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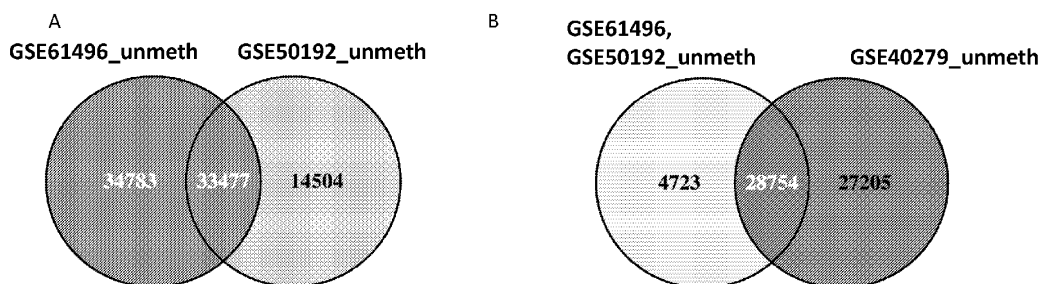


Figure 1.

(57) Abstract: A "binary-categorical differentiation" method for finding a combination of a small number of exquisite DNA methylation positions in the human genome (CG IDs) for detecting cancer in DNA in biological material derived from a patient and distinguishing it from other tissue cell free DNA and blood cells DNA is provided. Another method for detecting tissue of origin of tumor DNA using a combination of unique DNA methylation positions in the human genome (CG IDs) is also provided. Combinations of CG IDs derived from tumor DNA are disclosed for accurately detecting cancers by measuring the DNA methylation of a combination of specific CG IDs and deriving a "methylation score". Kits for predicting cancer using CG IDs are also provided.

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