Multimode whole genome approaches to plasma-based disease monitoring in triple-negative breast cancer

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Whole genome analysis of circulating tumour DNA fragments holds promise for highly sensitive monitoring and detection of cancer burden breast cancer patients. Furthermore, recent technology developments in methylation sequencing have advanced the possibility of single assay multi-mode monitoring of disease responses. To this end we are characterizing the genomes and plasma of patients from a cohort of 200 triple negative breast cancers, followed serially over a 5-year period with plasma collection. We have shown that whole genome sequencing of plasma provides sensitive detection of residual disease, anticipating relapse up to 27 months before clinical relapse. The approach and planned studies will be presented.