# R-RAS-2 AS A POTENTIAL PREDICTIVE TARGET IN TRIPLE-NEGATIVE BREAST CANCER

Justas Burauskas[1,2], Agnė Šeštokaitė[1,2], Monika Drobnienė[1], Rasa Sabaliauskaitė[1,2]

[1]Vilnius university
[2]National Cancer institute
justasb18@gmail.com

Breast cancer is the most commonly diagnosed neoplasm worldwide and is the leading cause of cancer deaths amongst women. Triple-negative breast cancer (TNBC) is the most aggressive subtype with the lowest 5-year survival rates accounting for 12-18% of all breast cancers. TNBCs have a much higher recurrence and metastasis as a result of not being eligible for current treatment options due to the lack of estrogen, progesterone receptor, and human epidermal growth factor receptor 2 . This aggressive cancer contributes to the overall shortened survival of patients diagnosed with TNBC.

Considering the absence of molecular targets, neoadjuvant chemotherapy (NAC) remains the standard of care for patient treatment. However, the effectiveness of treatment is unpredictable, as patients frequently develop resistance. For this reason, there is a growing need to develop novel non-invasive molecular predictive approaches for this disease . It has become evident that multiple signaling pathways are responsible for treatment resistance. Recent evidence from preclinical studies have marked a pivotal role of the R-RAS-2 gene which is involved in the STAT3 signaling pathway, in the progression, and chemoresistance of TNBC patients.

The aim of this study was to evaluate the expressions of STAT3, ALDH1A1, NFIB, UPF3A, BCL-2, and R-RAS-2 genes in serial plasma samples before and after NAC and determine their potential as predictive biomarkers.

In this study, we used reverse transcription quantitative PCR to determine gene expression in 81 TNBC patients ṕaired plasma samples before and after NAC. We determined that BCL-2, R-RAS-2, STAT3 and NFIB expression was higher after NAC (all $P<0.005$, respectfully). While R-RAS-2 higher expression of at least 10% was associated with partial response to NAC and residual disease ($P=0.013$ and $P=0.006$, respectfully).

In conclusion, understanding how the multiple signaling pathways influence the course response to NAC in TNBC is important. To date, we found that R-RAS2 could be used as a predictive biomarker for monitoring TNBC patient response to chemotherapy and treatment effectiveness.