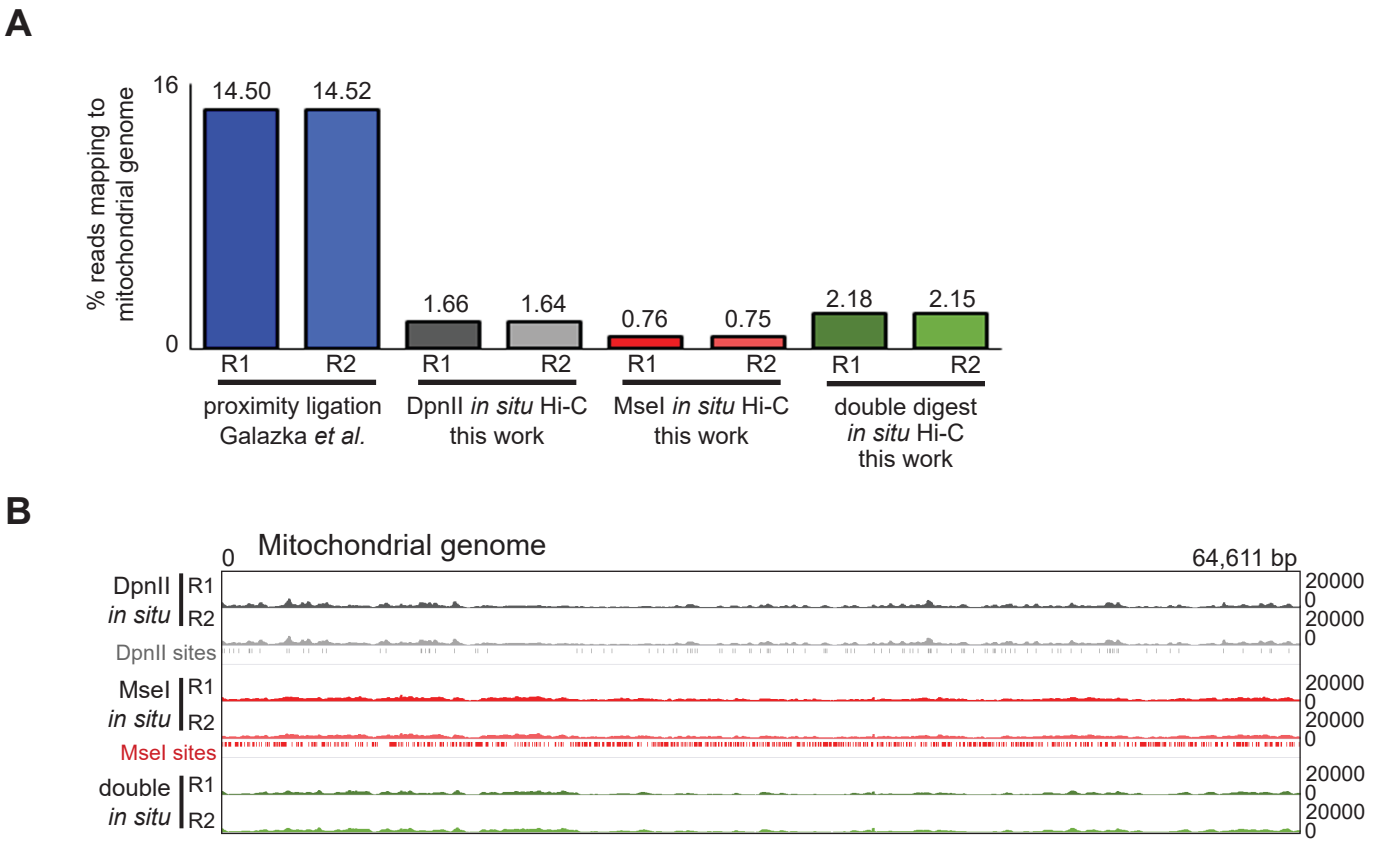

Figure S5. Comparison of proximal ligation and *in situ* Hi-C datasets of *Neurospora crassa* for aberrant, inter-organelle mitochondrial genome contacts. (A). Graph of the percent of reads from R1 and R2 fastq files of proximity ligation (Galazka et al. 2016) or *in situ* (DpnII, MseI, or DpnII+MseI double digest; this work) merged Hi-C datasets that map to the mitochondrial genome of *Neurospora crassa*; absolute percentage values reported at top of bars. (B). Image of IGV tracks of those reads that mapped to the mitochondrial genome from merged DpnII (gray), merged MseI (red), or merged DpnII+MseI double digest *in situ* Hi-C datasets. Tracks of DpnII and MseI restriction sites shown in gray and red, respectively, below the mapped read TDF tracks for DpnII and MseI.