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DNA Hypermethylation Biomarkers in Brain Cancer



DESCRIPTION

Astrocytomas are the most common and lethal type of human brain cancer and they are the primary malignancies of the central nervous system. It is known that aberrations in DNA methylation patterns have a critical affect on how aggressively tumors progress and their metastatic potential. COH's novel technology provides a global view of DNA hypermethylation events linked with human Astrocytomas, as compared with normal healthy brain tissue. COH is able to measure a patient's hypermethylation patterns by analyzing a blood sample, serum sample or plasma sample and then diagnosis Astrocytomas (most brain cancers) prior to the presentation of symptoms.

KEY ASPECTS

• The CpG clusters analyzed in the methylation pattern include homeobox genes selected from HOX gene clusters: HOXA, HOXB, HOXC, DLX1, BARHL2, PITX2, SIM1, NKX2-8, PAX9 and FOXA1

PUBLISHED DATA

• Wu X, Rauch TA, Zhong X, Bennett WP, Latif F, Krex D, Pfeifer GP. CpG island hypermethylation in human astrocytomas. Cancer Res. 2010 Apr 1;70(7):2718-27. Epub 2010 Mar 16.

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Title	US Application Number	Filed
DNA Hypermethylation Brain Cancer Markers	61/316,324	3/22/2010

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