

Identifying Potential Therapeutic Targets for Heart Failure through Systematic Transcriptome Analysis

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Heart failure is becoming increasingly prevalent as the global population ages. Once heart failure progresses, complete recovery becomes elusive, emphasizing the critical need for early detection. Current treatments primarily focus on supporting cardiac function or alleviating symptoms. Still, transcriptomic analysis could identify genes with differential expression in the early stages of the disease, offering valuable biomarkers for early diagnosis. These biomarkers could also inform the development of novel therapeutic approaches. In this study, we performed a comprehensive analysis of bulk RNA-seq data from both healthy individuals and heart failure patients to detect differentially expressed genes (DEGs). We further mapped DEGs onto the protein-protein interaction (PPI) network in order to identify key therapeutic targets. Based on these targets, we explored potential compounds through a drug discovery analysis, suggesting a set of candidates for further investigation.