# COVID-19 subject UPHS-0224

*2021-05-05*

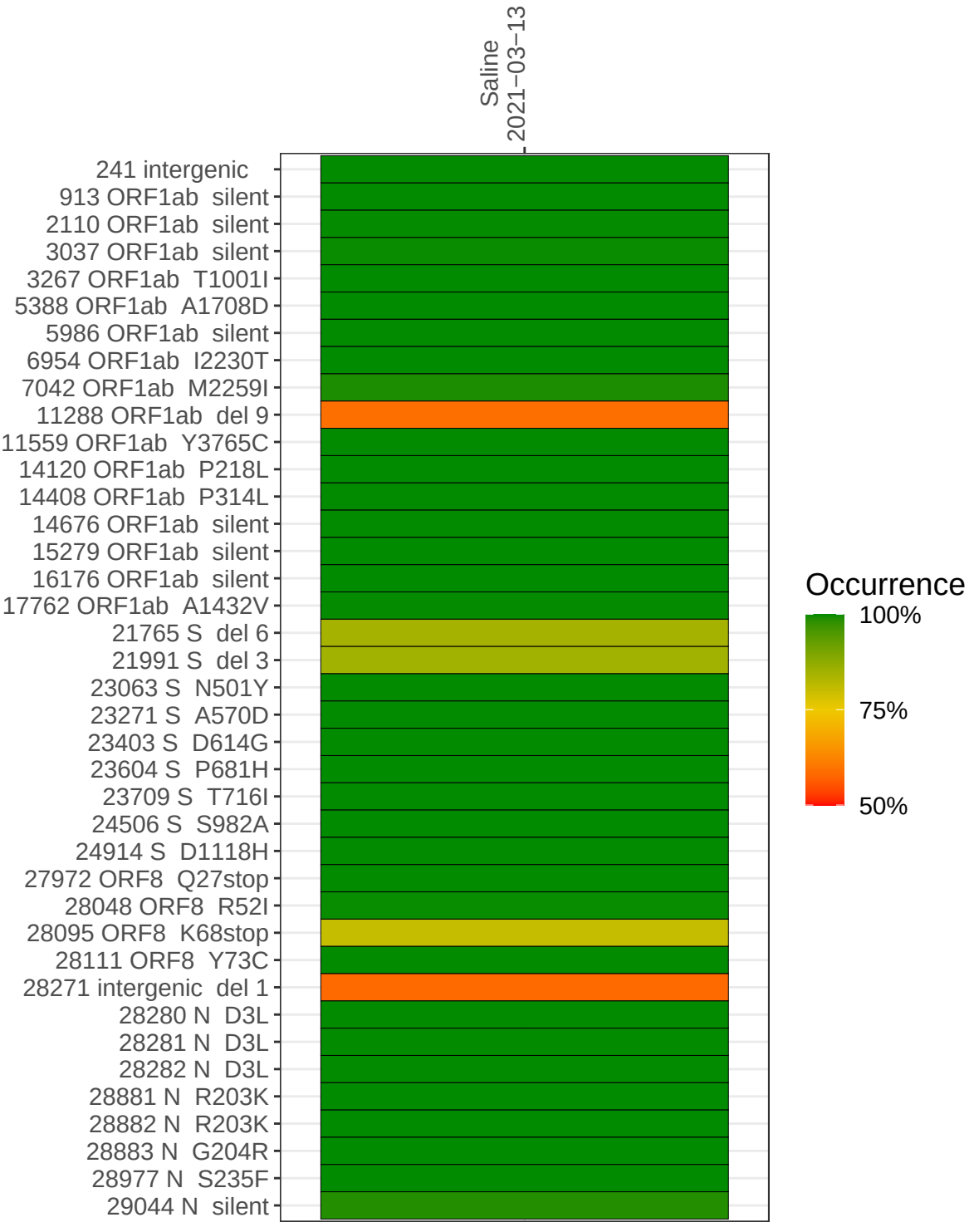
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

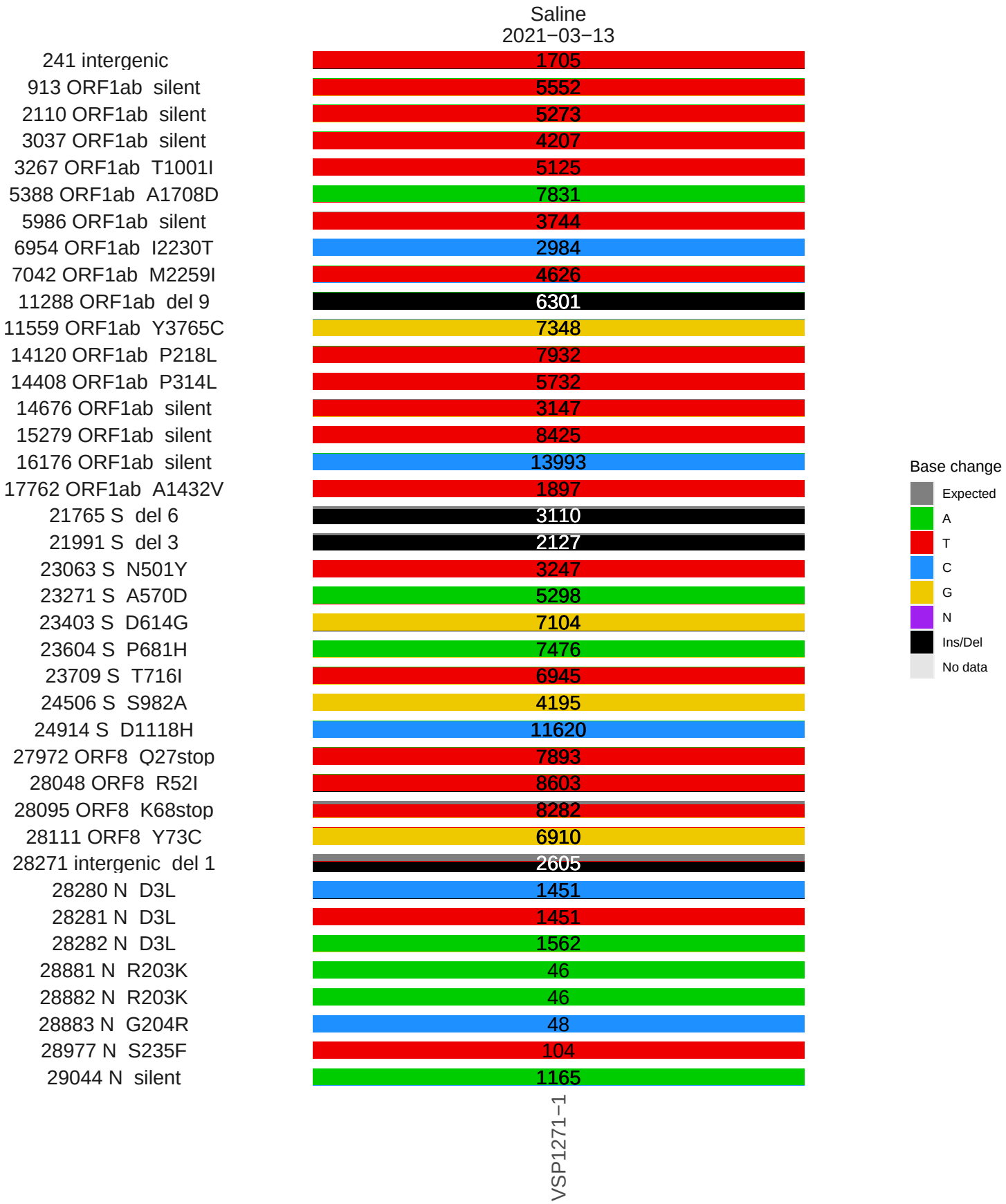
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1271-1 | single experiment | NA | Saline | 2021-03-13 | 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.

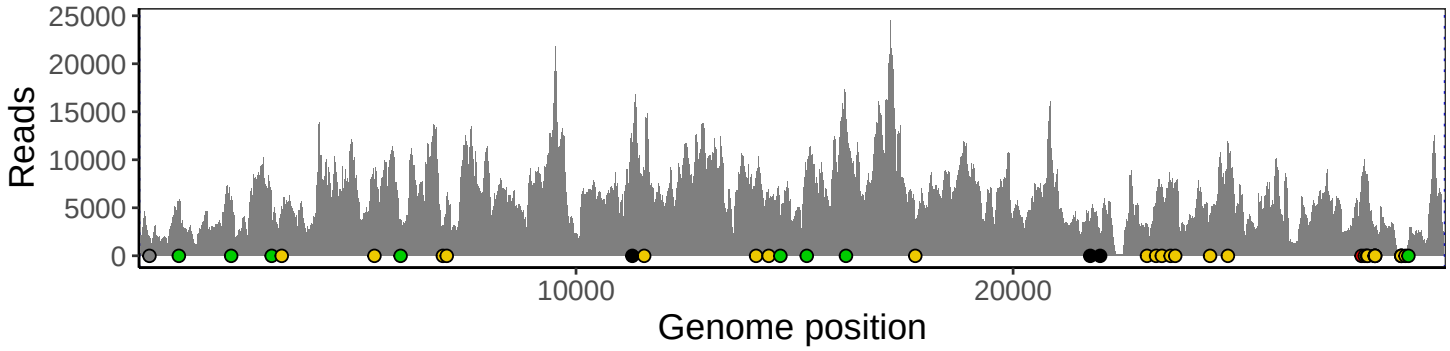



Saline
2021−03−13
241 intergenic 1705
913 ORF1ab silent 5552
2110 ORF1ab silent 5273
3037 ORF1ab silent 4207
3267 ORF1ab T1001I 5125
5388 ORF1ab A1708D 7831
5986 ORF1ab silent 3744
6954 ORF1ab I2230T 2984
7042 ORF1ab M2259I 4626
11288 ORF1ab del 9 6301
11559 ORF1ab Y3765C 7348
14120 ORF1ab P218L 7932
14408 ORF1ab P314L 5732
14676 ORF1ab silent 3147
15279 ORF1ab silent 8425
16176 ORF1ab silent 13993
17762 ORF1ab A1432V 1897
21765 S del 6 3110
21991 S del 3 2127
23063 S N501Y 3247
23271 S A570D 5298
23403 S D614G 7104
23604 S P681H 7476
23709 S T716I 6945
24506 S S982A 4195
24914 S D1118H 11620
27972 ORF8 Q27stop 7893
28048 ORF8 R52I 8603
28095 ORF8 K68stop 8282
28111 ORF8 Y73C 6910
28271 intergenic del 1 2605
28280 N D3L 1451
28281 N D3L 1451
28282 N D3L 1562
28881 N R203K 46
28882 N R203K 46
28883 N G204R 48
28977 N S235F 104
29044 N silent 1165
VSP1271−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

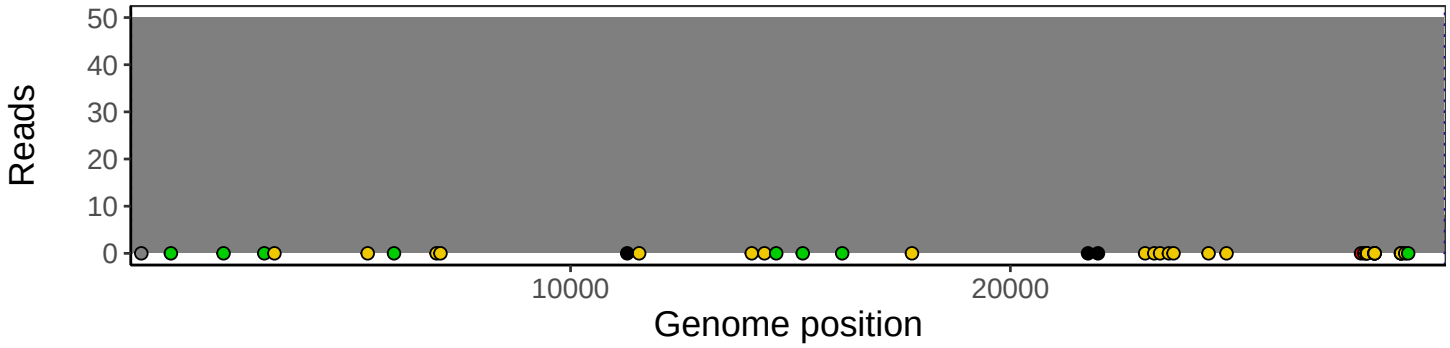
## Analyses of individual experiments and composite results

### VSP1271-1 | 2021-03-13 | Saline | UPHS-0224 | genomes | single experiment

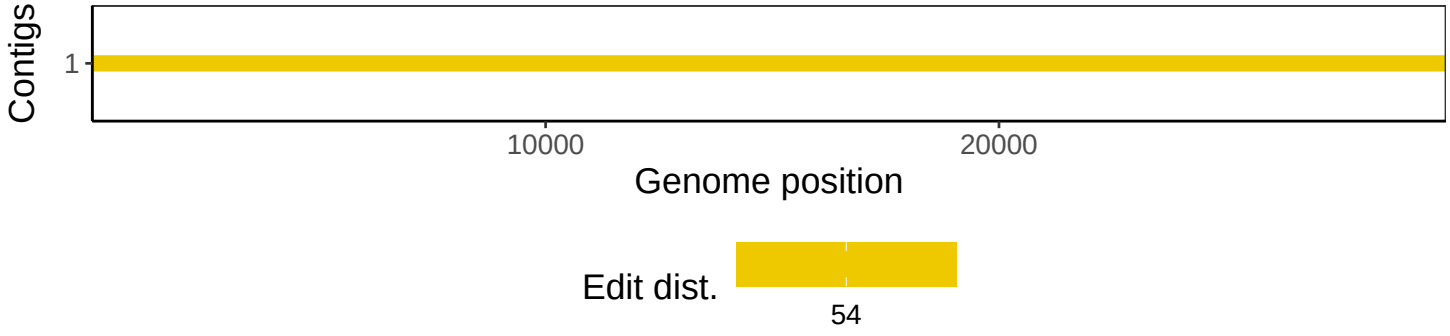
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 | 3.0.0 |
| 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 |