COVID-19 subject SARS_CoV_307

2021-06-29

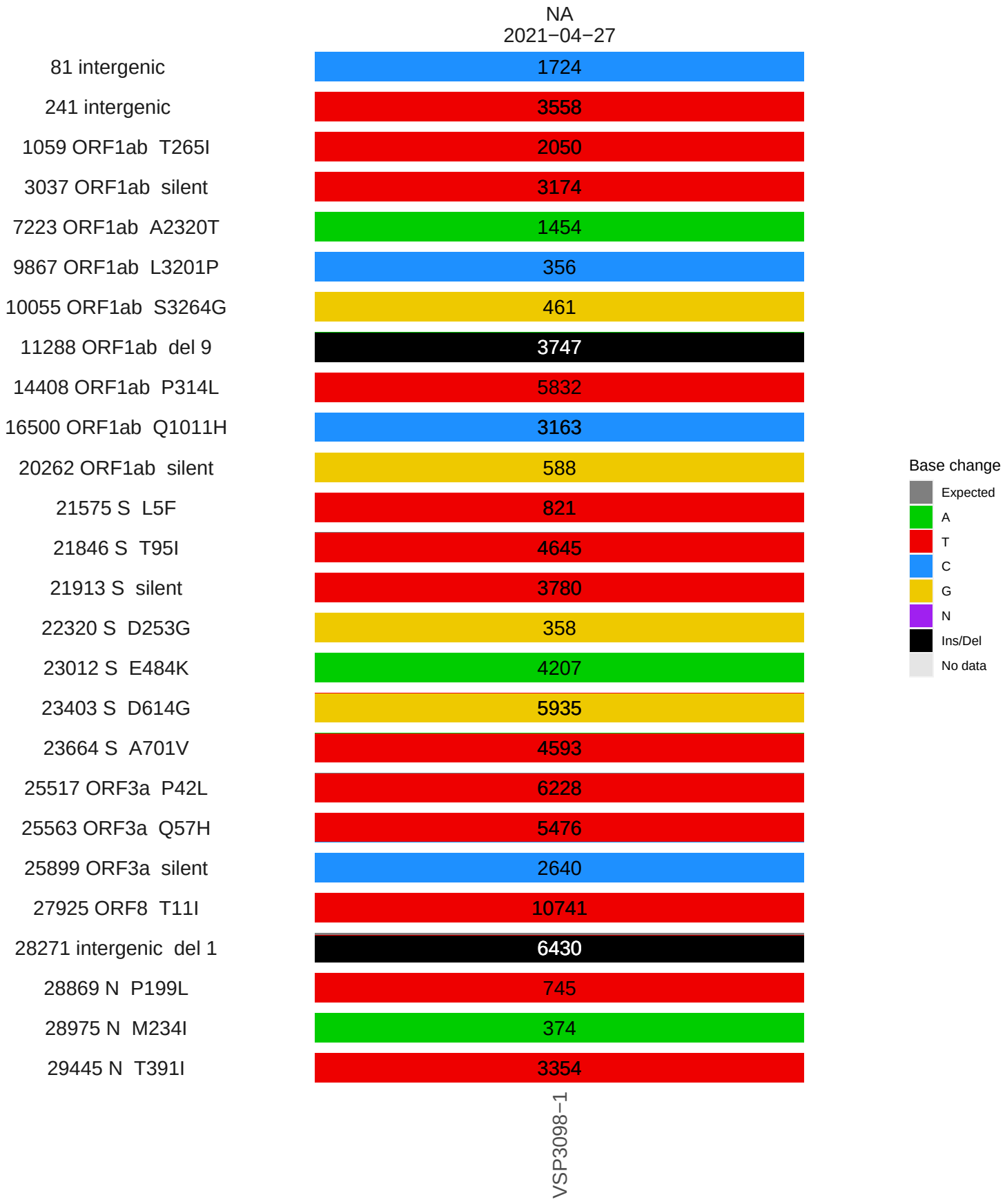
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP3098-1	single experiment	NA	NA	2021-04-27	29.81	B.1.526	99.8%	99.7%

Variants shared across samples

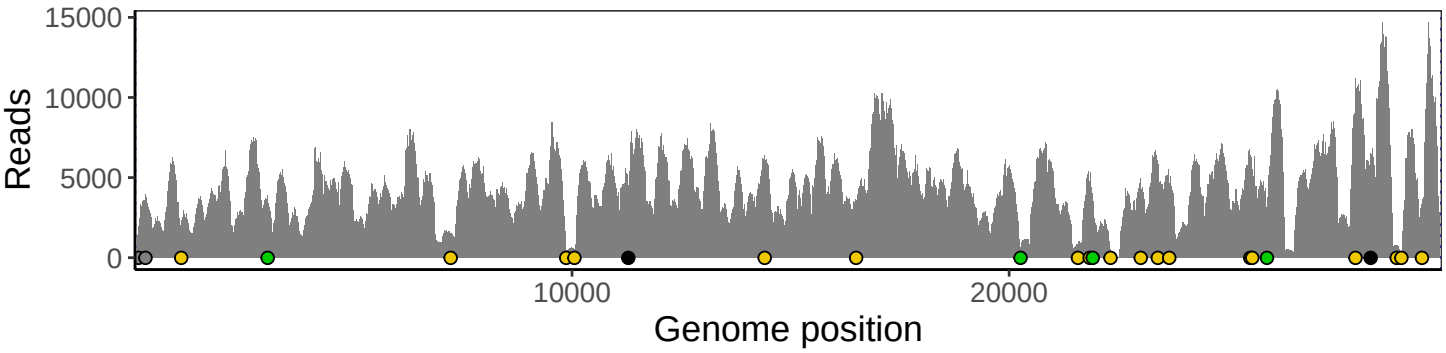
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/NC_04551 are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read pairs 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
2021−04−27
81 intergenic
1724
241 intergenic
3558
1059 ORF1ab T265I
2050
3037 ORF1ab silent
3174
7223 ORF1ab A2320T
1454
9867 ORF1ab L3201P
356
10055 ORF1ab S3264G
461
11288 ORF1ab del 9
3747
14408 ORF1ab P314L
5832
16500 ORF1ab Q1011H
3163
20262 ORF1ab silent
588
21575 S L5F
821
21846 S T95I
4645
21913 S silent
3780
22320 S D253G
358
23012 S E484K
4207
23403 S D614G
5935
23664 S A701V
4593
25517 ORF3a P42L
6228
25563 ORF3a Q57H
5476
25899 ORF3a silent
2640
27925 ORF8 T11I
10741
28271 intergenic del 1
6430
28869 N P199L
745
28975 N M234I
374
29445 N T391I
3354
VSP3098−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

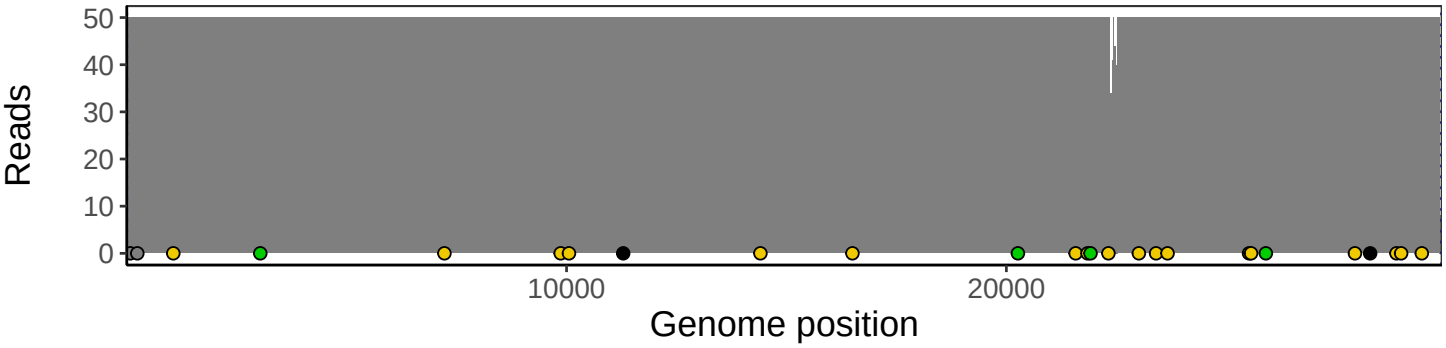
Analyses of individual experiments and composite results

VSP3098-1 | 2021-04-27 | NA | SARS_CoV_307 | genomes | single experiment

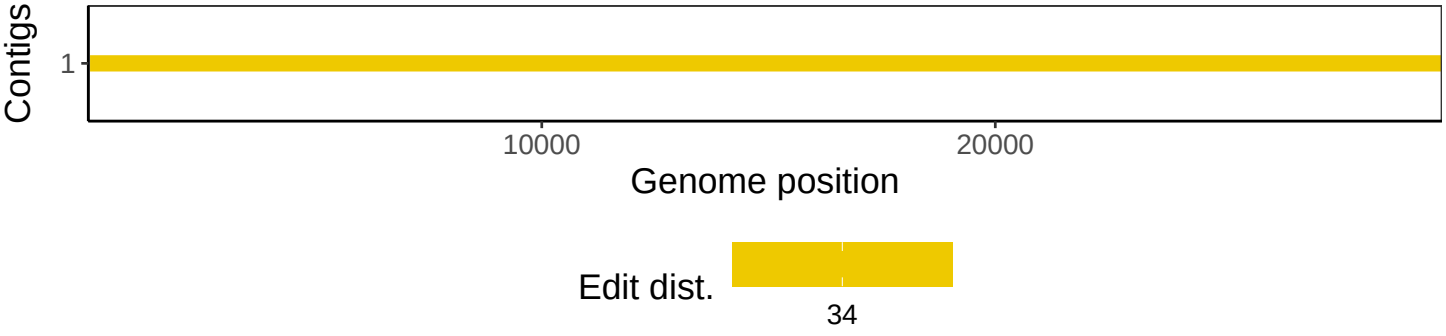
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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