Supplementary Table 1 | Oligonucleotides used in this study.

| Name	Length (nt/bp)	GC%	Sequence
ssDNA$_{16}$	16	50	TGT ACT TCT AGA GGC C
ssDNA$_{30}$	30	50	GCA TGT ATT GAA GTA CTT CTA GAG GCC GCC
dsDNA$_{30}$	30	50	same as above
RNA$_{16}$	16	50	rUrGrU rArCrU rUrCrU rArGrA rGrGrC rC
RNA$_{30}$	30	50	rGrCrA rUrGrU rArUrU rGrArA rGrUrA rCrUrU rCrUrA rGrArG rGrCrC rGrCrC
RNA$_{60}$	60	50	rGrCrA rUrGrU rArUrU rGrArA rGrUrA rCrUrU rCrUrA rGrArG rGrCrC rGrCrC rGrCrA rUrGrU rArUrU rGrArA rGrUrA rCrUrU rCrUrA rGrArG rGrCrC rGrCrC
ssDNA$_{70}$	70	50	GCA TGT ATT GAA GTA CTT CTA GAG GCC GCC GCA TGT ATT GAA GTA CTT CTA GAG GCC GCC TGC CTC TAG A
dsDNA$_{70}$	70	50	same as above
ssDNA$_{75}$	75	33	CCA AAA CTA ATC TTT ATA TAA ATG GGA GAC TCA CTA TCA TGG CTA CTA CGA CTA CTA AAC GAG GTT AAA ATG AAT
dsDNA$_{75}$	75	33	same as above
ssDNA$_{147}$	147	56	CT GGA GAA TCC CGG TGC CGA GGC CGC TCA ATT GGT CGT AGA CAG CTC TAG CAC CGC TTA AAC GCA CGT ACG CGC TGT CCC CCG CGT TTT AAC CGC CAA GGG GAT TAC TCC CTA GTC TCC AGG CAC GTG TCA GAT ATA TAC ATC CTG T
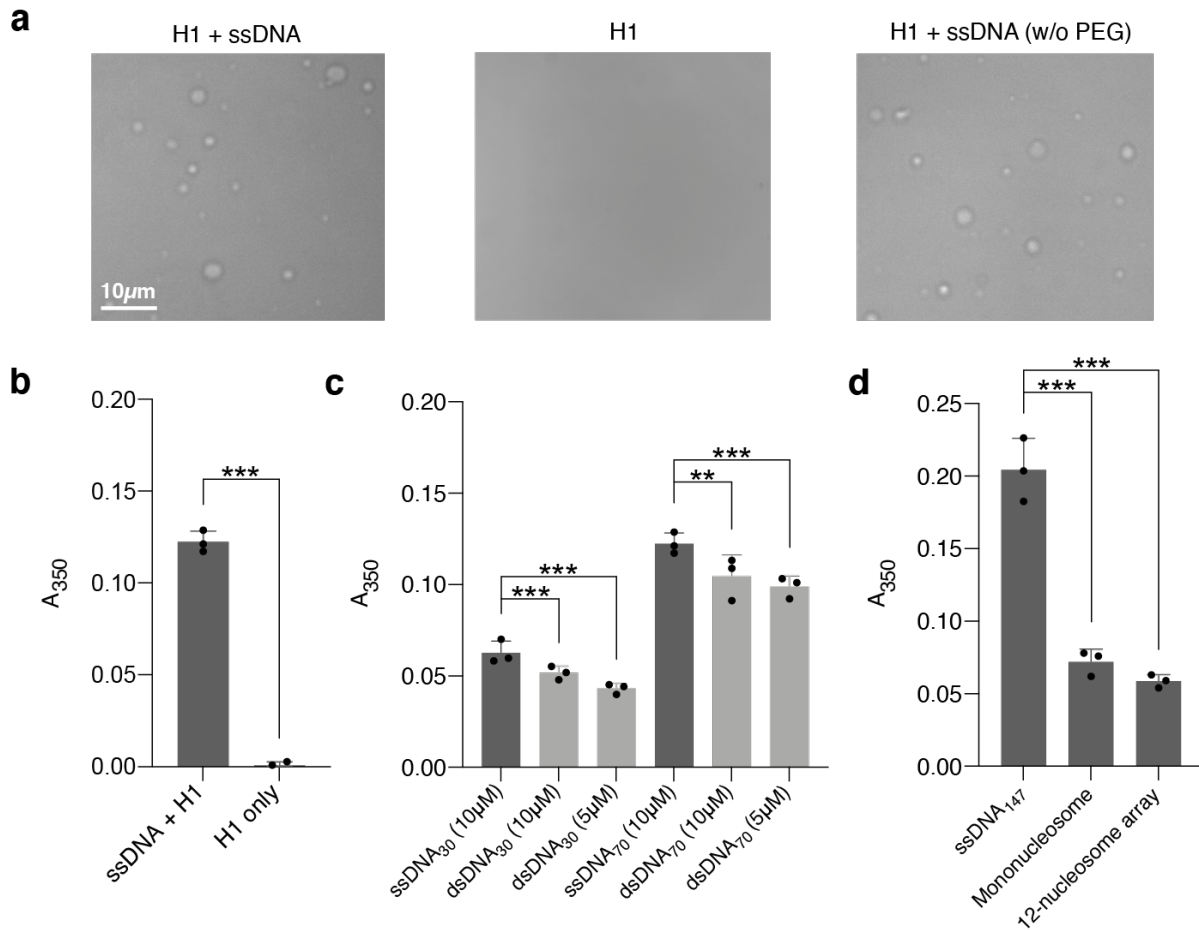
Supplementary Fig. 1 | Additional results from bulk phase separation assays. a, Representative brightfield images of H1 mixed with 10 µM ssDNA$_{75}$ (left), H1 alone (middle), and H1 mixed with and 10 µM ssDNA$_{75}$ in the absence of PEG (right) (among 3 independent experiments). **b**, Solution turbidity (A$_{350}$) measurements for H1 mixed with 10 µM ssDNA$_{70}$ and H1 alone. Significance calculated using an unpaired t-test (***$p<0.001$). **c**, A$_{350}$ measurements for H1 mixed with ss/ds DNA$_{30}$ or ss/ds DNA$_{70}$. Significance calculated using a one-way ANOVA with Dunnett's test for multiple comparisons (**$p<0.01$, ***$p<0.001$). **d**, A$_{350}$ measurements for H1 mixed with ssDNA$_{147}$ (5 µM), mononucleosomes (5 µM), or 12-nucleosome arrays (600 nM). Significance calculated using a one-way ANOVA with Dunnett's test for multiple comparisons (***$p<0.001$). All experiments were performed with 2.5 µM H1. All A$_{350}$ experiments performed with n=3 independent measurements. All data in bar charts presented as mean values ± SD.
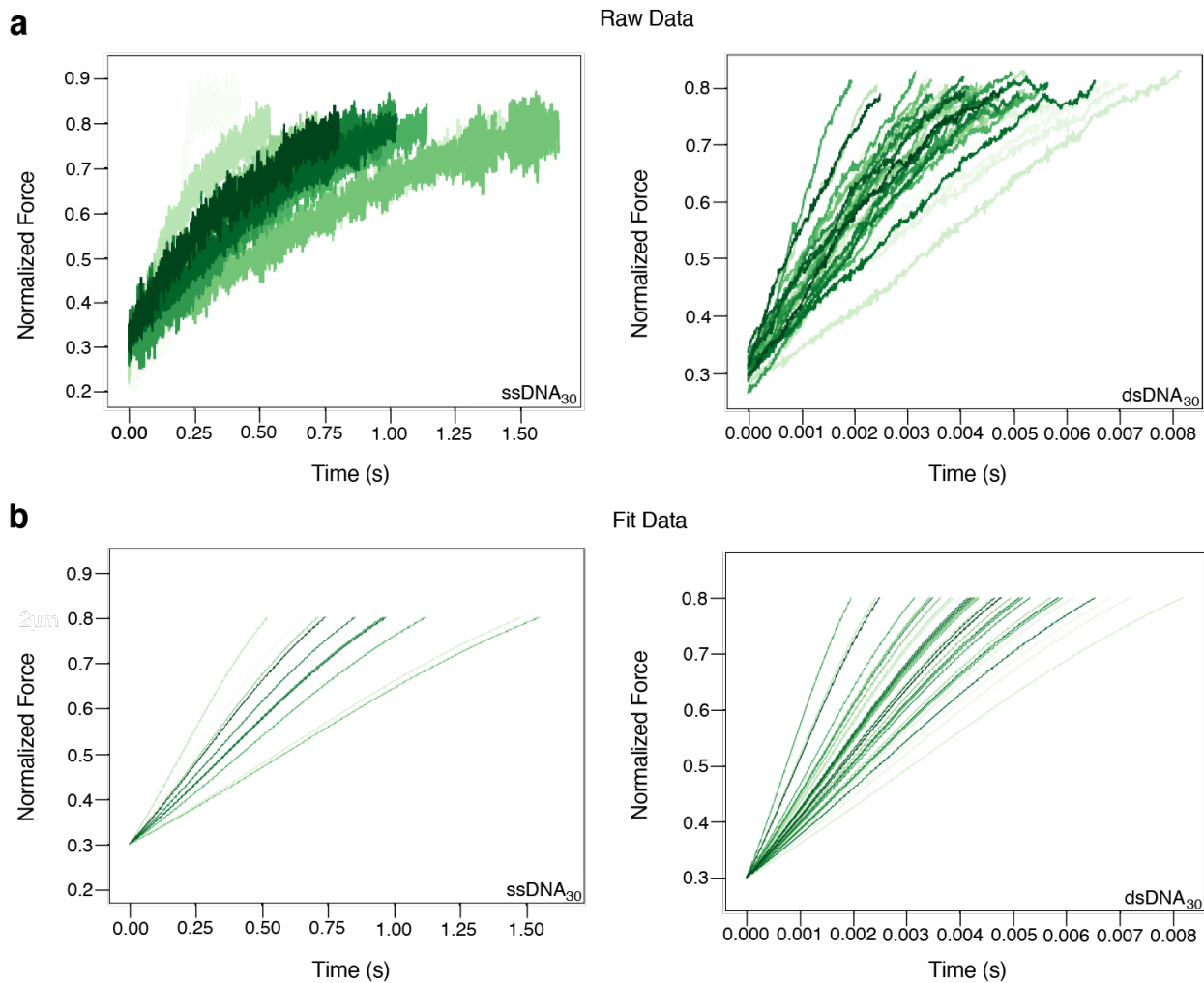
Supplementary Fig. 2 | Force profiles from droplet fusion experiments. a, Raw data between the normalized force values of 0.3 and 0.8 for H1:ssDNA$_{30}$ (Left) and H1:dsDNA$_{30}$ (Right) droplets. Each trace represents a fusion event between two optically trapped droplets. **b**, Corresponding sigmoidal fits of the force-time traces shown in **a**.

a eGFP-H1:ssDNA

b 2µm
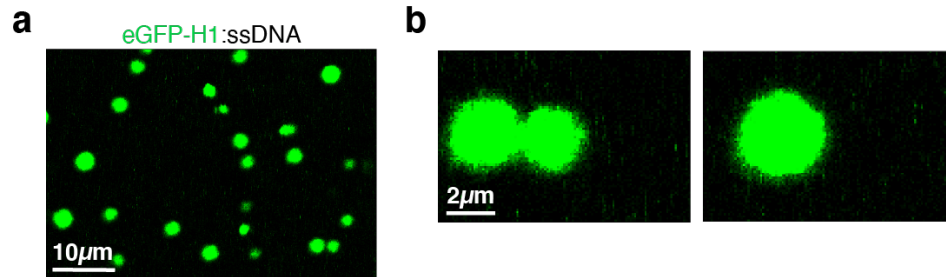
Supplementary Fig. 3 | eGFP-H1:ssDNA droplet formation and fusion *in vitro*. a, A representative image of droplets (among 3 independent experiments) formed with 2.5 µM recombinant eGFP-H1 and 10 µM ssDNA$_{75}$ visualized by GFP fluorescence. **b**, Representative snapshots of two eGFP-H1:ssDNA$_{75}$ droplets pre- and post-fusion (among 8 independent fusion events).
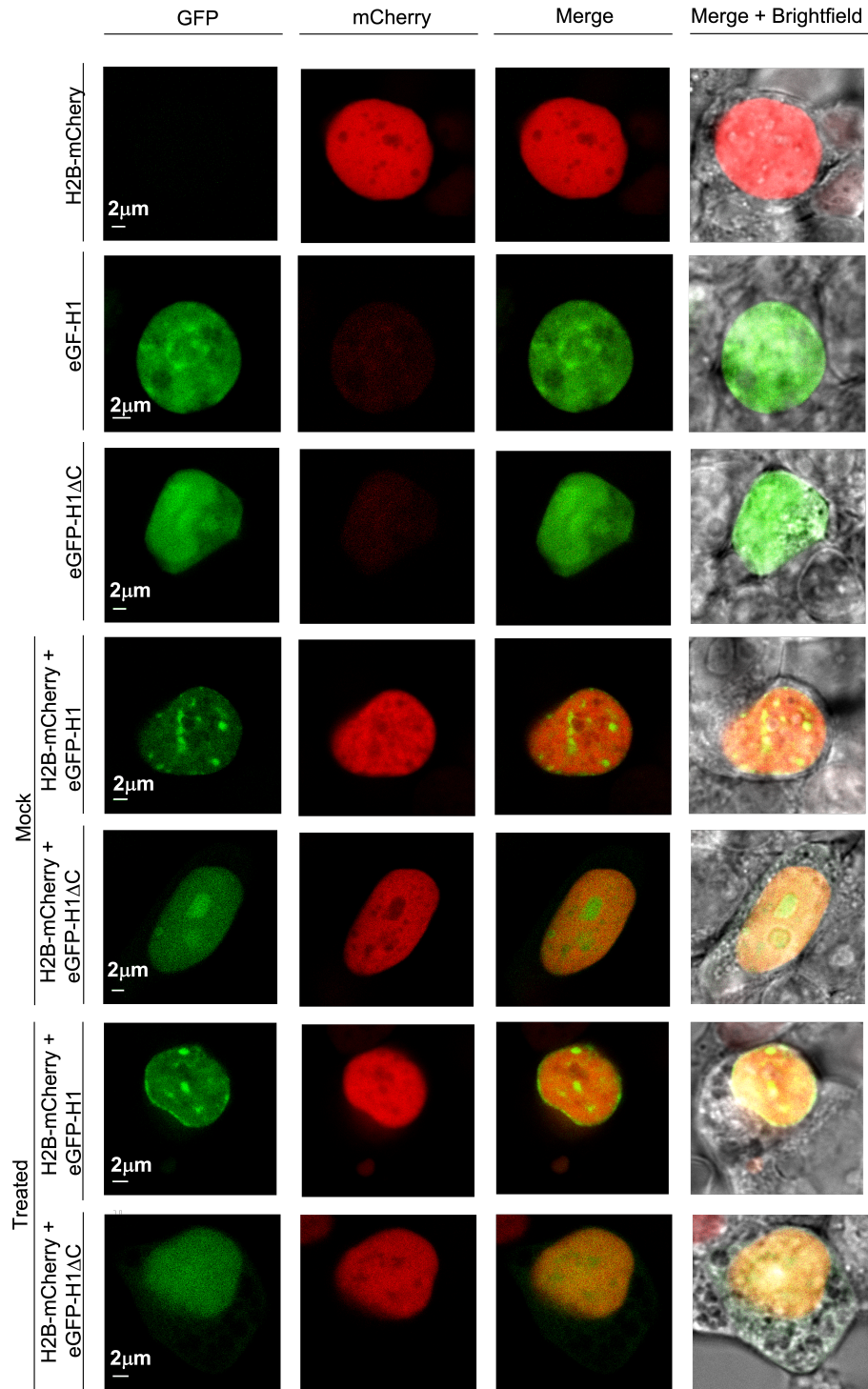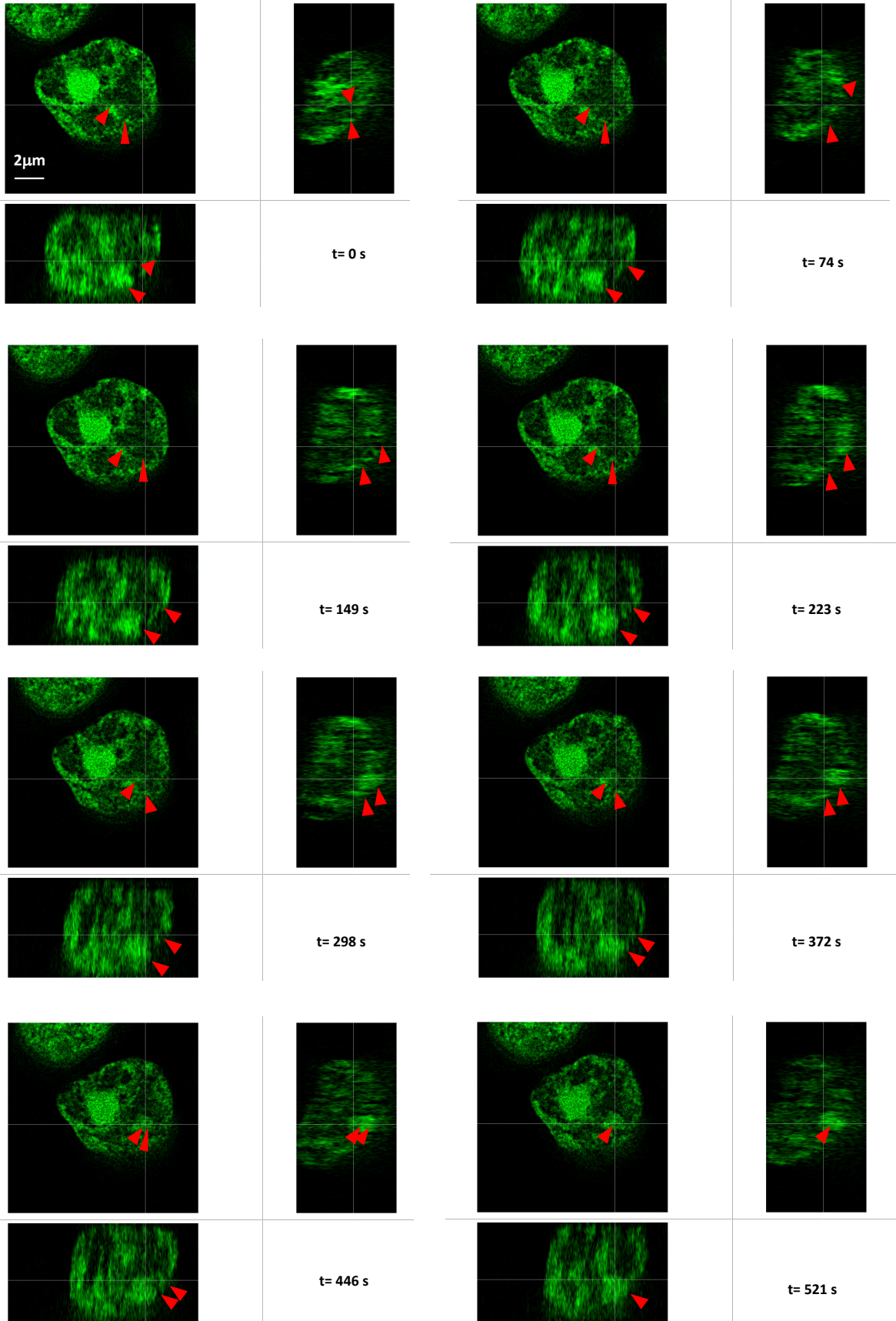
Supplementary Fig. 4 | Nuclear distributions of eGFP-H1 and H2B-mCherry.
Representative confocal images of HEK293T cells co-transfected with H2B-mCherry and either eGFP-H1 or eGFP-H1ΔC and treated with either mock or 2 mM HU + 20 μM AZD6738 for 18h. eGFP-H1, mock (n=16 independent nuclei); eGFP-H1ΔC, mock (n= 13); eGFP-H1, treated (n=20); eGFP-H1ΔC, treated (n= 12).
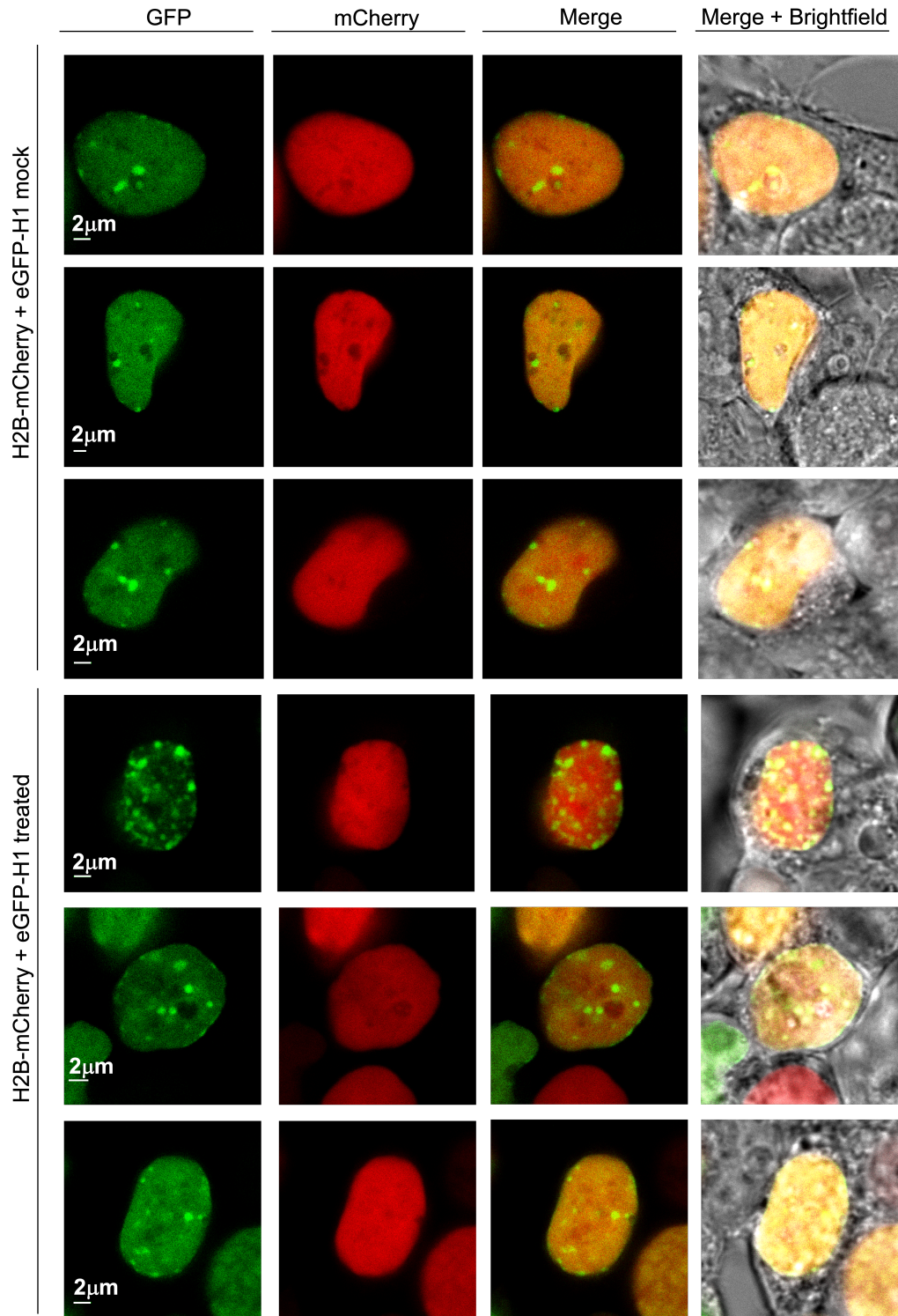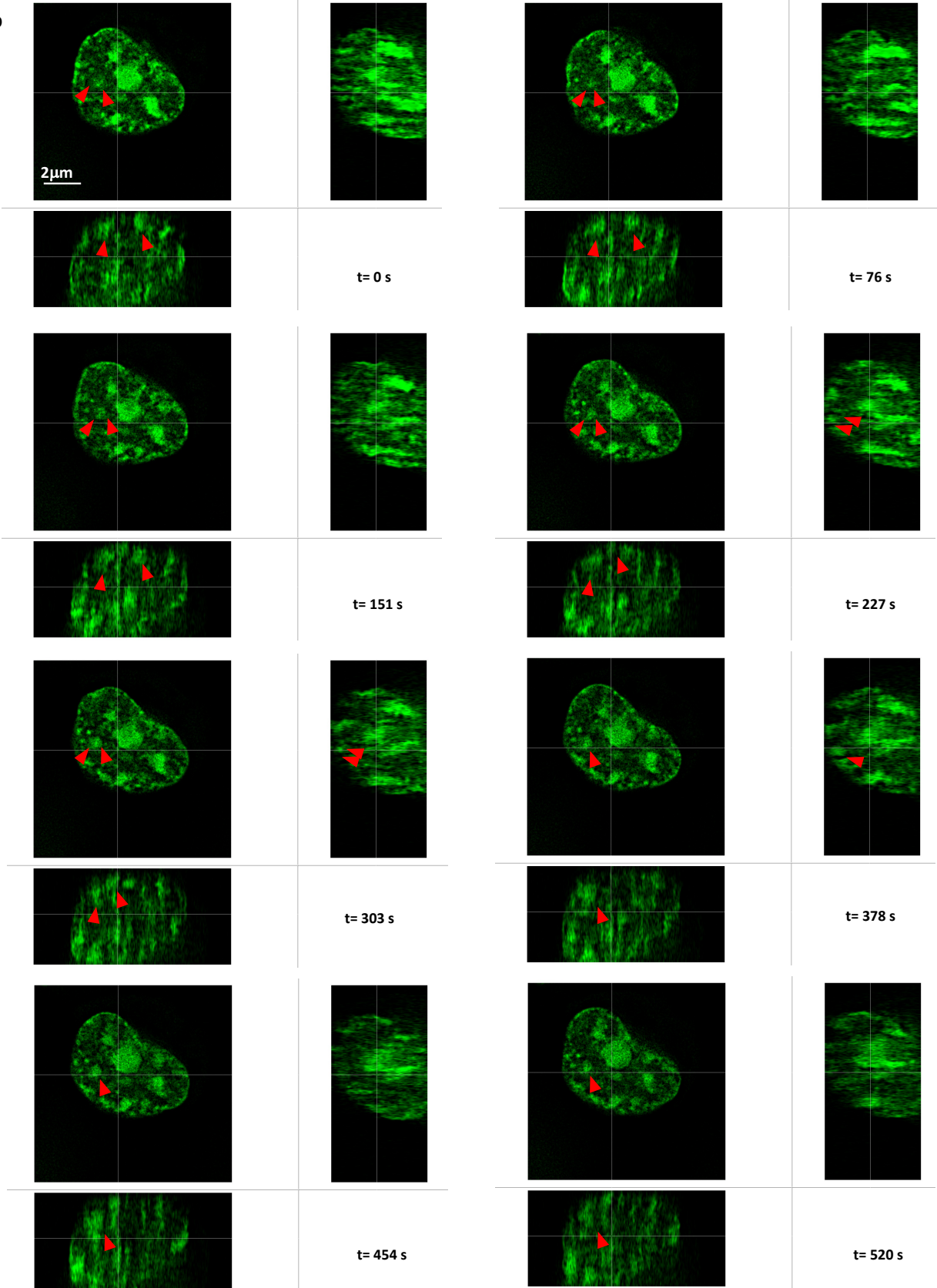
Supplementary Fig. 5 | Additional examples of eGFP-H1 and H2B-mCherry co-transfected cells. Representative confocal images of HEK293T cells co-transfected with H2B-mCherry and eGFP-H1 and treated with either mock or 2 mM HU + 20 μM AZD6738 for 18h. eGFP-H1, mock (n=16 independent nuclei); eGFP-H1, treated (n=20).
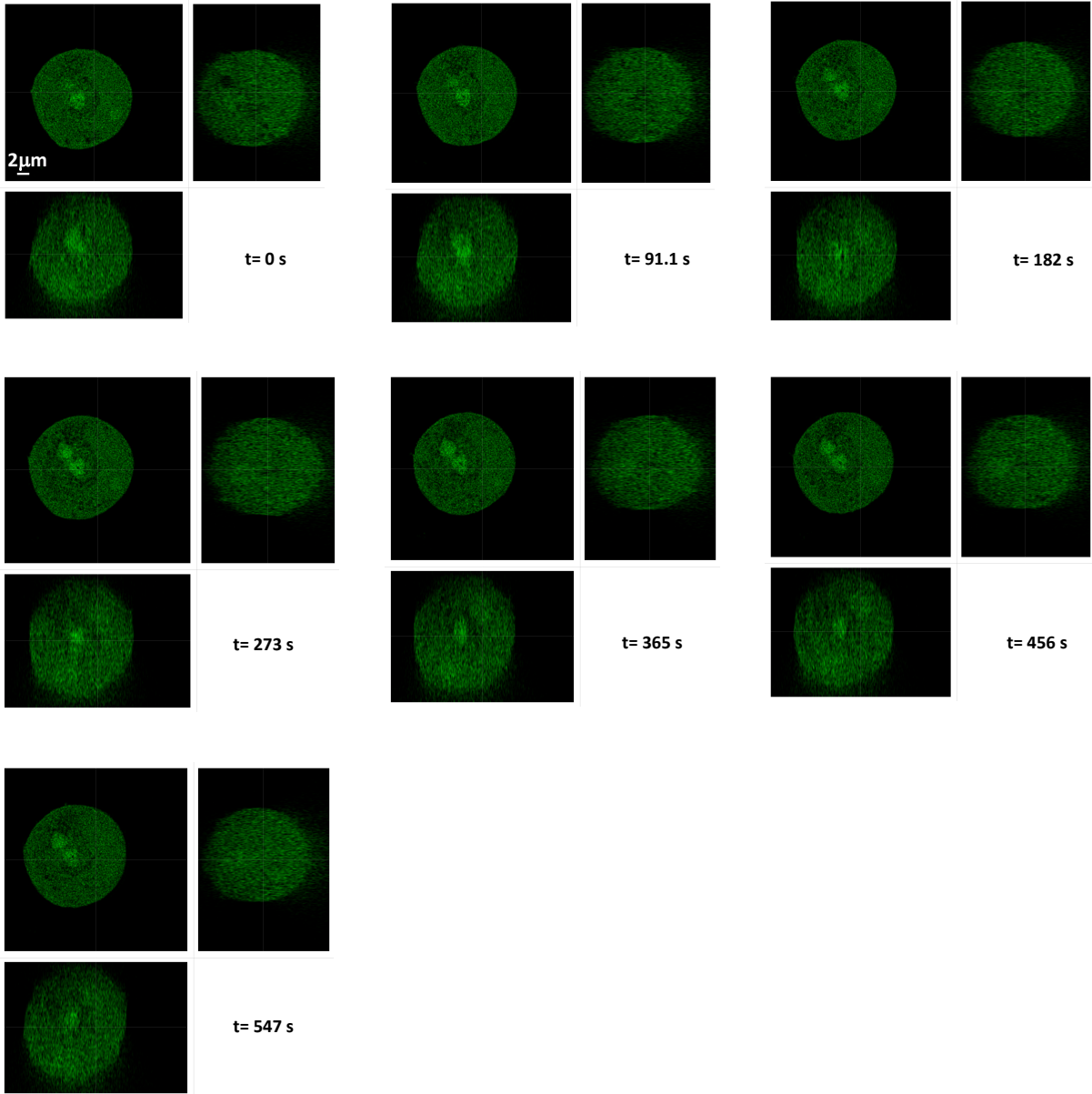
a

2μm
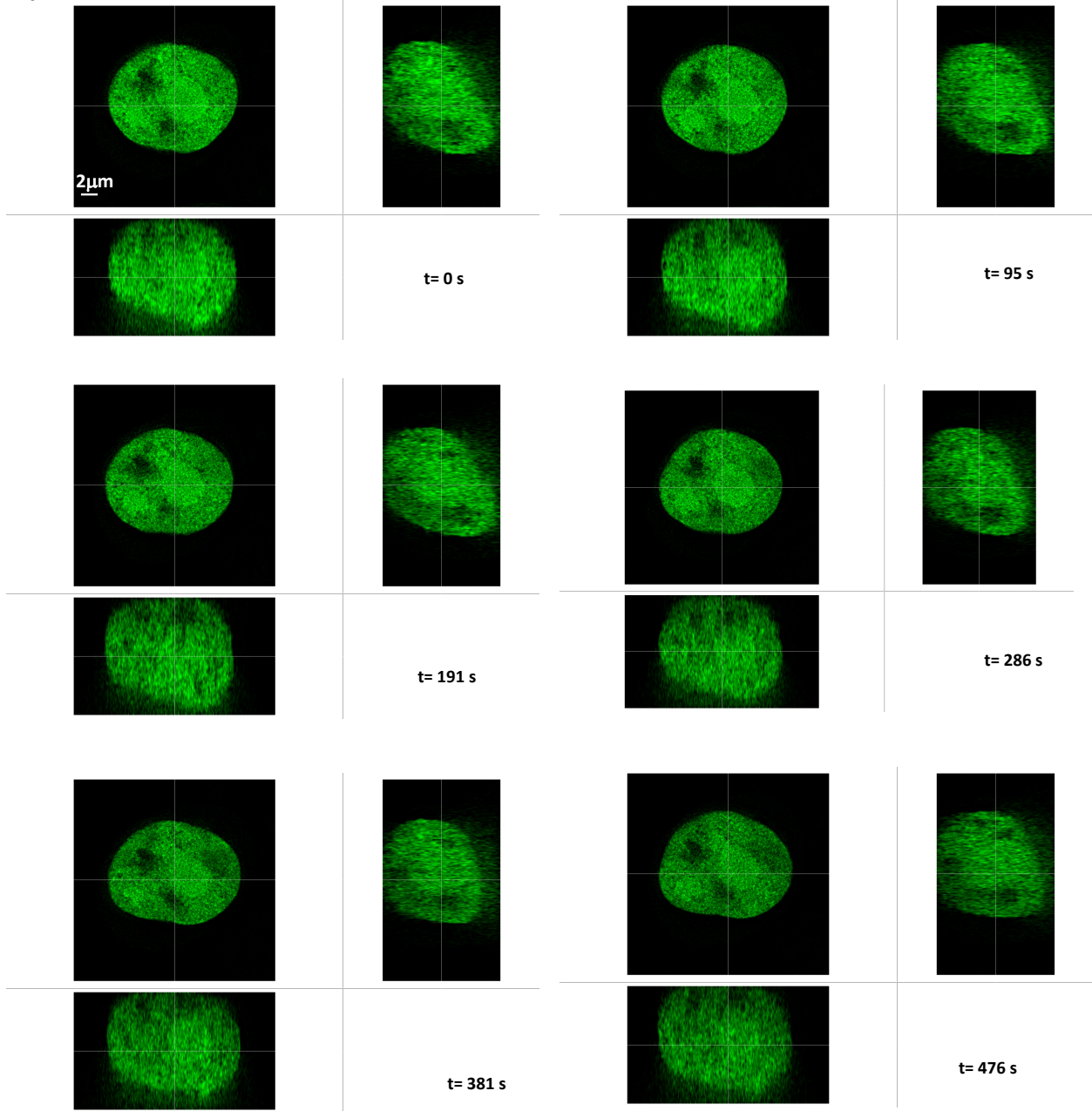
t= 0 s

t= 74 s

t= 149 s

t= 223 s

t= 298 s

t= 372 s

t= 446 s

t= 521 s

b

t= 0 s

t= 76 s

t= 151 s

t= 227 s

t= 303 s

t= 378 s

t= 454 s

t= 520 s

2µm

c

2μm

t= 0 s

t= 91.1 s

t= 182 s

t= 273 s

t= 365 s

t= 456 s

t= 547 s

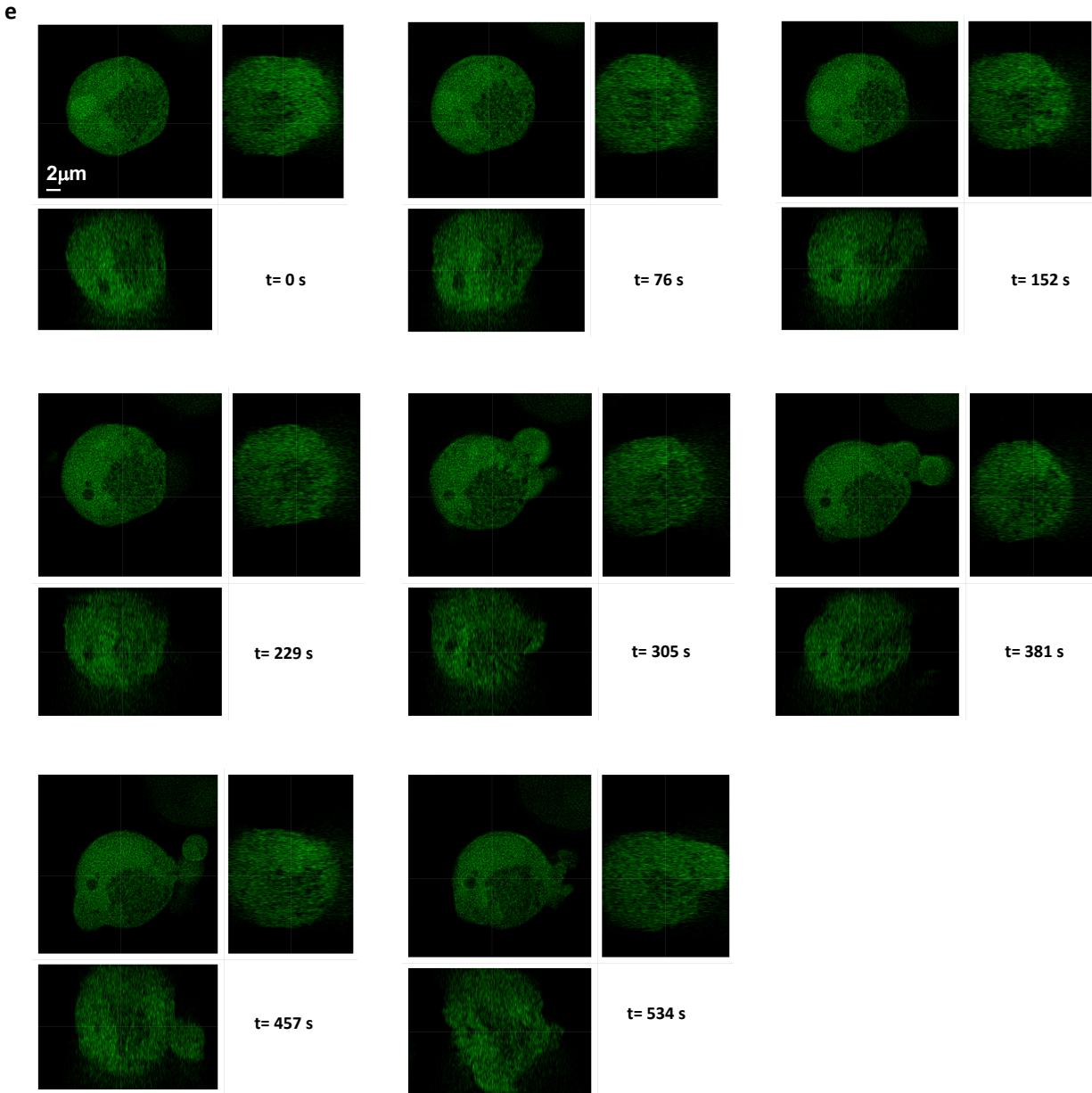**d**

2μm

t= 0 s

t= 95 s

t= 191 s

t= 286 s

t= 381 s

t= 476 s

e

Supplementary Fig. 6 | Timepoints from continuous Z-stack monitoring for merging eGFP-H1 puncta. Slices from continuous Z-stack imaging over 10 minutes of HEK293T cells transfected with eGFP-H1 or eGFP-H1ΔC and treated with either mock or 2 mM HU + 20 µM AZD6738 for 18h. At each timepoint, top left= x plane, top right= y plane, bottom left= z plane. **a-b,** Representative slices (among 6 imaging acquisitions on independent nuclei) of eGFP-H1 treated with 2 mM HU + 20 µM AZD6738. Red arrows highlight merging puncta. **c,** eGFP-H1ΔC treated with 2 mM HU + 20 µM AZD6738. **d,** eGFP-H1 with mock treatment. **e,** eGFP-H1ΔC with mock treatment.
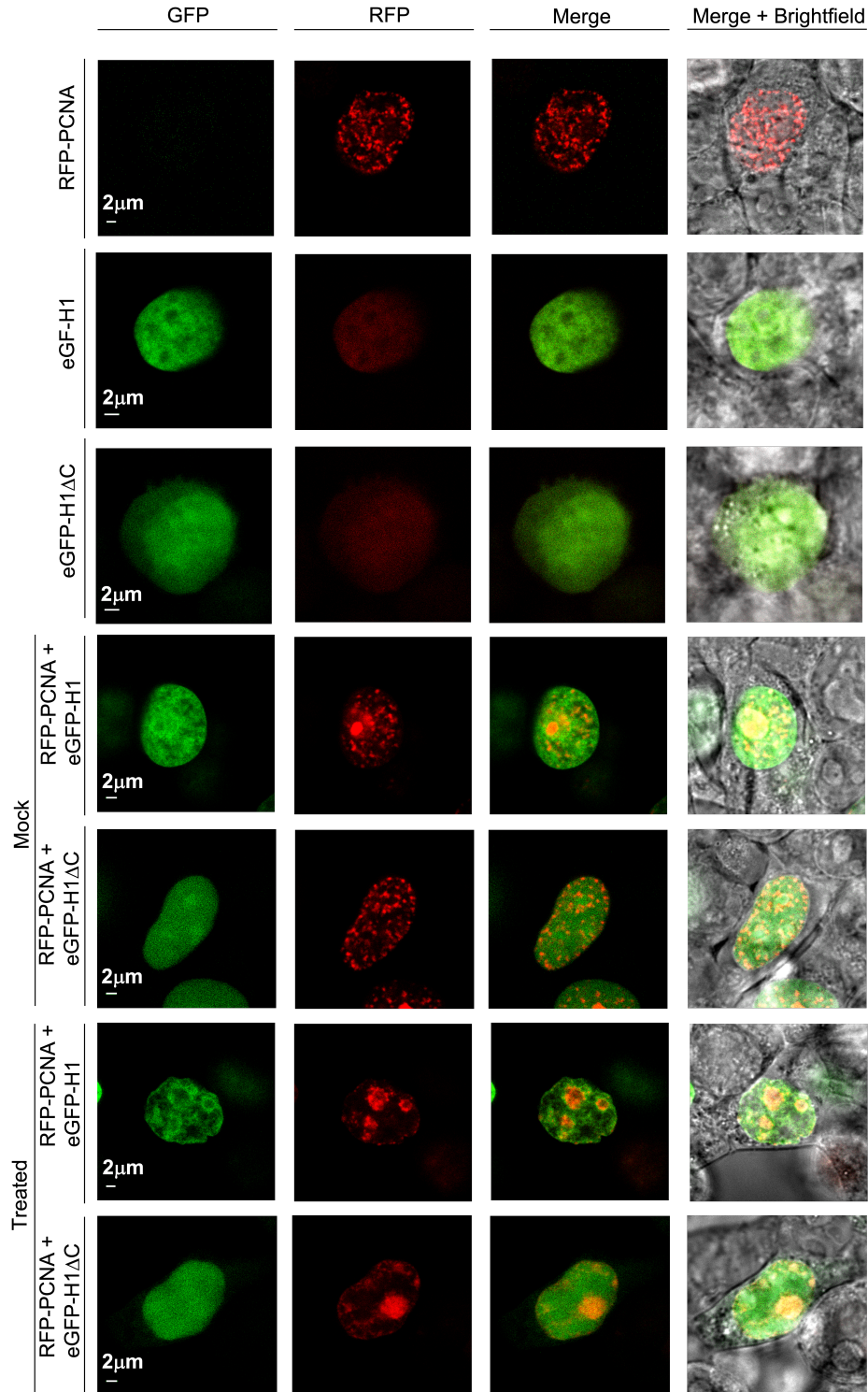
Supplementary Fig. 7 | Nuclear distributions of eGFP-H1 and RFP-PCNA. Representative confocal images and their corresponding brightfield images of HEK293T cells co-transfected with RFP-PCNA and either eGFP-H1 or eGFP-H1ΔC and treated with either mock or 2 mM HU + 20 μM AZD6738 for 18h. eGFP-H1, mock (n=12 independent nuclei); eGFP-H1ΔC, mock (n=9); eGFP-H1, treated (n=14); eGFP-H1ΔC, treated (n=12).
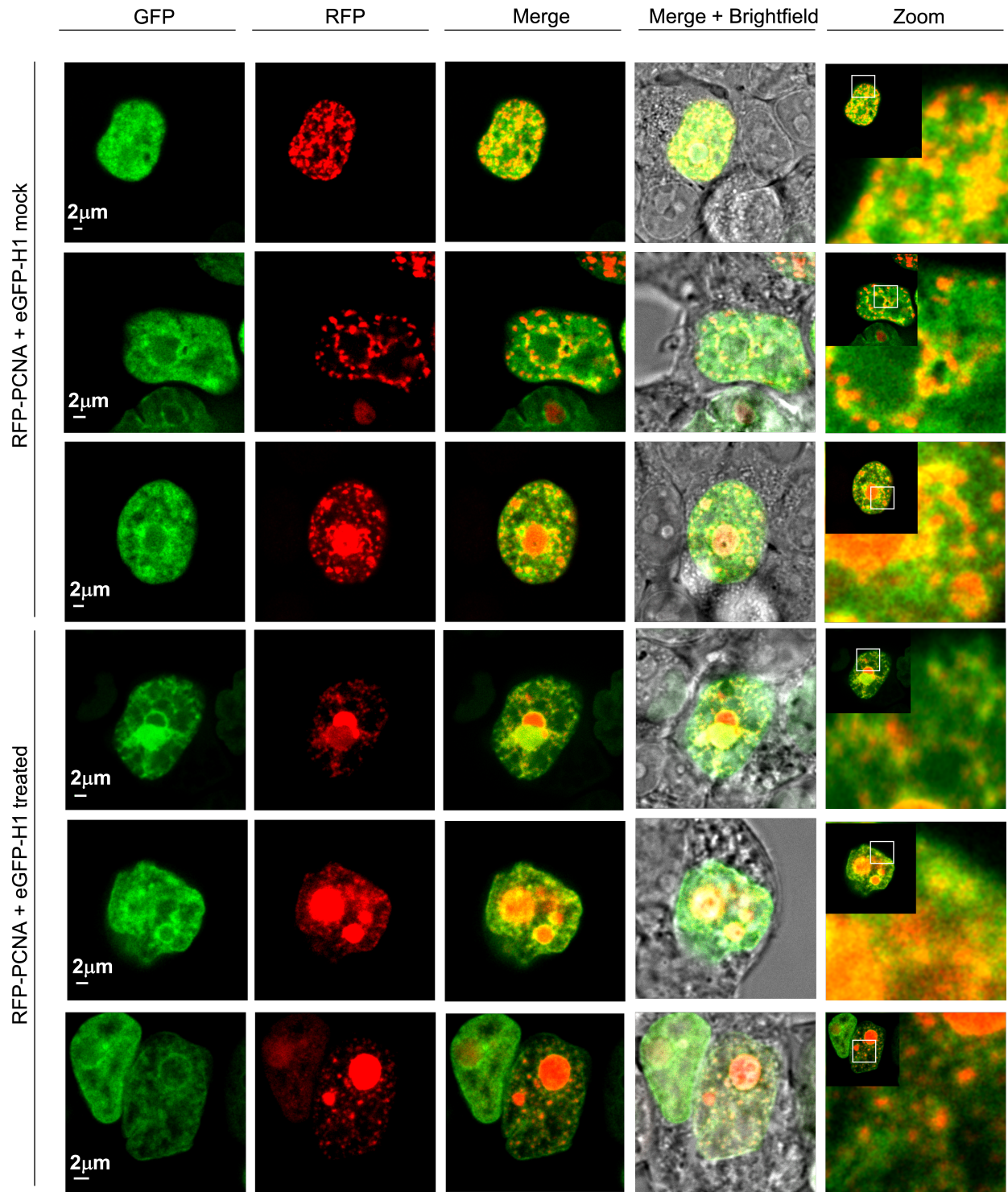
Supplementary Fig. 8 | Additional examples of eGFP-H1 and RFP-PCNA co-transfected cells. Representative confocal and brightfield images of HEK293T cells co-transfected with RFP-PCNA and eGFP-H1 and treated with either mock or 2 mM HU + 20 μM AZD6738 for 18h. eGFP-H1, mock (n=12 independent nuclei); eGFP-H1, treated (n=14).
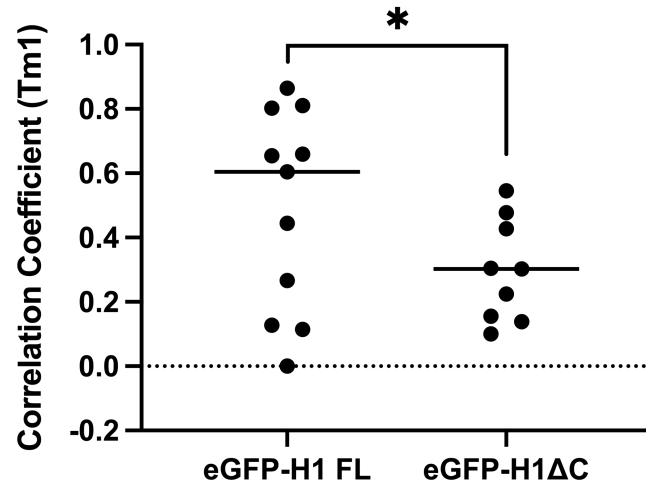
Supplementary Fig. 9 | Quantification of eGFP-H1 colocalization with RFP-PCNA.
Scatter plot showing the distribution of Mander's tM1 auto-thresholded correlation
coefficients for eGFP-H1 (n=11 independent nuclei) or eGFP-H1ΔC (n=9) (channel 1)
colocalizing with RFP-PCNA (channel 2). Each point represents the coefficient for one
nucleus. Significance calculated using Welch's t-test (*$p<0.05$).

Supplementary Data

A350	
ssDNA$_{70}$	H1 only
0.12133333	0.00266667
0.12866667	0.001
0.11733333	-0.0013333

Supplementary Fig. 1b

A350					
ssDNA$_{30}$ (10µM)	dsDNA$_{30}$ (10µM)	dsDNA$_{30}$ (5µM)	ssDNA$_{70}$ (10µM)	dsDNA$_{70}$ (10µM)	dsDNA$_{70}$ (5µM)
0.05833333	0.048	0.04	0.12133333	0.109	0.101
0.05966667	0.052	0.04533333	0.12866667	0.09133333	0.10333333
0.07	0.05533333	0.04433333	0.11733333	0.11333333	0.09233333

Supplementary Fig. 1c

A350		
ssDNA$_{147}$	Mononucleosome	12-nucleosome array
0.18266667	0.062	0.054
0.22633333	0.076	0.063
0.20366667	0.078	0.059

Supplementary Fig. 1d

Correlation Coefficient (Tm1)	
GFP-H1 FL	GFP-H1DC
0.864	0.1
0.654	0.302
0.552	0.545
0.605	0.478
0.659	0.138
0.444	0.427
0.592	0.304
0.81	0.155
0.266	0.224
0.127	
0	
0.114	
0.802	

Supplementary Fig. 9