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Kammerer, S; Roth, RB; Reneland, R; Marnellos, G; Hoyal, CR; Markward, NJ; Ebner, F; Kiechle, M; Schwarz-Boeger, U; Griffiths, LR; Ulbrich, C; Chrobok, K; Forster, G; Praetorius, GM; Meyer, P; Rehbock, J; Cantor, CR; Nelson, MR; Braun, A

Titel des Beitrags: Large-scale association study identifies ICAM gene region as breast and prostate cancer susceptibility locus.

Abstract: We conducted a large-scale association study to identify genes that influence nonfamilial breast cancer risk using a collection of German cases and matched controls and >25,000 single nucleotide polymorphisms located within 16,000 genes. One of the candidate loci identified was located on chromosome 19p13.2 [odds ratio (OR) = 1.5, P = 0.001]. The effect was substantially stronger in the subset of cases with reported family history of breast cancer (OR = 3.4, P = 0.001). The finding was subsequently replicated in two independent collections (combined OR = 1.4, P < 0.001) and was also associated with predisposition to prostate cancer in an independent sample set of prostate cancer cases and matched controls (OR = 1.4, P = 0.002). High-density single nucleotide polymorphism mapping showed that the extent of association spans 20 kb and includes the intercellular adhesion molecule genes ICAM1, ICAM4, and ICAM5. Although genetic variants in ICAM5 showed the strongest association with disease status, ICAM1 is expressed at highest levels in normal and tumor breast tissue. A variant in ICAM5 was also associated with disease progression and prognosis. Because ICAMs are suitable targets for
antibodies and small molecules, these findings may not only provide diagnostic and prognostic markers but also new therapeutic opportunities in breast and prostate cancer.