

MICRORNA SIGNATURES AS PREDICTIVE TOOLS FOR NEOADJUVANT CHEMOTHERAPY RESPONSES IN TNBC

Domas Šttilis^{1,3}, Adomas Vasiliauskas³, Linas Kunigėnas¹, Monika Drobniėnė^{1,2}, Eglė Strainienė^{1,3}, Kęstutis Sužiedėlis^{1,2}

¹National Cancer Institute

²Life Sciences Center

³Vilnius Gediminas Technical University

domas.sttilis@gmail.com

Breast cancer is the most common type of cancer among women. Triple-negative breast cancer (TNBC) is a subtype that is particularly aggressive and has limited treatment options, resulting in poor outcomes. This study focuses on the role of specific miRNAs in the progression of triple-negative breast cancer. Bioinformatics analysis of The Cancer Genome Atlas (TCGA) data identified 195 miRNAs that impact 57 genes associated with resistance to platinum-based therapies. Thus, we selected a subset of miRNAs and determined their expression levels through RT-PCR in triple-negative breast cancer (TNBC) patient samples, both before and after neoadjuvant therapy. Finally, the patients were stratified into a high-risk group and a low-risk group according to the median expression level of each miRNA.
