Accelerated case rates led to herd immunity but also elderly and male mortality in Amazonas, Brazil during the COVID-19 pandemic

Adam Zimmerman

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Background and Overview

What happened in the Amazon and São Paulo during COVID-19?

This exploratory analysis of tabular and genetic data shows that the city of Manaus, and its Northern Brazilian state, Amazonas, were hit harder per capita than the city and state of São Paulo through the second and third quarters (Q2; Q3) of 2020.

From Q2 into Q3, the intense period of infection correlated with the emergence of an antibody prevalence among Manaus blood donors that was approximately threefold greater than antibody prevalence among São Paulo blood donors (Figure 4; Buss *et al.*, 2020). This is an indication of good news and herd immunity for Manaus, heading into Q4. But the path to that antibody prevalence was characterized by a two- to three-fold increase in mortality for Manaus residents, especially those that were male and over 65 (Figure 6; Prowse *et al.*, 2020).

Additionally, a variant call analysis of 33 SARS-CoV-2 samples from patients across the Northern Brazilian states surrounding Manaus showed that the greatest numbers of high quality single nucleotide polymorphisms (SNPs) displayed substitutions of thymine with guanine.

Methods

Rstudio 4.0.2 and Ubuntu 20.04 powered two novel tabular data analyses (Figures 1-6), as well as a variant call analysis (Figures 7-8) developed by Dr. Naupaka Zimmerman.

Tabular data methods

TODO: tabular parsing walkthrough: trace piping especially:

Throughout 2020, Oxford hosted a large amount of tabular epidemiological COVID-19 data from across the world. This provided the demographics and case rates data of Manaus and São Paulo (Figures 1-3).

Buss and colleagues (Buss *et al.*, 2020)

In the final steps of data processing, I temporarily created a column in `Mortality_data.csv` that compared the ratios of mortality figures. I selected the age range 55-60 to show the maximum ratio seen between male and female excess mortality in Manaus, March through June, 2020.

Genetic data methods

Illumina NGS runs were collected as 33 .fasta files from the NCBI SRA website. Under the project number PRJNA662684, the runs came grouped by region, being specific to the Brazilian Amazon.
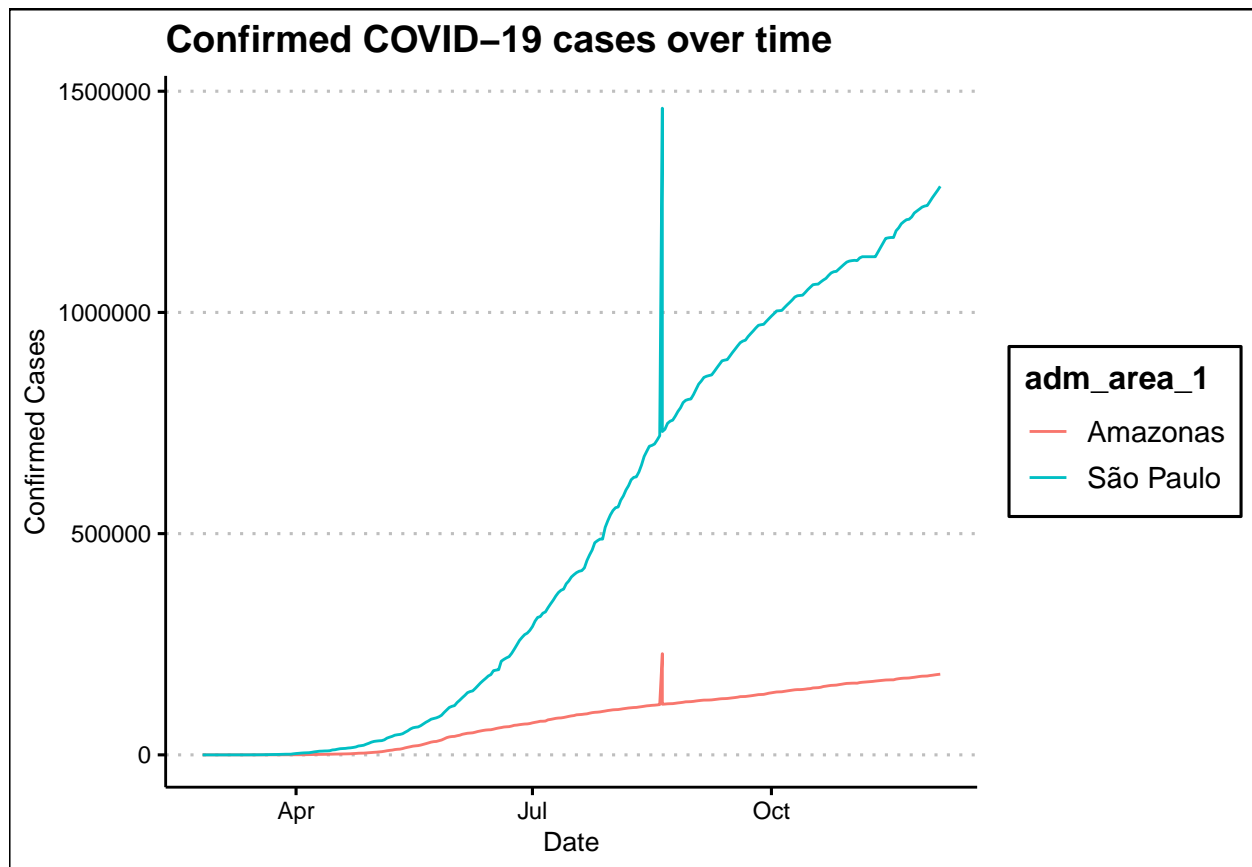
\textcolor{red}{TODO:Data were downloaded from the NCBI SRA archive from project numbers __ on date. Then processed with trimmomatic and run through a bwa variant calling pipeline (CITATION from bwa paper). ... That data was then brought into RStudio to analyze in combination. Include steps of modifying datatables, if applicable.)}

TODO: sequencing and bash walkthrough: trace scripts as sets by format; citations

Lastly, single nucleotide polymorphisms (SNPs) were tallied and grouped by region, gene, and quality (Table 1).

Results and Discussion

Tabular data analysis

Cities like Manaus track and report mortality on an ongoing basis, setting a baseline for deaths per week. Excess mortality is the observed number of deaths, minus the baseline expected mortality. Mortality is measured in deaths per 1000 people.

Total female mortality (996) was more than double (2.13x) expected mortality (468) in the oldest age group of patients, over 75 (not pictured; Prowse *et al.*, 2020). In fact, the situation was worse for slightly younger female patients, ages 65-70, who faced a total mortality (283) 2.78x expected mortality (102) (Figure 5; Prowse *et al.*, 2020).

In contrast, total male mortality (1208) were higher in raw numbers, as well as in proportion (3.16x) to expected mortality (382) in the oldest age group of patients, over 75 (not pictured; Prowse *et al.*, 2020). The ratio of expected (149) to observed mortality (510) was most severe at 3.42x in men, ages 65-70 (Figure 6; Prowse *et al.*, 2020).

In summary, living in Manaus, being over 65, and being male correlated with elevated mortality for Brazilians facing COVID-19 in Q2 and Q3 of 2020.

Genetic data analysis

Typical read quality was high across the 33 SARS-CoV-2 samples in the the Northern Brazil NCBI project analyzed 0 (Figure 7).

The majority of single nucleotide polymorphism mutations (SNPs) among Brazilian sample genomes were substitutions of thymine with guanine (Figure 8). While this trend is very clear, the implications of it would require further discovery to elucidate.

Figures

Figure 1: The state of São Paulo saw more total confirmed cases than the state of Amazonas.
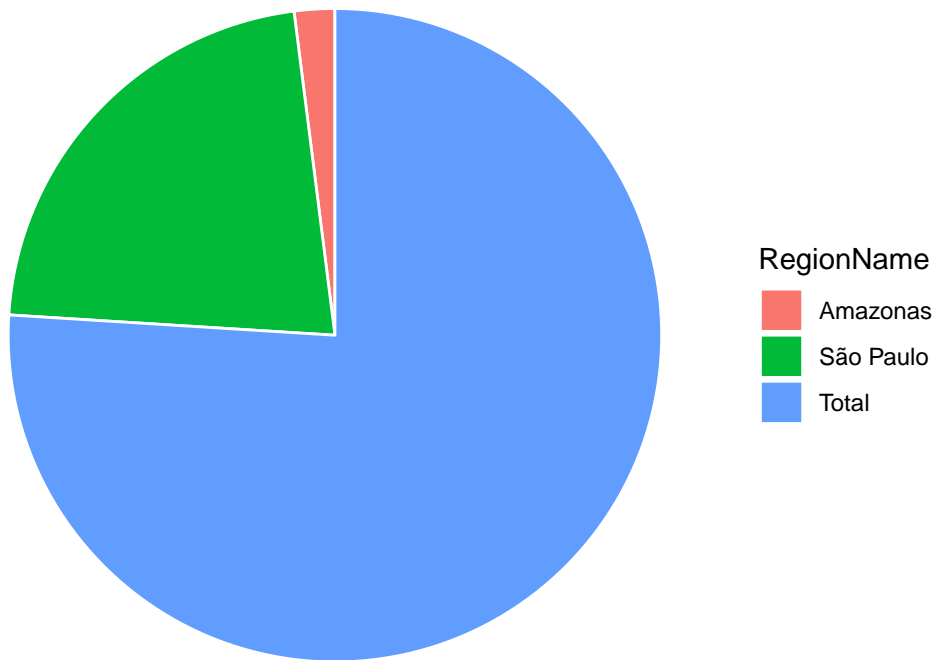
Population of Brazil

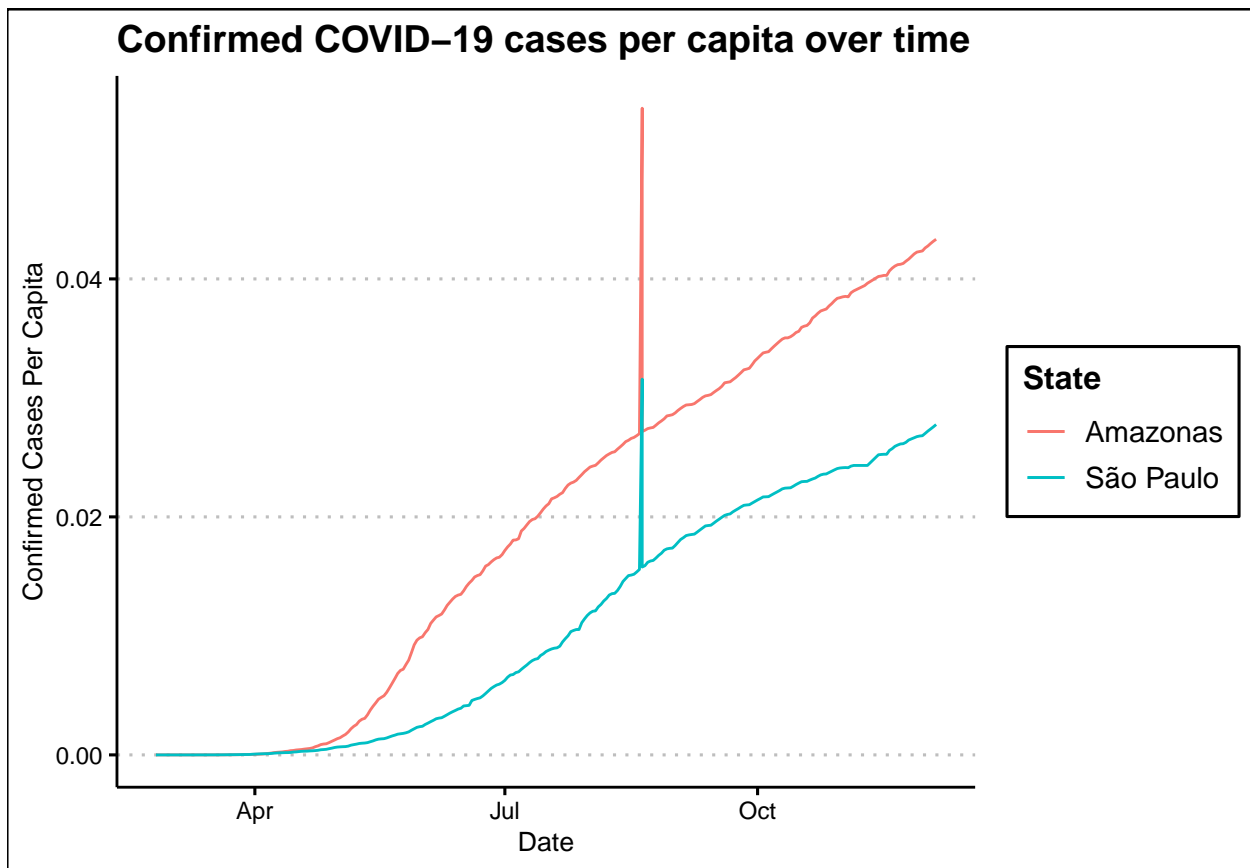**Figure 2**: The state of São Paulo is much larger than Amazonas by population at 46 million versus 4 million.

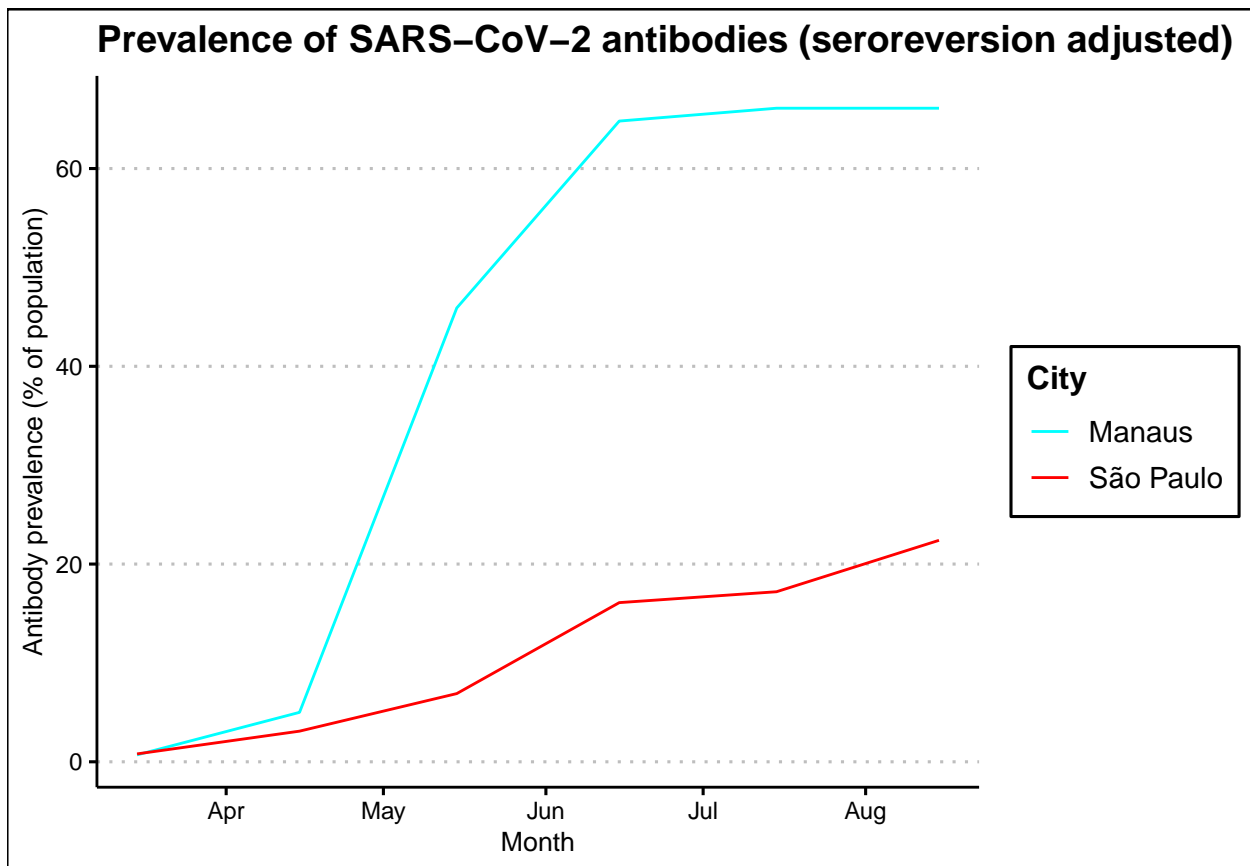**Figure 3**: Amazonas saw greater confirmed cases per capita than São Paulo.

Figure 4: Manaus saw more widespread prevalence of SARS-CoV-2 antibodies vs. São Paulo, up to 66% vs. 22% of the population respectively.
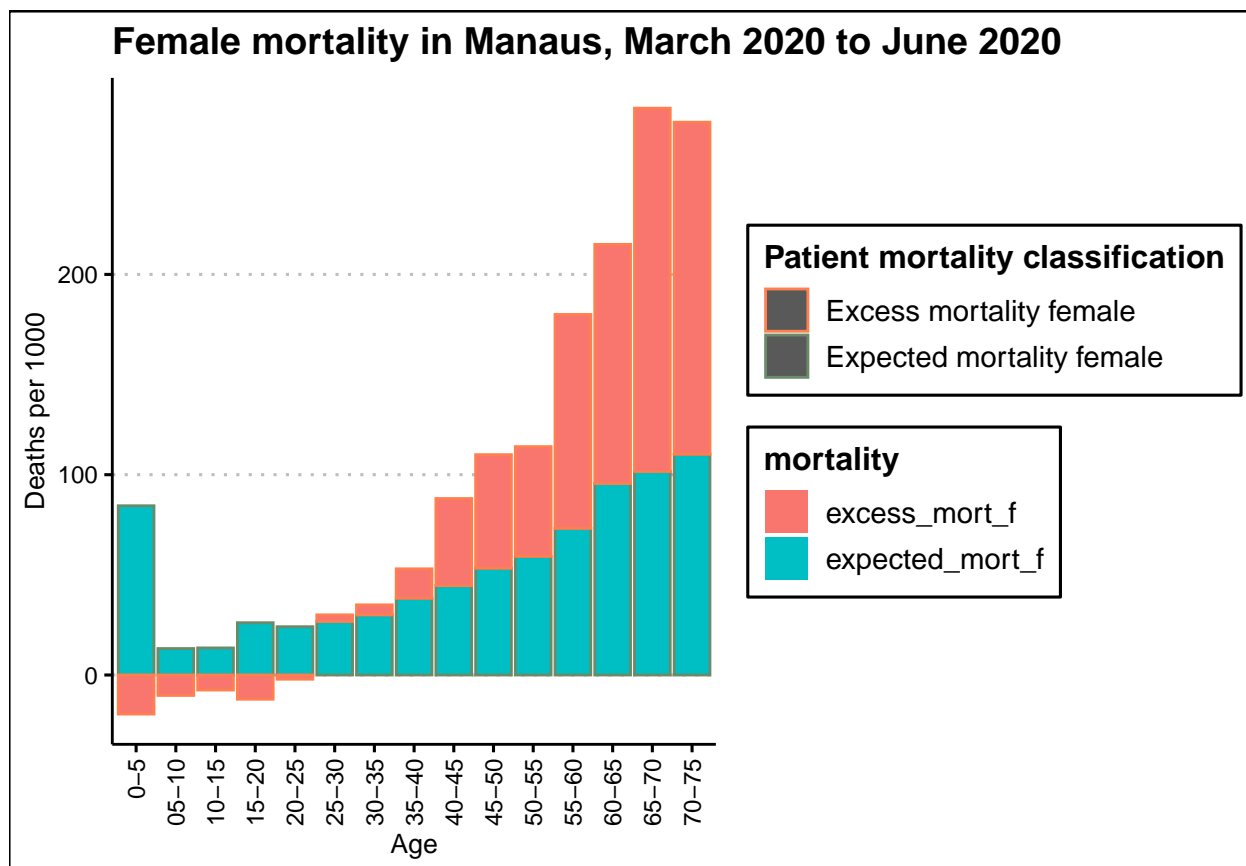
Figure 5: Excess female mortality reached a maximum of 2.13 times the expected mortality in female patients at .
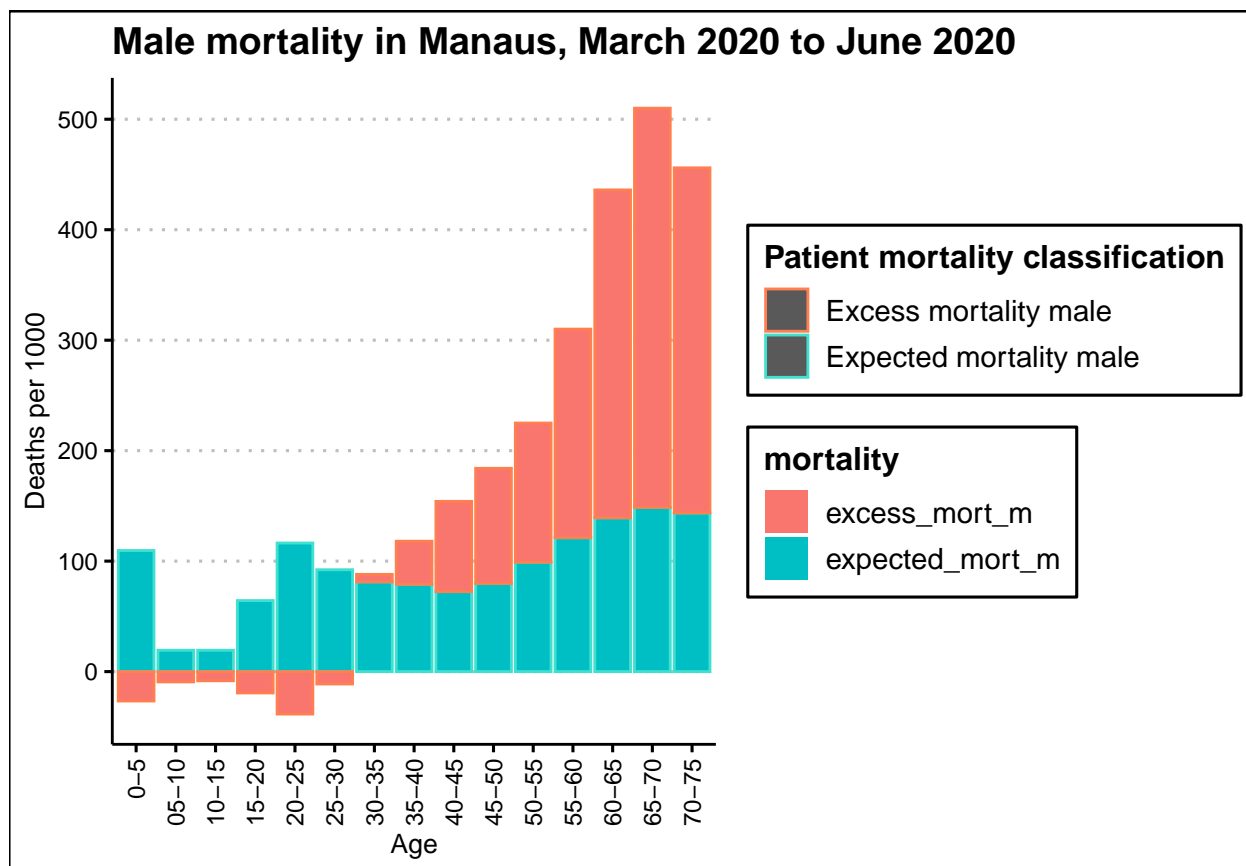
Figure 6: Excess mortality, unexpected deaths of any cause, reached a maximum of 2.49 times the expected mortality in female patients.
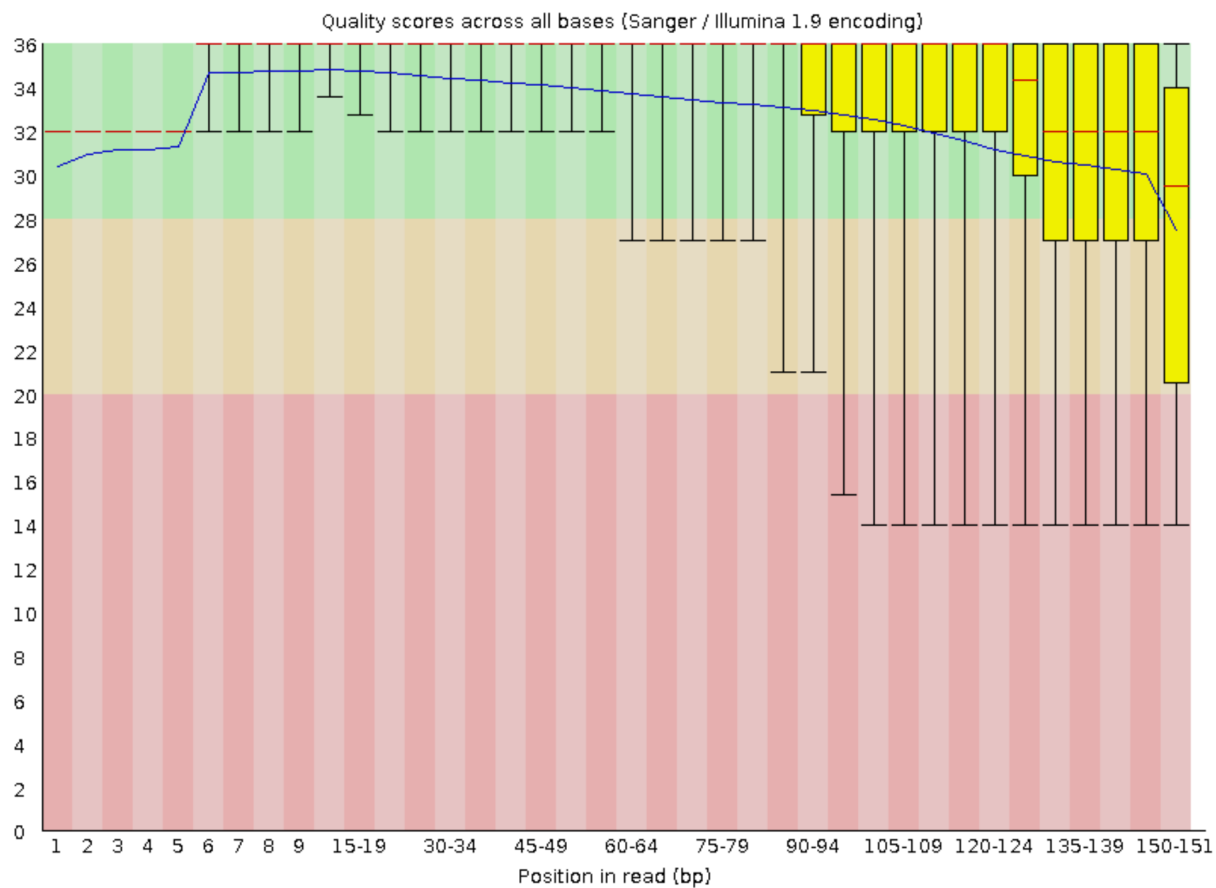
Figure 7: A typical fastq sample of SARS-CoV-2 from northern Brazil showed high read quality, with most reads scoring above 26.
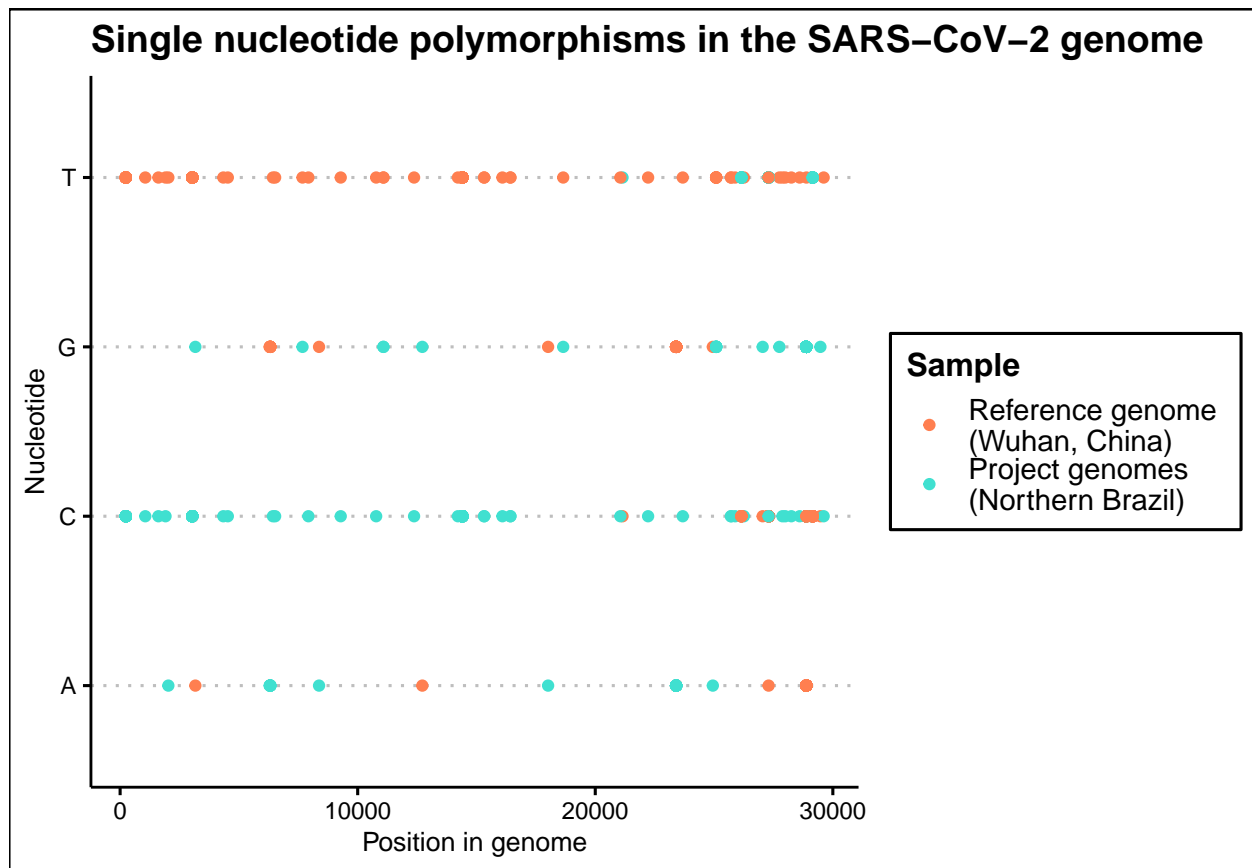
Figure 8: The majority of single nucleotide polymorphism mutations among Brazilian sample genomes were substitutions of thymine with guanine.

Sources Cited

Buss,L.F. *et al.* (2020) COVID-19 herd immunity in the brazilian amazon. *medRxiv.*

Prowse,T.A.A. *et al.* (2020) Inferred resolution through herd immmunity of first covid-19 wave in manaus, brazilian amazon. *medRxiv.*