COVID-19 subject patient_B1

2021-04-17

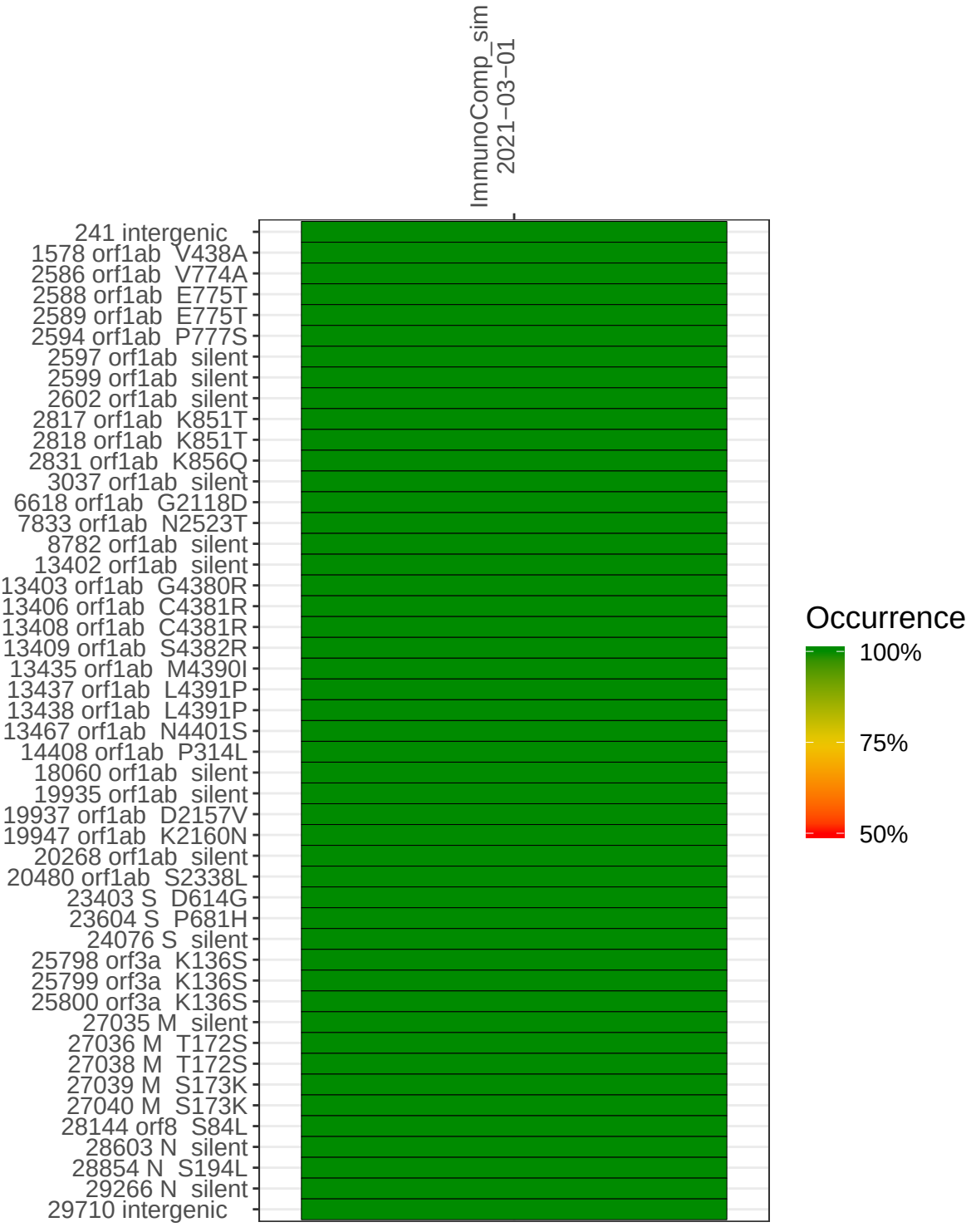
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

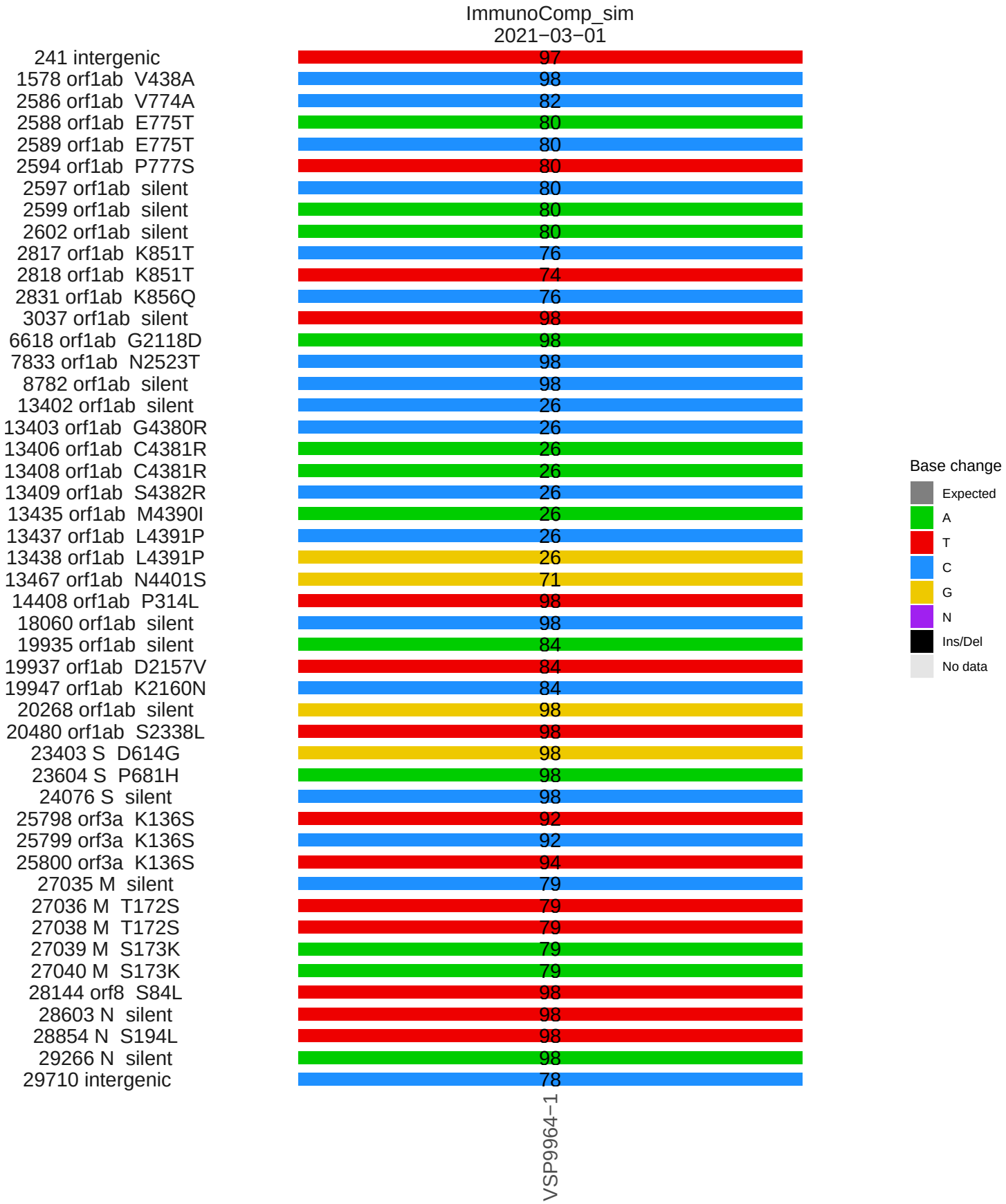
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP9964-1	single experiment	NA	ImmunoComp2021-Jun	2021-03-01	13.48	B.1.243	99.4%	99.4%

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.

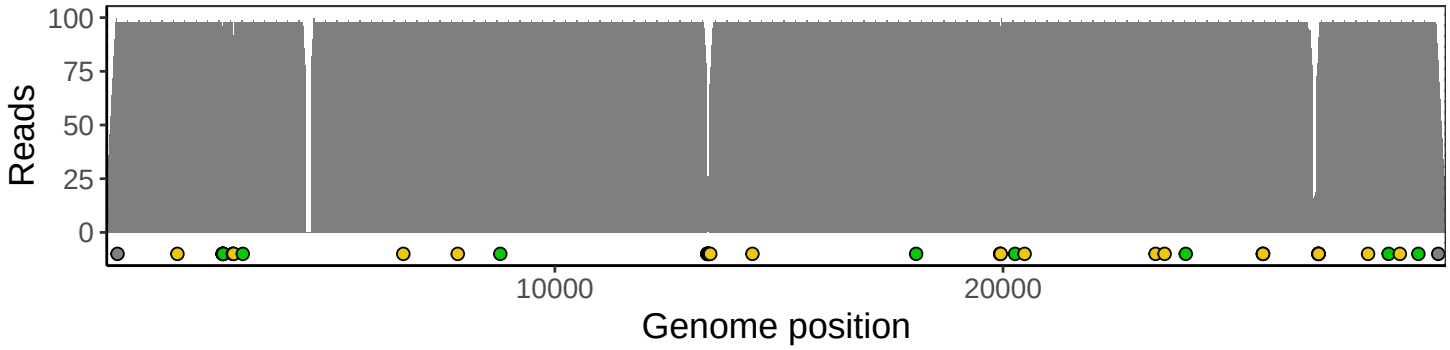



ImmunoComp_sim
2021−03−01
241 intergenic
1578 orf1ab V438A
2586 orf1ab V774A
2588 orf1ab E775T
2589 orf1ab E775T
2594 orf1ab P777S
2597 orf1ab silent
2599 orf1ab silent
2602 orf1ab silent
2817 orf1ab K851T
2818 orf1ab K851T
2831 orf1ab K856Q
3037 orf1ab silent
6618 orf1ab G2118D
7833 orf1ab N2523T
8782 orf1ab silent
13402 orf1ab silent
13403 orf1ab G4380R
13406 orf1ab C4381R
13408 orf1ab C4381R
13409 orf1ab S4382R
13435 orf1ab M4390I
13437 orf1ab L4391P
13438 orf1ab L4391P
13467 orf1ab N4401S
14408 orf1ab P314L
18060 orf1ab silent
19935 orf1ab silent
19937 orf1ab D2157V
19947 orf1ab K2160N
20268 orf1ab silent
20480 orf1ab S2338L
23403 S D614G
23604 S P681H
24076 S silent
25798 orf3a K136S
25799 orf3a K136S
25800 orf3a K136S
27035 M silent
27036 M T172S
27038 M T172S
27039 M S173K
27040 M S173K
28144 orf8 S84L
28603 N silent
28854 N S194L
29266 N silent
29710 intergenic
97
98
82
80
80
80
80
80
80
76
74
76
98
98
98
98
26
26
26
26
26
26
26
26
71
98
98
84
84
84
98
98
98
98
98
92
92
94
79
79
79
79
79
98
98
98
98
78
VSP9964−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

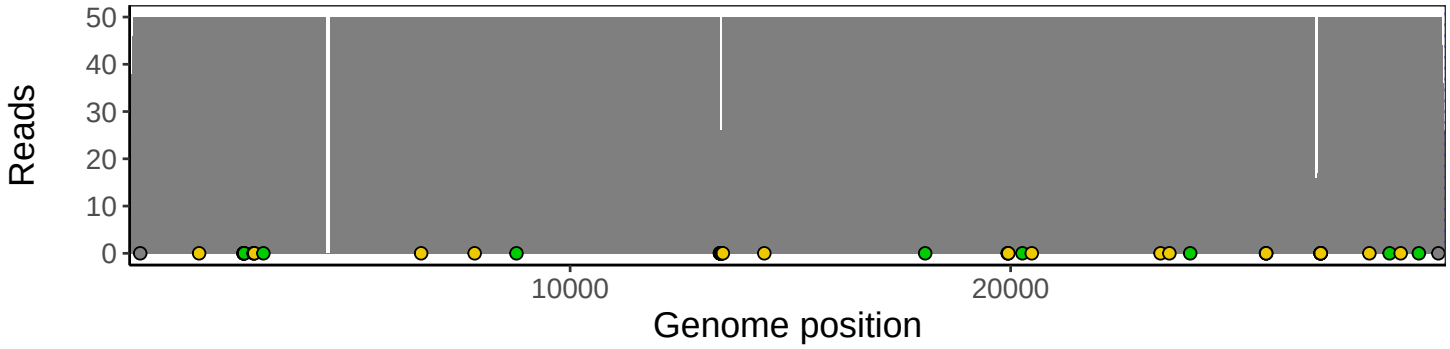
Analyses of individual experiments and composite results

VSP9964-1 | 2021-03-01 | ImmunoComp_sim | patient_B1 | genomes | single experiment

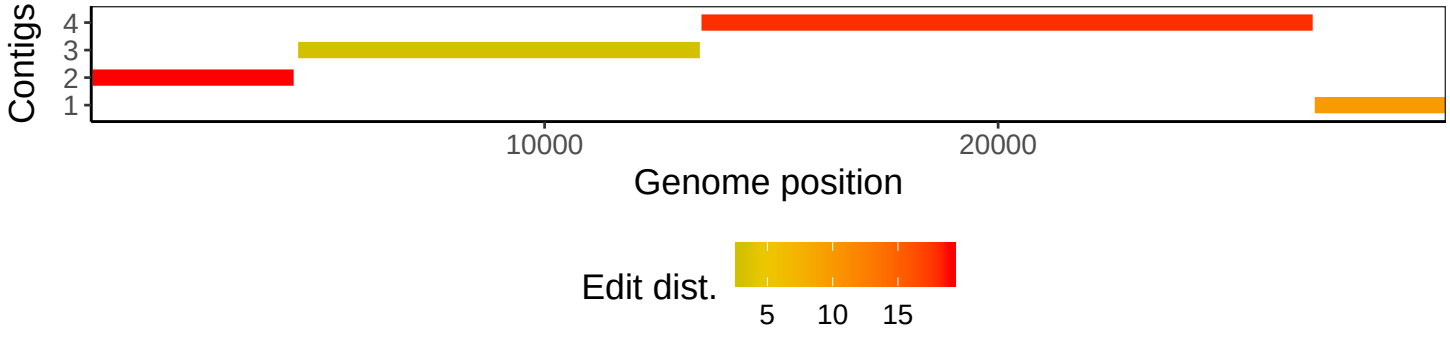
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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