I first used Sharon’s RNA-Seq data for Sorafenib treated cells, at all doses and timepoints, and used a published algorithm using fused lasso regression to generate a minimal network of genes that are best able to differentiate Sorafenib treated cells from DMSO treated cells. I ended up with a network of 172 genes, and I took this list of genes and fed it into INDRA to build a model of all mechanisms that we have found through automated reading that involve any of the genes in the list. This produced a new network that was still very large and highly connected, with a few small ‘islands’ with no connection to the main model. The attached image (indra\_generated\_model.png) shows a very messy visualization of this. I compiled a list of all the nodes in this network and manually filtered it, removing the small disconnected islands, as well as a number of indra-related errors. This left with me with a list of 78 genes of potential interest, which is also attached (gene\_list.txt). I then fed this list to PANTHER for pathway analysis, which produced a list of enriched pathways. I did some more manual filtering on this for pathways that seemed clearly to not be of interest (cell cycle, alzheimer’s-related pathways, T&B cell activation) as well as a number that only included one gene from my list. This left me with 35 enriched pathways. I’m attaching a spreadsheet (pathway\_list.csv) that includes all the names for these pathways, an accession number that can be searched on the pantherdb.org website to find the entire pathway, and HGNC and Uniprot IDs for all of the genes from the list I made that are present in the pathway. I think both the gene list and pathway list can be further filtered down to generate a good list of targets to follow up on, but I erred on including a lot of information for now.