COVID-19 subject UPHS-1035

2021-05-10

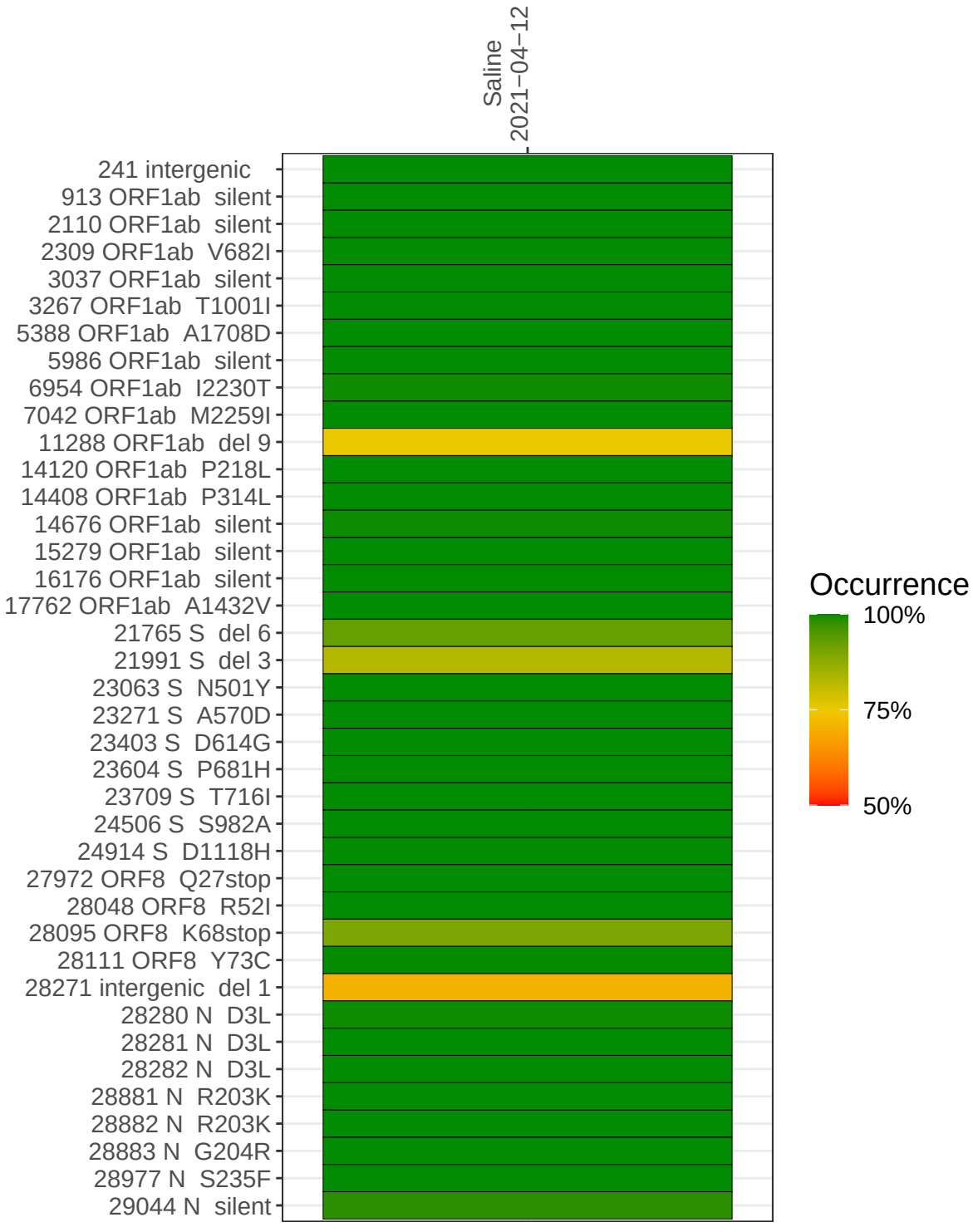
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

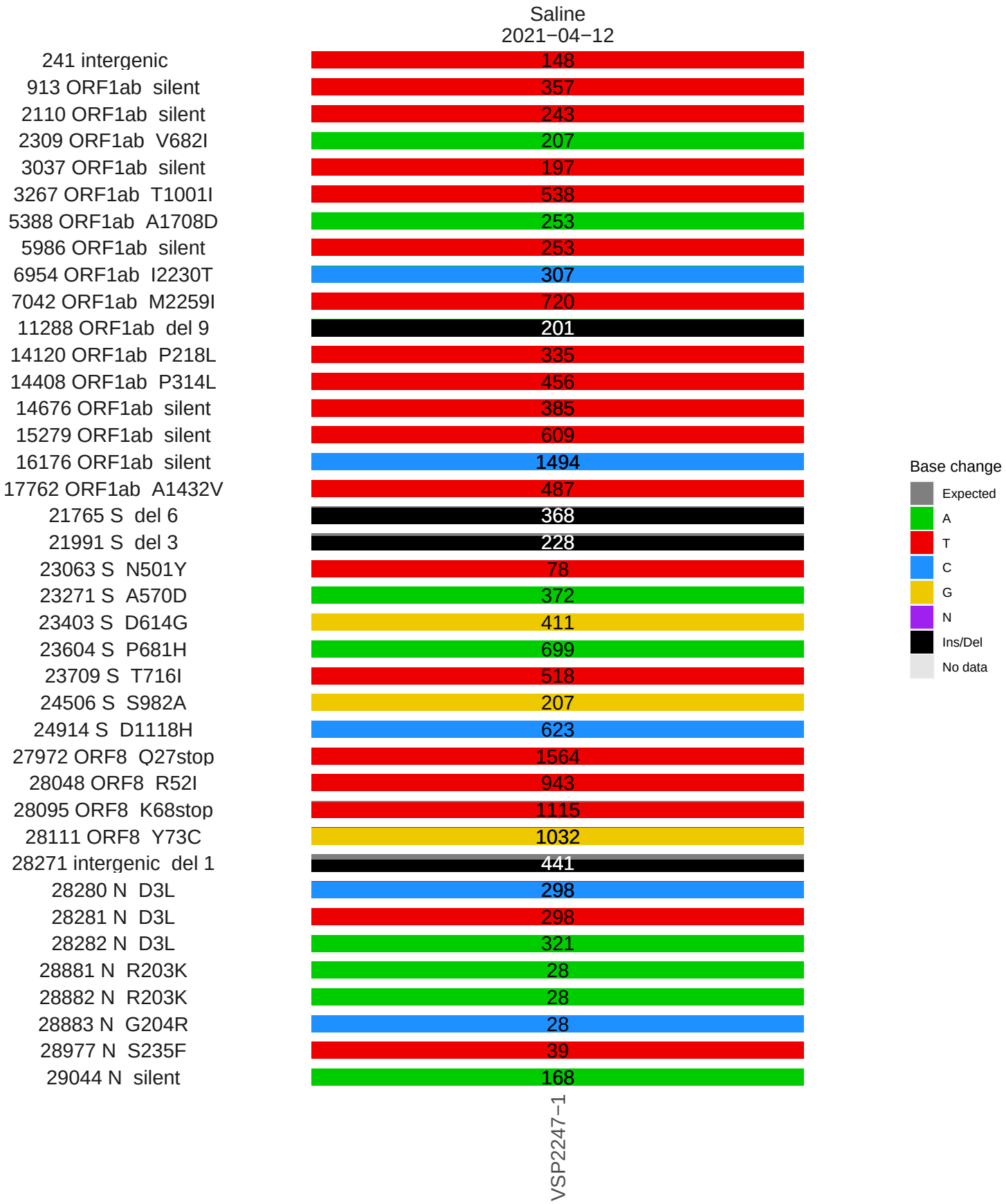
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2247-1	single experiment	NA	Saline	2021-04-12	29.64	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.

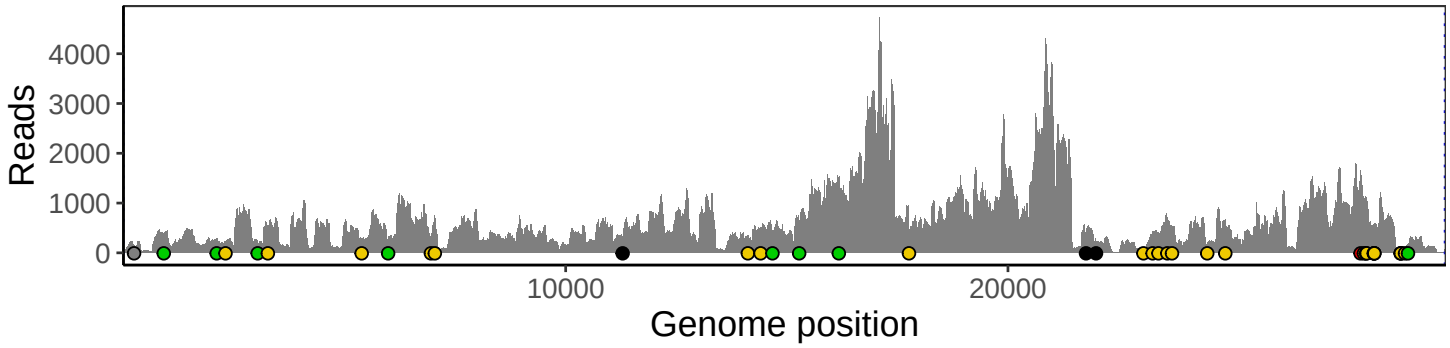



Saline
2021−04−12
241 intergenic 148
913 ORF1ab silent 357
2110 ORF1ab silent 243
2309 ORF1ab V682I 207
3037 ORF1ab silent 197
3267 ORF1ab T1001I 538
5388 ORF1ab A1708D 253
5986 ORF1ab silent 253
6954 ORF1ab I2230T 307
7042 ORF1ab M2259I 720
11288 ORF1ab del 9 201
14120 ORF1ab P218L 335
14408 ORF1ab P314L 456
14676 ORF1ab silent 385
15279 ORF1ab silent 609
16176 ORF1ab silent 1494
17762 ORF1ab A1432V 487
21765 S del 6 368
21991 S del 3 228
23063 S N501Y 78
23271 S A570D 372
23403 S D614G 411
23604 S P681H 699
23709 S T716I 518
24506 S S982A 207
24914 S D1118H 623
27972 ORF8 Q27stop 1564
28048 ORF8 R52I 943
28095 ORF8 K68stop 1115
28111 ORF8 Y73C 1032
28271 intergenic del 1 441
28280 N D3L 298
28281 N D3L 298
28282 N D3L 321
28881 N R203K 28
28882 N R203K 28
28883 N G204R 28
28977 N S235F 39
29044 N silent 168
VSP2247−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

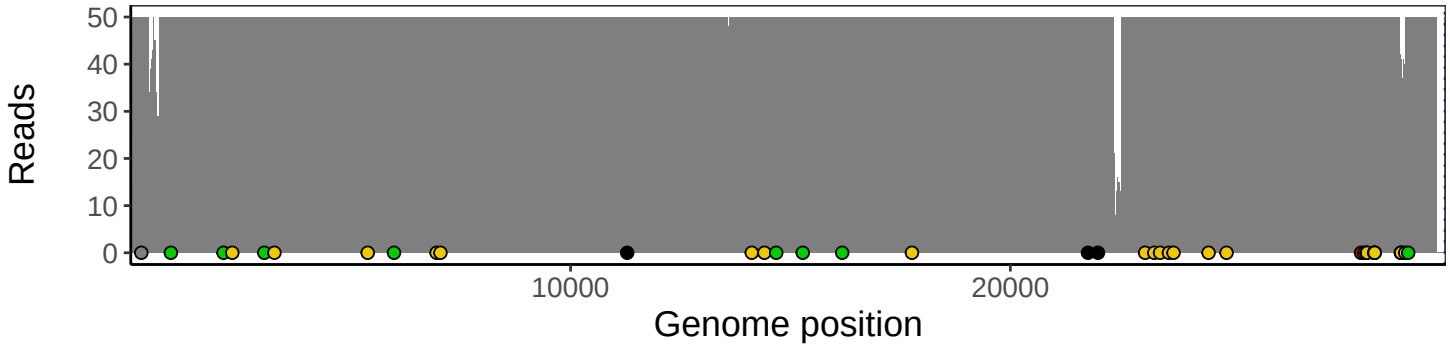
Analyses of individual experiments and composite results

VSP2247-1 | 2021-04-12 | Saline | UPHS-1035 | genomes | single experiment

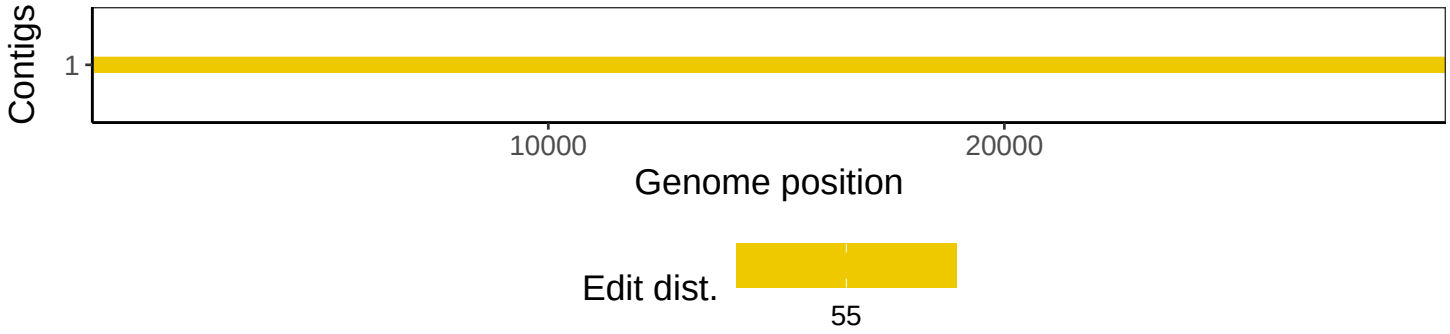
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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