

COVID-19 subject AHTMV3AFX2

2021-06-23

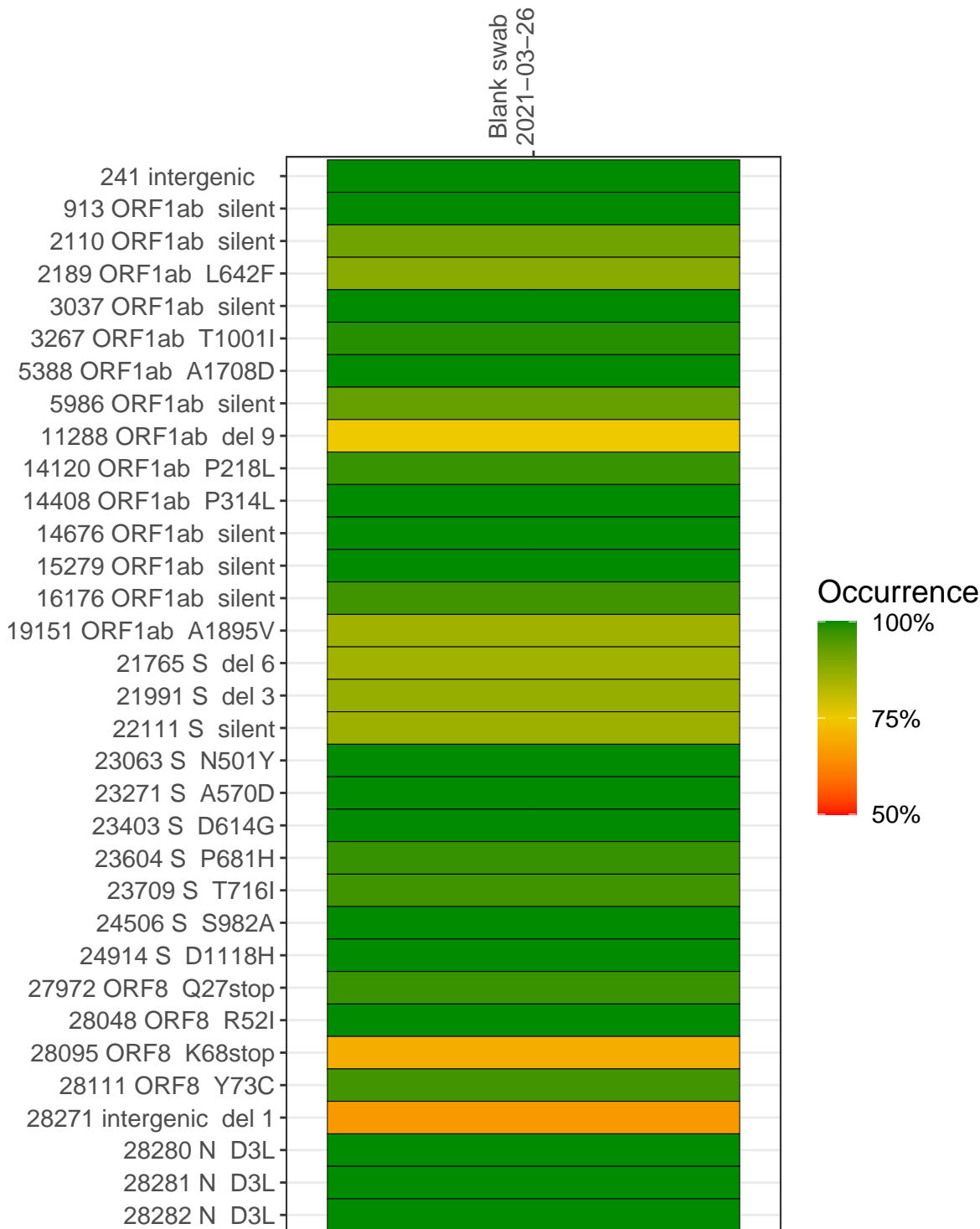
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP9959-1	single experiment	NA	Blank swab	2021-03-26	19.80	B.1.1.7	98.9%	97.0%

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.



Blank swab
2021-03-26

241 intergenic	35
913 ORF1ab silent	78
2110 ORF1ab silent	58
2189 ORF1ab L642F	17
3037 ORF1ab silent	35
3267 ORF1ab T1001I	72
5388 ORF1ab A1708D	50
5986 ORF1ab silent	27
11288 ORF1ab del 9	44
14120 ORF1ab P218L	72
14408 ORF1ab P314L	78
14676 ORF1ab silent	33
15279 ORF1ab silent	61
16176 ORF1ab silent	88
19151 ORF1ab A1895V	54
21765 S del 6	47
21991 S del 3	15
22111 S silent	35
23063 S N501Y	34
23271 S A570D	94
23403 S D614G	74
23604 S P681H	78
23709 S T716I	59
24506 S S982A	39
24914 S D1118H	130
27972 ORF8 Q27stop	70
28048 ORF8 R52I	54
28095 ORF8 K68stop	56
28111 ORF8 Y73C	55
28271 intergenic del 1	50
28280 N D3L	33
28281 N D3L	33
28282 N D3L	33

Base change

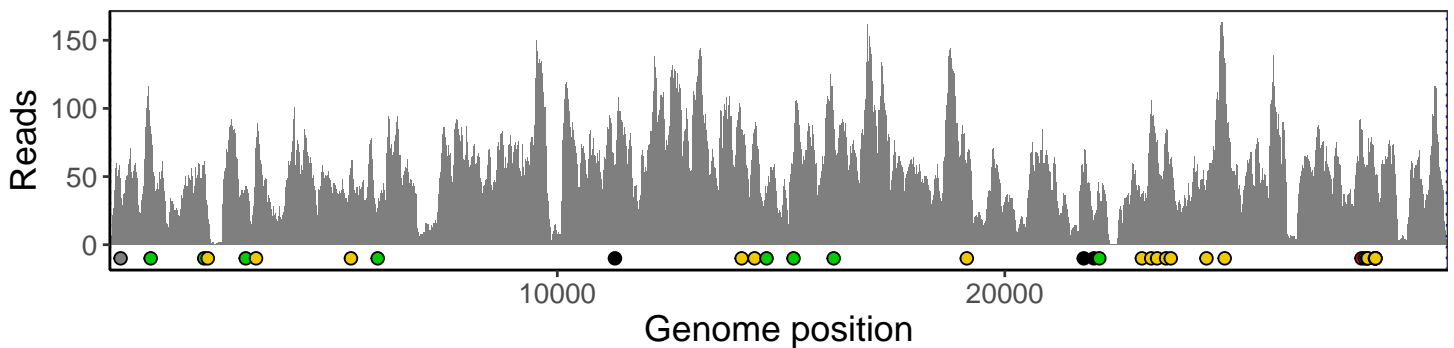
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP9959-1

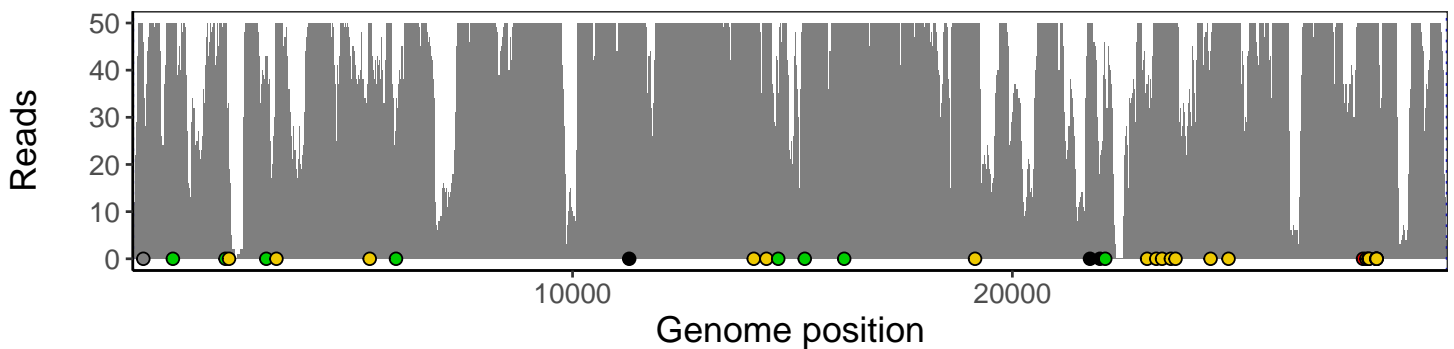
Analyses of individual experiments and composite results

VSP9959-1 | 2021-03-26 | Blank swab | AHTMV3AFX2 | genomes | single experiment

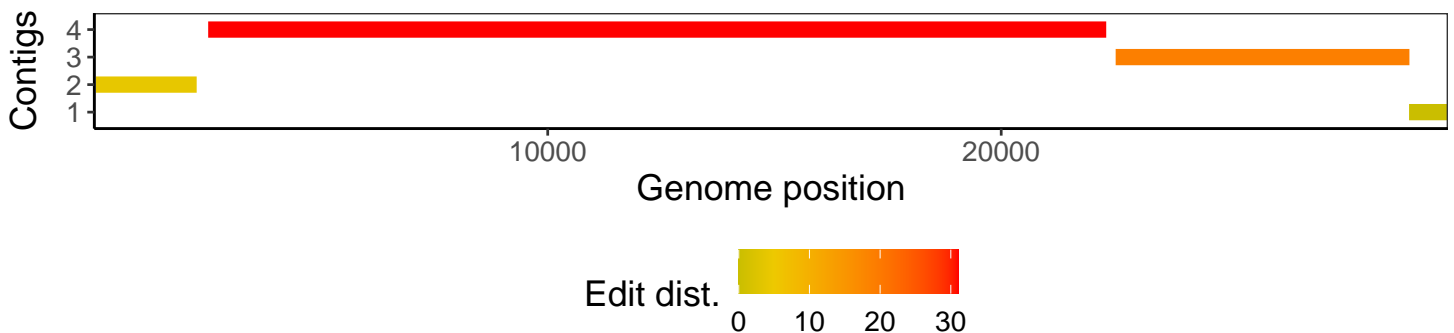
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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