COVID-19 subject UPHS-0680

2021-04-20

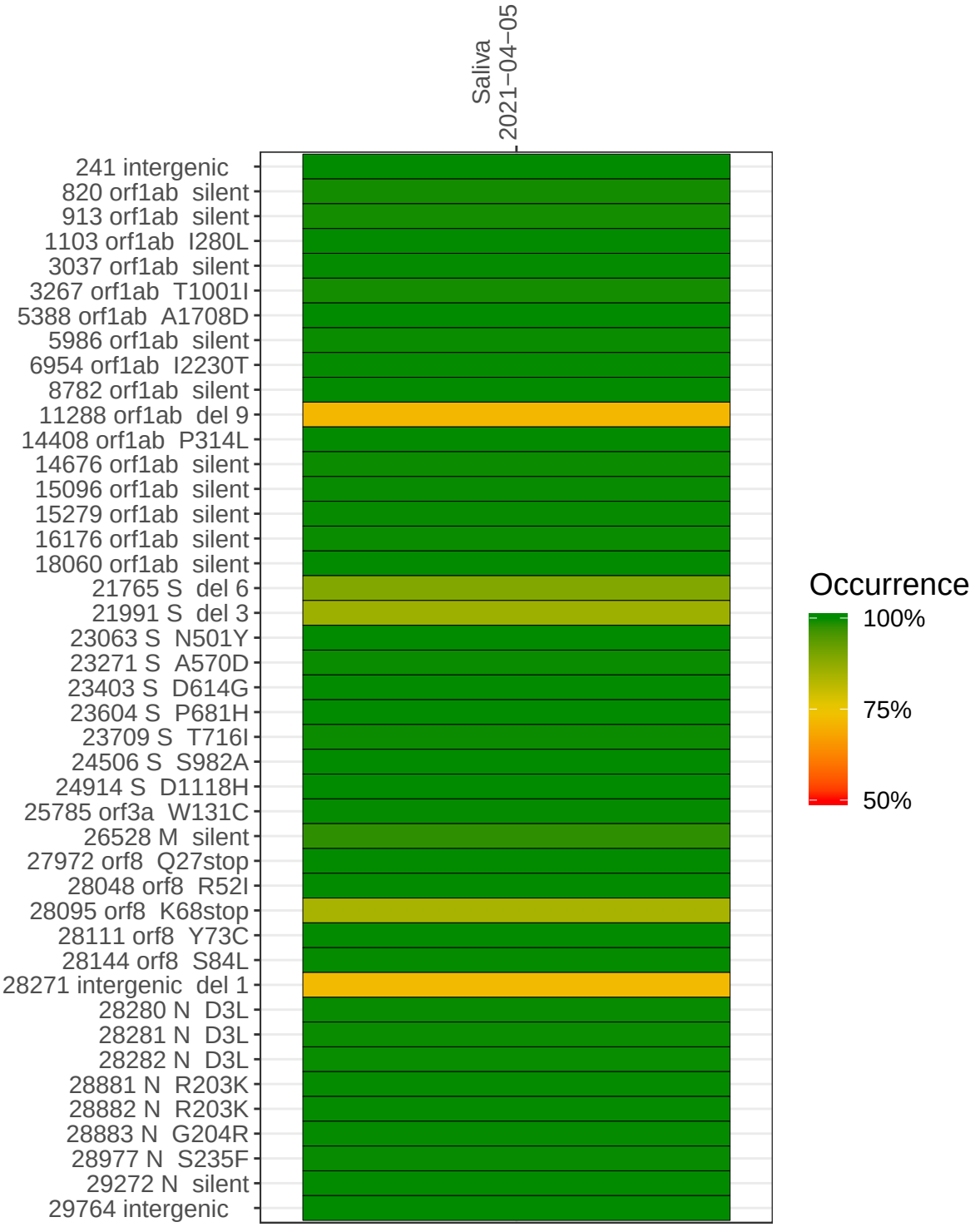
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

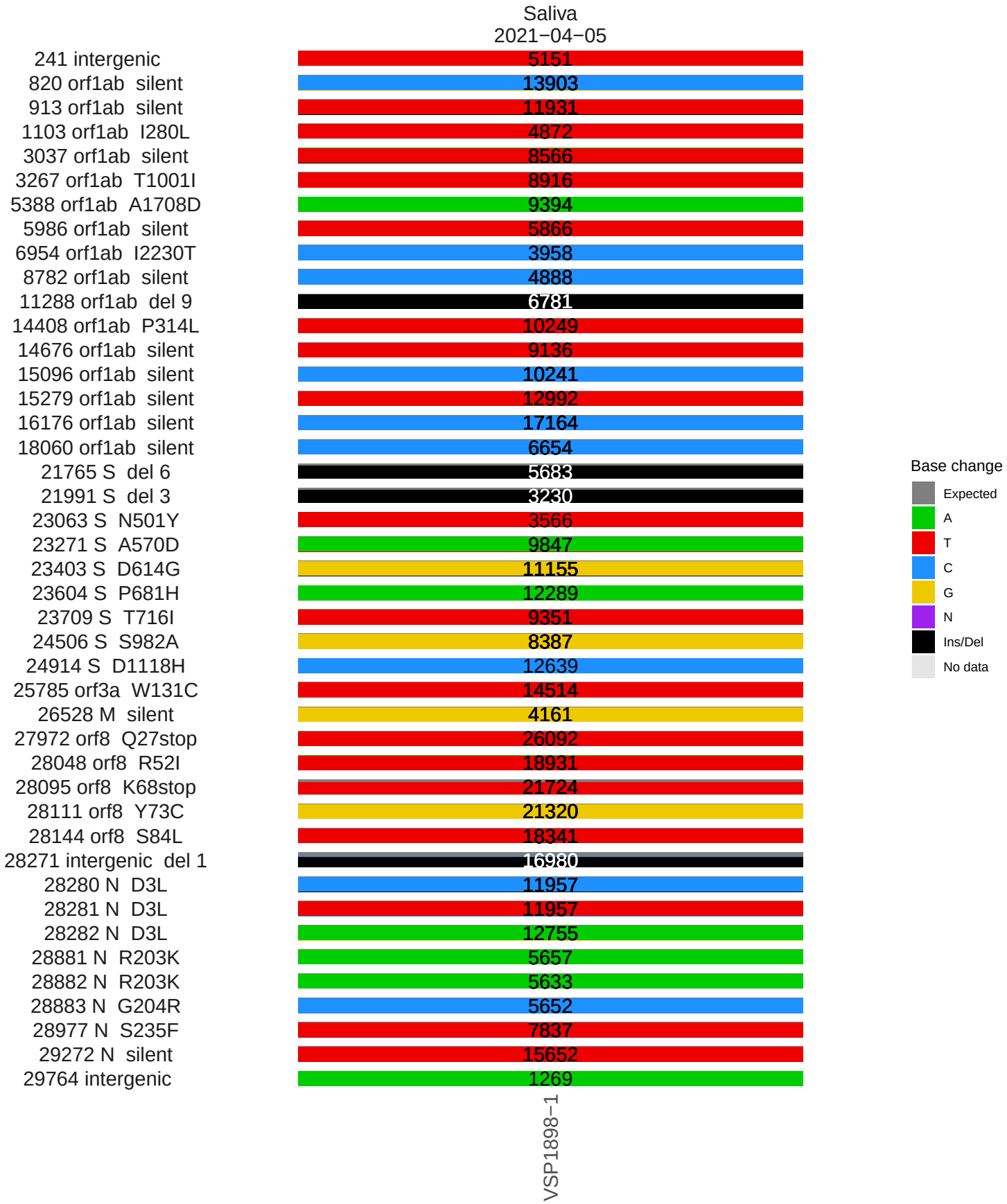
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1898-1	single experiment	NA	Saliva	2021-04-05	29.84	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.

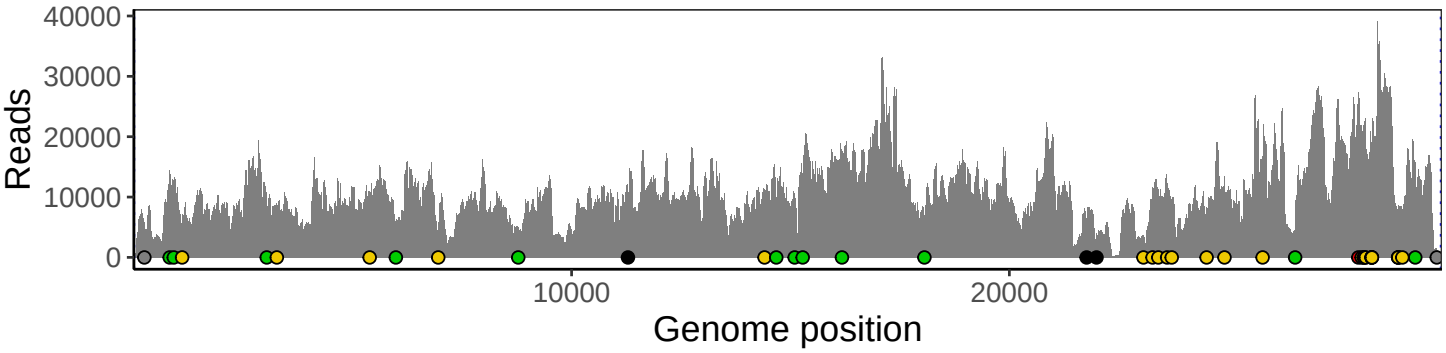



Saliva
2021−04−05
241 intergenic 5151
820 orf1ab silent 13903
913 orf1ab silent 11931
1103 orf1ab I280L 4872
3037 orf1ab silent 8566
3267 orf1ab T1001I 8916
5388 orf1ab A1708D 9394
5986 orf1ab silent 5866
6954 orf1ab I2230T 3958
8782 orf1ab silent 4888
11288 orf1ab del 9 6781
14408 orf1ab P314L 10249
14676 orf1ab silent 9136
15096 orf1ab silent 10241
15279 orf1ab silent 12992
16176 orf1ab silent 17164
18060 orf1ab silent 6654
21765 S del 6 5683
21991 S del 3 3230
23063 S N501Y 3566
23271 S A570D 9847
23403 S D614G 11155
23604 S P681H 12289
23709 S T716I 9351
24506 S S982A 8387
24914 S D1118H 12639
25785 orf3a W131C 14514
26528 M silent 4161
27972 orf8 Q27stop 26092
28048 orf8 R52I 18931
28095 orf8 K68stop 21724
28111 orf8 Y73C 21320
28144 orf8 S84L 18341
28271 intergenic del 1 16980
28280 N D3L 11957
28281 N D3L 11957
28282 N D3L 12755
28881 N R203K 5657
28882 N R203K 5633
28883 N G204R 5652
28977 N S235F 7837
29272 N silent 15652
29764 intergenic 1269
VSP1898−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

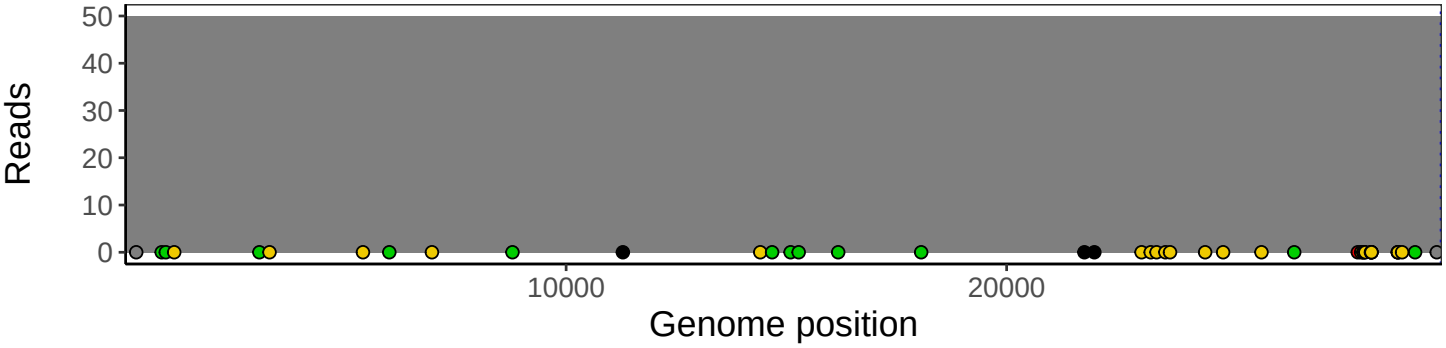
Analyses of individual experiments and composite results

VSP1898-1 | 2021-04-05 | Saliva | UPHS-0680 | genomes | single experiment

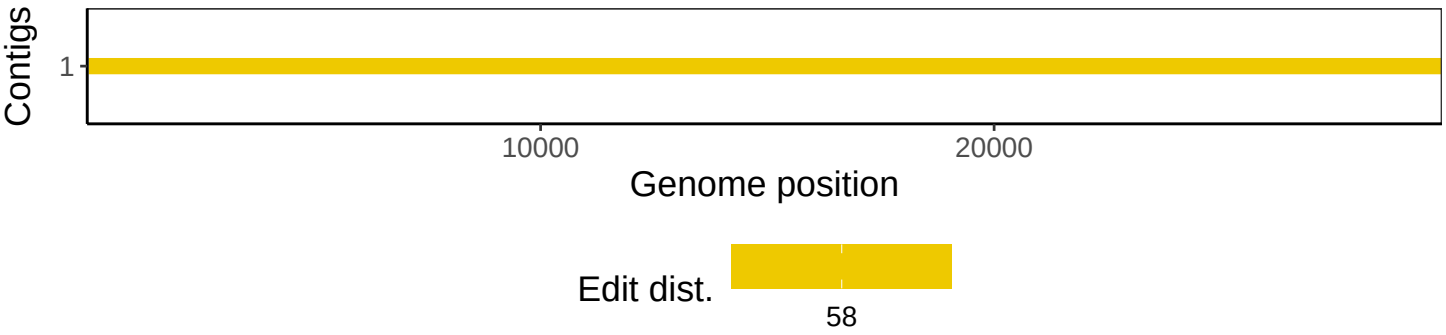
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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