

**Manuscript Title:** Phyloepidemiology and adaptive evolution of SARS-CoV2 during the first and second wave of COVID-19 in India

**The name(s) of the author(s):**Anuj Tewari, Rajesh Kumar

**The affiliation(s) and address(es) of the author(s):** Department of Veterinary Microbiology, College of Veterinary & Animal Sciences, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India.

**\*Corresponding author email:** anuj474@gmail.com

Figure S1

Figures showing amino acid substitution in NSP2 & NSP3 of SARS-CoV-2 under positive selective pressure

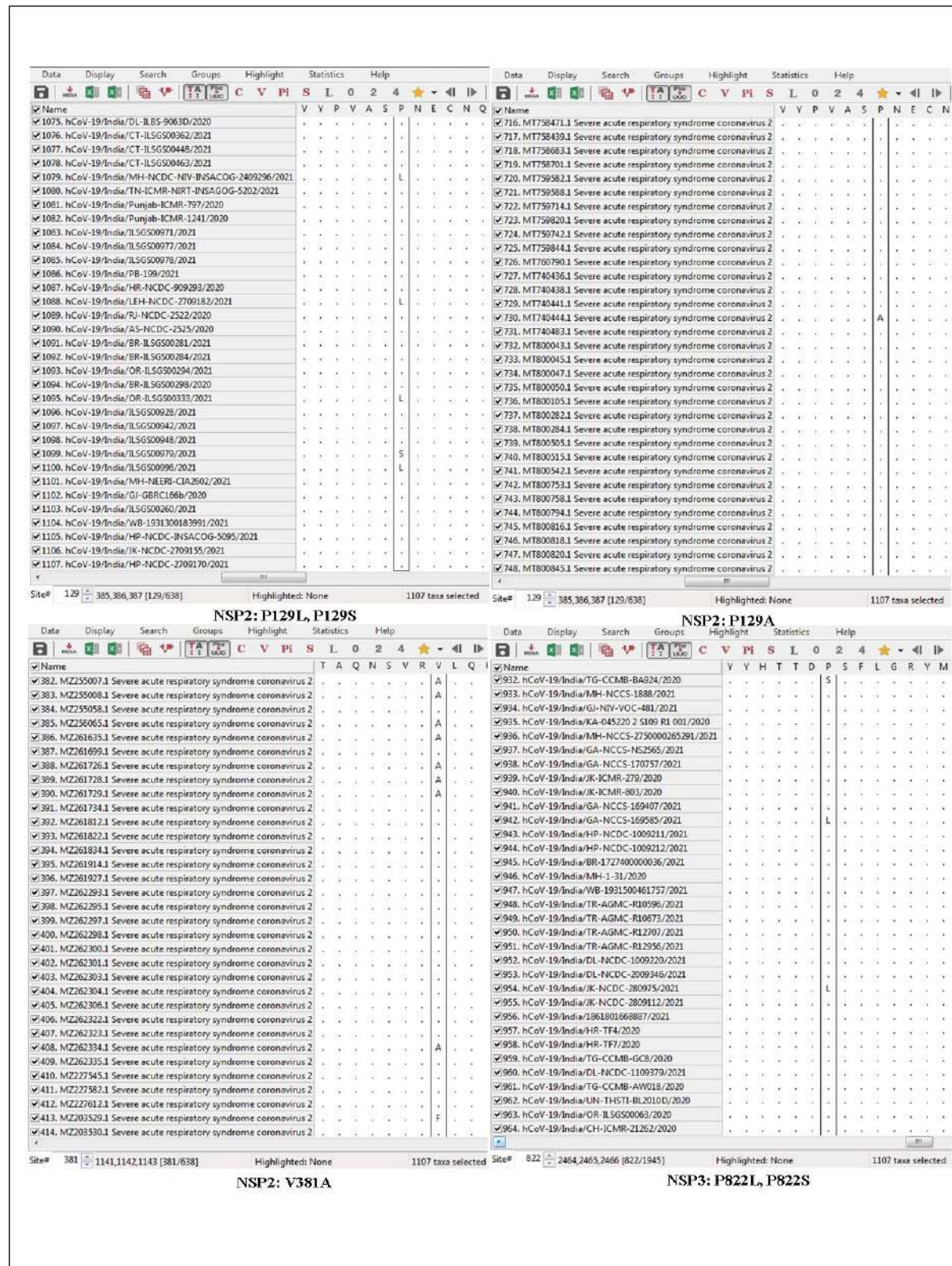


Figure S2

Figures showing amino acid substitution in NSP13 & S protein of SARS-CoV-2 under positive selective pressure

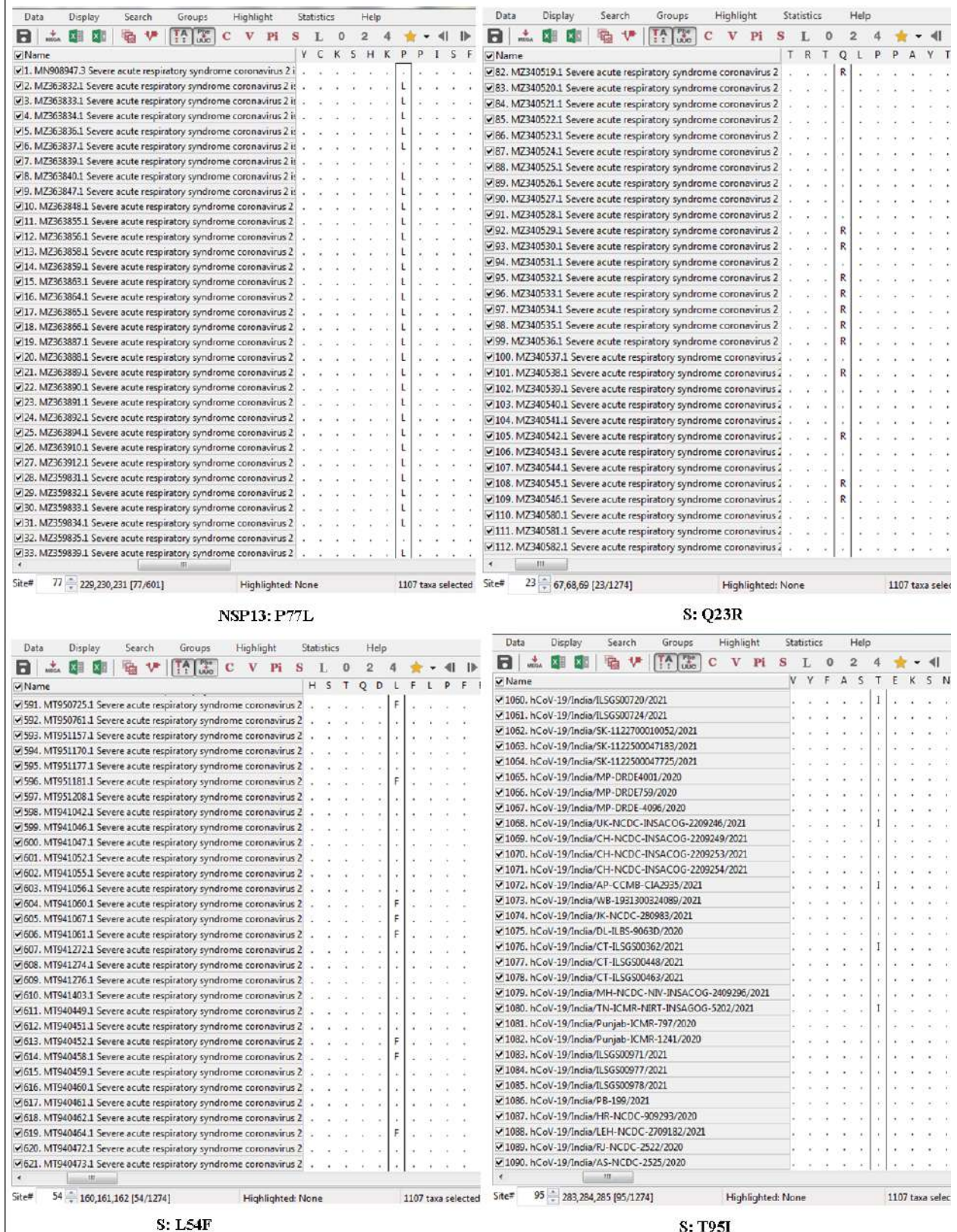
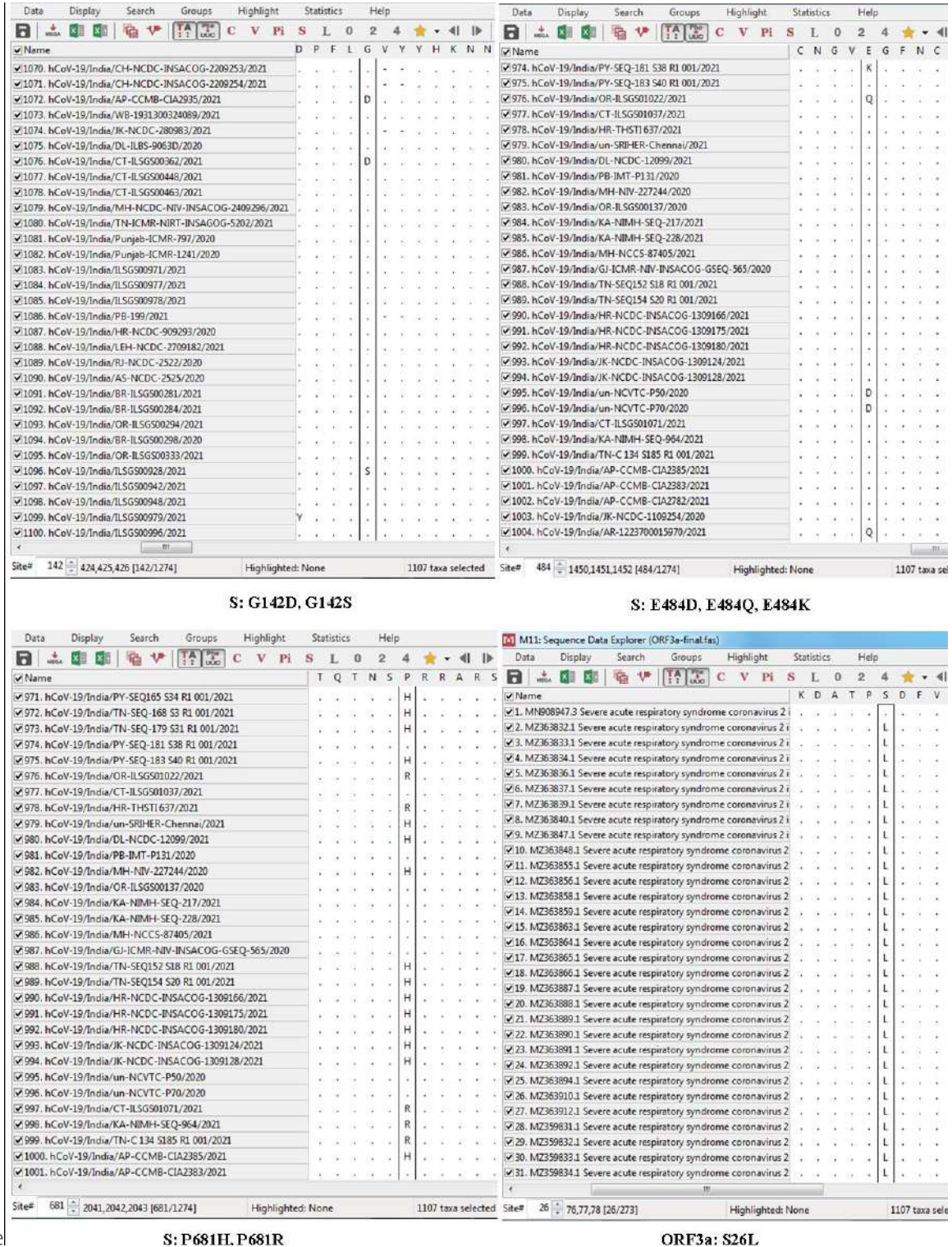


Figure S3

Figures showing amino acid substitution in S protein & ORF3a of SARS-CoV-2 under positive selective



pressure

S: P681H, P681R

ORF3a: S26L

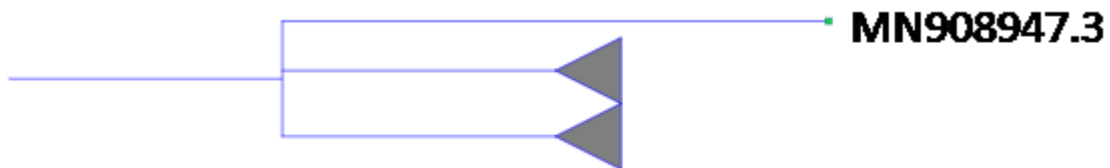
Figure S4

Figures showing amino acid substitution in ORF9 region of SARS-CoV-2 under positive selective pressure



Figure S5

Phylogenetic analysis of SARS-CoV-2 genomes using iTOL (<https://itol.embl.de/>). The tree initially got divided into three clades.



**Figure S6:** Phylogenetic analysis of SARS-CoV-2 genome using MEGA 11. The phylogenetic clusters are unlabelled lines. Sequences which didn't cluster with any of the sequences have been labeled and shown in the Phylogenetic Tree



Table S1

The purifying and diversifying selection in the genome of SARS-CoV-2 as assessed by FEL method

Protein	Site showing purifying selection	Site showing diversifying selection
NSP1	16, 90, 159, 172	33
NSP2	36, 75, 94, 107, 190, 260, 335, 357, 384, 470, 475, 563, 595, 598, 614, 629	381, 488, 489
NSP3	21, 39, 68, 85, 106, 111, 236, 246, 255, 297, 327, 352, 512, 527, 550, 551, 586, 629, 660, 700, 701, 705, 744, 763, 819, 875, 878, 938, 940, 951, 955, 963, 976, 978, 982, 991, 1003, 1055, 1089, 1092, 1113, 1159, 1193, 1216, 1225, 1325, 1342, 1671, 1703, 1813, 1820, 1823, 1857, 1915	183, 822, 1682
NSP4	15, 67, 78, 121, 177, 201, 212, 240, 400	Nil
NSP5	14, 81, 137, 301	Nil
NSP6	16, 28, 119, 120, 214, 215, 279, 285	37
NSP7	15, 23, 32, 60	Nil
NSP8	14, 146	Nil
NSP9	11, 112	Nil
NSP10	130	Nil
NSP11	Nil	Nil
NSP12	92, 103, 144, 302, 513, 626, 753	513
NSP14	17, 143, 183, 280, 338, 424, 425, 459, 495, 514	Nil
NSP15	53, 85, 192, 214, 247, 335	Nil
NSP16	97, 112, 122, 141, 191, 199, 204	126, 298
ORF3a	36, 78, 129, 252	26, 57, 93, 155, 172, 223
M gene	71, 93, 135	82
ORF6	7, 61	Nil
ORF7a	33	81
ORF7b	10, 36	Nil
ORF8	14, 31, 48, 49, 72	Nil
N gene	35, 36, 39, 61, 110, 157, 173, 234, 268, 287, 298, 302, 320, 321, 337	13, 18, 63, 194, 214, 215, 235, 251, 379
ORF 10	28	Nil
Spike:	32, 47, 61, 66, 81, 87, 111, 134, 146, 151, 206, 213, 227, 237, 238, 256, 294, 302, 321, 341, 342, 355, 372, 380, 386, 394, 433, 475, 518, 534, 555, 629, 636, 642, 679, 682, 693, 707, 789, 808, 820, 827, 852, 860, 881, 888, 905, 907, 912, 942, 948, 971, 995, 996, 1045, 1053, 1060, 1091, 1110, 1128, 1148, 1178, 1216, 1238, 1254, 1273	5, 23, 54, 95, 142, 452, 501, 681, 879, 950, 1118

Table S2

The purifying and diversifying selection in the genome of SARS-CoV-2 as assessed by MEME method

Protein	Site showing Episodic Positive/diversifying selection
NSP2	381
NSP3	183, 882, 1682
NSP6	37
NSP 12 polymerase	571
NSP 15	414
NSP 16	126, 298
ORF 3a	26, 57, 93, 155, 172, 223
M gene	82
Orf 7a	81-0.08, 1.82
Orf 8	73-0.01 0.719
Orf 9	3, 13, 63, 194, 204, 235, 251
Spike	23, 54, 95, 142, 152, 452, 501, 627, 681, 879, 943, 1118