

Supplementary Table

Table S1: Variants from peak to peak

Variants	2020		2021			2022	
	Aug-Sep	Oct-Nov	Jan-Mar	Apr-Jun	Jul-Sep	Oct-Nov	Jan-Mar
VOC_Alpha	0	0	2	5	0	0	0
VOC_Beta	0	0	1	3	0	0	0
VOI_Kappa	0	0	0	4	0	0	0
VOC_Delta	0	0	0	55	8	4	0
VOC_Omicron	0	0	0	0	0	0	25
Others	10	7	0	3	1	0	0

Supplementary Figures

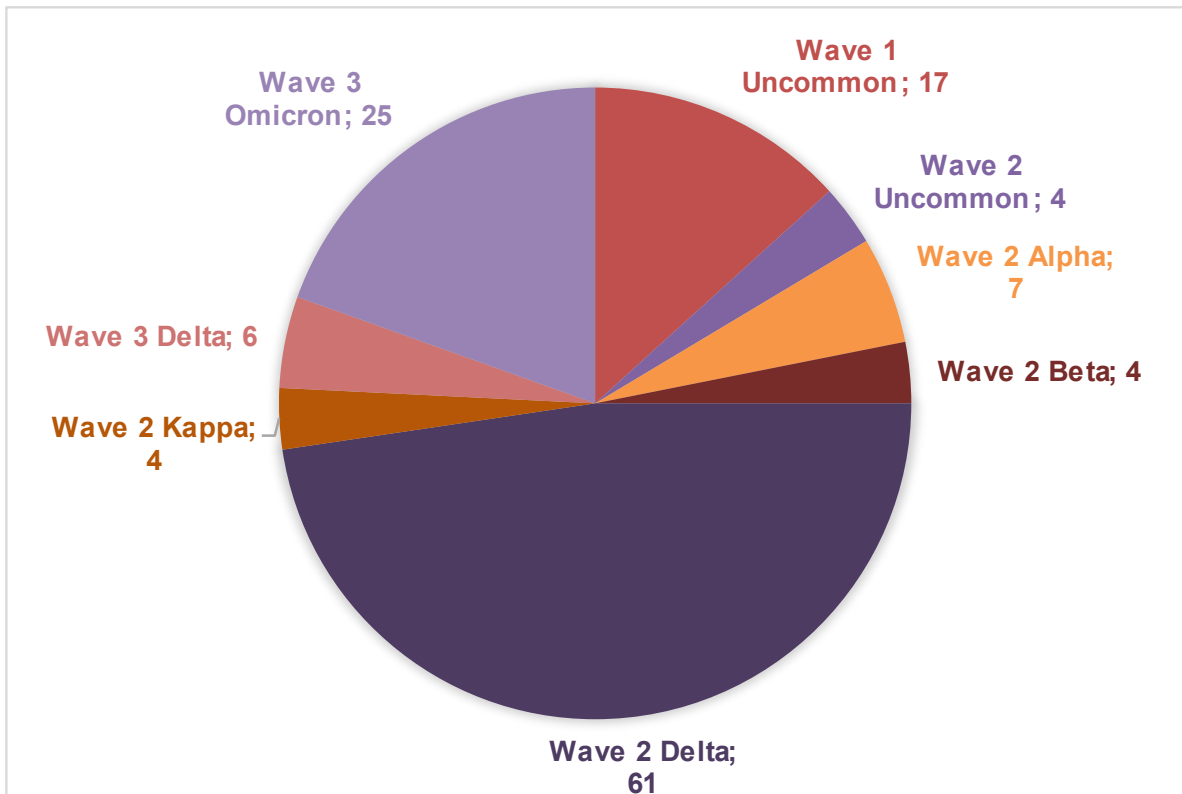


Figure S1: Distribution of Variants during three consecutive peaks

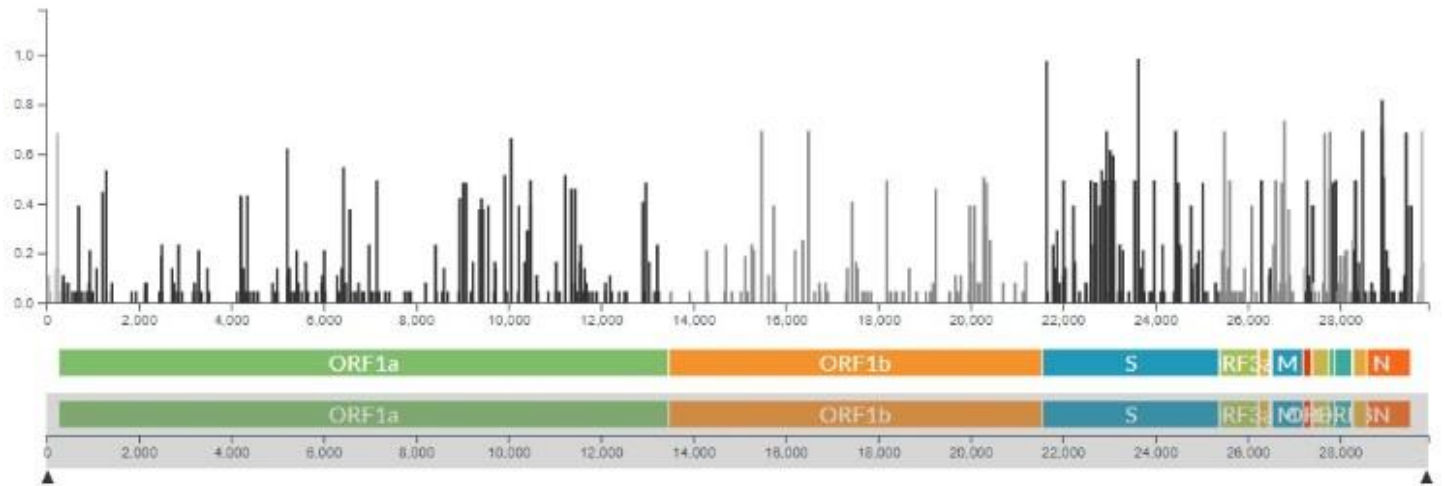


Figure S2: COVID-19 Genome wide coverage

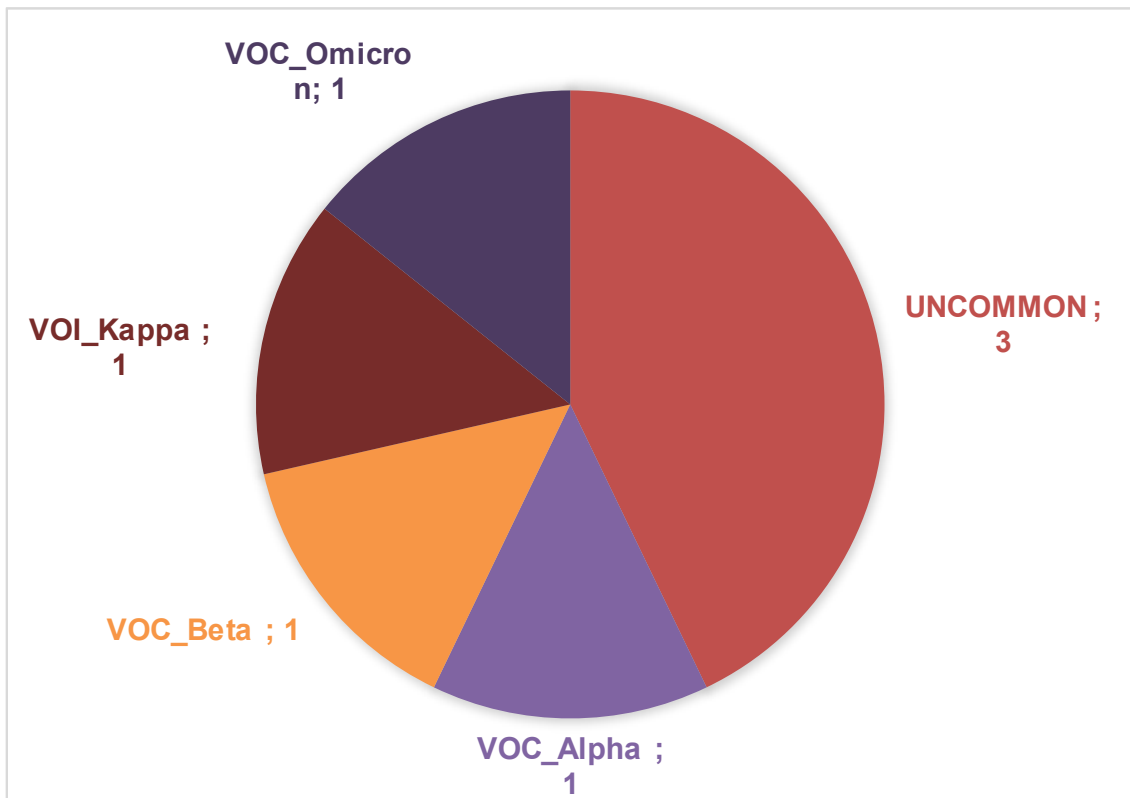


Figure S3: Breakthrough Infection in Second and Third wave

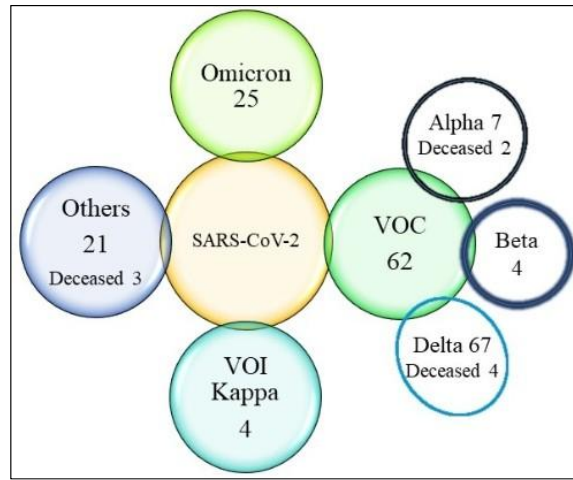


Figure S4: Overview of total variants and the outcome

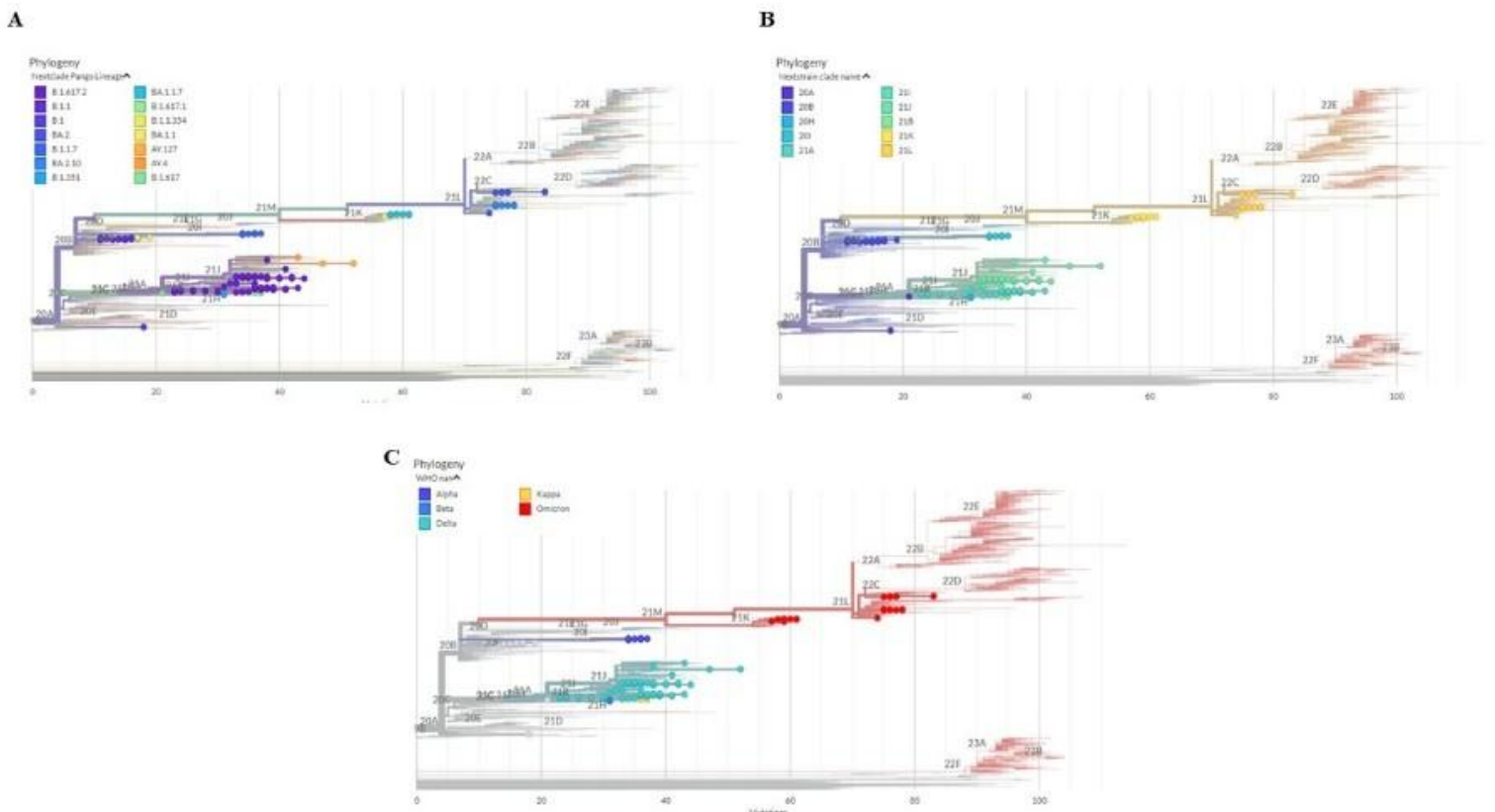


Figure S5: Phylogenetic analysis of 128 SARS-CoV-2 patient samples in Puducherry from August 2020 to March 2022. Dendrogram revealing the phylogenetic relationship between the SARS-CoV-2 genomes from 128 patient samples in Puducherry, aligned against the Wuhan Hu 1 (NC_045512.2) reference genome. The dendrogram was generated using FastTree, which infers approximately-maximum-likelihood phylogenetic trees from alignments of nucleotides. Major clades from pangolin lineages, Nextstrain and WHO lineages are indicated at the branch points.

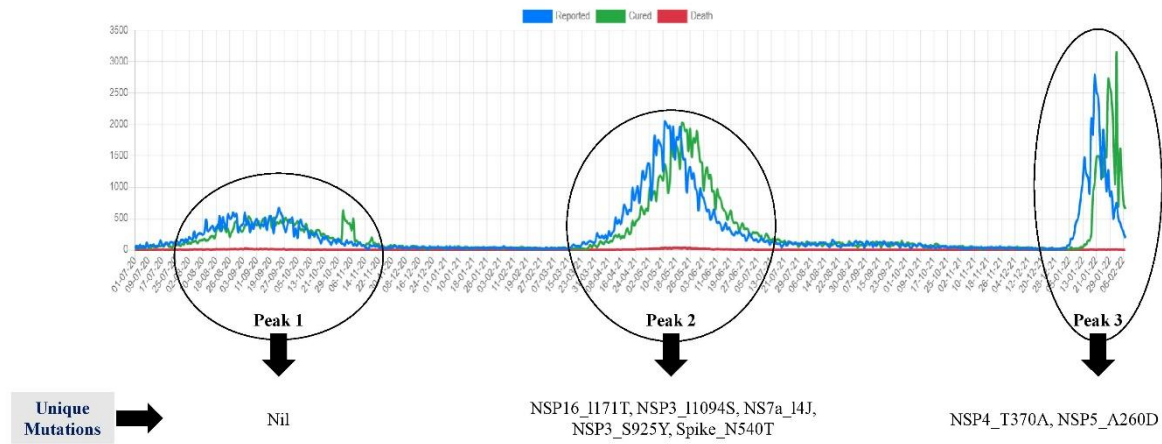


Figure S6: Distribution of unique mutants during three consecutive peaks in Puducherry. The sample collection during the peak 1 and peak 2 is similar to corresponding circle in the given image. Whereas the sample collection peak 3 was done during Sep 2021-Feb 2022.

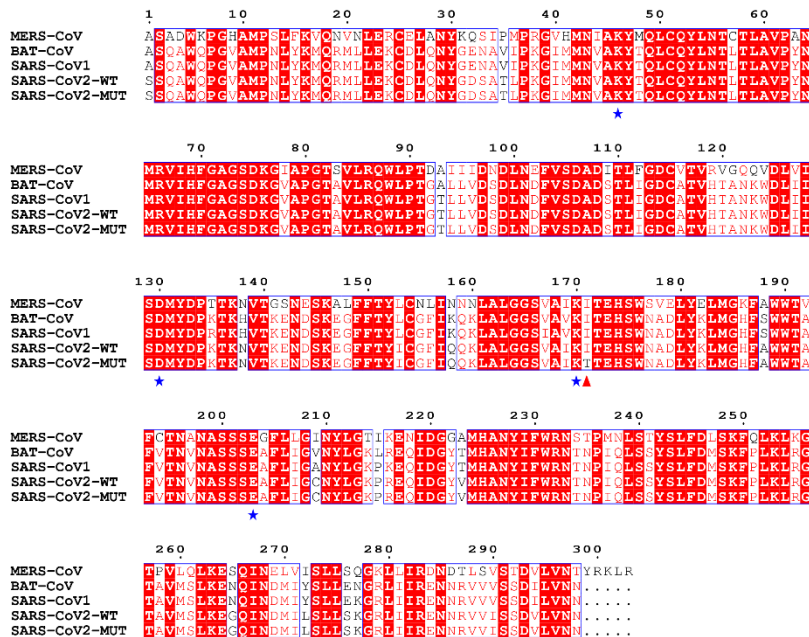


Figure S7: Multiple Sequence Alignment of nsp16 protein sequences from different sources (MERS-CoV: UniProt ID K9N7C7, Bat-CoV: UniProt ID P0C6V9, SARS-CoV1: UniProt ID P0C6X7, SARS-CoV2: UniProt ID P0DTD1) as indicated in the sequence names. The catalytic tetrad residues are indicated as blue stars, and the mutation site is indicated as red triangle.