

# COVID-19 subject 272

*2020-09-14*

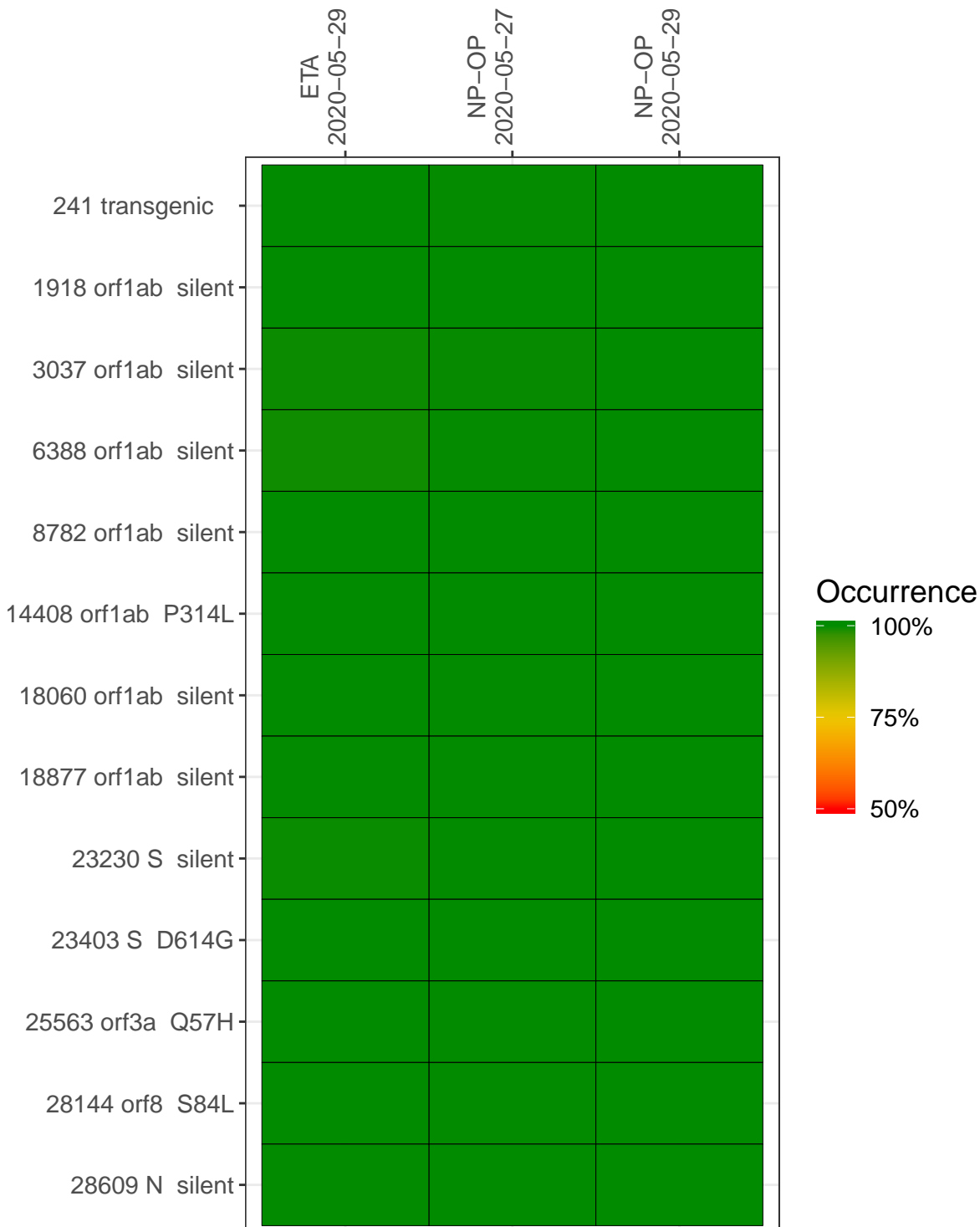
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0179-1	single experiment	14500	NP-OP	2020-05-27	29.41	99.8%	99.8%
VSP0195-1	single experiment	1530000	ETA	2020-05-29	25.63	99.7%	98.7%
VSP0196-1	single experiment	14300	NP-OP	2020-05-29	12.50	99.1%	97.7%
VSP0260-1	single experiment	NA	Stool	2020-06-17	NA	NA	NA

## 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.



	ETA 2020-05-29	NP-OP 2020-05-27	NP-OP 2020-05-29
241 transgenic	249	1781	21
1918 orf1ab silent	2840	1771	25
3037 orf1ab silent	1096	1494	24
6388 orf1ab silent	552	2731	89
8782 orf1ab silent	828	1429	17
14408 orf1ab P314L	931	2859	32
18060 orf1ab silent	462	1297	14
18877 orf1ab silent	1873	2488	29
23230 S silent	818	2793	104
23403 S D614G	1083	3659	117
25563 orf3a Q57H	2577	2002	16
28144 orf8 S84L	1135	4746	77
28609 N silent	1817	6263	124
	VSP0195-1	VSP0179-1	VSP0196-1

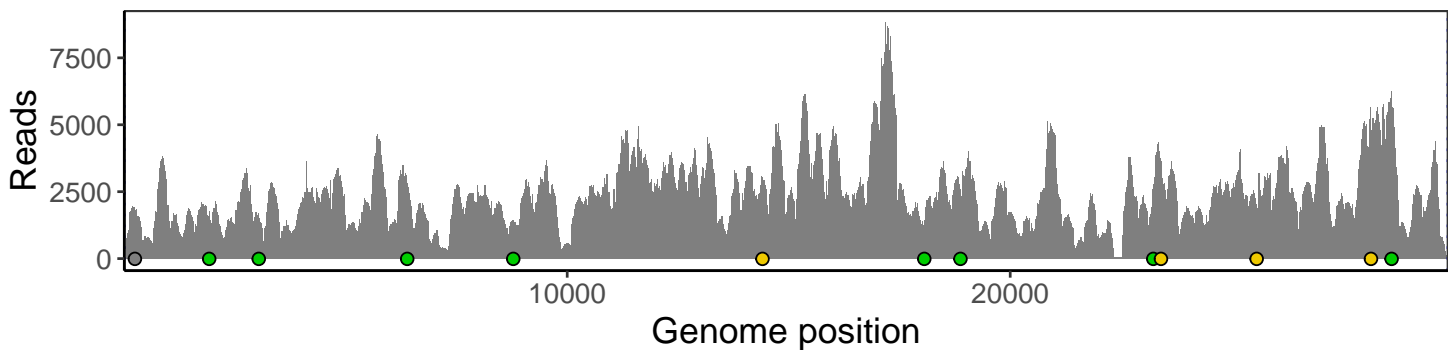
Base change

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

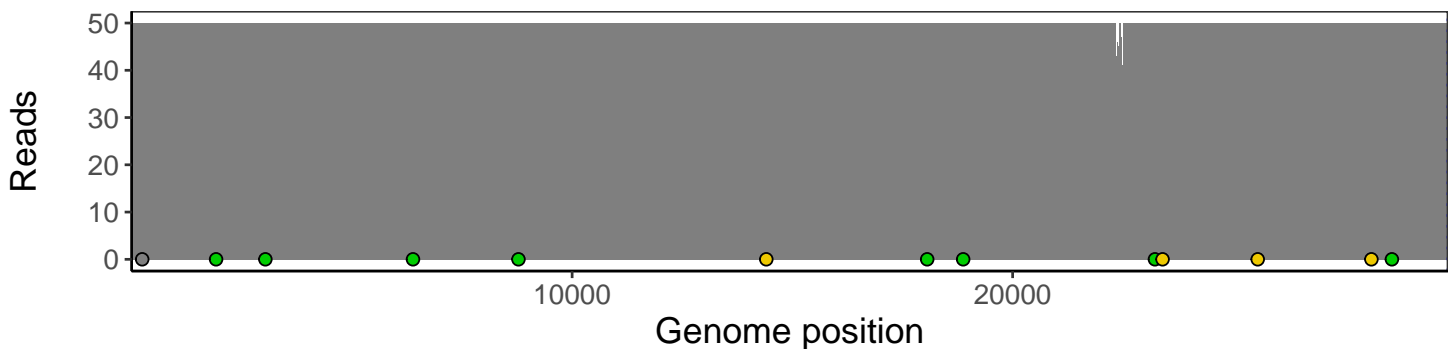
## Analyses of individual experiments and composite results.

VSP0179-1 | 2020-05-27 | NP-OP | 272no-q | 14500 genomes | single experiment

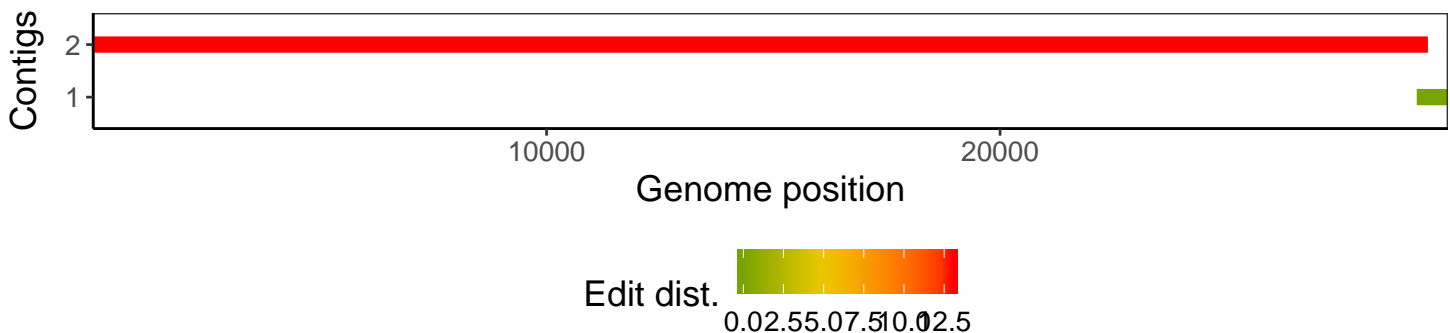
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



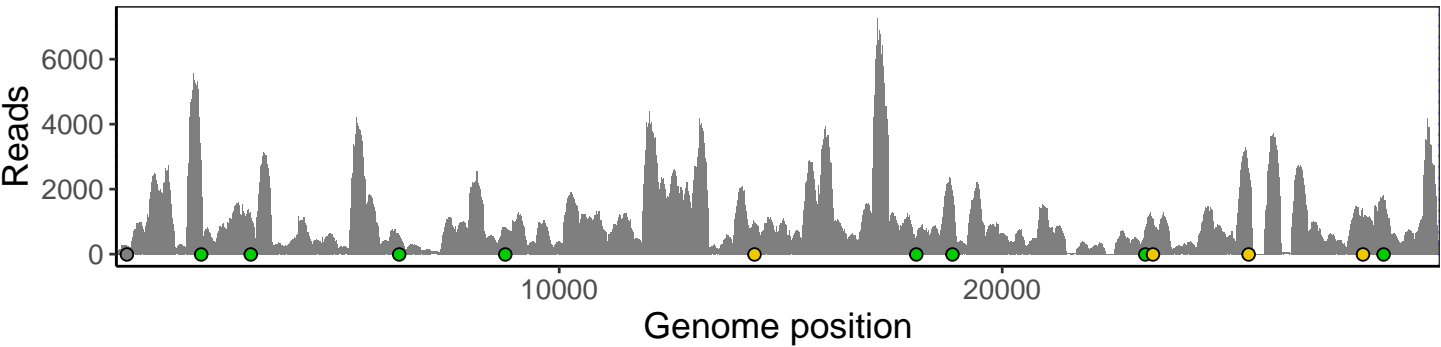
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



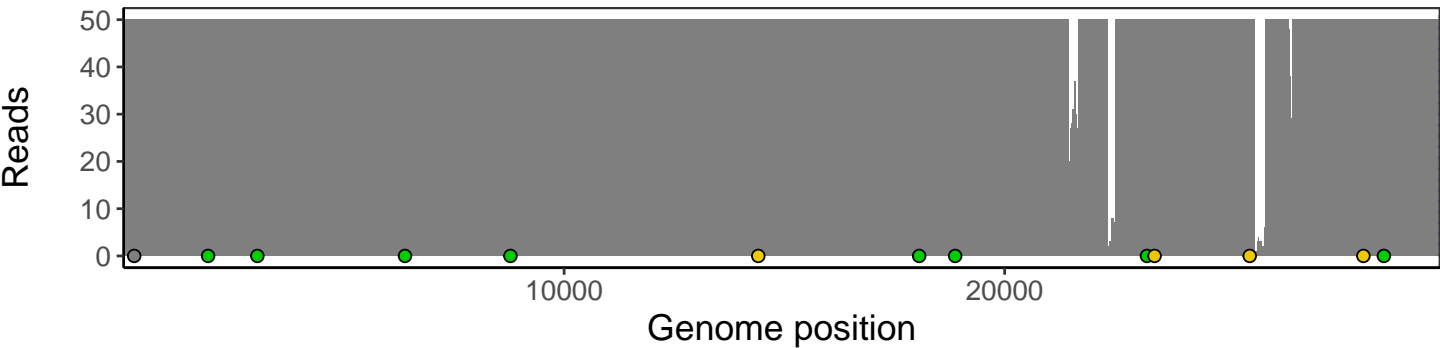
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



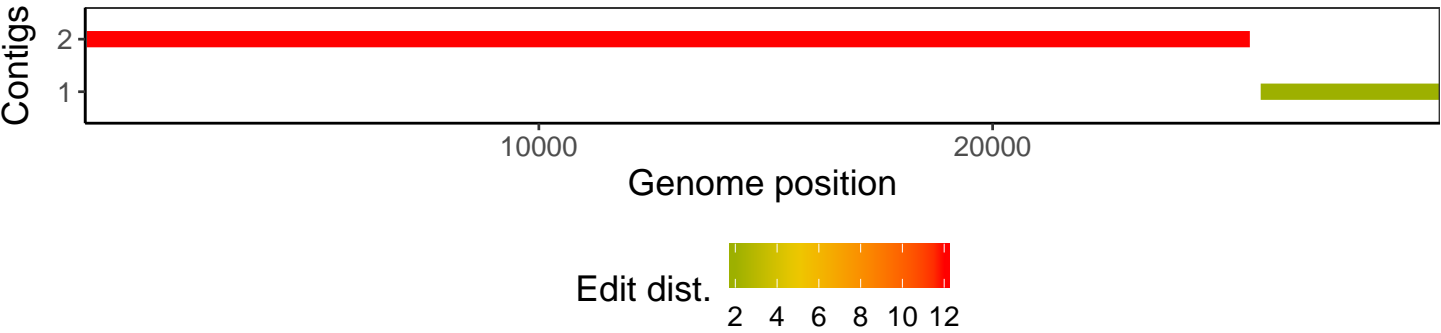
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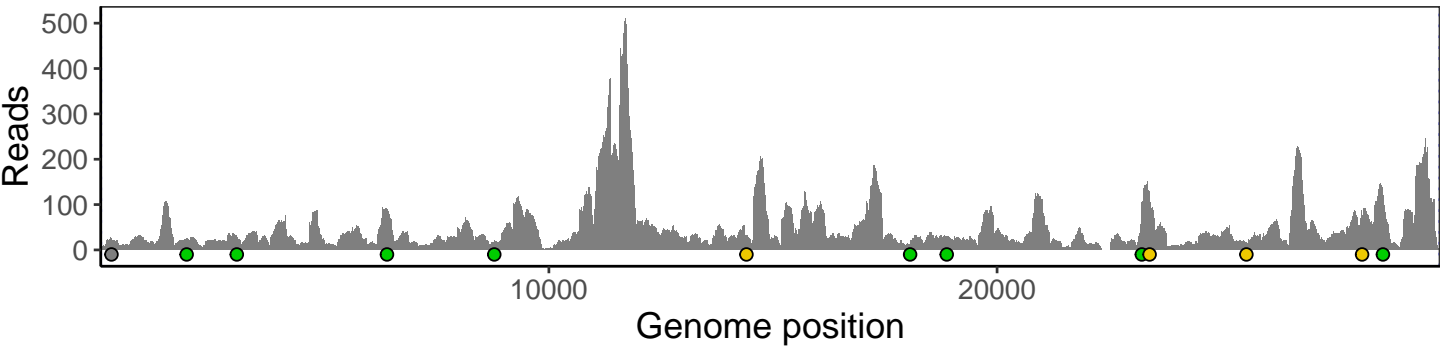
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



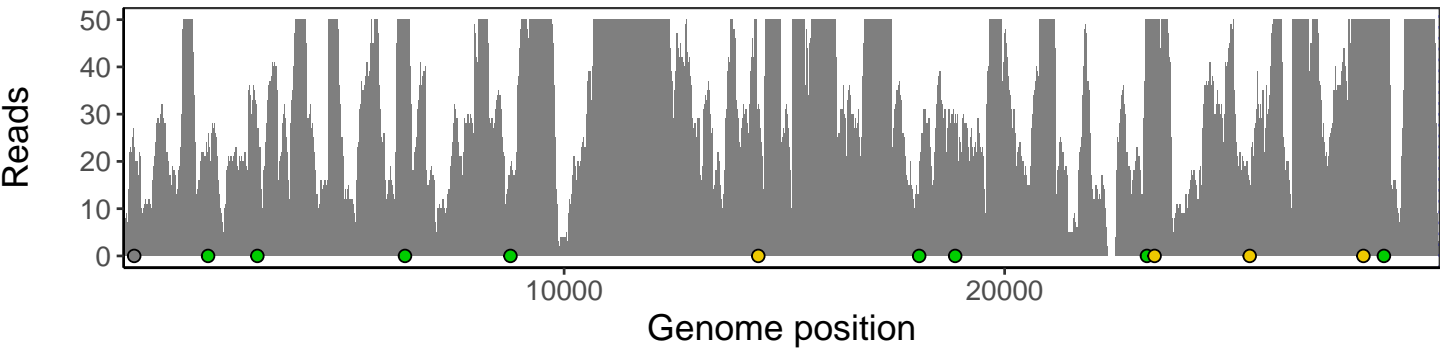
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



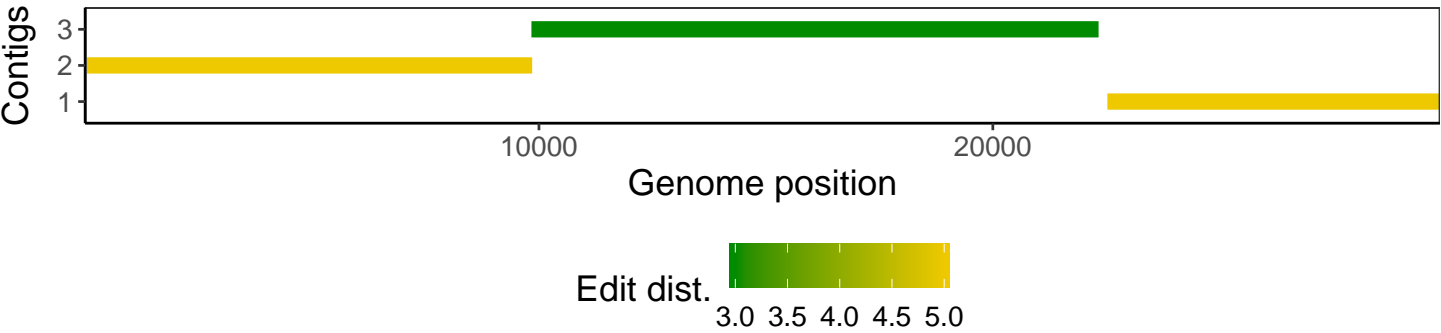
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



VSP0260-1 | 2020-06-17 | Stool | 272p | NA genomes | single experiment

No pileup data available.

No contig data available.