COVID-19 subject UPHS-1080

2021-05-10

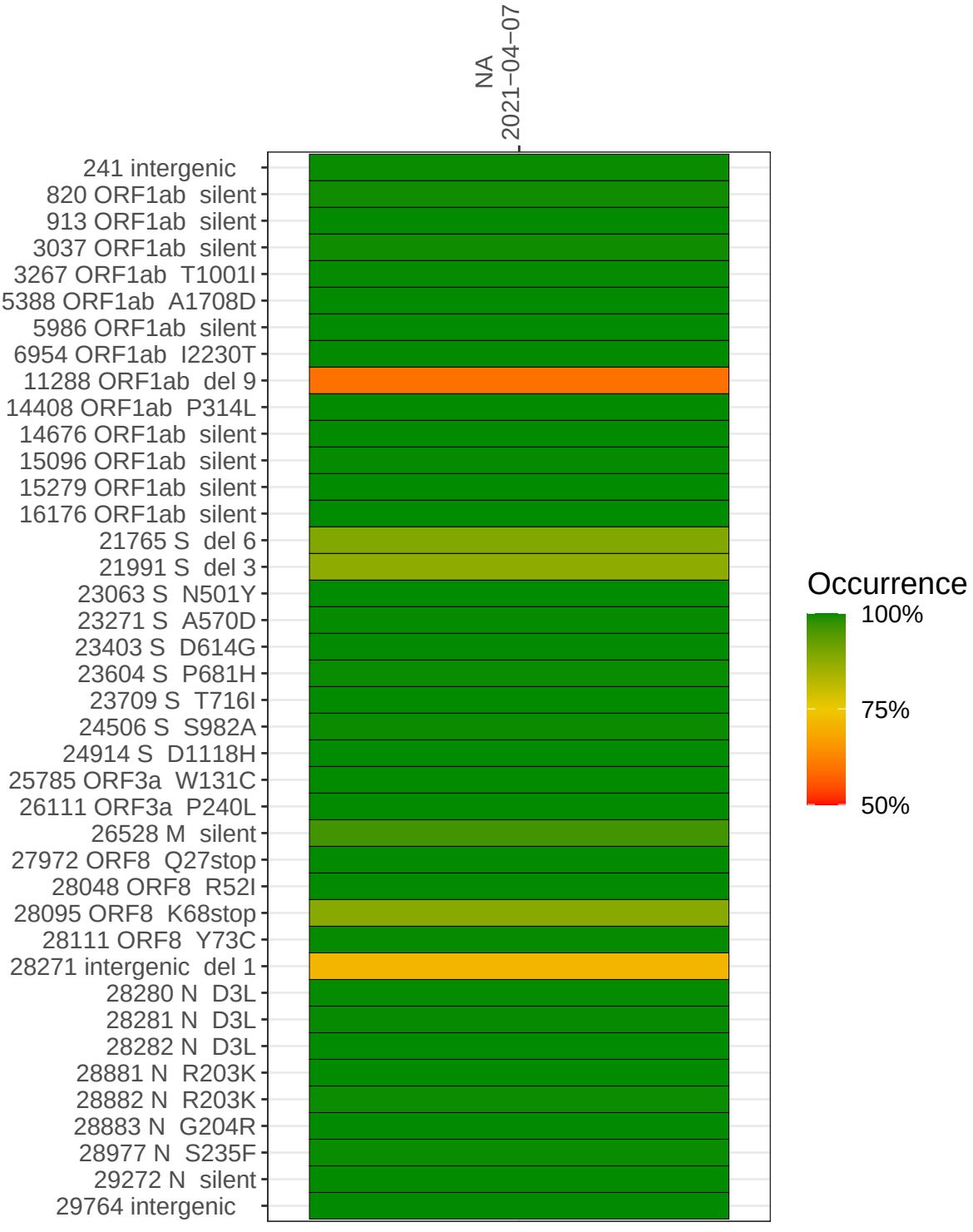
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

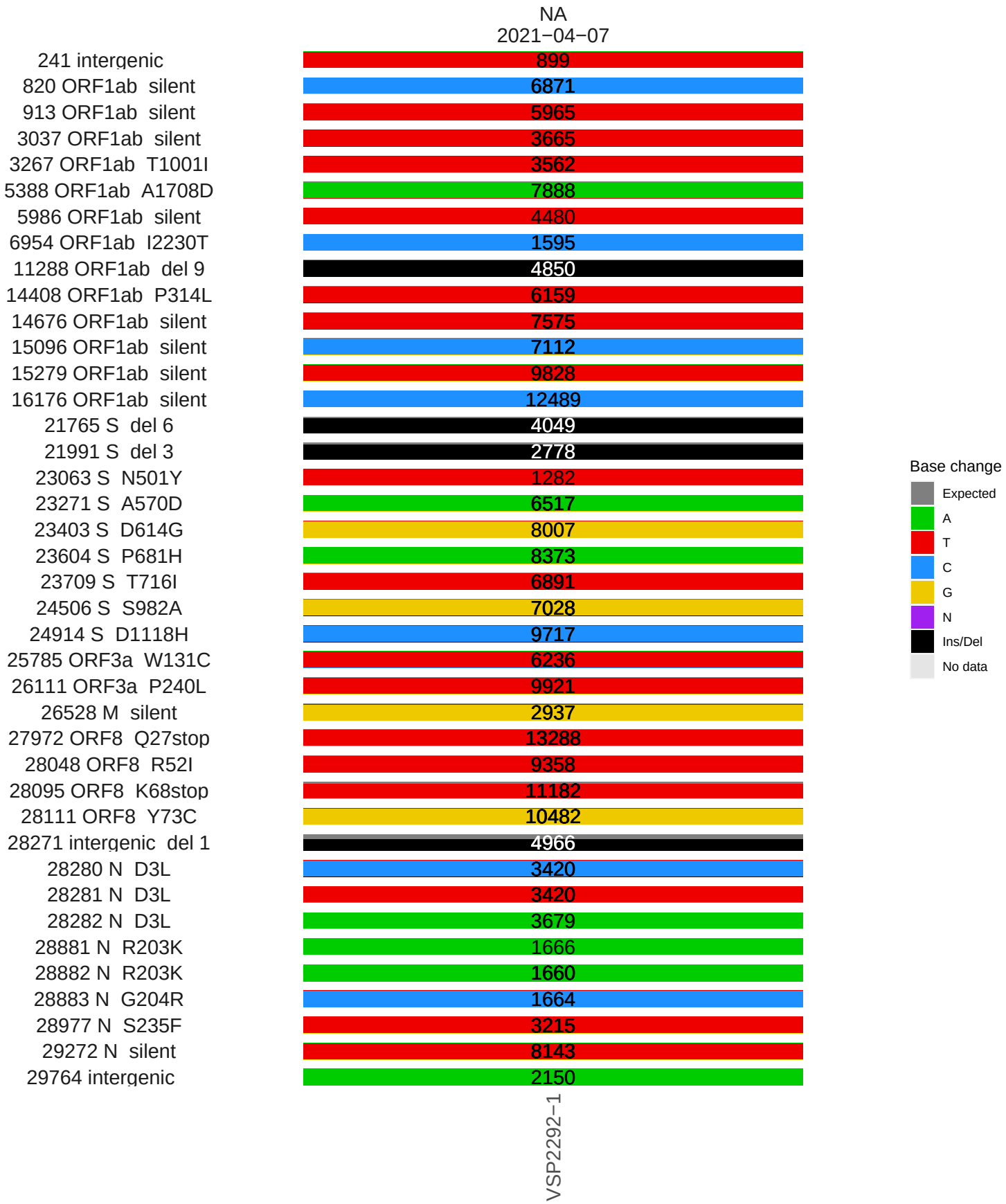
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2292-1	single experiment	NA	NA	2021-04-07	29.84	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.

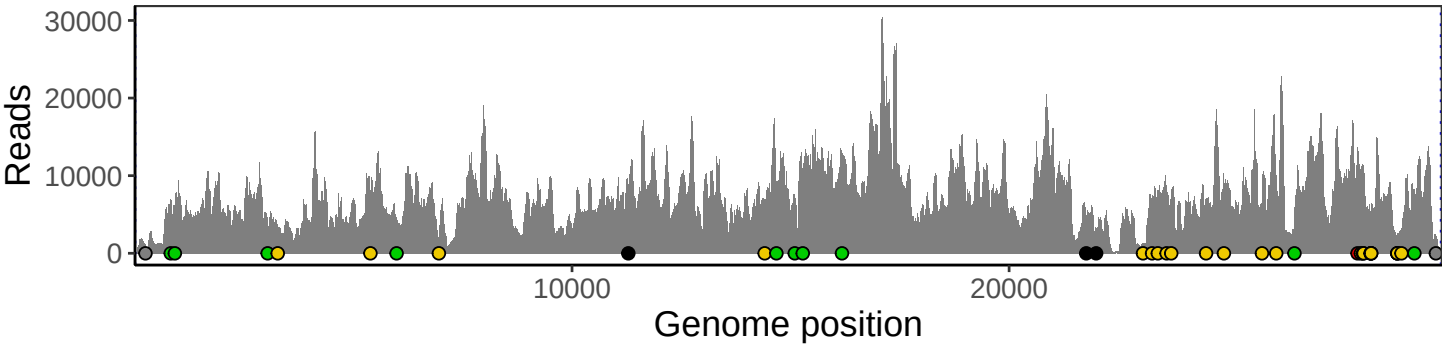



NA
2021−04−07
241 intergenic 899
820 ORF1ab silent 6871
913 ORF1ab silent 5965
3037 ORF1ab silent 3665
3267 ORF1ab T1001I 3562
5388 ORF1ab A1708D 7888
5986 ORF1ab silent 4480
6954 ORF1ab I2230T 1595
11288 ORF1ab del 9 4850
14408 ORF1ab P314L 6159
14676 ORF1ab silent 7575
15096 ORF1ab silent 7112
15279 ORF1ab silent 9828
16176 ORF1ab silent 12489
21765 S del 6 4049
21991 S del 3 2778
23063 S N501Y 1282
23271 S A570D 6517
23403 S D614G 8007
23604 S P681H 8373
23709 S T716I 6891
24506 S S982A 7028
24914 S D1118H 9717
25785 ORF3a W131C 6236
26111 ORF3a P240L 9921
26528 M silent 2937
27972 ORF8 Q27stop 13288
28048 ORF8 R52I 9358
28095 ORF8 K68stop 11182
28111 ORF8 Y73C 10482
28271 intergenic del 1 4966
28280 N D3L 3420
28281 N D3L 3420
28282 N D3L 3679
28881 N R203K 1666
28882 N R203K 1660
28883 N G204R 1664
28977 N S235F 3215
29272 N silent 8143
29764 intergenic 2150
VSP2292−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

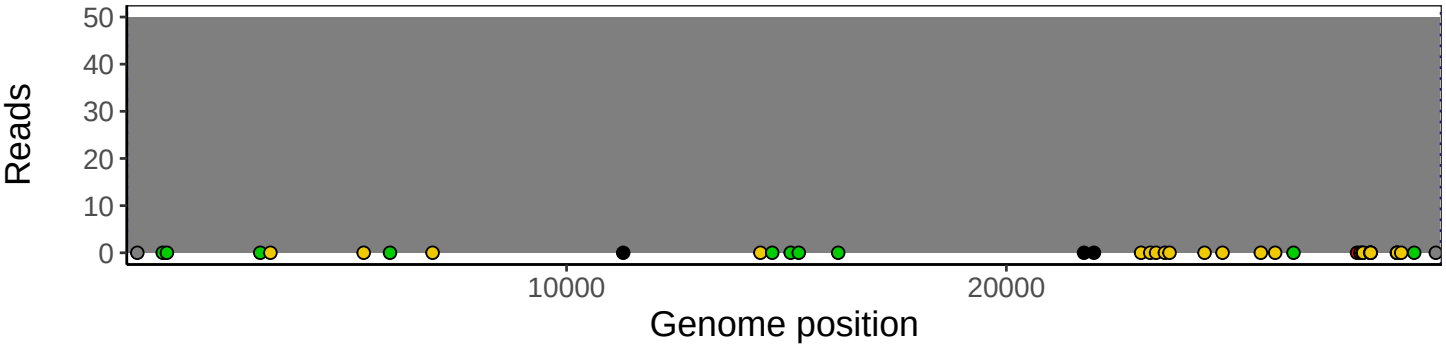
Analyses of individual experiments and composite results

VSP2292-1 | 2021-04-07 | NA | UPHS-1080 | genomes | single experiment

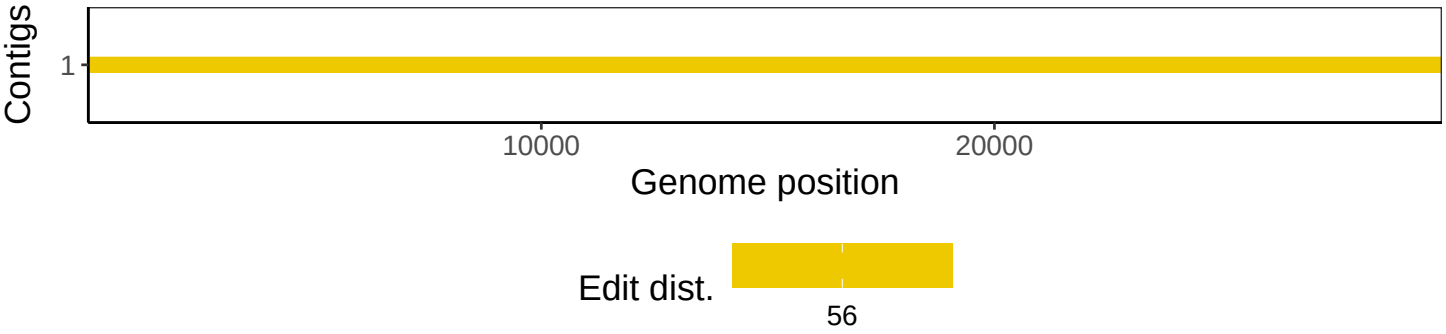
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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