

epigenomics

DNA Methylation Amplification

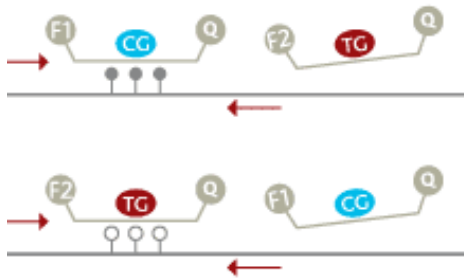
Epigenomics utilizes **MethyLight**, a fluorescence-based real-time PCR technology, for high-throughput methylation detection and quantification using DNA methylation specific probes. Epigenomics has customized MethyLight for:

- Quantitative methylation measurement: Quantitative MethyLight (QM).
- Sensitive methylation measurement: Heavy Methyl (HM).

Description

Quantitative MethyLight (QM)

After bisulfite conversion of genomic DNA, CpG sites are amplified by PCR using methylation-independent primers (red arrows). Detection probes for methylated (CG) and un-methylated (TG) sites allow for simultaneous quantitative measurement of un-methylated and methylated copies of the gene (F1, F2, fluorescence dyes; Q, quencher).



Heavy Methyl (HM)

On bisulfite converted genomic DNA, specific blockers (green) prevent amplification of un-methylated DNA by primers (red arrows). When genomic DNA is methylated, the blockers do not bind, allowing primers to bind and amplify the target sequence. The amplification is detected with a methylation specific oligonucleotide probe, labeled with fluorescent dye (F) and quencher (Q).

