COVID-19 subject 2749

2021-01-06

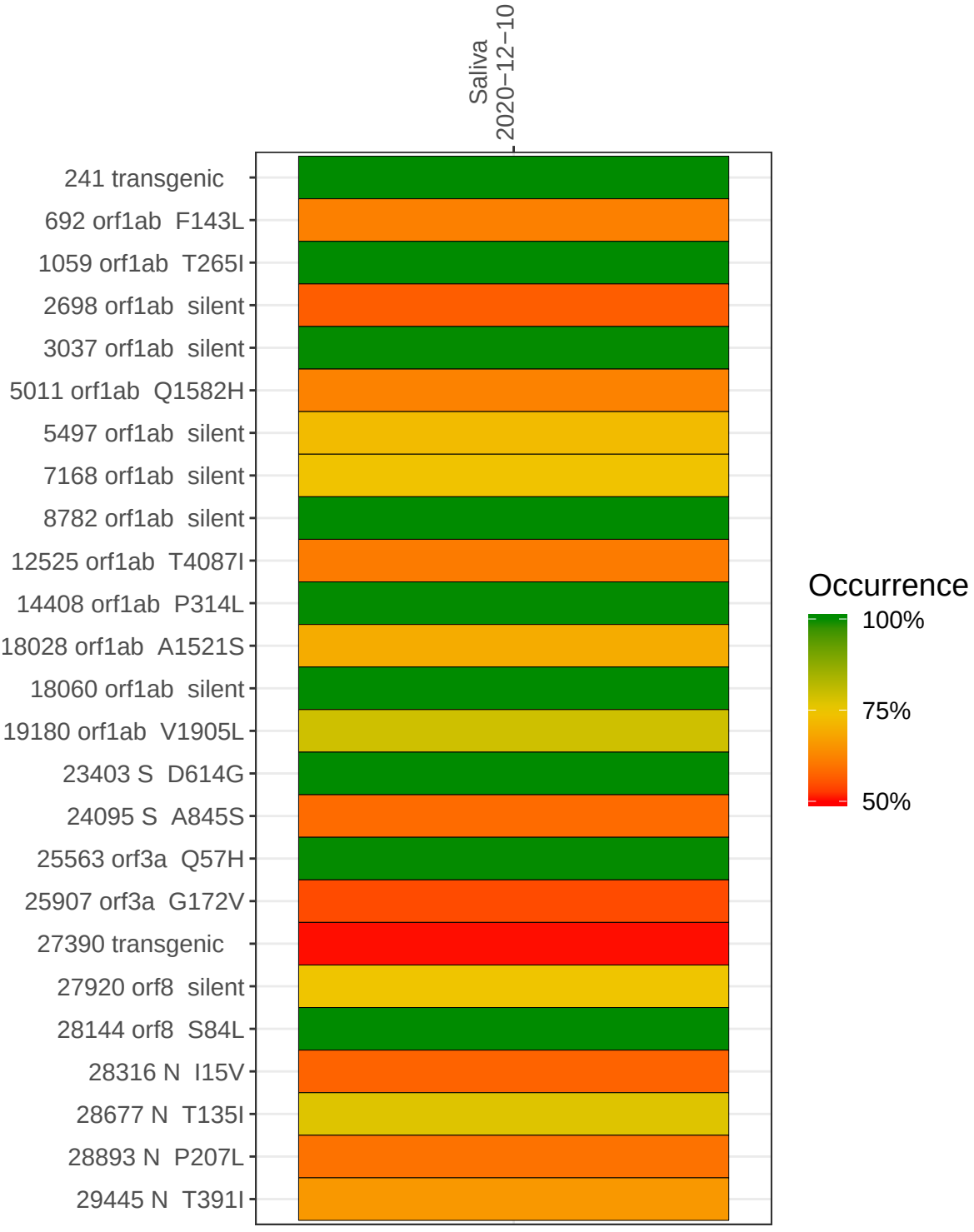
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

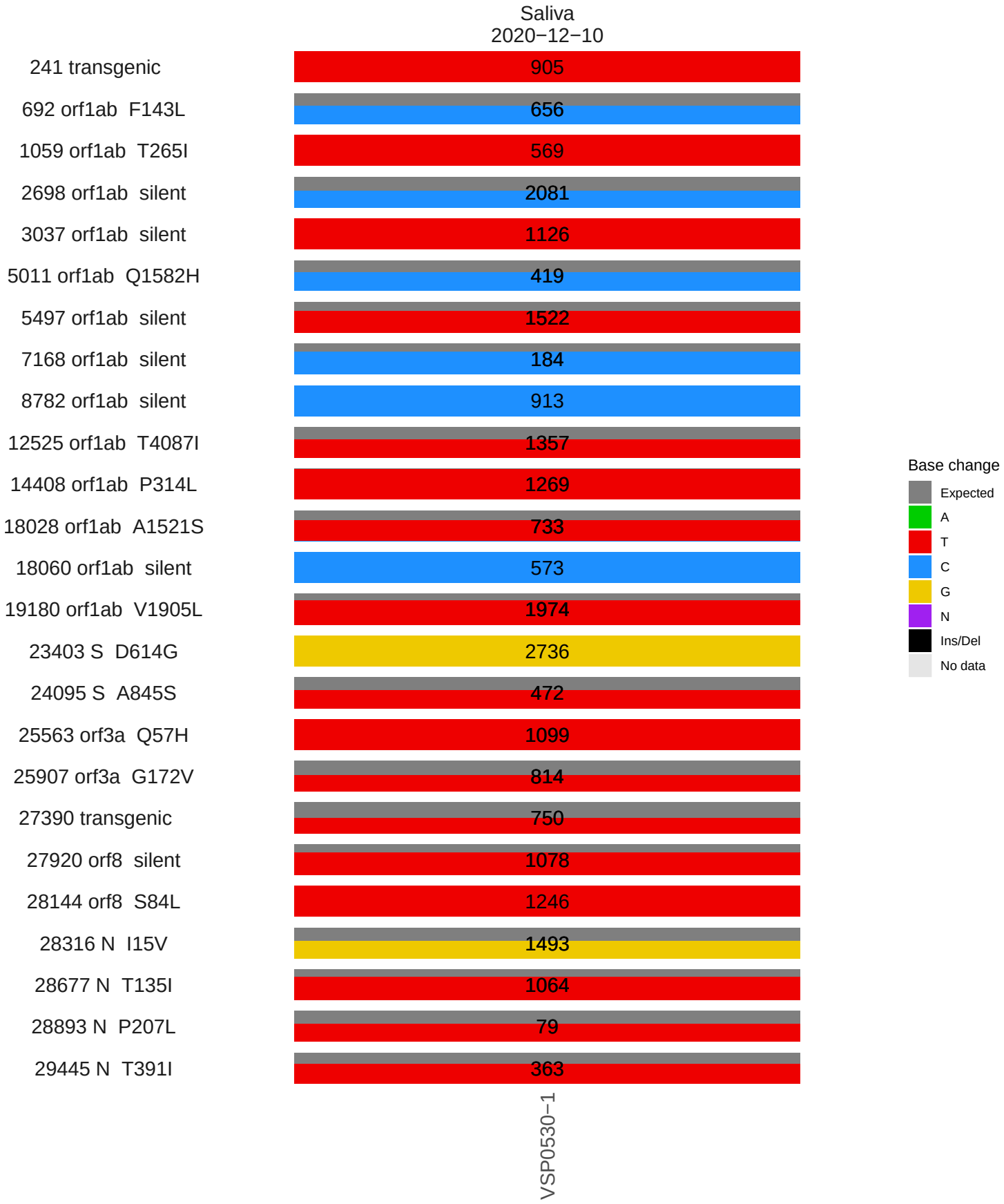
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0530-1	single experiment	NA	Saliva	2020-12-10	21.64	99.2%	99.2%

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.

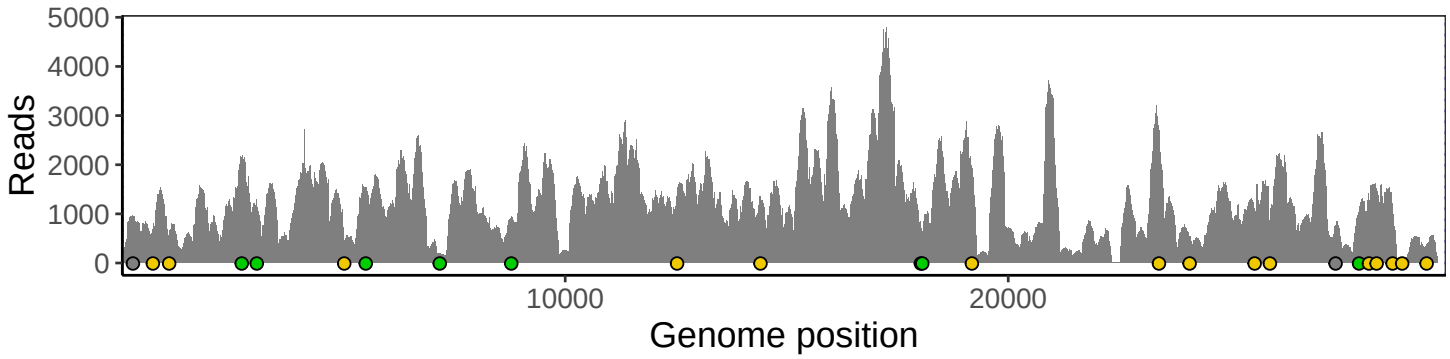



Saliva
2020−12−10
241 transgenic
905
692 orf1ab F143L
656
1059 orf1ab T265I
569
2698 orf1ab silent
2081
3037 orf1ab silent
1126
5011 orf1ab Q1582H
419
5497 orf1ab silent
1522
7168 orf1ab silent
184
8782 orf1ab silent
913
12525 orf1ab T4087I
1357
14408 orf1ab P314L
1269
18028 orf1ab A1521S
733
18060 orf1ab silent
573
19180 orf1ab V1905L
1974
23403 S D614G
2736
24095 S A845S
472
25563 orf3a Q57H
1099
25907 orf3a G172V
814
27390 transgenic
750
27920 orf8 silent
1078
28144 orf8 S84L
1246
28316 N I15V
1493
28677 N T135I
1064
28893 N P207L
79
29445 N T391I
363
VSP0530−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

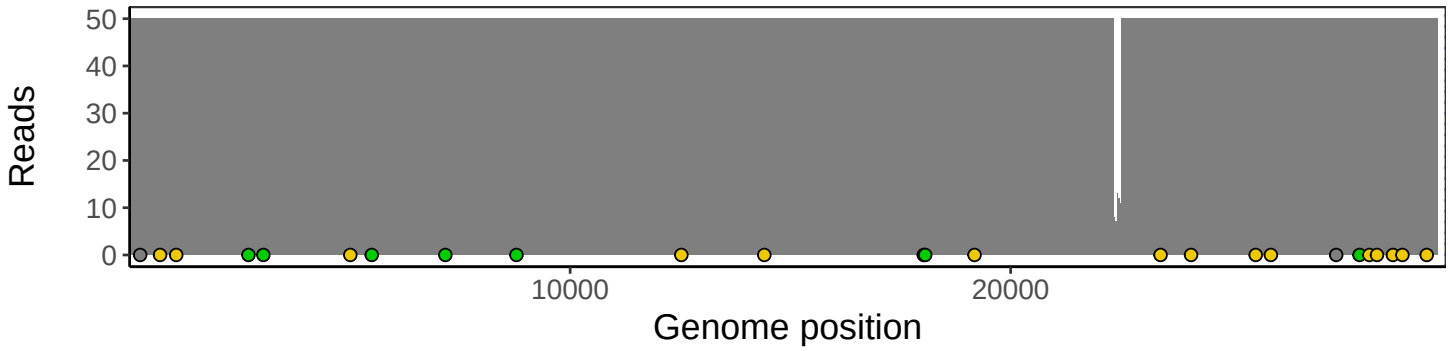
Analyses of individual experiments and composite results.

VSP0530-1 | 2020-12-10 | Saliva | 2749 | 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.