Dokumenttyp: journal article

Autor(en) des Beitrags: Holzscheiter, L; Biermann, JC; Kotzsch, M; Prezas, P; Farthmann, J; Baretton, G; Luther, T; Tjan-Heijnen, VC; Talieri, M; Schmitt, M; Sweep, FC; Span, PN; Magdolen, V

Titel des Beitrags: Quantitative reverse transcription-PCR assay for detection of mRNA encoding full-length human tissue kallikrein 7: prognostic relevance of KLK7 mRNA expression in breast cancer.

Abstract: BACKGROUND: The human tissue kallikrein gene family (KLK1 to KLK15) encodes a group of 15 serine proteases (hK1 to hK15), several of which have been implicated in cancer-related processes. METHODS: We established a specific quantitative reverse transcription-PCR assay for full-length KLK7 mRNA that excluded amplification of the exon 2 deletion splice variant (the latter does not encode a functional protease), and evaluated full-length KLK7 mRNA expression [normalized to human glucose-6-phosphate dehydrogenase (h-G6PDH)] in tumor tissue specimens from 155 breast cancer patients. RESULTS: High KLK7 mRNA expression (continuous) was significantly associated with a better patient outcome according to both univariate (P = 0.005) and multivariate (P = 0.046) Cox survival analysis. Separation of patients by optimized dichotomization revealed a significantly better prognosis for patients with high KLK7 mRNA status (n = 89) compared with patients with low KLK7 mRNA status (n = 66) [univariate hazard ratio (HR) = 0.45 (P = 0.001); multivariate HR = 0.50 (P = 0.005)]. In the subgroup of patients not receiving adjuvant treatment (n = 69), KLK7 mRNA status was a significant prognosticator [univariate HR = 0.29 (P = 0.002); multivariate...
HR = 0.40 (P = 0.034)]. This subgroup was least influenced by postoperative treatment and thus best showed the impact of KLK7 expression on the natural course of breast cancer disease. CONCLUSION: Expression of full-length KLK7 mRNA may represent a new prognostic marker in breast cancer disease.