

COVID-19 subject 1044999

2021-01-15

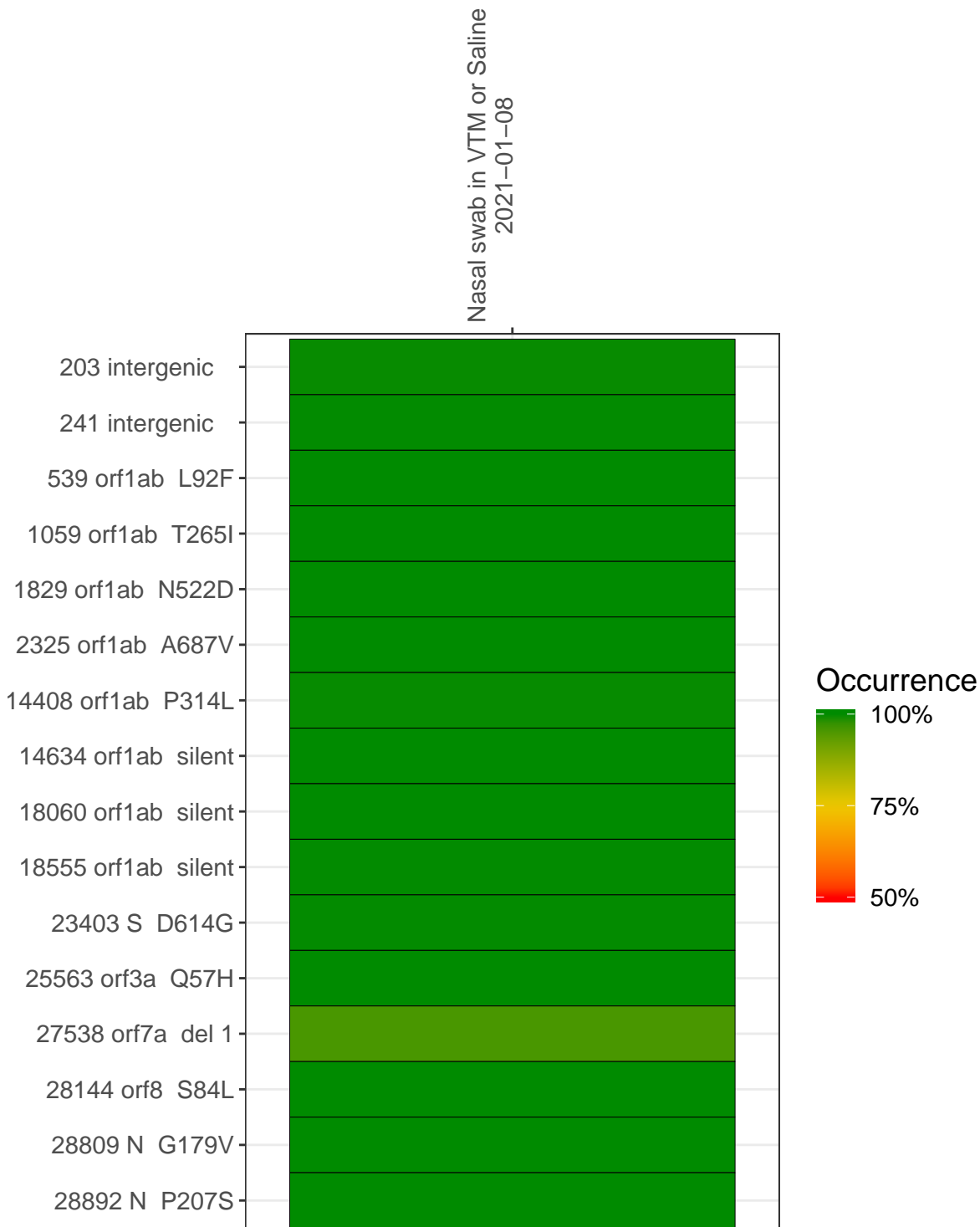
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0582	composite	NA	Nasal swab in VTM or Saline	2021-01-08	4.25	71.7%	69.1%
VSP0582-1	single experiment	NA	Nasal swab in VTM or Saline	2021-01-08	4.24	67.9%	64.5%
VSP0582-2	single experiment	NA	Nasal swab in VTM or Saline	2021-01-08	4.25	71.7%	69.1%

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

203 intergenic	75	1619
241 intergenic	65	1605
539 orf1ab L92F	6	318
1059 orf1ab T265I	6	332
1829 orf1ab N522D	13	420
2325 orf1ab A687V	9	306
14408 orf1ab P314L	29	691
14634 orf1ab silent	52	1676
18060 orf1ab silent	26	696
18555 orf1ab silent	87	2157
23403 S D614G	61	1541
25563 orf3a Q57H	12	436
27538 orf7a del 1		
28144 orf8 S84L	10	244
28809 N G179V	1	41
28892 N P207S	2	45

VSP0582-1

VSP0582-2

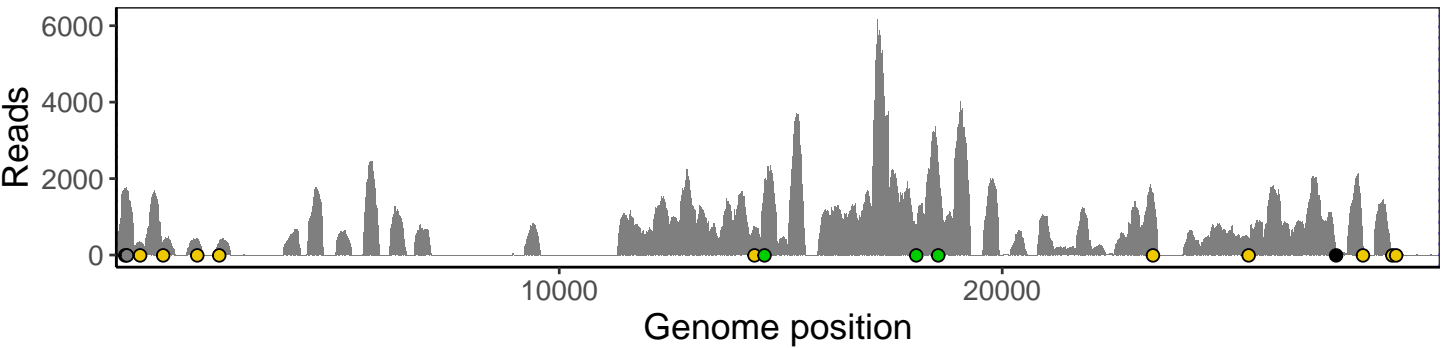
Base change

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

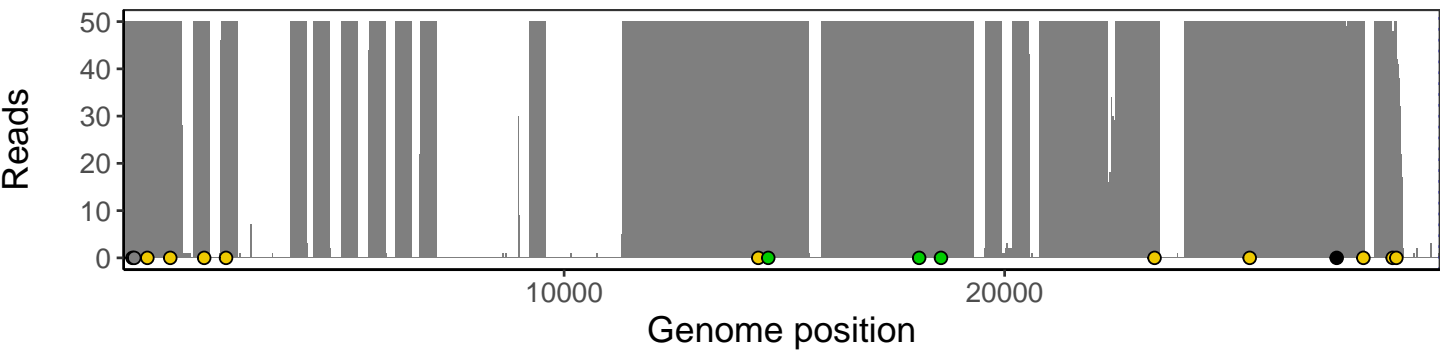
Analyses of individual experiments and composite results.

VSP0582 | 2021-01-08 | Nasal swab in VTM or Saline | E50701962-NR; 695215333 | 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 by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



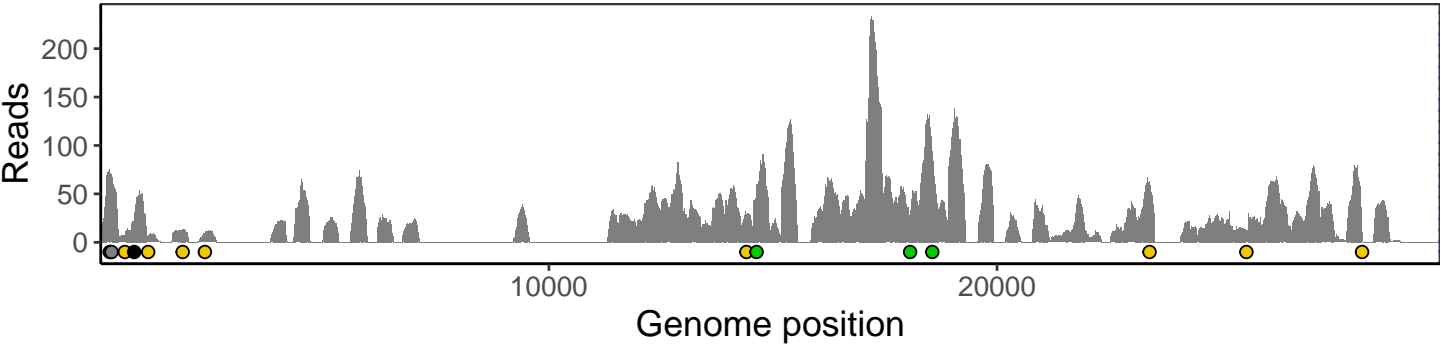
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



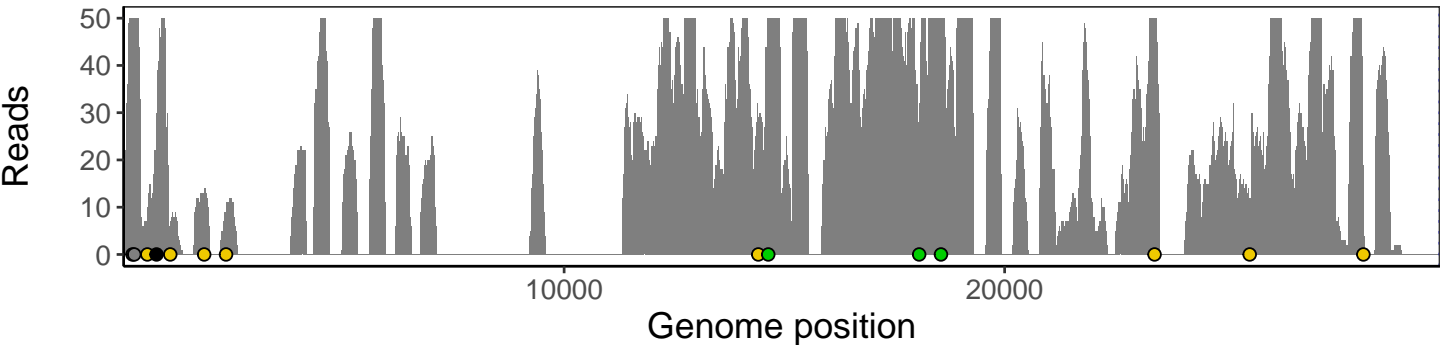
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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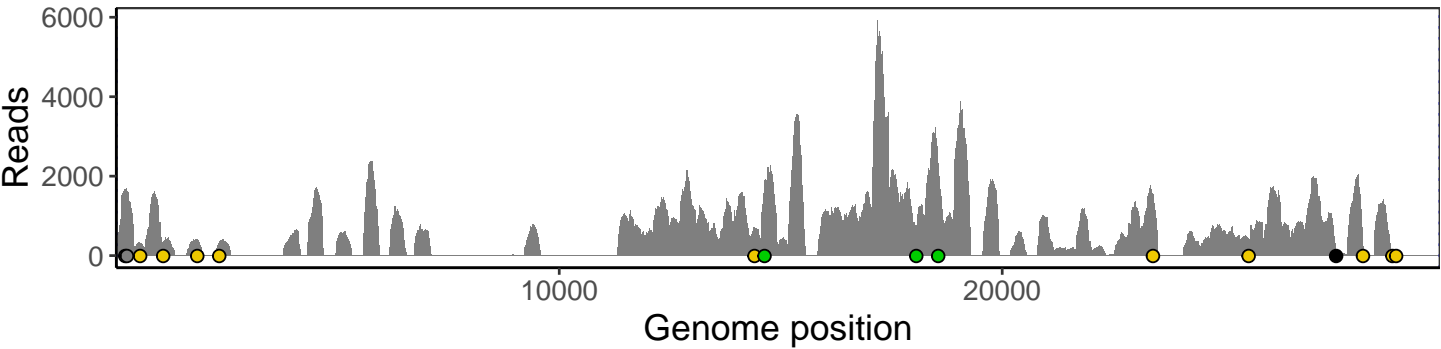
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



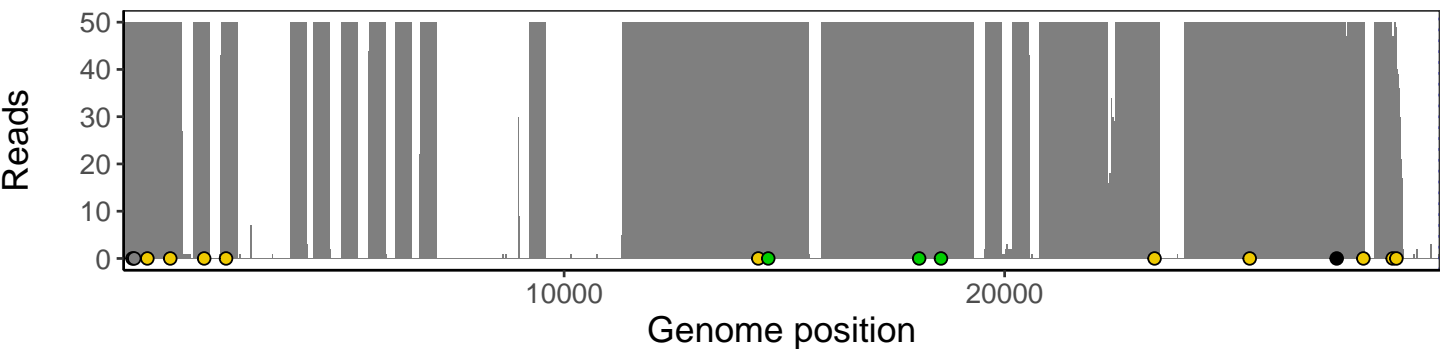
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