COVID-19 subject 463

2021-05-21

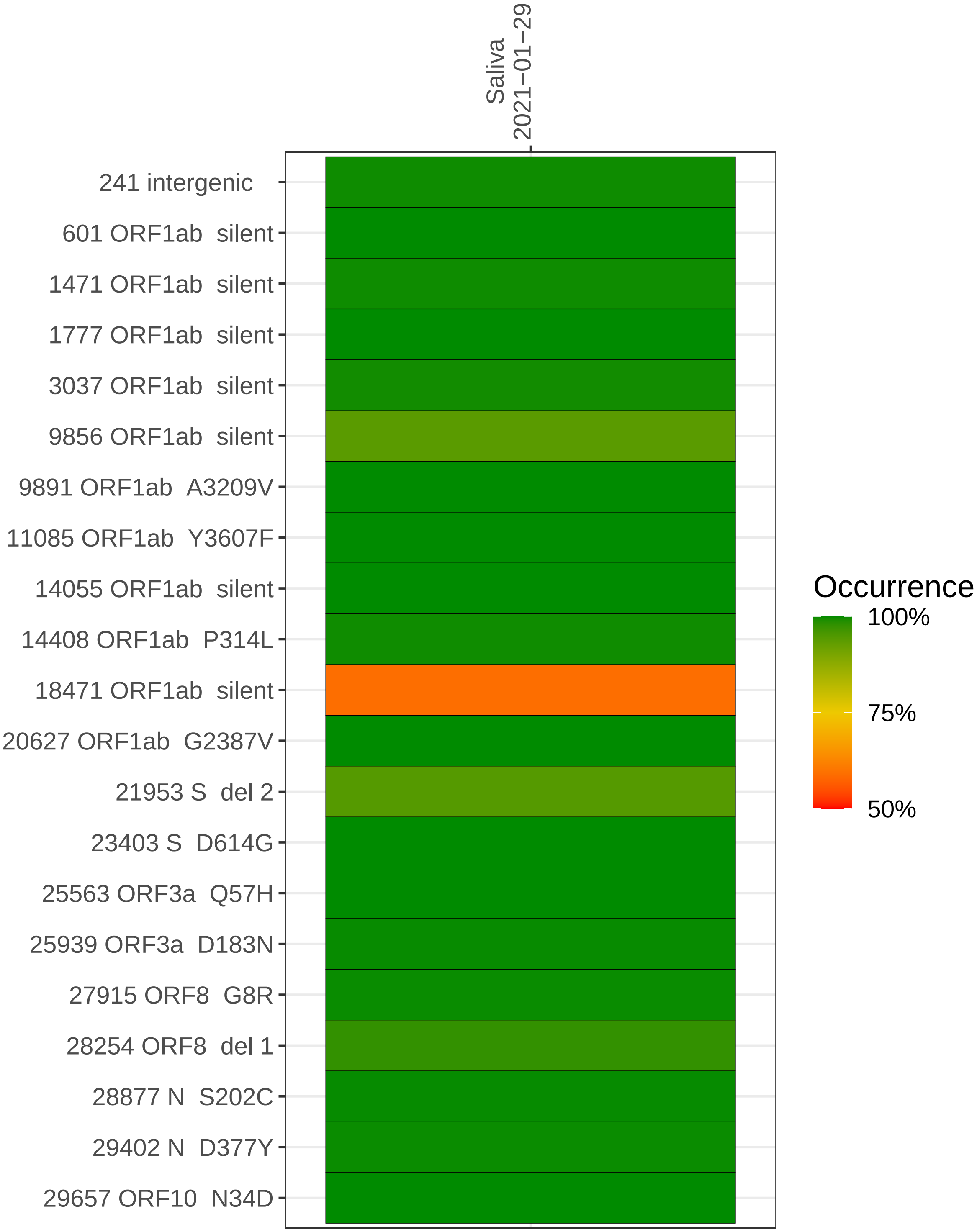
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

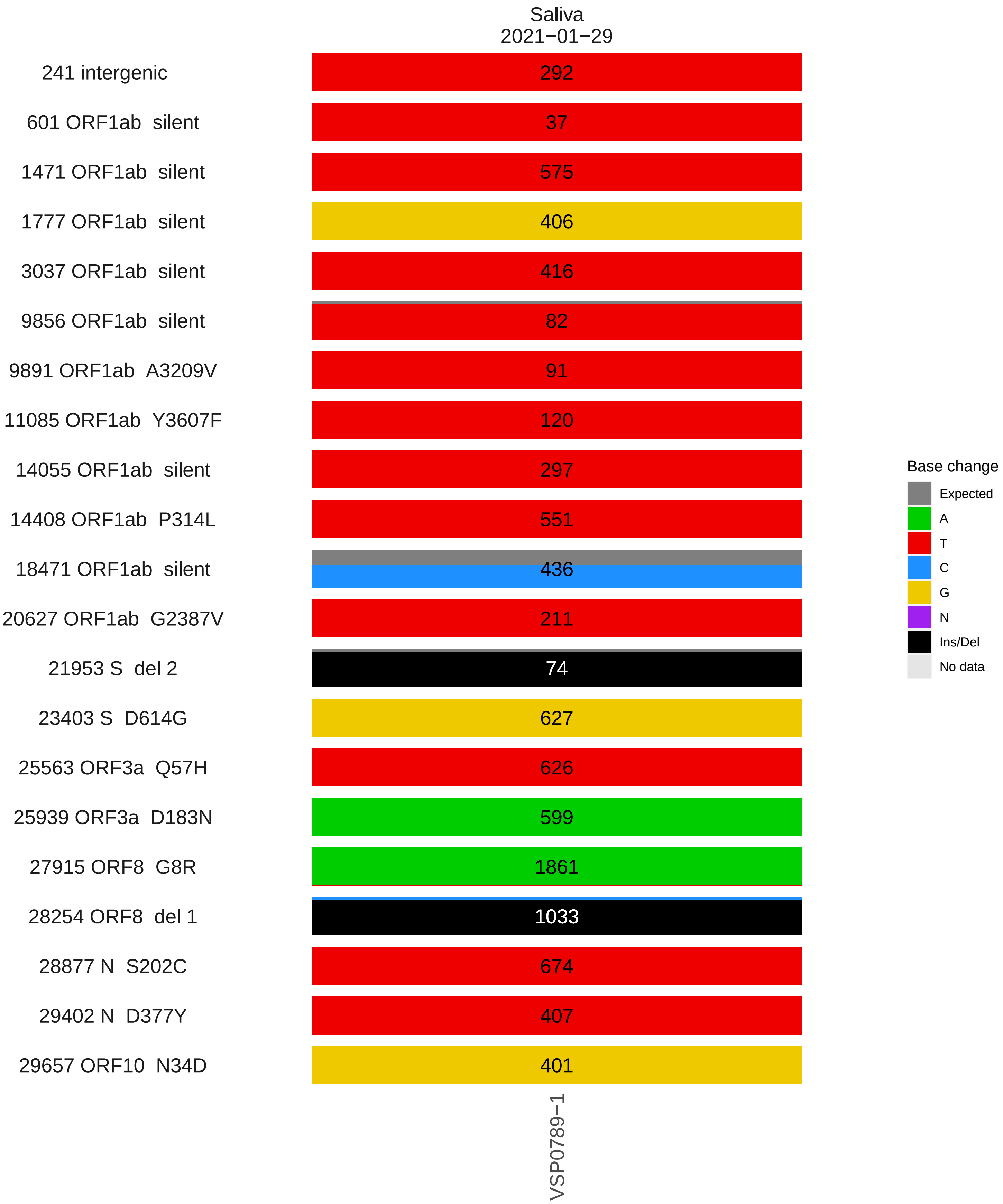
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0789-1	single experiment	NA	Saliva	2021-01-29	11.16	NA	94.9%	94.5%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

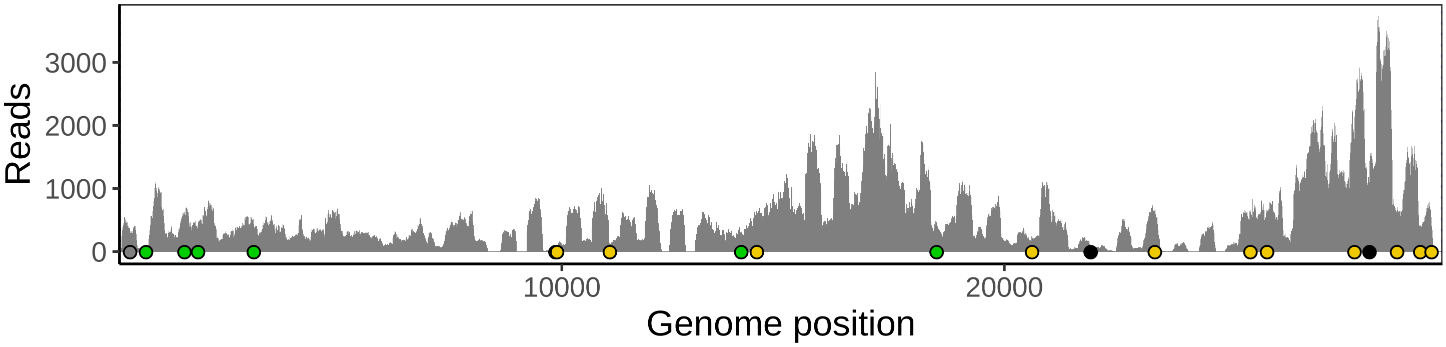



Saliva
2021−01−29
241 intergenic
292
601 ORF1ab silent
37
1471 ORF1ab silent
575
1777 ORF1ab silent
406
3037 ORF1ab silent
416
9856 ORF1ab silent
82
9891 ORF1ab A3209V
91
11085 ORF1ab Y3607F
120
14055 ORF1ab silent
297
14408 ORF1ab P314L
551
18471 ORF1ab silent
436
20627 ORF1ab G2387V
211
21953 S del 2
74
23403 S D614G
627
25563 ORF3a Q57H
626
25939 ORF3a D183N
599
27915 ORF8 G8R
1861
28254 ORF8 del 1
1033
28877 N S202C
674
29402 N D377Y
407
29657 ORF10 N34D
401
VSP0789−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

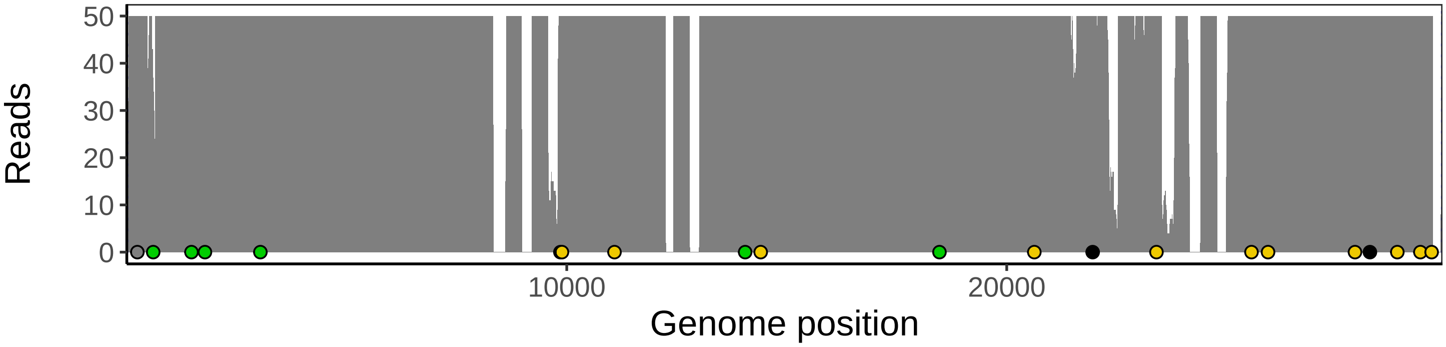
Analyses of individual experiments and composite results

VSP0789-1 | 2021-01-29 | Saliva | 463s | genomes | single experiment

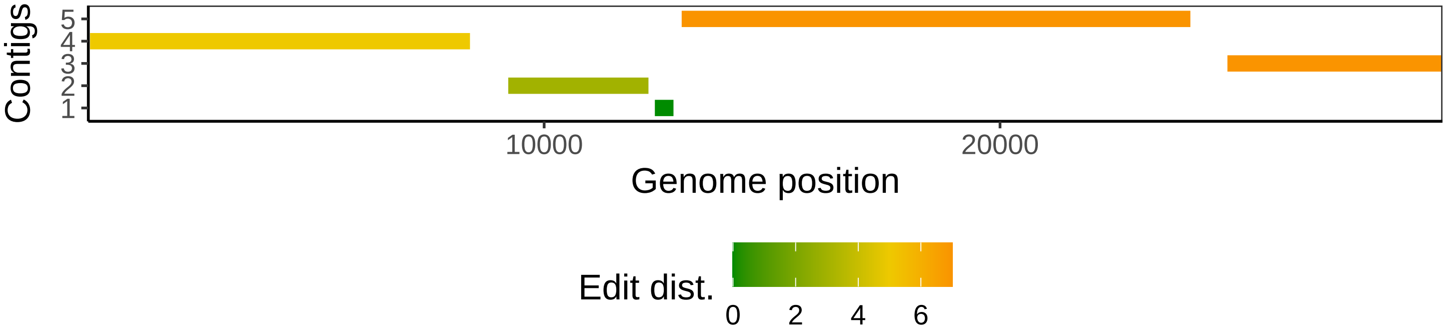
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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