COVID-19 subject 385

2021-01-11

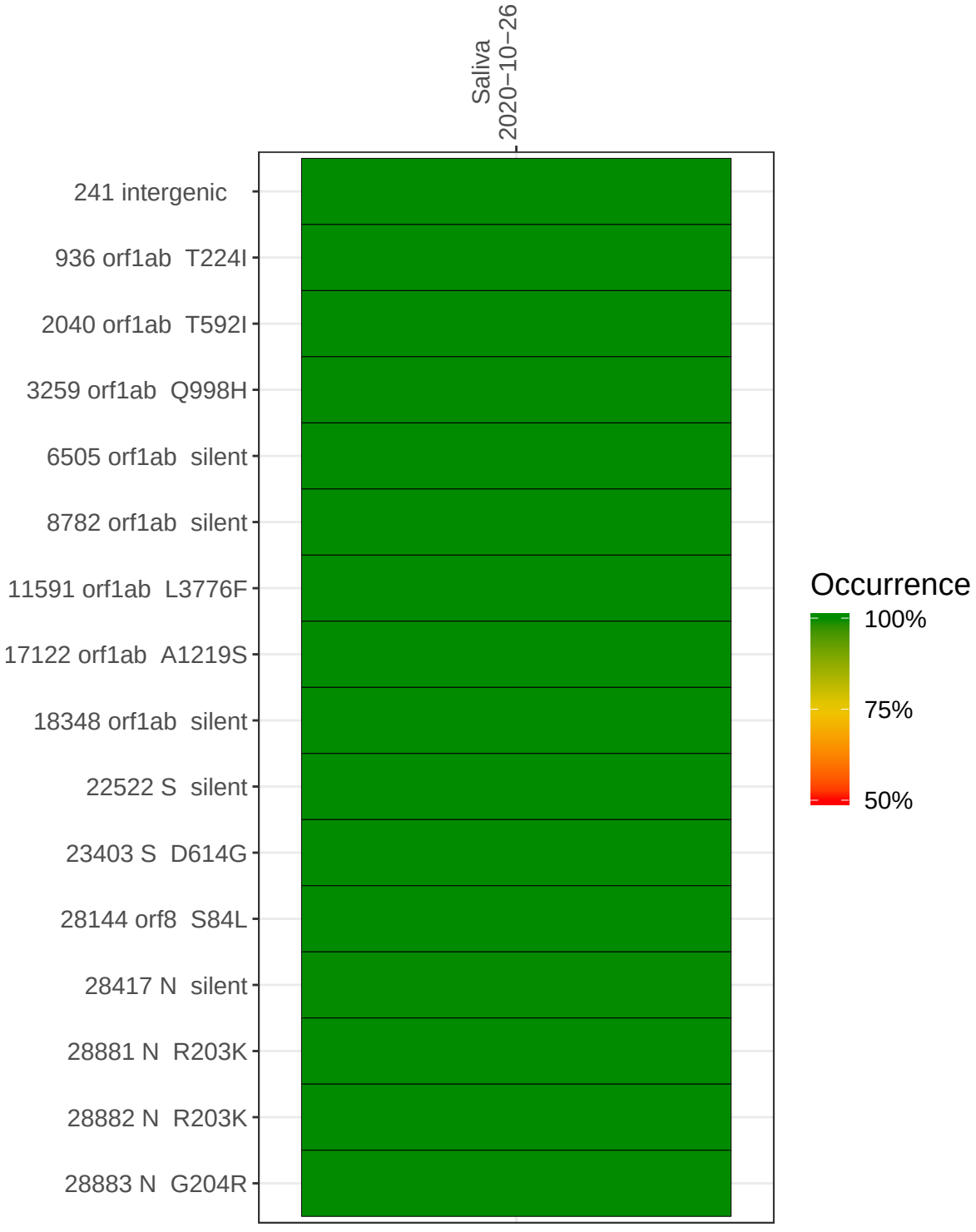
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

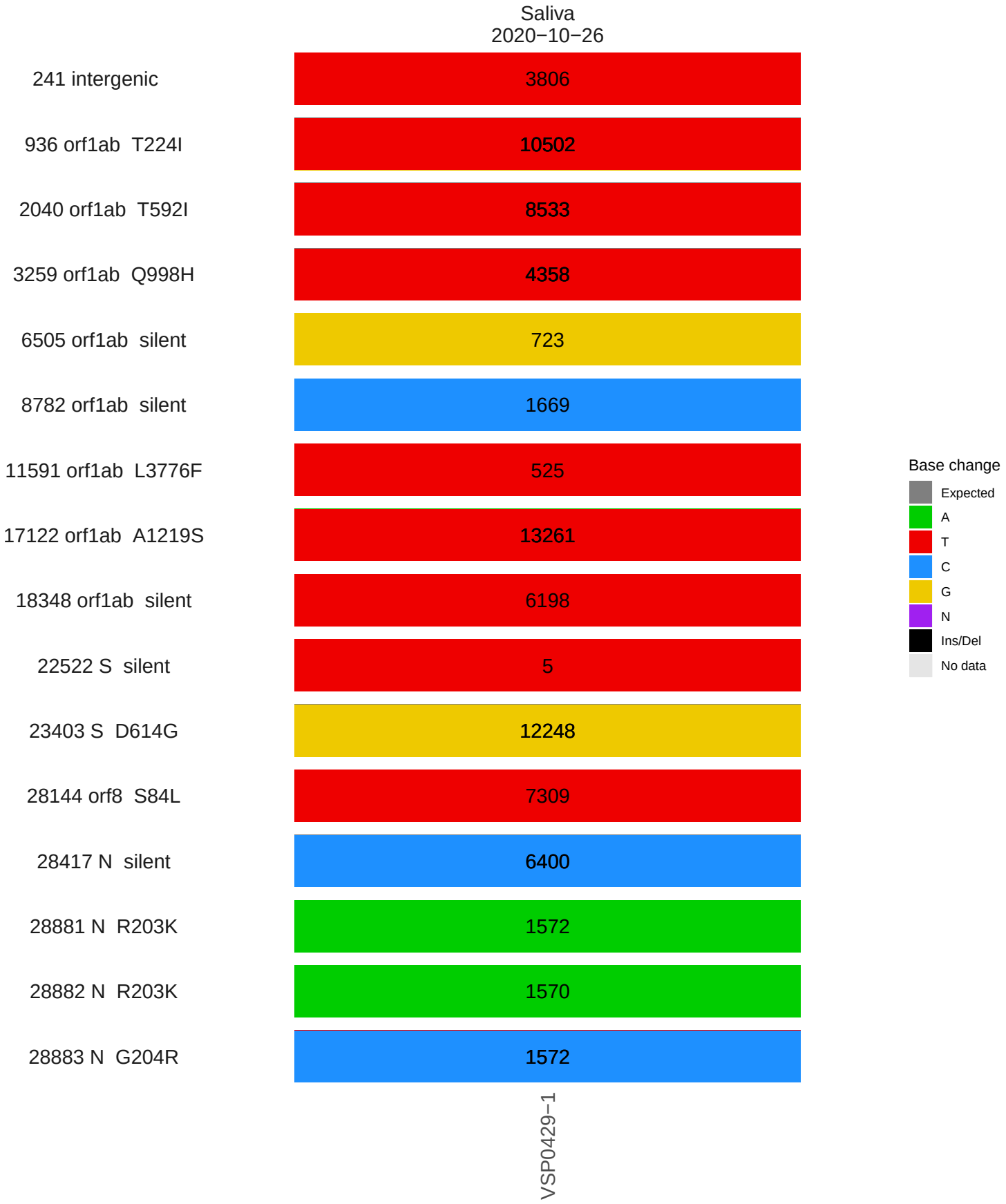
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0429-1	single experiment	NA	Saliva	2020-10-26	1.42	69.0%	64.3%

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.

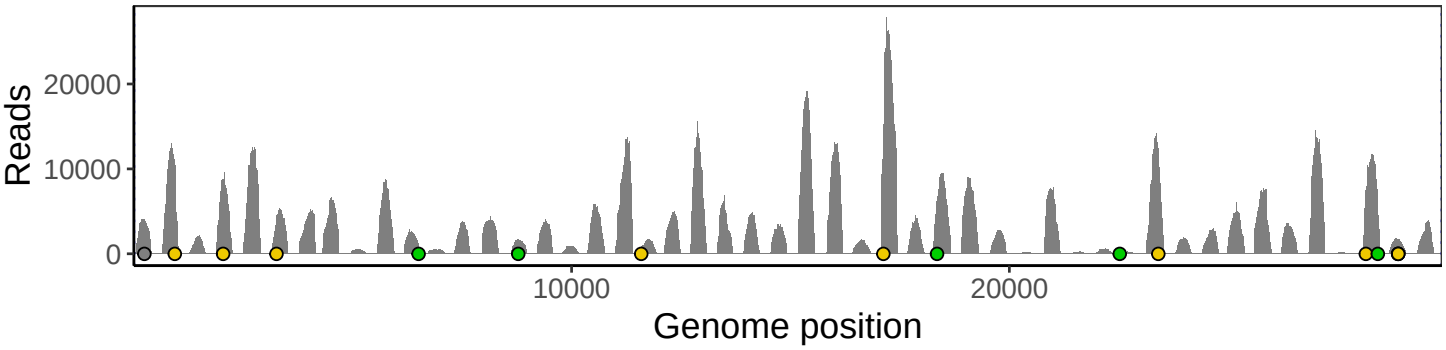



Saliva
2020−10−26
241 intergenic
3806
936 orf1ab T224I
10502
2040 orf1ab T592I
8533
3259 orf1ab Q998H
4358
6505 orf1ab silent
723
8782 orf1ab silent
1669
11591 orf1ab L3776F
525
17122 orf1ab A1219S
13261
18348 orf1ab silent
6198
22522 S silent
5
23403 S D614G
12248
28144 orf8 S84L
7309
28417 N silent
6400
28881 N R203K
1572
28882 N R203K
1570
28883 N G204R
1572
VSP0429−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

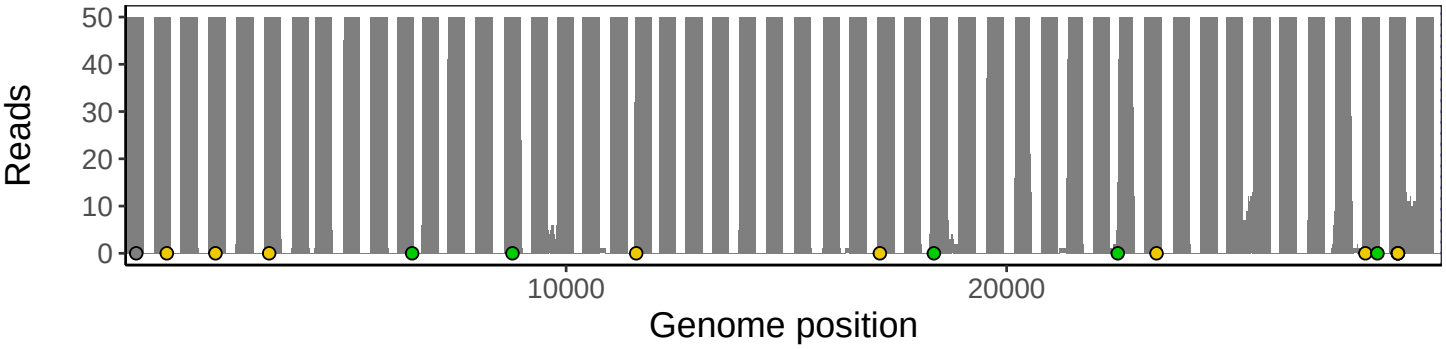
Analyses of individual experiments and composite results.

VSP0429-1 | 2020-10-26 | Saliva | 385s-q | 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.