

# **Distribution of Breast Cancer Molecular Subtypes among Jordanian Patients**

**By**

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## **Abstract**

In this study, the distribution of molecular subtypes of breast cancer was investigated in 102 samples from Jordanian patients who underwent biopsy or mastectomy at KHCC in 2006 and 2007. After optimization of the experimental conditions using 3 breast cancer cell lines (MCF7, MDA-MB-453, T-47D), gene expression profiles for Prediction Analysis of Microarray (PAM50) assay were obtained using qRT-PCR. Data analysis and molecular subtypes were obtained by SigClust and GeneFu algorithms. Gene expression profiles were produced for 54 out of the 102 samples tested and it was found that 28% of the samples were basal like subtype, 16.6% were human epidermal growth factor 2 (*HER2*) enriched, 27.7% were luminal A, 14.8% were luminal B and 12.9% were normal like. These data are in concordance with the reported subtypes using PAM50 assay in Caucasian populations, indicating ethnic biological similarities. Future correlation of these molecular subtypes with patients' immunohistochemical (IHC) profiles, treatment protocol plans applied and 5 years survival rates would help revise and establish new treatment protocols for future breast cancer patients according to their molecular subtype and thus enhance the prognosis of the disease.