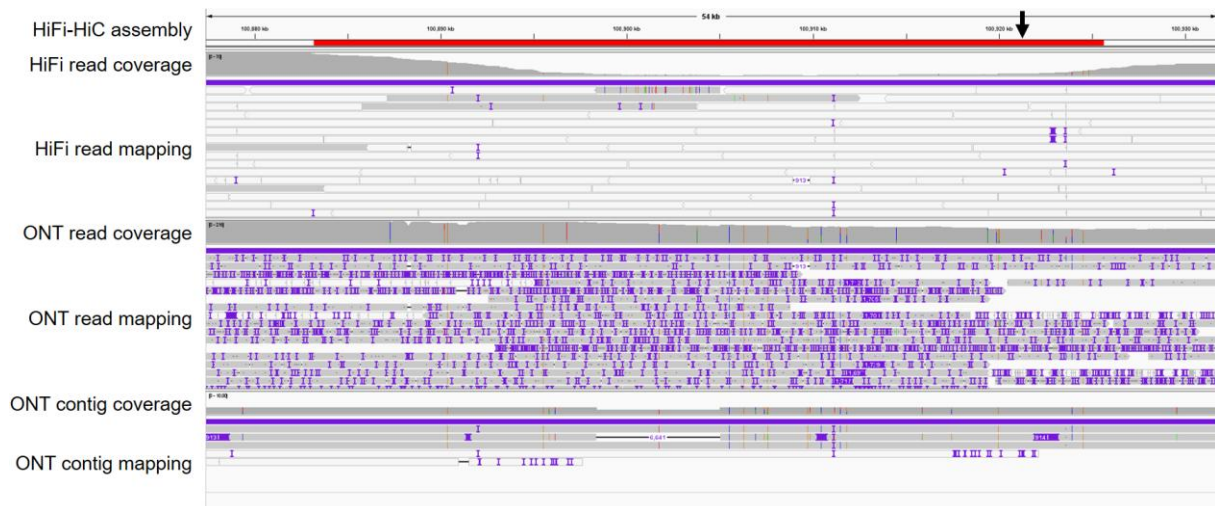




Supplementary Fig. 4 Gap filling of the HiFi assembly using the Oxford Nanopore Technologies (ONT) contigs spanning the gap. Integrative Genomics Viewer (IGV) screenshots show the PacBio HiFi reads, the ONT reads and the ONT contig alignments, which aligned to the final assemblies. The tracks represent the final assembly, HiFi reads coverage, HiFi reads mapping, ONT reads coverage, ONT reads mapping, ONT contig coverage, and ONT contig mapping, respectively. The black arrow represents the position of the gap. The results showed the reads supporting the assembly of *C. monnieri*.