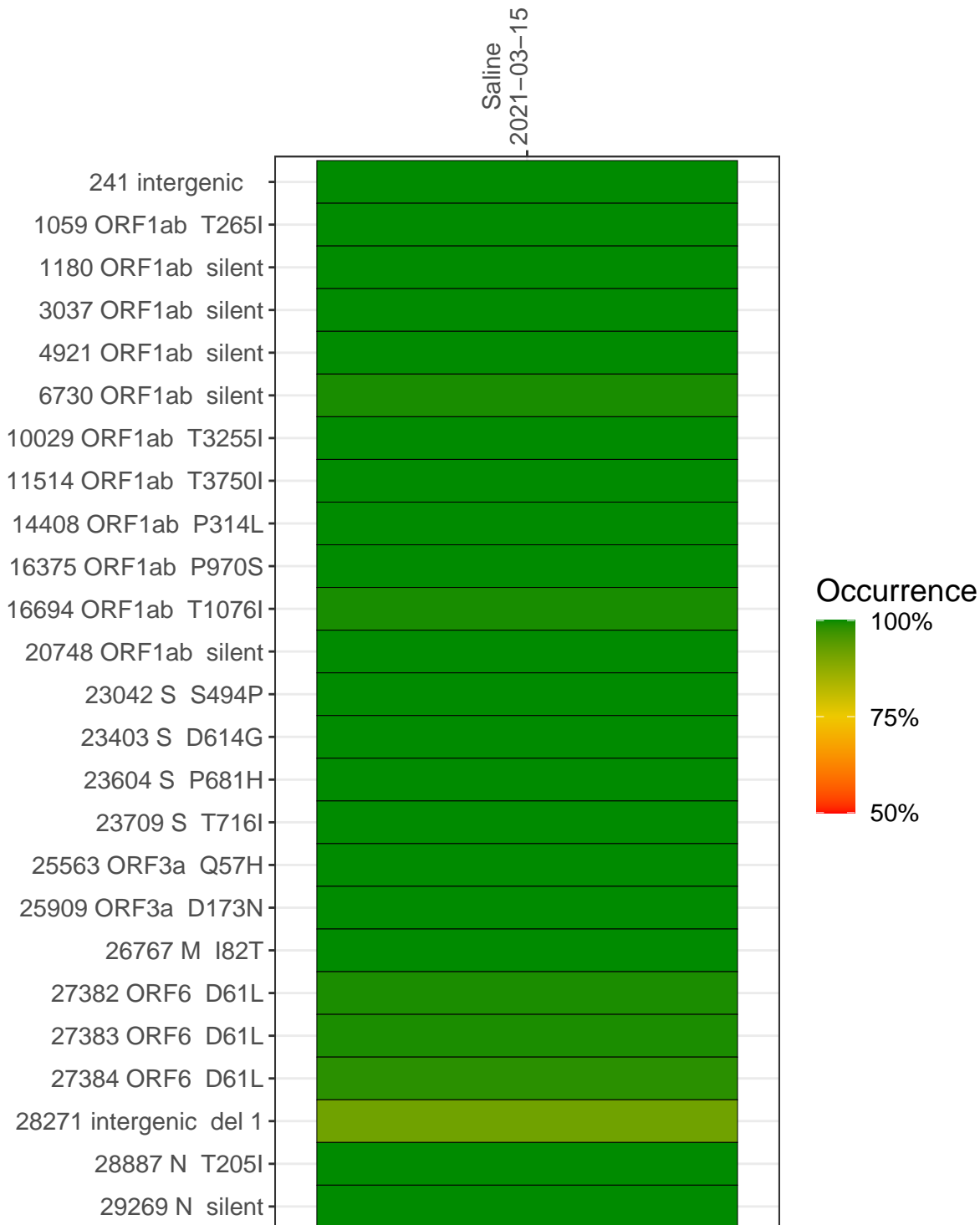# COVID-19 subject UPHS-0211

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.
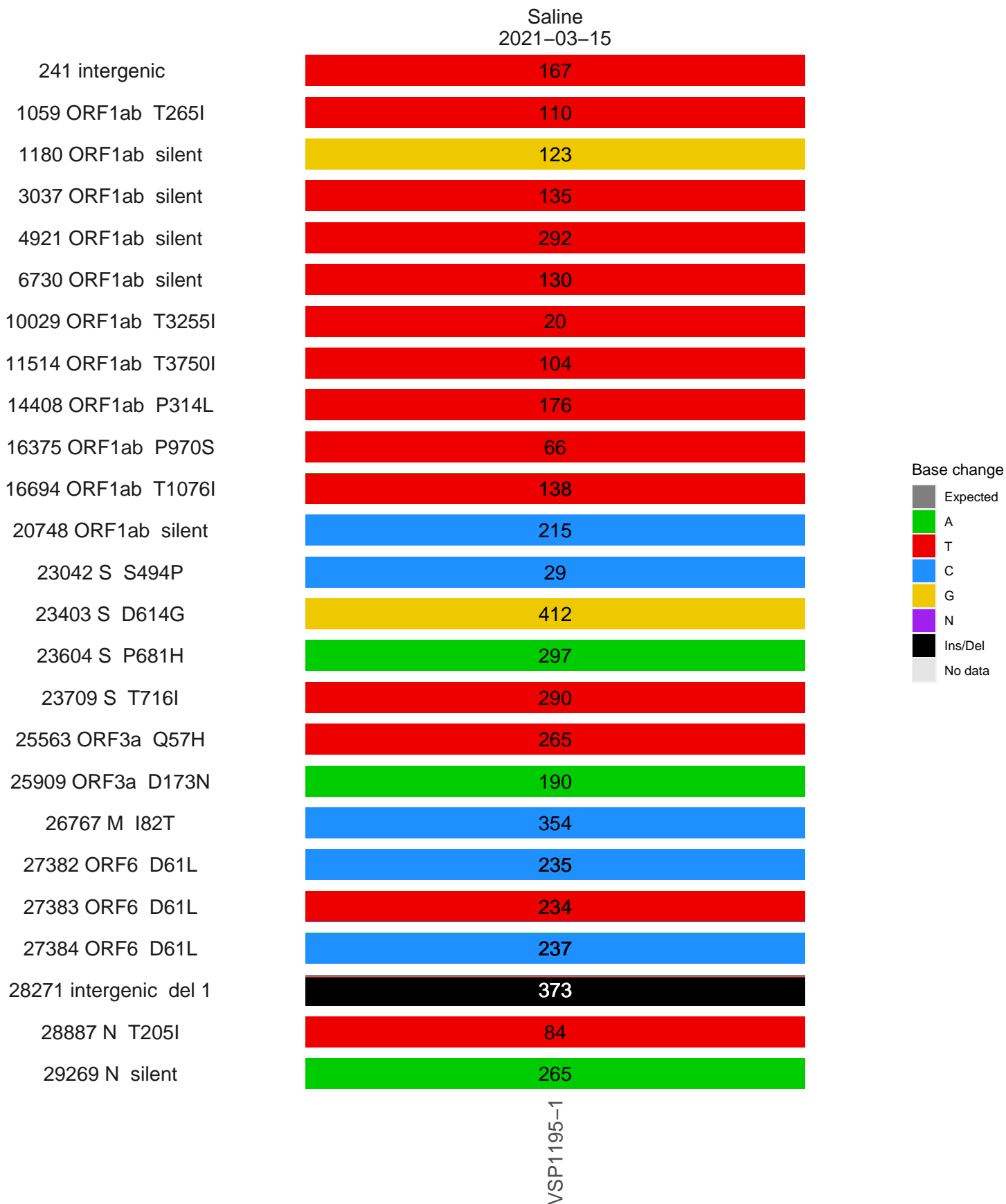
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1195-1	single experiment	NA	Saline	2021-03-15	22.35	B.1.575	99.6%	99.0%

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
2021−03−15

Position	VSP1195−1
241 intergenic	167
1059 ORF1ab T265I	110
1180 ORF1ab silent	123
3037 ORF1ab silent	135
4921 ORF1ab silent	292
6730 ORF1ab silent	130
10029 ORF1ab T3255I	20
11514 ORF1ab T3750I	104
14408 ORF1ab P314L	176
16375 ORF1ab P970S	66
16694 ORF1ab T1076I	138
20748 ORF1ab silent	215
23042 S S494P	29
23403 S D614G	412
23604 S P681H	297
23709 S T716I	290
25563 ORF3a Q57H	265
25909 ORF3a D173N	190
26767 M I82T	354
27382 ORF6 D61L	235
27383 ORF6 D61L	234
27384 ORF6 D61L	237
28271 intergenic del 1	373
28887 N T205I	84
29269 N silent	265

Base change

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

3

Analyses of individual experiments and composite results

**VSP1195-1 | 2021-03-15 | Saline | UPHS-0211 | 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.
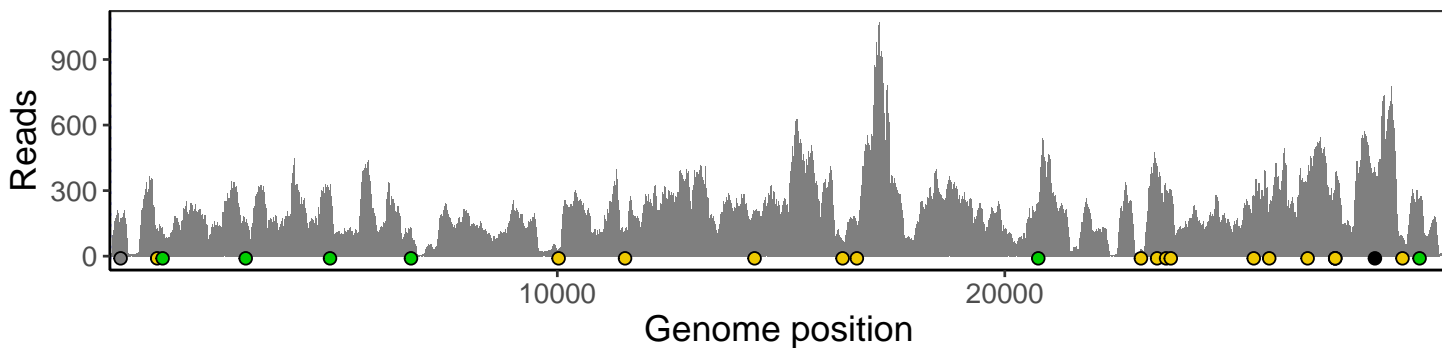
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
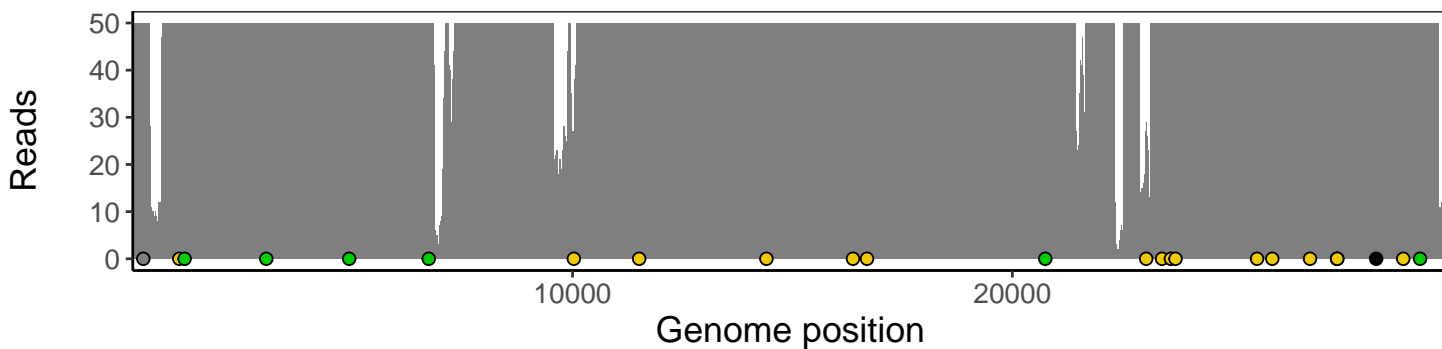
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
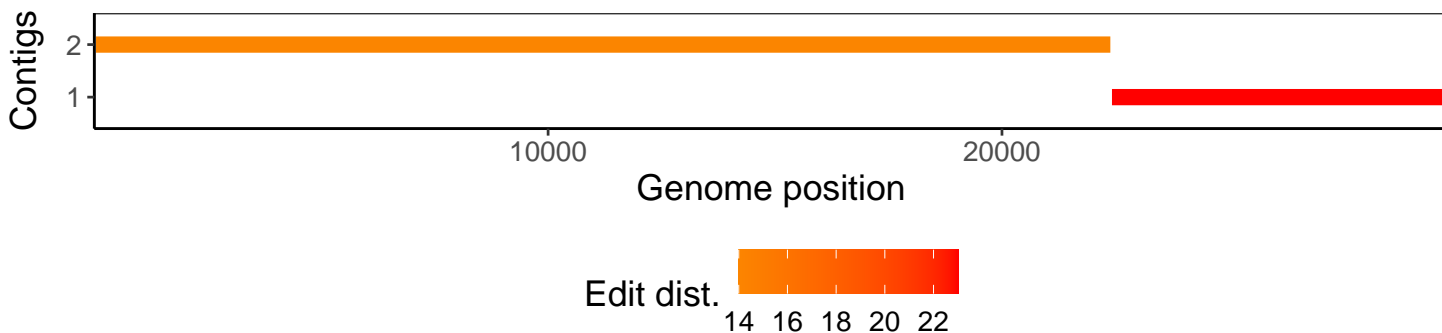
Software environment

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