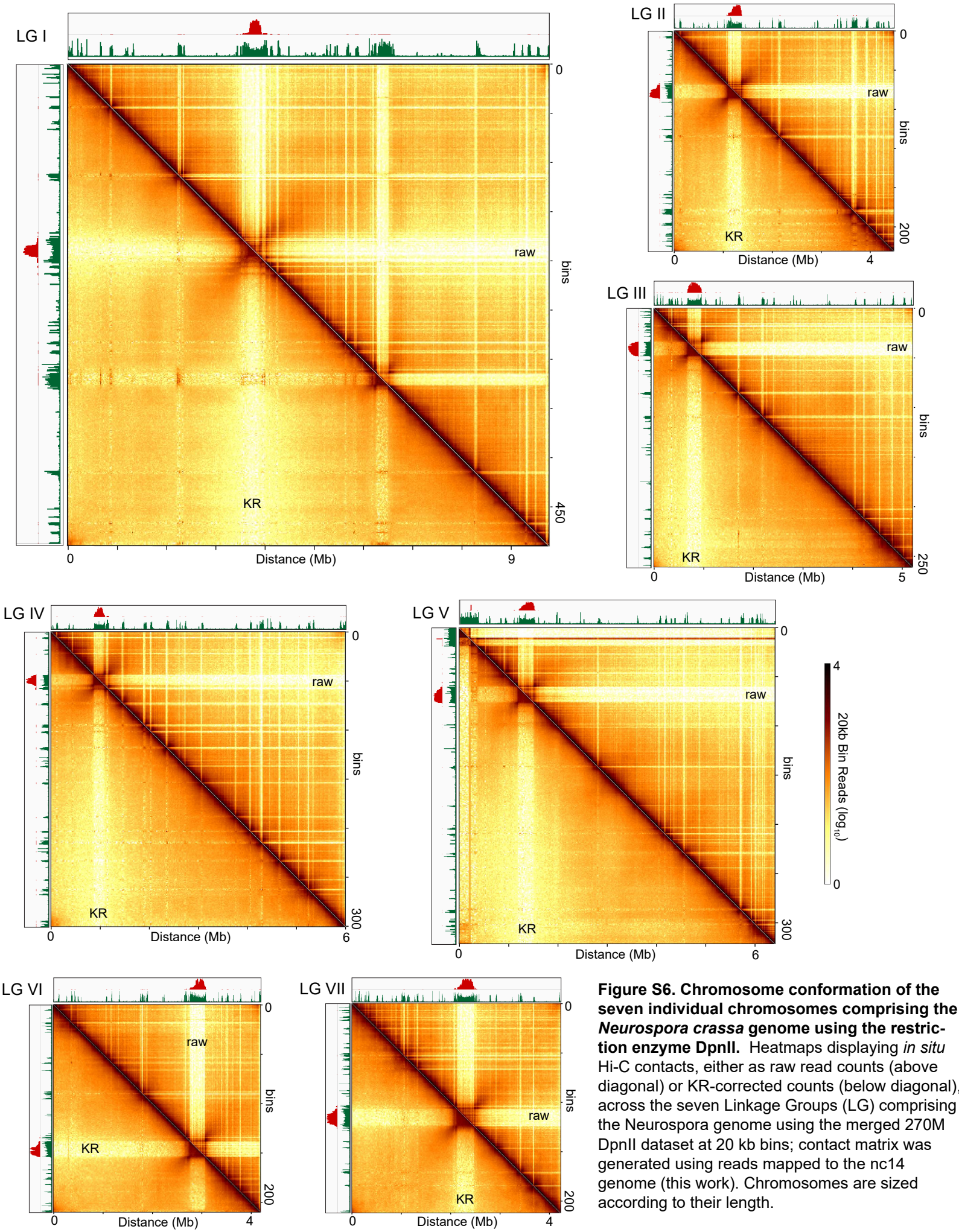

Figure S6. Chromosome conformation of the seven individual chromosomes comprising the *Neurospora crassa* genome using the restriction enzyme DpnII. Heatmaps displaying *in situ* Hi-C contacts, either as raw read counts (above diagonal) or KR-corrected counts (below diagonal), across the seven Linkage Groups (LG) comprising the Neurospora genome using the merged 270M DpnII dataset at 20 kb bins; contact matrix was generated using reads mapped to the nc14 genome (this work). Chromosomes are sized according to their length.