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Supplemental Information

Polymer Modeling Predicts Chromosome

Reorganization in Senescence

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SUPPLEMENTAL FIGURES

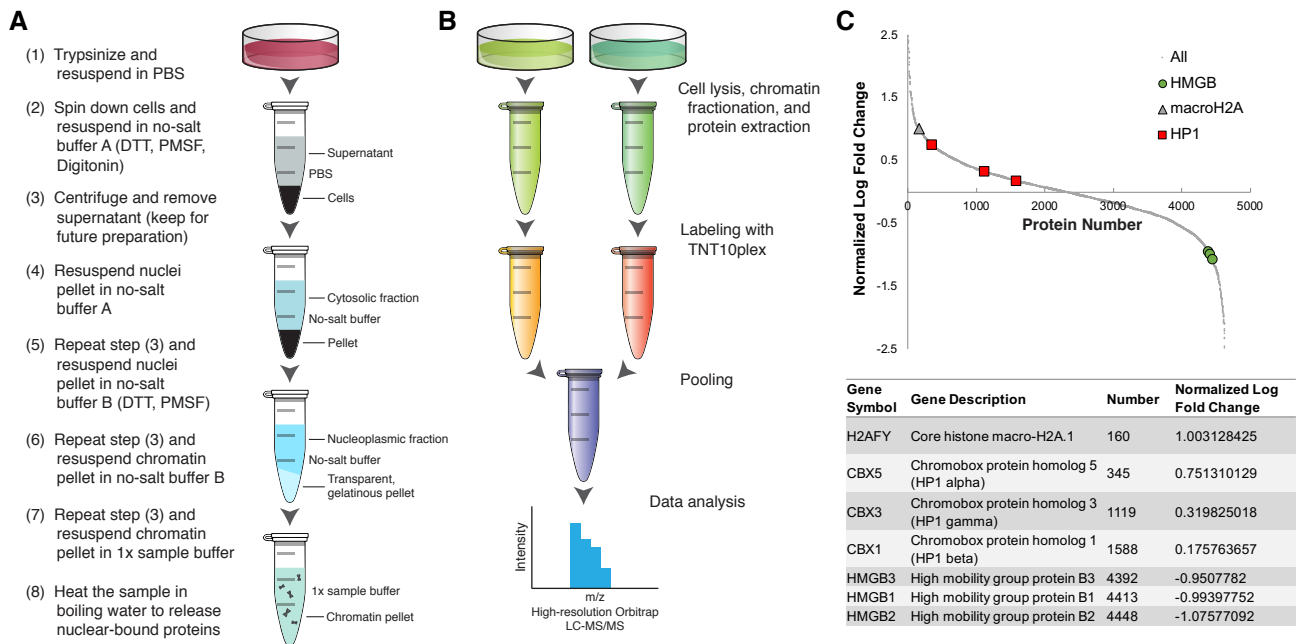


Figure S 1: Chromatin fractionation and mass spectrometry experiments investigating the change in protein abundance between growing and senescent cells, related to Figure 2 and STAR Methods. (A) The key stages for chromatin isolation of a single sample. (B) A schematic representation of chromatin fractionation from different samples followed by identification and quantitation of proteins based on high-resolution Orbitrap LC-MS/MS. (C) *Top*: A graph showing the normalized log fold change of individual protein abundance between growing and senescent cells. Proteins are numbered from the highest to the lowest ratio. *Bottom*: A table listing the normalized log fold change for macroH2A, HP1, and high mobility group proteins.

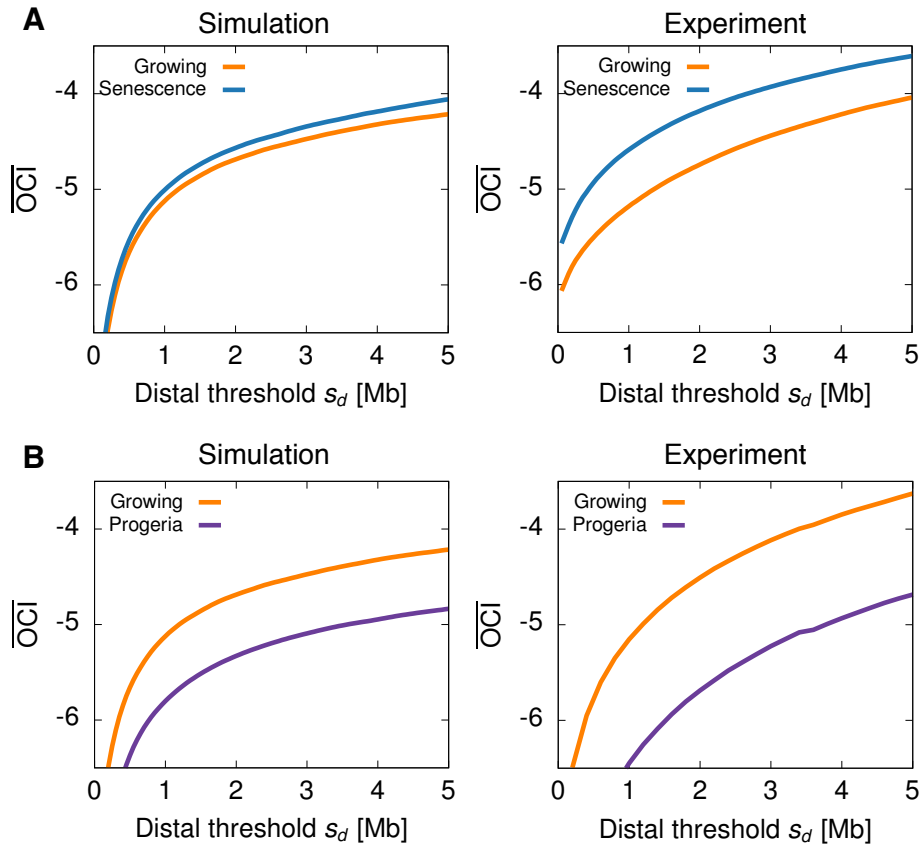


Figure S 2: Varying the threshold s_d which distinguishes local from distal contacts does not alter the general trends for the change in the open chromatin index (OCI) between different cell states, related to Figure 3. (A and B) The plots compare the average OCI value between (A) growing and senescent state and (B) growing and progeroid state for different thresholds s_d . Note that the OCI increases from growing to senescence and decreases from growing to progeria for different s_d , both in simulations and in experiments.

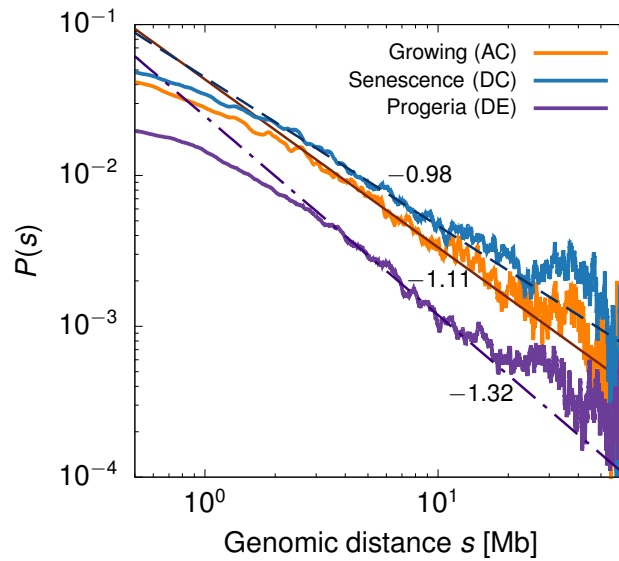


Figure S 3: Contact probability $P(s)$ as a function of genomic distance s , related to Figure 3. A log-log plot showing the decay in the contact probability $P(s)$ as the genomic distance s between two chromatin segments increases, for growing (adsorbed-collapsed, AC), senescence (desorbed-collapsed, DC), and progeria (desorbed-extended, DE). Straight lines are linear fits to the log-log curves with the measured exponents c shown for the different cell states.