1. Background (Draft)

Breast cancer is the most prevalent cancer in women, exhibits diverse subtypes characterized by distinct genetic aberrations. Within this spectrum the human epidermal growth factor receptor 2 amplified (ERBB2+) breast cancer subtype stands out as particularly aggressive. Despite the availability of targeted therapies, the response rate to these interventions remains at approximately 40%. One of the questions: What molecular characteristics distinguish ERBB2+ breast cancer from other subtypes?

The problem stems from the need to solve the molecular intricacies contributing to the aggressiveness of ERBB2+ breast cancer. The specific objective is to identify differentially expressed genes that play a pivotal role in distinguishing ERBB2+ tumors from other breast cancer subtypes. Leveraging TCGA RNASeq data and employing computational tools, this analysis seeks comprehensive insights into the genetic landscape, aiming to uncover potential biomarkers and shed light on the biological pathways that drive the aggressiveness of ERBB2+ breast cancer.

The rationale for undertaking this analysis is deeply rooted in the clinical significance of ERBB2+ breast cancer. Despite advancements in targeted therapeutic interventions, the limited response rate emphasizes the need for a more profound exploration of the underlying molecular landscape. By pinpointing differentially expressed genes associated with ERBB2+ tumors, scientists strive to identify potential biomarkers that may serve as targets for more effective treatments. This project has the potential to provide important new understandings of the complex molecular processes that underlie the aggressiveness of ERBB2+ breast cancer.

Methods (draft)