COVID-19 subject UPHS-0331

2021-04-17

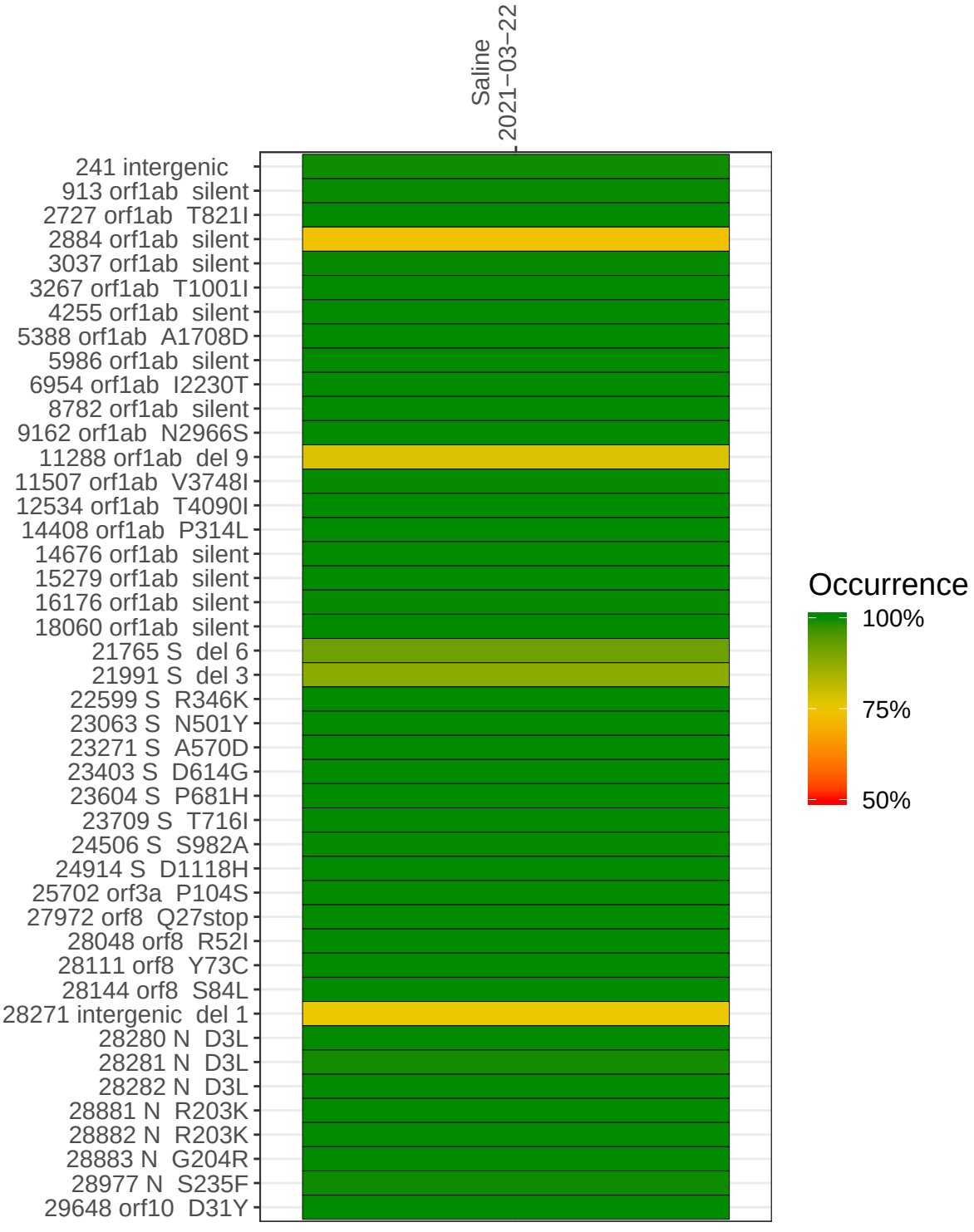
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

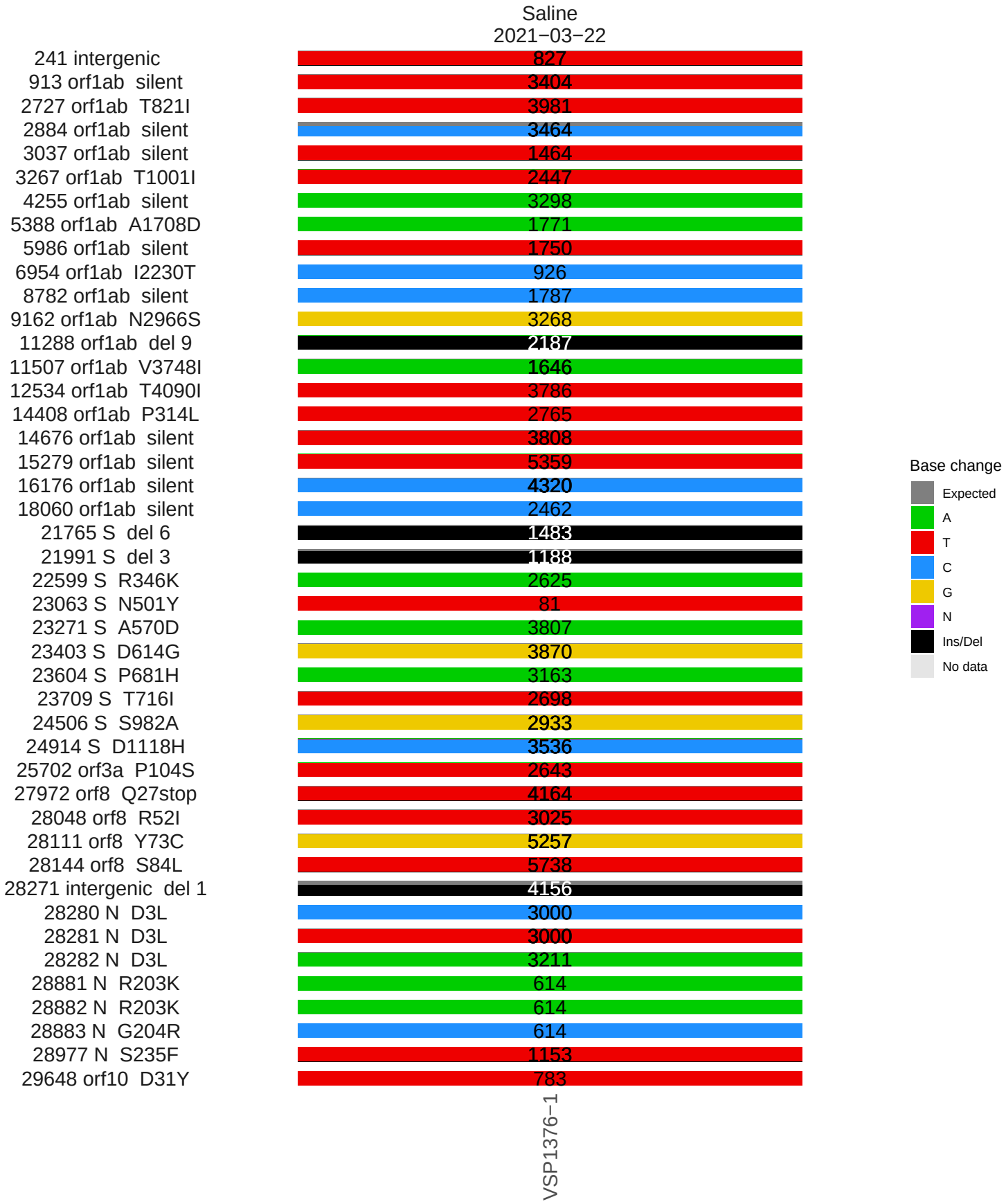
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1376-1	single experiment	NA	Saline	2021-03-22	29.81	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.

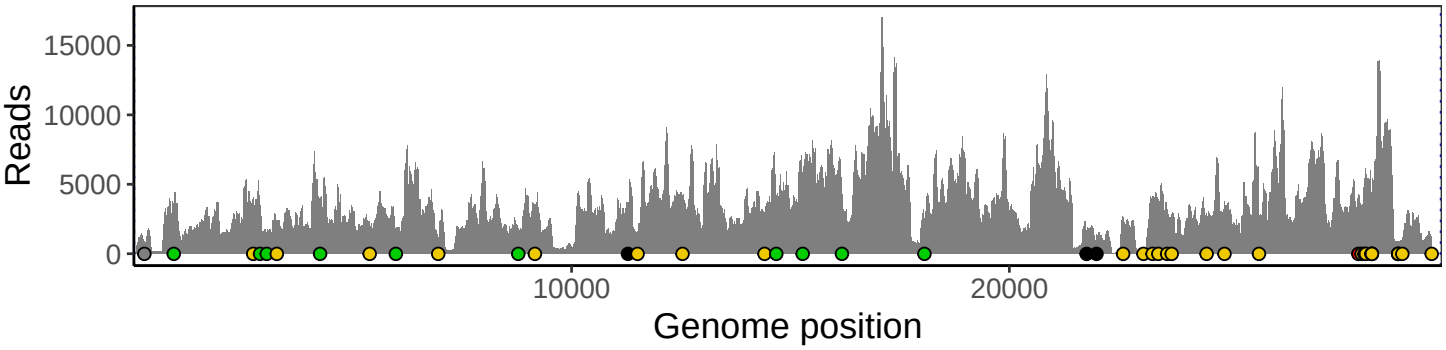



Saline
2021−03−22
241 intergenic 827
913 orf1ab silent 3404
2727 orf1ab T821I 3981
2884 orf1ab silent 3464
3037 orf1ab silent 1464
3267 orf1ab T1001I 2447
4255 orf1ab silent 3298
5388 orf1ab A1708D 1771
5986 orf1ab silent 1750
6954 orf1ab I2230T 926
8782 orf1ab silent 1787
9162 orf1ab N2966S 3268
11288 orf1ab del 9 2187
11507 orf1ab V3748I 1646
12534 orf1ab T4090I 3786
14408 orf1ab P314L 2765
14676 orf1ab silent 3808
15279 orf1ab silent 5359
16176 orf1ab silent 4320
18060 orf1ab silent 2462
21765 S del 6 1483
21991 S del 3 1188
22599 S R346K 2625
23063 S N501Y 81
23271 S A570D 3807
23403 S D614G 3870
23604 S P681H 3163
23709 S T716I 2698
24506 S S982A 2933
24914 S D1118H 3536
25702 orf3a P104S 2643
27972 orf8 Q27stop 4164
28048 orf8 R52I 3025
28111 orf8 Y73C 5257
28144 orf8 S84L 5738
28271 intergenic del 1 4156
28280 N D3L 3000
28281 N D3L 3000
28282 N D3L 3211
28881 N R203K 614
28882 N R203K 614
28883 N G204R 614
28977 N S235F 1153
29648 orf10 D31Y 783
VSP1376−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

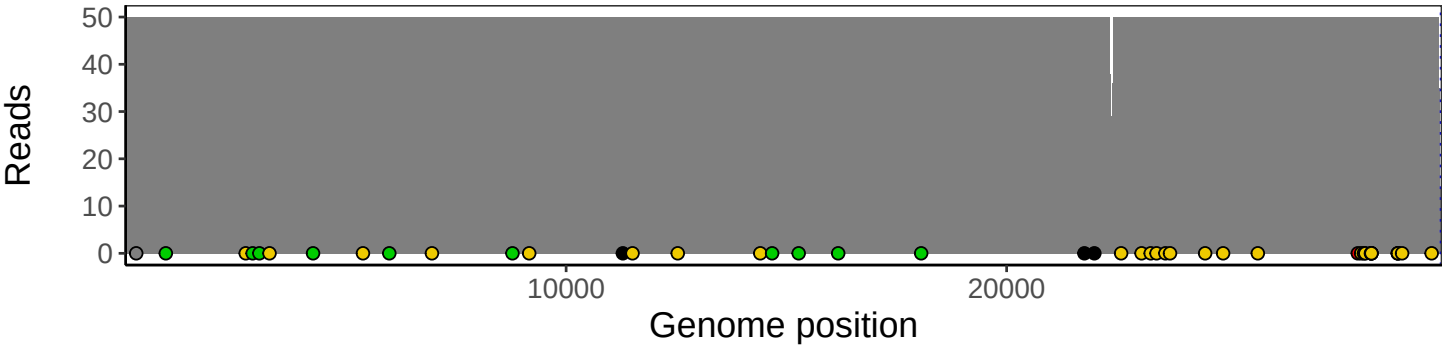
Analyses of individual experiments and composite results

VSP1376-1 | 2021-03-22 | Saline | UPHS-0331 | genomes | single experiment

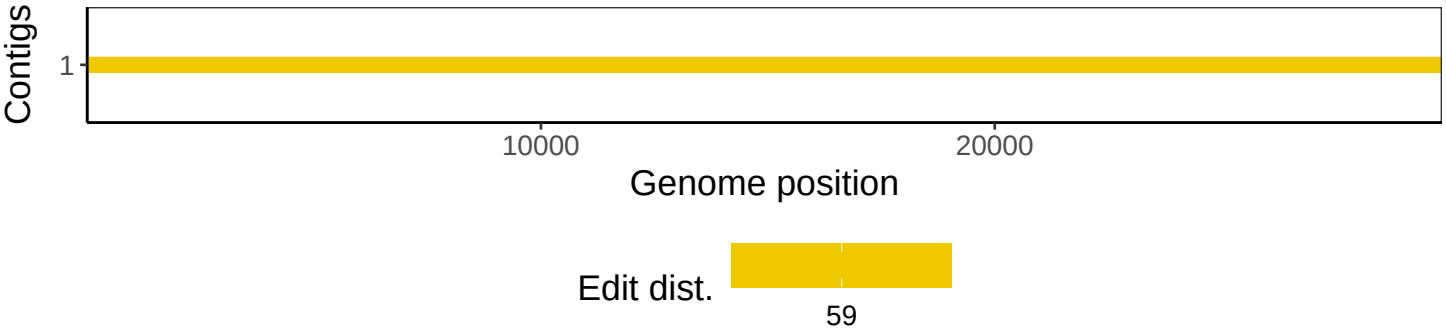
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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