An mre11 Mutation That Promotes Telomere Recombination and an Efficient Bypass of Senescence

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FIGURE S1.—Evolutionary invariance of Mre11-470A. (top) The map of the MRE11 gene, not drawn to scale, depicts the relative positions of the phosphodiesterase (PD), DNA binding (DNA A, DNA B), Mre11 dimerization (M/M), as well as the Mre11/Rad50 association domains (M/R). SF and MF refer to the signaling and meiotic functions of Mre11, respectively. The site of the 470A-482A motif is also depicted. (below) Protein motifs homologous to yeast amino acids 470A-482A among different eukaryotic organisms, accompanied by the deduced consensus sequence are shown. All eukaryotes that have the canonical C-terminal region of Mre11 maintain this homology. In the case of human MRE11A, the region begins with residue 457A.
Figure S2.—Bypass of senescence using subculturing on solid medium. Four spore products representing strains of MRE11, tlc1Δ, mre11-A470T, and mre11-A470T tlc1Δ were subjected to solid subculturing. The plate shown was incubated for 3 days of growth after subculturing at 30°C. Solid subculturing of all four spore colonies was conducted in at least two trials.
Figure S3.—Y’ elements are not essential for Type IA recombinant formation. (A) The structure of the left arm of chromosome III depicting the PCR-amplified probe (above fragment), the Eco RI (E) site, and the expected size of telomeric fragments (black) are shown. (B) Southern blot of DNA isolated from an I2lig4 spore colony, mre11-A470T tlc1Δ, at each stage of subculturing (s0-s7), as well as MRE11 TLC1 control strains, subjected to restriction digestion with EcoRI and probed with a 1053 bp telomere-proximal PCR-generated subtelomeric fragment on the left arm of chromosome III (cIII). This digest hybridizes to the telomeric species (see arrow on left) as well as multiple subtelomeric repeated fragments due to the homology of the probe with centromere proximal X-class repeats. Subtelomeric fragments, grey; telomeric fragments, black.