COVID-19 subject 9106

2021-04-17

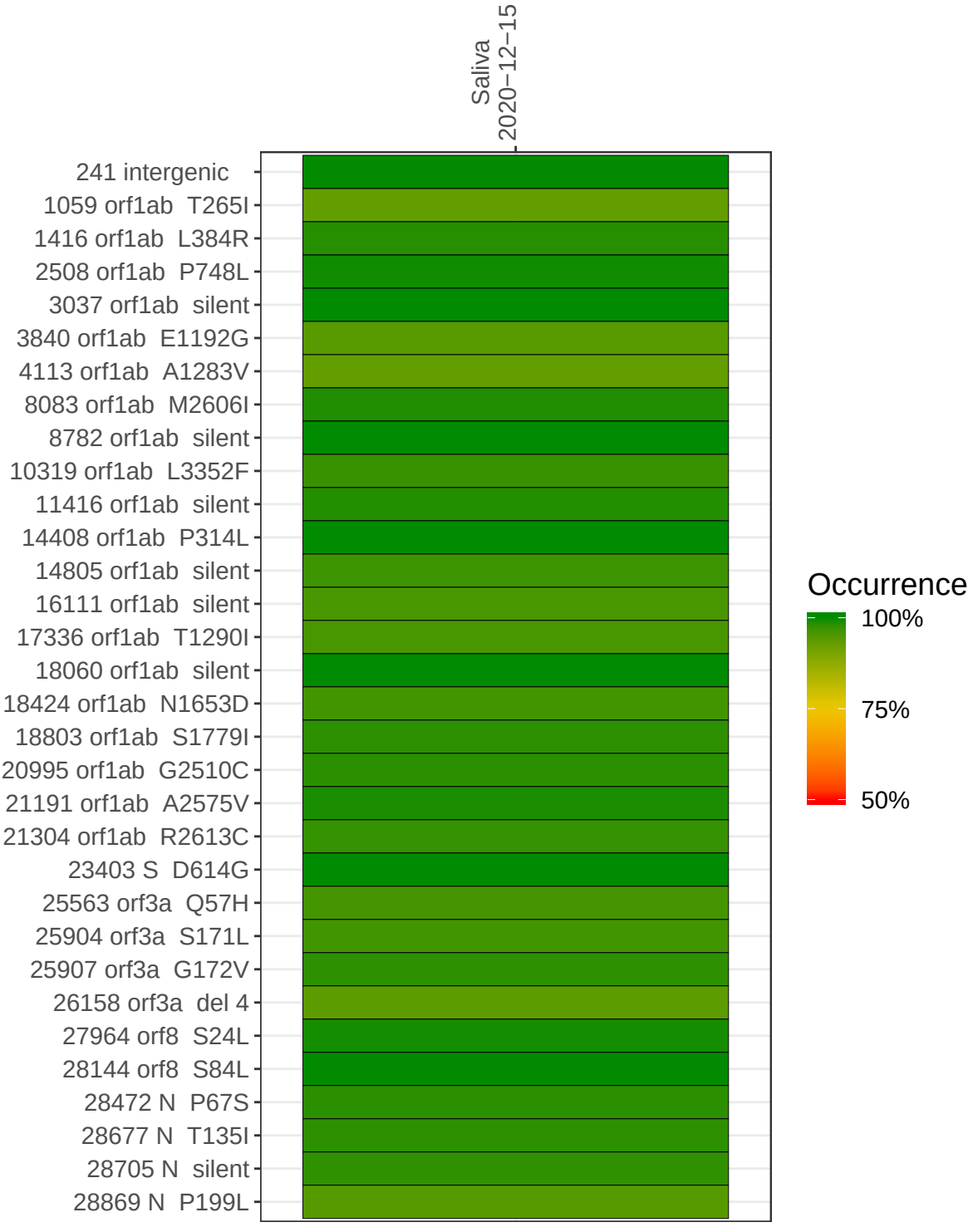
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

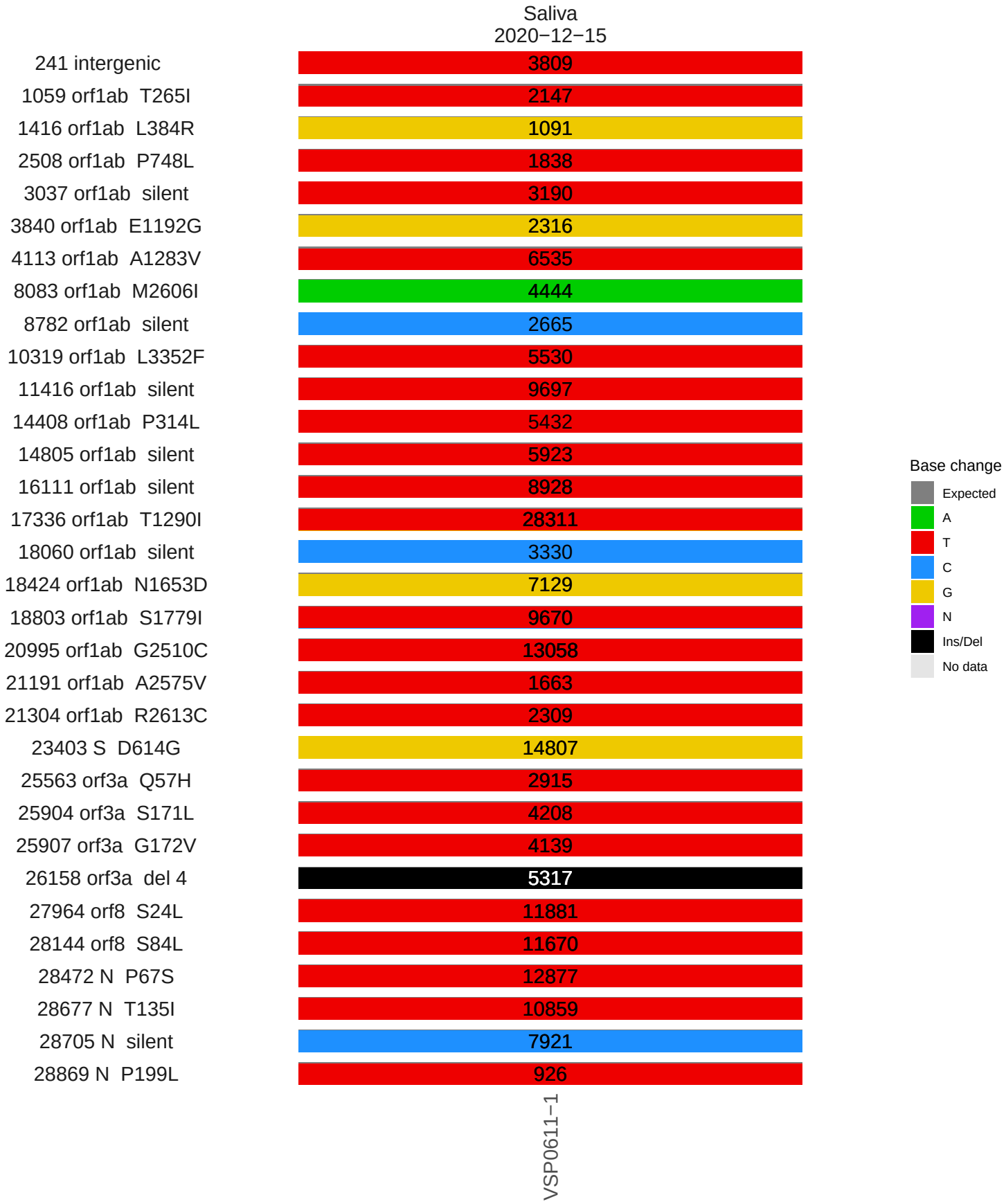
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0611-1	single experiment	NA	Saliva	2020-12-15	29.66	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.

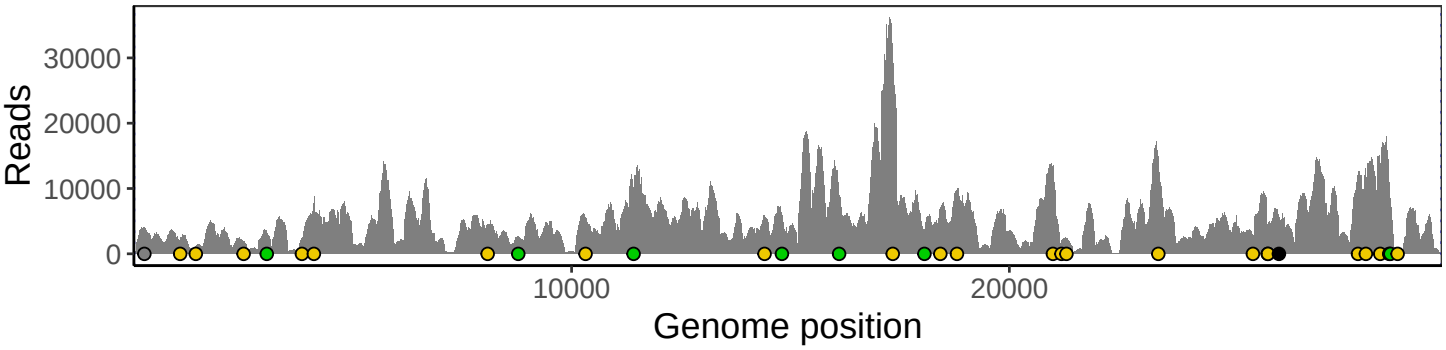



Saliva
2020−12−15
241 intergenic
1059 orf1ab T265I
1416 orf1ab L384R
2508 orf1ab P748L
3037 orf1ab silent
3840 orf1ab E1192G
4113 orf1ab A1283V
8083 orf1ab M2606I
8782 orf1ab silent
10319 orf1ab L3352F
11416 orf1ab silent
14408 orf1ab P314L
14805 orf1ab silent
16111 orf1ab silent
17336 orf1ab T1290I
18060 orf1ab silent
18424 orf1ab N1653D
18803 orf1ab S1779I
20995 orf1ab G2510C
21191 orf1ab A2575V
21304 orf1ab R2613C
23403 S D614G
25563 orf3a Q57H
25904 orf3a S171L
25907 orf3a G172V
26158 orf3a del 4
27964 orf8 S24L
28144 orf8 S84L
28472 N P67S
28677 N T135I
28705 N silent
28869 N P199L
3809
2147
1091
1838
3190
2316
6535
4444
2665
5530
9697
5432
5923
8928
28311
3330
7129
9670
13058
1663
2309
14807
2915
4208
4139
5317
11881
11670
12877
10859
7921
926
VSP0611−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

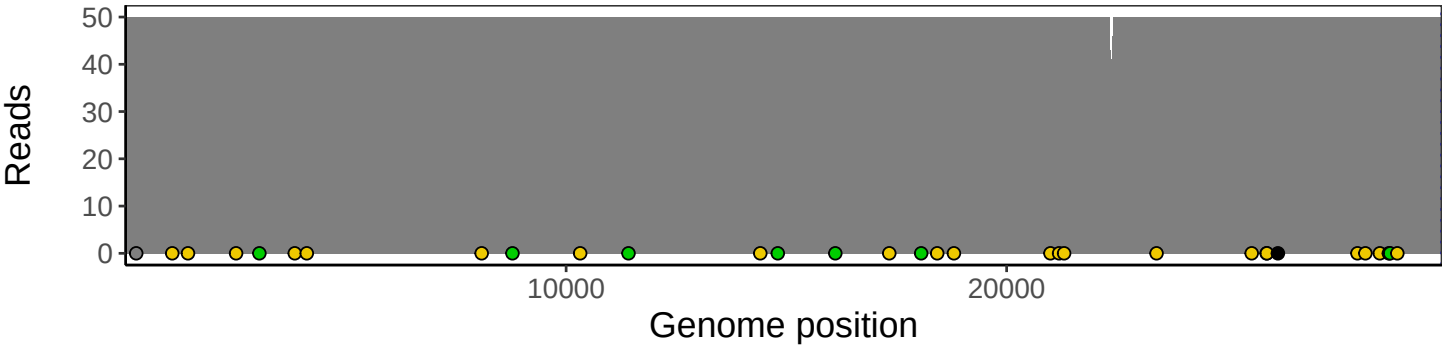
Analyses of individual experiments and composite results

VSP0611-1 | 2020-12-15 | Saliva | 9106 | genomes | single experiment

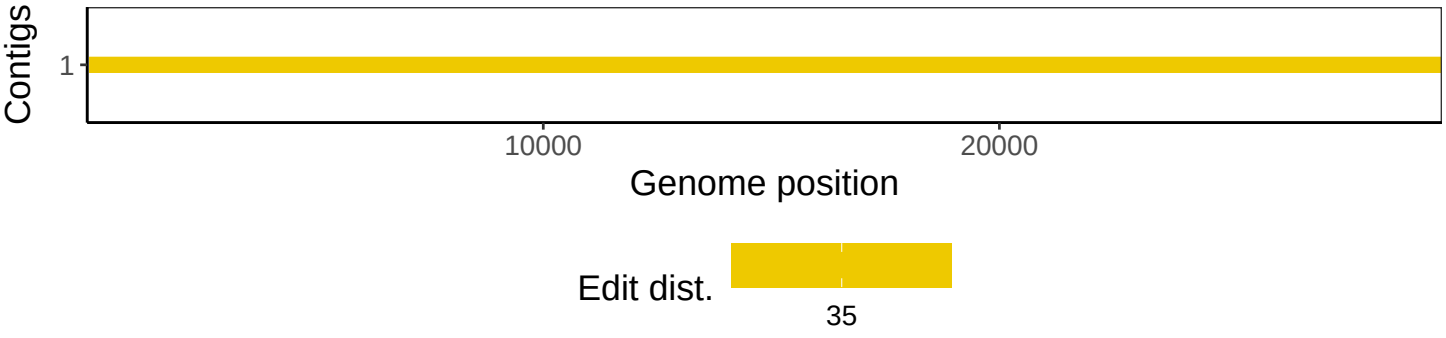
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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