

COVID-19 subject UPHS-0664

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.

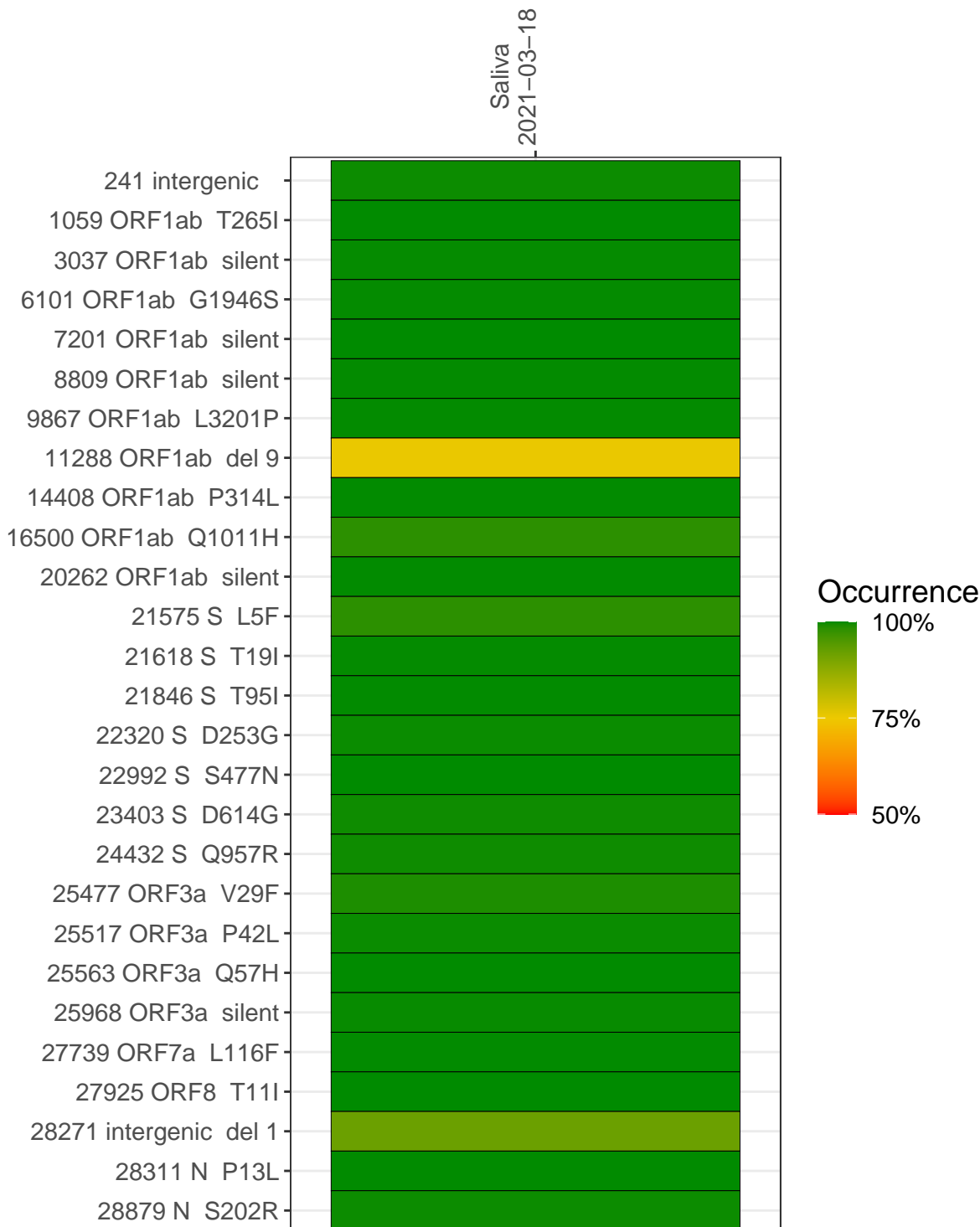
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP1882-1	single experiment	NA	Saliva	2021-03-18	29.88	B.1.526.2	99.9%	99.7%

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
2021-03-18

241 intergenic	4204
1059 ORF1ab T265I	7879
3037 ORF1ab silent	7957
6101 ORF1ab G1946S	7642
7201 ORF1ab silent	2403
8809 ORF1ab silent	3154
9867 ORF1ab L3201P	1501
11288 ORF1ab del 9	10883
14408 ORF1ab P314L	17543
16500 ORF1ab Q1011H	13634
20262 ORF1ab silent	6911
21575 S L5F	2737
21618 S T19I	2857
21846 S T95I	11471
22320 S D253G	1591
22992 S S477N	1058
23403 S D614G	16460
24432 S Q957R	8493
25477 ORF3a V29F	11670
25517 ORF3a P42L	11078
25563 ORF3a Q57H	14781
25968 ORF3a silent	16604
27739 ORF7a L116F	11994
27925 ORF8 T11I	26536
28271 intergenic del 1	13948
28311 N P13L	13877
28879 N S202R	4935

Base change

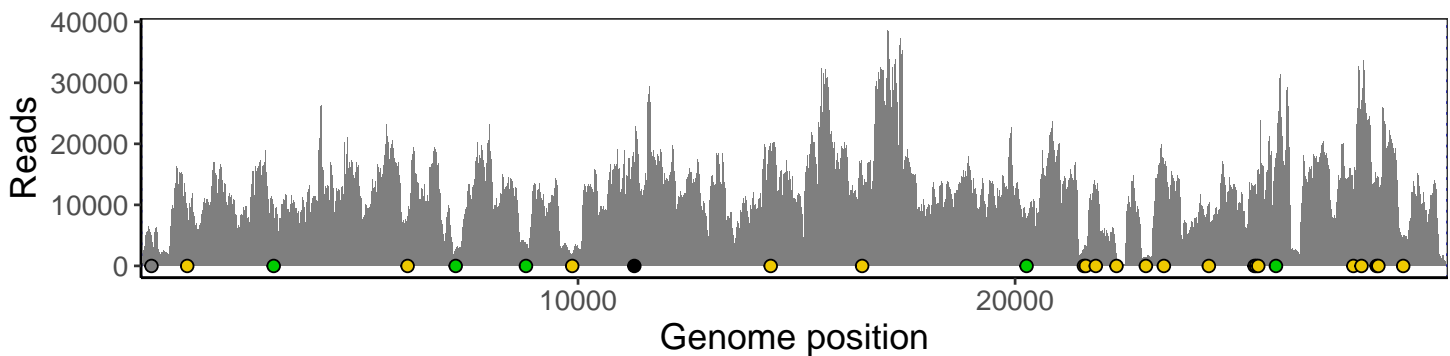
Expected
A
T
C
G
N
Ins/Del
No data

VSP1882-1

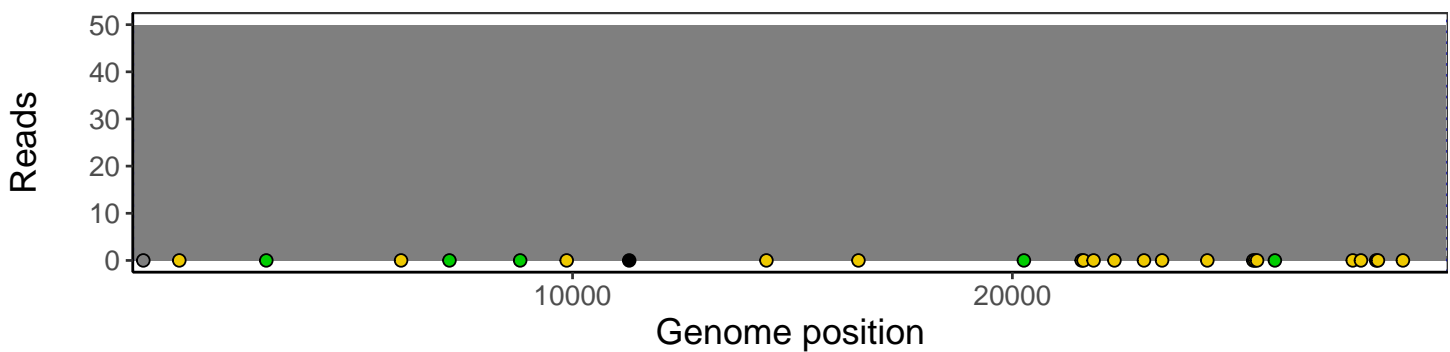
Analyses of individual experiments and composite results

VSP1882-1 | 2021-03-18 | Saliva | UPHS-0664 | genomes | single experiment

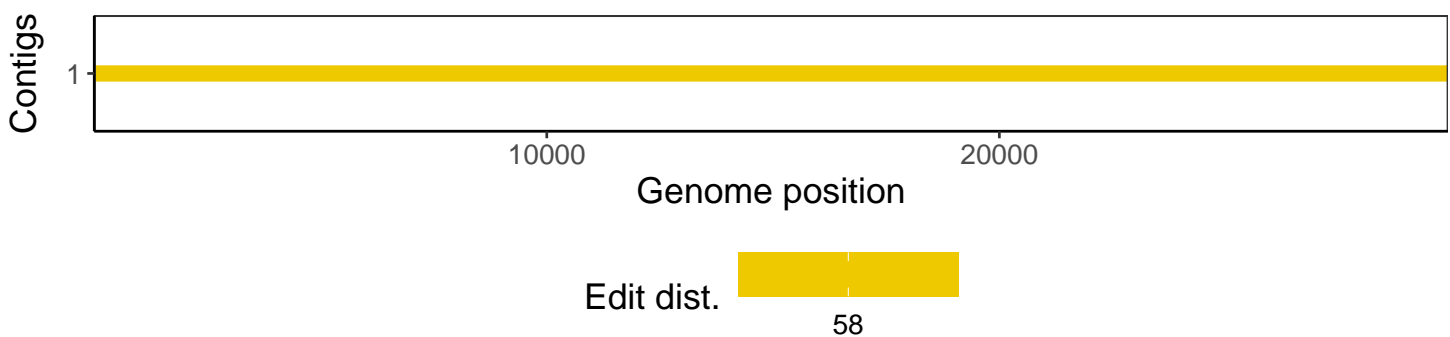
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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