COVID-19 subject HUP Q-0080

2021-04-17

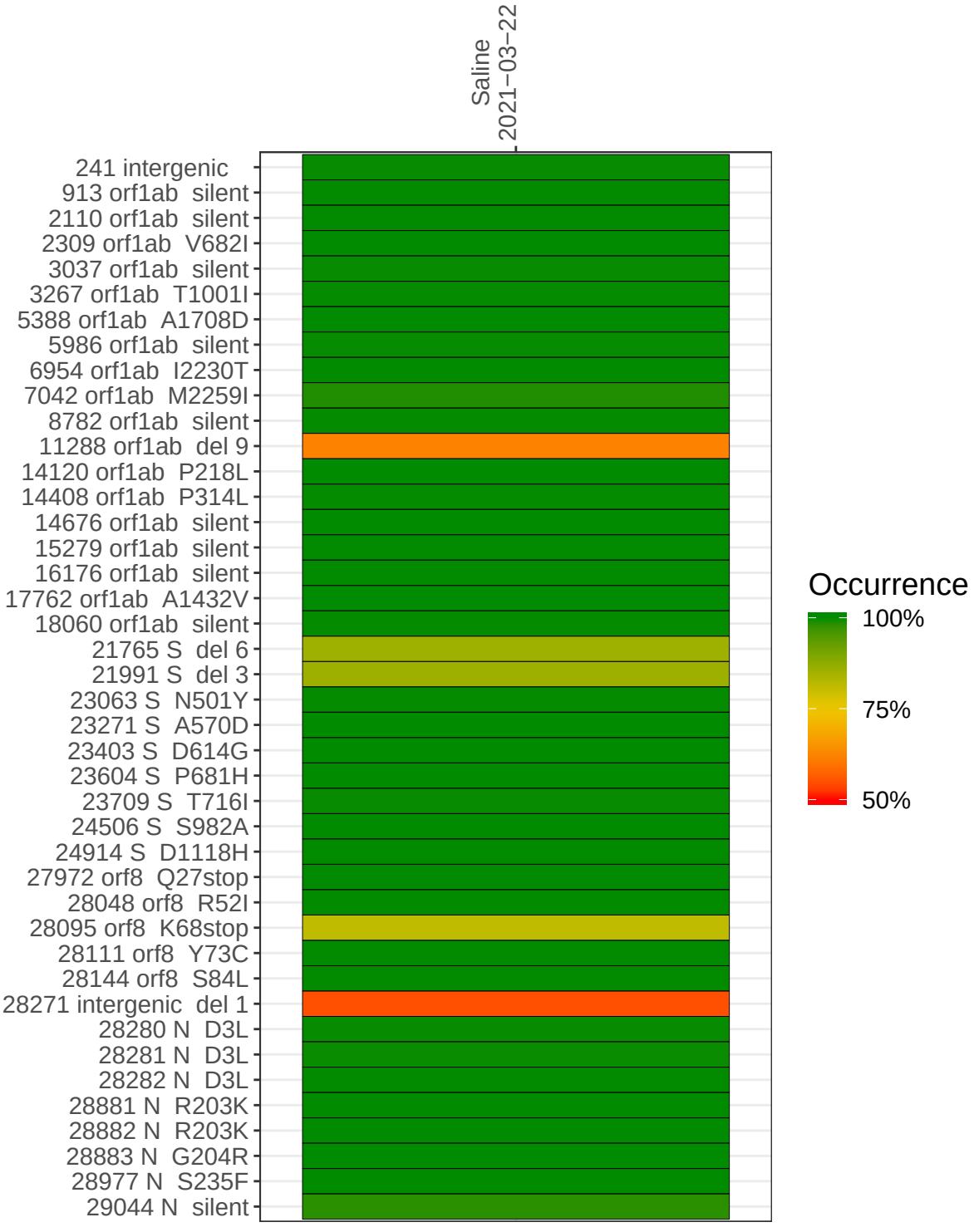
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

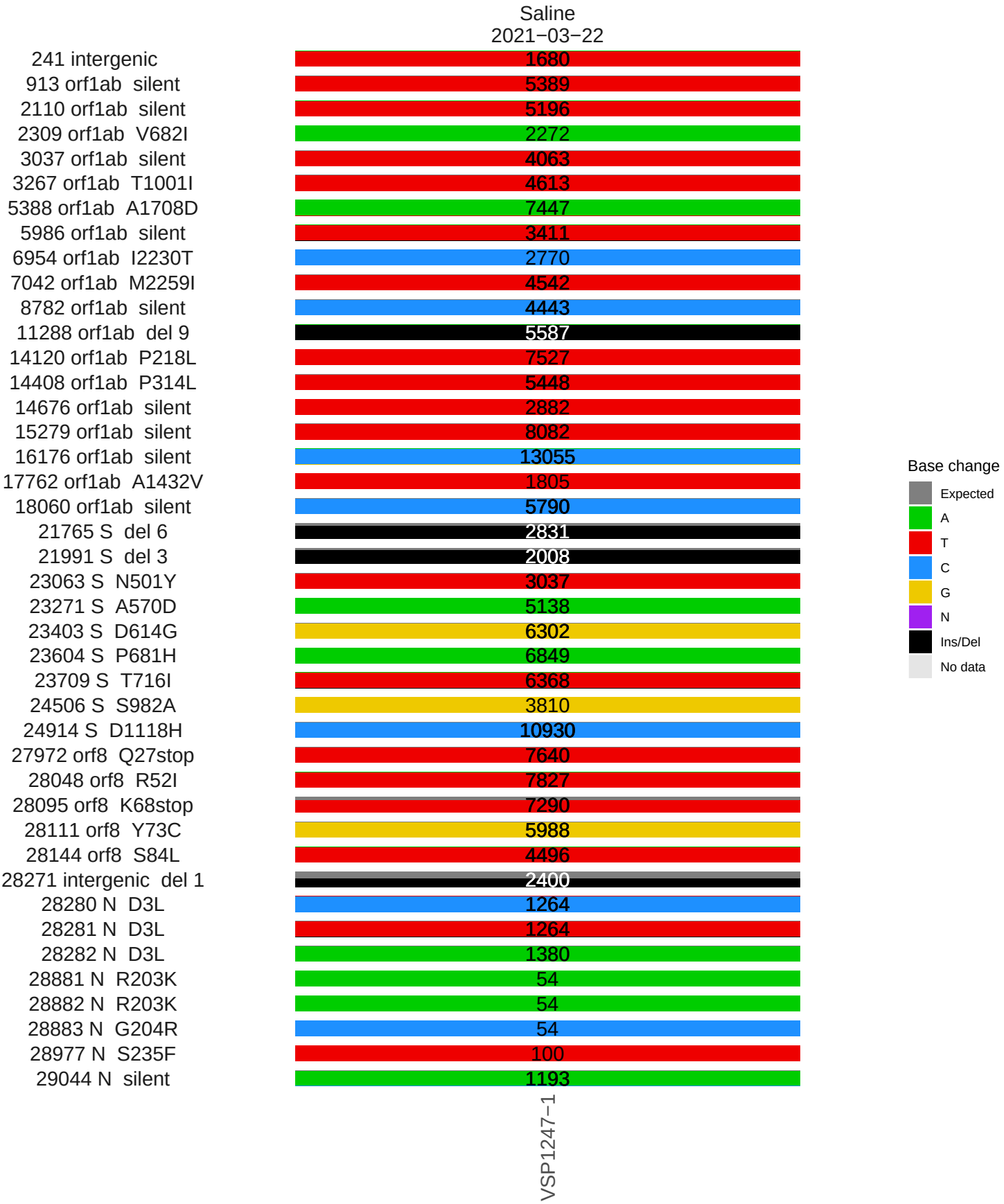
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1247-1	single experiment	NA	Saline	2021-03-22	29.85	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.

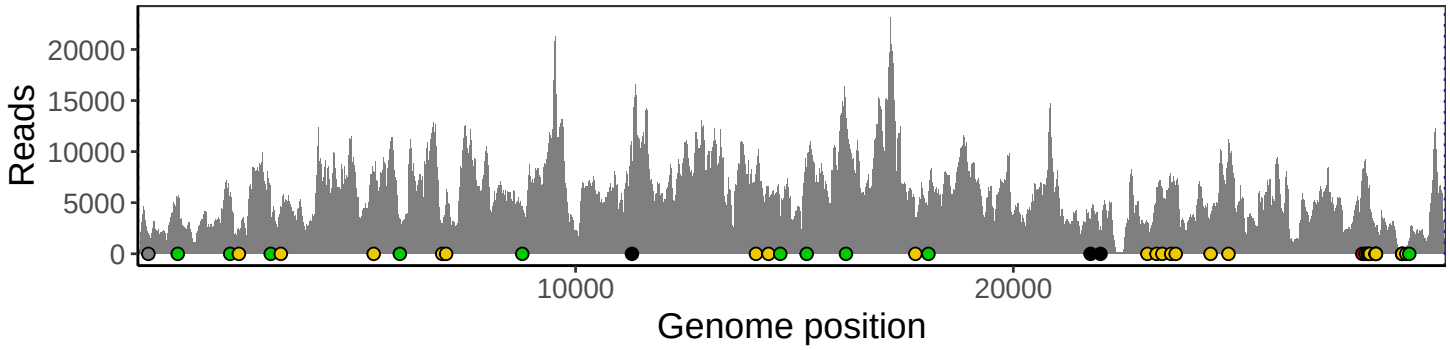



Saline
2021−03−22
241 intergenic 1680
913 orf1ab silent 5389
2110 orf1ab silent 5196
2309 orf1ab V682I 2272
3037 orf1ab silent 4063
3267 orf1ab T1001I 4613
5388 orf1ab A1708D 7447
5986 orf1ab silent 3411
6954 orf1ab I2230T 2770
7042 orf1ab M2259I 4542
8782 orf1ab silent 4443
11288 orf1ab del 9 5587
14120 orf1ab P218L 7527
14408 orf1ab P314L 5448
14676 orf1ab silent 2882
15279 orf1ab silent 8082
16176 orf1ab silent 13055
17762 orf1ab A1432V 1805
18060 orf1ab silent 5790
21765 S del 6 2831
21991 S del 3 2008
23063 S N501Y 3037
23271 S A570D 5138
23403 S D614G 6302
23604 S P681H 6849
23709 S T716I 6368
24506 S S982A 3810
24914 S D1118H 10930
27972 orf8 Q27stop 7640
28048 orf8 R52I 7827
28095 orf8 K68stop 7290
28111 orf8 Y73C 5988
28144 orf8 S84L 4496
28271 intergenic del 1 2400
28280 N D3L 1264
28281 N D3L 1264
28282 N D3L 1380
28881 N R203K 54
28882 N R203K 54
28883 N G204R 54
28977 N S235F 100
29044 N silent 1193
VSP1247−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

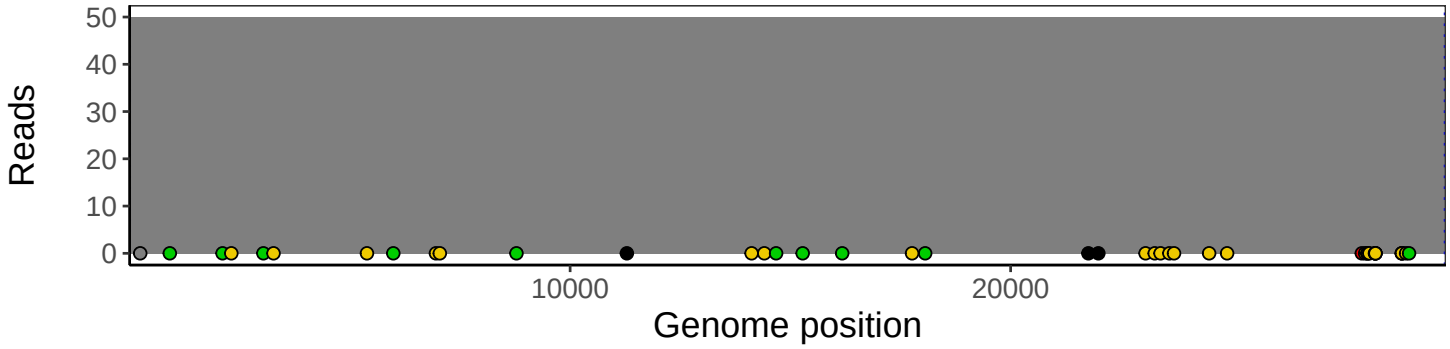
Analyses of individual experiments and composite results

VSP1247-1 | 2021-03-22 | Saline | HUP Q-0080 | genomes | single experiment

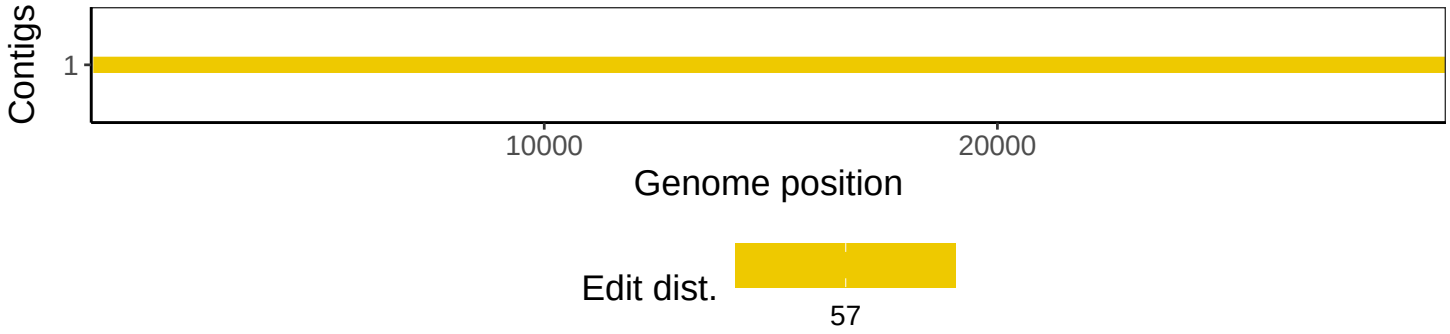
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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