Assembly of SARS-CoV-2 genome and sequence alignment

Alt-text Figure 7 - Two types of reads assembly methods

Schematic illustration describing two different methods for genome assembly. Resequencing aligns reads to a reference genome and identifies variants. *De novo* assembly constructs a genome sequence from overlaps between reads. Details in the main text.

Alt-text Figure 8 - Identification of a point mutation

Schematic illustration showing a reference genome and a query read being compared and highlighting a point mutation T>C. Details in the main text.