

COVID-19 subject 653685

2021-01-15

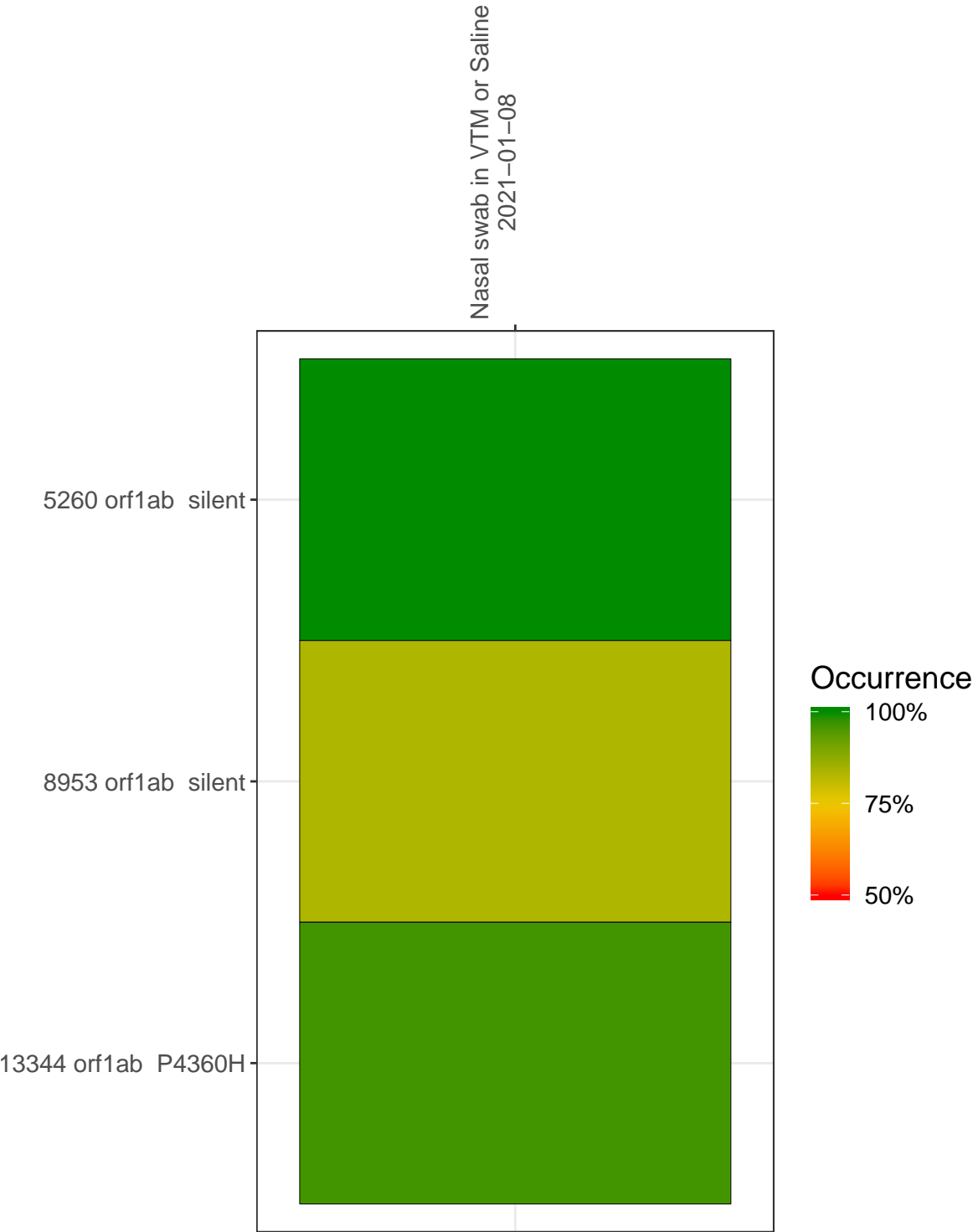
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0579	composite	NA	Nasal swab in VTM or Saline	2021-01-08	NA	7.2%	1.6%
VSP0579-1	single experiment	NA	Nasal swab in VTM or Saline	2021-01-08	NA	0.7%	0.2%
VSP0579-2	single experiment	NA	Nasal swab in VTM or Saline	2021-01-08	NA	7.4%	1.7%

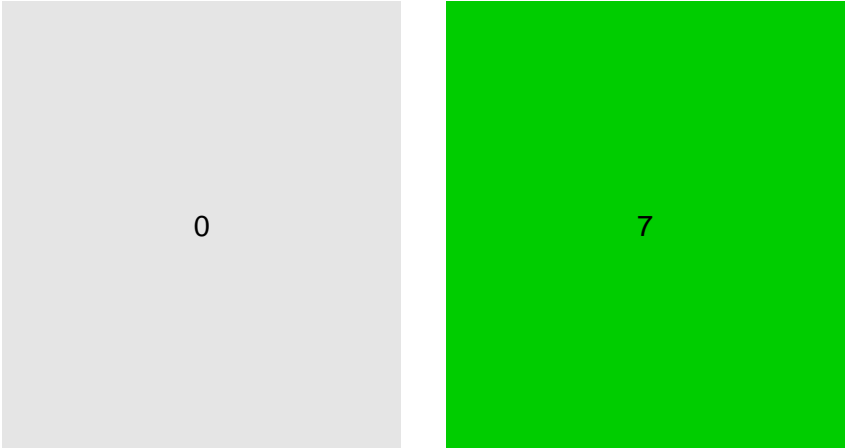
Variants shared across samples

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 or 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.

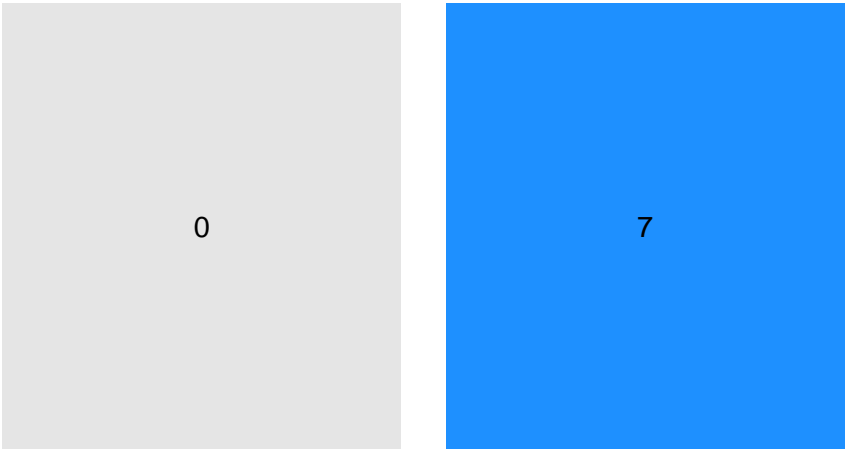


Nasal swab in VTM or Saline
2021-01-08

5260 orf1ab silent



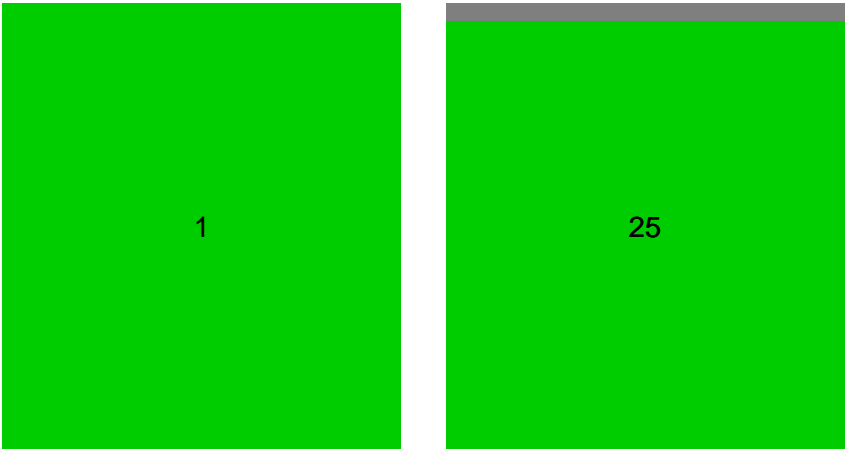
8953 orf1ab silent



Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

13344 orf1ab P4360H



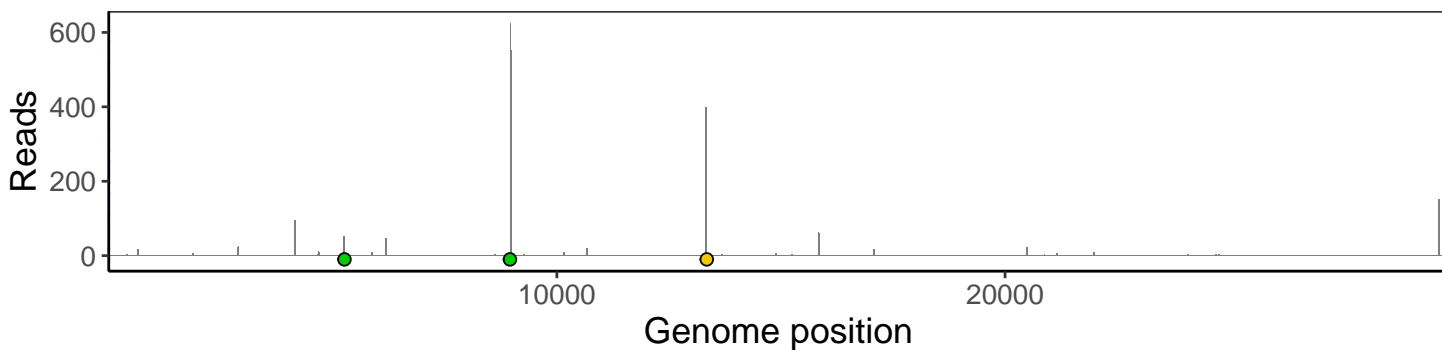
VSP0579-1

VSP0579-2

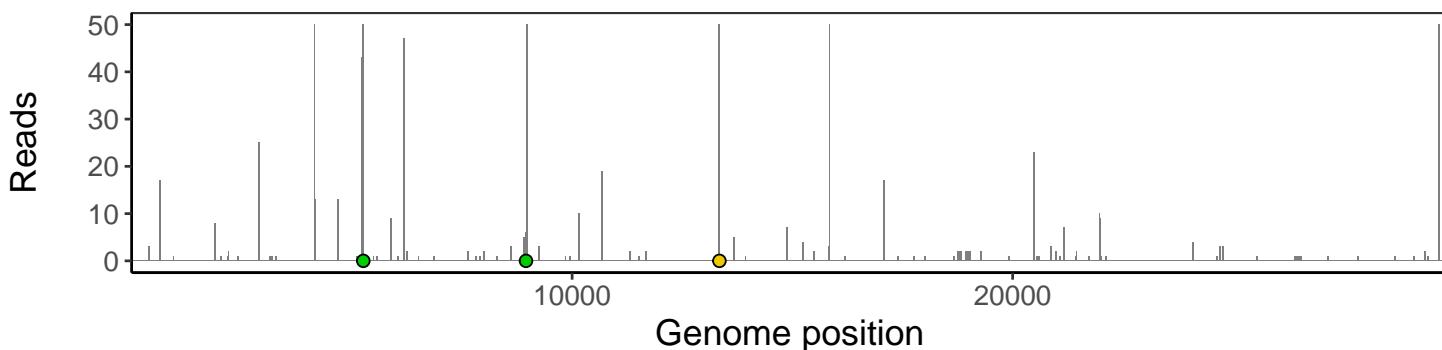
Analyses of individual experiments and composite results.

VSP0579 | 2021-01-08 | Nasal swab in VTM or Saline | E50703779-NR; 695237884 | composite result

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 to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.

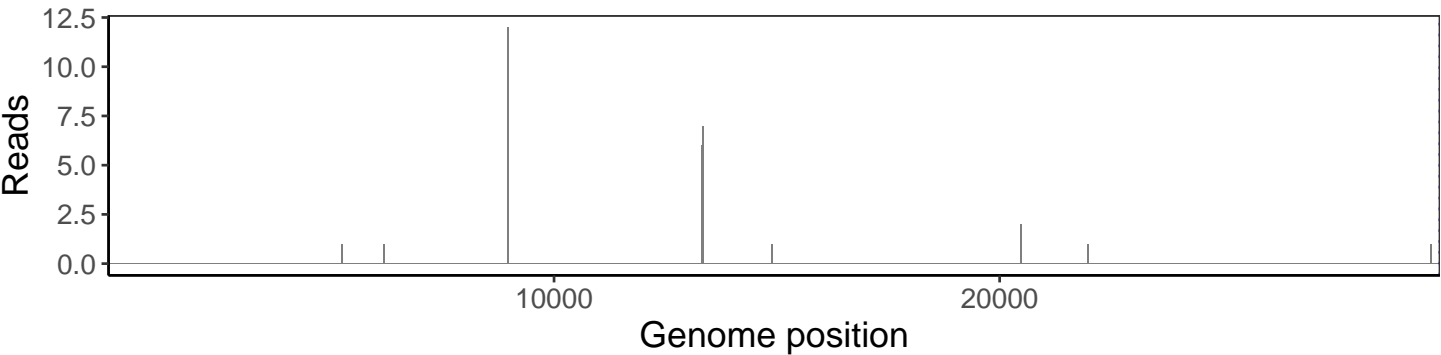


Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

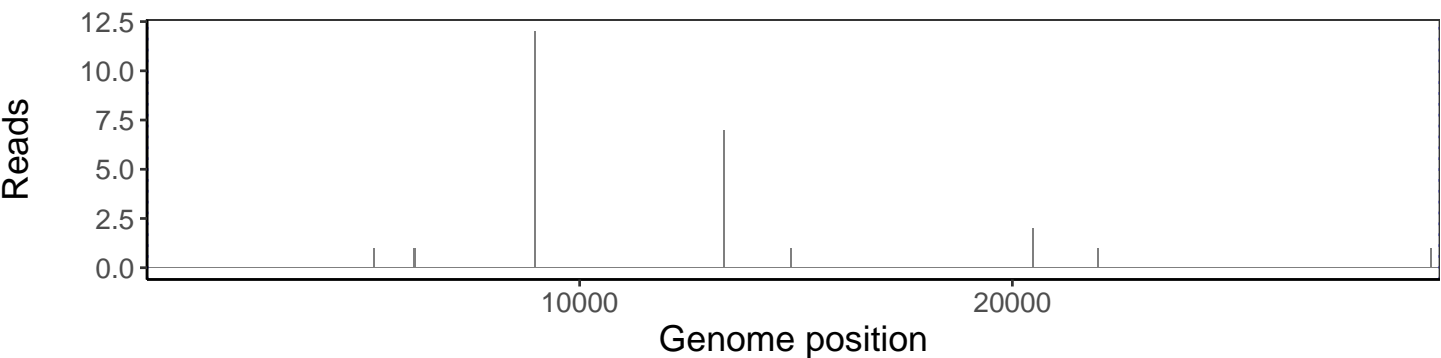


No contig data available.

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.



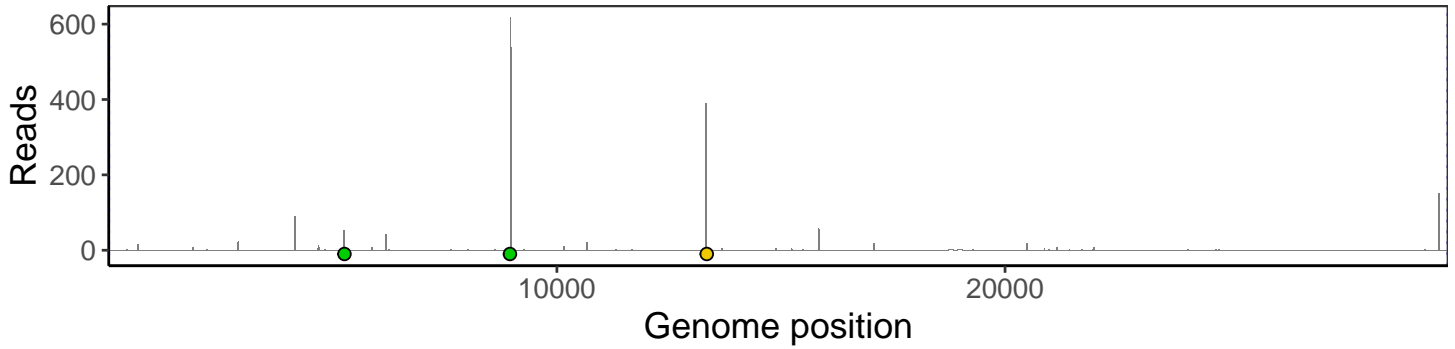
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



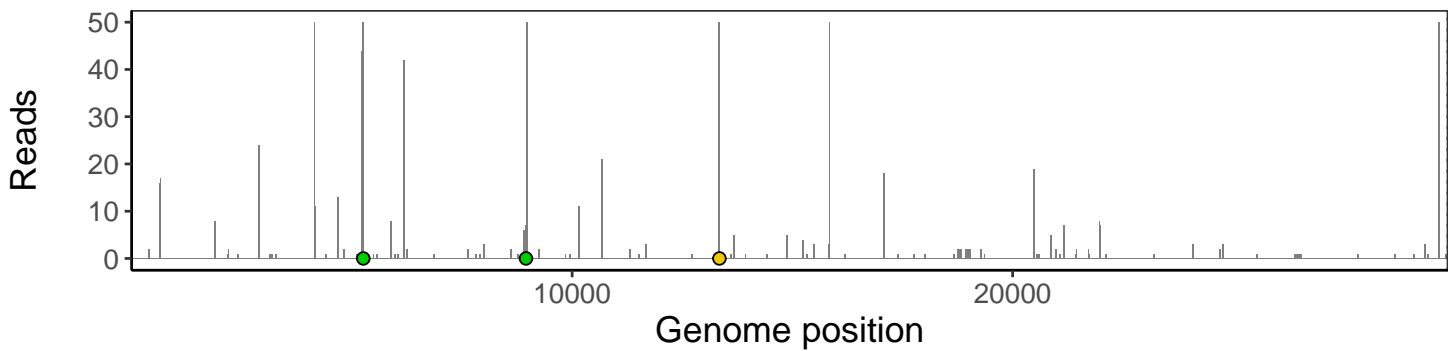
No contig data available.

VSP0579-2 | 2021-01-08 | Nasal swab in VTM or Saline | E50703779-NR; 695237884 | 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.



No contig data available.