Table S1. Gene set enrichment analysis of biological processes from Gene Ontology (GO) obtained from constructed PPI networks of the black module identified in the WGCNA. The table shows the GO terms identified, their cluster distribution according to ClueGO and the genes involved in each group cluster.

GOID	GOTerm	Term PValue	Term PValue Corrected with Bonferroni	Group PValue	Group PValue Corrected with Bonferroni	GOLevels	GOGroups	% Associated Genes	Nr. Genes	Associated Genes Found
GO:0000060	protein import into nucleus, translocation	12,0E-9	12,0E-6	12,0E-9	650,0E-9	[5, 6, 7, 8, 9, 10, 11, 12]	Group00	34,69	17,00	[BCL3, BCL6, CDK1, HSP90AB1, IPO4, IPO5, JAK2, KPNB1, MAPK1, NFKBIA, PHB2, POLA2, RAN, TNPO1, TNPO2, TXN, UBR5]
GO:0048008	platelet-derived growth factor receptor signaling pathway	10,0E-9	9,6E-6	10,0E-9	520,0E-9	[6, 7, 8]	Group01	33,33	18,00	[ABL1, BCAR1, BCR, CNTN1, GAB1, IQGAP1, JAK2, PDGFRA, PDGFRB, PIK3C2A, PTEN, PTPN1, PTPN11, PTPN12, PTPRJ, RAPGEF1, SNCA, SRC]
GO:0048041	focal adhesion assembly	15,0E-9	14,0E-6	15,0E-9	800,0E-9	[5, 7, 8]	Group02	27,50	22,00	[ACTN1, ARHGEF7, BCAS3, CFL1, CORO1C, CTTN, DYNLL1, FYN, IQGAP1, PDPK1, PPM1F, PTEN, PTK2, PTK2B, PTPRJ, PTPRK, RAC1, RCC2, SMAD3, SORBS1, SRC, TRIP6]
GO:0031958	corticosteroid receptor signaling pathway	690,0E-9	650,0E-6	690,0E-9	35,0E-6	[5, 6, 7, 8, 9]	Group03	50,00	9,00	[ARID1A, CALR, JAK2, NCOA6, NEDD4, NR3C1, PHB, RBM14, YWHAH]
GO:0071378	cellular response to growth hormone stimulus	240,0E-9	230,0E-6	240,0E-9	12,0E-6	[6, 7, 8]	Group04	40,00	12,00	[GHR, JAK2, JAK3, MAPK1, MAPK3, MYC, PIK3R1, PTK2, PTPN1, PXN, STAT3, STAT5B]
GO:1900024	regulation of substrate adhesion-dependent cell spreading	220,0E-9	210,0E-6	220,0E-9	11,0E-6	[4, 5, 6, 7, 8]	Group05	30,77	16,00	[ACTN4, ARHGEF7, C1QBP, CALR, CDC42, CORO1C, CRK, CRKL, DNM2, DOCK1, DOCK5, FLNA, PREX1, PTK2, RAC1, RCC2]
GO:0006607	NLS-bearing protein import into nucleus	540,0E-9	510,0E-6	540,0E-9	27,0E-6	[6, 7, 8, 9, 10, 11, 12]	Group06	45,45	10,00	[CBLB, IPO4, IPO5, KPNA2, KPNA3, KPNA4, KPNB1, RANBP2, TNPO1, TNPO2]
GO:0000186	activation of MAPKK activity	67,0E-9	62,0E-6	67,0E-9	3,4E-6	[6, 7, 8, 9, 10, 11, 12]	Group07	31,48	17,00	[CRK, CRKL, EGFR, EIF2AK2, FRS2, GNAI2, JAK2, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, PLCG1, RAF1, RAPGEF1]
GO:0007179	transforming growth factor beta receptor signaling pathway	150,0E-12	140,0E-9	150,0E-12	7,7E-9	[5, 6, 7, 8]	Group08	21,91	39,00	[ARRB2, CBL, CREB1, DNM2, DUSP22, FOS, HSP90AB1, HSPA1A, HSPA5, JUN, MAP3K7, MEN1, MTMR4, NEDD8, NKX2-1, PARP1, PDPK1, PIN1, PML, PTK2, PTPRK, PXN, RHOA, RPS27A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMURF1, SMURF2, SNW1, SRC, STK11, STRAP, STUB1, UBA52, USP9X, ZYX]
GO:0010001	glial cell differentiation	110,0E-9	100,0E-6	110,0E-9	5,7E-6	[5, 7, 8]	Group09	18,27	36,00	[ABL1, CDK1, CDK5, CLU, CSK, CTNNB1, DLL1, DTX1, EGFR, ERBB2, ERBB3, GSN, HDAC2, ID2, MAP2K1, MAPK1,

										MAPK3, MAPT, MTOR, NDRG1, NKX2-1, NLGN3, NOTCH1, PHGDH, PPARG, PRMT5, PTEN, PTPN11, RELA, S100A8, S100A9, S100B, SOD1, STAT3, VIM, VTN]
GO:0016202	regulation of striated muscle tissue development	110,0E-9	110,0E-6	110,0E-9	6,0E-6	[4, 5, 6, 7, 8]	Group10	21,60	27,00	[ARRB2, CDK1, CREB1, CTNNB1, DDX17, DDX5, DLL1, ERBB3, ERBB4, FGFR1, FRS2, GSK3B, MAPK14, MTOR, NACA, NOTCH1, PAK1, PIN1, PRKAA1, PTEN, RBPJ, RPS6KB1, S100B, SMAD3, SMAD4, TSC22D3, USP19]
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	660,0E-15	610,0E-12	660,0E-15	33,0E-12	[5, 6, 7, 8]	Group11	23,66	44,00	[ABL1, BRD4, C18orf32, CASP10, CASP8, CD4, CFLAR, CHUK, CTNNB1, EEF1D, FADD, FASLG, FLNA, FYN, IKBKB, IRAK1, MAP3K14, MAP3K3, MAP3K7, NEK6, NUP62, PELI2, PRKCB, PRKCE, PRKD1, PRKN, RBCK1, REL, RELA, RHOA, RIPK2, RPS27A, S100B, TAB2, TBK1, TFG, TNFRSF1A, TNIP2, TRADD, TRAF2, TRAF6, TRIP6, UBA52, UBE2I]
GO:0031295	T cell costimulation	290,0E-9	270,0E-6	68,0E-9	3,4E-6	[3, 6, 7, 8, 9]	Group12	23,66	22,00	[ARHGEF7, CD4, CDC42, CSK, FYN, GRB2, LCK, MAP3K14, MAP3K8, MLST8, MTOR, NCOR2, PAK1, PAK2, PDPK1, PIK3CA, PIK3R1, PTPN11, PTPN6, RAC1, SRC, VAV1]
GO:0050870	positive regulation of T cell activation	68,0E-9	63,0E-6	68,0E-9	3,4E-6	[5, 6, 7, 8]	Group12	17,75	41,00	[ANXA1, ARHGEF7, CD4, CDC42, CSK, DNAJA3, FADD, FYN, GRB2, HMGB1, HSPD1, HSPH1, JAK3, LCK, MAP3K14, MAP3K7, MAP3K8, MLST8, MTOR, NCK1, NCOR2, PAK1, PAK2, PDPK1, PIK3CA, PIK3R1, PTPN11, PTPN6, PTPRC, RAC1, RIPK2, RPS3, SPTA1, SRC, STAT5B, SYK, TRAF2, TRAF6, VAV1, ZAP70, ZBTB16]
GO:0051017	actin filament bundle assembly	170,0E-12	160,0E-9	170,0E-12	8,8E-9	[4, 6, 7, 8]	Group13	23,94	34,00	[ACTN1, ACTN4, ADD1, ARRB1, BAG4, CDC42, CFL1, CUL3, DYNLL1, EZR, HSP90B1, MET, MTOR, MYO1B, NEDD9, PAK1, PFN1, PIK3R1, PLEK, PLS3, PPM1F, PRKN, PTK2B, RAC1, RDX, RHOA, RNMT, SMAD3, SORBS1, SORBS3, SRC, SYNPO, WAS, ZYX]
GO:0043149	stress fiber assembly	360,0E-9	340,0E-6	170,0E-12	8,8E-9	[6, 7, 8, 9, 10]	Group13	23,40	22,00	[ARRB1, BAG4, CDC42, CUL3, DYNLL1, MET, MTOR, PAK1, PFN1, PIK3R1, PPM1F, PTK2B, RAC1, RHOA, RNMT, SMAD3, SORBS1, SORBS3, SRC, SYNPO, WAS, ZYX]
GO:0070646	protein modification by small protein removal	1,8E-18	1,7E-15	1,8E-18	95,0E-18	[5, 6, 7, 8]	Group14	22,15	72,00	[ACTB, ACTL6A, APC, AR, ARRB2, ATXN7, BABAM1, BARD1, BECN1, BRCA1, CDC20, CFTR, COPS2, COPS4, COPS5, COPS6, EP300, ESR1, HIF1A, ITCH, KAT2B, MAGI1, MAP3K7, MDM2, MYC, NEDD8, NFKBIA, PARK7, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, RAD23A, RHOA, RIPK2, RPS27A, RUVBL1, SHMT2, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMURF2, SUMO1, TNIP1, TNIP2, TP53, TRAF2, TRAF6, TRIM21, TRRAP, UBA52, UBE2D1, UBXN1, USP19, USP7, USP9X, VCP, YY1]

GO:0016579	protein deubiquitination	16,0E-18	15,0E-15	1,8E-18	95,0E-18	[6, 7, 8, 9]	Group14	22,15	68,00	[ACTB, ACTL6A, APC, AR, ARRB2, ATXN7, BABAM1, BARD1, BECN1, BRCA1, CDC20, CFTR, COPS5, EP300, ESR1, HIF1A, ITCH, KAT2B, MAGI1, MAP3K7, MDM2, MYC, NEDD8, NFKBIA, PARK7, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, RAD23A, RHOA, RIPK2, RPS27A, RUVBL1, SHMT2, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMURF2, TNIP1, TNIP2, TP53, TRAF2, TRAF6, TRIM21, TRRAP, UBA52, UBE2D1, UBXN1, USP19, USP7, USP9X, VCP, YY1]
GO:0032869	cellular response to insulin stimulus	400,0E-12	370,0E-9	400,0E-12	20,0E-9	[6, 7, 8]	Group15	20,00	43,00	[APC, BCAR1, CDK4, CFLAR, GAB1, GHR, GPR21, GRB10, GRB2, GSK3B, IGF1R, INSR, IRS4, KAT2B, MARS, MYC, MYO1C, PAK1, PARP1, PDPK1, PIK3C2A, PIK3CA, PIK3R1, PIK3R2, PIK3R3, PKM, PPARG, PRKAA1, PRKCB, PRKCI, PTPN1, PTPN11, RELA, RPS6KB1, SHC1, SMARCC1, SOCS1, SOCS3, SORBS1, SP1, SRC, SREBF1, YWHAG]
GO:0008286	insulin receptor signaling pathway	160,0E-9	150,0E-6	400,0E-12	20,0E-9	[6, 7, 8, 9]	Group15	21,26	27,00	[APC, BCAR1, CDK4, GAB1, GPR21, GRB10, GRB2, GSK3B, IGF1R, INSR, IRS4, PIK3C2A, PIK3CA, PIK3R1, PIK3R2, PIK3R3, PRKCB, PTPN1, RELA, RPS6KB1, SHC1, SMARCC1, SOCS1, SOCS3, SORBS1, SRC, SREBF1]
GO:0014065	phosphatidylinositol 3-kinase signaling	27,0E-12	25,0E-9	27,0E-12	1,3E-9	[6, 7, 8]	Group16	22,73	40,00	[BECN1, C1QBP, CBL, CD19, EGFR, ERBB2, ERBB3, ERBB4, FGFR1, FGR, FRS2, FYN, GAB1, GRB2, HAX1, IGF1R, JAK2, KIT, KLF4, LCK, MAPK1, MAPK3, MET, NEDD4, PDGFRA, PDGFRB, PIK3CA, PIK3CD, PIK3CG, PIK3R1, PIK3R2, PLXNB1, PTEN, PTK2, PTPN11, PTPN13, PTPN6, RNMT, SEMA4D, VAV1]
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	31,0E-12	29,0E-9	27,0E-12	1,3E-9	[5, 6, 7, 8, 9]	Group16	23,87	37,00	[BECN1, CBL, CD19, EGFR, ERBB2, ERBB3, ERBB4, FGFR1, FGR, FRS2, FYN, GAB1, GRB2, HAX1, JAK2, KIT, KLF4, LCK, MAPK1, MAPK3, MET, NEDD4, PDGFRA, PDGFRB, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLXNB1, PTEN, PTK2, PTPN11, PTPN13, PTPN6, RNMT, SEMA4D, VAV1]
GO:0010827	regulation of glucose transport	500,0E-12	470,0E-9	170,0E-9	8,6E-6	[4, 5, 8, 9]	Group17	25,21	30,00	[C3, CLTCL1, GNAI2, GRB10, HK2, INSR, MAPK14, MYC, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, PAK1, PEA15, PIK3R1, PIK3R2, PIK3R3, PRKAA1, PRKAG2, PRKCB, PRKCI, PTPN11, RAE1, RANBP2, RPS6KB1, SORBS1, TPR]
GO:0015758	glucose transport	170,0E-9	150,0E-6	170,0E-9	8,6E-6	[7, 8]	Group17	18,86	33,00	[C3, CLTCL1, EZR, GNAI2, GRB10, HK2, HNF1A, HOOK1, INSR, MAPK14, MYC, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, PAK1, PEA15, PIK3R1, PIK3R2, PIK3R3, PRKAA1, PRKAG2, PRKCB, PRKCI, PTPN11, RAE1, RANBP2, RPS6KB1, SORBS1, TPR]
GO:0006476	protein deacetylation	23,0E-9	22,0E-6	23,0E-9	1,1E-6	[7, 8]	Group18	24,51	25,00	[AKAP8L, BCL6, CCAR2, CHD4, CTBP1, EP300, HDAC1, HDAC2, HDAC3, JDP2, MAPK8, MBD3, MTA1, MTA2, PHB,

										PML, PRKD1, RBBP4, RBBP7, RBM14, SFPQ, SIN3A, SREBF1, TBL1X, TP53]
GO:0016575	histone deacetylation	27,0E-9	26,0E-6	23,0E-9	1,1E-6	[6, 7, 8, 9]	Group18	25,84	23,00	[AKAP8L, BCL6, CHD4, CTBP1, HDAC1, HDAC2, HDAC3, JDP2, MAPK8, MBD3, MTA1, MTA2, PHB, PML, PRKD1, RBBP4, RBBP7, RBM14, SFPQ, SIN3A, SREBF1, TBL1X, TP53]
GO:0030518	intracellular steroid hormone receptor signaling pathway	1,4E-12	1,3E-9	1,4E-12	75,0E-12	[4, 5, 6, 7, 8]	Group19	26,24	37,00	[AR, ARID1A, ARRB2, BRCA1, CALCOCO1, CALR, CARM1, CTNNB1, DAXX, DDX17, DDX5, DNAJA1, EP300, ESR1, HDAC1, JAK2, KAT5, NCOA1, NCOA6, NEDD4, NR3C1, NR6A1, PAK1, PARK7, PARP1, PHB, PHB2, PIAS2, POU4F2, RAN, RBFOX2, RBM14, SMARCA4, SRC, UBA5, UBR5, YWHAH]
GO:0030520	intracellular estrogen receptor signaling pathway	910,0E-9	850,0E-6	1,4E-12	75,0E-12	[5, 6, 7, 8, 9]	Group19	28,07	16,00	[AR, ARID1A, BRCA1, CARM1, DDX17, DDX5, ESR1, NCOA6, PAK1, PARP1, PHB2, POU4F2, RBFOX2, RBM14, SRC, UBA5]
GO:0043488	regulation of mRNA stability	1,8E-15	1,7E-12	1,0E-15	51,0E-15	[4, 7, 8]	Group20	28,57	42,00	[CARHSP1, DHX9, E2F1, ELAVL1, HNRNPA0, HNRNPC, HNRNPD, HNRNPR, HNRNPU, HSPA1A, HSPA8, HSPB1, IGF2BP1, KHSRP, MAPK14, MTOR, PABPC1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPS27A, SERBP1, SET, SYNCRIP, TARDBP, TNPO1, UBA52, XPO1, YBX1, YWHAB, YWHAZ]
GO:0043489	RNA stabilization	16,0E-9	15,0E-6	1,0E-15	51,0E-15	[4, 7, 8]	Group20	38,46	15,00	[DHX9, E2F1, ELAVL1, HNRNPA0, HNRNPC, HNRNPD, HNRNPU, IGF2BP1, MAPK14, MTOR, PABPC1, SYNCRIP, TARDBP, TNIP1, YBX1]
GO:0070934	CRD-mediated mRNA stabilization	940,0E-9	880,0E-6	1,0E-15	51,0E-15	[6, 9, 10]	Group20	100,00	5,00	[DHX9, HNRNPU, IGF2BP1, SYNCRIP, YBX1]
GO:0043299	leukocyte degranulation	240,0E-21	220,0E-18	490,0E-18	25,0E-15	[3, 6, 7, 8, 9]	Group21	18,12	106,00	[AGL, ALDOA, AMPD3, ANPEP, ANXA2, ATG7, BCR, BTK, C3, CBL, CCT2, CCT8, CD93, CLU, COPB1, CSTB, CTSD, DBNL, DDOST, DDX3X, DIAPH1, DNAJC5, DOCK2, DSP, DYNC1H1, DYNLL1, EEF1A1, EEF2, FGR, FLG2, GAB2, GDI2, GLB1, GSN, HCK, HLA-B, HMGB1, HSP90AA1, HSP90AB1, HSPA1A, HSPA6, HSPA8, IGF2R, ILF2, IMPDH2, IQGAP1, IQGAP2, ITGAM, ITGAX, ITGB2, KIT, KPNB1, KRT1, LAT, LYZ, MAPK1, MAPK14, MIF, MME, NFKB1, PA2G4, PDPK1, PFKL, PGAM1, PGM1, PGRMC1, PIK3CD, PIK3CG, PKM, PLAUR, PPIA, PRDX4, PRDX6, PSAP, PSMA2, PSMB1, PSMC2, PSMC3, PSMD13, PSMD2, PSMD3, PSMD7, PTPN6, PTPRB, PTPRC, PTPRJ, RAB24, RAC1, RAC2, RHOA, S100A7, S100A8, S100A9, SERPINB12, SPTAN1, SRP14, SURF4, SYK, TNFRSF1B, TOLLIP, TUBB, TUBB4B, UBR4, VCP, XRCC5, XRCC6]

GO:0045055	regulated exocytosis	490,0E-18	460,0E-15	490,0E-18	25,0E-15	[5, 6, 7, 8]	Group21	15,24	123,00	[ACTN1, ACTN4, AGL, ALB, ALDOA, AMPD3, ANPEP, ANXA2, APP, ATG7, BCR, BTK, C3, CACNA1A, CALM1, CBL, CCT2, CCT8, CD93, CDK5, CLU, COPB1, CSTB, CTSD, DBNL, DDOST, DDX3X, DIAPH1, DNAJC5, DOCK2, DSP, DYNC1H1, DYNLL1, EEF1A1, EEF2, FGR, FLG2, FLNA, GAB2, GDI2, GLB1, GSN, HCK, HLA-B, HMGB1, HSP90AA1, HSP90AB1, HSPA1A, HSPA6, HSPA8, IGF2R, ILF2, IMPDH2, IQGAP1, IQGAP2, ITGAM, ITGAX, ITGB2, KIT, KPNB1, KRT1, LAT, LGALS3BP, LYZ, MAPK1, MAPK14, MIF, MME, NFKB1, NOTCH1, PA2G4, PDPK1, PFKL, PGAM1, PGM1, PGRMC1, PIK3CD, PIK3CG, PKM, PLAUR, PLEK, PPIA, PRDX4, PRDX6, PSAP, PSMA2, PSMB1, PSMC2, PSMC3, PSMD13, PSMD2, PSMD3, PSMD7, PTPN6, PTPRB, PTPRC, PTPRJ, RAB24, RAC1, RAC2, RHOA, S100A7, S100A8, S100A9, SCRIB, SERPINB12, SOD1, SPTAN1, SRP14, SURF4, SYK, SYNJ1, TAGLN2, TLN1, TNFRSF1B, TOLLIP, TUBA4A, TUBB, TUBB4B, UBR4, VCP, XRCC5, XRCC6]
GO:0043312	neutrophil degranulation	24,0E-18	23,0E-15	490,0E-18	25,0E-15	[4, 6, 7, 8, 9, 10]	Group21	17,91	96,00	[AGL, ALDOA, AMPD3, ANPEP, ANXA2, ATG7, BCR, C3, CCT2, CCT8, CD93, CLU, COPB1, CSTB, CTSD, DBNL, DDOST, DDX3X, DIAPH1, DNAJC5, DOCK2, DSP, DYNC1H1, DYNLL1, EEF1A1, EEF2, FGR, FLG2, GDI2, GLB1, GSN, HLA-B, HMGB1, HSP90AA1, HSP90AB1, HSPA1A, HSPA6, HSPA8, IGF2R, ILF2, IMPDH2, IQGAP1, IQGAP2, ITGAM, ITGAX, ITGB2, KPNB1, KRT1, LYZ, MAPK1, MAPK14, MIF, MME, NFKB1, PA2G4, PFKL, PGAM1, PGM1, PGRMC1, PKM, PLAUR, PPIA, PRDX4, PRDX6, PSAP, PSMA2, PSMB1, PSMC2, PSMC3, PSMD13, PSMD2, PSMD3, PSMD7, PTPN6, PTPRB, PTPRC, PTPRJ, RAB24, RAC1, RHOA, S100A7, S100A8, S100A9, SERPINB12, SPTAN1, SRP14, SURF4, SYK, TNFRSF1B, TOLLIP, TUBB, TUBB4B, UBR4, VCP, XRCC5, XRCC6]
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	140,0E-15	130,0E-12	13,0E-21	670,0E-21	[2, 3, 4, 7, 8, 9, 10, 11, 12]	Group22	21,43	54,00	[ALK, AR, ATF2, BTK, CAMK2A, CARM1, CFLAR, CHUK, CLU, CRTC2, CTNNB1, DDIT3, EIF2AK2, EP300, ESR1, HSPA1A, IKBKB, IRAK1, ITGB2, JAK2, KIT, MAP3K7, NFKB1, NFKB2, NFKBIA, NFKBIB, NPM1, PARK7, PHB2, PPARG, PRDX3, PRKCB, PRKCI, PRKD1, PSMA6, PTEN, RBCK1, RELA, RIPK2, RPS27A, RPS3, RPS6KA4, S100A8, S100A9, SMARCA4, SMARCB1, STK3, TAB2, TCF7L1, TRADD, TRAF2, TRAF6, TRIM21, UBA52]
GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	13,0E-21	12,0E-18	13,0E-21	670,0E-21	[3, 6, 7, 8, 9, 10, 11]	Group22	21,46	85,00	[ALK, AR, ARRB1, ARRB2, ATF2, BTK, BTRC, CAMK2A, CARM1, CDK5RAP3, CDKN2A, CFLAR, CHUK, CLU, COMMD1, CRTC2, CTNNB1, DDIT3, DNAJA3, EIF2AK2, EP300, ESR1, EZH2, FANCA, FLNA, FOS, HCK, HDAC2,

										HSPA1A, ID2, IKBKB, IRAK1, ITCH, ITGB2, JAK2, JUN, KIT, KLF4, MAP3K7, MAPK1, MAPK10, MAPK14, MAPK3, MAPK8, MEN1, NFKB1, NFKB2, NFKBIA, NFKBIB, NPM1, PARK7, PHB2, PIAS2, POU4F2, PPARG, PRDX3, PRKCB, PRKCI, PRKD1, PSMA6, PTEN, RBCK1, RELA, RIPK2, RPS27A, RPS3, RPS6KA4, S100A8, S100A9, SGK1, SMAD7, SMARCA4, SMARCB1, STK3, SUMO1, SYK, TAB2, TCF7L1, TRADD, TRAF2, TRAF6, TRIM21, UBA52, USP7, WWP2]
GO:0051092	positive regulation of NF-kappaB transcription factor activity	1,4E-12	1,3E-9	13,0E-21	670,0E-21	[3, 4, 5, 8, 9, 10, 11, 12, 13]	Group22	26,24	37,00	[ALK, AR, BTK, CAMK2A, CARM1, CFLAR, CHUK, CLU, EIF2AK2, HSPA1A, IKBKB, IRAK1, ITGB2, MAP3K7, NFKB1, NFKB2, NFKBIA, NFKBIB, NPM1, PRDX3, PRKCB, PRKCI, PRKD1, PSMA6, RBCK1, RELA, RIPK2, RPS27A, RPS3, RPS6KA4, S100A8, S100A9, TAB2, TRADD, TRAF2, TRAF6, UBA52]
GO:0043550	regulation of lipid kinase activity	4,0E-12	3,7E-9	4,0E-12	200,0E-12	[5, 6, 8, 9]	Group23	40,00	22,00	[AMBRA1, ATG14, CDC42, EEF1A2, ERBB4, FGR, KIT, KLF4, NRBF2, PDGFRA, PDGFRB, PIK3R1, PIK3R2, PIK3R3, PRKD1, PTK2, PTK2B, RAC1, RBL1, SH3GLB1, SRC, VAV2]
GO:0090218	positive regulation of lipid kinase activity	740,0E-12	690,0E-9	4,0E-12	200,0E-12	[4, 5, 6, 7, 8, 9, 10]	Group23	43,24	16,00	[AMBRA1, ATG14, CDC42, EEF1A2, ERBB4, FGR, KIT, PDGFRA, PDGFRB, PRKD1, PTK2, PTK2B, RAC1, SH3GLB1, SRC, VAV2]
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	55,0E-12	52,0E-9	4,0E-12	200,0E-12	[6, 7, 8, 9, 10]	Group23	41,30	19,00	[AMBRA1, ATG14, CDC42, ERBB4, FGR, KIT, KLF4, PDGFRA, PDGFRB, PIK3R1, PIK3R2, PIK3R3, PRKD1, PTK2, PTK2B, RAC1, SH3GLB1, SRC, VAV2]
GO:1903146	regulation of mitophagy	330,0E-12	310,0E-9	31,0E-12	1,6E-9	[5, 6, 7, 8]	Group24	34,43	21,00	[ACTL6A, AMBRA1, ATG13, ATG14, BECN1, CAMKK2, CDC37, CSNK2A2, CTTN, FBXW7, HAX1, HIF1A, HK2, PARK7, PRKN, RPL28, RUVBL1, SMURF1, SQSTM1, SREBF1, SREBF2]
GO:0016239	positive regulation of macroautophagy	620,0E-9	580,0E-6	31,0E-12	1,6E-9	[6, 7, 8]	Group24	27,42	17,00	[AMBRA1, ATG13, ATG14, BECN1, CDC37, FYCO1, HIF1A, MAP3K7, MAPK3, PRKAA2, PRKN, RIPK2, SH3GLB1, SMURF1, SQSTM1, TBK1, UVRAG]
GO:1903599	positive regulation of mitophagy	150,0E-9	140,0E-6	31,0E-12	1,6E-9	[5, 6, 7, 8, 9]	Group24	41,38	12,00	[AMBRA1, ATG13, ATG14, BECN1, CAMKK2, CDC37, HIF1A, HK2, PARK7, PRKN, SMURF1, SQSTM1]
GO:2001235	positive regulation of apoptotic signaling pathway	19,0E-21	18,0E-18	71,0E-24	3,6E-21	[4, 5, 6, 7, 8]	Group25	29,02	56,00	[BAX, CASP8, CCM2, CLU, DDIT3, DEDD2, DYNLL1, E2F1, FADD, FASLG, FASN, FBXW7, GSK3B, GSN, ING5, JAK2, LCK, MAPK8, NCK1, PAK2, PARK7, PDIA3, PEA15, PLAUR, PML, PPP1CA, PPP2R1A, PPP2R1B, PRKN, PTEN, RACK1, RBCK1, RET, RPS3, S100A8, S100A9, SERINC3, SFN, SFPQ, SH3GLB1, SIAH1, SMAD3, SOD1, STK3, STK4, TP53, TP53BP2, TPD52L1, TRADD, TRAF2, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:2001242	regulation of intrinsic apoptotic signaling pathway	440,0E-12	410,0E-9	71,0E-24	3,6E-21	[5, 6, 7, 8]	Group25	21,89	37,00	[BAG5, BAX, CCAR2, CLU, DDIT3, DDX3X, DNAJA1, ENO1, FBXW7, HERPUD1, HIF1A, HSPA1A, HSPB1, HSPH1, LCK,

										MDM2, MIF, NCK1, NONO, P4HB, PARK7, PARP1, PLAUR, PRKN, PTPN1, RACK1, RPS3, S100A8, S100A9, SERINC3, SFPQ, SIAH1, SOD1, SRC, TP53, TRAP1, VDAC2]
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	280,0E-9	260,0E-6	71,0E-24	3,6E-21	[5, 6, 7, 8, 9]	Group25	28,81	17,00	[BAX, CLU, DDIT3, FBXW7, LCK, NCK1, PARK7, PRKN, RACK1, RPS3, S100A8, S100A9, SERINC3, SFPQ, SIAH1, SOD1, TP53]
GO:0006417	regulation of translation	18,0E-27	17,0E-24	18,0E-27	930,0E-27	[5, 6, 7, 8]	Group26	24,79	90,00	[ADAR, AGO1, AGO2, AGO4, AIRE, APP, ATF4, BCL3, C1QBP, CALR, CDK4, DAPK1, DDX1, DDX3X, DDX6, DNAJC5, EEF2, EGFR, EIF1B, EIF2AK2, EIF3I, EIF4A3, EIF5A, EIF5A2, EIF6, ELAVL1, EPRS, ERBB2, ESR1, FOXO3, GAPDH, GCN1, HNRNPA2B1, HNRNPD, HNRNPL, HNRNPR, HSPB1, IARS, IGF2BP1, IGF2BP2, IGF2BP3, ILF3, KHDRBS1, KHSRP, LARP4B, LRPPRC, MAP2K1, MAPK1, MAPK3, MKNK1, MOV10, MTOR, MYC, NCK1, NCL, NCOR1, NCOR2, NPM1, PA2G4, PABPC1, PML, PPP1CA, PTK2B, RACK1, RAN, RBM3, RPL30, RPL38, RPL5, RPS14, RPS27L, RPS3, RPS4X, RPS5, RPS6KA1, RPS6KA3, RPS6KB1, RPS9, S100A9, SMAD1, SMAD2, SMAD3, STAT3, SYNCRIP, TIA1, TNRC6B, TPR, TRAP1, VARS, XPO5]
GO:0017148	negative regulation of translation	12,0E-15	11,0E-12	18,0E-27	930,0E-27	[5, 6, 7, 8, 9]	Group26	26,71	43,00	[ADAR, AGO1, AGO2, AGO4, ATF4, CALR, DAPK1, DDX3X, DNAJC5, EGFR, EIF2AK2, EIF4A3, EIF6, ELAVL1, EPRS, ESR1, GAPDH, HNRNPA2B1, HNRNPD, HNRNPR, IGF2BP1, IGF2BP2, IGF2BP3, ILF3, KHSRP, MAP2K1, MOV10, NCL, NCOR1, NCOR2, PML, RACK1, RAN, RPS3, SMAD1, SMAD2, SMAD3, STAT3, SYNCRIP, TIA1, TNRC6B, TPR, XPO5]
GO:0045727	positive regulation of translation	200,0E-15	190,0E-12	18,0E-27	930,0E-27	[5, 6, 7, 8, 9]	Group26	29,82	34,00	[BCL3, C1QBP, CDK4, DDX3X, EEF2, EIF4A3, EIF5A, EIF5A2, EIF6, ELAVL1, EPRS, ERBB2, ESR1, HNRNPD, HNRNPL, KHDRBS1, LARP4B, MAPK1, MAPK3, MTOR, MYC, NCK1, NCOR1, NCOR2, NPM1, PABPC1, PTK2B, RBM3, RPL30, RPL5, RPS27L, RPS4X, RPS6KB1, RPS9]
GO:0018105	peptidyl-serine phosphorylation	3,8E-18	3,5E-15	430,0E-21	22,0E-18	[7, 8, 9]	Group27	22,74	68,00	[ARRB1, ARRB2, ATR, BAG4, BAX, CAMK2A, CAMK2G, CAMKK1, CAMKK2, CCM2, CDC42, CDK1, CDK5, CDK5R1, CHUK, GSK3B, HAX1, HIPK3, IKBKB, LMTK2, MAP4K1, MAPK1, MAPK13, MAPK14, MAPK3, MAPK8, MAST3, MIF, MKNK1, MTOR, MYLK2, NCK1, NEK6, PAK1, PAK2, PARK7, PDK3, PDPK1, PIK3CA, PLK1, PPM1F, PRKAA1, PRKAA2, PRKCB, PRKCE, PRKCI, PRKD1, RACK1, RAF1, RASSF2, RET, RIPK2, RPS6KA2, RPS6KA3, RPS6KA4, S100A8, S100A9, SGK1, SMAD7, SNCA, SRC, STK11, STK4, SYK, TBK1, TXN, ULK1, VRK2]
GO:0018107	peptidyl-threonine phosphorylation	1,1E-9	1,1E-6	430,0E-21	22,0E-18	[7, 8, 9]	Group27	25,00	29,00	[ACVR1B, CAD, CALM1, CAMK2A, CAMK2G, CAMKK1, CAMKK2, CDK1, CDK5, CDK5R1, CSNK2A1, CSNK2A2,

										GSK3B, HIPK3, LMTK2, MAPK1, MAPK8, MTOR, MYLK2, PDPK1, PLK1, PRKAG2, PRKCB, PRKD1, RIPK2, SMAD7, STK11, TBK1, ULK1]
GO:0033135	regulation of peptidyl-serine phosphorylation	170,0E-9	160,0E-6	430,0E-21	22,0E-18	[7, 8, 9, 10]	Group27	20,74	28,00	[ARRB1, ARRB2, BAG4, BAX, CCM2, CDC42, GSK3B, HAX1, MIF, NCK1, PAK1, PARK7, PIK3CA, PPM1F, PRKAA1, PRKD1, RACK1, RAF1, RASSF2, RET, RIPK2, S100A8, S100A9, SMAD7, SNCA, STK4, TBK1, TXN]
GO:2000142	regulation of DNA-templated transcription, initiation	230,0E-9	210,0E-6	98,0E-9	5,0E-6	[4, 5, 6, 7, 8, 9, 10, 11]	Group28	37,14	13,00	[CREB1, CTNNB1, ESR1, GTF2F2, HMGB1, HNF1A, JUN, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6]
GO:0006352	DNA-templated transcription, initiation	98,0E-9	92,0E-6	98,0E-9	5,0E-6	[6, 7, 8, 9, 10]	Group28	17,30	41,00	[AR, BRF2, CREB1, CREBBP, CTNNB1, E2F3, ESR1, GTF2F2, GTF3C1, HMGB1, HNF1A, JUN, KAT2B, MAML1, MAML3, MAPK3, MED31, MYC, NCOA6, NKX2-1, NOTCH1, NOTCH2, NR3C1, NR6A1, NRBF2, POLR2A, POLRMT, PPARG, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, RBPJ, SNW1, TFAM, TFB2M, TRIM28, VDR, YAP1]
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	380,0E-9	350,0E-6	98,0E-9	5,0E-6	[5, 6, 7, 8, 9, 10, 11, 12]	Group28	42,31	11,00	[CREB1, ESR1, GTF2F2, HMGB1, HNF1A, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6]
GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	13,0E-9	12,0E-6	98,0E-9	5,0E-6	[6, 7, 8, 9, 10, 11, 12, 13]	Group28	69,23	9,00	[CREB1, ESR1, HMGB1, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6]
GO:0002429	immune response-activating cell surface receptor signaling pathway	72,0E-24	68,0E-21	48,0E-27	2,4E-24	[4, 5, 6, 7, 8]	Group29	20,75	100,00	[ABI1, ABL1, ACTB, ACTG1, ARHGEF7, ARPC1A, BAX, BCAR1, BLK, BTK, BTRC, CD19, CD4, CDC42, CHUK, CREBBP, CRK, CSK, CUL1, DOCK1, DUSP22, ELMO1, EP300, EZR, FBXW11, FGR, FYN, GRB2, HCK, HSP90AA1, HSP90AB1, IKBKB, LAT, LCK, LCP2, MAP3K7, MAPK1, MAPK3, MYO1C, NCK1, NCOR2, NFKB1, NFKBIA, PAG1, PAK1, PAK2, PDPK1, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLCG1, PLCG2, PLSCR1, PRKCB, PRKCE, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTPN6, PTPRC, PTPRJ, RAC1, RAF1, RAPGEF1, RBCK1, RELA, RELB, RIPK2, RPS27A, RPS3, SKP1, SLC25A3, SRC, STK11, SYK, TAB2, TRAF6, UBA52, UBASH3A, UBE2D1, UBE2D2, VAV1, VAV2, WAS, WASL, ZAP70]
GO:0002431	Fc receptor mediated stimulatory signaling pathway	310,0E-12	290,0E-9	48,0E-27	2,4E-24	[5, 6, 7, 8, 9]	Group29	22,16	37,00	[ABI1, ABL1, ACTB, ACTG1, ARPC1A, CDC42, CRK, CSK, DOCK1, ELMO1, FGR, FYN, GRB2, HCK, HSP90AA1, HSP90AB1, MAPK1, MAPK3, MYO1C, NCK1, PAK1, PIK3CA, PIK3R1, PIK3R2, PLCG1, PLCG2, PLSCR1, PRKCE, PTK2, RAC1, RAPGEF1, SRC, SYK, VAV1, VAV2, WAS, WASL]

GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	1,5E-9	1,4E-6	48,0E-27	2,4E-24	[4, 5, 6, 7, 8, 9, 10]	Group29	21,74	35,00	[ABI1, ABL1, ACTB, ACTG1, ARPC1A, CDC42, CRK, DOCK1, ELMO1, FGR, FYN, GRB2, HCK, HSP90AA1, HSP90AB1, MAPK1, MAPK3, MYO1C, NCK1, PAK1, PIK3CA, PIK3R1, PIK3R2, PLCG1, PLCG2, PRKCE, PTK2, RAC1, RAPGEF1, SRC, SYK, VAV1, VAV2, WAS, WASL]
GO:0048010	vascular endothelial growth factor receptor signaling pathway	510,0E-18	480,0E-15	48,0E-27	2,4E-24	[6, 7, 8]	Group29	34,65	35,00	[ABI1, ACTB, ACTG1, BCAR1, CDC42, CRK, DOCK1, ELMO1, FYN, GRB10, HIF1A, HSP90AA1, HSPB1, MAPK13, MAPK14, NCF2, NCK1, NEDD4, PAK2, PIK3CA, PIK3R1, PIK3R2, PRKCB, PRKD1, PTK2, PTK2B, PTPN1, PXN, RAC1, RHOA, SHB, SRC, VAV1, VAV2, VTN]
GO:1901184	regulation of ERBB signaling pathway	35,0E-9	33,0E-6	56,0E-18	2,8E-15	[4, 5, 6, 7, 8, 9]	Group30	24,74	24,00	[APP, ARHGEF7, CBL, CBLB, CDC42, EGFR, EPS15L1, ERBB2, ERBB3, ERBB4, FASLG, FBXW7, GRB2, LGMN, NUP62, PLAUR, PTPN12, PTPRJ, RBPJ, RPS27A, SH3GL2, SH3KBP1, SHC1, UBA52]
GO:0038127	ERBB signaling pathway	56,0E-18	52,0E-15	56,0E-18	2,8E-15	[6, 7, 8]	Group30	29,41	45,00	[ABL1, APP, ARHGEF7, BCAR1, CBL, CBLB, CDC37, CDC42, CSK, EGFR, EPS15L1, ERBB2, ERBB3, ERBB4, FASLG, FBXW7, GAB1, GRB2, HSP90AA1, IQGAP1, LGMN, MAPK1, NUP62, PAG1, PDPK1, PIK3C2A, PIK3CA, PIK3R1, PLAUR, PLCG1, PTK2, PTK2B, PTPN11, PTPN12, PTPRJ, PXN, RASSF2, RBPJ, RPS27A, SH3GL2, SH3KBP1, SHC1, SRC, STUB1, UBA52]
GO:1901185	negative regulation of ERBB signaling pathway	7,3E-9	6,8E-6	56,0E-18	2,8E-15	[4, 5, 6, 7, 8, 9, 10]	Group30	33,96	18,00	[ARHGEF7, CBL, CBLB, CDC42, EGFR, EPS15L1, ERBB2, ERBB3, ERBB4, GRB2, LGMN, NUP62, PTPN12, PTPRJ, RPS27A, SH3GL2, SH3KBP1, UBA52]
GO:0007173	epidermal growth factor receptor signaling pathway	640,0E-15	600,0E-12	56,0E-18	2,8E-15	[7, 8, 9]	Group30	27,48	36,00	[ABL1, APP, ARHGEF7, BCAR1, CBL, CBLB, CDC42, CSK, EGFR, EPS15L1, FASLG, FBXW7, GAB1, GRB2, IQGAP1, NUP62, PAG1, PDPK1, PIK3C2A, PIK3CA, PIK3R1, PLAUR, PLCG1, PTK2, PTK2B, PTPN11, PTPN12, PTPRJ, PXN, RASSF2, RPS27A, SH3GL2, SH3KBP1, SHC1, SRC, UBA52]
GO:0038128	ERBB2 signaling pathway	2,9E-9	2,7E-6	56,0E-18	2,8E-15	[7, 8, 9]	Group30	40,00	16,00	[CDC37, EGFR, ERBB2, ERBB3, ERBB4, GAB1, GRB2, HSP90AA1, PIK3CA, PIK3R1, PTPN12, RPS27A, SHC1, SRC, STUB1, UBA52]
GO:0032271	regulation of protein polymerization	330,0E-15	310,0E-12	730,0E-15	37,0E-12	[4, 5, 6, 7, 8]	Group31	23,35	46,00	[ABL1, ADD1, ARF6, ARHGEF7, ARPC1A, AVIL, BAG4, CAPZA1, CAPZB, CDKN1B, CFL1, CLIP1, CTTN, DCTN1, DLG1, GRB2, GSN, HAX1, HCK, HSPA1A, IQGAP2, MAPT, MET, MLST8, MTOR, MYO1C, NCK1, PAK1, PFN1, PREX1, PRKCE, PTK2B, RAC1, RASA1, RDX, RNMT, RPS3, SNCA, SPTA1, SPTAN1, SPTBN1, TUBB4A, VASP, VDAC2, WAS, WASL]
GO:0032273	positive regulation of protein polymerization	7,6E-9	7,1E-6	730,0E-15	37,0E-12	[4, 5, 6, 7, 8, 9]	Group31	23,20	29,00	[ARF6, ARPC1A, BAG4, CDKN1B, CLIP1, CTTN, DCTN1, DLG1, GRB2, GSN, HCK, HSPA1A, IQGAP2, MAPT, MET, MLST8, MTOR, MYO1C, NCK1, PAK1, PFN1, PRKCE, PTK2B, RAC1, RNMT, RPS3, VASP, WAS, WASL]

GO:0008064	regulation of actin polymerization or depolymerization	24,0E-9	23,0E-6	730,0E-15	37,0E-12	[5, 6, 7, 8, 9]	Group31	19,66	35,00	[ADD1, ARF6, ARHGEF7, ARPC1A, AVIL, BAG4, CAPZA1, CAPZB, CFL1, CTTN, DLG1, GRB2, GSN, HAX1, HCK, IQGAP2, MLST8, MTOR, MYO1C, NCK1, PFN1, PLEK, PREX1, PRKCE, PTK2B, RAC1, RASA1, RDX, SPTA1, SPTAN1, SPTBN1, SSH2, VASP, WAS, WASL]
GO:0030041	actin filament polymerization	9,8E-9	9,2E-6	730,0E-15	37,0E-12	[6, 7, 8]	Group31	20,35	35,00	[ADD1, ARF6, ARHGEF7, ARPC1A, AVIL, BAG4, CAPZA1, CAPZB, CFL1, CTTN, DIAPH1, DLG1, GRB2, GSN, HAX1, HCK, IQGAP2, JAK2, MLST8, MTOR, MYO1C, NCK1, PFN1, PREX1, PRKCE, PTK2B, RAC1, RASA1, RDX, SPTA1, SPTAN1, SPTBN1, VASP, WAS, WASL]
GO:0030833	regulation of actin filament polymerization	12,0E-9	12,0E-6	730,0E-15	37,0E-12	[5, 6, 7, 8, 9, 10]	Group31	20,89	33,00	[ADD1, ARF6, ARHGEF7, ARPC1A, AVIL, BAG4, CAPZA1, CAPZB, CFL1, CTTN, DLG1, GRB2, GSN, HAX1, HCK, IQGAP2, MLST8, MTOR, MYO1C, NCK1, PFN1, PREX1, PRKCE, PTK2B, RAC1, RASA1, RDX, SPTA1, SPTAN1, SPTBN1, VASP, WAS, WASL]
GO:0031047	gene silencing by RNA	110,0E-12	100,0E-9	190,0E-30	10,0E-27	[4, 6, 7, 8]	Group32	24,29	34,00	[ADAR, AGO1, AGO2, AGO4, EGFR, EIF6, ELAVL1, ESR1, H3F3A, HIST2H3A, HNRNPA2B1, MAP2K1, MOV10, NCOR1, NCOR2, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, PABPC1, POLR2A, RAE1, RAN, RANBP2, SMAD1, SMAD2, SMAD3, STAT3, TNRC6B, TPR, XPO5]
GO:0006417	regulation of translation	18,0E-27	17,0E-24	190,0E-30	10,0E-27	[5, 6, 7, 8]	Group32	24,79	90,00	[ADAR, AGO1, AGO2, AGO4, AIRE, APP, ATF4, BCL3, C1QBP, CALR, CDK4, DAPK1, DDX1, DDX3X, DDX6, DNAJC5, EEF2, EGFR, EIF1B, EIF2AK2, EIF3I, EIF4A3, EIF5A, EIF5A2, EIF6, ELAVL1, EPRS, ERBB2, ESR1, FOXO3, GAPDH, GCN1, HNRNPA2B1, HNRNPD, HNRNPL, HNRNPR, HSPB1, IARS, IGF2BP1, IGF2BP2, IGF2BP3, ILF3, KHDRBS1, KHSRP, LARP4B, LRPPRC, MAP2K1, MAPK1, MAPK3, MKNK1, MOV10, MTOR, MYC, NCK1, NCL, NCOR1, NCOR2, NPM1, PA2G4, PABPC1, PML, PPP1CA, PTK2B, RACK1, RAN, RBM3, RPL30, RPL38, RPL5, RPS14, RPS27L, RPS3, RPS4X, RPS5, RPS6KA1, RPS6KA3, RPS6KB1, RPS9, S100A9, SMAD1, SMAD2, SMAD3, STAT3, SYNCRIP, TIA1, TNRC6B, TPR, TRAP1, VARS, XPO5]
GO:0017148	negative regulation of translation	12,0E-15	11,0E-12	190,0E-30	10,0E-27	[5, 6, 7, 8, 9]	Group32	26,71	43,00	[ADAR, AGO1, AGO2, AGO4, ATF4, CALR, DAPK1, DDX3X, DNAJC5, EGFR, EIF2AK2, EIF4A3, EIF6, ELAVL1, EPRS, ESR1, GAPDH, HNRNPA2B1, HNRNPD, HNRNPR, IGF2BP1, IGF2BP2, IGF2BP3, ILF3, KHSRP, MAP2K1, MOV10, NCL, NCOR1, NCOR2, PML, RACK1, RAN, RPS3, SMAD1, SMAD2, SMAD3, STAT3, SYNCRIP, TIA1, TNRC6B, TPR, XPO5]

GO:0035195	gene silencing by miRNA	1,6E-9	1,5E-6	190,0E-30	10,0E-27	[6, 7, 8, 9, 10]	Group32	33,33	20,00	[ADAR, AGO1, AGO2, AGO4, EGFR, EIF6, ELAVL1, ESR1, HNRNPA2B1, MAP2K1, MOV10, NCOR1, NCOR2, RAN, SMAD1, SMAD2, SMAD3, STAT3, TNRC6B, XPO5]
GO:0035196	production of miRNAs involved in gene silencing by miRNA	100,0E-9	95,0E-6	190,0E-30	10,0E-27	[6, 7, 8, 9, 10, 11]	Group32	39,39	13,00	[ADAR, AGO1, AGO2, AGO4, EGFR, ESR1, HNRNPA2B1, MAP2K1, NCOR1, NCOR2, SMAD1, SMAD2, SMAD3]
GO:0046777	protein autophosphorylation	200,0E-24	190,0E-21	6,4E-27	320,0E-27	[7, 8]	Group33	26,88	68,00	[ABL1, ACVR1B, ALK, ATR, BCR, BLK, BMX, BTK, CAD, CALM1, CAMK2A, CAMK2G, CAMKK2, CDK5, CSK, DAPK1, EGFR, EIF2AK2, EPHB1, ERBB2, ERBB4, FGFR1, FGR, FYN, GRB2, GSK3B, HCK, IGF1R, INSR, IQGAP1, IRAK1, JAK1, JAK2, JAK3, JUN, KIT, LCK, LMTK2, MAP3K3, MAP4K1, MAPK3, MKNK1, MTOR, MYLK2, NEK6, PAK1, PAK2, PDGFRA, PDGFRB, PDPK1, PRKD1, PTK2, PTK2B, RASSF2, SLA, SRC, STK11, STK4, SYK, TNK2, TOM1L1, TRIM28, TRPM7, TYK2, ULK1, ULK2, VRK2, ZAP70]
GO:0018108	peptidyl-tyrosine phosphorylation	9,8E-21	9,2E-18	6,4E-27	320,0E-27	[7, 8, 9]	Group33	21,39	86,00	[ABI1, ABL1, ALK, APP, ARRB2, BCR, BLK, BMX, BTK, CAMKK2, CBL, CBLB, CCM2, CD4, CDC37, CNTN1, CSF2RA, CSK, EGFR, EIF2AK2, EPHB1, ERBB2, ERBB3, ERBB4, FBXW7, FGFR1, FGR, FYN, GHR, GRB2, HAX1, HCK, HDAC2, HSP90AA1, HSPH1, IGF1R, INSR, IQGAP1, ITGB2, JAK1, JAK2, JAK3, KIT, LCK, LRRK1, MAP2K1, MAP2K3, MAPK3, MET, MIF, MLST8, MTOR, PAK2, PDGFRA, PDGFRB, PPP2CA, PPP2R1A, PRKCE, PTK2, PTK2B, PTPN1, PTPN6, RACK1, RET, RIPK2, RNMT, S100A8, S100A9, SEMA4D, SHC1, SLA, SOCS1, SOCS3, SRC, STAT3, STAT5B, STK11, SYK, TNFRSF1A, TNK2, TP53, TYK2, UNC119, VTN, WEE1, ZAP70]
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	5,4E-12	5,1E-9	6,4E-27	320,0E-27	[7, 8, 9, 10]	Group33	20,58	50,00	[ABI1, ABL1, APP, ARRB2, CBL, CBLB, CCM2, CD4, CNTN1, EGFR, ERBB3, ERBB4, FBXW7, FYN, GHR, HAX1, HDAC2, HSPH1, IQGAP1, ITGB2, JAK2, KIT, LRRK1, MIF, MLST8, MTOR, PAK2, PPP2CA, PPP2R1A, PRKCE, PTK2B, PTPN1, PTPN6, RACK1, RIPK2, S100A8, S100A9, SEMA4D, SHC1, SOCS1, SOCS3, SRC, STAT3, STK11, SYK, TNFRSF1A, TNK2, TP53, UNC119, VTN]
GO:0038083	peptidyl-tyrosine autophosphorylation	27,0E-18	26,0E-15	6,4E-27	320,0E-27	[8, 9, 10]	Group33	49,09	27,00	[ABL1, BLK, BMX, BTK, CSK, EGFR, ERBB4, FGR, FYN, GRB2, HCK, IGF1R, INSR, IQGAP1, JAK1, JAK2, JAK3, LCK, MAPK3, PTK2, PTK2B, SLA, SRC, SYK, TNK2, TYK2, ZAP70]
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	2,1E-9	1,9E-6	6,4E-27	320,0E-27	[7, 8, 9, 10, 11]	Group33	20,43	38,00	[ABI1, ABL1, ARRB2, CCM2, CD4, CNTN1, ERBB3, ERBB4, FBXW7, FYN, GHR, HAX1, HDAC2, HSPH1, IQGAP1, JAK2, KIT, LRRK1, MIF, MLST8, MTOR, PAK2, PTK2B, PTPN1, RIPK2, S100A8, S100A9, SEMA4D, SOCS3, SRC, STAT3, STK11, SYK, TNFRSF1A, TNK2, TP53, UNC119, VTN]

GO:1903706	regulation of hemopoiesis	100,0E-9	94,0E-6	86,0E-18	4,4E-15	[3, 4, 5, 6, 7, 8]	Group34	15,66	52,00	[ACIN1, ACVR1B, ANXA1, BCL6, BTK, CASP8, CD4, CDKN2A, CREB1, CTNNB1, DLL1, DTX1, EIF2AK2, EIF6, ERBB2, FADD, FANCA, FASN, FOS, FOXO3, HAX1, HIF1A, HLA-B, HMGB1, HSPA9, ID2, JAG1, JAK3, JUN, MAPK14, MTOR, MYC, NFKBIA, NOTCH1, PIK3R1, POU4F2, PRMT1, PTK2B, PTPN6, RASSF2, RBFOX2, RIPK2, RUNX1, SOD1, STAT5B, SYK, TFE3, TRAF6, UBASH3B, UNC45A, ZAP70, ZBTB16]
GO:0002521	leukocyte differentiation	180,0E-15	170,0E-12	86,0E-18	4,4E-15	[5, 6, 7, 8]	Group34	16,80	83,00	[ABL1, ACIN1, AIRE, ANXA1, ANXA2, ATG5, BAX, BCL3, BCL6, BLNK, BMX, BTK, CASP8, CD4, CDC42, CDKN2A, CLU, CREB1, CTNNB1, DLL1, DNAJA3, DOCK2, DTX1, EIF2AK2, EP300, ERBB2, FADD, FANCA, FASN, FOS, GAB2, HAX1, HLA-B, HMGB1, ID2, ITGB1, JAG2, JAK3, JUN, JUNB, KDELR1, KIT, KLF6, LCK, LRRK1, LYL1, MAPK14, MTOR, MYC, MYH9, NOTCH2, PARP1, PIK3CD, PIK3R1, PLCG2, POU4F2, PPARG, PREX1, PTK2B, PTPN6, PTPRC, RASSF2, RBPJ, RELB, RIPK2, RPL22, RPS6, RUNX1, SOD1, SRC, STAT3, STAT5B, STAT6, STK11, SYK, TCF7L1, TFE3, TPD52, TRAF6, UBASH3B, VAV1, ZAP70, ZBTB16]
GO:0030099	myeloid cell differentiation	120,0E-15	110,0E-12	86,0E-18	4,4E-15	[5, 6, 7, 8]	Group34	19,02	66,00	[ABI1, ACIN1, ACTN1, ACVR1B, ADAR, ADD1, ANXA2, BCL6, CASP3, CASP8, CD4, CDC42, CREB1, CTNNB1, DLL1, EIF2AK2, EIF6, EP300, FADD, FASN, FOS, FOXO3, GAB2, HAX1, HIF1A, HSPA9, ID2, JAG1, JAK2, JAK3, JUN, JUNB, KIT, LRRK1, MAPK14, MTOR, MYC, MYH9, NCOA6, NFKBIA, PARP1, PIK3CD, PIK3R1, PML, POU4F2, PPARG, PRDX3, PRMT1, PTK2B, PTPN11, PTPN6, RASSF2, RBFOX2, RBPJ, RELB, RPS14, RPS19, RPS6, RUNX1, SRC, STAT5B, TFE3, TRAF6, UBASH3B, UNC45A, ZBTB16]
GO:0045637	regulation of myeloid cell differentiation	100,0E-9	97,0E-6	86,0E-18	4,4E-15	[4, 5, 6, 7, 8, 9]	Group34	18,62	35,00	[ACIN1, ACVR1B, CASP8, CD4, CREB1, CTNNB1, DLL1, EIF6, FADD, FASN, FOS, FOXO3, HAX1, HIF1A, HSPA9, ID2, JAG1, JUN, MAPK14, MTOR, MYC, NFKBIA, PIK3R1, POU4F2, PRMT1, PTK2B, RASSF2, RBFOX2, RUNX1, STAT5B, TFE3, TRAF6, UBASH3B, UNC45A, ZBTB16]
GO:0030098	lymphocyte differentiation	1,1E-9	1,0E-6	86,0E-18	4,4E-15	[4, 6, 7, 8, 9]	Group34	17,13	56,00	[ABL1, AIRE, ANXA1, ATG5, BAX, BCL3, BCL6, BLNK, BMX, BTK, CD4, CDKN2A, CTNNB1, DLL1, DNAJA3, DOCK2, DTX1, EP300, ERBB2, FADD, FANCA, FASN, HMGB1, ID2, ITGB1, JAG2, JAK3, KDELR1, KIT, KLF6, LCK, LYL1, NOTCH2, PIK3CD, PIK3R1, PLCG2, PREX1, PTK2B, PTPN6, PTPRC, RBPJ, RELB, RIPK2, RPL22, RPS6, SOD1, STAT3, STAT5B, STAT6, STK11, SYK, TCF7L1, TPD52, VAV1, ZAP70, ZBTB16]
GO:0030217	T cell differentiation	46,0E-9	43,0E-6	86,0E-18	4,4E-15	[5, 7, 8, 9, 10]	Group34	17,86	40,00	[ABL1, AIRE, ANXA1, ATG5, BCL3, BCL6, BMX, CD4, CDKN2A, CTNNB1, DNAJA3, DOCK2, DTX1, ERBB2, FADD,

										FANCA, FASN, HMGB1, JAG2, JAK3, KDELR1, KIT, LCK, PIK3CD, PREX1, PTPRC, RELB, RIPK2, RPL22, RPS6, SOD1, STAT3, STAT5B, STAT6, STK11, SYK, TCF7L1, VAV1, ZAP70, ZBTB16]
GO:1903311	regulation of mRNA metabolic process	170,0E-9	160,0E-6	64,0E-18	3,2E-15	[5, 6, 7, 8]	Group35	20,74	28,00	[ACIN1, AGO2, BAG4, BARD1, C1QBP, CCNT1, DAZAP1, DDX17, DDX5, EIF4A3, HNRNPA1, HNRNPA2B1, HNRNPL, HNRNPR, HSPA1A, HSPA8, KHDRBS1, KHSRP, PABPC1, PTBP1, RBFOX2, RBMX, SNRPA, SNW1, SRSF3, SRSF7, TIA1, TNRC6B]
GO:0006397	mRNA processing	670,0E-18	630,0E-15	64,0E-18	3,2E-15	[6, 7, 8]	Group35	17,85	88,00	[ACIN1, ADAR, AKAP8L, APP, BARD1, C1QBP, CCAR2, CCNT1, CD2BP2, CDC5L, CMTR1, CPSF6, DAZAP1, DDX1, DDX17, DDX5, DHX15, DHX8, DHX9, EFTUD2, EIF4A3, ELAVL1, FUS, GEMIN4, GTF2F2, HNRNPA0, HNRNPA1, HNRNPA2B1, HNRNPA3, HNRNPC, HNRNPD, HNRNPF, HNRNPH1, HNRNPH2, HNRNPH3, HNRNPL, HNRNPM, HNRNPR, HNRNPU, HNRNPUL1, HSPA1A, HSPA8, KHDRBS1, KHSRP, LUC7L2, NONO, NUDT21, PABPC1, PCBP1, PCBP2, PIN1, POLR2A, PRMT5, PRPF8, PTBP1, PUF60, RALY, RBFOX2, RBM23, RBM39, RBMX, RBPMS, RNMT, SF1, SF3A2, SF3B3, SFPQ, SMNDC1, SNRNP200, SNRPA, SNRPB, SNRPC, SNRPD1, SNRPD3, SNRPF, SNRPG, SNW1, SRSF3, SRSF7, STRAP, SYNCRIP, TARDBP, TIA1, TUT1, WDR77, XRN2, YBX1, ZNF326]
GO:0008380	RNA splicing	4,3E-18	4,0E-15	64,0E-18	3,2E-15	[6, 7, 8]	Group35	19,68	85,00	[ACIN1, AKAP8L, C1QBP, CCAR2, CD2BP2, CDC5L, DAZAP1, DDX1, DDX17, DDX5, DHX15, DHX8, DHX9, EFTUD2, EIF4A3, ELAVL1, FAM98B, FUS, GEMIN4, GTF2F2, HNRNPA0, HNRNPA1, HNRNPA2B1, HNRNPA3, HNRNPC, HNRNPD, HNRNPF, HNRNPH1, HNRNPH2, HNRNPH3, HNRNPL, HNRNPM, HNRNPR, HNRNPU, HNRNPUL1, HSPA1A, HSPA8, KHDRBS1, KHSRP, LUC7L2, NONO, NUDT21, PABPC1, PCBP1, PCBP2, PIK3R1, PIN1, POLR2A, PPP2CA, PPP2R1A, PRMT5, PRPF8, PTBP1, PTEN, PUF60, RALY, RBFOX2, RBM39, RBMX, RBPMS, RPS13, RTCB, SF1, SF3A2, SF3B3, SFPQ, SMNDC1, SNRNP200, SNRPA, SNRPB, SNRPC, SNRPD1, SNRPD3, SNRPF, SNRPG, SNW1, SRSF3, SRSF7, STRAP, SYNCRIP, TARDBP, TIA1, WDR77, YBX1, ZNF326]
GO:0043484	regulation of RNA splicing	160,0E-9	150,0E-6	64,0E-18	3,2E-15	[5, 6, 7, 8, 9]	Group35	22,32	25,00	[ACIN1, C1QBP, DAZAP1, DDX17, DDX5, EIF4A3, HNRNPA1, HNRNPA2B1, HNRNPF, HNRNPH1, HNRNPL, HSPA1A, HSPA8, KHDRBS1, PIK3R1, POLR2A, PTBP1, RBFOX2, RBMX, RPS13, SNW1, SRSF3, SRSF7, TIA1, ZNF326]

GO:0000375	RNA splicing, via transesterification reactions	2,2E-18	2,1E-15	64,0E-18	3,2E-15	[7, 8, 9]	Group35	22,09	72,00	[ACIN1, C1QBP, CD2BP2, CDC5L, DAZAP1, DDX1, DDX17, DDX5, DHX15, DHX8, DHX9, EFTUD2, EIF4A3, ELAVL1, FUS, GEMIN4, GTF2F2, HNRNPA0, HNRNPA1, HNRNPA2B1, HNRNPA3, HNRNPC, HNRNPD, HNRNPF, HNRNPH1, HNRNPH2, HNRNPH3, HNRNPL, HNRNPM, HNRNPR, HNRNPU, HNRNPUL1, HSPA8, KHDRBS1, KHSRP, LUC7L2, NONO, NUDT21, PABPC1, PCBP1, PCBP2, PIN1, POLR2A, PRMT5, PRPF8, PTBP1, PUF60, RALY, RBFOX2, RBMX, RBPMS, SF1, SF3A2, SF3B3, SFPQ, SMNDC1, SNRNP200, SNRPA, SNRPB, SNRPC, SNRPD1, SNRPD3, SNRPF, SNRPG, SNW1, SRSF3, SRSF7, STRAP, SYNCRIP, TIA1, WDR77, YBX1]
GO:0000398	mRNA splicing, via spliceosome	5,0E-18	4,7E-15	64,0E-18	3,2E-15	[7, 8, 9, 10, 11]	Group35	21,98	71,00	[ACIN1, C1QBP, CD2BP2, CDC5L, DAZAP1, DDX1, DDX17, DDX5, DHX15, DHX8, DHX9, EFTUD2, EIF4A3, ELAVL1, FUS, GEMIN4, GTF2F2, HNRNPA0, HNRNPA1, HNRNPA2B1, HNRNPA3, HNRNPC, HNRNPD, HNRNPF, HNRNPH1, HNRNPH2, HNRNPH3, HNRNPL, HNRNPM, HNRNPR, HNRNPU, HNRNPUL1, HSPA8, KHDRBS1, LUC7L2, NONO, NUDT21, PABPC1, PCBP1, PCBP2, PIN1, POLR2A, PRMT5, PRPF8, PTBP1, PUF60, RALY, RBFOX2, RBMX, RBPMS, SF1, SF3A2, SF3B3, SFPQ, SMNDC1, SNRNP200, SNRPA, SNRPB, SNRPC, SNRPD1, SNRPD3, SNRPF, SNRPG, SNW1, SRSF3, SRSF7, STRAP, SYNCRIP, TIA1, WDR77, YBX1]
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	7,8E-12	7,3E-9	15,0E-30	770,0E-30	[7, 8, 9, 10, 11, 12, 13]	Group36	30,21	29,00	[AIFM1, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, DNAJA3, DYNLL1, FADD, FASLG, FASN, HSPD1, JAK2, LCK, MAPT, PML, PPARG, RACK1, RET, RIPK2, RPS27L, S100A8, S100A9, SMAD3, SNCA, TRADD, TRAF2, VCP]
GO:2001234	negative regulation of apoptotic signaling pathway	16,0E-12	15,0E-9	15,0E-30	770,0E-30	[4, 5, 6, 7, 8]	Group36	20,25	49,00	[AR, ARRB2, BAG5, BAX, BRCA1, CASP8, CCAR2, CFLAR, CLU, CTNNB1, CTTN, DAPK1, DDX3X, DNAJA1, ENO1, EPRS, FADD, FASLG, FASN, FYN, HERPUD1, HIF1A, HSPA1A, HSPB1, HSPH1, LMNA, MDM2, MEN1, MIF, NONO, PARK7, PEA15, PLAUR, PRKN, PTPN1, RAF1, RB1CC1, RELA, RFFL, RPS6KB1, S100A8, S100A9, SLC25A5, SRC, TRADD, TRAF2, TRAP1, VDAC2, YAP1]
GO:2001235	positive regulation of apoptotic signaling pathway	19,0E-21	18,0E-18	15,0E-30	770,0E-30	[4, 5, 6, 7, 8]	Group36	29,02	56,00	[BAX, CASP8, CCM2, CLU, DDIT3, DEDD2, DYNLL1, E2F1, FADD, FASLG, FASN, FBXW7, GSK3B, GSN, ING5, JAK2, LCK, MAPK8, NCK1, PAK2, PARK7, PDIA3, PEA15, PLAUR, PML, PPP1CA, PPP2R1A, PPP2R1B, PRKN, PTEN, RACK1, RBCK1, RET, RPS3, S100A8, S100A9, SERINC3, SFN, SFPQ, SH3GLB1, SIAH1, SMAD3, SOD1, STK3, STK4, TP53, TP53BP2, TPD52L1, TRADD, TRAF2, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]

GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	3,0E-9	2,8E-6	15,0E-30	770,0E-30	[5, 6, 7, 8]	Group36	26,88	25,00	[BAX, BRCA1, CASP8, CFLAR, DAPK1, DAXX, DDX3X, DEDD, DEDD2, ETFA, FADD, FASLG, FASN, GABARAP, PARK7, PEA15, PIK3R1, PTEN, RAF1, RFFL, STK3, STK4, TNFRSF1A, TRADD, TRAF2]
GO:2001236	regulation of extrinsic apoptotic signaling pathway	300,0E-12	280,0E-9	15,0E-30	770,0E-30	[5, 6, 7, 8]	Group36	21,43	39,00	[AR, BAX, BRCA1, CASP8, CFLAR, CTTN, DAPK1, DEDD2, ETFA, FADD, FASLG, FASN, FGFR1, FYN, HSPA1A, LMNA, MEN1, PAK2, PARK7, PDIA3, PEA15, PML, PPP1CA, PPP2R1A, PPP2R1B, PTEN, RAF1, RB1CC1, RBCK1, RELA, RET, RFFL, RPS6KB1, SRC, STK3, STK4, TRADD, TRAF2, YAP1]
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	370,0E-9	340,0E-6	15,0E-30	770,0E-30	[5, 6, 7, 8, 9]	Group36	28,33	17,00	[BAX, DEDD2, FADD, FASN, PAK2, PDIA3, PEA15, PML, PPP1CA, PPP2R1A, PPP2R1B, PTEN, RBCK1, RET, STK3, STK4, TRAF2]
GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	11,0E-9	10,0E-6	15,0E-30	770,0E-30	[5, 6, 7, 8, 9, 10, 11]	Group36	50,00	12,00	[BAX, CASP8, FADD, FASLG, FASN, GSN, JAK2, PARK7, PLAUR, SMAD3, TRADD, TRAF2]
GO:2001269	positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	93,0E-9	87,0E-6	15,0E-30	770,0E-30	[5, 6, 7, 8, 9, 10, 11, 12, 13]	Group36	52,63	10,00	[BAX, CASP8, FADD, FASLG, FASN, GSN, JAK2, SMAD3, TRADD, TRAF2]
GO:1903202	negative regulation of oxidative stress-induced cell death	12,0E-9	12,0E-6	1,4E-21	73,0E-21	[4, 5, 6, 7, 8]	Group37	34,69	17,00	[ATF4, ATG7, BAG5, CTNNB1, HIF1A, HSPB1, HSPH1, MET, NONO, NUP93, PARK7, PRKN, PSAP, RACK1, RNMT, TRAP1, TXN]
GO:2001234	negative regulation of apoptotic signaling pathway	16,0E-12	15,0E-9	1,4E-21	73,0E-21	[4, 5, 6, 7, 8]	Group37	20,25	49,00	[AR, ARRB2, BAG5, BAX, BRCA1, CASP8, CCAR2, CFLAR, CLU, CTNNB1, CTTN, DAPK1, DDX3X, DNAJA1, ENO1, EPRS, FADD, FASLG, FASN, FYN, HERPUD1, HIF1A, HSPA1A, HSPB1, HSPH1, LMNA, MDM2, MEN1, MIF, NONO, PARK7, PEA15, PLAUR, PRKN, PTPN1, RAF1, RB1CC1, RELA, RFFL, RPS6KB1, S100A8, S100A9, SLC25A5, SRC, TRADD, TRAF2, TRAP1, VDAC2, YAP1]
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	12,0E-9	12,0E-6	1,4E-21	73,0E-21	[5, 6, 7, 8]	Group37	34,69	17,00	[BAG5, FBXW7, HIF1A, HSPB1, HSPH1, JAK2, MAP3K5, NONO, P4HB, PARK7, PARP1, PDPK1, PML, PRKN, SFPQ, SOD1, TRAP1]
GO:1903203	regulation of oxidative stress-induced neuron death	23,0E-9	22,0E-6	1,4E-21	73,0E-21	[5, 6, 7, 8]	Group37	52,38	11,00	[ATF4, ATG7, CLU, CTNNB1, FBXW7, HIF1A, NONO, PARK7, PARP1, PRKN, RACK1]
GO:2001236	regulation of extrinsic apoptotic signaling pathway	300,0E-12	280,0E-9	1,4E-21	73,0E-21	[5, 6, 7, 8]	Group37	21,43	39,00	[AR, BAX, BRCA1, CASP8, CFLAR, CTTN, DAPK1, DEDD2, ETFA, FADD, FASLG, FASN, FGFR1, FYN, HSPA1A, LMNA, MEN1, PAK2, PARK7, PDIA3, PEA15, PML, PPP1CA, PPP2R1A, PPP2R1B, PTEN, RAF1, RB1CC1, RBCK1, RELA, RET, RFFL, RPS6KB1, SRC, STK3, STK4, TRADD, TRAF2, YAP1]

GO:2001242	regulation of intrinsic apoptotic signaling pathway	440,0E-12	410,0E-9	1,4E-21	73,0E-21	[5, 6, 7, 8]	Group37	21,89	37,00	[BAG5, BAX, CCAR2, CLU, DDIT3, DDX3X, DNAJA1, ENO1, FBXW7, HERPUD1, HIF1A, HSPA1A, HSPB1, HSPH1, LCK, MDM2, MIF, NCK1, NONO, P4HB, PARK7, PARP1, PLAUR, PRKN, PTPN1, RACK1, RPS3, S100A8, S100A9, SERINC3, SFPQ, SIAH1, SOD1, SRC, TP53, TRAP1, VDAC2]
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	100,0E-9	95,0E-6	1,4E-21	73,0E-21	[5, 6, 7, 8, 9]	Group37	39,39	13,00	[BAG5, FBXW7, HIF1A, HSPB1, HSPH1, NONO, P4HB, PARK7, PARP1, PRKN, SFPQ, SOD1, TRAP1]
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	1,0E-6	950,0E-6	1,4E-21	73,0E-21	[5, 6, 7, 8, 9]	Group37	21,50	23,00	[BAG5, CCAR2, CLU, DDX3X, DNAJA1, ENO1, HERPUD1, HIF1A, HSPA1A, HSPB1, HSPH1, MDM2, MIF, NONO, PARK7, PLAUR, PRKN, PTPN1, S100A8, S100A9, SRC, TRAP1, VDAC2]
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	280,0E-9	260,0E-6	1,4E-21	73,0E-21	[5, 6, 7, 8, 9]	Group37	28,81	17,00	[BAX, CLU, DDIT3, FBXW7, LCK, NCK1, PARK7, PRKN, RACK1, RPS3, S100A8, S100A9, SERINC3, SFPQ, SIAH1, SOD1, TP53]
GO:1905269	positive regulation of chromatin organization	340,0E-9	320,0E-6	21,0E-18	1,0E-15	[4, 5, 6, 7, 8]	Group38	22,77	23,00	[AKAP8L, ARRB1, BCL6, BRCA1, CTBP1, CTNNB1, JARID2, JDP2, MAPK3, NAP1L2, PML, PRKD1, RPS6KA4, RUVBL2, SIN3A, SMAD4, SMARCB1, SNW1, SREBF1, TP53, TPR, TRIM28, WBP2]
GO:0031056	regulation of histone modification	240,0E-9	220,0E-6	21,0E-18	1,0E-15	[5, 6, 7, 8]	Group38	20,00	29,00	[AKAP8L, ARRB1, ATG5, BCL6, BRCA1, CTBP1, CTNNB1, EHMT2, GFI1B, JARID2, JDP2, MAPK3, MAPK8, NAP1L2, PML, PRKD1, RPS6KA4, RUVBL2, SET, SIN3A, SMAD4, SMARCB1, SNCA, SNW1, SREBF1, TP53, UBE2B, UBR5, WBP2]
GO:0006611	protein export from nucleus	61,0E-12	57,0E-9	21,0E-18	1,0E-15	[5, 6, 7, 8, 9]	Group38	21,81	41,00	[ADAR, AKAP8L, BARD1, CALR, CDK5, CDKN2A, CSE1L, EIF4A3, EIF5A, EIF6, GSK3B, HNRNPA2B1, HSPA9, MDM2, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, NXF1, PARK7, PTPN11, RAE1, RAN, RANBP2, RANGAP1, RPSA, SFN, SMURF1, SRSF3, SRSF7, TP53, TPR, TXN, XPO1, XPO5, XPO6, XPOT, YWHAE]
GO:0018205	peptidyl-lysine modification	20,0E-12	18,0E-9	21,0E-18	1,0E-15	[7, 8]	Group38	17,05	67,00	[ACTL6A, ARRB1, ATF2, ATG5, BRCA1, CDKN2A, CREBBP, CRTC2, CTBP1, CTNNB1, EHMT2, EIF5A, EIF5A2, EP300, EZH2, GFI1B, HDAC2, HIST1H1C, HIST1H1D, HNF1A, ING5, JARID2, KAT2B, KAT5, MAP3K7, MAPK3, MBD3, MDM2, MEN1, MTA1, NAP1L2, NCOA1, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, PAG1, PARK7, PCNA, PIAS2, PIAS3, PLOD1, RAE1, RANBP2, RANGAP1, RPS6KA4, RUVBL1, RUVBL2, SET, SF3B3, SIN3A, SMAD4, SMARCB1, SNCA, SNW1, SUMO1, SUMO2, TOLLIP, TPR, TRIM28, TRRAP, UBE2I, VDAC2, WBP2]
GO:1901983	regulation of protein acetylation	1,0E-6	950,0E-6	21,0E-18	1,0E-15	[6, 7, 8, 9]	Group38	26,56	17,00	[ARRB1, ATG5, BRCA1, CTBP1, HDAC2, KAT5, MAPK3, NAP1L2, PARK7, RPS6KA4, RUVBL2, SET, SIN3A, SMAD4, SMARCB1, SNCA, WBP2]

GO:0046825	regulation of protein export from nucleus	55,0E-9	51,0E-6	21,0E-18	1,0E-15	[6, 7, 8, 9, 10]	Group38	35,71	15,00	[AKAP8L, BARD1, CDK5, CDKN2A, GSK3B, MDM2, PARK7, PTPN11, RANGAP1, SFN, TP53, TPR, TXN, XPO1, YWHAE]
GO:0006475	internal protein amino acid acetylation	260,0E-9	250,0E-6	21,0E-18	1,0E-15	[8, 9]	Group38	18,82	32,00	[ACTL6A, ARRB1, ATF2, ATG5, BRCA1, CREBBP, CRTC2, CTBP1, EP300, HNF1A, ING5, KAT2B, KAT5, MAP3K7, MAPK3, MBD3, MDH2, NAP1L2, NCOA1, PAG1, RPS6KA4, RUVBL1, RUVBL2, SET, SF3B3, SIN3A, SMAD4, SMARCB1, SNCA, TRRAP, VDAC2, WBP2]
GO:0016925	protein sumoylation	23,0E-9	21,0E-6	21,0E-18	1,0E-15	[8, 9]	Group38	25,26	24,00	[CDKN2A, CTNNB1, MDM2, MTA1, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, PARK7, PCNA, PIAS2, PIAS3, RAE1, RANBP2, RANGAP1, SUMO1, SUMO2, TOLLIP, TPR, TRIM28, UBE2I]
GO:0018394	peptidyl-lysine acetylation	260,0E-9	250,0E-6	21,0E-18	1,0E-15	[8, 9]	Group38	18,82	32,00	[ACTL6A, ARRB1, ATF2, ATG5, BRCA1, CREBBP, CRTC2, CTBP1, EP300, HDAC2, HNF1A, ING5, KAT2B, KAT5, MAP3K7, MAPK3, MBD3, NAP1L2, NCOA1, PAG1, RPS6KA4, RUVBL1, RUVBL2, SET, SF3B3, SIN3A, SMAD4, SMARCB1, SNCA, TRRAP, VDAC2, WBP2]
GO:0002218	activation of innate immune response	23,0E-21	22,0E-18	280,0E-27	14,0E-24	[3, 5, 6, 7, 8]	Group39	24,07	71,00	[ARHGEF7, ARRB2, BTK, BTRC, C1QBP, CASP8, CD300LF, CHUK, CREBBP, CUL1, EP300, ESR1, FADD, FBXW11, FYN, HCK, HMGB1, HSP90B1, HSPA1A, HSPD1, IKBKB, IRAK1, ITCH, ITGAM, ITGB2, LGMN, MAP3K1, MAP3K7, NFKB1, NFKBIA, PAK1, PAK2, PDPK1, PIK3C3, PLCG2, PRKCE, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAF1, RELA, RELB, RIPK2, RPS27A, RPS6KA3, RPSA, S100A8, S100A9, SIN3A, SKP1, SRC, SYK, TAB2, TBK1, TNIP1, TNIP2, TRAF6, UBA52, UBE2D1, UBE2D2]
GO:0002429	immune response-activating cell surface receptor signaling pathway	72,0E-24	68,0E-21	280,0E-27	14,0E-24	[4, 5, 6, 7, 8]	Group39	20,75	100,00	[ABI1, ABL1, ACTB, ACTG1, ARHGEF7, ARPC1A, BAX, BCAR1, BLK, BTK, BTRC, CD19, CD4, CDC42, CHUK, CREBBP, CRK, CSK, CUL1, DOCK1, DUSP22, ELMO1, EP300, EZR, FBXW11, FGR, FYN, GRB2, HCK, HSP90AA1, HSP90AB1, IKBKB, LAT, LCK, LCP2, MAP3K7, MAPK1, MAPK3, MYO1C, NCK1, NCOR2, NFKB1, NFKBIA, PAG1, PAK1, PAK2, PDPK1, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLCG1, PLCG2, PLSCR1, PRKCB, PRKCE, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTPN6, PTPRC, PTPRJ, RAC1, RAF1, RAPGEF1, RBCK1, RELA, RELB, RIPK2, RPS27A, RPS3, SKP1, SLC25A3, SRC, STK11, SYK, TAB2, TRAF6, UBA52, UBASH3A, UBE2D1, UBE2D2, VAV1, VAV2, WAS, WASL, ZAP70]
GO:0002431	Fc receptor mediated stimulatory signaling pathway	310,0E-12	290,0E-9	280,0E-27	14,0E-24	[5, 6, 7, 8, 9]	Group39	22,16	37,00	[ABI1, ABL1, ACTB, ACTG1, ARPC1A, CDC42, CRK, CSK, DOCK1, ELMO1, FGR, FYN, GRB2, HCK, HSP90AA1, HSP90AB1, MAPK1, MAPK3, MYO1C, NCK1, PAK1,

										PIK3CA, PIK3R1, PIK3R2, PLCG1, PLCG2, PLSCR1, PRKCE, PTK2, RAC1, RAPGEF1, SRC, SYK, VAV1, VAV2, WAS, WASL]
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	1,5E-9	1,4E-6	280,0E-27	14,0E-24	[4, 5, 6, 7, 8, 9, 10]	Group39	21,74	35,00	[ABI1, ABL1, ACTB, ACTG1, ARPC1A, CDC42, CRK, DOCK1, ELMO1, FGR, FYN, GRB2, HCK, HSP90AA1, HSP90AB1, MAPK1, MAPK3, MYO1C, NCK1, PAK1, PIK3CA, PIK3R1, PIK3R2, PLCG1, PLCG2, PRKCE, PTK2, RAC1, RAPGEF1, SRC, SYK, VAV1, VAV2, WAS, WASL]
GO:0050851	antigen receptor-mediated signaling pathway	1,5E-21	1,4E-18	280,0E-27	14,0E-24	[5, 6, 7, 8, 9]	Group39	24,91	72,00	[ABL1, ARHGEF7, BAX, BCAR1, BLK, BTK, BTRC, CD19, CD4, CHUK, CSK, CUL1, DUSP22, EZR, FBXW11, FYN, IKBKB, LAT, LCK, LCP2, MAP3K7, MAPK1, NCK1, NCOR2, NFKB1, NFKBIA, PAG1, PAK1, PAK2, PDPK1, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLCG1, PLCG2, PRKCB, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPN6, PTPRC, PTPRJ, RBCK1, RELA, RIPK2, RPS27A, RPS3, SKP1, SLC25A3, STK11, SYK, TAB2, TRAF6, UBA52, UBASH3A, UBE2D1, UBE2D2, WAS, ZAP70]
GO:0002221	pattern recognition receptor signaling pathway	180,0E-12	160,0E-9	280,0E-27	14,0E-24	[5, 6, 7, 8, 9, 10]	Group39	21,79	39,00	[ARRB2, BTK, C1QBP, CASP8, CD300LF, CHUK, ESR1, FADD, HMGB1, HSP90B1, HSPA1A, HSPD1, IKBKB, IRAK1, ITCH, ITGAM, ITGB2, LGMN, MAP3K1, MAP3K7, NFKBIA, PDPK1, PIK3C3, PRKCE, RELA, RIPK2, RPS27A, RPS6KA3, RPSA, S100A8, S100A9, TAB2, TBK1, TNIP1, TNIP2, TRAF6, UBA52, UBE2D1, UBE2D2]
GO:0050852	T cell receptor signaling pathway	980,0E-30	910,0E-27	280,0E-27	14,0E-24	[6, 7, 8, 9, 10]	Group39	33,85	65,00	[ARHGEF7, BCAR1, BTRC, CD4, CHUK, CSK, CUL1, DUSP22, EZR, FBXW11, FYN, IKBKB, LAT, LCK, LCP2, MAP3K7, MAPK1, NCK1, NCOR2, NFKB1, NFKBIA, PAG1, PAK1, PAK2, PDPK1, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLCG1, PLCG2, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPN6, PTPRC, PTPRJ, RBCK1, RELA, RIPK2, RPS27A, RPS3, SKP1, SLC25A3, STK11, TAB2, TRAF6, UBA52, UBASH3A, UBE2D1, UBE2D2, WAS, ZAP70]
GO:0002223	stimulatory C-type lectin receptor signaling pathway	9,5E-18	8,9E-15	280,0E-27	14,0E-24	[6, 7, 8, 9, 10, 11]	Group39	32,56	42,00	[ARHGEF7, BTRC, CHUK, CREBBP, CUL1, EP300, FBXW11, FYN, IKBKB, MAP3K7, NFKB1, NFKBIA, PAK1, PAK2, PDPK1, PLCG2, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAF1, RELA, RELB, RPS27A, SKP1, SRC, SYK, TAB2, TRAF6, UBA52, UBE2D1, UBE2D2]
GO:0002224	toll-like receptor signaling pathway	8,4E-12	7,8E-9	280,0E-27	14,0E-24	[6, 7, 8, 9, 10, 11]	Group39	25,93	35,00	[ARRB2, BTK, CASP8, CD300LF, CHUK, ESR1, FADD, HMGB1, HSP90B1, HSPD1, IKBKB, IRAK1, ITGAM, ITGB2, LGMN, MAP3K1, MAP3K7, NFKBIA, PDPK1, PIK3C3,

										PRKCE, RIPK2, RPS27A, RPS6KA3, RPSA, S100A8, S100A9, TAB2, TBK1, TNIP1, TNIP2, TRAF6, UBA52, UBE2D1, UBE2D2]
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	13,0E-9	12,0E-6	280,0E-27	14,0E-24	[7, 8, 9, 10, 11]	Group39	28,77	21,00	[BTRC, CUL1, FBXW11, FBXW7, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPS27A, SKP1, UBA52]
GO:1903749	positive regulation of establishment of protein localization to mitochondrion	110,0E-9	110,0E-6	450,0E-27	23,0E-24	[3, 4, 5, 6, 7, 8, 9]	Group40	21,60	27,00	[ACTL6A, ATG13, CASP8, CSNK2A2, DYNLL1, E2F1, FBXW7, HSPA1L, ITGAX, MAGI1, MAPK8, PIN1, RAC2, RPL28, RUVBL1, SFN, SH3GLB1, SREBF2, TP53, TP53BP2, UBE2L3, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:2001235	positive regulation of apoptotic signaling pathway	19,0E-21	18,0E-18	450,0E-27	23,0E-24	[4, 5, 6, 7, 8]	Group40	29,02	56,00	[BAX, CASP8, CCM2, CLU, DDIT3, DEDD2, DYNLL1, E2F1, FADD, FASLG, FASN, FBXW7, GSK3B, GSN, ING5, JAK2, LCK, MAPK8, NCK1, PAK2, PARK7, PDIA3, PEA15, PLAUR, PML, PPP1CA, PPP2R1A, PPP2R1B, PRKN, PTEN, RACK1, RBCK1, RET, RPS3, S100A8, S100A9, SERINC3, SFN, SFPQ, SH3GLB1, SIAH1, SMAD3, SOD1, STK3, STK4, TP53, TP53BP2, TPD52L1, TRADD, TRAF2, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:1903747	regulation of establishment of protein localization to mitochondrion	20,0E-12	19,0E-9	450,0E-27	23,0E-24	[5, 6, 7, 8]	Group40	25,18	35,00	[ACTL6A, ATG13, BAG4, CASP8, CDKN2A, CSNK2A2, DNAJA1, DYNLL1, E2F1, FBXW7, HAX1, HSPA1L, HSPH1, ITGAX, MAGI1, MAPK8, MAPT, PIN1, PRKN, RAC2, RPL28, RUVBL1, SFN, SH3GLB1, SREBF1, SREBF2, TP53, TP53BP2, UBE2L3, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:2001236	regulation of extrinsic apoptotic signaling pathway	300,0E-12	280,0E-9	450,0E-27	23,0E-24	[5, 6, 7, 8]	Group40	21,43	39,00	[AR, BAX, BRCA1, CASP8, CFLAR, CTTN, DAPK1, DEDD2, ETFA, FADD, FASLG, FASN, FGFR1, FYN, HSPA1A, LMNA, MEN1, PAK2, PARK7, PDIA3, PEA15, PML, PPP1CA, PPP2R1A, PPP2R1B, PTEN, RAF1, RB1CC1, RBCK1, RELA, RET, RFFL, RPS6KB1, SRC, STK3, STK4, TRADD, TRAF2, YAP1]
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	370,0E-9	340,0E-6	450,0E-27	23,0E-24	[5, 6, 7, 8, 9]	Group40	28,33	17,00	[BAX, DEDD2, FADD, FASN, PAK2, PDIA3, PEA15, PML, PPP1CA, PPP2R1A, PPP2R1B, PTEN, RBCK1, RET, STK3, STK4, TRAF2]
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	280,0E-9	260,0E-6	450,0E-27	23,0E-24	[5, 6, 7, 8, 9]	Group40	28,81	17,00	[BAX, CLU, DDIT3, FBXW7, LCK, NCK1, PARK7, PRKN, RACK1, RPS3, S100A8, S100A9, SERINC3, SFPQ, SIAH1, SOD1, TP53]
GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	2,8E-9	2,6E-6	450,0E-27	23,0E-24	[4, 5, 6, 7, 8, 9, 10, 11]	Group40	42,86	15,00	[BAX, CASP8, DYNLL1, E2F1, MAPK8, SFN, SH3GLB1, TP53, TP53BP2, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]

GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	2,4E-9	2,3E-6	450,0E-27	23,0E-24	[4, 5, 6, 7, 8, 9, 10, 11]	Group40	36,00	18,00	[BAX, CASP8, DYNLL1, E2F1, GSK3B, HSPA1A, MAPK8, SFN, SH3GLB1, SLC25A5, TP53, TP53BP2, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	6,9E-9	6,4E-6	450,0E-27	23,0E-24	[3, 4, 5, 6, 7, 8, 9, 10, 11, 12]	Group40	38,10	16,00	[BAX, CASP8, DYNLL1, E2F1, GSK3B, MAPK8, SFN, SH3GLB1, TP53, TP53BP2, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	26,0E-9	25,0E-6	450,0E-27	23,0E-24	[6, 7, 8, 9]	Group40	30,16	19,00	[ATF2, BAX, CASP8, DYNLL1, E2F1, GSK3B, HSPA1A, MAPK8, SFN, SH3GLB1, SLC25A5, TP53, TP53BP2, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:0048666	neuron development	7,2E-12	6,7E-9	27,0E-15	1,3E-12	[4, 5, 6, 8, 9]	Group41	12,88	137,00	[ABI1, ABL1, ALK, APP, ARF6, ARHGDIA, ARHGEF7, ARID1B, ASAP1, AVIL, BAG5, BECN1, CACNA1A, CAMK2A, CAPZB, CARM1, CDC20, CDC42, CDH1, CDK5, CDK5R1, CELSR2, CFL1, CFLAR, CNTN1, CNTNAP1, CREB1, CTTN, DBNL, DCC, DGKG, DLG4, DNM2, EGFR, EPHB1, ERBB2, EZH2, EZR, FGFR1, FRS2, FYCO1, FYN, GAB1, GAB2, GRB10, GRB2, GSK3B, HDAC2, HMGB1, HSPA5, ID2, IQGAP1, ISL2, ITGB1, JAK2, JUN, KLF4, MAP2K1, MAP4K4, MAPK1, MAPK10, MAPK3, MAPK8, MAPT, MCF2, MDM2, MTOR, MYH10, NCK1, NEDD4, NEFM, NKX2-1, NLGN3, NOTCH1, NUMB, PACSIN1, PAK1, PAK2, PAK4, PHGDH, PIK3CA, PIK3CD, PIK3R1, PLCG1, PLXNB1, POU4F2, PREX1, PRKCI, PRKD1, PRKN, PRMT1, PTEN, PTK2, PTK2B, PTN, PTPN11, PTPRG, PTPRK, PTPRO, RAB35, RAC1, RAP1GAP2, RAPGEF1, RBFOX2, RET, RHOA, RIPK2, RPGRIP1, RPL24, RUNX1, S100B, SCRIB, SEMA4D, SF3A2, SGK1, SH3GL2, SHC1, SIAH1, SMAD4, SMURF1, SOD1, SPTA1, SPTAN1, SPTBN1, SRC, SSH2, STK11, UBE4B, ULK1, ULK2, UQCRQ, USP9X, VASP, VIM, WASL, WEE1, YWHAH]
GO:0050767	regulation of neurogenesis	2,6E-9	2,4E-6	27,0E-15	1,3E-12	[5, 6, 7, 8]	Group41	13,22	97,00	[ABL1, APP, ARF6, ARHGDIA, ARHGEF7, ASAP1, AVIL, BAG5, BCL6, CACNA1A, CALR, CARM1, CDC20, CDK1, CDK5, CDK5R1, CDK5RAP3, CFL1, CFLAR, CNTN1, CREB1, CTNNB1, CTTN, DCC, DDX6, DLL1, DNM2, DTX1, ERBB4, EZH2, FGFR1, FLNA, FOXO3, FYCO1, FYN, GSK3B, HDAC2, HIF1A, HSPA5, ID2, IQGAP1, ISL2, JAG1, KIT, KLF4, MAP2K1, MAP4K4, MAPT, MDM2, MTOR, MYC, NAP1L2, NCK1, NCOA1, NEDD4, NLGN3, NOTCH1, NUMB, PACSIN1, PAK1, PLXNB1, POU4F2, PPARG, PREX1, PRKCI, PRKD1, PRKN, PRMT5, PTEN, PTK2, PTK2B, PTN, PTPRG, PTPRO, RAC1, RAP1GAP2, RAPGEF1, RELA, RET, RHOA,

										SEMA4D, SF3A2, SMURF1, SNW1, SORL1, SPAG9, SSH2, STAT3, STK11, SYNJ1, TCF7L1, ULK2, VIM, XRCC5, YAP1, YWHAG, YWHAH]
GO:0030182	neuron differentiation	310,0E-15	290,0E-12	27,0E-15	1,3E-12	[5, 7, 8]	Group41	12,53	167,00	[ABI1, ABL1, AIFM1, ALK, APP, ARF6, ARHGDIA, ARHGEF7, ARID1B, ASAP1, AVIL, BAG5, BCL6, BECN1, CACNA1A, CALR, CAMK2A, CAPZB, CARM1, CASP3, CDC20, CDC42, CDH1, CDK5, CDK5R1, CDK5RAP3, CELSR2, CFL1, CFLAR, CNTN1, CNTNAP1, COPS2, CREB1, CTNNB1, CTTN, DBNL, DCC, DDX6, DGKG, DLG4, DLL1, DNM2, DTX1, EGFR, EHMT2, EPHB1, ERBB2, ERBB4, EZH2, EZR, FGFR1, FOXO3, FRS2, FYCO1, FYN, GAB1, GAB2, GRB10, GRB2, GSK3B, HDAC2, HIF1A, HMGB1, HSPA5, ID2, IQGAP1, ISL2, ITGB1, JAG1, JAG2, JAK2, JUN, KLF4, MAP2K1, MAP4K4, MAPK1, MAPK10, MAPK3, MAPK8, MAPT, MCF2, MDM2, MTOR, MYH10, NAP1L2, NCK1, NCOA1, NEDD4, NEFM, NIF3L1, NKX2-1, NLGN3, NLGN4X, NOTCH1, NUMB, PACSIN1, PAK1, PAK2, PAK4, PHGDH, PIK3CA, PIK3CD, PIK3R1, PIN1, PLCG1, PLXNB1, POU4F2, PPP1CC, PREX1, PRKCI, PRKD1, PRKN, PRMT1, PTEN, PTK2, PTK2B, PTN, PTPN11, PTPRG, PTPRK, PTPRO, RAB35, RAC1, RAP1GAP2, RAPGEF1, RBFOX2, RBPJ, RET, RHOA, RIPK2, RPGRIP1, RPL24, RUNX1, S100B, SCRIB, SEMA4D, SF3A2, SGK1, SH3GL2, SHC1, SIAH1, SMAD4, SMARCC2, SMURF1, SOD1, SPAG9, SPTA1, SPTAN1, SPTBN1, SRC, SSH2, STAT3, STK11, TCF7L1, UBE4B, ULK1, ULK2, UNC119, UQCRQ, USP9X, VASP, VIM, WASL, WEE1, XRN2, YWHAG, YWHAH]
GO:0031175	neuron projection development	310,0E-15	290,0E-12	27,0E-15	1,3E-12	[4, 5, 6, 7, 9, 10]	Group41	13,91	126,00	[ABI1, ABL1, APP, ARF6, ARHGDIA, ARHGEF7, ARID1B, ASAP1, AVIL, BAG5, CACNA1A, CAMK2A, CAPZB, CARM1, CDC20, CDC42, CDH1, CDK5, CDK5R1, CELSR2, CFL1, CFLAR, CNTN1, CNTNAP1, CREB1, CTTN, DBNL, DCC, DLG4, DNM2, EGFR, EPHB1, ERBB2, EZH2, EZR, FGFR1, FRS2, FYCO1, FYN, GAB1, GAB2, GRB10, GRB2, GSK3B, HDAC2, HMGB1, HSPA5, IQGAP1, ISL2, ITGB1, JAK2, JUN, KLF4, MAP2K1, MAP4K4, MAPK1, MAPK3, MAPT, MCF2, MDM2, MTOR, MYH10, NCK1, NEDD4, NEFM, NKX2-1, NLGN3, NOTCH1, NUMB, PACSIN1, PAK1, PAK2, PAK4, PHGDH, PIK3CA, PIK3CD, PIK3R1, PLCG1, PLXNB1, POU4F2, PREX1, PRKCI, PRKD1, PRKN, PRMT1, PTEN, PTK2, PTK2B, PTN, PTPN11, PTPRG, PTPRK, PTPRO, RAB35, RAC1, RAP1GAP2, RAPGEF1, RBFOX2, RET, RHOA, RIPK2, RPL24, S100B, SEMA4D, SF3A2, SGK1, SH3GL2, SHC1, SIAH1, SMAD4, SMURF1, SPTA1, SPTAN1, SPTBN1,

										SRC, SSH2, STK11, UBE4B, ULK1, ULK2, USP9X, VASP, VIM, WASL, WEE1, YWHAH]
GO:0016358	dendrite development	520,0E-9	490,0E-6	27,0E-15	1,3E-12	[3, 5, 6, 7, 8, 10, 11]	Group41	16,81	38,00	[ABI1, APP, ARF6, ARHGEF7, ARID1B, ASAP1, CACNA1A, CAMK2A, CARM1, CDC20, CDC42, CDK5, CDK5R1, CELSR2, CFL1, DCC, DLG4, EPHB1, EZH2, FYN, HDAC2, IQGAP1, ITGB1, MCF2, MTOR, NEDD4, NLGN3, PACSIN1, PAK2, PAK4, PREX1, PTEN, RAC1, RBFOX2, SEMA4D, STK11, WASL, YWHAH]
GO:0045664	regulation of neuron differentiation	81,0E-9	76,0E-6	27,0E-15	1,3E-12	[6, 7, 8, 9]	Group41	13,28	79,00	[ABL1, APP, ARF6, ARHGDIA, ARHGEF7, ASAP1, AVIL, BAG5, BCL6, CACNA1A, CALR, CARM1, CDC20, CDK5, CDK5R1, CDK5RAP3, CFL1, CFLAR, CNTN1, CTTN, DCC, DDX6, DLL1, DNM2, DTX1, EZH2, FGFR1, FOXO3, FYCO1, FYN, GSK3B, HDAC2, HSPA5, ID2, IQGAP1, ISL2, JAG1, KLF4, MAP2K1, MAP4K4, MAPT, MDM2, MTOR, NAP1L2, NCK1, NCOA1, NEDD4, NLGN3, NOTCH1, PACSIN1, PAK1, PLXNB1, POU4F2, PREX1, PRKCI, PRKD1, PRKN, PTEN, PTK2, PTK2B, PTN, PTPRG, PTPRO, RAC1, RAP1GAP2, RAPGEF1, RET, RHOA, SEMA4D, SF3A2, SMURF1, SPAG9, SSH2, STK11, TCF7L1, ULK2, VIM, YWHAG, YWHAH]
GO:0048667	cell morphogenesis involved in neuron differentiation	71,0E-9	66,0E-6	27,0E-15	1,3E-12	[5, 6, 7, 8, 9, 10]	Group41	13,49	77,00	[ABI1, ABL1, APP, ARHGDIA, ARHGEF7, CACNA1A, CAMK2A, CDC42, CDK5, CDK5R1, CELSR2, CFL1, CREB1, CTTN, DCC, DLG4, DNM2, EPHB1, ERBB2, EZR, FRS2, FYCO1, FYN, GAB1, GAB2, GRB10, GRB2, GSK3B, ID2, ISL2, ITGB1, MAP2K1, MAPK1, MAPK3, MAPT, MYH10, NEDD4, NKX2-1, NLGN3, NOTCH1, NUMB, PAK1, PIK3CA, PIK3CD, PIK3R1, PLCG1, PLXNB1, POU4F2, PTEN, PTK2, PTPN11, PTPRO, RAC1, RBFOX2, RET, RHOA, RIPK2, RPL24, S100B, SCRIB, SEMA4D, SHC1, SIAH1, SMAD4, SOD1, SPTA1, SPTAN1, SPTBN1, SRC, SSH2, STK11, ULK1, ULK2, USP9X, VASP, WASL, YWHAH]
GO:0048812	neuron projection morphogenesis	9,0E-9	8,5E-6	27,0E-15	1,3E-12	[5, 6, 7, 8, 10, 11]	Group41	13,57	84,00	[ABI1, ABL1, APP, ARHGDIA, ARHGEF7, CACNA1A, CAMK2A, CDC42, CDK5, CDK5R1, CELSR2, CFL1, CNTNAP1, CREB1, CTTN, DBNL, DCC, DLG4, DNM2, EGFR, EPHB1, ERBB2, EZR, FRS2, FYCO1, FYN, GAB1, GAB2, GRB10, GRB2, GSK3B, IQGAP1, ISL2, ITGB1, MAP2K1, MAPK1, MAPK3, MAPT, MYH10, NEDD4, NKX2-1, NLGN3, NOTCH1, NUMB, PACSIN1, PAK1, PIK3CA, PIK3CD, PIK3R1, PLCG1, PLXNB1, POU4F2, PRKN, PTEN, PTK2, PTPN11, PTPRO, RAC1, RBFOX2, RET, RHOA, RIPK2, RPL24, S100B, SEMA4D, SGK1, SH3GL2, SHC1, SIAH1, SMAD4, SMURF1, SPTA1, SPTAN1, SPTBN1, SRC, SSH2, STK11, ULK1, ULK2, USP9X, VASP, WASL, WEE1, YWHAH]

GO:0061564	axon development	300,0E-9	280,0E-6	27,0E-15	1,3E-12	[5, 6, 7, 8, 10, 11]	Group41	13,57	68,00	[ABL1, APP, ARHGDIA, ARHGEF7, CACNA1A, CDK5, CDK5R1, CREB1, CTTN, DCC, DNM2, EPHB1, ERBB2, EZR, FRS2, FYCO1, FYN, GAB1, GAB2, GRB10, GRB2, GSK3B, ISL2, ITGB1, JAK2, JUN, KLF4, MAP2K1, MAPK1, MAPK3, MAPT, MYH10, NEFM, NKX2-1, NLGN3, NOTCH1, NUMB, PAK1, PIK3CA, PIK3CD, PIK3R1, PLCG1, PLXNB1, POU4F2, PTEN, PTK2, PTPN11, PTPRO, RAC1, RET, RHOA, RIPK2, RPL24, S100B, SEMA4D, SHC1, SIAH1, SMAD4, SPTA1, SPTAN1, SPTBN1, SRC, SSH2, STK11, ULK1, ULK2, USP9X, VASP]
GO:0010975	regulation of neuron projection development	230,0E-9	210,0E-6	27,0E-15	1,3E-12	[5, 6, 7, 8, 9, 10, 11]	Group41	14,06	62,00	[ABL1, ARF6, ARHGDIA, ARHGEF7, ASAP1, AVIL, BAG5, CACNA1A, CARM1, CDC20, CDK5, CDK5R1, CFL1, CFLAR, CNTN1, CTTN, DCC, DNM2, EZH2, FGFR1, FYCO1, FYN, GSK3B, HDAC2, HSPA5, IQGAP1, KLF4, MAP2K1, MAP4K4, MAPT, MDM2, MTOR, NCK1, NEDD4, NLGN3, PACSIN1, PAK1, PLXNB1, POU4F2, PREX1, PRKCI, PRKD1, PRKN, PTEN, PTK2, PTK2B, PTN, PTPRG, PTPRO, RAC1, RAP1GAP2, RAPGEF1, RET, RHOA, SEMA4D, SF3A2, SMURF1, SSH2, STK11, ULK2, VIM, YWHAH]
GO:0007409	axonogenesis	260,0E-9	240,0E-6	27,0E-15	1,3E-12	[6, 7, 8, 9, 10, 11, 12]	Group41	13,85	64,00	[ABL1, APP, ARHGDIA, ARHGEF7, CACNA1A, CDK5, CDK5R1, CREB1, CTTN, DCC, DNM2, EPHB1, ERBB2, EZR, FRS2, FYCO1, FYN, GAB1, GAB2, GRB10, GRB2, GSK3B, ISL2, ITGB1, MAP2K1, MAPK1, MAPK3, MAPT, MYH10, NKX2-1, NLGN3, NOTCH1, NUMB, PAK1, PIK3CA, PIK3CD, PIK3R1, PLCG1, PLXNB1, POU4F2, PTEN, PTK2, PTPN11, PTPRO, RAC1, RET, RHOA, RIPK2, RPL24, S100B, SEMA4D, SHC1, SIAH1, SMAD4, SPTA1, SPTAN1, SPTBN1, SRC, SSH2, STK11, ULK1, ULK2, USP9X, VASP]
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	7,8E-12	7,3E-9	22,0E-24	1,1E-21	[7, 8, 9, 10, 11, 12, 13]	Group42	30,21	29,00	[AIFM1, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, DNAJA3, DYNLL1, FADD, FASLG, FASN, HSPD1, JAK2, LCK, MAPT, PML, PPARG, RACK1, RET, RIPK2, RPS27L, S100A8, S100A9, SMAD3, SNCA, TRADD, TRAF2, VCP]
GO:0045862	positive regulation of proteolysis	440,0E-30	410,0E-27	22,0E-24	1,1E-21	[5, 6, 7, 8]	Group42	24,74	96,00	[AIFM1, ANAPC7, APP, ARRB1, BAX, BTRC, C3, CASP3, CASP8, CDC20, CDK1, CDKN1B, CDKN2A, CFL1, CLU, CNTN1, CUL1, DAPK1, DDX3X, DNAJA3, DYNLL1, ENO1, FADD, FASLG, FASN, FBXW11, FBXW7, GSK3B, GSN, HDAC2, HERPUD1, HMGB1, HSPA1A, HSPD1, JAK2, LCK, MAD2L1, MAP3K5, MAPK14, MAPK3, MAPT, MDM2, MEFV, MYC, MYH9, PACSIN3, PHB, PLK1, PML, PPARG, PPM1F, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RACK1, RAD23A, RET, RIPK2, RNF144B, RPS27A, RPS27L, RPS3,

										S100A8, S100A9, SKP1, SMAD3, SMAD7, SMURF1, SNCA, SOX7, SRC, STAT3, STUB1, SUMO1, SUMO2, TNFRSF1B, TRADD, TRAF2, UBA52, UBE2D1, VCP]
GO:0052548	regulation of endopeptidase activity	15,0E-12	14,0E-9	22,0E-24	1,1E-21	[6, 7, 8]	Group42	16,83	69,00	[AIFM1, APP, ARRB1, ARRB2, BAX, C3, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, COPS2, CSN2, CSNK2A1, CSNK2A2, CSTB, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HERPUD1, HMGB1, HSPD1, JAK2, KLF4, LCK, MAP3K5, MAPT, MDM2, MEFV, MICAL1, MYC, PAK2, PARK7, PEBP1, PLAUR, PML, PPARG, PPM1F, PRDX3, RACK1, RAF1, RET, RFFL, RIPK2, RPS27L, RPS3, RPS6KA1, RPS6KA3, S100A8, S100A9, SERPINB12, SFN, SMAD3, SNCA, SORL1, SOX7, SRC, STAT3, TRADD, TRAF2, VCP, VDAC2, VTN, YWHAE]
GO:0010952	positive regulation of peptidase activity	42,0E-15	39,0E-12	22,0E-24	1,1E-21	[6, 7, 8, 9]	Group42	25,43	44,00	[AIFM1, APP, ARRB1, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HMGB1, HSPD1, JAK2, LCK, MAP3K5, MAPK14, MAPK3, MAPT, MEFV, MYC, PML, PPARG, PPM1F, RACK1, RET, RIPK2, RPS27L, RPS3, S100A8, S100A9, SMAD3, SNCA, SOX7, STAT3, TRADD, TRAF2, VCP]
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	170,0E-21	160,0E-18	22,0E-24	1,1E-21	[6, 7, 8, 9, 10]	Group42	26,70	59,00	[AIFM1, APP, ARRB1, ARRB2, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, CSNK2A1, CSNK2A2, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HERPUD1, HMGB1, HSPD1, JAK2, KLF4, LCK, MAP3K5, MAPT, MDM2, MICAL1, MYC, PAK2, PARK7, PLAUR, PML, PPARG, PPM1F, PRDX3, RACK1, RAF1, RET, RFFL, RIPK2, RPS27L, RPS3, RPS6KA1, RPS6KA3, S100A8, S100A9, SFN, SMAD3, SNCA, SOX7, SRC, TRADD, TRAF2, VCP, VDAC2, YWHAE]
GO:2000116	regulation of cysteine-type endopeptidase activity	82,0E-21	77,0E-18	22,0E-24	1,1E-21	[7, 8, 9]	Group42	26,05	62,00	[AIFM1, APP, ARRB1, ARRB2, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, COPS2, CSN2, CSNK2A1, CSNK2A2, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HERPUD1, HMGB1, HSPD1, JAK2, KLF4, LCK, MAP3K5, MAPT, MDM2, MEFV, MICAL1, MYC, PAK2, PARK7, PLAUR, PML, PPARG, PPM1F, PRDX3, RACK1, RAF1, RET, RFFL, RIPK2, RPS27L, RPS3, RPS6KA1, RPS6KA3, S100A8, S100A9, SFN, SMAD3, SNCA, SOX7, SRC, TRADD, TRAF2, VCP, VDAC2, YWHAE]
GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	11,0E-9	10,0E-6	22,0E-24	1,1E-21	[5, 6, 7, 8, 9, 10, 11]	Group42	50,00	12,00	[BAX, CASP8, FADD, FASLG, FASN, GSN, JAK2, PARK7, PLAUR, SMAD3, TRADD, TRAF2]

GO:0010950	positive regulation of endopeptidase activity	23,0E-15	22,0E-12	22,0E-24	1,1E-21	[7, 8, 9, 10]	Group42	26,75	42,00	[AIFM1, APP, ARRB1, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HMGB1, HSPD1, JAK2, LCK, MAP3K5, MAPT, MEFV, MYC, PML, PPARG, PPM1F, RACK1, RET, RIPK2, RPS27L, RPS3, S100A8, S100A9, SMAD3, SNCA, SOX7, STAT3, TRADD, TRAF2, VCP]
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	18,0E-9	17,0E-6	22,0E-24	1,1E-21	[6, 7, 8, 9, 10, 11, 12]	Group42	25,53	24,00	[ARRB1, ARRB2, CASP8, CSNK2A1, CSNK2A2, DDX3X, DNAJA3, HERPUD1, KLF4, MDM2, MICAL1, PAK2, PARK7, PLAUR, PRDX3, RAF1, RFFL, RPS6KA1, RPS6KA3, SFN, SNCA, SRC, VDAC2, YWHAE]
GO:2001269	positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	93,0E-9	87,0E-6	22,0E-24	1,1E-21	[5, 6, 7, 8, 9, 10, 11, 12, 13]	Group42	52,63	10,00	[BAX, CASP8, FADD, FASLG, FASN, GSN, JAK2, SMAD3, TRADD, TRAF2]
GO:2000117	negative regulation of cysteine-type endopeptidase activity	5,1E-9	4,8E-6	22,0E-24	1,1E-21	[8, 9, 10, 11]	Group42	25,49	26,00	[ARRB1, ARRB2, CASP8, COPS2, CSN2, CSNK2A1, CSNK2A2, DDX3X, DNAJA3, HERPUD1, KLF4, MDM2, MICAL1, PAK2, PARK7, PLAUR, PRDX3, RAF1, RFFL, RPS6KA1, RPS6KA3, SFN, SNCA, SRC, VDAC2, YWHAE]
GO:1900182	positive regulation of protein localization to nucleus	500,0E-18	460,0E-15	160,0E-48	8,5E-45	[3, 4, 5, 6, 7, 8]	Group43	30,15	41,00	[CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CD2AP, CDH1, CDK1, CDK5RAP3, CDKN2A, EGFR, ERBB4, FLNA, FYN, HDAC3, HSP90AB1, IPO5, JAK2, MAPK1, MAPK14, NUP93, PARK7, PARP1, PIK3R1, PIK3R2, PLK1, PRKD1, RBCK1, RBPMS, RHOA, SMAD3, SMAD4, SRC, STK11, TCP1, TPR, TRIM28, TRIP6, UBR5]
GO:0006886	intracellular protein transport	900,0E-45	850,0E-42	160,0E-48	8,5E-45	[4, 5, 6, 7, 8]	Group43	18,49	225,00	[ACTL6A, ADAR, AKAP8L, ANXA2, ATG13, ATG3, ATG4B, ATG4C, BAG4, BARD1, BCAS3, BCL3, BCL6, BCR, CABP1, CACNA1A, CALR, CBLB, CDC37, CDC42, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CFL1, CLIP1, CLTC, CLTCL1, COPB1, COPB2, CSE1L, CSNK2A2, CTNNB1, CTTN, DYNC2LI1, DYNLL1, EGFR, EIF4A3, EIF5A, EIF6, ERBB2, ERBB4, FAU, FBXW11, FBXW7, FLNA, FYCO1, FYN, GABARAP, GGA1, GGA2, GGA3, GPN1, GSK3B, HAX1, HDAC3, HERC2, HERPUD1, HNRNPA2B1, HSP90AA1, HSP90AB1, HSP90B1, HSPA1L, HSPA4, HSPA8, HSPA9, HSPB1, HSPD1, IPO4, IPO5, ITGAX, JAK2, JAK3, JUN, KDELR1, KPNA2, KPNA3, KPNA4, KPNB1, LMNA, MAGI1, MAPK1, MAPK14, MAPK3, MDM2, MTOR, MYL12A, MYO1C, MYO6, NEDD4, NFKBIA, NFKBIE, NPM1, NSF, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, NXF1, OAZ2, PAK1, PARK7, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PIN1, PML, POLA2, PPM1B, PRDX1, PRKCI, PRKD1, PRKN, PTPN1, PTPN11, RAC2, RAE1, RAN, RANBP2, RANGAP1, RBCK1, RBPMS, RHOA, RILPL2,

										RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, RUVBL1, SFN, SH3GLB1, SLC25A6, SMAD3, SMAD4, SMURF1, SORL1, SPTBN1, SREBF1, SREBF2, SRP14, SRSF3, SRSF7, STAT3, SYK, TIMM50, TNPO1, TNPO2, TOM1L1, TP53, TPR, TRAF3IP1, TRIM28, TRIP6, TXN, UBA52, UBE2L3, UBR5, VCP, XPO1, XPO5, XPO6, XPOT, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:0017038	protein import	37,0E-18	34,0E-15	160,0E-48	8,5E-45	[4, 5, 6, 7, 8]	Group43	20,86	73,00	[ADAR, BCL3, BCL6, CABP1, CBLB, CDH1, CDK1, CFL1, CLU, CTNNB1, EGFR, ERBB4, FBXW11, FLNA, GPN1, GSK3B, HDAC3, HSP90AA1, HSP90AB1, HSPA4, HSPA8, HSPD1, IPO4, IPO5, JAK2, JAK3, JUN, KPNA2, KPNA3, KPNA4, KPNB1, LMNA, MAPK1, MAPK14, MAPK3, MTOR, NFKBIA, NFKBIE, NUP107, NUP155, NUP62, NUP88, NUP93, NUP98, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PML, POLA2, PPM1B, PRDX1, PRKD1, RAN, RANBP2, RBCK1, RBPMS, RHOA, RPL23, SMAD3, SMAD4, SPTBN1, STAT3, SYK, TIMM50, TNPO1, TNPO2, TPR, TRIM28, TRIP6, TXN, UBR5]
GO:0046824	positive regulation of nucleocytoplasmic transport	140,0E-12	130,0E-9	160,0E-48	8,5E-45	[4, 5, 6, 7, 8]	Group43	25,20	32,00	[CDH1, CDK1, EGFR, ERBB4, FLNA, GSK3B, HDAC3, HSP90AB1, IPO5, JAK2, KHDRBS1, MAPK1, MAPK14, MDM2, NEDD4, NUP93, PARP1, PIK3R1, PIK3R2, PRKD1, RBCK1, RBPMS, RHOA, SFN, SMAD3, SMAD4, TP53, TPR, TRIM28, TRIP6, UBR5, YWHAE]
GO:0051222	positive regulation of protein transport	5,0E-12	4,6E-9	160,0E-48	8,5E-45	[3, 4, 5, 6, 7, 8, 9]	Group43	15,95	82,00	[ABL1, ACTL6A, ARRB1, ATG13, BCAS3, BLK, CACNA1A, CDC42, CDH1, CDK1, CDK5, CDK5R1, CFTR, CHUK, CLU, CSNK2A2, EGFR, ERBB2, ERBB4, EZR, FBXW7, FGR, FLNA, FYCO1, FYN, GNAI2, GSK3B, HDAC3, HIF1A, HMGB1, HSP90AB1, HSPA1L, HSPD1, IL17RA, IPO5, ITGAX, JAK2, MAGI1, MAPK1, MAPK14, MAPK3, MDM2, MIF, MYO1C, NUP93, OAZ2, PAK1, PARP1, PFKFB2, PFKM, PIK3R1, PIK3R2, PIN1, PPIA, PRKCE, PRKD1, RAC2, RACK1, RBCK1, RBPMS, RHOA, RPL28, RUVBL1, S100A8, S100A9, SFN, SH3GLB1, SMAD3, SMAD4, SORL1, SPTBN1, SRC, SREBF2, SYK, TARDBP, TP53, TPR, TRIM28, TRIP6, UBE2L3, UBR5, YWHAE]

GO:0051223	regulation of protein transport	840,0E-18	790,0E-15	160,0E-48	8,5E-45	[5, 6, 7, 8]	Group43	15,14	124,00	[ABL1, ACTL6A, AKAP8L, ANXA1, ARRB1, ATG13, ATG5, BAG4, BARD1, BCAS3, BCL3, BLK, CABP1, CACNA1A, CDC42, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CFTR, CHUK, CLU, CSK, CSNK2A2, DNAJA1, EGFR, ERBB2, ERBB4, EZR, FBXW11, FBXW7, FGR, FLNA, FYCO1, FYN, GNAI2, GSK3B, HADHA, HAX1, HDAC3, HIF1A, HMGB1, HNF1A, HSP90AB1, HSPA1L, HSPA8, HSPD1, IL17RA, IL1R2, IPO5, ITGAX, JAK2, MAGI1, MAP4K4, MAPK1, MAPK14, MAPK3, MDM2, MIF, MTOR, MYO1C, NFKBIA, NFKBIE, NUP62, NUP93, OAZ2, PAK1, PARK7, PARP1, PFKFB2, PFKL, PFKM, PIK3C3, PIK3R1, PIK3R2, PIN1, PML, PPIA, PPM1B, PRDX1, PRKCE, PRKD1, PRKN, PTPN1, PTPN11, RAC2, RACK1, RANGAP1, RBCK1, RBPMS, RHOA, RPL28, RUVBL1, S100A8, S100A9, SFN, SH3GLB1, SLC16A1, SLC25A4, SLC25A5, SLC25A6, SMAD3, SMAD4, SOCS1, SORL1, SPTBN1, SRC, SREBF1, SREBF2, SYK, TARDBP, TP53, TPR, TRAF2, TRAF6, TRIM28, TRIP6, TXN, UBE2L3, UBR5, WWP2, XPO1, YWHAE]
GO:0090316	positive regulation of intracellular protein transport	1,2E-12	1,1E-9	160,0E-48	8,5E-45	[3, 4, 5, 6, 7, 8, 9, 10]	Group43	19,93	56,00	[ACTL6A, ATG13, BCAS3, CACNA1A, CDC42, CDH1, CDK1, CDK5, CDK5R1, CSNK2A2, EGFR, ERBB2, ERBB4, FBXW7, FLNA, FYCO1, FYN, GSK3B, HDAC3, HSP90AB1, HSPA1L, IPO5, ITGAX, JAK2, MAGI1, MAPK1, MAPK14, MDM2, MYO1C, NUP93, OAZ2, PAK1, PARP1, PIK3R1, PIK3R2, PIN1, PRKD1, RAC2, RBCK1, RBPMS, RHOA, RPL28, RUVBL1, SFN, SH3GLB1, SMAD3, SMAD4, SORL1, SREBF2, TP53, TPR, TRIM28, TRIP6, UBE2L3, UBR5, YWHAE]
GO:1902593	single-organism nuclear import	6,7E-18	6,3E-15	160,0E-48	8,5E-45	[5, 6, 7, 8]	Group43	22,52	68,00	[ADAR, BCL3, BCL6, CABP1, CBLB, CDH1, CDK1, CFL1, CTNNB1, EGFR, ERBB4, FBXW11, FLNA, GPN1, GSK3B, HDAC3, HSP90AB1, IPO4, IPO5, JAK2, JAK3, JUN, KPNA2, KPNA3, KPNA4, KPNB1, LMNA, MAPK1, MAPK14, MAPK3, MTOR, NFKBIA, NFKBIE, NUP107, NUP155, NUP62, NUP88, NUP93, NUP98, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PML, POLA2, PPM1B, PRDX1, PRKAG1, PRKD1, RAN, RANBP2, RBCK1, RBPMS, RHOA, RPL23, SMAD3, SMAD4, SPTBN1, STAT3, SYK, TNPO1, TNPO2, TPR, TRIM28, TRIP6, TXN, UBR5]
GO:0006605	protein targeting	1,1E-45	1,0E-42	160,0E-48	8,5E-45	[5, 6, 7, 8, 9]	Group43	23,20	171,00	[ACTL6A, ADAR, ANXA2, ATG13, ATG3, ATG4B, ATG4C, BAG4, BCL3, BCL6, CABP1, CACNA1A, CBLB, CDC37, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CFL1, CSNK2A2, CTNNB1, EGFR, ERBB2, ERBB4, FAU, FBXW11, FBXW7, FLNA, FYN, GABARAP, GPN1, GSK3B, HAX1, HDAC3, HSP90AA1, HSP90AB1, HSPA1L, HSPA4, HSPA8, HSPD1, IPO4, IPO5, ITGAX, JAK2, JAK3, JUN, KPNA2, KPNA3,

										KPNA4, KPNB1, LMNA, MAGI1, MAPK1, MAPK14, MAPK3, MTOR, MYL12A, MYO1C, NEDD4, NFKBIA, NFKBIE, NUP107, NUP155, NUP62, NUP88, NUP93, NUP98, PAK1, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PIN1, PML, POLA2, PPM1B, PRDX1, PRKCI, PRKD1, PRKN, RAC2, RAN, RANBP2, RBCK1, RBPMS, RHOA, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, RUVBL1, SH3GLB1, SLC25A6, SMAD3, SMAD4, SMURF1, SORL1, SPTBN1, SREBF1, SREBF2, SRP14, STAT3, SYK, TIMM50, TNPO1, TNPO2, TPR, TRIM28, TRIP6, TXN, UBA52, UBE2L3, UBR5, YWHAB, YWHAE, YWHAG, YWHAQ, YWHAZ]
GO:0033157	regulation of intracellular protein transport	650,0E-18	600,0E-15	160,0E-48	8,5E-45	[5, 6, 7, 8, 9]	Group43	19,07	78,00	[ACTL6A, AKAP8L, ATG13, BAG4, BARD1, BCAS3, BCL3, CABP1, CACNA1A, CDC42, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CSNK2A2, EGFR, ERBB2, ERBB4, FBXW11, FBXW7, FLNA, FYCO1, FYN, GSK3B, HAX1, HDAC3, HSP90AB1, HSPA1L, IPO5, ITGAX, JAK2, MAGI1, MAPK1, MAPK14, MDM2, MTOR, MYO1C, NFKBIA, NFKBIE, NUP62, NUP93, OAZ2, PAK1, PARK7, PARP1, PIK3R1, PIK3R2, PIN1, PPM1B, PRDX1, PRKD1, PRKN, PTPN1, PTPN11, RAC2, RANGAP1, RBCK1, RBPMS, RHOA, RPL28, RUVBL1, SFN, SH3GLB1, SMAD3, SMAD4, SORL1, SREBF1, SREBF2, TP53, TPR, TRIM28, TRIP6, TXN, UBE2L3, UBR5, XPO1, YWHAE]
GO:1904589	regulation of protein import	11,0E-9	10,0E-6	160,0E-48	8,5E-45	[5, 6, 7, 8, 9]	Group43	19,58	37,00	[BCL3, CABP1, CDH1, CDK1, EGFR, ERBB4, FBXW11, FLNA, GSK3B, HDAC3, HSP90AB1, HSPA8, IPO5, JAK2, MAPK1, MAPK14, MTOR, NFKBIA, NFKBIE, NUP62, NUP93, PARP1, PIK3R1, PIK3R2, PPM1B, PRDX1, PRKD1, RBCK1, RBPMS, RHOA, SMAD3, SMAD4, TPR, TRIM28, TRIP6, TXN, UBR5]
GO:1903533	regulation of protein targeting	690,0E-15	640,0E-12	160,0E-48	8,5E-45	[6, 7, 8, 9, 10]	Group43	19,02	62,00	[ACTL6A, ATG13, BAG4, BCL3, CABP1, CACNA1A, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CSNK2A2, EGFR, ERBB2, ERBB4, FBXW11, FBXW7, FLNA, FYN, GSK3B, HAX1, HDAC3, HSP90AB1, HSPA1L, IPO5, ITGAX, JAK2, MAGI1, MAPK1, MAPK14, MTOR, MYO1C, NFKBIA, NFKBIE, NUP62, NUP93, PAK1, PARP1, PIK3R1, PIK3R2, PIN1, PPM1B, PRDX1, PRKD1, PRKN, RAC2, RBCK1, RBPMS, RHOA, RPL28, RUVBL1, SH3GLB1, SMAD3, SMAD4,

										SREBF1, SREBF2, TPR, TRIM28, TRIP6, TXN, UBE2L3, UBR5]
GO:0042307	positive regulation of protein import into nucleus	35,0E-9	33,0E-6	160,0E-48	8,5E-45	[4, 5, 6, 7, 8, 9, 10, 11, 12, 13]	Group43	24,04	25,00	[CDH1, CDK1, EGFR, ERBB4, FLNA, HDAC3, HSP90AB1, IPO5, JAK2, MAPK1, MAPK14, NUP93, PARP1, PIK3R1, PIK3R2, PRKD1, RBCK1, RBPMS, RHOA, SMAD3, SMAD4, TPR, TRIM28, TRIP6, UBR5]
GO:0031400	negative regulation of protein modification process	18,0E-30	17,0E-27	16,0E-51	850,0E-51	[5, 6, 7, 8]	Group44	20,84	129,00	[ABL1, ADAR, ANAPC7, APC, ARRB1, ARRB2, ATG14, ATG5, BAG5, BAX, BRCA1, CALM1, CASP3, CBL, CBLB, CDC20, CDK1, CDK5, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, CTBP1, CTDSP2, CTNNB1, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, EIF6, EPRS, EZR, FYN, GPS2, HDAC2, HDAC3, HIPK3, HSPA1A, HSPB1, HSPH1, IGF1R, IKBKB, ITCH, JARID2, JUN, KAT2B, KLF4, LRRK1, MAD2L1, MEN1, MICAL1, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, PAK2, PARK7, PDPK1, PHB, PIAS3, PIN1, PLK1, PML, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAG2, PRKAR1A, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, RAPGEF1, RASSF2, RPL11, RPL23, RPL5, RPS27A, RPS3, SEMA4D, SET, SFN, SIN3A, SMAD4, SMAD7, SMARCB1, SNCA, SOCS1, SOCS3, SORL1, STRAP, SUMO1, TARDBP, TNIP1, TRAF3IP1, TRIM21, UBA52, UBASH3B, UBE2B, UBE2D1, UBR5, UBXN1, YWHAB, YWHAE, YWHAG]
GO:0001932	regulation of protein phosphorylation	140,0E-39	130,0E-36	16,0E-51	850,0E-51	[6, 7, 8]	Group44	16,90	234,00	[ABI1, ABL1, ACVR1B, ADAR, AKAP8L, AKTIP, ALK, ANXA2, APC, APP, AR, ARHGEF7, ARRB1, ARRB2, ATG14, BAG4, BAX, BRD4, C3, CALM1, CAMKK1, CAMKK2, CASP3, CBL, CBLB, CCM2, CCNT1, CD4, CDC37, CDC42, CDK1, CDK4, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CFLAR, CLU, CNTN1, COPS5, CORO1C, CRK, CRKL, CSK, CTDSP2, CTNNB1, DAXX, DBNL, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, EGFR, EIF2AK2, EIF6, EPHB1, EPRS, ERBB2, ERBB3, ERBB4, ETFA, EZH2, EZR, FASN, FBXW7, FGFR1, FGR, FRS2, FYN, GAB1, GCN1, GHR, GNAI2, GPS2, GRB2, GSK3B, HACD3, HAX1, HDAC2, HDAC3, HIPK3, HMGB1, HSP90AB1, HSPA5, HSPB1, HSPH1, IGF1R, INSR, IQGAP1, IRAK1, ITCH, ITGB2, JAK2, JUN, KAT2B, KIT, KLF4, LAT, LCP2, LRRK1, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAP4K4, MAPK1, MAPK10, MAPK14, MAPK3, MEN1, MICAL1, MIF, MLST8, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, OPRL1, PAK1, PAK2, PARK7,

										PDGFRA, PDGFRB, PDPK1, PEA15, PELI2, PHB, PHB2, PIK3CA, PIK3CG, PIN1, PLAUR, PLCG1, PLK1, PML, PPM1F, PPP2CA, PPP2R1A, PRDX1, PREX1, PRKAA1, PRKAB1, PRKAB2, PRKAG1, PRKAG2, PRKAR1A, PRKCE, PRKD1, PRKN, PRMT1, PRMT5, PSAP, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPN6, PTPRC, PTPRJ, RAC1, RAC2, RACK1, RAF1, RAPGEF1, RASSF2, RB1CC1, RBPMS, RET, RHOA, RIPK2, RPLP1, RPS27A, RPS3, RPS6KA4, S100A7, S100A8, S100A9, SEMA4D, SFN, SHC1, SMAD4, SMAD7, SNCA, SOCS1, SOCS3, SOD1, SORBS3, SORL1, SPAG9, SQSTM1, SRC, STAT3, STK11, STK3, STK4, STK40, STRAP, SUMO1, SYK, TAB2, TARDBP, TBK1, TNFRSF1A, TNIP1, TNK2, TOM1L1, TP53, TPD52L1, TRAF2, TRAF3IP1, TRAF6, TXN, UBA52, UBASH3B, UBE2B, UNC119, UVRAG, VRK2, VTN, XRCC5, XRCC6, YWHAG]
GO:0042326	negative regulation of phosphorylation	11,0E-18	10,0E-15	16,0E-51	850,0E-51	[6, 7, 8]	Group44	19,12	87,00	[ABL1, ADAR, APC, ARRB1, ARRB2, ATG14, ATXN7, BAX, CALM1, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, CTDSP2, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, DYNLL1, EIF6, EPRS, EZR, GPS2, GRB10, HDAC3, HIPK3, HSPB1, HSPH1, IGF1R, ITCH, JUN, KAT2B, KLF4, LRRK1, MAPT, MEN1, MICAL1, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, PAK2, PARK7, PDPK1, PHB, PIN1, PLK1, PPM1F, PPP2CA, PPP2R1A, PRDX3, PREX1, PRKAG2, PRKAR1A, PRKN, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, RAPGEF1, RASSF2, SEMA4D, SFN, SMAD4, SMAD7, SNCA, SOCS1, SOCS3, SORL1, STAT3, STRAP, TARDBP, TNIP1, TRAF3IP1, UBASH3B, UBE2B, YWHAG]
GO:1903320	regulation of protein modification by small protein conjugation or removal	15,0E-27	14,0E-24	16,0E-51	850,0E-51	[6, 7, 8]	Group44	27,21	80,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, BRCA1, BTRC, CDC20, CDK1, CDK5, CDK5RAP3, CDKN2A, CLU, COMMD1, CTNNB1, CUL1, DAXX, DNAJA1, DNAJA3, FANCI, FBXW7, FYN, HERPUD1, HSP90AA1, HSP90AB1, HSPA1A, HSPA5, ITCH, MAD2L1, MTA1, MTOR, MYO1C, NMI, PARK7, PIAS3, PIN1, PLK1, PML, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RASSF1, RIPK2, RPL11, RPL23, RPL5, RPS27A, RPS3, SKP1, SMAD7, SMURF1, STUB1, SUMO1, TOLLIP, TRAF6, TRIM21, UBA52, UBE2D1, UBE2I, UBE2L3, UBR5, UBXN1, VCP]
GO:0001933	negative regulation of protein phosphorylation	50,0E-18	47,0E-15	16,0E-51	850,0E-51	[6, 7, 8, 9]	Group44	19,47	81,00	[ABL1, ADAR, APC, ARRB1, ARRB2, ATG14, BAX, CALM1, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, CTDSP2, DLG1, DNAJA1, DNAJA3,

										DNAJC10, DUSP1, DUSP22, EIF6, EPRS, EZR, GPS2, HDAC3, HIPK3, HSPB1, HSPH1, IGF1R, ITCH, JUN, KAT2B, KLF4, LRRK1, MEN1, MICAL1, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, PAK2, PARK7, PDPK1, PHB, PIN1, PLK1, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAG2, PRKAR1A, PRKN, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, RAPGEF1, RASSF2, SEMA4D, SFN, SMAD4, SMAD7, SNCA, SOCS1, SOCS3, SORL1, STRAP, TARDBP, TNIP1, TRAF3IP1, UBASH3B, UBE2B, YWHAG]
GO:0033673	negative regulation of kinase activity	380,0E-12	350,0E-9	16,0E-51	850,0E-51	[6, 7, 8, 9]	Group44	18,38	50,00	[ABL1, ADAR, APC, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, DNAJA1, DNAJA3, DUSP1, DUSP22, EPRS, GPS2, HIPK3, HSPB1, IGF1R, KAT2B, MAPT, MEN1, NCK1, NPM1, NUP62, PAK2, PARK7, PDPK1, PLK1, PPM1F, PPP2CA, PPP2R1A, PRDX3, PREX1, PRKAG2, PRKAR1A, PRKN, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, SFN, SOCS1, SOCS3, SORL1, UBASH3B, YWHAG]
GO:0045859	regulation of protein kinase activity	11,0E-33	10,0E-30	16,0E-51	850,0E-51	[6, 7, 8, 9]	Group44	19,72	156,00	[ABI1, ABL1, ADAR, ALK, APC, APP, ARHGEF7, ARRB1, BAX, CALM1, CAMKK1, CAMKK2, CASP3, CBL, CBLB, CCNT1, CD4, CDC37, CDC42, CDK1, CDK4, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CLU, CORO1C, CRK, CRKL, CSK, DAXX, DBNL, DLG1, DNAJA1, DNAJA3, DUSP1, DUSP22, EGFR, EIF2AK2, EPRS, ERBB2, ERBB3, ETFA, EZH2, FBXW7, FGFR1, FGR, FRS2, GAB1, GCN1, GHR, GNAI2, GPS2, HACD3, HIPK3, HSP90AB1, HSPA5, HSPB1, HSPH1, IGF1R, INSR, IQGAP1, IRAK1, JAK2, KAT2B, KIT, LAT, LCP2, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MEN1, MIF, MLST8, MTOR, NCK1, NPM1, NUP62, PAK1, PAK2, PARK7, PDGFRB, PDPK1, PEA15, PIK3CA, PIK3CG, PLCG1, PLK1, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAA1, PRKAB1, PRKAB2, PRKAG1, PRKAG2, PRKAR1A, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPN6, PTPRC, PTPRJ, RAC2, RACK1, RAF1, RAPGEF1, RASSF2, RHOA, RIPK2, RPLP1, RPS27A, RPS3, S100A8, S100A9, SFN, SHC1, SNCA, SOCS1, SOCS3, SOD1, SORL1, SPAG9, SRC, STK11, STK3, STK4, SYK, TAB2, TOM1L1, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UBASH3B, UNC119, UVRAG, XRCC5, XRCC6, YWHAG]
GO:1903321	negative regulation of protein modification by small	7,3E-18	6,8E-15	16,0E-51	850,0E-51	[6, 7, 8, 9]	Group44	30,26	46,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, CDC20, CDK1, CDK5, CDKN2A, CTNNB1, DNAJA1, FYN, HSPA1A, MAD2L1, MTOR, PARK7, PIAS3, PML, PRKCE, PSMA2,

	protein conjugation or removal									PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPL11, RPL23, RPL5, RPS27A, RPS3, SMAD7, SUMO1, TRIM21, UBA52, UBE2D1, UBR5, UBXN1]
GO:0043409	negative regulation of MAPK cascade	920,0E-12	860,0E-9	16,0E-51	850,0E-51	[5, 6, 7, 8, 9, 10, 11]	Group44	22,15	35,00	[ABL1, ARRB1, CDK5RAP3, CSK, DLG1, DNAJA1, DUSP1, DUSP22, EIF6, EPRS, EZR, GPS2, HDAC3, HIPK3, HSPH1, IGF1R, ITCH, KLF4, MEN1, MYC, NCOR1, NUP62, PHB, PIN1, PPP2CA, PPP2R1A, PRKN, PTEN, PTPN1, PTPN6, PTPRJ, RAPGEF1, SMAD4, SORL1, TNIP1]
GO:0006469	negative regulation of protein kinase activity	2,6E-9	2,5E-6	16,0E-51	850,0E-51	[7, 8, 9, 10]	Group44	18,18	46,00	[ABL1, ADAR, APC, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, DNAJA1, DNAJA3, DUSP1, DUSP22, EPRS, GPS2, HIPK3, HSPB1, IGF1R, KAT2B, MEN1, NCK1, NPM1, NUP62, PAK2, PARK7, PDPK1, PLK1, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAG2, PRKAR1A, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, SFN, SOCS1, SOCS3, SORL1, UBASH3B, YWHAG]
GO:0031396	regulation of protein ubiquitination	3,8E-24	3,6E-21	16,0E-51	850,0E-51	[7, 8, 9, 10]	Group44	27,04	73,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, BRCA1, BTRC, CDC20, CDK1, CDK5, CDK5RAP3, CDKN2A, CLU, COMMD1, CUL1, DAXX, DNAJA1, DNAJA3, FANCI, FBXW7, FYN, HERPUD1, HSP90AA1, HSP90AB1, HSPA1A, HSPA5, MAD2L1, MTA1, MTOR, MYO1C, NMI, PARK7, PIN1, PLK1, PML, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RASSF1, RIPK2, RPL11, RPL23, RPL5, RPS27A, RPS3, SKP1, SMAD7, SMURF1, STUB1, SUMO1, TRAF6, UBA52, UBE2D1, UBE2L3, UBR5, UBXN1]
GO:0031397	negative regulation of protein ubiquitination	82,0E-18	77,0E-15	16,0E-51	850,0E-51	[7, 8, 9, 10, 11]	Group44	30,28	43,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, CDC20, CDK1, CDK5, CDKN2A, DNAJA1, FYN, HSPA1A, MAD2L1, MTOR, PARK7, PML, PRKCE, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPL11, RPL23, RPL5, RPS27A, RPS3, SMAD7, SUMO1, UBA52, UBE2D1, UBR5, UBXN1]
GO:0071901	negative regulation of protein serine/threonine kinase activity	270,0E-9	250,0E-6	16,0E-51	850,0E-51	[8, 9, 10, 11]	Group44	20,77	27,00	[ABL1, APC, CASP3, CDK5RAP3, CDKN1B, CDKN2A, DNAJA1, DUSP1, DUSP22, GPS2, HIPK3, HSPB1, KAT2B, MEN1, NUP62, PLK1, PPP2CA, PPP2R1A, PRKAG2, PRKAR1A, PTEN, PTPN1, PTPN6, PTPRJ, SFN, SORL1, YWHAG]
GO:0061621	canonical glycolysis	490,0E-9	460,0E-6	79,0E-9	4,0E-6	[5, 8, 9, 10, 11, 12, 13, 14, 15]	Group45	35,14	13,00	[ALDOA, ENO1, ENO2, GAPDH, HK2, HOOK1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PKM, TPI1]

GO:0009144	purine nucleoside triphosphate metabolic process	920,0E-9	860,0E-6	79,0E-9	4,0E-6	[6, 7, 8]	Group45	15,38	46,00	[AK2, ALDOA, AMPD2, AMPD3, ATP5A1, ATP5B, ATP5C1, ATP5O, CDK1, EIF6, ENO1, ENO2, GAPDH, GBAS, HIF1A, HK2, HOOK1, HSPA1A, HSPA8, IMPDH2, INSR, LDHA, MYC, NCOR1, NDUFA4, NME1, PARK7, PARP1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, SAMHD1, SDHA, SNCA, STAT3, TPI1, UQCRQ, VCP]
GO:0009161	ribonucleoside monophosphate metabolic process	4,2E-9	3,9E-6	79,0E-9	4,0E-6	[6, 7, 8]	Group45	16,62	54,00	[AK2, ALDOA, AMPD1, AMPD2, AMPD3, ATP5A1, ATP5B, ATP5C1, ATP5O, CAD, CDK1, DLG1, DLG3, DLG4, EIF6, ENO1, ENO2, GAPDH, GART, GBAS, HIF1A, HK2, HOOK1, HSPA1A, HSPA8, IMPDH2, INSR, LDHA, MYC, NCOR1, NDUFA4, NT5C2, PAICS, PARK7, PARP1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, PRPS1L1, SCRIB, SDHA, SNCA, STAT3, TPI1, UQCRQ, VCP]
GO:0009199	ribonucleoside triphosphate metabolic process	260,0E-9	250,0E-6	79,0E-9	4,0E-6	[6, 7, 8]	Group45	15,67	47,00	[AK2, ALDOA, AMPD2, AMPD3, ATP5A1, ATP5B, ATP5C1, ATP5O, CAD, CDK1, CTPS1, EIF6, ENO1, ENO2, GAPDH, GBAS, HIF1A, HK2, HOOK1, HSPA1A, HSPA8, IMPDH2, INSR, LDHA, MYC, NCOR1, NDUFA4, NME1, PARK7, PARP1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, SDHA, SNCA, STAT3, TPI1, UQCRQ, VCP]
GO:0046939	nucleotide phosphorylation	2,2E-9	2,1E-6	79,0E-9	4,0E-6	[6, 7, 8]	Group45	25,00	28,00	[AK2, AK6, ALDOA, EIF6, ENO1, ENO2, GAPDH, HIF1A, HK2, HOOK1, INSR, LDHA, MYC, NCOR1, NME1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, STAT3, TPI1]
GO:0006090	pyruvate metabolic process	2,5E-9	2,4E-6	79,0E-9	4,0E-6	[7, 8]	Group45	23,13	31,00	[ALDOA, DLAT, EIF6, ENO1, ENO2, GAPDH, HIF1A, HK2, HOOK1, INSR, LDHA, LDHB, MYC, NCOR1, PDHB, PDK3, PDPK1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, SLC16A1, STAT3, TPI1]
GO:0006165	nucleoside diphosphate phosphorylation	10,0E-9	9,3E-6	79,0E-9	4,0E-6	[6, 7, 8, 9]	Group45	24,76	26,00	[ALDOA, EIF6, ENO1, ENO2, GAPDH, HIF1A, HK2, HOOK1, INSR, LDHA, MYC, NCOR1, NME1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, STAT3, TPI1]
GO:0046496	nicotinamide nucleotide metabolic process	550,0E-9	520,0E-6	79,0E-9	4,0E-6	[6, 7, 8, 9]	Group45	18,56	31,00	[ALDOA, EIF6, ENO1, ENO2, GAPDH, HIF1A, HK2, HOOK1, INSR, LDHA, LDHB, MDH2, MYC, NCOR1, PDHB, PFKFB2, PFKL, PFKM, PGAM1, PGD, PGK1, PGM1, PHGDH, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, STAT3, TPI1, VCP]
GO:0009179	purine ribonucleoside diphosphate metabolic process	25,0E-12	23,0E-9	79,0E-9	4,0E-6	[7, 8, 9]	Group45	27,43	31,00	[AK2, ALDOA, AMPD3, DLG1, DLG3, DLG4, EIF6, ENO1, ENO2, GAPDH, HIF1A, HK2, HOOK1, INSR, LDHA, MYC, NCOR1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, SCRIB, STAT3, TPI1]

GO:0006096	glycolytic process	370,0E-12	350,0E-9	79,0E-9	4,0E-6	[5, 6, 7, 8, 9, 10, 11, 12]	Group45	29,41	25,00	[ALDOA, EIF6, ENO1, ENO2, GAPDH, HIF1A, HK2, HOOK1, INSR, LDHA, MYC, NCOR1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, STAT3, TPI1]
GO:0046031	ADP metabolic process	140,0E-12	130,0E-9	79,0E-9	4,0E-6	[7, 8, 9, 10]	Group45	28,72	27,00	[AK2, ALDOA, AMPD3, EIF6, ENO1, ENO2, GAPDH, HIF1A, HK2, HOOK1, INSR, LDHA, MYC, NCOR1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, STAT3, TPI1]
GO:0046034	ATP metabolic process	280,0E-9	260,0E-6	79,0E-9	4,0E-6	[7, 8, 9, 10]	Group45	16,29	43,00	[AK2, ALDOA, AMPD2, AMPD3, ATP5A1, ATP5B, ATP5C1, ATP5O, CDK1, EIF6, ENO1, ENO2, GAPDH, GBAS, HIF1A, HK2, HOOK1, HSPA1A, HSPA8, INSR, LDHA, MYC, NCOR1, NDUFA4, PARK7, PARP1, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PGM1, PKM, PRKAA1, PRKAA2, PRKAG1, PRKAG2, SDHA, SNCA, STAT3, TPI1, UQCRQ, VCP]
GO:1903578	regulation of ATP metabolic process	480,0E-9	450,0E-6	79,0E-9	4,0E-6	[7, 8, 9, 10, 11]	Group45	27,87	17,00	[CDK1, EIF6, ENO1, HIF1A, INSR, MYC, NCOR1, PARK7, PARP1, PGAM1, PRKAA1, PRKAA2, PRKAG1, PRKAG2, SNCA, STAT3, VCP]
GO:0006734	NADH metabolic process	410,0E-9	380,0E-6	79,0E-9	4,0E-6	[8, 9, 10, 11]	Group45	31,25	15,00	[ALDOA, ENO1, ENO2, GAPDH, HK2, HOOK1, MDH2, PFKFB2, PFKL, PFKM, PGAM1, PGK1, PKM, TPI1, VCP]
GO:0051253	negative regulation of RNA metabolic process	8,8E-27	8,3E-24	4,6E-33	230,0E-33	[4, 5, 6, 7, 8]	Group46	15,53	199,00	[ACIN1, AHRR, APP, AR, ARID1A, ATF2, ATN1, ATXN1, BACH1, BAG4, BARD1, BCL3, BCL6, BRCA1, BTRC, C1QBP, CALR, CCAR2, CCNT1, CDK5, CDK5R1, CDKN1B, CDKN2A, CDX2, CHD4, CNBP, COPS2, CREB1, CREBBP, CTBP1, CTNNB1, CUL3, DAXX, DDIT3, DDX5, DEDD, DEDD2, DLG1, DNAJA3, DNAJB1, DUSP22, E2F1, EHMT2, ENO1, EP300, EPRS, ESR1, EZH2, EZR, FASLG, FBXW11, FGFR1, FLNA, FOXO3, GFI1B, GPS2, H2AFX, H3F3A, HDAC1, HDAC2, HDAC3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HNRNPL, HSPA1A, HSPA8, ID2, IKZF4, ILF3, JARID2, JDP2, JUN, JUNB, JUND, KAT5, KDM5B, KHDRBS1, KLF4, KLF5, LRPPRC, MAF, MBD3, MDM2, MEN1, MEPCE, MTA1, MTA2, MYBBP1A, MYC, NACA, NCK1, NCOR1, NCOR2, NEDD4, NFKB1, NFKB2, NFX1, NIF3L1, NKRF, NKX2-1, NONO, NOTCH1, NR3C1, NR6A1, PA2G4, PABPC1, PARP1, PHB, PHB2, PLK1, PML, POU4F2, PPARG, PPM1F, PRKN, PRMT5, PSMC5, PTBP1, PTPRK, RBBP7, RBFOX2, RBL1, RBMX, RBPJ, REL, RELA, RELB, RPL15, RPL23, RPS13, RPS14, RPS27A, RUNX1, RYBP, SEMA4D, SET, SF1, SF3B3, SFPQ, SHC1, SIN3A, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCC2, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SOX7, SQSTM1, SRC, SREBF1, SREBF2, SRSF7, STAT1, STAT3, STAT6, STRAP, SUMO1, SUZ12, TARDBP, TBL1X, TCF7L1, TP53,

										TPR, TRAF6, TRIM21, TRIM28, TSC22D3, TSHZ3, TXN, UBA52, UBE2B, UBE2D1, UBE2I, UBR2, USP9X, VDR, VHL, WWC3, WWP2, XPO1, XRCC5, XRCC6, YAP1, YBX1, YWHAB, YWHAQ, YY1, ZBTB16]
GO:0051254	positive regulation of RNA metabolic process	240,0E-30	230,0E-27	4,6E-33	230,0E-33	[4, 5, 6, 7, 8]	Group46	14,88	229,00	[ACVR1B, AGO1, AGO2, AIRE, AKAP8L, APP, AR, ARHGEF11, ARID1A, ARID1B, ARID3A, ARRB1, ATF2, ATF4, ATXN7, BACH1, BANP, BCAS3, BCL3, BRCA1, BRD4, BTRC, CALCOCO1, CAMKK2, CARM1, CCM2, CCNT1, CD4, CDH1, CDK5RAP3, CDKN2A, CDX2, CHUK, CNBP, COPS5, CREB1, CREBBP, CRTC2, CTNNB1, DAZAP1, DDIT3, DDX17, DDX3X, DDX5, DLL1, DNAJC5, DNM2, E2F1, E2F3, EGFR, EIF4A3, ELOC, EP300, ERBB2, ERBB4, ESR1, EZH2, FADD, FBXW11, FBXW7, FOS, FOXO3, GCN1, GSK3B, GTF2F2, HAX1, HDAC1, HDAC2, HDAC3, HIF1A, HMGB1, HNF1A, HNRNPAB, HNRNPD, HNRNPR, HSPA1A, HSPA5, HSPA8, HSPH1, ID2, IKBKB, IKZF4, ILF2, ILF3, ING5, INSR, IRAK1, JAG1, JUN, JUNB, JUND, KAT2B, KAT5, KHSRP, KLF4, KLF5, KLF6, KRT6B, LMNA, LYL1, MAF, MAML1, MAML3, MAP2K1, MAP2K3, MAP3K5, MAPK1, MAPK14, MAPK3, MARS, MED19, MEN1, MET, MTA2, MTOR, MYC, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NFKB1, NFKB2, NFKBIA, NIF3L1, NKX2-1, NOTCH1, NPM1, NR3C1, NR6A1, NUFIP1, NUP62, PABPC1, PARK7, PARP1, PBX2, PCBD1, PCBP1, PELP1, PFN1, PHB, PIAS2, PIK3R1, PIK3R2, PIN1, PLSCR1, PML, POLR2A, POU2AF1, POU4F2, PPARG, PPP1R12A, PRKD1, PRKN, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, RAF1, RAN, RBL1, RBM14, RBMX, RBPJ, REL, RELA, RELB, RET, RIPK2, RNMT, RPL23, RPS27A, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL2, SFPQ, SHC1, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SNW1, SP1, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT5B, STAT6, SUMO1, SUMO2, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFB2M, TFE3, TNFRSF1A, TNIP1, TNIP2, TNRC6B, TP53, TRAF6, TRIM28, UBA52, VDR, VHL, WBP2, WWP2, XRCC6, YAP1, YBX1, YWHAH, ZBTB16]
GO:0006351	transcription, DNA-templated	260,0E-33	250,0E-30	4,6E-33	230,0E-33	[5, 6, 7, 8, 9]	Group46	11,60	456,00	[ABCG1, ABL1, ACTL6A, ACVR1B, AGO1, AGO2, AHRR, AIRE, AKAP8L, ALK, APP, AR, ARHGEF11, ARID1A, ARID1B, ARID3A, ARRB1, ARRB2, ASCC2, ASF1B, ATF2, ATF4, ATN1, ATXN1, ATXN7, BACH1, BANP, BCAS3, BCL3, BCL6, BRCA1, BRD4, BRF2, BTK, BTRC, BZW1, C1QBP, CALCOCO1, CALR, CAMK2A, CAMKK2, CARHSP1, CARM1, CBL, CCAR2, CCM2, CCNT1, CD4, CDC5L, CDH1, CDK1,

										CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CDX2, CELSR2, CFLAR, CHD4, CHUK, CLU, CNBP, COMMD1, COMMD10, COMMD2, COPS2, COPS5, CREB1, CREBBP, CRK, CRTC2, CSNK2A1, CSNK2A2, CTBP1, CTNNB1, CUL2, CUL3, DAXX, DCC, DDIT3, DDX1, DDX17, DDX21, DDX3X, DDX5, DEDD, DEDD2, DLG1, DLL1, DNAJA3, DNAJB1, DNAJC5, DNM2, DTX1, DUSP22, DYNLL1, E2F1, E2F3, EEF1A1, EEF1D, EGFR, EHMT2, EIF2AK2, EIF4A3, ELOC, ENO1, EP300, EPRS, ERBB2, ERBB4, ESF1, ESR1, EWSR1, EZH2, EZR, FADD, FANCA, FASLG, FBXW11, FBXW7, FGFR1, FLNA, FOS, FOXO3, GCN1, GFI1B, GPS2, GSK3B, GTF2F2, GTF3C1, H2AFX, H3F3A, HAX1, HCK, HDAC1, HDAC2, HDAC3, HIF1A, HINT1, HIPK3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HNRNPAB, HNRNPD, HNRNPDL, HNRNPUL1, HSPA1A, HSPA5, HSPA8, HSPD1, HSPH1, ID2, IKBKB, IKZF4, ILF2, ILF3, ING5, INSR, IRAK1, ISL2, ITCH, ITGB2, JAG1, JAK2, JARID2, JDP2, JUN, JUNB, JUND, KAT2B, KAT5, KDM2A, KDM3B, KDM5B, KHDRBS1, KHSRP, KIT, KLF4, KLF5, KLF6, KRT6B, LIN54, LMNA, LRPPRC, LYL1, MAF, MAML1, MAML3, MAP2K1, MAP2K3, MAP3K5, MAP3K7, MAPK1, MAPK10, MAPK13, MAPK14, MAPK3, MAPK8, MARS, MAX, MBD3, MDM2, MED13L, MED19, MED28, MED31, MEN1, MEPCE, MET, MOV10, MTA1, MTA2, MTOR, MYBBP1A, MYC, MYO1C, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NCOR1, NCOR2, NDRG1, NEDD4, NEDD8, NFKB1, NFKB2, NFKBIA, NFKBIB, NFKBIZ, NFX1, NIF3L1, NKRF, NKX2-1, NMI, NONO, NOTCH1, NOTCH2, NPM1, NR3C1, NR6A1, NRBF2, NUDT21, NUFIP1, NUP107, NUP62, PA2G4, PAG1, PARK7, PARP1, PBX2, PCBD1, PCBP1, PCNA, PDPK1, PELP1, PFDN1, PFN1, PHB, PHB2, PIAS2, PIAS3, PIK3R1, PIK3R2, PIN1, PLK1, PLSCR1, PML, POLR2A, POLRMT, POU2AF1, POU4F2, PPARG, PPM1F, PPP1R12A, PPP2CA, PPP2R1A, PRDX3, PRKAA1, PRKAA2, PRKAR1A, PRKCB, PRKCI, PRKD1, PRKN, PRMT5, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPRK, PUF60, RAF1, RALY, RAN, RB1CC1, RBBP4, RBBP7, RBCK1, RBFOX2, RBL1, RBM14, RBM39, RBMX, RBPJ, RBPMS, REL, RELA, RELB, RET, RHOXF2, RIPK2, RNMT, RPL15, RPL23, RPL6, RPS14, RPS27A, RPS3, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL1, RUVBL2, RYBP, S100A8, S100A9, SEMA4D, SET, SF1, SF3B3, SFPQ,

										SGK1, SHC1, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SMURF1, SMURF2, SNAI3, SNCA, SNRPB, SNRPD3, SNRPF, SNRPG, SNW1, SORBS3, SOX7, SP1, SQSTM1, SRC, SREBF1, SREBF2, SRSF3, SRSF7, STAT1, STAT3, STAT5B, STAT6, STK3, STRAP, SUMO1, SUMO2, SUZ12, SYK, TAB2, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFB2M, TFE3, TIAL1, TMPO, TNFRSF1A, TNIP1, TNIP2, TP53, TPR, TRADD, TRAF2, TRAF6, TRIM21, TRIM28, TRIP13, TRIP6, TROVE2, TRRAP, TSC22D1, TSC22D3, TSHZ3, TXN, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2I, UBE2L3, UBN1, UBR2, USP7, USP9X, VAV1, VDR, VHL, WASL, WBP2, WDR77, WWC3, WWP2, XPO1, XRCC5, XRCC6, XRN2, YAP1, YBX1, YWHAB, YWHAH, YWHAQ, YY1, ZBED1, ZBTB16, ZBTB47, ZNF326, ZNF512B, ZNF823, ZNFX1]
GO:0097659	nucleic acid-templated transcription	99,0E-33	93,0E-30	4,6E-33	230,0E-33	[6, 7, 8]	Group46	11,62	459,00	[ABCG1, ABL1, ACTL6A, ACTN1, ACTN4, ACVR1B, AGO1, AGO2, AHRR, AIRE, AKAP8L, ALK, APP, AR, ARHGEF11, ARID1A, ARID1B, ARID3A, ARRB1, ARRB2, ASCC2, ASF1B, ATF2, ATF4, ATN1, ATXN1, ATXN7, BACH1, BANP, BCAS3, BCL3, BCL6, BRCA1, BRD4, BRF2, BTK, BTRC, BZW1, C1QBP, CALCOCO1, CALR, CAMK2A, CAMKK2, CARHSP1, CARM1, CBL, CCAR2, CCM2, CCNT1, CD4, CDC5L, CDH1, CDK1, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CDX2, CELSR2, CFLAR, CHD4, CHUK, CLU, CNBP, COMMD1, COMMD10, COMMD2, COPS2, COPS5, CREB1, CREBBP, CRK, CRTC2, CSNK2A1, CSNK2A2, CTBP1, CTNNB1, CUL2, CUL3, DAXX, DCC, DDIT3, DDX1, DDX17, DDX21, DDX3X, DDX5, DEDD, DEDD2, DLG1, DLL1, DNAJA3, DNAJB1, DNAJC5, DNM2, DTX1, DUSP22, DYNLL1, E2F1, E2F3, EEF1A1, EEF1D, EGFR, EHMT2, EIF2AK2, EIF4A3, ELOC, ENO1, EP300, EPRS, ERBB2, ERBB4, ESF1, ESR1, EWSR1, EZH2, EZR, FADD, FANCA, FASLG, FBXW11, FBXW7, FGFR1, FLNA, FOS, FOXO3, FUS, GCN1, GFI1B, GPS2, GSK3B, GTF2F2, GTF3C1, H2AFX, H3F3A, HAX1, HCK, HDAC1, HDAC2, HDAC3, HIF1A, HINT1, HIPK3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HNRNPAB, HNRNPD, HNRNPDL, HNRNPUL1, HSPA1A, HSPA5, HSPA8, HSPD1, HSPH1, ID2, IKBKB, IKZF4, ILF2, ILF3, ING5, INSR, IRAK1, ISL2, ITCH, ITGB2, JAG1, JAK2, JARID2, JDP2, JUN, JUNB, JUND, KAT2B, KAT5, KDM2A, KDM3B, KDM5B, KHDRBS1, KHSRP, KIT, KLF4, KLF5, KLF6, KRT6B, LIN54, LMNA, LRPPRC, LYL1, MAF, MAML1, MAML3, MAP2K1, MAP2K3,

										MAP3K5, MAP3K7, MAPK1, MAPK10, MAPK13, MAPK14, MAPK3, MAPK8, MARS, MAX, MBD3, MDM2, MED13L, MED19, MED28, MED31, MEN1, MEPCE, MET, MOV10, MTA1, MTA2, MTOR, MYBBP1A, MYC, MYO1C, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NCOR1, NCOR2, NDRG1, NEDD4, NEDD8, NFKB1, NFKB2, NFKBIA, NFKBIB, NFKBIZ, NFX1, NIF3L1, NKRF, NKX2-1, NMI, NONO, NOTCH1, NOTCH2, NPM1, NR3C1, NR6A1, NRBF2, NUDT21, NUFIP1, NUP107, NUP62, PA2G4, PAG1, PARK7, PARP1, PBX2, PCBD1, PCBP1, PCNA, PDPK1, PELP1, PFDN1, PFN1, PHB, PHB2, PIAS2, PIAS3, PIK3R1, PIK3R2, PIN1, PLK1, PLSCR1, PML, POLR2A, POLRMT, POU2AF1, POU4F2, PPARG, PPM1F, PPP1R12A, PPP2CA, PPP2R1A, PRDX3, PRKAA1, PRKAA2, PRKAR1A, PRKCB, PRKCI, PRKD1, PRKN, PRMT5, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPRK, PUF60, RAF1, RALY, RAN, RB1CC1, RBBP4, RBBP7, RBCK1, RBFOX2, RBL1, RBM14, RBM39, RBMX, RBPJ, RBPMS, REL, RELA, RELB, RET, RHOXF2, RIPK2, RNMT, RPL15, RPL23, RPL6, RPS14, RPS27A, RPS3, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL1, RUVBL2, RYBP, S100A8, S100A9, SEMA4D, SET, SF1, SF3B3, SFPQ, SGK1, SHC1, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SMURF1, SMURF2, SNAI3, SNCA, SNRPB, SNRPD3, SNRPF, SNRPG, SNW1, SORBS3, SOX7, SP1, SQSTM1, SRC, SREBF1, SREBF2, SRSF3, SRSF7, STAT1, STAT3, STAT5B, STAT6, STK3, STRAP, SUMO1, SUMO2, SUZ12, SYK, TAB2, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFB2M, TFE3, TIAL1, TMPO, TNFRSF1A, TNIP1, TNIP2, TP53, TPR, TRADD, TRAF2, TRAF6, TRIM21, TRIM28, TRIP13, TRIP6, TROVE2, TRRAP, TSC22D1, TSC22D3, TSHZ3, TXN, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2I, UBE2L3, UBN1, UBR2, USP7, USP9X, VAV1, VDR, VHL, WASL, WBP2, WDR77, WWC3, WWP2, XPO1, XRCC5, XRCC6, XRN2, YAP1, YBX1, YWHAB, YWHAH, YWHAQ, YY1, ZBED1, ZBTB16, ZBTB47, ZNF326, ZNF512B, ZNF823, ZNFX1]
GO:1902679	negative regulation of RNA biosynthetic process	2,1E-24	2,0E-21	4,6E-33	230,0E-33	[5, 6, 7, 8, 9]	Group46	15,28	188,00	[AHRR, APP, AR, ARID1A, ATF2, ATN1, ATXN1, BACH1, BCL3, BCL6, BRCA1, BTRC, C1QBP, CALR, CCAR2, CDK5, CDK5R1, CDKN1B, CDKN2A, CDX2, CHD4, CNBP, COPS2, CREB1, CREBBP, CTBP1, CTNNB1, CUL3, DAXX, DDIT3, DDX5, DEDD, DEDD2, DLG1, DNAJA3, DNAJB1, DUSP22,

										E2F1, EHMT2, ENO1, EP300, EPRS, ESR1, EZH2, EZR, FASLG, FBXW11, FGFR1, FLNA, FOXO3, GFI1B, GPS2, H2AFX, H3F3A, HDAC1, HDAC2, HDAC3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HSPA1A, HSPA8, ID2, IKZF4, ILF3, JARID2, JDP2, JUN, JUNB, JUND, KAT5, KDM5B, KHDRBS1, KLF4, KLF5, MAF, MBD3, MDM2, MEN1, MEPCE, MTA1, MTA2, MYBBP1A, MYC, NACA, NCK1, NCOR1, NCOR2, NEDD4, NFKB1, NFKB2, NFX1, NIF3L1, NKRF, NKX2-1, NONO, NOTCH1, NR3C1, NR6A1, PA2G4, PARP1, PHB, PHB2, PLK1, PML, POU4F2, PPARG, PPM1F, PRKN, PRMT5, PSMC5, PTPRK, RBBP7, RBFOX2, RBL1, RBPJ, REL, RELA, RELB, RPL15, RPL23, RPS14, RPS27A, RUNX1, RYBP, SEMA4D, SET, SF1, SF3B3, SFPQ, SHC1, SIN3A, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCC2, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SOX7, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT6, STRAP, SUMO1, SUZ12, TARDBP, TBL1X, TCF7L1, TP53, TPR, TRAF6, TRIM21, TRIM28, TSC22D3, TSHZ3, TXN, UBA52, UBE2B, UBE2D1, UBE2I, UBR2, USP9X, VDR, VHL, WWC3, WWP2, XPO1, XRCC5, XRCC6, YAP1, YBX1, YWHAB, YWHAQ, YY1, ZBTB16]
GO:1902680	positive regulation of RNA biosynthetic process	3,0E-27	2,8E-24	4,6E-33	230,0E-33	[5, 6, 7, 8, 9]	Group46	14,87	222,00	[ACVR1B, AGO1, AGO2, AIRE, AKAP8L, APP, AR, ARHGEF11, ARID1A, ARID1B, ARID3A, ARRB1, ATF2, ATF4, ATXN7, BACH1, BANP, BCAS3, BCL3, BRCA1, BRD4, BTRC, CALCOCO1, CAMKK2, CARM1, CCM2, CCNT1, CD4, CDH1, CDK5RAP3, CDKN2A, CDX2, CHUK, CNBP, COPS5, CREB1, CREBBP, CRTC2, CTNNB1, DDIT3, DDX17, DDX3X, DDX5, DLL1, DNAJC5, DNM2, E2F1, E2F3, EGFR, EIF4A3, ELOC, EP300, ERBB2, ERBB4, ESR1, EZH2, FADD, FBXW11, FBXW7, FOS, FOXO3, GCN1, GSK3B, GTF2F2, HAX1, HDAC1, HDAC2, HDAC3, HIF1A, HMGB1, HNF1A, HNRNPAB, HNRNPD, HSPA5, HSPH1, ID2, IKBKB, IKZF4, ILF2, ILF3, ING5, INSR, IRAK1, JAG1, JUN, JUNB, JUND, KAT2B, KAT5, KLF4, KLF5, KLF6, KRT6B, LMNA, LYL1, MAF, MAML1, MAML3, MAP2K1, MAP2K3, MAP3K5, MAPK1, MAPK14, MAPK3, MARS, MED19, MEN1, MET, MTA2, MTOR, MYC, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NFKB1, NFKB2, NFKBIA, NIF3L1, NKX2-1, NOTCH1, NPM1, NR3C1, NR6A1, NUFIP1, NUP62, PARK7, PARP1, PBX2, PCBD1, PCBP1, PELP1, PFN1, PHB, PIAS2, PIK3R1, PIK3R2, PIN1, PLSCR1, PML, POLR2A, POU2AF1, POU4F2, PPARG, PPP1R12A, PRKD1, PRKN, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, RAF1, RAN,

										RBL1, RBM14, RBMX, RBPJ, REL, RELA, RELB, RET, RIPK2, RNMT, RPL23, RPS27A, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL2, SFPQ, SHC1, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SNW1, SP1, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT5B, STAT6, SUMO1, SUMO2, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFB2M, TFE3, TNFRSF1A, TNIP1, TNIP2, TP53, TRAF6, TRIM28, UBA52, VDR, VHL, WBP2, WWP2, XRCC6, YAP1, YBX1, YWHAH, ZBTB16]
GO:0006355	regulation of transcription, DNA-templated	580,0E-33	540,0E-30	4,6E-33	230,0E-33	[5, 6, 7, 8, 9, 10]	Group46	11,72	441,00	[ABCG1, ABL1, ACTL6A, ACVR1B, AGO1, AGO2, AHRR, AIRE, AKAP8L, ALK, APP, AR, ARHGEF11, ARID1A, ARID1B, ARID3A, ARRB1, ARRB2, ASCC2, ASF1B, ATF2, ATF4, ATN1, ATXN1, ATXN7, BACH1, BANP, BCAS3, BCL3, BCL6, BRCA1, BRD4, BRF2, BTK, BTRC, BZW1, C1QBP, CALCOCO1, CALR, CAMK2A, CAMKK2, CARHSP1, CARM1, CBL, CCAR2, CCM2, CCNT1, CD4, CDC5L, CDH1, CDK1, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CDX2, CELSR2, CFLAR, CHD4, CHUK, CLU, CNBP, COMMD1, COMMD10, COMMD2, COPS2, COPS5, CREB1, CREBBP, CRK, CRTC2, CSNK2A1, CSNK2A2, CTBP1, CTNNB1, CUL2, CUL3, DAXX, DCC, DDIT3, DDX1, DDX17, DDX3X, DDX5, DEDD, DEDD2, DLG1, DLL1, DNAJA3, DNAJB1, DNAJC5, DNM2, DUSP22, DYNLL1, E2F1, E2F3, EEF1A1, EEF1D, EGFR, EHMT2, EIF2AK2, EIF4A3, ELOC, ENO1, EP300, EPRS, ERBB2, ERBB4, ESF1, ESR1, EWSR1, EZH2, EZR, FADD, FANCA, FASLG, FBXW11, FBXW7, FGFR1, FLNA, FOS, FOXO3, GCN1, GFI1B, GPS2, GSK3B, GTF2F2, GTF3C1, H2AFX, H3F3A, HAX1, HCK, HDAC1, HDAC2, HDAC3, HIF1A, HINT1, HIPK3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HNRNPAB, HNRNPD, HNRNPDL, HNRNPUL1, HSPA1A, HSPA5, HSPA8, HSPD1, HSPH1, ID2, IKBKB, IKZF4, ILF2, ILF3, ING5, INSR, IRAK1, ISL2, ITCH, ITGB2, JAG1, JAK2, JARID2, JDP2, JUN, JUNB, JUND, KAT2B, KAT5, KDM2A, KDM3B, KDM5B, KHDRBS1, KHSRP, KIT, KLF4, KLF5, KLF6, KRT6B, LIN54, LMNA, LRPPRC, LYL1, MAF, MAML1, MAML3, MAP2K1, MAP2K3, MAP3K5, MAP3K7, MAPK1, MAPK10, MAPK13, MAPK14, MAPK3, MAPK8, MARS, MAX, MBD3, MDM2, MED13L, MED19, MED28, MED31, MEN1, MEPCE, MET, MOV10, MTA1, MTA2, MTOR, MYBBP1A, MYC, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NCOR1, NCOR2, NEDD4, NEDD8, NFKB1, NFKB2, NFKBIA, NFKBIB,

										NFKBIZ, NFX1, NIF3L1, NKRF, NKX2-1, NONO, NOTCH1, NOTCH2, NPM1, NR3C1, NR6A1, NRBF2, NUFIP1, NUP107, NUP62, PA2G4, PAG1, PARK7, PARP1, PBX2, PCBD1, PCBP1, PCNA, PDPK1, PELP1, PFDN1, PFN1, PHB, PHB2, PIAS2, PIAS3, PIK3R1, PIK3R2, PIN1, PLK1, PLSCR1, PML, POLR2A, POU2AF1, POU4F2, PPARG, PPM1F, PPP1R12A, PPP2CA, PPP2R1A, PRDX3, PRKAA1, PRKAA2, PRKAR1A, PRKCB, PRKCI, PRKD1, PRKN, PRMT5, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPRK, PUF60, RAF1, RALY, RAN, RB1CC1, RBBP4, RBBP7, RBCK1, RBFOX2, RBL1, RBM14, RBM39, RBMX, RBPJ, RBPMS, REL, RELA, RELB, RET, RHOXF2, RIPK2, RNMT, RPL15, RPL23, RPL6, RPS14, RPS27A, RPS3, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL1, RUVBL2, RYBP, S100A8, S100A9, SEMA4D, SET, SF1, SF3B3, SFPQ, SGK1, SHC1, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SMURF1, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SOX7, SP1, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT5B, STAT6, STK3, STRAP, SUMO1, SUMO2, SUZ12, SYK, TAB2, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFB2M, TFE3, TIAL1, TMPO, TNFRSF1A, TNIP1, TNIP2, TP53, TPR, TRADD, TRAF2, TRAF6, TRIM21, TRIM28, TRIP6, TRRAP, TSC22D1, TSC22D3, TSHZ3, TXN, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2I, UBE2L3, UBN1, UBR2, USP7, USP9X, VAV1, VDR, VHL, WASL, WBP2, WDR77, WWC3, WWP2, XPO1, XRCC5, XRCC6, XRN2, YAP1, YBX1, YWHAB, YWHAH, YWHAQ, YY1, ZBED1, ZBTB16, ZBTB47, ZNF326, ZNF512B, ZNF823, ZNFX1]
GO:1903506	regulation of nucleic acid-templated transcription	17,0E-33	15,0E-30	4,6E-33	230,0E-33	[6, 7, 8, 9]	Group46	11,82	448,00	[ABCG1, ABL1, ACTL6A, ACTN1, ACTN4, ACVR1B, AGO1, AGO2, AHRR, AIRE, AKAP8L, ALK, APP, AR, ARHGEF11, ARID1A, ARID1B, ARID3A, ARRB1, ARRB2, ASCC2, ASF1B, ATF2, ATF4, ATN1, ATXN1, ATXN7, BACH1, BANP, BCAS3, BCL3, BCL6, BRCA1, BRD4, BRF2, BTK, BTRC, BZW1, C1QBP, CALCOCO1, CALR, CAMK2A, CAMKK2, CARHSP1, CARM1, CBL, CCAR2, CCM2, CCNT1, CD4, CDC5L, CDH1, CDK1, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CDX2, CELSR2, CFLAR, CHD4, CHUK, CLU, CNBP, COMMD1, COMMD10, COMMD2, COPS2, COPS5, CREB1, CREBBP, CRK, CRTC2, CSNK2A1, CSNK2A2, CTBP1, CTNNB1, CUL2, CUL3, DAXX, DCC, DDIT3, DDX1, DDX17, DDX3X, DDX5, DEDD, DEDD2, DLG1, DLL1, DNAJA3,

										DNAJB1, DNAJC5, DNM2, DTX1, DUSP22, DYNLL1, E2F1, E2F3, EEF1A1, EEF1D, EGFR, EHMT2, EIF2AK2, EIF4A3, ELOC, ENO1, EP300, EPRS, ERBB2, ERBB4, ESF1, ESR1, EWSR1, EZH2, EZR, FADD, FANCA, FASLG, FBXW11, FBXW7, FGFR1, FLNA, FOS, FOXO3, FUS, GCN1, GFI1B, GPS2, GSK3B, GTF2F2, GTF3C1, H2AFX, H3F3A, HAX1, HCK, HDAC1, HDAC2, HDAC3, HIF1A, HINT1, HIPK3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HNRNPAB, HNRNPD, HNRNPDL, HNRNPUL1, HSPA1A, HSPA5, HSPA8, HSPD1, HSPH1, ID2, IKBKB, IKZF4, ILF2, ILF3, ING5, INSR, IRAK1, ISL2, ITCH, ITGB2, JAG1, JAK2, JARID2, JDP2, JUN, JUNB, JUND, KAT2B, KAT5, KDM2A, KDM3B, KDM5B, KHDRBS1, KHSRP, KIT, KLF4, KLF5, KLF6, KRT6B, LIN54, LMNA, LRPPRC, LYL1, MAF, MAML1, MAML3, MAP2K1, MAP2K3, MAP3K5, MAP3K7, MAPK1, MAPK10, MAPK13, MAPK14, MAPK3, MAPK8, MARS, MAX, MBD3, MDM2, MED13L, MED19, MED28, MED31, MEN1, MEPCE, MET, MOV10, MTA1, MTA2, MTOR, MYBBP1A, MYC, MYO1C, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NCOR1, NCOR2, NEDD4, NEDD8, NFKB1, NFKB2, NFKBIA, NFKBIB, NFKBIZ, NFX1, NIF3L1, NKRF, NKX2-1, NMI, NONO, NOTCH1, NOTCH2, NPM1, NR3C1, NR6A1, NRBF2, NUFIP1, NUP107, NUP62, PA2G4, PAG1, PARK7, PARP1, PBX2, PCBD1, PCBP1, PCNA, PDPK1, PELP1, PFDN1, PFN1, PHB, PHB2, PIAS2, PIAS3, PIK3R1, PIK3R2, PIN1, PLK1, PLSCR1, PML, POLR2A, POU2AF1, POU4F2, PPARG, PPM1F, PPP1R12A, PPP2CA, PPP2R1A, PRDX3, PRKAA1, PRKAA2, PRKAR1A, PRKCB, PRKCI, PRKD1, PRKN, PRMT5, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPRK, PUF60, RAF1, RALY, RAN, RB1CC1, RBBP4, RBBP7, RBCK1, RBFOX2, RBL1, RBM14, RBM39, RBMX, RBPJ, RBPMS, REL, RELA, RELB, RET, RHOXF2, RIPK2, RNMT, RPL15, RPL23, RPL6, RPS14, RPS27A, RPS3, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL1, RUVBL2, RYBP, S100A8, S100A9, SEMA4D, SET, SF1, SF3B3, SFPQ, SGK1, SHC1, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SMURF1, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SOX7, SP1, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT5B, STAT6, STK3, STRAP, SUMO1, SUMO2, SUZ12, SYK, TAB2, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFB2M, TFE3,

										TIAL1, TMPO, TNFRSF1A, TNIP1, TNIP2, TP53, TPR, TRADD, TRAF2, TRAF6, TRIM21, TRIM28, TRIP13, TRIP6, TRRAP, TSC22D1, TSC22D3, TSHZ3, TXN, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2I, UBE2L3, UBN1, UBR2, USP7, USP9X, VAV1, VDR, VHL, WASL, WBP2, WDR77, WWC3, WWP2, XPO1, XRCC5, XRCC6, XRN2, YAP1, YBX1, YWHAB, YWHAH, YWHAQ, YY1, ZBED1, ZBTB16, ZBTB47, ZNF326, ZNF512B, ZNF823, ZNFX1]
GO:0006366	transcription from RNA polymerase II promoter	22,0E-30	21,0E-27	4,6E-33	230,0E-33	[6, 7, 8, 9, 10]	Group46	13,47	297,00	[ABL1, ACTL6A, ACVR1B, AGO1, AGO2, AHRR, AIRE, AKAP8L, APP, AR, ARID1A, ARID3A, ARRB1, ARRB2, ATF2, ATF4, ATN1, ATXN7, BACH1, BCAS3, BCL3, BCL6, BRCA1, BRD4, C1QBP, CALCOCO1, CALR, CARM1, CCM2, CCNT1, CDC5L, CDK5RAP3, CDKN2A, CDX2, CHD4, CHUK, CNBP, COPS2, COPS5, CREB1, CREBBP, CRK, CRTC2, CTBP1, CTNNB1, CUL2, CUL3, DCC, DDIT3, DDX17, DDX21, DDX3X, DDX5, DLG1, DLL1, DNAJA3, DNAJB1, DNAJC5, DTX1, DUSP22, E2F1, E2F3, EGFR, EHMT2, EIF4A3, ELOC, ENO1, EP300, ERBB2, ESR1, EZH2, EZR, FADD, FASLG, FBXW7, FGFR1, FLNA, FOS, FOXO3, GCN1, GFI1B, GPS2, GSK3B, GTF2F2, HAX1, HDAC1, HDAC2, HDAC3, HIF1A, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HNRNPD, HSPA1A, HSPA5, HSPD1, HSPH1, ID2, IKBKB, IKZF4, JAG1, JARID2, JDP2, JUN, JUNB, JUND, KAT2B, KAT5, KDM5B, KIT, KLF4, KLF5, KLF6, KRT6B, LMNA, LYL1, MAF, MAML1, MAML3, MAPK14, MAPK3, MAX, MBD3, MDM2, MED13L, MED19, MED31, MEN1, MEPCE, MET, MTA2, MYC, MYO1C, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NCOR1, NCOR2, NEDD4, NEDD8, NFKB1, NFKB2, NFKBIA, NFKBIZ, NFX1, NKX2-1, NMI, NOTCH1, NOTCH2, NPM1, NR3C1, NR6A1, NRBF2, NUDT21, NUFIP1, PARK7, PARP1, PBX2, PCBP1, PELP1, PFN1, PHB, PIAS2, PIK3R1, PIK3R2, PIN1, PLK1, PLSCR1, PML, POLR2A, POU2AF1, POU4F2, PPARG, PPP1R12A, PRKAR1A, PRKCB, PRKD1, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAF1, RBBP7, RBL1, RBM14, RBMX, RBPJ, REL, RELA, RELB, RIPK2, RNMT, RPL15, RPL23, RPS14, RPS27A, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL1, RUVBL2, RYBP, SEMA4D, SF3B3, SFPQ, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SMURF1, SMURF2, SNAI3, SNCA, SNRPB, SNRPD3, SNRPF, SNRPG, SNW1, SORBS3, SP1, SQSTM1, SREBF1, SREBF2,

										SRSF3, SRSF7, STAT1, STAT3, STAT5B, STAT6, STRAP, SUMO1, SUMO2, SUZ12, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFE3, TIAL1, TNFRSF1A, TNIP1, TNIP2, TP53, TPR, TRAF6, TRIM28, TRIP13, TSC22D1, TSC22D3, TSHZ3, TXN, UBA52, UBE2D1, UBE2D2, UBE2I, UBN1, USP9X, VDR, VHL, WBP2, WDR77, WWC3, WWP2, XPO1, XRCC6, YAP1, YBX1, YY1, ZBED1, ZBTB16]
GO:0045892	negative regulation of transcription, DNA-templated	3,6E-24	3,4E-21	4,6E-33	230,0E-33	[5, 6, 7, 8, 9, 10, 11]	Group46	15,47	181,00	[AHRR, APP, AR, ARID1A, ATF2, ATN1, ATXN1, BACH1, BCL3, BCL6, BRCA1, BTRC, C1QBP, CALR, CCAR2, CDK5, CDK5R1, CDKN1B, CDKN2A, CDX2, CHD4, CNBP, COPS2, CREB1, CREBBP, CTBP1, CTNNB1, CUL3, DAXX, DDIT3, DDX5, DEDD, DEDD2, DLG1, DNAJA3, DNAJB1, DUSP22, E2F1, EHMT2, ENO1, EP300, EPRS, ESR1, EZH2, EZR, FASLG, FBXW11, FGFR1, FLNA, FOXO3, GFI1B, GPS2, H2AFX, H3F3A, HDAC1, HDAC2, HDAC3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HSPA1A, HSPA8, ID2, IKZF4, ILF3, JARID2, JDP2, JUN, JUNB, JUND, KAT5, KDM5B, KHDRBS1, KLF4, KLF5, MAF, MBD3, MDM2, MEN1, MEPCE, MTA2, MYBBP1A, MYC, NACA, NCK1, NCOR1, NCOR2, NEDD4, NFKB1, NFKB2, NFX1, NKRF, NKX2-1, NONO, NOTCH1, NR3C1, NR6A1, PA2G4, PARP1, PHB, PHB2, PLK1, PML, POU4F2, PPARG, PPM1F, PRKN, PSMC5, PTPRK, RBBP7, RBFOX2, RBL1, RBPJ, REL, RELA, RELB, RPL15, RPL23, RPS14, RPS27A, RUNX1, RYBP, SEMA4D, SET, SF3B3, SFPQ, SHC1, SIN3A, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCC2, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SOX7, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT6, STRAP, SUMO1, SUZ12, TBL1X, TCF7L1, TP53, TPR, TRAF6, TRIM28, TSC22D3, TSHZ3, TXN, UBA52, UBE2B, UBE2D1, UBE2I, UBR2, USP9X, VDR, VHL, WWC3, WWP2, XPO1, XRCC5, XRCC6, YBX1, YWHAB, YWHAQ, YY1, ZBTB16]
GO:0045893	positive regulation of transcription, DNA-templated	710,0E-30	670,0E-27	4,6E-33	230,0E-33	[5, 6, 7, 8, 9, 10, 11]	Group46	15,01	221,00	[ACVR1B, AGO1, AGO2, AIRE, AKAP8L, APP, AR, ARHGEF11, ARID1A, ARID1B, ARID3A, ARRB1, ATF2, ATF4, ATXN7, BACH1, BANP, BCAS3, BCL3, BRCA1, BRD4, BTRC, CALCOCO1, CAMKK2, CARM1, CCM2, CCNT1, CD4, CDH1, CDK5RAP3, CDKN2A, CDX2, CHUK, CNBP, COPS5, CREB1, CREBBP, CRTC2, CTNNB1, DDIT3, DDX17, DDX3X, DDX5, DLL1, DNAJC5, DNM2, E2F1, E2F3, EGFR, EIF4A3, ELOC, EP300, ERBB2, ERBB4, ESR1, EZH2, FADD, FBXW11, FBXW7, FOS, FOXO3, GCN1, GSK3B, GTF2F2, HAX1, HDAC1, HDAC2, HDAC3, HIF1A, HMGB1, HNF1A, HNRNPAB, HNRNPD, HSPA5, HSPH1, ID2, IKBKB, IKZF4,

										ILF2, ILF3, ING5, INSR, IRAK1, JAG1, JUN, JUNB, JUND, KAT2B, KAT5, KLF4, KLF5, KLF6, KRT6B, LMNA, LYL1, MAF, MAML1, MAML3, MAP2K1, MAP2K3, MAP3K5, MAPK1, MAPK14, MAPK3, MARS, MED19, MEN1, MET, MTA2, MTOR, MYC, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NFKB1, NFKB2, NFKBIA, NIF3L1, NKX2-1, NOTCH1, NPM1, NR3C1, NR6A1, NUFIP1, NUP62, PARK7, PARP1, PBX2, PCBD1, PCBP1, PELP1, PFN1, PHB, PIAS2, PIK3R1, PIK3R2, PIN1, PLSCR1, PML, POU2AF1, POU4F2, PPARG, PPP1R12A, PRKD1, PRKN, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, RAF1, RAN, RBL1, RBM14, RBMX, RBPJ, REL, RELA, RELB, RET, RIPK2, RNMT, RPL23, RPS27A, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL2, SFPQ, SHC1, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SNW1, SP1, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT5B, STAT6, SUMO1, SUMO2, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFB2M, TFE3, TNFRSF1A, TNIP1, TNIP2, TP53, TRAF6, TRIM28, UBA52, VDR, VHL, WBP2, WWP2, XRCC6, YAP1, YBX1, YWHAH, ZBTB16]
GO:1903507	negative regulation of nucleic acid-templated transcription	2,1E-24	2,0E-21	4,6E-33	230,0E-33	[6, 7, 8, 9, 10]	Group46	15,32	186,00	[AHRR, APP, AR, ARID1A, ATF2, ATN1, ATXN1, BACH1, BCL3, BCL6, BRCA1, BTRC, C1QBP, CALR, CCAR2, CDK5, CDK5R1, CDKN1B, CDKN2A, CDX2, CHD4, CNBP, COPS2, CREB1, CREBBP, CTBP1, CTNNB1, CUL3, DAXX, DDIT3, DDX5, DEDD, DEDD2, DLG1, DNAJA3, DNAJB1, DUSP22, E2F1, EHMT2, ENO1, EP300, EPRS, ESR1, EZH2, EZR, FASLG, FBXW11, FGFR1, FLNA, FOXO3, GFI1B, GPS2, H2AFX, H3F3A, HDAC1, HDAC2, HDAC3, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HSPA1A, HSPA8, ID2, IKZF4, ILF3, JARID2, JDP2, JUN, JUNB, JUND, KAT5, KDM5B, KHDRBS1, KLF4, KLF5, MAF, MBD3, MDM2, MEN1, MEPCE, MTA1, MTA2, MYBBP1A, MYC, NACA, NCK1, NCOR1, NCOR2, NEDD4, NFKB1, NFKB2, NFX1, NIF3L1, NKRF, NKX2-1, NONO, NOTCH1, NR3C1, NR6A1, PA2G4, PARP1, PHB, PHB2, PLK1, PML, POU4F2, PPARG, PPM1F, PRKN, PRMT5, PSMC5, PTPRK, RBBP7, RBFOX2, RBL1, RBPJ, REL, RELA, RELB, RPL15, RPL23, RPS14, RPS27A, RUNX1, RYBP, SEMA4D, SET, SF1, SF3B3, SFPQ, SHC1, SIN3A, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCC2, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SOX7, SQSTM1, SRC, SREBF1, SREBF2, STAT1, STAT3, STAT6, STRAP, SUMO1, SUZ12, TBL1X, TCF7L1, TP53, TPR, TRAF6, TRIM28, TSC22D3, TSHZ3,

										TXN, UBA52, UBE2B, UBE2D1, UBE2I, UBR2, USP9X, VDR, VHL, WWC3, WWP2, XPO1, XRCC5, XRCC6, YAP1, YBX1, YWHAB, YWHAQ, YY1, ZBTB16]
GO:0006357	regulation of transcription from RNA polymerase II promoter	25,0E-30	24,0E-27	4,6E-33	230,0E-33	[6, 7, 8, 9, 10, 11]	Group46	13,86	277,00	[ABL1, ACTL6A, ACVR1B, AGO1, AGO2, AHRR, AIRE, AKAP8L, APP, AR, ARID1A, ARID3A, ARRB1, ATF2, ATF4, ATN1, ATXN7, BACH1, BCAS3, BCL3, BCL6, BRCA1, BRD4, C1QBP, CALCOCO1, CALR, CARM1, CCM2, CCNT1, CDC5L, CDK5RAP3, CDKN2A, CDX2, CHD4, CHUK, CNBP, COPS2, COPS5, CREB1, CREBBP, CRK, CRTC2, CTBP1, CTNNB1, CUL2, CUL3, DCC, DDIT3, DDX17, DDX3X, DDX5, DLG1, DLL1, DNAJA3, DNAJB1, DNAJC5, DUSP22, E2F1, EGFR, EHMT2, EIF4A3, ELOC, ENO1, EP300, ERBB2, ESR1, EZH2, EZR, FADD, FASLG, FBXW7, FGFR1, FOS, FOXO3, GCN1, GFI1B, GPS2, GSK3B, GTF2F2, HAX1, HDAC1, HDAC2, HDAC3, HIF1A, HIRA, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HSPA1A, HSPA5, HSPD1, HSPH1, ID2, IKBKB, IKZF4, JAG1, JARID2, JDP2, JUN, JUNB, JUND, KAT2B, KAT5, KDM5B, KIT, KLF4, KLF5, KLF6, KRT6B, LMNA, LYL1, MAF, MAML1, MAML3, MAPK14, MAPK3, MAX, MBD3, MDM2, MED13L, MED19, MED31, MEN1, MEPCE, MET, MTA2, MYC, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NCOR1, NCOR2, NEDD4, NEDD8, NFKB1, NFKB2, NFKBIA, NFKBIZ, NFX1, NKX2-1, NOTCH1, NPM1, NR3C1, NR6A1, NUFIP1, PARK7, PARP1, PBX2, PCBP1, PELP1, PFN1, PHB, PIAS2, PIK3R1, PIK3R2, PIN1, PLK1, PLSCR1, PML, POU2AF1, POU4F2, PPARG, PPP1R12A, PRKAR1A, PRKCB, PRKD1, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAF1, RBBP7, RBL1, RBM14, RBMX, RBPJ, REL, RELA, RELB, RIPK2, RNMT, RPL15, RPL23, RPS14, RPS27A, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL1, RUVBL2, RYBP, SEMA4D, SF3B3, SFPQ, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SMURF1, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SP1, SQSTM1, SREBF1, SREBF2, STAT1, STAT3, STAT5B, STAT6, STRAP, SUMO1, SUMO2, SUZ12, TARDBP, TBK1, TBL1X, TCF7L1, TFAM, TFE3, TIAL1, TNFRSF1A, TNIP1, TNIP2, TP53, TPR, TRAF6, TRIM28, TSC22D3, TSHZ3, TXN, UBA52, UBE2D1, UBE2D2, UBE2I, UBN1, USP9X, VDR, VHL, WBP2, WDR77, WWC3, WWP2, XPO1, XRCC6, YAP1, YBX1, YY1, ZBED1, ZBTB16]

GO:0000122	negative regulation of transcription from RNA polymerase II promoter	2,6E-21	2,5E-18	4,6E-33	230,0E-33	[6, 7, 8, 9, 10, 11, 12]	Group46	16,79	136,00	[AHRR, APP, AR, ARID1A, ATF2, ATN1, BACH1, BCL6, C1QBP, CALR, CDX2, CHD4, CNBP, COPS2, CREBBP, CTBP1, CTNNB1, CUL3, DDIT3, DDX5, DLG1, DNAJA3, DNAJB1, DUSP22, E2F1, EHMT2, ENO1, EP300, ESR1, EZH2, EZR, FASLG, FGFR1, FOXO3, GFI1B, GPS2, HDAC1, HDAC2, HDAC3, HIST1H1C, HIST1H1D, HIST2H3A, HMGB1, HNF1A, HNRNPA2B1, HSPA1A, ID2, JARID2, JDP2, JUN, JUNB, JUND, KAT5, KLF4, KLF5, MAF, MBD3, MDM2, MEN1, MEPCE, MTA2, MYC, NACA, NCK1, NCOR1, NCOR2, NEDD4, NFKB1, NFKB2, NFX1, NKX2-1, NOTCH1, NR3C1, NR6A1, PARP1, PHB, PLK1, POU4F2, PPARG, PRKN, RBBP7, RBL1, RBPJ, REL, RELA, RELB, RPL15, RPL23, RPS14, RPS27A, RYBP, SEMA4D, SF3B3, SFPQ, SIN3A, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCC2, SMURF2, SNAI3, SNCA, SNW1, SORBS3, SQSTM1, SREBF1, SREBF2, STAT1, STAT3, STAT6, STRAP, SUMO1, SUZ12, TBL1X, TCF7L1, TP53, TPR, TRAF6, TRIM28, TSC22D3, TSHZ3, TXN, UBA52, UBE2D1, UBE2I, USP9X, VDR, VHL, WWC3, WWP2, XPO1, YBX1, YY1, ZBTB16]
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	1,8E-24	1,7E-21	4,6E-33	230,0E-33	[6, 7, 8, 9, 10, 11, 12]	Group46	15,69	179,00	[ACVR1B, AGO1, AGO2, AIRE, AKAP8L, APP, AR, ARID3A, ARRB1, ATF2, ATF4, ATXN7, BACH1, BCAS3, BCL3, BRCA1, BRD4, CALCOCO1, CARM1, CCM2, CCNT1, CDK5RAP3, CDKN2A, CHUK, CNBP, COPS5, CREB1, CREBBP, CRTC2, CTNNB1, DDIT3, DDX17, DDX3X, DDX5, DLL1, DNAJC5, E2F1, EGFR, EIF4A3, ELOC, EP300, ESR1, EZH2, FADD, FBXW7, FOS, FOXO3, GCN1, GSK3B, GTF2F2, HAX1, HDAC1, HDAC2, HDAC3, HIF1A, HMGB1, HNF1A, HSPA5, HSPH1, IKBKB, IKZF4, JAG1, JUN, JUNB, JUND, KAT2B, KAT5, KLF4, KLF5, KLF6, KRT6B, LMNA, MAF, MAML1, MAML3, MAPK14, MAPK3, MED19, MEN1, MET, MTA2, MYC, MYO6, MYT1, NACA, NCK1, NCL, NCOA1, NCOA6, NFKB1, NFKB2, NFKBIA, NKX2-1, NOTCH1, NPM1, NR3C1, NR6A1, NUFIP1, PARK7, PARP1, PBX2, PCBP1, PELP1, PFN1, PIAS2, PIK3R1, PIK3R2, PIN1, PLSCR1, PML, POU2AF1, POU4F2, PPARG, PPP1R12A, PRKD1, PRKN, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, RAF1, RBL1, RBM14, RBMX, RBPJ, REL, RELA, RELB, RIPK2, RNMT, RPL23, RPS27A, RPS6KA1, RPS6KA3, RPS6KA4, RUNX1, RUVBL2, SFPQ, SIN3A, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMARCA4, SMARCB1, SMARCC1, SNW1, SP1, SQSTM1, SREBF1, SREBF2, STAT1, STAT3, STAT5B, STAT6, SUMO1, SUMO2, TARDBP, TBK1, TBL1X, TCF7L1,

										TFAM, TFE3, TNFRSF1A, TNIP1, TNIP2, TP53, TRAF6, TRIM28, UBA52, VDR, WBP2, WWP2, XRCC6, YAP1, YBX1]
GO:0032204	regulation of telomere maintenance	10,0E-12	9,3E-9	5,9E-15	300,0E-15	[3, 4, 5, 6, 7, 8]	Group47	32,91	26,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPA2B1, HNRNPC, HNRNPD, HNRNPU, MAP3K4, MAPK1, MAPK3, MYC, PARP1, PML, SLX4, SRC, TCP1, TNIP1, USP7, XRCC5]
GO:0032206	positive regulation of telomere maintenance	2,9E-9	2,7E-6	5,9E-15	300,0E-15	[3, 4, 5, 6, 7, 8, 9]	Group47	33,93	19,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPA2B1, HNRNPD, MAP3K4, MAPK1, MAPK3, PML, SLX4, TCP1, TNIP1]
GO:0051054	positive regulation of DNA metabolic process	160,0E-15	150,0E-12	5,9E-15	300,0E-15	[4, 5, 6, 7, 8]	Group47	22,17	51,00	[ARHGEF7, ARRB2, ATR, BABAM1, BAX, BRCA1, CACYBP, CALR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CDC42, CDK1, CTNNB1, EGFR, FGFR1, H2AFX, HMGB1, HNRNPA1, HNRNPA2B1, HNRNPD, HSP90AA1, HSP90AB1, IGF1R, INSR, JUN, KLF4, MAP3K4, MAPK1, MAPK3, MYC, PCNA, PDGFRA, PDGFRB, PFN1, PML, PTK2B, RAC1, RPS3, SHC1, SLX4, SRC, STAT6, TCP1, TNIP1, TRIM28, UBE2B]
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	130,0E-9	120,0E-6	5,9E-15	300,0E-15	[3, 4, 5, 6, 7, 8, 9]	Group47	66,67	8,00	[CCT2, CCT4, CCT5, CCT6A, CCT7, CCT8, PML, TCP1]
GO:1904356	regulation of telomere maintenance via telomere lengthening	31,0E-12	29,0E-9	5,9E-15	300,0E-15	[4, 5, 6, 7, 8, 9]	Group47	36,67	22,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPA2B1, HNRNPC, HNRNPU, MAP3K4, MAPK1, MAPK3, PARP1, PML, SLX4, SRC, TCP1, TNIP1]
GO:2000278	regulation of DNA biosynthetic process	210,0E-15	190,0E-12	5,9E-15	300,0E-15	[5, 6, 7, 8]	Group47	30,56	33,00	[ARHGEF7, ARRB2, ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, DUSP1, HNRNPA1, HNRNPA2B1, HNRNPC, HNRNPD, HNRNPU, HSP90AA1, HSP90AB1, KLF4, MAP3K4, MAPK1, MAPK3, MEN1, MYC, PDGFRB, PML, PPARG, PTK2B, SRC, TCP1, TNIP1, TP53]
GO:0006278	RNA-dependent DNA biosynthetic process	7,2E-9	6,8E-6	5,9E-15	300,0E-15	[6, 7, 8]	Group47	28,57	22,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPC, HNRNPU, HSP90AA1, HSP90AB1, MAP3K4, MAPK1, MAPK3, PML, PPIA, PTEN, SRC, TCP1]
GO:0010833	telomere maintenance via telomere lengthening	390,0E-12	360,0E-9	5,9E-15	300,0E-15	[6, 7, 8]	Group47	30,38	24,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPA2B1, HNRNPC, HNRNPU, HSP90AA1, HSP90AB1, MAP3K4, MAPK1, MAPK3, PARP1, PML, SLX4, SRC, TCP1, TNIP1]
GO:0051972	regulation of telomerase activity	690,0E-12	640,0E-9	5,9E-15	300,0E-15	[5, 6, 7, 8, 9]	Group47	36,54	19,00	[CCT2, CCT4, CTNNB1, HNRNPA2B1, HNRNPD, HSP90AA1, HSP90AB1, KLF4, MAP3K4, MAPK1, MAPK3, MEN1, MYC, PML, PPARG, SRC, TCP1, TNIP1, TP53]
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	2,9E-9	2,7E-6	5,9E-15	300,0E-15	[4, 5, 6, 7, 8, 9, 10]	Group47	40,00	16,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPA2B1, MAP3K4, MAPK1, MAPK3, TCP1, TNIP1]

GO:2000573	positive regulation of DNA biosynthetic process	850,0E-15	800,0E-12	5,9E-15	300,0E-15	[5, 6, 7, 8, 9]	Group47	36,11	26,00	[ARHGEF7, ARRB2, ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPA2B1, HNRNPD, HSP90AA1, HSP90AB1, KLF4, MAP3K4, MAPK1, MAPK3, MYC, PDGFRB, PTK2B, SRC, TCP1, TNIP1]
GO:0032210	regulation of telomere maintenance via telomerase	1,7E-9	1,5E-6	5,9E-15	300,0E-15	[5, 6, 7, 8, 9, 10]	Group47	36,73	18,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPC, HNRNPU, MAP3K4, MAPK1, MAPK3, PML, SRC, TCP1]
GO:1904871	positive regulation of protein localization to Cajal body	340,0E-12	320,0E-9	5,9E-15	300,0E-15	[4, 5, 6, 7, 8, 9, 10, 11]	Group47	100,00	8,00	[CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, TCP1]
GO:0007004	telomere maintenance via telomerase	5,9E-9	5,6E-6	5,9E-15	300,0E-15	[7, 8, 9]	Group47	31,25	20,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, HNRNPC, HNRNPU, HSP90AA1, HSP90AB1, MAP3K4, MAPK1, MAPK3, PML, SRC, TCP1]
GO:0032212	positive regulation of telomere maintenance via telomerase	41,0E-9	38,0E-6	5,9E-15	300,0E-15	[5, 6, 7, 8, 9, 10, 11]	Group47	38,89	14,00	[ATR, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CTNNB1, HNRNPA1, MAP3K4, MAPK1, MAPK3, TCP1]
GO:0051973	positive regulation of telomerase activity	93,0E-9	87,0E-6	5,9E-15	300,0E-15	[6, 7, 8, 9, 10]	Group47	36,84	14,00	[CCT2, CCT4, CTNNB1, HNRNPA2B1, HNRNPD, HSP90AA1, HSP90AB1, KLF4, MAP3K4, MAPK1, MAPK3, MYC, TCP1, TNIP1]
GO:0006413	translational initiation	66,0E-39	61,0E-36	340,0E-45	17,0E-42	[3, 6, 7, 8]	Group48	38,35	79,00	[AGO2, ATF4, COPS5, DDX1, DDX3X, EIF1AX, EIF1B, EIF2AK2, EIF3I, EIF4A1, EIF6, FAU, HSPB1, KHDRBS1, NCK1, NPM1, PABPC1, PCBP2, PPP1CA, PTBP1, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS6KB1, RPS8, RPS9, RPSA, TPR, UBA52, YAE1D1]
GO:0006886	intracellular protein transport	900,0E-45	850,0E-42	340,0E-45	17,0E-42	[4, 5, 6, 7, 8]	Group48	18,49	225,00	[ACTL6A, ADAR, AKAP8L, ANXA2, ATG13, ATG3, ATG4B, ATG4C, BAG4, BARD1, BCAS3, BCL3, BCL6, BCR, CABP1, CACNA1A, CALR, CBLB, CDC37, CDC42, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CFL1, CLIP1, CLTC, CLTCL1, COPB1, COPB2, CSE1L, CSNK2A2, CTNNB1, CTTN, DYNC2LI1, DYNLL1, EGFR, EIF4A3, EIF5A, EIF6, ERBB2, ERBB4, FAU, FBXW11, FBXW7, FLNA, FYCO1, FYN, GABARAP, GGA1, GGA2, GGA3, GPN1, GSK3B, HAX1, HDAC3, HERC2, HERPUD1, HNRNPA2B1, HSP90AA1, HSP90AB1, HSP90B1, HSPA1L, HSPA4, HSPA8, HSPA9, HSPB1, HSPD1, IPO4, IPO5, ITGAX, JAK2, JAK3, JUN, KDELR1, KPNA2, KPNA3, KPNA4, KPNB1, LMNA, MAGI1, MAPK1, MAPK14, MAPK3, MDM2, MTOR, MYL12A, MYO1C, MYO6, NEDD4, NFKBIA, NFKBIE, NPM1, NSF,

										NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, NXF1, OAZ2, PAK1, PARK7, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PIN1, PML, POLA2, PPM1B, PRDX1, PRKCI, PRKD1, PRKN, PTPN1, PTPN11, RAC2, RAE1, RAN, RANBP2, RANGAP1, RBCK1, RBPMS, RHOA, RILPL2, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, RUVBL1, SFN, SH3GLB1, SLC25A6, SMAD3, SMAD4, SMURF1, SORL1, SPTBN1, SREBF1, SREBF2, SRP14, SRSF3, SRSF7, STAT3, SYK, TIMM50, TNPO1, TNPO2, TOM1L1, TP53, TPR, TRAF3IP1, TRIM28, TRIP6, TXN, UBA52, UBE2L3, UBR5, VCP, XPO1, XPO5, XPO6, XPOT, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ]
GO:0017038	protein import	37,0E-18	34,0E-15	340,0E-45	17,0E-42	[4, 5, 6, 7, 8]	Group48	20,86	73,00	[ADAR, BCL3, BCL6, CABP1, CBLB, CDH1, CDK1, CFL1, CLU, CTNNB1, EGFR, ERBB4, FBXW11, FLNA, GPN1, GSK3B, HDAC3, HSP90AA1, HSP90AB1, HSPA4, HSPA8, HSPD1, IPO4, IPO5, JAK2, JAK3, JUN, KPNA2, KPNA3, KPNA4, KPNB1, LMNA, MAPK1, MAPK14, MAPK3, MTOR, NFKBIA, NFKBIE, NUP107, NUP155, NUP62, NUP88, NUP93, NUP98, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PML, POLA2, PPM1B, PRDX1, PRKD1, RAN, RANBP2, RBCK1, RBPMS, RHOA, RPL23, SMAD3, SMAD4, SPTBN1, STAT3, SYK, TIMM50, TNPO1, TNPO2, TPR, TRIM28, TRIP6, TXN, UBR5]
GO:0019083	viral transcription	930,0E-45	870,0E-42	340,0E-45	17,0E-42	[4, 5, 6, 7, 8]	Group48	42,41	81,00	[CCNT1, EP300, FAU, GTF2F2, HDAC1, JUN, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, PFN1, POLR2A, PSMC3, RAE1, RANBP2, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, SMARCA4, SMARCB1, SNW1, SP1, TARDBP, TPR, TRIM21, UBA52]
GO:0006402	mRNA catabolic process	24,0E-27	23,0E-24	340,0E-45	17,0E-42	[5, 6, 7, 8]	Group48	29,83	71,00	[AGO1, AGO2, AGO4, DDX5, DDX6, EIF4A1, EIF4A3, FAU, HNRNPR, HSPA1A, KHSRP, PABPC1, PPP2CA, PPP2R1A,

										RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, TNRC6B, UBA52]
GO:1902593	single-organism nuclear import	6,7E-18	6,3E-15	340,0E-45	17,0E-42	[5, 6, 7, 8]	Group48	22,52	68,00	[ADAR, BCL3, BCL6, CABP1, CBLB, CDH1, CDK1, CFL1, CTNNB1, EGFR, ERBB4, FBXW11, FLNA, GPN1, GSK3B, HDAC3, HSP90AB1, IPO4, IPO5, JAK2, JAK3, JUN, KPNA2, KPNA3, KPNA4, KPNB1, LMNA, MAPK1, MAPK14, MAPK3, MTOR, NFKBIA, NFKBIE, NUP107, NUP155, NUP62, NUP88, NUP93, NUP98, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PML, POLA2, PPM1B, PRDX1, PRKAG1, PRKD1, RAN, RANBP2, RBCK1, RBPMS, RHOA, RPL23, SMAD3, SMAD4, SPTBN1, STAT3, SYK, TNPO1, TNPO2, TPR, TRIM28, TRIP6, TXN, UBR5]
GO:0006605	protein targeting	1,1E-45	1,0E-42	340,0E-45	17,0E-42	[5, 6, 7, 8, 9]	Group48	23,20	171,00	[ACTL6A, ADAR, ANXA2, ATG13, ATG3, ATG4B, ATG4C, BAG4, BCL3, BCL6, CABP1, CACNA1A, CBLB, CDC37, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CFL1, CSNK2A2, CTNNB1, EGFR, ERBB2, ERBB4, FAU, FBXW11, FBXW7, FLNA, FYN, GABARAP, GPN1, GSK3B, HAX1, HDAC3, HSP90AA1, HSP90AB1, HSPA1L, HSPA4, HSPA8, HSPD1, IPO4, IPO5, ITGAX, JAK2, JAK3, JUN, KPNA2, KPNA3, KPNA4, KPNB1, LMNA, MAGI1, MAPK1, MAPK14, MAPK3, MTOR, MYL12A, MYO1C, NEDD4, NFKBIA, NFKBIE, NUP107, NUP155, NUP62, NUP88, NUP93, NUP98, PAK1, PARP1, PDIA3, PHB2, PIK3R1, PIK3R2, PIN1, PML, POLA2, PPM1B, PRDX1, PRKCI, PRKD1, PRKN, RAC2, RAN, RANBP2, RBCK1, RBPMS, RHOA, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, RUVBL1, SH3GLB1, SLC25A6, SMAD3, SMAD4, SMURF1, SORL1, SPTBN1, SREBF1, SREBF2, SRP14, STAT3, SYK, TIMM50, TNPO1, TNPO2, TPR, TRIM28, TRIP6, TXN, UBA52, UBE2L3, UBR5, YWHAB, YWHAE, YWHAG, YWHAQ, YWHAZ]

GO:0016072	rRNA metabolic process	370,0E-27	340,0E-24	340,0E-45	17,0E-42	[6, 7, 8]	Group48	25,80	81,00	[CDKN2A, DDX21, DEDD, DEDD2, DNAJC5, EIF4A3, EIF6, FAU, GEMIN4, GTF3C1, IGF2BP3, MARS, MTOR, NCL, NEDD4, NOP58, PA2G4, PELP1, PIN4, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, RRP1B, SMARCA4, SMARCB1, TFB2M, TNIP1, UBA52, XRN2]
GO:0033157	regulation of intracellular protein transport	650,0E-18	600,0E-15	340,0E-45	17,0E-42	[5, 6, 7, 8, 9]	Group48	19,07	78,00	[ACTL6A, AKAP8L, ATG13, BAG4, BARD1, BCAS3, BCL3, CABP1, CACNA1A, CDC42, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CSNK2A2, EGFR, ERBB2, ERBB4, FBXW11, FBXW7, FLNA, FYCO1, FYN, GSK3B, HAX1, HDAC3, HSP90AB1, HSPA1L, IPO5, ITGAX, JAK2, MAGI1, MAPK1, MAPK14, MDM2, MTOR, MYO1C, NFKBIA, NFKBIE, NUP62, NUP93, OAZ2, PAK1, PARK7, PARP1, PIK3R1, PIK3R2, PIN1, PPM1B, PRDX1, PRKD1, PRKN, PTPN1, PTPN11, RAC2, RANGAP1, RBCK1, RBPMS, RHOA, RPL28, RUVBL1, SFN, SH3GLB1, SMAD3, SMAD4, SORL1, SREBF1, SREBF2, TP53, TPR, TRIM28, TRIP6, TXN, UBE2L3, UBR5, XPO1, YWHAE]
GO:0034470	ncRNA processing	360,0E-21	340,0E-18	340,0E-45	17,0E-42	[6, 7, 8]	Group48	20,43	85,00	[ADAR, AGO1, AGO2, AGO4, CDKN2A, DDX1, DDX21, EIF4A3, EIF6, FAM98B, FAU, GEMIN4, HNRNPA2B1, HSD17B10, IGF2BP3, NEDD4, NOP58, PA2G4, PELP1, PIN4, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, RRP1B, RTCB, SMAD1, SMAD2, SMAD3, TFB2M, TNIP1, TUT1, UBA52, XRN2]
GO:0006364	rRNA processing	64,0E-24	60,0E-21	340,0E-45	17,0E-42	[5, 7, 8, 9]	Group48	26,18	72,00	[CDKN2A, DDX21, EIF4A3, EIF6, FAU, GEMIN4, IGF2BP3, NEDD4, NOP58, PA2G4, PELP1, PIN4, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18,

										RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, RRP1B, TFB2M, TNIP1, UBA52, XRN2]
GO:0000956	nuclear-transcribed mRNA catabolic process	50,0E-27	47,0E-24	340,0E-45	17,0E-42	[6, 7, 8, 9]	Group48	31,02	67,00	[AGO1, AGO2, DDX5, DDX6, EIF4A1, EIF4A3, FAU, PABPC1, PPP2CA, PPP2R1A, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, TNRC6B, UBA52]
GO:0006612	protein targeting to membrane	750,0E-36	700,0E-33	340,0E-45	17,0E-42	[5, 6, 7, 8, 9, 10]	Group48	36,45	74,00	[ANXA2, ATG3, ATG4B, ATG4C, CACNA1A, CDK5, CDK5R1, ERBB2, FAU, FYN, MYL12A, MYO1C, NUP155, PAK1, PRKCI, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, SMURF1, SPTBN1, SRP14, UBA52]
GO:1903533	regulation of protein targeting	690,0E-15	640,0E-12	340,0E-45	17,0E-42	[6, 7, 8, 9, 10]	Group48	19,02	62,00	[ACTL6A, ATG13, BAG4, BCL3, CABP1, CACNA1A, CDH1, CDK1, CDK5, CDK5R1, CDKN2A, CSNK2A2, EGFR, ERBB2, ERBB4, FBXW11, FBXW7, FLNA, FYN, GSK3B, HAX1, HDAC3, HSP90AB1, HSPA1L, IPO5, ITGAX, JAK2, MAGI1, MAPK1, MAPK14, MTOR, MYO1C, NFKBIA, NFKBIE, NUP62, NUP93, PAK1, PARP1, PIK3R1, PIK3R2, PIN1, PPM1B, PRDX1, PRKD1, PRKN, RAC2, RBCK1, RBPMS, RHOA, RPL28, RUVBL1, SH3GLB1, SMAD3, SMAD4, SREBF1, SREBF2, TPR, TRIM28, TRIP6, TXN, UBE2L3, UBR5]
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	7,1E-36	6,7E-33	340,0E-45	17,0E-42	[7, 8, 9, 10]	Group48	47,29	61,00	[EIF4A3, FAU, PABPC1, PPP2CA, PPP2R1A, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, UBA52]

GO:0006614	SRP-dependent cotranslational protein targeting to membrane	200,0E-42	190,0E-39	340,0E-45	17,0E-42	[7, 8, 9, 10, 11, 12]	Group48	57,43	58,00	[FAU, RPL10A, RPL11, RPL13, RPL14, RPL15, RPL18, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL27, RPL27A, RPL28, RPL3, RPL30, RPL31, RPL35, RPL35A, RPL36, RPL38, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPLP0, RPLP1, RPLP2, RPS10, RPS11, RPS13, RPS14, RPS15A, RPS16, RPS18, RPS19, RPS2, RPS20, RPS21, RPS23, RPS24, RPS25, RPS27A, RPS3, RPS3A, RPS4X, RPS5, RPS6, RPS8, RPS9, RPSA, SRP14, UBA52]
GO:0000187	activation of MAPK activity	84,0E-12	79,0E-9	50,0E-63	2,5E-60	[7, 8, 9, 10, 11, 12, 13]	Group49	23,13	37,00	[ALK, APP, ARHGEF7, ARRB1, CDK1, DAXX, DBNL, ETFA, FRS2, GAB1, GHR, HACD3, INSR, IRAK1, KIT, MAP2K1, MAP2K3, MAP3K5, MAP3K7, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, PEA15, PRKAA1, PTPN1, PTPN11, RIPK2, RPS27A, SHC1, SOD1, SPAG9, SYK, TAB2, TRAF6, UBA52]
GO:0023014	signal transduction by protein phosphorylation	890,0E-39	830,0E-36	50,0E-63	2,5E-60	[3, 4, 5, 7, 8]	Group49	19,07	185,00	[ABL1, ACVR1B, ALK, APP, AR, ARHGEF7, ARRB1, ARRB2, BTRC, CALM1, CAMK2A, CAMK2G, CAMKK2, CCM2, CCR5, CD4, CDC42, CDK1, CDK5RAP3, CFLAR, CHUK, COPS5, CRK, CRKL, CSF2RA, CSK, CTNNB1, CUL1, CUL3, DAXX, DBNL, DLG1, DLG4, DNAJA1, DUSP1, DUSP22, EGFR, EIF2AK2, EIF6, EPHB1, EPRS, ERBB2, ERBB3, ERBB4, ETFA, EZH2, EZR, FASN, FBXW11, FBXW7, FGFR1, FRS2, FYN, GAB1, GHR, GNAI2, GPS2, GRB2, HACD3, HDAC3, HIPK3, HMGB1, HSPH1, IGF1R, IKBKB, INSR, IQGAP1, IRAK1, ITCH, JAK1, JAK2, JAK3, JUN, KBTBD7, KIT, KLF4, LAT, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAP4K4, MAPK1, MAPK10, MAPK13, MAPK14, MAPK3, MAPK8, MEN1, MET, MIF, MYC, NCOR1, NFKB1, NUP62, PAK1, PAK2, PAK4, PDGFRA, PDGFRB, PEA15, PEBP1, PELI2, PHB, PHB2, PIK3CG, PIN1, PLCG1, POU4F2, PPP2CA, PPP2R1A, PRDX1, PRKAA1, PRKCE, PRKN, PRMT1, PRMT5, PSAP, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPN6, PTPRJ, RAF1, RAPGEF1, RASA1, RASSF2, RB1CC1, RET, RIPK2, RNMT, RPS27A, RPS3, S100A7, S100A8, S100A9, SHC1, SKP1, SMAD1, SMAD4, SOD1, SORBS3, SORL1, SPAG9, SPTA1, SPTAN1, SPTBN1, SRC, STK3, STK4, STK40, SYK, TAB2, TNIP1, TNIP2, TPD52L1, TPR, TRAF2, TRAF6, UBA52, VRK2, YWHAB, YWHAE]
GO:0000165	MAPK cascade	640,0E-39	600,0E-36	50,0E-63	2,5E-60	[4, 5, 6, 8, 9]	Group49	19,38	181,00	[ABL1, ALK, APP, AR, ARHGEF7, ARRB1, ARRB2, BTRC, CALM1, CAMK2A, CAMK2G, CAMKK2, CCM2, CCR5, CD4,

										CDC42, CDK1, CDK5RAP3, CFLAR, CHUK, COPS5, CRK, CRKL, CSF2RA, CSK, CTNNB1, CUL1, CUL3, DAXX, DBNL, DLG1, DLG4, DNAJA1, DUSP1, DUSP22, EGFR, EIF2AK2, EIF6, EPHB1, EPRS, ERBB2, ERBB3, ERBB4, ETFA, EZH2, EZR, FASN, FBXW11, FBXW7, FGFR1, FRS2, FYN, GAB1, GHR, GNAI2, GPS2, GRB2, HACD3, HDAC3, HIPK3, HMGB1, HSPH1, IGF1R, IKBKB, INSR, IQGAP1, IRAK1, ITCH, JAK1, JAK2, JAK3, JUN, KBTBD7, KIT, KLF4, LAT, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAP4K4, MAPK1, MAPK10, MAPK13, MAPK14, MAPK3, MAPK8, MEN1, MET, MIF, MYC, NCOR1, NFKB1, NUP62, PAK1, PDGFRA, PDGFRB, PEA15, PEBP1, PELI2, PHB, PHB2, PIK3CG, PIN1, PLCG1, POU4F2, PPP2CA, PPP2R1A, PRDX1, PRKAA1, PRKCE, PRKN, PRMT1, PRMT5, PSAP, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPN6, PTPRJ, RAF1, RAPGEF1, RASA1, RASSF2, RB1CC1, RET, RIPK2, RNMT, RPS27A, RPS3, S100A7, S100A8, S100A9, SHC1, SKP1, SMAD1, SMAD4, SOD1, SORBS3, SORL1, SPAG9, SPTA1, SPTAN1, SPTBN1, SRC, STK3, STK40, SYK, TAB2, TNIP1, TNIP2, TPD52L1, TPR, TRAF2, TRAF6, UBA52, VRK2, YWHAB, YWHAE]
GO:0031400	negative regulation of protein modification process	18,0E-30	17,0E-27	50,0E-63	2,5E-60	[5, 6, 7, 8]	Group49	20,84	129,00	[ABL1, ADAR, ANAPC7, APC, ARRB1, ARRB2, ATG14, ATG5, BAG5, BAX, BRCA1, CALM1, CASP3, CBL, CBLB, CDC20, CDK1, CDK5, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, CTBP1, CTDSP2, CTNNB1, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, EIF6, EPRS, EZR, FYN, GPS2, HDAC2, HDAC3, HIPK3, HSPA1A, HSPB1, HSPH1, IGF1R, IKBKB, ITCH, JARID2, JUN, KAT2B, KLF4, LRRK1, MAD2L1, MEN1, MICAL1, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, PAK2, PARK7, PDPK1, PHB, PIAS3, PIN1, PLK1, PML, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAG2, PRKAR1A, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, RAPGEF1, RASSF2, RPL11, RPL23, RPL5, RPS27A, RPS3, SEMA4D, SET, SFN, SIN3A, SMAD4, SMAD7, SMARCB1, SNCA, SOCS1, SOCS3, SORL1, STRAP, SUMO1, TARDBP, TNIP1, TRAF3IP1, TRIM21, UBA52, UBASH3B, UBE2B, UBE2D1, UBR5, UBXN1, YWHAB, YWHAE, YWHAG]

GO:0031401	positive regulation of protein modification process	3,6E-42	3,4E-39	50,0E-63	2,5E-60	[5, 6, 7, 8]	Group49	18,34	225,00	[ABI1, ABL1, ACVR1B, AKAP8L, AKTIP, ALK, ANAPC7, ANXA2, APP, AR, ARHGEF7, ARRB1, ARRB2, ATG10, ATG14, ATG7, BAG4, BAX, BCL6, BRCA1, BTRC, C3, CALM1, CAMKK1, CAMKK2, CCM2, CCNT1, CD4, CDC20, CDC42, CDK1, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CFLAR, CLU, CNTN1, COMMD1, CRK, CRKL, CSK, CTBP1, CTNNB1, CUL1, DAXX, DBNL, DLG1, DNAJA3, DUSP22, DYNLL1, EGFR, EIF2AK2, ERBB2, ERBB3, ERBB4, ETFA, EZH2, FANCI, FASN, FBXW7, FGFR1, FRS2, FYN, GAB1, GHR, GNAI2, GSK3B, HACD3, HAX1, HDAC2, HDAC3, HMGB1, HSP90AB1, HSPA5, HSPH1, INSR, IQGAP1, IRAK1, JAK2, JARID2, JDP2, JUN, KAT5, KIT, LAT, LCP2, LRRK1, MAD2L1, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MIF, MLST8, MTA1, MTOR, MYO1C, NAP1L2, NMI, OPRL1, PAK1, PAK2, PARK7, PDGFRA, PDGFRB, PDPK1, PEA15, PELI2, PHB, PHB2, PIAS3, PIK3CA, PIK3CG, PIN1, PLAUR, PLCG1, PLK1, PML, PPP1R12A, PPP2CA, PRKAA1, PRKAG1, PRKAG2, PRKAR1A, PRKCE, PRKD1, PRKN, PRMT1, PSAP, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPRC, RAC1, RACK1, RAF1, RAPGEF1, RASSF1, RASSF2, RB1CC1, RBPMS, RET, RHOA, RIPK2, RPLP1, RPS27A, RPS3, RPS6KA4, RUVBL2, S100A7, S100A8, S100A9, SEMA4D, SHC1, SKP1, SMAD4, SMAD7, SMARCB1, SMURF1, SNCA, SNW1, SOCS1, SOCS3, SOD1, SORBS3, SPAG9, SQSTM1, SRC, SREBF1, STAT3, STK11, STK3, STK4, STUB1, SUMO1, SYK, TAB2, TBK1, TNFRSF1A, TNK2, TOLLIP, TOM1L1, TP53, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UBE2D1, UBE2I, UBE2L3, UNC119, VCP, VTN, WBP2, XRCC5, XRCC6]
GO:0043549	regulation of kinase activity	7,5E-39	7,0E-36	50,0E-63	2,5E-60	[5, 7, 8]	Group49	20,44	175,00	[ABI1, ABL1, ADAR, ALK, AMBRA1, APC, APP, ARHGEF7, ARRB1, ATG14, BAX, CALM1, CAMKK1, CAMKK2, CASP3, CBL, CBLB, CCNT1, CD4, CDC37, CDC42, CDK1, CDK4, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CLU, CORO1C, CRK, CRKL, CSK, DAXX, DBNL, DLG1, DNAJA1, DNAJA3, DUSP1, DUSP22, EEF1A2, EGFR, EIF2AK2, EPRS, ERBB2, ERBB3, ERBB4, ETFA, EZH2, FBXW7, FGFR1, FGR, FRS2, GAB1, GCN1, GHR, GNAI2, GPS2, HACD3, HIPK3, HSP90AB1, HSPA5, HSPB1, HSPH1, IGF1R, INSR, IQGAP1, IRAK1, JAK2, KAT2B, KIT, KLF4, LAT, LCP2, MAP2K1,

										MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MAPT, MEN1, MIF, MLST8, MTOR, NCK1, NPM1, NRBF2, NUP62, PAK1, PAK2, PARK7, PDGFRA, PDGFRB, PDPK1, PEA15, PFKFB2, PIK3CA, PIK3CG, PIK3R1, PIK3R2, PIK3R3, PLCG1, PLK1, PPM1F, PPP2CA, PPP2R1A, PRDX3, PREX1, PRKAA1, PRKAB1, PRKAB2, PRKAG1, PRKAG2, PRKAR1A, PRKD1, PRKN, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPN6, PTPRC, PTPRJ, RAC1, RAC2, RACK1, RAF1, RAPGEF1, RASSF2, RBL1, RHOA, RIPK2, RPLP1, RPS27A, RPS3, S100A8, S100A9, SFN, SH3GLB1, SHC1, SNCA, SOCS1, SOCS3, SOD1, SORL1, SPAG9, SRC, STK11, STK3, STK4, SYK, TAB2, TOM1L1, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UBASH3B, UNC119, UVRAG, VAV2, XRCC5, XRCC6, YWHAG]
GO:0001932	regulation of protein phosphorylation	140,0E-39	130,0E-36	50,0E-63	2,5E-60	[6, 7, 8]	Group49	16,90	234,00	[ABI1, ABL1, ACVR1B, ADAR, AKAP8L, AKTIP, ALK, ANXA2, APC, APP, AR, ARHGEF7, ARRB1, ARRB2, ATG14, BAG4, BAX, BRD4, C3, CALM1, CAMKK1, CAMKK2, CASP3, CBL, CBLB, CCM2, CCNT1, CD4, CDC37, CDC42, CDK1, CDK4, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CFLAR, CLU, CNTN1, COPS5, CORO1C, CRK, CRKL, CSK, CTDSP2, CTNNB1, DAXX, DBNL, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, EGFR, EIF2AK2, EIF6, EPHB1, EPRS, ERBB2, ERBB3, ERBB4, ETFA, EZH2, EZR, FASN, FBXW7, FGFR1, FGR, FRS2, FYN, GAB1, GCN1, GHR, GNAI2, GPS2, GRB2, GSK3B, HACD3, HAX1, HDAC2, HDAC3, HIPK3, HMGB1, HSP90AB1, HSPA5, HSPB1, HSPH1, IGF1R, INSR, IQGAP1, IRAK1, ITCH, ITGB2, JAK2, JUN, KAT2B, KIT, KLF4, LAT, LCP2, LRRK1, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAP4K4, MAPK1, MAPK10, MAPK14, MAPK3, MEN1, MICAL1, MIF, MLST8, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, OPRL1, PAK1, PAK2, PARK7, PDGFRA, PDGFRB, PDPK1, PEA15, PELI2, PHB, PHB2, PIK3CA, PIK3CG, PIN1, PLAUR, PLCG1, PLK1, PML, PPM1F, PPP2CA, PPP2R1A, PRDX1, PREX1, PRKAA1, PRKAB1, PRKAB2, PRKAG1, PRKAG2, PRKAR1A, PRKCE, PRKD1, PRKN, PRMT1, PRMT5, PSAP, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPN6, PTPRC, PTPRJ, RAC1, RAC2, RACK1, RAF1, RAPGEF1, RASSF2, RB1CC1, RBPMS, RET, RHOA, RIPK2, RPLP1, RPS27A, RPS3, RPS6KA4, S100A7, S100A8, S100A9, SEMA4D, SFN, SHC1, SMAD4, SMAD7, SNCA,

										SOCS1, SOCS3, SOD1, SORBS3, SORL1, SPAG9, SQSTM1, SRC, STAT3, STK11, STK3, STK4, STK40, STRAP, SUMO1, SYK, TAB2, TARDBP, TBK1, TNFRSF1A, TNIP1, TNK2, TOM1L1, TP53, TPD52L1, TRAF2, TRAF3IP1, TRAF6, TXN, UBA52, UBASH3B, UBE2B, UNC119, UVRAG, VRK2, VTN, XRCC5, XRCC6, YWHAG]
GO:0042326	negative regulation of phosphorylation	11,0E-18	10,0E-15	50,0E-63	2,5E-60	[6, 7, 8]	Group49	19,12	87,00	[ABL1, ADAR, APC, ARRB1, ARRB2, ATG14, ATXN7, BAX, CALM1, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, CTDSP2, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, DYNLL1, EIF6, EPRS, EZR, GPS2, GRB10, HDAC3, HIPK3, HSPB1, HSPH1, IGF1R, ITCH, JUN, KAT2B, KLF4, LRRK1, MAPT, MEN1, MICAL1, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, PAK2, PARK7, PDPK1, PHB, PIN1, PLK1, PPM1F, PPP2CA, PPP2R1A, PRDX3, PREX1, PRKAG2, PRKAR1A, PRKN, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, RAPGEF1, RASSF2, SEMA4D, SFN, SMAD4, SMAD7, SNCA, SOCS1, SOCS3, SORL1, STAT3, STRAP, TARDBP, TNIP1, TRAF3IP1, UBASH3B, UBE2B, YWHAG]
GO:0042327	positive regulation of phosphorylation	1,2E-33	1,2E-30	50,0E-63	2,5E-60	[6, 7, 8]	Group49	18,26	183,00	[ABI1, ABL1, ACVR1B, AKTIP, ALK, AMBRA1, ANXA2, APP, AR, ARHGEF7, ARRB1, ARRB2, ATG14, BAG4, BAX, BTBD10, C3, CALM1, CAMKK1, CAMKK2, CCM2, CCNT1, CD4, CDC42, CDK1, CDK5, CDK5R1, CDKN1B, CFLAR, CLU, CNTN1, CRK, CRKL, CSK, CTNNB1, DAXX, DBNL, DLG1, DUSP22, EEF1A2, EGFR, EIF2AK2, ERBB2, ERBB3, ERBB4, ETFA, EZH2, FASN, FBXW7, FGFR1, FGR, FRS2, FYN, GAB1, GCN1, GHR, GNAI2, GRB10, GSK3B, HACD3, HAX1, HDAC2, HDAC3, HIF1A, HMGB1, HSP90AB1, HSPA5, HSPH1, INSR, IQGAP1, IRAK1, ITSN1, JAK2, JUN, KIT, LAT, LCP2, LRRK1, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MAPT, MIF, MLST8, MTOR, MYC, OPRL1, PAK1, PAK2, PARK7, PDGFRA, PDGFRB, PDPK1, PEA15, PELI2, PFKFB2, PHB, PHB2, PIK3CA, PIK3CG, PIN1, PLAUR, PLCG1, PLK1, PPP2CA, PRKAA1, PRKAA2, PRKAG1, PRKAG2, PRKAR1A, PRKCE, PRKD1, PRMT1, PSAP, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPRC, RAC1, RACK1, RAF1, RAPGEF1, RASSF2, RB1CC1, RBPMS, RET, RHOA, RIPK2, RPLP1, RPS27A, RPS3, RPS6KA4, S100A7, S100A8, S100A9, SEMA4D, SH3GLB1, SHC1, SMAD4, SNCA, SOCS1, SOCS3, SOD1, SORBS3, SPAG9, SQSTM1, SRC, STAT3, STK11, STK3, STK4, SUMO1, SYK, TAB2, TBK1, TNFRSF1A, TNK2, TOM1L1,

										TP53, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UNC119, VAV2, VCP, VTN, XRCC5, XRCC6]
GO:0051403	stress-activated MAPK cascade	2,2E-21	2,0E-18	50,0E-63	2,5E-60	[5, 6, 7, 9, 10]	Group49	25,56	69,00	[BTRC, CCM2, CDC42, CHUK, COPS5, CRKL, CUL1, DAXX, DBNL, DLG1, DNAJA1, DUSP22, EGFR, EIF2AK2, EPHB1, EPRS, EZR, FASN, FBXW11, GAB1, GPS2, HACD3, HDAC3, HIPK3, HMGB1, HSPH1, IGF1R, IKBKB, IRAK1, ITCH, MAP2K1, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAP4K4, MAPK1, MAPK10, MAPK14, MAPK3, MAPK8, MEN1, MYC, NCOR1, NFKB1, PAK1, PRDX1, PRKN, PRMT1, PTK2B, PTPN1, RAPGEF1, RASSF2, RB1CC1, RIPK2, RPS27A, RPS3, SKP1, SPAG9, STK3, SYK, TAB2, TNIP2, TPD52L1, TRAF2, TRAF6, UBA52]
GO:0070371	ERK1 and ERK2 cascade	210,0E-9	190,0E-6	50,0E-63	2,5E-60	[5, 6, 7, 9, 10]	Group49	15,88	47,00	[ABL1, APP, ARRB1, ARRB2, CD4, CFLAR, CSK, DLG1, DUSP1, EGFR, EIF6, EPHB1, ERBB2, ERBB4, EZR, FBXW7, FRS2, HMGB1, JUN, KLF4, MAP2K1, MAPK1, MAPK3, MIF, MYC, PDGFRA, PDGFRB, PHB, PHB2, PIN1, PRMT5, PTEN, PTK2B, PTPN1, PTPN11, PTPN6, RAF1, RAPGEF1, RIPK2, S100A7, S100A8, S100A9, SHC1, SMAD4, SRC, SYK, TNIP1]
GO:0001933	negative regulation of protein phosphorylation	50,0E-18	47,0E-15	50,0E-63	2,5E-60	[6, 7, 8, 9]	Group49	19,47	81,00	[ABL1, ADAR, APC, ARRB1, ARRB2, ATG14, BAX, CALM1, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, CTDSP2, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, EIF6, EPRS, EZR, GPS2, HDAC3, HIPK3, HSPB1, HSPH1, IGF1R, ITCH, JUN, KAT2B, KLF4, LRRK1, MEN1, MICAL1, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, PAK2, PARK7, PDPK1, PHB, PIN1, PLK1, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAG2, PRKAR1A, PRKN, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, RAPGEF1, RASSF2, SEMA4D, SFN, SMAD4, SMAD7, SNCA, SOCS1, SOCS3, SORL1, STRAP, TARDBP, TNIP1, TRAF3IP1, UBASH3B, UBE2B, YWHAG]
GO:0001934	positive regulation of protein phosphorylation	110,0E-30	100,0E-27	50,0E-63	2,5E-60	[6, 7, 8, 9]	Group49	17,57	168,00	[ABI1, ABL1, ACVR1B, AKTIP, ALK, ANXA2, APP, AR, ARHGEF7, ARRB1, ARRB2, ATG14, BAG4, BAX, C3, CALM1, CAMKK1, CAMKK2, CCM2, CCNT1, CD4, CDC42, CDK1, CDK5, CDK5R1, CDKN1B, CFLAR, CLU, CNTN1, CRK, CRKL, CSK, CTNNB1, DAXX, DBNL, DLG1, DUSP22, EGFR, EIF2AK2, ERBB2, ERBB3, ERBB4, ETFA, EZH2, FASN, FBXW7, FGFR1, FRS2, FYN, GAB1, GHR, GNAI2, GSK3B, HACD3, HAX1, HDAC2, HDAC3, HMGB1, HSP90AB1, HSPA5, HSPH1, INSR, IQGAP1, IRAK1, JAK2, JUN, KIT, LAT, LCP2, LRRK1, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MIF, MLST8, MTOR, OPRL1, PAK1, PAK2, PARK7, PDGFRA,

										PDGFRB, PDPK1, PEA15, PELI2, PHB, PHB2, PIK3CA, PIK3CG, PIN1, PLAUR, PLCG1, PLK1, PPP2CA, PRKAA1, PRKAG1, PRKAG2, PRKAR1A, PRKCE, PRKD1, PRMT1, PSAP, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPRC, RAC1, RACK1, RAF1, RAPGEF1, RASSF2, RB1CC1, RBPMS, RET, RHOA, RIPK2, RPLP1, RPS27A, RPS3, RPS6KA4, S100A7, S100A8, S100A9, SEMA4D, SHC1, SMAD4, SNCA, SOCS1, SOCS3, SOD1, SORBS3, SPAG9, SQSTM1, SRC, STAT3, STK11, STK3, STK4, SUMO1, SYK, TAB2, TBK1, TNFRSF1A, TNK2, TOM1L1, TP53, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UNC119, VTN, XRCC5, XRCC6]
GO:0033673	negative regulation of kinase activity	380,0E-12	350,0E-9	50,0E-63	2,5E-60	[6, 7, 8, 9]	Group49	18,38	50,00	[ABL1, ADAR, APC, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, DNAJA1, DNAJA3, DUSP1, DUSP22, EPRS, GPS2, HIPK3, HSPB1, IGF1R, KAT2B, MAPT, MEN1, NCK1, NPM1, NUP62, PAK2, PARK7, PDPK1, PLK1, PPM1F, PPP2CA, PPP2R1A, PRDX3, PREX1, PRKAG2, PRKAR1A, PRKN, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, SFN, SOCS1, SOCS3, SORL1, UBASH3B, YWHAG]
GO:0033674	positive regulation of kinase activity	110,0E-33	100,0E-30	50,0E-63	2,5E-60	[6, 7, 8, 9]	Group49	22,36	125,00	[ABI1, ABL1, ALK, AMBRA1, APP, ARHGEF7, ARRB1, ATG14, BAX, CALM1, CAMKK1, CAMKK2, CCNT1, CD4, CDC42, CDK1, CDK5, CDK5R1, CDKN1B, CLU, CRK, CRKL, CSK, DAXX, DBNL, DLG1, EEF1A2, EGFR, EIF2AK2, ERBB2, ERBB3, ERBB4, ETFA, EZH2, FBXW7, FGFR1, FGR, FRS2, GAB1, GCN1, GHR, GNAI2, HACD3, HSP90AB1, HSPA5, HSPH1, INSR, IQGAP1, IRAK1, JAK2, KIT, LAT, LCP2, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MAPT, MIF, MLST8, PAK1, PAK2, PARK7, PDGFRA, PDGFRB, PDPK1, PEA15, PFKFB2, PIK3CA, PIK3CG, PLCG1, PPP2CA, PRKAA1, PRKAG1, PRKAG2, PRKAR1A, PRKD1, PTK2, PTK2B, PTPN1, PTPN11, PTPRC, RAC1, RAF1, RAPGEF1, RASSF2, RHOA, RIPK2, RPLP1, RPS27A, RPS3, S100A8, S100A9, SH3GLB1, SHC1, SNCA, SOCS1, SOD1, SPAG9, SRC, STK11, STK3, STK4, SYK, TAB2, TOM1L1, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UNC119, VAV2, XRCC5, XRCC6]
GO:0043408	regulation of MAPK cascade	56,0E-24	52,0E-21	50,0E-63	2,5E-60	[5, 6, 7, 8, 9, 10]	Group49	17,89	129,00	[ABL1, ALK, APP, AR, ARHGEF7, ARRB1, ARRB2, CCM2, CD4, CDC42, CDK1, CDK5RAP3, CFLAR, COPS5, CRK, CRKL, CSK, CTNNB1, DAXX, DBNL, DLG1, DNAJA1, DUSP1, DUSP22, EGFR, EIF2AK2, EIF6, EPHB1, EPRS, ERBB2, ERBB4, ETFA, EZH2, EZR, FASN, FBXW7, FGFR1, FRS2, GAB1, GHR, GNAI2, GPS2, GRB2, HACD3, HDAC3, HIPK3,

										HMGB1, HSPH1, IGF1R, INSR, IQGAP1, IRAK1, ITCH, JAK2, JUN, KIT, KLF4, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAP4K4, MAPK1, MAPK10, MAPK14, MAPK3, MEN1, MIF, MYC, NCOR1, NUP62, PAK1, PDGFRA, PDGFRB, PEA15, PELI2, PHB, PHB2, PIK3CG, PIN1, PLCG1, PPP2CA, PPP2R1A, PRDX1, PRKAA1, PRKCE, PRKN, PRMT1, PRMT5, PSAP, PTEN, PTK2B, PTPN1, PTPN11, PTPN6, PTPRJ, RAF1, RAPGEF1, RASSF2, RB1CC1, RIPK2, RPS27A, RPS3, S100A7, S100A8, S100A9, SHC1, SMAD4, SOD1, SORBS3, SORL1, SPAG9, SRC, STK3, STK40, SYK, TAB2, TNIP1, TPD52L1, TRAF2, TRAF6, UBA52, VRK2]
GO:0045859	regulation of protein kinase activity	11,0E-33	10,0E-30	50,0E-63	2,5E-60	[6, 7, 8, 9]	Group49	19,72	156,00	[ABI1, ABL1, ADAR, ALK, APC, APP, ARHGEF7, ARRB1, BAX, CALM1, CAMKK1, CAMKK2, CASP3, CBL, CBLB, CCNT1, CD4, CDC37, CDC42, CDK1, CDK4, CDK5, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CLU, CORO1C, CRK, CRKL, CSK, DAXX, DBNL, DLG1, DNAJA1, DNAJA3, DUSP1, DUSP22, EGFR, EIF2AK2, EPRS, ERBB2, ERBB3, ETFA, EZH2, FBXW7, FGFR1, FGR, FRS2, GAB1, GCN1, GHR, GNAI2, GPS2, HACD3, HIPK3, HSP90AB1, HSPA5, HSPB1, HSPH1, IGF1R, INSR, IQGAP1, IRAK1, JAK2, KAT2B, KIT, LAT, LCP2, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MEN1, MIF, MLST8, MTOR, NCK1, NPM1, NUP62, PAK1, PAK2, PARK7, PDGFRB, PDPK1, PEA15, PIK3CA, PIK3CG, PLCG1, PLK1, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAA1, PRKAB1, PRKAB2, PRKAG1, PRKAG2, PRKAR1A, PTEN, PTK2, PTK2B, PTPN1, PTPN11, PTPN6, PTPRC, PTPRJ, RAC2, RACK1, RAF1, RAPGEF1, RASSF2, RHOA, RIPK2, RPLP1, RPS27A, RPS3, S100A8, S100A9, SFN, SHC1, SNCA, SOCS1, SOCS3, SOD1, SORL1, SPAG9, SRC, STK11, STK3, STK4, SYK, TAB2, TOM1L1, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UBASH3B, UNC119, UVRAG, XRCC5, XRCC6, YWHAG]
GO:0032872	regulation of stress-activated MAPK cascade	11,0E-15	10,0E-12	50,0E-63	2,5E-60	[5, 6, 7, 8, 9, 10, 11]	Group49	23,61	51,00	[CDC42, COPS5, DAXX, DBNL, DLG1, DNAJA1, DUSP22, EGFR, EIF2AK2, EPHB1, EPRS, EZR, FASN, GAB1, GPS2, HACD3, HDAC3, HIPK3, HMGB1, HSPH1, IGF1R, ITCH, MAP2K1, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP4K1, MAP4K4, MAPK1, MAPK3, MEN1, MYC, NCOR1, PAK1, PRDX1, PRKN, PRMT1, PTK2B, PTPN1, RAPGEF1, RASSF2, RB1CC1, RIPK2, RPS3, SPAG9, STK3, SYK, TPD52L1, TRAF2, TRAF6]

GO:0043410	positive regulation of MAPK cascade	63,0E-18	59,0E-15	50,0E-63	2,5E-60	[5, 6, 7, 8, 9, 10, 11]	Group49	17,99	93,00	[ABL1, ALK, APP, AR, ARHGEF7, ARRB1, ARRB2, CCM2, CD4, CDC42, CDK1, CFLAR, CRK, CRKL, CSK, CTNNB1, DAXX, DBNL, DUSP22, EGFR, EIF2AK2, ERBB2, ERBB4, ETFA, EZH2, FBXW7, FGFR1, FRS2, GAB1, GHR, GNAI2, HACD3, HMGB1, INSR, IQGAP1, IRAK1, JAK2, JUN, KIT, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MIF, PAK1, PDGFRA, PDGFRB, PEA15, PELI2, PHB, PHB2, PIK3CG, PLCG1, PRKAA1, PRKCE, PRMT1, PSAP, PTEN, PTK2B, PTPN1, PTPN11, RAF1, RAPGEF1, RASSF2, RB1CC1, RIPK2, RPS27A, RPS3, S100A7, S100A8, S100A9, SHC1, SOD1, SORBS3, SPAG9, SRC, STK3, SYK, TAB2, TPD52L1, TRAF2, TRAF6, UBA52]
GO:0007254	JNK cascade	8,4E-12	7,9E-9	50,0E-63	2,5E-60	[6, 7, 8, 10, 11]	Group49	21,74	45,00	[CDC42, COPS5, CRKL, DAXX, DBNL, DNAJA1, DUSP22, EGFR, EPHB1, GAB1, GPS2, HACD3, HDAC3, HIPK3, HMGB1, IGF1R, IRAK1, ITCH, MAP3K4, MAP3K5, MAP3K7, MAP4K1, MAP4K4, MAPK10, MAPK8, MEN1, NCOR1, PAK1, PRKN, PTK2B, PTPN1, RAPGEF1, RASSF2, RB1CC1, RIPK2, RPS27A, RPS3, SPAG9, STK3, SYK, TAB2, TPD52L1, TRAF2, TRAF6, UBA52]
GO:0006469	negative regulation of protein kinase activity	2,6E-9	2,5E-6	50,0E-63	2,5E-60	[7, 8, 9, 10]	Group49	18,18	46,00	[ABL1, ADAR, APC, CASP3, CBL, CBLB, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, DNAJA1, DNAJA3, DUSP1, DUSP22, EPRS, GPS2, HIPK3, HSPB1, IGF1R, KAT2B, MEN1, NCK1, NPM1, NUP62, PAK2, PARK7, PDPK1, PLK1, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAG2, PRKAR1A, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, SFN, SOCS1, SOCS3, SORL1, UBASH3B, YWHAG]
GO:0043405	regulation of MAP kinase activity	2,9E-21	2,8E-18	50,0E-63	2,5E-60	[6, 7, 8, 9, 10, 11]	Group49	22,86	80,00	[ALK, APP, ARHGEF7, ARRB1, CDK1, CDK5RAP3, CRK, CRKL, CSK, DAXX, DBNL, DNAJA1, DUSP1, DUSP22, EGFR, EIF2AK2, ERBB2, ETFA, EZH2, FGFR1, FRS2, GAB1, GHR, GNAI2, GPS2, HACD3, HIPK3, IGF1R, INSR, IQGAP1, IRAK1, JAK2, KIT, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MIF, NUP62, PAK1, PDGFRB, PEA15, PIK3CG, PLCG1, PPP2CA, PPP2R1A, PRKAA1, PTK2B, PTPN1, PTPN11, PTPN6, PTPRJ, RAF1, RAPGEF1, RIPK2, RPS27A, RPS3, S100A8, S100A9, SHC1, SOD1, SORL1, SPAG9, SRC, SYK, TAB2, TPD52L1, TRAF2, TRAF6, UBA52]
GO:0045860	positive regulation of protein kinase activity	13,0E-27	12,0E-24	50,0E-63	2,5E-60	[7, 8, 9, 10]	Group49	21,47	111,00	[ABI1, ABL1, ALK, APP, ARHGEF7, ARRB1, BAX, CALM1, CAMKK1, CAMKK2, CCNT1, CD4, CDK1, CDK5, CDK5R1, CDKN1B, CLU, CRK, CRKL, CSK, DAXX, DBNL, DLG1, EGFR, EIF2AK2, ERBB2, ERBB3, ETFA, EZH2, FBXW7, FGFR1,

										FRS2, GAB1, GHR, GNAI2, HACD3, HSP90AB1, HSPA5, HSPH1, INSR, IQGAP1, IRAK1, JAK2, KIT, LAT, LCP2, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MIF, MLST8, PAK1, PAK2, PARK7, PDGFRB, PDPK1, PEA15, PIK3CA, PIK3CG, PLCG1, PPP2CA, PRKAA1, PRKAG1, PRKAG2, PRKAR1A, PTK2, PTK2B, PTPN1, PTPN11, PTPRC, RAF1, RAPGEF1, RASSF2, RHOA, RIPK2, RPLP1, RPS27A, RPS3, S100A8, S100A9, SHC1, SNCA, SOCS1, SOD1, SPAG9, SRC, STK11, STK3, STK4, SYK, TAB2, TOM1L1, TPD52L1, TRAF2, TRAF6, TXN, UBA52, UNC119, XRCC5, XRCC6]
GO:0070372	regulation of ERK1 and ERK2 cascade	120,0E-9	110,0E-6	50,0E-63	2,5E-60	[6, 7, 8, 9, 10, 11]	Group49	16,42	45,00	[ABL1, APP, ARRB1, ARRB2, CD4, CFLAR, CSK, DLG1, DUSP1, EGFR, EIF6, EPHB1, ERBB2, ERBB4, EZR, FBXW7, FRS2, HMGB1, JUN, KLF4, MAP2K1, MAPK3, MIF, PDGFRA, PDGFRB, PHB, PHB2, PIN1, PRMT5, PTEN, PTK2B, PTPN1, PTPN11, PTPN6, RAF1, RAPGEF1, RIPK2, S100A7, S100A8, S100A9, SHC1, SMAD4, SRC, SYK, TNIP1]
GO:0071900	regulation of protein serine/threonine kinase activity	1,5E-24	1,4E-21	50,0E-63	2,5E-60	[7, 8, 9, 10]	Group49	20,95	106,00	[ABL1, ALK, APC, APP, ARHGEF7, ARRB1, CALM1, CASP3, CCNT1, CDC37, CDK1, CDK5R1, CDK5RAP3, CDKN1B, CDKN2A, CRK, CRKL, CSK, DAXX, DBNL, DNAJA1, DUSP1, DUSP22, EGFR, EIF2AK2, ERBB2, ETFA, EZH2, FGFR1, FRS2, GAB1, GHR, GNAI2, GPS2, HACD3, HIPK3, HSP90AB1, HSPB1, IGF1R, INSR, IQGAP1, IRAK1, JAK2, KAT2B, KIT, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MEN1, MIF, MLST8, NUP62, PAK1, PDGFRB, PEA15, PIK3CG, PLCG1, PLK1, PPP2CA, PPP2R1A, PRKAA1, PRKAG2, PRKAR1A, PTEN, PTK2B, PTPN1, PTPN11, PTPN6, PTPRJ, RAF1, RAPGEF1, RHOA, RIPK2, RPS27A, RPS3, S100A8, S100A9, SFN, SHC1, SNCA, SOD1, SORL1, SPAG9, SRC, STK11, STK3, STK4, SYK, TAB2, TPD52L1, TRAF2, TRAF6, UBA52, UVRAG, YWHAG]
GO:0043406	positive regulation of MAP kinase activity	2,8E-15	2,6E-12	50,0E-63	2,5E-60	[6, 7, 8, 9, 10, 11, 12]	Group49	23,11	55,00	[ALK, APP, ARHGEF7, ARRB1, CDK1, CSK, DAXX, DBNL, EGFR, ERBB2, ETFA, EZH2, FGFR1, FRS2, GAB1, GHR, HACD3, INSR, IQGAP1, IRAK1, KIT, MAP2K1, MAP2K3, MAP3K4, MAP3K5, MAP3K7, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MIF, PAK1, PDGFRB, PEA15, PIK3CG, PRKAA1, PTK2B, PTPN1, PTPN11, RIPK2, RPS27A, RPS3, S100A8, S100A9, SHC1, SOD1, SPAG9, SRC, SYK, TAB2, TPD52L1, TRAF2, TRAF6, UBA52]

GO:0046328	regulation of JNK cascade	230,0E-12	220,0E-9	50,0E-63	2,5E-60	[6, 7, 8, 9, 10, 11, 12]	Group49	21,97	38,00	[CDC42, COPS5, DAXX, DBNL, DNAJA1, DUSP22, EGFR, EPHB1, GAB1, GPS2, HACD3, HDAC3, HIPK3, HMGB1, IGF1R, ITCH, MAP3K4, MAP3K5, MAP3K7, MAP4K1, MAP4K4, MEN1, NCOR1, PAK1, PRKN, PTK2B, PTPN1, RAPGEF1, RASSF2, RB1CC1, RIPK2, RPS3, SPAG9, STK3, SYK, TPD52L1, TRAF2, TRAF6]
GO:0032147	activation of protein kinase activity	2,5E-15	2,3E-12	50,0E-63	2,5E-60	[8, 9, 10, 11]	Group49	20,56	66,00	[ABL1, ALK, APP, ARHGEF7, ARRB1, CDK1, CRK, CRKL, DAXX, DBNL, DLG1, EGFR, EIF2AK2, ETFA, FRS2, GAB1, GHR, GNAI2, HACD3, INSR, IRAK1, JAK2, KIT, MAP2K1, MAP2K3, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K5, MAP3K7, MAP3K8, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, PARK7, PDPK1, PEA15, PIK3CA, PLCG1, PRKAA1, PRKAG2, PRKAR1A, PTK2B, PTPN1, PTPN11, RAF1, RAPGEF1, RIPK2, RPLP1, RPS27A, SHC1, SOCS1, SOD1, SPAG9, SRC, STK11, SYK, TAB2, TOM1L1, TRAF2, TRAF6, TXN, UBA52]
GO:0071902	positive regulation of protein serine/threonine kinase activity	1,5E-15	1,4E-12	50,0E-63	2,5E-60	[8, 9, 10, 11]	Group49	20,55	67,00	[ALK, APP, ARHGEF7, ARRB1, CALM1, CCNT1, CDK1, CDK5R1, CDKN1B, CSK, DAXX, DBNL, EGFR, ERBB2, ETFA, EZH2, FGFR1, FRS2, GAB1, GHR, HACD3, HSP90AB1, INSR, IQGAP1, IRAK1, KIT, MAP2K1, MAP2K3, MAP3K4, MAP3K5, MAP3K7, MAP4K1, MAPK1, MAPK10, MAPK14, MAPK3, MIF, MLST8, PAK1, PDGFRB, PEA15, PIK3CG, PPP2CA, PRKAA1, PTK2B, PTPN1, PTPN11, RHOA, RIPK2, RPS27A, RPS3, S100A8, S100A9, SHC1, SNCA, SOD1, SPAG9, SRC, STK11, STK3, STK4, SYK, TAB2, TPD52L1, TRAF2, TRAF6, UBA52]
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	7,8E-12	7,3E-9	210,0E-54	10,0E-51	[7, 8, 9, 10, 11, 12, 13]	Group50	30,21	29,00	[AIFM1, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, DNAJA3, DYNLL1, FADD, FASLG, FASN, HSPD1, JAK2, LCK, MAPT, PML, PPARG, RACK1, RET, RIPK2, RPS27L, S100A8, S100A9, SMAD3, SNCA, TRADD, TRAF2, VCP]
GO:1904667	negative regulation of ubiquitin protein ligase activity	160,0E-12	140,0E-9	210,0E-54	10,0E-51	[7, 9, 10, 11, 12, 13]	Group50	30,49	25,00	[ANAPC7, CDC20, CDK1, CDKN2A, MAD2L1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPL11, RPL23, RPL5, RPS27A, UBA52, UBE2D1]
GO:1904668	positive regulation of ubiquitin protein ligase activity	110,0E-12	100,0E-9	210,0E-54	10,0E-51	[7, 9, 10, 11, 12, 13]	Group50	29,89	26,00	[ANAPC7, BTRC, CDC20, CDK1, CUL1, MAD2L1, PLK1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, RPS27A, SKP1, UBA52, UBE2D1]
GO:0002218	activation of innate immune response	23,0E-21	22,0E-18	210,0E-54	10,0E-51	[3, 5, 6, 7, 8]	Group50	24,07	71,00	[ARHGEF7, ARRB2, BTK, BTRC, C1QBP, CASP8, CD300LF, CHUK, CREBBP, CUL1, EP300, ESR1, FADD, FBXW11, FYN, HCK, HMGB1, HSP90B1, HSPA1A, HSPD1, IKBKB, IRAK1, ITCH, ITGAM, ITGB2, LGMN, MAP3K1, MAP3K7, NFKB1, NFKBIA, PAK1, PAK2, PDPK1, PIK3C3, PLCG2, PRKCE,

										PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAF1, RELA, RELB, RIPK2, RPS27A, RPS6KA3, RPSA, S100A8, S100A9, SIN3A, SKP1, SRC, SYK, TAB2, TBK1, TNIP1, TNIP2, TRAF6, UBA52, UBE2D1, UBE2D2]
GO:0000077	DNA damage checkpoint	24,0E-9	23,0E-6	210,0E-54	10,0E-51	[4, 5, 6, 7, 8]	Group50	20,00	34,00	[ARID3A, ATF2, ATR, BABAM1, BAX, BRCA1, BRD4, CARM1, CCAR2, CDC5L, CDK1, CDK5RAP3, CDKN1B, E2F1, EP300, FANCI, H2AFX, MAPK14, MDM2, NEK6, NPM1, PCNA, PEA15, PLK1, PML, PRMT1, PTPN11, RPA2, RPS27A, RPS27L, SFN, TP53, UBA52, XPC]
GO:0002429	immune response-activating cell surface receptor signaling pathway	72,0E-24	68,0E-21	210,0E-54	10,0E-51	[4, 5, 6, 7, 8]	Group50	20,75	100,00	[ABI1, ABL1, ACTB, ACTG1, ARHGEF7, ARPC1A, BAX, BCAR1, BLK, BTK, BTRC, CD19, CD4, CDC42, CHUK, CREBBP, CRK, CSK, CUL1, DOCK1, DUSP22, ELMO1, EP300, EZR, FBXW11, FGR, FYN, GRB2, HCK, HSP90AA1, HSP90AB1, IKBKB, LAT, LCK, LCP2, MAP3K7, MAPK1, MAPK3, MYO1C, NCK1, NCOR2, NFKB1, NFKBIA, PAG1, PAK1, PAK2, PDPK1, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLCG1, PLCG2, PLSCR1, PRKCB, PRKCE, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTPN6, PTPRC, PTPRJ, RAC1, RAF1, RAPGEF1, RBCK1, RELA, RELB, RIPK2, RPS27A, RPS3, SKP1, SLC25A3, SRC, STK11, SYK, TAB2, TRAF6, UBA52, UBASH3A, UBE2D1, UBE2D2, VAV1, VAV2, WAS, WASL, ZAP70]
GO:0030111	regulation of Wnt signaling pathway	3,9E-9	3,6E-6	210,0E-54	10,0E-51	[4, 5, 6, 7, 8]	Group50	16,47	55,00	[ABL1, APC, BTRC, CCAR2, CSNK2A1, CSNK2A2, CUL3, DDIT3, FOXO3, G3BP1, GRB10, GSK3B, HDAC1, HNF1A, LRRK1, MAPK14, MCC, NFKB1, NOTCH1, PIN1, PPP1CA, PPP2CA, PPP2R1A, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTPRO, RACK1, RAPGEF1, RBPJ, RPS27A, SMARCA4, SMURF2, SOX7, SRC, STK11, STK3, STK4, SUMO1, TCF7L1, UBA52, UBR5, YAP1]
GO:0071158	positive regulation of cell cycle arrest	650,0E-9	600,0E-6	210,0E-54	10,0E-51	[4, 5, 6, 7, 8]	Group50	22,68	22,00	[ARID3A, BAX, BRCA1, CARM1, CDK1, CDK5R1, CDKN1B, CDKN2A, E2F1, EP300, ID2, MDM2, MYBBP1A, NPM1, PCNA, PML, PRMT1, RPL23, RPS27A, SFN, TP53, UBA52]
GO:0043488	regulation of mRNA stability	1,8E-15	1,7E-12	210,0E-54	10,0E-51	[4, 7, 8]	Group50	28,57	42,00	[CARHSP1, DHX9, E2F1, ELAVL1, HNRNPA0, HNRNPC, HNRNPD, HNRNPR, HNRNPU, HSPA1A, HSPA8, HSPB1, IGF2BP1, KHSRP, MAPK14, MTOR, PABPC1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPS27A, SERBP1, SET, SYNCRIP, TARDBP, TNPO1, UBA52, XPO1, YBX1, YWHAB, YWHAZ]

GO:0043489	RNA stabilization	16,0E-9	15,0E-6	210,0E-54	10,0E-51	[4, 7, 8]	Group50	38,46	15,00	[DHX9, E2F1, ELAVL1, HNRNPA0, HNRNPC, HNRNPD, HNRNPU, IGF2BP1, MAPK14, MTOR, PABPC1, SYNCRIP, TARDBP, TNIP1, YBX1]
GO:0010498	proteasomal protein catabolic process	190,0E-18	180,0E-15	210,0E-54	10,0E-51	[5, 6, 7, 8]	Group50	19,18	80,00	[ANAPC7, APC, ARRB1, ARRB2, BAG5, BTRC, CCAR2, CD2AP, CDC20, CDK1, CLU, COMMD1, CTNNB1, CUL1, CUL3, DDA1, DDB1, DDIT3, DNAJC10, FBXW11, FBXW7, GABARAPL2, GNA12, GSK3B, HERPUD1, HSP90AB1, HSP90B1, HSPA1A, HSPA5, KAT5, MAD2L1, MDM2, MTA1, NSFL1C, PARK7, PCBP2, PLK1, PML, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RACK1, RAD23A, RBCK1, RFFL, RNF144B, RPS27A, SIAH1, SKP1, SMAD7, SMARCC1, SMURF1, STUB1, SUMO1, SUMO2, TBL1X, TP53, UBA52, UBE2B, UBE2D1, UBE4B, UBQLN4, UBR1, UBR2, UBXN1, USP19, VCP, WWP2]
GO:0031400	negative regulation of protein modification process	18,0E-30	17,0E-27	210,0E-54	10,0E-51	[5, 6, 7, 8]	Group50	20,84	129,00	[ABL1, ADAR, ANAPC7, APC, ARRB1, ARRB2, ATG14, ATG5, BAG5, BAX, BRCA1, CALM1, CASP3, CBL, CBLB, CDC20, CDK1, CDK5, CDK5RAP3, CDKN1B, CDKN2A, CORO1C, CSK, CTBP1, CTDSP2, CTNNB1, DLG1, DNAJA1, DNAJA3, DNAJC10, DUSP1, DUSP22, EIF6, EPRS, EZR, FYN, GPS2, HDAC2, HDAC3, HIPK3, HSPA1A, HSPB1, HSPH1, IGF1R, IKBKB, ITCH, JARID2, JUN, KAT2B, KLF4, LRRK1, MAD2L1, MEN1, MICAL1, MTOR, MYC, NCK1, NCOR1, NPM1, NUP62, PAK2, PARK7, PDPK1, PHB, PIAS3, PIN1, PLK1, PML, PPM1F, PPP2CA, PPP2R1A, PREX1, PRKAG2, PRKAR1A, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPN1, PTPN6, PTPRC, PTPRJ, RACK1, RAPGEF1, RASSF2, RPL11, RPL23, RPL5, RPS27A, RPS3, SEMA4D, SET, SFN, SIN3A, SMAD4, SMAD7, SMARCB1, SNCA, SOCS1, SOCS3, SORL1, STRAP, SUMO1, TARDBP, TNIP1, TRAF3IP1, TRIM21, UBA52, UBASH3B, UBE2B, UBE2D1, UBR5, UBXN1, YWHAB, YWHAE, YWHAG]
GO:0045862	positive regulation of proteolysis	440,0E-30	410,0E-27	210,0E-54	10,0E-51	[5, 6, 7, 8]	Group50	24,74	96,00	[AIFM1, ANAPC7, APP, ARRB1, BAX, BTRC, C3, CASP3, CASP8, CDC20, CDK1, CDKN1B, CDKN2A, CFL1, CLU, CNTN1, CUL1, DAPK1, DDX3X, DNAJA3, DYNLL1, ENO1, FADD, FASLG, FASN, FBXW11, FBXW7, GSK3B, GSN, HDAC2, HERPUD1, HMGB1, HSPA1A, HSPD1, JAK2, LCK, MAD2L1, MAP3K5, MAPK14, MAPK3, MAPT, MDM2, MEFV, MYC, MYH9, PACSIN3, PHB, PLK1, PML, PPARG, PPM1F, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13,

										PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RACK1, RAD23A, RET, RIPK2, RNF144B, RPS27A, RPS27L, RPS3, S100A8, S100A9, SKP1, SMAD3, SMAD7, SMURF1, SNCA, SOX7, SRC, STAT3, STUB1, SUMO1, SUMO2, TNFRSF1B, TRADD, TRAF2, UBA52, UBE2D1, VCP]
GO:1901991	negative regulation of mitotic cell cycle phase transition	620,0E-15	580,0E-12	210,0E-54	10,0E-51	[5, 6, 7, 8]	Group50	22,33	48,00	[APC, ARID3A, BAX, CARM1, CDK1, CDK5RAP3, CDKN1B, CSNK2A1, CSNK2A2, CTDSP2, CUL1, DUSP1, E2F1, EP300, EZH2, FANCI, MAD1L1, MAD2L1, MDM2, NPM1, PCNA, PLK1, PML, PRMT1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, RPA2, RPS27A, RPS27L, SFN, SKP1, SMARCA4, TP53, TPR, UBA52]
GO:1902807	negative regulation of cell cycle G1/S phase transition	860,0E-9	800,0E-6	210,0E-54	10,0E-51	[5, 6, 7, 8]	Group50	21,70	23,00	[ARID3A, BAX, CARM1, CDK1, CDKN1B, CTDSP2, E2F1, EP300, EZH2, MDM2, MEN1, NPM1, PCNA, PML, PRMT1, PTEN, RPA2, RPS27A, RPS27L, SFN, SMARCA4, TP53, UBA52]
GO:1903364	positive regulation of cellular protein catabolic process	52,0E-15	49,0E-12	210,0E-54	10,0E-51	[5, 6, 7, 8]	Group50	24,10	47,00	[ANAPC7, BTRC, CDC20, CDK1, CLU, CUL1, EZR, FBXW7, GSK3B, HERPUD1, HSPA1A, MAD2L1, MDM2, MSN, PLK1, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RACK1, RAD23A, RDX, RNF144B, RPS27A, SKP1, SMAD7, SMURF1, STUB1, SUMO1, SUMO2, UBA52, UBE2D1, VCP]
GO:0010389	regulation of G2/M transition of mitotic cell cycle	39,0E-9	37,0E-6	210,0E-54	10,0E-51	[6, 7, 8]	Group50	22,69	27,00	[APP, BRD4, CDK1, CDK4, CDK5RAP3, CDKN2A, CUL1, FANCI, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RCC2, RPS27A, SIN3A, SKP1, UBA52]
GO:0035567	non-canonical Wnt signaling pathway	38,0E-12	35,0E-9	210,0E-54	10,0E-51	[6, 7, 8]	Group50	23,72	37,00	[ABL1, AGO1, AGO2, AGO4, ARRB2, CALM1, CAMK2A, CDC42, CELSR2, CLTC, CTNNB1, GNB1, MAP3K7, MOV10, PFN1, PLCB2, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAC1, RHOA, RPS27A, SMURF1, SMURF2, TNRC6B, UBA52]
GO:0050851	antigen receptor-mediated signaling pathway	1,5E-21	1,4E-18	210,0E-54	10,0E-51	[5, 6, 7, 8, 9]	Group50	24,91	72,00	[ABL1, ARHGEF7, BAX, BCAR1, BLK, BTK, BTRC, CD19, CD4, CHUK, CSK, CUL1, DUSP22, EZR, FBXW11, FYN, IKBKB, LAT, LCK, LCP2, MAP3K7, MAPK1, NCK1, NCOR2, NFKB1, NFKBIA, PAG1, PAK1, PAK2, PDPK1, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLCG1, PLCG2, PRKCB, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPN6, PTPRC, PTPRJ, RBCK1, RELA, RIPK2, RPS27A, RPS3, SKP1, SLC25A3, STK11, SYK, TAB2, TRAF6, UBA52, UBASH3A, UBE2D1, UBE2D2, WAS, ZAP70]

GO:0052548	regulation of endopeptidase activity	15,0E-12	14,0E-9	210,0E-54	10,0E-51	[6, 7, 8]	Group50	16,83	69,00	[AIFM1, APP, ARRB1, ARRB2, BAX, C3, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, COPS2, CSN2, CSNK2A1, CSNK2A2, CSTB, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HERPUD1, HMGB1, HSPD1, JAK2, KLF4, LCK, MAP3K5, MAPT, MDM2, MEFV, MICAL1, MYC, PAK2, PARK7, PEBP1, PLAUR, PML, PPARG, PPM1F, PRDX3, RACK1, RAF1, RET, RFFL, RIPK2, RPS27L, RPS3, RPS6KA1, RPS6KA3, S100A8, S100A9, SERPINB12, SFN, SMAD3, SNCA, SORL1, SOX7, SRC, STAT3, TRADD, TRAF2, VCP, VDAC2, VTN, YWHAE]
GO:0060070	canonical Wnt signaling pathway	1,3E-9	1,2E-6	210,0E-54	10,0E-51	[6, 7, 8]	Group50	17,26	53,00	[APC, BTRC, CCAR2, CDC42, CTNNB1, CUL3, DDIT3, FOXO3, G3BP1, GSK3B, HDAC1, KLF4, LRRK1, MAPK14, MCC, MYC, NFKB1, NOTCH1, PIN1, PPP1CA, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPRO, RAPGEF1, RBPJ, RPS27A, SMAD3, SMURF2, SOX7, SRC, STK11, STK3, STK4, TBL1X, TCF7L1, UBA52, UBE2B, UBR5, YAP1]
GO:0060828	regulation of canonical Wnt signaling pathway	79,0E-9	74,0E-6	210,0E-54	10,0E-51	[5, 6, 7, 8, 9]	Group50	16,93	43,00	[APC, BTRC, CCAR2, CUL3, DDIT3, FOXO3, G3BP1, GSK3B, HDAC1, LRRK1, MAPK14, MCC, NFKB1, NOTCH1, PIN1, PPP1CA, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTPRO, RAPGEF1, RBPJ, RPS27A, SMURF2, SOX7, SRC, STK3, STK4, UBA52, UBR5, YAP1]
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	1,8E-18	1,7E-15	210,0E-54	10,0E-51	[6, 7, 8]	Group50	24,90	61,00	[ANAPC7, BAG5, BTRC, CCAR2, CDC20, CDK1, CDKN2A, CLU, COMMD1, CUL1, DDA1, FBXW7, GABARAPL2, GNA12, GSK3B, HERPUD1, HSP90AB1, HSPA1A, MAD2L1, MDM2, PARK7, PLK1, PML, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RACK1, RAD23A, RNF144B, RPL11, RPL23, RPL5, RPS27A, SKP1, SMAD7, SMARCC1, SMURF1, STUB1, SUMO1, SUMO2, UBA52, UBE2D1, UBQLN4, UBXN1, USP19, VCP]
GO:1903320	regulation of protein modification by small protein conjugation or removal	15,0E-27	14,0E-24	210,0E-54	10,0E-51	[6, 7, 8]	Group50	27,21	80,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, BRCA1, BTRC, CDC20, CDK1, CDK5, CDK5RAP3, CDKN2A, CLU, COMMD1, CTNNB1, CUL1, DAXX, DNAJA1, DNAJA3, FANCI, FBXW7, FYN, HERPUD1, HSP90AA1, HSP90AB1, HSPA1A, HSPA5, ITCH, MAD2L1, MTA1, MTOR, MYO1C, NMI, PARK7, PIAS3, PIN1, PLK1, PML, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RASSF1, RIPK2, RPL11,

										RPL23, RPL5, RPS27A, RPS3, SKP1, SMAD7, SMURF1, STUB1, SUMO1, TOLLIP, TRAF6, TRIM21, UBA52, UBE2D1, UBE2I, UBE2L3, UBR5, UBXN1, VCP]
GO:2000045	regulation of G1/S transition of mitotic cell cycle	83,0E-9	78,0E-6	210,0E-54	10,0E-51	[6, 7, 8]	Group50	20,13	31,00	[ANXA1, ARID3A, BAX, CARM1, CDK1, CDKN1B, CTDSP2, DDX3X, E2F1, EGFR, EP300, EZH2, ID2, MDM2, MEPCE, NPM1, PCNA, PML, PRMT1, PTEN, PTPN6, RDX, RPA2, RPS27A, RPS27L, SFN, SMARCA4, SUMO1, TCF7L1, TP53, UBA52]
GO:0010952	positive regulation of peptidase activity	42,0E-15	39,0E-12	210,0E-54	10,0E-51	[6, 7, 8, 9]	Group50	25,43	44,00	[AIFM1, APP, ARRB1, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HMGB1, HSPD1, JAK2, LCK, MAP3K5, MAPK14, MAPK3, MAPT, MEFV, MYC, PML, PPARG, PPM1F, RACK1, RET, RIPK2, RPS27L, RPS3, S100A8, S100A9, SMAD3, SNCA, SOX7, STAT3, TRADD, TRAF2, VCP]
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	300,0E-9	280,0E-6	210,0E-54	10,0E-51	[6, 7, 8, 9]	Group50	24,42	21,00	[CDK1, CDK5RAP3, CUL1, FANCI, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPS27A, SKP1, UBA52]
GO:0032446	protein modification by small protein conjugation	14,0E-21	13,0E-18	210,0E-54	10,0E-51	[7, 8]	Group50	15,82	147,00	[ABL1, AKTIP, ANAPC7, ARRB1, ARRB2, ATG10, ATG3, ATG5, ATG7, BACH1, BAG5, BARD1, BRCA1, BTRC, CBL, CBLB, CDC20, CDC42, CDK1, CDK5, CDK5RAP3, CDKN2A, CLU, COMMD1, CTNNB1, CUL1, CUL2, CUL3, DAXX, DCAF7, DDB1, DNAJA1, DNAJA3, DTX1, DTX2, ELOC, FANCI, FBXO27, FBXW11, FBXW7, FYN, HERC2, HERPUD1, HIST1H2BK, HSP90AA1, HSP90AB1, HSPA1A, HSPA5, ITCH, KBTBD7, KLHL18, MAD2L1, MDM2, MED31, MTA1, MTOR, MYO1C, NEDD4, NEDD8, NMI, NUP107, NUP155, NUP210, NUP62, NUP88, NUP93, NUP98, PARK7, PCNA, PELI2, PIAS2, PIAS3, PIN1, PLK1, PML, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RAE1, RANBP2, RANGAP1, RASSF1, RBCK1, RFFL, RIPK2, RNF144B, RPL11, RPL23, RPL5, RPS27A, RPS3, RYBP, SIAH1, SKP1, SMAD7, SMURF1, SMURF2, SOCS1, SOCS3, STUB1, SUMO1, SUMO2, SUZ12, TOLLIP, TPR, TRAF2, TRAF6, TRIM21, TRIM28, UBA1, UBA5, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2D4, UBE2E3, UBE2I, UBE2L3, UBE4B, UBR1, UBR2, UBR4, UBR5, UBXN1, USP7, USP9X, VCP, VHL, WWP2, ZBTB16]
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	100,0E-9	100,0E-6	210,0E-54	10,0E-51	[6, 7, 8, 9]	Group50	22,22	26,00	[ABL1, ARRB2, CDC42, CELSR2, CLTC, PFN1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4,

										PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAC1, RHOA, RPS27A, SMURF1, SMURF2, UBA52]
GO:0061136	regulation of proteasomal protein catabolic process	440,0E-12	410,0E-9	210,0E-54	10,0E-51	[6, 7, 8, 9]	Group50	22,73	35,00	[BAG5, BTRC, CCAR2, CLU, COMMD1, DDA1, FBXW7, GABARAPL2, GNA12, GSK3B, HERPUD1, HSP90AB1, HSPA1A, MDM2, PARK7, PLK1, PRKN, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, RACK1, RAD23A, RNF144B, SMAD7, SMARCC1, STUB1, SUMO1, SUMO2, UBQLN4, UBXN1, USP19, VCP]
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	190,0E-15	180,0E-12	210,0E-54	10,0E-51	[6, 7, 8, 9]	Group50	24,44	44,00	[ANAPC7, BTRC, CDC20, CDK1, CLU, CUL1, FBXW7, GSK3B, HERPUD1, HSPA1A, MAD2L1, MDM2, PLK1, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RACK1, RAD23A, RNF144B, RPS27A, SKP1, SMAD7, SMURF1, STUB1, SUMO1, SUMO2, UBA52, UBE2D1, VCP]
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	7,3E-18	6,8E-15	210,0E-54	10,0E-51	[6, 7, 8, 9]	Group50	30,26	46,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, CDC20, CDK1, CDK5, CDKN2A, CTNNB1, DNAJA1, FYN, HSPA1A, MAD2L1, MTOR, PARK7, PIAS3, PML, PRKCE, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPL11, RPL23, RPL5, RPS27A, RPS3, SMAD7, SUMO1, TRIM21, UBA52, UBE2D1, UBR5, UBXN1]
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	340,0E-21	320,0E-18	210,0E-54	10,0E-51	[6, 7, 8, 9]	Group50	27,45	56,00	[ANAPC7, ARRB1, ARRB2, BRCA1, BTRC, CDC20, CDK1, CDK5RAP3, CDKN2A, CLU, COMMD1, CUL1, DNAJA3, FANCI, FBXW7, HSPA5, MAD2L1, MTA1, MYO1C, NMI, PIAS3, PIN1, PLK1, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RASSF1, RIPK2, RPS27A, SKP1, SMAD7, SMURF1, STUB1, SUMO1, TOLLIP, TRAF6, UBA52, UBE2D1, UBE2I, UBE2L3, VCP]
GO:0043620	regulation of DNA-templated transcription in response to stress	280,0E-18	260,0E-15	210,0E-54	10,0E-51	[4, 6, 7, 8, 9, 10, 11]	Group50	31,25	40,00	[ATF4, BACH1, CREBBP, CUL2, DDIT3, DNAJB1, ELOC, EP300, GCN1, HIF1A, HSPA1A, HSPA5, JUN, NCK1, NEDD4, NOTCH1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RBPJ, RPS27A, RPS6KA1, RPS6KA3, SIN3A, TP53, UBA52, UBE2D1, UBE2D2, VHL]
GO:0006511	ubiquitin-dependent protein catabolic process	170,0E-21	160,0E-18	210,0E-54	10,0E-51	[7, 8, 9]	Group50	18,28	106,00	[ANAPC7, APC, ARRB1, ARRB2, BAG5, BTRC, CBL, CCAR2, CD2AP, CDC20, CDK1, CDKN2A, CLU, COMMD1, CTNNB1, CUL1, CUL2, CUL3, DDA1, DDB1, DDIT3, DNAJC10, ELOC, FBXW11, FBXW7, GNA12, GSK3B, HERPUD1, HSP90AB1, HSP90B1, HSPA1A, HSPA5, ITCH, KAT5, MAD2L1, MAGI1, MDM2, MTA1, NEDD4, NEDD8, NSFL1C, PARK7, PCBP2,

										PLK1, PML, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RACK1, RAD23A, RANBP2, RBCK1, RFFL, RNF144B, RPL11, RPL23, RPL5, RPS27A, SIAH1, SKP1, SMAD7, SMARCC1, SMURF1, SMURF2, SQSTM1, STUB1, SUMO1, SUMO2, TBL1X, TOLLIP, TOM1L1, TP53, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2I, UBE2L3, UBE4B, UBQLN4, UBR1, UBR2, UBR4, UBR5, UBXN1, USP19, USP7, USP9X, VCP, VPS4A, WWP2]
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	170,0E-21	160,0E-18	210,0E-54	10,0E-51	[6, 7, 8, 9, 10]	Group50	26,70	59,00	[AIFM1, APP, ARRB1, ARRB2, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, CSNK2A1, CSNK2A2, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HERPUD1, HMGB1, HSPD1, JAK2, KLF4, LCK, MAP3K5, MAPT, MDM2, MICAL1, MYC, PAK2, PARK7, PLAUR, PML, PPARG, PPM1F, PRDX3, RACK1, RAF1, RET, RFFL, RIPK2, RPS27L, RPS3, RPS6KA1, RPS6KA3, S100A8, S100A9, SFN, SMAD3, SNCA, SOX7, SRC, TRADD, TRAF2, VCP, VDAC2, YWHAE]
GO:0050852	T cell receptor signaling pathway	980,0E-30	910,0E-27	210,0E-54	10,0E-51	[6, 7, 8, 9, 10]	Group50	33,85	65,00	[ARHGEF7, BCAR1, BTRC, CD4, CHUK, CSK, CUL1, DUSP22, EZR, FBXW11, FYN, IKBKB, LAT, LCK, LCP2, MAP3K7, MAPK1, NCK1, NCOR2, NFKB1, NFKBIA, PAG1, PAK1, PAK2, PDPK1, PIK3CA, PIK3CD, PIK3R1, PIK3R2, PLCG1, PLCG2, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTPN6, PTPRC, PTPRJ, RBCK1, RELA, RIPK2, RPS27A, RPS3, SKP1, SLC25A3, STK11, TAB2, TRAF6, UBA52, UBASH3A, UBE2D1, UBE2D2, WAS, ZAP70]
GO:1901800	positive regulation of proteasomal protein catabolic process	530,0E-9	500,0E-6	210,0E-54	10,0E-51	[6, 7, 8, 9, 10]	Group50	22,92	22,00	[CLU, FBXW7, GSK3B, HERPUD1, HSPA1A, MDM2, PLK1, PRKN, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, RACK1, RAD23A, RNF144B, SMAD7, STUB1, SUMO1, SUMO2, VCP]
GO:2000116	regulation of cysteine-type endopeptidase activity	82,0E-21	77,0E-18	210,0E-54	10,0E-51	[7, 8, 9]	Group50	26,05	62,00	[AIFM1, APP, ARRB1, ARRB2, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, COPS2, CSN2, CSNK2A1, CSNK2A2, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HERPUD1, HMGB1, HSPD1, JAK2, KLF4, LCK, MAP3K5, MAPT, MDM2, MEFV, MICAL1, MYC, PAK2, PARK7, PLAUR, PML, PPARG, PPM1F, PRDX3, RACK1, RAF1, RET, RFFL, RIPK2, RPS27L, RPS3, RPS6KA1, RPS6KA3, S100A8, S100A9, SFN, SMAD3, SNCA, SOX7, SRC, TRADD, TRAF2, VCP, VDAC2, YWHAE]

GO:0002223	stimulatory C-type lectin receptor signaling pathway	9,5E-18	8,9E-15	210,0E-54	10,0E-51	[6, 7, 8, 9, 10, 11]	Group50	32,56	42,00	[ARHGEF7, BTRC, CHUK, CREBBP, CUL1, EP300, FBXW11, FYN, IKBKB, MAP3K7, NFKB1, NFKBIA, PAK1, PAK2, PDPK1, PLCG2, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RAF1, RELA, RELB, RPS27A, SKP1, SRC, SYK, TAB2, TRAF6, UBA52, UBE2D1, UBE2D2]
GO:0010950	positive regulation of endopeptidase activity	23,0E-15	22,0E-12	210,0E-54	10,0E-51	[7, 8, 9, 10]	Group50	26,75	42,00	[AIFM1, APP, ARRB1, BAX, CASP3, CASP8, CDKN1B, CDKN2A, CNTN1, DAPK1, DDX3X, DNAJA3, DYNLL1, FADD, FASLG, FASN, GSN, HMGB1, HSPD1, JAK2, LCK, MAP3K5, MAPT, MEFV, MYC, PML, PPARG, PPM1F, RACK1, RET, RIPK2, RPS27L, RPS3, S100A8, S100A9, SMAD3, SNCA, SOX7, STAT3, TRADD, TRAF2, VCP]
GO:0016567	protein ubiquitination	570,0E-18	530,0E-15	210,0E-54	10,0E-51	[8, 9]	Group50	15,04	126,00	[ABL1, AKTIP, ANAPC7, ARRB1, ARRB2, ATG3, ATG5, ATG7, BACH1, BAG5, BARD1, BRCA1, BTRC, CBL, CBLB, CDC20, CDC42, CDK1, CDK5, CDK5RAP3, CDKN2A, CLU, COMMD1, CUL1, CUL2, CUL3, DAXX, DCAF7, DDB1, DNAJA1, DNAJA3, DTX1, DTX2, ELOC, FANCI, FBXO27, FBXW11, FBXW7, FYN, HERC2, HERPUD1, HIST1H2BK, HSP90AA1, HSP90AB1, HSPA1A, HSPA5, ITCH, KBTBD7, KLHL18, MAD2L1, MDM2, MED31, MTA1, MTOR, MYO1C, NEDD4, NMI, PARK7, PELI2, PIN1, PLK1, PML, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RASSF1, RBCK1, RFFL, RIPK2, RNF144B, RPL11, RPL23, RPL5, RPS27A, RPS3, RYBP, SIAH1, SKP1, SMAD7, SMURF1, SMURF2, SOCS1, SOCS3, STUB1, SUMO1, SUZ12, TRAF2, TRAF6, TRIM21, TRIM28, UBA1, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2D4, UBE2E3, UBE2L3, UBE4B, UBR1, UBR2, UBR4, UBR5, UBXN1, USP7, USP9X, VCP, VHL, WWP2, ZBTB16]
GO:0031396	regulation of protein ubiquitination	3,8E-24	3,6E-21	210,0E-54	10,0E-51	[7, 8, 9, 10]	Group50	27,04	73,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, BRCA1, BTRC, CDC20, CDK1, CDK5, CDK5RAP3, CDKN2A, CLU, COMMD1, CUL1, DAXX, DNAJA1, DNAJA3, FANCI, FBXW7, FYN, HERPUD1, HSP90AA1, HSP90AB1, HSPA1A, HSPA5, MAD2L1, MTA1, MTOR, MYO1C, NMI, PARK7, PIN1, PLK1, PML, PRKCE, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RASSF1, RIPK2, RPL11, RPL23, RPL5, RPS27A, RPS3, SKP1, SMAD7, SMURF1, STUB1, SUMO1, TRAF6, UBA52, UBE2D1, UBE2L3, UBR5, UBXN1]

GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	3,1E-9	2,9E-6	210,0E-54	10,0E-51	[4, 5, 6, 7, 10, 11, 12, 13]	Group50	29,73	22,00	[ANAPC7, CDC20, CDK1, MAD2L1, PLK1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPS27A, UBA52, UBE2D1]
GO:0051438	regulation of ubiquitin-protein transferase activity	17,0E-15	16,0E-12	210,0E-54	10,0E-51	[5, 8, 9, 10, 11]	Group50	29,23	38,00	[ABL1, ANAPC7, BAG5, BTRC, CDC20, CDK1, CDKN2A, CUL1, FBXW7, MAD2L1, PARK7, PIN1, PLK1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, RPL11, RPL23, RPL5, RPS27A, SKP1, SMAD7, STUB1, UBA52, UBE2D1, UBE2L3]
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	2,3E-15	2,1E-12	210,0E-54	10,0E-51	[5, 7, 8, 9, 10, 11, 12]	Group50	30,89	38,00	[ATF4, BACH1, CREBBP, CUL2, DDIT3, DNAJB1, ELOC, EP300, GCN1, HIF1A, HSPA1A, HSPA5, JUN, NCK1, NEDD4, NOTCH1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RBPJ, RPS27A, SIN3A, TP53, UBA52, UBE2D1, UBE2D2, VHL]
GO:0031145	anaphase-promoting complex-dependent catabolic process	5,0E-9	4,7E-6	210,0E-54	10,0E-51	[7, 8, 9, 10, 11]	Group50	28,05	23,00	[ANAPC7, CDC20, CDK1, CUL3, MAD2L1, PLK1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPS27A, UBA52, UBE2D1]
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	13,0E-9	12,0E-6	210,0E-54	10,0E-51	[7, 8, 9, 10, 11]	Group50	28,77	21,00	[BTRC, CUL1, FBXW11, FBXW7, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPS27A, SKP1, UBA52]
GO:0031397	negative regulation of protein ubiquitination	82,0E-18	77,0E-15	210,0E-54	10,0E-51	[7, 8, 9, 10, 11]	Group50	30,28	43,00	[ABL1, ANAPC7, ARRB1, ARRB2, ATG5, BAG5, CDC20, CDK1, CDK5, CDKN2A, DNAJA1, FYN, HSPA1A, MAD2L1, MTOR, PARK7, PML, PRKCE, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPL11, RPL23, RPL5, RPS27A, RPS3, SMAD7, SUMO1, UBA52, UBE2D1, UBR5, UBXN1]
GO:0031398	positive regulation of protein ubiquitination	17,0E-18	16,0E-15	210,0E-54	10,0E-51	[7, 8, 9, 10, 11]	Group50	27,27	51,00	[ANAPC7, ARRB1, ARRB2, BRCA1, BTRC, CDC20, CDK1, CDK5RAP3, CLU, COMMD1, CUL1, DNAJA3, FANCI, FBXW7, HSPA5, MAD2L1, MTA1, MYO1C, NMI, PIN1, PLK1, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RASSF1, RIPK2, RPS27A, SKP1, SMAD7, SMURF1, STUB1, SUMO1, TRAF6, UBA52, UBE2D1, UBE2L3]
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	290,0E-9	270,0E-6	210,0E-54	10,0E-51	[7, 8, 9, 10, 11]	Group50	21,74	25,00	[BAG5, CCAR2, CLU, COMMD1, DDA1, GNA12, GSK3B, HERPUD1, HSP90AB1, HSPA1A, MDM2, PARK7, PLK1, PRKN, RACK1, RAD23A, RNF144B, SMAD7, SMARCC1, STUB1, SUMO1, SUMO2, UBQLN4, UBXN1, VCP]

GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	480,0E-18	450,0E-15	210,0E-54	10,0E-51	[8, 9, 10]	Group50	25,00	52,00	[ANAPC7, BTRC, CBL, CDC20, CDK1, CDKN2A, CLU, CUL1, CUL2, CUL3, DDB1, ELOC, FBXW7, ITCH, MAD2L1, MDM2, NEDD4, PLK1, PML, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RFFL, RNF144B, RPL11, RPL23, RPL5, RPS27A, SIAH1, SKP1, SMURF1, STUB1, UBA52, UBE2D1, UBE2L3, UBE4B, UBR4]
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	10,0E-12	9,9E-9	210,0E-54	10,0E-51	[5, 6, 7, 8, 9, 10, 11, 12, 13]	Group50	31,76	27,00	[BACH1, CREBBP, CUL2, ELOC, EP300, HIF1A, NOTCH1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RBPJ, RPS27A, UBA52, UBE2D1, UBE2D2, VHL]
GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	1,6E-15	1,5E-12	210,0E-54	10,0E-51	[7, 8, 9, 10, 11]	Group50	32,73	36,00	[ANAPC7, BTRC, CDC20, CDK1, CDKN2A, CLU, CUL1, FBXW7, MAD2L1, PLK1, PML, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RPL11, RPL23, RPL5, RPS27A, SKP1, SMURF1, UBA52, UBE2D1]
GO:0051443	positive regulation of ubiquitin-protein transferase activity	28,0E-12	26,0E-9	210,0E-54	10,0E-51	[6, 8, 9, 10, 11, 12]	Group50	28,04	30,00	[ANAPC7, BTRC, CDC20, CDK1, CUL1, FBXW7, MAD2L1, PIN1, PLK1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, RPS27A, SKP1, STUB1, UBA52, UBE2D1, UBE2L3]
GO:0051444	negative regulation of ubiquitin-protein transferase activity	660,0E-15	610,0E-12	210,0E-54	10,0E-51	[6, 8, 9, 10, 11, 12]	Group50	32,95	29,00	[ABL1, ANAPC7, BAG5, CDC20, CDK1, CDKN2A, MAD2L1, PARK7, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RPL11, RPL23, RPL5, RPS27A, SMAD7, UBA52, UBE2D1]
GO:0000209	protein polyubiquitination	81,0E-12	75,0E-9	210,0E-54	10,0E-51	[9, 10]	Group50	18,37	54,00	[ANAPC7, BARD1, BRCA1, BTRC, CBL, CDKN2A, CUL1, CUL3, FBXO27, FBXW11, FBXW7, ITCH, MYO1C, NEDD4, NMI, PELI2, PRKN, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, RBCK1, RFFL, RNF144B, RPS27A, SIAH1, SKP1, SMURF1, SMURF2, STUB1, TRAF2, TRAF6, TRIM21, UBA52, UBE2B, UBE2D1, UBE2D2, UBE2D4, UBE2E3, UBE2L3, UBE4B, UBR2, UBR5, WWP2]
GO:2000060	positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	55,0E-15	51,0E-12	210,0E-54	10,0E-51	[7, 8, 9, 10, 11, 12]	Group50	33,70	31,00	[ANAPC7, BTRC, CDC20, CDK1, CLU, CUL1, FBXW7, MAD2L1, PLK1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, PTK2, PTK2B, RPS27A, SKP1, SMURF1, UBA52, UBE2D1]

GO:1904666	regulation of ubiquitin protein ligase activity	2,3E-12	2,2E-9	210,0E-54	10,0E-51	[6, 9, 10, 11, 12]	Group50	30,61	30,00	[ANAPC7, BTRC, CDC20, CDK1, CDKN2A, CUL1, MAD2L1, PLK1, PSMA2, PSMA6, PSMB1, PSMB5, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD13, PSMD2, PSMD3, PSMD7, PTEN, RPL11, RPL23, RPL5, RPS27A, SKP1, UBA52, UBE2D1]