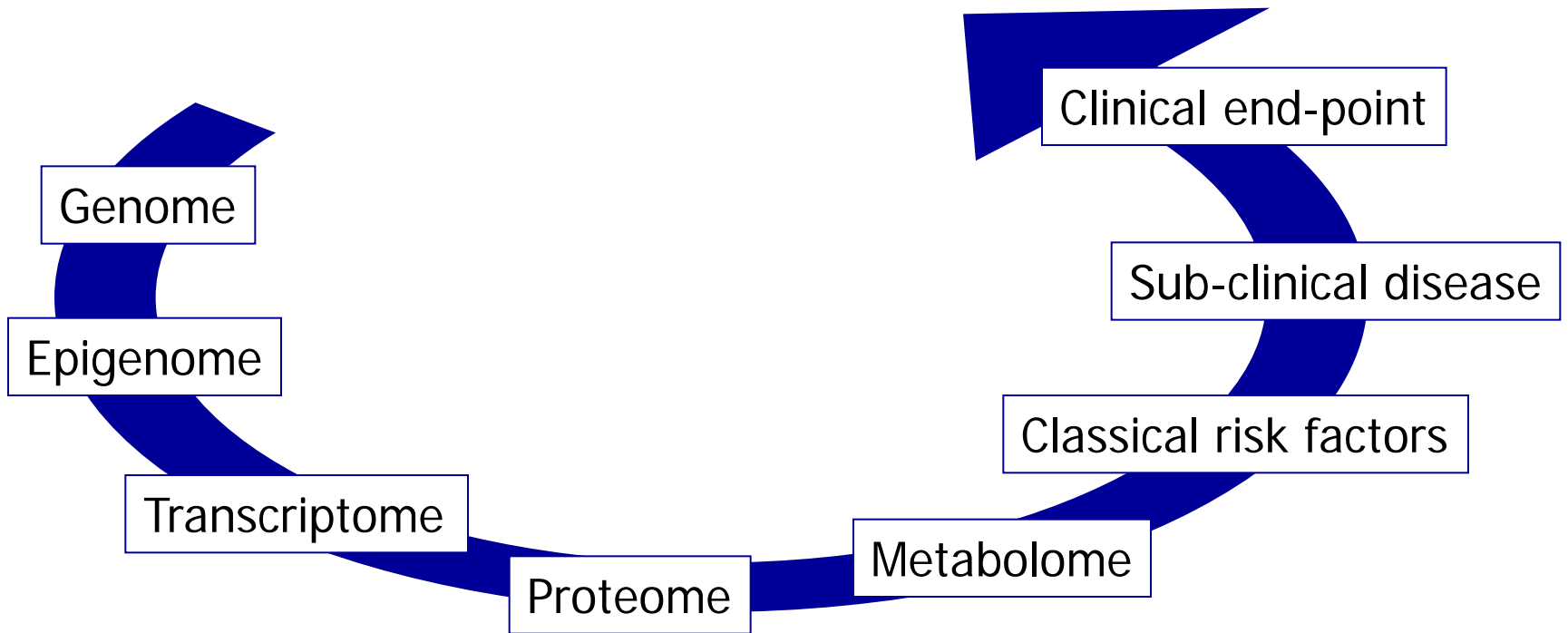


An introduction to the epigenome

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On offer for today

- The molecular basis of epigenetics
- The role of epigenetics in fundamental biology
- Epigenetics as integrator of environmental signals
- Epigenetics in disease mechanisms

The genetic code is not enough

AGTGCCGGGAAGTGGGGCTTGGC
CCAGGGCCCCCAAGACACACAGA
CGGCACAGCAGGGCTGGTTCAAG
GGCTTTATTCCATCTCTCTCGGT
GCAGGAGGCGGCGGGTGTGGGGC
TGCCTGCGGGCTGCGTCTAGTTG
CAGTAGTTCTCCAGCTGGTAGAG



The genetic code is not enough

A G T C

AGTGCCGGGAAGTGGGGCTTGGC
CCAGGGCCCCCAAGACACACAGA
CGGCACAGCAGGGCTGGTTCAAG
GGCTTTATTCCATCTCTCTCGGT
GCAGGAGGCGGCGGGTGTGGGGC
TGCCTGCGGGCTGCGTCTAGTTG
CAGTAGTTCTCCAGCTGGTAGAG



The genetic code is not enough

AGTGCCGGGAAGTGGGGCTTGGC
CCAGGGCCCCCAAGACACACAGA
CGGCACAGCAGG**GCTGGTTCAAG**
GGCTTTATTCCATCTCTCTCGGT
GCAGGAGGCGGCGGGTGTGGGGC
TGCCTGCGGGCTGCGTCTAGTTG
CAGTAGTTCTCCAGCTGGTAGAG



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AGTGCCGGGAAGTGGGGCTTGGC
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TGCCTGCGGGCTGCGTCTAGTTG
CAGTAGTTCTCCAGCTGGTAGAG



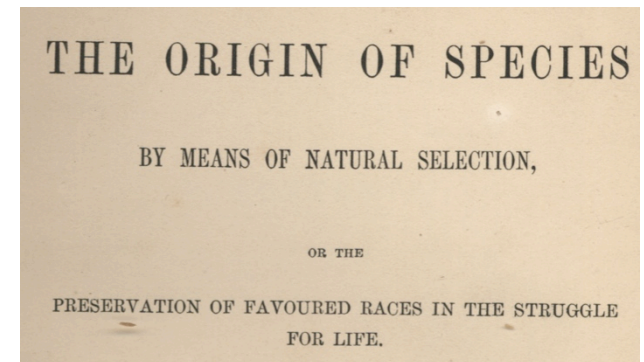
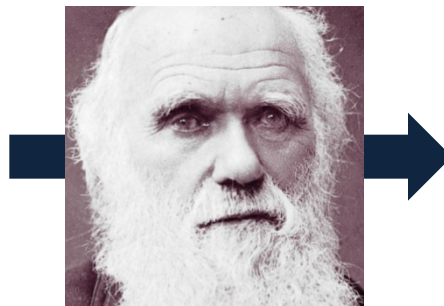
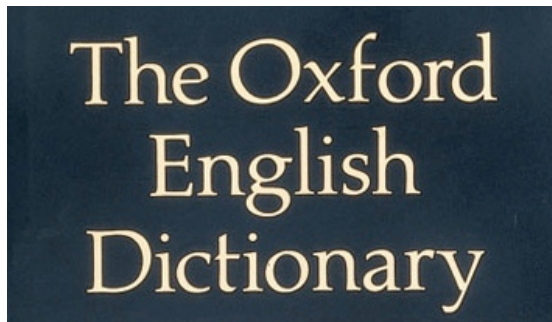
The Oxford
English
Dictionary



THE ORIGIN OF SPECIES
BY MEANS OF NATURAL SELECTION,
OR THE
PRESERVATION OF FAVOURED RACES IN THE STRUGGLE
FOR LIFE.

The genetic code is not enough

AGTGCCGGGAAGTGGGGCTTGGC
CCAGGGCCCCCAAGACACACAGA
CGGCACAGCAGG**GCTGGTTCAAG**
GGCTTTATTCCATCTCTCTCGGT
GCAGGAGGCGGCGGGTGTGGGGC
TGCCTGCGGGCTGCGTCTAGTTG
CAGTAGTTCTCCAGCTGGTAGAG



The genetic code is not enough

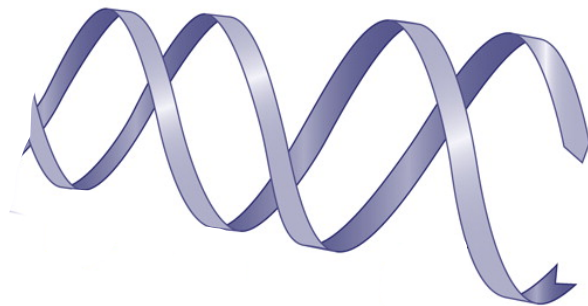
AGTGCCGGGAAGTGGGGCTTGGC
CCAGGGCCCCCAAGACACACAGA
CGGCACAGCAGG**GCTGGTTCAAG**
GGCTTTATTCCATCTCTCTCGGT
GCAGGAGGCGGCGGGTGTGGGGC
TGCCTGCGGGCTGCGTCTAGTTG
CAGTAGTTCTCCAGCTGGTAGAG

Epigenetics

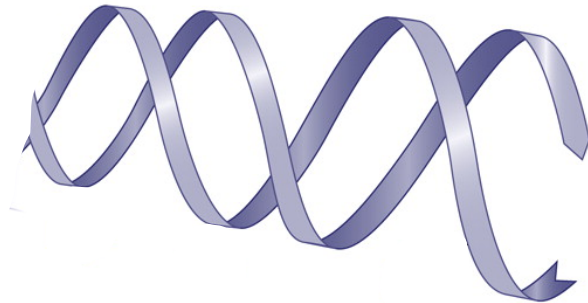
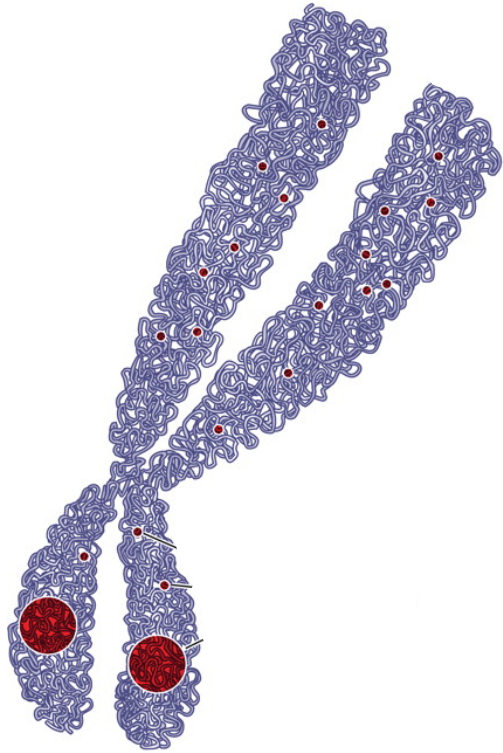


- Instructing the DNA where, when and how much to express a gene

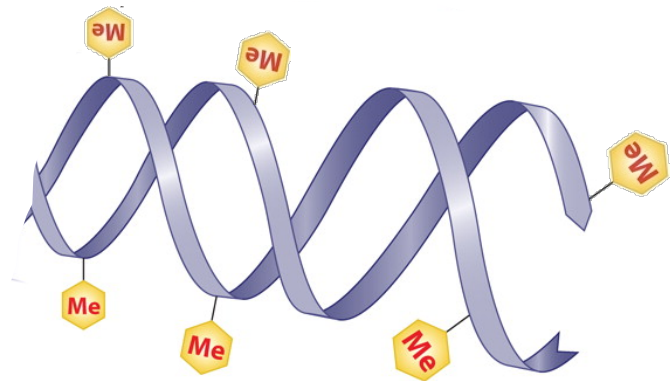
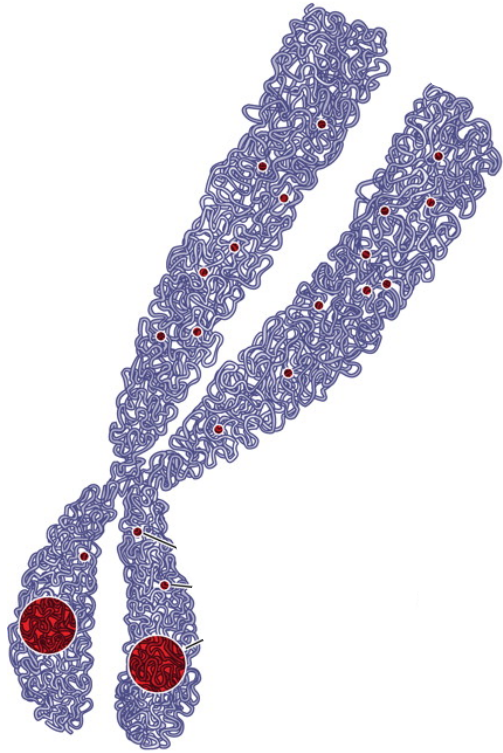
Molecular dimmers on the DNA



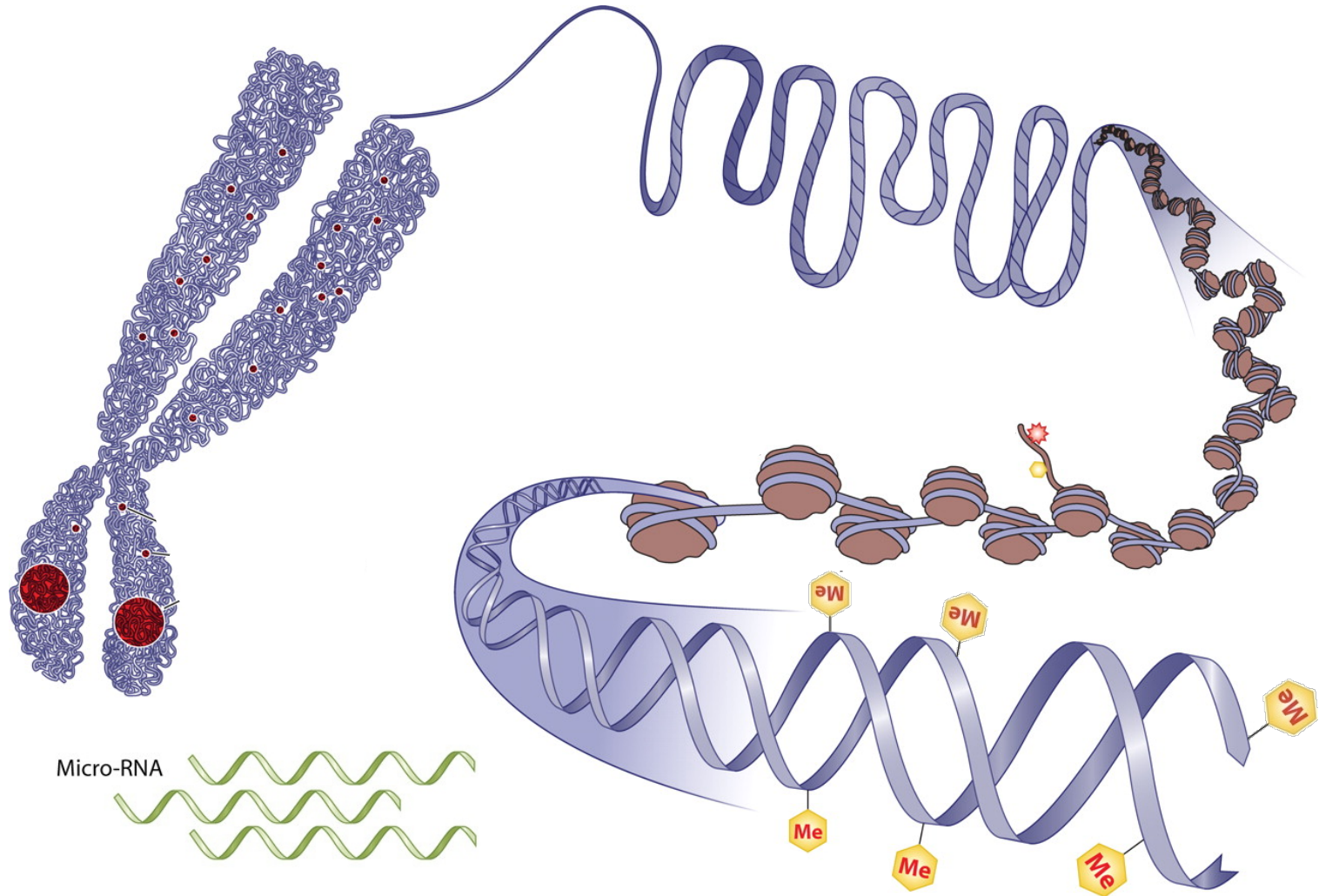
Molecular dimmers on the DNA



Molecular dimmers on the DNA



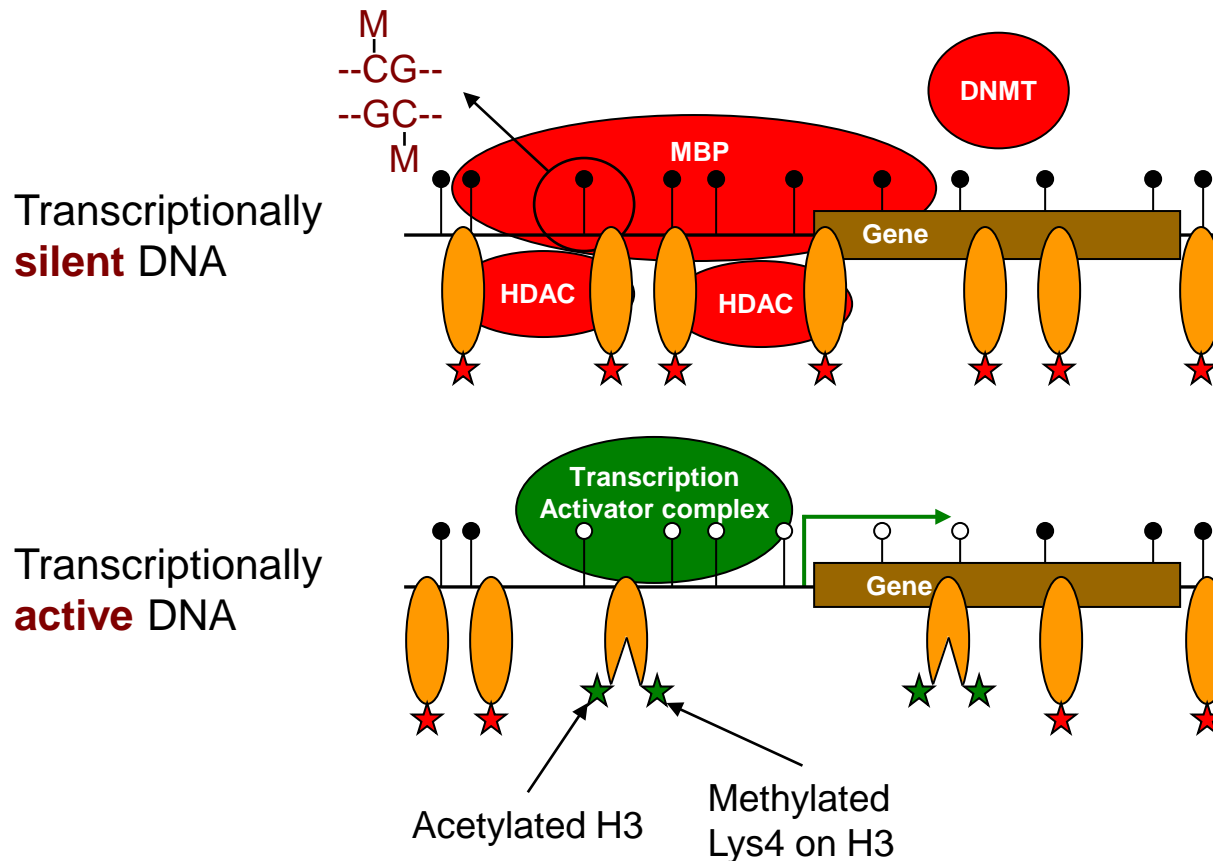
Molecular dimmers on the DNA



Roles for epigenetic mechanisms

- Controls gene expression by regulating accessibility and recruiting chromatin modifiers

The simplified (and outdated) text book view



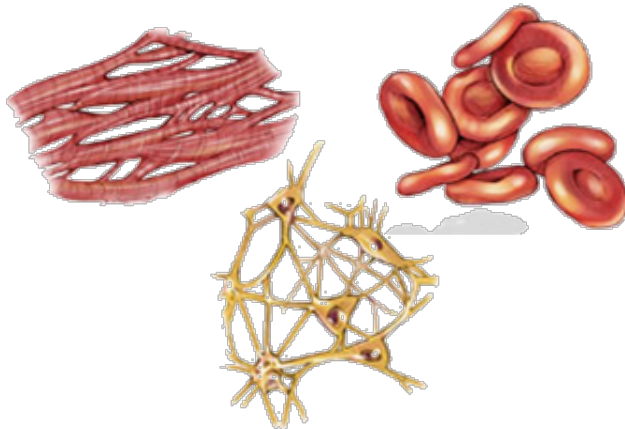
Note: The order of events (cause and consequence) is not known

Epigenetic mechanisms

Memory and variation

1. Controls gene expression by regulating accessibility and recruiting chromatin modifiers in interaction with transcription factors.
2. Stable, long-term, but in principle reversible.
3. Transmitted during cell division, particularly mitosis ('genetic').

Epigenome: the whole of epigenetics marks in a cell.



Human Epigenome Projects



International Human Epigenome Consortium

[Home](#) [Areas of focus](#) [Standard Operating Procedures](#) [Tools / Useful Information](#) [Policies and Guidelines](#) [IHEC Structure](#) [Outreach and Training](#) [Feedback](#) [Intranet](#)

Links



The focal point for the European epigenetics research community

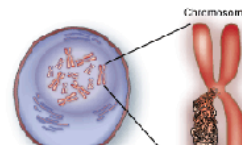


Centre of Excellence funded by The Danish National Research Foundation.

Overview

What is the International Human Epigenome Consortium?

The deciphering of the human genome sequence has helped our understanding of biological processes in health and diseases. However, the way in which the genomic information is organized within the cell, through epigenetic processes, is known to play a major role in regulating gene expression and in controlling specific cellular functions. Epigenetic processes



Consortium goals

Primary Goals

1. Coordinate the production of reference maps of human epigenomes for key cellular states relevant to health and diseases. To have a substantial coverage of the human epigenome, the IHEC sets the ambitious goal to decipher at least 1000 epigenomes within the next 7-10 years. To reach this goal, the consortium will use robust and validated technologies to generate:

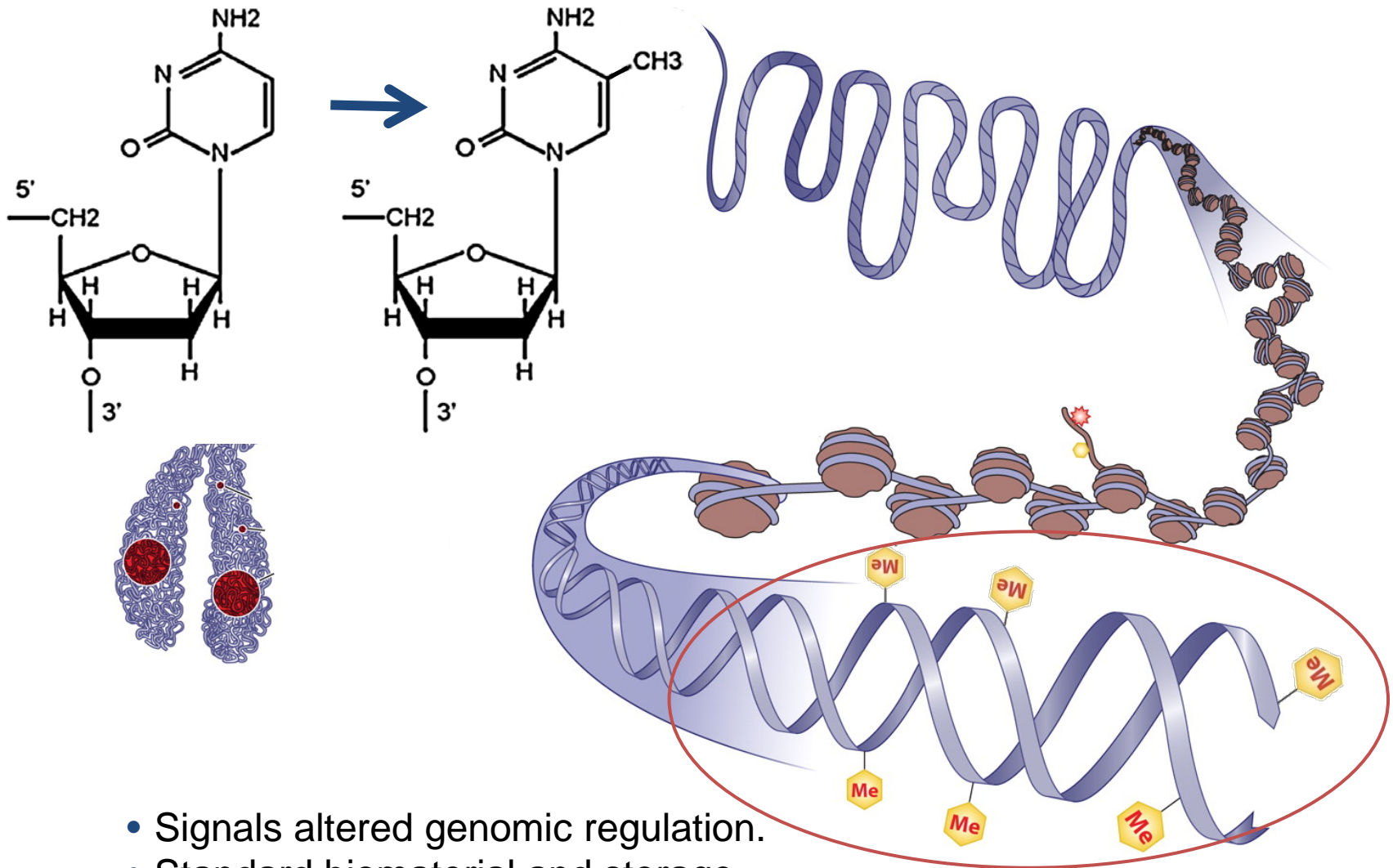
There is one human (reference) genome. How many epigenomes?

NIH Roadmap Epigenomics Mapping Consortium

BLUEPRINT epigenome

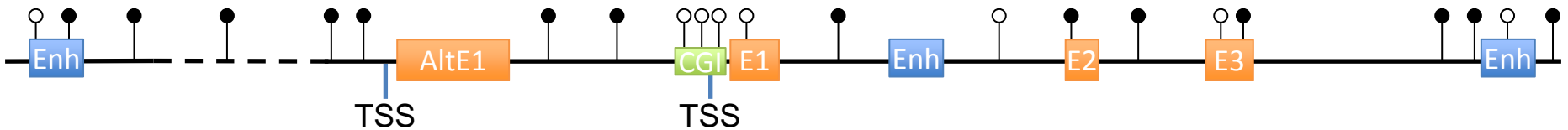
Insightful epigenetics BLUEPRINTs of innate immunity and hematopoiesis

Focus on DNA methylation



- Signals altered genomic regulation.
- Standard biomaterial and storage.
- High-throughput profiling.

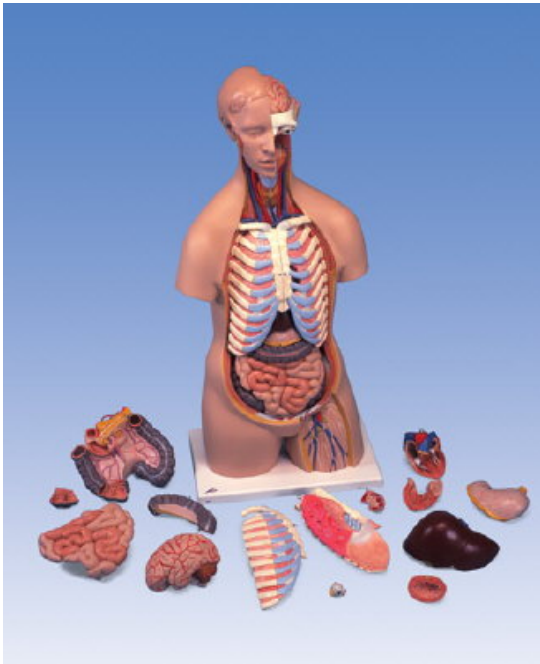
Effect methylation depends on genomic context



→ Genomic annotation is essential when interpreting DNA methylation data

First practical

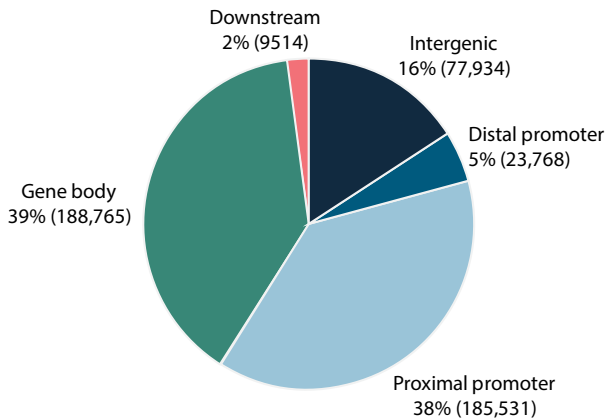
- Characterizing DNA methylation differences between tissues.
- Genome-wide methylation of close to 500 thousand CpG sites.



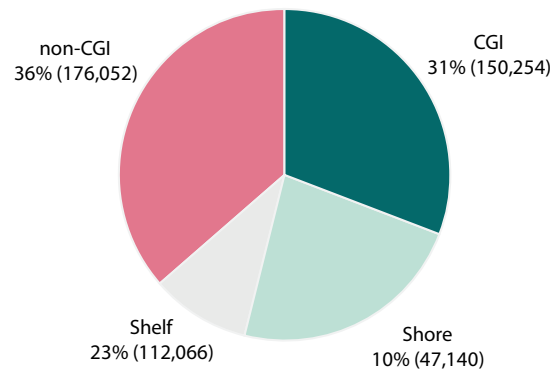
Illumina 450k DNA methylation array

- Informative: ~482,000 CpGs (<2%) but many annotations
- Affordable: ~200 euro per sample
- Fast: >1000 samples a week
- Data: easy to manage (amount and complexity)

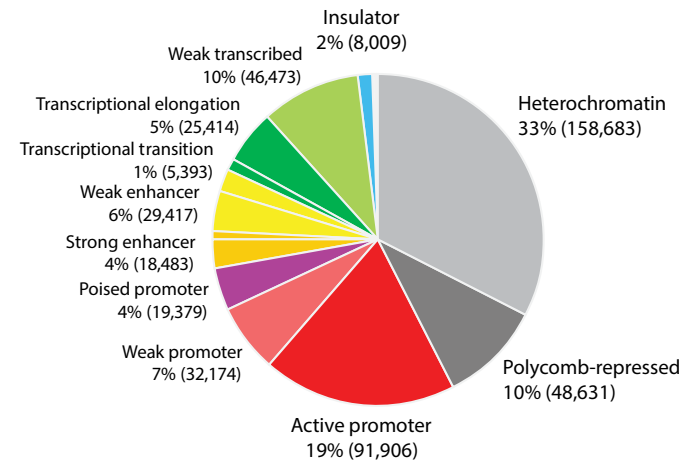
Genic



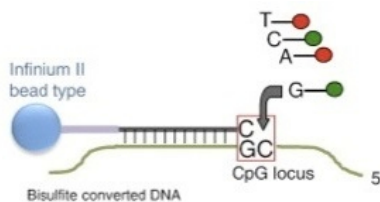
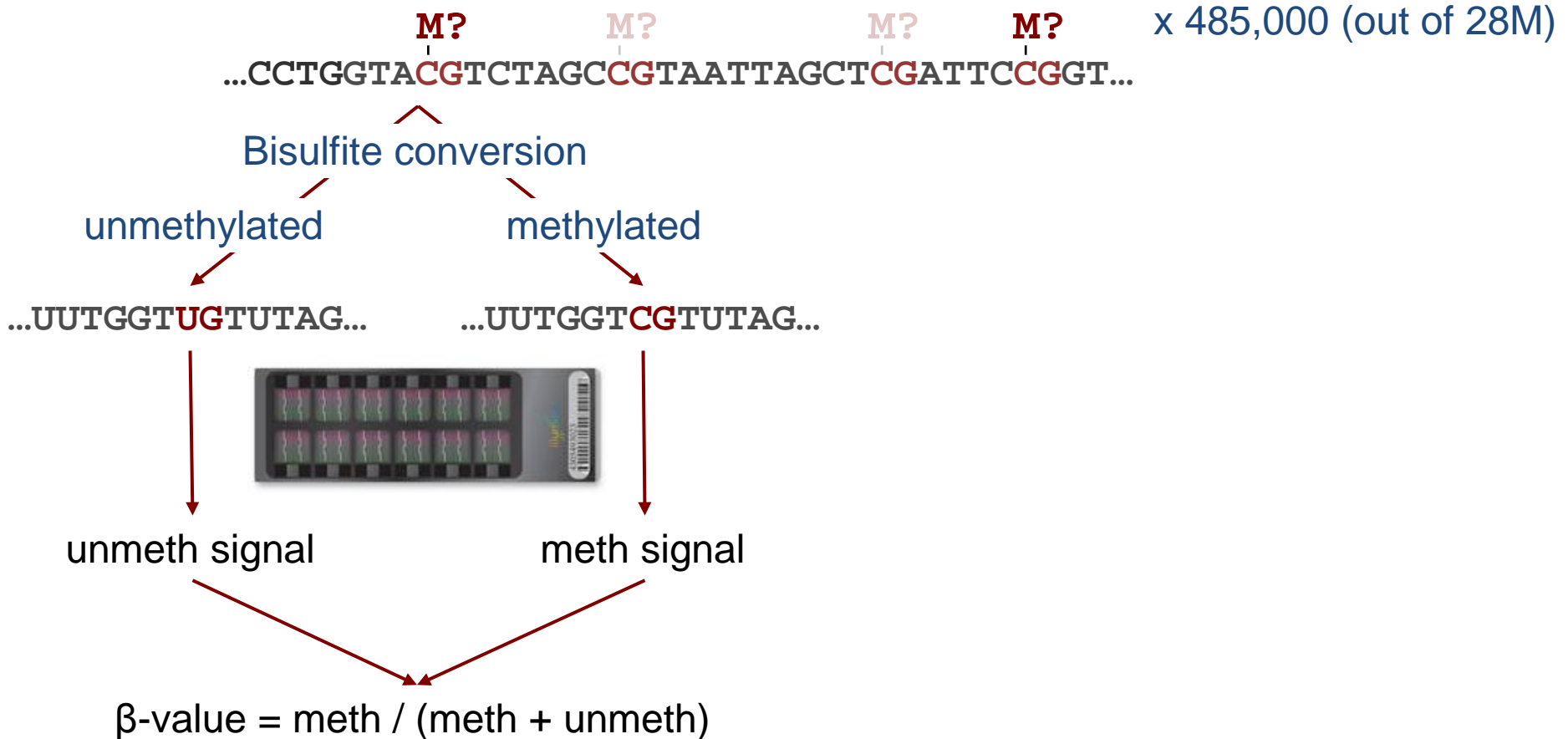
CpG island



Chromatin



Principle methylation array



DNA methylation levels

M?
...CCTGGTAC[|]GTCTAG...

$\beta\text{-value} = \text{meth} / (\text{meth} + \text{unmeth})$

- A DNA molecule?
- A cell?
- A population of cells?
- An organ?

Amazing DISCOVERIES

