COVID-19 subject UPHS-0395

2021-05-05

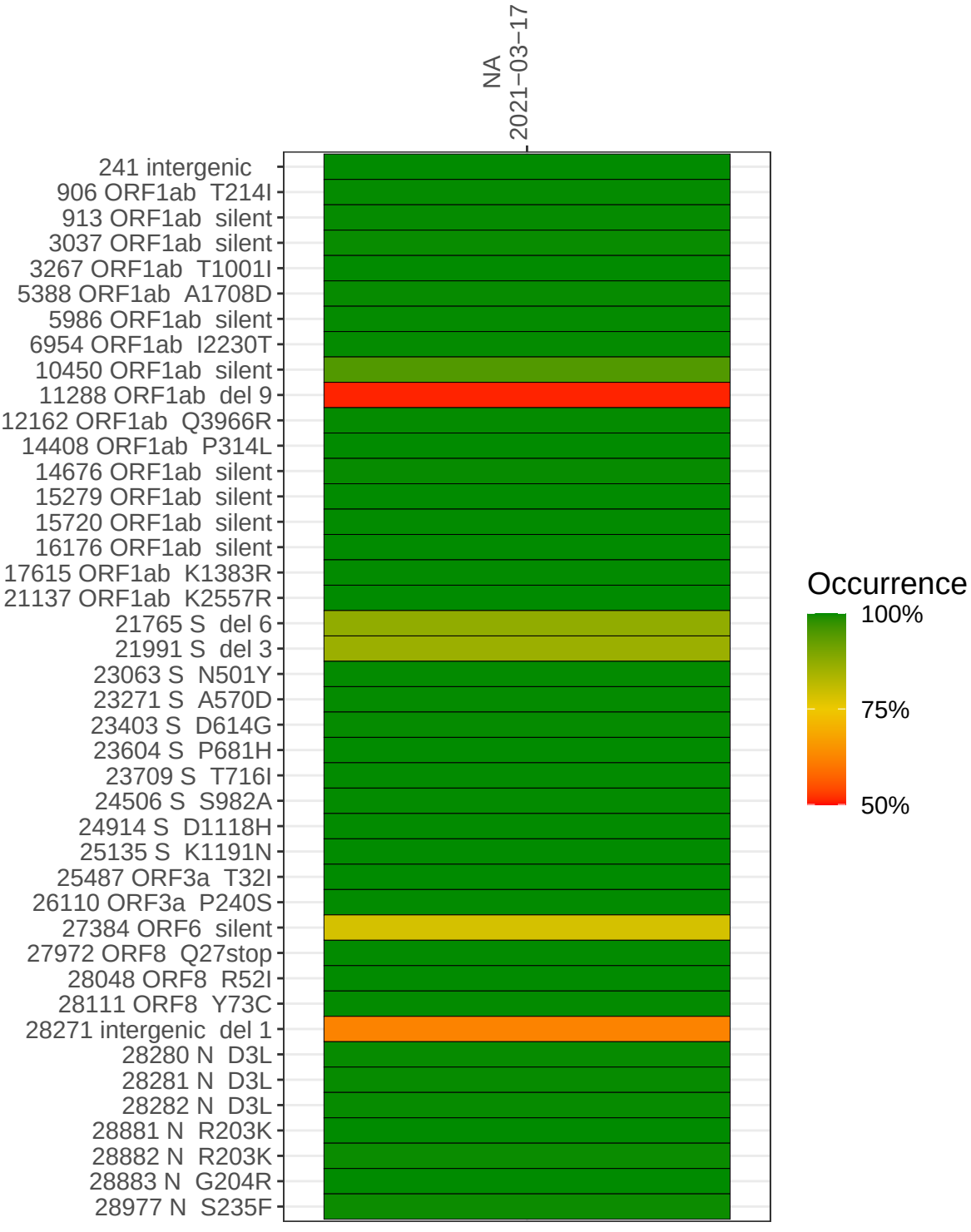
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

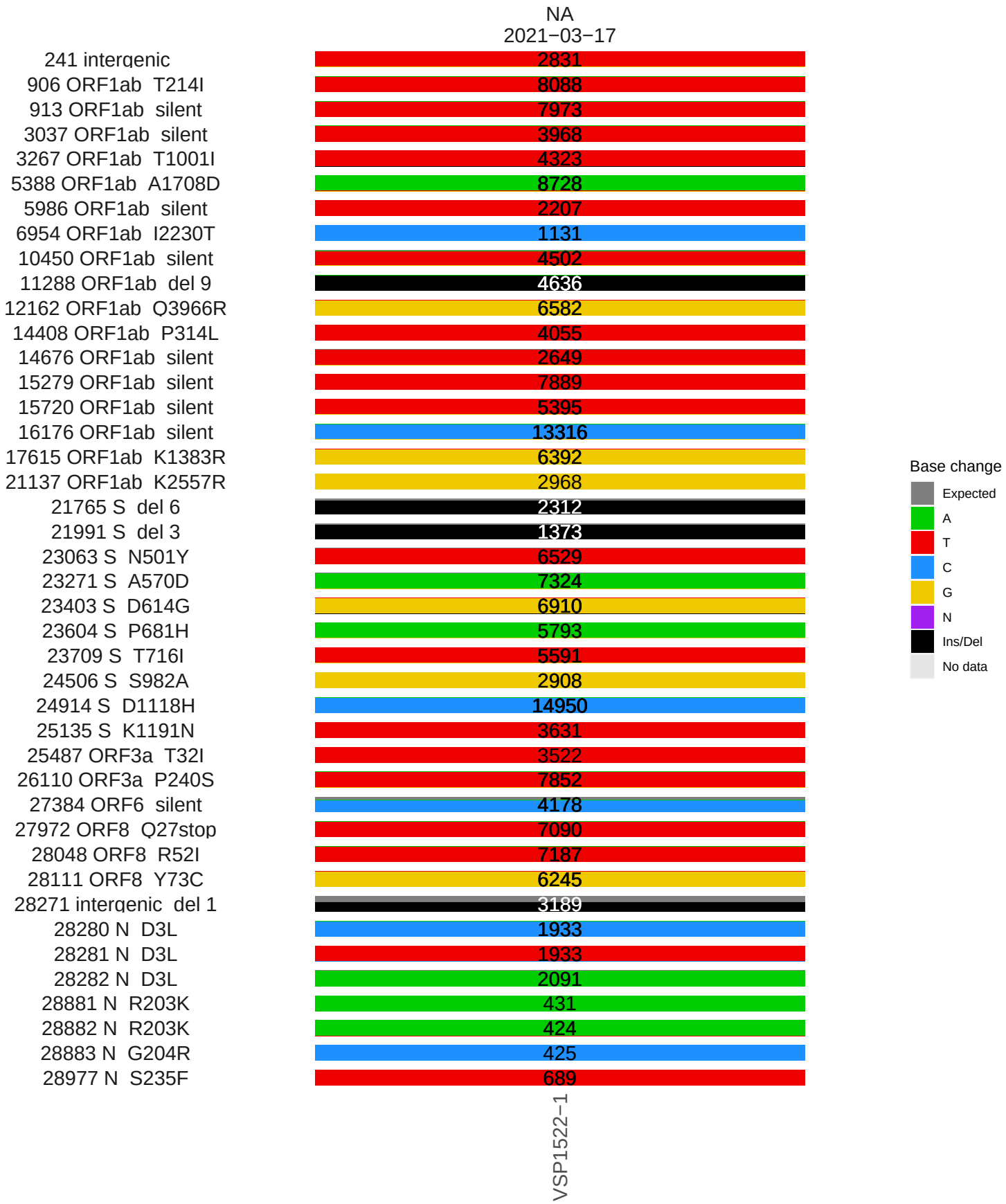
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1522-1	single experiment	NA	NA	2021-03-17	29.82	B.1.1.7	99.8%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

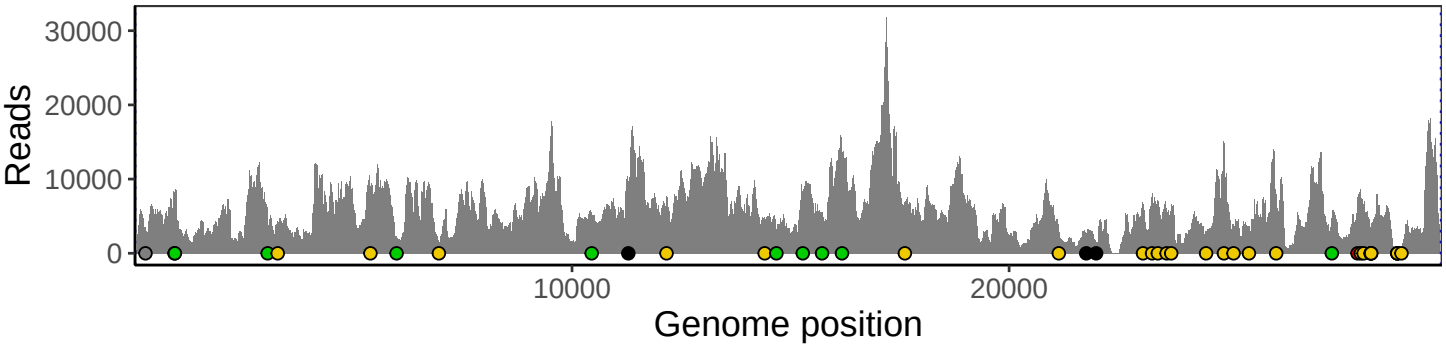



NA
2021−03−17
241 intergenic 2831
906 ORF1ab T214I 8088
913 ORF1ab silent 7973
3037 ORF1ab silent 3968
3267 ORF1ab T1001I 4323
5388 ORF1ab A1708D 8728
5986 ORF1ab silent 2207
6954 ORF1ab I2230T 1131
10450 ORF1ab silent 4502
11288 ORF1ab del 9 4636
12162 ORF1ab Q3966R 6582
14408 ORF1ab P314L 4055
14676 ORF1ab silent 2649
15279 ORF1ab silent 7889
15720 ORF1ab silent 5395
16176 ORF1ab silent 13316
17615 ORF1ab K1383R 6392
21137 ORF1ab K2557R 2968
21765 S del 6 2312
21991 S del 3 1373
23063 S N501Y 6529
23271 S A570D 7324
23403 S D614G 6910
23604 S P681H 5793
23709 S T716I 5591
24506 S S982A 2908
24914 S D1118H 14950
25135 S K1191N 3631
25487 ORF3a T32I 3522
26110 ORF3a P240S 7852
27384 ORF6 silent 4178
27972 ORF8 Q27stop 7090
28048 ORF8 R52I 7187
28111 ORF8 Y73C 6245
28271 intergenic del 1 3189
28280 N D3L 1933
28281 N D3L 1933
28282 N D3L 2091
28881 N R203K 431
28882 N R203K 424
28883 N G204R 425
28977 N S235F 689
VSP1522−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

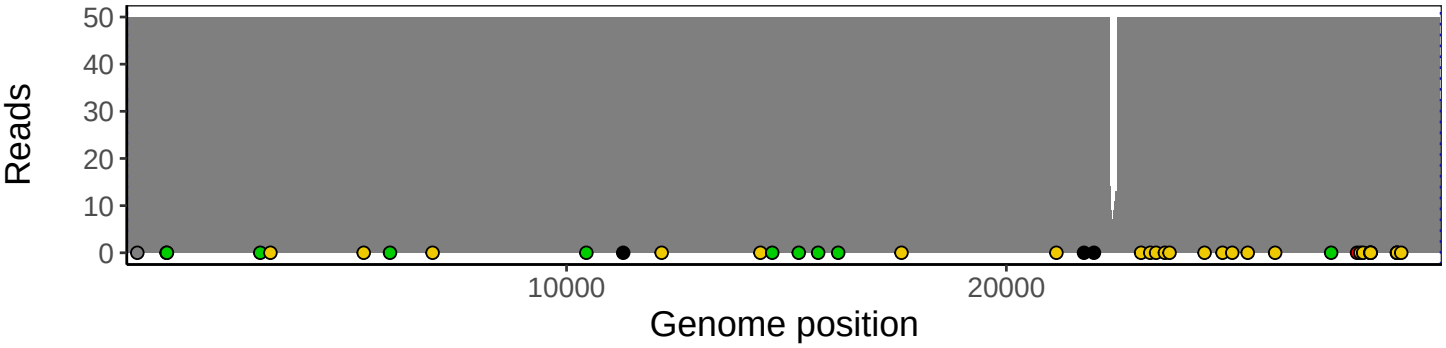
Analyses of individual experiments and composite results

VSP1522-1 | 2021-03-17 | NA | UPHS-0395 | genomes | single experiment

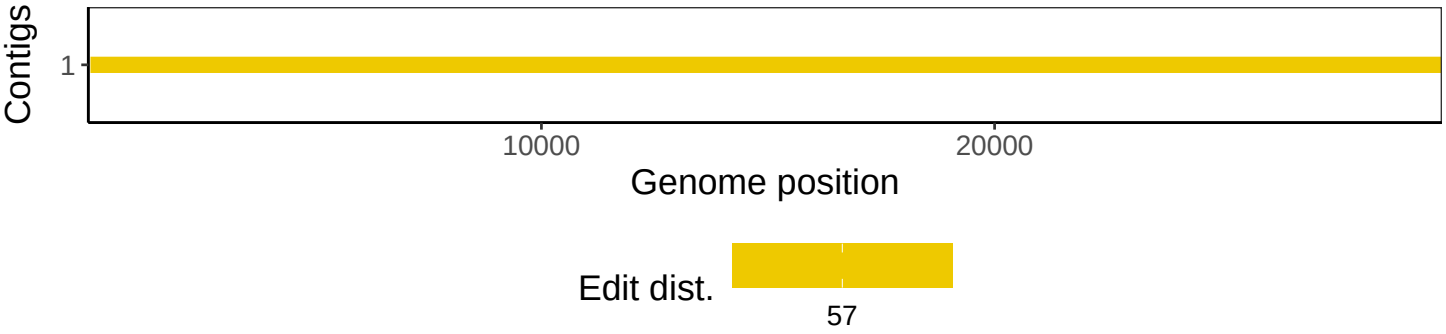
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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