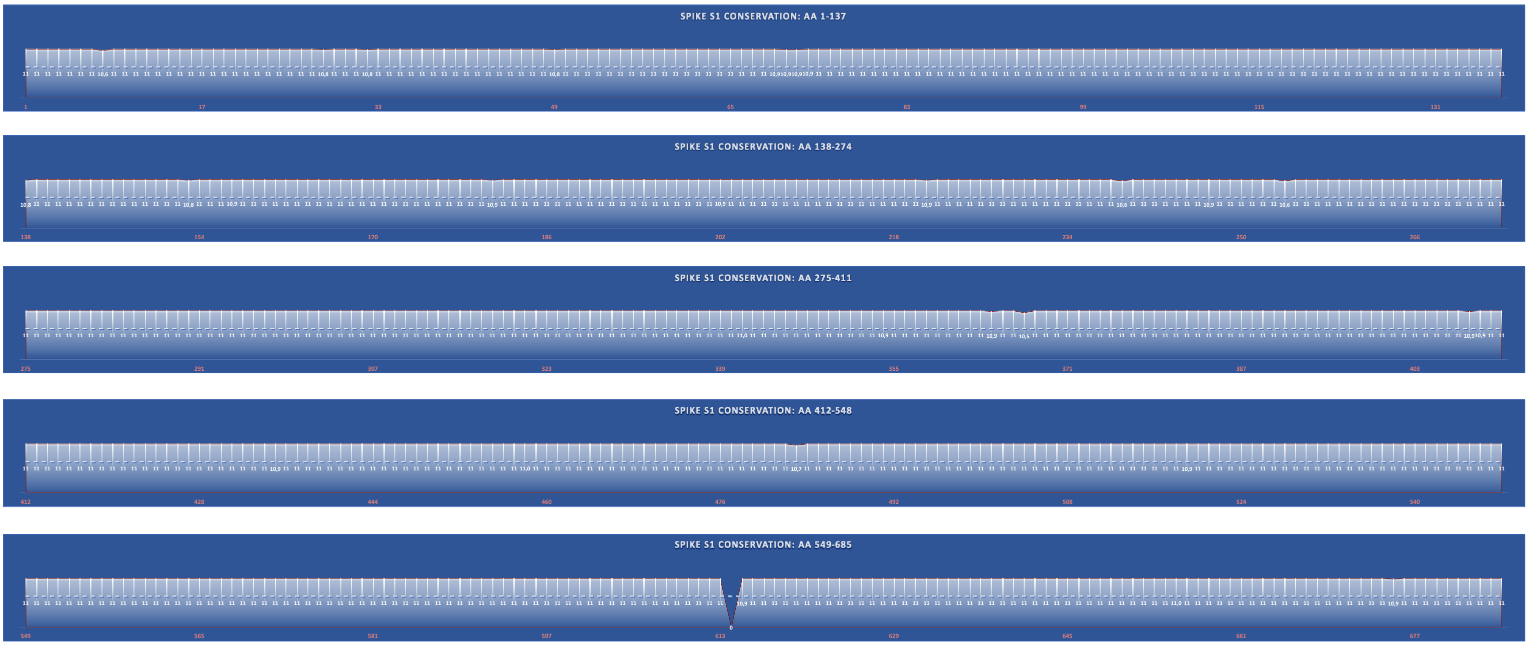
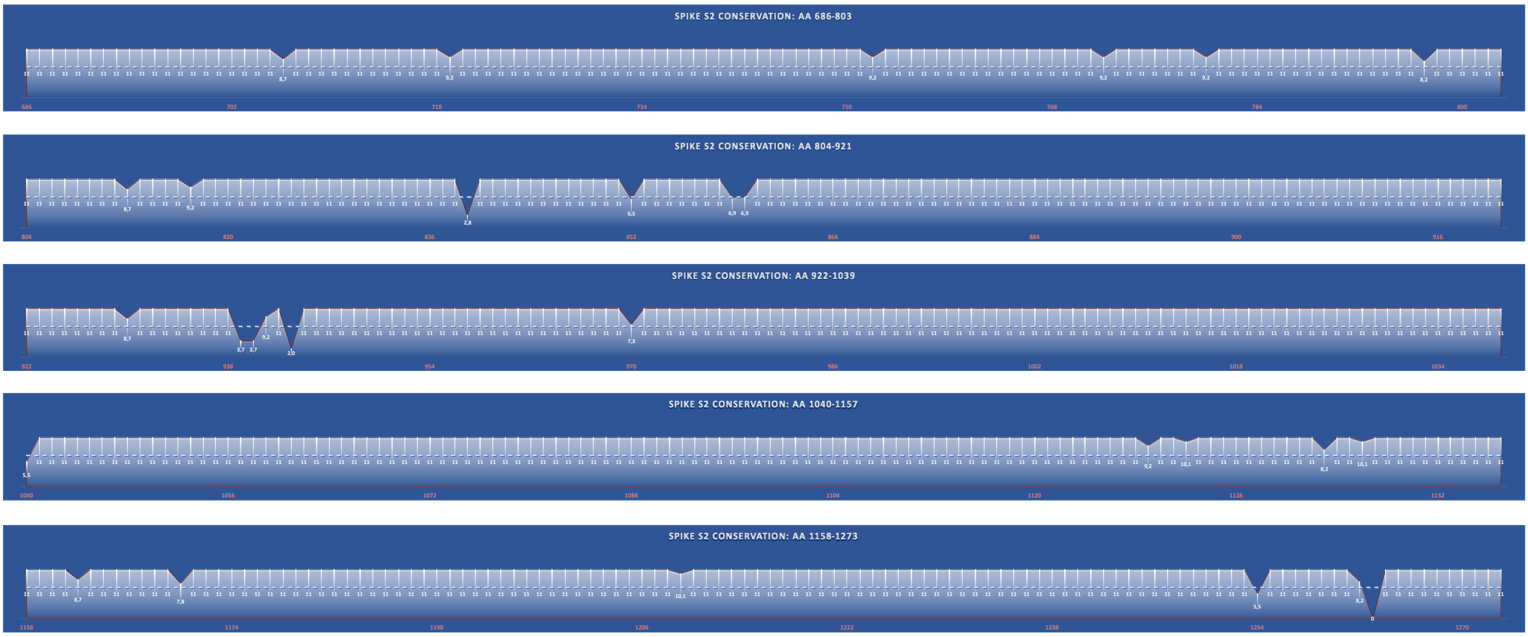
(a) SARS-CoV-2

S1

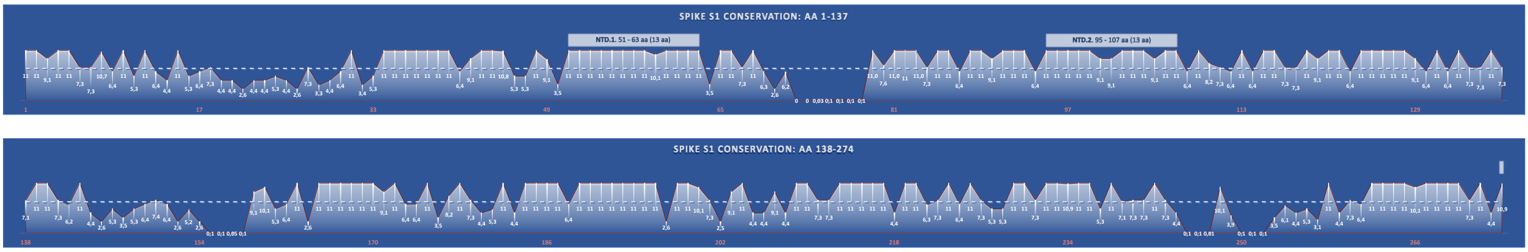


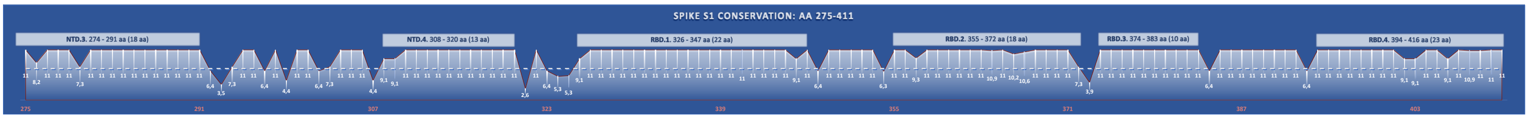
S2

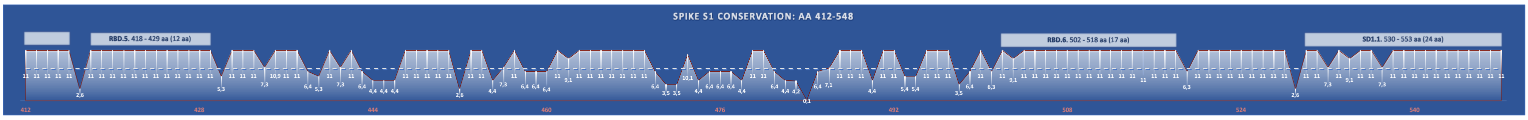


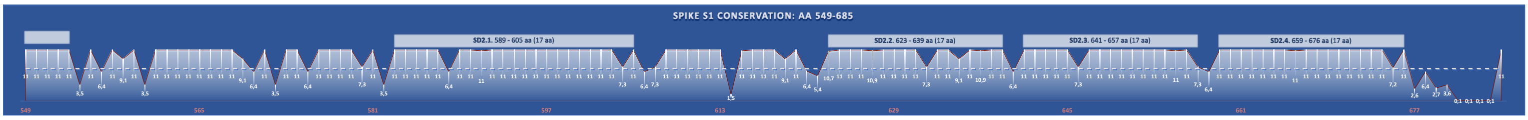
(b) human SARSr-CoV

S1

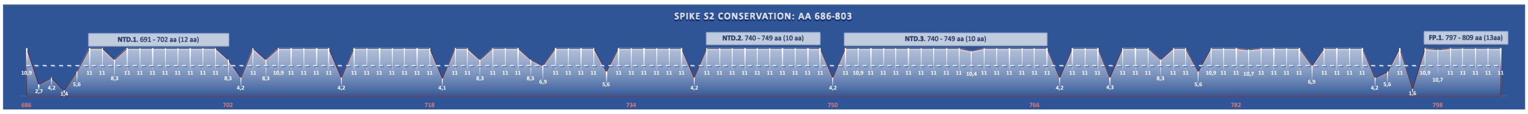


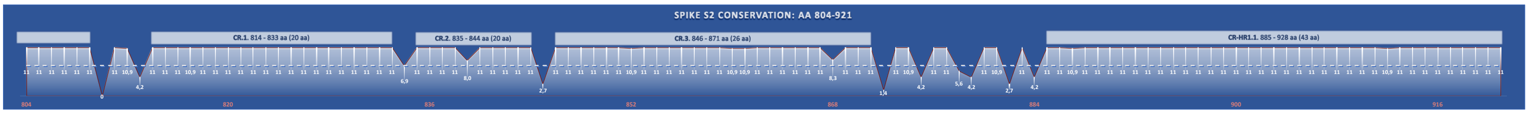


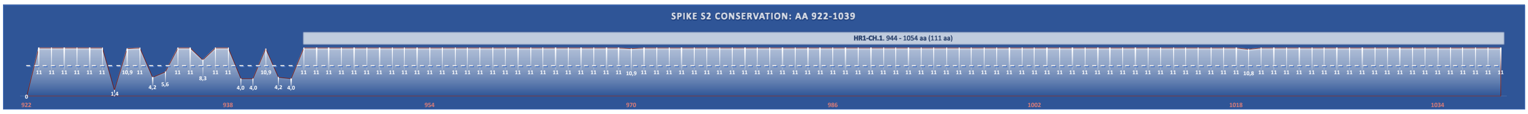


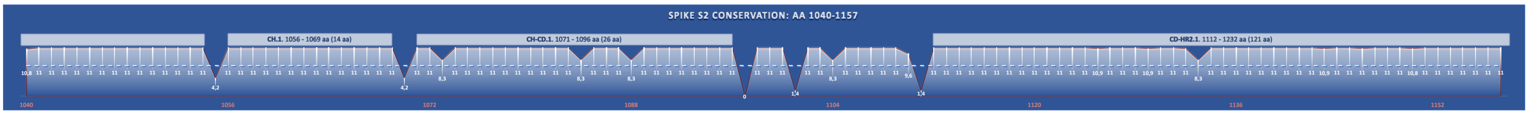


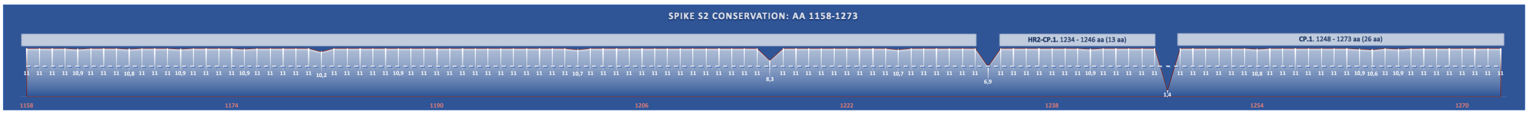
S2





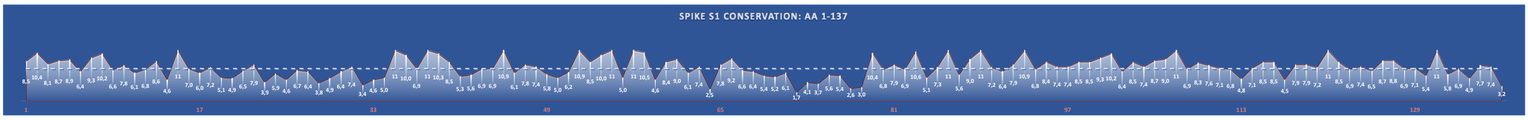


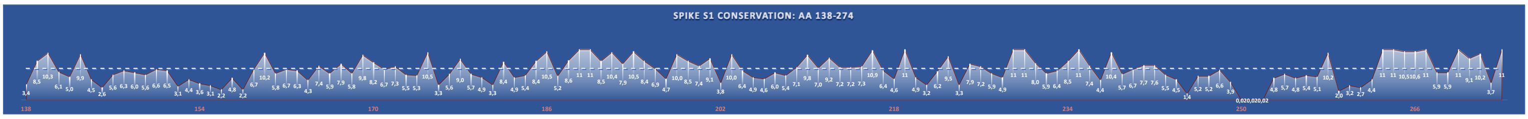


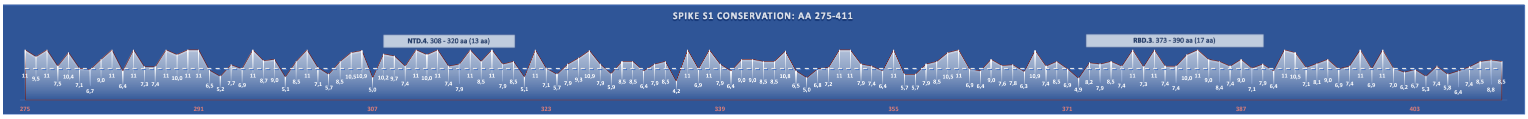


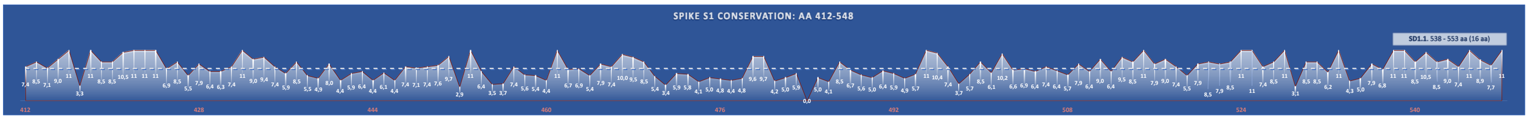
(c) SARSr and MERSr-CoV

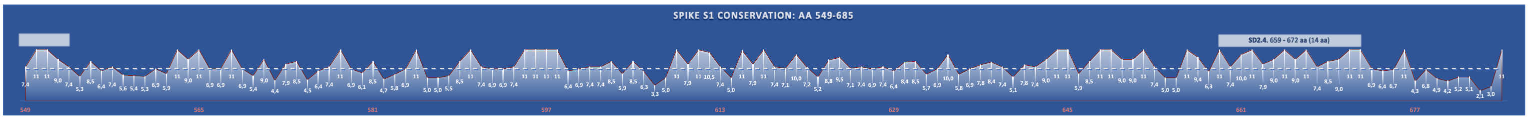
S1











S2

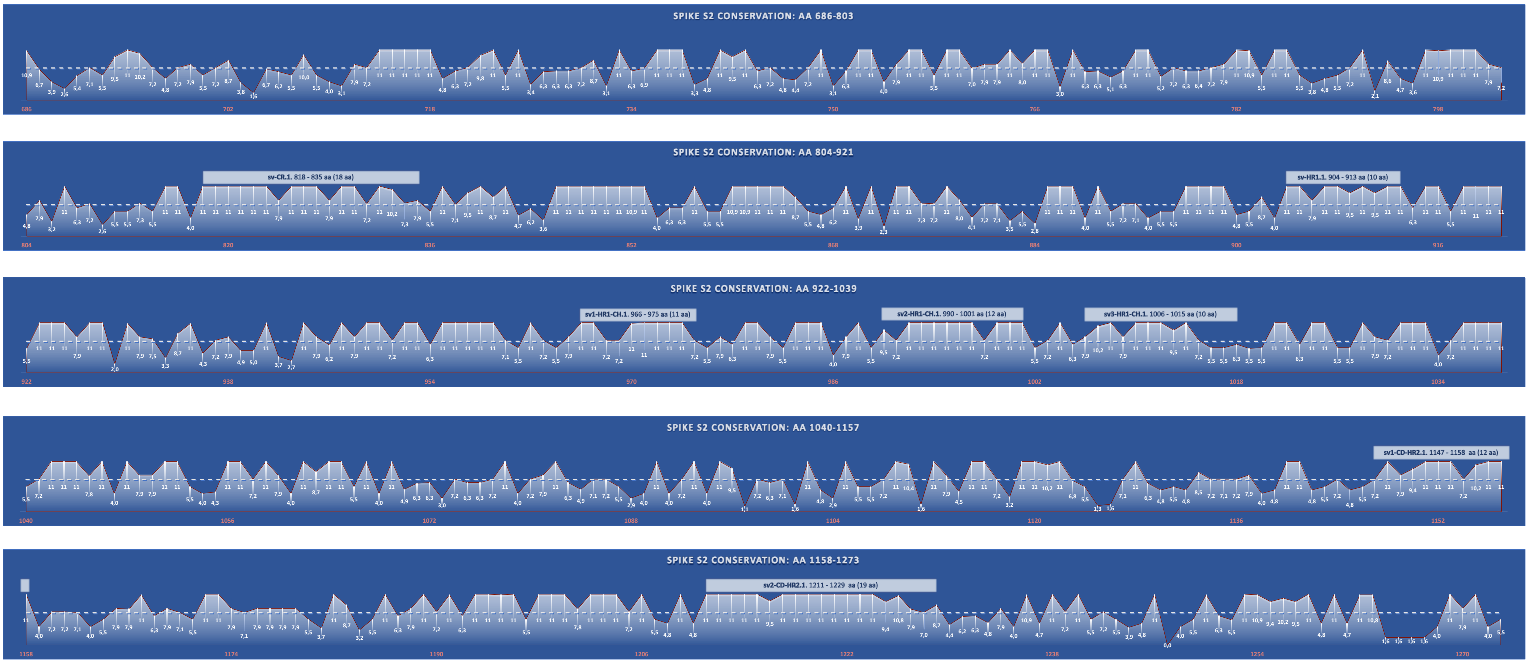


Figure S-1. Representation of the conservation-score distribution of the Spike S1 and S2 residues. The conservation scores (cs) were calculated for each aa position within the S protein for three different groups: **(a)** SARS-CoV-2; **(b)** human SARSr-CoV; and **(c)** SARSr and MERSr-CoV**.** The white numbers (below each aa position) represent the cs of each individual aa, on a scale varying from 0 (most variable) to 11 (most conserved); a score of 11 indicates 100% identity across the considered beta-CoVs. In (b) and (c) the regions composed of ≥ 10 continuous conserved aa (score >7) are displayed above the conservation-score bars.