COVID-19 subject HUP PH-0031

2021-05-05

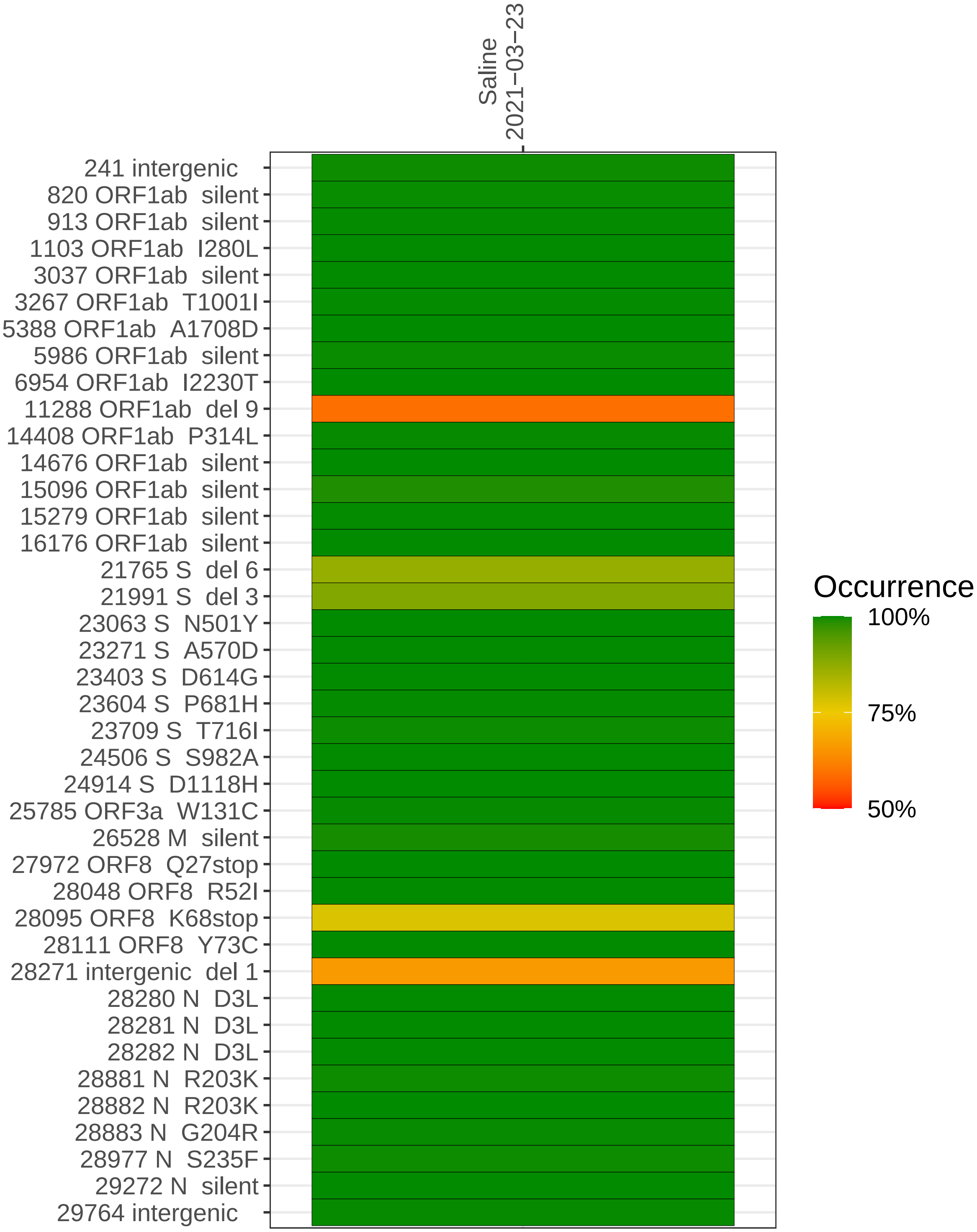
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

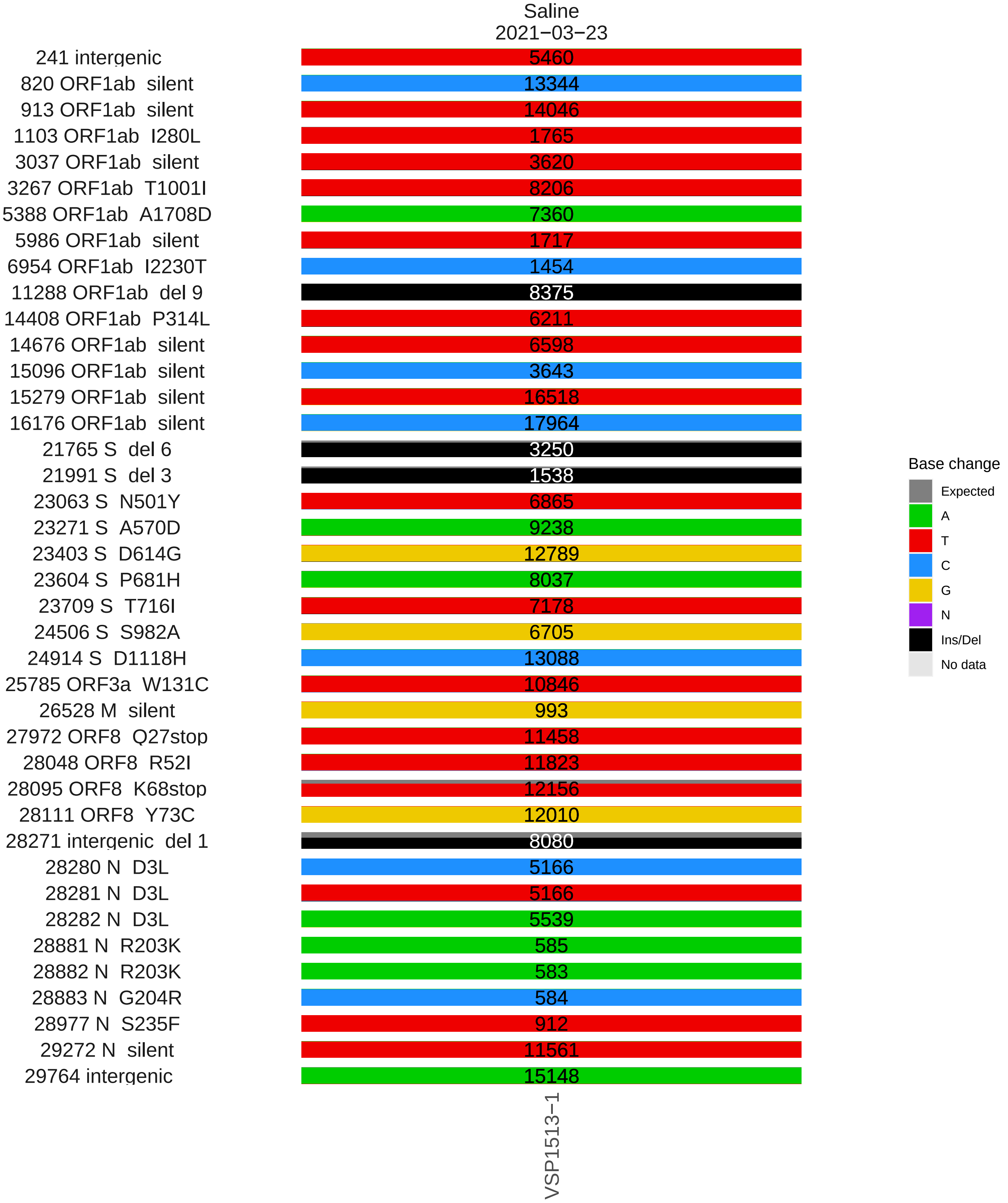
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1513-1	single experiment	NA	Saline	2021-03-23	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/Wuhan-Hu-1) 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.

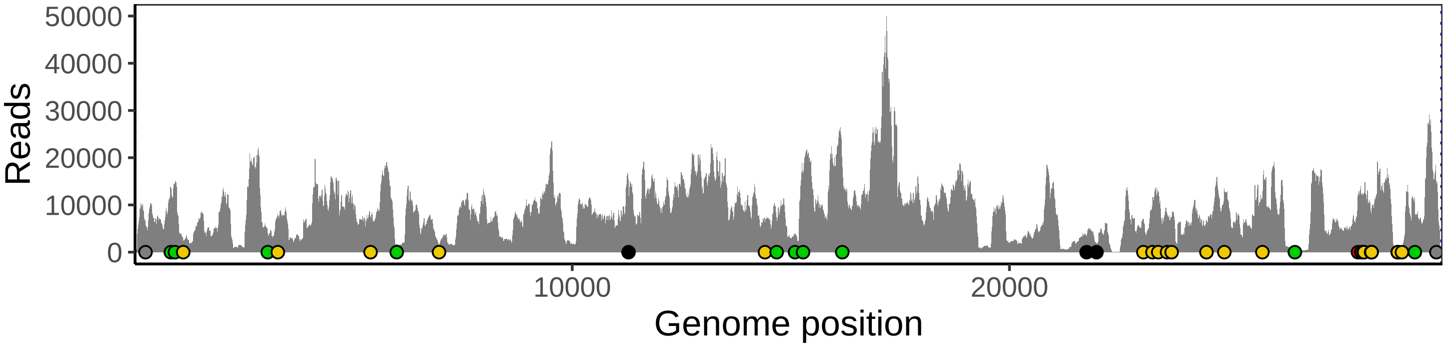



Saline
2021−03−23
241 intergenic 5460
820 ORF1ab silent 13344
913 ORF1ab silent 14046
1103 ORF1ab I280L 1765
3037 ORF1ab silent 3620
3267 ORF1ab T1001I 8206
5388 ORF1ab A1708D 7360
5986 ORF1ab silent 1717
6954 ORF1ab I2230T 1454
11288 ORF1ab del 9 8375
14408 ORF1ab P314L 6211
14676 ORF1ab silent 6598
15096 ORF1ab silent 3643
15279 ORF1ab silent 16518
16176 ORF1ab silent 17964
21765 S del 6 3250
21991 S del 3 1538
23063 S N501Y 6865
23271 S A570D 9238
23403 S D614G 12789
23604 S P681H 8037
23709 S T716I 7178
24506 S S982A 6705
24914 S D1118H 13088
25785 ORF3a W131C 10846
26528 M silent 993
27972 ORF8 Q27stop 11458
28048 ORF8 R52I 11823
28095 ORF8 K68stop 12156
28111 ORF8 Y73C 12010
28271 intergenic del 1 8080
28280 N D3L 5166
28281 N D3L 5166
28282 N D3L 5539
28881 N R203K 585
28882 N R203K 583
28883 N G204R 584
28977 N S235F 912
29272 N silent 11561
29764 intergenic 15148
VSP1513−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

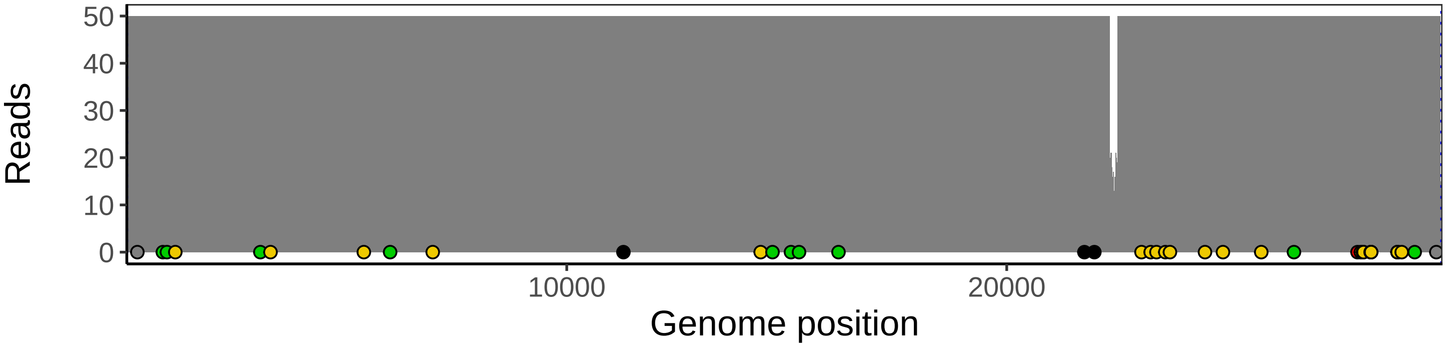
Analyses of individual experiments and composite results

VSP1513-1 | 2021-03-23 | Saline | HUP PH-0031 | genomes | single experiment

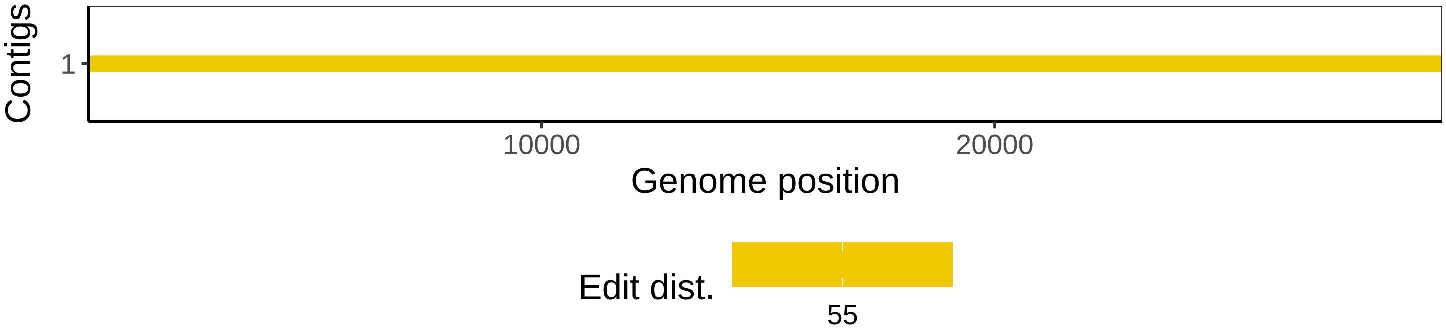
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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