COVID-19 subject HUP Q-0019

2021-06-23

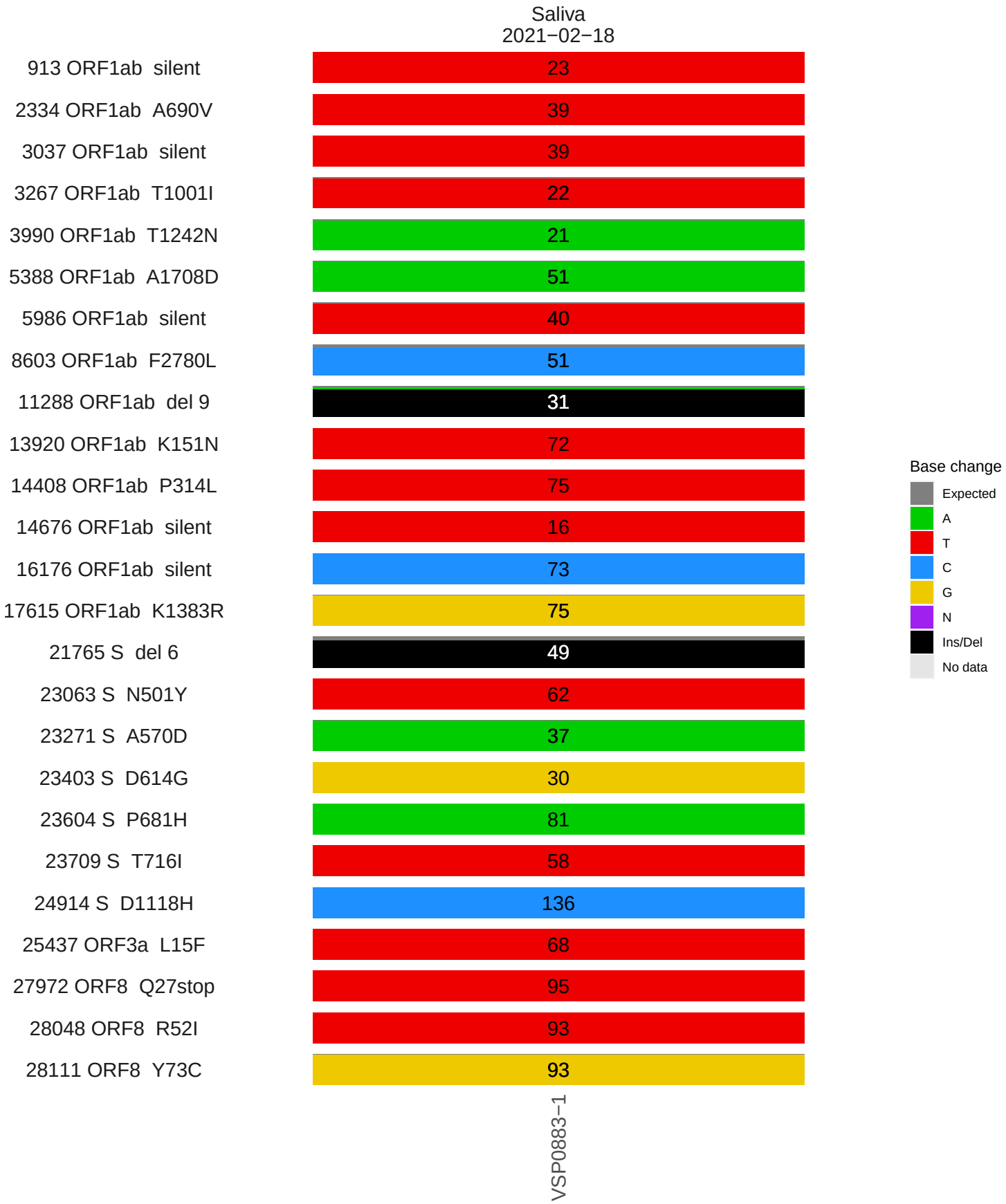
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0883-1	single experiment	NA	Saliva	2021-02-18	10.39	B.1.1.7	99.1%	97.0%

Variants shared across samples

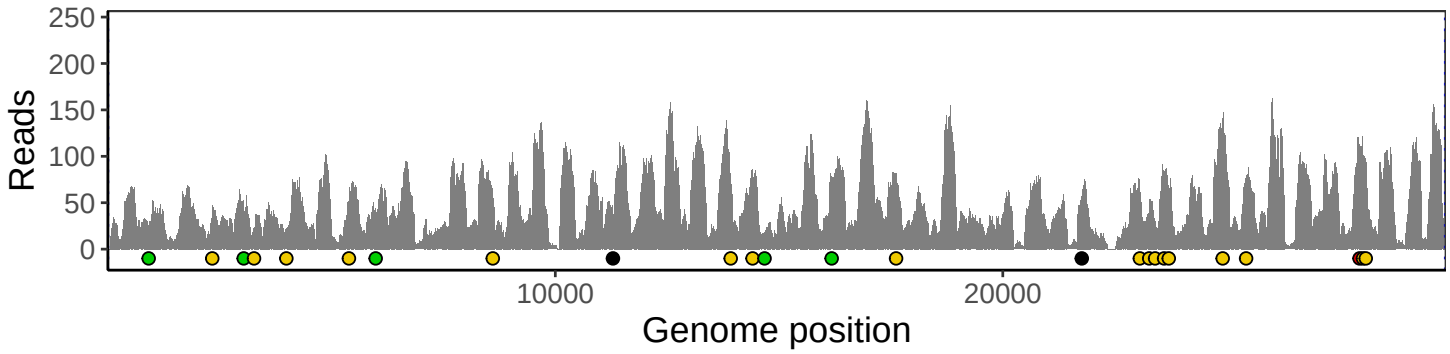
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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
2021−02−18
913 ORF1ab silent
23
2334 ORF1ab A690V
39
3037 ORF1ab silent
39
3267 ORF1ab T1001I
22
3990 ORF1ab T1242N
21
5388 ORF1ab A1708D
51
5986 ORF1ab silent
40
8603 ORF1ab F2780L
51
11288 ORF1ab del 9
31
13920 ORF1ab K151N
72
14408 ORF1ab P314L
75
14676 ORF1ab silent
16
16176 ORF1ab silent
73
17615 ORF1ab K1383R
75
21765 S del 6
49
23063 S N501Y
62
23271 S A570D
37
23403 S D614G
30
23604 S P681H
81
23709 S T716I
58
24914 S D1118H
136
25437 ORF3a L15F
68
27972 ORF8 Q27stop
95
28048 ORF8 R52I
93
28111 ORF8 Y73C
93
VSP0883−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

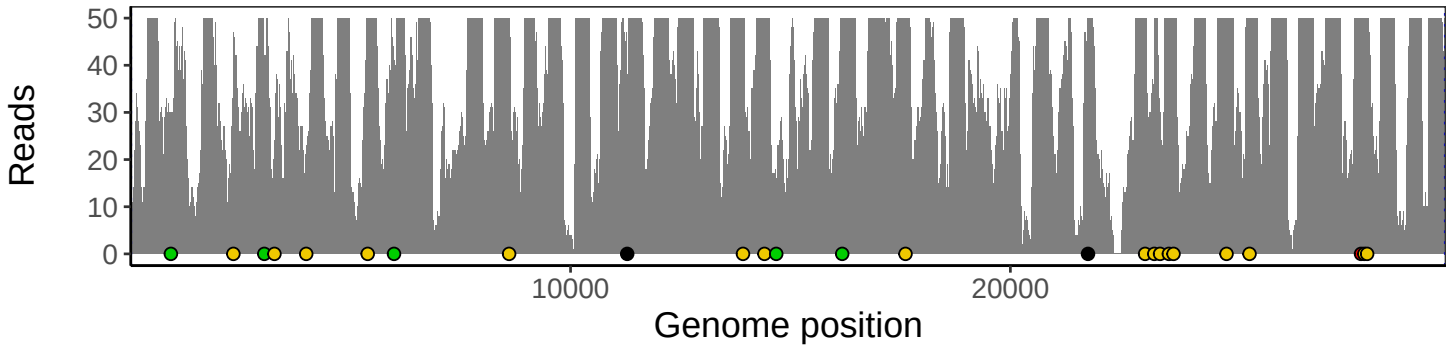
Analyses of individual experiments and composite results

VSP0883-1 | 2021-02-18 | Saliva | HUP Q-0019 | genomes | single experiment

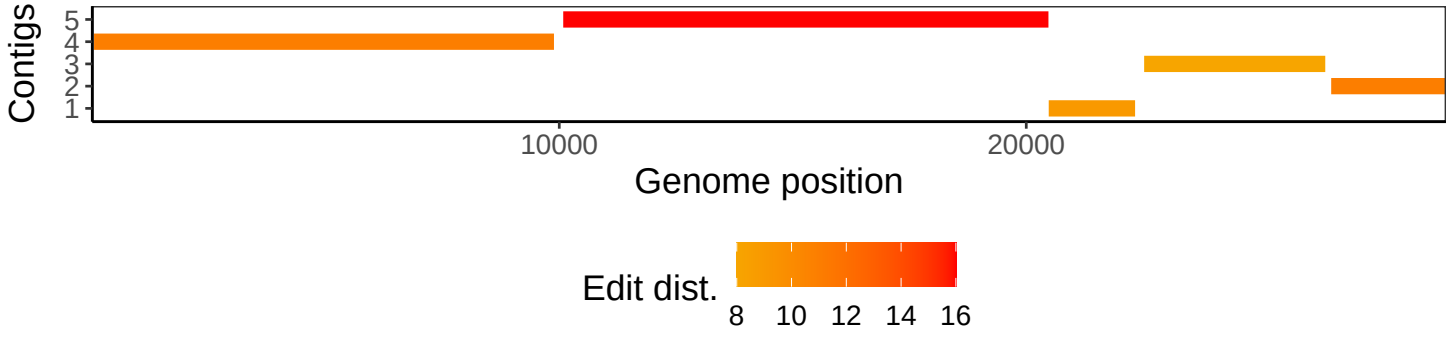
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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