COVID-19 subject 425

2021-01-11

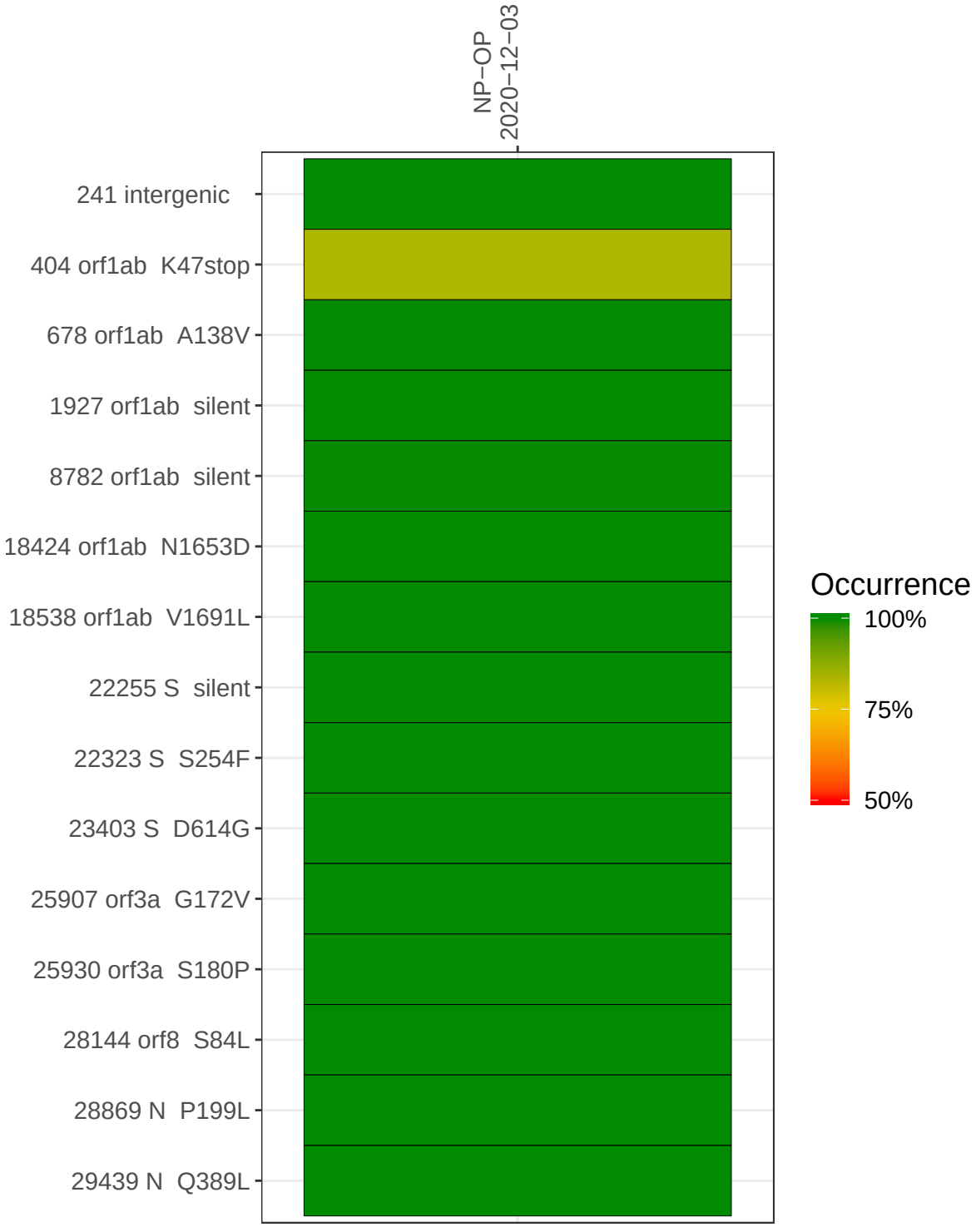
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

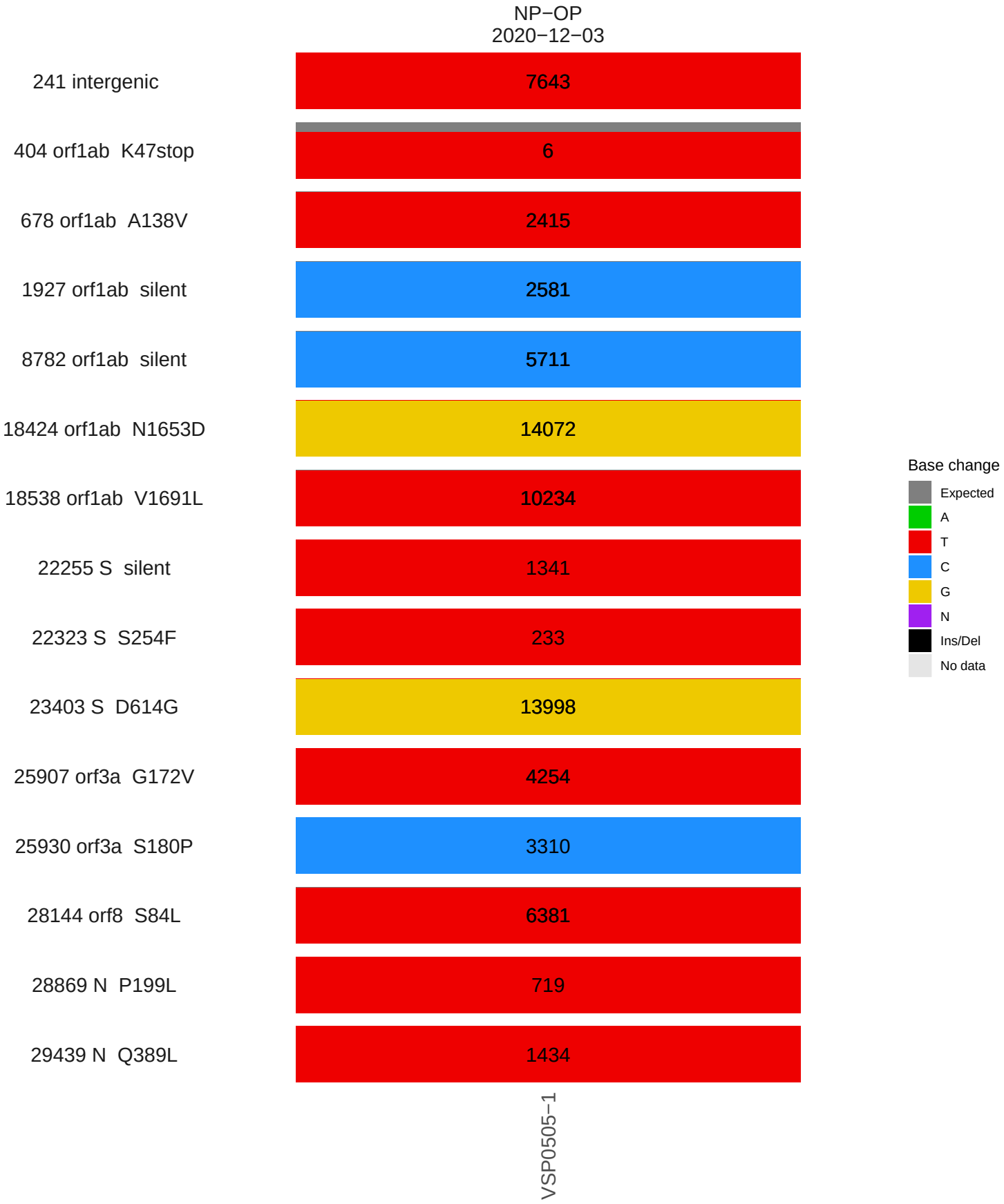
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0505-1	single experiment	NA	NP-OP	2020-12-03	1.22	66.6%	64.5%

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.

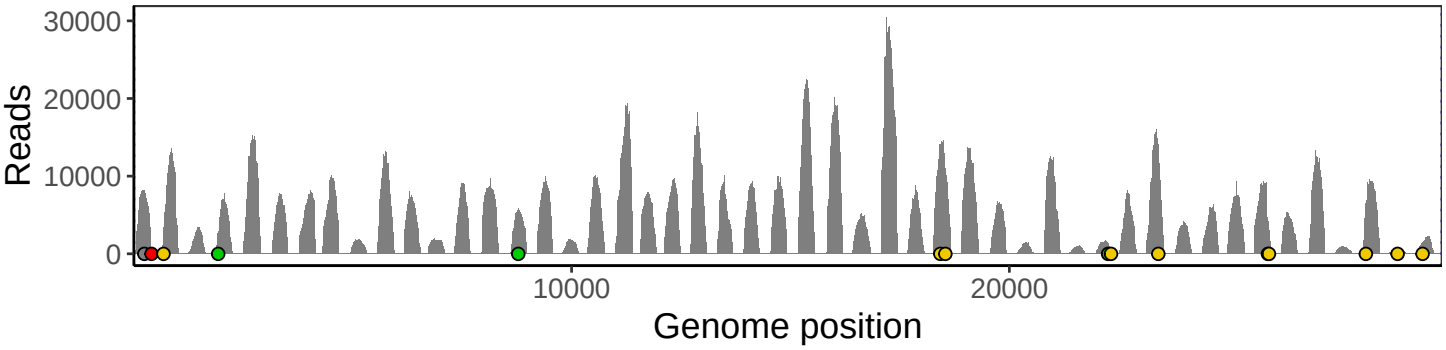



NP−OP
2020−12−03
241 intergenic
7643
404 orf1ab K47stop
6
678 orf1ab A138V
2415
1927 orf1ab silent
2581
8782 orf1ab silent
5711
18424 orf1ab N1653D
14072
18538 orf1ab V1691L
10234
22255 S silent
1341
22323 S S254F
233
23403 S D614G
13998
25907 orf3a G172V
4254
25930 orf3a S180P
3310
28144 orf8 S84L
6381
28869 N P199L
719
29439 N Q389L
1434
VSP0505−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

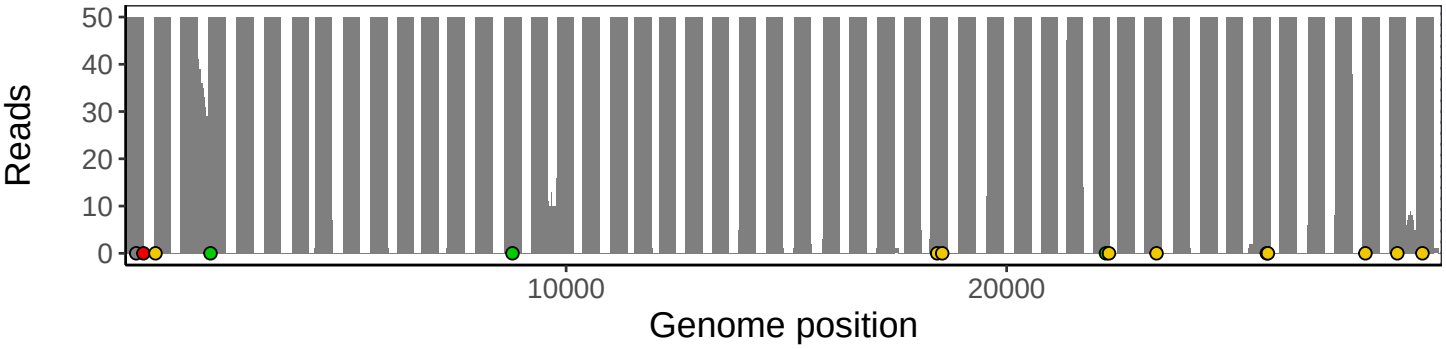
Analyses of individual experiments and composite results.

VSP0505-1 | 2020-12-03 | NP-OP | 425no-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.