



Innovating Epigenetics Solutions



# WELCOME TO DIAGENODE

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DNA-methylation Workshop

January 2022

# Objectives

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## Overview of DNA methylation analysis methods

### MeDIP workflow

MeDIP-qPCR

MeDIP-seq

MeDIP-seq: analysis

### RRBS Workflow

Sample & Library preparation

Early Sample Pooling

Bisulfite conversion

Library amplification & QC

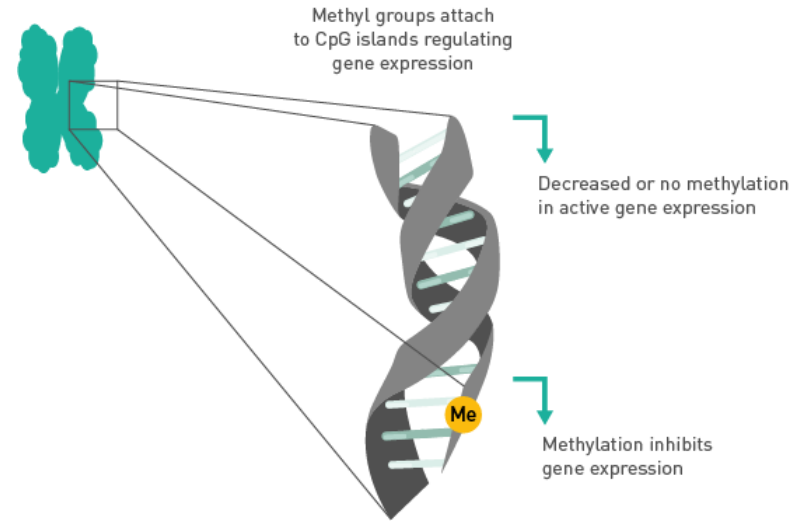
Sequencing recommendations

NGS analysis



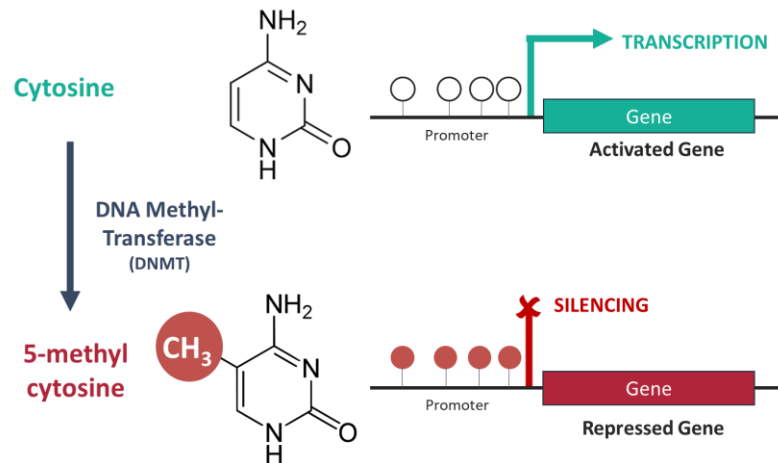
# What is DNA methylation?

- DNA methylation is an epigenetic mechanism that occurs by the addition of a methyl (CH<sub>3</sub>) group to DNA
- Occurs at different genome locations:
  - Gene bodies
  - Promoters
  - Non-coding areas (e.g. repetitive regions, small RNAs, pericentromeric regions)
- DNA-methylation often modifies expression and function of genes



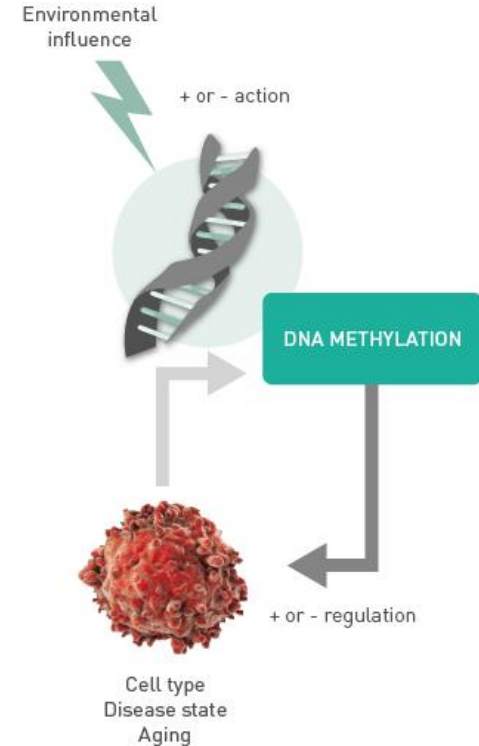
# What is DNA methylation?

- The most abundant and widely characterized DNA methylation is at the 5-carbon of the cytosine ring resulting in 5-methylcytosine: **5-mC**
- In somatic cells, most 5-mC occurs as paired symmetrical methylation of CpG sites
- In embryonic stem cells, a substantial amount of 5-mC is also observed in non-CpG contexts



# Application to human diseases

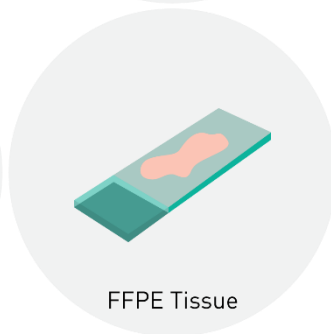
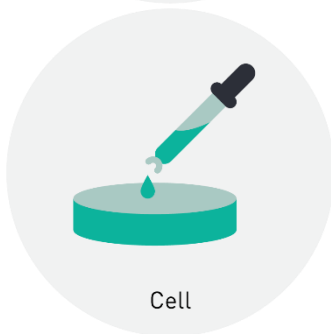
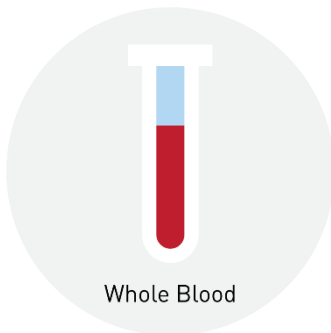
- DNA methylation profiles is cell type and tissue specific
- Aberrations in methylation marks is implicated in various diseases. For example, abnormal changes in DNA methylation are markers for cancer formation:
  - Global loss of DNA methylation (hypomethylation) resulting in genomic instability
  - Increased DNA methylation (hypermethylation) in CpG-rich regions inducing transcriptional repression
- Specific DNA methylation aberrations can be used as biomarkers for disease detection





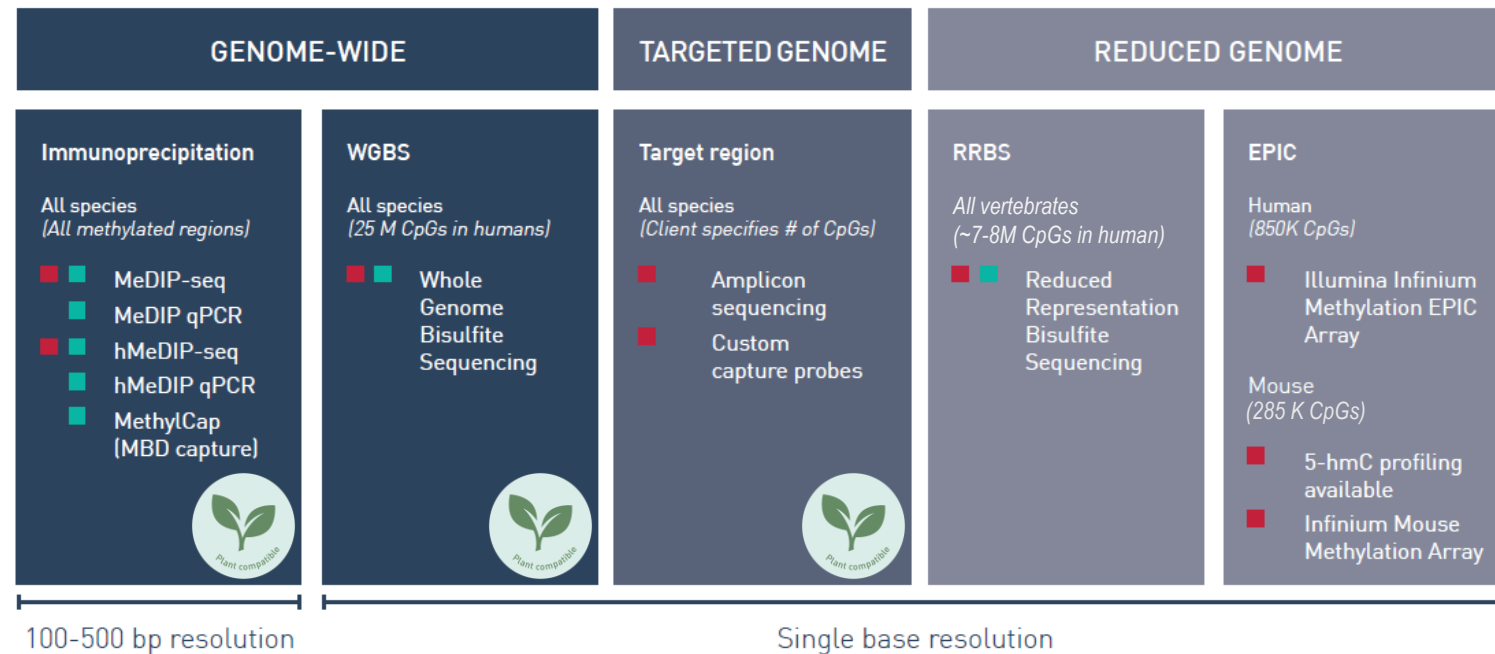
# DNA methylation analysis

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# DNA methylation analysis



■ Service  
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