COVID-19 subject HUP Q-0133

2021-06-23

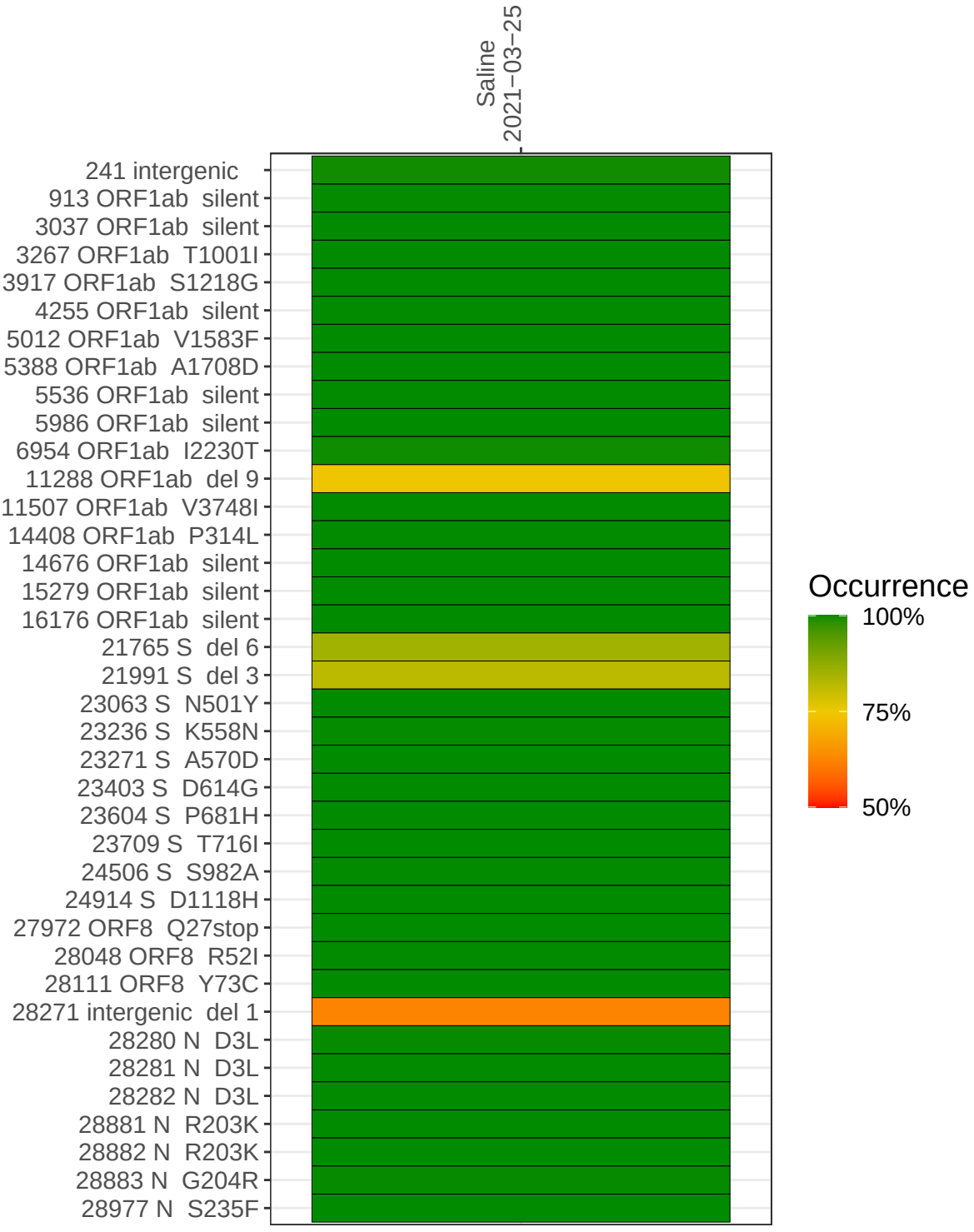
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

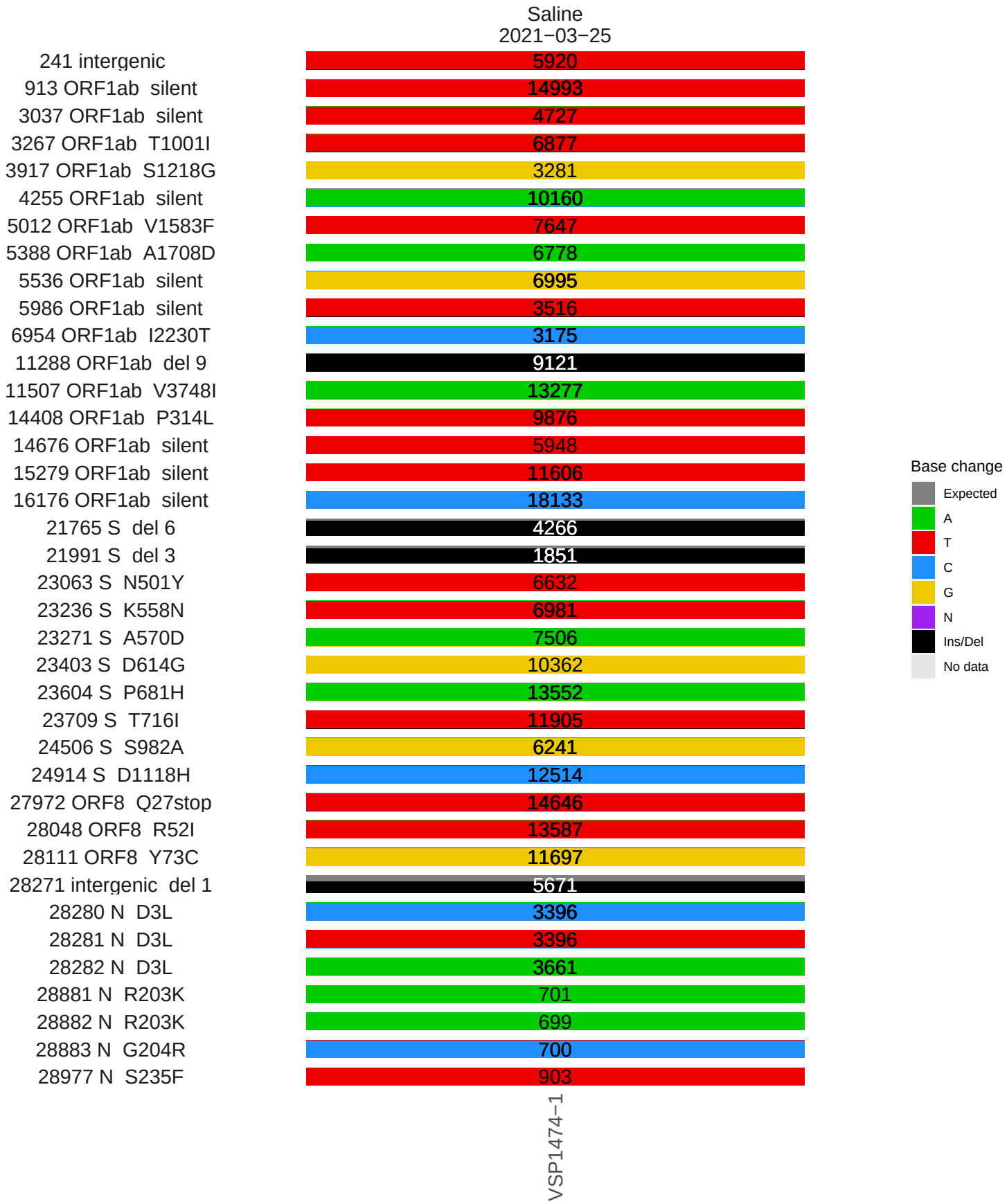
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1474-1	single experiment	NA	Saline	2021-03-25	29.87	B.1.1.7	100.0%	99.9%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

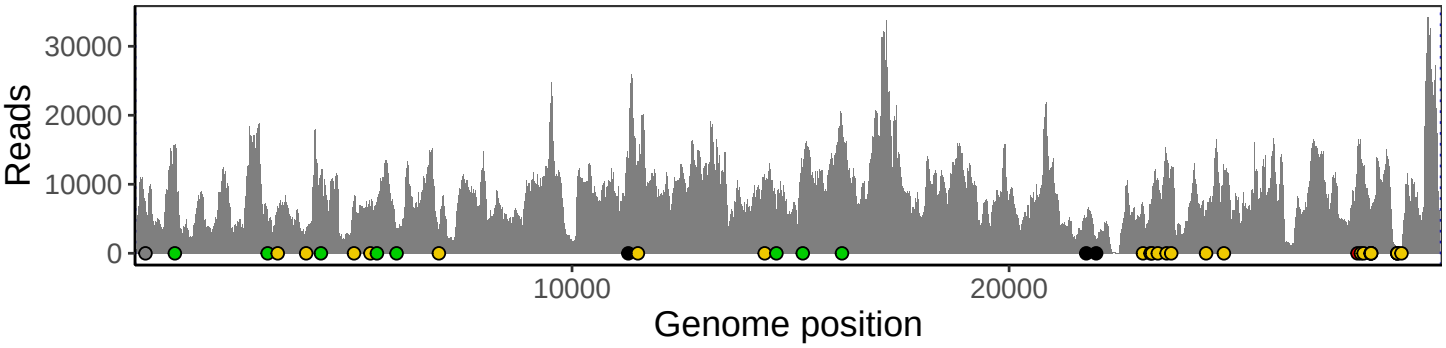



Saline
2021−03−25
241 intergenic 5920
913 ORF1ab silent 14993
3037 ORF1ab silent 4727
3267 ORF1ab T1001I 6877
3917 ORF1ab S1218G 3281
4255 ORF1ab silent 10160
5012 ORF1ab V1583F 7647
5388 ORF1ab A1708D 6778
5536 ORF1ab silent 6995
5986 ORF1ab silent 3516
6954 ORF1ab I2230T 3175
11288 ORF1ab del 9 9121
11507 ORF1ab V3748I 13277
14408 ORF1ab P314L 9876
14676 ORF1ab silent 5948
15279 ORF1ab silent 11606
16176 ORF1ab silent 18133
21765 S del 6 4266
21991 S del 3 1851
23063 S N501Y 6632
23236 S K558N 6981
23271 S A570D 7506
23403 S D614G 10362
23604 S P681H 13552
23709 S T716I 11905
24506 S S982A 6241
24914 S D1118H 12514
27972 ORF8 Q27stop 14646
28048 ORF8 R52I 13587
28111 ORF8 Y73C 11697
28271 intergenic del 1 5671
28280 N D3L 3396
28281 N D3L 3396
28282 N D3L 3661
28881 N R203K 701
28882 N R203K 699
28883 N G204R 700
28977 N S235F 903
VSP1474−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

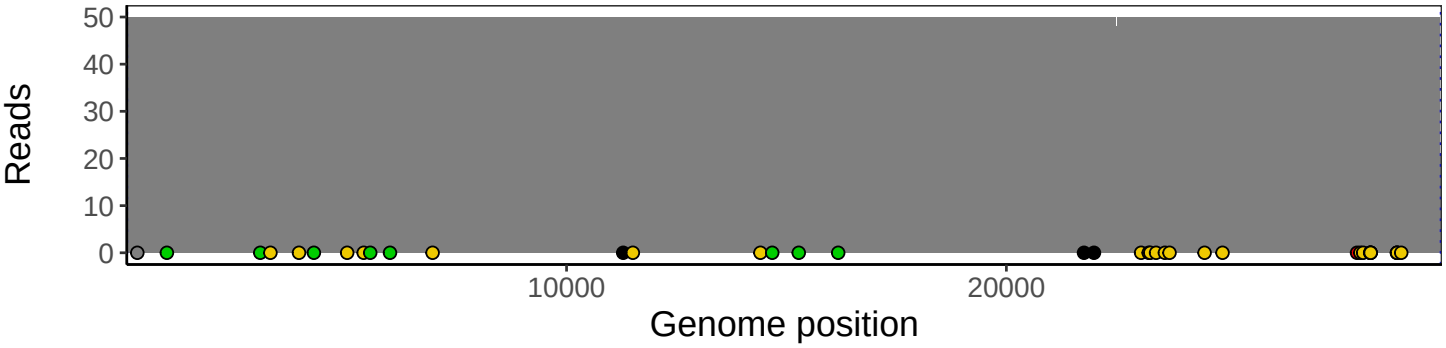
Analyses of individual experiments and composite results

VSP1474-1 | 2021-03-25 | Saline | HUP Q-0133 | genomes | single experiment

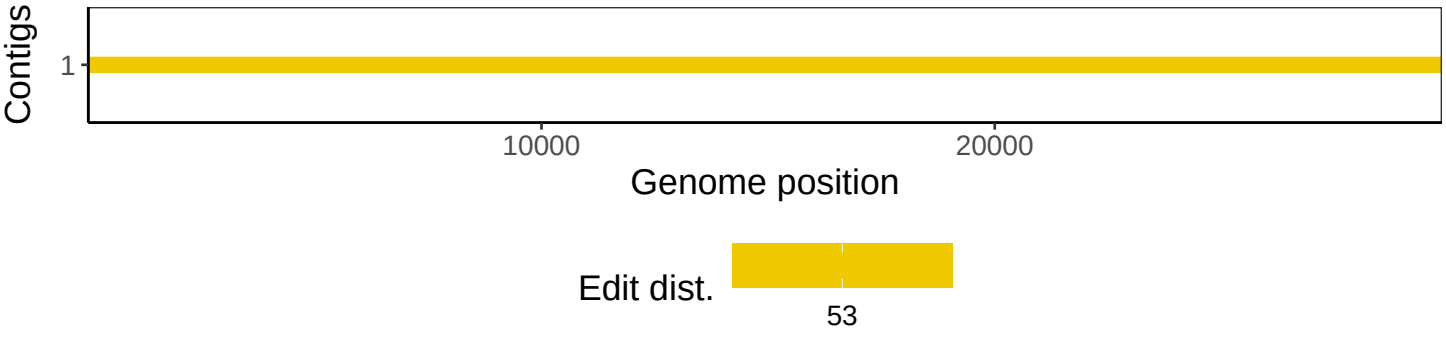
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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