

Influence of Epigenetic Variation on Marine Invertebrate Physiology

Steven Roberts



Epigenetics: Background and Fish

Background

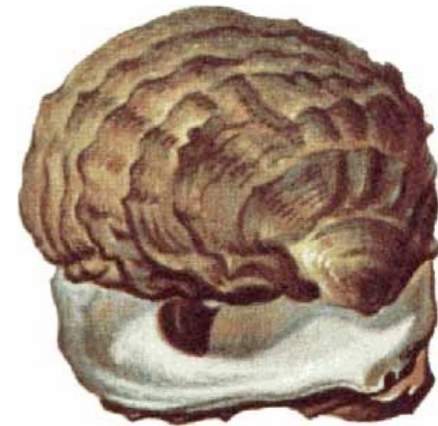
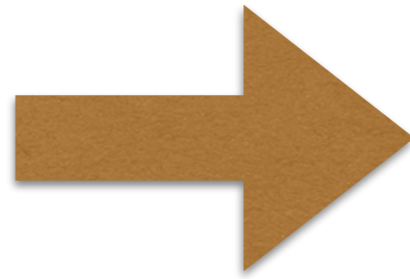
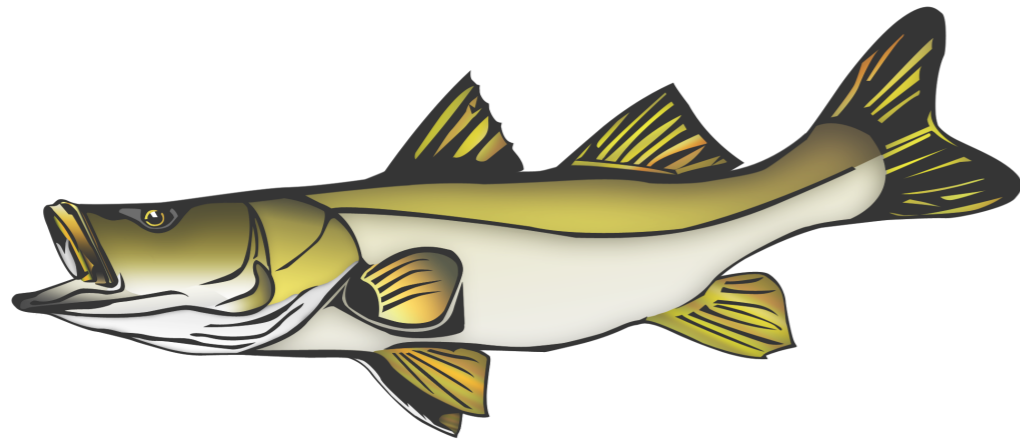
Physiology

How fundamental processes work in aquatic species

Background

Physiology

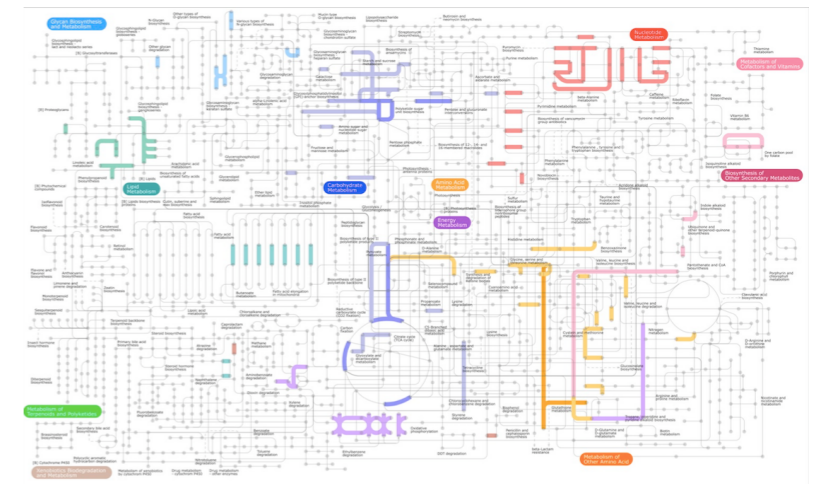
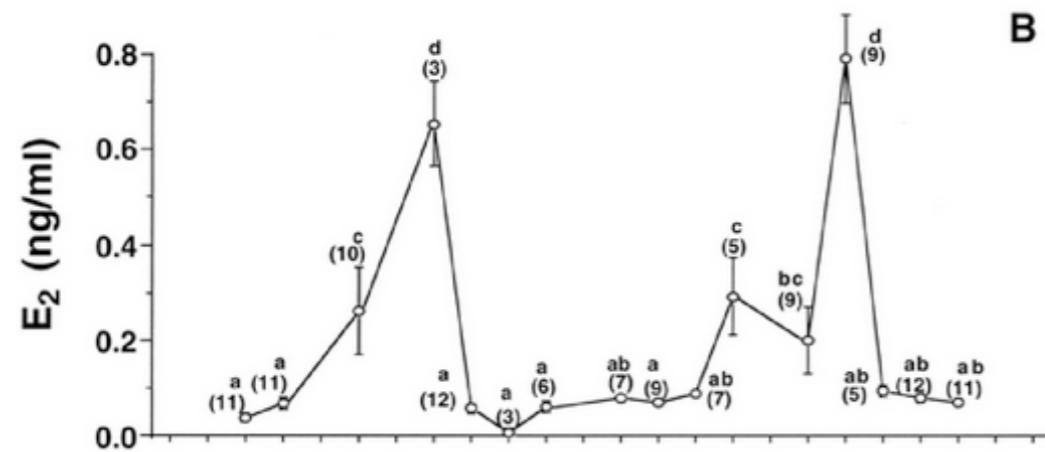
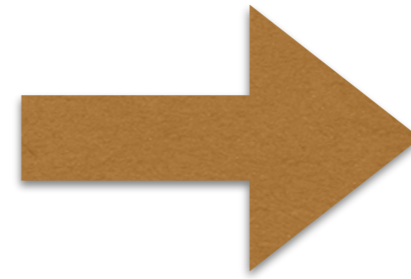
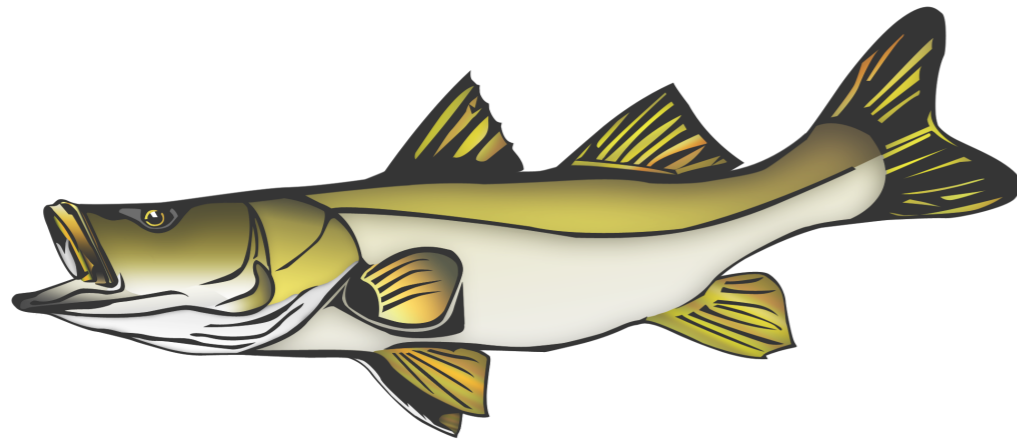
How fundamental processes work in aquatic species



Background

Physiology

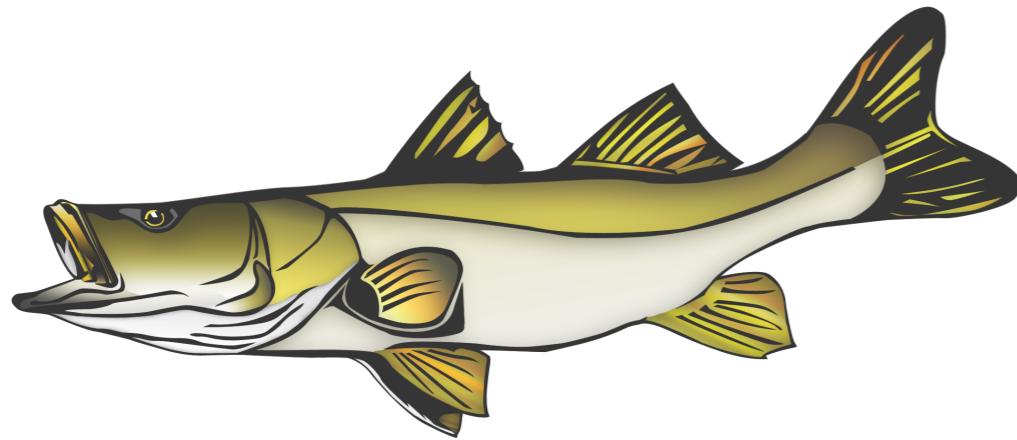
How fundamental processes work in aquatic species



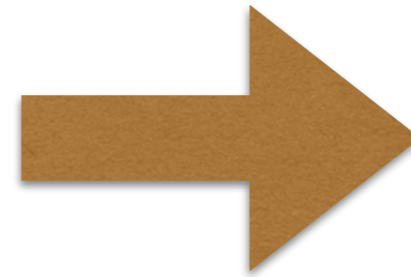
Background

Physiology

How fundamental processes work in aquatic species

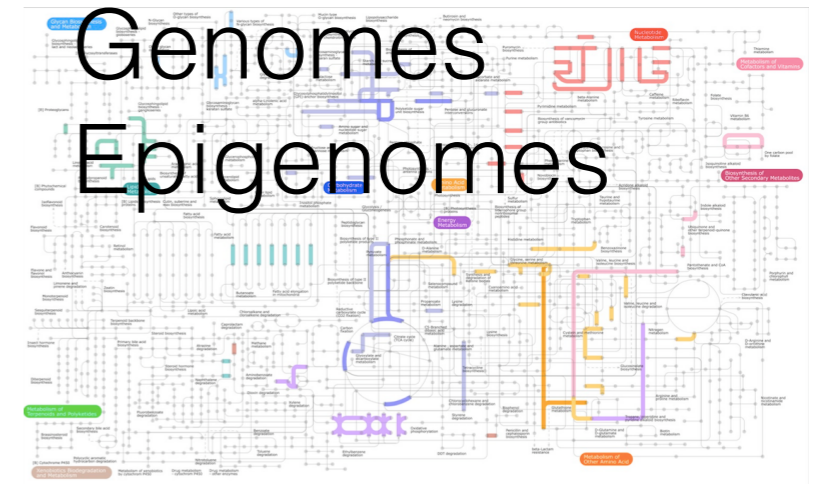
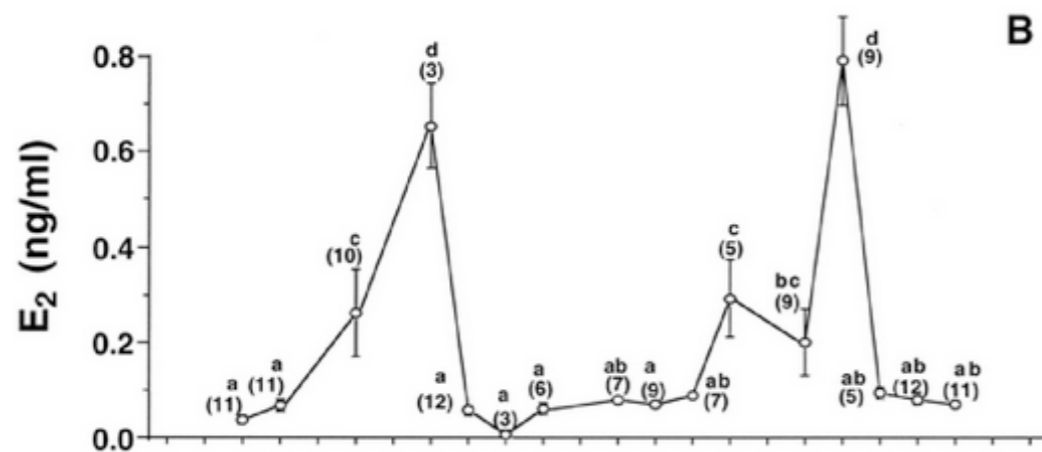


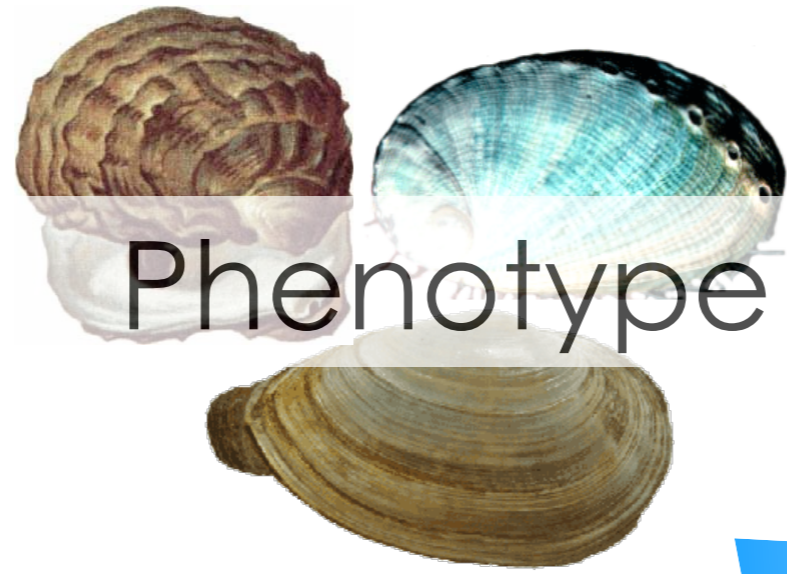
Hormones
Proteins



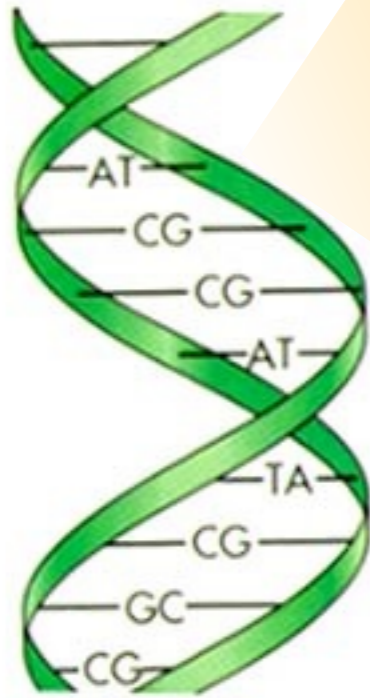
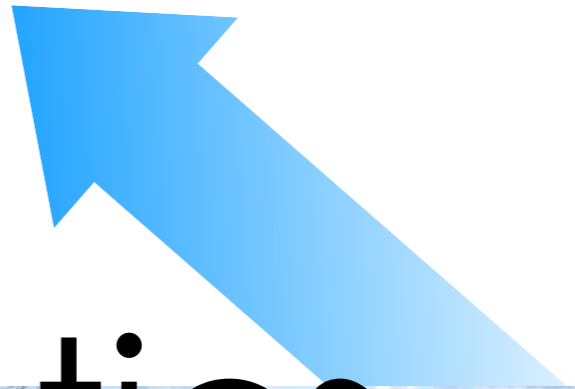
Transcriptomes
Proteomes

Genomes
Epigenomes





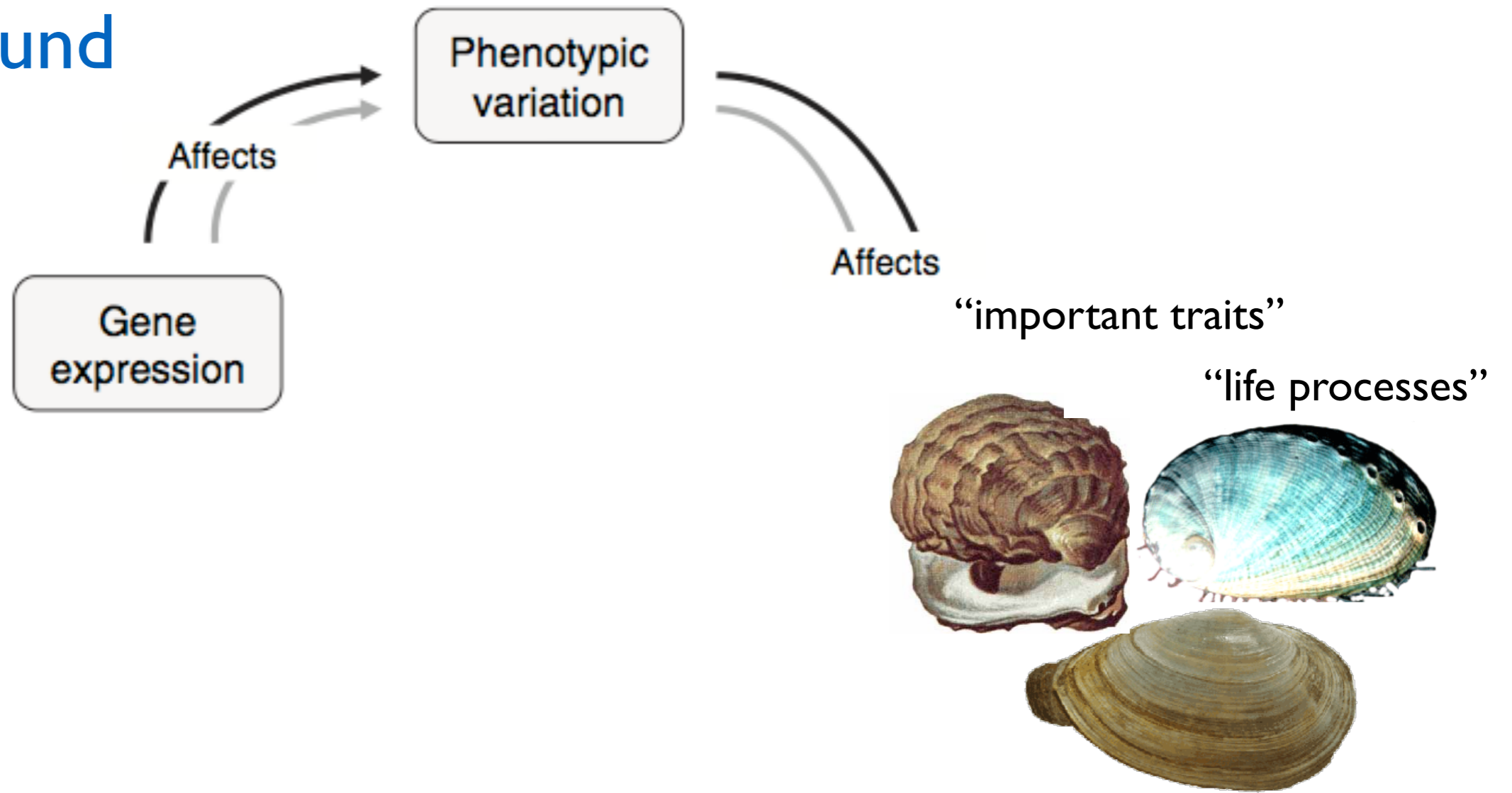
Phenotype

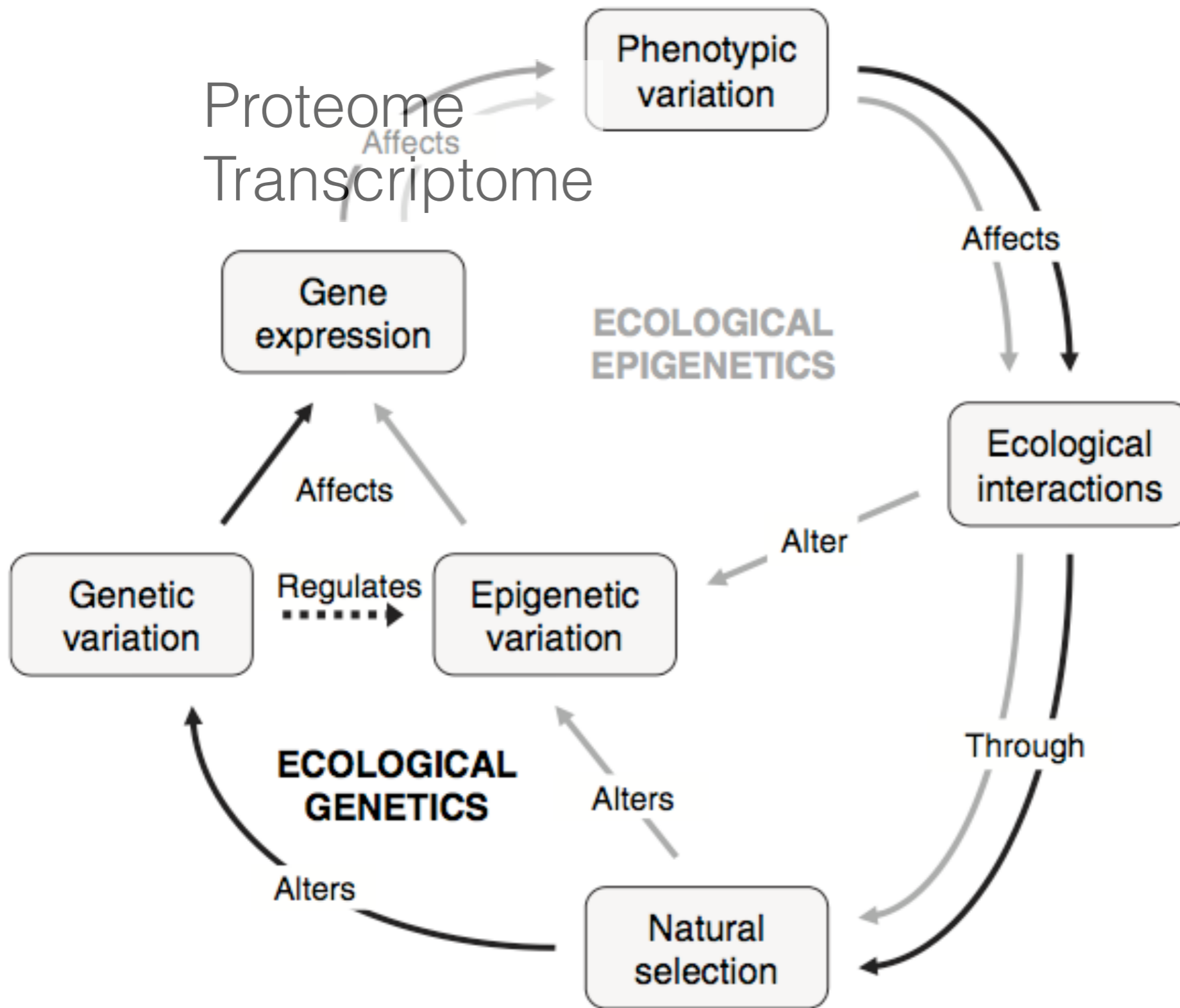


Epigenetics

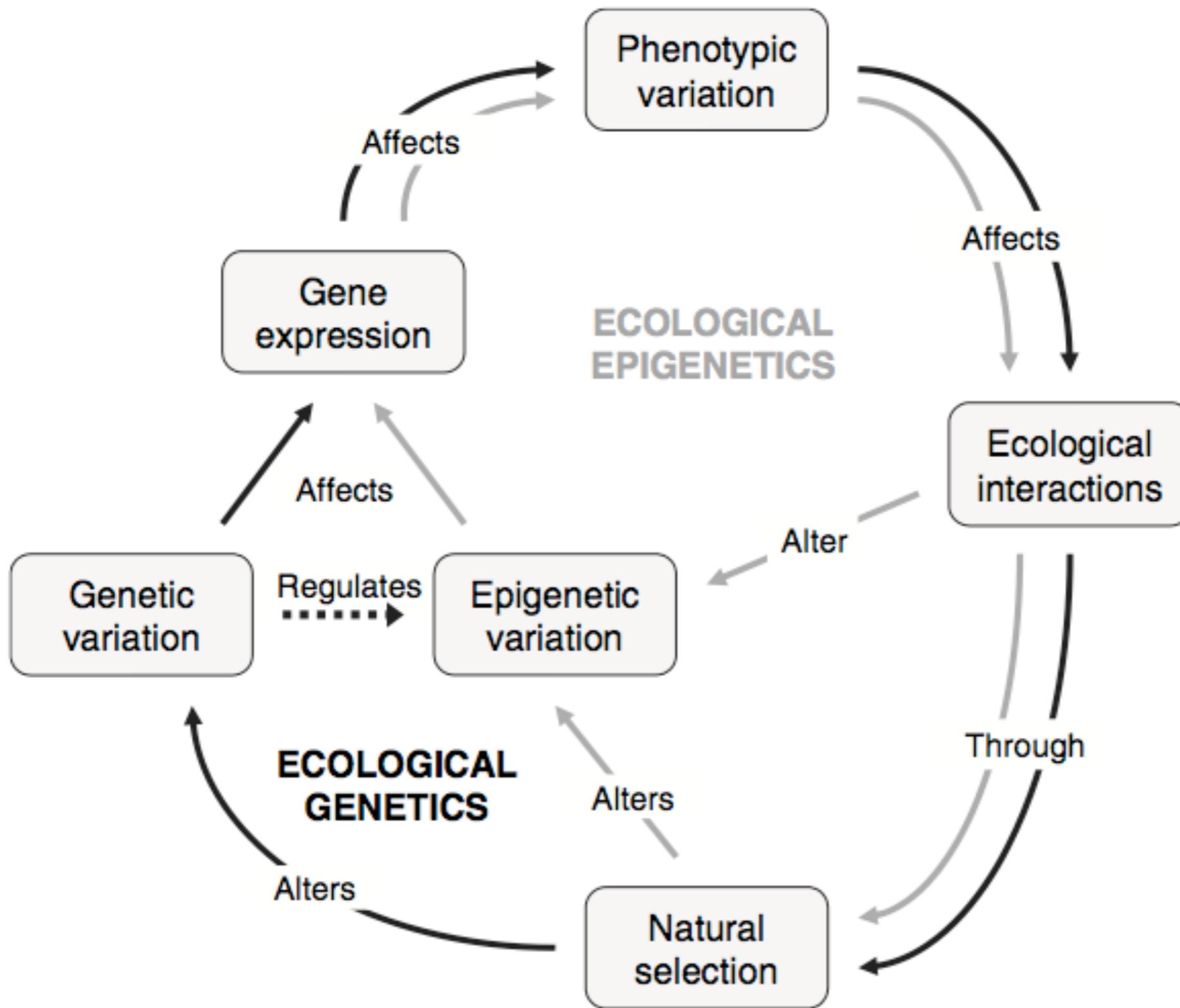


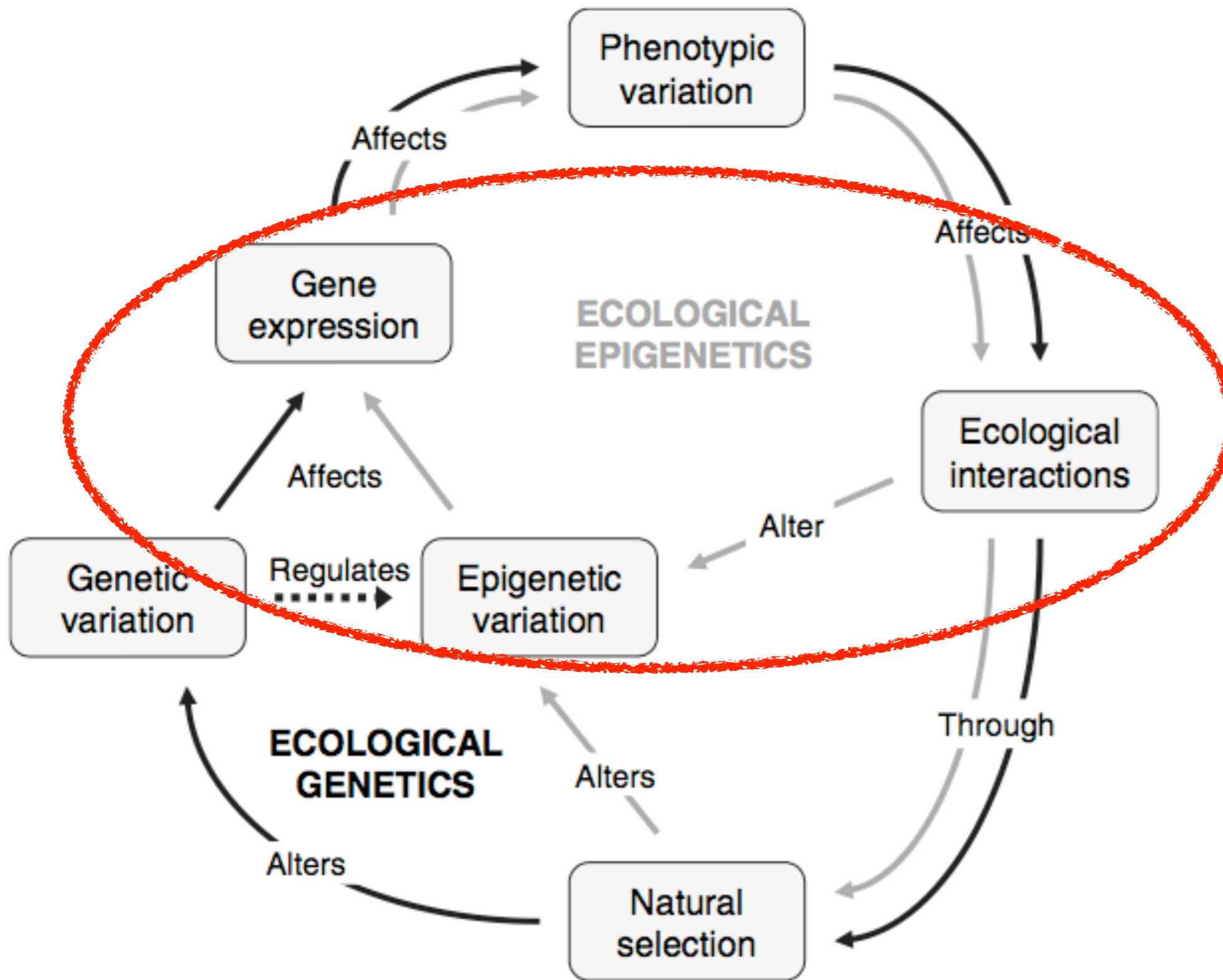
Background

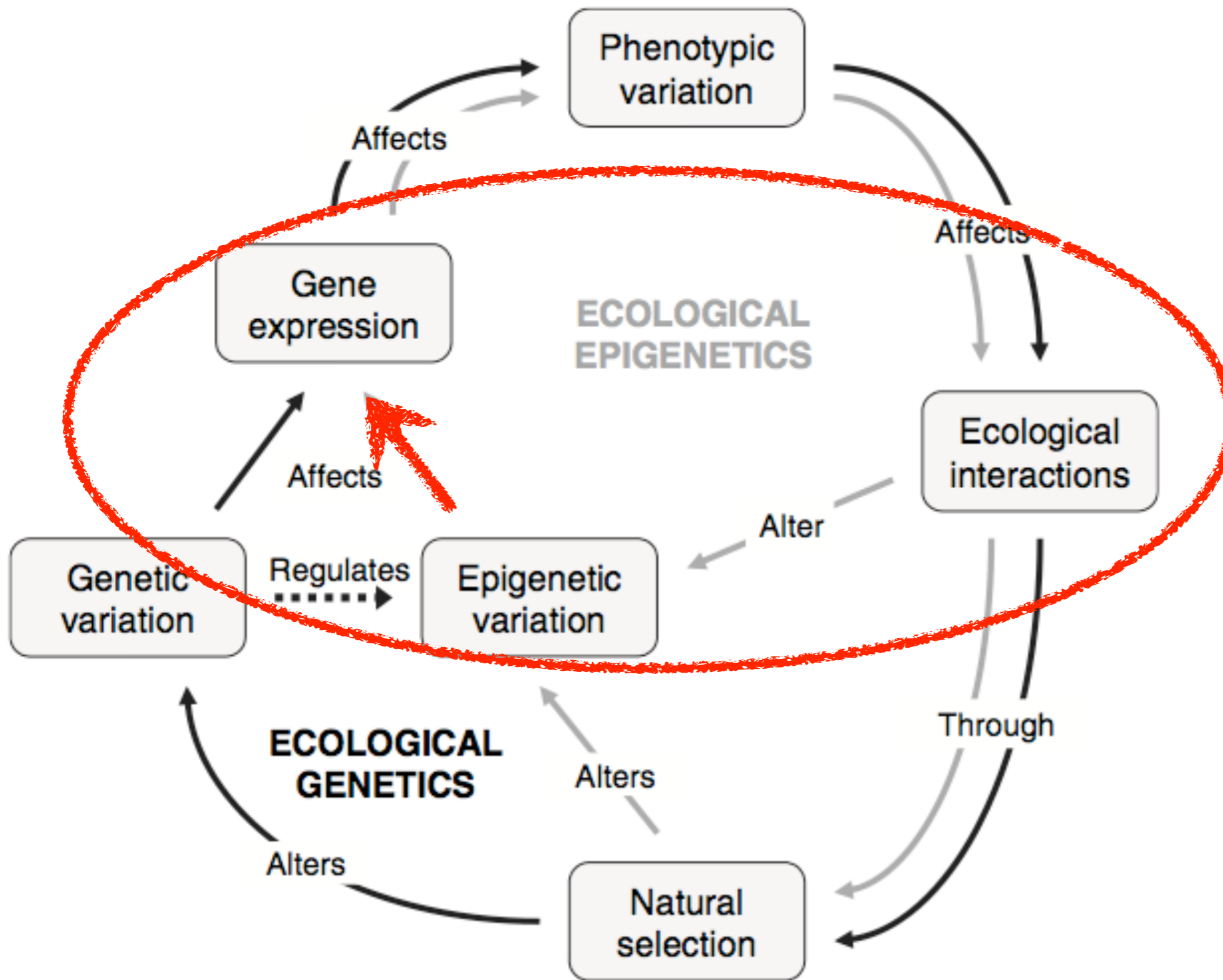




Proteome
Transcriptome







Epigenetics



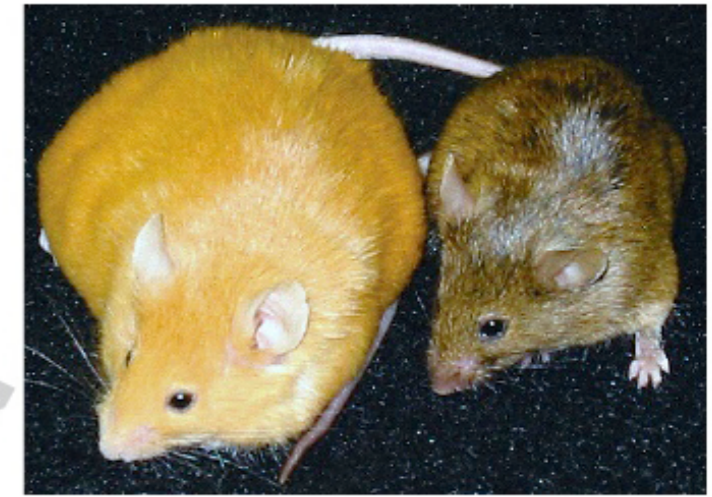
Photo credit: Flickr, Creative Commons, he-boden



Epigenetics



These Two Mice are Genetically Identical and the Same Age



While pregnant, both of their mothers were fed Bisphenol A (BPA) but **DIFFERENT DIETS**:

The mother of this mouse received a **normal mouse diet**

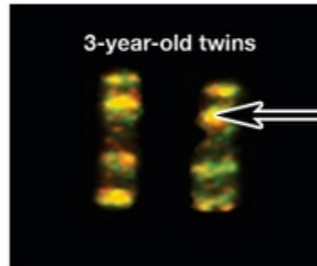
The mother of this mouse received a diet **supplemented** with choline, folic acid, betaine and vitamin B12

Nature AND Nurture

Chromosome 3 Pairs

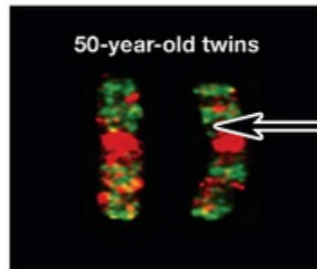
3-year old twins vs. 50-year-old twins

3-year-old twins



Yellow shows where the twins have epigenetic tags in the same place.

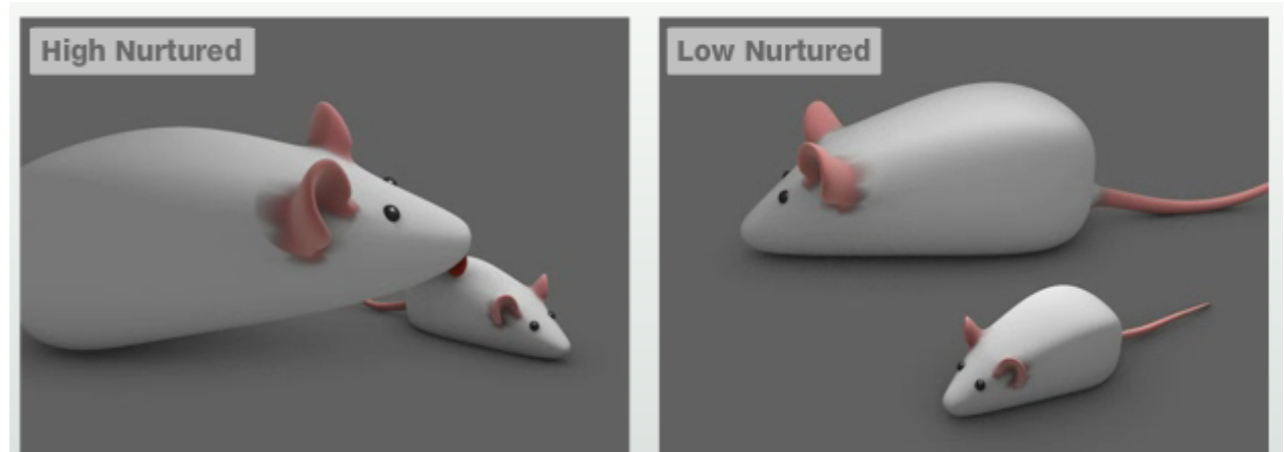
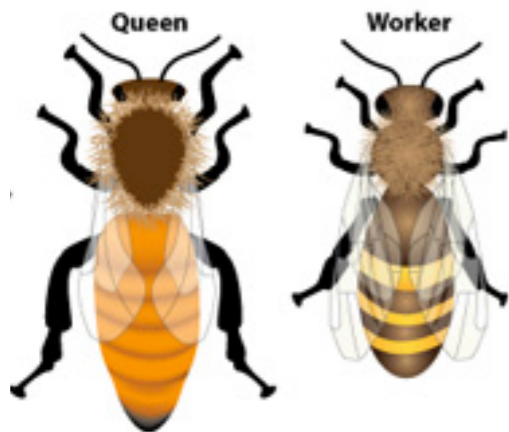
50-year-old twins



Red and green show where the twins have epigenetic tags in different places.



Queen Bee Larvae: Queens are raised in specially constructed cells called "queen cups," which are filled with royal jelly.



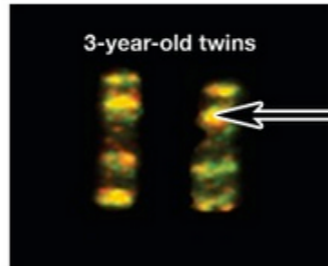
These mothers come from a long line of inbred rats, so their genomes are highly similar. But they care for their pups very differently.

AUDIO



Nature AND Nurture

Chromosome 3 Pairs 3-year old twins vs. 50-year-old twins

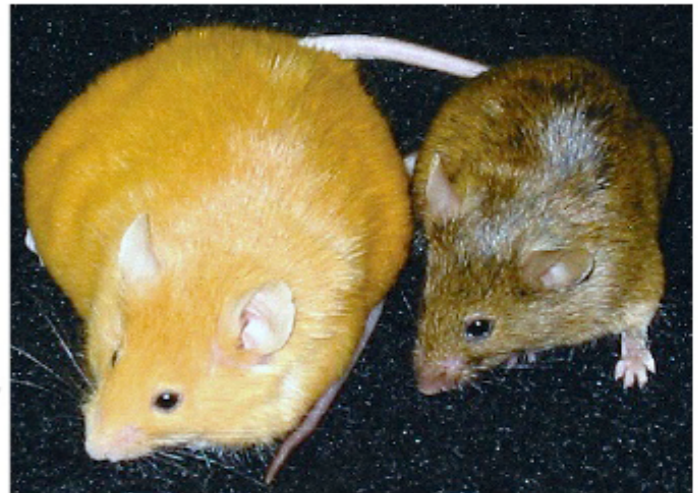


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These Two Mice are Genetically Identical and the Same Age



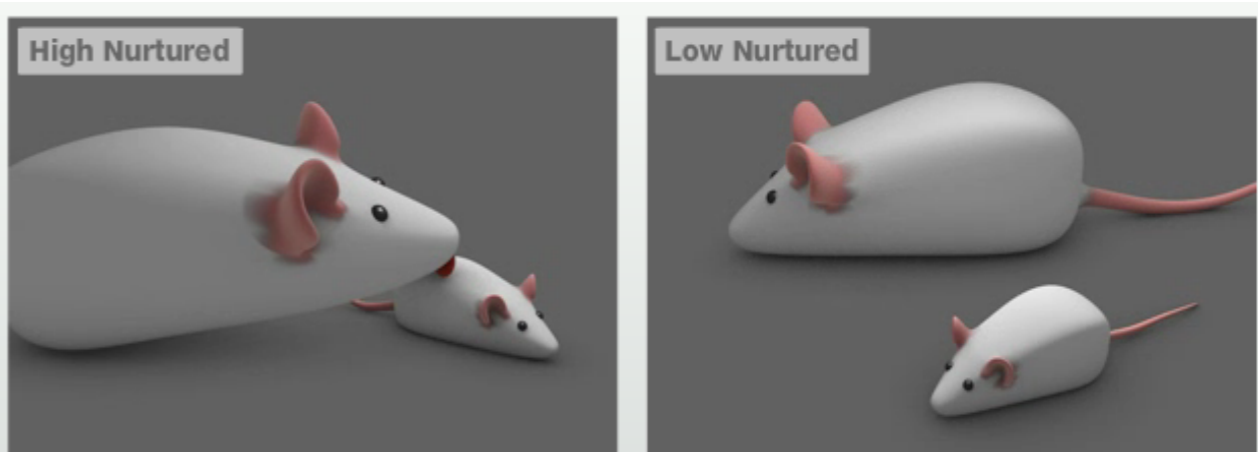
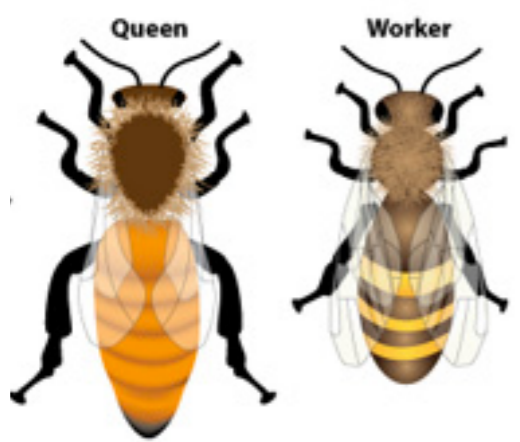
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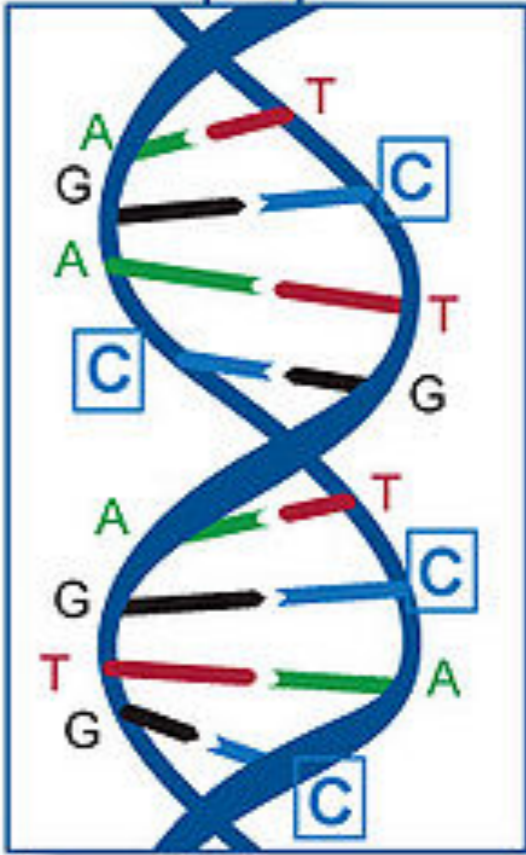
Epigenetics



Histone Modification

short RNAs

DNA Methylation



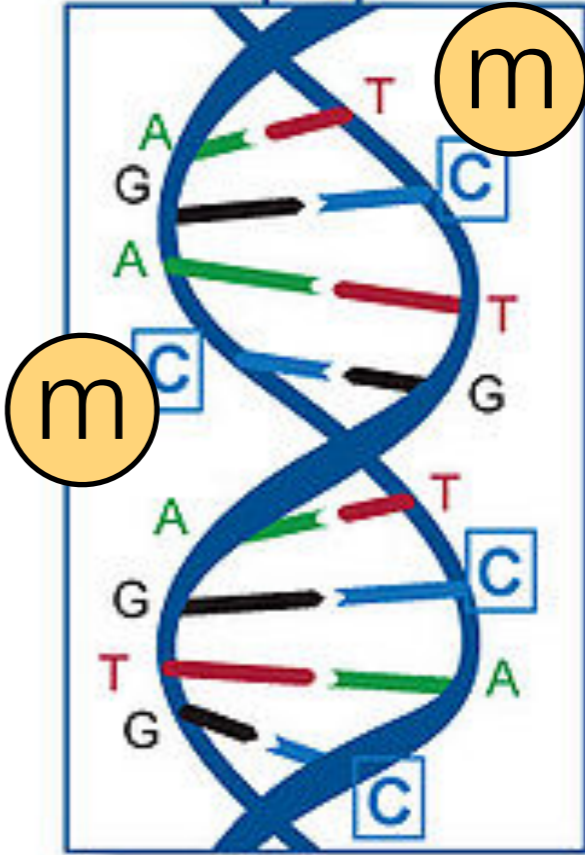
Epigenetics

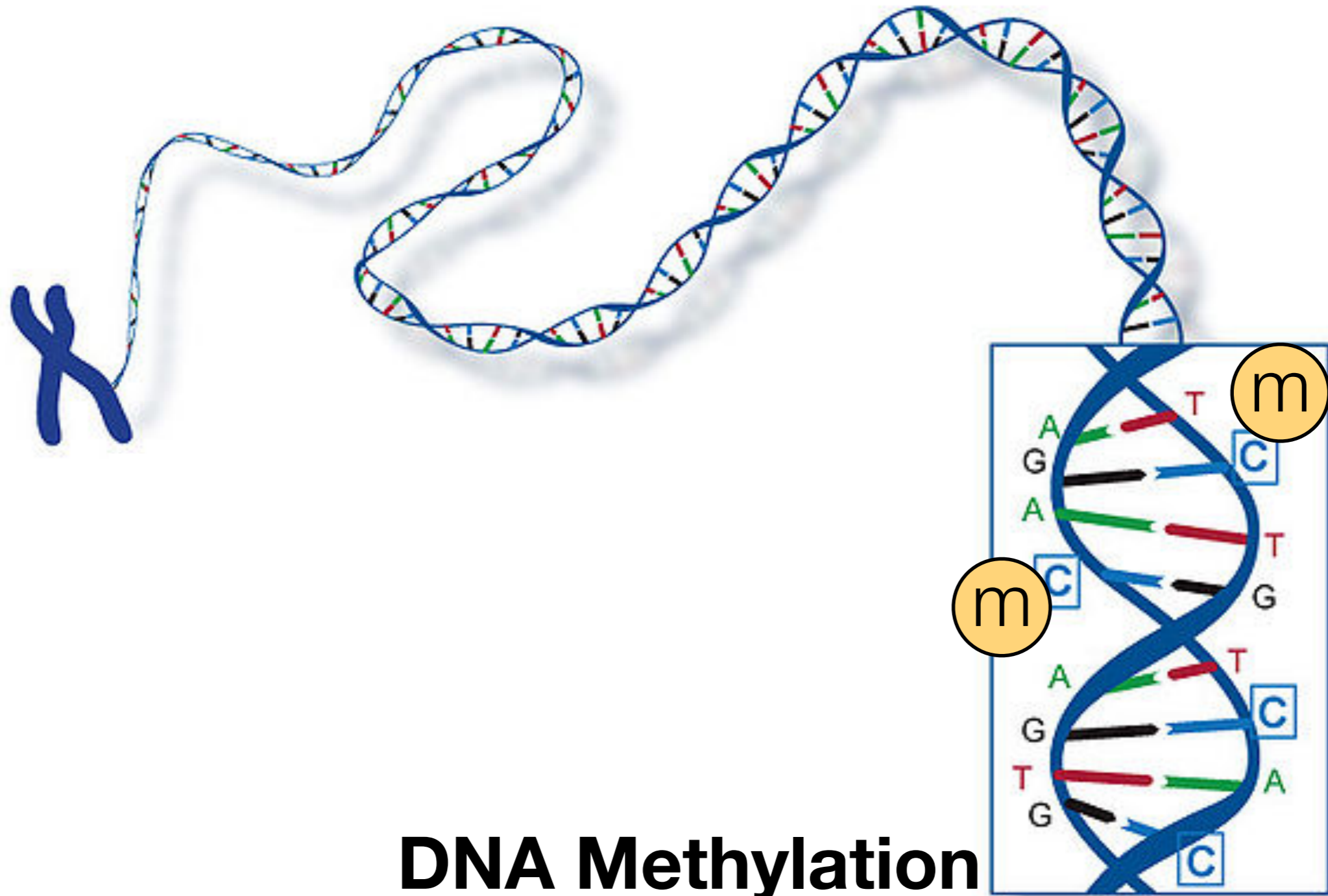


Histone Modification

short RNAs

DNA Methylation




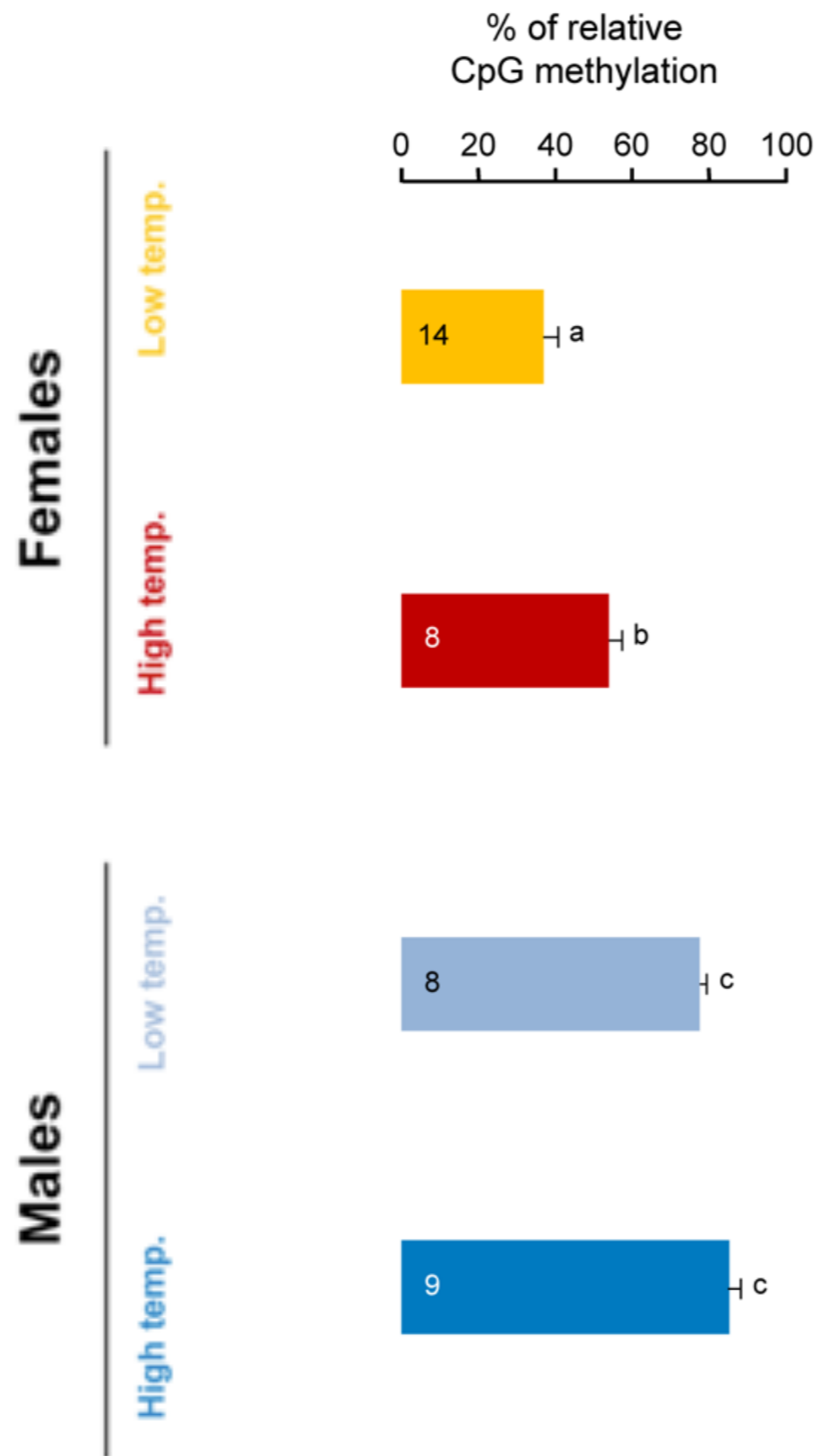


DNA Methylation


Function?

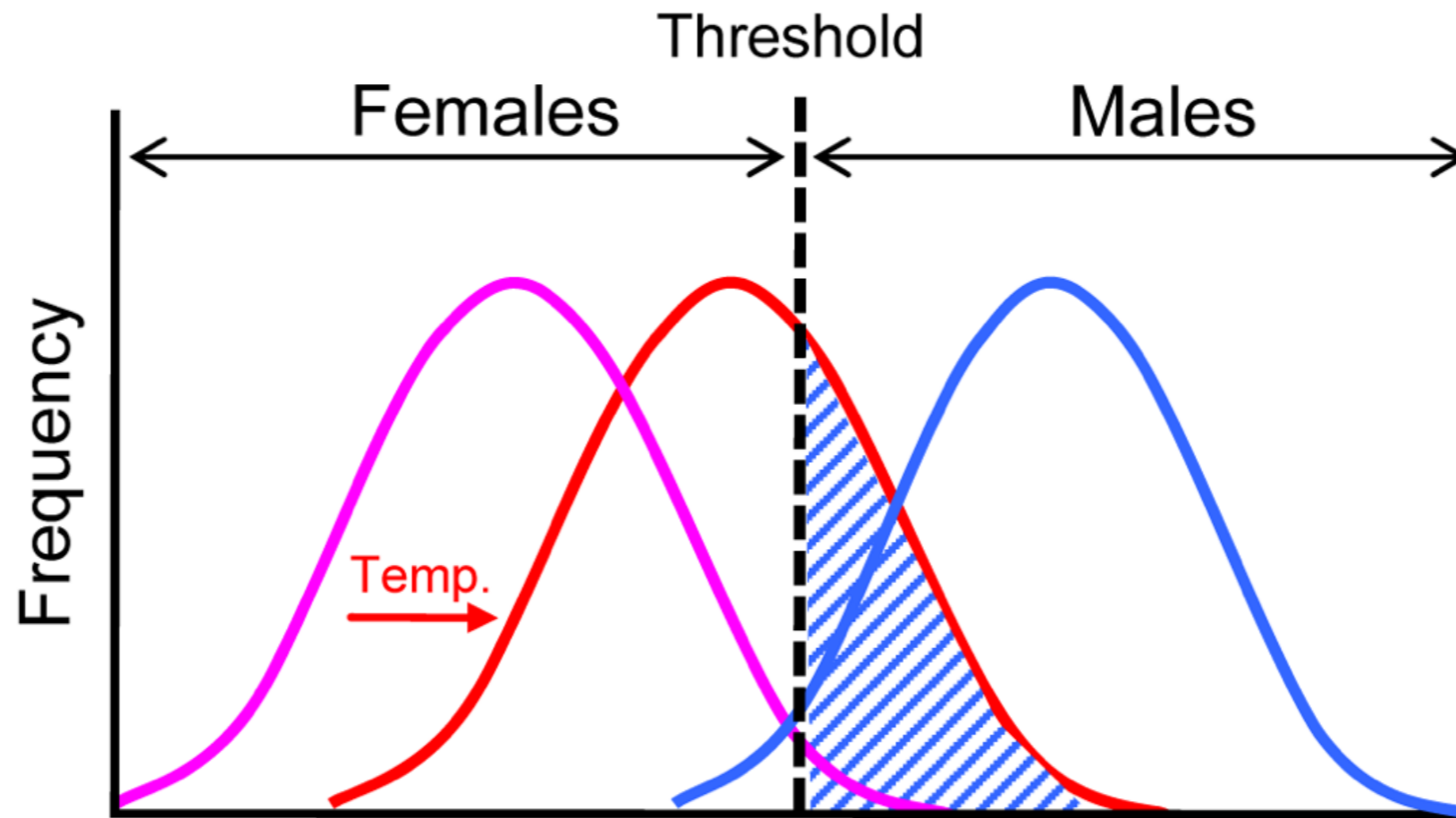
DNA Methylation of the Gonadal Aromatase (*cyp19a*) Promoter Is Involved in Temperature-Dependent Sex Ratio Shifts in the European Sea Bass

Laia Navarro-Martín, Jordi Viñas, Laia Ribas, Noelia Díaz, Arantxa Gutiérrez, Luciano Di Croce, Francesc Piferrer 



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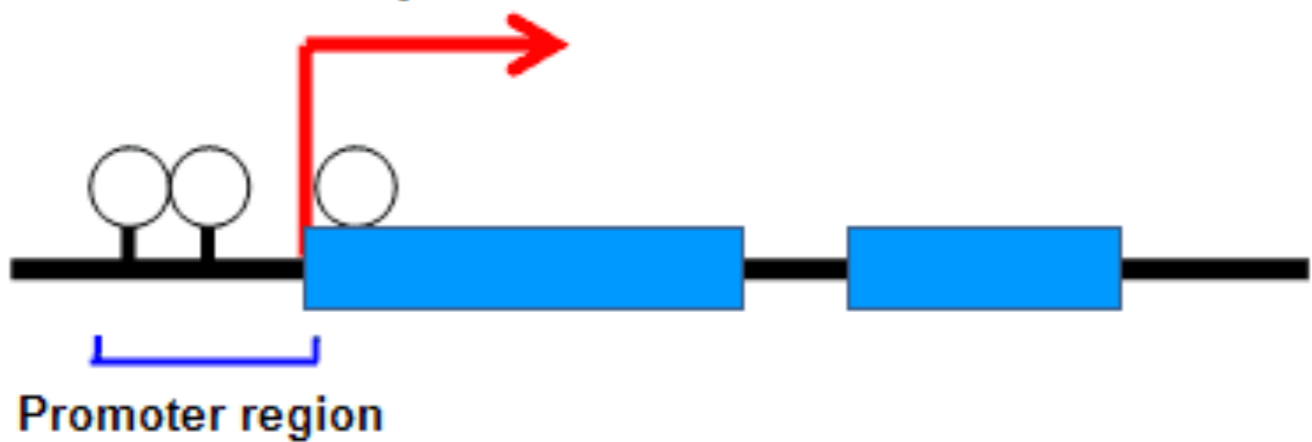


cyp19a promoter methylation level

- Low temperature females
- High temperature females
- Males

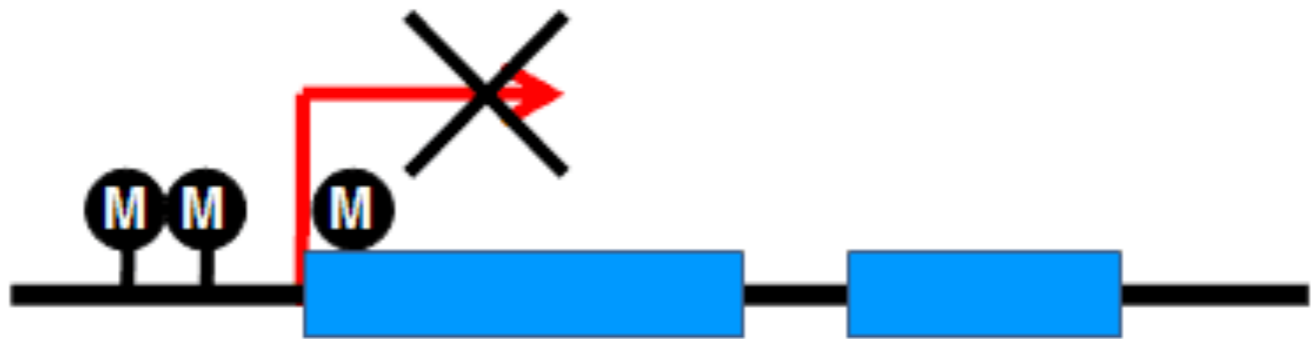
Genes that can be expressed

Low temp.



Genes inactivated by DNA methylation

High temp.



- M** Methylated
- Unmethylated

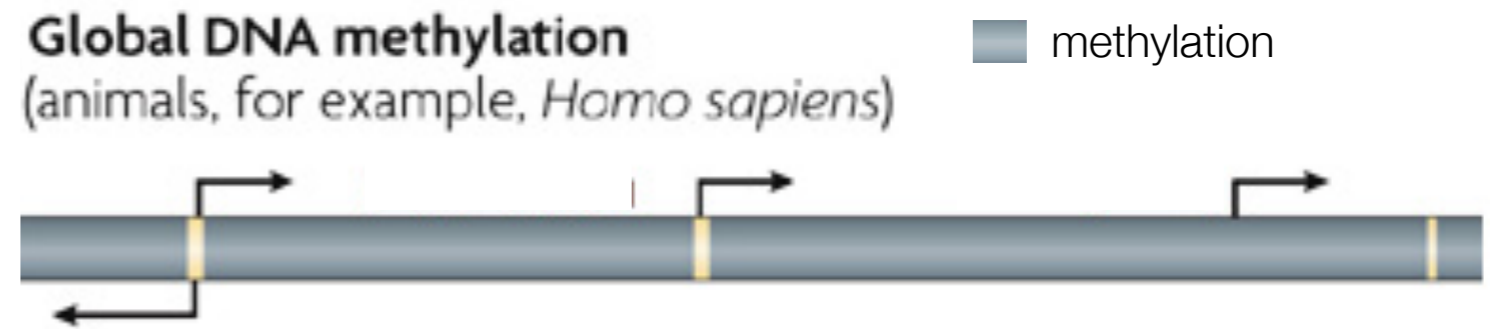
Transcriptome



Epigenetics

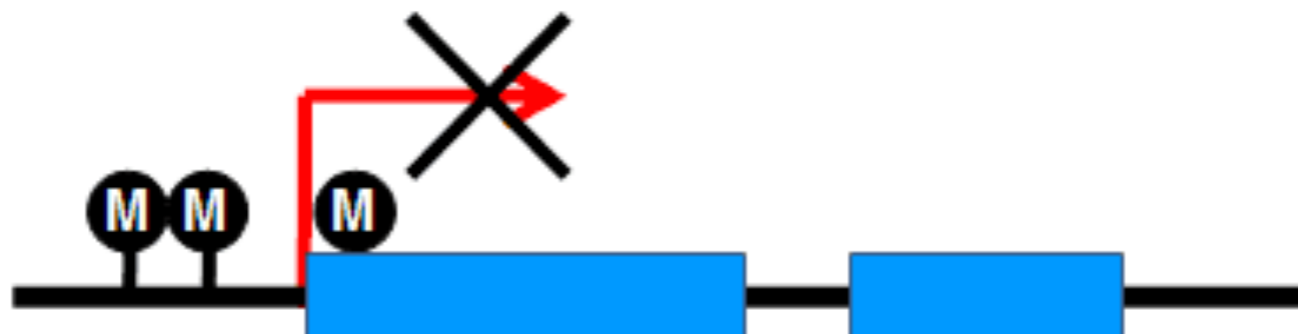


traditional - vertebrate model



Nature Reviews Genetics 9, 465-476 (June 2008)

Genes inactivated by DNA methylation



- M Methylated
- Unmethylated

Epigenetics: Marine Invertebrates

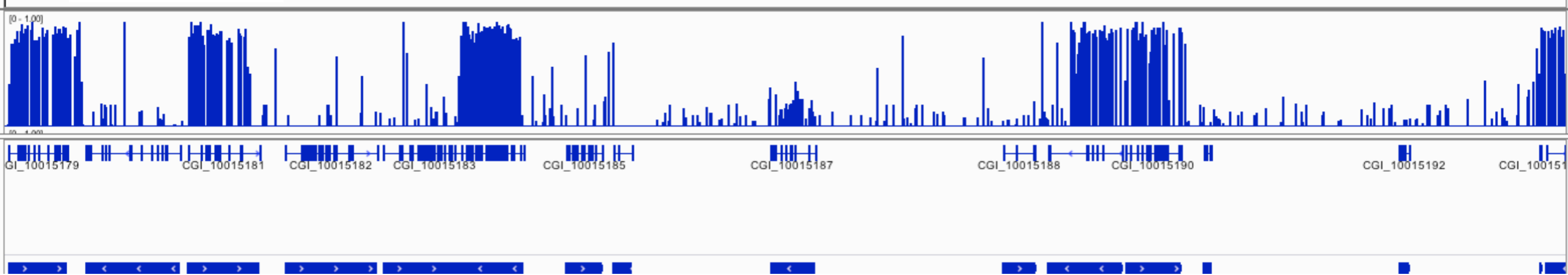
Non-
Vertebrates?

Absent in
several
model
organisms



Shellfish?

Epigenetic variation **1**

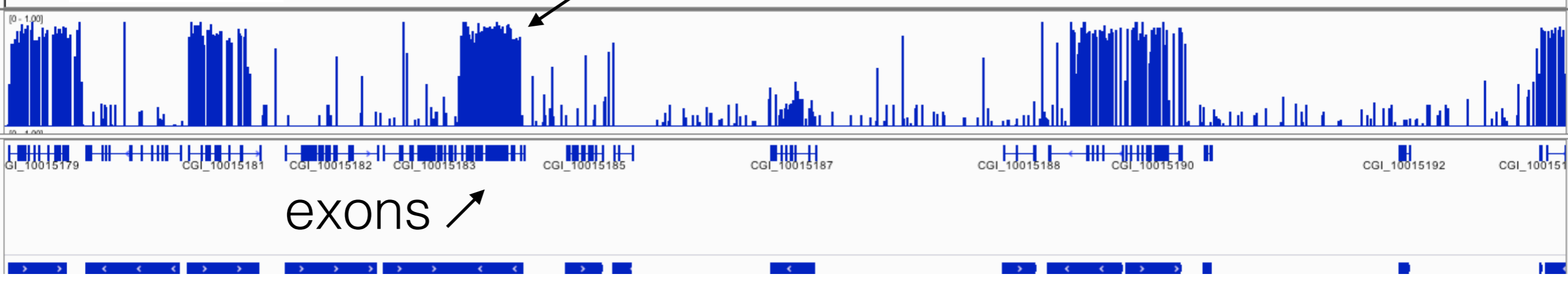


mosaic

associated with gene bodies

Epigenetic variation **1**

DNA methylation level (0-100%) @ cytosines



exons ↗

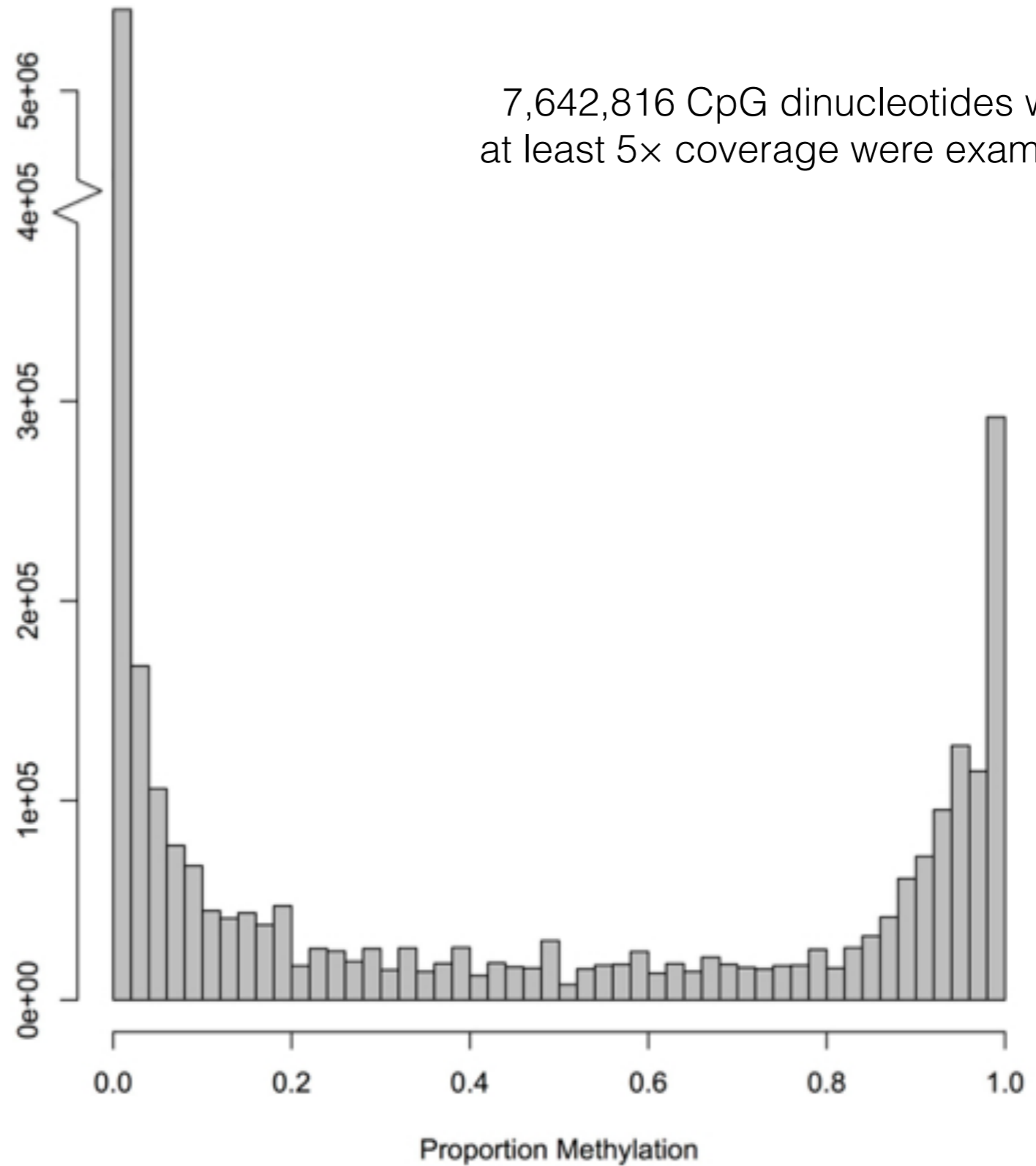
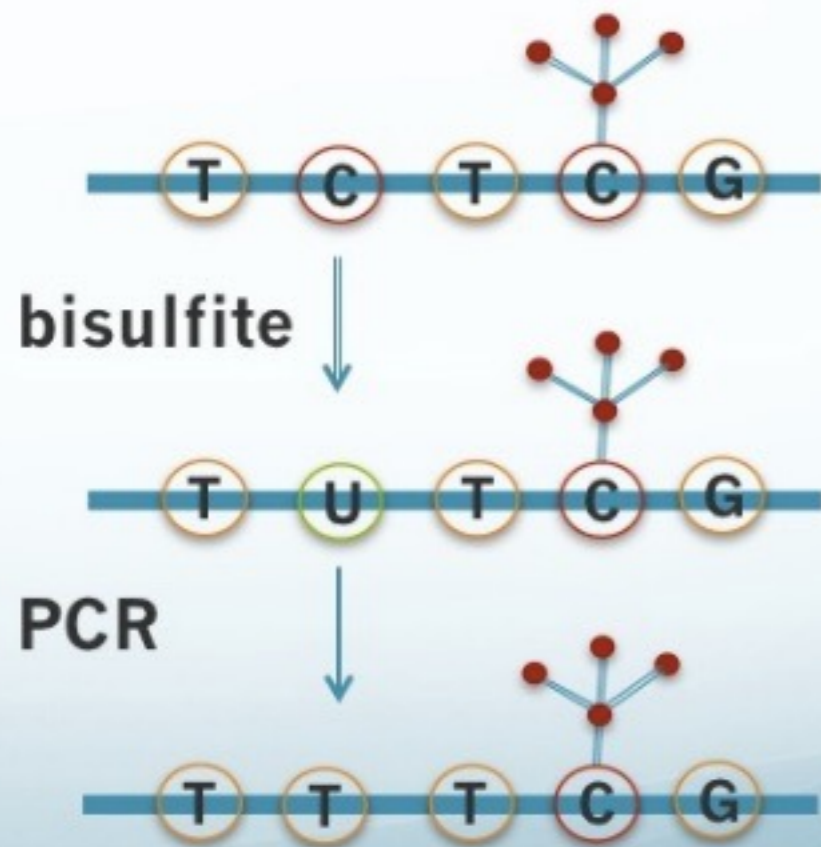
gene ↗

mosaic

associated with gene bodies

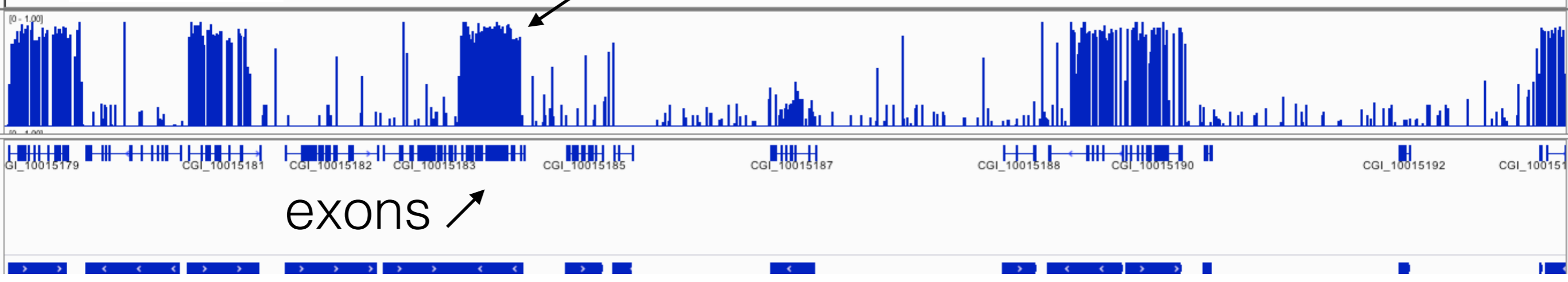
Epigenetic variation **1**

- Bisulfite conversion



Epigenetic variation **1**

DNA methylation level (0-100%) @ cytosines



exons ↗

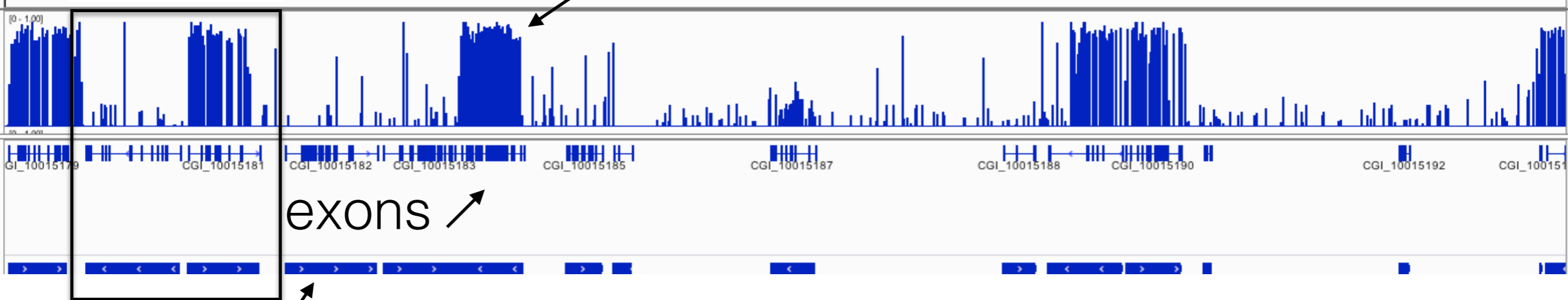
gene ↗

mosaic

associated with gene bodies

DNA methylation level (0-100%) @ cytosines

Epigenetic variation **1**



gene

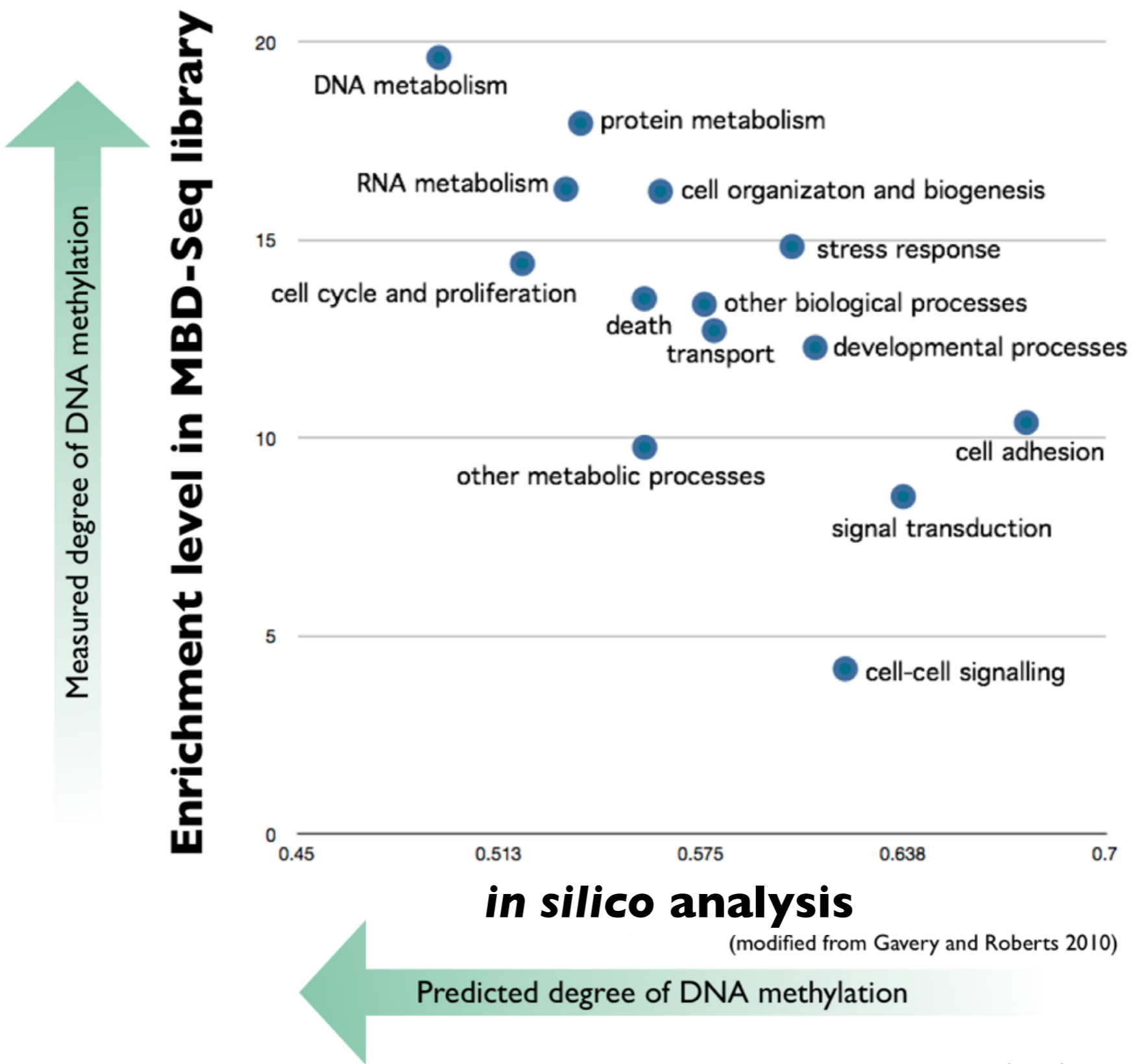
exons

mosaic

Why are only a subset of genes methylated?

associated with gene bodies

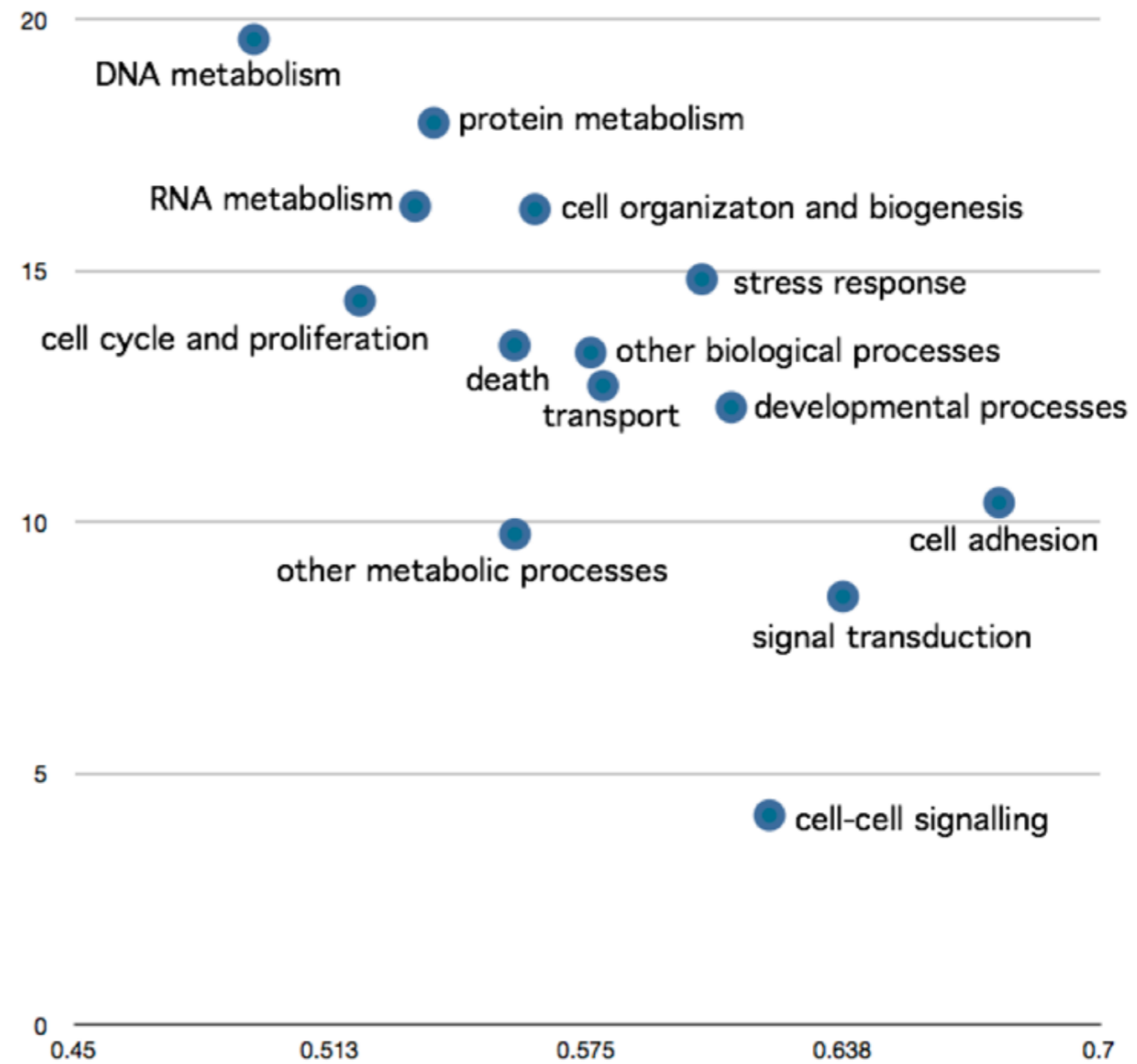
Epigenetic variation **1**



Epigenetic variation **1**

Measured degree of DNA methylation

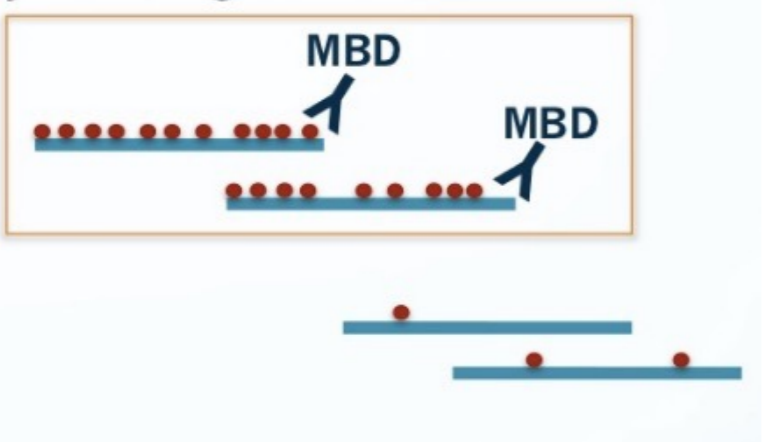
Enrichment level in MBD-Seq library

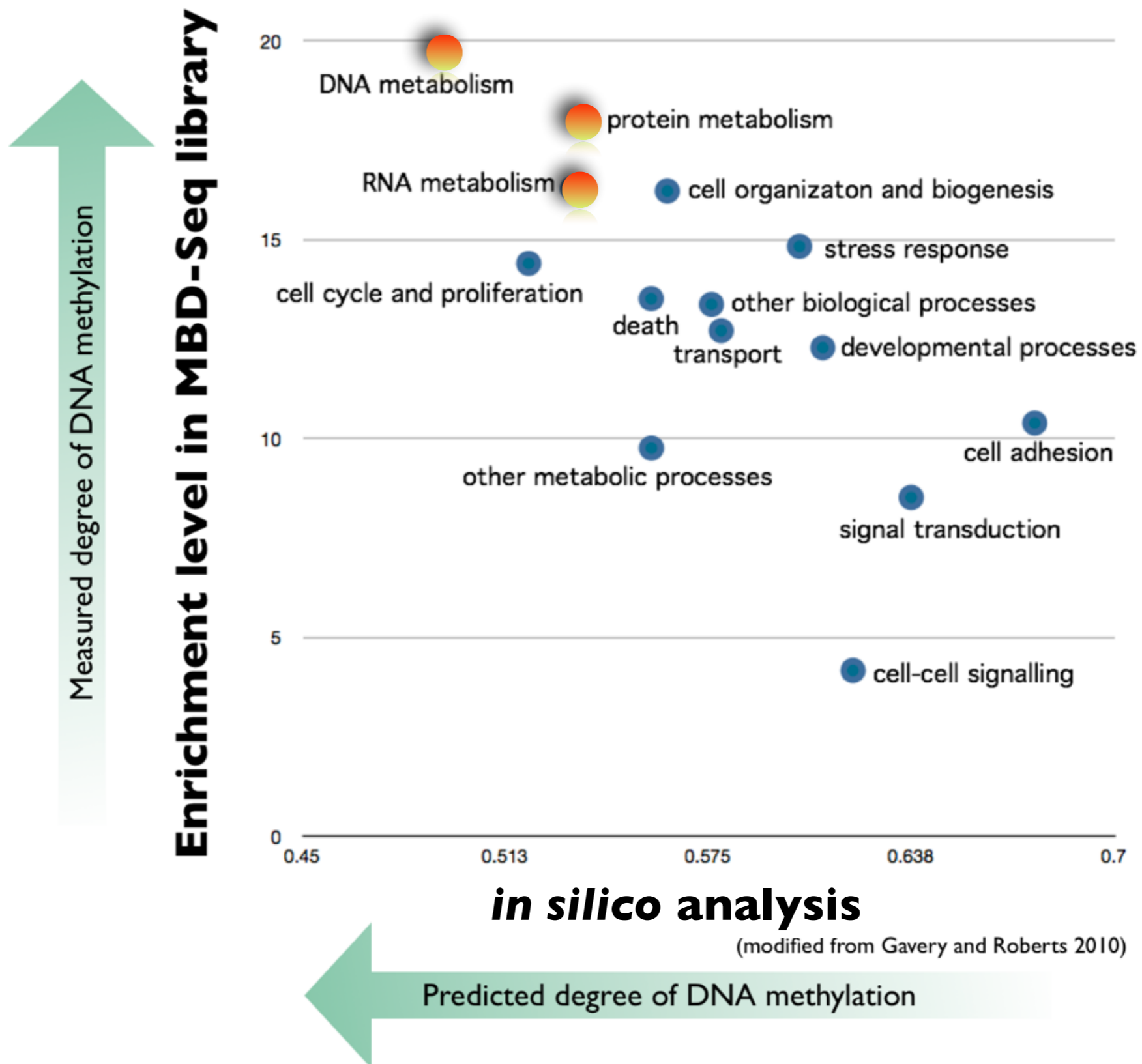


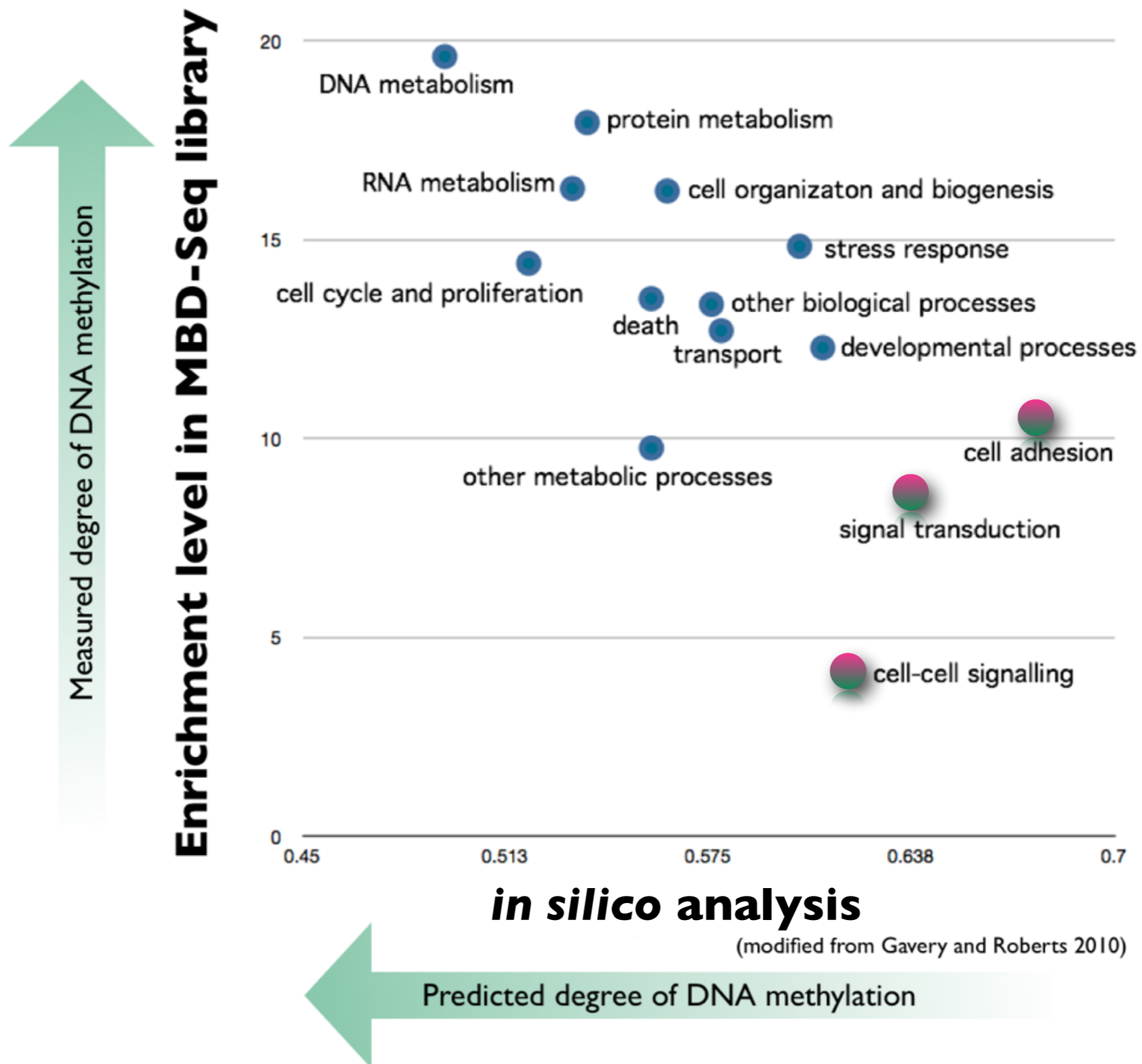
in silico analysis

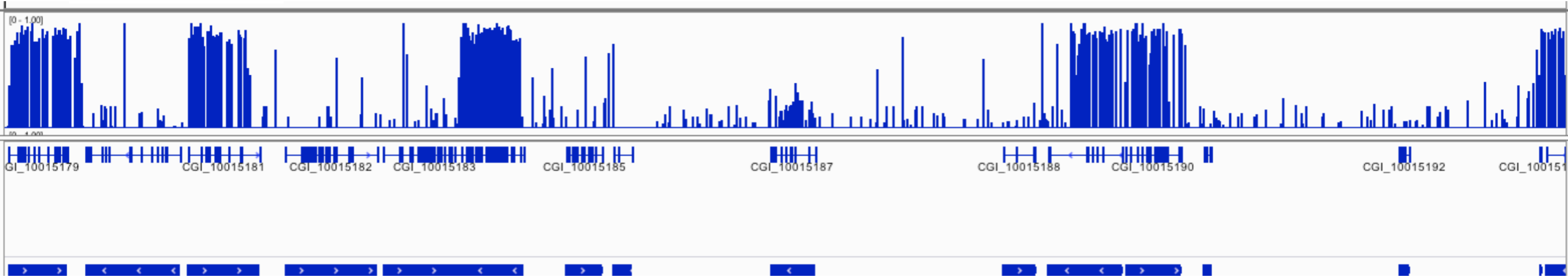
(modified from Gavery and Roberts 2010)

Predicted degree of DNA methylation









mosaic

associated with gene bodies
based on gene function

explanation?

1 Summary

- Sparsely (~16 %), mosaic methylated genome
- Gene body methylation correlated with function
- DNA methylation patterns are inherited
- DMRs are predominant in transposable elements

DNA Methylation Function in Marine Invertebrates

Gene
expression



2

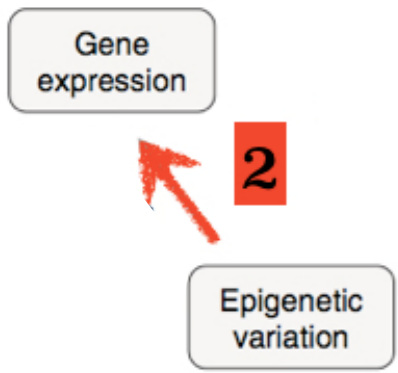
Epigenetic
variation

Function?



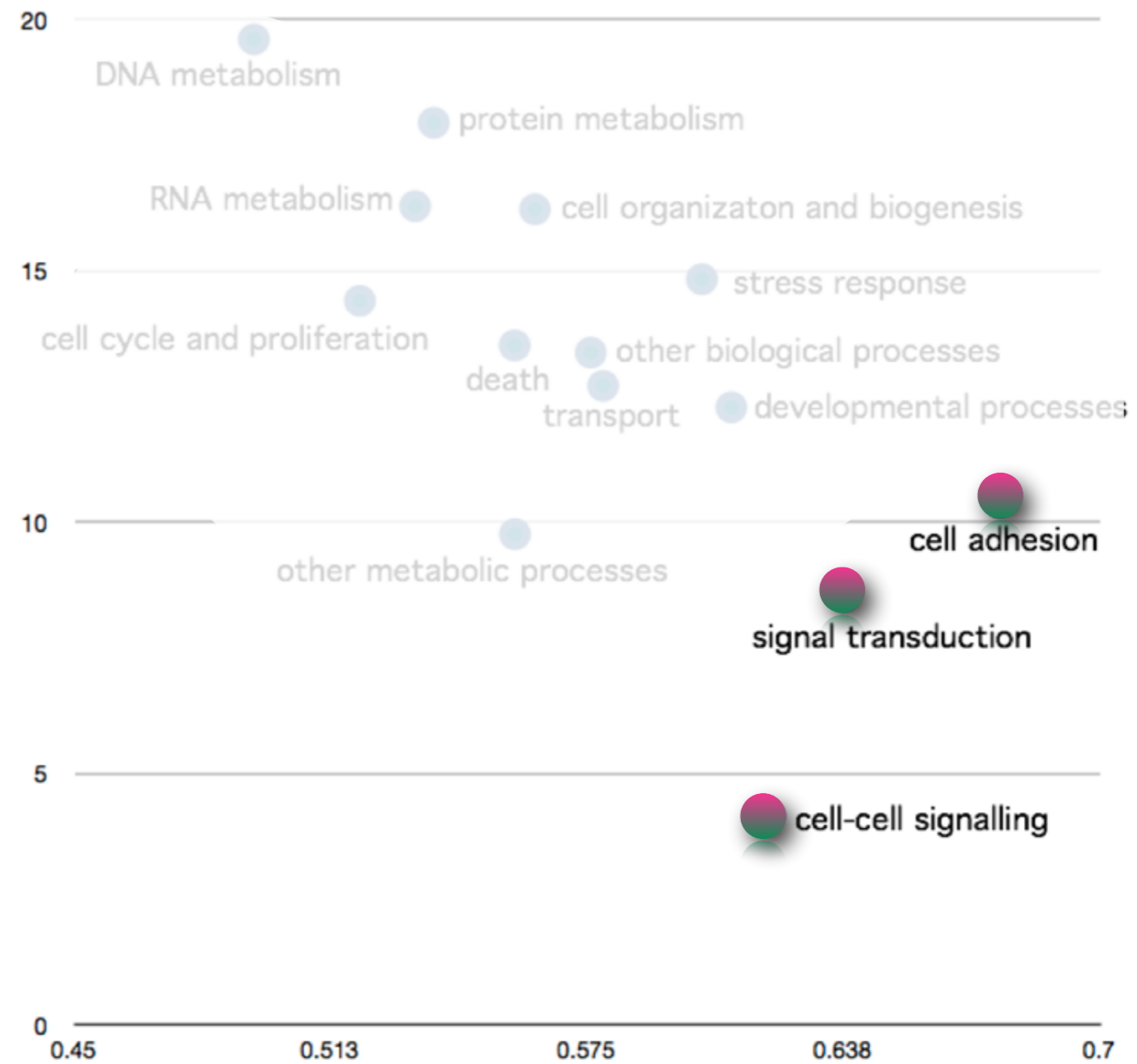
In species that experience a diverse range of environmental conditions, processes have evolved to increase the number of potential phenotypes in a population in order to improve the chances for an individual's survival.





Measured degree of DNA methylation

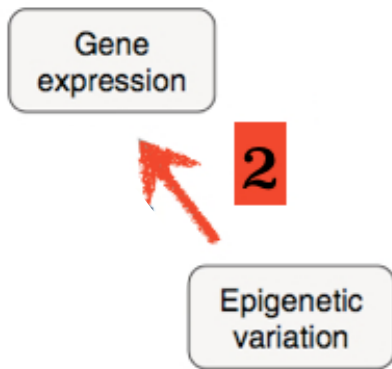
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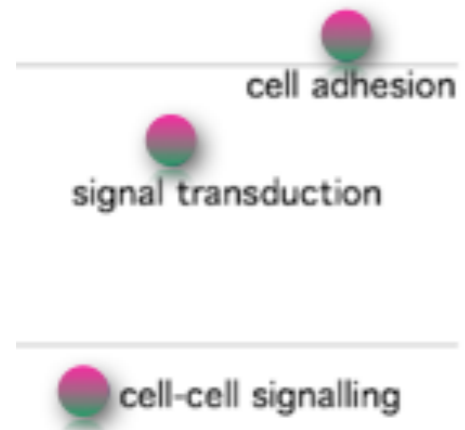
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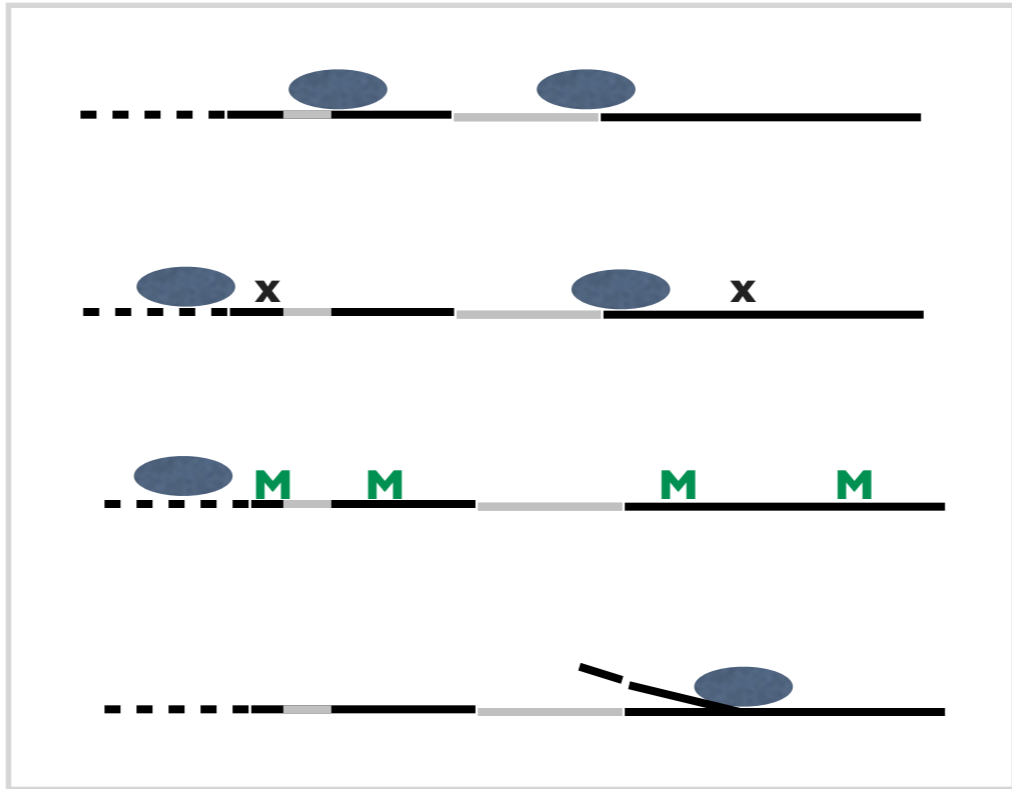
Predicted degree of DNA methylation



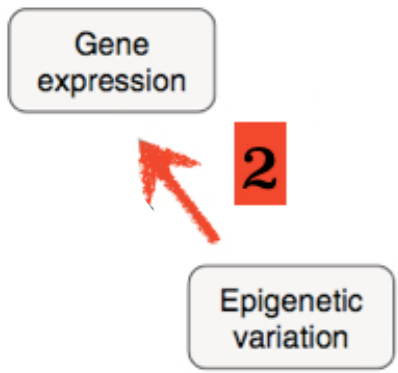
Transcriptional opportunities

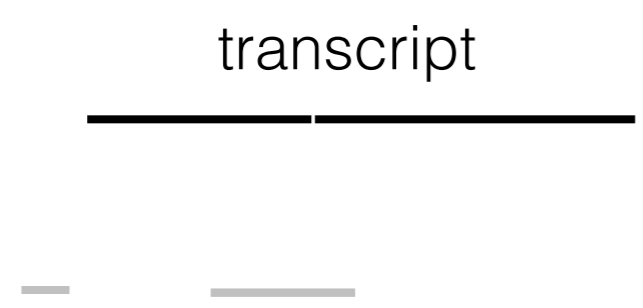
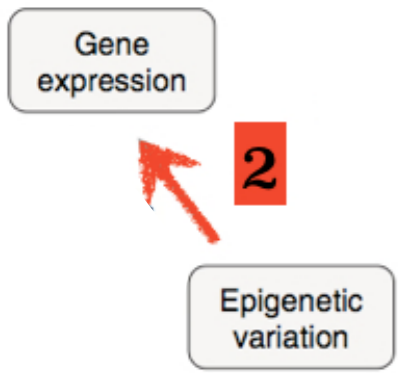


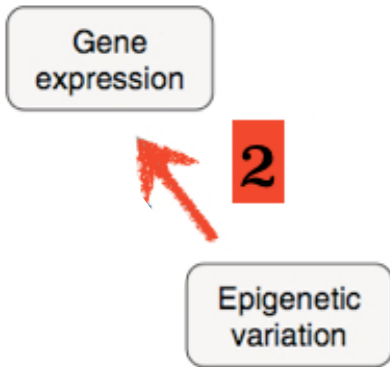
sparse methylation
tissue / temporal specific and inducible genes



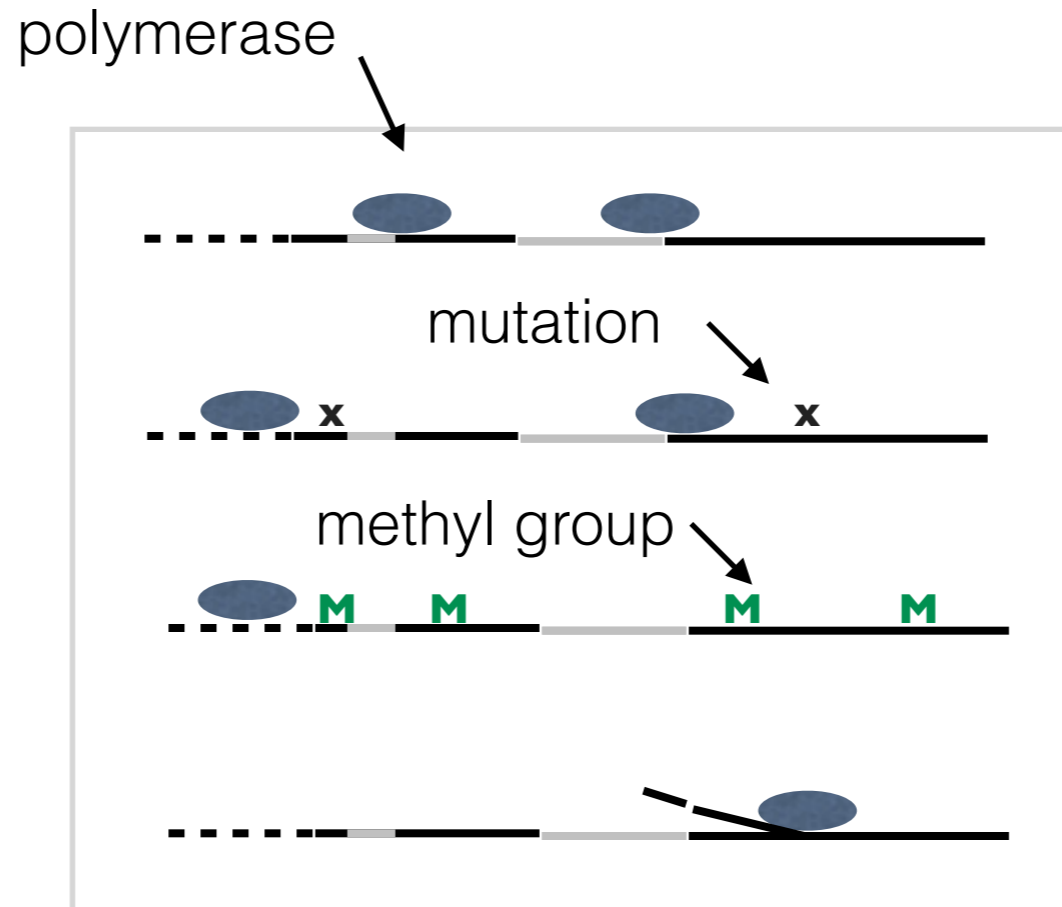
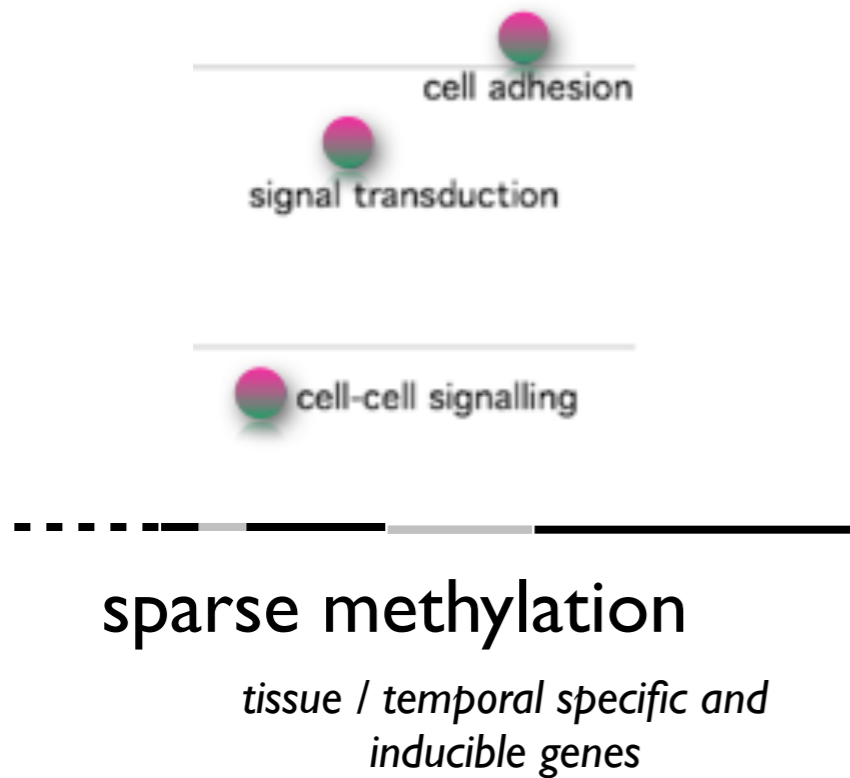
- alternative start sites
- sequence mutation
change AA, premature stop codon
- conventional transcription
transient methylation
- alternate transcript
exon skipping



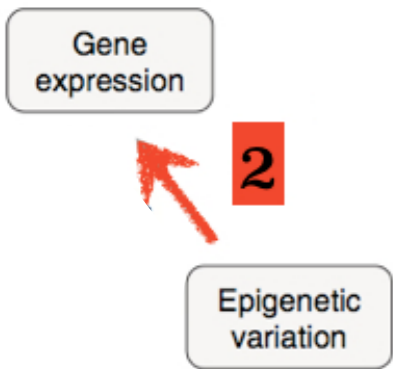




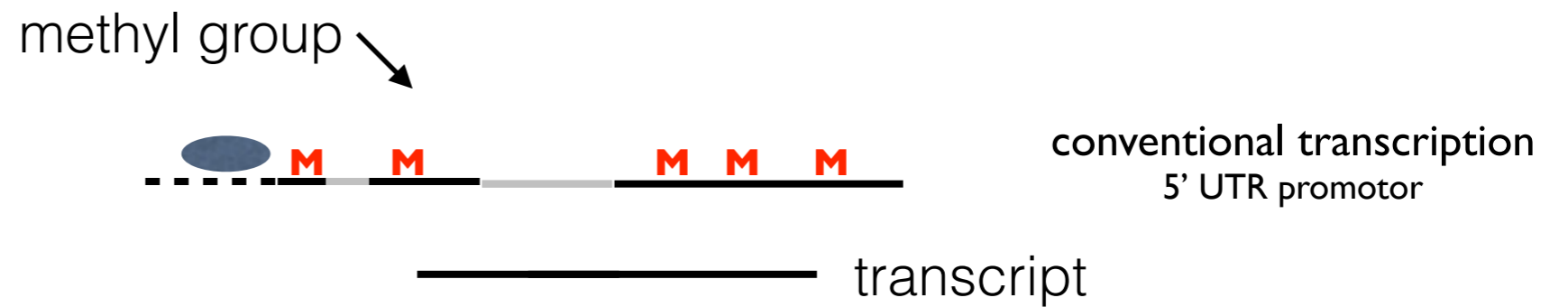
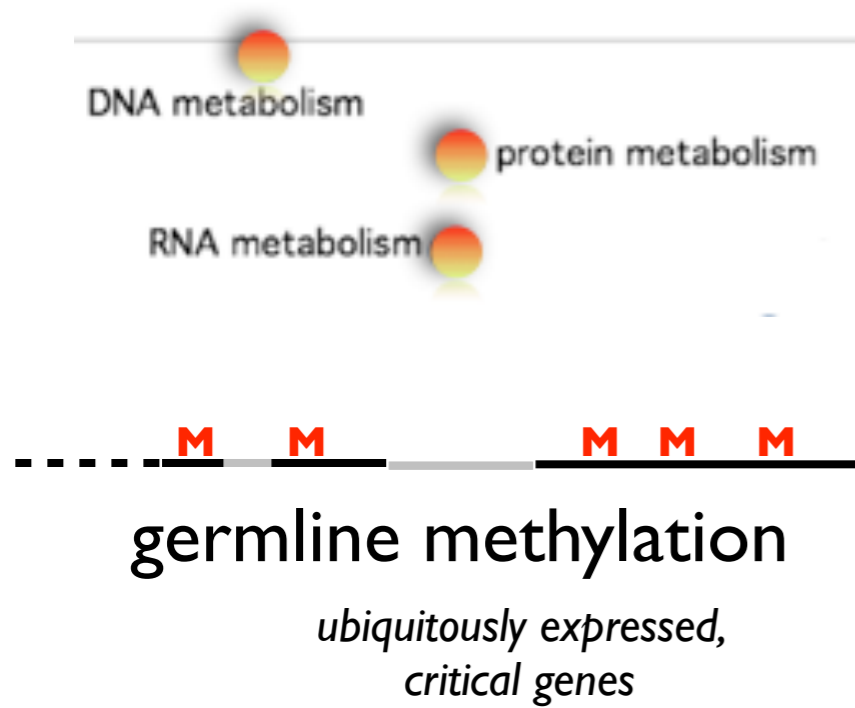
Transcriptional opportunities



- alternative start sites
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Transcriptional opportunities



A context dependent role for DNA methylation in bivalves

Mackenzie R. Gavery and Steven B. Roberts

Advance Access publication date 7 January 2014

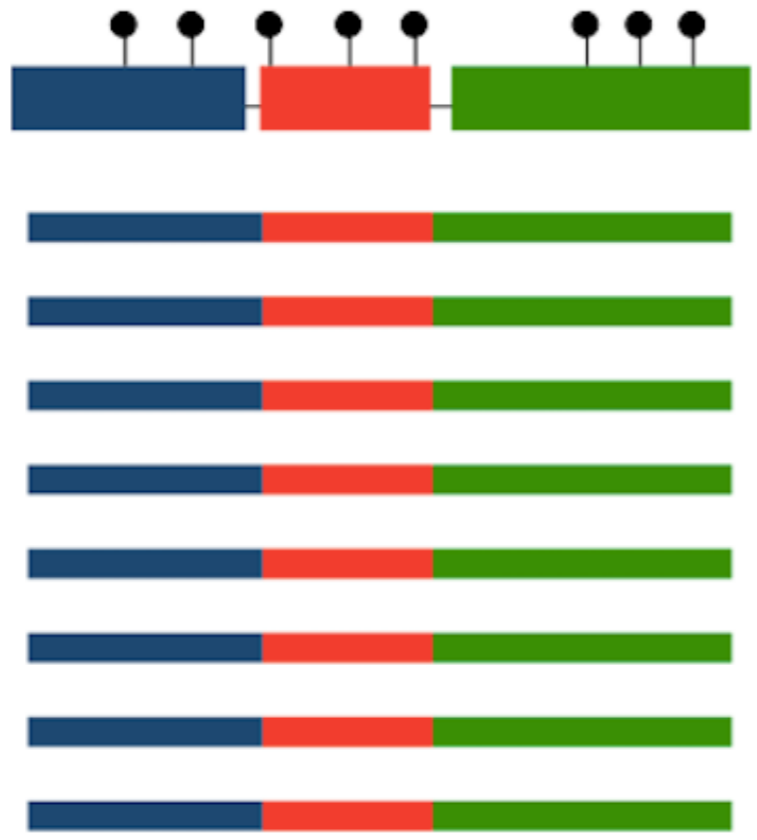
Stochastic Variation

Gene expression

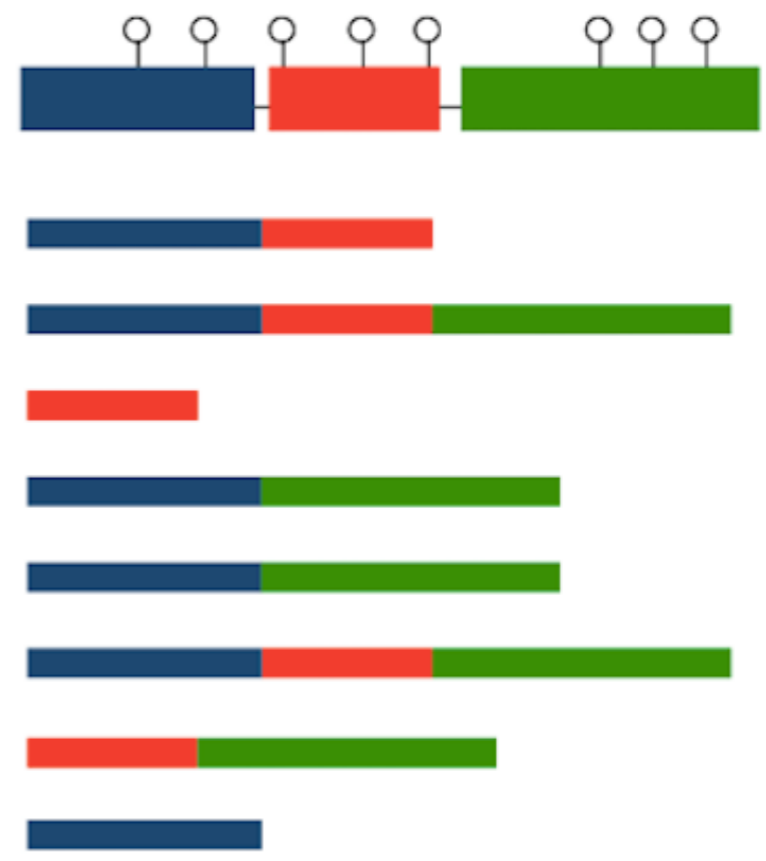
2



Epigenetic variation



housekeeping



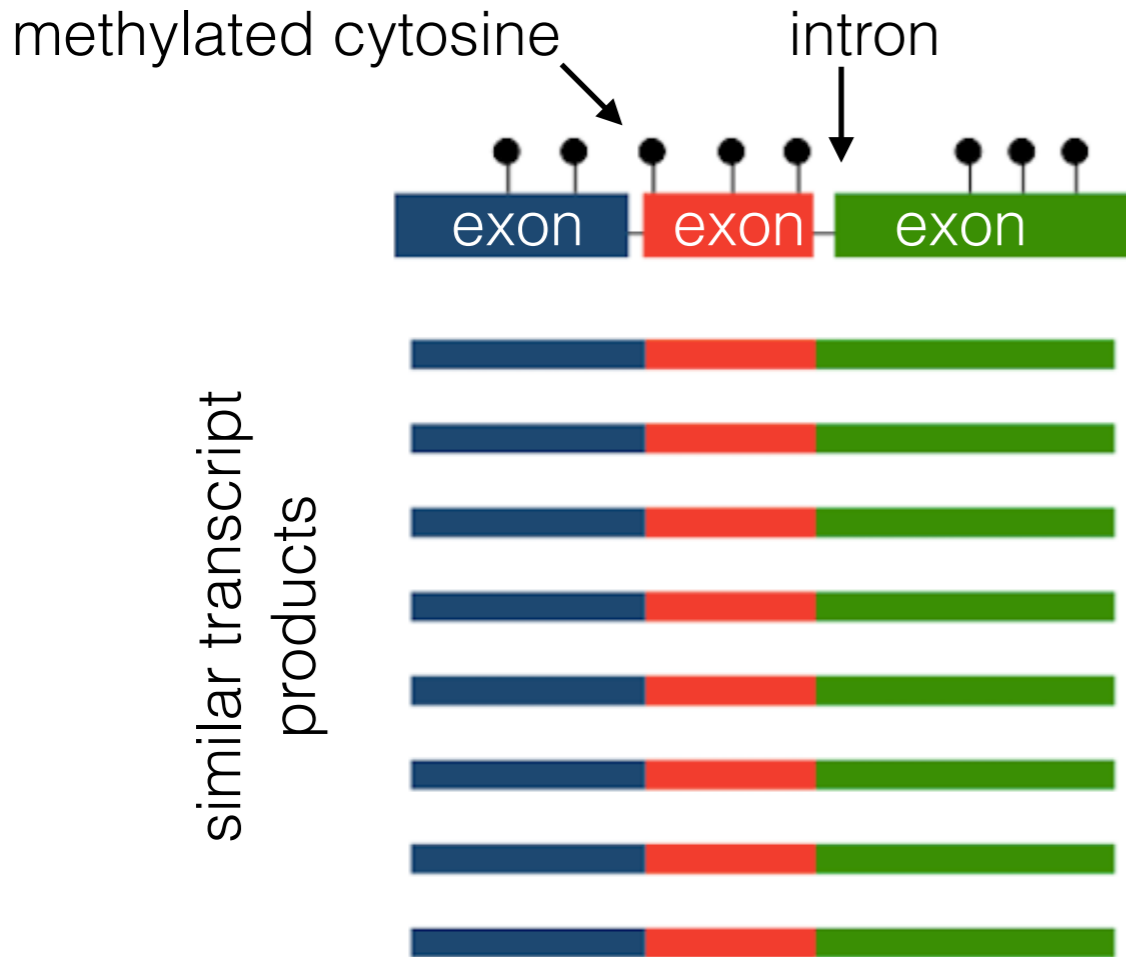
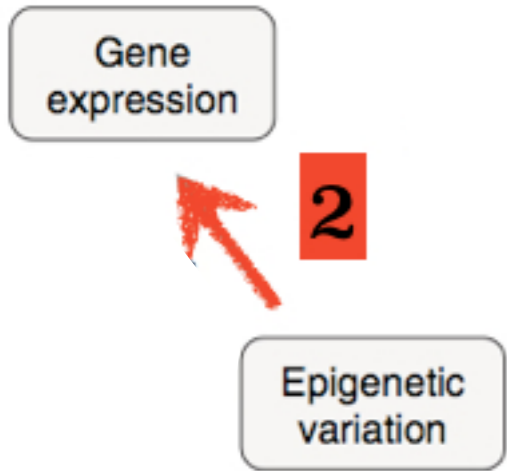
response to change

A context dependent role for DNA methylation in bivalves

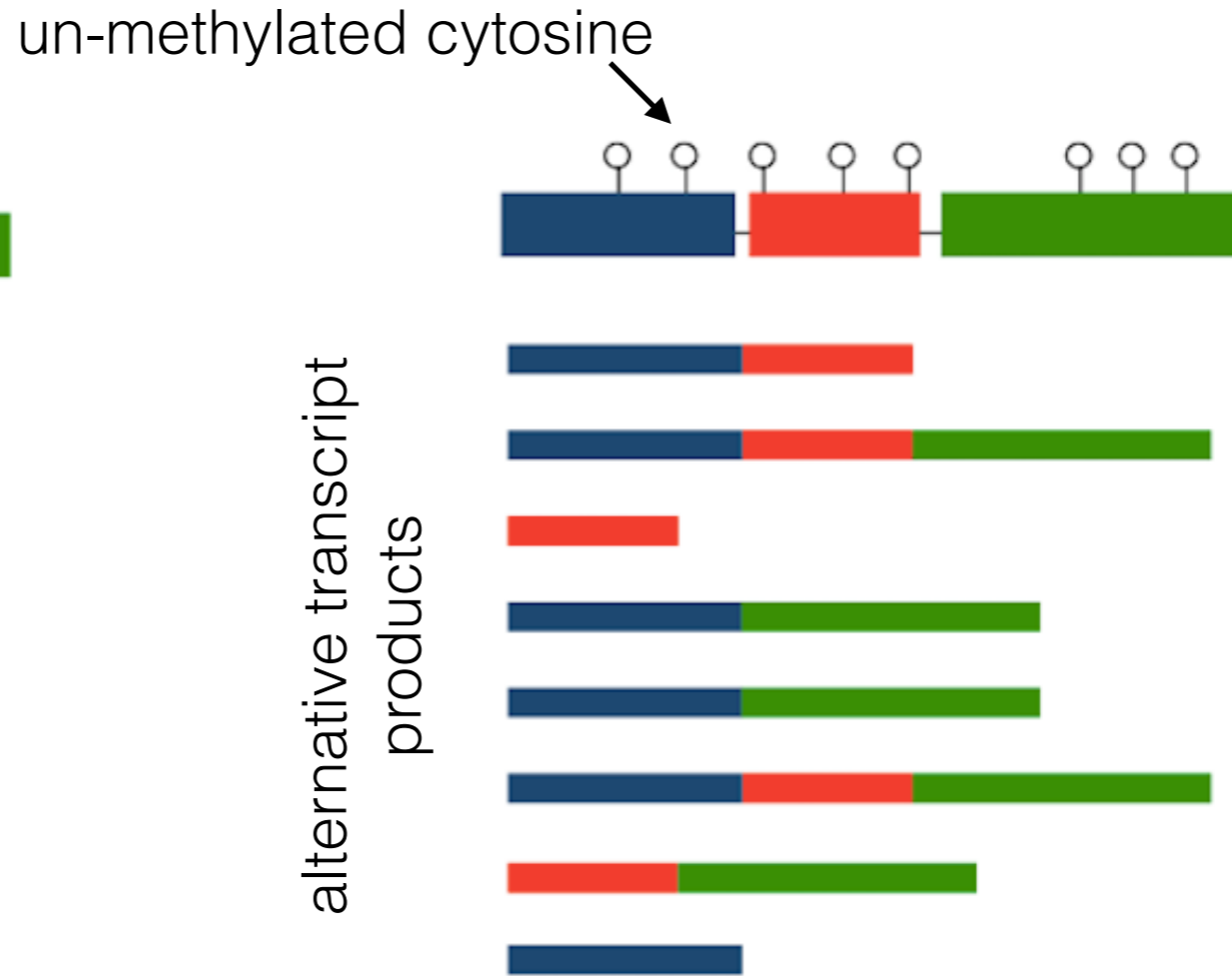
Mackenzie R. Gavery and Steven B. Roberts

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Stochastic Variation



housekeeping

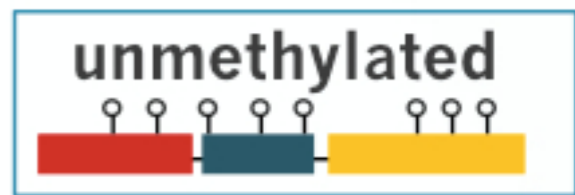


response to change

Gene expression

2

Epigenetic variation



inducible



disease

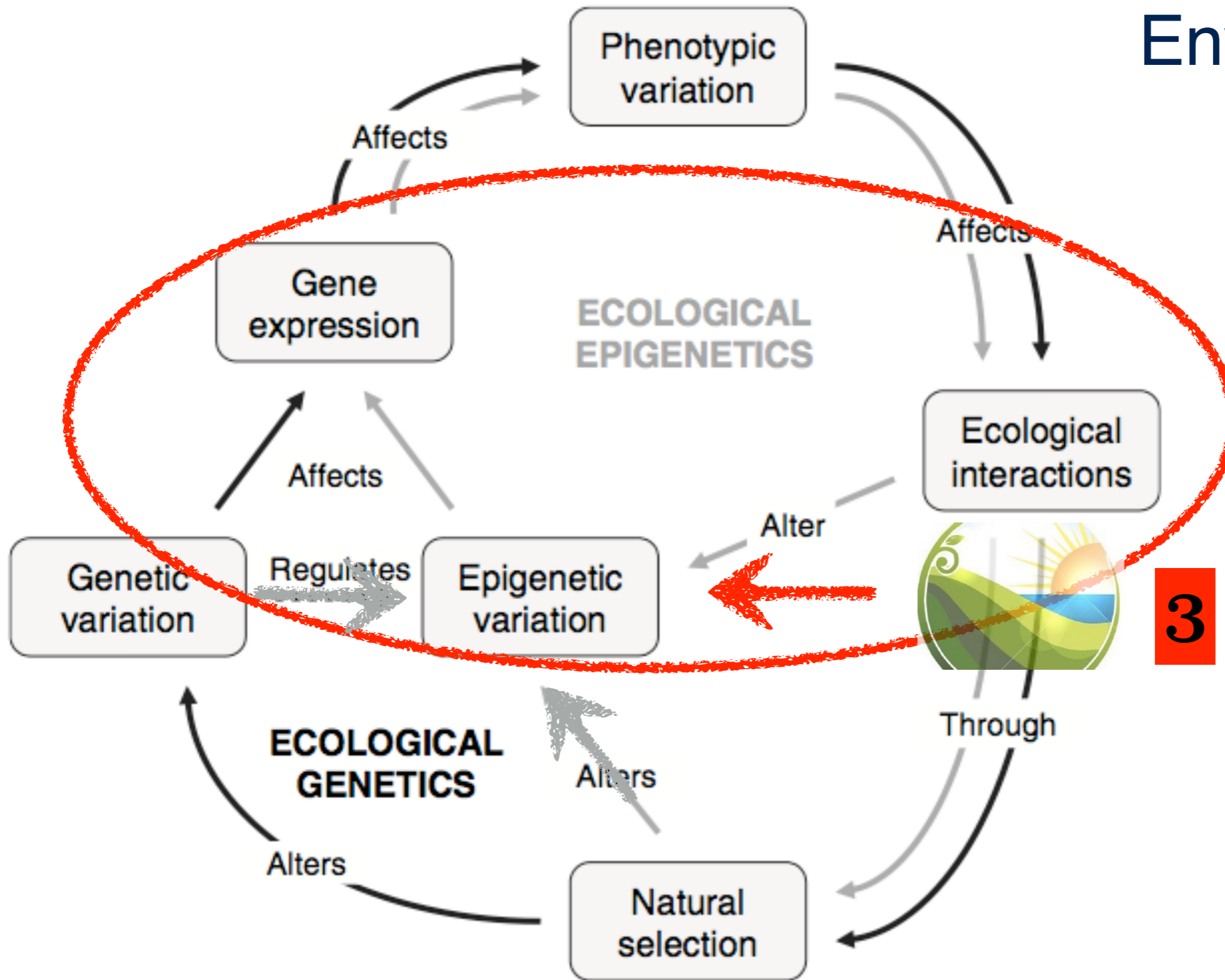
temperature

dessication

salinity

Mackenzie Gavery

Environmental Influence



Ecology Letters, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

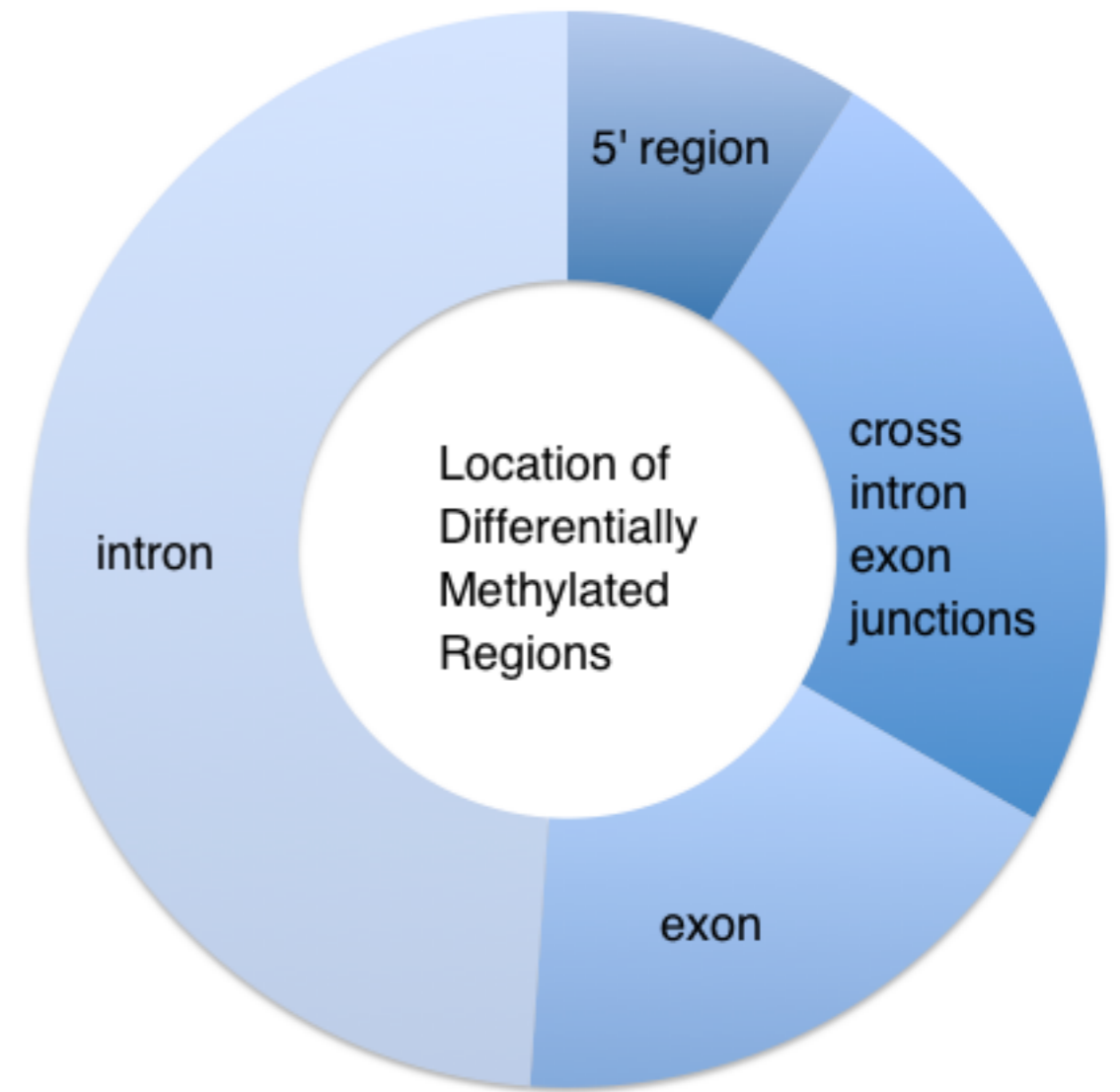
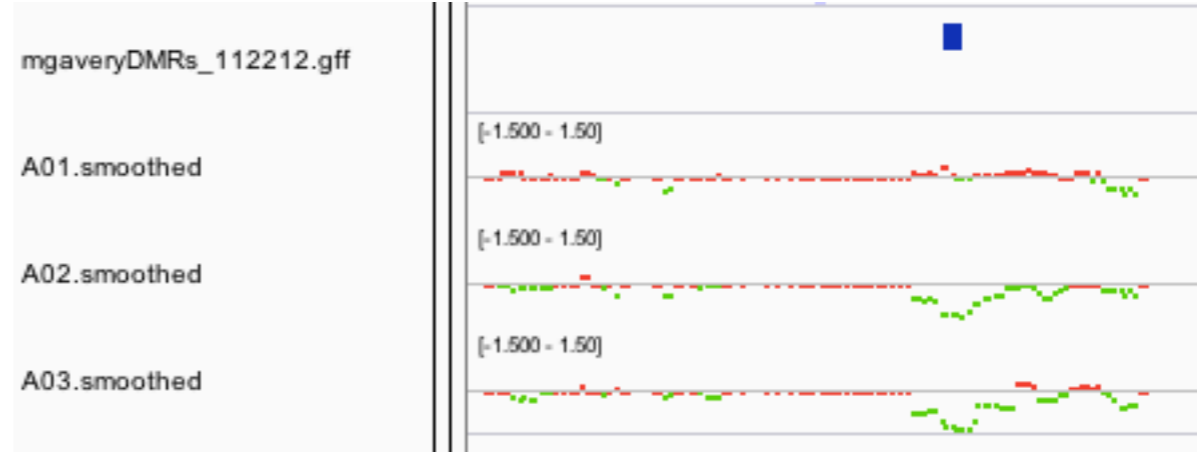
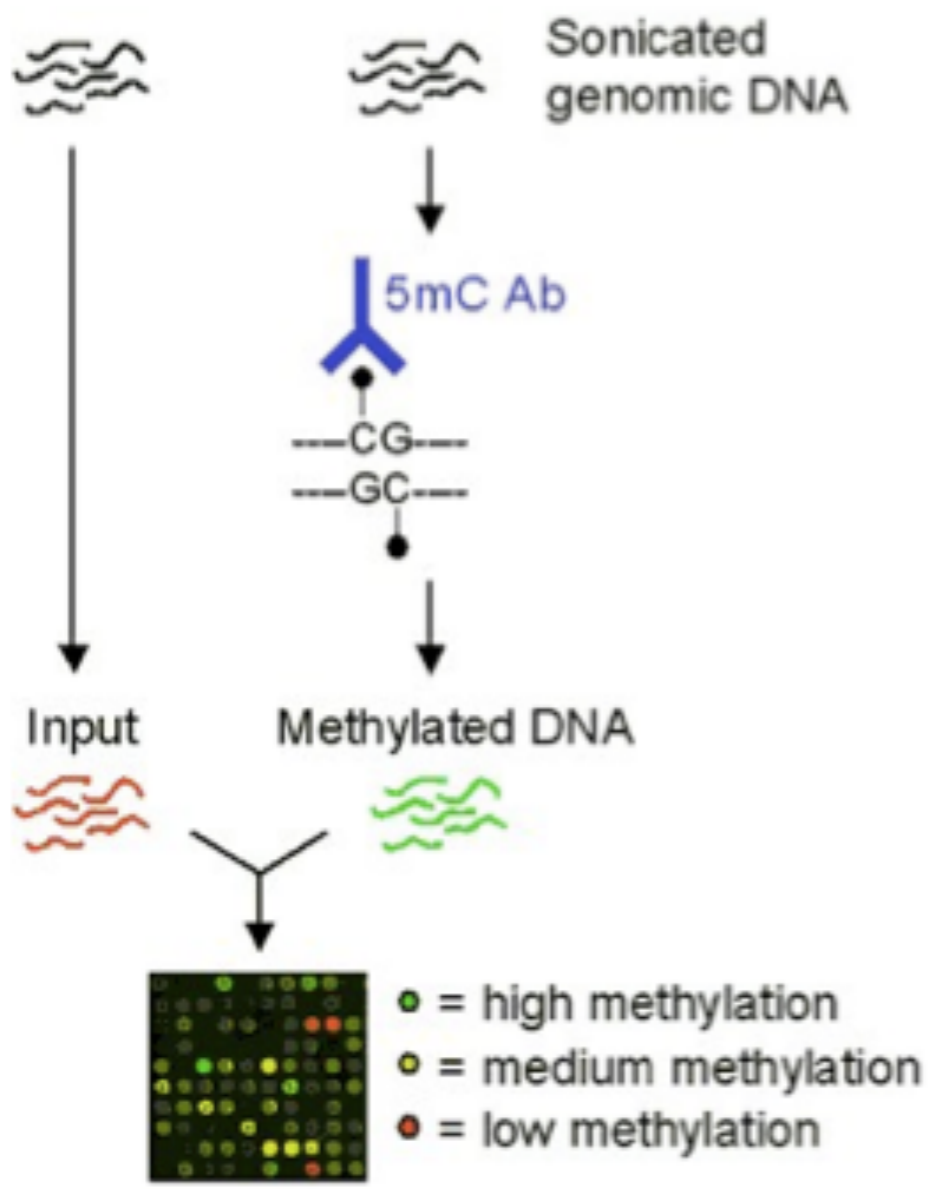
modified from

**IDEA AND
PERSPECTIVE**

Epigenetics for ecologists

Oliver Bosdorf,^{1*} Christina L. Richards² and Massimo Pigliucci³

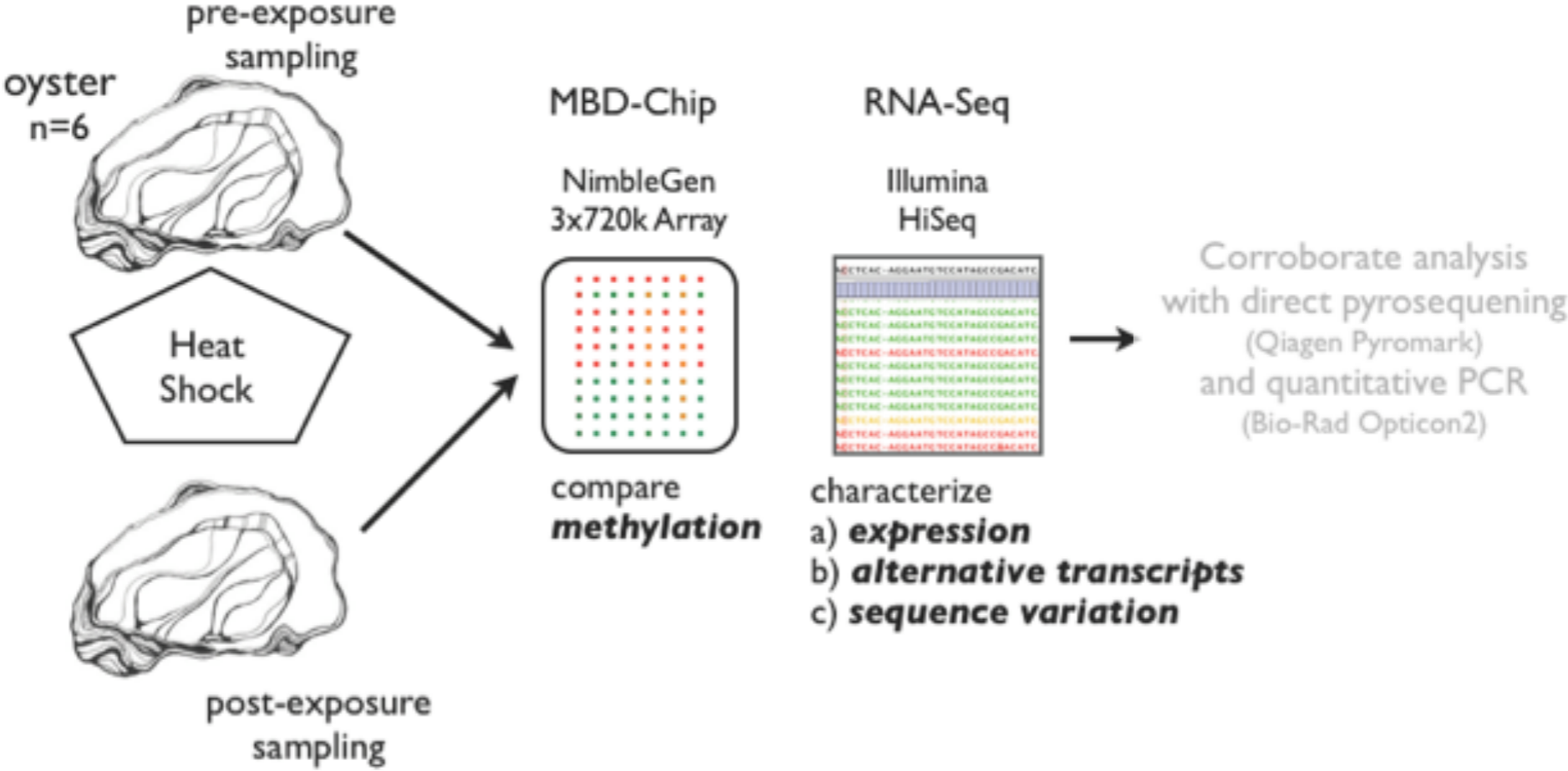
Environmental impact (Estrogens)



Environment and gene expression



stochastic or targeted?



Take Home

Oyster genome has a fantastic degree of diversity contributing to phenotypic plasticity & adaptation potential.

Take Home

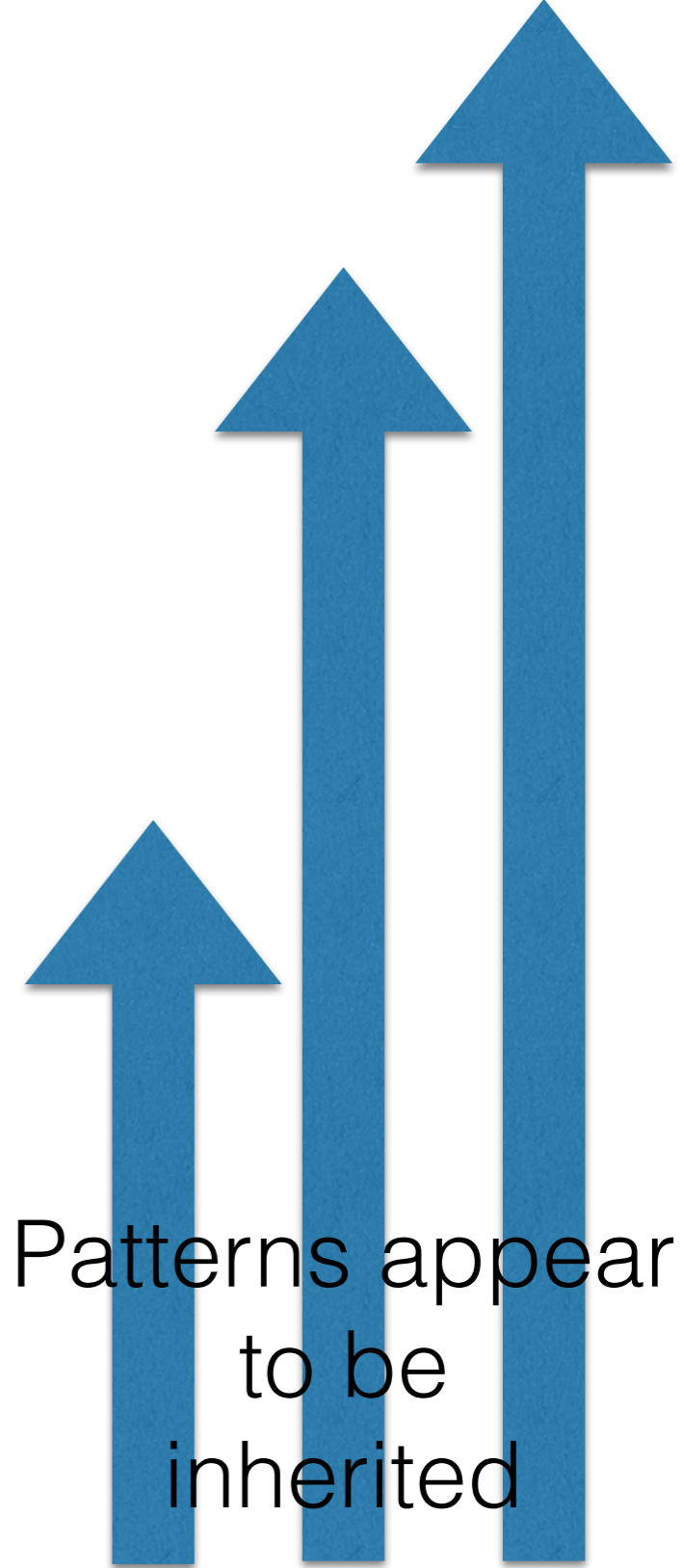
Oyster genome has a fantastic degree of diversity contributing to phenotypic plasticity & adaptation potential.

- large gene families
- very high mutation rate (snp/50bp)
- numerous exons per gene (potential for alternatives)
- genome full of repeats region
- high number of transposable elements
- lack of methylation of transposable suggest mobility
- family variation of methylation
- limited methylation environmental response genes is associated with spurious transcription
- inheritance of epigenetic marks as mechanism of improved adaptation

Considerations



Environmental perturbation impacts DNA methylation (predominantly demethylation)



Patterns appear to be inherited



Germline methylation encoded with a pattern product of evolutionary forces

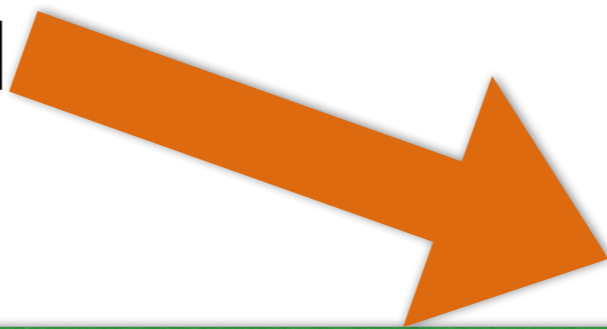
Considerations



Environmental perturbation impacts DNA methylation (predominantly demethylation)



Possibly incorporated into germline

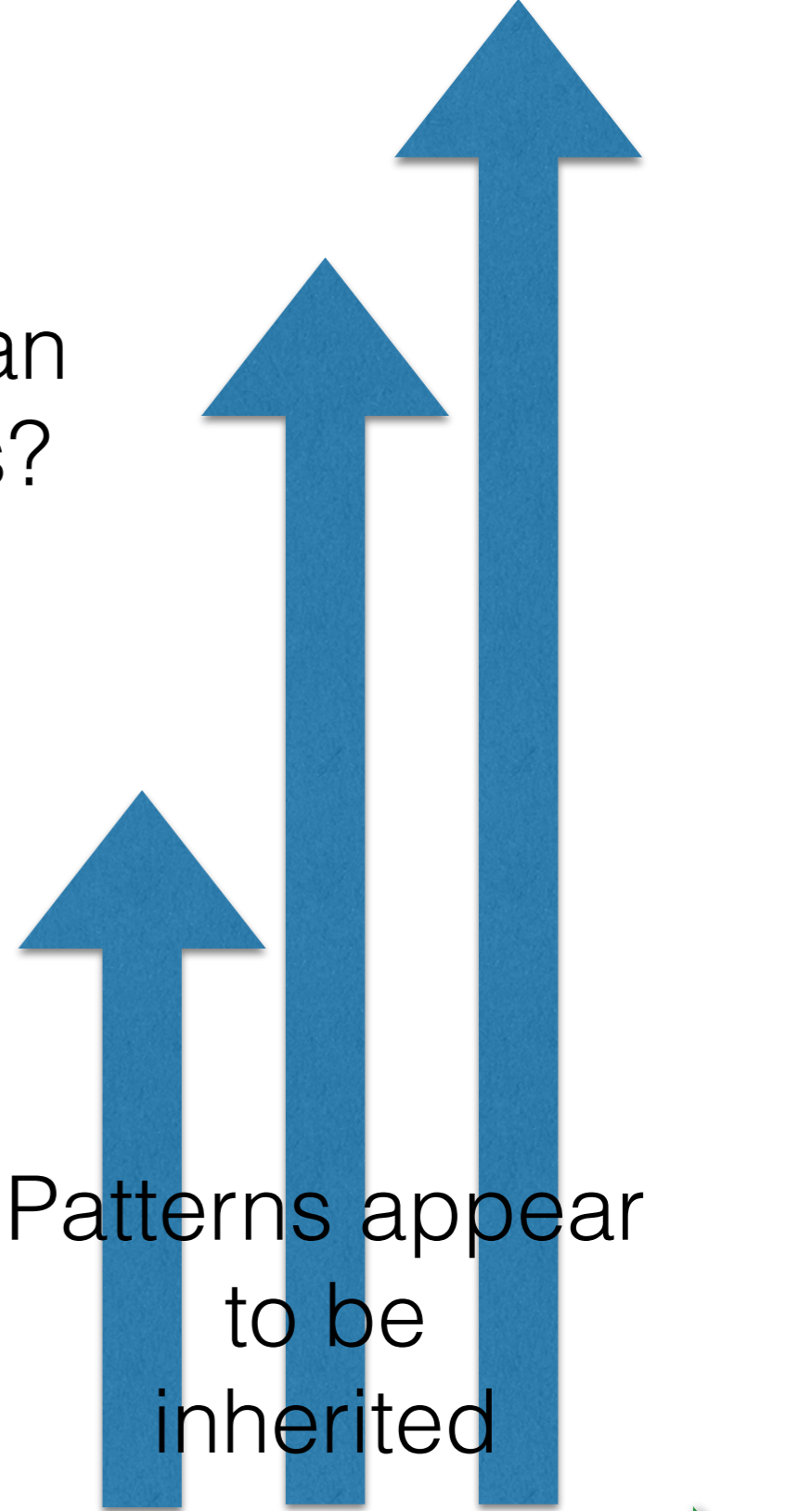


Germline methylation encoded with a pattern

Lifespan or less?

?

Patterns appear to be inherited



Considerations

Could this provide a “memory” for subsequent exposure?

Lifespan or less?

Environmental perturbation impacts DNA methylation (predominantly demethylation)

Possibly incorporated into germline

Patterns appear to be inherited

Germline methylation

Transgenerational Impact

