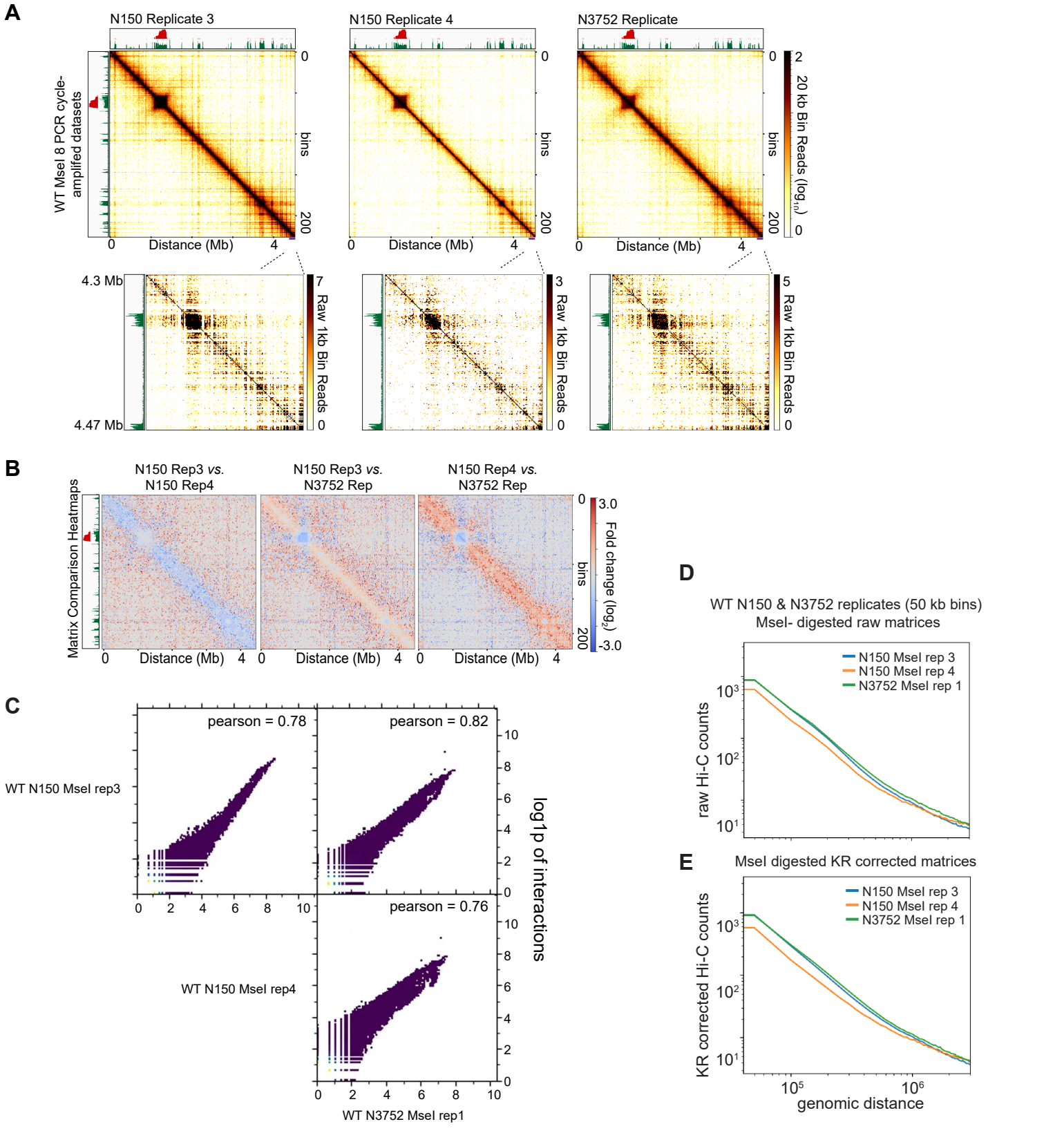

Figure S8. Replicate analysis of *in situ* Hi-C genome organization datasets using MseI restriction enzyme, with libraries amplified by eight PCR cycles, of strains of *Neurospora crassa*. (A). Top: Raw count Hi-C heatmaps of genomic interactions across LG II of MseI-derived *in situ* Hi-C replicate datasets at 20 kb bin resolution. Purple line indicates region highlighted in 1 kb bin resolution images below. Below: Raw count Hi-C heatmaps of genomic interactions at 1 kb bin resolution within the ~150 kb region highlighted above. IGV images of H3K9me3 (green) ChIP-seq enrichment track to the left. (B). Heatmaps comparing genomic interactions across LG II of MseI-derived *in situ* Hi-C replicate datasets at 20 kb bin resolution. (C) Scatter plots comparing interactions between each WT MseI replicate matrix at 20kb bin resolution; log1p values of interactions presented. Pearson correlation values of each binary comparison shown at the upper right. Image produced by hicCorrelate program in hicExplorer. (D-E) Genomic distance vs. contact strength plots of the MseI *in situ* Hi-C replicates. Plots were generated using the raw (D) or KR-corrected (E) contact matrices at 50 kb bin resolution using the hicExplorer command hicPlotDistVsCounts.