COVID-19 subject UPHS-1175

2021-06-23

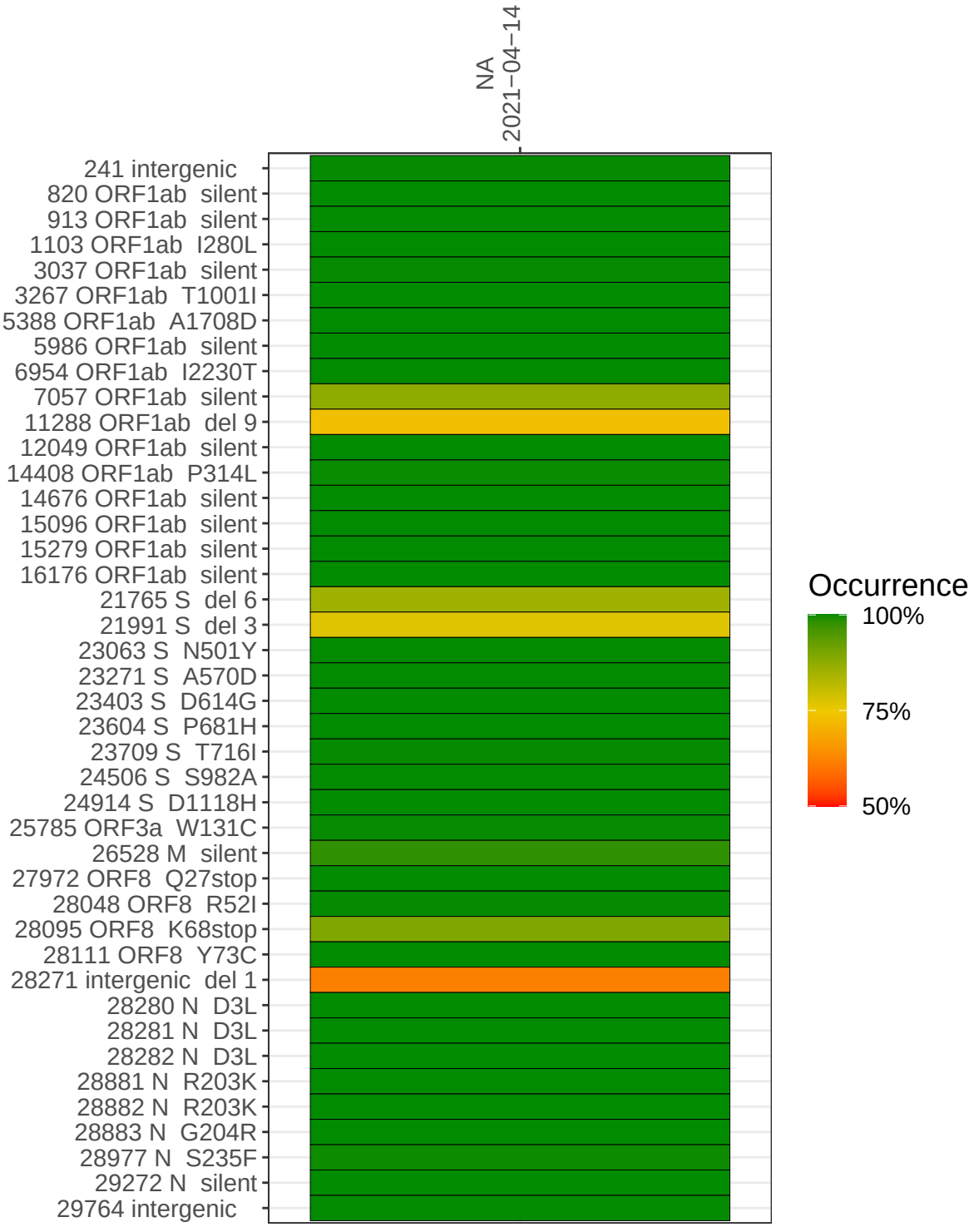
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

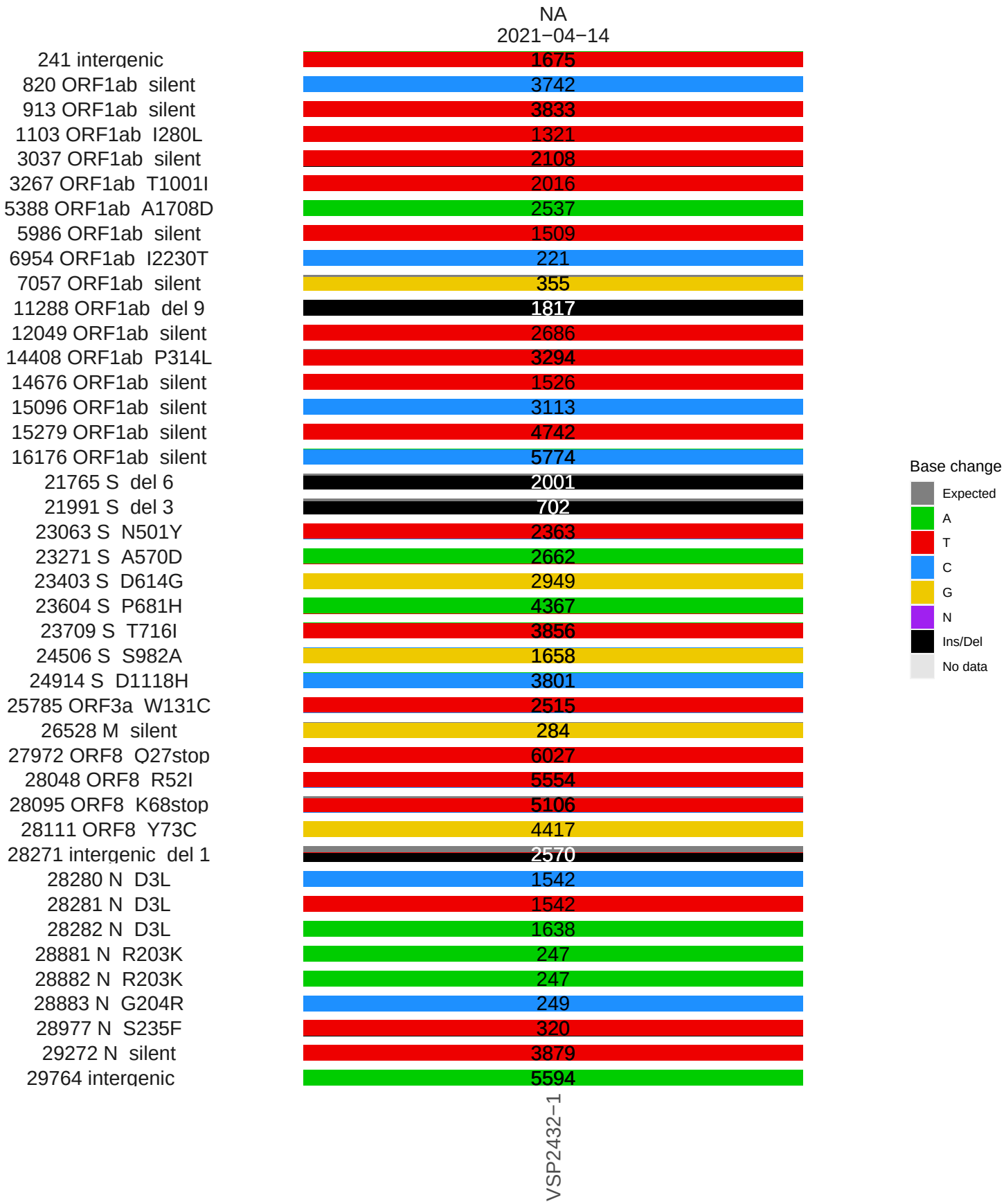
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2432-1	single experiment	NA	NA	2021-04-14	29.83	B.1.1.7	99.7%	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.

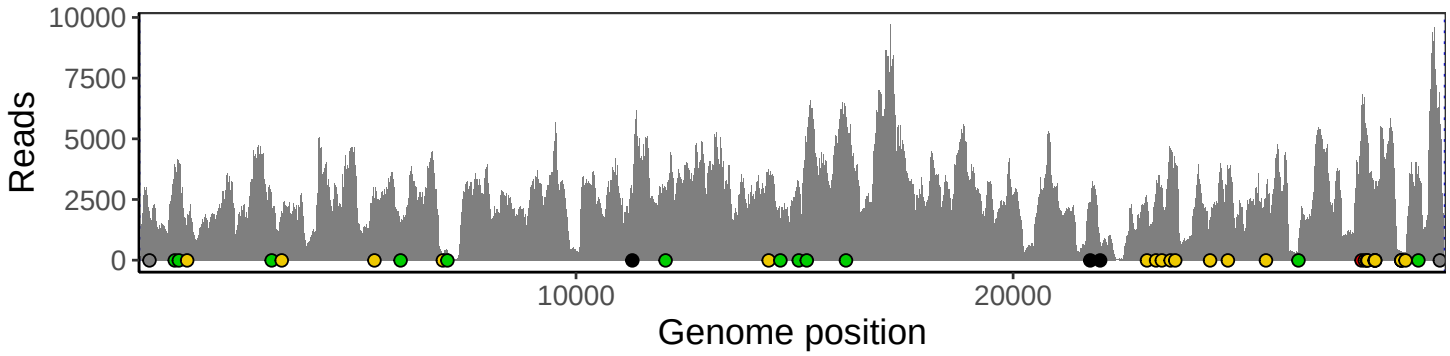



NA
2021−04−14
241 intergenic 1675
820 ORF1ab silent 3742
913 ORF1ab silent 3833
1103 ORF1ab I280L 1321
3037 ORF1ab silent 2108
3267 ORF1ab T1001I 2016
5388 ORF1ab A1708D 2537
5986 ORF1ab silent 1509
6954 ORF1ab I2230T 221
7057 ORF1ab silent 355
11288 ORF1ab del 9 1817
12049 ORF1ab silent 2686
14408 ORF1ab P314L 3294
14676 ORF1ab silent 1526
15096 ORF1ab silent 3113
15279 ORF1ab silent 4742
16176 ORF1ab silent 5774
21765 S del 6 2001
21991 S del 3 702
23063 S N501Y 2363
23271 S A570D 2662
23403 S D614G 2949
23604 S P681H 4367
23709 S T716I 3856
24506 S S982A 1658
24914 S D1118H 3801
25785 ORF3a W131C 2515
26528 M silent 284
27972 ORF8 Q27stop 6027
28048 ORF8 R52I 5554
28095 ORF8 K68stop 5106
28111 ORF8 Y73C 4417
28271 intergenic del 1 2570
28280 N D3L 1542
28281 N D3L 1542
28282 N D3L 1638
28881 N R203K 247
28882 N R203K 247
28883 N G204R 249
28977 N S235F 320
29272 N silent 3879
29764 intergenic 5594
VSP2432−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

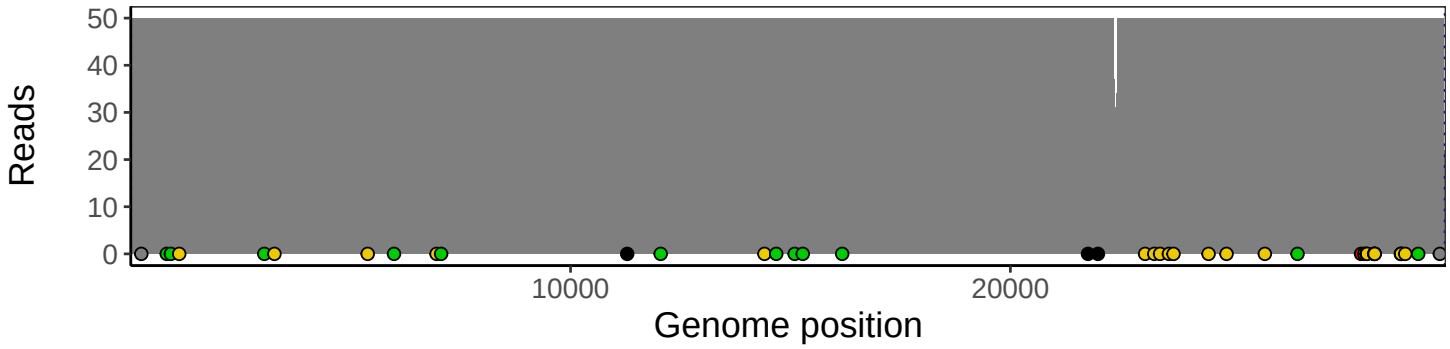
Analyses of individual experiments and composite results

VSP2432-1 | 2021-04-14 | NA | UPHS-1175 | genomes | single experiment

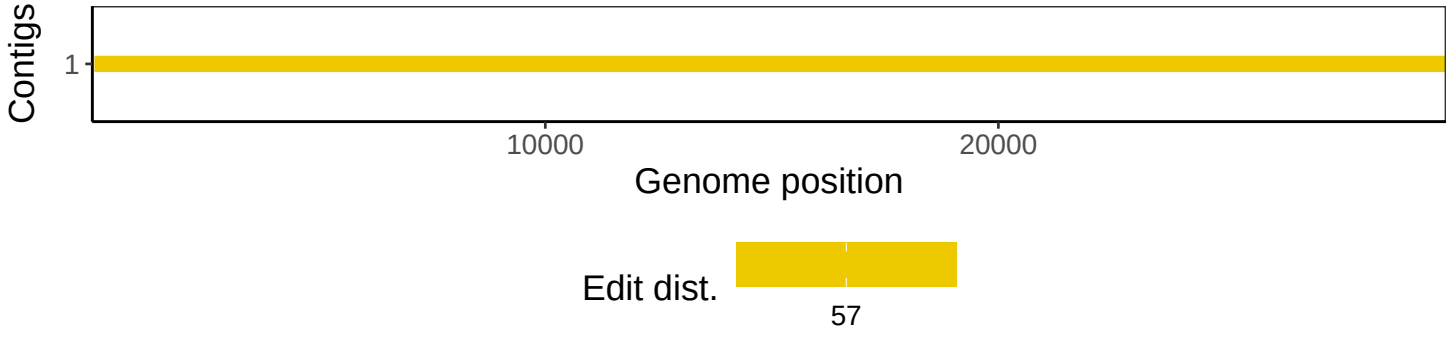
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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