COVID-19 subject SARS_CoV_265

2021-06-29

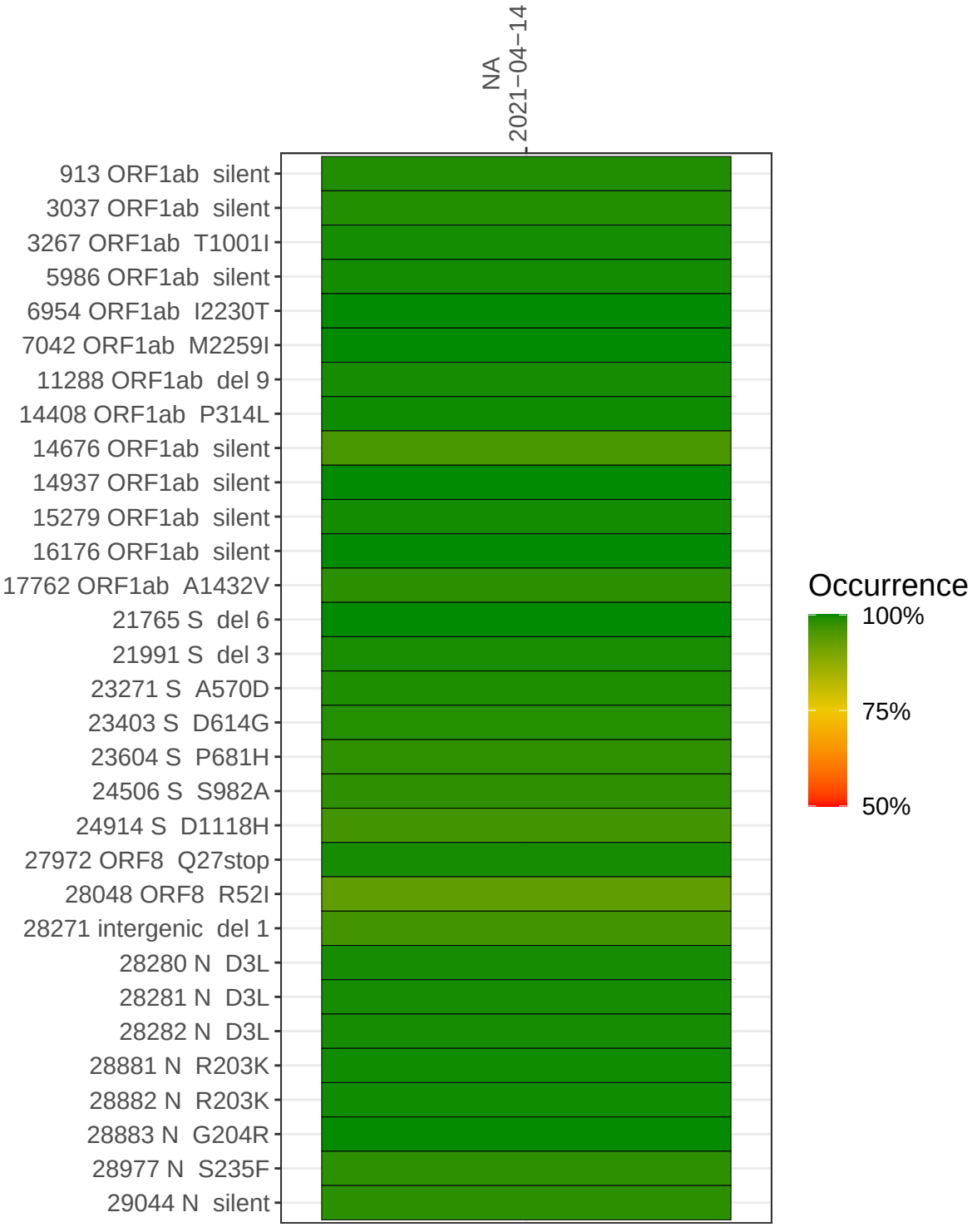
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

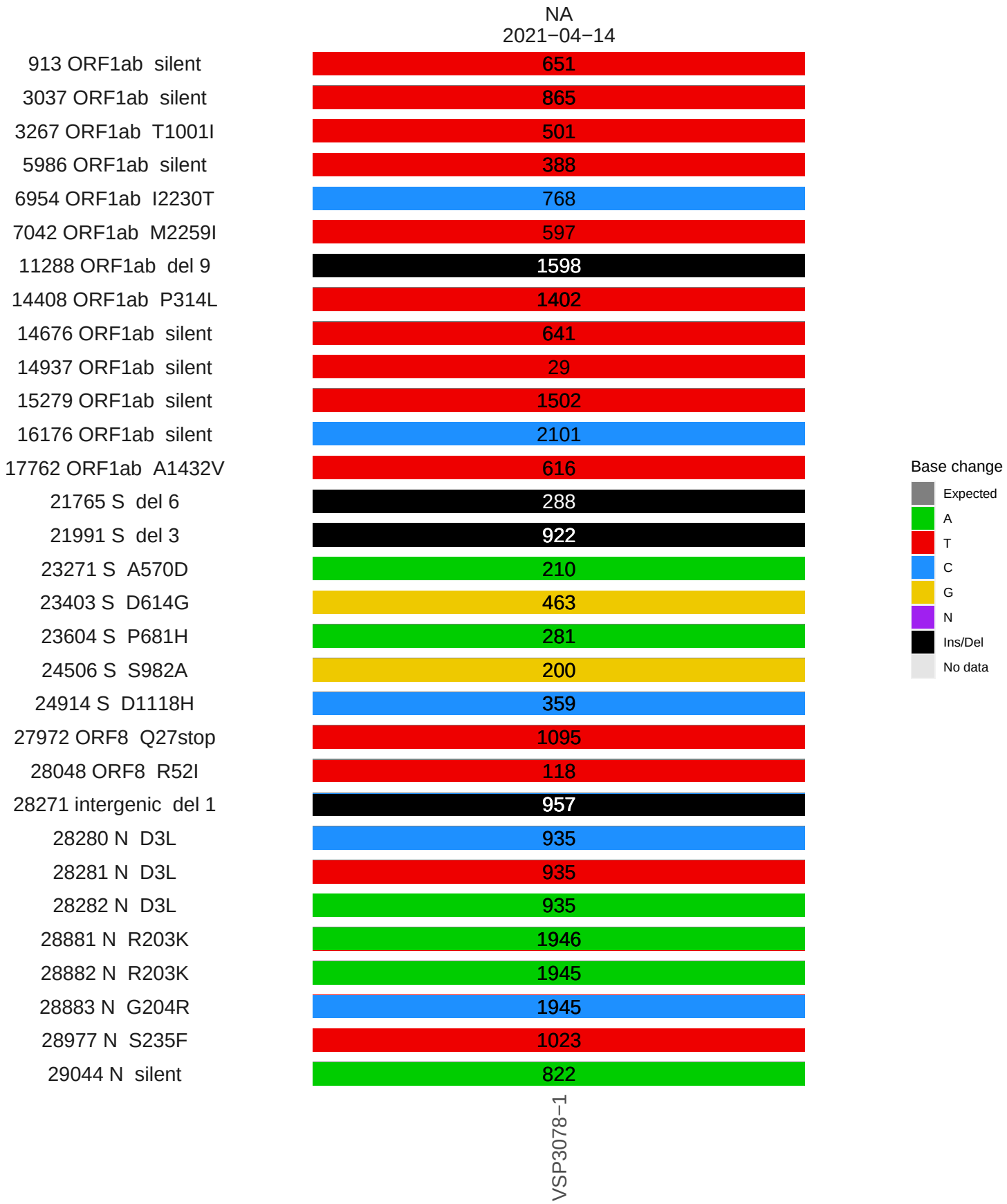
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP3078-1	single experiment	NA	NA	2021-04-14	22.87	B.1.1.7	99.6%	99.6%

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.

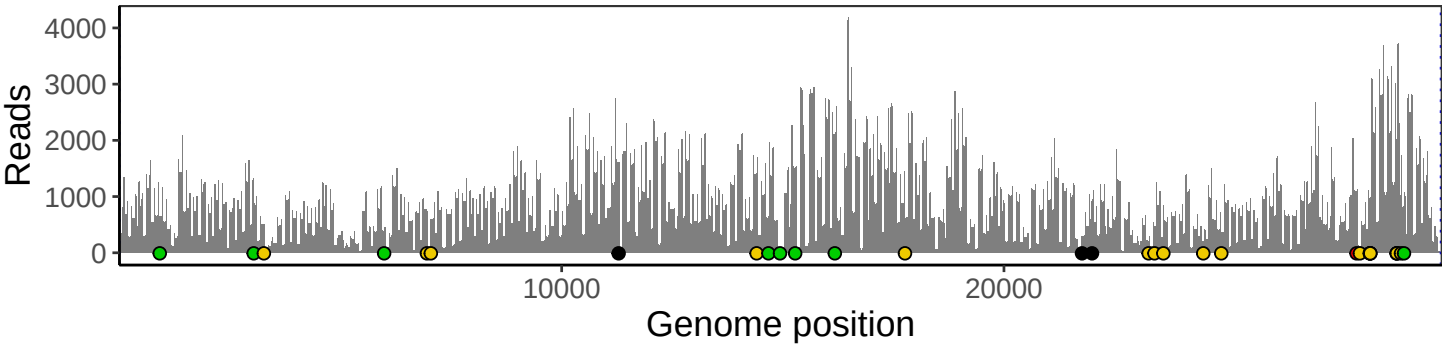



NA
2021−04−14
913 ORF1ab silent
651
3037 ORF1ab silent
865
3267 ORF1ab T1001I
501
5986 ORF1ab silent
388
6954 ORF1ab I2230T
768
7042 ORF1ab M2259I
597
11288 ORF1ab del 9
1598
14408 ORF1ab P314L
1402
14676 ORF1ab silent
641
14937 ORF1ab silent
29
15279 ORF1ab silent
1502
16176 ORF1ab silent
2101
17762 ORF1ab A1432V
616
21765 S del 6
288
21991 S del 3
922
23271 S A570D
210
23403 S D614G
463
23604 S P681H
281
24506 S S982A
200
24914 S D1118H
359
27972 ORF8 Q27stop
1095
28048 ORF8 R52I
118
28271 intergenic del 1
957
28280 N D3L
935
28281 N D3L
935
28282 N D3L
935
28881 N R203K
1946
28882 N R203K
1945
28883 N G204R
1945
28977 N S235F
1023
29044 N silent
822
VSP3078−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

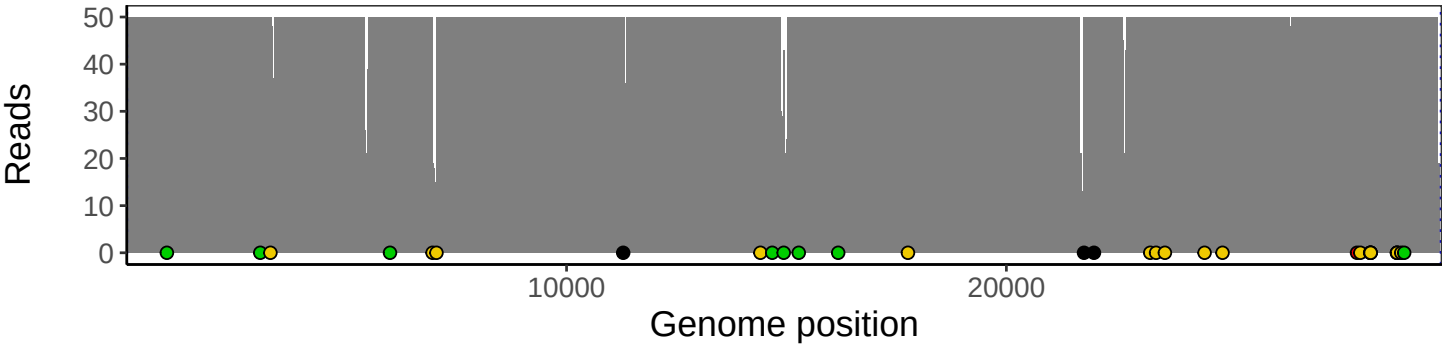
Analyses of individual experiments and composite results

VSP3078-1 | 2021-04-14 | NA | SARS_CoV_265 | genomes | single experiment

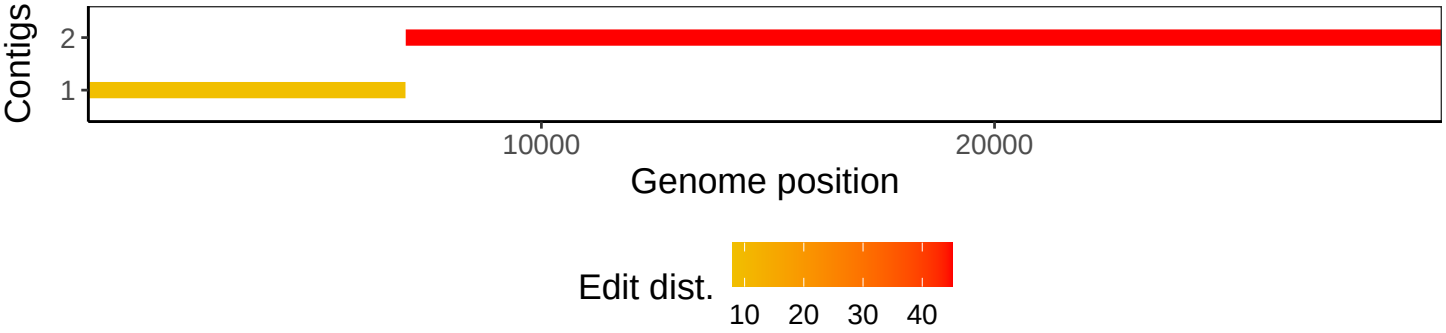
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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