COVID-19 subject SARS_CoV_171

2021-06-29

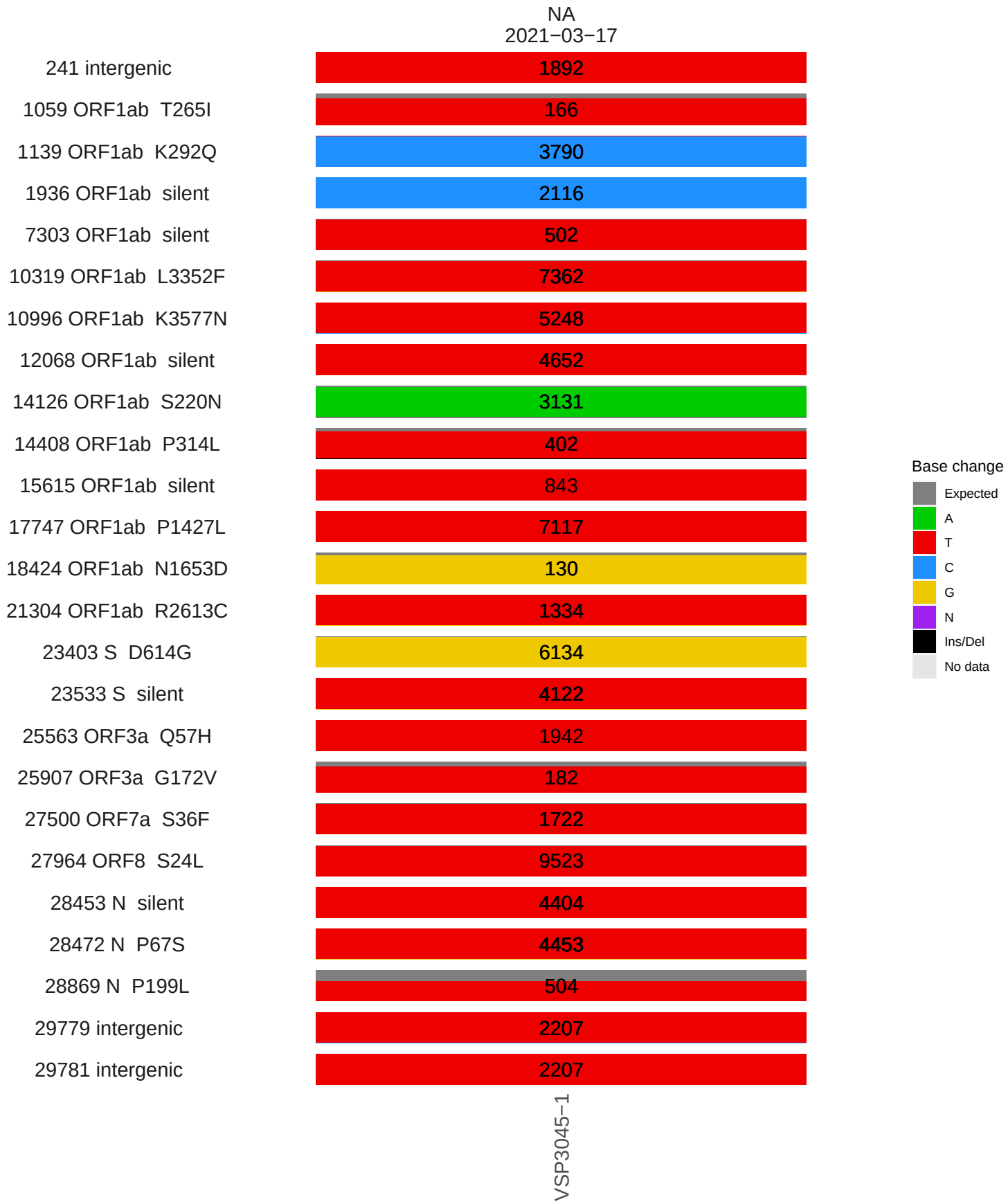
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP3045-1	single experiment	NA	NA	2021-03-17	4.03	B.1.2	99.9%	99.8%

Variants shared across samples

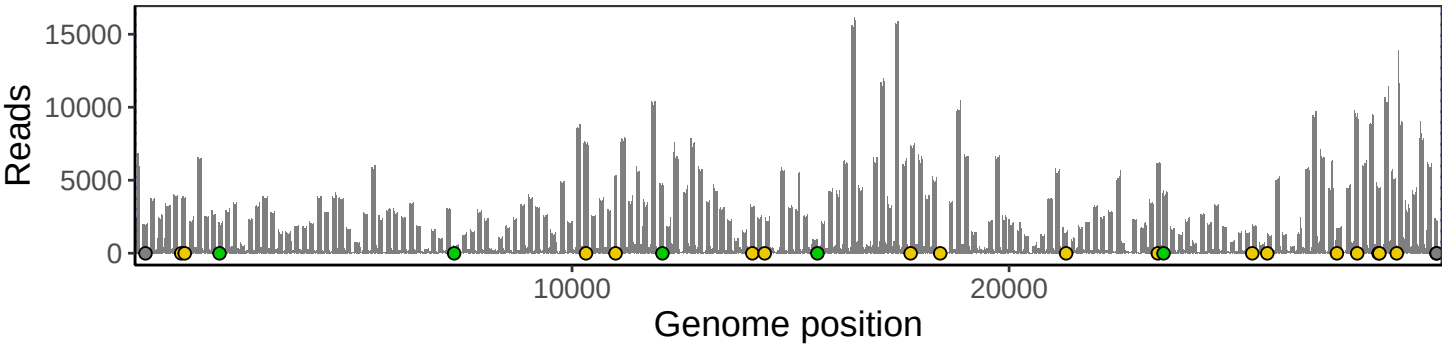
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/NC_04551 are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read pairs and the variant yields a PHRED score > 20. Gray tiles denote positions where the variant was not the major variant or no variants were found. The relative base compositions of each experiment used to calculate tiles are shown in the following plot where the total number of position reads are shown atop of each plot.


NA
2021−03−17
241 intergenic
1892
1059 ORF1ab T265I
166
1139 ORF1ab K292Q
3790
1936 ORF1ab silent
2116
7303 ORF1ab silent
502
10319 ORF1ab L3352F
7362
10996 ORF1ab K3577N
5248
12068 ORF1ab silent
4652
14126 ORF1ab S220N
3131
14408 ORF1ab P314L
402
15615 ORF1ab silent
843
17747 ORF1ab P1427L
7117
18424 ORF1ab N1653D
130
21304 ORF1ab R2613C
1334
23403 S D614G
6134
23533 S silent
4122
25563 ORF3a Q57H
1942
25907 ORF3a G172V
182
27500 ORF7a S36F
1722
27964 ORF8 S24L
9523
28453 N silent
4404
28472 N P67S
4453
28869 N P199L
504
29779 intergenic
2207
29781 intergenic
2207
VSP3045−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

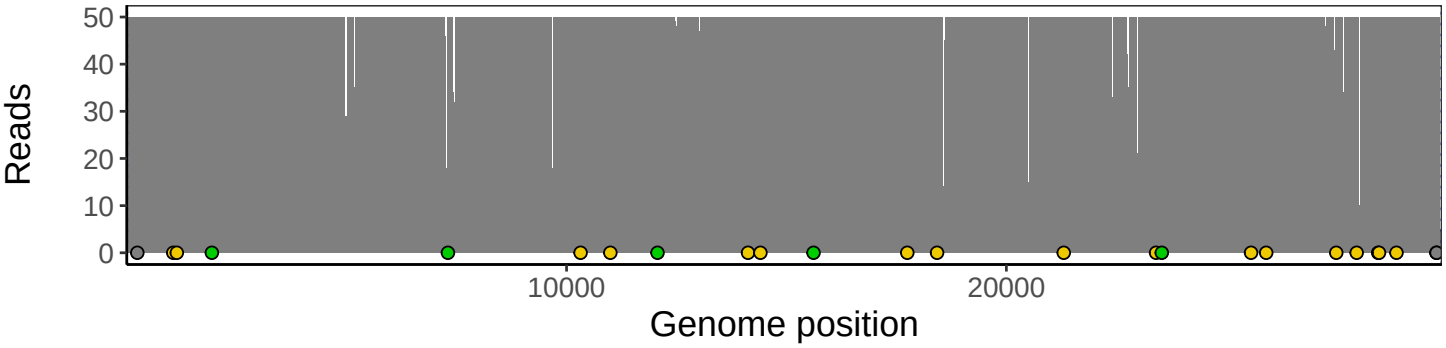
Analyses of individual experiments and composite results

VSP3045-1 | 2021-03-17 | NA | SARS_CoV_171 | genomes | single experiment

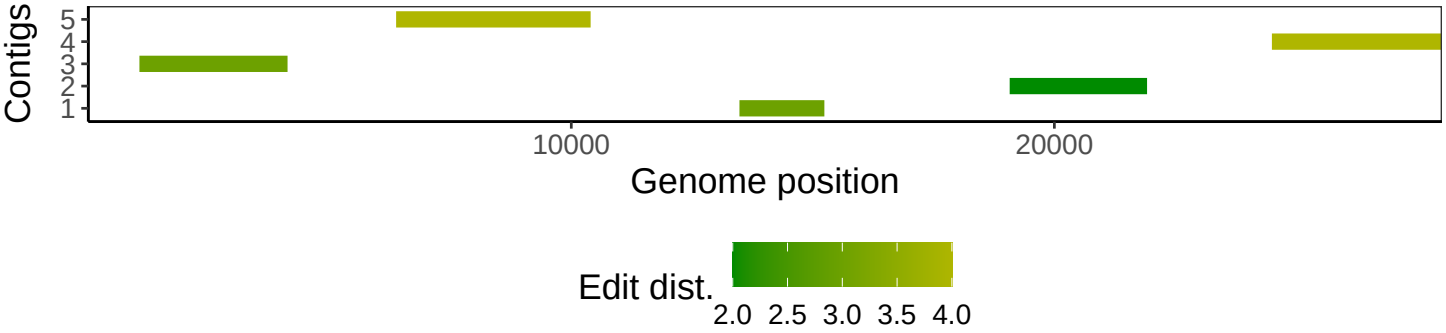
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htslib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htslib 1.10.2-57-gf58a6f3
pangolin	3.1.3
genbankr	1.4.0
optparse	1.6.0
forcats	0.3.0
stringr	1.4.0
dplyr	0.8.1
purrr	0.2.5
readr	1.1.1
tidyr	0.8.1
tibble	2.1.2
ggplot2	3.3.3
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
GenomeInfoDb	1.12.3
Biostrings	2.44.2
XVector	0.16.0
IRanges	2.10.5
S4Vectors	0.14.7
BiocParallel	1.10.1
BiocGenerics	0.22.1