COVID-19 subject HUP Q-0083

2021-04-17

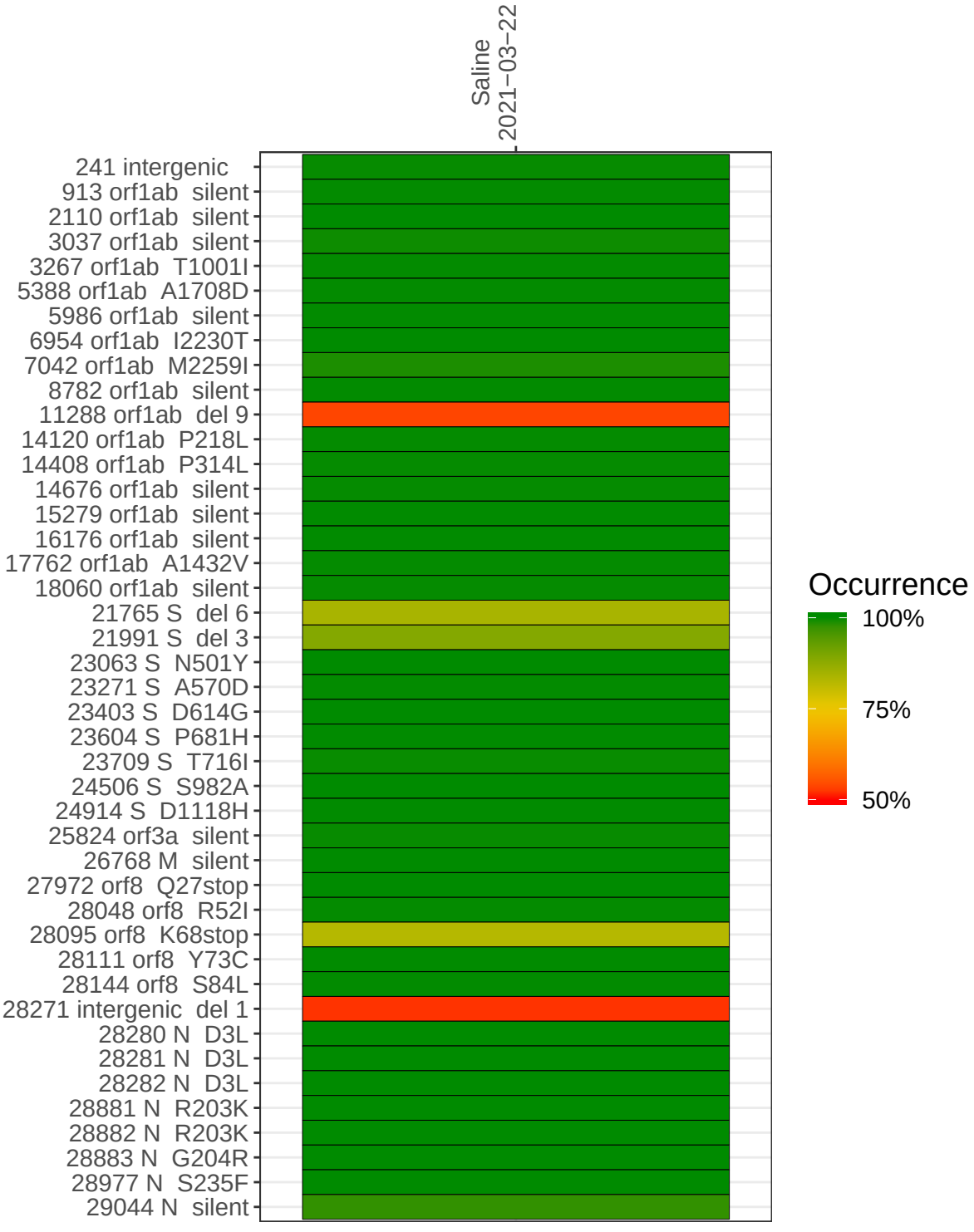
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

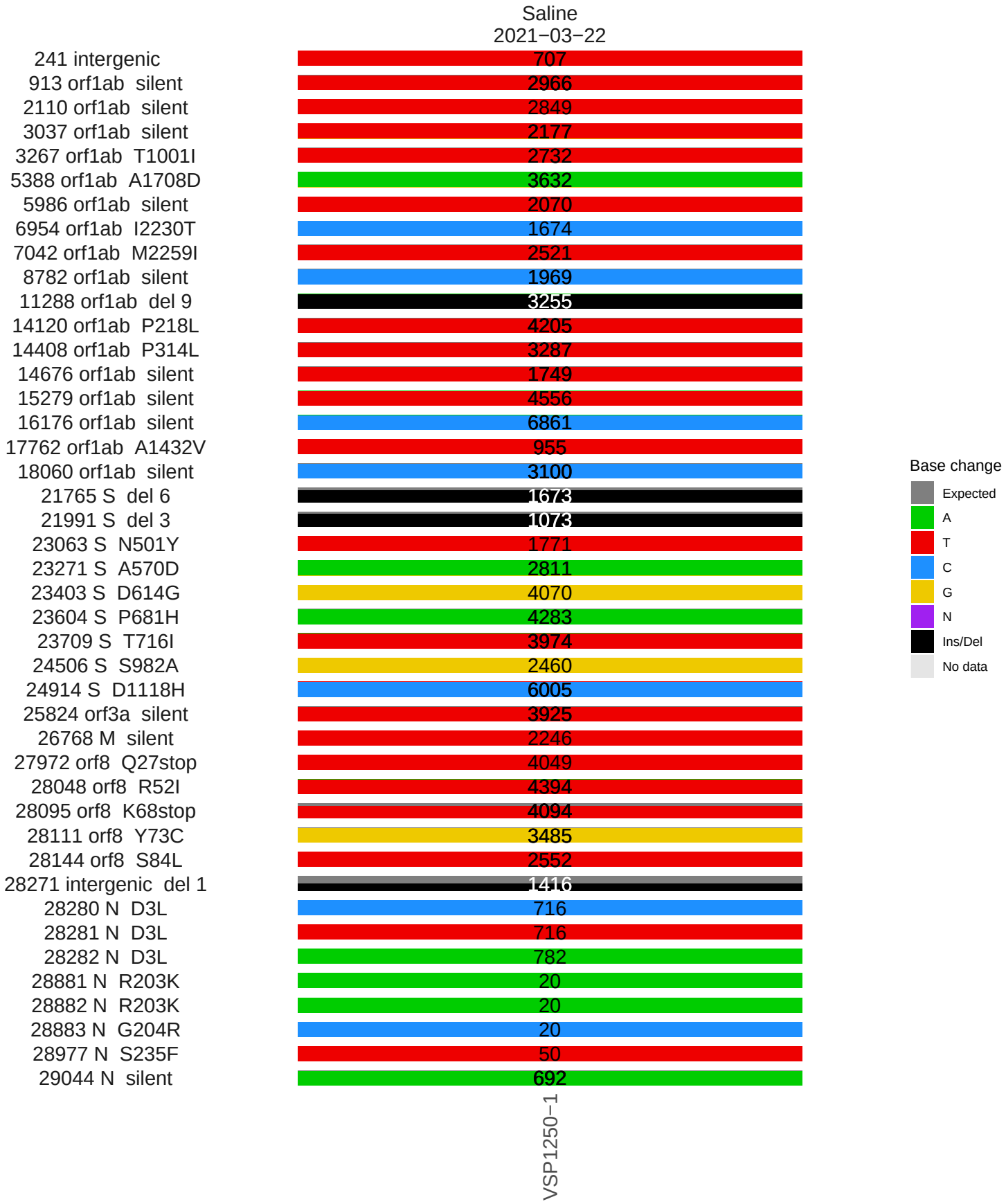
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1250-1	single experiment	NA	Saline	2021-03-22	29.86	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.

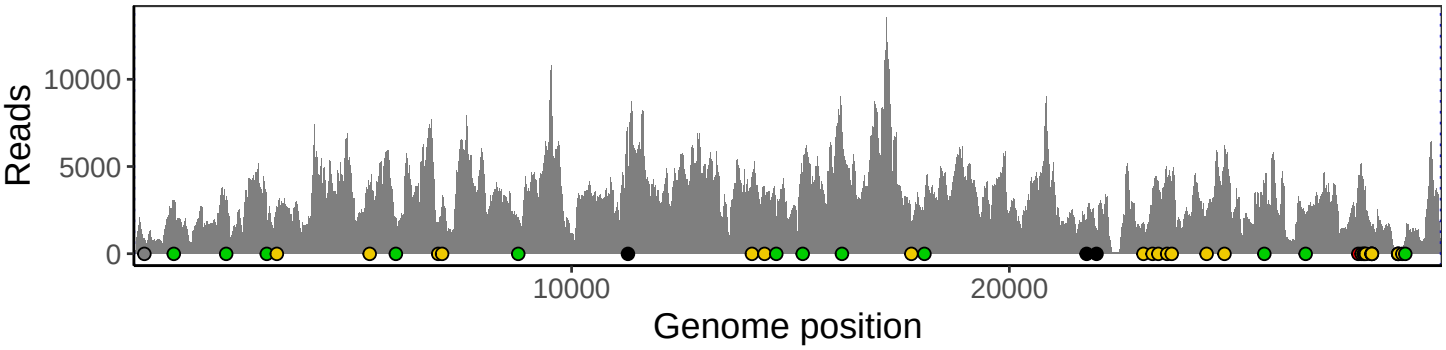



Saline
2021−03−22
241 intergenic 707
913 orf1ab silent 2966
2110 orf1ab silent 2849
3037 orf1ab silent 2177
3267 orf1ab T1001I 2732
5388 orf1ab A1708D 3632
5986 orf1ab silent 2070
6954 orf1ab I2230T 1674
7042 orf1ab M2259I 2521
8782 orf1ab silent 1969
11288 orf1ab del 9 3255
14120 orf1ab P218L 4205
14408 orf1ab P314L 3287
14676 orf1ab silent 1749
15279 orf1ab silent 4556
16176 orf1ab silent 6861
17762 orf1ab A1432V 955
18060 orf1ab silent 3100
21765 S del 6 1673
21991 S del 3 1073
23063 S N501Y 1771
23271 S A570D 2811
23403 S D614G 4070
23604 S P681H 4283
23709 S T716I 3974
24506 S S982A 2460
24914 S D1118H 6005
25824 orf3a silent 3925
26768 M silent 2246
27972 orf8 Q27stop 4049
28048 orf8 R52I 4394
28095 orf8 K68stop 4094
28111 orf8 Y73C 3485
28144 orf8 S84L 2552
28271 intergenic del 1 1416
28280 N D3L 716
28281 N D3L 716
28282 N D3L 782
28881 N R203K 20
28882 N R203K 20
28883 N G204R 20
28977 N S235F 50
29044 N silent 692
VSP1250−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

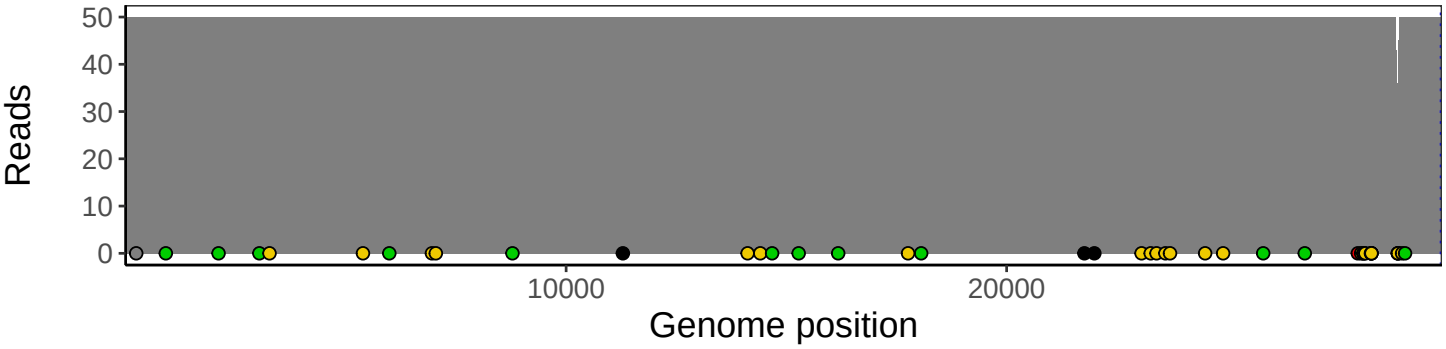
Analyses of individual experiments and composite results

VSP1250-1 | 2021-03-22 | Saline | HUP Q-0083 | genomes | single experiment

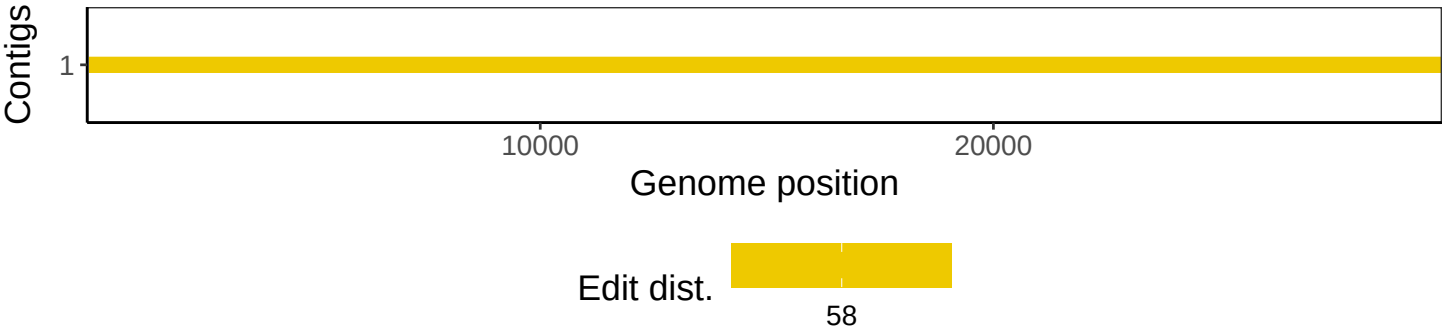
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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