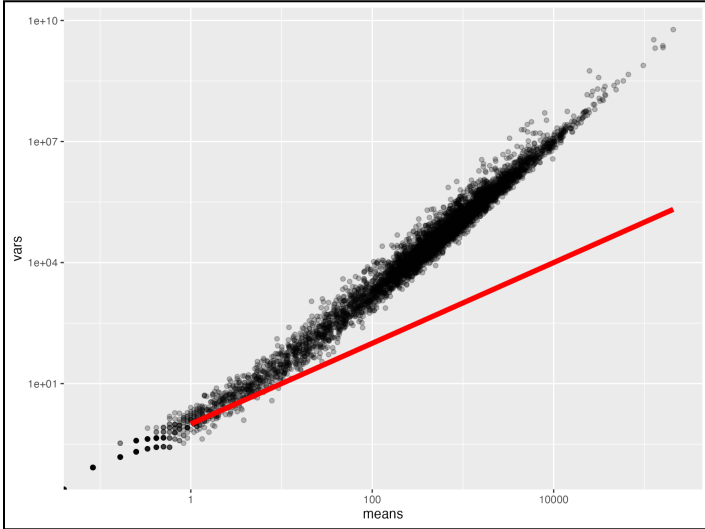
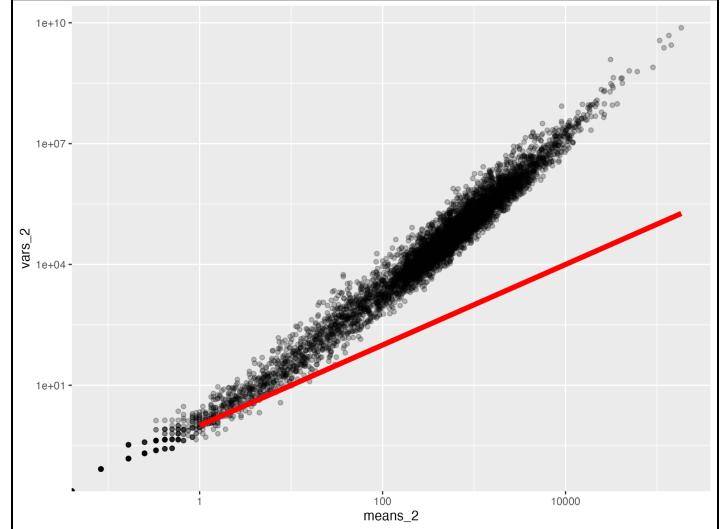


Part A:



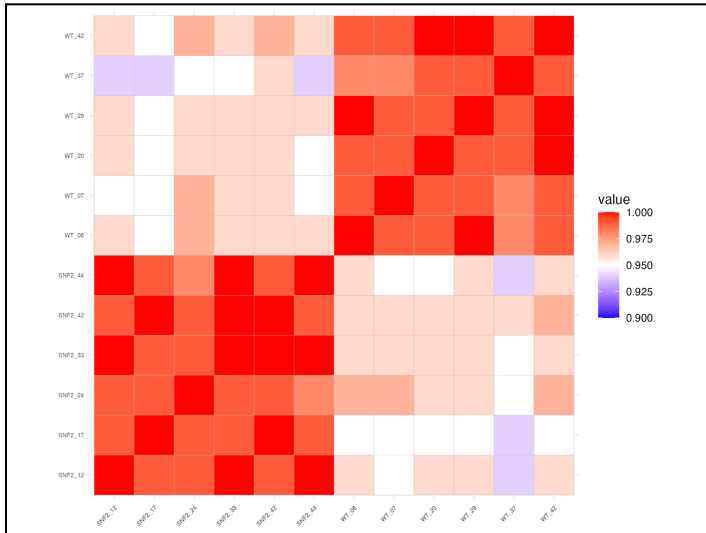
Scatterplot for given data



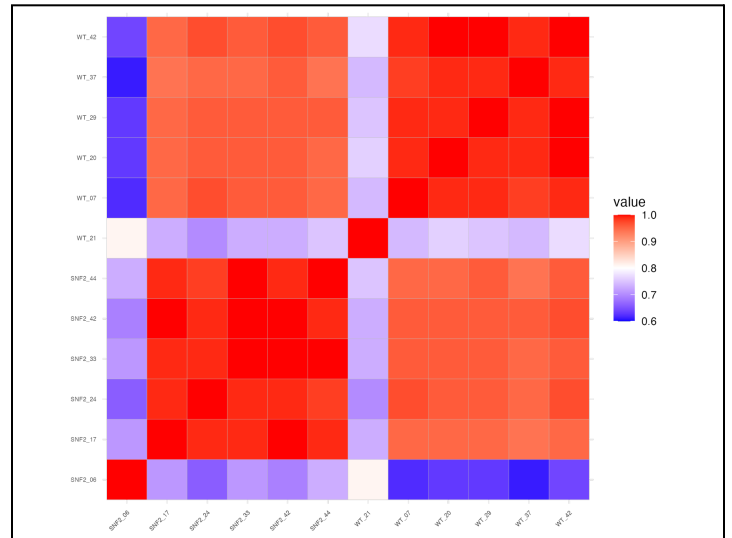
Scatterplot with replaced samples

The insertion of the two bad replicates, SNF2_06 and WT_21, did not cause any significant difference in the mean-variance scatter plot of the total count data. While one can point out the slightly greater amount of variance represented as a wider distribution of points, the general trend from the count data is still present and strong. This is surprising considering how the bad replicate data demonstrated a less uniform distribution of reads compared to the other samples.

Part B:



Correlation matrix for given data



Correlation plot with replaced samples

The insertion of the two bad replicates, SNF2_06 and WT_21, required a change in the scale in order to better visualize these data. It is evident to see that the bad replicates, confirmed by their atypical distribution of reads most likely due to uneven priming during PCR amplification, have much lower correlation values to the other biological replicates in their corresponding condition and even more so in the opposite condition. This is evident from the greater presence of blue, the lower level of the correlation scale, throughout the correlation plot. The lower level of correlation from these replaced samples is not made as apparent in the scatter plots in comparison to the correlation matrix, most likely due to the gradient scale highlighting even small differences.