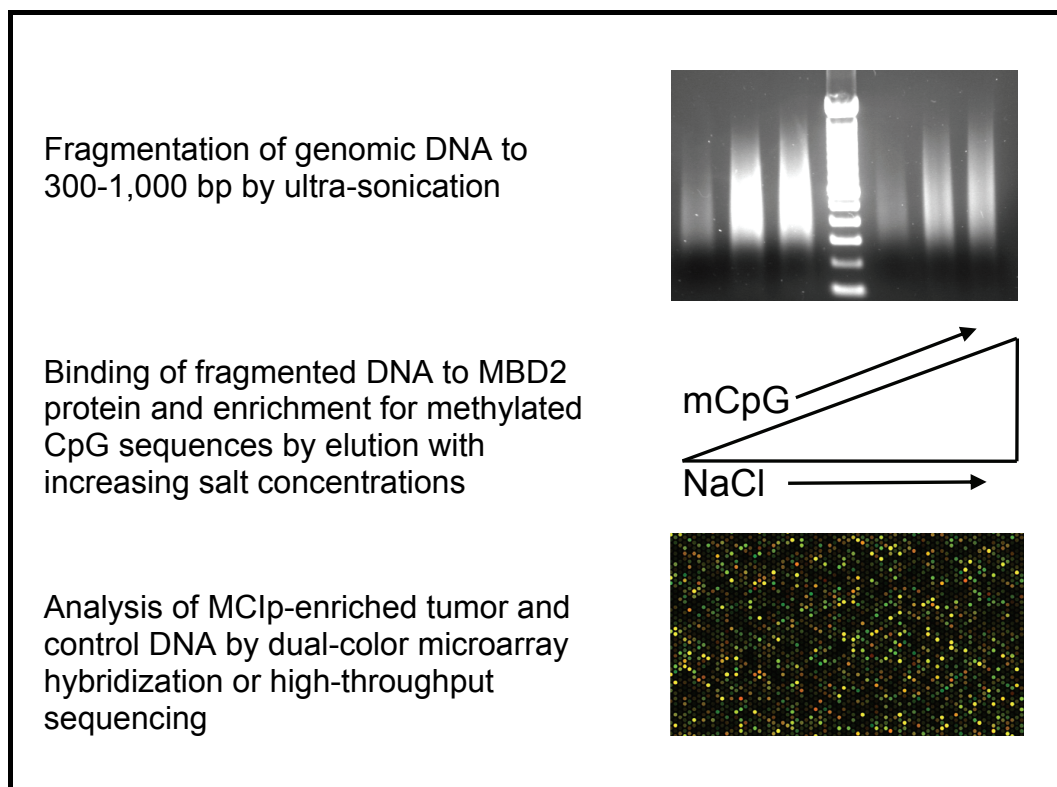


Genome-wide methylation analysis

A common hallmark in tumorigenesis is the silencing of tumor suppressor genes by hypermethylation of promoter CpG islands. To facilitate the identification of novel hypermethylated tumor suppressor genes, we apply **methyl-CpG immunoprecipitation (MCIp)** enabling the enrichment of methylated CpG-rich sequences (Gebhard et al., 2006).

MCIp employs a recombinant methyl-CpG-binding domain protein, MBD2, whose affinity for double-stranded methylated DNA can be modulated by differing salt concentrations. Non- or weakly methylated DNA elutes at low, while highly methylated DNA elutes at high salt concentrations. MCIp-enriched methylated DNA of tumor and control tissue is either analysed by dual-color CpG island microarray hybridization or by parallel next-generation high-throughput sequencing.



Gebhard C, Schwarzfischer L, Pham TH, Schilling E, Klug M, Andreessen R, Rehli M, Genome-wide profiling of CpG methylation identifies novel targets of aberrant hypermethylation in myeloid leukemia. *Cancer Res.* 2006; 66: 6118-28.