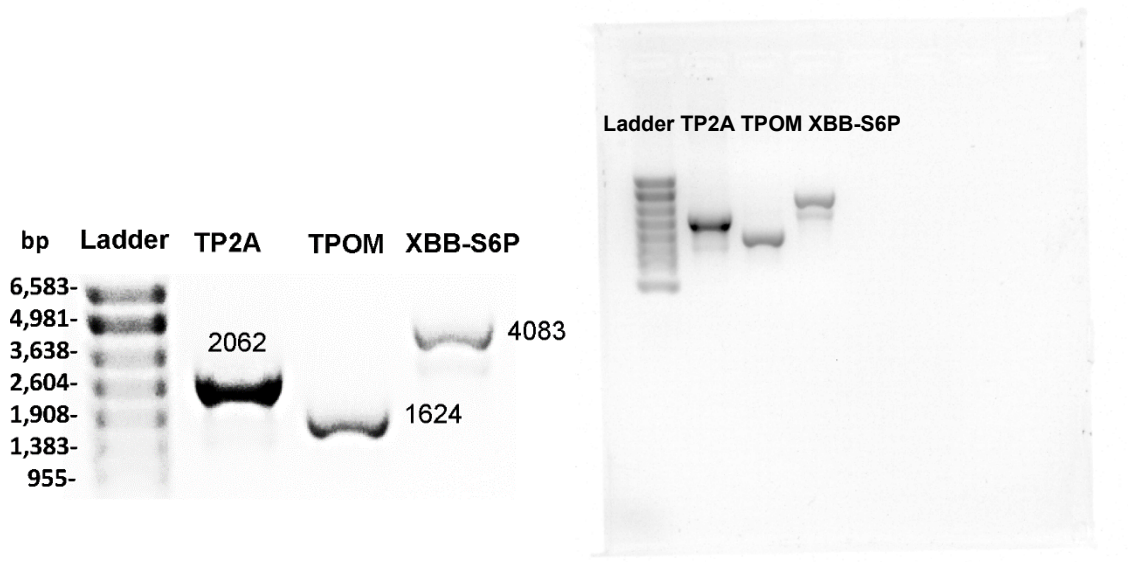
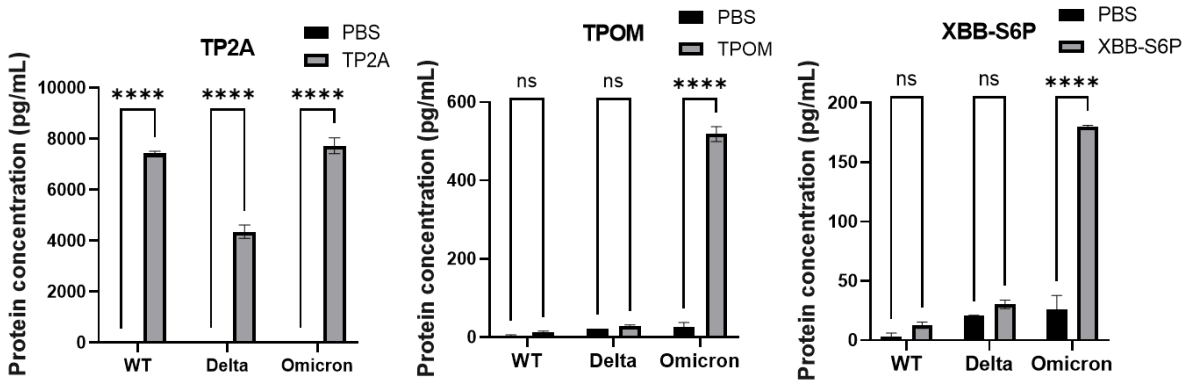
Supplementary information

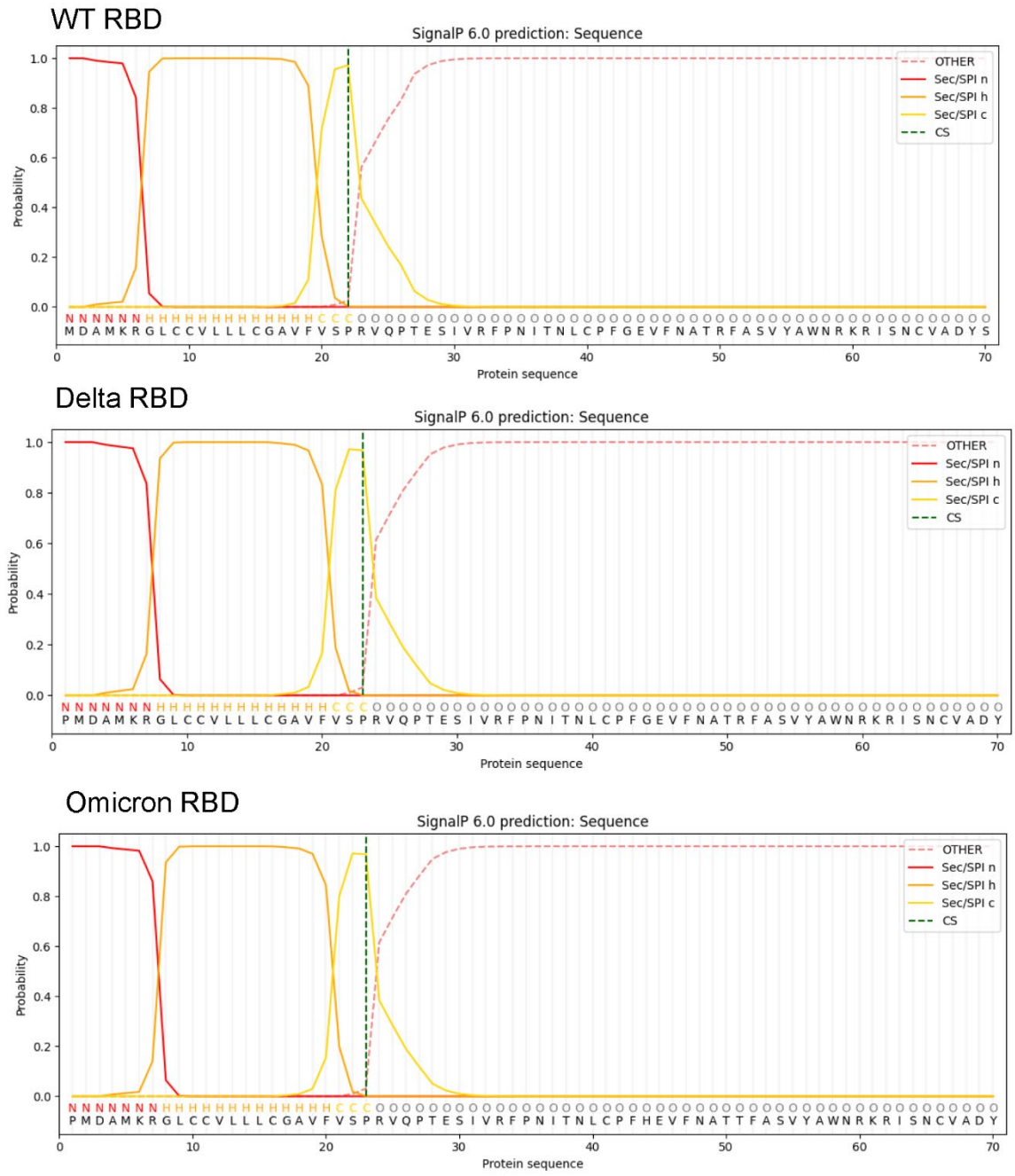
A **B**



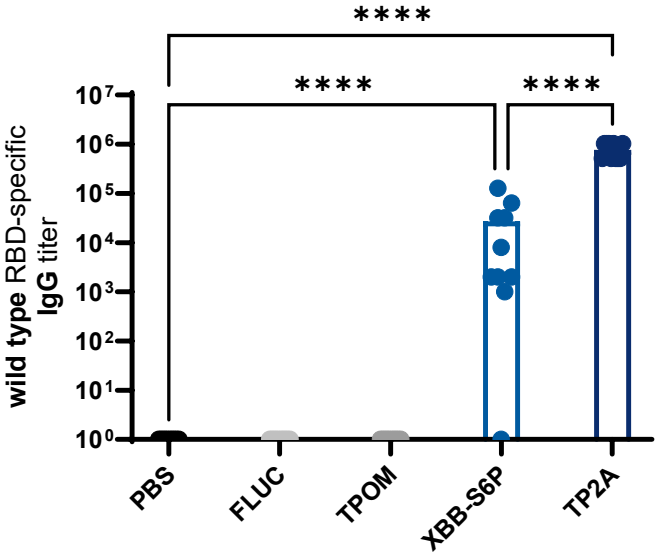
Supplementary Figure 1: **(A)** Agarose gel electrophoresis of *in vitro* transcribed RNA. RNA samples were transcribed *in vitro* and purified using lithium chloride precipitation. Lane 1: RNA ladder; Lane 2 – 4: *in vitro* transcribed RNA samples. The RNA was separated on a 1 % denaturing agarose gel. **(B)** The original uncropped gel.



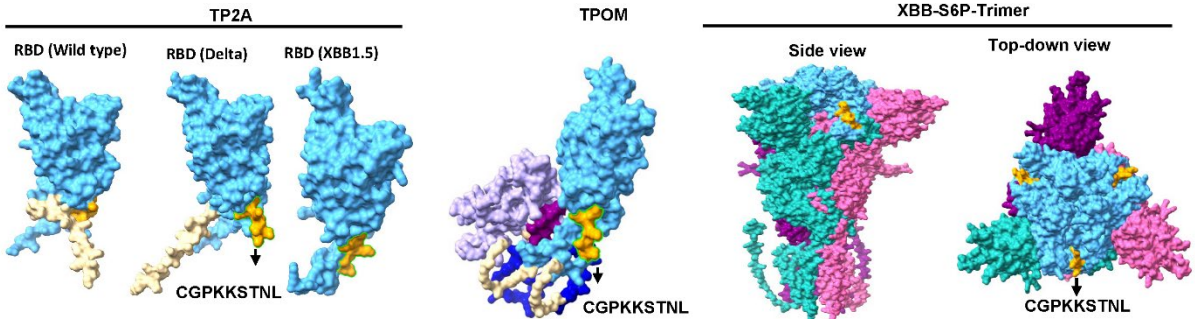
Supplementary Figure 2: The protein concentration of different vaccine candidates after transfected into 293T cells. Results are presented as mean ± SEM (n = 3). Adjusted P values were determined by a two-way ANOVA followed by Tukey's multiple comparisons test. ****p < 0.0001.



Supplementary Figure 3: The additional proline residue (P) that left at the N-terminus due to P2A has no effect on signal peptide activity predicted by SignalP-6.0.



Supplementary Figure 4: Total IgG titers specific for the WT receptor binding domain (RBD) protein. Mice were immunized three times in a two-week interval with LNP-encapsulated mRNA constructs encoding TP2A, TPOM, or XBB-S6P. Sera were collected on day 42 and analyzed by ELISA. RBD-specific total IgG levels were measured using serial dilutions against recombinant WT RBD proteins. Results represent mean ± SEM (n = 10 mice/group). Statistical analysis was performed using lognormal one-way ANOVA followed by Tukey's multiple comparisons test (**** $p < 0.0001$).



Supplementary Figure 5: The predicted position of the H-2D^d-restricted peptide epitope CGPKKSTNL (yellow) within RBD region (light blue) of the protein structure in mRNA vaccine candidates.