COVID-19 subject HUP Q-0057

2021-04-17

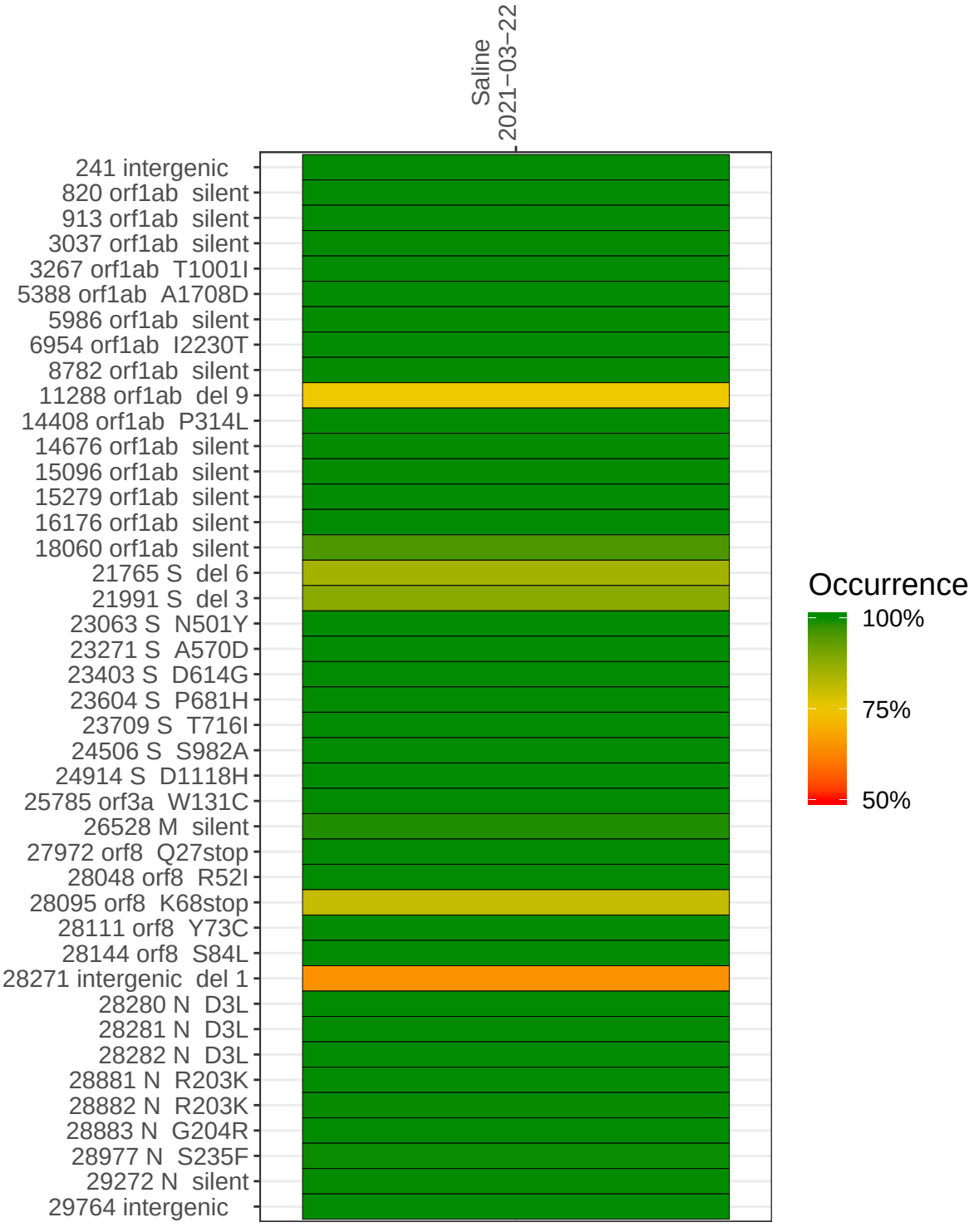
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

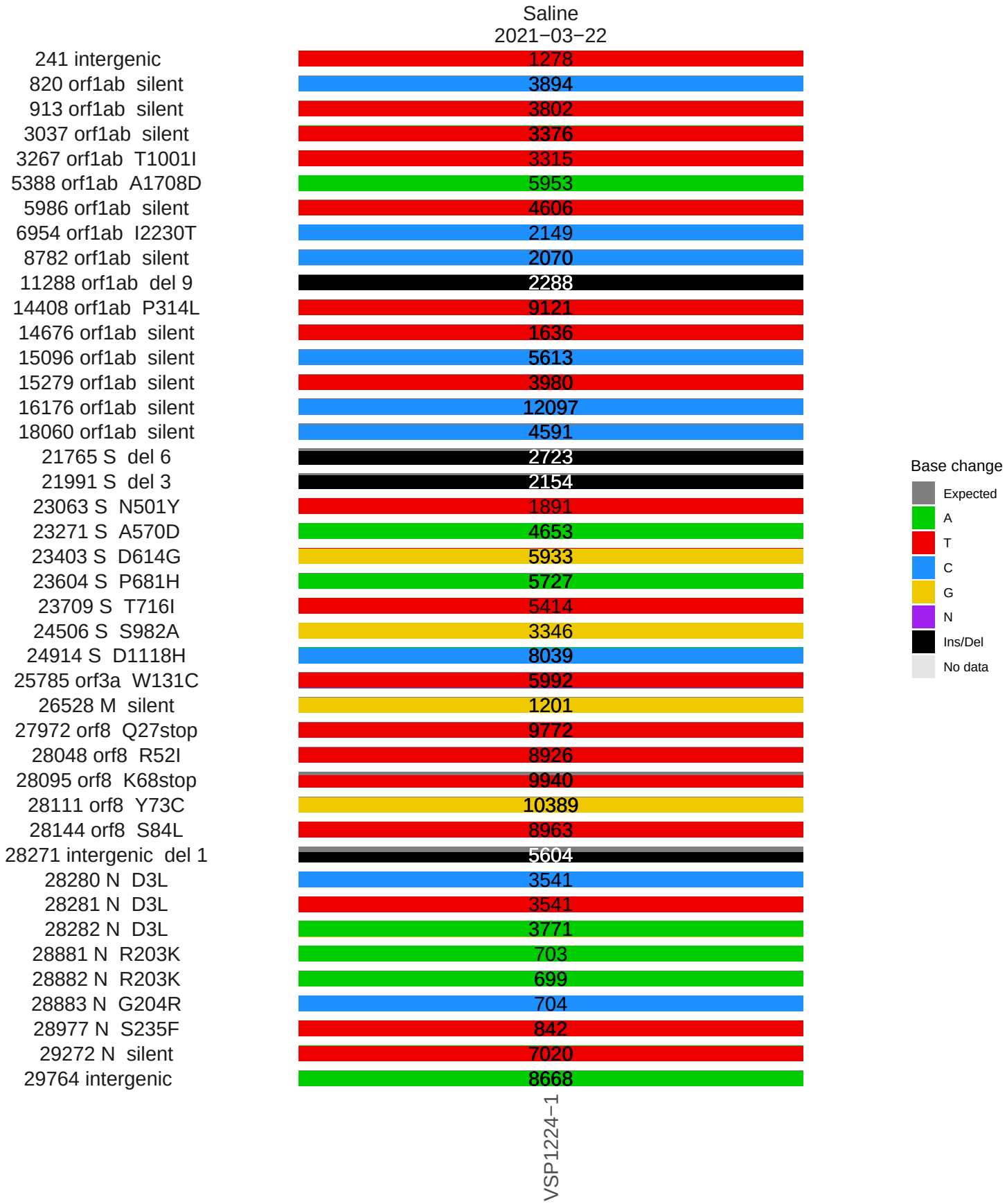
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1224-1	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.

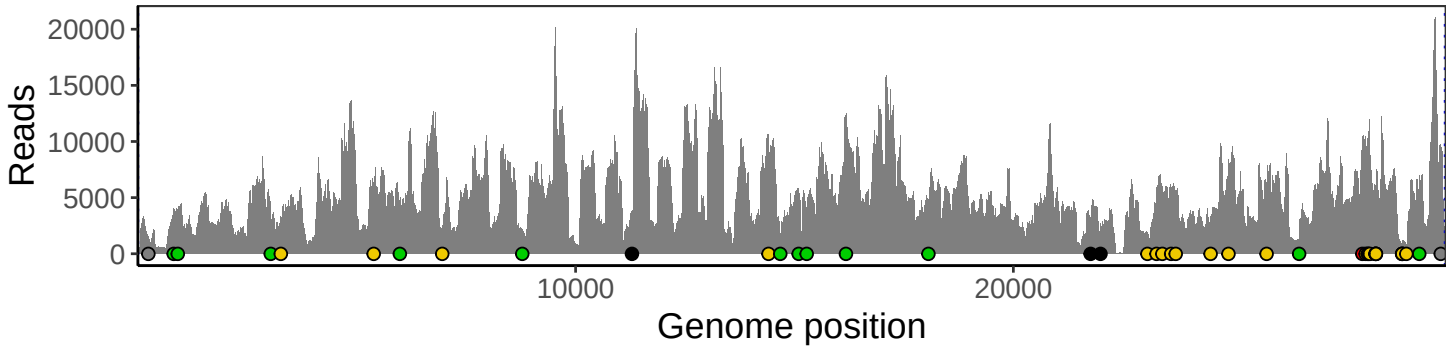



Saline
2021−03−22
241 intergenic 1278
820 orf1ab silent 3894
913 orf1ab silent 3802
3037 orf1ab silent 3376
3267 orf1ab T1001I 3315
5388 orf1ab A1708D 5953
5986 orf1ab silent 4606
6954 orf1ab I2230T 2149
8782 orf1ab silent 2070
11288 orf1ab del 9 2288
14408 orf1ab P314L 9121
14676 orf1ab silent 1636
15096 orf1ab silent 5613
15279 orf1ab silent 3980
16176 orf1ab silent 12097
18060 orf1ab silent 4591
21765 S del 6 2723
21991 S del 3 2154
23063 S N501Y 1891
23271 S A570D 4653
23403 S D614G 5933
23604 S P681H 5727
23709 S T716I 5414
24506 S S982A 3346
24914 S D1118H 8039
25785 orf3a W131C 5992
26528 M silent 1201
27972 orf8 Q27stop 9772
28048 orf8 R52I 8926
28095 orf8 K68stop 9940
28111 orf8 Y73C 10389
28144 orf8 S84L 8963
28271 intergenic del 1 5604
28280 N D3L 3541
28281 N D3L 3541
28282 N D3L 3771
28881 N R203K 703
28882 N R203K 699
28883 N G204R 704
28977 N S235F 842
29272 N silent 7020
29764 intergenic 8668
VSP1224−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

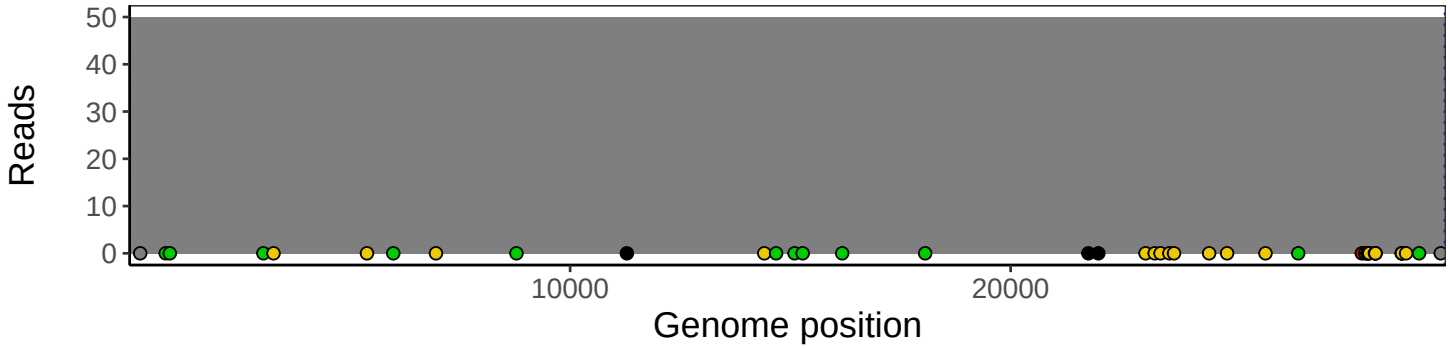
Analyses of individual experiments and composite results

VSP1224-1 | 2021-03-22 | Saline | HUP Q-0057 | genomes | single experiment

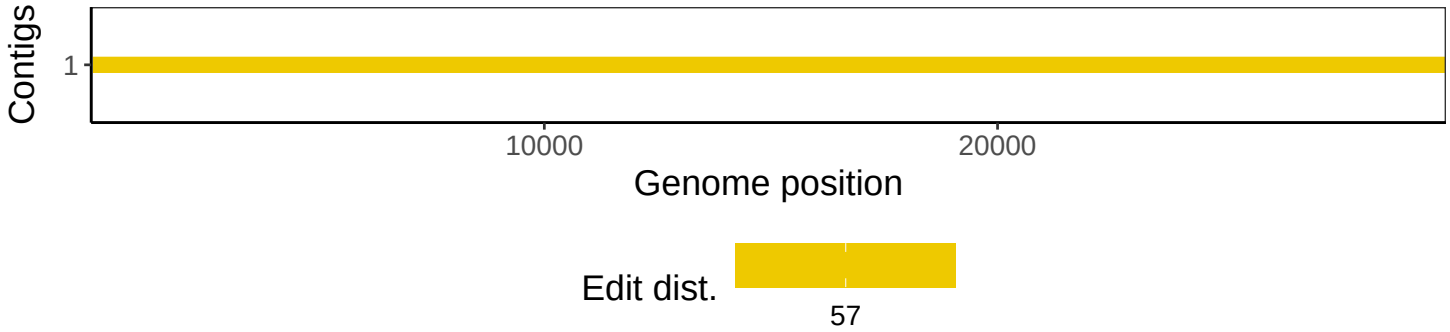
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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