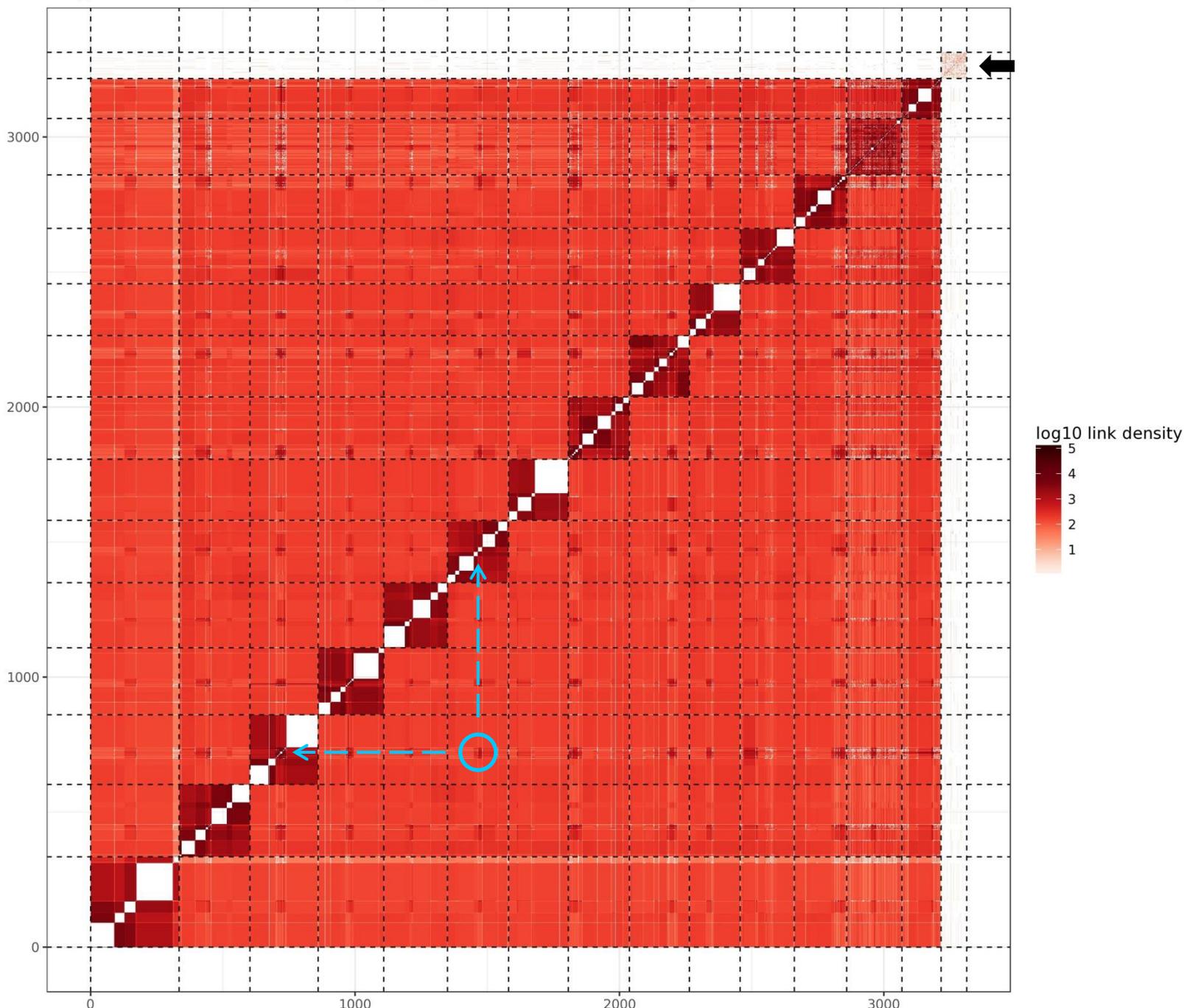


Ant_6 Post-Scaffolding Heatmap by length, chunk size = 75778 bp



Supplementary Figure S1: Heat map of HiC linkage between contigs within the clonal raider ant genome (before filtering bacterial sequences and gap filling and polishing steps). One large cluster (black arrow) shows extremely low coverage and virtually no linkage to the rest of the genome, and was found to belong to a *Sphingomonas* bacterium based on BLAST similarity to sequences in the NCBI non-redundant protein database. Centromeres can be observed as areas of high pan-chromosomal linkage (many interactions with specific areas on all chromosomes). One such interaction hotspot is circled in blue and the corresponding putatively centromeric contigs are indicated with blue arrows.