COVID-19 subject 391

2021-01-11

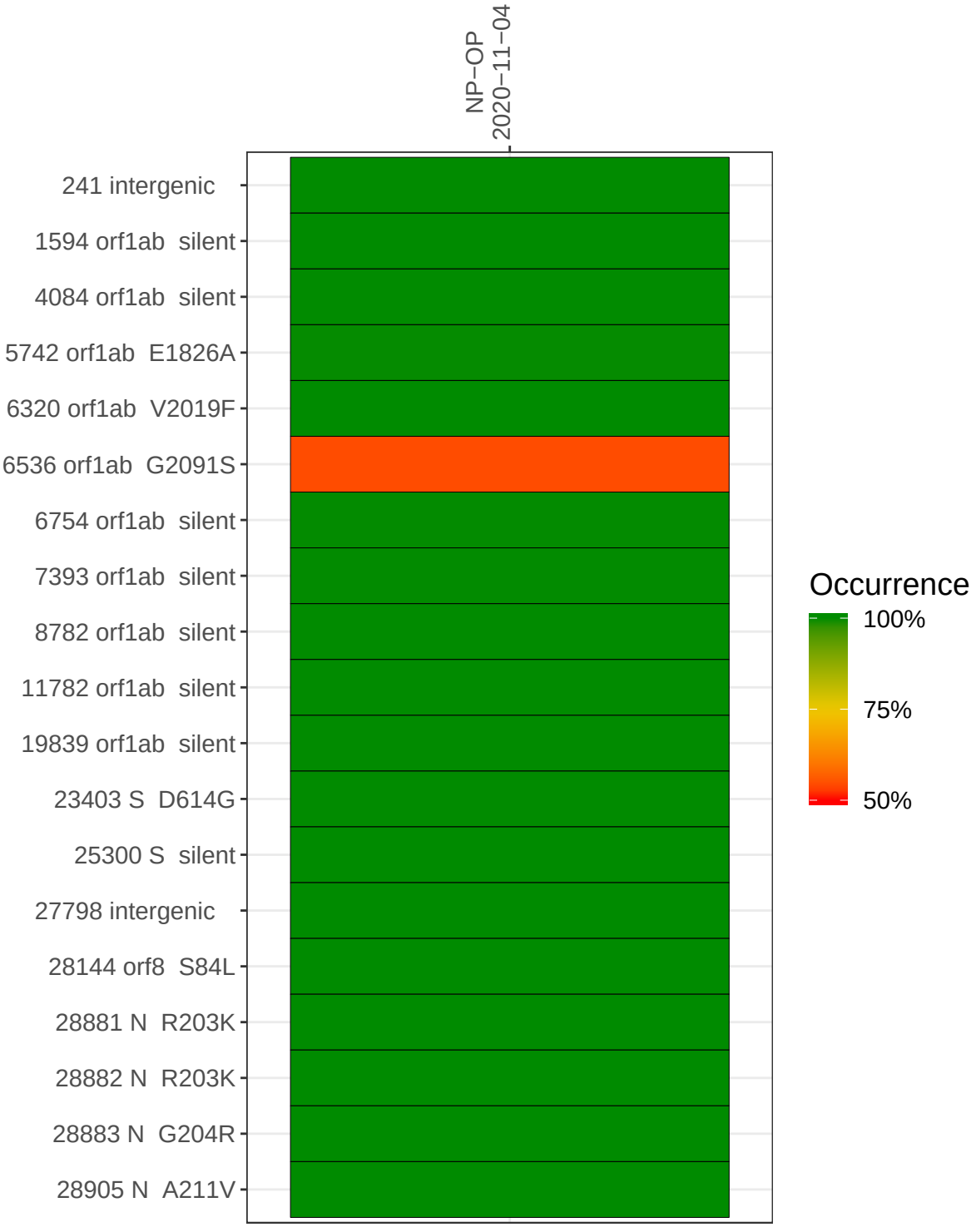
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

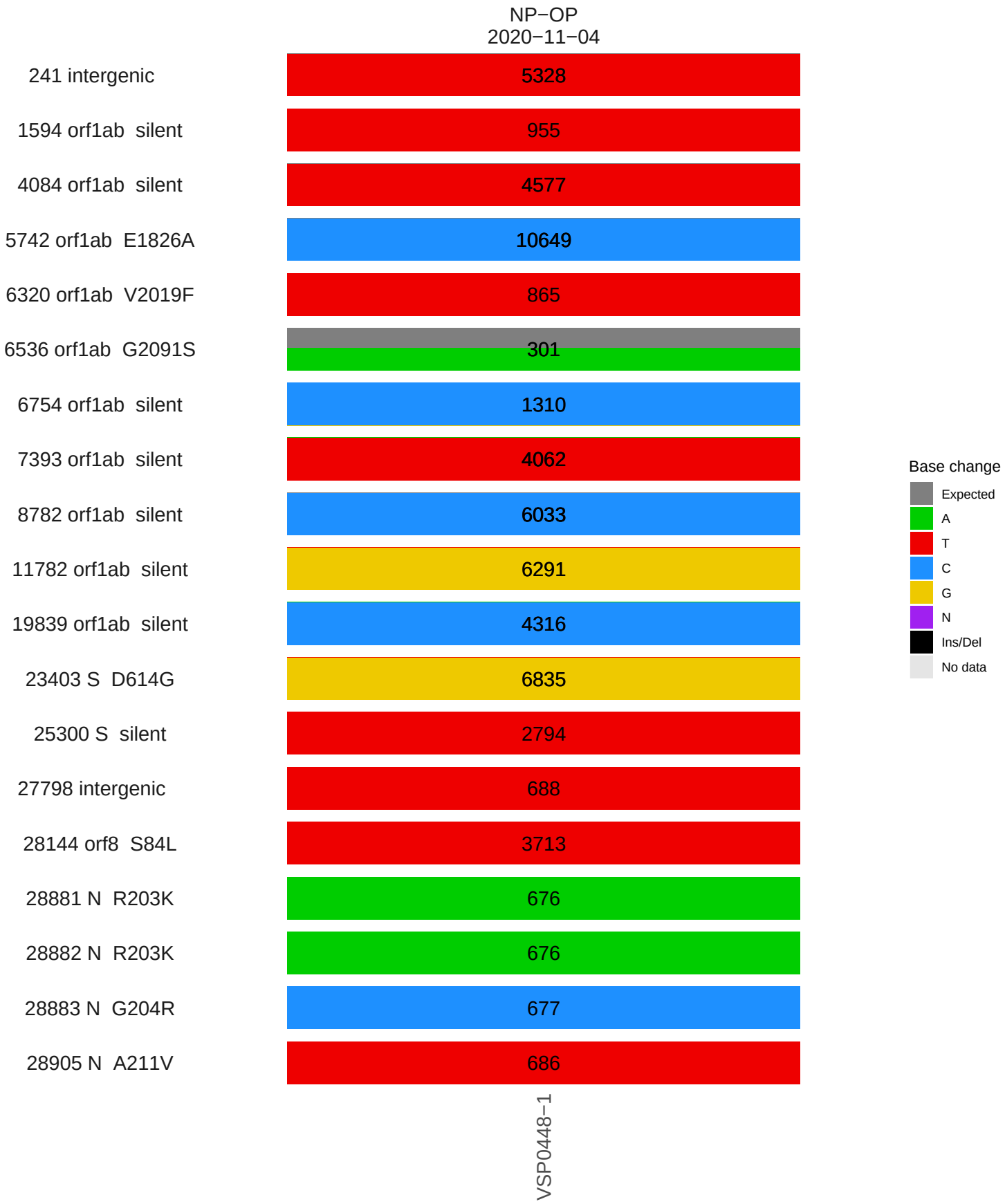
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0448-1	single experiment	NA	NP-OP	2020-11-04	1.16	74.6%	64.7%

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.

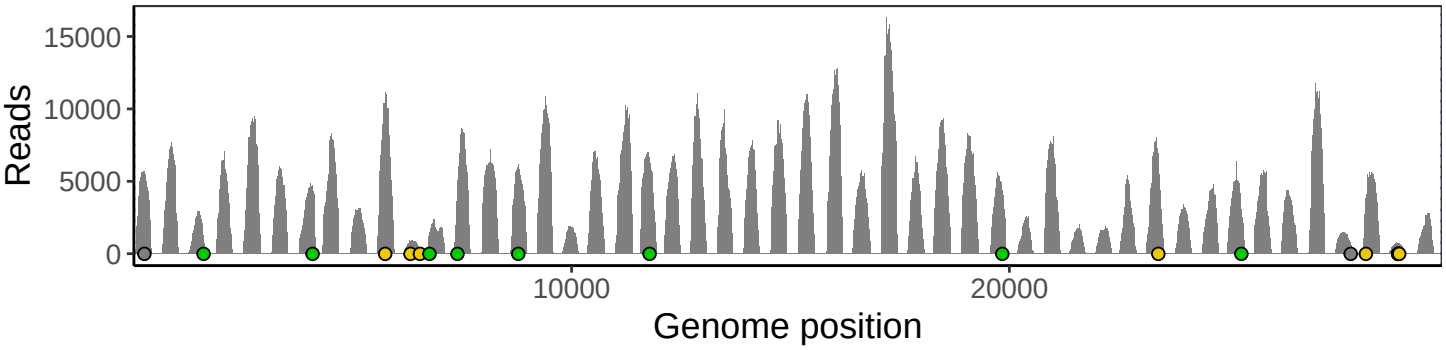



NP−OP
2020−11−04
241 intergenic
5328
1594 orf1ab silent
955
4084 orf1ab silent
4577
5742 orf1ab E1826A
10649
6320 orf1ab V2019F
865
6536 orf1ab G2091S
301
6754 orf1ab silent
1310
7393 orf1ab silent
4062
8782 orf1ab silent
6033
11782 orf1ab silent
6291
19839 orf1ab silent
4316
23403 S D614G
6835
25300 S silent
2794
27798 intergenic
688
28144 orf8 S84L
3713
28881 N R203K
676
28882 N R203K
676
28883 N G204R
677
28905 N A211V
686
VSP0448−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

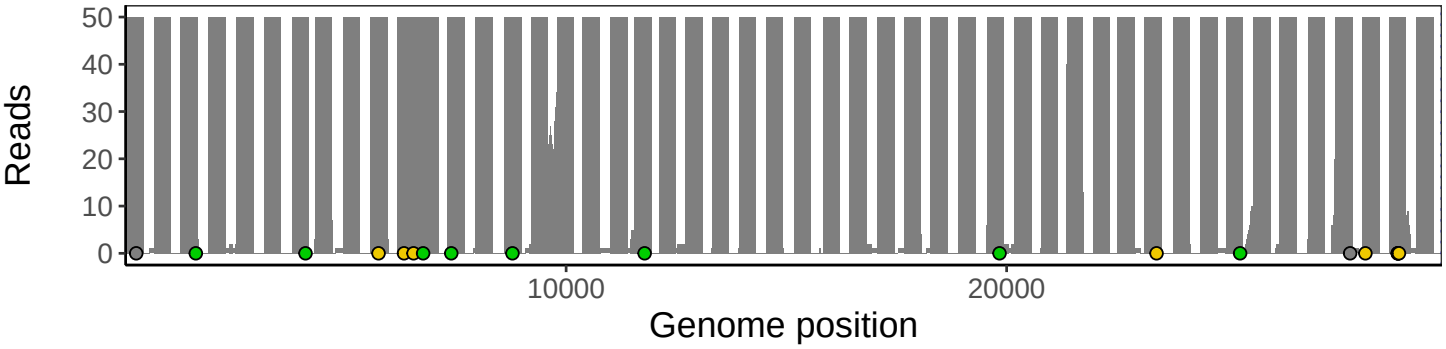
Analyses of individual experiments and composite results.

VSP0448-1 | 2020-11-04 | NP-OP | 391no-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.