# Investigating Racial Disparities in Cancer by Assessing Transcriptomic and Proteomic Biomarkers in Various Carcinomas using TCGA Database and Web-based Analysis Tools

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In the United States, epidemiological studies have highlighted a disparity in cancer incidence and outcome rates between racial groups. This disparity is attributed to numerous factors, including gene polymorphisms, differences in lifestyle and environmental exposures, and socioeconomic factors. Although an abundance of tumor molecular data exists, the effect of race on gene expression signatures often remains unexplored. In my project, I investigated racial molecular differences in tumors of 10 carcinoma types. I used publicly available data from The Cancer Genome Atlas and online analysis tools such as the Kaplan Meier plotter, cBioPortal, and Reactome to identify patterns of differential gene expression in tumors obtained from White, Black/African American, and Asian patients. I identified race-dependent expression of numerous genes whose mRNA transcript levels were significantly correlated with patient survival outcomes. A small subset of these genes was differentially expressed in multiple carcinomas, including genes involved in cell cycle progression such as CCNB1, CCNE1, CCNE2, and FOXM1. This suggests that cell cycle dysregulation is a major culprit in the health disparity. In contrast, genes such as transcriptional factor ETS1 and apoptotic gene BAK1 were differentially expressed and clinically significant only in specific cancer types. Additionally, in numerous cancer types I identified race-dependent regulation of cancer-relevant biological pathways, especially DNA repair mechanisms. This large-scale pan-cancer study refines our understanding of the molecular basis for the cancer racial disparity and can help inform the use of novel biomarkers in clinical settings as well as the future development of precision therapies.

**Awards Won:**

American Statistical Association: Certificate of Honorable Mention