

# COVID-19 subject PQ-Seq15

*2021-03-01*

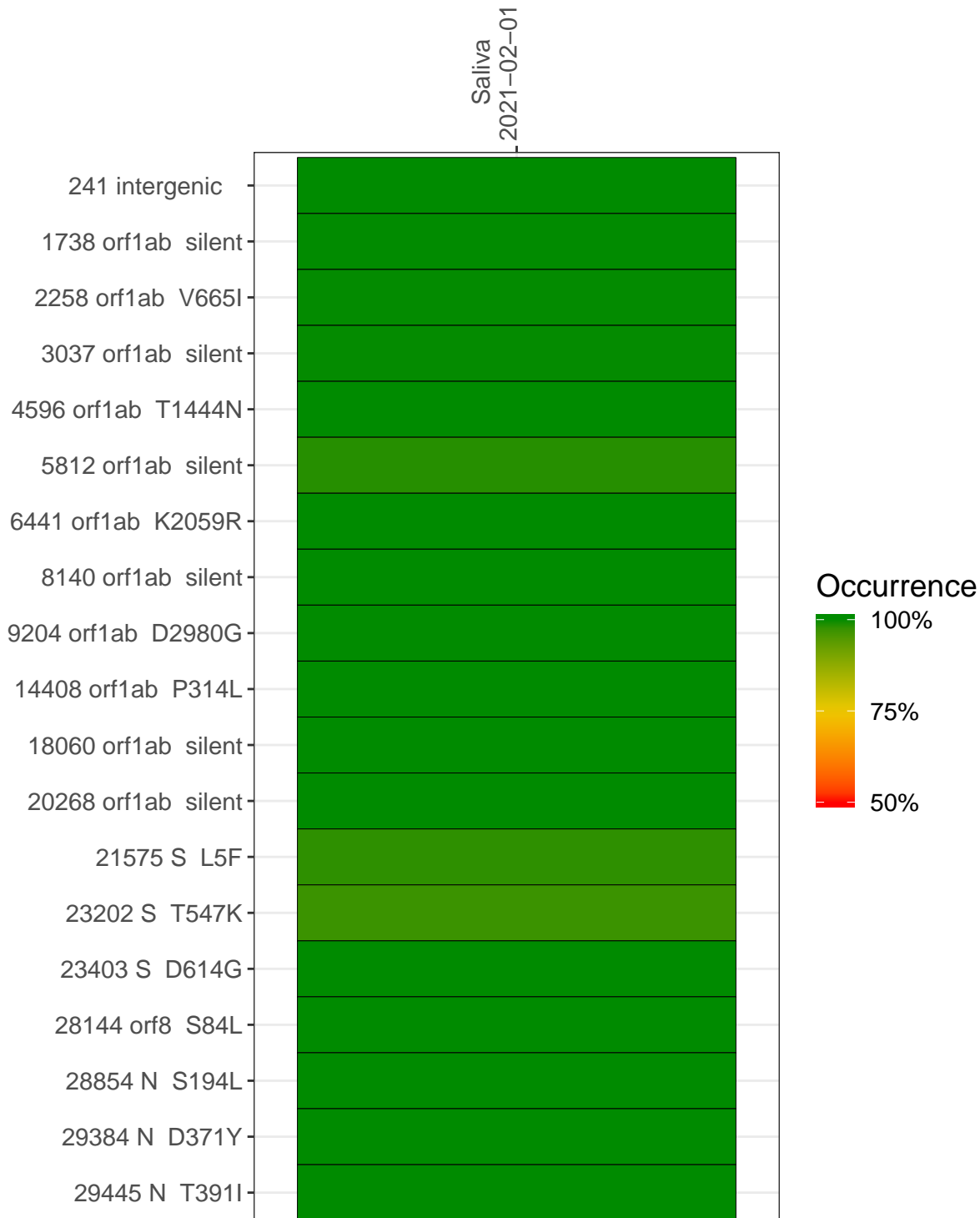
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 ( $\geq 5$ reads) |
|------------|-------------------|---------|-------------|-------------|---------------------|---------|-------------------------|---|
| VSP0784    | composite         | NA      | Saliva      | 2021-02-01  | 15.05               | B.1.234 | 99.8%                   | 98.6%                                     |
| VSP0784-1  | single experiment | NA      | Saliva      | 2021-02-01  | 2.28                | B.1.234 | 94.7%                   | 80.4%                                     |
| VSP0784-2  | single experiment | NA      | Saliva      | 2021-02-01  | 12.86               | B.1.234 | 98.0%                   | 91.3%                                     |

## Variants shared across samples

The heat map below shows how variants (reference genome USA-WA1-2020) 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.



Saliva  
2021-02-01

|                     |       |     |
|---------------------|-------|-----|
| 241 intergenic      | 6     | 36  |
| 1738 orf1ab silent  | 13391 | 108 |
| 2258 orf1ab V665I   | 3724  | 15  |
| 3037 orf1ab silent  | 9128  | 7   |
| 4596 orf1ab T1444N  | 3     | 89  |
| 5812 orf1ab silent  | 4     | 65  |
| 6441 orf1ab K2059R  | 16    | 82  |
| 8140 orf1ab silent  | 6     | 46  |
| 9204 orf1ab D2980G  | 11448 | 49  |
| 14408 orf1ab P314L  | 17845 | 42  |
| 18060 orf1ab silent | 9382  | 67  |
| 20268 orf1ab silent | 4     | 53  |
| 21575 S L5F         | 6     | 145 |
| 23202 S T547K       | 63    | 363 |
| 23403 S D614G       | 61    | 177 |
| 28144 orf8 S84L     | 1311  | 263 |
| 28854 N S194L       | 2     | 120 |
| 29384 N D371Y       | 0     | 50  |
| 29445 N T391I       | 0     | 22  |

VSP0784-1

VSP0784-2

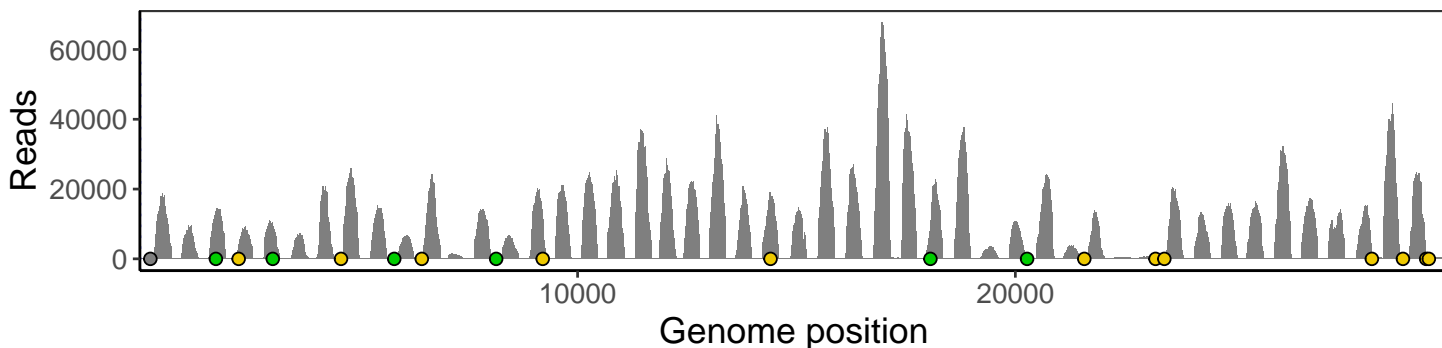
Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

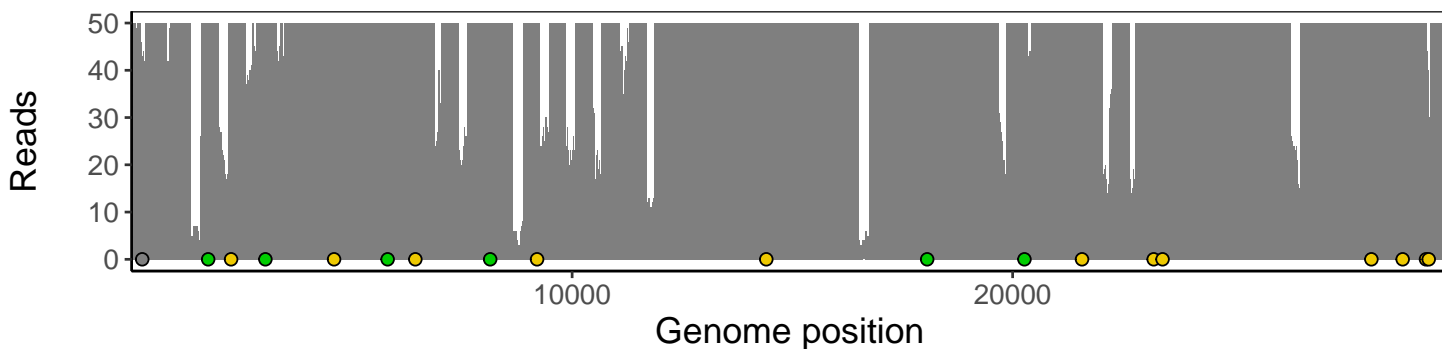
## Analyses of individual experiments and composite results

VSP0784 | 2021-02-01 | Saliva | PQ-Seq15 | composite result

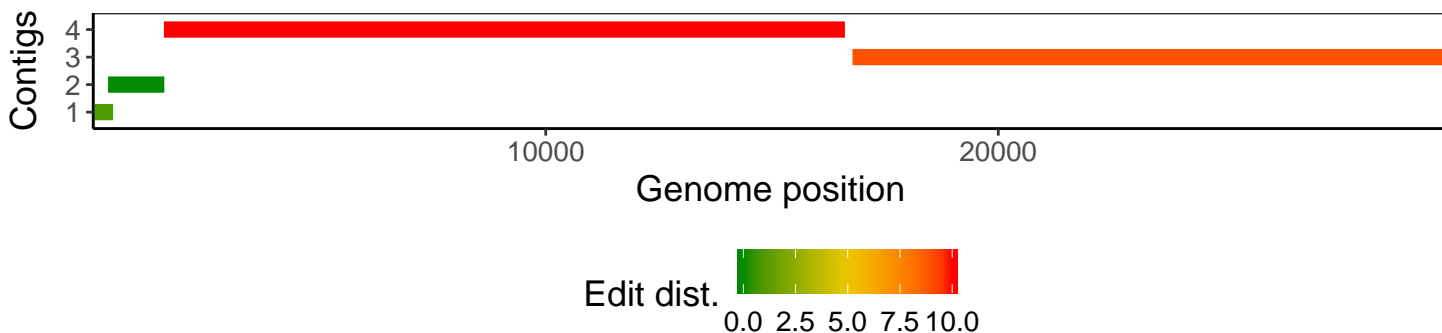
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



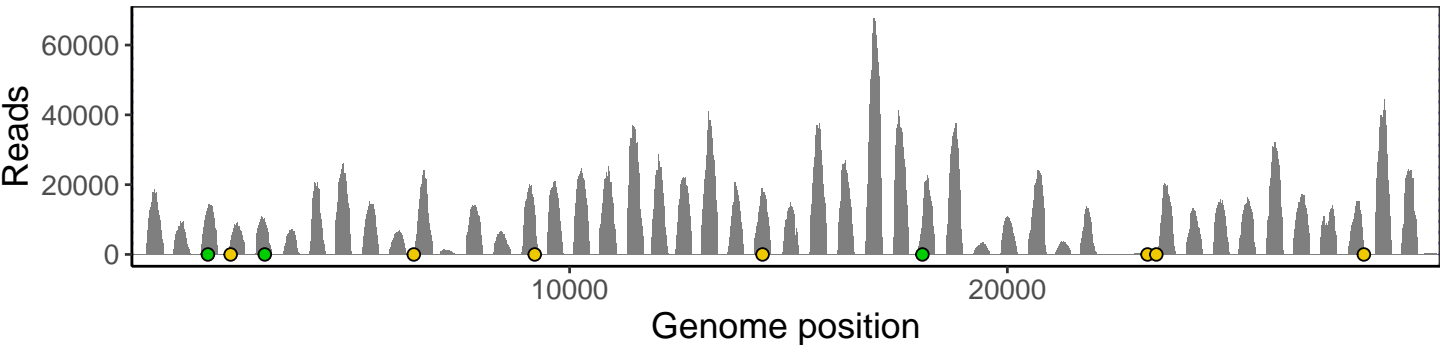
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



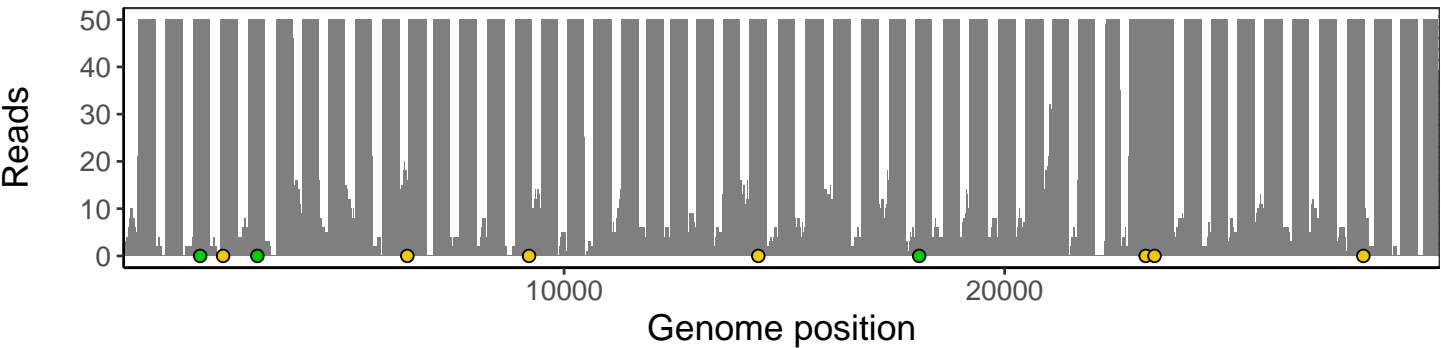
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.



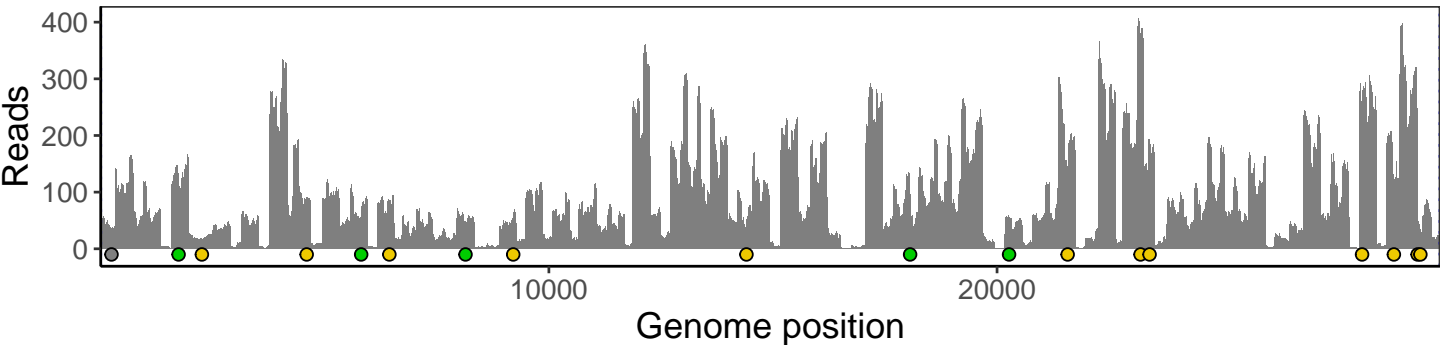
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



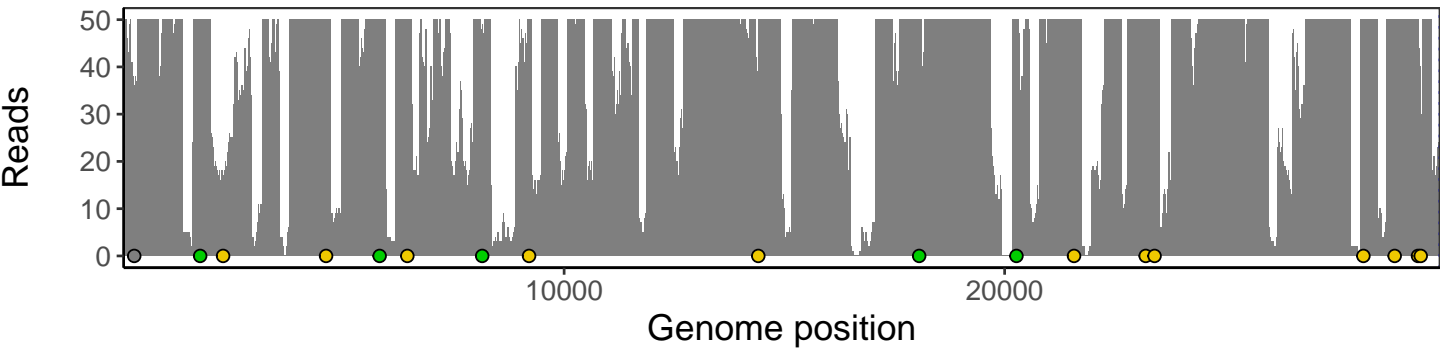
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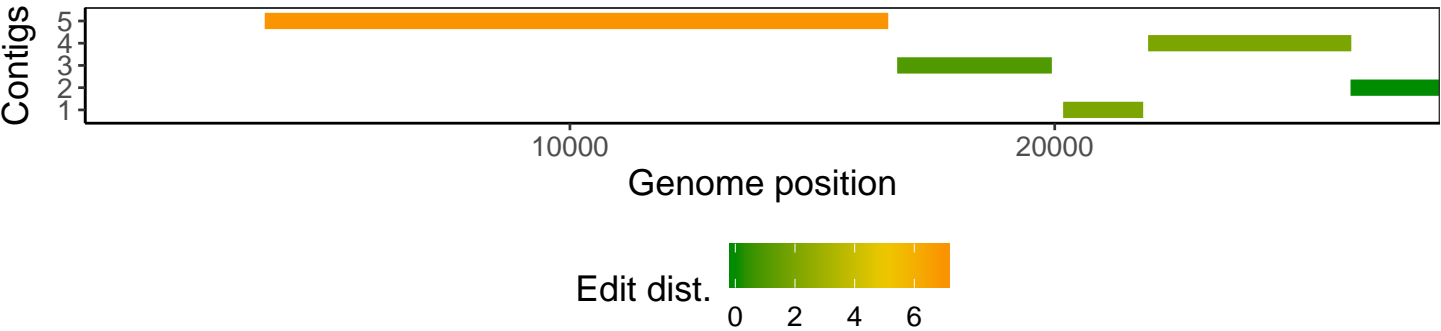
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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 htlib 1.10                                   |
| bcftools             | 1.10.2-34-g1a12af0-dirty Using htlib 1.10.2-57-gf58a6f3 |
| pangolin             | 2.3.3   |
| 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              | 3.0.0   |
| 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  |