COVID-19 subject 2748

2021-01-19

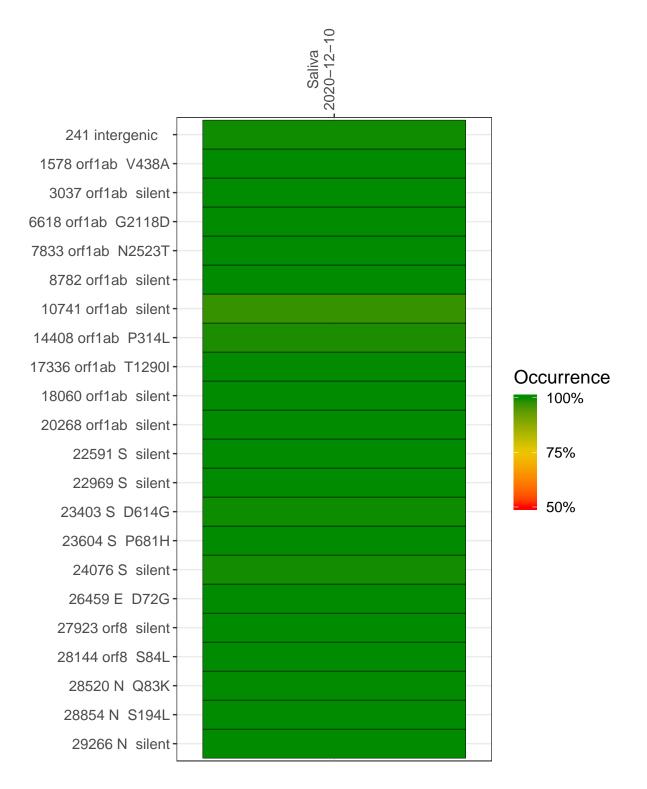
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

Table 1. Sample summary.

Experiment	Туре	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0529-1	single experiment	NA	Saliva	2020-12-10	29.82	99.8%	99.7%

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 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

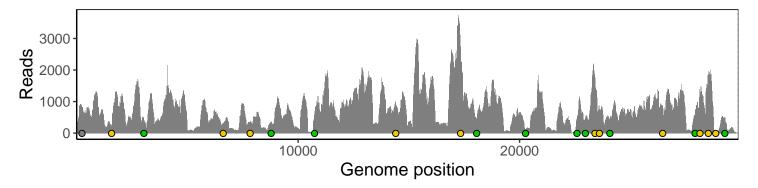
241 intergenic	817
1578 orf1ab V438A	141
3037 orf1ab silent	422
6618 orf1ab G2118D	284
7833 orf1ab N2523T	374
8782 orf1ab silent	356
10741 orf1ab silent	599
14408 orf1ab P314L	903
17336 orf1ab T1290I	2590
18060 orf1ab silent	459
20268 orf1ab silent	115
22591 S silent	459
22969 S silent	468
23403 S D614G	1782
23604 S P681H	829
24076 S silent	403
26459 E D72G	786
27923 orf8 silent	702
28144 orf8 S84L	1287
28520 N Q83K	1759
28854 N S194L	77
29266 N silent	481
	VSP0529-1



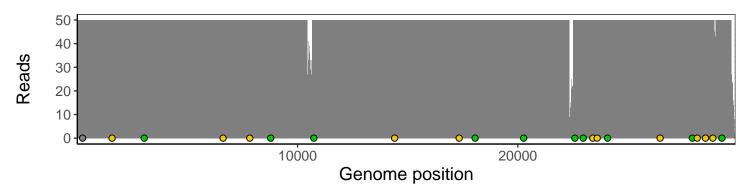
Analyses of individual experiments and composite results.

VSP0529-1 | 2020-12-10 | Saliva | 2748 | 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.

