COVID-19 subject UPHS-0059

2021-03-25

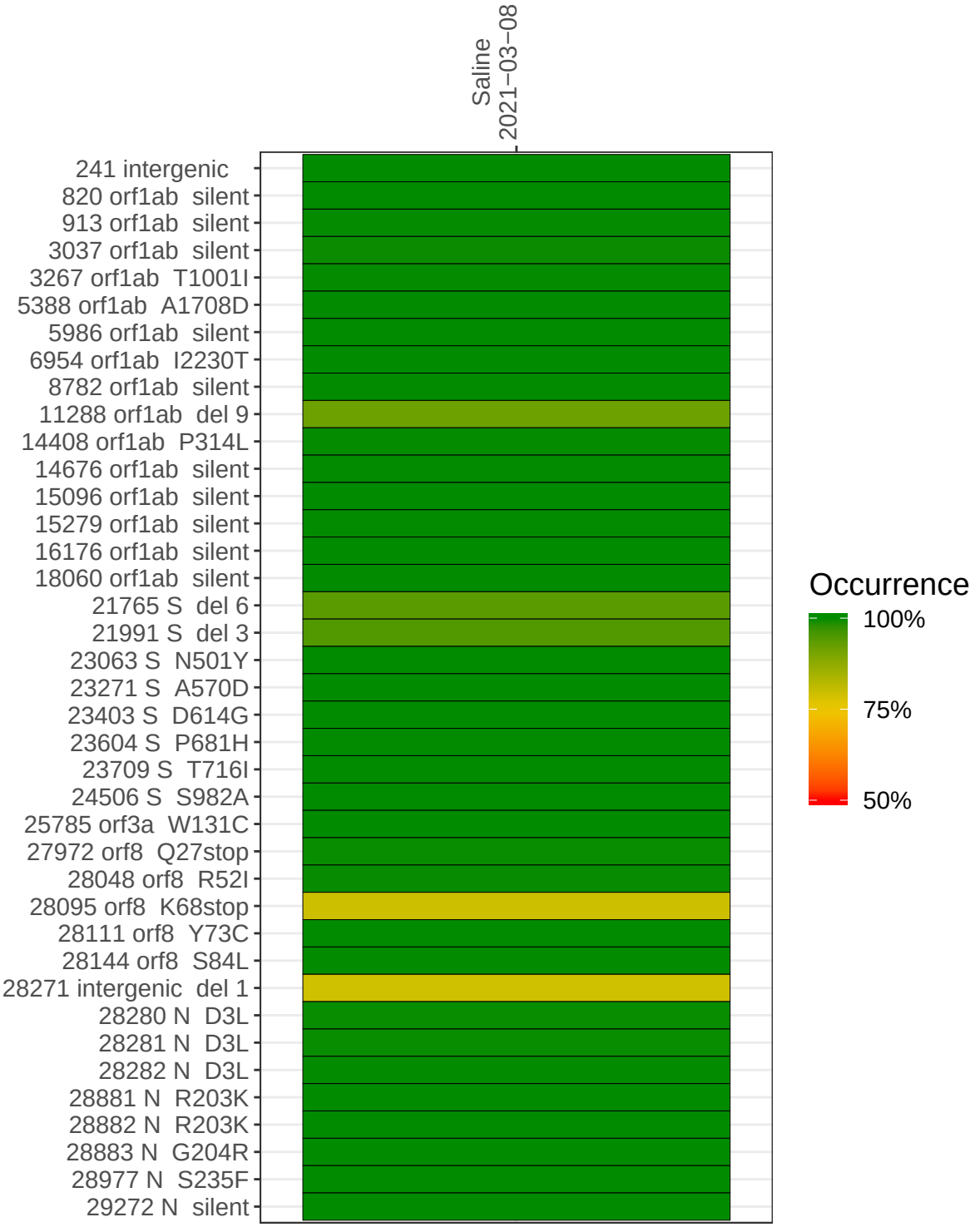
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

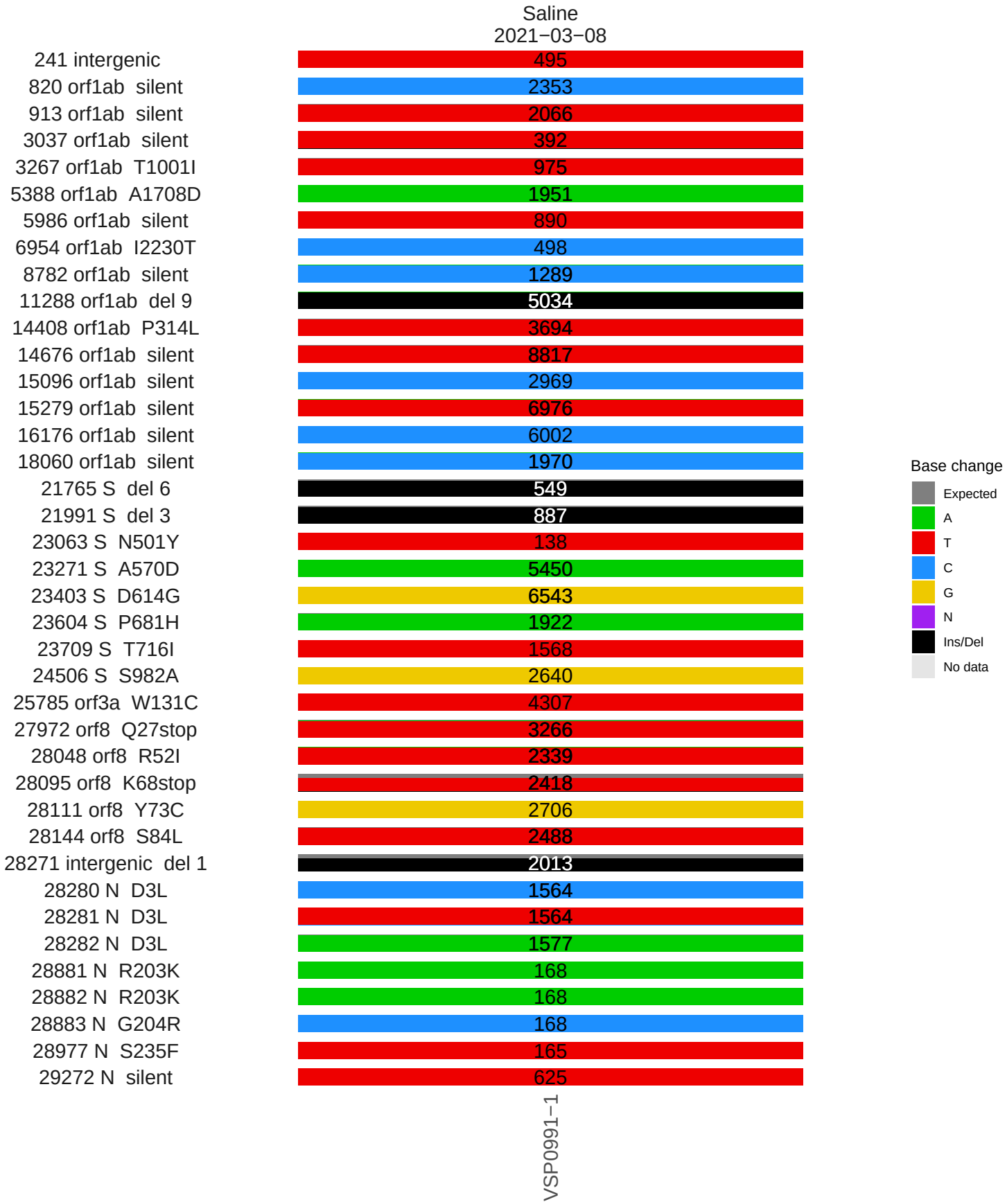
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0991-1	single experiment	NA	Saline	2021-03-08	15.90	B.1.1.7	93.2%	93.1%

Variants shared across samples

The heat map below shows how variants (reference genome 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.

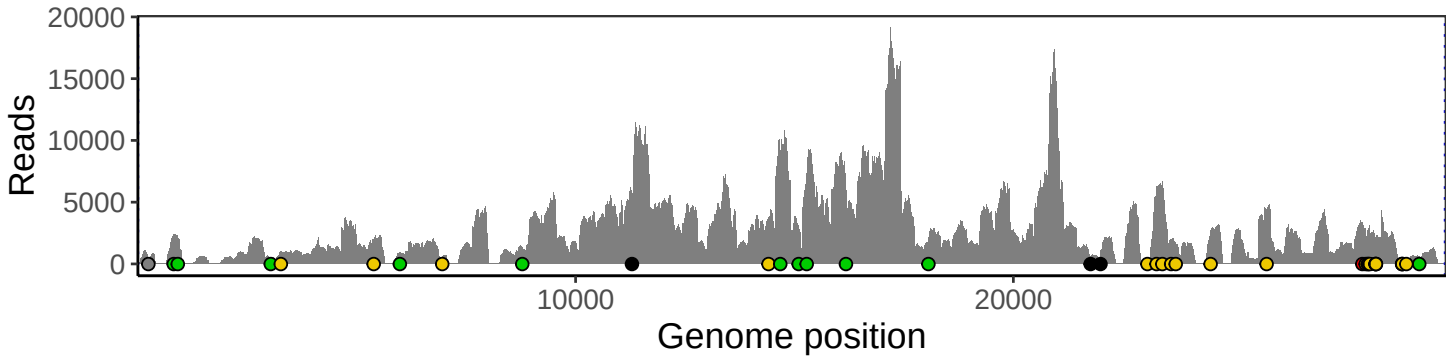



Saline
2021−03−08
241 intergenic 495
820 orf1ab silent 2353
913 orf1ab silent 2066
3037 orf1ab silent 392
3267 orf1ab T1001I 975
5388 orf1ab A1708D 1951
5986 orf1ab silent 890
6954 orf1ab I2230T 498
8782 orf1ab silent 1289
11288 orf1ab del 9 5034
14408 orf1ab P314L 3694
14676 orf1ab silent 8817
15096 orf1ab silent 2969
15279 orf1ab silent 6976
16176 orf1ab silent 6002
18060 orf1ab silent 1970
21765 S del 6 549
21991 S del 3 887
23063 S N501Y 138
23271 S A570D 5450
23403 S D614G 6543
23604 S P681H 1922
23709 S T716I 1568
24506 S S982A 2640
25785 orf3a W131C 4307
27972 orf8 Q27stop 3266
28048 orf8 R52I 2339
28095 orf8 K68stop 2418
28111 orf8 Y73C 2706
28144 orf8 S84L 2488
28271 intergenic del 1 2013
28280 N D3L 1564
28281 N D3L 1564
28282 N D3L 1577
28881 N R203K 168
28882 N R203K 168
28883 N G204R 168
28977 N S235F 165
29272 N silent 625
VSP0991−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

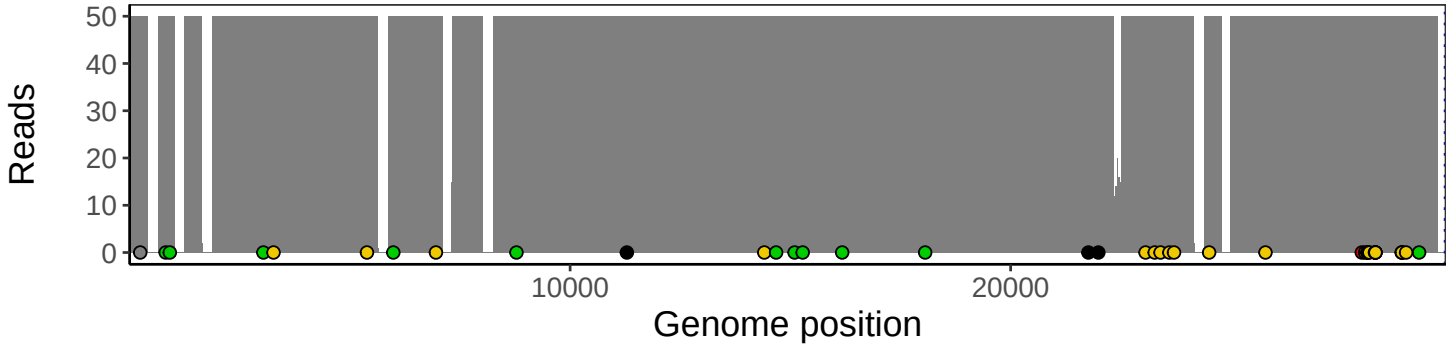
Analyses of individual experiments and composite results

VSP0991-1 | 2021-03-08 | Saline | UPHS-0059 | genomes | single experiment

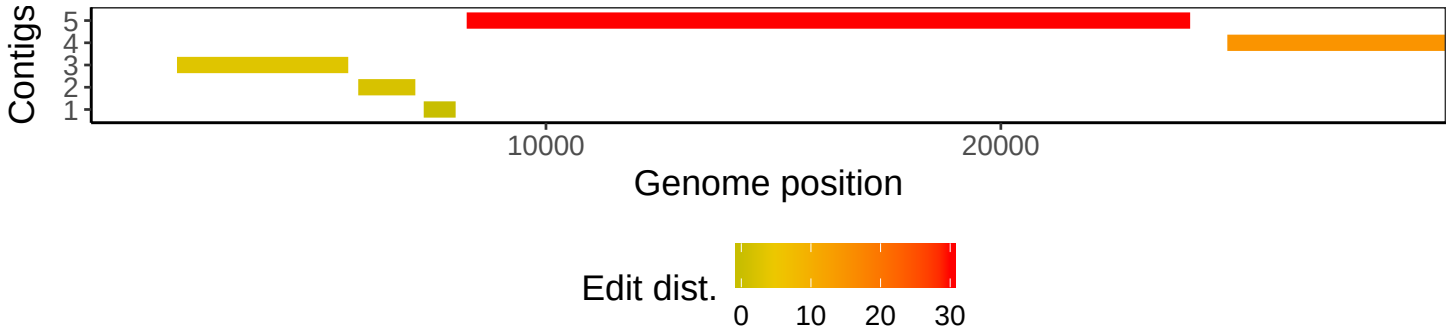
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
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