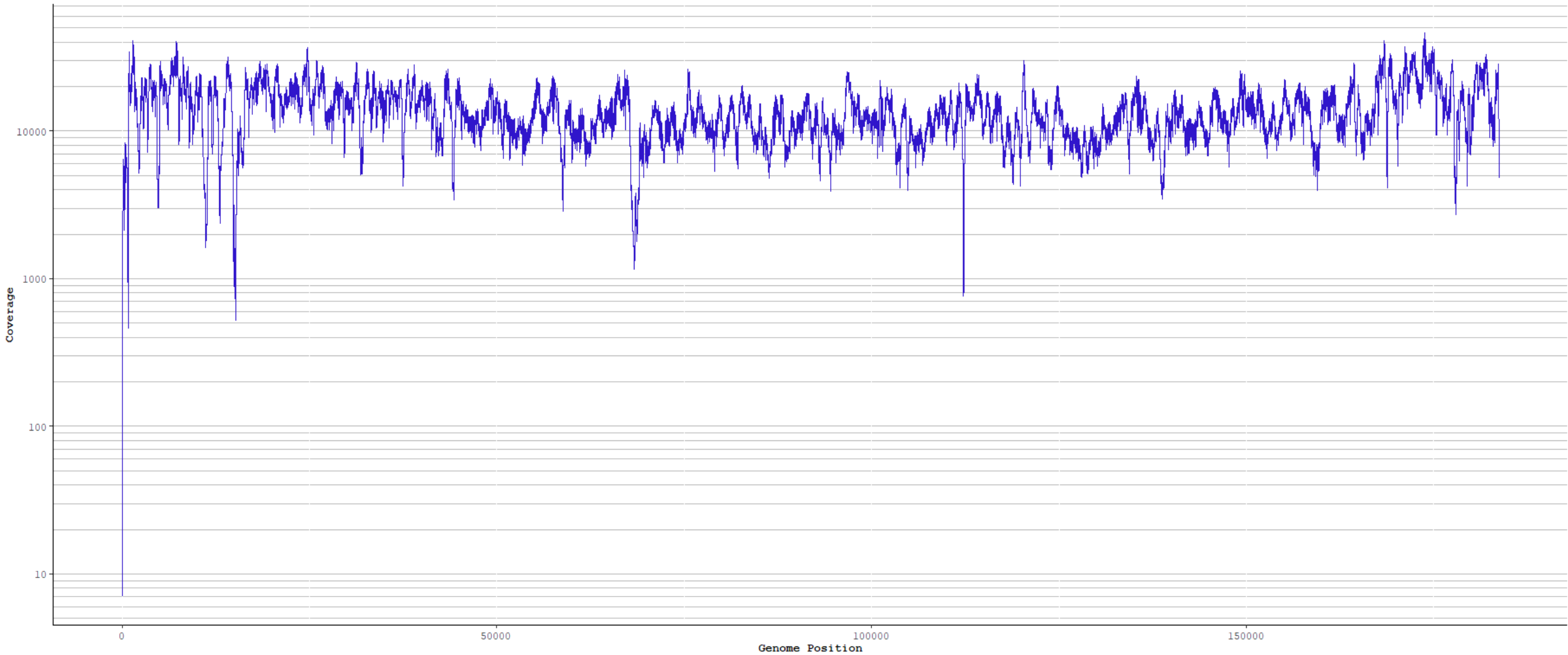Supplemental Figure 2. Trimmed Illumina reads were mapped backed to the DR-1980 genome using the default parameters of the Map Reads to Contigs module of CLC Genomics Workbench. The depth of coverage (y) is indicated at each position of the genome (x).