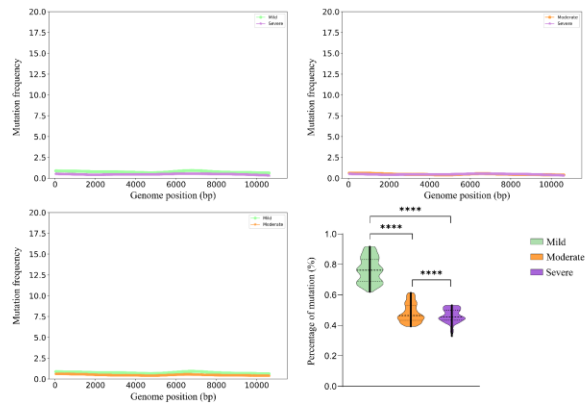
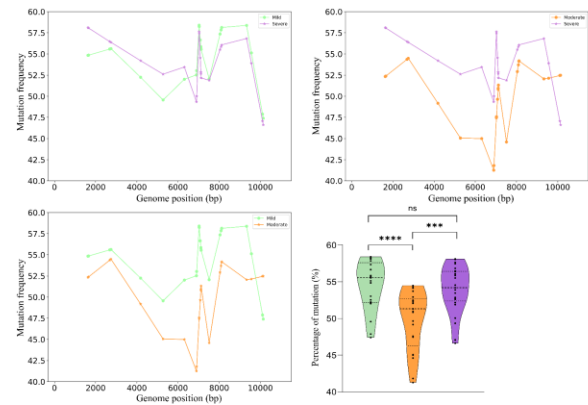


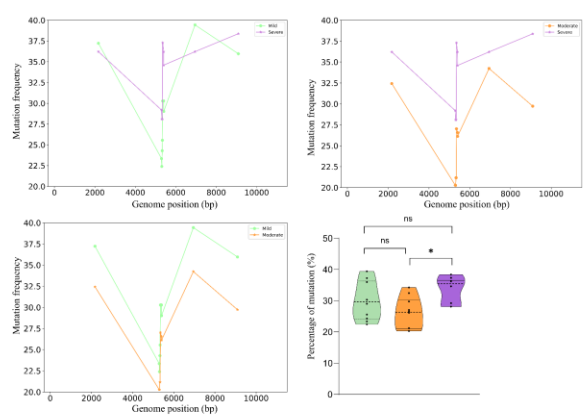
A 0-20 % (Cluster E)



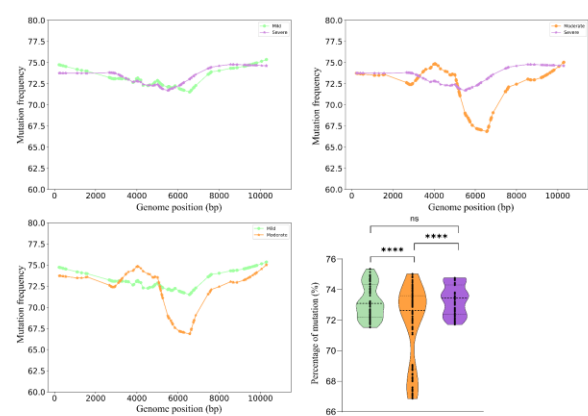
C 40-60 % (Cluster C)



B 20-40 % (Cluster D)

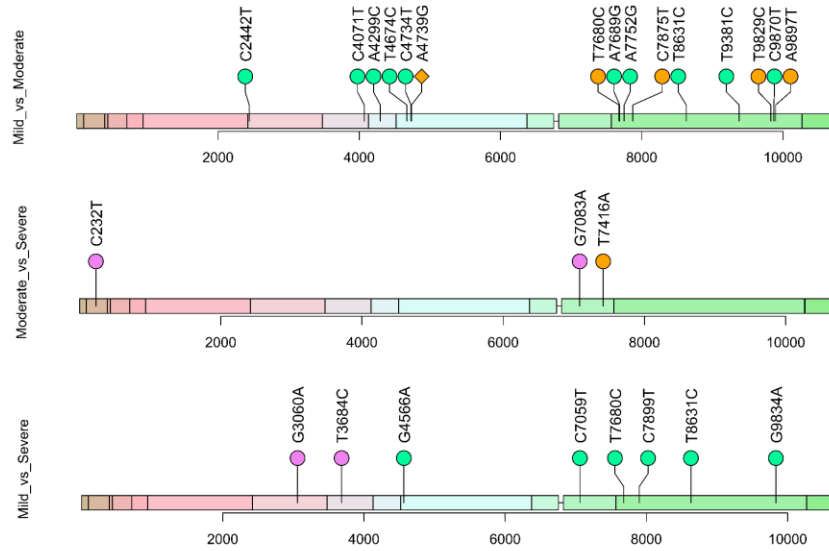


D 60-80 % (Cluster B)

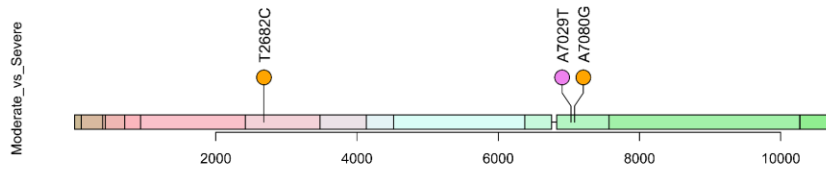


Supplementary Figure 1: (A-D) Line plots showing mutation frequency across the DENV-2. genome for Cluster B-E and Violin plot showing significant differences between percentage of mutation and severity cohort.

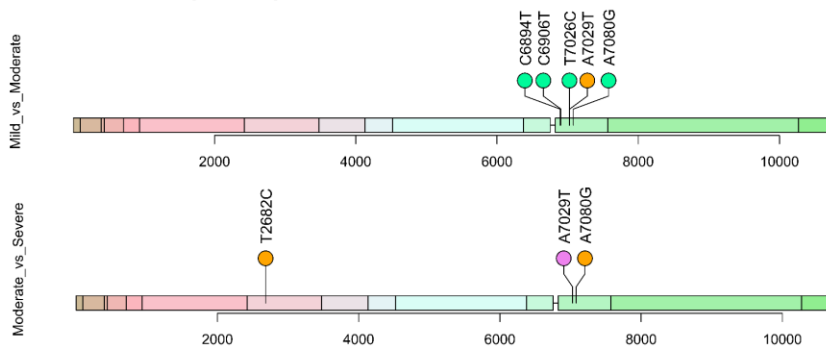
A) Cluster - E (0-20)



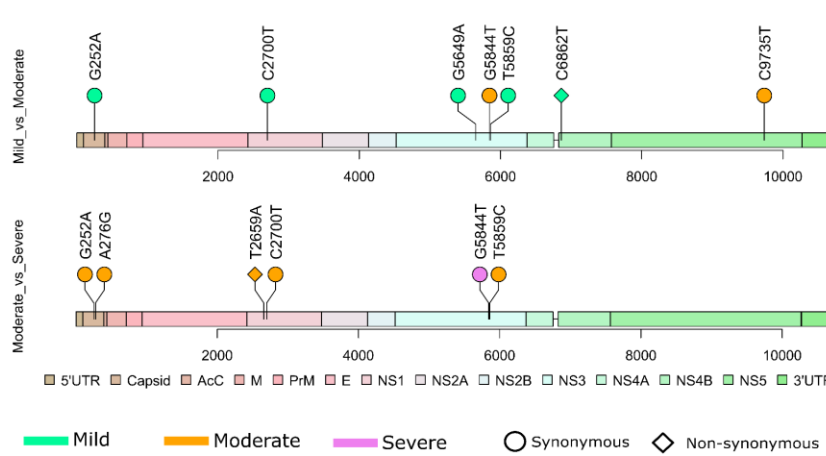
B) Cluster - D (20-40)



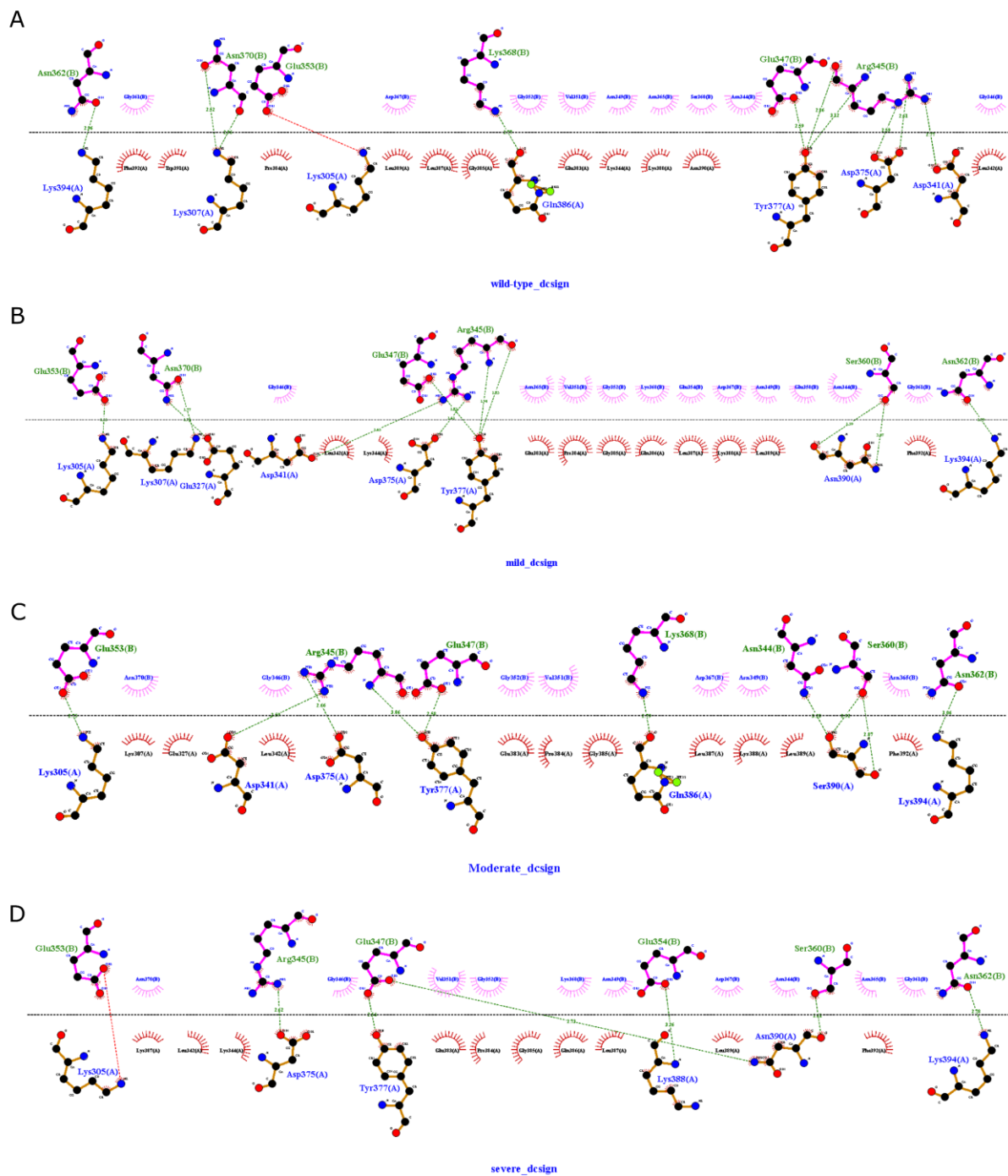
C) Cluster - C (40-60)



D) Cluster - B (60-80)



Supplementary Figure 2: (A-D) Lollipop plot representing significant synonymous and non-synonymous mutations between severity groups.



Supplementary Figure 3: (A-D) Interaction plot between E-protein and DC-SIGN.