Table S2. Gene set enrichment analysis of biological processes from Gene Ontology (GO) obtained from constructed PPI networks of the light cyan 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:0010001	glial cell differentiation	39,0E-9	17,0E-6	39,0E-9	1,2E-6	[5, 7, 8]	Group00	7,61	15,00	[ABL1, AKT1, CDH2, CTNNB1, EGFR, ERBB2, HDAC2, IL6ST, MAPK1, MTOR, PTPN11, RELA, SKI, SRSF1, STAT3]
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	16,0E-12	7,3E-9	16,0E-12	540,0E-12	[5, 6, 7, 8, 9]	Group01	10,97	17,00	[AKT1, CBL, EGFR, ERBB2, GRB2, HCLS1, IRS1, JAK2, MAPK1, MET, PDGFRB, PIK3R1, PTPN11, SIRT1, SLC9A3R1, TSC2, VAV1]
GO:0014911	positive regulation of smooth muscle cell migration	31,0E-9	13,0E-6	31,0E-9	1,0E-6	[5, 6, 7, 8, 9]	Group02	19,51	8,00	[BCL2, HDAC4, IQGAP1, MDM2, PAK1, PDGFRB, PKN1, SRC]
GO:0016579	protein deubiquitination	2,2E-12	960,0E-12	2,2E-12	71,0E-12	[6, 7, 8, 9]	Group03	7,82	24,00	[AR, ARRB2, ATXN3, AXIN1, BAP1, BRCA1, ESR1, HCFC1, IKBKG, MAP3K7, MDM2, NFKBIA, PSME3, RHOA, SMAD1, SMAD2, SMAD3, SMAD7, TP53, TRAF2, TRAF6, USP3, USP46, WDR48]
GO:0001568	blood vessel development	200,0E-9	89,0E-6	200,0E-9	6,6E-6	[3, 5, 6, 7, 8]	Group04	4,16	26,00	[AKT1, AMOT, BRCA1, CAV1, CDC42, CDH2, CTNNB1, DNM2, EPHA2, ERBB2, FASLG, HDAC7, HSPG2, MAP3K3, MAPK1, MAPK14, MDM2, MEN1, NTRK1, PDGFRB, PLCG1, PML, RHOA, SIRT1, SMAD7, TCF7L2]
GO:0030111	regulation of Wnt signaling pathway	78,0E-9	34,0E-6	78,0E-9	2,5E-6	[4, 5, 6, 7, 8]	Group05	5,69	19,00	[ABL1, AXIN1, BTRC, CAV1, CDH2, CHD8, GSK3B, MAPK14, MCC, NFKB1, PPP2CA, PPP2R1A, PSME3, RACK1, SKI, SMARCA4, SRC, TCF7L2, TSC2]
GO:0031113	regulation of microtubule polymerization	20,0E-9	9,0E-6	20,0E-9	660,0E-9	[5, 6, 7, 8, 9]	Group06	20,51	8,00	[ABL1, CDKN1B, CLIP1, HSPA1A, MECP2, MET, PAK1, PKN1]
GO:0033120	positive regulation of RNA splicing	830,0E-9	360,0E-6	830,0E-9	26,0E-6	[5, 6, 7, 8, 9, 10]	Group07	21,43	6,00	[HSPA1A, HSPA8, PIK3R1, POLR2A, SRSF1, U2AF2]
GO:0043488	regulation of mRNA stability	390,0E-9	170,0E-6	390,0E-9	12,0E-6	[4, 7, 8]	Group08	8,16	12,00	[AKT1, DCP1A, HSPA1A, HSPA8, MAPK14, MTOR, PABPC1, PSME3, SET, YBX1, YWHAB, YWHAZ]
GO:1902893	regulation of pri-miRNA transcription from RNA polymerase II promoter	1,0E-6	450,0E-6	1,0E-6	33,0E-6	[7, 8, 9, 10, 11, 12]	Group09	20,69	6,00	[HDAC4, RELA, SMAD1, SMAD3, SMARCA4, STAT3]

GO:0007179	transforming growth factor beta receptor signaling pathway	1,8E-12	790,0E-12	1,8E-12	58,0E-12	[5, 6, 7, 8]	Group10	10,67	19,00	[ADAM17, ARRB2, CAV1, CBL, DNM2, HSPA1A, HSPA5, MAP3K7, MEN1, PML, RHOA, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SRC]
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	90,0E-9	39,0E-6	1,8E-12	58,0E-12	[5, 6, 7, 8, 9]	Group10	10,48	11,00	[ADAM17, CAV1, DNM2, HSPA1A, HSPA5, MEN1, SIRT1, SKI, SMAD2, SMAD3, SMAD7]
GO:0060443	mammary gland morphogenesis	190,0E-9	82,0E-6	1,3E-9	41,0E-9	[5, 6, 7, 8]	Group11	15,69	8,00	[AR, BTRC, CAV1, EPHA2, ESR1, PML, SRC, VDR]
GO:0061180	mammary gland epithelium development	2,8E-9	1,2E-6	1,3E-9	41,0E-9	[5, 6, 7, 8]	Group11	14,47	11,00	[AKT1, AR, BTRC, CEBPB, EPHA2, ESR1, JAK2, MAPK1, PML, SRC, VDR]
GO:0060444	branching involved in mammary gland duct morphogenesis	19,0E-9	8,4E-6	1,3E-9	41,0E-9	[5, 6, 7, 8, 9, 10]	Group11	26,92	7,00	[AR, BTRC, EPHA2, ESR1, PML, SRC, VDR]
GO:0002521	leukocyte differentiation	34,0E-9	15,0E-6	130,0E-12	4,3E-9	[5, 6, 7, 8]	Group12	4,86	24,00	[ABL1, ADAM17, BCL2, BLNK, CASP8, CDC42, CEBPB, CTNNB1, EPHA2, ERBB2, HCLS1, HDAC4, MAPK14, MTOR, NTRK1, PIK3R1, RB1, RIPK3, SIRT1, SRC, STAT3, STAT5B, TRAF6, VAV1]
GO:0030099	myeloid cell differentiation	5,6E-9	2,4E-6	130,0E-12	4,3E-9	[5, 6, 7, 8]	Group12	6,05	21,00	[CASP8, CDC42, CEBPB, CSF3R, CTNNB1, EPHA2, HCLS1, JAK2, MAPK14, MTOR, NFKBIA, PIK3R1, PML, PTPN11, RB1, SIRT1, SMAD5, SNRK, SRC, STAT5B, TRAF6]
GO:0002573	myeloid leukocyte differentiation	2,1E-6	940,0E-6	130,0E-12	4,3E-9	[6, 7, 8, 9]	Group12	6,40	13,00	[CASP8, CDC42, CEBPB, CTNNB1, EPHA2, HCLS1, MAPK14, MTOR, PIK3R1, RB1, SIRT1, SRC, TRAF6]
GO:0051054	positive regulation of DNA metabolic process	300,0E-9	130,0E-6	9,5E-9	300,0E-9	[4, 5, 6, 7, 8]	Group13	6,52	15,00	[AKT1, ARRB2, BRCA1, CDC42, CTNNB1, EGFR, H2AFX, HSP90AA1, MAP2K7, MAPK1, PDGFRB, PML, SIRT1, SRC, TOP2A]
GO:2000278	regulation of DNA biosynthetic process	120,0E-9	52,0E-6	9,5E-9	300,0E-9	[5, 6, 7, 8]	Group13	10,19	11,00	[ARRB2, CTNNB1, DACH1, HSP90AA1, MAP2K7, MAPK1, MEN1, PDGFRB, PML, SRC, TP53]
GO:0051972	regulation of telomerase activity	220,0E-9	96,0E-6	9,5E-9	300,0E-9	[5, 6, 7, 8, 9]	Group13	15,38	8,00	[CTNNB1, HSP90AA1, MAP2K7, MAPK1, MEN1, PML, SRC, TP53]
GO:0031295	T cell costimulation	12,0E-12	5,5E-9	5,6E-12	180,0E-12	[3, 6, 7, 8, 9]	Group14	15,05	14,00	[AKT1, CAV1, CDC42, GRB2, MAP3K14, MTOR, NCOR2, PAK1, PAK2, PIK3R1, PKN1, PTPN11, SRC, VAV1]
GO:0018105	peptidyl-serine phosphorylation	2,3E-9	1,0E-6	5,6E-12	180,0E-12	[7, 8, 9]	Group14	6,69	20,00	[AKT1, ARRB2, AXIN1, BCL2, CAV1, CDC42, GSK3B, HCLS1, IKBKB, MAPK1, MAPK14, MTOR, PAK1, PAK2, PKN1, RACK1, RAF1, SMAD7, SPRY2, SRC]
GO:0033135	regulation of peptidyl-serine phosphorylation	2,0E-9	890,0E-9	5,6E-12	180,0E-12	[7, 8, 9, 10]	Group14	10,37	14,00	[AKT1, ARRB2, AXIN1, BCL2, CAV1, CDC42, GSK3B, HCLS1, PAK1, PKN1, RACK1, RAF1, SMAD7, SPRY2]
GO:0033138	positive regulation of peptidyl-serine phosphorylation	5,1E-9	2,2E-6	5,6E-12	180,0E-12	[7, 8, 9, 10, 11]	Group14	12,00	12,00	[AKT1, ARRB2, AXIN1, BCL2, CAV1, CDC42, GSK3B, HCLS1, PAK1, PKN1, RAF1, SPRY2]
GO:1900078	positive regulation of cellular response to insulin stimulus	44,0E-9	19,0E-6	230,0E-15	7,5E-12	[3, 4, 5, 7, 8, 9, 10]	Group15	24,14	7,00	[IRS1, PAK1, PIK3R1, PKN1, PTPN11, SIRT1, SRC]

GO:0031295	T cell costimulation	12,0E-12	5,5E-9	230,0E-15	7,5E-12	[3, 6, 7, 8, 9]	Group15	15,05	14,00	[AKT1, CAV1, CDC42, GRB2, MAP3K14, MTOR, NCOR2, PAK1, PAK2, PIK3R1, PKN1, PTPN11, SRC, VAV1]
GO:0043149	stress fiber assembly	28,0E-9	12,0E-6	230,0E-15	7,5E-12	[6, 7, 8, 9, 10]	Group15	11,70	11,00	[AMOT, CDC42, MET, MTOR, PAK1, PIK3R1, PKN1, RHOA, SMAD3, SORBS3, SRC]
GO:0051496	positive regulation of stress fiber assembly	160,0E-9	70,0E-6	230,0E-15	7,5E-12	[4, 5, 6, 7, 8, 9, 10, 11, 12]	Group15	16,00	8,00	[AMOT, CDC42, MTOR, PAK1, PKN1, RHOA, SMAD3, SORBS3]
GO:0030518	intracellular steroid hormone receptor signaling pathway	38,0E-12	16,0E-9	310,0E-15	10,0E-12	[4, 5, 6, 7, 8]	Group16	11,35	16,00	[AR, ARRB2, BRCA1, CTNNB1, DAXX, ESR1, FHL2, JAK2, NR3C1, PAK1, PKN1, RB1, SAFB2, SIRT1, SMARCA4, SRC]
GO:1900076	regulation of cellular response to insulin stimulus	180,0E-9	79,0E-6	310,0E-15	10,0E-12	[3, 4, 7, 8, 9]	Group16	13,04	9,00	[IRS1, PAK1, PIK3R1, PKN1, PTPN11, RELA, SIRT1, SRC, TSC2]
GO:1900078	positive regulation of cellular response to insulin stimulus	44,0E-9	19,0E-6	310,0E-15	10,0E-12	[3, 4, 5, 7, 8, 9, 10]	Group16	24,14	7,00	[IRS1, PAK1, PIK3R1, PKN1, PTPN11, SIRT1, SRC]
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	330,0E-9	140,0E-6	310,0E-15	10,0E-12	[4, 5, 6, 7, 8, 9]	Group16	12,16	9,00	[AR, ARRB2, BRCA1, PAK1, PKN1, SAFB2, SIRT1, SMARCA4, SRC]
GO:0030521	androgen receptor signaling pathway	24,0E-9	10,0E-6	310,0E-15	10,0E-12	[5, 6, 7, 8, 9]	Group16	13,70	10,00	[AR, ARRB2, BRCA1, CTNNB1, DAXX, FHL2, RB1, SAFB2, SIRT1, SMARCA4]
GO:0002429	immune response-activating cell surface receptor signaling pathway	43,0E-15	18,0E-12	7,8E-18	240,0E-18	[4, 5, 6, 7, 8]	Group17	6,64	32,00	[ABL1, ACTG1, BCAR1, BCL2, BTRC, CDC42, DOCK1, GRB2, HSP90AA1, IKBKB, IKBKG, LAT, MAP3K7, MAPK1, MUC1, NCOR2, NFKB1, NFKBIA, PAK1, PAK2, PIK3R1, PKN1, PLCG1, PLD2, PSME3, RAF1, RELA, SKP1, SRC, TRAF6, VAV1, WASL]
GO:0031295	T cell costimulation	12,0E-12	5,5E-9	7,8E-18	240,0E-18	[3, 6, 7, 8, 9]	Group17	15,05	14,00	[AKT1, CAV1, CDC42, GRB2, MAP3K14, MTOR, NCOR2, PAK1, PAK2, PIK3R1, PKN1, PTPN11, SRC, VAV1]
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2,5E-9	1,0E-6	7,8E-18	240,0E-18	[4, 5, 6, 7, 8, 9, 10]	Group17	9,32	15,00	[ABL1, ACTG1, CDC42, DOCK1, GRB2, HSP90AA1, MAPK1, PAK1, PIK3R1, PKN1, PLCG1, PLD2, SRC, VAV1, WASL]
GO:0038127	ERBB signaling pathway	9,6E-15	4,1E-12	7,8E-18	240,0E-18	[6, 7, 8]	Group17	13,07	20,00	[ABL1, ADAM17, AKT1, BCAR1, CBL, CBLB, CDC42, EGFR, ERBB2, FASLG, GRB2, HSP90AA1, IQGAP1, MAPK1, PIK3C2A, PIK3R1, PLCG1, PTPN11, SPRY2, SRC]
GO:0048667	cell morphogenesis involved in neuron differentiation	1,7E-6	770,0E-6	7,8E-18	240,0E-18	[5, 6, 7, 8, 9, 10]	Group17	4,03	23,00	[ABL1, ARHGDIA, BCL2, CDC42, DNM2, ERBB2, GRB2, GSK3B, MAP2, MAPK1, MAPK8IP3, NTRK1, PAK1, PARD6B, PIK3R1, PKN1, PLCG1, PTPN11, RB1, RHOA, SLC9A3R1, SRC, WASL]
GO:0000077	DNA damage checkpoint	1,8E-6	800,0E-6	14,0E-15	470,0E-15	[4, 5, 6, 7, 8]	Group18	7,06	12,00	[BRCA1, CDKN1B, H2AFX, MAPK14, MDM2, MUC1, PEA15, PML, PTPN11, SFN, TP53, WAC]
GO:1905269	positive regulation of chromatin organization	560,0E-9	240,0E-6	14,0E-15	470,0E-15	[4, 5, 6, 7, 8]	Group18	9,90	10,00	[BRCA1, CTNNB1, KMT2A, MECP2, MUC1, PML, SIN3A, SIRT1, SMARCB1, TP53]

GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	1,2E-6	540,0E-6	14,0E-15	470,0E-15	[5, 6, 7, 8]	Group18	9,09	10,00	[ABL1, BRCA1, EPHA2, MUC1, PIK3R1, PML, SFN, SIRT1, TNFRSF1A, TP53]
GO:0031056	regulation of histone modification	330,0E-9	140,0E-6	14,0E-15	470,0E-15	[5, 6, 7, 8]	Group18	8,28	12,00	[BRCA1, CTNNB1, KMT2A, MECP2, MUC1, PML, SET, SIN3A, SIRT1, SKI, SMARCB1, TP53]
GO:1902807	negative regulation of cell cycle G1/S phase transition	890,0E-9	380,0E-6	14,0E-15	470,0E-15	[5, 6, 7, 8]	Group18	9,43	10,00	[BCL2, CDKN1B, MDM2, MEN1, MUC1, PML, RB1, SFN, SMARCA4, TP53]
GO:2000045	regulation of G1/S transition of mitotic cell cycle	90,0E-9	39,0E-6	14,0E-15	470,0E-15	[6, 7, 8]	Group18	8,44	13,00	[ADAM17, AKT1, BCL2, CDKN1B, EGFR, MDM2, MUC1, PML, PSME3, RB1, SFN, SMARCA4, TP53]
GO:0048666	neuron development	510,0E-12	220,0E-9	4,6E-27	140,0E-27	[4, 5, 6, 8, 9]	Group19	3,85	41,00	[ABL1, AKT1, ALK, ARHGDIA, ASAP1, BCL2, CDC42, CDH1, DNM2, EGFR, ERBB2, FBXO38, GRB2, GSK3B, HDAC2, HSPA5, IQGAP1, JAK2, MAP2, MAPK1, MAPK8IP3, MDM2, MECP2, MTOR, NTRK1, PAK1, PAK2, PARD6B, PIK3R1, PKN1, PLCG1, PTPN11, PTPRF, RAC3, RB1, RHOA, SKI, SLC9A3R1, SRC, WASL, WDR5]
GO:0031295	T cell costimulation	12,0E-12	5,5E-9	4,6E-27	140,0E-27	[3, 6, 7, 8, 9]	Group19	15,05	14,00	[AKT1, CAV1, CDC42, GRB2, MAP3K14, MTOR, NCOR2, PAK1, PAK2, PIK3R1, PKN1, PTPN11, SRC, VAV1]
GO:0046777	protein autophosphorylation	17,0E-12	7,3E-9	4,6E-27	140,0E-27	[7, 8]	Group19	8,30	21,00	[ABL1, AKT1, ALK, BCR, CAV1, EGFR, ERBB2, GRB2, GSK3B, IQGAP1, JAK2, MAP3K3, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PKN1, RIPK3, SRC, TOM1L1]
GO:0018108	peptidyl-tyrosine phosphorylation	4,3E-18	1,8E-15	4,6E-27	140,0E-27	[7, 8, 9]	Group19	8,46	34,00	[ABL1, ADAM17, ALK, ARRB2, BCR, CAV1, CBL, CBLB, EGFR, EPHA2, ERBB2, GHR, GRB2, HCLS1, HDAC2, HSP90AA1, IL6ST, IQGAP1, JAK2, MAP2K7, MET, MTOR, NTRK1, PAK2, PDGFRB, PPP2CA, PPP2R1A, RACK1, SRC, STAT3, STAT5A, STAT5B, TNFRSF1A, TP53]
GO:0045860	positive regulation of protein kinase activity	210,0E-24	92,0E-21	4,6E-27	140,0E-27	[7, 8, 9, 10]	Group19	8,32	43,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CDKN1B, DAXX, EGFR, ERBB2, GHR, HSPA5, IKBKG, IQGAP1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PRKAR1A, PTPN11, RAF1, RHOA, RIPK3, SIRT1, SPRY2, SRC, TOM1L1, TRAF2, TRAF6]
GO:0038083	peptidyl-tyrosine autophosphorylation	350,0E-9	150,0E-6	4,6E-27	140,0E-27	[8, 9, 10]	Group19	14,55	8,00	[ABL1, CAV1, EGFR, GRB2, IQGAP1, JAK2, NTRK1, SRC]
GO:2001234	negative regulation of apoptotic signaling pathway	900,0E-15	390,0E-12	1,3E-15	41,0E-15	[4, 5, 6, 7, 8]	Group20	9,09	22,00	[AKT1, AR, ARRB2, BCL2, BRCA1, CASP8, CTNNB1, FASLG, HSPA1A, HTT, MDM2, MEN1, MUC1, PEA15, PSME3, RAF1, RB1CC1, RELA, SIRT1, SRC, TCF7L2, TRAF2]
GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	25,0E-9	10,0E-6	1,3E-15	41,0E-15	[5, 6, 7, 8]	Group20	11,83	11,00	[BCL2, BRCA1, CASP8, DAXX, FASLG, GABARAP, PEA15, PIK3R1, RAF1, TNFRSF1A, TRAF2]

GO:2001236	regulation of extrinsic apoptotic signaling pathway	2,4E-15	1,0E-12	1,3E-15	41,0E-15	[5, 6, 7, 8]	Group20	12,09	22,00	[AKT1, AR, BCL2, BRCA1, CASP8, CAV1, FASLG, HSPA1A, HTT, MEN1, PAK2, PEA15, PML, PPP2R1A, PSME3, RAF1, RB1CC1, RELA, SRC, TCF7L2, TRAF1, TRAF2]
GO:0052548	regulation of endopeptidase activity	430,0E-9	190,0E-6	1,3E-15	41,0E-15	[6, 7, 8]	Group20	4,88	20,00	[AKT1, ARRB2, ATXN3, CASP8, CDKN1B, FASLG, JAK2, LXN, MDM2, PAK2, PML, PSME3, RACK1, RAF1, SFN, SIRT1, SMAD3, SRC, STAT3, TRAF2]
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	180,0E-15	79,0E-12	1,3E-15	41,0E-15	[5, 6, 7, 8, 9]	Group20	14,41	17,00	[AKT1, AR, BCL2, BRCA1, CASP8, FASLG, HSPA1A, HTT, MEN1, PEA15, PSME3, RAF1, RB1CC1, RELA, SRC, TCF7L2, TRAF2]
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	29,0E-9	12,0E-6	1,3E-15	41,0E-15	[6, 7, 8, 9, 10]	Group20	7,24	16,00	[AKT1, ARRB2, CASP8, CDKN1B, FASLG, JAK2, MDM2, PAK2, PML, RACK1, RAF1, SFN, SIRT1, SMAD3, SRC, TRAF2]
GO:0031400	negative regulation of protein modification process	57,0E-15	25,0E-12	29,0E-33	930,0E-33	[5, 6, 7, 8]	Group21	5,82	36,00	[ABL1, AKT1, ARRB2, BRCA1, CAV1, CBL, CBLB, CDKN1B, CTNNB1, HDAC2, HSPA1A, IKBKB, MECP2, MEN1, MTOR, PAK2, PKN1, PML, PPP2CA, PPP2R1A, PRKAR1A, PSME3, RACK1, RB1, SET, SFN, SIN3A, SIRT1, SKI, SLC9A3R1, SMAD7, SMARCB1, SPRY2, TSC2, YWHAB, YWHAG]
GO:0043549	regulation of kinase activity	19,0E-27	8,5E-24	29,0E-33	930,0E-33	[5, 7, 8]	Group21	6,89	59,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CAV1, CBL, CBLB, CDC42, CDKN1B, DAXX, EGFR, ERBB2, GHR, HSPA5, IKBKG, IQGAP1, IRS1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PIK3R1, PKN1, PLCG1, PPP2CA, PPP2R1A, PRKAB1, PRKAR1A, PTPN11, RACK1, RAF1, RB1, RHOA, RIPK3, SFN, SIRT1, SLC9A3R1, SPRY2, SRC, TOM1L1, TRAF2, TRAF6, TSC2, YWHAG]
GO:0042326	negative regulation of phosphorylation	1,5E-9	650,0E-9	29,0E-33	930,0E-33	[6, 7, 8]	Group21	5,49	25,00	[ABL1, AKT1, ARRB2, CAV1, CBL, CBLB, CDKN1B, HDAC4, MEN1, MTOR, PAK2, PKN1, PPP2CA, PPP2R1A, PRKAR1A, RACK1, RB1, SFN, SIRT1, SLC9A3R1, SMAD7, SPRY2, STAT3, TSC2, YWHAG]
GO:0001933	negative regulation of protein phosphorylation	6,0E-9	2,6E-6	29,0E-33	930,0E-33	[6, 7, 8, 9]	Group21	5,53	23,00	[ABL1, AKT1, ARRB2, CAV1, CBL, CBLB, CDKN1B, MEN1, MTOR, PAK2, PKN1, PPP2CA, PPP2R1A, PRKAR1A, RACK1, RB1, SFN, SIRT1, SLC9A3R1, SMAD7, SPRY2, TSC2, YWHAG]
GO:0045859	regulation of protein kinase activity	17,0E-27	7,4E-24	29,0E-33	930,0E-33	[6, 7, 8, 9]	Group21	7,21	57,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CAV1, CBL, CBLB, CDC42, CDKN1B, DAXX, EGFR, ERBB2, GHR, HSPA5, IKBKG, IQGAP1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PPP2R1A, PRKAB1, PRKAR1A, PTPN11, RACK1, RAF1,

										RB1, RHOA, RIPK3, SFN, SIRT1, SLC9A3R1, SPRY2, SRC, TOM1L1, TRAF2, TRAF6, TSC2, YWHAG]
GO:0006469	negative regulation of protein kinase activity	840,0E-12	360,0E-9	29,0E-33	930,0E-33	[7, 8, 9, 10]	Group2 1	7,51	19,00	[ABL1, AKT1, CAV1, CBL, CBLB, CDKN1B, MEN1, PAK2, PKN1, PPP2CA, PPP2R1A, PRKAR1A, RACK1, RB1, SFN, SIRT1, SPRY2, TSC2, YWHAG]
GO:0071901	negative regulation of protein serine/threonine kinase activity	800,0E-9	340,0E-6	29,0E-33	930,0E-33	[8, 9, 10, 11]	Group2 1	8,46	11,00	[ABL1, CAV1, CDKN1B, MEN1, PPP2CA, PPP2R1A, PRKAR1A, SFN, SIRT1, SPRY2, YWHAG]
GO:1901184	regulation of ERBB signaling pathway	380,0E-9	160,0E-6	1,0E-18	34,0E-18	[4, 5, 6, 7, 8, 9]	Group2 2	10,31	10,00	[ADAM17, AKT1, CBL, CBLB, CDC42, EGFR, ERBB2, FASLG, GRB2, SPRY2]
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2,5E-9	1,0E-6	1,0E-18	34,0E-18	[4, 5, 6, 7, 8, 9, 10]	Group2 2	9,32	15,00	[ABL1, ACTG1, CDC42, DOCK1, GRB2, HSP90AA1, MAPK1, PAK1, PIK3R1, PKN1, PLCG1, PLD2, SRC, VAV1, WASL]
GO:0038127	ERBB signaling pathway	9,6E-15	4,1E-12	1,0E-18	34,0E-18	[6, 7, 8]	Group2 2	13,07	20,00	[ABL1, ADAM17, AKT1, BCAR1, CBL, CBLB, CDC42, EGFR, ERBB2, FASLG, GRB2, HSP90AA1, IQGAP1, MAPK1, PIK3C2A, PIK3R1, PLCG1, PTPN11, SPRY2, SRC]
GO:0048008	platelet-derived growth factor receptor signaling pathway	1,1E-9	500,0E-9	1,0E-18	34,0E-18	[6, 7, 8]	Group2 2	18,52	10,00	[ABL1, BCAR1, BCR, IQGAP1, JAK2, PDGFRB, PIK3C2A, PTPN11, SLC9A3R1, SRC]
GO:0046777	protein autophosphorylation	17,0E-12	7,3E-9	1,0E-18	34,0E-18	[7, 8]	Group2 2	8,30	21,00	[ABL1, AKT1, ALK, BCR, CAV1, EGFR, ERBB2, GRB2, GSK3B, IQGAP1, JAK2, MAP3K3, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PKN1, RIPK3, SRC, TOM1L1]
GO:0007173	epidermal growth factor receptor signaling pathway	1,0E-12	460,0E-12	1,0E-18	34,0E-18	[7, 8, 9]	Group2 2	12,98	17,00	[ABL1, ADAM17, AKT1, BCAR1, CBL, CBLB, CDC42, EGFR, FASLG, GRB2, IQGAP1, PIK3C2A, PIK3R1, PLCG1, PTPN11, SPRY2, SRC]
GO:0038083	peptidyl-tyrosine autophosphorylation	350,0E-9	150,0E-6	1,0E-18	34,0E-18	[8, 9, 10]	Group2 2	14,55	8,00	[ABL1, CAV1, EGFR, GRB2, IQGAP1, JAK2, NTRK1, SRC]
GO:0048666	neuron development	510,0E-12	220,0E-9	17,0E-15	560,0E-15	[4, 5, 6, 8, 9]	Group2 3	3,85	41,00	[ABL1, AKT1, ALK, ARHGDIA, ASAP1, BCL2, CDC42, CDH1, DNM2, EGFR, ERBB2, FBXO38, GRB2, GSK3B, HDAC2, HSPA5, IQGAP1, JAK2, MAP2, MAPK1, MAPK8IP3, MDM2, MECP2, MTOR, NTRK1, PAK1, PAK2, PARD6B, PIK3R1, PKN1, PLCG1, PTPN11, PTPRF, RAC3, RB1, RHOA, SKI, SLC9A3R1, SRC, WASL, WDR5]
GO:0050767	regulation of neurogenesis	120,0E-9	53,0E-6	17,0E-15	560,0E-15	[5, 6, 7, 8]	Group2 3	3,95	29,00	[ABL1, AKT1, ARHGDIA, ASAP1, BCL2, CDH2, CTNNB1, DNM2, FBXO38, FLNA, GSK3B, HDAC2, HSPA5, IL6ST, IQGAP1, MAPK8IP3, MDM2, MTOR, NTRK1, PAK1, PKN1, PTPRF, RAC3, RELA, RHOA, SKI, STAT3, TCF7L2, YWHAG]
GO:0030182	neuron differentiation	42,0E-12	18,0E-9	17,0E-15	560,0E-15	[5, 7, 8]	Group2 3	3,68	49,00	[ABL1, AKT1, ALK, ARHGDIA, ASAP1, AXIN1, BCL2, CDC42, CDH1, CEBPB, CTNNB1, DNM2, EGFR, EPHA2, ERBB2, FBXO38, GRB2, GSK3B, HDAC2, HSPA5, IQGAP1, JAK2, MAP2, MAPK1, MAPK8IP3, MDM2, MECP2,

										MTOR, NTRK1, PAK1, PAK2, PARD6B, PIK3R1, PKN1, PLCG1, PTPN11, PTPRF, RAC3, RB1, RHOA, SKI, SLC9A3R1, SMARCC2, SRC, STAT3, TCF7L2, WASL, WDR5, YWHAG]
GO:0031175	neuron projection development	210,0E-12	95,0E-9	17,0E-15	560,0E-15	[4, 5, 6, 7, 9, 10]	Group2 3	4,19	38,00	[ABL1, AKT1, ARHGDIA, ASAP1, BCL2, CDC42, CDH1, DNM2, EGFR, ERBB2, FBXO38, GRB2, GSK3B, HDAC2, HSPA5, IQGAP1, JAK2, MAP2, MAPK1, MAPK8IP3, MDM2, MECP2, MTOR, NTRK1, PAK1, PAK2, PARD6B, PIK3R1, PKN1, PLCG1, PTPN11, PTPRF, RAC3, RB1, RHOA, SRC, WASL, WDR5]
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2,5E-9	1,0E-6	17,0E-15	560,0E-15	[4, 5, 6, 7, 8, 9, 10]	Group2 3	9,32	15,00	[ABL1, ACTG1, CDC42, DOCK1, GRB2, HSP90AA1, MAPK1, PAK1, PIK3R1, PKN1, PLCG1, PLD2, SRC, VAV1, WASL]
GO:0046777	protein autophosphorylation	17,0E-12	7,3E-9	17,0E-15	560,0E-15	[7, 8]	Group2 3	8,30	21,00	[ABL1, AKT1, ALK, BCR, CAV1, EGFR, ERBB2, GRB2, GSK3B, IQGAP1, JAK2, MAP3K3, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PKN1, RIPK3, SRC, TOM1L1]
GO:0048667	cell morphogenesis involved in neuron differentiation	1,7E-6	770,0E-6	17,0E-15	560,0E-15	[5, 6, 7, 8, 9, 10]	Group2 3	4,03	23,00	[ABL1, ARHGDIA, BCL2, CDC42, DNM2, ERBB2, GRB2, GSK3B, MAP2, MAPK1, MAPK8IP3, NTRK1, PAK1, PARD6B, PIK3R1, PKN1, PLCG1, PTPN11, RB1, RHOA, SLC9A3R1, SRC, WASL]
GO:0042516	regulation of tyrosine phosphorylation of Stat3 protein	1,5E-6	650,0E-6	3,4E-21	100,0E-21	[8, 9, 10, 11, 12]	Group2 4	14,89	7,00	[GHR, HDAC2, IL6ST, JAK2, PPP2CA, PPP2R1A, STAT3]
GO:0046425	regulation of JAK-STAT cascade	970,0E-9	420,0E-6	3,4E-21	100,0E-21	[6, 7, 8]	Group2 4	7,50	12,00	[CAV1, ELP2, GHR, HCLS1, HDAC2, IKBKB, IL6ST, JAK2, PPP2CA, PPP2R1A, STAT3, TNFRSF1A]
GO:0046777	protein autophosphorylation	17,0E-12	7,3E-9	3,4E-21	100,0E-21	[7, 8]	Group2 4	8,30	21,00	[ABL1, AKT1, ALK, BCR, CAV1, EGFR, ERBB2, GRB2, GSK3B, IQGAP1, JAK2, MAP3K3, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PKN1, RIPK3, SRC, TOM1L1]
GO:0060396	growth hormone receptor signaling pathway	14,0E-9	6,2E-6	3,4E-21	100,0E-21	[6, 7, 8, 9]	Group2 4	28,00	7,00	[GHR, JAK2, MAPK1, PIK3R1, STAT3, STAT5A, STAT5B]
GO:0018108	peptidyl-tyrosine phosphorylation	4,3E-18	1,8E-15	3,4E-21	100,0E-21	[7, 8, 9]	Group2 4	8,46	34,00	[ABL1, ADAM17, ALK, ARRB2, BCR, CAV1, CBL, CBLB, EGFR, EPHA2, ERBB2, GHR, GRB2, HCLS1, HDAC2, HSP90AA1, IL6ST, IQGAP1, JAK2, MAP2K7, MET, MTOR, NTRK1, PAK2, PDGFRB, PPP2CA, PPP2R1A, RACK1, SRC, STAT3, STAT5A, STAT5B, TNFRSF1A, TP53]
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	980,0E-15	420,0E-12	3,4E-21	100,0E-21	[7, 8, 9, 10]	Group2 4	9,05	22,00	[ABL1, ADAM17, ARRB2, CAV1, CBL, CBLB, EGFR, GHR, HCLS1, HDAC2, IL6ST, IQGAP1, JAK2, MTOR, PAK2, PPP2CA, PPP2R1A, RACK1, SRC, STAT3, TNFRSF1A, TP53]
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	28,0E-9	12,0E-6	3,4E-21	100,0E-21	[7, 8, 9, 10, 11]	Group2 4	13,51	10,00	[CAV1, GHR, HCLS1, HDAC2, IL6ST, JAK2, PPP2CA, PPP2R1A, STAT3, TNFRSF1A]

GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	18,0E-9	7,9E-6	3,4E-21	100,0E-21	[7, 8, 9, 10, 11]	Group2 4	8,06	15,00	[ABL1, ADAM17, ARRB2, GHR, HCLS1, HDAC2, IL6ST, IQGAP1, JAK2, MTOR, PAK2, SRC, STAT3, TNFRSF1A, TP53]
GO:0051253	negative regulation of RNA metabolic process	840,0E-24	360,0E-21	27,0E-24	870,0E-24	[4, 5, 6, 7, 8]	Group2 5	5,07	65,00	[AR, AXIN1, BRCA1, BTRC, CAV1, CDKN1B, CEBPB, CHD8, CTNNB1, DACH1, DAXX, ESR1, FASLG, FHL2, FLNA, H2AFX, HCFC1, HCLS1, HDAC2, HDAC4, HDAC7, HSPA1A, HSPA8, KHDRBS1, LRRFIP1, MDM2, MECP2, MEN1, MUC1, NCOR2, NFKB1, NFKB2, NR3C1, PABPC1, PML, RB1, RELA, RNPS1, RUNX1T1, SET, SIN3A, SIRT1, SKI, SMAD2, SMAD3, SMAD7, SMARCA4, SMARCC2, SORBS3, SQSTM1, SRC, SRSF4, STAT3, TCF7L2, TOB1, TP53, TRAF6, U2AF2, UBE2I, USP3, VDR, YBX1, YWHAB, YWHAQ, ZHX1]
GO:0051254	positive regulation of RNA metabolic process	2,6E-24	1,1E-21	27,0E-24	870,0E-24	[4, 5, 6, 7, 8]	Group2 5	4,87	75,00	[AKT1, AR, AXIN1, BRCA1, BTRC, CDH1, CEBPB, CHD8, CTNNB1, DNM2, EGFR, ERBB2, ESR1, FHL2, GSK3B, HCFC1, HCLS1, HDAC2, HDAC4, HSPA1A, HSPA5, HSPA8, IKBKB, IKBKG, KMT2A, MAP3K2, MAPK1, MAPK14, MECP2, MEN1, MET, MTOR, MUC1, MYBL2, NFKB1, NFKB2, NFKBIA, NR3C1, PABPC1, PHF20, PIK3R1, PML, POLR2A, RAF1, RB1, RELA, SIN3A, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SQSTM1, SRC, SRSF1, STAT3, STAT5B, TBP, TCF7L2, TNFRSF1A, TOB1, TOP2A, TP53, TRAF6, U2AF2, VDR, WAC, WDR5, YBX1]
GO:0006351	transcription, DNA-templated	33,0E-24	14,0E-21	27,0E-24	870,0E-24	[5, 6, 7, 8, 9]	Group2 5	3,10	122,00	[ABL1, AFF4, AKT1, ALK, AR, ARRB2, ATXN3, AXIN1, BRCA1, BTRC, CAV1, CBL, CDH1, CDKN1B, CEBPB, CHD8, CTNNB1, DACH1, DAXX, DNM2, EGFR, ELP2, ERBB2, ESR1, FASLG, FHL2, FLNA, GSK3B, H2AFX, HCFC1, HCLS1, HDAC2, HDAC4, HDAC7, HSPA1A, HSPA5, HSPA8, IKBKB, IKBKG, JAK2, KHDRBS1, KMT2A, LRRFIP1, MAP3K2, MAP3K7, MAPK1, MAPK14, MDM2, MECP2, MED28, MEN1, MET, MTOR, MUC1, MYBL2, NCOR2, NFKB1, NFKB2, NFKBIA, NR3C1, NTRK1, PHF20, PIK3R1, PKN1, PML, POLR2A, PPP2CA, PPP2R1A, PRKAR1A, PSME3, RAF1, RB1, RB1CC1, RBBP5, RELA, RIPK3, RNPS1, RUNX1T1, SAFB2, SET, SIN3A, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SORBS3, SP110, SQSTM1, SRC, SRSF1, SRSF4, STAT3, STAT5A, STAT5B, TBP, TCF7L2, TNFRSF1A, TOB1, TOP2A, TP53, TRAF1, TRAF2, TRAF6, U2AF2, UBE2I, USP3, VAV1, VDR, WAC, WASL, WDR5, YBX1, YWHAB, YWHAQ, ZHX1]

GO:1902680	positive regulation of RNA biosynthetic process	6,2E-21	2,7E-18	27,0E-24	870,0E-24	[5, 6, 7, 8, 9]	Group2 5	4,62	69,00	[AKT1, AR, AXIN1, BRCA1, BTRC, CDH1, CEBPB, CHD8, CTNNB1, DNM2, EGFR, ERBB2, ESR1, FHL2, GSK3B, HCFC1, HCLS1, HDAC2, HDAC4, HSPA5, IKBKB, IKBKG, KMT2A, MAP3K2, MAPK1, MAPK14, MECP2, MEN1, MET, MTOR, MUC1, MYBL2, NFKB1, NFKB2, NFKBIA, NR3C1, PHF20, PIK3R1, PML, POLR2A, RAF1, RB1, RELA, SIN3A, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SQSTM1, SRC, STAT3, STAT5B, TBP, TCF7L2, TNFRSF1A, TOP2A, TP53, TRAF6, VDR, WAC, WDR5, YBX1]
GO:0006355	regulation of transcription, DNA-templated	79,0E-24	34,0E-21	27,0E-24	870,0E-24	[5, 6, 7, 8, 9, 10]	Group2 5	3,14	118,00	[ABL1, AFF4, AKT1, ALK, AR, ARRB2, ATXN3, AXIN1, BRCA1, BTRC, CAV1, CBL, CDH1, CDKN1B, CEBPB, CHD8, CTNNB1, DACH1, DAXX, DNM2, EGFR, ELP2, ERBB2, ESR1, FASLG, FHL2, FLNA, GSK3B, H2AFX, HCFC1, HCLS1, HDAC2, HDAC4, HDAC7, HSPA1A, HSPA5, HSPA8, IKBKB, IKBKG, JAK2, KHDRBS1, KMT2A, LRRFIP1, MAP3K2, MAP3K7, MAPK1, MAPK14, MDM2, MECP2, MED28, MEN1, MET, MTOR, MUC1, MYBL2, NCOR2, NFKB1, NFKB2, NFKBIA, NR3C1, NTRK1, PHF20, PIK3R1, PKN1, PML, POLR2A, PPP2CA, PPP2R1A, PRKAR1A, PSME3, RAF1, RB1, RB1CC1, RBBP5, RELA, RIPK3, RUNX1T1, SAFB2, SET, SIN3A, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SORBS3, SP110, SQSTM1, SRC, STAT3, STAT5A, STAT5B, TBP, TCF7L2, TNFRSF1A, TOB1, TOP2A, TP53, TRAF1, TRAF2, TRAF6, UBE2I, USP3, VAV1, VDR, WAC, WASL, WDR5, YBX1, YWHAB, YWHAQ, ZHX1]
GO:0006366	transcription from RNA polymerase II promoter	76,0E-24	33,0E-21	27,0E-24	870,0E-24	[6, 7, 8, 9, 10]	Group2 5	3,99	88,00	[ABL1, AFF4, AKT1, AR, ARRB2, AXIN1, BRCA1, CAV1, CEBPB, CHD8, CTNNB1, DACH1, EGFR, ELP2, ERBB2, ESR1, FASLG, FHL2, FLNA, GSK3B, HCFC1, HCLS1, HDAC2, HDAC4, HDAC7, HSPA1A, HSPA5, IKBKB, IKBKG, KMT2A, LRRFIP1, MAPK14, MDM2, MECP2, MEN1, MET, MUC1, MYBL2, NCOR2, NFKB1, NFKB2, NFKBIA, NR3C1, PHF20, PIK3R1, PKN1, PML, POLR2A, PRKAR1A, PSME3, RAF1, RB1, RELA, RNPS1, SAFB2, SIN3A, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SORBS3, SQSTM1, SRSF1, SRSF4, STAT3, STAT5A, STAT5B, TBP, TCF7L2, TNFRSF1A, TOB1, TOP2A, TP53, TRAF6, U2AF2, UBE2I, USP3, VDR, WDR5, YBX1, ZHX1]

GO:0045893	positive regulation of transcription, DNA-templated	13,0E-21	5,8E-18	27,0E-24	870,0E-24	[5, 6, 7, 8, 9, 10, 11]	Group2 5	4,62	68,00	[AKT1, AR, AXIN1, BRCA1, BTRC, CDH1, CEBPB, CHD8, CTNNB1, DNM2, EGFR, ERBB2, ESR1, FHL2, GSK3B, HCFC1, HCLS1, HDAC2, HDAC4, HSPA5, IKBKB, IKBKG, KMT2A, MAP3K2, MAPK1, MAPK14, MECP2, MEN1, MET, MTOR, MUC1, MYBL2, NFKB1, NFKB2, NFKBIA, NR3C1, PHF20, PIK3R1, PML, RAF1, RB1, RELA, SIN3A, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SQSTM1, SRC, STAT3, STAT5B, TBP, TCF7L2, TNFRSF1A, TOP2A, TP53, TRAF6, VDR, WAC, WDR5, YBX1]
GO:1903507	negative regulation of nucleic acid-templated transcription	34,0E-21	14,0E-18	27,0E-24	870,0E-24	[6, 7, 8, 9, 10]	Group2 5	5,02	61,00	[AR, AXIN1, BRCA1, BTRC, CAV1, CDKN1B, CEBPB, CHD8, CTNNB1, DACH1, DAXX, ESR1, FASLG, FHL2, FLNA, H2AFX, HCFC1, HCLS1, HDAC2, HDAC4, HDAC7, HSPA1A, HSPA8, KHDRBS1, LRRFIP1, MDM2, MECP2, MEN1, MUC1, NCOR2, NFKB1, NFKB2, NR3C1, PML, RB1, RELA, RUNX1T1, SET, SIN3A, SIRT1, SKI, SMAD2, SMAD3, SMAD7, SMARCA4, SMARCC2, SORBS3, SQSTM1, SRC, STAT3, TCF7L2, TOB1, TP53, TRAF6, UBE2I, USP3, VDR, YBX1, YWHAB, YWHAQ, ZHX1]
GO:0006357	regulation of transcription from RNA polymerase II promoter	57,0E-21	24,0E-18	27,0E-24	870,0E-24	[6, 7, 8, 9, 10, 11]	Group2 5	3,95	79,00	[ABL1, AKT1, AR, AXIN1, BRCA1, CAV1, CEBPB, CHD8, CTNNB1, DACH1, EGFR, ELP2, ERBB2, ESR1, FASLG, FHL2, GSK3B, HCFC1, HCLS1, HDAC2, HDAC4, HDAC7, HSPA1A, HSPA5, IKBKB, IKBKG, KMT2A, LRRFIP1, MAPK14, MDM2, MECP2, MEN1, MET, MUC1, MYBL2, NCOR2, NFKB1, NFKB2, NFKBIA, NR3C1, PHF20, PIK3R1, PKN1, PML, PRKAR1A, PSME3, RAF1, RB1, RELA, SAFB2, SIN3A, SIRT1, SKI, SMAD1, SMAD2, SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCC2, SORBS3, SQSTM1, STAT3, STAT5A, STAT5B, TCF7L2, TNFRSF1A, TOB1, TOP2A, TP53, TRAF6, UBE2I, USP3, VDR, WDR5, YBX1, ZHX1]
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	4,1E-15	1,7E-12	27,0E-24	870,0E-24	[6, 7, 8, 9, 10, 11, 12]	Group2 5	5,31	43,00	[AR, AXIN1, CAV1, CHD8, CTNNB1, DACH1, ESR1, FASLG, FHL2, HCFC1, HCLS1, HDAC2, HDAC4, HDAC7, HSPA1A, MDM2, MECP2, MEN1, NCOR2, NFKB1, NFKB2, NR3C1, RB1, RELA, SIN3A, SIRT1, SKI, SMAD2, SMAD3, SMAD7, SMARCA4, SMARCC2, SORBS3, SQSTM1, STAT3, TCF7L2, TP53, TRAF6, UBE2I, USP3, VDR, YBX1, ZHX1]
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	100,0E-18	45,0E-15	27,0E-24	870,0E-24	[6, 7, 8, 9, 10, 11, 12]	Group2 5	4,73	54,00	[AKT1, AR, BRCA1, CEBPB, CHD8, CTNNB1, EGFR, ESR1, GSK3B, HCFC1, HCLS1, HDAC2, HDAC4, HSPA5, IKBKB, IKBKG, KMT2A, MAPK14, MEN1, MET, MUC1, MYBL2, NFKB1, NFKB2, NFKBIA, NR3C1, PHF20, PIK3R1, PML, RAF1, RB1, RELA, SIN3A, SIRT1, SKI, SMAD1, SMAD2,

										SMAD3, SMAD5, SMAD7, SMARCA4, SMARCB1, SMARCC1, SQSTM1, STAT3, STAT5B, TCF7L2, TNFRSF1A, TOP2A, TP53, TRAF6, VDR, WDR5, YBX1]
GO:0043984	histone H4-K16 acetylation	45,0E-9	19,0E-6	79,0E-12	2,5E-9	[8, 9, 10, 12, 13]	Group2 6	33,33	6,00	[BRCA1, HCFC1, KMT2A, PHF20, SIRT1, WDR5]
GO:1905269	positive regulation of chromatin organization	560,0E-9	240,0E-6	79,0E-12	2,5E-9	[4, 5, 6, 7, 8]	Group2 6	9,90	10,00	[BRCA1, CTNNB1, KMT2A, MECP2, MUC1, PML, SIN3A, SIRT1, SMARCB1, TP53]
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	1,2E-6	540,0E-6	79,0E-12	2,5E-9	[5, 6, 7, 8]	Group2 6	9,09	10,00	[ABL1, BRCA1, EPHA2, MUC1, PIK3R1, PML, SFN, SIRT1, TNFRSF1A, TP53]
GO:0031056	regulation of histone modification	330,0E-9	140,0E-6	79,0E-12	2,5E-9	[5, 6, 7, 8]	Group2 6	8,28	12,00	[BRCA1, CTNNB1, KMT2A, MECP2, MUC1, PML, SET, SIN3A, SIRT1, SKI, SMARCB1, TP53]
GO:0031057	negative regulation of histone modification	570,0E-9	240,0E-6	79,0E-12	2,5E-9	[5, 6, 7, 8, 9]	Group2 6	17,07	7,00	[BRCA1, MECP2, SET, SIN3A, SIRT1, SKI, SMARCB1]
GO:0018205	peptidyl-lysine modification	49,0E-9	21,0E-6	79,0E-12	2,5E-9	[7, 8]	Group2 6	5,34	21,00	[BRCA1, CTNNB1, HCFC1, HDAC2, HDAC4, HDAC7, KMT2A, MAP3K7, MDM2, MECP2, MEN1, MUC1, PHF20, RBBP5, SET, SIN3A, SIRT1, SMARCB1, TOP2A, UBE2I, WDR5]
GO:0016573	histone acetylation	910,0E-9	390,0E-6	79,0E-12	2,5E-9	[6, 7, 8, 10, 11]	Group2 6	7,55	12,00	[BRCA1, HCFC1, KMT2A, MAP3K7, MECP2, MUC1, PHF20, SET, SIN3A, SIRT1, SMARCB1, WDR5]
GO:0018394	peptidyl-lysine acetylation	280,0E-9	120,0E-6	79,0E-12	2,5E-9	[8, 9]	Group2 6	7,65	13,00	[BRCA1, HCFC1, HDAC2, KMT2A, MAP3K7, MECP2, MUC1, PHF20, SET, SIN3A, SIRT1, SMARCB1, WDR5]
GO:2000756	regulation of peptidyl-lysine acetylation	27,0E-9	12,0E-6	79,0E-12	2,5E-9	[7, 8, 9, 10]	Group2 6	16,07	9,00	[BRCA1, HDAC2, KMT2A, MECP2, MUC1, SET, SIN3A, SIRT1, SMARCB1]
GO:2000757	negative regulation of peptidyl-lysine acetylation	65,0E-9	28,0E-6	79,0E-12	2,5E-9	[7, 8, 9, 10, 11]	Group2 6	31,58	6,00	[BRCA1, HDAC2, MECP2, SET, SIN3A, SIRT1]
GO:0043967	histone H4 acetylation	1,4E-6	640,0E-6	79,0E-12	2,5E-9	[7, 8, 9, 11, 12]	Group2 6	12,12	8,00	[BRCA1, HCFC1, KMT2A, MUC1, PHF20, SIRT1, SMARCB1, WDR5]
GO:0002218	activation of innate immune response	6,7E-12	2,9E-9	440,0E-30	14,0E-27	[3, 5, 6, 7, 8]	Group2 7	7,80	23,00	[ARRB2, BTRC, CASP8, CAV1, ESR1, HSPA1A, IKBKB, IKBKG, MAP3K1, MAP3K7, MUC1, NFKB1, NFKBIA, PAK1, PAK2, PKN1, PSME3, RAF1, RELA, SIN3A, SKP1, SRC, TRAF6]
GO:0002429	immune response-activating cell surface receptor signaling pathway	43,0E-15	18,0E-12	440,0E-30	14,0E-27	[4, 5, 6, 7, 8]	Group2 7	6,64	32,00	[ABL1, ACTG1, BCAR1, BCL2, BTRC, CDC42, DOCK1, GRB2, HSP90AA1, IKBKB, IKBKG, LAT, MAP3K7, MAPK1, MUC1, NCOR2, NFKB1, NFKBIA, PAK1, PAK2, PIK3R1, PKN1, PLCG1, PLD2, PSME3, RAF1, RELA, SKP1, SRC, TRAF6, VAV1, WASL]
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2,5E-9	1,0E-6	440,0E-30	14,0E-27	[4, 5, 6, 7, 8, 9, 10]	Group2 7	9,32	15,00	[ABL1, ACTG1, CDC42, DOCK1, GRB2, HSP90AA1, MAPK1, PAK1, PIK3R1, PKN1, PLCG1, PLD2, SRC, VAV1, WASL]

GO:0050851	antigen receptor-mediated signaling pathway	200,0E-12	89,0E-9	440,0E-30	14,0E-27	[5, 6, 7, 8, 9]	Group27	7,27	21,00	[ABL1, BCAR1, BCL2, BTRC, IKBKB, IKBKG, LAT, MAP3K7, MAPK1, NCOR2, NFKB1, NFKBIA, PAK1, PAK2, PIK3R1, PKN1, PLCG1, PSME3, RELA, SKP1, TRAF6]
GO:0043433	negative regulation of sequence-specific DNA binding transcription factor activity	310,0E-9	130,0E-6	440,0E-30	14,0E-27	[2, 3, 4, 7, 8, 9, 10, 11, 12]	Group27	8,33	12,00	[ARRB2, BTRC, ESR1, FLNA, HDAC2, HDAC4, MEN1, NFKBIA, RB1, SIRT1, SMAD7, TCF7L2]
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	250,0E-15	100,0E-12	440,0E-30	14,0E-27	[2, 3, 4, 7, 8, 9, 10, 11, 12]	Group27	9,13	23,00	[AKT1, ALK, AR, CTNNB1, ESR1, HDAC4, HSPA1A, IKBKB, IKBKG, JAK2, LRRFIP1, MAP3K7, NFKB1, NFKB2, NFKBIA, NTRK1, RELA, RIPK3, SMARCA4, SMARCB1, TRAF1, TRAF2, TRAF6]
GO:0051403	stress-activated MAPK cascade	1,0E-12	460,0E-12	440,0E-30	14,0E-27	[5, 6, 7, 9, 10]	Group27	8,52	23,00	[AKT1, AXIN1, BTRC, CDC42, DAXX, EGFR, IKBKB, IKBKG, MAP2K7, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, NFKB1, PAK1, PKN1, RB1CC1, SKP1, TRAF2, TRAF6]
GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	2,7E-18	1,1E-15	440,0E-30	14,0E-27	[3, 6, 7, 8, 9, 10, 11]	Group27	8,59	34,00	[AKT1, ALK, AR, ARRB2, BTRC, CTNNB1, ESR1, FLNA, HDAC2, HDAC4, HSPA1A, IKBKB, IKBKG, JAK2, LRRFIP1, MAP3K7, MAPK1, MAPK14, MEN1, NFKB1, NFKB2, NFKBIA, NTRK1, RB1, RELA, RIPK3, SIRT1, SMAD7, SMARCA4, SMARCB1, TCF7L2, TRAF1, TRAF2, TRAF6]
GO:0050852	T cell receptor signaling pathway	7,1E-12	3,0E-9	440,0E-30	14,0E-27	[6, 7, 8, 9, 10]	Group27	9,90	19,00	[BCAR1, BTRC, IKBKB, IKBKG, LAT, MAP3K7, MAPK1, NCOR2, NFKB1, NFKBIA, PAK1, PAK2, PIK3R1, PKN1, PLCG1, PSME3, RELA, SKP1, TRAF6]
GO:0051092	positive regulation of NF-kappaB transcription factor activity	38,0E-12	16,0E-9	440,0E-30	14,0E-27	[3, 4, 5, 8, 9, 10, 11, 12, 13]	Group27	11,35	16,00	[ALK, AR, HSPA1A, IKBKB, IKBKG, LRRFIP1, MAP3K7, NFKB1, NFKB2, NFKBIA, NTRK1, RELA, RIPK3, TRAF1, TRAF2, TRAF6]
GO:0002223	stimulatory C-type lectin receptor signaling pathway	9,8E-12	4,2E-9	440,0E-30	14,0E-27	[6, 7, 8, 9, 10, 11]	Group27	12,40	16,00	[BTRC, IKBKB, IKBKG, MAP3K7, MUC1, NFKB1, NFKBIA, PAK1, PAK2, PKN1, PSME3, RAF1, RELA, SKP1, SRC, TRAF6]
GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	8,2E-9	3,6E-6	440,0E-30	14,0E-27	[5, 6, 7, 8, 9, 10, 11, 12]	Group27	22,86	8,00	[CASP8, HSPA1A, IKBKB, IKBKG, MAP3K7, NFKBIA, RELA, TRAF6]
GO:1900076	regulation of cellular response to insulin stimulus	180,0E-9	79,0E-6	1,0E-27	33,0E-27	[3, 4, 7, 8, 9]	Group28	13,04	9,00	[IRS1, PAK1, PIK3R1, PKN1, PTPN11, RELA, SIRT1, SRC, TSC2]
GO:1900078	positive regulation of cellular response to insulin stimulus	44,0E-9	19,0E-6	1,0E-27	33,0E-27	[3, 4, 5, 7, 8, 9, 10]	Group28	24,14	7,00	[IRS1, PAK1, PIK3R1, PKN1, PTPN11, SIRT1, SRC]
GO:0031295	T cell costimulation	12,0E-12	5,5E-9	1,0E-27	33,0E-27	[3, 6, 7, 8, 9]	Group28	15,05	14,00	[AKT1, CAV1, CDC42, GRB2, MAP3K14, MTOR, NCOR2, PAK1, PAK2, PIK3R1, PKN1, PTPN11, SRC, VAV1]

GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	330,0E-9	140,0E-6	1,0E-27	33,0E-27	[4, 5, 6, 7, 8, 9]	Group28	12,16	9,00	[AR, ARRB2, BRCA1, PAK1, PKN1, SAFB2, SIRT1, SMARCA4, SRC]
GO:0050870	positive regulation of T cell activation	180,0E-12	78,0E-9	1,0E-27	33,0E-27	[5, 6, 7, 8]	Group28	8,23	19,00	[AKT1, CAV1, CDC42, GRB2, IL6ST, MAP3K14, MAP3K7, MTOR, NCOR2, PAK1, PAK2, PIK3R1, PKN1, PTPN11, SRC, STAT5B, TRAF2, TRAF6, VAV1]
GO:0032869	cellular response to insulin stimulus	400,0E-12	170,0E-9	1,0E-27	33,0E-27	[6, 7, 8]	Group28	8,37	18,00	[AKT1, BCAR1, GHR, GRB2, GSK3B, IRS1, MYO5A, PAK1, PIK3C2A, PIK3R1, PKN1, PTPN11, RELA, SIRT1, SMARCC1, SRC, TSC2, YWHAG]
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2,5E-9	1,0E-6	1,0E-27	33,0E-27	[4, 5, 6, 7, 8, 9, 10]	Group28	9,32	15,00	[ABL1, ACTG1, CDC42, DOCK1, GRB2, HSP90AA1, MAPK1, PAK1, PIK3R1, PKN1, PLCG1, PLD2, SRC, VAV1, WASL]
GO:0008286	insulin receptor signaling pathway	78,0E-9	34,0E-6	1,0E-27	33,0E-27	[6, 7, 8, 9]	Group28	9,45	12,00	[AKT1, BCAR1, GRB2, GSK3B, IRS1, PIK3C2A, PIK3R1, RELA, SIRT1, SMARCC1, SRC, TSC2]
GO:0046777	protein autophosphorylation	17,0E-12	7,3E-9	1,0E-27	33,0E-27	[7, 8]	Group28	8,30	21,00	[ABL1, AKT1, ALK, BCR, CAV1, EGFR, ERBB2, GRB2, GSK3B, IQGAP1, JAK2, MAP3K3, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PKN1, RIPK3, SRC, TOM1L1]
GO:0018105	peptidyl-serine phosphorylation	2,3E-9	1,0E-6	1,0E-27	33,0E-27	[7, 8, 9]	Group28	6,69	20,00	[AKT1, ARRB2, AXIN1, BCL2, CAV1, CDC42, GSK3B, HCLS1, IKBKB, MAPK1, MAPK14, MTOR, PAK1, PAK2, PKN1, RACK1, RAF1, SMAD7, SPRY2, SRC]
GO:0043149	stress fiber assembly	28,0E-9	12,0E-6	1,0E-27	33,0E-27	[6, 7, 8, 9, 10]	Group28	11,70	11,00	[AMOT, CDC42, MET, MTOR, PAK1, PIK3R1, PKN1, RHOA, SMAD3, SORBS3, SRC]
GO:2001275	positive regulation of glucose import in response to insulin stimulus	820,0E-9	350,0E-6	1,0E-27	33,0E-27	[4, 5, 6, 7, 8, 9, 10, 11, 12]	Group28	31,25	5,00	[IRS1, PAK1, PIK3R1, PKN1, PTPN11]
GO:1900182	positive regulation of protein localization to nucleus	160,0E-9	72,0E-6	35,0E-15	1,1E-12	[3, 4, 5, 6, 7, 8]	Group29	8,82	12,00	[AKT1, CDH1, EGFR, FLNA, HCLS1, JAK2, MAPK1, MAPK14, PIK3R1, RHOA, SMAD3, SRC]
GO:0006886	intracellular protein transport	110,0E-15	48,0E-12	35,0E-15	1,1E-12	[4, 5, 6, 7, 8]	Group29	4,19	51,00	[AKT1, AP1B1, BAP1, BCR, CBLB, CDC42, CDH1, CLIP1, CTNNB1, EGFR, ERBB2, FLNA, GABARAP, GSK3B, HCLS1, HSP90AA1, HSPA8, JAK2, MAPK1, MAPK14, MDM2, MTOR, MUC1, NFKBIA, PAK1, PDZK1, PIK3R1, PKN1, PML, PTPN11, RHOA, RNPS1, SEC23B, SFN, SIRT1, SLC9A3R1, SMAD3, SRSF1, SRSF4, STAT3, TCF7L2, TNPO3, TOB1, TOM1L1, TP53, TSC2, U2AF2, YWHAB, YWHAG, YWHAQ, YWHAZ]
GO:0017038	protein import	5,7E-12	2,4E-9	35,0E-15	1,1E-12	[4, 5, 6, 7, 8]	Group29	7,14	25,00	[AKT1, CBLB, CDH1, CTNNB1, EGFR, FLNA, GSK3B, HCLS1, HSP90AA1, HSPA8, JAK2, MAPK1, MAPK14, MTOR, NFKBIA, PIK3R1, PML, RHOA, SIRT1, SLC9A3R1, SMAD3, STAT3, TNPO3, TOB1, TSC2]

GO:0046824	positive regulation of nucleocytoplasmic transport	7,7E-12	3,3E-9	35,0E-15	1,1E-12	[4, 5, 6, 7, 8]	Group2 9	12,60	16,00	[CDH1, EGFR, FLNA, GSK3B, HCLS1, JAK2, KHDRBS1, MAPK1, MAPK14, MDM2, PIK3R1, RHOA, SFN, SMAD3, TCF7L2, TP53]
GO:0051222	positive regulation of protein transport	890,0E-12	380,0E-9	35,0E-15	1,1E-12	[3, 4, 5, 6, 7, 8, 9]	Group2 9	5,25	27,00	[ABL1, BAP1, CDC42, CDH1, EGFR, ERBB2, FLNA, GSK3B, HCLS1, JAK2, MAPK1, MAPK14, MDM2, MPC2, MUC1, PAK1, PDZK1, PIK3R1, PKN1, RACK1, RHOA, SFN, SMAD3, SRC, TCF7L2, TP53, U2AF2]
GO:0051223	regulation of protein transport	2,7E-12	1,1E-9	35,0E-15	1,1E-12	[5, 6, 7, 8]	Group2 9	4,76	39,00	[ABL1, BAP1, CDC42, CDH1, EGFR, ERBB2, FLNA, GOPC, GSK3B, HCLS1, HSPA8, IRS1, ITPR1, JAK2, MAPK1, MAPK14, MDM2, MPC2, MTOR, MUC1, NFKBIA, PAK1, PDZK1, PIK3R1, PKN1, PML, PTPN11, RACK1, RHOA, SFN, SIRT1, SLC9A3R1, SMAD3, SRC, TCF7L2, TP53, TRAF2, TRAF6, U2AF2]
GO:0090316	positive regulation of intracellular protein transport	2,4E-12	1,0E-9	35,0E-15	1,1E-12	[3, 4, 5, 6, 7, 8, 9, 10]	Group2 9	8,19	23,00	[BAP1, CDC42, CDH1, EGFR, ERBB2, FLNA, GSK3B, HCLS1, JAK2, MAPK1, MAPK14, MDM2, MUC1, PAK1, PDZK1, PIK3R1, PKN1, RHOA, SFN, SMAD3, TCF7L2, TP53, U2AF2]
GO:0006605	protein targeting	2,1E-12	950,0E-12	35,0E-15	1,1E-12	[5, 6, 7, 8, 9]	Group2 9	5,02	37,00	[AKT1, BAP1, CBLB, CDH1, CTNNB1, EGFR, ERBB2, FLNA, GABARAP, GSK3B, HCLS1, HSP90AA1, HSPA8, JAK2, MAPK1, MAPK14, MTOR, MUC1, NFKBIA, PAK1, PDZK1, PIK3R1, PKN1, PML, RHOA, SIRT1, SLC9A3R1, SMAD3, STAT3, TNPO3, TOB1, TSC2, U2AF2, YWHAB, YWHAG, YWHAQ, YWHAZ]
GO:0033157	regulation of intracellular protein transport	840,0E-15	360,0E-12	35,0E-15	1,1E-12	[5, 6, 7, 8, 9]	Group2 9	6,85	28,00	[BAP1, CDC42, CDH1, EGFR, ERBB2, FLNA, GSK3B, HCLS1, JAK2, MAPK1, MAPK14, MDM2, MTOR, MUC1, NFKBIA, PAK1, PDZK1, PIK3R1, PKN1, PTPN11, RHOA, SFN, SIRT1, SLC9A3R1, SMAD3, TCF7L2, TP53, U2AF2]
GO:1904589	regulation of protein import	3,1E-9	1,3E-6	35,0E-15	1,1E-12	[5, 6, 7, 8, 9]	Group2 9	8,47	16,00	[CDH1, EGFR, FLNA, GSK3B, HCLS1, HSPA8, JAK2, MAPK1, MAPK14, MTOR, NFKBIA, PIK3R1, RHOA, SIRT1, SLC9A3R1, SMAD3]
GO:0006606	protein import into nucleus	8,9E-12	3,8E-9	35,0E-15	1,1E-12	[5, 6, 7, 8, 9, 10, 11]	Group2 9	7,69	23,00	[AKT1, CBLB, CDH1, CTNNB1, EGFR, FLNA, GSK3B, HCLS1, JAK2, MAPK1, MAPK14, MTOR, NFKBIA, PIK3R1, PML, RHOA, SIRT1, SLC9A3R1, SMAD3, STAT3, TNPO3, TOB1, TSC2]
GO:1903533	regulation of protein targeting	310,0E-12	130,0E-9	35,0E-15	1,1E-12	[6, 7, 8, 9, 10]	Group2 9	6,75	22,00	[BAP1, CDH1, EGFR, ERBB2, FLNA, GSK3B, HCLS1, JAK2, MAPK1, MAPK14, MTOR, MUC1, NFKBIA, PAK1, PDZK1, PIK3R1, PKN1, RHOA, SIRT1, SLC9A3R1, SMAD3, U2AF2]
GO:0042307	positive regulation of protein import into nucleus	740,0E-9	320,0E-6	35,0E-15	1,1E-12	[4, 5, 6, 7, 8, 9, 10, 11, 12, 13]	Group2 9	9,62	10,00	[CDH1, EGFR, FLNA, HCLS1, JAK2, MAPK1, MAPK14, PIK3R1, RHOA, SMAD3]

GO:0097296	activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	570,0E-9	240,0E-6	84,0E-21	2,7E-18	[6, 7, 8, 9, 10, 11, 12, 13, 14]	Group3 0	33,33	5,00	[CASP8, FASLG, JAK2, SMAD3, TRAF2]
GO:1903749	positive regulation of establishment of protein localization to mitochondrion	540,0E-9	230,0E-6	84,0E-21	2,7E-18	[3, 4, 5, 6, 7, 8, 9]	Group3 0	8,80	11,00	[BAP1, BCL2, CASP8, MUC1, SFN, TP53, U2AF2, YWHAB, YWHAG, YWHAQ, YWHAZ]
GO:2001234	negative regulation of apoptotic signaling pathway	900,0E-15	390,0E-12	84,0E-21	2,7E-18	[4, 5, 6, 7, 8]	Group3 0	9,09	22,00	[AKT1, AR, ARRB2, BCL2, BRCA1, CASP8, CTNNB1, FASLG, HSPA1A, HTT, MDM2, MEN1, MUC1, PEA15, PSME3, RAF1, RB1CC1, RELA, SIRT1, SRC, TCF7L2, TRAF2]
GO:2001235	positive regulation of apoptotic signaling pathway	8,3E-15	3,6E-12	84,0E-21	2,7E-18	[4, 5, 6, 7, 8]	Group3 0	11,40	22,00	[BCL2, CASP8, CAV1, FASLG, GSK3B, JAK2, PAK2, PEA15, PML, PPP2R1A, RACK1, RIPK3, SFN, SIRT1, SLC9A3R1, SMAD3, TP53, TRAF2, YWHAB, YWHAG, YWHAQ, YWHAZ]
GO:0010498	proteasomal protein catabolic process	6,3E-9	2,7E-6	84,0E-21	2,7E-18	[5, 6, 7, 8]	Group3 0	5,52	23,00	[AKT1, ARRB2, ATXN3, AXIN1, BTRC, CAV1, CTNNB1, DDA1, GABARAPL2, GSK3B, HSPA1A, HSPA5, MDM2, NSFL1C, PML, PSME3, RACK1, SIRT1, SKP1, SMAD7, SMARCC1, TP53, WAC]
GO:0045862	positive regulation of proteolysis	1,6E-9	690,0E-9	84,0E-21	2,7E-18	[5, 6, 7, 8]	Group3 0	5,93	23,00	[AKT1, AXIN1, BTRC, CASP8, CAV1, CDKN1B, FASLG, GSK3B, HDAC2, HSPA1A, JAK2, MAPK14, MDM2, PML, PSME3, RACK1, SIRT1, SKP1, SMAD3, SMAD7, SRC, STAT3, TRAF2]
GO:2001242	regulation of intrinsic apoptotic signaling pathway	1,7E-6	760,0E-6	84,0E-21	2,7E-18	[5, 6, 7, 8]	Group3 0	7,10	12,00	[AKT1, BCL2, CAV1, HSPA1A, MDM2, MUC1, RACK1, RIPK3, SIRT1, SLC9A3R1, SRC, TP53]
GO:0052548	regulation of endopeptidase activity	430,0E-9	190,0E-6	84,0E-21	2,7E-18	[6, 7, 8]	Group3 0	4,88	20,00	[AKT1, ARRB2, ATXN3, CASP8, CDKN1B, FASLG, JAK2, LXN, MDM2, PAK2, PML, PSME3, RACK1, RAF1, SFN, SIRT1, SMAD3, SRC, STAT3, TRAF2]
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	120,0E-9	53,0E-6	84,0E-21	2,7E-18	[6, 7, 8]	Group3 0	6,53	16,00	[AKT1, AXIN1, BTRC, CAV1, DDA1, GABARAPL2, GSK3B, HSPA1A, MDM2, PML, PSME3, RACK1, SKP1, SMAD7, SMARCC1, WAC]
GO:1903320	regulation of protein modification by small protein conjugation or removal	280,0E-12	120,0E-9	84,0E-21	2,7E-18	[6, 7, 8]	Group3 0	7,14	21,00	[ABL1, ARRB2, AXIN1, BRCA1, BTRC, CAV1, CTNNB1, DAXX, HDAC4, HSP90AA1, HSPA1A, HSPA5, MTOR, PML, PSME3, SKP1, SMAD7, TRAF6, UBE2I, WDR48, ZYG11B]
GO:0010952	positive regulation of peptidase activity	350,0E-9	150,0E-6	84,0E-21	2,7E-18	[6, 7, 8, 9]	Group3 0	7,51	13,00	[CASP8, CAV1, CDKN1B, FASLG, JAK2, MAPK14, PML, PSME3, RACK1, SIRT1, SMAD3, STAT3, TRAF2]
GO:0032446	protein modification by small protein conjugation	62,0E-9	26,0E-6	84,0E-21	2,7E-18	[7, 8]	Group3 0	3,66	34,00	[ABL1, AKT1, ARRB2, ASB7, AXIN1, BCL2, BRCA1, BTRC, CAV1, CBL, CBLB, CDC42, CTNNB1, DAXX, HDAC4, HDAC7, HERC3, HSP90AA1, HSPA1A, HSPA5, MDM2,

										MTOR, PML, PSME3, SIRT1, SKP1, SMAD7, TOP2A, TRAF2, TRAF6, UBE2I, WAC, WDR48, ZYG11B]
GO:0061136	regulation of proteasomal protein catabolic process	90,0E-9	39,0E-6	84,0E-21	2,7E-18	[6, 7, 8, 9]	Group30	8,44	13,00	[AKT1, BTRC, CAV1, DDA1, GABARAPL2, GSK3B, HSPA1A, MDM2, PSME3, RACK1, SMAD7, SMARCC1, WAC]
GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	520,0E-12	220,0E-9	84,0E-21	2,7E-18	[4, 5, 6, 7, 8, 9, 10, 11]	Group30	20,00	10,00	[BCL2, CASP8, GSK3B, HSPA1A, SFN, TP53, YWHAB, YWHAG, YWHAQ, YWHAZ]
GO:0006511	ubiquitin-dependent protein catabolic process	650,0E-12	280,0E-9	84,0E-21	2,7E-18	[7, 8, 9]	Group30	5,00	29,00	[AKT1, ARRB2, ATXN3, AXIN1, BAP1, BTRC, CAV1, CBL, CTNNB1, DDA1, GSK3B, HSPA1A, HSPA5, MDM2, NSFL1C, PML, PSME3, RACK1, SIRT1, SKP1, SMAD7, SMARCC1, SQSTM1, TOM1L1, TP53, UBE2I, USP3, USP46, WAC]
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	29,0E-9	12,0E-6	84,0E-21	2,7E-18	[6, 7, 8, 9, 10]	Group30	7,24	16,00	[AKT1, ARRB2, CASP8, CDKN1B, FASLG, JAK2, MDM2, PAK2, PML, RACK1, RAF1, SFN, SIRT1, SMAD3, SRC, TRAF2]
GO:0016567	protein ubiquitination	1,8E-6	800,0E-6	84,0E-21	2,7E-18	[8, 9]	Group30	3,46	29,00	[ABL1, AKT1, ARRB2, ASB7, AXIN1, BCL2, BRCA1, BTRC, CAV1, CBL, CBLB, CDC42, DAXX, HERC3, HSP90AA1, HSPA1A, HSPA5, MDM2, MTOR, PML, PSME3, SIRT1, SKP1, SMAD7, TRAF2, TRAF6, WAC, WDR48, ZYG11B]
GO:0031396	regulation of protein ubiquitination	15,0E-9	6,6E-6	84,0E-21	2,7E-18	[7, 8, 9, 10]	Group30	6,67	18,00	[ABL1, ARRB2, AXIN1, BRCA1, BTRC, CAV1, DAXX, HSP90AA1, HSPA1A, HSPA5, MTOR, PML, PSME3, SKP1, SMAD7, TRAF6, WDR48, ZYG11B]
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	1,8E-6	820,0E-6	84,0E-21	2,7E-18	[7, 8, 9, 10, 11]	Group30	8,70	10,00	[AKT1, CAV1, DDA1, GSK3B, HSPA1A, MDM2, RACK1, SMAD7, SMARCC1, WAC]
GO:0000187	activation of MAPK activity	2,3E-9	1,0E-6	29,0E-33	950,0E-33	[7, 8, 9, 10, 11, 12, 13]	Group31	9,38	15,00	[ALK, AXIN1, DAXX, GHR, IKBKG, MAP2K7, MAP3K2, MAP3K7, MAPK1, MAPK14, MAPK8IP3, PEA15, PKN1, PTPN11, TRAF6]
GO:0043507	positive regulation of JUN kinase activity	18,0E-9	8,1E-6	29,0E-33	950,0E-33	[7, 8, 9, 10, 11, 12, 13, 14]	Group31	14,08	10,00	[AXIN1, DAXX, MAP2K7, MAP3K2, MAP3K7, MAPK8IP3, PAK1, PKN1, TRAF2, TRAF6]
GO:0023014	signal transduction by protein phosphorylation	440,0E-24	190,0E-21	29,0E-33	950,0E-33	[3, 4, 5, 7, 8]	Group31	5,88	57,00	[ABL1, AKT1, ALK, AR, ARRB2, AXIN1, BTRC, CAV1, CDC42, CDH2, CTNNB1, DAXX, EGFR, EPHA2, ERBB2, GHR, GRB2, IKBKB, IKBKG, IQGAP1, IRS1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, MET, NFKB1, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PPP2R1A, PSME3, PTPN11, RAF1,

										RB1CC1, SKP1, SLC9A3R1, SMAD1, SORBS3, SPRY2, SRC, TRAF2, TRAF6, YWHAB]
GO:0031401	positive regulation of protein modification process	9,0E-30	3,9E-27	29,0E-33	950,0E-33	[5, 6, 7, 8]	Group3 1	6,03	74,00	[ABL1, ADAM17, AKT1, ALK, AR, ARRB2, AXIN1, BCL2, BRCA1, BTRC, CAV1, CDC42, CDH2, CDKN1B, CTNNB1, DAXX, EGFR, ERBB2, GHR, GSK3B, HCLS1, HDAC2, HDAC4, HSPA5, IKBKG, IL6ST, IQGAP1, JAK2, KMT2A, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MECP2, MTOR, MUC1, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PML, PPP2CA, PRKAR1A, PSME3, PTPN11, RACK1, RAF1, RB1CC1, RHOA, RIPK3, SIRT1, SKP1, SMAD7, SMARCB1, SORBS3, SPRY2, SQSTM1, SRC, STAT3, TNFRSF1A, TOM1L1, TP53, TRAF2, TRAF6, UBE2I]
GO:0043549	regulation of kinase activity	19,0E-27	8,5E-24	29,0E-33	950,0E-33	[5, 7, 8]	Group3 1	6,89	59,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CAV1, CBL, CBLB, CDC42, CDKN1B, DAXX, EGFR, ERBB2, GHR, HSPA5, IKBKG, IQGAP1, IRS1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PIK3R1, PKN1, PLCG1, PPP2CA, PPP2R1A, PRKAB1, PRKAR1A, PTPN11, RACK1, RAF1, RB1, RHOA, RIPK3, SFN, SIRT1, SLC9A3R1, SPRY2, SRC, TOM1L1, TRAF2, TRAF6, TSC2, YWHAG]
GO:0001932	regulation of protein phosphorylation	590,0E-30	250,0E-27	29,0E-33	950,0E-33	[6, 7, 8]	Group3 1	5,49	76,00	[ABL1, ADAM17, AKT1, ALK, AR, ARRB2, AXIN1, BCL2, CAV1, CBL, CBLB, CDC42, CDH2, CDKN1B, CTNNB1, DAXX, EGFR, EPHA2, ERBB2, GHR, GRB2, GSK3B, HCLS1, HDAC2, HSPA5, IKBKG, IL6ST, IQGAP1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PML, PPP2CA, PPP2R1A, PRKAB1, PRKAR1A, PTPN11, RACK1, RAF1, RB1, RB1CC1, RHOA, RIPK3, SFN, SIRT1, SLC9A3R1, SMAD7, SORBS3, SPRY2, SQSTM1, SRC, STAT3, TNFRSF1A, TOM1L1, TP53, TRAF2, TRAF6, TSC2, YWHAG]
GO:0042326	negative regulation of phosphorylation	1,5E-9	650,0E-9	29,0E-33	950,0E-33	[6, 7, 8]	Group3 1	5,49	25,00	[ABL1, AKT1, ARRB2, CAV1, CBL, CBLB, CDKN1B, HDAC4, MEN1, MTOR, PAK2, PKN1, PPP2CA, PPP2R1A, PRKAR1A, RACK1, RB1, SFN, SIRT1, SLC9A3R1, SMAD7, SPRY2, STAT3, TSC2, YWHAG]
GO:0042327	positive regulation of phosphorylation	44,0E-27	19,0E-24	29,0E-33	950,0E-33	[6, 7, 8]	Group3 1	6,29	63,00	[ABL1, ADAM17, AKT1, ALK, AR, ARRB2, AXIN1, BCL2, CAV1, CDC42, CDH2, CDKN1B, CTNNB1, DAXX, EGFR, ERBB2, GHR, GSK3B, HCLS1, HDAC2, HSPA5, IKBKG, IL6ST, IQGAP1, IRS1, JAK2, LAT, MAP2K7, MAP3K1,

										MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PRKAR1A, PTPN11, RACK1, RAF1, RB1CC1, RHOA, RIPK3, SIRT1, SORBS3, SPRY2, SQSTM1, SRC, STAT3, TNFRSF1A, TOM1L1, TP53, TRAF2, TRAF6]
GO:0051403	stress-activated MAPK cascade	1,0E-12	460,0E-12	29,0E-33	950,0E-33	[5, 6, 7, 9, 10]	Group3 1	8,52	23,00	[AKT1, AXIN1, BTRC, CDC42, DAXX, EGFR, IKBKB, IKBKG, MAP2K7, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, NFKB1, PAK1, PKN1, RB1CC1, SKP1, TRAF2, TRAF6]
GO:0001933	negative regulation of protein phosphorylation	6,0E-9	2,6E-6	29,0E-33	950,0E-33	[6, 7, 8, 9]	Group3 1	5,53	23,00	[ABL1, AKT1, ARRB2, CAV1, CBL, CBLB, CDKN1B, MEN1, MTOR, PAK2, PKN1, PPP2CA, PPP2R1A, PRKAR1A, RACK1, RB1, SFN, SIRT1, SLC9A3R1, SMAD7, SPRY2, TSC2, YWHAG]
GO:0033674	positive regulation of kinase activity	76,0E-24	33,0E-21	29,0E-33	950,0E-33	[6, 7, 8, 9]	Group3 1	8,05	45,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CDC42, CDKN1B, DAXX, EGFR, ERBB2, GHR, HSPA5, IKBKG, IQGAP1, IRS1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PRKAR1A, PTPN11, RAF1, RHOA, RIPK3, SIRT1, SPRY2, SRC, TOM1L1, TRAF2, TRAF6]
GO:0043408	regulation of MAPK cascade	310,0E-21	130,0E-18	29,0E-33	950,0E-33	[5, 6, 7, 8, 9, 10]	Group3 1	6,38	46,00	[ABL1, AKT1, ALK, AR, ARRB2, AXIN1, CAV1, CDC42, CDH2, CTNNB1, DAXX, EGFR, EPHA2, ERBB2, GHR, GRB2, IKBKG, IQGAP1, JAK2, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, NTRK1, PAK1, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PPP2R1A, PTPN11, RAF1, RB1CC1, SLC9A3R1, SORBS3, SPRY2, SRC, TRAF2, TRAF6]
GO:0045859	regulation of protein kinase activity	17,0E-27	7,4E-24	29,0E-33	950,0E-33	[6, 7, 8, 9]	Group3 1	7,21	57,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CAV1, CBL, CBLB, CDC42, CDKN1B, DAXX, EGFR, ERBB2, GHR, HSPA5, IKBKG, IQGAP1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PPP2R1A, PRKAB1, PRKAR1A, PTPN11, RACK1, RAF1, RB1, RHOA, RIPK3, SFN, SIRT1, SLC9A3R1, SPRY2, SRC, TOM1L1, TRAF2, TRAF6, TSC2, YWHAG]
GO:0046777	protein autophosphorylation	17,0E-12	7,3E-9	29,0E-33	950,0E-33	[7, 8]	Group3 1	8,30	21,00	[ABL1, AKT1, ALK, BCR, CAV1, EGFR, ERBB2, GRB2, GSK3B, IQGAP1, JAK2, MAP3K3, MTOR, NTRK1, PAK1, PAK2, PDGFRB, PKN1, RIPK3, SRC, TOM1L1]

GO:0032872	regulation of stress-activated MAPK cascade	3,1E-9	1,3E-6	29,0E-33	950,0E-33	[5, 6, 7, 8, 9, 10, 11]	Group3 1	7,87	17,00	[AKT1, AXIN1, CDC42, DAXX, EGFR, MAP2K7, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK8IP3, MEN1, PAK1, PKN1, RB1CC1, TRAF2, TRAF6]
GO:0043410	positive regulation of MAPK cascade	4,9E-18	2,1E-15	29,0E-33	950,0E-33	[5, 6, 7, 8, 9, 10, 11]	Group3 1	7,35	38,00	[ABL1, ALK, AR, ARRB2, AXIN1, CDC42, CDH2, CTNNB1, DAXX, EGFR, ERBB2, GHR, IKBKG, IQGAP1, JAK2, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, NTRK1, PAK1, PDGFRB, PEA15, PKN1, PLCG1, PTPN11, RAF1, RB1CC1, SORBS3, SPRY2, SRC, TRAF2, TRAF6]
GO:0050852	T cell receptor signaling pathway	7,1E-12	3,0E-9	29,0E-33	950,0E-33	[6, 7, 8, 9, 10]	Group3 1	9,90	19,00	[BCAR1, BTRC, IKBKB, IKBKG, LAT, MAP3K7, MAPK1, NCOR2, NFKB1, NFKBIA, PAK1, PAK2, PIK3R1, PKN1, PLCG1, PSME3, RELA, SKP1, TRAF6]
GO:0007254	JNK cascade	11,0E-9	5,0E-6	29,0E-33	950,0E-33	[6, 7, 8, 10, 11]	Group3 1	7,73	16,00	[AKT1, AXIN1, CDC42, DAXX, EGFR, IKBKG, MAP2K7, MAP3K2, MAP3K7, MAPK8IP3, MEN1, PAK1, PKN1, RB1CC1, TRAF2, TRAF6]
GO:0002223	stimulatory C-type lectin receptor signaling pathway	9,8E-12	4,2E-9	29,0E-33	950,0E-33	[6, 7, 8, 9, 10, 11]	Group3 1	12,40	16,00	[BTRC, IKBKB, IKBKG, MAP3K7, MUC1, NFKB1, NFKBIA, PAK1, PAK2, PKN1, PSME3, RAF1, RELA, SKP1, SRC, TRAF6]
GO:0006469	negative regulation of protein kinase activity	840,0E-12	360,0E-9	29,0E-33	950,0E-33	[7, 8, 9, 10]	Group3 1	7,51	19,00	[ABL1, AKT1, CAV1, CBL, CBLB, CDKN1B, MEN1, PAK2, PKN1, PPP2CA, PPP2R1A, PRKAR1A, RACK1, RB1, SFN, SIRT1, SPRY2, TSC2, YWHAG]
GO:0043405	regulation of MAP kinase activity	500,0E-21	220,0E-18	29,0E-33	950,0E-33	[6, 7, 8, 9, 10, 11]	Group3 1	9,43	33,00	[ALK, AXIN1, CAV1, DAXX, EGFR, ERBB2, GHR, IKBKG, IQGAP1, JAK2, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, NTRK1, PAK1, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PPP2R1A, PTPN11, RAF1, SPRY2, SRC, TRAF2, TRAF6]
GO:0045860	positive regulation of protein kinase activity	210,0E-24	92,0E-21	29,0E-33	950,0E-33	[7, 8, 9, 10]	Group3 1	8,32	43,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CDKN1B, DAXX, EGFR, ERBB2, GHR, HSPA5, IKBKG, IQGAP1, JAK2, LAT, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, NTRK1, PAK1, PAK2, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PRKAR1A, PTPN11, RAF1, RHOA, RIPK3, SIRT1, SPRY2, SRC, TOM1L1, TRAF2, TRAF6]
GO:0071900	regulation of protein serine/threonine kinase activity	91,0E-24	39,0E-21	29,0E-33	950,0E-33	[7, 8, 9, 10]	Group3 1	8,50	43,00	[ABL1, ADAM17, AKT1, ALK, AXIN1, CAV1, CDKN1B, DAXX, EGFR, ERBB2, GHR, IKBKG, IQGAP1, JAK2, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, MEN1, NTRK1, PAK1, PDGFRB, PEA15, PKN1, PLCG1, PPP2CA, PPP2R1A, PRKAR1A, PTPN11, RAF1, RHOA, SFN, SIRT1, SPRY2, SRC, TRAF2, TRAF6, YWHAG]
GO:0000186	activation of MAPKK activity	1,1E-9	500,0E-9	29,0E-33	950,0E-33	[6, 7, 8, 9, 10, 11, 12]	Group3 1	18,52	10,00	[EGFR, JAK2, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, NTRK1, PLCG1, RAF1]

GO:0032874	positive regulation of stress-activated MAPK cascade	51,0E-9	22,0E-6	29,0E-33	950,0E-33	[6, 7, 8, 9, 10, 11, 12]	Group3 1	8,84	13,00	[AXIN1, CDC42, DAXX, MAP2K7, MAP3K2, MAP3K3, MAP3K7, MAPK8IP3, PAK1, PKN1, RB1CC1, TRAF2, TRAF6]
GO:0043406	positive regulation of MAP kinase activity	640,0E-15	270,0E-12	29,0E-33	950,0E-33	[6, 7, 8, 9, 10, 11, 12]	Group3 1	9,24	22,00	[ALK, AXIN1, DAXX, EGFR, ERBB2, GHR, IKBKG, IQGAP1, MAP2K7, MAP3K2, MAP3K7, MAPK1, MAPK14, MAPK8IP3, PAK1, PDGFRB, PEA15, PKN1, PTPN11, SRC, TRAF2, TRAF6]
GO:0032147	activation of protein kinase activity	230,0E-18	100,0E-15	29,0E-33	950,0E-33	[8, 9, 10, 11]	Group3 1	9,03	29,00	[ABL1, ALK, AXIN1, DAXX, EGFR, GHR, IKBKG, JAK2, MAP2K7, MAP3K1, MAP3K14, MAP3K2, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK8IP3, NTRK1, PEA15, PKN1, PLCG1, PRKAR1A, PTPN11, RAF1, RIPK3, SRC, TOM1L1, TRAF2, TRAF6]
GO:0071902	positive regulation of protein serine/threonine kinase activity	360,0E-18	150,0E-15	29,0E-33	950,0E-33	[8, 9, 10, 11]	Group3 1	8,90	29,00	[ADAM17, AKT1, ALK, AXIN1, CDKN1B, DAXX, EGFR, ERBB2, GHR, IKBKG, IQGAP1, MAP2K7, MAP3K2, MAP3K7, MAPK1, MAPK14, MAPK8IP3, PAK1, PDGFRB, PEA15, PKN1, PPP2CA, PTPN11, RHOA, SIRT1, SPRY2, SRC, TRAF2, TRAF6]