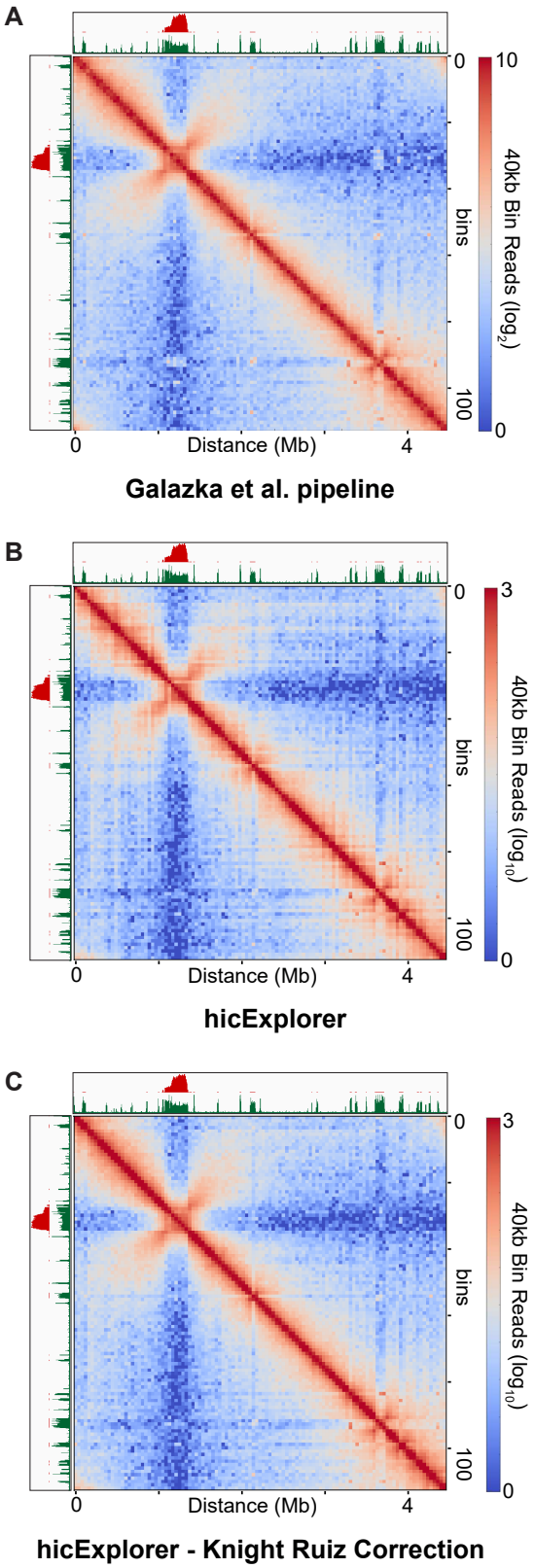

Figure S1. Confirmation of hicExplorer software package for Hi-C data analysis. (A). Unpublished image of LG II interactions at 40 kb bin resolution within the Hi-C dataset from (Galazka et al. 2016) produced with the computational pipeline described within, which was derived from the original Hi-C analyses (Lieberman-Aiden et al. 2009); bin numbers and genomic distance (in Megabases) shown to the left and below, respectively. Here, and in all supplemental figures unless indicated, IGV images of CenH3 (red) and H3K9me3 (green) ChIP-seq enrichment tracks flank the heatmaps. (B-C). Images of the LG II interactions within the Hi-C dataset from (Galazka et al. 2016) produced by re-processing the original fastq files using the hicExplorer suite of programs; images of Hi-C raw read counts (B) or Knight-Ruiz corrected read counts (C) are shown.