COVID-19 subject HUP-Q-0027

2021-03-29

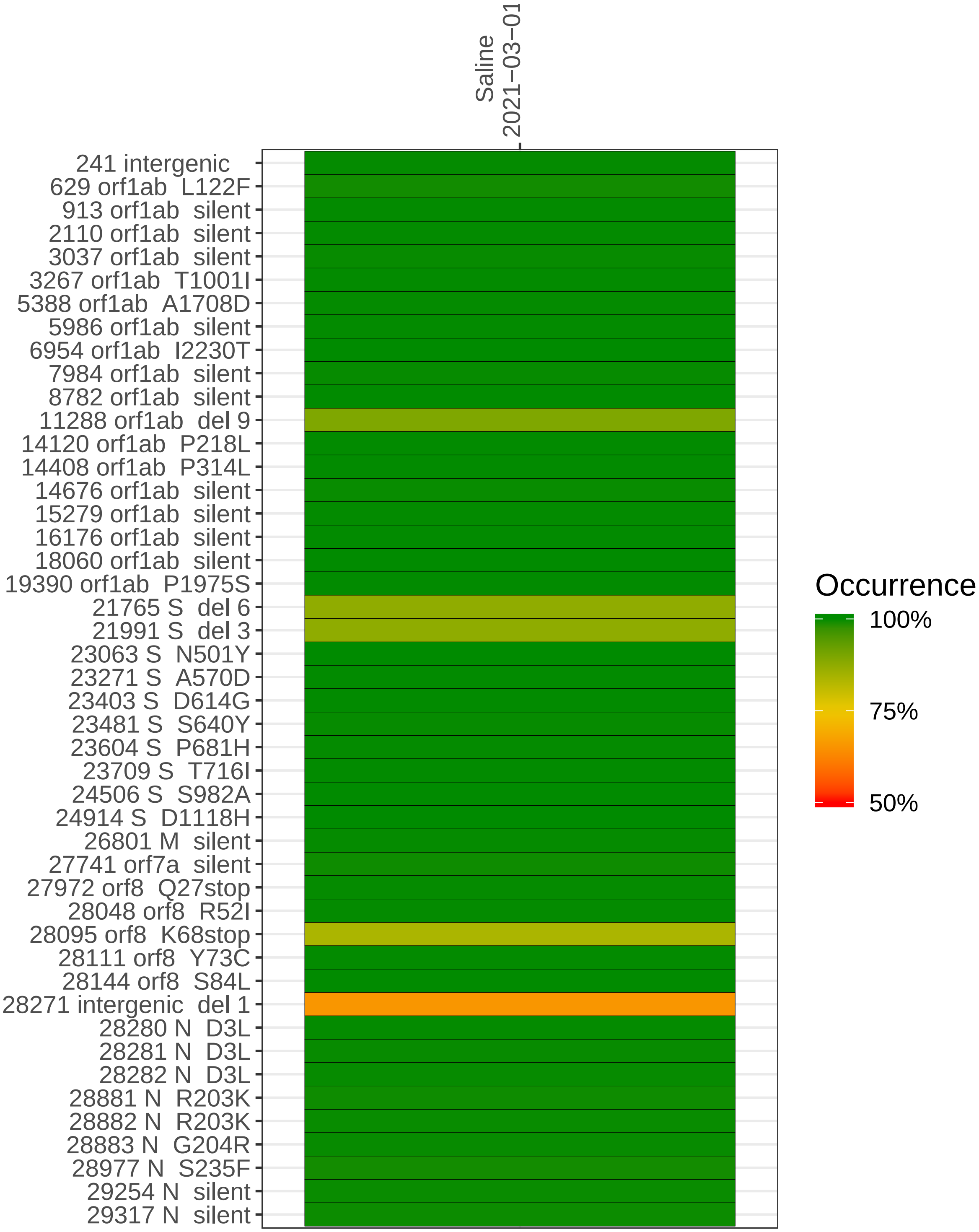
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

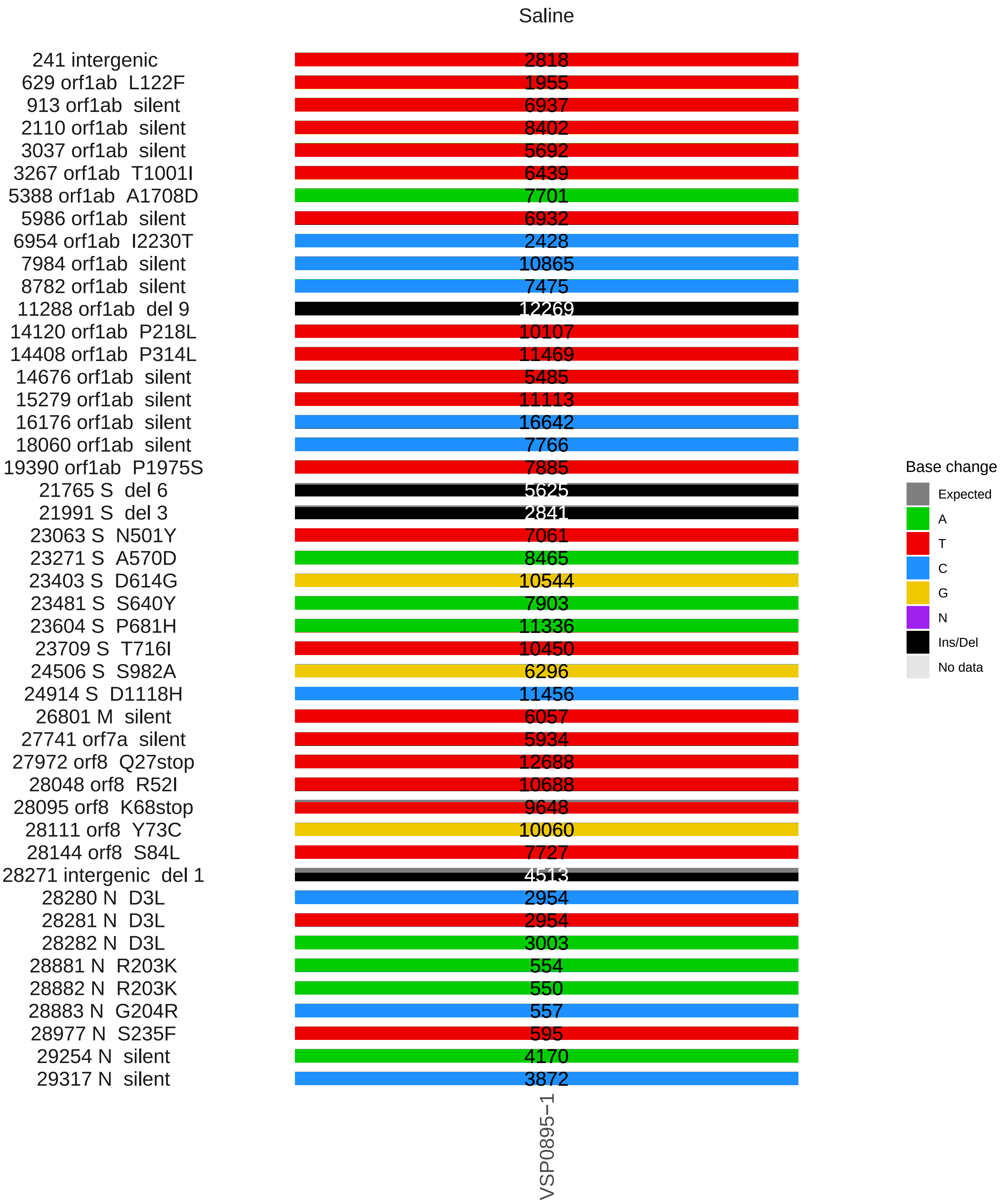
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0895-1	single experiment	NA	Saline	2021-03-01	29.81	B.1.1.7	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome 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.

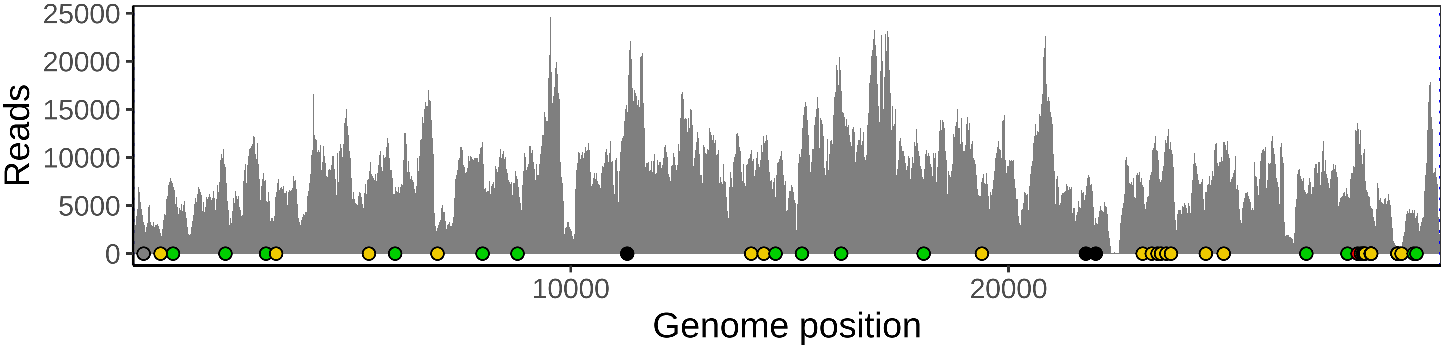



Saline
241 intergenic 2818
629 orf1ab L122F 1955
913 orf1ab silent 6937
2110 orf1ab silent 8402
3037 orf1ab silent 5692
3267 orf1ab T1001I 6439
5388 orf1ab A1708D 7701
5986 orf1ab silent 6932
6954 orf1ab I2230T 2428
7984 orf1ab silent 10865
8782 orf1ab silent 7475
11288 orf1ab del 9 12269
14120 orf1ab P218L 10107
14408 orf1ab P314L 11469
14676 orf1ab silent 5485
15279 orf1ab silent 11113
16176 orf1ab silent 16642
18060 orf1ab silent 7766
19390 orf1ab P1975S 7885
21765 S del 6 5625
21991 S del 3 2841
23063 S N501Y 7061
23271 S A570D 8465
23403 S D614G 10544
23481 S S640Y 7903
23604 S P681H 11336
23709 S T716I 10450
24506 S S982A 6296
24914 S D1118H 11456
26801 M silent 6057
27741 orf7a silent 5934
27972 orf8 Q27stop 12688
28048 orf8 R52I 10688
28095 orf8 K68stop 9648
28111 orf8 Y73C 10060
28144 orf8 S84L 7727
28271 intergenic del 1 4513
28280 N D3L 2954
28281 N D3L 2954
28282 N D3L 3003
28881 N R203K 554
28882 N R203K 550
28883 N G204R 557
28977 N S235F 595
29254 N silent 4170
29317 N silent 3872
VSP0895–1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

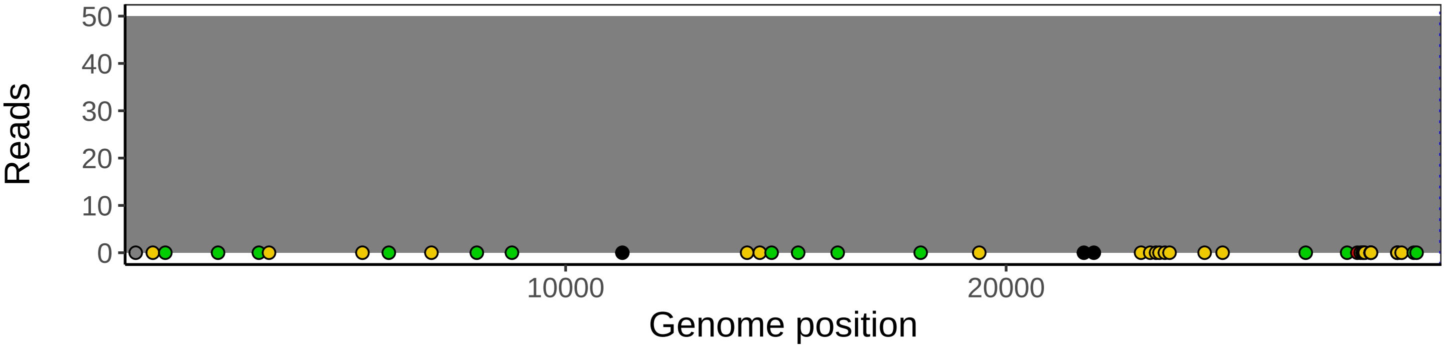
Analyses of individual experiments and composite results

VSP0895-1 | 2021-03-01 | Saline | HUP-Q-0027 | genomes | single experiment

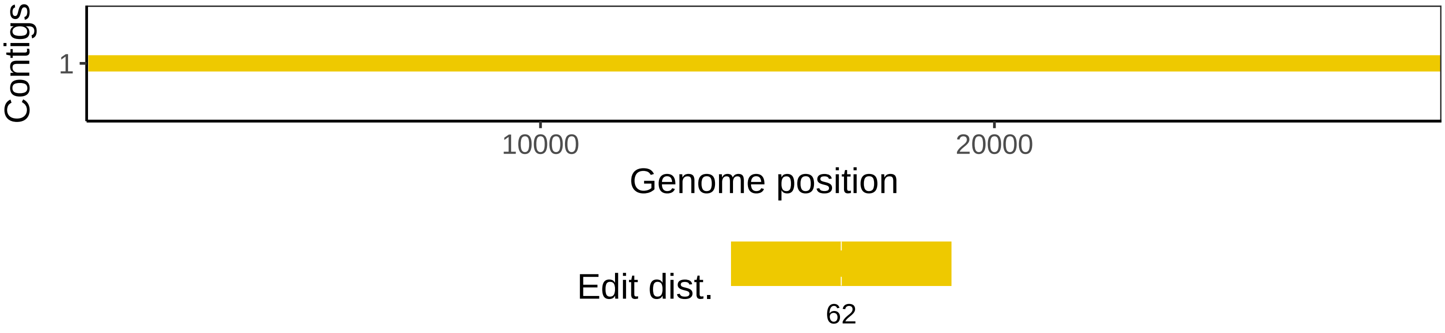
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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