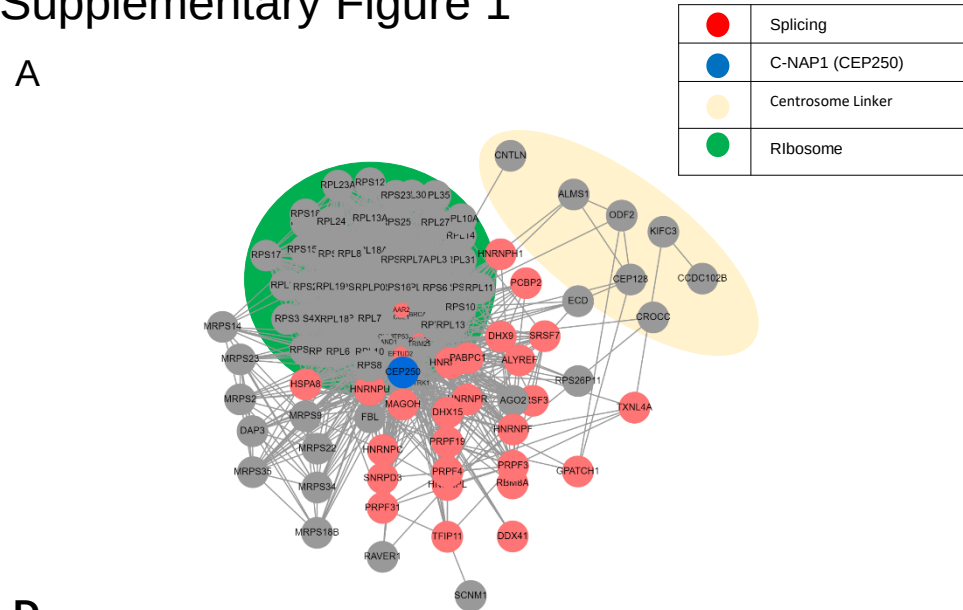
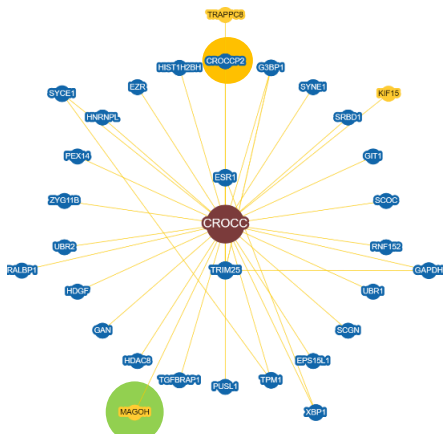


Supplementary Figure 1

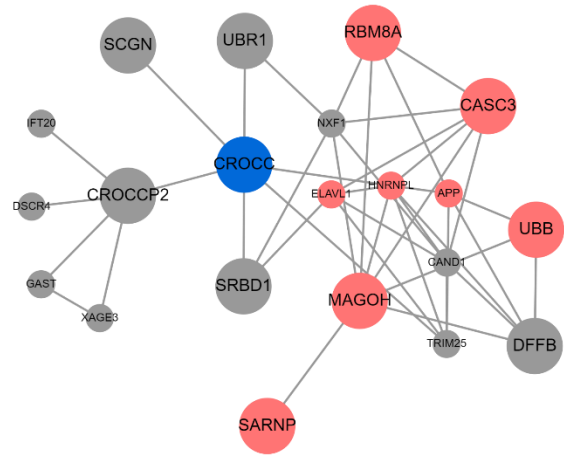
A



B



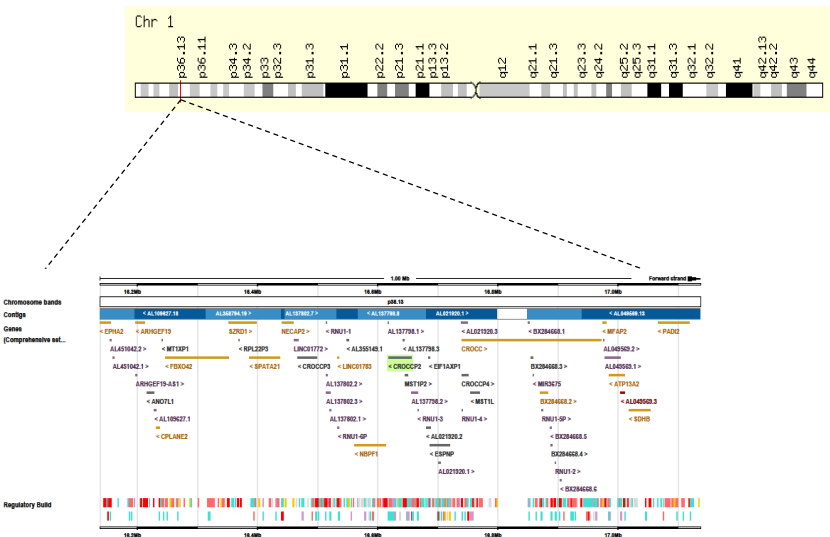
C



Top Ranking Neighbors

Gene Symbol	Random Walk Probability
XAGE3	5.10E-03
GAST	5.04E-03
IFT20	4.86E-03
DSCR4	4.82E-03
HNRNPL	3.40E-03
APP	2.17E-03
NXF1	2.14E-03
TRIM25	1.93E-03
CAND1	1.86E-03
ELAVL1	1.71E-03

D



E

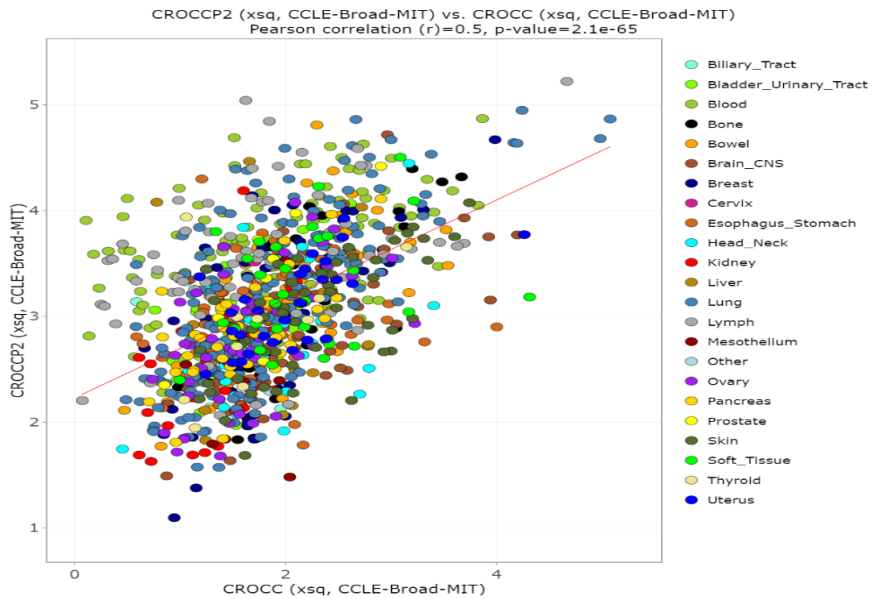


Figure S1. Centrosome cohesion and splicing partners. **A)** Protein-Protein interaction network analysis integrating Ribosome, splicing and centrosome linker proteins; The different categories are indicated by colours. **B)** Left, Protein-Protein network analysis for Rootletin (CROCC) derived from BioGRID database. Right, Top-ranking neighbours interactors derived from the analysis of CROCC-interacting partners. **C)** Enlarged image of Chromosome 1 at 1p36.3 band indicate the adjacent positioning or overlapping between U1 snRNP components, *CROCCP2* and *CROCC* gene. **D)** Up, the graph shows the major pathways derived from C-NAP1 interactome (see Table S2); Down, Protein-Protein interaction network for C-NAP1 (BioGRID database). **E)** The graphs shows the strong co-expression of *CROCCP2* and *CROCC* transcripts; RNA-seq data from cancer cell line encyclopedia (CCLE) database.

Supplementary Figure 2

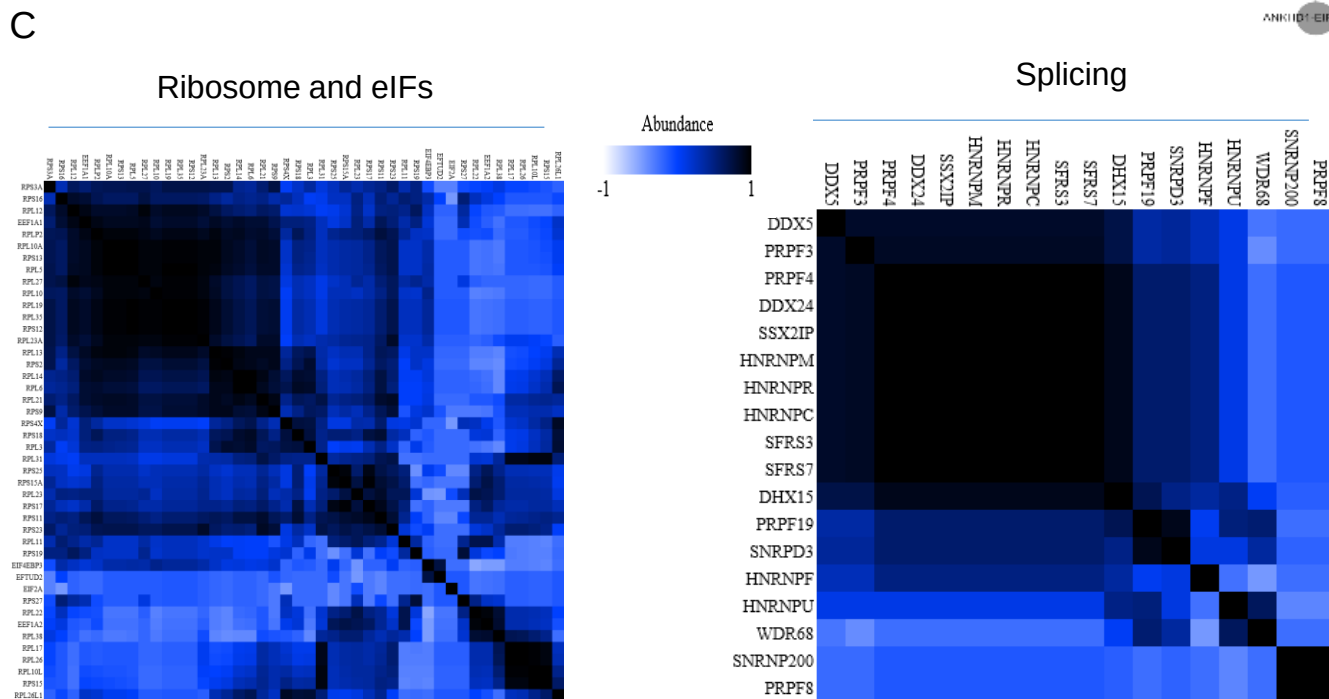
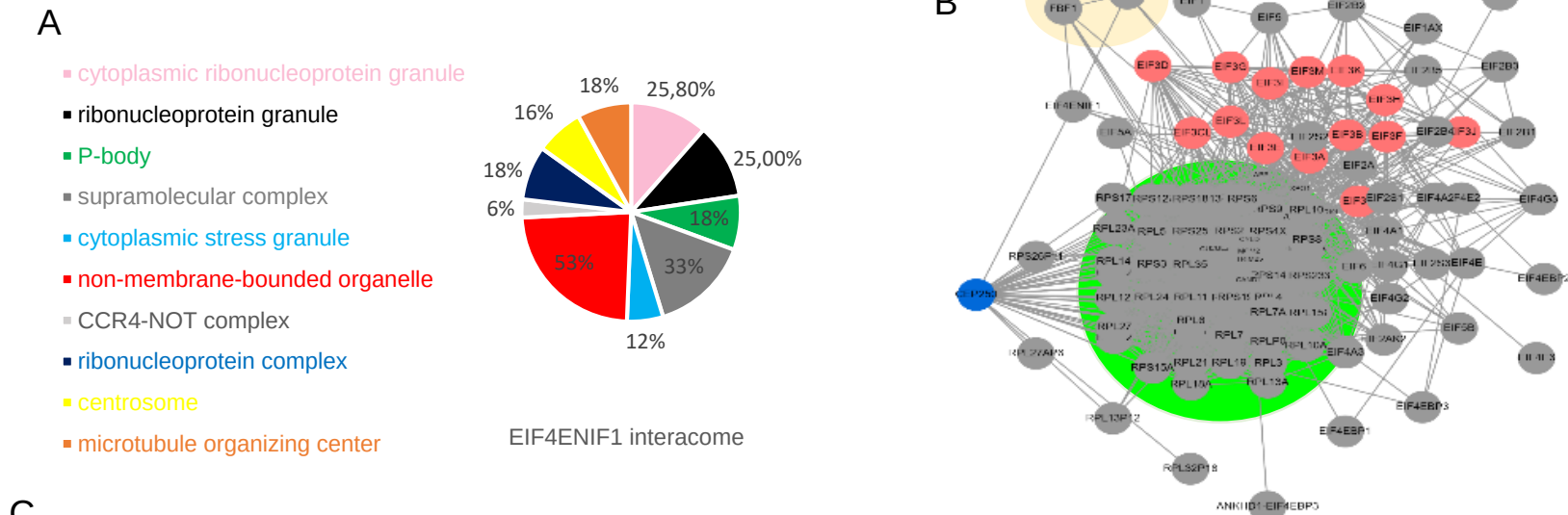


Figure S2. Abundance and features of ribonucleoproteins interacting with centrosome molecules. **A)** Gene Ontology analysis of the most significant pathways of EIF4ENIF1 interactome. Protein-Protein interaction network of EIF4ENIF1 was extracted from BioGRID database. **B)** Protein-Protein interaction Network analysis to show the spatial proximity between ciliogenic factors FBF1 and ODF1 and EIFs factors. **C)** Correlation matrix for Ribosome and splicing proteins interacting with centrosome proteins.

Supplementary Figure 3

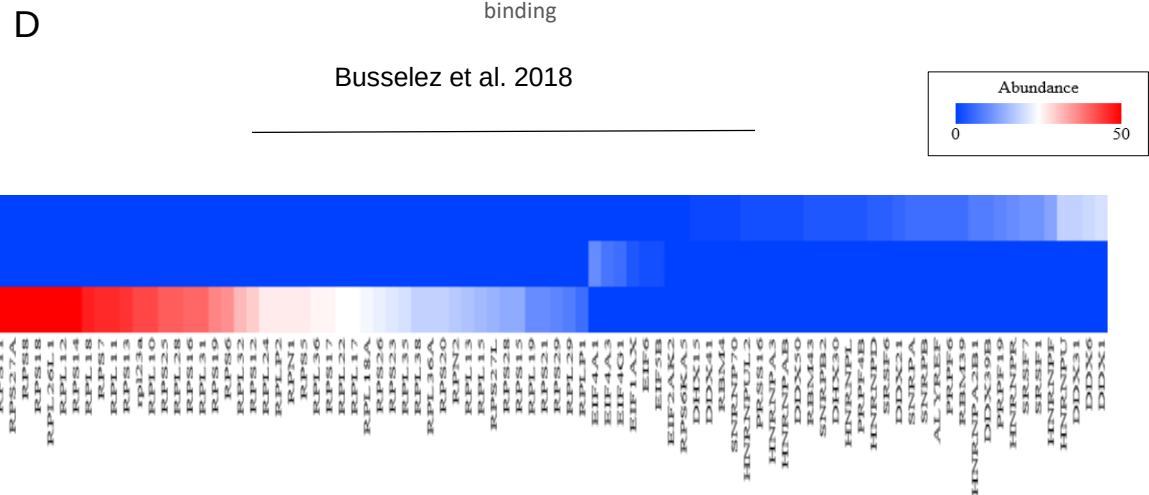
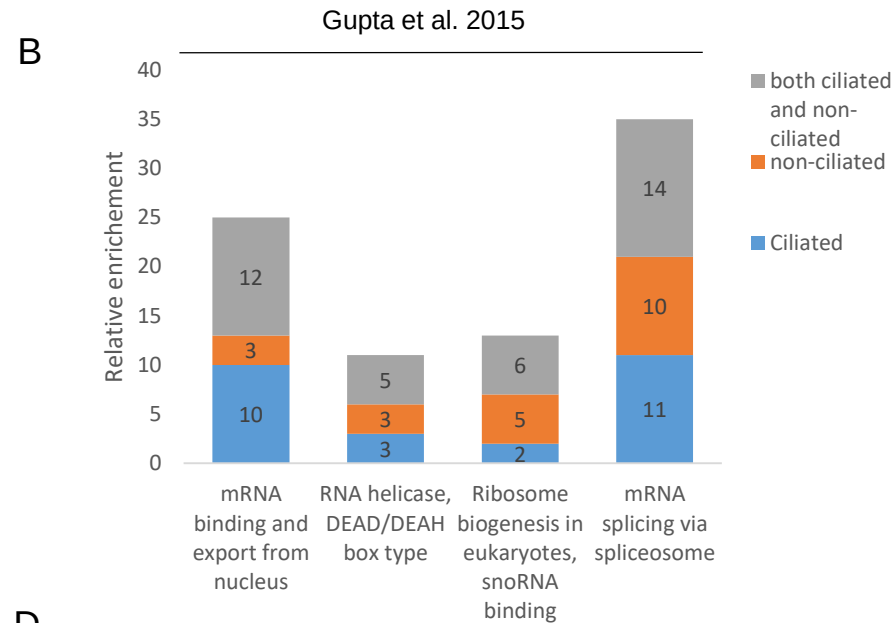
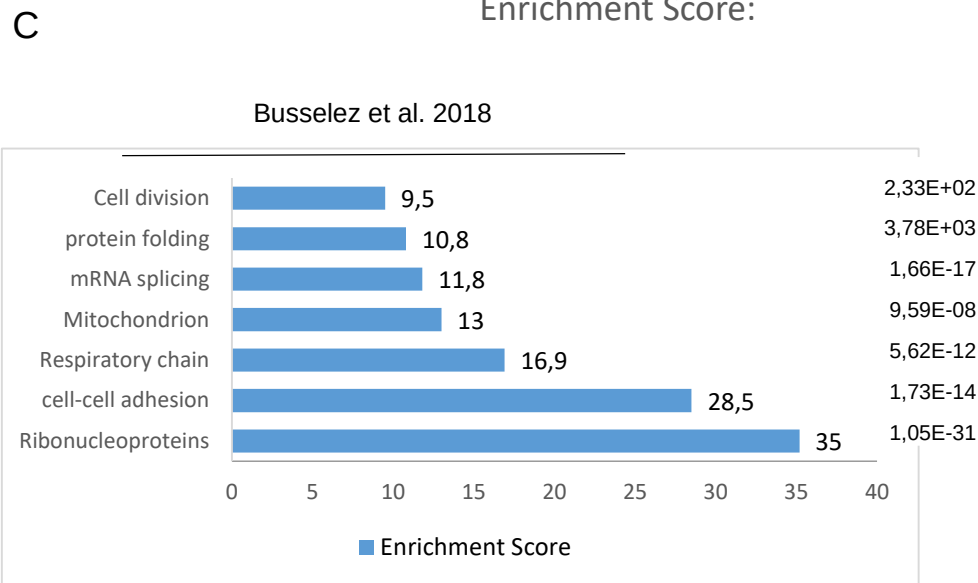
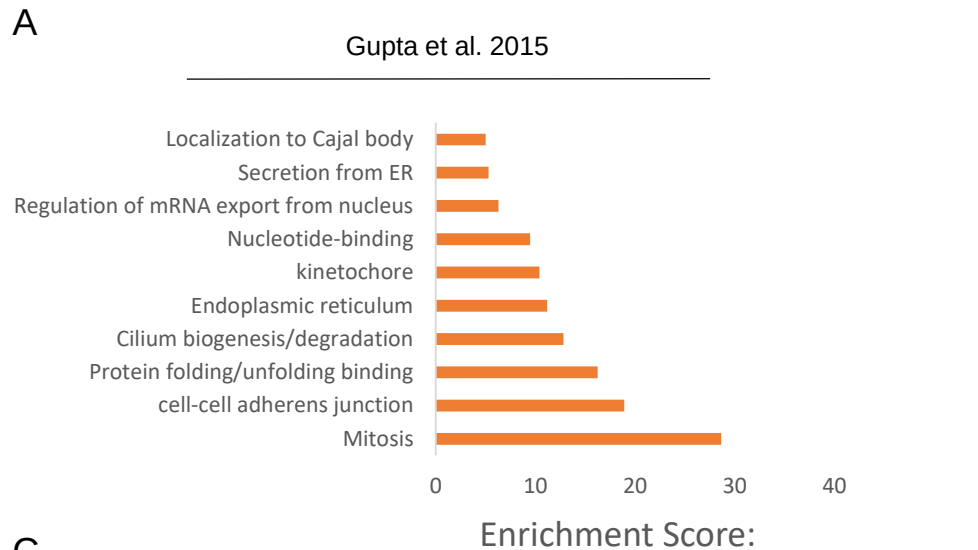


Figure S3. Independent proteomic data reveal spatial interactions between splicing and centrosome proteins **A)** The graph shows the top-10 most significant pathways. Gene ontology analysis on 6000 interactions using 58 bait centrosome proteins detected by proximity dependent biotinylation (BioID) according with Gupta et al, 2015. **B)** The graph shows that Splicing and mRNA export proteins are the most represented centrosome-interacting partners among Ribonucleoproteins, Gupta et al, 2015. **C)** Gene ontology analysis on 814 high-confident proteins identified (100% probability) in centrosomes isolated from the young lamb thymus according to Busselez et al. 2018. **D)** Heatmap shows the quantitative value of high-confident ribonucleoproteins identified in centrosome isolated according to Busselez et al. 2018. The colors indicate the relative abundance of identified proteins.

Supplementary Figure 4

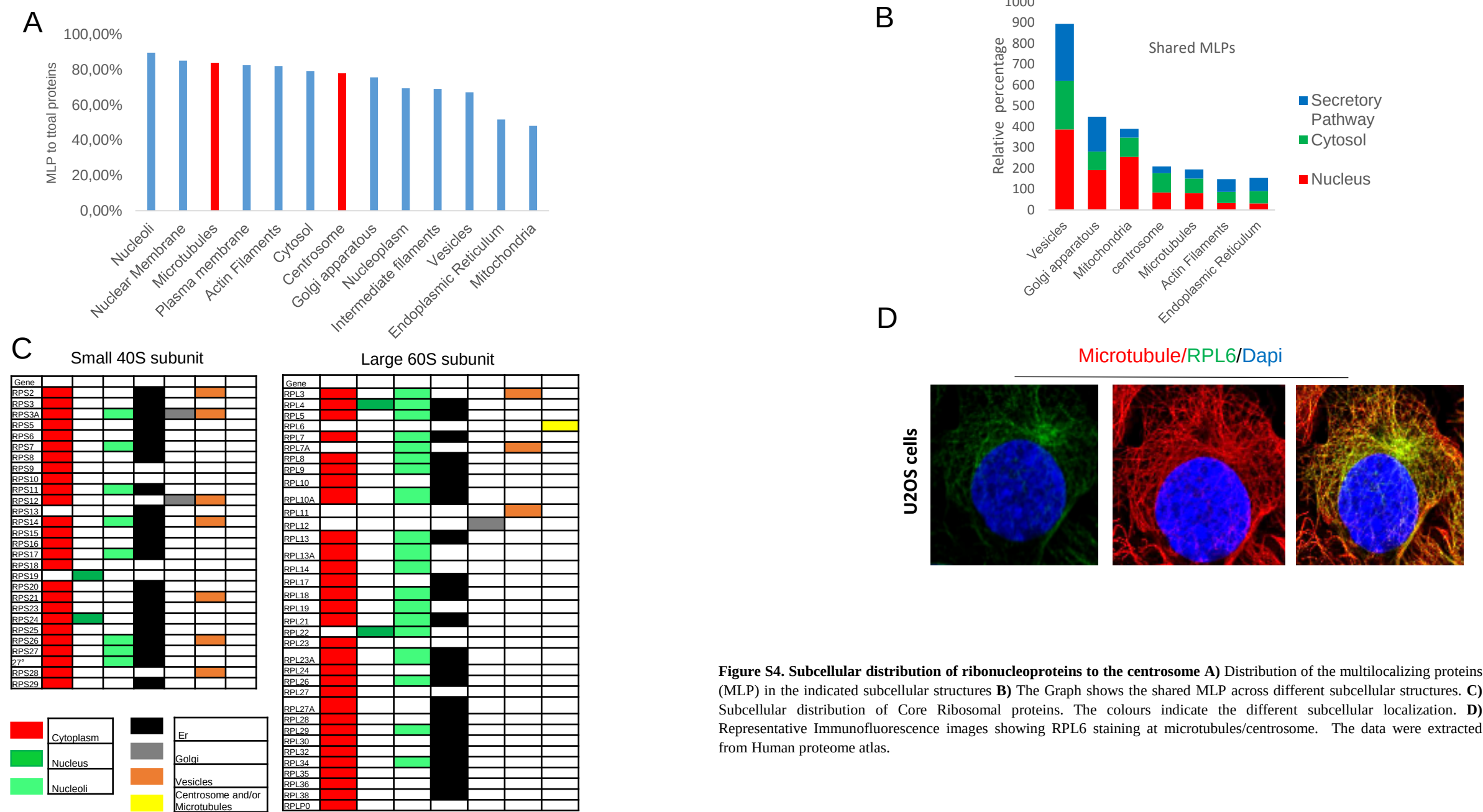


Figure S4. Subcellular distribution of ribonucleoproteins to the centrosome **A)** Distribution of the multilocalizing proteins (MLP) in the indicated subcellular structures **B)** The Graph shows the shared MLP across different subcellular structures. **C)** Subcellular distribution of Core Ribosomal proteins. The colours indicate the different subcellular localization. **D)** Representative Immunofluorescence images showing RPL6 staining at microtubules/centrosome. The data were extracted from Human proteome atlas.

Supplementary Figure 5

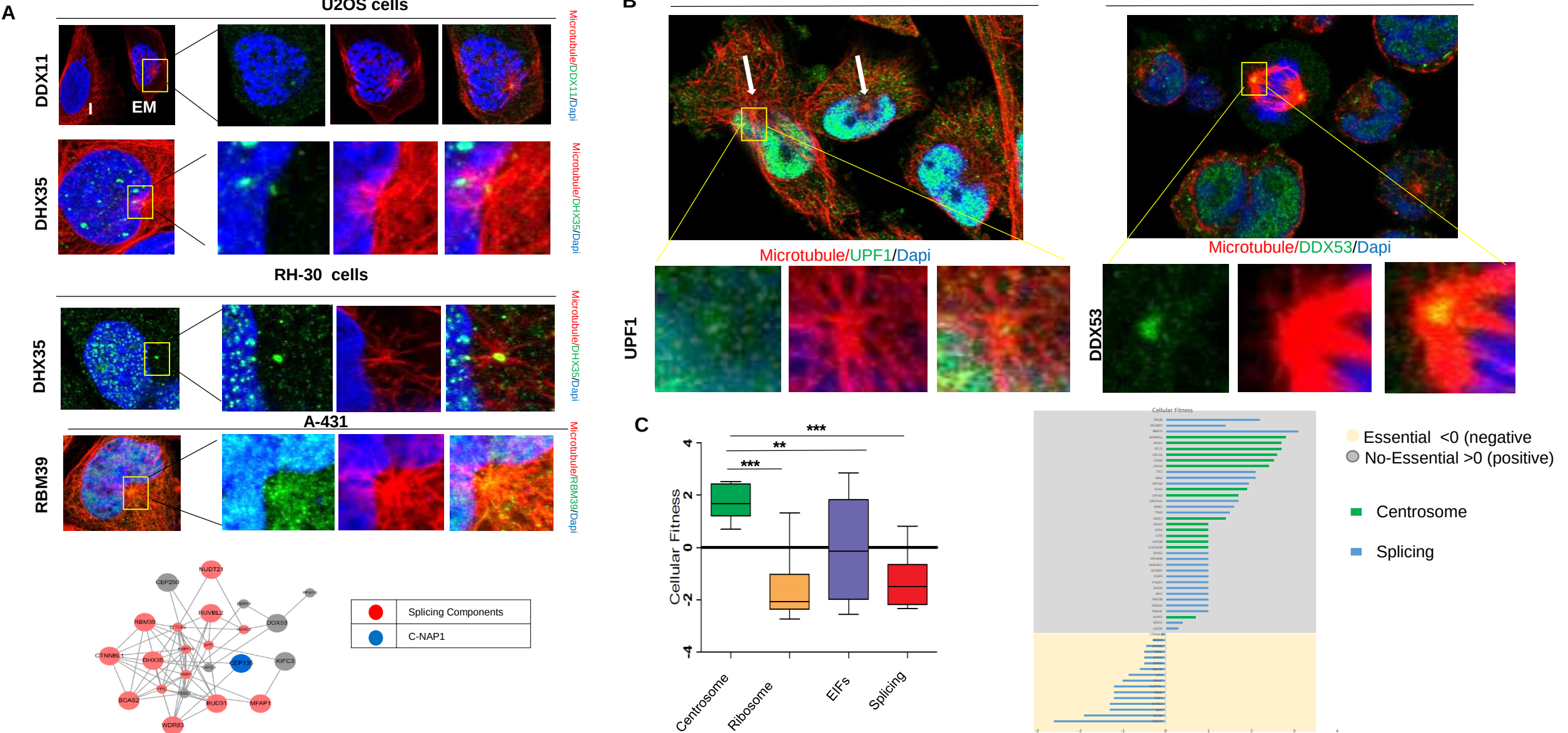


Figure S5. Key splicing proteins localize to the centrosome refining the protein-protein interaction network data. **A)** Up, A subset of proteins involved in splicing localize to the centrosome as indicated by high-resolution IF-images. Down, Protein-Protein network analysis of splicing factors localizing to centrosome and their relation with C-NAP1. **B)** High-resolution IF images reveal that UPF1 and DDX53 localize in interphase and mitotic centrosomes, respectively. **C)** Left, The box plot shows the distribution of cellular fitness growing significance of cellular targets for the indicated categories derived from the telomerase-immortalized RPE1 cell line hTERT-RPE1. $**P \leq 0.01$, $***P \leq 0.001$; Student's t-test. Right, the values of cellular fitness for each gene are reported comparing canonical and splicing genes relevant to centrosome.

Supplementary Figure 6

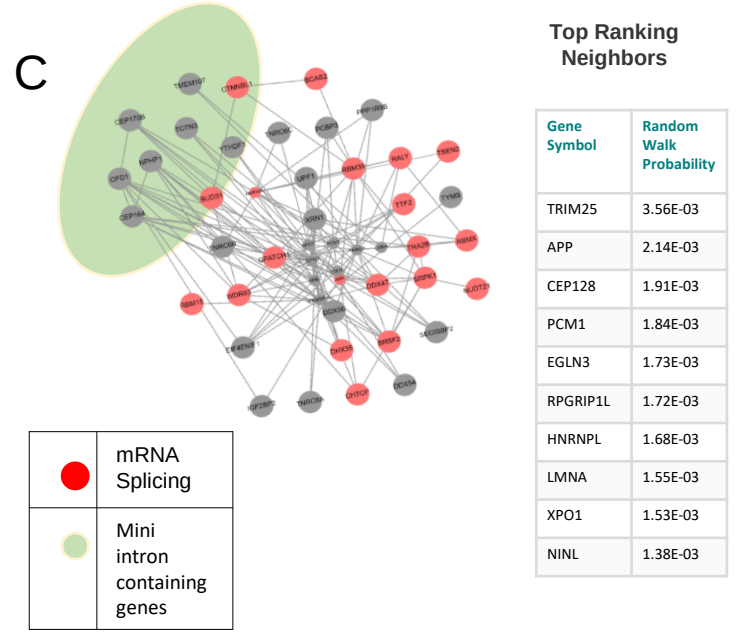
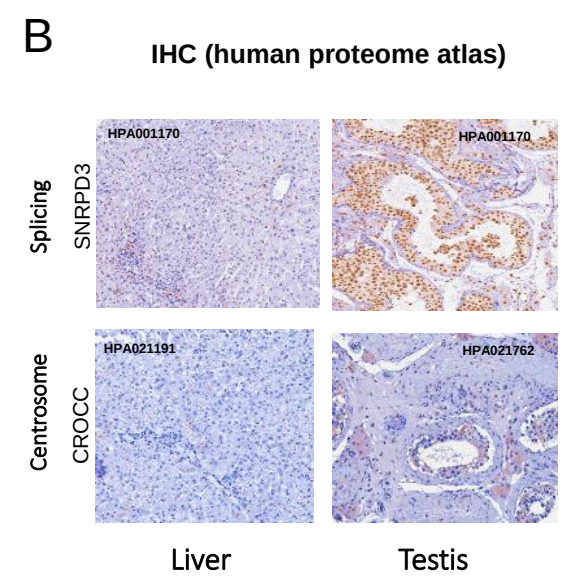
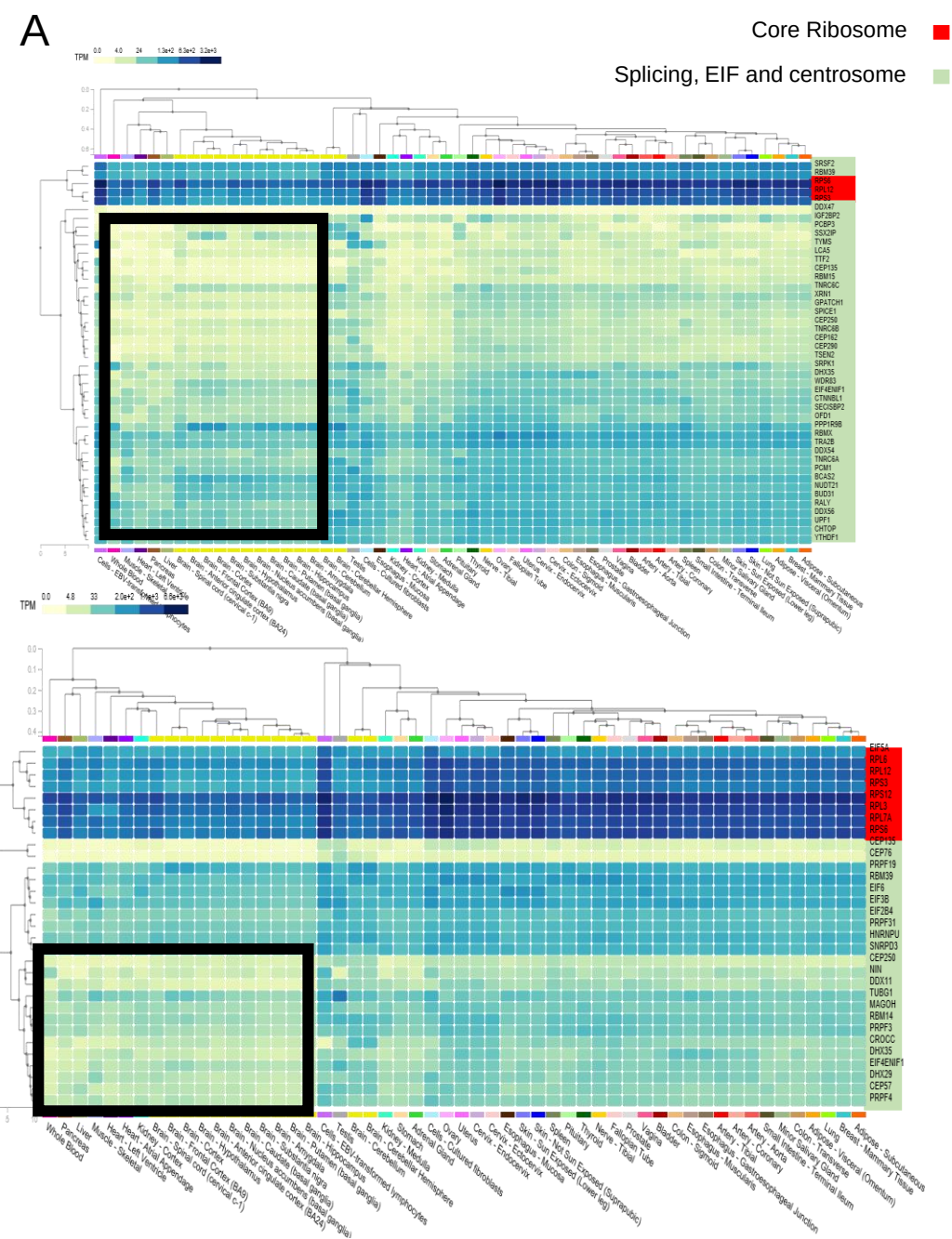
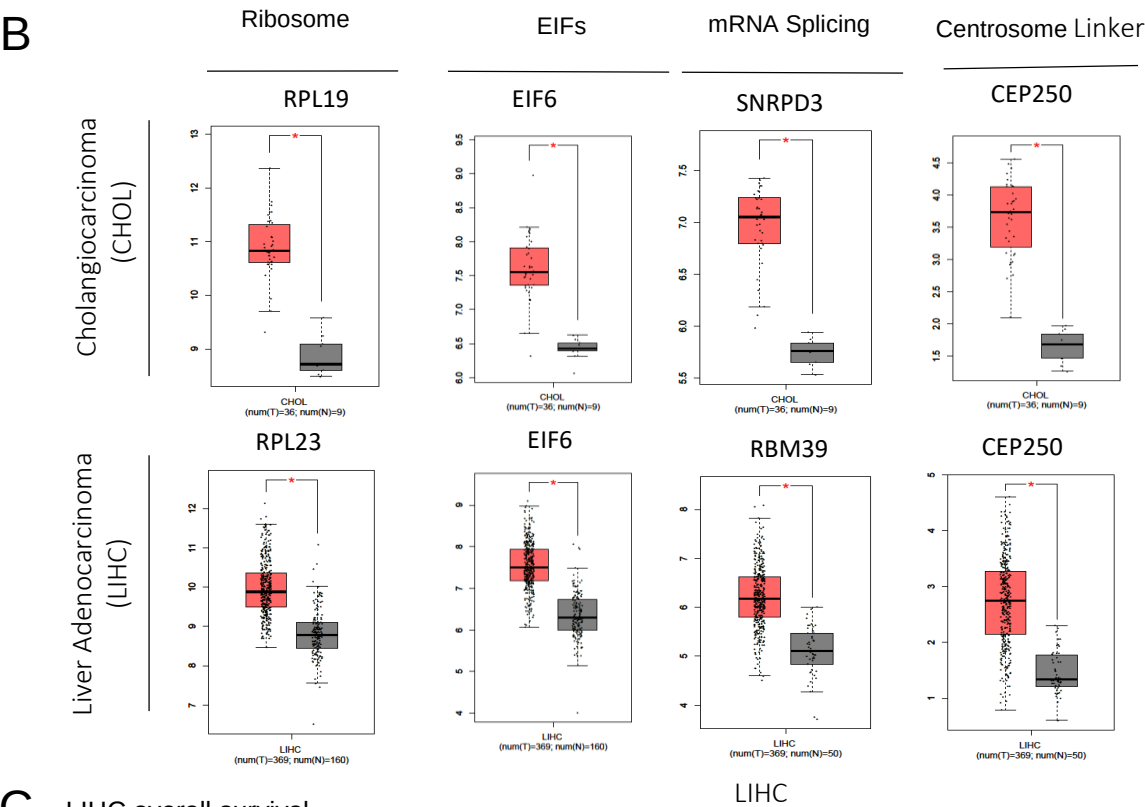
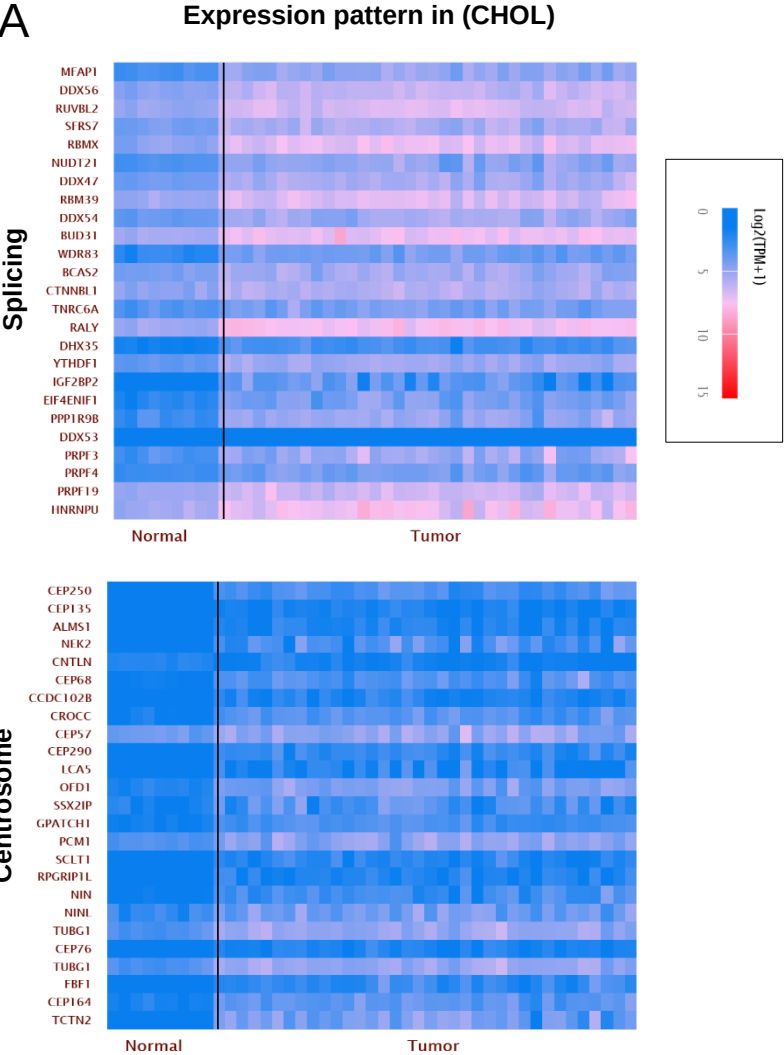


Figure S6. Gene expression profile of splicing and centrosome encoding genes are coordinated in tissue-specific manner **A)** Gene expression profile for the indicated categories across 54 non-diseased human tissues from the GTEx portal (Ref). Expression values are shown in TPM (transcripts per million). **B)** Representative IHC labelling for SNRPD3 and Rootletin (CROCC) in liver and testis tissues, respectively. **C)** Protein-Protein interaction map reveals a close proximity of ciliogenic mini intron containing genes and splicing regulators.

Supplementary Figure 7



C LIHC overall survival

Splicing Factor	HR(high)	Logrank p value
PRPF3	1,6	p=0.0093
PRPF31	1,7	p=0.003
PRPF19	1,8	P=0.0015
SNRPD1	2	p=0.00011
DHX35	1,5	p=0.015
RBM39	1,6	p=0.01

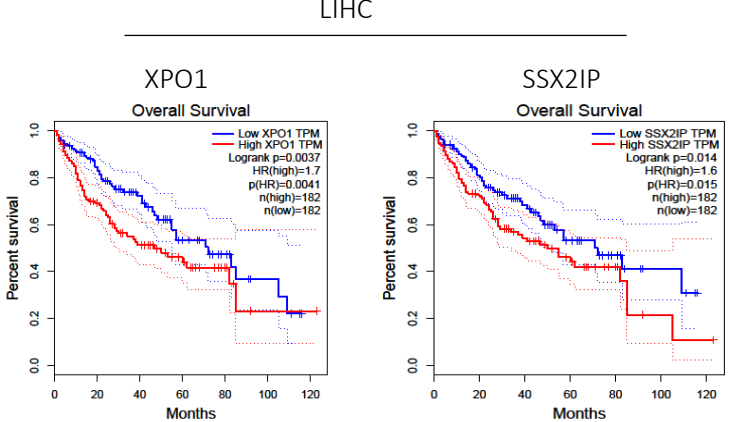
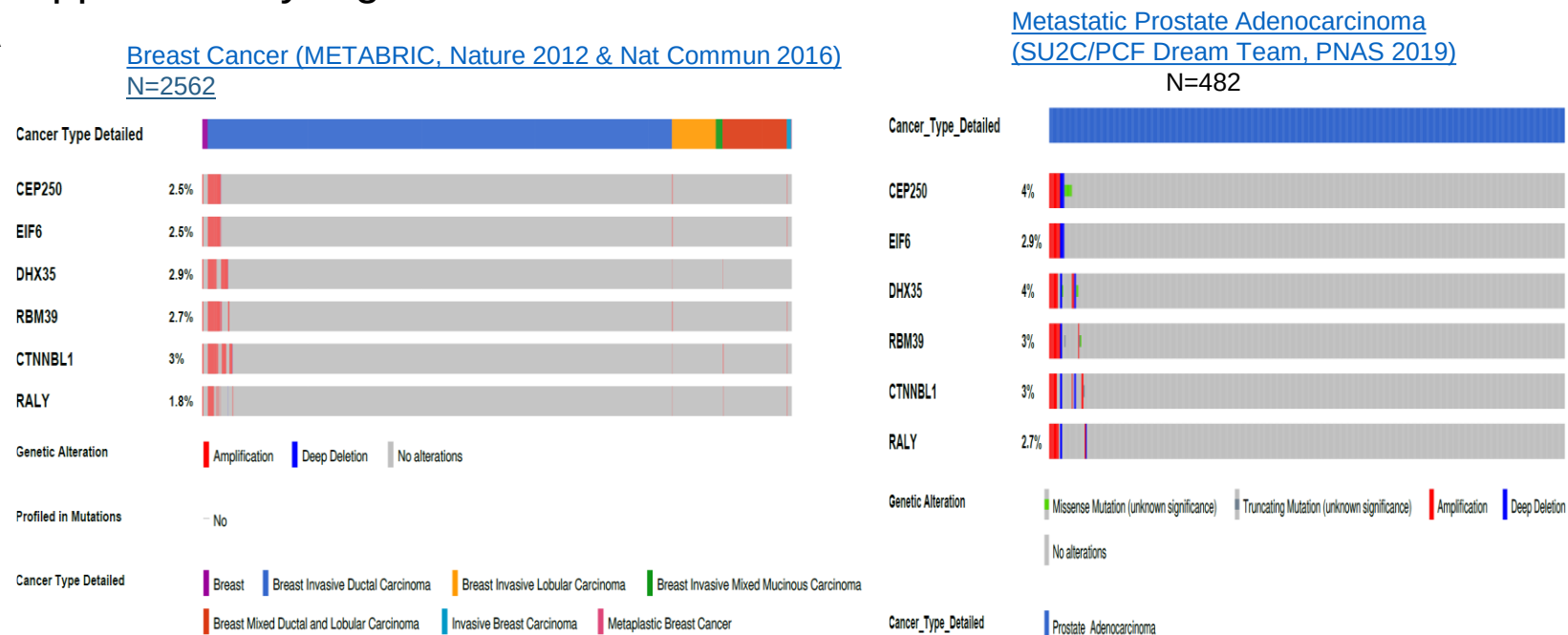


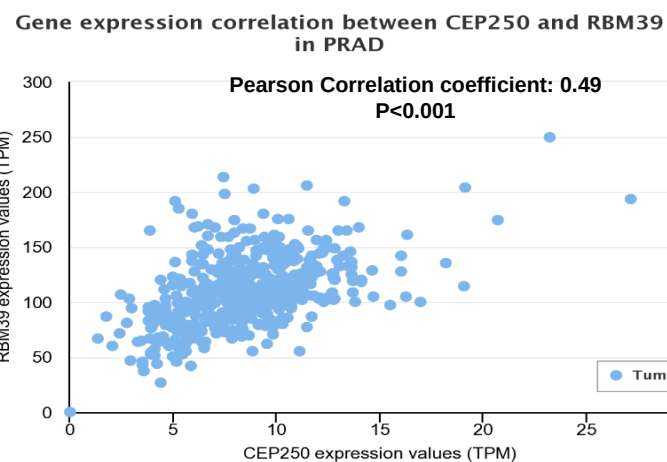
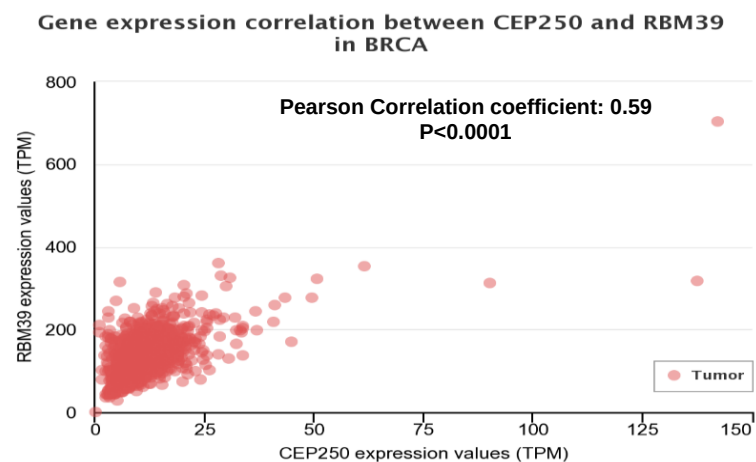
Figure S7. Co-alteration of Splicing and centrosome gene expression program in human diseases **A)** Heat maps showing the coordinated alteration of gene expression profile for splicing and centrosome genes in cholangiocarcinoma versus Non-tumoral tissues. **B)** The expression profile of the indicated genes in liver cancers and normal tissues is shown by Box-plot; *P<0,05. **C)** Left, the table shows over-expression of different splicing factors correlated with worse overall survival (OS) in LIHC. Right, LIHC patients with with high mRNA level of XPO1 and SSX2IP had poor prognosis by Kaplan–Meier analysis. HR: hazard ratio; OS: overall survival.

Supplementary Figure 8

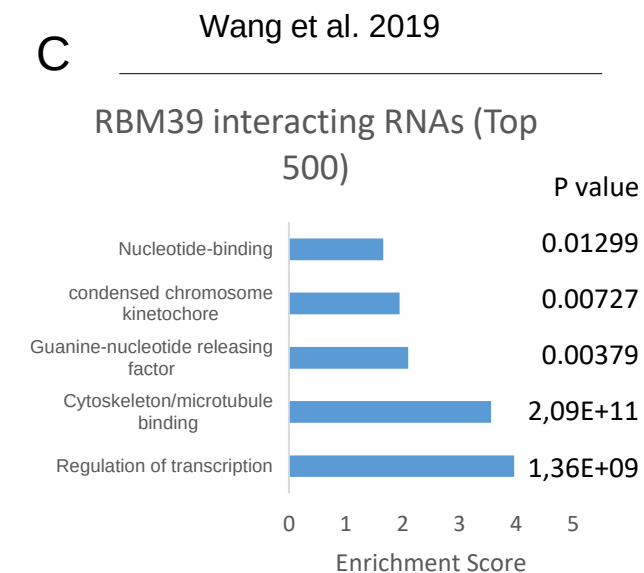
A



B



C



D

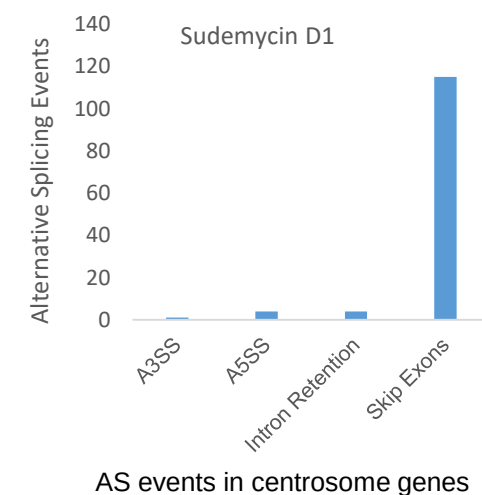


Figure S8. Whole genome amplification of identified gene module and effect of splicing inhibition on centrosome genes processing **A)** Co-amplification of gene module characterizes a subgroup of breast and prostate cancers, Data were extracted from cbiportal platform. **B)** Correlation between *CEP250* and *RBM39* expression levels in breast (BRCA) and prostate (PRAD) cancers. **C)** Gene ontology pathways analysis of the top-500 *RBM39* interacting RNAs. **D)** Alternative splicing events in centrosome genes following Sudemycin D1 treatment.

Table S1. A list of the Informatics Tools, software and publically available databases used for the work.

Database	Source	Approach	Ref
Proteome and Protein-Protein interaction			
BioGRID	https://thebiogrid.org/	Protein-Protein Interactions, chemical associations, and post-translational modifications (PTM) from 76,264 publications	Oughtred R et al. 2020
The Human Protein Atlas	https://www.proteinatlas.org/	To map all the human proteins in cells in tissues and organs various omics technologies, including antibody-based imaging, mass spectrometry-based proteomics, transcriptomics and systems biology.	Thul PJ et al. 2018
Protein Interaction of the Human Centrosome-Cilium Interface	http://prohits-web.hafenfeld.ca	protein interaction map of the human centrosome-cilium complexes using in vivo proximity-dependent biotinylation (BioID)	Gupta GD et al. 2015
Proteome on isolated centrosomes from HeLa S3 cells	www.landesbioscience.com/journals/cc/article/28896	Quantified centrosomal proteins during S and M phases using stable isotope labeling by amino acids in cell culture (SILAC) coupled with liquid chromatography-tandem mass spectrometry (LC-MS/MS)	Kimura H et al.2014
Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines	discover.nci.nih.gov/cellmineradb	Transcriptome and proteome for the NCI-60 together with relevant software tools	Guo T et al. 2019
To identify proteins from biochemically purified centrosomes in "Human lymphoblastic KE37" proteomics and spatial immune localization in isolated centrosomes from the young lamb thymus.	(http://www.embojournal.org). PXD003928	MS-based proteomics and SILAC Mass spectrometry, cryo Electron Tomography and immunogold assay	Jacobsen L. et al. 2011 Busselez J et al. 2019
Protein-protein interaction network of major centrosome proteins	https://thebiogrid.org/165943/publication/fgals3bp-regulates-centriole-biogenesis-and-centrosome-hypertrophy-in-cancer-cells.html	Tandem affinity purification and MS in human embryonic kidney cells (HEK293)	Fogeron ML et la. 2013
Transcriptomic			
Comparison of slow versus fasting cycling MCF10A cells	GSE122927	Gene expression based on RNA-seq data	Min M et al. 2019
GTEx: Genetic variation and gene expression across human tissues	https://gtexportal.org/home/	Gene expression based on RNA-seq data	GTEx Consortium, 2019
Profiles from PRPF31-mutated patient-derived retinal organoids and retinal pigment epithelium (RPE)	PRUEB22885 (human) and PRUNA417002 (mouse)	RNA-seq	Buskin A et al. 2018
GEPIA: cancer and normal gene expression profiling and interactive analyses	http://gepia.cancer-pku.cn/	A web-based tool to deliver results based on TCGA and GTEx data.	Tang Z et al. 2017
UALCAN: A portal for facilitating tumor subgroup gene expression and survival analyses.	http://ualcan.path.uab.edu/	a comprehensive, user-friendly, and interactive web resource for analyzing cancer OMICS data	Chandrashekar DS et al. 2017
cBioPorta: A Web Platform of Gene-Based Data Exploration on a significant of tumours	https://www.cbioportal.org/	genomic profile(s), such as mutations and copy number alterations, patient case set and gene sets of interest	Cerami E et al. 2012
Genetic			
Tool to identify minor intron-containing genes	https://midb.pnh.uconn.edu	position-weight matrices (PWM) of the consensus sequences of all annotated introns	Olthof, AM et al. 2019
DepMap: A portal to discover genetic dependencies related to cancer vulnerabilities	https://depmap.org/portal/	CRISPR-Cas9 approach to selectively knock out approximately 7460 genes in 324 genomically characterized cell lines representing 19 cancer tissues and assayed the requirement of each gene for the cellular fitness (viability) of cancer cells	Dempster, JM et al 2019
Pharmacological			
Cancer Therapeutics Response Portal (CTRP): links genetic and cellular features of cancer cell lines to small-molecule sensitivity	https://portals.broadinstitute.org/ctrp/	quantitatively measured the sensitivity (viability) of 860 characterized cancer-cell lines to Informer Set compounds	Basu, Bodycombe, Cheah, et al. 2013
CRISPR/Cas9 screen and Pharmacological targeting of RBM39 and other classical RNAbinding proteins (RBPs) in acute myeloid leukemia (AML)	GSE114558	RNA-seq data	Wang E et al. 2019
Splicing inhibition by spliceostatin A in HeLa cells	GSE72156	RNA-seq data	Yoshimoto R et al. 2017
Treatment of Rh18 cells with selenite, an SF3B1 inhibitor" leads to aberrant splicing event.	GSE102539	A poly(A) enriched RNA-seq transcriptome analyses.	Wu G et al. 2018
Mouse			
Gene expression pattern of single mouse embryonic stem cells (mESM) during cell cycle stages	E-MTAB-2805	single-cell RNA-seq data from mESCs	Buettner F et al. 2015

Table S2. Gene Ontology analysis of CNAP-1 interactome

CNAP-1 interactome (from BioGRID database)											
Annotatio Enrichment Score: 56.44891618546402											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini FDR
UP_KEYW	Ribonucleoprotein	67	#####	9,83E-52	RPL4, RPL5	239	296	20581	#####	2,24E-49	2,24E-49 1,95E-49
UP_KEYW	Ribosomal protein	57	#####	1,19E-48	RPL4, RPL5	239	185	20581	#####	2,71E-47	1,35E-47 1,18E-46
GOTERM	_GO:0019083~viral transcription	50	#####	1,10E-46	RPL4, RPL5	229	112	16792	#####	1,14E-43	1,14E-43 1,10E-43
GOTERM	_GO:0006614~SRP-dependent cotrans	47	#####	9,85E-47	RPL4, RPL5	229	94	16792	#####	1,02E-42	5,11E-44 4,93E-43
GOTERM	_GO:0000184~nuclear-transcribed mR	48	#####	1,83E-41	RPL4, RPL5	229	119	16792	#####	1,89E-38	6,32E-40 6,10E-40
GOTERM	_GO:0005840~ribosome	52	#####	3,07E-41	RPL4, RPL5	232	166	18224	#####	1,02E-38	1,02E-38 9,24E-40
GOTERM	_GO:0006413~translational initiation	49	#####	1,15E-39	RPL4, RPL5	229	137	16792	#####	1,19E-36	2,97E-37 2,87E-38
GOTERM	_GO:0003735~structural constituent o	56	#####	4,01E-38	RPL4, RPL5	233	222	16881	#####	1,31E-35	6,54E-37 6,10E-36
KEGG_PATH	hsa03010:Ribosome	50	#####	6,28E-36	RPL4, RPL5	140	136	6879	#####	6,91E-34	6,91E-34 6,72E-34
GOTERM	_GO:0006364~rRNA processing	52	#####	1,83E-34	RPL4, RPL5	229	214	16792	#####	1,89E-30	3,79E-32 3,66E-31
GOTERM	_GO:0006412~translation	54	#####	3,09E-33	RPL4, RPL5	229	253	16792	#####	3,21E-30	5,34E-31 5,16E-31
Annotatio Enrichment Score: 11.8706517417852											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini FDR
GOTERM	_GO:0005913~cell-cell adherens juncti	27	#####	6,61E+00	YWHAE, H	232	323	18224	#####	2,20E+04	2,00E+03 1,81E+04
GOTERM	_GO:0098641~cadherin binding involv	25	#####	1,92E+03	YWHAE, H	233	290	16881	#####	6,26E+05	1,25E+05 1,17E+06
GOTERM	_GO:0098609~cell-cell adhesion	23	#####	1,93E+05	YWHAE, V	229	271	16792	#####	2,00E+07	2,50E+07 2,41E+06
Annotatio Enrichment Score: 10.359223750542602											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini FDR
GOTERM	_GO:0000398~mRNA splicing, via splic	22	#####	3,06E+04	HSPA8, DC	229	222	16792	#####	3,17E+06	4,53E+06 4,38E+05
UP_KEYW	Spliceosome	16	#####	2,10E+05	HSPA8, DC	239	127	20581	#####	4,80E+06	4,80E+05 4,17E+05
UP_KEYW	mRNA splicing	21	#####	2,74E+04	HSPA8, DC	239	260	20581	#####	6,26E+06	5,69E+05 4,94E+05
UP_KEYW	mRNA processing	21	#####	2,07E+06	HSPA8, DC	239	332	20581	#####	4,72E+09	2,78E+08 2,41E+08
Annotatio Enrichment Score: 6.33314018114846											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini FDR
INTERPRO	IPR018316:Tubulin/FtsZ, 2-layer sand	9	#####	1,45E+05	TUBA1C, T	233	22	18559	#####	8,11E+05	3,08E+08 2,98E+08
SMART	_SM00865:SM00865	9	#####	1,72E+06	TUBA1C, T	131	22	10057	#####	2,14E+08	2,14E+07 2,10E+07
INTERPRO	IPR023123:Tubulin, C-terminal	9	#####	2,20E+06	TUBA1C, T	233	23	18559	#####	1,23E+07	3,08E+08 2,98E+08
INTERPRO	IPR008280:Tubulin/FtsZ, C-terminal	9	#####	2,20E+06	TUBA1C, T	233	23	18559	#####	1,23E+07	3,08E+08 2,98E+08
INTERPRO	IPR017975:Tubulin, conserved site	9	#####	2,20E+06	TUBA1C, T	233	23	18559	#####	1,23E+07	3,08E+08 2,98E+08
INTERPRO	IPR000217:Tubulin	9	#####	3,27E+06	TUBA1C, T	233	24	18559	#####	1,83E+09	3,65E+08 3,54E+07
SMART	_SM00864:SM00864	9	#####	3,88E+05	TUBA1C, T	131	24	10057	#####	4,81E+08	2,41E+08 2,37E+08
INTERPRO	IPR003008:Tubulin/FtsZ, GTPase dom	9	#####	4,76E+05	TUBA1C, T	233	25	18559	#####	2,66E+09	4,43E+08 4,29E+08
GOTERM	_GO:0007017~microtubule-based pro	8	#####	4,63E+08	TUBA1C, T	229	36	16792	#####	4,80E+11	4,37E+09 4,22E+11
KEGG_PATH	hsa05130:Pathogenic Escherichia coli	10	#####	6,41E+07	TUBA1C, T	140	51	6879	#####	7,05E+10	2,35E+11 2,29E+11
GOTERM	_GO:0005200~structural constituent o	10	#####	2,09E+11	TUBA1C, T	233	110	16881	#####	0.0067794	6,68E+11 6,23E+11
KEGG_PATH	hsa04540:Gap junction	8	#####	0.0019211	TUBA1C, T	140	88	6879	#####	0.19065110.0528305	0.0513896
UP_SEQ_F	nucleotide phosphate-binding region	11	#####	0.0042085	EEF1A1, TI	240	310	20063	#####	0.97762680.2711499	0.2681438
GOTERM	_GO:0003924~GTPase activity	10	#####	0.0051162	EEF1A1, TI	233	234	16881	#####	0.81215960.0725166	0.0676228
UP_KEYW	GTP-binding	11	#####	0.0068966	EEF1A1, TI	239	343	20581	#####	0.79358960.0507239	0.0440497
GOTERM	_GO:0005525~GTP binding	13	#####	0.0070211	HSP90AA1	233	384	16881	#####	0.89943770.0915562	0.0853775
KEGG_PATH	hsa04145:Phagosome	9	#####	0.0107755	TUBA1C, T	140	150	6879	#####	0.69630930.19755220.1921644	
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INTERPRO	IPR012677:Nucleotide-binding, alpha	17	#####	2,28E+08	RBM14, AI	233	264	18559	#####	1,27E+12	1,42E+11 1,37E+10
SMART	_SM00360:RRM	13	#####	1,83E+11	RBM14, AI	131	212	10057	#####	0.0022663	7,56E+11 7,44E+11
GOTERM	_GO:0000166~nucleotide binding	17	#####	2,65E+11	RBM14, H	233	348	16881	#####	0.0085937	7,19E+10 6,71E+11
INTERPRO	IPR000504:RNA recognition motif doi	13	#####	2,87E+11	RBM14, AI	233	226	18559	#####	0.01590670.0010689	0.0010363
Annotatio Enrichment Score: 2.8639676434030377											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini FDR
INTERPRO	IPR011545:DNA/RNA helicase, DEAD/	7	#####	2,22E+12	DDX17, D	233	69	18559	#####	0.11664660.0077510	0.0075148
GOTERM	_GO:0004004~ATP-dependent RNA he	7	#####	2,65E+10	DDX17, D	233	65	16881	#####	0.08281910.0061742	0.0057575
UP_SEQ_F	domain:Helicase C-terminal	7	#####	0.0018684	DDX17, D	240	108	20063	#####	0.81456670.1872615	0.1851854
INTERPRO	IPR001650:Helicase, C-terminal	7	#####	0.0023714	DDX17, D	233	108	18559	#####	0.73415120.0696450	0.0675232
UP_SEQ_F	domain:Helicase ATP-binding	7	#####	0.0024552	DDX17, D	240	114	20063	#####	0.89083720.2144431	0.2120657
SMART	_SM00490:HELICc	7	#####	0.0025881	DDX17, D	131	107	10057	#####	0.27482480.0704317	0.0692957
INTERPRO	IPR014001:Helicase, superfamily 1/2,	7	#####	0.0026003	DDX17, D	233	110	18559	#####	0.76610280.0725491	0.0703389
SMART	_SM00487:DEXDc	7	#####	0.0028399	DDX17, D	131	109	10057	#####	0.29718380.0704317	0.0692957