COVID-19 subject UPHS-0996

2021-05-10

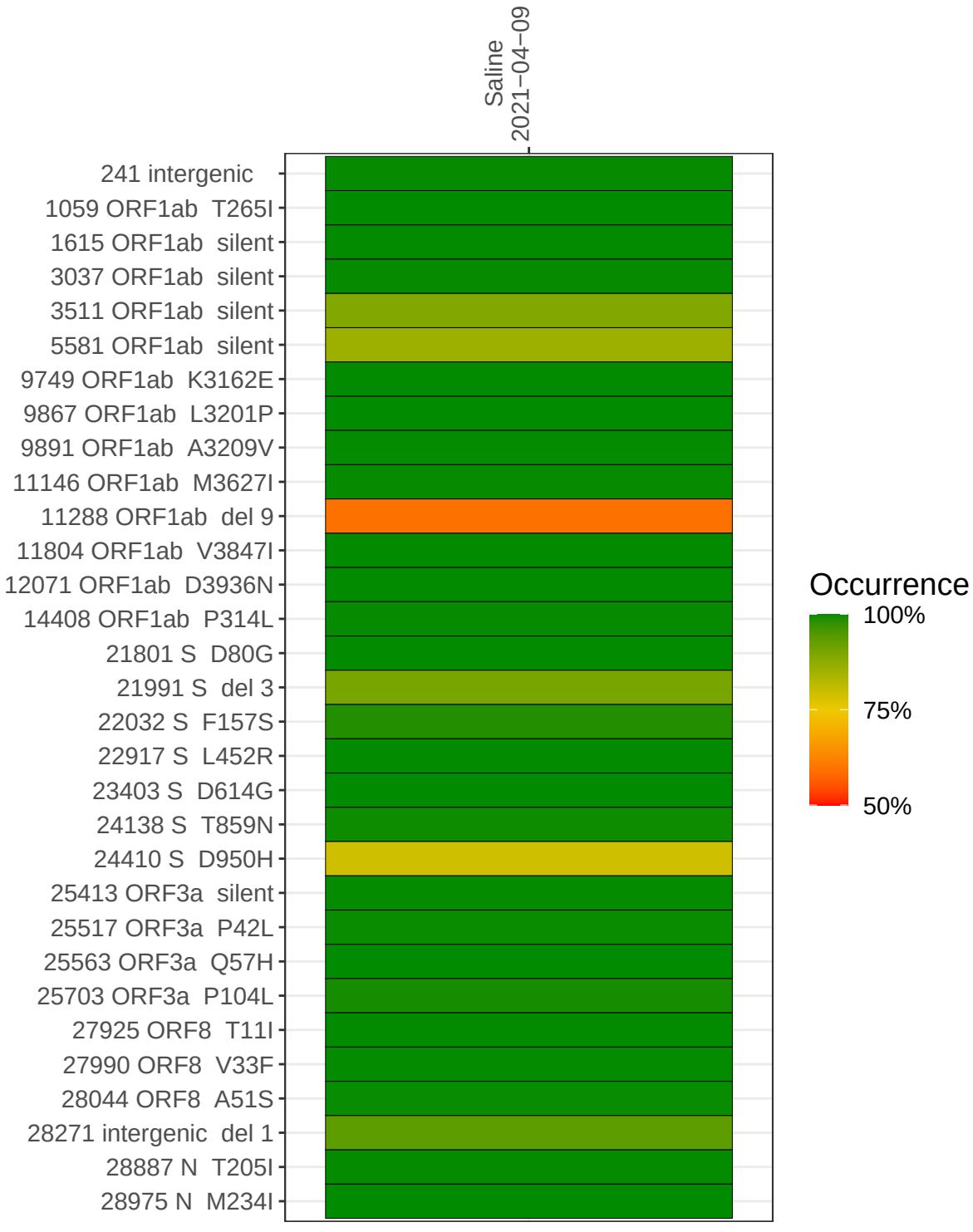
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

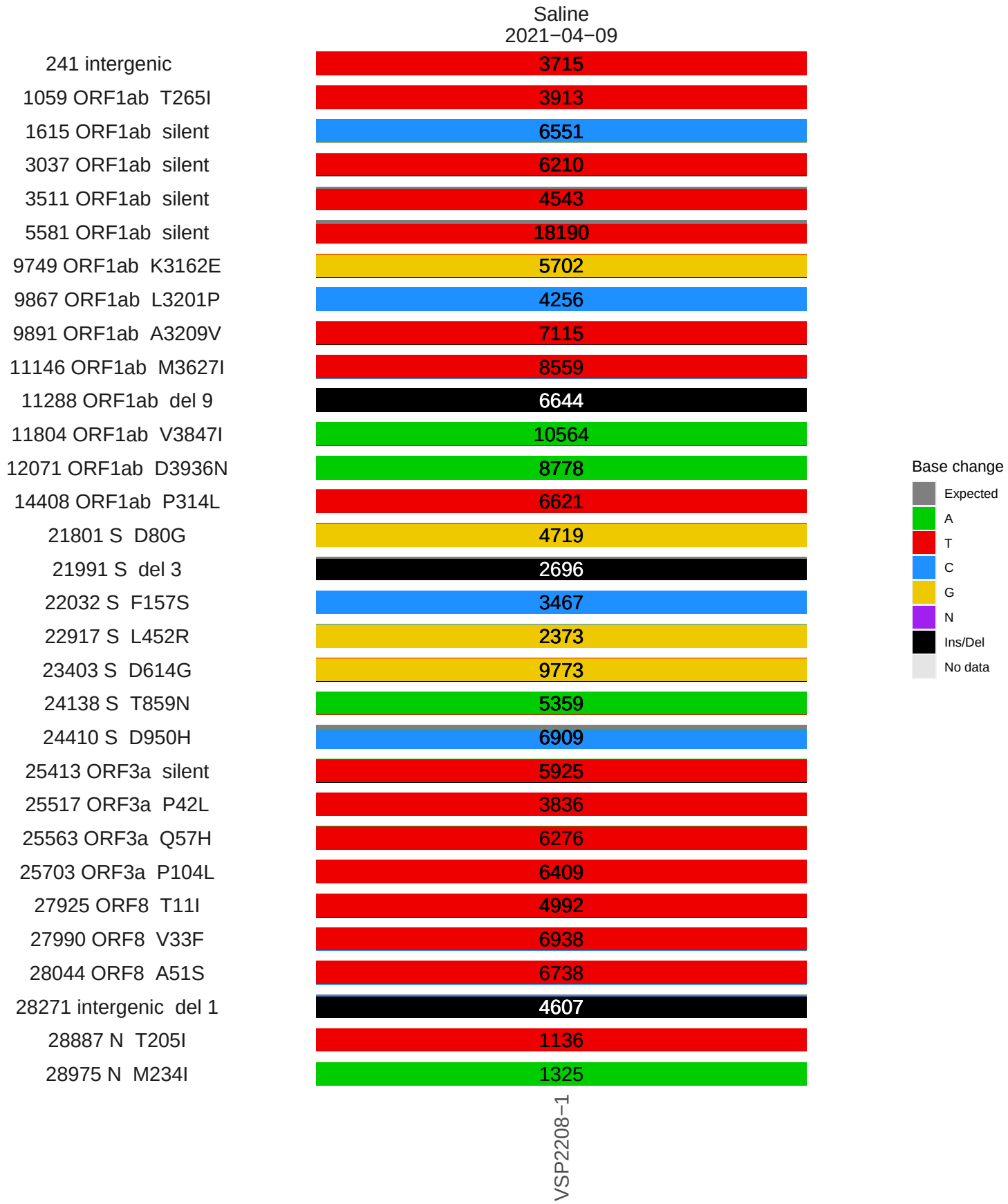
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2208-1	single experiment	NA	Saline	2021-04-09	29.82	B.1.526.1	99.9%	99.7%

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.

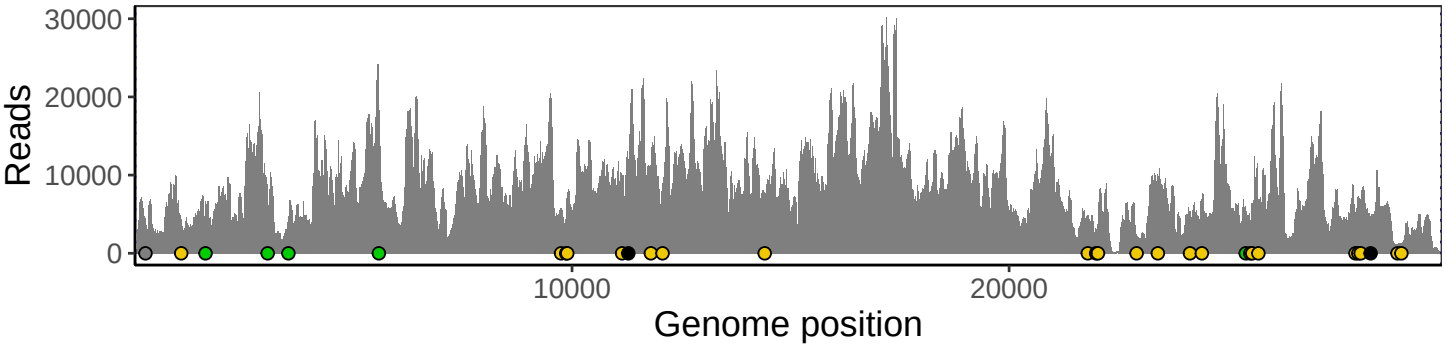



Saline
2021−04−09
241 intergenic
3715
1059 ORF1ab T265I
3913
1615 ORF1ab silent
6551
3037 ORF1ab silent
6210
3511 ORF1ab silent
4543
5581 ORF1ab silent
18190
9749 ORF1ab K3162E
5702
9867 ORF1ab L3201P
4256
9891 ORF1ab A3209V
7115
11146 ORF1ab M3627I
8559
11288 ORF1ab del 9
6644
11804 ORF1ab V3847I
10564
12071 ORF1ab D3936N
8778
14408 ORF1ab P314L
6621
21801 S D80G
4719
21991 S del 3
2696
22032 S F157S
3467
22917 S L452R
2373
23403 S D614G
9773
24138 S T859N
5359
24410 S D950H
6909
25413 ORF3a silent
5925
25517 ORF3a P42L
3836
25563 ORF3a Q57H
6276
25703 ORF3a P104L
6409
27925 ORF8 T11I
4992
27990 ORF8 V33F
6938
28044 ORF8 A51S
6738
28271 intergenic del 1
4607
28887 N T205I
1136
28975 N M234I
1325
VSP2208−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

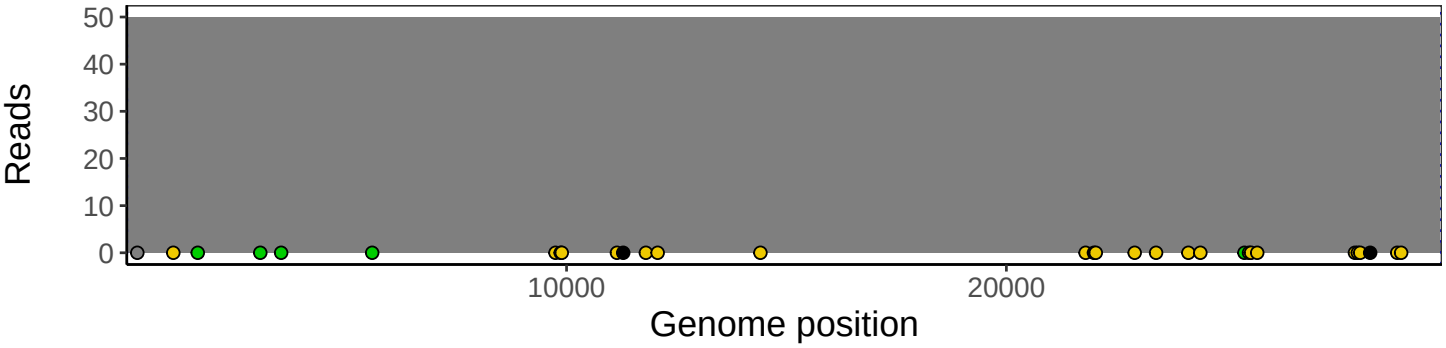
Analyses of individual experiments and composite results

VSP2208-1 | 2021-04-09 | Saline | UPHS-0996 | genomes | single experiment

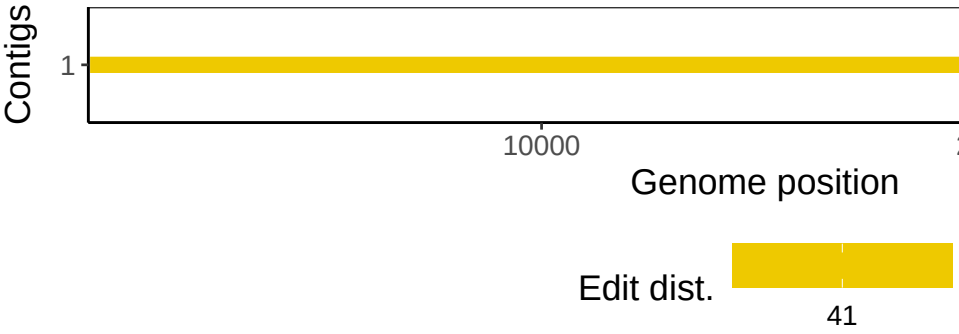
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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