COVID-19 subject 306

2020-08-28

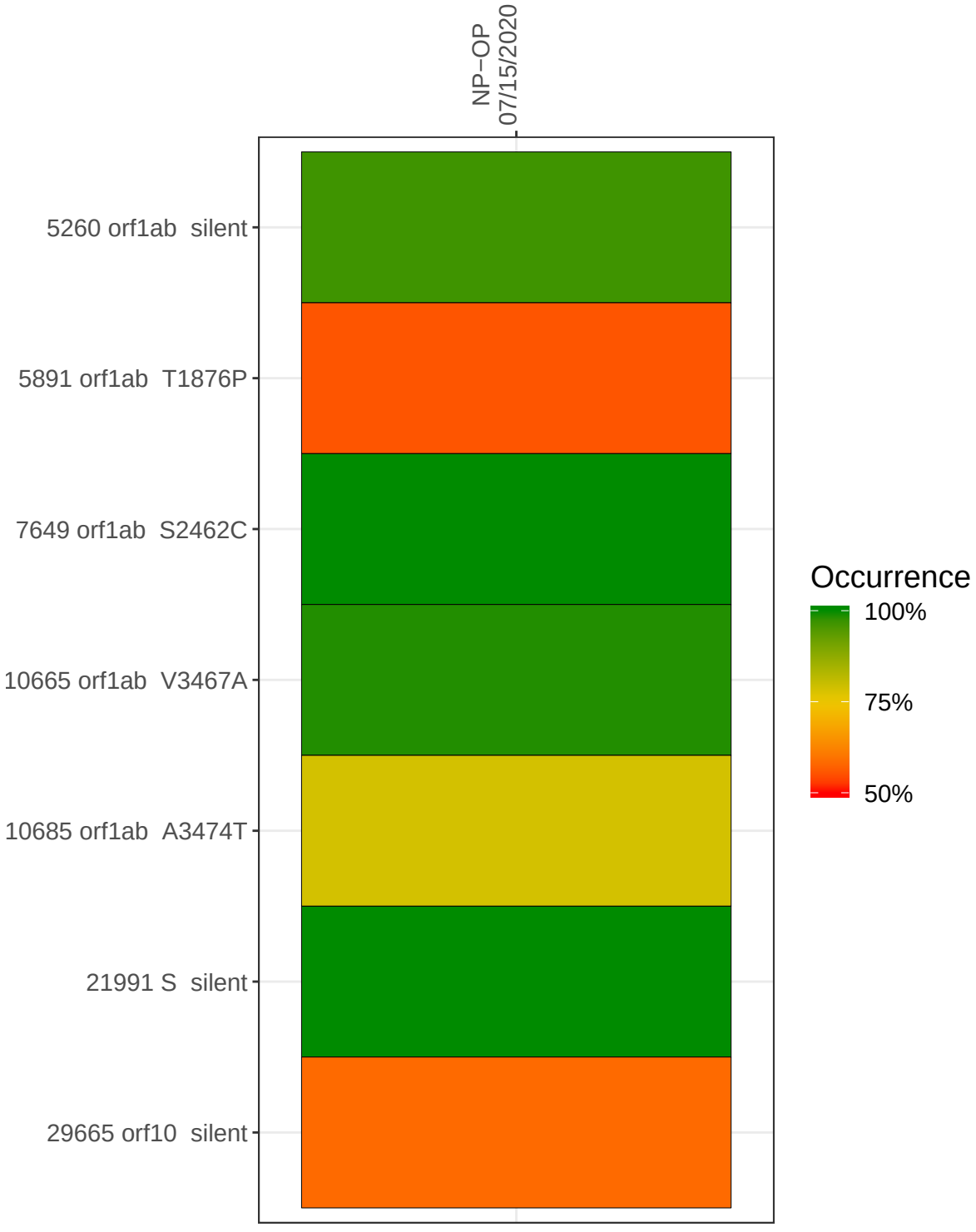
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

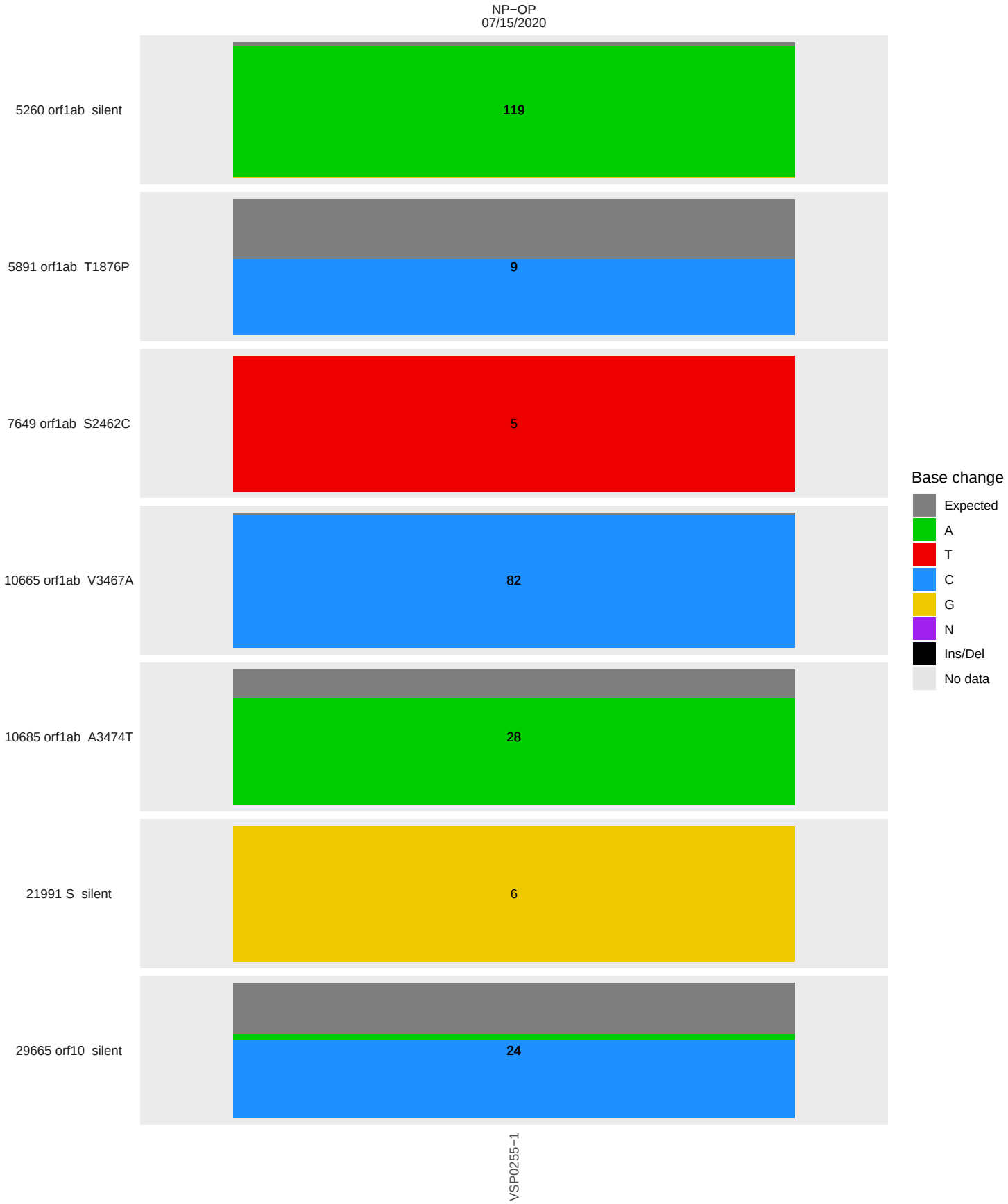
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0255-1	single experiment	NA	NP-OP	07/15/2020	NA	5.5%	3.0%

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.

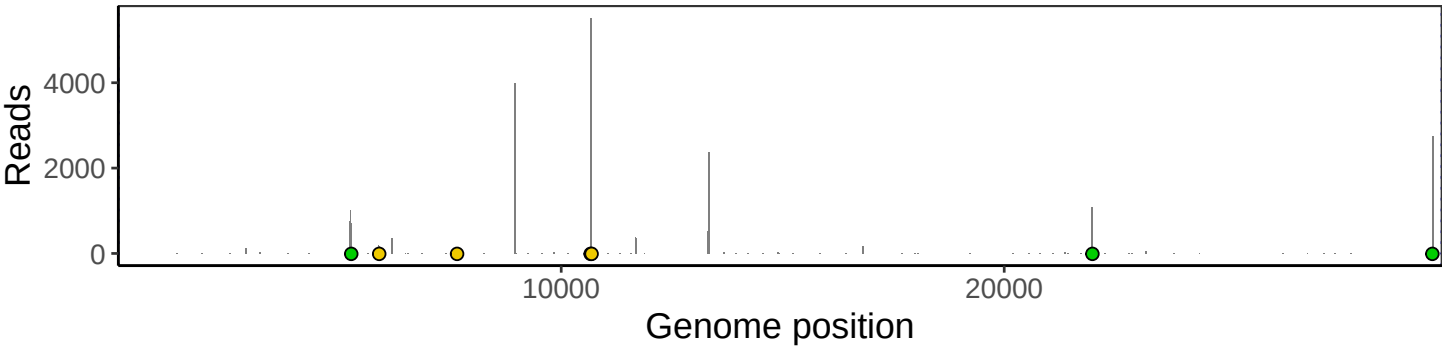



NP−OP
07/15/2020
5260 orf1ab silent
119
5891 orf1ab T1876P
9
7649 orf1ab S2462C
5
10665 orf1ab V3467A
82
10685 orf1ab A3474T
28
21991 S silent
6
29665 orf10 silent
24
VSP0255−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

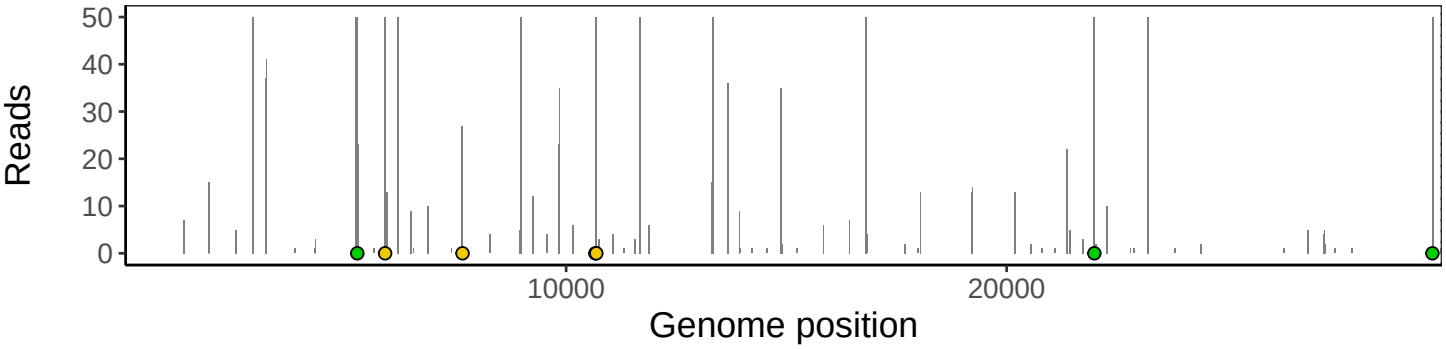
Analyses of individual experiments and composite results.

VSP0255-1 | 07/15/2020 | NP-OP | 306no-q | NA 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.