

Table SI. NLS oligos.

Oligo name	Sequence (5'-3')
NLS-for	<u>CGCGTCCTAAAAAGAAACGTAAAGTTTAAACTAGTC</u>
NLS-rev	<b><u>TCGAGACTAGTTTAAACTTTACGTTTCTTTT</u></b> <u>AGGA</u>
NLS-GFP FOR	<u>CGCGTCCTAAAAAGAAACGTAAAGTTACTAGTC</u>
NLS-GFP REV	<b><u>TCGAGACTAGTAACTTTACGTTTCTTTT</u></b> <u>AGGA</u>

Underlined, *Mlu*I site (part); bold underlined, *Xho*I site (part); Bold, *Spe*I site. For, forward;

Rev, reverse; NLS nuclear localization signal; GFP, green fluorescence protein.

Table SII. Primer sequences for qPCR.

Target gene	Forward (direction 5'-3')	Reverse (direction 5'-3')
ABCG2	AGA TGG GTT TCC AAG CGT CCA GTC CCA GTA CGA CTG TCA T	TGA CA
$\beta$ 2M	CTC CGT GGC CTT AGC TGT G	TTG GGA GTA CGC TGG ATA GCC T
C-MYC	AAT GAA AAG GCC CCC AAG GTA GTT ATC C	GTC GTT TCC GCA ACA AGT CCT CTT C
CXCR4	GCA TGA CGG ACA AGT ACA GGC T	AAA GTA CCA GTT TGC CAC GGC
CXCL12	TCA GCC TGA GCT ACA GAT GC	CTT TAG CTT CGG GTC AAT GC
E-cadherin	CCC GGG ACA ACG TTT ATT AC	GCT GGC TCA AGT CAA AGT CC
N-cadherin	GGT GGA GGA GAA GAA GAC CAG	GGC ATC AGG CTC CAC AGT
NR2F1	TTC GTC CGT TTG GTA GGT AAA A	GGA AGC GCC CAA GGT CTA G
COUP-TFII (both variants)	TTC GTC CGT TTG GTA GGT AAA A	TCT GTT TCA CTC CCC C CTT CTT ATT T
COUP-TFII_V1	GCA AGC ACT ACG GCC AGT T	CTG CGC TTG AAG AAG CTC TT

COUP-TFII_V2	AGCA GGG AAA TAT ATC CGG TTT TGC GGT GCA GAG GGG ACA GG
GAPDH	AAC AGC CTC AAG ATC ATC CAG TCT GGG TGG CAG TGA AGC AA T
KLF-4	GAA ATT CGC CCG CTC CGA CTG TGT GTT TGC GGT AGT TGA GCC
KLF-6	CGG ACG CAC ACA GGA GAA CGG TGT GCT TTC GGA AGT AA G
LIN28	GGT GAG TCA AAG GAA CTC TAA TCA TTT CAC TCT GGC CAA C ATG G
MMP2	ACC CAG ATG TGG CCA ACT TAC TTT TAA GGC CCG AGC AC AA
MMP9	GAA CCA ATC TCA CCG ACA GCC ACC CGA GTG TAA CCA GG TA
Nanog	TGG GAT TTA CAG GCG TGA AAG CAA AGC CTC CCA ATC GCC AC CCA AAC
Nestin	GGC GCA CCT CAA GAT GTC C CTT GGG GTC CTG AAA GCT G
POU5F1	Quantitect Primer Assay Qiagen GeneGlobe ID - QT00210840
RPL13A	CCT GGA GGA GAA GAG GAA TTG AGG ACC TCT GTG TAT AGA G TTG TCA A
SNAIL1	TTC CAG CAG CCC TAC GAC GCC TTT CCC ACT GTC CTC CAG ATC

Sox2	TCA GGA GTT GTC AAG GCA GCC GCC GCC GAT GAT TGT GAG AAG	TAT TAT
hTERT	Quantitect Primer Assay Qiagen	GeneGlobe ID - QT00073409
TGFβ	TAC CTG AAC CCG TGT TGC GTT GCT GAG GTA TCG CCA TCT C	GGA A
Vimentin	TGG ATT CAC TCC CTC TGG TT	GGT CAT CGT GAT GCT GAG AA
CTNNB1	TGC AGT TCG CCT TCA CTA TG	ACT AGT CGT GGA ATG GCA CC
PCNA	GCC AGA GCT CTT CCC TTA CG	TAG CTG GTT TCG GCT TCA GG
Ki67	GAG GTG TGC AGA AAA TCC AAA	CTG TCC CTA TGA CTT CTG GT T CT
AMPK	GGG TGA AGA TCG GCC ACT	TTG CCA ACC TTC ACT TTG AC CC
TGFβ receptor	CGA GTG CCA AAT GAA GAG GAC C	AAA CCT GAG CCA GAA CCT GAC G

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ABCG2, ATP-binding cassette sub-family G member 2; CTNNB1, β-catenin; hTERT, human telomerase reverse transcriptase; NR2F1, COUP-TFI; RPL13A, ribosomal protein L13a; KLF4, Kruppel-like factor 4; KLF6, Kruppel-like factor 6; PCNA, proliferating cell nuclear antigen.

Table SIII. Scoring table for *in vivo* experiments.

TNMP stage	Score
<b>T-Stage</b>	
T0	0
T1	2
T2	3
T3	4
T4	5
<b>N-stage: Lymph node metastasis</b>	
Yes	2
No	0
<b>M-stage: Liver metastasis</b>	
Yes	3
No	0
<b>P-stage: Other metastasis (abdominal wall, kidney, spleen)</b>	
No	0
In one	2
In two	3
In all	4

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The overall score is additive.

Table SIV. Sequences of Cy3-labeled oligos.

Direction	Sequence (5'-3')
NHE sense	[Cy3]GGGTCTCCCTACTGACCTCAGCCTGGTCTAGAACTCACTTG
NHE antisense	[Cy3]CAAAGTGAGTTCTAGACCAGGCTGAGGTCAGTAGGGAGACCC

Cy3, cyanine 3; NHE, sodium-hydrogen exchanger.

Table SV. Cox univariate analysis.

Variable/comparison	HR (95%CI)	P-value <sup>a</sup>
Age ( $\geq 70$ vs. $< 70$ years)	0.95 (0.4-2.3)	NS
Sex (male vs. female)	0.7 (0.28-1.7)	NS
T (T <sub>3</sub> vs. T <sub>1-2</sub> )	2.1 (0.74-5.9)	NS
N (N+ vs. N-)	2.4 (0.78-7.6)	NS
Differentiation		
Poor vs. moderate	4.3 (1.4-13)	<0.05
Well-differentiated vs. moderate	0.45 (0.058-3.5)	NS
COUP-TFII_V2 (low vs. high)	0.37 (0.14-1)	<0.05

<sup>a</sup>Likelihood ratio P-value. HR, hazard ratio; TF, transcription factor; NS, not significant.

Table SVI. 2D-DIGE COUP-TFII\_V2 with protein score  $\geq 30$ .

Protein name	Abbreviation	Score
ATP-binding cassette sub-family E member 1	ABCE1	35
ATP-binding cassette sub-family F member 1	ABCF1	44
Abhydrolase Domain Containing 14A	ABHD14A	37
Actin Related Protein 10	ACTR10	30
Fructose-bisphosphate aldolase A	ALDOA	46
Angiopoietin-1	ANGPT1	32
Ankyrin repeat and SAM domain-containing protein 3	ANKS3	40
Apolipoprotein E	APOE	51
Activity Regulated Cytoskeleton Associated Protein	ARC	30
Rho guanine nucleotide exchange factor 19	ARHGEF19	35
Rho guanine nucleotide exchange factor 3	ARHGEF3	32
ADP-ribosylation factor-like protein 6	ARL6	39
Activating signal cointegrator 1 complex subunit 2	ASCC2	30
Mitochondrial inner membrane protease ATP23 homolog	ATP23	36
Ataxin-10	ATXN10	50
Beta-1,4-galactosyltransferase 2	B4GALT2	53
B melanoma antigen 4	BAGE4	31
Bromodomain-containing protein 1	BRD1	52
Peregrin OS=Homo sapiens	BRPF1	39
Putative uncharacterized protein C17orf82	C17orf82	34
Uncharacterized protein C1orf105	C1orf105	63
Protein CASC2, isoform 3	CASC2	37
Caspase-5	CASP5	37
Chromatin licensing and DNA replication factor 1	CDT1	37
Citron Rho-interacting kinase	CIT	54
Conserved oligomeric Golgi complex subunit 8	COG8	39
Cytochrome c oxidase subunit 6C	COX6C	30
Complexin 1	CPLX1	49
Chondroitin sulfate N-acetylgalactosaminyltransferase 1	CSGALNACT1	43
Casein kinase I isoform delta	CSNK1D	35
Cystatin-SA	CST2	35
Cytochrome b5 reductase 4	CYB5R4	33
DEXD-Box Helicase 50	DDXH50	37
DiGeorge Syndrome Critical Region Gene 6 Like	DGCR6L	34
Disrupted in schizophrenia 1 protein	DISC1	37
Dynamamin-binding protein	DNMBP	32
2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1	38
Eukaryotic Translation Elongation Factor 2	EEF2	48
Probable crossover junction endonuclease EME2	EME2	35
Exonuclease mut-7 homolog	EXD3	43
Protein FAM76A	FAM76A	33
Protein FAM81B	FAM81B	44
Putative uncharacterized protein FRMD6-AS1	FRMD6-AS1	38
Frizzled-2	FZD2	32
G protein subunit alpha 11	GNA11	34
Nucleolar GTP-binding protein 2	GNL2	32
Glutathione S-transferase A2	GSTA2	36
Histone H2B type F-S	H2BF6	35
Haloacid dehalogenase-like hydrolase domain-containing protein 3	HDHD3	33
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	38
Heterogeneous nuclear ribonucleoprotein C-like 1	HNRNPCL1	37
Heterogeneous nuclear ribonucleoprotein C-like 2	HNRNPCL2	38



Heterogeneous nuclear ribonucleoprotein K	HNRNPK	44
Heat shock 70 kDa protein 14	HSPA14	31
Intermediate filament family orphan 2	IFFO2	42
Pro-interleukin-16	IL16	33
Junction-mediating and -regulatory protein	JMY	47
Junctional sarcoplasmic reticulum protein 1	JSRP1	49
ATP-sensitive inward rectifier potassium channel 12	KCNJ12	32
Inward rectifier potassium channel 18	KCNJ18	32
Uncharacterized protein kiaa1211	KIAA1211	36
Uncharacterized protein kiaa2012	KIAA2012	49
Keratin, type II cytoskeletal 1	KRT1	58
Keratin, type I cytoskeletal 18	KRT18	71
Keratin, type II cytoskeletal 8	KRT8	115
Kynureninase	KYNU	43
Lipocalin-1	LCN1	31
Protein lin-7 homolog C	LIN7C	45
Leucine-rich repeat-containing protein 3	LRRC3	37
Melanoma-associated antigen B18	MAGEB18	35
Methyltransferase-like protein 2A	METTL2A	31
Mitochondrial pyruvate carrier 2	MPC2	41
MRN Complex Interacting Protein	MRNIP	35
39S ribosomal protein L17, mitochondrial	MRPL17	40
28S ribosomal protein S14, mitochondrial	MRPS14	34
Mitochondrial fission regulator 1-like	MTFR1L	34
Metaxin-3	MTX3	38
N-Deacetylase And N-Sulfotransferase 1	NDST1	49
Nuclear factor 1 C-type	NFIC	30
Dehydrololichyl diphosphate synthase complex subunit NUS1	NUS1	34
Optic atrophy 3 protein	OPA3	30
Protein deglycase DJ-1	PARK7	38
Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	32
Peroxisome biogenesis factor 1	PEX1	57
Pleckstrin homology-like domain family A member 2	PHLDA2	35
Phosphatidylinositol Glycan Anchor Biosynthesis Class K	PIGK	32
Pyruvate kinase PKM	PKM	42
Plakophilin-1	PKP1	33
PRELI domain-containing protein 1, mitochondrial	PRELID1	39
cAMP-dependent protein kinase catalytic subunit alpha	PRKACA	30
Proline/serine-rich coiled-coil protein 1	PSRC1	40
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	42
Focal adhesion kinase 1	PTK2	41
Rab GTPase-activating protein 1-like	RABGAP1L	40
Rap Guanine Nucleotide Exchange Factor 2	RAPGEF2	38
RAS Like Family 11 Member A	RASL11A	31
Replication factor C subunit 1	RFC1	31
Serine/threonine-protein kinase RIO2	RIOK2	35
RBPJ-interacting and tubulin-associated protein 1	RITA1	30
E3 ubiquitin-protein ligase	E3 ligase	38
Ring Finger Protein 20	RNF20	44
Ribonuclease P protein subunit p14	RPP14	32
40S ribosomal protein S28	RPS28	35
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	32
Semaphorin 6D	SEMA6D	39
Septin-1	SEPT1	38

Serine hydroxymethyltransferase, mitochondrial	SHMT2	45
Protein Shroom3	SHROOM3	42
Shootin-1	SHTN1	44
Signal-induced proliferation-associated 1-like protein 1	SIPA1L1	45
Calcium-binding mitochondrial carrier protein SCaMC-3	SLC25A23	36
Phosphate carrier protein, mitochondrial	SLC25A3	31
Solute Carrier Family 25 Member 35	SLC25A35	50
Solute carrier family 25 member 41	SLC25A41	39
Long-chain fatty acid transport protein 4	SLC27A4	39
SMC5-SMC6 complex localization factor protein 1	SLF1	48
Small proline-rich protein 4	SPR44	40
Small proline-rich protein 3	SPRR3	31
SRC kinase signaling inhibitor 1	SRCIN1	35
Lactosylceramide alpha-2,3-sialyltransferase	ST3GAL5	54
Serine/threonine-protein kinase 32C	STK32C	39
O(6)-methylguanine-induced apoptosis 2	STPG1	40
Synaptonemal complex central element protein 1	SYCE1	37
Synaptonemal complex central element protein 1	SYCE1	37
SUZ RNA Binding Domain Containing 1	SZRD1	37
Protein TANC2	TANC2	48
Transcription elongation factor A protein-like 2	TCEAL2	39
Dimethyladenosine transferase 2, mitochondrial	TFB2M	38
Transmembrane protein 191B	TMEM191B	30
Tumor necrosis factor alpha-induced protein 8-like protein 3	TNFAIP8L3	37
E3 ubiquitin-protein ligase TRIM63	TRIM63	36
Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1	TSTD1	32
Mitochondrial uncoupling protein 2	UCP2	36
Ubiquitin carboxyl-terminal hydrolase 14	USP14	36
UDP-glucuronic acid decarboxylase 1	UXS1	30
vinculin	VCL	123
Vimentin	VIM	97
XK-related protein 3	XKR3	30
Putative uncharacterized protein FLJ43343	FLJ43343	36
Putative uncharacterized protein FLJ32790	FLJ32790	45
Palmitoyltransferase ZDHHC23	ZDHHC23	47
Zinc finger protein 385A	ZNF385	33
Zinc finger protein 391	ZNF391	31
Zinc finger protein 420	ZNF420	41
Zinc Finger Protein 525	ZNF525	55
Zinc finger protein 780A	ZNF780A	32
Zinc finger protein 843	ZNF843	38

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Table SVII. COUP-TFII\_V2 GO terms.

GO term	Ontology source	Term P-value corrected with Benjamini-Hochberg	Associated genes found
Protein localization to cell surface	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ANGPT1, PIGK, VCL
Metaphase plate congression	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, PSRC1, SEPT1
Response to electrical stimulus	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	BRD1, NDUFA2, TRIM63
Glycolysis	REACTOME_Pathways_04.0 9.2018	0.01	ALDOA, PKM, PRKACA
Protein homotetramerization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ALDOA, KCNJ12, PKM, SAMHD1, SHMT2
Heparin metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	ANGPT1, CSGALNACT1, NDST1
Heparin biosynthetic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	ANGPT1, CSGALNACT1, NDST1
Insulin secretion involved in cellular response to glucose stimulus	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	KRT1, MPC2, UCP2
Regulation of insulin secretion involved in cellular response to glucose stimulus	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	KRT1, MPC2, UCP2
Response to nerve growth factor	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CSNK1D, EEF2, RAPGEF2
Cellular response to nerve growth factor stimulus	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CSNK1D, EEF2, RAPGEF2
Regulation of cellular respiration	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	PARK7, PRELID1, SHMT2, SLC25A23
Phospholipid transport	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, PRELID1, SLC25A23, TNFAIP8L3
Regulation of oxidative phosphorylation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	PARK7, SHMT2, SLC25A23
Regulation of dendrite morphogenesis	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ARC, RAPGEF2, SIPA1L1, SLC25A23, SRCIN1
Regulation of dendritic spine development	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, ARC, SIPA1L1, SRCIN1
Regulation of dendritic spine morphogenesis	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ARC, SIPA1L1, SRCIN1

Apoptotic cleavage of cellular proteins	REACTOME_Pathways_04.0 9.2018	0.01	PKP1, PTK2, VIM
Apoptotic execution phase	REACTOME_Pathways_04.0 9.2018	0.01	PKP1, PTK2, VIM
Intermediate filament cytoskeleton organization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	KRT18, PKP1, VIM
Cornification	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	KRT1, KRT18, KRT8, PKP1, SPRR3
Negative regulation of RNA catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HNRNPC, HNRNPK, PKP1, SEPT1
Negative regulation of mRNA metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	HNRNPC, HNRNPK, PKP1, RNF20, SEPT1
RNA stabilization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	HNRNPC, HNRNPK, SEPT1
Negative regulation of mRNA catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	HNRNPC, HNRNPK, PKP1, SEPT1
mRNA stabilization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	HNRNPC, HNRNPK, SEPT1
Metaphase/anaphase transition of cell cycle	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, RIOK2, SLC25A41
Regulation of mitotic sister chromatid segregation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, RIOK2, SLC25A41, SLF1
Regulation of mitotic sister chromatid separation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, RIOK2, SLC25A41
Regulation of metaphase/anaphase transition of cell cycle	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, RIOK2, SLC25A41
Metaphase/anaphase transition of mitotic cell cycle	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, RIOK2, SLC25A41
Regulation of mitotic metaphase/anaphase transition	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, RIOK2, SLC25A41
Plasma lipoprotein particle organization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, PRKACA, SLC25A23
Positive regulation of oxidoreductase activity	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, NUS1, PARK7
Protein-lipid complex subunit organization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, PRKACA, SLC25A23
Plasma lipoprotein particle assembly	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, PRKACA, SLC25A23
Organophosphate ester transport	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, PRELID1, SLC25A23, SLC25A41, TNFAIP8L3

Positive regulation of monoxygenase activity	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, NUS1, PARK7
Protein-lipid complex assembly	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, PRKACA, SLC25A23
Regulation of cellular respiration	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	PARK7, PRELID1, SHMT2, SLC25A23
Phospholipid transport	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, PRELID1, SLC25A23, TNFAIP8L3
Regulation of sterol transport	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, NUS1, SLC25A23
Positive regulation of phospholipid metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	PTK2, SLC25A23, TNFAIP8L3
Regulation of cholesterol transport	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, NUS1, SLC25A23

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GO, gene ontology.



Table SVIII. 2D-Dige COUP-TFII\_V1 with protein score  $\geq 30$ .

Protein name	Abbreviation	Score
ATP binding cassette sub-family f member 1	ABCF1	44
Abhydrolase domain containing 14a	ABHD14A	37
Actin, cytoplasmic 1	ACTB	43
Actin, cytoplasmic 2	ACTG	43
Apoptosis-inducing factor 2	AIFM2	31
Ah receptor-interacting protein	AIP	53
Aldo-keto reductase family 1 member c3	AKR1C3	40
Angiopoietin-1	ANGPT1	32
Putative ankyrin repeat domain-containing protein 26-like protein	ANKRD26P1	34
Ankyrin repeat and sam domain-containing protein 3	ANKS3	40
DNA dc->du-editing enzyme apobec-3a	APOBEC-3A	31
Apolipoprotein e	APOE	40
Apolipoprotein I domain-containing protein 1	APOLD1	32
Activity regulated cytoskeleton associated protein	ARC	30
Rho guanine nucleotide exchange factor 19	ARHGEF19	35
Rho guanine nucleotide exchange factor 3	ARHGEF3	32
Adp-ribosylation factor-like protein 6	ARL6	39
Activating signal cointegrator 1 complex subunit 2	ASCC2	30
Argininosuccinate synthase 1	ASS1	31
Ataxin-10	ATXN10	52
Beta-1,4-galactosyltransferase 2	B4GALT2	53
Bromodomain-containing protein 1	BRD1	52
Peregrin os=homo sapiens	BRPF1	39
Blood vessel epicardial substance	BVES	59
Putative uncharacterized protein c17orf82	C17orf82	34
Uncharacterized protein c1orf64	C1orf64	41
Complement c1q tumor necrosis factor-related protein 1	C1QTNF1	44
Uncharacterized protein c4orf17	C4orf17	43
Uncharacterized protein c8orf76	C8orf76	30
Putative uncharacterized protein encoded by cactin-as	CACTIN-AS1	32
Caspase recruitment domain-containing protein 11	CARD11	42
Caspase-5	CASP5	37
Coiled-coil domain-containing protein 12	CCDC12	35
DNA replication factor cdt1	CDT1	43
Citron rho-interacting kinase	CIT	54
Conserved oligomeric golgi complex subunit 8	COG8	39
Complexin 1	CPLX1	49
Ef-hand calcium-binding domain-containing protein 4a	CRACR2B	30
Chondroitin sulfate n-acetylgalactosaminyltransferase 1	CSGALNACT1	43
Cystatin-sa	CST2	35
Catenin beta-1	CTNNB1	48
Cytochrome b5 reductase 4	CYB5R4	33
Beta-defensin 136	DEFB136	37
Protein dger6l	DGCR6L	36
Disrupted in schizophrenia 1 protein	DISC1	37
2'-deoxynucleoside 5'-phosphate n-hydrolase 1	DNPH1	38
Eukaryotic translation elongation factor 2	EEF2	48
Probable crossover junction endonuclease eme2	EME2	44
Exonuclease mut-7 homolog	EXD3	43
Protein fam76a	FAM76A	33
Protein fam81b	FAM81B	44
F-box/lrr-repeat protein 8	FBXL8	31

Fibroblast growth factor 20	FGF20	32
Fibrinogen silencer-binding protein	FSBP	32
Frizzled-2	FZD2	32
Ga-binding protein subunit beta-1	GABPB1	36
Chondroitin sulfate n-acetylgalactosaminyltransferase 1	GALNACT1	36
GTPase imap family member gimd1	GIMD1	34
Pdz domain-containing protein gipc1	GIPC1	31
G protein subunit alpha 11	GNA11	34
G protein subunit alpha q	GNAQ	35
Nucleolar gtp-binding protein 2	GNL2	32
Glutathione s-transferase a2	GSTA2	32
Histone h1oo	H1FOO	37
Histone h2b type f-s	H2BF6	35
Hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase	H6PD	45
Haloacid dehalogenase-like hydrolase domain-containing protein 3	HDHD3	33
Heterogeneous nuclear ribonucleoproteins c1/c2	HNRNPC	38
Heterogeneous nuclear ribonucleoprotein c-like 1	HNRNPCL1	38
Heterogeneous nuclear ribonucleoprotein c-like 2	HNRNPCL2	37
Heterogeneous nuclear ribonucleoprotein k	HNRNPK	44
Heat shock transcription factor 4	HSF4	31
Heat shock 70 kda protein 1a	HSPA1A	33
Heat shock 70 kda protein 1b	HSPA1B	33
78 kda glucose-regulated protein	HSPA5	30
Heat shock cognate 71 kda protein	HSPA8	44
Intermediate filament family orphan 2	IFFO2	43
Interferon-induced protein with tetratricopeptide repeats 1	IFIT1	59
Pro-interleukin-16	IL16	33
Junction-mediating and -regulatory protein	JMY	47
Junctional sarcoplasmic reticulum protein 1	JSRP1	49
Uncharacterized protein kiaa1143	KIAA1143	35
Uncharacterized protein kiaa1211	KIAA1211	36
Uncharacterized protein kiaa2012	KIAA2012	42
Kelch like family member 2	KLHL2	41
Keratin, type ii cytoskeletal 1	KRT1	58
Keratin, type i cytoskeletal 10	KRT10	60
Keratin, type i cytoskeletal 18	KRT18	71
Keratin, type ii cytoskeletal 8	KRT8	115
Kynureninase	KYNU	43
Leucine-rich repeat neuronal protein 2	LRRN2	32
Melanoma-associated antigen b18	MAGEB18	35
Mitochondrial coiled-coil domain protein 1	MCCD1	39
Mediator of RNA polymerase ii transcription subunit 9	MED9	40
MRN complex interacting protein	MRNIP	35
mRNA turnover protein 4 homolog	MRTO4	34
Mitochondrial fission regulator 1-like	MTFR1L	34
Metaxin-3	MTX3	38
Nuclear distribution protein nude-like 1	NDEL1	41
Neurensin-1	NRSN1	31
Neuron-specific protein family member 1	NSG1	43
One cut homeobox 2	ONECUT2	40
Protein disulfide-isomerase	P4HB	31
Protein deglycase dj-1	PARK7	38
Pds5 cohesin associated factor b	PDS5B	40
Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	32



Peroxisome biogenesis factor 1	PEX1	57
Peroxisomal biogenesis factor 10	PEX10	32
Pleckstrin homology-like domain family a member 2	PHLDA2	35
Phosphatidylinositol glycan anchor biosynthesis class k	PIGK	32
Pyruvate kinase pkm	PKM	42
Plakophilin-1	PKP1	33
Centrosomal protein poc5	POC5	36
Peptidyl-prolyl cis-trans isomerase-like 6	PPIL6	35
Prame family member 10	PRAMEF10	30
Peroxisiredoxin-1	PRDX1	42
Camp-dependent protein kinase catalytic subunit alpha	PRKACA	30
Proteasome subunit alpha type-1	PSMA1	36
Proline/serine-rich coiled-coil protein 1	PSRC1	40
Focal adhesion kinase 1	PTK2	41
Rab gtpase-activating protein 1-like	RABGAP1L	40
Ankyrin	RAI14	37
Ras-like protein family member 11a	RASL11A	39
Protein rd3	RD3	34
Receptor expression-enhancing protein 1	REEP1	32
Replication factor c subunit 1	RFC1	31
Serine/threonine-protein kinase rio2	RIOK2	35
Rbpj-interacting and tubulin-associated protein 1	RITA1	30
Regulator of microtubule dynamics protein 2	RMDN2	39
E3 ubiquitin-protein ligase	RNF130	38
Deoxynucleoside triphosphate triphosphohydrolase samhd1	SAMHD1	32
Sodium channel and clathrin linker 1	SCLT1	42
Semaphorin 6d	SEMA6D	39
Septin-1	SEPT1	38
Serine hydroxymethyltransferase, mitochondrial	SHMT2	45
Protein shroom3	SHROOM3	42
Signal-induced proliferation-associated 1-like protein 1	SIPA1L1	45
Calcium-binding mitochondrial carrier protein scamc-3	SLC25A23	36
Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	31
Sra stem-loop-interacting rna-binding protein, mitochondrial	SLIRP	42
Sperm-associated antigen 1	SPAG1	30
Spermatogenesis-associated protein 5	SPATA5	35
Signal recognition particle 9	SRP9	36
Lactosylceramide alpha-2,3-sialyltransferase	ST3GAL5	53
Star-related lipid transfer protein 7, mitochondrial	STARD7	39
Serine/threonine-protein kinase 32c	STK32C	39
Synaptonemal complex central element protein 1	SYCE1	37
Synaptonemal complex protein 1	SYCP1	37
Protein tanc2	TANC2	48
Tbc1 domain family member 20	TBC1D20	30
Transcription elongation factor a protein-like 2	TCEAL2	39
Transmembrane emp24 domain-containing protein 2	TMED2	36
Transmembrane protein 191b	TMEM191B	30
Transmembrane protein 97	TMEM97	37
Tumor necrosis factor alpha-induced protein 8-like protein 3	TNFAIP8L3	37
Tripartite motif-containing protein 5	TRIM5	33
E3 ubiquitin-protein ligase trim63	TRIM63	33
Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1	TSTD1	32
Tubulin alpha-1a chain	TUBA1A	75

Tubulin alpha-1b chain	TUBA1B	86
Tubulin alpha-1c chain	TUBA1C	64
Tubulin alpha-3c/d chain	TUBA3C	56
Tubulin beta chain	TUBB	32
Tubulin beta-2a	TUBB2A	42
Tubulin beta-2b chain	TUBB2B	42
Twinfilin-2	TWF2	30
Ubiquitin carboxyl-terminal hydrolase 14	USP14	36
Udp-glucuronic acid decarboxylase 1	UXS1	30
Xk-related protein 3	XKR3	30
Zinc fingers and homeoboxes protein 1, isoform 2	ZHX1-C8orf76	37
Zinc finger protein 385a	ZNF385	33
Zinc finger protein 420	ZNF420	41
Zinc finger protein 525	ZNF525	55
Zinc finger protein 780a	ZNF780A	32
Zinc finger protein 843	ZNF843	38

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Table SIX. COUP-TFII\_V1 GO levels.

GO Term	Ontology source	Term P-value corrected with Benjamini-Hochberg	Associated genes found
Positive regulation of axon extension	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	NDEL1, SLC25A23, TWF2
Response to electrical stimulus	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	BRD1, NDUFA2, TRIM63
Protein trimerization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ATXN10, C1QTNF1, HSF4
Nuclear envelope organization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	HSPA8, NDEL1, PRKACA
Positive regulation of phospholipid metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	PTK2, SLC25A23, TNFAIP8L3
Substantia nigra development	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ACTB, CASP5, HSPA5
Protein localization to cell surface	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ANGPT1, CTNNB1, PIGK
Regulation of insulin secretion	REACTOME_Pathways_04. 09.2018 GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	GNA11, GNAQ, PRKACA, SLC2A1
Dopamine receptor signaling pathway	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	GNA11, GNAQ, NSG1
Protein transmembrane transport	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HSPA8, PEX1, PEX10, SRP9
Intracellular protein transmembrane transport	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	PEX1, PEX10, SRP9
Intrinsic apoptotic signaling pathway in response to oxidative stress	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ARC, P4HB, PARK7
Regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ARC, P4HB, PARK7
Regulation of cellular respiration	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	PARK7, SHMT2, SLC25A23
Regulation of oxidative phosphorylation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	PARK7, SHMT2, SLC25A23
Regulation of receptor internalization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ANGPT1, ARC, LRRN2
Regulation of receptor-mediated endocytosis	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	ANGPT1, ARC, HNRNPK, LRRN2, SLC25A23

Long-term synaptic potentiation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, ARC, C1QTNF1, LRRN2, NSG1
Chromosome localization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, NDEL1, PSRC1, SEPT1
Establishment of chromosome localization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, NDEL1, PSRC1, SEPT1
Metaphase plate congression	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	CDT1, PSRC1, SEPT1
Microtubule polymerization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, NDEL1, PSRC1, TUBB
Interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Superoxide metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	AIFM2, CYB5R4, PARK7, PRDX1
Regulation of interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Hydrogen peroxide metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	GIPC1, PARK7, PRDX1
Positive regulation of interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Regulation of postsynaptic membrane neurotransmitter receptor levels	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ARC, CPLX1, NSG1
Establishment of protein localization to plasma membrane	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ARL6, KRT18, NSG1
Protein transport within lipid bilayer	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	ARL6, CPLX1, NSG1
Long-term synaptic potentiation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, ARC, C1QTNF1, LRRN2, NSG1
Regulation of long-term synaptic potentiation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, ARC, NSG1
Apoptotic cleavage of cellular proteins	REACTOME_Pathways_04. 09.2018	<0.01	CTNNB1, PKP1, PTK2, VIM
Signaling by VEGF	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, ACTG1, CTNNB1, PRKACA, PTK2
Vegfa-vegfr2 pathway	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, ACTG1, CTNNB1, PRKACA, PTK2
Apoptotic execution phase	REACTOME_Pathways_04. 09.2018	<0.01	CTNNB1, PKP1, PTK2, VIM
Intermediate filament cytoskeleton organization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	KRT18, NDEL1, PKP1, VIM

Cornification	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	KRT1, KRT10, KRT18, KRT8, PKP1
Interleukin-12 family signaling	REACTOME_Pathways_04. 09.2018	0.01	AIP, GSTA2, P4HB
Interleukin-12 signaling	REACTOME_Pathways_04. 09.2018	0.01	AIP, GSTA2, P4HB
Response to interleukin-12	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	AIP, GSTA2, P4HB
Interleukin-12-mediated signaling pathway	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	AIP, GSTA2, P4HB
Cellular response to interleukin-12	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	AIP, GSTA2, P4HB
Peptidyl-proline modification	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	AIP, P4HB, PPIL6
Superoxide metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	AIFM2, CYB5R4, PARK7, PRDX1
Hydrogen peroxide metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	GIPC1, PARK7, PRDX1
Negative regulation of response to endoplasmic reticulum stress	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA5, PARK7, USP14
Positive regulation of reactive oxygen species metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	AKR1C3, ASS1, GIPC1, HNRNPK, PARK7
Negative regulation of proteasomal protein catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	GIPC1, PARK7, USP14
Negative regulation of ubiquitin-dependent protein catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	GIPC1, PARK7, USP14
Negative regulation of proteasomal ubiquitin-dependent protein catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	GIPC1, PARK7, USP14 HNRNPC, HNRNPK,
Regulation of RNA stability	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA8, PRKACA, SEPT1, VIM HNRNPC, HNRNPK,
Regulation of mRNA catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA8, PKP1, PRKACA, SEPT1, VIM
Negative regulation of RNA catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HNRNPC, HNRNPK, PKP1, SEPT1, SLIRP
Negative regulation of mRNA metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	HNRNPC, HNRNPK, PKP1, SEPT1
Regulation of mRNA stability	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HNRNPC, HNRNPK, HSPA1A, HSPA8, PRKACA, SEPT1, VIM
RNA stabilization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	HNRNPC, HNRNPK, SEPT1

Negative regulation of mRNA catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HNRNPC, HNRNPK, PKP1, SEPT1
mRNA stabilization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	HNRNPC, HNRNPK, SEPT1
Regulation of HSF1-mediated heat shock response	REACTOME_Pathways_04. 09.2018	<0.01	HSPA1A, HSPA1B, HSPA5, HSPA8
Cellular response to heat stress	REACTOME_Pathways_04. 09.2018	0.01	HSPA1A, HSPA1B, HSPA5, HSPA8
Interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Regulation of interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Positive regulation of interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Negative regulation of response to endoplasmic reticulum stress	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA5, PARK7, USP14
Negative regulation of proteasomal protein catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	GIPC1, PARK7, USP14
Negative regulation of ubiquitin-dependent protein catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	GIPC1, PARK7, USP14
Negative regulation of proteasomal ubiquitin-dependent protein catabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	GIPC1, PARK7, USP14
Apoptotic cleavage of cellular proteins	REACTOME_Pathways_04. 09.2018	<0.01	CTNNB1, PKP1, PTK2, VIM ACTB, ACTG1, CTNNB1, PRKACA, PTK2
Signaling by VEGF	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, ACTG1, PTK2
Regulation of actin dynamics for phagocytic cup formation	REACTOME_Pathways_04. 09.2018	0.02	ACTB, ACTG1, PTK2
EPHB-mediated forward signaling	REACTOME_Pathways_04. 09.2018	0.01	ACTB, ACTG1, PTK2
Adherens junctions interactions	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, ACTG1, CTNNB1
Cell-cell junction organization	REACTOME_Pathways_04. 09.2018	0.02	ACTB, ACTG1, CTNNB1
Vegfa-vegfr2 pathway	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, ACTG1, CTNNB1, PRKACA, PTK2 ACTB, ACTG1, CTNNB1, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
RHO GTPases activate iqgaps	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, ACTG1, PTK2
RHO gtpases Activate wasps and waves	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, ACTG1, PTK2
Apoptotic execution phase	REACTOME_Pathways_04. 09.2018	<0.01	CTNNB1, PKP1, PTK2, VIM
Retina homeostasis	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ACTB, ACTG1, KRT1, PRDX1

Platelet aggregation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ACTB, ACTG1, C1QTNF1, PRKACA
Regulation of platelet activation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, C1QTNF1, PRKACA
Ephrin receptor signaling pathway	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	ACTB, ACTG1, KRT1, PTK2, SIPA1L1
Plasma lipoprotein assembly, remodeling, and clearance	REACTOME_Pathways_04. 09.2018	0.02	APOE, P4HB, PRKACA
Plasma lipoprotein assembly	REACTOME_Pathways_04. 09.2018	<0.01	APOE, P4HB, PRKACA
Regulation of plasma lipoprotein particle levels	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, HNRNPK, P4HB, PRKACA, SLC25A23
Regulation of postsynaptic membrane neurotransmitter receptor levels	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ARC, CPLX1, NSG1
Plasma lipoprotein particle organization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, P4HB, PRKACA, SLC25A23
Negative regulation of coagulation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	APOE, C1QTNF1, KRT1
Protein-lipid complex subunit organization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, P4HB, PRKACA, SLC25A23
Negative regulation of hemostasis	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	APOE, C1QTNF1, KRT1
Plasma lipoprotein particle assembly	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, P4HB, PRKACA, SLC25A23
Positive regulation of viral process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, IFIT1, P4HB, SEPT1, TBC1D20
Protein-lipid complex assembly	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, P4HB, PRKACA, SLC25A23
Platelet aggregation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ACTB, ACTG1, C1QTNF1, PRKACA
Negative regulation of blood coagulation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	APOE, C1QTNF1, KRT1
Chylomicron assembly	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, P4HB, SLC25A23
Positive regulation of viral life cycle	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	IFIT1, P4HB, SEPT1, TBC1D20
Regulation of receptor internalization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	ANGPT1, ARC, LRRN2
Regulation of platelet activation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, C1QTNF1, PRKACA

Acylglycerol homeostasis	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, C1QTNF1, SLC25A23
Lipopolysaccharide-mediated signaling pathway	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	HNRNPK, NDUFA2, PRKACA, TRIM5
Positive regulation of viral genome replication	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	IFIT1, SEPT1, TBC1D20
Long-term synaptic potentiation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	APOE, ARC, C1QTNF1, LRRN2, NSG1
Triglyceride homeostasis	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, C1QTNF1, SLC25A23
Regulation of long-term synaptic potentiation	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	APOE, ARC, NSG1
Regulation of HSF1-mediated heat shock response	REACTOME_Pathways_04.09.2018	<0.01	HSPA1A, HSPA1B, HSPA5, HSPA8, HSPA1A, HSPA1B, HSPA8, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
HSP90 chaperone cycle for steroid hormone receptors (SHR)	REACTOME_Pathways_04.09.2018	<0.01	HSPA1A, HSPA1B, HSPA5, HSPA8
Cellular response to heat stress	REACTOME_Pathways_04.09.2018	0.01	HSPA1A, HSPA1B, HSPA8
Attenuation phase	REACTOME_Pathways_04.09.2018	<0.01	HSPA1A, HSPA1B, HSPA8
HSF1-dependent transactivation	REACTOME_Pathways_04.09.2018	<0.01	HSPA1A, HSPA1B, HSPA8
AUF1 (hnmp D0) binds and destabilizes mRNA	REACTOME_Pathways_04.09.2018	<0.01	HSPA1A, HSPA1B, HSPA8, PSMA1
Regulation of mRNA stability by proteins that bind AU-rich elements	REACTOME_Pathways_04.09.2018	0.01	HSPA1A, HSPA1B, HSPA8, PSMA1
Response to ischemia	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	ARC, BVES, EEF2
Interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Protein refolding	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, HSPA8
Superoxide metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	AIFM2, CYB5R4, PARK7, PRDX1
Chromosome localization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, NDEL1, PSRC1, SEPT1
Natural killer cell mediated immunity	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.02	PRDX1, TUBB, TUBB2A
Regulation of interleukin-8 production	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
Establishment of chromosome localization	GO_BiologicalProcess-EBI- UniProt- GOA_04.09.2018_00h00	0.01	CDT1, NDEL1, PSRC1, SEPT1



	GO_BiologicalProcess-EBI- UniProt-		
Natural killer cell mediated cytotoxicity	GOA_04.09.2018_00h00	0.02	PRDX1, TUBB, TUBB2A
	GO_BiologicalProcess-EBI- UniProt-		
Positive regulation of interleukin-8 production	GOA_04.09.2018_00h00	<0.01	AIFM2, HSPA1A, HSPA1B, NDUFA2, PARK7
	GO_BiologicalProcess-EBI- UniProt-		
Regulation of cellular response to heat	GOA_04.09.2018_00h00	0.02	HSPA1A, HSPA1B, HSPA8
	GO_BiologicalProcess-EBI- UniProt-		
Negative regulation of response to endoplasmic reticulum stress	GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA5, PARK7, USP14
	GO_BiologicalProcess-EBI- UniProt-		
Microtubule polymerization	GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, NDEL1, PSRC1, TUBB
	GO_BiologicalProcess-EBI- UniProt-		
Spindle assembly	GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, SEPT1, TUBB, TUBB2A
	GO_BiologicalProcess-EBI- UniProt-		
Microtubule nucleation	GOA_04.09.2018_00h00	0.01	HSPA1A, HSPA1B, NDEL1
	GO_BiologicalProcess-EBI- UniProt-		
Regulation of spindle organization	GOA_04.09.2018_00h00	0.01	HSPA1A, HSPA1B, PSRC1
	GO_BiologicalProcess-EBI- UniProt-		
Regulation of tumor necrosis factor-mediated signaling pathway	GOA_04.09.2018_00h00	0.01	ARC, BVES, HSPA1A, HSPA1B
	GO_BiologicalProcess-EBI- UniProt-		
Regulation of microtubule polymerization or depolymerization	GOA_04.09.2018_00h00	0.01	HSPA1A, HSPA1B, PSRC1, TUBB
	GO_BiologicalProcess-EBI- UniProt-		
Regulation of erythrocyte differentiation	GOA_04.09.2018_00h00	0.02	HNRNPK, HSPA1A, HSPA1B
	GO_BiologicalProcess-EBI- UniProt-		
Positive regulation of microtubule polymerization or depolymerization	GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, PSRC1
	GO_BiologicalProcess-EBI- UniProt-		
Regulation of microtubule polymerization	GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, PSRC1, TUBB
	GO_BiologicalProcess-EBI- UniProt-		
Regulation of mitotic spindle organization	GOA_04.09.2018_00h00	0.01	HSPA1A, HSPA1B, PSRC1
	GO_BiologicalProcess-EBI- UniProt-		
Positive regulation of microtubule polymerization	GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, PSRC1
	GO_BiologicalProcess-EBI- UniProt-		
Positive regulation of erythrocyte differentiation	GOA_04.09.2018_00h00	0.01	HNRNPK, HSPA1A, HSPA1B, ACTB, ACTG1, TUBA1A, TUBA1B, TUBA1C,
Translocation of SLC2A4 (GLUT4) to the plasma membrane	REACTOME_Pathways_04.09.2018	<0.01	TUBA3C, TUBB2A, TUBB2B, ACTB, ACTG1, TUBA1A, TUBA1B, TUBA1C,
Gap junction trafficking and regulation	REACTOME_Pathways_04.09.2018	<0.01	TUBA3C, TUBB2A, TUBB2B, ACTB, ACTG1, TUBA1A, TUBA1B, TUBA1C,
Gap junction trafficking	REACTOME_Pathways_04.09.2018	<0.01	TUBA3C, TUBB2A, TUBB2B

Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Gap junction assembly	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Transport of connexons to the plasma membrane	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B COG8, TBC1D20, TMED2,
ER to Golgi anterograde transport	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
MHC class II antigen presentation	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B NDEL1, PDS5B, PSMA1,
Separation of sister chromatids	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B NDEL1, PDS5B, TUBA1A,
Resolution of sister chromatid cohesion	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B NDEL1, PDS5B, PSMA1,
Mitotic Metaphase and Anaphase	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Regulation of HSF1-mediated heat shock response	REACTOME_Pathways_04. 09.2018	<0.01	HSPA1A, HSPA1B, HSPA5, HSPA8 HSPA1A, HSPA1B, HSPA8,
HSP90 chaperone cycle for steroid hormone receptors (SHR)	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Cellular response to heat stress	REACTOME_Pathways_04. 09.2018	0.01	HSPA1A, HSPA1B, HSPA5, HSPA8
Attenuation phase	REACTOME_Pathways_04. 09.2018	<0.01	HSPA1A, HSPA1B, HSPA8
HSF1-dependent transactivation	REACTOME_Pathways_04. 09.2018	<0.01	HSPA1A, HSPA1B, HSPA8 ACTB, ACTG1, HSPA8, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
L1CAM interactions	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Loss of Nlp from mitotic centrosomes	REACTOME_Pathways_04. 09.2018	0.02	PRKACA, TUBA1A, TUBB
Loss of proteins required for interphase microtubule organization from the centrosome	REACTOME_Pathways_04. 09.2018	0.02	PRKACA, TUBA1A, TUBB PRKACA, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB, TUBB2A, TUBB2B
Recruitment of numa to mitotic centrosomes	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, TUBA1A, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Prefoldin mediated transfer of substrate to CCT/tric	REACTOME_Pathways_04. 09.2018	<0.01	ACTB, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Cooperation of Prefoldin and tric/CCT in actin and tubulin folding	REACTOME_Pathways_04. 09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B

Formation of tubulin folding intermediates by CCT/tric	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Post-chaperonin tubulin folding pathway	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Chaperonin-mediated protein folding	REACTOME_Pathways_04.09.2018	<0.01	ACTB, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Protein folding	REACTOME_Pathways_04.09.2018	<0.01	ACTB, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Adherens junctions interactions	REACTOME_Pathways_04.09.2018	<0.01	ACTB, ACTG1, CTNNB1
Cell-cell junction organization	REACTOME_Pathways_04.09.2018	0.02	ACTB, ACTG1, CTNNB1
Recycling pathway of L1	REACTOME_Pathways_04.09.2018	<0.01	ACTB, ACTG1, TUBA1A, TUBA1B, TUBA1C,
AUF1 (hnrnp D0) binds and destabilizes mrna	REACTOME_Pathways_04.09.2018	<0.01	TUBA3C, TUBB2A, TUBB2B
Regulation of mRNA stability by proteins that bind AU-rich elements	REACTOME_Pathways_04.09.2018	0.01	HSPA1A, HSPA1B, HSPA8, PSMA1
Mitotic G2-G2/M phases	REACTOME_Pathways_04.09.2018	<0.01	HSPA1A, HSPA1B, HSPA8, PSMA1
Signaling by Hedgehog	REACTOME_Pathways_04.09.2018	<0.01	PRKACA, PSMA1, TUBA1A, TUBA1B, TUBA1C,
Hedgehog 'off' state	REACTOME_Pathways_04.09.2018	<0.01	TUBA3C, TUBB2A, TUBB2B
Cilium assembly	REACTOME_Pathways_04.09.2018	<0.01	ARL6, PRKACA, SCLT1, TUBA1A, TUBA1B,
Anchoring of the basal body to the plasma membrane	REACTOME_Pathways_04.09.2018	0.01	TUBA1C, TUBA3C, TUBB, TUBB2A, TUBB2B
Intraflagellar transport	REACTOME_Pathways_04.09.2018	<0.01	PRKACA, SCLT1, TUBA1A, TUBB
RHO GTPases activate iqgaps	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
RHO GTPases activate formins	REACTOME_Pathways_04.09.2018	<0.01	ACTB, ACTG1, CTNNB1, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
COPI-mediated anterograde transport	REACTOME_Pathways_04.09.2018	<0.01	ACTB, ACTG1, NDEL1, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
COPI-dependent Golgi-to-ER retrograde traffic	REACTOME_Pathways_04.09.2018	<0.01	COG8, TMED2, TUBA1A, TUBA1B, TUBA1C,

COPI-independent Golgi-to-ER retrograde traffic	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B, NDEL1, PDS5B, PRKACA, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB, TUBB2A, TUBB2B
Mitotic prometaphase	REACTOME_Pathways_04.09.2018	<0.01	NDEL1, PDS5B, PSMA1, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB, TUBB2A, TUBB2B
Mitotic anaphase	REACTOME_Pathways_04.09.2018	<0.01	PRKACA, PSMA1, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB, TUBB2A, TUBB2B
G2/M transition	REACTOME_Pathways_04.09.2018	<0.01	PSMA1, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB, TUBB2A, TUBB2B
The role of GTSE1 in G2/M progression after G2 checkpoint	REACTOME_Pathways_04.09.2018	<0.01	TUBA1C, TUBA3C, TUBB2A, TUBB2B
AURKA Activation by TPX2	REACTOME_Pathways_04.09.2018	0.02	PRKACA, TUBA1A, TUBB, TMED2, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Golgi-to-ER retrograde transport	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Carboxyterminal post-translational modifications of tubulin	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B, B4GALT2, COG8, TBC1D20, TMED2, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Transport to the Golgi and subsequent modification	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Kinesins	REACTOME_Pathways_04.09.2018	<0.01	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B, ACTB, PRKACA, TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBB2A, TUBB2B
Factors involved in megakaryocyte development and platelet production	REACTOME_Pathways_04.09.2018	<0.01	TUBA3C, TUBB2A, TUBB2B
Protein refolding	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	<0.01	HSPA1A, HSPA1B, HSPA8
Regulation of cellular response to heat	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	0.02	HSPA1A, HSPA1B, HSPA8

GO, gene ontology.