

Evaluation of Glis2 Gene Expression in Samples of Breast Cancer

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Abstract

Introduction: The GLIS family members are the Krüppel-like zinc finger proteins with transcriptional repression and activation function. Glis2 is one of these family members which its relation revealed with some diseases such as Nephronophthisis (NPHP), an autosomal recessive renal disease, and in non-Down syndrome acute megakaryoblastic leukemia and meningiomas cancers. Regarding to the connection of this factor with other cancers and Hedgehog and Wnt/ β -catenin signalling pathways-important pathways that involve in both normal and tumor genesis of breast tissue-the aim of this study is investigating the alteration of Glis2 mRNA expression level in breast cancer.

Materials and Methods: Real-Time PCR performed with Glis2 and GAPDH gene primers on the RNA which extracted from 25 fresh frozen breast tumor tissue samples and also 25 normal samples with slight distance from site of tumor.

Results: The relative expression of Glis2 in breast cancer tissues revealed a six times decrease comparing normal breast tissues; with a significant differences between cancer and normal samples ($P=0.002$), and in tissues that had Her2- and ER-/PR- statuses.

Conclusions: Our study suggested a probable relationship between down regulated of Glis2 expression and breast cancer. Also detection of a probable association between down regulated of Glis2 and breast cancers without Her2 and ER/PR receptors might be useful for prognostic and diagnostic uses or as probable target for treatment of these patients.