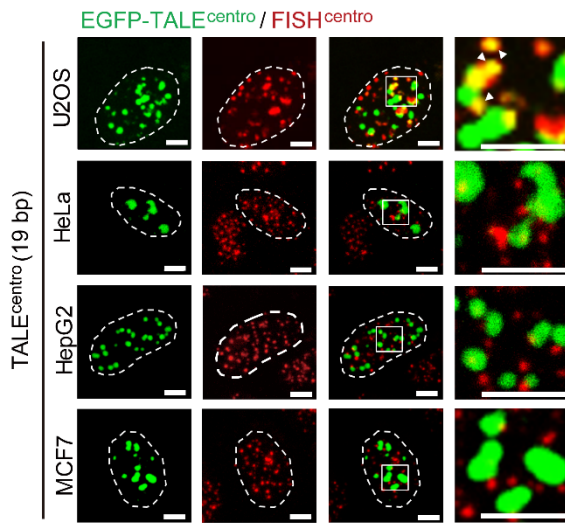
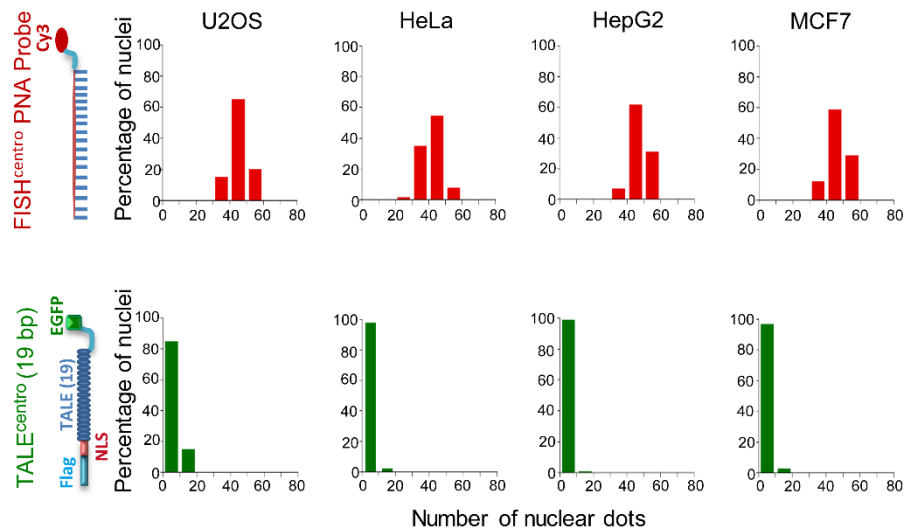


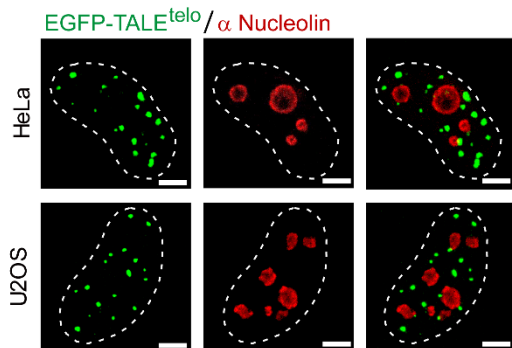
A



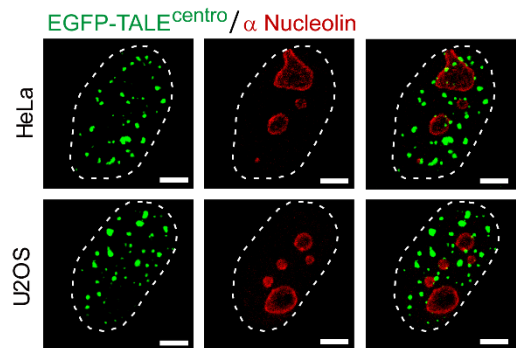
B



C



D



Supplementary information, Figure S1 Unmodified TALEs were insufficient to visualize centromeres in four tumor cell lines. **(A)** Co-localization analysis of EGFP-TALE^{centro} (green) and centromeric FISH (red) signals in U2OS, HeLa, HepG2, and MCF7 cells. EGFP-TALE^{centro} was designed using a 19-bp centromeric DNA sequence. Dashed lines indicate the nuclear boundary; arrowheads indicate overlapping signals. Scale bars, 5 μ m. **(B)** Histograms showing numbers of centromeric FISH- or EGFP-TALE^{centro} (19 bp)-positive dots in nuclei of indicated cell lines. $n = 50$ nuclei per line. **(C)** The absence of co-localization between EGFP-TALE^{telo} (green) and nucleolin (red, IF) in U2OS and HeLa cells, respectively. Dashed lines indicate the nuclear boundary. Scale bars, 5 μ m. **(D)** The absence of co-localization between EGFP-TALE^{centro} (green) and nucleolin (red, IF) in U2OS and HeLa cells, respectively. Dashed lines indicate the nuclear boundary. Scale bars, 5 μ m.