About DNA Methylation
It is well demonstrated that DNA methylation plays an important role in normal human development and is associated with the regulation of gene expression, tumorigenesis, and other genetic and epigenetic diseases. DNA methylation involves the addition of a methyl group to DNA nucleotide, namely attached to a carbon atom on cytosine or a nitrogen atom on adenine. The addition of a methyl group to these nucleotides can be an integral part of important biological processes, though aberrant methylation patterns can also be associated with cancer and genetically related diseases. Such information may contribute to a greater understanding of suspect genes in diseased cells and may lead to a method of discrimination of the disease. Subsequently, it is important to quantify DNA methylation levels in order to further study development and disease at an epigenetic level.

Methods of DNA Methylation Analysis
There are three major approaches to a DNA methylation study: global, gene-specific, or genome wide. It is important to determine whether to study global (total) methylation or gene-specific (locus-specific) methylation in a DNA sample. A comparative study in global DNA methylation levels between various DNA samples is useful for evaluating the effects of exposure to certain conditions or treatment with certain drugs/chemicals. For researchers interested in detecting methylation in a certain gene and its association in certain symptoms or diseases, a gene-specific methylation approach is needed. The following table can help a researcher determine which Epigentek products are suitable for his or her DNA methylation studies:

	Global DNA Methylation	DNA Bisulfite Modification	Methylated DNA Immunoprecipitation
Representative Kit	P-1034, P-1035	P-1001, P-1016, P-1026	P-1015, P-2019, P-2020
Format	96 strip-well plate	Vial/column	96 strip-well plate
Input materials	DNA	DNA/cells	DNA/cells
Processing time	3 to 4 hours	30 min to 2 hours	2 to 3 hours
Applications	Direct quantification of global DNA methylation	Preparation of bisulfite treated DNA	Enrich methylated DNA fractions from genomic DNA
Study-based selection	When global (total) DNA methylation status is to be examined. Suitable for using in comparative study of DNA methylation status of the samples that may be exposed to drugs, nutrients, or chemicals.	When gene-specific methylation is to be detected. Most suitable for using in PCR or sequencing-based methylation analysis. Can also be used with array-based methylation scanning (Illumina).	When genome-wide DNA methylation is to be profiled. Most suitable for use in microarray-based methylation analysis. Can also be used for PCR and sequencing-based methylation analysis.

Decision Flowchart for DNA Methylation Study Approaches

Global or Gene-Specific Study?

Global

Gene-Specific

MethylFlash Methylated DNA Quantification Kit *(Cat # P-1034 or P-1035)*

or

Bisulfite Sequencing of Repetitive Elements

or

HPLC/Mass Spectrometry

Individual Candidate Gene or Genome Wide?

Individual Candidate Gene

Genome Wide

Bisulfite Treatment of DNA with **BisulFlash DNA Modification Kit** *(Cat #P-1026)*

Array-based?

Yes

No

Single Base Resolution or Qualitative?

Single Base Resolution

Qualitative

Allele specific?

Yes

No

Methylation Specific PCR (qMSP) with **Methylamp MS-qPCR Fast Kit** *(Cat # P-1028)*

Bisulfite Cloning and Sequencing

Direct Bisulfite Sequencing (pyrosequencing, manual sequencing, or mass array)

Immunoprecipitation-enabled enrichment of methylated DNA fractions with a **5-methylcytosine antibody** *(Cat # A-1014)*, or with **Methylamp Methylated DNA Capture Kit** *(Cat #P-1015)* for DNA samples, **EpiQuik MeDIP Kit** *(Cat #P-2019)* for cell culture samples, or **EpiQuik Tissue MeDIP Kit** *(Cat #P-2020)* for tissue samples, followed by microarray (MeDIP-chip)

or

Methylation-sensitive restriction enzyme

RGLS (Restriction Landmark Genomic Scanning)

or

Digital Karyotyping

or

Library & Sequencing