COVID-19 subject UPHS-0240

2021-04-17

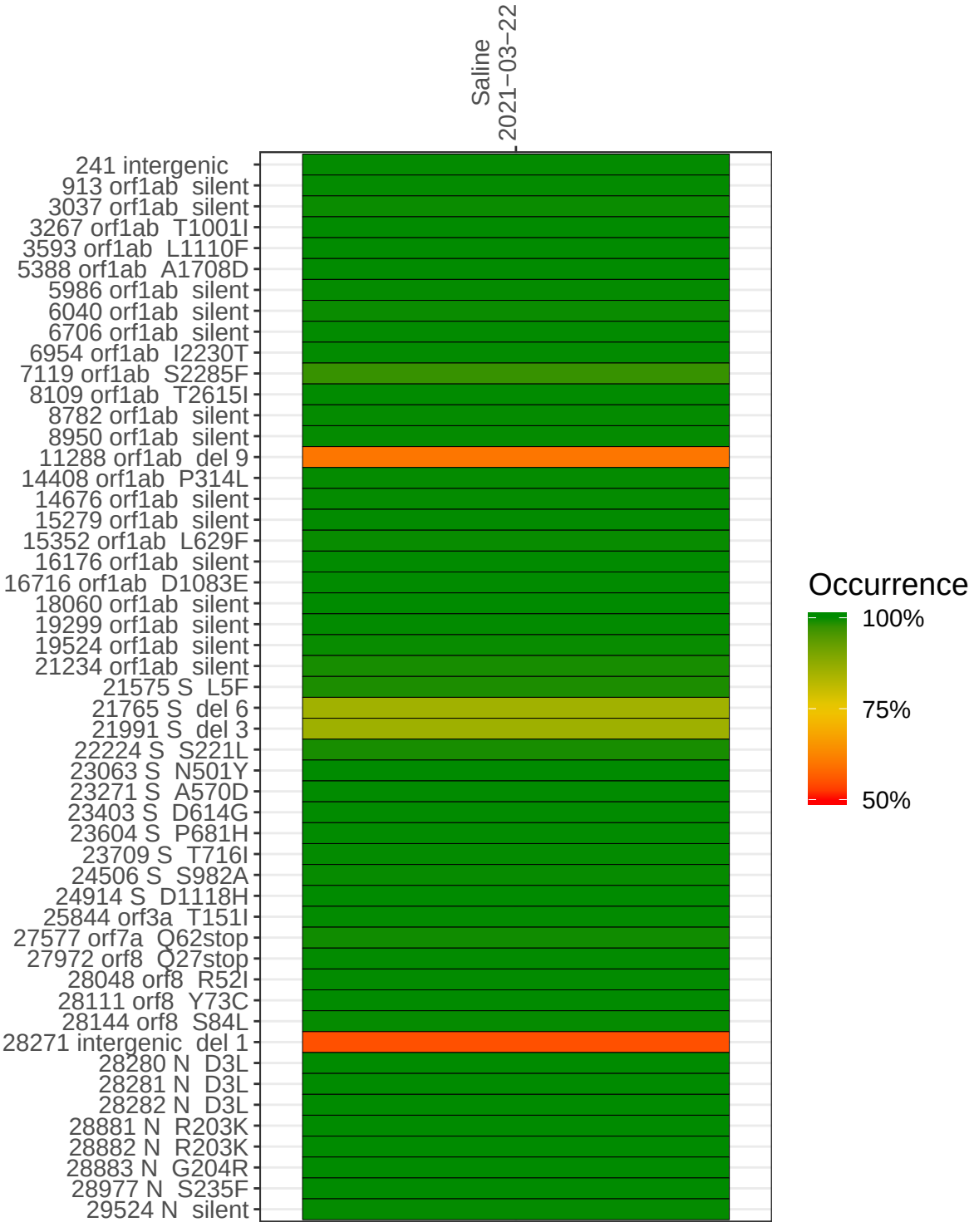
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

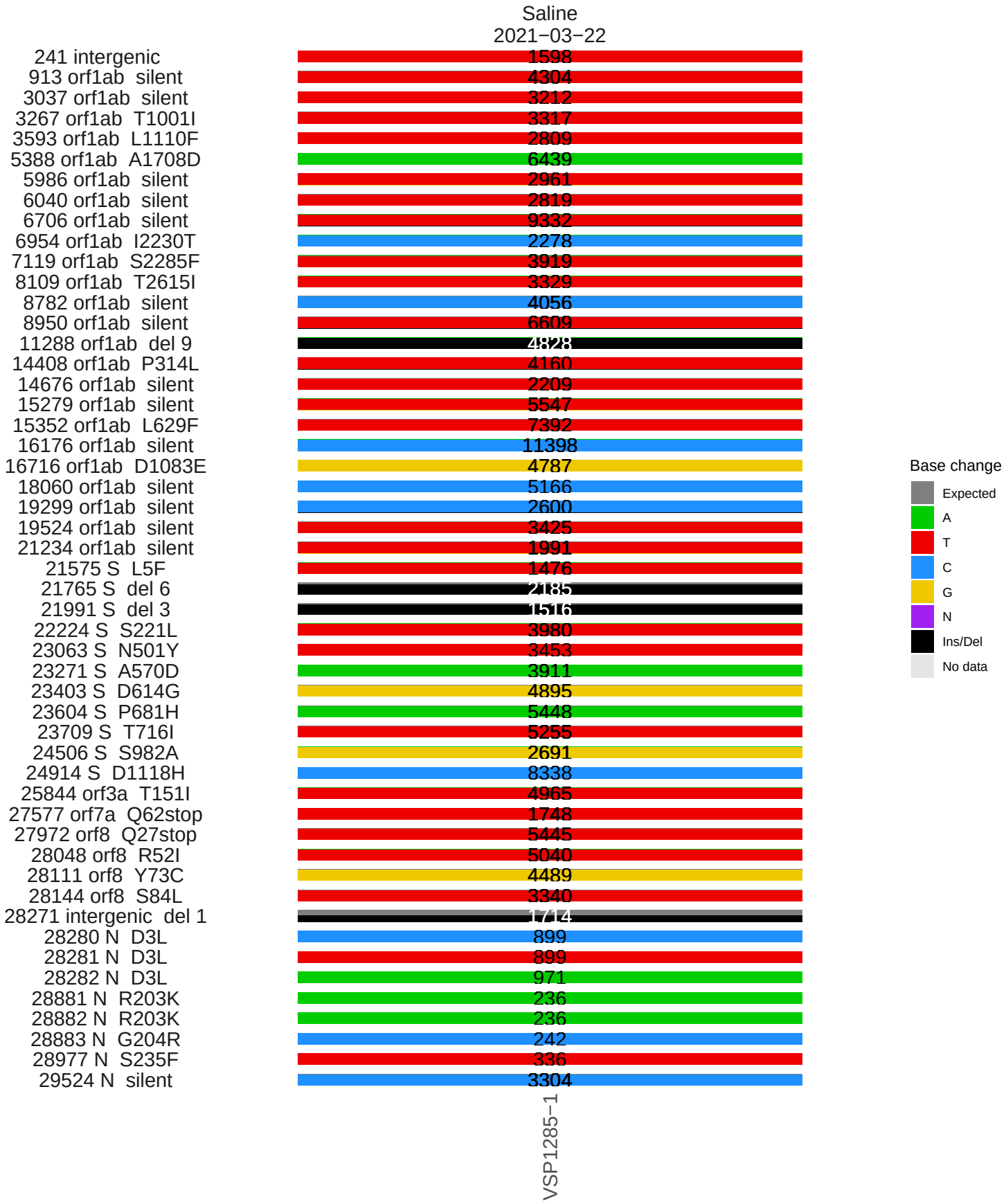
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1285-1	single experiment	NA	Saline	2021-03-22	29.85	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.

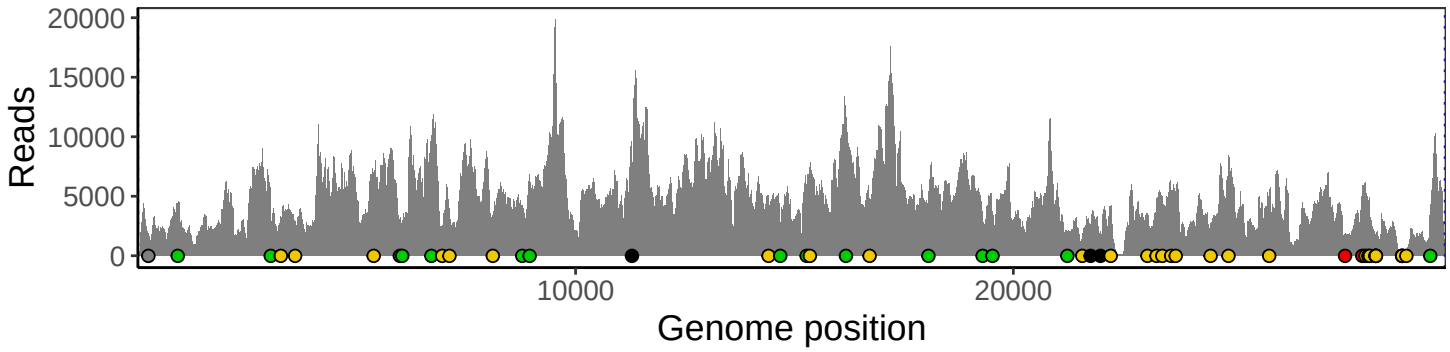



Saline
2021−03−22
241 intergenic 1598
913 orf1ab silent 4304
3037 orf1ab silent 3212
3267 orf1ab T1001I 3317
3593 orf1ab L1110F 2809
5388 orf1ab A1708D 6439
5986 orf1ab silent 2961
6040 orf1ab silent 2819
6706 orf1ab silent 9332
6954 orf1ab I2230T 2278
7119 orf1ab S2285F 3919
8109 orf1ab T2615I 3329
8782 orf1ab silent 4056
8950 orf1ab silent 6609
11288 orf1ab del 9 4828
14408 orf1ab P314L 4160
14676 orf1ab silent 2209
15279 orf1ab silent 5547
15352 orf1ab L629F 7392
16176 orf1ab silent 11398
16716 orf1ab D1083E 4787
18060 orf1ab silent 5166
19299 orf1ab silent 2600
19524 orf1ab silent 3425
21234 orf1ab silent 1991
21575 S L5F 1476
21765 S del 6 2185
21991 S del 3 1516
22224 S S221L 3980
23063 S N501Y 3453
23271 S A570D 3911
23403 S D614G 4895
23604 S P681H 5448
23709 S T716I 5255
24506 S S982A 2691
24914 S D1118H 8338
25844 orf3a T151I 4965
27577 orf7a Q62stop 1748
27972 orf8 Q27stop 5445
28048 orf8 R52I 5040
28111 orf8 Y73C 4489
28144 orf8 S84L 3340
28271 intergenic del 1 1714
28280 N D3L 899
28281 N D3L 899
28282 N D3L 971
28881 N R203K 236
28882 N R203K 236
28883 N G204R 242
28977 N S235F 336
29524 N silent 3304
VSP1285−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

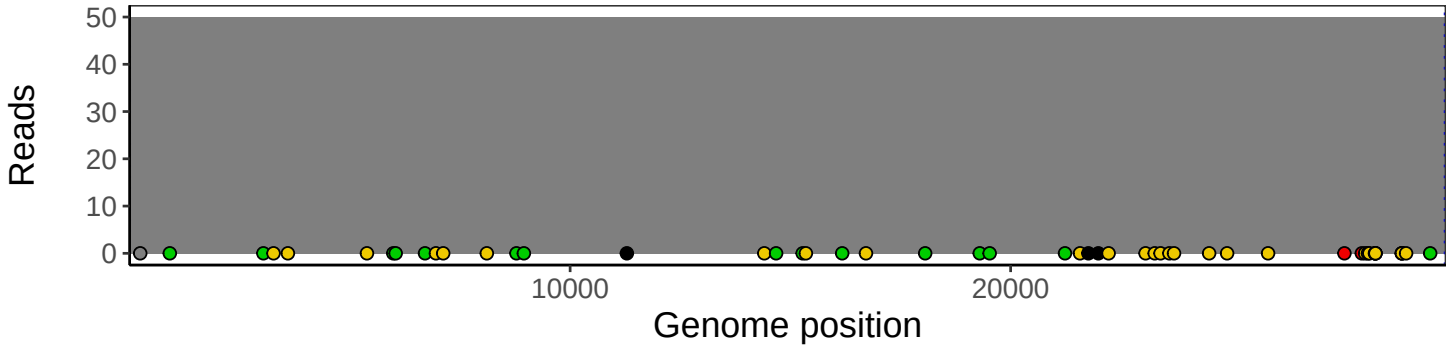
Analyses of individual experiments and composite results

VSP1285-1 | 2021-03-22 | Saline | UPHS-0240 | genomes | single experiment

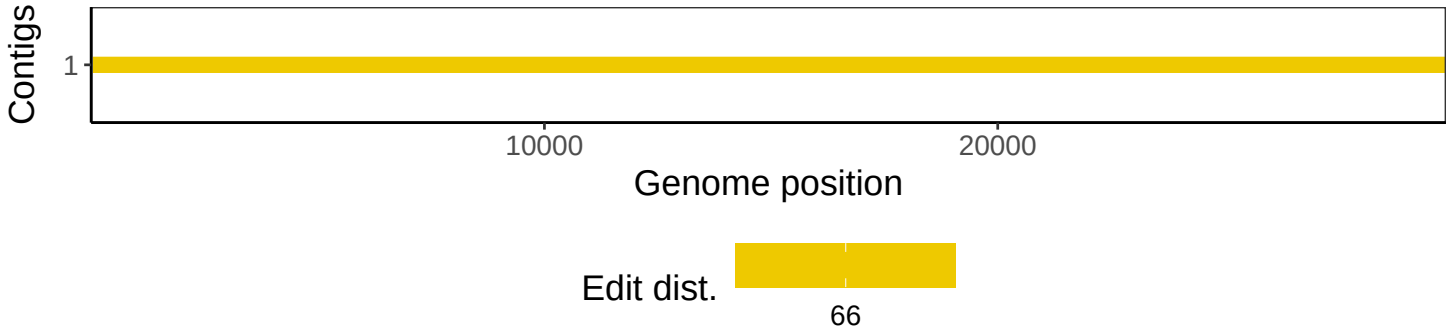
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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