COVID-19 subject UPHS-0083

2021-04-17

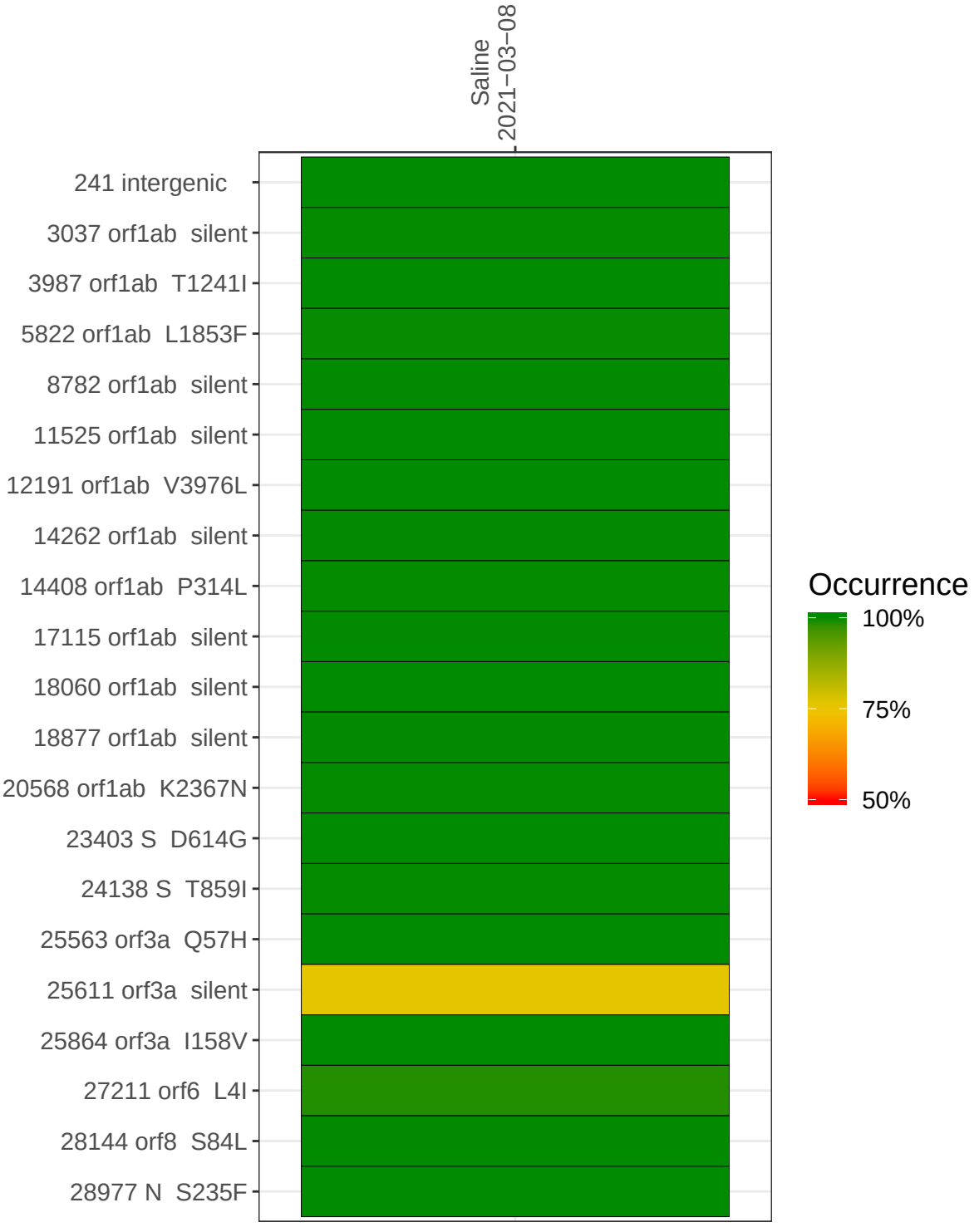
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

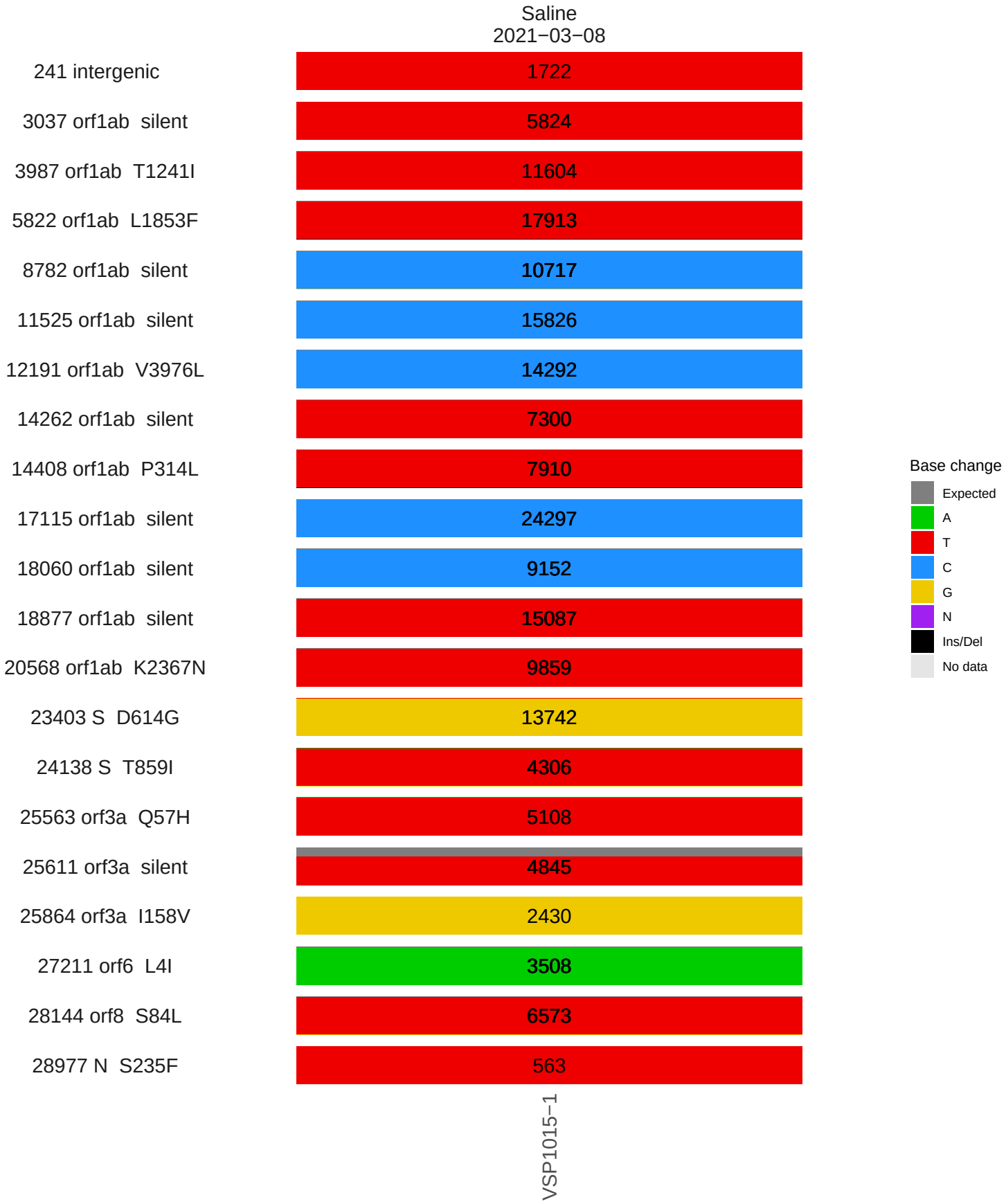
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1015-1	single experiment	NA	Saline	2021-03-08	29.88	B.1.170	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.

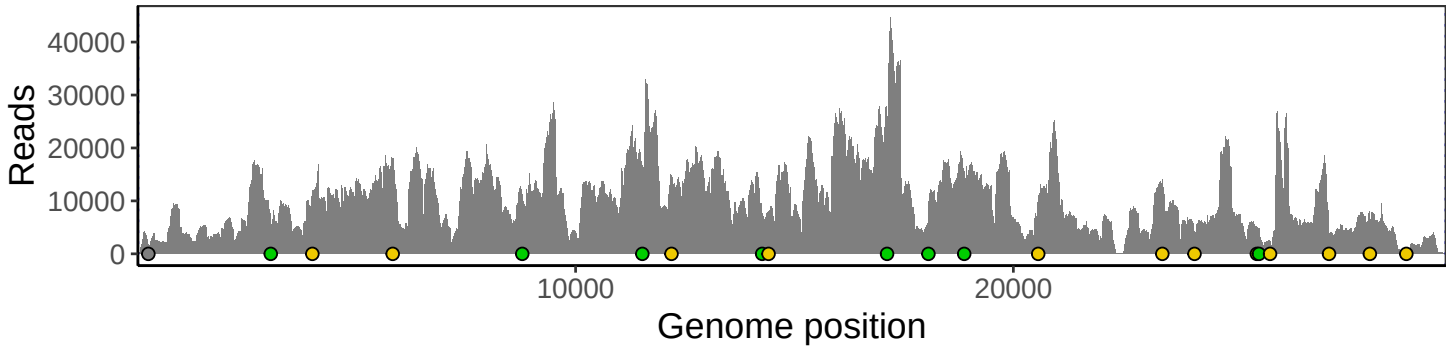



Saline
2021−03−08
241 intergenic
1722
3037 orf1ab silent
5824
3987 orf1ab T1241I
11604
5822 orf1ab L1853F
17913
8782 orf1ab silent
10717
11525 orf1ab silent
15826
12191 orf1ab V3976L
14292
14262 orf1ab silent
7300
14408 orf1ab P314L
7910
17115 orf1ab silent
24297
18060 orf1ab silent
9152
18877 orf1ab silent
15087
20568 orf1ab K2367N
9859
23403 S D614G
13742
24138 S T859I
4306
25563 orf3a Q57H
5108
25611 orf3a silent
4845
25864 orf3a I158V
2430
27211 orf6 L4I
3508
28144 orf8 S84L
6573
28977 N S235F
563
VSP1015−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

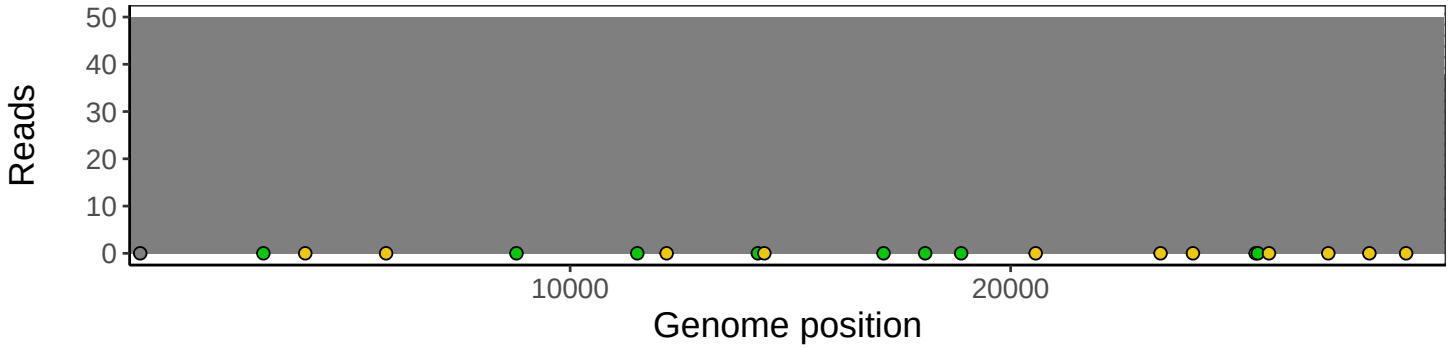
Analyses of individual experiments and composite results

VSP1015-1 | 2021-03-08 | Saline | UPHS-0083 | genomes | single experiment

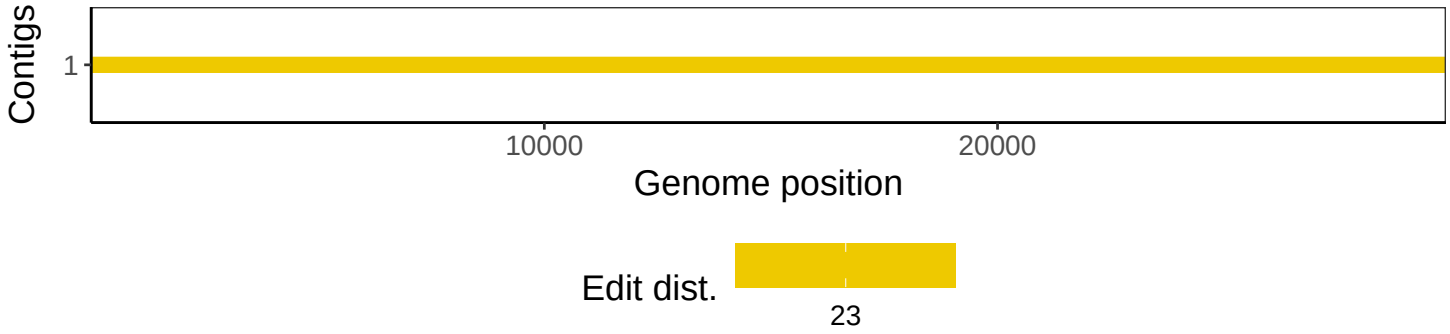
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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