COVID-19 subject UPHS-0696

2021-04-20

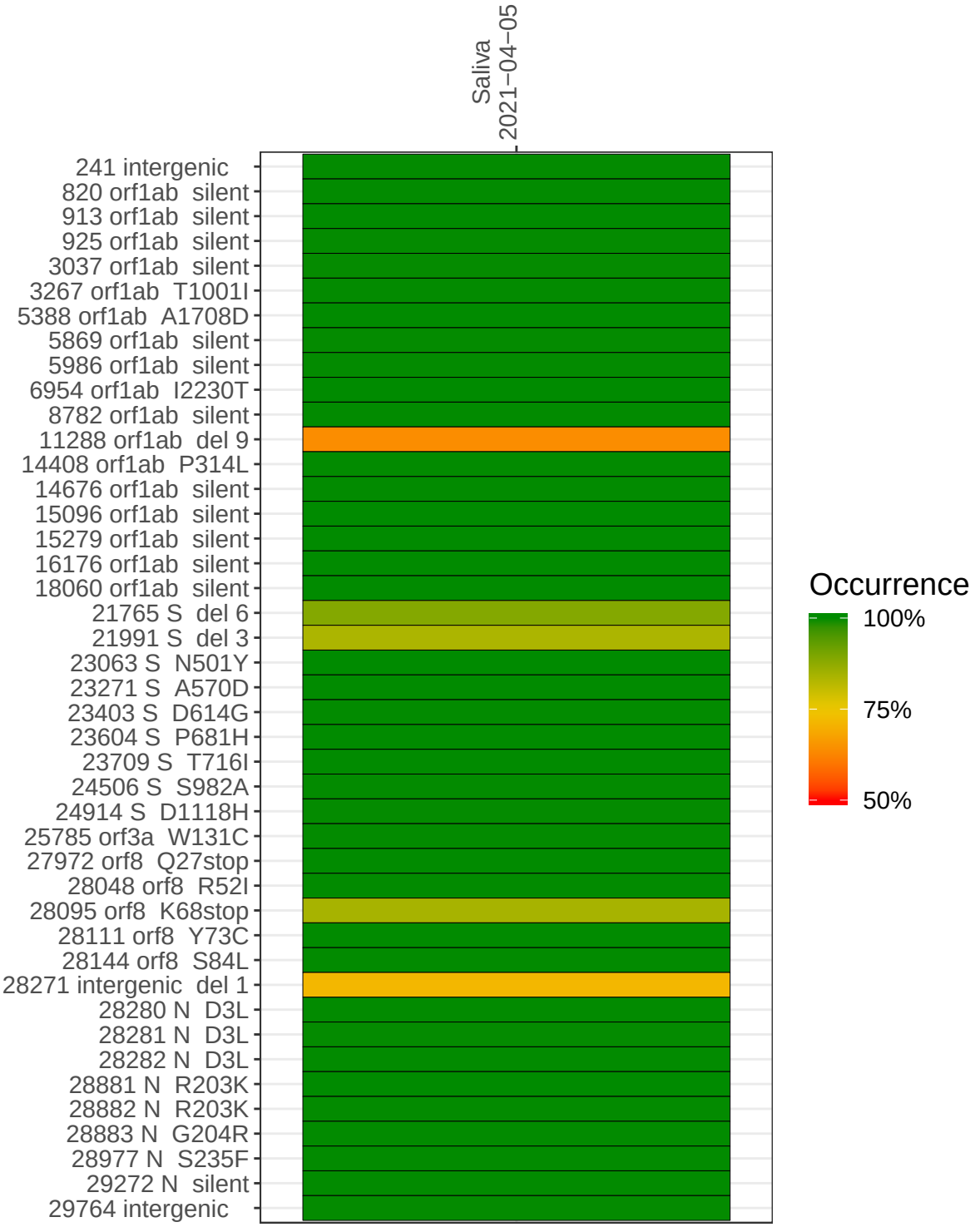
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

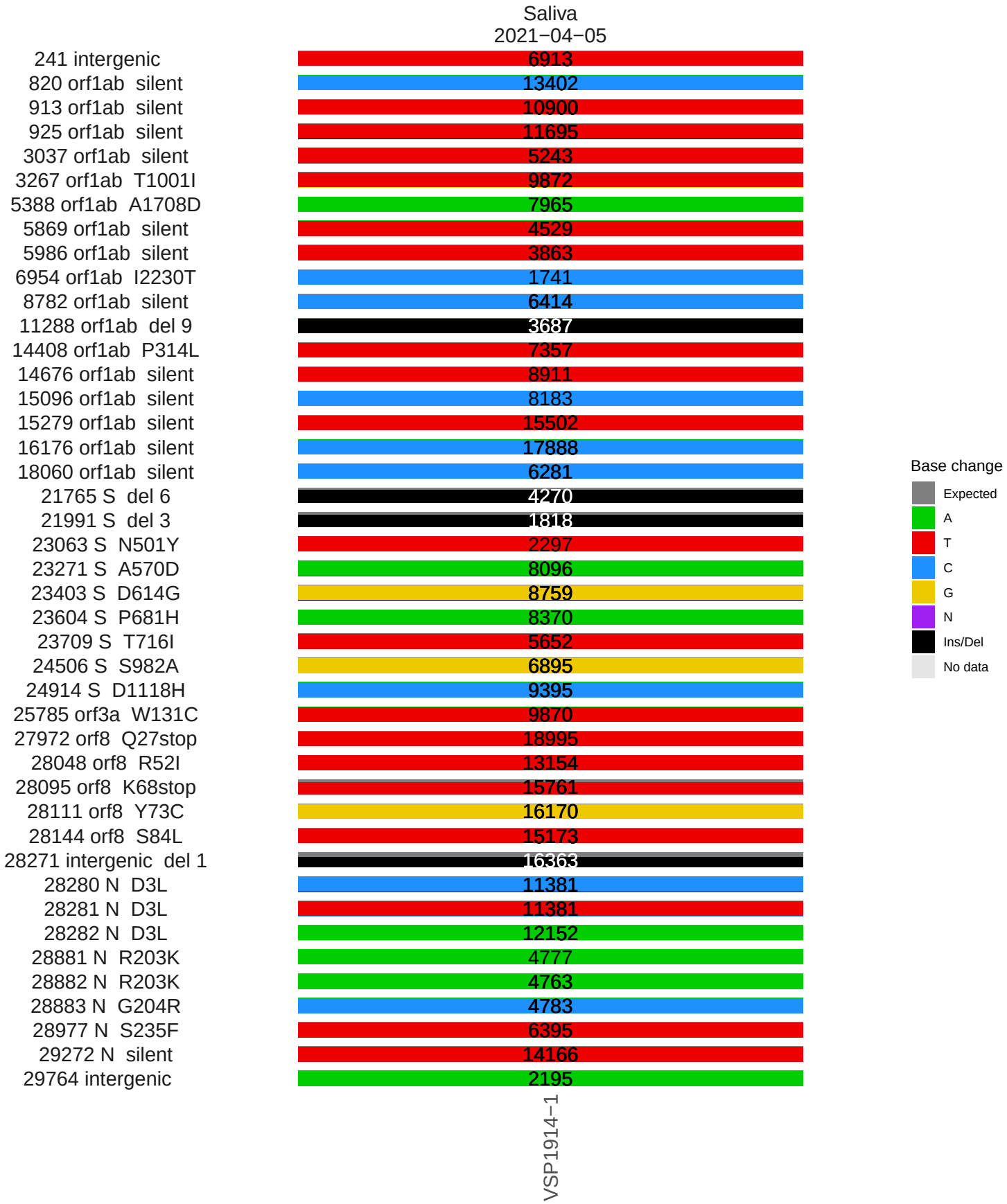
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1914-1	single experiment	NA	Saliva	2021-04-05	29.83	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.

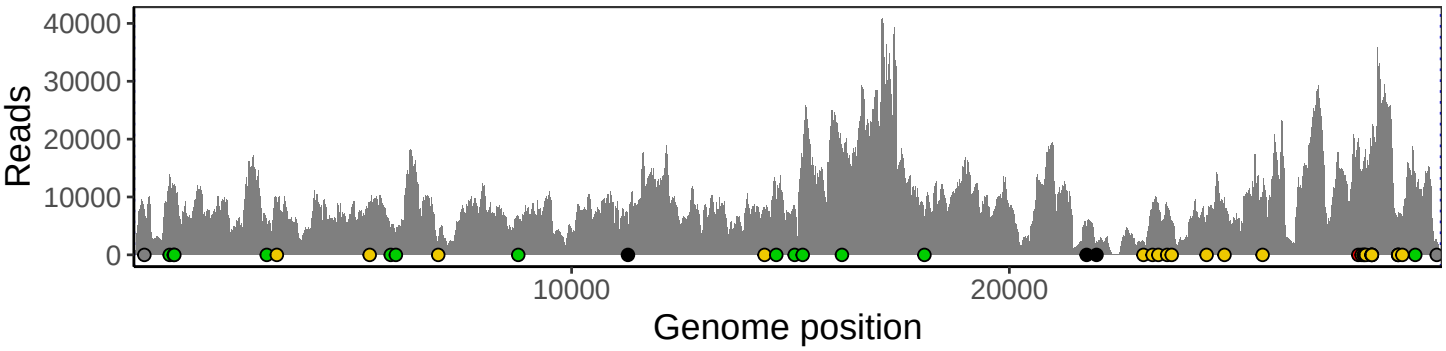



Saliva
2021−04−05
241 intergenic 6913
820 orf1ab silent 13402
913 orf1ab silent 10900
925 orf1ab silent 11695
3037 orf1ab silent 5243
3267 orf1ab T1001I 9872
5388 orf1ab A1708D 7965
5869 orf1ab silent 4529
5986 orf1ab silent 3863
6954 orf1ab I2230T 1741
8782 orf1ab silent 6414
11288 orf1ab del 9 3687
14408 orf1ab P314L 7357
14676 orf1ab silent 8911
15096 orf1ab silent 8183
15279 orf1ab silent 15502
16176 orf1ab silent 17888
18060 orf1ab silent 6281
21765 S del 6 4270
21991 S del 3 1818
23063 S N501Y 2297
23271 S A570D 8096
23403 S D614G 8759
23604 S P681H 8370
23709 S T716I 5652
24506 S S982A 6895
24914 S D1118H 9395
25785 orf3a W131C 9870
27972 orf8 Q27stop 18995
28048 orf8 R52I 13154
28095 orf8 K68stop 15761
28111 orf8 Y73C 16170
28144 orf8 S84L 15173
28271 intergenic del 1 16363
28280 N D3L 11381
28281 N D3L 11381
28282 N D3L 12152
28881 N R203K 4777
28882 N R203K 4763
28883 N G204R 4783
28977 N S235F 6395
29272 N silent 14166
29764 intergenic 2195
VSP1914−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

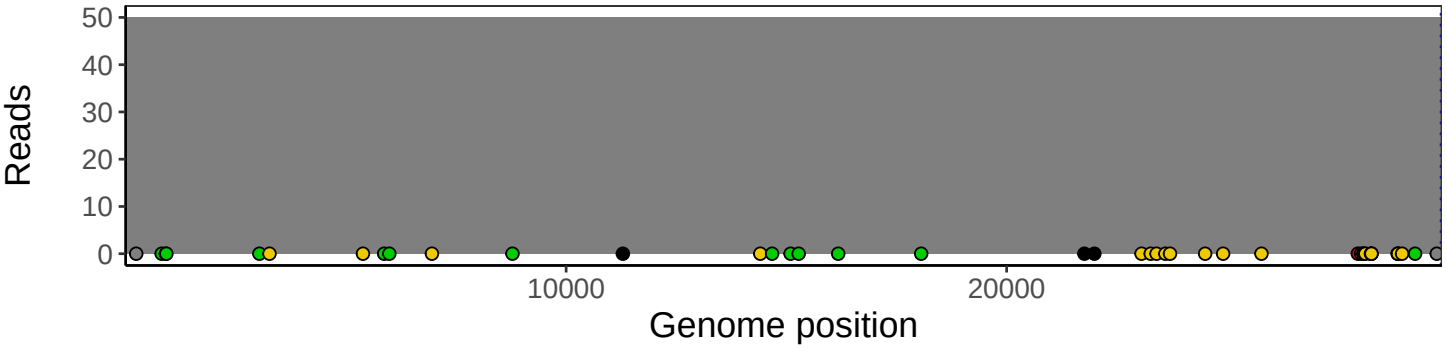
Analyses of individual experiments and composite results

VSP1914-1 | 2021-04-05 | Saliva | UPHS-0696 | genomes | single experiment

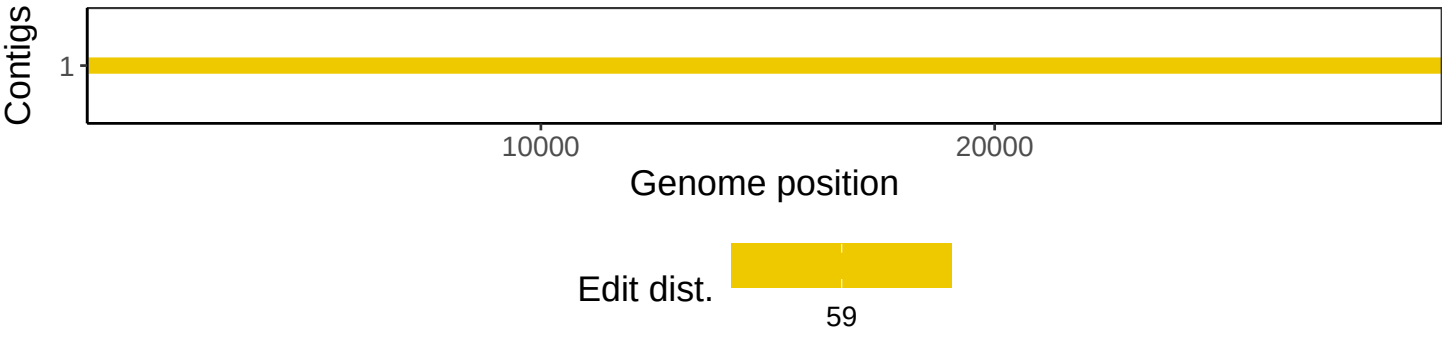
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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