COVID-19 subject 459

2021-04-17

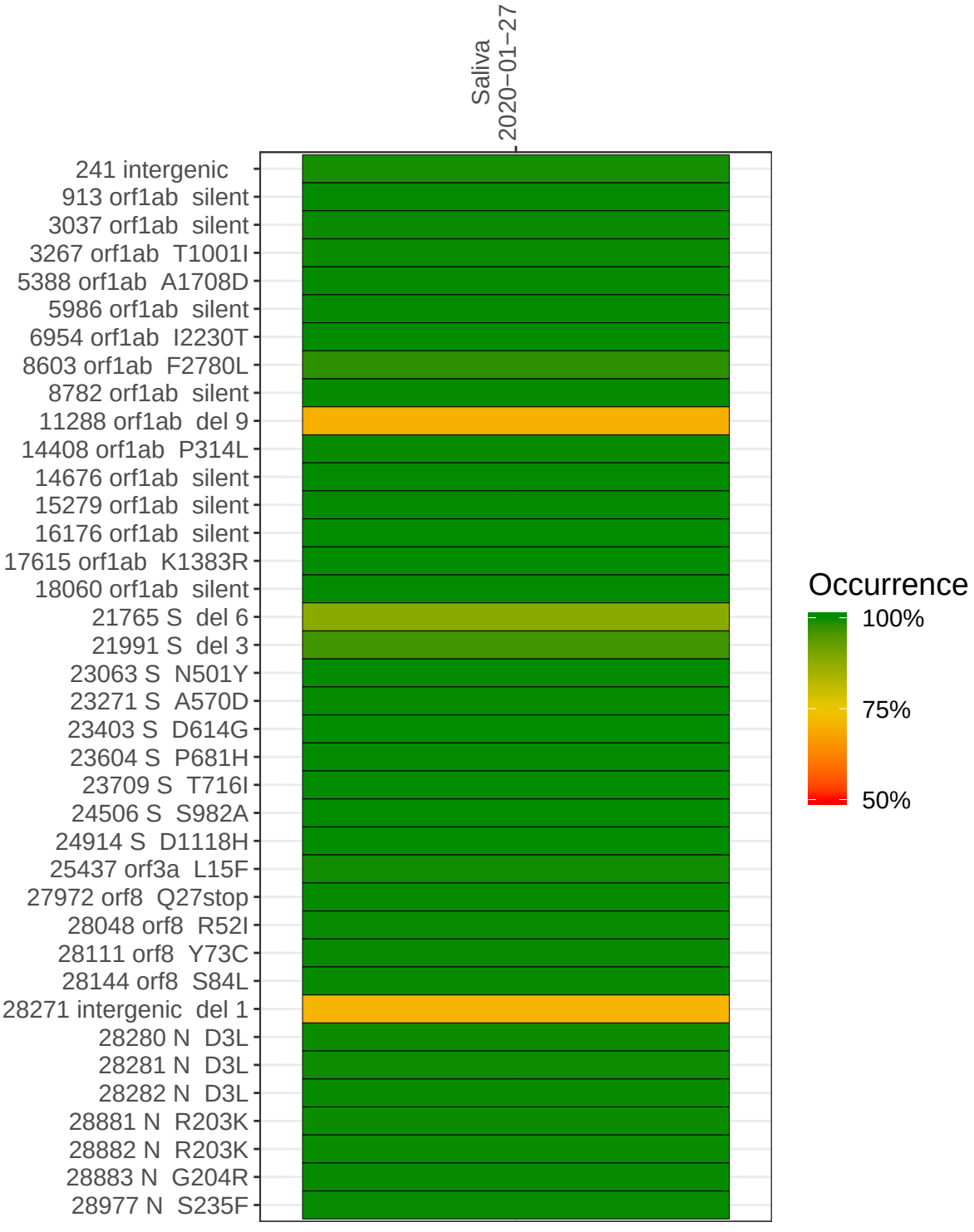
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

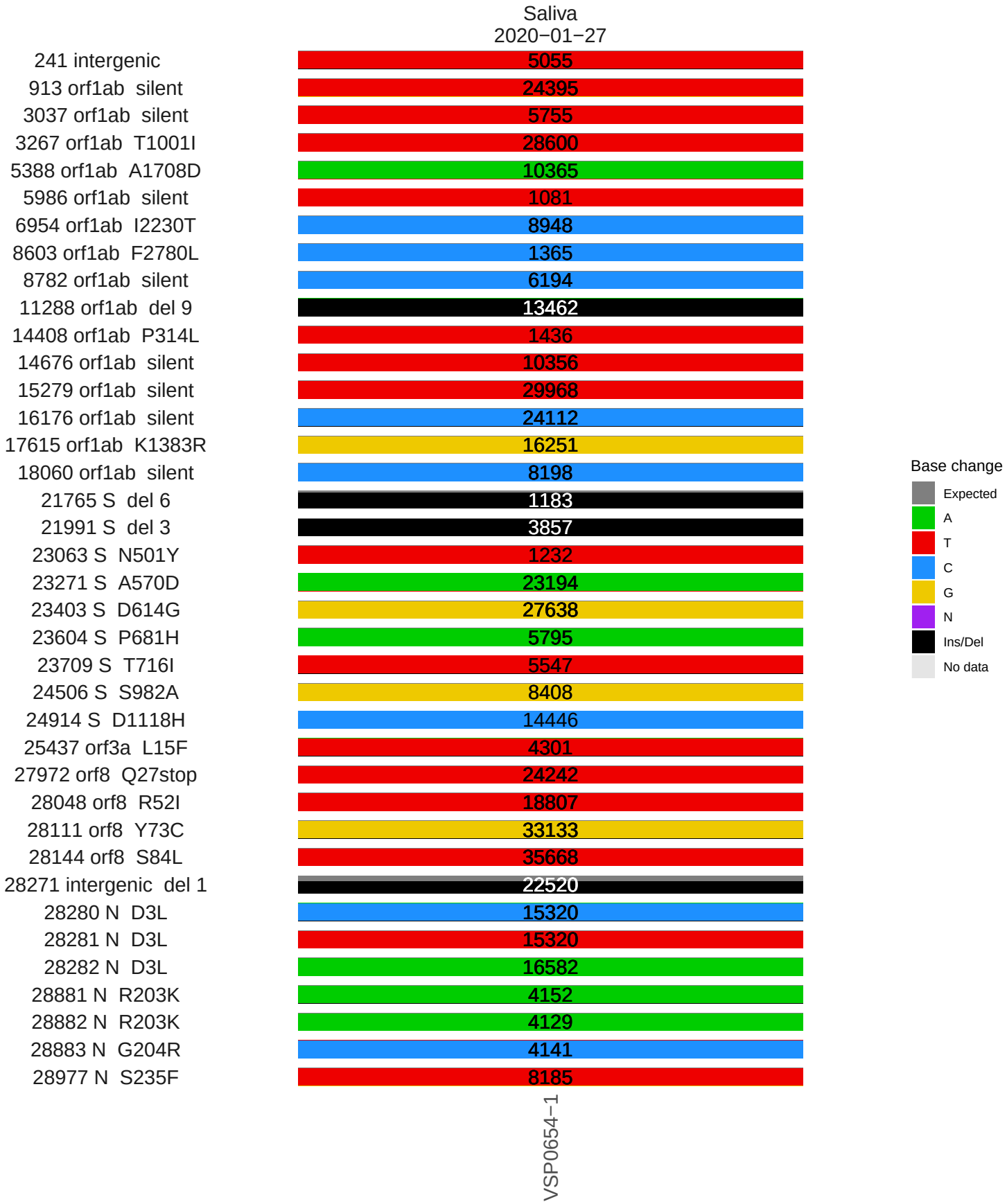
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0654-1	single experiment	NA	Saliva	2020-01-27	29.86	B.1.1.7	99.9%	99.9%

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.

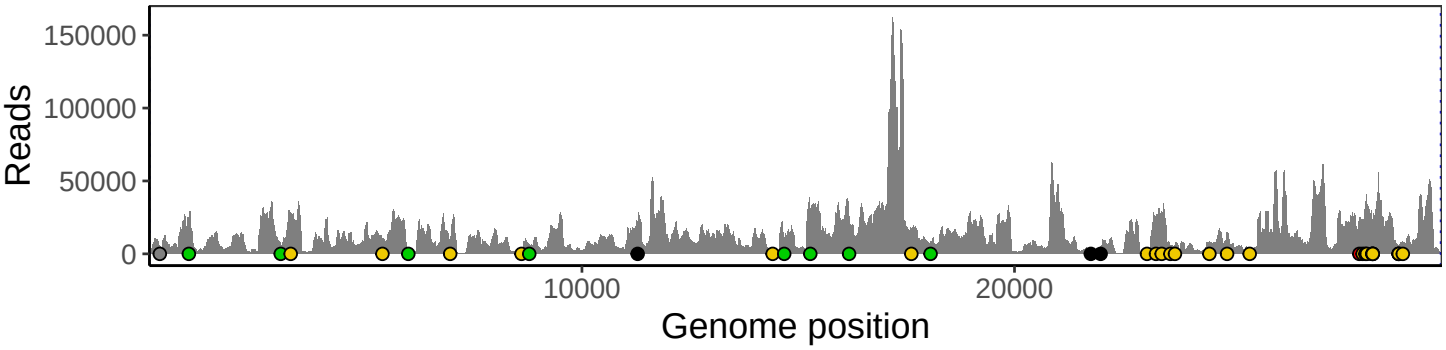



Saliva
2020−01−27
241 intergenic 5055
913 orf1ab silent 24395
3037 orf1ab silent 5755
3267 orf1ab T1001I 28600
5388 orf1ab A1708D 10365
5986 orf1ab silent 1081
6954 orf1ab I2230T 8948
8603 orf1ab F2780L 1365
8782 orf1ab silent 6194
11288 orf1ab del 9 13462
14408 orf1ab P314L 1436
14676 orf1ab silent 10356
15279 orf1ab silent 29968
16176 orf1ab silent 24112
17615 orf1ab K1383R 16251
18060 orf1ab silent 8198
21765 S del 6 1183
21991 S del 3 3857
23063 S N501Y 1232
23271 S A570D 23194
23403 S D614G 27638
23604 S P681H 5795
23709 S T716I 5547
24506 S S982A 8408
24914 S D1118H 14446
25437 orf3a L15F 4301
27972 orf8 Q27stop 24242
28048 orf8 R52I 18807
28111 orf8 Y73C 33133
28144 orf8 S84L 35668
28271 intergenic del 1 22520
28280 N D3L 15320
28281 N D3L 15320
28282 N D3L 16582
28881 N R203K 4152
28882 N R203K 4129
28883 N G204R 4141
28977 N S235F 8185
VSP0654−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

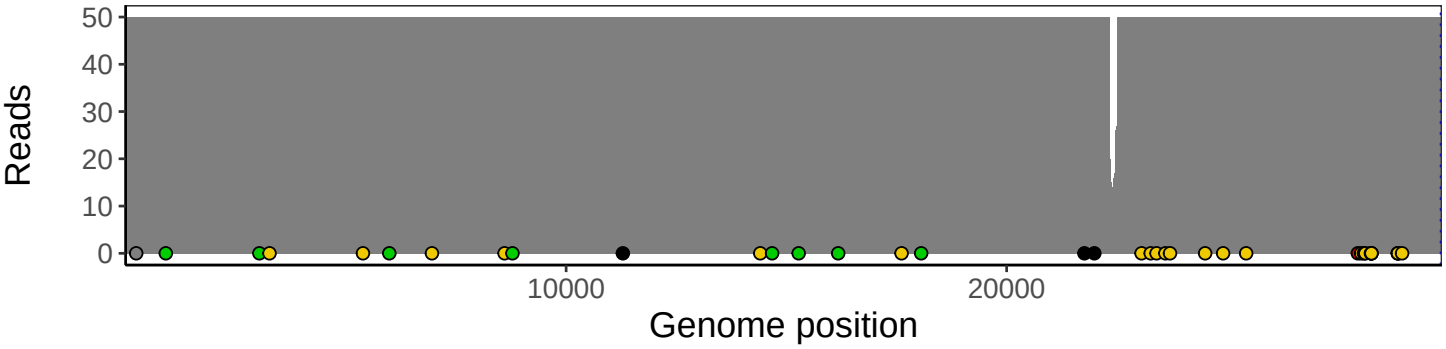
Analyses of individual experiments and composite results

VSP0654-1 | 2020-01-27 | Saliva | 459s | genomes | single experiment

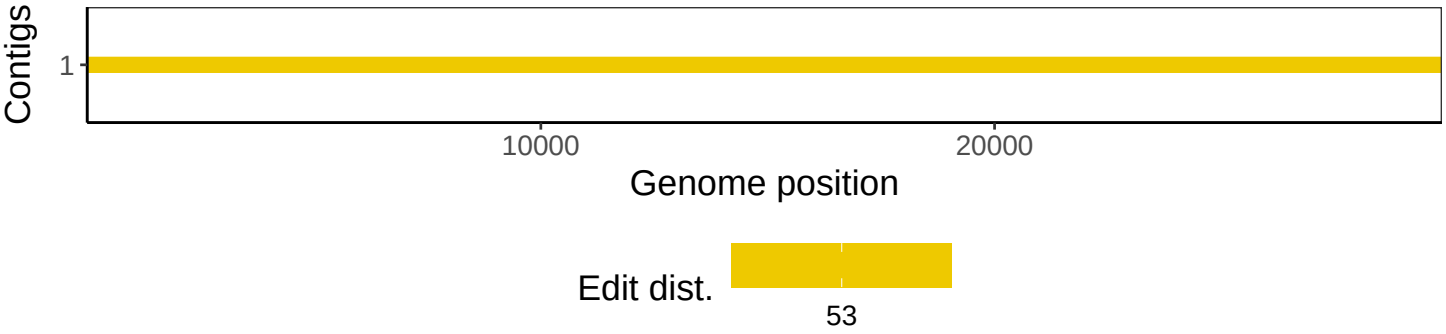
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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