COVID-19 subject S-210-12-03128

2021-06-03

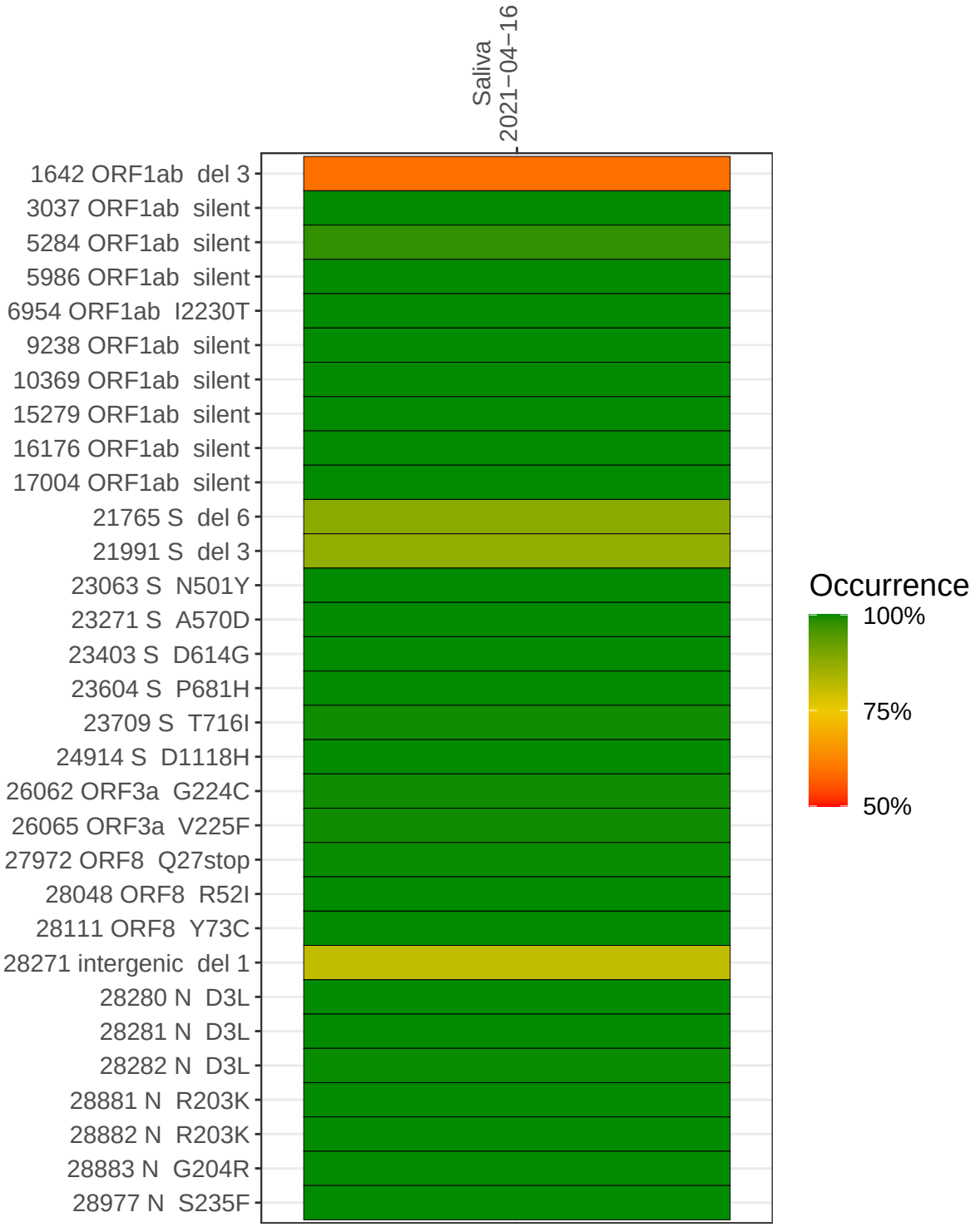
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

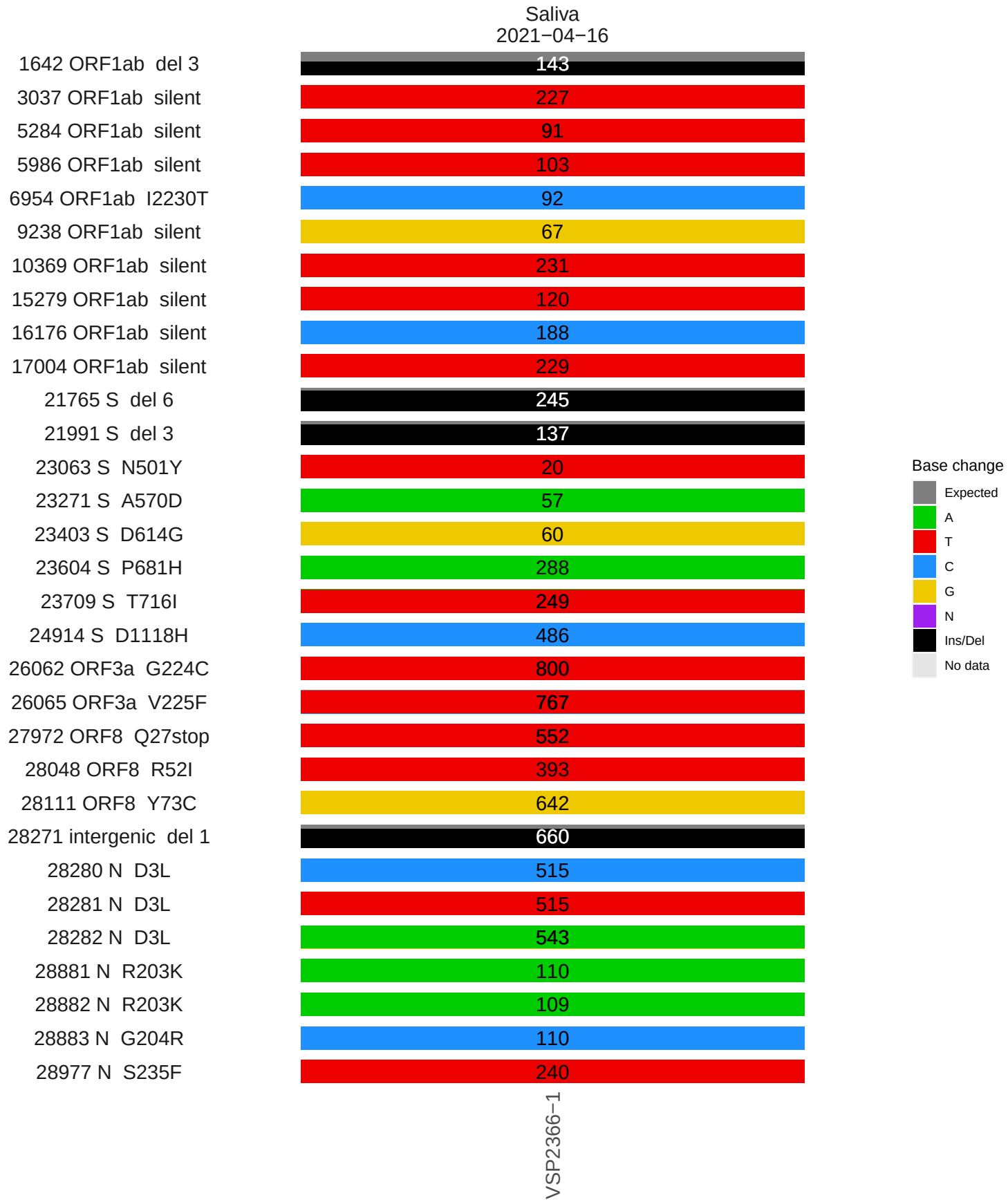
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2366-1	single experiment	NA	Saliva	2021-04-16	4.08	NA	77.7%	76.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

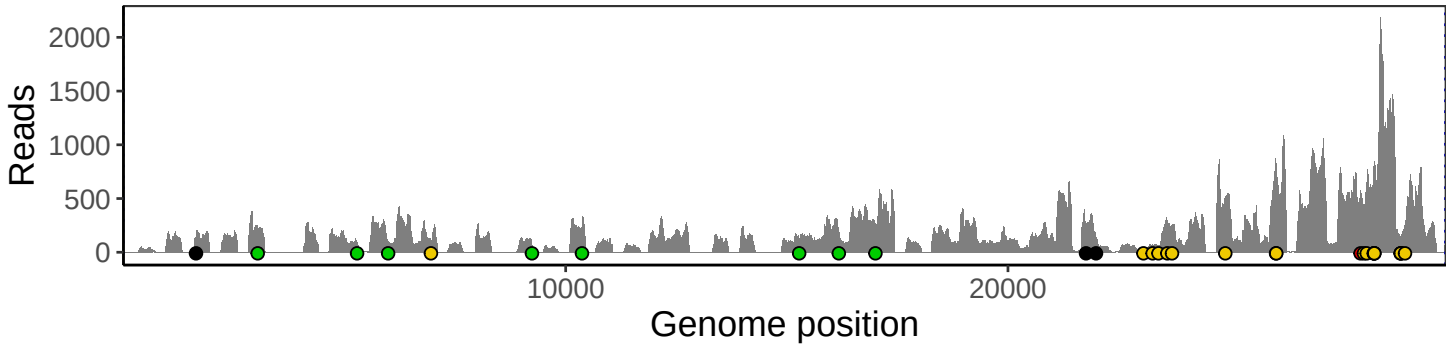



Saliva
2021−04−16
1642 ORF1ab del 3
143
3037 ORF1ab silent
227
5284 ORF1ab silent
91
5986 ORF1ab silent
103
6954 ORF1ab I2230T
92
9238 ORF1ab silent
67
10369 ORF1ab silent
231
15279 ORF1ab silent
120
16176 ORF1ab silent
188
17004 ORF1ab silent
229
21765 S del 6
245
21991 S del 3
137
23063 S N501Y
20
23271 S A570D
57
23403 S D614G
60
23604 S P681H
288
23709 S T716I
249
24914 S D1118H
486
26062 ORF3a G224C
800
26065 ORF3a V225F
767
27972 ORF8 Q27stop
552
28048 ORF8 R52I
393
28111 ORF8 Y73C
642
28271 intergenic del 1
660
28280 N D3L
515
28281 N D3L
515
28282 N D3L
543
28881 N R203K
110
28882 N R203K
109
28883 N G204R
110
28977 N S235F
240
VSP2366−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

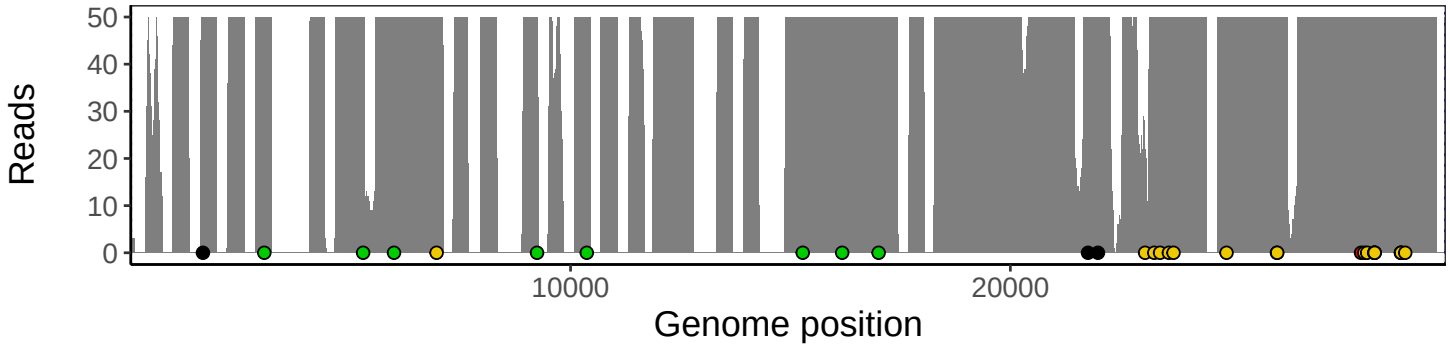
Analyses of individual experiments and composite results

VSP2366-1 | 2021-04-16 | Saliva | PMBBCCC-2 | genomes | single experiment

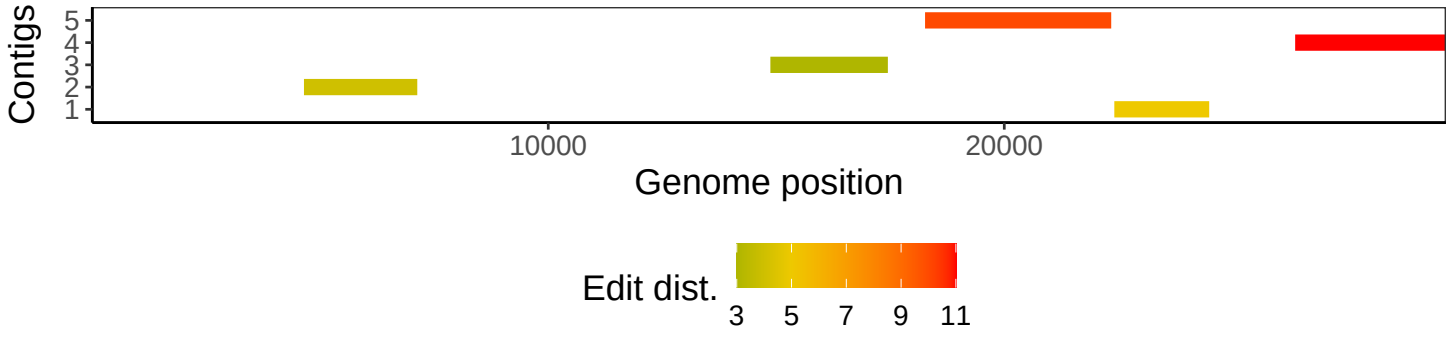
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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	3.3.3
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