COVID-19 subject UPHS-0223

2021-04-17

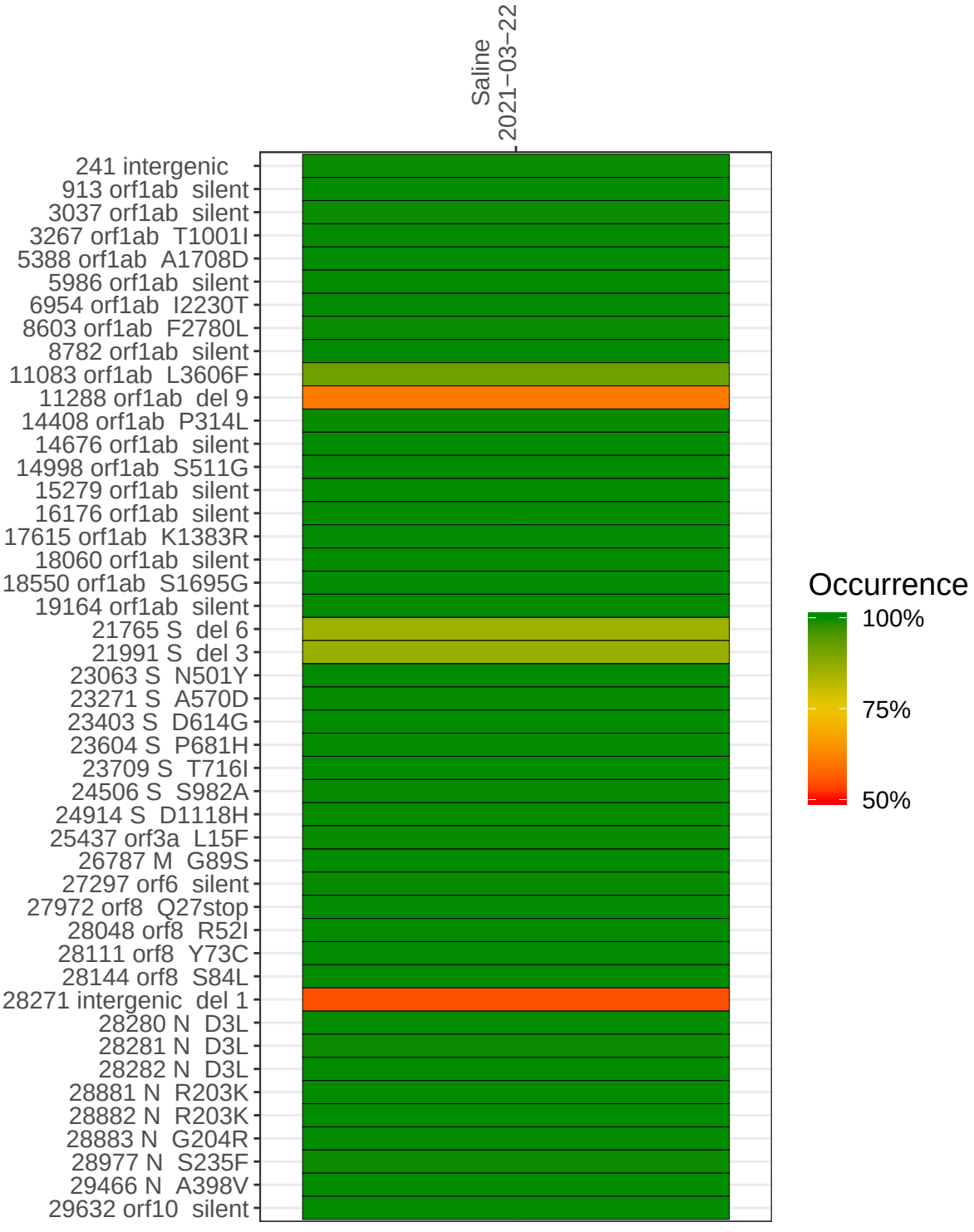
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

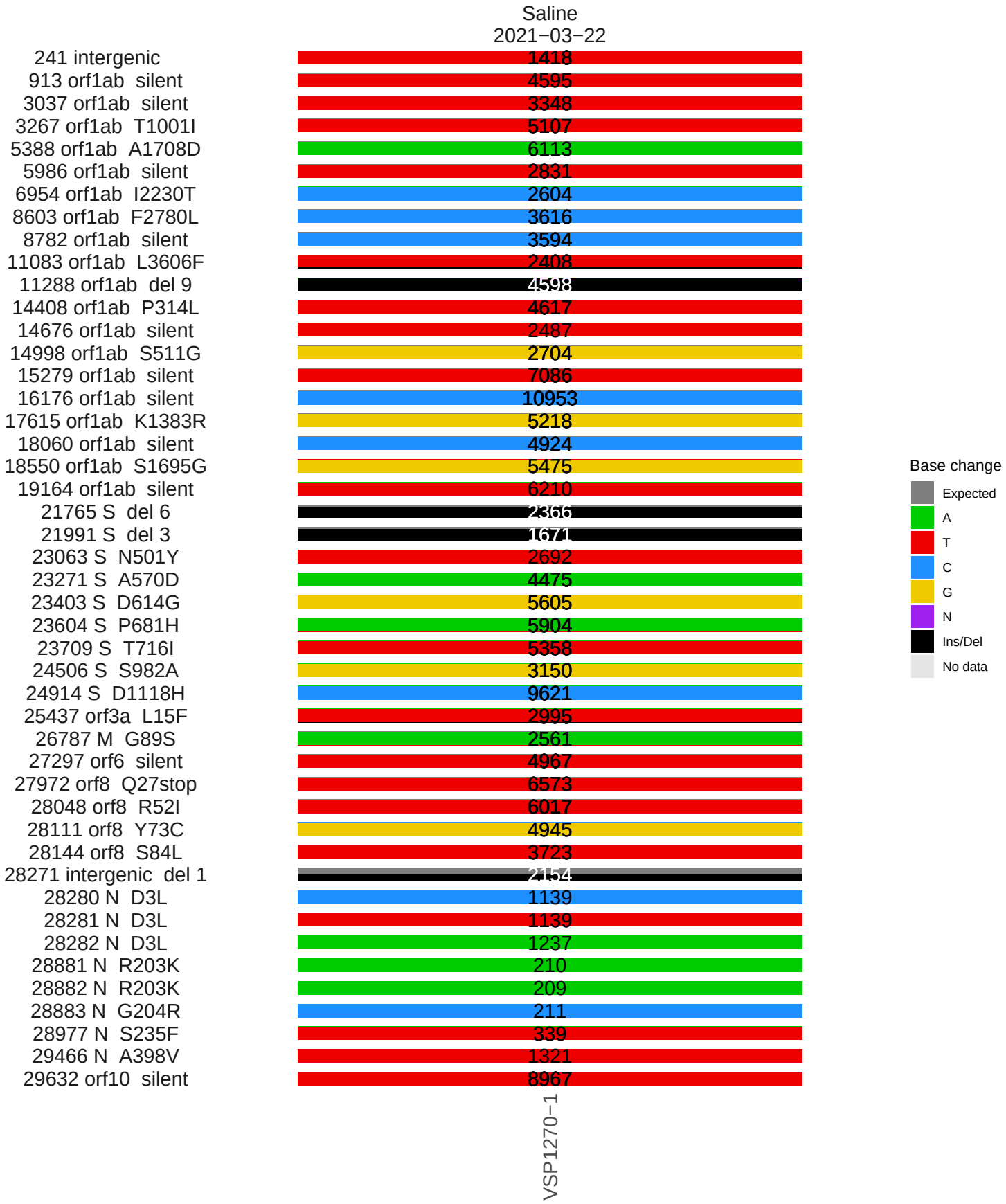
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1270-1	single experiment	NA	Saline	2021-03-22	29.88	B.1.1.7	99.9%	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.

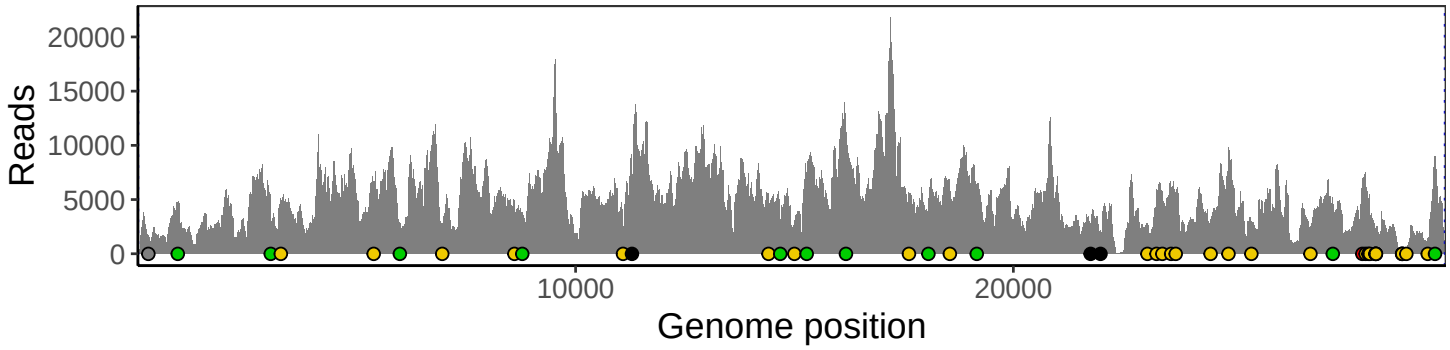



Saline
2021−03−22
241 intergenic 1418
913 orf1ab silent 4595
3037 orf1ab silent 3348
3267 orf1ab T1001I 5107
5388 orf1ab A1708D 6113
5986 orf1ab silent 2831
6954 orf1ab I2230T 2604
8603 orf1ab F2780L 3616
8782 orf1ab silent 3594
11083 orf1ab L3606F 2408
11288 orf1ab del 9 4598
14408 orf1ab P314L 4617
14676 orf1ab silent 2487
14998 orf1ab S511G 2704
15279 orf1ab silent 7086
16176 orf1ab silent 10953
17615 orf1ab K1383R 5218
18060 orf1ab silent 4924
18550 orf1ab S1695G 5475
19164 orf1ab silent 6210
21765 S del 6 2366
21991 S del 3 1671
23063 S N501Y 2692
23271 S A570D 4475
23403 S D614G 5605
23604 S P681H 5904
23709 S T716I 5358
24506 S S982A 3150
24914 S D1118H 9621
25437 orf3a L15F 2995
26787 M G89S 2561
27297 orf6 silent 4967
27972 orf8 Q27stop 6573
28048 orf8 R52I 6017
28111 orf8 Y73C 4945
28144 orf8 S84L 3723
28271 intergenic del 1 2154
28280 N D3L 1139
28281 N D3L 1139
28282 N D3L 1237
28881 N R203K 210
28882 N R203K 209
28883 N G204R 211
28977 N S235F 339
29466 N A398V 1321
29632 orf10 silent 8967
VSP1270−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

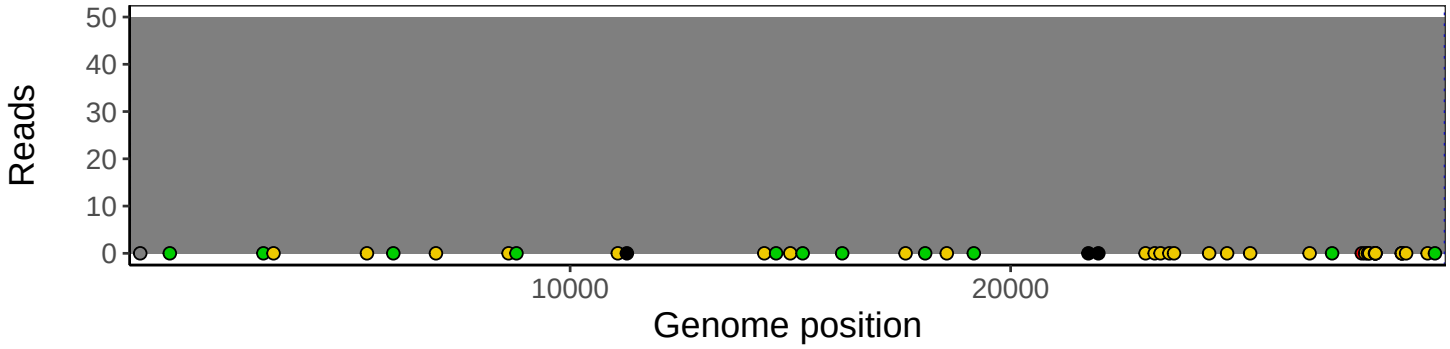
Analyses of individual experiments and composite results

VSP1270-1 | 2021-03-22 | Saline | UPHS-0223 | genomes | single experiment

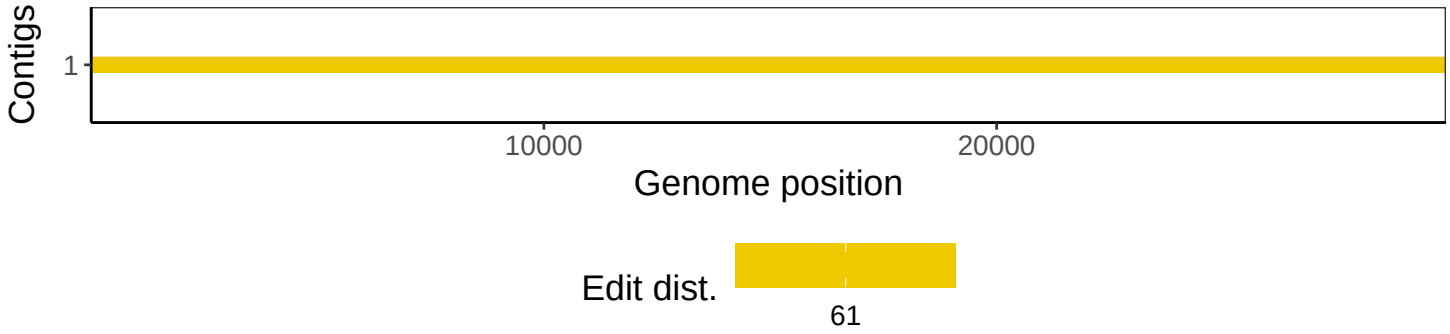
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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