



**Fig. S5. Comparison of transcription of different SARS-CoV-2 genes in wild-type (WT) versus  $\Delta 382$  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  $\Delta 382$  to WT (\*:  $p \leq 0.05$  \*\*:  $p \leq 0.01$ ).