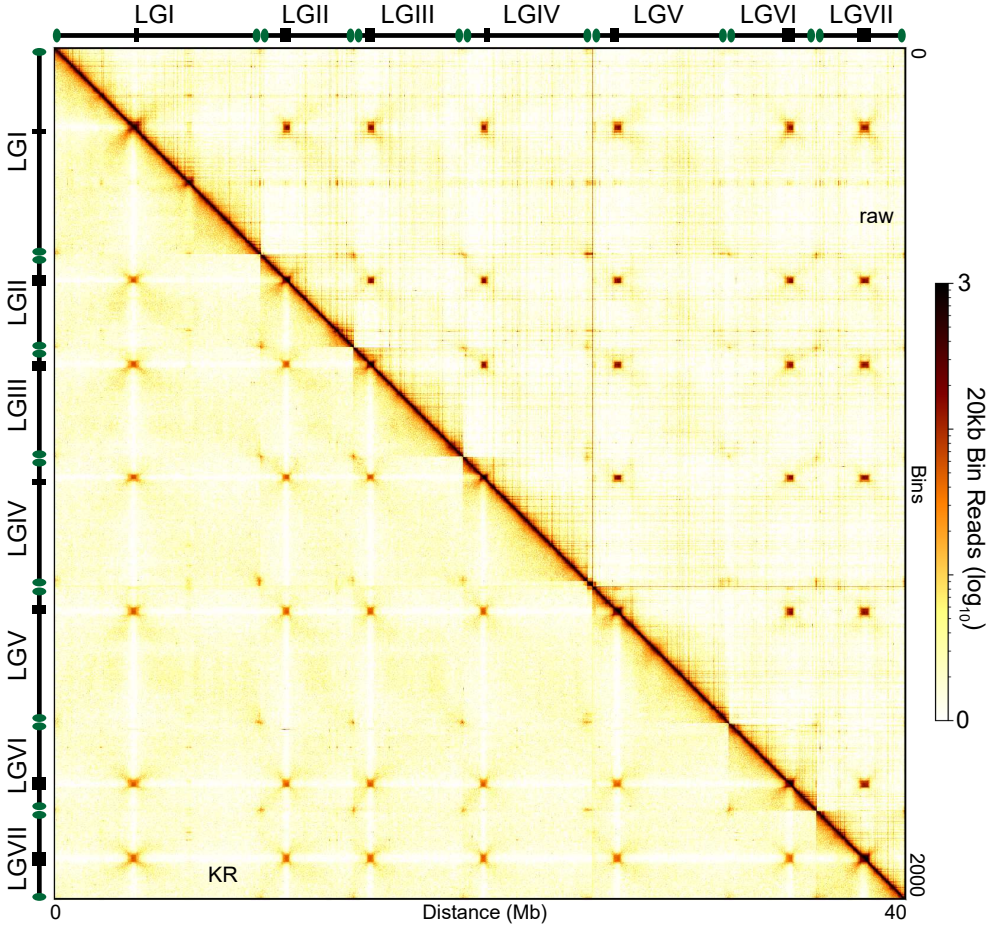

Figure S11. Chromosome conformation of the entire *Neurospora crassa* genome using the restriction enzyme MseI. Heatmap displaying *in situ* Hi-C contacts, either as raw read counts (above diagonal) or KR-corrected counts (below diagonal), across the entire Neurospora genome of the merged 72M MseI dataset at 20 kb bins; contact matrix was generated using reads mapped to the nc14 genome (this work). Schematics of the seven Neurospora chromosomes above and to the left; green circles indicate telomeres while black boxes show centromere positions.