COVID-19 subject HUP Q-0065

2021-04-17

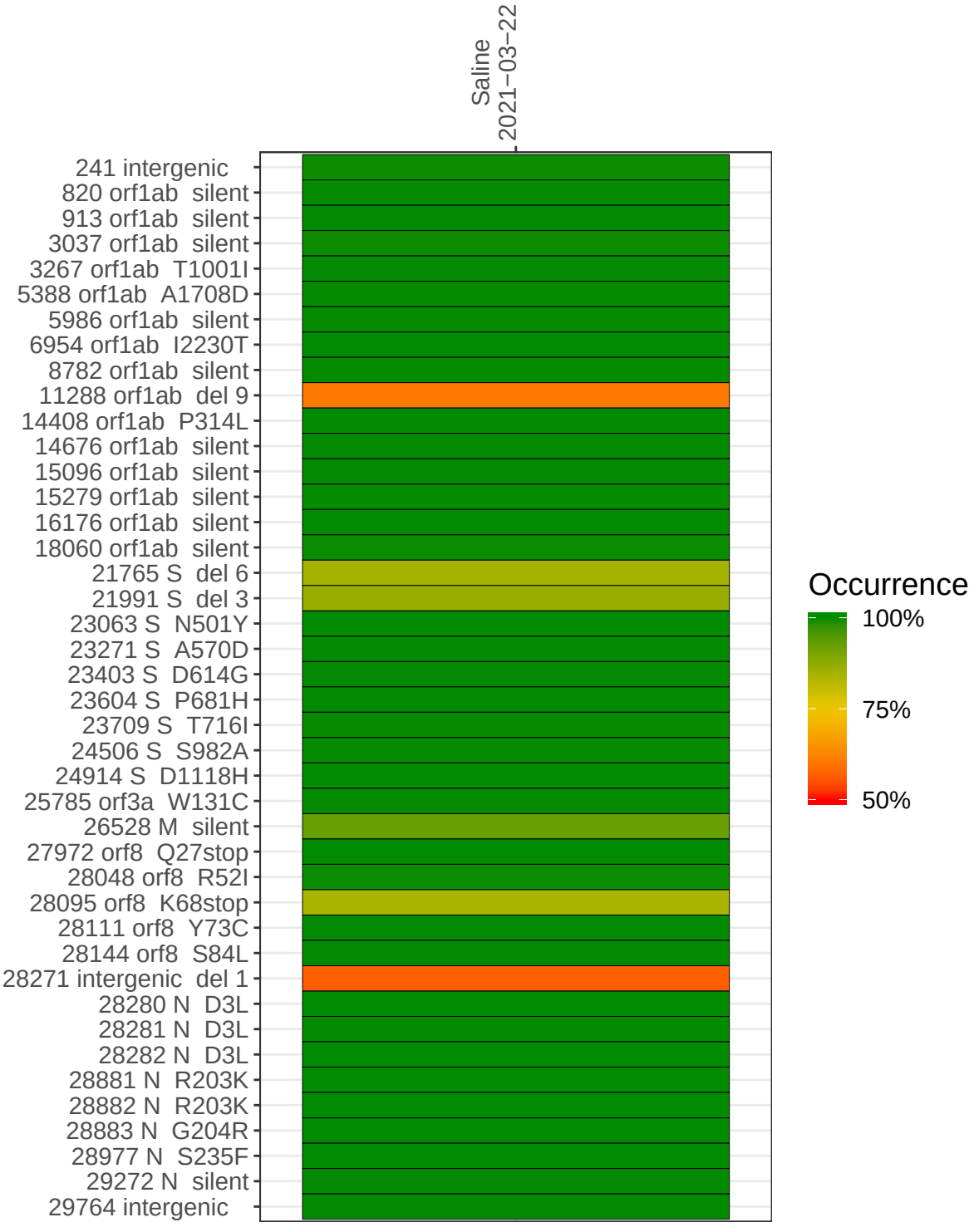
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

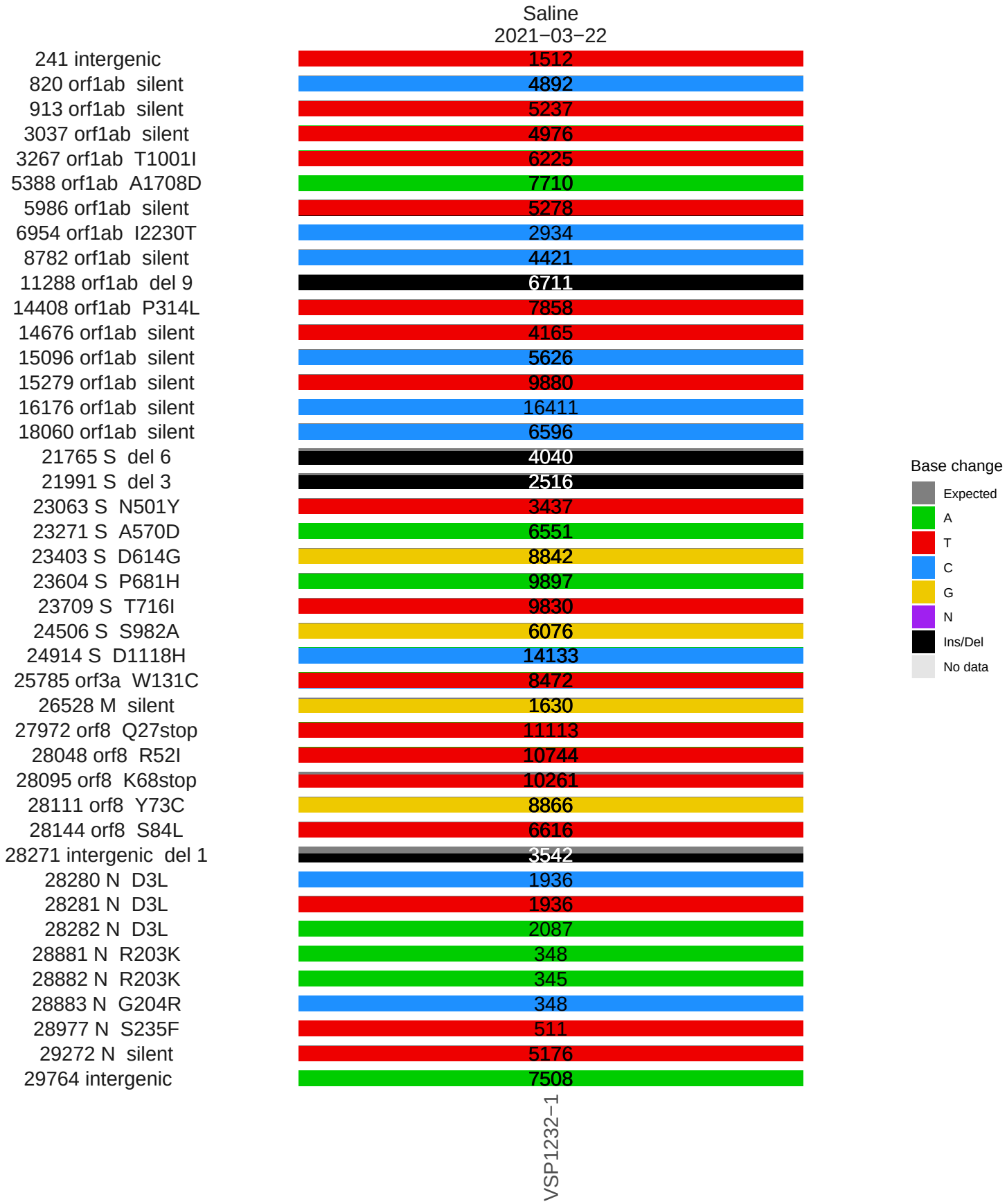
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1232-1	single experiment	NA	Saline	2021-03-22	29.86	B.1.1.7	99.9%	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.

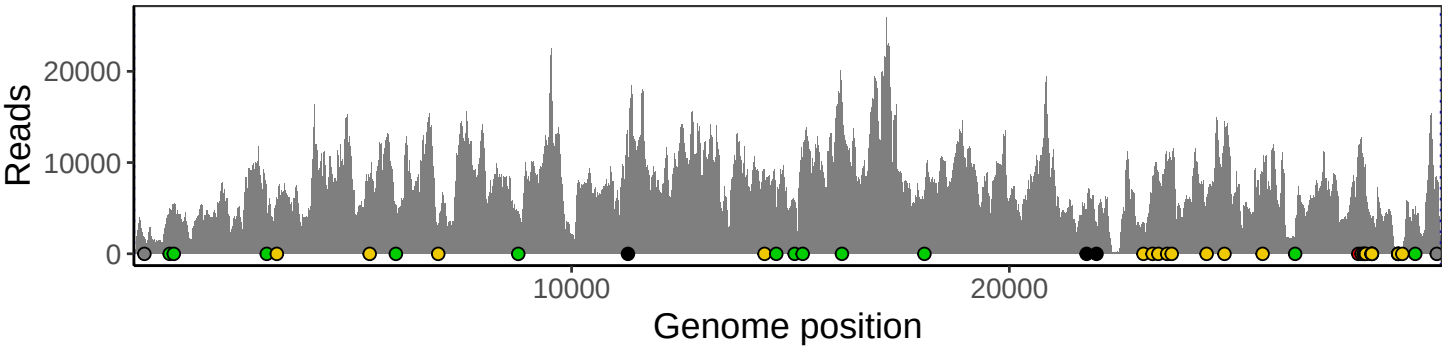



Saline
2021−03−22
241 intergenic 1512
820 orf1ab silent 4892
913 orf1ab silent 5237
3037 orf1ab silent 4976
3267 orf1ab T1001I 6225
5388 orf1ab A1708D 7710
5986 orf1ab silent 5278
6954 orf1ab I2230T 2934
8782 orf1ab silent 4421
11288 orf1ab del 9 6711
14408 orf1ab P314L 7858
14676 orf1ab silent 4165
15096 orf1ab silent 5626
15279 orf1ab silent 9880
16176 orf1ab silent 16411
18060 orf1ab silent 6596
21765 S del 6 4040
21991 S del 3 2516
23063 S N501Y 3437
23271 S A570D 6551
23403 S D614G 8842
23604 S P681H 9897
23709 S T716I 9830
24506 S S982A 6076
24914 S D1118H 14133
25785 orf3a W131C 8472
26528 M silent 1630
27972 orf8 Q27stop 11113
28048 orf8 R52I 10744
28095 orf8 K68stop 10261
28111 orf8 Y73C 8866
28144 orf8 S84L 6616
28271 intergenic del 1 3542
28280 N D3L 1936
28281 N D3L 1936
28282 N D3L 2087
28881 N R203K 348
28882 N R203K 345
28883 N G204R 348
28977 N S235F 511
29272 N silent 5176
29764 intergenic 7508
VSP1232−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

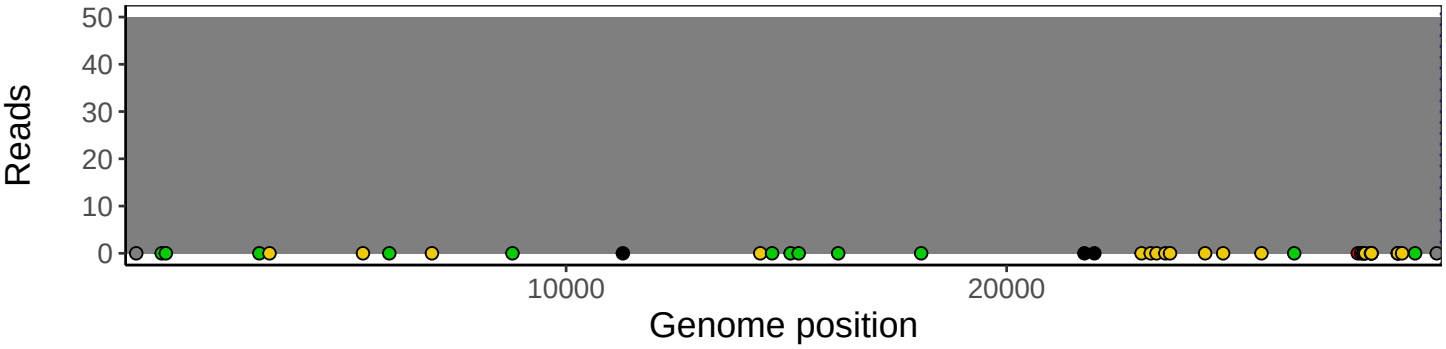
Analyses of individual experiments and composite results

VSP1232-1 | 2021-03-22 | Saline | HUP Q-0065 | genomes | single experiment

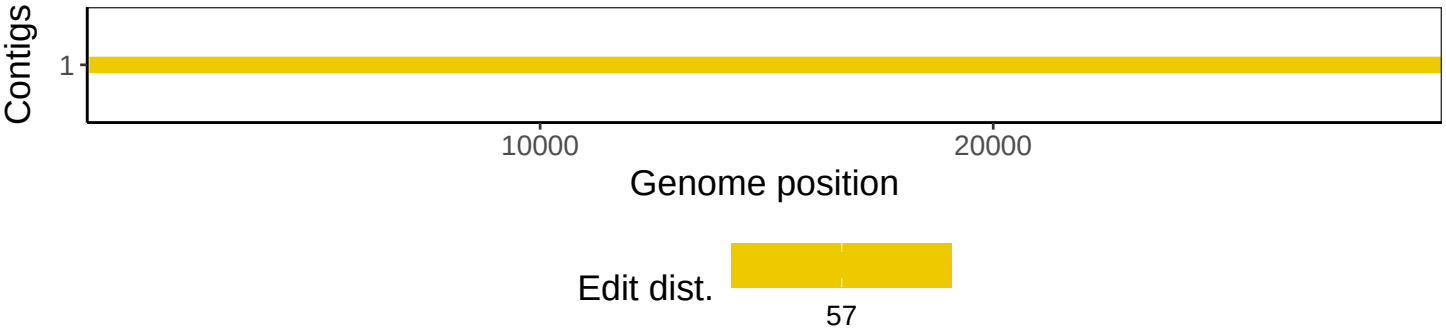
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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