# COVID-19 subject UPHS-1372

*2021-05-21*

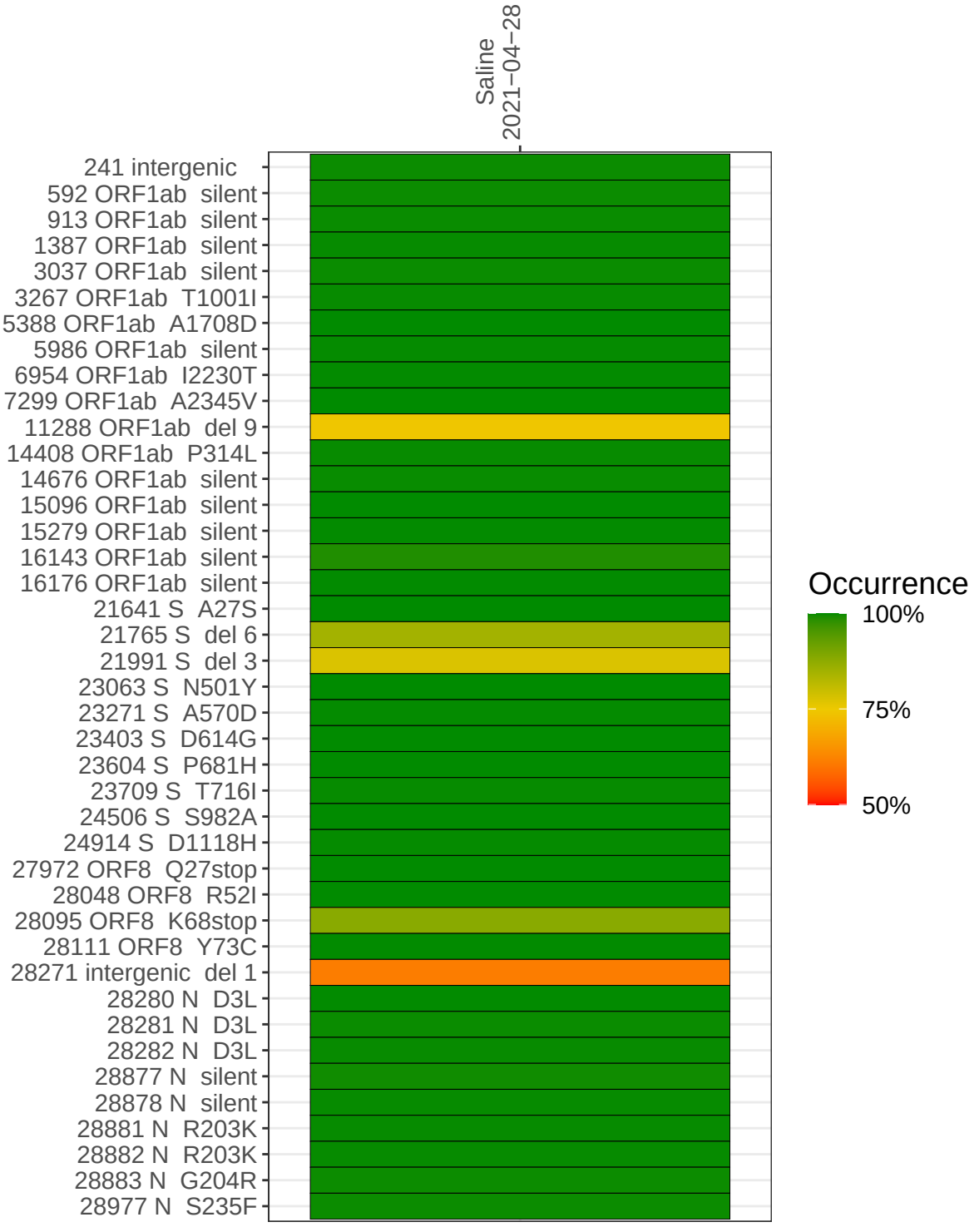
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

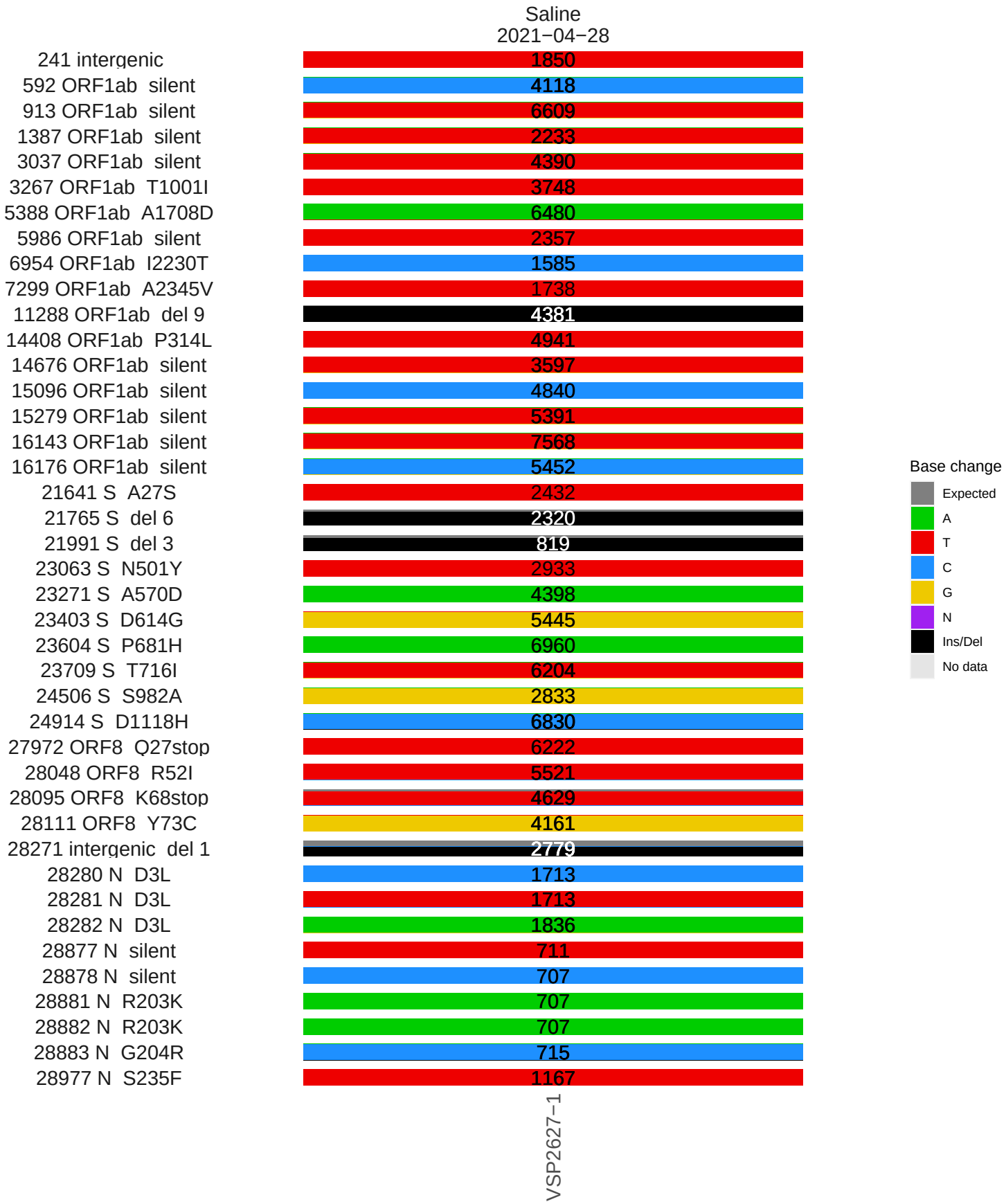
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP2627-1 | single experiment | NA | Saline | 2021-04-28 | 29.86 | B.1.1.7 | 99.9% | 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.

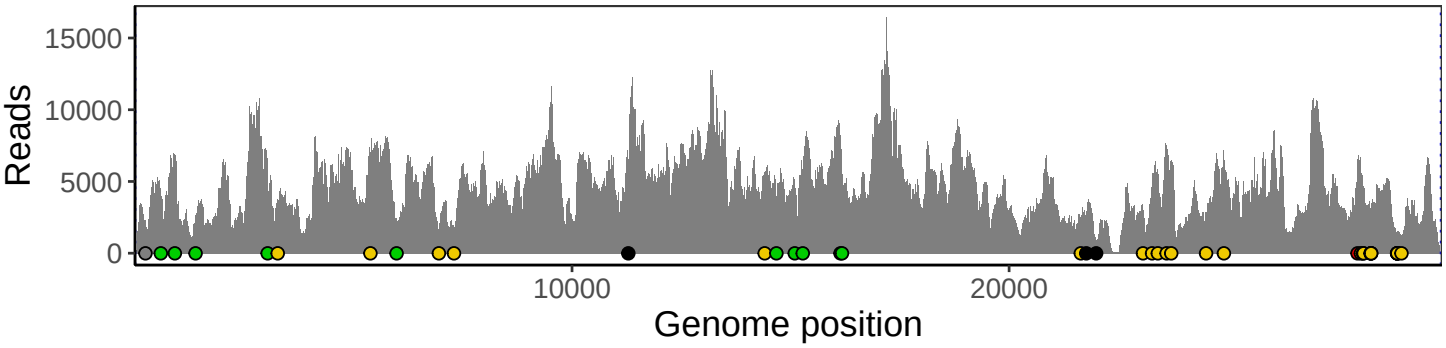



Saline
2021−04−28
241 intergenic 1850
592 ORF1ab silent 4118
913 ORF1ab silent 6609
1387 ORF1ab silent 2233
3037 ORF1ab silent 4390
3267 ORF1ab T1001I 3748
5388 ORF1ab A1708D 6480
5986 ORF1ab silent 2357
6954 ORF1ab I2230T 1585
7299 ORF1ab A2345V 1738
11288 ORF1ab del 9 4381
14408 ORF1ab P314L 4941
14676 ORF1ab silent 3597
15096 ORF1ab silent 4840
15279 ORF1ab silent 5391
16143 ORF1ab silent 7568
16176 ORF1ab silent 5452
21641 S A27S 2432
21765 S del 6 2320
21991 S del 3 819
23063 S N501Y 2933
23271 S A570D 4398
23403 S D614G 5445
23604 S P681H 6960
23709 S T716I 6204
24506 S S982A 2833
24914 S D1118H 6830
27972 ORF8 Q27stop 6222
28048 ORF8 R52I 5521
28095 ORF8 K68stop 4629
28111 ORF8 Y73C 4161
28271 intergenic del 1 2779
28280 N D3L 1713
28281 N D3L 1713
28282 N D3L 1836
28877 N silent 711
28878 N silent 707
28881 N R203K 707
28882 N R203K 707
28883 N G204R 715
28977 N S235F 1167
VSP2627−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

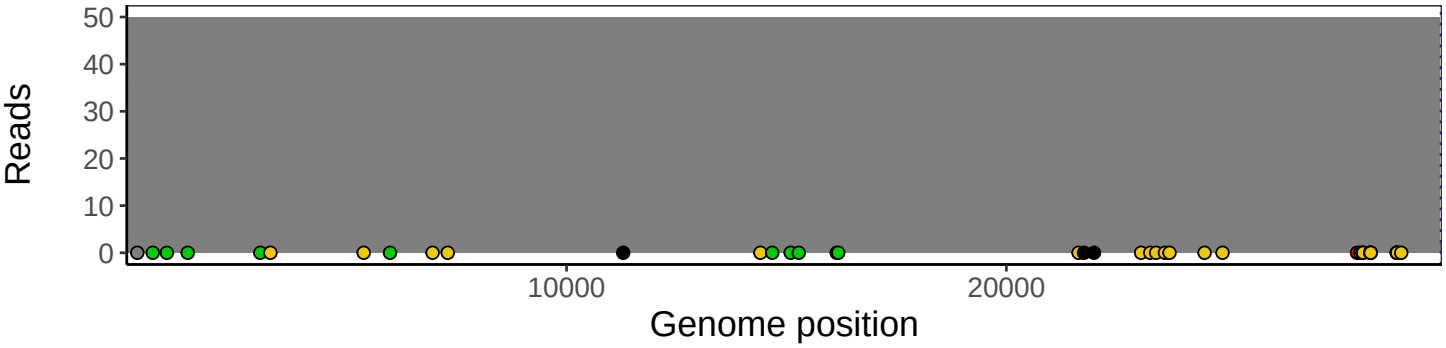
## Analyses of individual experiments and composite results

### VSP2627-1 | 2021-04-28 | Saline | UPHS-1372 | genomes | single experiment

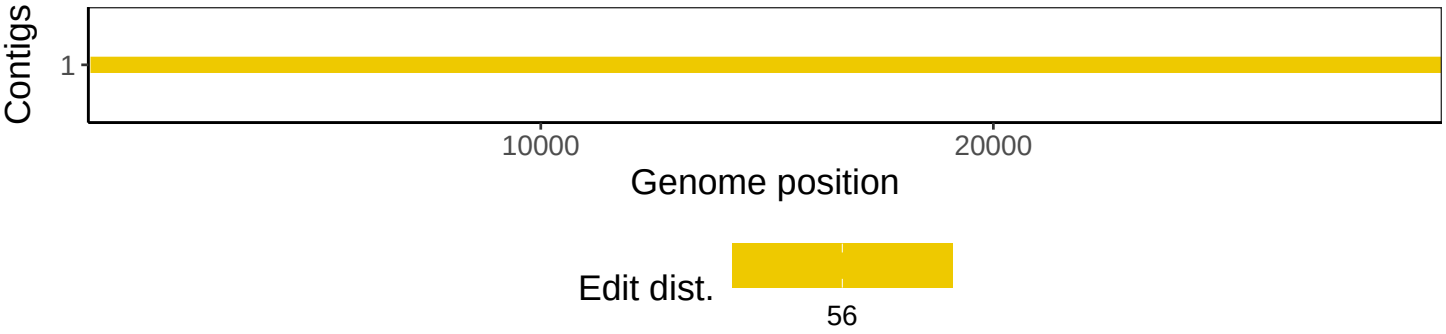
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 | 3.3.3 |
| 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 |