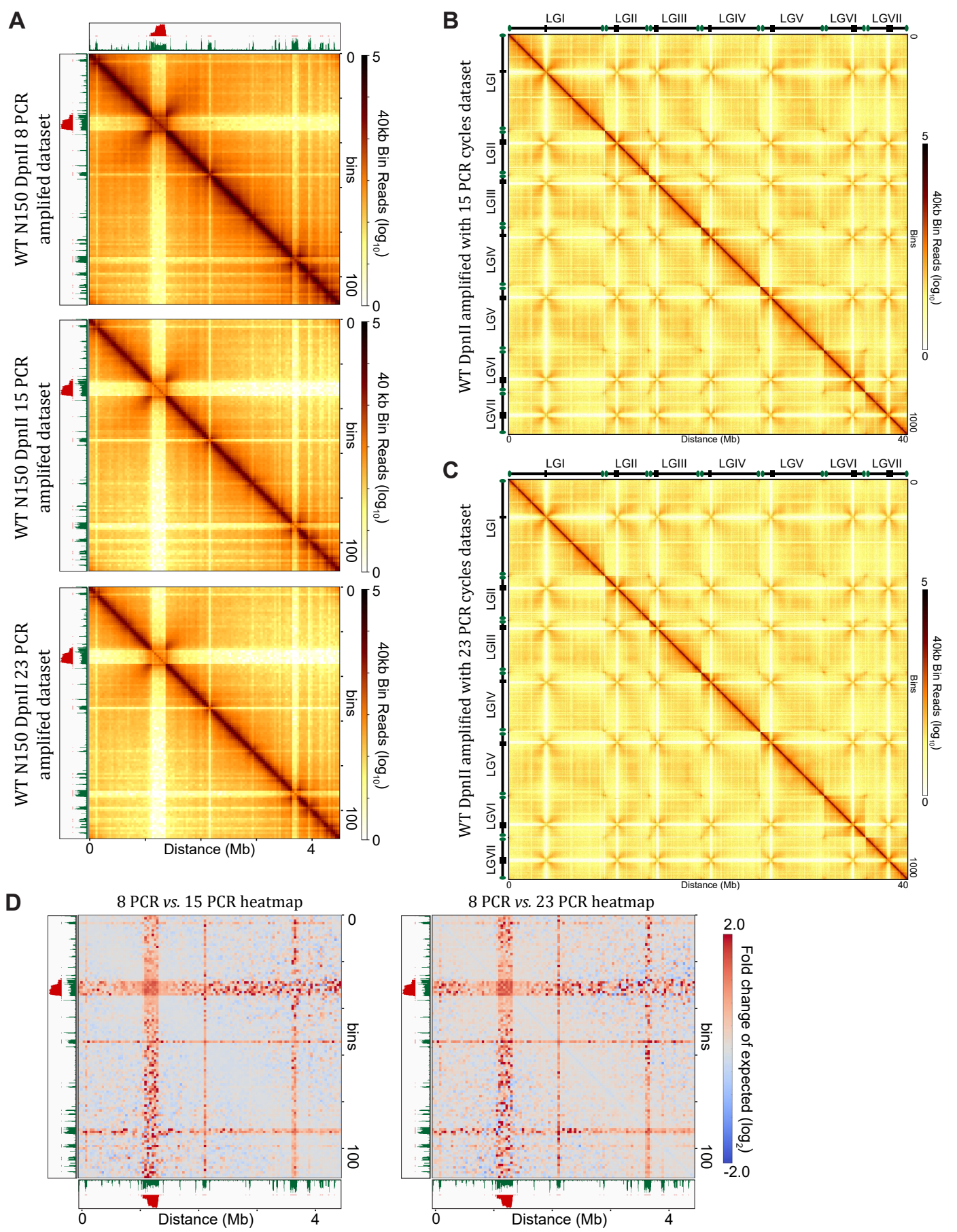

Figure S3. Comparison of merged DpnII *in situ* Hi-C datasets of libraries amplified with 8, 15, and 23 PCR cycles. (A). Raw count Hi-C heatmaps of genomic interactions across LG II of DpnII-derived *in situ* Hi-C datasets, in which all replicates from wild type strain N150 were merged at 40 kb bin resolution amplified with eight (top), 15 (middle), or 23 (fifteen cycles initially, then another eight cycles; bottom) PCR cycles. (B-C). Raw count Hi-C heatmap of genomic interactions across the entire Neurospora genome of DpnII-derived, replicate-merged *in situ* Hi-C datasets at 40 kb bin resolution amplified with 15 (B), or 23 (C) PCR cycles. Schematics of the seven Neurospora chromosomes above and to the left; green circles indicate telomeres while black boxes show centromere positions. (D). Heatmaps comparing genomic interactions across LG II of the DpnII-derived, replicate-merged *in situ* Hi-C dataset amplified with eight PCR cycles to the replicate-merged datasets amplified with 15 (left) or 23 (right) PCR cycles at 40 kb bin resolution; only replicates from wild type strain N150 were merged for this comparison.