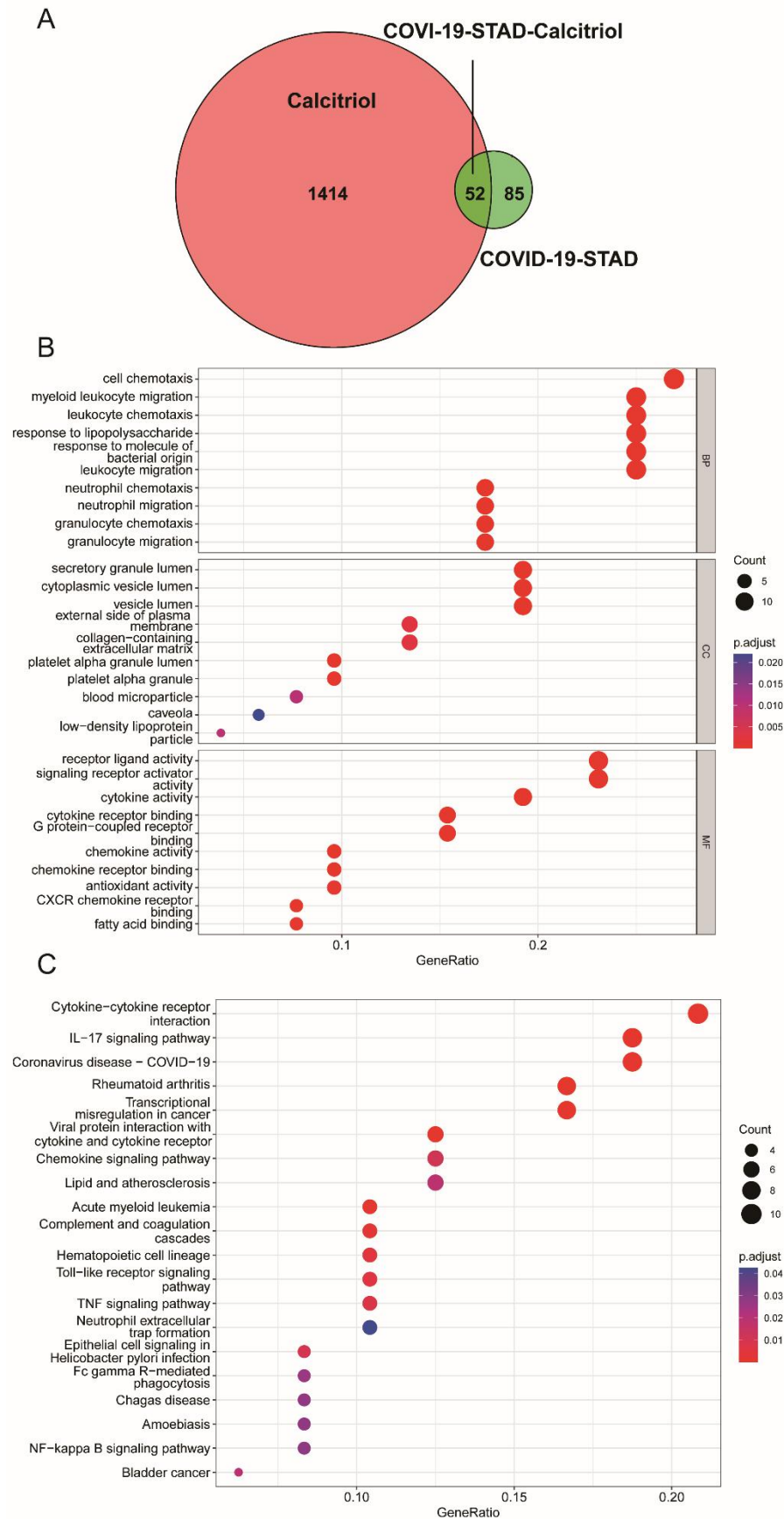
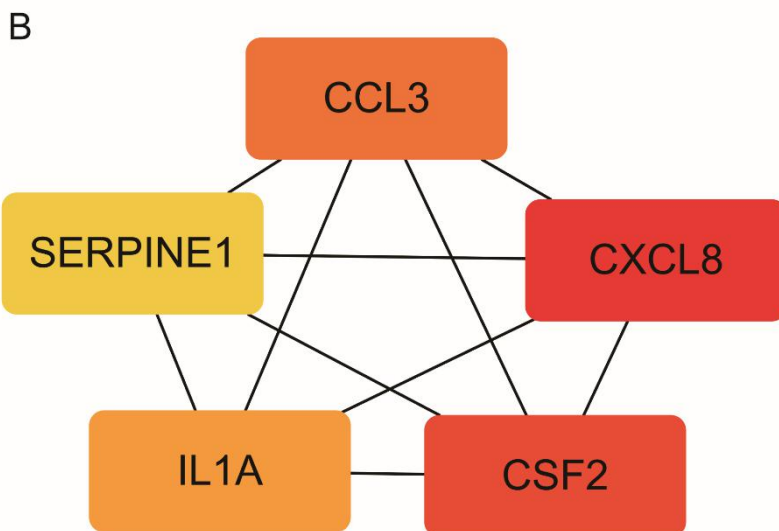
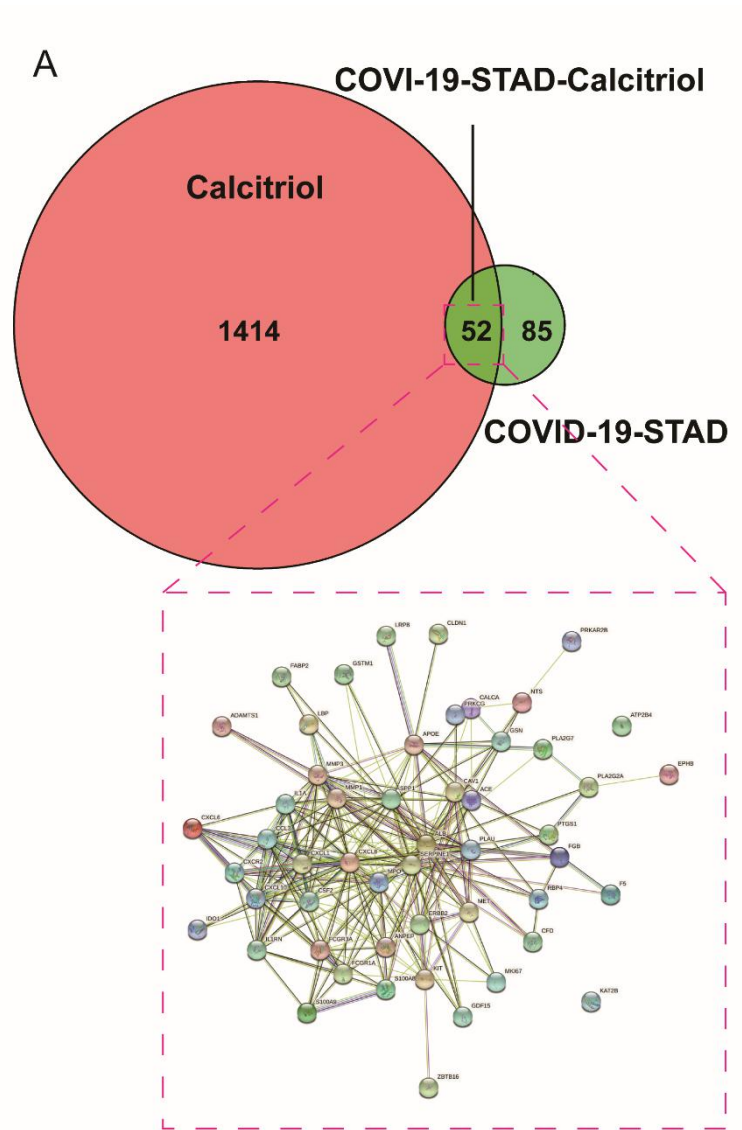


Supplementary figure 1. Univariate cox analysis and multivariate cox analysis for five characteristics

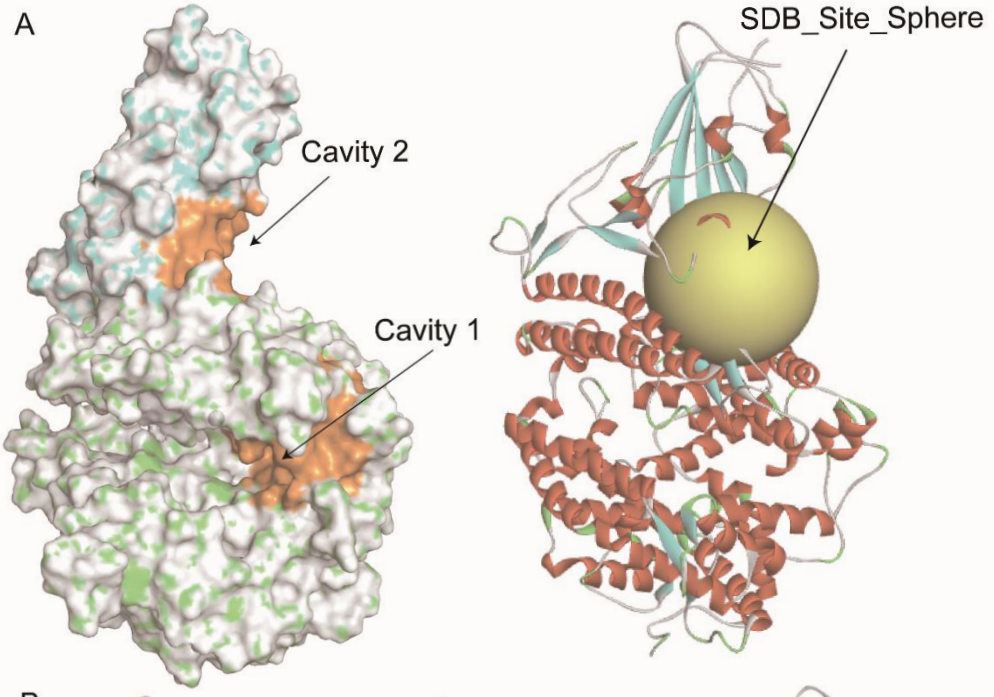


Supplementary figure 2. **(A)** Venn diagram of calcitriol and STAD/COVID-19 Intersecting genes. **(B)** GO analysis of intersecting genes of calcitriol and STAD/COVID-19. **(C)** KEGG pathway enrichment analysis of intersecting genes of calcitriol and STAD/COVID-19.

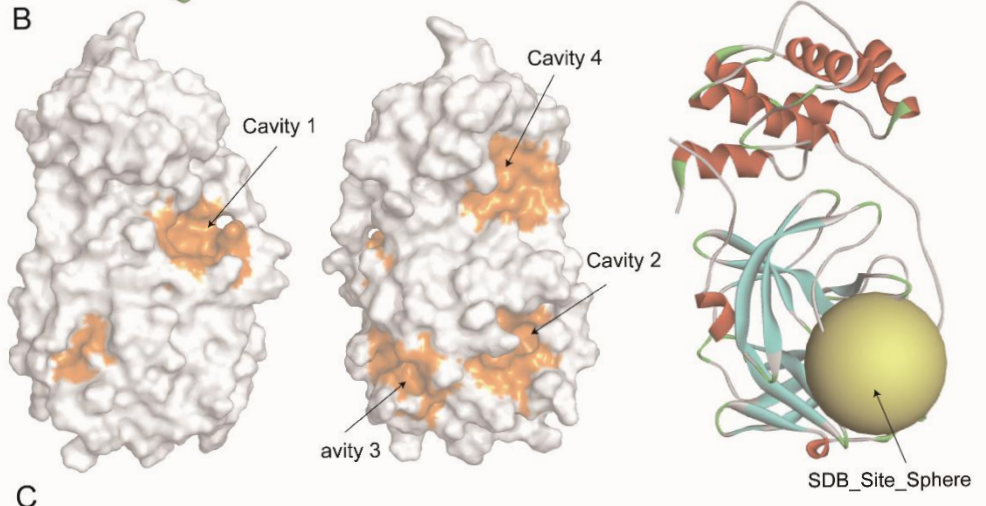


Supplementary figure 3. **(A)** STRING analysis of calcitriol and STAD/COVID-19 intersecting genes. **(B)** Cytoscape analysis of protein interaction networks associated with calcitriol anti-STAD/COVID-19.

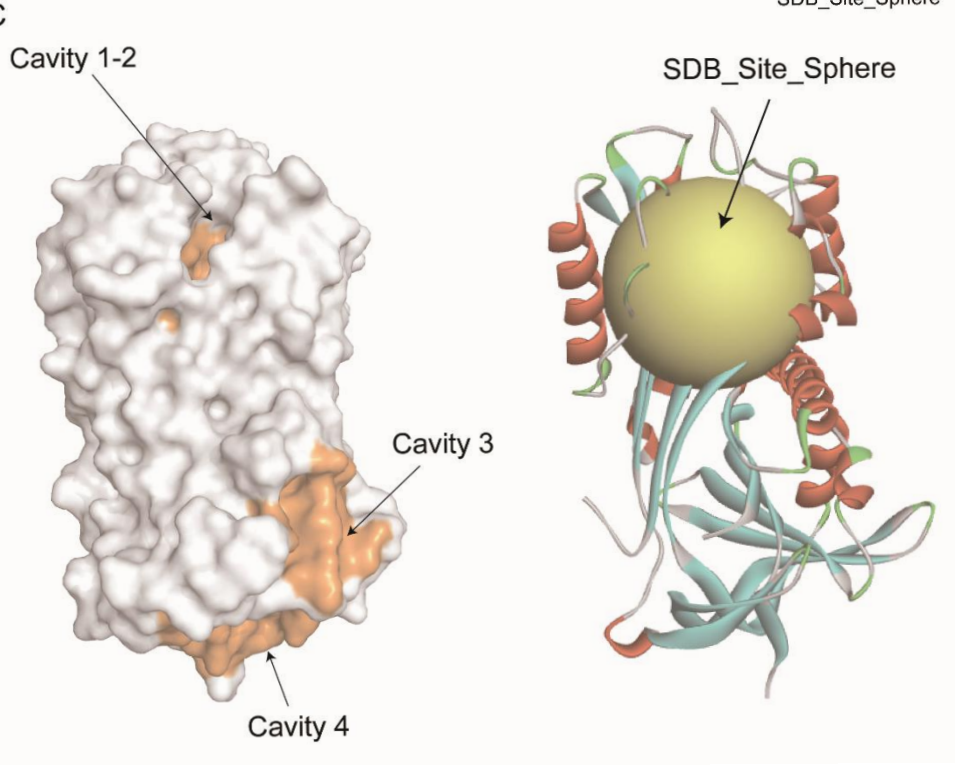
A



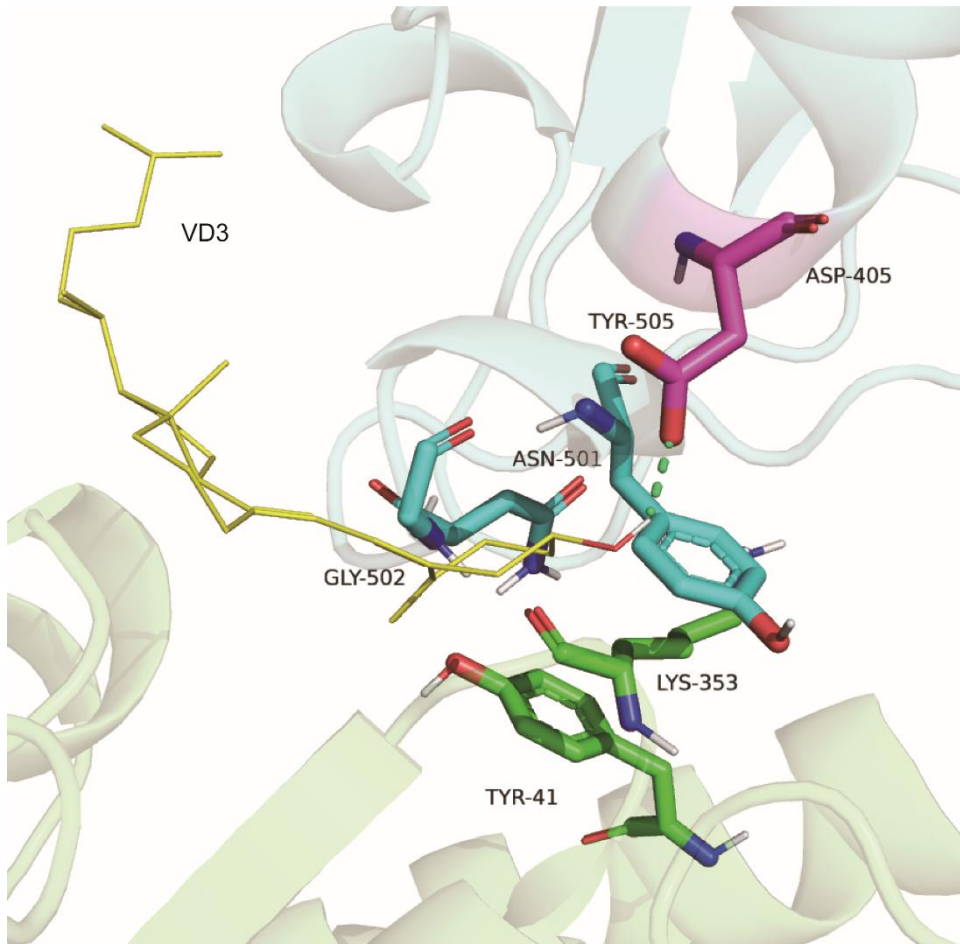
B



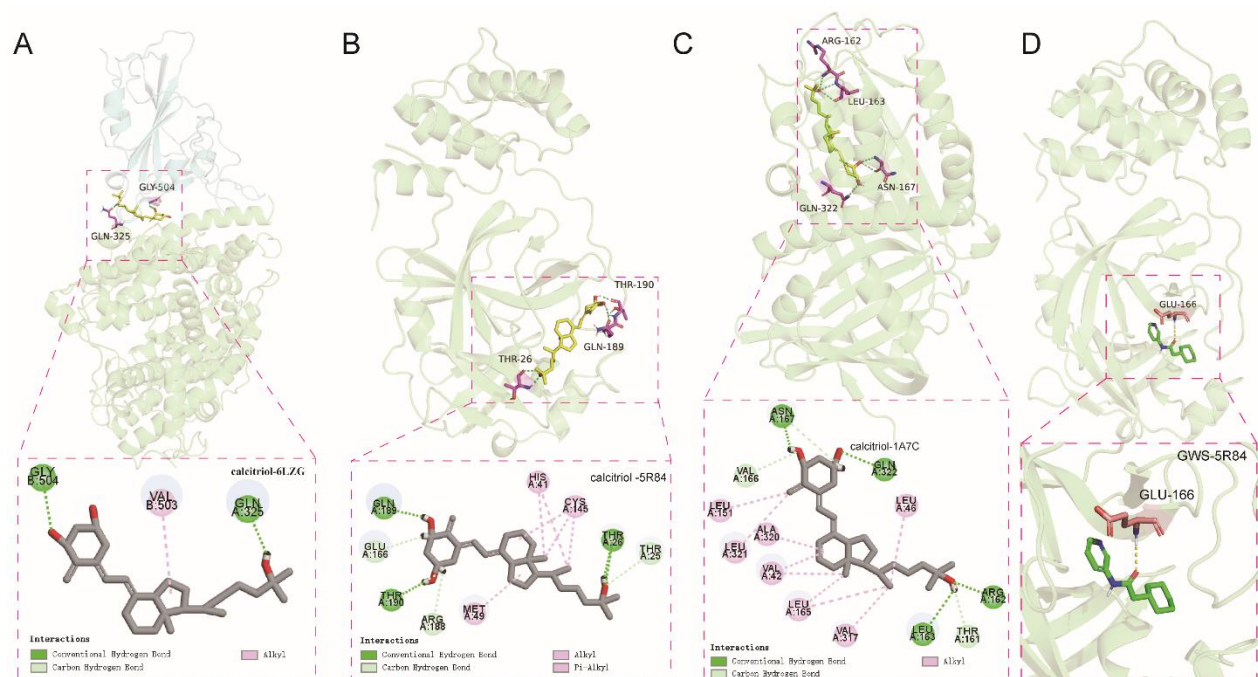
C



Supplementary figure 4. Identified protein cavity and site information in SARS-COV-2 RBD/ACE2 (A), Mpro (B) and PAI1 (C).



Supplementary figure 5. Partial structure of the SARS-CoV-2 spike receptor-binding domain bound to the ACE2 receptor. ACE2 is shown in green. The SARS-CoV-2 RBD is shown in cyan. VD3 is shown in yellow.



Supplementary figure 6. **(A)** Molecular docking model of calcitriol with SARS-COV-2 Spike RBD/ACE2 complex (PDB: 6LZG, ACE2(green), SARS-CoV-2 RBD (cyan)) and 2D patterns of bonds in the model. **(B)** Molecular docking model of calcitriol with SARS-CoV-2 major protease (PDB: 5R84) and 2D patterns of bonds in the model. **(C)** Molecular docking model of calcitriol with PAI-1 (PDB: 1A7C) and 2D patterns of bonds in the model. **(D)** Molecular docking model of the original non-specific ligands GWS with 5R84 and 3D patterns of bonds in the model.