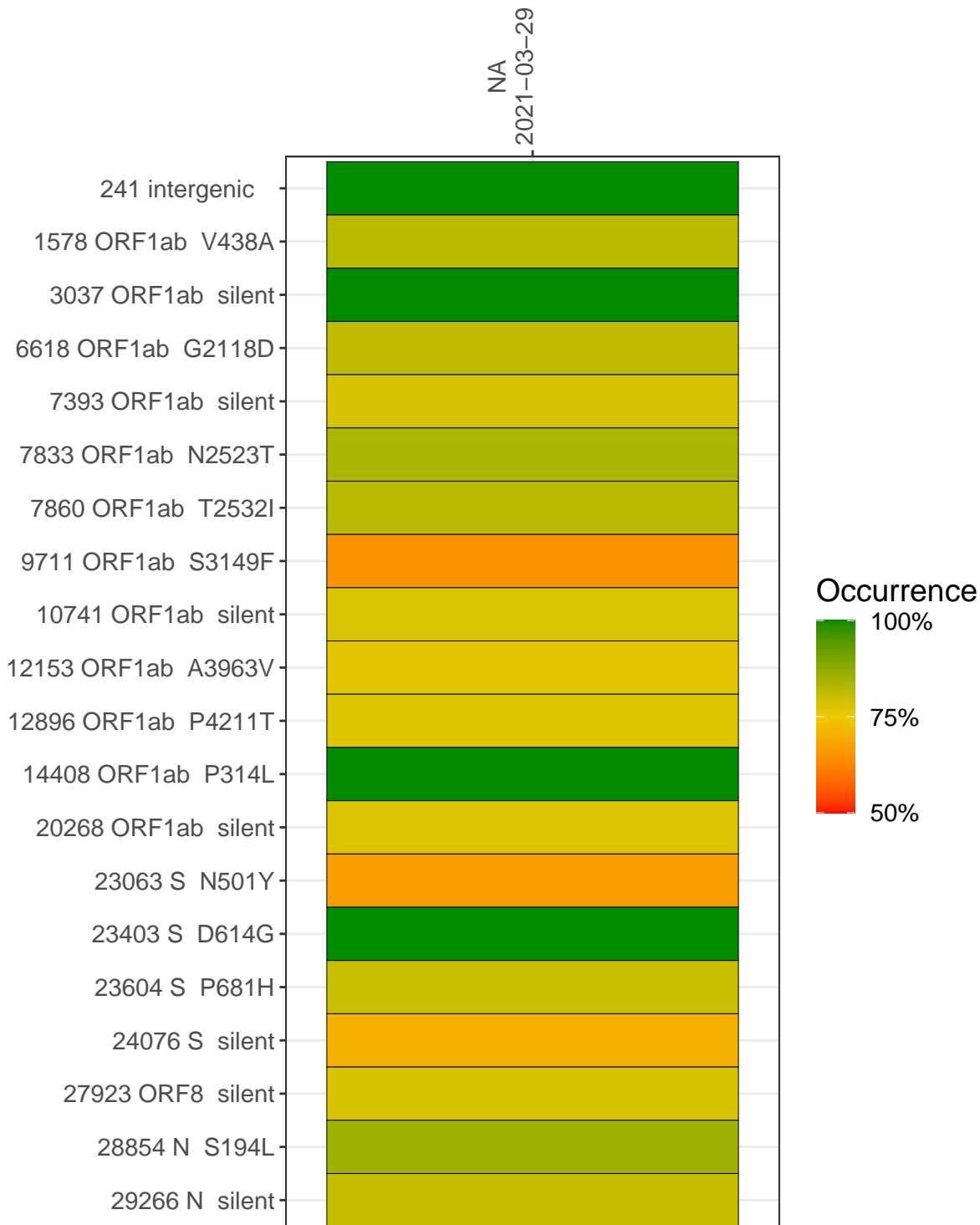# COVID-19 subject UPHS-0578

2021-06-03

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.
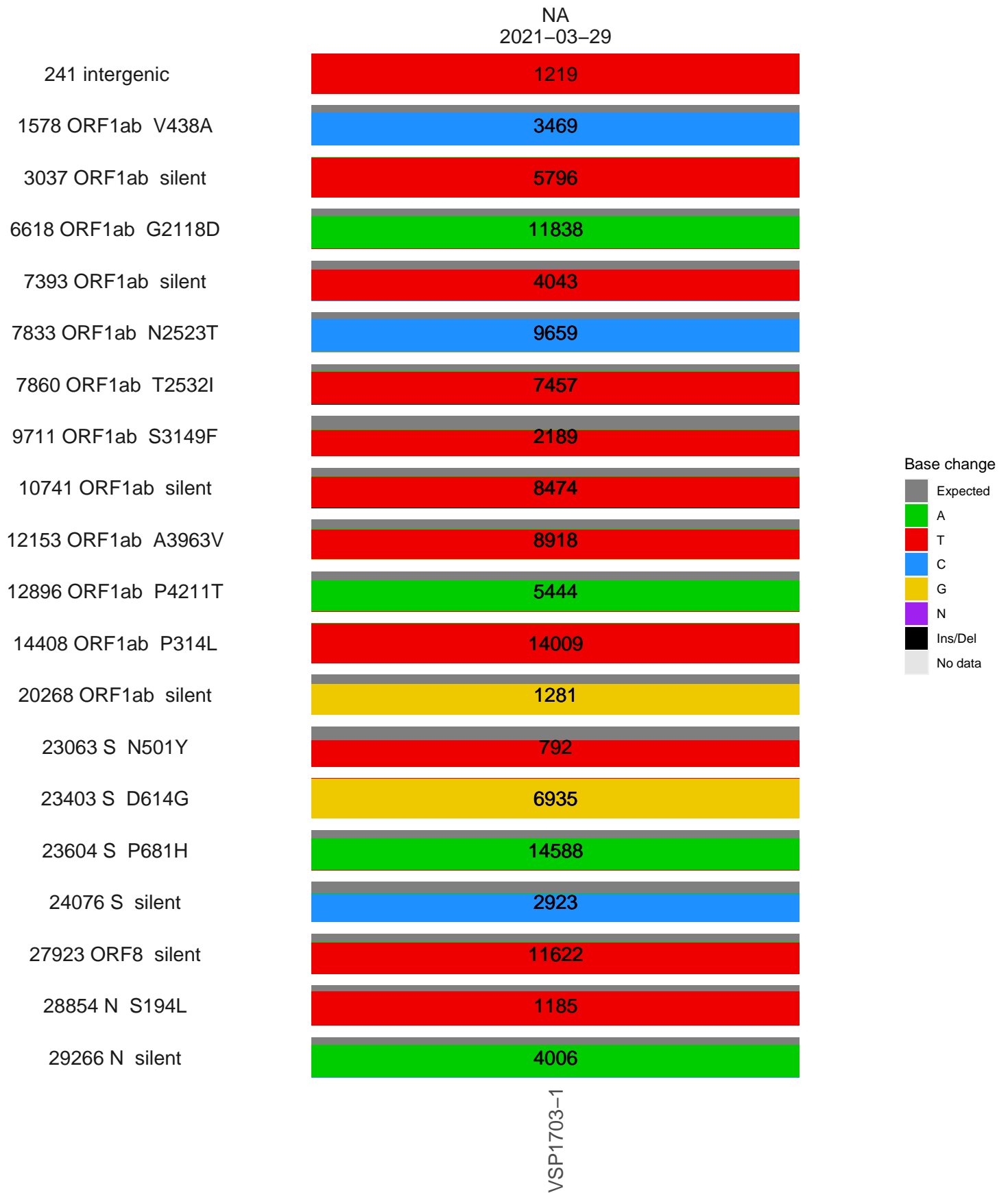
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1703-1	single experiment	NA	NA	2021-03-29	29.72	B.1.243	99.3%	99.2%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

NA
2021−03−29

Position	VSP1703−1
241 intergenic	1219
1578 ORF1ab V438A	3469
3037 ORF1ab silent	5796
6618 ORF1ab G2118D	11838
7393 ORF1ab silent	4043
7833 ORF1ab N2523T	9659
7860 ORF1ab T2532I	7457
9711 ORF1ab S3149F	2189
10741 ORF1ab silent	8474
12153 ORF1ab A3963V	8918
12896 ORF1ab P4211T	5444
14408 ORF1ab P314L	14009
20268 ORF1ab silent	1281
23063 S N501Y	792
23403 S D614G	6935
23604 S P681H	14588
24076 S silent	2923
27923 ORF8 silent	11622
28854 N S194L	1185
29266 N silent	4006

Base change

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

VSP1703−1

3

Analyses of individual experiments and composite results

## VSP1703-1 | 2021-03-29 | NA | UPHS-0578 | 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.
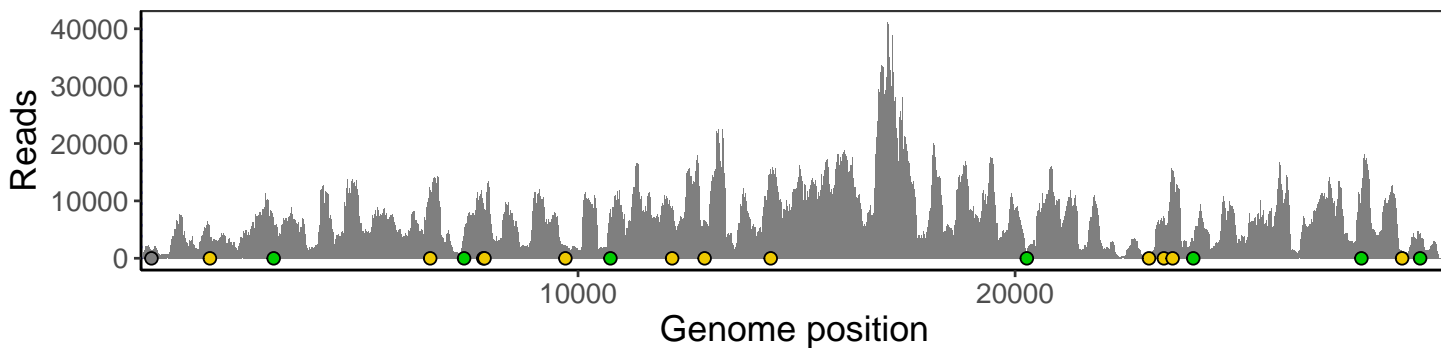
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
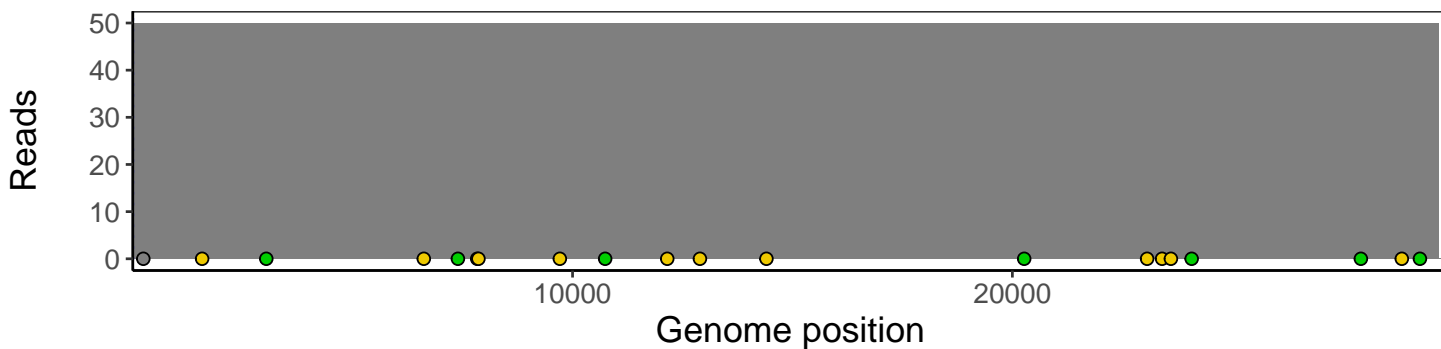
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
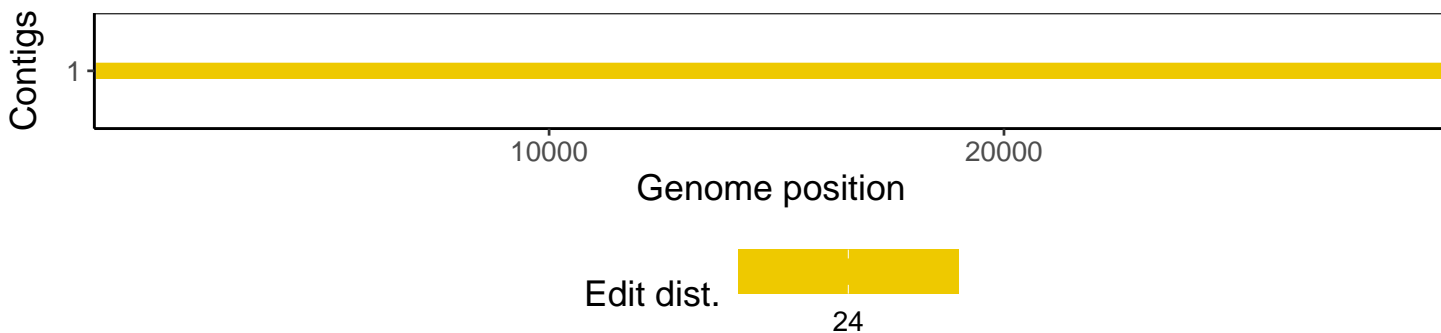
Software environment

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