# COVID-19 subject J3R26

*2020-11-30*

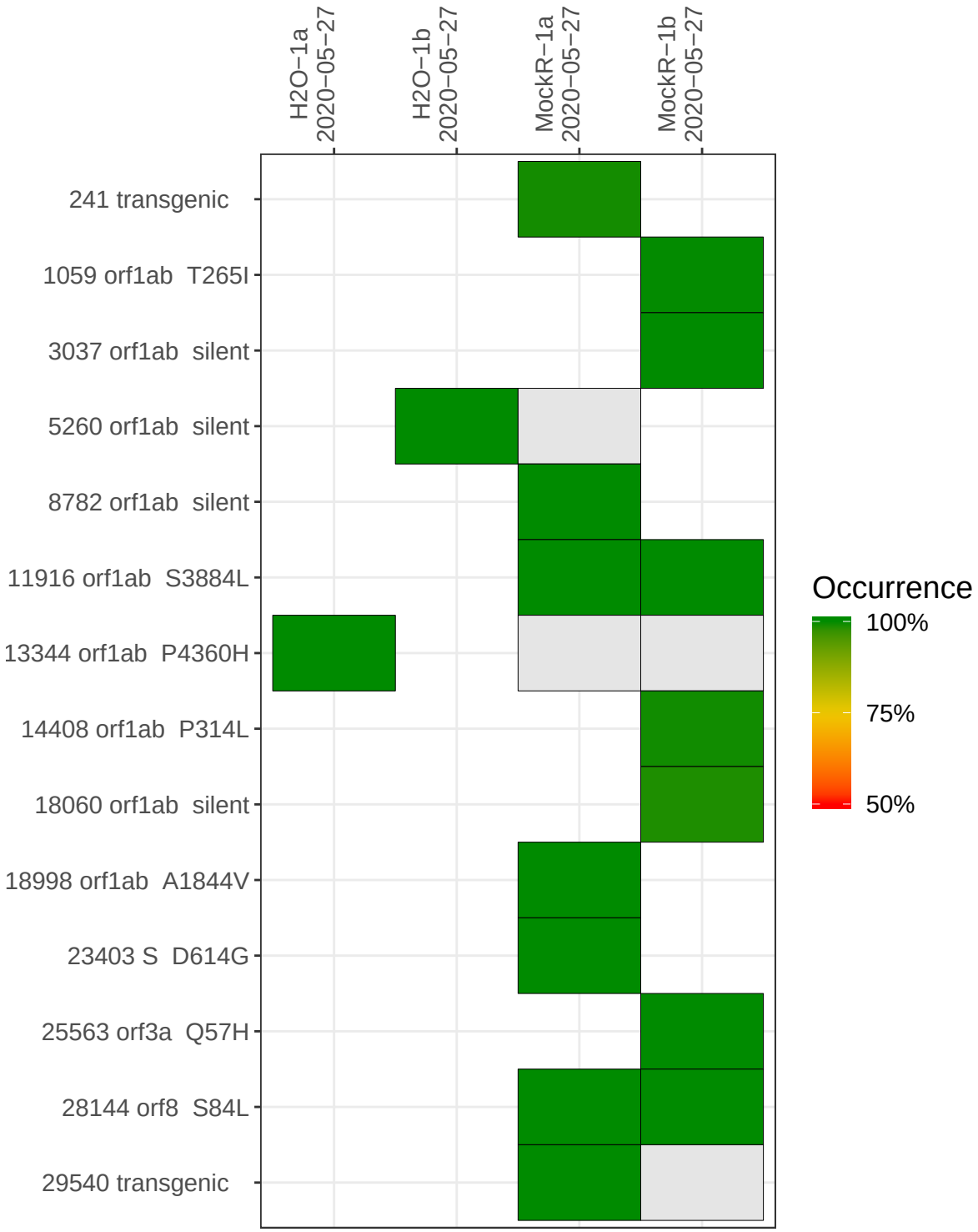
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

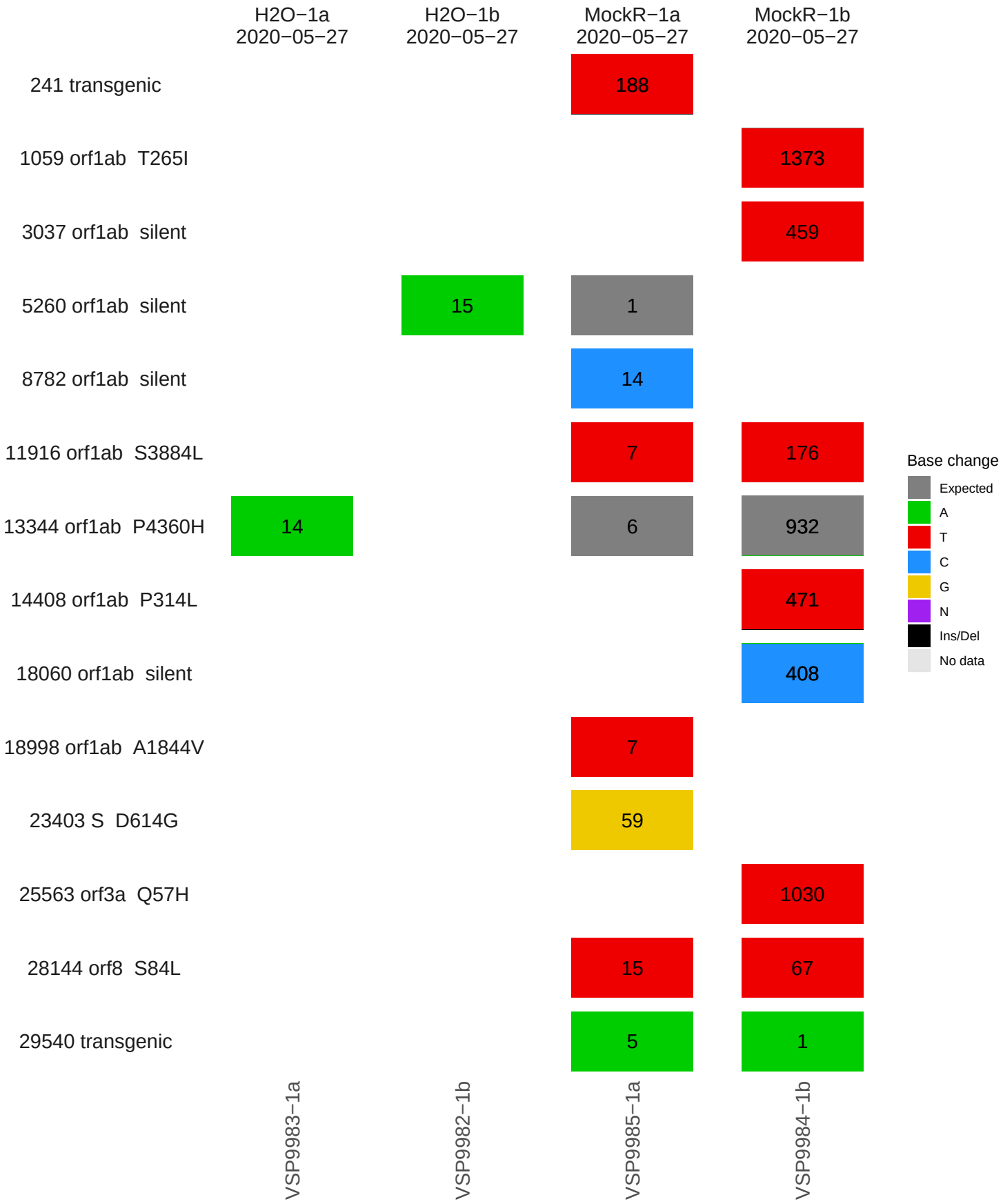
Table 1. Sample summary.

| 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.

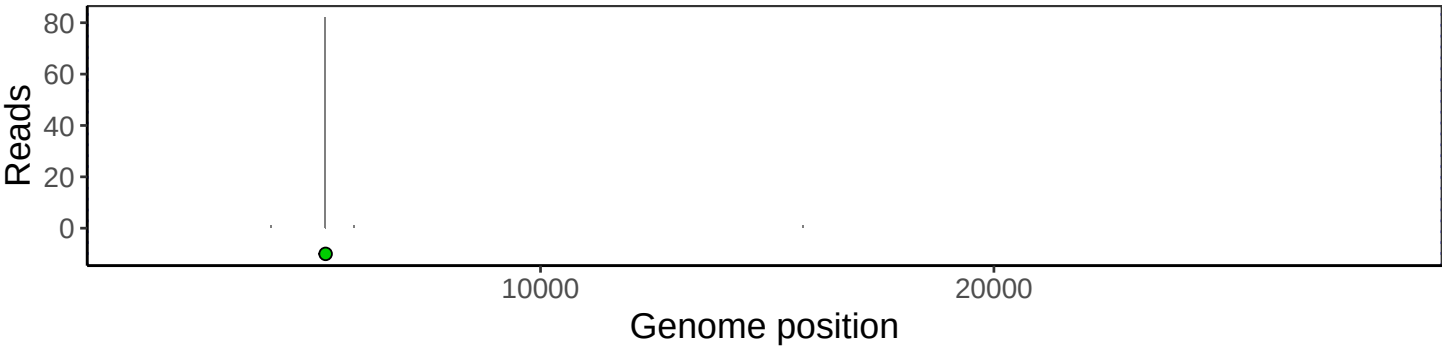



H2O−1a 2020−05−27
H2O−1b 2020−05−27
MockR−1a 2020−05−27
MockR−1b 2020−05−27
241 transgenic
1059 orf1ab T265I
3037 orf1ab silent
5260 orf1ab silent
8782 orf1ab silent
11916 orf1ab S3884L
13344 orf1ab P4360H
14408 orf1ab P314L
18060 orf1ab silent
18998 orf1ab A1844V
23403 S D614G
25563 orf3a Q57H
28144 orf8 S84L
29540 transgenic
188
1373
459
15
1
14
7
176
14
6
932
471
408
7
59
1030
15
67
5
1
Base change
Expected
A
T
C
G
N
Ins/Del
No data
VSP9983−1a
VSP9982−1b
VSP9985−1a
VSP9984−1b

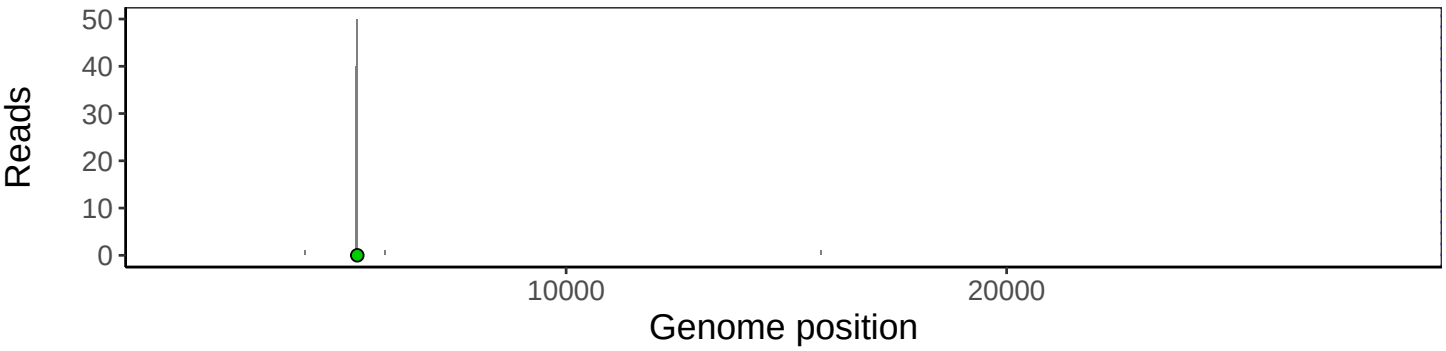
## Analyses of individual experiments and composite results.

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



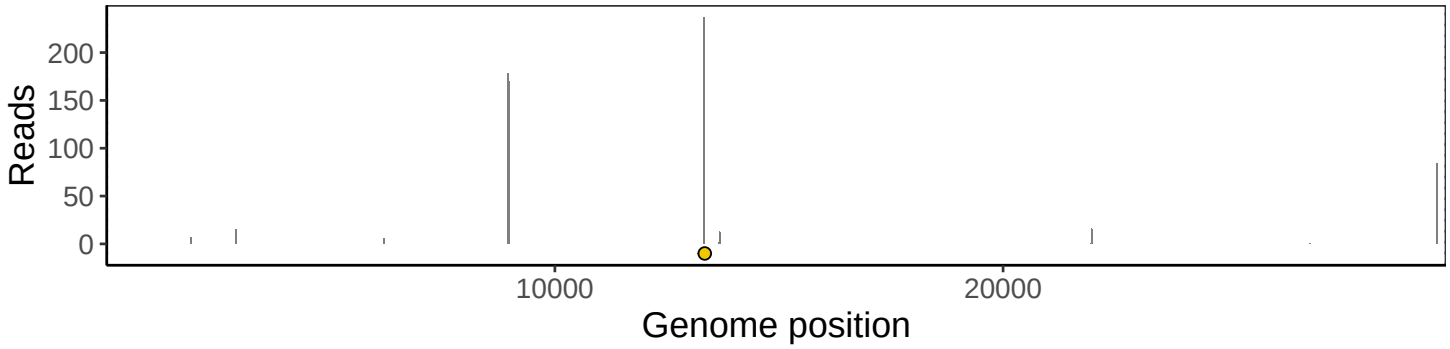

Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



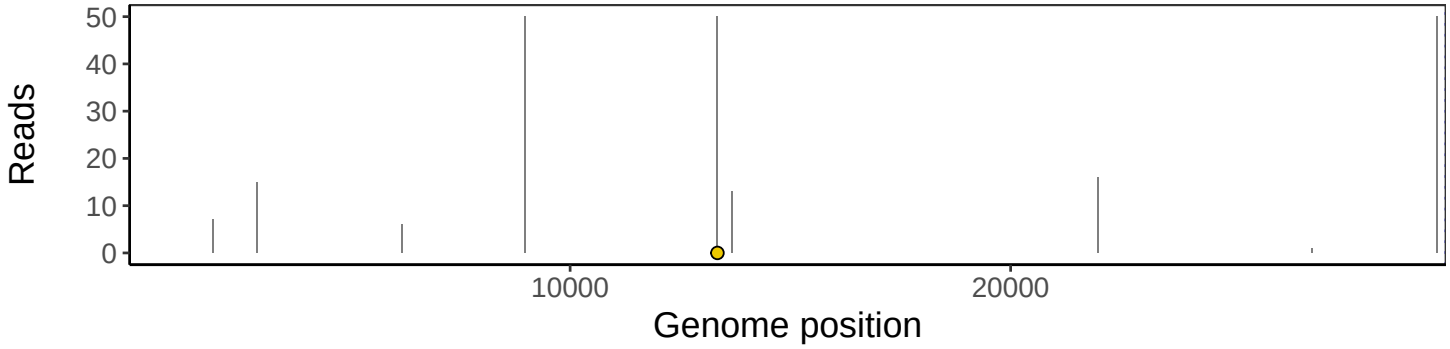

## No contig data available.

**VSP9983-1a | 2020-05-27 | H2O-1a | 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 by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



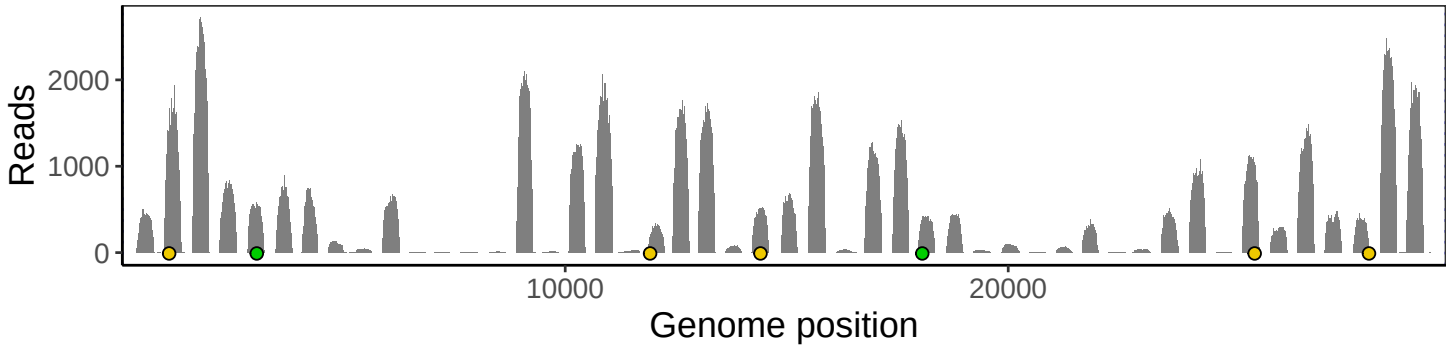

Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



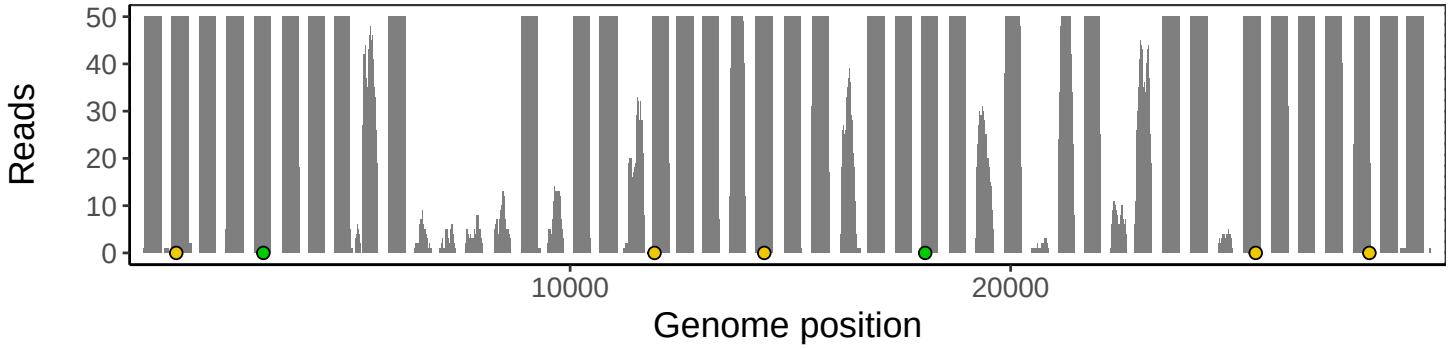

## No contig data available.

**VSP9984-1b | 2020-05-27 | MockR-1b | J3R26 | genomes | single experiment**

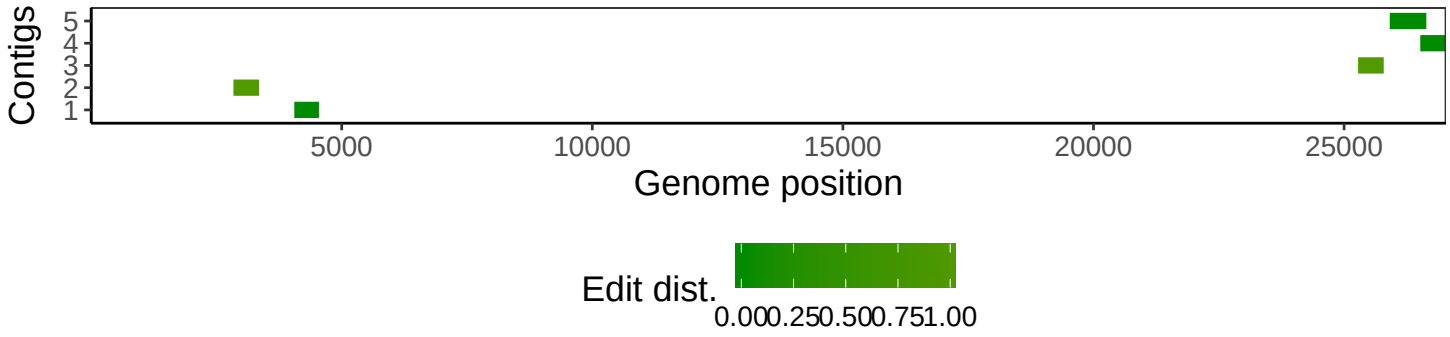
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

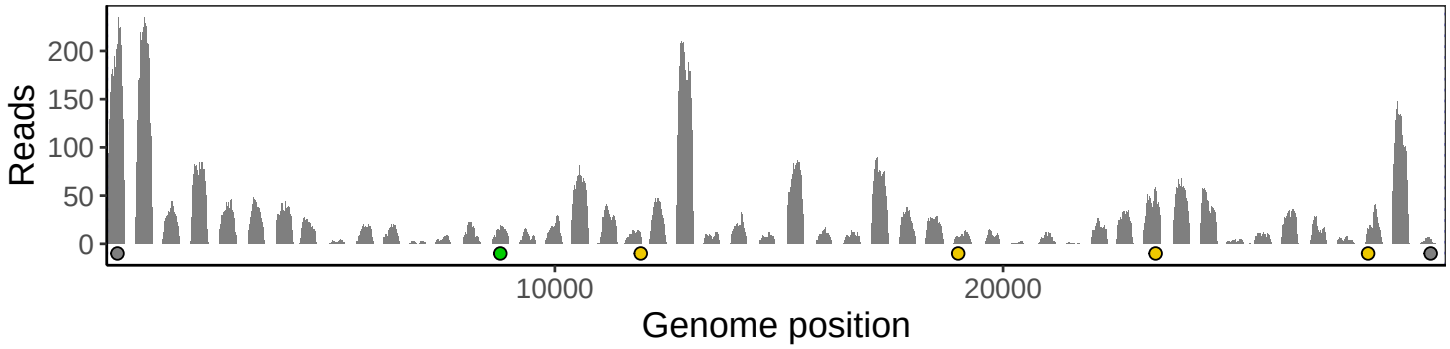



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

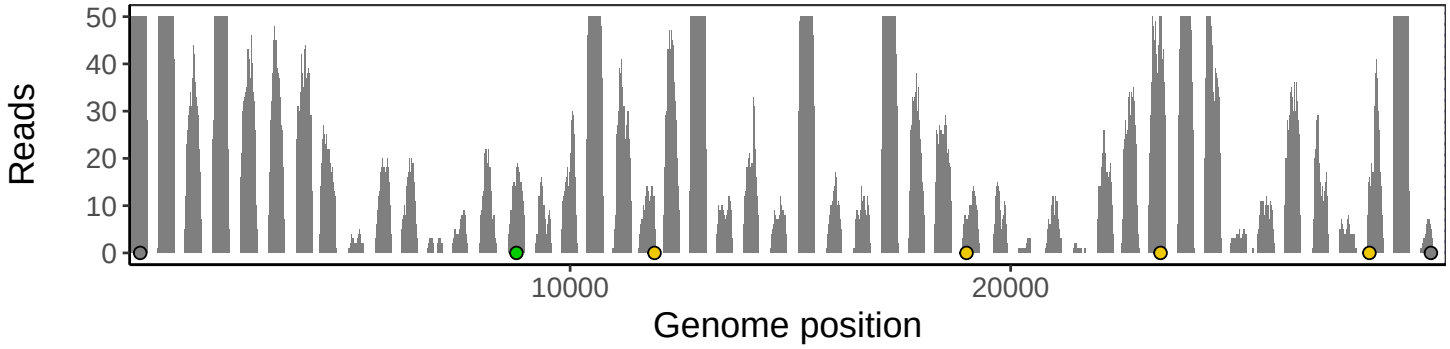


**VSP9985-1a | 2020-05-27 | MockR-1a | J3R26 | genomes | single experiment**

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 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.