COVID-19 subject UPHS-1093

2021-06-23

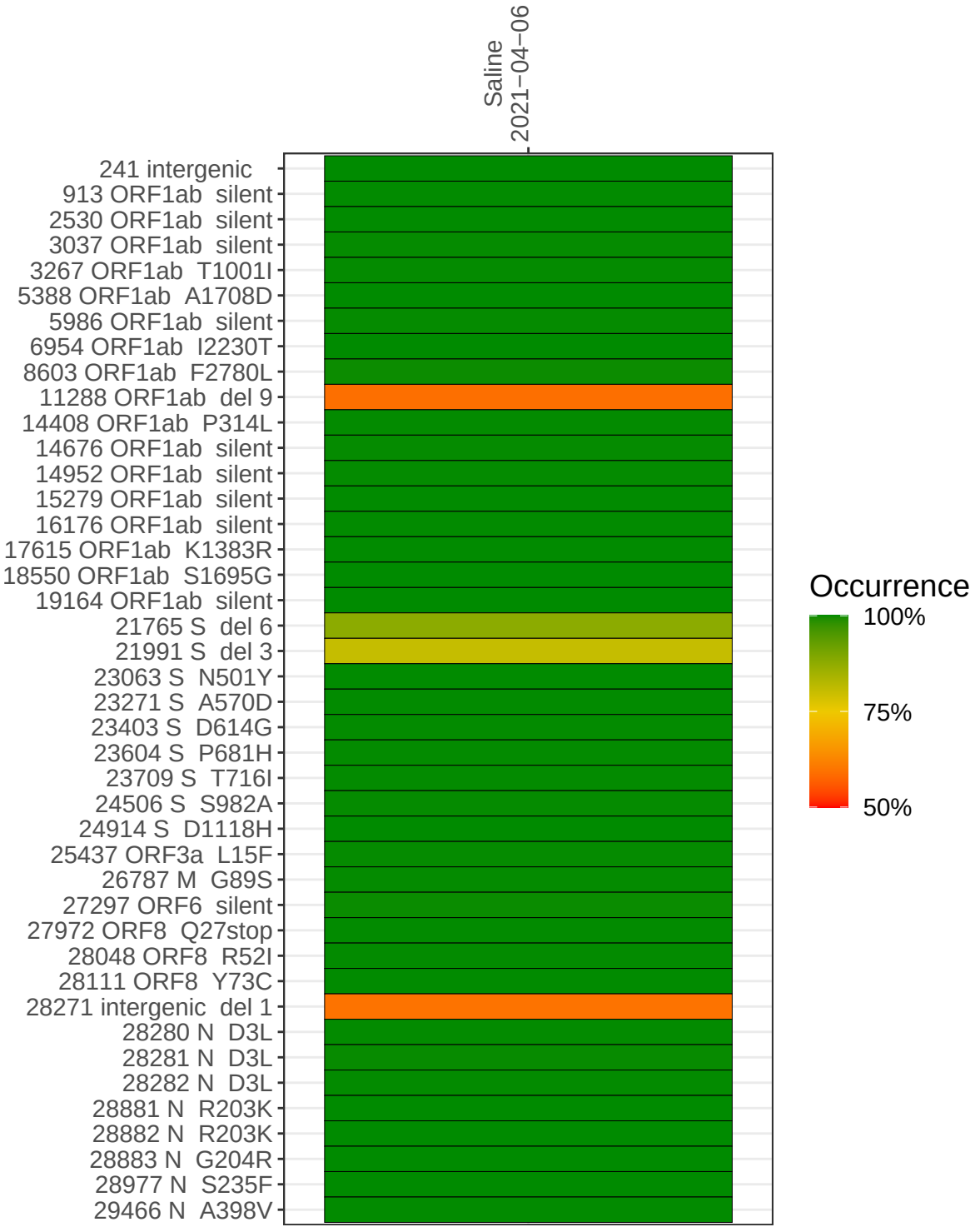
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

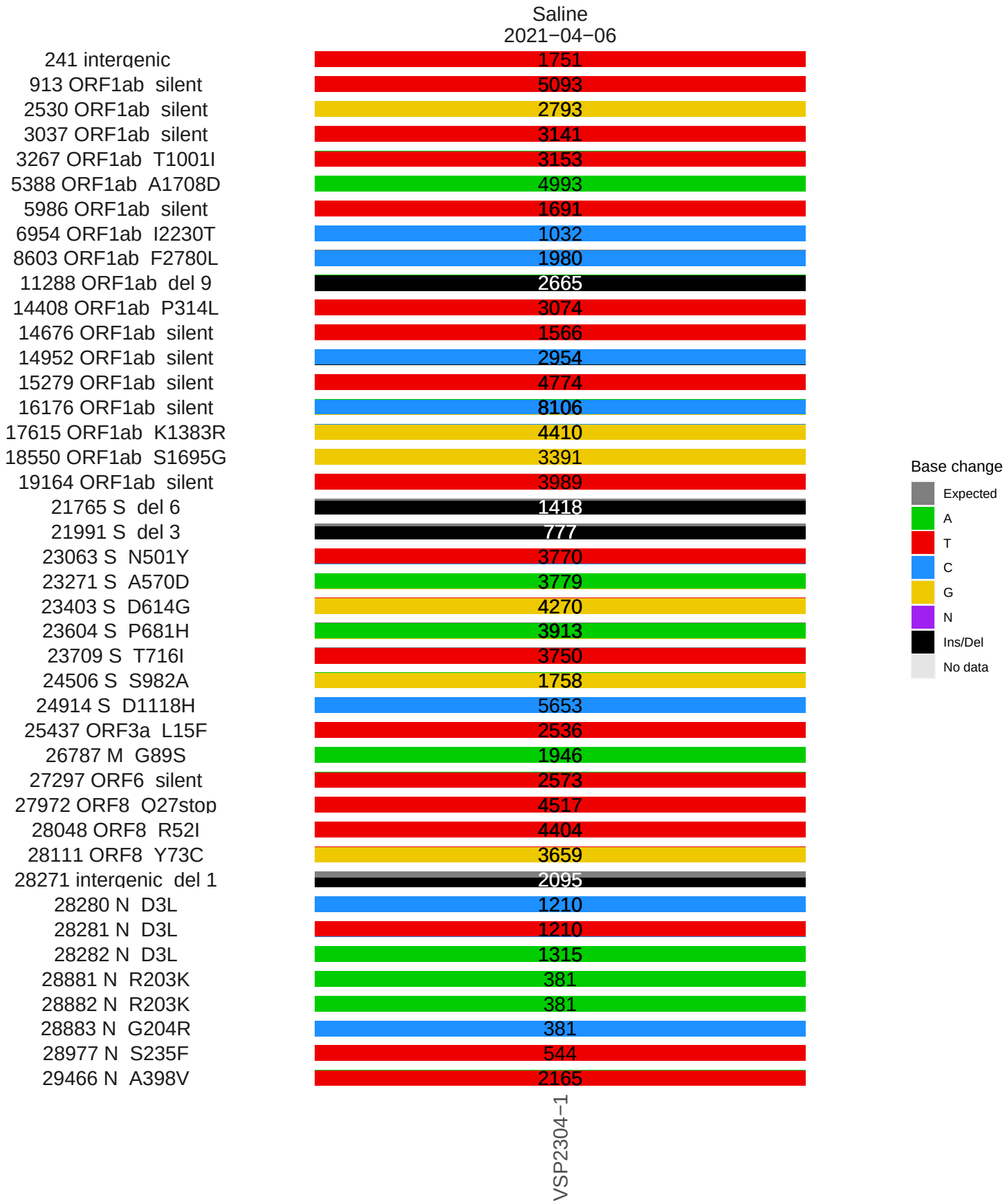
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2304-1	single experiment	NA	Saline	2021-04-06	29.84	B.1.1.7	99.9%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

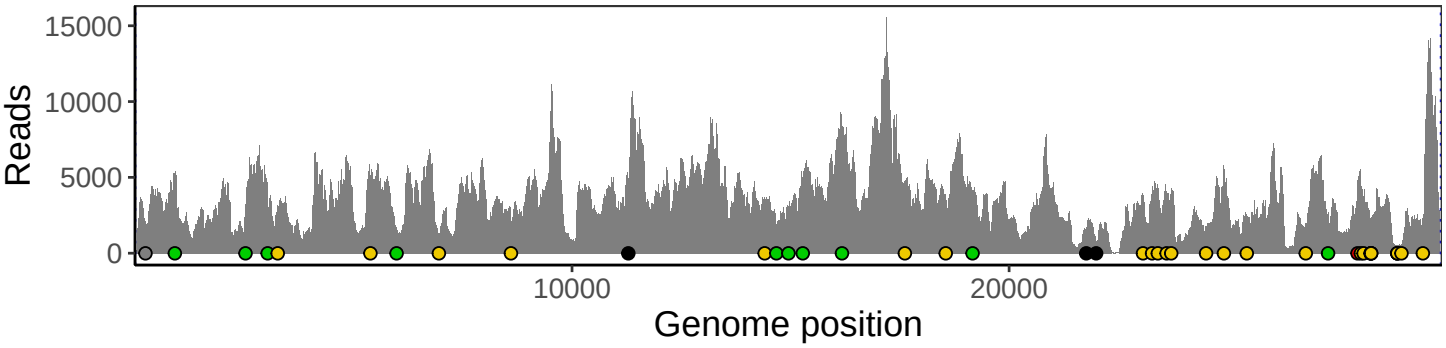



Saline
2021−04−06
241 intergenic 1751
913 ORF1ab silent 5093
2530 ORF1ab silent 2793
3037 ORF1ab silent 3141
3267 ORF1ab T1001I 3153
5388 ORF1ab A1708D 4993
5986 ORF1ab silent 1691
6954 ORF1ab I2230T 1032
8603 ORF1ab F2780L 1980
11288 ORF1ab del 9 2665
14408 ORF1ab P314L 3074
14676 ORF1ab silent 1566
14952 ORF1ab silent 2954
15279 ORF1ab silent 4774
16176 ORF1ab silent 8106
17615 ORF1ab K1383R 4410
18550 ORF1ab S1695G 3391
19164 ORF1ab silent 3989
21765 S del 6 1418
21991 S del 3 777
23063 S N501Y 3770
23271 S A570D 3779
23403 S D614G 4270
23604 S P681H 3913
23709 S T716I 3750
24506 S S982A 1758
24914 S D1118H 5653
25437 ORF3a L15F 2536
26787 M G89S 1946
27297 ORF6 silent 2573
27972 ORF8 Q27stop 4517
28048 ORF8 R52I 4404
28111 ORF8 Y73C 3659
28271 intergenic del 1 2095
28280 N D3L 1210
28281 N D3L 1210
28282 N D3L 1315
28881 N R203K 381
28882 N R203K 381
28883 N G204R 381
28977 N S235F 544
29466 N A398V 2165
VSP2304−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

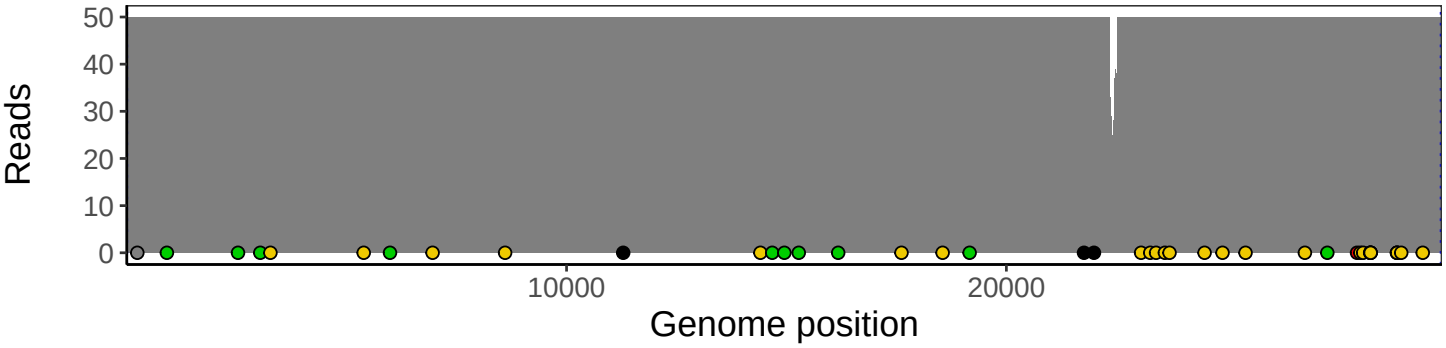
Analyses of individual experiments and composite results

VSP2304-1 | 2021-04-06 | Saline | UPHS-1093 | genomes | single experiment

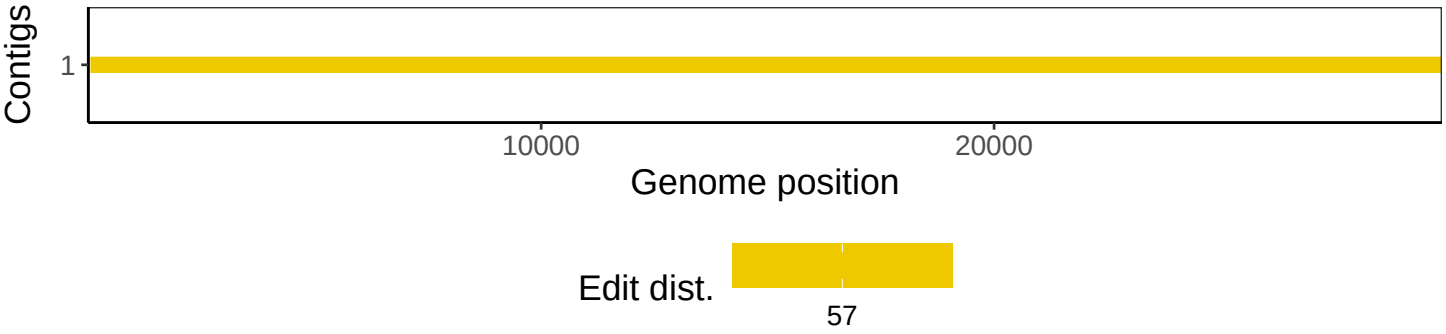
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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