

# COVID-19 subject 263

*2021-01-10*

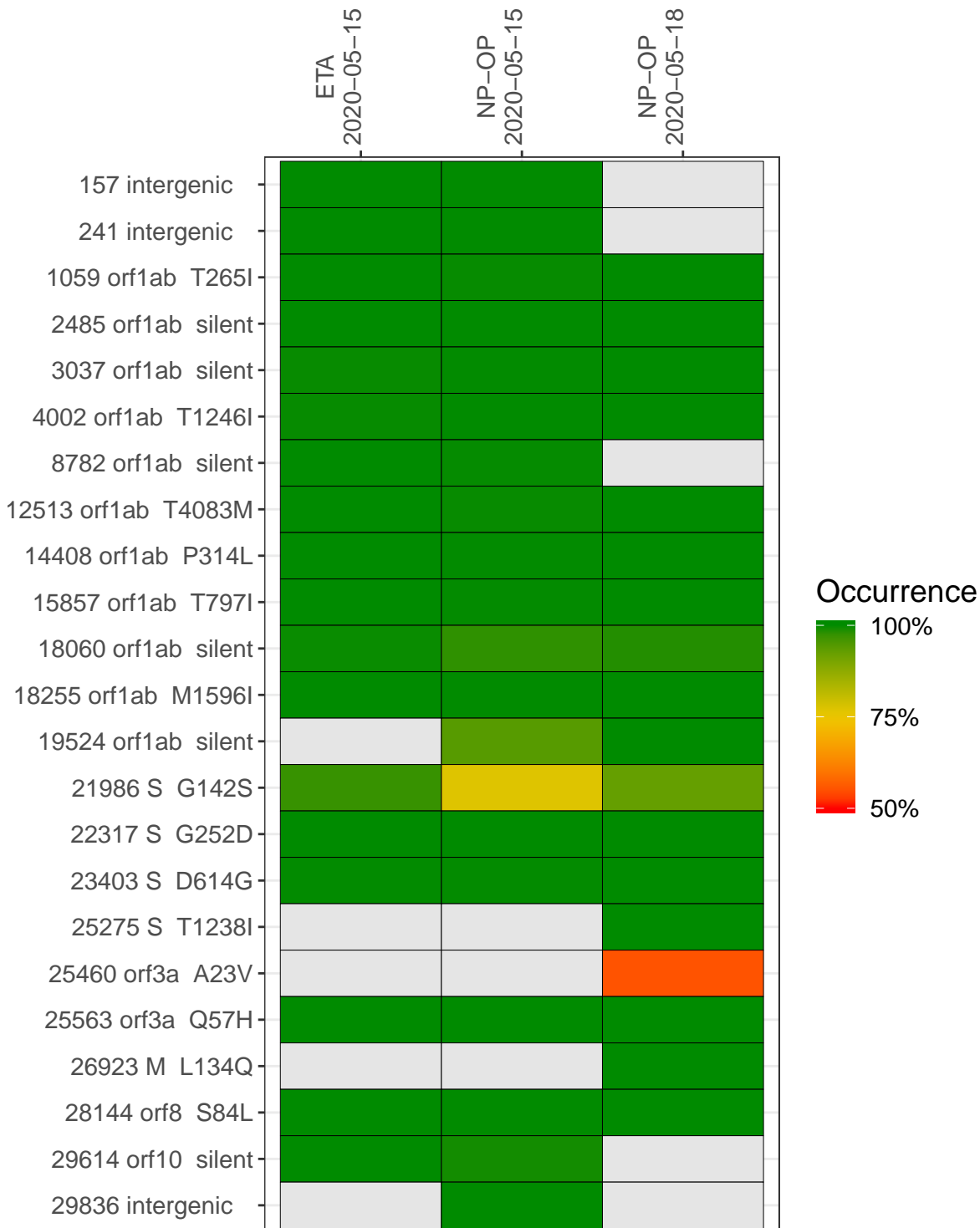
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0142-1	single experiment	NA	ETA	2020-05-15	29.81	99.7%	99.6%
VSP0143-1	single experiment	172000	NP-OP	2020-05-15	29.87	99.8%	99.8%
VSP0148-1	single experiment	NA	NP-OP	2020-05-18	8.68	90.7%	89.5%

## 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.



	ETA 2020-05-15	NP-OP 2020-05-15	NP-OP 2020-05-18
157 intergenic	679	3447	
241 intergenic	702	3797	
1059 orf1ab T265I	404	2869	42
2485 orf1ab silent	393	3139	32
3037 orf1ab silent	609	2364	81
4002 orf1ab T1246I	749	4062	138
8782 orf1ab silent	475	3021	
12513 orf1ab T4083M	964	3063	215
14408 orf1ab P314L	1072	4170	240
15857 orf1ab T797I	1218	4955	296
18060 orf1ab silent	440	2921	80
18255 orf1ab M1596I	613	2741	100
19524 orf1ab silent	142	2168	14
21986 S G142S	188	1570	41
22317 S G252D	17	478	6
23403 S D614G	1892	6347	273
25275 S T1238I	313	2836	29
25460 orf3a A23V	724	4749	103
25563 orf3a Q57H	689	4079	87
26923 M L134Q	969	5061	57
28144 orf8 S84L	855	5801	24
29614 orf10 silent	135	1347	
29836 intergenic	1	158	
	VSP0142-1	VSP0143-1	VSP0148-1

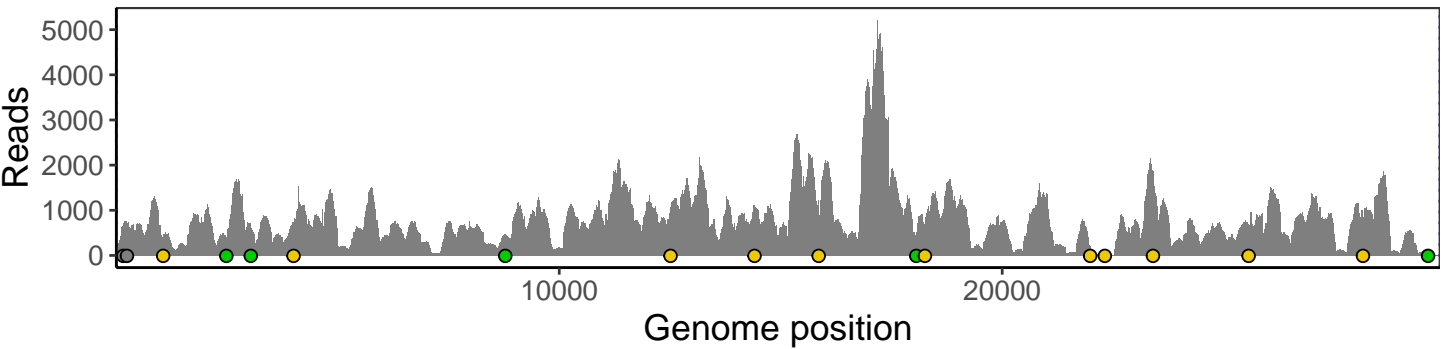
Base change

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

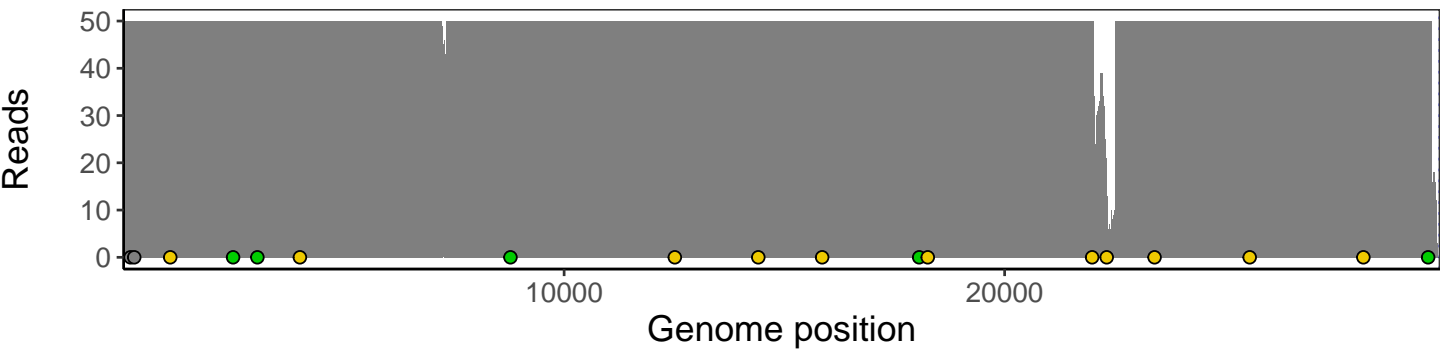
Analyses of individual experiments and composite results.

VSP0142-1 | 2020-05-15 | ETA | 263e-q1 | genomes | single experiment

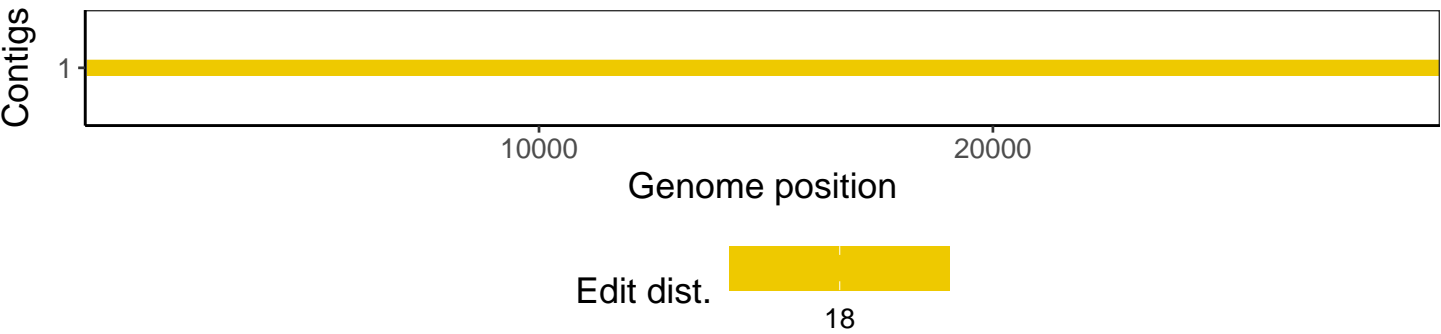
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



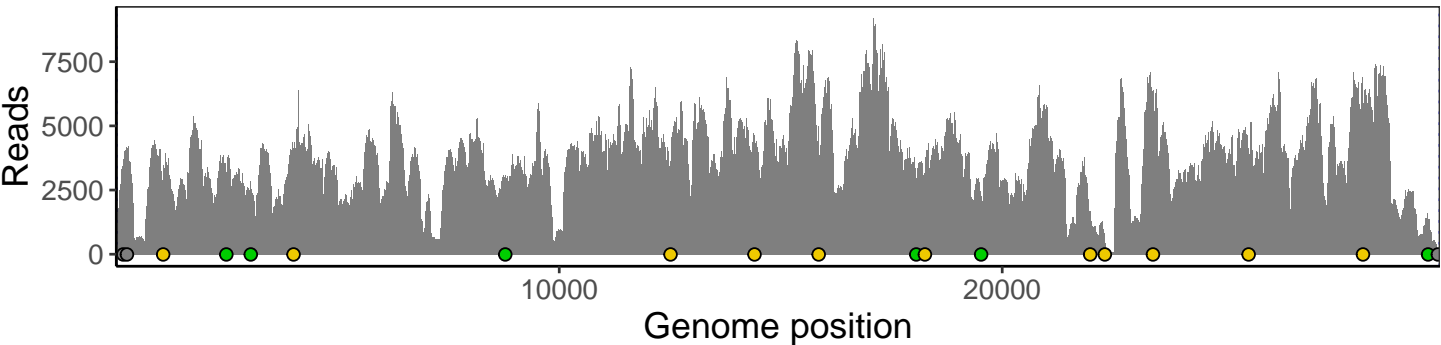
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



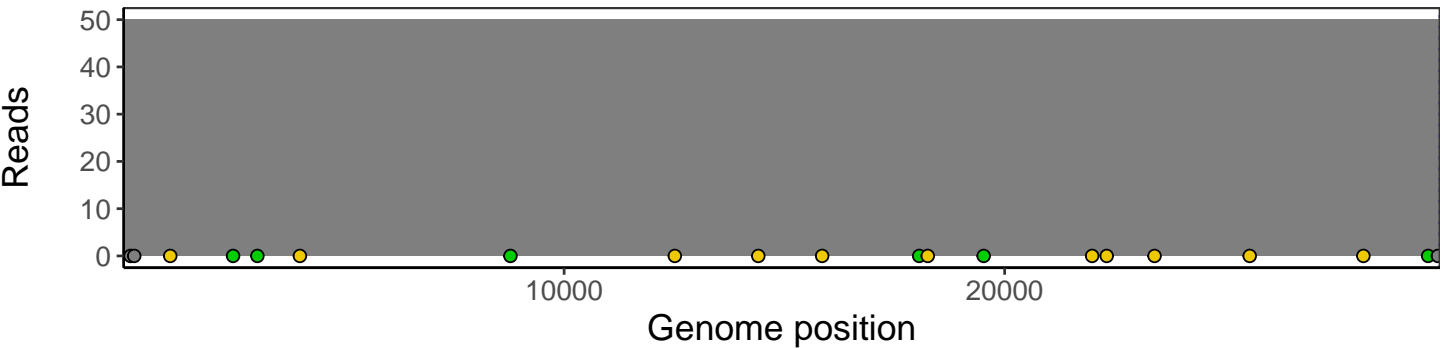
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



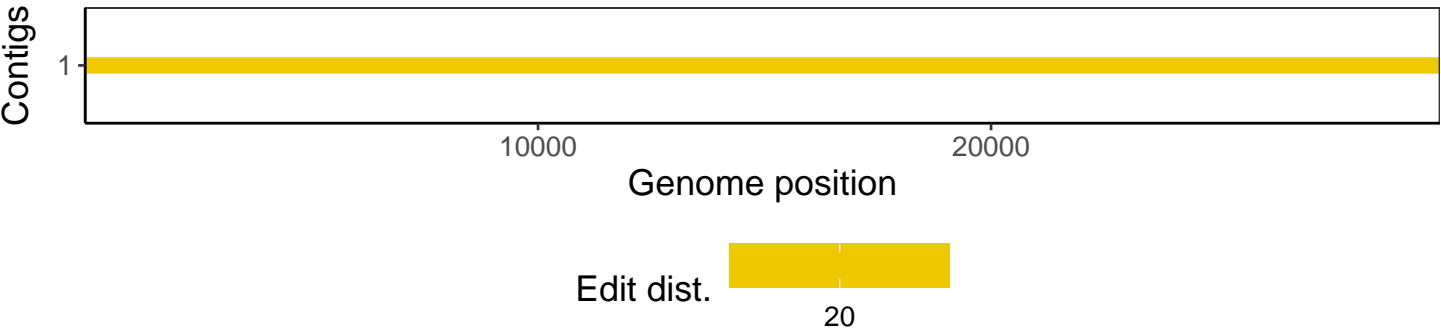
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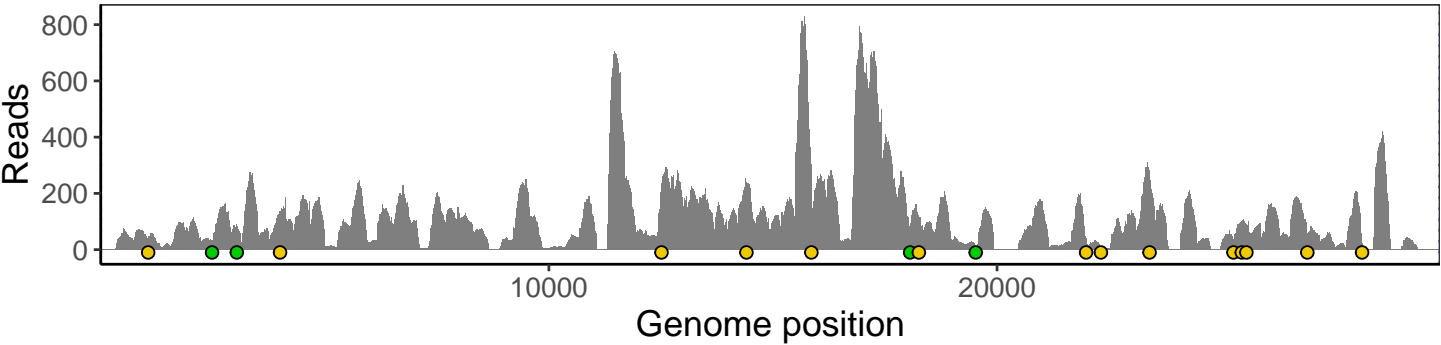
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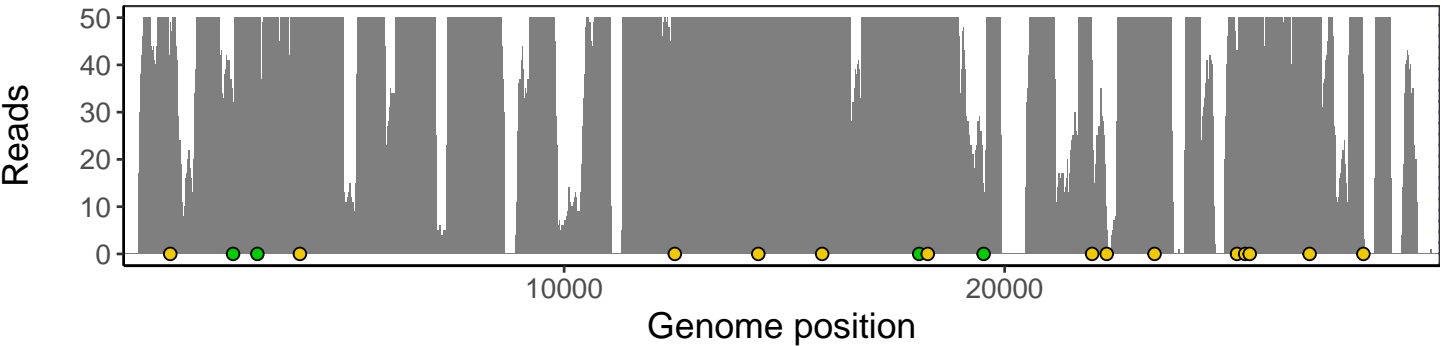
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