# COVID-19 subject 2750

2021-01-06

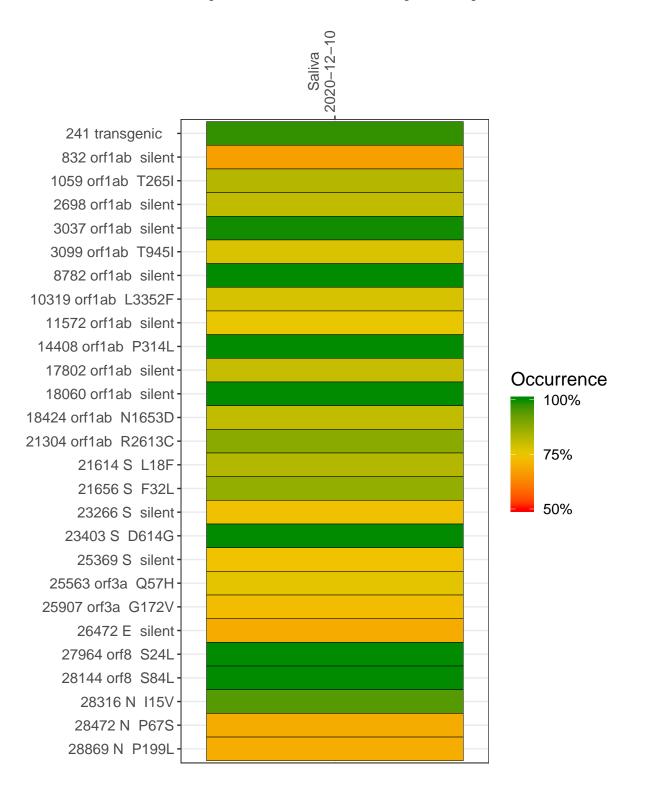
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

Table 1. Sample summary.

Experiment	Туре	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0531-1	single experiment	NA	Saliva	2020-12-10	29.83	99.8%	99.6%

#### 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

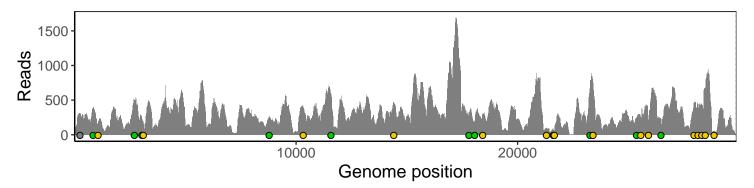
	2020-12-10				
241 transgenic	299				
832 orf1ab silent	379				
1059 orf1ab T265I	162				
2698 orf1ab silent	485				
3037 orf1ab silent	236				
3099 orf1ab T945I	193				
8782 orf1ab silent	262				
10319 orf1ab L3352F	399				
11572 orf1ab silent	558				
14408 orf1ab P314L	444				
17802 orf1ab silent	315				
18060 orf1ab silent	194				
18424 orf1ab N1653D	303				
21304 orf1ab R2613C	93				
21614 S L18F	70				
21656 S F32L	53				
23266 S silent	670				
23403 S D614G	771				
25369 S silent	208				
25563 orf3a Q57H	252				
25907 orf3a G172V	210				
26472 E silent	224				
27964 orf8 S24L	446				
28144 orf8 S84L	392				
28316 N I15V	432				
28472 N P67S	628				
28869 N P199L	46				
	0531–1				
	053				



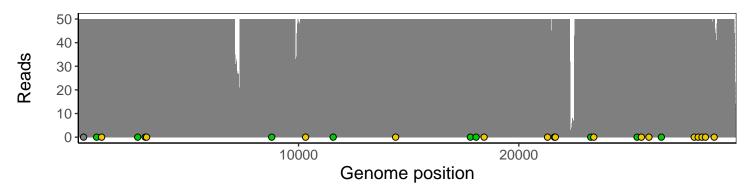
# Analyses of individual experiments and composite results.

## VSP0531-1 | 2020-12-10 | Saliva | 2750 | 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.

