

User-friendly tools for quality control

Alt-text Figure 2 - Example read alignment

Illustrative example of a read alignment. Detailed description in the figure legend: Each read has been independently aligned to the reference sequence. Mutations within each read and with respect to the reference sequence are highlighted in red. Based on all the read alignments combined we can calculate a consensus sequence – the most frequent base observed at each genome position. As the majority of reads contain the two highlighted mutations, these are incorporated in the consensus sequence. This is an example with a short genome and low coverage with only between one and three reads covering each position