COVID-19 subject UPHS-1379

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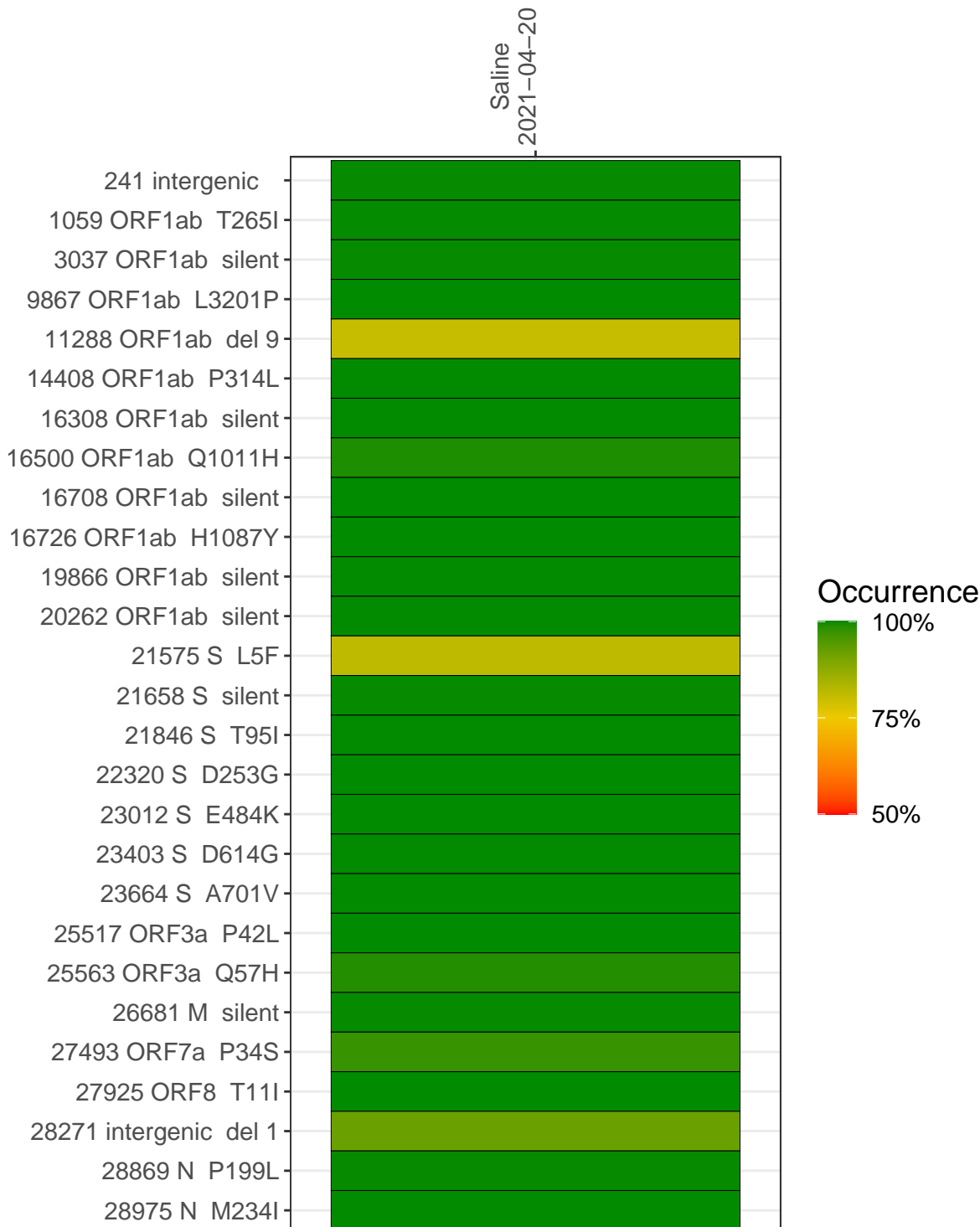 sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.
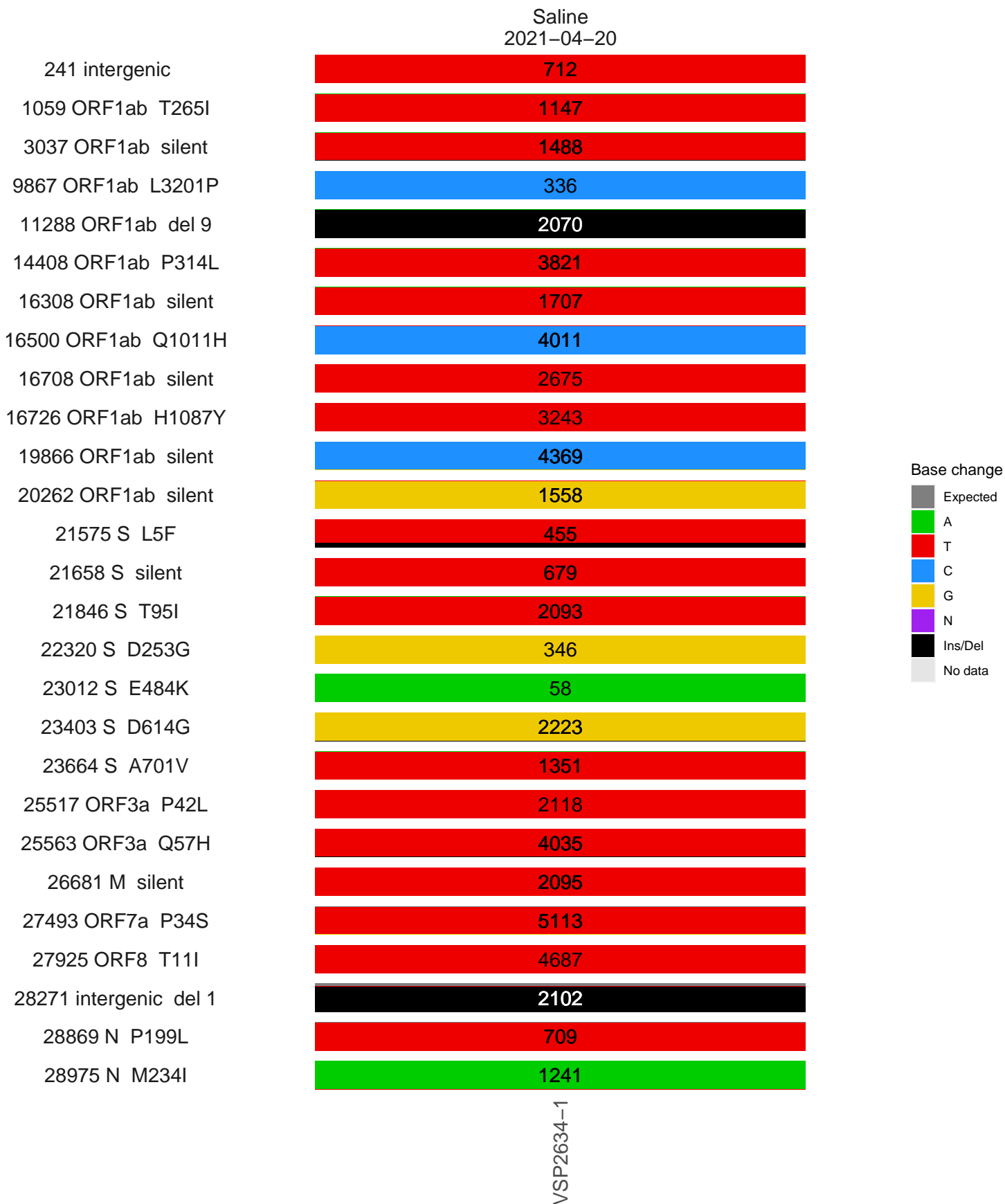
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2634-1	single experiment	NA	Saline	2021-04-20	29.81	B.1.526	99.8%	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
2021−04−20

Position	Value
241 intergenic	712
1059 ORF1ab T265I	1147
3037 ORF1ab silent	1488
9867 ORF1ab L3201P	336
11288 ORF1ab del 9	2070
14408 ORF1ab P314L	3821
16308 ORF1ab silent	1707
16500 ORF1ab Q1011H	4011
16708 ORF1ab silent	2675
16726 ORF1ab H1087Y	3243
19866 ORF1ab silent	4369
20262 ORF1ab silent	1558
21575 S L5F	455
21658 S silent	679
21846 S T95I	2093
22320 S D253G	346
23012 S E484K	58
23403 S D614G	2223
23664 S A701V	1351
25517 ORF3a P42L	2118
25563 ORF3a Q57H	4035
26681 M silent	2095
27493 ORF7a P34S	5113
27925 ORF8 T11I	4687
28271 intergenic del 1	2102
28869 N P199L	709
28975 N M234I	1241

VSP2634−1

Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

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Analyses of individual experiments and composite results

**VSP2634-1 | 2021-04-20 | Saline | UPHS-1379 | 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.
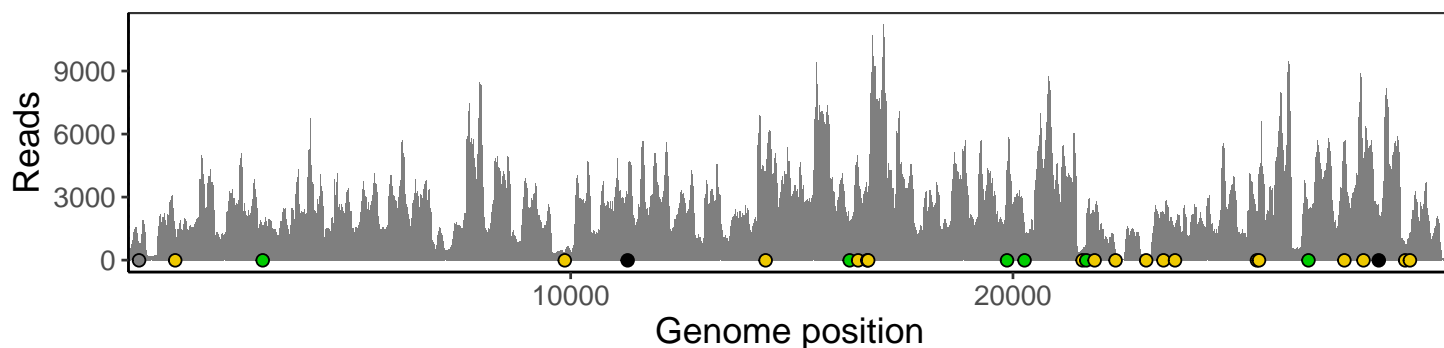
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
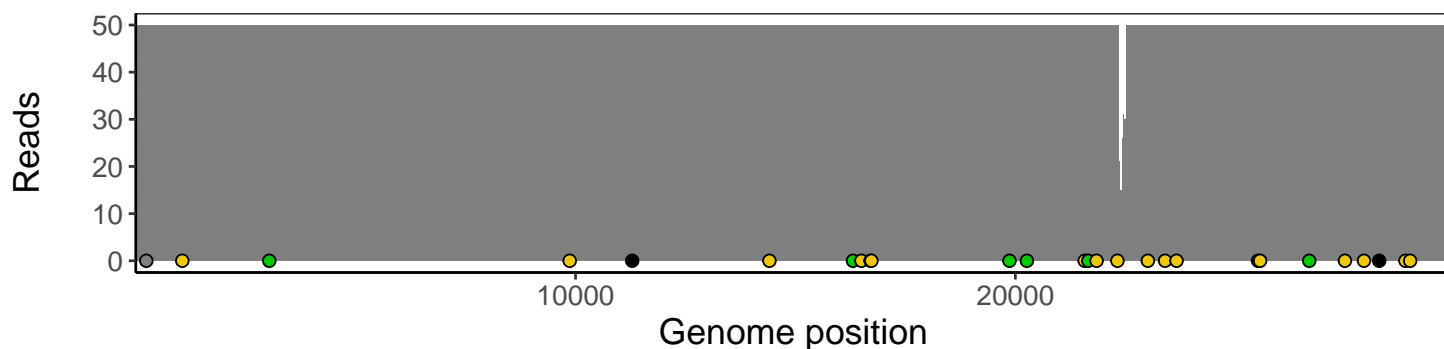
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
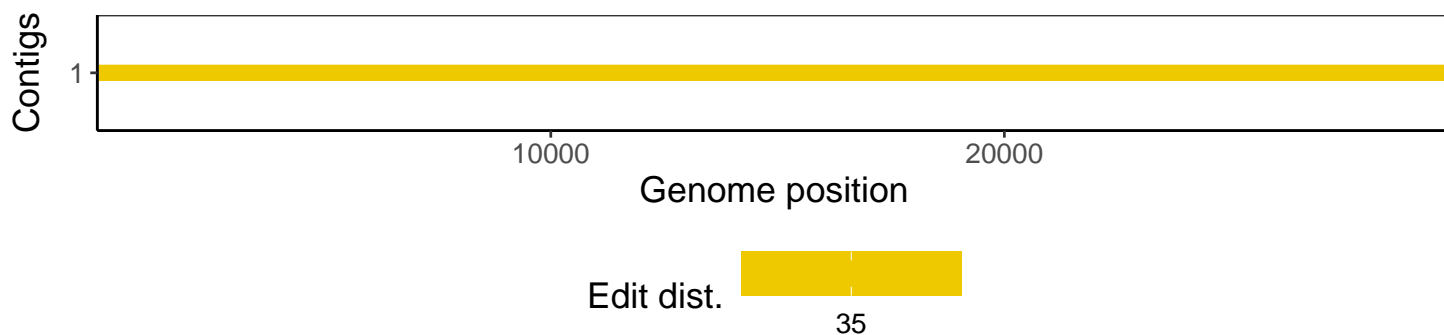
Software environment

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