

# COVID-19 subject H2101300054

*2021-04-17*

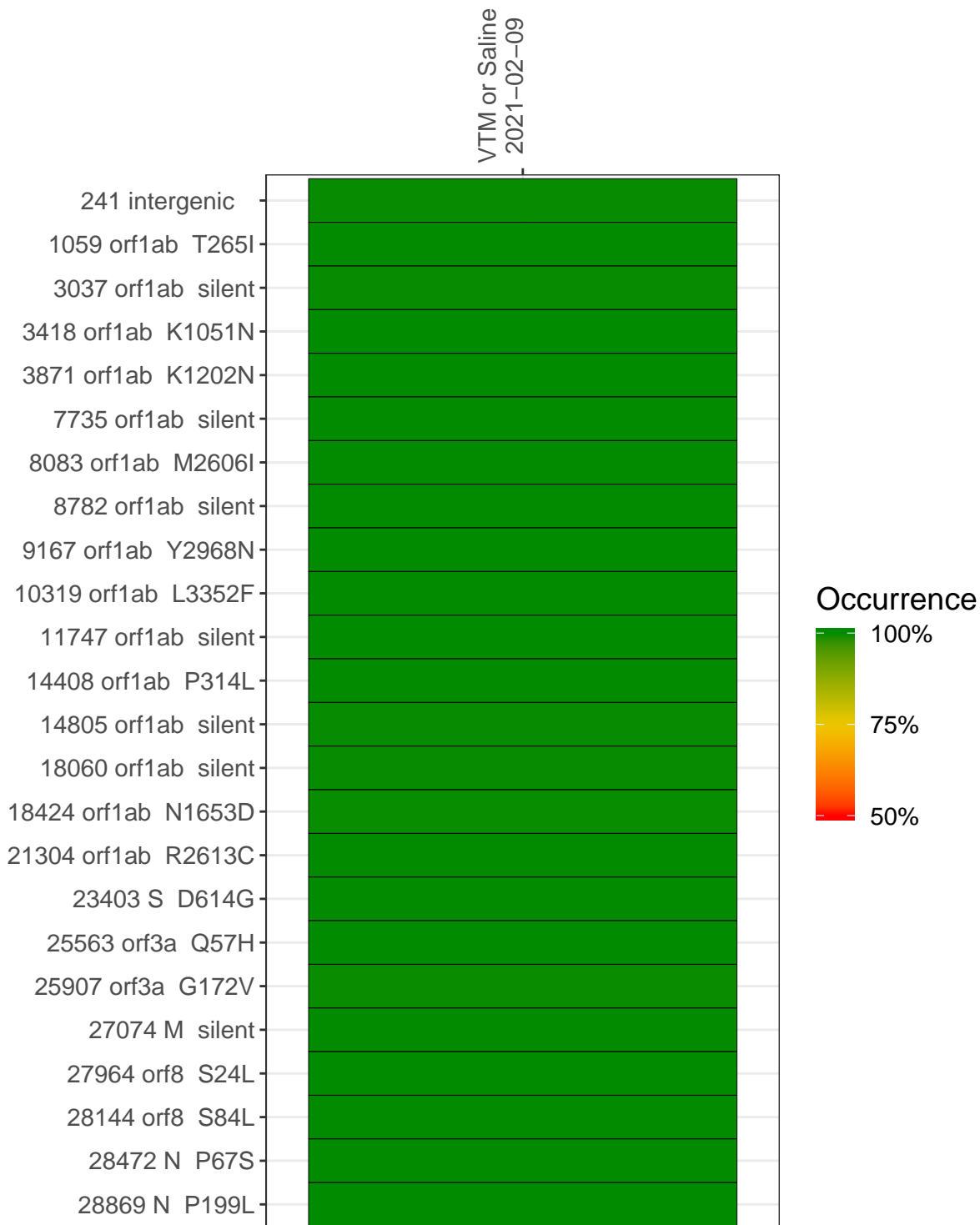
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP0659	composite	NA	VTM or Saline	2021-02-09	29.97	B.1.2	99.9%	99.8%
VSP0659-1	single experiment	NA	VTM or Saline	2021-02-09	29.99	B.1.2	99.9%	99.8%
VSP0659-2	single experiment	NA	VTM or Saline	2021-02-09	29.85	B.1.2	99.8%	99.8%

## Variants shared across samples

The heat map below shows how variants (reference genome `/home/everett/projects/SARS-CoV-2-Philadelphia/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 or 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.



VTM or Saline  
2021-02-09

241 intergenic	30195	2424	
1059 orf1ab T265I	18482	4018	
3037 orf1ab silent	26927	1956	
3418 orf1ab K1051N	28920	3770	
3871 orf1ab K1202N	15387	3693	
7735 orf1ab silent	28477	3041	
8083 orf1ab M2606I	37749	3211	
8782 orf1ab silent	41001	3128	
9167 orf1ab Y2968N	33587	3626	
10319 orf1ab L3352F	41801	3758	
11747 orf1ab silent	38245	2708	
14408 orf1ab P314L	41134	3187	
14805 orf1ab silent	42022	4008	
18060 orf1ab silent	26513	3573	
18424 orf1ab N1653D	45603	3162	
21304 orf1ab R2613C	8883	726	
23403 S D614G	41290	4850	
25563 orf3a Q57H	25676	3913	
25907 orf3a G172V	16278	2984	
27074 M silent	60299	4301	
27964 orf8 S24L	23461	2524	
28144 orf8 S84L	23702	4837	
28472 N P67S	29355	4479	
28869 N P199L	7200	1007	

Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

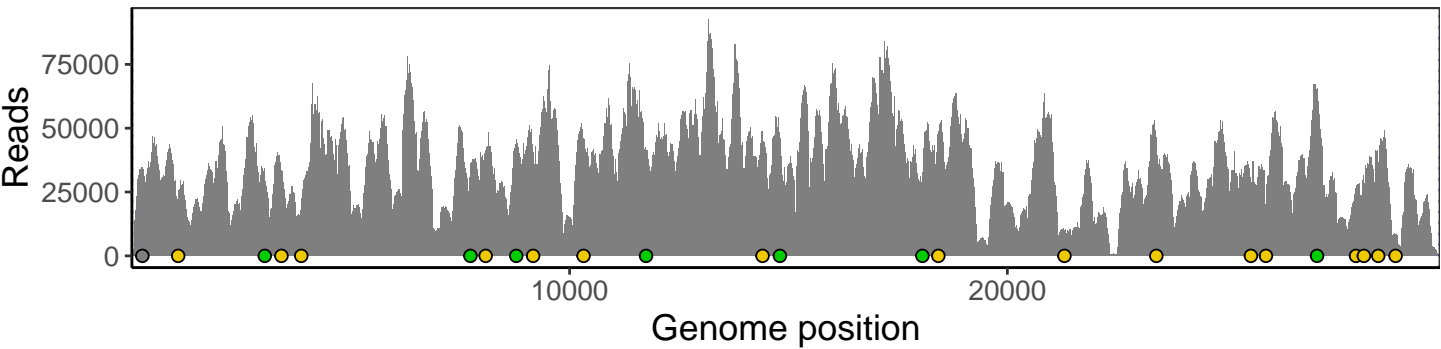
VSP0659-1

VSP0659-2

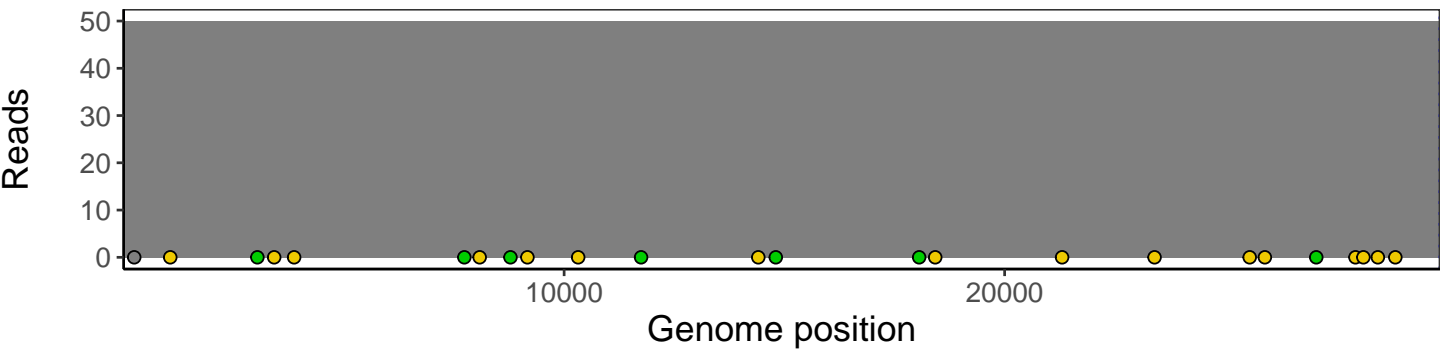
# Analyses of individual experiments and composite results

VSP0659 | 2021-02-09 | VTM or Saline | H2101300054 | composite result

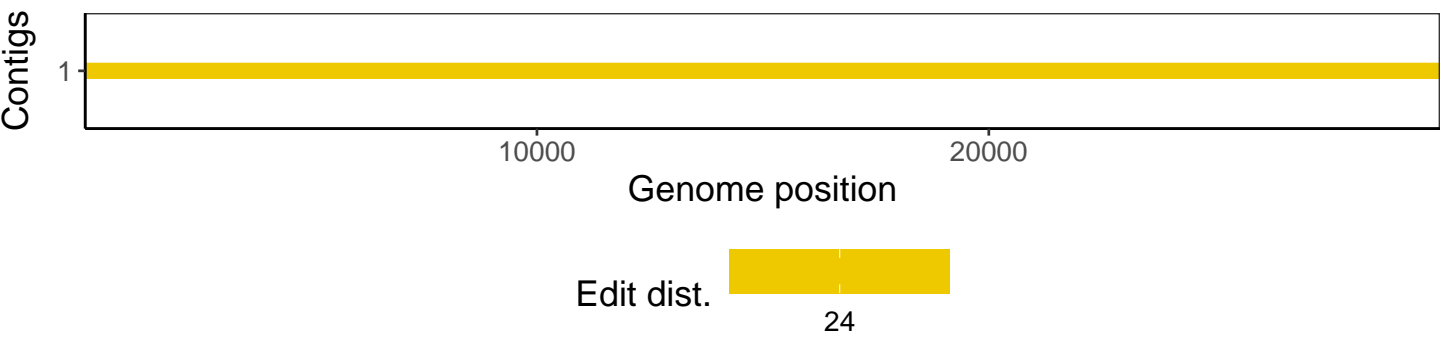
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



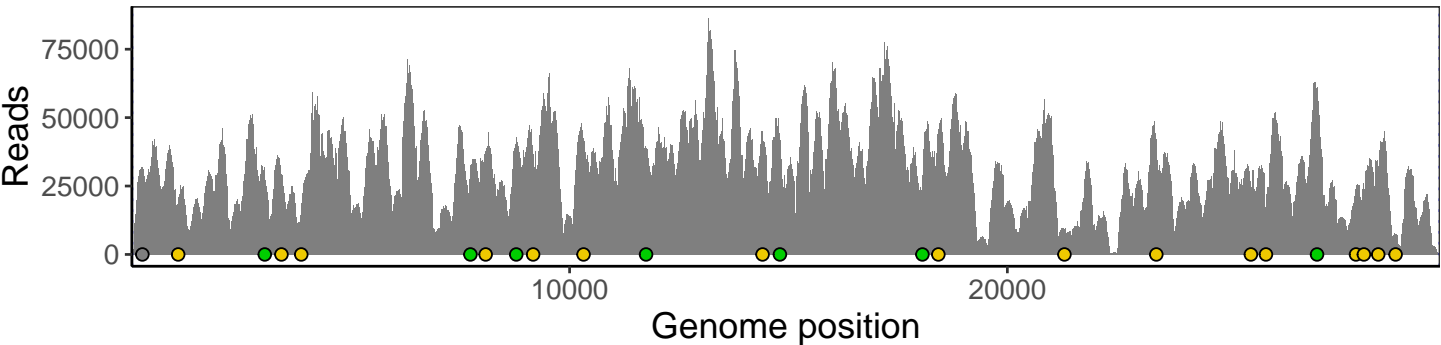
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



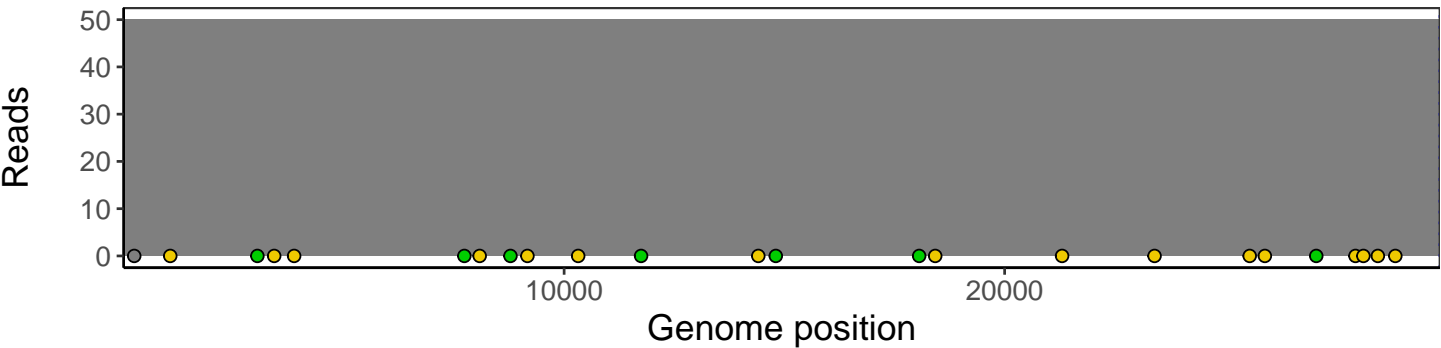
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



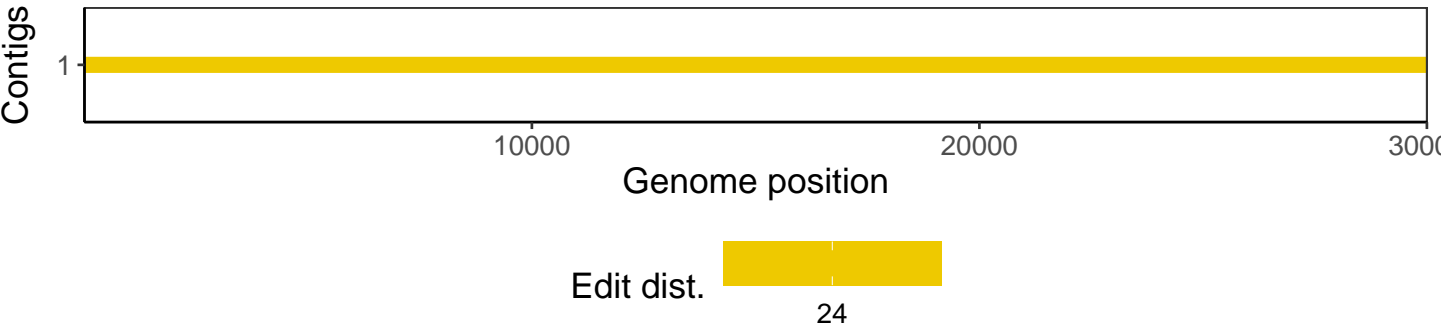
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



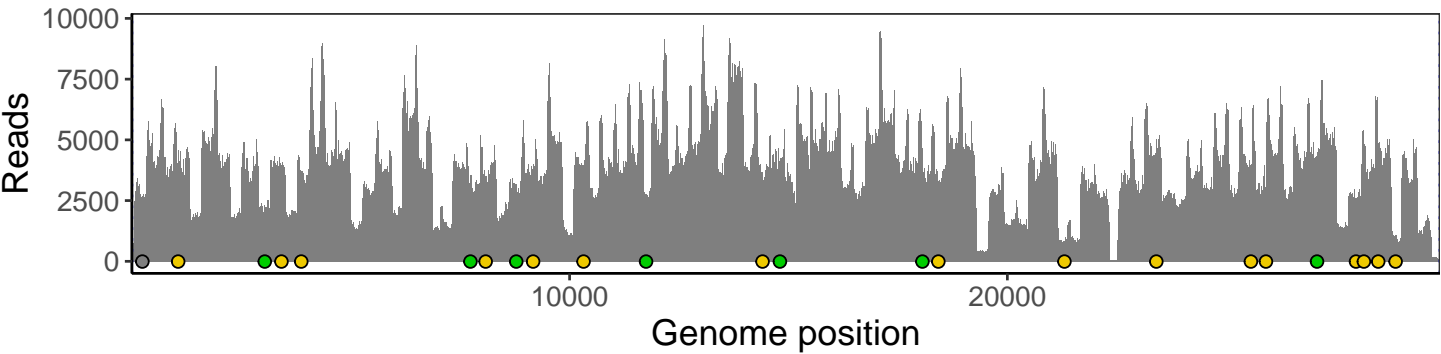
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



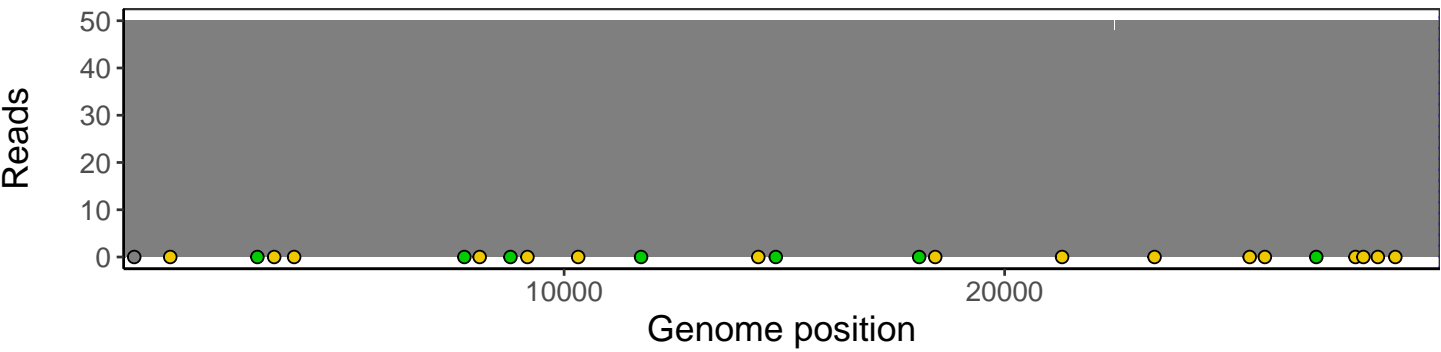
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



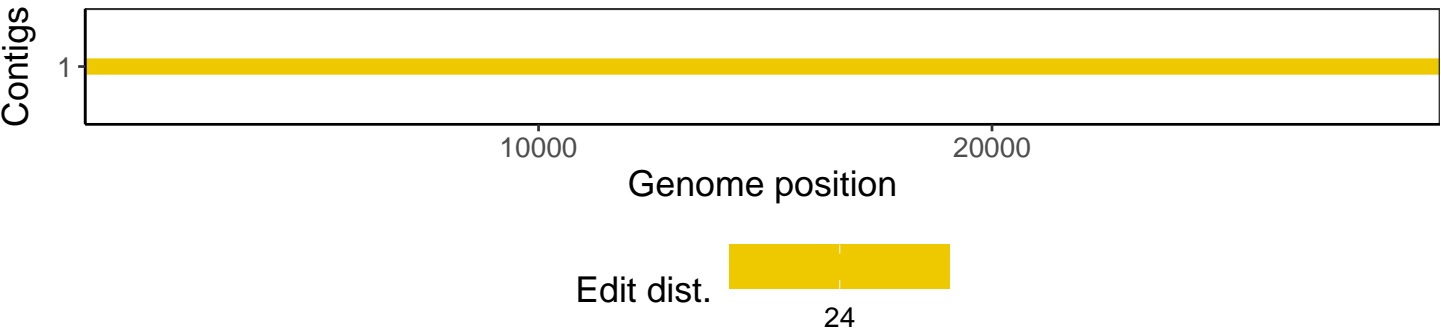
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



## Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 1.10.2-57-gf58a6f3
pangolin	2.3.8
genbankr	1.4.0
optparse	1.6.0
forcats	0.3.0
stringr	1.4.0
dplyr	0.8.1
purrr	0.2.5
readr	1.1.1
tidyr	0.8.1
tibble	2.1.2
ggplot2	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
GenomeInfoDb	1.12.3
Biostrings	2.44.2
XVector	0.16.0
IRanges	2.10.5
S4Vectors	0.14.7
BiocParallel	1.10.1
BiocGenerics	0.22.1