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**Universal microarray for analysis of breast cancer**

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**Background:** L-DNA is an artificial left turning enantiomer of the naturally occurring D -conformation of DNA. Therefore, L-DNA duplexes have the same physical characteristics in terms of solubility, duplex stability and selectivity as D-DNA but form a left-helical double-helix. Because of its chiral difference, L-DNA does not bind to its naturally occurring D-DNA counterpart. Breast cancer is a complex disease; clinically there is a need of new and more precise diagnostic tools. **Objective:** establishment of a universal microarray based on L-DNA molecules that permits the analysis of different kinds of molecular diagnostic information in breast cancer. **Methods:** based on microarray technology protocols an L-DNA platform was developed and applied to analyze markers related to breast cancer in 18 breast cancer samples as well as in 3 cell lines with different phenotypes. **Results:** The establishment of an L-DNA microarray platform was applied to obtain information of both SNPs and expression profiling genes in breast cancer. From merging the data generated, specific SNP-haplotypes related to different metastasis outcomes in breast cancer were identified. **Conclusion:** The benefits of analyze different molecular levels at once enlarge the understanding of biological processes. In practice specific metastasis haplotypes could detect high risk individuals early on and patient-specific treatment plans could be drawn up.