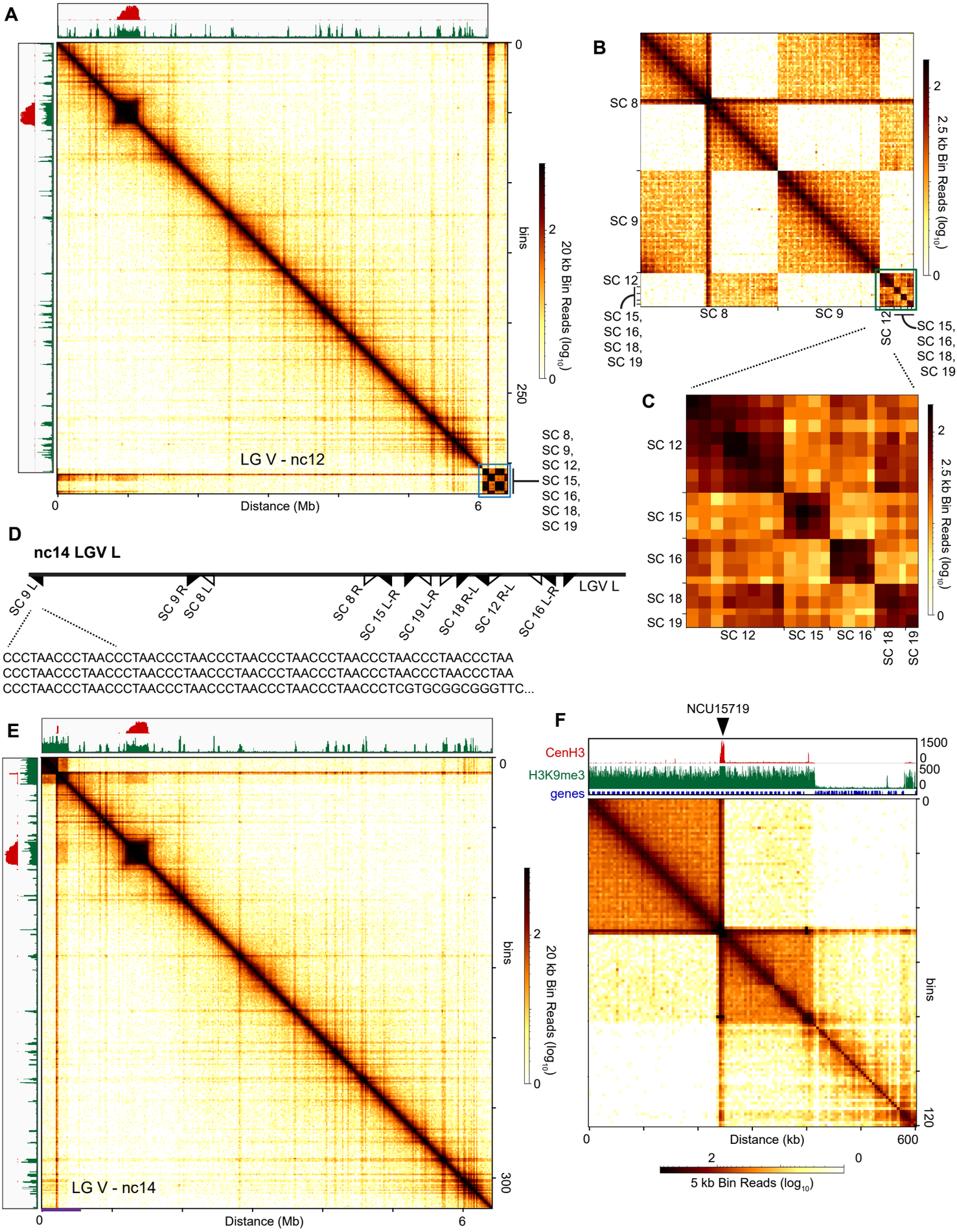

Figure S13. High resolution MseI Hi-C data allowed Linkage Group V to be corrected. (A) Heatmap displaying raw read count *in situ* Hi-C contacts across Linkage Group V (LG V) and the previously unplaced Supercontigs (SC) 8, 9, 12, 15, 16, 18, and 19 using the merged 72M MseI dataset at 20 kb bins; reads were mapped to the Neurospora genome version 12 (nc12). Blue box shows region highlighted in B. IGV images of CenH3 (red) and H3K9me3 (green) ChIP-seq enrichment tracks above and to the left of the heatmap. (B). Heatmap displaying raw read count *in situ* Hi-C contacts, mapped to nc12, between SCs 8, 9, 12, 15, 16, 18, and 19 using the merged 72M MseI dataset at 2.5 kb bins. Green box shows region highlighted in C of the smaller SCs 12, 15, 16, 18, and 19. (C). Heatmap displaying raw read count *in situ* Hi-C contacts, mapped to nc12, between SCs 12, 15, 16, 18, and 19 using the merged 72M MseI dataset at 2.5 kb bins. (D). Top: Schematic of the direction and orientation of the previously unmapped SCs 8, 9, 12, 15, 16, 18, and 19 now placed at the heterochromatic region within the left telomere of LG V (starting at 0 Mb for SC 9), as established by the strong contacts between those LGs and LG V in panel B-C heatmaps. Bottom: DNA sequence of the left side of SC 9 showing the telomeric repeat sequences found on that SC, showing SC 9 must be the terminal sequence of LG V within the nc14 genome. (E). Heatmap displaying raw read count *in situ* Hi-C contacts across Linkage Group V (LG V), as in A, except that reads were mapped to the corrected Neurospora genome version 14 (nc14). Purple line shows the region magnified in panel F. (F). Magnified heatmap displaying raw read count *in situ* Hi-C contacts across the left end of Linkage Group V (LG V). IGV image of CenH3 (red) or H3K9me3 (green) ChIP-seq enrichment tracks, mapped to nc14, above the heatmap. Black arrowhead shows the location of the ribosomal DNA gene NCU15719 that is amplified ~46 to 71 times at that location, as calculated from the amplified CenH3 signal (~1500) relative to "background" CenH3 signal (21-32) across nearby, single copy rDNA genes at that location. Note, the sequence of SC 20 is identical to a portion of the rDNA gene sequence and was excluded from placement in the nc14 genome.