA, ATP2B1, ATP6V1B2, ATP7A, DST, CD44, CDK6, CFL1, CTNNA1, CTNNB1, CTNND1, DAG1, DIAPH1, EEF1A1, EPS8, FAT1, FER, FLOT2, ILK, INSR, ITGA5, ITGAV, ITGB1, KCNC1, KCNC4, ABLIM1, LIMK1, MAPT, KITLG, MKLN1, MPP2, MYH9, MYH10, MYO1C, MYO1D, MYO5A, MYO6, MYO10, NEDD9, NF2, NHS, PAFAH1B1, PODXL, PKN2, TWF1, PTPRJ, PTPRK, PXN, RAB5A, RASA1, RDX, RPS3, SLC1A2, SLC9A1, SNX1, SPTBN1, SRC, STX3, VAMP7, ADAM17, TIAM1, TLN1, TSC1, SORBS2, ITGA8, PDLIM4, IQGAP1, KSR1, LDB1, WASF1, WASL, LDB2, ARHGEF2, PDLIM7, CYTH3, AKAP5, SLK, C2CD5, ARPC5, ACTR2, ARPC2, ABI2, WASF2, DLC1, RAPGEF3, IGF2BP1, NCKAP1, IQGAP2, FAM107A, AAK1, PALLD, PLXND1, KANK1, WWC1, PSD3, PIP5K1C, CORO1C, CD2AP, ARFIP2, SLC39A6, CNTNAP2, APPL1, SSH1, VEZT, FERMT1, INPP5E, RAB22A, EPB41L5, PLEKHA1, RAPH1, MTMR9, SPRY4, ANTXR1, PHLDB2, MYADM, RAB3IP, SSX2IP, FGD4, JMY, EXOC8, AMOT, AMOTL1, SPATA13, SCIMP
CC	GO:0005769	early endosome	109/3499	6.95E-08	ADRB1, AKT2, ARF6, RHOB, CAV1, CLCN4, EGFR, EPHA4, GJA1, RAPGEF1, HLA-B, IGF2R, LDLR, LNPEP, LRP1, LRP6, MME, MYO1B, MYO1D, MYO5A, NF2, SLC11A2, PML, MAPK1, MAPK3, PTPN1, RAB1A, RAB5A, RAB5B, SORT1, SH3GL2, SIAH1, SIAH2, SNX1, SORL1, TFRC, UVRAG, VCAM1, PTP4A1, FZD5, PTP4A2, RND2, PDLIM4, NUMB, SNX3, NRP1, MTMR4, ATP6V0D1, RABEP1, ZFYVE16, SNX17, RABGAP1L, ATP9A, WASF2, GPNMB, SLC9A6, STAMBP, PRDX3, RAB31, LMTK2, TRAK1, DKK1, RAB21, SNX13, ATP11B, ATP11A, MGRN1, DNAJC13, VPS8, NCSTN, STX12, SGK3, PARM1, CLIP3, CNTNAP2, APPL1, LDLRAP1, RNF11, EHD4, DERL2, APH1A, ANKFY1, RAB14, NEURL1B, CMTM6, LAPTM4B, TMEM127, VPS35, TMEM165, RCC2, TMEM9B, PMEPA1, RAB22A, ARRDC3, WDFY1, GPR107, RAB17, TRAK2, PLEKHF2, HPS6, NIPA2, ITCH, ARRDC4, MMGT1, NIPA1, WDR81, MIB2, STEAP2, SNX19
CC	GO:0044798	nuclear transcription factor complex	72/3499	6.95E-08	BCL9, RUNX1, RUNX3, CBFB, CEBPB, CREB1, ATF6B, CTNNB1, E2F3, E2F5, E2F6, ERCC2, NR5A2, KAT2A, GTF2A1, GTF2E1, GTF2H3, BRF1, GTF3C1, HIF1A, HMGA1, HNRNPAB, HNRNPU, JUN, JUND, SMAD2, SMAD4, MAX, MXI1, NFYA, NFYB, PBX1, POU2F1, PPARA, PPARD, RARG, RB1, SNAPC1, SOX4, SOX11, SOX12, STAT3, TAF1, TAF4B, TCF4, TCF3, TCF7L2, TEAD1, TFDP1, TFDP2, THRA, TLE1, TLE4, TP53, NR1H2, VDR, LDB1, KLF4, GTF3C4, GTF3C3, HAND1, NR1D2, NFAT5, SOX21, HIPK2, SOX8, TAF9B, BRF2, BDP1, MXD3, SOX7, E2F7

CC	GO:0000151	ubiquitin ligase complex	92/3499	8.43E-08	AMFR, BRCA1, CCNF, CDKN1B, MKLN1, NEDD4, RNF2, SEL1L, SKP1, TNFAIP1, UBE2D2, UBE2D3, UBE2L3, UBE2N, UBE2V1, VHL, CUL5, GAN, SPOP, DYRK2, CUL4B, CUL3, CUL2, ENC1, CBX4, BTRC, UBE4A, RNF144A, KLHL21, DCAF7, UBE4B, PCGF3, ARIH2, ZER1, RBCK1, USP33, CBX7, KCTD2, ARIH1, ARMC8, DCAF12, RNF19A, FBXL3, KLHL3, FBXO9, RNF11, DERL2, DTL, YPEL5, DCUN1D1, ANKIB1, FBXL19, KLHL24, FBXL12, BCOR, GID8, USP47, FBXW7, DCAF6, CAND1, KLHL7, KLHL42, ZSWIM6, ZSWIM4, DDA1, GID4, BRCC3, DCAF10, ZYG11B, KCTD17, CBLL1, PHC3, SPSB1, WDR26, KLHL15, ABTB1, KCTD10, MED10, PCGF5, SYVN1, KBTBD8, CBX2, KLHL13, DCUN1D3, UBR3, MIB2, RNF217, RNF168, UBR1, FBXO45, RNF144B, SPOPL
CC	GO:0010008	endosome membrane	137/3499	1.84E-07	ARF6, RHOB, ARHGAP1, CAV1, SCARB2, AP2M1, CLCN4, EGFR, EPHA4, ERBB2, HLA-B, INSR, IRAK1, IRAK2, LAMP2, LDLR, LRP6, RAB8A, MYO1B, NPC1, SLC11A2, FURIN, PLD1, PML, RAB5A, RAB5B, RAP2A, RAP2B, SORT1, SNX1, SORL1, VAMP7, TFRC, UBE2D3, FZD5, PDLIM4, SNX3, CD164, AP1G2, AP3D1, MTMR4, ATP6V0D1, RABEP1, RAB11B, TM9SF2, ITM2B, SCAMP1, VPS4B, GOSR2, LAPTM4A, ZFYVE16, RNF144A, SNX17, PLEKHM1, SCAMP2, ATP9A, TAB1, GPNMB, SLC9A6, RAB31, SNF8, RAB11FIP2, DKK1, RAB21, TAB2, SNX13, ATP11B, DNAJC13, NCSTN, PIP5K1C, ACAP2, MMD, CORO1C, STX12, PARM1, CLIP3, APPL1, CDIP1, EHD4, VPS36, ABHD17B, APH1A, UBAP1, ANKFY1, CHMP5, RAB14, RAB23, RAB8B, TPCN1, WDR44, TMEM106B, LEPROT, CMTM6, PLEKHB2, VPS37C, STEAP3, LAPTM4B, SLC48A1, VPS35, TMEM165, RCC2, TMEM9B, PMEPA1, CHMP1B, RAB22A, RAP2C, ABHD17C, KIF13A, TMBIM1, RAB17, GNPNAT1, ATG9A, PLEKHF2, HPS6, APH1B, ITCH, ANTXR1, RAB11FIP4, SLC9A7, SPPL2A, MICALL1, CHMP7, MMGT1, RFFL, ANTXR2, WDR81, ARL8A, ATP6V0E2, VPS37D, RAB12, TPCN2, CYB561A3, ZNRF2, MCOLN2, STEAP2, RAB15, SNX19
CC	GO:0005938	cell cortex	97/3499	1.94E-07	ACTB, ACTN4, AKT2, ARF6, RHOA, RHOB, ASPH, DST, FMNL1, CALD1, CAPN2, CAPZA2, CAV1, CDC42, CFL1, CTNNB1, CTNND1, CTSZ, EEF1A1, EPB41, EPS8, FER, FGF1, FLNB, FLOT2, GYPC, HIP1, ITPR2, LAMC2, LASP1, MARCKS, MKLN1, MPP1, MYH9, MYH10, MYO1D, MYO6, MYO10, NEDD4, NEDD9, NF2, PAFAH1B1, PXN, RDX, SNCA, SPTAN1, SPTBN1, STIM1, TPM4, TSC1, RND2, BSN, WASL, AKAP12, RIMS3, MELK, C2CD5, ACTR2, FRY, DLC1, RAPGEF3, CAP2, CAP1, UNC13B, EXOC5, DSTN, AKAP13, RHOBTB3, TRAK1, FNBP1, PHLDB1, EXOC6B, CLASP1, COTL1, RHOQ, CORO1C, ARFIP2, NSMF, RAI14, DCTN4, ANLN, FNBP1L, PARD3, FMN2, SPIRE1, SHROOM3, RHOU, MLPH, MED28, PARD6B, PHLDB2, MYADM, SHROOM1, RIMS4, WIPF2, EXOC8, FAM110C
CC	GO:0005667	transcription factor complex	110/3499	2.56E-07	ZFHX3, BCL9, RUNX2, RUNX1, RUNX3, CBFB, CEBPB, CREB1, ATF6B, CTNNB1, DACH1, E2F3, E2F5, E2F6, EP300, EPAS1, ERCC2, NR5A2, GATA6, KAT2A, NR6A1, GTF2A1, GTF2E1, GTF2H3, BRF1, GTF3C1, HIF1A, HMGA1, HNRNPAB, HNRNPU, HOXA9, RBPJ, JUN, JUND, LMO2, SMAD2, SMAD4, SMAD6, SMAD7, MAX, MEF2A, MXI1, NFYA, NFYB, PBX1, PKNOX1, POU2F1, POU3F2, PPARA, PPARD, RARG, RB1, RBL2, RFX3, SKI, SNAPC1, SOX4, SOX11, SOX12, STAT3, TAF1, TAF4B, TAL1, TCF4, HNF1B, TCF3, TCF7, TCF7L2, ZEB1, TEAD1, TEAD3, TFDP1, TFDP2, THRA, TLE1, TLE4, TP53, NR1H2, VDR, YY1, NR4A3, LDB1, LIMD1, LDB2, KLF4, GTF3C4, GTF3C3, HAND1, CLOCK, HDAC9, NR1D2, NFAT5, SUB1, SOX21, SNF8, KDM1A, RCOR1, SATB2, SIN3A, HIPK2, SOX8, TAF9B, SIX4, BRF2, HES6, ATF7IP, BDP1, MXD3, SOX7, E2F7
CC	GO:0030496	midbody	62/3499	5.97E-07	ARF6, RHOA, CDC42, CTNND1, CYLD, ECT2, GDI1, GNAI2, GNAI3, HNRNPU, HSPA5, INCENP, RAB8A, MYH10, PIK3CB, PIN1, PPP1CC, PKN2, PTCH1, RALB, RAN, RAP2A, RDX, AURKA, TACC1, UVRAG, PKP4, IQGAP1, PRC1, AURKB, KIF3B, KIF23, VPS4B, PDCD6IP, EXOC5, JTB, CNTRL, CIT, DCTN3, MAPRE3, ZFYVE26, ARL2BP, CLIC4, SH3GLB1, YPEL5, SSH1, ANLN, ALKBH4, CDCA8, CEP55, RCC2, CHMP1B, BIRC6, WIZ, KIF13A, SHCBP1, RAB11FIP4, LZTS2, KLHL13, ARL8A, KLHDC8B, FLCN
CC	GO:0001726	ruffle	61/3499	1.13E-06	AKT2, APC, ARF6, RHOA, ATP6V1B2, CDK6, CFL1, DIAPH1, EEF1A1, EPS8, ITGA5, ITGAV, ITGB1, MKLN1, MYH9, MYO1C, MYO5A, MYO6, MYO10, NF2, PODXL, TWF1, PTPRJ, RAB5A, RASA1, RDX, RPS3, SRC, ADAM17, TIAM1, TLN1, IQGAP1, KSR1, ARHGEF2, PDLIM7, CYTH3, C2CD5, WASF2, DLC1, NCKAP1, FAM107A, PALLD, KANK1, WWC1, PSD3, PIP5K1C, CORO1C, CD2AP, ARFIP2, APPL1, FERMT1, INPP5E, RAB22A, EPB41L5, PLEKHA1, MTMR9, SPRY4, MYADM, FGD4, AMOT, SPATA13
CC	GO:0036464	cytoplasmic ribonucleoprotein granule	71/3499	1.17E-06	ACTB, ZFP36L1, CDC42, DDX3X, DDX6, EIF2S1, EIF4E, ELAVL1, FMR1, HNRNPK, HNRNPU, LIG4, CAPRIN1, MAPT, MBNL1, PABPC3, POLR2D, PSMA2, PSMC2, UPF1, RPL28, ATXN2, STAU1, VCP, ZFP36, FXR1, SOCS1, DDX3Y, PABPC4, IQGAP1, SQSTM1, LIMD1, CNOT8, ROCK2, CLOCK, SNCAIP, PUM1, G3BP2, G3BP1, IGF2BP1, DDX19B, ATXN2L, CNOT1, SAMD4A, TNRC6B, LARP4B, ICOSLG, LARP1, TARDBP, LSM4, UPF2, GIGYF2, LSM14A, AGO1, PABPC1, TNRC6A, YTHDF2, XRN1, SAMD4B, RBM23, DDX19A, DCP1A, NUFIP2, TNRC6C, EDC3, MEX3A, LARP4, TRIM71, AGO3, AGO4, PATL1
CC	GO:0016607	nuclear speck	114/3499	1.92E-06	AR, BDNF, CDC5L, CDC34, CRY2, MAPK14, DDX3X, DYRK1A, EPAS1, NR3C1, HIF1A, HNRNPU, IK, LIMK1, MAPT, MEF2C, FOXO4, MPP1, OGG1, PIN1, PNN, POLR2D, PPP1CC, PRKAA1, RBBP6, RREB1, SRSF1, SRSF2, SRSF4, SRSF7, SNRPB2, SON, TCF3, TERT, TKT, ZNF217, KAT6A, PABPN1, SF3A2, NRIP1, AKAP17A, SPOP, CBX4, PRPF4, STK17A, TRIP12, TRIP11, EFTUD2, CTR9, PUM1, SETD1A, DAZAP2, DDX46, RBM19, AP5Z1, THRAP3, TENM1, TRIM22, PIAS3, TAB1, NXF1, DDX17, SRSF10, RNPS1, CPSF6, FAM107A, DUSP10, ATXN2L, U2AF2, PSME4, KAZN, FNBP4, TARDBP, PNISR, PPP1R16B, RBM15B, HP1BP3, RSRC1, WAC, CDC40, LUC7L3, RBM27, HAUS6, GATAD2A, ALKBH5, NCAPG2, SMU1, BMP2K, PRPF40A, KMT2E, YLPM1, ZMIZ1, THOC2, GATAD2B, USP36, EP400, SFMBT2, RBM25, SAP130, SMC6, AAGAB, CBLL1, SYNPO2L, GLYR1, GLIS2, EAF1, ZNF830, TIMM50, ARHGAP18, RMI2, SREK1, E2F7, HIPK1, PATL1
CC	GO:0010494	cytoplasmic stress granule	31/3499	2.08E-06	DDX3X, DDX6, EIF2S1, EIF4E, ELAVL1, FMR1, HNRNPK, CAPRIN1, MBNL1, PABPC3, ATXN2, STAU1, VCP, ZFP36, PABPC4, PUM1, G3BP2, G3BP1, IGF2BP1, DDX19B, ATXN2L, LARP4B, LARP1, TARDBP, GIGYF2, LSM14A, PABPC1, RBM23, DDX19A, NUFIP2, LARP4

CC	GO:0005819	spindle	102/3499	2.45E-06	ATM, CALM1, CALM2, CALM3, CDC42, MAPK14, CSNK1D, CTNNB1, CYLD, DIAPH1, ECT2, ERCC2, KAT2A, NR3C1, HNRNPU, HSPA2, IK, INCENP, KIF2A, MAD2L1, MAP4, MID1, MYH9, MYH10, NEDD9, PAFAH1B1, PPP2CA, MAPK1, RAD21, RB1, RPS3, AURKA, TBL1X, DYNLT3, TPT1, PTP4A1, EVI5, SMC1A, CUL3, PKP4, CDC14B, DYNLL1, TNKS, PRC1, LATS1, ARHGEF2, AURKB, KIF3B, CIAO1, KIF23, VPS4B, NCOR1, CEP350, KLHL21, NUBP2, FRY, STAG2, PLK2, JTB, SPIN1, KIF3A, DCTN3, CBX3, MAPRE3, MAPKBP1, CLASP1, ARL2BP, LATS2, DCTN4, NIN, YPEL5, INO80, HAUS6, NDE1, PINX1, HAUS2, CDCA8, RIF1, MAP7D1, RCC2, NSFL1C, FMN2, BIRC6, MTUS1, HECW2, KLHL42, CEP85, BRCC3, TBL1XR1, SHCBP1, RAB11FIP4, KBTBD8, WDR73, CEP19, CCSAP, ARL8A, UBXN2B, CKAP2L, TMEM201, BOD1L1, SKA2, FAM110C
CC	GO:0098562	cytoplasmic side of membrane	61/3499	3.43E-06	ACP1, ANK1, RHOA, ATP2A2, ATP2B1, CYLD, DTNA, EEF1A1, EPB41, FER, FKBP1A, G6PD, GM2A, GNAI2, GNAI3, GNAL, GNAQ, GNAS, GNB1, GNG7, HIP1, DNAJA1, IKBKB, JUP, KIT, KRAS, LYN, CDK16, PPP3CA, PTEN, PTPN1, PTPN4, PTPRC, RAB5A, RGS2, SNAP25, SRC, TIAM1, TRAF3, PTP4A1, PKP4, IQGAP1, CYTH3, CYTH1, AKAP5, EPM2AIP1, FARP1, GNA13, RASA3, RAB21, CBX6, NPTXR, LDLRAP1, HTRA2, CDIP1, ERRFI1, CISD1, ESYT2, PLEKHA4, SPPL2A, SPPL3
CC	GO:0035770	ribonucleoprotein granule	72/3499	3.52E-06	ACTB, ZFP36L1, CDC42, DDX3X, DDX6, EIF2S1, EIF4E, ELAVL1, FMR1, HNRNPK, HNRNPU, LIG4, CAPRIN1, MAPT, MBNL1, PABPC3, POLR2D, PSMA2, PSMC2, UPF1, RPL28, ATXN2, STAU1, VCP, ZFP36, FXR1, SOCS1, DDX3Y, PABPC4, IQGAP1, SQSTM1, LIMD1, CNOT8, ROCK2, CLOCK, SNCAIP, PUM1, G3BP2, G3BP1, IGF2BP1, DDX19B, ATXN2L, FASTKD2, CNOT1, SAMD4A, TNRC6B, LARP4B, ICOSLG, LARP1, TARDBP, LSM4, UPF2, GIGYF2, LSM14A, AGO1, PABPC1, TNRC6A, YTHDF2, XRN1, SAMD4B, RBM23, DDX19A, DCP1A, NUFIP2, TNRC6C, EDC3, MEX3A, LARP4, TRIM71, AGO3, AGO4, PATL1
CC	GO:0005774	vacuolar membrane	116/3499	3.52E-06	AP1G1, ABCC6, TRIM23, ARRB1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, SCARB2, AP2M1, AP1S1, CLCN7, CTNS, DAB2, EEF1A1, STOM, GAA, GNAI3, GNAQ, GNB1, IGF2R, LAMP2, LDLR, LNPEP, LRP1, M6PR, MYO6, NPC1, SLC11A2, NSF, ENPP1, PLD1, PRCP, RAP1B, SORT1, SLC12A4, SURF4, VAMP7, TRPM2, UVRAG, VLDLR, ULK1, ABCC3, CD164, NAPA, CPNE3, AP3D1, SPAG9, SYT7, ATP6V0D1, SYNGR1, VAPA, ENTPD4, LAPTM4A, PLEKHM1, TSPAN1, ATP8A1, HPSE, GLIPR1, SLC2A6, GABARAPL2, ATG14, ATP11B, ATP11A, DNAJC13, SZT2, NCSTN, ZFYVE26, MMD, SLC17A5, AP3M1, CDIP1, SLC2A8, SH3GLB1, ATP6V1D, ANKFY1, RAB14, TPCN1, TMEM106B, GDAP2, CMTM6, STX17, ATG16L1, DRAM1, LAPTM4B, SLC48A1, VPS35, TMEM165, TMEM9B, SLC7A14, RRAGD, GNB4, TMBIM1, RRAGC, AHNAK, HPS6, LPCAT1, CYBRD1, DNAJC5, ITM2C, MAP1LC3B, SEH1L, SPPL2A, WDR81, MFSD12, ARL8A, AP1S3, TMEM199, TMEM74, RAB12, TMEM192, SLC36A1, TPCN2, CYB561A3, ZNRF2, ATP11C
CC	GO:0090575	RNA polymerase II transcription factor complex	57/3499	3.52E-06	BCL9, RUNX1, RUNX3, CBFB, CEBPB, CREB1, ATF6B, CTNNB1, E2F3, E2F5, E2F6, ERCC2, NR5A2, KAT2A, GTF2A1, GTF2E1, GTF2H3, HIF1A, HMGA1, HNRNPAB, HNRNPU, JUN, JUND, SMAD2, SMAD4, MAX, MXI1, NFYA, NFYB, PBX1, POU2F1, PPARA, PPARD, RARG, RB1, STAT3, TAF1, TAF4B, TCF4, TCF3, TCF7L2, TEAD1, TFDP1, TFDP2, THRA, TLE1, TLE4, TP53, NR1H2, VDR, LDB1, HAND1, NR1D2, HIPK2, TAF9B, MXD3, E2F7
CC	GO:0034708	methyltransferase complex	43/3499	8.25E-06	CLNS1A, E2F6, EZH1, EZH2, HCFC1, HDAC2, JARID2, MAX, MEN1, KMT2A, KDM5A, RNF2, SNRPF, TAF1, KDM6A, KMT2D, KDM4A, HDAC9, SETD1A, KMT2B, KDM5B, MTF2, ZNF507, POGZ, KDM6B, MGA, SIRT1, CBX5, SUZ12, ZNF451, RBM15B, TRMT6, WDR5B, PRDM10, METTL14, ZNF462, KMT2C, WDR77, CBLL1, DPY30, TRMT61A, AEBP2, ZNF827
CC	GO:0030426	growth cone	58/3499	8.25E-06	AMFR, APBB2, CALM3, CBL, CTNND1, CTSZ, CXADR, DLG3, EPHA4, EPS8, FKBP4, FMR1, ITGA3, KIF5B, L1CAM, LRP1, MAP1B, MAPT, MYH10, MYO5A, PAFAH1B1, PCDH9, PTCH1, SNAP25, SNCA, STX3, TIAM1, TIMP2, TSC1, YWHAE, USP9X, IQGAP1, NRP1, TAOK2, LRIG2, ARPC5, SIGMAR1, OLFM1, IGF2BP1, LMTK2, TRAK1, SHANK2, PALLD, MAPK8IP3, DICER1, CBX6, NPTXR, AUTS2, TMOD2, NIN, SSH1, PARD3, NDRG2, TRAK2, ORAI2, CPEB4, GPRIN1, EXOC8
CC	GO:0005765	lysosomal membrane	101/3499	9.86E-06	AP1G1, TRIM23, ARRB1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, SCARB2, AP2M1, AP1S1, CLCN7, CTNS, DAB2, EEF1A1, STOM, GAA, GNAI3, GNAQ, GNB1, IGF2R, LAMP2, LDLR, LNPEP, LRP1, M6PR, MYO6, NPC1, SLC11A2, NSF, ENPP1, PLD1, PRCP, RAP1B, SORT1, SLC12A4, SURF4, VAMP7, TRPM2, VLDLR, CD164, CPNE3, AP3D1, SPAG9, SYT7, ATP6V0D1, SYNGR1, VAPA, LAPTM4A, PLEKHM1, TSPAN1, ATP8A1, HPSE, GLIPR1, SLC2A6, ATP11B, ATP11A, DNAJC13, SZT2, NCSTN, ZFYVE26, MMD, SLC17A5, AP3M1, CDIP1, SLC2A8, ATP6V1D, ANKFY1, RAB14, TPCN1, TMEM106B, GDAP2, CMTM6, DRAM1, LAPTM4B, SLC48A1, VPS35, TMEM165, TMEM9B, SLC7A14, GNB4, TMBIM1, AHNAK, HPS6, LPCAT1, CYBRD1, DNAJC5, ITM2C, SEH1L, SPPL2A, WDR81, MFSD12, ARL8A, AP1S3, TMEM74, RAB12, TMEM192, SLC36A1, TPCN2, CYB561A3, ZNRF2, ATP11C
CC	GO:0098852	lytic vacuole membrane	101/3499	1.10E-05	AP1G1, TRIM23, ARRB1, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, SCARB2, AP2M1, AP1S1, CLCN7, CTNS, DAB2, EEF1A1, STOM, GAA, GNAI3, GNAQ, GNB1, IGF2R, LAMP2, LDLR, LNPEP, LRP1, M6PR, MYO6, NPC1, SLC11A2, NSF, ENPP1, PLD1, PRCP, RAP1B, SORT1, SLC12A4, SURF4, VAMP7, TRPM2, VLDLR, CD164, CPNE3, AP3D1, SPAG9, SYT7, ATP6V0D1, SYNGR1, VAPA, LAPTM4A, PLEKHM1, TSPAN1, ATP8A1, HPSE, GLIPR1, SLC2A6, ATP11B, ATP11A, DNAJC13, SZT2, NCSTN, ZFYVE26, MMD, SLC17A5, AP3M1, CDIP1, SLC2A8, ATP6V1D, ANKFY1, RAB14, TPCN1, TMEM106B, GDAP2, CMTM6, DRAM1, LAPTM4B, SLC48A1, VPS35, TMEM165, TMEM9B, SLC7A14, GNB4, TMBIM1, AHNAK, HPS6, LPCAT1, CYBRD1, DNAJC5, ITM2C, SEH1L, SPPL2A, WDR81, MFSD12, ARL8A, AP1S3, TMEM74, RAB12, TMEM192, SLC36A1, TPCN2, CYB561A3, ZNRF2, ATP11C
CC	GO:0005911	cell-cell junction	124/3499	1.18E-05	ACTN4, ADCYAP1R1, ADD1, APC, RHOA, ATP1B1, ATP2A2, CCND1, BMPR2, CDH6, CFL1, CNN2, CSK, CTNNA1, CTNNB1, CTNND1, CXADR, DAG1, DDX6, DLG3, DSC2, ECT2, EIF4G2, FAT1, FLOT2, GAB1, GJA1, GJB1, GRB2, ILK, ITGA6, ITGA5, ITGB1, JUP, KCNJ2, KIT, LYN, SMAD7, MYH9, NCK1, NHS, CLDN11, PCDH9, PKP1, PNN, PODXL, PPP1CA, PPP3CA, PKN2, TWF1, PTPRJ, PTPRK, RAP1B, RAP2B, RDX, SLC8A1, SLC9A1, STRN, STX3, ADAM17, TGFBR1, TIAM1, VCL, VEGFA, FZD5, FZD4, PKP4, PDLIM4, MPDZ, IQGAP1, LIMD1, ARHGEF2, VAPA, DLG5, PDLIM7, CYTH3, CYTH1, TJP2, AKAP6, TRAF4, RAPGEF2, SV2A, PDCD6IP, GJC1, WASF2, PDLIM5, FRS2, PDZD2, NFASC, KAZN, CD2AP, CADM1, FLRT2, CLIC4, CNTNAP2, PDLIM3, EPB41L4B, KLHL24, AHI1, ARHGAP17,

					FRMD4A, PARD3, PANX2, VANGL2, HEG1, SHROOM3, RAP2C, JAM2, AHNAK, CLMP, TMEM47, PARD6B, CGNL1, MYADM, MTDH, SSX2IP, IQGAP3, SHROOM1, CLDN23, AMOT, AMOTL1, TMEM65, FLCN, CCDC85C
CC	GO:0031256	leading edge membrane	57/3499	1.33E-05	AKT2, ANK1, APC, RHOA, ATP2B1, CD44, CFL1, DIAPH1, EEF1A1, EPS8, INSR, ITGA5, ITGAV, ITGB1, KCNC1, KCNC4, MAPT, MPP2, MYO1C, MYO1D, MYO6, NF2, TWF1, PTPRJ, PTPRK, RPS3, SLC1A2, SPTBN1, SRC, ADAM17, TIAM1, TLN1, ITGA8, KSR1, ARHGEF2, AKAP5, C2CD5, DLC1, NCKAP1, FAM107A, PLXND1, KANK1, WWC1, PSD3, PIP5K1C, CORO1C, SLC39A6, CNTNAP2, VEZT, FERMT1, EPB41L5, PLEKHA1, MTMR9, SPRY4, ANTXR1, SPATA13, SCIMP
CC	GO:0035097	histone methyltransferase complex	35/3499	1.33E-05	E2F6, EZH1, EZH2, HCFC1, HDAC2, JARID2, MAX, MEN1, KMT2A, KDM5A, RNF2, TAF1, KDM6A, KMT2D, KDM4A, HDAC9, SETD1A, KMT2B, KDM5B, MTF2, ZNF507, POGZ, KDM6B, MGA, SIRT1, CBX5, SUZ12, ZNF451, WDR5B, PRDM10, ZNF462, KMT2C, DPY30, AEBP2, ZNF827
CC	GO:0030427	site of polarized growth	58/3499	1.94E-05	AMFR, APBB2, CALM3, CBL, CTNND1, CTSZ, CXADR, DLG3, EPHA4, EPS8, FKBP4, FMR1, ITGA3, KIF5B, L1CAM, LRP1, MAP1B, MAPT, MYH10, MYO5A, PAFAH1B1, PCDH9, PTCH1, SNAP25, SNCA, STX3, TIAM1, TIMP2, TSC1, YWHAE, USP9X, IQGAP1, NRP1, TAOK2, LRIG2, ARPC5, SIGMAR1, OLFM1, IGF2BP1, LMTK2, TRAK1, SHANK2, PALLD, MAPK8IP3, DICER1, CBX6, NPTXR, AUTS2, TMOD2, NIN, SSH1, PARD3, NDRG2, TRAK2, ORAI2, CPEB4, GPRIN1, EXOC8
CC	GO:0032587	ruffle membrane	36/3499	4.86E-05	AKT2, APC, RHOA, CFL1, DIAPH1, EEF1A1, EPS8, ITGA5, ITGAV, ITGB1, MYO1C, MYO6, NF2, TWF1, PTPRJ, RPS3, SRC, ADAM17, TIAM1, TLN1, KSR1, ARHGEF2, C2CD5, DLC1, FAM107A, KANK1, WWC1, PSD3, PIP5K1C, CORO1C, FERMT1, EPB41L5, PLEKHA1, MTMR9, SPRY4, SPATA13
CC	GO:0009898	cytoplasmic side of plasma membrane	51/3499	7.02E-05	ACP1, ANK1, RHOA, ATP2A2, ATP2B1, CYLD, DTNA, EPB41, FER, G6PD, GM2A, GNAI2, GNAI3, GNAL, GNAQ, GNAS, GNB1, GNG7, HIP1, IKBKB, JUP, KIT, KRAS, LYN, CDK16, PPP3CA, PTEN, PTPN4, PTPRC, RGS2, SNAP25, SRC, TIAM1, TRAF3, PTP4A1, PKP4, IQGAP1, CYTH3, CYTH1, AKAP5, FARP1, GNA13, RASA3, RAB21, CBX6, NPTXR, LDLRAP1, HTRA2, ERRFI1, ESYT2, PLEKHA4
CC	GO:0098978	glutamatergic synapse	96/3499	8.24E-05	ACTB, ADAM10, ADCY1, ADORA2B, ARF1, ARF6, RHOA, ATP2B1, ATP2B4, CAMK4, CANX, MAPK14, CTNND1, DAG1, DLG3, EFNB2, EIF4E, ELAVL1, EPHA4, EPHA7, EPHB2, EPS8, FLOT2, GSK3B, NRG1, HIP1, IL1RAP, ITGB1, KPNA1, LYN, RAB8A, MYH10, MYO5A, NPTX1, NTRK3, OPHN1, P2RY1, PAK2, PAK3, PIN1, PPP1CA, PPP1CC, PPP2R1A, PPP2R2A, PPP3CA, PRKAR1A, PTPRD, PURA, SH3GL2, SLC1A2, SNAP25, SPARC, SPTBN1, SRC, STAT3, STAU1, STX3, VAMP1, SYT1, TIAM1, VCP, YWHAE, FXR1, FZD4, DGKE, NUMB, NAPA, NRP1, SYNGAP1, BSN, AP3D1, ARHGEF2, NOS1AP, SV2A, GPC6, ARPC2, AKAP9, UNC13B, NLGN1, NCS1, NPTXR, RNF19A, TANC2, NPTN, PCDH17, ABHD17B, ADAM22, VPS35, PPM1H, ABHD17C, DLGAP3, LRRC4, ARHGAP39, SLITRK4, FBXO45, RGS7BP
CC	GO:0055037	recycling endosome	56/3499	8.99E-05	AP1G1, ARF6, SLC31A2, HLA-B, ITGB1, KCNK1, RAB8A, MYO5A, SLC11A2, RAN, RAP2A, RAP2B, SORL1, TFRC, ULK1, PDLIM4, RABEP1, RAB11B, SCAMP1, FCHSD2, SCAMP2, ATP9A, SLC9A6, ARFGEF2, SNF8, RAB11FIP2, LMTK2, AVL9, ATP11B, SYT11, ATP11A, STX12, SGK3, CLIP3, LDLRAP1, RNF11, EHD4, ABHD17B, RAB14, RAB8B, CMTM6, PLEKHB2, RAP2C, ABHD17C, RAB17, ATG9A, RAB11FIP1, TMUB1, RAB11FIP4, SLC9A7, MICALL1, RFFL, RAB12, DENND6A, MCOLN2, ATP11C
CC	GO:0033267	axon part	103/3499	9.20E-05	ACTB, AMFR, ANK1, APBB2, DST, CALM3, CBL, AP1S1, CTNND1, CTSZ, CXADR, DAG1, DLG3, ELK1, EPHA4, EPS8, FKBP4, FMR1, HIF1A, ILK, ITGA3, KCNC1, KCNC4, KIF5B, L1CAM, LRP1, MAP1A, MAP1B, MAPT, MBP, MYH10, MYO1D, MYO5A, OPA1, OPHN1, PAFAH1B1, PCDH9, PTCH1, PTPRN2, RAB5A, SCN8A, SLC1A2, SNAP25, SNCA, SPTBN1, AURKA, STX3, TIAM1, TIMP2, TNFRSF1B, TSC1, YWHAE, USP9X, DYNLL1, IQGAP1, NRP1, SYNJ1, AP3D1, ATP6V0D1, TAOK2, KIF3B, LRIG2, ARPC5, AP3S2, SIGMAR1, TUBB4A, OLFM1, SLC9A6, UNC13B, IGF2BP1, KIF3A, AAK1, LMTK2, TRAK1, SHANK2, RAB21, PALLD, KIF1B, NFASC, MAPK8IP3, SYT11, DICER1, NCS1, CBX6, NPTXR, CNTNAP2, AUTS2, AP3M1, GIT1, TMOD2, NIN, SSH1, PARD3, NDRG2, TBC1D24, TRAK2, ORAI2, CPEB4, NAV1, GPRIN1, TPRG1L, ARL8A, EXOC8
CC	GO:0030135	coated vesicle	82/3499	1.06E-04	AP1G1, ARCN1, ARF1, ATP7A, SCARB2, CD59, AP2M1, AP1S1, COPB1, CTSZ, DAB2, HBEGF, EDN1, EGFR, HIP1, HLA-B, IGF2R, IL7R, LDLR, LRP1, M6PR, RAB8A, MYO6, FURIN, PIK3C2A, RAB5A, SORT1, SH3GL2, SREBF2, VAMP2, VAMP7, SYT1, TFRC, TGFA, MALL, FZD5, FZD4, USO1, NUMB, SNX3, AP1G2, SCAMP1, GOSR2, SEC24C, BCAP31, CNIH1, TNK2, SEC23A, TGOLN2, SEC24A, TMED10, SYNRG, AAK1, SEC31B, NECAP1, LDLRAP1, SLC2A8, TMED5, TMED7, ERGIC2, RAB14, RAB8B, STX17, PACS1, NECAP2, SAR1A, VANGL2, GPR107, DNAJC5, YIPF5, PITPNM3, SGIP1, STON2, YIF1B, TEX261, FCHO2, SYT2, TMEM199, VMA21, TMED4, EPGN, STEAP2
CC	GO:0005635	nuclear envelope	120/3499	1.34E-04	ABL1, ANXA7, BCL2, BCL2L1, BNIP2, DST, CALR, CCND2, CETN2, RCC1, EGFR, GAPDH, GATA6, GNAQ, HOXA7, DNAJB2, IGF2R, IL15RA, INSR, ITPR1, KPNA1, KPNA3, IPO5, LBR, MAD2L1, MYO1C, MYO6, NPC1, NUP88, NUP98, PAFAH1B1, PDE4D, POLA1, MAPK3, RAN, RANBP2, SORT1, TRA2B, SNCA, SORL1, MLX, TMPO, TYRO3, XPO1, ZNF224, YEATS4, TNKS, MTA1, VAPA, GTF3C3, AKAP6, NOS1AP, MRPL19, POM121, NUTF2, SIGMAR1, CEPT1, PGRMC2, NXF1, NUP50, SPIN1, XPOT, DDX19B, CBX3, SEPHS1, XPO7, RAP1GAP2, PHF8, LPIN1, UBXN4, ATP11B, PHLPP1, BICD2, SIRT1, CBX5, KPNA6, NSMF, MYOF, TOR1B, RBM15B, DTL, DNAJB12, TMEM33, RIF1, DDX19A, IPO9, NDC1, NUP133, TXLNG, PCID2, EIF5A2, AGPAT3, DNAJC1, XPO4, AEN, TMEM43, AKIRIN1, EPC1, SEH1L, DCTN5, LMNB2, NAV3, CHMP7, MTDH, DTX2, OSBPL8, TMEM170A, TBC1D20, TMEM18, TMEM120B, TOR1AIP2, PRICKLE2, QSOX2, TMEM201, CERS6, CNEP1R1, RNF180, DPY19L4, NUP43, POM121C
CC	GO:0098984	neuron to neuron synapse	95/3499	1.43E-04	ADAM10, ADCY1, ADD1, ARF1, ARRB1, ARRB2, BMPR2, CACNA1C, CAMK2A, CTNNB1, CTNND1, DLG3, EFNB2, EPB41, EPHA4, EPHA7, EPS8, FMR1, ITPR1, KPNA1, LYN, MAP1B, MAP4, RAB8A, MPP2, NEFH, NSF, P2RY1, PAK2, PAK3, MAPK1, PTCH1, RPS3, SH3GL2, SLC6A9, SOS1, SPTBN1, SRC, STAT3, STRN, VAMP7, SYT1, TIAM1, TSC1, FXR1, NCK2, PKP4, ITGA8, EIF3A, MPDZ,

					SYNGAP1, BSN, SYT7, ARHGEF2, DCLK1, DLG5, AKAP5, ACTR2, AKAP9, SIGMAR1, CAP2, UNC13B, ARFGEF2, PDLIM5, CPEB3, NLGN1, SHANK2, SYT11, ARHGEF9, PSD3, NCS1, RNF19A, NSMF, SIPA1L1, TANC2, NPTN, MINK1, ABHD17B, BCL11A, ADAM22, SEMA4C, CAMK2N1, VPS35, ARFGAP1, PRR12, MIB1, NLGN2, ABHD17C, DLGAP3, LRRC4, CPEB4, NETO2, FBXO45, RGS7BP, IQSEC3
CC	GO:0032154	cleavage furrow	24/3499	1.43E-04	ARF6, RHOA, RHOB, ECT2, ITGB1, MEN1, MYH9, MYH10, NF2, PPP1CC, PKN2, RDX, STAMBP, CIT, DCTN3, RAB21, SSH1, NDE1, CEP55, SPIRE1, RAB11FIP4, WDR73, PLCD3, KLHDC8B
CC	GO:0098589	membrane region	90/3499	1.50E-04	ADCY1, ADCYAP1R1, ADD1, FAS, ATP1B1, ATP2B1, ATP2B4, ATP7A, BMPR1A, BMPR2, CAPN2, CASP3, CAV1, CBL, CNTN1, CRK, CSK, CTNNA1, CTNNB1, CXADR, DAG1, S1PR1, EFNA5, EFNB1, EGFR, EMP2, STOM, FLOT2, GJA1, GNAI2, GNAI3, HK1, IKBKB, INSR, ITGB1, KRAS, LAMP2, LRP6, LYN, MAPT, MME, MYO1C, MYO1D, NPC1, OLR1, FURIN, PODXL, PPP2CA, PRKAR1A, PRKAR2A, MAPK1, MAPK3, PTCH1, PTGIS, PTPRC, RAB5A, RANBP2, RAP2B, SDC4, SLC9A1, SRC, STIM1, ADAM17, TFPI, TGFBR1, TNFRSF1B, XPO1, MALL, FADD, IQGAP1, SYNJ2, TRIP11, AKAP6, AKAP5, NOS1AP, DLC1, HPSE, ERLIN2, BICD2, RHOQ, CORO1C, STX12, CLIP3, MYOF, PAG1, AHNAK, EFHD2, MYADM, MAL2, SPRED1
CC	GO:0030863	cortical cytoskeleton	40/3499	2.09E-04	ACTB, ACTN4, CALD1, CAPN2, CAPZA2, CFL1, EEF1A1, EPB41, FLOT2, GYPC, HIP1, LASP1, MPP1, MYH9, NF2, RDX, SPTAN1, SPTBN1, TPM4, BSN, WASL, RIMS3, ACTR2, DLC1, RAPGEF3, CAP2, CAP1, DSTN, AKAP13, CLASP1, COTL1, NSMF, ANLN, SHROOM3, MLPH, MED28, MYADM, SHROOM1, RIMS4, WIPF2
CC	GO:0016363	nuclear matrix	38/3499	2.49E-04	RUNX1T1, CEBPB, CFL1, CFL2, DNMT3A, ATN1, HNRNPU, MEN1, ATXN3, MYB, HNRNPM, OGG1, PML, POLA1, RAD21, SATB1, ATXN1, ATXN7, SPARC, TP53, YY1, YEATS4, SMC1A, ENC1, TENM1, DCAF7, STAG2, XPOT, MORC2, SATB2, MORC3, CLIC4, NSMF, PIAS4, FIGN, PRPF40A, SMARCAD1, ZNF350
CC	GO:0098644	complex of collagen trimers	12/3499	2.49E-04	COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL4A5, COL4A6, COL5A1, COL5A2, COL11A1, COL5A3, COL27A1
CC	GO:0045121	membrane raft	86/3499	2.63E-04	ADCY1, ADCYAP1R1, ADD1, FAS, ATP1B1, ATP2B1, ATP2B4, ATP7A, BMPR1A, BMPR2, CAPN2, CASP3, CAV1, CBL, CNTN1, CRK, CSK, CTNNA1, CTNNB1, CXADR, DAG1, S1PR1, EFNA5, EFNB1, EGFR, EMP2, STOM, FLOT2, GJA1, GNAI2, GNAI3, HK1, IKBKB, INSR, ITGB1, KRAS, LAMP2, LRP6, LYN, MAPT, MME, MYO1C, MYO1D, NPC1, OLR1, FURIN, PODXL, PPP2CA, PRKAR1A, PRKAR2A, MAPK1, MAPK3, PTCH1, PTGIS, PTPRC, RAB5A, RAP2B, SDC4, SLC9A1, SRC, STIM1, ADAM17, TFPI, TGFBR1, TNFRSF1B, MALL, FADD, IQGAP1, SYNJ2, AKAP6, AKAP5, NOS1AP, DLC1, HPSE, ERLIN2, RHOQ, CORO1C, STX12, CLIP3, MYOF, PAG1, AHNAK, EFHD2, MYADM, MAL2, SPRED1
CC	GO:0031463	Cul3-RING ubiquitin ligase complex	18/3499	2.75E-04	TNFAIP1, GAN, SPOP, CUL3, ENC1, KLHL21, KCTD2, ARIH1, KLHL3, KLHL24, KLHL7, KLHL42, KCTD17, KLHL15, KCTD10, KBTBD8, KLHL13, SPOPL
CC	GO:0098857	membrane microdomain	86/3499	2.75E-04	ADCY1, ADCYAP1R1, ADD1, FAS, ATP1B1, ATP2B1, ATP2B4, ATP7A, BMPR1A, BMPR2, CAPN2, CASP3, CAV1, CBL, CNTN1, CRK, CSK, CTNNA1, CTNNB1, CXADR, DAG1, S1PR1, EFNA5, EFNB1, EGFR, EMP2, STOM, FLOT2, GJA1, GNAI2, GNAI3, HK1, IKBKB, INSR, ITGB1, KRAS, LAMP2, LRP6, LYN, MAPT, MME, MYO1C, MYO1D, NPC1, OLR1, FURIN, PODXL, PPP2CA, PRKAR1A, PRKAR2A, MAPK1, MAPK3, PTCH1, PTGIS, PTPRC, RAB5A, RAP2B, SDC4, SLC9A1, SRC, STIM1, ADAM17, TFPI, TGFBR1, TNFRSF1B, MALL, FADD, IQGAP1, SYNJ2, AKAP6, AKAP5, NOS1AP, DLC1, HPSE, ERLIN2, RHOQ, CORO1C, STX12, CLIP3, MYOF, PAG1, AHNAK, EFHD2, MYADM, MAL2, SPRED1
CC	GO:0031519	PcG protein complex	21/3499	2.75E-04	EZH1, EZH2, HDAC2, JARID2, RNF2, SKP1, YY1, BAP1, CBX4, UBAP2L, PCGF3, SCML2, MTF2, SIRT1, CBX6, CBX7, SUZ12, PHC3, PCGF5, CBX2, AEBP2
CC	GO:0030667	secretory granule membrane	82/3499	2.75E-04	ADAM10, ANXA7, RHOA, CAV1, CD44, CD47, CD59, COPB1, DIAPH1, STOM, FLOT2, GAA, NCKAP1L, IGF2R, ITGAV, ITPR1, ITPR2, LAMP2, MME, NRAS, OLR1, PCDH7, PKP1, PLD1, PRCP, PTAFR, PTPRB, PTPRC, PTPRJ, PTPRN2, RAB5B, RAP1B, RAP2B, SNAP25, SNCA, SPARC, STK10, STX3, SURF4, VAMP1, VAMP2, VAMP7, SYT1, TNFRSF1B, TRPM2, RND2, DYNLL1, IQGAP1, CPNE3, SYNGR1, VAPA, TRIP11, SCAMP1, PHACTR2, MLEC, ATP6AP2, LHFPL2, ATP8A1, IQGAP2, PGRMC1, TMED10, GLIPR1, RAB31, NFASC, ATP11B, ATP11A, DNAJC13, NCSTN, ATP6V1D, RAB14, TMX3, CMTM6, RAP2C, TMBIM1, LPCAT1, DNAJC5, FRMPD3, ORMDL3, ARL8A, SYT2, CD109, SIRPA
CC	GO:0070603	SWI/SNF superfamily-type complex	29/3499	3.18E-04	CHD3, CHD4, BPTF, HDAC2, RB1, SMARCA2, SMARCC2, SMARCD2, SMARCE1, SS18, YY1, DPF3, DPF1, ARID1A, MTA1, HMGXB4, SRCAP, SUZ12, SS18L1, CECR2, UCHL5, RSF1, ING3, INO80, GATAD2A, GATAD2B, ARID1B, EP400, ANP32E
CC	GO:0016605	PML body	35/3499	3.21E-04	ATR, ATRX, ELF4, MKNK2, MAX, PML, PTEN, RAD51, RB1, RNF4, SATB1, SKI, SP3, SP100, TCF7L2, TERT, TP53, ZMYM2, KAT6A, SQSTM1, HIPK3, SIRT1, CBX5, MORC3, ZNF451, HIPK2, PIAS4, RNF111, TP53INP2, HMBOX1, SMC6, RPAIN, TP53INP1, HIPK1, PATL1
CC	GO:0034399	nuclear periphery	43/3499	3.22E-04	RUNX1T1, CEBPB, CFL1, CFL2, DAG1, DNMT3A, ATN1, HNRNPU, MAPT, MEN1, ATXN3, MYB, HNRNPM, NUP98, OGG1, PML, POLA1, RAD21, SATB1, ATXN1, ATXN7, SPARC, SUV39H1, TP53, YY1, YEATS4, SMC1A, ENC1, TENM1, DCAF7, STAG2, XPOT, MORC2, SATB2, MORC3, CLIC4, NSMF, PIAS4, FIGN, PRPF40A, SMARCAD1, ZNF350, LMNB2
CC	GO:0000932	P-body	31/3499	3.42E-04	ZFP36L1, DDX6, EIF4E, CAPRIN1, POLR2D, PSMA2, PSMC2, UPF1, ZFP36, SQSTM1, LIMD1, CNOT8, PUM1, CNOT1, SAMD4A, TNRC6B, LSM4, LSM14A, AGO1, TNRC6A, YTHDF2, XRN1, SAMD4B, DCP1A, TNRC6C, EDC3, MEX3A, TRIM71, AGO3, AGO4, PATL1

CC	GO:0032279	asymmetric synapse	88/3499	3.58E-04	ADAM10, ADCY1, ADD1, ARF1, ARRB1, ARRB2, BMPR2, CACNA1C, CAMK2A, CTNNB1, CTNND1, DLG3, EFNB2, EPB41, EPHA4, EPHA7, EPS8, FMR1, ITPR1, KPNA1, LYN, MAP1B, MAP4, RAB8A, MPP2, NEFH, NSF, P2RY1, PAK2, PAK3, MAPK1, PTCH1, RPS3, SLC6A9, SOS1, SPTBN1, SRC, STAT3, STRN, TIAM1, TSC1, FXR1, NCK2, PKP4, ITGA8, EIF3A, MPDZ, SYNGAP1, BSN, ARHGEF2, DCLK1, DLG5, AKAP5, ACTR2, AKAP9, SIGMAR1, CAP2, ARFGEF2, PDLIM5, CPEB3, NLGN1, SHANK2, SYT11, ARHGEF9, PSD3, NCS1, NSMF, SIPA1L1, TANC2, NPTN, MINK1, ABHD17B, BCL11A, ADAM22, SEMA4C, CAMK2N1, VPS35, ARFGAP1, PRR12, MIB1, ABHD17C, DLGAP3, LRRC4, CPEB4, NETO2, FBXO45, RGS7BP, IQSEC3
CC	GO:0014069	postsynaptic density	87/3499	3.76E-04	ADAM10, ADCY1, ADD1, ARF1, ARRB1, ARRB2, BMPR2, CACNA1C, CAMK2A, CTNNB1, CTNND1, DLG3, EFNB2, EPB41, EPHA4, EPHA7, EPS8, FMR1, ITPR1, KPNA1, LYN, MAP1B, MAP4, RAB8A, MPP2, NEFH, NSF, P2RY1, PAK2, PAK3, MAPK1, PTCH1, RPS3, SLC6A9, SOS1, SPTBN1, SRC, STAT3, STRN, TIAM1, TSC1, FXR1, NCK2, PKP4, ITGA8, EIF3A, MPDZ, SYNGAP1, BSN, ARHGEF2, DCLK1, DLG5, AKAP5, ACTR2, AKAP9, SIGMAR1, CAP2, PDLIM5, CPEB3, NLGN1, SHANK2, SYT11, ARHGEF9, PSD3, NCS1, NSMF, SIPA1L1, TANC2, NPTN, MINK1, ABHD17B, BCL11A, ADAM22, SEMA4C, CAMK2N1, VPS35, ARFGAP1, PRR12, MIB1, ABHD17C, DLGAP3, LRRC4, CPEB4, NETO2, FBXO45, RGS7BP, IQSEC3
CC	GO:0030175	filopodium	36/3499	3.79E-04	ARF6, CDC42, CXADR, DAG1, EPHA4, FAT1, FMR1, UBE2K, ITGA6, ITGA3, ITGAV, ITGB1, KITLG, MYO1B, MYO5A, MYO6, MYO10, NF2, PODXL, TWF1, RDX, VCAM1, FZD3, ABI2, FARP1, RAPGEF3, IGF2BP1, IQGAP2, NLGN1, CBX6, NPTXR, UBE2Q1, RAPH1, ANTXR1, FGD4, SPATA13
CC	GO:0043025	neuronal cell body	124/3499	3.84E-04	ABL1, ADA, ADAM10, ALCAM, AMFR, ATP2B1, ATP7A, BMPR1A, BMPR2, CACNA1B, CACNA1C, CANX, CAPN2, CASP3, CDC42, DLG3, DMWD, ELK1, EPHA4, EPHA7, EPHB2, ACSL4, FKBP4, FLNB, FMR1, FUS, GDI1, GOT2, GRIA4, HCFC1, IL6ST, ILK, INSR, KCNC1, KCNC4, KCNJ2, KCNK1, KCNN3, L1CAM, LRP1, LRP6, MAP1A, MAP1B, MAPT, MBP, RAB8A, MME, MYH10, MYO1D, MYO5A, MYO10, PAFAH1B1, PCSK2, PDE1B, PMM2, PPP1CA, PRKAA1, MAPK1, PTPRF, PTPRK, PURA, RAB5A, SORT1, CX3CL1, MAP2K4, SH3GL2, SIAH2, SLC1A4, SNCA, SOS1, STAU1, AURKA, STRN, TIAM1, TIMP2, TNFRSF1B, TRPM2, FZD5, FZD3, FXR1, ITGA8, NRP1, ARHGEF2, SLC4A8, AKAP12, SNCAIP, RAPGEF2, LRIG2, SV2A, AKAP9, G3BP1, TUBB4A, OLFM1, PGRMC1, CIT, LMTK2, SHANK2, NCDN, CBX6, NPTXR, TMEM50A, TXN2, ZNF385A, NSMF, CNTNAP2, GIGYF2, CNNM4, STRN3, SLC38A2, XRN1, KLHL24, CAMK2N1, VPS35, PARD3, DPYSL5, SMURF1, KLHL14, ELOVL5, RAB17, TRAK2, MUL1, TTLL7, KREMEN1, DAB2IP
CC	GO:0008287	protein serine/threonine phosphatase complex	20/3499	3.94E-04	ITPR1, PPP1R12A, NCK1, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PPP3R1, SHOC2, TOX4, CYCS, PPP2R2D, PPP1R15B, PPP4R2, CNEP1R1
CC	GO:1903293	phosphatase complex	20/3499	3.94E-04	ITPR1, PPP1R12A, NCK1, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PPP3R1, SHOC2, TOX4, CYCS, PPP2R2D, PPP1R15B, PPP4R2, CNEP1R1
CC	GO:0150034	distal axon	78/3499	4.30E-04	ACTB, AMFR, APBB2, CALM3, CBL, AP1S1, CTNND1, CTSZ, CXADR, DLG3, ELK1, EPHA4, EPS8, FKBP4, FMR1, ILK, ITGA3, KCNC1, KCNC4, KIF5B, L1CAM, LRP1, MAP1B, MAPT, MYH10, MYO5A, OPHN1, PAFAH1B1, PCDH9, PTCH1, PTPRN2, RAB5A, SNAP25, SNCA, STX3, TIAM1, TIMP2, TSC1, YWHAE, USP9X, IQGAP1, NRP1, SYNJ1, AP3D1, ATP6V0D1, TAOK2, LRIG2, ARPC5, SIGMAR1, OLFM1, SLC9A6, UNC13B, IGF2BP1, AAK1, LMTK2, TRAK1, SHANK2, PALLD, MAPK8IP3, SYT11, DICER1, NCS1, CBX6, NPTXR, AUTS2, GIT1, TMOD2, NIN, SSH1, PARD3, NDRG2, TBC1D24, TRAK2, ORAI2, CPEB4, GPRIN1, TPRG1L, EXOC8
CC	GO:0005802	trans-Golgi network	67/3499	4.30E-04	ADAM10, AP1G1, ARF1, ARL1, ATP7A, AP1S1, GOLGA1, GOLGA4, IGF2R, M6PR, CHST6, RAB8A, MME, MYO1B, FURIN, ATXN2, SNAP25, SORL1, VAMP2, VAMP7, CHST1, SCAMP1, PREPL, USP6NL, SCAMP2, ATP9A, ARFRP1, ATP8A1, ARFGEF2, TGOLN2, POSTN, RAB31, RHOBTB3, RAB21, NMNAT2, ATP11B, ATP11A, AP4E1, ARFIP2, BACE2, CLIP3, NBEA, RAB30, VPS54, RAB14, SYT17, GOLPH3L, PI4K2B, TMEM165, CHST7, BIRC6, KIF13A, ATG9A, C16orf70, COG3, SLC10A7, COG8, DPY30, SLC9A7, PLEKHA8, AP1S3, FAM91A1, RAB12, ARL5B, ATP11C, ATP9B, MYO18A
CC	GO:0032155	cell division site part	25/3499	4.30E-04	ARF6, RHOA, RHOB, ECT2, ITGB1, MEN1, MYH9, MYH10, NF2, PPP1CC, PKN2, RDX, STAMBP, CIT, DCTN3, RAB21, SSH1, ANLN, NDE1, CEP55, SPIRE1, RAB11FIP4, WDR73, PLCD3, KLHDC8B
CC	GO:0030027	lamellipodium	57/3499	4.69E-04	APBB2, APC, RHOA, CD44, CFL1, CTNNA1, CTNNB1, CTNND1, DAG1, FAT1, FER, FLOT2, ILK, ITGAV, ITGB1, ABLIM1, LIMK1, KITLG, MYH10, MYO10, NEDD9, NF2, NHS, PODXL, PKN2, PXN, RDX, SLC9A1, SNX1, STX3, VAMP7, TSC1, SORBS2, PDLIM4, WASF1, WASL, ARPC5, ACTR2, ARPC2, ABI2, WASF2, RAPGEF3, IGF2BP1, NCKAP1, IQGAP2, PALLD, PLXND1, CORO1C, SLC39A6, SSH1, RAPH1, ANTXR1, RAB3IP, FGD4, AMOT, AMOTL1, SPATA13
CC	GO:0032153	cell division site	26/3499	6.23E-04	ARF6, RHOA, RHOB, ECT2, ITGB1, MEN1, MYH9, MYH10, NF2, PPP1CC, PKN2, RDX, RND2, STAMBP, CIT, DCTN3, RAB21, SSH1, ANLN, NDE1, CEP55, SPIRE1, RAB11FIP4, WDR73, PLCD3, KLHDC8B
CC	GO:0017053	transcriptional repressor complex	30/3499	7.61E-04	CCND1, CHD3, CHD4, DR1, ETV3, HDAC2, HDGF, RBPJ, JUN, SKI, SP3, SUV39H1, TBL1X, ZNF224, MTA1, NCOR1, SPEN, RCOR1, SIRT1, CBX5, SIN3A, RLIM, GATAD2A, AKIRIN2, DEPDC1, GATAD2B, MIER1, ZNF350, TBL1XR1, JAZF1
CC	GO:0030133	transport vesicle	100/3499	7.65E-04	ADAM10, AP1G1, ARCN1, ATP7A, BCL2L1, BDNF, CALM3, CD59, AP1S1, COPB1, EDN1, FGFR3, HLA-B, IGF2R, ITPR1, M6PR, RAB8A, MME, NPTX1, FURIN, PCSK1, PCSK2, CDK16, PTPRN2, RAB1A, RAB3B, RAB5A, RAB5B, SORT1, SH3GL2, SLC6A9, SNAP25, SNCA, SNTB2, SREBF2, STX3, SURF4, VAMP1, VAMP2, VAMP7, SYT1, TGFA, VDAC2, TMEM187, USO1, AP1G2, BSN, SYT7, ATP6V0D1, SYNGR3, SYNGR1, RAB11B, TRIP11, SCAMP1, GOSR1, GOSR2, SNCAIP, SEC24C, SV2A, GOLGA5, SCAMP2, CNIH1, SEC23A, UNC13B, TGOLN2, SEC24A, TMED10, SYNRG, SYT11, NCSTN, STX12, SEC31B, SLC17A5, SLC2A8, TMED7,

					APH1A, TRAPPC4, RAB14, SYT17, RAB8B, SYTL2, SEMA4C, STX17, SAR1A, MFF, ATG9A, PLEKHF2, C16orf70, DNAJC5, APH1B, ZNRF1, STON2, TPRG1L, SYT2, SYNPR, STXBP5, SPRED2, VMA21, STEAP2, RAB15
CC	GO:0031227	intrinsic component of endoplasmic reticulum membrane	48/3499	8.07E-04	AMFR, CALR, CANX, ATF6B, HLA-B, DNAJB2, HSPA5, INSIG1, RRBP1, SCD, SREBF2, ELOVL4, STIM1, XBP1, SGPL1, EDEM1, RCE1, BCAP31, SACM1L, ANKLE2, ARL6IP1, TRAM1, SPCS1, SEC61A1, SLC35B3, DERL2, INSIG2, BFAR, ERGIC2, DNAJB12, TMEM33, ACER3, EMC7, ESYT2, ELOVL5, ELOVL6, RHBDD1, SLC37A3, SYVN1, SPPL2A, PGAP3, MMGT1, TEX261, SPPL3, SAMD8, SGMS2, EMC10, RNF180
CC	GO:0031965	nuclear membrane	79/3499	8.62E-04	ABL1, BCL2, BCL2L1, CCND2, RCC1, EGFR, GAPDH, GATA6, GNAQ, HOXA7, DNAJB2, IL15RA, ITPR1, LBR, MYO6, NUP98, PAFAH1B1, PDE4D, RANBP2, SORT1, TRA2B, SNCA, MLX, XPO1, ZNF224, YEATS4, TNKS, VAPA, GTF3C3, AKAP6, NOS1AP, MRPL19, POM121, NUTF2, SIGMAR1, CEPT1, NUP50, SPIN1, DDX19B, CBX3, SEPHS1, RAP1GAP2, PHF8, LPIN1, ATP11B, PHLPP1, SIRT1, NSMF, MYOF, TOR1B, DTL, DNAJB12, RIF1, DDX19A, NDC1, NUP133, TXLNG, DNAJC1, AEN, TMEM43, AKIRIN1, EPC1, DCTN5, LMNB2, NAV3, MTDH, DTX2, OSBPL8, TBC1D20, TMEM18, TMEM120B, TOR1AIP2, PRICKLE2, QSOX2, TMEM201, CERS6, CNEP1R1, DPY19L4, POM121C
CC	GO:0055038	recycling endosome membrane	29/3499	8.95E-04	ARF6, HLA-B, RAB8A, RAP2A, RAP2B, PDLIM4, RAB11B, SCAMP1, SCAMP2, SLC9A6, RAB11FIP2, ATP11B, STX12, CLIP3, EHD4, ABHD17B, RAB14, RAB8B, CMTM6, PLEKHB2, RAP2C, ABHD17C, RAB17, RAB11FIP4, SLC9A7, MICALL1, RFFL, RAB12, MCOLN2
CC	GO:0005583	fibrillar collagen trimer	8/3499	1.05E-03	COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COL11A1, COL5A3, COL27A1
CC	GO:0098643	banded collagen fibril	8/3499	1.05E-03	COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COL11A1, COL5A3, COL27A1
CC	GO:0000792	heterochromatin	28/3499	1.07E-03	ATRX, CENPA, DDX6, DNMT3A, FOXC1, HMGA1, INCENP, MECP2, PML, RNF2, SATB1, SNAI1, SUV39H1, TOP2B, HMGA2, MBD2, BAZ1B, CBX3, MORC2, RRP1B, SIRT1, CBX6, CBX5, SUZ12, SMARCAD1, BEND3, WDR76, CBX2
CC	GO:0030136	clathrin-coated vesicle	54/3499	1.41E-03	AP1G1, ATP7A, SCARB2, AP2M1, AP1S1, DAB2, HBEGF, EDN1, EGFR, HIP1, IGF2R, IL7R, LDLR, LRP1, M6PR, RAB8A, MYO6, FURIN, PIK3C2A, RAB5A, SORT1, SH3GL2, VAMP2, VAMP7, SYT1, TFRC, TGFA, MALL, FZD5, FZD4, NUMB, SNX3, AP1G2, SCAMP1, BCAP31, TNK2, TGOLN2, TMED10, SYNRG, AAK1, NECAP1, LDLRAP1, SLC2A8, RAB14, RAB8B, NECAP2, GPR107, DNAJC5, SGIP1, STON2, FCHO2, SYT2, EPGN, STEAP2
CC	GO:0031300	intrinsic component of organelle membrane	65/3499	1.41E-03	BAK1, CPT1A, GALNT2, LAMP2, LBR, NPC1, FURIN, PEX13, SLC25A3, PTPRN2, RAB3B, RAB5A, RAB5B, SLC6A9, VAMP1, VAMP7, SYT1, SYNGR1, RAB11B, ITM2B, ENTPD4, TOMM20, SV2A, MFN2, MICU1, TIMM17A, SLC25A17, SLC35A1, SYT11, STX12, PISD, SLC35B3, ABHD17B, ERGIC2, ARMCX3, CHCHD3, ACER3, CSGALNACT2, POMGNT1, MFN1, PEX26, DNAJC11, CSGALNACT1, MFF, CASD1, TMEM43, MUL1, L2HGDH, DNAJC5, VOPP1, FAR1, YIF1B, SFXN1, TEX261, SLC35A4, TBC1D20, SYNPR, SAMD8, SGMS2, QSOX2, TMEM201, ZDHHC20, STEAP2, ACER2, CHCHD10
CC	GO:0044309	neuron spine	50/3499	1.49E-03	ADAM10, RHOA, ARRB1, ARRB2, ATP2B1, CAMK2A, CANX, CDC42, COMT, CTNND1, EPHA4, FMR1, FUS, GRIA4, ITGB1, KCNJ2, MAP1B, MAPT, RAB8A, MPP2, MYH10, NEDD4, OPHN1, PPP1CA, PPP1CC, PPP3CA, PSMC2, PTEN, SLC8A1, STRN, TIAM1, FXR1, ITGA8, PDLIM4, AKAP5, ABI2, FARP1, SLC9A6, ARFGEF2, IGF2BP1, NLGN1, SHANK2, SYT11, SIPA1L1, STRN4, ASAP1, ABHD17B, ABHD17C, LRRC4, CPEB4
CC	GO:0000775	chromosome, centromeric region	55/3499	1.49E-03	APC, ATRX, CEBPB, CENPA, DNMT3A, FMR1, HNRNPU, INCENP, MAD2L1, PPP1R12A, NUP98, PAFAH1B1, PPP1CC, PPP2CA, PPP2R1A, RAD21, SNAI1, AURKA, SUV39H1, DYNLT3, UVRAG, XPO1, SMC1A, DYNLL1, KAT2B, BAZ1B, AURKB, RASSF2, CTCF, STAG2, KIF2C, DCTN3, CBX3, PDS5B, FBXO28, PDS5A, CLASP1, CBX5, SIN3A, SS18L1, DCTN4, NDE1, PINX1, CDCA8, NUP133, RCC2, ZNFX1, MEAF6, SEH1L, DCTN5, CENPL, ZNF276, BOD1L1, SKA2, NUP43
CC	GO:1904949	ATPase complex	33/3499	2.01E-03	ATP1B1, CHD3, CHD4, BPTF, HDAC2, RB1, RFC1, SLC9A1, SMARCA2, SMARCC2, SMARCD2, SMARCE1, SS18, VCP, YY1, DPF3, DPF1, ARID1A, MTA1, HMGXB4, SRCAP, SUZ12, SS18L1, CECR2, UCHL5, RSF1, ING3, INO80, GATAD2A, GATAD2B, ARID1B, EP400, ANP32E
CC	GO:0030662	coated vesicle membrane	52/3499	2.01E-03	AP1G1, ARCN1, SCARB2, CD59, AP2M1, AP1S1, COPB1, DAB2, HBEGF, EGFR, HIP1, HLA-B, IGF2R, IL7R, LDLR, M6PR, MYO6, RAB5A, SH3GL2, SREBF2, VAMP2, VAMP7, SYT1, TFRC, TGFA, FZD5, FZD4, USO1, AP1G2, GOSR2, SEC24C, CNIH1, SEC23A, TGOLN2, SEC24A, TMED10, SYNRG, SEC31B, NECAP1, LDLRAP1, SLC2A8, TMED7, STX17, NECAP2, SAR1A, DNAJC5, SGIP1, FCHO2, SYT2, TMEM199, VMA21, EPGN
CC	GO:0043296	apical junction complex	43/3499	2.01E-03	ADCYAP1R1, APC, RHOA, CCND1, CTNNA1, CTNNB1, CTNND1, CXADR, DLG3, ECT2, JUP, NHS, CLDN11, PKN2, RAP2B, STRN, TGFBR1, FZD5, MPDZ, ARHGEF2, VAPA, CYTH3, CYTH1, TJP2, TRAF4, RAPGEF2, PDCD6IP, EPB41L4B, ARHGAP17, FRMD4A, PARD3, SHROOM3, RAP2C, JAM2, CLMP, PARD6B, CGNL1, MTDH, SHROOM1, CLDN23, AMOT, AMOTL1, CCDC85C
CC	GO:0043197	dendritic spine	49/3499	2.01E-03	ADAM10, RHOA, ARRB1, ARRB2, ATP2B1, CAMK2A, CANX, CDC42, COMT, CTNND1, EPHA4, FMR1, FUS, GRIA4, ITGB1, KCNJ2, MAP1B, MAPT, RAB8A, MPP2, MYH10, NEDD4, OPHN1, PPP1CA, PPP1CC, PPP3CA, PSMC2, PTEN, SLC8A1, STRN, TIAM1, FXR1, ITGA8, PDLIM4, AKAP5, ABI2, FARP1, ARFGEF2, IGF2BP1, NLGN1, SHANK2, SYT11, SIPA1L1, STRN4, ASAP1, ABHD17B, ABHD17C, LRRC4, CPEB4

CC	GO:0005643	nuclear pore	30/3499	2.01E-03	CETN2, KPNA1, KPNA3, IPO5, MAD2L1, MYO1C, NUP88, NUP98, RAN, RANBP2, TNKS, POM121, NUTF2, NXF1, NUP50, XPOT, DDX19B, XPO7, BICD2, KPNA6, TMEM33, DDX19A, NDC1, NUP133, PCID2, EIF5A2, XPO4, SEH1L, NUP43, POM121C
CC	GO:0005798	Golgi-associated vesicle	51/3499	2.04E-03	ADAM10, AP1G1, ARCN1, ARF1, ATP7A, CD59, AP1S1, COPB1, CTSZ, GJA1, HLA-B, IGF2R, RAB8A, FURIN, PKD1, SORT1, SREBF2, TGFA, USO1, AP1G2, ITM2B, GOSR2, SEC24C, CNIH1, SEC23A, TGOLN2, SEC24A, TMED10, SYNRG, ZDHHC17, RHOQ, SEC31B, TMED5, TMED7, ERGIC2, RAB14, RAB8B, STX17, PACS1, SAR1A, VANGL2, YIPF5, PITPNM3, SPPL2A, YIF1B, TEX261, SPPL3, TMEM199, VMA21, TMED4, STEAP2
CC	GO:0061695	transferase complex, transferring phosphorus-containing groups	69/3499	2.04E-03	ACVR1B, ACVR2B, CCND1, CCNA2, CCND2, CCNF, CCNG2, CCNT1, CCNT2, CDK6, CDKN1A, ERCC2, KAT2A, GTF2A1, GTF2E1, GTF2H3, IGF1R, IKBKB, INSR, MCM3, MYO6, PHKA1, PHKG2, PIK3C2A, PIK3CB, PKM, POLA1, POLR2D, POLR2K, PRKAA1, PRKAB2, PRKAR1A, PRKAR2A, PRPSAP2, RB1, REV3L, TAF1, TAF4B, TERT, TGFBR1, TP53, UVRAG, ULK1, SOCS1, SOCS2, CCNE2, SOCS6, CTR9, SOCS5, ATG13, POLR3G, POLR3A, ATG14, ERC1, RPRD2, POLR1A, SOCS7, TAF9B, CCNJ, RPRD1A, SETD5, ZNFX1, CDC73, ZNF768, SESN2, POLR1B, ACVR1C, SMCR8, SIK1
CC	GO:0099572	postsynaptic specialization	88/3499	2.17E-03	ADAM10, ADCY1, ADD1, ARF1, ARRB1, ARRB2, BMPR2, CACNA1C, CAMK2A, CTNNB1, CTNND1, DLG3, EFNB2, EPB41, EPHA4, EPHA7, EPS8, FMR1, ITPR1, KPNA1, LYN, MAP1B, MAP4, RAB8A, MPP2, NEFH, NSF, P2RY1, PAK2, PAK3, MAPK1, PTCH1, RPS3, SLC6A9, SOS1, SPTBN1, SRC, STAT3, STRN, TIAM1, TSC1, FXR1, NCK2, PKP4, ITGA8, EIF3A, MPDZ, SYNGAP1, BSN, ARHGEF2, DCLK1, DLG5, AKAP5, ACTR2, AKAP9, SIGMAR1, CAP2, PDLIM5, CPEB3, NLGN1, SHANK2, SYT11, ARHGEF9, PSD3, NCS1, NSMF, SIPA1L1, TANC2, NPTN, MINK1, ABHD17B, BCL11A, ADAM22, SEMA4C, CAMK2N1, VPS35, ARFGAP1, PRR12, MIB1, NLGN2, ABHD17C, DLGAP3, LRRC4, CPEB4, NETO2, FBXO45, RGS7BP, IQSEC3
CC	GO:0032009	early phagosome	8/3499	2.17E-03	RAB5A, SYK, SNX3, SYT7, UNC13B, RAB31, SYT11, APPL1
CC	GO:0042470	melanosome	34/3499	2.17E-03	ATP6V1B2, CALU, CANX, TPP1, CTNS, CTSB, STOM, HSPA5, ITGB1, MMP14, MYO5A, NAP1L1, PRDX1, RAB1A, RAB5A, RAB5B, RAN, SLC1A4, SLC1A5, STX3, TFRC, YWHAE, SYNGR1, PDCD6IP, GPNMB, GNA13, TMED10, GANAB, NCSTN, SND1, SYTL2, TMEM33, RAB17, DNAJC5
CC	GO:0048770	pigment granule	34/3499	2.17E-03	ATP6V1B2, CALU, CANX, TPP1, CTNS, CTSB, STOM, HSPA5, ITGB1, MMP14, MYO5A, NAP1L1, PRDX1, RAB1A, RAB5A, RAB5B, RAN, SLC1A4, SLC1A5, STX3, TFRC, YWHAE, SYNGR1, PDCD6IP, GPNMB, GNA13, TMED10, GANAB, NCSTN, SND1, SYTL2, TMEM33, RAB17, DNAJC5
CC	GO:0098687	chromosomal region	88/3499	2.30E-03	APC, ATM, ATR, ATRX, CEBPB, CENPA, CHEK1, DNMT3A, EZH1, EZH2, FMR1, HNRNPU, INCENP, LIG4, MAD2L1, MCM3, MCM4, MCM7, MEN1, PPP1R12A, NUP98, ORC5, PAFAH1B1, PML, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PURA, RAD21, RAD51, UPF1, SNAI1, SP100, AURKA, SUV39H1, DYNLT3, TERT, UVRAG, XPO1, XRCC5, SMC1A, DYNLL1, TNKS, KAT2B, BAZ1B, AURKB, RASSF2, TOX4, CTCF, STAG2, KIF2C, DCTN3, CBX3, KDM1A, PDS5B, FBXO28, PDS5A, CLASP1, CBX5, SIN3A, SS18L1, DCTN4, RTEL1, NDE1, PINX1, CDCA8, RIF1, NUP133, RCC2, ZNFX1, THOC2, MEAF6, DCLRE1B, NABP1, NABP2, CDC73, HMBOX1, SMC6, SEH1L, SLX4, DCTN5, CENPL, ZNF276, BOD1L1, SKA2, NUP43
CC	GO:0005795	Golgi stack	44/3499	2.39E-03	FUT8, GALNT1, GALNT2, GOLGA3, GOLGB1, MAN2A1, NSF, SORT1, ST3GAL1, SORL1, USO1, B4GALT2, B4GALT6, GOSR1, GOLGA5, BCAP31, AKAP9, CIT, LYPLA2, RAB21, GOLGA8A, MOB4, TMEM87A, CLIP3, RAB30, APH1A, TRAPPC4, RAB14, ZFYVE1, GOLPH3L, CSGALNACT2, CSGALNACT1, SULF2, NSFL1C, INPP5E, VCPIP1, COG3, SLC10A7, ST6GAL2, FUT10, CANT1, B4GALNT3, HID1, GOLGA8B
CC	GO:0044322	endoplasmic reticulum quality control compartment	12/3499	2.65E-03	AMFR, CALR, CANX, SEL1L, RNF103, EDEM1, TRIM13, DERL2, UGGT1, EDEM3, RHBDD1, SYVN1
CC	GO:0101002	ficolin-1-rich granule	52/3499	2.66E-03	ACLY, ALAD, RHOA, ASAH1, COPB1, MAPK14, CTSB, CTSS, CTSZ, DDX3X, DIAPH1, EEF1A1, GAA, GPI, NCKAP1L, IMPDH1, JUP, LAMP2, LTA4H, PAFAH1B2, PGAM1, PKM, PKP1, PRCP, MAPK1, PSMA2, PSMC2, PSMD3, PSMD13, PTPRN2, TIMP2, TNFAIP6, TRPM2, VCL, VCP, DYNLL1, ARPC5, ACTR2, ATP6AP2, PSMD14, ATG7, PDAP1, NFASC, COTL1, OSTF1, YPEL5, CAND1, KCMF1, PLEKHO2, CANT1, ARL8A, SIRPA
CC	GO:0031248	protein acetyltransferase complex	31/3499	2.66E-03	ACTB, CREBBP, DR1, EP300, KAT2A, HCFC1, KAT6A, YEATS4, DPF3, DPF1, KAT2B, MORF4L2, UBAP2L, KAT7, ZZZ3, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, ATXN7L3, EP400, NAA35, MEAF6, NAA25, NAA50, EPC1, TADA2B, NAA30
CC	GO:1902493	acetyltransferase complex	31/3499	2.66E-03	ACTB, CREBBP, DR1, EP300, KAT2A, HCFC1, KAT6A, YEATS4, DPF3, DPF1, KAT2B, MORF4L2, UBAP2L, KAT7, ZZZ3, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, ATXN7L3, EP400, NAA35, MEAF6, NAA25, NAA50, EPC1, TADA2B, NAA30
CC	GO:0030176	integral component of endoplasmic reticulum membrane	44/3499	2.66E-03	AMFR, CALR, CANX, ATF6B, HLA-B, HSPA5, INSIG1, RRBP1, SCD, SREBF2, ELOVL4, STIM1, XBP1, SGPL1, EDEM1, RCE1, BCAP31, SACM1L, ANKLE2, ARL6IP1, TRAM1, SPCS1, SEC61A1, SLC35B3, DERL2, INSIG2, BFAR, ERGIC2, DNAJB12, TMEM33, ACER3, EMC7, ELOVL5, ELOVL6, RHBDD1, SLC37A3, SYVN1, SPPL2A, MMGT1, TEX261, SPPL3, SAMD8, SGMS2, EMC10
CC	GO:0098858	actin-based cell projection	57/3499	2.79E-03	ADCY6, ARF6, ATP6V1A, ATP6V1B2, ATP6V1E1, ATP7A, CD44, CDC42, CTNNB1, CXADR, DAG1, EPHA4, EPS8, FAT1, FMR1, UBE2K, FOXA1, ITGA6, ITGA3, ITGAV, ITGB1, KITLG, MPP1, MYO1B, MYO1C, MYO5A, MYO6, MYO10, NF2, PAFAH1B1, PDGFA, PDGFRA, ATP8B1, PODXL, TWF1, RDX, VCAM1, FZD3, SLC4A7, FCHSD2, ABI2, FARP1, RAPGEF3, IGF2BP1, IQGAP2, NLGN1, NFASC, CBX6, NPTXR, CLIC4, UBE2Q1, VEZT, FMN2, RAPH1, ANTXR1, FGD4, SPATA13

CC	GO:0030140	trans-Golgi network transport vesicle	14/3499	3.04E-03	AP1G1, ATP7A, AP1S1, IGF2R, RAB8A, FURIN, SORT1, AP1G2, TGOLN2, TMED10, SYNRG, RAB14, RAB8B, STEAP2
CC	GO:0005741	mitochondrial outer membrane	50/3499	3.24E-03	BAK1, BCL2, BCL2L1, CPT1A, ATF2, DDX3X, CYB5R3, EPHA4, ACSL4, FOXO3, GJA1, HK1, HK2, MCL1, SLC11A2, OPA1, PGR, PPP1CC, RPS6KB1, SNCA, VAMP1, VDAC2, SNN, ULK1, WASF1, TOMM20, MFN2, BCL2L11, MLXIP, LPIN1, ACSL6, SLC44A1, LETMD1, SH3GLB1, ARMCX3, MIEF1, VPS13C, MFN1, DNAJC11, CISD1, MFF, MAVS, MOAP1, MUL1, CYB5B, BMF, FAM210B, MIEF2, PLD6, MTX3
CC	GO:0120111	neuron projection cytoplasm	28/3499	3.24E-03	ADA, DST, CANX, FLOT2, FMR1, HIF1A, HNRNPU, KIF5B, MAP1A, MAPT, OPA1, PAFAH1B1, MAPK1, PURA, MAP2K4, DYNLL1, WASF1, AP3D1, KIF3B, AP3S2, KIF3A, TRAK1, RAB21, KIF1B, MAPK8IP3, AP3M1, TRAK2, ARL8A
CC	GO:0031301	integral component of organelle membrane	58/3499	3.24E-03	BAK1, CPT1A, GALNT2, LAMP2, LBR, NPC1, FURIN, PEX13, SLC25A3, PTPRN2, SLC6A9, VAMP1, VAMP7, SYT1, SYNGR1, ITM2B, ENTPD4, TOMM20, SV2A, MICU1, TIMM17A, SLC25A17, SLC35A1, SYT11, STX12, PISD, SLC35B3, ERGIC2, ARMCX3, CHCHD3, ACER3, CSGALNACT2, POMGNT1, MFN1, PEX26, DNAJC11, CSGALNACT1, MFF, CASD1, TMEM43, MUL1, L2HGDH, VOPP1, FAR1, YIF1B, SFXN1, TEX261, SLC35A4, TBC1D20, SYNPR, SAMD8, SGMS2, QSOX2, TMEM201, ZDHHC20, STEAP2, ACER2, CHCHD10
CC	GO:1902911	protein kinase complex	34/3499	3.34E-03	ACVR1B, ACVR2B, CCND1, CCNA2, CCND2, CCNF, CCNG2, CCNT1, CCNT2, CDK6, CDKN1A, ERCC2, GTF2H3, IGF1R, IKBKB, INSR, PHKA1, PHKG2, PRKAA1, PRKAB2, PRKAR1A, PRKAR2A, RB1, TGFBR1, UVRAG, ULK1, CCNE2, ATG13, ERC1, CCNJ, SESN2, ACVR1C, SMCR8, SIK1
CC	GO:0044295	axonal growth cone	13/3499	3.34E-03	EPHA4, FKBP4, KIF5B, L1CAM, LRP1, PTCH1, TIAM1, TAOK2, OLFM1, TRAK1, NIN, PARD3, TRAK2
CC	GO:0044448	cell cortex part	51/3499	3.87E-03	ACTB, ACTN4, ASPH, CALD1, CAPN2, CAPZA2, CFL1, CTNNB1, CTNND1, CTSZ, EEF1A1, EPB41, FLOT2, GYPC, HIP1, LASP1, MPP1, MYH9, NF2, RDX, SPTAN1, SPTBN1, STIM1, TPM4, BSN, WASL, RIMS3, ACTR2, DLC1, RAPGEF3, CAP2, CAP1, UNC13B, EXOC5, DSTN, AKAP13, PHLDB1, EXOC6B, CLASP1, COTL1, NSMF, ANLN, SHROOM3, MLPH, MED28, PHLDB2, MYADM, SHROOM1, RIMS4, WIPF2, EXOC8
CC	GO:0044233	Mitochondria-associated ER Membrane	8/3499	3.98E-03	CANX, ACSL4, ATG5, TOMM20, ATG14, ZFYVE1, STX17, PDZD8
CC	GO:0031461	cullin-RING ubiquitin ligase complex	45/3499	4.19E-03	CCNF, CDKN1B, SKP1, TNFAIP1, CUL5, GAN, SPOP, CUL4B, CUL3, CUL2, ENC1, BTRC, KLHL21, DCAF7, ARIH2, ZER1, KCTD2, ARIH1, DCAF12, FBXL3, KLHL3, FBXO9, DTL, FBXL19, KLHL24, FBXL12, USP47, FBXW7, DCAF6, CAND1, KLHL7, KLHL42, ZSWIM6, ZSWIM4, DDA1, DCAF10, ZYG11B, KCTD17, SPSB1, KLHL15, KCTD10, KBTBD8, KLHL13, FBXO45, SPOPL
CC	GO:0001650	fibrillar center	39/3499	4.30E-03	ACACA, CAMK4, KLF6, DAB2, DKC1, E2F5, ESRRA, FHIT, FOXA1, HOXB5, SMAD7, NFIB, NFIC, PAFAH1B2, RREB1, SNRPB2, TAF4B, UBE2N, UBTF, COIL, USO1, KDM4A, IP6K1, SPATA2, DDX46, NUAK1, SAMD4A, RAI14, HERC4, AFF4, FBLIM1, CC2D1A, WDR33, FOXJ2, UTP15, MRI1, RPAIN, MTDH, JAZF1
CC	GO:0030864	cortical actin cytoskeleton	29/3499	4.50E-03	CALD1, CAPN2, CAPZA2, CFL1, EEF1A1, FLOT2, HIP1, LASP1, MYH9, NF2, RDX, SPTAN1, SPTBN1, WASL, ACTR2, DLC1, RAPGEF3, CAP2, CAP1, DSTN, AKAP13, COTL1, ANLN, SHROOM3, MLPH, MED28, MYADM, SHROOM1, WIPF2
CC	GO:1904813	ficolin-1-rich granule lumen	37/3499	4.68E-03	ACLY, ALAD, ASAH1, MAPK14, CTSB, CTSS, CTSZ, DDX3X, EEF1A1, GPI, IMPDH1, JUP, LTA4H, PAFAH1B2, PGAM1, PKM, MAPK1, PSMA2, PSMC2, PSMD3, PSMD13, TIMP2, TNFAIP6, VCL, VCP, ARPC5, ACTR2, PSMD14, ATG7, PDAP1, COTL1, OSTF1, YPEL5, CAND1, KCMF1, PLEKHO2, CANT1
CC	GO:0044420	extracellular matrix component	19/3499	5.27E-03	COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL4A5, COL4A6, COL5A1, COL5A2, COL11A1, COL12A1, FBN1, FBN2, LAMC1, LAMC2, LTBP1, COL5A3, THSD4, COL27A1
CC	GO:0005876	spindle microtubule	21/3499	5.67E-03	CALM1, CALM2, CALM3, CSNK1D, HNRNPU, KIF2A, PAFAH1B1, AURKA, DYNLT3, CUL3, PRC1, AURKB, KIF3B, KLHL21, KIF3A, MAPRE3, CLASP1, HAUS2, CCSAP, BOD1L1, SKA2
CC	GO:0033116	endoplasmic reticulum-Golgi intermediate compartment membrane	24/3499	5.79E-03	CALR, CD59, CSNK1D, CTSZ, CLN8, ROBO1, SURF4, TGFA, GOSR2, BCAP31, CNIH1, TMED10, TMED5, TMED7, ERGIC2, STX17, ERGIC1, GORASP1, PRRG4, SPPL3, WHAMM, TBC1D20, TMEM199, VMA21
CC	GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	37/3499	6.27E-03	CALR, CD59, COPB1, CSNK1D, CTSZ, CLN8, FN1, GOLGB1, HSPA5, LRPAP1, ROBO1, SURF4, TGFA, STK17B, GOSR2, BCAP31, CNIH1, TMED10, DICER1, TMED5, TMED7, ERGIC2, RAB6B, STX17, UGGT1, ERGIC1, GORASP1, GNPNAT1, PRRG4, YIF1B, SPPL3, WHAMM, TBC1D20, TMEM199, VMA21, TMED4, MYO18A
CC	GO:1990907	beta-catenin-TCF complex	7/3499	6.35E-03	BCL9, CTNNB1, TCF4, TCF7L2, TLE1, TLE4, LDB1
CC	GO:0002102	podosome	13/3499	6.70E-03	HNRNPK, PTPN12, SRC, TPM4, VCAM1, VCL, ARHGEF2, SH3PXD2A, ACTR2, PALLD, ASAP1, RHOU, SH3PXD2B

CC	GO:0030173	integral component of Golgi membrane	21/3499	6.91E-03	GALNT2, FURIN, ENTPD4, SLC35A1, SLC35B3, ERGIC2, ACER3, CSGALNACT2, POMGNT1, CSGALNACT1, CASD1, YIF1B, TEX261, SLC35A4, TBC1D20, SAMD8, SGMS2, QSOX2, ZDHHC20, STEAP2, ACER2
CC	GO:0019867	outer membrane	54/3499	6.91E-03	BAK1, BCL2, BCL2L1, CPT1A, ATF2, DDX3X, CYB5R3, EPHA4, ACSL4, FOXO3, GJA1, HK1, HK2, MCL1, SLC11A2, OPA1, PGR, PPP1CC, RPS6KB1, SNCA, VAMP1, VDAC2, SNN, ULK1, WASF1, TOMM20, MFN2, BCL2L11, NUTF2, SIGMAR1, MLXIP, LPIN1, ACSL6, SLC44A1, LETMD1, SH3GLB1, ARMCX3, MIEF1, VPS13C, MFN1, DNAJC11, CISD1, ANKH, MFF, MAVS, MOAP1, MUL1, CYB5B, NAV3, BMF, FAM210B, MIEF2, PLD6, MTX3
CC	GO:0030658	transport vesicle membrane	55/3499	7.20E-03	AP1G1, BCL2L1, CALM3, CD59, AP1S1, HLA-B, ITPR1, PTPRN2, RAB1A, RAB3B, RAB5A, RAB5B, SH3GL2, SLC6A9, SNCA, SNTB2, SREBF2, VAMP1, VAMP2, VAMP7, SYT1, TGFA, USO1, AP1G2, BSN, SYT7, SYNGR3, SYNGR1, RAB11B, SCAMP1, GOSR2, SEC24C, SV2A, CNIH1, SEC23A, UNC13B, SEC24A, TMED10, SYNRG, SYT11, STX12, SEC31B, SLC17A5, TMED7, SEMA4C, STX17, SAR1A, C16orf70, DNAJC5, ZNRF1, TPRG1L, SYT2, SYNPR, SPRED2, VMA21
CC	GO:0005923	bicellular tight junction	36/3499	7.39E-03	ADCYAP1R1, APC, CCND1, CTNNB1, CXADR, DLG3, ECT2, NHS, CLDN11, RAP2B, STRN, TGFBR1, FZD5, MPDZ, ARHGEF2, VAPA, CYTH3, CYTH1, TJP2, TRAF4, RAPGEF2, PDCD6IP, EPB41L4B, ARHGAP17, FRMD4A, PARD3, RAP2C, JAM2, CLMP, PARD6B, CGNL1, MTDH, CLDN23, AMOT, AMOTL1, CCDC85C
CC	GO:0000123	histone acetyltransferase complex	27/3499	7.79E-03	ACTB, CREBBP, DR1, EP300, KAT2A, HCFC1, KAT6A, YEATS4, DPF3, DPF1, KAT2B, MORF4L2, UBAP2L, KAT7, ZZZ3, BRPF3, ING4, TAF9B, RSF1, ING3, KANSL2, MSL2, ATXN7L3, EP400, MEAF6, EPC1, TADA2B
CC	GO:0030665	clathrin-coated vesicle membrane	34/3499	8.11E-03	AP1G1, SCARB2, AP2M1, AP1S1, DAB2, HBEGF, EGFR, HIP1, IGF2R, IL7R, LDLR, M6PR, MYO6, RAB5A, SH3GL2, VAMP2, VAMP7, SYT1, TFRC, TGFA, FZD5, FZD4, AP1G2, TGOLN2, SYNRG, NECAP1, LDLRAP1, SLC2A8, NECAP2, DNAJC5, SGIP1, FCHO2, SYT2, EPGN
CC	GO:0008021	synaptic vesicle	51/3499	8.20E-03	ADAM10, BCL2L1, BDNF, CALM3, RAB8A, MME, CDK16, PTPRN2, RAB3B, RAB5A, RAB5B, SH3GL2, SLC6A9, SNAP25, SNCA, STX3, VAMP1, VAMP2, VAMP7, SYT1, VDAC2, BSN, SYT7, ATP6V0D1, SYNGR3, SYNGR1, RAB11B, SCAMP1, SNCAIP, SV2A, UNC13B, SYT11, NCSTN, STX12, SLC17A5, SLC2A8, APH1A, TRAPPC4, RAB8B, SEMA4C, MFF, ATG9A, C16orf70, DNAJC5, ZNRF1, STON2, TPRG1L, SYT2, SYNPR, STXBP5, RAB15
CC	GO:1904115	axon cytoplasm	20/3499	8.22E-03	DST, FMR1, HIF1A, KIF5B, MAP1A, MAPT, OPA1, PAFAH1B1, DYNLL1, AP3D1, KIF3B, AP3S2, KIF3A, TRAK1, RAB21, KIF1B, MAPK8IP3, AP3M1, TRAK2, ARL8A
CC	GO:0005905	clathrin-coated pit	23/3499	8.22E-03	ARRB1, ARRB2, AP2M1, AP1S1, DAB2, HIP1, LDLR, LRP1, LRP3, MYO6, SORT1, TFRC, VLDLR, SYNJ1, FCHSD2, TNK2, AAK1, FNBP1, NECAP1, NECAP2, SGIP1, FCHO2, AP1S3
CC	GO:0000922	spindle pole	45/3499	8.25E-03	CALM1, CALM2, CALM3, MAPK14, CTNNB1, HNRNPU, IK, KIF2A, MAD2L1, NEDD9, PPP2CA, RAD21, AURKA, TPT1, SMC1A, CUL3, PKP4, CDC14B, TNKS, PRC1, LATS1, AURKB, VPS4B, KLHL21, NUBP2, FRY, STAG2, PLK2, MAPKBP1, LATS2, DCTN4, NIN, YPEL5, NDE1, NSFL1C, BIRC6, CEP85, BRCC3, WDR73, CEP19, UBXN2B, CKAP2L, TMEM201, BOD1L1, FAM110C
CC	GO:0031968	organelle outer membrane	53/3499	8.76E-03	BAK1, BCL2, BCL2L1, CPT1A, ATF2, DDX3X, CYB5R3, EPHA4, ACSL4, FOXO3, GJA1, HK1, HK2, MCL1, SLC11A2, OPA1, PGR, PPP1CC, RPS6KB1, SNCA, VAMP1, VDAC2, SNN, ULK1, WASF1, TOMM20, MFN2, BCL2L11, NUTF2, SIGMAR1, MLXIP, LPIN1, ACSL6, SLC44A1, LETMD1, SH3GLB1, ARMCX3, MIEF1, VPS13C, MFN1, DNAJC11, CISD1, MFF, MAVS, MOAP1, MUL1, CYB5B, NAV3, BMF, FAM210B, MIEF2, PLD6, MTX3
CC	GO:0000118	histone deacetylase complex	20/3499	1.02E-02	RERE, CHD3, CHD4, HDAC2, TAL1, TBL1X, ZNF217, NRIP1, MBD2, MTA1, NCOR1, HDAC9, SATB2, CBX5, SIN3A, GATAD2A, GATAD2B, SAP130, TBL1XR1, BRMS1L
CC	GO:0005913	cell-cell adherens junction	34/3499	1.04E-02	ADD1, APC, ATP2A2, BMPR2, CDH6, CTNNA1, CTNNB1, CTNND1, CXADR, DAG1, DDX6, DSC2, EIF4G2, FLOT2, GJA1, ITGA6, JUP, LYN, SMAD7, MYH9, PKP1, PPP1CA, RDX, VCL, VEGFA, PKP4, PDLIM4, DLG5, PDLIM7, PDLIM5, FRS2, PDLIM3, PARD3, SSX2IP
CC	GO:0030672	synaptic vesicle membrane	31/3499	1.04E-02	BCL2L1, CALM3, PTPRN2, RAB3B, RAB5A, RAB5B, SH3GL2, SLC6A9, SNCA, VAMP1, VAMP2, VAMP7, SYT1, BSN, SYT7, SYNGR3, SYNGR1, RAB11B, SCAMP1, SV2A, UNC13B, SYT11, STX12, SLC17A5, SEMA4C, C16orf70, DNAJC5, ZNRF1, TPRG1L, SYT2, SYNPR
CC	GO:0099501	exocytic vesicle membrane	31/3499	1.04E-02	BCL2L1, CALM3, PTPRN2, RAB3B, RAB5A, RAB5B, SH3GL2, SLC6A9, SNCA, VAMP1, VAMP2, VAMP7, SYT1, BSN, SYT7, SYNGR3, SYNGR1, RAB11B, SCAMP1, SV2A, UNC13B, SYT11, STX12, SLC17A5, SEMA4C, C16orf70, DNAJC5, ZNRF1, TPRG1L, SYT2, SYNPR
CC	GO:0042641	actomyosin	25/3499	1.12E-02	ACTN4, CNN2, FLNB, ILK, ABLIM1, LPP, MYH9, MYH10, MYO5A, PXN, TPM3, TPM4, PDLIM4, KAT2B, PDLIM7, PDCD6IP, NEBL, PDLIM5, FAM107A, LIMCH1, PDLIM3, DCTN4, FBLIM1, VANGL2, MYO18A
CC	GO:0071565	nBAF complex	8/3499	1.12E-02	SMARCA2, SMARCC2, SMARCE1, DPF3, DPF1, ARID1A, SS18L1, ARID1B
CC	GO:0031901	early endosome membrane	41/3499	1.16E-02	ARF6, CAV1, CLCN4, EGFR, EPHA4, HLA-B, LRP6, PML, RAB5A, RAB5B, SNX1, FZD5, PDLIM4, SNX3, MTMR4, RABEP1, ZFYVE16, ATP9A, GPNMB, SLC9A6, RAB31, DKK1, RAB21, SNX13, DNAJC13, STX12, CLIP3, APPL1, EHD4, RAB14, CMTM6, TMEM165, RCC2, TMEM9B, PMEPA1, PLEKHF2, HPS6, ITCH, MMGT1, WDR81, SNX19
CC	GO:0000407	phagophore assembly site	13/3499	1.17E-02	NBR1, ULK1, SQSTM1, ATG5, ATG13, ATG7, ATG14, ATG2A, STX12, ZFYVE1, ATG16L1, ATG2B, ATG9A

CC	GO:0005770	late endosome	64/3499	1.21E-02	ARF1, RHOB, ATP7A, SCARB2, CLCN4, SLC31A2, CTNS, CTSS, EGFR, GJA1, HTT, IFNAR1, IGF2R, LAMP2, LDLR, M6PR, NBR1, MYO5A, NPC1, SLC11A2, PLD1, MAPK1, MAPK3, SORL1, SRC, VAMP7, TPT1, UVRAG, SQSTM1, VPS4B, GOSR2, RAPGEF2, LAPTM4A, SLC9A6, SNF8, NMNAT2, MMD, PARM1, CDIP1, DERL2, VPS36, RAB14, TMEM106B, VPS37C, STEAP3, LAPTM4B, VPS35, TMEM165, CHMP1B, RAB22A, KIDINS220, GNPNAT1, ATG9A, FYCO1, SPPL2A, MICALL1, ANKRD13A, WDR81, ARL8A, EXOC8, VPS37D, TMEM192, CYB561A3, MCOLN2
CC	GO:1902554	serine/threonine protein kinase complex	27/3499	1.21E-02	ACVR1B, ACVR2B, CCND1, CCNA2, CCND2, CCNF, CCNG2, CCNT1, CCNT2, CDK6, CDKN1A, ERCC2, GTF2H3, IKBKB, PHKA1, PHKG2, RB1, TGFBR1, UVRAG, ULK1, CCNE2, ATG13, ERC1, CCNJ, SESN2, ACVR1C, SMCR8
CC	GO:0098793	presynapse	112/3499	1.29E-02	ACTB, ADAM10, ARF6, ATP2B1, ATP2B4, BCL2L1, BDNF, CACNA1B, CALM3, CANX, AP1S1, CNTN1, CTNNB1, CTNND1, EFNB2, ELK1, EPHA4, EPHB2, CLN8, FLOT2, FMR1, HTT, HIP1, ILK, KCNC1, KCNC4, KCNJ3, KCNJ10, RAB8A, MME, OPHN1, P2RY1, CDK16, PPP1CA, PPP1CC, PTPRN2, RAB3B, RAB5A, RAB5B, SH3GL2, SLC1A2, SLC6A9, SNAP25, SNCA, STX3, VAMP1, VAMP2, VAMP7, SYT1, VDAC2, YWHAG, FZD3, FOSL1, NAPA, SYNJ1, SYNJ2, BSN, AP3D1, SYT7, ATP6V0D1, SYNGR3, SYNGR1, RAB11B, SCAMP1, SNCAIP, RIMS3, SV2A, SLC9A6, UNC13B, AAK1, NLGN1, ERC1, SYT11, NCSTN, ZDHHC17, PIP5K1C, NCS1, STX12, PNISR, SLC17A5, NPTN, PCDH17, GIT1, SLC2A8, APH1A, TRAPPC4, RAB6B, SYT17, RAB8B, SEMA4C, VPS35, MFF, TBC1D24, KCTD16, NLGN2, ATG9A, C16orf70, DNAJC5, KIAA1109, ZNRF1, STON2, KCTD12, FCHO2, TPRG1L, SYT2, SYNPR, STXBP5, RIMS4, FBXO45, ZNRF2, RAB15, RGS7BP
CC	GO:0005901	caveola	25/3499	1.29E-02	ADCYAP1R1, ATP1B1, ATP2B4, BMPR1A, BMPR2, CAV1, CBL, CTNNA1, CTNNB1, EFNA5, FLOT2, INSR, LRP6, MAPK1, MAPK3, PTCH1, PTGIS, SRC, TFPI, AKAP6, NOS1AP, DLC1, CORO1C, MYOF, SPRED1
CC	GO:0031594	neuromuscular junction	24/3499	1.33E-02	COL4A5, CRKL, DLG3, EPHA4, EPHA7, NRG1, ITGB1, KCNC4, MYH9, MYH10, SERPINE2, PRKAR1A, VAMP1, SYNGR3, SYNGR1, FCHSD2, SV2A, UNC13B, POSTN, PDZRN3, TBC1D24, DLGAP3, DNAJC5, STXBP5
CC	GO:0005776	autophagosome	28/3499	1.33E-02	HTT, LAMP2, NBR1, TBC1D25, PIP4K2A, UVRAG, ULK1, SQSTM1, ATG5, ENTPD4, GABARAPL2, ATG14, UBQLN2, UBQLN1, SH3GLB1, RAB23, ZFYVE1, STX17, ATG16L1, UBQLN4, TP53INP2, ATG9A, FYCO1, MAP1LC3B, TP53INP1, WDR81, TMEM74, RAB12
CC	GO:0070160	tight junction	36/3499	1.33E-02	ADCYAP1R1, APC, CCND1, CTNNB1, CXADR, DLG3, ECT2, NHS, CLDN11, RAP2B, STRN, TGFBR1, FZD5, MPDZ, ARHGEF2, VAPA, CYTH3, CYTH1, TJP2, TRAF4, RAPGEF2, PDCD6IP, EPB41L4B, ARHGAP17, FRMD4A, PARD3, RAP2C, JAM2, CLMP, PARD6B, CGNL1, MTDH, CLDN23, AMOT, AMOTL1, CCDC85C
CC	GO:0005844	polysome	23/3499	1.34E-02	CALR, EIF2S1, EIF4B, EIF4G1, FMR1, FUS, MSI1, MYH10, PSMA1, RPS3, RPS23, ATXN2, FXR1, LARP4B, LARP1, UPF2, AGO1, NUFIP2, NAA35, UNK, LARP4, NAA30, MSI2
CC	GO:0044452	nucleolar part	47/3499	1.34E-02	ACACA, CAMK4, KLF6, DAB2, DKC1, E2F5, ESRRA, FHIT, FOXA1, HOXB5, SMAD7, NFIB, NFIC, PAFAH1B2, POLR2K, RREB1, SNRPB2, TAF4B, UBE2N, UBTF, COIL, USO1, BTRC, KDM4A, IP6K1, SPATA2, DDX46, NUAK1, POP1, WDR37, SAMD4A, RRP1B, POLR1A, RAI14, HERC4, AFF4, FBLIM1, CC2D1A, WDR33, FOXJ2, UTP15, POLR1B, MRI1, RPAIN, MTDH, WDR36, JAZF1
CC	GO:0070382	exocytic vesicle	53/3499	1.52E-02	ADAM10, BCL2L1, BDNF, CALM3, RAB8A, MME, CDK16, PTPRN2, RAB3B, RAB5A, RAB5B, SH3GL2, SLC6A9, SNAP25, SNCA, STX3, VAMP1, VAMP2, VAMP7, SYT1, VDAC2, BSN, SYT7, ATP6V0D1, SYNGR3, SYNGR1, RAB11B, SCAMP1, SNCAIP, SV2A, UNC13B, SYT11, NCSTN, STX12, SLC17A5, SLC2A8, APH1A, TRAPPC4, SYT17, RAB8B, SYTL2, SEMA4C, MFF, ATG9A, C16orf70, DNAJC5, ZNRF1, STON2, TPRG1L, SYT2, SYNPR, STXBP5, RAB15
CC	GO:0031228	intrinsic component of Golgi membrane	21/3499	1.71E-02	GALNT2, FURIN, ENTPD4, SLC35A1, SLC35B3, ERGIC2, ACER3, CSGALNACT2, POMGNT1, CSGALNACT1, CASD1, YIF1B, TEX261, SLC35A4, TBC1D20, SAMD8, SGMS2, QSOX2, ZDHHC20, STEAP2, ACER2
CC	GO:0035098	ESC/E(Z) complex	8/3499	1.71E-02	EZH1, EZH2, HDAC2, JARID2, MTF2, SIRT1, SUZ12, AEBP2
CC	GO:0000164	protein phosphatase type 1 complex	6/3499	1.78E-02	NCK1, PPP1CA, PPP1CB, PPP1CC, SHOC2, PPP1R15B
CC	GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	27/3499	1.87E-02	RHOA, ATP2A2, CYLD, DTNA, FER, GNAI2, GNAI3, GNAL, GNAQ, GNAS, GNB1, GNG7, HIP1, KRAS, LYN, CDK16, SNAP25, SRC, TIAM1, IQGAP1, CYTH3, CYTH1, FARP1, GNA13, ERRFI1, ESYT2, PLEKHA4
CC	GO:0044853	plasma membrane raft	31/3499	2.00E-02	ADCYAP1R1, ADD1, ATP1B1, ATP2B4, BMPR1A, BMPR2, CAV1, CBL, CTNNA1, CTNNB1, DAG1, EFNA5, FLOT2, INSR, LRP6, MYO1D, PRKAR1A, PRKAR2A, MAPK1, MAPK3, PTCH1, PTGIS, SRC, STIM1, TFPI, AKAP6, NOS1AP, DLC1, CORO1C, MYOF, SPRED1
CC	GO:0072686	mitotic spindle	31/3499	2.00E-02	CDC42, DIAPH1, ECT2, KAT2A, HNRNPU, IK, MAD2L1, MAP4, MAPK1, RPS3, AURKA, TBL1X, DYNLT3, SMC1A, PKP4, CDC14B, DYNLL1, TNKS, AURKB, KIF23, NCOR1, STAG2, MAPRE3, MAPKBP1, NIN, YPEL5, RCC2, HECW2, TBL1XR1, CCSAP, CKAP2L
CC	GO:0031253	cell projection membrane	81/3499	2.01E-02	AKT2, ANK1, APC, ARF6, RHOA, ATP2B1, ATP7A, CD44, CFL1, CTNNB1, DIAPH1, EEF1A1, EPS8, GNB1, INSR, ITGA3, ITGA5, ITGAV, ITGB1, KCNC1, KCNC4, KCNK1, MAPT, MPP2, MYO1C, MYO1D, MYO6, MYO10, NF2, SLC11A2, ATP8B1, PKD1, PODXL, PTCH1, TWF1, PTPRJ, RPS3, SLC1A2, SPTBN1, SRC, ADAM17, TIAM1, TLN1, SHOC2, ITGA8, KSR1, SLC5A6, ARHGEF2, AKAP5, C2CD5, ARPC2, DLC1, GNA13, NCKAP1, FAM107A, SHANK2, PHLPP2, PLXND1, KANK1, PHLPP1, WWC1, IQCE, PSD3, PIP5K1C, CORO1C,

					SLC7A11, SLC39A6, CNTNAP2, ASAP1, VEZT, FERMT1, EPB41L5, PLEKHA1, NDRG4, MTMR9, CYBRD1, SPRY4, ANTXR1, SLC46A1, SPATA13, SCIMP
CC	GO:0030117	membrane coat	28/3499	2.02E-02	AP1G1, ARCN1, AP2M1, AP1S1, COPB1, HIP1, IGF2R, SYNJ1, AP1G2, AP3D1, SEC24C, AP5Z1, AP3S2, SEC23A, SEC24A, SYNRG, AP4E1, SEC31B, NECAP1, AP3M1, TMED7, NECAP2, KCNQ5, SAR1A, CHMP1B, SGIP1, FCHO2, AP1S3
CC	GO:0048475	coated membrane	28/3499	2.02E-02	AP1G1, ARCN1, AP2M1, AP1S1, COPB1, HIP1, IGF2R, SYNJ1, AP1G2, AP3D1, SEC24C, AP5Z1, AP3S2, SEC23A, SEC24A, SYNRG, AP4E1, SEC31B, NECAP1, AP3M1, TMED7, NECAP2, KCNQ5, SAR1A, CHMP1B, SGIP1, FCHO2, AP1S3
CC	GO:0035577	azurophil granule membrane	19/3499	2.08E-02	STOM, GAA, LAMP2, PRCP, RAP1B, SURF4, VAMP7, CPNE3, SYNGR1, VAPA, ATP8A1, GLIPR1, ATP11B, DNAJC13, NCSTN, CMTM6, LPCAT1, DNAJC5, ARL8A
CC	GO:0044232	organelle membrane contact site	9/3499	2.17E-02	CANX, ACSL4, ATG5, TOMM20, ATG14, ZFYVE1, STX17, ESYT2, PDZD8
CC	GO:0032432	actin filament bundle	23/3499	2.17E-02	ACTN4, CNN2, FLNB, ILK, ABLIM1, LPP, MARCKS, MYH9, MYH10, PLS3, PXN, TPM3, TPM4, PDLIM4, PDLIM7, NEBL, PDLIM5, FAM107A, LIMCH1, PDLIM3, DCTN4, FBLIM1, VANGL2
CC	GO:0044291	cell-cell contact zone	22/3499	2.26E-02	ATP1B1, CTNNA1, CTNNB1, DSC2, FLOT2, GJA1, ITGB1, JUP, KCNJ2, PCDH9, RAP2B, SLC8A1, SLC9A1, TIAM1, VCL, PKP4, AKAP6, GJC1, RAP2C, AHNAK, TMEM65, FLCN
CC	GO:0019897	extrinsic component of plasma membrane	43/3499	2.30E-02	APC, RHOA, ATP2A2, CDH6, CRKL, CTNNA1, CTNNB1, CTNND1, CYLD, DTNA, FER, FMR1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, GNB1, GNG7, HIP1, JUP, KRAS, LYN, SMAD7, CDK16, SERPINE2, SNAP25, SRC, TIAM1, NUMB, IQGAP1, CYTH3, CYTH1, AKAP9, FARP1, GNA13, AAK1, ERRFI1, SYTL2, ESYT2, PLEKHA4, PRSS22, STXBP5
CC	GO:0001725	stress fiber	21/3499	2.30E-02	ACTN4, CNN2, FLNB, ILK, ABLIM1, LPP, MYH9, MYH10, PXN, TPM3, TPM4, PDLIM4, PDLIM7, NEBL, PDLIM5, FAM107A, LIMCH1, PDLIM3, DCTN4, FBLIM1, VANGL2
CC	GO:0097517	contractile actin filament bundle	21/3499	2.30E-02	ACTN4, CNN2, FLNB, ILK, ABLIM1, LPP, MYH9, MYH10, PXN, TPM3, TPM4, PDLIM4, PDLIM7, NEBL, PDLIM5, FAM107A, LIMCH1, PDLIM3, DCTN4, FBLIM1, VANGL2
CC	GO:0016323	basolateral plasma membrane	54/3499	2.35E-02	ANK1, ABCC6, ARRB1, ARRB2, ATP1B1, ATP2B1, ATP2B4, ATP7A, BMPR2, DST, CD44, CTNNB1, CXADR, DAG1, DLG3, EGFR, EPB41, ERBB2, FLOT2, GM2A, IL6R, ITGA6, ITGA3, KCNJ10, LDLR, LRP1, MET, MYO1C, MYO1D, P2RY1, PDGFB, ENPP1, PKD1, SLC4A2, SLC9A1, TFRC, TGFA, NUMB, SLC4A4, ADAM9, MAP7, SLC7A6, SLC4A7, SLC23A2, SLC12A6, NOD1, CADM1, DSTYK, LDLRAP1, CNNM4, VANGL2, RAB17, NDRG4, SLC16A10
CC	GO:0030014	CCR4-NOT complex	8/3499	2.45E-02	CNOT4, ZFP36, CNOT8, TOB1, CPEB3, CNOT1, CNOT6, PATL1
CC	GO:0019898	extrinsic component of membrane	70/3499	2.53E-02	APC, RHOA, ATP2A2, CDH6, CRKL, CTNNA1, CTNNB1, CTNND1, CYLD, DTNA, FER, FKBP1A, FMR1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, GNB1, GNG7, GOLGA3, HIP1, JUP, KRAS, LYN, SMAD7, OPA1, CDK16, SERPINE2, PIK3C2A, PIK3CB, PML, SNAP25, SRC, TIAM1, ULK1, NUMB, SOCS1, IQGAP1, SOCS2, MTMR3, CYTH3, CYTH1, SOCS6, SOCS5, ATG13, BCL2L11, AKAP9, FARP1, SEC23A, GNA13, MGLL, AAK1, ATG14, ATG2A, VPS13A, SOCS7, ZFYVE1, ERRFI1, VPS13C, SYTL2, ATG2B, VPS13D, ESYT2, PLEKHA4, PRSS22, MICALL1, WDR81, STXBP5, HID1
CC	GO:1902562	H4 histone acetyltransferase complex	15/3499	2.53E-02	ACTB, DR1, KAT2A, HCFC1, YEATS4, KAT2B, MORF4L2, UBAP2L, ZZZ3, ING3, KANSL2, MSL2, EP400, MEAF6, EPC1
CC	GO:0031985	Golgi cisterna	32/3499	2.62E-02	FUT8, GALNT1, GALNT2, GOLGA3, MAN2A1, SORT1, ST3GAL1, SORL1, B4GALT2, B4GALT6, GOSR1, GOLGA5, BCAP31, CIT, RAB21, GOLGA8A, MOB4, TMEM87A, RAB30, APH1A, GOLPH3L, CSGALNACT2, CSGALNACT1, INPP5E, COG3, SLC10A7, ST6GAL2, FUT10, CANT1, B4GALNT3, HID1, GOLGA8B
CC	GO:0030673	axolemma	7/3499	2.71E-02	ANK1, KCNC1, MAPT, MYO1D, SLC1A2, SPTBN1, CNTNAP2
CC	GO:0038201	TOR complex	7/3499	2.71E-02	LARP1, MLST8, MAPKAP1, SESN2, AKT1S1, SESN3, RICTOR
CC	GO:0070821	tertiary granule membrane	22/3499	3.03E-02	ADAM10, CD47, CD59, COPB1, STOM, GAA, NRAS, OLR1, PLD1, PTAFR, PTPRB, RAP2B, SNAP25, VAMP1, TRPM2, DYNLL1, ATP6AP2, ATP11A, RAB14, RAP2C, FRMPD3, SIRPA
CC	GO:0030139	endocytic vesicle	71/3499	3.15E-02	ARF6, ARRB2, ATP7A, FMNL1, CALR, CAMK2A, CAMK2D, CAV1, SCARB2, AP2M1, HBEGF, EGFR, FLNB, FLOT2, RAPGEF1, GRIA4, HIP1, HLA-B, IGF2R, ITGAV, KIF5B, LAMP2, LDLR, LRP1, RAB8A, MYO1C, MYO6, PLD1, PTCH1, RAB5A, RAB5B, SH3GL2, SPARC, VAMP7, SYK, UVRAG, WNT7B, FZD5, FZD4, SNX3, WASL, SYT7, ATP6V0D1, RABEP1, RAB11B, ATG5, RAPGEF2, CDC42EP2, UNC13B, HYOU1, RAB31, ATG14, SYT11, CD2AP, STX12, APPL1, RAB14, RAB23, RAB8B, WNT4, HEATR5B, RAB22A, RAB17, RAB11FIP1, SGIP1, RAB11FIP4, FCHO2, DAB2IP, AMOT, ATP6V0E2, RAB12
CC	GO:0005788	endoplasmic reticulum lumen	72/3499	3.41E-02	ADAM10, CALR, CALU, CANX, COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL4A5, COL4A6, COL5A1, COL5A2, COL6A2, COL11A1, COL12A1, COL19A1, CSF1, CTSZ, DAG1, EDN1, ESD, FBN1, FN1, SERPIND1, HSPA5, IGFBP1, IGFBP5, LAMC1, LRPAP1, LTBP1, DNAJB9, MEN1, P4HA1, PDGFA, PDGFB, PRKCSH, PTPRN2, RCN1, RCN2, SDC2, THBS1, WNT7B, STC2, H6PD, FSTL3,

					CRTAP, HYOU1, TGOLN2, ADAMTS5, FSTL1, GANAB, TOR1B, COL5A3, TXNDC12, GOLM1, ERAP1, WNT4, DNAJC10, TMEM132A, FKBP14, UGGT1, FAM20C, ANO8, TMEM43, ARSJ, VCPIP1, EDEM3, TXNDC5, COL27A1, EOGT, MIA3
CC	GO:1990752	microtubule end	11/3499	3.64E-02	DST, MYO5A, CLIP2, KIF2C, MAPRE3, CAMSAP2, CLASP1, NIN, SLAIN2, NAV3, CAMSAP1
CC	GO:0035102	PRC1 complex	7/3499	4.18E-02	RNF2, CBX4, PCGF3, CBX7, PHC3, PCGF5, CBX2
CC	GO:0030120	vesicle coat	18/3499	4.28E-02	AP1G1, ARCN1, AP2M1, AP1S1, COPB1, HIP1, AP1G2, SEC24C, SEC23A, SEC24A, SYNRG, SEC31B, NECAP1, TMED7, NECAP2, SAR1A, SGIP1, FCHO2
CC	GO:0090576	RNA polymerase III transcription factor complex	6/3499	4.77E-02	BRF1, GTF3C1, GTF3C4, GTF3C3, BRF2, BDP1
CC	GO:0000791	euchromatin	13/3499	4.87E-02	CREB1, CTNNB1, DNMT3A, JUN, RNF2, TCF7, KLF4, CBX3, RRP1B, SIRT1, NSMF, RBMX, CBX2
MF	GO:0003713	transcription coactivator activity	115/3415	1.32E-09	ABL1, ACTN4, RERE, BCL9, BRCA1, CBFB, CREBBP, CTNNB1, DR1, EP300, ESR2, FGF2, FHL2, FOXC1, FUS, GABPA, GATA3, KAT2A, GTF2A1, HCFC1, HMGA1, ISL1, JUN, JUND, JUP, MAX, MEF2A, MNT, MTF1, NPAT, NUP98, PML, PRRX1, POU3F2, POU4F1, PPARA, PPARD, RARG, RB1, KDM5A, RNF4, SMARCA2, SMARCC2, SMARCD2, SMARCE1, SOX4, SOX11, SOX12, SS18, TAF1, TCF3, ZEB1, TCF20, TFDP1, THRA, NR2C2, UBE2L3, NR1H2, VDR, YY1, KAT6A, KMT2D, NCOA3, NRIP1, ARID1A, KAT2B, PER2, MTA1, DYRK1B, TRIP11, HAND1, LPIN2, SERTAD2, MED24, THRAP3, MED13, NR1D2, YAF2, CITED2, SLC30A9, ZBTB18, NCOA2, DDX17, GMEB1, SRCAP, TCERG1, SUB1, KDM1A, RRP1B, LPIN1, WWC1, WBP2, ARL2BP, HINFP, SS18L1, MYCBP, USP21, HIPK2, ING4, DCAF6, ATXN7L3, ZMIZ1, ARID1B, CALCOCO1, RAP2C, KMT2C, WDR77, ZMIZ2, ARID5B, SETD3, MTDH, TADA2B, MYSM1, MED12L, JMY
MF	GO:0019787	ubiquitin-like protein transferase activity	134/3415	1.74E-08	AMFR, TRIM23, BRCA1, CBL, CDC34, CDC42, UBE2K, NEDD4, CNOT4, RAG1, RANBP2, RBBP6, RNF2, RNF4, SEL1L, SIAH1, SIAH2, SKP1, TAF1, TNFAIP1, TRAF3, TTC3, UBE2D2, UBE2D3, UBE2G1, UBE2G2, UBE2H, UBE2L3, UBE2N, UBE2V1, VHL, TRIM25, RNF103, CUL5, CUL3, CBX4, HERC3, BTRC, TRIP12, UBE4A, RNF144A, AREL1, KLHL21, RNF10, TRIM13, UBE4B, PIAS3, ARIH2, UBE2E3, RBCK1, PDZRN3, MYCBP2, MGRN1, TRIM2, UFL1, MKRN1, ARIH1, HECTD1, RNF19A, ZNF451, LTN1, HERC4, FBXW2, FBXL3, FBXO22, FBXO9, RNF11, MYLIP, RNF141, RLIM, BFAR, UBR5, UBE2J1, DTL, PIAS4, TRIM33, FBXO40, ANKIB1, NEURL1B, RNF111, FBXL12, BCOR, UBE2R2, RNF125, ATG16L1, MSL2, TRIM62, UBE2W, TRIM36, UBE2Q1, G2E3, KCMF1, SMURF1, PELI1, ZMIZ1, BIRC6, HECW2, MIB1, KLHL42, RNF213, RMND5B, UBE2Z, GID4, MUL1, CBLL1, ZFP91, RNF170, TRIM56, ZMIZ2, ATG10, ITCH, KCTD10, FBXO30, ZNRF3, MED10, SYVN1, ZNRF1, KLHL13, RFFL, UBR3, TRIM71, MIB2, RNF187, RNF38, RNF145, RNF217, RNF168, UBR1, ZNRF2, RNF144B, SHPRH, RNF180, SH3RF3, RNF165
MF	GO:0019903	protein phosphatase binding	60/3415	4.78E-08	ANK1, ATP2B4, BCL2, CDC5L, CDKN1B, MAPK14, CSK, CTNNB1, DLG3, EGFR, ENSA, ERBB2, FER, FOXO1, FLT4, KAT2A, GRB2, HMGCR, JUP, MAPT, MET, PPP1CA, PPP1CC, PPP1R3C, PPP2R2A, PTPN1, PXN, SLC9A1, STAT1, STAT3, STAU1, STRN, TP53, TRAF3, VCP, SHOC2, PDLIM4, IRS2, SNX3, IQGAP1, MTMR3, MTMR4, AKAP5, SMG7, ARPP19, PTPRT, KIF3A, AKAP11, PPP6R1, ANKLE2, SMG5, STRN4, STRN3, STX17, PPP6R3, PARD3, MTMR9, SIRPA, DAB2IP, BOD1L1
MF	GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	139/3415	6.84E-08	AR, RUNX2, RUNX1, CDC5L, CEBPB, CEBPD, CEBPG, KLF6, CREB1, ATF2, ATF6B, DLX2, E2F3, EGR1, ELF4, ELK1, ELK3, ELK4, EP300, EPAS1, ESRRA, ESRRG, ETV1, FOXC1, FOXO3, FOSB, FOSL2, NR5A2, GABPA, GATA2, GATA3, NR6A1, NR3C1, HCFC1, HIF1A, FOXA1, HNF4A, HNRNPK, HOXA5, HOXA7, HOXB3, HOXB5, HOXC4, HOXD13, RBPJ, FOXK2, IRF1, IRF4, ISL1, JUN, JUND, LMO2, SMAD2, SMAD4, MAFG, MEF2A, MEF2C, MEF2D, MEIS2, FOXO4, MSX1, MTF1, MYB, MYBL2, MYC, MYCN, NFIA, NFIB, NFIC, NFKB1, NRF1, OTX1, PAX6, PAX9, PBX1, PGR, PKNOX1, PLAGL2, POU2F2, POU3F2, POU4F1, PPARA, RORA, RORB, RREB1, SALL2, SOX4, SOX11, SOX12, SRF, STAT1, STAT2, STAT3, STAT5B, TCF4, TBX3, TFDP1, TFDP2, KLF10, TP53, NR2C2, NR1H2, ZNF24, ZNF131, VEZF1, PRDM2, NR4A3, FOSL1, HMGA2, TP63, KLF4, ONECUT2, CLOCK, CTCF, GMEB1, NFAT5, SUB1, SOX21, MLXIP, FOXJ3, MGA, SATB2, SIRT1, TARDBP, MAFF, EHF, HEYL, GRHL1, SOX8, ZNF639, SIX4, FOXJ2, NUCKS1, CREB3L2, BCL11B, GLIS2, EBF3, MACC1, IRF2BP2
MF	GO:0019902	phosphatase binding	72/3415	6.84E-08	ANK1, ATP2B4, BCL2, CDC5L, CDKN1B, CRY2, MAPK14, CSK, CTNNB1, DLG3, EGFR, ENSA, ERBB2, FER, FOXO1, FLT4, KAT2A, GRB2, HMGCR, JUP, SMAD2, MAPT, MET, PPARA, PPP1CA, PPP1CC, PPP1R3C, PPP2R2A, PPP3R1, MAPK1, MAPK3, PTPN1, PXN, SLC9A1, STAT1, STAT3, STAU1, STRN, SYK, TP53, TRAF3, VCP, SHOC2, PDLIM4, IRS2, SNX3, IQGAP1, MTMR3, MTMR4, AKAP5, SMG7, ARPP19, PTPRT, KIF3A, AKAP11, PPP6R1, ANKLE2, SMG5, STRN4, STRN3, SYTL2, CHCHD3, STX17, PPP6R3, PARD3, WNK1, MTMR9, PVRIG, SIRPA, DAB2IP, SPRED1, BOD1L1
MF	GO:0004842	ubiquitin-protein transferase activity	124/3415	6.84E-08	AMFR, TRIM23, BRCA1, CBL, CDC34, CDC42, UBE2K, NEDD4, CNOT4, RAG1, RBBP6, RNF2, RNF4, SEL1L, SIAH1, SIAH2, SKP1, TAF1, TNFAIP1, TRAF3, TTC3, UBE2D2, UBE2D3, UBE2G1, UBE2G2, UBE2H, UBE2L3, UBE2N, UBE2V1, VHL, TRIM25, RNF103, CUL5, CUL3, HERC3, BTRC, TRIP12, UBE4A, RNF144A, AREL1, KLHL21, RNF10, TRIM13, UBE4B, ARIH2, UBE2E3, RBCK1, PDZRN3, MYCBP2, MGRN1, TRIM2, MKRN1, ARIH1, HECTD1, RNF19A, LTN1, HERC4, FBXW2, FBXL3, FBXO22, FBXO9, RNF11, MYLIP, RNF141, RLIM, BFAR, UBR5, UBE2J1, DTL, TRIM33, FBXO40, ANKIB1, NEURL1B, RNF111, FBXL12, BCOR, UBE2R2, RNF125, MSL2, TRIM62, UBE2W, TRIM36, UBE2Q1, G2E3, KCMF1, SMURF1, PELI1, BIRC6, HECW2, MIB1, KLHL42, RNF213, RMND5B, UBE2Z, GID4, MUL1, CBLL1, ZFP91, RNF170, TRIM56, ITCH, KCTD10, FBXO30, ZNRF3, MED10, SYVN1, ZNRF1, KLHL13, RFFL, UBR3, TRIM71, MIB2, RNF187, RNF38, RNF145, RNF217, RNF168, UBR1, ZNRF2, RNF144B, SHPRH, RNF180, SH3RF3, RNF165

MF	GO:0004721	phosphoprotein phosphatase activity	71/3415	6.84E-08	ACP1, CDC25A, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EYA4, PPM1B, PPP1CA, PPP1CB, PPP1CC, PPP1R3C, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PPP3R1, PPP6C, PTEN, PTPN1, PTPN4, PTPN11, PTPN12, PTPN14, PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRJ, PTPRK, PTPRN2, PTPRR, STYX, PTP4A1, SHOC2, PTP4A2, PPM1D, CDC14B, MTMR3, MTMR7, MTMR4, CTDSP2, CTDSPL, TAB1, DUSP14, PTPN21, PTPRT, DUSP10, PHLPP2, PHLPP1, PTPN18, PALD1, CYCS, SSH1, DUSP23, PPP2R2D, PPM1H, PDP2, CTDSP1, DUSP16, SSH2, TIMM50, PPM1M, DUSP18, PPM1L, PPTC7
MF	GO:0050839	cell adhesion molecule binding	153/3415	6.84E-08	ACTN4, ADAM10, ADD1, ANXA7, ARHGAP1, BMPR2, DST, CALD1, CALR, CBL, CDH6, CNN2, COL3A1, COL5A1, CRKL, CSNK1D, CTNNA1, CTNNB1, CTNND1, CXADR, DDX3X, DDX6, S1PR3, EGFR, EIF2S3, EIF4G2, EIF5, MARK2, EMP2, FBN1, FGF1, FGF2, FLNB, FN1, GOLGA3, HCFC1, HDLBP, NRG1, HNRNPK, HSPA5, IGF2, ILK, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, JUP, KIF5B, LASP1, LDHA, LYN, MMP14, MYO1B, MYH9, NCK1, PRDX1, PAK2, PKM, PKP1, PLEC, PPP1CA, PRKCA, PKN2, TWF1, PTPN1, PTPN11, PTPRB, PTPRD, PTPRF, PTPRJ, PXN, RAB1A, RAN, RDX, RPL15, RPL34, CX3CL1, SNX1, SPTAN1, SPTBN1, SRC, STAT1, SYK, ADAM17, THBS1, TIMP2, TLN1, TMPO, VCAM1, VCL, YWHAE, TRIM25, STK24, SEMA7A, PPFIBP1, PKP4, USO1, NUMB, ADAM9, IQGAP1, GPRC5A, VAPB, VAPA, RAB11B, TJP2, SLK, WASF2, TENM1, GPNMB, PAICS, PDLIM5, POSTN, ADAMTS5, PTPRT, ATXN2L, LYPLA2, STK38, NLGN1, PDXDC1, ERC1, MPRIP, DOCK9, LARP1, CD2AP, ARFIP2, GIGYF2, SERBP1, TES, RSL1D1, NPTN, SND1, EHD4, ASAP1, SH3GLB1, CHMP5, ADAM22, ANLN, CC2D1A, FNBP1L, TENM3, UBFD1, ZC3HAV1, ESYT2, NLGN2, KLC2, AHNAK, EFHD2, MICALL1, PHLDB2, ARHGAP18, DAB2IP
MF	GO:0031625	ubiquitin protein ligase binding	99/3415	1.69E-07	ACVR1B, APC, ARRB1, ARRB2, BAG1, BCL2, BRCA1, CALR, CASP10, CDKN1A, DBT, DLG3, EGFR, FHIT, FOXO1, GPI, GSK3B, HIF1A, UBE2K, DNAJA1, HSPA5, JUN, LYN, SMAD2, SMAD6, SMAD7, MID1, ATXN3, PA2G4, PAX6, PML, PRKAR1A, PRKAR2A, PXN, RALB, RB1, SKI, SRC, AURKA, TMBIM6, TNFRSF1B, TP53, TRAF1, TRAF3, UBE2D2, UBE2D3, UBE2G1, UBE2L3, UBE2N, VCL, VCP, XRCC5, YWHAE, FZD5, CUL5, FZD4, FZD6, SPOP, CUL4B, CUL3, CUL2, PER3, SQSTM1, USP13, USP2, BAG4, TRAF4, SNCAIP, KDM4A, MFN2, ABI2, TNK2, TRIB1, ERLIN2, GABARAPL2, SYT11, SMG5, HSPBP1, ARIH1, UBXN7, TRIB2, USP25, UBE2J1, PIAS4, NLK, UBE2W, FBXW7, LAPTM4B, YOD1, NPLOC4, MOAP1, MUL1, SMC6, MAP1LC3B, RFFL, CACUL1, ZNF675, SHPRH, SPOPL
MF	GO:0044389	ubiquitin-like protein ligase binding	103/3415	2.56E-07	ACVR1B, APC, ARRB1, ARRB2, BAG1, BCL2, BRCA1, CALR, CASP10, CDKN1A, CEBPB, DBT, DLG3, EGFR, FHIT, FOXO1, GPI, GSK3B, HIF1A, UBE2K, DNAJA1, HSPA5, JUN, LYN, SMAD2, SMAD6, SMAD7, MID1, ATXN3, PA2G4, PAX6, PML, PRKAR1A, PRKAR2A, PXN, RALB, RB1, SKI, SRC, STAT1, STAT2, AURKA, TMBIM6, TNFRSF1B, TP53, TRAF1, TRAF3, UBE2D2, UBE2D3, UBE2G1, UBE2L3, UBE2N, VCL, VCP, XRCC5, YWHAE, FZD5, CUL5, FZD4, FZD6, SPOP, CUL4B, CUL3, CUL2, PER3, SQSTM1, USP13, USP2, BAG4, TRAF4, SNCAIP, KDM4A, MFN2, ABI2, TNK2, TRIB1, ERLIN2, GABARAPL2, SYT11, SMG5, HSPBP1, ARIH1, UBXN7, TRIB2, USP25, UBE2J1, PIAS4, NLK, UBE2W, FBXW7, LAPTM4B, YOD1, NPLOC4, MOAP1, MUL1, SMC6, MAP1LC3B, ITCH, RFFL, CACUL1, ZNF675, SHPRH, SPOPL
MF	GO:0042393	histone binding	73/3415	3.92E-07	ATRX, RCC1, CHD2, EZH1, FMR1, KMT2A, MLLT3, MLLT6, PTMA, RAG1, KDM5A, SET, SMARCA2, SMARCC2, SNCA, SSRP1, STAT1, TAF1, TBL1X, KAT6A, BRD3, MLLT10, KMT2D, DPF3, ANP32A, DPF1, CBX4, TNKS, BAZ1B, KDM4A, ANP32B, KDM5B, ZMYND11, SRCAP, SPIN1, KAT7, SUPT16H, MTF2, WDTC1, PHF8, PSME4, SIRT1, CBX5, SUZ12, USP49, HINFP, ING4, SFMBT1, RSF1, ATAD2B, WDR5B, ING3, INO80, MBTD1, NCAPG2, PHIP, IPO9, ASF1B, KMT2E, SFMBT2, KMT2C, TBL1XR1, ANP32E, GLYR1, CBX2, MYSM1, PWWP2A, SPIN4, SPTY2D1, PHF13, USP51, RNF168, KDM1B
MF	GO:0045296	cadherin binding	108/3415	4.14E-07	ADD1, ARHGAP1, BMPR2, CALD1, CBL, CDH6, CNN2, CRKL, CSNK1D, CTNNA1, CTNNB1, CTNND1, DDX3X, DDX6, EGFR, EIF2S3, EIF4G2, EIF5, MARK2, FLNB, GOLGA3, HCFC1, HDLBP, HNRNPK, HSPA5, ITGA6, ITGB1, JUP, KIF5B, LASP1, LDHA, MYO1B, MYH9, NCK1, PRDX1, PAK2, PKM, PKP1, PLEC, PPP1CA, PKN2, TWF1, PTPN1, PTPRB, PTPRJ, RAB1A, RAN, RDX, RPL15, RPL34, SNX1, SPTAN1, SPTBN1, SRC, STAT1, TLN1, TMPO, VCL, YWHAE, TRIM25, STK24, PPFIBP1, PKP4, USO1, NUMB, IQGAP1, GPRC5A, VAPB, VAPA, RAB11B, TJP2, SLK, WASF2, PAICS, PDLIM5, PTPRT, ATXN2L, LYPLA2, STK38, PDXDC1, ERC1, MPRIP, DOCK9, LARP1, CD2AP, ARFIP2, GIGYF2, SERBP1, TES, RSL1D1, SND1, EHD4, ASAP1, SH3GLB1, CHMP5, ANLN, CC2D1A, FNBP1L, UBFD1, ZC3HAV1, ESYT2, KLC2, AHNAK, EFHD2, MICALL1, PHLDB2, ARHGAP18, DAB2IP
MF	GO:0031267	small GTPase binding	135/3415	6.77E-07	ADCYAP1R1, ADRB1, AP1G1, ARHGAP1, ARHGDIA, ATP7A, FMNL1, CAV1, RCC1, DIAPH1, DOCK3, DVL3, ECT2, EPS8, GDI1, RAPGEF1, NCKAP1L, TNPO1, IPO5, RAB8A, MYO1C, MYO5A, NSF, TBC1D25, PAK2, PAK3, PKN2, PEX5, RABGGTB, RANBP2, SORL1, SOS1, TIAM1, TNFAIP1, TRIO, XPO1, EVI5, ULK1, MADD, IQGAP1, WASF1, KALRN, ARHGEF2, KIF3B, ROCK2, RALGPS1, RAPGEF2, USP6NL, RIMS3, ARHGEF17, TBC1D4, DENND4B, RABGAP1L, GOLGA5, ABI2, FARP1, NUTF2, NET1, RAPGEF3, CDC42EP2, VAV3, UNC13B, EXOC5, NUP50, NCKAP1, IQGAP2, KIF3A, TBC1D8, AKAP13, XPOT, RHOBTB3, RAB11FIP2, PPP6R1, DENND3, USP33, XPO7, TBC1D9B, MYCBP2, ERC1, TBC1D2B, RGL1, ARHGEF9, BICD2, ARHGEF12, ACAP2, CORO1C, RABGAP1, ARFIP2, RAB3GAP2, TBC1D10B, PLEKHG3, AP3M1, STRN3, TRAPPC4, ANKFY1, PEX5L, ERRFI1, ANLN, WDR44, SYTL2, ARHGAP17, TBC1D22B, TMEM127, IPO9, RCC2, CDC42SE1, XPO5, PLEKHG2, MLPH, MAPKAP1, HPS6, SIKE1, RAB11FIP1, PREX2, SH3BP5L, KCTD10, RAB11FIP4, PARD6B, ARHGEF39, MICALL1, FMNL3, RAB3IP, FGD4, WHAMM, IQGAP3, TBC1D20, STXBP5, RIMS4, SMCR8, EXOC8, PLEKHG4B, DENND5B, DENND6A, SPATA13, RILPL1
MF	GO:0003714	transcription corepressor activity	83/3415	7.52E-07	RERE, CCND1, RUNX1T1, CREBBP, DNMT3A, DNMT3B, DR1, ATN1, E2F6, ERF, EZH1, EZH2, ARHGAP35, HDGF, HNRNPU, HSBP1, ID4, MXD1, MECP2, MEIS2, MNT, MXI1, NPAT, PAWR, POU4F1, SRSF2, SIAH2, SKI, TBL1X, ZEB1, NR2F2, TGIF1, TLE1, TLE4, YY1, SF1, NRIP1, CBX4, BHLHE40, LDB1, LIMD1, MTA1, COPS2, NCOR1, HDAC9, YAF2, TOB1, TRIM22, CITED2, MXD4, CTCF, KDM5B, TOB2, ZMYND11, TCERG1, ZHX1, KLF12, SPEN, SIRT1, RBFOX2, SIN3A, ZNF451, HEYL, HIPK2, LMCD1, RLIM, SFMBT1, PIAS4, TAF9B, SUFU, WNT4, BCOR, ATF7IP, MIER1, SFMBT2, NSD1, TBL1XR1, AEBP2, NACC2, E2F7, PARP15, MIER3, JAZF1

MF	GO:0046332	SMAD binding	38/3415	7.66E-07	ACVR1B, ACVR2B, BMPR1A, BMPR2, COL1A2, COL3A1, COL5A2, CTNNB1, DAB2, DDX5, FKBP1A, JUN, SMAD2, SMAD4, SMAD6, SMAD7, MEF2A, MEN1, PAX6, PML, PURA, PURB, SKI, SKIL, TGFBR1, TGFBR3, TGIF1, YY1, HMGA2, USP9X, TOB1, ZC3H3, HIPK2, TRIM33, RNF111, PMEPA1, SMURF1, ACVR1C
MF	GO:0001085	RNA polymerase II transcription factor binding	59/3415	2.65E-06	AR, RERE, CHD4, CREB1, ATF2, CREBBP, CTNNB1, ATN1, ELK1, EP300, GATA6, GSK3B, GTF2A1, GTF2E1, HDAC2, HNF4A, HNRNPU, ID4, RBPJ, ISL1, JUN, LMO2, SMAD4, MEF2A, PPARA, PPARD, RB1, RBL2, SRF, STAT3, TAF1, TAL1, TCF4, TBX3, TCF7L2, TEAD1, TEAD3, TP53, BHLHE40, LDB1, LDB2, MTA1, KLF4, NCOR1, PIAS3, TCERG1, SPEN, KDM1A, MGA, SIN3A, HIPK2, PIAS4, ZNHIT6, ZMIZ1, MIER1, ZMIZ2, SETD3, MTDH, MIER3
MF	GO:0017016	Ras GTPase binding	129/3415	2.65E-06	ADRB1, AP1G1, ARHGAP1, ARHGDIA, ATP7A, FMNL1, CAV1, RCC1, DIAPH1, DOCK3, DVL3, ECT2, EPS8, GDI1, RAPGEF1, NCKAP1L, TNPO1, IPO5, RAB8A, MYO1C, MYO5A, NSF, TBC1D25, PAK2, PAK3, PKN2, RABGGTB, RANBP2, SOS1, TIAM1, TNFAIP1, TRIO, XPO1, EVI5, ULK1, MADD, IQGAP1, WASF1, KALRN, ARHGEF2, KIF3B, ROCK2, RALGPS1, RAPGEF2, USP6NL, RIMS3, ARHGEF17, TBC1D4, DENND4B, RABGAP1L, GOLGA5, ABI2, FARP1, NUTF2, NET1, RAPGEF3, CDC42EP2, VAV3, UNC13B, EXOC5, NUP50, NCKAP1, IQGAP2, KIF3A, TBC1D8, AKAP13, XPOT, RHOBTB3, RAB11FIP2, PPP6R1, DENND3, USP33, XPO7, TBC1D9B, MYCBP2, ERC1, TBC1D2B, RGL1, ARHGEF9, BICD2, ARHGEF12, ACAP2, CORO1C, RABGAP1, ARFIP2, RAB3GAP2, TBC1D10B, PLEKHG3, AP3M1, STRN3, TRAPPC4, ANKFY1, ANLN, WDR44, SYTL2, ARHGAP17, TBC1D22B, TMEM127, IPO9, RCC2, CDC42SE1, XPO5, PLEKHG2, MLPH, MAPKAP1, HPS6, SIKE1, RAB11FIP1, PREX2, SH3BP5L, KCTD10, RAB11FIP4, PARD6B, ARHGEF39, MICALL1, FMNL3, RAB3IP, FGD4, WHAMM, IQGAP3, TBC1D20, STXBP5, RIMS4, SMCR8, EXOC8, PLEKHG4B, DENND5B, DENND6A, SPATA13
MF	GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	82/3415	3.10E-06	ZFHX3, BCL6, PRDM1, CEBPB, DACH1, E2F6, ELK3, ERF, ESRRA, ETV3, FOXM1, FOXO1, FOXO3, GATA3, ARHGAP35, HIVEP1, HES1, FOXK2, JARID2, MXD1, MAX, MECP2, MNT, MSX1, MXI1, MYC, NFKB1, PAX6, PRRX1, PPARA, PPARD, PROX1, PURA, PURB, SATB1, SKIL, SNAI2, SNAI1, SP3, SREBF2, TBX3, TCF3, TCF7, ZEB1, MLX, TGIF1, TRPS1, YY1, CNBP, ZNF131, ZNF140, ZNF148, ZNF217, ZNF224, BTG2, MAFK, HMGA2, BHLHE40, HAND1, NR1D2, CTCF, KLF12, KLF8, HIC2, RCOR1, HINFP, HEYL, PURG, BCL11A, CC2D1A, CHCHD3, HES6, ZBTB2, ZBTB4, ZNF350, BACH2, HMBOX1, MXD3, ARID5B, AEBP2, E2F7, FOXK1
MF	GO:0008013	beta-catenin binding	37/3415	5.10E-06	APC, AR, BCL9, CTNNA1, CXADR, DVL3, EP300, FOXO1, FOXO3, GSK3B, SMAD7, FOXO4, PIN1, PTPRJ, PTPRK, PXN, RORA, SKP1, TBL1X, TCF7, TCF7L2, VCL, NUMB, BTRC, DLG5, KLF4, SETD1A, PTPRT, KDM6B, KANK1, CD2AP, SUFU, CALCOCO1, TBL1XR1, LZIC, MED12L, AMER1
MF	GO:0004722	protein serine/threonine phosphatase activity	35/3415	5.75E-06	DUSP1, PPM1B, PPP1CA, PPP1CB, PPP1CC, PPP1R3C, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP3CA, PPP3R1, PPP6C, PTEN, SHOC2, PPM1D, CDC14B, MTMR3, MTMR4, CTDSP2, CTDSPL, TAB1, PHLPP2, PHLPP1, PALD1, CYCS, DUSP23, PPP2R2D, PPM1H, PDP2, CTDSP1, TIMM50, PPM1M, PPM1L, PPTC7
MF	GO:0004725	protein tyrosine phosphatase activity	42/3415	7.77E-06	ACP1, CDC25A, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EYA4, PTEN, PTPN1, PTPN4, PTPN11, PTPN12, PTPN14, PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRJ, PTPRK, PTPRN2, PTPRR, PTP4A1, PTP4A2, CDC14B, MTMR3, MTMR7, MTMR4, DUSP14, PTPN21, PTPRT, DUSP10, PTPN18, PALD1, SSH1, DUSP23, DUSP16, SSH2, TIMM50, DUSP18
MF	GO:0019003	GDP binding	34/3415	8.50E-06	TRIM23, ARF1, RHOA, RHOB, GBP1, GNAI3, KRAS, RAB8A, NRAS, RAB3B, RAB5A, RAB5B, RALB, RAN, RAP1B, RAP2A, RAP2B, SUCLG2, RAB11B, RAB28, RAB31, RAB21, RAB14, RAB8B, MIEF1, DIRAS2, RAB22A, RAB40C, RAP2C, RRAGD, RRAGC, RAB17, DIRAS1, RAB12
MF	GO:0016791	phosphatase activity	87/3415	1.24E-05	ACP1, CDC25A, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EYA4, IMPA2, NT5E, PFKFB2, PFKFB3, PFKFB4, PPM1B, PPP1CA, PPP1CB, PPP1CC, PPP1R3C, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PPP3R1, PPP6C, PTEN, PTPN1, PTPN4, PTPN11, PTPN12, PTPN14, PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRJ, PTPRK, PTPRN2, PTPRR, STYX, PTP4A1, SHOC2, PTP4A2, PPM1D, CDC14B, INPP4B, SYNJ1, SYNJ2, MTMR3, MTMR7, MTMR4, LPIN2, CTDSP2, CTDSPL, TAB1, DUSP14, PTPN21, PTPRT, DUSP10, SACM1L, PHLPP2, LPIN1, PHLPP1, PTPN18, PALD1, NT5DC3, CYCS, SSH1, DUSP23, PPP2R2D, INPP5E, PPM1H, PDP2, CTDSP1, ENOPH1, DUSP16, SGPP1, SSH2, TIMM50, PPM1M, NANP, DUSP18, PPM1L, PPTC7
MF	GO:0060090	molecular adaptor activity	78/3415	1.89E-05	AMFR, ANK1, ARHGAP1, ARRB1, ARRB2, CAV1, AP2M1, COL1A2, COL11A1, COL19A1, CRK, CRKL, CUX1, DAB2, EIF4G1, EPS8, ERCC2, FKBP4, GAB1, GRB2, HCFC1, HIP1, LASP1, MAP1A, MAPT, MEN1, NCK1, NEFH, PTPN11, SH3BP2, SHC1, SLC9A1, SRC, NCK2, SORBS2, IQGAP1, SOCS2, KSR1, SPAG9, TJP2, AKAP6, HERPUD1, SH2B3, TOB1, AKAP9, ABI2, TRIM22, VAV3, FRS2, AKAP13, CNOT1, MAPK8IP3, WWC1, BICD2, CBX5, ISCU, FLRT2, SH2B1, LDLRAP1, NMD3, BFAR, OTUD4, GATAD2A, CHCHD3, FBXW7, FRMD4A, PAG1, WWC3, MAVS, SERINC1, MLPH, WWC2, SPSB1, AFAP1L2, ARRDC4, TEX261, PPP4R2, DAB2IP
MF	GO:0004674	protein serine/threonine kinase activity	127/3415	2.43E-05	ACVR1B, ACVR2B, AKT2, ATM, ATR, BMPR1A, BMPR2, CAMK4, CAMK2A, CAMK2D, CDK6, CHEK1, MAPK14, CSNK1D, CSNK1E, CSNK1G3, DAPK1, DYRK1A, EGFR, MARK2, ERCC2, GRK6, MKNK2, GSK3B, GTF2H3, IKBKB, ILK, IRAK1, IRAK2, LIMK1, LTBP1, MARK1, MAP3K1, MAP3K3, MAP3K4, MAP3K9, PAK2, PAK3, CDK16, PDK3, PHKA1, PHKG2, PIM1, PRKAA1, PRKAB2, PRKCA, PRKCE, PKN2, MAPK1, MAPK3, MAPK6, MAPK8, MAPK9, EIF2AK2, RPS6KA3, RPS6KB1, MAP2K4, STK4, AURKA, STK10, SYK, TAF1, TESK1, TGFBR1, TGFBR3, TRIO, ULK1, STK24, DYRK2, PPM1D, CDK10, MKNK1, SQSTM1, CPNE3, RPS6KA4, KALRN, LATS1, DYRK1B, DCLK1, AURKB, RPS6KA5, STK17B, STK17A, TAOK2, MAP4K4, ROCK2, SLK, MELK, NUAK1, AKT3, HIPK3, TNK2, MAP3K2, PLK2, TLK2, CIT, AKAP13, STK38, AAK1, LMTK2, STK38L, SMG1, CDK19, PASK, SGK3, DSTYK, LATS2, EIF2AK1, HIPK2, HUNK, MINK1, NLK, SNRK, BMP2K, RIOK2, FAM20C, CAMK1D, ALPK3, TAOK1, WNK1, NUAK2, STK40, ACVR1C, TTBK2, SIK1, HIPK1, MAST4

MF	GO:0001158	enhancer sequence-specific DNA binding	46/3415	3.00E-05	ACTB, CHD4, CREB1, ATF2, ATF6B, NR5A2, GATA2, GATA3, HDAC2, HIVEP1, HMGA1, HNRNPC, HOXA5, HOXA7, HOXB5, HOXC4, HOXD13, ISL1, JUN, MEF2C, KMT2A, NFKB1, NFYA, NFYB, POU4F1, SMARCC2, SMARCD2, SMARCE1, SOX11, TAL1, TP53, XBP1, YY1, BHLHE40, LDB1, MBD2, MTA1, CLOCK, THRAP3, NR1D2, SIRT1, ZNF395, GATAD2B, CALCOCO1, BACH2, ZNF704
MF	GO:0008022	protein C-terminus binding	64/3415	3.94E-05	ABL1, ATP1B1, DST, CACNA1B, FOXN3, CSK, CTNNB1, DAB2, DLG3, EP300, EPB41, ERBB2, ERCC2, ERCC6, FN1, KCNK3, KPNA3, LIG4, MAD2L1, MYO1C, NPAT, PPP1CC, PPP2CA, PRKAA1, RAD51, ATXN1, ATXN2, SH3GL2, SIAH1, SRC, SREBF2, SYT1, TBL1X, TCF4, TERT, TESK1, TOP2B, XRCC5, YEATS4, COIL, DYNLL1, MPDZ, KSR1, VPS4B, CEP135, SNX17, PIAS3, PRDX3, CEP250, SNF8, MAPRE3, HIC2, PRRC2C, SIRT1, CD2AP, NIPBL, CNRIP1, PABPC1, VPS36, PIAS4, FIGN, PEX26, CALCOCO1, CEP120
MF	GO:0051219	phosphoprotein binding	35/3415	5.55E-05	ABL1, ABL2, ARRB1, CBL, CRK, CRKL, EPB41, FKBP4, GRB2, IGF2R, LYN, MID1, NEDD4, PAFAH1B1, PIN1, PRKCSH, MAPK1, MAPK3, PTPN11, RASA1, RB1, SH3BP2, SHC1, SNCA, SRC, SYK, YWHAE, NCK2, CBX4, BTRC, THRAP3, LDLRAP1, FBXW7, SCAF4, GPRIN1
MF	GO:0035326	enhancer binding	49/3415	6.22E-05	ACTB, CHD4, CREB1, ATF2, ATF6B, NR5A2, GATA2, GATA3, HDAC2, HIVEP1, HMGA1, HNRNPC, HOXA5, HOXA7, HOXB5, HOXC4, HOXD13, ISL1, JUN, SMAD2, MEF2C, KMT2A, MSX1, NFKB1, NFYA, NFYB, POU4F1, SMARCC2, SMARCD2, SMARCE1, SOX11, TAL1, TCF3, TP53, XBP1, YY1, BHLHE40, LDB1, MBD2, MTA1, CLOCK, THRAP3, NR1D2, SIRT1, ZNF395, GATAD2B, CALCOCO1, BACH2, ZNF704
MF	GO:0060589	nucleoside-triphosphatase regulator activity	102/3415	7.78E-05	ARHGAP1, ARHGDIA, ARRB1, ATP1B1, BAG1, BNIP2, ECT2, EIF5, GDI1, GNAQ, ARHGAP35, NCKAP1L, AGFG2, DNAJB2, DNAJA1, JUN, IPO5, TBC1D25, OPHN1, RALGDS, RANBP2, RAP1GDS1, RASA1, RGS2, RGS4, RGS16, RP2, SOS1, TSC1, EVI5, RGS5, IQGAP1, NRP1, SYNGAP1, WASL, RABEP1, ARHGAP29, RASAL2, RAPGEF2, USP6NL, GIT2, TBC1D4, RABGAP1L, TNK2, DNAJA2, DLC1, CDC42EP2, VAV3, SEC23A, NUP50, IQGAP2, ADAP1, DNAJB4, TBC1D8, RASA3, TBC1D9B, TBC1D2B, RAP1GAP2, ARHGEF12, ACAP2, ARL2BP, RABGAP1, HSPBP1, RAB3GAP2, TBC1D10B, SIPA1L1, GIT1, DNAJC15, ASAP1, ERRFI1, DNAJC10, ARHGAP17, TBC1D22B, DEPDC1, ARFGAP1, CDC42SE1, RALGAPA2, TBC1D24, SIPA1L2, FNIP2, RIC8A, DNAJC1, ARHGAP28, PREX2, GRPEL1, ARHGAP39, SESN2, SYDE2, ARHGAP18, ARHGAP12, FNIP1, ARAP2, AGAP1, DNAJC24, TBC1D20, CPEB2, GRPEL2, STXBP5, SIRPA, DAB2IP, TOR1AIP2, FLCN
MF	GO:0030674	protein binding, bridging	58/3415	1.21E-04	AMFR, ANK1, ARHGAP1, ARRB1, CAV1, AP2M1, COL1A2, COL11A1, COL19A1, CRK, CRKL, CUX1, DAB2, ERCC2, FKBP4, GAB1, GRB2, HCFC1, HIP1, LASP1, MAP1A, MAPT, MEN1, NCK1, NEFH, PTPN11, SH3BP2, SHC1, SLC9A1, SRC, NCK2, SORBS2, SOCS2, TJP2, HERPUD1, SH2B3, TOB1, ABI2, TRIM22, VAV3, FRS2, BICD2, CBX5, FLRT2, SH2B1, LDLRAP1, NMD3, BFAR, GATAD2A, FBXW7, FRMD4A, PAG1, SERINC1, MLPH, SPSB1, ARRDC4, TEX261, PPP4R2
MF	GO:0051721	protein phosphatase 2A binding	18/3415	1.32E-04	BCL2, ENSA, FOXO1, HMGCR, MAPT, PPP2R2A, PTPN1, STAT1, STRN, TP53, SMG7, ARPP19, ANKLE2, SMG5, STRN4, STRN3, DAB2IP, BOD1L1
MF	GO:0003779	actin binding	121/3415	1.72E-04	ABL1, ABL2, ACTN4, ADD1, DST, FMNL1, CALD1, CAPZA2, CFL1, CFL2, CNN2, CTNNA1, DAG1, DIAPH1, EGFR, EPB41, EPS8, FLNB, GBP1, HIP1, HNRNPU, IPP, ITGB1, LASP1, ABLIM1, MARCKS, MAP1A, MAP1B, MAPT, MYO1B, MYO1F, MYH9, MYH10, MYO1C, MYO1D, MYO5A, MYO6, MYO10, NF2, OPHN1, PAWR, PLEC, PLS3, PRKCE, TWF1, RDX, SNCA, SNTB1, SNTB2, SPTAN1, SPTBN1, TAGLN, TLN1, TNS1, TPM3, TPM4, VCL, ZNF185, ENC1, PDLIM4, WASF1, WASL, PDLIM7, PHACTR2, ARPC5, ACTR2, ARPC2, WASF2, CAP2, CAP1, NEBL, PDLIM5, IQGAP2, DSTN, FAM107A, VASH1, LIMCH1, STK38L, PALLD, MPRIP, COTL1, CORO1C, KLHL3, PDLIM3, TMOD2, KLHL5, HOOK1, SSH1, ANLN, INO80, ALKBH4, FERMT1, MYO5C, KLHL4, FMN2, SPIRE1, SHROOM3, AFAP1, PKNOX2, MARCKSL1, MLPH, SYNPO2L, MED28, ANTXR1, SETD3, DIXDC1, FHDC1, SSH2, FMNL3, MYOZ3, RCSD1, FGD4, WHAMM, JMY, SHROOM1, MIB2, WIPF2, TMEM201, GAS2L3, FMN1, MYO18A
MF	GO:0046875	ephrin receptor binding	16/3415	1.72E-04	ABL1, CBL, CRK, EFNA3, EFNA5, EFNB1, EFNB2, EPHA4, EPHA7, GRB2, LYN, NCK1, PTPN1, SHC1, SRC, SIPA1L1
MF	GO:0061659	ubiquitin-like protein ligase activity	72/3415	2.67E-04	AMFR, CBL, CDC42, UBE2K, NEDD4, RAG1, RBBP6, RNF2, SIAH1, SIAH2, SKP1, VHL, TRIM25, RNF103, BTRC, UBE4A, RNF144A, AREL1, TRIM13, UBE4B, PIAS3, ARIH2, PDZRN3, MYCBP2, MGRN1, TRIM2, MKRN1, ARIH1, RNF19A, ZNF451, LTN1, FBXL3, MYLIP, RLIM, BFAR, UBR5, PIAS4, FBXO40, ANKIB1, NEURL1B, RNF111, FBXL12, RNF125, MSL2, KCMF1, SMURF1, PELI1, ZMIZ1, HECW2, GID4, CBLL1, RNF170, ZMIZ2, ITCH, FBXO30, ZNRF3, MED10, SYVN1, ZNRF1, RFFL, UBR3, TRIM71, MIB2, RNF145, RNF217, UBR1, ZNRF2, RNF144B, SHPRH, RNF180, SH3RF3, RNF165
MF	GO:0035257	nuclear hormone receptor binding	52/3415	3.00E-04	ACTN4, ARRB1, BRCA1, CALR, CEBPB, CTNNB1, DDX5, EP300, FHL2, FKBP4, FUS, HIF1A, HMGA1, ISL1, JUND, JUP, NKX3-1, PROX1, RAN, RARG, RB1, RNF4, SMARCE1, SRC, STAT1, STAT3, STAT5B, STRN, TACC1, TAF1, TCF7L2, VDR, NR4A3, NCOA3, NRIP1, ARID1A, LATS1, TRIP12, NCOR1, MED24, THRAP3, MED13, SLC30A9, NCOA2, TOB2, CNOT1, KDM1A, SIRT1, WBP2, FOXP1, NSD1, JMJD1C
MF	GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	10/3415	3.42E-04	DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, DUSP14, DUSP10, DUSP16, DUSP18
MF	GO:0003707	steroid hormone receptor activity	25/3415	3.89E-04	AR, ESR2, ESRRA, ESRRG, NR5A2, NR6A1, NR3C1, HNF4A, NKX3-1, PGR, PPARA, PPARD, RARG, RORA, RORB, NR2F2, THRA, NR2C2, NR1H2, VDR, NR4A3, NR1D2, PGRMC2, ABHD2, PAQR8

MF	GO:0000980	RNA polymerase II distal enhancer sequence-specific DNA binding	37/3415	5.78E-04	ACTB, CHD4, CREB1, ATF2, ATF6B, NR5A2, GATA2, HDAC2, HIVEP1, HNRNPC, HOXA5, HOXA7, HOXB5, HOXC4, JUN, MEF2C, KMT2A, NFKB1, NFYA, NFYB, POU4F1, SMARCC2, SMARCD2, SMARCE1, TAL1, TP53, YY1, BHLHE40, MBD2, MTA1, CLOCK, THRAP3, NR1D2, SIRT1, GATAD2B, CALCOCO1, BACH2
MF	GO:0005516	calmodulin binding	63/3415	6.72E-04	ADCY1, ADD1, FAS, ATP2B1, ATP2B4, CACNA1C, CALD1, CAMK4, CAMK2A, CAMK2D, CNN2, DAPK1, DDX5, EEF1A1, EGFR, EPB41, MKNK2, ITPKB, KCNN3, MARCKS, MBP, MYO1B, MYO1F, MYH9, MYH10, MYO1C, MYO1D, MYO5A, MYO6, MYO10, PDE1B, PHKA1, PHKG2, PPP3CA, PPP3R1, RGS2, RGS4, RGS16, SLC8A1, SLC9A1, SNTB1, SNTB2, SPTAN1, SPTBN1, STRN, VAMP2, SYT1, MKNK1, IQGAP1, SYT7, AKAP5, UNC13B, IQGAP2, CAMSAP2, STRN4, STRN3, MYO5C, KCNQ5, CAMK1D, MARCKSL1, CEP97, IQGAP3, CAMSAP1
MF	GO:0017124	SH3 domain binding	45/3415	7.30E-04	ABL1, ADAM10, ARHGAP1, CBL, CRK, DOCK3, FUT8, GJA1, GRB2, RAPGEF1, ILK, LYN, MAPT, PAK3, PTPN12, SH3BP2, SOS1, ADAM17, UVRAG, CCDC6, ADAM12, ADAM9, SYNGAP1, SYNJ1, SYNJ2, QKI, AKAP5, ABI2, WASF2, LANCL1, CIT, SHANK2, CD2AP, OSTF1, SOCS7, ERRFI1, ARHGAP17, RUFY2, PLSCR4, AFAP1, SGIP1, AFAP1L2, SIRPA, DAB2IP, FMN1
MF	GO:0048185	activin binding	10/3415	8.72E-04	ACVR1B, ACVR2B, FKBP1A, SMAD7, TGFBR1, TGFBR3, FSTL3, FST, SMURF1, ACVR1C
MF	GO:0003730	mRNA 3'-UTR binding	34/3415	1.13E-03	ZFP36L1, ZFP36L2, CRYZ, DDX5, ELAVL2, ELAVL1, FMR1, HNRNPC, HNRNPD, HNRNPU, PABPC3, PARN, RBMS2, TP53, ZFP36, FXR1, PABPC4, PUM1, SECISBP2L, IGF2BP1, IGF2BP3, RNPS1, HNRNPA0, CPEB3, LARP1, TARDBP, ZNF385A, SERBP1, RSL1D1, DAZAP1, PABPC1, RBM38, CPEB4, CPEB2
MF	GO:0061630	ubiquitin protein ligase activity	67/3415	1.33E-03	AMFR, CBL, CDC42, UBE2K, NEDD4, RAG1, RBBP6, RNF2, SIAH1, SIAH2, SKP1, VHL, TRIM25, RNF103, BTRC, UBE4A, RNF144A, AREL1, TRIM13, UBE4B, ARIH2, PDZRN3, MYCBP2, MGRN1, TRIM2, MKRN1, ARIH1, RNF19A, LTN1, FBXL3, MYLIP, RLIM, BFAR, UBR5, FBXO40, ANKIB1, NEURL1B, RNF111, FBXL12, RNF125, MSL2, KCMF1, SMURF1, PELI1, HECW2, GID4, CBLL1, RNF170, ITCH, FBXO30, ZNRF3, MED10, SYVN1, ZNRF1, RFFL, UBR3, TRIM71, MIB2, RNF145, RNF217, UBR1, ZNRF2, RNF144B, SHPRH, RNF180, SH3RF3, RNF165
MF	GO:0004879	nuclear receptor activity	21/3415	1.53E-03	AR, ESR2, ESRRA, ESRRG, NR5A2, NR6A1, NR3C1, NKX3-1, PGR, PPARA, PPARD, RARG, RORA, RORB, STAT3, NR2F2, THRA, NR1H2, VDR, NR4A3, NR1D2
MF	GO:0098531	transcription factor activity, direct ligand regulated sequence-specific DNA binding	21/3415	1.53E-03	AR, ESR2, ESRRA, ESRRG, NR5A2, NR6A1, NR3C1, NKX3-1, PGR, PPARA, PPARD, RARG, RORA, RORB, STAT3, NR2F2, THRA, NR1H2, VDR, NR4A3, NR1D2
MF	GO:0042578	phosphoric ester hydrolase activity	101/3415	1.67E-03	ACP1, CDC25A, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EYA4, GNB1, IMPA2, NT5E, PDE3A, PDE4D, PDE7A, PDE1B, ENPP1, PFKFB2, PFKFB3, PFKFB4, PLCL1, PLD1, PPM1B, PPP1CA, PPP1CB, PPP1CC, PPP1R3C, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PPP3R1, PPP6C, PRKAR1A, PRKAR2A, PTEN, PTPN1, PTPN4, PTPN11, PTPN12, PTPN14, PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRJ, PTPRK, PTPRN2, PTPRR, STYX, PTP4A1, SHOC2, PTP4A2, PPM1D, CDC14B, INPP4B, SYNJ1, SYNJ2, MTMR3, MTMR7, MTMR4, LPIN2, CTDSP2, CTDSPL, TAB1, DUSP14, PTPN21, PTPRT, DUSP10, SACM1L, PHLPP2, LPIN1, PHLPP1, PTPN18, PALD1, NT5DC3, CYCS, SSH1, DUSP23, PPP2R2D, GPCPD1, INPP5E, PPM1H, PDP2, CTDSP1, ENOPH1, PGAP1, DUSP16, SGPP1, SSH2, TIMM50, PLCD3, PPM1M, NANP, DUSP18, PPM1L, PPTC7, PLD6
MF	GO:0019207	kinase regulator activity	63/3415	1.76E-03	APC, CCND1, CALM1, CALM2, CALM3, CASP3, CCNA2, CCNC, CCND2, CCNF, CCNG2, CCNT1, CCNT2, CDKN1A, CDKN1B, DDX3X, EFNA5, MARK2, ERCC6, NCKAP1L, NRG1, IGF2, LRP6, NCK1, PAK2, PKIA, PRKAR1A, PRKAR2A, STK4, YWHAG, MADD, SOCS1, IQGAP1, SOCS2, KAT2B, GPRC5A, CCNE2, SOCS6, KLF4, SOCS5, ATG13, DAZAP2, TRIB1, TAB1, IBTK, GREM1, TRIB2, SOCS7, ETAA1, CCNJ, DUS2, CAMK2N1, KIDINS220, TAOK1, MLST8, WNK1, SH3BP5L, AFAP1L2, ITPRIP, WDR81, SMCR8, SPRED1, SPRED2
MF	GO:0033549	MAP kinase phosphatase activity	10/3415	1.80E-03	DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, DUSP14, DUSP10, DUSP16, DUSP18
MF	GO:0045309	protein phosphorylated amino acid binding	22/3415	1.80E-03	ABL1, ABL2, ARRB1, CBL, CRK, CRKL, GRB2, NEDD4, PIN1, MAPK1, MAPK3, PTPN11, RASA1, SH3BP2, SHC1, SYK, YWHAE, NCK2, BTRC, LDLRAP1, FBXW7, SCAF4
MF	GO:0061631	ubiquitin conjugating enzyme activity	18/3415	1.80E-03	CDC34, UBE2K, TAF1, UBE2D2, UBE2D3, UBE2G1, UBE2G2, UBE2H, UBE2L3, UBE2N, UBE2V1, UBE2E3, UBE2J1, UBE2R2, UBE2W, UBE2Q1, BIRC6, UBE2Z
MF	GO:0019887	protein kinase regulator activity	56/3415	2.07E-03	APC, CCND1, CALM1, CALM2, CALM3, CASP3, CCNA2, CCNC, CCND2, CCNF, CCNG2, CCNT1, CCNT2, CDKN1A, CDKN1B, DDX3X, EFNA5, MARK2, ERCC6, NCKAP1L, NRG1, IGF2, NCK1, PAK2, PKIA, PRKAR1A, PRKAR2A, STK4, YWHAG, MADD, SOCS1, IQGAP1, KAT2B, GPRC5A, CCNE2, ATG13, DAZAP2, TRIB1, TAB1, IBTK, GREM1, TRIB2, ETAA1, CCNJ, DUS2, CAMK2N1, KIDINS220, TAOK1, MLST8, WNK1, SH3BP5L, AFAP1L2, ITPRIP, SMCR8, SPRED1, SPRED2
MF	GO:0017048	Rho GTPase binding	55/3415	2.42E-03	ARHGDIA, ATP7A, FMNL1, CAV1, DIAPH1, DOCK3, DVL3, ECT2, EPS8, NCKAP1L, PAK2, PAK3, PKN2, SOS1, TIAM1, TNFAIP1, TRIO, IQGAP1, WASF1, KALRN, ARHGEF2, KIF3B, ROCK2, ARHGEF17, ABI2, FARP1, NET1, CDC42EP2, VAV3, NCKAP1, IQGAP2, AKAP13,

					PPP6R1, ARHGEF9, ARHGEF12, CORO1C, ARFIP2, PLEKHG3, STRN3, ANLN, ARHGAP17, RCC2, CDC42SE1, PLEKHG2, SIKE1, PREX2, KCTD10, PARD6B, ARHGEF39, FMNL3, FGD4, WHAMM, IQGAP3, PLEKHG4B, SPATA13
MF	GO:0008179	adenylate cyclase binding	9/3415	2.54E-03	ADCYAP1R1, CALM1, CALM2, CALM3, AKAP6, AKAP5, AKAP12, CAP2, CAP1
MF	GO:0042169	SH2 domain binding	17/3415	2.75E-03	ABL1, CRK, DAG1, KIT, SRC, SYK, SQSTM1, SYNGR3, CTR9, DLC1, NLK, LAX1, PAG1, AFAP1, SHCBP1, AFAP1L2, SH3PXD2B
MF	GO:0030695	GTPase regulator activity	85/3415	2.83E-03	ARHGAP1, ARHGDIA, ARRB1, BNIP2, ECT2, EIF5, GDI1, GNAQ, ARHGAP35, NCKAP1L, AGFG2, JUN, IPO5, TBC1D25, OPHN1, RALGDS, RANBP2, RAP1GDS1, RASA1, RGS2, RGS4, RGS16, RP2, SOS1, EVI5, RGS5, IQGAP1, NRP1, SYNGAP1, WASL, RABEP1, ARHGAP29, RASAL2, RAPGEF2, USP6NL, GIT2, TBC1D4, RABGAP1L, TNK2, DLC1, CDC42EP2, VAV3, SEC23A, NUP50, IQGAP2, ADAP1, TBC1D8, RASA3, TBC1D9B, TBC1D2B, RAP1GAP2, ARHGEF12, ACAP2, ARL2BP, RABGAP1, RAB3GAP2, TBC1D10B, SIPA1L1, GIT1, ASAP1, ERRFI1, ARHGAP17, TBC1D22B, DEPDC1, ARFGAP1, CDC42SE1, RALGAPA2, TBC1D24, SIPA1L2, RIC8A, ARHGAP28, PREX2, ARHGAP39, SESN2, SYDE2, ARHGAP18, ARHGAP12, ARAP2, AGAP1, TBC1D20, CPEB2, STXBP5, SIRPA, DAB2IP, FLCN
MF	GO:0048407	platelet-derived growth factor binding	8/3415	3.51E-03	COL1A1, COL1A2, COL3A1, COL4A1, COL5A1, PDGFA, PDGFB, PDGFRA
MF	GO:0061650	ubiquitin-like protein conjugating enzyme activity	18/3415	3.59E-03	CDC34, UBE2K, TAF1, UBE2D2, UBE2D3, UBE2G1, UBE2G2, UBE2H, UBE2L3, UBE2N, UBE2V1, UBE2E3, UBE2J1, UBE2R2, UBE2W, UBE2Q1, BIRC6, UBE2Z
MF	GO:0034212	peptide N-acetyltransferase activity	28/3415	3.81E-03	ATF2, CREBBP, EP300, KAT2A, HCFC1, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, SRCAP, KAT7, TAF9B, RSF1, ING3, KANSL2, NAA35, MEAF6, NAA40, NAA25, NAA50, EPC1, TADA2B, ESCO1, NAA30
MF	GO:0019199	transmembrane receptor protein kinase activity	29/3415	4.08E-03	ACVR1B, ACVR2B, AXL, BMPR1A, BMPR2, EFNA3, EGFR, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, FGFR3, FLT4, IGF1R, IGF2R, INSR, KIT, LTBP1, MET, NTRK3, PDGFRA, TGFBR1, TGFBR3, TYRO3, NRP1, LMTK2, ACVR1C
MF	GO:0019838	growth factor binding	44/3415	4.32E-03	ACVR1B, ACVR2B, BMPR1A, BMPR2, COL1A1, COL1A2, COL3A1, COL4A1, COL5A1, DUSP1, EGFR, ERBB2, FGFR3, FLT4, IGF1R, IGF2R, IGFBP1, IGFBP5, IL1R1, IL6R, IL6ST, INSR, ITGA6, ITGAV, LIFR, LTBP1, NTRK3, FURIN, PCSK6, PDGFA, PDGFB, PDGFRA, SORT1, SHC1, TGFBR1, TGFBR3, THBS1, PXDN, NRP1, OSMR, FSTL4, WFIKKN2, ACVR1C, CD109
MF	GO:0003727	single-stranded RNA binding	33/3415	4.99E-03	DDX3X, DLX2, EIF4B, FMR1, HNRNPC, HNRNPU, MSI1, PABPC3, POLR2D, RBMS2, ATXN1, CNBP, FXR1, CBX4, PABPC4, HNRNPDL, SYNCRIP, U2AF2, ZFR2, TARDBP, CBX6, LSM14A, AGO1, DAZAP1, PABPC1, RBMX, ZFR, STRBP, LARP4, MSI2, AGO3, AGO4, PATL1
MF	GO:0004713	protein tyrosine kinase activity	43/3415	4.99E-03	ABL1, ABL2, AXL, CSK, DYRK1A, EFNA3, EGFR, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, FER, FGFR3, FLT4, IGF1R, IGF2R, INSR, KIT, LYN, MET, NTRK3, PDGFRA, EIF2AK2, MAP2K4, SRC, SYK, TESK1, TYRO3, DYRK2, NRP1, BAZ1B, DYRK1B, MELK, HIPK3, TNK2, LMTK2, DSTYK, HIPK2, PEAK1, PKDCC, HIPK1
MF	GO:0001047	core promoter binding	22/3415	5.34E-03	CEBPB, DR1, ELK4, EZH2, NR3C1, MYC, NRF1, PAX6, POU2F1, STAT1, KLF10, TP53, UBTF, ZNF507, POGZ, ZNF451, AGO1, SOX8, RRN3, PRDM10, ZNF462, ZNF827
MF	GO:0042826	histone deacetylase binding	37/3415	5.45E-03	CCND1, PRDM1, CEBPB, CHD4, DNMT3B, KAT2A, HDAC2, HIF1A, HNRNPD, HES1, MEF2A, MEF2C, MEF2D, NKX3-1, PKN2, MAPK8, SRF, TAL1, TOP2B, TP53, YWHAE, NRIP1, KAT2B, MTA1, KLF4, NCOR1, HDAC9, WDTC1, SMG5, CBX5, NIPBL, BCOR, UHRF1BP1, MIER1, BRMS1L, NACC2, MIER3
MF	GO:0061733	peptide-lysine-N-acetyltransferase activity	25/3415	5.66E-03	ATF2, CREBBP, EP300, KAT2A, HCFC1, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, SRCAP, KAT7, TAF9B, RSF1, ING3, KANSL2, MEAF6, NAA40, NAA50, EPC1, TADA2B, ESCO1
MF	GO:0048156	tau protein binding	19/3415	5.72E-03	ACTB, DYRK1A, MARK2, EP300, FKBP4, GSK3B, HSPA2, SMAD2, MAP1A, MARK1, PIN1, PPP2CA, PPP2R2A, PRKAA1, SNCA, TAOK2, ROCK2, TAOK1, TTBK2
MF	GO:0031624	ubiquitin conjugating enzyme binding	15/3415	6.05E-03	PPARA, SIAH1, SIAH2, ZMYM2, RNF144A, ARIH2, ARIH1, RNF19A, DCUN1D1, ANKIB1, RNF125, DCUN1D3, RNF217, RNF144B, RNF180
MF	GO:0033613	activating transcription factor binding	30/3415	6.15E-03	CREB1, ATF2, CREBBP, CTNNB1, EP300, GABPA, HCFC1, HNF4A, HOXC4, ISL1, JUN, LMO2, SMAD2, MEF2A, MEF2C, MEF2D, MYC, PTMA, RB1, RBL2, TBX3, BHLHE40, LDB1, LDB2, NCOR1, ZNF516, MGA, SIN3A, HIPK2, SETD3
MF	GO:0051427	hormone receptor binding	55/3415	6.41E-03	ACTN4, ARRB1, BRCA1, CALR, CEBPB, CTNNB1, DDX5, EP300, FHL2, FKBP4, FUS, GNAS, HIF1A, HMGA1, ISL1, JUND, JUP, NKX3-1, PROX1, PTPN11, RAN, RARG, RB1, RNF4, SMARCE1, SRC, STAT1, STAT3, STAT5B, STRN, TACC1, TAF1, TCF7L2, VDR, NR4A3,

					NCOA3, NRIP1, ARID1A, SOCS2, LATS1, TRIP12, NCOR1, MED24, THRAP3, MED13, SLC30A9, NCOA2, TOB2, CNOT1, KDM1A, SIRT1, WBP2, FOXP1, NSD1, JMJD1C
MF	GO:0051019	mitogen-activated protein kinase binding	13/3415	6.50E-03	ABL1, ARRB2, MAPK14, DUSP1, NBR1, PTAFR, PTPRJ, PPM1D, IQGAP1, TNIP1, TAB1, DUSP10, SIRT1
MF	GO:0030374	nuclear receptor transcription coactivator activity	25/3415	6.77E-03	ACTN4, FGF2, HMGA1, PPARA, PPARD, RARG, RNF4, SS18, THRA, NR1H2, VDR, NCOA3, MED24, THRAP3, MED13, NR1D2, SLC30A9, NCOA2, KDM1A, DCAF6, ATXN7L3, ZMIZ1, CALCOCO1, WDR77, ZMIZ2
MF	GO:0061578	Lys63-specific deubiquitinase activity	8/3415	6.82E-03	CYLD, ATXN3, PSMD14, STAMBP, DESI2, OTUD4, YOD1, BRCC3
MF	GO:0035091	phosphatidylinositol binding	69/3415	6.89E-03	EPB41, HIP1, ITPR1, ITPR2, KCNJ2, MAPT, MARK1, MYO1B, MYO10, PIK3C2A, PITPNA, PLD1, TWF1, SLC9A1, SNX1, SYT1, TLN1, SNX3, IQGAP1, SYT7, CYTH3, SH3PXD2A, ZFYVE16, SNX17, FCHSD2, IQGAP2, ADAP1, SNX13, ZCCHC14, PASK, ZFYVE26, ACAP2, PHLDA3, ARFIP2, SGK3, PITPNB, APPL1, LDLRAP1, PITPNC1, DAPP1, ASAP1, VPS36, ANKFY1, ZFYVE1, TPCN1, SYTL2, ZCCHC2, PLEKHB2, GOLPH3L, LAPTM4B, PARD3, ESYT2, WDFY1, PITPNM2, PLEKHA4, PLEKHA1, AIDA, MAPKAP1, PLEKHF2, PLEKHA8, SESTD1, OSBPL8, FCHO2, ARAP2, AMER1, DAB2IP, SH3PXD2B, SNX19, SNX30
MF	GO:0047485	protein N-terminus binding	36/3415	6.89E-03	ACOX1, ACTN4, ARF6, ATM, CALM1, CALM2, CALM3, DCN, EPB41, ERCC2, ERCC6, GTF2H3, RBPJ, MECP2, MEN1, NPAT, PPP1CC, PEX5, SMARCE1, SNCA, SUV39H1, TERT, TP53, TSC1, RND2, NCOA3, SYNGR3, PIAS3, PDLIM5, EXOC5, SNF8, MAU2, HYPK, NIPBL, DCTN4, TBL1XR1
MF	GO:0070491	repressing transcription factor binding	26/3415	6.98E-03	RUNX2, CHD4, CTNNB1, EIF4E, GATA6, GTF2A1, HDAC2, RBPJ, MYC, NFYB, PPARA, PPARD, SKI, STAT1, STAT3, TCF3, TCF7L2, TLE1, TLE4, MTA1, HDAC9, TCERG1, CBX5, SIN3A, MIER1, MIER3
MF	GO:0008080	N-acetyltransferase activity	31/3415	7.22E-03	ATF2, CREBBP, EP300, KAT2A, HCFC1, SMARCE1, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, SRCAP, KAT7, TAF9B, RSF1, ING3, KANSL2, NAA35, MEAF6, GNPNAT1, NAA40, NAA25, NAA50, EPC1, TADA2B, ESCO1, NAA30, NAT8L
MF	GO:0003725	double-stranded RNA binding	27/3415	7.31E-03	ADAR, ADARB1, DDX3X, EIF4A1, EIF4B, ELAVL1, FMR1, HNRNPU, MBNL1, OAS2, EIF2AK2, STAU1, TFRC, FXR1, DDX21, ZFR2, DICER1, LSM14A, AGO1, STAU2, ZFR, DUS2, STRBP, YRDC, MTDH, AGO3, AGO4
MF	GO:0004402	histone acetyltransferase activity	24/3415	7.33E-03	ATF2, CREBBP, EP300, KAT2A, HCFC1, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, SRCAP, KAT7, TAF9B, RSF1, ING3, KANSL2, MEAF6, NAA40, NAA50, EPC1, TADA2B
MF	GO:0051087	chaperone binding	34/3415	7.47E-03	AMFR, ATP7A, BAG1, BAK1, CALR, SCARB2, CDC25A, CDKN1B, FN1, HES1, DNAJB2, DNAJA1, HSPA2, HSPA5, MAPT, DNAJB9, TERT, TP53, TSC1, KSR1, USP13, BAG4, DNAJA2, SLC25A17, HYOU1, DNAJB4, GET4, DNAJC10, FNIP2, DNAJC1, GRPEL1, SYVN1, FNIP1, GRPEL2
MF	GO:0001221	transcription cofactor binding	18/3415	7.47E-03	CCNT2, CDC5L, CREB1, FOXC1, FOXO1, FOXO3, HDGF, PPARA, RORA, TEAD1, TERT, MAFK, NR4A3, PER3, PER2, KLF4, VGLL4, CHD6
MF	GO:0005154	epidermal growth factor receptor binding	15/3415	7.47E-03	CBL, HBEGF, FER, GRB2, HIP1, ITGA5, ATXN2, SHC1, SNX1, TGFA, SOCS5, TNK2, VAV3, AGR2, EPGN
MF	GO:0097718	disordered domain specific binding	15/3415	7.47E-03	CALM1, CALM2, CALM3, CTNNB1, DFFB, FN1, GAPDH, GJA1, HSPA2, SMAD2, MYO5A, RB1, TP53, NCOA3, PPIL1
MF	GO:0016407	acetyltransferase activity	36/3415	7.47E-03	ATF2, CREBBP, DBT, EP300, KAT2A, HADHA, HCFC1, PAFAH1B2, SMARCE1, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, SRCAP, KAT7, TAF9B, RSF1, ING3, KANSL2, NAA35, MEAF6, GNPNAT1, CASD1, NAA40, LPCAT1, NAA25, NAA50, EPC1, TADA2B, ESCO1, NAA30, NAT8L
MF	GO:0070851	growth factor receptor binding	42/3415	7.50E-03	CBL, HBEGF, FER, FGF1, FGF2, FGF5, GATA3, GRB2, HIP1, IL1R1, IL1RAP, IL6R, IL6ST, ITGA5, LYN, PDGFA, PDGFB, PDGFRA, PTEN, PTPRJ, ATXN2, SHC1, SNX1, SRC, ADAM17, TGFA, VEGFA, SOCS5, FGF19, TNK2, VAV3, AGR2, FRS2, CD2AP, FLRT2, GREM1, NPTN, ERAP1, TIMM50, DAB2IP, TXLNA, EPGN
MF	GO:0005161	platelet-derived growth factor receptor binding	9/3415	7.65E-03	IL1R1, ITGA5, LYN, PDGFA, PDGFB, PDGFRA, PTEN, PTPRJ, VEGFA
MF	GO:0060590	ATPase regulator activity	17/3415	8.16E-03	ATP1B1, BAG1, DNAJB2, DNAJA1, TSC1, DNAJA2, DNAJB4, HSPBP1, DNAJC15, DNAJC10, FNIP2, DNAJC1, GRPEL1, FNIP1, DNAJC24, GRPEL2, TOR1AIP2

MF	GO:0035591	signaling adaptor activity	28/3415	8.66E-03	ARHGAP1, CRK, CRKL, EPS8, GAB1, GRB2, LASP1, NCK1, PTPN11, SH3BP2, SHC1, SRC, NCK2, SOCS2, KSR1, SPAG9, SH2B3, TOB1, VAV3, FRS2, AKAP13, MAPK8IP3, SH2B1, LDLRAP1, PAG1, MAVS, AFAP1L2, DAB2IP
MF	GO:0044390	ubiquitin-like protein conjugating enzyme binding	16/3415	9.01E-03	PPARA, RPS3, SIAH1, SIAH2, ZMYM2, RNF144A, ARIH2, ARIH1, RNF19A, DCUN1D1, ANKIB1, RNF125, DCUN1D3, RNF217, RNF144B, RNF180
MF	GO:0048365	Rac GTPase binding	25/3415	9.01E-03	ARHGDIA, ATP7A, FMNL1, CAV1, DOCK3, DVL3, EPS8, NCKAP1L, PAK2, PAK3, TIAM1, IQGAP1, WASF1, ARHGEF2, ABI2, FARP1, VAV3, NCKAP1, IQGAP2, CORO1C, ARFIP2, ARHGAP17, RCC2, PREX2, SPATA13
MF	GO:0005178	integrin binding	41/3415	9.90E-03	ACTN4, ADAM10, ANXA7, DST, CALR, COL3A1, COL5A1, CXADR, S1PR3, EGFR, EMP2, FBN1, FGF1, FGF2, FN1, NRG1, IGF2, ILK, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, LYN, MMP14, MYH9, PRKCA, PXN, CX3CL1, SRC, SYK, ADAM17, THBS1, TIMP2, TLN1, VCAM1, SEMA7A, ADAM9, GPNMB, ADAMTS5, ADAM22
MF	GO:0005096	GTPase activator activity	74/3415	1.18E-02	ARHGAP1, ARHGDIA, ARRB1, BNIP2, ECT2, GDI1, GNAQ, ARHGAP35, NCKAP1L, AGFG2, JUN, TBC1D25, OPHN1, RANBP2, RAP1GDS1, RASA1, RGS2, RGS4, RGS16, RP2, SOS1, EVI5, RGS5, IQGAP1, NRP1, SYNGAP1, RABEP1, ARHGAP29, RASAL2, RAPGEF2, USP6NL, GIT2, TBC1D4, RABGAP1L, DLC1, CDC42EP2, VAV3, SEC23A, NUP50, ADAP1, TBC1D8, RASA3, TBC1D9B, TBC1D2B, RAP1GAP2, ARHGEF12, ACAP2, RABGAP1, RAB3GAP2, TBC1D10B, SIPA1L1, GIT1, ASAP1, ERRFI1, ARHGAP17, TBC1D22B, DEPDC1, ARFGAP1, RALGAPA2, TBC1D24, SIPA1L2, RIC8A, ARHGAP28, PREX2, ARHGAP39, SYDE2, ARHGAP18, ARHGAP12, ARAP2, AGAP1, TBC1D20, STXBP5, DAB2IP, FLCN
MF	GO:0043425	bHLH transcription factor binding	13/3415	1.21E-02	RUNX2, CREBBP, ISL1, LMO2, TCF4, TCF3, TWIST1, USF2, BHLHE40, HAND1, KDM1A, SIRT1, NCAPG2
MF	GO:0017137	Rab GTPase binding	51/3415	1.25E-02	AP1G1, ARHGAP1, GDI1, RAB8A, MYO5A, NSF, TBC1D25, RABGGTB, EVI5, ULK1, MADD, USP6NL, RIMS3, TBC1D4, DENND4B, RABGAP1L, GOLGA5, UNC13B, KIF3A, TBC1D8, RHOBTB3, RAB11FIP2, DENND3, TBC1D9B, ERC1, TBC1D2B, BICD2, ACAP2, RABGAP1, RAB3GAP2, TBC1D10B, AP3M1, TRAPPC4, ANKFY1, WDR44, SYTL2, TBC1D22B, TMEM127, MLPH, HPS6, RAB11FIP1, SH3BP5L, RAB11FIP4, MICALL1, RAB3IP, TBC1D20, STXBP5, RIMS4, SMCR8, DENND5B, DENND6A
MF	GO:0005159	insulin-like growth factor receptor binding	9/3415	1.31E-02	ARRB1, CRK, GNAS, IGF2, INSR, SHC1, YWHAG, SOCS1, SOCS2
MF	GO:0050321	tau-protein kinase activity	11/3415	1.34E-02	CSNK1D, DYRK1A, MARK2, GSK3B, MARK1, PHKG2, PRKAA1, TAOK2, ROCK2, TAOK1, TTBK2
MF	GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	64/3415	1.48E-02	ALAS1, CPT1A, ATF2, CREBBP, DBT, EP300, KAT2A, HADHA, HCFC1, PAFAH1B2, ACSM3, SCP2, SMARCE1, SOAT1, ELOVL4, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, LPGAT1, LPCAT3, SPTLC1, CERS1, SRCAP, KAT7, ZDHHC17, ZDHHC5, ZDHHC8, ABHD5, TAF9B, RSF1, ING3, KANSL2, SPTLC3, ZDHHC7, AGPAT3, ELOVL5, NAA35, ZDHHC6, MEAF6, GNPNAT1, CASD1, ELOVL6, NAA40, LPCAT1, NAA25, NAA50, EPC1, ZDHHC18, TADA2B, ESCO1, NAA30, MBOAT2, LCLAT1, CERS6, ZDHHC20, ZDHHC23, ZDHHC22, NAT8L, ZDHHC21
MF	GO:0001102	RNA polymerase II activating transcription factor binding	20/3415	1.53E-02	CREB1, ATF2, CREBBP, CTNNB1, EP300, HNF4A, ISL1, JUN, LMO2, RB1, RBL2, TBX3, BHLHE40, LDB1, LDB2, NCOR1, MGA, SIN3A, HIPK2, SETD3
MF	GO:0005547	phosphatidylinositol-3,4,5-trisphosphate binding	16/3415	1.62E-02	MYO1B, MYO10, IQGAP1, CYTH3, ZFYVE16, FCHSD2, IQGAP2, ADAP1, PHLDA3, DAPP1, ASAP1, ZFYVE1, PLEKHB2, PARD3, MAPKAP1, ARAP2
MF	GO:1901981	phosphatidylinositol phosphate binding	47/3415	1.71E-02	HIP1, KCNJ2, MAPT, MARK1, MYO1B, MYO10, TWF1, SLC9A1, SYT1, SNX3, IQGAP1, SYT7, CYTH3, SH3PXD2A, ZFYVE16, FCHSD2, IQGAP2, ADAP1, SNX13, ZFYVE26, ACAP2, PHLDA3, ARFIP2, LDLRAP1, DAPP1, ASAP1, VPS36, ANKFY1, ZFYVE1, TPCN1, SYTL2, PLEKHB2, GOLPH3L, LAPTM4B, PARD3, PLEKHA4, PLEKHA1, MAPKAP1, PLEKHA8, SESTD1, OSBPL8, FCHO2, ARAP2, AMER1, DAB2IP, SH3PXD2B, SNX19
MF	GO:0070411	I-SMAD binding	7/3415	1.71E-02	CTNNB1, SMAD2, SMAD4, SMAD6, SMAD7, TGFBR1, SMURF1
MF	GO:0001882	nucleoside binding	99/3415	1.71E-02	ACTN4, ADA, AK4, TRIM23, ARF1, ARF6, RHOA, RHOB, ARL1, CDC42, DAPK1, DRG2, EEF1A1, EIF2S3, EIF5, FKBP4, GBP1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, ARHGAP35, GSPT1, GUCY1A2, INSR, KRAS, RAB8A, NRAS, OPA1, POLA1, RAB1A, RAB3B, RAB5A, RAB5B, RALB, RAN, RAP1B, RAP2A, RAP2B, RP2, SCG5, RND2, SUCLG2, RAB11B, EFTUD2, RAB28, RAB36, EIF5B, MFN2, ARFRP1, TUBB4A, GNA13, HBS1L, IFI44L, RAB31, RHOBTB3, SEPHS1, RAB21, RHOQ, ARFIP2, ATL3, RAB30, NKIRAS2, NKIRAS1, EHD4, AK3, NIN, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, MIEF1, GNL3L, DIRAS2, MFN1, SAR1A, RAB22A, RAB40C, RAP2C, RHOU, RRAGD, RRAGC, ATL2, RAB17, POLR1B, GFM1, RASL10B, RAB39B, AGAP1, IRGQ, ARL8A, DIRAS1, GIMAP1, RAB12, ARL5B, OARD1, RAB15
MF	GO:0051018	protein kinase A binding	19/3415	1.73E-02	CSK, GSK3B, PKIA, PRKAR1A, PRKAR2A, RDX, RPS3, AKAP17A, WASF1, AKAP6, AKAP5, AKAP12, AKAP9, WASF2, ARFGEF2, AKAP13, AKAP11, AKAP10, ACBD3

MF	GO:0043394	proteoglycan binding	15/3415	1.78E-02	COL5A1, CTSB, CTSS, FN1, LRP1, NID1, PTPRC, PTPRF, THBS1, CHRD, GPNMB, FST, HPSE, COL5A3, AGRN
MF	GO:0004712	protein serine/threonine/tyrosine kinase activity	17/3415	1.78E-02	ACVR2B, MAPK14, DYRK1A, MAP3K9, PAK3, MAPK1, MAPK3, MAPK9, RPS6KB1, MAP2K4, AURKA, TESK1, DYRK2, DYRK1B, AURKB, TNK2, DSTYK
MF	GO:0043021	ribonucleoprotein complex binding	40/3415	1.91E-02	DDX3X, DDX5, EIF2S1, EIF4B, ETF1, EZH2, FMR1, HNRNPU, HSPA5, LETM1, PIM1, PPP1CA, ABCE1, SNRPA, SNRPB2, UNG, SECISBP2L, EIF1, CPSF6, CPEB3, LARP1, CBX5, LETMD1, LTN1, SND1, SEC61A1, NMD3, MTRF1L, YTHDF1, PTCD3, RBM23, EIF5A2, XPO5, CPEB4, ITCH, UNK, TIMM50, CPEB2, RICTOR, YTHDF3
MF	GO:0070412	R-SMAD binding	11/3415	1.91E-02	DDX5, JUN, SMAD2, SMAD4, SMAD6, MEN1, PAX6, ZC3H3, TRIM33, PMEPA1, SMURF1
MF	GO:0005001	transmembrane receptor protein tyrosine phosphatase activity	9/3415	1.98E-02	PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRK, PTPRN2, PTPRR, PTPRT
MF	GO:0019198	transmembrane receptor protein phosphatase activity	9/3415	1.98E-02	PTPRB, PTPRC, PTPRD, PTPRF, PTPRG, PTPRK, PTPRN2, PTPRR, PTPRT
MF	GO:0043024	ribosomal small subunit binding	9/3415	1.98E-02	DDX3X, EIF4B, PIM1, ABCE1, UNG, EIF1, LARP1, PTCD3, CPEB2
MF	GO:0051010	microtubule plus-end binding	9/3415	1.98E-02	APC, DST, PAFAH1B1, STIM1, CLIP2, KIF2C, MAPRE3, CLASP1, TTBK2
MF	GO:0070717	poly-purine tract binding	13/3415	2.19E-02	DDX3X, FMR1, HNRNPU, PABPC3, RBMS2, ATXN1, PABPC4, HNRNPDL, SYNCRIP, DAZAP1, PABPC1, LARP4, PATL1
MF	GO:0032452	histone demethylase activity	12/3415	2.47E-02	JARID2, KDM5A, KDM6A, KDM4A, KDM5B, KDM2A, KDM1A, PHF8, KDM6B, KDM3B, JMJD1C, KDM1B
MF	GO:0001883	purine nucleoside binding	96/3415	2.47E-02	ADA, AK4, TRIM23, ARF1, ARF6, RHOA, RHOB, ARL1, CDC42, DAPK1, DRG2, EEF1A1, EIF2S3, EIF5, FKBP4, GBP1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, ARHGAP35, GSPT1, GUCY1A2, INSR, KRAS, RAB8A, NRAS, OPA1, RAB1A, RAB3B, RAB5A, RAB5B, RALB, RAN, RAP1B, RAP2A, RAP2B, RP2, SCG5, RND2, SUCLG2, RAB11B, EFTUD2, RAB28, RAB36, EIF5B, MFN2, ARFRP1, TUBB4A, GNA13, HBS1L, IFI44L, RAB31, RHOBTB3, SEPHS1, RAB21, RHOQ, ARFIP2, ATL3, RAB30, NKIRAS2, NKIRAS1, EHD4, AK3, NIN, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, MIEF1, GNL3L, DIRAS2, MFN1, SAR1A, RAB22A, RAB40C, RAP2C, RHOU, RRAGD, RRAGC, ATL2, RAB17, GFM1, RASL10B, RAB39B, AGAP1, IRGQ, ARL8A, DIRAS1, GIMAP1, RAB12, ARL5B, OARD1, RAB15
MF	GO:0005543	phospholipid binding	106/3415	2.54E-02	JAG1, ANXA7, AXL, SCARB2, EPB41, NR5A2, GOT2, ARHGAP35, HIP1, ITPR1, ITPR2, KCNJ2, MAP1B, MAPT, MARK1, MME, MYO1B, MYO10, NME4, OPA1, OPHN1, ATP8B1, PIK3C2A, PITPNA, PLD1, PTAFR, TWF1, SHC1, SLC9A1, SNCA, SNX1, SPTBN1, VAMP2, SYT1, THBS1, TLN1, SNX3, IQGAP1, CPNE3, SYT7, CYTH3, PCYT1B, SH3PXD2A, RAPGEF2, ZFYVE16, SNX17, C2CD5, FCHSD2, UNC13B, IQGAP2, ADAP1, SNX13, ZCCHC14, PASK, SYT11, ZFYVE26, ACAP2, PHLDA3, ARFIP2, SGK3, PITPNB, APPL1, LDLRAP1, PITPNC1, MYOF, DAPP1, ASAP1, VPS36, GLTP, ANKFY1, SYT17, ZFYVE1, TPCN1, SYTL2, ZCCHC2, PLEKHB2, GOLPH3L, LAPTM4B, NSFL1C, PARD3, SMURF1, GRAMD1B, ESYT2, WDFY1, PITPNM2, PLEKHA4, PLEKHA1, AIDA, MAPKAP1, PLEKHF2, SGIP1, PLEKHA8, MICALL1, SESTD1, OSBPL8, FCHO2, ARAP2, AGAP1, SYT2, AMER1, CPNE8, DAB2IP, CPNE2, SH3PXD2B, SNX19, SNX30
MF	GO:0031490	chromatin DNA binding	36/3415	2.59E-02	ACTB, ACTN4, BCL6, PRDM1, CENPA, RCC1, CHD4, EP300, EZH2, FOXO3, HDAC2, HMGN2, HNRNPC, HNRNPU, KDM5A, SMARCC2, SMARCD2, SMARCE1, SRF, STAT3, THRA, KDM6A, ZNF711, PRDM2, HMGA2, MBD2, CLOCK, HMGN4, CTCF, KDM6B, SUZ12, WBP2, GRHL1, KDM3B, GATAD2B, JMJD1C
MF	GO:0140030	modification-dependent protein binding	42/3415	2.59E-02	ATRX, FMR1, DNAJB2, LYN, KMT2A, MLLT3, RAD23B, KDM5A, TAF1, VCP, BRD3, CBX4, SQSTM1, KDM4A, TNIP1, ZMYND11, SPIN1, MTF2, TAB2, PHF8, PSME4, CBX5, SUZ12, UBQLN2, UBQLN1, ING4, ATAD2B, ING3, MBTD1, NCAPG2, PHIP, KMT2E, UBQLN4, OTUD7B, BRCC3, GLYR1, CBX2, ANKRD13A, WDR81, SPIN4, PHF13, RNF168
MF	GO:0003924	GTPase activity	83/3415	2.76E-02	TRIM23, ARF1, ARF6, RHOA, RHOB, ARL1, CDC42, DDX3X, DRG2, EEF1A1, EIF2S3, EIF5, GBP1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, GNB1, GNG7, ARHGAP35, GSPT1, KRAS, RAB8A, NRAS, OPA1, RAB1A, RAB3B, RAB5A, RAB5B, RALB, RAN, RAP1B, RAP2A, RAP2B, RASA1, RGS2, RGS4, RGS16, RND2, RGS5, RAB11B, EFTUD2, RAB28, RAB36, EIF5B, MFN2, ARFRP1, TUBB4A, GNA13, HBS1L, RAB31, RHOBTB3, RAB21, RHOQ, ATL3, RAB30, NKIRAS2, NKIRAS1, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, DIRAS2, MFN1, SAR1A, RAB22A, RAB40C, RAP2C, RHOU, RRAGD, RRAGC, ATL2, RAB17, GFM1, RASL10B, RAB39B, AGAP1, ARL8A, DIRAS1, RAB12, RAB15

MF	GO:0001046	core promoter sequence-specific DNA binding	17/3415	2.76E-02	CEBPB, EZH2, NRF1, PAX6, POU2F1, STAT1, KLF10, TP53, UBTF, ZNF507, POGZ, ZNF451, SOX8, RRN3, PRDM10, ZNF462, ZNF827
MF	GO:0008138	protein tyrosine/serine/threonine phosphatase activity	17/3415	2.76E-02	DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, PTEN, STYX, PTP4A1, CDC14B, DUSP14, DUSP10, SSH1, DUSP23, DUSP16, SSH2, DUSP18
MF	GO:0005024	transforming growth factor beta-activated receptor activity	8/3415	3.07E-02	ACVR1B, ACVR2B, BMPR1A, BMPR2, LTBP1, TGFBR1, TGFBR3, ACVR1C
MF	GO:0070063	RNA polymerase binding	25/3415	3.09E-02	BRCA1, CCNT1, CCNT2, STOM, ERBB2, GTF2E1, HNRNPU, NEDD4, PKN2, ZFP36, PABPN1, NCOA3, CTR9, ANP32B, RPRD2, AGO1, WAC, RRN3, RPRD1A, SCAF4, SCAF1, PCIF1, CDC73, ELOF1, SPTY2D1
MF	GO:0019208	phosphatase regulator activity	30/3415	3.09E-02	CALM1, CALM2, CALM3, ENSA, PPP1R12A, PPP1R12B, PPP1R2, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, EIF2AK2, SET, STYX, SHOC2, PHACTR2, ARPP19, FRS2, LMTK2, ANKLE2, PPP1R16B, PPP1R12C, BMP2K, PPP2R2D, ANP32E, PPP1R15B, FAM122A, PPP4R2, BOD1L1, PPP1R37
MF	GO:0030295	protein kinase activator activity	26/3415	3.09E-02	CALM1, CALM2, CALM3, CCNT1, CCNT2, CDKN1A, DDX3X, EFNA5, MARK2, ERCC6, NCKAP1L, NRG1, IGF2, PAK2, STK4, MADD, IQGAP1, GPRC5A, DAZAP2, TAB1, GREM1, ETAA1, TAOK1, MLST8, WNK1, AFAP1L2
MF	GO:0035258	steroid hormone receptor binding	29/3415	3.09E-02	ARRB1, BRCA1, CALR, CEBPB, CTNNB1, DDX5, EP300, FHL2, FKBP4, FUS, ISL1, NKX3-1, RAN, RB1, RNF4, SRC, STAT3, STAT5B, STRN, TACC1, NR4A3, NCOA3, NRIP1, LATS1, CNOT1, KDM1A, WBP2, FOXP1, NSD1
MF	GO:0001103	RNA polymerase II repressing transcription factor binding	14/3415	3.28E-02	CHD4, GATA6, GTF2A1, HDAC2, RBPJ, PPARA, PPARD, STAT3, TCF7L2, MTA1, TCERG1, SIN3A, MIER1, MIER3
MF	GO:0016410	N-acyltransferase activity	34/3415	3.36E-02	ALAS1, ATF2, CREBBP, EP300, KAT2A, HCFC1, SMARCE1, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, CERS1, SRCAP, KAT7, TAF9B, RSF1, ING3, KANSL2, NAA35, MEAF6, GNPNAT1, NAA40, NAA25, NAA50, EPC1, TADA2B, ESCO1, NAA30, CERS6, NAT8L
MF	GO:0032549	ribonucleoside binding	95/3415	3.47E-02	AK4, TRIM23, ARF1, ARF6, RHOA, RHOB, ARL1, CDC42, DAPK1, DRG2, EEF1A1, EIF2S3, EIF5, FKBP4, GBP1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, ARHGAP35, GSPT1, GUCY1A2, INSR, KRAS, RAB8A, NRAS, OPA1, RAB1A, RAB3B, RAB5A, RAB5B, RALB, RAN, RAP1B, RAP2A, RAP2B, RP2, SCG5, RND2, SUCLG2, RAB11B, EFTUD2, RAB28, RAB36, EIF5B, MFN2, ARFRP1, TUBB4A, GNA13, HBS1L, IFI44L, RAB31, RHOBTB3, SEPHS1, RAB21, RHOQ, ARFIP2, ATL3, RAB30, NKIRAS2, NKIRAS1, EHD4, AK3, NIN, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, MIEF1, GNL3L, DIRAS2, MFN1, SAR1A, RAB22A, RAB40C, RAP2C, RHOU, RRAGD, RRAGC, ATL2, RAB17, POLR1B, GFM1, RASL10B, RAB39B, AGAP1, IRGQ, ARL8A, DIRAS1, GIMAP1, RAB12, ARL5B, RAB15
MF	GO:1990782	protein tyrosine kinase binding	29/3415	3.56E-02	BMPR2, CBL, CRK, EPHA4, FNTA, GJA1, NRG1, NCK1, NEDD9, PTEN, PTPN1, PTPN11, PTPN14, SHC1, TIAM1, TP53, YWHAG, EIF3A, SQSTM1, CPNE3, SOCS5, DAZAP2, SH2B3, TOB1, FRS2, SH2B1, PITPNM2, PITPNM3, SIRPA
MF	GO:0032550	purine ribonucleoside binding	94/3415	3.58E-02	AK4, TRIM23, ARF1, ARF6, RHOA, RHOB, ARL1, CDC42, DAPK1, DRG2, EEF1A1, EIF2S3, EIF5, FKBP4, GBP1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, ARHGAP35, GSPT1, GUCY1A2, INSR, KRAS, RAB8A, NRAS, OPA1, RAB1A, RAB3B, RAB5A, RAB5B, RALB, RAN, RAP1B, RAP2A, RAP2B, RP2, SCG5, RND2, SUCLG2, RAB11B, EFTUD2, RAB28, RAB36, EIF5B, MFN2, ARFRP1, TUBB4A, GNA13, HBS1L, IFI44L, RAB31, RHOBTB3, SEPHS1, RAB21, RHOQ, ARFIP2, ATL3, RAB30, NKIRAS2, NKIRAS1, EHD4, AK3, NIN, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, MIEF1, GNL3L, DIRAS2, MFN1, SAR1A, RAB22A, RAB40C, RAP2C, RHOU, RRAGD, RRAGC, ATL2, RAB17, GFM1, RASL10B, RAB39B, AGAP1, IRGQ, ARL8A, DIRAS1, GIMAP1, RAB12, ARL5B, RAB15
MF	GO:0005525	GTP binding	93/3415	3.72E-02	AK4, TRIM23, ARF1, ARF6, RHOA, RHOB, ARL1, CDC42, DAPK1, DRG2, EEF1A1, EIF2S3, EIF5, FKBP4, GBP1, GNAI2, GNAI3, GNAL, GNAQ, GNAS, ARHGAP35, GSPT1, GUCY1A2, INSR, KRAS, RAB8A, NRAS, OPA1, RAB1A, RAB3B, RAB5A, RAB5B, RALB, RAN, RAP1B, RAP2A, RAP2B, RP2, SCG5, RND2, SUCLG2, RAB11B, EFTUD2, RAB28, RAB36, EIF5B, MFN2, ARFRP1, TUBB4A, GNA13, HBS1L, IFI44L, RAB31, RHOBTB3, SEPHS1, RAB21, RHOQ, ARFIP2, ATL3, RAB30, NKIRAS2, NKIRAS1, EHD4, AK3, NIN, DNAJC27, RAB14, RAB6B, RAB23, RAB8B, GNL3L, DIRAS2, MFN1, SAR1A, RAB22A, RAB40C, RAP2C, RHOU, RRAGD, RRAGC, ATL2, RAB17, GFM1, RASL10B, RAB39B, AGAP1, IRGQ, ARL8A, DIRAS1, GIMAP1, RAB12, ARL5B, RAB15
MF	GO:0005158	insulin receptor binding	10/3415	3.94E-02	IGF1R, IGF2, ENPP1, PTPN1, PTPN11, SHC1, SNX1, SRC, IRS2, PHIP
MF	GO:0004714	transmembrane receptor protein tyrosine kinase activity	21/3415	3.98E-02	AXL, EFNA3, EGFR, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, ERBB2, FGFR3, FLT4, IGF1R, IGF2R, INSR, KIT, MET, NTRK3, PDGFRA, TYRO3, NRP1, LMTK2

MF	GO:0035035	histone acetyltransferase binding	12/3415	4.21E-02	CEBPB, CREB1, EGR1, EPAS1, HIF1A, MEF2A, MTF1, PAX6, STAT1, TP53, NR4A3, CITED2
MF	GO:0071889	14-3-3 protein binding	12/3415	4.21E-02	ARRB2, ZFP36L1, PPP1R12A, PRKCE, ZFP36, IRS2, KSR1, DDIT4, TBC1D22B, SIK1, DAB2IP, FOXK1
MF	GO:0031690	adrenergic receptor binding	9/3415	4.23E-02	ADRB1, ARRB1, ARRB2, GNAS, NEDD4, PDE4D, AKAP5, RAPGEF2, ARRDC3
MF	GO:0002162	dystroglycan binding	6/3415	4.25E-02	DAG1, VCL, AGR2, CLASP1, FKRP, AGRN
MF	GO:0070016	armadillo repeat domain binding	6/3415	4.25E-02	STRN, TCF7L2, CNOT1, STRN4, STRN3, CALCOCO1
MF	GO:0071837	HMG box domain binding	8/3415	4.43E-02	GATA3, HOXA3, HOXC4, JUN, MEF2C, PAX3, PAX6, PRRX1
MF	GO:0001784	phosphotyrosine residue binding	15/3415	4.43E-02	ABL1, ABL2, CBL, CRK, CRKL, GRB2, MAPK1, MAPK3, PTPN11, RASA1, SH3BP2, SHC1, SYK, NCK2, LDLRAP1
MF	GO:0031434	mitogen-activated protein kinase kinase binding	7/3415	4.48E-02	ARRB1, PIN1, KSR1, TAOK2, TRIB1, TRIB2, DAB2IP
MF	GO:0016746	transferase activity, transferring acyl groups	68/3415	4.54E-02	ACLY, ALAS1, CPT1A, ATF2, CREBBP, DBT, EP300, KAT2A, HADHA, HCFC1, HMGCS2, PAFAH1B2, ACSM3, SCP2, SMARCE1, SOAT1, ELOVL4, TAF1, KAT6A, DPF3, DPF1, NCOA3, KAT2B, GTF3C4, CLOCK, LPGAT1, LPCAT3, SPTLC1, CERS1, SRCAP, ATE1, KAT7, ZDHHC17, ZDHHC5, ZDHHC8, ABHD5, TAF9B, RSF1, ING3, KANSL2, SPTLC3, ZDHHC7, AGPAT3, KMT2C, ELOVL5, NAA35, ZDHHC6, MEAF6, GNPNAT1, CASD1, ELOVL6, NAA40, LPCAT1, NAA25, NAA50, EPC1, ZDHHC18, TADA2B, ESCO1, NAA30, MBOAT2, LCLAT1, CERS6, ZDHHC20, ZDHHC23, ZDHHC22, NAT8L, ZDHHC21
MF	GO:0004860	protein kinase inhibitor activity	21/3415	4.54E-02	CASP3, CDKN1A, CDKN1B, NCK1, PKIA, PRKAR1A, PRKAR2A, YWHAG, SOCS1, KAT2B, TRIB1, IBTK, TRIB2, DUS2, CAMK2N1, WNK1, SH3BP5L, ITPRIP, SMCR8, SPRED1, SPRED2
MF	GO:0005088	Ras guanyl-nucleotide exchange factor activity	39/3415	4.54E-02	ADRB1, RCC1, DOCK3, ECT2, EPS8, RAPGEF1, SOS1, TIAM1, TRIO, MADD, KALRN, ARHGEF2, RALGPS1, RAPGEF2, ARHGEF17, DENND4B, FARP1, NET1, RAPGEF3, VAV3, AKAP13, DENND3, RGL1, ARHGEF9, ARHGEF12, RAB3GAP2, PLEKHG3, TRAPPC4, PLEKHG2, PREX2, SH3BP5L, ARHGEF39, RAB3IP, FGD4, SMCR8, PLEKHG4B, DENND5B, DENND6A, SPATA13
MF	GO:0008187	poly-pyrimidine tract binding	13/3415	4.54E-02	FMR1, HNRNPC, HNRNPU, MSI1, PABPC3, RBMS2, ATXN1, PABPC4, U2AF2, DAZAP1, PABPC1, MSI2, PATL1
MF	GO:0019210	kinase inhibitor activity	22/3415	4.54E-02	CASP3, CDKN1A, CDKN1B, LRP6, NCK1, PKIA, PRKAR1A, PRKAR2A, YWHAG, SOCS1, KAT2B, TRIB1, IBTK, TRIB2, DUS2, CAMK2N1, WNK1, SH3BP5L, ITPRIP, SMCR8, SPRED1, SPRED2
MF	GO:0018024	histone-lysine N-methyltransferase activity	16/3415	4.56E-02	EZH1, EZH2, MEN1, KMT2A, SUV39H1, PRDM2, KMT2D, SETD1A, KMT2B, SUZ12, SETD5, KMT2C, NSD1, SETD7, SETDB2, SETD3
MF	GO:1990841	promoter-specific chromatin binding	17/3415	4.81E-02	PRDM1, DDX5, EGR1, EZH2, FOXC1, HDAC2, HNRNPU, ISL1, FOXO4, NUP98, RBL2, STAT1, TP53, KLF4, SUZ12, CHD7, PRDM15
MF	GO:0032451	demethylase activity	14/3415	4.97E-02	JARID2, KDM5A, KDM6A, KDM4A, KDM5B, KDM2A, KDM1A, PHF8, KDM6B, KDM3B, ALKBH4, ALKBH5, JMJD1C, KDM1B
KEGG	hsa05205	Proteoglycans in cancer	86/1652	3.71E-10	ACTB, AKT2, ANK1, FAS, RHOA, CCND1, CAMK2A, CAMK2D, CASP3, CAV1, CBL, CD44, CDC42, CDKN1A, COL1A1, COL1A2, MAPK14, CTNNB1, DCN, DDX5, HBEGF, EGFR, EIF4B, ELK1, ERBB2, FGF2, FLNB, FN1, GAB1, GRB2, HIF1A, IGF1R, IGF2, ITGA5, ITGAV, ITGB1, ITPR1, ITPR2, KRAS, SMAD2, MET, MYC, PPP1R12A, PPP1R12B, NRAS, PIK3CB, PPP1CA, PPP1CB, PPP1CC, PRKCA, MAPK1, MAPK3, PTCH1, PTPN11, PXN, RDX, RPS6KB1, SDC2, SDC4, SLC9A1, SOS1, SRC, STAT3, THBS1, TIAM1, TIMP3, TP53, TWIST1, VEGFA, WNT7B, WNT2B, FZD5, FZD3, FZD1, FZD4, FZD6, IQGAP1, ROCK2, AKT3, VAV3, FRS2, HPSE, ARHGEF12, PDCD4, WNT4, PPP1R12C
KEGG	hsa04510	Focal adhesion	78/1652	1.88E-07	ACTB, ACTN4, AKT2, RHOA, CCND1, BCL2, CAPN2, CAV1, CCND2, CDC42, COL1A1, COL1A2, COL4A1, COL4A2, COL4A5, COL4A6, COL6A2, CRK, CRKL, CTNNB1, DIAPH1, EGFR, ELK1, ERBB2, FLNB, FLT4, FN1, GRB2, RAPGEF1, ARHGAP35, GSK3B, IGF1R, ILK, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, JUN, LAMA4, LAMC1, LAMC2, MET, PPP1R12A, PPP1R12B, PAK2, PAK3, PDGFA, PDGFB, PDGFRA, PIK3CB, PPP1CA, PPP1CB, PPP1CC, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, PTEN, PXN, RAP1B, SHC1, SOS1, SRC, THBS1, THBS3, TLN1, VCL, VEGFA, ITGA8, ROCK2, AKT3, VAV3, MYL12A, PIP5K1C, PPP1R12C
KEGG	hsa04520	Adherens junction	37/1652	3.16E-07	ACP1, ACTB, ACTN4, RHOA, CDC42, CREBBP, CTNNA1, CTNNB1, CTNND1, EGFR, EP300, ERBB2, FER, IGF1R, INSR, SMAD4, MET, MAPK1, MAPK3, PTPN1, PTPRB, PTPRF, PTPRJ, SNAI2, SNAI1, SRC, TCF7, TCF7L2, TGFBR1, VCL, IQGAP1, WASF1, WASL, WASF2, NLK, PARD3, SSX2IP

KEGG	hsa04012	ErbB signaling pathway	41/1652	6.05E-07	ABL1, ABL2, AKT2, CAMK2A, CAMK2D, CBL, CDKN1A, CDKN1B, CRK, CRKL, HBEGF, EGFR, ELK1, ERBB2, GAB1, GRB2, GSK3B, NRG1, JUN, KRAS, MYC, NCK1, NRAS, PAK2, PAK3, PIK3CB, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, RPS6KB1, MAP2K4, SHC1, SOS1, SRC, STAT5B, TGFA, NCK2, AKT3, NRG4
KEGG	hsa05165	Human papillomavirus infection	111/1652	6.05E-07	JAG1, AKT2, APC, FAS, ATM, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, ATR, BAK1, CCND1, CASP3, CCNA2, CCND2, CDC42, CDK6, CDKN1A, CDKN1B, CHD4, COL1A1, COL1A2, COL4A1, COL4A2, COL4A5, COL4A6, COL6A2, CREB1, CREBBP, CTNNB1, DLG3, DVL3, EGFR, EP300, FOXO1, FN1, GNAS, GRB2, GSK3B, HDAC2, HLA-B, HES1, IFNAR1, IFNAR2, RBPJ, IKBKB, ITGA6, IRF1, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, KRAS, LAMA4, LAMC1, LAMC2, NFKB1, NOTCH2, NRAS, PIK3CB, PKM, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, MAPK1, MAPK3, EIF2AK2, PTEN, PTGER4, PXN, RB1, RBL2, RPS6KB1, SOS1, STAT1, STAT2, TCF7, TCF7L2, TERT, THBS1, THBS3, TP53, TRAF3, TSC1, VEGFA, WNT7B, WNT2B, FZD5, FZD3, FZD1, FZD4, FZD6, ITGA8, FADD, ATP6V0D1, CCNE2, CREB5, AKT3, BCAP31, HEYL, ATP6V1D, WNT4, HES6, PPP2R2D, PARD3, CREB3L2, PARD6B, ATP6V0E2
KEGG	hsa04010	MAPK signaling pathway	100/1652	1.24E-06	AKT2, FAS, ARRB1, ARRB2, BDNF, CACNA1B, CACNA1C, CACNA1E, CACNA2D1, CACNB1, CASP3, CDC42, ATF2, CRK, CRKL, MAPK14, CSF1, DUSP1, DUSP5, DUSP6, DUSP7, DUSP8, DUSP9, EFNA3, EFNA5, EGFR, ELK1, ELK4, ERBB2, FGF1, FGF2, FGF5, FGFR3, FLNB, FLT4, MKNK2, GRB2, HSPA2, IGF1R, IGF2, IKBKB, IL1R1, IL1RAP, INSR, IRAK1, JUN, JUND, KIT, KRAS, MAPT, MAX, MEF2C, MAP3K1, MAP3K3, MAP3K4, MET, KITLG, MYC, NFKB1, NRAS, PAK2, PDGFA, PDGFB, PDGFRA, PPM1B, PPP3CA, PPP3R1, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, PTPRR, RAP1B, RASA1, RPS6KA3, MAP2K4, SOS1, SRF, STK4, TGFA, TGFBR1, TP53, VEGFA, MKNK1, RPS6KA4, RPS6KA5, TAOK2, MAP4K4, RAPGEF2, FGF19, AKT3, TAB1, MAP3K2, DUSP10, TAB2, MAPK8IP3, NLK, TAOK1, DUSP16
KEGG	hsa04722	Neurotrophin signaling pathway	50/1652	2.79E-06	ABL1, AKT2, RHOA, ARHGDIA, BCL2, BDNF, CALM1, CALM2, CALM3, CAMK4, CAMK2A, CAMK2D, CDC42, CRK, CRKL, MAPK14, FOXO3, GAB1, GRB2, RAPGEF1, GSK3B, IKBKB, IRAK1, IRAK2, JUN, KRAS, MAP3K1, MAP3K3, NFKB1, NRAS, NTRK3, PIK3CB, MAPK1, MAPK3, MAPK8, MAPK9, PTPN11, RAP1B, RPS6KA3, SORT1, SHC1, SOS1, TP53, YWHAE, RPS6KA5, AKT3, SH2B3, FRS2, SH2B1, KIDINS220
KEGG	hsa04141	Protein processing in endoplasmic reticulum	65/1652	2.91E-06	AMFR, BAG1, BAK1, BCL2, CALR, CANX, CAPN2, ATF6B, EIF2S1, DNAJB2, DNAJA1, HSPA2, HSPA5, ATXN3, PRKCSH, MAPK8, MAPK9, EIF2AK2, RAD23B, RRBP1, SEL1L, SKP1, SSR1, SSR3, UBE2D2, UBE2D3, UBE2G1, UBE2G2, VCP, XBP1, SEC24C, EDEM1, HERPUD1, BCAP31, UBE4B, DNAJA2, SEC23A, HYOU1, SEC24A, MAN1A2, SEC63, UBXN4, GANAB, TRAM1, HSPBP1, SEC31B, EIF2AK1, SEC61A1, UBQLN2, UBQLN1, DERL2, UBE2J1, DNAJC10, DNAJB12, YOD1, NPLOC4, NSFL1C, SAR1A, UGGT1, UBQLN4, DNAJC1, EDEM3, DNAJC5, TXNDC5, SYVN1
KEGG	hsa05211	Renal cell carcinoma	33/1652	1.08E-05	AKT2, CDC42, CDKN1A, CREBBP, CRK, CRKL, EP300, EPAS1, GAB1, GRB2, RAPGEF1, HIF1A, JUN, KRAS, MET, NRAS, PAK2, PAK3, PDGFB, PIK3CB, MAPK1, MAPK3, PTPN11, RAP1B, SOS1, TGFA, VEGFA, VHL, CUL2, AKT3, EGLN2, EGLN3, FLCN
KEGG	hsa04360	Axon guidance	66/1652	1.13E-05	ABL1, RHOA, BMP7, BMPR2, CAMK2A, CAMK2D, CDC42, CFL1, CFL2, EFNA3, EFNA5, EFNB1, EFNB2, EPHA4, EPHA7, EPHB2, EPHB3, EPHB4, GNAI2, GNAI3, GSK3B, ILK, ITGB1, KRAS, L1CAM, ABLIM1, LIMK1, MET, NCK1, NEO1, NRAS, PAK2, PAK3, PIK3CB, PPP3CA, PPP3R1, PRKCA, MAPK1, MAPK3, PTCH1, PTPN11, RASA1, ROBO1, SRC, FZD3, NCK2, SEMA7A, NRP1, NTN1, ROCK2, SEMA3E, SEMA3A, SEMA4B, MYL12A, ARHGEF12, WNT4, SSH1, SEMA4C, PARD3, DPYSL5, RGMA, SEMA6A, LRRC4, PARD6B, SSH2, PLXNA4
KEGG	hsa01521	EGFR tyrosine kinase inhibitor resistance	36/1652	1.17E-05	AKT2, AXL, BCL2, BCL2L1, EGFR, EIF4E, ERBB2, FGF2, FGFR3, FOXO3, GAB1, GRB2, GSK3B, NRG1, IGF1R, IL6R, KRAS, MET, NRAS, PDGFA, PDGFB, PDGFRA, PIK3CB, PRKCA, MAPK1, MAPK3, PTEN, RPS6KB1, SHC1, SOS1, SRC, STAT3, TGFA, VEGFA, AKT3, BCL2L11
KEGG	hsa05210	Colorectal cancer	38/1652	1.36E-05	AKT2, APC, RHOA, BAK1, CCND1, BCL2, CASP3, CDKN1A, CTNNB1, EGFR, GRB2, GSK3B, JUN, KRAS, SMAD2, SMAD4, MLH1, MYC, NRAS, PIK3CB, MAPK1, MAPK3, MAPK8, MAPK9, RALB, RALGDS, RPS6KB1, SOS1, TCF7, TCF7L2, TGFA, TGFBR1, TP53, AKT3, BCL2L11, APPL1, BBC3, CYCS
KEGG	hsa04933	AGE-RAGE signaling pathway in diabetic complications	42/1652	1.73E-05	AKT2, CCND1, BCL2, CASP3, CDC42, CDKN1B, COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL4A5, COL4A6, MAPK14, DIAPH1, EDN1, EGR1, FOXO1, FN1, JUN, KRAS, SMAD2, SMAD4, NFKB1, NRAS, SERPINE1, PIK3CB, PIM1, PRKCA, PRKCE, MAPK1, MAPK3, MAPK8, MAPK9, STAT1, STAT3, STAT5B, TGFBR1, VCAM1, VEGFA, AKT3, PLCD3
KEGG	hsa04068	FoxO signaling pathway	51/1652	1.73E-05	AKT2, ATM, CCND1, BCL6, CCND2, CCNG2, CDKN1A, CDKN1B, CREBBP, MAPK14, CSNK1E, S1PR1, EGFR, EP300, FOXO1, FOXO3, GRB2, IGF1R, IKBKB, IL7R, INSR, KRAS, SMAD4, FOXO4, NRAS, PIK3CB, PRKAA1, PRKAB2, MAPK1, MAPK3, MAPK8, MAPK9, PTEN, RAG1, RBL2, SOD2, SOS1, STAT3, STK4, TGFBR1, IRS2, TNFSF10, AKT3, BCL2L11, KLF2, PLK2, GABARAPL2, SIRT1, SGK3, NLK, SETD7
KEGG	hsa04810	Regulation of actin cytoskeleton	75/1652	1.73E-05	ACTB, ACTN4, APC, RHOA, CDC42, CFL1, CFL2, CRK, CRKL, DIAPH1, EGFR, FGF1, FGF2, FGF5, FGFR3, FN1, ARHGAP35, NCKAP1L, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, KRAS, LIMK1, MYH9, MYH10, PPP1R12A, PPP1R12B, NRAS, PAK2, PAK3, PDGFA, PDGFB, PDGFRA, PIK3CB, PIP4K2A, PPP1CA, PPP1CB, PPP1CC, MAPK1, MAPK3, PXN, RDX, SLC9A1, SOS1, SRC, TIAM1, VCL, ITGA8, IQGAP1, WASF1, WASL, ROCK2, FGF19, ARPC5, ACTR2, ARPC2, ABI2, WASF2, VAV3, MYL12A, GNA13, NCKAP1, IQGAP2, ARHGEF12, PIP5K1C, CYFIP2, GIT1, SSH1, PPP1R12C, SSH2, IQGAP3, SPATA13
KEGG	hsa04218	Cellular senescence	58/1652	1.73E-05	AKT2, SLC25A6, ATM, ATR, CCND1, ZFP36L1, ZFP36L2, CALM1, CALM2, CALM3, CAPN2, CCNA2, CCND2, CDC25A, CDK6, CDKN1A, CHEK1, MAPK14, E2F3, E2F5, FOXM1, FOXO1, FOXO3, HLA-B, ITPR1, ITPR2, KRAS, SMAD2, MYBL2, MYC, NFKB1, NRAS,

					SERPINE1, PIK3CB, PPP1CA, PPP1CB, PPP1CC, PPP3CA, PPP3R1, MAPK1, MAPK3, PTEN, RAD1, RB1, RBL2, TGFBR1, TP53, TSC1, VDAC2, SQSTM1, BTRC, CCNE2, AKT3, HIPK3, SIRT1, HIPK2, LIN54, HIPK1
KEGG	hsa05130	Pathogenic Escherichia coli infection	69/1652	1.89E-05	ABL1, ACTB, FAS, ARF1, ARF6, RHOA, BAK1, CASP3, CDC42, MAPK14, GAPDH, NCKAP1L, IKBKB, IL1R1, IL18, IRAK1, ITGB1, JUN, MYO1B, MYO1F, MYH9, MYH10, MYO1C, MYO1D, MYO5A, MYO6, MYO10, NCK1, NFKB1, CLDN11, PAK2, PAK3, MAPK1, MAPK3, MAPK8, MAPK9, PTPN11, RAB1A, RPS3, SRC, TMBIM6, NCK2, TNFSF10, FADD, WASF1, WASL, ARHGEF2, CYTH3, CYTH1, ROCK2, SEC24C, ABCF2, ARPC5, ACTR2, ARPC2, WASF2, TUBB4A, TAB1, GNA13, NCKAP1, SEC24A, TMED10, TAB2, ARHGEF12, CYFIP2, CYCS, MYO5C, CLDN23, WIPF2
KEGG	hsa04390	Hippo signaling pathway	58/1652	1.89E-05	ACTB, APC, CCND1, BMP7, BMPR1A, BMPR2, CCND2, CSNK1D, CSNK1E, CTNNA1, CTNNB1, DLG3, DVL3, FGF1, GSK3B, SMAD2, SMAD4, SMAD7, MYC, NF2, SERPINE1, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, SNAI2, TCF7, TCF7L2, TEAD1, TEAD3, TGFBR1, WNT7B, WNT2B, YWHAE, YWHAG, FZD5, FZD3, FZD1, FZD4, FZD6, BTRC, LIMD1, LATS1, DLG5, WWC1, LATS2, BBC3, WNT4, MOB1A, PPP2R2D, PARD3, PARD6B, AMOT, CRB2, BMP8A
KEGG	hsa05131	Shigellosis	82/1652	1.89E-05	ACTB, ACTN4, AKT2, ARF1, ARF6, RHOA, ATM, BCL2, BCL2L1, CAPN2, CD44, CDC42, CRK, CRKL, MAPK14, DIAPH1, EGFR, FOXO1, FOXO3, GSK3B, HK1, HK2, IKBKB, IL1R1, IL18, ILK, ITGA5, ITGB1, ITPR1, ITPR2, JUN, FOXO4, NFKB1, PIK3CB, PRKCE, MAPK1, MAPK3, MAPK8, MAPK9, PXN, RPS6KB1, SKP1, SRC, TLN1, TP53, UBE2D2, UBE2D3, UBE2N, UBE2V1, VCL, SQSTM1, WASF1, BTRC, WASL, ARHGEF2, RPS6KA5, CYTH3, CYTH1, ATG5, ROCK2, AKT3, ARPC5, ACTR2, ARPC2, WASF2, TNIP1, NOD1, TAB1, RBCK1, MYL12A, CBX3, GABARAPL2, ATG14, FNBP1, TAB2, CYCS, FNBP1L, ATG16L1, RRAGD, RRAGC, AKT1S1, PLCD3
KEGG	hsa05224	Breast cancer	55/1652	2.10E-05	JAG1, AKT2, APC, BAK1, CCND1, BRCA1, CDK6, CDKN1A, CTNNB1, DVL3, E2F3, EGFR, ERBB2, ESR2, FGF1, FGF2, FGF5, FLT4, GRB2, GSK3B, HES1, IGF1R, JAG2, JUN, KIT, KRAS, LRP6, MYC, NOTCH2, NRAS, PGR, PIK3CB, MAPK1, MAPK3, PTEN, RB1, RPS6KB1, SHC1, SOS1, TCF7, TCF7L2, TP53, WNT7B, WNT2B, FZD5, FZD3, NCOA3, FZD1, FZD4, FZD6, FGF19, AKT3, HEYL, WNT4, DLL4
KEGG	hsa04140	Autophagy - animal	52/1652	2.24E-05	AKT2, BCL2, BCL2L1, CTSB, DAPK1, EIF2S1, HIF1A, IGF1R, ITPR1, KRAS, LAMP2, RAB8A, NRAS, PIK3CB, PPP2CA, PRKAA1, MAPK1, MAPK3, MAPK8, MAPK9, PTEN, RAB1A, RPS6KB1, TSC1, UVRAG, ULK1, IRS2, SQSTM1, MTMR3, MTMR4, ATG5, ATG13, AKT3, ATG7, GABARAPL2, ATG14, ATG2A, SH3GLB1, ZFYVE1, DDIT4, STX17, ATG16L1, ATG2B, TP53INP2, RRAGD, RRAGC, MLST8, ATG9A, ATG10, AKT1S1, RAB39B, SMCR8
KEGG	hsa04910	Insulin signaling pathway	52/1652	2.24E-05	ACACA, AKT2, CALM1, CALM2, CALM3, CBL, CRK, CRKL, EIF4E, ELK1, FOXO1, FLOT2, MKNK2, GRB2, RAPGEF1, GSK3B, GYS1, HK1, HK2, IKBKB, INSR, KRAS, NRAS, PHKA1, PHKG2, PIK3CB, PPP1CA, PPP1CB, PPP1CC, PPP1R3C, PRKAA1, PRKAB2, PRKAR1A, PRKAR2A, MAPK1, MAPK3, MAPK8, MAPK9, PTPN1, PTPRF, PYGB, RPS6KB1, SHC1, SOS1, TSC1, MKNK1, SOCS1, IRS2, SOCS2, AKT3, RHOQ, SOCS4
KEGG	hsa04151	PI3K-Akt signaling pathway	109/1652	2.41E-05	AKT2, CCND1, BCL2, BCL2L1, BDNF, BRCA1, CCND2, CDK6, CDKN1A, CDKN1B, COL1A1, COL1A2, COL4A1, COL4A2, COL4A5, COL4A6, COL6A2, CREB1, ATF2, ATF6B, CSF1, EFNA3, EFNA5, EGFR, EIF4B, EIF4E, ERBB2, FGF1, FGF2, FGF5, FGFR3, FOXO3, FLT4, FN1, GNB1, GNG7, GRB2, GSK3B, GYS1, IFNAR1, IFNAR2, IGF1R, IGF2, IKBKB, IL6R, IL7R, INSR, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, KIT, KRAS, LAMA4, LAMC1, LAMC2, MCL1, MET, KITLG, MYB, MYC, NFKB1, NRAS, PDGFA, PDGFB, PDGFRA, PIK3CB, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PRKAA1, PRKCA, PKN2, MAPK1, MAPK3, PRLR, PTEN, RBL2, RPS6KB1, SOS1, SYK, TGFA, THBS1, THBS3, TP53, TSC1, VEGFA, YWHAE, YWHAG, ITGA8, CCNE2, OSMR, CREB5, FGF19, AKT3, BCL2L11, PHLPP2, PHLPP1, SGK3, DDIT4, PPP2R2D, GNB4, MLST8, CREB3L2, PIK3AP1
KEGG	hsa05215	Prostate cancer	40/1652	3.00E-05	AKT2, AR, CCND1, BCL2, CDKN1A, CDKN1B, CREB1, CREBBP, CTNNB1, E2F3, EGFR, EP300, ERBB2, FOXO1, GRB2, GSK3B, IGF1R, IKBKB, KRAS, NFKB1, NKX3-1, NRAS, PDGFA, PDGFB, PDGFRA, PIK3CB, MAPK1, MAPK3, PTEN, RB1, SOS1, TCF7, TCF7L2, ZEB1, TGFA, TP53, CCNE2, CREB5, AKT3, CREB3L2
KEGG	hsa04350	TGF-beta signaling pathway	39/1652	3.21E-05	ACVR1B, ACVR2B, RHOA, BMP7, BMPR1A, BMPR2, CREBBP, DCN, E2F5, EP300, FBN1, ID4, LTBP1, SMAD2, SMAD4, SMAD6, SMAD7, MYC, NEO1, PPP2CA, PPP2R1A, MAPK1, MAPK3, RPS6KB1, SKP1, TFDP1, TGFBR1, TGIF1, THBS1, CHRD, ZFYVE16, FST, GREM1, RGMA, SMURF1, TGIF2, THSD4, ACVR1C, BMP8A
KEGG	hsa05225	Hepatocellular carcinoma	60/1652	3.25E-05	ACTB, AKT2, APC, BAK1, CCND1, BCL2L1, CDK6, CDKN1A, CTNNB1, DVL3, E2F3, EGFR, ELK1, GAB1, GRB2, GSK3B, GSTM3, IGF1R, IGF2, KRAS, LRP6, SMAD2, SMAD4, MET, MYC, NRAS, PIK3CB, PRKCA, MAPK1, MAPK3, PTEN, RB1, RPS6KB1, SHC1, SMARCA2, SMARCC2, SMARCD2, SMARCE1, SOS1, TCF7, TCF7L2, TERT, TGFA, TGFBR1, TP53, WNT7B, WNT2B, FZD5, FZD3, DPF3, DPF1, ARID1A, FZD1, FZD4, FZD6, AKT3, WNT4, ARID1B, TXNRD3, ARID2
KEGG	hsa04550	Signaling pathways regulating pluripotency of stem cells	53/1652	3.37E-05	ACVR1B, ACVR2B, AKT2, APC, ZFHX3, BMPR1A, BMPR2, MAPK14, CTNNB1, DUSP9, DVL3, FGF2, FGFR3, GRB2, GSK3B, ID4, IGF1R, IL6ST, ISL1, JARID2, KRAS, LIFR, SMAD2, SMAD4, MYC, NRAS, OTX1, PAX6, PIK3CB, MAPK1, MAPK3, SKIL, STAT3, TBX3, TCF3, TCF7, WNT7B, WNT2B, FZD5, FZD3, KAT6A, FZD1, FZD4, FZD6, KLF4, HAND1, AKT3, PCGF3, WNT4, RIF1, SMARCAD1, PCGF5, ACVR1C
KEGG	hsa04211	Longevity regulating pathway	37/1652	4.88E-05	ADCY1, ADCY6, ADCY9, AKT2, CAMK4, CREB1, ATF2, ATF6B, EIF4E, FOXO1, FOXO3, IGF1R, INSR, KRAS, NFKB1, NRAS, PIK3CB, PRKAA1, PRKAB2, RPS6KB1, SOD2, TP53, TSC1, ULK1, IRS2, ATG5, CREB5, ATG13, AKT3, SIRT1, APPL1, ADIPOR1, CREB3L2, ADIPOR2, SESN2, AKT1S1, SESN3

KEGG	hsa05212	Pancreatic cancer	33/1652	5.00E-05	AKT2, BAK1, CCND1, BCL2L1, CDC42, CDK6, CDKN1A, E2F3, EGFR, ERBB2, IKBKB, KRAS, SMAD2, SMAD4, NFKB1, PIK3CB, PLD1, MAPK1, MAPK3, MAPK8, MAPK9, RAD51, RALB, RALGDS, RB1, RPS6KB1, STAT1, STAT3, TGFA, TGFBR1, TP53, VEGFA, AKT3
KEGG	hsa04917	Prolactin signaling pathway	31/1652	5.70E-05	AKT2, CCND1, CCND2, MAPK14, ESR2, FOXO3, GRB2, GSK3B, IRF1, KRAS, NFKB1, NRAS, PIK3CB, MAPK1, MAPK3, MAPK8, MAPK9, PRLR, SHC1, SOS1, SRC, STAT1, STAT3, STAT5B, SOCS1, SOCS2, SOCS6, SOCS5, AKT3, SOCS7, SOCS4
KEGG	hsa03015	mRNA surveillance pathway	39/1652	6.47E-05	ETF1, FUS, GSPT1, MSI1, NCBP1, PABPC3, PNN, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, UPF1, PABPN1, PABPC4, SMG7, NXF1, HBS1L, PAPOLA, RNPS1, CPSF6, DDX19B, SMG1, CSTF2T, SMG5, TARDBP, UPF2, DAZAP1, PABPC1, CPSF2, DDX19A, WDR33, PPP2R2D, CPSF7, MSI2, BCL2L2-PABPN1
KEGG	hsa05213	Endometrial cancer	27/1652	6.85E-05	AKT2, APC, BAK1, CCND1, CDKN1A, CTNNA1, CTNNB1, EGFR, ELK1, ERBB2, FOXO3, GRB2, GSK3B, ILK, KRAS, MLH1, MYC, NRAS, PIK3CB, MAPK1, MAPK3, PTEN, SOS1, TCF7, TCF7L2, TP53, AKT3
KEGG	hsa05214	Glioma	32/1652	9.55E-05	AKT2, BAK1, CCND1, CALM1, CALM2, CALM3, CAMK4, CAMK2A, CAMK2D, CDK6, CDKN1A, E2F3, EGFR, GRB2, IGF1R, KRAS, NRAS, PDGFA, PDGFB, PDGFRA, PIK3CB, PRKCA, MAPK1, MAPK3, PTEN, RB1, SHC1, SOS1, TGFA, TP53, AKT3, CAMK1D
KEGG	hsa05222	Small cell lung cancer	37/1652	1.01E-04	AKT2, BAK1, CCND1, BCL2, BCL2L1, CASP3, CDK6, CDKN1A, CDKN1B, COL4A1, COL4A2, COL4A5, COL4A6, E2F3, FHIT, FN1, IKBKB, ITGA6, ITGA3, ITGAV, ITGB1, LAMA4, LAMC1, LAMC2, MAX, MYC, NFKB1, PIK3CB, PTEN, RB1, TP53, TRAF1, TRAF3, CCNE2, TRAF4, AKT3, CYCS
KEGG	hsa05220	Chronic myeloid leukemia	32/1652	1.25E-04	ABL1, AKT2, BAK1, CCND1, BCL2L1, RUNX1, CBL, CDK6, CDKN1A, CDKN1B, CRK, CRKL, E2F3, GRB2, HDAC2, IKBKB, KRAS, SMAD4, MYC, NFKB1, NRAS, PIK3CB, MAPK1, MAPK3, PTPN11, RB1, SHC1, SOS1, STAT5B, TGFBR1, TP53, AKT3
KEGG	hsa04912	GnRH signaling pathway	37/1652	1.27E-04	ADCY1, ADCY6, ADCY9, CACNA1C, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, CDC42, MAPK14, HBEGF, EGFR, EGR1, ELK1, GNAQ, GNAS, GRB2, ITPR1, ITPR2, JUN, KRAS, MAP3K1, MAP3K3, MAP3K4, MMP14, NRAS, PLD1, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, MAP2K4, SOS1, SRC, MAP3K2
KEGG	hsa01522	Endocrine resistance	38/1652	1.90E-04	ADCY1, ADCY6, ADCY9, JAG1, AKT2, CCND1, BCL2, CDKN1A, CDKN1B, MAPK14, HBEGF, E2F3, EGFR, ERBB2, ESR2, GNAS, GRB2, IGF1R, JAG2, JUN, KRAS, NOTCH2, NRAS, PIK3CB, MAPK1, MAPK3, MAPK8, MAPK9, RB1, RPS6KB1, SHC1, SOS1, SRC, TP53, NCOA3, NCOR1, AKT3, DLL4
KEGG	hsa05163	Human cytomegalovirus infection	72/1652	2.08E-04	ADCY1, ADCY6, ADCY9, AKT2, FAS, RHOA, BAK1, CCND1, CALM1, CALM2, CALM3, CALR, CASP3, CDK6, CDKN1A, CREB1, ATF2, ATF6B, CRK, CRKL, MAPK14, CTNNB1, E2F3, EGFR, ELK1, GNAI2, GNAI3, GNAQ, GNAS, GNB1, GNG7, GRB2, GSK3B, HLA-B, IKBKB, IL1R1, IL6R, ITGAV, ITPR1, ITPR2, KRAS, MYC, NFKB1, NRAS, PDGFRA, PIK3CB, PPP3CA, PPP3R1, PRKCA, MAPK1, MAPK3, PTGER4, PXN, RB1, RPS6KB1, CX3CL1, SOS1, SRC, STAT3, TP53, TSC1, VEGFA, FADD, ROCK2, CREB5, AKT3, GNA13, AKAP13, ARHGEF12, CYCS, GNB4, CREB3L2
KEGG	hsa04926	Relaxin signaling pathway	46/1652	3.23E-04	ADCY1, ADCY6, ADCY9, AKT2, ARRB1, ARRB2, COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL4A5, COL4A6, CREB1, ATF2, ATF6B, MAPK14, EDN1, EGFR, GNAI2, GNAI3, GNAS, GNB1, GNG7, GRB2, JUN, KRAS, SMAD2, NFKB1, NRAS, PIK3CB, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, MAP2K4, SHC1, SOS1, SRC, TGFBR1, VEGFA, CREB5, AKT3, GNB4, CREB3L2
KEGG	hsa04150	mTOR signaling pathway	53/1652	3.23E-04	AKT2, RHOA, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, DVL3, EIF4B, EIF4E, GRB2, GSK3B, IGF1R, IKBKB, INSR, KRAS, LRP6, NRAS, PIK3CB, PRKAA1, PRKCA, MAPK1, MAPK3, PTEN, RPS6KA3, RPS6KB1, SOS1, TSC1, WNT7B, WNT2B, FZD5, FZD3, SLC7A5, FZD1, FZD4, FZD6, ULK1, LPIN2, AKT3, LPIN1, ATP6V1D, WNT4, DDIT4, FNIP2, RRAGD, RRAGC, MLST8, MAPKAP1, SEH1L, SESN2, AKT1S1, FNIP1, FLCN, RICTOR
KEGG	hsa04144	Endocytosis	78/1652	3.32E-04	ARF1, ARF6, RHOA, ARRB1, ARRB2, CAPZA2, CAV1, CBL, CDC42, AP2M1, DAB2, EGFR, FGFR3, GRK6, HLA-B, HSPA2, IGF1R, IGF2R, KIF5B, LDLR, SMAD2, RAB8A, NEDD4, PDGFRA, PLD1, PML, RAB5A, RAB5B, SH3GL2, SNX1, SRC, TFRC, TGFBR1, SNX3, WASL, RABEP1, RAB11B, CYTH3, CYTH1, VPS4B, ZFYVE16, GIT2, PDCD6IP, ARPC5, ACTR2, ARPC2, ARFGEF2, STAMBP, RAB31, SNF8, RAB11FIP2, PSD3, PIP5K1C, ACAP2, LDLRAP1, GIT1, EHD4, ASAP1, VPS36, SH3GLB1, CHMP5, VPS37C, VPS35, ARFGAP1, PARD3, CHMP1B, SMURF1, RAB22A, RAB11FIP1, ITCH, RAB11FIP4, PARD6B, CHMP7, ARAP2, AGAP1, WIPF2, VPS37D, IQSEC3
KEGG	hsa05226	Gastric cancer	51/1652	4.10E-04	AKT2, APC, BAK1, CCND1, BCL2, CDKN1A, CDKN1B, CTNNA1, CTNNB1, DVL3, E2F3, EGFR, ERBB2, FGF1, FGF2, FGF5, GAB1, GRB2, GSK3B, JUP, KRAS, LRP6, SMAD2, SMAD4, MET, MLH1, MYC, NRAS, PIK3CB, MAPK1, MAPK3, RB1, RPS6KB1, SHC1, SOS1, TCF7, TCF7L2, TERT, TGFBR1, TP53, WNT7B, WNT2B, FZD5, FZD3, FZD1, FZD4, FZD6, CCNE2, FGF19, AKT3, WNT4
KEGG	hsa05221	Acute myeloid leukemia	28/1652	4.10E-04	AKT2, CCND1, RUNX1, RUNX1T1, CCNA2, DUSP6, GRB2, IKBKB, JUP, KIT, KRAS, MYC, NFKB1, NRAS, PIK3CB, PIM1, PML, PPARD, MAPK1, MAPK3, RPS6KB1, SOS1, STAT3, STAT5B, TCF7, TCF7L2, PER2, AKT3
KEGG	hsa05166	Human T-cell leukemia virus 1 infection	69/1652	4.59E-04	ADCY1, ADCY6, ADCY9, AKT2, SLC25A6, ATM, ATR, CCND1, BCL2L1, CALR, CANX, CCNA2, CCND2, CDKN1A, CHEK1, CREB1, ATF2, CREBBP, ATF6B, E2F3, EGR1, ELK1, ELK4, EP300, KAT2A, HLA-B, IKBKB, IL1R1, IL15RA, JUN, KRAS, MAD2L1, SMAD2, SMAD4, MAP3K1, MAP3K3, MSX1, MYC, NFKB1, NFYB, NRAS, PIK3CB, PPP3CA, PPP3R1, MAPK1, MAPK3, MAPK8, MAPK9, PTEN, RAN, RB1, MAP2K4, SRF, STAT5B, TCF3, TERT, TGFBR1, TLN1, TP53, VDAC2, XPO1, ZFP36, FOSL1, NRP1, KAT2B, CCNE2, CREB5, AKT3, CREB3L2
KEGG	hsa05161	Hepatitis B	54/1652	5.28E-04	AKT2, FAS, BCL2, CASP3, CASP10, CCNA2, CDKN1A, CREB1, ATF2, CREBBP, ATF6B, MAPK14, DDX3X, E2F3, EGR3, ELK1, EP300, GRB2, IFNAR1, IKBKB, IRAK1, JUN, KRAS, SMAD4, MAP3K1, MYC, NFKB1, NRAS, PIK3CB, PRKCA, MAPK1, MAPK3, MAPK8,

					MAPK9, RB1, MAP2K4, SOS1, SRC, STAT1, STAT2, STAT3, STAT5B, TGFBR1, TP53, TRAF3, FADD, CCNE2, CREB5, AKT3, TAB1, TAB2, CYCS, MAVS, CREB3L2
KEGG	hsa04728	Dopaminergic synapse	46/1652	5.28E-04	AKT2, ARRB1, ARRB2, CACNA1B, CACNA1C, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, COMT, CREB1, ATF2, ATF6B, MAPK14, GNAI2, GNAI3, GNAL, GNAQ, GNAS, GNB1, GNG7, GRIA4, GSK3B, ITPR1, ITPR2, KCNJ3, KIF5B, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PPP3CA, PRKCA, MAPK8, MAPK9, CLOCK, CREB5, AKT3, PPP2R2D, GNB4, CREB3L2
KEGG	hsa05167	Kaposi sarcoma-associated herpesvirus infection	62/1652	5.35E-04	AKT2, FAS, BAK1, CCND1, CALM1, CALM2, CALM3, CASP3, CDK6, CDKN1A, CREB1, CREBBP, MAPK14, CTNNB1, E2F3, EP300, FGF2, GNB1, GNG7, GSK3B, HIF1A, HLA-B, IFNAR1, IFNAR2, IKBKB, IL6ST, ITPR1, ITPR2, JUN, KRAS, LYN, MYC, NFKB1, NRAS, PDGFB, PIK3CB, PPP3CA, PPP3R1, MAPK1, MAPK3, MAPK8, MAPK9, EIF2AK2, RB1, MAP2K4, SRC, STAT1, STAT2, STAT3, SYK, TCF7, TCF7L2, TP53, TRAF3, VEGFA, ZFP36, FADD, AKT3, GABARAPL2, ATG14, CYCS, GNB4
KEGG	hsa05132	Salmonella infection	76/1652	5.94E-04	ACTB, AKT2, ARF1, ARF6, RHOA, RHOB, BAK1, BCL2, CASP3, CDC42, MAPK14, CTNNB1, FLNB, GAPDH, NCKAP1L, IKBKB, IL18, IRAK1, JUN, KIF5B, KPNA1, KPNA3, M6PR, MYC, MYO6, NFKB1, PAK3, PIK3C2A, PIK3CB, PODXL, MAPK1, MAPK3, MAPK8, MAPK9, PTPRC, RAB5A, RAB5B, RPS3, MAP2K4, SKP1, TCF7, TCF7L2, DYNLT3, TXN, DYNLL1, TNFSF10, FADD, WASL, CYTH3, CYTH1, ROCK2, PLEKHM1, AKT3, ARPC5, ACTR2, ARPC2, TUBB4A, NOD1, TAB1, MYL12A, EXOC5, NCKAP1, DCTN3, TAB2, TXN2, FBXO22, CYFIP2, DCTN4, DYNC2LI1, CYCS, ACBD3, KLC2, AHNAK, FYCO1, DCTN5, ARL8A
KEGG	hsa04931	Insulin resistance	39/1652	7.10E-04	AKT2, CPT1A, CREB1, FOXO1, GFPT1, GSK3B, GYS1, IKBKB, INSR, NFKB1, PIK3CB, PPARA, PPP1CA, PPP1CB, PPP1CC, PPP1R3C, PRKAA1, PRKAB2, PRKCE, MAPK8, MAPK9, PTEN, PTPN1, PTPN11, PTPRF, PYGB, RPS6KA3, RPS6KB1, STAT3, MLX, NR1H2, IRS2, CREB5, TBC1D4, GFPT2, AKT3, MLXIP, CREB3L2, SLC27A1
KEGG	hsa04935	Growth hormone synthesis, secretion and action	42/1652	7.10E-04	ADCY1, ADCY6, ADCY9, AKT2, CACNA1C, CREB1, ATF2, CREBBP, ATF6B, CRK, CRKL, MAPK14, EP300, GNAI2, GNAI3, GNAQ, GNAS, GRB2, GSK3B, ITPR1, ITPR2, KRAS, MAP3K1, NRAS, PIK3CB, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, MAP2K4, SHC1, SOS1, STAT1, STAT3, STAT5B, SOCS1, IRS2, SOCS2, CREB5, AKT3, CREB3L2
KEGG	hsa04916	Melanogenesis	37/1652	7.30E-04	ADCY1, ADCY6, ADCY9, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, CREB1, CREBBP, CTNNB1, DVL3, EDN1, EP300, GNAI2, GNAI3, GNAQ, GNAS, GSK3B, KIT, KRAS, KITLG, NRAS, PRKCA, MAPK1, MAPK3, TCF7, TCF7L2, WNT7B, WNT2B, FZD5, FZD3, FZD1, FZD4, FZD6, WNT4, CREB3L2
KEGG	hsa04668	TNF signaling pathway	40/1652	7.35E-04	JAG1, AKT2, FAS, CASP3, CASP10, CEBPB, CREB1, ATF2, ATF6B, MAPK14, CSF1, EDN1, IKBKB, IRF1, JUN, MMP14, NFKB1, PIK3CB, MAPK1, MAPK3, MAPK8, MAPK9, CXCL5, CX3CL1, MAP2K4, TNFRSF1B, TRAF1, TRAF3, VCAM1, FADD, RPS6KA4, RPS6KA5, BAG4, CREB5, AKT3, TAB1, TAB2, CREB3L2, ITCH, DAB2IP
KEGG	hsa04115	p53 signaling pathway	29/1652	7.37E-04	FAS, ATM, ATR, CCND1, BCL2, BCL2L1, CASP3, CCND2, CCNG2, CDK6, CDKN1A, CHEK1, MDM4, SERPINE1, PTEN, RRM2, SIAH1, THBS1, TP53, PPM1D, CCNE2, BBC3, RRM2B, CYCS, STEAP3, RPRM, ZMAT3, SESN2, SESN3
KEGG	hsa04152	AMPK signaling pathway	42/1652	7.90E-04	ACACA, AKT2, CCND1, CCNA2, CPT1A, CREB1, ELAVL1, FOXO1, FOXO3, GYS1, HMGCR, HNF4A, IGF1R, INSR, RAB8A, PFKFB2, PFKFB3, PFKFB4, PIK3CB, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PRKAA1, PRKAB2, RPS6KB1, SCD, TSC1, ULK1, IRS2, RAB11B, CREB5, AKT3, SIRT1, ADIPOR1, RAB14, PPP2R2D, CREB3L2, ADIPOR2, SCD5, AKT1S1
KEGG	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	28/1652	7.90E-04	ADAM10, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1E1, CASP3, CDC42, MAPK14, CSK, HBEGF, EGFR, IKBKB, JUN, LYN, MET, NFKB1, MAPK8, MAPK9, PTPN11, MAP2K4, SRC, ADAM17, ATP6V0D1, NOD1, GIT1, ATP6V1D, JAM2, ATP6V0E2
KEGG	hsa05230	Central carbon metabolism in cancer	28/1652	7.90E-04	AKT2, EGFR, ERBB2, FGFR3, G6PD, GLS, HIF1A, HK1, HK2, IDH2, KIT, KRAS, LDHA, MET, MYC, NRAS, NTRK3, PDGFRA, PGAM1, PIK3CB, PKM, MAPK1, MAPK3, PTEN, SLC1A5, TP53, SLC7A5, AKT3
KEGG	hsa04928	Parathyroid hormone synthesis, secretion and action	38/1652	8.98E-04	ADCY1, ADCY6, ADCY9, RHOA, ARRB1, ARRB2, BCL2, RUNX2, CDKN1A, CREB1, ATF2, ATF6B, HBEGF, EGFR, EGR1, GATA3, GNAI2, GNAI3, GNAQ, GNAS, ITPR1, ITPR2, JUND, LRP6, MEF2A, MEF2C, MEF2D, MMP14, PDE4D, PLD1, PRKCA, MAPK1, MAPK3, VDR, CREB5, GNA13, AKAP13, CREB3L2
KEGG	hsa04919	Thyroid hormone signaling pathway	42/1652	9.21E-04	ACTB, AKT2, ATP1B1, ATP2A2, CCND1, CREBBP, CTNNB1, EP300, FOXO1, KAT2A, GSK3B, HDAC2, HIF1A, ITGAV, KRAS, MYC, NOTCH2, NRAS, PFKFB2, PIK3CB, PRKCA, MAPK1, MAPK3, SLC9A1, SRC, STAT1, THRA, TP53, NCOA3, KAT2B, NCOR1, MED24, TBC1D4, MED13, AKT3, NCOA2, MED13L, SIN3A, WNT4, PLCD3, MED12L, SLC16A10
KEGG	hsa05219	Bladder cancer	19/1652	9.21E-04	CCND1, CDKN1A, DAPK1, HBEGF, E2F3, EGFR, ERBB2, FGFR3, KRAS, MYC, NRAS, MAPK1, MAPK3, RB1, SRC, THBS1, TP53, VEGFA, RPS6KA5
KEGG	hsa04071	Sphingolipid signaling pathway	41/1652	1.28E-03	AKT2, RHOA, ASAH1, BCL2, MAPK14, S1PR1, S1PR3, GNAI2, GNAI3, GNAQ, KRAS, NFKB1, NRAS, PIK3CB, PLD1, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PRKCA, PRKCE, MAPK1, MAPK3, MAPK8, MAPK9, PTEN, TP53, NSMAF, SGPL1, ROCK2, AKT3, SPTLC1, GNA13, CERS1, SPTLC3, PPP2R2D, SGPP1, SGMS2, CERS6, ACER2
KEGG	hsa04014	Ras signaling pathway	70/1652	1.28E-03	ABL1, ABL2, AKT2, ARF6, RHOA, BCL2L1, BDNF, CALM1, CALM2, CALM3, CDC42, CSF1, EFNA3, EFNA5, EGFR, ELK1, FGF1, FGF2, FGF5, FGFR3, FLT4, GAB1, GNB1, GNG7, GRB2, IGF1R, IGF2, IKBKB, INSR, KIT, KRAS, MET, KITLG, FOXO4, NFKB1, NRAS, PAK2,

					PAK3, PDGFA, PDGFB, PDGFRA, PIK3CB, PLD1, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, PTPN11, RAB5A, RAB5B, RALB, RALGDS, RAP1B, RASA1, SHC1, SOS1, STK4, TGFA, TIAM1, VEGFA, SHOC2, SYNGAP1, KSR1, RASAL2, FGF19, AKT3, RASA3, RGL1, GNB4
KEGG	hsa04066	HIF-1 signaling pathway	38/1652	1.59E-03	AKT2, BCL2, CAMK2A, CAMK2D, CDKN1A, CDKN1B, CREBBP, EDN1, EGFR, EIF4E, EP300, ERBB2, GAPDH, MKNK2, HIF1A, HK1, HK2, IGF1R, IL6R, INSR, LDHA, NFKB1, SERPINE1, PFKFB3, PIK3CB, PRKCA, MAPK1, MAPK3, RPS6KB1, STAT3, TFRC, VEGFA, VHL, CUL2, MKNK1, AKT3, EGLN2, EGLN3
KEGG	hsa04015	Rap1 signaling pathway	64/1652	1.67E-03	ACTB, ADCY1, ADCY6, ADCY9, ADORA2B, AKT2, RHOA, CALM1, CALM2, CALM3, CDC42, CRK, CRKL, MAPK14, CSF1, CTNNB1, CTNND1, EFNA3, EFNA5, EGFR, FGF1, FGF2, FGF5, FGFR3, FLT4, GNAI2, GNAI3, GNAQ, GNAS, RAPGEF1, IGF1R, INSR, ITGB1, KIT, KRAS, MET, KITLG, NRAS, P2RY1, PDGFA, PDGFB, PDGFRA, PIK3CB, PRKCA, MAPK1, MAPK3, RALB, RALGDS, RAP1B, SRC, THBS1, TIAM1, TLN1, VEGFA, F2RL3, RAPGEF2, FGF19, AKT3, RAPGEF3, VAV3, SIPA1L1, PARD3, SIPA1L2, PARD6B
KEGG	hsa04120	Ubiquitin mediated proteolysis	46/1652	1.81E-03	BRCA1, CBL, CDC34, UBE2K, MAP3K1, MID1, NEDD4, PML, SIAH1, SKP1, UBE2D2, UBE2D3, UBE2G1, UBE2G2, UBE2H, UBE2L3, UBE2N, VHL, CUL5, CUL4B, CUL3, CUL2, SOCS1, HERC3, BTRC, TRIP12, UBE4A, UBE4B, PIAS3, UBE2E3, MGRN1, HERC4, UBR5, UBE2J1, PIAS4, UBE2R2, UBA6, UBE2W, FBXW7, UBE2Q1, SMURF1, BIRC6, UBE2Z, ITCH, SYVN1, KLHL13
KEGG	hsa04720	Long-term potentiation	26/1652	2.06E-03	ADCY1, CACNA1C, CALM1, CALM2, CALM3, CAMK4, CAMK2A, CAMK2D, CREBBP, EP300, GNAQ, ITPR1, ITPR2, KRAS, NRAS, PPP1CA, PPP1CB, PPP1CC, PPP3CA, PPP3R1, PRKCA, MAPK1, MAPK3, RAP1B, RPS6KA3, RAPGEF3
KEGG	hsa04710	Circadian rhythm	15/1652	2.23E-03	CREB1, CRY2, CSNK1D, CSNK1E, PRKAA1, PRKAB2, RORA, RORB, SKP1, BHLHE40, PER3, PER2, BTRC, CLOCK, FBXL3
KEGG	hsa04921	Oxytocin signaling pathway	49/1652	2.61E-03	ACTB, ADCY1, ADCY6, ADCY9, RHOA, CCND1, CACNA1C, CACNA2D1, CACNB1, CALM1, CALM2, CALM3, CAMK4, CAMK2A, CAMK2D, CDKN1A, EGFR, ELK1, GNAI2, GNAI3, GNAQ, GNAS, GUCY1A2, ITPR1, ITPR2, JUN, KCNJ2, KCNJ3, KRAS, MEF2C, PPP1R12A, PPP1R12B, NRAS, PPP1CA, PPP1CB, PPP1CC, PPP3CA, PPP3R1, PRKAA1, PRKAB2, PRKCA, MAPK1, MAPK3, RGS2, SRC, TRPM2, ROCK2, PPP1R12C, CAMK1D
KEGG	hsa05223	Non-small cell lung cancer	27/1652	2.90E-03	AKT2, BAK1, CCND1, CDK6, CDKN1A, E2F3, EGFR, ERBB2, FHIT, FOXO3, GRB2, KIF5B, KRAS, MET, NRAS, PIK3CB, PRKCA, MAPK1, MAPK3, RB1, SOS1, STAT3, STAT5B, STK4, TGFA, TP53, AKT3
KEGG	hsa04934	Cushing syndrome	49/1652	2.98E-03	ADCY1, ADCY6, ADCY9, APC, CCND1, CACNA1C, CAMK2A, CAMK2D, CDK6, CDKN1A, CDKN1B, CREB1, ATF2, ATF6B, CTNNB1, DVL3, E2F3, EGFR, GNAI2, GNAI3, GNAQ, GNAS, GSK3B, ITPR1, ITPR2, KCNK3, LDLR, MEN1, KMT2A, PBX1, MAPK1, MAPK3, RAP1B, RB1, TCF7, TCF7L2, WNT7B, WNT2B, FZD5, FZD3, KMT2D, FZD1, FZD4, FZD6, CCNE2, CREB5, WNT4, WDR5B, CREB3L2
KEGG	hsa05231	Choline metabolism in cancer	34/1652	3.16E-03	AKT2, CHKA, EGFR, GRB2, HIF1A, JUN, KRAS, NRAS, PDGFA, PDGFB, PDGFRA, PIK3CB, PLD1, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, RALGDS, RPS6KB1, SOS1, TSC1, DGKE, DGKD, WASF1, PCYT1B, AKT3, WASF2, LYPLA1, PIP5K1C, SLC44A1, GPCPD1, CHPT1, DGKH
KEGG	hsa05203	Viral carcinogenesis	61/1652	3.47E-03	ACTN4, RHOA, BAK1, CCND1, CASP3, CCNA2, CCND2, CDC42, CDK6, CDKN1A, CDKN1B, CHD4, CHEK1, CREB1, ATF2, CREBBP, ATF6B, DDX3X, EGR3, EP300, KAT2A, GRB2, GTF2A1, GTF2E1, GTF2H3, HDAC2, HLA-B, HNRNPK, RBPJ, IL6ST, JUN, KRAS, LYN, NFKB1, NRAS, PIK3CB, PKM, MAPK1, MAPK3, EIF2AK2, PXN, RB1, RBL2, SP100, SRC, SRF, STAT3, STAT5B, SYK, TP53, TRAF1, TRAF3, YWHAE, YWHAG, KAT2B, ATP6V0D1, CCNE2, CREB5, HDAC9, SND1, CREB3L2
KEGG	hsa05202	Transcriptional misregulation in cancer	58/1652	3.47E-03	ATM, BAK1, BCL2L1, BCL6, RUNX2, RUNX1, RUNX1T1, CCNA2, CCND2, CCNT1, CCNT2, CDKN1A, CDKN1B, CEBPB, DDX5, DUSP6, ELK4, ETV1, FOXO1, FUS, FUT8, HDAC2, HOXA9, IGF1R, JUP, LMO2, MAX, MEF2C, MEN1, MET, KMT2A, AFF1, MLLT3, MYC, MYCN, NFKB1, PAX3, PBX1, PDGFA, PML, SS18, TCF3, ZEB1, TSPAN7, TP53, TRAF1, KDM6A, NR4A3, HMGA2, LDB1, PER2, NCOR1, SIN3A, KLF3, SIX4, BMP2K, BCL11B, JMJD1C
KEGG	hsa05160	Hepatitis C	49/1652	3.88E-03	AKT2, FAS, BAK1, CCND1, CASP3, CDK6, CDKN1A, CTNNB1, E2F3, EGFR, EIF2S1, GRB2, GSK3B, IFNAR1, IFNAR2, IKBKB, KRAS, LDLR, MYC, NFKB1, NRAS, OAS2, CLDN11, PIK3CB, PPARA, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, MAPK1, MAPK3, EIF2AK2, RB1, SOS1, STAT1, STAT2, STAT3, TP53, TRAF3, YWHAE, YWHAG, FADD, AKT3, PSME3, EIF2AK1, CYCS, PPP2R2D, MAVS, CLDN23
KEGG	hsa04530	Tight junction	52/1652	3.90E-03	ACTB, ACTN4, RHOA, CCND1, RUNX1, CDC42, DLG3, ERBB2, HSPA4, ITGB1, JUN, MAP3K1, RAB8A, MYH9, MYH10, NEDD4, NF2, CLDN11, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PRKAA1, PRKAB2, PRKCE, MAPK8, MAPK9, RDX, SRC, TIAM1, MPDZ, ARHGEF2, TJP2, ROCK2, RAPGEF2, ARPC5, ACTR2, ARPC2, MYL12A, RAB8B, EPB41L4B, ARHGAP17, PPP2R2D, PARD3, RAP2C, JAM2, PARD6B, CGNL1, WHAMM, CLDN23, AMOT, AMOTL1
KEGG	hsa04261	Adrenergic signaling in cardiomyocytes	47/1652	4.34E-03	ADCY1, ADCY6, ADCY9, ADRB1, AKT2, ATP1B1, ATP2A2, ATP2B1, ATP2B4, BCL2, CACNA1C, CACNA2D1, CACNB1, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, CREB1, ATF2, ATF6B, MAPK14, GNAI2, GNAI3, GNAQ, GNAS, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PPP2R2A, PPP2R2C, PPP2R5D, PRKCA, MAPK1, MAPK3, SLC8A1, SLC9A1, TPM3, TPM4, RPS6KA5, CREB5, AKT3, RAPGEF3, PPP2R2D, CREB3L2
KEGG	hsa04330	Notch signaling pathway	21/1652	4.49E-03	JAG1, CREBBP, DVL3, EP300, KAT2A, HDAC2, HES1, RBPJ, JAG2, NOTCH2, ATXN1, ADAM17, NUMB, KAT2B, NCSTN, HEYL, APH1A, DLL4, APH1B, DTX2, ATXN1L
KEGG	hsa04340	Hedgehog signaling pathway	20/1652	5.03E-03	ARRB1, ARRB2, CCND1, BCL2, CCND2, CSNK1D, CSNK1E, CSNK1G3, MEGF8, GSK3B, PTCH1, SPOP, CUL3, BTRC, KIF3A, MGRN1, CDON, SUFU, SMURF1, SPOPL

KEGG	hsa05135	Yersinia infection	43/1652	6.45E-03	ACTB, AKT2, ARF6, RHOA, CDC42, CRK, CRKL, MAPK14, FN1, GNAQ, GSK3B, IKBKB, IL18, IRAK1, ITGA5, ITGB1, JUN, LIMK1, NFKB1, PIK3CB, PKN2, MAPK1, MAPK3, MAPK8, MAPK9, PXN, RPS6KA3, MAP2K4, SRC, WASL, ROCK2, GIT2, AKT3, ARPC5, ACTR2, ARPC2, WASF2, VAV3, TAB1, TAB2, ARHGEF12, PIP5K1C, WIPF2
KEGG	hsa05100	Bacterial invasion of epithelial cells	27/1652	8.04E-03	ACTB, RHOA, CAV1, CBL, CDC42, CRK, CRKL, CTNNA1, CTNNB1, FN1, GAB1, ILK, ITGA5, ITGB1, MET, PIK3CB, PXN, SHC1, SRC, VCL, WASF1, WASL, ARPC5, ACTR2, ARPC2, WASF2, CD2AP
KEGG	hsa04022	cGMP-PKG signaling pathway	50/1652	8.50E-03	ADCY1, ADCY6, ADCY9, ADRB1, AKT2, SLC25A6, RHOA, ATP1B1, ATP2A2, ATP2B1, ATP2B4, CACNA1C, CALM1, CALM2, CALM3, CREB1, ATF2, ATF6B, GNAI2, GNAI3, GNAQ, GTF2I, GUCY1A2, INSR, ITPR1, ITPR2, MEF2A, MEF2C, MEF2D, PPP1R12A, PDE3A, PPP1CA, PPP1CB, PPP1CC, PPP3CA, PPP3R1, PRKCE, MAPK1, MAPK3, RGS2, SLC8A1, SRF, VDAC2, IRS2, ROCK2, CREB5, AKT3, GNA13, KCNMB4, CREB3L2
KEGG	hsa05418	Fluid shear stress and atherosclerosis	43/1652	8.50E-03	ACTB, ACVR2B, AKT2, RHOA, BCL2, BMPR1A, BMPR2, CALM1, CALM2, CALM3, CAV1, MAPK14, CTNNB1, DUSP1, EDN1, GSTM3, IKBKB, IL1R1, ITGAV, JUN, MEF2A, MEF2C, NFKB1, PDGFA, PDGFB, PIK3CB, PRKAA1, MAPK8, MAPK9, SDC2, SDC4, MAP2K4, SRC, TP53, TXN, VCAM1, VEGFA, SQSTM1, ARHGEF2, AKT3, KLF2, TXN2, PIAS4
KEGG	hsa04611	Platelet activation	39/1652	9.51E-03	ACTB, ADCY1, ADCY6, ADCY9, AKT2, RHOA, COL1A1, COL1A2, COL3A1, MAPK14, GNAI2, GNAI3, GNAQ, GNAS, ARHGAP35, GUCY1A2, ITGB1, ITPR1, ITPR2, LYN, PPP1R12A, P2RY1, PIK3CB, PPP1CA, PPP1CB, PPP1CC, MAPK1, MAPK3, RAP1B, SRC, STIM1, SYK, TLN1, F2RL3, ROCK2, AKT3, MYL12A, GNA13, ARHGEF12
KEGG	hsa04310	Wnt signaling pathway	48/1652	9.61E-03	APC, RHOA, CCND1, CAMK2A, CAMK2D, CCND2, CREBBP, CSNK1E, CTNNB1, DVL3, EP300, GSK3B, JUN, LRP6, SMAD4, MYC, PPARD, PPP3CA, PPP3R1, PRKCA, MAPK8, MAPK9, SFRP1, SIAH1, SKP1, TBL1X, TCF7, TCF7L2, TP53, WNT7B, WNT2B, FZD5, FZD3, FOSL1, FZD1, FZD4, FZD6, BTRC, ROCK2, DKK1, NLK, WNT4, LGR4, VANGL2, TBL1XR1, VANGL1, ZNRF3, PRICKLE2
KEGG	hsa04930	Type II diabetes mellitus	18/1652	1.07E-02	CACNA1B, CACNA1C, CACNA1E, HK1, HK2, IKBKB, INSR, PIK3CB, PKM, PRKCE, MAPK1, MAPK3, MAPK8, MAPK9, SOCS1, IRS2, SOCS2, SOCS4
KEGG	hsa05218	Melanoma	25/1652	1.25E-02	AKT2, BAK1, CCND1, CDK6, CDKN1A, E2F3, EGFR, FGF1, FGF2, FGF5, IGF1R, KRAS, MET, NRAS, PDGFA, PDGFB, PDGFRA, PIK3CB, MAPK1, MAPK3, PTEN, RB1, TP53, FGF19, AKT3
KEGG	hsa05170	Human immunodeficiency virus 1 infection	60/1652	1.32E-02	AP1G1, AKT2, FAS, ATM, ATR, BAK1, BCL2, BCL2L1, CALM1, CALM2, CALM3, CALR, CASP3, CFL1, CFL2, CHEK1, AP1S1, CRK, CRKL, MAPK14, GNAI2, GNAI3, GNAQ, GNB1, GNG7, HLA-B, IKBKB, IRAK1, ITPR1, ITPR2, JUN, KRAS, LIMK1, NFKB1, NRAS, PAK2, PAK3, PIK3CB, PPP3CA, PPP3R1, PRKCA, MAPK1, MAPK3, MAPK8, MAPK9, PXN, RPS6KB1, SKP1, TNFRSF1B, CUL5, CUL4B, FADD, AP1G2, BTRC, AKT3, TAB1, TAB2, CYCS, GNB4, AP1S3
KEGG	hsa04922	Glucagon signaling pathway	34/1652	1.37E-02	ACACA, AKT2, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, CPT1A, CREB1, ATF2, CREBBP, EP300, FOXO1, GNAQ, GNAS, GYS1, ITPR1, ITPR2, LDHA, PGAM1, PHKA1, PHKG2, PKM, PPARA, PPP3CA, PPP3R1, PRKAA1, PRKAB2, PYGB, CREB5, AKT3, SIRT1, CREB3L2, SIK1
KEGG	hsa05031	Amphetamine addiction	24/1652	1.41E-02	CACNA1C, CALM1, CALM2, CALM3, CAMK4, CAMK2A, CAMK2D, CREB1, ATF2, ATF6B, FOSB, GNAS, GRIA4, HDAC2, JUN, PPP1CA, PPP1CB, PPP1CC, PPP3CA, PPP3R1, PRKCA, CREB5, SIRT1, CREB3L2
KEGG	hsa04213	Longevity regulating pathway - multiple species	22/1652	1.52E-02	ADCY1, ADCY6, ADCY9, AKT2, FOXO1, FOXO3, HDAC2, HSPA2, IGF1R, INSR, KRAS, NRAS, PIK3CB, PRKAA1, PRKAB2, RPS6KB1, SOD2, IRS2, ATG5, AKT3, SIRT1, AKT1S1
KEGG	hsa00534	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	11/1652	1.57E-02	EXTL2, EXTL3, NDST1, NDST3, HS2ST1, HS3ST3A1, HS3ST1, GLCE, XYLT2, HS6ST2, HS6ST3
KEGG	hsa04210	Apoptosis	41/1652	1.57E-02	ACTB, AKT2, FAS, ATM, BAK1, BCL2, BCL2L1, CAPN2, CASP3, CASP10, CTSB, CTSS, CTSZ, DFFB, EIF2S1, IKBKB, ITPR1, ITPR2, JUN, KRAS, MCL1, NFKB1, NRAS, PIK3CB, MAPK1, MAPK3, MAPK8, MAPK9, SPTAN1, TP53, TRAF1, CTSF, TNFSF10, FADD, AKT3, BCL2L11, BBC3, HTRA2, CYCS, LMNB2, DAB2IP
KEGG	hsa04110	Cell cycle	38/1652	1.57E-02	ABL1, ATM, ATR, CCND1, CCNA2, CCND2, CDC25A, CDK6, CDKN1A, CDKN1B, CHEK1, CREBBP, E2F3, E2F5, EP300, GSK3B, HDAC2, MAD2L1, SMAD2, SMAD4, MCM3, MCM4, MCM7, MYC, ORC5, RAD21, RB1, RBL2, SKP1, TFDP1, TFDP2, TP53, YWHAE, YWHAG, SMC1A, CDC14B, CCNE2, STAG2
KEGG	hsa03013	RNA transport	53/1652	1.75E-02	CLNS1A, EEF1A1, EIF2S1, EIF2S3, EIF4A1, EIF4B, EIF4E, EIF4G1, EIF4G2, EIF5, FMR1, FUS, NCBP1, NUP88, NUP98, PABPC3, PNN, RAN, RANBP2, UPF1, XPO1, FXR1, EIF3A, PABPC4, EIF5B, POM121, EIF1, NXF1, PAIP1, NUP50, POP4, RNPS1, POP1, RPP14, XPOT, DDX19B, TARDBP, UPF2, PABPC1, CYFIP2, GEMIN4, NMD3, TRNT1, RPP25, DDX19A, NDC1, NUP133, THOC2, XPO5, SEH1L, TGS1, NUP43, POM121C
KEGG	hsa04371	Apelin signaling pathway	41/1652	1.77E-02	ADCY1, ADCY6, ADCY9, JAG1, AKT2, CCND1, CALM1, CALM2, CALM3, CAMK4, EGR1, GNAI2, GNAI3, GNAQ, GNB1, GNG7, ITPR1, ITPR2, KRAS, SMAD2, SMAD4, MEF2A, MEF2C, MEF2D, NRAS, NRF1, SERPINE1, PRKAA1, PRKAB2, PRKCE, MAPK1, MAPK3, RPS6KB1, SLC8A1, SLC9A1, TGFBR1, AKT3, KLF2, GNA13, GABARAPL2, GNB4

KEGG	hsa05206	MicroRNAs in cancer	82/1652	1.92E-02	ABL1, APC, RHOA, ATM, BAK1, CCND1, BCL2, BMPR2, BRCA1, CASP3, CCND2, CD44, CDC25A, CDK6, CDKN1A, CDKN1B, CREBBP, CRK, CRKL, DNMT3A, DNMT3B, E2F3, EFNA3, EFNA5, EGFR, EP300, ERBB2, EZH2, FGFR3, GLS, GRB2, HDAC2, HNRNPK, IKBKB, ITGA5, KRAS, MARCKS, MCL1, MDM4, MET, MYC, NFKB1, NOTCH2, NRAS, PDGFA, PDGFB, PDGFRA, PIK3CB, PIM1, PRKCA, PRKCE, MAPK1, MAPK3, PTEN, RDX, SHC1, SLC7A1, SOS1, SOX4, STAT3, ZEB1, THBS1, TIMP3, TP53, VEGFA, FZD3, HMGA2, TP63, SOCS1, IRS2, CCNE2, RPS6KA5, KIF23, BCL2L11, IGF2BP1, DICER1, SIRT1, FOXP1, PDCD4, DDIT4, BMF, TRIM71
KEGG	hsa05169	Epstein-Barr virus infection	56/1652	2.52E-02	AKT2, FAS, BAK1, CCND1, BCL2, CALR, CASP3, RUNX3, CCNA2, CCND2, ENTPD1, CD44, CDK6, CDKN1A, CDKN1B, MAPK14, E2F3, HDAC2, HLA-B, HES1, IFNAR1, IFNAR2, RBPJ, IKBKB, IRAK1, JUN, LYN, MYC, NEDD4, NFKB1, OAS2, PIK3CB, MAPK8, MAPK9, EIF2AK2, PSMC2, PSMD3, PSMD13, RB1, MAP2K4, STAT1, STAT2, STAT3, SYK, TP53, TRAF3, FADD, CCNE2, AKT3, BCL2L11, PSMD14, TAB1, TAB2, SIN3A, CYCS, MAVS
KEGG	hsa04392	Hippo signaling pathway - multiple species	12/1652	2.72E-02	CSNK1E, NF2, TEAD1, TEAD3, DCHS1, LIMD1, LATS1, RASSF2, WWC1, LATS2, MOB1A, RASSF4
KEGG	hsa04924	Renin secretion	23/1652	2.72E-02	ADCY6, ADCYAP1R1, ADRB1, CACNA1C, CALM1, CALM2, CALM3, CREB1, CTSB, EDN1, GNAI2, GNAI3, GNAQ, GNAS, GUCY1A2, ITPR1, ITPR2, KCNJ2, PDE3A, PDE1B, PPP3CA, PPP3R1, PTGER4
KEGG	hsa04070	Phosphatidylinositol signaling system	30/1652	3.02E-02	CALM1, CALM2, CALM3, CDS1, IMPA2, ITPK1, ITPKB, ITPR1, ITPR2, PIK3C2A, PIK3CB, PIP4K2A, PRKCA, PTEN, DGKE, DGKD, INPP4B, SYNJ1, SYNJ2, MTMR3, MTMR7, MTMR4, IP6K1, SACM1L, PPIP5K2, PIP5K1C, PI4K2B, INPP5E, PLCD3, DGKH
KEGG	hsa04666	Fc gamma R-mediated phagocytosis	30/1652	3.02E-02	AKT2, ARF6, CDC42, CFL1, CFL2, CRK, CRKL, LIMK1, LYN, MARCKS, MYO10, PIK3CB, PLD1, PRKCA, PRKCE, MAPK1, MAPK3, PTPRC, RPS6KB1, SYK, WASF1, AKT3, ARPC5, ACTR2, ARPC2, WASF2, VAV3, PIP5K1C, ASAP1, MARCKSL1
KEGG	hsa04915	Estrogen signaling pathway	40/1652	3.24E-02	ADCY1, ADCY6, ADCY9, AKT2, BCL2, CALM1, CALM2, CALM3, CREB1, ATF2, ATF6B, HBEGF, EGFR, ESR2, FKBP4, GNAI2, GNAI3, GNAQ, GNAS, GRB2, HSPA2, ITPR1, ITPR2, JUN, KCNJ3, KRAS, NRAS, PGR, PIK3CB, MAPK1, MAPK3, SHC1, SOS1, SRC, TGFA, NCOA3, CREB5, AKT3, NCOA2, CREB3L2
KEGG	hsa04962	Vasopressin-regulated water reabsorption	16/1652	3.33E-02	ADCY6, ADCY9, ARHGDIA, CREB1, GNAS, NSF, RAB5A, RAB5B, VAMP2, DYNLL1, RAB11B, CREB5, DCTN4, DYNC2LI1, CREB3L2, DCTN5
KEGG	hsa05216	Thyroid cancer	14/1652	3.48E-02	BAK1, CCND1, CDKN1A, CTNNB1, KRAS, MYC, NRAS, MAPK1, MAPK3, TCF7, TCF7L2, TP53, TPM3, CCDC6
KEGG	hsa00520	Amino sugar and nucleotide sugar metabolism	17/1652	3.53E-02	CYB5R3, GFPT1, GPI, HK1, HK2, MPI, PGM3, PMM2, UGDH, UGP2, GFPT2, GNPDA1, GNE, GMPPA, GNPNAT1, UAP1L1, NANP
KEGG	hsa04625	C-type lectin receptor signaling pathway	31/1652	4.43E-02	AKT2, RHOA, CALM1, CALM2, CALM3, MAPK14, CYLD, EGR3, IKBKB, IRF1, ITPR1, ITPR2, JUN, KRAS, NFKB1, NRAS, PIK3CB, PPP3CA, PPP3R1, MAPK1, MAPK3, MAPK8, MAPK9, PTPN11, SRC, STAT1, STAT2, SYK, KSR1, AKT3, ARHGEF12
KEGG	hsa04512	ECM-receptor interaction	27/1652	4.43E-02	CD44, CD47, COL1A1, COL1A2, COL4A1, COL4A2, COL4A5, COL4A6, COL6A2, DAG1, FN1, ITGA6, ITGA3, ITGA5, ITGAV, ITGB1, ITGB8, LAMA4, LAMC1, LAMC2, SDC4, THBS1, THBS3, ITGA8, SV2A, FREM2, AGRN
KEGG	hsa04540	Gap junction	27/1652	4.43E-02	ADCY1, ADCY6, ADCY9, ADRB1, CSNK1D, EGFR, GJA1, GNAI2, GNAI3, GNAQ, GNAS, GRB2, GUCY1A2, ITPR1, ITPR2, KRAS, NRAS, PDGFA, PDGFB, PDGFRA, PRKCA, MAPK1, MAPK3, SOS1, SRC, TUBB4A, MAP3K2
KEGG	hsa04630	JAK-STAT signaling pathway	45/1652	4.43E-02	AKT2, CCND1, BCL2, BCL2L1, CCND2, CDKN1A, CREBBP, EGFR, EP300, FHL1, GRB2, IFNAR1, IFNAR2, IL6R, IL6ST, IL7R, IL12RB2, IL13RA1, IL15RA, LIFR, MCL1, MYC, PDGFA, PDGFB, PDGFRA, PIK3CB, PIM1, PRLR, PTPN11, SOS1, STAT1, STAT2, STAT3, STAT5B, SOCS1, SOCS2, OSMR, SOCS6, SOCS5, AKT3, PIAS3, IL24, SOCS7, PIAS4, SOCS4
KEGG	hsa04114	Oocyte meiosis	37/1652	4.58E-02	ADCY1, ADCY6, ADCY9, AR, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, MAPK14, IGF1R, ITPR1, ITPR2, MAD2L1, PGR, PPP1CA, PPP1CB, PPP1CC, PPP2CA, PPP2R1A, PPP2R5D, PPP3CA, PPP3R1, MAPK1, MAPK3, RPS6KA3, SKP1, AURKA, YWHAE, YWHAG, SMC1A, BTRC, CCNE2, SLK, CPEB3, CPEB4, CPEB2
KEGG	hsa01524	Platinum drug resistance	23/1652	4.95E-02	AKT2, FAS, ATM, ATP7A, BAK1, BCL2, BCL2L1, BRCA1, CASP3, CDKN1A, ERBB2, GSTM3, MLH1, PIK3CB, MAPK1, MAPK3, REV3L, TOP2B, TP53, FADD, AKT3, BBC3, CYCS
KEGG	hsa04713	Circadian entrainment	29/1652	4.95E-02	ADCY1, ADCY6, ADCY9, ADCYAP1R1, CACNA1C, CALM1, CALM2, CALM3, CAMK2A, CAMK2D, CREB1, GNAI2, GNAI3, GNAQ, GNAS, GNB1, GNG7, GRIA4, GUCY1A2, ITPR1, KCNJ3, PRKCA, MAPK1, MAPK3, PER3, PER2, RPS6KA5, NOS1AP, GNB4

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.