

COVID-19 subject J3R26

2020-10-23

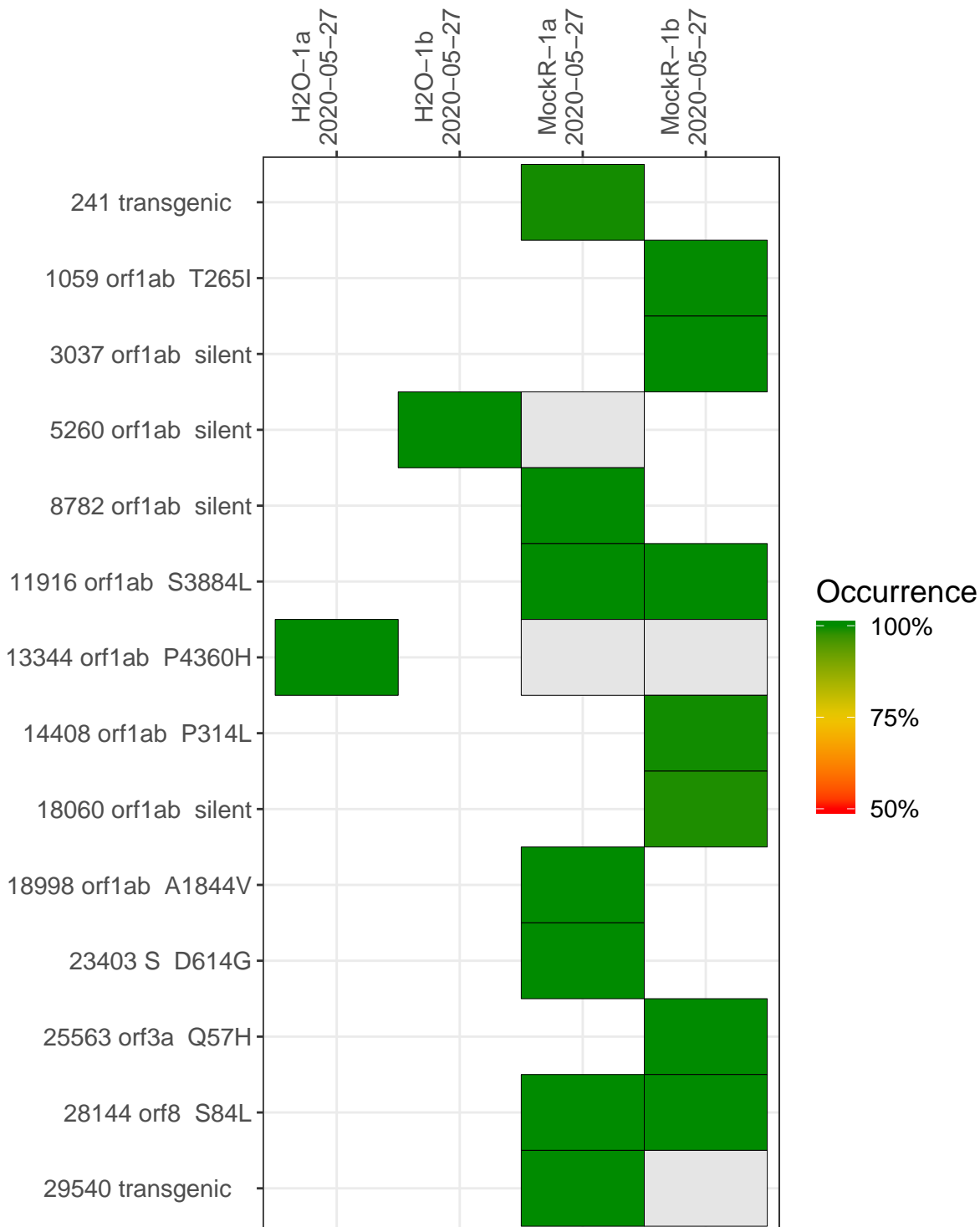
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP9982-1b	single experiment	NA	H2O-1b	2020-05-27	NA	0.4%	0.1%
VSP9983-1a	single experiment	NA	H2O-1a	2020-05-27	NA	0.8%	0.6%
VSP9984-1b	single experiment	NA	MockR-1b	2020-05-27	0.73	63.2%	54.3%
VSP9985-1a	single experiment	NA	MockR-1a	2020-05-27	0.62	59.7%	48.6%

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.



	H2O-1a 2020-05-27	H2O-1b 2020-05-27	MockR-1a 2020-05-27	MockR-1b 2020-05-27	
241 transgenic			188		
1059 orf1ab T265I				1373	
3037 orf1ab silent				459	
5260 orf1ab silent		15	1		
8782 orf1ab silent			14		
11916 orf1ab S3884L			7	176	
13344 orf1ab P4360H	14		6	932	
14408 orf1ab P314L				471	
18060 orf1ab silent				408	
18998 orf1ab A1844V			7		
23403 S D614G			59		
25563 orf3a Q57H				1030	
28144 orf8 S84L			15	67	
29540 transgenic			5	1	
	VSP9983-1a	VSP9982-1b	VSP9985-1a	VSP9984-1b	

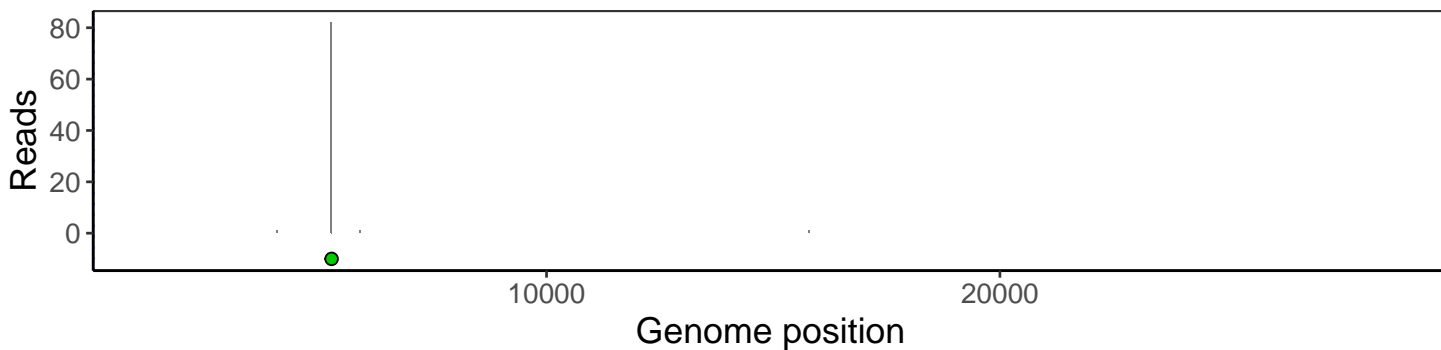
Base change

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

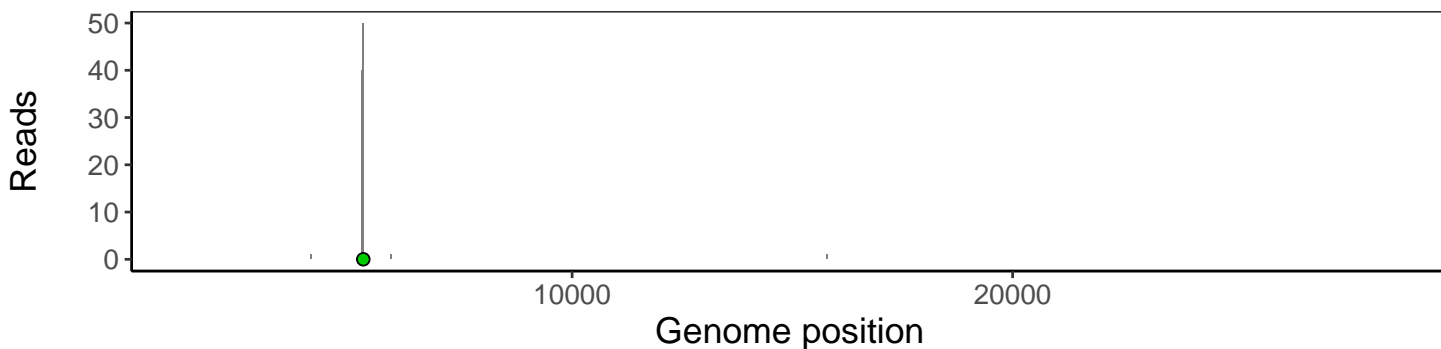
Analyses of individual experiments and composite results.

VSP9982-1b | 2020-05-27 | H2O-1b | J3R26 | 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.

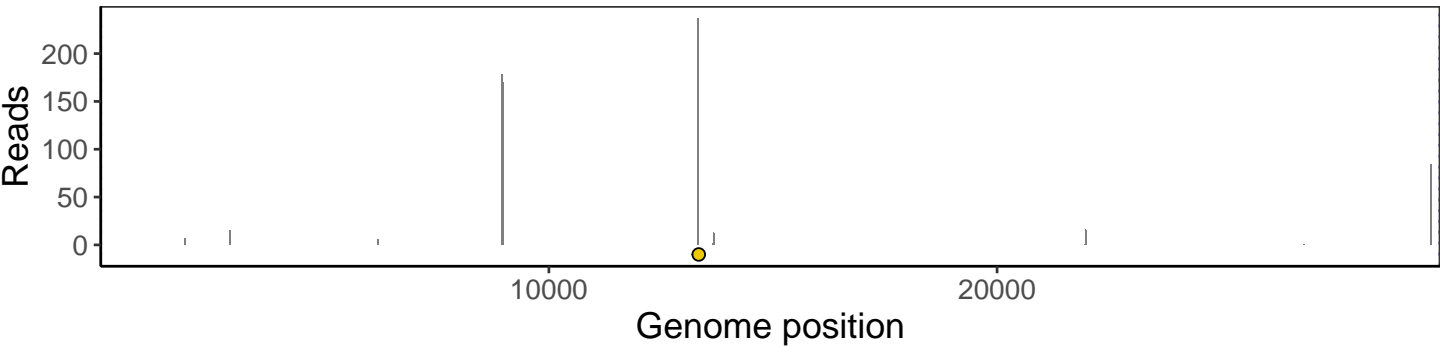


Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

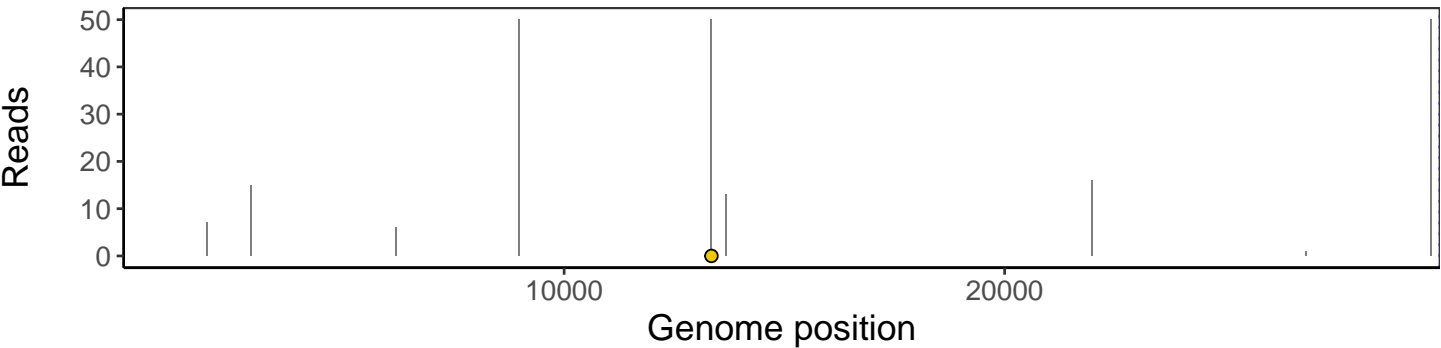


No contig data available.

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.

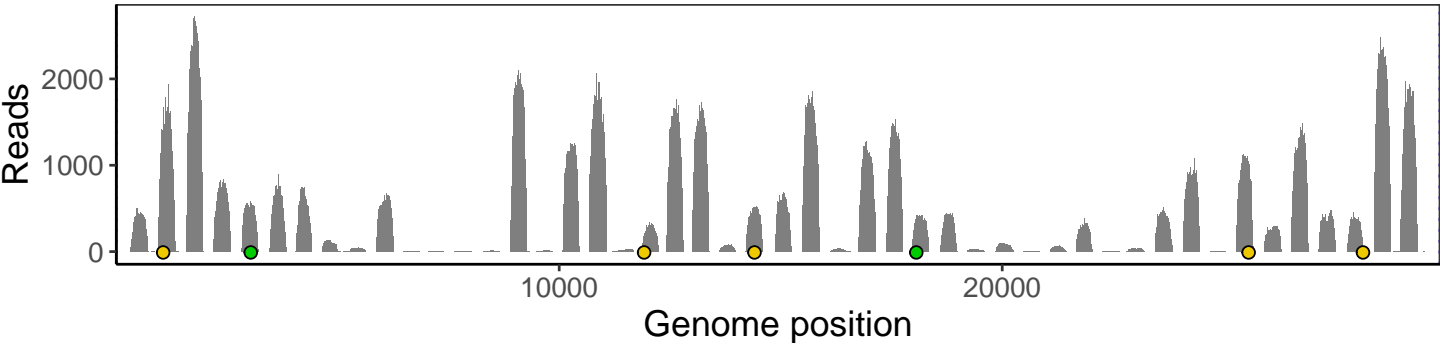


Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

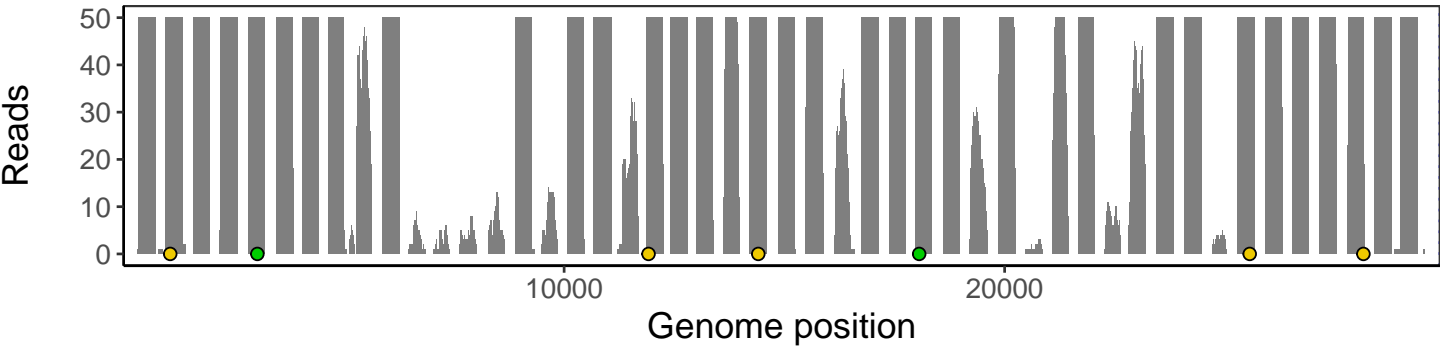


No contig data available.

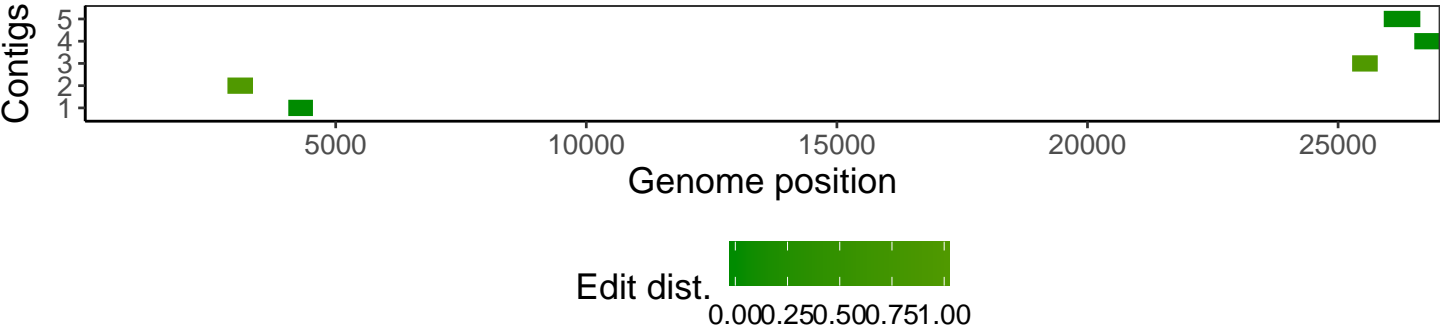
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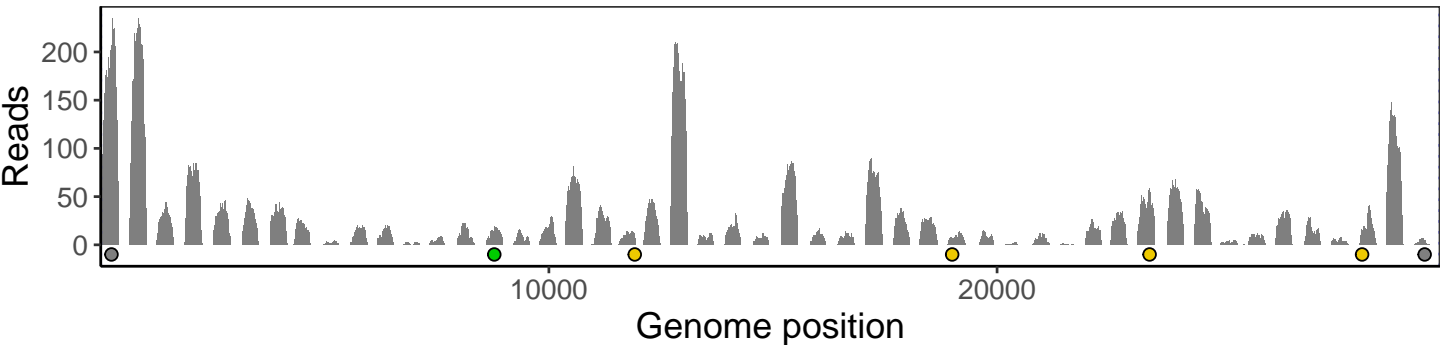
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



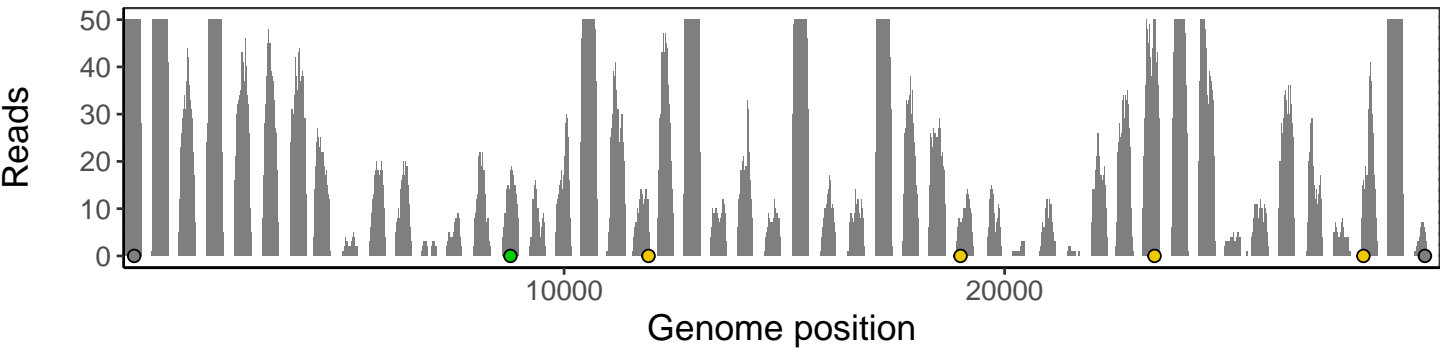
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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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.

