

Supplementary information, Figure S9 TTALE-based imaging of attrition of NOR-rDNAs in senescent hMSCs. (A) Quantitative PCR analysis showing no significant difference of *GAPDH* gene copy number in WS-MSCs relative to WT-MSCs. Data were presented as mean  $\pm$  SEM; n = 3; NS, not significant. (B, E) SIM images showing diminished mCherry-TTALE<sup>rDNA</sup> fluorescence in HGPS-MSCs (passage 8) compared to HGPS-GC-MSCs (passage 8) (B) and LP-WT-MSCs (passage 12) compared to EP-WT-MSCs (passage 6) (E) . NLS-EGFP was co-transfected as an internal control. Dashed lines indicate the nuclear boundary. Scale bars, 5  $\mu$ m. (C, F) Intensity profiles across TTALE<sup>rDNA</sup>-labeled rDNAs in HGPS-GC-MSCs and HGPS-MSCs (C) and EP-WT-MSCs and LP-WT-MSCs (F) as indicated by solid lines in Figure S9B and S9E, respectively. Solid lines represent 10  $\mu$ m in length. (D, G) qPCR analysis indicating a reduction in rDNA copy number in HGPS-MSCs relative to WT control cells (D) and LP-WT-MSCs (passage 12) compared to EP-WT-MSCs (passage 6) (G) . Data were presented as mean  $\pm$  SEM; n = 3; \*\*p < 0.01; \*\*\*\*p < 0.001.