COVID-19 subject UPHS-0094

2021-04-17

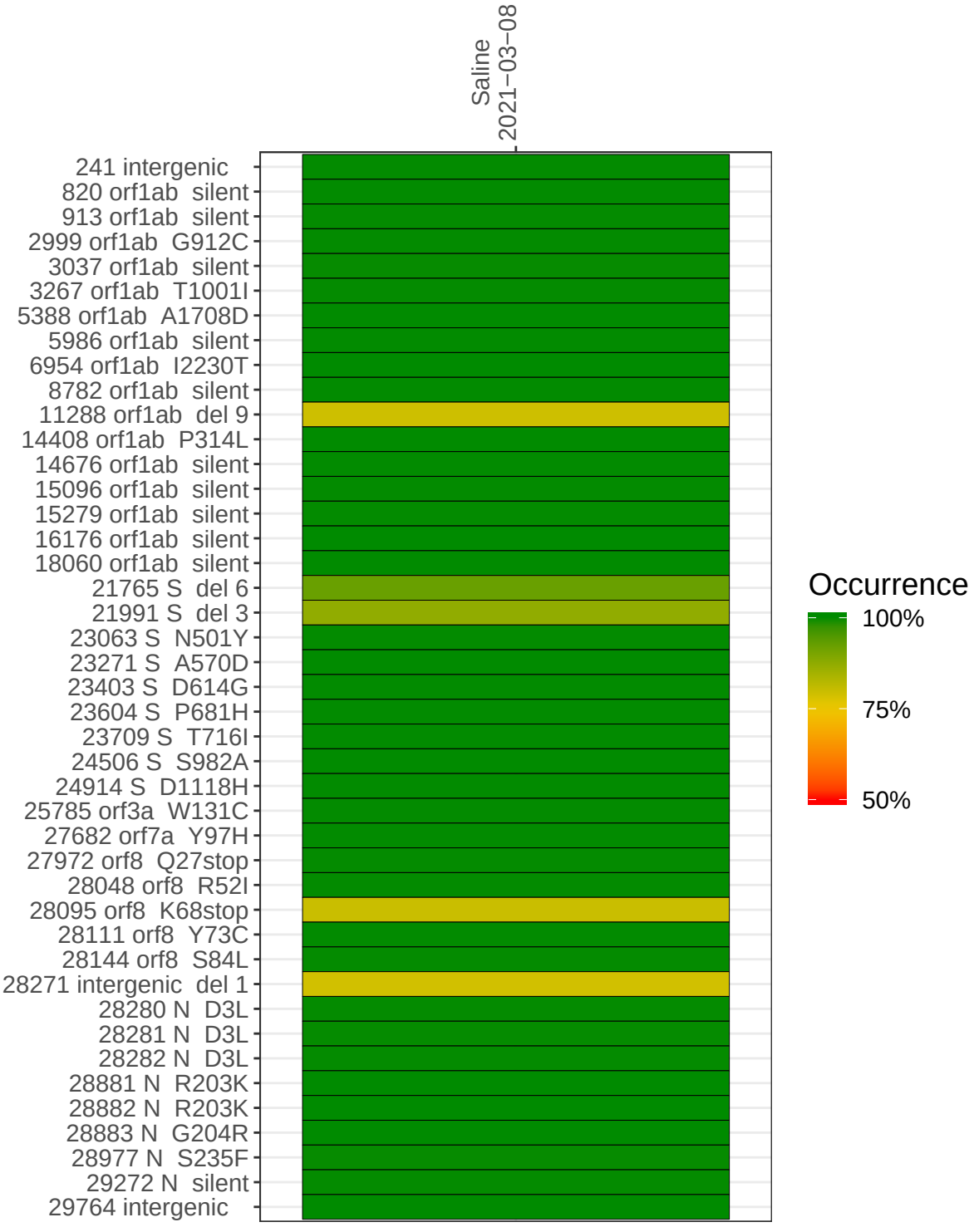
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

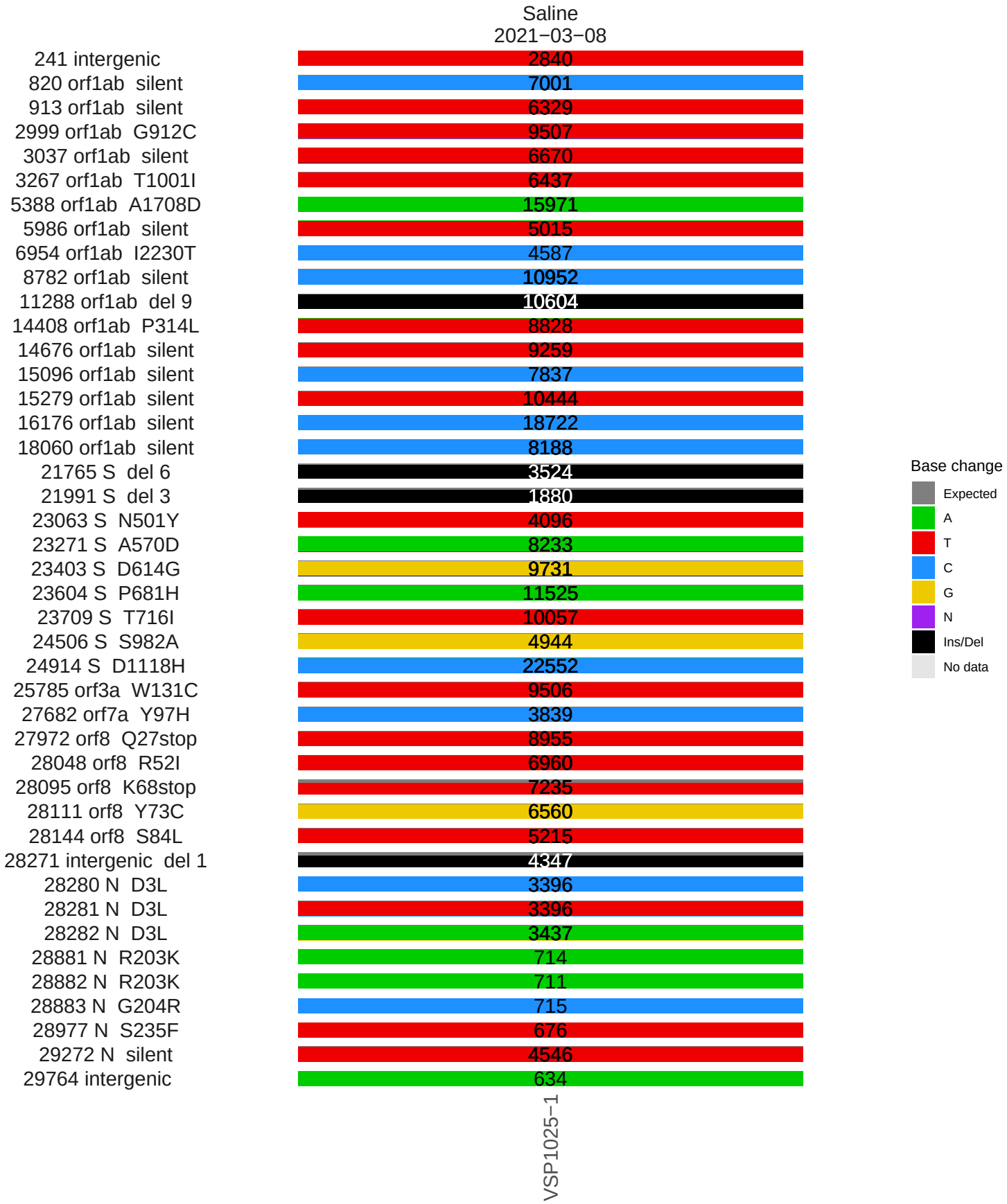
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1025-1	single experiment	NA	Saline	2021-03-08	29.88	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.

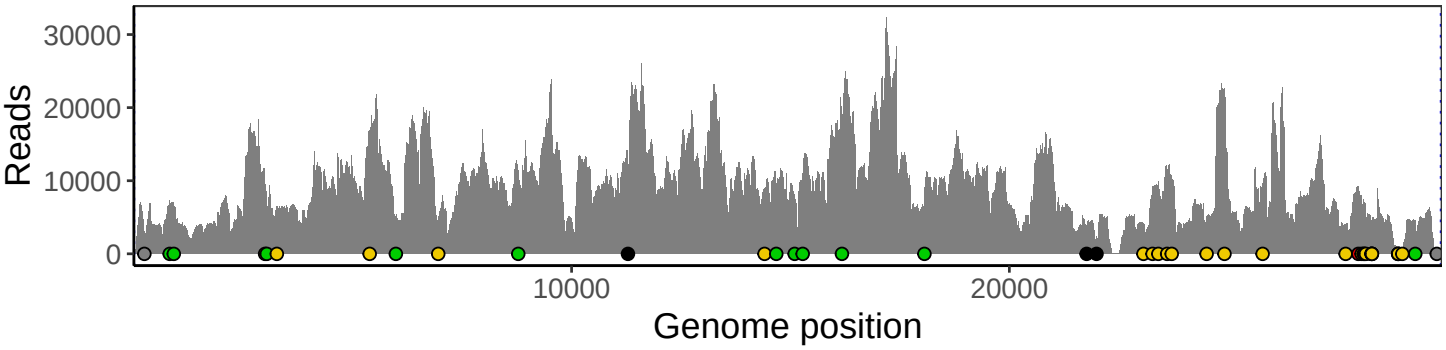



Saline
2021−03−08
241 intergenic 2840
820 orf1ab silent 7001
913 orf1ab silent 6329
2999 orf1ab G912C 9507
3037 orf1ab silent 6670
3267 orf1ab T1001I 6437
5388 orf1ab A1708D 15971
5986 orf1ab silent 5015
6954 orf1ab I2230T 4587
8782 orf1ab silent 10952
11288 orf1ab del 9 10604
14408 orf1ab P314L 8828
14676 orf1ab silent 9259
15096 orf1ab silent 7837
15279 orf1ab silent 10444
16176 orf1ab silent 18722
18060 orf1ab silent 8188
21765 S del 6 3524
21991 S del 3 1880
23063 S N501Y 4096
23271 S A570D 8233
23403 S D614G 9731
23604 S P681H 11525
23709 S T716I 10057
24506 S S982A 4944
24914 S D1118H 22552
25785 orf3a W131C 9506
27682 orf7a Y97H 3839
27972 orf8 Q27stop 8955
28048 orf8 R52I 6960
28095 orf8 K68stop 7235
28111 orf8 Y73C 6560
28144 orf8 S84L 5215
28271 intergenic del 1 4347
28280 N D3L 3396
28281 N D3L 3396
28282 N D3L 3437
28881 N R203K 714
28882 N R203K 711
28883 N G204R 715
28977 N S235F 676
29272 N silent 4546
29764 intergenic 634
VSP1025−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

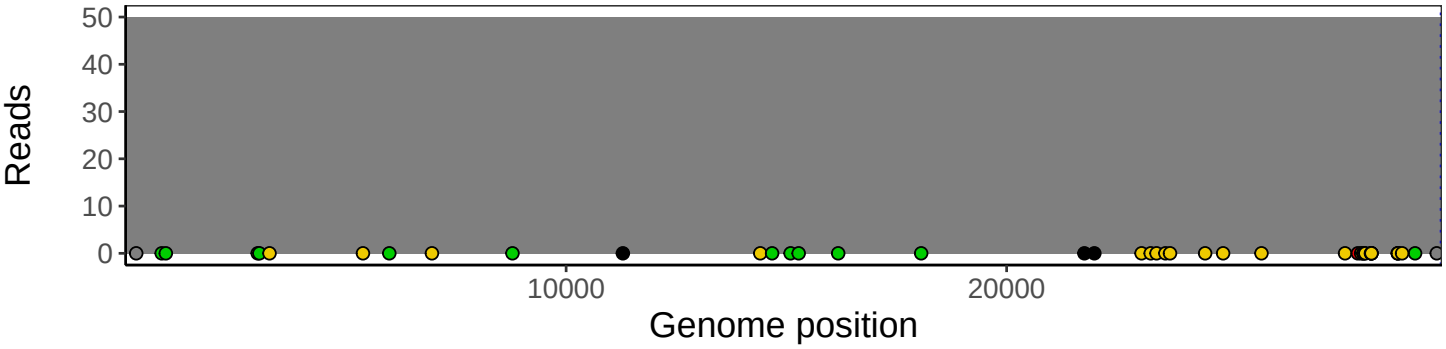
Analyses of individual experiments and composite results

VSP1025-1 | 2021-03-08 | Saline | UPHS-0094 | genomes | single experiment

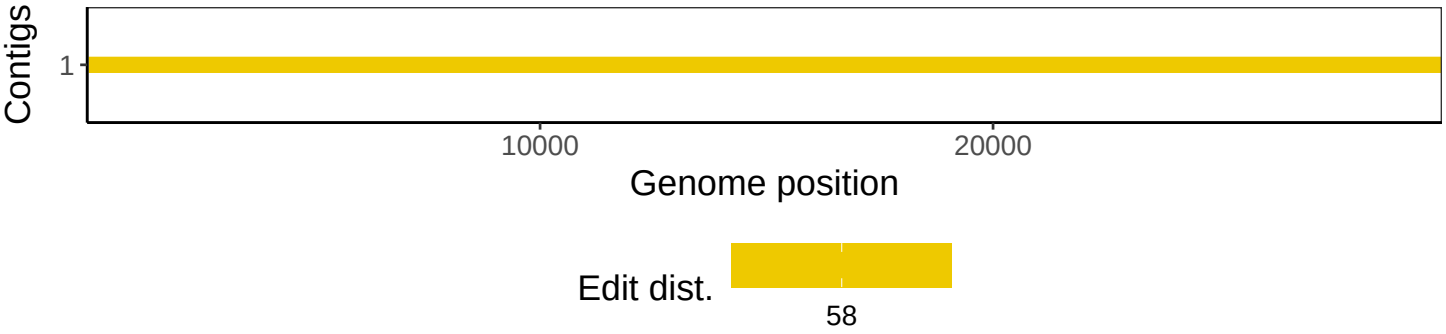
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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