

epigenomics

DNA Methylation

DNA methylation is a fundamental and tightly controlled biological process that naturally serves the regulation of genes and the stability of the genome. Cytosine, one of the four chemical bases of our genetic code, can be modified by the addition of a chemical methyl group. DNA methylation in gene regulatory regions (i.e. gene promoters) usually shuts off gene activity either by directly interfering with the binding of transcription factors or by allowing chromatin condensation. As different cells shut off different genes, every cell type has its unique DNA methylation “fingerprint”. Originally identified as a fundamental mechanism underlying cell determination and differentiation in embryonic development, today virtually thousands of scientific publications show that this „fingerprint“ changes specifically in aging and many common diseases, in particular cancer providing a rich source for highly specific biomarkers for organ-specific disease diagnosis and disease classification.

Compared to other biomarkers, DNA methylation biomarkers have multiple advantages. Thus, cancer specific DNA methylation patterns can be used to sensitively detect tumor DNA shed to body fluids such as blood or urine. This is the underlying principle of our organ-specific early detection tests for colorectal, prostate and lung cancer with non- or minimally invasive test procedures. Further, DNA-Methylation can easily be quantified as the unmethylated DNA of the same gene in the sample can serve as an internal reference. As DNA methylation is stable in routine clinical sample processing, it can be analyzed in tissue samples fixed and paraffin embedded for histological analysis by the pathologists. Thus, no extra sample is required for our tissue-based cancer molecular classification tests.

Epigenomics has the technology and the know-how to identify and validate DNA methylation biomarkers and use them for the development of molecular diagnostic tests.