

# COVID-19 subject SRR11783591

*2020-09-29*

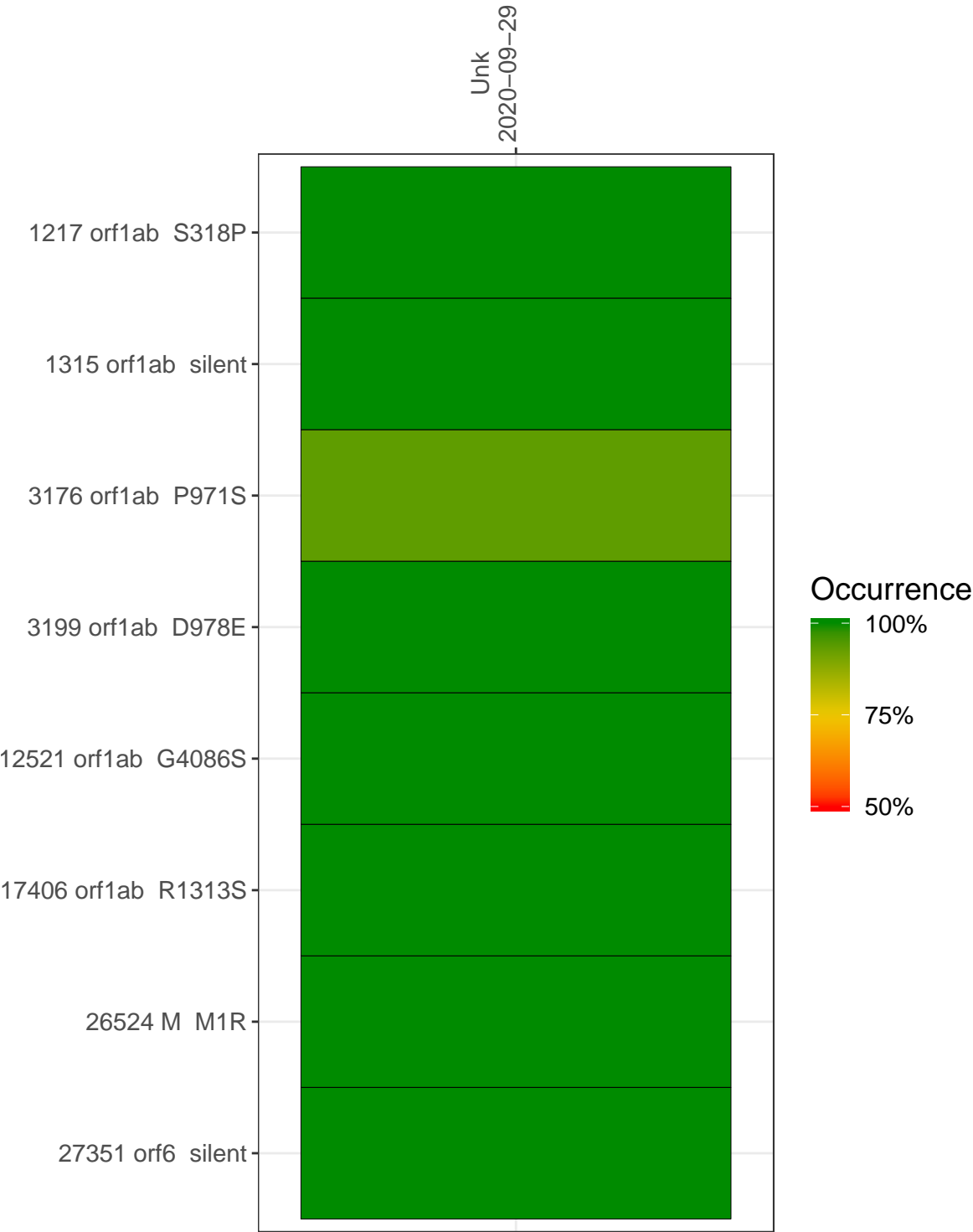
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8002-1	single experiment	NA	Unk	2020-09-29	NA	9.4%	8.8%

**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.



Unk  
2020-09-29

1217 orf1ab S318P

570

1315 orf1ab silent

15

3176 orf1ab P971S

15

3199 orf1ab D978E

272

12521 orf1ab G4086S

7

17406 orf1ab R1313S

9

26524 M M1R

6

27351 orf6 silent

1484

Base change

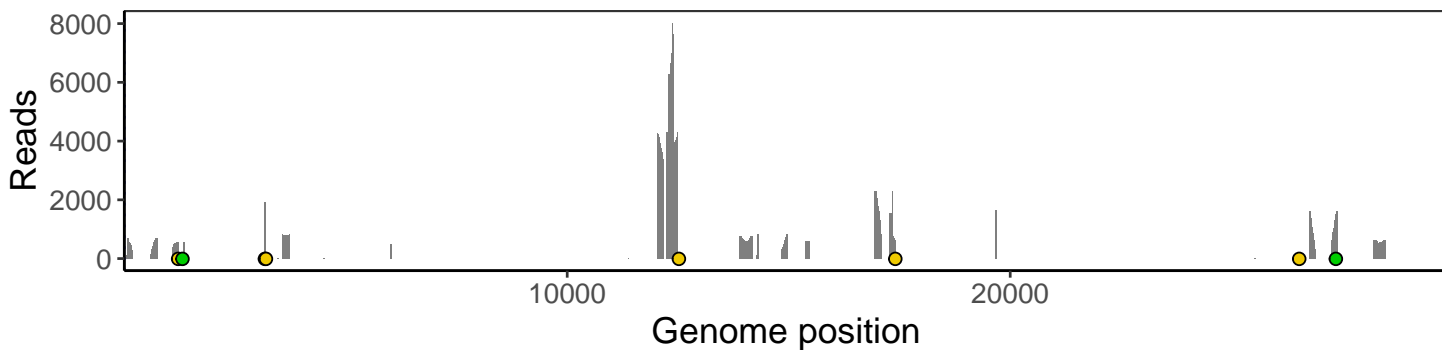


VSP8002-1

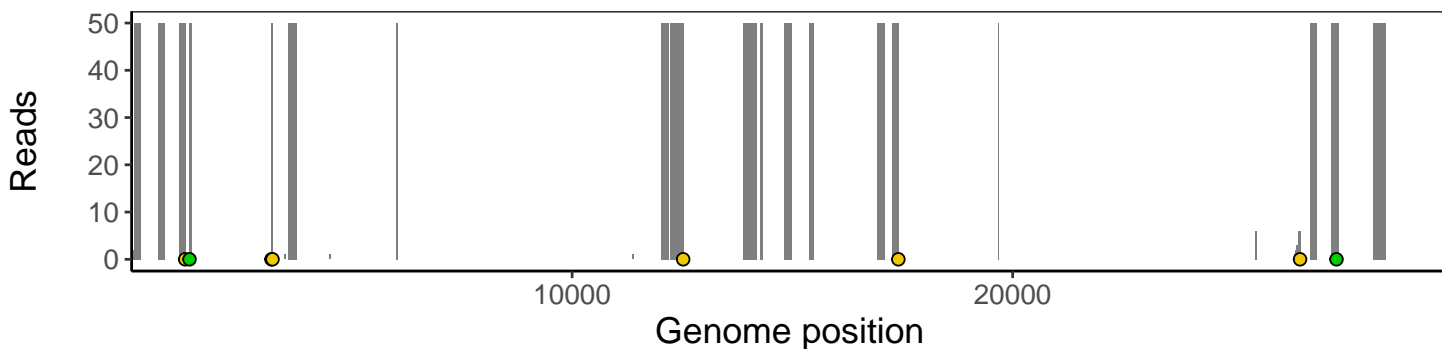
## Analyses of individual experiments and composite results.

VSP8002-1 | 2020-09-29 | Unk | SRR11783591 | 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.



No contig data available.