COVID-19 subject 408

2021-01-11

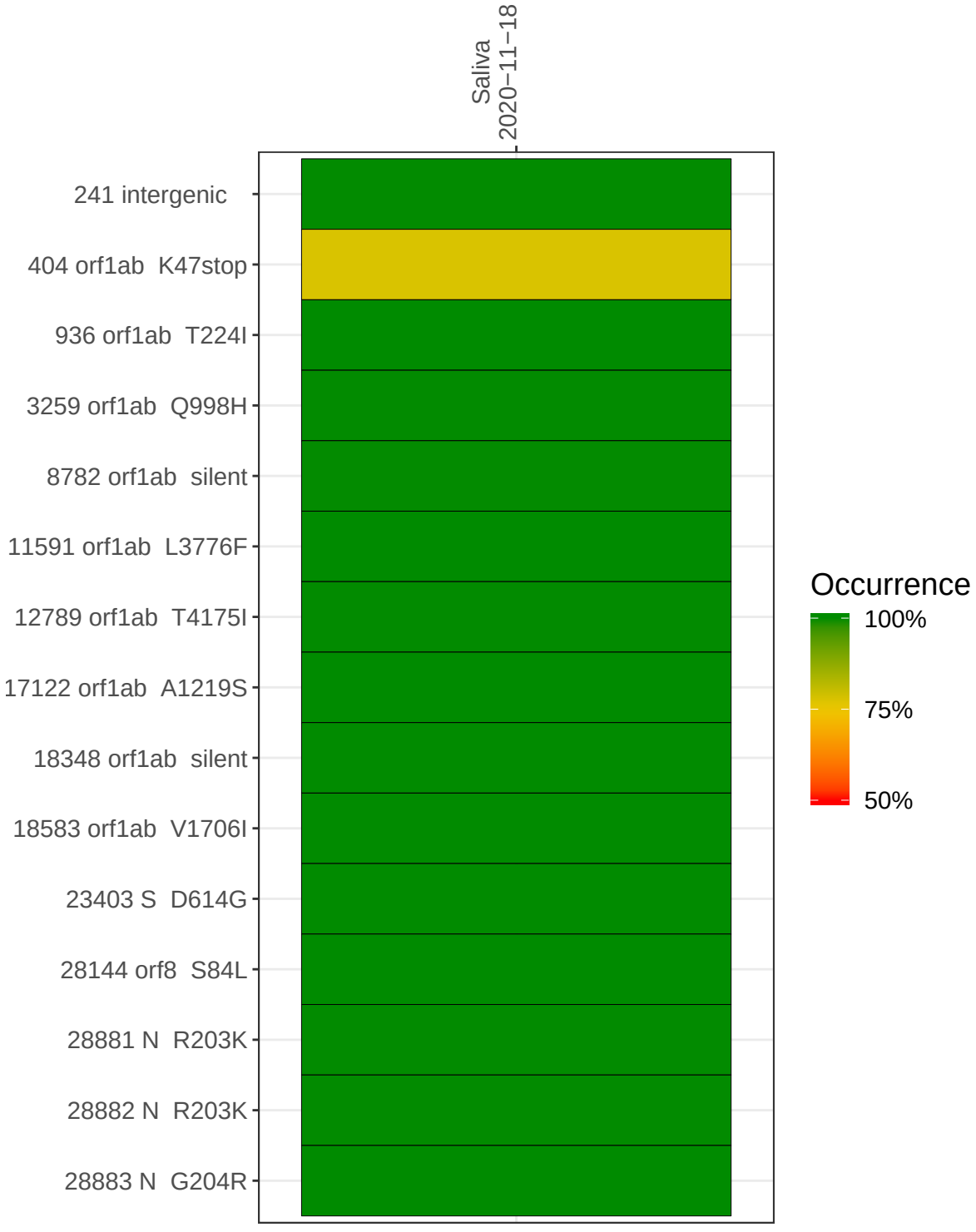
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

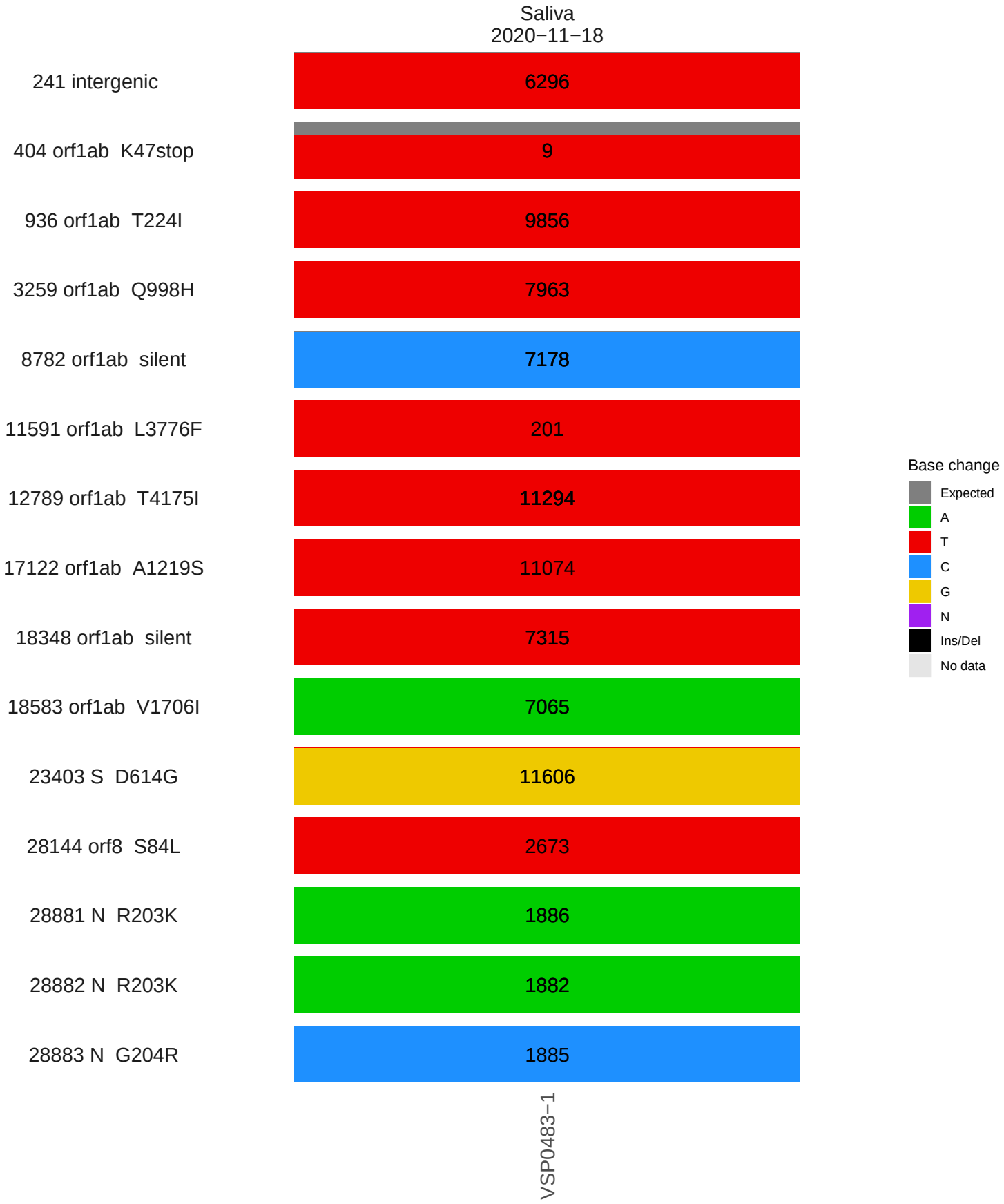
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0483-1	single experiment	NA	Saliva	2020-11-18	1.32	72.9%	64.4%

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.

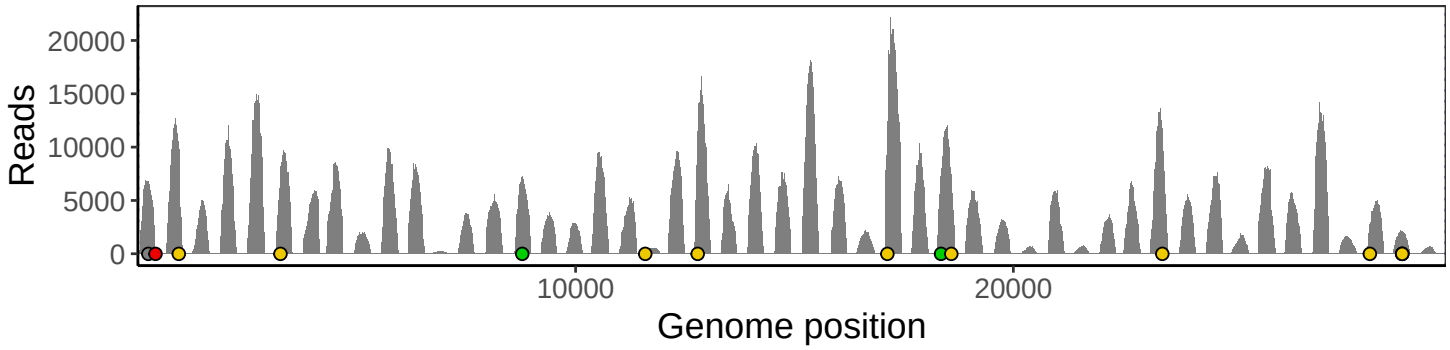



Saliva
2020−11−18
241 intergenic
6296
404 orf1ab K47stop
9
936 orf1ab T224I
9856
3259 orf1ab Q998H
7963
8782 orf1ab silent
7178
11591 orf1ab L3776F
201
12789 orf1ab T4175I
11294
17122 orf1ab A1219S
11074
18348 orf1ab silent
7315
18583 orf1ab V1706I
7065
23403 S D614G
11606
28144 orf8 S84L
2673
28881 N R203K
1886
28882 N R203K
1882
28883 N G204R
1885
VSP0483−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

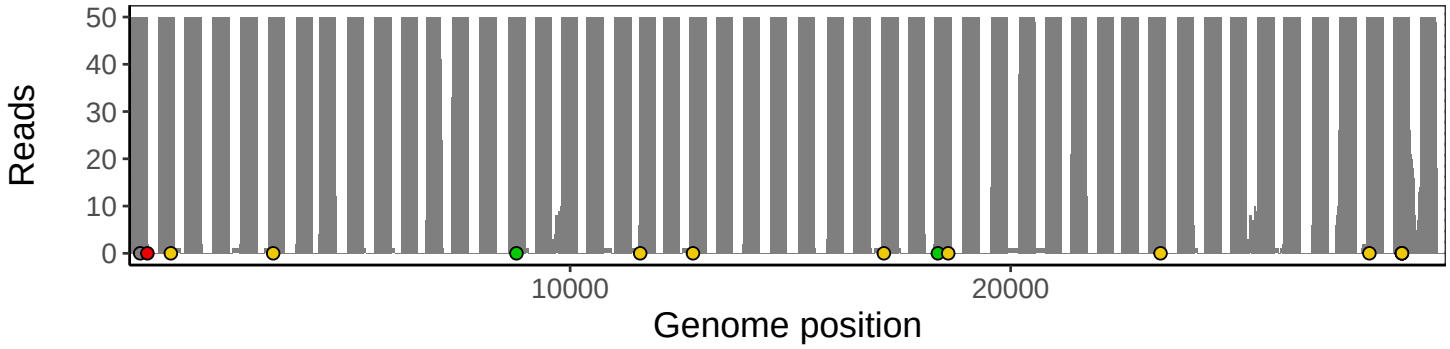
Analyses of individual experiments and composite results.

VSP0483-1 | 2020-11-18 | Saliva | 408s-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.