COVID-19 subject UPHS-1209

2021-06-23

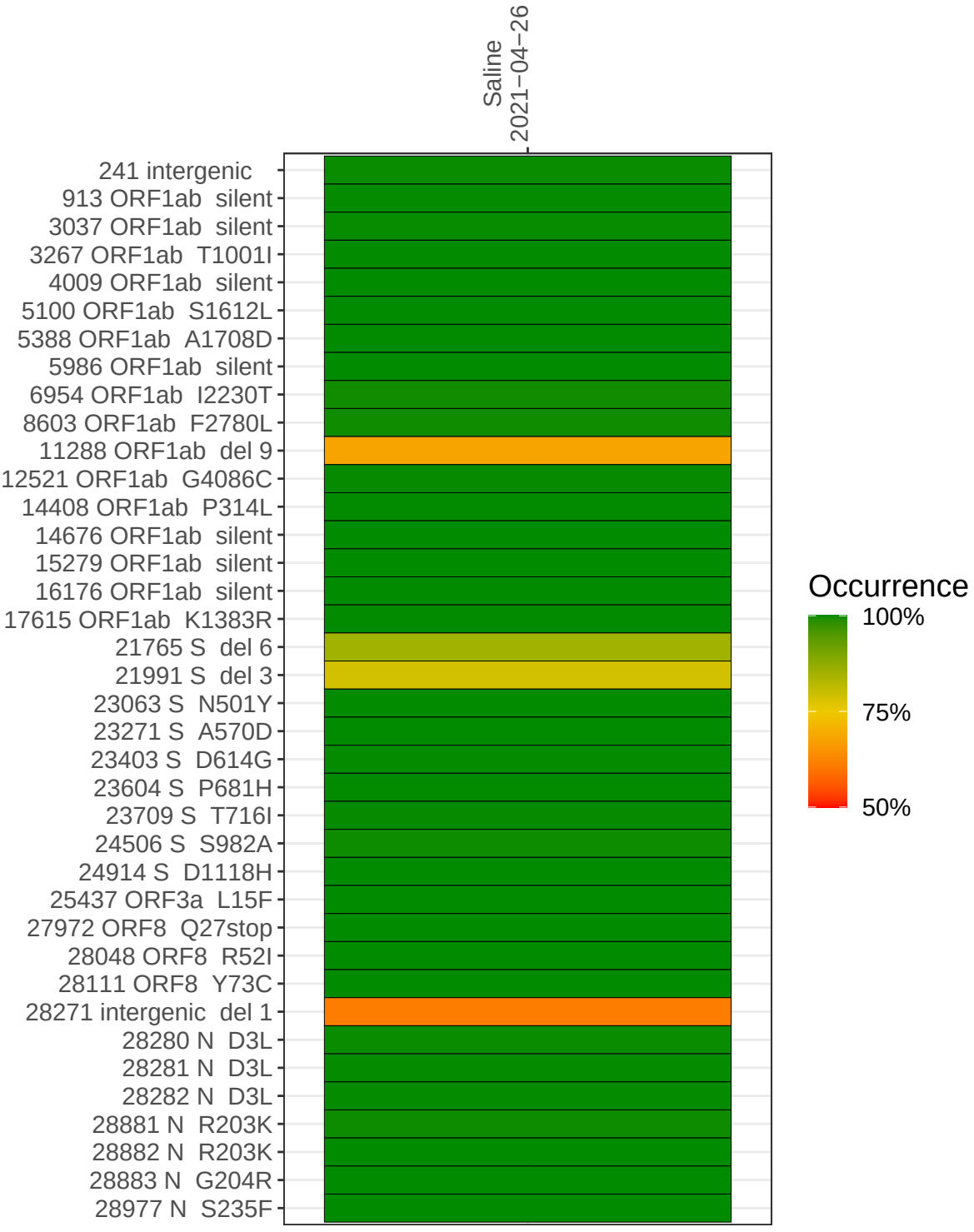
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

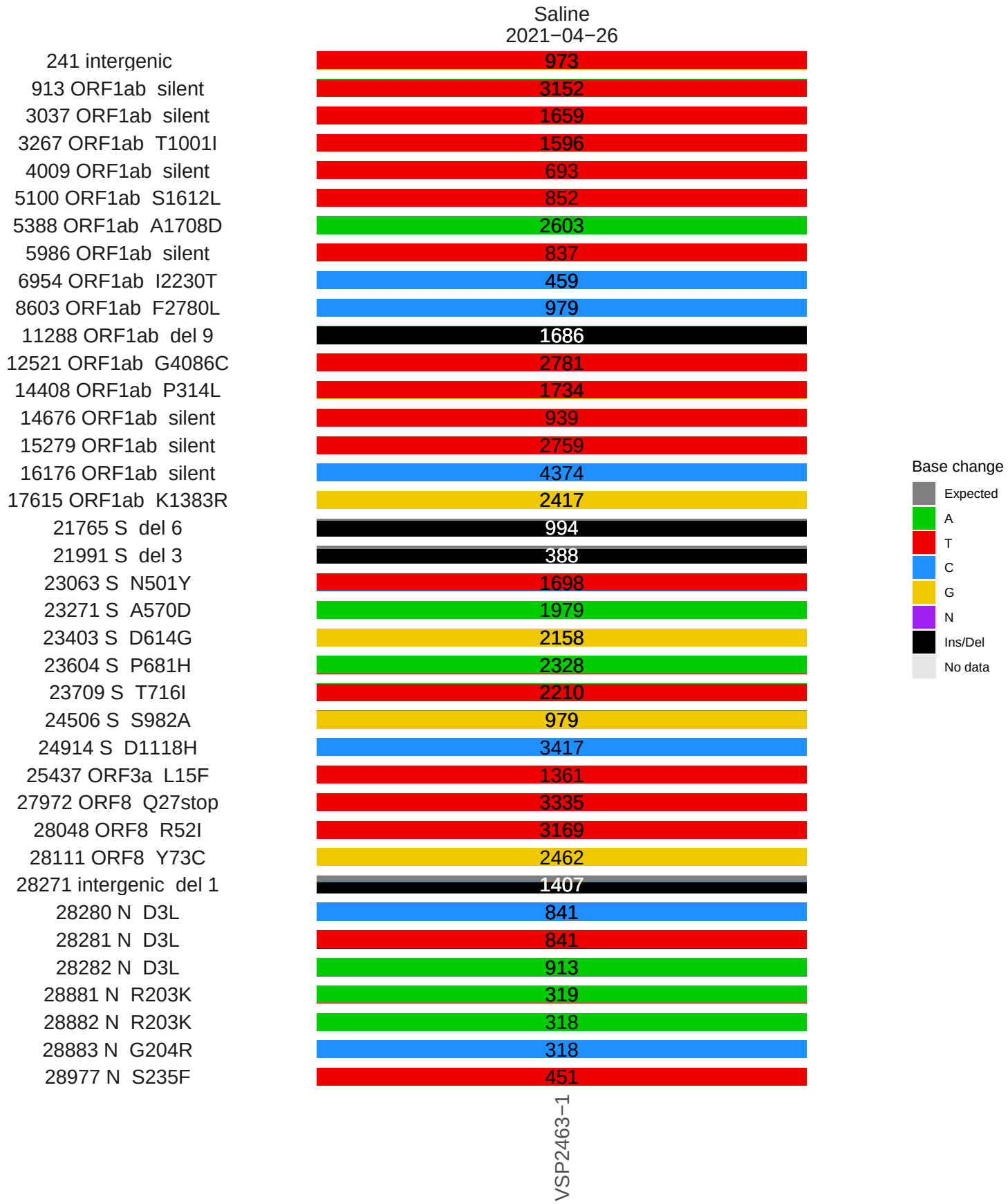
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2463-1	single experiment	NA	Saline	2021-04-26	29.86	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.

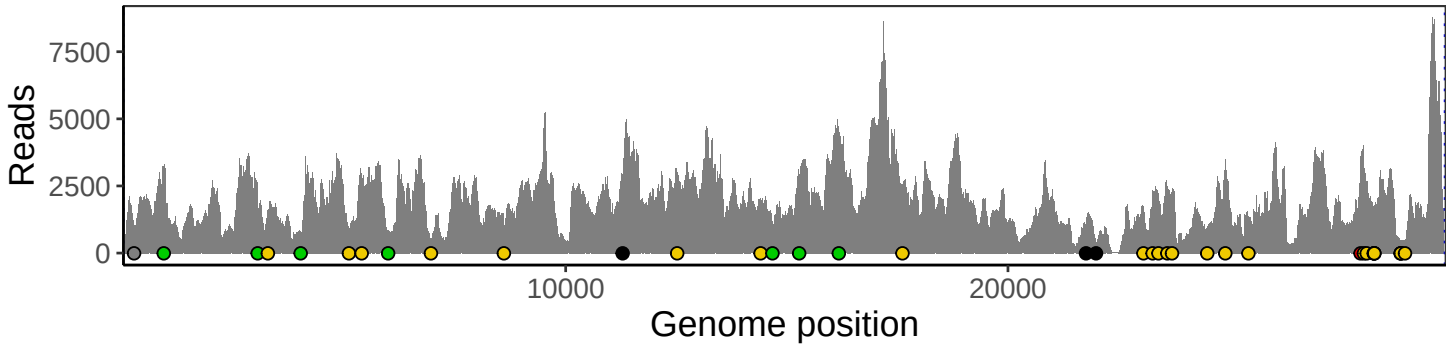



Saline
2021−04−26
241 intergenic 973
913 ORF1ab silent 3152
3037 ORF1ab silent 1659
3267 ORF1ab T1001I 1596
4009 ORF1ab silent 693
5100 ORF1ab S1612L 852
5388 ORF1ab A1708D 2603
5986 ORF1ab silent 837
6954 ORF1ab I2230T 459
8603 ORF1ab F2780L 979
11288 ORF1ab del 9 1686
12521 ORF1ab G4086C 2781
14408 ORF1ab P314L 1734
14676 ORF1ab silent 939
15279 ORF1ab silent 2759
16176 ORF1ab silent 4374
17615 ORF1ab K1383R 2417
21765 S del 6 994
21991 S del 3 388
23063 S N501Y 1698
23271 S A570D 1979
23403 S D614G 2158
23604 S P681H 2328
23709 S T716I 2210
24506 S S982A 979
24914 S D1118H 3417
25437 ORF3a L15F 1361
27972 ORF8 Q27stop 3335
28048 ORF8 R52I 3169
28111 ORF8 Y73C 2462
28271 intergenic del 1 1407
28280 N D3L 841
28281 N D3L 841
28282 N D3L 913
28881 N R203K 319
28882 N R203K 318
28883 N G204R 318
28977 N S235F 451
VSP2463−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

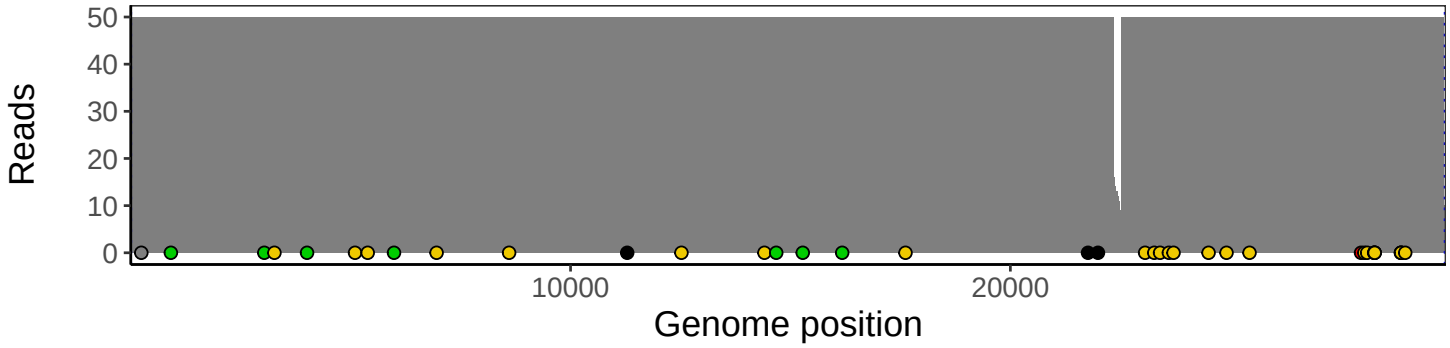
Analyses of individual experiments and composite results

VSP2463-1 | 2021-04-26 | Saline | UPHS-1209 | genomes | single experiment

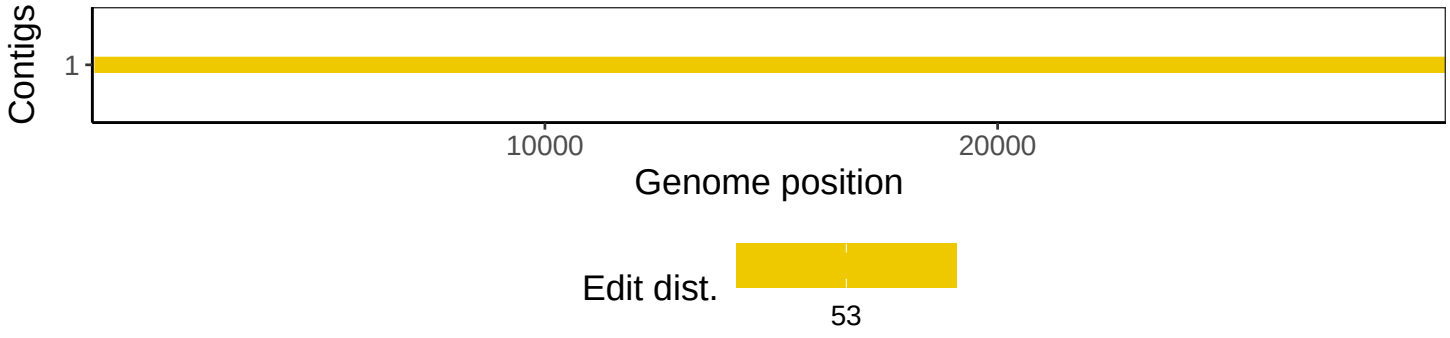
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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