COVID-19 subject UPHS-0439

2021-06-23

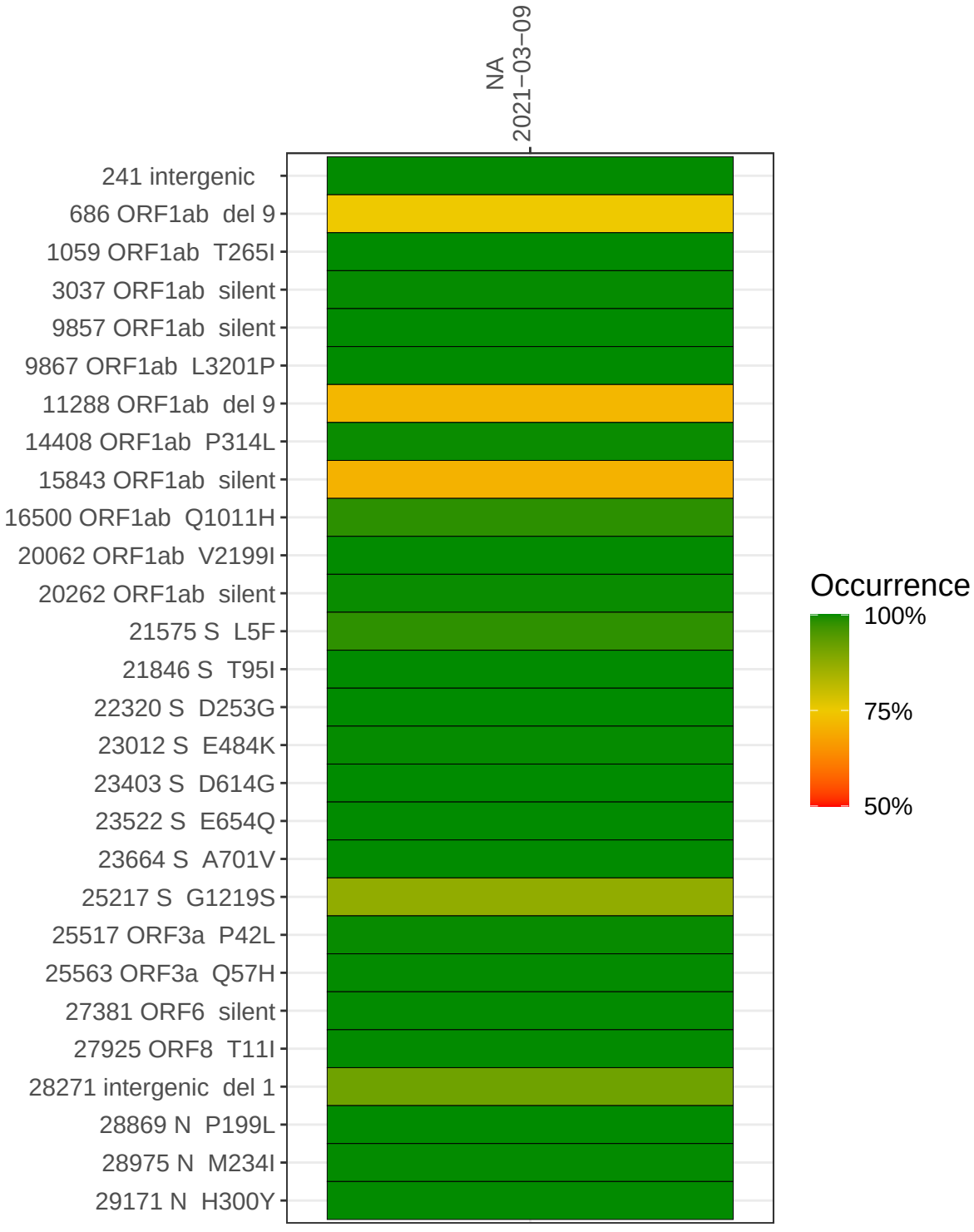
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

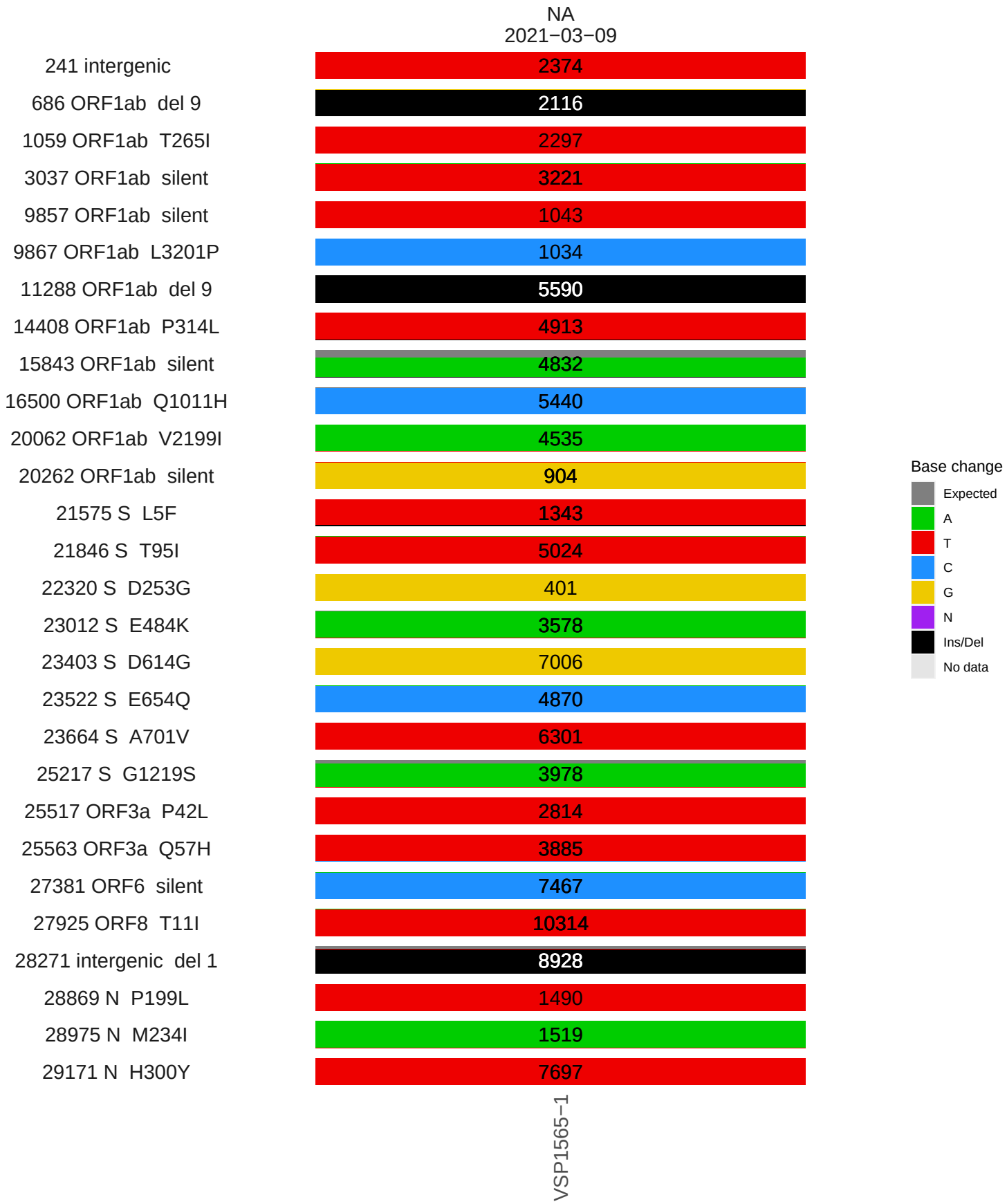
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1565-1	single experiment	NA	NA	2021-03-09	29.84	B.1.526	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

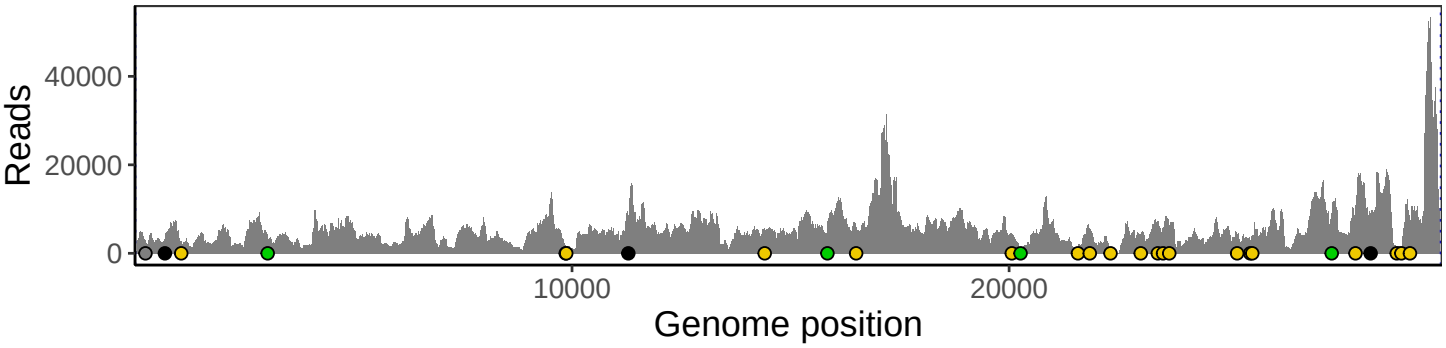



NA
2021−03−09
241 intergenic
2374
686 ORF1ab del 9
2116
1059 ORF1ab T265I
2297
3037 ORF1ab silent
3221
9857 ORF1ab silent
1043
9867 ORF1ab L3201P
1034
11288 ORF1ab del 9
5590
14408 ORF1ab P314L
4913
15843 ORF1ab silent
4832
16500 ORF1ab Q1011H
5440
20062 ORF1ab V2199I
4535
20262 ORF1ab silent
904
21575 S L5F
1343
21846 S T95I
5024
22320 S D253G
401
23012 S E484K
3578
23403 S D614G
7006
23522 S E654Q
4870
23664 S A701V
6301
25217 S G1219S
3978
25517 ORF3a P42L
2814
25563 ORF3a Q57H
3885
27381 ORF6 silent
7467
27925 ORF8 T11I
10314
28271 intergenic del 1
8928
28869 N P199L
1490
28975 N M234I
1519
29171 N H300Y
7697
VSP1565−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

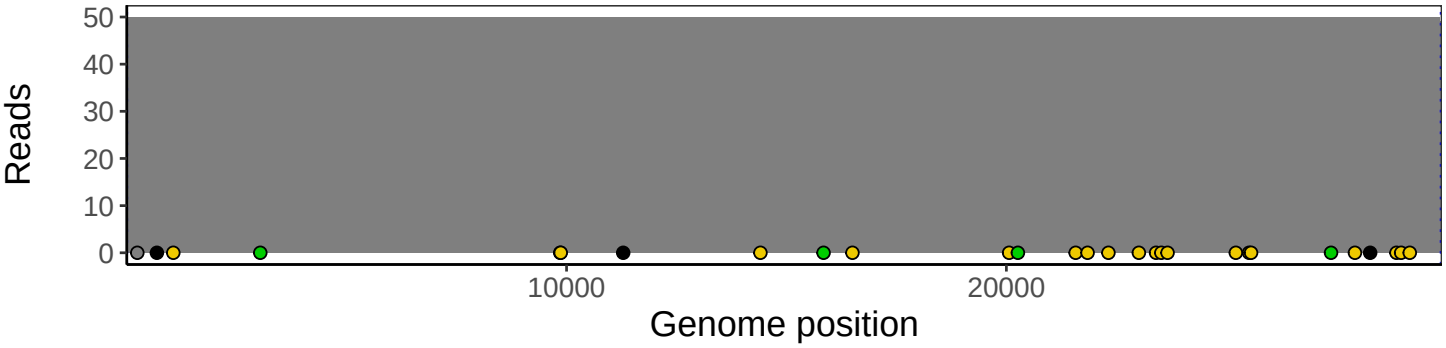
Analyses of individual experiments and composite results

VSP1565-1 | 2021-03-09 | NA | UPHS-0439 | genomes | single experiment

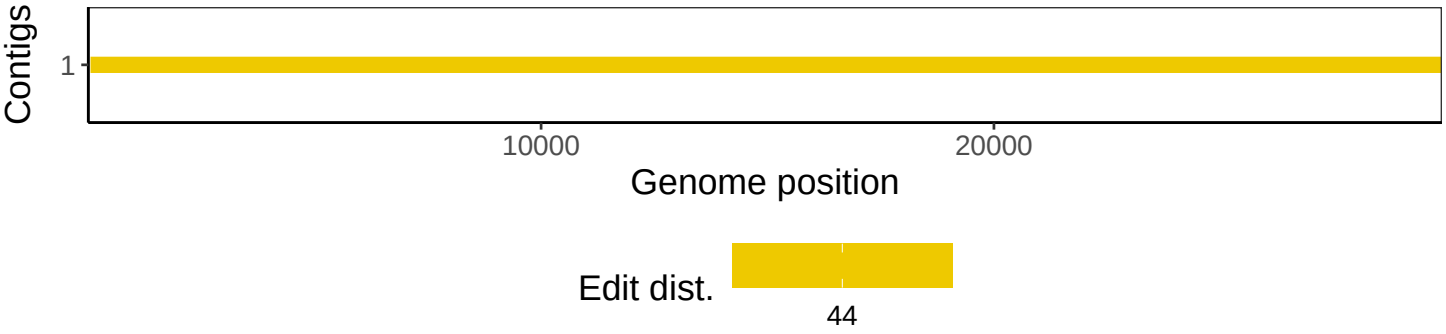
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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