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Blood-based methylation as biomarker for breast cancer

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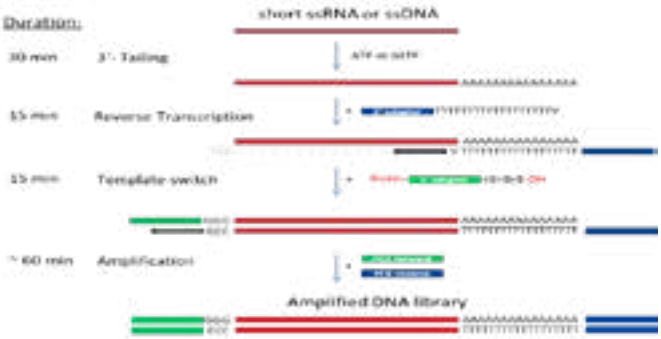
Multiple studies have investigated global DNA methylation profiles and gene-specific DNA methylation in blood DNA-either from blood cells or from circulating free (cf) DNA-to develop powerful screening markers for cancer. We give an overview including examples for blood cell methylation and cfDNA methylation 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

1. Tang Q, Holland-Letz T, Slynko A, Cuk K, Marme F, Schott S, Heil J, Qu B, Golatta M, Bewerunge-Hudler M, Sutter C, Surowy H, Wappenschmidt B, Schmutzler R, Hoth M, Bugert P, Bartram CR, Sohn C, Schneeweiss A, Yang R and Burwinkel B. DNA methylation array analysis identifies breast cancer associated-RPTOR, MGRN1 and RAPSN hypomethylation in peripheral blood DNA. Oncotarget 7(39):64191-64202
2. Tang Q, Cheng J, Cao X, Surowy H and Burwinkel B (2016) Blood-based DNA methylation as biomarker for breast cancer: a systematic review. Clinical Epigenetics 8:115.
3. Yang R, Pfütze K, Zucknick M, Sutter C, Wappenschmidt B, Marme F, Qu B, Cuk K, Engel C, Schott S, Schneeweiss A, Brenner H, Claus R, Plass C, Bugert P, Hoth M, Sohn C, Schmutzler R, Bartram CR, Burwinkel B (2015) DNA methylation array analyses identified breast cancer-associated HYAL2 methylation in peripheral blood. International Journal of Cancer 136(8):1845-55.
4. Pfütze K, Benner A, Hoffmeister M, Jansen L, Yang R, Bläker H, Herpel E, Ulrich A, Ulrich CM, Chang-Claude J, Brenner H, Burwinkel B (2015) Methylation status at HYAL2 predicts overall and progression-free survival of colon cancer patients under 5-FU chemotherapy. Genomics 106(6):348-54.
5. Turchinovich A, Surowy H, Serva A, Zapatka M, Lichter P, Burwinkel B (2014)Capture and Amplification by Tailing and Switching (CATS). An ultrasensitive ligation-independent method for generation of DNA libraries for deep sequencing from picogram amounts of DNA and RNA. RNA Biol. 11(7):817-28.

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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