

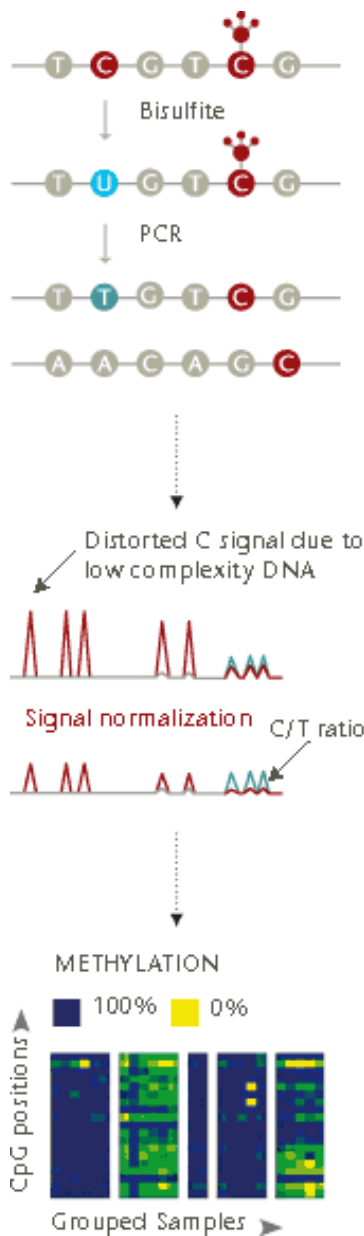
epigenomics

Bisulfit-Sequenzierung

Die deutsche Seite befindet sich im Aufbau und wird in Kürze fertiggestellt.

Epigenomics uses its proprietary bisulfite conversion protocols in combination with in-house developed sequence analysis software for **direct sequencing of bisulfite converted genomic DNA**. The main features of this technology are:

- Highly efficient bisulfite conversion.
- Direct sequencing of genomic DNA (no sub-cloning steps required).
- Quantitative methylation information at each CpG over up to 500 bp.
- Suitable for methylation analysis of paraffin-embedded tissue samples.



Description

1. Genomic DNA is converted using Epigenomics' proprietary bisulfite pre-analytics workflow
2. PCR products are directly sequenced. Sequencing trace file are normalized. Relative methylation levels are calculated by determining the ratios between C (red) and T (green) signals at individual CpG positions.
3. Calculated methylation ratios at individual CpG positions are translated into a color-coded data matrix