COVID-19 subject HUP PH-0028

2021-05-05

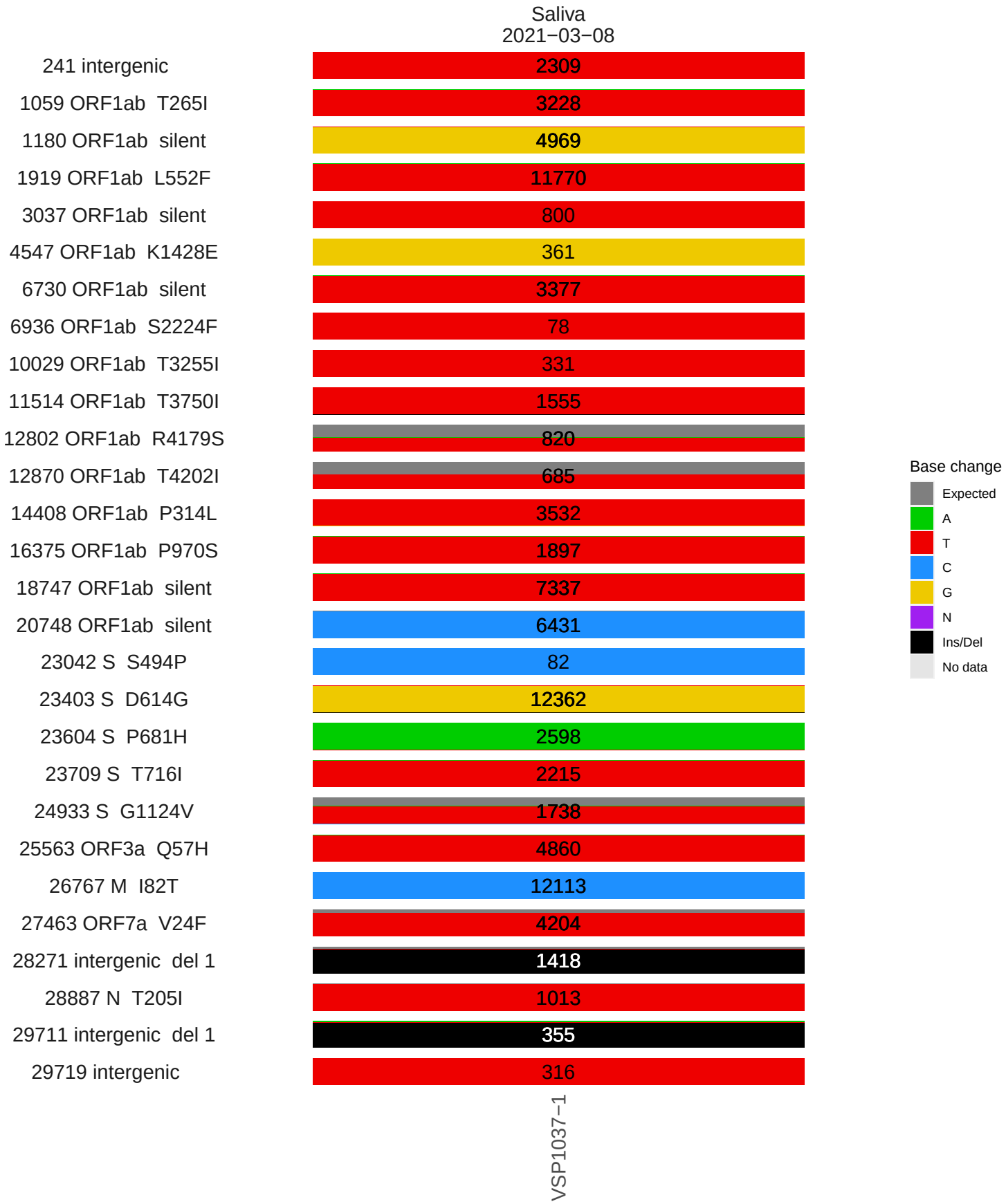
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1037-1	single experiment	NA	Saliva	2021-03-08	26.15	B.1.575	99.0%	99.0%

Variants shared across samples

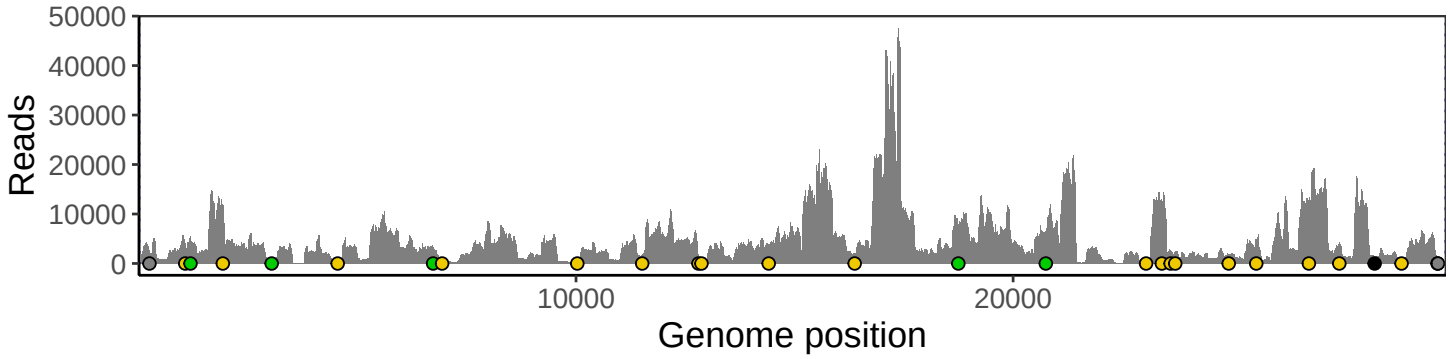
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of 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
2021−03−08
241 intergenic
2309
1059 ORF1ab T265I
3228
1180 ORF1ab silent
4969
1919 ORF1ab L552F
11770
3037 ORF1ab silent
800
4547 ORF1ab K1428E
361
6730 ORF1ab silent
3377
6936 ORF1ab S2224F
78
10029 ORF1ab T3255I
331
11514 ORF1ab T3750I
1555
12802 ORF1ab R4179S
820
12870 ORF1ab T4202I
685
14408 ORF1ab P314L
3532
16375 ORF1ab P970S
1897
18747 ORF1ab silent
7337
20748 ORF1ab silent
6431
23042 S S494P
82
23403 S D614G
12362
23604 S P681H
2598
23709 S T716I
2215
24933 S G1124V
1738
25563 ORF3a Q57H
4860
26767 M I82T
12113
27463 ORF7a V24F
4204
28271 intergenic del 1
1418
28887 N T205I
1013
29711 intergenic del 1
355
29719 intergenic
316
VSP1037−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

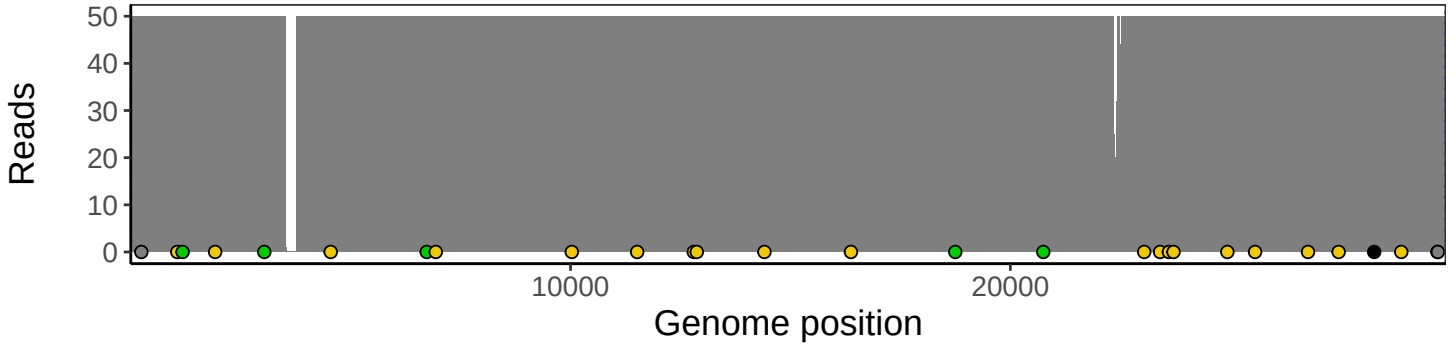
Analyses of individual experiments and composite results

VSP1037-1 | 2021-03-08 | Saliva | HUP PH-0028 | genomes | single experiment

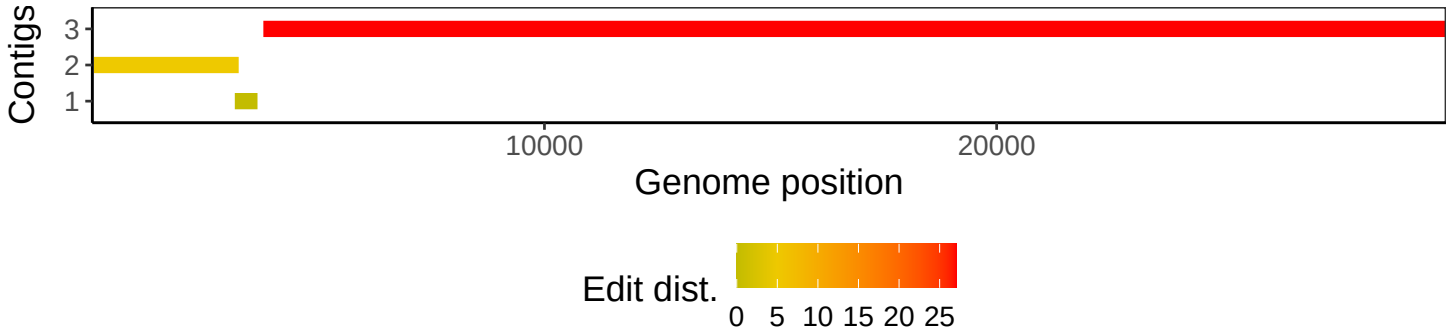
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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