COVID-19 subject 381

2021-01-11

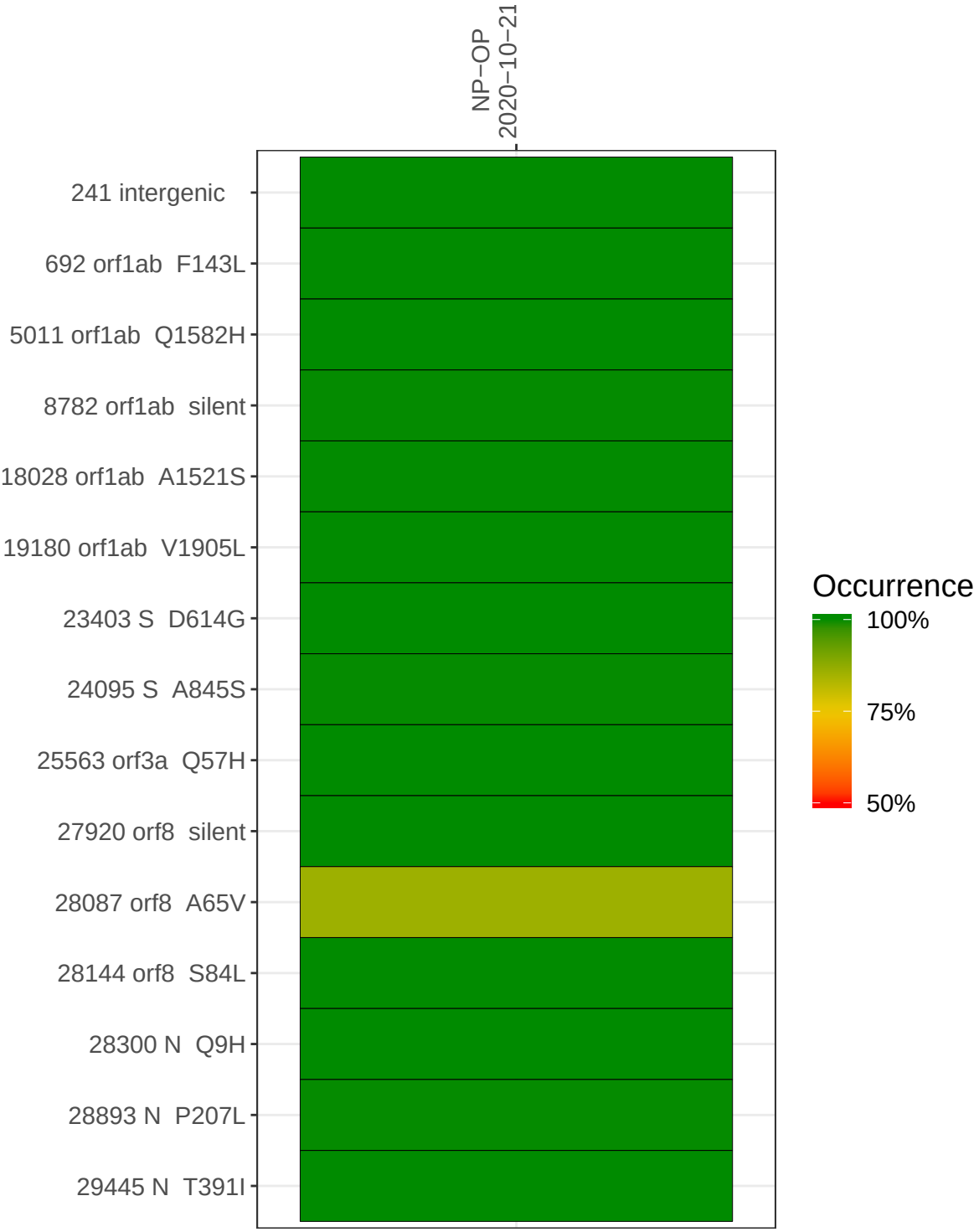
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

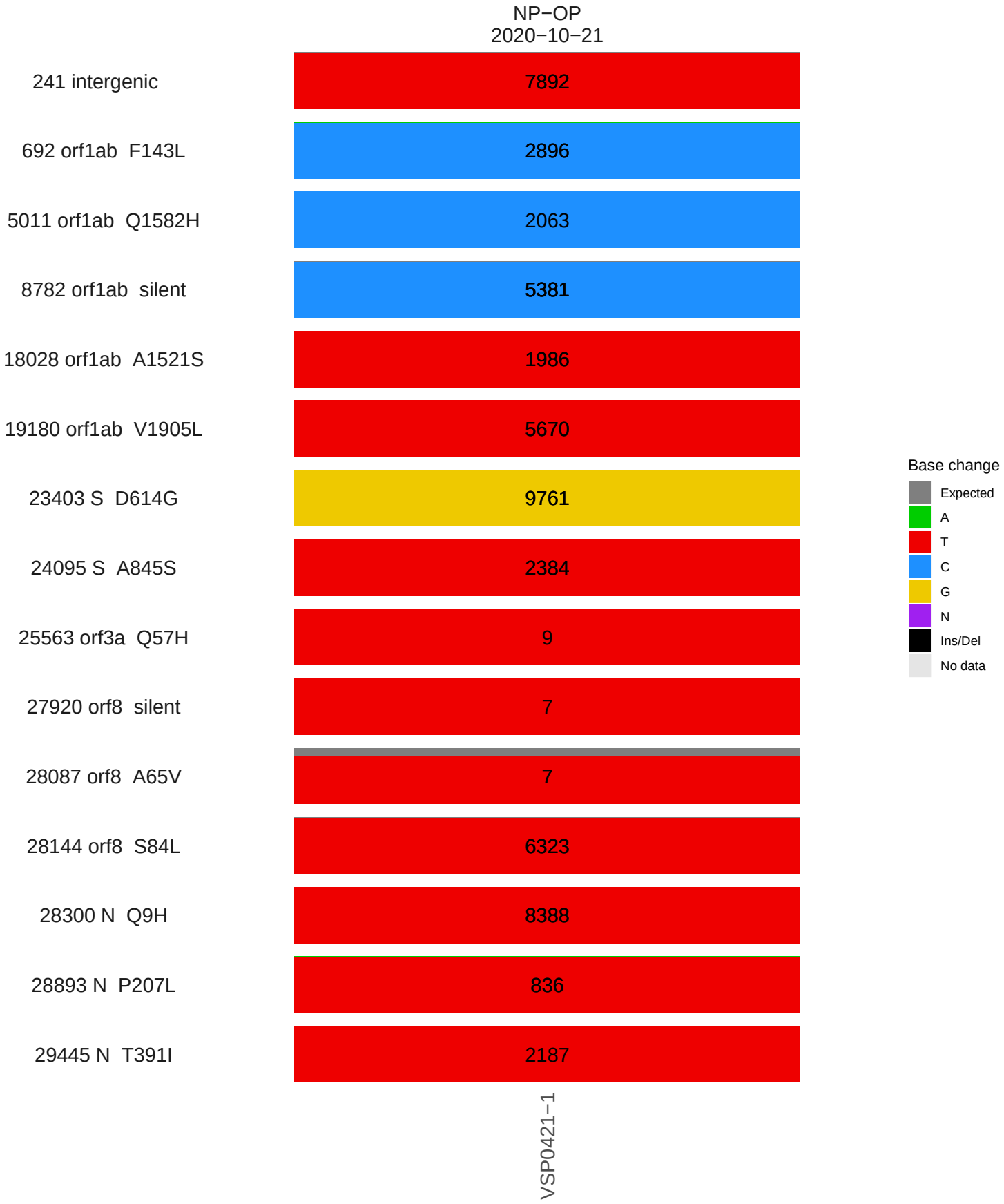
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0421-1	single experiment	NA	NP-OP	2020-10-21	1.19	70.3%	64.9%

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.

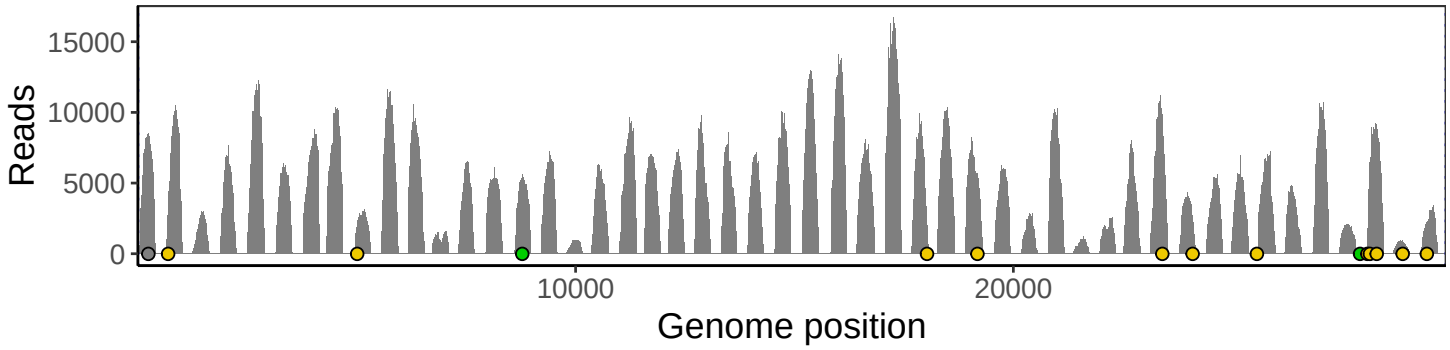



NP−OP
2020−10−21
241 intergenic
7892
692 orf1ab F143L
2896
5011 orf1ab Q1582H
2063
8782 orf1ab silent
5381
18028 orf1ab A1521S
1986
19180 orf1ab V1905L
5670
23403 S D614G
9761
24095 S A845S
2384
25563 orf3a Q57H
9
27920 orf8 silent
7
28087 orf8 A65V
7
28144 orf8 S84L
6323
28300 N Q9H
8388
28893 N P207L
836
29445 N T391I
2187
VSP0421−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

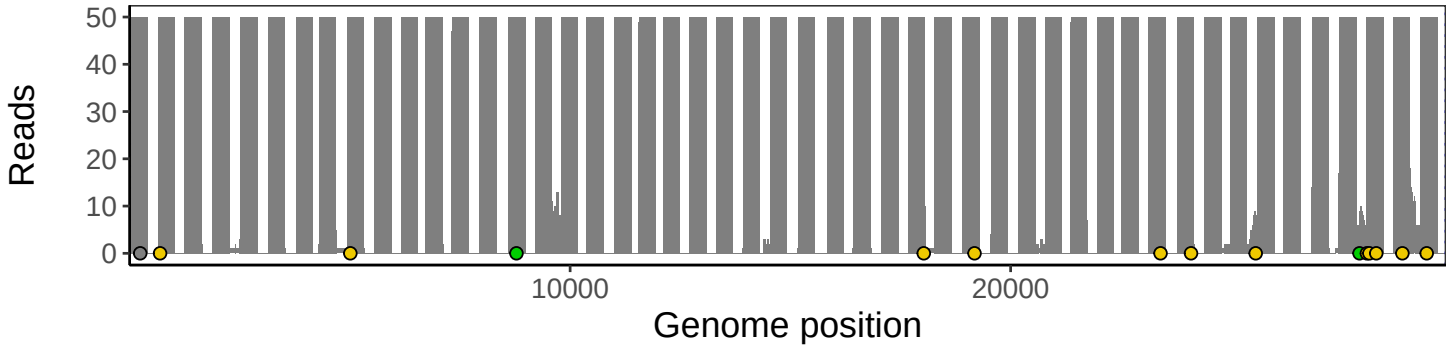
Analyses of individual experiments and composite results.

VSP0421-1 | 2020-10-21 | NP-OP | 381no-q | 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.