



Figure S16. Chromosome conformation of the seven individual chromosomes comprising the *Neurospora crassa* genome of the combined 342M total read (106M valid read) dataset. 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 of the combined DpnII (270M total reads) and MseI (72M reads) dataset at 10 kb bins; contact matrix was generated by merging DpnII and MseI fastq files and mapping reads to the nc14 genome (this work). Chromosomes are sized according to their length. IGV images of CenH3 (red), H3K9me3 (green), and H3K27me2/3 (purple) ChIP-seq enrichment tracks above and to the left of each heatmap.