FastQC: Mean Quality Scores
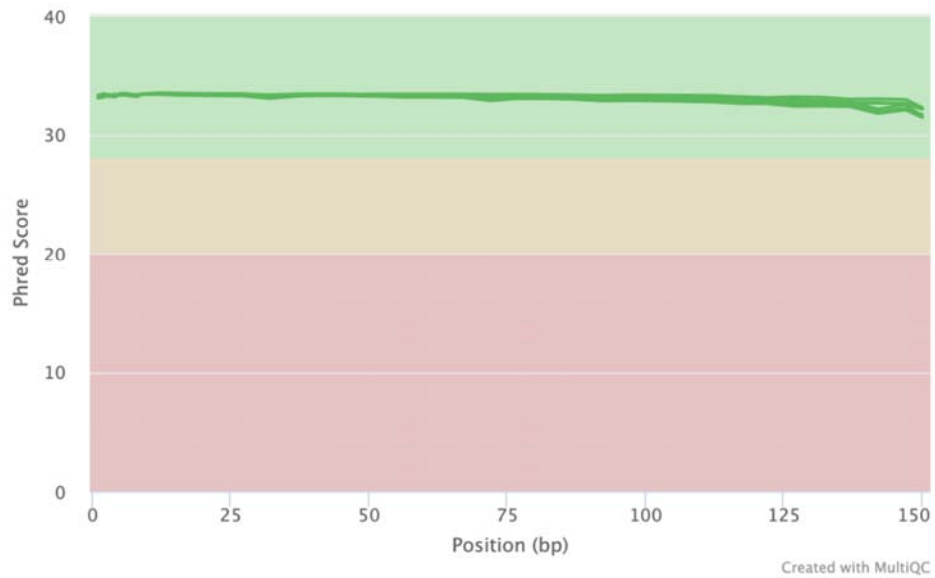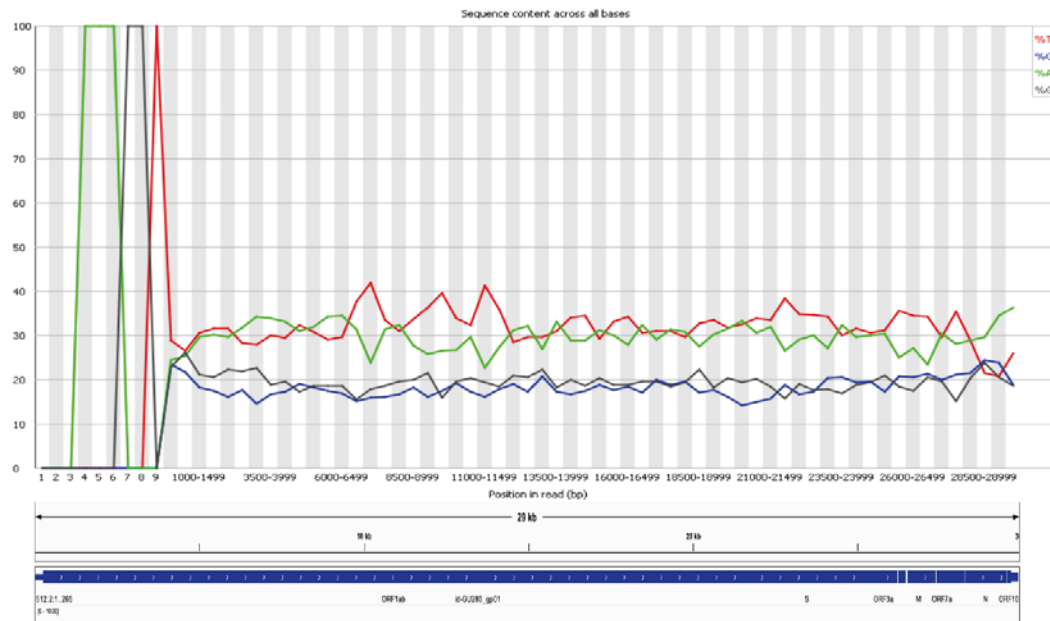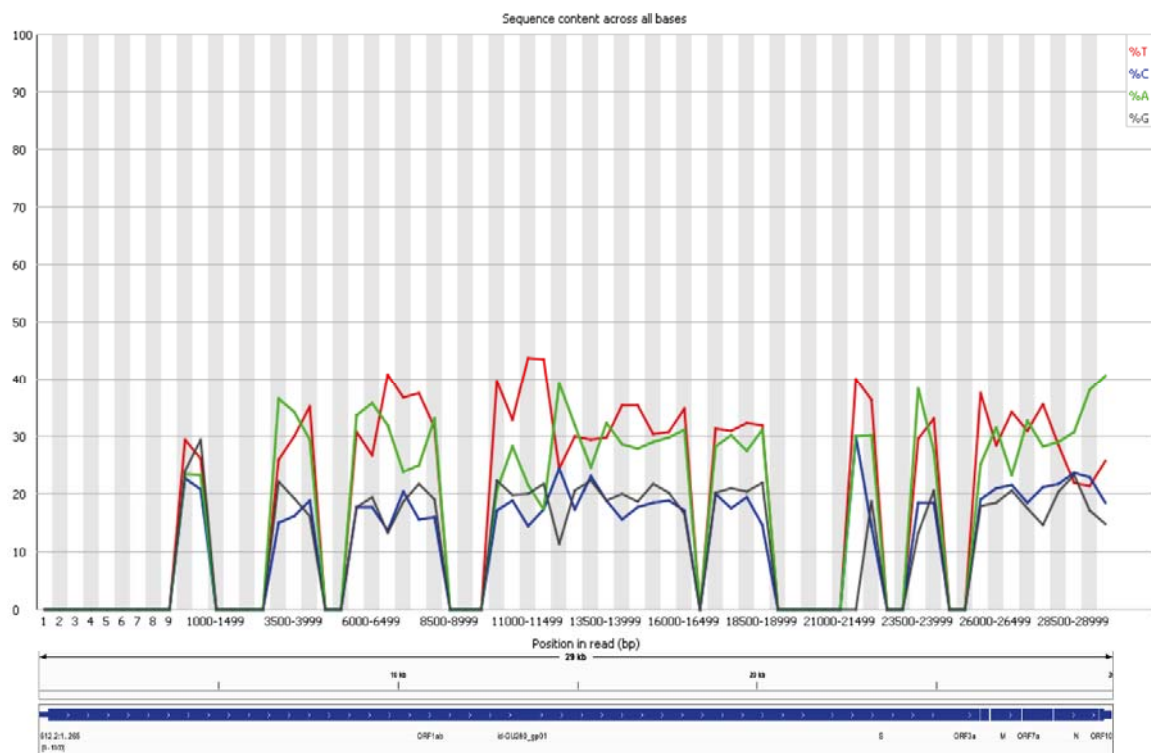

Supplementary Figure S1. Sequence quality score of the two positive samples sequenced (0806-191 and 230921-099). Mean sequence quality (Phred Score) y-axis. The graph is divided into the sequencing of excellent quality (green), acceptable quality (orange), and poor quality (red) concerning the number of bp on the x-axis. Both samples optimum sequencing quality. The quality analyzes were created with the MultiQC software

Supplementary Figure S2. Coverage of NGS in the SARS-CoV-2 genome of sample 0806-191.
Sequence content for all bases (T in red, C in blue, A in green, and G in black) and their position in
the read (bp) of sample 0806-191 (at 99.1% coverage). The coverage of the sequenced genes of the
SARS-CoV-2 genome (29 kbp) is shown. The quality analyzes were created with the FastQC software.

Supplementary Figure S3. Coverage of NGS in the SARS-CoV-2 genome of sample 230921-099. Sequence content for all bases (T in red, C in blue, A in green, and G in black) and their position in the read (bp) of sample 230921-099 (at 37.4% coverage). The coverage of the sequenced genes of the SARS-CoV-2 genome (29 kbp) is shown. The quality analyzes were created with the FastQC software.