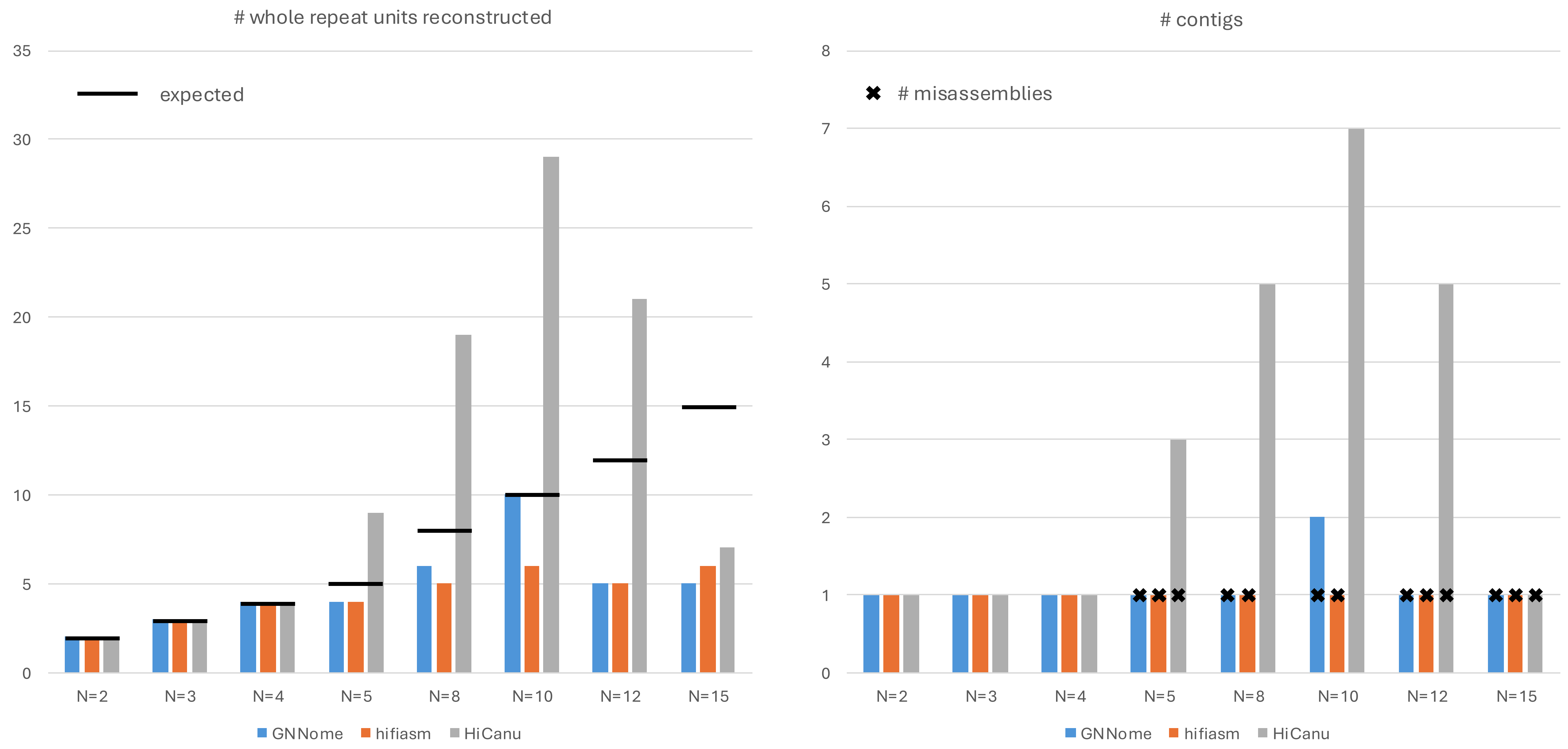

Supplemental Figure S4: Analysis of assemblies of simulated genomes with a varying number of perfect repeat units (N). The assemblers shown are GNNome (blue), hifiasm (orange), and HiCanu (grey). Left: number of whole repeat units reconstructed for each assembler and each genome, together with the expected number of units (black line). Right: Number of contigs produced by each assembler for each genome, together with the number of misassemblies (black cross).