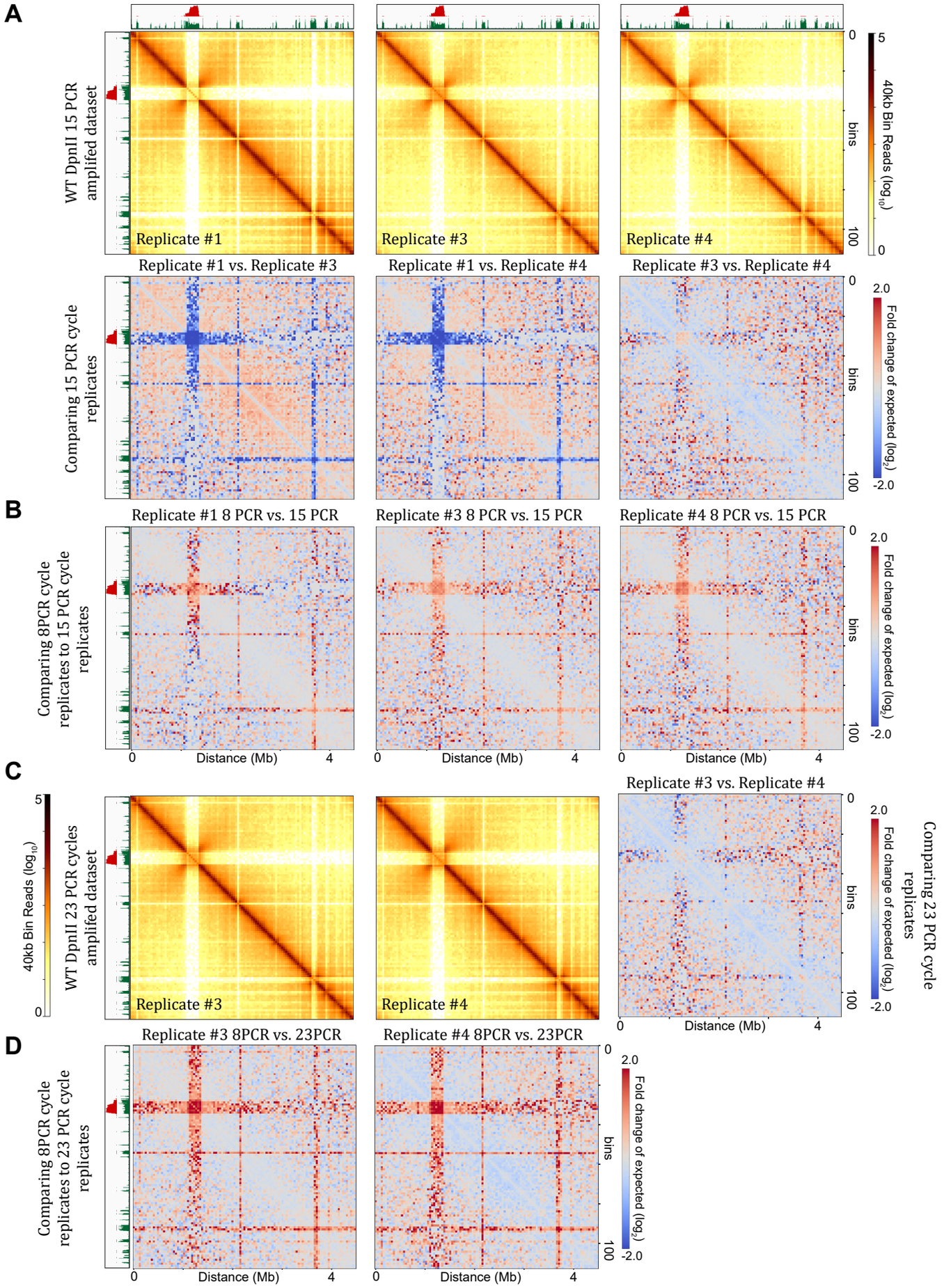

Figure S2. Replicate analysis of DpnII in situ Hi-C datasets amplified with 15 or 23 PCR cycles compared to DpnII *in situ* Hi-C replicates amplified with eight PCR cycles. (A). Top: Raw count Hi-C heatmaps of genomic interactions across LG II of DpnII-derived *in situ* Hi-C replicate datasets at 40 kb bin resolution amplified with 15 PCR cycles. Below: Heatmaps comparing genomic interactions across LG II of those three DpnII-derived *in situ* Hi-C replicate datasets amplified with 15 PCR cycles at 40 kb bin resolution. (B). Heatmaps comparing genomic interactions across LG II of DpnII-derived *in situ* Hi-C replicate datasets amplified with eight PCR cycles to the replicates amplified with 15 PCR cycles at 40 kb bin resolution; only directly comparable datasets from strain N150 were examined. (C). Left: Raw count Hi-C heatmaps of genomic interactions across LG II of two DpnII-derived *in situ* Hi-C replicate datasets at 40 kb bin resolution amplified with a total of 23 PCR cycles. Right: Heatmaps comparing genomic interactions across LG II of those two DpnII-derived *in situ* Hi-C replicate datasets amplified with 23 total PCR cycles at 40 kb bin resolution. (D). Heatmaps comparing genomic interactions across LG II of DpnII-derived *in situ* Hi-C replicate datasets amplified with eight PCR cycles to the replicates amplified with a total of 23 PCR cycles at 40 kb bin resolution; only directly comparable datasets from strain N150 were examined.