

Bioinformatics team requires partner to quickly analyze & visualize bulk transcriptomic data

CASE STUDY

SITUATION

- A U.S. discovery-stage biotech company with less than 100 employees, pursuing genetic biomarker discovery
- R&D team had initially performed large scale experiments which yielded a list of potential gene biomarkers
- To further analyze the relation of those markers to the corresponding physiological pathways, an investigative sequencing experiment had been designed
- Bioinformatics Manager, who led a small team of bioinformaticians, concluded that further data analysis would take their team months to complete while maintaining the team's day-to-day activities
- Thus, the company sought an outsourcing partner who could rapidly conduct the analysis and visualize the results

AT A GLANCE

Primary Challenges

- Internal team lacked bandwidth to quickly conduct analysis
- Manager required results to be visualized to facilitate internal understanding across wider R&D team

Why Bridge Informatics

Team of computational biologists with experience at the bench whose core specialty is understanding and analyzing biological data

STRATEGY & PROCESS

- Bridge's team of bioinformaticians and engineers customized a plan which included best practices for library preparation, the sequencing platform that would generate the highest quality data, and data transfer conditions
- Once data was transferred, Client granted Bridge access to their sequencing data for pre-processing, processing, and analysis
- Bridge's bioinformaticians pre-processed the sequencing data by read trimming prior to alignment and sorting and indexing the aligned file prior to normalization
- To apply research context to the pre-processed data, Bridge conducted an investigative study of how gene expression has been altered under examined conditions through the following steps:
 - Normalized read count data to account for differences in library depth and composition
 - Performed dimensional reduction and hierarchical clustering of the dataset
 - Identified the differentially expressed genes (DEGs) and computed p-value and False Discovery Rate (FDR) adjusted p-value for each gene
 - Created a subset of DEGs that pass desired FDR and fold-change cut-off(s)
 - Conducted pathway analysis using KEGG and Reactome databases, and performed gene set enrichment analysis
 - Organized findings in tables and visualizations per Client's request
 - Suggested a list of candidate genes for validation via quantitative PCR (qPCR) or Western blot analysis; Assisted with primer design for qPCR and antibody selection strategies for proteomics validation

RESULTS

- Within a month of receiving the sequencing data from Client, Bridge conducted the analysis and summarized the most compelling findings to help the Bioinformatics Manager determine subsequent research approach
- Bioinformatics Manager received the data in their desired format alongside a thorough explanation of how Bridge generated the results