



The Realisation of Research

DNA Methylation Markers for Prediction of Cancer Risk

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Category(s):

Cancer/Oncology
Medical

Description:

Markers for Prediction of Cancer Risk

Available for: Co-development and licensing

Summary

UCL researchers have identified unique DNA methylation signatures in patient serum that have the potential to indicate breast cancer risk up to five years in advance of clinical diagnosis.

The Technology and its Advantages

Aberrant DNA methylation is a hallmark of cancer. UCL researchers have demonstrated for the first time that DNA methylation present in a subset of genes is predictive of cancer risk.

These markers were measured in serum DNA from healthy postmenopausal women (aged 50-75 years) of low genetic breast cancer risk in a nested prospective case control design within the UK Collaborative Trial for Ovarian Cancer Screening encompassing serum DNA samples from over 200,000 women.

Importantly UCL researchers have identified unique DNA methylation signatures in patient serum that have the potential to indicate breast cancer risk up to five years in advance of clinical diagnosis.

Market Opportunity

The markers developed by UCL serve as a solid basis to develop DNA methylation based tests to predict chronic diseases like cancer. Currently SNP and epidemiological models are of limited value when predicting breast cancer risk. As well as being independent risk predictors there is potential of the DNA methylation tests to complement genetic and epidemiological models to predict breast cancer risk.

Intellectual Property Status

A GB patent application was filed on 4th February 2011.

Further Information

Further Information

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