COVID-19 subject 1044999

2021-01-14

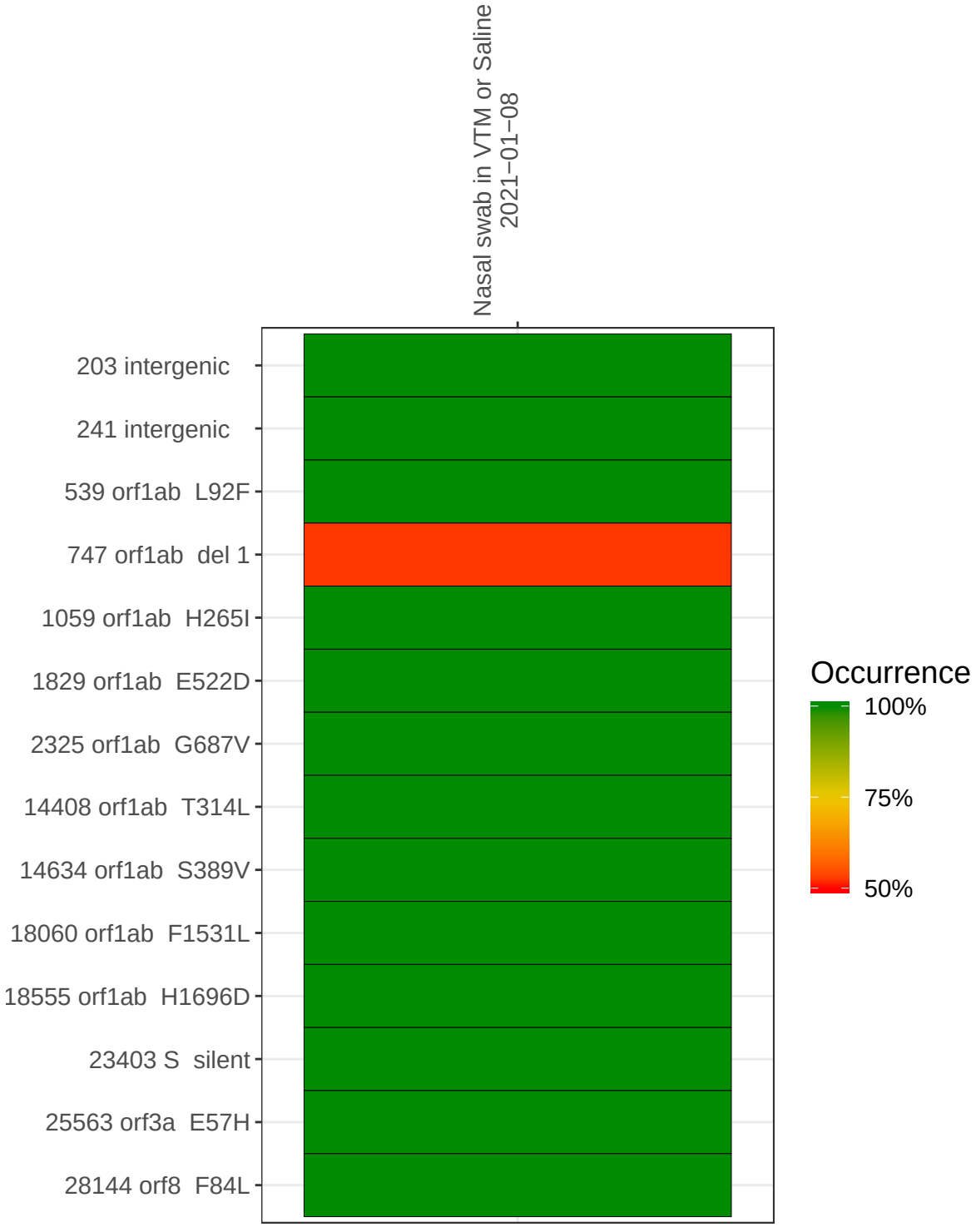
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

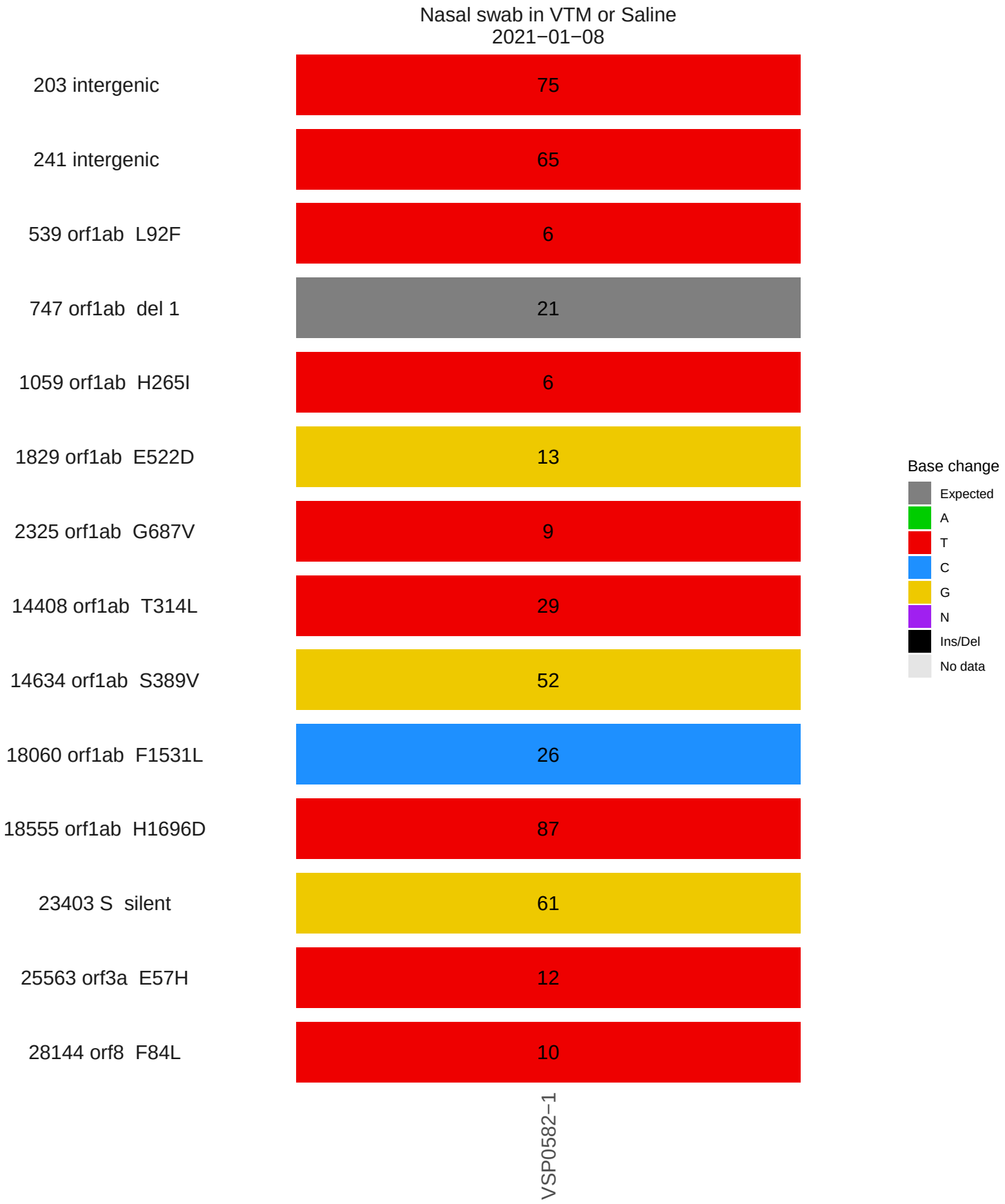
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0582-1	single experiment	NA	Nasal swab in VTM or Saline	2021-01-08	4.24	67.9%	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.

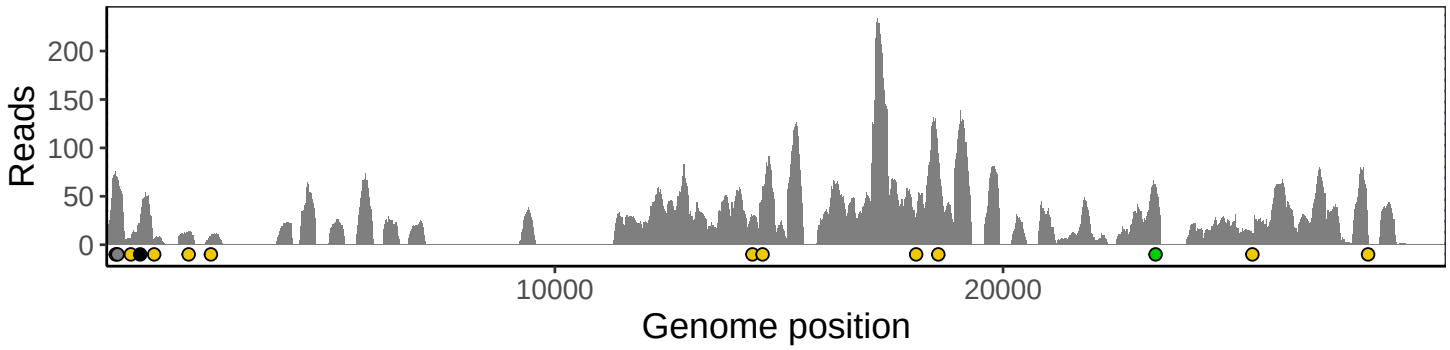



Nasal swab in VTM or Saline
2021−01−08
203 intergenic
75
241 intergenic
65
539 orf1ab L92F
6
747 orf1ab del 1
21
1059 orf1ab H265I
6
1829 orf1ab E522D
13
2325 orf1ab G687V
9
14408 orf1ab T314L
29
14634 orf1ab S389V
52
18060 orf1ab F1531L
26
18555 orf1ab H1696D
87
23403 S silent
61
25563 orf3a E57H
12
28144 orf8 F84L
10
VSP0582−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

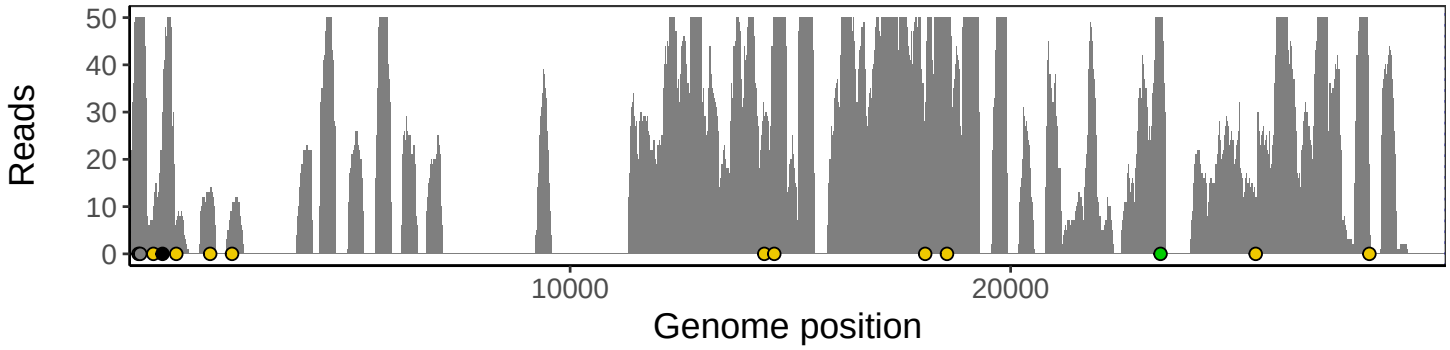
Analyses of individual experiments and composite results.

VSP0582-1 | 2021-01-08 | Nasal swab in VTM or Saline | E50701962-NR; 695215333 | 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.