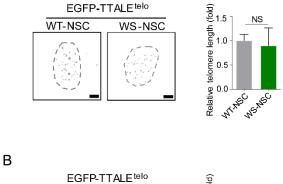
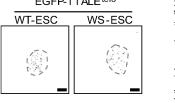
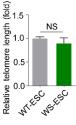
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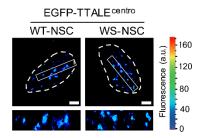


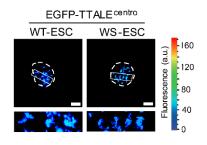




D

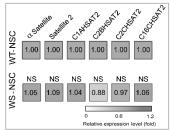
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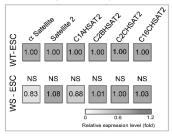
Е

Centromere repetitive sequence transcripts



F

Centromere repetitive sequence transcripts



Supplementary information, Figure S8 TTALE-mediated visualization of telomeres and centromeres in WRN-deficient ESCs and NSCs. (A-B) Left: EGFP-TTALE^{telo}-based SIM imaging showing comparable telomere lengths between WS-NSCs and WT-NSCs (A) and between WS-ESCs and WT-ESCs (B). Dashed lines indicate the nuclear boundary. Scale bars, 5 μ m. Right: Telomere length detected by qPCR. Values were normalized to 36B4. Data were presented as mean \pm SEM; n = 3; NS, not significant. (C-D) Top: SIM images showing centromeres labeled by EGFP-TTALE^{centro} in NSCs (C) and ESCs (D). Bottom: Magnified images of boxed regions from top panels. Dashed lines indicate the nuclear boundary. Scale bars, 5 μ m. (E-F) RT-qPCR analysis of centromeric repetitive sequence transcripts in NSCs (E) and ESCs (F). Values were normalized to GAPDH. Data were presented as mean \pm SEM; n = 3; NS, not significant.