COVID-19 subject UPHS-0476

2021-06-23

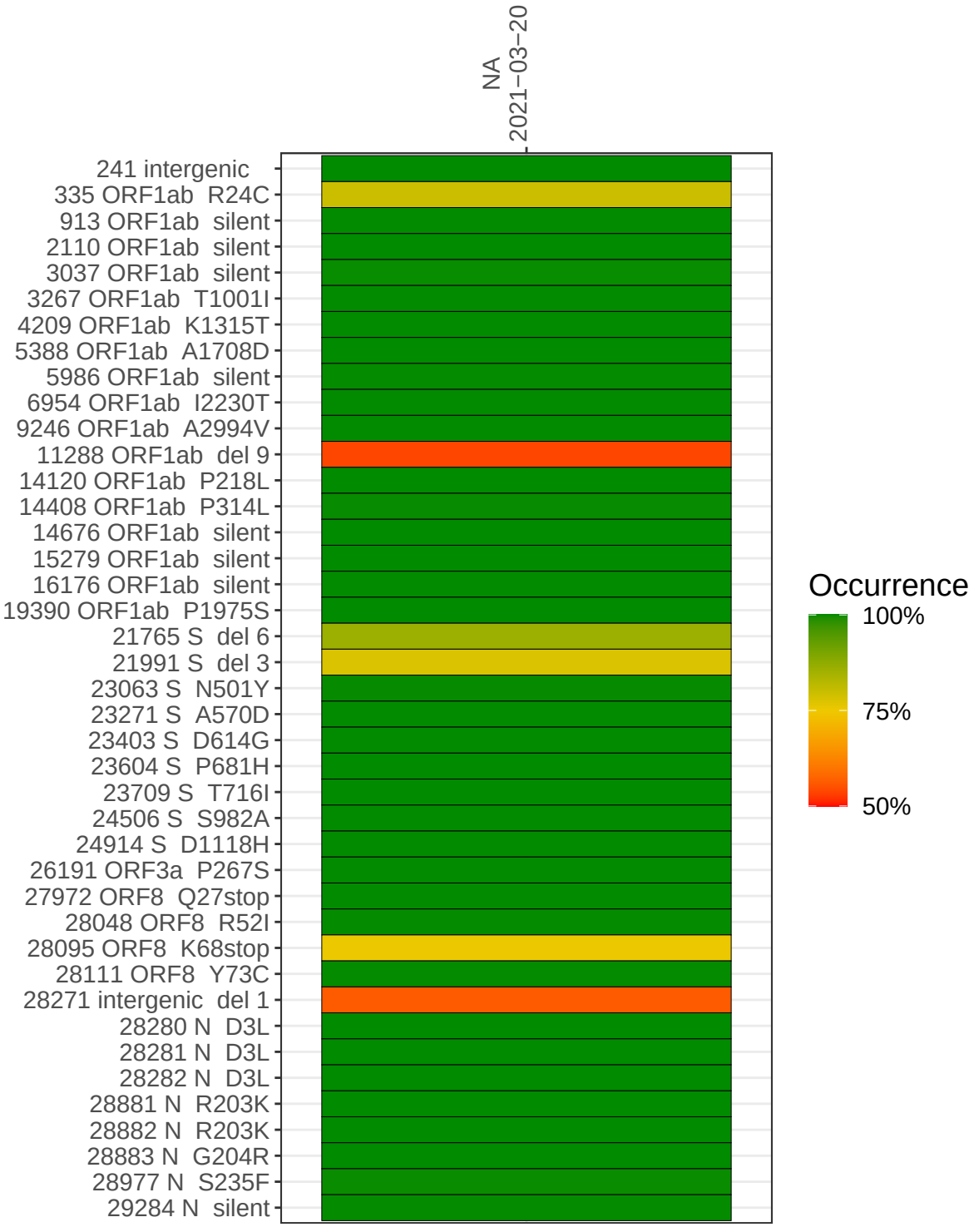
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

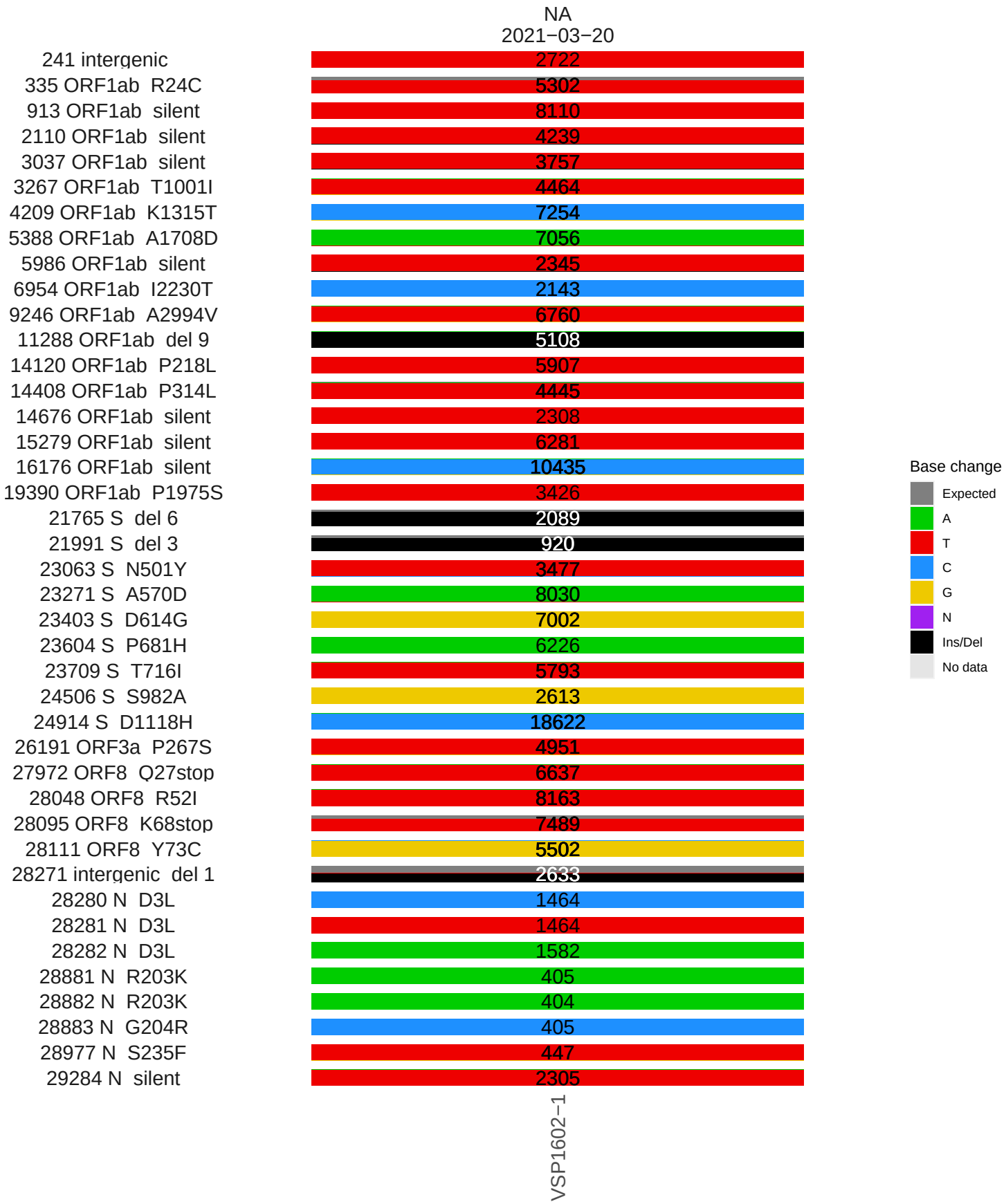
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1602-1	single experiment	NA	NA	2021-03-20	29.81	B.1.1.7	99.8%	99.7%

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.

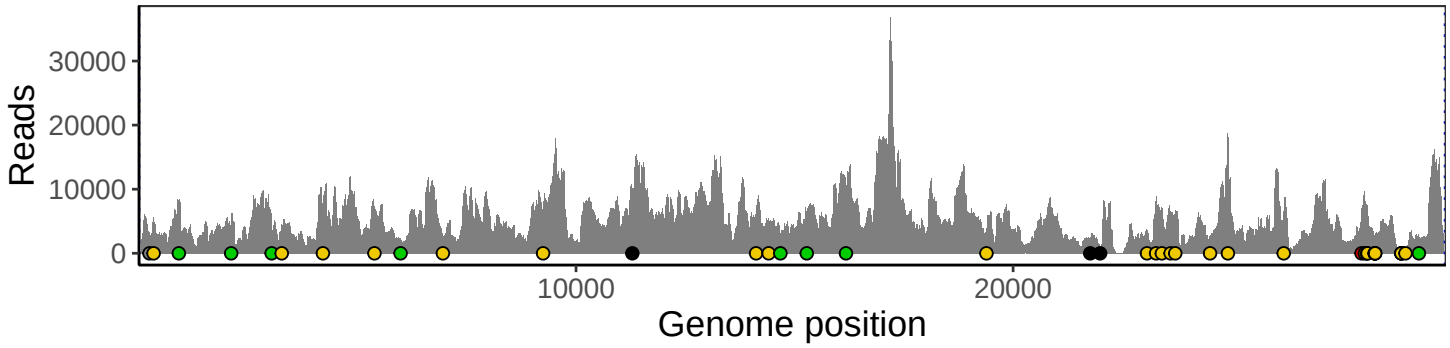



NA
2021−03−20
241 intergenic 2722
335 ORF1ab R24C 5302
913 ORF1ab silent 8110
2110 ORF1ab silent 4239
3037 ORF1ab silent 3757
3267 ORF1ab T1001I 4464
4209 ORF1ab K1315T 7254
5388 ORF1ab A1708D 7056
5986 ORF1ab silent 2345
6954 ORF1ab I2230T 2143
9246 ORF1ab A2994V 6760
11288 ORF1ab del 9 5108
14120 ORF1ab P218L 5907
14408 ORF1ab P314L 4445
14676 ORF1ab silent 2308
15279 ORF1ab silent 6281
16176 ORF1ab silent 10435
19390 ORF1ab P1975S 3426
21765 S del 6 2089
21991 S del 3 920
23063 S N501Y 3477
23271 S A570D 8030
23403 S D614G 7002
23604 S P681H 6226
23709 S T716I 5793
24506 S S982A 2613
24914 S D1118H 18622
26191 ORF3a P267S 4951
27972 ORF8 Q27stop 6637
28048 ORF8 R52I 8163
28095 ORF8 K68stop 7489
28111 ORF8 Y73C 5502
28271 intergenic del 1 2633
28280 N D3L 1464
28281 N D3L 1464
28282 N D3L 1582
28881 N R203K 405
28882 N R203K 404
28883 N G204R 405
28977 N S235F 447
29284 N silent 2305
VSP1602−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

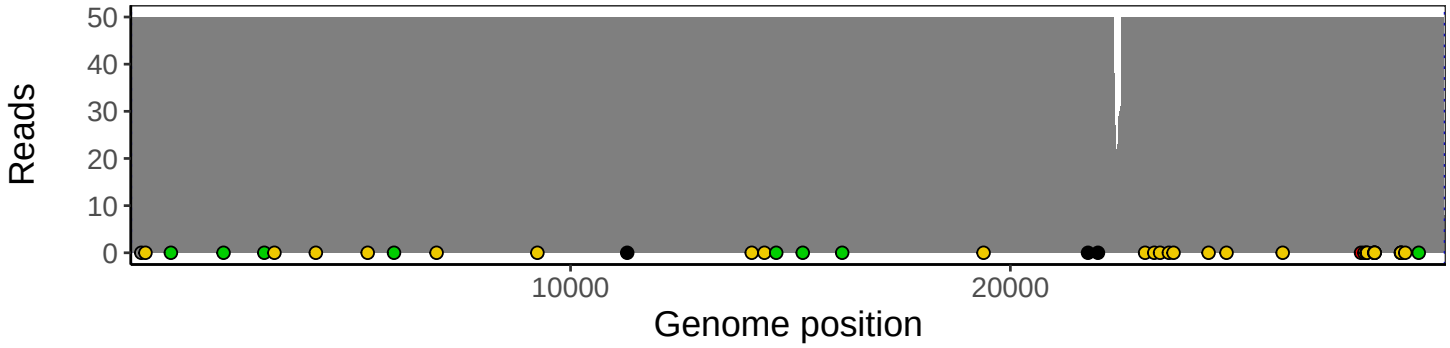
Analyses of individual experiments and composite results

VSP1602-1 | 2021-03-20 | NA | UPHS-0476 | genomes | single experiment

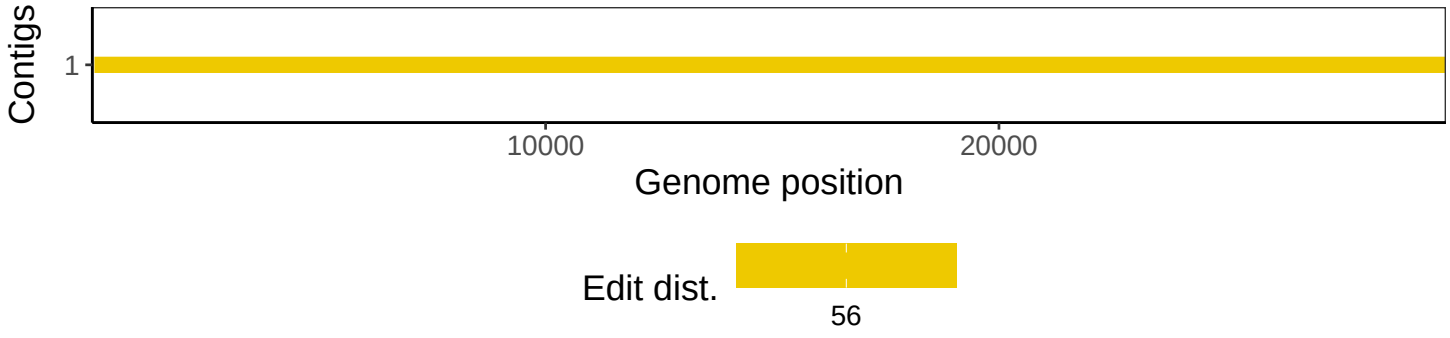
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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