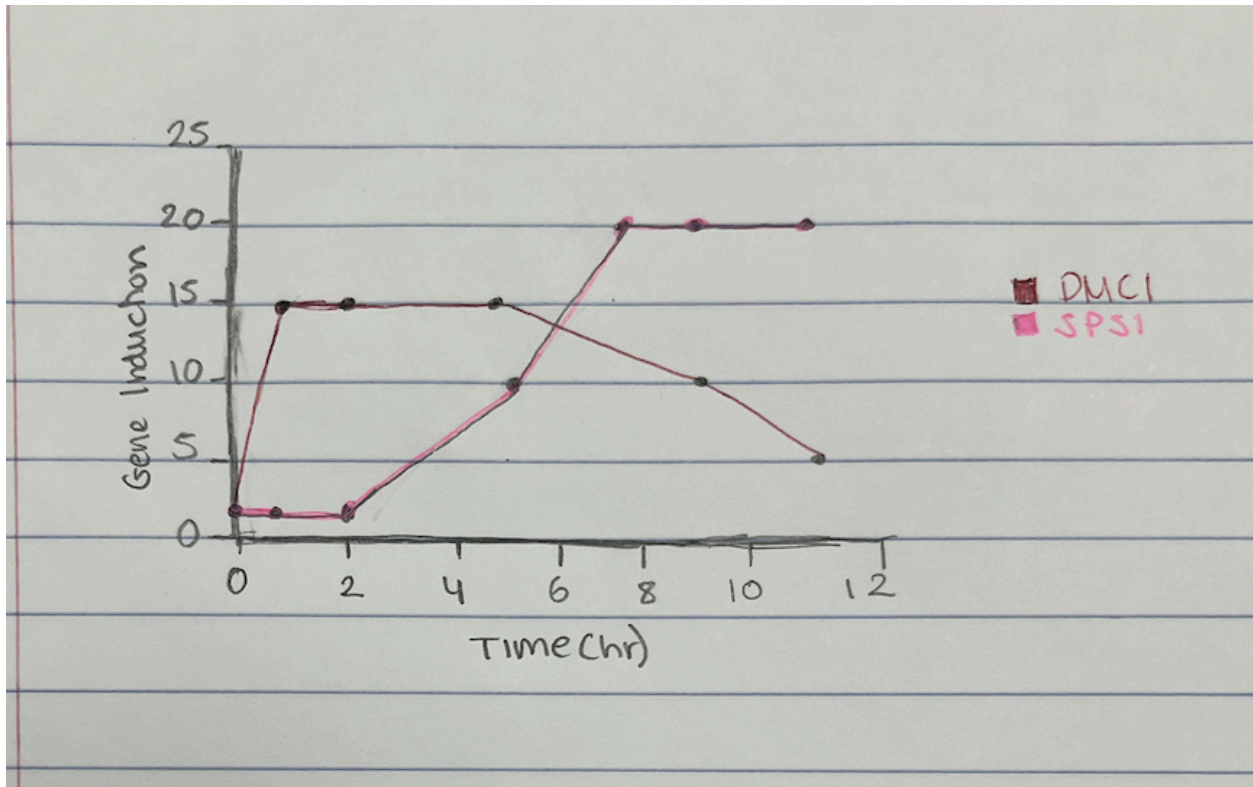


1.



- Gene X - 1 hour: Black, 3 hour - medium red, 5 hour - black, 9 hour - dim green
Gene Y - 1 hour: black, 3 hour: bright red, 5 hour: black, 9 hour: dim green
Gene Z - 1 hour: black, 3 hour: dim red, 5 hour - medium red, 9 hour- medium red
- I think that Gene X and Gene Y are transcribed similarly because the only difference is that at hour 3, Gene X is dim red and Gene Z is bright red. All of the Genes start the same with Black at hour 1 but then Gene Z remains red.
- Some of the spots are yellow because the microarrays have a color scale that runs from red to green. When they are merged together they appear yellow because the system reads it as one color since its hard to separate, therefore, the yellow spots are created.
- The TEF4 gene is green which indicates that it is being repressed. The change in expression that's seen in TEF4 is due to the reduction because TEF4 is involved in elongation. This alters the genes response mechanism and as a result it can't adequately produce glucose which results in a reliance on stored energy.
- TCA genes would be induced if the glucose supply is running out because the genes need to find another energy source in order to produce ATP and other cellular functions. When TCA genes are induced it allows them to use different substrates to produce energy which ensures they are able to survive on a low glucose supply.

7. The mechanism the gene could use is known as the 'guilt by association'. This derives the function of genes based on their expression patterns. This method assumes that genes with similar expression profiles share similar promoters and vice versa. Using this method, it can allow researchers to see the functions and mechanisms of a gene.
8. There would be spots changing from green to red over time to show that the glucose is being depleted over time.
9. The spots would be also red at later points of the experiment with the Yap1p gene. This is because the Yap1p gene is a transcription factor and it activates in response to different stressors such as glucose depletion. In this case, as the glucose is depleted, Yap1p activity increases resulting in high intensity red meaning that the gene is overexpressed.
10. I could verify that the TUP1 gene is truly deleted by doing an analysis to see how the changes of gene expression throughout the experiment. If there were changes, the spots would represent these changes. Similarly, for the Yap1p gene, I could do an analysis to see the changes in gene expression. They could be compared to controls and if the gene is overexpressed there would be a lot more red spots.