# ABSTRACT

The worldwide impact of breast cancer (BRCA) has received a lot of attention due to its poor prognosis which leads to the high mortality and morbidity rate. Studies suggest that the high morbidity rate is mainly due to ineffectiveness of existing conventional therapies including chemotherapy, surgery as well as radiation therapy. Consequently, researchers are investigating gene therapy as a promising treatment for BRCA. An effective gene therapy involves the prognostic gene biomarkers associated with BRCA. Despite all of the identified prognosis biomarkers of BRCA, reports indicate that the current prognostic gene biomarker is ineffective and does not meet the requirements of clinical procedures. Therefore, it is essential to explore novel prognostic biomarkers associated with the poor prognosis of BRCA. These explorations involve in-silico studies through the data mining process utilizing various bioinformatics tools to analyze gene expression, prognostic value, correlation analysis and enrichment pathways analysis. Several analyses have identified the overexpression of gene *Y* in tumor samples and its association with the poor prognosis of BRCA. Moreover, it has been identified that gene *Y* also contributes to cell cycle regulation through enrichment pathway analysis.

Keywords: BRCA, gene *Y*, *In-silico*, data mining, gene biomarker