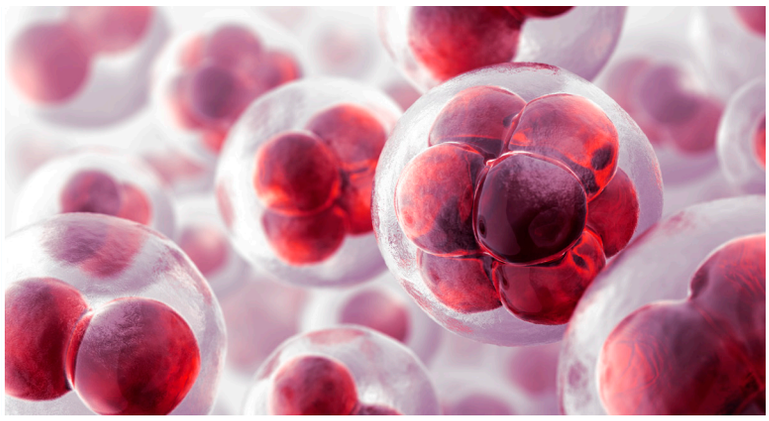
DNA METHYLATION

Empowering Australian Genomics

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

illumina CSPro CERTIFIED SERVICE PROVIDER

Agena CERTIFIED SERVICE PROVIDER

NATA WORLD RECOGNISED ACCREDITATION

REDUCED REPRESENTATION BUSULFITE 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 methylC) 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.

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 cohort

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 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 on 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

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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.

RESEARCH

A small sample of AGRF authored work using our methylation service.

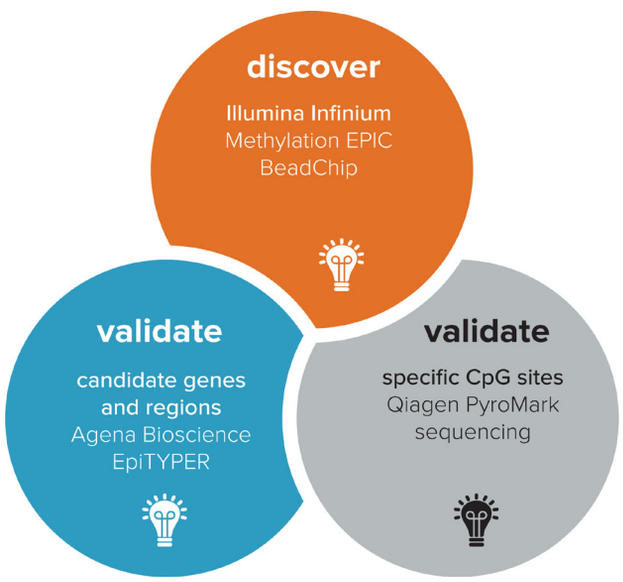
Maksimovic J, Gordon L, Oshlack A. SWAN: Subset-quantile within array normalization for illumina infinium HumanMethylation450 BeadChips. Genome Biol.2012 Jun 15;13(6):R44.

Saffery R, Gordon L. Time for a standardized system of reporting sites ofgenomic methylation. Genome Biol. 2015 Apr 30;16:85.

Martino D, Loke YJ, Gordon L, Ollikainen M, Cruickshank MN, Saffery R, Craig JM. Longitudinal, genome-scale analysis of DNA methylation in twins from birth to18 months of age reveals rapid epigenetic change in early life and pair-specific effects of discordance. Genome Biol. 2013 May 22;14(5):R42.

BIOINFORMATCS

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



Our funding partners

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

NCRIS National Research Infrastructure for Australia
An Australian Government Initiative

BIOPLATFORMS AUSTRALIA

Contact us:

1300 247 301

info@agrf.org.au

www.agrf.org.au/services