COVID-19 subject 303

2020-09-04

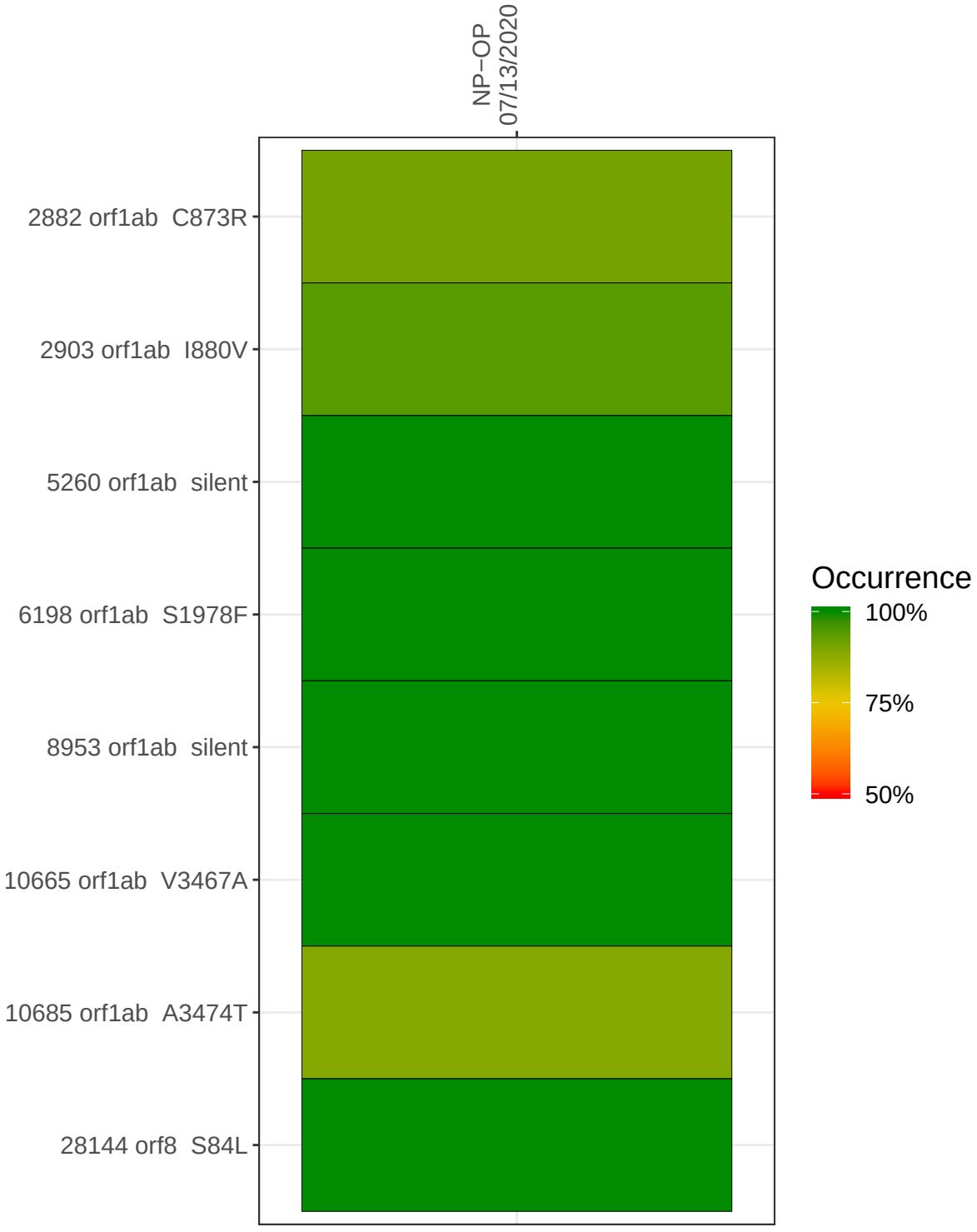
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

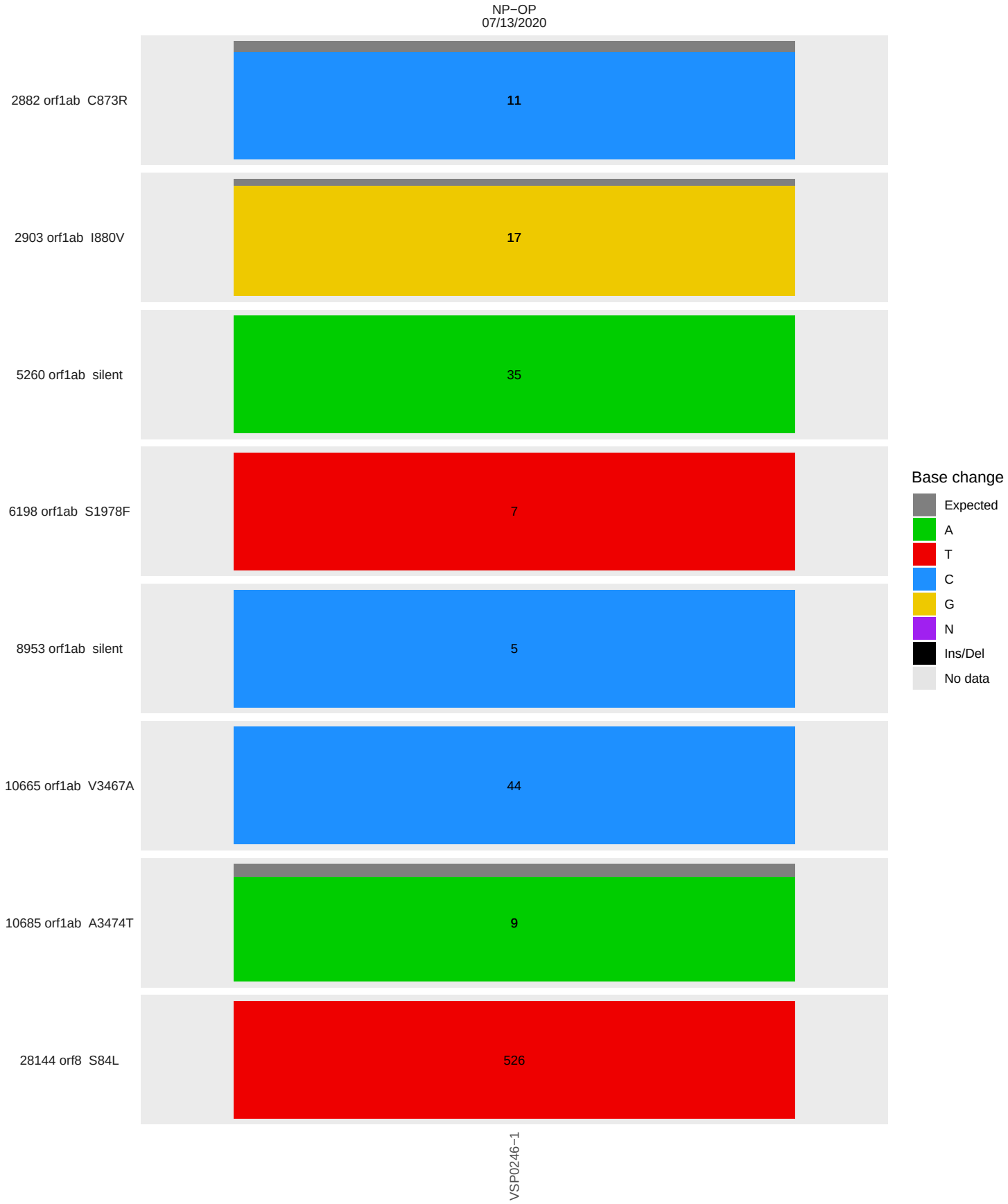
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0246-1	single experiment	37.55	NP-OP	07/13/2020	0.52	7.5%	4.2%

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.

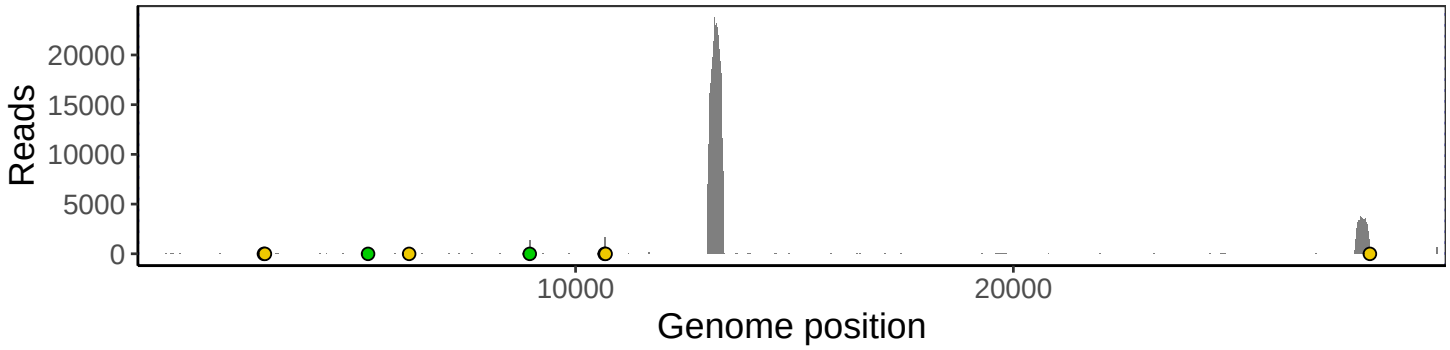



NP−OP
07/13/2020
2882 orf1ab C873R
11
2903 orf1ab I880V
17
5260 orf1ab silent
35
6198 orf1ab S1978F
7
8953 orf1ab silent
5
10665 orf1ab V3467A
44
10685 orf1ab A3474T
9
28144 orf8 S84L
526
VSP0246−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

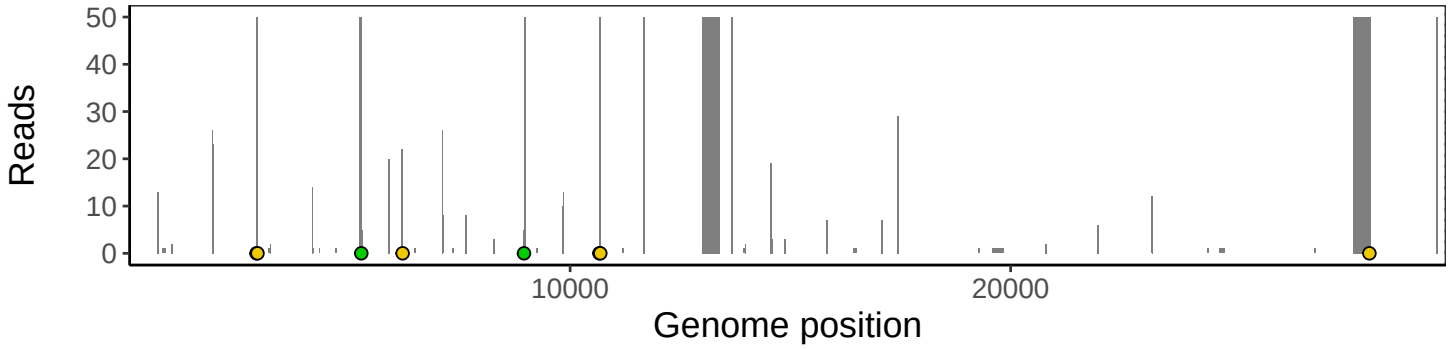
Analyses of individual experiments and composite results.

VSP0246-1 | 07/13/2020 | NP-OP | 303no-q | 37.55 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.