# COVID-19 subject 2752

2021-01-06

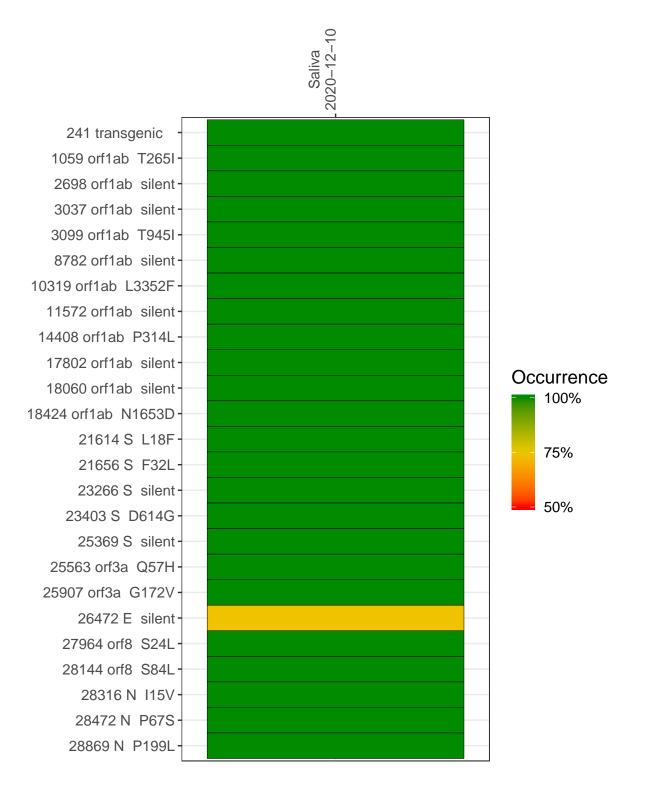
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

Table 1. Sample summary.

| Experiment | Туре              | Input genomes | Sample type | Sample date | Largest contig<br>(KD) | Reference read<br>coverage | Reference read coverage (>= 5 reads) |
|------------|-------------------|---------------|-------------|-------------|------------------------|----------------------------|--------------------------------------|
| VSP0533-1  | single experiment | NA            | Saliva      | 2020-12-10  | 19.25                  | 99.4%                      | 96.7%                                |

#### 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 for 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 2020–12–10

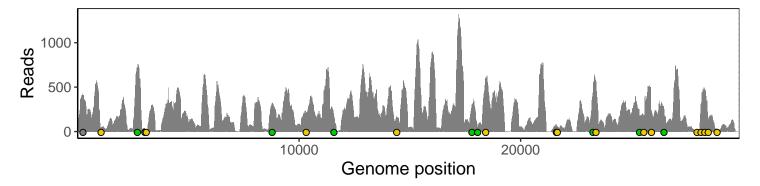
|                     | 2020-12-10 |  |  |  |  |
|---------------------|------------|--|--|--|--|
| 241 transgenic      | 403        |  |  |  |  |
| 1059 orf1ab T265I   | 43         |  |  |  |  |
| 2698 orf1ab silent  | 713        |  |  |  |  |
| 3037 orf1ab silent  | 30         |  |  |  |  |
| 3099 orf1ab T945I   | 22         |  |  |  |  |
| 8782 orf1ab silent  | 314        |  |  |  |  |
| 10319 orf1ab L3352F | 210        |  |  |  |  |
| 11572 orf1ab silent | 168        |  |  |  |  |
| 14408 orf1ab P314L  | 163        |  |  |  |  |
| 17802 orf1ab silent | 299        |  |  |  |  |
| 18060 orf1ab silent | 48         |  |  |  |  |
| 18424 orf1ab N1653D | 604        |  |  |  |  |
| 21614 S L18F        | 64         |  |  |  |  |
| 21656 S F32L        | 49         |  |  |  |  |
| 23266 S silent      | 434        |  |  |  |  |
| 23403 S D614G       | 563        |  |  |  |  |
| 25369 S silent      | 150        |  |  |  |  |
| 25563 orf3a Q57H    | 180        |  |  |  |  |
| 25907 orf3a G172V   | 226        |  |  |  |  |
| 26472 E silent      | 249        |  |  |  |  |
| 27964 orf8 S24L     | 22         |  |  |  |  |
| 28144 orf8 S84L     | 307        |  |  |  |  |
| 28316 N I15V        | 469        |  |  |  |  |
| 28472 N P67S        | 133        |  |  |  |  |
| 28869 N P199L       | 31         |  |  |  |  |
|                     | 33-1       |  |  |  |  |



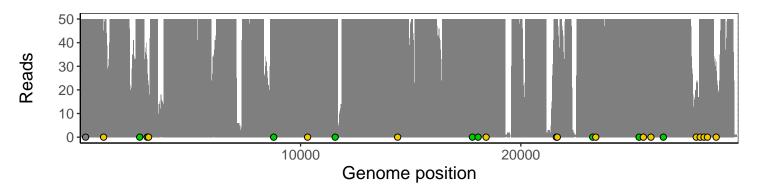
## Analyses of individual experiments and composite results.

# VSP0533-1 | 2020-12-10 | Saliva | 2752 | 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.

