COVID-19 subject 3110

2021-04-17

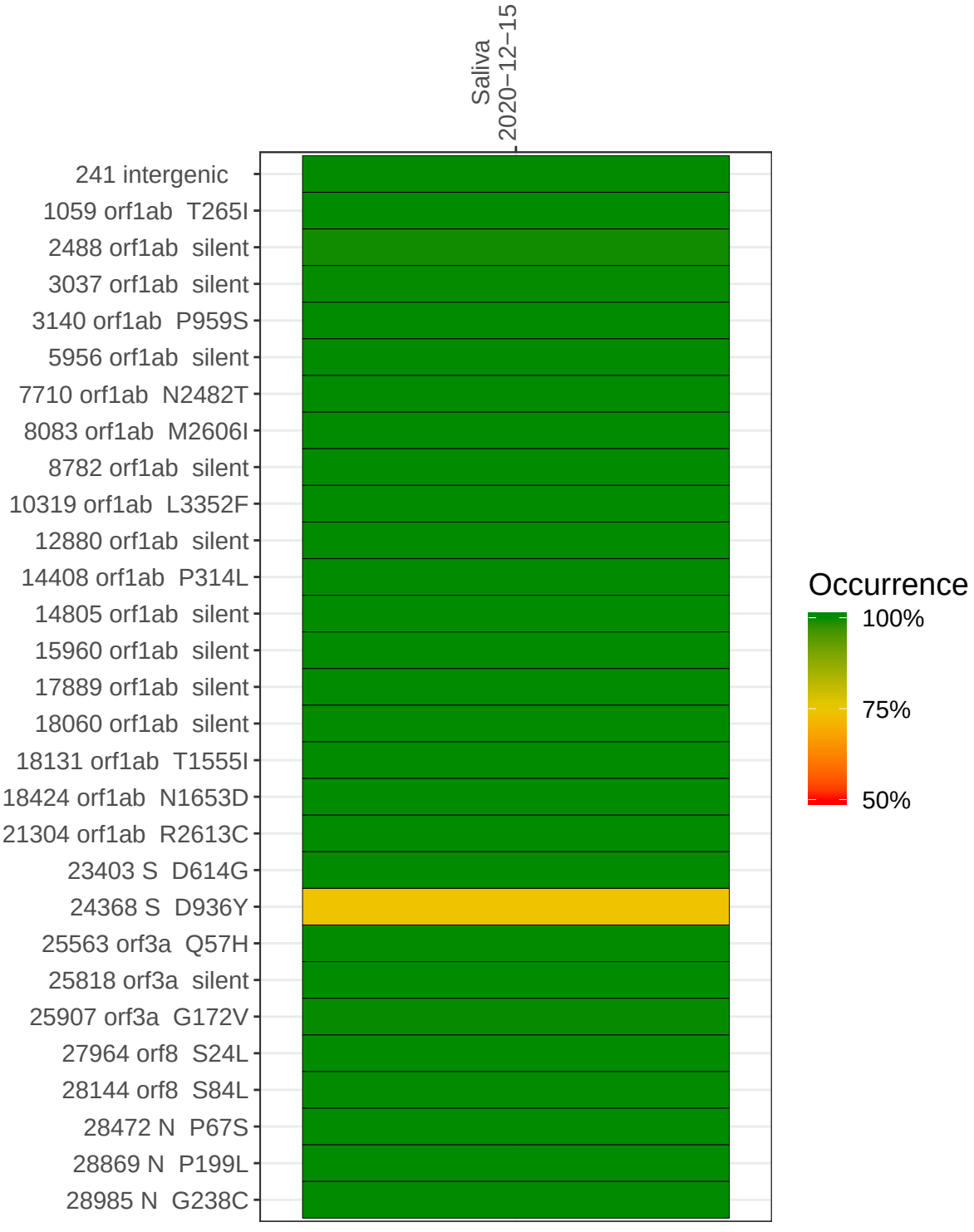
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

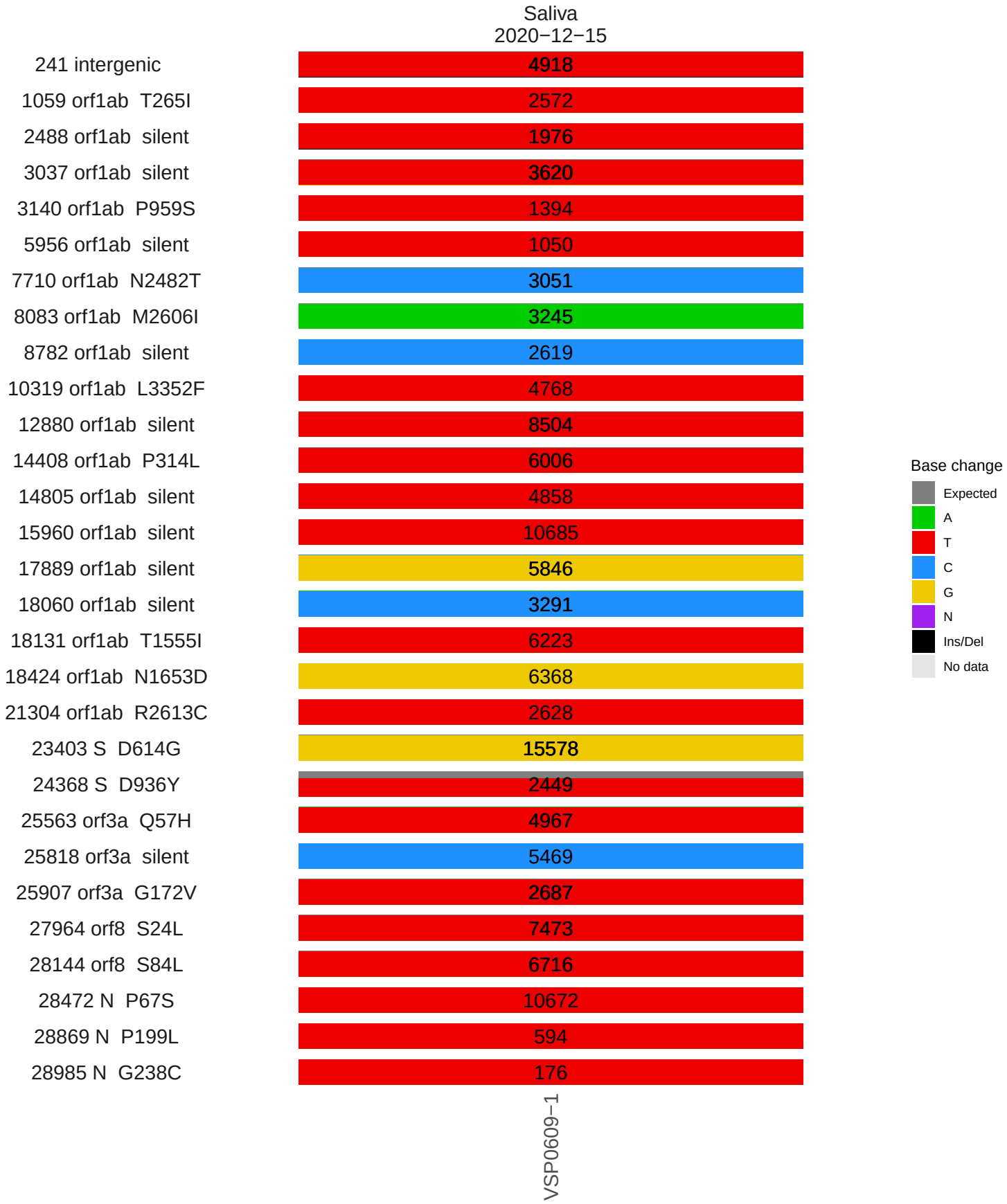
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0609-1	single experiment	NA	Saliva	2020-12-15	29.82	B.1.2	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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.

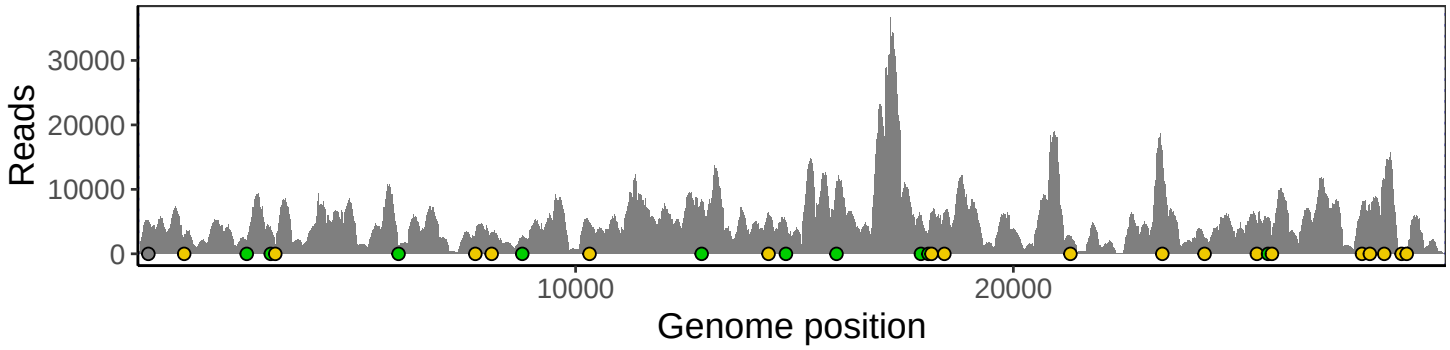



Saliva
2020−12−15
241 intergenic
1059 orf1ab T265I
2488 orf1ab silent
3037 orf1ab silent
3140 orf1ab P959S
5956 orf1ab silent
7710 orf1ab N2482T
8083 orf1ab M2606I
8782 orf1ab silent
10319 orf1ab L3352F
12880 orf1ab silent
14408 orf1ab P314L
14805 orf1ab silent
15960 orf1ab silent
17889 orf1ab silent
18060 orf1ab silent
18131 orf1ab T1555I
18424 orf1ab N1653D
21304 orf1ab R2613C
23403 S D614G
24368 S D936Y
25563 orf3a Q57H
25818 orf3a silent
25907 orf3a G172V
27964 orf8 S24L
28144 orf8 S84L
28472 N P67S
28869 N P199L
28985 N G238C
4918
2572
1976
3620
1394
1050
3051
3245
2619
4768
8504
6006
4858
10685
5846
3291
6223
6368
2628
15578
2449
4967
5469
2687
7473
6716
10672
594
176
VSP0609−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

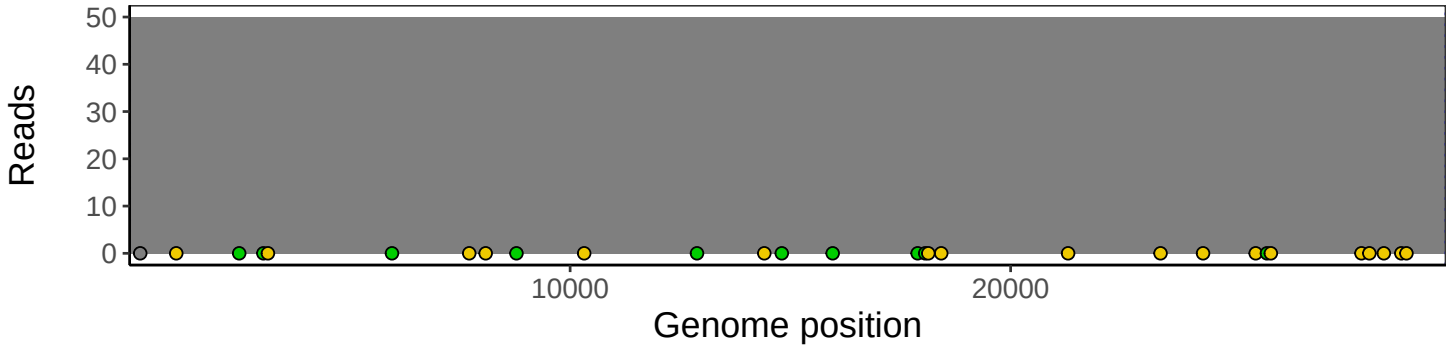
Analyses of individual experiments and composite results

VSP0609-1 | 2020-12-15 | Saliva | 3110 | genomes | single experiment

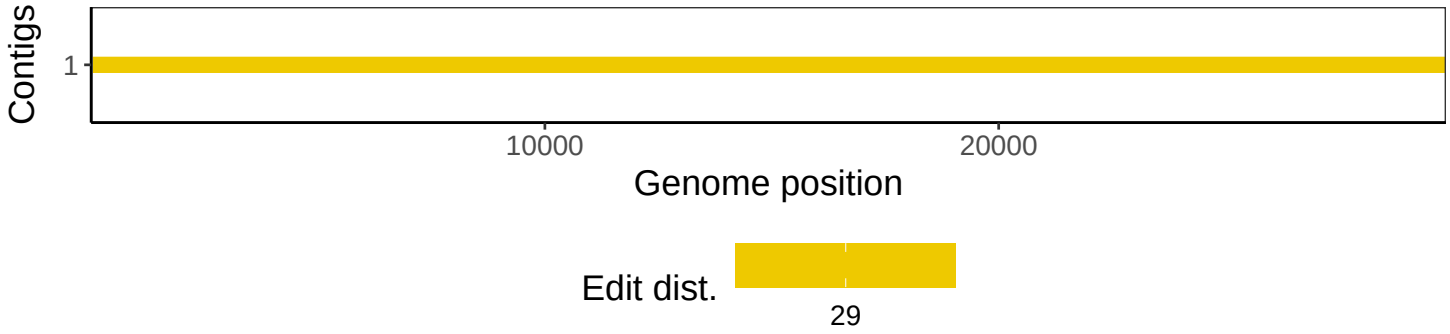
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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