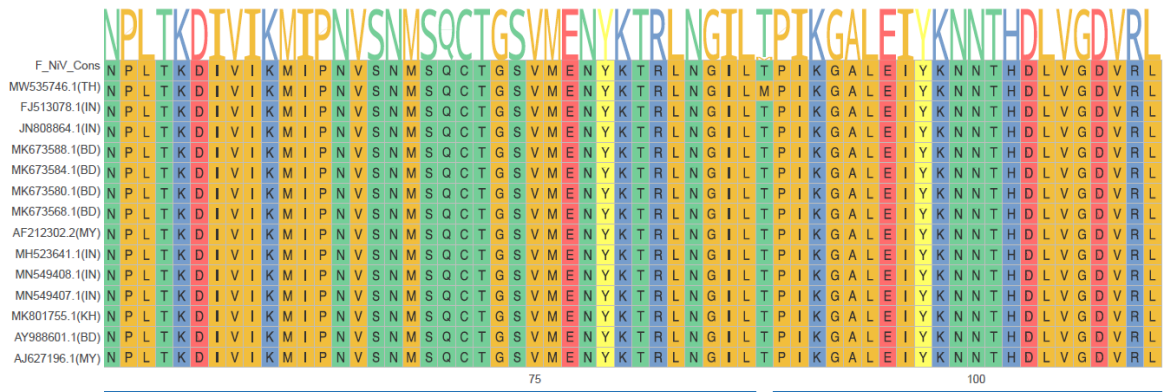


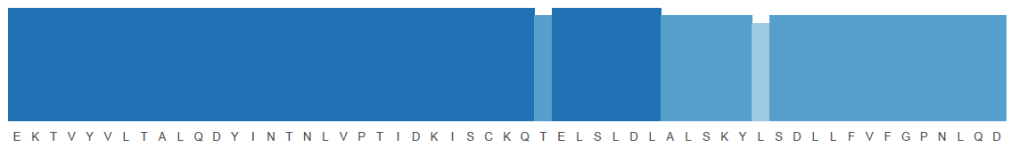
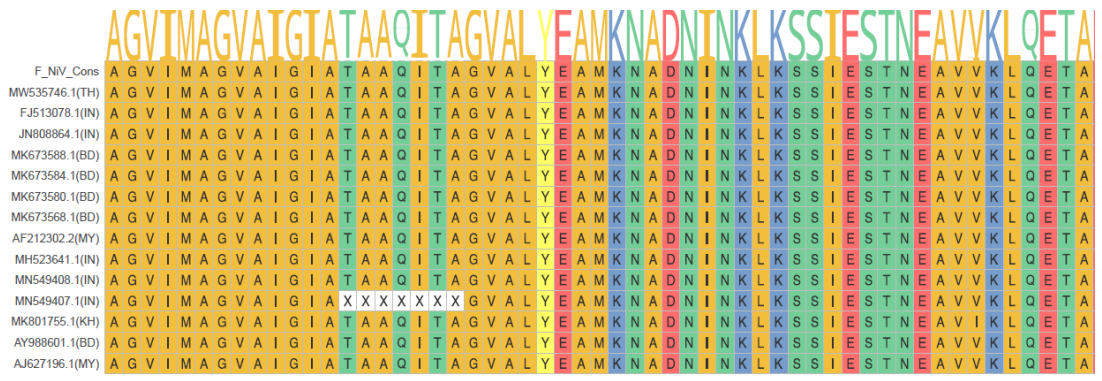
A



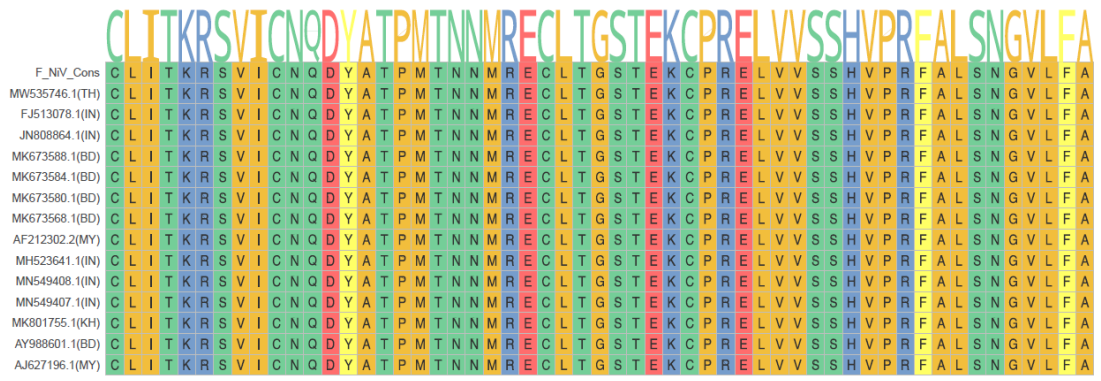
consensus

N P L T K D I V I K M I P N V S N M S Q C T G S V M E N Y K T R L N G I L T P I K G A L E I Y K N N T H D L V G D V R L

B



D

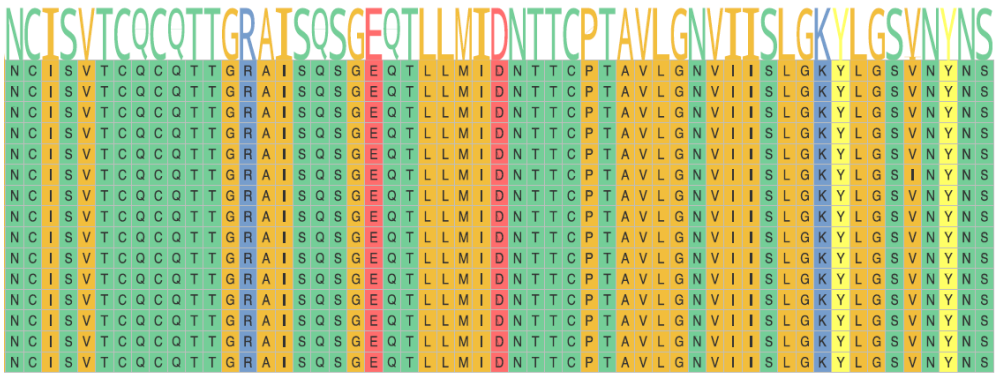


360

consensus



C L I T K R S V I C N Q D Y A T P M T N N M R E C L T G S T E K C P R E L V V S S H V P R F A L S N G V L F A



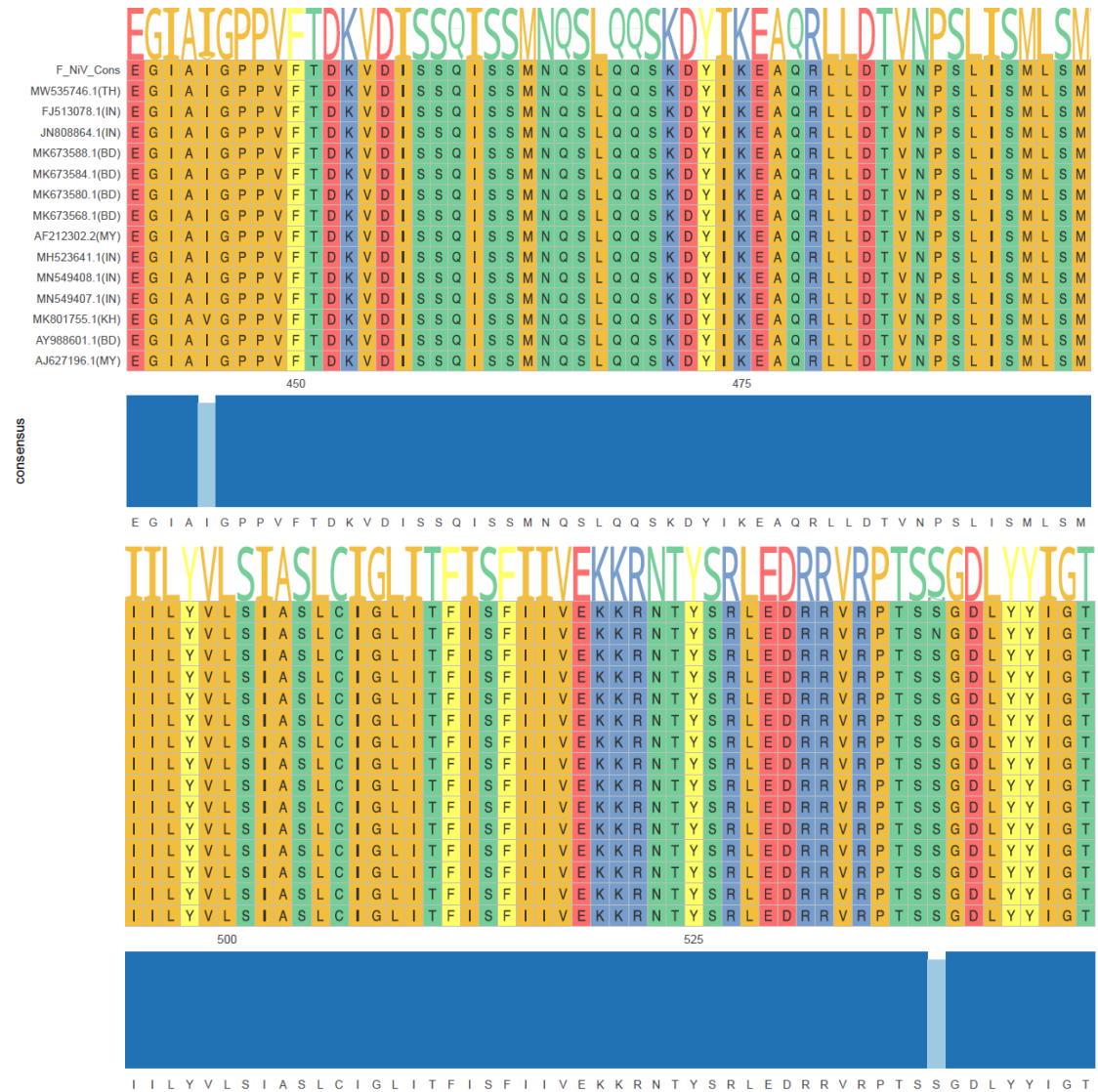
390

420



N C I S V T C Q C Q T T G R A I S S Q S G E Q T L L M I D N T T C P T A V L G N V I I S L G K Y L G S V N Y N S

E



Supplemental Figure 1 The consensus sequence of the F protein in the vaccine study by bioinformatics analysis. In addition to the sequences presented in the text. (A) 51-110 aa, (B) 111-220aa, (C) 221-330aa, (D) 331-440aa, (E) 441-546aa. Sequences were shown by ggmsa function analysis in the R software package obtained amino acid consistency results.