COVID-19 subject UPHS-0672

2021-04-20

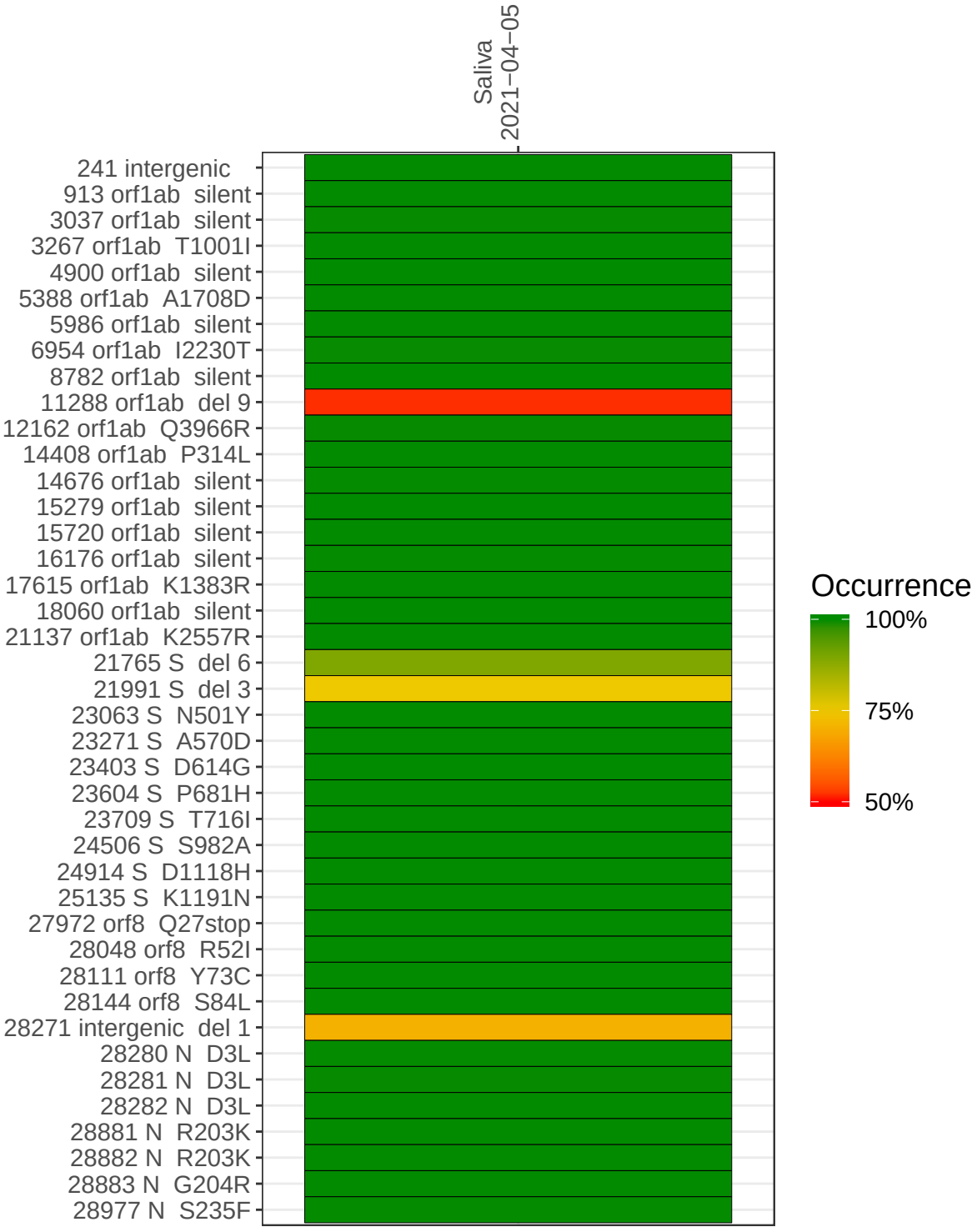
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

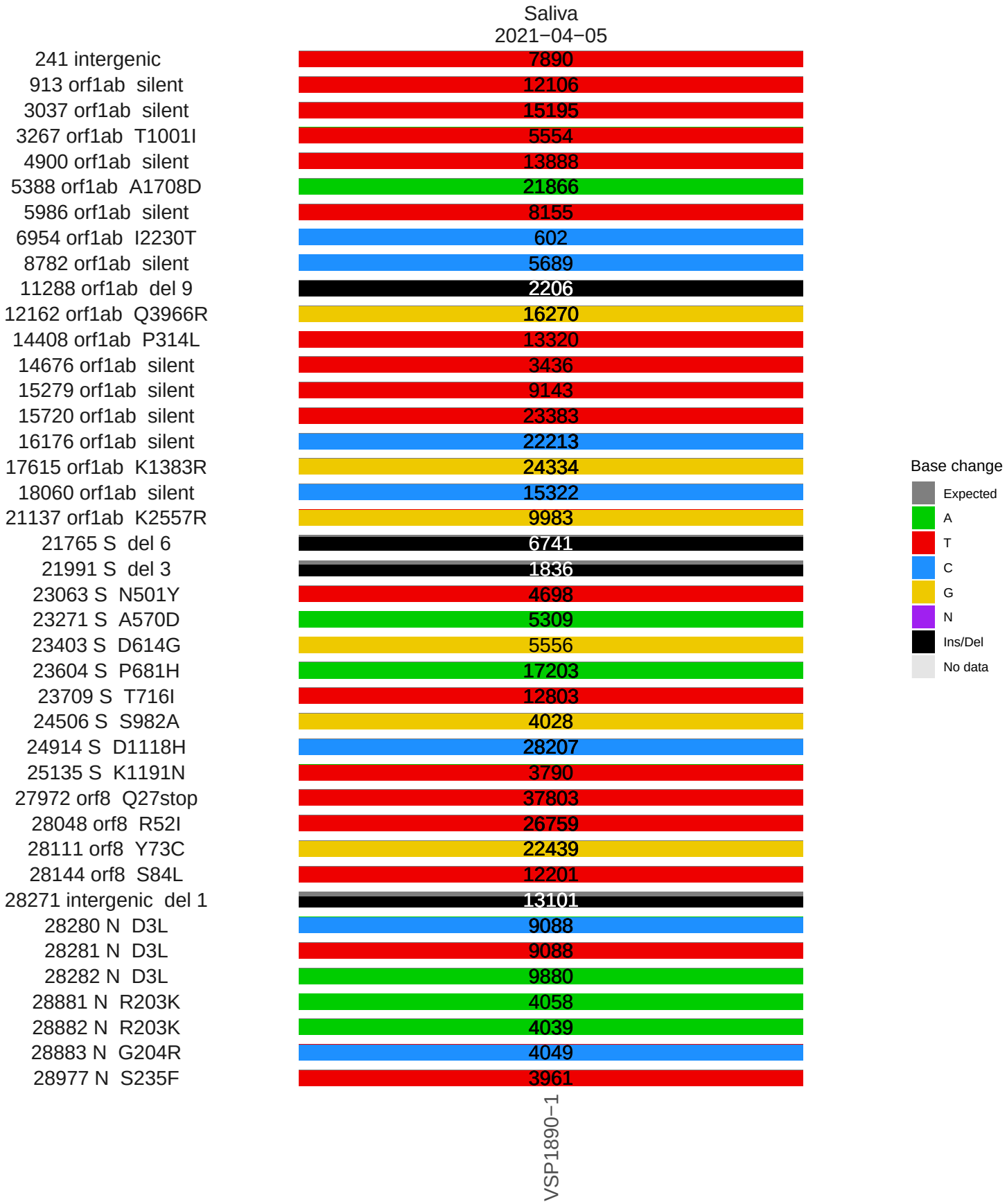
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1890-1	single experiment	NA	Saliva	2021-04-05	29.88	B.1.1.7	99.9%	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.

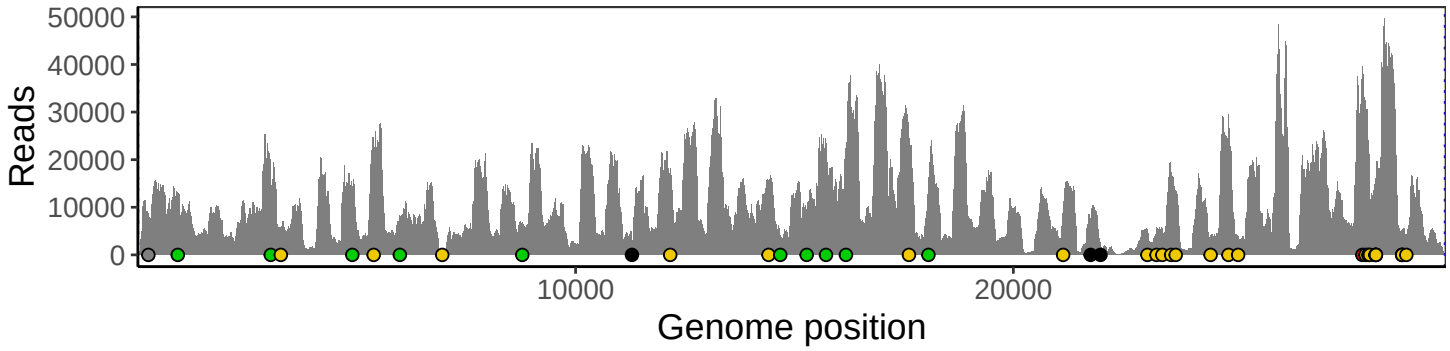



Saliva
2021−04−05
241 intergenic 7890
913 orf1ab silent 12106
3037 orf1ab silent 15195
3267 orf1ab T1001I 5554
4900 orf1ab silent 13888
5388 orf1ab A1708D 21866
5986 orf1ab silent 8155
6954 orf1ab I2230T 602
8782 orf1ab silent 5689
11288 orf1ab del 9 2206
12162 orf1ab Q3966R 16270
14408 orf1ab P314L 13320
14676 orf1ab silent 3436
15279 orf1ab silent 9143
15720 orf1ab silent 23383
16176 orf1ab silent 22213
17615 orf1ab K1383R 24334
18060 orf1ab silent 15322
21137 orf1ab K2557R 9983
21765 S del 6 6741
21991 S del 3 1836
23063 S N501Y 4698
23271 S A570D 5309
23403 S D614G 5556
23604 S P681H 17203
23709 S T716I 12803
24506 S S982A 4028
24914 S D1118H 28207
25135 S K1191N 3790
27972 orf8 Q27stop 37803
28048 orf8 R52I 26759
28111 orf8 Y73C 22439
28144 orf8 S84L 12201
28271 intergenic del 1 13101
28280 N D3L 9088
28281 N D3L 9088
28282 N D3L 9880
28881 N R203K 4058
28882 N R203K 4039
28883 N G204R 4049
28977 N S235F 3961
VSP1890−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

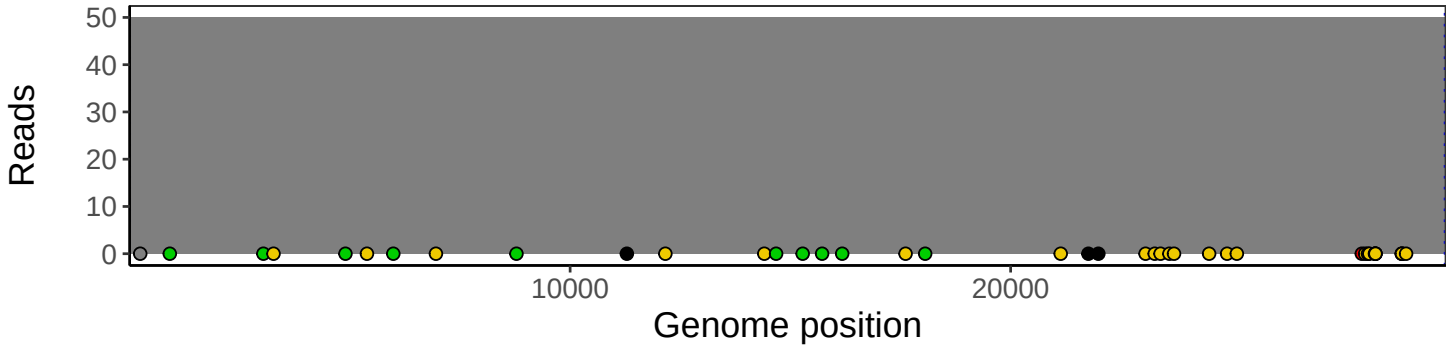
Analyses of individual experiments and composite results

VSP1890-1 | 2021-04-05 | Saliva | UPHS-0672 | genomes | single experiment

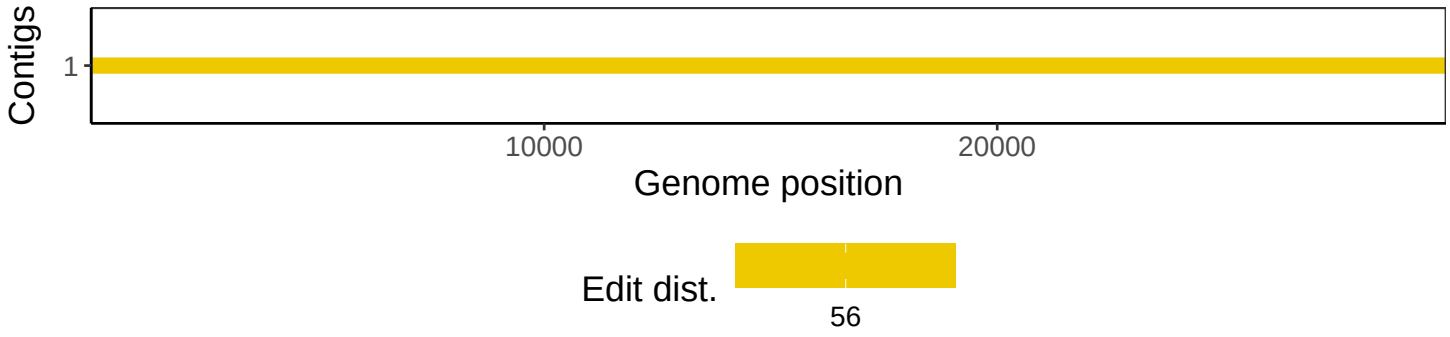
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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