COVID-19 subject UPHS-1169

2021-06-23

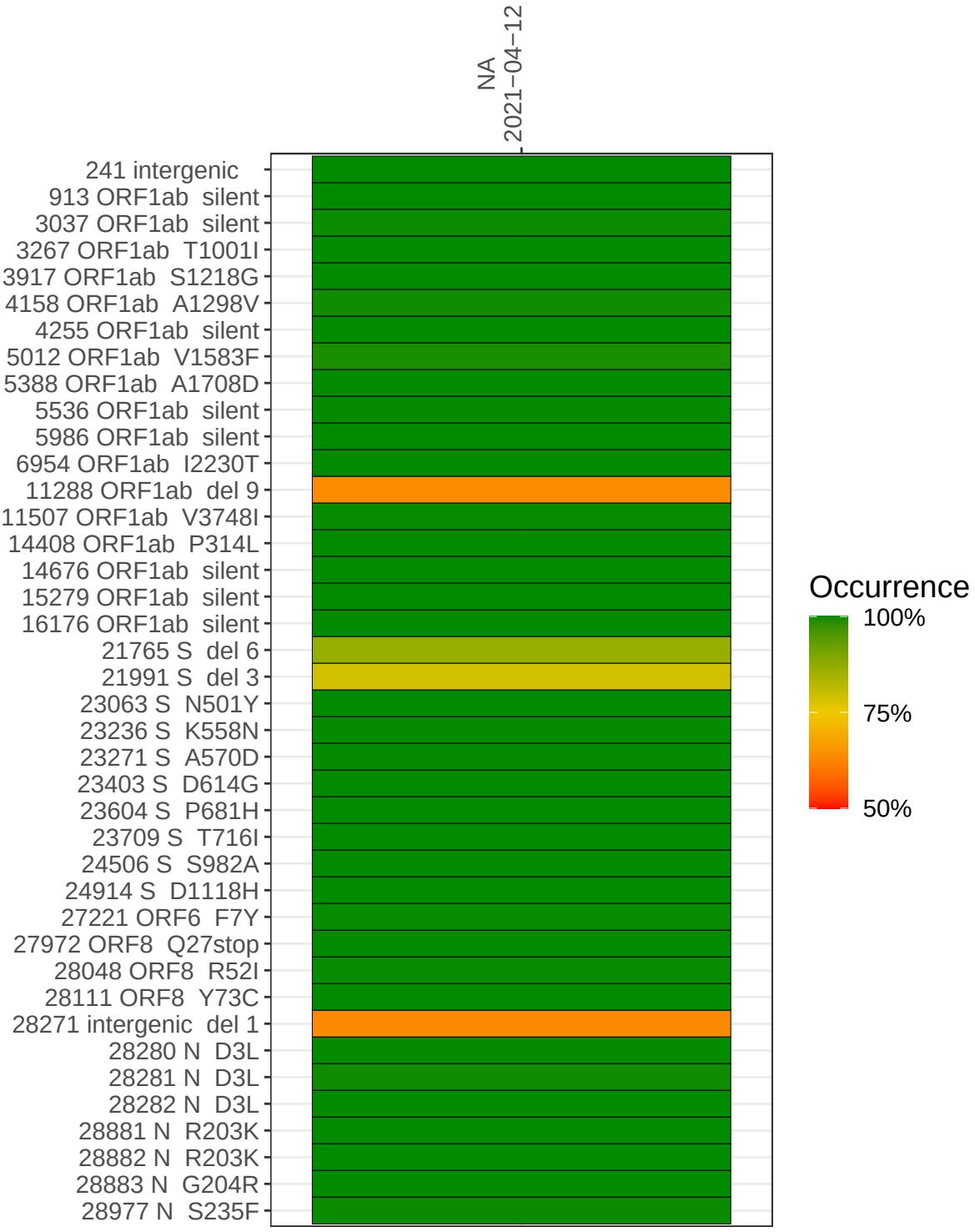
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

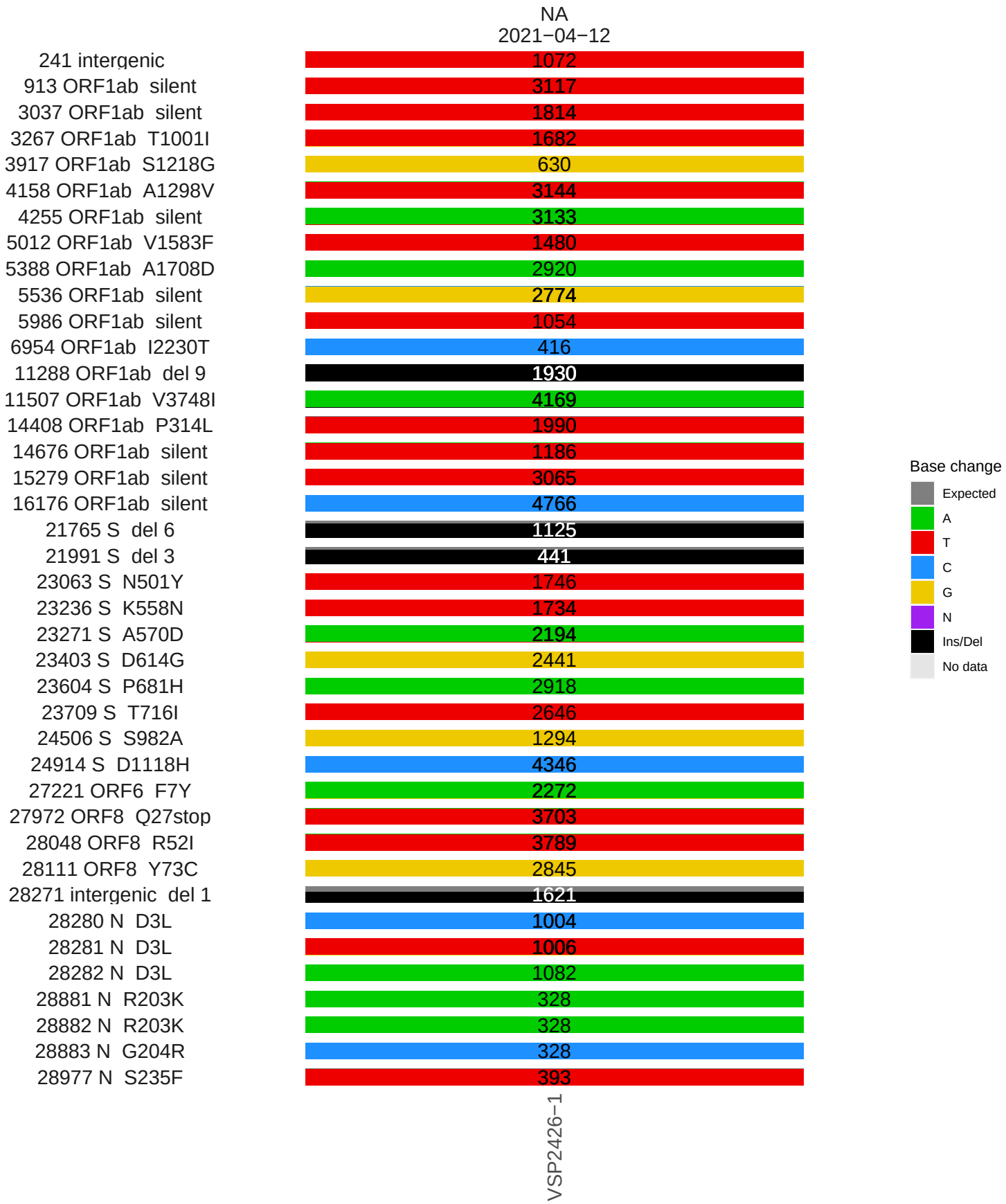
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2426-1	single experiment	NA	NA	2021-04-12	29.86	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.

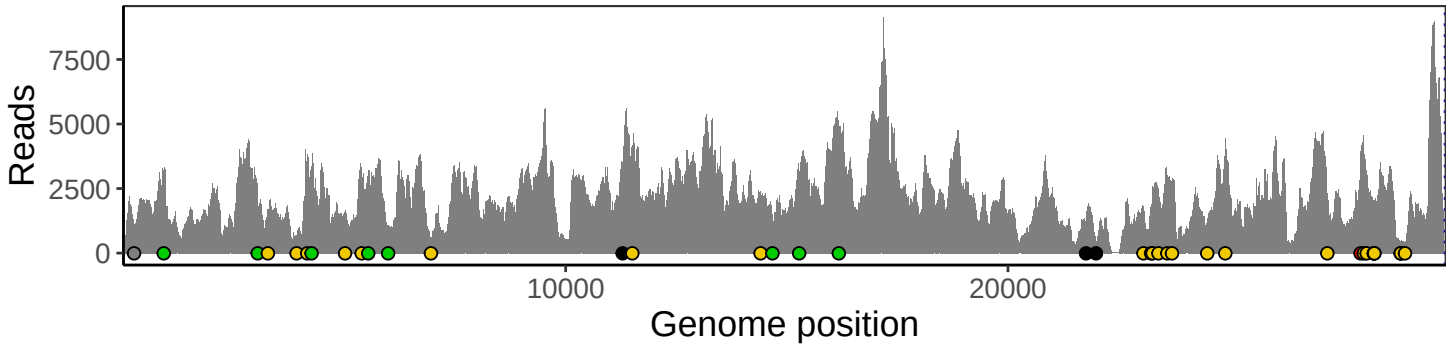



NA
2021−04−12
241 intergenic 1072
913 ORF1ab silent 3117
3037 ORF1ab silent 1814
3267 ORF1ab T1001I 1682
3917 ORF1ab S1218G 630
4158 ORF1ab A1298V 3144
4255 ORF1ab silent 3133
5012 ORF1ab V1583F 1480
5388 ORF1ab A1708D 2920
5536 ORF1ab silent 2774
5986 ORF1ab silent 1054
6954 ORF1ab I2230T 416
11288 ORF1ab del 9 1930
11507 ORF1ab V3748I 4169
14408 ORF1ab P314L 1990
14676 ORF1ab silent 1186
15279 ORF1ab silent 3065
16176 ORF1ab silent 4766
21765 S del 6 1125
21991 S del 3 441
23063 S N501Y 1746
23236 S K558N 1734
23271 S A570D 2194
23403 S D614G 2441
23604 S P681H 2918
23709 S T716I 2646
24506 S S982A 1294
24914 S D1118H 4346
27221 ORF6 F7Y 2272
27972 ORF8 Q27stop 3703
28048 ORF8 R52I 3789
28111 ORF8 Y73C 2845
28271 intergenic del 1 1621
28280 N D3L 1004
28281 N D3L 1006
28282 N D3L 1082
28881 N R203K 328
28882 N R203K 328
28883 N G204R 328
28977 N S235F 393
VSP2426−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

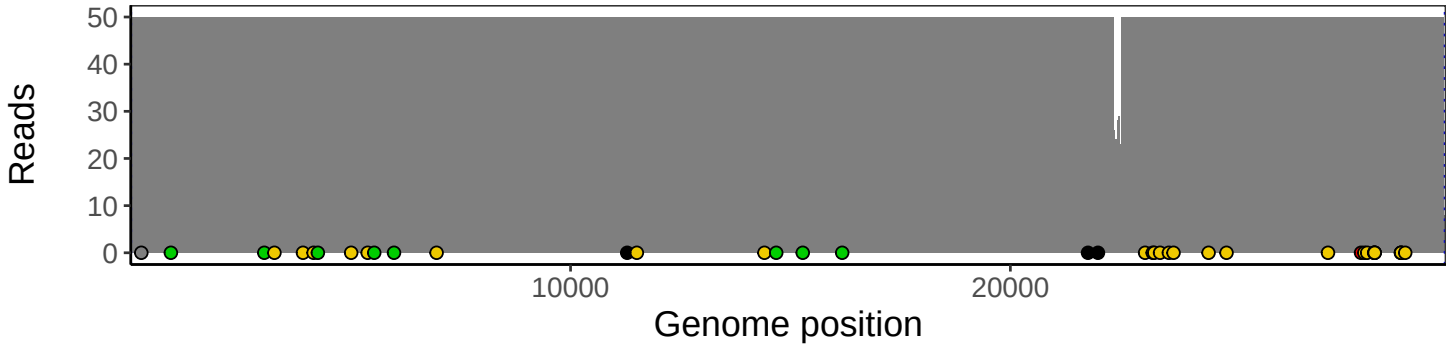
Analyses of individual experiments and composite results

VSP2426-1 | 2021-04-12 | NA | UPHS-1169 | genomes | single experiment

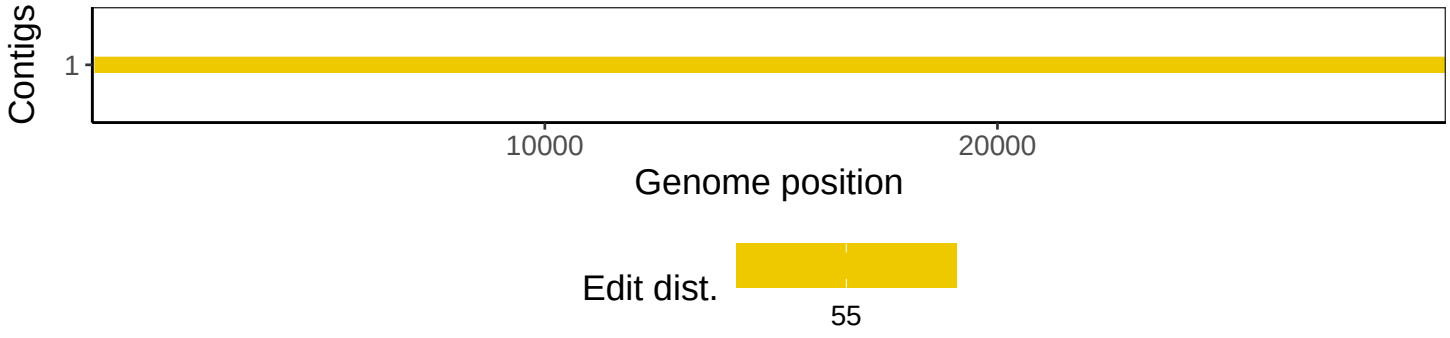
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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