



# Gene expression profile in breast cancer comprising predictive markers for metastatic risk

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**ABSTRACT.** Quantitative multiplex reverse transcriptase-polymerase chain reaction was developed for the simultaneous detection of multiple-gene expression levels of formalin-fixed, paraffin-embedded breast cancer samples. Candidate genes were selected from previous microarray data relevant to breast cancer markers that had the potential to serve as predictive markers for metastatic risk. This multiplex gene set included 11 candidate and 3 housekeeping genes, and the aim was to predict breast cancer progression based on lymph node involvement status. Our study demonstrated that the system generated a good standard curve fit ( $R^2 = 0.9901-0.9998$ ) correlated with RNA concentration. The multiplex gene expression profile indicated significantly downregulated levels of G protein-coupled receptor kinase interacting ArfGAP 2 (*GIT2*) and mitochondrial transcription termination factor (*MTERF*)

genes in a lymph node-positive group of patients, with P values of 0.004 and 0.038, respectively. Therefore, this in-house method using multiple genes of interest might be an alternative tool for prediction of breast cancer metastasis.

**Key words:** Multiplex RT-PCR; Breast cancer; Metastasis; *GIT2*; *MTERF*