# COVID-19 subject HUP Q-0122

*2021-05-05*

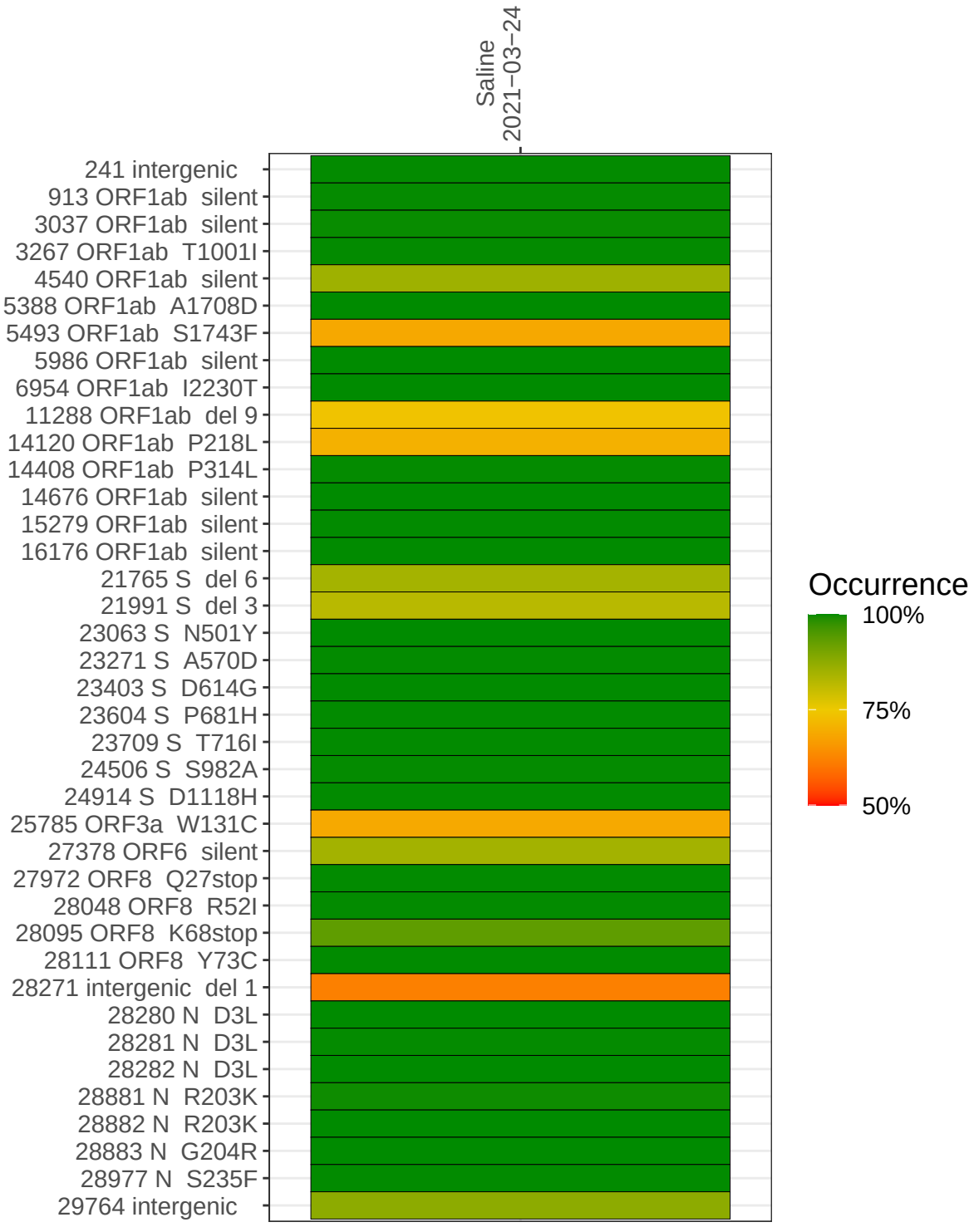
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

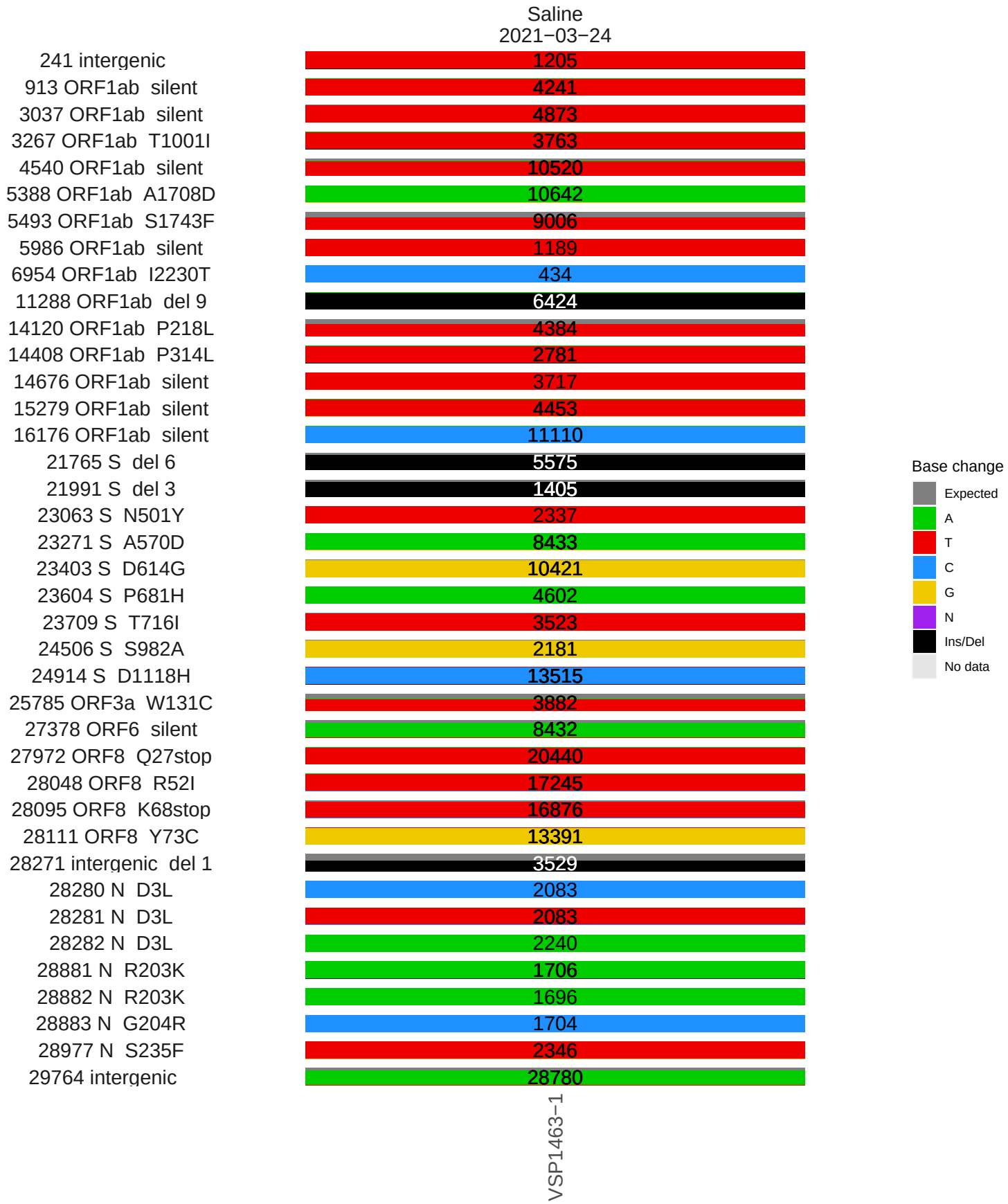
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1463-1 | single experiment | NA | Saline | 2021-03-24 | 29.83 | B.1.1.7 | 99.9% | 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.

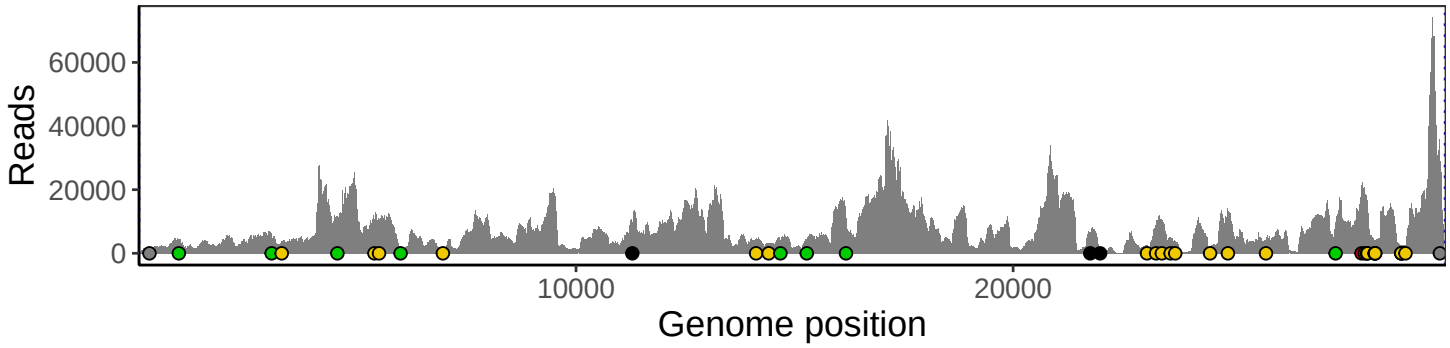



Saline
2021−03−24
241 intergenic 1205
913 ORF1ab silent 4241
3037 ORF1ab silent 4873
3267 ORF1ab T1001I 3763
4540 ORF1ab silent 10520
5388 ORF1ab A1708D 10642
5493 ORF1ab S1743F 9006
5986 ORF1ab silent 1189
6954 ORF1ab I2230T 434
11288 ORF1ab del 9 6424
14120 ORF1ab P218L 4384
14408 ORF1ab P314L 2781
14676 ORF1ab silent 3717
15279 ORF1ab silent 4453
16176 ORF1ab silent 11110
21765 S del 6 5575
21991 S del 3 1405
23063 S N501Y 2337
23271 S A570D 8433
23403 S D614G 10421
23604 S P681H 4602
23709 S T716I 3523
24506 S S982A 2181
24914 S D1118H 13515
25785 ORF3a W131C 3882
27378 ORF6 silent 8432
27972 ORF8 Q27stop 20440
28048 ORF8 R52I 17245
28095 ORF8 K68stop 16876
28111 ORF8 Y73C 13391
28271 intergenic del 1 3529
28280 N D3L 2083
28281 N D3L 2083
28282 N D3L 2240
28881 N R203K 1706
28882 N R203K 1696
28883 N G204R 1704
28977 N S235F 2346
29764 intergenic 28780
VSP1463−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

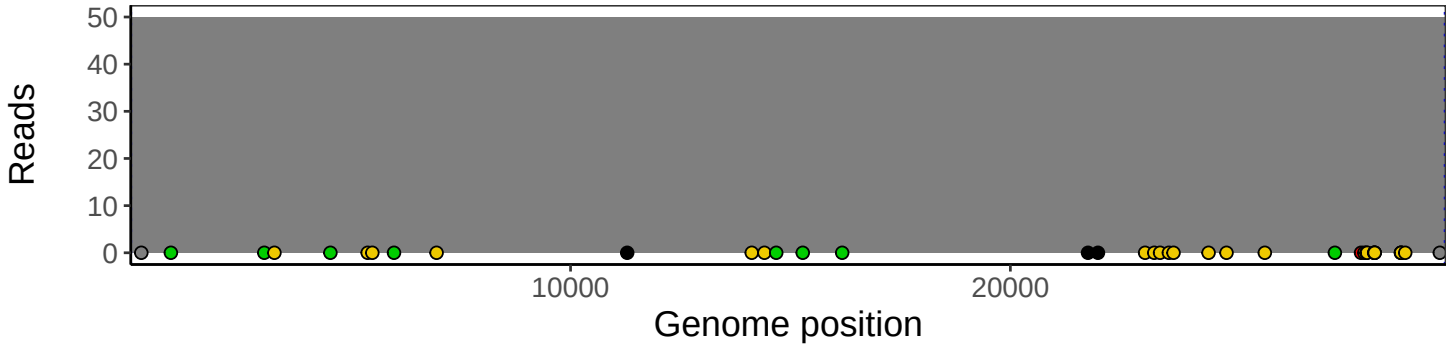
## Analyses of individual experiments and composite results

### VSP1463-1 | 2021-03-24 | Saline | HUP Q-0122 | genomes | single experiment

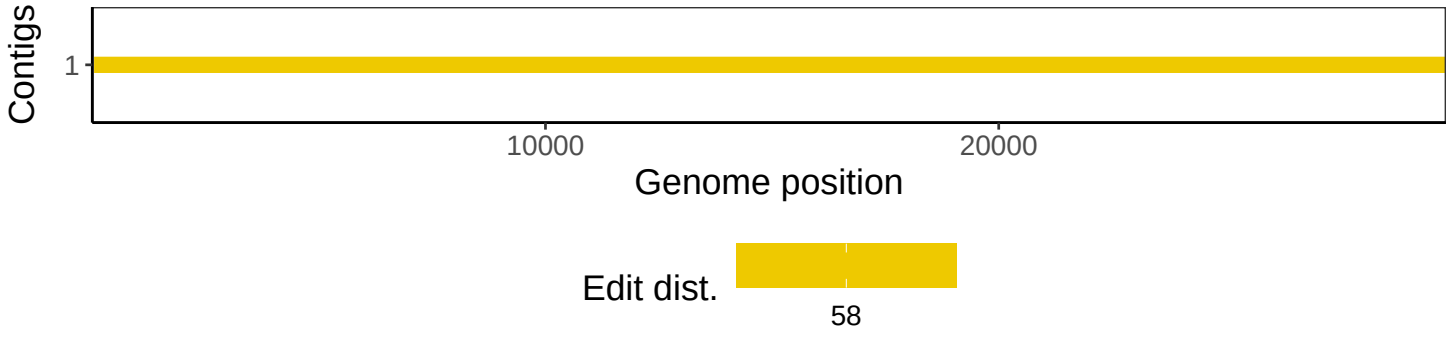
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |