

Supplementary Figures & Tables

Figure S1: The distribution of predominant PangoLIN lineages in the labelled districts of Maharashtra. The size of the pie charts is proportional to the number of genome sequences from the particular district.

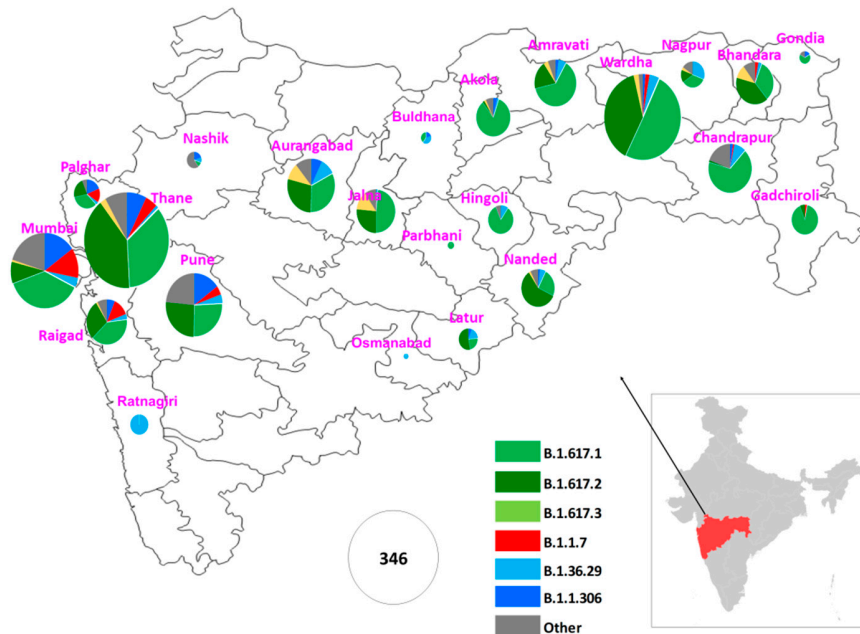
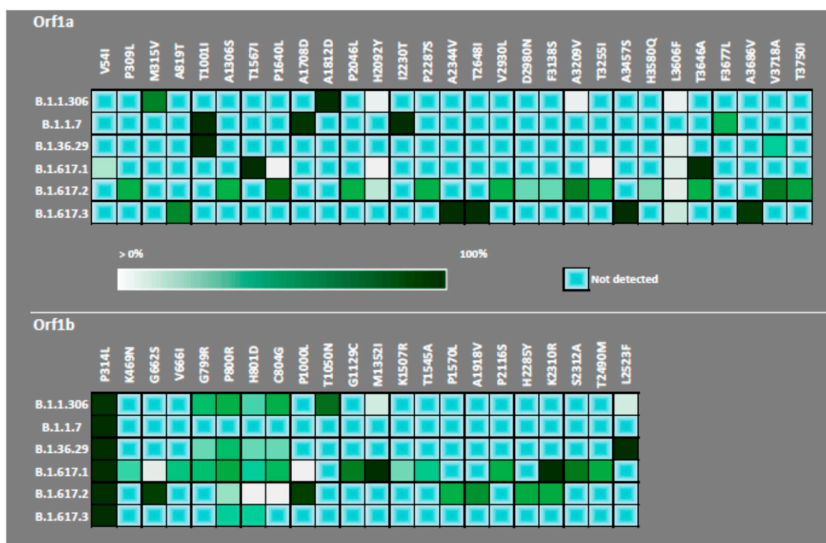
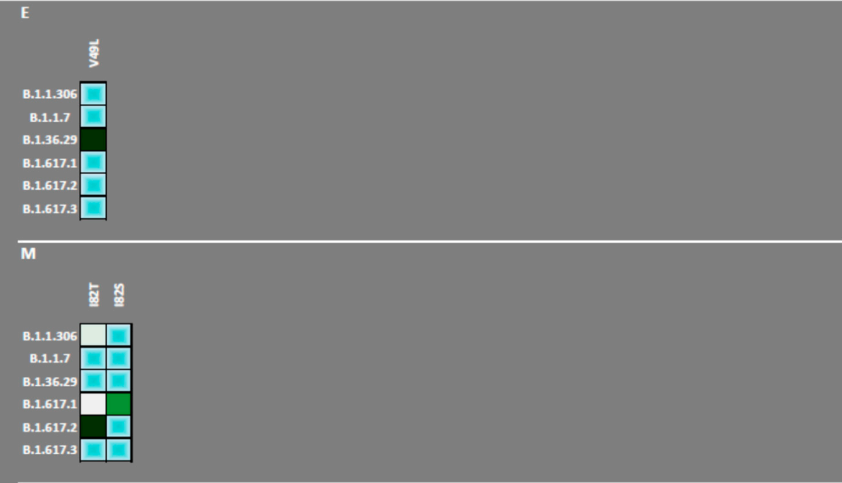
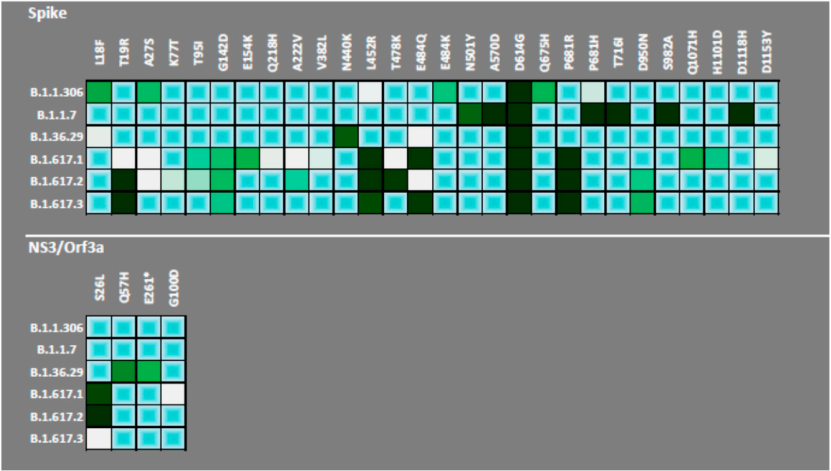


Figure S2: Heat map of major mutations in the different proteins of the predominant lineages from November, 2020 to May, 2021





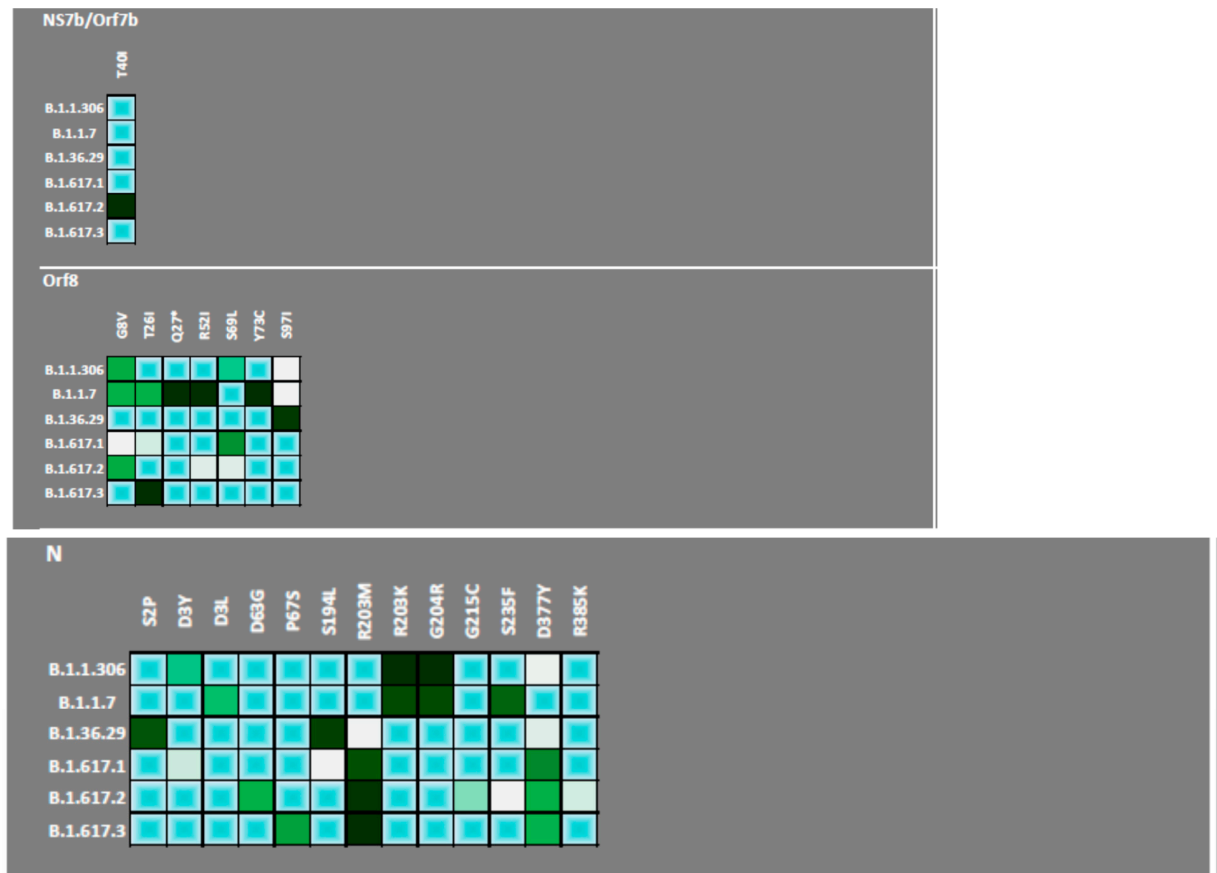


Figure S3: Structural complexes of RBD-ACE2 and RBD-Fab. **A.** RBD - ACE2 (PDB Id-6LZG), **B.** RBD - mAb REGN10933(PDB Id-6XDXG) **C.** RBD - mAb P2B-2F6(7bwj)

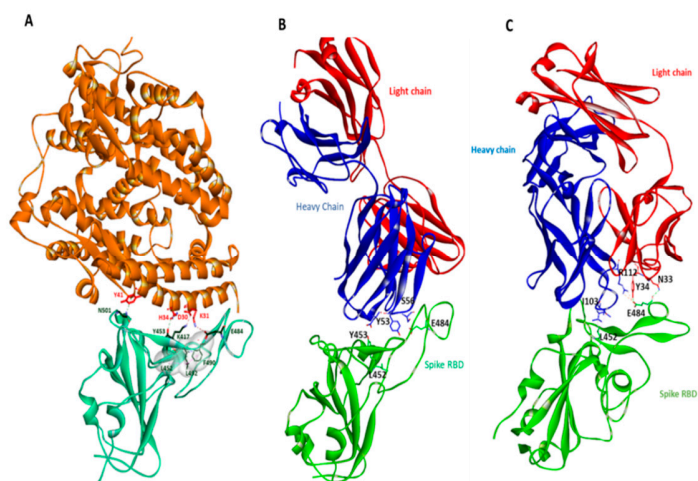


Figure S4: Modeling of the SARS-CoV-2 spike protein (with the furin cleavage motif) and effect of P681R mutation (A) Complete spike protein with the residues in the furin cleavage site labelled (B) Wild-type strain with P681 (C) Mutant strain with P681R

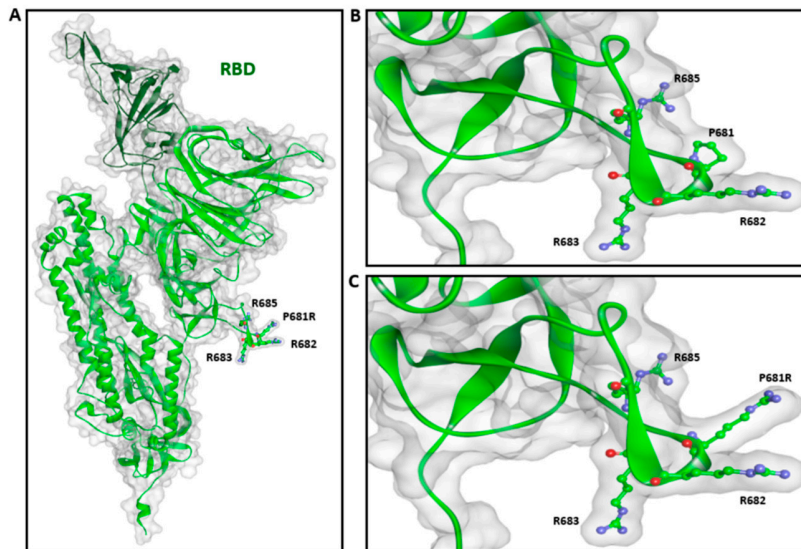
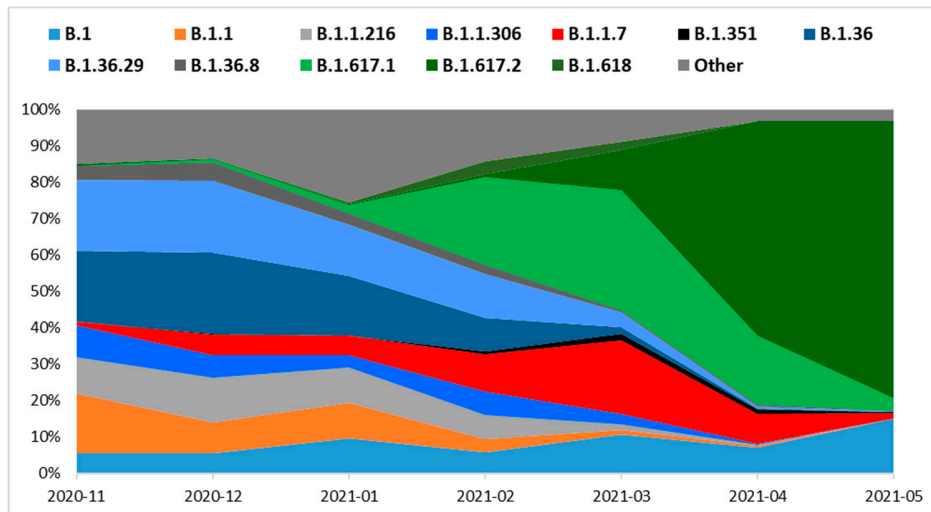
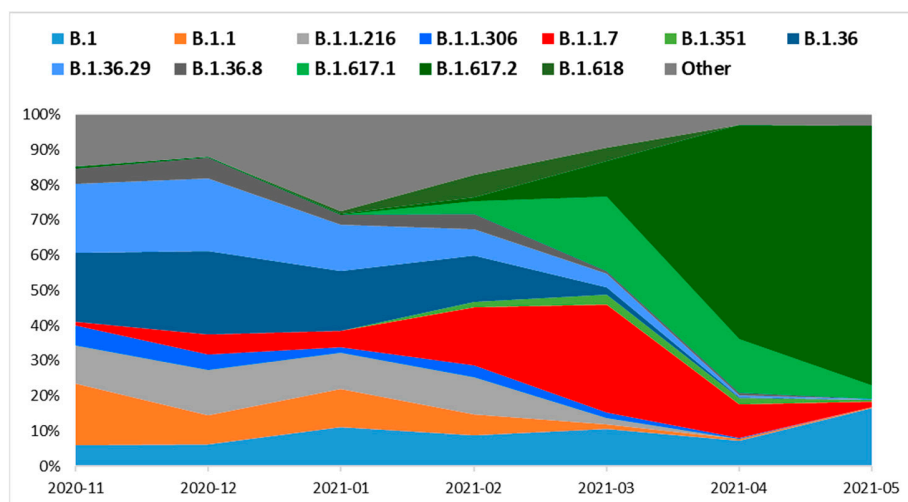


Figure S5: Temporal trend of major lineages (top twelve) in India based on sequences from GISAID (As of June 6, 2021) from November, 2020 to May, 2021 (A) India inclusive of Maharashtra (n= 9495) (B) India excluding Maharashtra (n=6949).

(A)



(B)



Supplementary Table S1

Supplementary Table S1: Intra and inter-molecular interactions of the wild-type and mutant spike RBD of SARS-CoV-2 with ACE2. The bonds that are made bold in the wild-type indicate those that are disrupted in the mutant strain while the bonds that are bold in the mutant indicate those that are additional when compared to the wild-type strain. Mutant1 indicates the strain of lineage B.1.617.1 and mutant2 indicates a strain of lineage B.1.617.2.

Spike RBD with ACE2 (6LZG.pdb) (wild-type)			
Interactions			
Sr. No.	RBD-Wild Type	ACE2	Type
1	K417	D30	Hydrogen Bond; Electrostatic
2	E484	K31	Electrostatic
3	A475	S19	Hydrogen Bond
4	N487	Q24	Hydrogen Bond
5	T500	Y41	Hydrogen Bond
6	G496	K353	Hydrogen Bond
7	Y449	D38	Hydrogen Bond
8	Y449	Q42	Hydrogen Bond
9	N487	Y83	Hydrogen Bond
10	Q493	E35	Hydrogen Bond
11	Q498	Q42	Hydrogen Bond
12	Q498	Q42	Hydrogen Bond
13	G502	K353	Hydrogen Bond
14	Y453	H34	Hydrogen Bond
15	F486	Y83	Hydrogen Bond
16	N501	Y41	Hydrogen Bond

17	L455	H34	Hydrophobic
18	F486	Y83	Hydrophobic
19	Y505	K353	Hydrophobic
20	F486	M82	Hydrophobic
21	Y489	K31	Hydrophobic
22	Y505	K353	Hydrophobic
23	L452-L492	-	Hydrophobic
24	F490-L492	-	Hydrophobic

Spike RBD with ACE2 (6LZG.pdb) (L452R & E484Q Mutant1)

Interactions			
Sr. No.	RBD-Mutant Type	ACE2	Type
1	K417	D30	Hydrogen Bond; Electrostatic
2	A475	S19	Hydrogen Bond
3	N487	Q24	Hydrogen Bond
4	T500	Y41	Hydrogen Bond
5	G496	K353	Hydrogen Bond
6	Y449	D38	Hydrogen Bond
7	Y449	Q42	Hydrogen Bond
8	N487	Y83	Hydrogen Bond
9	Q493	E35	Hydrogen Bond
10	Q498	Q42	Hydrogen Bond
11	Q498	Q42	Hydrogen Bond
12	G502	K353	Hydrogen Bond
13	Y453	H34	Hydrogen Bond
14	F486	Y83	Hydrogen Bond
15	N501	Y41	Hydrogen Bond
16	L455	H34	Hydrophobic
17	F486	Y83	Hydrophobic
18	Y505	K353	Hydrophobic
19	F486	M82	Hydrophobic
20	Y489	K31	Hydrophobic
21	Y505	K353	Hydrophobic
22	F490-L492	-	Hydrophobic

Spike RBD with ACE2 (6LZG.pdb) (L452R & T478K Mutant2)

Interactions			
1	K417	D30	Hydrogen Bond; Electrostatic
2	A475	S19	Hydrogen Bond
3	N487	Q24	Hydrogen Bond
4	T500	Y41	Hydrogen Bond
5	G496	K353	Hydrogen Bond
6	Y449	D38	Hydrogen Bond
7	Y449	Q42	Hydrogen Bond
8	N487	Y83	Hydrogen Bond

9	Q493	E35	Hydrogen Bond
10	Q498	Q42	Hydrogen Bond
11	Q498	Q42	Hydrogen Bond
12	G502	K353	Hydrogen Bond
13	Y453	H34	Hydrogen Bond
14	F486	Y83	Hydrogen Bond
15	N501	Y41	Hydrogen Bond
16	L455	H34	Hydrophobic
17	F486	Y83	Hydrophobic
18	Y505	K353	Hydrophobic
19	F486	M82	Hydrophobic
20	Y489	K31	Hydrophobic
21	Y505	K353	Hydrophobic
22	F490-L492	-	Hydrophobic
23	K478-F486	-	Hydrogen Bond
24	K478-F486	-	Hydrogen Bond
25	K478-F486	-	Hydrogen Bond

Supplementary Table S2: Intermolecular interaction of neutralizing antibodies with wild-type and mutant spike RBD of SARS-CoV-2

A	Spike RBD with Antibody REGN10933 (Wild-type)		
	Interactions		
	RBD	Antibody	Type
1	GLU484	H: TYR53	Hydrogen Bond
		H:SER56	
2	LYS417	H:ASP31	Hydrogen Bond
		H:THR28	
3	PHE486	L: LEU94	Hydrophobic
		H: ARG100	Electrostatic
		H:TYR59	Hydrogen bond
4	TYR489	H: TYR53	Hydrophobic
	TYR489	H:TYR33	Hydrogen Bond
5	TYR453	H:ASP31	Hydrogen Bond
6	LYS417	H:ASP31	Hydrogen Bond
7	ALA475	H:MET104	Hydrophobic bond
B	Spike RBD with Antibody REGN10933 (Mutant)		
	Interactions		
	RBD	Antibody	Type

1	LYS417	H:ASP31	Hydrogen Bond
		H: THR28	
2	TYR453	H :ASP31	Hydrogen Bond
3	PHE486	H: ARG100	Hydrogen Bond
		L: LEU94	
		H:TYR59	
4	ALA475	H:MET104	Hydrophobic bond
5	TYR489	H:TYR53	Hydrophobic
6	GLN484	H:SER56	Hydrogen bond
7	CYS488	H:TYR33	Hydrogen bond
C	Spike RBD with Antibody P2B-2F6(Wild-type)		
	Interactions		
	RBD	Antibody	Type
1	LEU452	H: ILE103	Hydrophobic
		H:VAL105	
2	GLU484	L: ASN33	Hydrogen bond
		L:TYR34	
3	GLU484	H:ARG112	Hydrogen bond; Electrostatic
4	PHE490	H: VAL106	Hydrophobic
		H:PRO107	
5	TYR449	H: SER31	Hydrogen bond
6	ASN450	H: SER30	Hydrogen bond
		H:SER31	
7	GLY447	H: TYR27	Hydrogen bond
D	Spike RBD with Antibody P2B-2F6 A(Mutant)		
	Interactions		
	RBD	Antibody	Type
1	GLN484	L: ASN33	Hydrogen bond
		L: TYR34	
2	ASN450	H: SER30	Hydrogen bond
		H:SER31	
3	PHE490	H: VAL106	Hydrophobic
		H: PRO107	

Supplementary Table S3: Major spike protein mutations defining the B.1.617 lineages and proposed effect on structural aspects

S.No.	Mutations	Lineage/s	Proposed Effect on structural aspects	Available Reference/s
1.	E484Q	B.1.617.1, B.1.617.3	Decreased binding to select mAb [#]	32,33
2.	L452R	B.1.617.1, B.1.617.2, B.1.617.3	Decreased binding to select mAb [#]	26, 32, 34, 35, 36
3.	L452R and E484Q	B.1.617.1, B.1.617.3	Enhanced ACE2 [§] binding	24, 32, 36, 37,
4.	L452R and T478K	B.1.617.2	Enhanced ACE2 [§] binding	38
5.	P681R	B.1.617.1, B.1.617.2, B.1.617.3	Enhanced binding to furin	24

[#] Monoclonal antibody

[§]Angiotensin converting enzyme