# COVID-19 subject 2751

2021-01-19

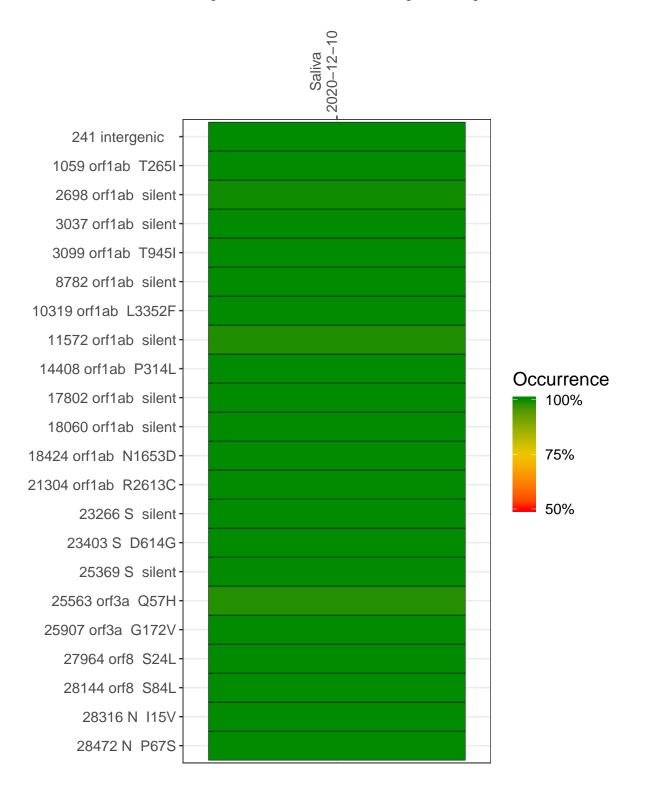
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

Table 1. Sample summary.

Experiment	Туре	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0532-1	single experiment	NA	Saliva	2020-12-10	22.30	98.6%	98.1%

#### 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 2020–12–10

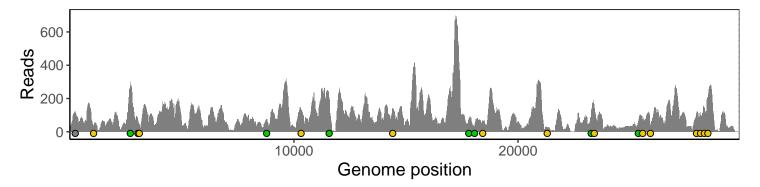
	2020 12 10			
241 intergenic	116			
1059 orf1ab T265I	39			
2698 orf1ab silent	274			
3037 orf1ab silent	69			
3099 orf1ab T945I	44			
8782 orf1ab silent	76			
10319 orf1ab L3352F	126			
11572 orf1ab silent	196			
14408 orf1ab P314L	137			
17802 orf1ab silent	78			
18060 orf1ab silent	45			
18424 orf1ab N1653D	65			
21304 orf1ab R2613C	26			
23266 S silent	106			
23403 S D614G	150			
25369 S silent	52			
25563 orf3a Q57H	75			
25907 orf3a G172V	38			
27964 orf8 S24L	109			
28144 orf8 S84L	95			
28316 N I15V	147			
28472 N P67S	200			
	7			



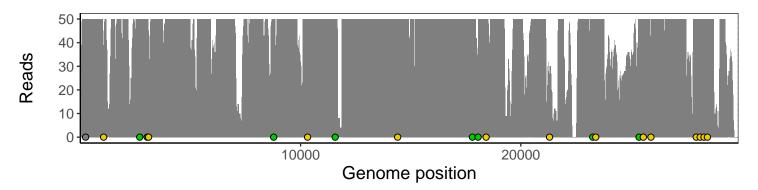
## Analyses of individual experiments and composite results.

#### VSP0532-1 | 2020-12-10 | Saliva | 2751 | 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.

