

# Influence of Epigenetic Variation on Marine Invertebrate Physiology

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Associate Professor  
University of Washington  
School of Aquatic and Fishery Sciences  
**robertslab.info**  
**@sr320**



# Background

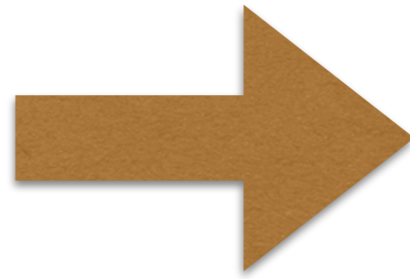
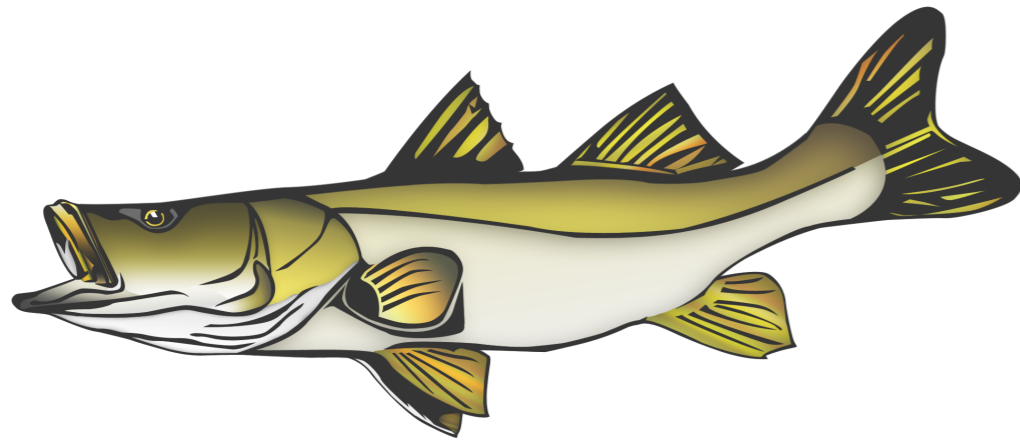
## **Physiology**

*How fundamental processes work in aquatic species*

# Background

## Physiology

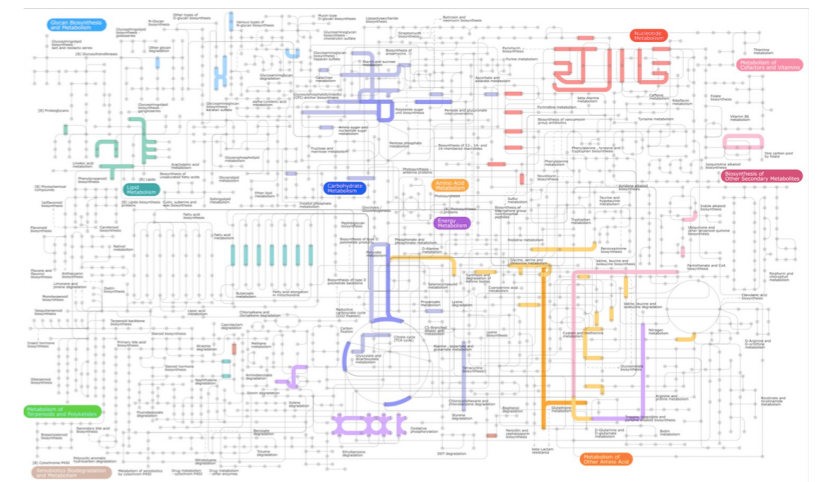
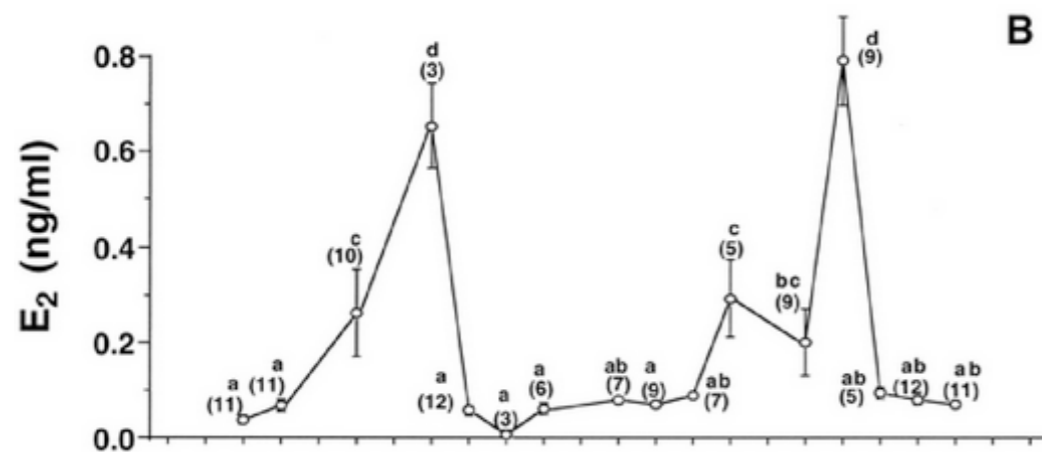
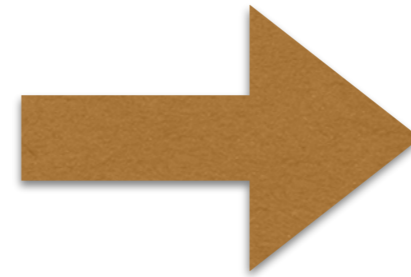
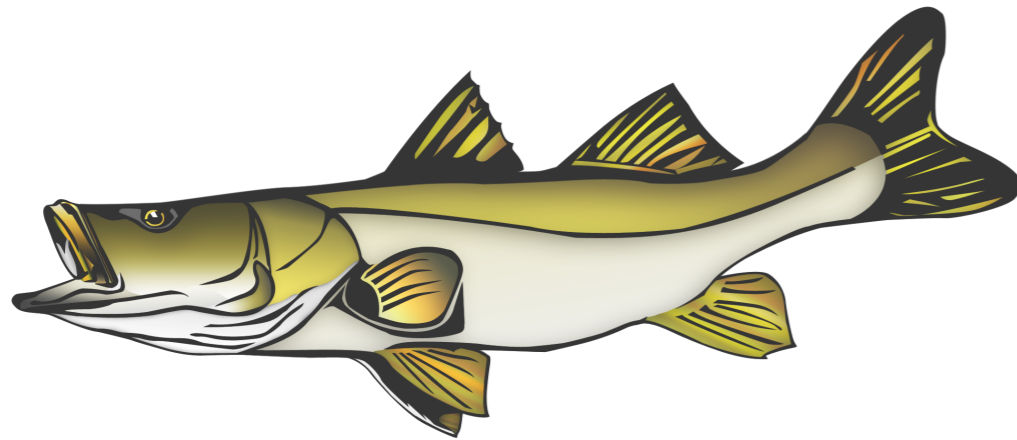
*How fundamental processes work in aquatic species*



# Background

## Physiology

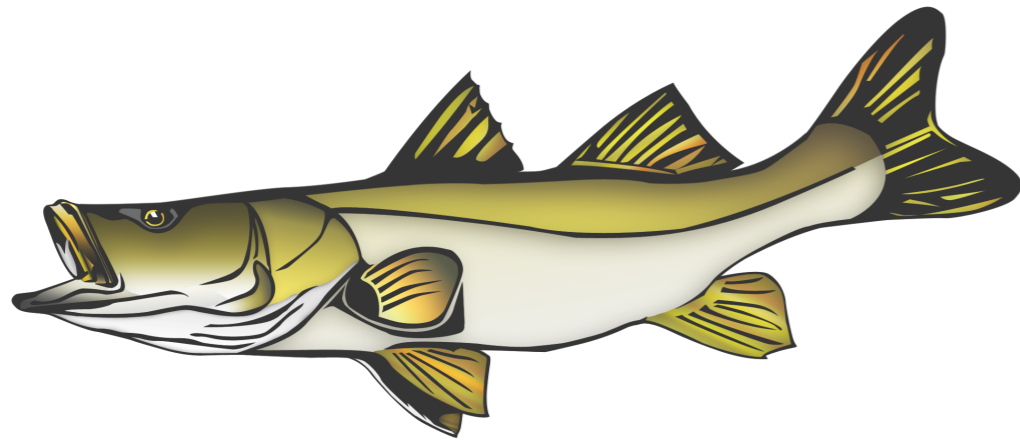
*How fundamental processes work in aquatic species*



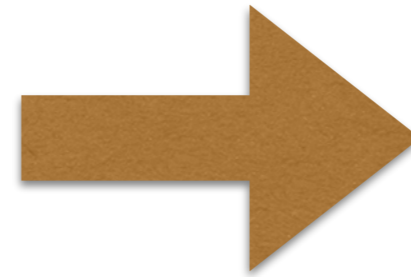
# Background

## Physiology

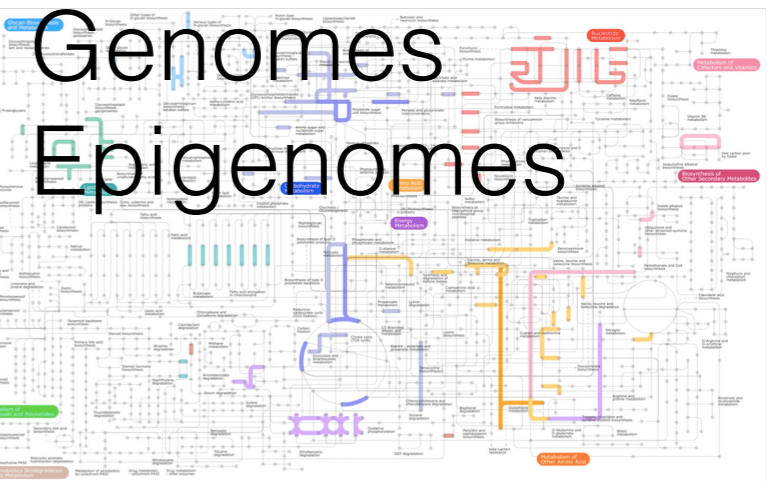
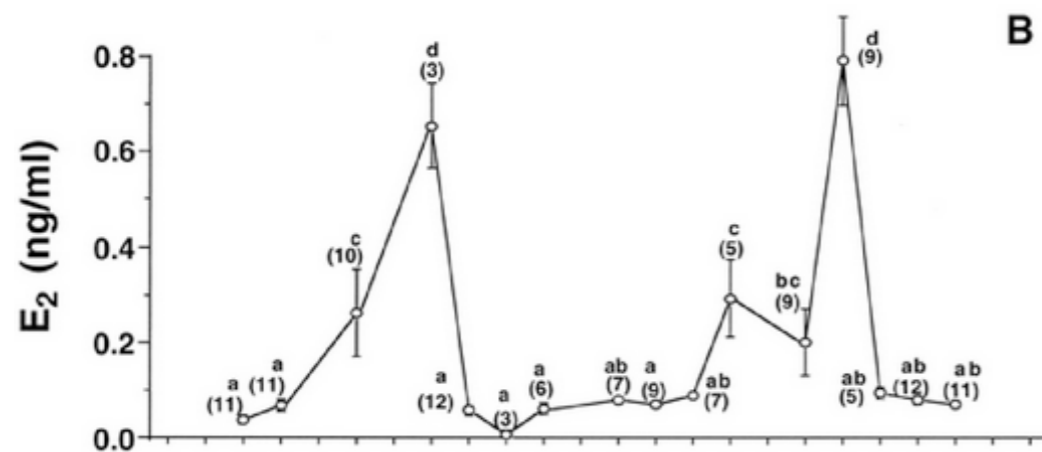
*How fundamental processes work in aquatic species*



Hormones  
Proteins



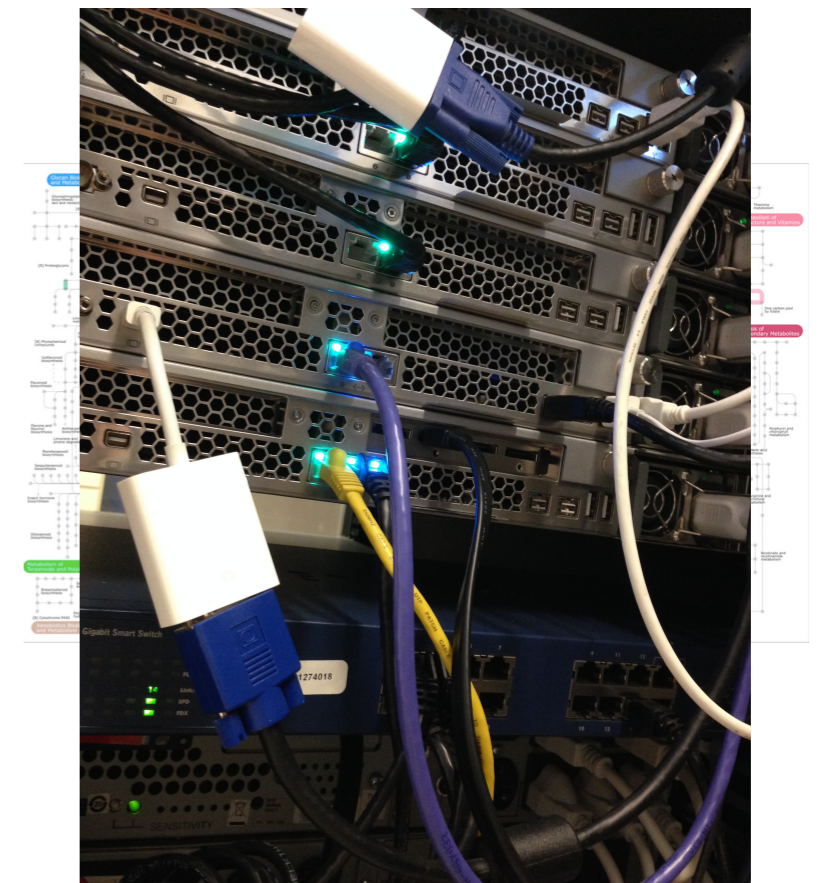
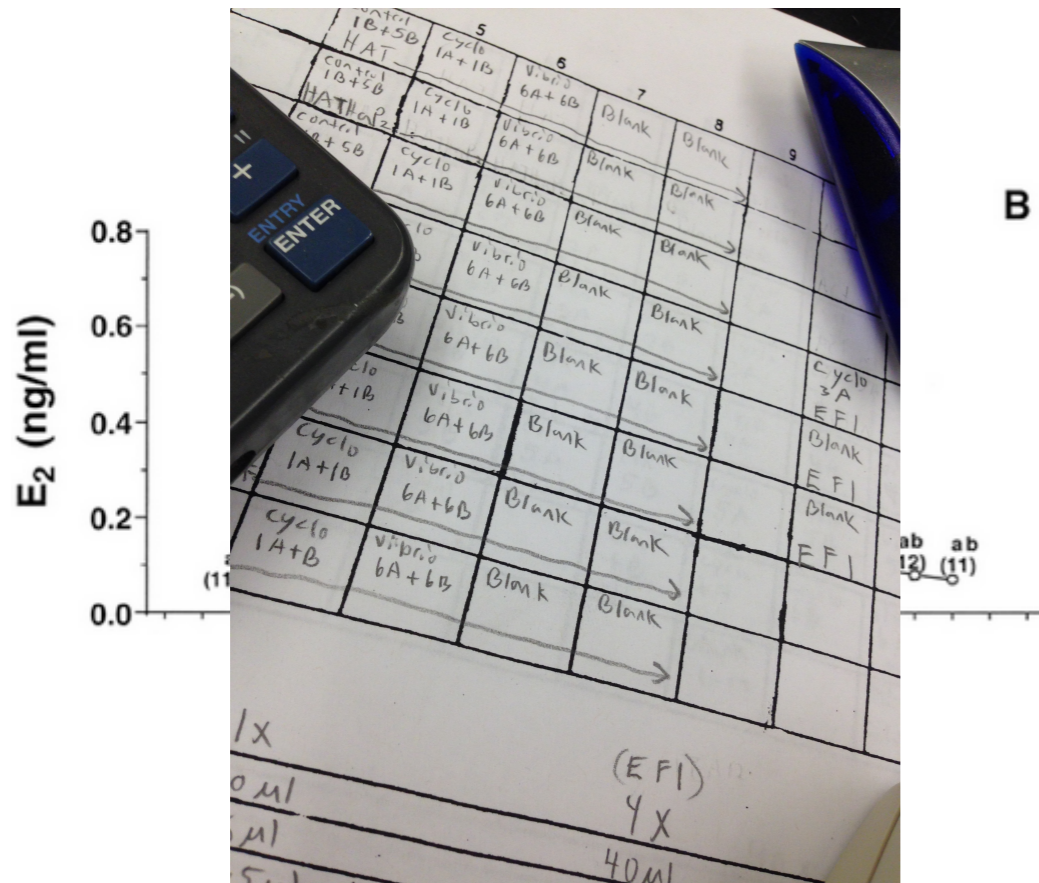
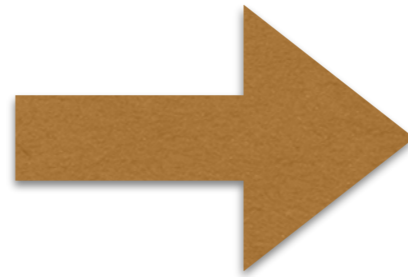
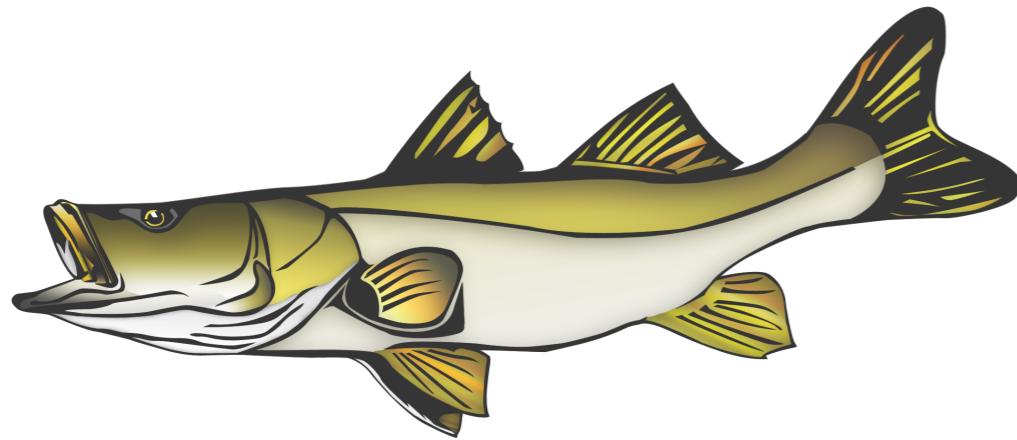
Transcriptomes  
Proteomes



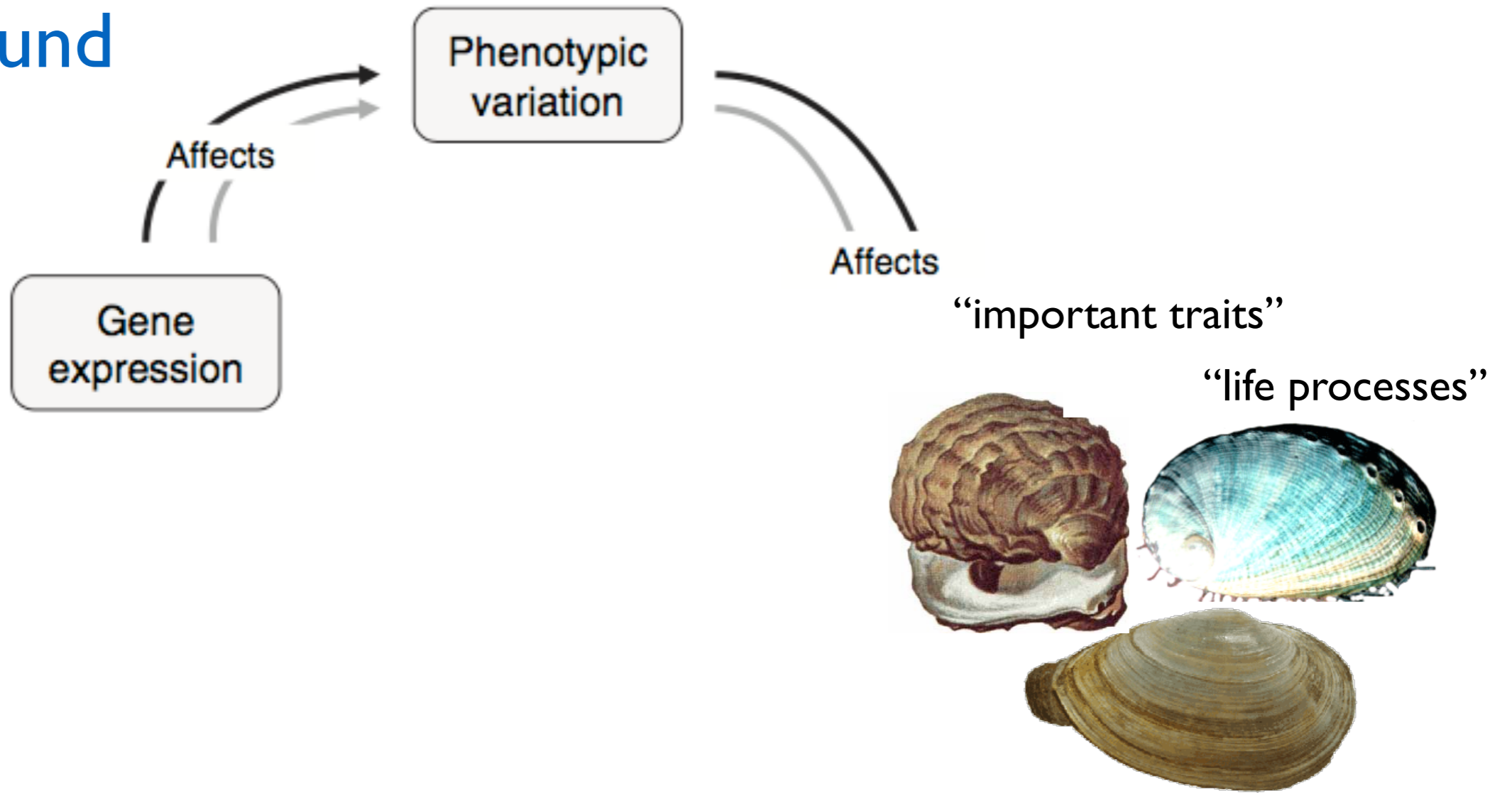
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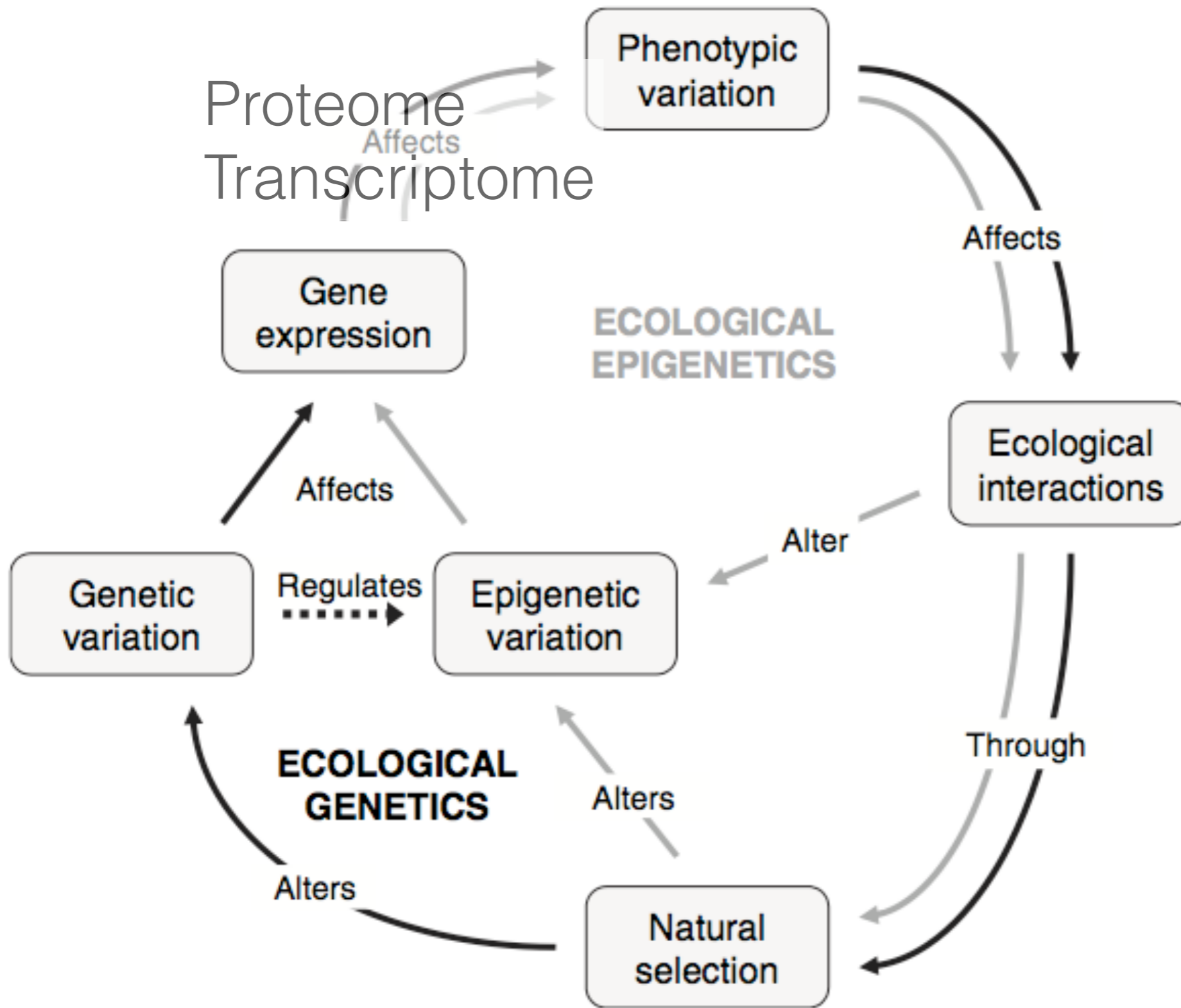
## Physiology

*How fundamental processes work in aquatic species*



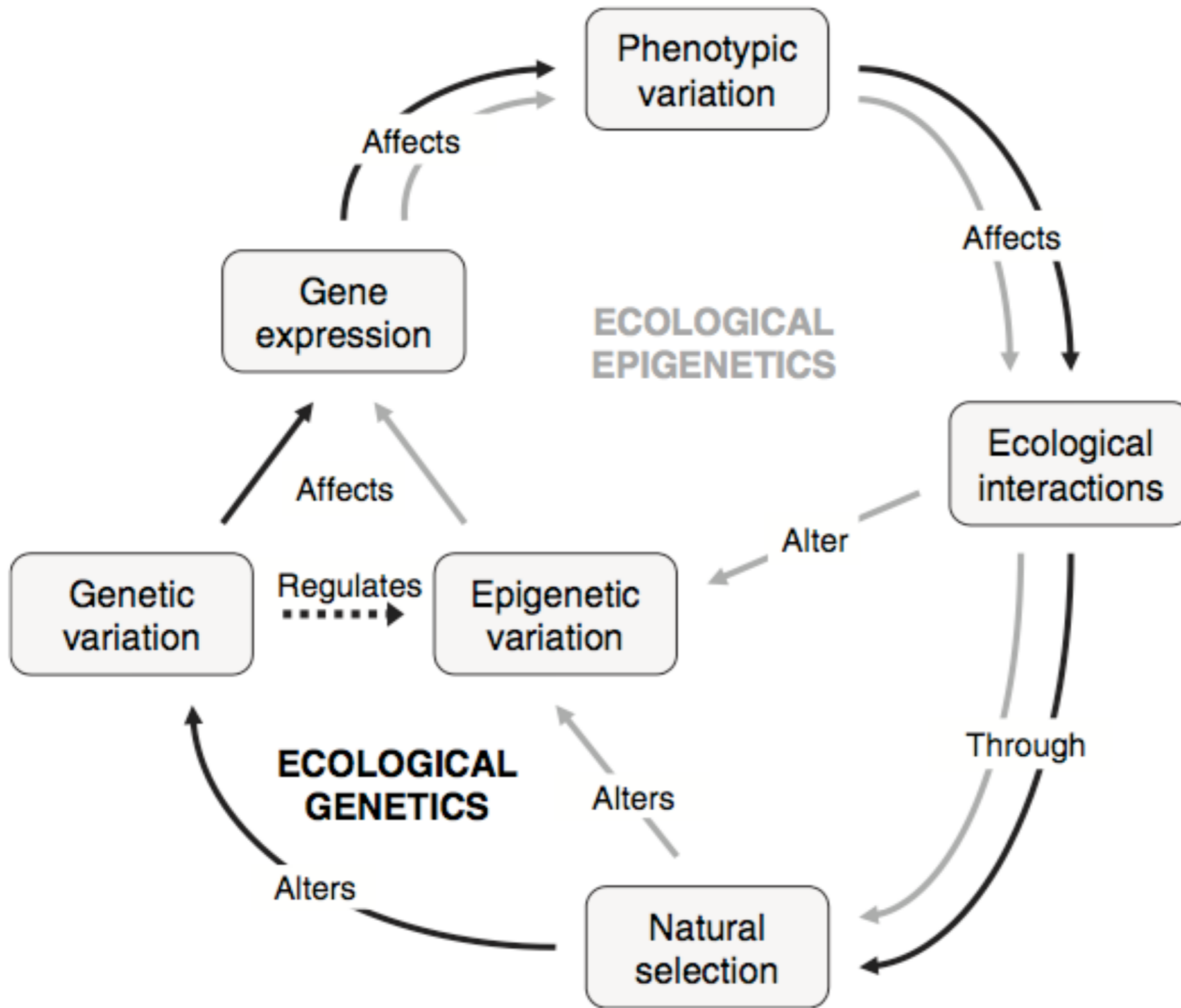
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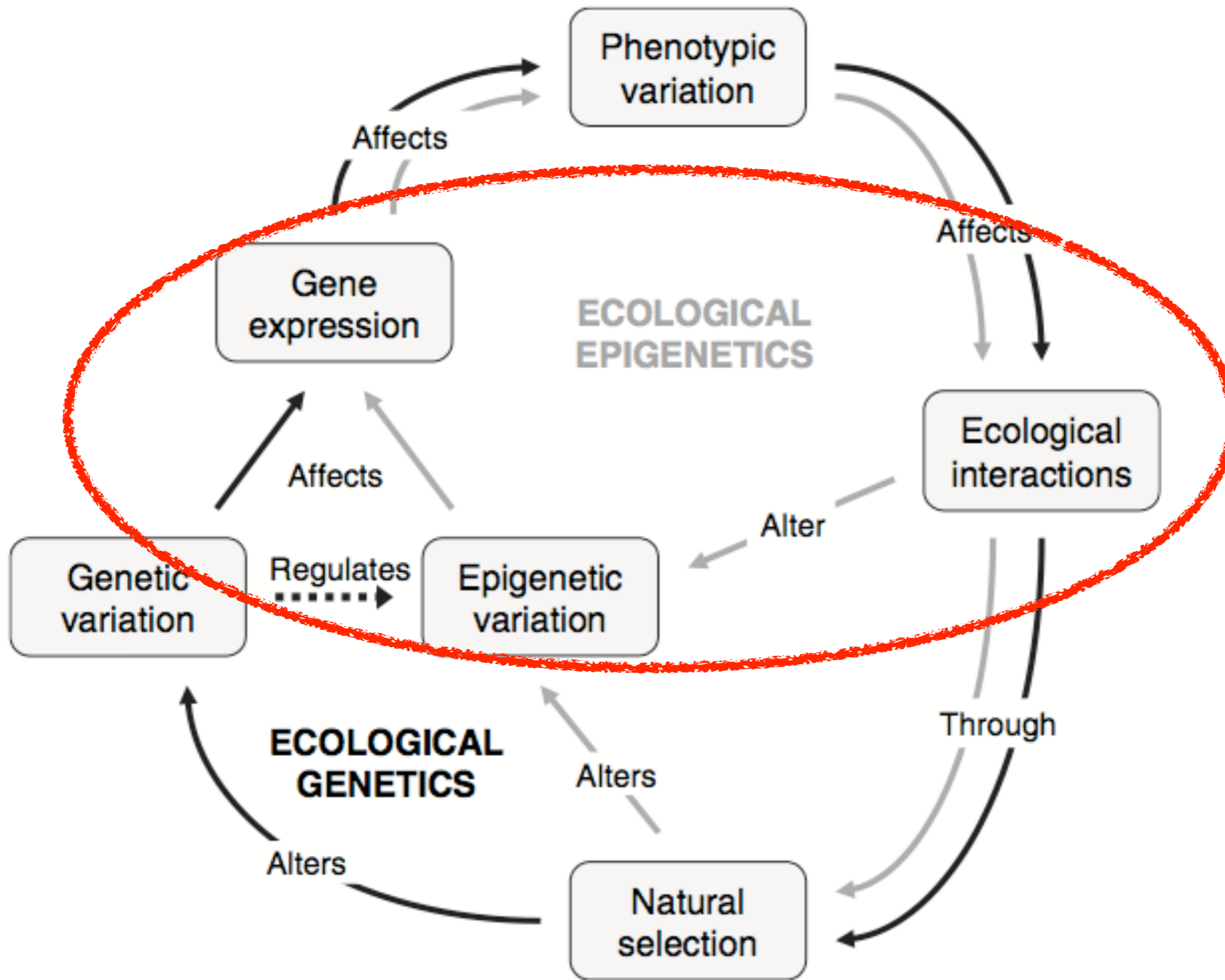


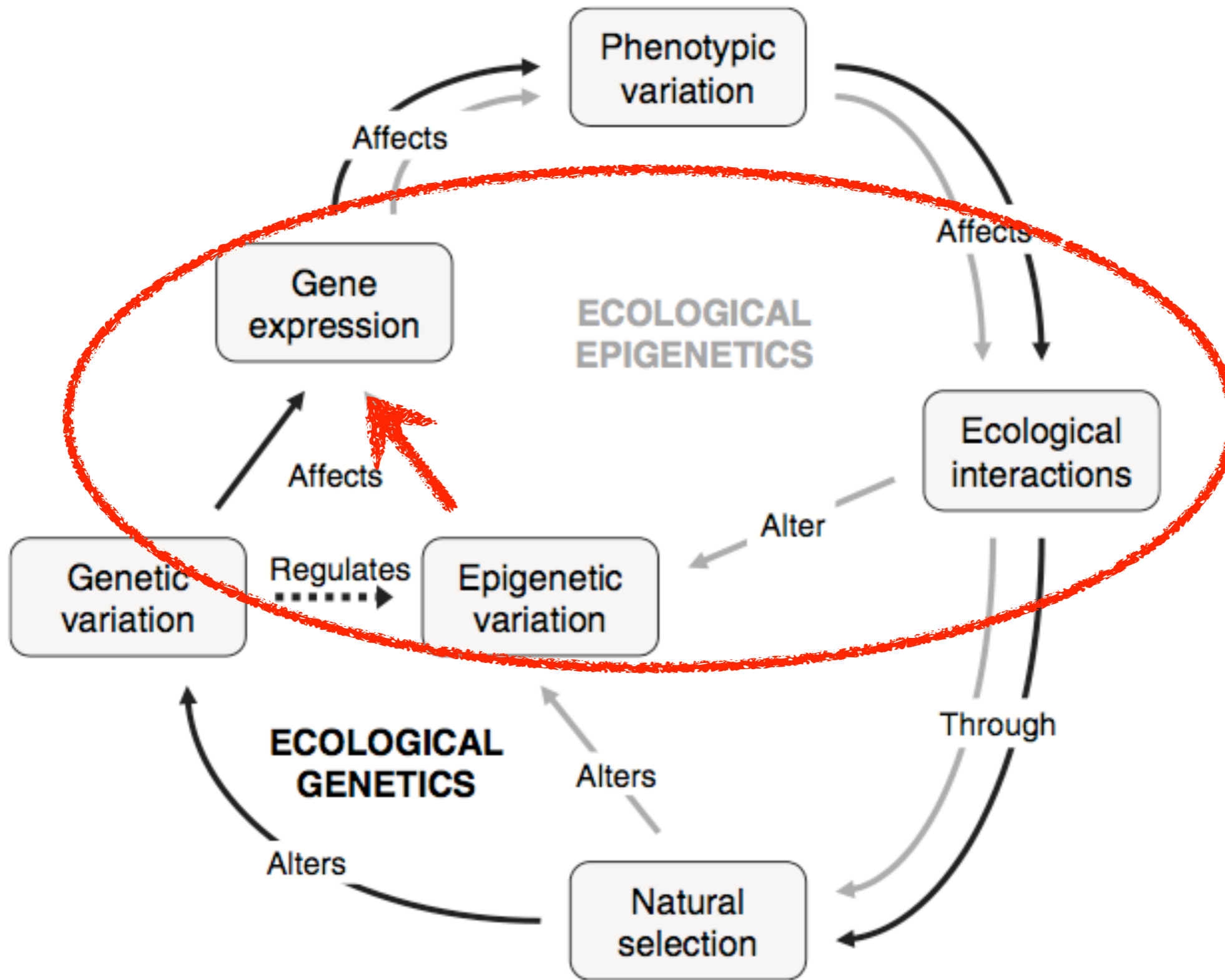


Proteome  
Transcriptome

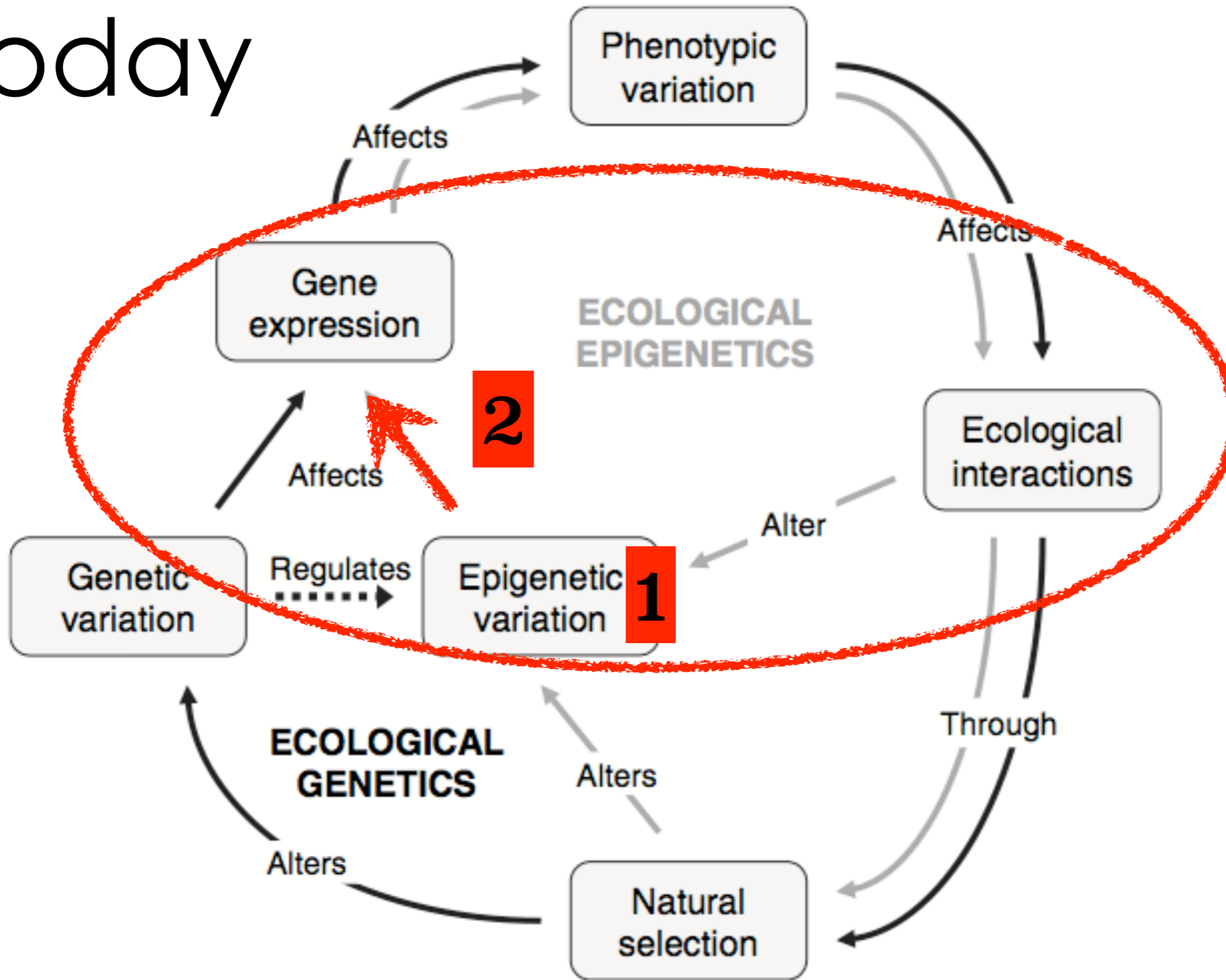








# Today



*Ecology Letters*, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

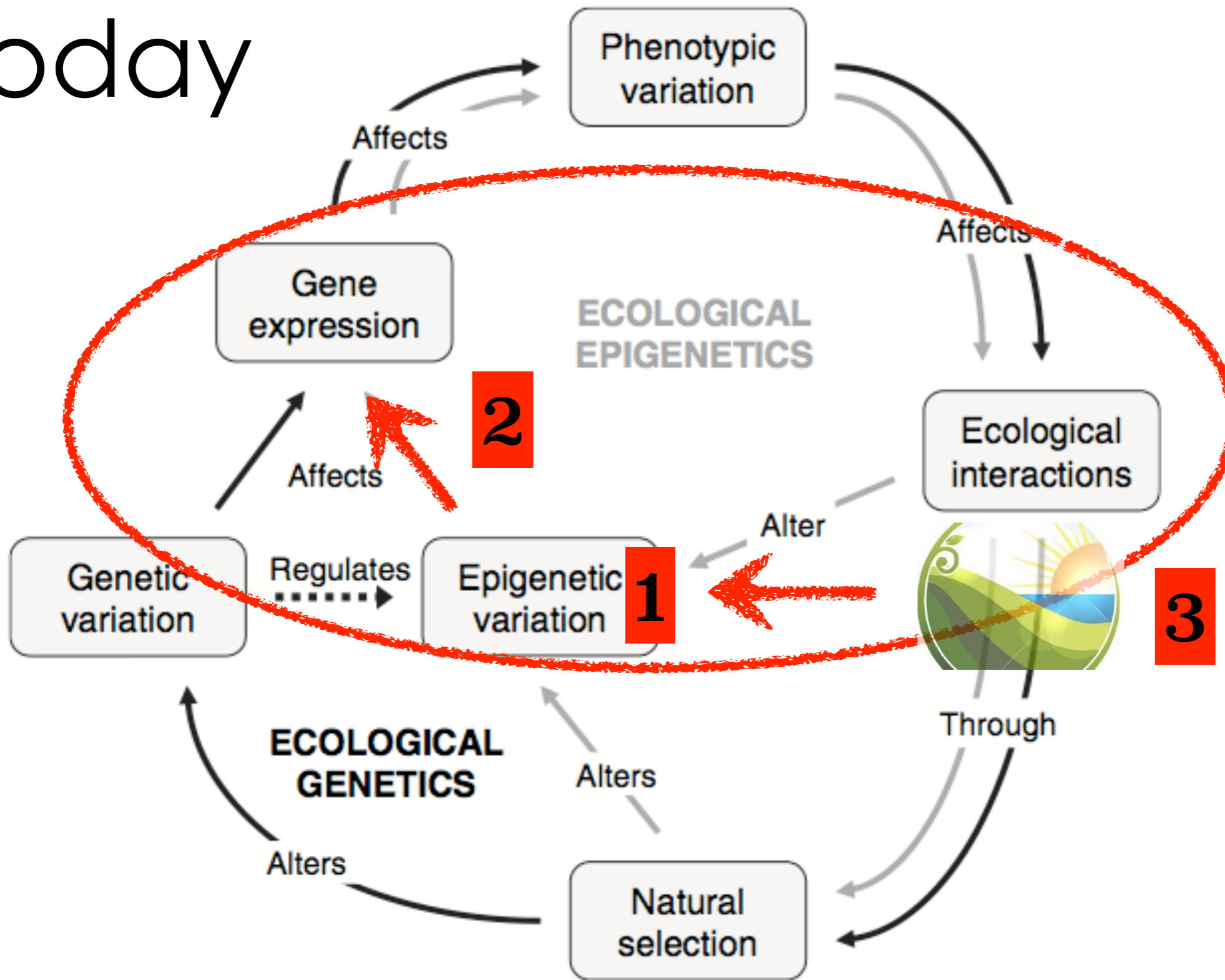
modified from

**IDEA AND  
PERSPECTIVE**

**Epigenetics for ecologists**

Oliver Bossdorf,<sup>1\*</sup> Christina L. Richards<sup>2</sup> and Massimo Pigliucci<sup>3</sup>

# Today



Ecology Letters, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

modified from

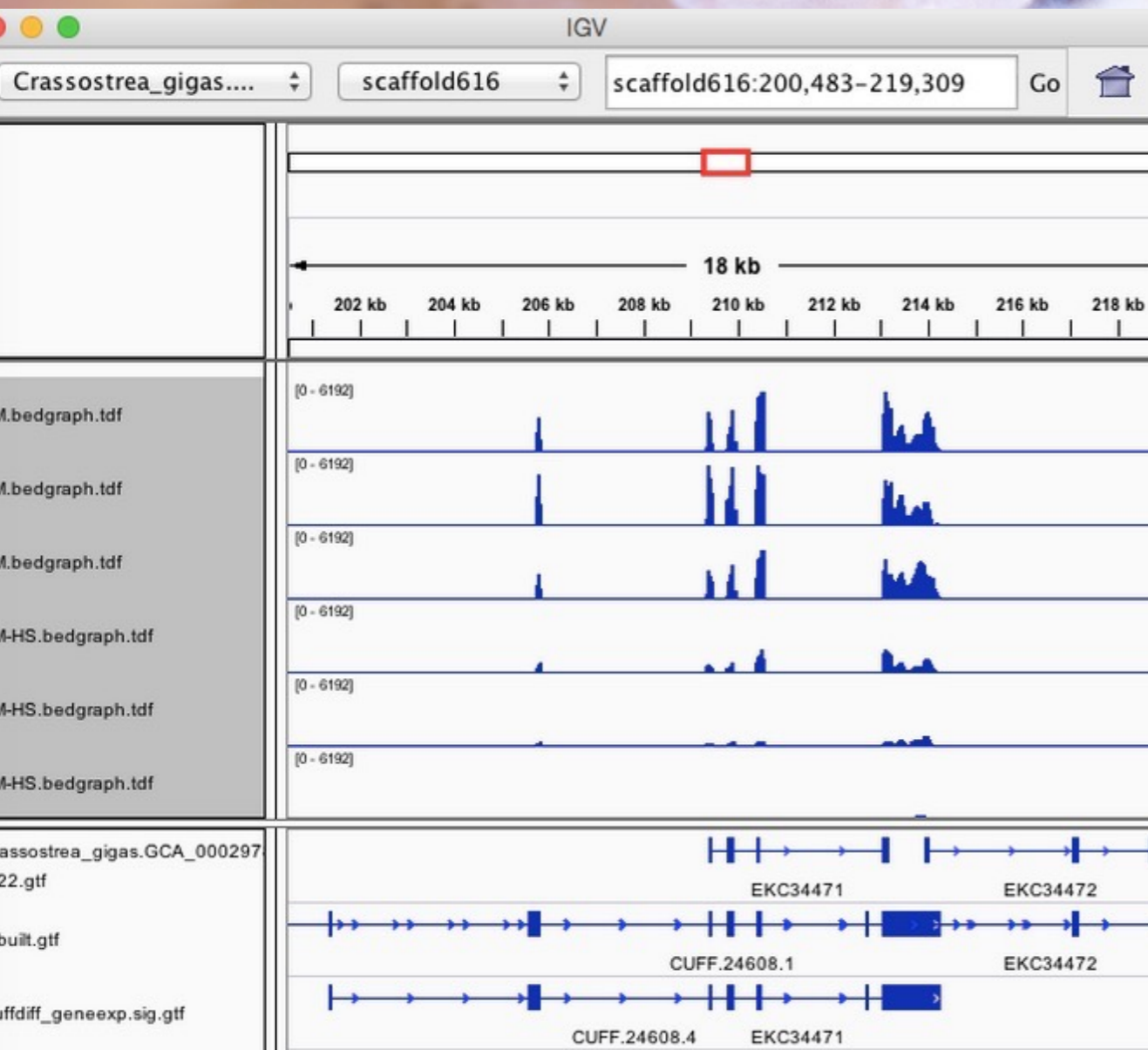
**IDEA AND  
PERSPECTIVE**

**Epigenetics for ecologists**

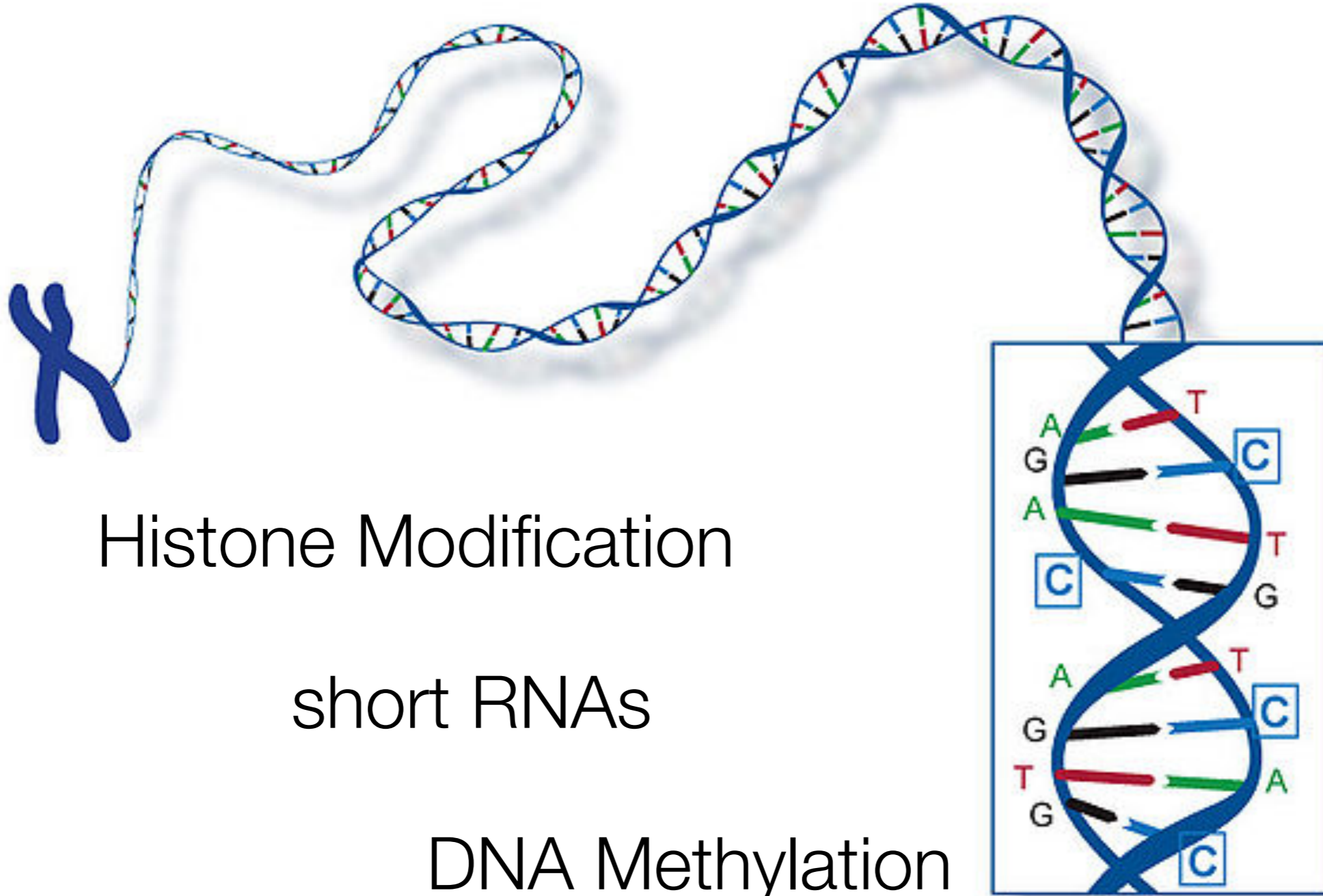
Oliver Bosdorf,<sup>1\*</sup> Christina L. Richards<sup>2</sup> and Massimo Pigliucci<sup>3</sup>



# Genome Resources



# Epigenetics



Histone Modification

short RNAs

DNA Methylation



# Epigenetics



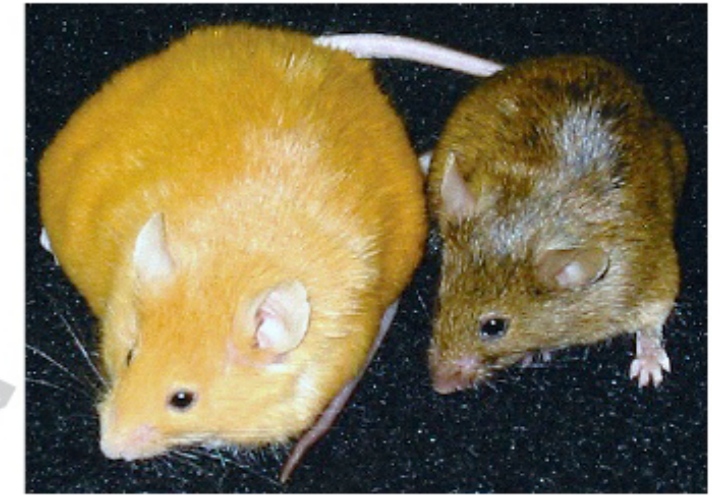
Photo credit: Flickr, Creative Commons, he-boden



**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

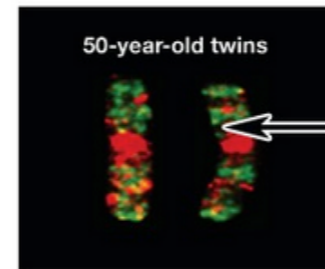
#### Chromosome 3 Pairs

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.

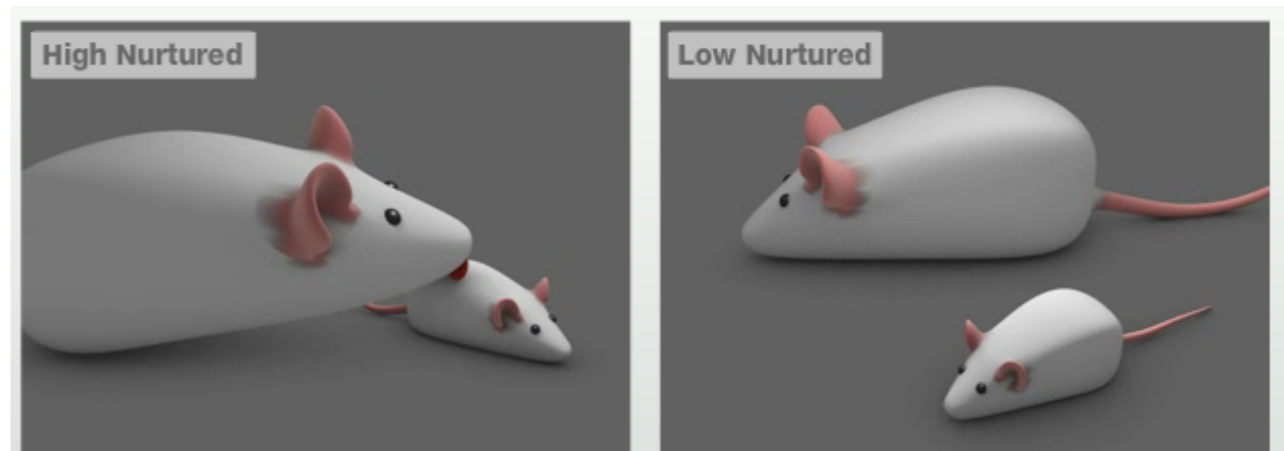
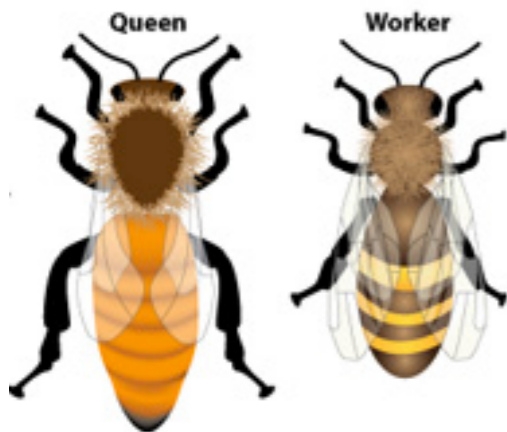


50-year-old twins

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

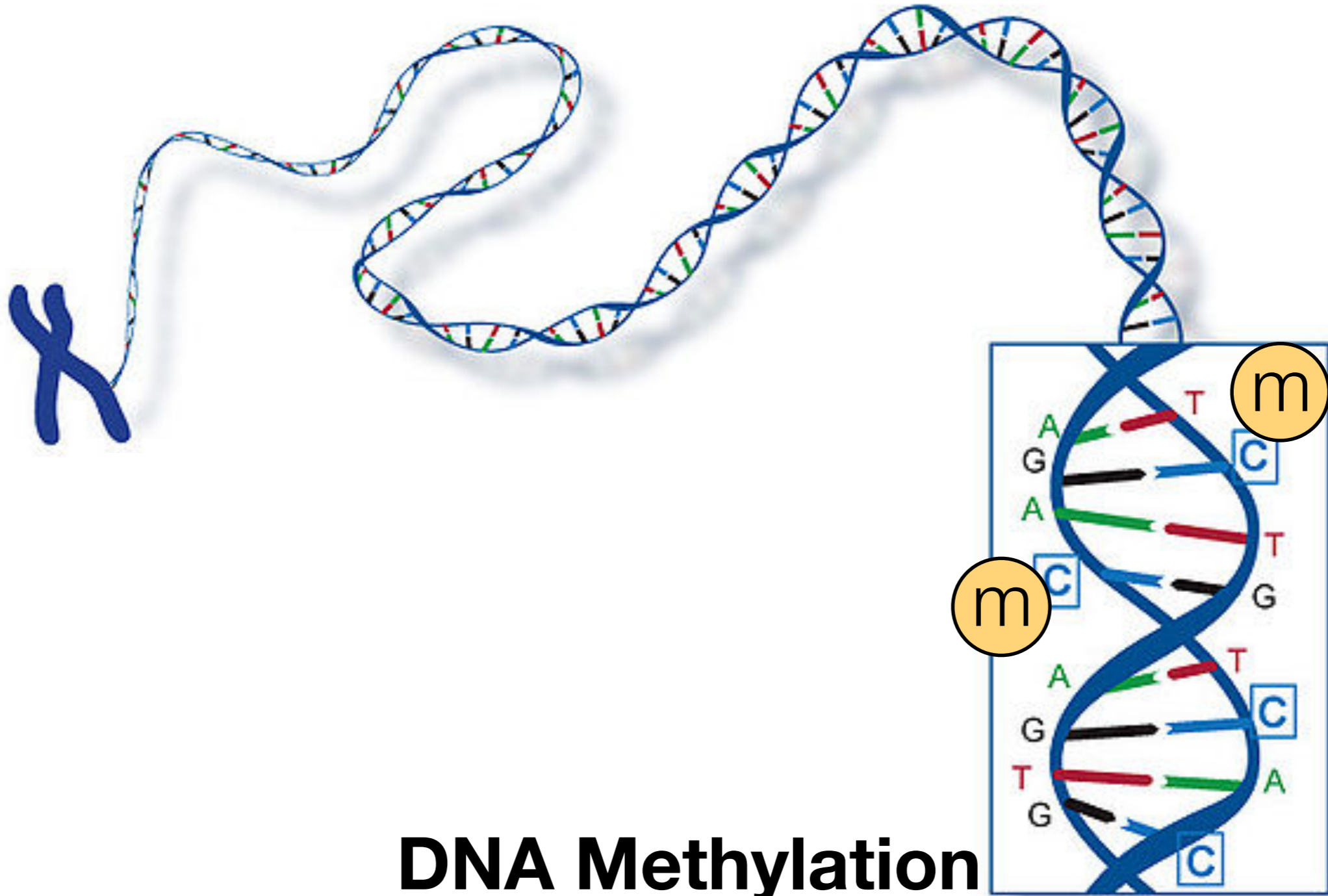


Queen Bee Larvae: Queens are raised in specially constructed cells called "queen cups," which are filled with royal jelly.



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




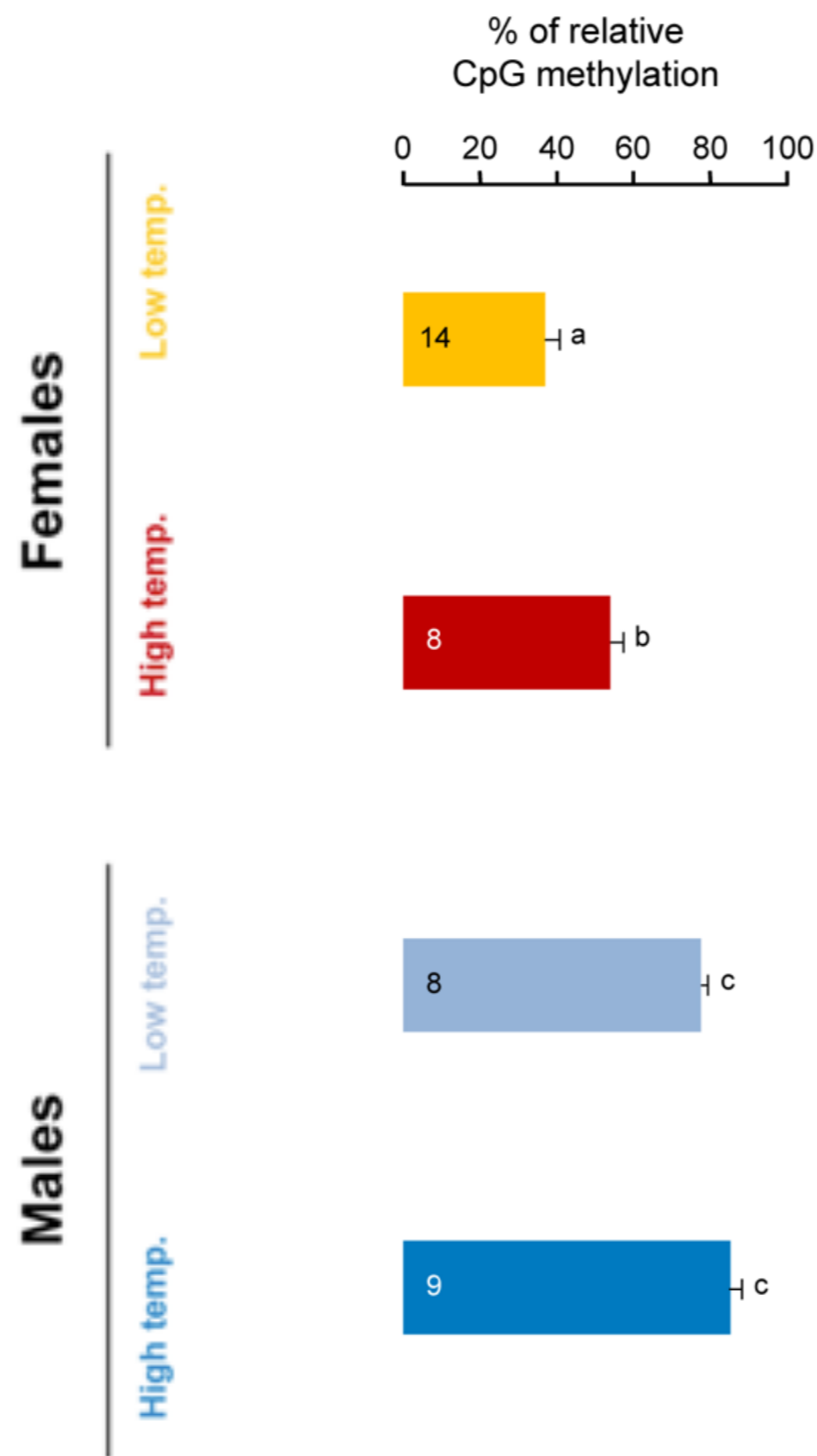


**DNA Methylation**

Mechanism?

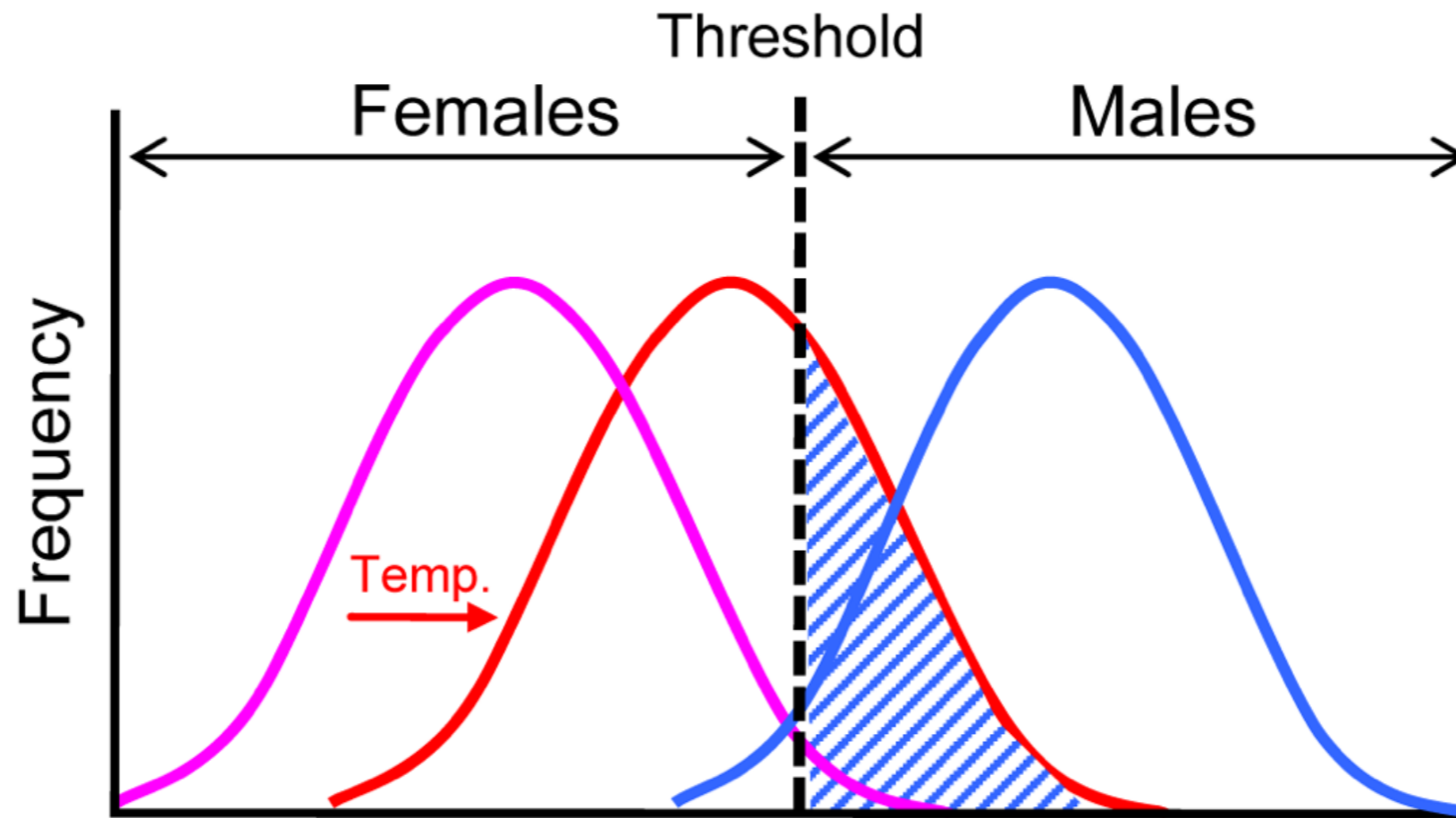
# DNA Methylation of the Gonadal Aromatase (*cyp19a*) Promoter Is Involved in Temperature-Dependent Sex Ratio Shifts in the European Sea Bass

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



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

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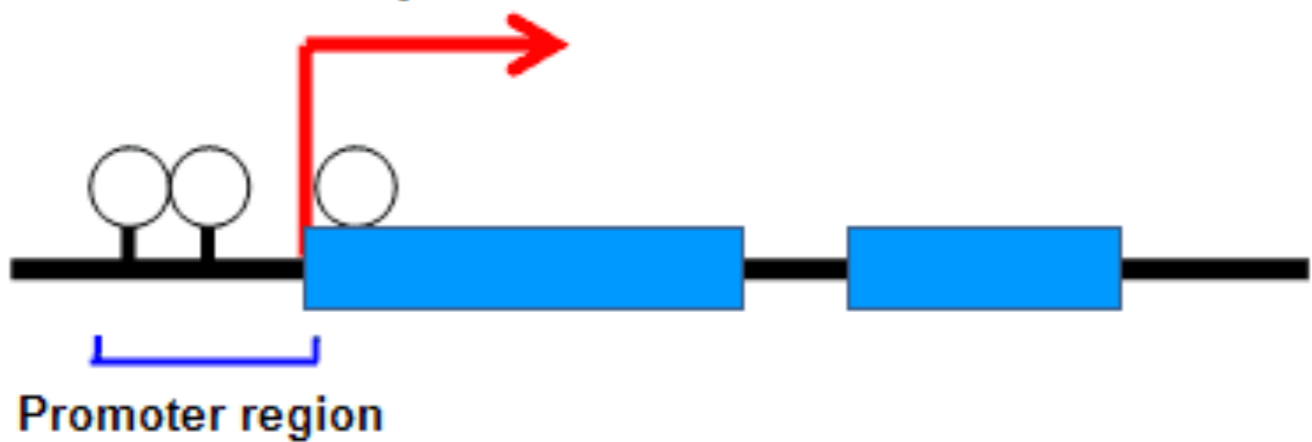
*cyp19a* promoter methylation level

- Low temperature females
- High temperature females
- Males



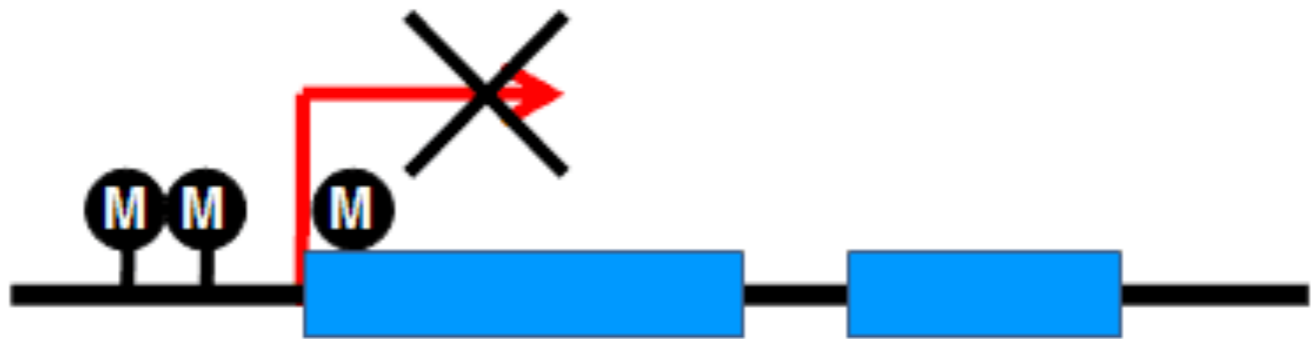
**Genes that can be expressed**

Low temp.



**Genes inactivated by DNA methylation**

High temp.



- M** Methylated
- Unmethylated

Non-  
Vertebrates?

The image displays a complex genomic visualization. At the top, a horizontal axis is marked with numerical values from 1,000 to 10,000. Below this, several tracks are visible: a track with orange and green bars, a track with a red bar and a green bar, a track with orange arrows, a track with purple and green bars, and a track with blue and white characters. A large, semi-transparent grey hand icon is positioned in the upper left quadrant, pointing towards the genomic data. The text 'Non-Vertebrates?' is overlaid in the center in a large, black, sans-serif font. At the bottom, a red rectangular box contains the text 'landscape and function is very different than what is observed in vertebrates' in a black, sans-serif font.

# Non-Vertebrates?

landscape and function is very different than what is observed in vertebrates

The background of the slide is a complex genomic visualization. At the top, there are several tracks showing gene models with orange and green boxes. Below these are tracks with colored bars (green, red, yellow) and a track with orange arrows. A large, semi-transparent grey hand icon is positioned in the upper left. In the lower left, there is a semi-transparent image of a mouse. The central text 'Non-Vertebrates?' is overlaid on these tracks. At the bottom, a green box contains text.

# Non-Vertebrates?

landscape and function is very different than what is observed in vertebrates

The background features a complex genomic visualization. At the top, a horizontal axis is marked with values from 1,000 to 10,000. Below this, several tracks are visible: a track with orange and green bars, a track with a red bar and a green bar, a track with orange arrows, a track with purple and green bars, and a track with blue and white text. A vertical line is drawn at the 3,754 position. Two semi-transparent images of animals are overlaid: a grey seal at the top and a yellow lizard at the bottom. The text 'Non-Vertebrates?' is centered over the tracks.

# Non-Vertebrates?

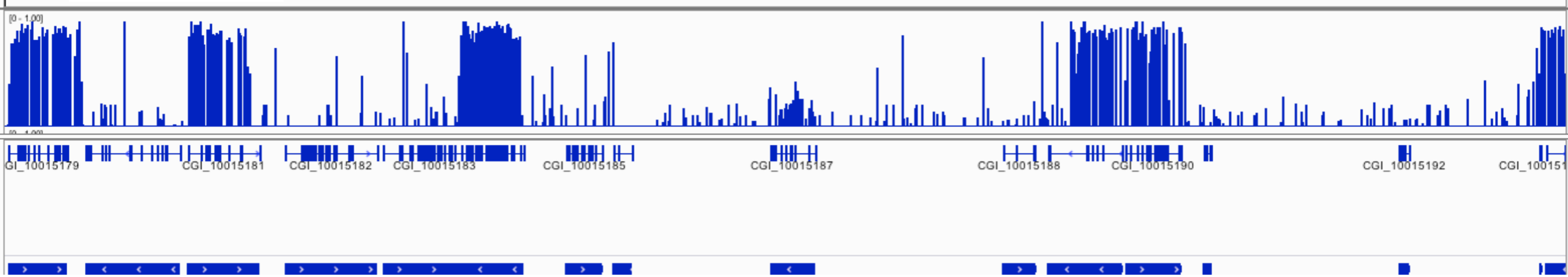
landscape and function is very different than what is observed in vertebrates

*Absent* in  
several  
model  
organisms

Oysters?



Epigenetic variation **1**



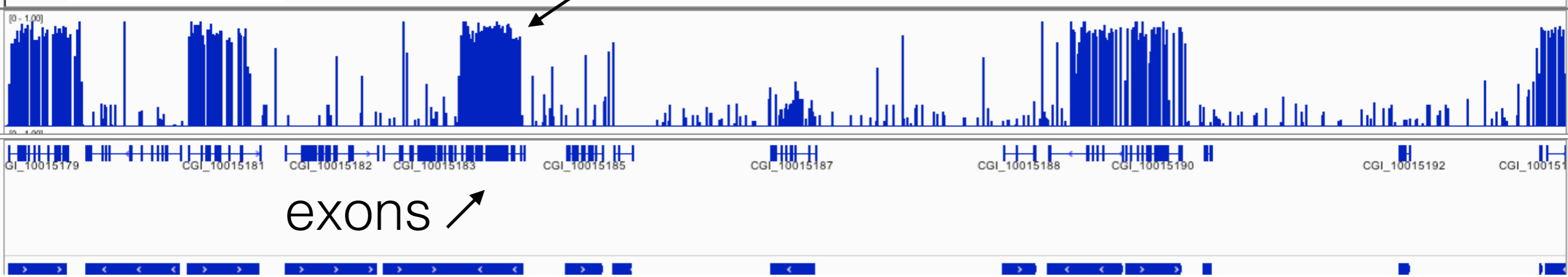
*mosaic*

associated with gene bodies



Epigenetic variation **1**

DNA methylation level (0-100%) @ cytosines



exons ↗

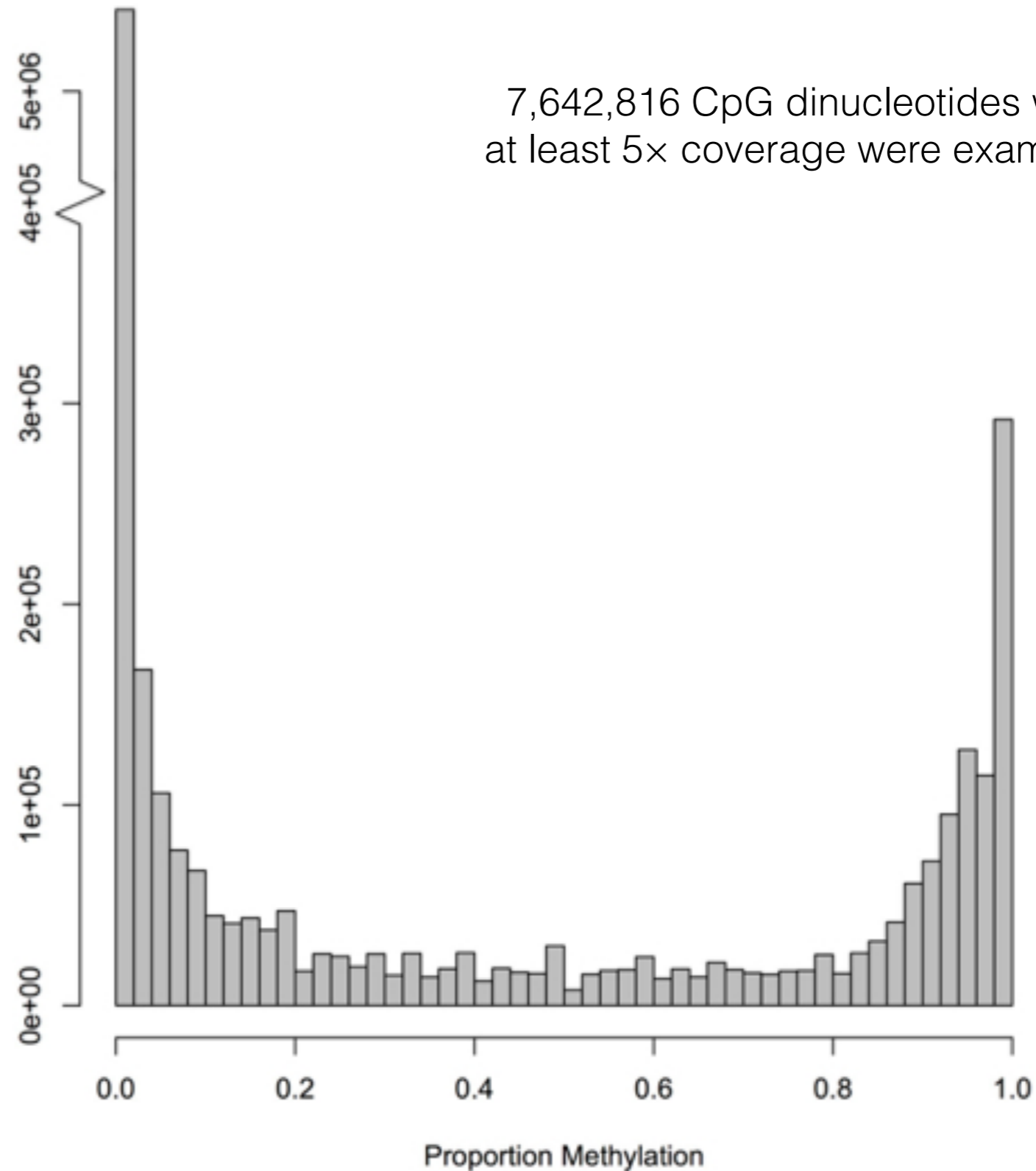
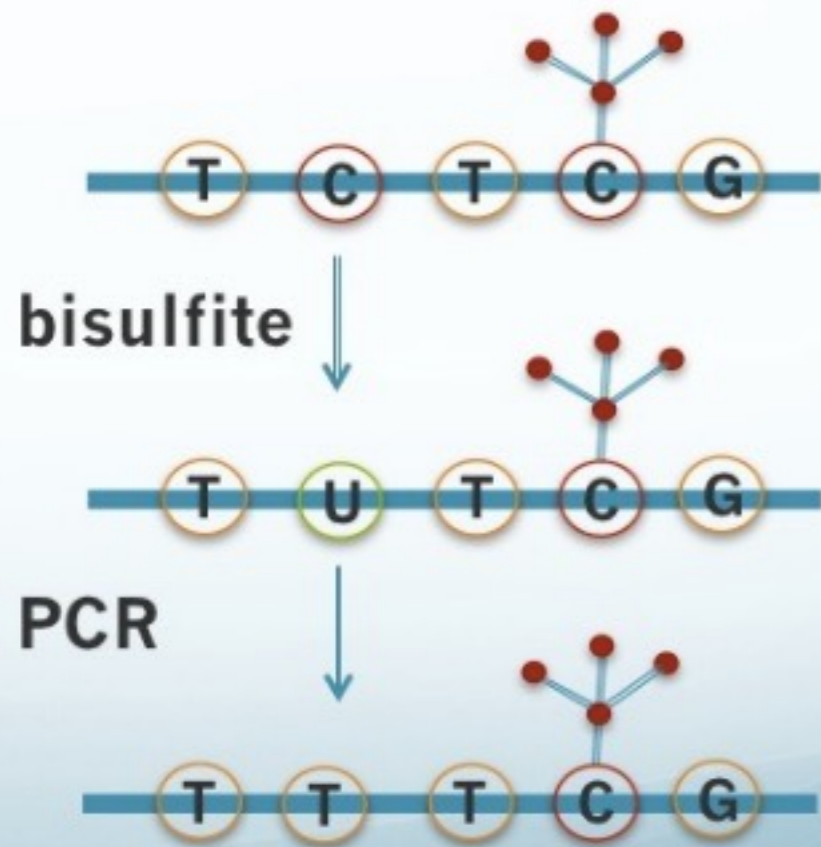
gene ↗

*mosaic*

associated with gene bodies

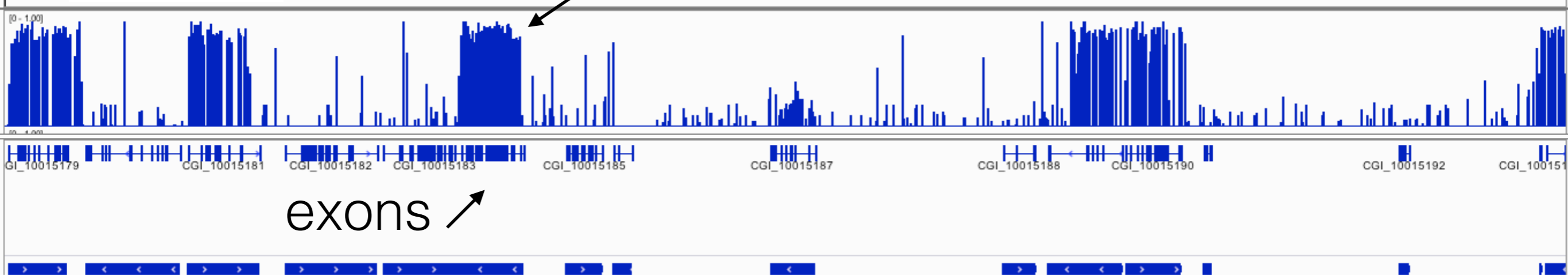
Epigenetic variation **1**

- Bisulfite conversion



Epigenetic variation **1**

DNA methylation level (0-100%) @ cytosines



exons ↗

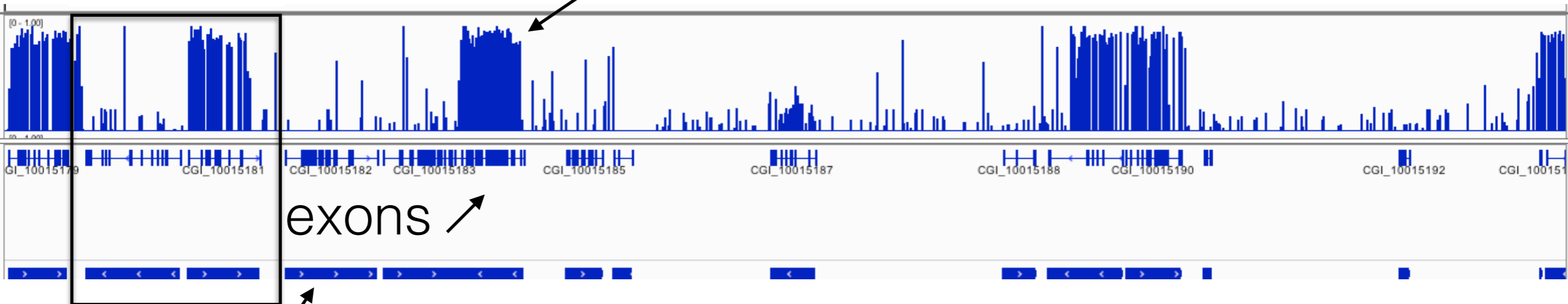
gene ↗

*mosaic*

associated with gene bodies

DNA methylation level (0-100%) @ cytosines

Epigenetic variation **1**



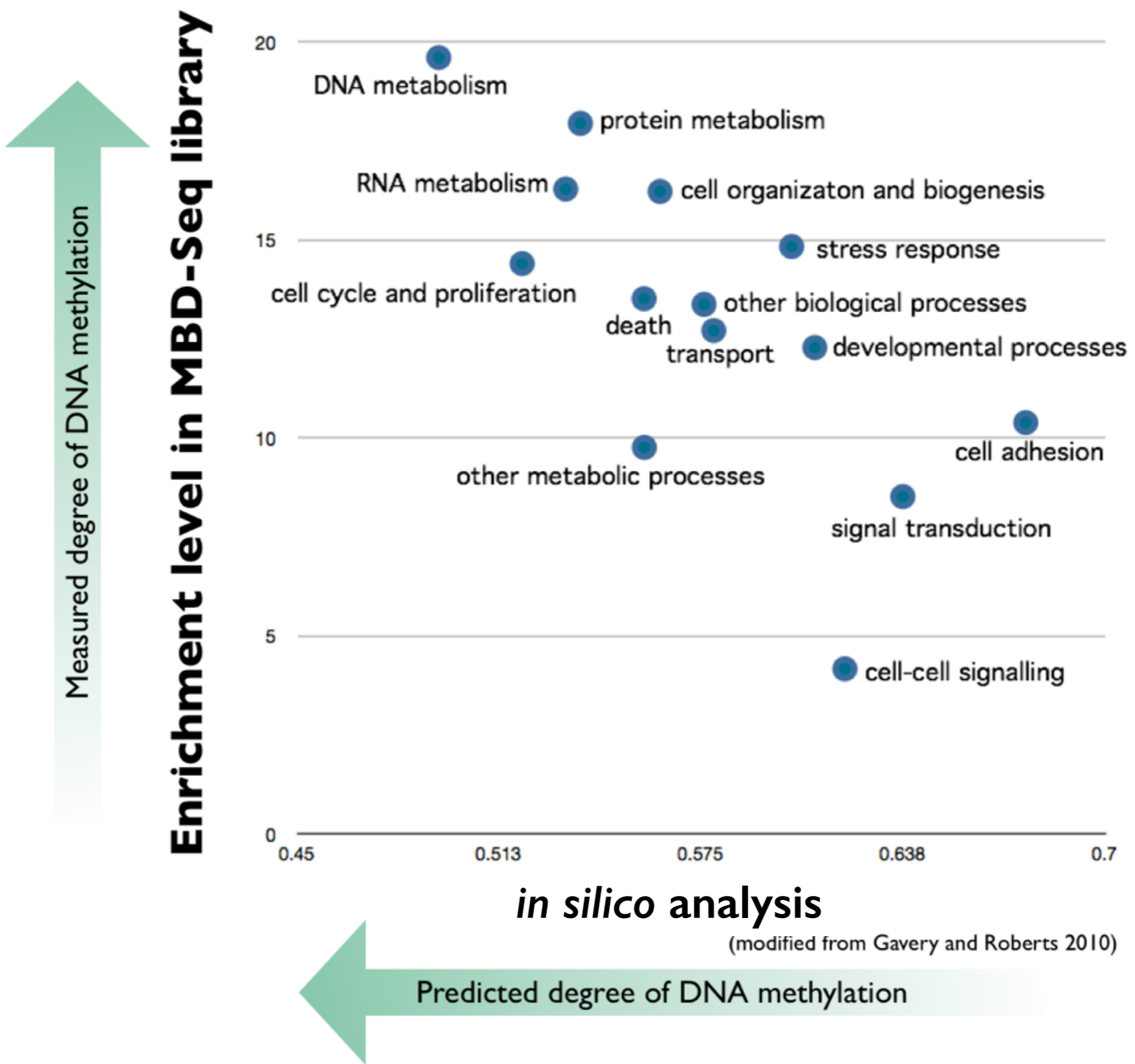
gene

exons

*mosaic*

**Why are only a subset of genes methylated?**

associated with gene bodies

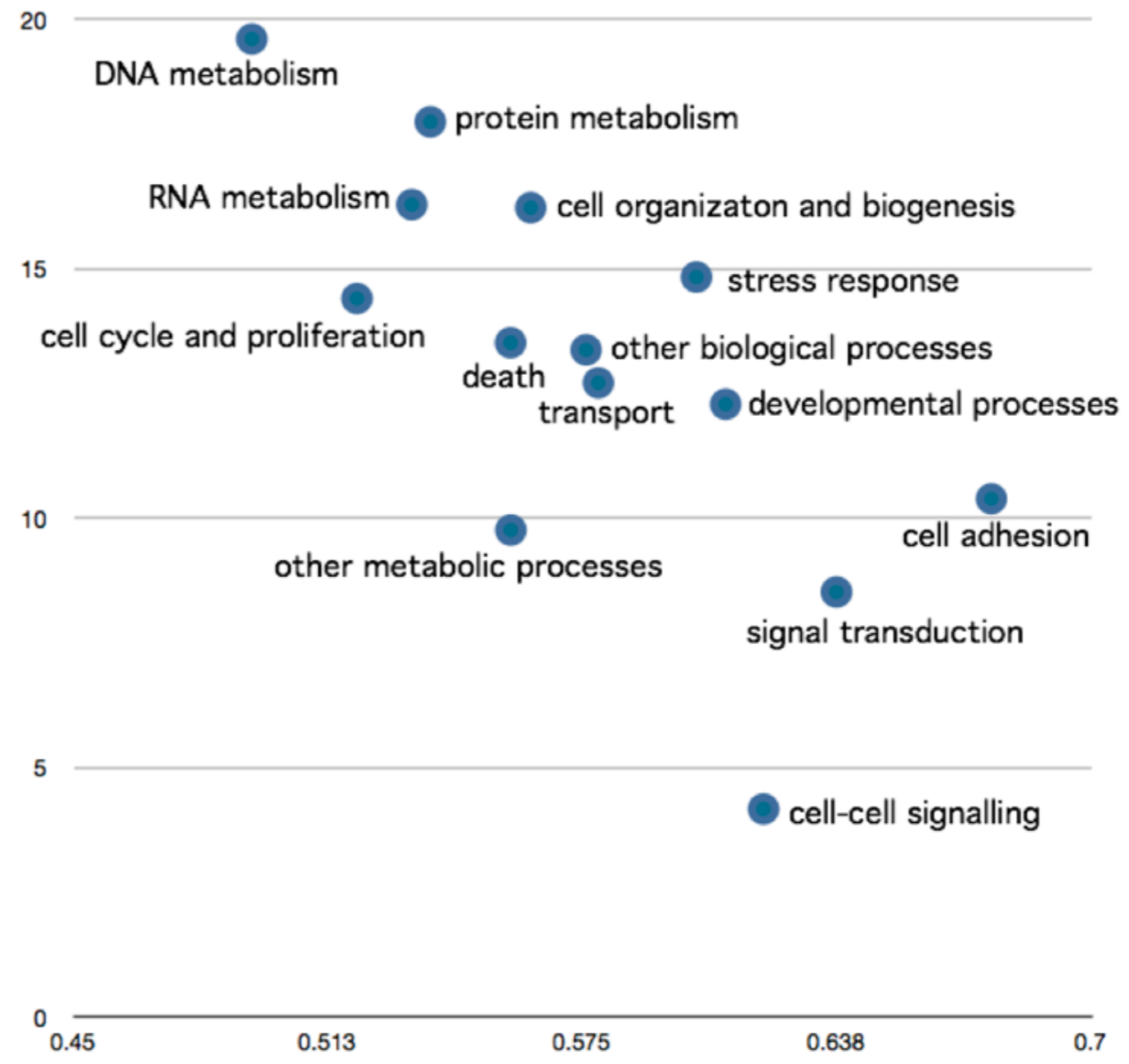
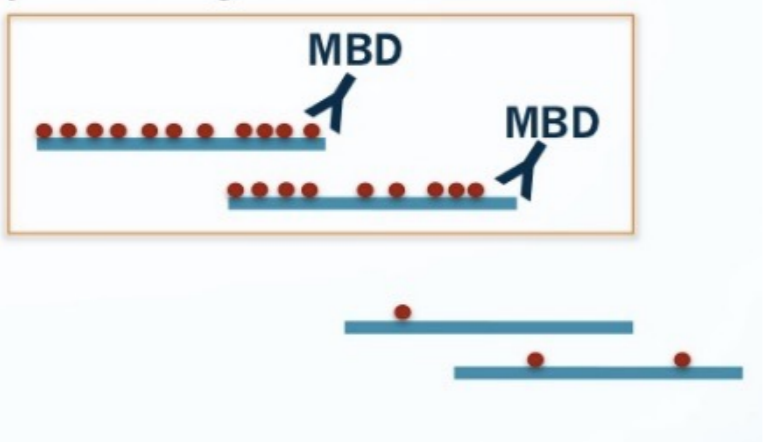


(modified from Gavery and Roberts 2010)

Epigenetic variation **1**

Measured degree of DNA methylation

Enrichment level in MBD-Seq library

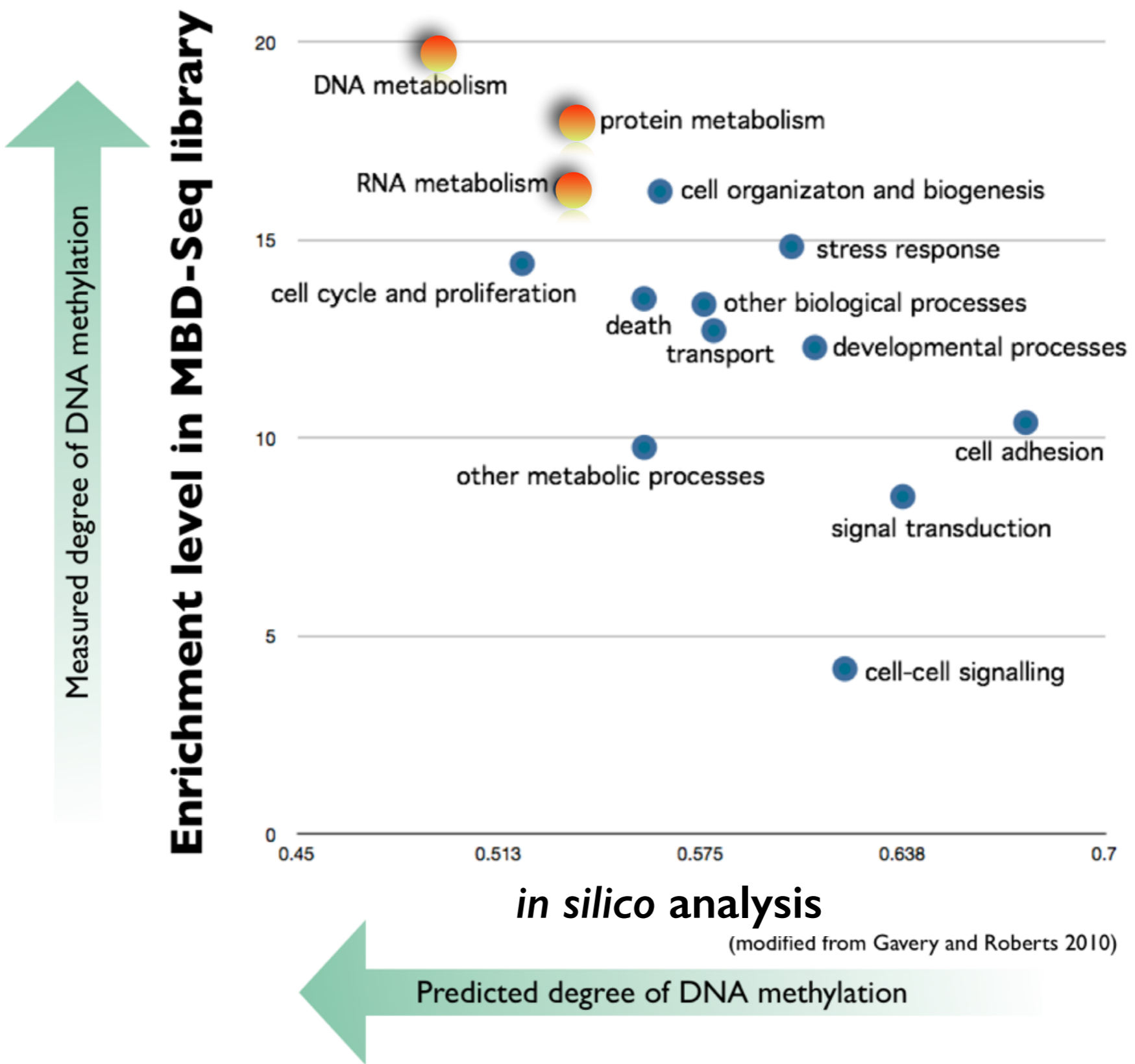


*in silico analysis*

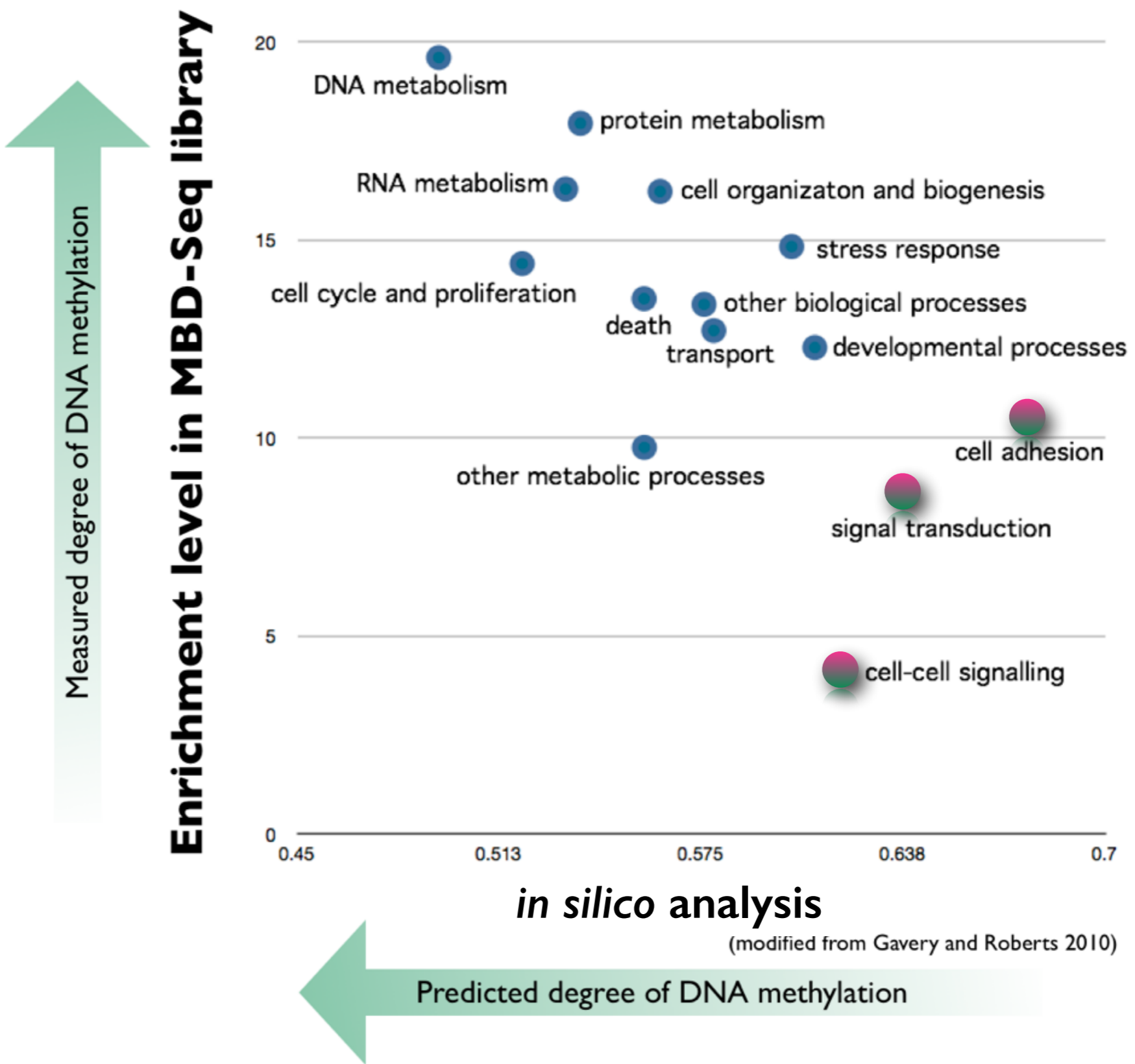
(modified from Gavery and Roberts 2010)

Predicted degree of DNA methylation

Epigenetic variation **1**



(modified from Gavery and Roberts 2010)



(modified from Gavery and Roberts 2010)



Jay Dimond

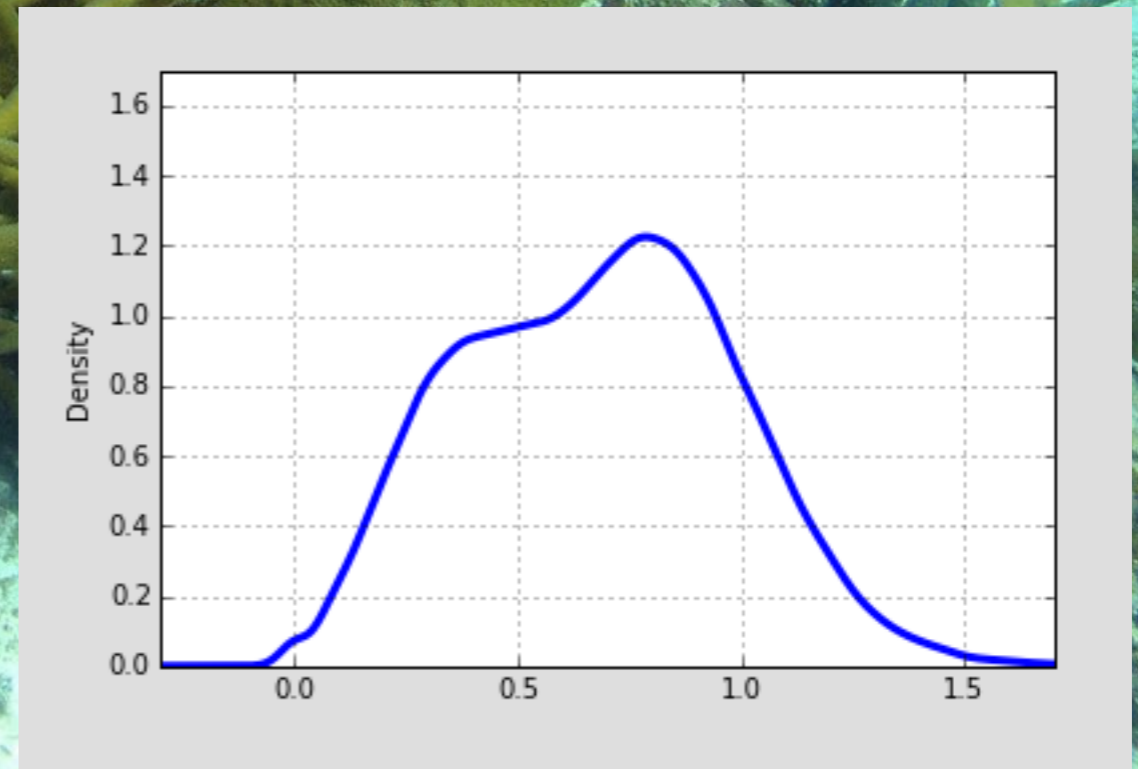
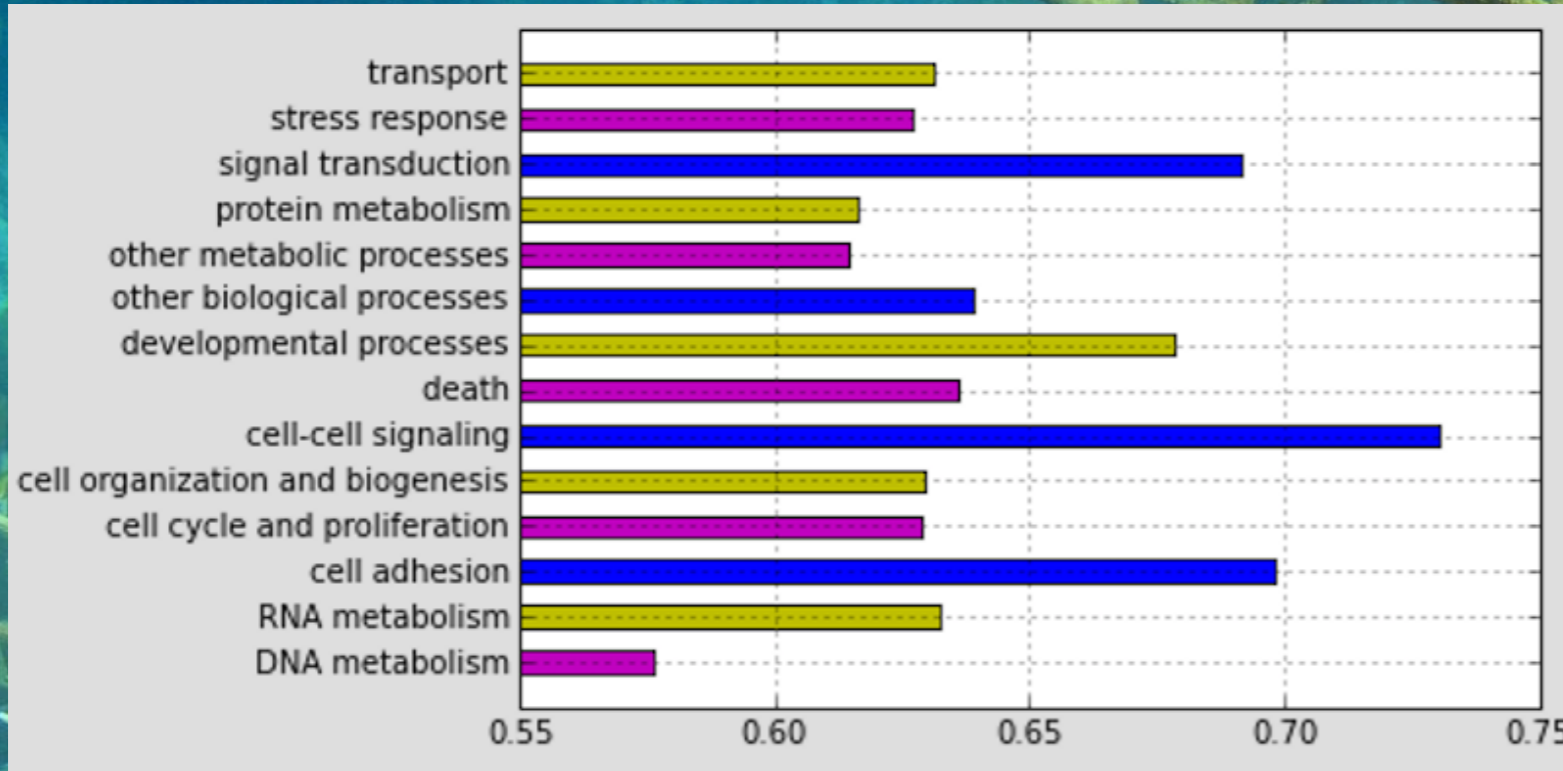
*Acropora palmata*

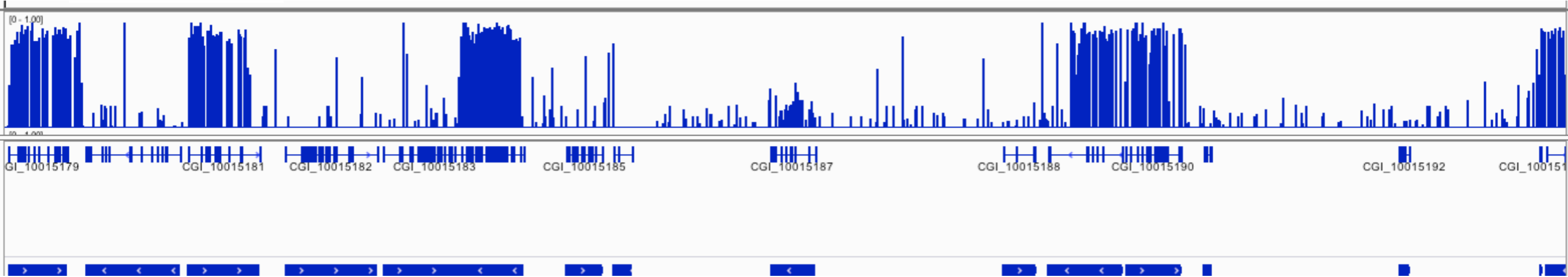
*Acropora cervicornis*



Jay Dimond

*Acropora palmata*





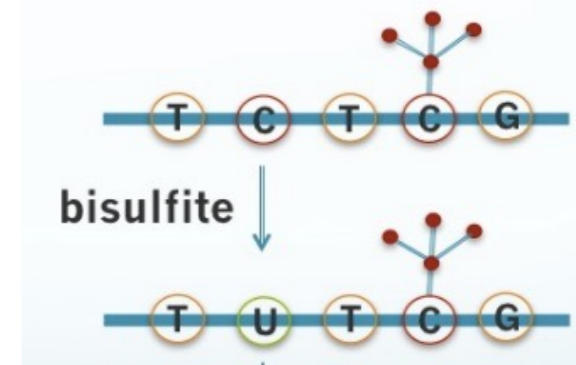
*mosaic*

associated with gene bodies  
based on gene function

*explanation?*

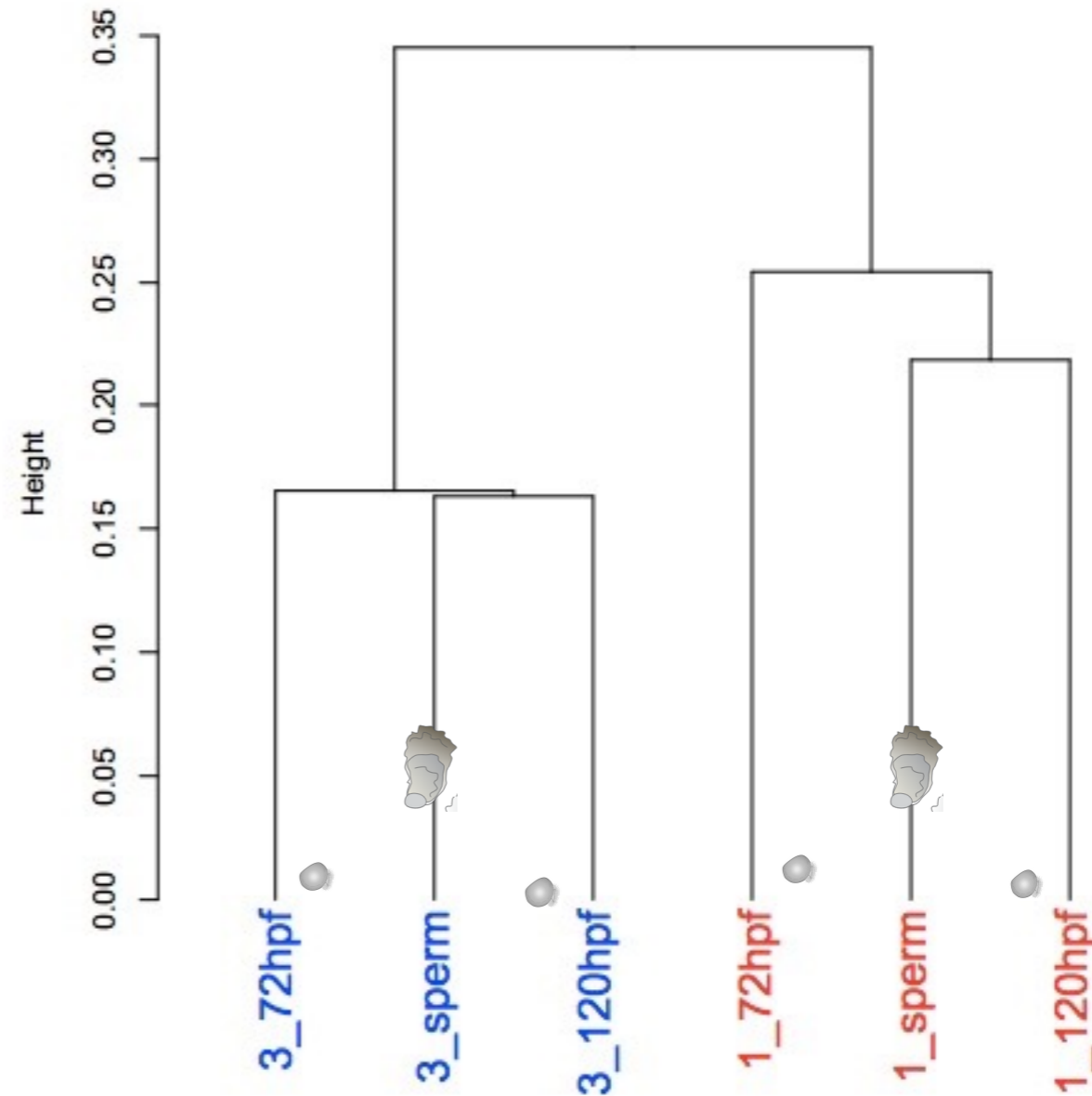
Epigenetic variation **1**

# Family and Developmental Variation



## Sperm & Larvae (72h & 120h)

CpG methylation clustering



bioRxiv  
beta  
THE PREPRINT SERVER FOR BIOLOGY

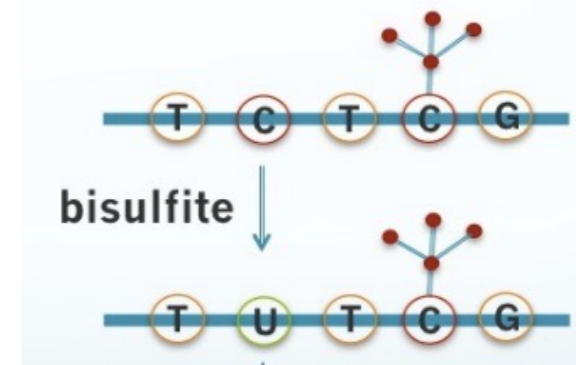
New Results

Indication of family-specific DNA methylation patterns in developing oysters

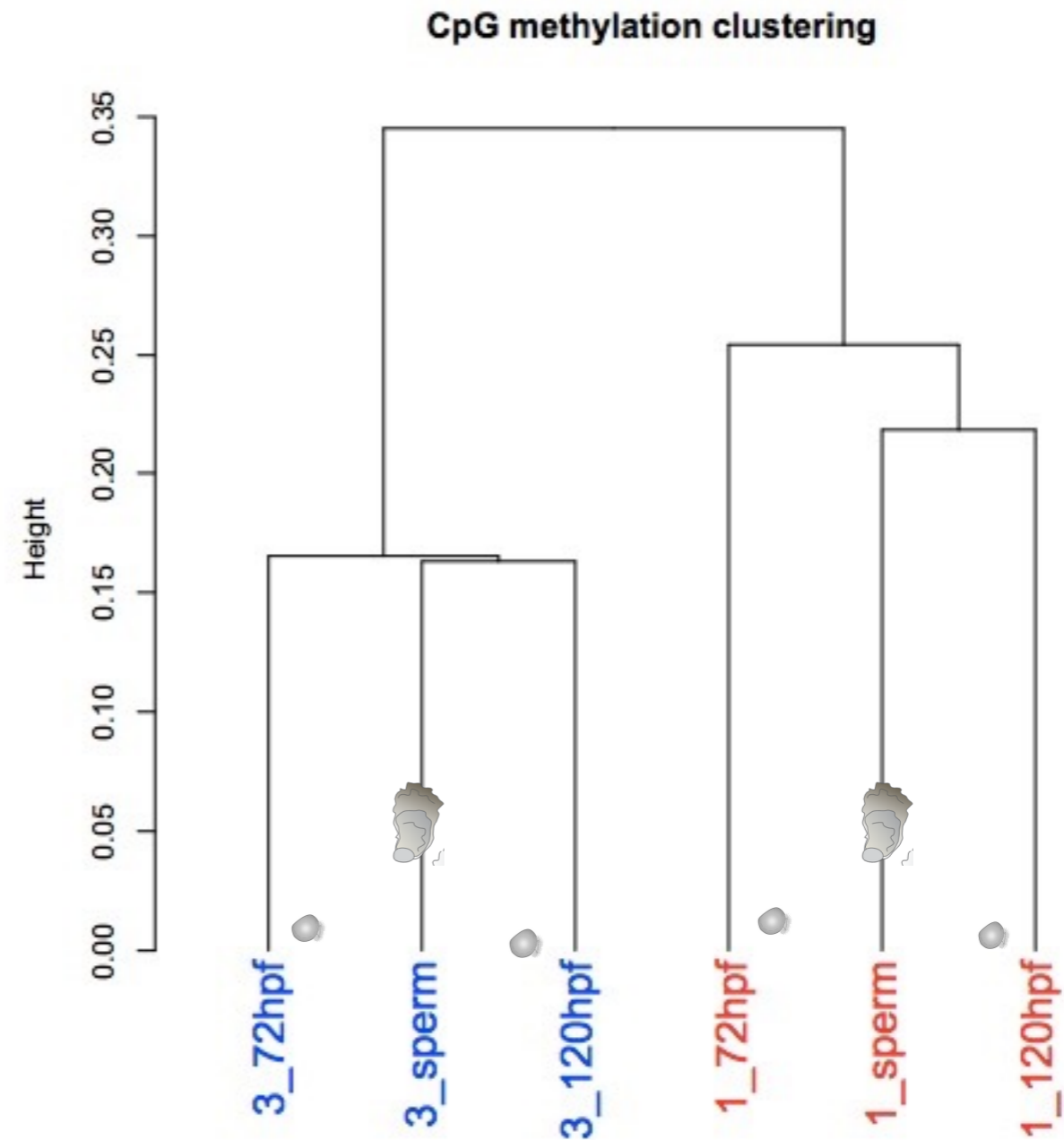
Claire E. Olson , Steven B. Roberts

doi: <http://dx.doi.org/10.1101/012831>

# Family and Developmental Variation

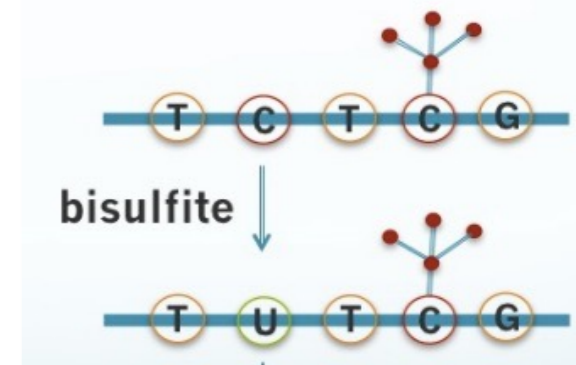


## Inheritance



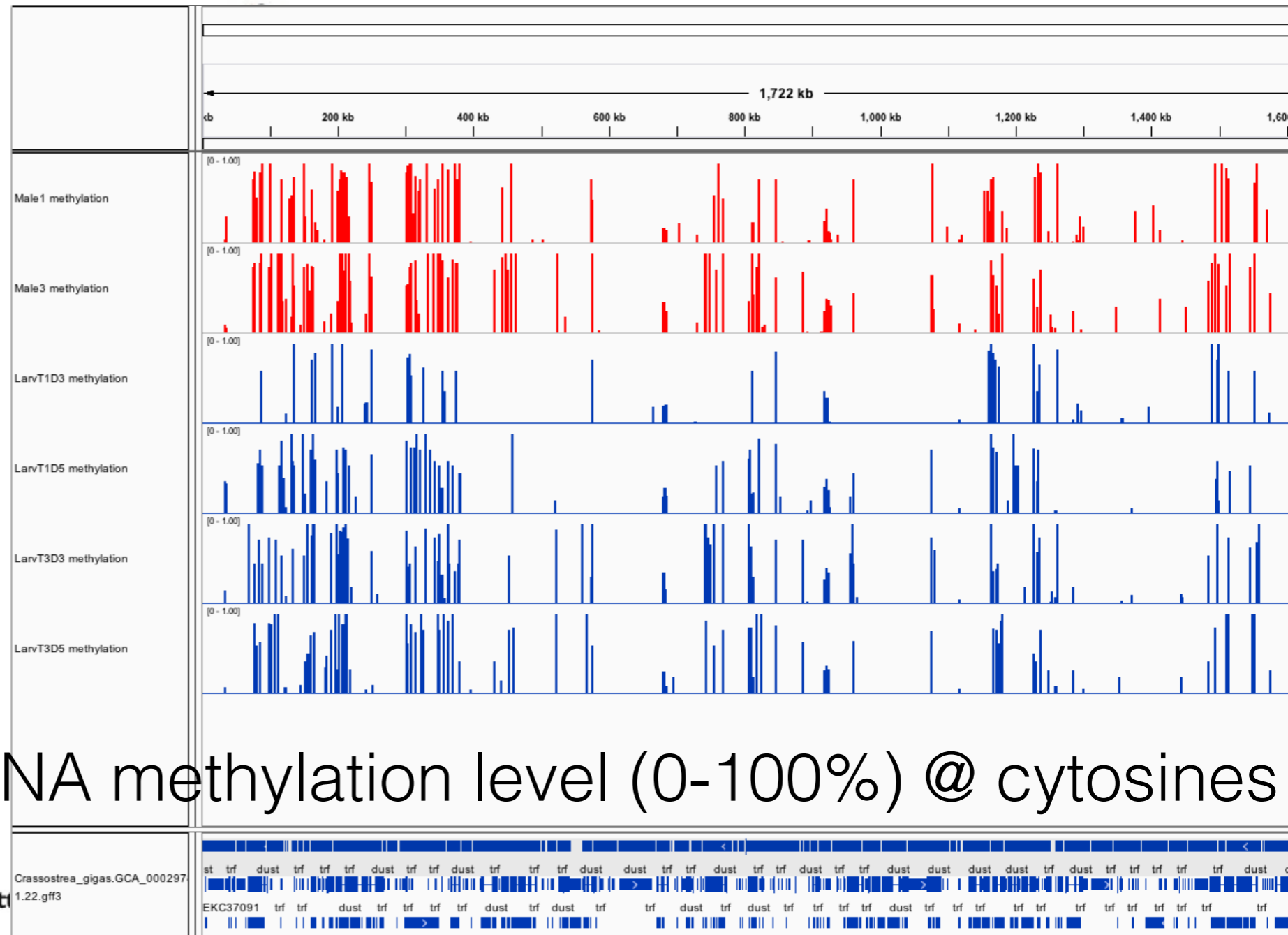
Epigenetic variation **1**

# Family and Developmental Variation



CpG methylation clustering

## Sperm & Larvae (72h & 120h)



bioRxiv beta  
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DNA methylation level (0-100%) @ cytosines

New Results

Indication of family-specific DNA methylation patterns in developing oysters

Claire E. Olson, Steven B. Roberts

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# 1 Summary

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

Gene  
expression



2

Epigenetic  
variation

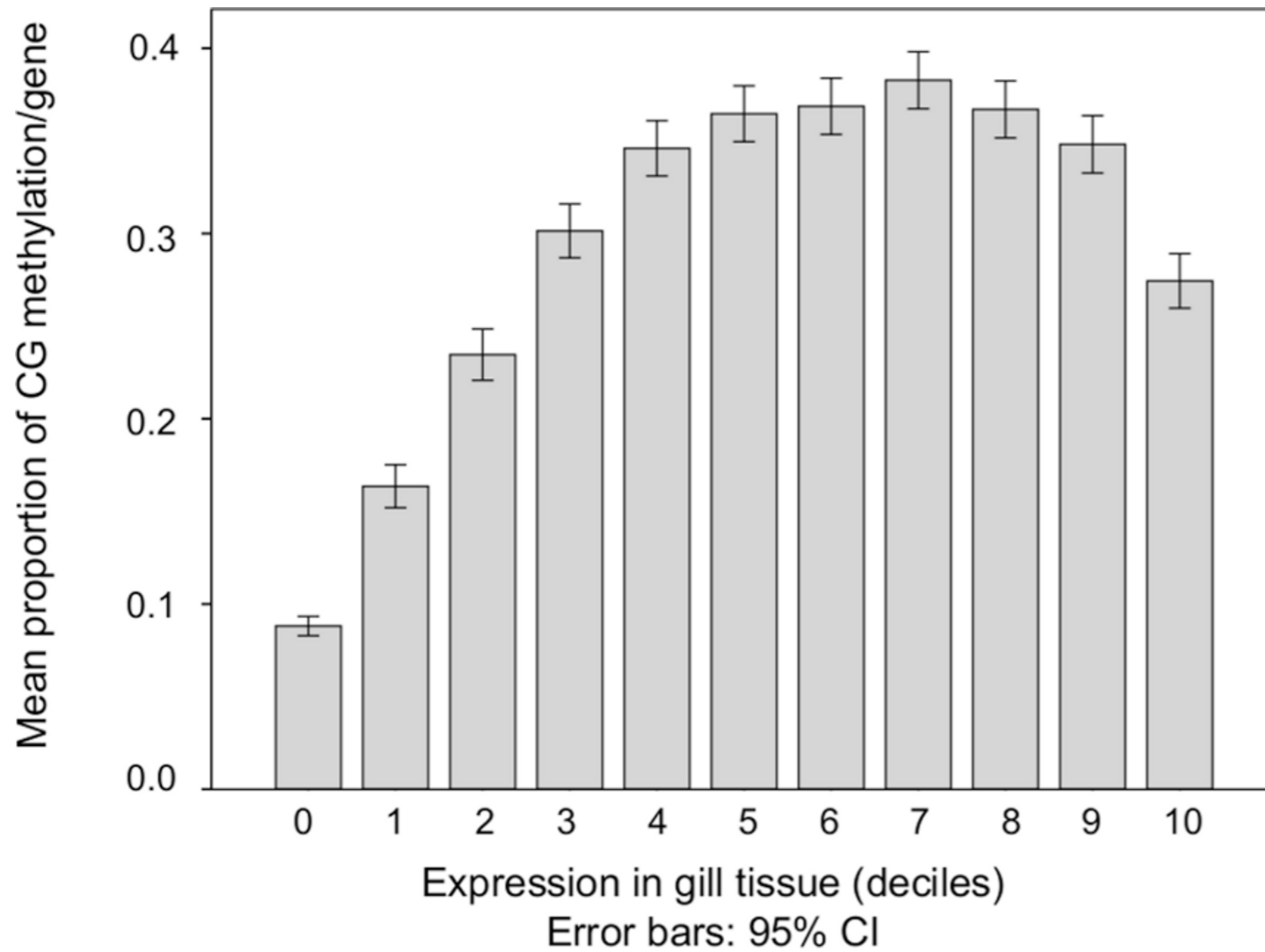
# Function?



Gene  
expression

2

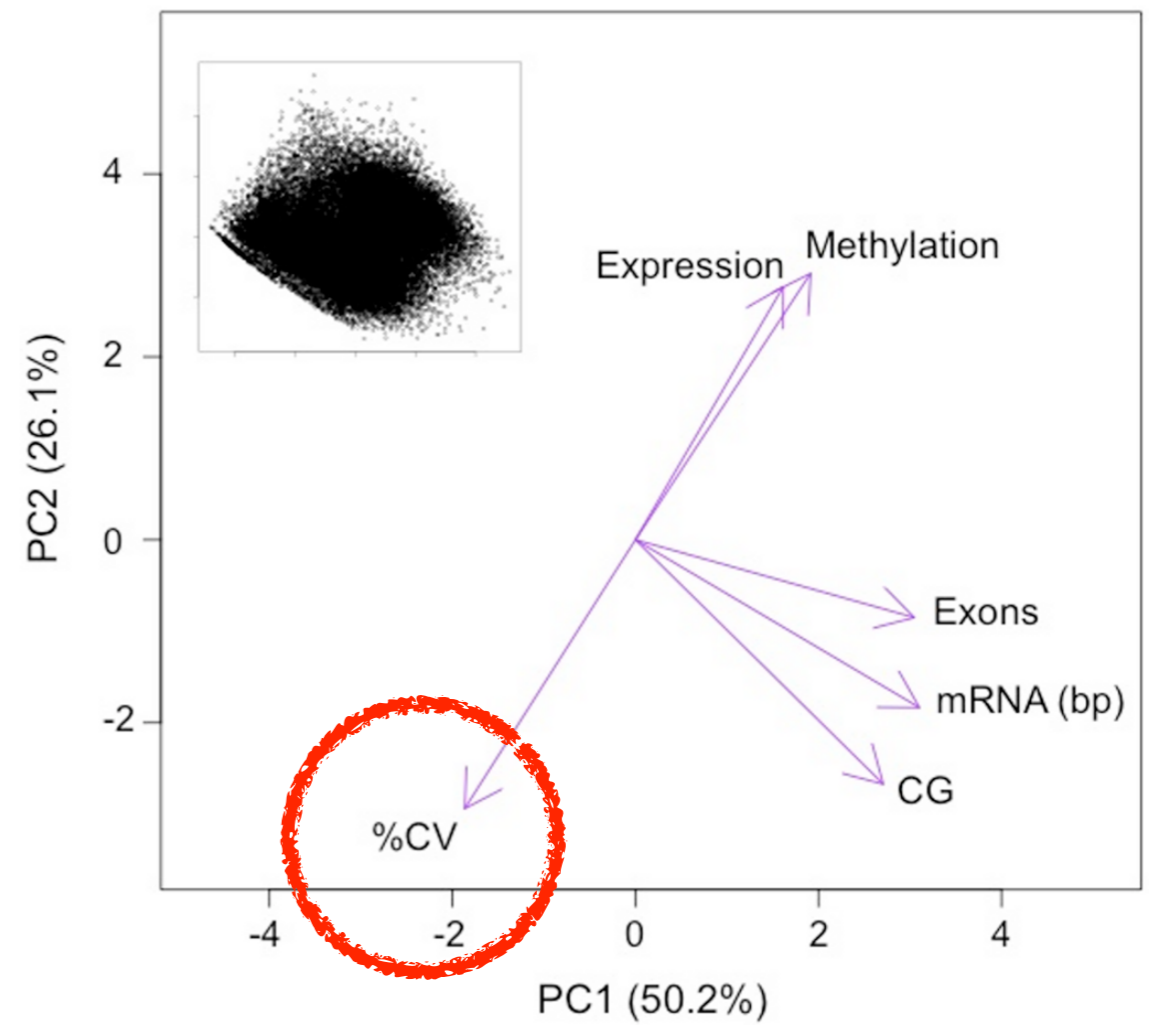
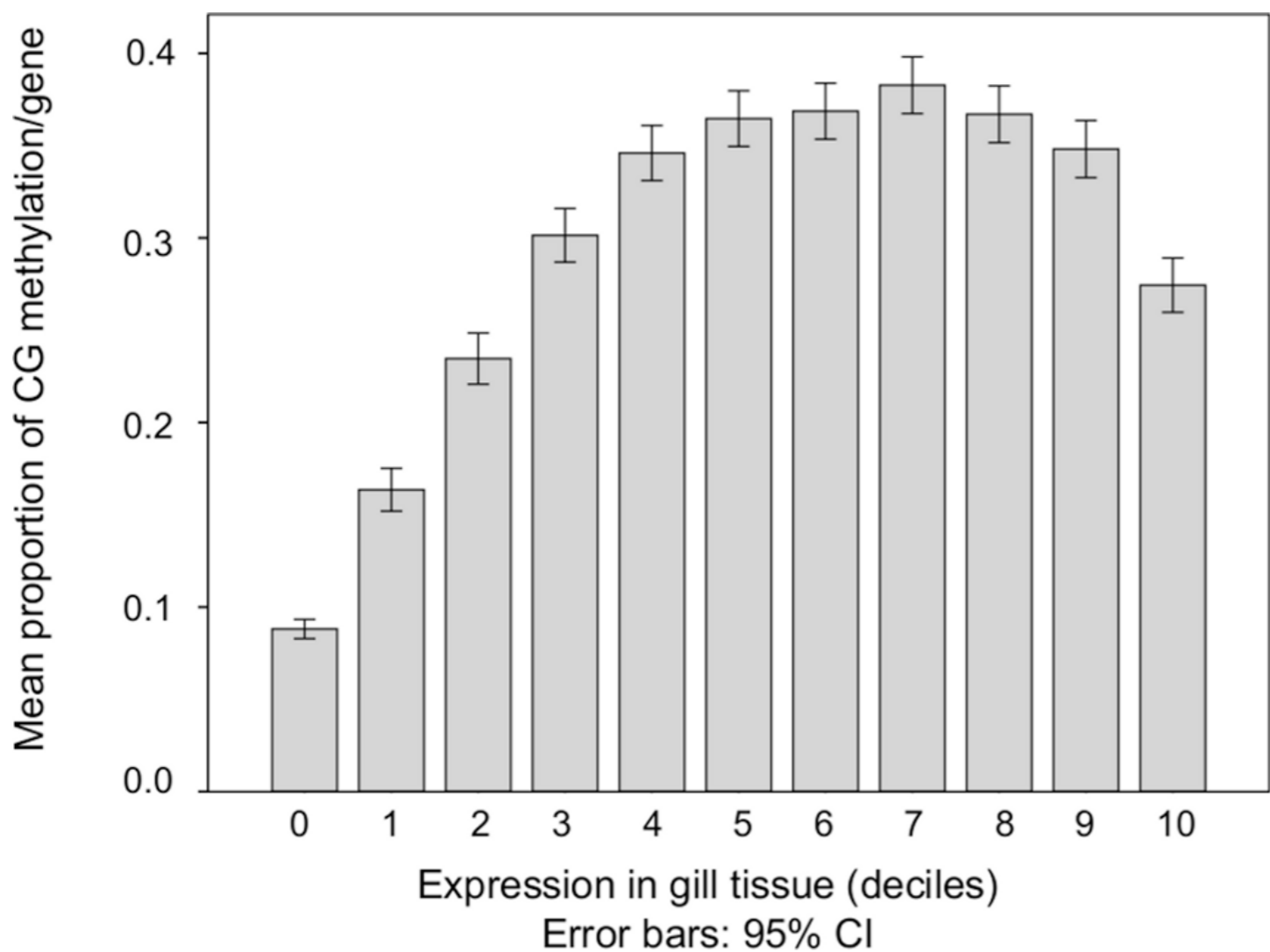
Epigenetic  
variation



Gene expression

2

Epigenetic variation



### Predominant intragenic methylation is associated with gene expression characteristics in a bivalve mollusc

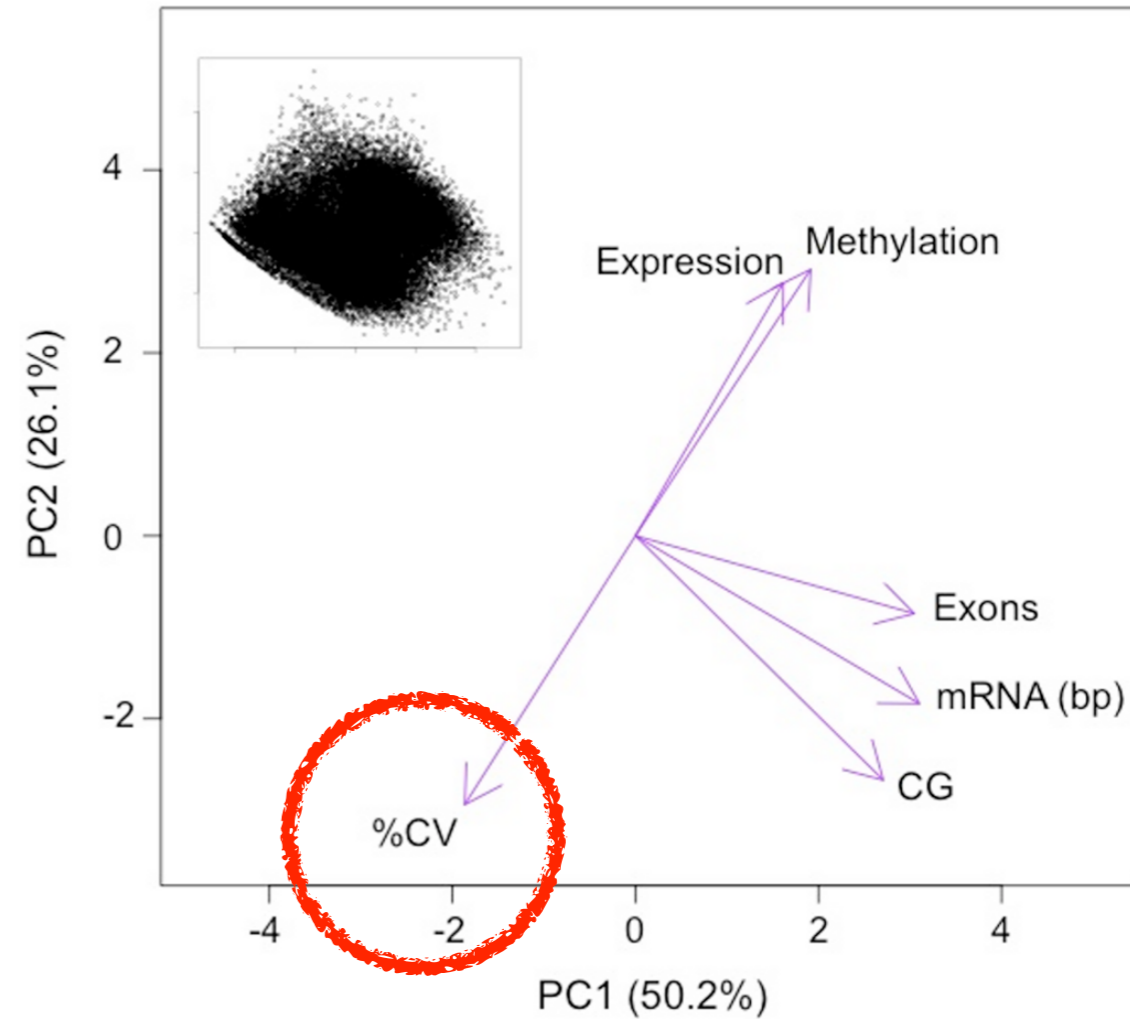
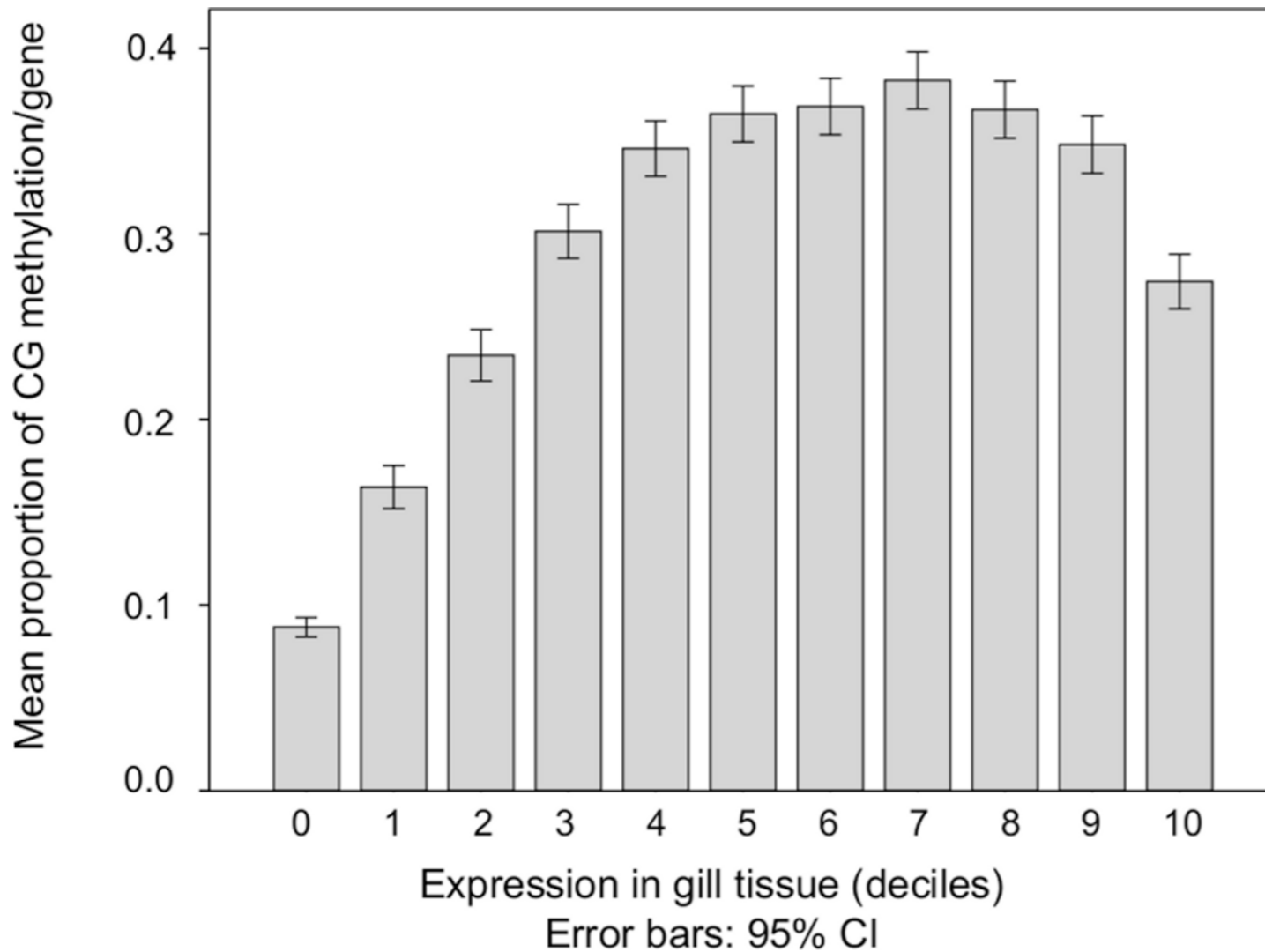
Mackenzie R. Gavery and Steven B. Roberts  
School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA

Gene expression

2

Epigenetic variation

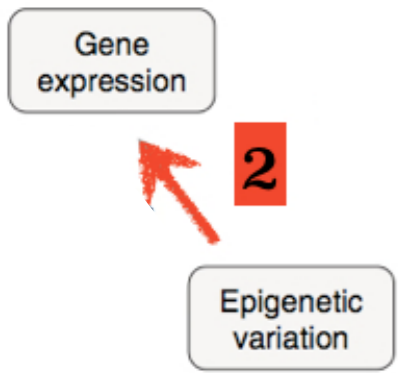
Theory: **Does not** influence expression level but rather alternative splicing.





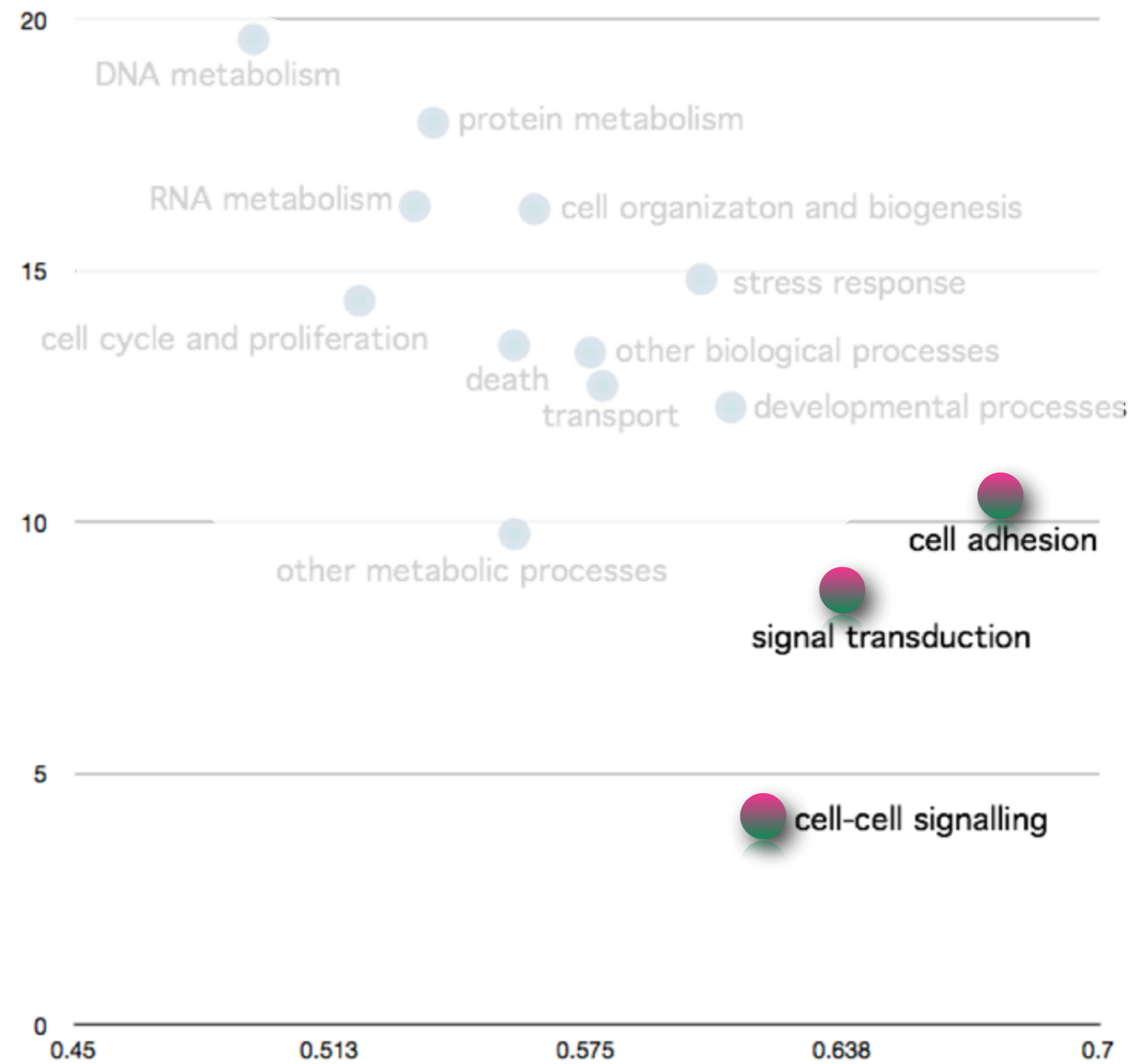
In species that experience a diverse range of environmental conditions, processes have evolved to increase the number of potential phenotypes in a population in order to improve the chances for an individual's survival.





Measured degree of DNA methylation

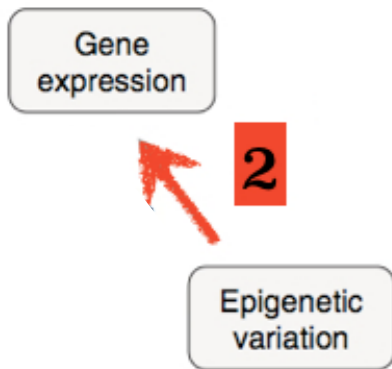
**Enrichment level in MBD-Seq library**



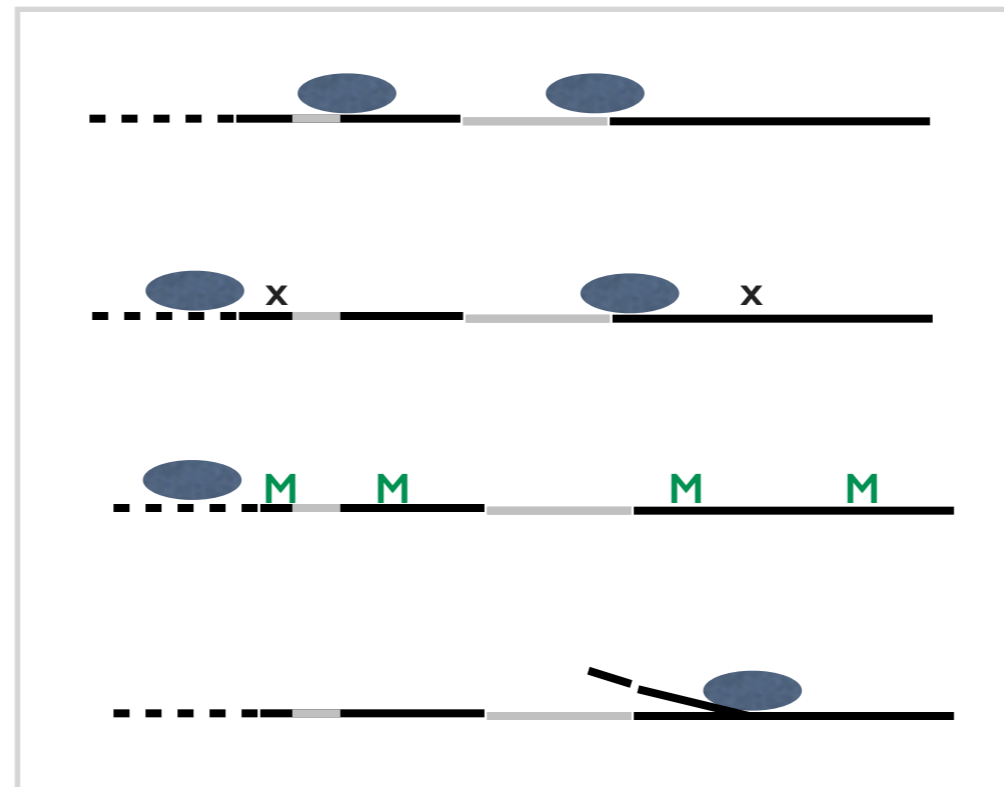
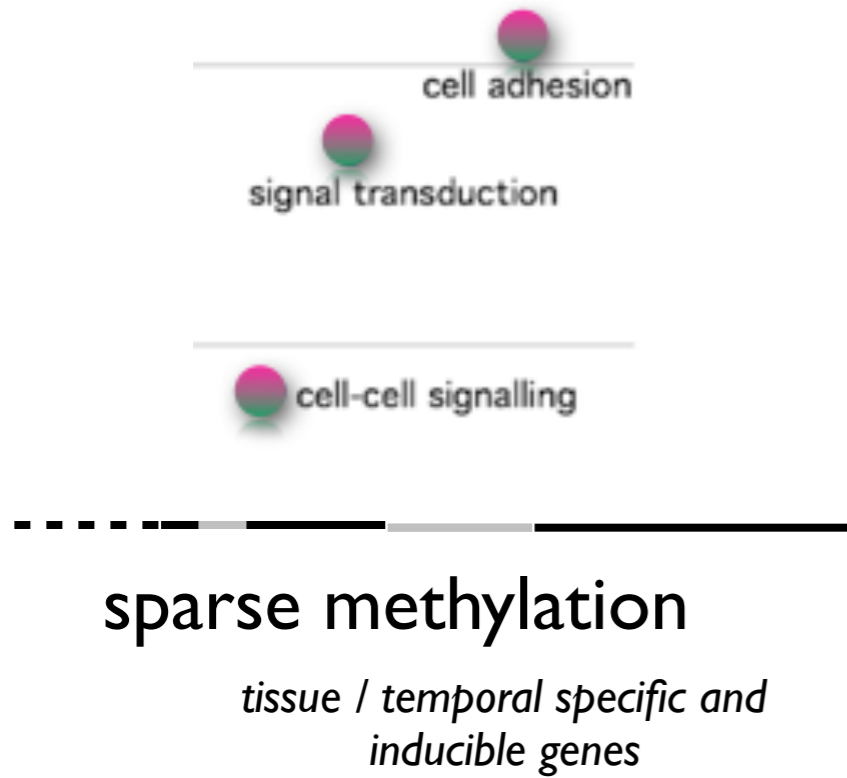
**in silico analysis**

(modified from Gavery and Roberts 2010)

Predicted degree of DNA methylation



# Transcriptional opportunities

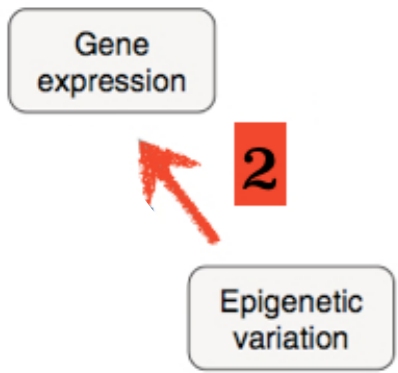


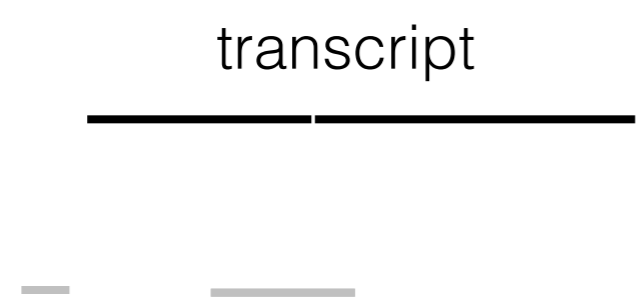
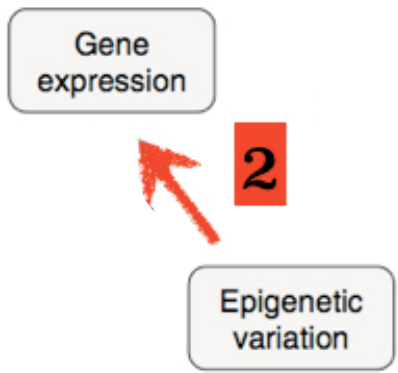
alternative start sites

sequence mutation  
change AA, premature stop codon

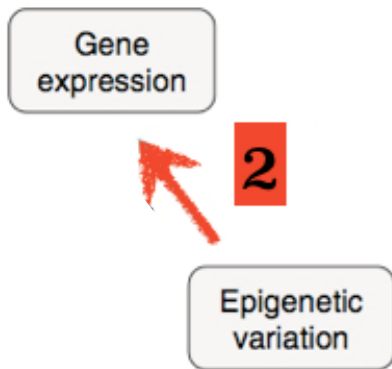
conventional transcription  
*transient methylation*

alternate transcript  
exon skipping

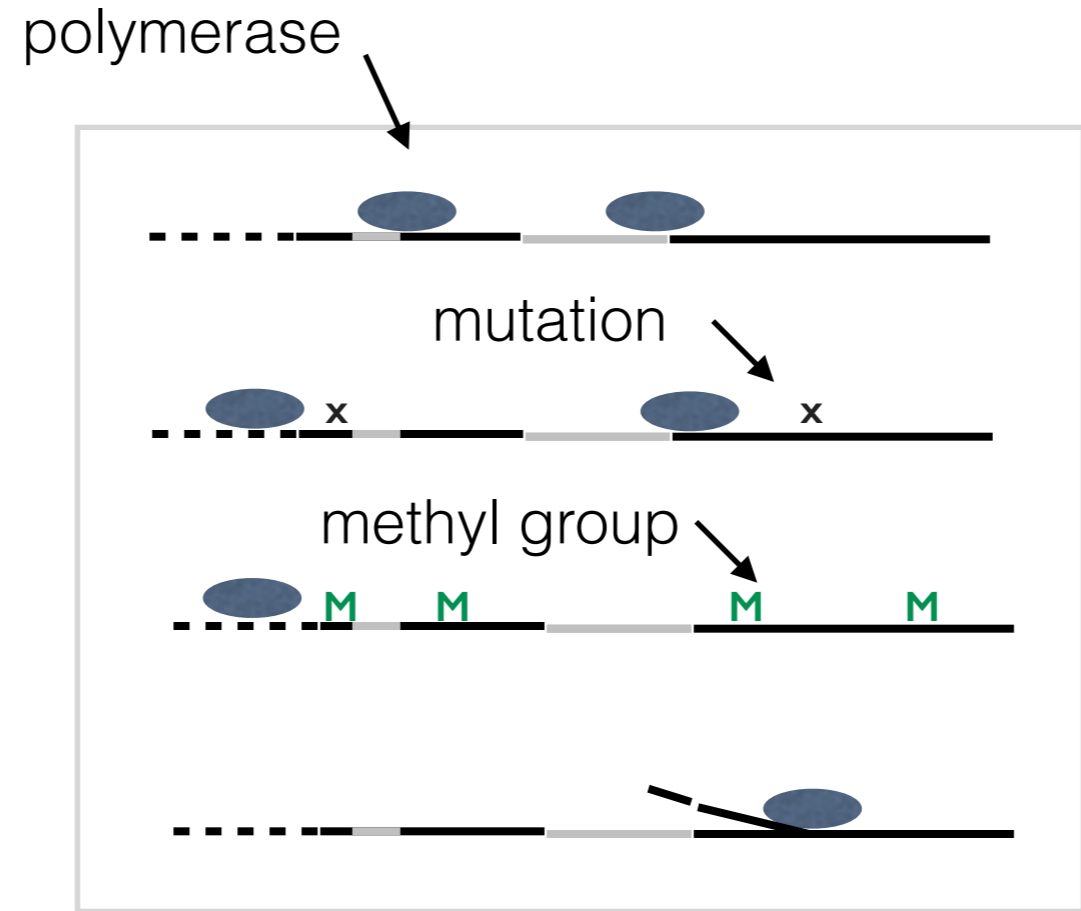
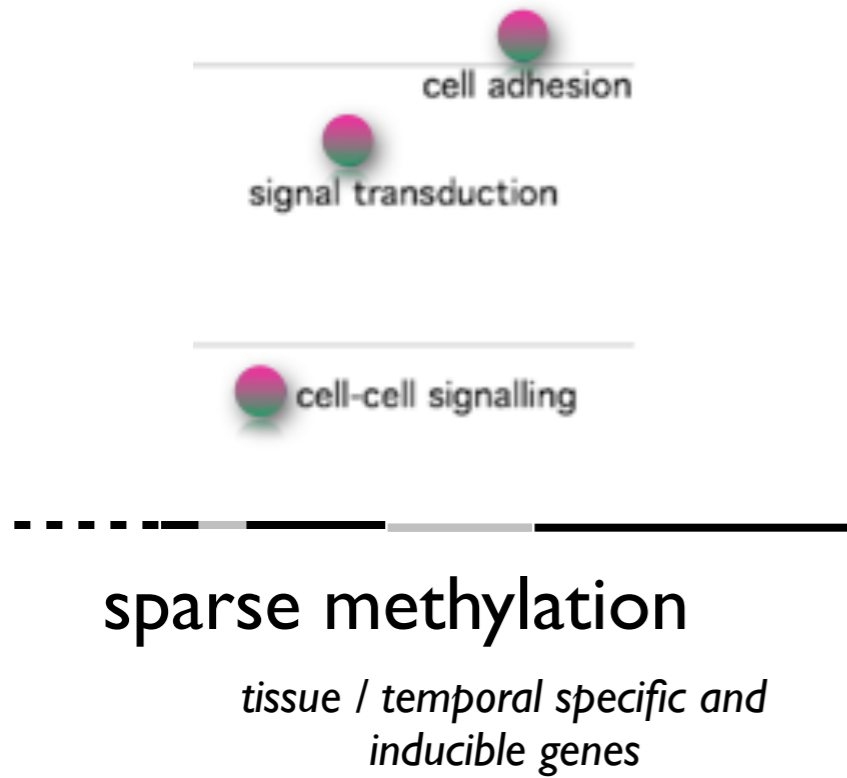




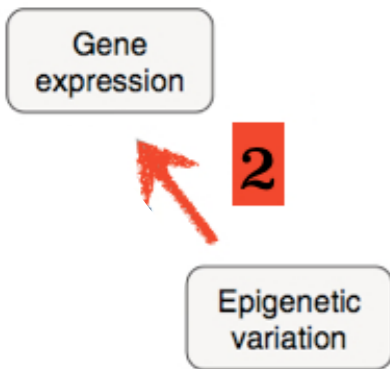




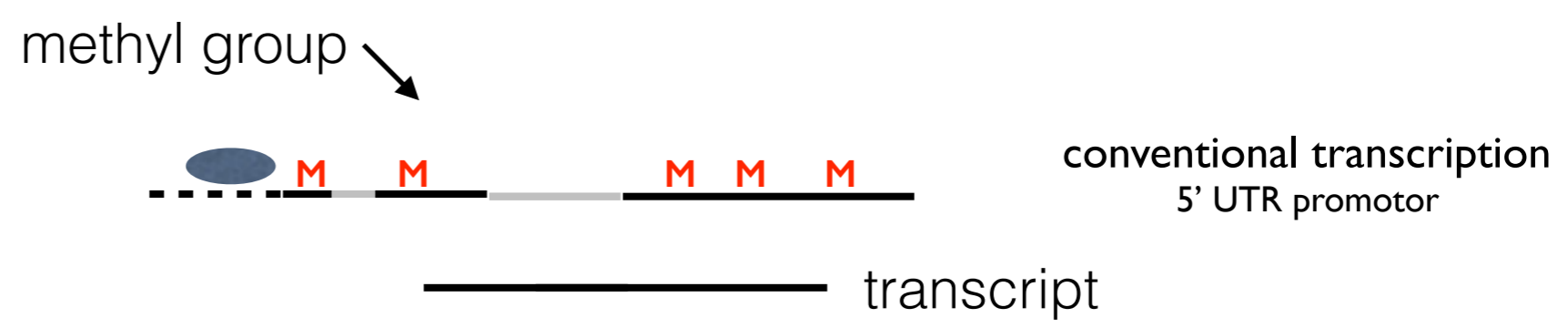
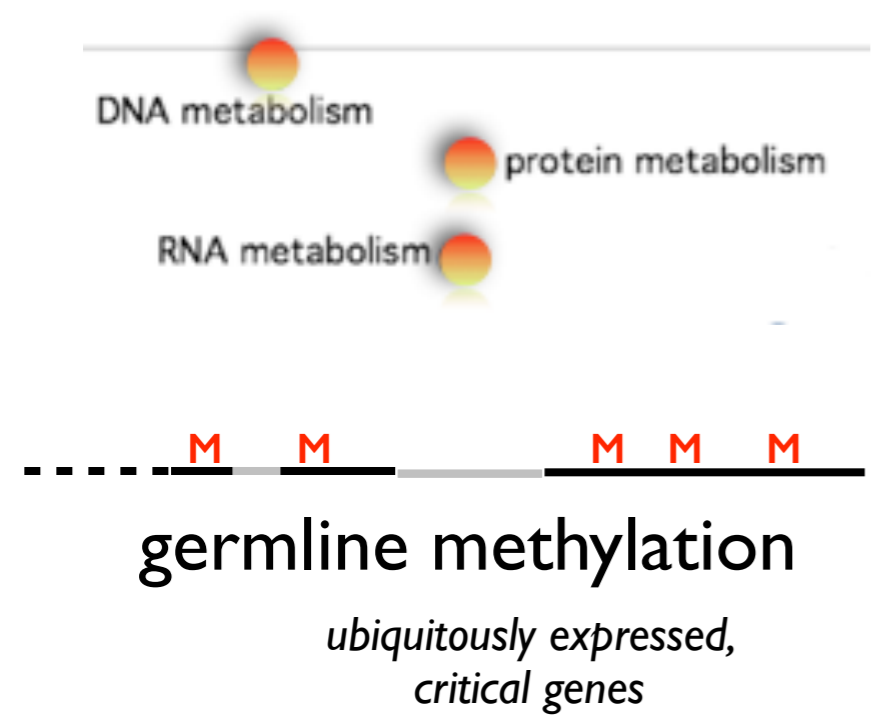
# Transcriptional opportunities



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



# 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

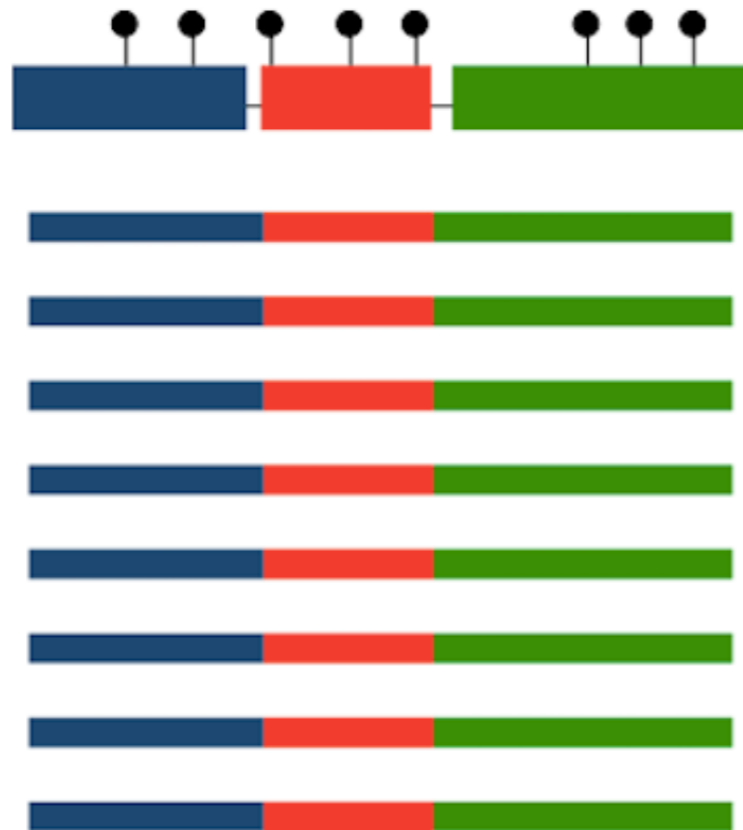
## Stochastic Variation

Gene expression

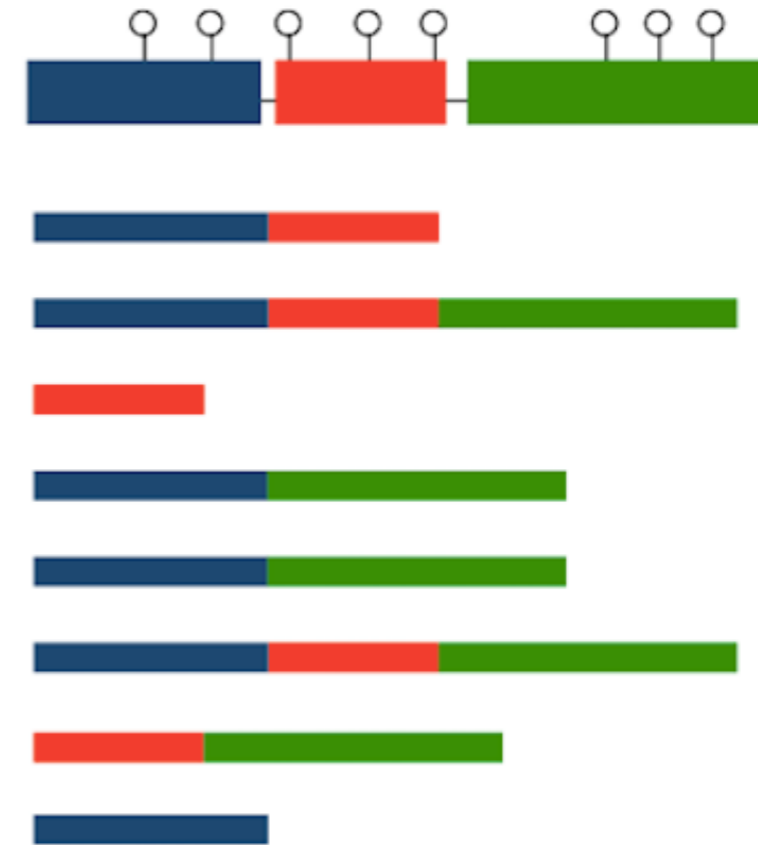
2



Epigenetic variation



housekeeping



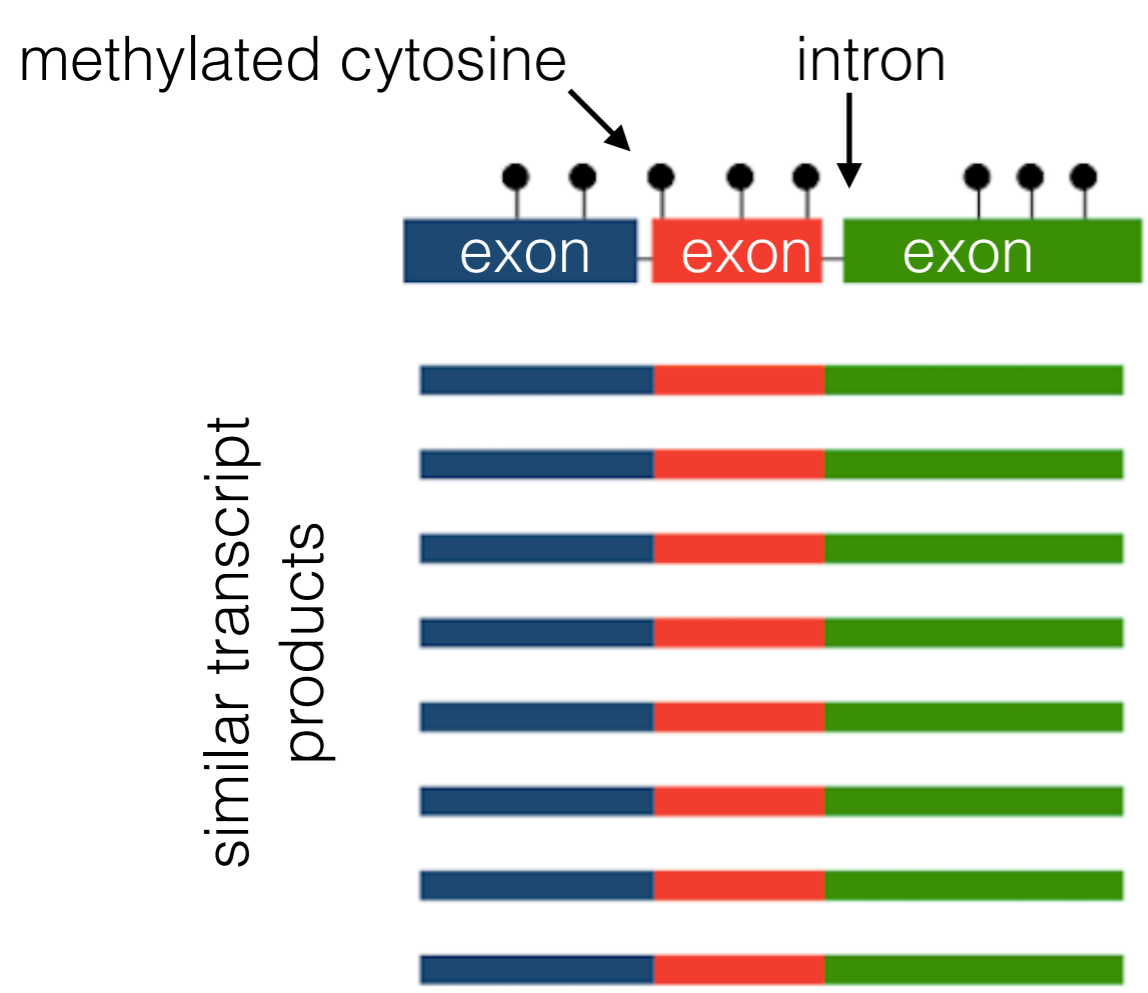
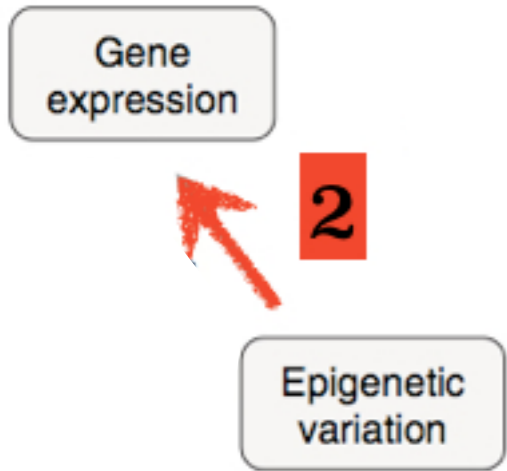
response to change

# A context dependent role for DNA methylation in bivalves

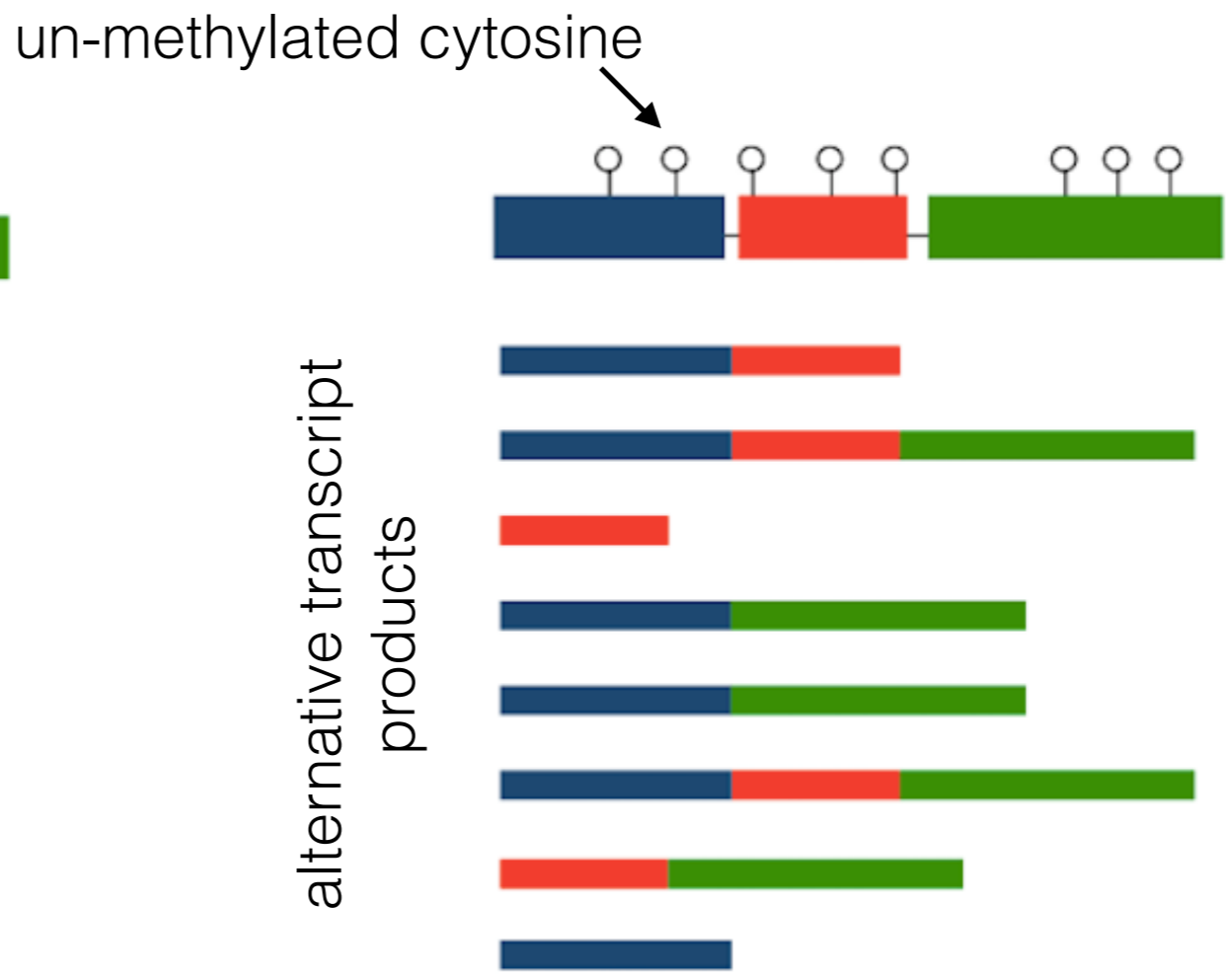
Mackenzie R. Gavery and Steven B. Roberts

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## Stochastic Variation



housekeeping



response to change

Gene expression

2

Epigenetic variation



inducible



disease

temperature

dessication

salinity

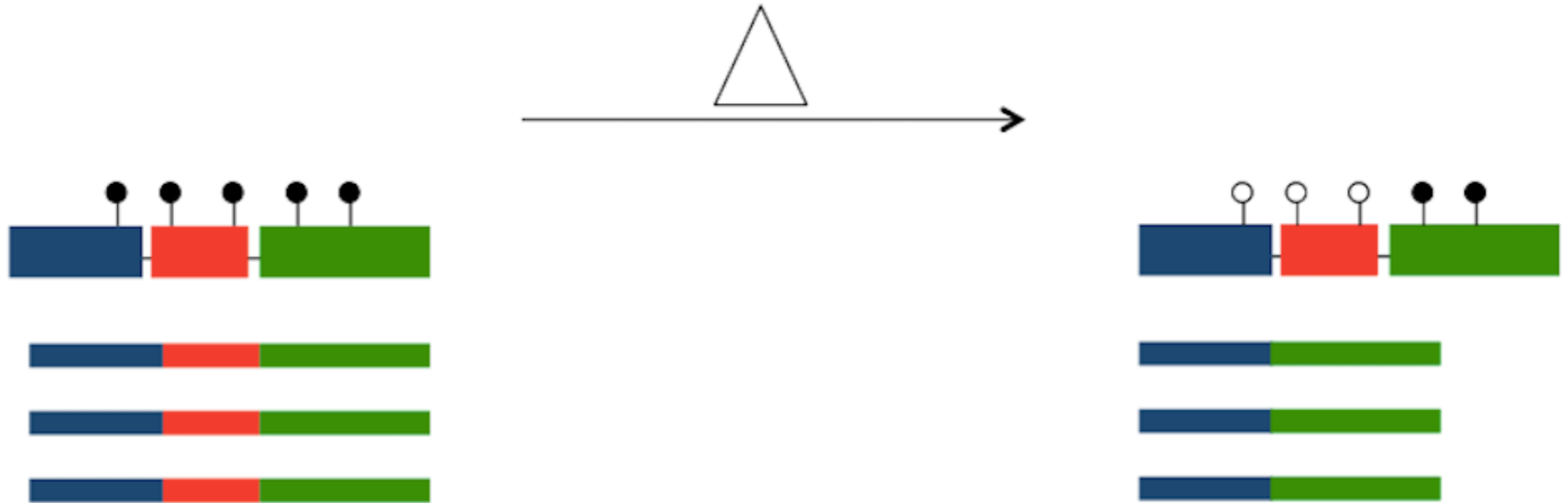
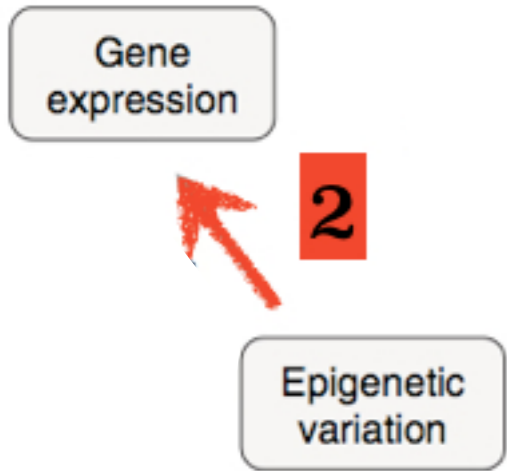
Mackenzie Gavery

# A context dependent role for DNA methylation in bivalves

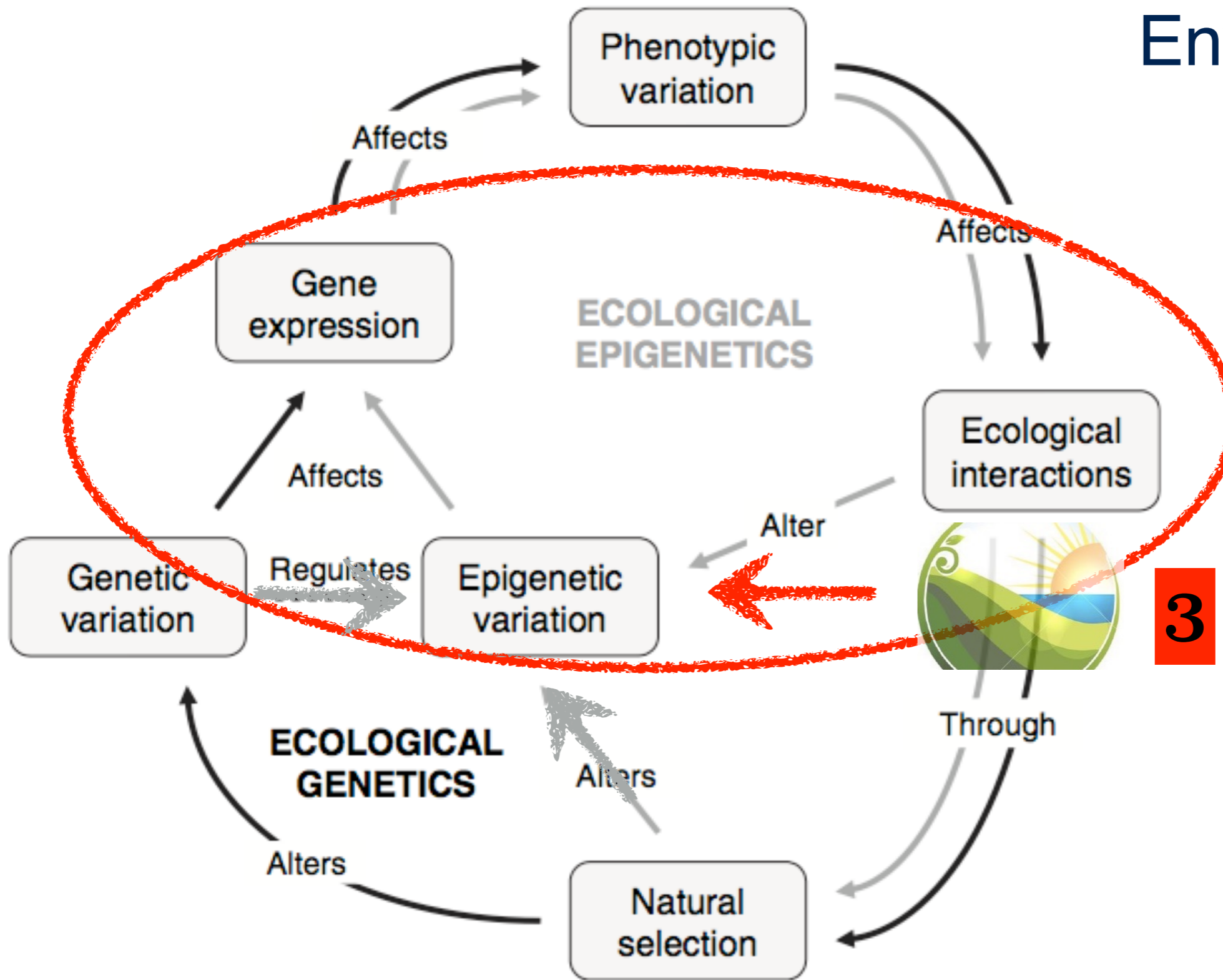
Mackenzie R. Gavery and Steven B. Roberts

Advance Access publication date 7 January 2014

# Targeted Regulation



# Environmental Influence



Ecology Letters, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

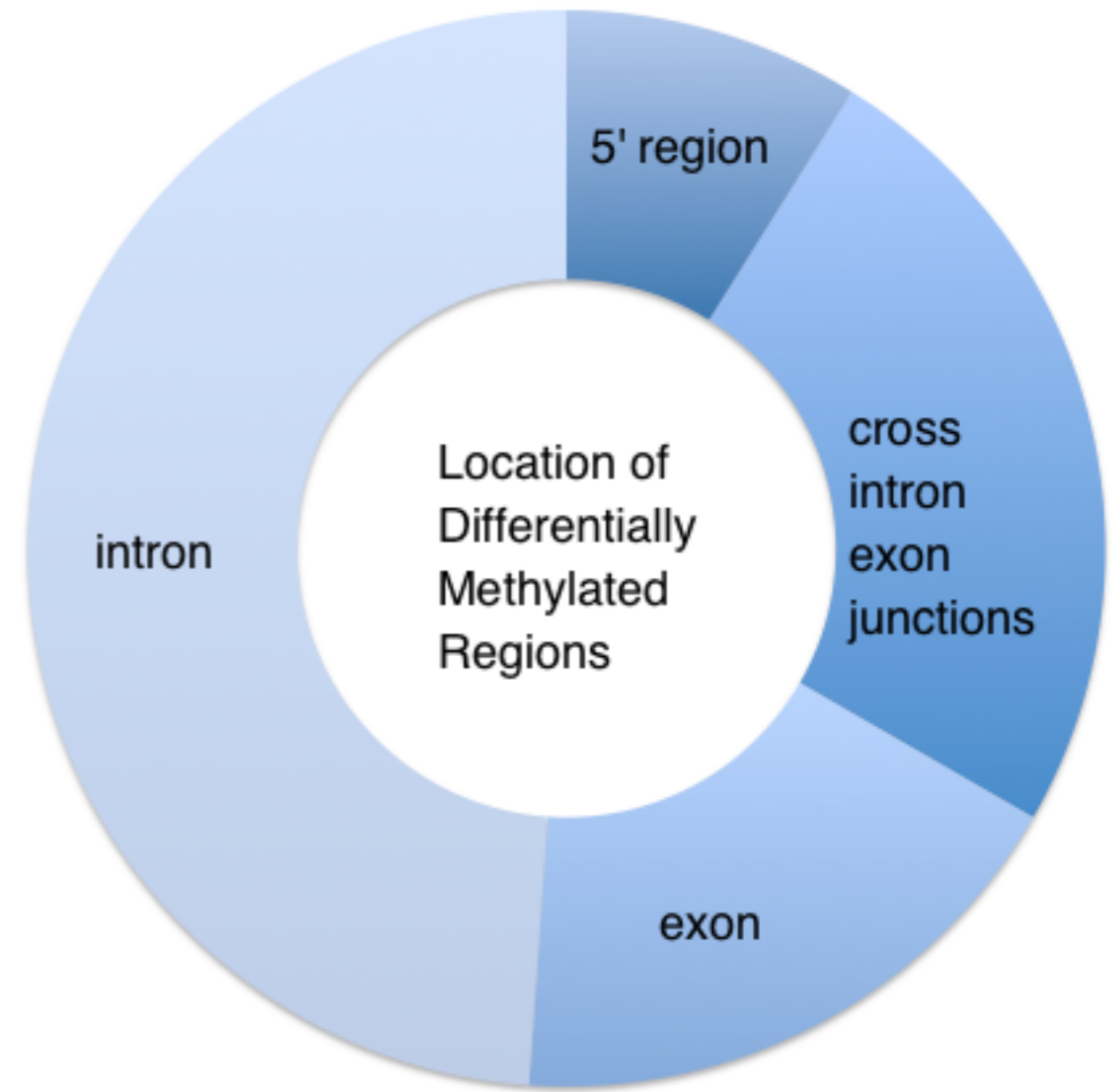
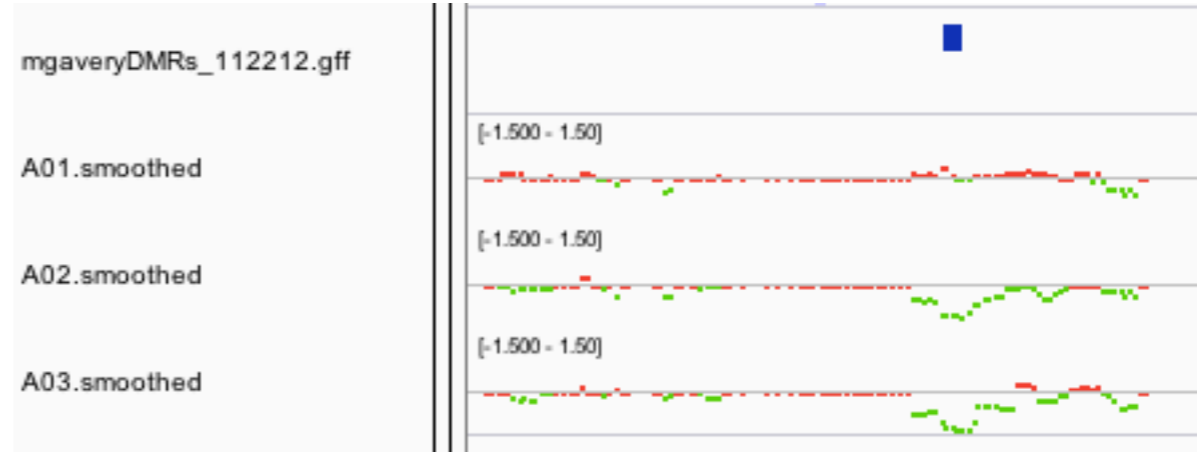
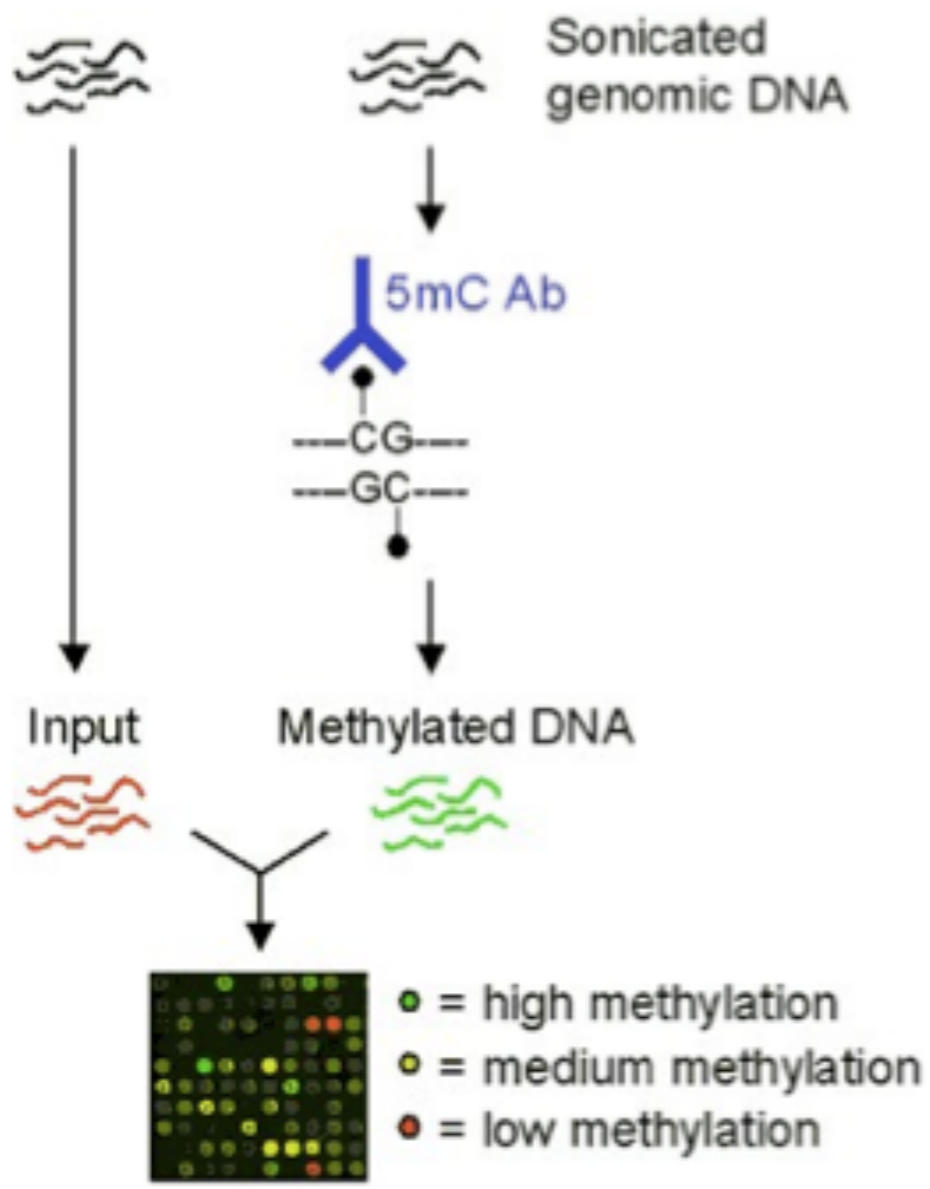
modified from

**IDEA AND  
PERSPECTIVE**

**Epigenetics for ecologists**

Oliver Bosdorf,<sup>1\*</sup> Christina L. Richards<sup>2</sup> and Massimo Pigliucci<sup>3</sup>

# Environmental impact (Estrogens)

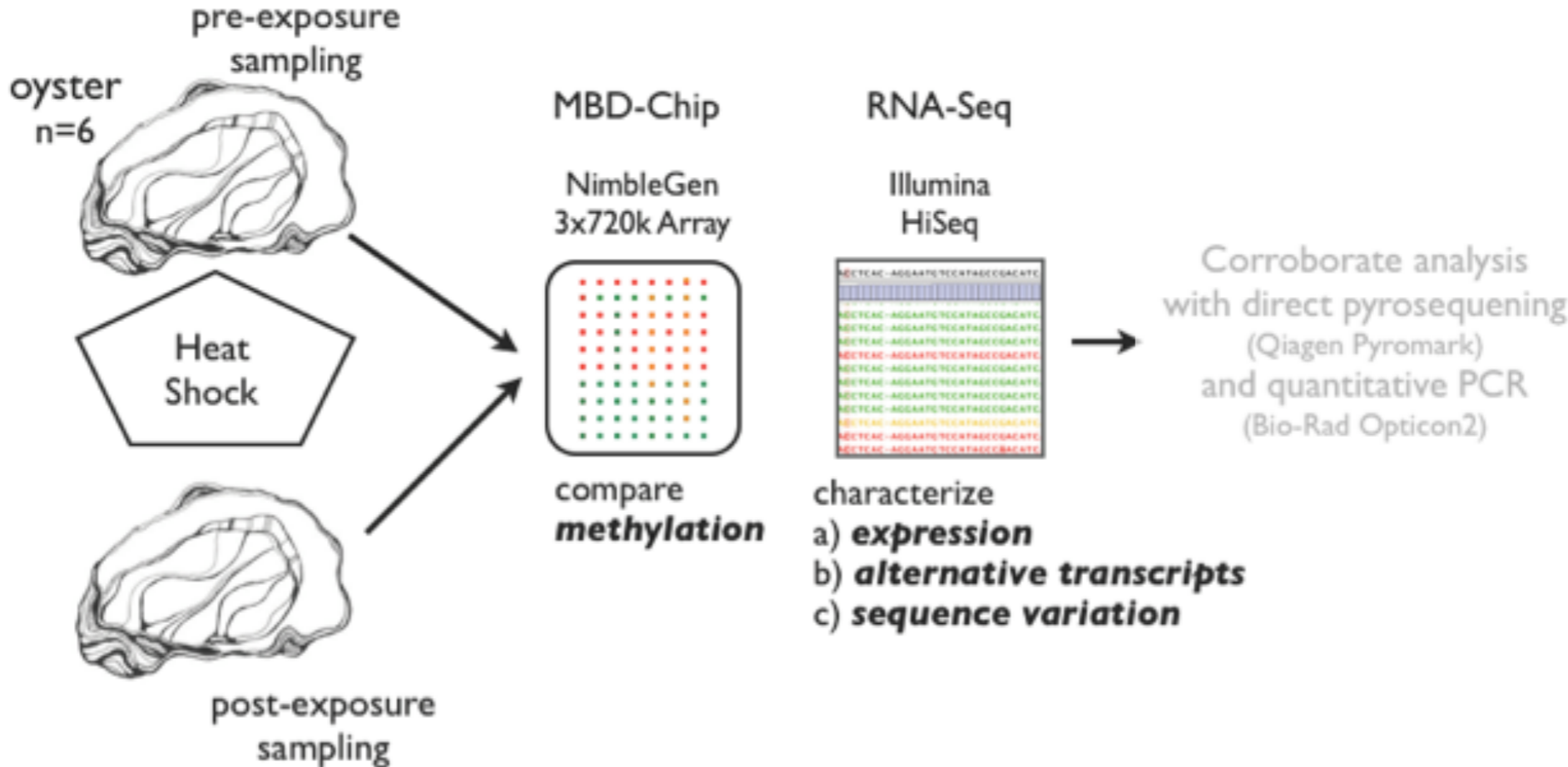




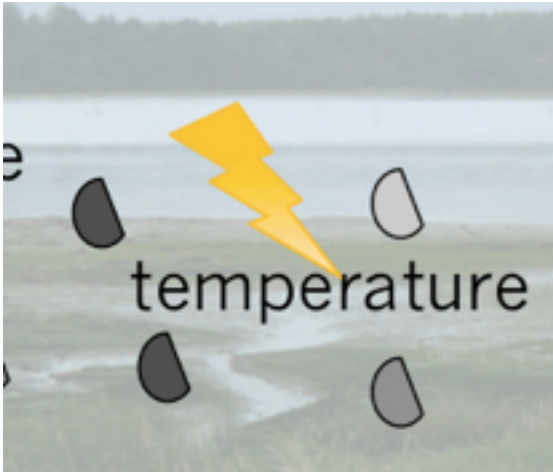
# Environment and gene expression



*stochastic or targeted?*



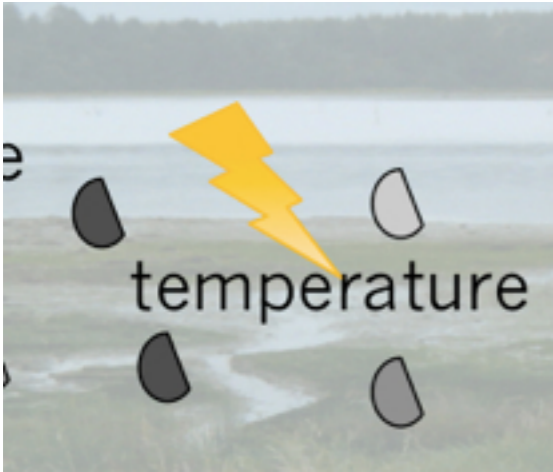
# Environment and gene expression



*stochastic or targeted?*

Oyster	Hypo-methylated	Hyper-methylated
2	7224	2803
4	6560	3587
6	7645	4044

# Environment and gene expression

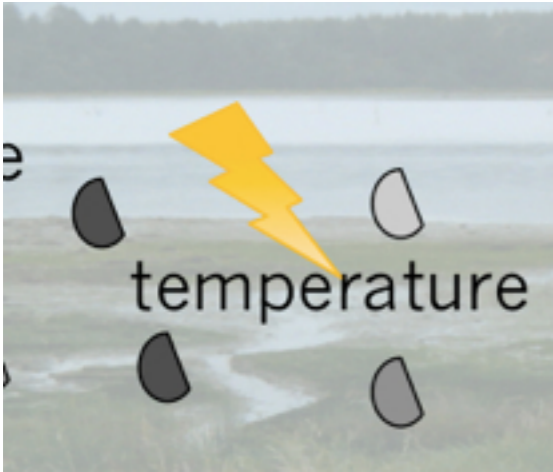


*stochastic or targeted?*

Oyster	Hypo-methylated	Hyper-methylated
2	7224	2803
4	6560	3587
6	7645	4044

No obvious association with genome feature including *differentially expressed genes*

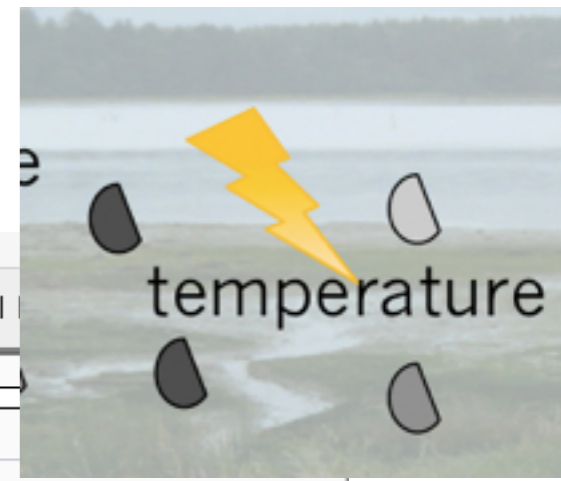
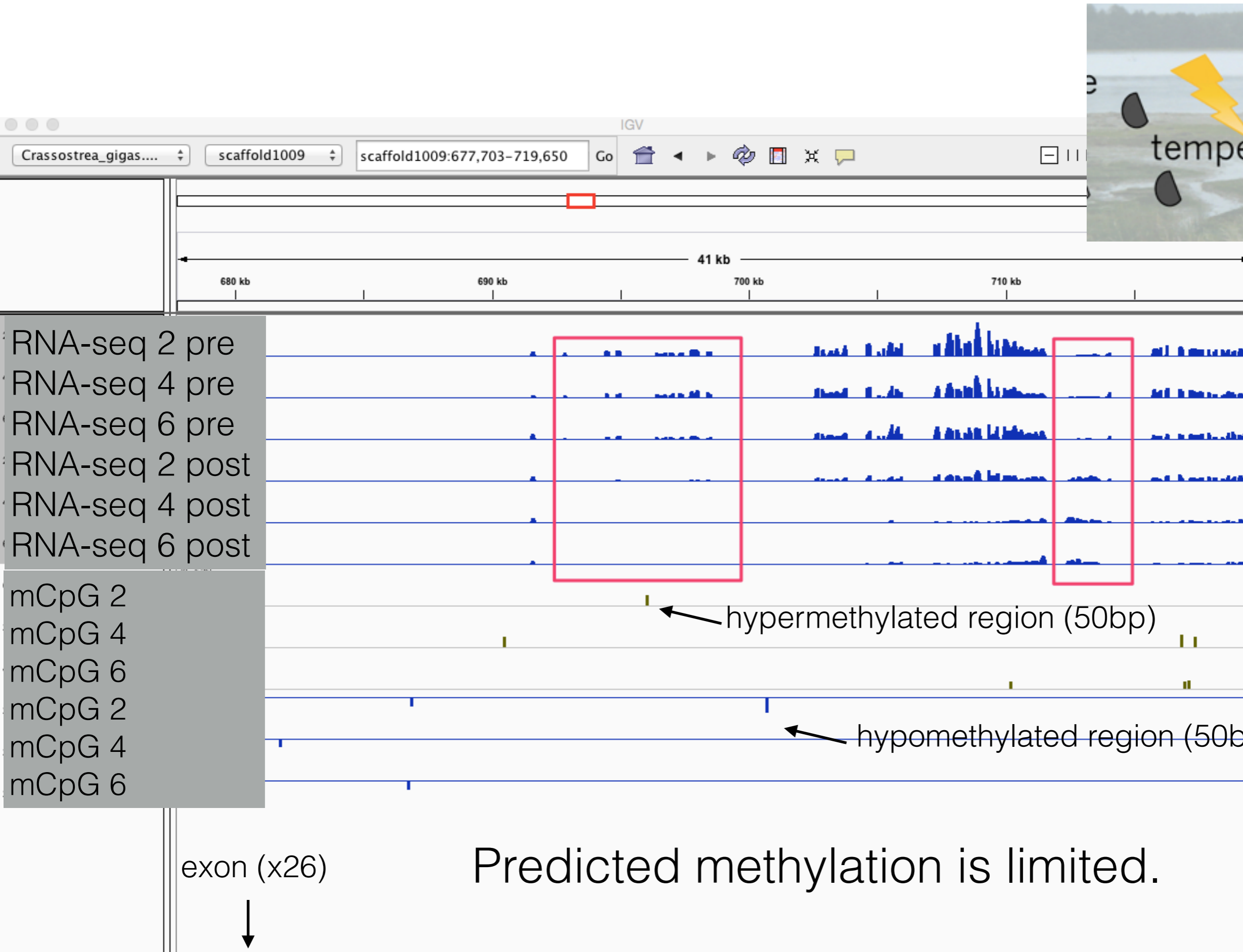
# Environment and gene expression



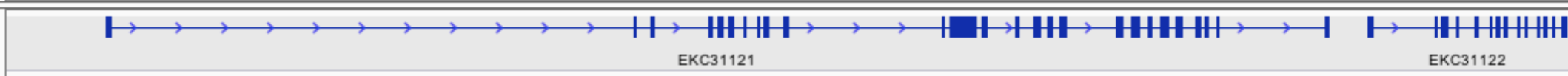
*stochastic or targeted  
or ..?*

Oyster	Hypo-methylated	Hyper-methylated
2	7224	2803
4	6560	3587
6	7645	4044

Changes in methylation (either direction) are more prevalent in introns, repeats, and transposable elements.



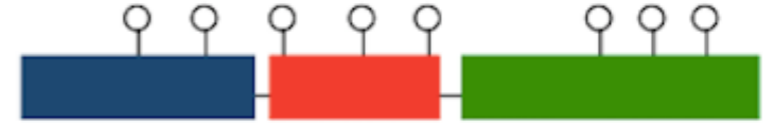
Crassostrea\_gigas.GCA\_000297.1.22.gtf  
 Cuffdiff\_geneexp.sig.gtf



Gene expression

2

Epigenetic variation



more questions....  
interesting but what is controlling?

# 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





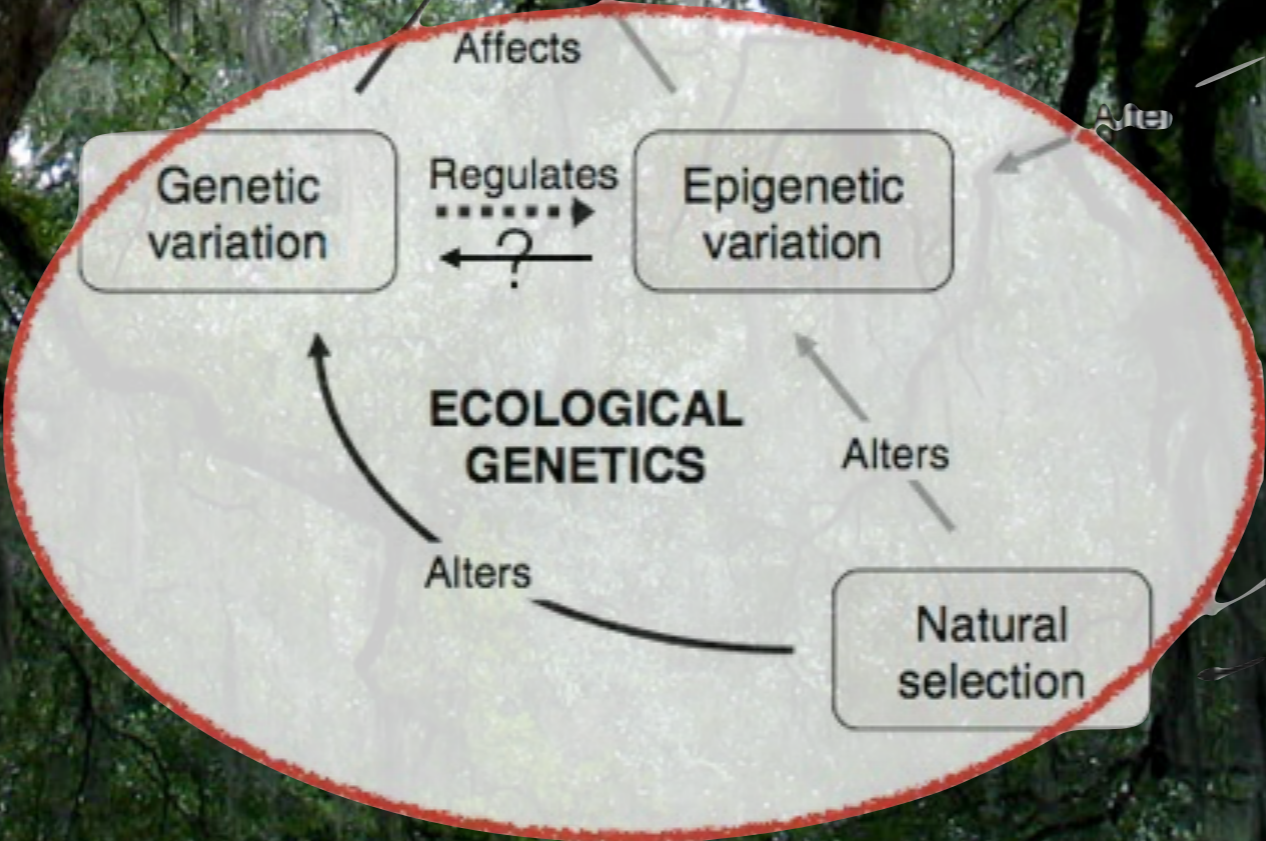
## Next Steps

Transposable  
Elements

Consider other  
epigenetic process

Photo credit: Flickr, Creative Commons, cseessums

# Next Steps



~~Very new data~~  
Heritability  
Plasticity  
Local Adaptation

*Genetics  
versus  
Epigenetics*

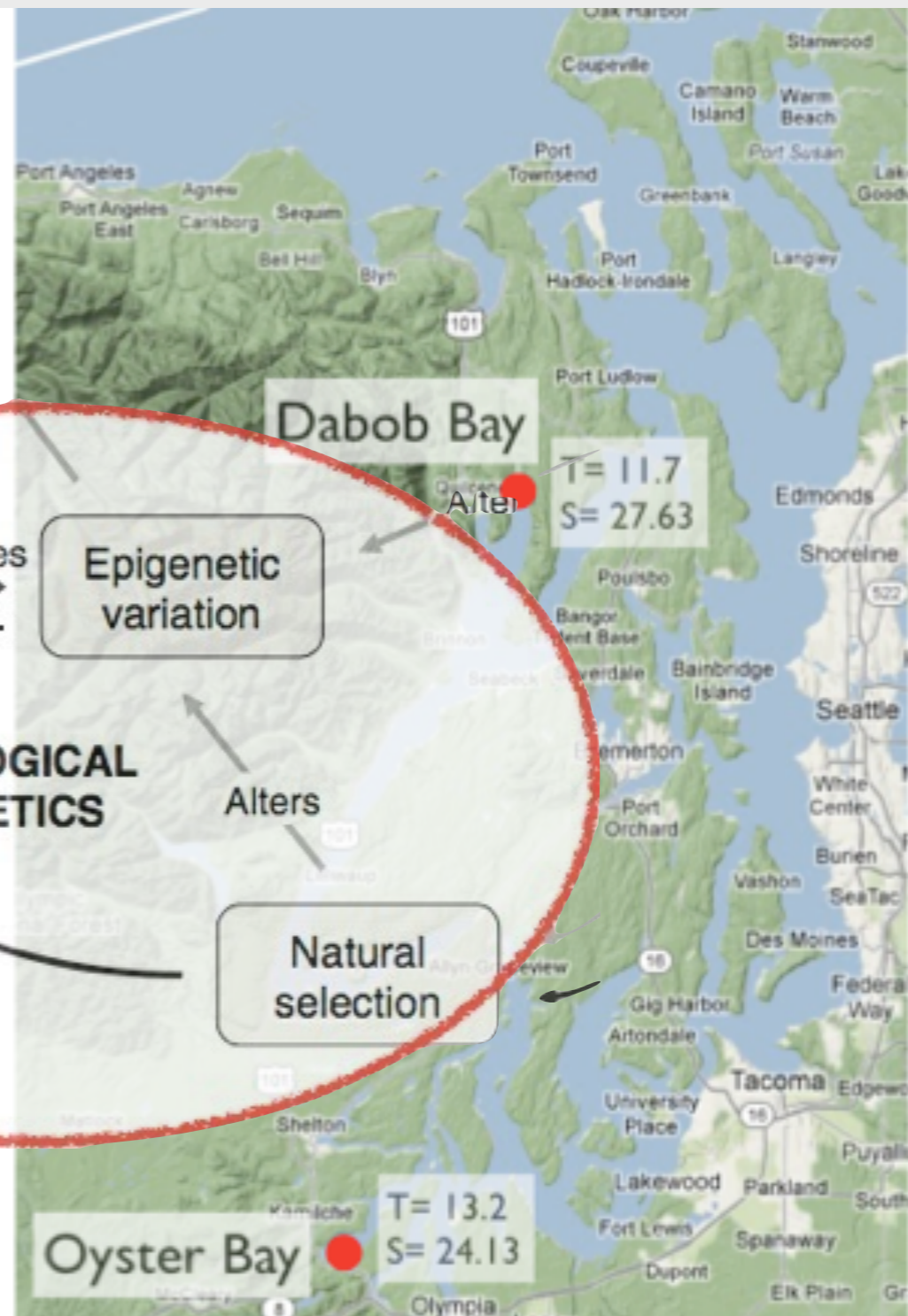
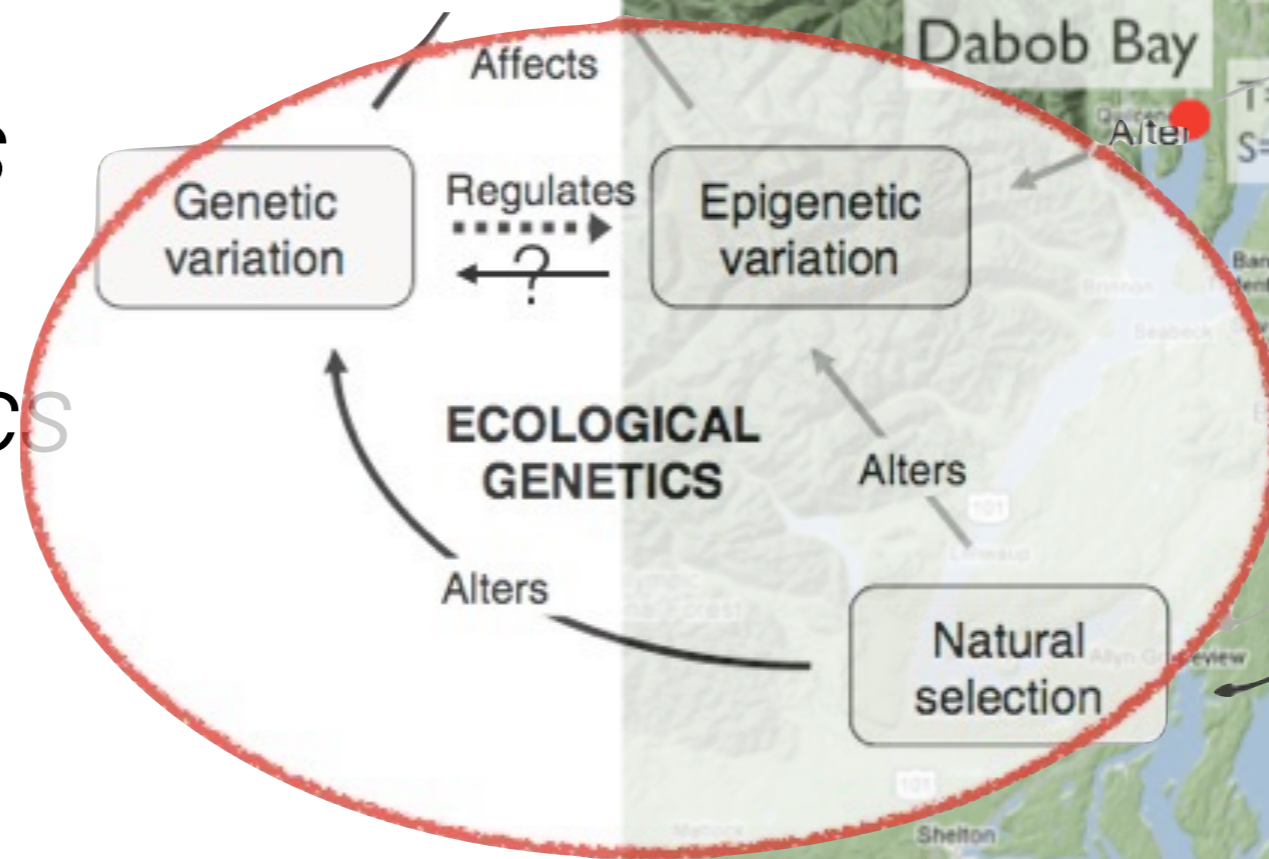
**Reciprocal Transplant Experiment**



~~Very new data~~  
Heritability  
Plasticity  
Local Adaptation

*Genetics  
versus  
Epigenetics*

## Reciprocal Transplant Experiment



# Acknowledgements

Mackenzie Gavery

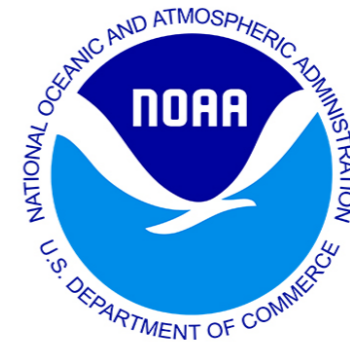
Claire Olson

Sam White

Brent Vadopalas

Jake Heare

Jay Dimond



Bill Howe

Dan Halperin



slides, data & more @  
[github.com/sr320/talk-CICESE-2015](https://github.com/sr320/talk-CICESE-2015)