COVID-19 subject SRR11783578

2020-09-29

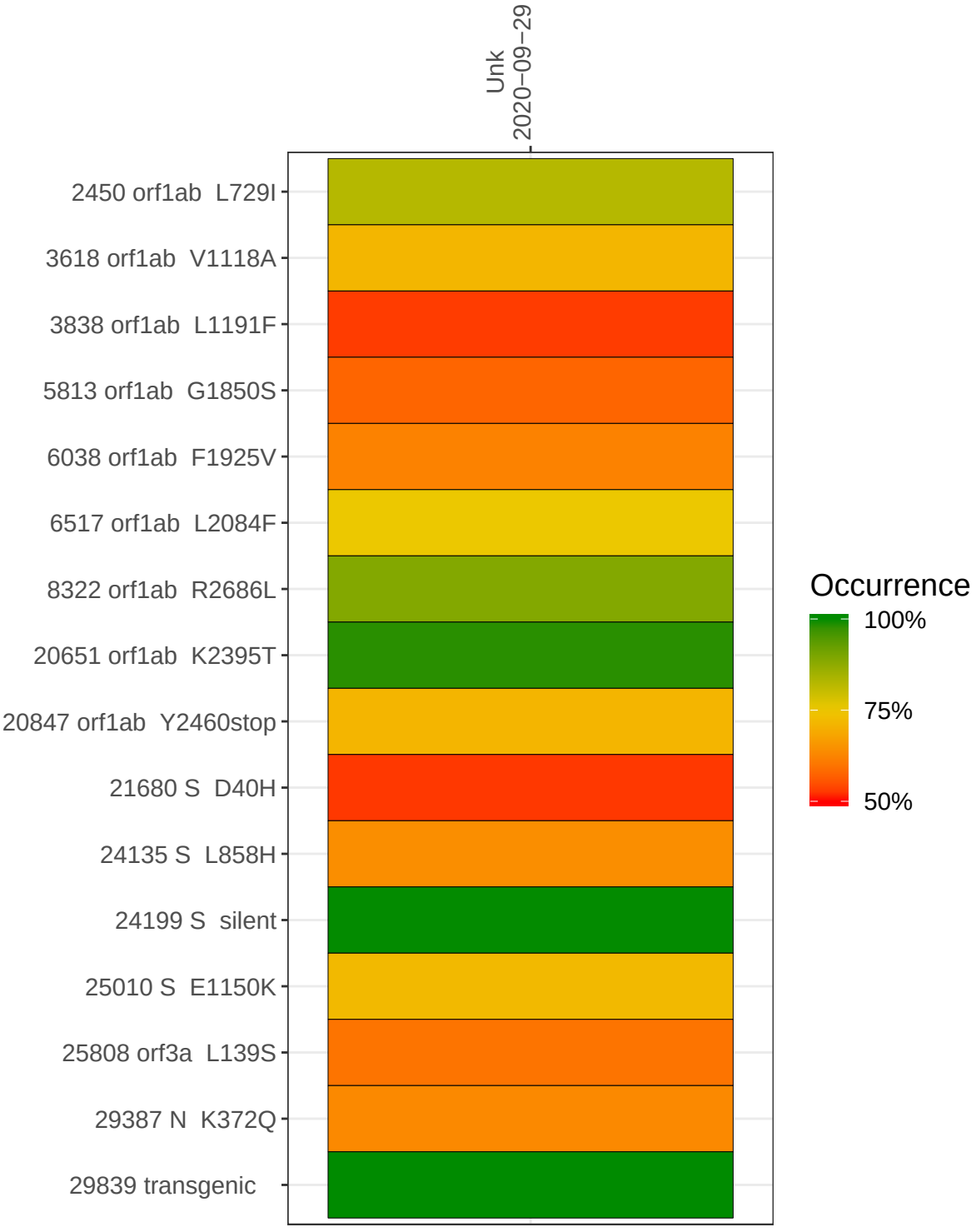
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

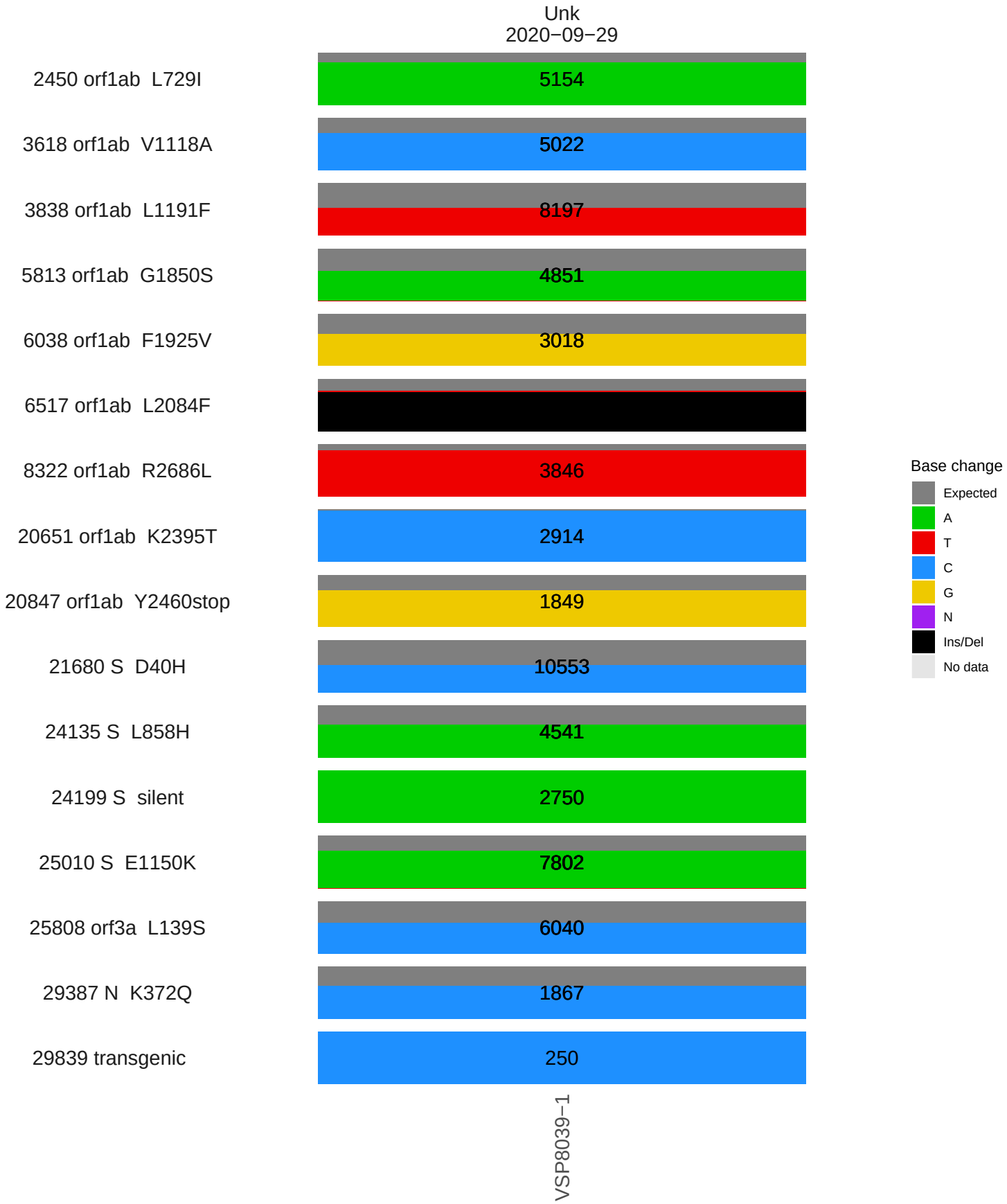
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8039-1	single experiment	NA	Unk	2020-09-29	6.55	99.0%	98.9%

Variants shared across samples

The heat map below shows how variants (reference genome 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 for 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.

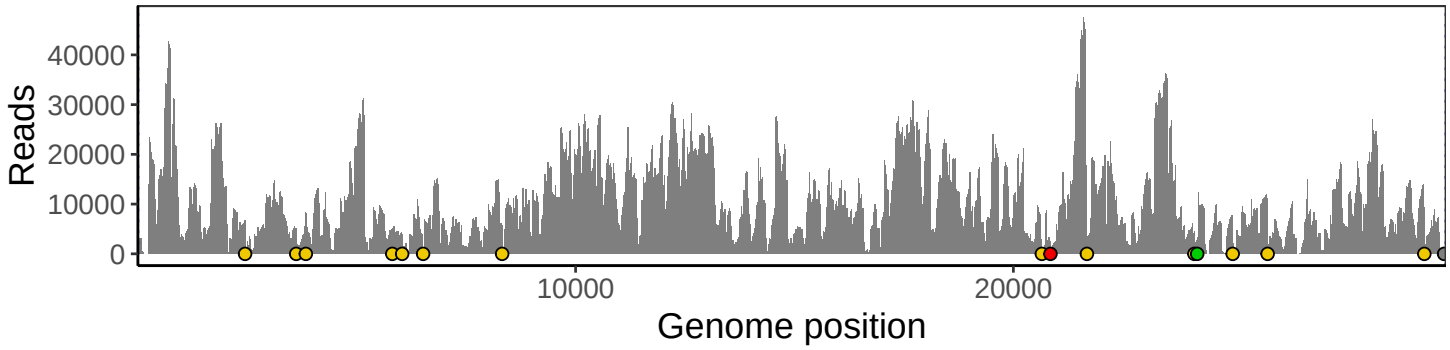



Unk
2020−09−29
2450 orf1ab L729I
5154
3618 orf1ab V1118A
5022
3838 orf1ab L1191F
8197
5813 orf1ab G1850S
4851
6038 orf1ab F1925V
3018
6517 orf1ab L2084F
8322 orf1ab R2686L
3846
20651 orf1ab K2395T
2914
20847 orf1ab Y2460stop
1849
21680 S D40H
10553
24135 S L858H
4541
24199 S silent
2750
25010 S E1150K
7802
25808 orf3a L139S
6040
29387 N K372Q
1867
29839 transgenic
250
VSP8039−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

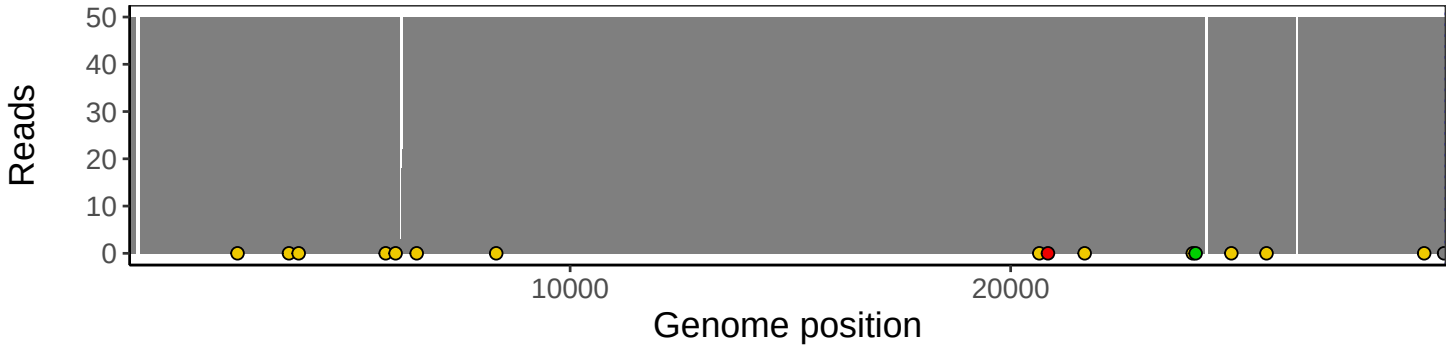
Analyses of individual experiments and composite results.

VSP8039-1 | 2020-09-29 | Unk | SRR11783578 | 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.