

# COVID-19 subject 261

*2020-08-28*

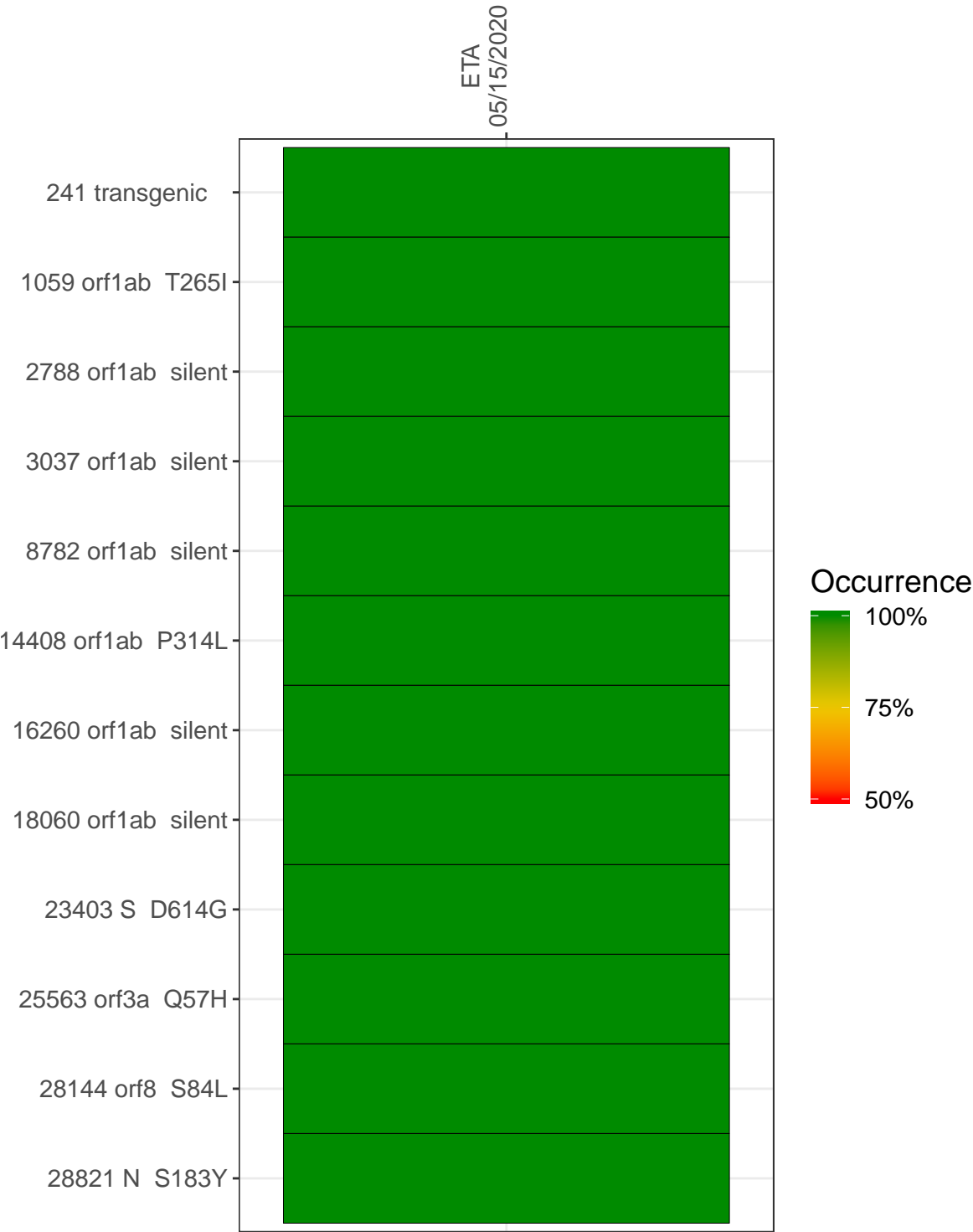
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0140-1	single experiment	NA	ETA	05/15/2020	7.26	98.1%	95.0%

**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.



ETA  
05/15/2020

241 transgenic

32

1059 orf1ab T265I

36

2788 orf1ab silent

56

3037 orf1ab silent

18

8782 orf1ab silent

30

14408 orf1ab P314L

61

16260 orf1ab silent

75

18060 orf1ab silent

15

23403 S D614G

93

25563 orf3a Q57H

52

28144 orf8 S84L

37

28821 N S183Y

9

Base change

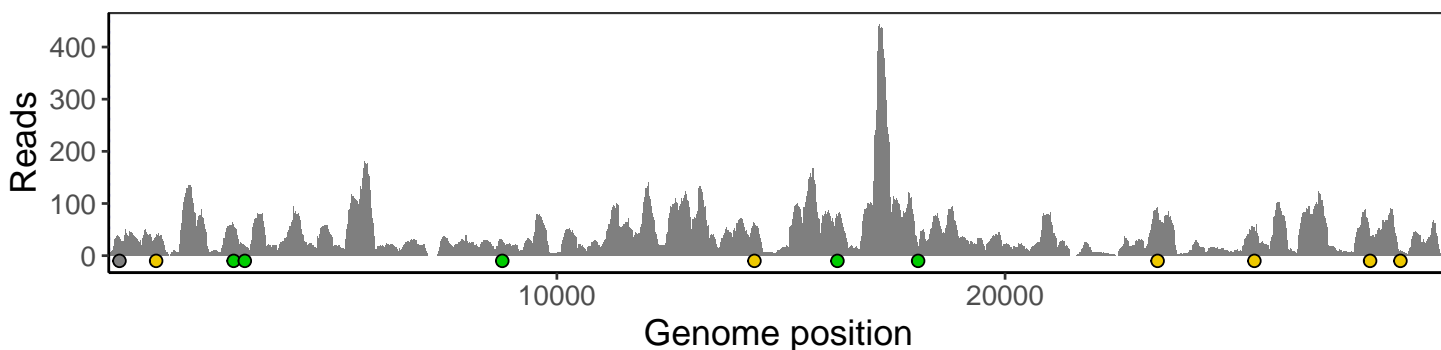


VSP0140-1

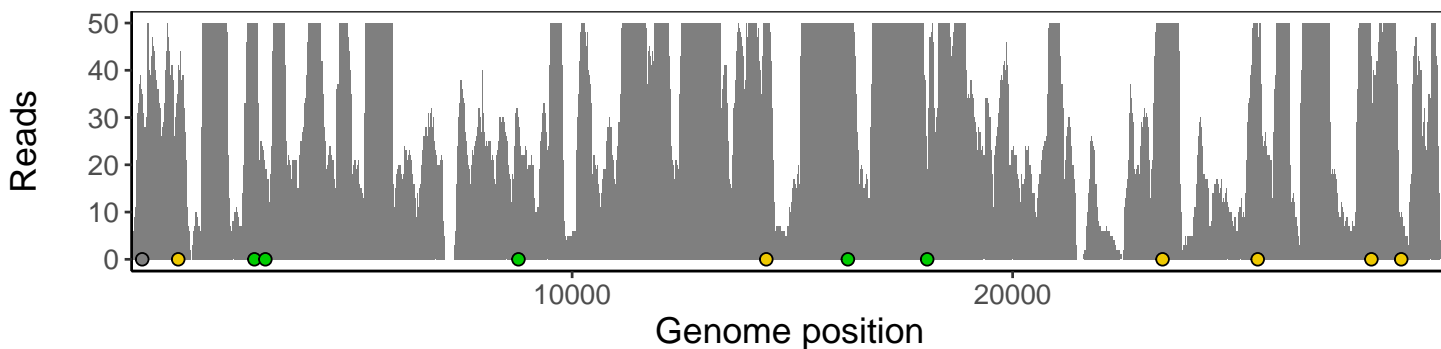
## Analyses of individual experiments and composite results.

VSP0140-1 | 05/15/2020 | ETA | 261e-q1 | 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.

