

Supplementary Table 2
Gene ontology (GO) analysis generated from up-regulated and down-regulated DE-genes

Category		Gene numbers	p-value	Genes
GO - Biological Process				
GO:0010467	Gene expression	141	6.47E-04	MORF4L1, STAT5A, LOC100158121, NAA15, SYNCRIP, RPS6KB1, FOXO3, ENPEP, NR2E3, NF1L1, SART1, CITED2, KDM1B, APP, MDPIC, WWP1, ZNF445, RARB, EIF2B2, SAMD4A, GNL3, PPP1CC, TBR1, HHEX, EP300, EIF2S1, MED17, TFAP2A, TNFAIP3, TDRD7, NFKBIA, KEAP1, MYBL2, CCL4, UHMK1, NR2C2, RPS27, HNRNPK, DD46, KLKB1, LEO1, HELLS, TRAF3, TAF2, ZNF398, IKZF4, DNMT3A, TAF5, SMAD7, KLF11, MPHOSPH10, LOC100154071, DENR, FXR2, RBMX, FOXF1, ATM, RNFB, ATFB, SFRP5, ETS1, PHEX, COPP5, CCNT1, ZNF518A, LOC100627422, DDR2, CDC45, NOS2, MSN, CASP1, KDM5B, FANCA, LOC100621389, CHUK, FTSJ3, LOC100153329, ABCE1, TBL1XR1, SNAPC5, CCNK, ACTA1, ARID5B, LDB1, SAA3, TLE4, EIF4G1, TARS, INHBA, FANCD2, HIPK3, UCHL5, CUX2, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NR3C1, NEO1, VARS, DTNBP1, ZFP36L1, TFAM, SF3B1, TNFRSF1B, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, INPP5B, BCL9, CHD3, CEBPA, BRD2, KATZB, CEBPB, ZNF667, SIRT2, RGS14, SIRT2, SOD2, ATXN1, RPS6KA3, PAPOLA, HBZ, IRF1, NOP58, NOP56, ZBTB1, BMPR1A, RNF111
*GO:0006351	Transcription, DNA-templated	91	4.38E-05	MORF4L1, COPP5, STAT5A, LOC100158121, CCNT1, NAA15, FOXO3, NR2E3, ZNF518A, NF1L1, LOC100627422, DDR2, CITED2, CDC45, APP, MDPIC, WWP1, ZNF445, RARB, KDM5B, FANCA, LOC100153329, LOC100621389, CHUK, GNL3, SNAPC5, TBL1XR1, CCNK, LDB1, ARID5B, SAA3, TLE4, TBR1, INHBA, HHEX, EP300, FANCD2, HIPK3, MED17, UCHL5, TFAP2A, CUX2, TNFAIP3, MTDH, UBE3A, SAV1, NFKBIA, KEAP1, NR3C1, NEO1, MYBL2, NR2C2, TFAM, HNRNPK, MAP3K2, AGO1, LEO1, KDM3A, BCL9, CEBPA, TAF2, DNMT3A, IKZF4, KATZB, TAF5, SMAD7, KLF11, RBMX, SIRT2, FOXF1, RNFB, ATFB, CEBPB, SMAD7, TAF5, KLF11, ZNF667, LOC100154071, RBMX, FOXF1, RGS14, SIRT2, SOD2, SFRP5, ATFB, RNFB, ATXN1, RPS6KA3, ETS1, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0006366	Transcription from RNA polymerase II promoter	51	3.77E-03	COPP5, STAT5A, CCNT1, NR2E3, NF1L1, LOC100627422, CITED2, APP, RARB, CHUK, GNL3, SNAPC5, TBL1XR1, CCNK, LDB1, TLE4, TBR1, INHBA, HHEX, EP300, MED17, TFAP2A, MTDH, UBE3A, NFKBIA, NEO1, NR3C1, NR2C2, AGO1, LEO1, KDM3A, BCL9, CEBPA, TAF2, DNMT3A, IKZF4, KATZB, TAF5, SMAD7, KLF11, RBMX, SIRT2, FOXF1, RNFB, ATFB, RPS6KA3, ETS1, HBZ, IRF1, ZBTB1, BMPR1A
GO:0034645	Cellular macromolecule biosynthetic process	131	5.09E-04	MORF4L1, STAT5A, LOC100158121, NAA15, SYNCRIP, RPS6KB1, FOXO3, NR2E3, NF1L1, CITED2, ST3GAL1, APP, APOA1, MDPIC, ST3GAL4, WWP1, ZNF445, RARB, EIF2B2, SAMD4A, GNL3, POLS1, TBR1, HHEX, EP300, EIF2S1, MED17, MCMBP, TFAP2A, TNFAIP3, ENP1, NFKBIA, KEAP1, MYBL2, NR2C2, UHMK1, RPS27, HNRNPK, LEO1, HELLS, TRAF3, TAF2, ZNF398, IKZF4, DNMT3A, SMAD7, TAF5, KLF11, LOC100154071, DENR, FXR2, RBMX, FOXF1, ATM, SFRP5, ATFB, RNFB, ETS1, PHEX, GRB7, ALG12, ABCF1, CPFB2, COPP5, CPFB4, CCNT1, DPY19L4, ZNF518A, LOC100627422, DDR2, CDC45, KDM5B, TNIP1, FANCA, LOC100621389, CHUK, LOC100153329, ABCE1, TBL1XR1, SNAPC5, CCNK, ARID5B, LDB1, PIK3V, SAA3, CHS13, TLE4, EIF4G1, TARS, INHBA, FANCD2, HIPK3, UCHL5, CHSY1, CUX2, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NR3C1, NEO1, VARS, ZFP36L1, TFAM, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, BCL9, CHD3, CEBPA, BRD2, KATZB, CEBPB, ZNF667, RGS14, SIRT2, SOD2, ATXN1, RPS6KA3, HBZ, CSGALNACT2, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0018130	Heterocycle biosynthetic process	107	1.66E-03	MORF4L1, STAT5A, LOC100158121, NAA15, FOXO3, NR2E3, NF1L1, CITED2, TPX1, APP, MDPIC, WWP1, RARB, ZNF445, ATFB, SAMD4A, GNL3, TBR1, HHEX, EP300, MED17, TFAP2A, TNFAIP3, PRPS2, NFKBIA, KEAP1, MRAP2, MYBL2, CCL4, NR2C2, HNRNPK, LEO1, HELLS, TRAF3, ZNF398, TAF2, IKZF4, DNMT3A, SMAD7, TAF5, KLF11, LOC100154071, RBMX, FOXF1, RNFB, ATFB, SFRP5, ETS1, PHEX, COPP5, CCNT1, ZNF518A, DDR2, LOC100627422, CDC45, ATP5Q, FANCA, KDM5B, LOC100153329, CHUK, LOC100621389, TBL1XR1, SNAPC5, CCNK, LDB1, ARID5B, SAA3, TLE4, INHBA, FANCD2, HIPK3, UCHL5, CUX2, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, TFAM, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, CHD3, BCL9, CEBPA, BRD2, KATZB, CEBPB, ZNF667, AMPD3, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0034654	Nucleobase-containing compound biosynthetic process	106	1.30E-03	MORF4L1, STAT5A, LOC100158121, NAA15, FOXO3, NR2E3, NF1L1, CITED2, APP, MDPIC, WWP1, RARB, ZNF445, ATFB, SAMD4A, GNL3, TBR1, HHEX, EP300, MED17, TFAP2A, TNFAIP3, PRPS2, NFKBIA, KEAP1, MRAP2, MYBL2, CCL4, NR2C2, HNRNPK, LEO1, HELLS, TRAF3, ZNF398, TAF2, IKZF4, DNMT3A, SMAD7, TAF5, KLF11, LOC100154071, RBMX, FOXF1, RNFB, ATFB, SFRP5, ETS1, PHEX, COPP5, CCNT1, ZNF518A, DDR2, LOC100627422, CDC45, ATP5Q, FANCA, KDM5B, LOC100153329, CHUK, LOC100621389, TBL1XR1, SNAPC5, CCNK, LDB1, ARID5B, SAA3, TLE4, INHBA, FANCD2, HIPK3, UCHL5, CUX2, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, TFAM, MAP3K2, CHD2, AGO1, MYCBP, KDM3A, PHF20L1, CHD3, BCL9, CEBPA, BRD2, KATZB, CEBPB, ZNF667, AMPD3, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
**GO:0019438	Aromatic compound biosynthetic process	107	1.82E-03	MORF4L1, STAT5A, LOC100158121, NAA15, FOXO3, NR2E3, NF1L1, CITED2, TPX1, APP, MDPIC, WWP1, RARB, ZNF445, ATFB, SAMD4A, GNL3, TBR1, HHEX, EP300, MED17, TFAP2A, TNFAIP3, PRPS2, NFKBIA, KEAP1, MRAP2, MYBL2, CCL4, NR2C2, HNRNPK, LEO1, HELLS, TRAF3, ZNF398, TAF2, IKZF4, DNMT3A, SMAD7, TAF5, KLF11, LOC100154071, RBMX, FOXF1, RNFB, ATFB, SFRP5, ETS1, PHEX, COPP5, CCNT1, ZNF518A, DDR2, LOC100627422, CDC45, ATP5Q, FANCA, KDM5B, LOC100153329, CHUK, LOC100621389, TBL1XR1, SNAPC5, CCNK, LDB1, ARID5B, SAA3, TLE4, INHBA, FANCD2, HIPK3, UCHL5, CUX2, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, TFAM, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, CHD3, BCL9, CEBPA, BRD2, KATZB, CEBPB, ZNF667, AMPD3, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
GO:0010468	Regulation of gene expression	118	7.30E-06	MORF4L1, STAT5A, LOC100158121, NAA15, SYNCRIP, RPS6KB1, FOXO3, NR2E3, CITED2, KDM1B, APP, MDPIC, WWP1, RARB, EIF2B2, SAMD4A, GNL3, PPP1CC, TBR1, HHEX, EP300, EIF2S1, MED17, TFAP2A, TNFAIP3, TDRD7, NFKBIA, KEAP1, MYBL2, CCL4, NR2C2, UHMK1, DD46, HNRNPK, LEO1, HELLS, TRAF3, TAF2, ZNF398, IKZF4, DNMT3A, SMAD7, KLF11, LOC100154071, FXR2, RBMX, FOXF1, ATM, RNFB, ATFB, SFRP5, ETS1, PHEX, GRB7, ABCF1, CPFB2, COPP5, CPFB4, CCNT1, LOC100627422, DDR2, CDC45, NOS2, MSN, KDM5B, FANCA, CHUK, LOC100153329, TBL1XR1, CCNK, ACTA1, ARID5B, LDB1, SAA3, TLE4, EIF4G1, INHBA, FANCD2, UCHL5, CUX2, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NR3C1, NEO1, DTNBP1, ZFP36L1, TFAM, TNFRSF1B, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, INPP5B, BCL9, CHD3, CEBPA, BRD2, KATZB, CEBPB, ZNF667, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, PAPOLA, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0010628	Positive regulation of gene expression	53	7.62E-04	ABCF1, COPP5, STAT5A, CCNT1, NAA15, RPS6KB1, NR2E3, APP, MDPIC, RARB, MSN, KDM5B, SAMD4A, CHUK, GNL3, TBL1XR1, CCNK, ACTA1, LDB1, TBR1, HHEX, INHBA, EP300, MED17, TFAP2A, CUX2, UBE3A, NFKBIA, NR3C1, DTNBP1, NR2C2, UHMK1, TFAM, MAP3K2, AGO1, LEO1, KDM3A, BCL9, CEBPA, TAF2, IKZF4, KATZB, CEBPB, RBMX, SIRT2, FOXF1, ATFB, RPS6KA3, ETS1, IRF1, RNF111, BMPR1A
*GO:0010629	Negative regulation of gene expression	43	7.43E-03	MORF4L1, MTDH, CPFB2, CPFB4, CCNT1, LOC100158121, SYNCRIP, NR2E3, LOC100627422, CCL4, ZFP36L1, CDC45, MDPIC, WWP1, AGO1, RARB, NOS2, KDM5B, LOC100153329, SAMD4A, HELLS, CEBPA, TBL1XR1, DNMT3A, IKZF4, SMAD7, LDB1, KLF11, LOC100154071, SAA3, TLE4, FXR2, FOXF1, SIRT2, ATXN1, RNFB, EP300, EIF2S1, HBZ, IRF1, TFAP2A, GRB7, ZBTB1
*GO:0016458	Gene silencing	8	5.08E-02	MORF4L1, DNMT3A, CDC45, LOC100158121, AGO1, LOC100154071, HELLS, LOC100153329
*GO:0006342	Chromatin silencing	7	1.10E-02	MORF4L1, DNMT3A, CDC45, LOC100158121, LOC100154071, HELLS, LOC100153329
*GO:0045814	Negative regulation of gene expression	7	1.45E-02	MORF4L1, DNMT3A, CDC45, LOC100158121, LOC100154071, HELLS, LOC100153329
*GO:0010608	Posttranscriptional regulation of gene expression	18	2.23E-03	ABCF1, CPFB2, TDRD7, CPFB4, SYNCRIP, RPS6KB1, FOXO3, FXR2, UHMK1, EIF4G1, ZFP36L1, TNFRSF1B, APP, EIF2S1, AGO1, EIF2B2, GRB7, SAMD4A
*GO:0006417	Regulation of translation	16	2.27E-03	ABCF1, CPFB2, CPFB4, SYNCRIP, RPS6KB1, FOXO3, FXR2, UHMK1, EIF4G1, ZFP36L1, APP, EIF2S1, AGO1, EIF2B2, GRB7, SAMD4A
**GO:0017148	Negative regulation of translation	9	8.77E-03	ZFP36L1, CPFB2, EIF2S1, CPFB4, AGO1, SYNCRIP, FXR2, GRB7, SAMD4A
*GO:0040029	Regulation of gene expression, epigenetic	9	5.98E-02	MORF4L1, KDM1B, DNMT3A, CDC45, LOC100158121, AGO1, LOC100154071, HELLS, LOC100153329

GO:0051171	Regulation of nitrogen compound metabolic process	117	1,77E-05	MORF4L1, STAT5A, LOC100158121, NAA15, SYNCRIP, RPS6KB1, FOXO3, NR2E3, CITED2, KDM1B, APP, MDFIC, WWP1, RARB, EIF2B2, SAMD4A, GNL3, FBP1, TBR1, HHEX, EP300, EIF2F5, MED17, TFAP2A, TNFAIP3, MEI1, ASS1, NFKBIA, KEAP1, MRAP2, MYBL2, CCL4, NR2C2, UHMK1, HNRNPK, LPCAT1, LEO1, HELLS, TRAF3, TAF2, ZNF398, IKZF4, DNMT3A, SMAD7, KLF11, LOC100154071, FOXJ2, RBMX, FOXP1, RNFB, ATF6, SFRP5, ETS1, PARPBP, PHEX, GRB7, ABCF1, CPEB2, COP55, CPEB4, CCNT1, DDR2, LOC100627422, CDC45, KDM5B, FANCA, CHUK, LOC100153329, TBL1XR1, CCNK, ARID5B, LDB1, SAA3, TLE4, RAD52, EPF4G1, INHBA, FANCD2, UCHL5, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, ZFP36L1, TFAM, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, ACSL3, TRIP12, BCL9, CHD3, CEBPA, BRD2, KATZB, CEBPB, ZNF667, SIRT2, RGS14, SOD2, ATXN1, SAMD5, RPS6KA3, PAPOLA, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0019219	Regulation of nucleobase-containing compound metabolic process	101	1,50E-03	MORF4L1, STAT5A, LOC100158121, NAA15, NR2E3, CITED2, KDM1B, APP, MDFIC, WWP1, RARB, SAMD4A, GNL3, FBP1, TBR1, HHEX, EP300, MED17, TFAP2A, TNFAIP3, MEI1, NFKBIA, KEAP1, MRAP2, MYBL2, CCL4, NR2C2, UHMK1, HNRNPK, LEO1, HELLS, TRAF3, ZNF398, TAF2, IKZF4, DNMT3A, SMAD7, KLF11, LOC100154071, RBMX, FOXP1, RNFB, ATF6, SFRP5, ETS1, PARPBP, PHEX, COP55, CCNT1, DDR2, LOC100627422, CDC45, FANCA, KDM5B, LOC100153329, CHUK, TBL1XR1, CCNK, LDB1, ARID5B, SAA3, TLE4, TBR1, INHBA, HHEX, EP300, FANCD2, MED17, UCHL5, TFAP2A, TNFAIP3, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NFKBIA, KEAP1, NR3C1, NEO1, MYBL2, CCL4, NR2C2, UHMK1, TFAM, HNRNPK, MAP3K2, AGO1, CHD2, LEO1, MYCBP, KDM3A, PHF20L1, HELLS, BCL9, CHD3, TRAF3, CEBPA, ZNF398, TAF2, IKZF4, DNMT3A, BRD2, KATZB, CEBPB, SMAD7, KLF11, LOC100154071, ZNF667, RBMX, FOXP1, RGS14, SIRT2, SOD2, SFRP5, ATF6, RNFB, ATXN1, RPS6KA3, PAPOLA, ETS1, HBZ, IRF1, PHEX, ZBTB1, RNF111, BMPR1A
*GO:0051252	Regulation of RNA metabolic process	94	6,65E-04	MORF4L1, COP55, STAT5A, LOC100158121, CCNT1, NAA15, NR2E3, LOC100627422, DDR2, CITED2, CDC45, APP, MDFIC, WWP1, RARB, KDM5B, FANCA, LOC100153329, CHUK, SAMD4A, GNL3, TBL1XR1, CCNK, LDB1, ARID5B, SAA3, TLE4, TBR1, INHBA, HHEX, EP300, FANCD2, MED17, UCHL5, TFAP2A, TNFAIP3, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NFKBIA, KEAP1, NR3C1, NEO1, MYBL2, CCL4, NR2C2, UHMK1, TFAM, HNRNPK, MAP3K2, AGO1, CHD2, LEO1, MYCBP, KDM3A, PHF20L1, HELLS, BCL9, CHD3, TRAF3, CEBPA, ZNF398, TAF2, IKZF4, DNMT3A, BRD2, KATZB, CEBPB, SMAD7, KLF11, LOC100154071, ZNF667, RBMX, FOXP1, RGS14, SIRT2, SOD2, SFRP5, ATF6, RNFB, ATXN1, RPS6KA3, PAPOLA, ETS1, HBZ, IRF1, PHEX, ZBTB1, RNF111, BMPR1A
*GO:2001141	Regulation of RNA biosynthetic process	92	3,29E-04	MORF4L1, COP55, STAT5A, LOC100158121, CCNT1, NAA15, NR2E3, LOC100627422, DDR2, CITED2, CDC45, APP, MDFIC, WWP1, RARB, KDM5B, FANCA, LOC100153329, CHUK, SAMD4A, GNL3, TBL1XR1, CCNK, LDB1, ARID5B, SAA3, TLE4, TBR1, INHBA, HHEX, EP300, FANCD2, MED17, UCHL5, TFAP2A, TNFAIP3, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NFKBIA, KEAP1, NR3C1, NEO1, MYBL2, CCL4, NR2C2, UHMK1, TFAM, HNRNPK, MAP3K2, AGO1, CHD2, LEO1, MYCBP, KDM3A, PHF20L1, HELLS, BCL9, CHD3, TRAF3, CEBPA, ZNF398, TAF2, IKZF4, DNMT3A, BRD2, KATZB, CEBPB, SMAD7, KLF11, ZNF667, LOC100154071, RBMX, FOXP1, RGS14, SIRT2, SOD2, SFRP5, ATF6, RNFB, ATXN1, RPS6KA3, ETS1, HBZ, IRF1, PHEX, ZBTB1, RNF111, BMPR1A
*GO:1903506		91	4,60E-04	MORF4L1, COP55, STAT5A, LOC100158121, CCNT1, NAA15, NR2E3, LOC100627422, DDR2, CITED2, CDC45, APP, MDFIC, WWP1, RARB, KDM5B, FANCA, LOC100153329, CHUK, SAMD4A, GNL3, TBL1XR1, CCNK, LDB1, ARID5B, SAA3, TLE4, TBR1, INHBA, HHEX, EP300, FANCD2, MED17, UCHL5, TFAP2A, TNFAIP3, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NFKBIA, KEAP1, NR3C1, NEO1, MYBL2, NR2C2, TFAM, HNRNPK, MAP3K2, AGO1, CHD2, LEO1, MYCBP, KDM3A, PHF20L1, HELLS, BCL9, CHD3, TRAF3, CEBPA, ZNF398, TAF2, IKZF4, DNMT3A, BRD2, KATZB, CEBPB, SMAD7, KLF11, ZNF667, LOC100154071, RBMX, FOXP1, RGS14, SIRT2, SOD2, SFRP5, ATF6, RNFB, ATXN1, RPS6KA3, ETS1, HBZ, IRF1, PHEX, ZBTB1, RNF111, BMPR1A
*GO:0006355	Regulation of transcription, DNA-templated	91	4,36E-04	MORF4L1, COP55, STAT5A, LOC100158121, CCNT1, NAA15, NR2E3, LOC100627422, DDR2, CITED2, CDC45, APP, MDFIC, WWP1, RARB, KDM5B, FANCA, LOC100153329, CHUK, SAMD4A, GNL3, TBL1XR1, CCNK, LDB1, ARID5B, SAA3, TLE4, TBR1, INHBA, HHEX, EP300, FANCD2, MED17, UCHL5, TFAP2A, TNFAIP3, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NFKBIA, KEAP1, NR3C1, NEO1, MYBL2, NR2C2, TFAM, HNRNPK, MAP3K2, AGO1, CHD2, LEO1, MYCBP, KDM3A, PHF20L1, HELLS, BCL9, CHD3, TRAF3, CEBPA, ZNF398, TAF2, IKZF4, DNMT3A, BRD2, KATZB, CEBPB, SMAD7, KLF11, ZNF667, LOC100154071, RBMX, FOXP1, RGS14, SIRT2, SOD2, SFRP5, ATF6, RNFB, ATXN1, RPS6KA3, ETS1, HBZ, IRF1, PHEX, ZBTB1, RNF111, BMPR1A
*GO:0006357	Regulation of transcription from RNA polymerase II promoter	54	4,19E-03	COP55, STAT5A, CCNT1, NR2E3, LOC100627422, CITED2, APP, RARB, CHUK, GNL3, TBL1XR1, CCNK, LDB1, ARID5B, TLE4, TBR1, INHBA, HHEX, EP300, MED17, TFAP2A, MTDH, UBE3A, NFKBIA, ATXN1, NR3C1, MYBL2, NR2C2, HNRNPK, AGO1, LEO1, KDM3A, BCL9, CEBPA, TAF2, DNMT3A, IKZF4, BRD2, KATZB, SMAD7, KLF11, ZNF667, LOC100154071, RBMX, FOXP1, RGS14, SIRT2, SOD2, RNFB, ATF6, RPS6KA3, ETS1, HBZ, IRF1, ZBTB1, BMPR1A
*GO:0051090	Regulation of sequence-specific DNA binding transcription factor activity	15	2,97E-02	SFRP5, MTDH, CEBPB, EP300, FANCD2, SMAD7, SAV1, ARID5B, NFKBIA, KEAP1, TNFAIP3, FANCA, DDR2, TRAF3
**GO:0051173	Positive regulation of nitrogen compound metabolic process	53	3,05E-03	ABCF1, COP55, STAT5A, CCNT1, NAA15, RPS6KB1, NR2E3, APP, MDFIC, RARB, SAMD4A, CHUK, GNL3, TBL1XR1, CCNK, LDB1, TBR1, HHEX, INHBA, EP300, MED17, TFAP2A, ASS1, UBE3A, NFKBIA, MRAP2, NR3C1, NR2C2, UHMK1, TFAM, MAP3K2, AGO1, LEO1, KDM3A, ACSL3, BCL9, CEBPA, TAF2, IKZF4, KATZB, CEBPB, RBMX, SIRT2, FOXP1, SOD2, RNFB, ATF6, RPS6KA3, ETS1, IRF1, RNF111, BMPR1A
*GO:0045935	Positive regulation of nucleobase-containing compound metabolic process	46	2,25E-02	COP55, UBE3A, STAT5A, CCNT1, NAA15, NFKBIA, MRAP2, NR2E3, NR3C1, NR2C2, TFAM, APP, MDFIC, MAP3K2, AGO1, LEO1, KDM3A, RARB, CHUK, GNL3, BCL9, CEBPA, TAF2, TBL1XR1, IKZF4, CCNK, KATZB, CEBPB, LDB1, TBR1, RBMX, FOXP1, SIRT2, RNFB, ATF6, HHEX, INHBA, RPS6KA3, EP300, ETS1, MED17, IRF1, TFAP2A, BMPR1A, RNF111
*GO:0051254	Positive regulation of RNA metabolic process	44	2,98E-03	COP55, UBE3A, STAT5A, CCNT1, NAA15, NFKBIA, NR2E3, NR3C1, NR2C2, TFAM, APP, MDFIC, MAP3K2, AGO1, LEO1, KDM3A, RARB, CHUK, GNL3, BCL9, CEBPA, TAF2, TBL1XR1, IKZF4, CCNK, KATZB, CEBPB, LDB1, TBR1, RBMX, FOXP1, SIRT2, ATF6, HHEX, INHBA, RPS6KA3, EP300, ETS1, MED17, IRF1, TFAP2A, BMPR1A, RNF111
*GO:1902690	Positive regulation of RNA biosynthetic process	44	1,41E-03	COP55, UBE3A, STAT5A, CCNT1, NAA15, NFKBIA, NR2E3, NR3C1, NR2C2, TFAM, APP, MDFIC, MAP3K2, AGO1, LEO1, KDM3A, RARB, CHUK, GNL3, BCL9, CEBPA, TAF2, TBL1XR1, IKZF4, CCNK, KATZB, CEBPB, LDB1, TBR1, RBMX, FOXP1, SIRT2, ATF6, HHEX, INHBA, RPS6KA3, EP300, ETS1, MED17, IRF1, TFAP2A, BMPR1A, RNF111
*GO:1903508	Positive regulation of nucleic acid-templated transcription	43	2,18E-03	COP55, UBE3A, STAT5A, CCNT1, NAA15, NFKBIA, NR2E3, NR3C1, NR2C2, TFAM, APP, MAP3K2, AGO1, LEO1, KDM3A, RARB, CHUK, GNL3, BCL9, CEBPA, TAF2, IKZF4, TBL1XR1, CCNK, KATZB, CEBPB, LDB1, TBR1, RBMX, FOXP1, SIRT2, ATF6, HHEX, INHBA, RPS6KA3, EP300, ETS1, MED17, IRF1, TFAP2A, BMPR1A, RNF111
*GO:0045893	Positive regulation of transcription, DNA-templated	43	2,18E-03	COP55, UBE3A, STAT5A, CCNT1, NAA15, NFKBIA, NR2E3, NR3C1, NR2C2, TFAM, APP, MAP3K2, AGO1, LEO1, KDM3A, RARB, CHUK, GNL3, BCL9, CEBPA, TAF2, TBL1XR1, CCNK, KATZB, CEBPB, LDB1, TBR1, RBMX, FOXP1, SIRT2, ATF6, HHEX, INHBA, RPS6KA3, EP300, ETS1, MED17, IRF1, TFAP2A, BMPR1A, RNF111
*GO:0045944	Positive regulation of transcription from RNA polymerase II promoter	36	4,39E-04	COP55, UBE3A, STAT5A, CCNT1, NFKBIA, NR2E3, NR3C1, NR2C2, APP, AGO1, LEO1, KDM3A, RARB, CHUK, GNL3, BCL9, TAF2, IKZF4, TBL1XR1, CCNK, KATZB, LDB1, TBR1, RBMX, FOXP1, SIRT2, ATF6, HHEX, INHBA, RPS6KA3, EP300, ETS1, MED17, IRF1, TFAP2A, BMPR1A
**GO:0051172	Negative regulation of nitrogen compound metabolic process	46	1,85E-03	MORF4L1, MTDH, CPEB2, CPEB4, CCNT1, NR2E3, CCL4, LOC100627422, SYNCRIP, NR2E3, LOC100627422, CCL4, ZFP36L1, CDC45, LPCAT1, MDFIC, WWP1, AGO1, RARB, KDM5B, LOC100153329, TRIP12, SAMD4A, HELLS, CEBPA, TBL1XR1, DNMT3A, IKZF4, SMAD7, LDB1, KLF11, FBP1, LOC100154071, SAA3, TLE4, FOXJ2, FOXO1, SIRT2, ATXN1, RNFB, EP300, EIF2B1, PARPBP, HBZ, IRF1, TFAP2A, GRB7, ZBTB1
*GO:0045934	Negative regulation of nucleobase-containing compound metabolic process	36	4,22E-02	MORF4L1, MTDH, LOC100158121, CCNT1, NR2E3, CCL4, LOC100627422, CDC45, MDFIC, WWP1, RARB, KDM5B, LOC100153329, TRIP12, HELLS, CEBPA, IKZF4, DNMT3A, TBL1XR1, SMAD7, LDB1, KLF11, FBP1, LOC100154071, SAA3, TLE4, FOXO1, SIRT2, ATXN1, RNFB, EP300, PARPBP, HBZ, IRF1, TFAP2A, ZBTB1
*GO:0051253	Negative regulation of RNA metabolic process	33	4,13E-02	MORF4L1, MTDH, LOC100158121, CCNT1, NR2E3, CCL4, LOC100627422, CDC45, MDFIC, WWP1, RARB, KDM5B, LOC100153329, HELLS, CEBPA, IKZF4, DNMT3A, TBL1XR1, SMAD7, LDB1, KLF11, LOC100154071, SAA3, TLE4, FOXO1, SIRT2, ATXN1, RNFB, EP300, HBZ, IRF1, TFAP2A, ZBTB1
*GO:1902679	Negative regulation of RNA biosynthetic process	32	3,99E-02	MORF4L1, MTDH, LOC100158121, NR2E3, CCL4, LOC100627422, CDC45, MDFIC, WWP1, RARB, KDM5B, LOC100153329, HELLS, CEBPA, IKZF4, DNMT3A, TBL1XR1, SMAD7, LDB1, KLF11, LOC100154071, SAA3, TLE4, FOXO1, SIRT2, ATXN1, RNFB, EP300, HBZ, IRF1, TFAP2A, ZBTB1
*GO:1903507	Negative regulation of nucleic acid-templated transcription	31	5,16E-02	MORF4L1, MTDH, LOC100158121, NR2E3, LOC100627422, CDC45, MDFIC, WWP1, RARB, KDM5B, LOC100153329, HELLS, CEBPA, IKZF4, DNMT3A, TBL1XR1, SMAD7, LDB1, KLF11, LOC100154071, SAA3, TLE4, FOXO1, SIRT2, ATXN1, RNFB, EP300, HBZ, IRF1, TFAP2A, ZBTB1
*GO:0045892	Negative regulation of transcription, DNA-templated	31	4,89E-02	MORF4L1, MTDH, LOC100158121, NR2E3, LOC100627422, CDC45, MDFIC, WWP1, RARB, KDM5B, LOC100153329, HELLS, CEBPA, IKZF4, DNMT3A, TBL1XR1, SMAD7, LDB1, KLF11, LOC100154071, SAA3, TLE4, FOXO1, SIRT2, ATXN1, RNFB, EP300, HBZ, IRF1, TFAP2A, ZBTB1

GO:0016070	RNA metabolic process	117	2,63E-03	MORF4L1, STAT5A, LOC100158121, NAA15, FOXO3, NR2E3, NFXL1, SART3, CITED2, APP, MDR1C, WWP1, RARB, ZNF445, SAMD4A, GNL3, TBR1, HHEX, EP300, MED17, TFAP2A, TNFAIP3, NFKBIA, KEAP1, MYBL2, CCL4, NR2C2, UHMK1, DDXX46, HNRNP, LEO1, HELLS, TRAF3, TAF2, ZNF398, IKZF4, DNMT3A, SMAD7, TAF5, KLF11, MPHOSPH10, LOC100154071, RBMX, FOXP1, ATM, RNFB, ATF6, SFRP5, ETS1, WDR3, PABPC1L, PHEX, COPP5, CCNT1, ZNF518A, LOC100627422, DDR2, CDC45, KDM5B, FANCA, LOC100621389, CHUK, FTSJ3, LOC100153329, TBL1XR1, SNAPC5, CCNK, ARID5B, LDB1, SAA3, TLE4, TARS, INHBA, FANCD2, HPK3, UCHL5, CUX2, KIAA1429, SBN01, MTDH, UBE3A, ZBTB11, SAV1, NR3C1, NEO1, VARS, ZFP36L1, TFAM, SF3B1, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, BCL9, CHD3, CEBPA, BRD2, KAT2B, CEBPB, ZNF667, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, PAPOLA, HBZ, IRF1, NOP56, NOP56, ZBTB1, RNF111, BMPR1A
*GO:0032774	RNA biosynthetic process	101	1,04E-04	MORF4L1, STAT5A, LOC100158121, NAA15, FOXO3, NR2E3, NFXL1, CITED2, APP, MDR1C, WWP1, RARB, ZNF445, SAMD4A, GNL3, TBR1, HHEX, EP300, MED17, TFAP2A, TNFAIP3, NFKBIA, KEAP1, MYBL2, CCL4, NR2C2, HNRNP, LEO1, HELLS, TRAF3, ZNF398, TAF2, IKZF4, DNMT3A, SMAD7, TAF5, KLF11, LOC100154071, RBMX, FOXO1, RNFB, ATF6, SFRP5, ETS1, PHEX, COPP5, CCNT1, ZNF518A, DDR2, LOC100627422, CDC45, FANCA, KDM5B, LOC100153329, CHUK, LOC100621389, TBL1XR1, SNAPC5, CCNK, LDB1, ARID5B, SAA3, TLE4, INHBA, FANCD2, HPK3, UCHL5, CUX2, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, TFAM, MAP3K2, CHD2, AGO1, KDM3A, MYCBP, PHF20L1, CHD3, BCL9, CEBPA, BRD2, KAT2B, CEBPB, ZNF667, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0097659	Nucleic acid-templated transcription	100	1,36E-04	MORF4L1, STAT5A, LOC100158121, NAA15, FOXO3, NR2E3, NFXL1, CITED2, APP, MDR1C, WWP1, RARB, ZNF445, SAMD4A, GNL3, TBR1, HHEX, EP300, MED17, TFAP2A, TNFAIP3, NFKBIA, KEAP1, MYBL2, NR2C2, HNRNP, LEO1, HELLS, TRAF3, ZNF398, TAF2, IKZF4, DNMT3A, SMAD7, TAF5, KLF11, LOC100154071, RBMX, FOXO1, RNFB, ATF6, SFRP5, ETS1, PHEX, COPP5, CCNT1, ZNF518A, DDR2, LOC100627422, CDC45, FANCA, KDM5B, LOC100153329, CHUK, LOC100621389, TBL1XR1, SNAPC5, CCNK, LDB1, ARID5B, SAA3, TLE4, INHBA, FANCD2, HPK3, UCHL5, CUX2, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, TFAM, MAP3K2, CHD2, AGO1, KDM3A, MYCBP, PHF20L1, CHD3, BCL9, CEBPA, BRD2, KAT2B, CEBPB, ZNF667, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0043631	RNA polyadenylation	5	7,77E-03	APP, PAPOLA, CCNT1, LEO1, PABPC1L
*GO:0006378	mRNA polyadenylation	5	6,49E-03	APP, PAPOLA, CCNT1, LEO1, PABPC1L
*GO:0031123	RNA 3'-end processing	5	7,76E-02	APP, PAPOLA, CCNT1, LEO1, PABPC1L
*GO:0031124	mRNA 3'-end processing	5	1,08E-02	APP, PAPOLA, CCNT1, LEO1, PABPC1L
*GO:0031440	Regulation of mRNA 3'-end processing	3	3,57E-02	PAPOLA, CCNT1, LEO1
GO:0010556	Regulation of macromolecule biosynthetic process	110	1,67E-05	MORF4L1, STAT5A, LOC100158121, NAA15, SYNCRIP, RPS6KB1, FOXO3, NR2E3, CITED2, APP, MDR1C, WWP1, RARB, EIF2B2, SAMD4A, GNL3, TBR1, HHEX, EP300, EIF2S1, MED17, TFAP2A, TNFAIP3, ENPP1, NFKBIA, KEAP1, MYBL2, CCL4, NR2C2, UHMK1, HNRNP, LEO1, HELLS, TRAF3, TAF2, ZNF398, IKZF4, DNMT3A, SMAD7, KLF11, LOC100154071, FXR2, RBMX, FOXP1, RNFB, ATF6, SFRP5, ETS1, PHEX, GRB7, ABCF1, SEC24A, CPEB2, COPP5, CPEB4, CCNT1, DDR2, LOC100627422, CDC45, FANCA, KDM5B, CHUK, LOC100153329, TBL1XR1, CCNK, ARID5B, LDB1, ELANE, SAA3, TLE4, EIF4G1, INHBA, FANCD2, UCHL5, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, ZFP36L1, TFAM, MAP3K2, AGO1, CHD2, MYCBP, KDM3A, PHF20L1, BCL9, CHD3, CEBPA, BRD2, KAT2B, CEBPB, IL5, ZNF667, SIRT2, RGS14, SOD2, ATXN1, SAMD9, RPS6KA3, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
**GO:0010557	Positive regulation of macromolecule biosynthetic process	50	1,71E-03	ABCF1, COPP5, STAT5A, CCNT1, NAA15, RPS6KB1, NR2E3, APP, MDR1C, RARB, SAMD4A, CHUK, GNL3, TBL1XR1, CCNK, LDB1, ELANE, TBR1, HHEX, INHBA, EP300, MED17, TFAP2A, UBE3A, NFKBIA, NR3C1, NR2C2, UHMK1, TFAM, MAP3K2, AGO1, LEO1, KDM3A, BCL9, CEBPA, IKZF4, CEBPB, KAT2B, IL5, RBMX, SIRT2, FOXO1, ATF6, RPS6KA3, ETS1, IRF1, BMPR1A, RNF111
**GO:0010558	Negative regulation of macromolecule biosynthetic process	43	2,69E-03	MORF4L1, MTDH, ENPP1, CPEB2, CPEB4, LOC100158121, SYNCRIP, NR2E3, LOC100627422, CCL4, ZFP36L1, CDC45, MDR1C, WWP1, AGO1, RARB, KDM5B, LOC100153329, SAMD4A, HELLS, CEBPA, DNMT3A, TBL1XR1, IKZF4, SMAD7, LDB1, ELANE, KLF11, LOC100154071, SAA3, TLE4, FXR2, FOXO1, SIRT2, ATXN1, RNFB, EP300, EIF2S1, HBZ, IRF1, TFAP2A, GRB7, ZBTB1
*GO:2000112	Regulation of cellular macromolecule biosynthetic process	105	6,94E-05	MORF4L1, STAT5A, LOC100158121, NAA15, SYNCRIP, RPS6KB1, FOXO3, NR2E3, CITED2, APP, MDR1C, WWP1, RARB, EIF2B2, SAMD4A, GNL3, TBR1, HHEX, EP300, EIF2S1, MED17, TFAP2A, TNFAIP3, ENPP1, NFKBIA, KEAP1, MYBL2, NR2C2, UHMK1, HNRNP, LEO1, HELLS, TRAF3, ZNF398, TAF2, IKZF4, DNMT3A, SMAD7, KLF11, LOC100154071, RBMX, FOXO1, RNFB, ATF6, SFRP5, ETS1, PHEX, GRB7, ABCF1, CPEB2, COPP5, CPEB4, CCNT1, DDR2, LOC100627422, CDC45, FANCA, KDM5B, CHUK, LOC100153329, TBL1XR1, CCNK, LDB1, ARID5B, SAA3, TLE4, EIF4G1, INHBA, FANCD2, UCHL5, SBN01, MTDH, UBE3A, SAV1, ZBTB11, NR3C1, NEO1, ZFP36L1, TFAM, MAP3K2, CHD2, AGO1, MYCBP, KDM3A, PHF20L1, CHD3, BCL9, CEBPA, BRD2, KAT2B, CEBPB, ZNF667, SIRT2, RGS14, SOD2, ATXN1, RPS6KA3, HBZ, IRF1, ZBTB1, RNF111, BMPR1A
*GO:0031328	Positive regulation of cellular biosynthetic process	55	5,11E-04	ABCF1, COPP5, STAT5A, CCNT1, NAA15, RPS6KB1, NR2E3, APP, APOA1, MDR1C, RARB, SAMD4A, CHUK, GNL3, TBL1XR1, CCNK, LDB1, ELANE, MDR1P1, TBR1, HHEX, INHBA, EP300, MED17, TFAP2A, ASS1, UBE3A, NFKBIA, UBRAP2, NR3C1, NR2C2, UHMK1, TFAM, MAP3K2, AGO1, LEO1, KDM3A, BCL9, CEBPA, TAF2, IKZF4, KAT2B, CEBPB, IL5, RBMX, FOXO1, SIRT2, SOD2, ATF6, RPS6KA3, ETS1, IRF1, RNF111, BMPR1A
*GO:0031327	Negative regulation of cellular biosynthetic process	43	5,95E-03	MORF4L1, MTDH, ENPP1, CPEB2, CPEB4, LOC100158121, SYNCRIP, NR2E3, LOC100627422, CCL4, ZFP36L1, CDC45, MDR1C, WWP1, AGO1, RARB, KDM5B, LOC100153329, SAMD4A, HELLS, CEBPA, DNMT3A, TBL1XR1, IKZF4, SMAD7, LDB1, ELANE, KLF11, LOC100154071, SAA3, TLE4, FXR2, FOXO1, SIRT2, ATXN1, RNFB, EP300, EIF2S1, HBZ, IRF1, TFAP2A, GRB7, ZBTB1
*GO:2000113	Negative regulation of cellular macromolecule biosynthetic process	41	4,19E-03	MORF4L1, MTDH, ENPP1, CPEB2, CPEB4, LOC100158121, SYNCRIP, NR2E3, LOC100627422, ZFP36L1, CDC45, MDR1C, WWP1, AGO1, RARB, KDM5B, LOC100153329, SAMD4A, HELLS, CEBPA, DNMT3A, TBL1XR1, IKZF4, SMAD7, LDB1, KLF11, LOC100154071, SAA3, TLE4, FXR2, FOXO1, SIRT2, ATXN1, RNFB, EP300, EIF2S1, HBZ, IRF1, TFAP2A, GRB7, ZBTB1
*GO:0009893	Positive regulation of metabolic process	83	7,06E-03	ABCF1, COPP5, STAT5A, CCNT1, NAA15, RPS6KB1, NR2E3, DDR2, TNFRSF11B, APP, APOA1, MDR1C, TGFA, MEN, RARB, KDM5B, SAMD4A, CHUK, GNL3, TBL1XR1, CCNK, ACTA1, ANP32B, LDB1, SOCS1, ELANE, SAA3, SOCS4, MDR1P1, TBR1, INHBA, HHEX, EP300, MED17, TFAP2A, CUX2, TNFAIP3, ASS1, UBE3A, NFKBIA, NR3C1, MDRAP2, TNFRSF4, CCL4, NR2C2, UHMK1, TFAM, TNFRSF11B, ACSL1, MAP3K2, AGO1, LEO1, PKR35, KDM3A, BCL9, CEBPA, TAF2, IKZF4, KAT2B, CEBPB, SMAD7, IL5, CHIL1, RBMX, FOXO1, SIRT2, RNFB, ATF6, EPHA4, RPS6KA3, PRLR, ETS1, IRF1, HSPD1, SH3D19, RNF111, BMPR1A
*GO:0010604	Positive regulation of macromolecule metabolic process	76	1,65E-02	ABCF1, COPP5, STAT5A, CCNT1, NAA15, RPS6KB1, NR2E3, DDR2, TNFRSF11B, APP, MDR1C, TGFA, MEN, RARB, KDM5B, SAMD4A, CHUK, GNL3, TBL1XR1, CCNK, ACTA1, ANP32B, LDB1, SOCS1, ELANE, SAA3, SOCS4, TBR1, INHBA, HHEX, EP300, MED17, TFAP2A, CUX2, TNFAIP3, UBE3A, NFKBIA, NR3C1, TNFRSF4, CCL4, DTNBP1, NR2C2, UHMK1, TFAM, TNFRSF11B, ACSL1, MAP3K2, AGO1, LEO1, PKR35, KDM3A, BCL9, CEBPA, TAF2, IKZF4, KAT2B, CEBPB, SMAD7, IL5, CHIL1, RBMX, FOXO1, SIRT2, RNFB, ATF6, EPHA4, RPS6KA3, PRLR, ETS1, IRF1, HSPD1, SH3D19, RNF111, BMPR1A
*GO:0031325	Positive regulation of cellular metabolic process	76	1,65E-02	ABCF1, COPP5, STAT5A, CCNT1, NAA15, RPS6KB1, NR2E3, DDR2, TNFRSF11B, APP, APOA1, MDR1C, TGFA, MEN, RARB, SAMD4A, CHUK, GNL3, TBL1XR1, CCNK, ANP32B, LDB1, SOCS1, ELANE, SAA3, SOCS4, MDR1P1, TBR1, INHBA, HHEX, EP300, MED17, TFAP2A, TNFAIP3, ASS1, UBE3A, NFKBIA, NR3C1, UBRAP2, TNFRSF4, CCL4, NR2C2, UHMK1, TFAM, TNFRSF11B, ACSL1, MAP3K2, AGO1, LEO1, PKR35, KDM3A, BCL9, CEBPA, TAF2, IKZF4, KAT2B, CEBPB, SMAD7, IL5, CHIL1, RBMX, FOXO1, SIRT2, ATF6, RNFB, EPHA4, RPS6KA3, PRLR, ETS1, IRF1, HSPD1, SH3D19, RNF111, BMPR1A
GO:0006793	Phosphorus metabolic process	81	7,95E-03	NUAK2, COPP5, CCNT1, DDR2, ST3GAL1, TPK1, TNFRSF11B, APP, APOA1, EIF2K3, TGFA, ATP5G, TNIP1, ATF6, CLN3, TBL1XR1, CCNK, NUOT12, LDB1, SOCS1, P6V1, EBP1, SAA3, PKN2, OL1, SOCS4, CDKL5, INHBA, HHEX, CKM, HPK3, EIF2S1, DLD, TNFAIP3, PRPS2, CROT, PPP2R2A, ME1, PHLPP1, ENPP1, BCLIP, MRRAP2, TNFRSF4, CCL4, DTNBP1, NR2C2, UHMK1, TNFRSF11B, ACSL1, LPICAT1, SNRK, DCLK3, PKR35, RPIA, INPP5B, MYOC, KAT2B, NRBF2, NCEH1, PCIF1, SMAD7, CBL, CHIL1, MPHOSPH10, TKT, CDC25C, CDKN3, AMPD3, ATM, RGS14, SIRT2, EPHA4, PPP1R9B, CBLB, PRLR, JAK3, PIP4K2A, PHEX, ABL2, MYLK, BMPR1A

*GO:0006796	Phosphate-containing compound metabolic process			80	1.06E-02	COPSS, NUAK2, CNT1, DDR2, ST3GAL1, TPK1, TNFRSF11B, APP, APOA1, EEF2K, TGFA, ATP5G, TNIP1, ATP8, CLN3, TBL1XR1, CCNK, NUDT12, LDB1, SOCS1, PIGV, FBP1, SAA3, PKN2, OLA1, SOCS4, CDKL5, INHBA, HHEX, CKM, HIPK3, EIF2S1, CLD, TNFAIP3, PRPS2, CROT, PPP2R2A, ME1, PHLP1, ENPP1, BCCIP, IRRAP2, TNFRSF4, DTNBP1, CCL4, TNFAIP3, PHLP1, UHMK1, TNFRSF1B, ACSL1, LPCAT1, SNRK, DCLK3, PKGSR5, RPA, RPP5B, MYOC, KAT2B, NRBF2, NCEH1, PCIF1, SMAD7, CBL, CH3L1, MPHOSPH10, TKT, CDC25C, CDKN3, AMPO3, ATM, RGS14, SIRT2, EPHA4, PPP1R9B, CBLB, PRLR, JAK3, PIP4K2A, ABL2, MYLK, BMPR1A
*GO:0016310	Phosphorylation			57	2.54E-02	COPSS, NUAK2, CNT1, DDR2, ST3GAL1, APP, TNFRSF11B, APOA1, EEF2K, TGFA, TNIP1, CCNK, LDB1, SOCS1, FBP1, PKN2, SAA3, SOCS4, CDKL5, HHEX, INHBA, CKM, HIPK3, EIF2S1, CLD, TNFAIP3, PRPS2, CROT, PPP2R2A, ME1, ENPP1, BCCIP, TNFRSF4, DTNBP1, CCL4, NR2C2, UHMK1, TNFRSF1B, ACSL1, SNRK, DCLK3, PKGSR5, MYOC, KAT2B, SMAD7, CBL, CH3L1, ATM, SIRT2, RGS14, PPP1R9B, EPHA4, CBLB, PRLR, JAK3, PIP4K2A, ABL2, MYLK, BMPR1A
*GO:0006468	Protein amino acid phosphorylation			49	4.29E-02	COPSS, NUAK2, CNT1, DDR2, ST3GAL1, APP, TNFRSF11B, EEF2K, TGFA, TNIP1, CCNK, SOCS1, PKN2, SAA3, SOCS4, CDKL5, HHEX, INHBA, HIPK3, EIF2S1, TNFAIP3, PHLP1, ENPP1, BCCIP, DTNBP1, CCL4, TNFRSF4, NR2C2, UHMK1, TNFRSF1B, ACSL1, SNRK, DCLK3, PKGSR5, MYOC, KAT2B, SMAD7, CBL, CH3L1, SIRT2, RGS14, ATM, EPHA4, CBLB, PRLR, JAK3, ABL2, MYLK, BMPR1A
*GO:0042325	Regulation of phosphorylation			41	9.26E-02	PHLP1, ENPP1, COPSS, CNT1, BCCIP, TNFRSF4, DTNBP1, CCL4, DDR2, TNFRSF11B, APP, APP, TNFRSF1B, ACSL1, APOA1, EEF2K, TGFA, PKGSR5, TNIP1, MYOC, CCNK, KAT2B, NRBF2, SMAD7, LDB1, SOCS1, FBP1, CH3L1, SAA3, SOCS4, RGS14, SIRT2, HHEX, INHBA, EPHA4, PPP1R9B, CBLB, PRLR, HIPK3, TNFAIP3, BMPR1A
*GO:0043549	Regulation of kinase activity			23	5.86E-02	CCNK, KAT2B, NRBF2, LDB1, SOCS1, CNT1, CBL, CH3L1, SOCS4, BCCIP, DDR2, DTNBP1, RGS14, EPHA4, HHEX, CBLB, APP, ACSL1, PRLR, HIPK3, TGFA, PKGSR5, TNFAIP3
*GO:0045859	Regulation of protein kinase activity			21	6.98E-02	CCNK, KAT2B, SOCS1, CNT1, CBL, CH3L1, SOCS4, BCCIP, DDR2, DTNBP1, RGS14, EPHA4, HHEX, CBLB, APP, ACSL1, PRLR, HIPK3, TGFA, PKGSR5, TNFAIP3
*GO:0006469	Negative regulation of protein kinase activity			10	6.94E-02	HHEX, CBLB, KAT2B, HIPK3, SOCS1, CBL, SOCS4, TNFAIP3, DTNBP1, RGS14
*GO:1904029	Regulation of cyclin-dependent protein kinase activity			6	5.65E-02	HHEX, CCNK, KAT2B, CNT1, BCCIP, TNFAIP3
*GO:0000079	Regulation of cyclin-dependent protein kinase activity			6	5.28E-02	HHEX, CCNK, KAT2B, CNT1, BCCIP, TNFAIP3
*GO:0061097	Regulation of protein tyrosine kinase activity			5	3.35E-02	APP, CBLB, CBL, TGFA, SOCS4
*GO:0061099	Negative regulation of protein tyrosine kinase activity			3	9.97E-02	CBLB, CBL, SOCS4
*GO:0050732	Negative regulation of peptidyl-tyrosine phosphorylation			4	5.71E-02	CBLB, SOCS1, CBL, SOCS4
GO:0051246	Regulation of protein metabolic process			79	5.36E-04	ABCF1, SEC24A, CPEB2, COPSS, CPEB4, STAT5A, CNTN1, SYNCRIP, RPS6KB1, FOXO3, ENPEP, DDR2, TNFRSF11B, APP, APOA1, EEF2K, TGFA, MSN, NOS2, EIF2B2, TNIP1, SAMD4A, GNL3, CCNK, ANP32B, SOCS1, ELANE, SAA3, SOCS4, EIF4G1, INHBA, HHEX, RENBP, EP300, HIPK3, EIF2S1, SERPINB1, TNFAIP3, PHLP1, RAD23B, SSH1, ENPP1, UBE3A, NFKBIA, AZIN1, BCCIP, TNFRSF4, CCL4, DTNBP1, UHMK1, ZFP36L1, TNFRSF1B, ACSL1, LPCAT1, AGO1, PKGSR5, KDM3A, NTFP5B, TRIP12, MYOC, TRAF3, KAT2B, SMAD7, CBL, IL9, CH3L1, FXR2, RGS14, SIRT2, EPHA4, PPP1R9B, CBLB, PRLR, IRF1, HSPD1, SH3D19, GRB7, RNF111, BMPR1A
*GO:0032268	Regulation of cellular protein metabolic process			68	1.05E-02	ABCF1, CPEB2, COPSS, CPEB4, CNT1, SYNCRIP, RPS6KB1, FOXO3, DDR2, TNFRSF11B, APP, APOA1, EEF2K, TGFA, MSN, EIF2B2, TNIP1, SAMD4A, GNL3, CCNK, ANP32B, SOCS1, SAA3, SOCS4, EIF4G1, INHBA, HHEX, RENBP, EP300, HIPK3, EIF2S1, SERPINB1, TNFAIP3, PHLP1, RAD23B, SSH1, ENPP1, UBE3A, NFKBIA, BCCIP, TNFRSF4, DTNBP1, CCL4, UHMK1, ZFP36L1, TNFRSF1B, ACSL1, AGO1, PKGSR5, KDM3A, TRIP12, MYOC, KAT2B, SMAD7, CBL, CH3L1, FXR2, SIRT2, RGS14, EPHA4, PPP1R9B, CBLB, PRLR, HSPD1, SH3D19, GRB7, RNF111, BMPR1A
GO:0070887	Cellular response to chemical stimulus			76	2.82E-04	GGA, FGF7, CPEB2, COPSS, STAT5A, CPEB4, SYNCRIP, RPS6KB1, FOXO3, CITED2, APOA1, CXCR4, IL4R, MSN, NOS2, CASP1, CHUK, LY96, SOCS1, FBP1, SAA3, SOCS4, UBR1, RAD52, IFNAR1, HHEX, RAB11FIP2, EP300, GNAQ, FANCD2, MED17, RYR1, RAB14, TFAP2A, RAB13, CUX2, TNFAIP3, JAM3, AMCF-I, MTDH, SSH1, ENPP1, UBE3A, DIAPH1, CXCL2, NFKBIA, CXCL8, NR3C1, NED1, CCL4, CCL28, TNFRSF1B, ACSL1, AGO1, KDM3A, TRAF3, CEBPA, PDK1, DNMT3A, KAT2B, MLC1, NCEH1, SMAD7, CH3L1, ACACA, RBMX, SIRT2, SOD2, ATF6, PPP1R9B, PRLR, IRF1, JAK3, LHB, ABL2, RNF111
*GO:0010033	Response to organic substance			76	2.91E-04	GGA, FGF7, CPEB2, COPSS, STAT5A, CPEB4, SYNCRIP, RPS6KB1, FOXO3, AQP3, CITED2, TNFRSF11B, APOA1, CXCR4, IL4R, MSN, NOS2, CASP1, CHUK, LY96, SOCS1, ELANE, SOCS4, UBR1, IFNAR1, HHEX, RAB11FIP2, EP300, GNAQ, MED17, RYR1, RAB14, CUX2, TNFAIP3, PPP2R2A, AMCF-I, ME1, MTDH, SSH1, ENPP1, UBE3A, DIAPH1, FFAR1, GDAPI, CXCL2, NFKBIA, CXCL8, ABHD2, NR3C1, NED1, TNFRSF4, CCL4, TNFRSF1B, ACSL1, AGO1, KDM3A, TRAF3, CEBPA, DNMT3A, KAT2B, MLC1, SMAD7, CH3L1, ACACA, RBMX, SIRT2, ATF6, PPP1R9B, RPS6KB3, PRLR, IRF1, HSPD1, JAK3, LHB, ABL2, RNF111
*GO:0071310	Cellular response to organic substance			64	2.83E-04	GGA, FGF7, COPSS, CPEB2, STAT5A, CPEB4, SYNCRIP, RPS6KB1, FOXO3, CITED2, APOA1, CXCR4, IL4R, MSN, NOS2, CASP1, CHUK, LY96, SOCS1, SOCS4, UBR1, IFNAR1, HHEX, RAB11FIP2, EP300, MED17, RYR1, RAB14, CUX2, TNFAIP3, AMCF-I, MTDH, ENPP1, SSH1, DIAPH1, UBE3A, CXCL2, NFKBIA, CXCL8, NR3C1, NED1, CCL4, TNFRSF1B, ACSL1, AGO1, KDM3A, TRAF3, CEBPA, DNMT3A, KAT2B, MLC1, SMAD7, ACACA, CH3L1, RBMX, SIRT2, ATF6, PPP1R9B, PRLR, IRF1, JAK3, LHB, ABL2, RNF111
*GO:0033993	Response to lipid			27	6.34E-04	AMCF-II, MTDH, UBE3A, CXCL2, FFAR1, GDAPI, CXCL8, NFKBIA, ABHD2, NR3C1, TNFRSF4, AQP3, TNFRSF1B, TNFRSF1B, KDM3A, NOS2, MSN, CASP1, MLC1, LY96, ELANE, IFNAR1, RPS6KB3, EP300, MED17, TNFAIP3, ABL2
*GO:0071396	Cellular response to lipid			14	9.36E-02	MTDH, MLC1, LY96, UBE3A, NFKBIA, NR3C1, TNFRSF1B, EP300, MED17, KDM3A, NOS2, MSN, TNFAIP3, ABL2
*GO:0034097	Response to cytokine			22	3.97E-02	AMCF-II, STAT5A, SOCS1, CXCL2, CH3L1, SYNCRIP, CXCL8, SOCS4, FOXO3, CCL4, RBMX, IFNAR1, APOA1, ACSL1, PRLR, CXCR4, IL4R, RFI1, NOS2, JAK3, CHUK, TRAF3
*GO:0071345	Cellular response to cytokine stimulus			22	1.06E-02	AMCF-II, STAT5A, SOCS1, CXCL2, CH3L1, SYNCRIP, CXCL8, SOCS4, FOXO3, CCL4, RBMX, IFNAR1, APOA1, ACSL1, PRLR, CXCR4, IL4R, RFI1, NOS2, JAK3, CHUK, TRAF3
*GO:0010243	Response to organonitrogen compound			17	7.98E-02	DNMT3A, KAT2B, SSH1, CPEB2, ENPP1, DIAPH1, CPEB4, SOCS1, NFKBIA, RPS6KB1, UBR1, SIRT2, PPP1R9B, RYR1, CASP1, TNFAIP3, PPP2R2A
*GO:0032870	Cellular response to hormone stimulus			16	9.35E-02	GGA, KAT2B, CPEB2, ENPP1, UBE3A, STAT5A, SOCS1, ACACA, RPS6KB1, NR3C1, ACSL1, EP300, PRLR, MED17, KDM3A, LHB
*GO:0009755	Hormone-mediated signaling pathway			9	4.65E-02	EP300, ACSL1, PRLR, UBE3A, STAT5A, MED17, KDM3A, NR3C1, LHB
*GO:0071407	Cellular response to organic cyclic compound			15	4.74E-02	CEBPA, MLC1, SSH1, UBE3A, DIAPH1, RPS6KB1, NR3C1, SIRT2, PPP1R9B, EP300, MED17, AGO1, RYR1, KDM3A, MSN
*GO:1901700	Response to oxygen-containing compound			39	2.04E-03	AMCF-II, MTDH, ENPP1, SSH1, CPEB2, CPEB4, CXCL2, FFAR1, GDAPI, CXCL8, NFKBIA, ABHD2, RPS6KB1, TNFRSF4, AQP3, TNFRSF1B, TNFRSF11B, NOS2, MSN, CASP1, DNMT3A, KAT2B, MLC1, STX2, LY96, ELANE, SOCS1, ACACA, APTX, UBR1, SIRT2, IFNAR1, SOD2, RAB11FIP2, RPS6KB3, GNAQ, TXNRD1, TNFAIP3, ABL2
*GO:1901701	Cellular response to oxygen-containing compound			23	6.52E-02	DNMT3A, KAT2B, MTDH, MLC1, SSH1, ENPP1, CPEB2, LY96, CPEB4, SOCS1, ACACA, NFKBIA, RPS6KB1, UBR1, SIRT2, SOD2, RAB11FIP2, TNFRSF1B, GNAQ, NOS2, MSN, TNFAIP3, ABL2
*GO:1901699	Cellular response to nitrogen compound			15	7.37E-02	DNMT3A, PPP1R9B, KAT2B, SSH1, GNAQ, ENPP1, CPEB2, DIAPH1, CPEB4, SOCS1, AGO1, RYR1, RPS6KB1, UBR1, SIRT2
GO:0071417	Cellular response to organonitrogen compound			13	7.06E-02	DNMT3A, PPP1R9B, KAT2B, SSH1, ENPP1, CPEB2, DIAPH1, CPEB4, SOCS1, RYR1, RPS6KB1, UBR1, SIRT2
GO:0044085	Cellular component biogenesis			72	7.72E-02	ABCF1, TLN1, ATL2, ATL3, SART3, WHAMM, TRIM4, CDC45, APP, APOA1, MSN, WDR35, FTSJ3, LOC100621389, GNL3, ABCE1, STX1A, STX2, ACTA1, ANP32B, LDB1, FBP1, PKN2, DECY1, MID1P1, RAD52, TMEM67, ARPC1B, RAB14, RAB13, CUX2, SNAP29, ME1, CALY, SSH1, DIAPH1, GPM6B, ARPC5, MYBL2, SF3B1, RPS27, ATXN2L, DNAAF1, AGO1, DNAJA4, ACSL3, MYOC, HELLS, HSD17B8, LOC100156127, SELP, BRD2, MLC1, SMAD7, ACACA, MPHOSPH10, ARFIP1, DENR, FOXF1, SIRT2, NCKAP1, SAMD8, PRLR, CABIN1, WDR3, NOP58, DNAJB1, NOP56, PIP4K2A, ZBTB1, GRB7, TBC1D20
GO:0009892	Negative regulation of metabolic process			67	5.54E-03	MORF4L1, CPEB2, CPEB4, CCNT1, LOC100158121, SYNCRIP, NR1E3, LOC10057422, CDC45, APP, MDC1C, WWI, NOS2, RARB, KDM5B, TNIP1, LOC100153329, SAMD4A, TBL1XR1, LDB1, SOCS1, ELANE, FBP1, SAA3, TLE4, SOCS4, HHEX, RENBP, EP300, HIPK3, EIF2S1, SERPINB1, TFAP2A, TNFAIP3, MTDH, ENPP1, AZIN1, DTNBP1, CCL4, ZFP36L1, LPCAT1, AGO1, KDM3A, TRIP12, HELLS, CEBPA, DNMT3A, IKZF4, KAT2B, PCIF1, SMAD7, CBL, KLF11, LOC100154071, MPHOSPH10, FXR2, FOXF1, SIRT2, RGS14, RNFB, ATXN1, CBLB, PARPBP, HBZ, IRF1, ZBTB1, GRB7

GO:0031324	Negative regulation of cellular metabolic process				64	5.48E-03	MORF4L1, CPEB2, CPEB4, CNTN1, LOC100158121, SYNCRIP, NR2E3, LOC100827422, CDC45, APP, MDR1C, WWP1, RARB, KDM5B, TNIP1, LOC100155329, SAMDA4, TBL1XR1, LDB1, SOCS1, ELANE, FBP1, SAA3, TLE4, SOCS4, HHEX, RENBP, EP300, HIPK3, EIF2S1, SERPBN1, TFAP2A, TNFAIP3, MTDH, ENPP1, DTNBP1, CCL4, ZFP36L1, AGO1, KDM3A, TRIP12, HELLS, CEBPA, DNMT3A, IKZF4, KAT2B, PCF1, SMAD7, CBL, KLF11, LOC100154071, MPHOSPH10, FXR2, FOXF1, SIRT2, RGS14, RNFB, ATXN1, CBLB, PARPBP, HBZ, IRF1, ZBTB1, GRB7	
	*GO:0032269	Negative regulation of cellular protein metabolic process			28	5.78E-02	CPEB2, ENPP1, CPEB4, SYNCRIP, DTNBP1, ZFP36L1, APP, AGO1, KDM3A, TNIP1, SAMDA4, TRIP12, KAT2B, SMAD7, SOCS1, CBL, SOCS4, FXR2, RGS14, SIRT2, HHEX, RENBP, CBLB, HIPK3, EIF2S1, SERPBN1, TNFAIP3, GRB7	
*GO:0010605	Negative regulation of macromolecule metabolic process				63	4.06E-03	MORF4L1, CPEB2, CPEB4, CNTN1, LOC100158121, SYNCRIP, NR2E3, LOC100827422, CDC45, APP, MDR1C, WWP1, NOS2, RARB, KDM5B, TNIP1, LOC100155329, SAMDA4, TBL1XR1, LDB1, SOCS1, ELANE, SAA3, TLE4, SOCS4, HHEX, RENBP, EP300, HIPK3, EIF2S1, SERPBN1, TFAP2A, TNFAIP3, MTDH, ENPP1, AZN1, DTNBP1, CCL4, ZFP36L1, AGO1, KDM3A, TRIP12, HELLS, CEBPA, DNMT3A, IKZF4, KAT2B, SMAD7, CBL, KLF11, LOC100154071, FXR2, FOXF1, SIRT2, RGS14, RNFB, ATXN1, CBLB, PARPBP, HBZ, IRF1, ZBTB1, GRB7	
	*GO:0051248	Negative regulation of protein metabolic process			31	2.84E-02	CPEB2, ENPP1, CPEB4, SYNCRIP, AZN1, DTNBP1, ZFP36L1, APP, AGO1, KDM3A, NOS2, TNIP1, SAMDA4, TRIP12, KAT2B, SMAD7, ELANE, SOCS1, CBL, SOCS4, FXR2, RGS14, SIRT2, HHEX, RENBP, CBLB, HIPK3, EIF2S1, SERPBN1, TNFAIP3, GRB7	
GO:0007166	Cell surface receptor signaling pathway				64	5,65E-02	FGF7, STAT5A, RPS6KB1, FOXO3, CITED2, APP, APOA1, CXCR4, IL4R, TGFA, INSR, TBL1XR1, STX1A, LY96, LDB1, ARID5B, SOCS1, TLE4, SOCS4, PTPRU, IFNAR1, HHEX, INHBA, GNAQ, RAB14, CHSY1, CUX2, TNFAIP3, AMCF-II, ITGAL, MTDH, ENPP1, PITCHD1, CD247, CXCL2, NFKBIA, CXCL8, NEO1, GCLM, CCL4, PE415, IL17D, TNFRSF1B, ACSL1, ITGB7, MYOC, BCL9, TRAF3, CEBPA, NCEH1, SMAD7, CBL, SIRT2, SFRP5, CBLB, RNF115, PRLR, PLN, IRF1, JAK3, CD79A, ABL2, RNF111, BMP1A	
*GO:0007167	Enzyme linked receptor protein signaling pathway				26	5.33E-02	FGF7, ENPP1, RPS6KB1, NEO1, CITED2, APP, TGFA, INSR, MYOC, NCEH1, SMAD7, ARID5B, SOCS1, CBL, SOCS4, SIRT2, INHBA, HHEX, CBLB, RNF115, PRLR, RAB14, JAK3, ABL2, RNF111, BMP1A	
*GO:0007169	Transmembrane receptor protein tyrosine kinase signaling pathway				19	2.45E-02	FGF7, ENPP1, ARID5B, SOCS1, CBL, SOCS4, RPS6KB1, SIRT2, HHEX, CBLB, APP, RNF115, PRLR, RAB14, TGFA, JAK3, INSR, ABL2, MYOC	
	*GO:0038127	ERBB signaling pathway			7	1.88E-02	APP, CBLB, RNF115, CBL, TGFA, SOCS4, MYOC	
	**GO:1901184	Regulation of ERBB signaling pathway			6	3.95E-03	APP, CBLB, RNF115, CBL, TGFA, SOCS4	
				*GO:1901185	Negative regulation of ERBB signaling pathway	4	7.48E-03	CBLB, RNF115, CBL, SOCS4
				*GO:0007173	Epidermal growth factor receptor signaling pathway	6	3.40E-02	APP, CBLB, RNF115, CBL, TGFA, SOCS4
				**GO:0042058	Regulation of epidermal growth factor receptor signaling pathway	6	2.81E-03	APP, CBLB, RNF115, CBL, TGFA, SOCS4
				*GO:0042059	Negative regulation of epidermal growth factor receptor signaling pathway	4	7.48E-03	CBLB, RNF115, CBL, SOCS4
	*GO:0019221	Cytokine-mediated signaling pathway			17	2.63E-02	AMCF-II, STAT5A, SOCS1, CXCL2, CXCL8, SOCS4, FOXO3, CCL4, IFNAR1, APOA1, ACSL1, PRLR, CXCR4, IL4R, IRF1, JAK3, TRAF3	
	*GO:0070098	Chemokine-mediated signaling pathway			5	7.23E-02	AMCF-II, CXCR4, CXCL2, CXCL8, CCL4	
GO:0043933	Macromolecular complex subunit organization				63	8.96E-03	MORF4L1, ATL2, ATL3, LOC100158121, SART3, DDR2, WHAMM, TRIM4, CDC45, APOA1, MSN, LOC100153329, LOC100621389, TBL1XR1, ABCE1, STX1A, ANP32B, STX2, LDB1, FBP1, DECR1, MID1IP1, RAD52, ARPC1B, EP300, KDM2A, SMARCA1, ME1, SNAP29, CALY, DIAPH1, ARPC5, NR3C1, SFRB1, RPS27, ATXN2L, AGO1, LEO1, KDM3A, ACSL3, TRIP12, HELLS, HSD17B8, CHD3, LOC100156127, DNMT3A, SELP, BRD2, KAT2B, MLC1, LOC100154071, ACACA, ARFIP1, DENR, ATM, SIRT2, NCKAP1, RNFB, PRLR, CABIN1, ZBTB1, GRB7, TBC1D20	
*GO:0006325	Chromatin organization				27	2.81E-03	MORF4L1, LOC100158121, NR3C1, CDC45, LEO1, KDM3A, LOC100153329, LOC100621389, HELLS, TRIP12, CHD3, LOC100156127, DNMT3A, TBL1XR1, BRD2, KAT2B, ANP32B, LDB1, LOC100154071, SIRT2, ATM, RNFB, EP300, KDM2A, CABIN1, SMARCA1, ZBTB1	
*GO:0016569	Covalent chromatin modification				15	6.43E-02	MORF4L1, TBL1XR1, DNMT3A, KAT2B, LDB1, NR3C1, SIRT2, ATM, RNFB, EP300, KDM2A, LEO1, KDM3A, HELLS, TRIP12	
*GO:0005003	Macromolecular complex assembly				43	4.79E-02	ME1, SNAP29, CALY, ATL2, DIAPH1, ATL3, ARPC5, SART3, WHAMM, TRIM4, SFRB1, RPS27, CDC45, APOA1, ATXN2L, AGO1, MSN, ACSL3, LOC100621389, HELLS, HSD17B8, LOC100156127, SELP, BRD2, STX1A, MLC1, STX2, ANP32B, FBP1, ACACA, DECR1, MID1IP1, ARFIP1, DENR, RAD52, SIRT2, NCKAP1, ARPC1B, PRLR, CABIN1, GRB7, ZBTB1, TBC1D20	
	*GO:0051262	Protein tetramerization			6	8.12E-02	ME1, ACACA, FBP1, DECR1, LOC100621389, HSD17B8	
GO:0009605	Response to external stimulus				58	2,53E-02	NUAK2, STAT5A, TNFRSF11B, APP, APOA1, CXCR4, IL4R, SLC22A3, NOS2, CASP1, FANCA, TNIP1, TBL1XR1, STX2, LY96, ELANE, SAA3, CHST3, PPP1CC, TBR1, PROC, IFNAR1, GNAQ, FANCD2, CLIC5, EIF2S1, RAB14, RAB15, TNFAIP3, JAM3, AMCF-II, PHLPP1, MTDH, CXCL2, ENPP4, NFKBIA, CXCL8, NEO1, TNFRSF4, CCL28, CCL4, TNFRSF1B, MAP3K2, KLB1, SERPINB10, MYOC, IQSEC2, CHD3, PDK1, MAP1A, ARFIP1, DENR, RGS14, ATM, FOXF1, NCKAP1, PPP1R9B, CEP68, SYNM, TBC1D20, ABL2, GFR2	
**GO:0009607	Response to biotic stimulus				28	6.31E-02	AMCF-II, MTDH, CXCL2, CXCL8, NFKBIA, TNFRSF4, TNFRSF11B, TNFRSF1B, IL4R, SERPINB10, NOS2, CASP1, TRAF3, CEBPE, LY96, ELANE, LGALS8, CHST3, FXR2, SIRT2, IFNAR1, RPS6KA3, EIF2S1, APOA1, HSPD1, TNFAIP3, TMC01	
	*GO:0071216	Cellular response to biotic stimulus			8	7.09E-02	TNFRSF1B, MTDH, LY96, NFKBIA, NOS2, TNFAIP3, TMC01, SIRT2	
	*GO:0009617	Response to bacterium			18	1.63E-02	AMCF-II, MTDH, CEBPE, LY96, ELANE, CXCL2, NFKBIA, CXCL8, TNFRSF4, SIRT2, IFNAR1, TNFRSF11B, TNFRSF1B, RPS6KA3, RAB14, NOS2, CASP1, TNFAIP3	
	*GO:0002237	Response to molecule of bacterial origin			16	7.28E-04	AMCF-II, MTDH, LY96, ELANE, CXCL2, NFKBIA, CXCL8, TNFRSF4, SIRT2, IFNAR1, TNFRSF1B, RPS6KA3, TNFRSF11B, NOS2, CASP1, TNFAIP3	
	*GO:0071219	Cellular response to molecule of bacterial origin			7	6.03E-02	TNFRSF1B, MTDH, LY96, NFKBIA, NOS2, TNFAIP3, SIRT2	
	*GO:0032496	Response to lipopolysaccharide			15	1.17E-03	AMCF-II, MTDH, LY96, ELANE, CXCL2, NFKBIA, CXCL8, TNFRSF4, IFNAR1, TNFRSF1B, RPS6KA3, TNFRSF11B, NOS2, CASP1, TNFAIP3	
GO:0005009	Regulation of molecular function				57	9,58E-02	COPB5, CNTN1, DDR2, TBC1D16, APP, APOA1, TGFA, NQO1, FANCA, CCKN, SCN2B, ANP32B, LDB1, ARID5B, SOCS1, SOCS4, MID1IP1, HHEX, RENBP, SSGM1, EP300, GNAQ, FANCD2, HIPK3, SERPINB1, TNFAIP3, MTDH, SAV1, NFKBIA, BCCIP, KEAP1, DTNBP1, GCLM, CCL4, ACSL1, PIK3R5, TRAF3, KAT2B, NRBF2, CEBPB, PCGF1, SMAD7, CBL, MPHOSPH10, CH3L1, SIRT2, RGS14, SOD2, SFRP5, EPHA4, CBLB, PRLR, PLN, HSPD1, ABL2, CSN2	
*GO:0043086	Negative regulation of catalytic activity				20	7.73E-02	KAT2B, PCGF1, SMAD7, SOCS1, CBL, MPHOSPH10, SOCS4, DTNBP1, RGS14, HHEX, CBLB, APP, RENBP, APOA1, HIPK3, PLN, SERPINB1, TNFAIP3, NQO1, CSN2	
GO:0051348	Negative regulation of transferase activity				11	6.98E-02	HHEX, CBLB, KAT2B, SMAD7, HIPK3, SOCS1, CBL, SOCS4, TNFAIP3, DTNBP1, RGS14	
*GO:0010469	Regulation of receptor activity				6	7.24E-02	APP, CBLB, PLN, CBL, TGFA, SOCS4	
*GO:0007176	Regulation of epidermal growth factor-activated receptor activity				5	8.47E-04	APP, CBLB, CBL, TGFA, SOCS4	
	*GO:0007175	Negative regulation of epidermal growth factor-activated receptor activity			3	2.01E-02	CBLB, CBL, SOCS4	
GO:1902589	Single-organism organelle organization				52	5,08E-02	TLN1, NUAK2, SLC6A1, POLM3, WHAMM, APOA1, CAMSAP2, SLC22A3, MCOLN1, WDR35, STX1A, ACTA1, STX2, CHST3, MID1IP1, TACC2, TMEM67, ARPC1B, SPATA18, EIF2S1, MCMBP, JAM3, ANKYF1, SNAP29, SSH1, DIAPH1, GDAF1, EEA1, ARPC5, MYBL2, DTNBP1, TPM1, NR2C2, DNAAF1, SERPINB10, MYOC, IQSEC2, CHD3, PDK1, MAP1A, ARFIP1, DENR, RGS14, ATM, FOXF1, NCKAP1, PPP1R9B, CEP68, SYNM, TBC1D20, ABL2, GFR2	
GO:0042592	Homeostatic process				51	8,14E-03	SEC24A, STAT5A, FOXO3, AQP3, CITED2, APP, APOA1, SLC22A5, GNJ3, CLN3, SITI1, SCN2B, LDB1, INHBA, DCLRE1A, RAB11FIP2, RHOG, TNFSF13B, DLD, RYR1, TXNRD1, TNFAIP3, JAM3, TMC01, AMCF-II, ENPP1, DIAPH1, TMX4, FFAR1, NEO1, MRAP2, GCLM, CCL28, LPCAT1, SLC31A2, MYOC, ETFA, CEBPA, KLF13, ACACA, AMPD3, ATM, SOD2, ABCG8, ETS1, PYGL, PLN, HBZ, JAK3, TBC1D20, ABL2	
*GO:0048872	Homeostasis of number of cells				16	3.79E-04	AMCF-II, SITI1, KLF13, LDB1, STAT5A, FOXO3, AMPD3, CITED2, INHBA, TNFSF13B, ETS1, HBZ, SLC22A5, JAK3, TNFAIP3, JAM3	
*GO:0002262	Myeloid cell homeostasis				10	3.58E-03	INHBA, ETS1, KLF13, LDB1, STAT5A, HBZ, FOXO3, AMPD3, JAM3, CITED2	
*GO:0034101	Erythrocyte homeostasis				9	4.09E-03	INHBA, ETS1, KLF13, LDB1, STAT5A, HBZ, FOXO3, AMPD3, CITED2	
*GO:0001776	Leukocyte homeostasis				7	9.94E-03	AMCF-II, SITI1, TNFSF13B, STAT5A, JAK3, TNFAIP3, JAM3	

		*GO:0002260	Lymphocyte homeostasis	5	5.76E-02	SIT1, TNFSF13B, STAT5A, JAK3, TNFAIP3
GO:0048584	Positive regulation of response to stimulus			50	7.47E-02	MASP1, STAT5A, CITED2, TNFRSF11B, APOA1, IL4R, TGFA, CASP1, TNIP1, STX1A, LY96, SOCS1, ELANE, SAA3, HHEX, INHBA, TNFSF13B, CHSY1, CUX2, TNFAIP3, AMCF-II, MTDH, UBES3A, CXCL2, ENPP4, CD247, NFKBIA, CXCL8, NEO1, CCL4, TNFRSF4, PEA15, TNFRSF18, AGO1, PIK3R5, MYOC, TRAF3, SELP, CBL, CH3L1, RNF8, EPHA4, RPS6KA3, ETS1, IRF1, HSPD1, CD79A, ZBTB1, BMPR1A, RNF111
*GO:0031349	Positive regulation of defense response			11	6.28E-02	RPS6KA3, ETS1, LY96, STAT5A, IRF1, NFKBIA, HSPD1, TNFAIP3, TNIP1, CCL4, TRAF3
GO:0044248	Cellular catabolic process			49	9.02E-03	RAD23B, ENPP1, UBES3A, KEAP1, ABHD2, ENPEP, ALDH1L2, UHMK1, ZFP36L1, DDHD2, CYLD, CUL5, TNFRSF18, APOA1, WWP1, AGO1, NOS2, MSN, FBXO9, TRIP12, SAMD4A, ETFA, HECTD1, TBL1XR1, NUDT12, SMAD7, CBL, SAA3, SOCS4, DECR1, UBR1, ATM, PSMB8, CLPX, SIRT2, RNF8, CTSK, RENBP, RNF115, PYGM, PYGL, SPATA18, UCHL5, SH3D19, TNFAIP3, CROT, RNF111
*GO:0009057	Macromolecule catabolic process			42	2.48E-03	RAD23B, UBES3A, KEAP1, AZIN1, UHMK1, ZFP36L1, CYLD, CUL5, TNFRSF18, LPCAT1, WWP1, AGO1, NOS2, MSN, FBXO9, TRIP12, SAMD4A, HECTD1, TBL1XR1, SMAD7, CBL, CH3L1, SOCS4, UBR1, PAG6, ATM, PSMB8, CLPX, SIRT2, RNF8, LYVE1, CTSK, RNF115, PYGM, PYGL, SPATA18, UCHL5, SH3D19, TNFAIP3, RNF111
*GO:0044265	Cellular macromolecule catabolic process			32	3.15E-02	RAD23B, UBES3A, KEAP1, UHMK1, ZFP36L1, CYLD, CUL5, WWP1, AGO1, MSN, FBXO9, SAMD4A, TRIP12, HECTD1, TBL1XR1, SMAD7, CBL, SOCS4, UBR1, PSMB8, CLPX, SIRT2, ATM, RNF8, CTSK, RNF115, SPATA18, UCHL5, TNFAIP3, RNF111
*GO:0030163	Protein catabolic process			33	6.74E-03	RAD23B, UBES3A, KEAP1, AZIN1, CYLD, TNFRSF18, CUL5, LPCAT1, WWP1, NOS2, MSN, FBXO9, TRIP12, HECTD1, TBL1XR1, SMAD7, CBL, SOCS4, UBR1, PAG6, PSMB8, CLPX, SIRT2, RNF8, CTSK, RNF115, SPATA18, UCHL5, SH3D19, TNFAIP3, RNF111
		*GO:0044257	Cellular protein catabolic process	27	2.48E-02	RAD23B, UBES3A, KEAP1, CYLD, CUL5, WWP1, MSN, FBXO9, TRIP12, HECTD1, TBL1XR1, SMAD7, CBL, SOCS4, UBR1, PSMB8, CLPX, SIRT2, RNF8, CTSK, RNF115, SPATA18, UCHL5, TNFAIP3, RNF111
		**GO:0005008	Proteolysis	42	6.79E-02	RAD23B, COPPS, UBES3A, KEAP1, ENPEP, CYLD, CUL5, APP, TNFRSF18, WWP1, KLKB1, CASP1, FBXO9, NPP5B, TRIP12, HECTD1, TBL1XR1, ANP32B, SMAD7, CBL, SOCS4, UBR1, PAG6, RBMX, SIRT2, CLPX, PSMB8, PROC, RNF1, CBLB, CTSK, RENBP, RNF115, DLD, UCHL5, SERPINEB1, SH3D19, HSPD1, TNFAIP3, RNF111
		*GO:0051603	Proteolysis involved in cellular protein catabolic process	25	4.35E-02	RAD23B, TBL1XR1, UBES3A, SMAD7, CBL, KEAP1, SOCS4, UBR1, CLPX, PSMB8, SIRT2, RNF8, CYLD, CUL5, CTSK, RNF115, WWP1, UCHL5, TNFAIP3, FBXO9, TRIP12, RNF111, HECTD1
		*GO:0043632	Modification-dependent macromolecule catabolic process	21	7.44E-02	RAD23B, TBL1XR1, SMAD7, UBES3A, CBL, KEAP1, SOCS4, UBR1, SIRT2, RNF8, CYLD, CUL5, RNF115, WWP1, UCHL5, TNFAIP3, FBXO9, TRIP12, HECTD1, RNF111
		*GO:0019941	Modification-dependent protein catabolic process	21	6.52E-02	RAD23B, TBL1XR1, SMAD7, UBES3A, CBL, KEAP1, SOCS4, UBR1, SIRT2, RNF8, CYLD, CUL5, RNF115, WWP1, UCHL5, TNFAIP3, FBXO9, TRIP12, HECTD1, RNF111
		*GO:0006511	Ubiquitin-dependent protein catabolic process	21	5.43E-02	RAD23B, TBL1XR1, SMAD7, UBES3A, CBL, KEAP1, SOCS4, UBR1, SIRT2, RNF8, CYLD, CUL5, RNF115, WWP1, UCHL5, TNFAIP3, FBXO9, TRIP12, HECTD1, RNF111
		*GO:0042787	Protein ubiquitination involved in ubiquitin-dependent protein catabolic process	9	2.41E-02	CUL5, RNF115, UBES3A, WWP1, CBL, KEAP1, TRIP12, RNF111, HECTD1
GO:0033554	Cellular response to stress			49	6.02E-02	MORF4L1, PHLP1, RAD23B, CPB2, NUA2, COPPS, SLC6A1, ASS1, TMX4, BCCIP, FOXO3, DTNBP1, NR2C2, PEA15, CDC45, TNFRSF18, APOA1, SERPINB10, CHD2, SLC22A3, TRIP12, PDK1, CCMK, NR2F2, POLG, CHST3, APTX, RAD52, ATM, RGS14, SIRT2, SOD2, ATRF, RNF8, EPHA4, DCLRE1A, EP300, KDM2A, FANCD2, HIPK3, SPATA18, EIF2S1, PARPBP, UCHL5, TNFAIP3, ZBTB1, TMC01, BMPR1A
*GO:0071495	Cellular response to endogenous stimulus			30	7.42E-02	CSF3, FGF7, SSH1, CPB2, ENPP1, UBES3A, DIAPH1, CPB2A, STAT5A, RPS6KB1, NEO1, NR3C1, CITED2, ACSL1, KDM3A, DNMT3A, KAT2B, SMAD7, SOCS1, ACACA, UBR1, SIRT2, PPP1R9B, EP300, PRLR, MED17, RAB14, RYR1, LHB, RNF111
*GO:0006974	Cellular response to DNA damage stimulus			25	7.17E-02	MORF4L1, RAD23B, CCMK, POLG, APTX, BCCIP, FOXO3, RAD52, ATM, SOD2, RNF8, PEA15, DCLRE1A, CDC45, TNFRSF18, EP300, KDM2A, FANCD2, SPATA18, PARPBP, UCHL5, CHD2, ZBTB1, TRIP12
GO:0006952	Defense response			48	2.11E-03	AMCF-II, MASP1, STAT5A, CXCL2, PTGS1, SYNCRIP, NFKBIA, CXCL8, RPS6KB1, TNFRSF4, CCL4, IL17D, TNFRSF18, TNFRSF11B, APOA1, IL4R, SERPINB10, NOS2, CASP1, FBXO9, FANCA, TNIP1, TRAF3, SELP, CEBPE, LY96, ELANE, SOCS1, SAA3, CH3L1, CHST3, LGALS8, FXR2, SIRT2, PROC, IFNAR1, EIF4G1, RPS6KA3, ETS1, FANCD2, EIF2S1, IRF1, RAB14, HSPD1, JAK3, TNFAIP3, ABL2, JAM3
*GO:0006955	Immune response			40	1.24E-02	AMCF-II, CSF3, ITGAL, MASP1, ENPP1, CXCL2, CD247, CXCL8, NFKBIA, SYNCRIP, TNFRSF4, CCL2B, CCL4, SLA-B, TNFRSF11B, TNFRSF18, APOA1, IL4R, NOS2, FBXO9, TNIP1, TRAF3, LY96, ELANE, SOCS1, L8, FOXP1, IFNAR1, RPS6KA3, TNFSF13B, IRF1, JAK3, HSPD1, CD79A, TNFAIP3, JAM3, ZBTB1, ABL2, BMPR1A
		*GO:0002764	Immune response-regulating signaling pathway	10	9.54E-02	RPS6KA3, LY96, CD247, IRF1, NFKBIA, CD79A, HSPD1, TNFAIP3, TNIP1, TRAF3
		*GO:0002757	Immune response-activating signal transduction	10	8.03E-02	RPS6KA3, LY96, CD247, IRF1, NFKBIA, CD79A, HSPD1, TNFAIP3, TNIP1, TRAF3
		*GO:0002218	Activation of innate immune response	8	2.07E-02	RPS6KA3, LY96, IRF1, NFKBIA, HSPD1, TNFAIP3, TNIP1, TRAF3
		*GO:0002758	Innate immune response-activating signal transduction	8	1.55E-02	RPS6KA3, LY96, IRF1, NFKBIA, HSPD1, TNFAIP3, TNIP1, TRAF3
*GO:0009719	Response to endogenous stimulus			36	4.38E-02	ME1, CSF3, FGF7, ENPP1, SSH1, CPB2, DIAPH1, UBES3A, CPB2A, STAT5A, NFKBIA, ABHD2, RPS6KB1, NEO1, NR3C1, CITED2, ACSL1, KDM3A, CASP1, DNMT3A, KAT2B, SMAD7, SOCS1, ACACA, UBR1, SIRT2, PPP1R9B, EP300, PRLR, MED17, RAB14, RYR1, TNFAIP3, LHB, RNF111, PPP2R2A
*GO:0009628	Response to abiotic stimulus			28	1.35E-02	CPB2B, TRPV2, NFKBIA, DDHD2, APP, MAP3K2, CXCR4, NOS2, CASP1, DNAAJ4, PDK1, ELANE, CH3L1, PPP1CC, SIRT2, ATM, SOD2, RNF8, RHDH1, EP300, CCMK, GNAQ, FANCD2, EIF2S1, RYR1, IRF1, HSPD1, ZBTB1
		*GO:0006979	Response to oxidative stress	16	3.54E-03	PDK1, STX2, PTGS1, APTX, FOXO3, RAD52, GCLM, SIRT2, SOD2, GPX2, GPX1, APP, FANCD2, TXNRD1, TNFAIP3, NOD1
		*GO:0070482	Response to oxygen levels	9	8.28E-02	PDK1, EP300, CPB2, CXCR4, RYR1, NOS2, CASP1, SIRT2, SOD2
*GO:0006954	Inflammatory response			21	3.53E-02	AMCF-II, SELP, STAT5A, ELANE, CXCL2, PTGS1, CH3L1, SAA3, CXCL8, CCL4, TNFRSF4, PROC, IL1D, TNFRSF11B, TNFRSF18, APOA1, ETS1, LHB, NOS2, TNFAIP3, JAM3
GO:2000026	Regulation of multicellular organismal development			48	3.87E-02	PHLP1, CSF3, MTDH, SSH1, SAV1, TRPV2, STAT5A, NFKBIA, GPM6B, FOXO3, DDHD2, NR2F2, CITED2, APP, APOA1, IL4R, LE01, RAR8, GOLGA4, KDM5B, FANCA, LOC10621389, MYOC, KLF13, SMAD7, LDB1, CH3L1, TBR1, FOXP1, SIRT2, PROC, EIF4G1, SFRP5, HHEX, INHBA, EPHA4, PRLR, ETS1, FANCD2, IRF1, TFAP2A, CUX2, TNFAIP3, ZBTB1, ABL2, BMPR1A, CSN2
GO:1903706	Regulation of hemopoiesis			16	4.60E-03	CSF3, KLF13, STAT5A, LDB1, NFKBIA, FOXO3, INHBA, ETS1, FANCD2, IL4R, IRF1, LE01, ZBTB1, FANCA, LOC10621389
*GO:1903708	Positive regulation of hemopoiesis			8	8.09E-02	CSF3, INHBA, ETS1, IL4R, STAT5A, FOXO3, ZBTB1
*GO:1903707	Negative regulation of hemopoiesis			8	1.67E-02	KLF13, IL4R, LDB1, STAT5A, IRF1, LE01, NFKBIA, LOC10621389
*GO:0045637	Regulation of myeloid cell differentiation			11	8.80E-03	CSF3, INHBA, ETS1, KLF13, LDB1, STAT5A, LE01, NFKBIA, FOXO3, LOC10621389
*GO:0045646	Regulation of erythrocyte differentiation			6	2.81E-03	INHBA, ETS1, KLF13, LDB1, STAT5A, FOXO3
*GO:0045638	Negative regulation of myeloid cell differentiation			6	2.20E-02	KLF13, LDB1, STAT5A, LE01, NFKBIA, LOC10621389
*GO:0045647	Negative regulation of erythrocyte differentiation			3	2.74E-02	KLF13, LDB1, STAT5A
*GO:0045589	Regulation of regulatory T cell differentiation			3	4.47E-02	FANCD2, IRF1, FANCA
GO:0002682	Regulation of immune system process			46	1.69E-04	PHLP1, AMCF-II, CSF3, MASP1, STAT5A, CXCL2, CD247, NFKBIA, CXCL8, FOXO3, CCL2B, CCL4, AOP3, APOA1, IL4R, SERPINB10, LE01, MSN, FANCA, TNIP1, LOC10621389, TRAF3, SELP, SIT1, LY96, KLF13, LDB1, ELANE, SOCS1, CHST3, FXR2, FOXP1, INHBA, RPS6KA3, TNFSF13B, ETS1, FANCD2, EIF2S1, IRF1, JAK3, HSPD1, CD79A, TNFAIP3, JAM3, ZBTB1
*GO:0002684	Positive regulation of immune system process			29	4.59E-03	CSF3, AMCF-II, MASP1, STAT5A, CD247, CXCL2, CXCL8, NFKBIA, FOXO3, CCL4, AOP3, IL4R, TNIP1, TRAF3, SELP, LY96, ELANE, FOXP1, INHBA, RPS6KA3, TNFSF13B, ETS1, IRF1, JAK3, HSPD1, CD79A, TNFAIP3, ZBTB1
*GO:0045088	Regulation of innate immune response			9	9.95E-02	RPS6KA3, LY96, SOCS1, IRF1, NFKBIA, HSPD1, TNFAIP3, TNIP1, TRAF3
*GO:0045089	Positive regulation of innate immune response			8	7.75E-02	RPS6KA3, LY96, IRF1, NFKBIA, HSPD1, TNFAIP3, TNIP1, TRAF3
*GO:0002685	Regulation of leukocyte migration			8	9.16E-02	AMCF-II, SELP, CXCL2, CXCL8, MSN, JAM3, CCL2B, CCL4

*GO:0045137	Development of primary sexual characteristics	*GO:0008406	Gonad development	10	1.69E-02	CGA, INHBA, UBE3A, STAT5A, ARID5B, FOXO3, EIF2B2, FANCA, TBC1D20, CITED2
		*GO:0046545	Development of primary female sexual characteristics	10	1.50E-02	CGA, INHBA, UBE3A, STAT5A, ARID5B, FOXO3, EIF2B2, FANCA, TBC1D20, CITED2
				7	1.21E-02	INHBA, UBE3A, STAT5A, ARID5B, FOXO3, EIF2B2, FANCA
		*GO:0008585	Female gonad development	7	1.21E-02	INHBA, UBE3A, STAT5A, ARID5B, FOXO3, EIF2B2, FANCA
		*GO:0001541	Ovarian follicle development	4	9.97E-02	INHBA, UBE3A, FOXO3, EIF2B2
	*GO:0046660	Female sex differentiation		7	2.38E-02	INHBA, UBE3A, STAT5A, ARID5B, FOXO3, EIF2B2, FANCA
GO:0030155	Regulation of cell adhesion			21	3.53E-02	SIT1, ASS1, SMAD7, LDB1, STAT5A, GPM6B, CCL28, CITED2, APOA1, TNFSF13B, PRLR, ETS1, FANCD2, IL4R, IRF1, HSPD1, JAK3, FANCA, ZBTB1, ABL2, MYOC
**GO:0045785	Positive regulation of cell adhesion			13	8.43E-02	SMAD7, STAT5A, LDB1, CCL28, CITED2, APOA1, TNFSF13B, ETS1, IL4R, HSPD1, JAK3, ZBTB1, MYOC
*GO:0022407	Regulation of cell-cell adhesion			16	1.21E-02	SIT1, ASS1, SMAD7, STAT5A, CCL28, CITED2, APOA1, TNFSF13B, ETS1, FANCD2, IL4R, IRF1, HSPD1, JAK3, FANCA, ZBTB1
	**GO:0022409	Positive regulation of cell-cell adhesion		9	9.95E-02	TNFSF13B, ETS1, SMAD7, IL4R, STAT5A, JAK3, HSPD1, ZBTB1, CITED2
	*GO:1903037	Regulation of leukocyte cell-cell adhesion		13	2.30E-02	SIT1, ASS1, STAT5A, CCL28, TNFSF13B, ETS1, FANCD2, IL4R, IRF1, HSPD1, JAK3, ZBTB1, FANCA
GO:0048589	Developmental growth			20	7.08E-02	CGA, TBL1XR1, UBE3A, ARID5B, STAT5A, TRPV2, SAV1, FOXO3, RAPH1, DDR2, FOXP1, ZFP361, HHEX, APP, PRLR, RARB, GOLGA4, KDM5B, BMPR1A, BCL9
*GO:0035265	Organ growth			7	8.03E-02	CGA, PRLR, UBE3A, SAV1, RARB, DDR2, FOXP1
*GO:0043900	Regulation of multi-organism process			18	2.63E-02	AMCF-II, CCNK, LY96, ELANE, PKN2, CHST3, FXR2, CCL4, SIRT2, INHBA, EP300, MDFIC, EIF251, SERPINB10, NOS2, TNFAIP3, TBC1D20, TRAF3
*GO:0043903	Regulation of symbiosis, encompassing mutation through parasitism			13	6.64E-02	AMCF-II, CCNK, EP300, MDFIC, EIF251, ELANE, SERPINB10, PKN2, CHST3, FXR2, CCL4, TBC1D20, TRAF3
	*GO:0051702	Interaction with symbiont		6	1.64E-02	AMCF-II, CCNK, EP300, ELANE, CCL4, TBC1D20
*GO:0035821	Modification of morphology or physiology of other organism			8	4.49E-03	AMCF-II, CCNK, EP300, ELANE, NOS2, TNP1, CCL4, TBC1D20
	*GO:0051817	Modification of morphology or physiology of other organism involved in symbiotic interaction		7	1.21E-02	AMCF-II, CCNK, EP300, ELANE, TNP1, CCL4, TBC1D20
	*GO:0044364	Disruption of cells of other organism		3	7.60E-02	AMCF-II, ELANE, NOS2
	*GO:0031640	Killing of cells of other organism		3	7.60E-02	AMCF-II, ELANE, NOS2
	*GO:0051851	Modification by host of symbiont morphology or physiology		6	1.47E-02	AMCF-II, CCNK, EP300, ELANE, CCL4, TBC1D20
	*GO:0043902	Positive regulation of multi-organism process		8	6.47E-02	INHBA, EP300, LY96, MDFIC, PKN2, NOS2, TBC1D20, SIRT2
GO:0048732	Gland development			17	1.20E-02	CEBPA, CGA, UBE3A, ARID5B, STAT5A, SOD2, CITED2, HHEX, APOA1, PRLR, TGFA, MSN, TNFAIP3, ZBTB1, KDM5B, BMPR1A, CSN2
*GO:0001889	Liver development			6	2.20E-02	CEBPA, HHEX, TGFA, TNFAIP3, CITED2, SOD2
*GO:0003325	Adrenal gland development			3	6.49E-02	APOA1, ARID5B, CITED2
GO:0006914	Autophagy			17	7.09E-02	SNAP29, PDK1, NRBF2, MTDH, SLC6A1, LGALS8, CHST3, FXR2, SIRT2, NR2C2, CTSK, SPATA18, EIF251, SERPINB10, SLC22A3, MCOLN1, PI4KA2A
GO:0010876	Lipid localization			14	1.88E-02	ARV1, ENPP1, STAT5A, NFKBIA, ABCA3, ABCG8, INHBA, APOA1, ACSL1, NOS2, ACSL3, KDM5B, SLC27A2, CROT
GO:0007517	Muscle organ development			13	3.58E-02	FAM65B, EP300, ACTA1, SMAD7, SAV1, ARID5B, CHD2, RYR1, SIRT2, FOXP1, MYOC, CITED2, BCL9
*GO:0005637	Muscle tissue development			13	9.95E-02	FAM65B, EP300, ACTA1, SMAD7, PLN, SAV1, RYR1, RARB, FOXP1, SIRT2, MYOC, CITED2, BCL9
	*GO:0014706	Striated muscle tissue development		13	7.50E-02	FAM65B, EP300, ACTA1, SMAD7, PLN, SAV1, RYR1, RARB, FOXP1, SIRT2, MYOC, CITED2, BCL9
GO:0045444	Fat cell differentiation			12	7.04E-03	CEBPA, TBL1XR1, EP300, ENPP1, SAV1, ARID5B, LRRC8C, SOCS1, FBXO9, PSM88, SIRT2, SOD2
GO:0031589	Cell-substrate adhesion			12	5.67E-02	ITGAL, APOA1, TMEM8B, SNED1, ITGB7, LDB1, GPM6B, JAM3, CCL28, WHAMM, MYOC, MUC4
*GO:0007160	Cell-matrix adhesion			11	6.35E-03	ITGAL, TMEM8B, SNED1, ITGB7, LDB1, GPM6B, JAM3, CCL28, WHAMM, MYOC, MUC4
GO:0050878	Regulation of body fluid levels			12	6.94E-02	SELP, TLN1, STX2, PRLR, STAT5A, KLKB1, ENPP4, ADRA2B, DTNBP1, AQP3, CSN2, PROC
GO:0006790	Sulfur compound metabolic process			11	9.09E-02	PDK1, TPX1, ENPP1, CSGALNACT2, GDAP1, ACACA, CHST3, MAT2B, CHSY1, GCLM, SOD2
	*GO:0044272	Sulfur compound biosynthetic process		6	9.54E-02	PDK1, CSGALNACT2, CHST3, MAT2B, CHSY1, GCLM
	*GO:0050650	Chondroitin sulfate proteoglycan biosynthetic process		3	8.76E-02	CSGALNACT2, CHST3, CHSY1
GO:0048511	Rhythmic process			10	7.47E-02	PHLPP1, INHBA, EP300, GNAQ, UBE3A, STAT5A, FOXO3, NOS2, PPP1CC, EIF2B2
GO:0048469	Cell maturation			9	4.33E-02	CEBPA, APP, DLD, HBZ, ABHD2, FOXO3, PABPC1L, SIRT2, MYOC
GO:0046822	Regulation of nucleocytoplasmic transport			9	8.28E-02	SFRP5, ANP32B, MDFIC, NFKBIA, KEAP1, PPP1CC, ZIC1, UHMK1, BMPR1A
GO:0002221	Pattern recognition receptor signaling pathway			8	1.33E-02	RPS6KA3, LY96, IRF1, NFKBIA, HSPD1, TNFAIP3, TNIP1, TRAF3
	*GO:0002224	Toll-like receptor signaling pathway		8	4.04E-03	RPS6KA3, LY96, IRF1, NFKBIA, HSPD1, TNFAIP3, TNIP1, TRAF3
	*GO:0070427	Nucleotide-binding oligomerization domain containing 1 signaling pathway		2	7.57E-02	NFKBIA, TNFAIP3
GO:0043491	Protein kinase B signaling			8	4.56E-02	PHLPP1, SFRP5, MTDH, CH3L1, PIK3R5, RPS6KB1, SIRT2, MYOC
GO:0034329	Cell junction assembly			8	5.60E-02	TLN1, SMAD7, LDB1, PKN2, GPM6B, RAB13, WHAMM, MYOC
*GO:0007044	Cell-substrate junction assembly			5	5.31E-02	TLN1, LDB1, GPM6B, WHAMM, MYOC
GO:0001101	Response to acid chemical			8	8.09E-02	DNMT3A, CPEB4, SOCS1, FFAR1, GDAP1, UBR1, ABL2, AQP3
GO:0006575	Cellular modified amino acid metabolic process			7	6.92E-02	CGA, CKM, ASS1, GDAP1, ALDH1L2, GCLM, SOD2
	*GO:0006474	N-terminal protein amino acid acetylation		3	8.78E-02	KAT2B, EP300, NAA15
GO:0048017	Inositol lipid-mediated signaling			7	8.03E-02	SELP, UBE3A, CBL, PI4KA, PIK3R5, SIRT2, MYOC
	*GO:0048015	Phosphatidylinositol-mediated signaling		7	7.28E-02	SELP, UBE3A, CBL, PI4KA, PIK3R5, SIRT2, MYOC
	*GO:0014955	Phosphatidylinositol 3-kinase signaling		6	6.82E-02	SELP, UBE3A, CBL, PIK3R5, SIRT2, MYOC
GO:0007050	Cell cycle arrest			7	7.28E-02	INHBA, CCNK, CDKN1A, IRF1, CDKN3, P14ARF, UHMK1
GO:0098727	Maintenance of cell number			7	8.43E-02	FANCD2, LDB1, MED17, LEOT1, FOXO3, BCL9, BMPR1A
*GO:0015807	Stem cell population maintenance			7	7.69E-02	FANCD2, LDB1, MED17, LEOT1, FOXO3, BCL9, BMPR1A
GO:0061008	Hepaticobiliary system development			6	2.88E-02	CEBPA, HHEX, TGFA, TNFAIP3, CITED2, SOD2
GO:0006413	Translational initiation			6	7.24E-02	ABCF1, ABCE1, EIF251, RPS6KB1, DENR, UHMK1
GO:0006081	Cellular aldehyde metabolic process			5	2.71E-02	RDH11, TKT, SDR16C5, KDM3A, RPIA
GO:0051781	Positive regulation of cell division			5	5.76E-02	FGF7, PKN2, TGFA, IGFB, SIRT2
GO:0051899	Membrane depolarization			5	6.72E-02	SCN9B, CACSPER2, CASP1, GCLM, MYOC
GO:1900181	Negative regulation of protein localization to nucleus			5	9.46E-02	SFRP5, MDFIC, DCLK3, NFKBIA, KEAP1
GO:0048048	Embryonic eye morphogenesis			4	4.54E-02	TFAP2A, MFAP2, RARB, CITED2
*GO:0002089	Lens morphogenesis in camera-type eye			3	5.45E-02	TDRD7, TBC1D20, CITED2
GO:2000348	Regulation of CD40 signaling pathway			3	1.38E-02	FANCD2, TNFAIP3, FANCA
GO:0042026	Protein refolding			3	2.74E-02	DNAJB1, HSPD1, DNAJAA
GO:0006656	Phosphatidylcholine biosynthetic process			3	6.49E-02	APOA1, LPCAT1, ACSL3
*GO:2001245	Regulation of phosphatidylcholine biosynthetic process			2	7.57E-02	LPCAT1, ACSL3
GO:0031629	Synaptic vesicle fusion to presynaptic active zone membrane			3	9.97E-02	SNAP29, STX1A, STX2
*subset	**part of					

Category	GO - Cellular Component	Gene numbers	p-value	Genes
GO:0044421	Extracellular region part	109	7.48E-02	MASP1, LTBP2, PTGS1, ENPEP, ALDH1L2, ST3GAL1, APP, APOA1, STAG4A, WWP1, ZNF445, NOS1, GNL3, POLG, FBP1, OLA1, ARPC1B, RENBP, RHCG, EIF2S1, SLC37A2, RAB1A, RYR1, MFAP2, RAB13, TNFAIP3, ANKFY1, VPS26A, PRPS2, AMCF-II, ITGAL, ASS1, ENPP1, ARPC5, COL4, IL17D, ITGB7, KLKB1, SLCOC1, PCF1, ACACA, LOC100154071, CH3L1, LGALS8, TKT, FXR2, RBMX, NOKAP1, LYVE1, DNAJB1, HSPD1, PABPC1L, LHB, TLN1, DDR2, GPX2, CXCR4, TGFA, SLC22A5, MSN, GOLGA4, LOC100153329, LOC100621389, SIT1, STX2, ANP32B, ARMD2, ACTA1, ELANE, SAK3, PI4KA, DEGR1, PROC, TAR5, INHBA, CTSK, CKM, CLIC5, GRN, CYBRD1, SERPINB1, TXNRD1, CUX2, JAM3, CSF3, CXCL2, ADAMTS15, CXCL8, EEZ1, ATP6V101, CCL28, APLP2, SERPINB10, CHD2, MYOC, ETFA, SELP, SLC12A2, IL9, IGFB, KLK1, PAG6, PYGM, SNED1, PYGL, HBZ, MAT2B, CSN2

GO:0031988	Membrane-bounded vesicle	95	4.84E-02	TLN1, SEC24A, LTBP2, COP55, PTGS1, ENPEP, ALDH1L2, DDR2, ST3GAL1, GPX2, APP, APOA1, CXCR4, ST3GAL4, WWP1, SV2B, ZNF445, SLC22A5, MSN, NOD1, GOLGA4, LOC100153329, LOC100621389, SCAMP1, CLN3, STX1A, SIT1, STX2, ACTA1, ANP32B, POLG, ELANE, FBP1, PHKA, OLA1, DECR1, TAR5, ARPC1B, RENBP, KIF1B, RHCG, CLIC5, EF2S1, GRN, SLC37A2, DLD, RAB14, RYR1, CYBRD1, TXNRD1, RAB13, CUX2, TNFAIP3, ANKFY1, VPS26A, PRPS2, ITGAL, ASS1, EEA1, ABHD2, ATP6V1G1, ARPC5, CCL28, DTNBP1, APLP2, DDHD2, SYN1, KLKB1, ITGB7, CHD2, MYOC, ETFA, SLC04C1, SLC12A2, OPR1, CHIBL1, ACACA, LOC100154071, LGALS8, TKT, KLK1, FXR2, RBMX, ATM, NCKAP1, LYVE1, SNED1, PYGM, PYGL, HBZ, MAT2B, DNAJB1, HSPD1, PABPC1L
GO:0070062	Extracellular exosome	80	5.05E-02	TLN1, LTBP2, PTGS1, ENPEP, ALDH1L2, DDR2, ST3GAL1, GPX2, APP, APOA1, CXCR4, ST3GAL4, WWP1, ZNF445, MSN, SLC22A5, NOD1, GOLGA4, LOC100153329, LOC100621389, SIT1, STX2, ACTA1, ANP32B, POLG, ELANE, FBP1, PHKA, OLA1, DECR1, TAR5, ARPC1B, RENBP, RHCG, CLIC5, EIF2S1, GRN, SLC37A2, RAB14, CYBRD1, RYR1, TXNRD1, RAB13, CUX2, TNFAIP3, VPS26A, ANKFY1, PRPS2, ITGAL, ASS1, EEA1, ATP6V1G1, ARPC5, CCL28, APLP2, KLKB1, ITGB7, CHD2, MYOC, ETFA, SLC04C1, SLC12A2, CHIBL1, LOC100154071, ACACA, LGALS8, TKT, KLK1, FXR2, RBMX, NCKAP1, LYVE1, SNED1, PYGM, PYGL, HBZ, MAT2B, DNAJB1, HSPD1, PABPC1L
GO:1903561	Extracellular vesicle	80	5.90E-02	TLN1, LTBP2, PTGS1, ENPEP, ALDH1L2, DDR2, ST3GAL1, GPX2, APP, APOA1, CXCR4, ST3GAL4, WWP1, ZNF445, MSN, SLC22A5, NOD1, GOLGA4, LOC100153329, LOC100621389, SIT1, STX2, ACTA1, ANP32B, POLG, ELANE, FBP1, PHKA, OLA1, DECR1, TAR5, ARPC1B, RENBP, RHCG, CLIC5, EIF2S1, GRN, SLC37A2, RAB14, CYBRD1, RYR1, TXNRD1, RAB13, CUX2, TNFAIP3, VPS26A, ANKFY1, PRPS2, ITGAL, ASS1, EEA1, ATP6V1G1, ARPC5, CCL28, APLP2, KLKB1, ITGB7, CHD2, MYOC, ETFA, SLC04C1, SLC12A2, CHIBL1, LOC100154071, ACACA, LGALS8, TKT, KLK1, FXR2, RBMX, NCKAP1, LYVE1, SNED1, PYGM, PYGL, HBZ, MAT2B, DNAJB1, HSPD1, PABPC1L
GO:0043230	Extracellular organelle	80	5.97E-02	TLN1, LTBP2, PTGS1, ENPEP, ALDH1L2, DDR2, ST3GAL1, GPX2, APP, APOA1, CXCR4, ST3GAL4, WWP1, ZNF445, MSN, SLC22A5, NOD1, GOLGA4, LOC100153329, LOC100621389, SIT1, STX2, ACTA1, ANP32B, POLG, ELANE, FBP1, PHKA, OLA1, DECR1, TAR5, ARPC1B, RENBP, RHCG, CLIC5, EIF2S1, GRN, SLC37A2, RAB14, CYBRD1, RYR1, TXNRD1, RAB13, CUX2, TNFAIP3, VPS26A, ANKFY1, PRPS2, ITGAL, ASS1, EEA1, ATP6V1G1, ARPC5, CCL28, APLP2, KLKB1, ITGB7, CHD2, MYOC, ETFA, SLC04C1, SLC12A2, CHIBL1, LOC100154071, ACACA, LGALS8, TKT, KLK1, FXR2, RBMX, NCKAP1, LYVE1, SNED1, PYGM, PYGL, HBZ, MAT2B, DNAJB1, HSPD1, PABPC1L
GO:0005654	Nucleoplasm	74	1.06E-02	MORF4L1, ABCF1, COP55, CCNT1, RPS6KB1, FOXO3, ZIC1, SART3, CDC45, SMAP2, RARB, TNBP1, FANCA, GOLGA4, CHUK, GNL3, SCAMP1, TBL1XR1, CCNK, PKN2, RAI14, APTX, DECR1, PPP1CC, CLPX, CDKL5, RAB11FIP2, EP300, HIPK3, MED17, DLD, MCMBP, KPN47, FBXL4, TFAP2A, KPN45, KIAA1429, RAD23B, MTDH, SSH1, ZBTB11, HCF2, NR3C1, MYB2, NR2C2, SF3B1, ATXN2L, MAP3K2, CHD2, LEO1, KDM3A, TRIP12, CHD3, TAF2, DNMT3A, IKZF4, SELP, KAT2B, CEBPE, PCIF1, KANSL1, SMAD7, TAF5, TKT, RGS14, ATXN1, CBLB, PAPOLA, PP1G, ETS1, PARBP, NOP58, SH3D19, ZBTB1
GO:0097458	Neuron part	32	3.40E-02	SNAP29, CPEB2, SLC6A1, COP55, CPEB4, TRPV2, PTGS1, EEA1, DTNBP1, UHMK1, MBP, APP, TMEM57, SYN1, SV2B, MYOC, SCAMP1, CLN3, STX1A, STX2, OPR1, LGALS8, SIRT2, EPHA4, RDIH1, PPP1R9B, KIF1B, GNAQ, CLIC5, SYNM, RAB13
GO:0043005	Neuron projection	22	6.81E-02	CLN3, STX1A, CPEB2, SLC6A1, OPR1, CPEB4, TRPV2, EEA1, PDYN, DTNBP1, RGS14, UHMK1, MBP, EPHA4, PPP1R9B, APP, KIF1B, TMEM57, SYN1, SV2B, RAB13, MYOC
GO:0044454	Nuclear chromosome part	20	5.06E-02	MORF4L1, LOC100156127, DNMT3A, LDB1, LOC100158121, LOC100154071, APTX, PPP1CC, RBMX, CITED2, DCLRE1A, CDC45, SYN1, IRF1, MCMBP, UCHL5, SMARCA1, LOC100153329, LOC100621389
GO:0000228	Nuclear chromosome	20	9.12E-02	MORF4L1, LOC100156127, DNMT3A, LDB1, LOC100158121, LOC100154071, APTX, PPP1CC, RBMX, CITED2, DCLRE1A, CDC45, SYN1, IRF1, MCMBP, UCHL5, SMARCA1, LOC100153329, LOC100621389
GO:0000785	Chromatin	19	5.15E-02	MORF4L1, LOC100156127, DNMT3A, LDB1, LOC100158121, LOC100154071, APTX, RBMX, CITED2, PARBP, IRF1, MCMBP, UCHL5, KDM3A, SMARCA1, LOC100153329, HELLS, LOC100621389
GO:0044431	Golgi apparatus part	19	6.56E-02	SCAMP1, CLN3, SLC35A5, CHST3, ARFIP1, WHAMM, SLC35A3, ST3GAL1, SAMD8, SLC35D1, ST3GAL4, IGF2R, ATP9A, CSGALNACT2, RAB14, CHSY1, RAB13, TBC1D20, TMC01
GO:0000790	Nuclear chromatin	15	1.94E-02	MORF4L1, LOC100156127, DNMT3A, LDB1, LOC100158121, LOC100154071, APTX, RBMX, CITED2, IRF1, MCMBP, UCHL5, SMARCA1, LOC100153329
GO:0000139	Golgi membrane	14	3.30E-02	SLC35A5, CHST3, ARFIP1, WHAMM, SLC35A3, SAMD8, ST3GAL1, SLC35D1, ST3GAL4, CSGALNACT2, RAB14, CHSY1, TBC1D20, TMC01
GO:0030424	Axon	13	2.42E-02	EPHA4, APP, KIF1B, TMEM57, SYN1, SLC6A1, TRPV2, EEA1, PDYN, DTNBP1, MYOC, UHMK1, MBP
GO:0005769	Early endosome	12	7.50E-03	TBC1D16, EPHA4, CLN3, MLC1, CXCR4, RUSC1, ATP9A, RAB14, EEA1, HSPD1, ANKFY1, VPS26A
GO:0030133	Transport vesicle	11	5.62E-02	SCAMP1, DDHD2, CLN3, APP, STX1A, SEC24A, SYN1, STX2, COP55, SV2B, DTNBP1
GO:0031984	Organelle subcompartment	11	5.62E-02	SCAMP1, ST3GAL1, CLN3, ARV1, IGF2R, ATP9A, CSGALNACT2, RAB14, CHSY1, ARFIP1, RAB13
GO:0098791	Golgi subcompartment	10	8.43E-02	SCAMP1, ST3GAL1, CLN3, IGF2R, ATP9A, CSGALNACT2, RAB14, CHSY1, ARFIP1, RAB13
GO:0043209	Myelin sheath	10	8.75E-02	SYN1, DLD, ATP5O, TKT, MSN, HSPD1, JAM3, SIRT2, MBP, SOD2
GO:0008021	Synaptic vesicle	8	1.21E-02	SCAMP1, CLN3, STX1A, SYN1, STX2, COP55, SV2B, DTNBP1
GO:0070382	Exocytic vesicle	8	3.23E-02	SCAMP1, CLN3, STX1A, SYN1, STX2, COP55, SV2B, DTNBP1
GO:0033267	Axon part	7	4.41E-02	KIF1B, TRPV2, EEA1, PDYN, DTNBP1, MYOC, MBP
GO:0030658	Transport vesicle membrane	6	4.53E-02	SCAMP1, STX1A, SEC24A, SYN1, SV2B, DTNBP1
GO:0099572	Postsynaptic specialization	5	2.17E-02	PPP1R9B, SYN1, CPEB4, DTNBP1, RGS14
GO:0014069	Postsynaptic density	5	2.17E-02	PPP1R9B, SYN1, CPEB4, DTNBP1, RGS14
GO:0030672	Synaptic vesicle membrane	5	2.76E-02	SCAMP1, STX1A, SYN1, SV2B, DTNBP1
GO:0090501	Exocytic vesicle membrane	5	2.78E-02	SCAMP1, STX1A, SYN1, SV2B, DTNBP1
GO:0060076	Excitatory synapse	5	4.29E-02	PPP1R9B, SYN1, CPEB4, DTNBP1, RGS14
GO:0000307	Cyclin-dependent protein kinase holoenzyme complex	4	6.20E-02	CCNK, CCNT1, BCCIP, HSPD1
GO:0044309	Neuron spine	4	6.20E-02	APP, EEA1, DTNBP1, RGS14
GO:0043218	Compact myelin	3	5.17E-02	JAM3, SIRT2, MBP
GO:0019208	Nuclear cyclin-dependent protein kinase holoenzyme complex	3	5.17E-02	CCNT1, BCCIP, HSPD1

Category		Gene numbers	p-value	Genes
GO - Molecular Process				
GO:0005524	ATP binding	55	6.70E-03	ABCF1, NUAK2, RPS6KB1, DDR2, TPK1, CSNK2A2, EEF2K, EF2B2, INSR, CHUK, ABCE1, ACTA1, PKN2, OLA1, COT6A, CLPX, CDKL5, TAR5, KIF1B, CKM, NAV2, HIPK3, ATP9A, LOC102162987, SMARCA1, ENPP1, ASS1, VARS, ABCA3, UHMK1, CHD8, DD46, SYN1, SNRK, MAP3K2, DCLK3, CHD2, IKZF1A, LOC780419, DNAJA4, HELLS, CHD3, ACACA, ATM, ABCG8, EPHA4, RPS6KA3, PYGL, HSPD1, JAK3, PIP4K2A, ABL2, MYLK, GFRA2, BMPR1A
GO:0003677	DNA binding	28	2.76E-02	ZFAND5, SSH1, STAT5A, LOC100158121, NR3C1, LOC100627422, KDM1B, CHD8, APP, HNRNP, RARB, KDM5B, LOC100153329, LOC100621389, CHD3, LOC100156127, DNMT3A, CEBPB, AFR2, POLG, LOC100154071, APTX, RAD52, ATM, KDM2A, SMARCA1, TNFAIP3
GO:0003682	Chromatin binding	20	1.83E-03	MORF4L1, TAF2, DNMT3A, BRD2, KAT2B, POLG, LDB1, CCNT1, TLE4, APTX, RBMX, FOXD1, SIRT2, CITED2, RNH8, TFAM, HHEX, CDC45, MCMBP, HELLS
GO:0004674	Protein serine/threonine kinase activity	13	4.63E-02	NUAK2, PKN2, RPS6KB1, UHMK1, ATM, CSNK2A2, RPS6KA3, SNRK, HIPK3, EEF2K, DCLK3, GFRA2, MYLK
GO:0004842	Ubiquitin-protein transferase activity	11	1.82E-02	RNF8, CBLB, UBE3A, UBR5, WWP1, FBXL4, KEAP1, TNFAIP3, TRIP12, TRAF3, HECTD1
GO:0003713	Transcription coactivator activity	10	1.29E-02	CEBPA, KAT2B, EP300, MTDH, UBE3A, ARID5B, MED17, TFAP2A, MYCBP, MYOC
GO:0016887	ATPase activity	9	7.75E-03	ABCG8, ABCF1, ABCE1, KIF1B, OLA1, KIF21A, SMARCA1, ABCA3, ATP9
GO:0044212	Transcription regulatory region DNA binding	9	2.63E-02	TAF2, IKZF4, TBL1XR1, SMAD7, TAF5, ARID5B, KLF11, CCNT1, MYBL2
GO:0016874	Ligase activity	7	5.30E-03	RNF8, CBLB, UBE3A, UBR5, WWP1, TRIP12, HECTD1
GO:0043022	Ribosome binding	6	8.34E-03	ABCF1, CPEB2, EIF2S1, CPEB4, NAA15, OLA1
GO:0008083	Growth factor activity	6	4.37E-02	CSF3, INHBA, FGF7, TGFA, IGF2

GO:0050660	Flavin adenine dinucleotide binding	6	6.96E-02	KDM1B, AIFM2, DLD, TXNRP1, NOS2, ETFA
GO:0001047	Core promoter binding	5	4.54E-02	KANSL1, AGO1, KDM3A, FOXO3, RBMX
GO:0003725	Double-stranded RNA binding	5	6.83E-02	MITD1, AGO1, APTX, MSN, HSPD1
GO:0000030	Mannosyltransferase activity	3	3.61E-02	PIGV, DPY19L4, ALG12
GO:0044467	Long-chain fatty acid-CoA ligase activity	3	6.56E-02	ACSL1, SLC27A2, ACSL3
GO:0008307	Structural constituent of muscle	3	8.85E-02	PDLIM3, SYNM, TPM1
GO:0006184	Glycogen phosphorylase activity	2	7.62E-02	PYGM, PYGL
GO:0005130	Granulocyte colony-stimulating factor receptor binding	2	7.62E-02	CSF3