COVID-19 subject UPHS-1054

2021-05-10

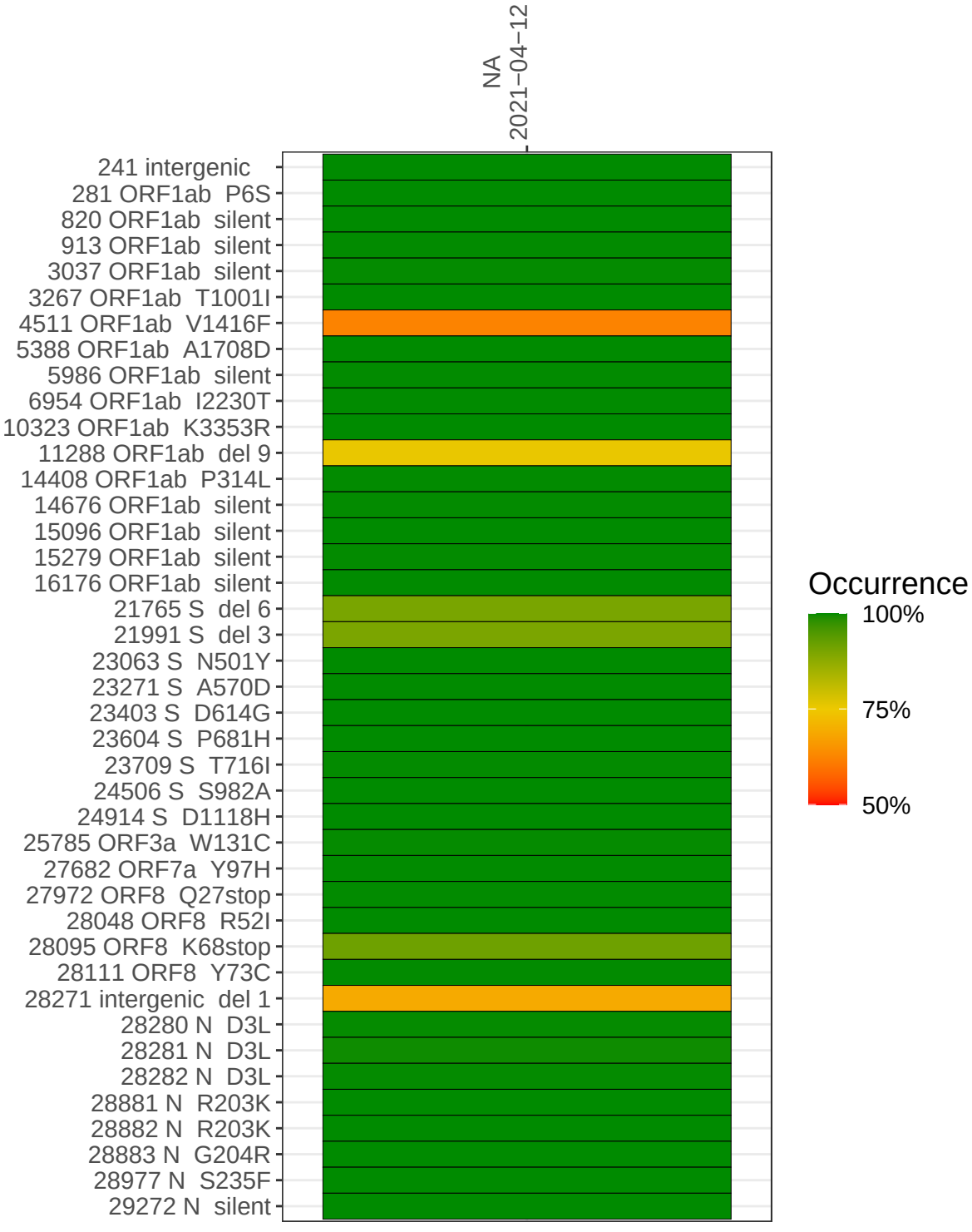
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

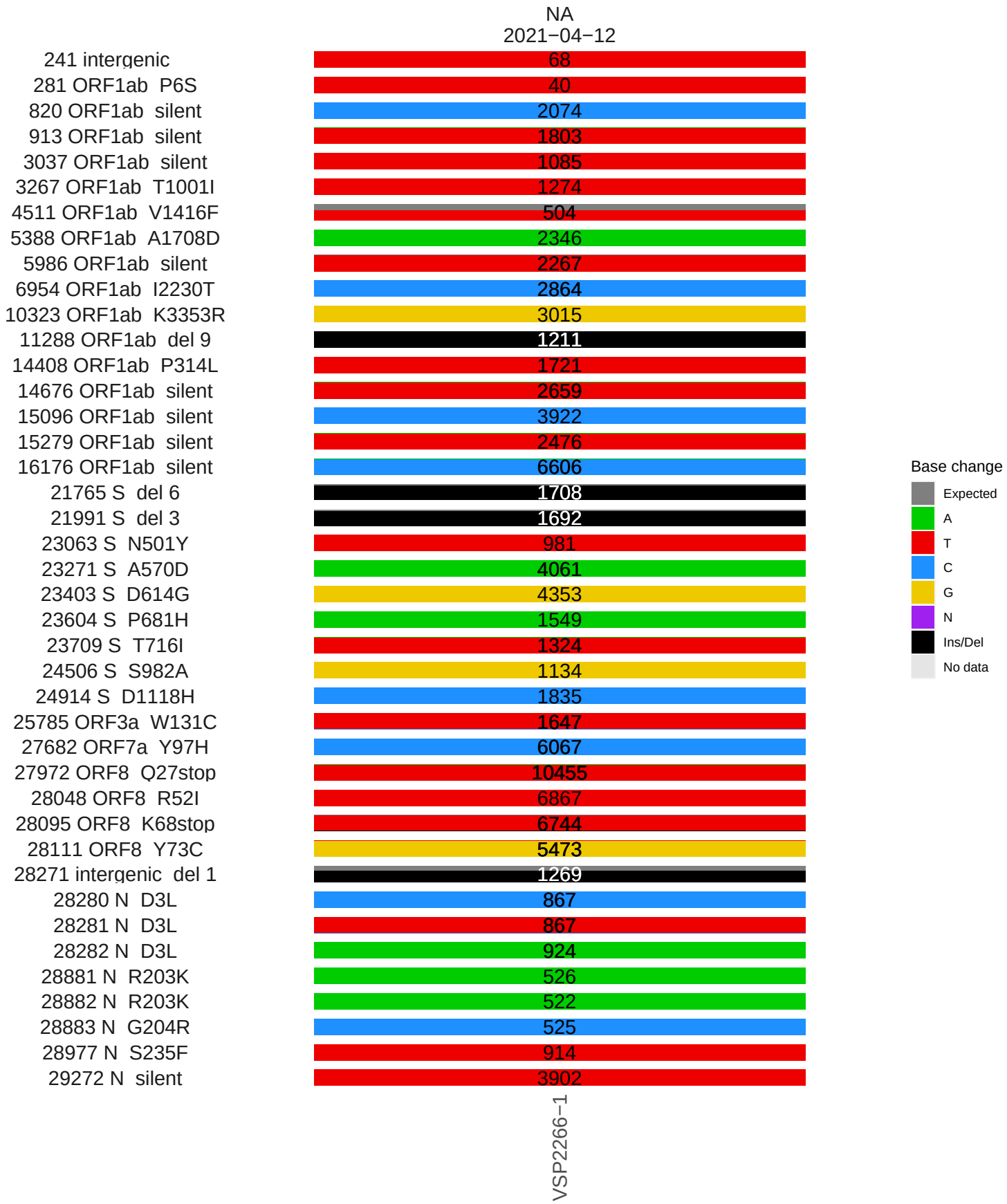
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2266-1	single experiment	NA	NA	2021-04-12	29.65	B.1.1.7	99.3%	99.3%

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.

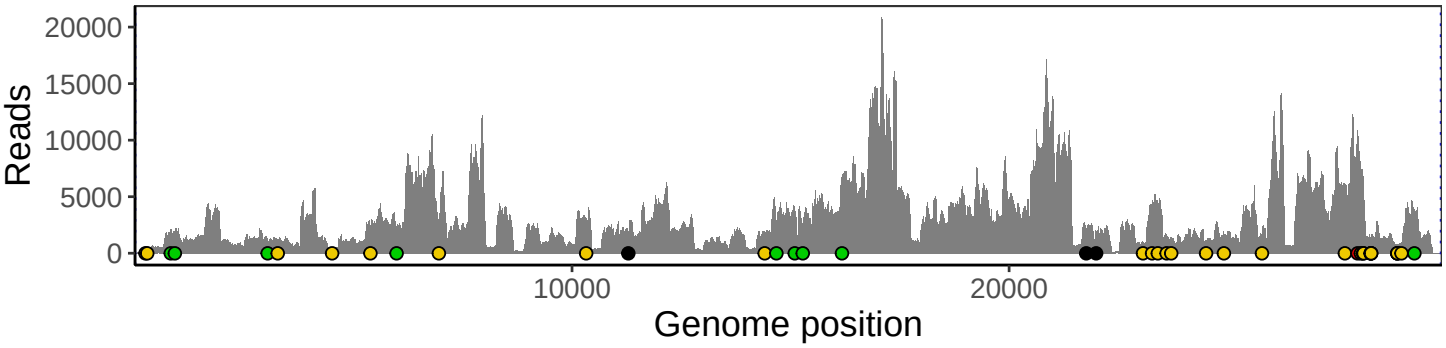



NA
2021−04−12
241 intergenic 68
281 ORF1ab P6S 40
820 ORF1ab silent 2074
913 ORF1ab silent 1803
3037 ORF1ab silent 1085
3267 ORF1ab T1001I 1274
4511 ORF1ab V1416F 504
5388 ORF1ab A1708D 2346
5986 ORF1ab silent 2267
6954 ORF1ab I2230T 2864
10323 ORF1ab K3353R 3015
11288 ORF1ab del 9 1211
14408 ORF1ab P314L 1721
14676 ORF1ab silent 2659
15096 ORF1ab silent 3922
15279 ORF1ab silent 2476
16176 ORF1ab silent 6606
21765 S del 6 1708
21991 S del 3 1692
23063 S N501Y 981
23271 S A570D 4061
23403 S D614G 4353
23604 S P681H 1549
23709 S T716I 1324
24506 S S982A 1134
24914 S D1118H 1835
25785 ORF3a W131C 1647
27682 ORF7a Y97H 6067
27972 ORF8 Q27stop 10455
28048 ORF8 R52I 6867
28095 ORF8 K68stop 6744
28111 ORF8 Y73C 5473
28271 intergenic del 1 1269
28280 N D3L 867
28281 N D3L 867
28282 N D3L 924
28881 N R203K 526
28882 N R203K 522
28883 N G204R 525
28977 N S235F 914
29272 N silent 3902
VSP2266−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

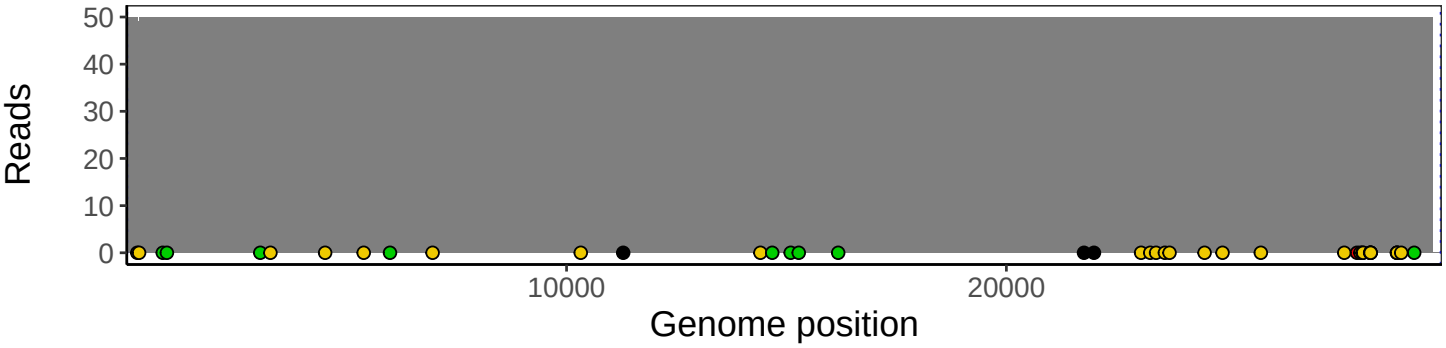
Analyses of individual experiments and composite results

VSP2266-1 | 2021-04-12 | NA | UPHS-1054 | genomes | single experiment

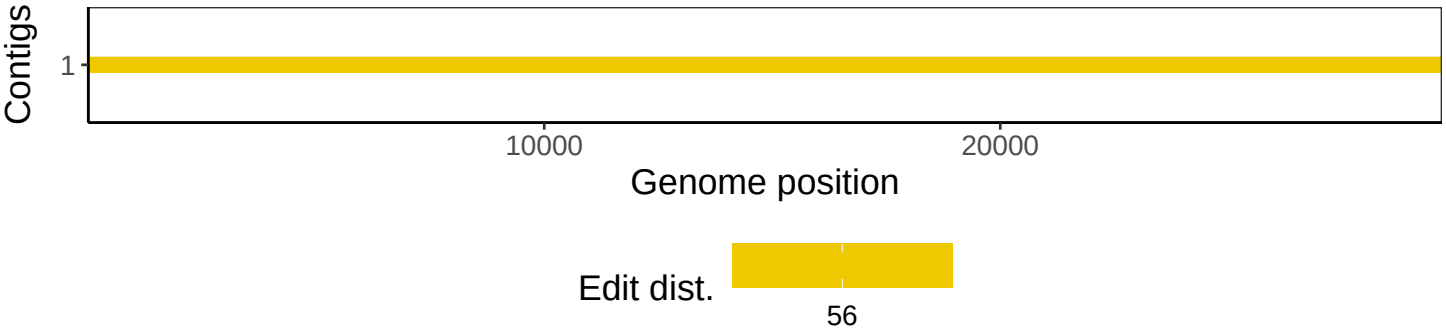
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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