# COVID-19 subject UPHS-1365

*2021-05-21*

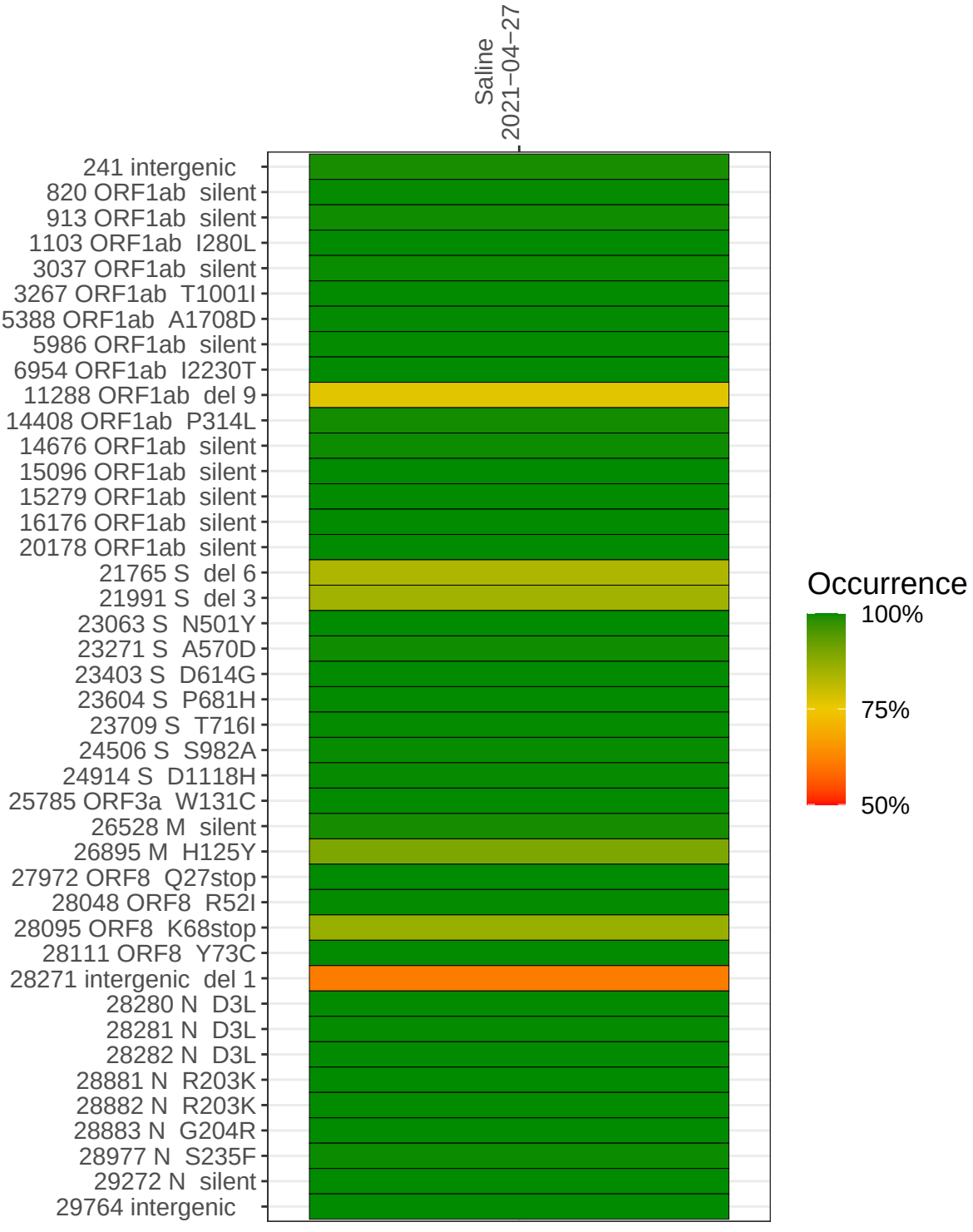
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

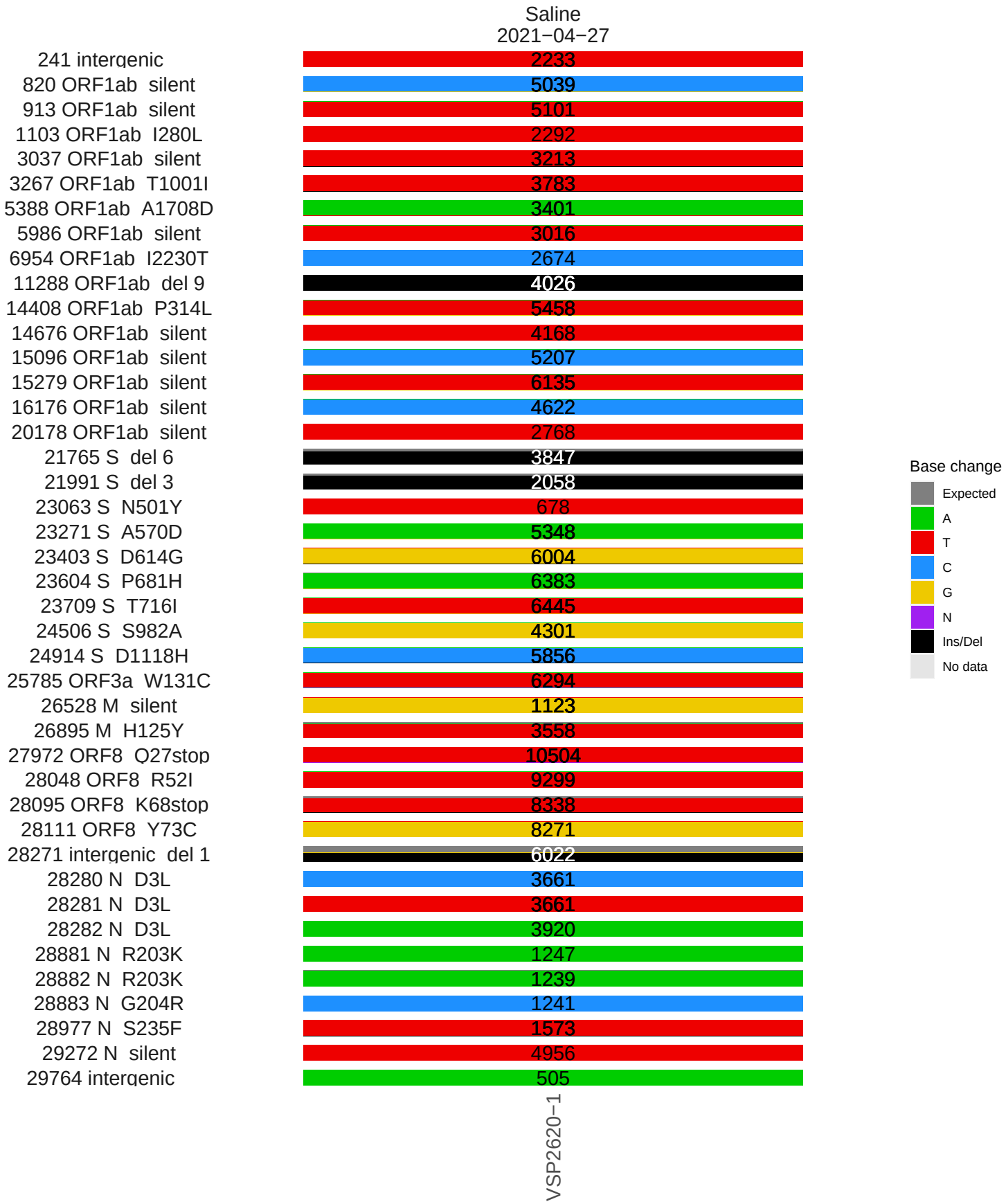
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP2620-1 | single experiment | NA | Saline | 2021-04-27 | 29.83 | B.1.1.7 | 99.8% | 99.8% |

**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.

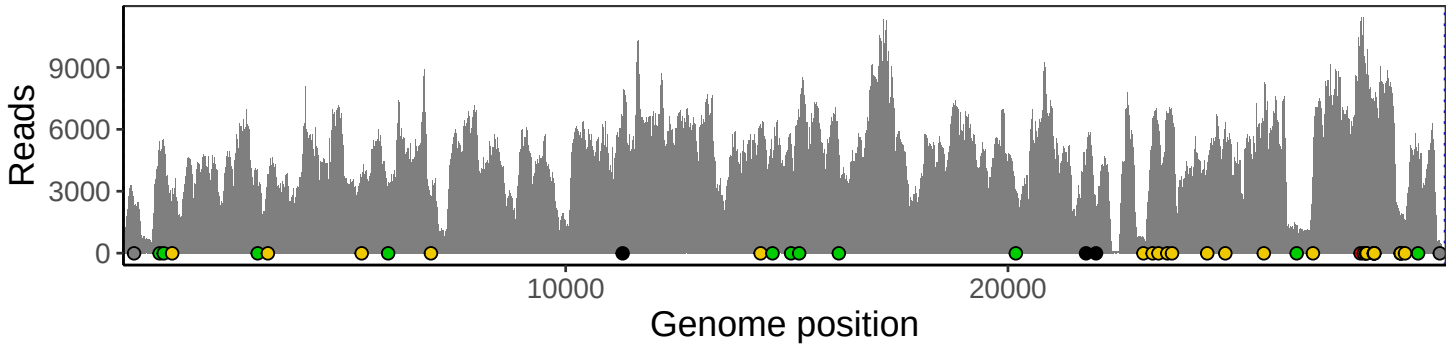



Saline
2021−04−27
241 intergenic 2233
820 ORF1ab silent 5039
913 ORF1ab silent 5101
1103 ORF1ab I280L 2292
3037 ORF1ab silent 3213
3267 ORF1ab T1001I 3783
5388 ORF1ab A1708D 3401
5986 ORF1ab silent 3016
6954 ORF1ab I2230T 2674
11288 ORF1ab del 9 4026
14408 ORF1ab P314L 5458
14676 ORF1ab silent 4168
15096 ORF1ab silent 5207
15279 ORF1ab silent 6135
16176 ORF1ab silent 4622
20178 ORF1ab silent 2768
21765 S del 6 3847
21991 S del 3 2058
23063 S N501Y 678
23271 S A570D 5348
23403 S D614G 6004
23604 S P681H 6383
23709 S T716I 6445
24506 S S982A 4301
24914 S D1118H 5856
25785 ORF3a W131C 6294
26528 M silent 1123
26895 M H125Y 3558
27972 ORF8 Q27stop 10504
28048 ORF8 R52I 9299
28095 ORF8 K68stop 8338
28111 ORF8 Y73C 8271
28271 intergenic del 1 6022
28280 N D3L 3661
28281 N D3L 3661
28282 N D3L 3920
28881 N R203K 1247
28882 N R203K 1239
28883 N G204R 1241
28977 N S235F 1573
29272 N silent 4956
29764 intergenic 505
VSP2620−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

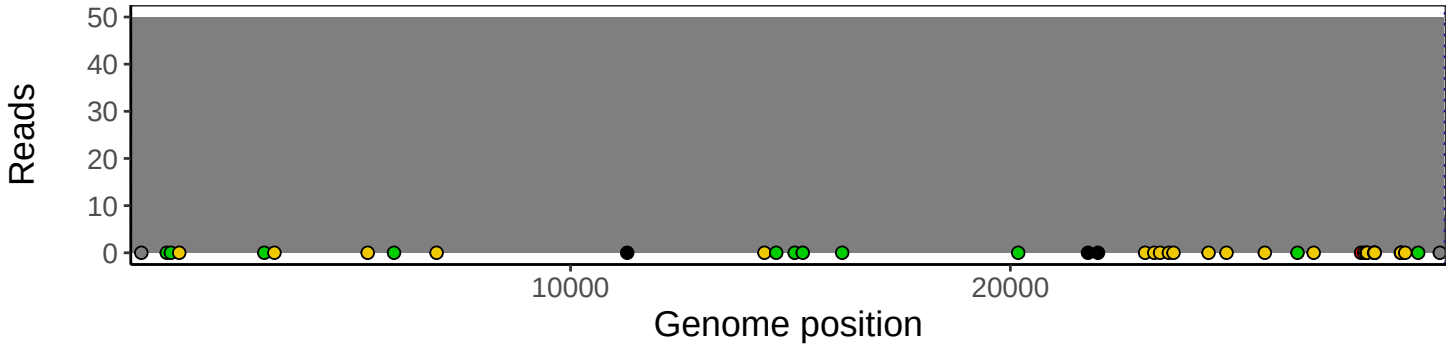
## Analyses of individual experiments and composite results

### VSP2620-1 | 2021-04-27 | Saline | UPHS-1365 | genomes | single experiment

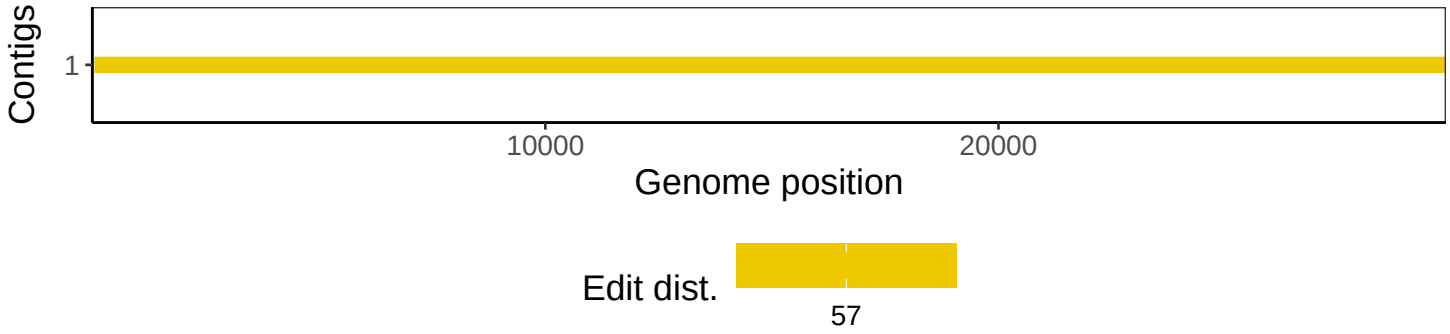
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |