COVID-19 subject 506

2021-05-21

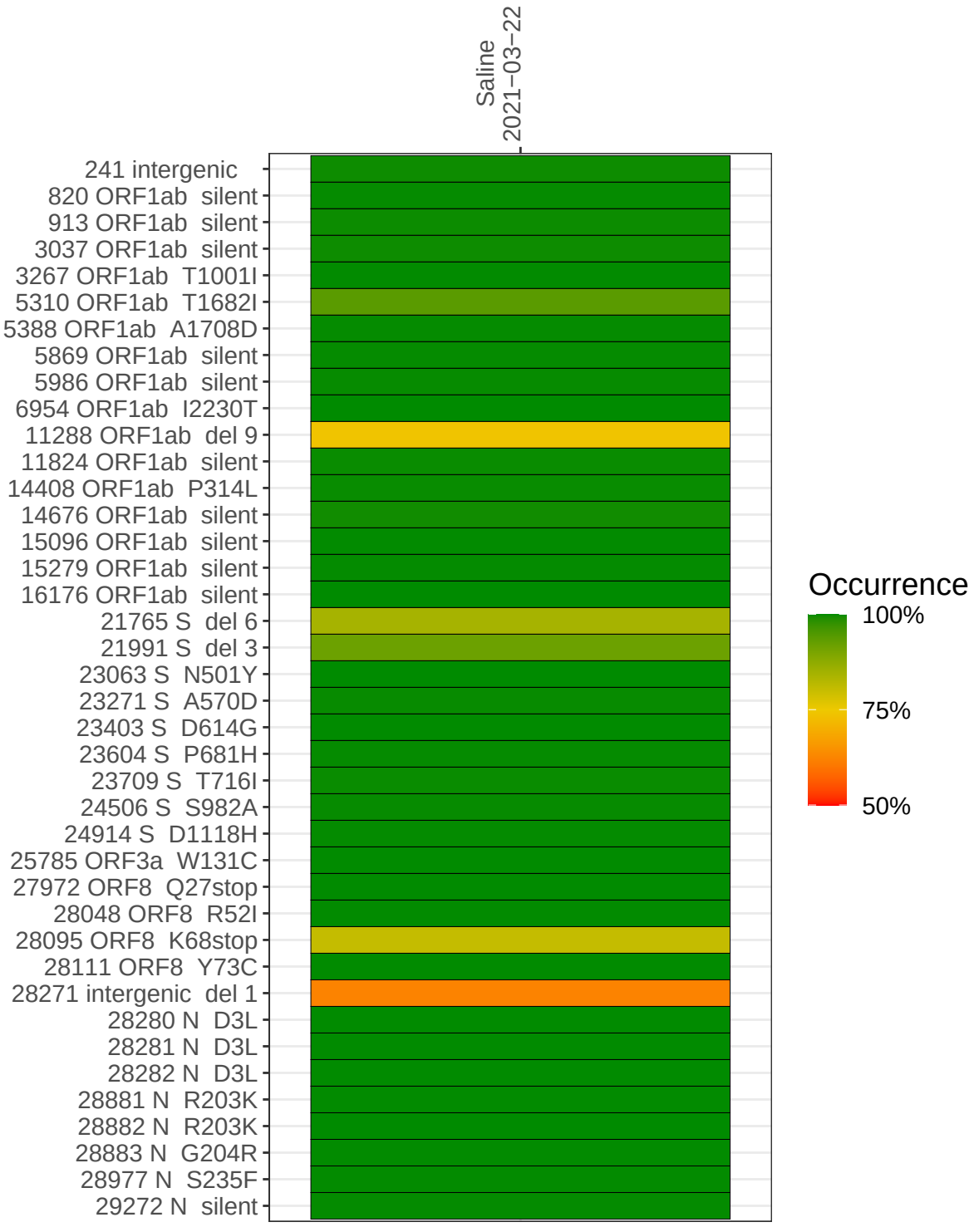
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

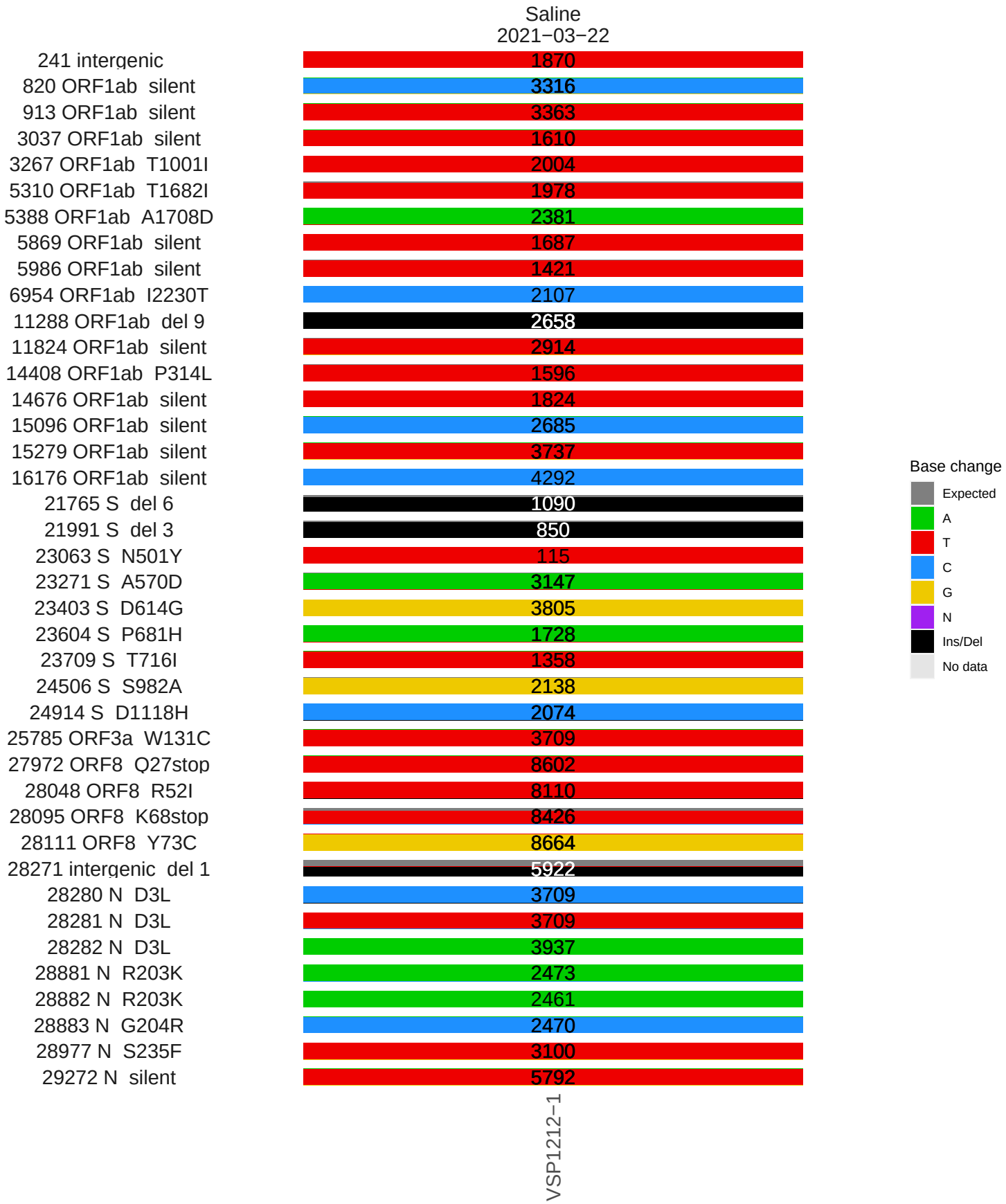
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1212-1	single experiment	NA	Saline	2021-03-22	29.69	B.1.1.7	99.3%	99.3%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

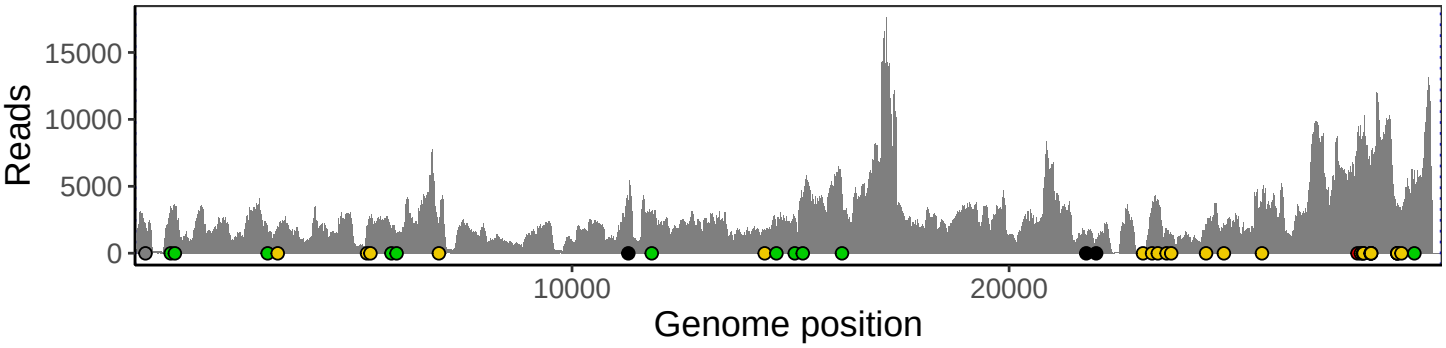



Saline
2021−03−22
241 intergenic 1870
820 ORF1ab silent 3316
913 ORF1ab silent 3363
3037 ORF1ab silent 1610
3267 ORF1ab T1001I 2004
5310 ORF1ab T1682I 1978
5388 ORF1ab A1708D 2381
5869 ORF1ab silent 1687
5986 ORF1ab silent 1421
6954 ORF1ab I2230T 2107
11288 ORF1ab del 9 2658
11824 ORF1ab silent 2914
14408 ORF1ab P314L 1596
14676 ORF1ab silent 1824
15096 ORF1ab silent 2685
15279 ORF1ab silent 3737
16176 ORF1ab silent 4292
21765 S del 6 1090
21991 S del 3 850
23063 S N501Y 115
23271 S A570D 3147
23403 S D614G 3805
23604 S P681H 1728
23709 S T716I 1358
24506 S S982A 2138
24914 S D1118H 2074
25785 ORF3a W131C 3709
27972 ORF8 Q27stop 8602
28048 ORF8 R52I 8110
28095 ORF8 K68stop 8426
28111 ORF8 Y73C 8664
28271 intergenic del 1 5922
28280 N D3L 3709
28281 N D3L 3709
28282 N D3L 3937
28881 N R203K 2473
28882 N R203K 2461
28883 N G204R 2470
28977 N S235F 3100
29272 N silent 5792
VSP1212−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

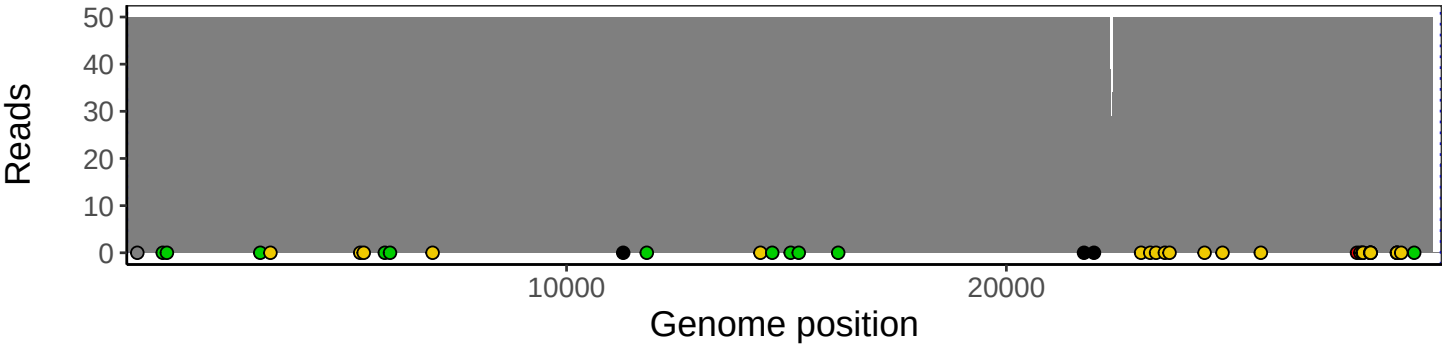
Analyses of individual experiments and composite results

VSP1212-1 | 2021-03-22 | Saline | 506s | genomes | single experiment

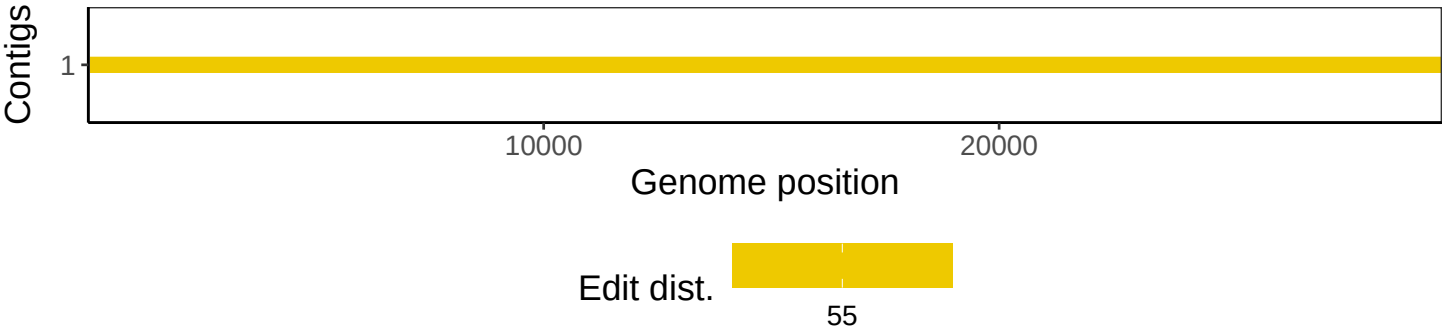
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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