Blood-based methylation as biomarker for breast cancer

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Multiple studies have investigated global DNA methylation profiles and gene-specific DNA methylation in blood DNA—either from blood cells or from circulating free (cf) DNA—to develop powerful screening markers for cancer. We give an overview including examples for blood cell methylation and cfDNA methylation differences between healthy controls and breast cancer patients. Further, we developed a method, capture, and amplification by tailing and switching (CATS), which is very powerful to generate libraries of ng amounts of strongly fragmented and bisulfite treated cfDNA for methylation analysis via NGS or array-based approaches. One advantage of CATS is that it also targets single-stranded DNA. Furthermore, it is time efficient and as one tube approach easy to automate. First results of our breast cancer study applying CATS and 850k methylation arrays are shown. Even so, blood-based DNA methylation marker holds great promises as a marker for BC risk stratification, the evidence is still limited. Optimal marker sets are yet to be identified and promising results need to be validated in prospective study cohorts and tested in a large screening population.

Recent Publications

Biography

Barbara Burwinkel is the Head of the Molecular Epidemiology Group at the German Cancer Research Center, DKFZ, and Head of the founder professorship “Molecular Biology of Breast Cancer” at the University Clinic Heidelberg. She has working experience in both biotech and academia and has been awarded several research awards. Her research focus is on the development of blood-based molecular marker sets for diagnosis, early detection, prognosis and prediction of breast and ovarian cancer including the development of new methods like CATS (Capture and Amplification by Tailing and Switching) for NGS library generation.

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