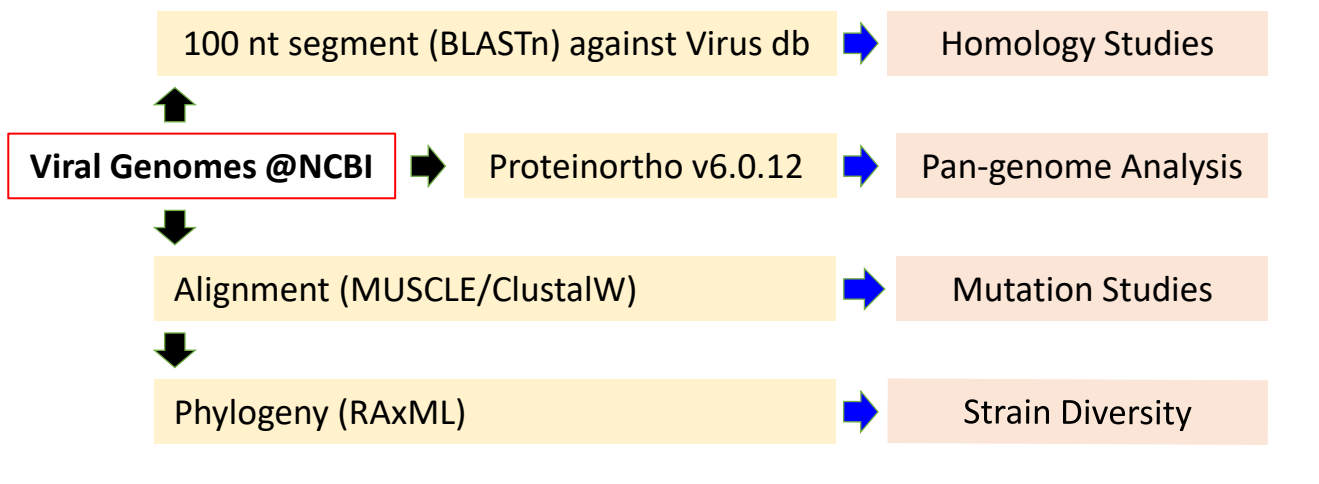
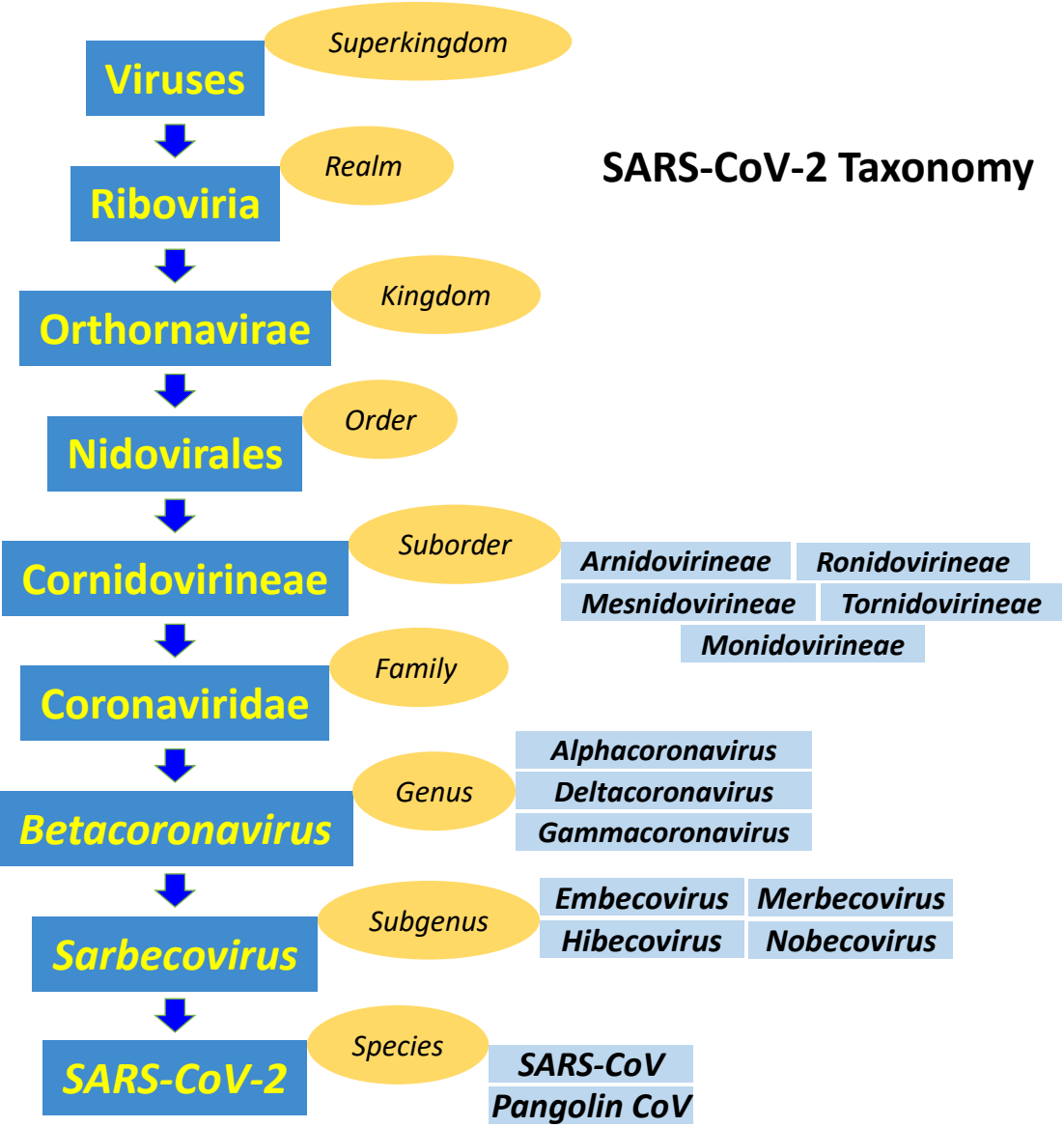


Methodology at a glance



SARS-CoV-2 Taxonomy



Strain diversity amongst 56 reference strains (*Figure-S1*)

19 reference strains-based Pan-genome analysis (*Figure-5, S5*)

Strain diversity amongst 23 reference strains (*Figure-S2*)

Strain diversity amongst 420 SARS-CoV-2 & SARS-CoV strains (*Figure-1, S3*)

Strain diversity amongst 167 SARS-CoV-2 strains (*Figure-2, S4*)

Mutation hotspot analysis based on 167 SARS-CoV-2 strains (*Figure-3*)

Evolutionary origin identification of SARS-CoV-2, SARS-CoV, Pangolin CoV, & MERS, (*Figure-4*)

Workflow