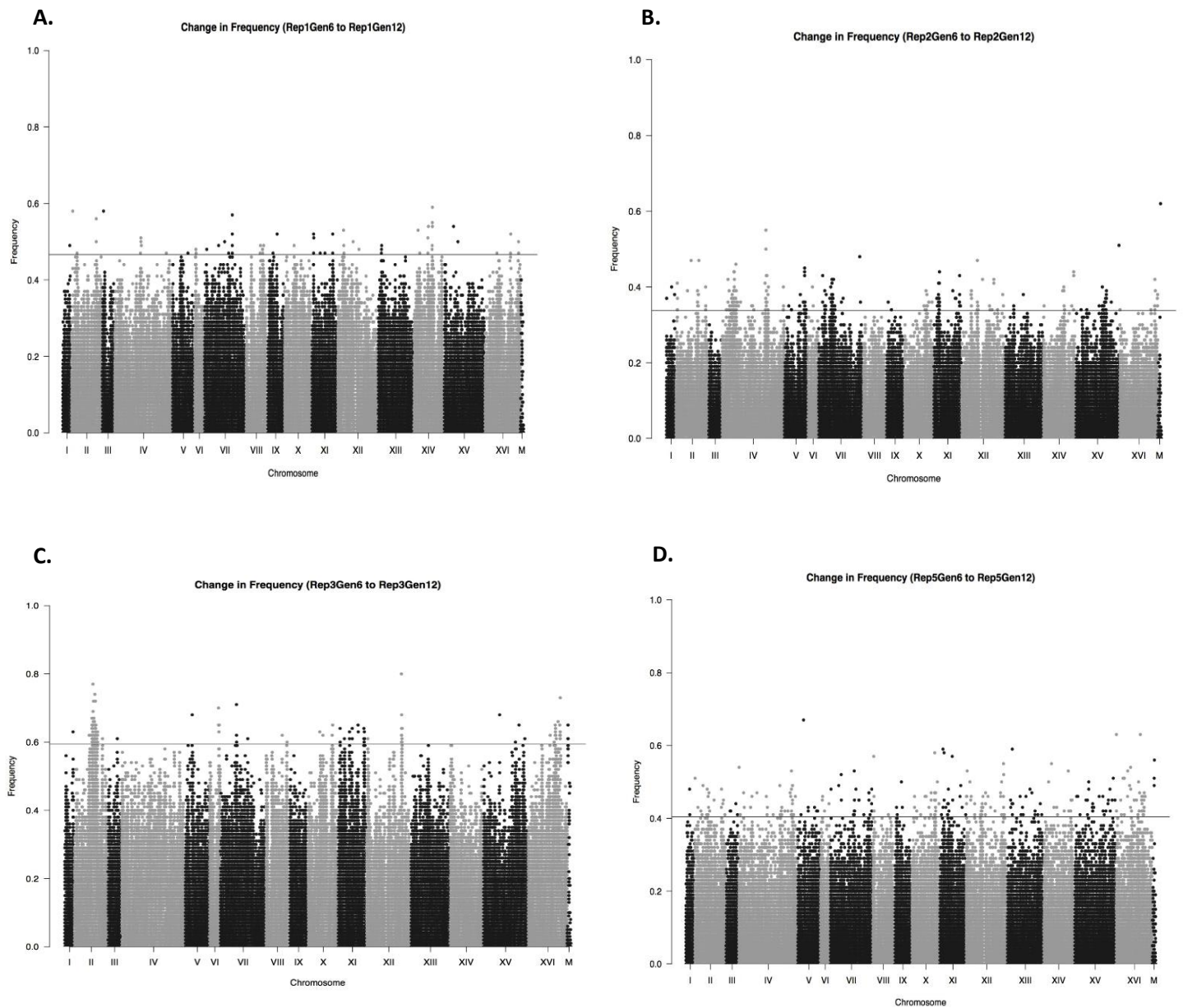


Conclusion from Group Project Step 5:

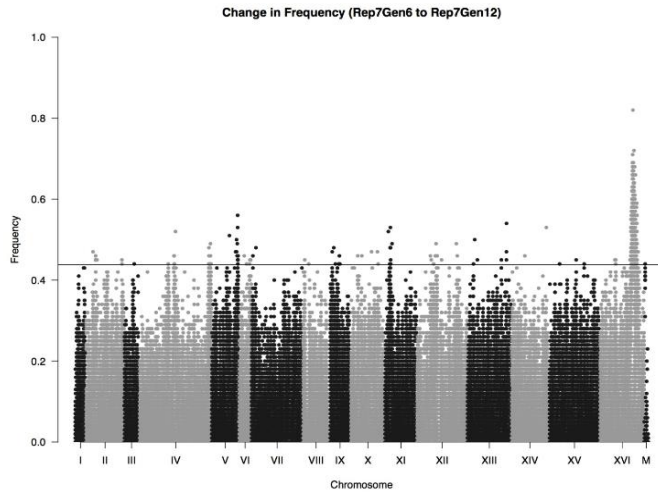
Change in Allele Frequency between Generation 6 and Generation 12:

After generating the Manhattan-like plots, the Mad Scientists selected an appropriate cut off (mean plus four times the standard deviation) to determine which SNPs were most significant across the genome.

Figure 1: Manhattan-like plot for the change in allele frequency for (A) Rep1Gen6 to Rep1Gen12, (B) Rep2Gen6 to Rep2Gen12, (C) Rep3Gen6 to Rep3Gen12, (D) Rep5Gen6 to Rep5Gen12, and (E) Rep7Gen6 to Rep7Gen12.

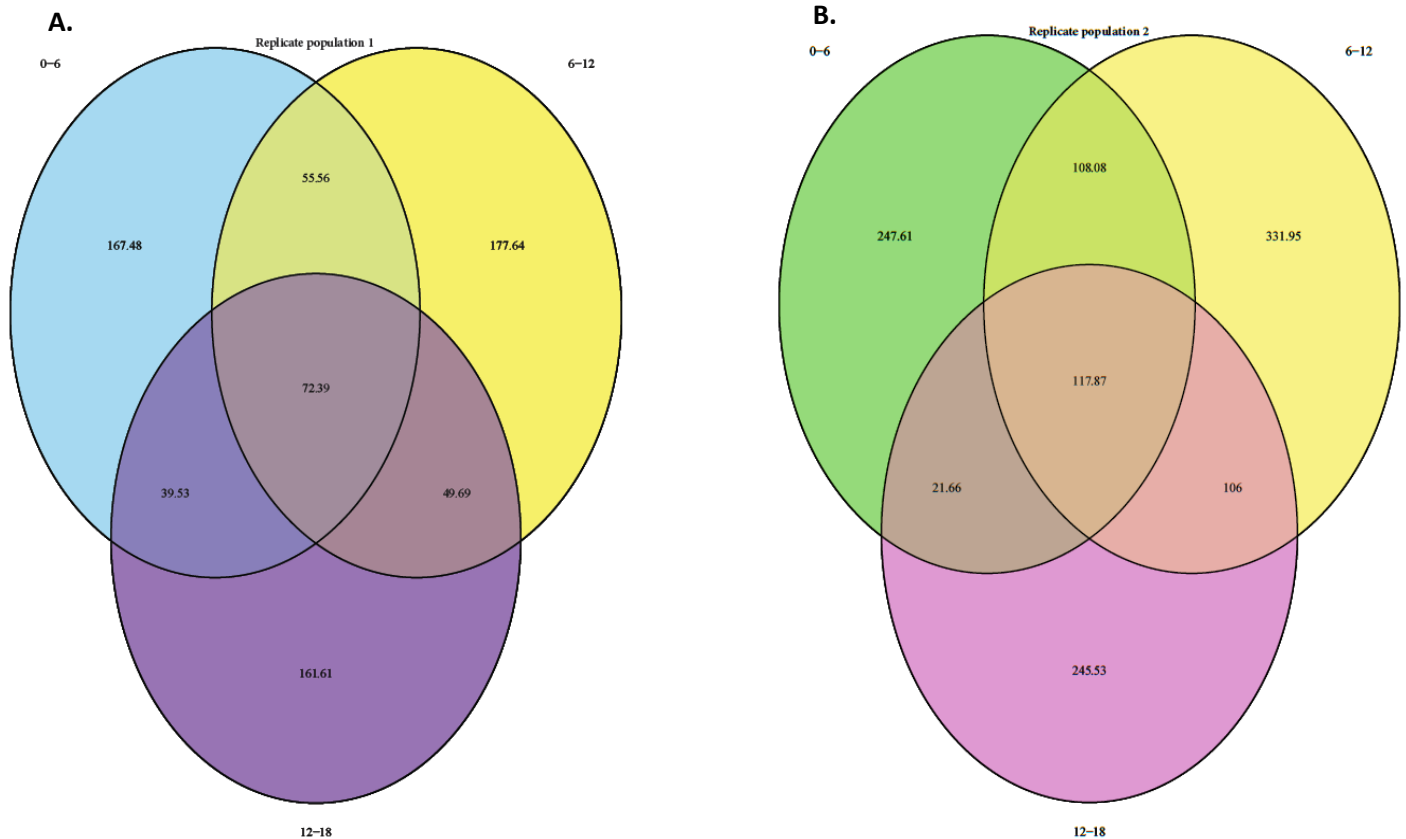


E.

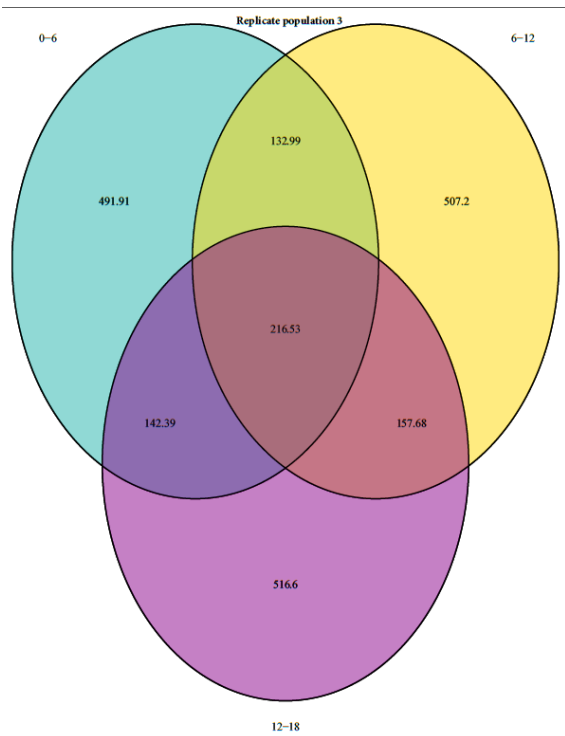


The Mad Scientists specified to “Snapes on a Plane” and “The Ladies” to apply the same cut off for their significant SNPs at their time point, so the genomic positions with the greatest change in allele frequency could be compared across all generations for each replicate population. Additionally, the top SNPs with the greatest change in allele frequency from **all** of the populations at the time points were compiled for a larger comparison.

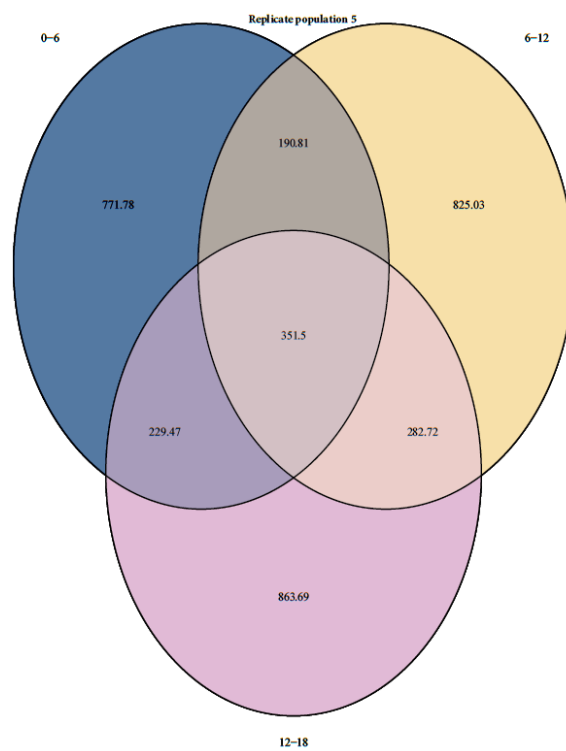
Figure 2: Venn diagram for comparison of genomic positions for SNPs with the greatest change in allele frequency at all time points for (A) replicate population 1, (B) replicate population 2, (C) replicate population 3, (D) replicate population 5, (E) replicate population 7, and (F) top SNPs from all populations.



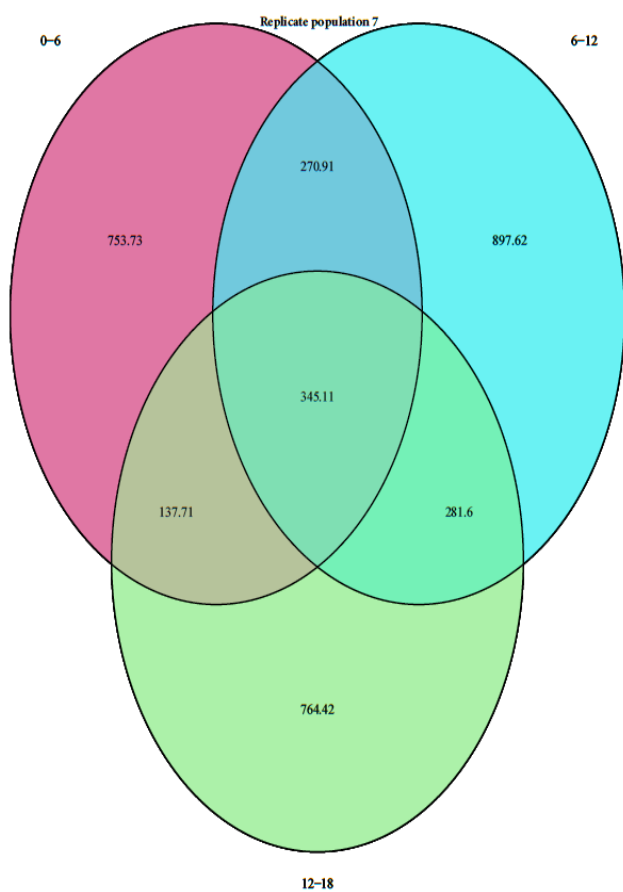
C.



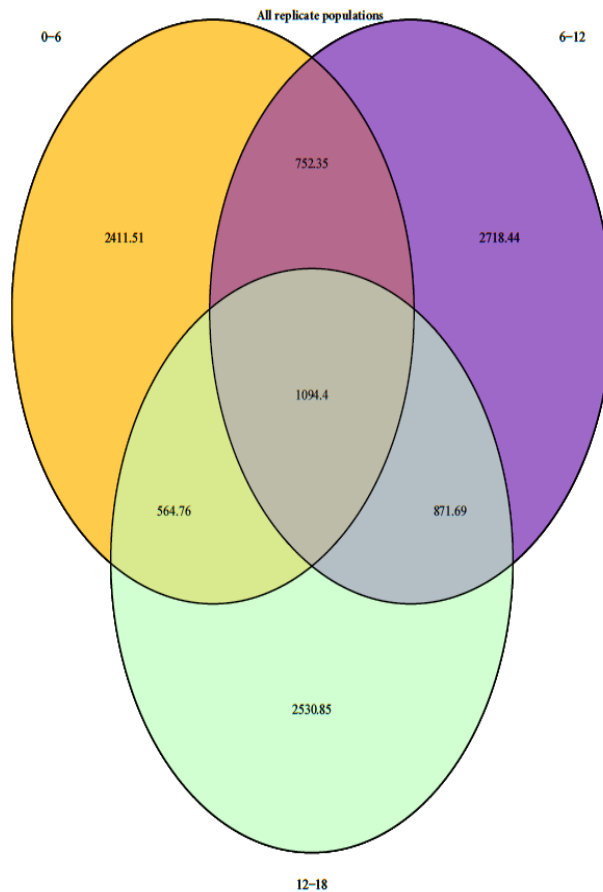
D.



E.



F.



After the data was visually depicted using Venn diagrams, it was determined that SNPs that changed most significantly across all time points occurred **at specific genomic positions**, not randomly throughout the genome, for each replicate populations (Figure2A-E) and across all parallel replicate populations (Figure2F). Using this data, the localized regions in the genome that change most significantly over time (the overlapping center portion of the Venn diagrams) can be determined.