

Supplementary Table 3
The most significantly enriched gene ontologies (biological process)

GO - Biological Process					
Up-regulated			Count	p-value	Altered genes
GO:0006396	RNA processing		12	1,72E-02	SF3B1, PAPOLA, PPIG, TRMT11, TRDMT1, MPHOSPH10, SYNCRIP, WDR3, NOP58, NOP56, ALG11, KIAA1429
	*GO:0034470	ncRNA processing	7	9,69E-03	TRMT11, TRDMT1, MPHOSPH10, WDR3, NOP58, NOP56, ALG11
	*GO:0006364	rRNA processing	5	1,22E-02	MPHOSPH10, WDR3, NOP58, NOP56, ALG11
GO:0022403	Cell cycle phase		11	6,96E-03	TAF2, CCDC99, DCLRE1A, CUL5, PRC1, DBF4, ALG11, FANCA, SMC2, ATM, HELLS
	*GO:0000279	M phase	8	4,09E-02	CCDC99, DCLRE1A, PRC1, ALG11, FANCA, SMC2, ATM, HELLS
GO:0022402	Cell cycle process		11	4,77E-02	TAF2, CCDC99, DCLRE1A, CUL5, PRC1, DBF4, ALG11, FANCA, SMC2, ATM, HELLS
GO:0003006	Developmental process involved in reproduction		9	3,97E-03	HOOK1, PLA2G4A, FGF7, TDRD7, DLD, RQCD1, RPS6KB1, FANCA, BMPR1A
GO:0019953	Sexual reproduction		9	7,68E-02	HOOK1, PLA2G4A, TDRD7, DLD, MYCBP, RPS6KB1, SEPP1, ALG11, ATM
GO:0034660	ncRNA metabolic process		8	7,05E-03	TRMT11, TRDMT1, MPHOSPH10, WDR3, NOP58, NOP56, ALG11, VARS
	*GO:0016072	rRNA metabolic process	5	1,41E-02	MPHOSPH10, WDR3, NOP58, NOP56, ALG11
*GO:0007276	Gamete generation		8	8,92E-02	HOOK1, PLA2G4A, TDRD7, DLD, MYCBP, RPS6KB1, ALG11, ATM
	*GO:0007281	Germ cell development	4	7,47E-02	HOOK1, TDRD7, DLD, RPS6KB1
GO:0000278	Mitotic cell cycle		8	6,82E-02	TAF2, CCDC99, DCLRE1A, CUL5, PRC1, DBF4, SMC2, HELLS
GO:0022613	Ribonucleoprotein complex biogenesis		6	3,07E-02	MPHOSPH10, WDR3, NOP58, NOP56, ALG11, BMS1
	*GO:0042254	Ribosome biogenesis	6	6,63E-03	MPHOSPH10, WDR3, NOP58, NOP56, ALG11, BMS1
GO:0006457	Protein folding		6	2,88E-02	PPIG, FKBP3, CCT6A, HSPD1, UGGT1, CLPX
GO:0014070	Response to organic cyclic substance		5	3,00E-02	TAF2, RYR1, ACACA, RPS6KB1, PPP2R2A
GO:0009141	Nucleoside triphosphate metabolic process		5	3,84E-02	ENPP1, ATP9A, OLA1, ATP5O, ATP8
	*GO:0009143	Nucleoside triphosphate catabolic process	3	2,23E-02	ENPP1, OLA1, ATP5O
GO:0007548	Sex differentiation		5	5,90E-02	PLA2G4A, FGF7, RQCD1, FANCA, BMPR1A
GO:0006352	Transcription initiation		4	4,66E-02	TAF2, SNAPC5, TAF5, MED23
GO:0008654	Phospholipid biosynthetic process		4	7,65E-02	SAMD8, PLA2G4A, FGF7, MBOAT1
GO:0009166	Nucleotide catabolic		3	8,73E-02	ENPP1, OLA1, ATP5O
	*GO:0046034	ATP metabolic process	4	8,18E-02	ATP9A, OLA1, ATP5O, ATP8
GO:0070167	Regulation of biomineral formation		3	3,82E-02	PLA2G4A, ENPP1, BMPR1A
	GO:0030500	Regulation of bone mineralization	3	3,39E-02	PLA2G4A, ENPP1, BMPR1A
GO:0050679	Positive regulation of epithelial cell proliferation		3	5,97E-02	FGF7, TGFA, BMPR1A
GO:0015780	Nucleotide-sugar transport		2	5,67E-02	SLC35A5, SLC35A3
GO:0045022	Early endosome to late endosome transport		2	9,28E-02	HOOK1, EEA1
GO:0048875	Chemical homeostasis within a tissue		2	9,28E-02	PLA2G4A, FGF7
	*GO:0043129	Surfactant homeostasis	2	9,28E-02	PLA2G4A, FGF7
Down-regulated			Count	p-value	Altered genes
GO:0006793	Phosphorus metabolic process		45	1,43E-04	SSH1, NUA2, STAT5A, CCNT1, SSH2, DDR2, UHMK1, CSNK2A2, APP, SNRK, CXCR4, MAP3K2, MDFIC, PTPLA, DCLK3, EEF2K, IL1B, DYRK3, ADRA2B, MTMR9, INSR, PDK1, PAN3, NCEH1, SMAD7, PI4KA, PKN2, PTPRU, CDKN3, CDC25C, PPP1CC, CDKL5, DAPK1, SACM1L, EPHA4, RPS6KA3, MTMR14, PRLR, HIPK1, HIPK3, CDC42BPA, JAK3, PIP4K2A, MAP3K13, MYLK
*GO:0006796	Phosphate-containing compound metabolic process		45	1,43E-04	SSH1, NUA2, STAT5A, CCNT1, SSH2, DDR2, UHMK1, CSNK2A2, APP, SNRK, CXCR4, MAP3K2, MDFIC, PTPLA, DCLK3, EEF2K, IL1B, DYRK3, ADRA2B, MTMR9, INSR, PDK1, PAN3, NCEH1, SMAD7, PI4KA, PKN2, PTPRU, CDKN3, CDC25C, PPP1CC, CDKL5, DAPK1, SACM1L, EPHA4, RPS6KA3, MTMR14, PRLR, HIPK1, HIPK3, CDC42BPA, JAK3, PIP4K2A, MAP3K13, MYLK
	*GO:0016310	Phosphorylation	34	4,33E-03	NUAK2, STAT5A, CCNT1, DDR2, UHMK1, CSNK2A2, APP, SNRK, CXCR4, MAP3K2, MDFIC, EEF2K, DCLK3, IL1B, DYRK3, ADRA2B, INSR, PDK1, PAN3, SMAD7, PI4KA, PKN2, CDKL5, DAPK1, EPHA4, RPS6KA3, PRLR, HIPK1, HIPK3, CDC42BPA, JAK3, PIP4K2A, MAP3K13, MYLK
	*GO:0006468	Protein amino acid phosphorylation	32	9,01E-04	NUAK2, STAT5A, CCNT1, DDR2, UHMK1, CSNK2A2, APP, SNRK, CXCR4, MAP3K2, MDFIC, DCLK3, EEF2K, IL1B, DYRK3, ADRA2B, INSR, PDK1, PAN3, SMAD7, PKN2, CDKL5, DAPK1, EPHA4, RPS6KA3, PRLR, HIPK1, HIPK3, CDC42BPA, JAK3, MAP3K13, MYLK
	*GO:0001932	Regulation of protein amino acid phosphorylation	11	1,33E-02	PPP1R9B, APOA1, MDFIC, MAP3K2, SMAD7, HIPK3, SOCS1, IL1B, BDKRB1, IGF2, INSR
	*GO:0001933	Negative regulation of protein amino acid phosphorylation	4	4,70E-02	SMAD7, SOCS1, BDKRB1, INSR
	*GO:0051174	Regulation of phosphorus metabolic process	29	4,92E-05	CCNT1, BDKRB1, BCCIP, TNFRSF4, APLP2, APP, APOA1, CXCR4, MDFIC, MAP3K2, IL1B, ADRA2B, INSR, CNK, SMAD7, SOCS1, ELANE, IGF2, CDC25C, CDKN3, SIRT2, ATXN1, PPP1R9B, INHBA, CDKN1A, PPP1R2, PRLR, HIPK3, MAP3K13
	*GO:0019220	Regulation of phosphate metabolic process	29	4,92E-05	CCNT1, BDKRB1, BCCIP, TNFRSF4, APLP2, APP, APOA1, CXCR4, MDFIC, MAP3K2, IL1B, ADRA2B, INSR, CNK, SMAD7, SOCS1, ELANE, IGF2, CDC25C, CDKN3, SIRT2, ATXN1, PPP1R9B, INHBA, CDKN1A, PPP1R2, PRLR, HIPK3, MAP3K13
	*GO:0042325	Regulation of phosphorylation	28	6,30E-05	CCNT1, BDKRB1, BCCIP, TNFRSF4, APLP2, APP, APOA1, CXCR4, MDFIC, MAP3K2, IL1B, ADRA2B, INSR, CNK, SMAD7, SOCS1, ELANE, IGF2, CDC25C, CDKN3, SIRT2, ATXN1, INHBA, PPP1R9B, CDKN1A, PRLR, HIPK3, MAP3K13

		*GO:0043549	Regulation of kinase activity	21	8,63E-04	CCNK, CCNT1, ELANE, BCCIP, IGF2, BDKRB1, CDC25C, CDKN3, TNFRSF4, APLP2, APP, CDKN1A, PRLR, CXCR4, MDIC, MAP3K2, HIPK3, IL1B, ADRA2B, INSR, MAP3K13
		*GO:0045859	Regulation of protein kinase activity	21	5,59E-04	CCNK, CCNT1, ELANE, BCCIP, IGF2, BDKRB1, CDC25C, CDKN3, TNFRSF4, APLP2, APP, CDKN1A, PRLR, CXCR4, MDIC, MAP3K2, HIPK3, IL1B, ADRA2B, INSR, MAP3K13
		**GO:0000079	Regulation of cyclin-dependent protein kinase activity	6	1,19E-02	CDKN1A, CCNK, CCNT1, BCCIP, CDKN3, CDC25C
		*GO:0042326	Negative regulation of phosphorylation	7	9,27E-04	ATXN1, INHBA, CDKN1A, SMAD7, SOCS1, BDKRB1, INSR
		*GO:0010563	Negative regulation of phosphorus metabolic process	7	1,31E-03	ATXN1, INHBA, CDKN1A, SMAD7, SOCS1, BDKRB1, INSR
		*GO:0045936	Negative regulation of phosphate metabolic process	7	1,31E-03	ATXN1, INHBA, CDKN1A, SMAD7, SOCS1, BDKRB1, INSR
	*GO:0016311	Dephosphorylation		11	6,13E-03	MTMR14, NCEH1, SSH1, SSH2, PTPLA, PTPRU, MTMR9, PPP1CC, CDKN3, CDC25C, SACM1L
GO:0007242	Intracellular signaling cascade			44	2,79E-02	STAT5A, RASGEF1B, NFKBIA, RRAD, TP63, MYO9B, NR3C1, GNG12, APOA1, MCTP2, CXCR4, MAP3K2, MDIC, RHOB1, IL1B, KDM3A, NOS2, ADRA2B, INSR, PDK1, ARHGEF3, IL8, OPR1, LY96, SMAD7, SOCS1, PI4KA, IGF2, IFNAR1, DAPK1, CBLB, RPS6KA3, PRLR, GNAQ, HIPK1, NCOA4, MED17, UBR5, RAB14, CDC42BPA, JAK3, RAB13, MAP3K13, PHLD82
*GO:0030522	Intracellular receptor-mediated signaling pathway			6	4,20E-02	NCOA4, MED17, UBR5, KDM3A, NOS2, NR3C1
*GO:0016055	Wnt receptor signaling pathway			10	7,03E-03	CSNK2A2, SFRP5, HHEX, TBL1XR1, CHD8, LDB1, FBXW4, TLE3, TLE4, PTPRU
*GO:0051897	Positive regulation of protein kinase B signaling cascade			3	3,05E-02	GPX1, IGF2, INSR
GO:0042592	Homeostatic process			40	1,85E-05	STAT5A, TMX4, FFAR1, BDKRB1, FOXO3, CCL28, GCLM, APLP2, MBP, GPX2, GSR, GPX1, APP, APOA1, CXCR4, IL1B, DYRK3, SLC22A5, EIF2B2, INSR, CLN3, SLC12A2, OPR1, SMAD7, ELANE, IGF2, SOD2, ABCG8, ATXN1, INHBA, CTSK, EP300, TNFSF13B, RHCG, PYGM, GNAQ, PYGL, PLN, HBZ, TXNRD1
*GO:0048878	Chemical homeostasis			26	1,47E-03	FFAR1, BDKRB1, FOXO3, GCLM, CCL28, APLP2, MBP, APP, APOA1, CXCR4, IL1B, EIF2B2, INSR, CLN3, SMAD7, OPR1, ELANE, IGF2, SOD2, ATXN1, ABCG8, RHCG, GNAQ, PYGM, PYGL, PLN
	*GO:0050801	Ion homeostasis		19	1,79E-02	CLN3, OPR1, SMAD7, ELANE, BDKRB1, CCL28, GCLM, APLP2, SOD2, MBP, ATXN1, APP, GNAQ, RHCG, PYGM, CXCR4, PLN, IL1B, EIF2B2
	*GO:0033500	Carbohydrate homeostasis		5	3,55E-02	PYGL, FFAR1, IGF2, FOXO3, INSR
		*GO:0042593	Glucose homeostasis	5	3,55E-02	PYGL, FFAR1, IGF2, FOXO3, INSR
*GO:0019725	Cellular homeostasis			24	1,96E-03	CLN3, SLC12A2, OPR1, SMAD7, TMX4, ELANE, BDKRB1, GCLM, CCL28, APLP2, SOD2, MBP, ATXN1, GPX1, GSR, APP, GNAQ, RHCG, PYGM, CXCR4, PLN, IL1B, TXNRD1, EIF2B2
	*GO:0055082	Cellular chemical homeostasis		19	9,00E-03	CLN3, OPR1, SMAD7, ELANE, BDKRB1, CCL28, GCLM, APLP2, SOD2, MBP, ATXN1, APP, GNAQ, RHCG, PYGM, CXCR4, PLN, IL1B, EIF2B2
	*GO:0006873	Cellular ion homeostasis		19	7,57E-03	CLN3, OPR1, SMAD7, ELANE, BDKRB1, CCL28, GCLM, APLP2, SOD2, MBP, ATXN1, APP, GNAQ, RHCG, PYGM, CXCR4, PLN, IL1B, EIF2B2
GO:0010604	Positive regulation of macromolecule metabolic process			40	3,10E-04	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, APP, CHD8, MDIC, KLB1, IL1B, KDM3A, RARB, NFATC3, INSR, SAMD4A, CEBPA, TBL1XR1, CEBPB, SMAD7, KLF13, ELANE, IL9, IGF2, TBR1, PSMB8, ATF6, RNFB, ATXN1, INHBA, HHEX, CBLB, EP300, TNFSF13B, ETS1, NCOA4, MED17, IRF1, SH3D19, JAK3
*GO:0009891	Positive regulation of biosynthetic process			34	4,39E-04	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, CHD8, APP, MDIC, IL1B, KDM3A, RARB, INSR, NFATC3, SAMD4A, CEBPA, TBL1XR1, CEBPB, KLF13, ELANE, IL9, IGF2, TBR1, SOD2, ATXN1, ATF6, INHBA, HHEX, EP300, ETS1, NCOA4, MED17, IRF1, JAK3
	*GO:0031328	Positive regulation of cellular biosynthetic process		34	3,38E-04	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, CHD8, APP, MDIC, IL1B, KDM3A, RARB, INSR, NFATC3, SAMD4A, CEBPA, TBL1XR1, CEBPB, KLF13, ELANE, IL9, IGF2, TBR1, SOD2, ATXN1, ATF6, INHBA, HHEX, EP300, ETS1, NCOA4, MED17, IRF1, JAK3
	*GO:0010557	Positive regulation of macromolecule biosynthetic process		33	3,18E-04	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, CHD8, APP, MDIC, IL1B, KDM3A, RARB, INSR, NFATC3, SAMD4A, CEBPA, TBL1XR1, CEBPB, KLF13, ELANE, IL9, IGF2, TBR1, ATXN1, ATF6, INHBA, HHEX, EP300, ETS1, NCOA4, MED17, IRF1, JAK3
*GO:0010628	Positive regulation of gene expression			28	1,94E-03	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, APP, CHD8, MDIC, KDM3A, RARB, NFATC3, CEBPA, TBL1XR1, CEBPB, KLF13, TBR1, ATF6, ATXN1, HHEX, INHBA, EP300, TNFSF13B, NCOA4, ETS1, MED17, IRF1, JAK3
	*GO:0045941	Positive regulation of transcription		27	2,65E-03	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, APP, CHD8, MDIC, KDM3A, RARB, NFATC3, CEBPA, TBL1XR1, CEBPB, KLF13, TBR1, ATF6, ATXN1, HHEX, INHBA, EP300, NCOA4, ETS1, MED17, IRF1, JAK3
	*GO:0045893	Positive regulation of transcription, DNA-dependent		26	5,30E-04	STAT5A, TP63, NFKBIA, FOXO3, NR2E3, CITED2, APP, CHD8, MDIC, RARB, NFATC3, CEBPA, TBL1XR1, CEBPB, KLF13, TBR1, ATF6, ATXN1, HHEX, INHBA, EP300, NCOA4, ETS1, MED17, IRF1, JAK3
	*GO:0051254	Positive regulation of RNA metabolic process		26	6,15E-04	STAT5A, TP63, NFKBIA, FOXO3, NR2E3, CITED2, APP, CHD8, MDIC, RARB, NFATC3, CEBPA, TBL1XR1, CEBPB, KLF13, TBR1, ATF6, ATXN1, HHEX, INHBA, EP300, NCOA4, ETS1, MED17, IRF1, JAK3

GO:0010941	Regulation of cell death			36	1,73E-03	NUAK2, STAT5A, NFKBIA, TP63, PMAIP1, NR3C1, FOXO3, TNFRSF4, GCLM, CITED2, PEA15, GPX1, CHD8, APP, IL1B, RARB, CASP1, NQO1, TRAF3, CLN3, ARHGEF3, CEBPB, AIFM2, IGF2, SOD2, PROC, DAPK1, INHBA, CDKN1A, TNFSF13B, PRLR, HIPK1, ETS1, IGF2R, HIPK3, TNFAIP3	
*GO:0043067	Regulation of programmed cell death			36	1,63E-03	NUAK2, STAT5A, NFKBIA, TP63, PMAIP1, NR3C1, FOXO3, TNFRSF4, GCLM, CITED2, PEA15, GPX1, CHD8, APP, IL1B, RARB, CASP1, NQO1, TRAF3, CLN3, ARHGEF3, CEBPB, AIFM2, IGF2, SOD2, PROC, DAPK1, INHBA, CDKN1A, TNFSF13B, PRLR, HIPK1, ETS1, IGF2R, HIPK3, TNFAIP3	
	*GO:0042981	Regulation of apoptosis		36	1,38E-03	NUAK2, STAT5A, NFKBIA, TP63, PMAIP1, NR3C1, FOXO3, TNFRSF4, GCLM, CITED2, PEA15, GPX1, CHD8, APP, IL1B, RARB, CASP1, NQO1, TRAF3, CLN3, ARHGEF3, CEBPB, AIFM2, IGF2, SOD2, PROC, DAPK1, INHBA, CDKN1A, TNFSF13B, PRLR, HIPK1, ETS1, IGF2R, HIPK3, TNFAIP3	
		*GO:0043065	Positive regulation of apoptosis	19	2,75E-02	ARHGEF3, CEBPB, AIFM2, TP63, NR3C1, PMAIP1, FOXO3, DAPK1, INHBA, GPX1, CDKN1A, APP, HIPK1, ETS1, IL1B, RARB, NQO1, CASP1, TRAF3	
		*GO:0012502	Induction of programmed cell death	15	3,46E-02	ARHGEF3, CEBPB, AIFM2, TP63, PMAIP1, FOXO3, DAPK1, INHBA, GPX1, APP, CDKN1A, HIPK1, ETS1, CASP1, TRAF3	
		*GO:0006917	Induction of apoptosis	15	3,50E-02	ARHGEF3, CEBPB, AIFM2, TP63, PMAIP1, FOXO3, DAPK1, INHBA, GPX1, APP, CDKN1A, HIPK1, ETS1, CASP1, TRAF3	
		*GO:0060548	Negative regulation of cell death	21	9,21E-04	CLN3, CEBPB, NUAK2, STAT5A, NFKBIA, TP63, IGF2, GCLM, PROC, SOD2, DAPK1, CITED2, GPX1, PEA15, CDKN1A, CHD8, TNFSF13B, PRLR, HIPK3, IL1B, TNFAIP3	
		*GO:0043069	Negative regulation of programmed cell death	21	9,48E-04	CLN3, CEBPB, NUAK2, STAT5A, NFKBIA, TP63, IGF2, GCLM, PROC, SOD2, DAPK1, CITED2, GPX1, PEA15, CDKN1A, CHD8, TNFSF13B, PRLR, HIPK3, IL1B, TNFAIP3	
			*GO:0043066	Negative regulation of apoptosis	21	7,74E-04	CLN3, CEBPB, NUAK2, STAT5A, NFKBIA, TP63, IGF2, GCLM, PROC, SOD2, DAPK1, CITED2, GPX1, PEA15, CDKN1A, CHD8, TNFSF13B, PRLR, HIPK3, IL1B, TNFAIP3
GO:0010033	Response to organic substance			35	4,04E-04	ME1, CGA, SLC6A1, STAT5A, PTGS1, NFKBIA, BDKRB1, PMAIP1, NR3C1, GNG12, TNFRSF11B, ACSL1, PLIN2, IL1B, KDM3A, CASP1, EIF2B2, INSR, SELP, APCS, KAT2B, ACTA1, LY96, ATP4B, SOCS1, FBP1, IGF2, PTPRU, APPL1, ATF6, CDKN1A, EP300, PYGM, DNAJB1, HSPB3	
*GO:0009719	Response to endogenous stimulus			21	3,77E-03	ME1, CGA, KAT2B, SLC6A1, ACTA1, ATP4B, STAT5A, SOCS1, PTGS1, FBP1, IGF2, GNG12, PTPRU, APPL1, TNFRSF11B, CDKN1A, EP300, IL1B, KDM3A, EIF2B2, INSR	
	*GO:0009725	Response to hormone stimulus		20	2,76E-03	ME1, CGA, KAT2B, SLC6A1, ACTA1, STAT5A, PTGS1, SOCS1, FBP1, IGF2, GNG12, PTPRU, APPL1, TNFRSF11B, CDKN1A, EP300, IL1B, KDM3A, EIF2B2, INSR	
		*GO:0032870	Cellular response to hormone stimulus	9	2,06E-02	CGA, KAT2B, STAT5A, FBP1, KDM3A, IGF2, GNG12, APPL1, INSR	
*GO:0032101	Regulation of response to external stimulus			11	7,63E-03	GPX2, SELP, CLN3, GPX1, MASP1, IL8, STAT5A, KLKB1, ELANE, IGF2, PROC	
	*GO:0009617	Response to bacterium		12	1,07E-02	CFP, GPX2, SELP, GPX1, CEBPE, ATP4B, LY96, SOCS1, NFKBIA, IL1B, BDKRB1, NOS2	
		*GO:0032496	Response to lipopolysaccharide	7	1,37E-02	SELP, ATP4B, LY96, SOCS1, NFKBIA, IL1B, BDKRB1	
GO:0006357	Regulation of transcription from RNA polymerase II promoter			34	9,46E-04	SUPT3H, STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, CHD8, APP, RARB, NFATC3, CHD3, CEBPA, DNMT3A, TBL1XR1, CEBPB, SMAD7, KLF13, KLF11, TBR1, FOXO1, SOD2, ATXN1, ATF6, INHBA, HHEX, EP300, ETS1, MED17, HBZ, IRF1, TFAP2A, PHF21A, JAK3	
*GO:0045944	Positive regulation of transcription from RNA polymerase II promoter			24	7,66E-05	CEBPA, TBL1XR1, CEBPB, KLF13, STAT5A, NFKBIA, TP63, NR2E3, FOXO3, TBR1, CITED2, ATXN1, ATF6, INHBA, HHEX, CHD8, APP, EP300, ETS1, MED17, IRF1, RARB, JAK3, NFATC3	
*GO:0000122	Negative regulation of transcription from RNA polymerase II promoter			13	3,97E-02	CEBPA, DNMT3A, TBL1XR1, SMAD7, KLF11, TP63, NR2E3, FOXO1, CITED2, HHEX, HBZ, PHF21A, RARB	
GO:0010605	Negative regulation of macromolecule metabolic process			33	2,11E-03	EIF2C1, MASP1, TP63, BDKRB1, NR2E3, TNFRSF4, CITED2, WWP1, SERPINB10, RARB, KDM5B, INSR, CEBPA, DNMT3A, CLN3, TBL1XR1, SMAD7, ARID5B, LDB1, ELANE, KLF11, SOCS1, IGF2, PTPRU, FOXO1, PSMB8, SIRT2, ATXN1, INHBA, HHEX, TRPS1, HBZ, PHF21A	
*GO:0010558	Negative regulation of macromolecule biosynthetic process			25	6,70E-03	EIF2C1, TP63, NR2E3, TNFRSF4, CITED2, WWP1, RARB, KDM5B, CEBPA, DNMT3A, TBL1XR1, SMAD7, LDB1, ARID5B, KLF11, ELANE, PTPRU, SIRT2, FOXO1, ATXN1, HHEX, INHBA, TRPS1, HBZ, PHF21A	
GO:0009611	Response to wounding			33	5,54E-06	ABCF1, ITGAL, PLDN, MASP1, F13A1, CXCL2, BDKRB1, ABHD2, TNFRSF4, DTNBP1, CCL4, TPM1, CFP, GPX1, IL17D, CXCR4, IL10RB, KLKB1, IL1B, NFATC3, SELP, CEBPB, APCS, IL8, LY96, IL9, STXBP1, CHST3, IGF2, SOD2, PROC, LYVE1, GNAQ	
*GO:0006954	Inflammatory response			21	2,62E-04	ABCF1, SELP, ITGAL, APCS, CEBPB, MASP1, IL8, LY96, CXCL2, IL9, IGF2, BDKRB1, TNFRSF4, CCL4, CFP, IL17D, CXCR4, IL10RB, KLKB1, IL1B, NFATC3	
	*GO:0050727	Regulation of inflammatory response		7	1,29E-02	GPX2, GPX1, MASP1, STAT5A, KLKB1, ELANE, IGF2	
		*GO:0050728	Negative regulation of inflammatory response	4	4,37E-02	GPX2, GPX1, ELANE, IGF2	
GO:0030888	Regulation of B cell proliferation			4	3,34E-02	CDKN1A, TNFSF13B, IL13RA1, TNFRSF4	
	*GO:0030890	Positive regulation of B cell proliferation		4	1,35E-02	CDKN1A, TNFSF13B, IL13RA1, TNFRSF4	
GO:0051173	Positive regulation of nitrogen compound metabolic process			32	5,21E-04	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, CHD8, APP, MDIC, IL1B, KDM3A, RARB, INSR, NFATC3, CEBPA, TBL1XR1, CEBPB, KLF13, IGF2, TBR1, SOD2, RNF8, ATF6, ATXN1, INHBA, HHEX, EP300, ETS1, NCOA4, MED17, IRF1, JAK3	
*GO:0045935	Positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process			30	1,35E-03	STAT5A, NFKBIA, TP63, FOXO3, NR2E3, CITED2, APP, CHD8, MDIC, KDM3A, RARB, INSR, NFATC3, CEBPA, TBL1XR1, CEBPB, KLF13, IGF2, TBR1, ATF6, RNF8, ATXN1, HHEX, INHBA, EP300, NCOA4, ETS1, MED17, IRF1, JAK3	

GO:0016265	Death			29	1,82E-02	PHLPP1, NUA2, NFKBIA, TP63, FOXO3, PMAIP1, GPX1, PEA15, TNFRSF11B, APP, CXCR4, IL1B, CASP1, TRAF3, CLN3, ARHGEF3, AIFM2, KLF11, APTX, IGF2, IL24, SOD2, DAPK1, ATXN1, SFRP5, EP300, HIPK3, TNFAIP3, DRAM1
*GO:0008219	Cell death			29	1,70E-02	PHLPP1, NUA2, NFKBIA, TP63, FOXO3, PMAIP1, GPX1, PEA15, TNFRSF11B, APP, CXCR4, IL1B, CASP1, TRAF3, CLN3, ARHGEF3, AIFM2, KLF11, APTX, IGF2, IL24, SOD2, DAPK1, ATXN1, SFRP5, EP300, HIPK3, TNFAIP3, DRAM1
	*GO:0012501	Programmed cell death		25	2,39E-02	PHLPP1, NUA2, TP63, NFKBIA, FOXO3, PMAIP1, GPX1, PEA15, TNFRSF11B, APP, CXCR4, IL1B, CASP1, TRAF3, ARHGEF3, AIFM2, KLF11, IL24, SOD2, DAPK1, SFRP5, EP300, HIPK3, TNFAIP3, DRAM1
	*GO:0006915	Apoptosis		25	2,05E-02	PHLPP1, NUA2, TP63, NFKBIA, FOXO3, PMAIP1, GPX1, PEA15, TNFRSF11B, APP, CXCR4, IL1B, CASP1, TRAF3, ARHGEF3, AIFM2, KLF11, IL24, SOD2, DAPK1, SFRP5, EP300, HIPK3, TNFAIP3, DRAM1
		*GO:0008637	Apoptotic mitochondrial changes	4	4,33E-02	GPX1, AIFM2, PMAIP1, SOD2
GO:0032268	Regulation of cellular protein metabolic process			27	2,10E-04	EIF2C1, MASP1, NFKBIA, BDKRB1, MTF13, ZFP36L1, APP, APOA1, MDFIC, MAP3K2, KLKB1, SERPINB10, IL1B, EIF2B2, INSR, SAMD4A, CLN3, SMAD7, SOCS1, IGF2, PSMB8, EIF4G1, PPP1R9B, EIF4G3, EP300, HIPK3, SH3D19
*GO:0051248	Negative regulation of protein metabolic process			10	4,97E-02	CLN3, EIF2C1, MASP1, SMAD7, SOCS1, SERPINB10, BDKRB1, IGF2, INSR, PSMB8
	*GO:0032269	Negative regulation of cellular protein metabolic process		10	4,07E-02	CLN3, EIF2C1, MASP1, SMAD7, SOCS1, SERPINB10, BDKRB1, IGF2, INSR, PSMB8
*GO:0030162	Regulation of proteolysis			9	5,37E-05	CLN3, EP300, MASP1, SMAD7, KLKB1, SERPINB10, IL1B, IGF2, SH3D19
	*GO:0045862	Positive regulation of proteolysis		5	3,44E-03	EP300, SMAD7, KLKB1, IL1B, SH3D19
	*GO:0045861	Negative regulation of proteolysis		4	1,75E-02	CLN3, MASP1, SERPINB10, IGF2
GO:0009890	Negative regulation of biosynthetic process			26	4,86E-03	EIF2C1, TP63, NR2E3, TNFRSF4, CITED2, WWP1, RARB, KDM5B, CEBPA, DNMT3A, TBL1XR1, SMAD7, LDB1, ARID5B, KLF11, ELANE, IGF2, PTPRU, SIRT2, FOXP1, ATXN1, HHEX, INHBA, TRPS1, HBZ, PHF21A
*GO:0031327	Negative regulation of cellular biosynthetic process			26	6,15E-03	EIF2C1, TP63, NR2E3, TNFRSF4, CITED2, WWP1, RARB, KDM5B, CEBPA, DNMT3A, TBL1XR1, SMAD7, LDB1, ARID5B, KLF11, ELANE, IGF2, PTPRU, SIRT2, FOXP1, ATXN1, HHEX, INHBA, TRPS1, HBZ, PHF21A
GO:0010629	Negative regulation of gene expression			24	4,98E-03	CEBPA, DNMT3A, TBL1XR1, EIF2C1, SMAD7, ARID5B, LDB1, KLF11, TP63, NR2E3, PTPRU, TNFRSF4, FOXF1, SIRT2, CITED2, ATXN1, HHEX, WWP1, TRPS1, HBZ, PHF21A, RARB, INSR, KDM5B
*GO:0016481	Negative regulation of transcription			22	7,05E-03	CEBPA, DNMT3A, TBL1XR1, SMAD7, ARID5B, LDB1, KLF11, TP63, NR2E3, PTPRU, TNFRSF4, SIRT2, FOXF1, CITED2, ATXN1, HHEX, WWP1, TRPS1, HBZ, PHF21A, RARB, KDM5B
	*GO:0045892	Negative regulation of transcription, DNA-dependent		19	4,48E-03	CEBPA, DNMT3A, TBL1XR1, SMAD7, ARID5B, LDB1, KLF11, TP63, NR2E3, TNFRSF4, SIRT2, FOXF1, CITED2, HHEX, TRPS1, HBZ, PHF21A, RARB, KDM5B
GO:0033554	Cellular response to stress			24	1,90E-02	MORF4L1, RAD23B, CLN3, NUA2, POLG, CHST3, APTX, TP63, BCCIP, FOXO3, RAD52, TPM1, SOD2, RNFB, ATF6, GPX1, CDKN1A, HIPK1, MDFIC, MAP3K2, FANCD2, UBR5, MYOF, MAP3K13
*GO:0006979	Response to oxidative stress			11	9,21E-03	ANGPTL7, GPX2, GPX1, EP300, PTGS1, APTX, CA3, NQO1, TPM1, GCLM, SOD2
*GO:0006952	Defense response			25	2,56E-02	ABCF1, ITGAL, MASP1, CXCL2, BDKRB1, TNFRSF4, CCL4, CFP, IL17D, IL10RB, CXCR4, KLKB1, IL1B, NOS2, TNIP1, NFATC3, SELP, APC5, CEBPB, IL8, CEBPE, LY96, IL9, IGF2, INHBA
GO:0051172	Negative regulation of nitrogen compound metabolic process			22	2,55E-02	CEBPA, DNMT3A, TBL1XR1, SMAD7, ARID5B, LDB1, KLF11, TP63, NR2E3, PTPRU, TNFRSF4, SIRT2, FOXF1, CITED2, ATXN1, HHEX, WWP1, TRPS1, HBZ, PHF21A, RARB, KDM5B
*GO:0045934	Negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process			22	2,15E-02	CEBPA, DNMT3A, TBL1XR1, SMAD7, ARID5B, LDB1, KLF11, TP63, NR2E3, PTPRU, TNFRSF4, SIRT2, FOXF1, CITED2, ATXN1, HHEX, WWP1, TRPS1, HBZ, PHF21A, RARB, KDM5B
	*GO:0051253	Negative regulation of RNA metabolic process		19	5,29E-03	CEBPA, DNMT3A, TBL1XR1, SMAD7, ARID5B, LDB1, KLF11, TP63, NR2E3, TNFRSF4, SIRT2, FOXF1, CITED2, HHEX, TRPS1, HBZ, PHF21A, RARB, KDM5B
GO:0051338	Regulation of transferase activity			22	5,87E-04	CCNK, CCNT1, ELANE, BCCIP, IGF2, BDKRB1, CDC25C, CDKN3, TNFRSF4, APLP2, APP, CDKN1A, APOA1, PRLR, CXCR4, MDFIC, MAP3K2, HIPK3, IL1B, ADRA2B, INSR, MAP3K13
GO:0006928	Cell motion			21	1,95E-02	SELP, ITGAL, ZFAND5, TLN1, IL8, ARID5B, ELANE, ARPC5, CCL4, TPM1, TBR1, ARPC1B, GPX1, EPHA4, LYVE1, APP, APOA1, CXCR4, ETS1, IL1B, MSN
*GO:0051270	Regulation of cell motion			13	3,89E-03	SELP, SMAD7, CHST3, IGF2, BDKRB1, ABHD2, PTPRU, TPM1, CITED2, ETS1, CLIC4, CXCR4, INSR
	*GO:0030334	Regulation of cell migration		11	1,12E-02	SELP, CXCR4, SMAD7, CLIC4, ABHD2, BDKRB1, IGF2, PTPRU, INSR, TPM1, CITED2
		*GO:0030336	Negative regulation of cell migration	6	1,47E-02	SMAD7, CLIC4, ABHD2, PTPRU, TPM1, CITED2
		**GO:0051271	Negative regulation of cell motion	6	2,18E-02	SMAD7, CLIC4, ABHD2, PTPRU, TPM1, CITED2
GO:0051276	Chromosome organization			20	4,15E-02	MORF4L1, SUPT3H, DNMT3A, TBL1XR1, DPF3, KAT2B, AIFM2, NR3C1, SIRT2, RNFB, CHD8, EP300, KDM2A, FANCD2, CABIN1, PHF21A, KDM3A, KDM5B, CHD3, SUV420H1
*GO:0006325	Chromatin organization			18	1,69E-02	MORF4L1, SUPT3H, DNMT3A, TBL1XR1, DPF3, KAT2B, NR3C1, SIRT2, RNFB, CHD8, EP300, KDM2A, CABIN1, PHF21A, KDM3A, KDM5B, CHD3, SUV420H1
	*GO:0016568	Chromatin modification		18	6,57E-04	MORF4L1, SUPT3H, DNMT3A, TBL1XR1, DPF3, KAT2B, NR3C1, SIRT2, RNFB, CHD8, EP300, KDM2A, CABIN1, PHF21A, KDM3A, KDM5B, CHD3, SUV420H1
		*GO:0016569	Covalent chromatin modification	9	1,51E-02	RNFB, MORF4L1, SUPT3H, DNMT3A, EP300, KAT2B, KDM3A, SIRT2, SUV420H1
		*GO:0016570	Histone modification	8	3,62E-02	RNFB, MORF4L1, SUPT3H, EP300, KAT2B, KDM3A, SIRT2, SUV420H1
GO:0002684	Positive regulation of immune system process			19	3,97E-05	PLDN, MASP1, STAT5A, CD247, NFKBIA, BDKRB1, TNFRSF4, AQP3, FOXF1, CFP, CBLB, CDKN1A, TNFSF13B, IL4R, IL1B, CD79A, NOS2, IL13RA1, CD226

*GO:0002697	Regulation of immune effector process		10	1,09E-03	APOA1, MASP1, STAT5A, IL1B, IGF2, NOS2, IL13RA1, TNFRSF4, CD226, FOXP1
*GO:0002699	Positive regulation of immune effector process		6	5,03E-03	STAT5A, IL1B, NOS2, IL13RA1, CD226, FOXP1
GO:0032774	RNA biosynthetic process		17	3,81E-03	BATF3, CEBPA, SUPT3H, CCNK, CEBPB, KLF13, CCNT1, KLF11, NR3C1, NR2E3, PRDM4, ETS1, MED17, TRPS1, IRF1, GTF3C1, NFATC3
*GO:0006351	Transcription, DNA-dependent		17	3,33E-03	BATF3, CEBPA, SUPT3H, CCNK, CEBPB, KLF13, CCNT1, KLF11, NR3C1, NR2E3, PRDM4, ETS1, MED17, TRPS1, IRF1, GTF3C1, NFATC3
*GO:0006366	Transcription from RNA polymerase II promoter		16	9,69E-04	BATF3, CEBPA, SUPT3H, CCNK, CEBPB, KLF13, CCNT1, KLF11, NR2E3, NR3C1, PRDM4, ETS1, MED17, TRPS1, IRF1, NFATC3
GO:0051726	Regulation of cell cycle		18	4,99E-03	CCNK, STAT5A, CCNT1, BCCIP, IGF2, CDC25C, CDKN3, SIRT2, CITED2, CSNK2A2, PPP1R9B, INHBA, APP, CDKN1A, PRDM4, ETS1, IL1B, INSR
*GO:0045787	Positive regulation of cell cycle		6	4,95E-02	APP, STAT5A, TGFA, IGF2, INSR, CITED2
GO:0040008	Regulation of growth		16	2,82E-02	MORF4L1, CGA, STAT5A, SOCS1, TP63, BDKRB1, TKT, IGF2, DDR2, PPP1R9B, INHBA, CDKN1A, APP, EP300, PRDM4, INSR
GO:0046903	Secretion		14	4,35E-02	SNAP29, SCAMP1, CGA, PLDN, LTBP2, STX2, FFAR1, STXBP1, AQP3, ABCG8, TNFSF13B, SYN1, SCFD2, RAB14
*GO:0032940	Secretion by cell		12	1,70E-02	SCAMP1, SNAP29, CGA, PLDN, TNFSF13B, STX2, SYN1, LTBP2, SCFD2, FFAR1, STXBP1, RAB14
*GO:0050707	Regulation of cytokine secretion		4	3,99E-02	APOA1, IGF2, CASP1, TNFRSF4
GO:0040012	Regulation of locomotion		13	3,73E-03	SELP, IL8, CXCR4, SMAD7, CLIC4, ELANE, ABHD2, BDKRB1, IGF2, PTPRU, INSR, TPM1, CITED2
*GO:0040013	Negative regulation of locomotion		7	4,49E-03	SMAD7, CLIC4, ELANE, ABHD2, PTPRU, TPM1, CITED2
GO:0006916	Anti-apoptosis		14	2,44E-03	CEBPB, STAT5A, TP63, NFKBIA, DAPK1, CITED2, SOD2, PEA15, GPX1, TNFSF13B, PRLR, HIPK3, IL1B, TNFAIP3
GO:0007507	Heart development		13	8,99E-03	SMAD7, PDLIM3, TPM1, FOXP1, SOD2, CITED2, HHEX, EP300, GNAQ, PLN, RARB, NFATC3, INSR
GO:0003006	Developmental process involved in reproduction		13	3,60E-02	CGA, DZIP1, STAT5A, TP63, FOXO3, NR2C2, CITED2, INHBA, CXCR4, NCOA4, EIF2B2, LHB, INSR
*GO:0048608	Reproductive structure development		8	4,19E-02	CGA, INHBA, NCOA4, STAT5A, TP63, FOXO3, EIF2B2, LHB
*GO:0045137	Development of primary sexual characteristics		8	4,34E-02	CGA, INHBA, NCOA4, STAT5A, TP63, FOXO3, EIF2B2, LHB
GO:0050865	Regulation of cell activation		13	1,78E-03	SELP, INHBA, CDKN1A, CBLB, PLDN, SIT1, TNFSF13B, STAT5A, IL4R, IL1B, IL13RA1, TNFRSF4, CD226
*GO:0002694	Regulation of leukocyte activation		12	3,55E-03	INHBA, CDKN1A, CBLB, PLDN, SIT1, TNFSF13B, STAT5A, IL4R, IL1B, IL13RA1, TNFRSF4, CD226
**GO:0051249	Regulation of lymphocyte activation		11	4,65E-03	INHBA, CDKN1A, CBLB, PLDN, SIT1, TNFSF13B, STAT5A, IL4R, IL1B, IL13RA1, TNFRSF4
*GO:0050864	Regulation of B cell activation		6	9,31E-03	INHBA, CDKN1A, TNFSF13B, STAT5A, IL13RA1, TNFRSF4
GO:0007517	Muscle organ development		12	1,93E-02	FAM65B, ZFAND5, APP, EP300, ACTA1, SMAD7, PLN, ARID5B, TP63, RARB, TPM1, FOXP1
*GO:0060537	Muscle tissue development		10	4,62E-03	ZFAND5, APP, EP300, ACTA1, SMAD7, PLN, TP63, RARB, TPM1, FOXP1
*GO:0014706	Striated muscle tissue development		8	3,22E-02	APP, EP300, ACTA1, SMAD7, PLN, RARB, TPM1, FOXP1
*GO:0048745	Smooth muscle tissue development		3	2,06E-02	ZFAND5, TP63, FOXP1
GO:0009991	Response to extracellular stimulus		12	2,53E-02	PPP1R9B, CLN3, CDKN1A, TNFRSF11B, ACSL1, ACTA1, NUAK2, GDAPI1, SLC22A3, INSR, AQP3, SOD2
GO:0030029	Actin filament-based process		12	4,44E-02	PPP1R9B, TLN1, SSH1, ACTA1, NUAK2, DIAPH1, SSH2, CDC42BPA, PDLIM3, MYO9B, ARPC5, TPM1
*GO:0030036	Actin cytoskeleton organization		12	3,00E-02	PPP1R9B, TLN1, SSH1, ACTA1, NUAK2, DIAPH1, SSH2, CDC42BPA, PDLIM3, MYO9B, ARPC5, TPM1
GO:0030097	Hemopoiesis		12	3,94E-02	CEBPA, CSF3, INHBA, SNRK, CEBPE, STAT5A, HBZ, IRF1, DYRK3, CD79A, FOXP1, SOD2
GO:0032844	Regulation of homeostatic process		10	2,49E-03	INHBA, TNFRSF11B, ETS1, SMAD7, LDB1, STAT5A, BDKRB1, FOXO3, SLC22A5, GCLM
*GO:0001817	Regulation of cytokine production		11	1,75E-02	INHBA, CEBPB, APOA1, STAT5A, IL9, ELANE, IRF1, IGF2, CASP1, TNFRSF4, IFNAR1
GO:0010035	Response to inorganic substance		11	3,70E-02	GPX1, CDKN1A, TNFRSF11B, EP300, SLC6A1, CYBRD1, APTX, INSR, TPM1, AQP3, SOD2
GO:0010608	Posttranscriptional regulation of gene expression		11	4,36E-02	ZFP36L1, EIF4G1, EIF4G3, APP, APOA1, EIF2C1, SMAD7, APTX, EIF2B2, MTIF3, SAMD4A
GO:0005976	Polysaccharide metabolic process		10	2,08E-03	LYVE1, PPP1R2, SLC35D1, PYGM, PYGL, CSGALNACT2, CHI3L1, CHST3, MAT2B, PPP1CC
*GO:0044264	Cellular polysaccharide metabolic process		6	1,09E-02	PPP1R2, PYGM, PYGL, CSGALNACT2, MAT2B, PPP1CC
*GO:0000272	Polysaccharide catabolic process		4	3,34E-02	LYVE1, PYGM, PYGL, CHI3L1
GO:0006790	Sulfur metabolic process		10	2,65E-03	TPK1, GSR, GPX1, SLC35D1, STAT5A, CSGALNACT2, CHST3, MAT2B, GCLM, SOD2
*GO:0044272	Sulfur compound biosynthetic process		6	8,57E-03	TPK1, SLC35D1, CSGALNACT2, CHST3, MAT2B, GCLM
*GO:0050650	Chondroitin sulfate proteoglycan biosynthetic process		3	3,05E-02	SLC35D1, CSGALNACT2, CHST3
*GO:0006749	Glutathione metabolic process		4	3,34E-02	GSR, GPX1, GCLM, SOD2
GO:0003013	Circulatory system process		10	4,84E-02	GPX1, RENBP, PLN, PTGS1, BDKRB1, NOS2, MYOF, TPM1, GCLM, SOD2
*GO:0008015	Blood circulation		10	4,84E-02	GPX1, RENBP, PLN, PTGS1, BDKRB1, NOS2, MYOF, TPM1, GCLM, SOD2
GO:0050867	Positive regulation of cell activation		9	7,36E-03	SELP, CDKN1A, PLDN, TNFSF13B, STAT5A, IL4R, IL13RA1, TNFRSF4, CD226
*GO:0002696	Positive regulation of leukocyte activation		8	1,85E-02	CDKN1A, PLDN, TNFSF13B, STAT5A, IL4R, IL13RA1, TNFRSF4, CD226
*GO:0051251	Positive regulation of lymphocyte		7	3,72E-02	CDKN1A, PLDN, TNFSF13B, STAT5A, IL4R, IL13RA1, TNFRSF4
*GO:0042110	T cell activation		9	1,51E-02	ITGAL, CBLB, PRLR, CXCR4, STAT5A, IRF1, IGF2, TNFRSF4, IFNAR1
*GO:0050871	Positive regulation of B cell activation		5	9,40E-03	CDKN1A, TNFSF13B, STAT5A, IL13RA1, TNFRSF4

GO:0002683	Negative regulation of immune system process	7	1,90E-02	GPX2, INHBA, GPX1, CBLB, MASP1, IL4R, IGF2
GO:0030099	Myeloid cell differentiation	7	3,11E-02	CEBPA, CSF3, INHBA, SNRK, CEBPE, HBZ, DYRK3
*GO:0045637	Regulation of myeloid cell differentiation	6	3,26E-02	INHBA, ETS1, LDB1, STAT5A, NFKBIA, FOXO3
	*GO:0045638 Negative regulation of myeloid cell differentiation	4	3,99E-02	INHBA, LDB1, STAT5A, NFKBIA
GO:0048585	Negative regulation of response to stimulus	7	4,21E-02	GPX2, CLN3, GPX1, MASP1, SOCS1, ELANE, IGF2
*GO:0032102	Negative regulation of response to external stimulus	5	3,79E-02	GPX2, CLN3, GPX1, ELANE, IGF2
*GO:0050777	Negative regulation of immune response	4	5,61E-02	GPX2, GPX1, MASP1, IGF2
GO:0050817	Coagulation	7	4,57E-02	PLDN, GNAQ, KLKB1, F13A1, STXBP1, DTNBP1, PROC
*GO:0007596	Blood coagulation	7	4,57E-02	PLDN, GNAQ, KLKB1, F13A1, STXBP1, DTNBP1, PROC
GO:0007050	Cell cycle arrest	7	4,75E-02	PPP1R9B, INHBA, CDKN1A, KAT2B, IL8, CDKN3, UHMK1
GO:0042035	Regulation of cytokine biosynthetic process	6	4,00E-02	INHBA, CEBPB, STAT5A, IL9, ELANE, IRF1
GO:0045646	Regulation of erythrocyte differentiation	5	9,48E-04	INHBA, ETS1, LDB1, STAT5A, FOXO3
*GO:0045648	Positive regulation of erythrocyte differentiation	3	3,05E-02	INHBA, ETS1, FOXO3
GO:0018212	Peptidyl-tyrosine modification	5	3,33E-02	PRLR, STAT5A, JAK3, INSR, DDR2
*GO:0018108	Peptidyl-tyrosine phosphorylation	5	2,90E-02	PRLR, STAT5A, JAK3, INSR, DDR2
GO:0009896	Positive regulation of catabolic process	5	3,55E-02	CBLB, SMAD7, IGF2, SH3D19, INSR
GO:0045444	Fat cell differentiation	5	4,54E-02	CEBPA, GPX1, CEBPB, SOCS1, INSR
GO:0001889	Liver development	5	4,54E-02	CEBPA, HHEX, EP300, SOD2, CITED2
GO:0045682	Regulation of epidermis development	4	1,75E-02	INHBA, TP63, KEAP1, AQP3
GO:0015695	Organic cation transport	4	4,55E-02	RHCG, SLC12A2, SLC22A3, SLC22A5
GO:0000272	Polysaccharide catabolic process	4	3,34E-02	LYVE1, PYGM, PYGL, CHI3L1
GO:0030856	Regulation of epithelial cell differentiation	4	3,66E-02	PRLR, STAT5A, TP63, AQP3
GO:0022406	Membrane docking	4	4,33E-02	PLDN, SCFD2, STXBP1, MSN
GO:0030325	Adrenal gland development	3	2,54E-02	APOA1, NR3C1, CITED2
GO:0044058	Regulation of digestive system process	3	3,05E-02	ABCG8, APOA1, SLC22A5
GO:0045604	Regulation of epidermal cell differentiation	3	4,80E-02	TP63, KEAP1, AQP3
*Subset	**Part of			