COVID-19 subject UPHS-1026

2021-06-23

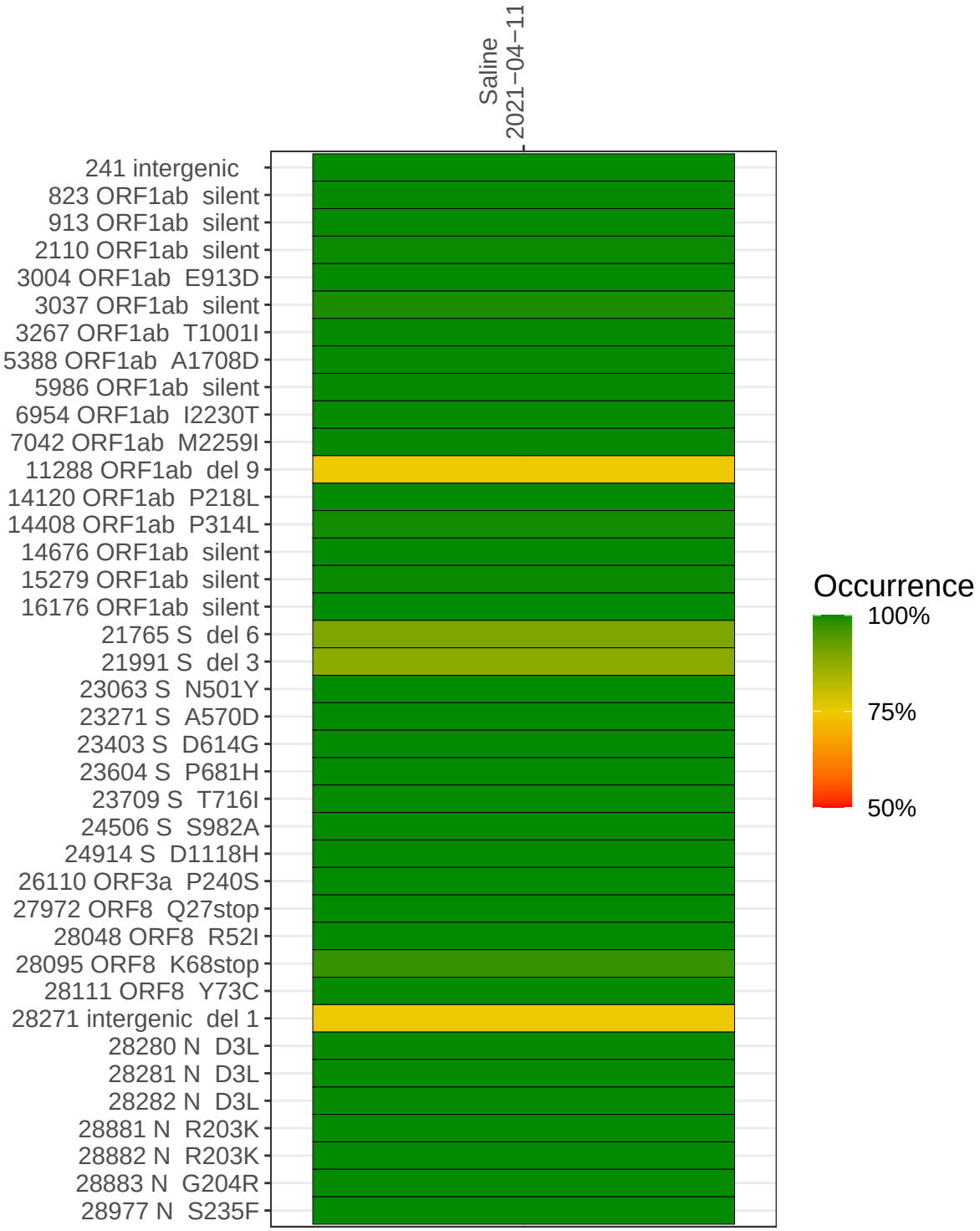
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

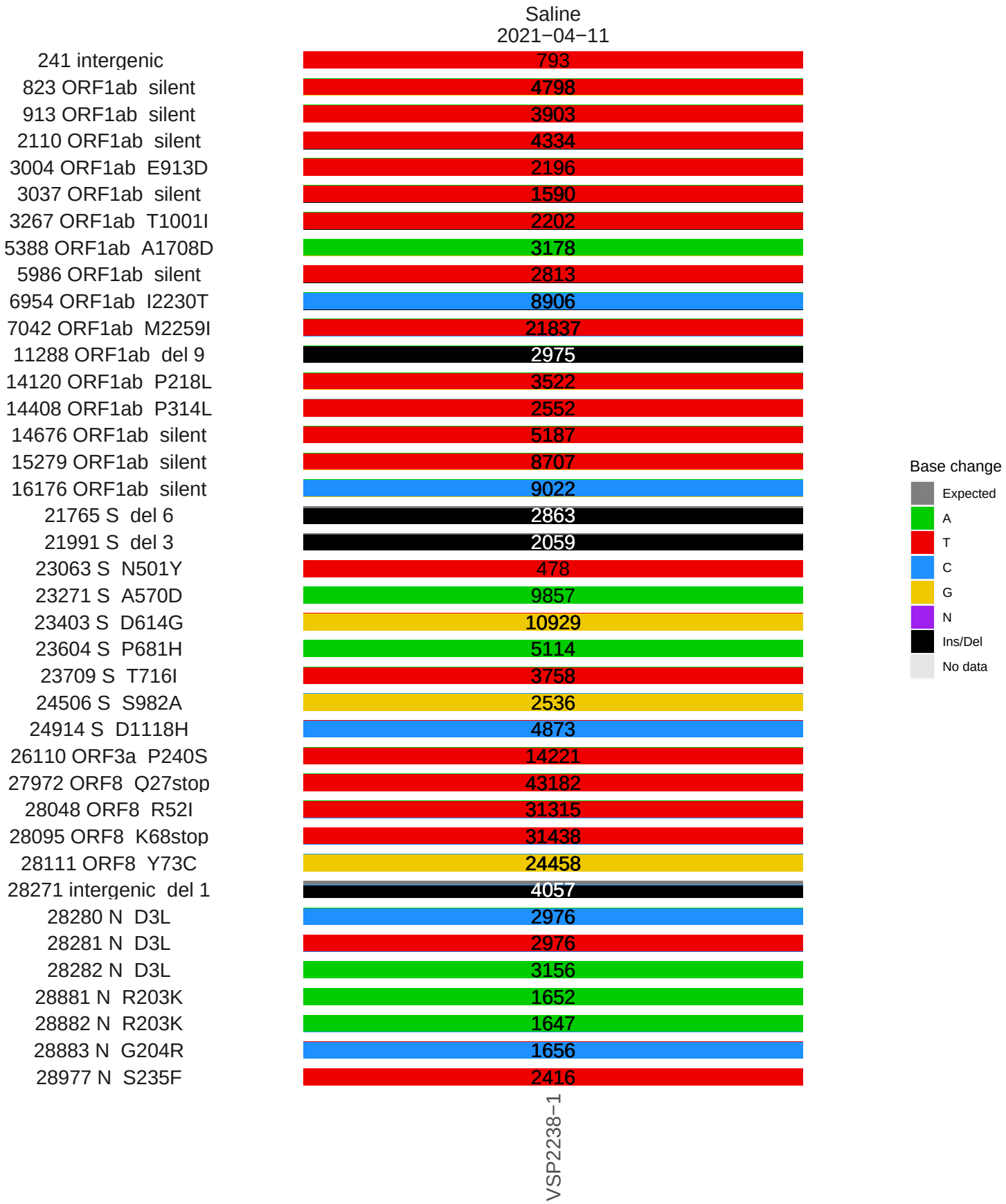
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2238-1	single experiment	NA	Saline	2021-04-11	29.85	B.1.1.7	99.8%	99.8%

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.

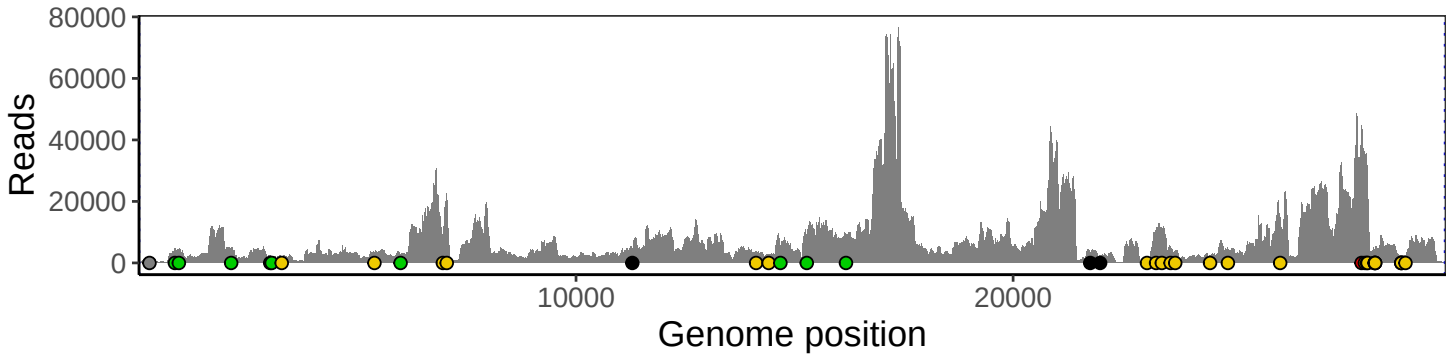



Saline
2021−04−11
241 intergenic 793
823 ORF1ab silent 4798
913 ORF1ab silent 3903
2110 ORF1ab silent 4334
3004 ORF1ab E913D 2196
3037 ORF1ab silent 1590
3267 ORF1ab T1001I 2202
5388 ORF1ab A1708D 3178
5986 ORF1ab silent 2813
6954 ORF1ab I2230T 8906
7042 ORF1ab M2259I 21837
11288 ORF1ab del 9 2975
14120 ORF1ab P218L 3522
14408 ORF1ab P314L 2552
14676 ORF1ab silent 5187
15279 ORF1ab silent 8707
16176 ORF1ab silent 9022
21765 S del 6 2863
21991 S del 3 2059
23063 S N501Y 478
23271 S A570D 9857
23403 S D614G 10929
23604 S P681H 5114
23709 S T716I 3758
24506 S S982A 2536
24914 S D1118H 4873
26110 ORF3a P240S 14221
27972 ORF8 Q27stop 43182
28048 ORF8 R52I 31315
28095 ORF8 K68stop 31438
28111 ORF8 Y73C 24458
28271 intergenic del 1 4057
28280 N D3L 2976
28281 N D3L 2976
28282 N D3L 3156
28881 N R203K 1652
28882 N R203K 1647
28883 N G204R 1656
28977 N S235F 2416
VSP2238−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

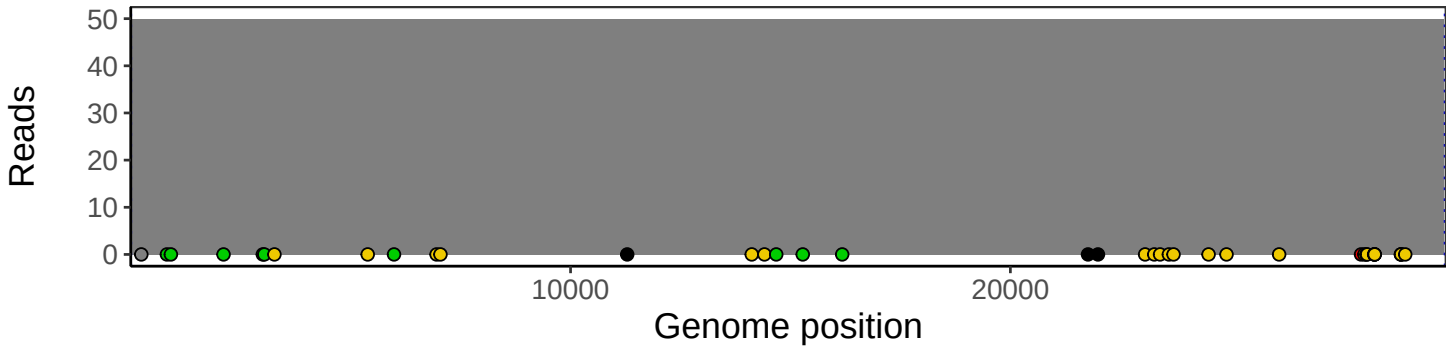
Analyses of individual experiments and composite results

VSP2238-1 | 2021-04-11 | Saline | UPHS-1026 | genomes | single experiment

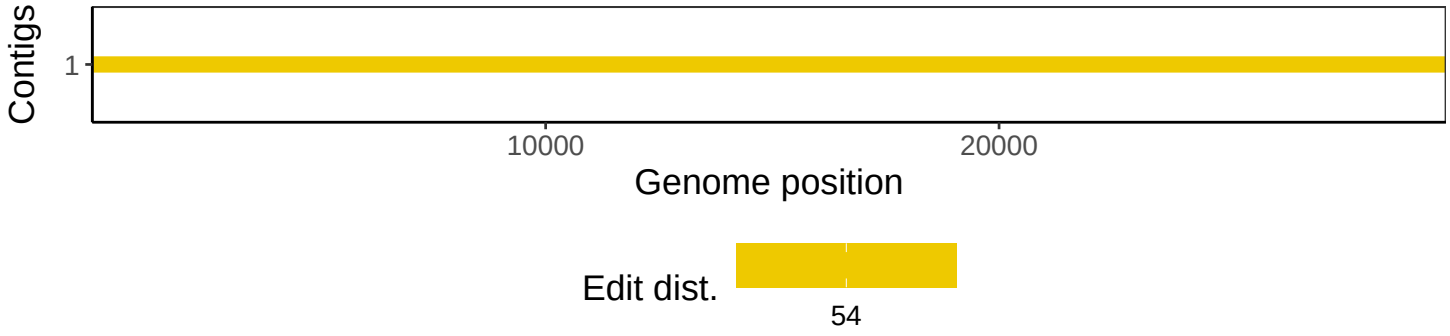
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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