COVID-19 subject UPHS-0479

2021-06-23

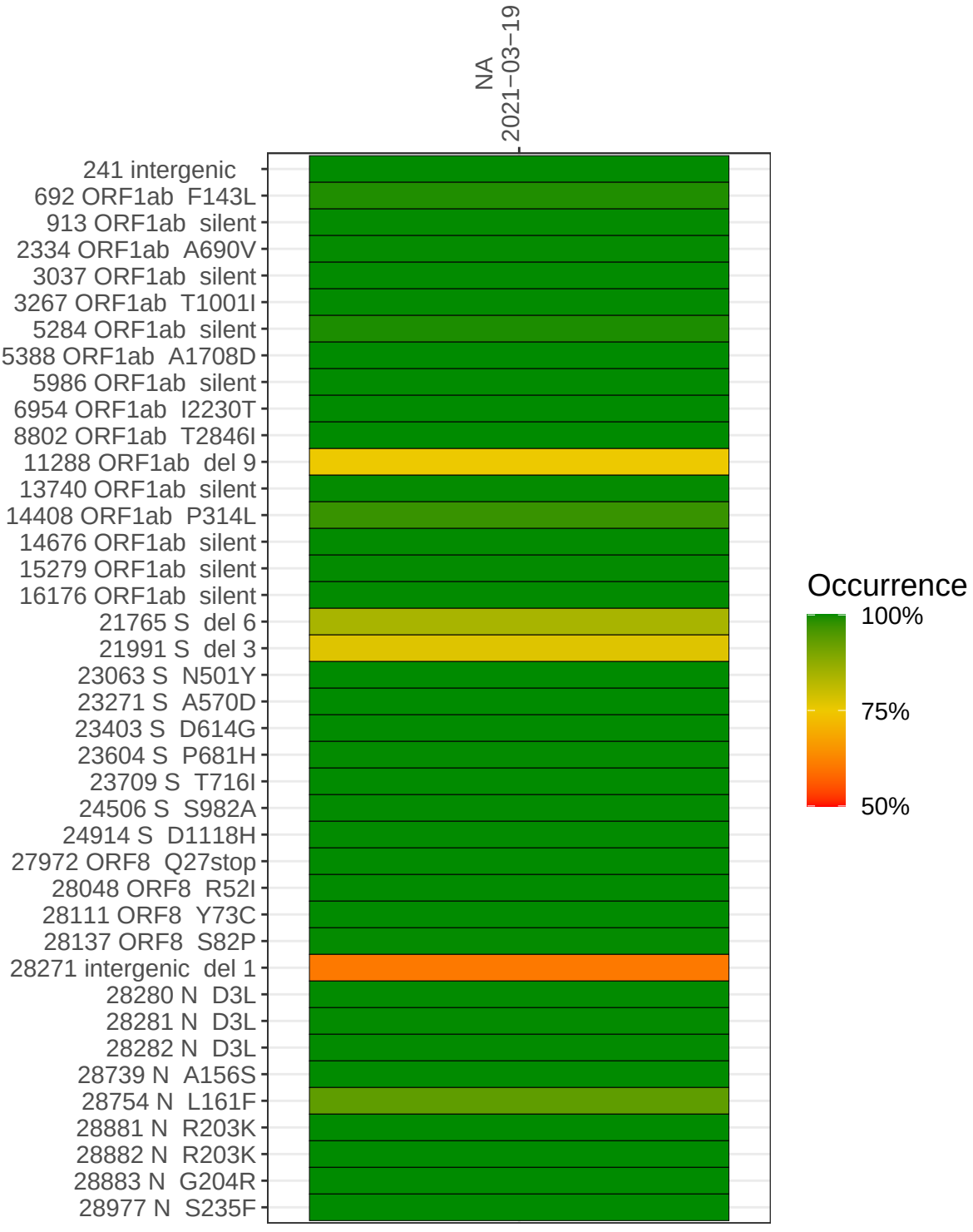
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

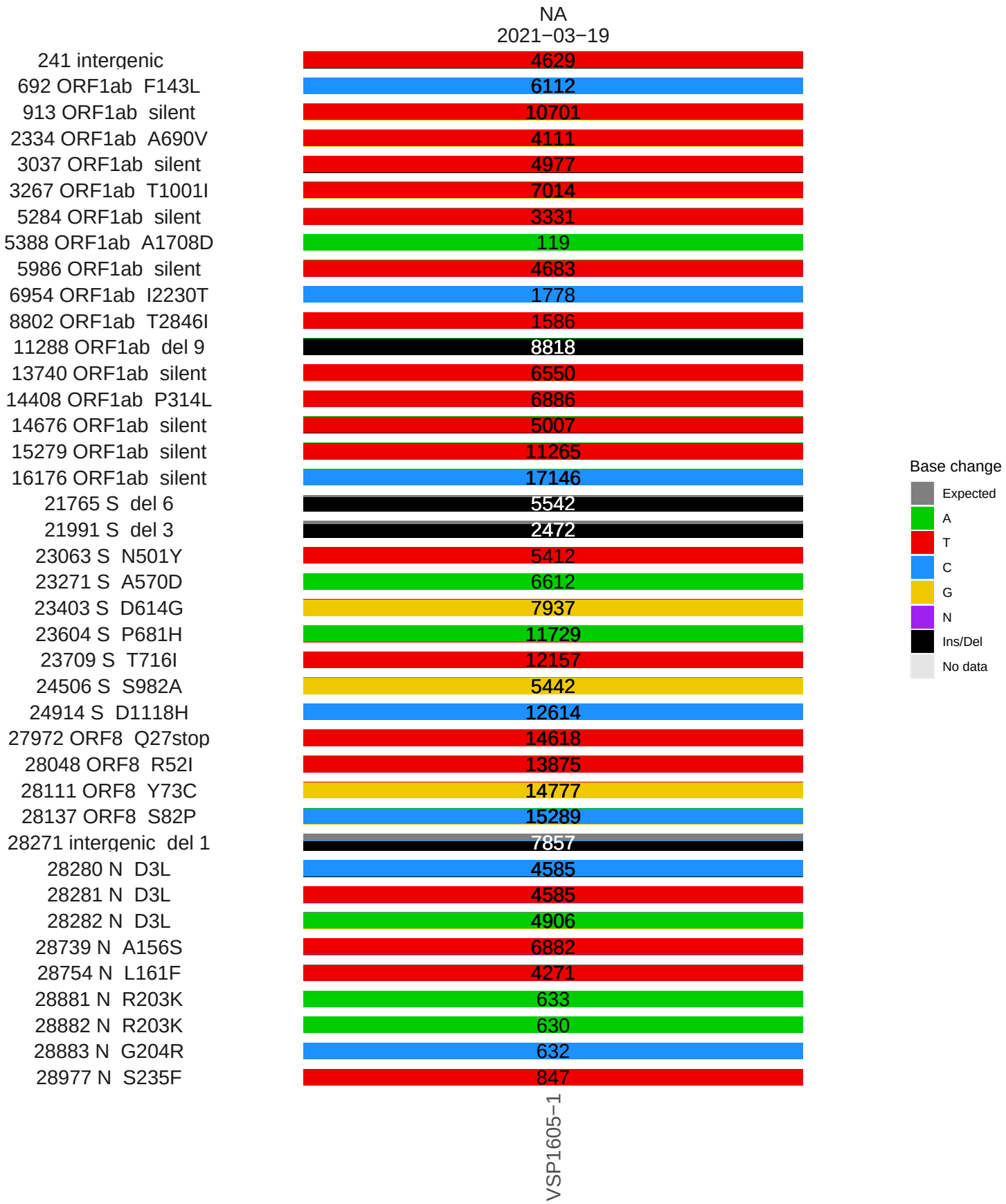
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1605-1	single experiment	NA	NA	2021-03-19	29.84	B.1.1.7	99.9%	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.

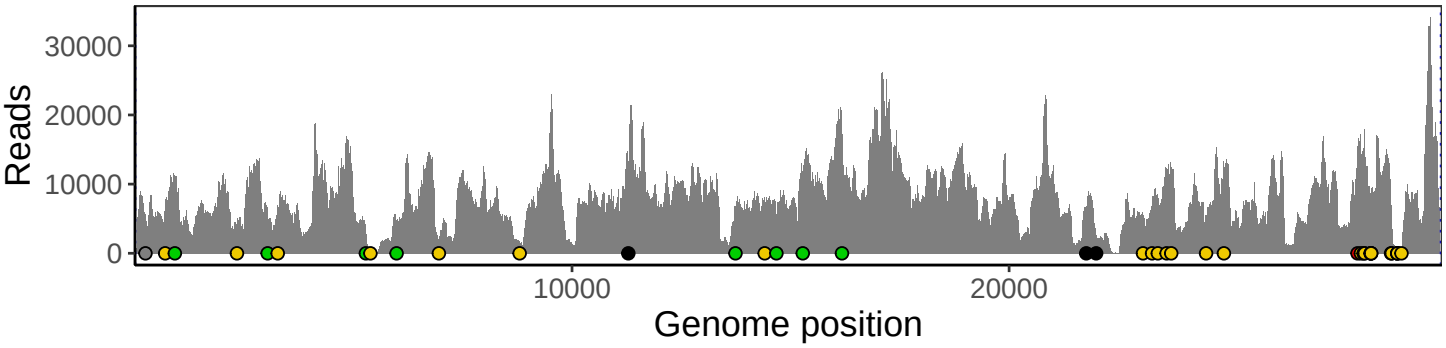



NA
2021−03−19
241 intergenic 4629
692 ORF1ab F143L 6112
913 ORF1ab silent 10701
2334 ORF1ab A690V 4111
3037 ORF1ab silent 4977
3267 ORF1ab T1001I 7014
5284 ORF1ab silent 3331
5388 ORF1ab A1708D 119
5986 ORF1ab silent 4683
6954 ORF1ab I2230T 1778
8802 ORF1ab T2846I 1586
11288 ORF1ab del 9 8818
13740 ORF1ab silent 6550
14408 ORF1ab P314L 6886
14676 ORF1ab silent 5007
15279 ORF1ab silent 11265
16176 ORF1ab silent 17146
21765 S del 6 5542
21991 S del 3 2472
23063 S N501Y 5412
23271 S A570D 6612
23403 S D614G 7937
23604 S P681H 11729
23709 S T716I 12157
24506 S S982A 5442
24914 S D1118H 12614
27972 ORF8 Q27stop 14618
28048 ORF8 R52I 13875
28111 ORF8 Y73C 14777
28137 ORF8 S82P 15289
28271 intergenic del 1 7857
28280 N D3L 4585
28281 N D3L 4585
28282 N D3L 4906
28739 N A156S 6882
28754 N L161F 4271
28881 N R203K 633
28882 N R203K 630
28883 N G204R 632
28977 N S235F 847
VSP1605−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

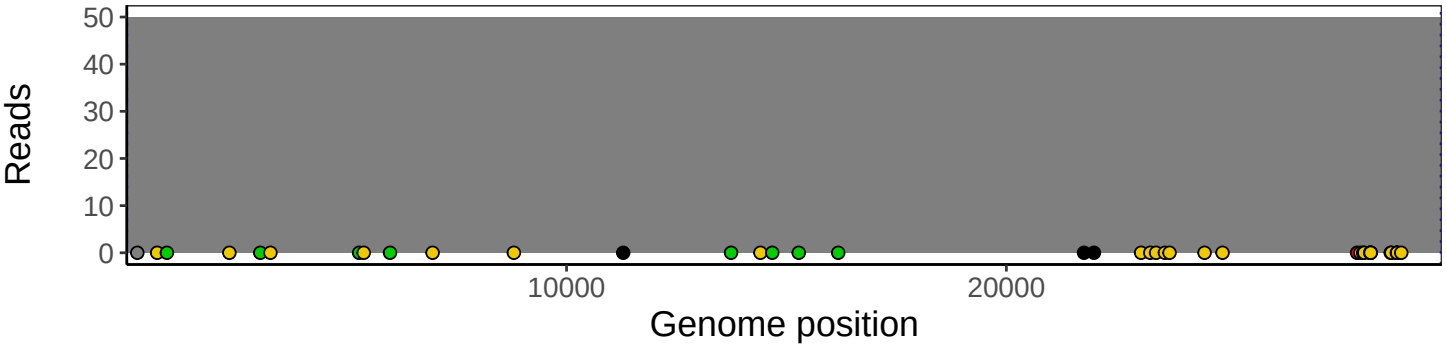
Analyses of individual experiments and composite results

VSP1605-1 | 2021-03-19 | NA | UPHS-0479 | genomes | single experiment

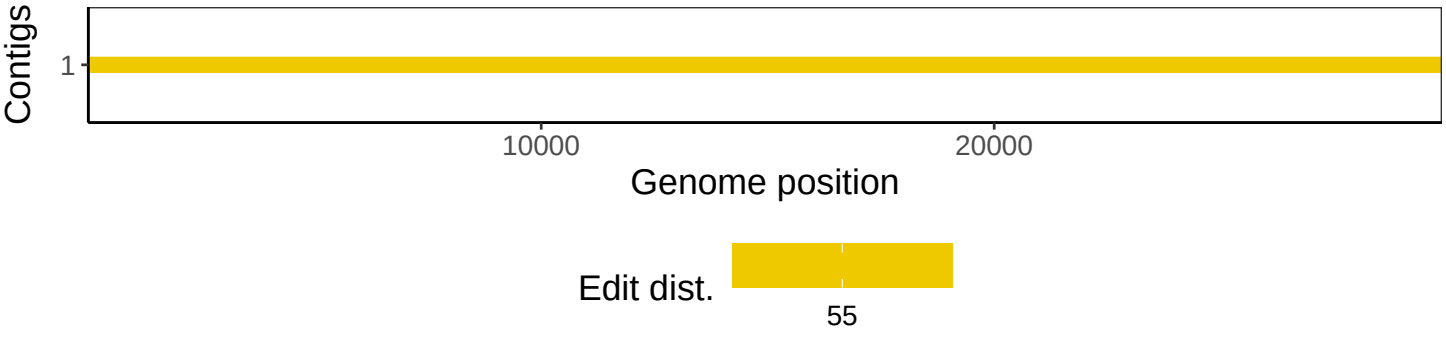
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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