**TGFb Project to do**

1. Perform DE analysis on RNA seq data
   1. Redone for better analysis
2. Validate effective RNA seq data
   1. Compare results to prior RNA seq analysis
   2. Review other qc metrics
3. Validate effective treatment
   1. Use Pathways analysis to validate treatments
      1. Do we see TGFb signaling?
      2. Do we see ECM development
      3. Reduction with A485 ( broad CBP/bromo-domain inhibitor)
      4. Reduction with PF-CBP1 (selective CBP/bromo-domain inhibitor)
   2. Use rtPCR results to validate gene expression(
      1. Acta2, Postn, TGFb, etc..
4. GSEA analysis of TFs
5. Create a report of current analysis for Tim and Katerina to see.

**6/5/20**

1. Finally approaching additional data for this project! Yay!
2. This may be the first of many new era RNA seq experiments! (for me and the lab)
3. New set of mouse samples are to be used for follow up.
   1. 4 mice
   2. Each of the 4 mice will have heart samples extracted and tested with each of the 4 conditions.
   3. 4 mice total X 4 conditions each
4. We may merge with previous data but it will likely cluster differently by batch effect but if needed we can do some diagnostic measurements to and see if plausible
5. Regardless we ultimately want to overlap the results of the two treatments in an attempt to find the subset of genes contributing to the reduction of the fibrotic state.
6. Timeline is as soon as possible but the Marcello should be able to get these samples ready in two weeks.
7. NOVa seq
8. Barcoded 2x150bp paired end reads
9. 40 million each read for a total of 80 million fragments
10. An alternate experiment will be performed with Rats but more details will be revealed soon.