COVID-19 subject UPHS-0682

2021-04-20

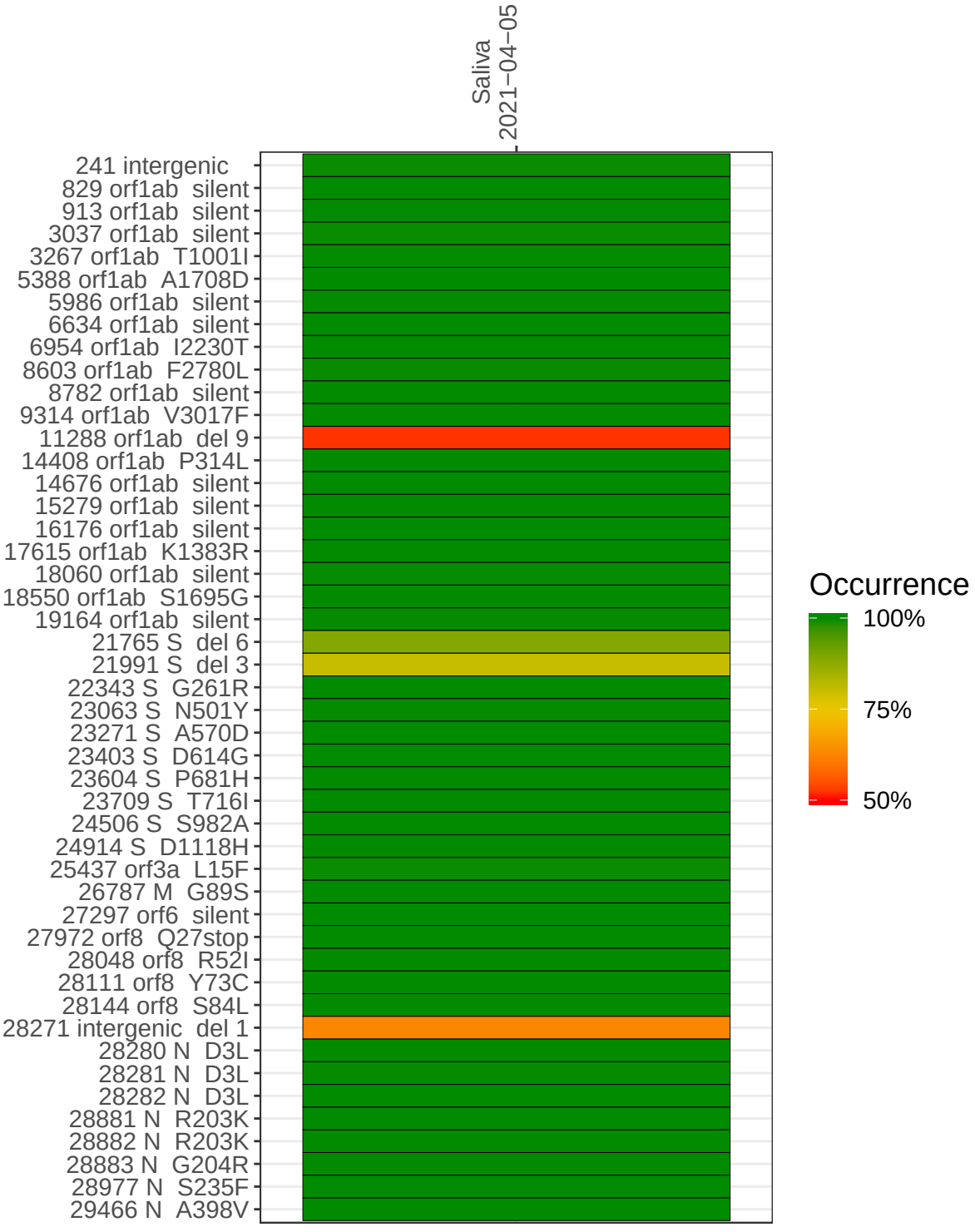
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

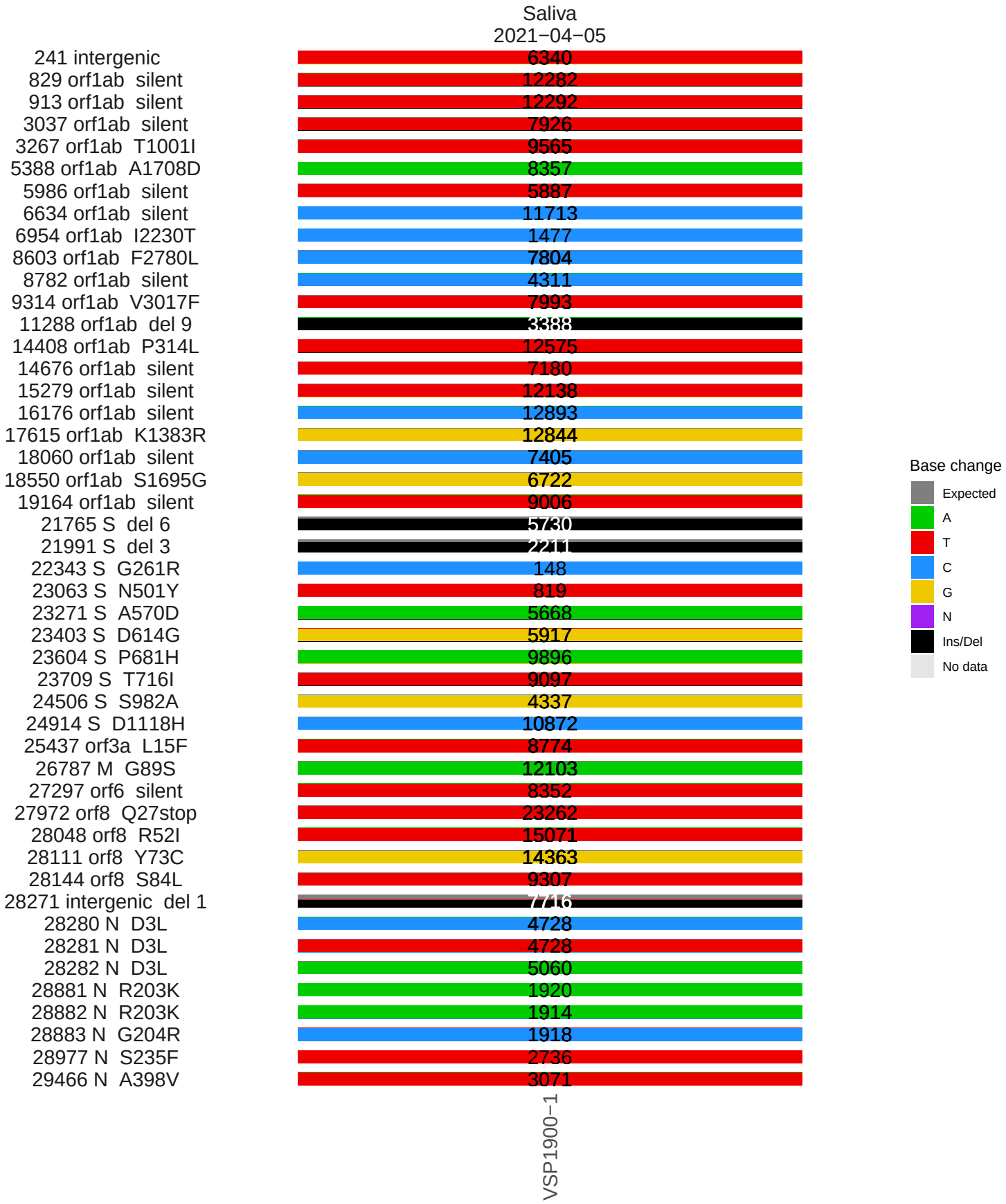
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1900-1	single experiment	NA	Saliva	2021-04-05	29.82	B.1.1.7	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.

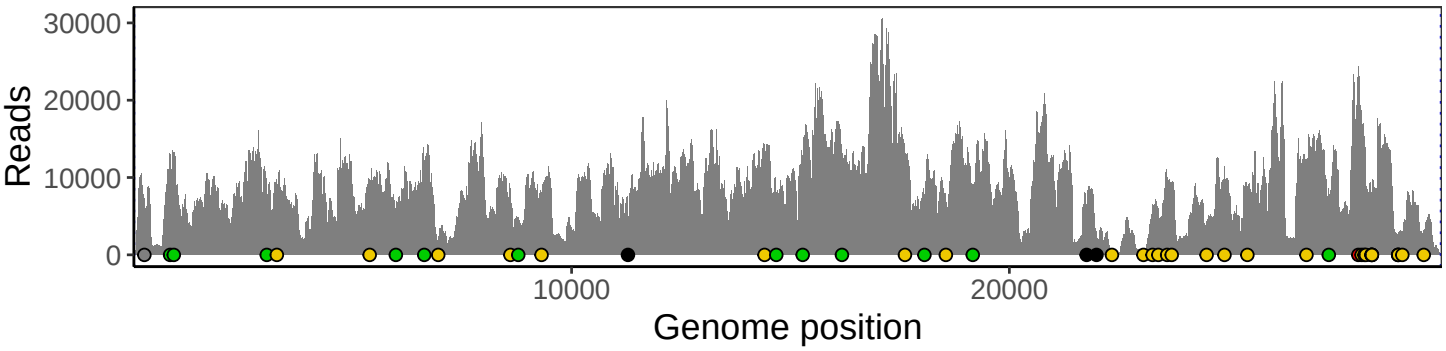



Saliva
2021−04−05
241 intergenic
829 orf1ab silent
913 orf1ab silent
3037 orf1ab silent
3267 orf1ab T1001I
5388 orf1ab A1708D
5986 orf1ab silent
6634 orf1ab silent
6954 orf1ab I2230T
8603 orf1ab F2780L
8782 orf1ab silent
9314 orf1ab V3017F
11288 orf1ab del 9
14408 orf1ab P314L
14676 orf1ab silent
15279 orf1ab silent
16176 orf1ab silent
17615 orf1ab K1383R
18060 orf1ab silent
18550 orf1ab S1695G
19164 orf1ab silent
21765 S del 6
21991 S del 3
22343 S G261R
23063 S N501Y
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24506 S S982A
24914 S D1118H
25437 orf3a L15F
26787 M G89S
27297 orf6 silent
27972 orf8 Q27stop
28048 orf8 R52I
28111 orf8 Y73C
28144 orf8 S84L
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
29466 N A398V
6340
12282
12292
7926
9565
8357
5887
11713
1477
7804
4311
7993
3388
12575
7180
12138
12893
12844
7405
6722
9006
5730
2211
148
819
5668
5917
9896
9097
4337
10872
8774
12103
8352
23262
15071
14363
9307
7716
4728
4728
5060
1920
1914
1918
2736
3071
VSP1900−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

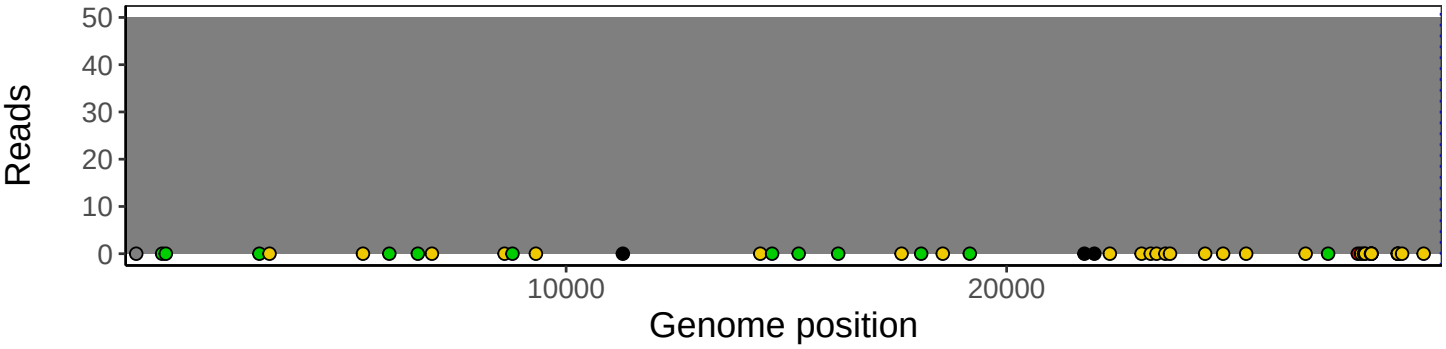
Analyses of individual experiments and composite results

VSP1900-1 | 2021-04-05 | Saliva | UPHS-0682 | genomes | single experiment

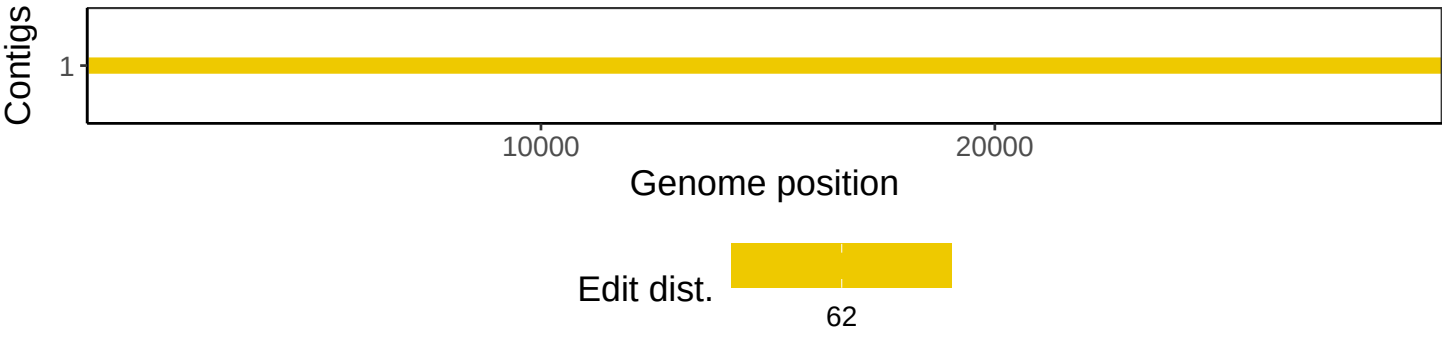
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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