NRF2 gene signature in human esophageal epithelial cells and NRF2 Activity Index\_mRNA

Comments (JYL) before all these can be achieve, here are some of my requests:

1. I will determine a group of DEGs from the titrated siRNA knockout samples
2. I hope that you keep those “knockout lines”, I do need experimental validation at least on those genes with the strongest signals.
3. If there are proteins expressed, I would like to see similar western results.
4. **To develop an NRF2 gene signature and an algorithm of NRF2 Activity Index\_mRNA**
5. Use “KYSE70 NRF2 siRNA dose-dependent RNAseq data” to identify an “human esophagus NRF2 gene list” which correlates with siRNA doses
6. Overalp “human esophagus NRF2 gene list” with “KYSE70 NRF2 ChIPseq data”
7. Refer to “mouse NRF2 ChIPseq data” (1542 genes) and “human NRF2high ESCC gene list (244 genes)”
8. Use “human esophagus NRF2 gene list” to develop an algorithm for calculation of “NRF2 Activity Index\_mRNA”
9. Calculate “NRF2 Activity Index\_mRNA” of 4 PYR-treated samples
10. Calculate “NRF2 Activity Index\_mRNA” of 22 human ESCC cell lines using their RNAseq data
11. **To use NRF2 Activity Index\_mRNA to discover drug sensitivity**
12. Correlate “NRF2 Activity Index\_mRNA” and “Drug Sensitivity screen data” of 22 human ESCC cell lines
13. Identify drug candidates
14. **To use NRF2 Activity Index\_mRNA to discover gene dependency**
15. Correlate “NRF2 Activity Index\_mRNA” and “Gene Dependency screen data” of 22 human ESCC cell lines
16. Identify gene dependency