COVID-19 subject HUP Q-0101

2021-04-17

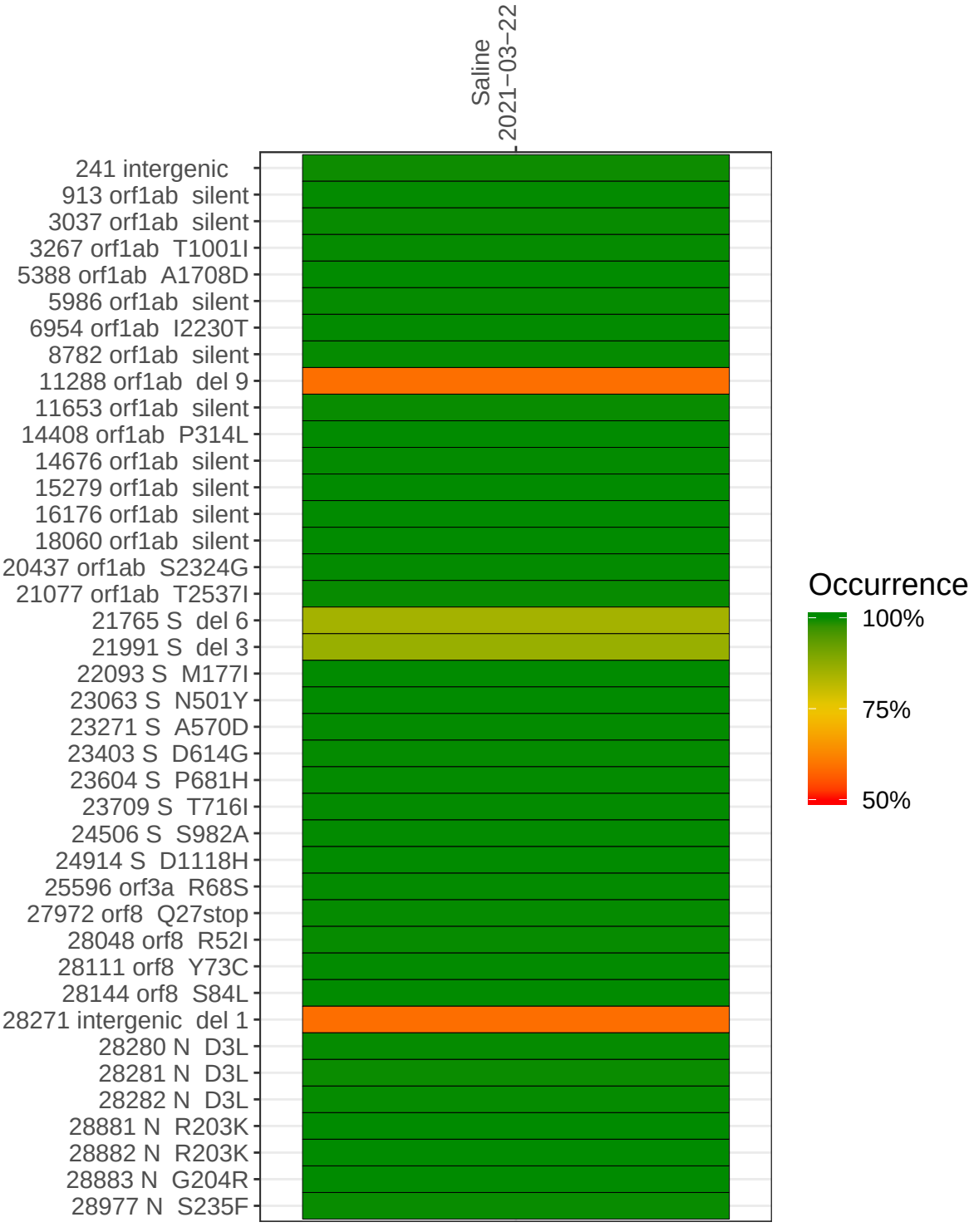
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

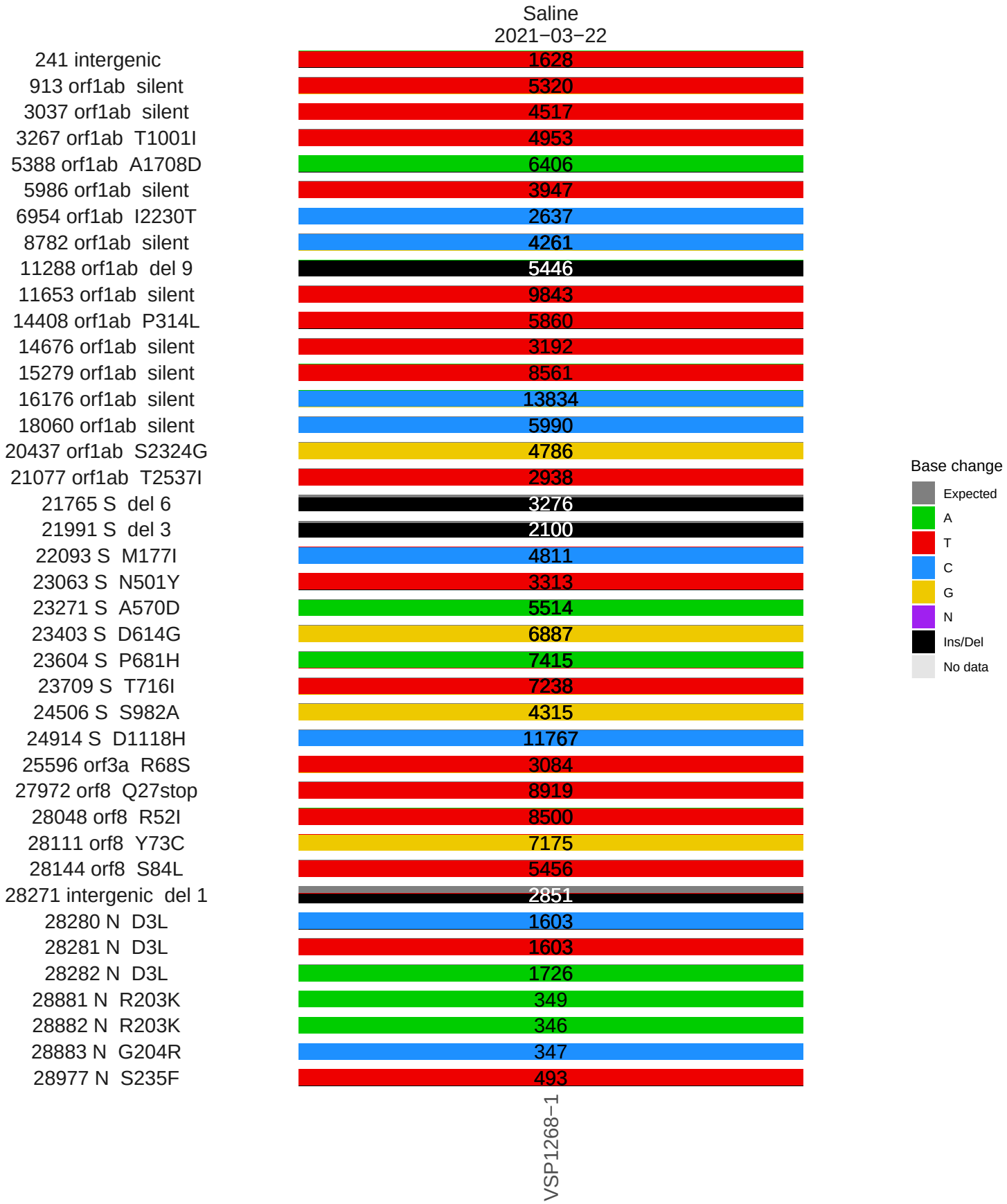
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1268-1	single experiment	NA	Saline	2021-03-22	29.92	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.

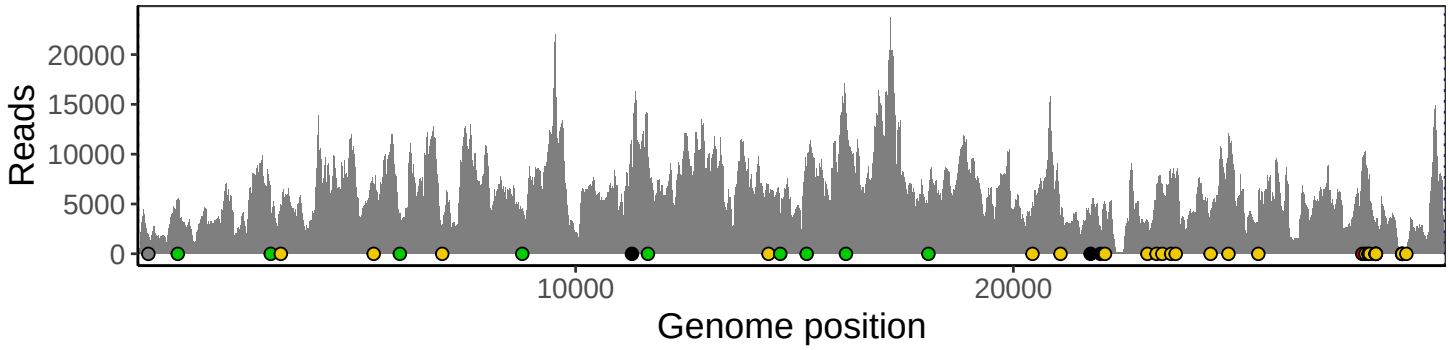



Saline
2021−03−22
241 intergenic 1628
913 orf1ab silent 5320
3037 orf1ab silent 4517
3267 orf1ab T1001I 4953
5388 orf1ab A1708D 6406
5986 orf1ab silent 3947
6954 orf1ab I2230T 2637
8782 orf1ab silent 4261
11288 orf1ab del 9 5446
11653 orf1ab silent 9843
14408 orf1ab P314L 5860
14676 orf1ab silent 3192
15279 orf1ab silent 8561
16176 orf1ab silent 13834
18060 orf1ab silent 5990
20437 orf1ab S2324G 4786
21077 orf1ab T2537I 2938
21765 S del 6 3276
21991 S del 3 2100
22093 S M177I 4811
23063 S N501Y 3313
23271 S A570D 5514
23403 S D614G 6887
23604 S P681H 7415
23709 S T716I 7238
24506 S S982A 4315
24914 S D1118H 11767
25596 orf3a R68S 3084
27972 orf8 Q27stop 8919
28048 orf8 R52I 8500
28111 orf8 Y73C 7175
28144 orf8 S84L 5456
28271 intergenic del 1 2851
28280 N D3L 1603
28281 N D3L 1603
28282 N D3L 1726
28881 N R203K 349
28882 N R203K 346
28883 N G204R 347
28977 N S235F 493
VSP1268−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

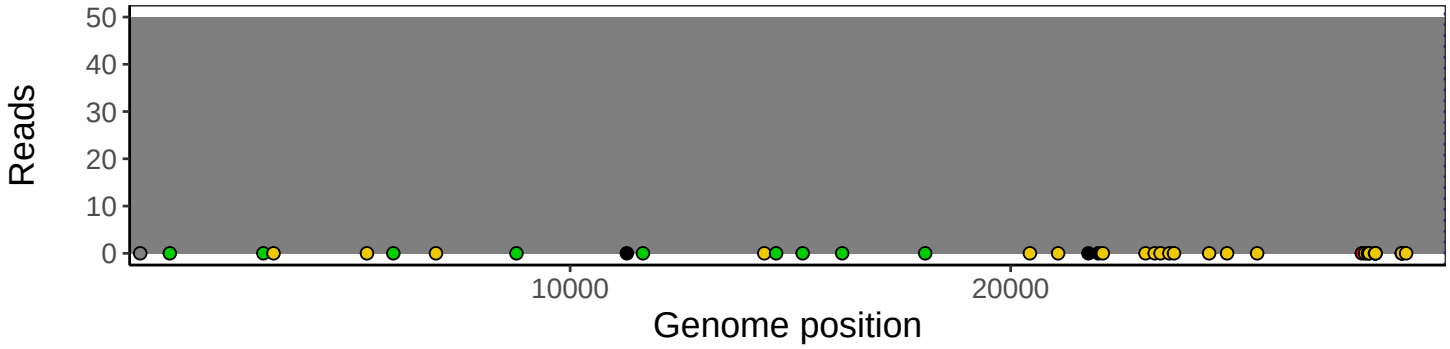
Analyses of individual experiments and composite results

VSP1268-1 | 2021-03-22 | Saline | HUP Q-0101 | genomes | single experiment

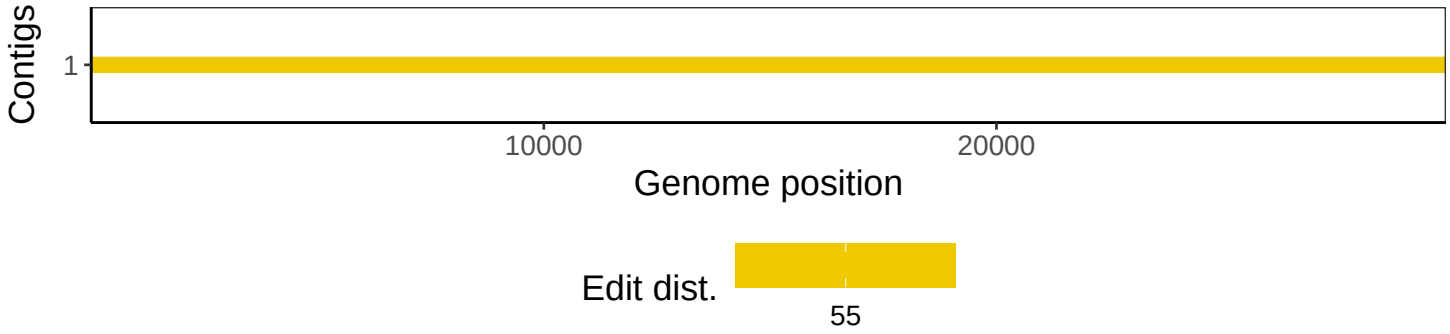
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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