

Fig. S1 Predicted kinases for the phosphorylation in position N501Y of mutated SARS-CoV-2 spike receptor-binding domain by NetPhos 3.1. Arrow shows the phosphorylation at N501Y but not at N501 wild type (WT).

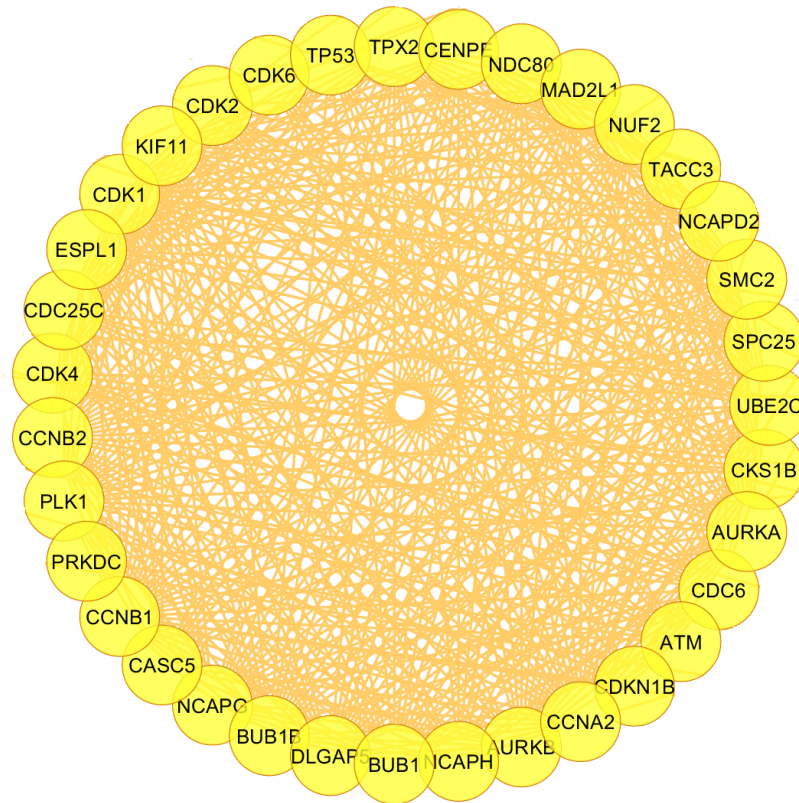


Fig. S2. Possible gain of phosphorylation of B.1.1.7 lineage. Protein-protein interaction Analysis. (a) The network of PPI was derived from STRING database and retrieved by Cytoscape 7.3 software. ClusterONE plug-in of Cytoscape 7.3 was used to identify the most significant cluster (nodes - 35; density – 0.699; p-value - <0.000). Proteins are represented by nodes, while their associations are by edges.

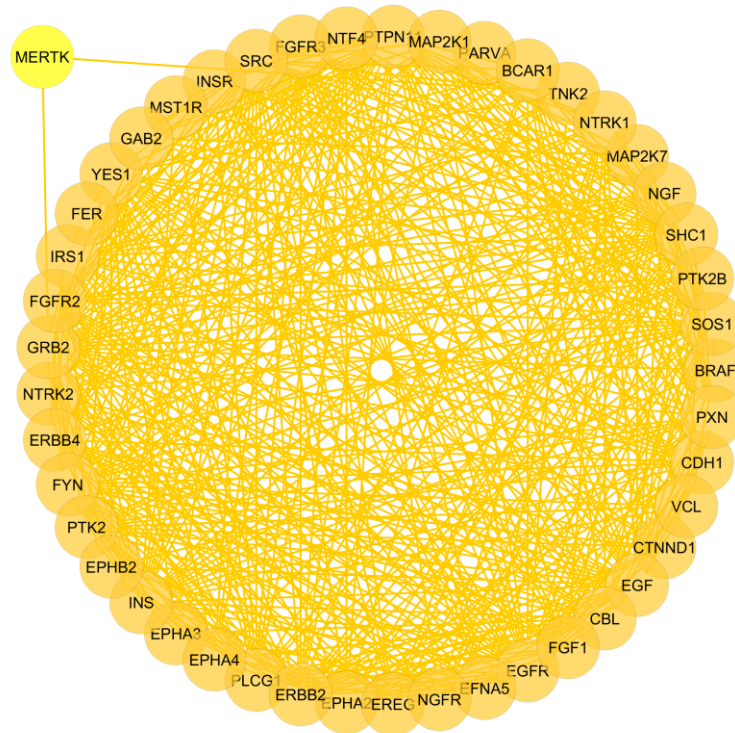


Fig. S3. Possible gain of phosphorylation of B.1.351 lineage. Protein-protein interaction analysis of the network of was derived from STRING database [1] and retrieved by Cytoscape 7.3 software [2]. ClusterONE plug-in of Cytoscape 7.3 was used to identify the most significant cluster (nodes - 45; density – 0.498; p-value - <0.000). Proteins are represented by nodes, while their associations are by edges.

Reference

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