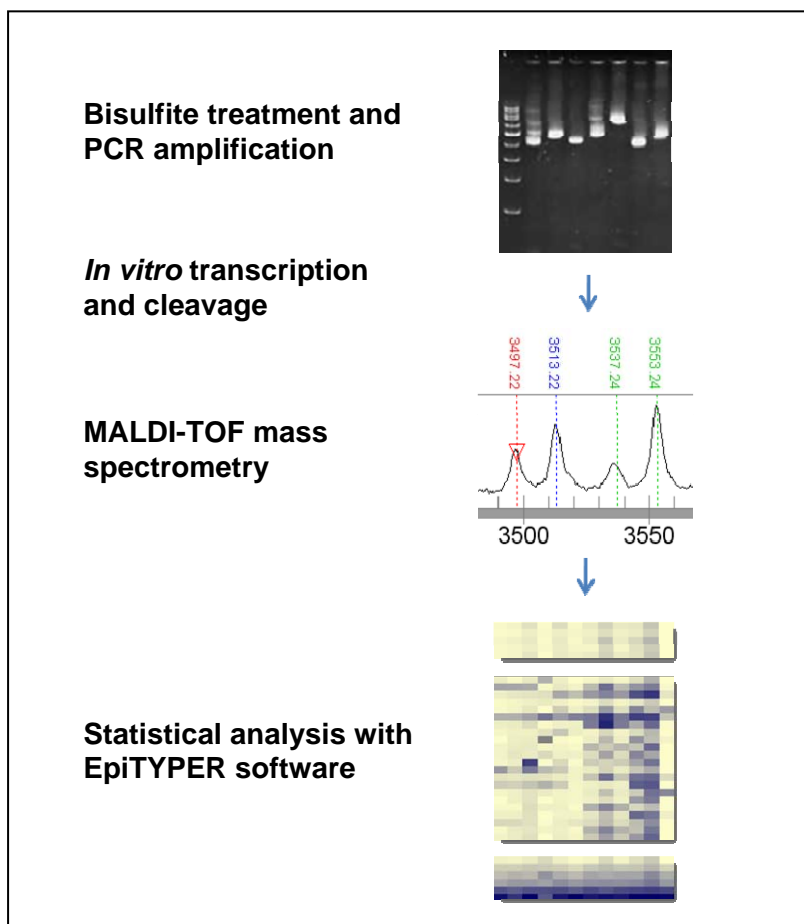


## High-throughput quantitative DNA methylation analysis

The EpiTYPER - MassARRAY assay (Sequenom Inc.) is a candidate approach that allows high-throughput quantitative methylation analysis of multiple CpG sites. The assay uses bisulfite-treated DNA in which unmethylated cytosines have been converted to thymines while methylated cytosines remain unaltered. Selected DNA regions are amplified by PCR with tagged primers, *in vitro* transcribed into RNA and cleaved base-specifically by endoribonuclease. Mass spectra of cleavage products are obtained by MassARRAY analyses based on MALDI-TOF mass spectrometry. Fragments differ in mass depending on the sequence changes introduced by the initial bisulfite treatment. The assay is used for validations of whole epigenome screening experiments (e.g. MCIp combined with array technology) and candidate gene promoter analyses and is even suitable for analyses of DNA extracted from formalin-fixed paraffin-embedded tissues.



Ehrich M, Nelson MR, Stanssens P, Zabeau M, Liloglou T, Xinarianos G, Cantor CR, Field JK, van den Boom D. Quantitative high-throughput analysis of DNA methylation patterns by base-specific cleavage and mass spectrometry. Proc. Natl. Acad. Sci USA 2005; 102: 15785-90.