

乳腺癌组织中Id1基因mRNA的表达及其与临床病理的关系

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Id1 mRNA Expression in Breast Cancer and Its Relation to Clinicopathological Features

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全文: PDF (1055 KB) HTML (0 KB) 输出: BibTeX | EndNote (RIS) 背景资料

摘要 Id1基因; 乳腺癌; 实时荧光定量逆转录聚合酶链反应

关键词:

Abstract: Objective To investigate the expression of inhibitor of differentiation/DNA binding 1(Id1) in breast cancer tissue and its relation to clinicopathological and other molecular parameters. Methods The mRNA expression of Id1 in tissue and MCF-7 cell line of breast cancer were detected by fqRT-PCR. The protein expression of Id1, VEGF in 48 cases of breast carcinoma and 20 cases of breast fibroadenoma tissues of breast were detected by SABC immunohistochemistry. Results By Real-time RT-PCR method, the $2^{-\Delta CT}$ values of the breast carcinoma tissue and breast fibroadenoma tissue were (3.4581 ± 1.3644) and (1.1042 ± 0.0125) respectively. The positive rates of Id1 were significantly higher in breast carcinoma than those in breast fibroadenoma tissues, there were significant difference between the two groups ($p < 0.05$). Spearman rank correlation analysis revealed that the protein expression of Id1 was positively correlated with that of VEGF ($r = 0.303, p = 0.037$). No statistical correlation existed among the patients as grouped by age, lymph nodes metastasis, tumor size, histological grading, pTNM stages ($p > 0.05$). Conclusion Over-expression of Id1 exists in the patients with breast cancer. The expression of Id1 is positively correlated with that of VEGF which may be related to blood vessel formation.

Key words:

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