COVID-19 subject UPHS-0522

2021-06-03

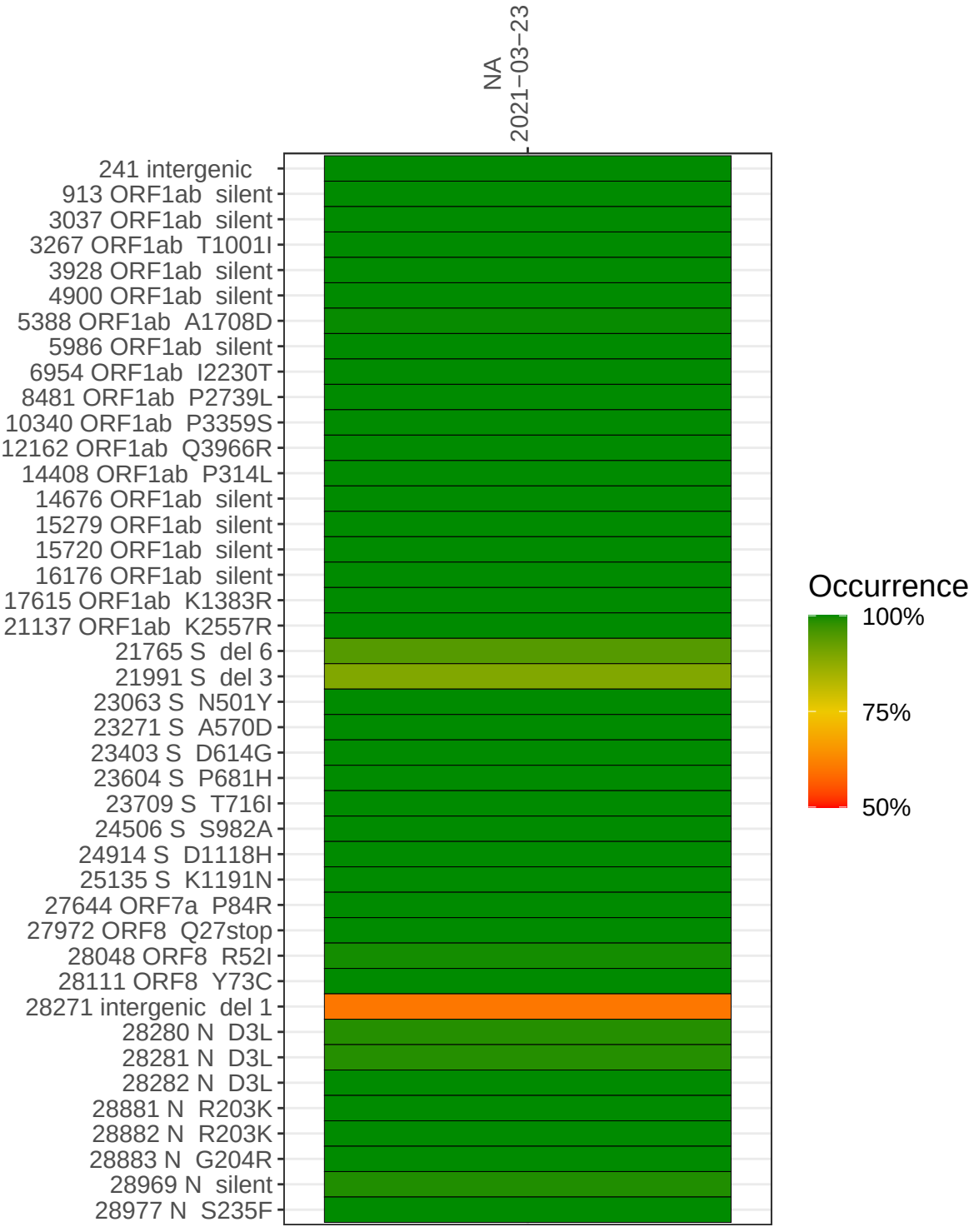
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

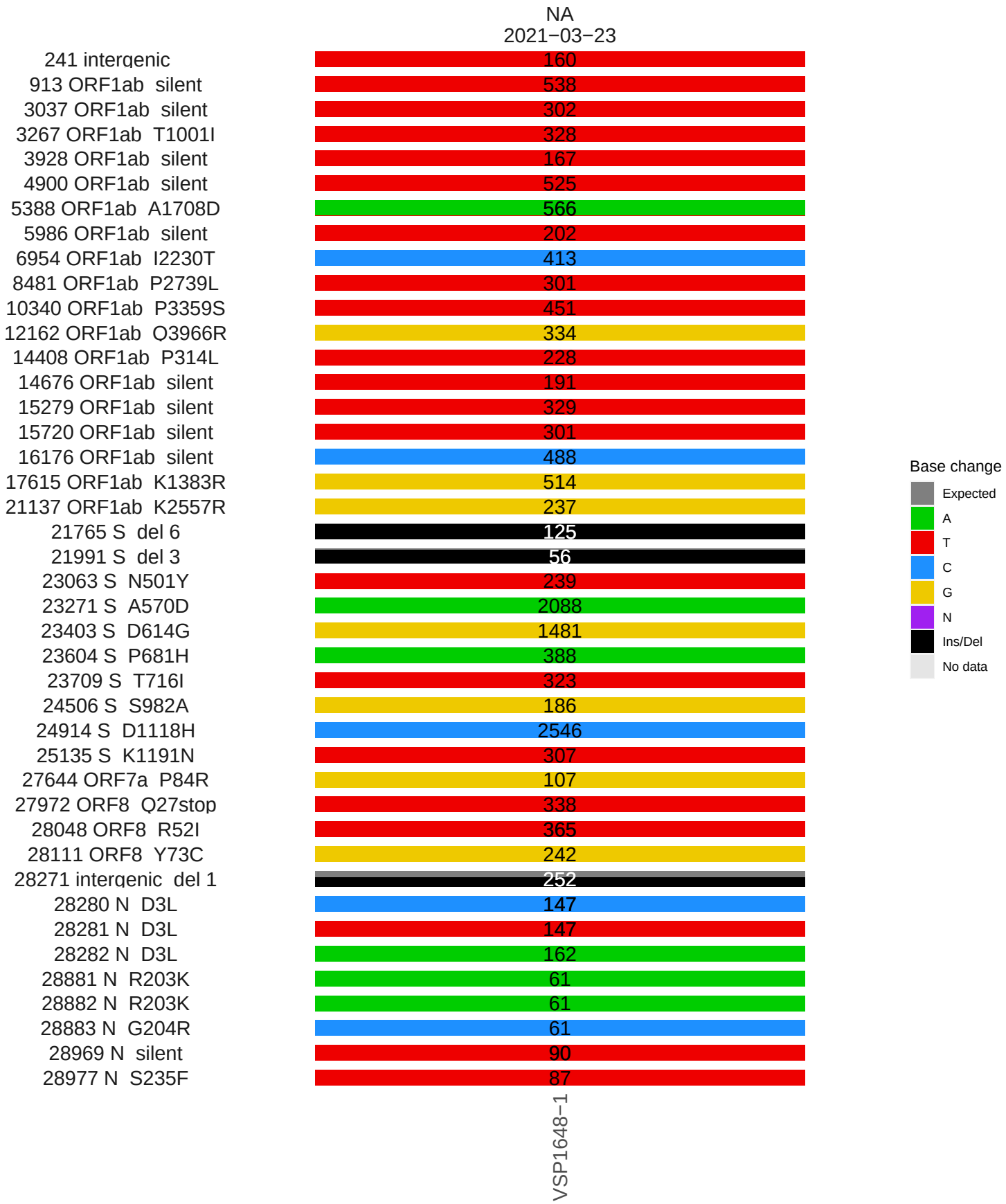
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1648-1	single experiment	NA	NA	2021-03-23	29.85	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.

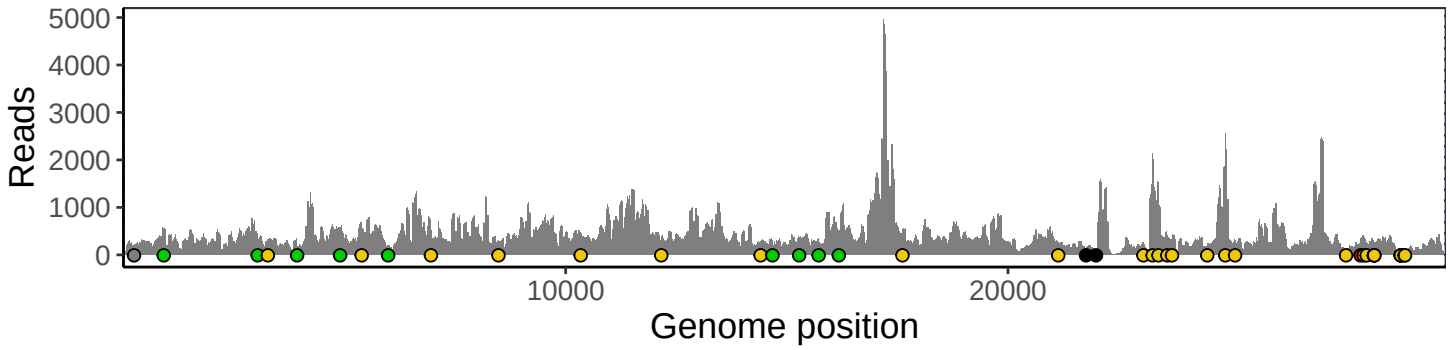



NA
2021−03−23
241 intergenic 160
913 ORF1ab silent 538
3037 ORF1ab silent 302
3267 ORF1ab T1001I 328
3928 ORF1ab silent 167
4900 ORF1ab silent 525
5388 ORF1ab A1708D 566
5986 ORF1ab silent 202
6954 ORF1ab I2230T 413
8481 ORF1ab P2739L 301
10340 ORF1ab P3359S 451
12162 ORF1ab Q3966R 334
14408 ORF1ab P314L 228
14676 ORF1ab silent 191
15279 ORF1ab silent 329
15720 ORF1ab silent 301
16176 ORF1ab silent 488
17615 ORF1ab K1383R 514
21137 ORF1ab K2557R 237
21765 S del 6 125
21991 S del 3 56
23063 S N501Y 239
23271 S A570D 2088
23403 S D614G 1481
23604 S P681H 388
23709 S T716I 323
24506 S S982A 186
24914 S D1118H 2546
25135 S K1191N 307
27644 ORF7a P84R 107
27972 ORF8 Q27stop 338
28048 ORF8 R52I 365
28111 ORF8 Y73C 242
28271 intergenic del 1 252
28280 N D3L 147
28281 N D3L 147
28282 N D3L 162
28881 N R203K 61
28882 N R203K 61
28883 N G204R 61
28969 N silent 90
28977 N S235F 87
VSP1648−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

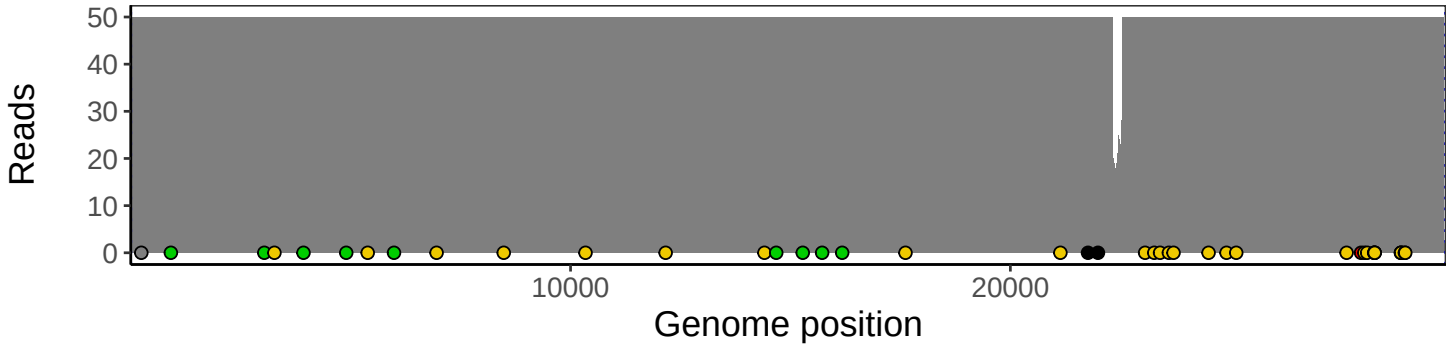
Analyses of individual experiments and composite results

VSP1648-1 | 2021-03-23 | NA | UPHS-0522 | genomes | single experiment

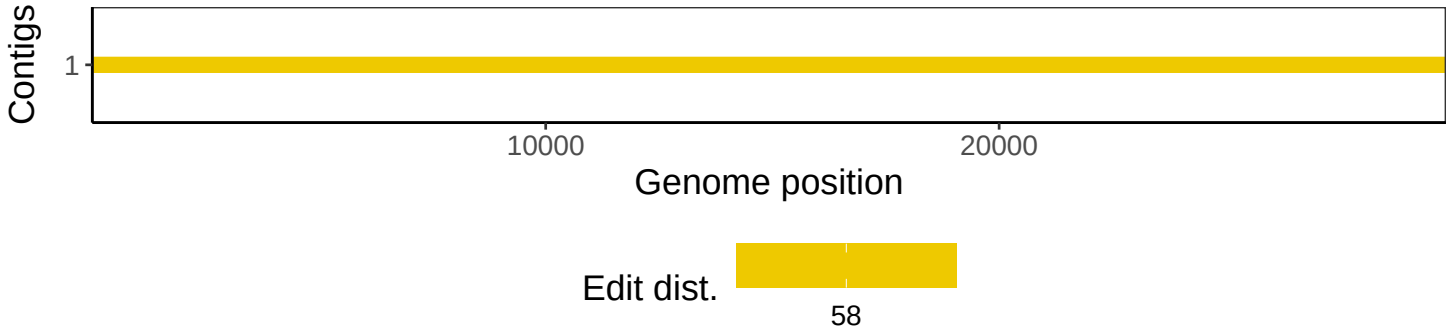
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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