

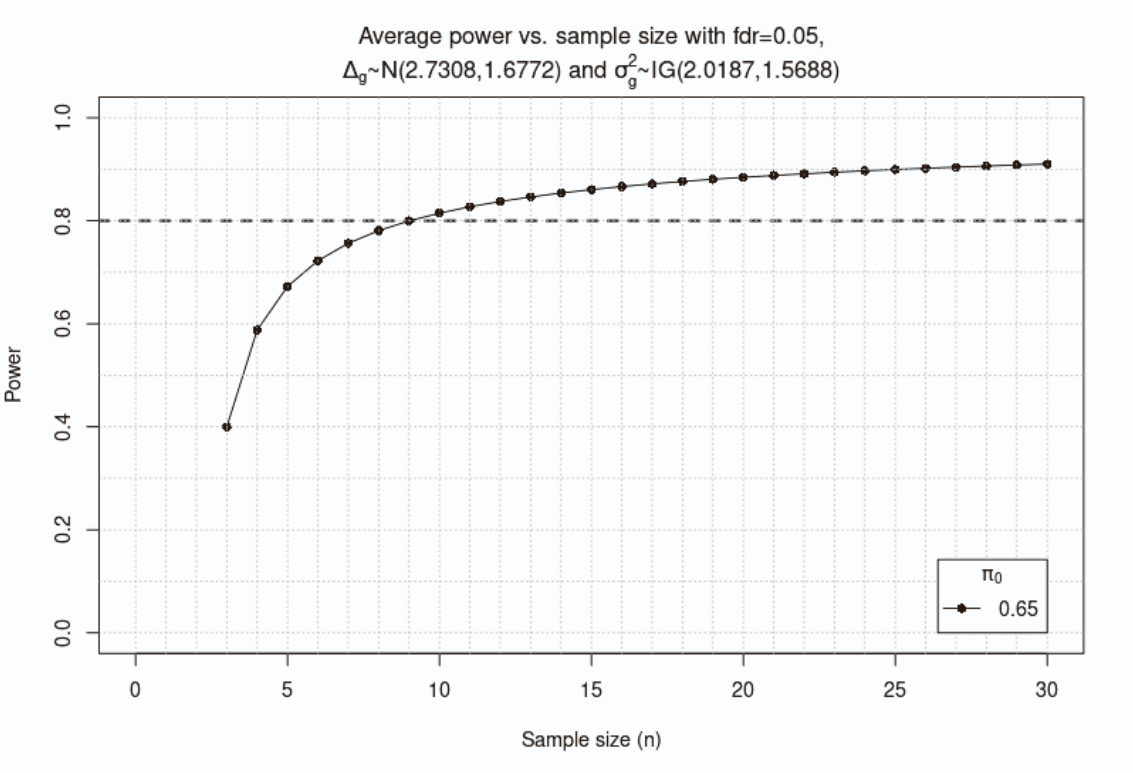
iScience, Volume 27

Supplemental information

**Unveiling the pathophysiology
of restless legs syndrome through
transcriptome analysis**

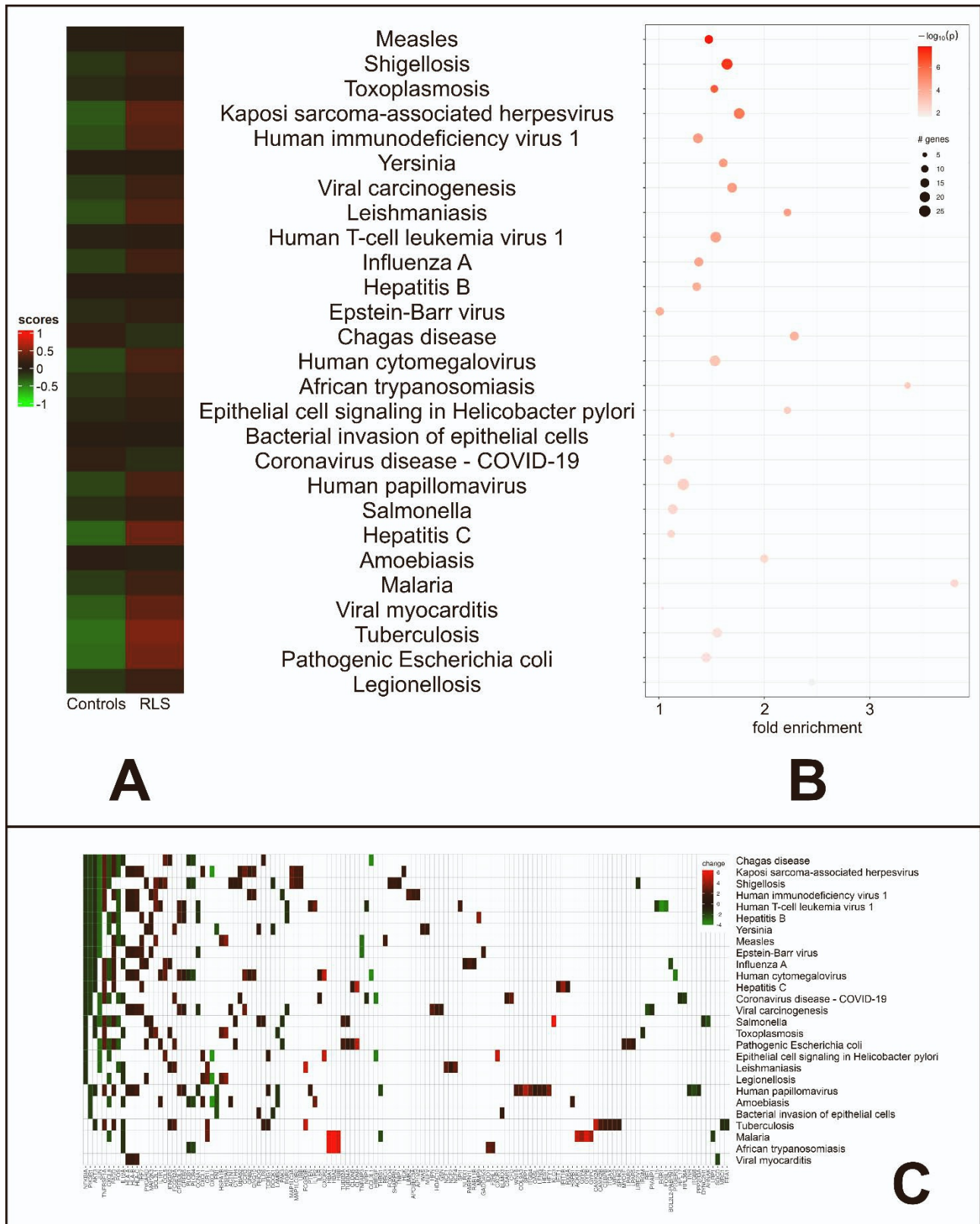
Maria P. Mogavero, Michele Salemi, Giuseppe Lanza, Antonio Rinaldi, Giovanna Marchese, Maria Ravo, Maria Grazia Salluzzo, Amedeo Antoci, Lourdes M. DelRosso, Oliviero Bruni, Luigi Ferini-Strambi, and Raffaele Ferri

Supplemental Figure S1 (related to Methods). Statistical power calculation based on our data.



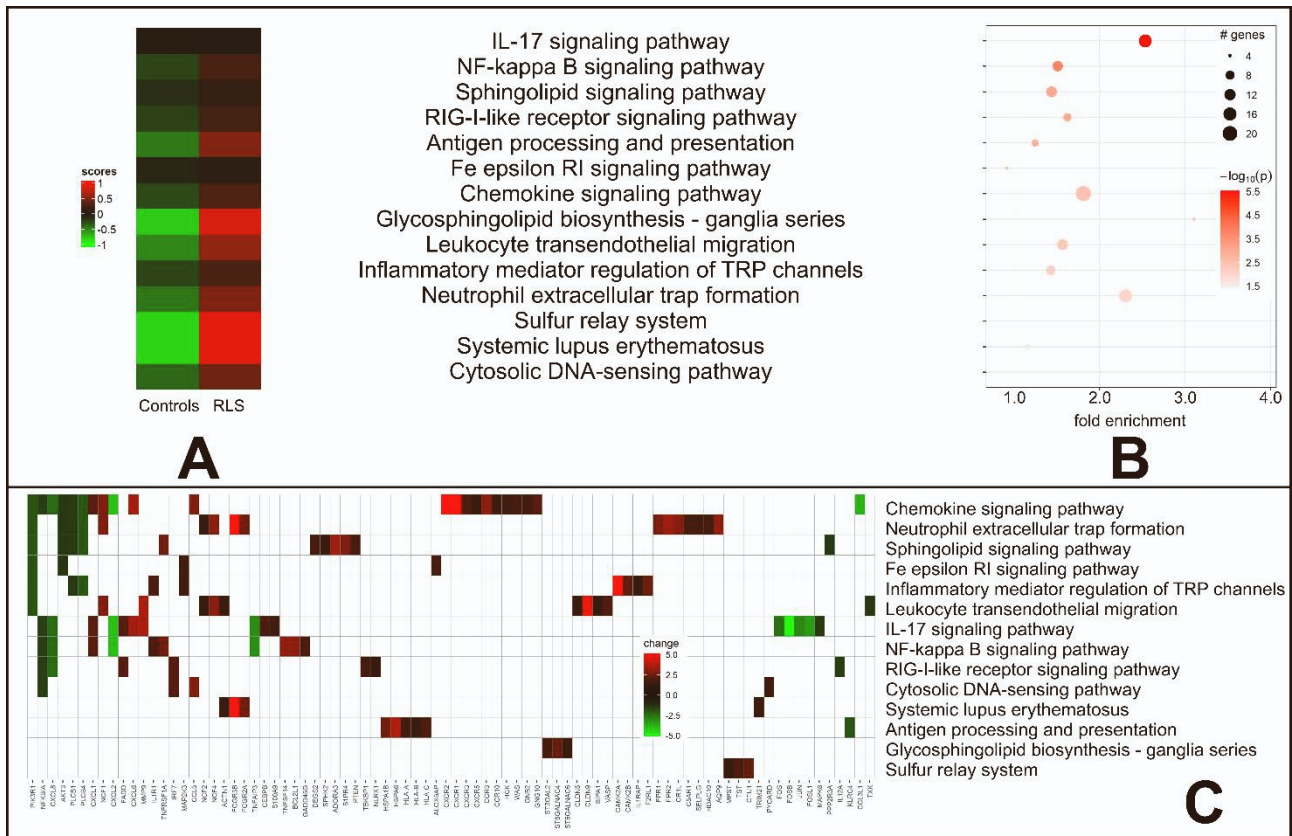
Supplemental Figure S2 (related to Table1).

Statistically significant pathways found by pathfinder involved in infections. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Tem-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



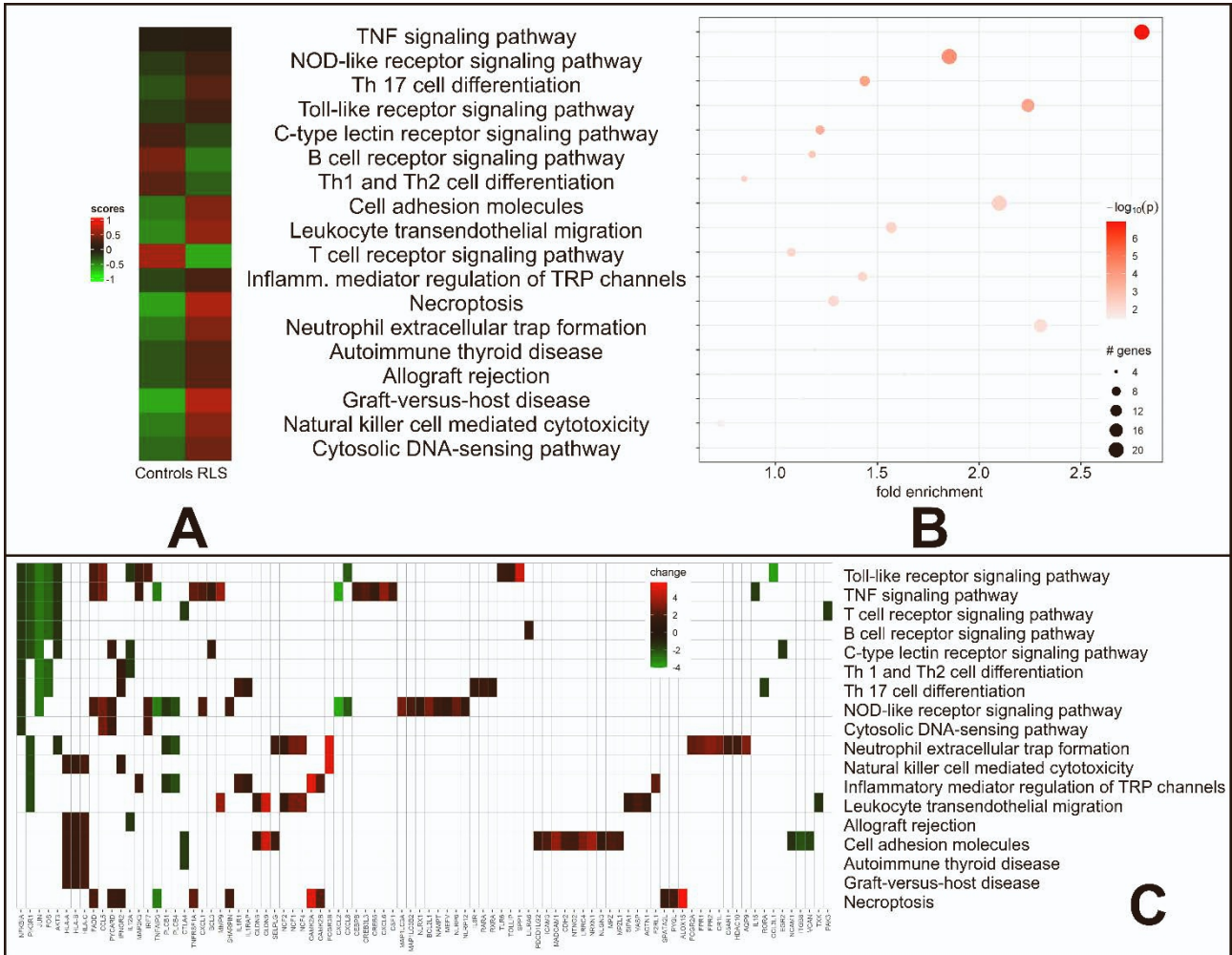
Supplemental Figure S3 (related to Table1).

Statistically significant pathways found by pathfinder involved in inflammation. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



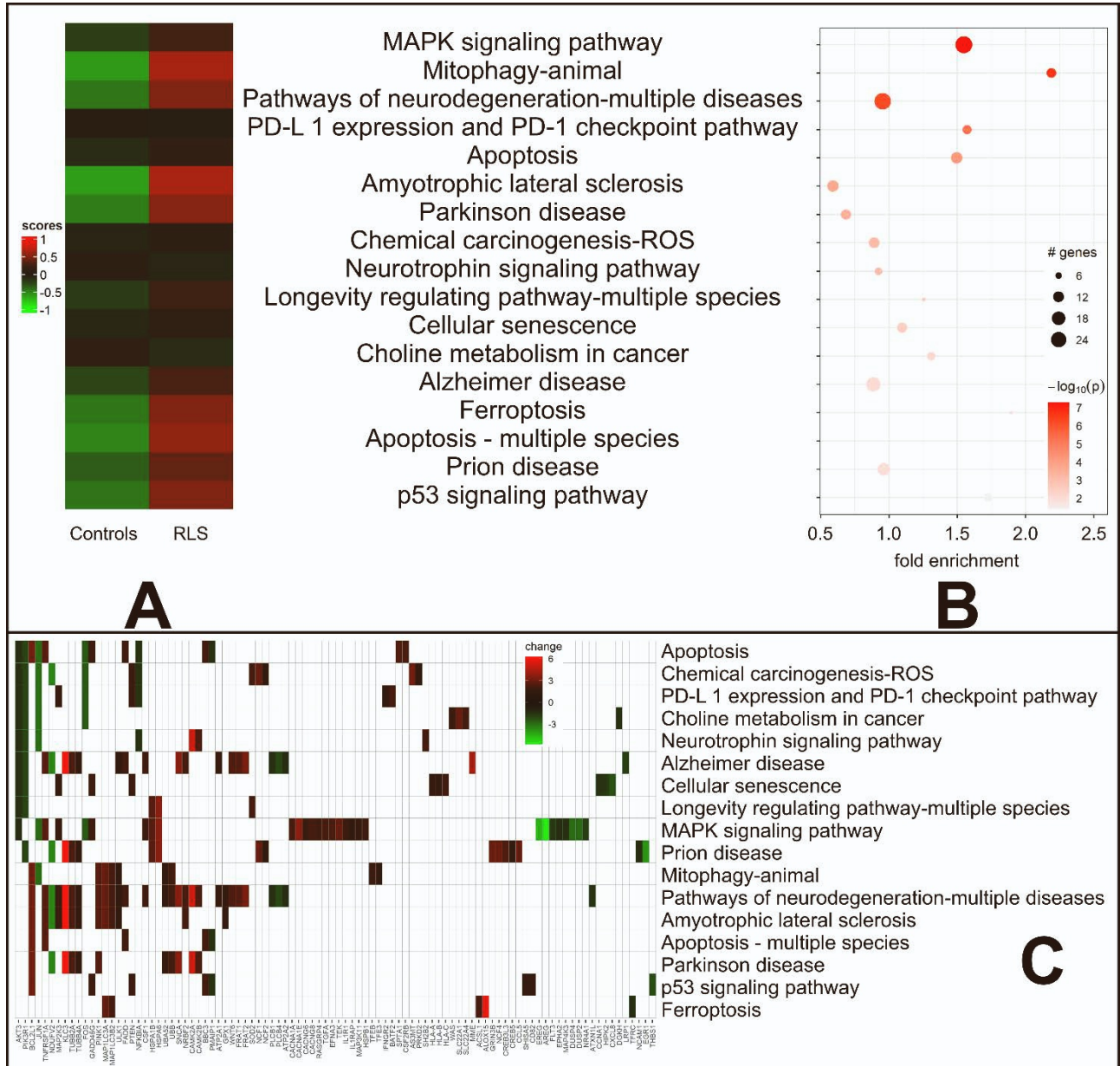
Supplemental Figure S4 (related to Table1).

Statistically significant pathways found by pathfinder involved in immunology. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



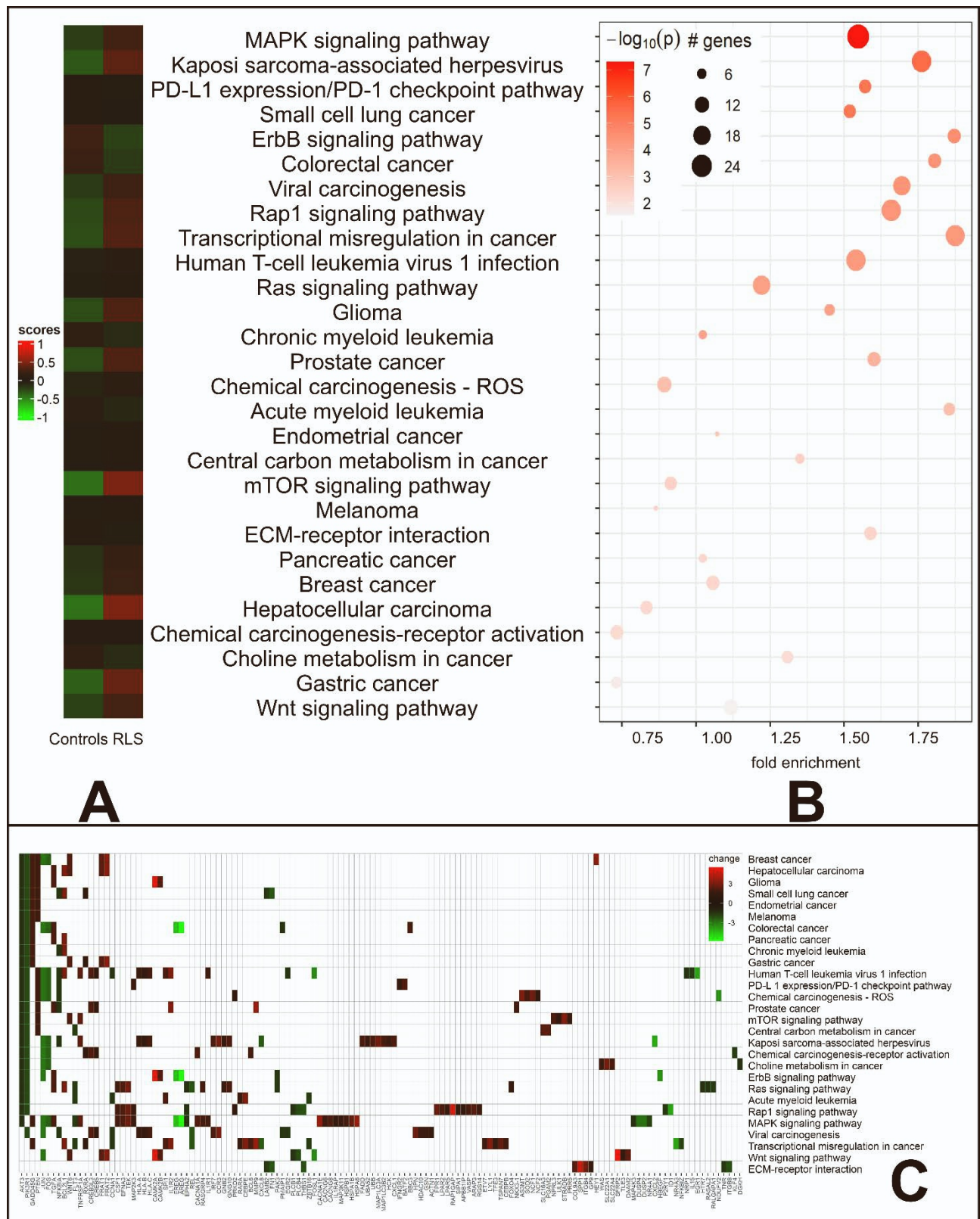
Supplementary Figure S5 (related to Table1).

Statistically significant pathways found by pathfinder involved in neurodegeneration. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



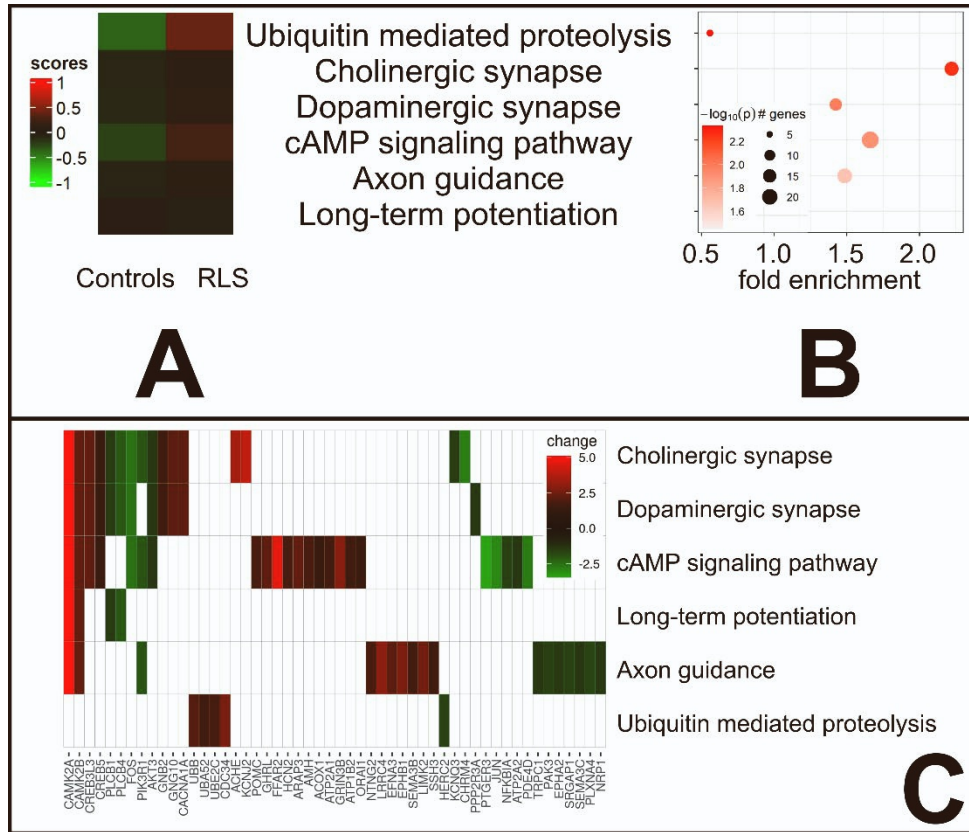
Supplemental Figure S6 (related to Table1).

Statistically significant pathways found by pathfinder involved in cancer. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



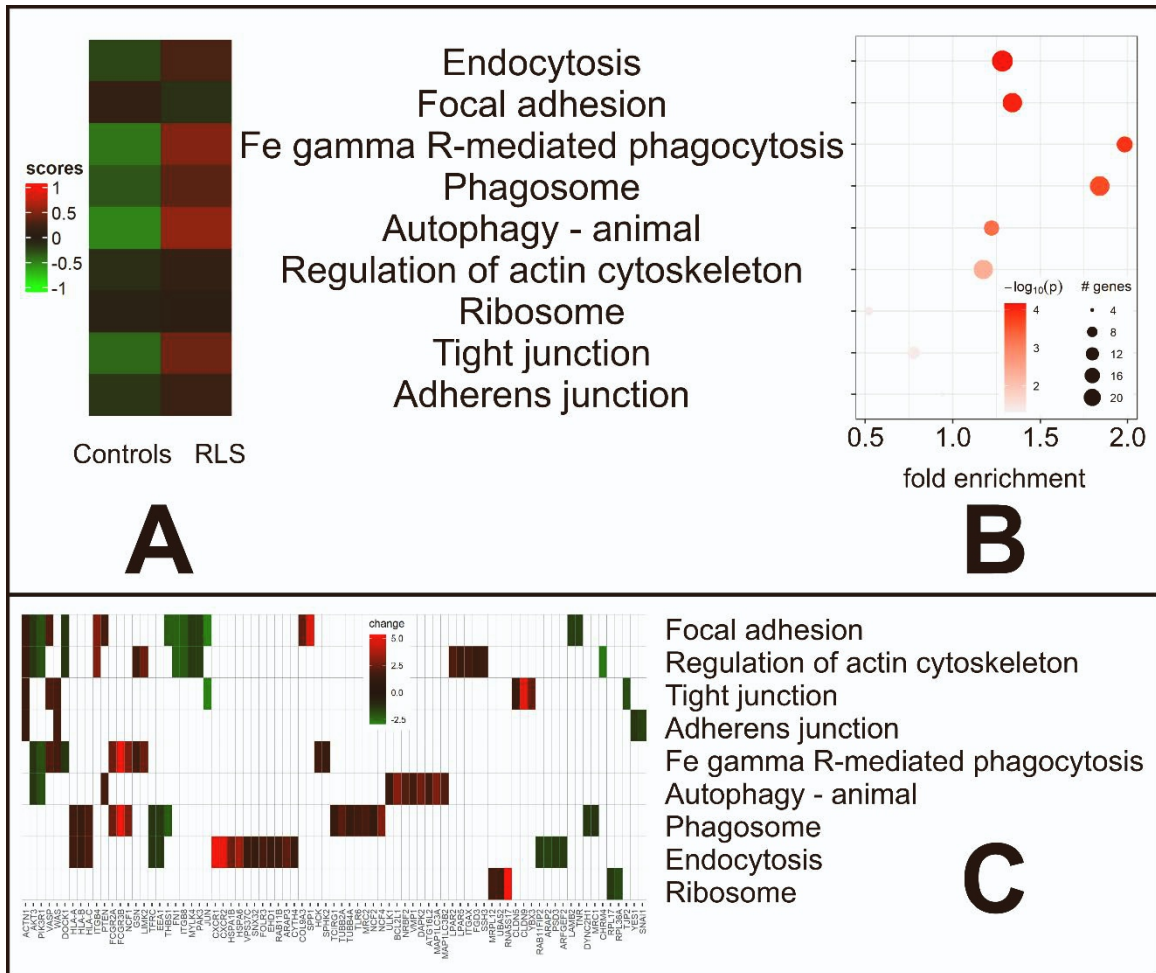
Supplemental Figure S7 (related to Table1).

Statistically significant pathways found by pathfinder involved in neurotransmitters. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



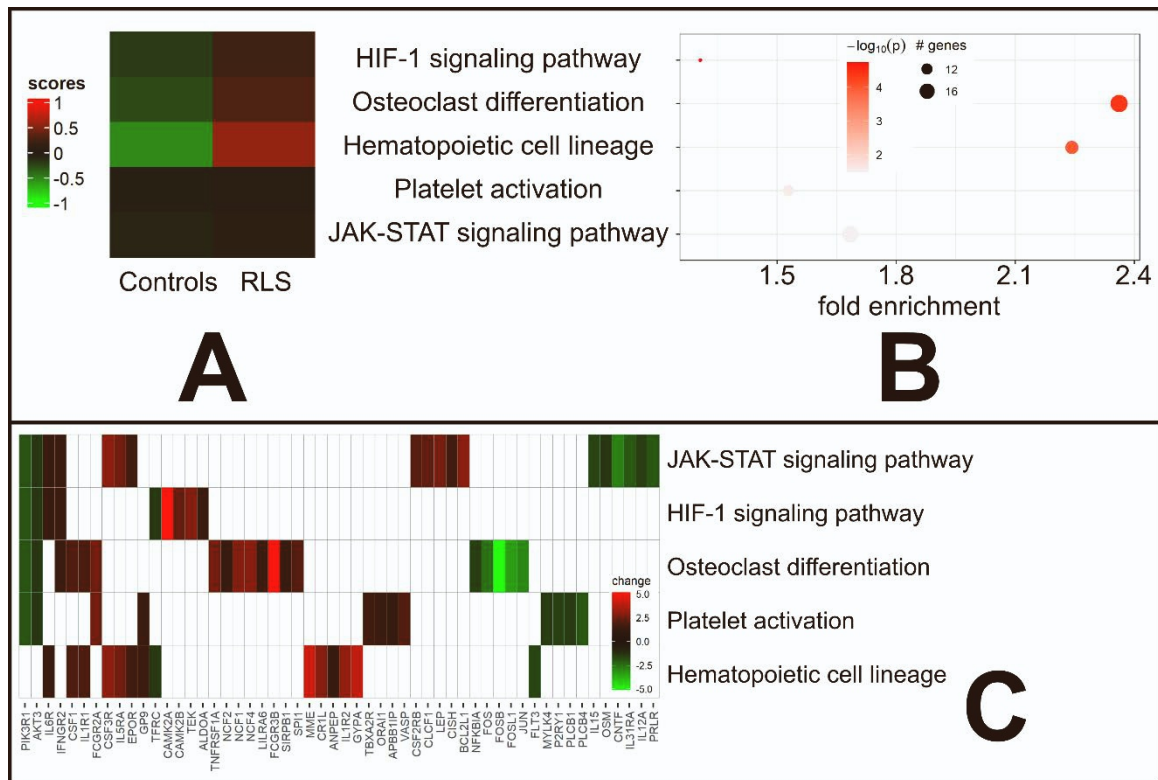
Supplemental Figure S8 (related to Table1).

Statistically significant pathways found by pathfinder involved in cellular processes. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



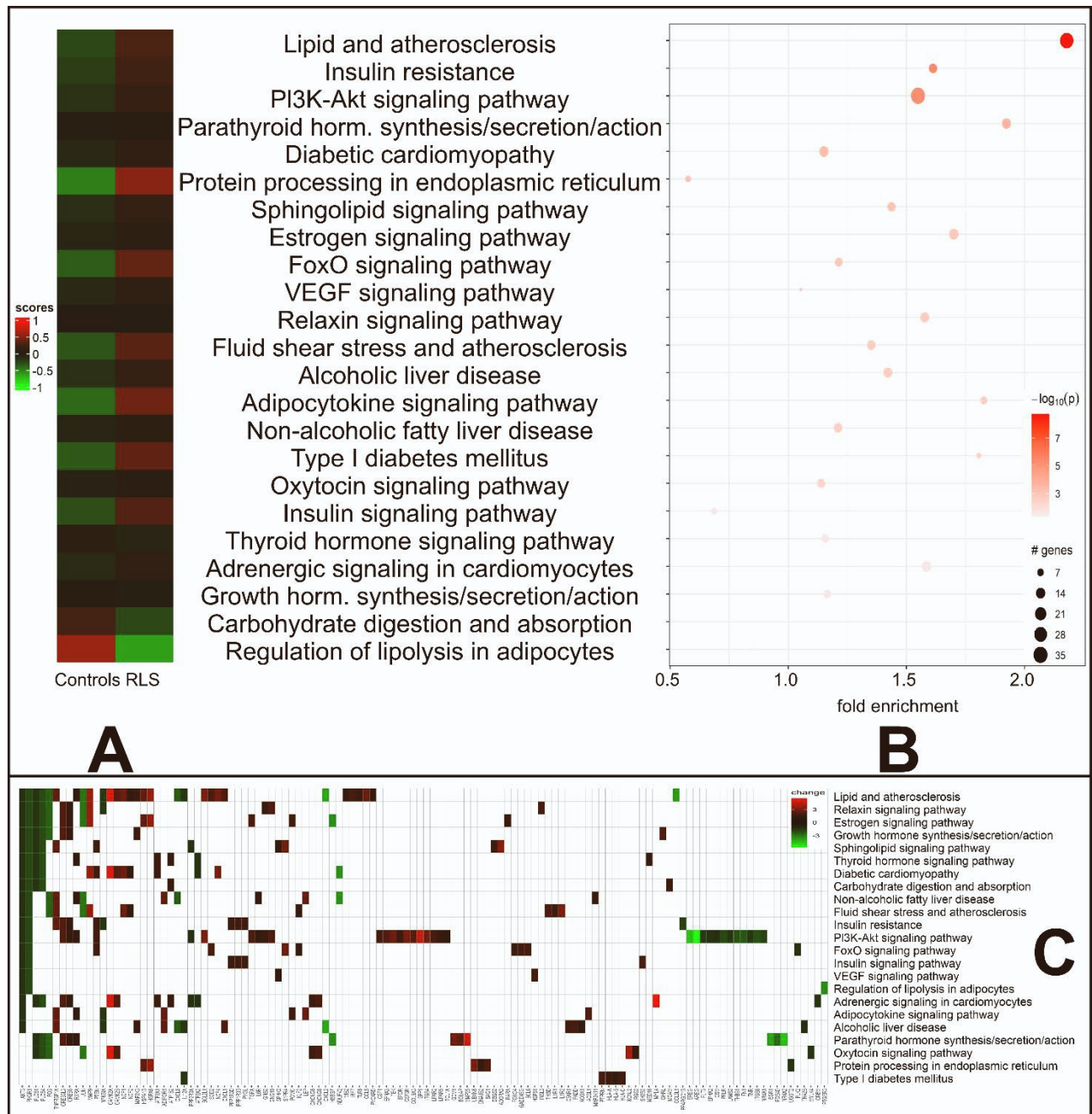
Supplemental Figure S9 (related to Table1).

Statistically significant pathways found by pathfinder involved in blood. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



Supplemental Figure S10 (related to Table1).

Statistically significant pathways found by pathfinder involved in metabolism. Panel A: The heatmap shows the average of aggregated term scores per sample for patients with RLS and healthy controls (CTRL). Panel B: Bubble plot of selected enrichment KEGG pathways. P values were shown by different colors, the size of bubbles indicates the gene count of each pathway. Panel C: Term-Gene Heatmap, shows the heatmap of genes that are involved in the enriched terms, as well as the common or distinct genes between different terms. The tile colors indicate the change values.



Supplemental Table S2. Gene ontology enrichment analysis: molecular functions, related to Figure 2.

ID	Molecular Functions (MF)	Fold_Enrichment	occurrence	support	lowest_p	highest_p	Up_regulated	Down_regulated
GO:0003700	DNA-binding transcription factor activity	1.96198	10	0.07692	2.30078E-16	1.98818E-12	BCL6, NR2F6, FOXD2, GATA1, FOXO4, NFE2, NFIX, NKX3-1, RARA, RFX2, RXRA, SPI1, TAL1, TFE3, TFEB, GCM1, CREB5, KLF2, KLF1, HEY1, SOX6, ZNF746	ATF3, KLF9, EGR1, EGR2, ELF3, FOS, JUN, PLAG1, RORA, KLF10, TRPS1, FOSL1, KLF11, NFAT5, KLF12
GO:0000978	RNA polymerase II cis-regulatory region sequence-specific DNA binding	1.94850	10	0.07490	4.06737E-15	9.9223E-14	CEBPE, GATA1, IRF7, MXD1, NKX3-1, OTX1, RARA, RFX2, RXRA, SPI1, GCM1, LITAF, KLF1, PRDM5, WBP2, ZNF746, MYPOP, MEF2B	ZFXH3, ATF3, EGR1, EGR2, FOS, JUN, MYBL1, PER1, PLAG1, REL, RORA, KLF10, ZNF711, ZBTB16, FOSL1, NRIP1, KLF4, NFAT5, KLF12, GLIS3
GO:0000976	transcription cis-regulatory region binding	2.19712	10	0.09400	1.96294E-11	5.53382E-10	CEBPB, GATA1, NKX3-1, RXRA, SNCA, SPI1, TAL1, TFE3, TFEB, RNF10, BASP1, KLF1, PRDM5, SOX6, CREB3L3, ZNF746, ZNF579	ATF3, EGR1, EGR2, FOS, JUN, TAF9, KLF11, KLF4, ZBED4, ZBTB20, ZBED6
GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	2.13979	10	0.07794	1.0731E-10	4.08266E-09	BCL6, CEBPB, ERF, MXD1, MXI1, PRDM5, HEY1, ETV7, ZNF746, MYPOP	ZFXH3, ATF3, CREM, JUN, SNAI1, TRPS1, ZBTB16, KLF12, TFEC, ZBTB21, ZBTB10, GLIS3, ZBED6
GO:0005096	GTPase activator activity	2.64700	10	0.03133	3.31001E-09	0.000898102	RAP1GAP, RGS2, SIPA1, NPRL3, CDC42EP2, RGS14, ADAP1, SH3BP1, ARHGAP9, ARAP3	DOCK1, JUN, RGS1, NRIP1, ARHGAP32, PLCB1, ARHGAP8, ERFF1, ARHGAP31, SRGAP1, ARHGAP21, SYDE2, RALGAP1
GO:0000977	RNA polymerase II transcription regulatory region sequence-specific DNA binding	1.71361	10	0.03038	8.06687E-09	2.48163E-05	CEBPB, GATA1, MXI1, RARA, RXRA, ETV7, CREB3L3	ATF3, CREM, EGR1, RORA, SNAI1, TRPS1, ZBED4, ZBTB10
GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	1.00888	10	0.04103	1.99995E-08	6.72228E-05	GATA1, HSPB1, SPI1, TAL1, HEY1	EGR2, FOS, JUN, KLF4, HIPK2
GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	1.61721	10	0.04568	1.19603E-07	9.06924E-06	CEBPE, FOXD2, GATA1, FOXO4, OTX1, GCM1, LITAF, CREB3L3, SCX, MEF2B	ATF3, EGR1, EGR2, ELF3, FOS, NR4A1, JUN, MYBL1, NR4A2, PLAG1, REL, KLF10, NR4A3, KLF4, ZBED4, NFAT5, TFEC, GLIS3
GO:0004674	protein serine/threonine kinase activity	1.39514	10	0.00524	1.64912E-07	0.027582621	CAMK2A, LIMK2, MAP3K11, ULK1, DYRK3, DAPK2, PRKD2, PINK1, WNK2, ALPK1, NUAQ2, TSSK6	PAK3, MAPK6, MAP4K3, NUAQ1, AKT3, PLK2, HIPK2, ACVR1C, TTBK2, SIK1
GO:0003779	actin binding	2.52306	10	0.06635	3.80783E-07	7.94145E-07	ALDOA, CEACAM1, DMTN, GSN, HPCA, MEFV, SNCA, SPTB, TMOD1, AVIL, PLEKHG3, MSRB1, FHDC1	SPTBN1, SYNE2, MACF1, CCDC88A, VASH2, GAS2L3
GO:0003677	DNA binding	1.08590	10	0.03210	6.92225E-07	1.19676E-06	CEBPB, GATA1, IMPDH1, IRF7, LYL1, FOXO4, NFE2, RFX2, SLPI, GCM1, OASL, KLF2, MAP15, ISL2, MBD6, SCX	EGR1, FMR1, FOSB, NR4A1, JUN, NR4A2, RORA, TAF9, ZBTB16, KLF12
GO:0004601	peroxidase activity	4.43907	7	0.00552	2.66742E-06	0.00169606	HBA1, HBA2, HBB, PRDX5	
GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	1.98017	10	0.02618	3.32953E-06	7.92434E-06	CEBPB, IRF7, NKX3-1, SPI1, GCM1, KLF2, HEY1, ZNF579	ZFXH3, EGR2, JUN, ZNF711, KLF11
GO:0001221	transcription coregulator binding	3.21450	10	0.02073	7.87504E-06	2.56345E-05	GATA1, RXRA	FOS, RORA, CHD6, ZNF618
GO:0043565	sequence-specific DNA binding	1.28841	7	0.00552	8.50191E-06	0.028126561	BCL6, NR2F6, ERF, FOXD2, GATA1, HLX, FOXO4, NFE2, NKX3-1, RXRA, SPI1, PRDM5, SCX	EGR1, EGR2, RORA, ZNF711
GO:0140297	DNA-binding transcription factor binding	1.03578	10	0.00524	2.35796E-05	0.000635591	BCL3, BCL6, FOXO4, NKX3-1, SPI1, PRDM5, NFE4, ZNF653	TAF9
GO:0042826	histone deacetylase binding	1.66465	10	0.00524	3.7554E-05	0.001387723	BCL3, HSPA1B, NKX3-1, SPI1, TAL1, GCM1, HDAC10, MEF2B	UHRF1BP1
GO:0004713	protein tyrosine kinase activity	1.03578	10	0.01519	0.000119964	0.005997275	HCK, TEK	FLT3, YES1
GO:0051011	microtubule minus-end binding	7.76838	10	0.02564	0.000125701	0.001460066		CAMSAP2, MACF1, CEP290
GO:0043422	protein kinase B binding	5.82628	10	0.00534	0.000351045	0.00037731	RARA, PINK1	CCDC88A
GO:0051082	unfolded protein binding	0.89635	8	0.00548	0.000696395	0.047179577	DNAJB2, HSPA1B, HSPA6	
GO:0019899	enzyme binding	1.22256	10	0.06283	0.001177021	0.005774696	ANK1, CBS, HSPA1B, HSPA6, IL6R, FOXO4, PTEN, RARA, RXRA, SPI1, ZBTB7B, SOX6	ZFXH3, ATP2A2, FN1, JUN, NFKBIA, PDE4D, YES1, PPF22, SACS
GO:0001217	DNA-binding transcription repressor activity, RNA polymerase II-specific	6.21470	10	0.00524	0.001202127	0.001440964	RARA, SPI1, ZBTB7B, SOX6	
GO:0051010	microtubule plus-end binding	2.58946	7	0.00521	0.001371919	0.001474368		DST, TTBK2
GO:0044548	S100 protein binding	3.58540	10	0.01047	0.002199423	0.007708244	S100A11	ATP2A2, AHNAK
GO:0002020	protease binding	1.64507	9	0.00524	0.002812034	0.003331847	F2RL1, INSL3, FADD, PYCARD, CD177, PINK1	FN1, TNFAIP3, SLC2A13
GO:0044325	transmembrane transporter binding	1.36587	10	0.01538	0.002874712	0.028677641	ACTN1, FGF13, TCAP	ATP2A2, FMR1, PDE4D, YES1, AKAP9
GO:0004842	ubiquitin-protein transferase activity	0.96014	9	0.00565	0.00300452	0.006107998	CDC34, TRIM21, KLHL21, UBE2C, FBXO7, TRIM47, RNF182, RNF508	TNFAIP3, RNF217, SHPRH
GO:0004714	transmembrane receptor protein tyrosine kinase activity	3.10735	10	0.01334	0.003257946	0.01220986		EPHA2, FLT3, DDR2
GO:0070412	R-SMAD binding	1.55368	10	0.00524	0.003360715	0.003360715		FOS, JUN
GO:0008017	microtubule binding	1.84961	7	0.00524	0.003852576	0.004339937	FGF13, S100A9, RGS14, MAP15, ENKD1, SGIP1, FHDC1, NIPA1, NIPA2, NIPA3	FMR1, SBDS, CCDC88A, VASH2, MAP9, JMY, GAS2L3
GO:0004385	guanylate kinase activity	7.76838	5	0.00543	0.003882767	0.034406042	GUK1, MPP1	TJP2
GO:0051020	GTPase binding	1.86441	10	0.00534	0.005031357	0.005566329	GNB2, ULK1	SPTBN1
GO:0061630	ubiquitin protein ligase activity	1.43247	10	0.01047	0.005219565	0.005219565	PEX12, TRIM21, RNF10, UBE2C, IRF2BP1, IRF2BPL, NFE2L3, TRIM18, TRIM6, RNF67	HERC2, MYCBP2, SHPRH
GO:0005509	calcium ion binding	1.69358	10	0.01644	0.005373903	0.01186094	AOC1, ADAM8, ALPL, ATP2A1, CDH2, DNASE1L2, GSN, NIPA1, NIPA2, NIPA3, TRAP1, TRAP2, TRAP3, TRAP6, TRAP7, TRAP8	ATP2A2, LRP1
GO:0003729	mRNA binding	1.10977	1	0.00500	0.005498369	0.005498369	SLPI	EIF4A1, FMR1, TRA2B, PEG10
GO:0043130	ubiquitin binding	1.29473	10	0.01047	0.00558299	0.008527822	DNAJB2, HSPB1, FBXO7	TNFAIP3
GO:0004879	nuclear receptor activity	2.30174	10	0.00524	0.006387017	0.011178324	NKX3-1, RARA, RXRA	NR4A2
GO:0043236	laminin binding	4.78054	2	0.00545	0.006416855	0.006416855	ACHE, BCAM	THBS1, ADAM9
GO:0043027	cysteine-type endopeptidase inhibitor	2.91314	1	0.00500	0.00746682	0.00746682	SNCA, TNFSF14, PRDX5	
GO:0044183	protein folding chaperone	1.60725	10	0.01090	0.007964448	0.013933495	HSPA1B, HSPB1, FKBP8	
GO:0031625	ubiquitin protein ligase binding	0.89145	10	0.01067	0.008068633	0.043344395	BAG1, CBS, HSPA1B, SLC22A18, FBXO7, PINK1, NIPA1, NIPA2, NIPA3	EGR2, JUN, NFKBIA, PER1, HERC2, SHPRH
GO:0005178	integrin binding	1.65285	6	0.01013	0.008634079	0.009835887	ACTN1, ICAM3, ITGAX, SFRP2, SPP1, CD177	DST, FN1, THBS1, ADAM9
GO:0005085	guanyl-nucleotide exchange factor activity	1.54459	5	0.00546	0.008839371	0.048677822	RAB3IL1, TBXA2R, DENND3, PLEKHG3, CYTH4, SH3BP5L, NIPA1, NIPA2, NIPA3	DOCK1, MCF2, TRIO, ARFGEF2, MYCBP2, CCDC88A, FGD6, PIP5K1A, RHOGEF, RHOGEF2
GO:0004672	protein kinase activity	1.13182	9	0.00524	0.009325366	0.010495328	MAP3K11, CCL5, TEK, DYRK3, PRKD2, STRADB, PINK1	MAP4K3, AKT3, HIPK2, TTBK2
GO:0019838	growth factor binding	3.45261	9	0.00524	0.010843138	0.028054681		EPHA2, NRP2, NRP1, ACVR1C
GO:0003725	double-stranded RNA binding	1.36287	8	0.00524	0.011153306	0.013852135	ACTN1, OASL, NLRP6	EIF4A1, TFRC
GO:0008373	sialyltransferase activity	5.54884	9	0.00524	0.011632326	0.014241075	ST3GAL2, ST3GAL4, ST6GALNAC2, ST6GALNAC4, ST6GALNAC5	
GO:0003730	mRNA 3'-UTR binding	0.71270	10	0.01334	0.013572564	0.031863305	YBX3, IGF2BP2, MIR106B, MIR93	FMR1
GO:0030297	transmembrane receptor protein tyrosine kinase activity	5.82628	3	0.00552	0.015267736	0.020844166		AREG, HBEGF, EREG
GO:0030331	nuclear estrogen receptor binding	2.58946	8	0.00524	0.015650228	0.028006737	NKX3-1, PADI2, WBP2	NRIP1, PPARGC1B
GO:0030544	Hsp70 protein binding	2.21954	10	0.00524	0.015967072	0.017247262	DNAJB2, SNCA	PPEF2, SACS
GO:0004722	protein serine/threonine phosphatase	1.88324	10	0.00524	0.017394537	0.024423839	PPP1R3D, PTEN	CDC14A, PPM1L
GO:0042605	peptide antigen binding	2.58946	10	0.01117	0.017488823	0.036572528	FCGRT, HLA-A, HLA-B, HLA-C	
GO:0001222	transcription corepressor binding	1.22659	9	0.00524	0.018238596	0.018238596	BCL6	RORA, ZBTB16
GO:0008013	beta-catenin binding	0.92757	10	0.00524	0.01972891	0.021259418	CDH2, FOXO4, SLC9A3R1	NR4A2
GO:0004715	non-membrane spanning protein tyrosine kinase activity	1.66465	10	0.00524	0.021489357	0.023042461	BMX	YES1, PEAK1
GO:0003711	transcription elongation factor activity	3.10735	10	0.00524	0.021610608	0.02295922		EAF2
GO:0042809	nuclear vitamin D receptor binding	3.10735	1	0.00524	0.021610608	0.021610608	RXRA	
GO:0003723	RNA binding	0.48807	1	0.00500	0.022731475	0.022731475	IFIT1, MRPL12	FMR1, TRA2B, ZBED4, SRSF10
GO:0097718	disordered domain specific binding	1.35102	10	0.00524	0.023333366	0.048795073	FKBP8	FN1
GO:0140444	cytoskeleton-nuclear membrane anchor	3.10735	9	0.00524	0.024348512	0.024348512		SYNE2
GO:0055131	C3HC4-type RING finger domain binding	5.17892	10	0.01614	0.026691195	0.047803099	HSPA1B, PINK1	
GO:0001784	phosphotyrosine residue binding	1.37089	10	0.01538	0.026756086	0.031271022	HCK	PIK3R1, YES1
GO:0016176	superoxide-generating NADPH oxidase	6.21470	10	0.00524	0.027249095	0.027249095	NCF2, NCF4	
GO:0003682	chromatin binding	0.96556	1	0.00500	0.028334327	0.028334327	BCL6, RARA, SPI1, TAL1, MBD6, LRWD1	EGR2, FMR1, MLLT10, NFAT5, AUTS2
GO:0003714	transcription corepressor activity	0.97869	10	0.00524	0.028343984	0.0322514	BCL3, CBFA2T3, BASP1, IRF2BP1, ZNF653	NRIP1, AASS, HIPK2
GO:0031267	small GTPase binding	1.35947	2	0.00506	0.029375456	0.029375456	RAP1GAP, WAS, ULK1, YBX3, CDC42EP2, EHD1, FGD3	CHML, RABGGTB, MYCBP2, EXPH5, DMXL2, FGD6, RIC1
GO:0031490	chromatin DNA binding	2.48588	1	0.00500	0.030199842	0.030199842	GATA1, RARA, WBP2	PER1
GO:0043120	tumor necrosis factor binding	3.10735	10	0.00524	0.031904801	0.033537947	TNFRSF1A	

Supplemental Table S4. Gene ontology enrichment analysis: cellular components, related to Figure 2.

ID	Cellular Component	Fold_Enrichment	occurrence	support	lowest_p	highest_p	Up_regulated	Down_regulated
GO:0005813	centrosome	1.23744	10	0.02632	2.62069E-14	4.58249E-12	BCL2L1, HSPA1B, LIMK2, MAK, MAP3K11, RGS14, CCDC85B, DCAF12, MAP1S, MZT2B, ALPK1, B9D2, ENKD1, CEP19, TPGS1, CFAP58, HEPACAM2	PLAG1, XRCC2, LUZP1, ALMS1, CDC14A, PDE4DIP, AKAP9, PLK2, ANKRD26, CAMSAP2, RTTN, AHI1, CNTLN, ODF2L, CCDC14, CEP290, SPICE1, CEP112, CEP85L
GO:0090575	RNA polymerase II transcription regulator complex	2.26578	10	0.07857	1.07967E-08	1.87034E-08	CEBPB, CEBPD, CEBPE, MXI1, NFE2, RARA, RXRA, BATF2	ATF3, FOS, JUN, FOSL1, HIPK2, BACH2
GO:0015629	actin cytoskeleton	1.83299	10	0.06433	1.64303E-08	2.35803E-08	ALDOA, DBN1, DMTN, RARA, SNCA, SPTA1, SPTB, VASP, WAS, PDLIM7, SLC9A3R1, CORIN, MSRB1	NEB, DDR2, AUTS2, ARHGAP21, AHNAK, PEAK1, DGKH, GAS2L3
GO:0000785	chromatin	1.22123	10	0.02717	4.00845E-08	7.51291E-08	MXD1, RARA, RXRA, SPI1, TAL1, TGM2, KLF2, KLF1, WBP2, PINK1	EGR1, TRPS1, ZNF711, NRIP1, KLF4, PLCB1, ZNF618, ZNF827
GO:0005814	centriole	2.08225	10	0.03085	6.02772E-08	0.000415387	HSPA1B, HSPA6, ENKD1, CEP19	ALMS1, PLK2, RTTN, AHI1, CNTLN, CCDC88A, CEP290, TTBK2, SPICE1
GO:0034451	centriolar satellite	1.65927	10	0.00606	2.99075E-06	0.000315058	MPP1, TEK, DYSF, CYTH4, ZMYND10, RPP25	ODF2L, CCDC14, CEP290, CCDC18, ZBED6
GO:0009986	cell surface	1.65842	10	0.01124	3.72535E-06	0.001119497	ADAM8, CEACAM1, CA4, CDH2, CCR10, HLA-A, HLA-B, HLA-C, HPN, CXCR2, ITGAX, ITGB4, TEK, TGFA, THBD, AOC3, LPAR2, NRXN1, SIRPB1, ABCA7, TSPEAR, NLGN3, RTN4R, TREM1, PLVAP, CLEC9A, SMIM1	AREG, HBEGF, EPHA2, ITGB8, NCAM1, PRLR, TFRC, TGFBR3, THBS1, SLC4A4, ADAM9
GO:0005833	hemoglobin complex	12.08414	10	0.03548	3.91824E-06	0.000233836	HBA1, HBA2, HBB, HBD, HBG1, HBG2, HBZ	
GO:0032010	phagolysosome	12.42940	10	0.00543	2.56991E-05	2.79648E-05	ADAM8, NCF2, NCF4, NCF1	
GO:0005925	focal adhesion	1.62324	10	0.01729	2.682E-05	0.002347353	ACTN1, HCK, TNS1, VASP, PDLIM7, AVIL, LIM2, CASS4	EPHA2, KLF11, NRP1, IL1RL1, SYNE2, PEAK1
GO:0005743	mitochondrial inner membrane	0.51633	6	0.00536	3.58606E-05	4.28075E-05	ALAS2, FECH, MRPL12, GCAT, MTG2, AURKAIP1, PINK1	NDUFV2, NDUFAF5, ACAD11, MICU3
GO:1904813	ficolin-1-rich granule lumen	2.13004	10	0.03700	5.66063E-05	0.016277186	ALDOA, CDA, CFD, GSN, HBB, HSPA1B, HSPA6, IMPDH1, KRT1, MMP9, MND, PYGL, TNFAIP6, QPCT, PLEKHO2, IRLG1, CANT1	
GO:0031410	cytoplasmic vesicle	1.59937	10	0.01078	6.54532E-05	0.038662527	DMTN, MME, TGFA, PRDX5, WLS, ANKRD9	DST, TFRC, NRP1, ARFGF2, MYOF, CCDC88A, JMY, STARD4
GO:0016323	basolateral plasma membrane	2.01195	8	0.01028	7.60244E-05	0.037091014	AQP1, C5AR1, CA4, SLC29A1, SLC4A1, SLC6A9, SLC19A1, TEK, TGFA, BEST1, SLC16A3, HEPH, CALHM1	LRP1, TFRC, SLC4A4, SLC16A7, SLC4A7
GO:0030667	secretory granule membrane	3.65571	10	0.01687	8.76325E-05	0.000572167	ANPEP, RHOG, C5AR1, CA4, FCGR2A, FCGR3B, FPR1, HLA-B, HLA-C, CXCR1, CXCR2, ITGAX, MME, PTAFR, SIGLEC5, SIRPB1, RAB24, CD177, DOK3	ABCA13
GO:0043020	NADPH oxidase complex	5.82628	10	0.00543	0.000143438	0.000156069	NCF2, NCF4, NCF1	
GO:0030670	phagocytic vesicle membrane	1.89473	9	0.01075	0.000172725	0.000198052	ANXA3, HLA-A, HLA-B, HLA-C, TCIRG1	
GO:0042612	MHC class I protein complex	7.76838	10	0.06612	0.000178035	0.000258142	HLA-A, HLA-B, HLA-C	
GO:0031095	platelet dense tubular network membrane	7.76838	10	0.03373	0.00019835	0.032645283	ATP2A1, DMTN, EHD1	ATP2A2
GO:0034774	secretory granule lumen	1.92491	10	0.03030	0.000339282	0.000523446	ALDOA, CDA, CFD, GSN, HSPA6, IMPDH1, POMC, PYGL, S100A9, S100A11, S100P, PYCARD, GHRL, ARHGAP9	
GO:0098978	glutamatergic synapse	1.29473	2	0.00514	0.000377976	0.000377976	ACTN1, SPTB	TRIO, AKAP9
GO:0031901	early endosome membrane	1.28138	10	0.01720	0.000434593	0.011028712	EPHB1, HLA-A, HLA-B, HLA-C, IFITM3, EHD1, WLS, UBXN6	
GO:0055038	recycling endosome membrane	1.52821	10	0.02424	0.0004915	0.009182286	HLA-A, HLA-B, HLA-C, RAB11B, EHD1, PACSIN2	
GO:0000932	P-body	0.83233	10	0.01087	0.000617777	0.000707984	IGF2BP2, LSM14A	TNRC6A
GO:0005667	transcription regulator complex	1.72631	10	0.01687	0.000620252	0.000838227	GATA1, RARA, RXRA, SPI1, TAL1, GCM1, SCX, MEF2B	ZFXH3
GO:0035102	PRC1 complex	2.58946	1	0.00510	0.000717443	0.000717443	PHC2	PHC3
GO:0005741	mitochondrial outer membrane	1.40085	10	0.01078	0.000740882	0.016744412	BCL2L1, ACSL1, UBA52, UBB, ULK1, PINK1, NLRX1, FAM210B	PMAIP1, VPS13A, VPS13C
GO:0031093	platelet alpha granule lumen	1.91222	10	0.00543	0.000998654	0.00115695	ACTN1, ALDOA, SERPING1, CFD, ORM1, TOR4A	FN1, THBS1
GO:0071682	endocytic vesicle lumen	2.58946	5	0.00541	0.001178976	0.011893833	HBA1, HBA2, HBB	
GO:0005788	endoplasmic reticulum lumen	1.27066	10	0.00606	0.001455869	0.002706124	BGLAP, SERPING1, CDH2, COL9A3, CSF1, PROC, SPP1, WNT6, RNASET2, TSPAN5, SHISA5, GHRL, COL18A1	COL19A1, VCAN, FN1, IL12A, KTN1, LAMB2, THBS1, UGGT2, COL24A1
GO:0005882	intermediate filament	3.27090	9	0.00546	0.001547808	0.001707011	RTN2	KRT5, PNN, SYNM
GO:0042995	cell projection	4.94351	10	0.02796	0.001602149	0.002216997	ACTN1, CACNA1A, PTEN, AVIL, MAP1S	FMR1, SLC2A13
GO:0005856	cytoskeleton	1.48612	10	0.02710	0.002288726	0.014330526	DBN1, EPB42, HSPB1, KRT1, S100A9, BASP1, IGF2BP2, PINK1	MCF2, AKAP9, TENM1
GO:0035580	specific granule lumen	3.56581	10	0.00543	0.002574622	0.003482318	AOC1, CHI3L1, CNN2, FOLR3, CXCL1, ORM1, SLPI, PGLYRP1, QPCT, TOLLIP, IRLG1, CANT1	PTX3, CEP290
GO:0005759	mitochondrial matrix	0.86616	7	0.00578	0.003367373	0.02468337	ALAS2, FECH, GPX1, MPST, SOD2, TST, MTHFS, PRDX5, MTG2, GLRX5, NT5M, ACS3, MRM1, ALKBH7, NAGS	AASS
GO:0043235	receptor complex	1.47429	1	0.00606	0.004199929	0.004199929	CR1L, ITGB4, RXRA, TNFRSF1A, TLR6, ITLN1	LRP1, TGFBR3, TRPC1, LRP8, CUBN, NRP1, NT5DC3

GO:0031519	PcG protein complex	1.47969	1	0.00510	0.004290476	0.004290476	PHC2	PHC3
GO:0016234	inclusion body	2.07157	10	0.00543	0.004699361	0.005216977	HSPA1B, SNCA	
GO:0030669	clathrin-coated endocytic vesicle membrane	1.35102	8	0.00562	0.005032529	0.007245398	TGFA, KIAA0319	AREG, HBEGF, EREG, TFRC
GO:0016324	apical plasma membrane	1.90077	5	0.00541	0.005874448	0.041956711	AQP1, ATP1B2, CEACAM1, CA4, SLC29A1, IL6R, SLC22A18, PTEN, SLC6A8, SLC6A9, SLC19A1, SLC22A1, SLC22A4, STX3, TEK, MGAM, SLC16A3, SLC9A3R1, TCIRG1, ZMYND10, CYP4F12, SLC6A19	CUBN
GO:0098797	plasma membrane protein complex	4.66103	10	0.01072	0.006438709	0.03063426	SLC9A3R1	LRP1, AHNAK
GO:0045171	intercellular bridge	1.32631	9	0.00546	0.006787162	0.007564576	TUBB2A, TUBB4A, FAM50B, CYTH4, KLHDC8B	PRC1, RBM44
GO:0031463	Cul3-RING ubiquitin ligase complex	1.37089	10	0.01087	0.006960868	0.01141622	KLHL21, KBTBD7	ENC1
GO:0019005	SCF ubiquitin ligase complex	1.07150	10	0.01087	0.007006152	0.007006152	FBXO7, FBXL15	
GO:0009897	external side of plasma membrane	1.69212	1	0.00510	0.007033553	0.007033553	ATP1B2, CA4, RTN4R	CTLA4, MCAM, NCAM1, TFRC, TGFBR3, THBS1, ADAM9, CD163
GO:0005874	microtubule	1.60725	10	0.00606	0.008586774	0.014338712	FGF13, MAP3K11, TUBB2A, CDK2AP2, TUBB4A, MAP1S, FHDC1	MACF1, DYNC2H1
GO:0072686	mitotic spindle	1.41243	10	0.00592	0.010156551	0.012813351	CXCR2, LIMK2, MAK, TUBB2A, TUBB4A, LSM14A, HECW2, HEPACAM2	MAP9
GO:0001725	stress fiber	1.25974	9	0.00541	0.011035138	0.014778958	ACTN1, CNN2, TEK	
GO:0035976	transcription factor AP-1 complex	6.21470	10	0.04348	0.013324871	0.013324871		FOS, JUN
GO:0016529	sarcoplasmic reticulum	2.82486	4	0.00576	0.01333921	0.015705578		ATP2A2, THBS1, SYNE2, CMYA5
GO:0010008	endosome membrane	1.05496	1	0.00606	0.014285424	0.014285424	IRF7, NCF4, UBA52, UBB, TCIRG1, EHD1, VPS37C	FLT3, MRC1, TFRC, VPS13A
GO:0034993	meiotic nuclear membrane microtubule tethering complex	3.10735	8	0.00539	0.015980188	0.015980188		SYNE2
GO:0030424	axon	1.22337	10	0.00543	0.01860246	0.01860246	FGF13, MME, SNCA, GHRL, PINK1	FMR1, KCNA2, NRP1, SACS, MAP9
GO:0005776	autophagosome	1.08396	10	0.01543	0.019274145	0.038770019	ULK1, MAP1LC3A, ATG16L2	
GO:0015630	microtubule cytoskeleton	1.58770	9	0.00546	0.021013999	0.032252673	CXCR2, TUBB2A, SPAG6, TUBB4A, CDC42EP2, MID1IP1, ENKD1, LRRC25	DST, CCNA1, PRC1, KLF4, NUA1, GAS2L3
GO:0005811	lipid droplet	1.96945	2	0.00522	0.021778659	0.03039155	ALOX15, EHD1, HSD3B7, DGAT2, PLIN5, PLIN4	VPS13A, GOS2, VPS13C
GO:0012507	ER to Golgi transport vesicle membrane	2.07157	9	0.01075	0.022120423	0.024374476	HLA-A, HLA-B, HLA-C, TGFA, CNIH3	AREG
GO:0031252	cell leading edge	2.91314	2	0.00606	0.022771594	0.022771594	ITGB4, SH3BP1, CADM4	DST, LDB2, JMY
GO:1990752	microtubule end	6.21470	4	0.00528	0.023109814	0.024234956	NAV3	CAMSAP2
GO:0030122	AP-2 adaptor complex	2.58946	10	0.00543	0.023946749	0.025352361	SGIP1	
GO:0070062	extracellular exosome	1.32793	7	0.00541	0.024721591	0.027606766	AOC1, ALDOA, ANPEP, AQP1, CA4, WNT6, WLS	FN1, CUBN, AHNAK
GO:0048471	perinuclear region of cytoplasm	0.94881	8	0.00543	0.025195538	0.028515932	ACHE, CA4, CSF1, DMTN, GNB2, HSPA1B, INHBB, SNCA, TGFA, YBX3, SLC9A3R1, PRDX5, MAP1S, HHATL, PINK1, GDPD3, DGAT2	CTLA4, FMR1, PIK3R1, TFRC, GALNT4, TENM1, CMYA5
GO:0031012	extracellular matrix	1.98342	2	0.00514	0.025229827	0.025229827	LTBP2, PI3, TGM2	FN1, MATN1, THBS1
GO:0017053	transcription repressor complex	0.63415	1	0.00538	0.025884041	0.025884041	GATA1	ZBTB16
GO:0000139	Golgi membrane	1.43785	9	0.00546	0.026098301	0.034991485	BSG, FUT7, HLA-A, HLA-B, HLA-C, LFN3, ST3GAL2, ST3GAL4, TNFRSF1A, ST8SIA4, B3GALT2, RAB33A, RAB36, AP1M2, ST6GALNAC2, GALNT5, ST6GALNAC4, CYTH4, PYCARD, ST6GALNAC6, CHST7, GALNT14, WLS, CREB3L3, ZDHHC19, CHST13, B3GNT8	NCAM1, GALNT4, ARFGF2, ABCA6, RAB39A, XYLT1, B3GNT7, ZDHHC21, IRGM
GO:0036064	ciliary basal body	1.34453	4	0.00528	0.02894533	0.0318006	B9D2, ENKD1, CEP19	CAMSAP2, RTTN, AHI1, CCDC88A, ODF2L, TTBK2
GO:0019897	extrinsic component of plasma membrane	3.88419	9	0.00546	0.02924932	0.047932135		FMR1, EEA1, SYTL2
GO:0005577	fibrinogen complex	3.88419	10	0.00592	0.032645283	0.034890449		FN1, THBS1
GO:0030056	hemidesmosome	5.17892	10	0.00543	0.032978663	0.034623471	ITGB4	DST
GO:1904724	tertiary granule lumen	3.95481	9	0.00546	0.036658566	0.036658566	ALDOA, CDA, CNN2, FOLR3, CXCL1, HBB, MMP9, ORM1, TNFAIP6, PGLYRP1, QPCT, LRG1, CANT1	PTX3
GO:0022625	cytosolic large ribosomal subunit	0.95123	10	0.00562	0.037916244	0.045102026	UBA52	RPL17, RPL36A
GO:0014731	spectrin-associated cytoskeleton	8.87815	10	0.00543	0.039554183	0.04168604	ANK1, DMTN, SPTA1, SPTB	
GO:0097386	glial cell projection	3.88419	10	0.00543	0.042071087	0.042071087	ABCA7	FMR1
GO:0055037	recycling endosome	0.79676	1	0.00510	0.043976172	0.043976172	ULK1, RAB11B	TFRC, ARFGF2
GO:0030426	growth cone	2.21954	2	0.00606	0.047109871	0.047109871	DBN1, FGF13, SNCA, STX3	FMR1, AUTS2, ZNF804A, SLC2A13