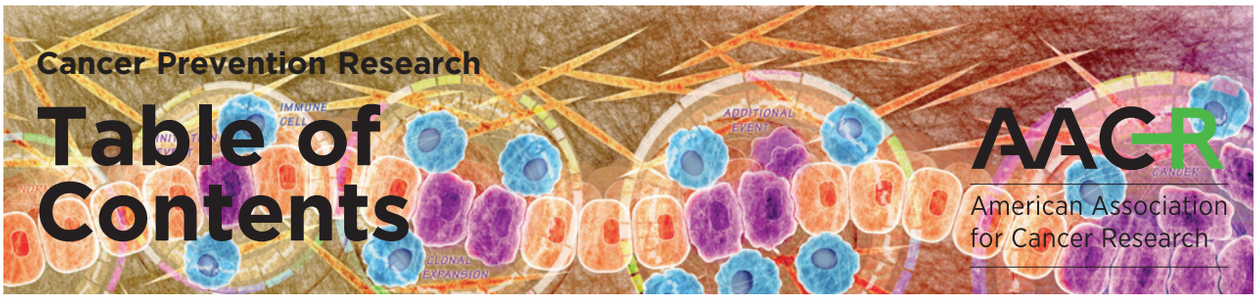

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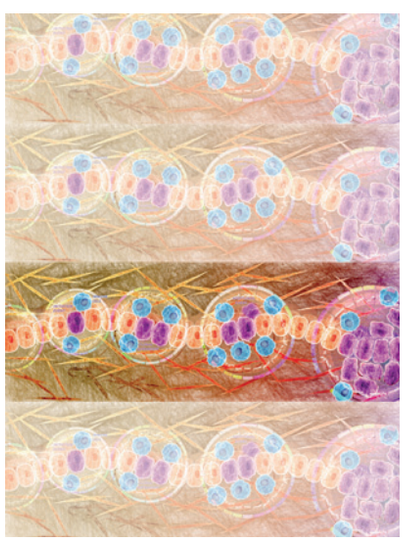
LETTER TO THE EDITOR

CORRECTION

ABOUT THE COVER

The molecular alterations associated with early pathological steps preceding the development of invasive carcinoma have not been well characterized. A Premalignant Cancer Genome Atlas (PCGA) is needed to both support the collection and molecular profiling (circus plot) of premalignant lesions (purple cells) to identify the sequence of initial driver events that cause normal cells (orange cells) to acquire cancer hallmarks that enable lesions (purple cells) to progress to fully invasive carcinoma, including the critical "additional genomic events" (e.g., checkpoint/tumor suppressor loss or other co-activating event) that transform premalignancy (purple cells in the fourth circle to the right) to cancer (far right). In addition to defining the sequence of site-specific genomic driving events, characterizing the premalignant inflammatory microenvironment, including the contribution of the stroma and immune cell (blue) regulation, will provide a better understanding of the selective forces that drive premalignant lesions to become invasive cancer. This figure appears in the Special Report by Kensler and colleagues (beginning on page 2), which sets out a brief agenda for the immediate future of cancer prevention, involving the inter-related fields of precision medicine and immunoprevention, driven by transformative approaches like PCGA, pivotal elements in a broader domain of personalized public health.



Cancer Prevention Research

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Cancer Prev Res 2016;9:1-117.