# COVID-19 subject HUP Q-0124

*2021-05-05*

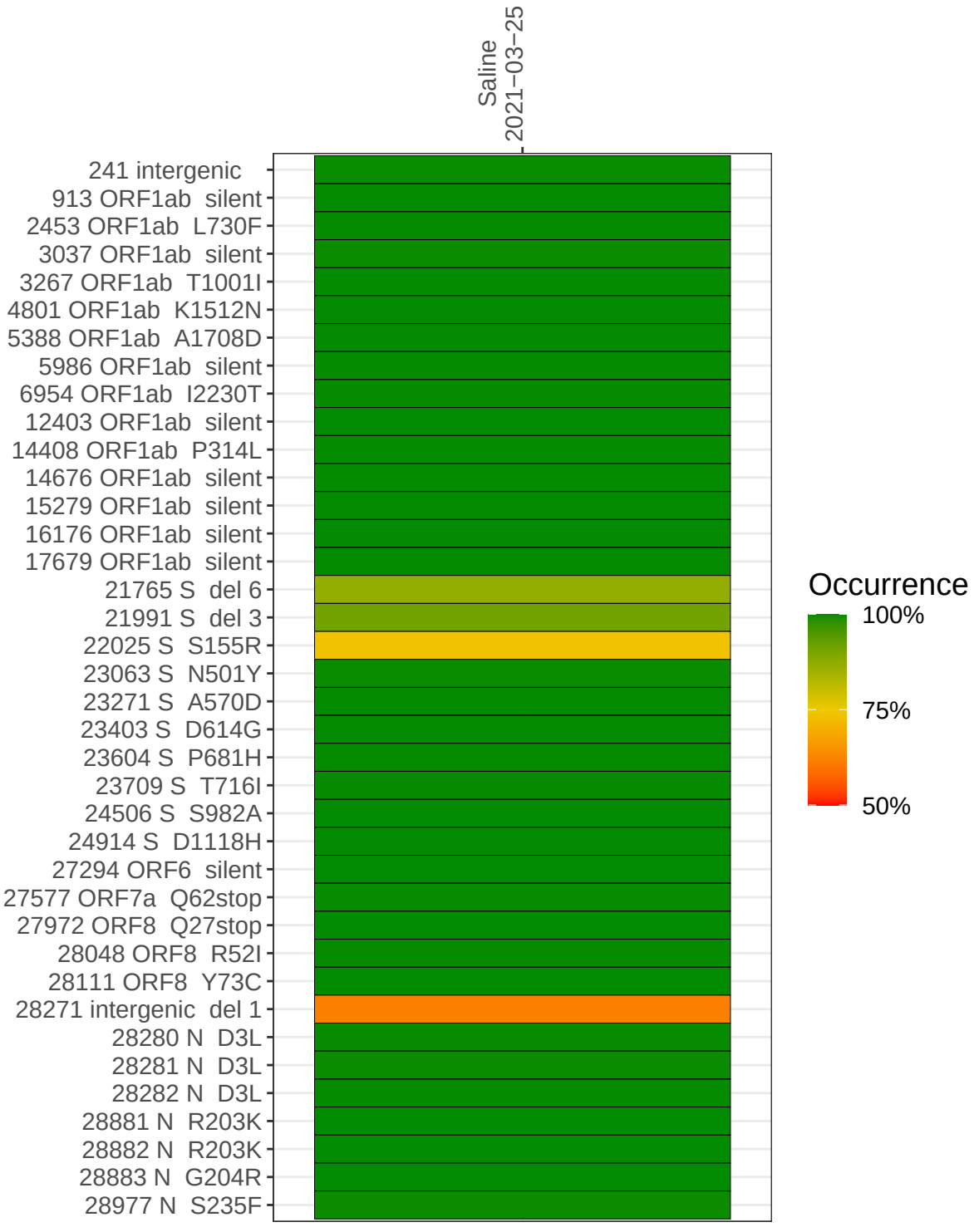
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

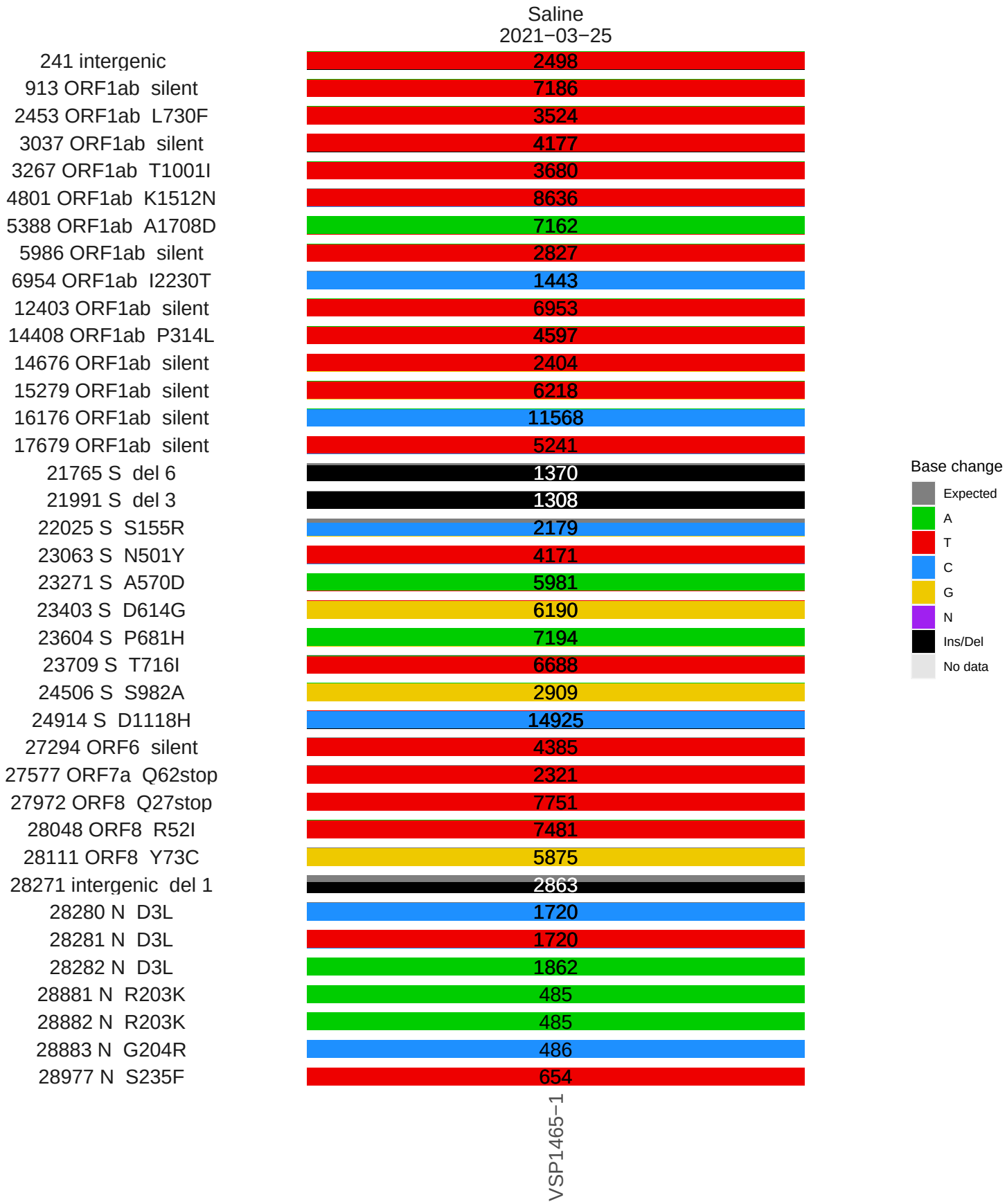
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1465-1 | single experiment | NA | Saline | 2021-03-25 | 29.83 | B.1.1.7 | 99.8% | 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.

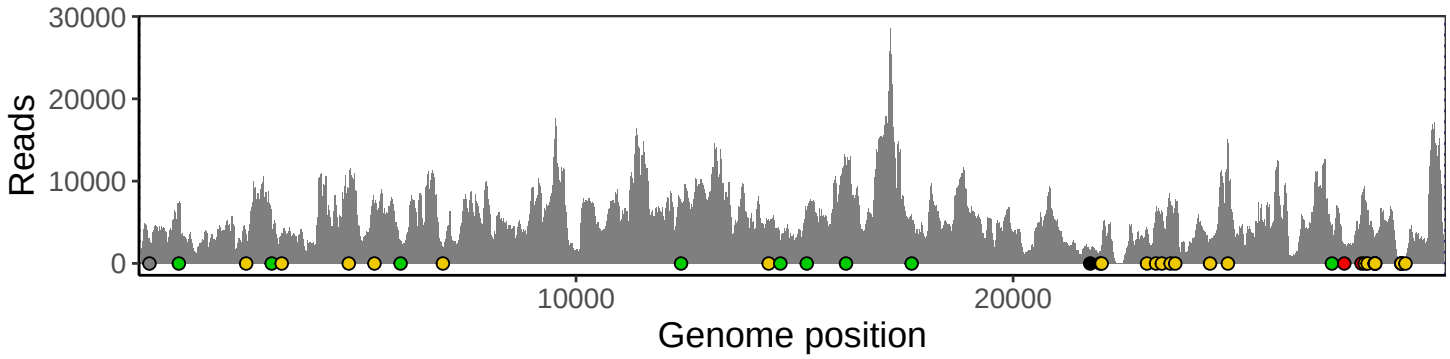



Saline
2021−03−25
241 intergenic
913 ORF1ab silent
2453 ORF1ab L730F
3037 ORF1ab silent
3267 ORF1ab T1001I
4801 ORF1ab K1512N
5388 ORF1ab A1708D
5986 ORF1ab silent
6954 ORF1ab I2230T
12403 ORF1ab silent
14408 ORF1ab P314L
14676 ORF1ab silent
15279 ORF1ab silent
16176 ORF1ab silent
17679 ORF1ab silent
21765 S del 6
21991 S del 3
22025 S S155R
23063 S N501Y
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24506 S S982A
24914 S D1118H
27294 ORF6 silent
27577 ORF7a Q62stop
27972 ORF8 Q27stop
28048 ORF8 R52I
28111 ORF8 Y73C
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
2498
7186
3524
4177
3680
8636
7162
2827
1443
6953
4597
2404
6218
11568
5241
1370
1308
2179
4171
5981
6190
7194
6688
2909
14925
4385
2321
7751
7481
5875
2863
1720
1720
1862
485
485
486
654
VSP1465−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

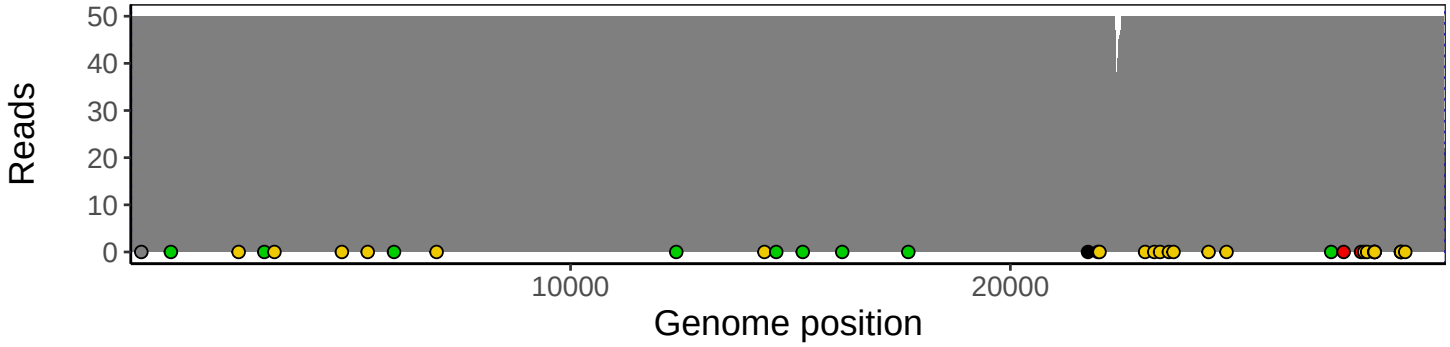
## Analyses of individual experiments and composite results

### VSP1465-1 | 2021-03-25 | Saline | HUP Q-0124 | genomes | single experiment

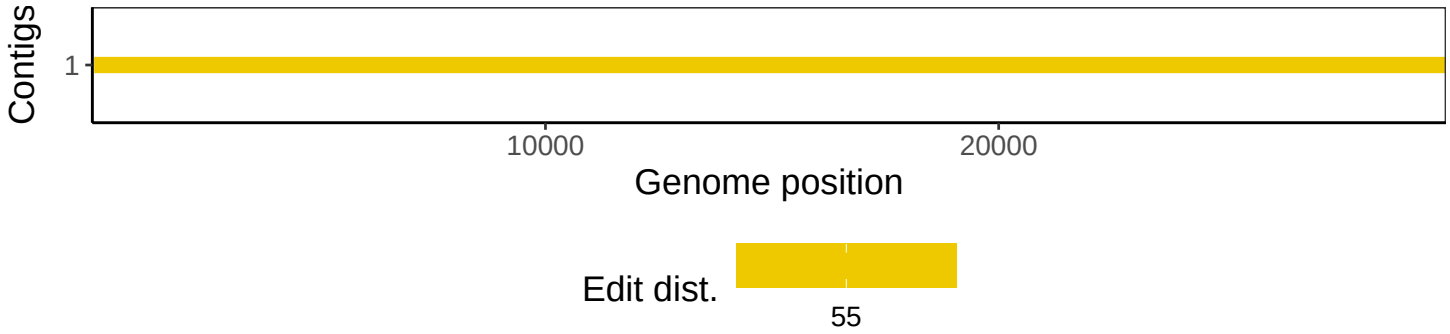
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |