COVID-19 subject UPHS-0407

2021-05-05

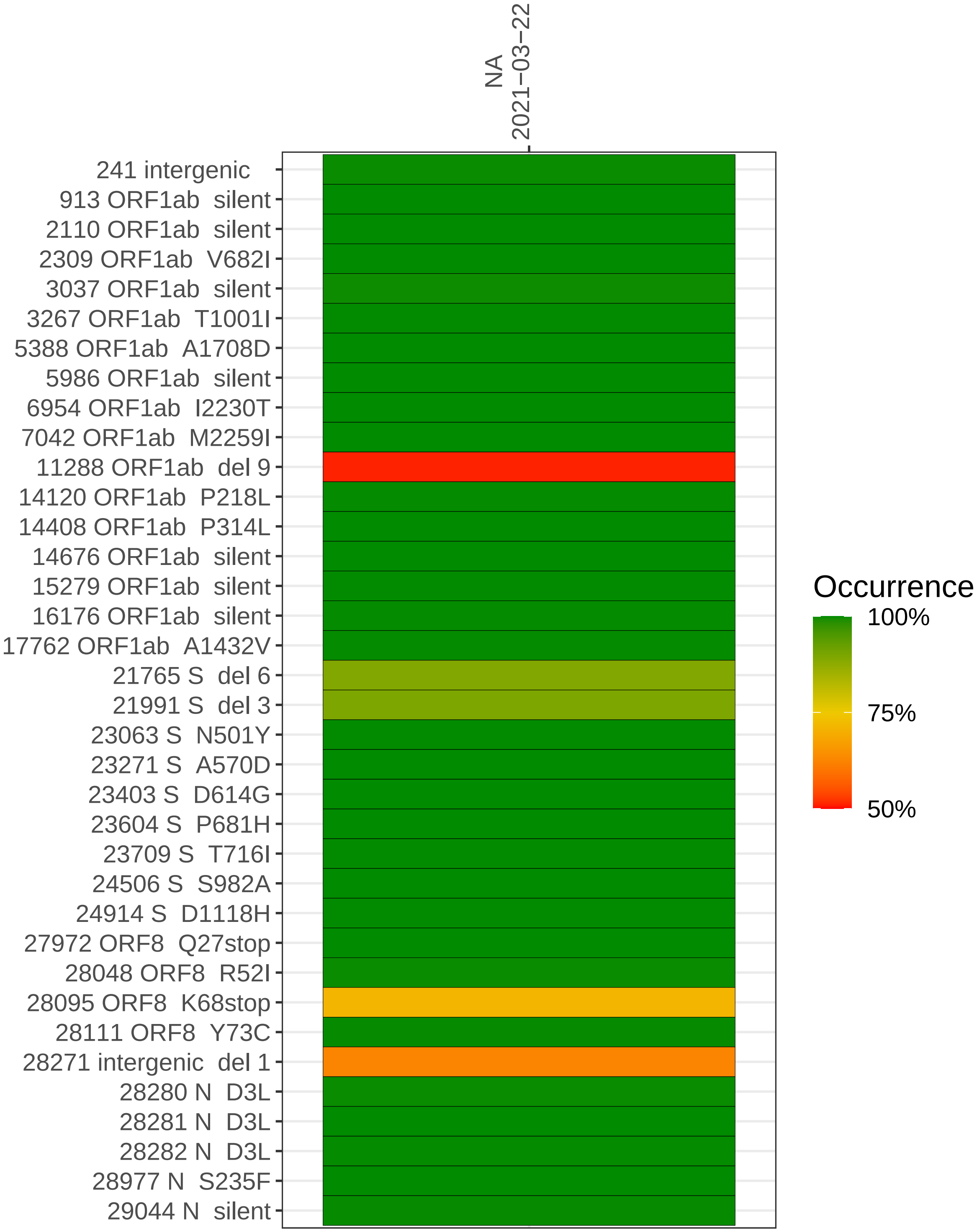
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

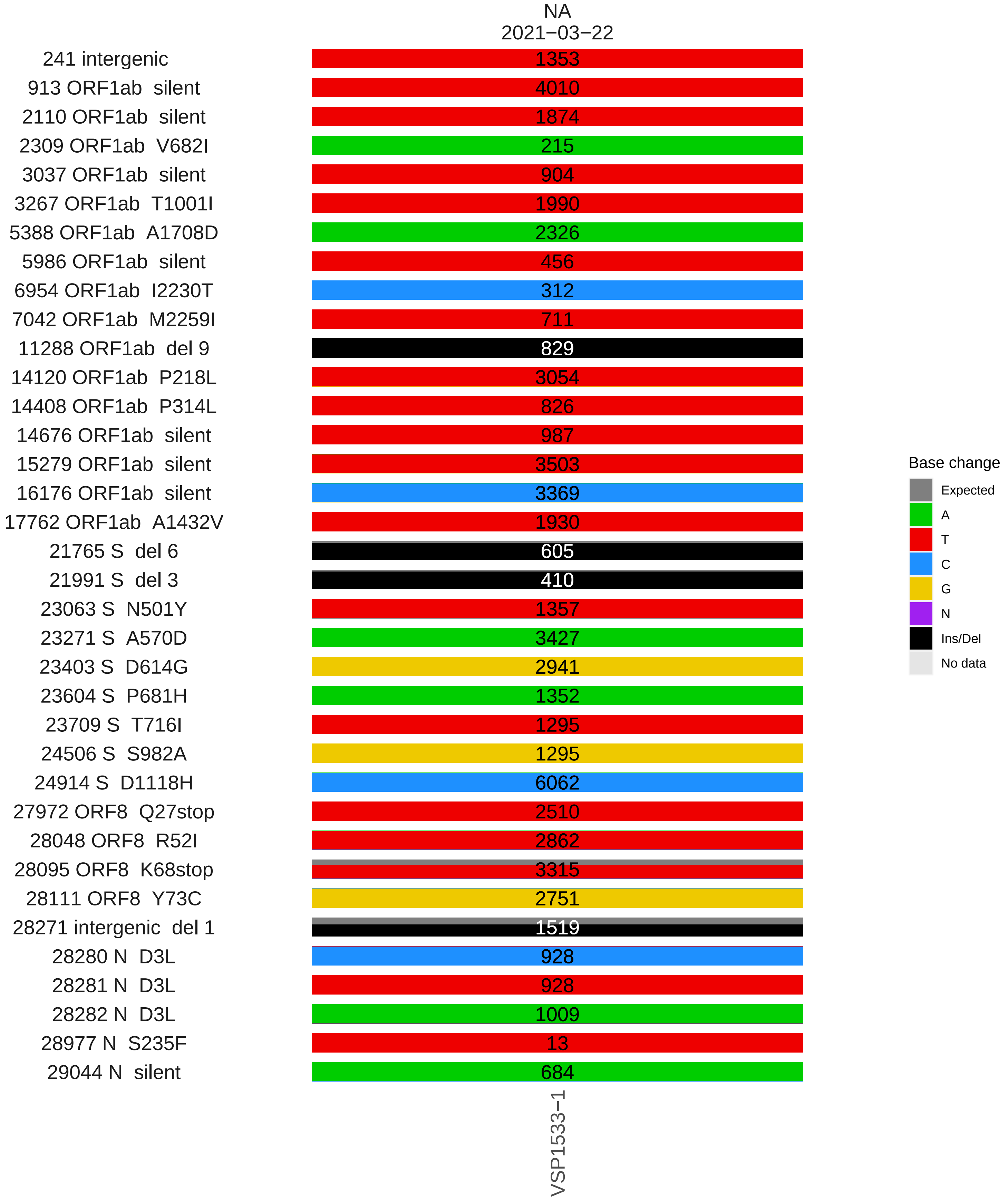
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1533-1	single experiment	NA	NA	2021-03-22	22.46	B.1.1.7	99.7%	99.2%

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.

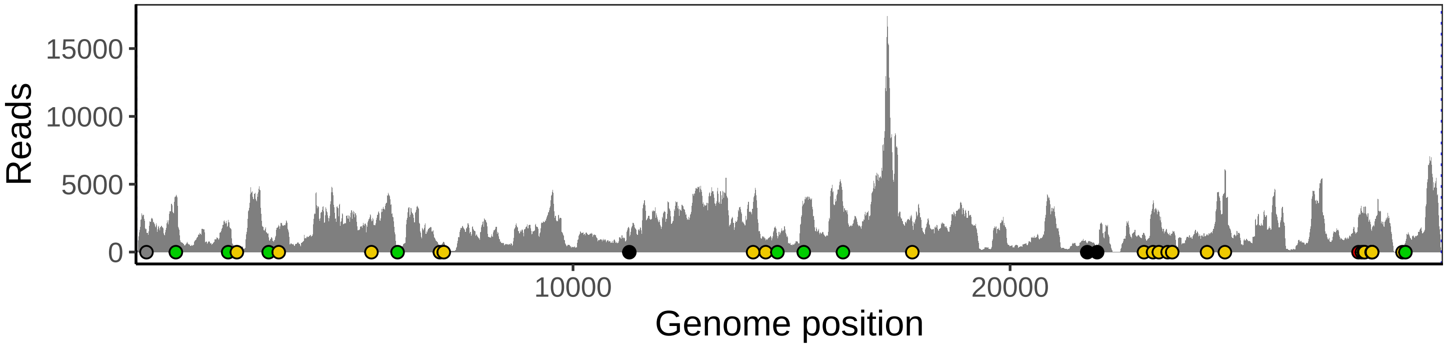



NA
2021−03−22
241 intergenic
1353
913 ORF1ab silent
4010
2110 ORF1ab silent
1874
2309 ORF1ab V682I
215
3037 ORF1ab silent
904
3267 ORF1ab T1001I
1990
5388 ORF1ab A1708D
2326
5986 ORF1ab silent
456
6954 ORF1ab I2230T
312
7042 ORF1ab M2259I
711
11288 ORF1ab del 9
829
14120 ORF1ab P218L
3054
14408 ORF1ab P314L
826
14676 ORF1ab silent
987
15279 ORF1ab silent
3503
16176 ORF1ab silent
3369
17762 ORF1ab A1432V
1930
21765 S del 6
605
21991 S del 3
410
23063 S N501Y
1357
23271 S A570D
3427
23403 S D614G
2941
23604 S P681H
1352
23709 S T716I
1295
24506 S S982A
1295
24914 S D1118H
6062
27972 ORF8 Q27stop
2510
28048 ORF8 R52I
2862
28095 ORF8 K68stop
3315
28111 ORF8 Y73C
2751
28271 intergenic del 1
1519
28280 N D3L
928
28281 N D3L
928
28282 N D3L
1009
28977 N S235F
13
29044 N silent
684
VSP1533−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

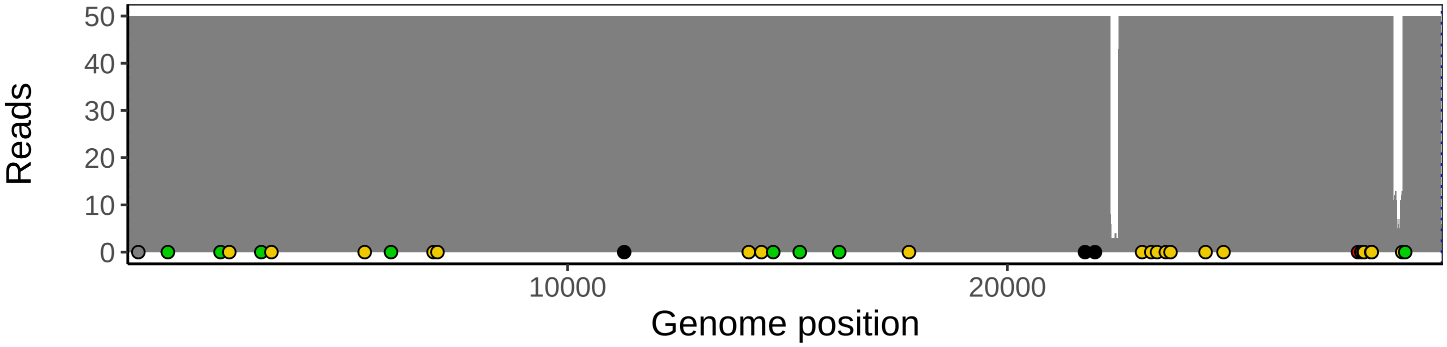
Analyses of individual experiments and composite results

VSP1533-1 | 2021-03-22 | NA | UPHS-0407 | genomes | single experiment

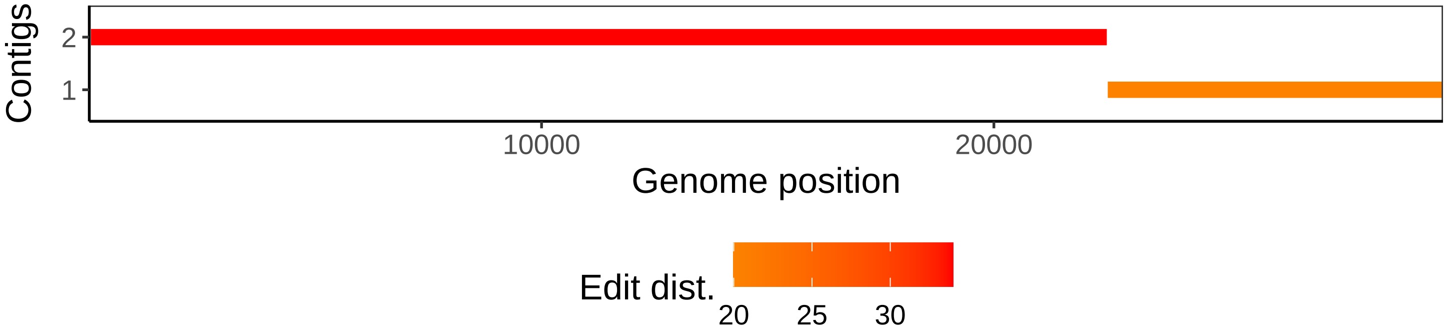
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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