COVID-19 subject UPHS-0842

2021-05-21

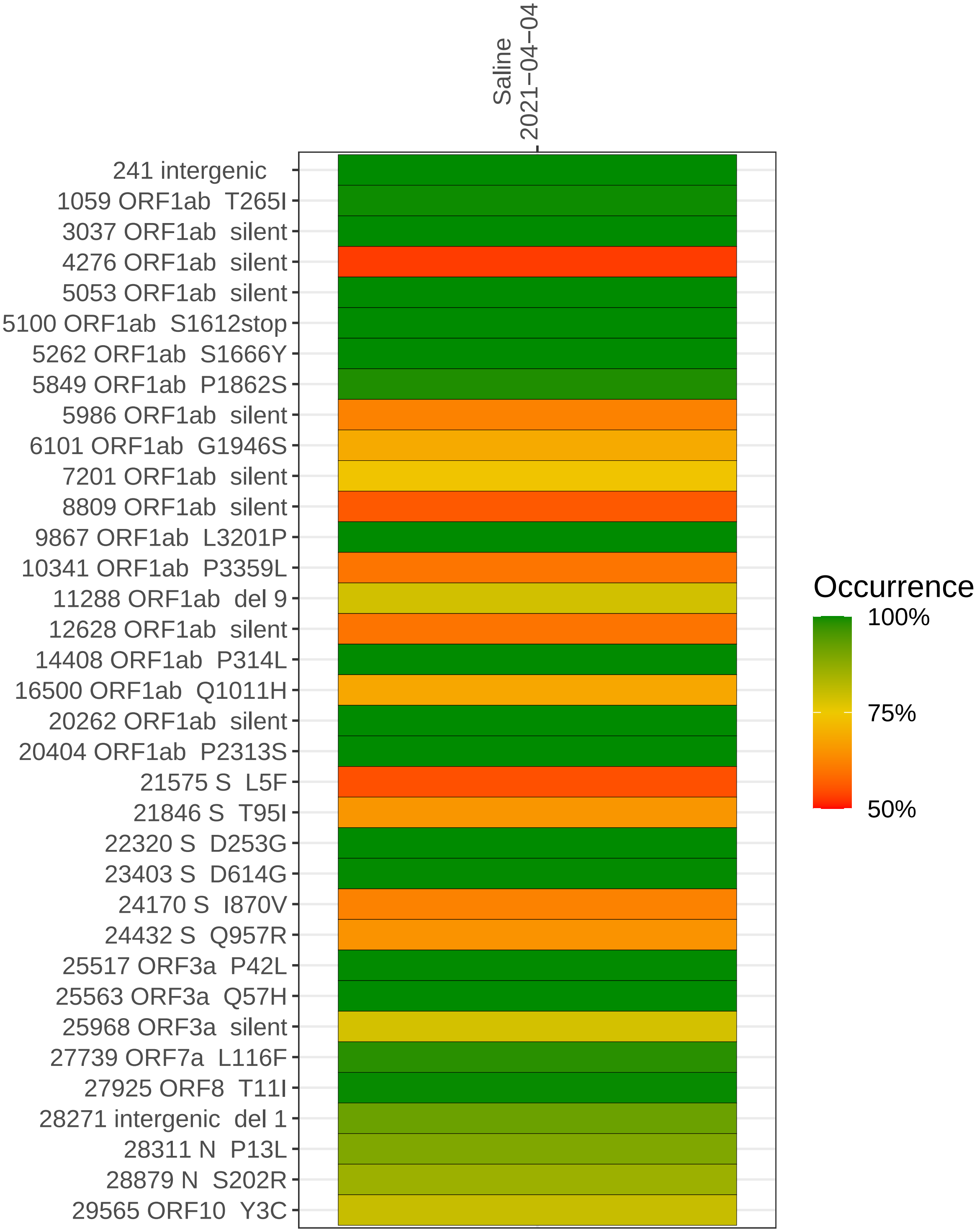
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

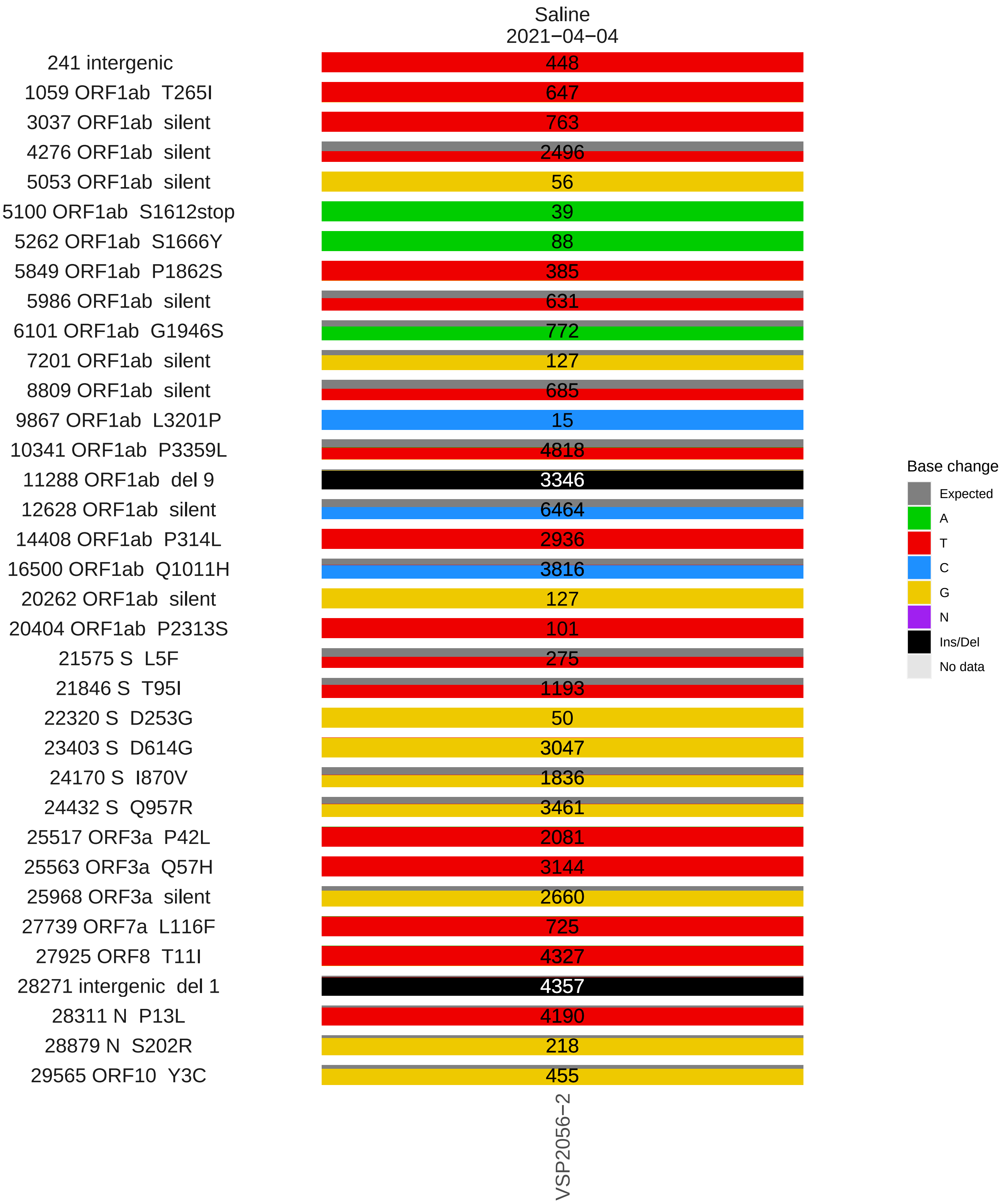
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2056-2	single experiment	NA	Saline	2021-04-04	12.52	B.1.526.2	96.6%	96.3%

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.

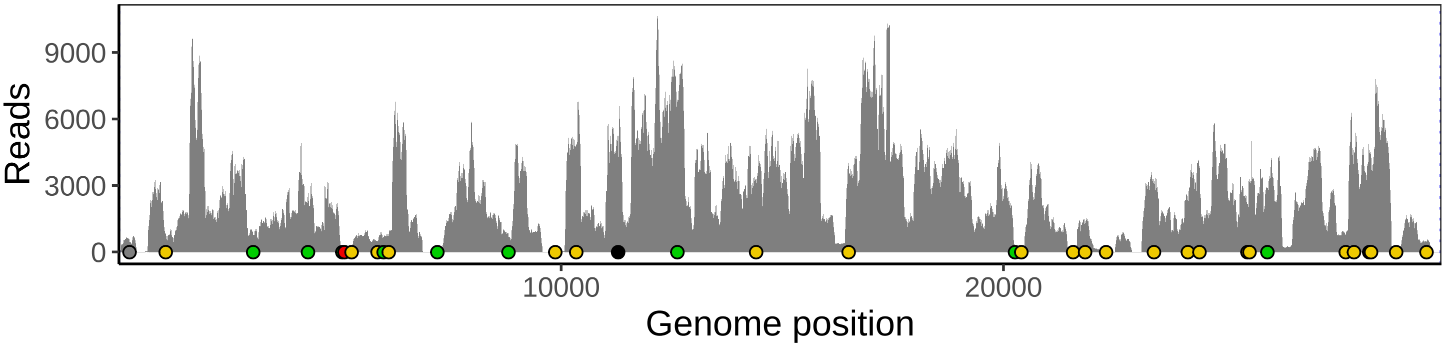



Saline
2021−04−04
241 intergenic
1059 ORF1ab T265I
3037 ORF1ab silent
4276 ORF1ab silent
5053 ORF1ab silent
5100 ORF1ab S1612stop
5262 ORF1ab S1666Y
5849 ORF1ab P1862S
5986 ORF1ab silent
6101 ORF1ab G1946S
7201 ORF1ab silent
8809 ORF1ab silent
9867 ORF1ab L3201P
10341 ORF1ab P3359L
11288 ORF1ab del 9
12628 ORF1ab silent
14408 ORF1ab P314L
16500 ORF1ab Q1011H
20262 ORF1ab silent
20404 ORF1ab P2313S
21575 S L5F
21846 S T95I
22320 S D253G
23403 S D614G
24170 S I870V
24432 S Q957R
25517 ORF3a P42L
25563 ORF3a Q57H
25968 ORF3a silent
27739 ORF7a L116F
27925 ORF8 T11I
28271 intergenic del 1
28311 N P13L
28879 N S202R
29565 ORF10 Y3C
448
647
763
2496
56
39
88
385
631
772
127
685
15
4818
3346
6464
2936
3816
127
101
275
1193
50
3047
1836
3461
2081
3144
2660
725
4327
4357
4190
218
455
VSP2056−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

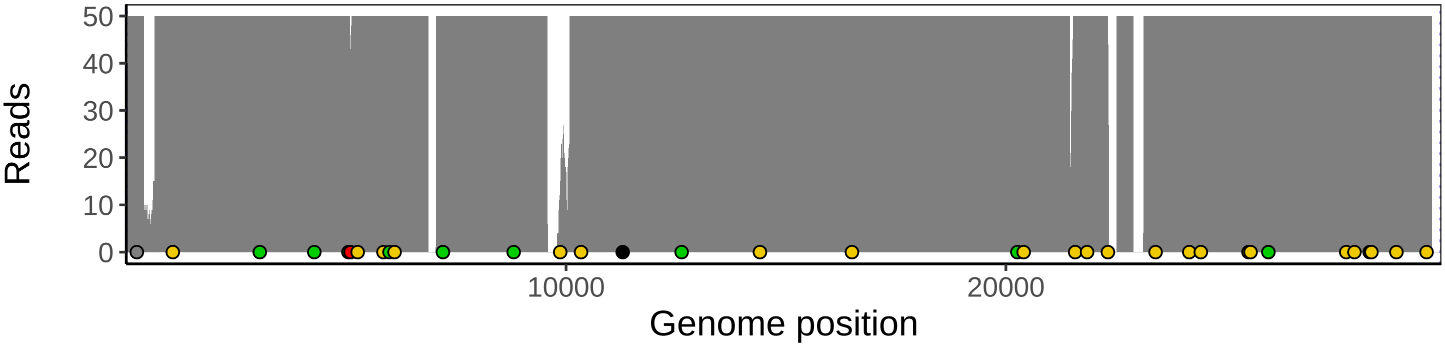
Analyses of individual experiments and composite results

VSP2056-2 | 2021-04-04 | Saline | UPHS-0842 | genomes | single experiment

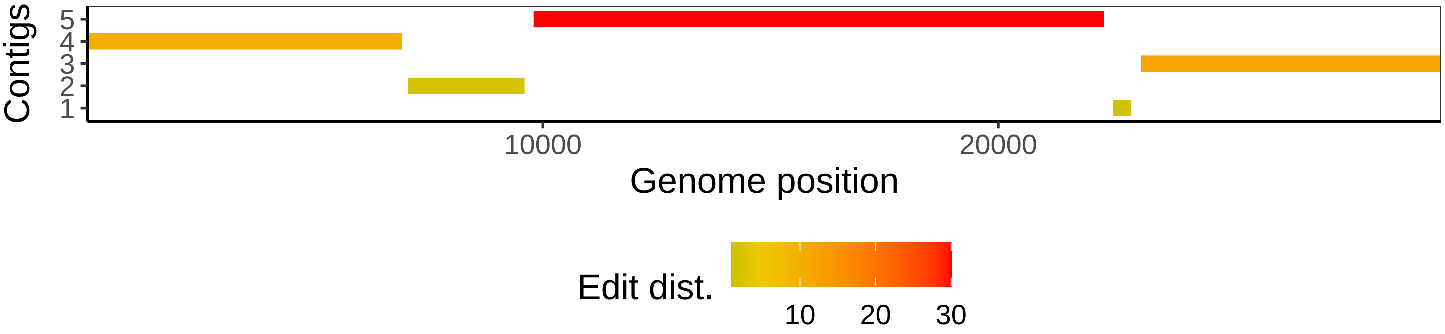
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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