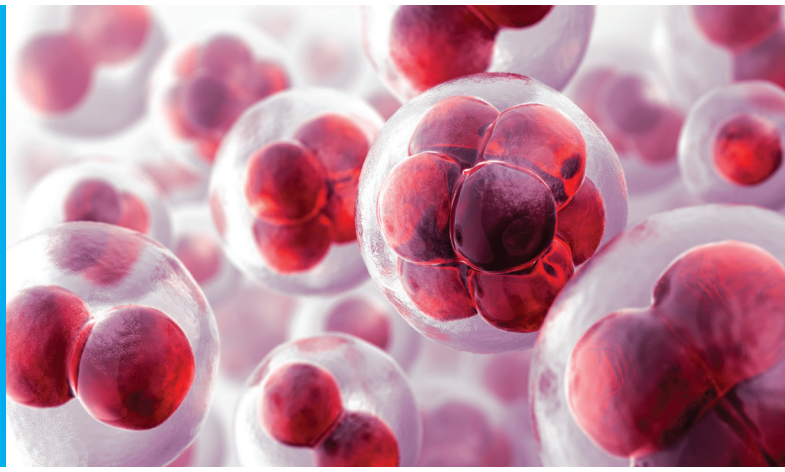
DNA METHYLATION

Analysis of DNA methylation, DNA demethylation, and the functional effects in these changes are of increasing interest to epigenetics researchers in developmental programming, cell differentiation, disease identification, and therapeutic development.



DNA Methylation analysis is widely recognised as a critical component of any study into the function of genes. Changes in methylation can modify gene expression, impacting a range of biological processes including developmental programming, cell differentiation, disease identification and therapeutic development.

Whole Genome Methylation Screening

Illumina Infinium MethylationEPIC BeadChip

- A powerful discovery tool to identify epigenetic changes
- Comprehensive coverage of methylation sites across the human genome at single-nucleotide resolution
- Economical screening of multiple samples in parallel

Start your methylation study by screening the human genome's key methylated sites to advance the understanding of variable regions contributing to gene expression variation or the phenotypic outcome.

Key Highlights

- Uses the Illumina MethylationEPIC BeadChip, containing over 850,000 methylation sites
- Contains > 90% original content from the broadly used Infinium HumanMethylation450K plus a significant increase in enhancer sites to deliver a comprehensive genome overview
- Provides quantitative analysis at single-nucleotide resolution
- Multiple samples can be analysed in parallel to deliver high-throughput power while minimising the cost per sample

For non-human whole genome methylation, our Next Generation Sequencing service can be considered.

Reduced Representation Bisulfite Sequencing (RRBS-Seq)

Reduced Representation Bisulfite Sequencing (RRBS) is an economical alternative to whole genome bisulfite sequencing, requiring ~50-fold fewer sequencing reads. It provides single-base resolution of DNA methylation (5-methylcytosine) across a genome. The method employs restriction digestion of genomic DNA with the methylation-insensitive restriction enzyme MspI (recognition site CCGG) to enrich the sample for genomic fragments with a high frequency of MspI sites and potential CpG methylation sites.

DNA METHYLATION

Gene and Promoter Methylation Discovery

Agena Bioscience EpiTYPER

- Targeted and quantitative methylation profiling
- Ideal for methylation discovery in candidate genes or promoter/enhancer regions
- Flexible in design and high throughput for sizable cohorts

Agena Bioscience EpiTYPER is an ideal tool for screening candidate genes or regions, for differentially methylated regions. It can be used to verify existing results or to refine the location of predictive CpG sites. It is applicable with most organisms and large or small sample sets.

Key Highlights

- Rapid discovery of multiple methylated CpG positions in regions of 200-500 bp
- Quantitative assessment of the degree of methylation for most sites
- Detection of methylation levels as low as 5%
- Compatible with many sample types, including formalin-fixed paraffin-embedded tissue
- Cost-effectively investigate promoter regions

Targeted Sites and Methylation Validations

Qiagen PyroMark sequencing

- Targets specific CpG sites for high accuracy methylation quantification
- Detects and quantifies even small changes in methylation levels
- Assay design flexibility to enable higher success rates in design and analysis
- Ideal for validation of key CpG sites from whole genome methylation studies

Qiagen PyroMark sequencing is used for a high resolution result by targeting known sites for methylation quantification on specific CpG's.

Key Highlights

- Measure specific CpG site methylation levels, even in close proximity
- Simple and flexible design giving the highest percentage of customisable targets
- Routinely measures methylation values with a sensitivity of 5%
- Bisulphite conversion quality indication measuring non-CpG cytosine conversion to thymine

At AGRF Pyrosequencing and EpiTyper are complementary technologies and the decision to use one over the other is based on project requirements.

Bioinformatics

Analysis options are available with every service, from detection of differentially methylated probes, to visualisation of results.

Our funding partners

AGRF is a not-for-profit organisation supported by the Commonwealth Government infrastructure schemes administered through Bioplatforms Australia.

These schemes include NCRIS, EIF, Super Science Initiative CRIS and NCRIS 2.

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