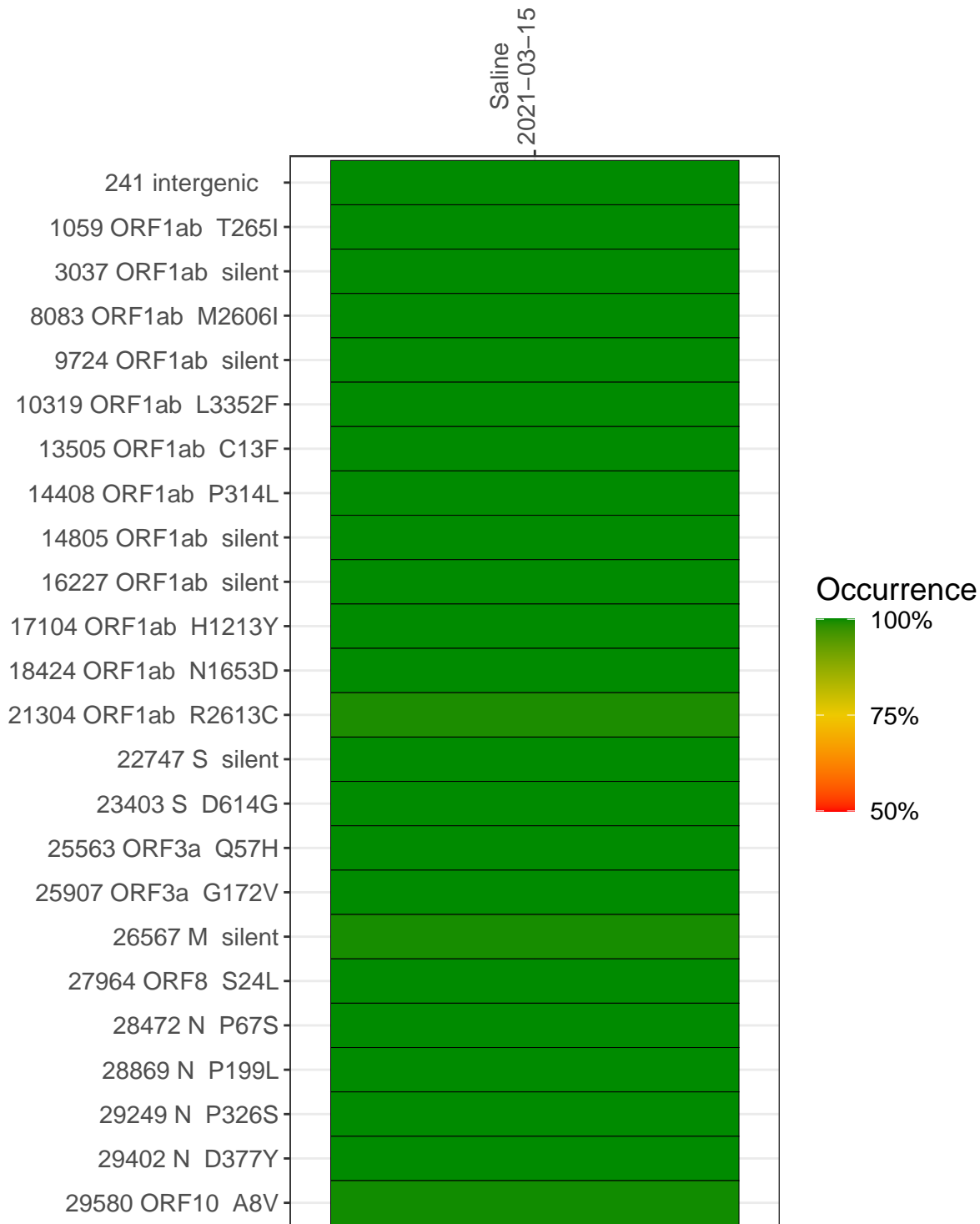# COVID-19 subject UPHS-0206

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.
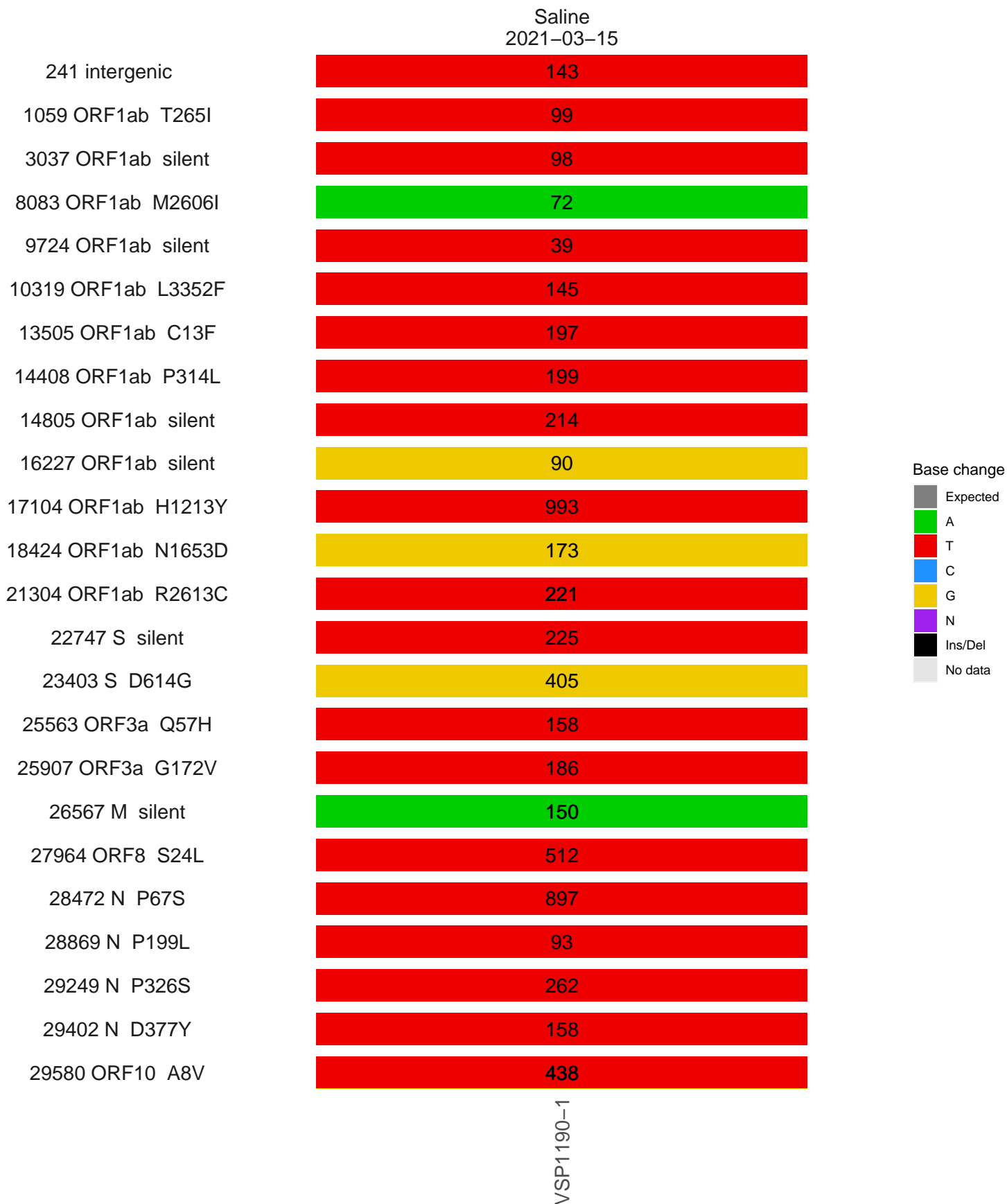
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1190-1	single experiment	NA	Saline	2021-03-15	22.30	B.1.2	99.6%	99.1%

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

	VSP1190−1
241 intergenic	143
1059 ORF1ab T265I	99
3037 ORF1ab silent	98
8083 ORF1ab M2606I	72
9724 ORF1ab silent	39
10319 ORF1ab L3352F	145
13505 ORF1ab C13F	197
14408 ORF1ab P314L	199
14805 ORF1ab silent	214
16227 ORF1ab silent	90
17104 ORF1ab H1213Y	993
18424 ORF1ab N1653D	173
21304 ORF1ab R2613C	221
22747 S silent	225
23403 S D614G	405
25563 ORF3a Q57H	158
25907 ORF3a G172V	186
26567 M silent	150
27964 ORF8 S24L	512
28472 N P67S	897
28869 N P199L	93
29249 N P326S	262
29402 N D377Y	158
29580 ORF10 A8V	438

Base change

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

Analyses of individual experiments and composite results

**VSP1190-1 | 2021-03-15 | Saline | UPHS-0206 | 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.
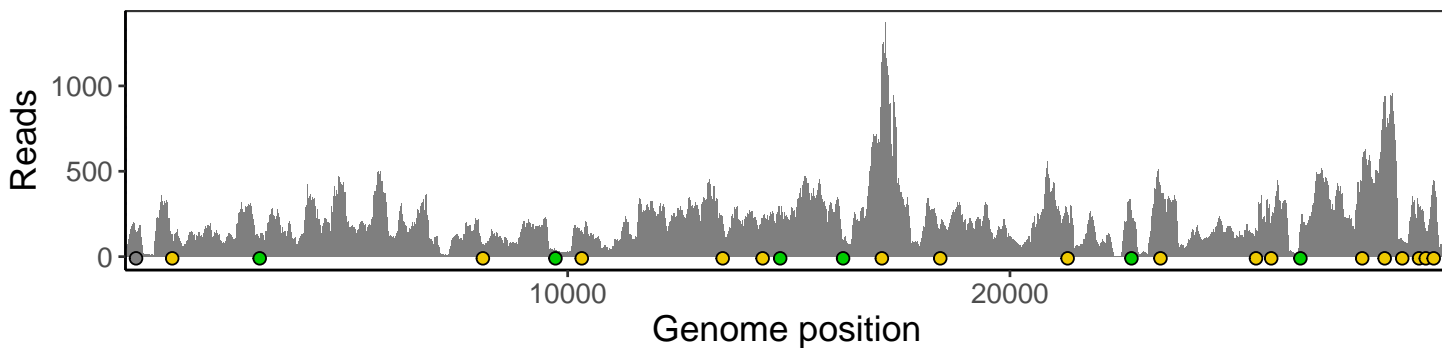
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
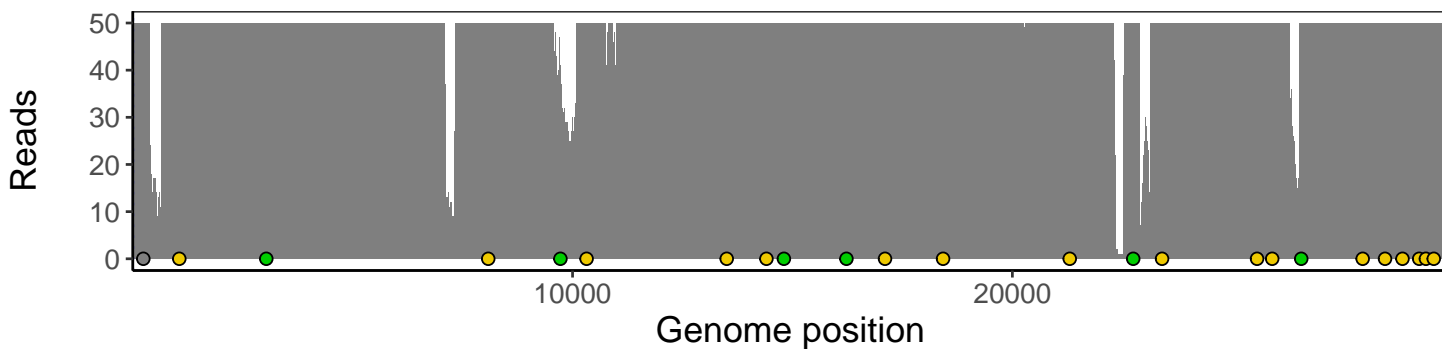
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
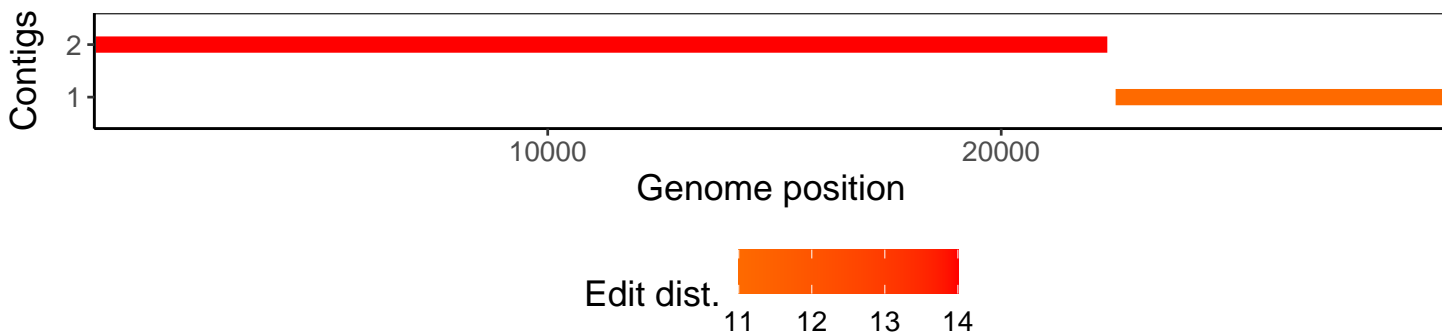
Software environment

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