



Figure S4. Homology modeling predicts the 3D structure of S protein of IBT/VN/2018 through sequence alignment of the known 3D structure strain (6U7K). No changes were observed in the 3D structure of the S protein of IBT/VN/2018 at mutated sites p.P766L, p.L1009M, and p.S1089L as compared to 6U7K strain.