# COVID-19 subject UPHS-1129

*2021-06-23*

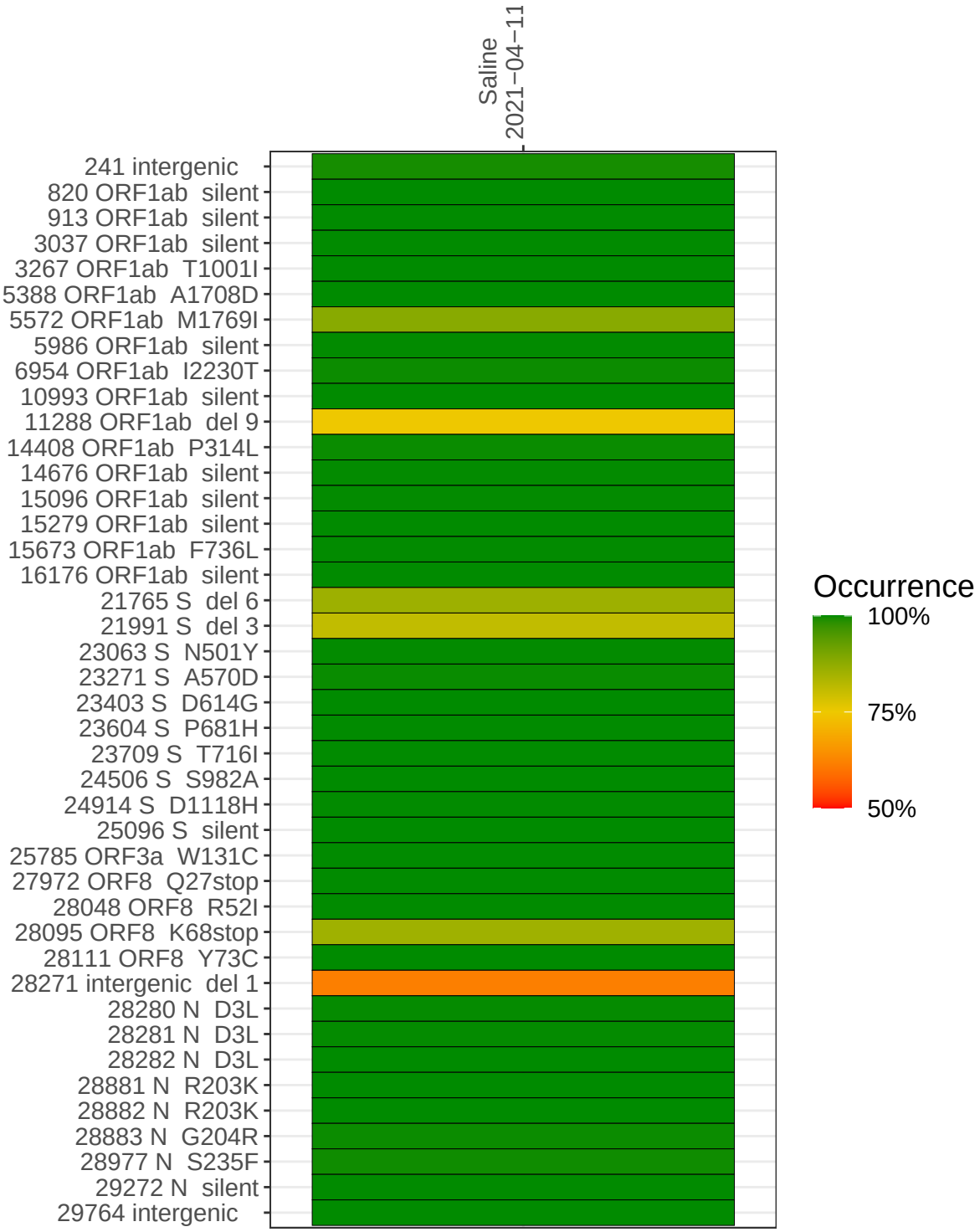
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

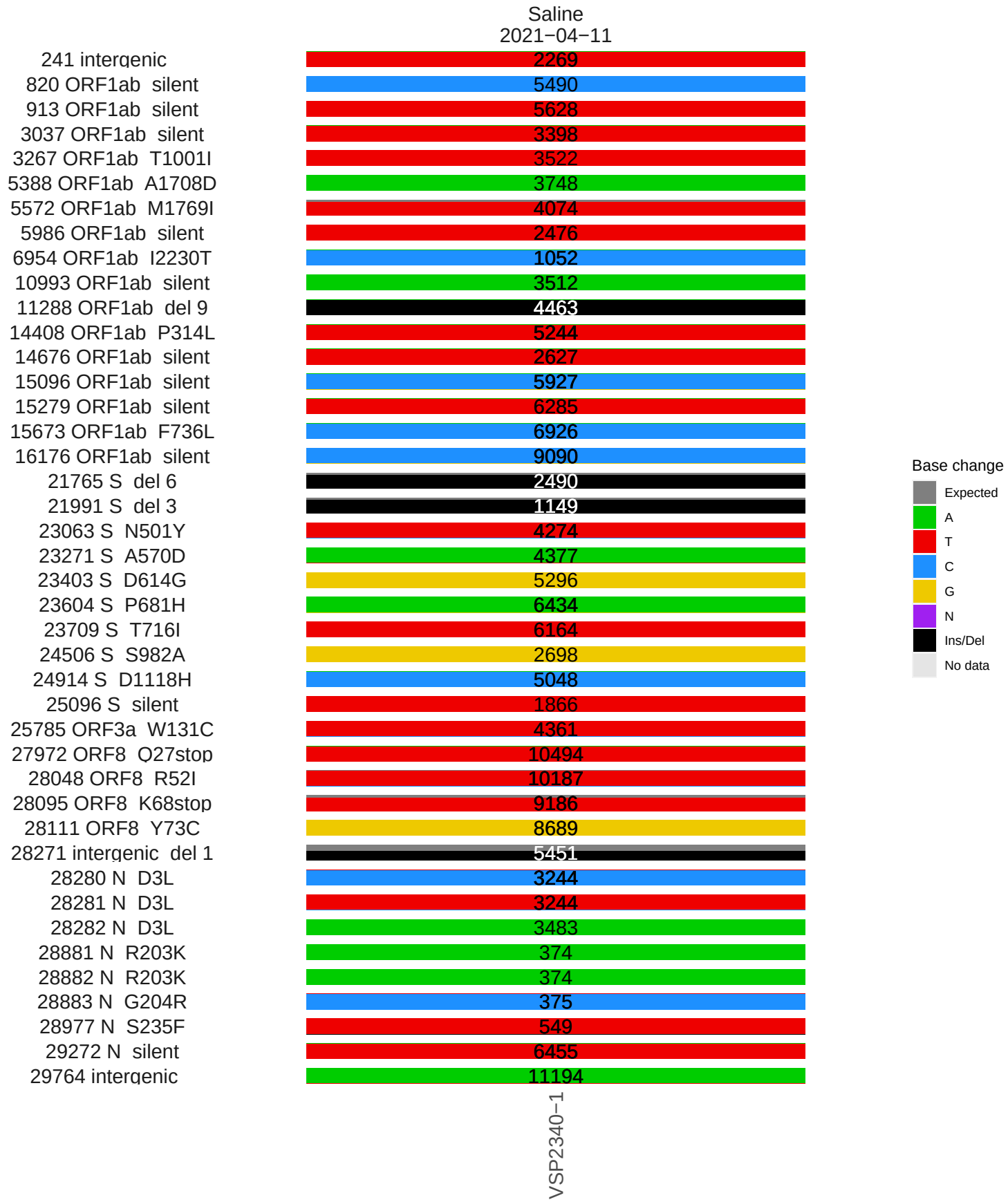
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP2340-1 | single experiment | NA | Saline | 2021-04-11 | 29.82 | B.1.1.7 | 99.7% | 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.

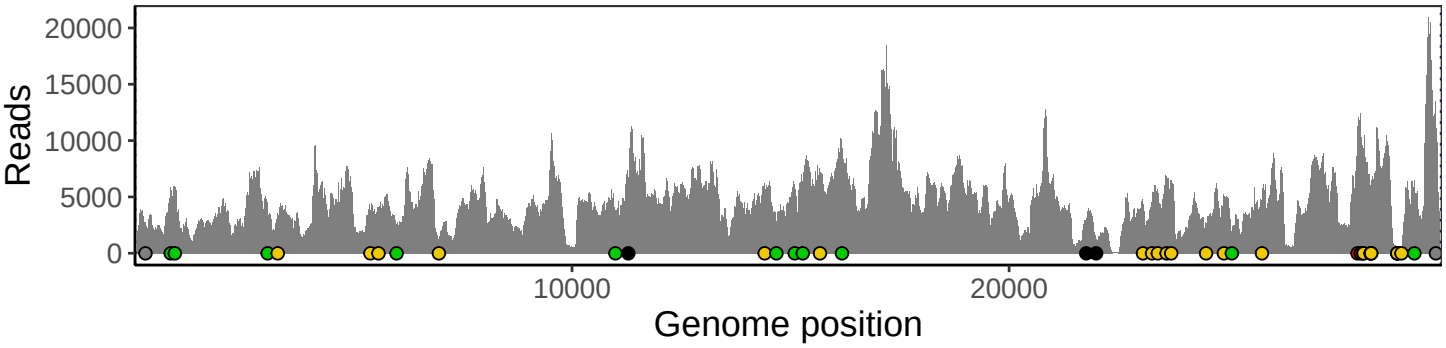



Saline
2021−04−11
241 intergenic 2269
820 ORF1ab silent 5490
913 ORF1ab silent 5628
3037 ORF1ab silent 3398
3267 ORF1ab T1001I 3522
5388 ORF1ab A1708D 3748
5572 ORF1ab M1769I 4074
5986 ORF1ab silent 2476
6954 ORF1ab I2230T 1052
10993 ORF1ab silent 3512
11288 ORF1ab del 9 4463
14408 ORF1ab P314L 5244
14676 ORF1ab silent 2627
15096 ORF1ab silent 5927
15279 ORF1ab silent 6285
15673 ORF1ab F736L 6926
16176 ORF1ab silent 9090
21765 S del 6 2490
21991 S del 3 1149
23063 S N501Y 4274
23271 S A570D 4377
23403 S D614G 5296
23604 S P681H 6434
23709 S T716I 6164
24506 S S982A 2698
24914 S D1118H 5048
25096 S silent 1866
25785 ORF3a W131C 4361
27972 ORF8 Q27stop 10494
28048 ORF8 R52I 10187
28095 ORF8 K68stop 9186
28111 ORF8 Y73C 8689
28271 intergenic del 1 5451
28280 N D3L 3244
28281 N D3L 3244
28282 N D3L 3483
28881 N R203K 374
28882 N R203K 374
28883 N G204R 375
28977 N S235F 549
29272 N silent 6455
29764 intergenic 11194
VSP2340−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

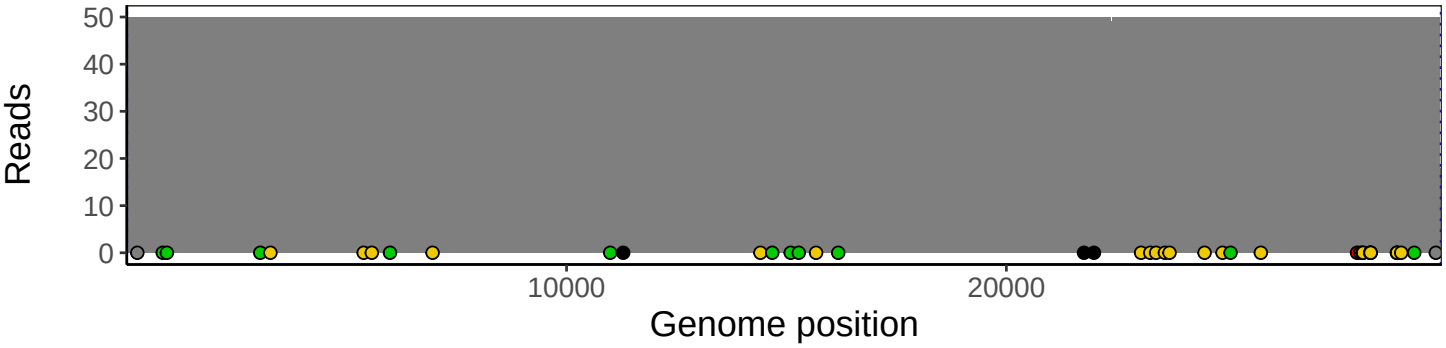
## Analyses of individual experiments and composite results

### VSP2340-1 | 2021-04-11 | Saline | UPHS-1129 | genomes | single experiment

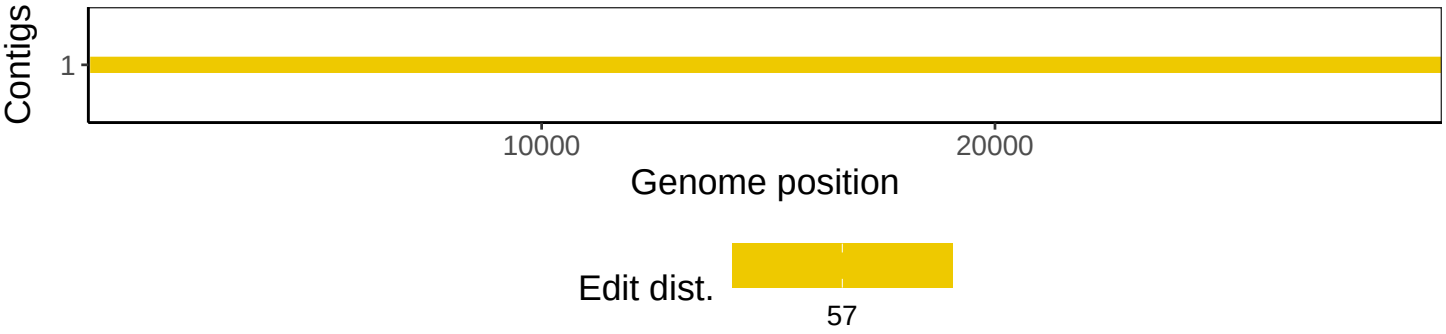
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |