COVID-19 subject HUP-PH-0009

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.

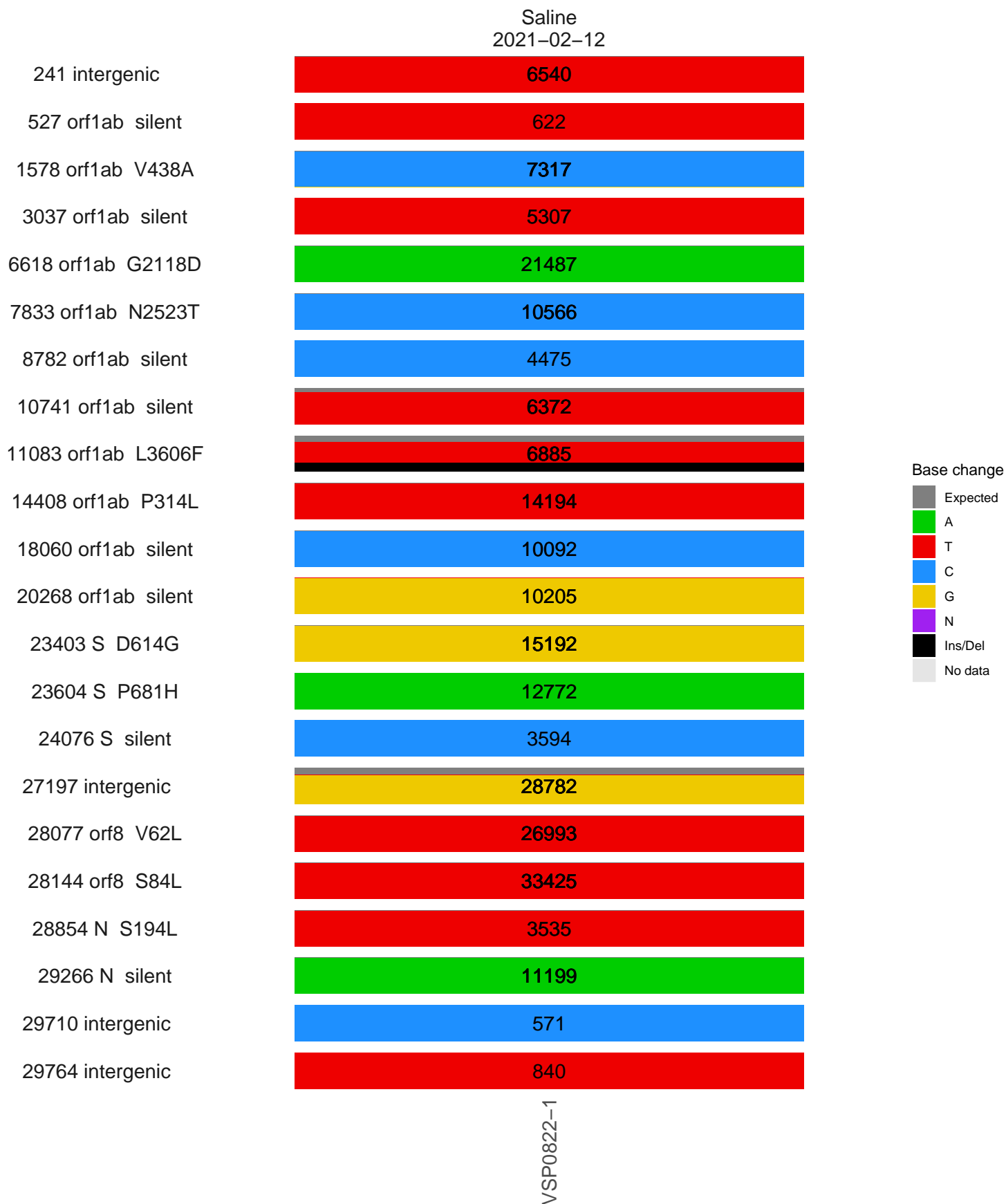Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0822-1	single experiment	NA	Saline	2021-02-12	29.86	B.1.243	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
2021−02−12

Position	VSP0822−1
241 intergenic	6540
527 orf1ab silent	622
1578 orf1ab V438A	7317
3037 orf1ab silent	5307
6618 orf1ab G2118D	21487
7833 orf1ab N2523T	10566
8782 orf1ab silent	4475
10741 orf1ab silent	6372
11083 orf1ab L3606F	6885
14408 orf1ab P314L	14194
18060 orf1ab silent	10092
20268 orf1ab silent	10205
23403 S D614G	15192
23604 S P681H	12772
24076 S silent	3594
27197 intergenic	28782
28077 orf8 V62L	26993
28144 orf8 S84L	33425
28854 N S194L	3535
29266 N silent	11199
29710 intergenic	571
29764 intergenic	840

Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

Analyses of individual experiments and composite results

## VSP0822-1 | 2021-02-12 | Saline | HUP-PH-0009 | 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.
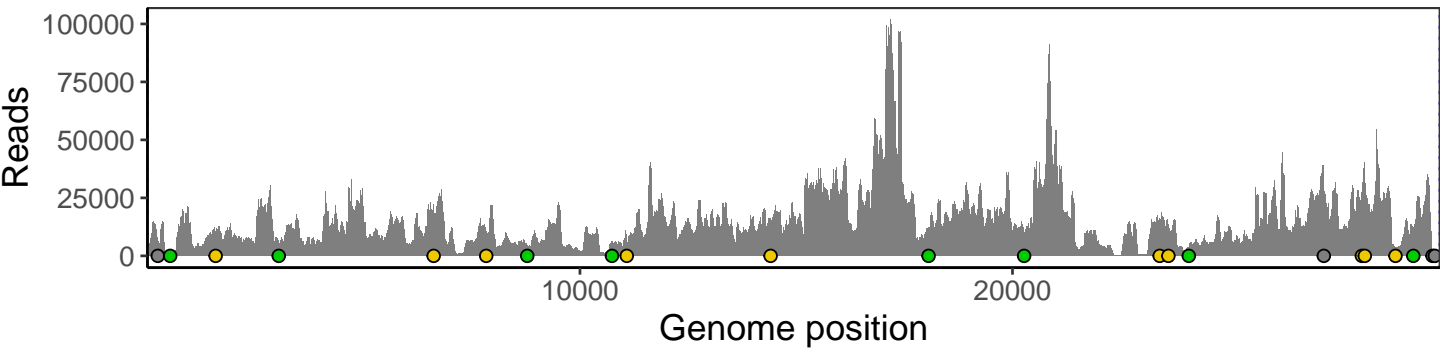
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
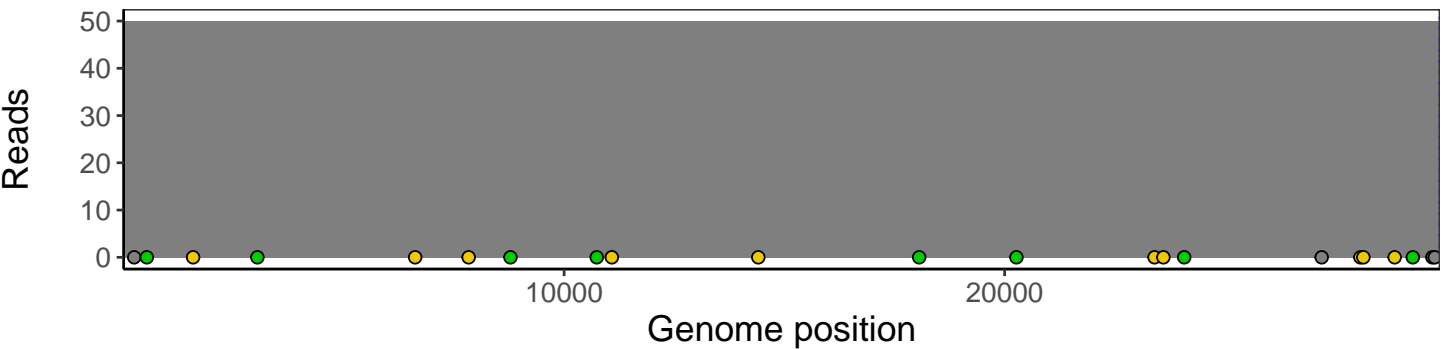
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
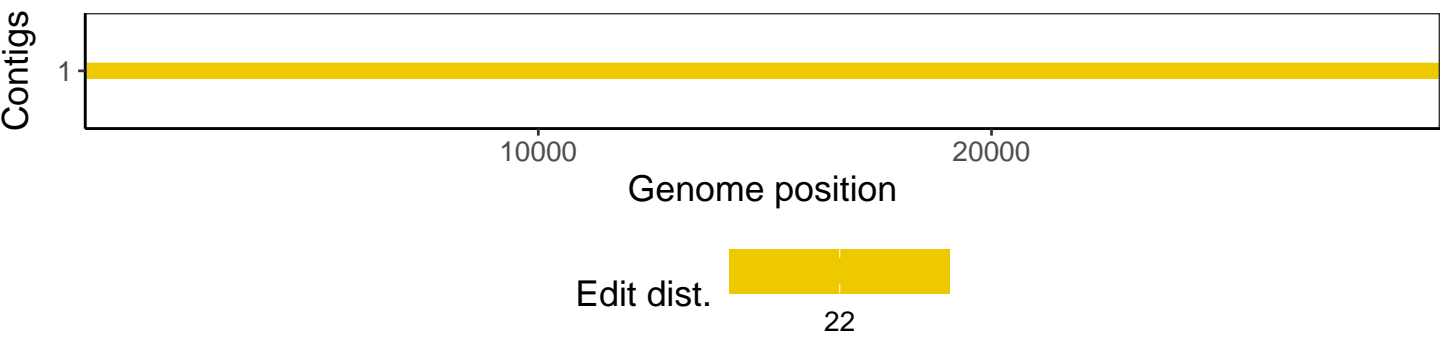
Software environment

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