COVID-19 subject UPHS-0686

2021-06-23

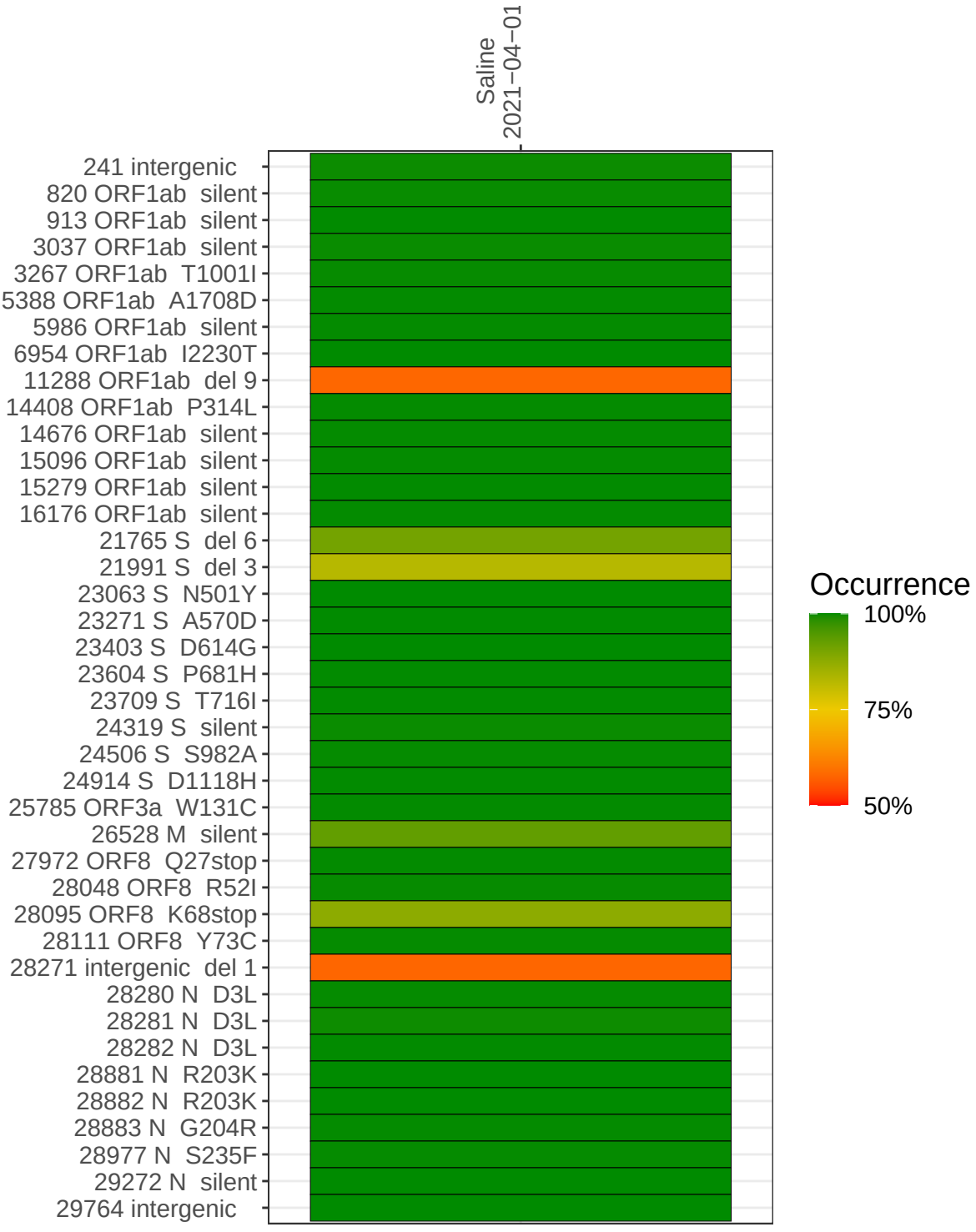
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

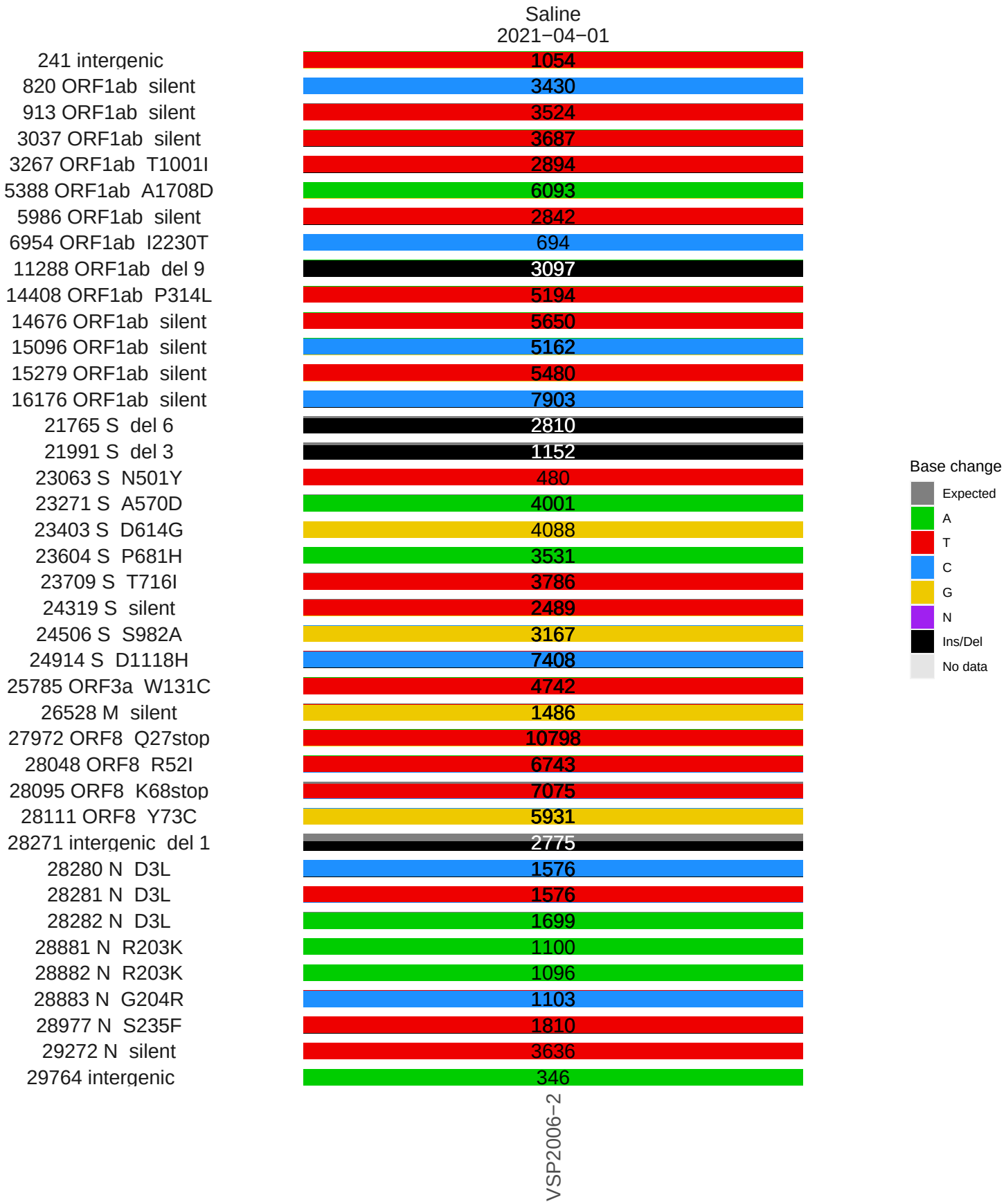
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2006-2	single experiment	NA	Saline	2021-04-01	29.80	B.1.1.7	99.7%	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.

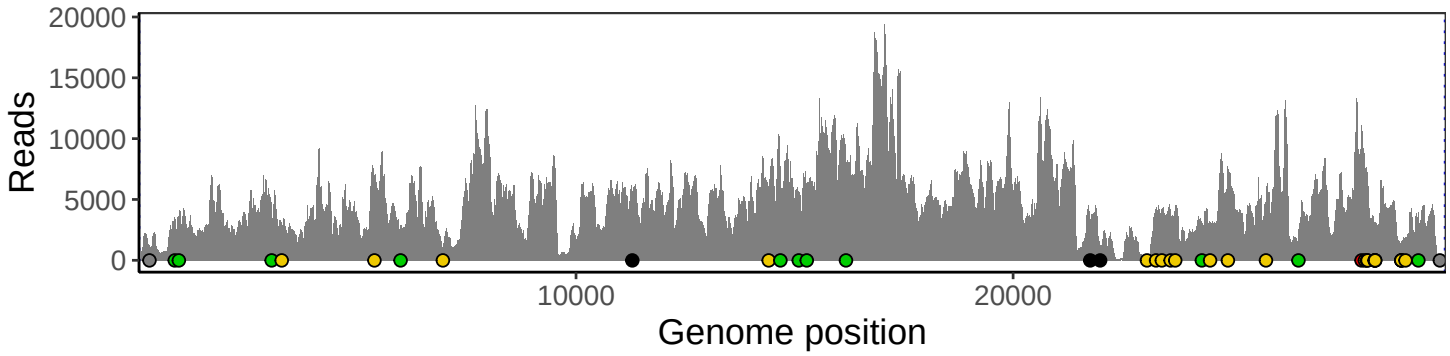



Saline
2021−04−01
241 intergenic 1054
820 ORF1ab silent 3430
913 ORF1ab silent 3524
3037 ORF1ab silent 3687
3267 ORF1ab T1001I 2894
5388 ORF1ab A1708D 6093
5986 ORF1ab silent 2842
6954 ORF1ab I2230T 694
11288 ORF1ab del 9 3097
14408 ORF1ab P314L 5194
14676 ORF1ab silent 5650
15096 ORF1ab silent 5162
15279 ORF1ab silent 5480
16176 ORF1ab silent 7903
21765 S del 6 2810
21991 S del 3 1152
23063 S N501Y 480
23271 S A570D 4001
23403 S D614G 4088
23604 S P681H 3531
23709 S T716I 3786
24319 S silent 2489
24506 S S982A 3167
24914 S D1118H 7408
25785 ORF3a W131C 4742
26528 M silent 1486
27972 ORF8 Q27stop 10798
28048 ORF8 R52I 6743
28095 ORF8 K68stop 7075
28111 ORF8 Y73C 5931
28271 intergenic del 1 2775
28280 N D3L 1576
28281 N D3L 1576
28282 N D3L 1699
28881 N R203K 1100
28882 N R203K 1096
28883 N G204R 1103
28977 N S235F 1810
29272 N silent 3636
29764 intergenic 346
VSP2006−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

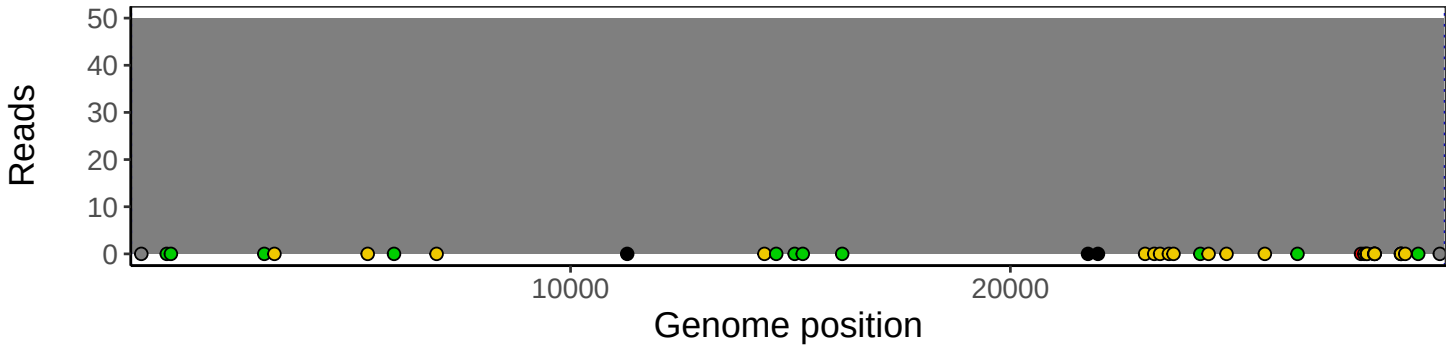
Analyses of individual experiments and composite results

VSP2006-2 | 2021-04-01 | Saline | UPHS-0686 | genomes | single experiment

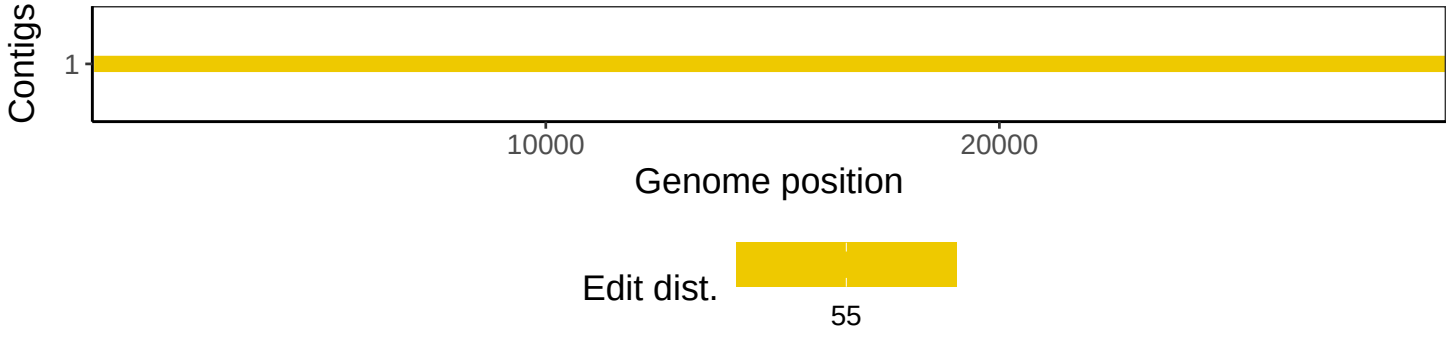
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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