Supplemental Materials

Molecular Biology of the Cell

Viganó et al.

Supplemental Material

Figure S1: Comparison of randomly selected CIN and MIN cells.

(A) Table lists ploidy and chromosome numbers for 8 human cancer cell lines used in (B), including diploid telomerase-immortalized (hTERT) RPE1 cells, diploid microsatellite instable (MIN) and aneuploid chromosomally instable (CIN) cells. Chromosome counts were obtained from the American Tissue Culture Consortium (ATCC). (B) Hierarchical clustering based on the LC-MS/MS results for the cell lines listed in (A), using the tandem mass tag (TMT)-labeling approach. The vertical dimension depicts ~7.500 proteins detected in the indicated cell lines. The heat map shows the degree of deregulation versus the diploid control cell line hTERT-RPE1. Data are from a single biological replicate, conceived as a pilot experiment (see table S1).

Figure S2: Establishment of DLD-1-derived cell lines differing in ploidy.

(A) Left panel: micrographs show mitotic spreads stained with whole-chromosome DNA probes for the indicated chromosomes (chromosomes 3 and 4 in 2N, 4N and PTA; chromosomes 5 and 7 in Tr7 clones). Scale bars represent 10 μm. Right panel: histogram shows the frequencies of chromosome copy number counts. Values are normalized for the number of counted cells (n). Data are from two biological replicates. (B) Histograms shows the frequencies of chromosome mis-segregation events in trisomic clones. Data relate to Fig. 2A. Error bars represent SD. Values indicate the number of counted cells, data are from three biological replicates, unpaired two-tailed t-test. (C) Upper panel: Spindle geometry

measurements in metaphase cells. Scale bar represents 5 μm, DNA was stained with DAPI. Lower left panel: representative α-tubulin staining and schematic showing spindle geometry measurement approach. Lower right panels: dot plots showing mitotic spindle length, width and angle measurements for indicated cell lines. Horizontal bars show mean values, the numbers of counted cells are indicated, data are from two biological replicates. Two-tailed *t*-test: **P*<0.05, ***P*<0.01, ****P*<0.001 and *****P*<0.0001. (D) Left panel: micrographs of fixed cells stained with antibodies raised against the centriole maker CP110 and α-tubulin. Scale bar represents 5 μm, DNA was stained with DAPI. Right panel: dot plots show centrioles and centrosomes numbers in the indicated cell lines, using CP110 and Cep135 as markers for centrioles and centrosomes, respectively. Horizontal bars indicate mean values, numbers of counted cells are indicated, data are from two biological replicates.

Figure S3: Comparative proteomic analysis of DLD-1 derived cells.

(A) Box whisker plot shows the relative abundance of proteins (*versus* parental diploid DLD-1 cells) functionally associated with protein proteolysis, protein folding, autophagy, DNA damage and oxidative stress response. Each dot represents an incident of a significant ($p<0.1$) deregulation that was observed in the 4N clone or in at least one PTA clone or Tr7 clone. Tables on the right describe the GO terms that were considered for the analysis. (B) Box whisker plot showing the relative abundance (versus parental diploid DLD-1 cells) of proteins functionally related to type I interferon signaling. P-values for the proteins shown are below 0.05. Data relate to experiment shown in Fig. 4B, C and D. Data compiled in panels A and B are from biological triplicates (table S2). (C) Left panel: micrographs of cells treated

with BrdU and stained with anti-BrdU antibodies and DAPI. Acid denaturing of DNA was omitted to avoid prevalent nuclear staining; extra-nuclear BrdU foci represent cytoplasmic DNA. Scale bar represents 10 μm. Right panel: box whisker plot showing the number of cytoplasmic BrdU foci for the indicated cell lines. Data come from biological duplicates.

Figure S4: Targeted analysis of protein expression in DLD-1-derived cells.

(A, B) Tables show an enrichment analysis of the 500 most deregulated phospho-peptides per cell line based on the TSG/OG and CIN/cell division inclusion lists. The number of inclusion list matches (signlList) and non-matches (totSign) were compared to random inclusion list matches (nonSignlList) and non-matches (totNonSign) in a human proteome background. Significance (ftPValue) was calculated using Fisher's exact test. Shaded areas highlight the most significant enrichments. We note that one of the two trisomic clones showed an apparently significant enrichment, but because this was seen in only one of two near-identical clones, the significance, if any, of this observation is difficult to assess (C) Dot plots show the relative abundance of selected mitotic proteins in 4N, PTA and Tr7 clones. Note that a less stringent p-value cut off of 0.1 was applied. (D) Dot plots show the relative abundance of proteins belonging to the MCM and ORC complexes in 4N, PTA and Tr7 clones. Data compiled in panels C and D come from biological triplicates (table S4)

Figure S5: Comparative phospho-proteomic analysis of DLD-1 derived cells.

(A, B) Tables list the results of a gene ontology (GO)-term enrichment analysis of phospho-peptides up-regulated across 4N and PTA clones (A) or 4N and Tr7 clones (B). Enrichment

analysis was carried out for the 500 most deregulated phospho-peptides per condition ($p>0.05$), the 20 most significant enrichments are shown.

Figure S6: Targeted analysis of protein phosphorylation in DLD-1-derived cells.

(A, B) STRING functional network analysis of the phospho-peptides belonging to clusters shown in (Fig. 5E). Nodal connections are based on a confidence value of 0.9 using experimental and database evidence. Solid lines indicate intra-network, dashed lines inter-network connections. (C, D) STRING functional network analysis of the phospho-peptides obtained by clustering through the fuzzy C-means algorithm, as shown in Fig. 5F. Nodal connections are based on a confidence value of 0.9 using experimental and database evidence. Solid lines indicate intra-network, dashed lines inter-network connections.

Figure S7: Targeted analysis of protein phosphorylation in DLD-1-derived cells.

(A) Tables show an enrichment analysis of the 500 most deregulated phospho-peptides per cell line, using the CIN/cell division inclusion list. The number of inclusion list matches (signlList) and non-matches (totSign) were compared to random inclusion list matches (nonSignlList) and non-matches (totNonSign) in a human proteome background. Significance (ftPvalue) was calculated using Fisher's exact test. Shaded areas highlight the most significant enrichments. (B) Dot plot shows selected detection ratios of regulatory phosphorylation sites of the centrosome and mitotic spindle kinase Aurora A (AURKA P-T288), the mitotic kinase Cdk1 (CDK1 P-T14, P-Y15), the cell cycle checkpoint kinase Chk1 (CHK1 P-S286, CHK1 P-S301) and the mitotic spindle kinase Plk1 (Plk1 P-T210). Dashed lines indicate a 2-fold cutoff. (C) Table lists the p-values for phospho-peptide measurements

shown in (B), without applying a p-value cutoff. Data compiled in panels A and B come from biological triplicates (table S4).

Table S1: Raw data (spreadsheet) summarizing results from TMT of 8 CIN and MIN cell lines. The first three columns describe the accession number (AC), gene name and protein description of each identified protein. The columns in grey show the relative abundance (log2 ratio versus RPE1) for each entrance in all the considered cell lines. Note that this pilot experiment was only carried out once; hence, no statistical tests for deregulation could be applied.

Table S2: Raw data (spreadsheets) summarizing analyses of TMT data. The first spreadsheet contains TMT data of diploid, tetraploid and PTA clones. The first three columns describe the accession number (AC), gene name and protein description of each identified protein. TRUE or FALSE refer to membership of a given protein to CIN/Cell Division, TSGs or OGs list. GO indicate the Gene Ontology annotation relative to Cellular Component (cc), Molecular Function (mf) and Biological Process (bp). The columns in grey show the relative abundance (log2 ratio versus diploid DLD-1) for each entrance in all the considered cell lines, and respective p-values and q-values (False discovery rates). Note that this experiment was performed in biological triplicates. The second spreadsheet contains the same analysis, as described above, for diploid, tetraploid and two trisomic clones. Relative abundance was calculated versus the diploid cell line. The third spreadsheet lists the 18 commonly deregulated proteins (between 4N and two trisomic clones).

Table S3: Table refers to Figure 4A and lists only significant proteins, with at least a 1.5 fold change *versus* 2N (p-value cut-off <0.1). Spreadsheets one to four are related to oxidative stress, protein folding, protein lysis and autophagy GO terms, respectively.

Table S4: The first spreadsheet contains the components that make up the inclusion lists of tumor suppressor genes (TSGs) and oncogenes (OGs), used for targeted analyses. The second spreadsheet contains the components that make up the CIN/Cell Division inclusion list, used for targeted analysis. These inclusion lists were generated as described in the Materials and methods section.

Table S5: Raw data (spreadsheet) summarizing the results of the analyses of phospho-enrichment experiments. The first spreadsheet lists phospho-enriched peptides of diploid, tetraploid and PTA clones. The first four columns describe the identified peptide, the accession number (AC) of the corresponding protein, protein descriptions and type of post-translational modifications (ptm). The subsequent columns indicate the numbers of ptms per identified peptide, the modified residue (*), and the position of the ptm within the protein. TRUE or FALSE refer to the membership of each protein in the CIN/Cell Division, TSG or OG inclusion lists. GO indicate the Gene Ontology annotation relative to Cellular Component (cc), Molecular Function (mf) and Biological Process (bp). The columns in grey show the relative phosphorylation level (log2 ratio versus diploid DLD-1) for each entrance in all considered cell lines, and respective p-values and q-values (False discovery rates). Note that this experiment was performed in biological triplicates. The second spreadsheet

contains the same analysis, as described above, for diploid, tetraploid and two trisomic clones. Relative abundance was calculated versus the diploid cell line.

Table S6: Venn diagram analyses. TRUE or FALSE in the spreadsheets refer to membership of a given protein to the Venn diagram in 4N plus PTA clones (first spreadsheet) or 4N plus trisomic clones (second spreadsheet). Venn diagrams were obtained by selecting the 500 most deregulated phospho-peptides per cell line (based on an FDR of <10%, yielding a total of 1410 phospho-peptides from 807 proteins). Note that this experiment was performed in biological triplicates.

Table S7: Fuzzy C-means algorithm analysis. Data for this analysis were obtained from the same biological experiments (in triplicate) as used for Table S5. The first and second spreadsheets list phospho-peptides referring to Figure 5E. The third, fourth and fifth spreadsheets list phospho-peptides referring to Figure 5F. The first columns describe the properties of phosphopeptides as described in Table S5. In subsequent columns, log2 ratios (sample abundance versus 2N) were normalized to have a standard deviation of 1 and a mean of 0 (z-score). The last columns represent mFuzz cluster membership values.

Table S8: Drug screening assay spreadsheet. List of targets, incubation time, IC_{50} and IC_{50} average for each of the tested compounds. Note that biological triplicates were performed only for the compounds that showed a significant IC_{50} difference in the first run. Two-tailed *t*-test was used for the significance analysis. NA: no activity was detectable at highest dose of compound.

Figure S1

A

	Name	Ploidy	Chromosome Number
hTERT	RPE1	Diploid	46
MIN	HCT116	Diploid	46
	DLD-1	Diploid	46
	RKO	Diploid	46-50
CIN	SW480	Aneuploid	Hypotriploid
	HT29	Aneuploid	71
	Hela-S3	Aneuploid	76-80
Other	Sw837	Hypodiploid	40

B

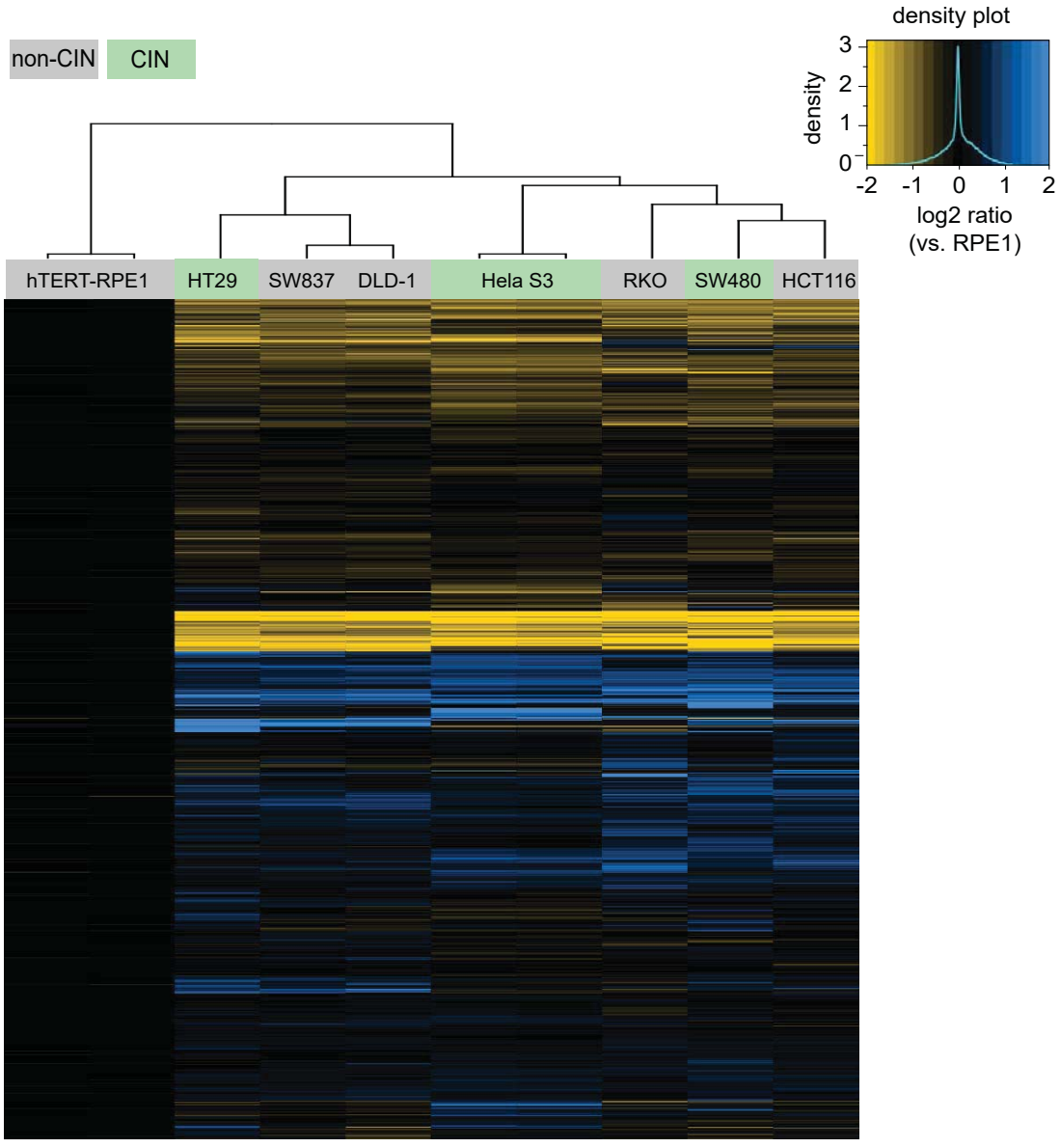


Figure S2

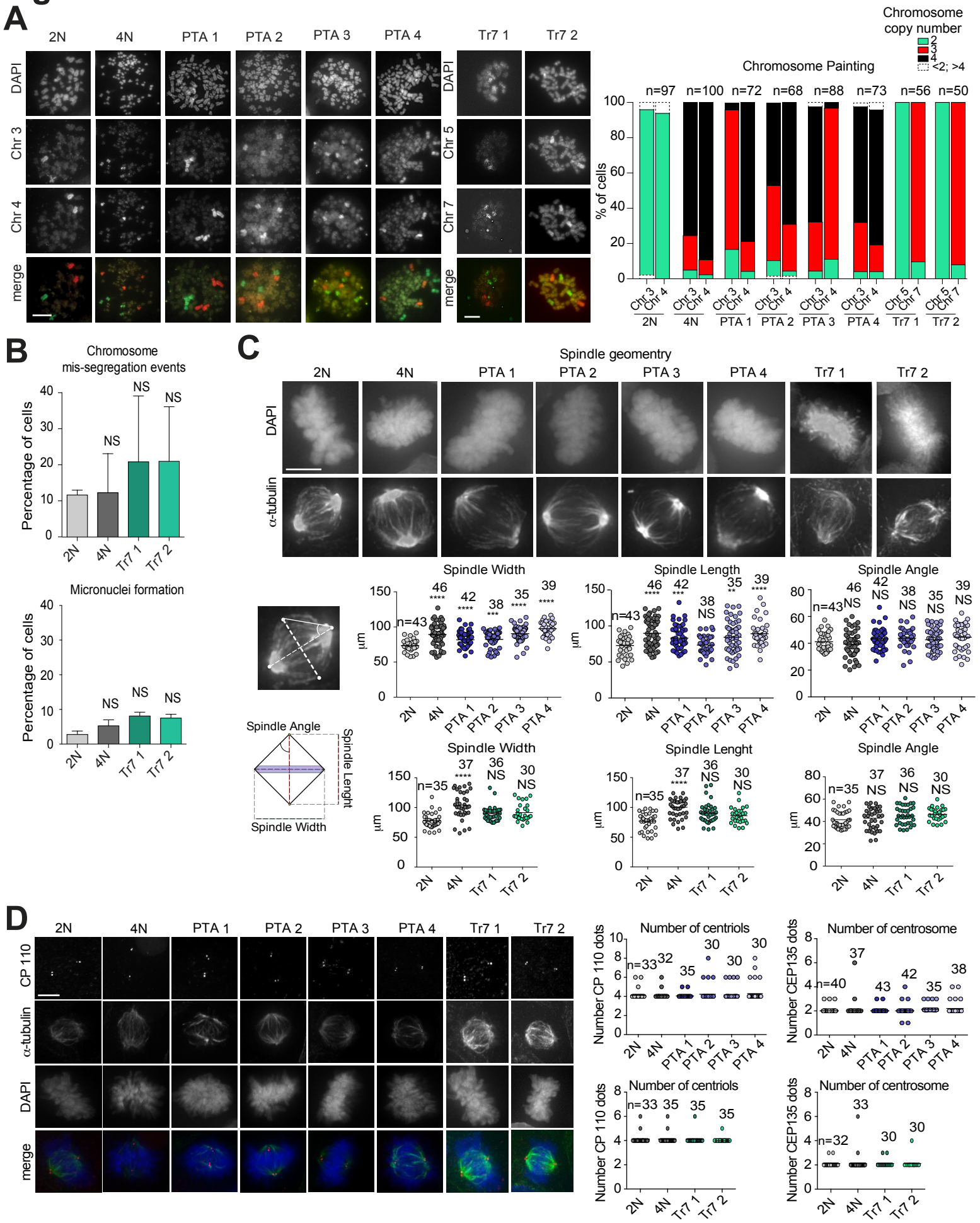
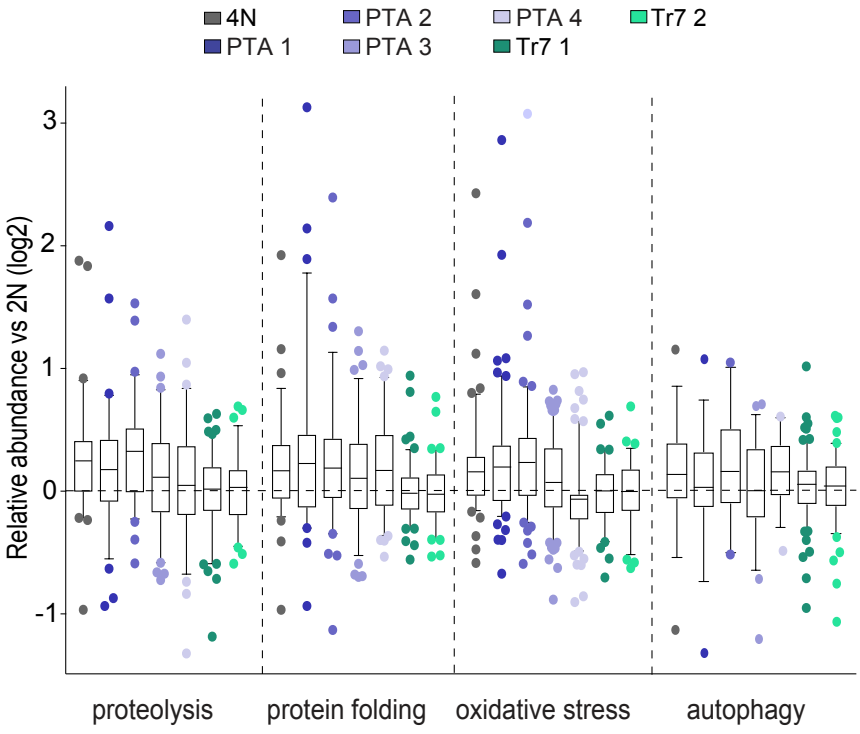

A
2N
4N
PTA 1
PTA 2
PTA 3
PTA 4
Tr7 1
Tr7 2
DAPI
Chr 3
Chr 4
Chr 5
Chr 7
merge
Chromosome copy number
2
3
4
<2; >4
Chromosome Painting
n=97
n=100
n=72
n=68
n=88
n=73
n=56
n=50
% of cells
B
Chromosome mis-segregation events
Percentage of cells
NS
Micronuclei formation
C
Spindle geometry
α-tubulin
Spindle Width
Spindle Length
Spindle Angle
Spindle Lenght
µm
n=43
n=35
D
CP 110
Number of centriols
Number CP 110 dots
Number of centrosome
Number CEP135 dots

Figure S3

A



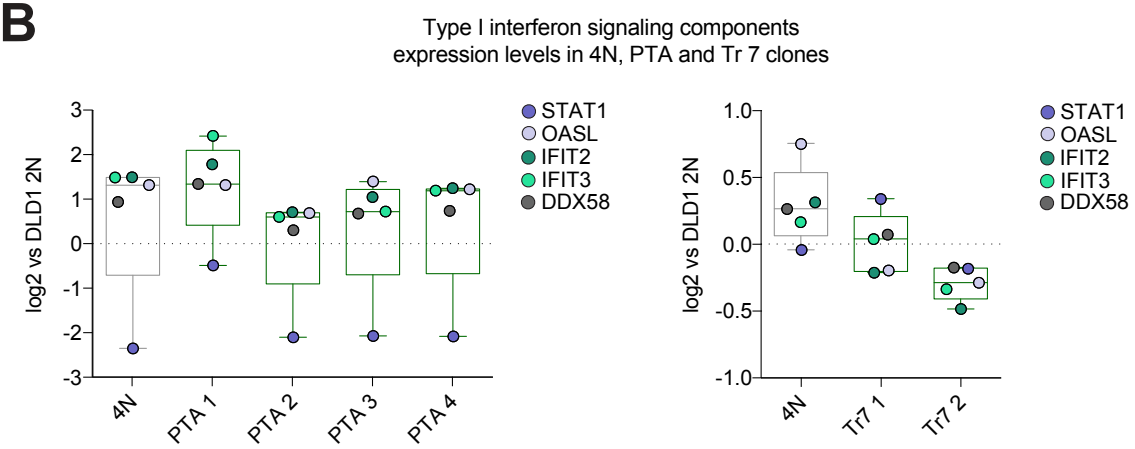
GO term Proteolysis	
GO:0006508	proteolysis

GO term Protein Folding	
GO:0006457	protein folding
GO:0034975	protein folding in endoplasmic reticulum

GO term Oxidative Stress	
GO:0006979	response to oxidative stress
GO:0034599	cellular response to oxidative stress
GO:1902882	regulation of response to oxidative stress
GO:1902883	negative regulation of response to oxidativ stress
GO:1902884	positive regulation of response to oxidative stress
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress
GO:0043619	regulation of transcription from RNA polymeras II promoter in response to oxidative stress
GO:0032938	negative regulation of translation response to oxidative stress
GO:0036475	neuron death in response to oxidative stress
GO:1900407	regulation of cellular response to oxidativ stress
GO:0001306	age-dependent response to oxidative stress

GO term Autophagy	
GO:0006914	autophagy
GO:0016236	macroautophagy
GO:0016241	regulation of macroautophagy
GO:0010506	regulation of autophagy
GO:0075044	autophagy of host cells involved in interaction with symbiont
GO:0039521	suppression by virus of host autophagy
GO:0034727	picemeal microautophagy of nucleus

B



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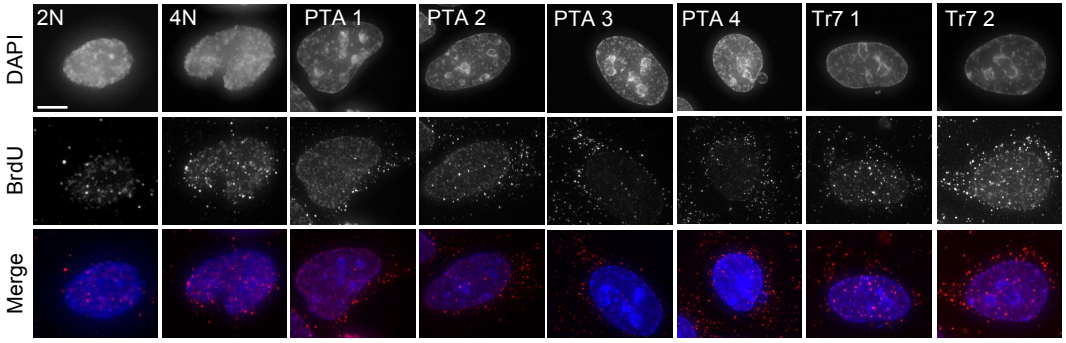


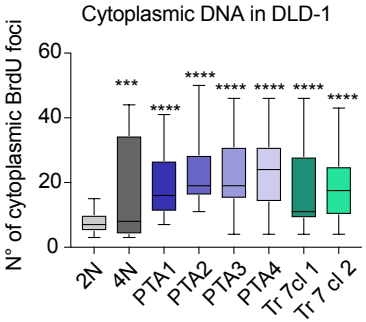


Figure S4

A

Tumour suppressor genes (TSG)

TSG enrichment analysis of proteins up-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	6	145	175	5486	0.3374176
PTA 1	3	128	182	5479	0.7905782
PTA 2	3	143	181	5480	0.8425621
PTA 3	0	108	182	5479	1.0000000
PTA 4	2	156	181	5480	0.9593175

TSG enrichment analysis of proteins down-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	4	145	175	5486	0.6771092
PTA 1	0	169	182	5479	1.0000000
PTA 2	1	153	181	5480	0.9920951
PTA 3	3	189	182	5479	0.9425012
PTA 4	2	140	181	5480	0.9387884

TSG enrichment analysis of proteins up-regulated in 4N and Tr 7 cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	3	157	213	7160	0.8381178
Tr7 d1	1	155	213	7160	0.9882724
Tr7 d2	2	132	215	7158	0.8997608

TSG enrichment analysis of proteins down-regulated in 4N and Tr 7 cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	3	137	213	7160	0.7682216
Tr7 d1	5	139	213	7160	0.4109171
Tr7 d2	2	164	215	7158	0.9520510

Oncogenes (OG)

OG enrichment analysis of proteins up-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	1	150	87	5574	0.9011513
PTA1	1	131	88	5573	1.0000000
PTA 2	0	146	89	5572	1.0000000
PTA 3	0	108	89	5572	1.0000000
PTA 4	2	156	89	5572	0.7117185

OG enrichment analysis of proteins down-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSig	ftPValue
4N	4	145	87	5574	0.2099882
PTA1	4	165	88	5573	0.2815287
PTA 2	3	151	89	5572	0.4444776
PTA 3	3	189	89	5572	0.5862782
PTA 4	1	141	89	5572	0.8922519

OG enrichment analysis of proteins up-regulated in 4N and Tr 7 cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	4	156	104	7269	0.2017603
Tr7 d1	4	152	105	7268	0.1946339
Tr7 d2	4	130	105	7268	0.1353750

OG enrichment analysis of proteins down-regulated in 4N and Tr 7 cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	1	139	104	7269	0.8612769
Tr7 d1	0	144	105	7268	1.0000000
Tr7 d2	0	166	105	7268	1.0000000

B

CIN/Cell division inclusion list

Enrichment analysis of proteins up-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	13	138	711	4950	0.9289159
PTA 1	15	116	699	4962	0.6477453
PTA 2	21	125	700	4961	0.2957998
PTA 3	9	99	706	4955	0.9108165
PTA 4	10	148	706	4955	0.9916212

Enrichment analysis of proteins down-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSIgn	ftPValue
4N	11	137	711	4962	0.4440535
PTA 1	22	147	699	4962	0.4440535
PTA 2	15	139	700	4961	0.8415546
PTA 3	21	171	706	4955	0.7450646
PTA 4	20	122	706	4955	0.3435905

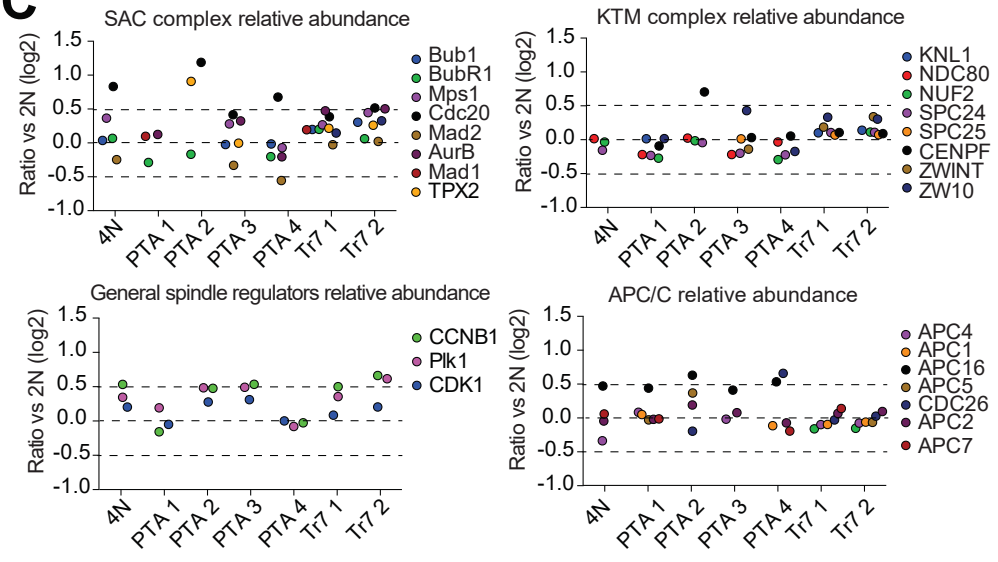
Enrichment analysis of proteins up-regulated in 4N and Tr 7 cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	11	149	681	6692	0.8624752
Tr7 d1	20	136	679	6694	0.1097800
Tr7 d2	19	115	680	6693	0.0605936

Enrichment analysis of proteins down-regulated in 4N and Tr 7 cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	12	128	681	6692	0.6403011
Tr7 d1	5	139	679	6694	0.9959316
Tr7 d2	5	161	680	6693	0.9990127

C



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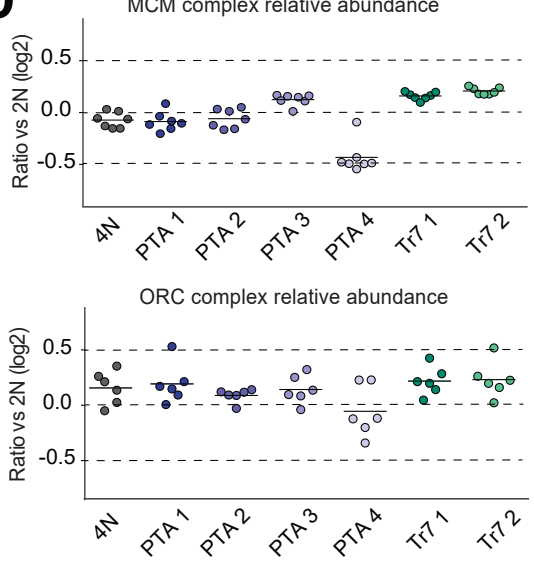


Figure S5

A

Cell cycle and cytoskeleton-related processes RNA-related processes Nucelar pore-related processes

Enrichment analysis on cluster of up-regulations in PTA cells

GO.ID	Term	Significant	weight01Fisher
GO:0045944	positive reg. of transcription from RNA Poll II promoter	19	2.0e-11
GO:0016925	protein sumoylation	7	1.8e-07
GO:0007186	G-protein coupled receptor signaling	8	1.0e-06
GO:0045892	negative regulation of transcription	22	1.2e-06
GO:0008284	positive regulation of cell proliferation	10	1.9e-06
GO:0070527	platelet aggregation	4	5.6e-06
GO:0035329	hippo signaling	4	1.5e-05
GO:1904951	positive regulation of establ. of protein localizaition	10	1.7e-05
GO:0030261	chromosome condensation	4	2.6e-05
GO:0007267	cell-cell signaling	11	3.5e-05
GO:0000281	mitotic cytokinesis	4	7.6e-05
GO:0000122	negative reg. of transcription from RNA Poll II promoter	10	7.7e-05
GO:0031032	actomyosin structure organization	7	8.5e-05
GO:0006260	DNA replication	8	9.1e-05
GO:0060560	developmental growth involved in morphogenesis	6	0.00013
GO:0006999	nuclear pore organization	3	0.00013
GO:0043066	negative regulation of apoptotic process	12	0.00014
GO:0031047	gene silencing by RNA	7	0.00014
GO:0015031	protein transport	26	0.00016
GO:1902589	single-organism organelle organization	58	0.00017

Enrichment analysis on cluster of up-regulations in 4N and PTA cells

GO.ID	Term	Significant	weight01Fisher
GO:0051301	cell division	28	2.0e-14
GO:0000226	microtubule cytoskeleton organization	24	1.7e-10
GO:0030261	chromosome condensation	7	1.5e-09
GO:0006406	mRNA export from nucleus	10	4.5e-08
GO:0006355	regulation of transcription	54	5.2e-08
GO:0006325	chromatin organization	23	3.7e-07
GO:0000281	mitotic cytokinesis	6	5.4e-07
GO:0007077	mitotic nuclear envelope disassembly	6	1.2e-06
GO:0007018	microtubule-based movement	9	1.4e-06
GO:0045944	positive reg. of transcription from RNA Poll II promoter	15	2.2e-06
GO:0000070	mitotic sister chromatid segregation	11	4.2e-06
GO:0007049	cell cycle	62	6.3e-06
GO:0000381	regulation of alternative mRNA splicing	5	8.2e-06
GO:0006606	protein import into nucleus	12	1.2e-05
GO:0070925	organelle assembly	21	1.3e-05
GO:0030154	cell differentiation	51	2.0e-05
GO:0006998	nuclear envelope organization	10	2.1e-05
GO:1900034	regulation of cellular response to heat	6	2.2e-05
GO:0031047	gene silencing by RNA	7	2.4e-05
GO:0001764	neuron migration	5	2.5e-05

B

Cell cycle and cytoskeleton-related processes RNA-related processes

Enrichment analysis on cluster of up-regulations in Tr 7 cells

GO.ID	Term	Significant	weight01Fisher
GO:0045944	positive reg. of transcription from RNA Poll II promoter	14	1.7e-06
GO:0000902	cell morphogenesis	14	2.8e-05
GO:0031397	negative regulation of protein ubiquitination	5	6.1e-05
GO:0043065	positive regulation of apoptotic process	10	7.8e-05
GO:0006355	regulation of transcription	33	0.00019
GO:0008283	cell proliferation	21	0.00026
GO:0008285	negative regulation of cell proliferation	8	0.00045
GO:0007507	heart development	10	0.00060
GO:1902041	regulation of extrinsic apoptotic signaling	3	0.00073
GO:0030433	ER-assoc. ubiquitin-dependent protein breakdown	3	0.00073
GO:0001892	embryonic placenta development	4	0.00090
GO:0001510	RNA methylation	3	0.00092
GO:0035329	hippo signaling	3	0.00092
GO:0032990	cell part morphogenesis	6	0.00115
GO:2000045	regulation of G1/S transition of mitotic cell cycle	4	0.00136
GO:0051028	mRNA transport	6	0.00157
GO:0030216	keratinocyte differentiation	4	0.00163
GO:0043623	cellular protein complex assembly	8	0.00168
GO:0016925	protein sumoylation	4	0.00180
GO:0035023	regulation of Rho protein signal transdu...	4	0.00180

Enrichment analysis on cluster of up-regulations in 4N and Tr 7 cells

GO.ID	Term	Significant	weight01Fisher
GO:0042733	embryonic digit morphogenesis	3	2.5e-05
GO:0043266	regulation of potassium ion transport	3	3.5e-05
GO:0031532	actin cytoskeleton reorganization	4	3.5e-05
GO:0086003	cardiac muscle cell contraction	3	4.6e-05
GO:0071805	potassium ion transmembrane transport	3	4.6e-05
GO:0032663	regulation of interleukin-2 production	3	4.6e-05
GO:0086001	cardiac muscle cell action potential	3	6.0e-05
GO:0000281	mitotic cytokinesis	3	0.00012
GO:0016032	viral process	8	0.00015
GO:0043066	negative regulation of apoptotic process	7	0.00032
GO:0048589	developmental growth	5	0.00042
GO:0008283	cell proliferation	10	0.00073
GO:0007010	cytoskeleton organization	11	0.00131
GO:0030216	keratinocyte differentiation	3	0.00135
GO:1902305	regulation of sodium ion transmembrane transport	2	0.00161
GO:1903115	regulation of actin filament-based movement	2	0.00161
GO:0086065	cell communication involved in cardiac conduction	2	0.00161
GO:2000106	regulation of leukocyte apoptotic processes	2	0.00161
GO:0032456	endocytic recycling	2	0.00161
GO:0034766	negative regulation of ion transmembrane transoport	2	0.00161

Figure S6

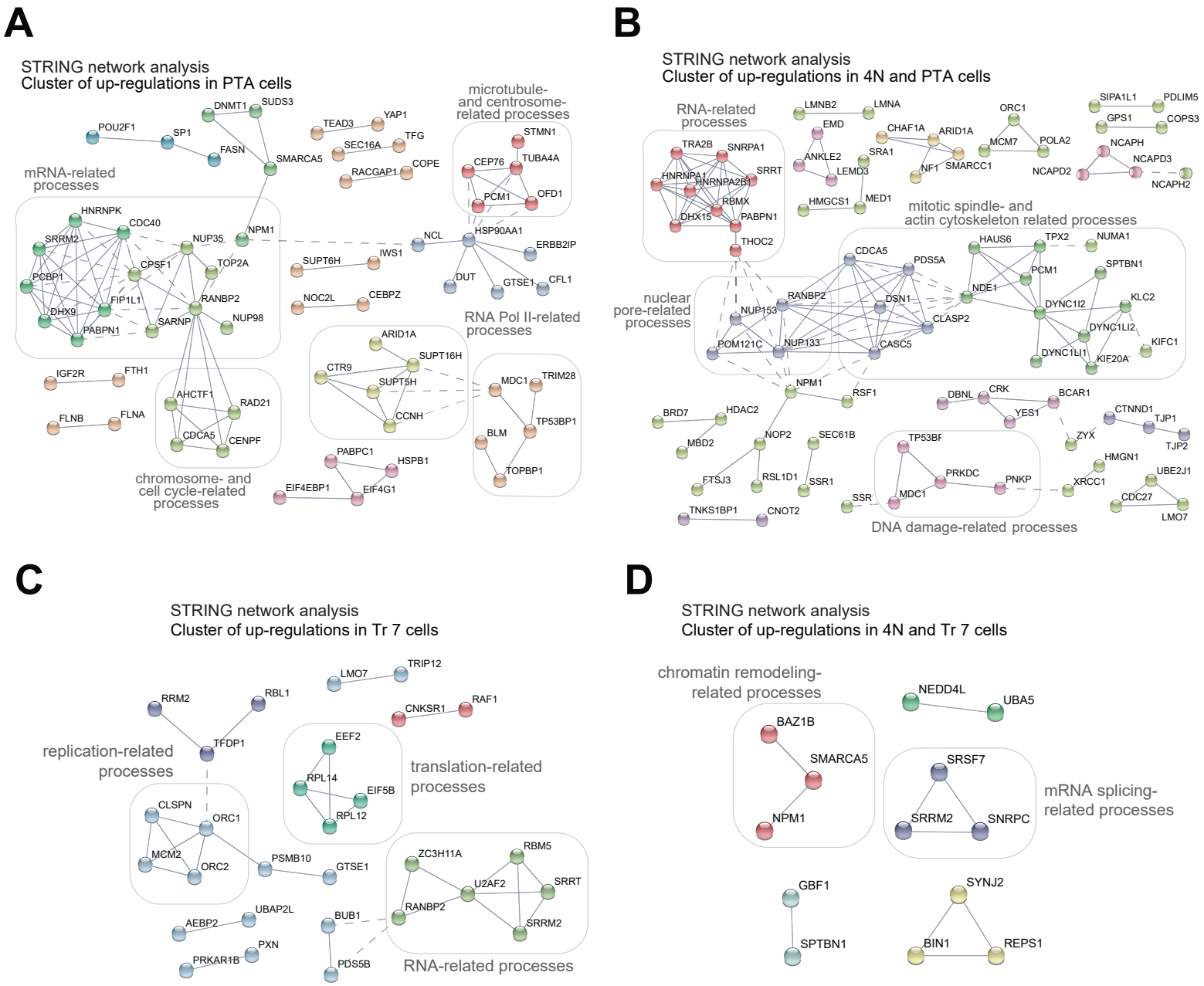

A
STRING network analysis
Cluster of up-regulations in PTA cells
mRNA-related processes
microtubule- and centrosome-related processes
RNA Pol II-related processes
chromosome- and cell cycle-related processes
B
STRING network analysis
Cluster of up-regulations in 4N and PTA cells
RNA-related processes
mitotic spindle- and actin cytoskeleton related processes
nuclear pore-related processes
DNA damage-related processes
C
STRING network analysis
Cluster of up-regulations in Tr 7 cells
replication-related processes
translation-related processes
RNA-related processes
D
STRING network analysis
Cluster of up-regulations in 4N and Tr 7 cells
chromatin remodeling-related processes
mRNA splicing-related processes

Figure S7

A

CIN/cell division inclusion list enrichment analysis of the most deregulated phospho-peptides (500 phospho-peptides per condition)

phospho-peptides up-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	80	324	2563	12305	0.1466766
PTA 1	94	322	2551	12317	0.0119480
PTA 3	79	260	2556	12312	0.0113770
PTA 4	62	214	2562	12306	0.0393165

phospho-peptides up-regulated in Tr7cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	55	223	1326	7133	0.0735379
Tr7d1	57	204	1342	7117	0.5997863
Tr7d2	56	216	1319	7140	0.0405239

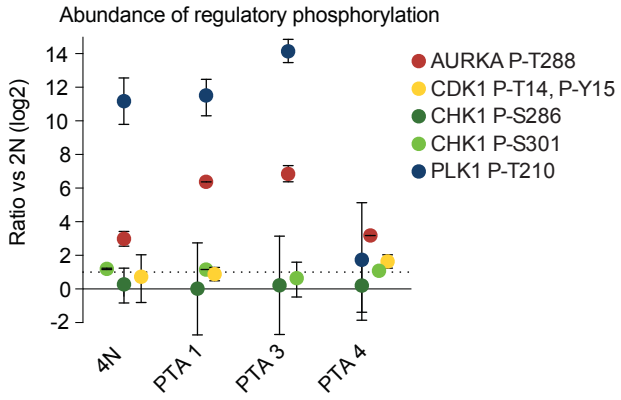
phospho-peptides down-regulated in 4N and PTA cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	14	82	2563	12305	0.7590456
PTA 1	12	72	2551	12317	0.7648565
PTA 3	32	139	2556	12312	0.8686990
PTA 4	33	191	2562	12306	0.8217455

phospho-peptides down-regulated in Tr7cells

	signIList	totSign	nonSignIList	totNonSign	ftPValue
4N	37	185	1326	7133	0.3941695
Tr7d1	39	220	1342	7117	0.6436645
Tr7d2	43	185	1319	7140	0.1498234

B



C

p-values for selected phopho-peptides

Kinase,	P-site	role of P-site	4N	PTA 1	PTA 3	PTA 4
AURKA	P-T288	activating, T-loop	0.025	0.000	0.021	0.002
CDK1	P-T14/ P-Y15	inhibitory	0.207	0.027	0.013	0.027
CHK1	P-S301	upon stalled replication and DNA damage	0.001	0.002	0.187	0.016
CHK1	P-S286	upon stalled replication and DNA damage	0.158	0.469	0.479	0.297
PLK1	P-T210	activating, T-loop	0.195	0.168	0.055	0.554