COVID-19 subject SRR11783576

2020-09-29

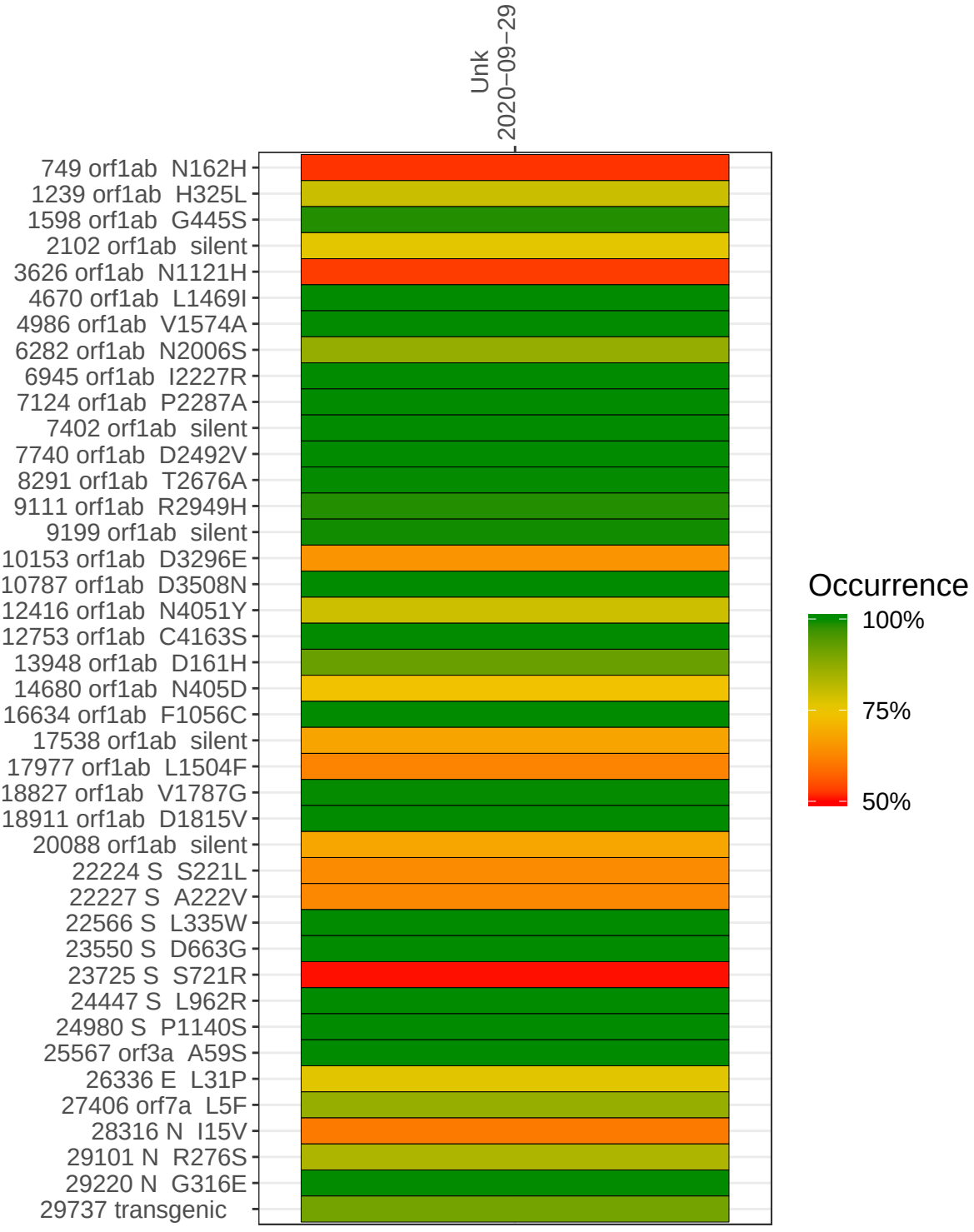
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

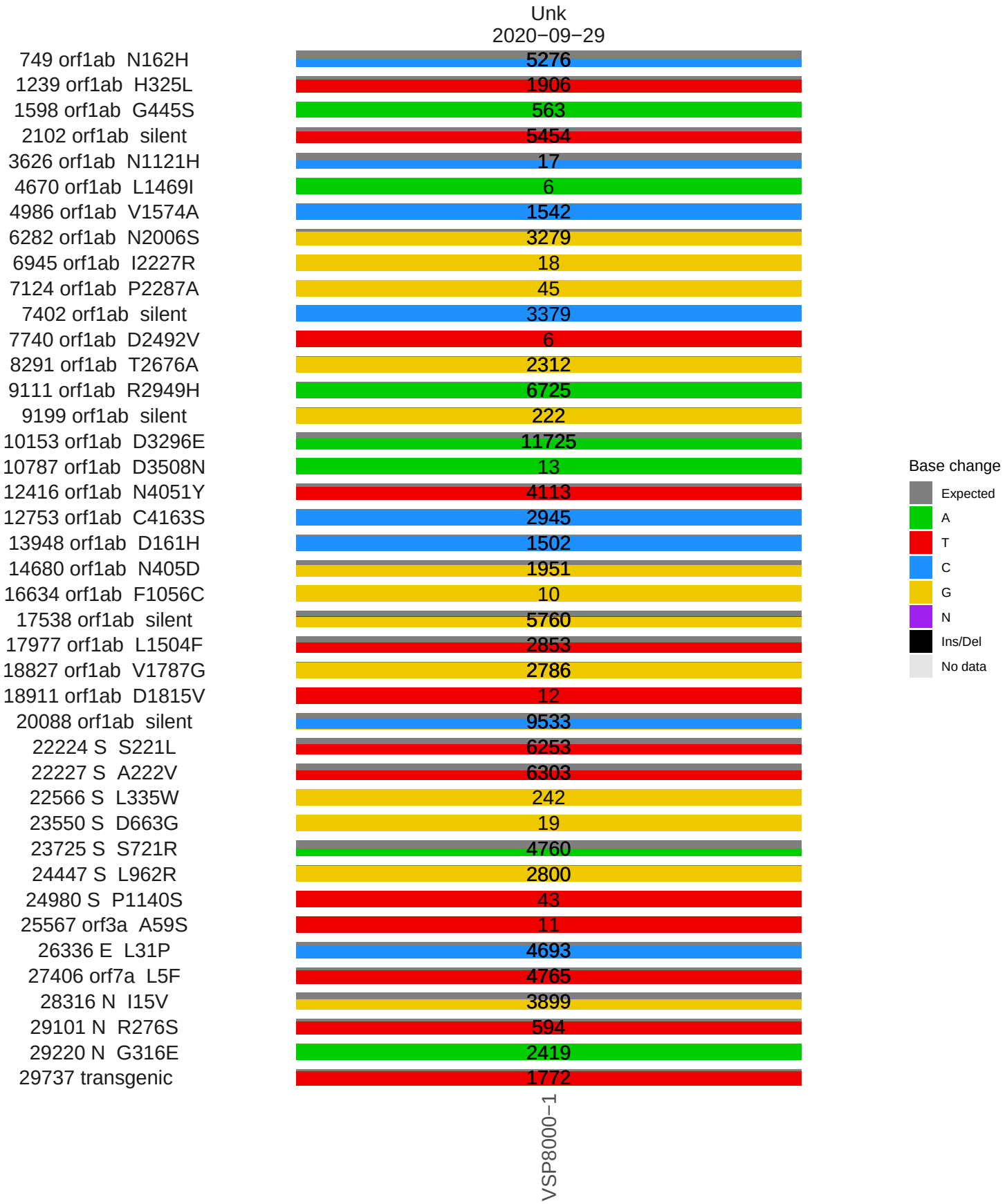
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8000-1	single experiment	NA	Unk	2020-09-29	1.38	85.7%	83.7%

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.

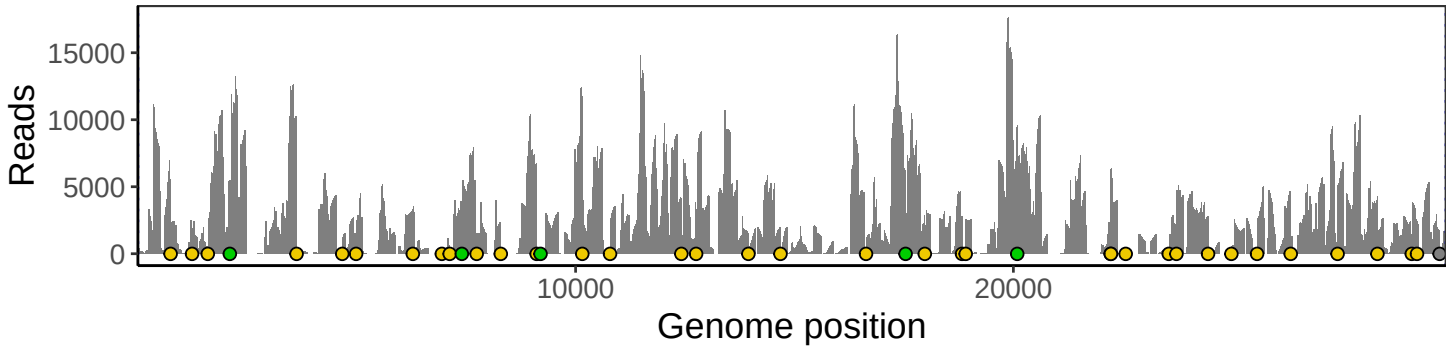



Unk
2020−09−29
749 orf1ab N162H
1239 orf1ab H325L
1598 orf1ab G445S
2102 orf1ab silent
3626 orf1ab N1121H
4670 orf1ab L1469I
4986 orf1ab V1574A
6282 orf1ab N2006S
6945 orf1ab I2227R
7124 orf1ab P2287A
7402 orf1ab silent
7740 orf1ab D2492V
8291 orf1ab T2676A
9111 orf1ab R2949H
9199 orf1ab silent
10153 orf1ab D3296E
10787 orf1ab D3508N
12416 orf1ab N4051Y
12753 orf1ab C4163S
13948 orf1ab D161H
14680 orf1ab N405D
16634 orf1ab F1056C
17538 orf1ab silent
17977 orf1ab L1504F
18827 orf1ab V1787G
18911 orf1ab D1815V
20088 orf1ab silent
22224 S S221L
22227 S A222V
22566 S L335W
23550 S D663G
23725 S S721R
24447 S L962R
24980 S P1140S
25567 orf3a A59S
26336 E L31P
27406 orf7a L5F
28316 N I15V
29101 N R276S
29220 N G316E
29737 transgenic
5276
1906
563
5454
17
6
1542
3279
18
45
3379
6
2312
6725
222
11725
13
4113
2945
1502
1951
10
5760
2853
2786
12
9533
6253
6303
242
19
4760
2800
43
11
4693
4765
3899
594
2419
1772
VSP8000−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

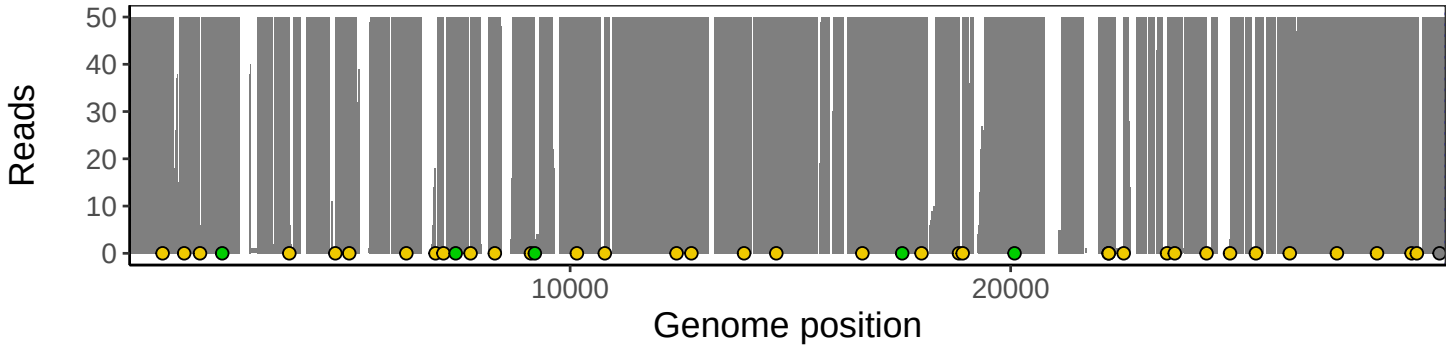
Analyses of individual experiments and composite results.

VSP8000-1 | 2020-09-29 | Unk | SRR11783576 | 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.