

Supplementary Information

Hits	Control	Bait proteins	
	BirA ^{R118G}	NHA9-BioID	SN214-BioID
BirA ^{R118G} *	10	8	5
A*	15	2	15

*Numbers represent LFQ values of each hit determined by MS in each bait condition

1. Internal normalization of protein A (LFQ_i)
 $LFQ_i (A_{BirA(R118G)}) = 15/10 = 1,5$
 $LFQ_i (A_{NHA9-BioID}) = 2/8 = 0,25$
 $LFQ_i (A_{SN214-BioID}) = 15/5 = 3$

2. External normalization of protein A (LFQ_e): bait LFQ_{iA} / control LFQ_{iA}
 $LFQ_e (A_{BirA(R118G)}) = 1,5/1,5 = 1$
 $LFQ_e (A_{NHA9-BioID}) = 0,25/1,5 = 0,167$
 $LFQ_e (A_{SN214-BioID}) = 3/1,5 = 2$

Log₂ Transformed values (Fold Change, F.C.)
 $Log_2 (A_{BirA(R118G)}) = 0$ (No change)
 $Log_2 (A_{NHA9-BioID}) = -2,58$ (less abundant in NHA9-BioID than in control BioID)
 $Log_2 (A_{SN214-BioID}) = 1$ (twice more abundant in SN214-BioID than in control BioID)

Figure S1: Normalization strategy of BioID results. Normalization of protein MS-Label Free Quantification (LFQ) values between NHA9-BioID and BirA^{R118G} and SN214-BioID and BirA^{R118G}. A two-step normalization approach was used to account for the differences in protein expression between the BioID fusion proteins and the control BirA^{R118G}. **1. Internal normalization (LFQ_i):** for each condition, the ratio between the LFQ value of each protein (protein A) and the LFQ value of the BirA^{R118G} within the same condition (i.e. the BirA portion from the respective BioID fusion protein). **2. External normalization (LFQ_e):** the LFQ_i value of each protein (protein A) in NHA9-BioID or SN214-BioID was divided by the corresponding LFQ_i value in the control condition (BirA). The results are expressed as a fold-change, which corresponds to log₂.

Function	Group Genes
cytoskeletal response to stress	ABLIM1 ACTB BAG3 ELMO3 PTK2 SEPT11
deactivation of the beta-catenin transactivating complex	BCL9L SOX9 TLE3
estrogen-dependent gene expression	CALM3 CDC23 DVL1 JUN NCOA3 POLR2E SCRIB TLE3 TNRC6A TNRC6B
MAPK6/MAPK4 signaling	IPO8 JUN NCOA3 NUP58 POLR2E PSMB6 RAE1 TLE3 TNRC6A TNRC6B
mitochondrial protein import	BCS1L MTX1 SLC25A13 TOMM7
TP53 Regulates Transcription of DNA Repair Genes	CTDP1 JUN POLR2E
basal RNA polymerase II transcription machinery binding	CTDP1 NCOA3 SOX9
RNA processing	BAG3 CALM3 CLPB EIF2A GNPDA1 IPO8 MAPT NCOA3 NUP58 PIAS2 POLR2E RAE1 SLBP SLC25A13 SLU7 TNRC6A TNRC6B
inner ear morphogenesis	CEP290 DVL1 SCRIB SOX9 TFAP2A TRIOBP KIF3A SCRIB TRIOBP
mitochondrial respiratory chain complex assembly	BCS1L LYRM7 NDUFA2 NDUFA3
mitotic metaphase plate congression	CDC23 CHMP6 ZW10
negative regulation of EGFR signaling pathway	CHMP6 EPS15 SLBP
neural nucleus development	ACTB AKAP9 CALM3 GNAQ KIF3A SCRIB ZNF148
cell proliferation and mitophagy	JUN MEF2D MFN2 TOMM7

Figure S2: Clustered Pathway Analysis of NUP98-HOXA9-BioID proximal interactors. Functionally grouped NHA9-BioID interactors. Statistical analysis was performed with the Cytoscape plugin ClueGo (v2.5.5) using hypergeometric test and the following parameters: $p < 0.01$, kappa-score (k) = 0.4; (min/%) genes = 3/4%, GO tree levels: 3-11. Ontology databases: GOBP, GOCC, and GOMF, Reactome Pathways and KEGG.

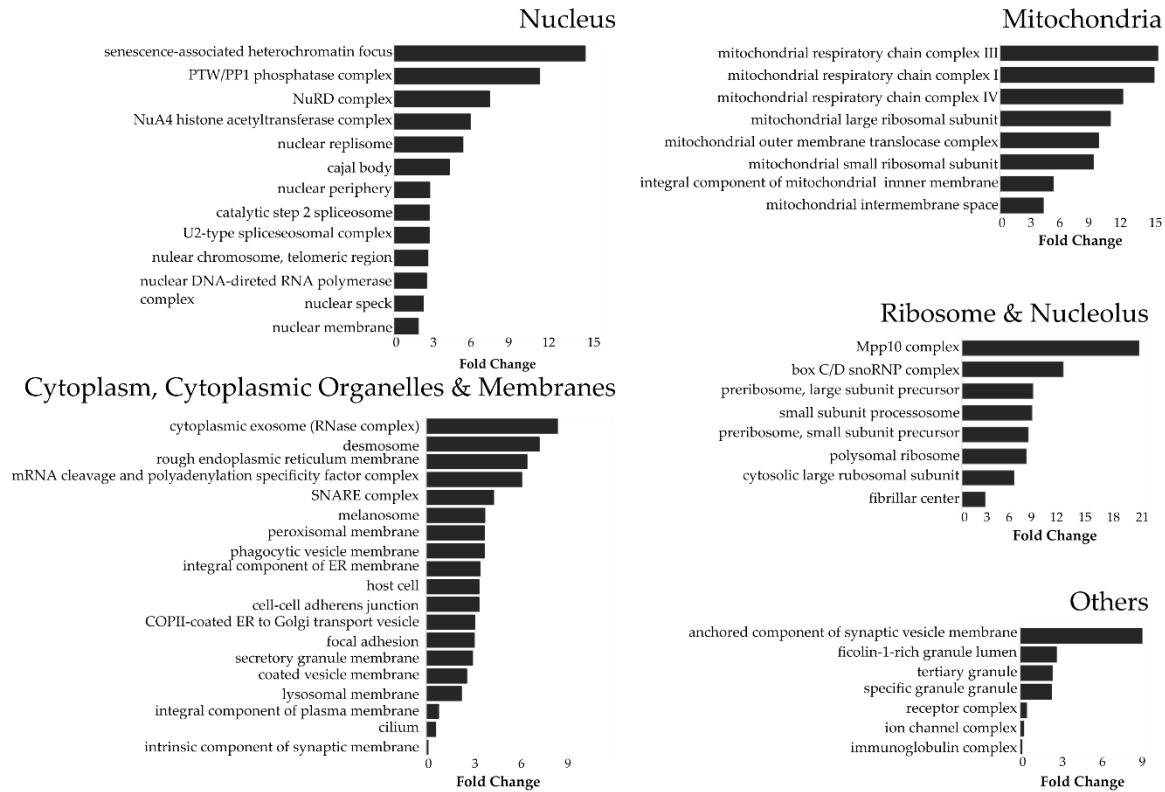


Figure S3: Most represented cellular compartments (GOCC) among SN214-BioID proximal interactors. Statistical analysis of the overrepresented proteins in the SN214-BioID fraction (total 1125 proteins) with PANTHER classification online software (v14.1) using Fisher's exact test. Results are displayed for FDR $p < 0.05$.

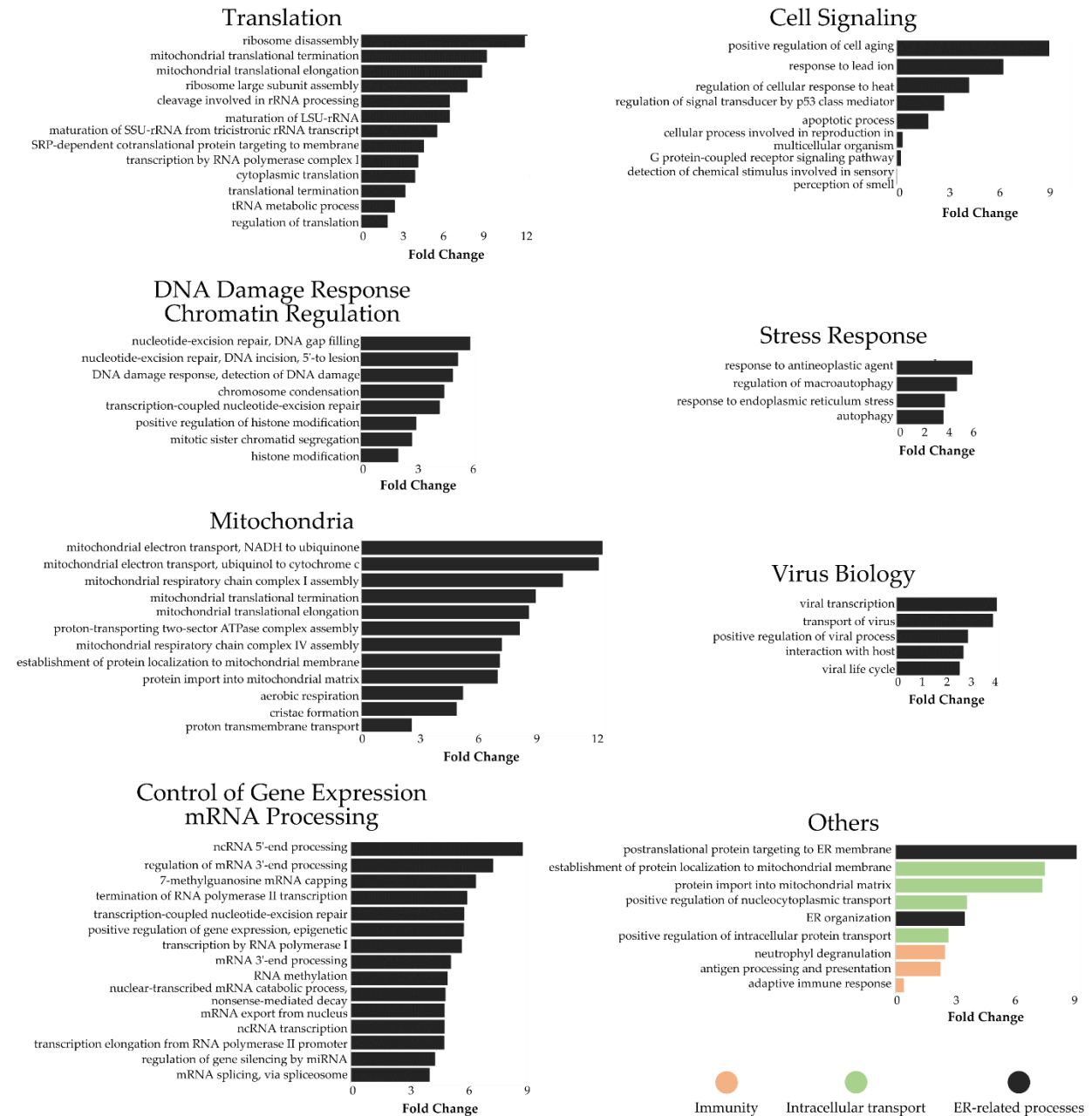
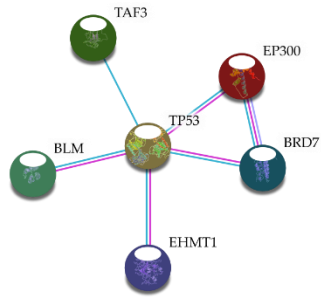


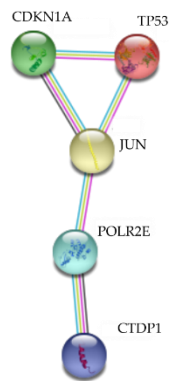
Figure S4: Most represented biological processes (GOBP) among SN214-BioID proximal interactors. Statistical analysis of the overrepresented proteins in the SN214-BioID fraction (total 1125 proteins) with PANTHER classification online software (v14.1) using Fisher's exact test. Results are displayed for FDR $p < 0.05$.

A.



Protein name	Gene	SN214-BioID (F.C.)
Bloom syndrome protein	BLM	29,42
Histone acetyltransferase p300	EP300	26,67
Transcription initiation factor TFIID subunit 3	TAF3	1,72
Histone-lysine N-methyltransferase EHMT1	EHMT1	26,68
Bromodomain-containing protein 7	BRD7	27,01

B.



Protein name	Gene	NHA9-BioID (F.C.)
Transcription factor AP-1	JUN	28,64
DNA-directed RNA polymerase II subunit E	POLR2E	26,06
RNA polymerase II subunit A C-terminal domain phosphatase	CTDP1	27.50

Figure S5: **Network of direct p53 binding proteins in SN214-BioID and NHA9-BioID proximal interactors.** STRING (<https://string-db.org/>) network of direct p53 binding proteins found in the pool of **A.** SN214-BioID and **B.** NHA9-BioID proximal interactors, and the corresponding fold change values relative to control BirAR118G. TP53 and CDKN1A were included to illustrate protein-protein interactions.

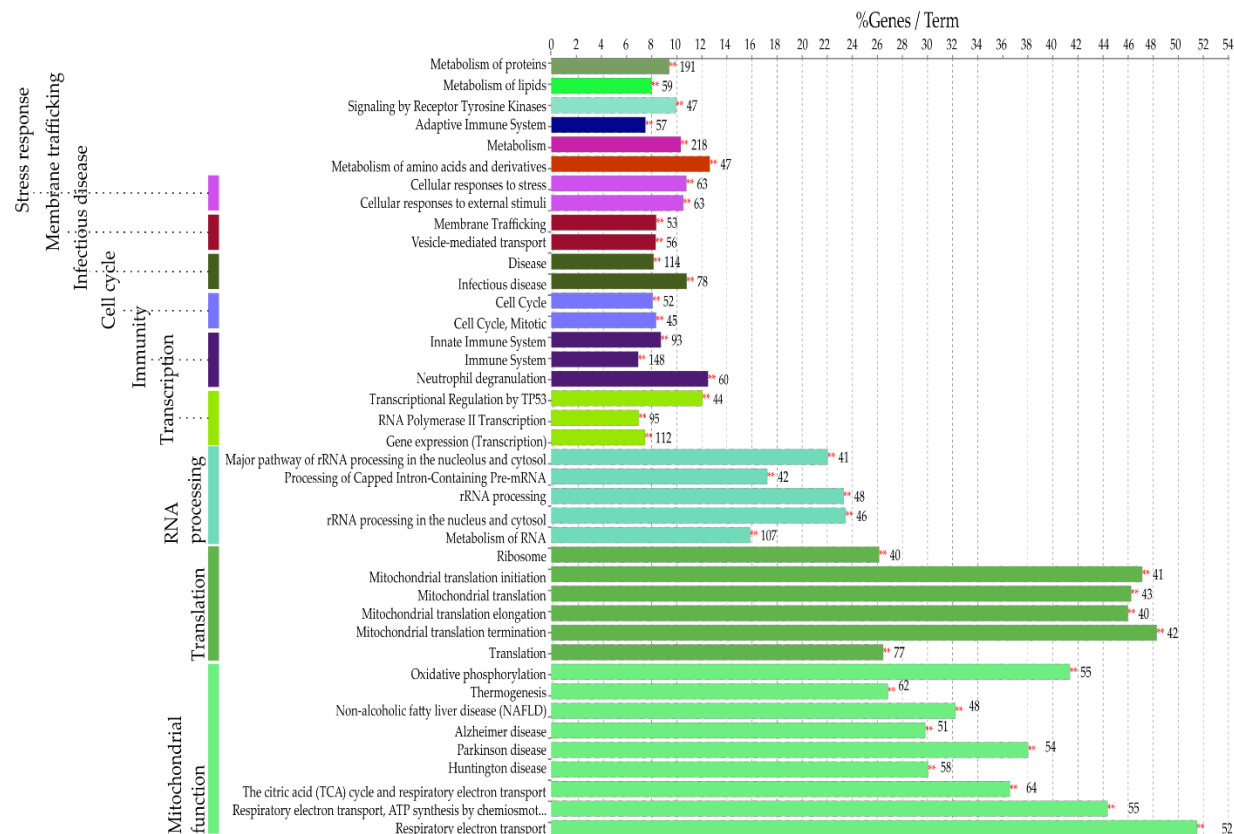


Figure S6: Clustered Pathway Analysis of SET-NUP2147-BioID proximal interactors. Graphic representation of functional groups. The of number of genes within each group is shown after each bar. The X axis corresponds to the percentage of genes/term that is present in the protein set, by comparison to the reference organism (*Homo sapiens* genome). Statistical analysis was performed with the Cytoscape plugin ClueGo (v2.5.5) using the following parameters: $p < 0.01$, kappa-score (k) = 0.5; (min/%) genes = 40/4%, GO tree levels: 13-15. Ontology databases: GOBP, GOCC, and GOMF, Reactome Pathways and KEGG.

Table S1List of biotinylated proteins found exclusively in the biotinylated fraction of BirA^{R118G}

Protein name	UniPROT ID	Gene	Cellular localization*
Ubiquitin family domain containing 1	O14562	UBFD1	N/A
Sperm associated antigen 9	O60271	SPAG9	Lysosome
Methyltransferase like 18	O95568	METTL18	n/a
Polypyrimidine tract binding protein 3	O95758	PTBP3	Nucleus
Thioredoxin domain containing 12	O95881	TXNDC12	Endoplasmic reticulum
Interferon induced protein 35	P80217	IFI35	Nucleus
Epidermal growth factor receptor pathway substrate 8	Q12929	EPS8	Plasma membrane
Cytosolic thiouridylase subunit 2	Q2VPK5	CTU2	Cytoplasm
Poly(ADP-ribose) polymerase family member 14	Q460N5	PARP14	Nucleus
Programmed cell death 4	Q53EL6	PDCD4	Nucleus
Zinc finger protein 787	Q6DD87	ZNF787	Nucleus
Solute carrier family 27 member 1	Q6PCB7	SLC27A1	Plasma membrane
THO complex 6	Q86W42	THOC6	Nucleus
Exoribonuclease 1	Q8IV48	ERI1	Nucleus
AVL9 cell migration associated	Q8NBF6	AVL9	Endosome
Atpase family AAA domain containing 1	Q8NBU5	ATAD1	Peroxisome / Plasma membrane
Zinc finger CCHC-type containing 10	Q8TBK6	ZCCHC10	N/A
Myosin XVIIIa	Q92614	MYO18A	Golgi / Cytoskeleton
Fumarylacetoacetate hydrolase domain containing 2A	Q96GK7	FAHD2A	N/A
Tubulin folding cofactor B	Q99426	TBCB	Golgi / Cytoskeleton
WD repeat domain 26	Q9H7D7	WDR26	Nucleus / Mitochondria
Helicase, lymphoid specific	Q9NRZ9	HELLS	Nucleus
RNA binding fox-1 homolog 1	Q9NWB1	RBFOX1	Nucleus
Histone parylation factor 1	Q9NWX4	HPF1	Nucleus
Disco interacting protein 2 homolog B	Q9P265	DIP2B	Nucleus / Extracellular regions or secreted
Protein phosphatase 6 regulatory subunit 1	Q9UPN7	PPP6R1	Cytoplasm
Transportin 3	Q9Y5L0	TNPO3	Nucleus / Cytoplasm

* Cellular localization according to the UniPROT database

Table S2

List of overrepresented proteins in the biotinylated fraction of NHA9-BioID (NHA9-BioID proximal interactors) and respective fold-change relative to control BirA^{R118G}

Protein name	UniProt ID	Gene name	LFQ _e
Dedicator of cytokinesis 6	Q96HP0	DOCK6	33,239
Dynein axonemal heavy chain 5	Q8TE73	DNAH5	30,201
ATPase 13A1	Q9HD20	ATP13A1	29,197
SUB1 regulator of transcription	P53999	SUB1	29,113
Eukaryotic translation initiation factor 2A	Q9BY44	EIF2A	28,994
Jun proto-oncogene, AP-1 transcription factor subunit	P05412	JUN	28,639
Stathmin 1	P16949	STMN1	28,622
Calmodulin 3	P0DP25	CALM3	28,516
Adenylate kinase 3	Q9UIJ7	AK3	28,499
Glutamate-ammonia ligase	P15104	GLUL	28,413
Zinc finger protein 384	Q8TF68	ZNF384	28,340
RNA binding motif protein 33	Q96EV2	RBM33	28,318
Golgi reassembly stacking protein 2	Q9H8Y8	GORASP2	28,305
Epidermal growth factor receptor pathway substrate 15	P42566	EPS15	28,137
Dishevelled segment polarity protein 1	O14640	DVL1	28,105
Translational activator of cytochrome c oxidase I	Q9BSH4	TACO1	28,089
Cold inducible RNA binding protein	Q14011	CIRBP	28,027
Translocase of outer mitochondrial membrane 7	Q9P0U1	TOMM7	27,822
Mannose phosphate isomerase	P34949	MPI	27,775
Methylmalonyl-CoA mutase	P22033	MMUT	27,758
NADH:ubiquinone oxidoreductase subunit A3	O95167	NDUFA3	27,749
Cystatin A	P01040	CSTA	27,738
Coiled-coil domain containing 124	Q96CT7	CCDC124	27,695
DDB1 and CUL4 associated factor 7	P61962	DCAF7	27,593
NDRG family member 3	Q9UGV2	NDRG3	27,531
NADH:ubiquinone oxidoreductase subunit A2	O43678	NDUFA2	27,530
Prenylcysteine oxidase 1	Q9UHG3	PCYOX1	27,504
CTD phosphatase subunit 1	Q9Y5B0	CTDP1	27,500
Centrosomal protein 290	O15078	CEP290	27,448
Nuclear receptor subfamily 2 group C member 2	P49116	NR2C2	27,441
Transcription factor AP-2 alpha	P05549	TFAP2A	27,398
Gasdermin A	Q96QA5	GSDMA	27,396
Proteasome subunit beta 6	P28072	PSMB6	27,371
Microtubule associated protein tau	P10636	MAPT	27,358
TLE family member 3, transcriptional corepressor	Q04726	TLE3	27,345
TOX high mobility group box family member 3	O15405	TOX3	27,278
BRCA1/BRCA2-containing complex subunit 3	P46736	BRCC3	27,239
NAD(P)HX epimerase	Q8NCW5	NAXE	27,205
Nudix hydrolase 19	A8MXV4	NUDT19	27,195
Scribble planar cell polarity protein	Q14160	SCRIB	27,173
Metaxin 1	Q13505	MTX1	27,166
Programmed cell death 10	Q9BUL8	PDCD10	27,149
Protein tyrosine kinase 2	Q05397	PTK2	27,074
SRY-box transcription factor 9	P48436	SOX9	27,074

LYR motif containing 7	Q5U5X0	LYRM7	27,071
Syntaxin 10	O60499	STX10	27,049
Mitochondrial calcium uniporter	Q8NE86	MCU	26,975
FLYWCH family member 2	Q96CP2	FLYWCH2	26,974
Non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	Q6ZVX7	NCCRP1	26,956
Septin 11	Q9NVA2	SEPTIN11	26,933
Fatty acyl-CoA reductase 1	Q8WVX9	FAR1	26,902
Rho guanine nucleotide exchange factor 10	O15013	ARHGEF10	26,876
Hippocalcin like 1	P37235	HPCAL1	26,869
3-hydroxybutyrate dehydrogenase 1	Q02338	BDH1	26,865
BBX high mobility group box domain containing	Q8WY36	BBX	26,858
Trinucleotide repeat containing adaptor 6A	Q8NDV7	TNRC6A	26,847
ATPase H ⁺ transporting V0 subunit d1	P61421	ATP6V0D1	26,838
Mitochondrial ribosomal protein S12	O15235	MRPS12	26,821
Acidic nuclear phosphoprotein 32 family member E	Q9BTT0	ANP32E	26,768
stem-loop binding protein	Q14493	SLBP	26,767
F-box protein 22	Q8NEZ5	FBXO22	26,705
Mitofusin 2	O95140	MFN2	26,677
F-box protein 2	Q9UK22	FBXO2	26,628
Eukaryotic translation initiation factor 2D	P41214	EIF2D	26,590
Decapping mRNA 1A	Q9NPI6	DCP1A	26,584
Activating transcription factor 3	P18847	ATF3	26,511
Nuclear factor I A	Q12857	NFIA	26,502
Kelch domain containing 4	Q8TBB5	KLHDC4	26,472
Zw10 kinetochore protein	O43264	ZW10	26,415
Pleckstrin homology like domain family B member 2	Q86SQ0	PHLDB2	26,409
Nucleoporin 58	Q9BVL2	NUP58	26,380
Protein inhibitor of activated STAT 2	O75928	PIAS2	26,358
Protein kinase C and casein kinase substrate in neurons 3	Q9UKS6	PACSIN3	26,319
A-kinase anchoring protein 9	Q99996	AKAP9	26,305
3-hydroxyacyl-CoA dehydratase 2	Q6Y1H2	HACD2	26,302
Actin binding LIM protein 1	O14639	ABLIM1	26,293
Spermatogenesis associated 5 like 1	Q9BVQ7	SPATA5L1	26,178
Cap methyltransferase 1	Q8N1G2	CMTR1	26,136
Zinc finger protein 148	Q9UQR1	ZNF148	26,107
DNA polymerase delta 3, accessory subunit	Q15054	POLD3	26,089
RNA polymerase II subunit E	P19388	POLR2E	26,062
TRIO and F-actin binding protein	Q9H2D6	TRIOBP	26,009
BCL9 like	Q86UU0	BCL9L	26,005
Novel protein	H7C1D1	AC037459.1	25,908
WD repeat and HMG-box DNA binding protein 1	O75717	WDHD1	25,897
C-X9-C motif containing 1	Q7Z7K0	CMC1	25,888
Eukaryotic translation initiation factor 4E nuclear import factor 1	Q9NRA8	EIF4ENIF1	25,885
Phosphomevalonate kinase	Q15126	PMVK	25,883
SKI proto-oncogene	P12755	SKI	25,868
FKBP prolyl isomerase 10	Q96AY3	FKBP10	25,814
Isochorismatase domain containing 1	Q96CN7	ISOC1	25,781

KIAA1671	Q9BY89	KIAA1671	25,781
Chromosome 19 open reading frame 44	Q9H6X5	C19orf44	25,731
Charged multivesicular body protein 6	Q96FZ7	CHMP6	25,731
SET domain containing 3, actin histidine methyltransferase	Q86TU7	SETD3	25,692
Cell division cycle 23	Q9UJX2	CDC23	25,614
SLU7 homolog, splicing factor	O95391	SLU7	25,612
BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone	Q9Y276	BCS1L	25,563
Amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	P35573	AGL	25,521
Zinc finger CCHC-type containing 8	Q6NZY4	ZCCHC8	25,421
ClpB homolog, mitochondrial AAA ATPase chaperonin	Q9H078	CLPB	25,276
Peptidase M20 domain containing 2	Q8IYS1	PM20D2	25,252
Coiled-coil domain containing 50	Q8IVM0	CCDC50	25,249
Origin recognition complex subunit 4	O43929	ORC4	25,218
TELO2 interacting protein 1	O43156	TTI1	25,145
Glucosamine-6-phosphate deaminase 1	P46926	GNPDA1	25,143
Engulfment and cell motility 3	Q96BJ8	ELMO3	25,109
Kinesin family member 3A	Q9Y496	KIF3A	25,018
Solute carrier family 25 member 13	Q9UJS0	SLC25A13	24,847
Thiosulfate sulfurtransferase like domain containing 1	Q8NFU3	TSTD1	24,814
Nuclear factor of activated T cells 5	O94916	NFAT5	24,812
TGF-beta activated kinase 1 (MAP3K7) binding protein 2	Q9NYJ8	TAB2	24,803
NSFL1 cofactor	Q9UNZ2	NSFL1C	24,783
2-oxoglutarate and iron dependent oxygenase domain containing 3	Q6PK18	OGFOD3	24,749
Dynein light chain roadblock-type 1	Q9NP97	DYNLRB1	24,736
Lysophosphatidylcholine acyltransferase 4	Q643R3	LPCAT4	24,635
Nuclear receptor coactivator 3	Q9Y6Q9	NCOA3	24,603
SLIT-ROBO Rho GTPase activating protein 2B	P0DMP2	SRGAP2B	24,475
Signal transducer and activator of transcription 2	P52630	STAT2	24,429
BCL2 associated athanogene 3	O95817	BAG3	24,320
ER membrane protein complex subunit 1	Q8N766	EMC1	24,185
G protein subunit alpha q	P50148	GNAQ	23,202
WD repeat containing, antisense to TP73	Q9P2S5	WRAP73	22,894
Actin beta	P60709	ACTB	22,586
NUP98-HOXA9	<i>bait</i>	None	8,518
Ribonucleic acid export 1	P78406	RAE1	6,395
Nucleus accumbens associated 1	Q96RE7	NACC1	1,365
Importin 8	O15397	IPO8	1,010
Trinucleotide repeat containing adaptor 6B	Q9UPQ9	TNRC6B	0,874
Myocyte enhancer factor 2D	Q14814	MEF2D	0,841
JunB proto-oncogene, AP-1 transcription factor subunit	P17275	JUNB	0,697

Proteins highlighted in blue were exclusively detected in the NHA9-BioID pool of biotinylated proteins.

Table S3

Presence of classical nuclear export signals (NES) in NHA9-BioID proximal interactors

Protein name	Gene	F.C	NES finder 0.2	LocNES
Dedicator of cytokinesis 6	DOCK6	33,239	Y	Y
Dynein axonemal heavy chain 5	DNAH5	30,201	Y	Y
ATPase 13A1	ATP13A1	29,197	Y	Y
SUB1 regulator of transcription	SUB1	29,113	N	Y
Eukaryotic translation initiation factor 2A	EIF2A	28,994	Y	Y
Jun proto-oncogene, AP-1 transcription factor subunit	JUN	28,639	N	Y
Stathmin 1	STMN1	28,622	N	N
Calmodulin 3	CALM3	28,516	Y	Y
Adenylate kinase 3	AK3	28,499	Y	Y
Glutamate-ammonia ligase	GLUL	28,413	Y	Y
Zinc finger protein 384	ZNF384	28,34	N	Y
RNA binding motif protein 33	RBM33	28,318	Y	Y
Golgi reassembly stacking protein 2	GORASP2	28,305	Y	Y
Epidermal growth factor receptor pathway substrate 15	EPS15	28,137	Y	Y
Dishevelled segment polarity protein 1	DVL1	28,105	Y	Y
Translational activator of cytochrome c oxidase I	TACO1	28,089	Y	Y
Cold inducible RNA binding protein	CIRBP	28,027	N	Y
Translocase of outer mitochondrial membrane 7	TOMM7	27,822	Y	Y
Mannose phosphate isomerase	MPI	27,775	Y	Y
Methylmalonyl-CoA mutase	MMUT	27,758	Y	Y
NADH:ubiquinone oxidoreductase subunit A3	NDUFA3	27,749	Y	Y
Cystatin A	CSTA	27,738	N	N
Coiled-coil domain containing 124	CCDC124	27,695	Y	Y
DDB1 and CUL4 associated factor 7	DCAF7	27,593	N	Y
NDRG family member 3	NDRG3	27,531	Y	Y
NADH:ubiquinone oxidoreductase subunit A2	NDUFA2	27,53	N	Y
Prenylcysteine oxidase 1	PCYOX1	27,504	Y	Y
CTD phosphatase subunit 1	CTDP1	27,5	Y	Y
Centrosomal protein 290	CEP290	27,448	Y	Y
Nuclear receptor subfamily 2 group C member 2	NR2C2	27,441	Y	Y
Transcription factor AP-2 alpha	TFAP2A	27,398	Y	Y
Gasdermin A	GSDMA	27,396	Y	Y
Proteasome subunit beta 6	PSMB6	27,371	Y	Y
Microtubule associated protein tau	MAPT	27,358	Y	Y
TLE family member 3, transcriptional corepressor	TLE3	27,345	N	Y
TOX high mobility group box family member 3	TOX3	27,278	N	Y
BRCA1/BRCA2-containing complex subunit 3	BRCC3	27,239	N	Y
NAD(P)HX epimerase	NAXE	27,205	Y	Y
Nudix hydrolase 19	NUDT19	27,195	Y	N
Scribble planar cell polarity protein	SCRIB	27,173	Y	Y
Metaxin 1	MTX1	27,166	N	Y
Programmed cell death 10	PDCD10	27,149	N	Y
Protein tyrosine kinase 2	PTK2	27,074	Y	Y

SRY-box transcription factor 9	SOX9	27,074	Y	Y
LYR motif containing 7	LYRM7	27,071	Y	Y
Syntaxin 10	STX10	27,049	Y	Y
Mitochondrial calcium uniporter	MCU	26,975	Y	Y
FLYWCH family member 2	FLYWCH2	26,974	Y	N
Non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	NCCRP1	26,956	Y	N
Septin 11	SEPTIN11	26,933	Y	Y
Fatty acyl-CoA reductase 1	FAR1	26,902	Y	Y
Rho guanine nucleotide exchange factor 10	ARHGEF10	26,876	Y	Y
Hippocalcin like 1	HPCAL1	26,869	Y	Y
3-hydroxybutyrate dehydrogenase 1	BDH1	26,865	Y	Y
BBX high mobility group box domain containing	BBX	26,858	Y	Y
Trinucleotide repeat containing adaptor 6A	TNRC6A	26,847	Y	Y
ATPase H ⁺ transporting V0 subunit d1	ATP6V0D1	26,838	Y	Y
Mitochondrial ribosomal protein S12	MRPS12	26,821	N	Y
Acidic nuclear phosphoprotein 32 family member E	ANP32E	26,768	Y	Y
stem-loop binding protein	SLBP	26,767	N	N
F-box protein 22	FBXO22	26,705	Y	Y
Mitofusin 2	MFN2	26,677	Y	Y
F-box protein 2	FBXO2	26,628	N	Y
Eukaryotic translation initiation factor 2D	EIF2D	26,59	N	Y
Decapping mRNA 1A	DCP1A	26,584	Y	Y
Activating transcription factor 3	ATF3	26,511	N	Y
Nuclear factor I A	NFIA	26,502	Y	Y
Kelch domain containing 4	KLHDC4	26,472	Y	Y
Zw10 kinetochore protein	ZW10	26,415	Y	Y
Pleckstrin homology like domain family B member 2	PHLDB2	26,409	Y	Y
Nucleoporin 58	NUPL1	26,38	Y	Y
Protein inhibitor of activated STAT 2	PIAS2	26,358	Y	Y
Protein kinase C and casein kinase substrate in neurons 3	PACSIN3	26,319	Y	Y
A-kinase anchoring protein 9	AKAP9	26,305	Y	Y
3-hydroxyacyl-CoA dehydratase 2	HACD2	26,302	Y	Y
Actin binding LIM protein 1	ABLIM1	26,293	Y	Y
Spermatogenesis associated 5 like 1	SPATA5L1	26,178	Y	Y
Cap methyltransferase 1	CMTR1	26,136	Y	Y
Zinc finger protein 148	ZNF148	26,107	N	Y
DNA polymerase delta 3, accessory subunit	POLD3	26,089	Y	N
RNA polymerase II subunit E	POLR2E	26,062	N	N
TRIO and F-actin binding protein	TRIOBP	26,009	Y	Y
BCL9 like	BCL9L	26,005	N	Y
Novel protein	AC037459.1	25,908	Y	Y
WD repeat and HMG-box DNA binding protein 1	WDHD1	25,897	Y	Y
C-X9-C motif containing 1	CMC1	25,888	N	Y

Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	25,885	Y	Y
Phosphomevalonate kinase	PMVK	25,883	N	Y
SKI proto-oncogene	SKI	25,868	Y	Y
FKBP prolyl isomerase 10	FKBP10	25,814	Y	Y
Isochorismatase domain containing 1	ISOC1	25,781	Y	Y
KIAA1671	KIAA1671	25,781	Y	Y
Chromosome 19 open reading frame 44	C19orf44	25,731	Y	Y
Charged multivesicular body protein 6	CHMP6	25,731	Y	Y
SET domain containing 3, actin histidine methyltransferase	SETD3	25,692	Y	Y
Cell division cycle 23	CDC23	25,614	Y	Y
SLU7 homolog, splicing factor	SLU7	25,612	Y	Y
BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone	BCS1L	25,563	Y	Y
Amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	AGL	25,521	Y	Y
Zinc finger CCHC-type containing 8	ZCCHC8	25,421	Y	Y
ClpB homolog, mitochondrial AAA ATPase chaperonin	CLPB	25,276	Y	Y
Peptidase M20 domain containing 2	PM20D2	25,252	Y	Y
Coiled-coil domain containing 50	CCDC50	25,249	Y	Y
Origin recognition complex subunit 4	ORC4	25,218	Y	Y
TELO2 interacting protein 1	TTI1	25,145	Y	Y
Glucosamine-6-phosphate deaminase 1	GNPDA1	25,143	Y	Y
Engulfment and cell motility 3	ELMO3	25,109	Y	Y
Kinesin family member 3A	KIF3A	25,018	Y	Y
Solute carrier family 25 member 13	SLC25A13	24,847	Y	Y
Thiosulfate sulfurtransferase like domain containing 1	TSTD1	24,814	Y	Y
Nuclear factor of activated T cells 5	NFAT5	24,812	Y	Y
TGF-beta activated kinase 1 (MAP3K7) binding protein 2	TAB2	24,803	Y	Y
NSFL1 cofactor	NSFL1C	24,783	N	Y
2-oxoglutarate and iron dependent oxygenase domain containing 3	OGFOD3	24,749	N	Y
Dynein light chain roadblock-type 1	DYNLRB1	24,736	N	Y
Lysophosphatidylcholine acyltransferase 4	LPCAT4	24,635	Y	Y
Nuclear receptor coactivator 3	NCOA3	24,603	Y	Y
SLIT-ROBO Rho GTPase activating protein 2B	SRGAP2B	24,475	Y	Y
Signal transducer and activator of transcription 2	STAT2	24,429	Y	Y
BCL2 associated athanogene 3	BAG3	24,32	N	Y
ER membrane protein complex subunit 1	EMC1	24,185	Y	Y
G protein subunit alpha q	GNAQ	23,202	Y	Y
WD repeat containing, antisense to TP73	WRAP73	22,894	Y	Y
Actin beta	ACTB	22,586	Y	Y
Ribonucleic acid export 1	RAE1	6,395	Y	N
Nucleus accumbens associated 1	NACC1	1,365	N	Y
Importin 8	IPO8	1,01	Y	Y
Trinucleotide repeat containing adaptor 6B	TNRC6B	0,874	Y	Y

Myocyte enhancer factor 2D	MEF2D	0,841	Y	Y
JunB proto-oncogene, AP-1 transcription factor subunit	JUNB	0,697	N	Y

F.C. – Fold Change; Y - presence of at least one potential NES peptide sequence; N - absence of potential NES peptide sequences

Table S5

List of functional groups with corresponding genes of SN214-BioID proximal interactors generated by the ClueGO Cytoscape plugin

Functional Cluster	Genes
Adaptive Immune System	ACTR1B AHCYL1 ANAPC7 AP1S1 AP2A2 AP2M1 B2M BLMH CALM3 CD81 CD99 CDC27 CDH1 CHUK CSK CTSA CTSB CUL5 CYBA DTX3L DYNC1I2 DYNLL2 FBXO22 GAN HERC4 HLA-G KIF23 LRSAM1 LYN NEDD4 NFKB1 NRAS PIK3CB PIK3R2 PPP2CA PSMB4 PSMB7 PVR RAC1 RACGAP1 RAP1A RBBP6 RBX1 RNF126 SEC13 SEC22B SEC61A1 SEC61B SNAP23 TAB2 TAP2 TRIM21 UBA3 UBE2A UBE2L6 UBE2V2 UBE4A
Cell Cycle	AKAP9 ANAPC7 ATRIP BABAM2 BLM CDC27 CENPC CEP290 CLASP2 CSNK1D DHFR DYNC1I2 DYNLL2 EP300 GORASP2 H2AFV HIST2H2AC KIF23 LCMT1 LEMD3 LIG1 LMNA LYN MAD2L1 NCAPG NEK9 NHP2 NIPBL NUP153 NUP58 NUP62 PHLDA1 POLD1 POLD2 POLD3 PPP1CB PPP1R12A PPP2CA PSMB4 PSMB7 RAE1 RANBP2 RBBP7 RBX1 RFC1 RPA2 RPA3 SEC13 STAG2 SUN2 TPX2 UBE2V2
Stress response	AKT1S1 ANAPC7 ASF1A ATP6V0D1 ATP6V1E1 ATP6V1G1 CAMK2G CAT CBX4 CDC27 CYBA DNAJB6 DYNC1I2 DYNLL2 EHMT1 EP300 H2AFV HIGD1A HIST1H1C HIST1H1E HIST2H2AC HMGA1 HMGA2 HSPA6 LAMTOR3 LIMD1 NFKB1 NUP153 NUP58 NUP62 PHC2 PSMB4 PSMB7 RAE1 RANBP2 RBBP7 RBX1 RNF2 RPA2 RPA3 RPL13 RPL14 RPL18 RPL22L1 RPL23A RPL24 RPL26L1 RPL29 RPL31 RPL32 RPL34 RPL35 RPL36A RPL6 RPL7A RPLP1 RPS19BP1 RPS24 RPS26 RPTOR SEC13 TNRC6B TXNRD1
Infectious disease	ACACA AGK AKAP9 AKT1S1 AP1S1 AP2A2 AP2M1 B2M BAD BSG C1QBP CALM3 CAMK2G CAST CCNT1 CD9 CDH1 CHMP2A CHMP4B CHUK CPSF4 CREB1 CSK CTSA CUL5 DERL2 DPM3 DYNC1I2 DYNLL2 ELL EP300 EPS15 ERCC2 EREG GBE1 GRSF1 GTF2E2 HIST2H2AB HIST2H2AC HMGA1 ISG15 LIG1 LMNA MECP2 MPI MUCL1 MVB12A NCBP2 NCOR2 NELFE NFKB1 NMT1 NRAS NUP153 NUP58 NUP62 PABPN1 PAH PEBP1 PHB PIK3CB PIK3R2 PML POLR2E POLR2G POLR2I POLR2L PPP2CA PSMB4 PSMB7 RAB5A RAC1 RAC2 RAE1 RANBP2 RAP1A RBBP7 RBPJ RBX1 RCC1 RPL13 RPL14 RPL18 RPL22L1 RPL23A RPL24 RPL26L1 RPL29 RPL31 RPL32 RPL34 RPL35 RPL36A RPL6 RPL7A RPLP1 RPS24 RPS26 SDC4 SEC13 SFPQ SLC16A1 SLC25A4 SLC27A4 SLC2A1 SMAD3 SYT1 TAF2 TAF3 TBP TXNRD1 VPS25 VTA1 XRCC4
Metabolism	AASDHPPT ABCC1 ACACA ACACB ACAD8 ACADVL ACAT2 ACOT13 ACSF3 AGK AGPAT5 AHCYL1 AKR7A2 ALDH2 ALDH4A1 APOC3 ARG1 ATP5MG ATP5PF ATP6 AUH AZIN2 B4GALT5 BSG CALM3 CDIPT CDS2 CERS2 CHPF COASY COL4A3BP COX1 COX2 COX20 COX4I1 COX5B COX6C COX7A2L CPOX CTSA CYB5A CYB5R3 CYC1 CYP2S1 DCTD DGAT1 DHCR7 DHFR DHRS7B DLAT DLST ELOVL1 ELOVL5 ELOVL7 EP300 ERCC2 ESD ESYT2 ETFB FABP5 GAPDH GBE1 GCDH GLRX GNA11 GNG12 GOT1 GPAT3 GPD1L GSTK1 HACD2 HELZ2 HSD17B10 ITPA IVD KYAT3 LBR LCLAT1 LHPP LPCAT1 LPCAT3 MARCKS MBOAT7 MCAT MDH1 MDH2 ME1 MED19 MGST1 MGST2 MGST3 MLXIPL MPST MRI1 MSMO1 MTHFD2 NAXE NCOR2 ND1 ND2 ND4 ND5 NDUFA1 NDUFA10 NDUFA12 NDUFA13 NDUFA2 NDUFA3 NDUFA4 NDUFA7 NDUFA9 NDUFAF2 NDUFB1 NDUFB10 NDUFB11 NDUFB3 NDUFB4 NDUFB5 NDUFB6 NDUFB7 NDUFB8 NDUFB9 NDUFC2 NDUFS1 NDUFS2 NDUFS5 NDUFS6 NDUFS7 NDUFS8 NDUFV1 NDUFV2 NFS1 NFYA NUDT1 NUDT19 NUP153 NUP58 NUP62 PAH PCBD1 PCK2 PCYT1A PCYT2 PDHB PGLS PIK3CB PIK3R2 PIP4P1 PIP5K1A PISD POLD1 PON2 PPCS PPP1CA PPP1CB PPP2CA PRSS3 PSMB4 PSMB7 PTDS1 PXMP2 PYCR3 RAB4A RAB5A RAE1 RANBP2 RAP1A RDH11 RPL13 RPL14 RPL18 RPL22L1 RPL23A RPL24 RPL26L1 RPL29 RPL31 RPL32 RPL34 RPL35 RPL36A RPL6 RPL7A RPLP1 RPS24 RPS26 SACM1L SCO1 SDC4 SDHA SEC13 SERINC1

	SGPP1 SLC16A1 SLC25A10 SLC25A11 SLC25A13 SLC2A1 SLC35B2 SLC7A5 SMPD4 SMS SPTLC2 SQOR SUCLA2 SURF1 THRAP3 TIMMDC1 TM7SF2 TST TXNRD1 UQCR10 UQCR11 UQCRC1 UQCRC2 UQCRFS1 UQCRQ VDAC1
Metabolism of RNA	BCAS2 BUD31 CDC5L CLNS1A CPSF2 CPSF3 CPSF4 CSNK1D CTNBNB1 DIMT1 EBNA1BP2 EIF4B ERCC2 EXOSC2 EXOSC6 EXOSC7 FCF1 FIP1L1 FTSJ3 GEMIN7 GNL3 GSPT2 GTPBP3 HNRNPH1 HNRNPH2 HNRNPR HSD17B10 IMP3 IMP4 KRR1 LSM4 MPHOSPH10 MRM1 MTO1 NAT10 NCBP2 NHP2 NOP10 NOP2 NOP58 NUP153 NUP58 NUP62 PABPN1 PAPOLA PELP1 PHF5A POLR2E POLR2G POLR2I POLR2L POP4 PPIL4 PPP2CA PPWD1 PRKCD PRPF40A PSMB4 PSMB7 RAE1 RANBP2 R1OK2 RNPS1 RPL13 RPL14 RPL18 RPL22L1 RPL23A RPL24 RPL26L1 RPL29 RPL31 RPL32 RPL34 RPL35 RPL36A RPL6 RPL7A RPLP1 RPP38 RPP40 RPS24 RPS26 RRP9 SART1 SEC13 SLBP SMNDC1 SNRPC SNU13 SRRM1 SRRM2 SRSF3 SUGP1 THOC3 TRMT5 TRMT6 TRMT61A TSEN2 TSEN34 UPF3B UTP20 UTP3 UTP6 WBP11 WDR61 WDR75
Amino acid metabolism	ACAD8 ALDH4A1 ARG1 AUH AZIN2 DLAT DLST GCDH GOT1 HSD17B10 IVD KYAT3 MPST MRI1 PAH PCBD1 PDHB PSMB4 PSMB7 PXMP2 PYCR3 RPL13 RPL14 RPL18 RPL22L1 RPL23A RPL24 RPL26L1 RPL29 RPL31 RPL32 RPL34 RPL35 RPL36A RPL6 RPL7A RPLP1 RPS24 RPS26 SERINC1 SLC25A10 SLC25A13 SLC7A5 SMS SQOR TST TXNRD1
Metabolism of lipids	ABCC1 ACACA ACACB ACADVL ACAT2 ACOT13 ACSF3 AGK AGPAT5 CDIPT CDS2 CERS2 COL4A3BP CTSA DGAT1 DHCR7 DHR57B ELOVL1 ELOVL5 ELOVL7 EP300 ESYT2 FABP5 GPAT3 GPD1L HACD2 HELZ2 LBR LCLAT1 LPCAT1 LPCAT3 MBOAT7 MCAT ME1 MED19 MSMO1 NCOR2 NFYA NUDT19 PCYT1A PCYT2 PIK3CB PIK3R2 PIP4P1 PIP5K1A PISD PON2 PPP1CA PPP1CB PTDS51 RAB4A RAB5A SACM1L SGPP1 SMPD4 SPTLC2 THRAP3 TM7SF2 TXNRD1
Metabolism of proteins	ACADVL ACTL6A ATP6V0D1 AURKAIP1 B2M B4GALT5 BABAM2 BET1L BLM CALM3 CBX4 CHCHD1 CHD3 CKAP4 CMAS COG3 COPS7A CREBRF CSNK1D CTR9 CTSA CUL4A CUL5 DAD1 DCUN1D5 DERL2 DPM3 DYNC112 DYNLL2 EIF1AX EIF4B EIF5B EP300 ETFB EXOC4 EXOSC2 EXOSC6 EXOSC7 F10 FBXO22 FKBP8 FOXK2 GADD45GIP1 GALNT2 GAN GFM2 GMPPA GNG12 GPAA1 GSPT2 HARS2 HDGF HIST2H2AB HIST2H2AC KTN1 LMAN2 LMNA MAGT1 MAVS MLEC MPI MRPL11 MRPL13 MRPL14 MRPL15 MRPL16 MRPL17 MRPL2 MRPL21 MRPL22 MRPL23 MRPL24 MRPL27 MRPL28 MRPL30 MRPL32 MRPL34 MRPL40 MRPL41 MRPL42 MRPL43 MRPL46 MRPL48 MRPL54 MRPL55 MRPL58 MRPS10 MRPS12 MRPS15 MRPS21 MRPS23 MRPS24 MRPS25 MRPS30 MRPS31 MRPS33 MRPS34 MRPS5 MRRF MTIF2 MUCL1 NARS2 NCOR2 NFYA NOP58 NUP153 NUP58 NUP62 OGT PFDN2 PHC2 PIGT PIGU PML PPP6R3 PSMB4 PSMB7 PTRH2 RAB22A RAB2B RAB35 RAB3A RAB3B RAB4A RAB4B RAB5A RAB5B RAB6A RABGGTB RAE1 RANBP2 RBBP7 RBX1 RHOT1 RNF2 RNF20 RPL13 RPL14 RPL18 RPL22L1 RPL23A RPL24 RPL26L1 RPL29 RPL31 RPL32 RPL34 RPL35 RPL36A RPL6 RPL7A RPLP1 RPS24 RPS26 SARS2 SEC11A SEC13 SEC22B SEC61A1 SEC61B SMAD3 SPCS2 SPTBN1 SRP19 SRP72 SSR1 SSR3 STAG2 TGOLN2 TMED10 TOP1 TRAM1 TRRAP TTF1 TTLL11 UBA3 UBE2A UBE2L6 UBE2T UBE2V2 UCHL3 USP16 USP19 USP42 VDAC1 VDAC2 VDAC3 WDR61 WFS1 XRCC4 YIF1A
Neutrophil degranulation	ACTR1B AHCYL1 ANAPC7 AP1S1 AP2A2 AP2M1 ARG1 ARPC1A ARPC1B ATP6V0A1 ATP6V0D1 ATP6V1E1 ATP6V1G1 B2M BLMH C1orf35 CAB39 CALM3 CALML5 CAMK2G CAT CD81 CD99 CDC27 CDH1 CEP290 CHUK CKAP4 CREB1 CRK CRKL CSK CTSA CTSB CUL5 CYB5R3 CYBA CYFIP2 CYSTM1 DCD DGAT1 DSC1 DSG1 DTX3L DYNC112 DYNLL2 DYNLT1 EP300 EREG FABP5 FBXO22 GAN GSDMD HBB HERC4 HLA-G HSPA6 IFITM3 IL18 ISG15 IST1 JUP KCMF1 KIF23 LAMTOR3 LPCAT1 LRSAM1 LYN MAGT1 MAVS MGST1 MIF MLEC MUCL1 MYO1C NDUFC2 NEDD4 NFKB1 NRAS NUP153 NUP58 NUP62 OASL OSTF1 PDAP1 PEA15 PEBP1 PGRMC1 PHB PIK3CB

	PIK3R2 PKP1 PML POLR2E POLR2L POLR3C PPP2CA PPP5C PRDX4 PRKCD PRSS3 PSMB4 PSMB7 PTK2 PVR RAB3A RAB4B RAB5B RAB6A RAC1 RAC2 RACGAP1 RAE1 RALA RANBP2 RANBP9 RAP1A RAP2B RAP2C RBBP6 RBX1 RNF126 S100A8 S100A9 SCAMP1 SEC13 SEC22B SEC61A1 SEC61B SERPINB12 SMAD3 SNAP23 SNAP29 SPTBN1 SQSTM1 STOM STX3 TAB2 TAP2 TOLLIP TRIM21 TRIM56 UBA3 UBE2A UBE2L6 UBE2V2 UBE4A VIM
Respiratory electron transport	ACTL6A AKT1S1 AP2A2 AP2M1 ARID1B ATP5MG ATP5PF ATP6 ATP6V0A1 ATP6V0D1 ATP6V1E1 ATP6V1G1 BAD BSG CALM3 CALML5 COA3 COX1 COX17 COX2 COX20 COX4I1 COX5B COX6C COX7A2L CREB1 CYC1 DLAT DLST DNAH5 EP300 ETFB GAPDH HSD17B10 HTRA2 LHPP MAPT MDH2 ME1 MLXIPL ND1 ND2 ND4 ND5 NDUFA1 NDUFA10 NDUFA12 NDUFA13 NDUFA2 NDUFA3 NDUFA4 NDUFA7 NDUFA9 NDUFAF2 NDUFB1 NDUFB10 NDUFB11 NDUFB3 NDUFB4 NDUFB5 NDUFB6 NDUFB7 NDUFB8 NDUFB9 NDUFC2 NDUF51 NDUF52 NDUF55 NDUF56 NDUF57 NDUF58 NDUFV1 NDUFV2 NFKB1 NRAS PDHB PIK3CB PIK3R2 POLR2E POLR2G POLR2I POLR2L PRKAA1 RAC1 RPS6KB1 RPTOR RTN3 SCO1 SDHA SIRT6 SLC16A1 SLC25A4 SUCLA2 SURF1 TBP TIMMDC1 UBE2L6 UQCR10 UQCR11 UQCRC1 UQCRC2 UQCRFS1 UQCRQ VDAC1 VDAC2 VDAC3
Signaling by Receptor Tyrosine Kinases	AHCYL1 AP2A2 AP2M1 ATP6V0A1 ATP6V0D1 ATP6V1E1 ATP6V1G1 CALM3 CREB1 CRK CRKL CSK CUL5 CYBA CYFIP2 EPS15 EPS15L1 EREG GRB7 HNRNPH1 ITGA2 ITGA3 JUP LAMB3 LYN MEMO1 NCBP2 NEDD4 NRAS PIK3CB PIK3R2 POLR2E POLR2G POLR2I POLR2L PPP2CA PRKCD PTK2 RAB4A RAB4B RAC1 RALA RALB RANBP9 RAP1A SPINT1 TAB2
Transcriptional Regulation by TP53	ACTL6A AIFM2 ANAPC7 ARID1B ATRIP BAZ2A BLM BRD7 CALM3 CAMK2G CAT CBFβ CBX3 CBX4 CCNT1 CDC27 CHD3 COX1 COX2 COX20 COX4I1 COX5B COX6C COX7A2L CPSF2 CPSF3 CPSF4 CREB1 CTR9 EHMT1 ELL EP300 ERCC2 FANCI FIP1L1 GTF2E2 GTF3C2 GTF3C4 GTF3C5 H2AFV HIST2H2AC INTS2 INTS9 IWS1 LAMTOR3 LBR MBD2 MECP2 MTA2 MTA3 MYO1C NCBP2 NCOR2 NDUFA4 NELFE NFKB1 NFYA NOP2 NUP153 NUP58 NUP62 OCLN PABPN1 PAPOLA PHC2 PIP4P1 PML POLR1A POLR1B POLR2E POLR2G POLR2I POLR2L POLR3C PPP2CA PRKAA1 PSMB4 PSMB7 RABGGTB RAE1 RANBP2 RBBP7 RBM14 RBPJ RBX1 RNF2 RNPS1 RPA2 RPA3 RPTOR SCO1 SEC13 SLBP SMAD3 SOX9 SRRM1 SRSF3 SSU72 SURF1 TAF2 TAF3 TBP TFAP2D THOC3 TMEM219 TNRC6B TPX2 TRIM33 TTF1 TXNRD1 UPF3B WDR61
Translation	AURKAIP1 CHCHD1 EIF1AX EIF4B EIF5B GADD45GIP1 GFM2 GSPT2 HARS2 MRPL11 MRPL13 MRPL14 MRPL15 MRPL16 MRPL17 MRPL2 MRPL21 MRPL22 MRPL23 MRPL24 MRPL27 MRPL28 MRPL30 MRPL32 MRPL34 MRPL40 MRPL41 MRPL42 MRPL43 MRPL46 MRPL48 MRPL54 MRPL55 MRPL58 MRPS10 MRPS12 MRPS15 MRPS21 MRPS23 MRPS24 MRPS25 MRPS30 MRPS31 MRPS33 MRPS34 MRPS5 MRRF MTIF2 NARS2 RPL13 RPL14 RPL18 RPL22L1 RPL23A RPL24 RPL26L1 RPL29 RPL31 RPL32 RPL34 RPL35 RPL36A RPL6 RPL7A RPLP1 RPS24 RPS26 RSL24D1 SARS2 SEC11A SEC61A1 SEC61B SPCS2 SRP19 SRP72 SSR1 SSR3 TRAM1
Vesicle-mediated transport	API51 AP2A2 AP2M1 ARPC1A BET1L BNIP1 CALM3 CHMP2A CHMP4B COG3 COPS7A CSNK1D DYNC112 DYNLL2 EPS15 EPS15L1 EREG EXOC4 GAK GALNT2 GCC2 HBB HPX KIF18B KIF23 KIFC1 LMAN2 MVB12A MYO1C NECAP2 PPP6R3 RAB35 RAB3A RAB4A RAB5A RAB5B RAB6A RAC1 RACGAP1 RALA RIN1 SCARB1 SCARB2 SEC13 SEC22B SNAP23 SNAP29 SPTBN1 STX6 SYT1 TGOLN2 TMED10 TPD52 VPS25 VTA1 YIPF6