COVID-19 subject HWMYMAFX2-1

2021-06-23

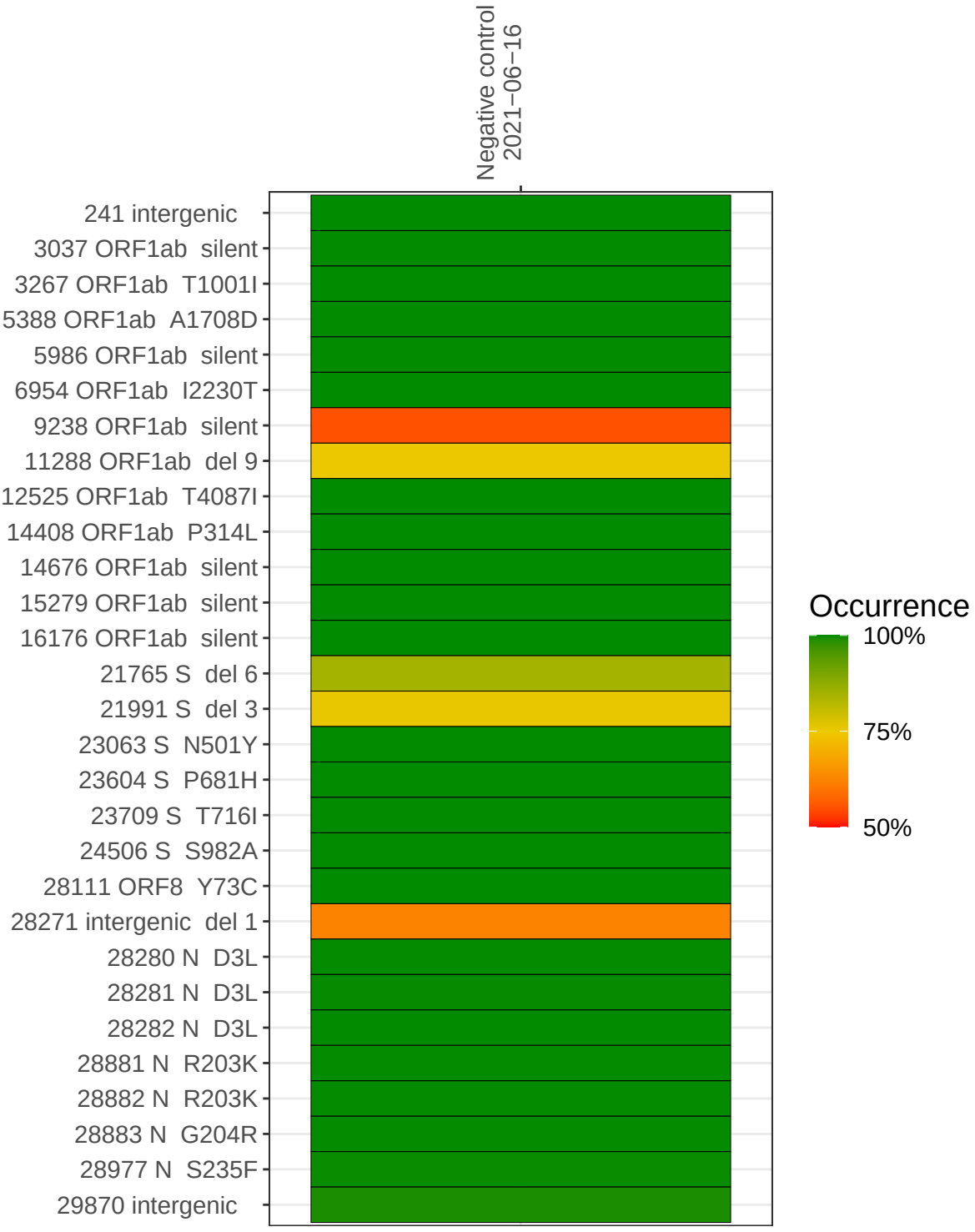
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

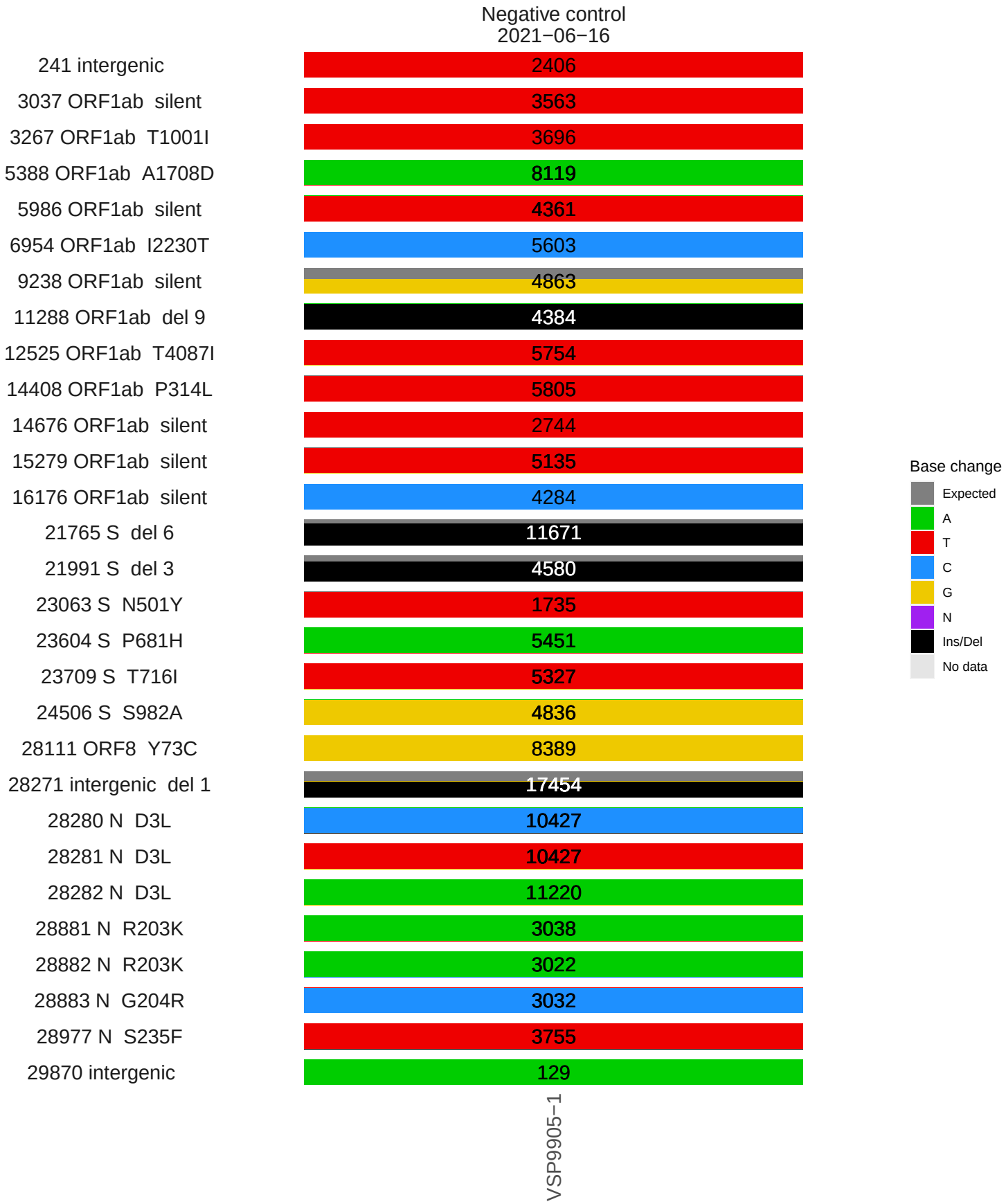
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP9905-1	single experiment	NA	Negative control	2021-06-16	9.01	NA	91.2%	89.7%

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.

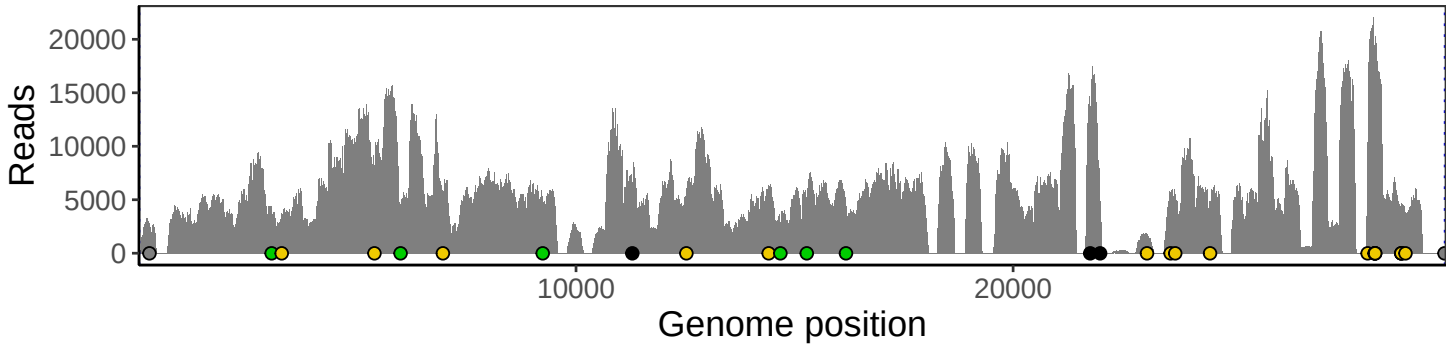



Negative control
2021−06−16
241 intergenic
2406
3037 ORF1ab silent
3563
3267 ORF1ab T1001I
3696
5388 ORF1ab A1708D
8119
5986 ORF1ab silent
4361
6954 ORF1ab I2230T
5603
9238 ORF1ab silent
4863
11288 ORF1ab del 9
4384
12525 ORF1ab T4087I
5754
14408 ORF1ab P314L
5805
14676 ORF1ab silent
2744
15279 ORF1ab silent
5135
16176 ORF1ab silent
4284
21765 S del 6
11671
21991 S del 3
4580
23063 S N501Y
1735
23604 S P681H
5451
23709 S T716I
5327
24506 S S982A
4836
28111 ORF8 Y73C
8389
28271 intergenic del 1
17454
28280 N D3L
10427
28281 N D3L
10427
28282 N D3L
11220
28881 N R203K
3038
28882 N R203K
3022
28883 N G204R
3032
28977 N S235F
3755
29870 intergenic
129
VSP9905−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

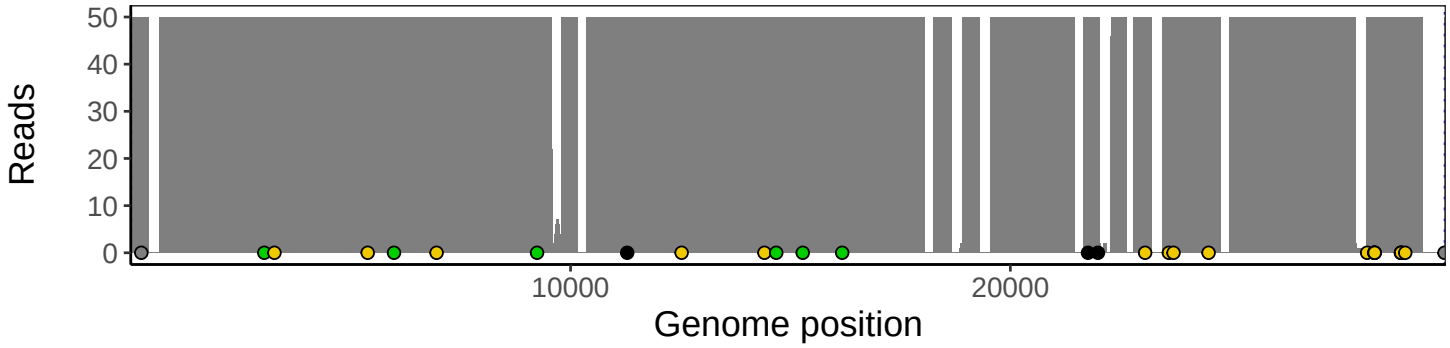
Analyses of individual experiments and composite results

VSP9905-1 | 2021-06-16 | Negative control | HWMYMAFX2-1 | genomes | single experiment

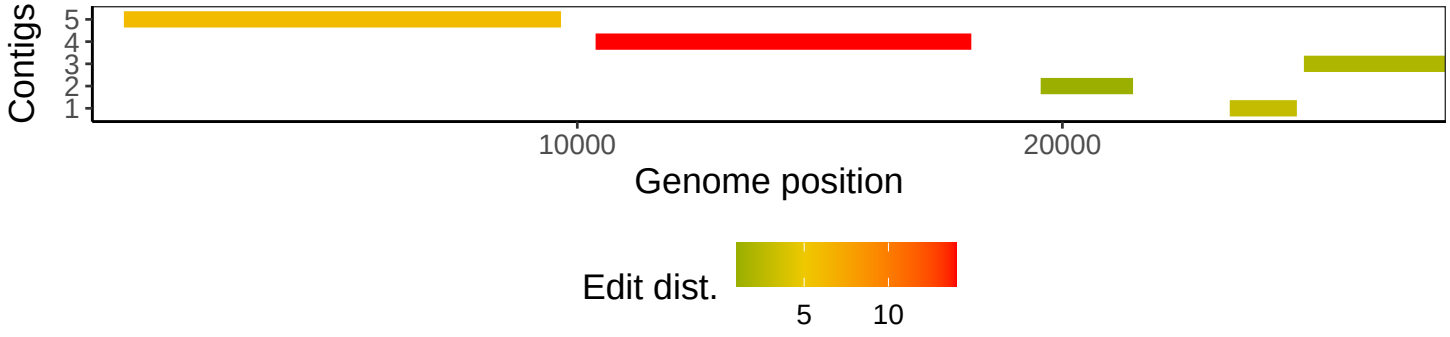
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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