COVID-19 subject UPHS-0443

2021-06-23

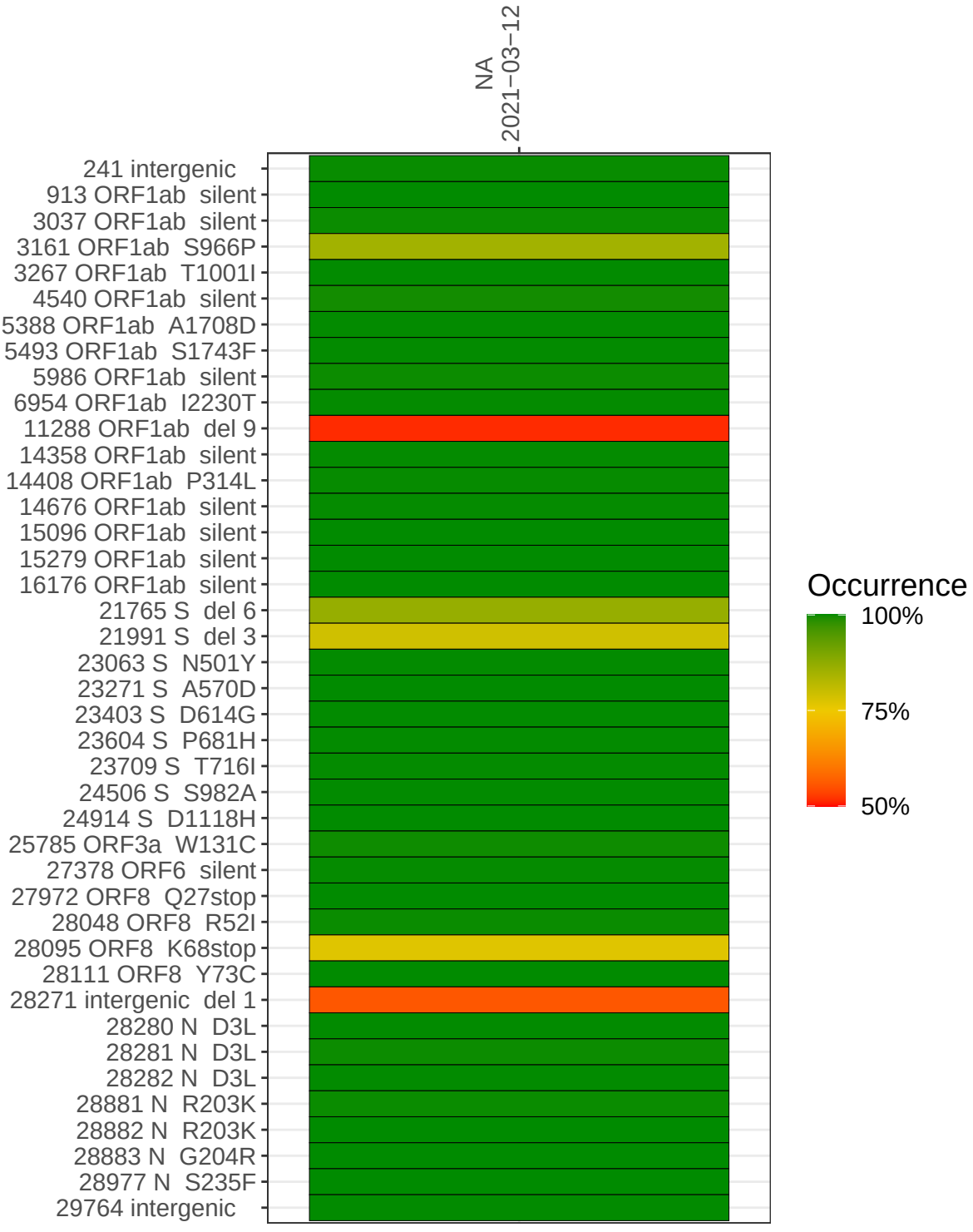
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

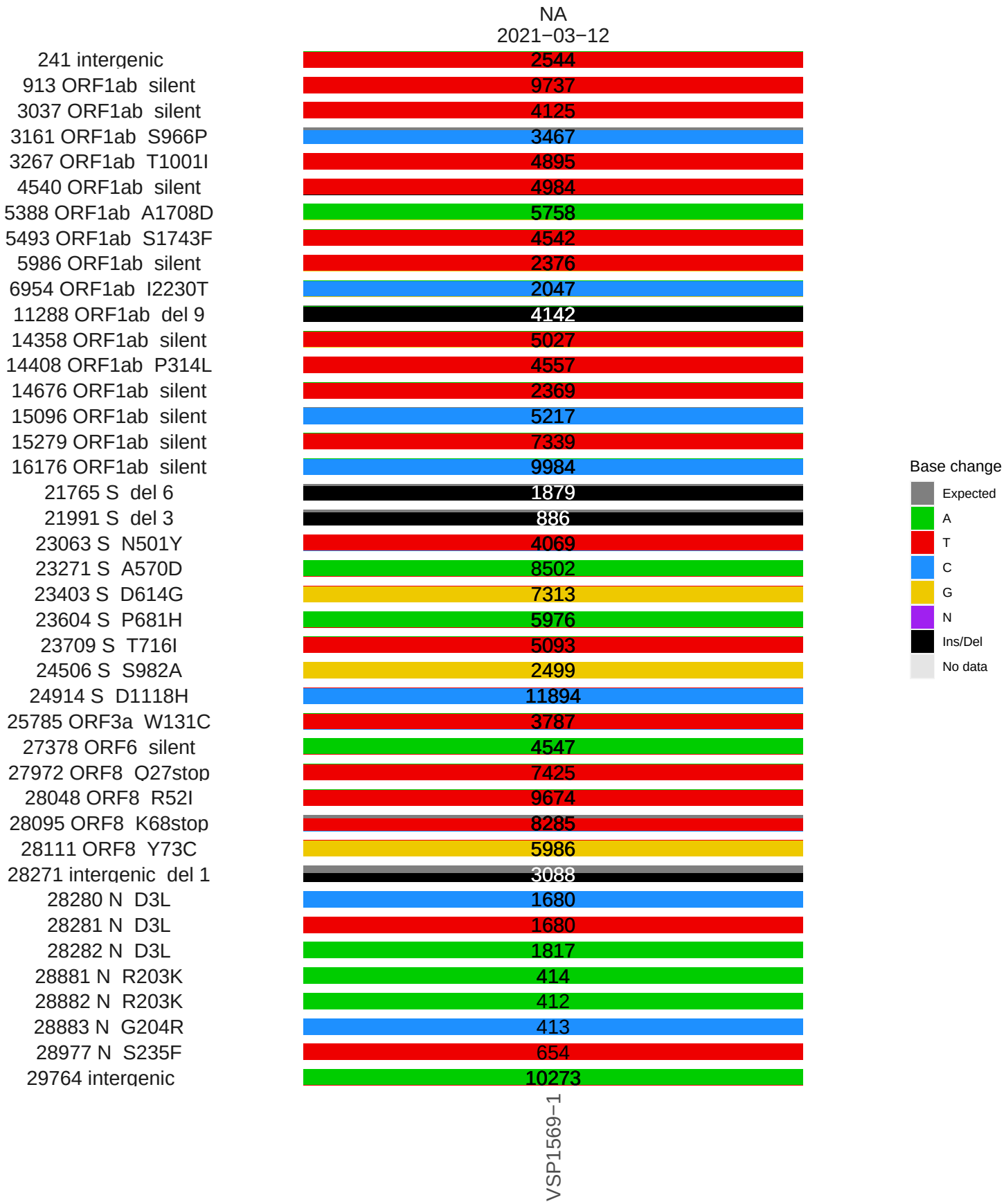
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1569-1	single experiment	NA	NA	2021-03-12	29.91	B.1.1.7	100.0%	99.9%

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.

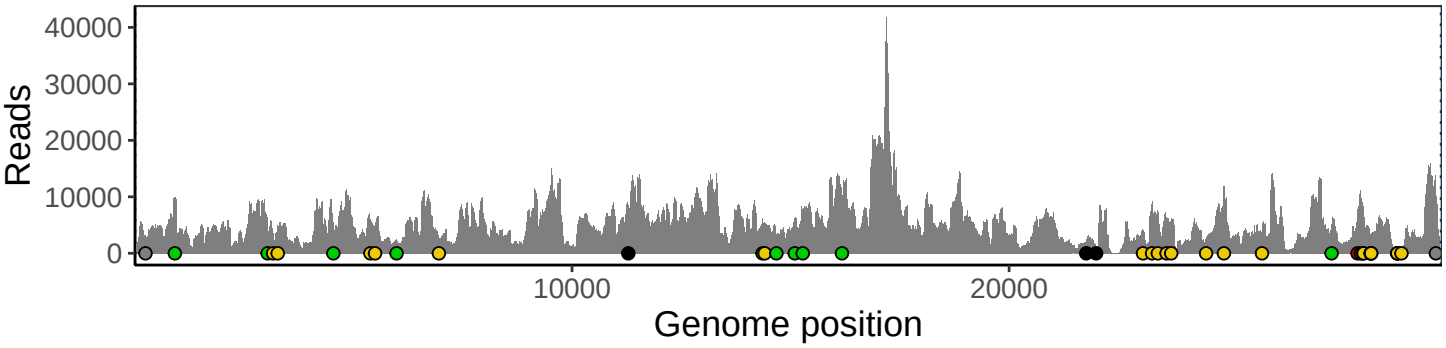



NA
2021−03−12
241 intergenic
913 ORF1ab silent
3037 ORF1ab silent
3161 ORF1ab S966P
3267 ORF1ab T1001I
4540 ORF1ab silent
5388 ORF1ab A1708D
5493 ORF1ab S1743F
5986 ORF1ab silent
6954 ORF1ab I2230T
11288 ORF1ab del 9
14358 ORF1ab silent
14408 ORF1ab P314L
14676 ORF1ab silent
15096 ORF1ab silent
15279 ORF1ab silent
16176 ORF1ab silent
21765 S del 6
21991 S del 3
23063 S N501Y
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24506 S S982A
24914 S D1118H
25785 ORF3a W131C
27378 ORF6 silent
27972 ORF8 Q27stop
28048 ORF8 R52I
28095 ORF8 K68stop
28111 ORF8 Y73C
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
29764 intergenic
2544
9737
4125
3467
4895
4984
5758
4542
2376
2047
4142
5027
4557
2369
5217
7339
9984
1879
886
4069
8502
7313
5976
5093
2499
11894
3787
4547
7425
9674
8285
5986
3088
1680
1680
1817
414
412
413
654
10273
VSP1569−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

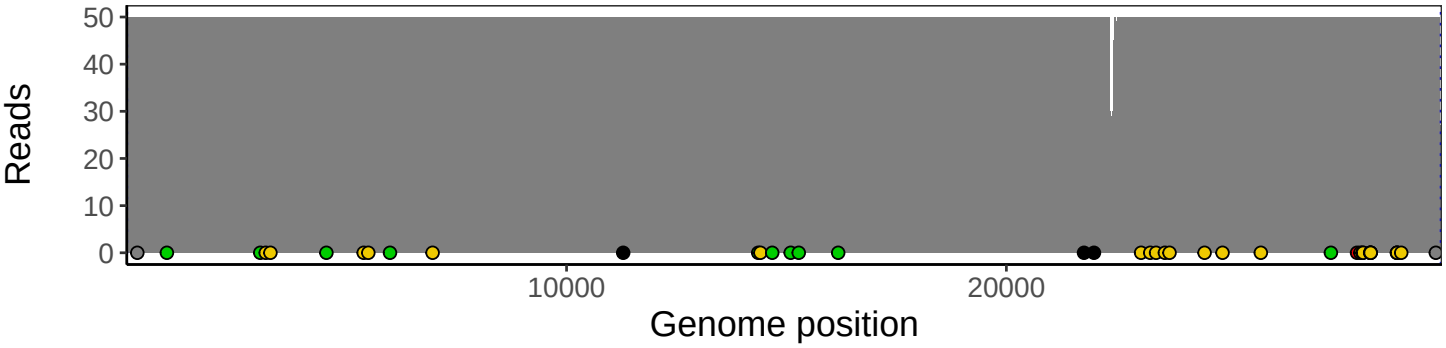
Analyses of individual experiments and composite results

VSP1569-1 | 2021-03-12 | NA | UPHS-0443 | genomes | single experiment

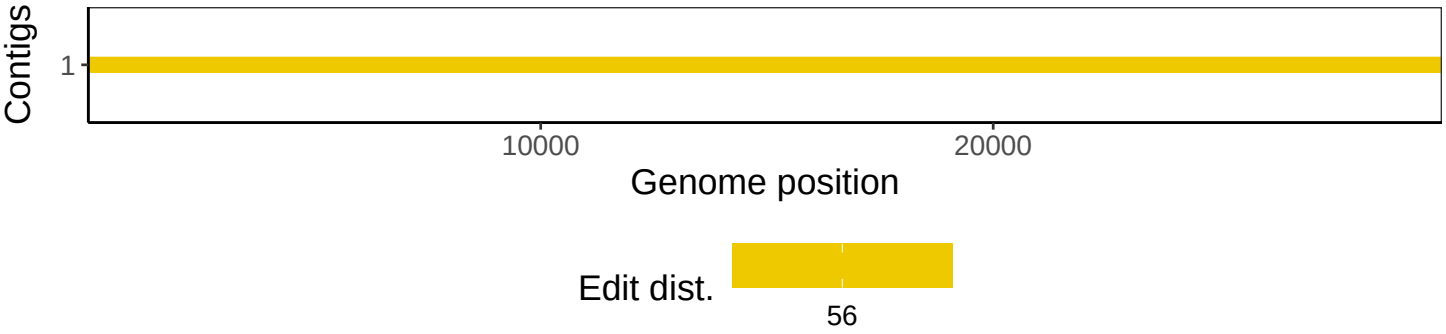
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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