

The methylome in health and disease: survey of unmethylated CpGs
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Amongst dinucleotides, CpGs are unique in that they are severely underrepresented in the genomes of higher eukaryotes and can operate as on-off switches depending on their methylation status. Methylation of CpGs constitutes an epigenetic mark that is at the core of cellular differentiation. Changes in these marks are necessary for the differentiation of the one cell fertilized egg into all of the body's cell types and organs. Once applied, methylation marks may be stable and replete of information that we are only beginning to glimpse at. Abnormal removal or abnormal deposition of methylation marks occur in diseases such as cancer and complex syndromes such as allergic asthma and may include pre-obesity and the metabolic syndrome. But, it is not known whether the methylation marks are cause or consequence. It is also thought that behavioral imprinting is associated with changes in the methylation status of selected genes as is the case with genetic imprinting and allelic exclusion. The goal of the project is to test if we can define tissue and cell specific DNA methylation patterns.

