COVID-19 subject UPHS-0098

2021-04-17

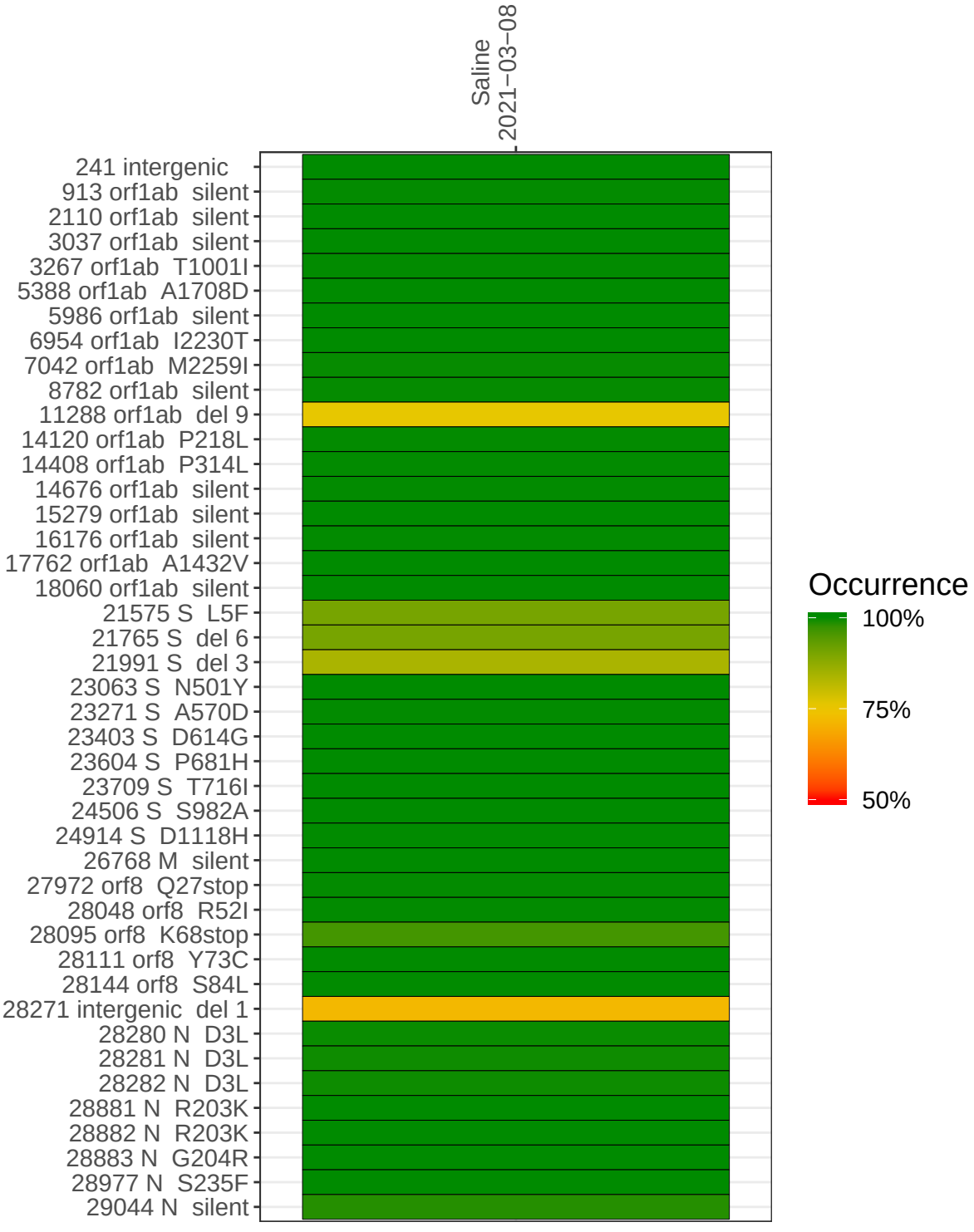
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

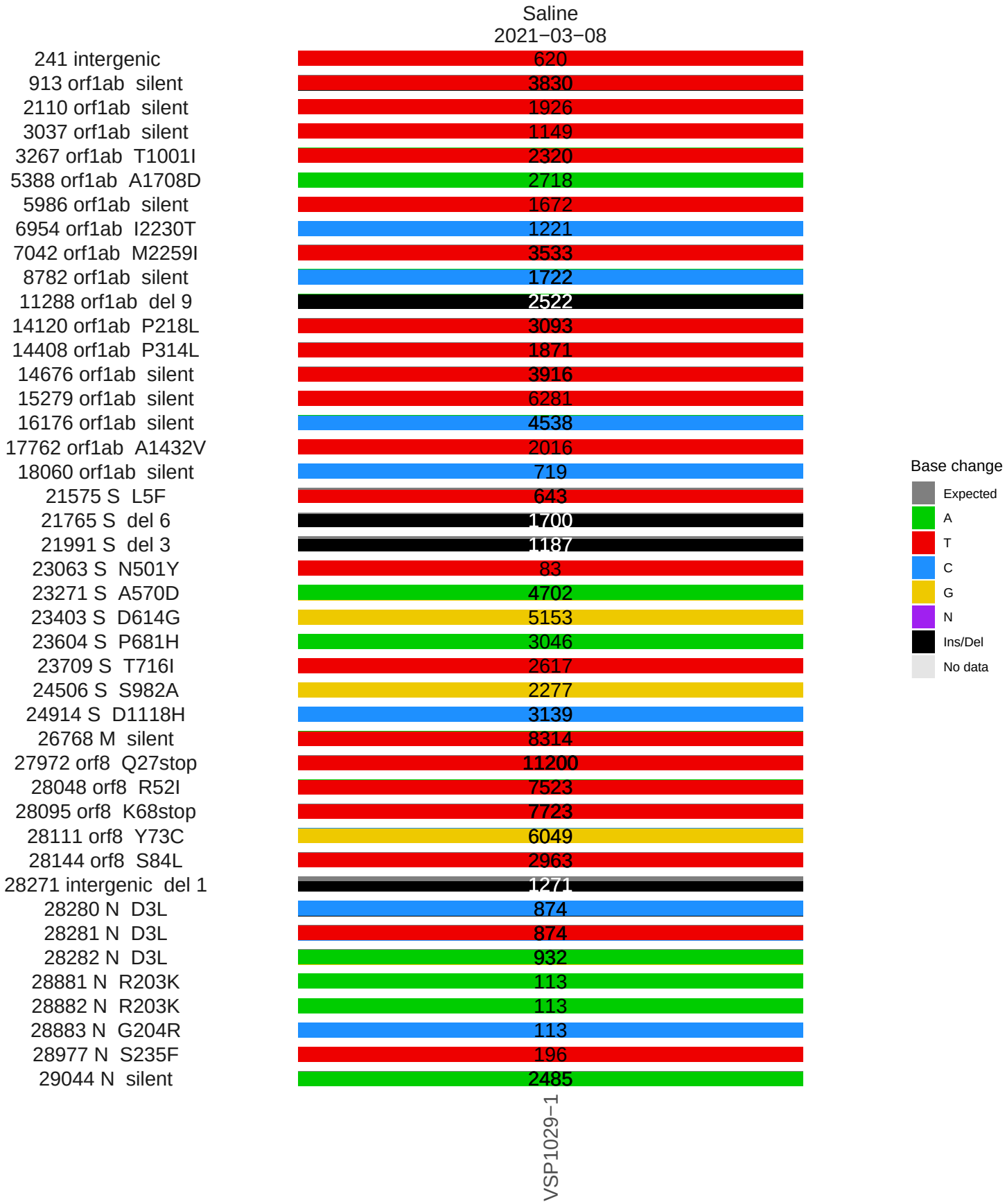
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1029-1	single experiment	NA	Saline	2021-03-08	29.87	B.1.1.7	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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.

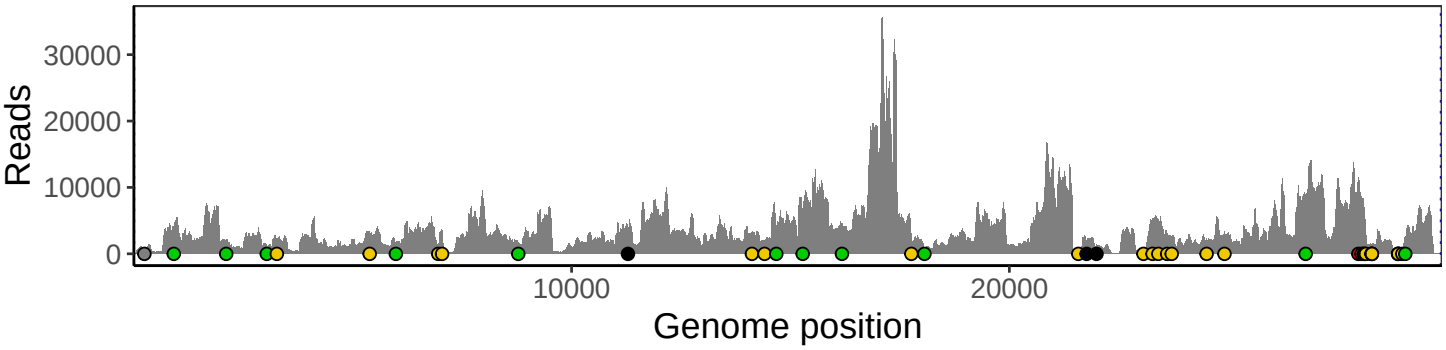



Saline
2021−03−08
241 intergenic 620
913 orf1ab silent 3830
2110 orf1ab silent 1926
3037 orf1ab silent 1149
3267 orf1ab T1001I 2320
5388 orf1ab A1708D 2718
5986 orf1ab silent 1672
6954 orf1ab I2230T 1221
7042 orf1ab M2259I 3533
8782 orf1ab silent 1722
11288 orf1ab del 9 2522
14120 orf1ab P218L 3093
14408 orf1ab P314L 1871
14676 orf1ab silent 3916
15279 orf1ab silent 6281
16176 orf1ab silent 4538
17762 orf1ab A1432V 2016
18060 orf1ab silent 719
21575 S L5F 643
21765 S del 6 1700
21991 S del 3 1187
23063 S N501Y 83
23271 S A570D 4702
23403 S D614G 5153
23604 S P681H 3046
23709 S T716I 2617
24506 S S982A 2277
24914 S D1118H 3139
26768 M silent 8314
27972 orf8 Q27stop 11200
28048 orf8 R52I 7523
28095 orf8 K68stop 7723
28111 orf8 Y73C 6049
28144 orf8 S84L 2963
28271 intergenic del 1 1271
28280 N D3L 874
28281 N D3L 874
28282 N D3L 932
28881 N R203K 113
28882 N R203K 113
28883 N G204R 113
28977 N S235F 196
29044 N silent 2485
VSP1029−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

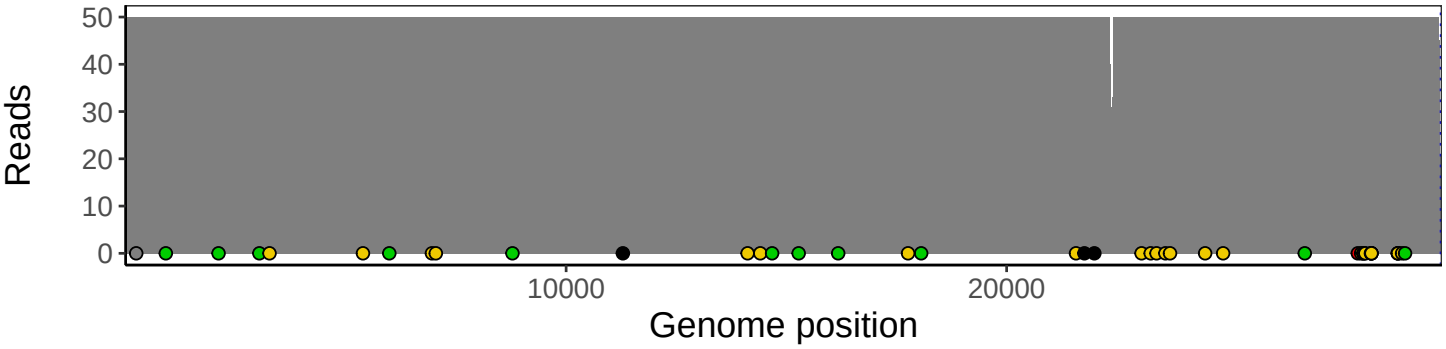
Analyses of individual experiments and composite results

VSP1029-1 | 2021-03-08 | Saline | UPHS-0098 | genomes | single experiment

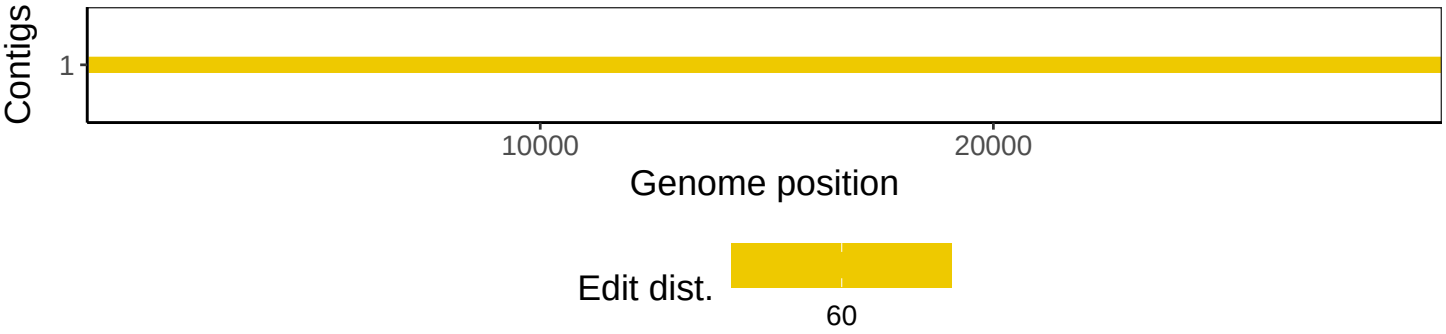
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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