COVID-19 subject 95-267

2021-01-10

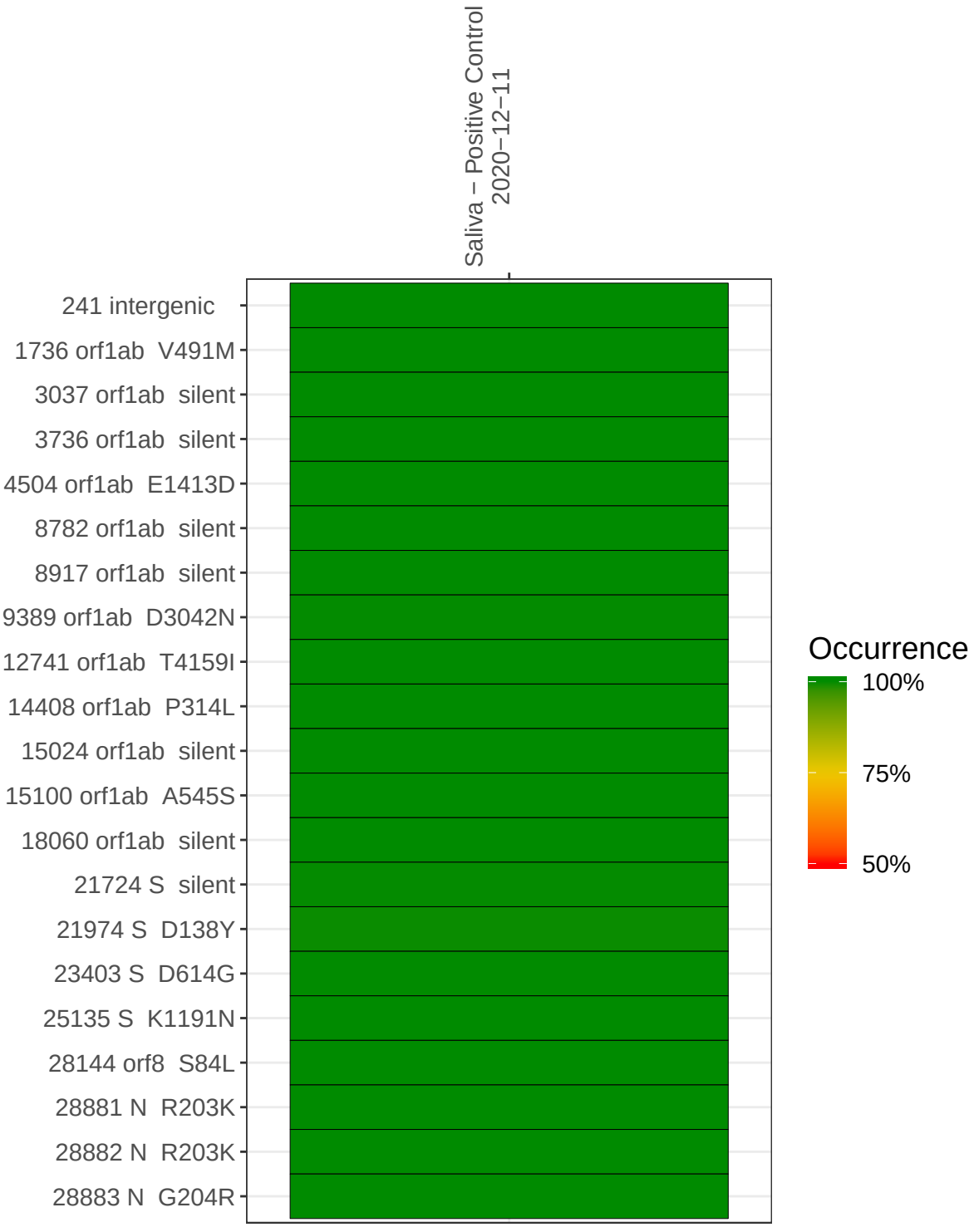
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

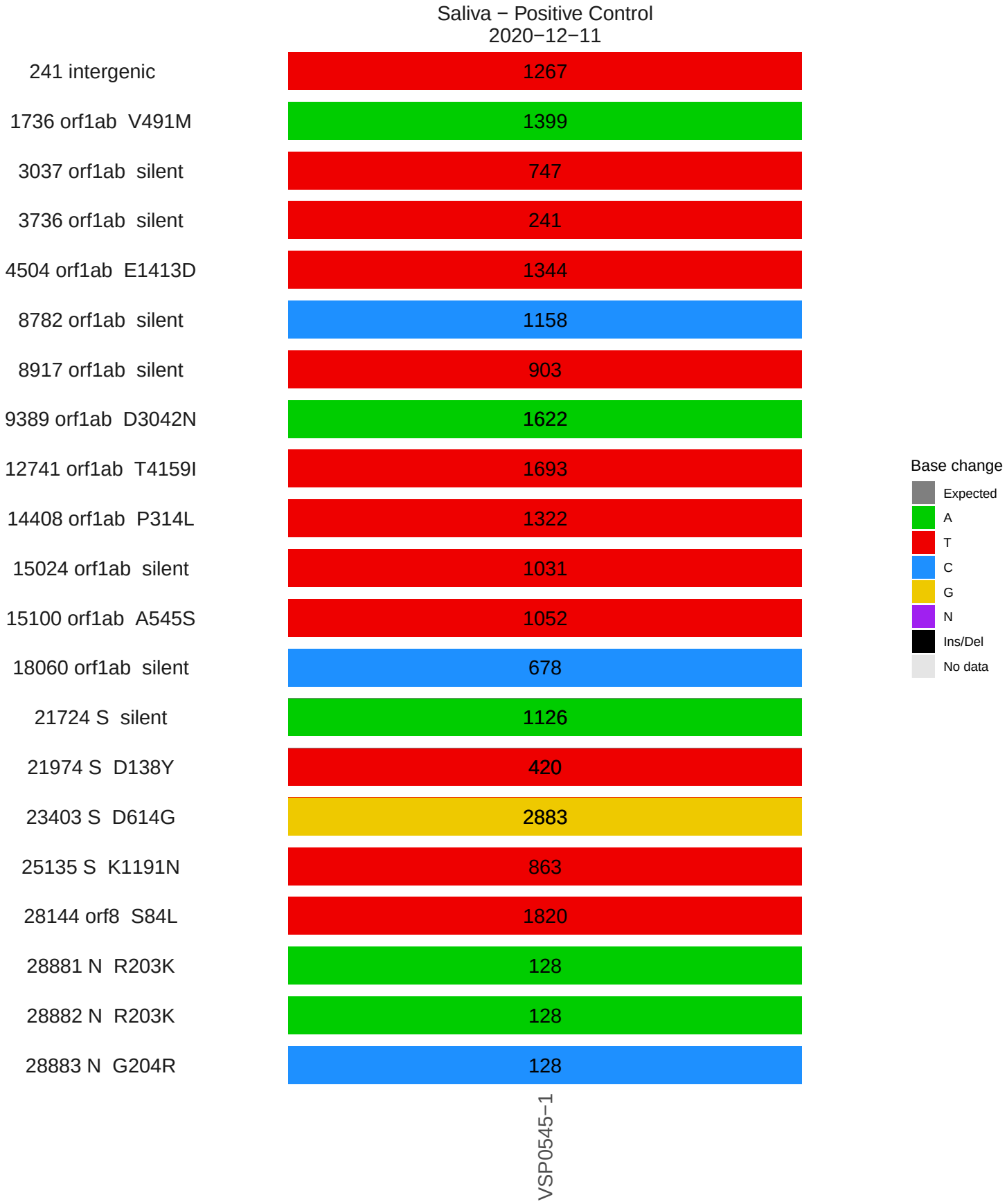
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0545-1	single experiment	NA	Saliva - Positive Control	2020-12-11	22.41	98.9%	97.9%

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.

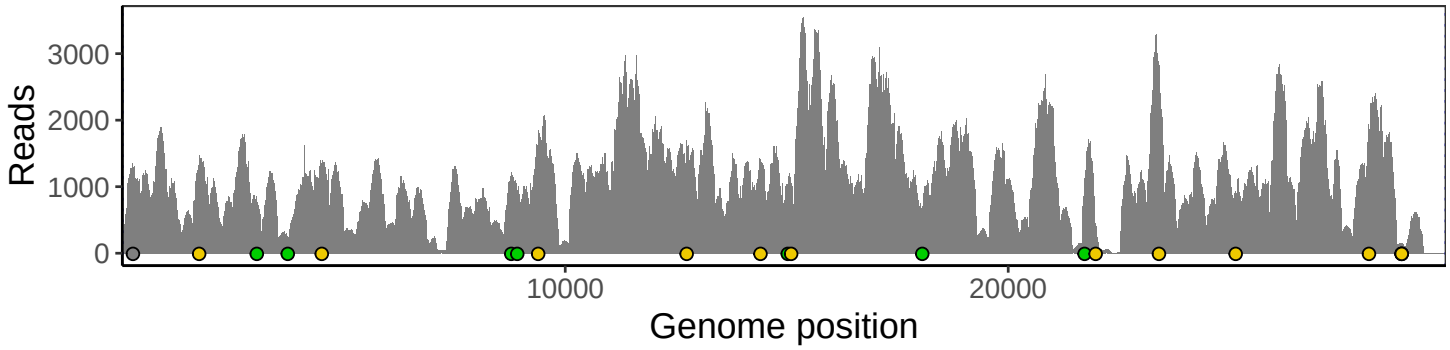



Saliva − Positive Control
2020−12−11
241 intergenic
1267
1736 orf1ab V491M
1399
3037 orf1ab silent
747
3736 orf1ab silent
241
4504 orf1ab E1413D
1344
8782 orf1ab silent
1158
8917 orf1ab silent
903
9389 orf1ab D3042N
1622
12741 orf1ab T4159I
1693
14408 orf1ab P314L
1322
15024 orf1ab silent
1031
15100 orf1ab A545S
1052
18060 orf1ab silent
678
21724 S silent
1126
21974 S D138Y
420
23403 S D614G
2883
25135 S K1191N
863
28144 orf8 S84L
1820
28881 N R203K
128
28882 N R203K
128
28883 N G204R
128
VSP0545−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

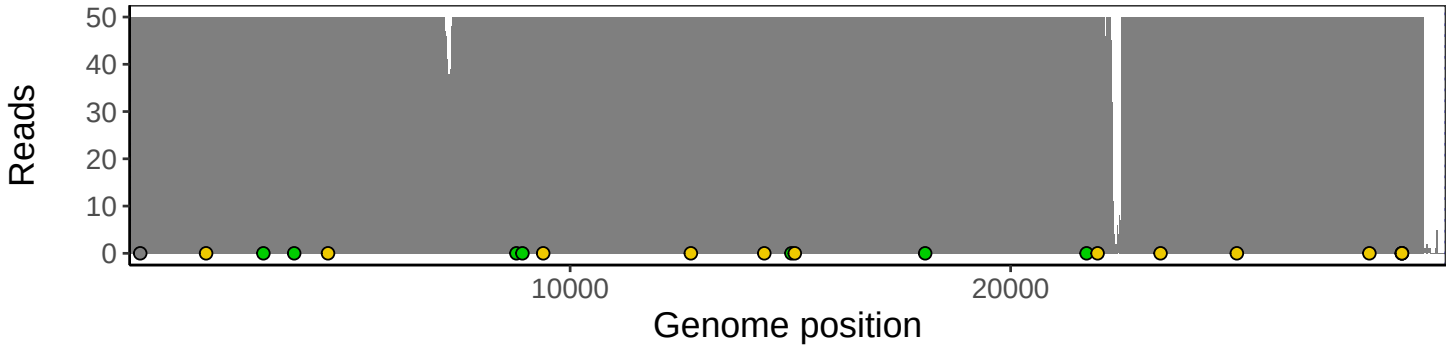
Analyses of individual experiments and composite results.

VSP0545-1 | 2020-12-11 | Saliva - Positive Control | 95-267 | 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.