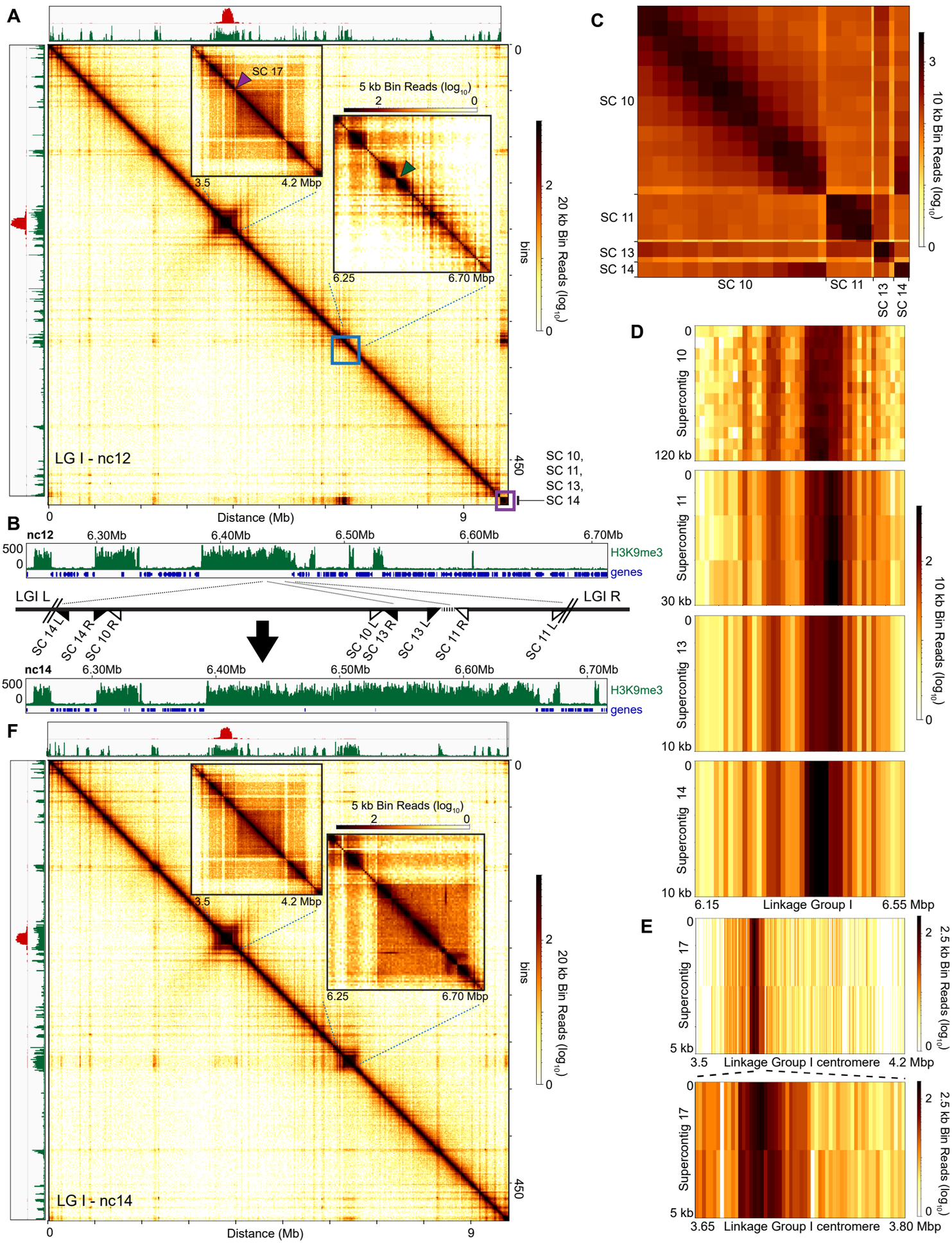

Figure S12. High resolution MseI Hi-C data allowed Linkage Group I to be corrected. (A) Heatmap displaying raw read count *in situ* Hi-C contacts across Linkage Group I (LG I) and the previously unplaced Supercontigs (SC) 10, 11, 13, and 14 using the merged 72M MseI dataset at 20 kb bins; reads were mapped to the Neurospora genome version 12 (nc12). Insets show the LG I centromere and a heterochromatic region at ~6.40 Mb. Blue box shows the expanded area in the inset for the heterochromatic region at ~6.40 Mb, purple and green arrows highlight where the unmapped linkage groups were inserted. Purple 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). Top and bottom: IGV images of H3K9me3 ChIP-seq tracks of the heterochromatic region starting at ~6.40 Mb, with reads mapped to either nc12 (top) or nc14 (bottom). Center: schematic of the direction and orientation of the previously unmapped SCs 10, 11, 13, and 14 now placed in the heterochromatic region of LG I starting at ~6.40 Mb, as established by the strong contacts between those SCs and LG I in panel C heatmaps. (C). Heatmap displaying raw read count *in situ* Hi-C contacts, mapped to nc12, between SCs 10, 11, 13, and 14 using the merged 72M MseI dataset at 10 kb bins. (D). Heatmap comparing the raw read count *in situ* Hi-C contacts between LG I, between 6.15 and 6.55 Mb, to the SCs 10, 11, 13, and 14 using the merged 72M MseI dataset at 10 kb bins to determine where and how these unplaced SCs contact this heterochromatic region in LG I. (E). Heatmap comparing the raw read count *in situ* Hi-C contacts between the LG I centromere to the previously unplaced SC 17 using the merged 72M MseI dataset at 2.5 kb bins. Bottom heatmap is a further magnified area of the entire LG I centromeric region (top heatmap, from ~3.5 Mb to ~4.2 Mb) to determine where SC 17 interacts. (F). Heatmap displaying raw read count *in situ* Hi-C contacts across Linkage Group I (LG I), as in A, except that reads were mapped to the corrected Neurospora genome version 14 (nc14). Insets show the LG I centromere and a heterochromatic region at ~6.40 Mb.