Fig. S5. Comparison of transcription of different SARS-CoV-2 genes in wild-type (WT) versus ∆382 viruses. Abundance of mapped reads relative to transcriptional regulatory sequence (TRS) positions across the genome. Transcripts per million (TPM) reads were calculated from reads mapped specifically to each leader-TRS region and a whisker and scatter plot was drawn for each gene. A Wilcoxon test was applied to the TPM for each gene of ∆382 to WT (*: p ≤ 0.05  **: p ≤ 0.01).