COVID-19 subject MPCluster2-Seq12

2021-04-17

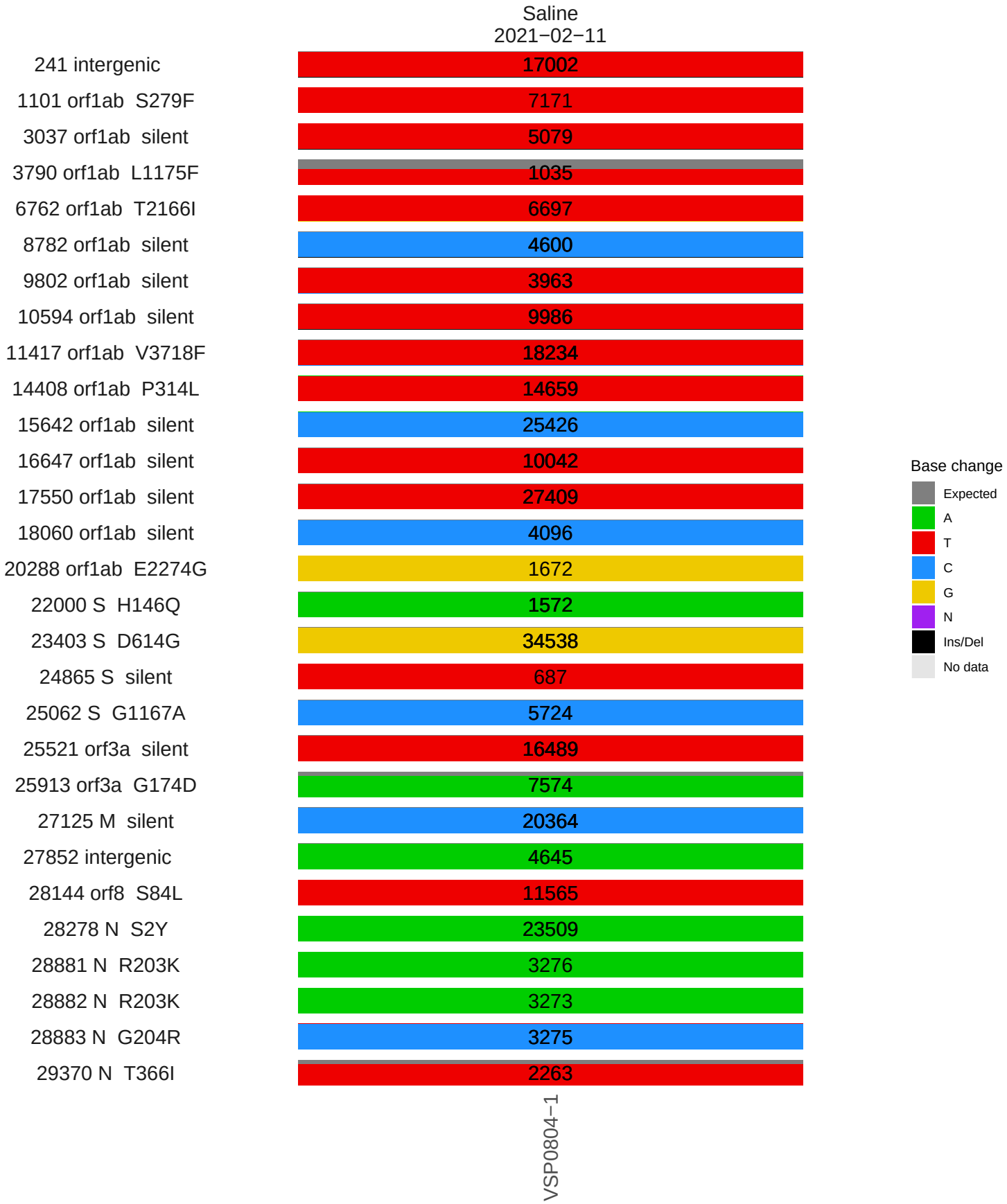
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0804-1	single experiment	NA	Saline	2021-02-11	24.84	B.1.1.348	99.8%	99.8%

Variants shared across samples

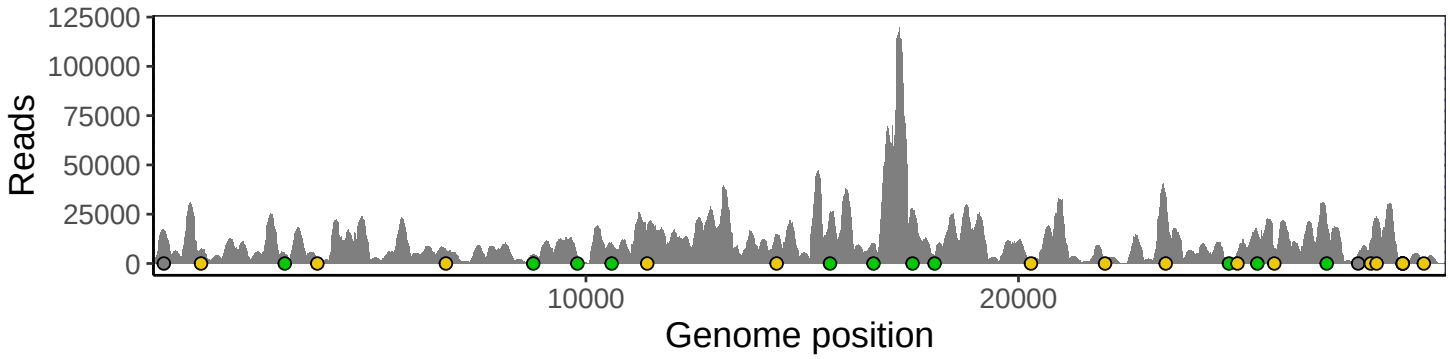
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% 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
2021−02−11
241 intergenic
1101 orf1ab S279F
3037 orf1ab silent
3790 orf1ab L1175F
6762 orf1ab T2166I
8782 orf1ab silent
9802 orf1ab silent
10594 orf1ab silent
11417 orf1ab V3718F
14408 orf1ab P314L
15642 orf1ab silent
16647 orf1ab silent
17550 orf1ab silent
18060 orf1ab silent
20288 orf1ab E2274G
22000 S H146Q
23403 S D614G
24865 S silent
25062 S G1167A
25521 orf3a silent
25913 orf3a G174D
27125 M silent
27852 intergenic
28144 orf8 S84L
28278 N S2Y
28881 N R203K
28882 N R203K
28883 N G204R
29370 N T366I
17002
7171
5079
1035
6697
4600
3963
9986
18234
14659
25426
10042
27409
4096
1672
1572
34538
687
5724
16489
7574
20364
4645
11565
23509
3276
3273
3275
2263
VSP0804−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

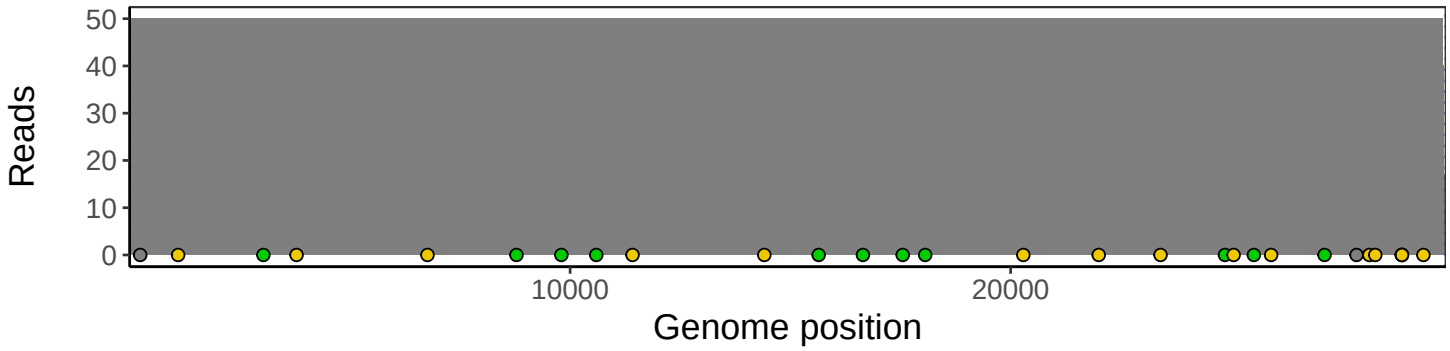
Analyses of individual experiments and composite results

VSP0804-1 | 2021-02-11 | Saline | MPCluster2-Seq12 | genomes | single experiment

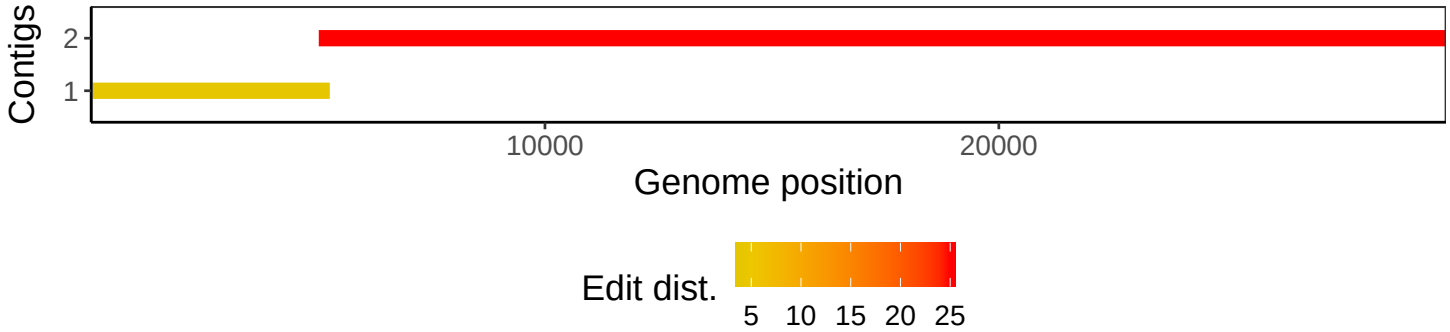
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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