# COVID-19 subject SARS_CoV_298

*2021-06-29*

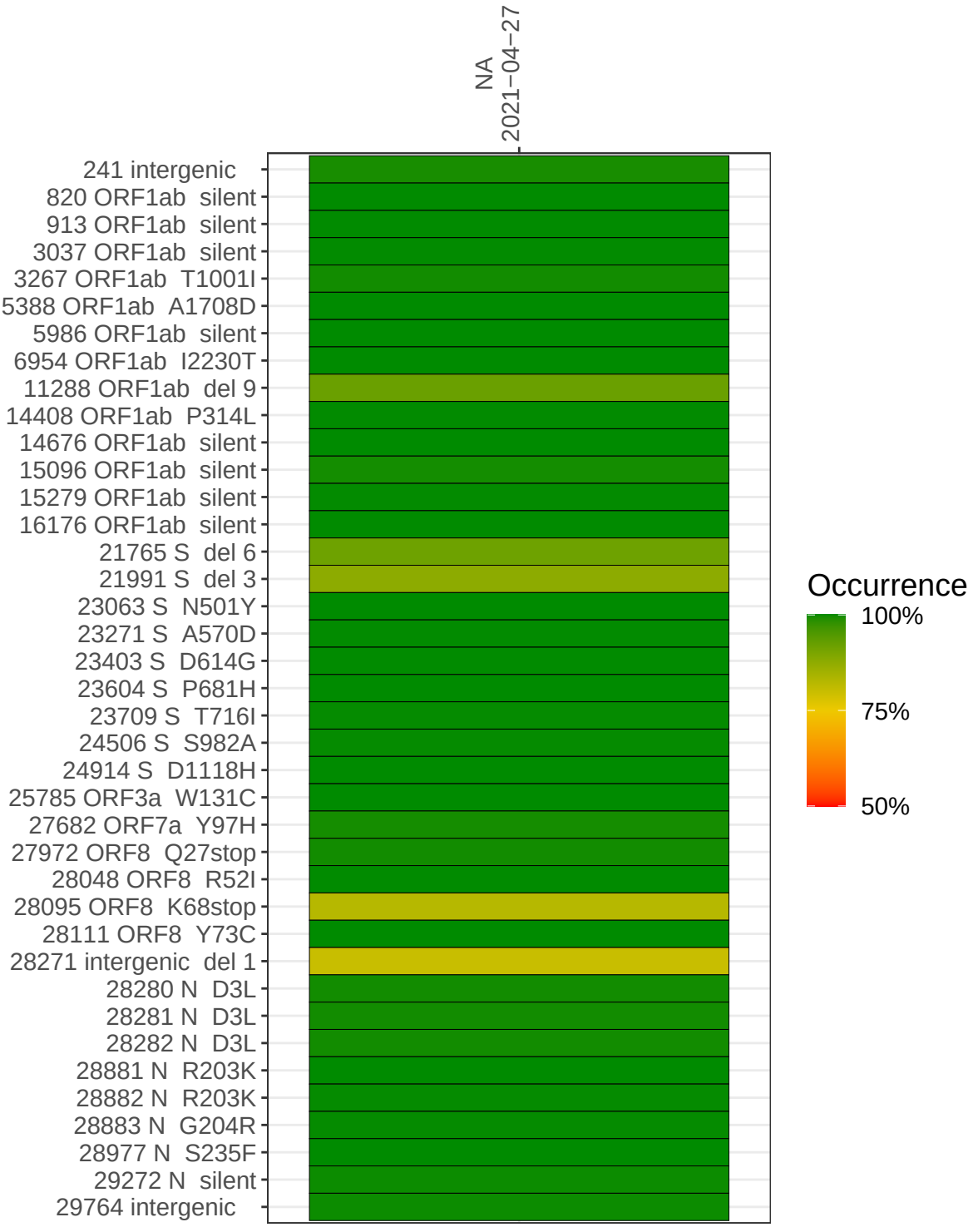
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

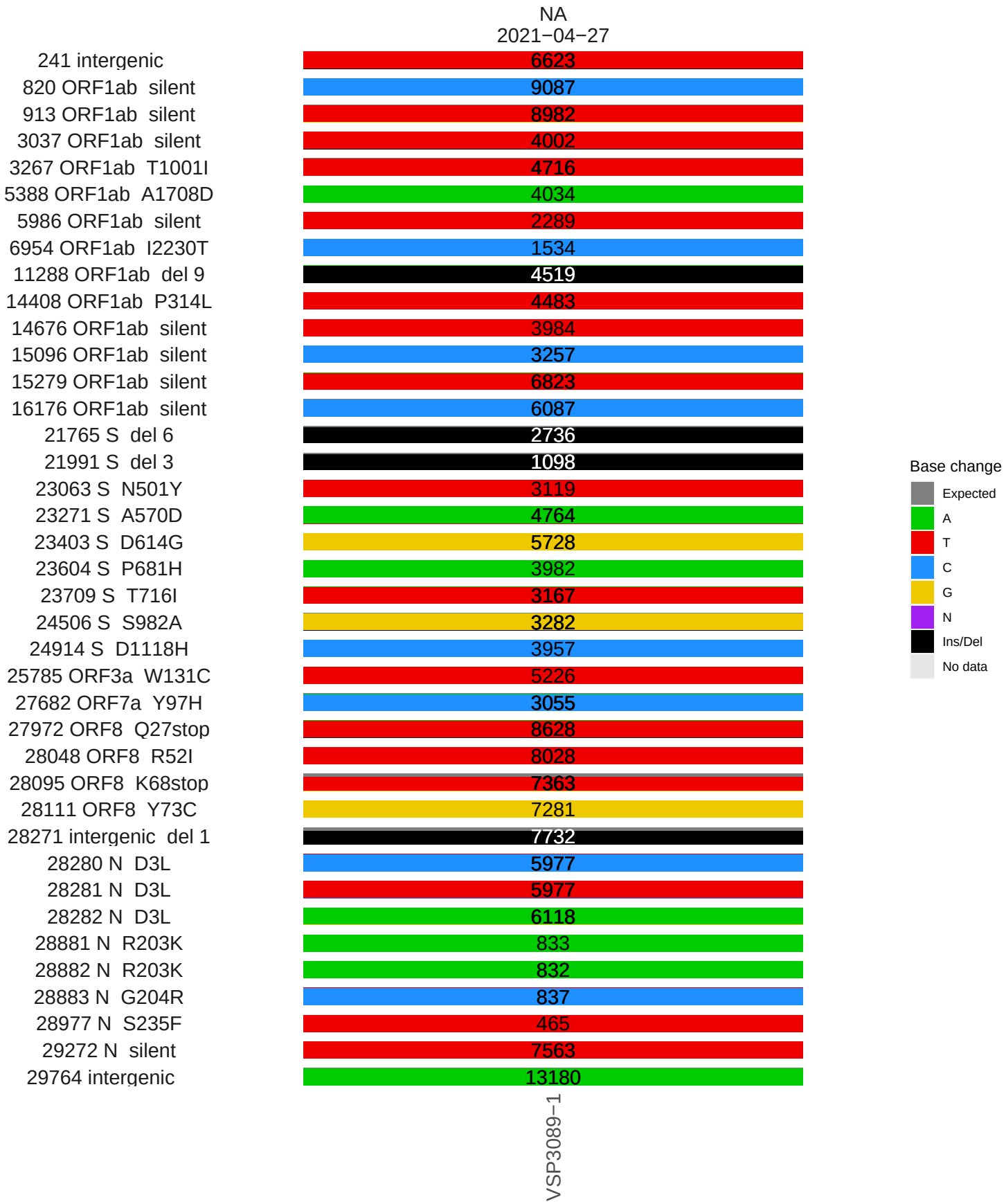
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP3089-1 | single experiment | NA | NA | 2021-04-27 | 29.84 | B.1.1.7 | 100.0% | 99.8% |

### Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/NC_04551 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.

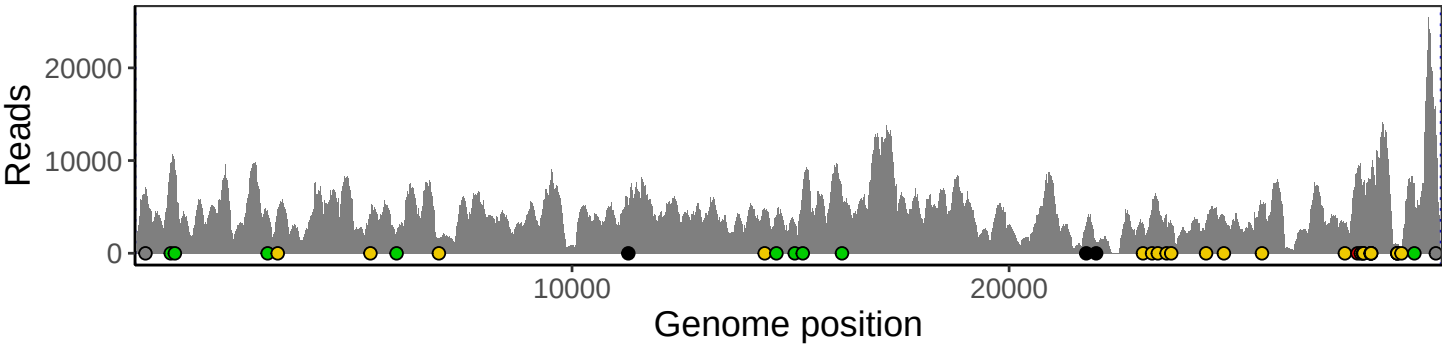



NA
2021−04−27
241 intergenic
820 ORF1ab silent
913 ORF1ab silent
3037 ORF1ab silent
3267 ORF1ab T1001I
5388 ORF1ab A1708D
5986 ORF1ab silent
6954 ORF1ab I2230T
11288 ORF1ab del 9
14408 ORF1ab P314L
14676 ORF1ab silent
15096 ORF1ab silent
15279 ORF1ab silent
16176 ORF1ab silent
21765 S del 6
21991 S del 3
23063 S N501Y
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24506 S S982A
24914 S D1118H
25785 ORF3a W131C
27682 ORF7a Y97H
27972 ORF8 Q27stop
28048 ORF8 R52I
28095 ORF8 K68stop
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
29272 N silent
29764 intergenic
6623
9087
8982
4002
4716
4034
2289
1534
4519
4483
3984
3257
6823
6087
2736
1098
3119
4764
5728
3982
3167
3282
3957
5226
3055
8628
8028
7363
7281
7732
5977
5977
6118
833
832
837
465
7563
13180
VSP3089−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

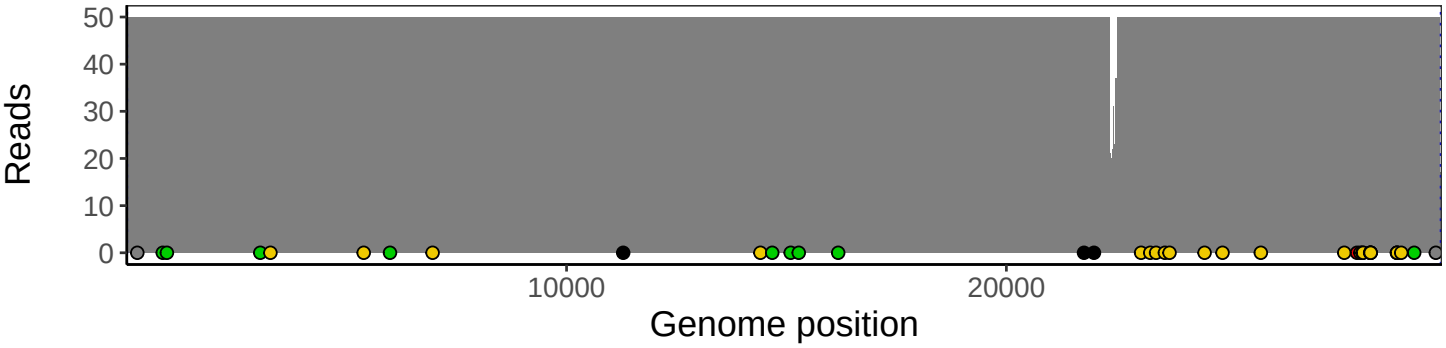
## Analyses of individual experiments and composite results

### VSP3089-1 | 2021-04-27 | NA | SARS_CoV_298 | genomes | single experiment

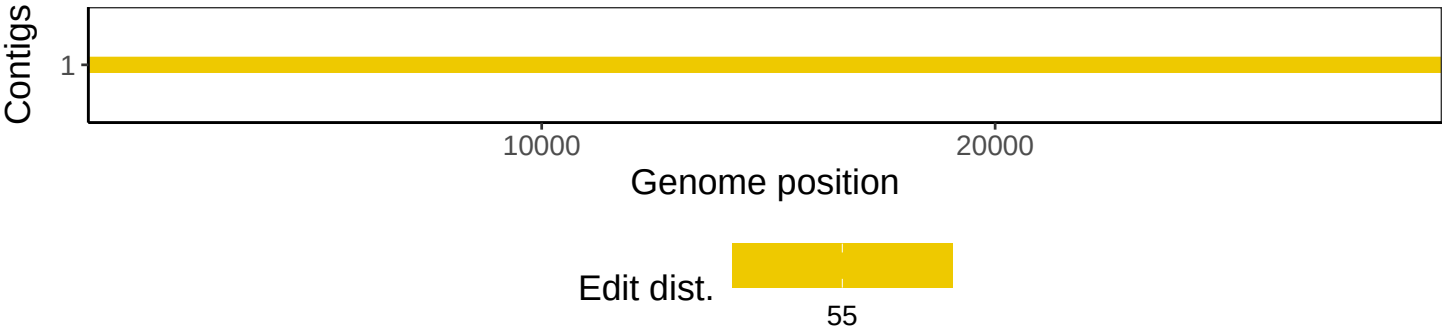
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |