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

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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 state, Amazonas, were hit harder per capita than the city and state of São Paulo through the second (Q2) and third quarters (Q3) of 2020 TODO: additional citations. Deaths were especially high for elderly patients, as well as male patients in Manaus.

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 (Buss *et al.*, 2020). This is an indication of good news and herd immunity for Manaus, heading into Q4.

Additionally, a variant call analysis of 33 SARS-CoV-2 samples showed that the greatest numbers of high quality, distinct SNPs in the named genes originated in the Amazonian states of Maranhao and Para.

Methods

Tabular data analysis

TODO: tabular parsing walkthrough: trace piping especially.

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 this year.

Genetic data analysis

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 Brazillian 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

This analysis indicates that living in Manaus, being elderly, and being male were risk factors for Brazillians facing COVID-19 in Q2 and Q3 of 2020. It surprised me to see that male patients in Manaus were at such markedly higher risk of death than female patients, to the order of TODO: insert ratio.

TODO: tabular parsing; refer to figures; 66Fix fill for col.

Excess mortality in 50-55 year old male patients reached a maximum of 126 deaths/1000, 1.30 times their expected mortality of 99 deaths/1000, as well as 2.49 times the excess mortality of female patients of the same age at 54.8 deaths/1000 (Figure 5).

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).

Figures

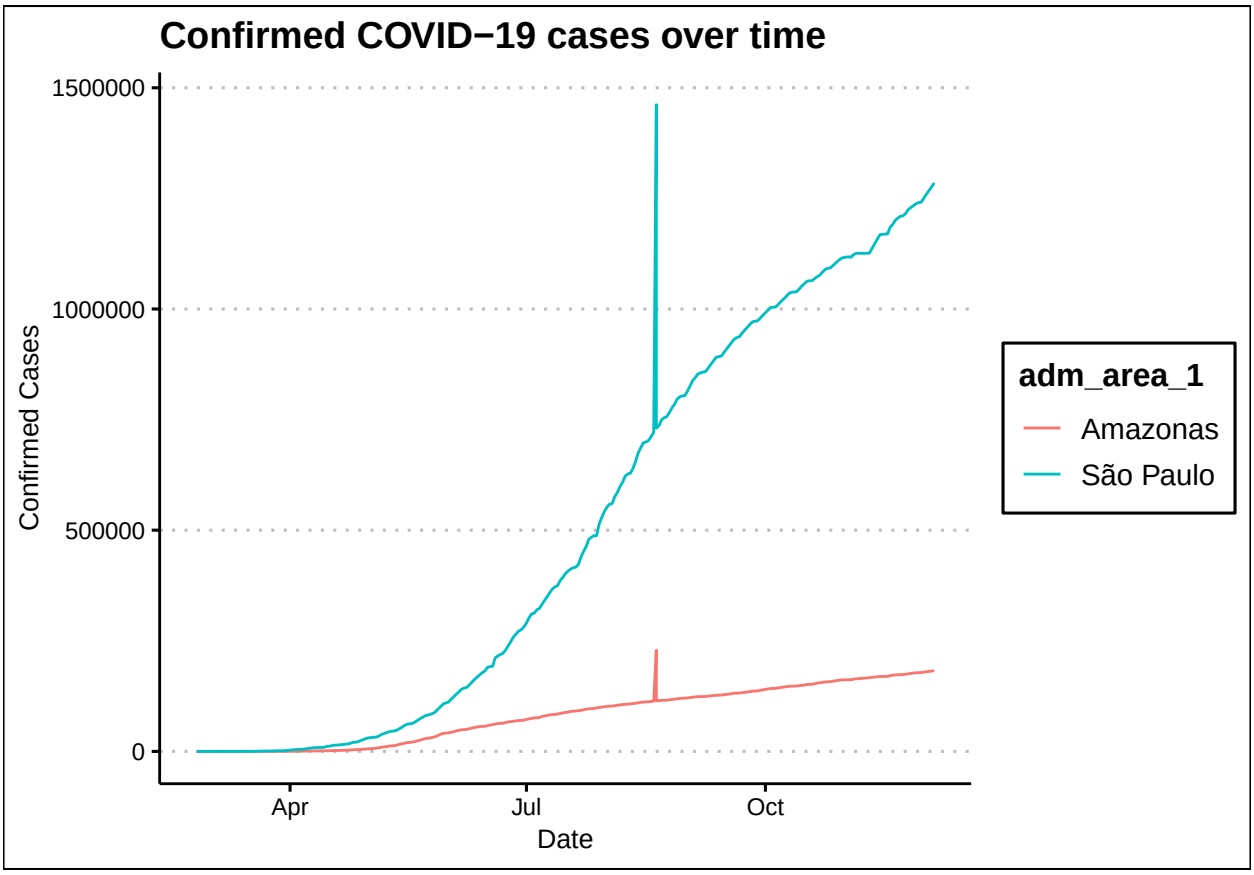

Figure 1: The state of São Paulo saw more total confirmed cases than the state of Amazonas.

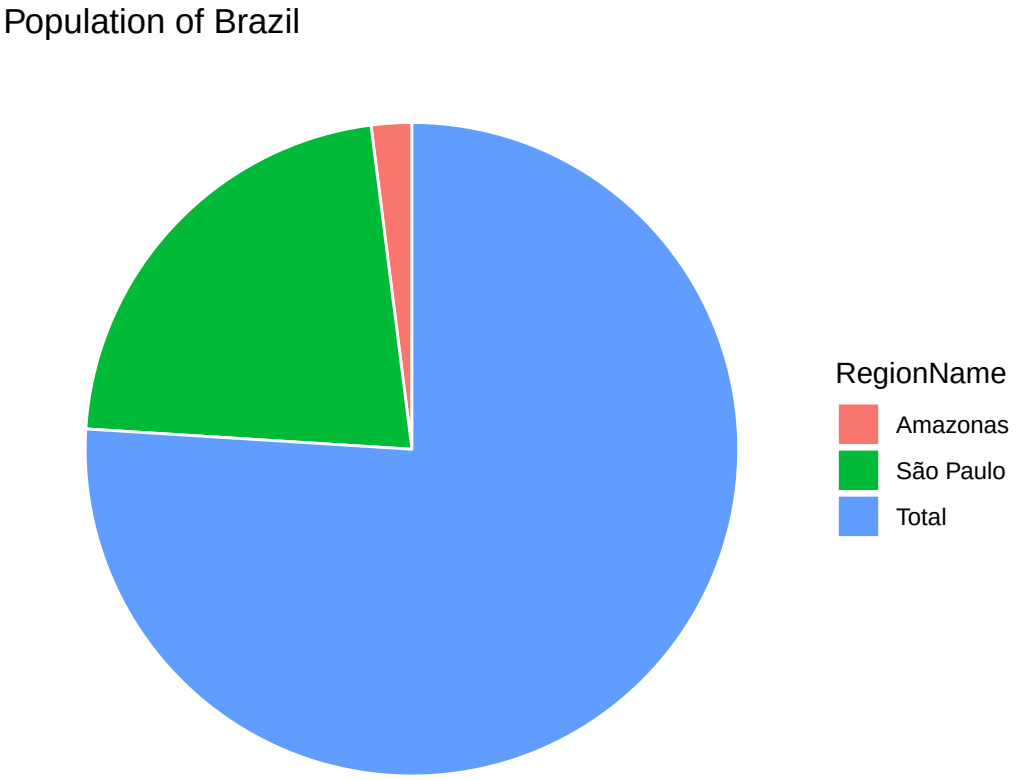

Figure 2: The state of São Paulo is much larger than Amazonas by population at 46 million versus 4 million.

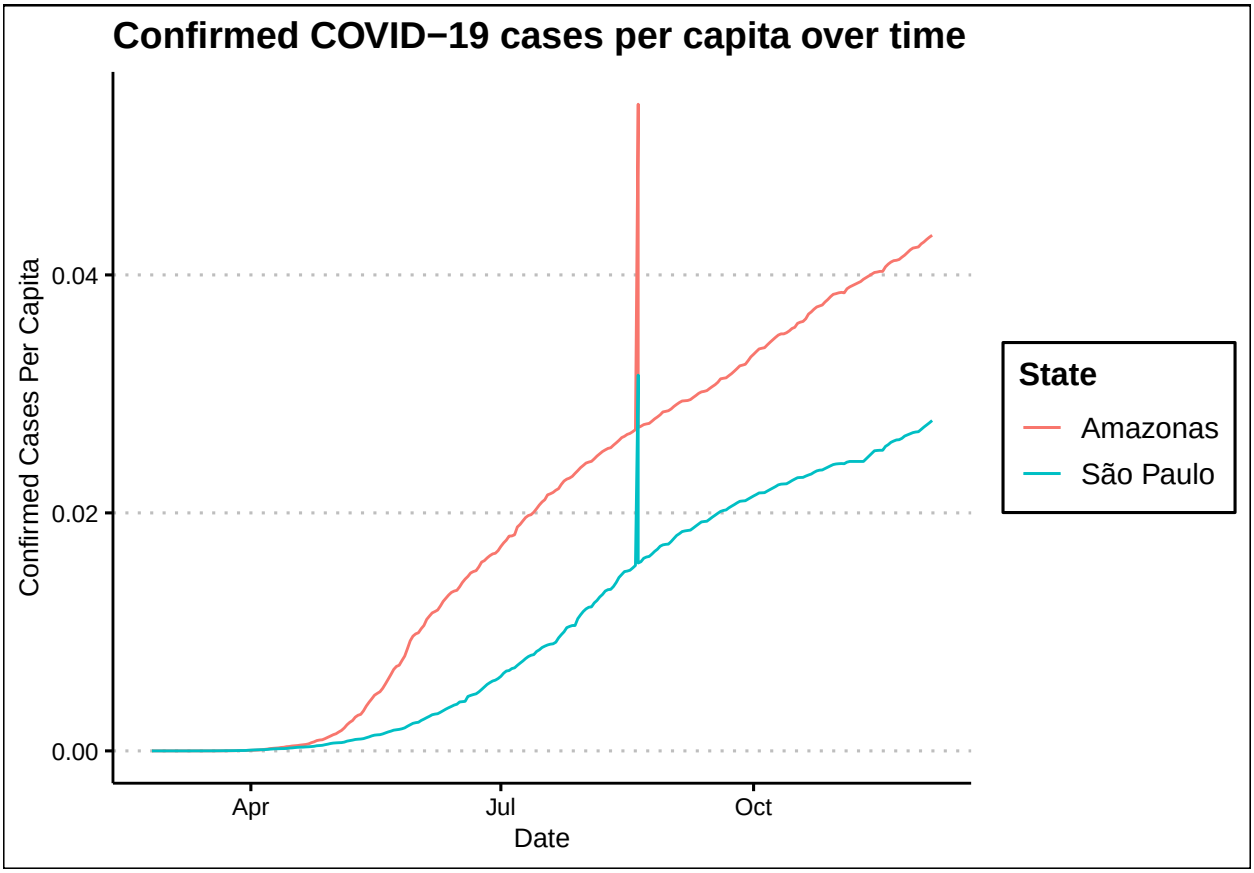

Figure 3: Amazonas saw greater confirmed cases per capita than São Paulo.

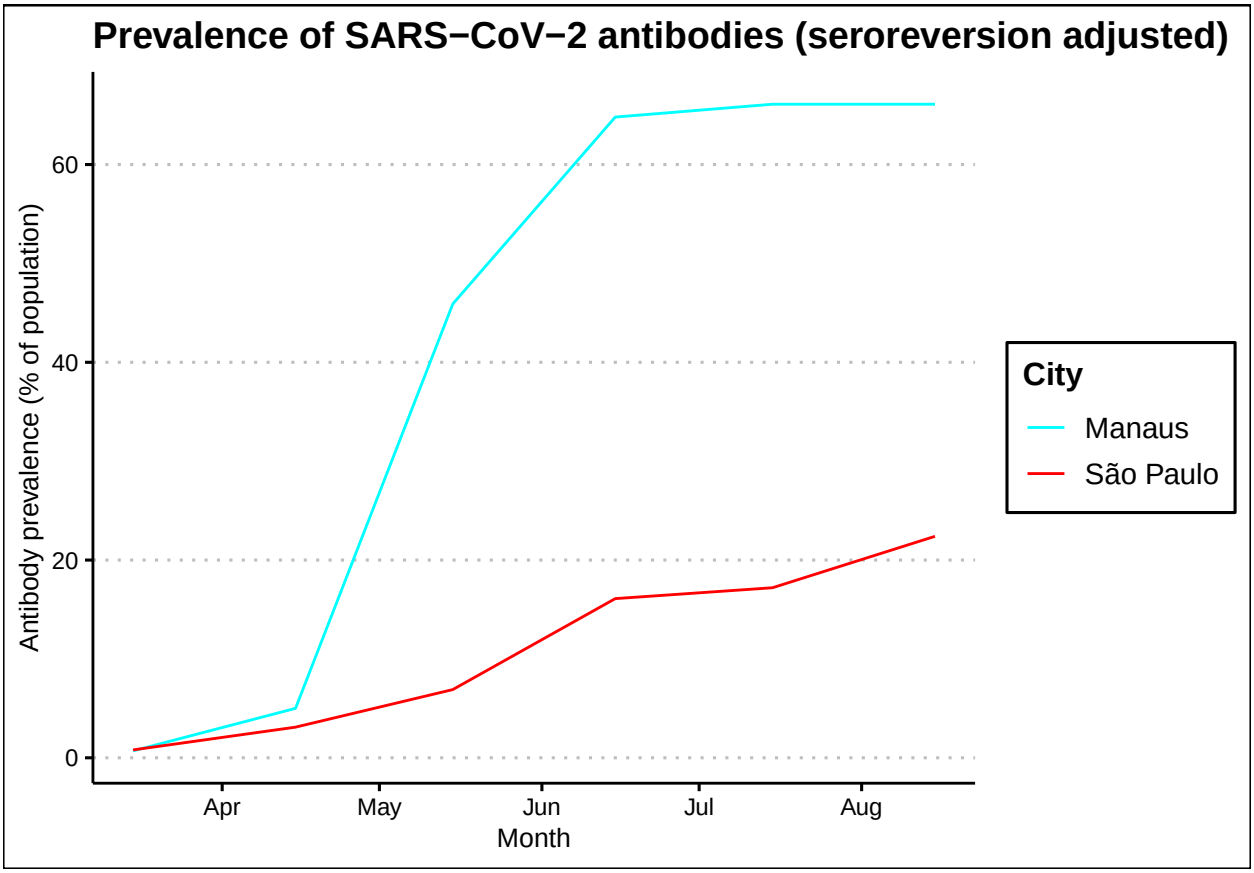

Figure 4: Manaus saw more widespread prevalence of SARS-CoV-2 antibodies vs. São Paulo, up to 66% vs. 22% of the population respectively.

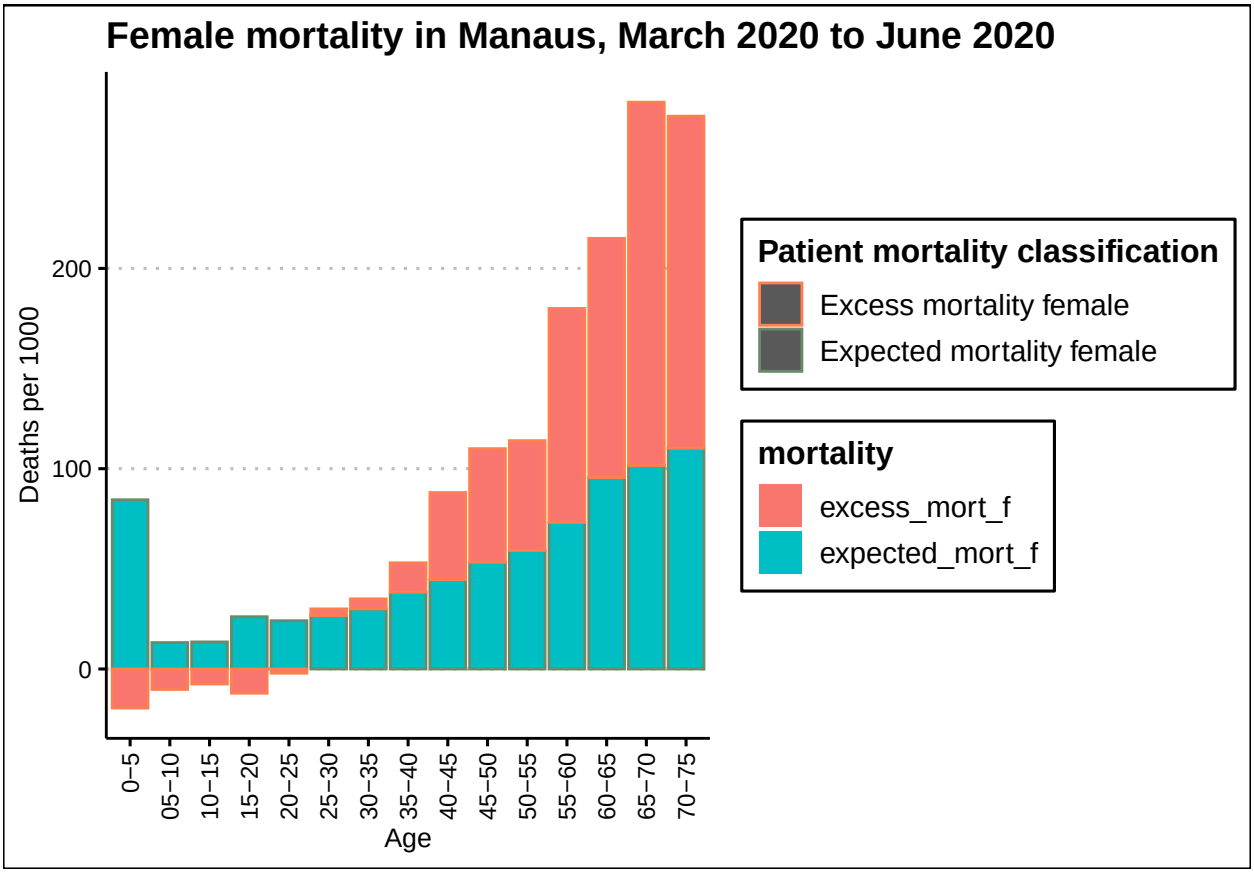

Figure 5: Excess mortality, unexpected deaths of any cause, reached a maximum of 2.49 times the expected mortality in female patients.

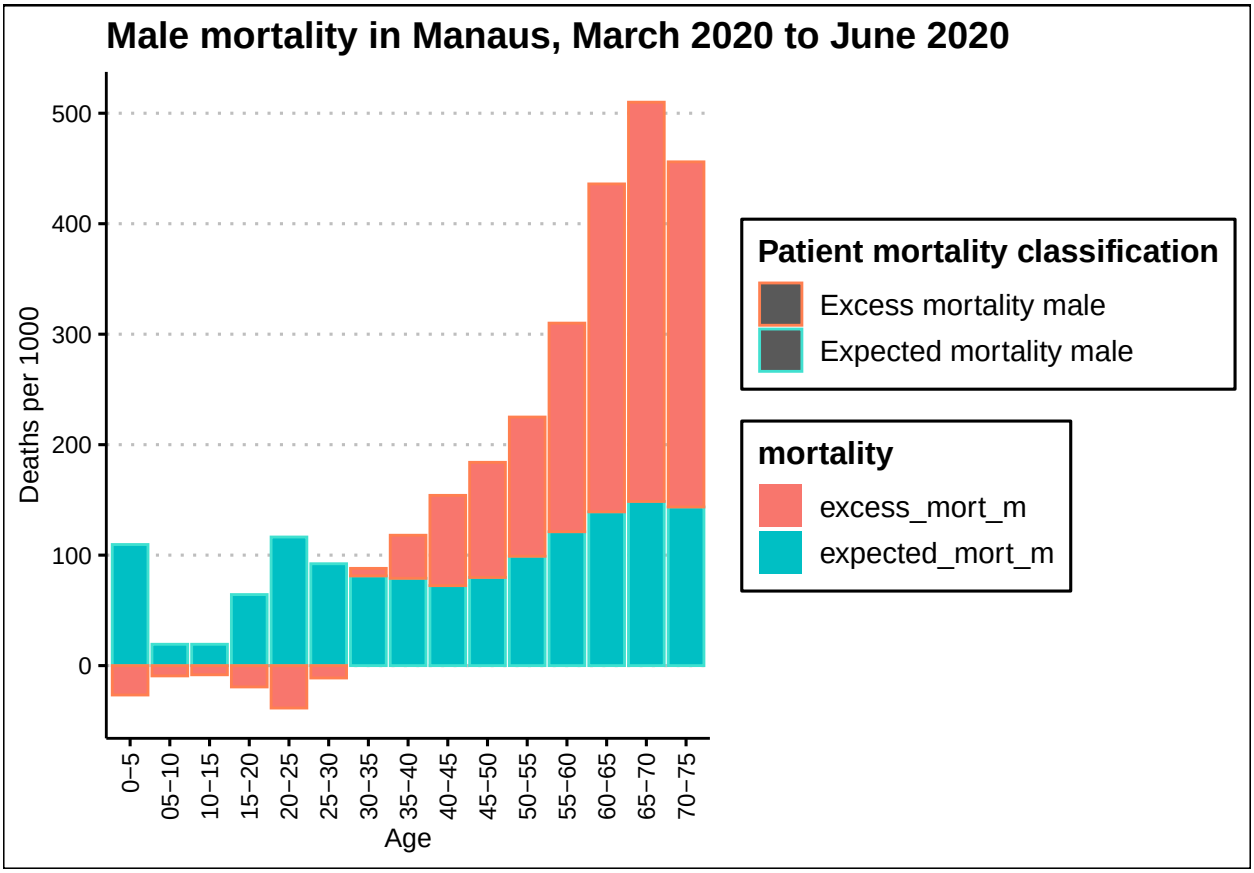

Figure 6: Excess mortality, unexpected deaths of any cause, reached a maximum of 2.49 times the expected mortality in female patients.

TODO: unique caption

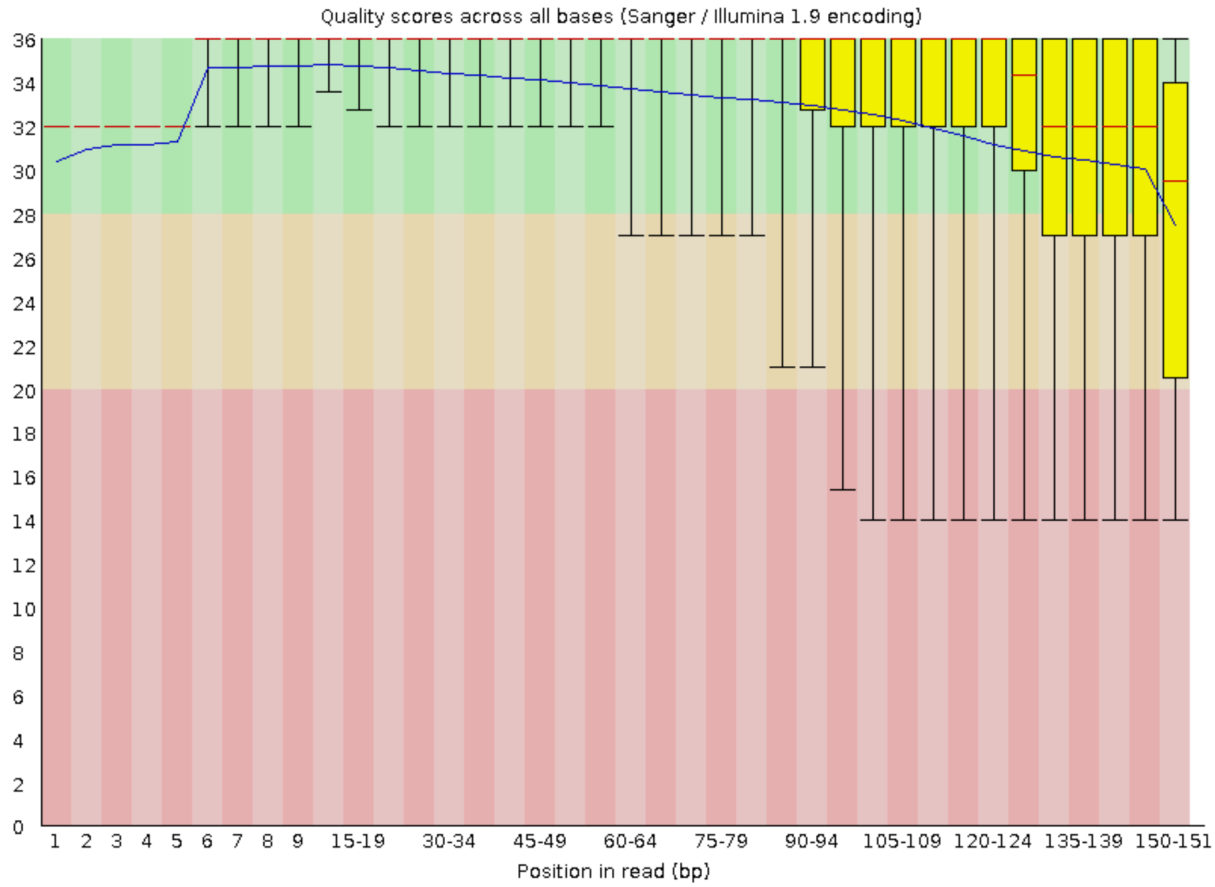

Figure 7: A typical fastq sample of SARS-CoV-2 from northern Brazil showed high read quality, with most reads scoring above 26.

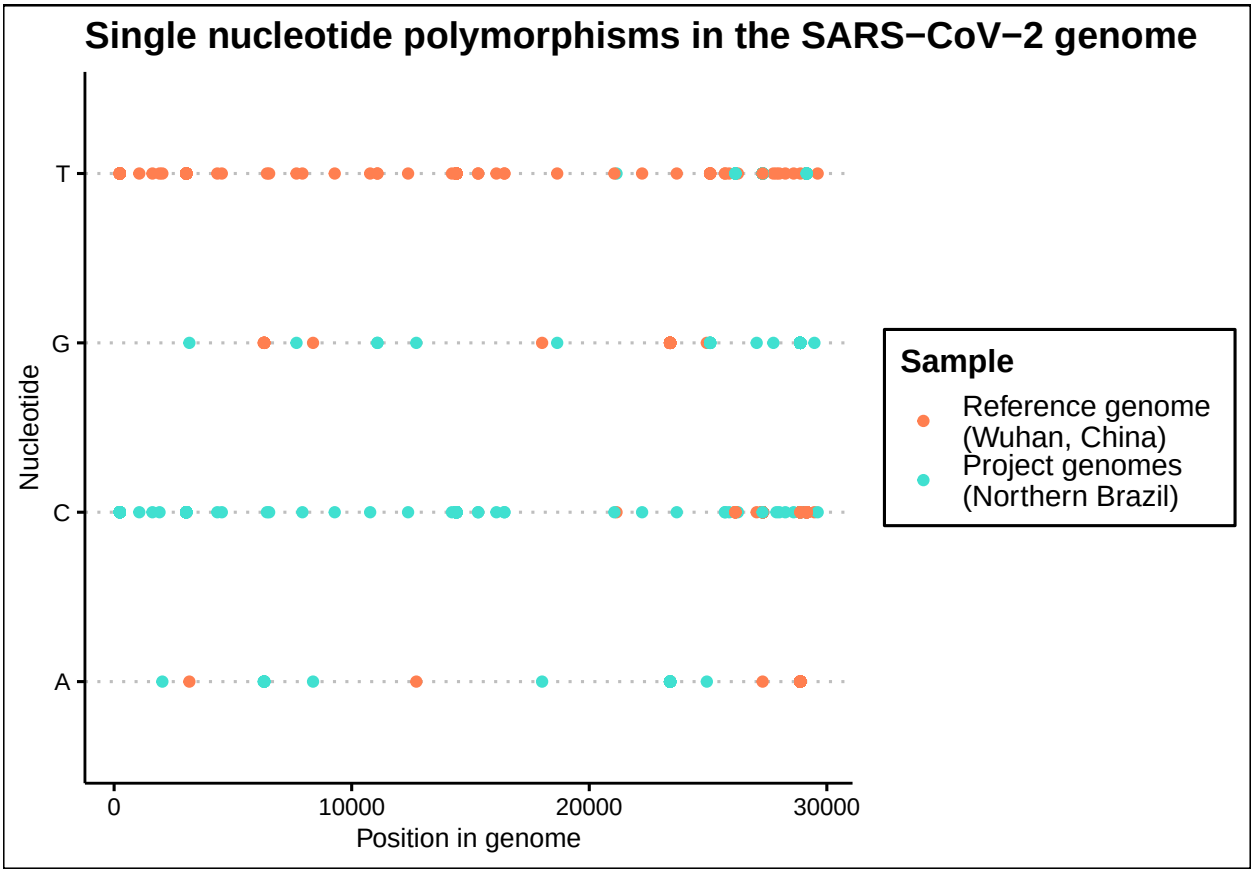

Figure 8: The majority of single nucleotide polymorphism mutations among Brazilian sample genomes were substitutions of thymine with guanine.

Sources Cited

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