COVID-19 subject SARS_CoV_274

2021-06-29

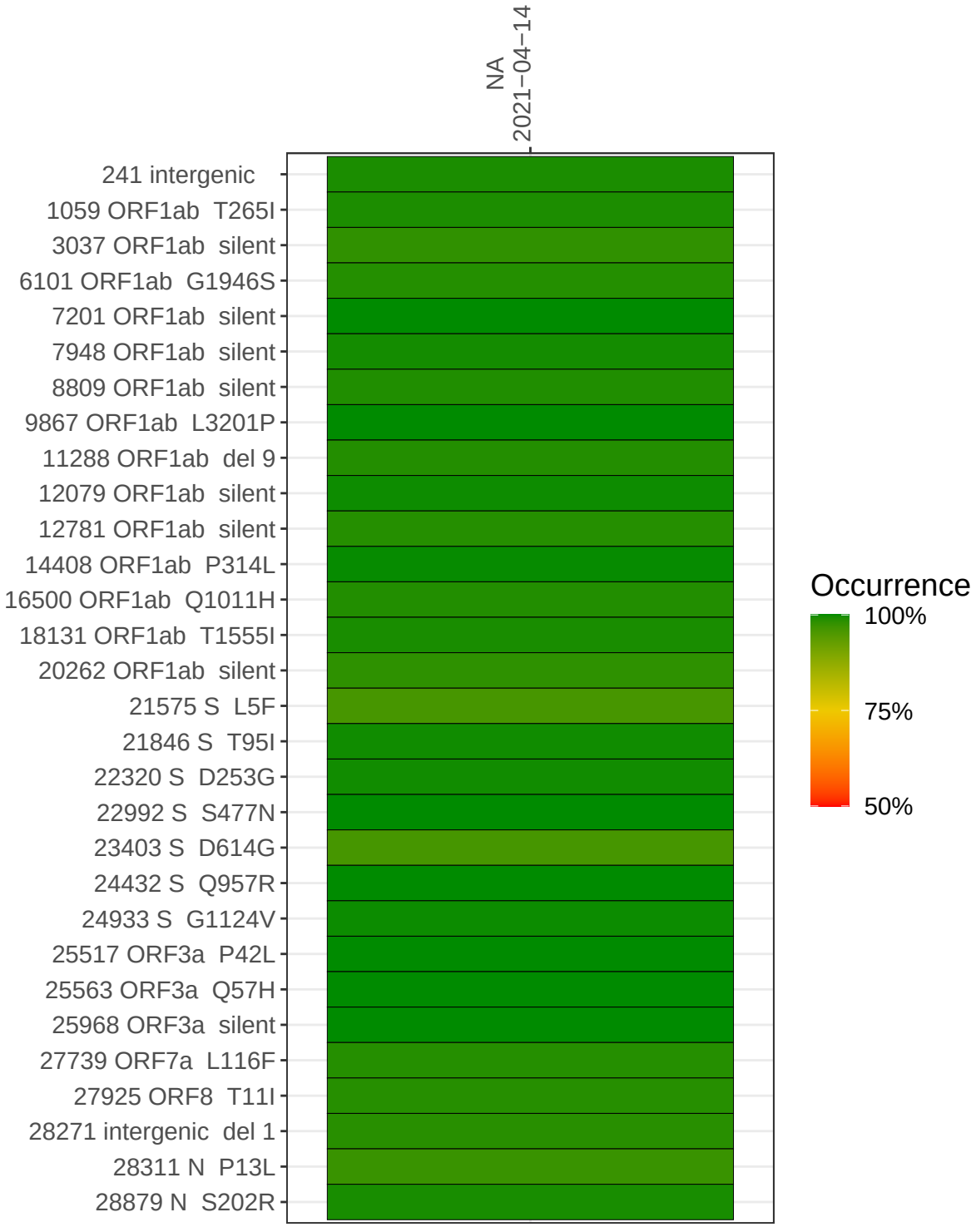
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

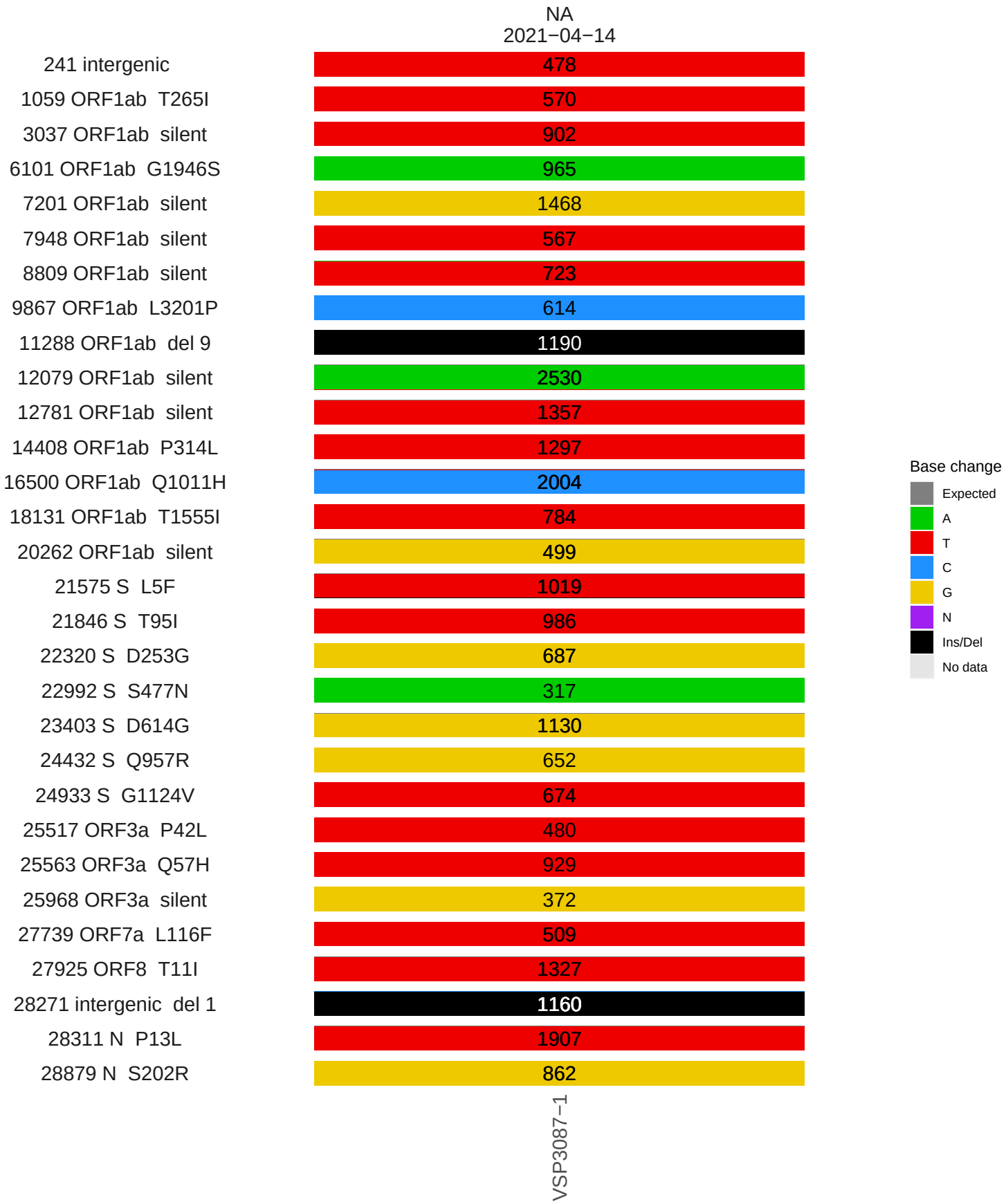
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP3087-1	single experiment	NA	NA	2021-04-14	29.69	B.1.526	99.9%	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.

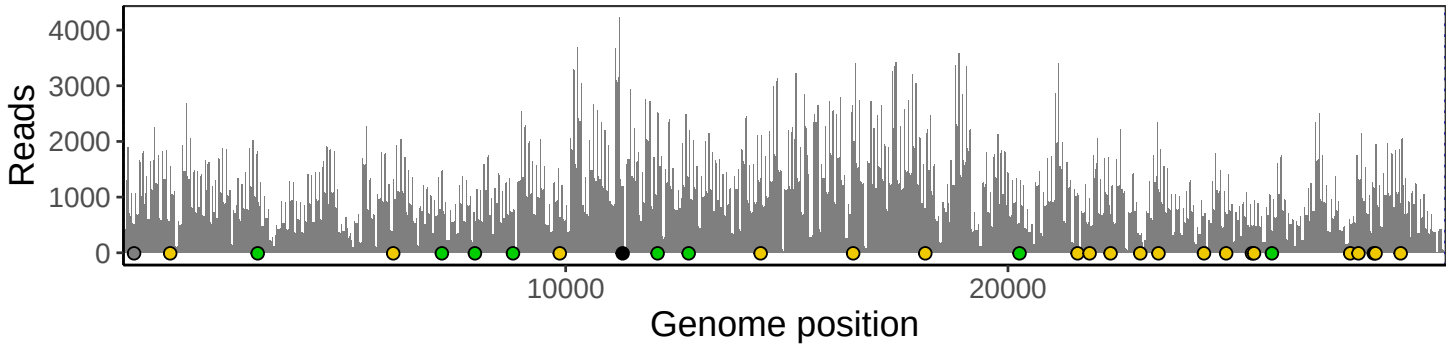



NA
2021−04−14
241 intergenic
478
1059 ORF1ab T265I
570
3037 ORF1ab silent
902
6101 ORF1ab G1946S
965
7201 ORF1ab silent
1468
7948 ORF1ab silent
567
8809 ORF1ab silent
723
9867 ORF1ab L3201P
614
11288 ORF1ab del 9
1190
12079 ORF1ab silent
2530
12781 ORF1ab silent
1357
14408 ORF1ab P314L
1297
16500 ORF1ab Q1011H
2004
18131 ORF1ab T1555I
784
20262 ORF1ab silent
499
21575 S L5F
1019
21846 S T95I
986
22320 S D253G
687
22992 S S477N
317
23403 S D614G
1130
24432 S Q957R
652
24933 S G1124V
674
25517 ORF3a P42L
480
25563 ORF3a Q57H
929
25968 ORF3a silent
372
27739 ORF7a L116F
509
27925 ORF8 T11I
1327
28271 intergenic del 1
1160
28311 N P13L
1907
28879 N S202R
862
VSP3087−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

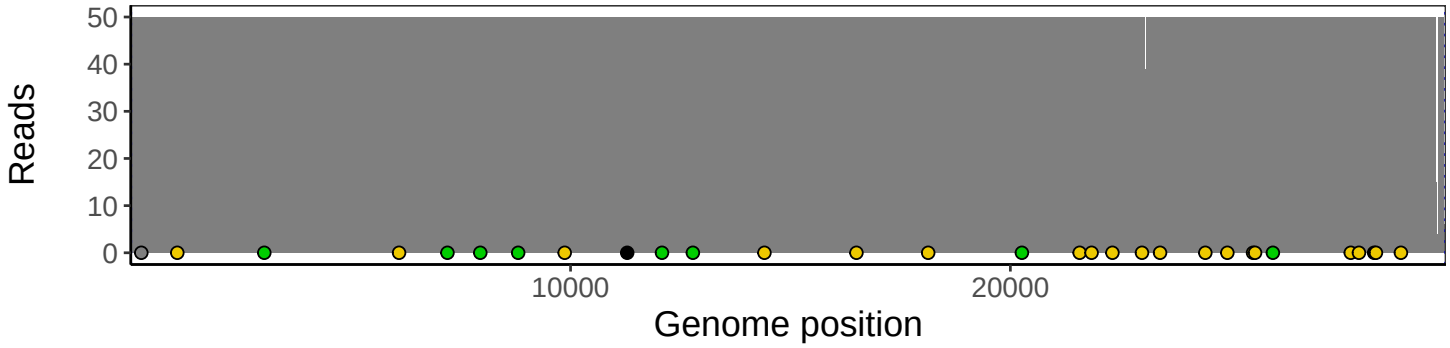
Analyses of individual experiments and composite results

VSP3087-1 | 2021-04-14 | NA | SARS_CoV_274 | genomes | single experiment

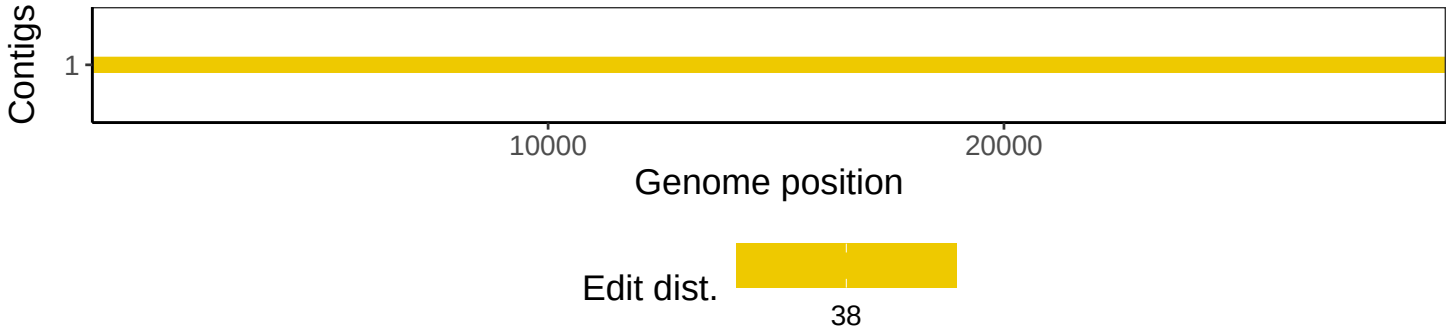
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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