Development of Transcriptomics Analysis Pipeline for mTOR Signaling in Human Cancer

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The goal of this project was to construct a working RNA-sequencing analysis pipeline that would (1) produce visuals to demonstrate differentially expressed genes via PCA plots, correlation and expression heatmaps, and differentially expressed gene plots, and (2) provide insight into key metabolic pathways for wet-lab scientists to validate. FASTQ files from an RNA-seq experiment with mTOR complex knockouts were provided by the NCI's Lab of Cancer Biology and Genetics and processed in the computer terminal using command-line tools. Then, differential expression analysis was conducted in RStudio using the DESeq2 negative binomial model. The plots produced by the analysis pipeline were validated by running the data through Ingenuity Pathways Analysis and comparing the results. The plots served to visualize and highlight which genes were differentially expressed across the different signaling pathway knockouts. Many of the highlighted genes play roles in metabolism and immunity and have been previously observed to be involved in cancer. Further investigation of those genes could aid in the development of more targeted cancer drug treatments. An extension of this project is to integrate the RNA-seq data with data from other omics experiments conducted with the same knockout cell line in order to determine overlap in the phosphorylation sites and metabolites of each mTOR signaling complex.

Awards Won:
Fourth Award of $500