# COVID-19 subject 2745

2021-01-10

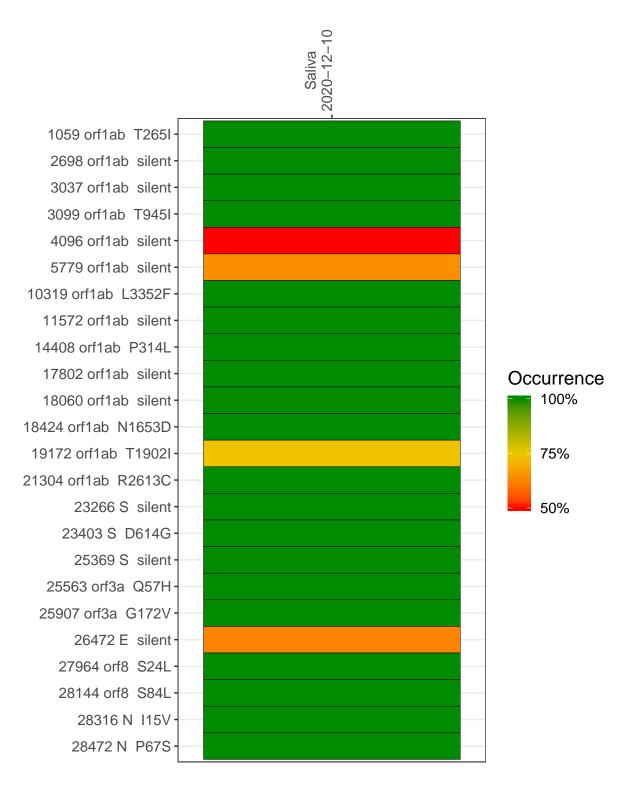
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

Table 1. Sample summary.

Experiment	Туре	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0526-1	single experiment	NA	Saliva	2020-12-10	4.98	86.4%	73.9%

#### 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

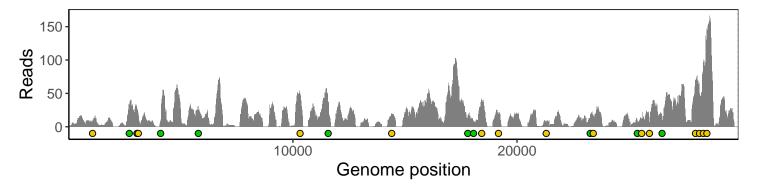
	2020-12-10
1059 orf1ab T265I	8
2698 orf1ab silent	33
3037 orf1ab silent	29
3099 orf1ab T945I	20
4096 orf1ab silent	8
5779 orf1ab silent	28
10319 orf1ab L3352F	50
11572 orf1ab silent	36
14408 orf1ab P314L	18
17802 orf1ab silent	16
18060 orf1ab silent	7
18424 orf1ab N1653D	42
19172 orf1ab T1902I	19
21304 orf1ab R2613C	7
23266 S silent	16
23403 S D614G	18
25369 S silent	8
25563 orf3a Q57H	13
25907 orf3a G172V	5
26472 E silent	16
27964 orf8 S24L	65
28144 orf8 S84L	50
28316 N I15V	93
28472 N P67S	127
	0526-1
	055



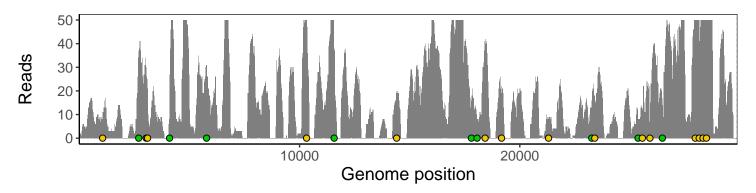
## Analyses of individual experiments and composite results.

# $VSP0526\text{-}1 \mid 2020\text{-}12\text{-}10 \mid Saliva \mid 2745 \mid genomes \mid single \ experiment$

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.

