

COVID-19 subject sdrop1__molpath

2021-01-15

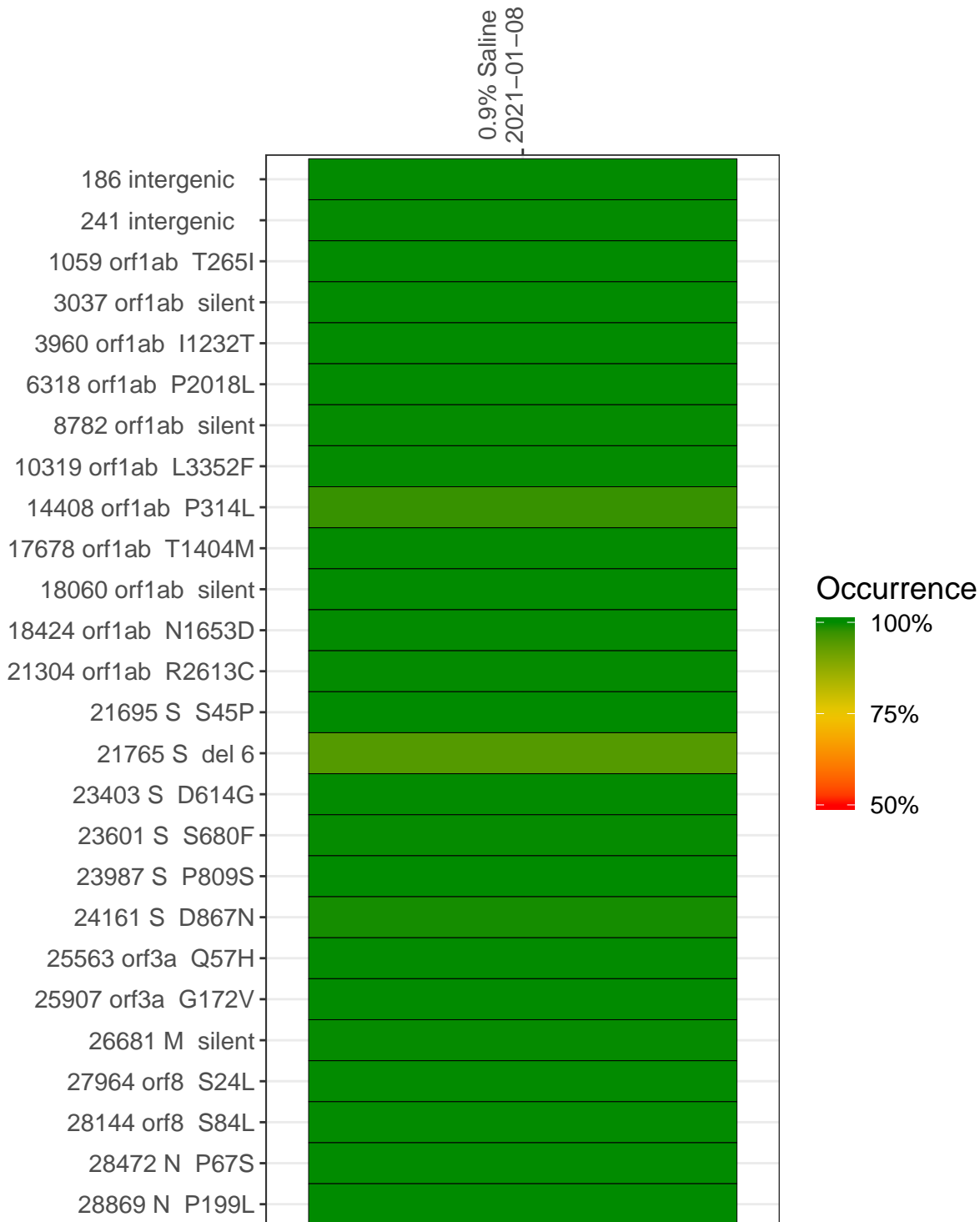
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0571	composite	NA	0.9% Saline	2021-01-08	29.91	99.9%	99.9%
VSP0571-1	single experiment	NA	0.9% Saline	2021-01-08	29.82	99.9%	99.2%
VSP0571-2	single experiment	NA	0.9% Saline	2021-01-08	29.91	99.9%	99.9%

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.



0.9% Saline
2021-01-08

186 intergenic	614	12070
241 intergenic	543	11039
1059 orf1ab T265I	215	3492
3037 orf1ab silent	339	5203
3960 orf1ab I1232T	418	5703
6318 orf1ab P2018L	652	10506
8782 orf1ab silent	460	6897
10319 orf1ab L3352F	581	9329
14408 orf1ab P314L	934	13495
17678 orf1ab T1404M	519	8544
18060 orf1ab silent	306	5092
18424 orf1ab N1653D	881	14501
21304 orf1ab R2613C	164	2959
21695 S S45P	136	2412
21765 S del 6		
23403 S D614G	786	13765
23601 S S680F	507	8896
23987 S P809S	59	972
24161 S D867N	215	3930
25563 orf3a Q57H	353	6295
25907 orf3a G172V	361	5762
26681 M silent	469	7569
27964 orf8 S24L	538	8431
28144 orf8 S84L	534	8962
28472 N P67S	643	11702
28869 N P199L	55	1095

Base change

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

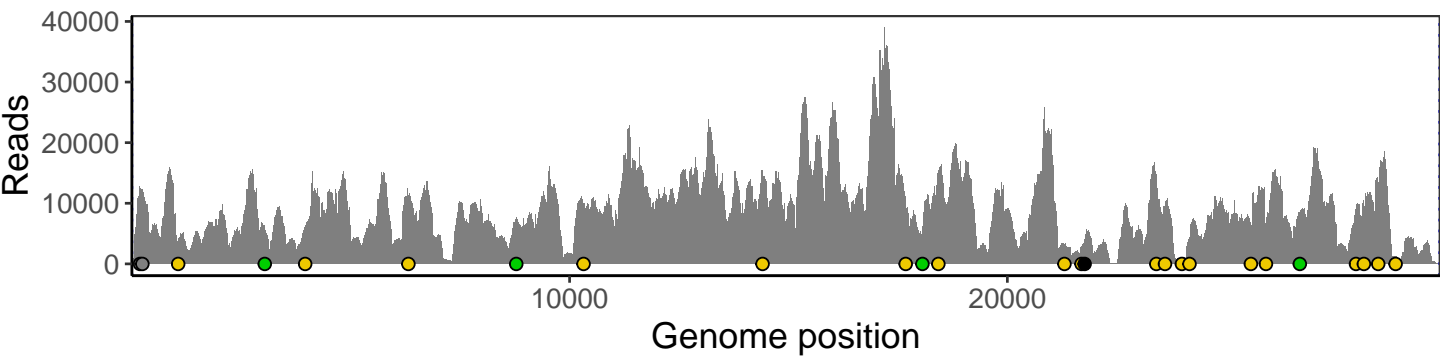
VSP0571-1

VSP0571-2

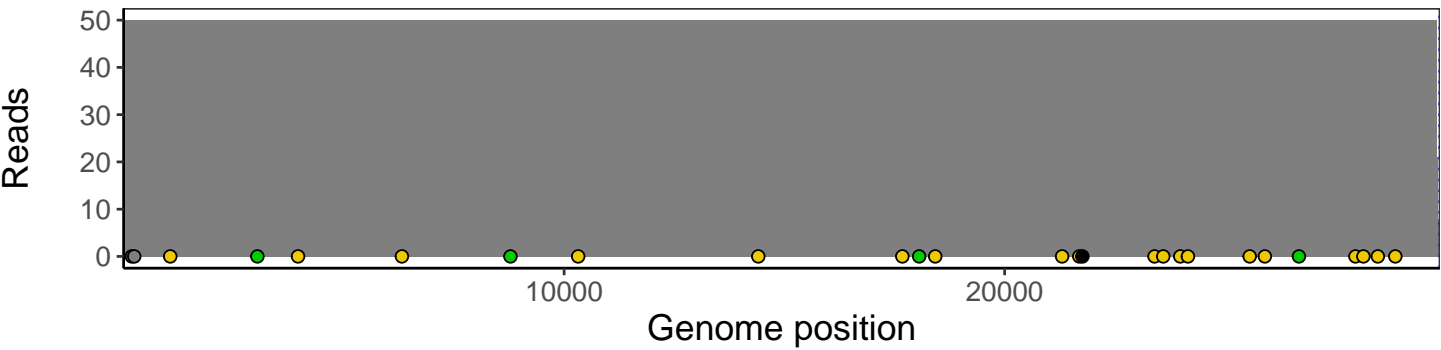
Analyses of individual experiments and composite results.

VSP0571 | 2021-01-08 | 0.9% Saline | sdrop1_molpath | composite result

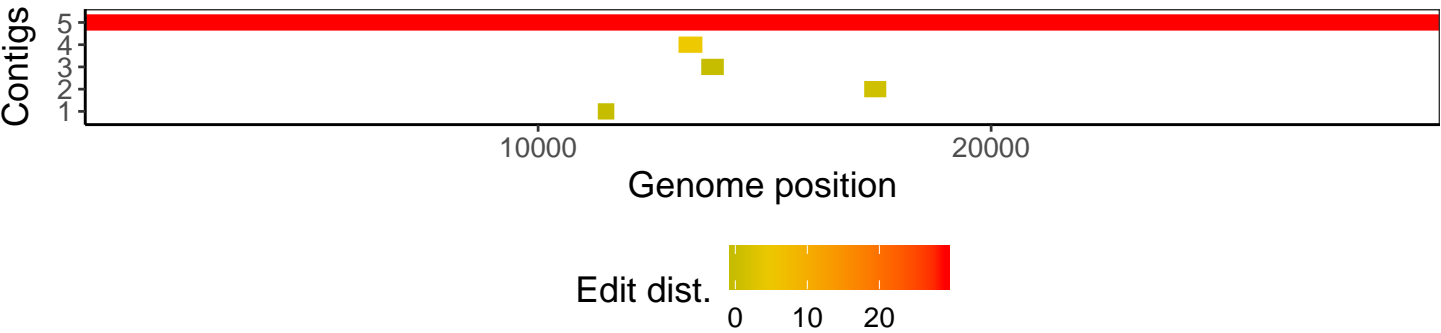
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



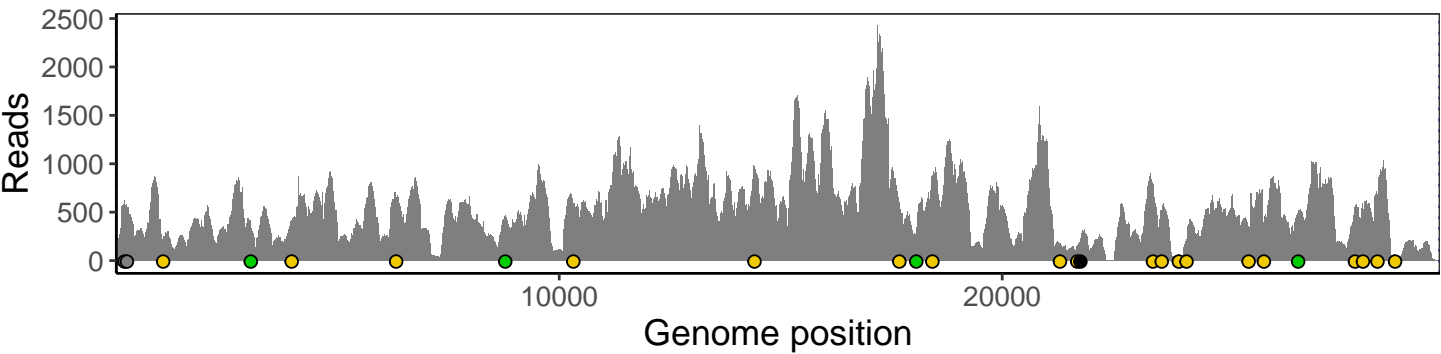
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



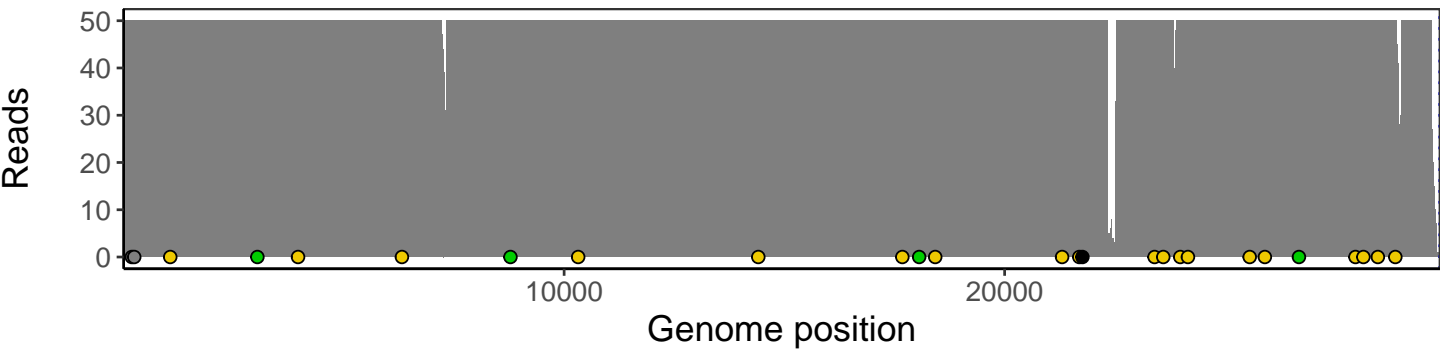
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



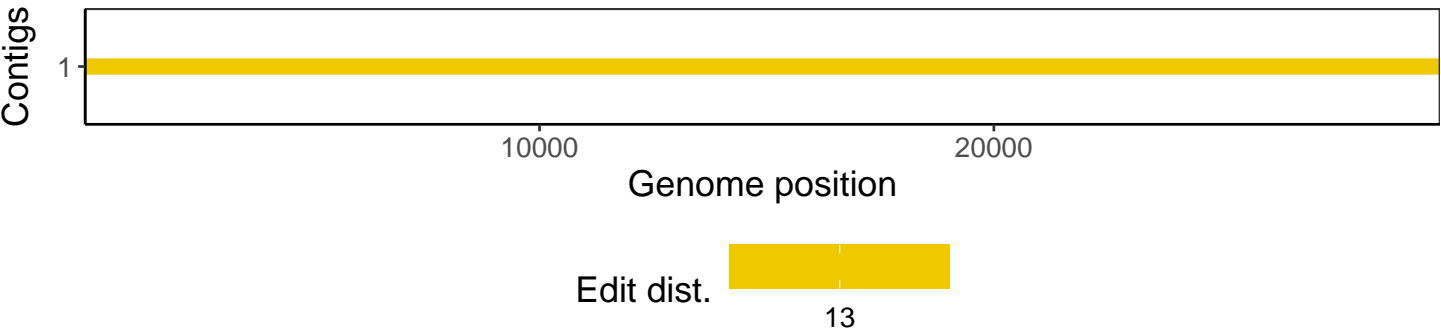
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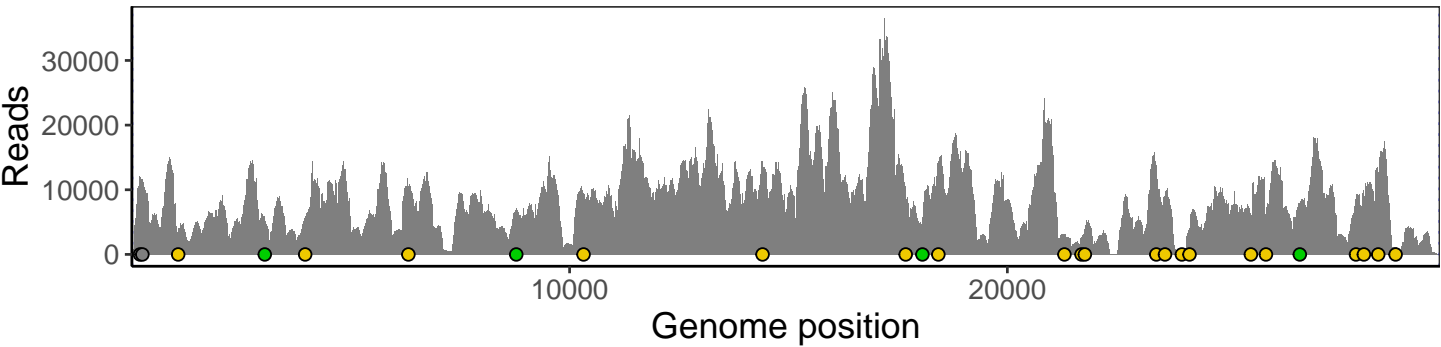
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



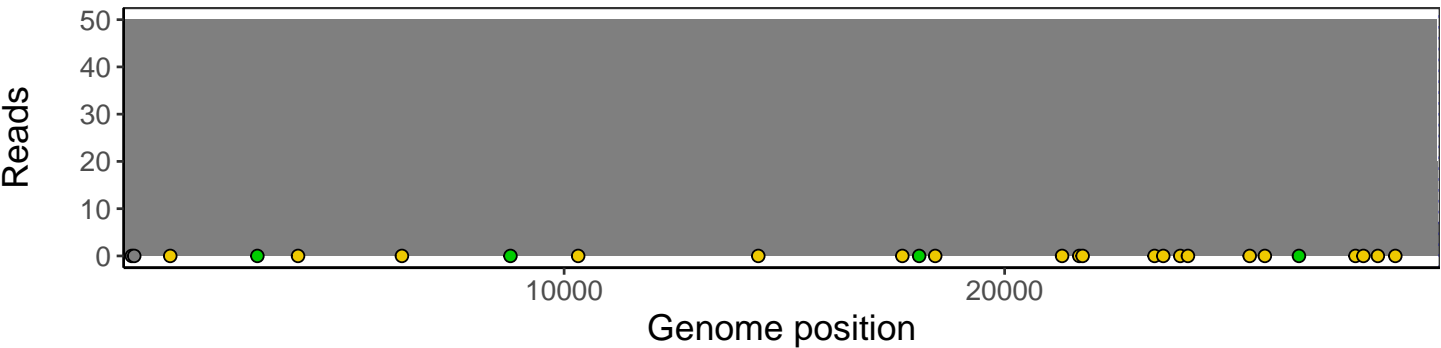
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