Figure S1: Selective enrichment of other tRNA with modification profiles.
(a) Mutation fractions of tRNA$^{\text{Ser}}$(AGA) isodecoders from uninfected Vero cell ($n=3$, red) or viral preparations ($n=6$, blue) of the wobble anticodon position (I34).
(b) Mutation fractions of tRNA$^{\text{Lys}}$(TTT) isodecoders of position m1A58.
Figure S2: Subgenomic junction sites used in our large RNA analysis. Residue numbers are according to the Wuhan SARS-CoV-2 reference genome. Residues linking the 5’ leader and the subgenomic regions are indicated.
Figure S3: Stop signatures of the five sites in Fig. 6b.