COVID-19 subject UPHS-1342

2021-05-21

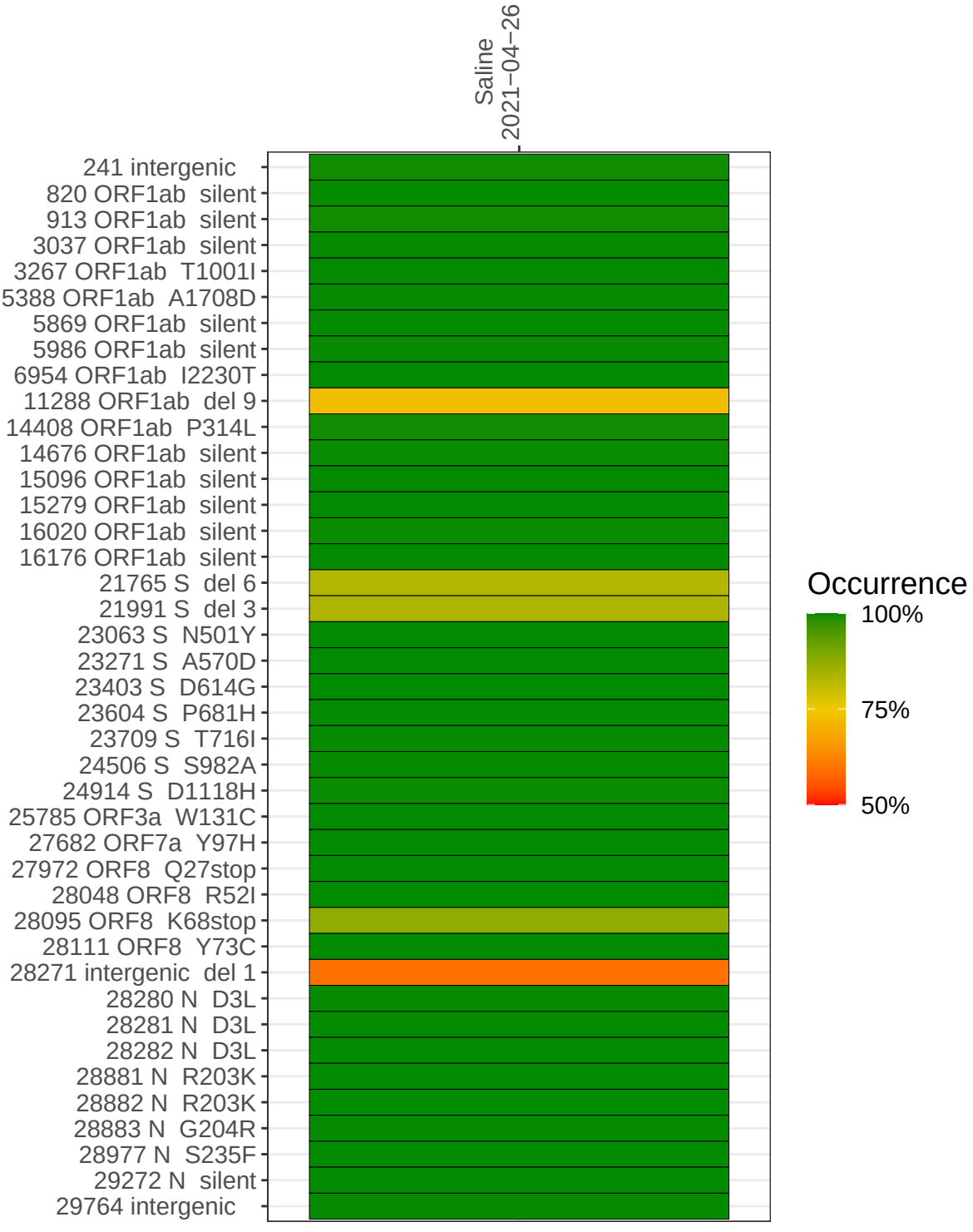
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

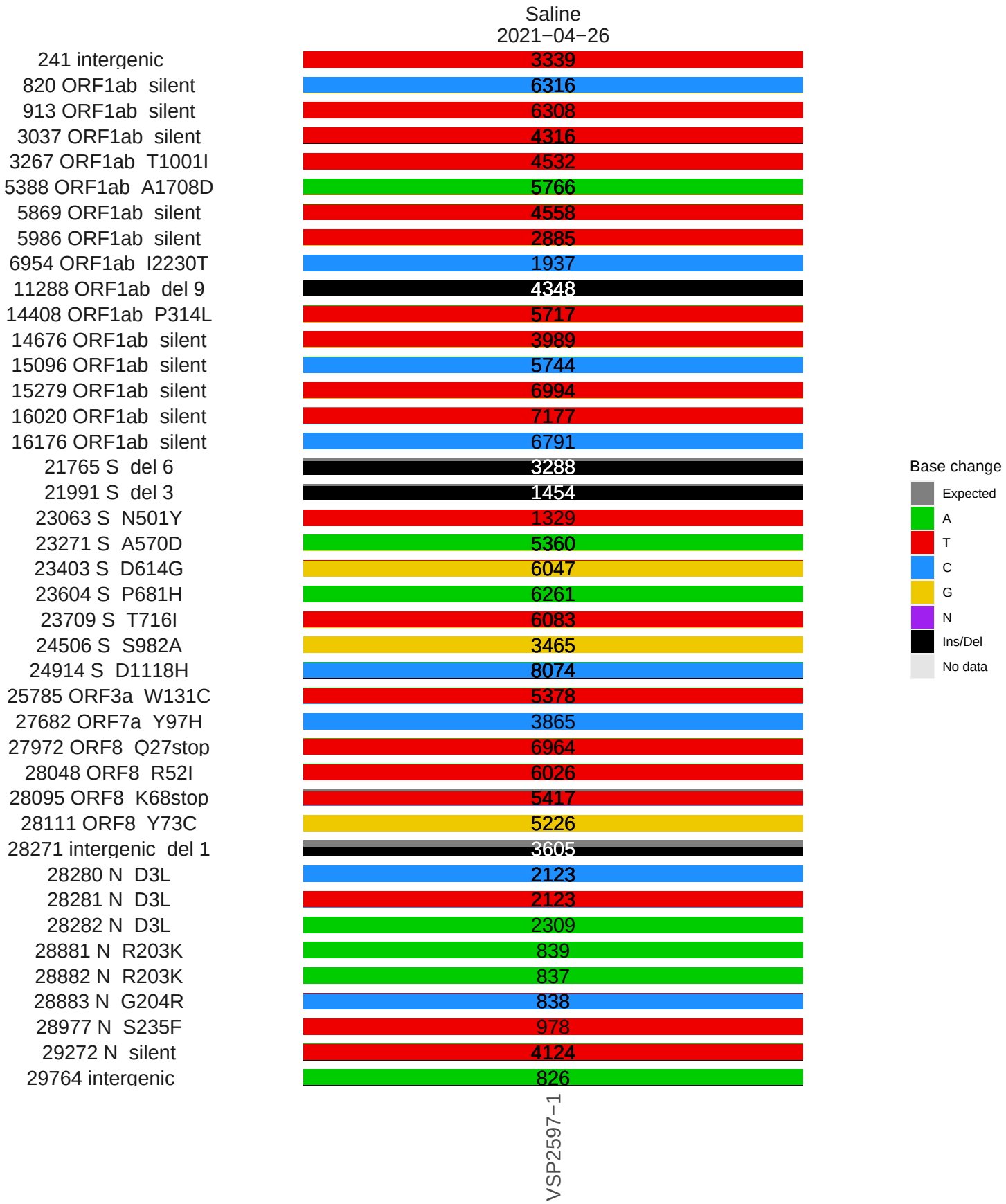
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2597-1	single experiment	NA	Saline	2021-04-26	29.82	B.1.1.7	99.7%	99.7%

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.

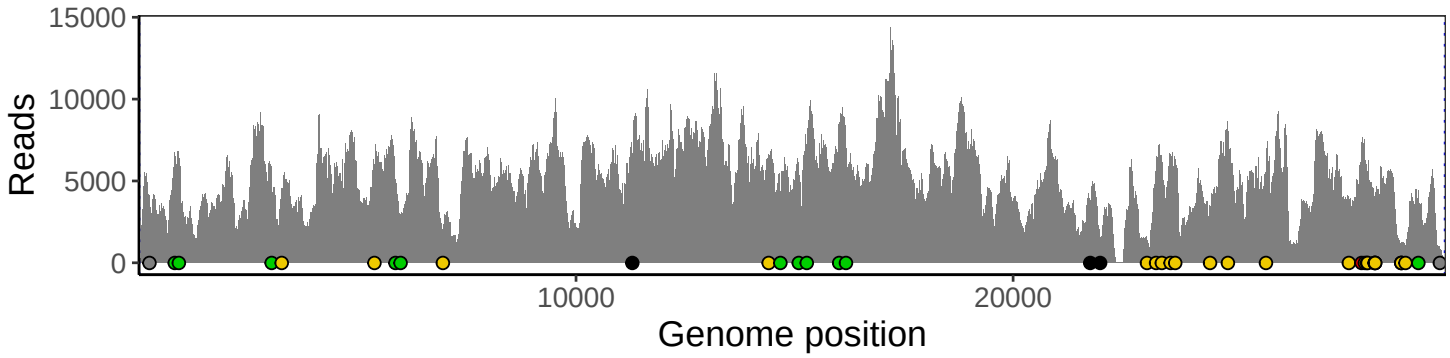



Saline
2021−04−26
241 intergenic 3339
820 ORF1ab silent 6316
913 ORF1ab silent 6308
3037 ORF1ab silent 4316
3267 ORF1ab T1001I 4532
5388 ORF1ab A1708D 5766
5869 ORF1ab silent 4558
5986 ORF1ab silent 2885
6954 ORF1ab I2230T 1937
11288 ORF1ab del 9 4348
14408 ORF1ab P314L 5717
14676 ORF1ab silent 3989
15096 ORF1ab silent 5744
15279 ORF1ab silent 6994
16020 ORF1ab silent 7177
16176 ORF1ab silent 6791
21765 S del 6 3288
21991 S del 3 1454
23063 S N501Y 1329
23271 S A570D 5360
23403 S D614G 6047
23604 S P681H 6261
23709 S T716I 6083
24506 S S982A 3465
24914 S D1118H 8074
25785 ORF3a W131C 5378
27682 ORF7a Y97H 3865
27972 ORF8 Q27stop 6964
28048 ORF8 R52I 6026
28095 ORF8 K68stop 5417
28111 ORF8 Y73C 5226
28271 intergenic del 1 3605
28280 N D3L 2123
28281 N D3L 2123
28282 N D3L 2309
28881 N R203K 839
28882 N R203K 837
28883 N G204R 838
28977 N S235F 978
29272 N silent 4124
29764 intergenic 826
VSP2597−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

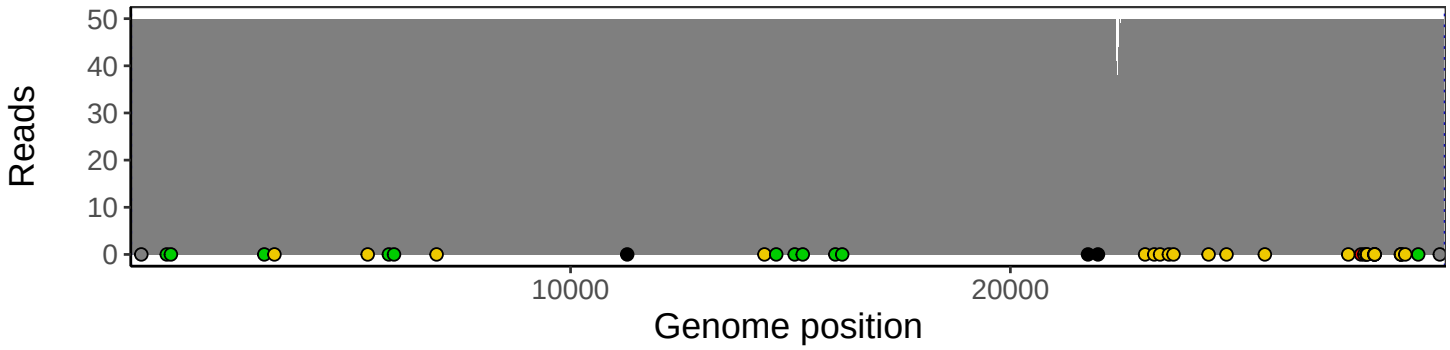
Analyses of individual experiments and composite results

VSP2597-1 | 2021-04-26 | Saline | UPHS-1342 | genomes | single experiment

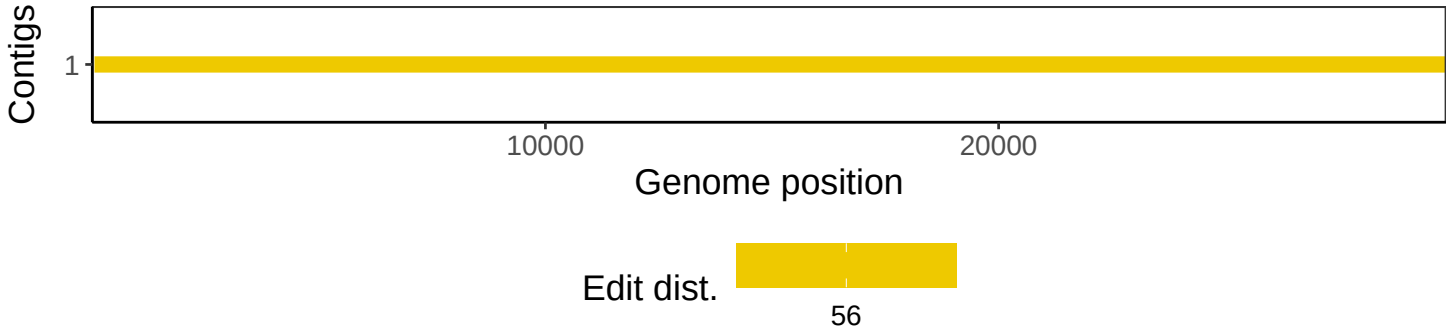
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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