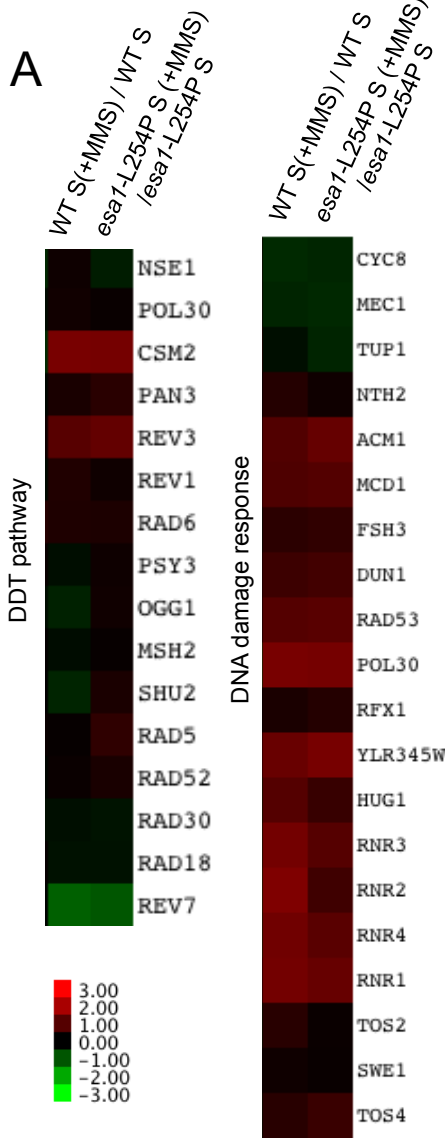
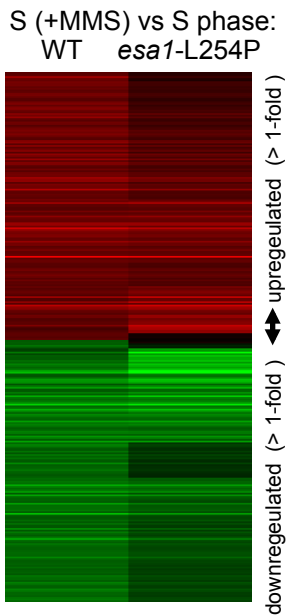


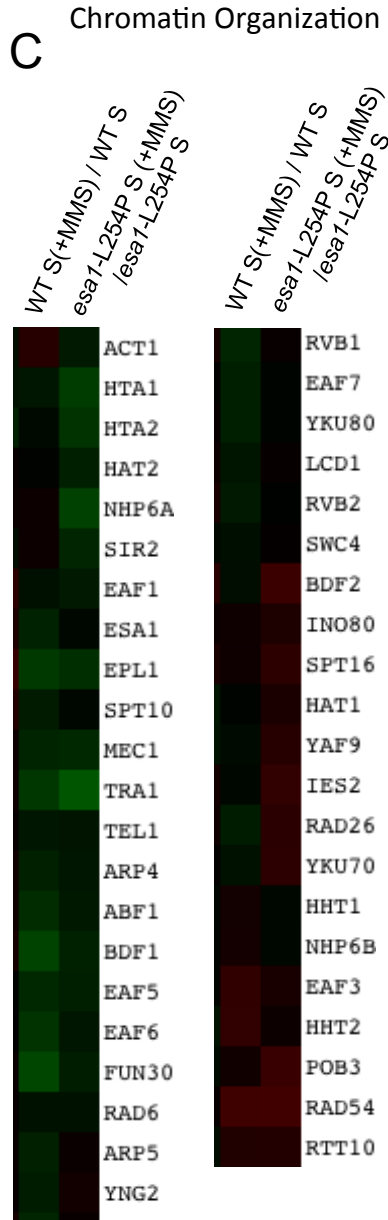
A



B



C



D

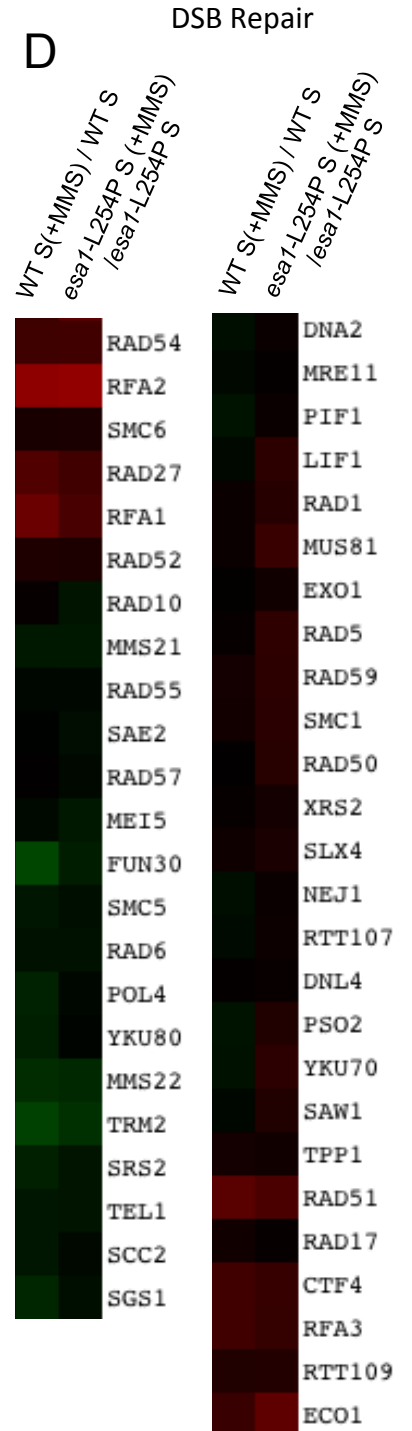


Figure S6 Transcriptional comparison of Gene Upregulation in MMS vs. Untreated S phase samples . Cells arrested in α -factor were released into normal YPAD or YPAD/0.05% MMS for 1hr. RNA was extracted followed by microarray. (A) Transcriptome analysis was performed as described in the Materials and Methods. Heat maps of the genome-wide expression profile of 0.05% MMS vs. untreated samples of wild type and *esa1*-L254P in S phase. Sample genes from the DNA damage tolerance pathway and genes upregulated as part of the transcriptional DNA damage response from derepression of Crt1/Rfx1 and Nrm1. (B) Heat map of the genome-wide expression profile of 0.05% MMS vs. untreated samples indicated that the NuA4 allele, *esa1*-L254P, had a similar transcriptional profile compared to wild type cells. Data looking at specific subsets of genes associated with (C) Chromatin Organization and (D) Double-Strand Break Repair shows few differences between strains.