COVID-19 subject PQ-Seq1

2021-03-01

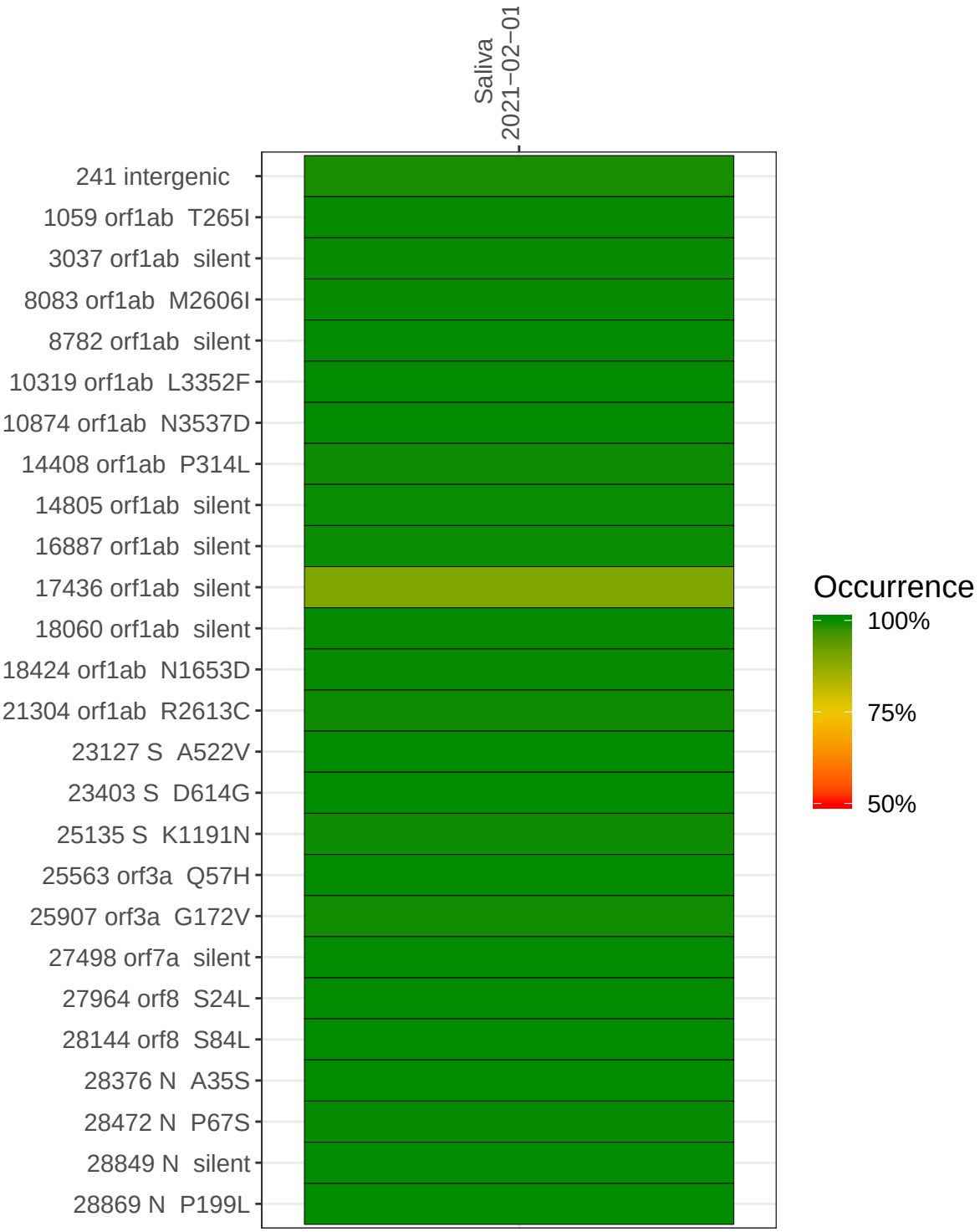
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

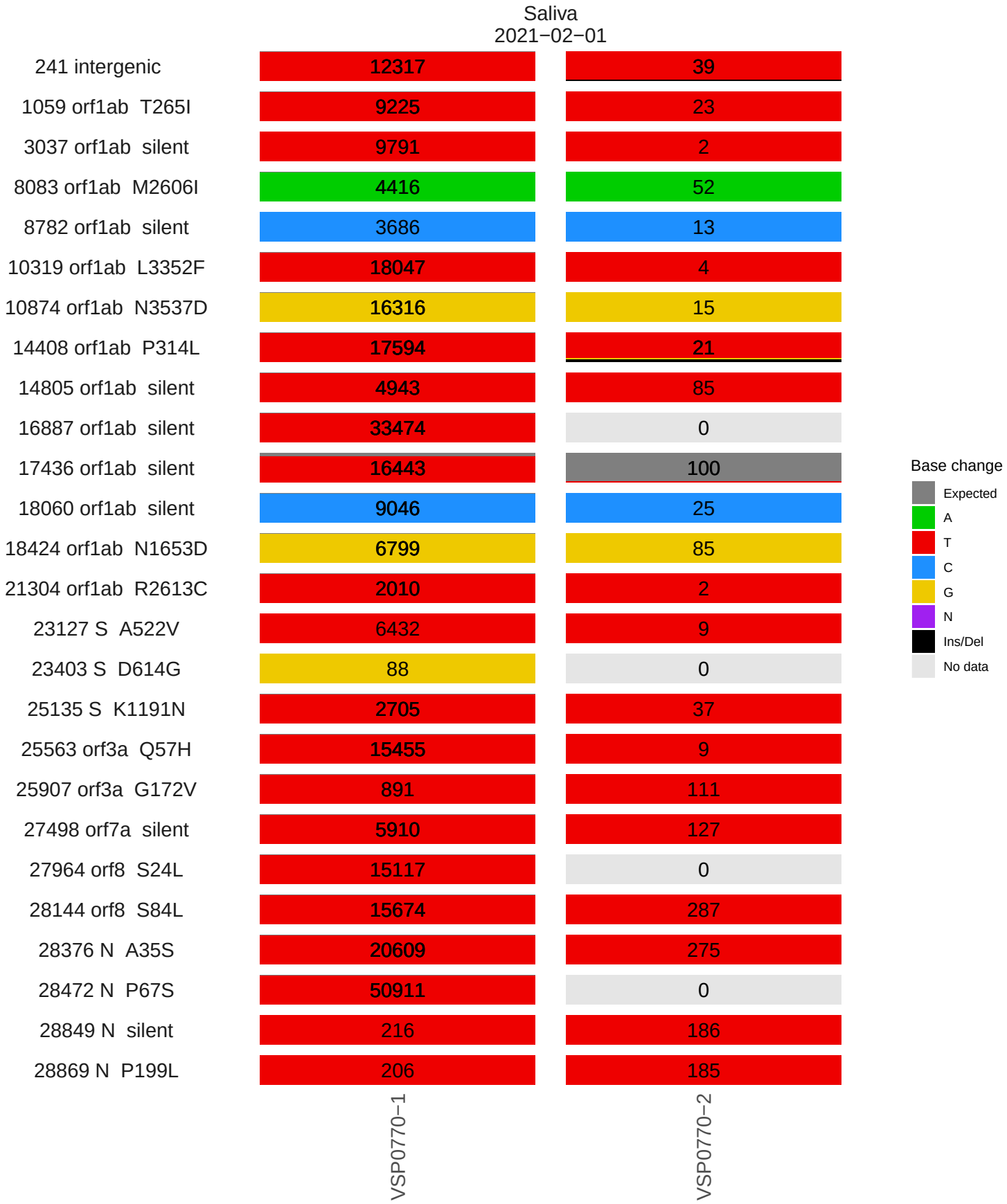
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0770	composite	NA	Saliva	2021-02-01	29.94	B.1.2	99.9%	99.9%
VSP0770-1	single experiment	NA	Saliva	2021-02-01	29.94	B.1.2	99.9%	99.9%
VSP0770-2	single experiment	NA	Saliva	2021-02-01	3.90	NA	86.0%	77.6%

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 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.

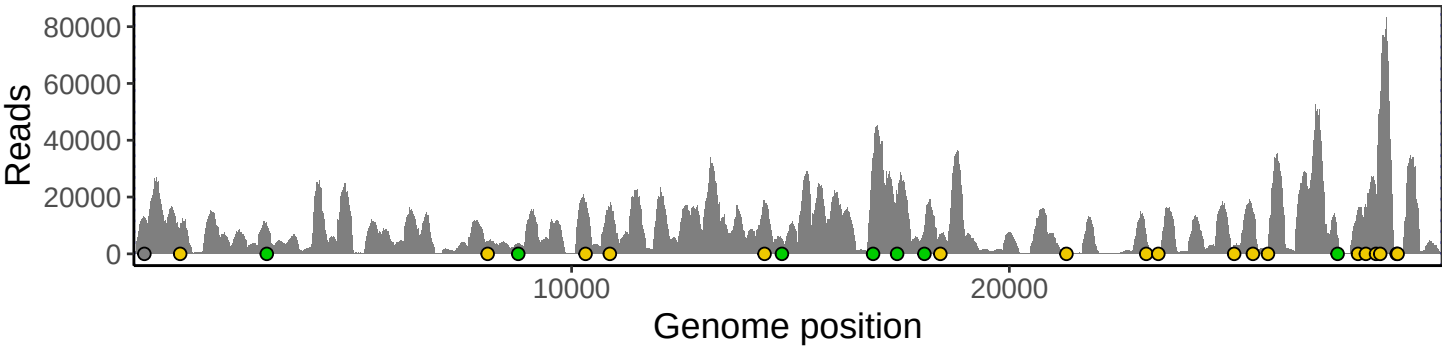



Saliva
2021−02−01
241 intergenic
1059 orf1ab T265I
3037 orf1ab silent
8083 orf1ab M2606I
8782 orf1ab silent
10319 orf1ab L3352F
10874 orf1ab N3537D
14408 orf1ab P314L
14805 orf1ab silent
16887 orf1ab silent
17436 orf1ab silent
18060 orf1ab silent
18424 orf1ab N1653D
21304 orf1ab R2613C
23127 S A522V
23403 S D614G
25135 S K1191N
25563 orf3a Q57H
25907 orf3a G172V
27498 orf7a silent
27964 orf8 S24L
28144 orf8 S84L
28376 N A35S
28472 N P67S
28849 N silent
28869 N P199L
12317
9225
9791
4416
3686
18047
16316
17594
4943
33474
16443
9046
6799
2010
6432
88
2705
15455
891
5910
15117
15674
20609
50911
216
206
39
23
2
52
13
4
15
21
85
0
100
25
85
2
9
0
37
9
111
127
0
287
275
0
186
185
VSP0770−1
VSP0770−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

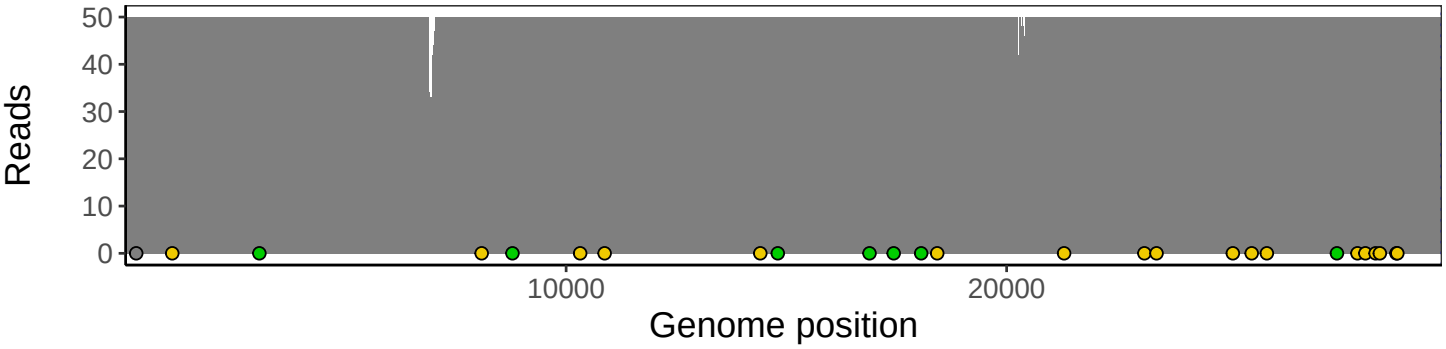
Analyses of individual experiments and composite results

VSP0770 | 2021-02-01 | Saliva | PQ-Seq1 | 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.



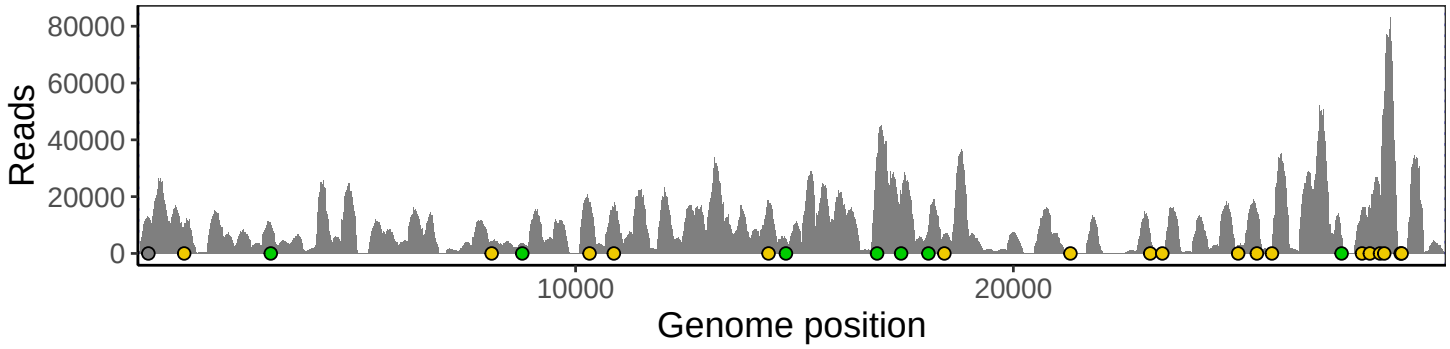
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



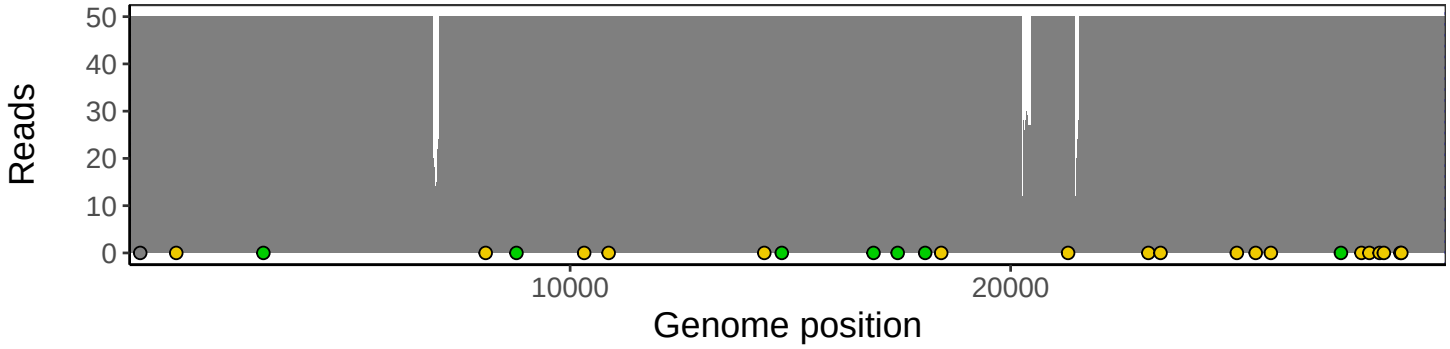
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

VSP0770-1 | 2021-02-01 | Saliva | PQ-Seq1 | genomes | single experiment

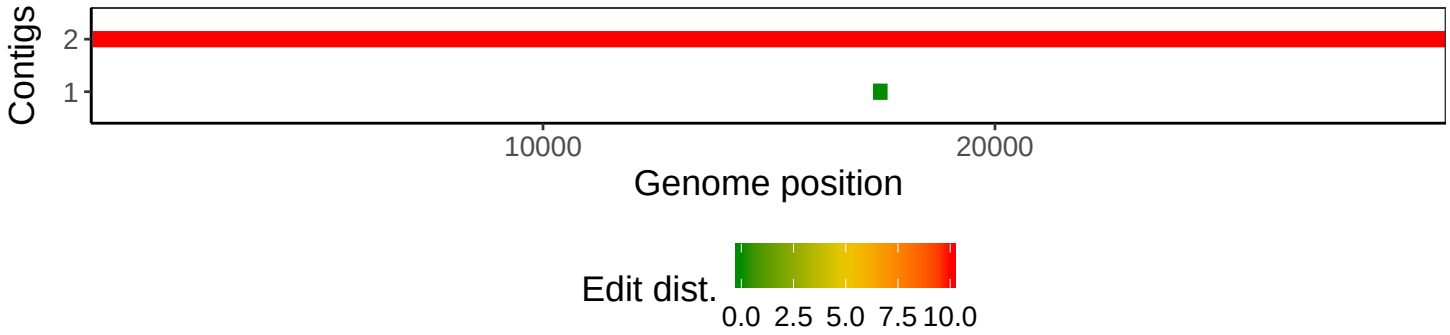
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

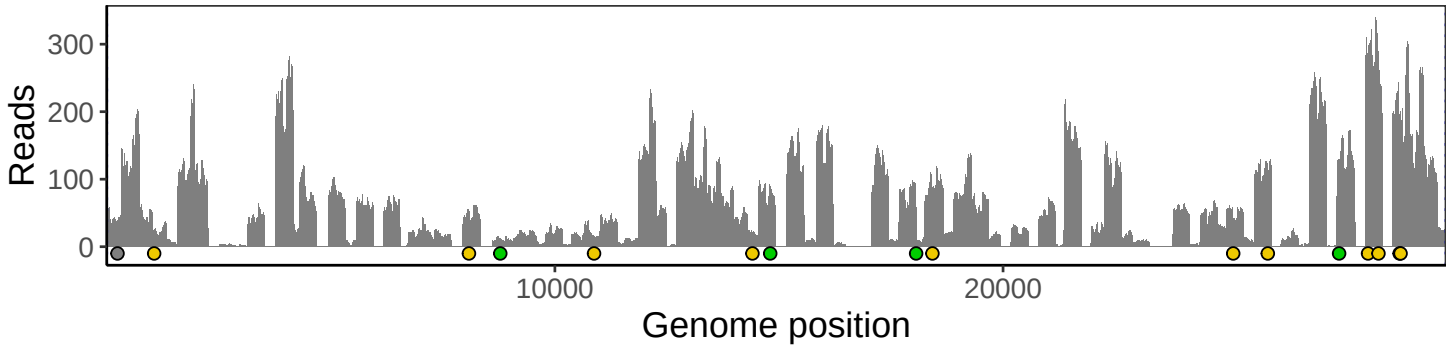


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

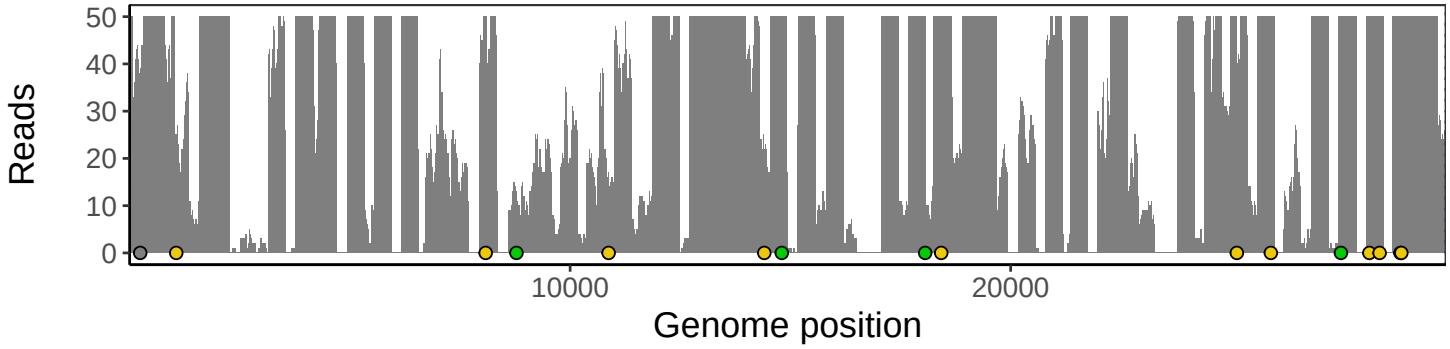


VSP0770-2 | 2021-02-01 | Saliva | PQ-Seq1 | genomes | single experiment

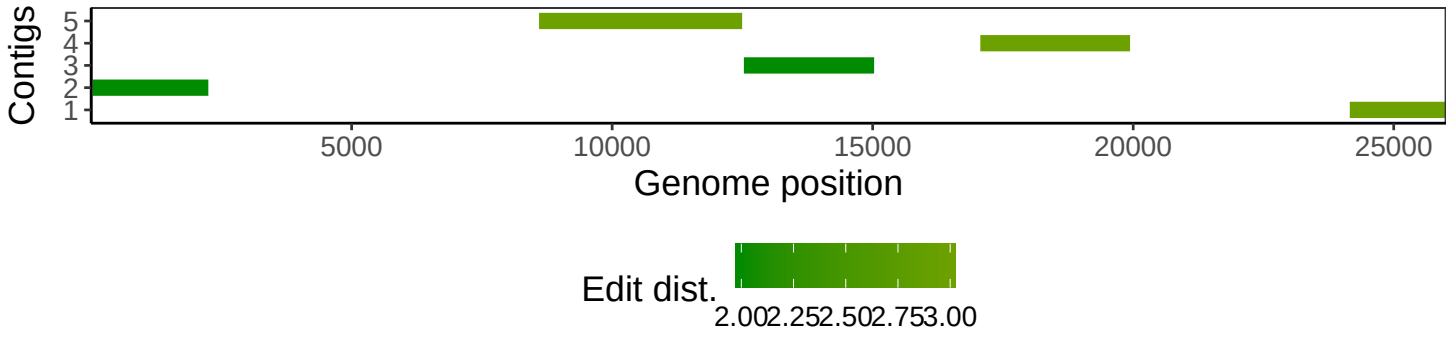
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htslib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htslib 1.10.2-57-gf58a6f3
pangolin	2.3.3
genbankr	1.4.0
optparse	1.6.0
forcats	0.3.0
stringr	1.4.0
dplyr	0.8.1
purrr	0.2.5
readr	1.1.1
tidyr	0.8.1
tibble	2.1.2
ggplot2	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
GenomeInfoDb	1.12.3
Biostrings	2.44.2
XVector	0.16.0
IRanges	2.10.5
S4Vectors	0.14.7
BiocParallel	1.10.1
BiocGenerics	0.22.1