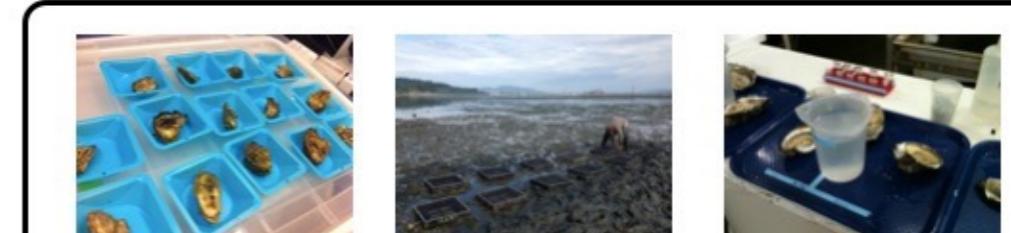


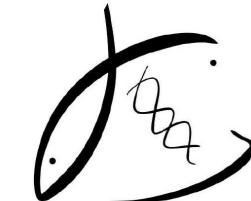
# Environmental influences on DNA methylation patterns in oysters and the relationship with phenotypic variation

Steven Roberts  
Kenneth K. Chew Endowed Professor  
University of Washington  
School of Aquatic and Fishery Sciences

December 5, 2016 - University of Chicago



latest online genetics responses relationship live addition DNA includes weekly Lab check strive page Data use process notebooks functional practice sure focuses Resource highlights adaptive science open maintaining dependent Sharing new Research component developed organismal investigating members resources meetings sure focuses Plan one Meeting Check impacts core change environmental lab list nucleotide electronic organisms blogs potential Acidification approaches context transcription marine role Mac level view developed newest members follow proteome Facebook resources nucleotide electronic organisms blogs potential Acidification approaches context transcription

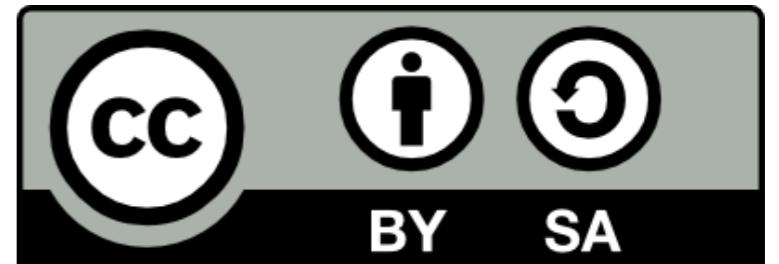


[robertslab.info](http://robertslab.info) | @sr320

# Open Science

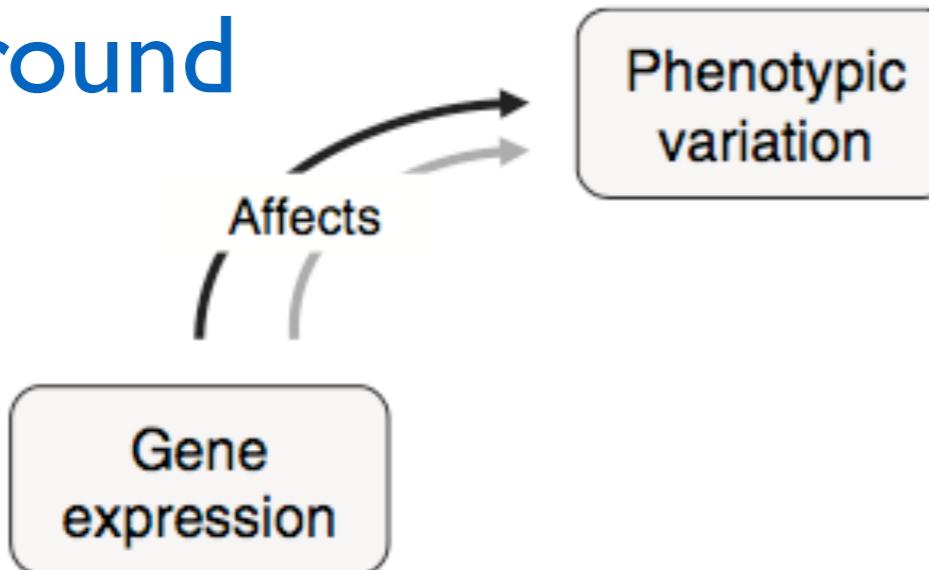
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- You are free to Share!
- Our lab practices open notebook science
- Data, Preprints, Proposals, Lab Meetings, Web Cams, Slidedecks

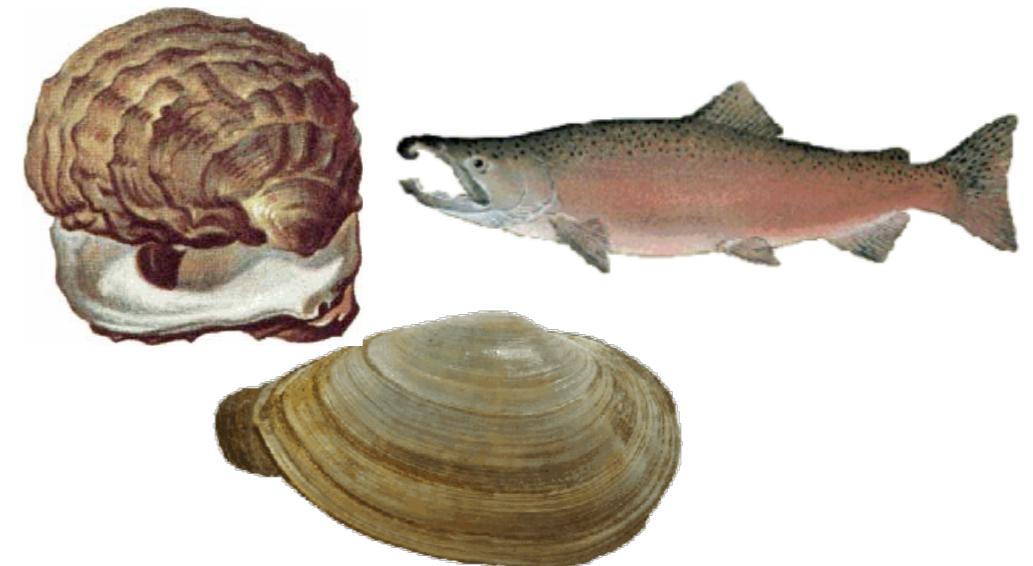


These slides plus links @  
[github.com/sr320/talk-Chicago-eed-2016](https://github.com/sr320/talk-Chicago-eed-2016)

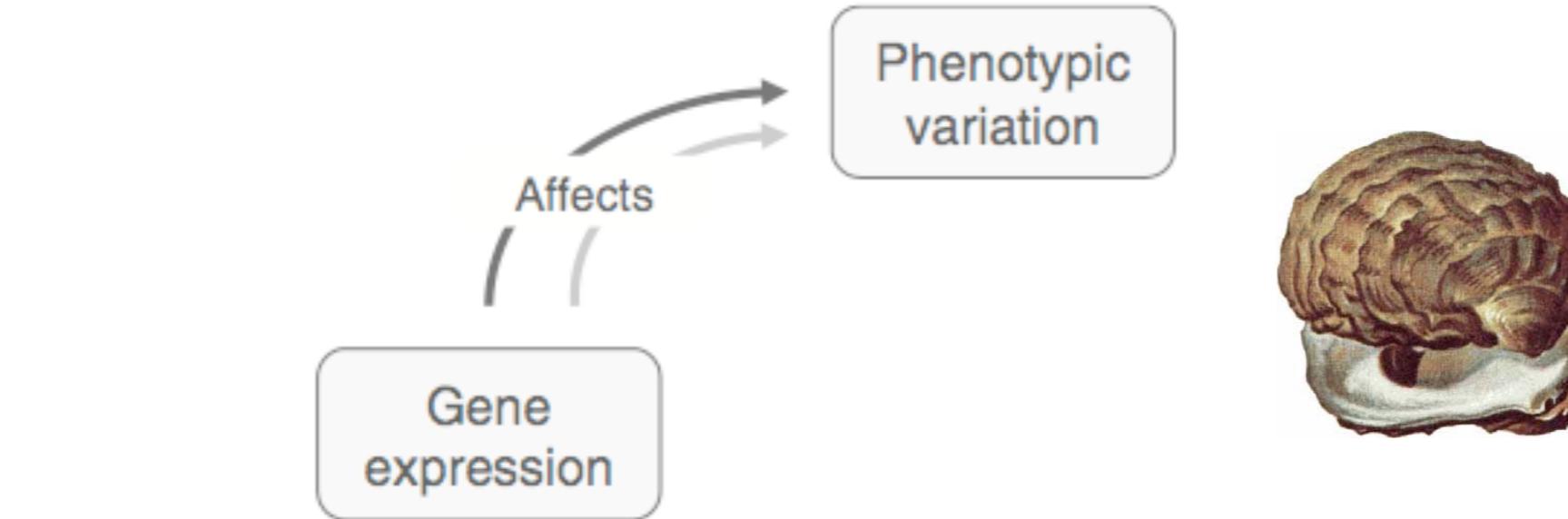
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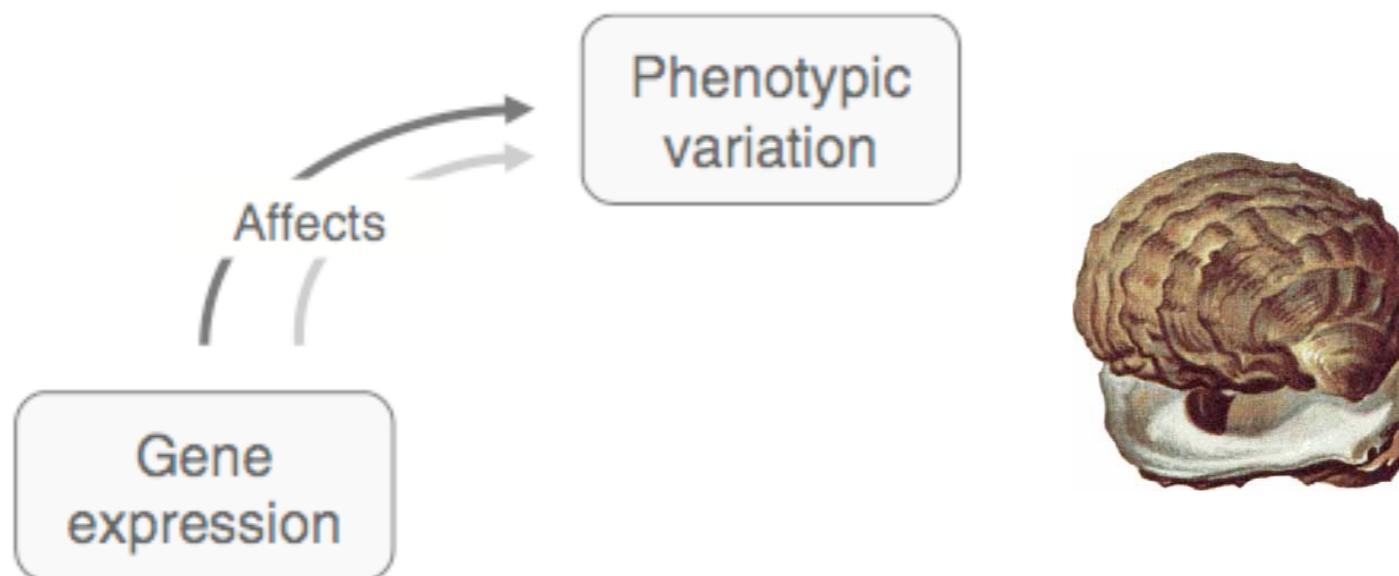
"relevant traits"



# Conceptual Models for a functional role of DNA methylation



# Conceptual Models for a functional role of DNA methylation

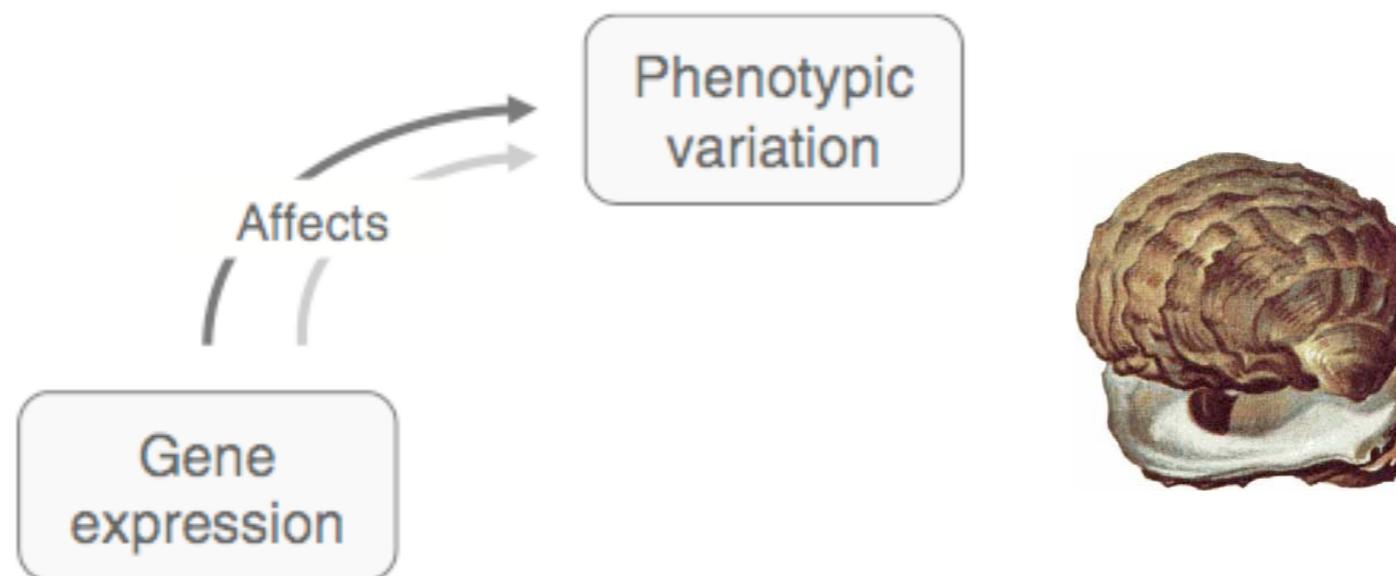


## Stochastic Variation

increased transcriptional opportunities  
increased likelihood of suitable phenotype

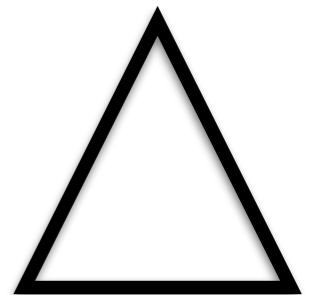


# Conceptual Models for a functional role of DNA methylation

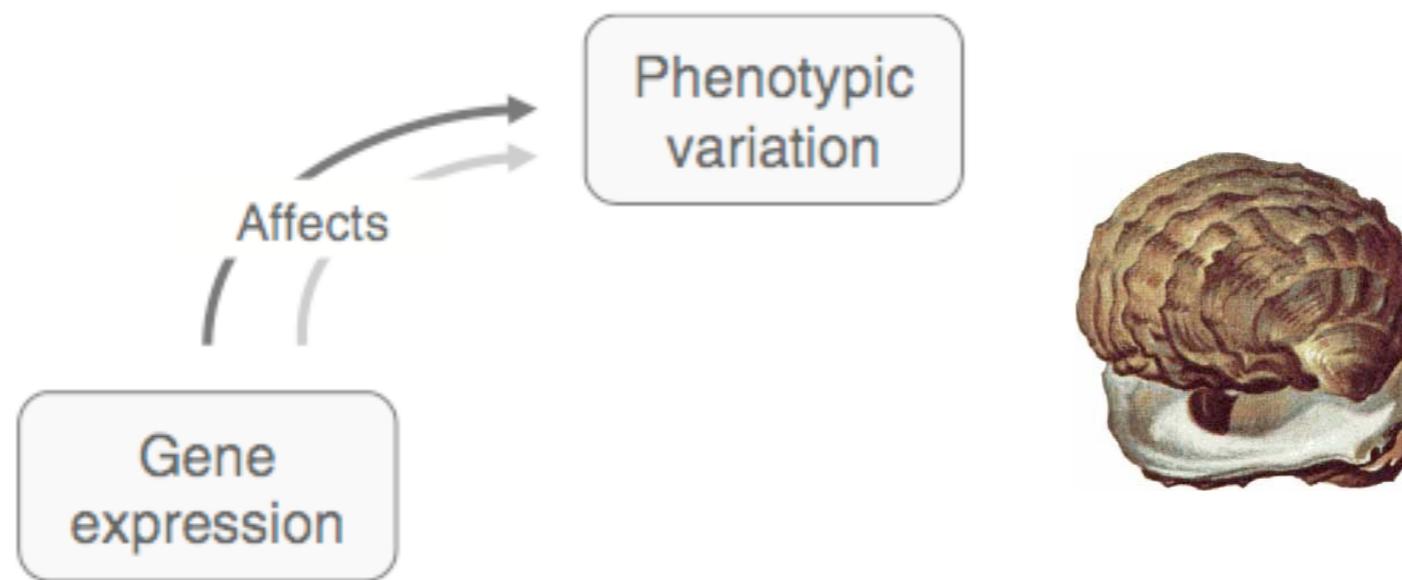


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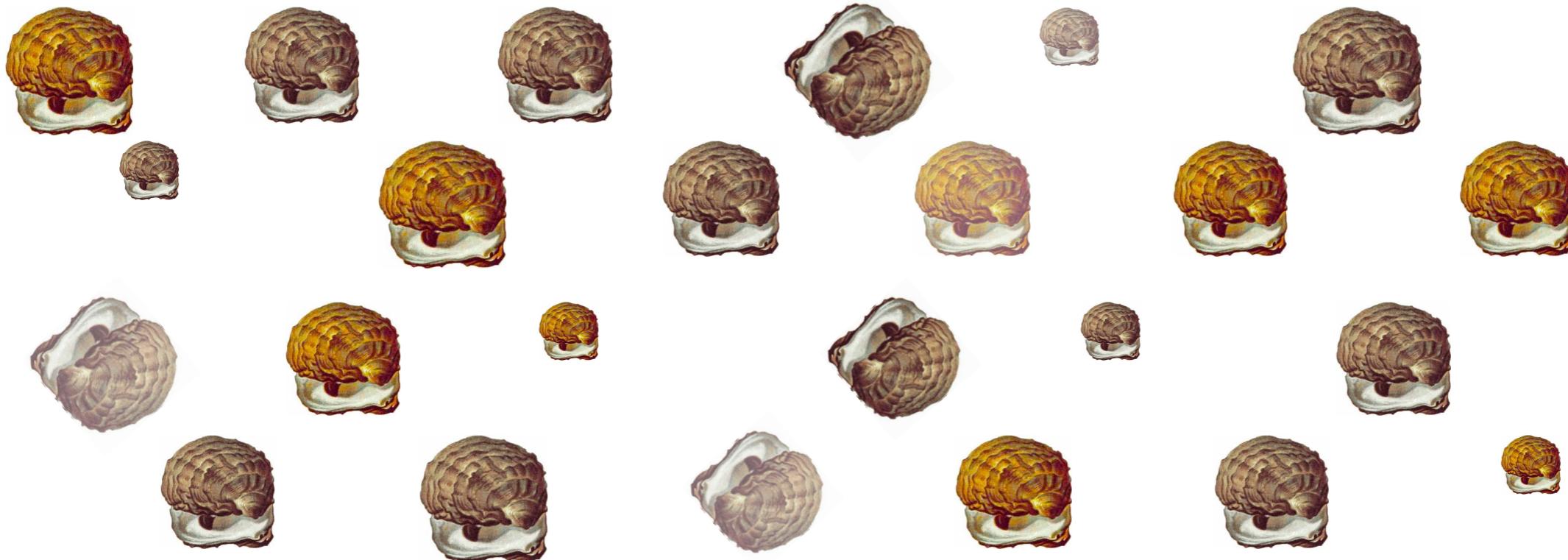


# Conceptual Models for a functional role of DNA methylation

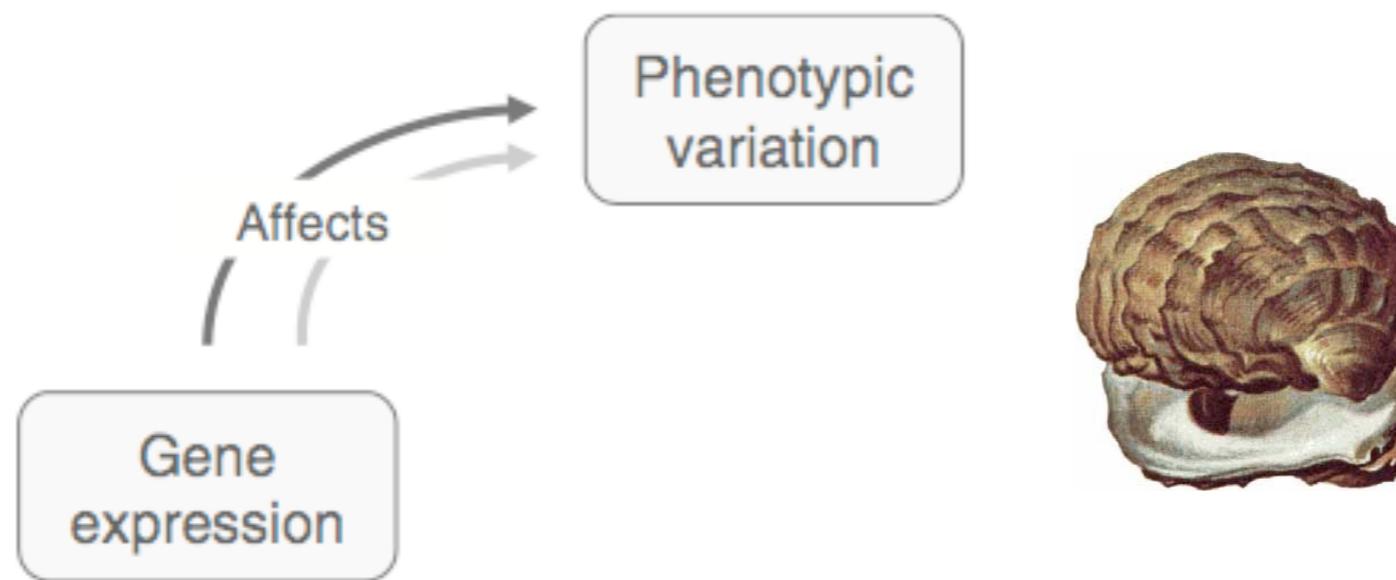


## Stochastic Variation

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# Conceptual Models for a functional role of DNA methylation



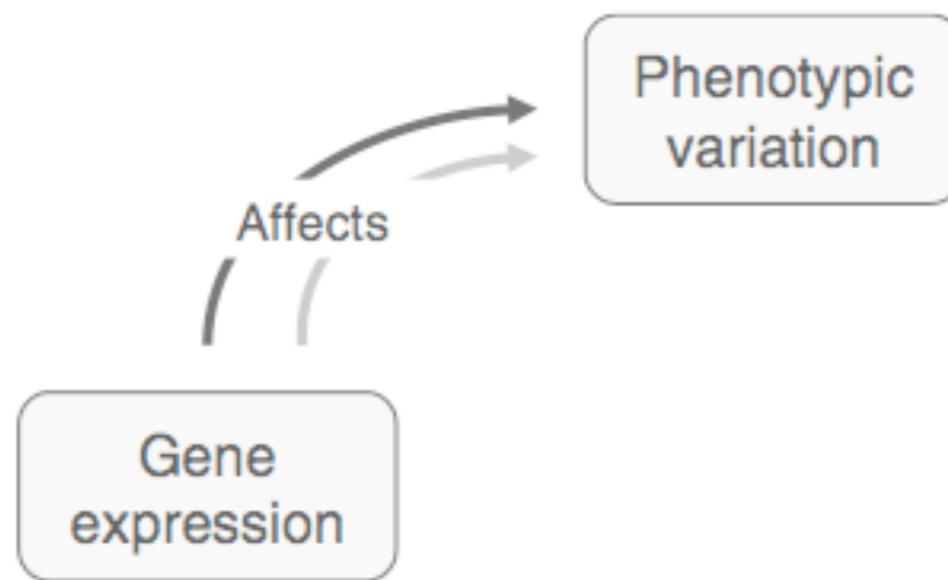
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# Conceptual Models for a functional role of DNA methylation



## Stochastic Variation

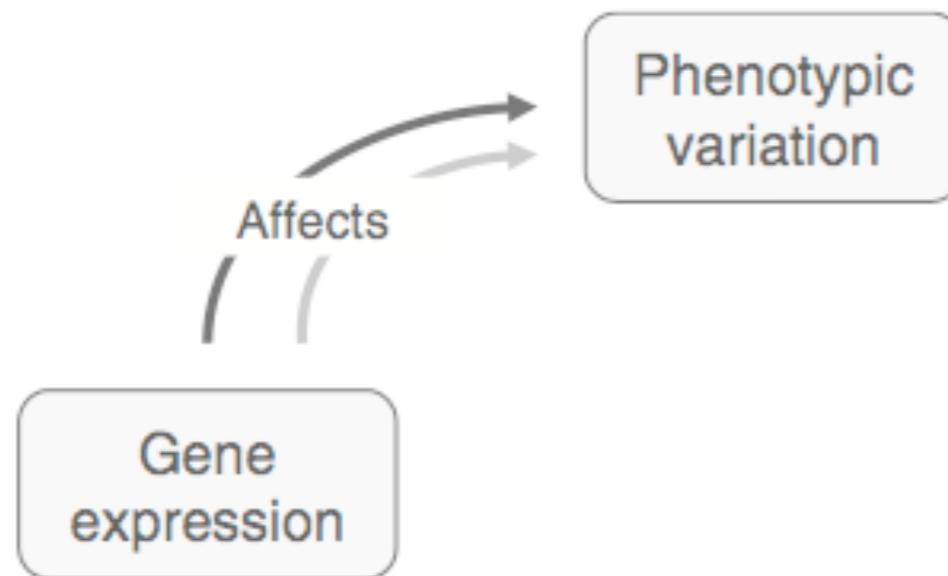
increased transcriptional opportunities

increased likelihood of suitable phenotype



\*

# Conceptual Models for a functional role of DNA methylation



## Stochastic Variation

increased transcriptional opportunities

increased likelihood of suitable phenotype

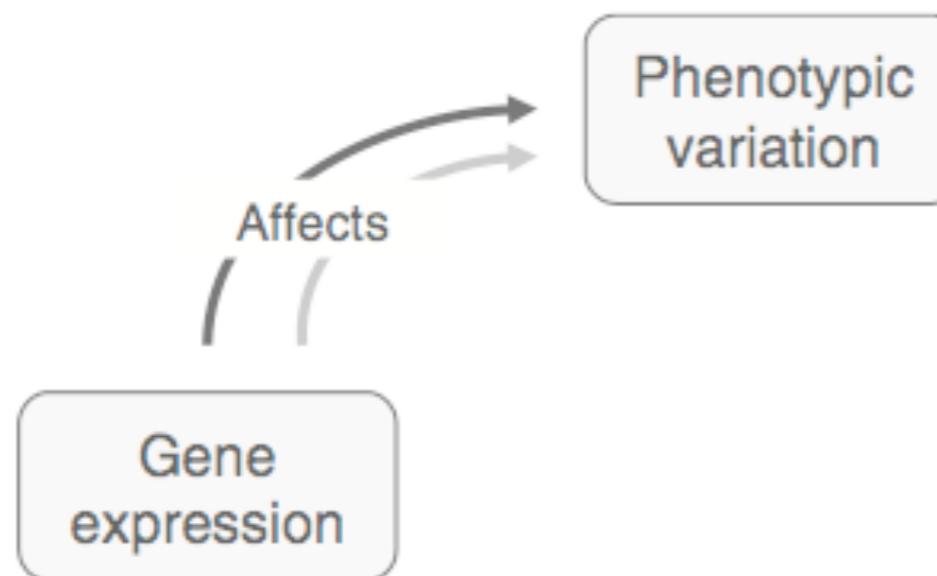


Biological Scale?  
Organism  
Cell  
Tissue

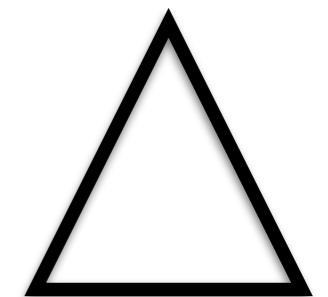


\*

# Conceptual Models for a functional role of DNA methylation

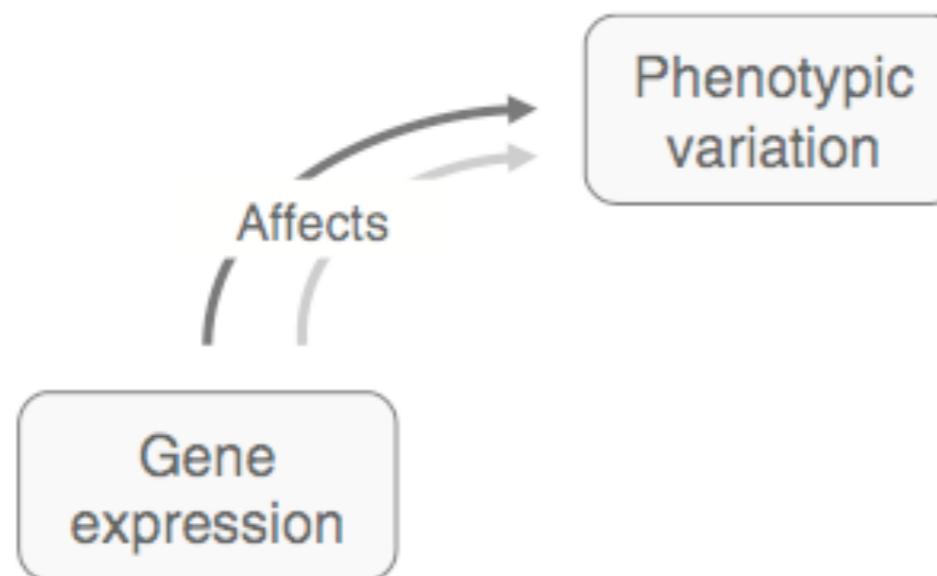


**Target Regulation**  
results in beneficial phenotype



\*

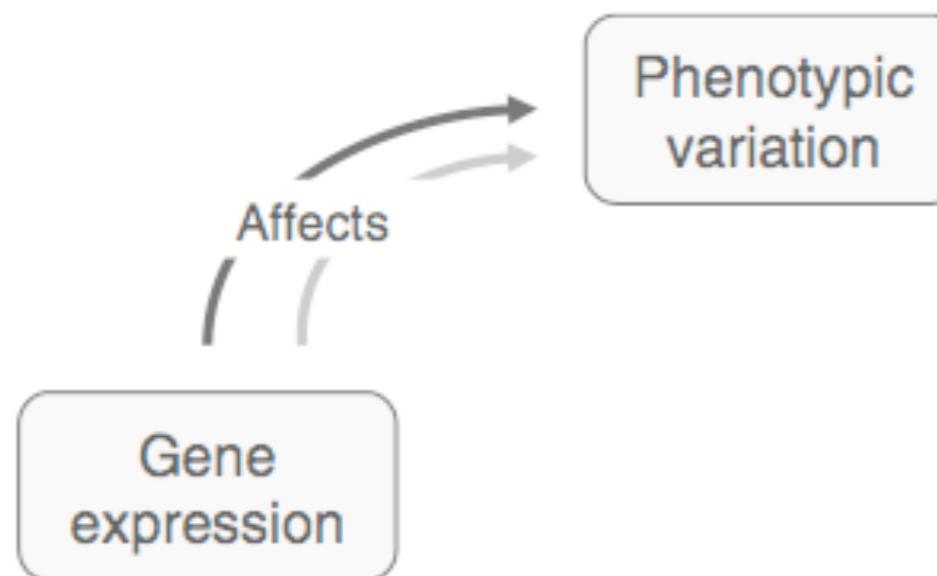
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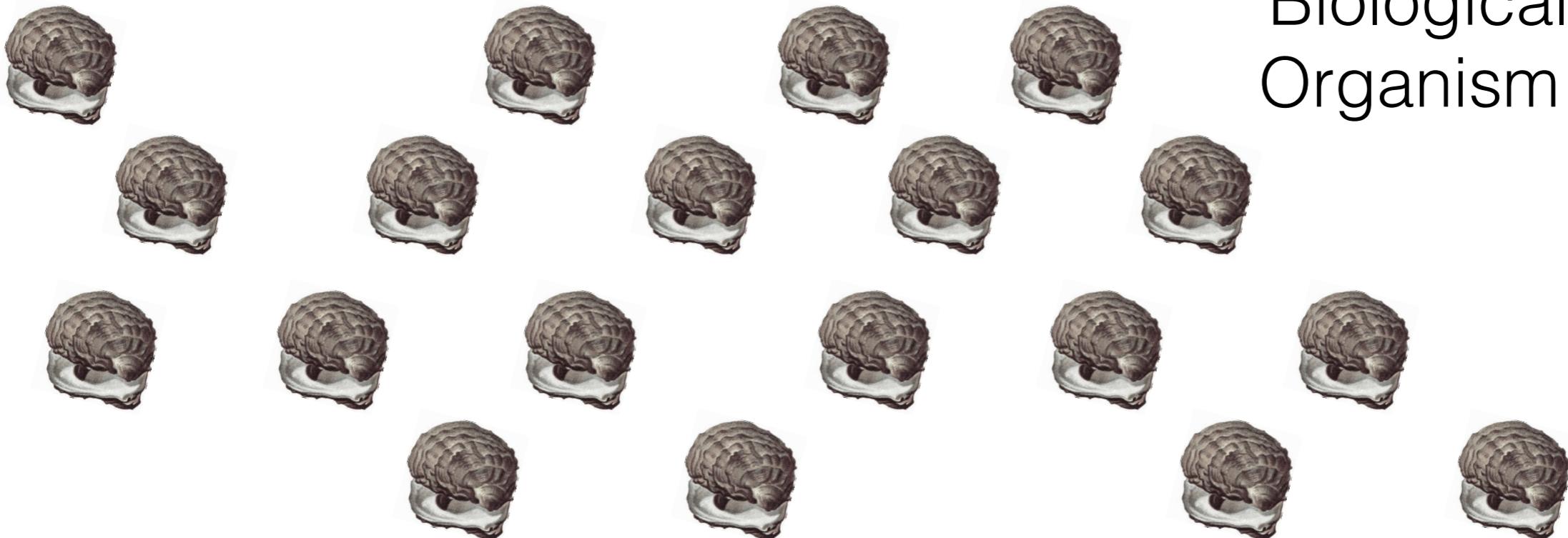
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# Conceptual Models for a functional role of DNA methylation



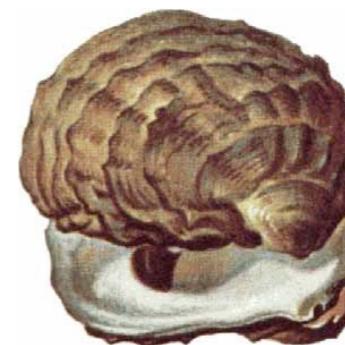
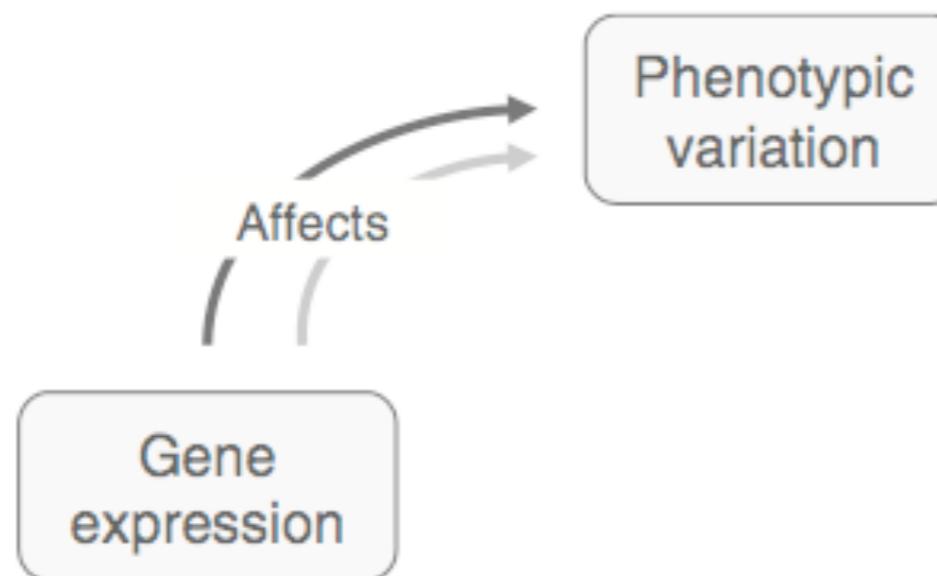
**Target Regulation**  
results in beneficial phenotype



Biological Scale?  
Organism

\*

# Conceptual Models for a functional role of DNA methylation

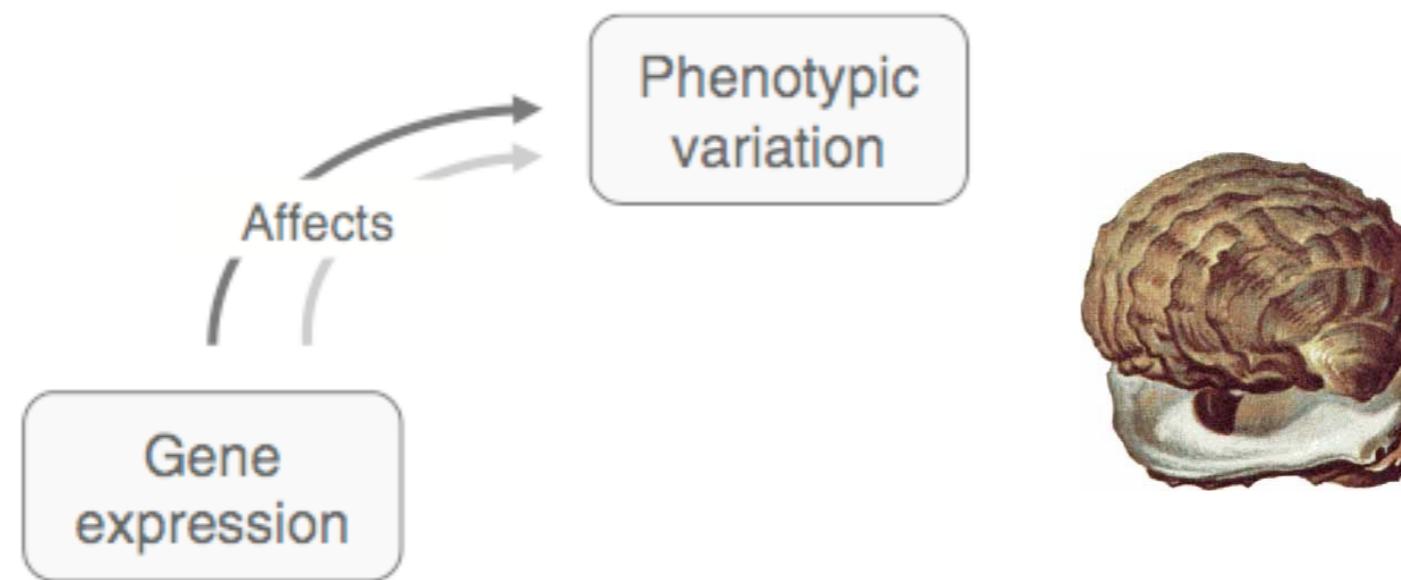


## Mystery - Natural Epigenetic Variation Exists



\*

# Conceptual Models for a functional role of DNA methylation

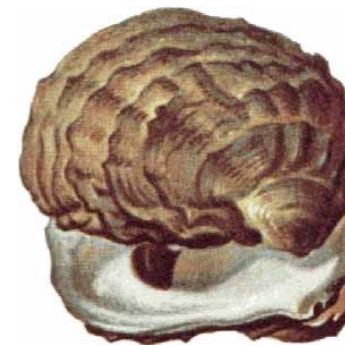
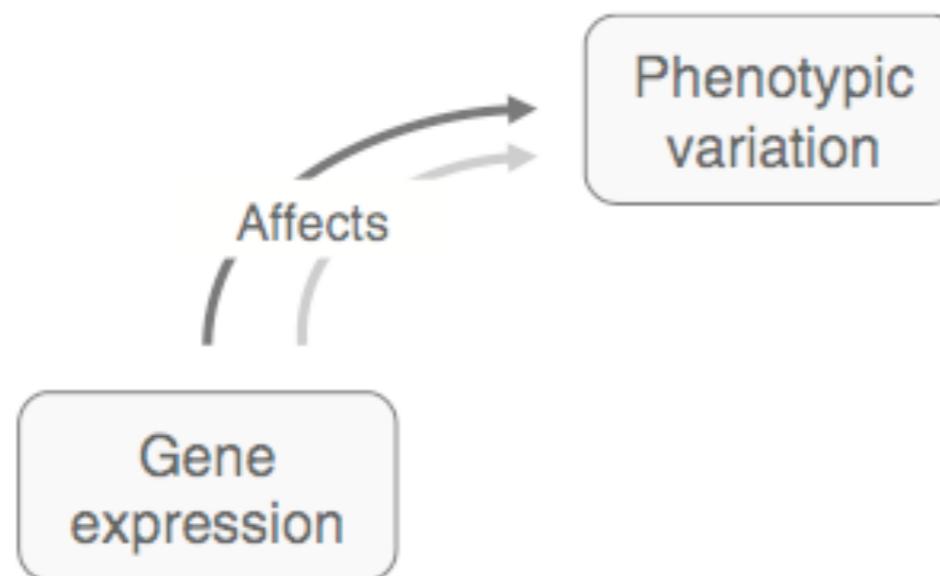


## Mystery - Natural Epigenetic Variation Exist

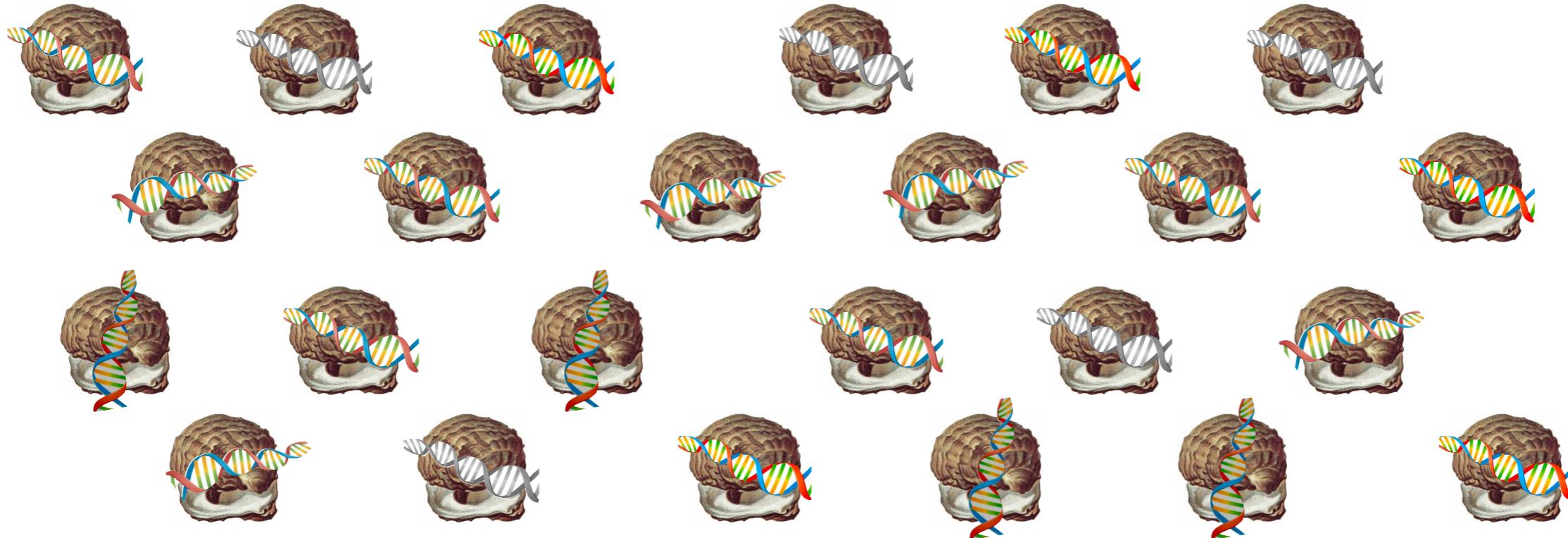
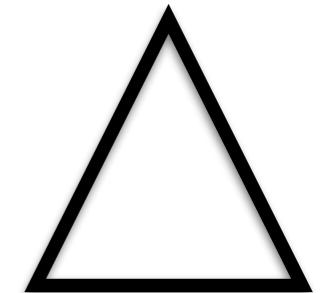


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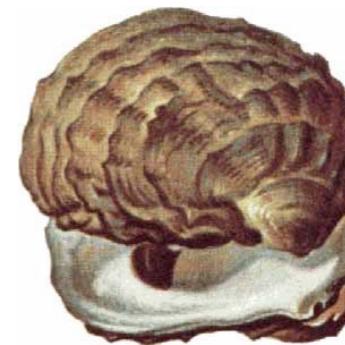
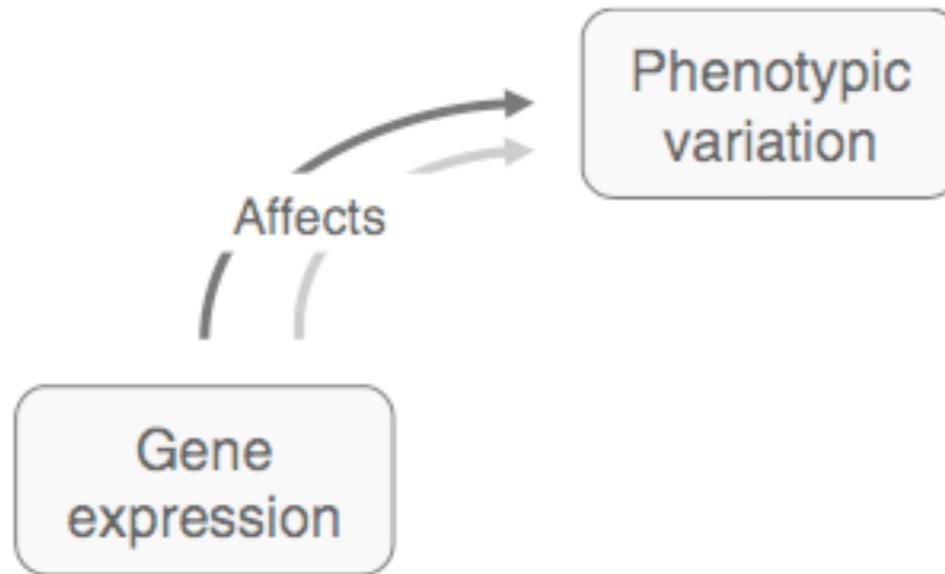
# Conceptual Models for a functional role of DNA methylation



**Mystery - Natural Epigenetic Variation Exist**  
that is subject selection



\*

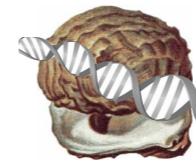


# Conceptual Models for a functional role of DNA methylation

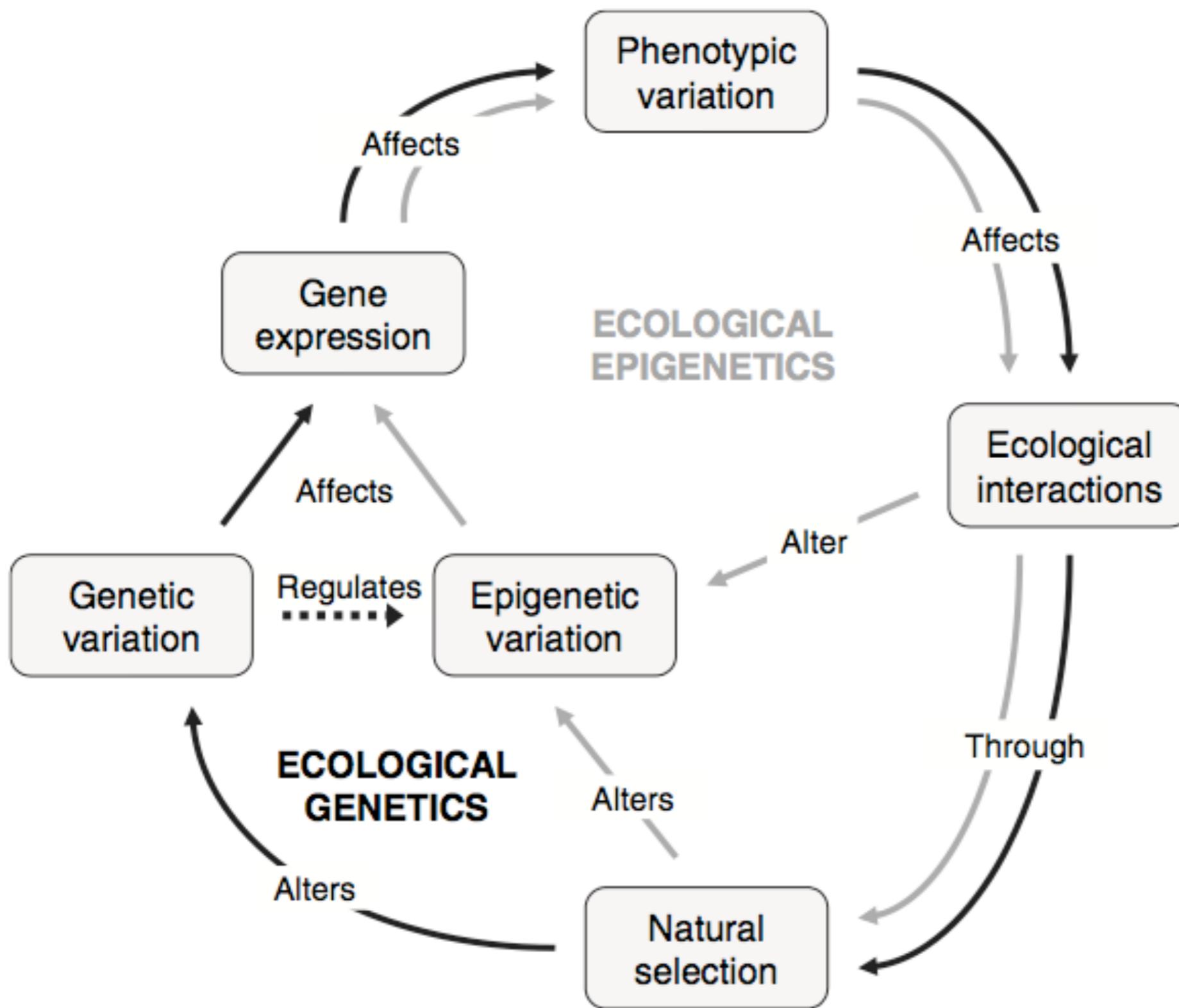
**Mystery - Natural Epigenetic Variation Exist**

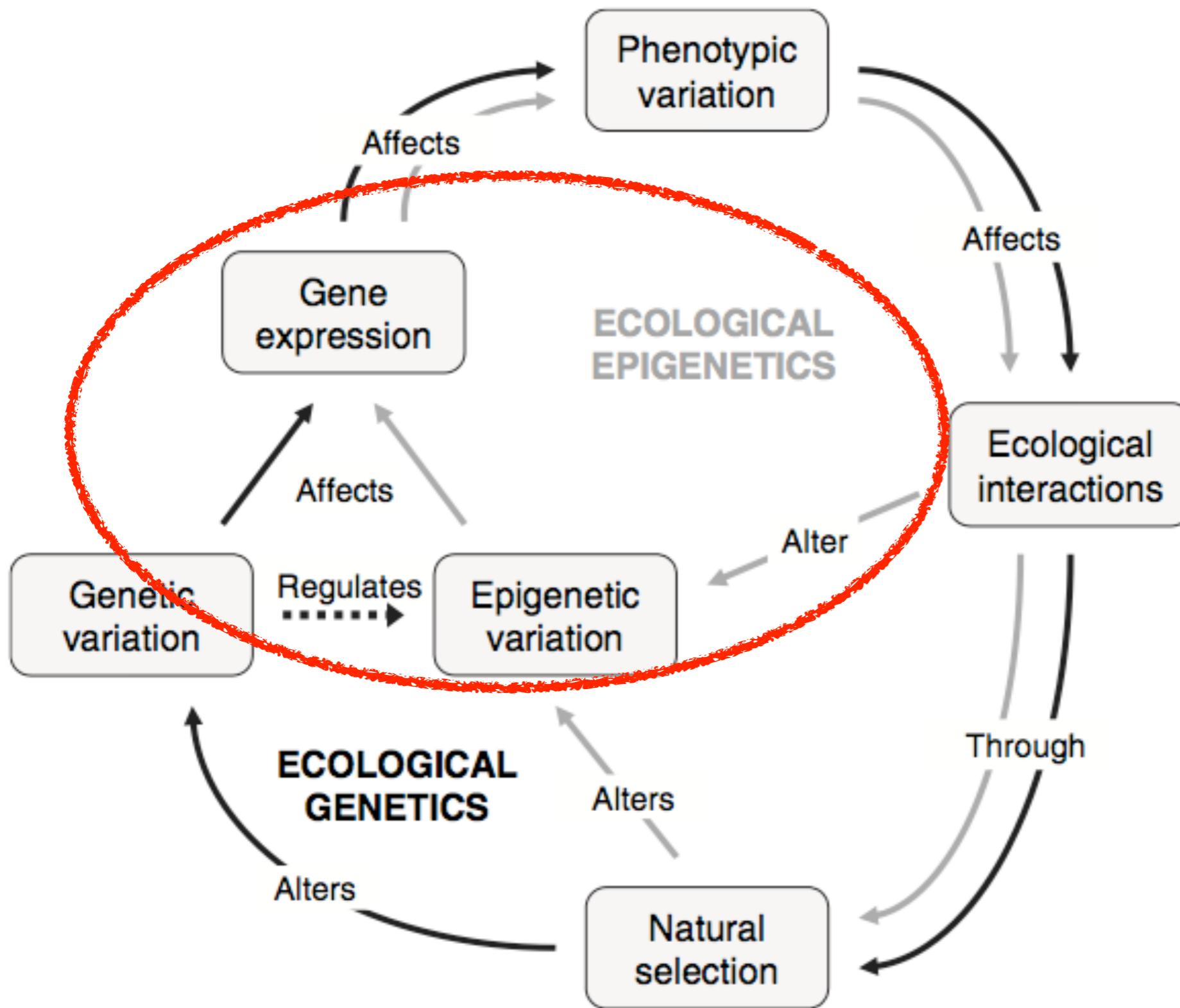


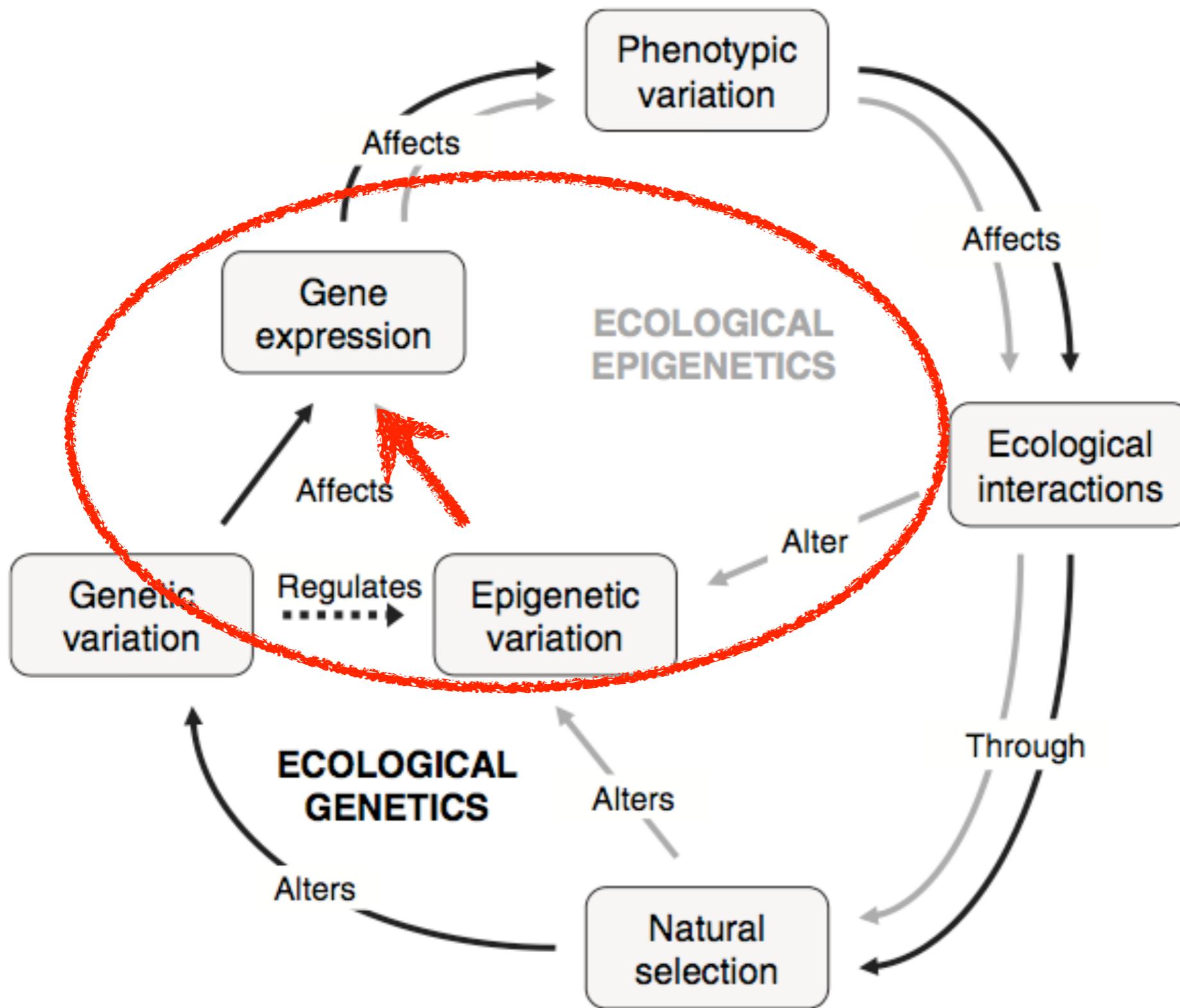
Biological Scale?  
Population



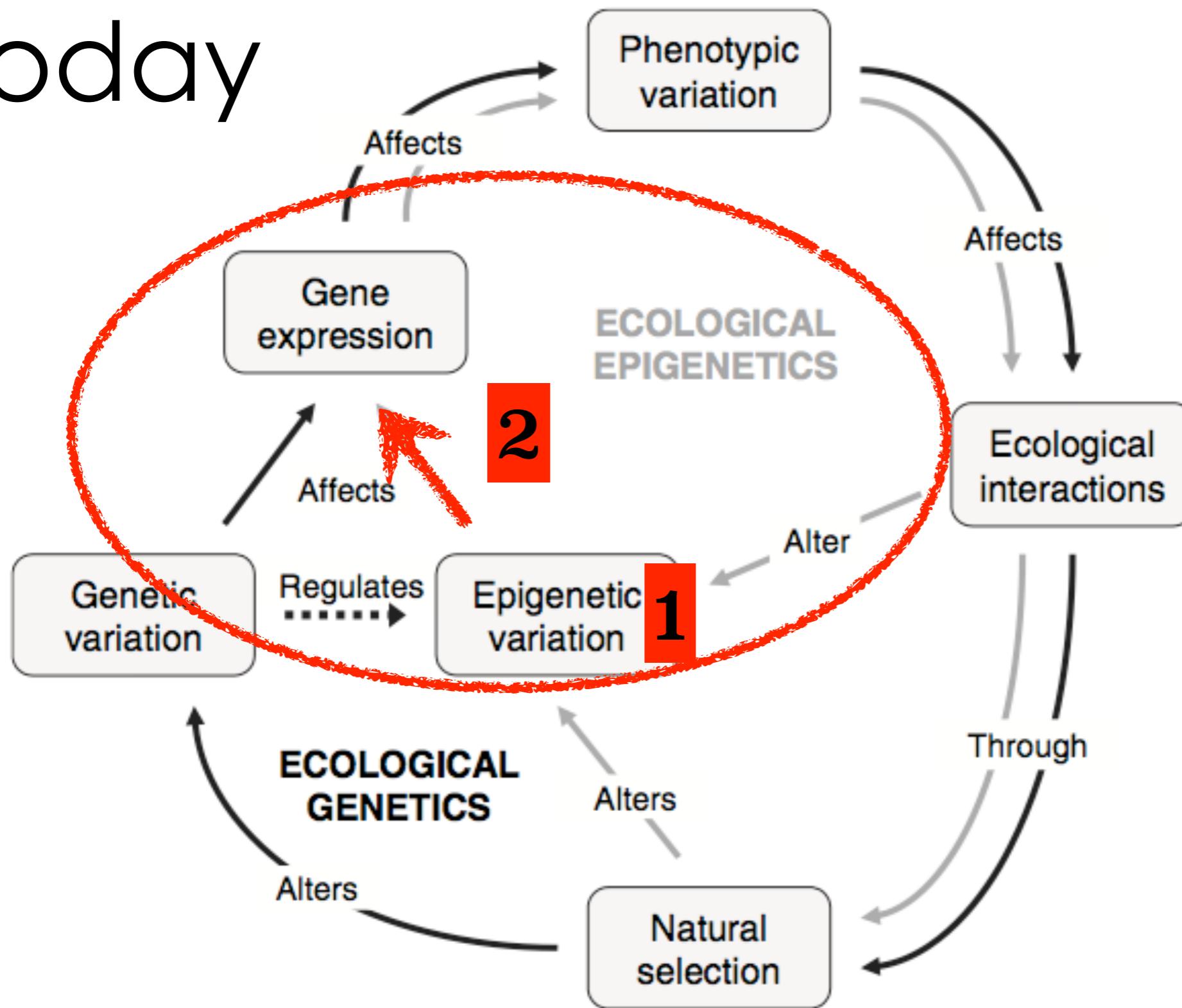
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# Today



*Ecology Letters*, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

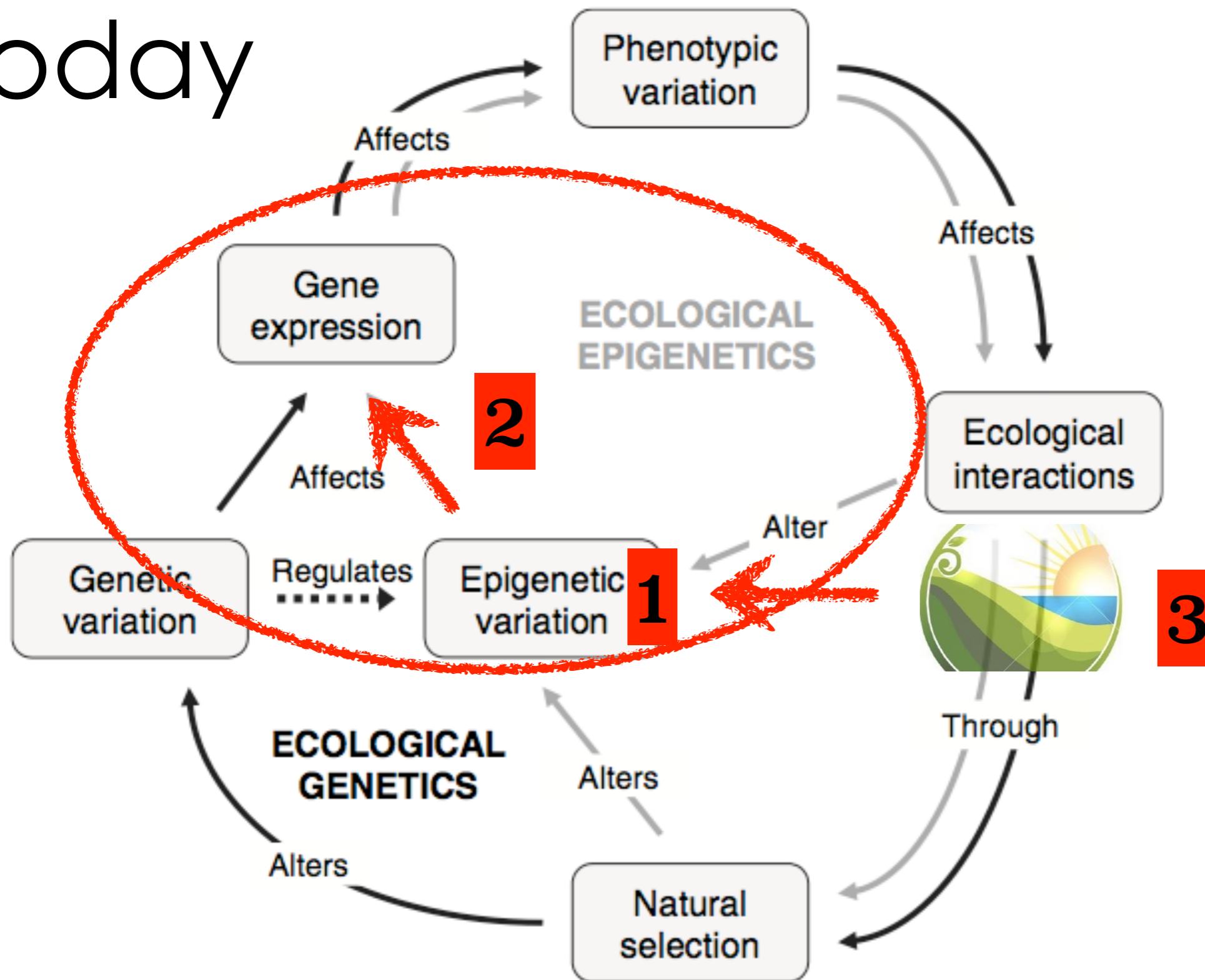
modified from

IDEA AND  
PERSPECTIVE

Epigenetics for ecologists

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

# Today



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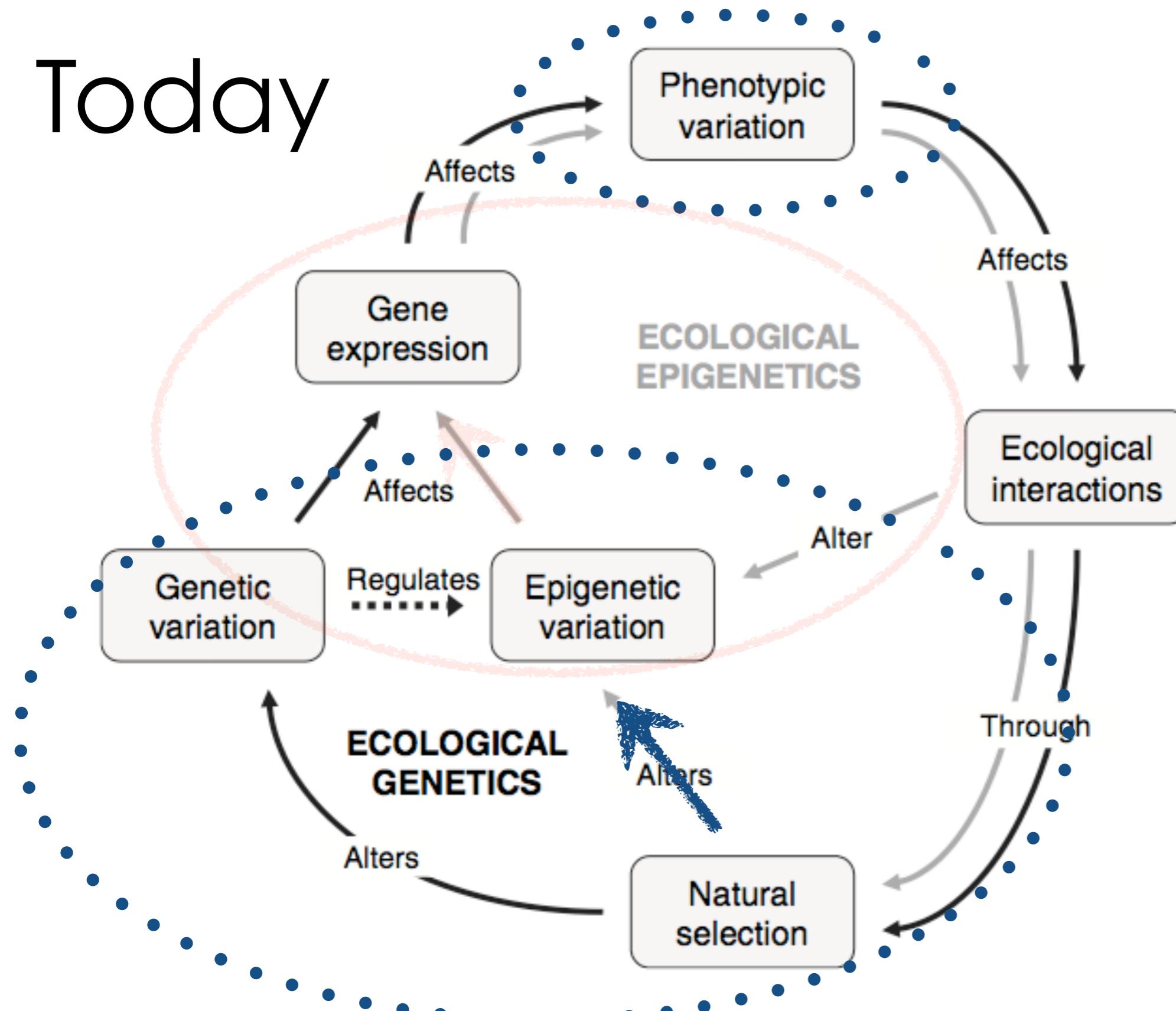
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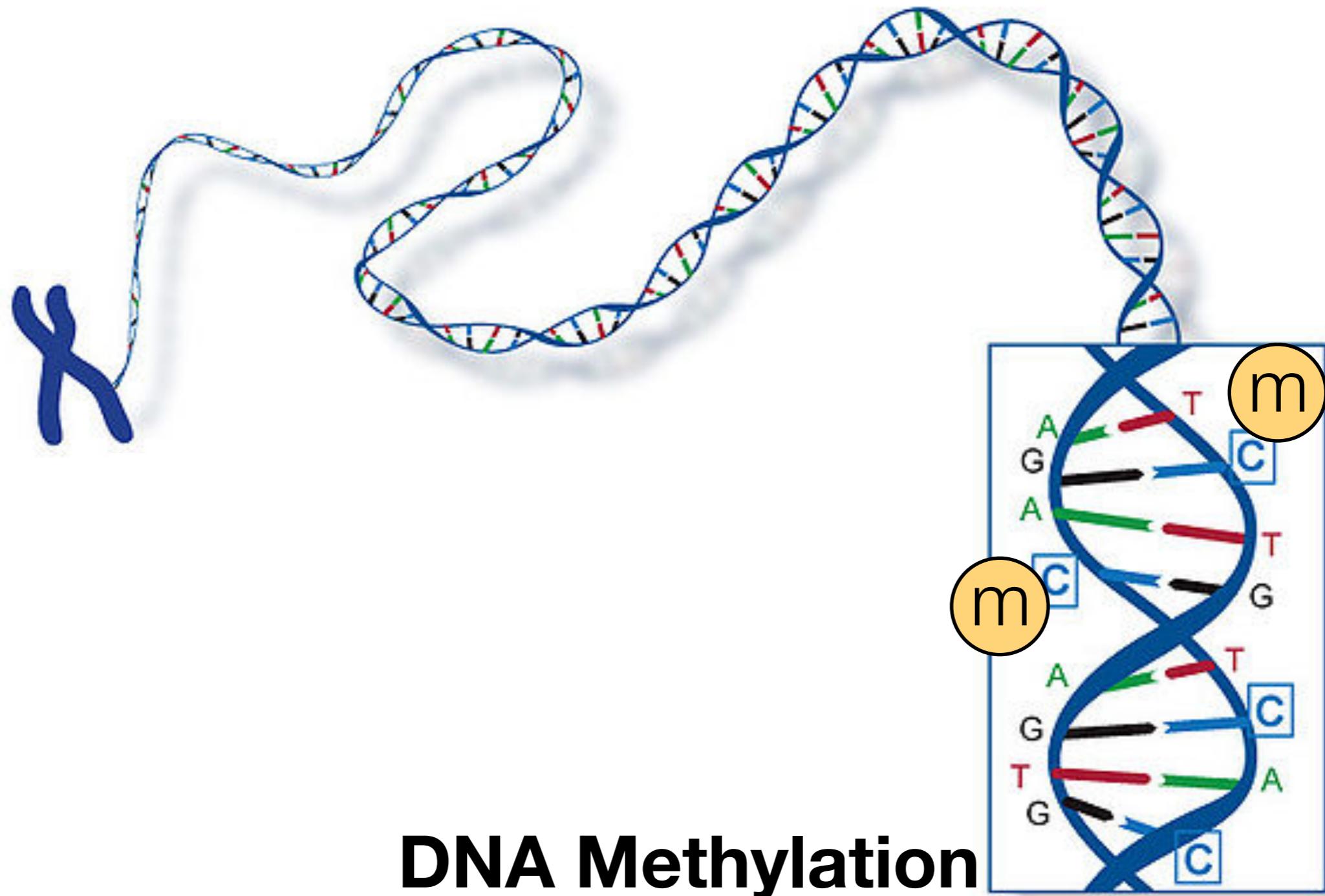
# Genome Resources



# Genome Resources

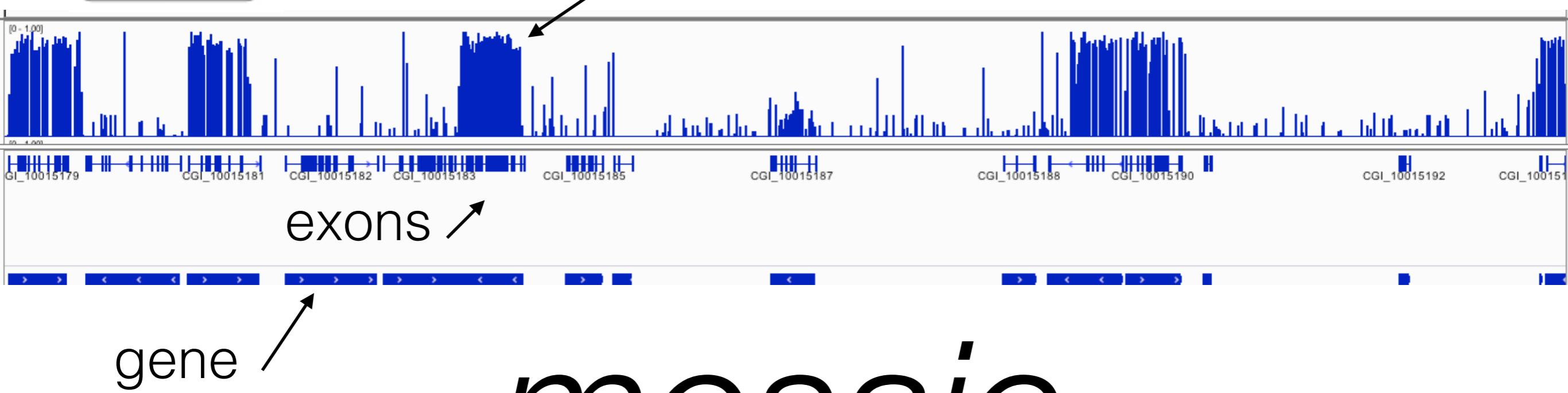






Epigenetic variation **1**

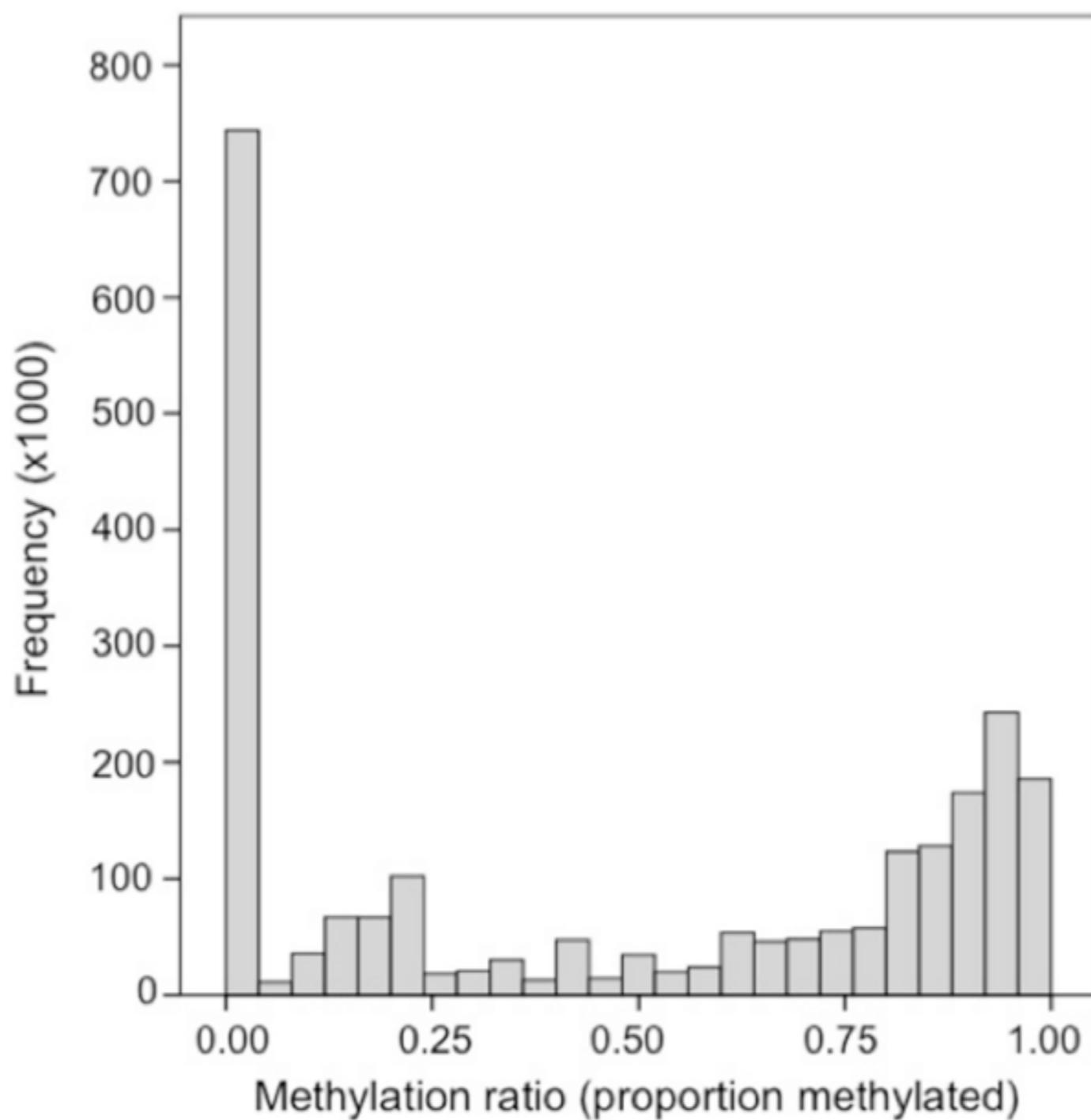
DNA methylation level (0-100%) @ cytosines



*mosaic*

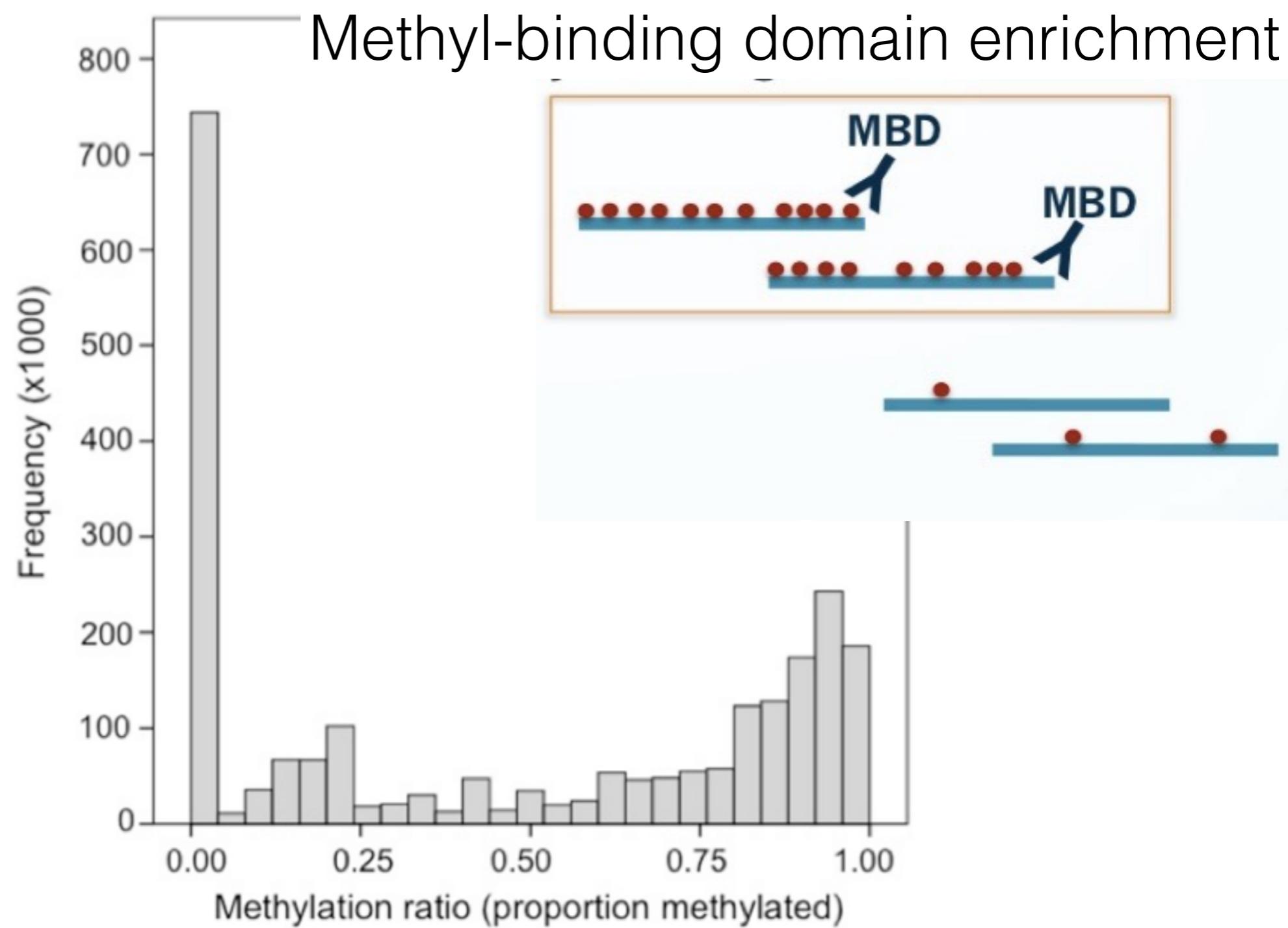
associated with gene bodies

Epigenetic variation **1**



**Figure 1** Frequency distribution of methylation ratios for CpG dinucleotides in oyster gill tissue. A total of 2,625,745 CpG dinucleotides with  $\geq 5 \times$  coverage are represented.

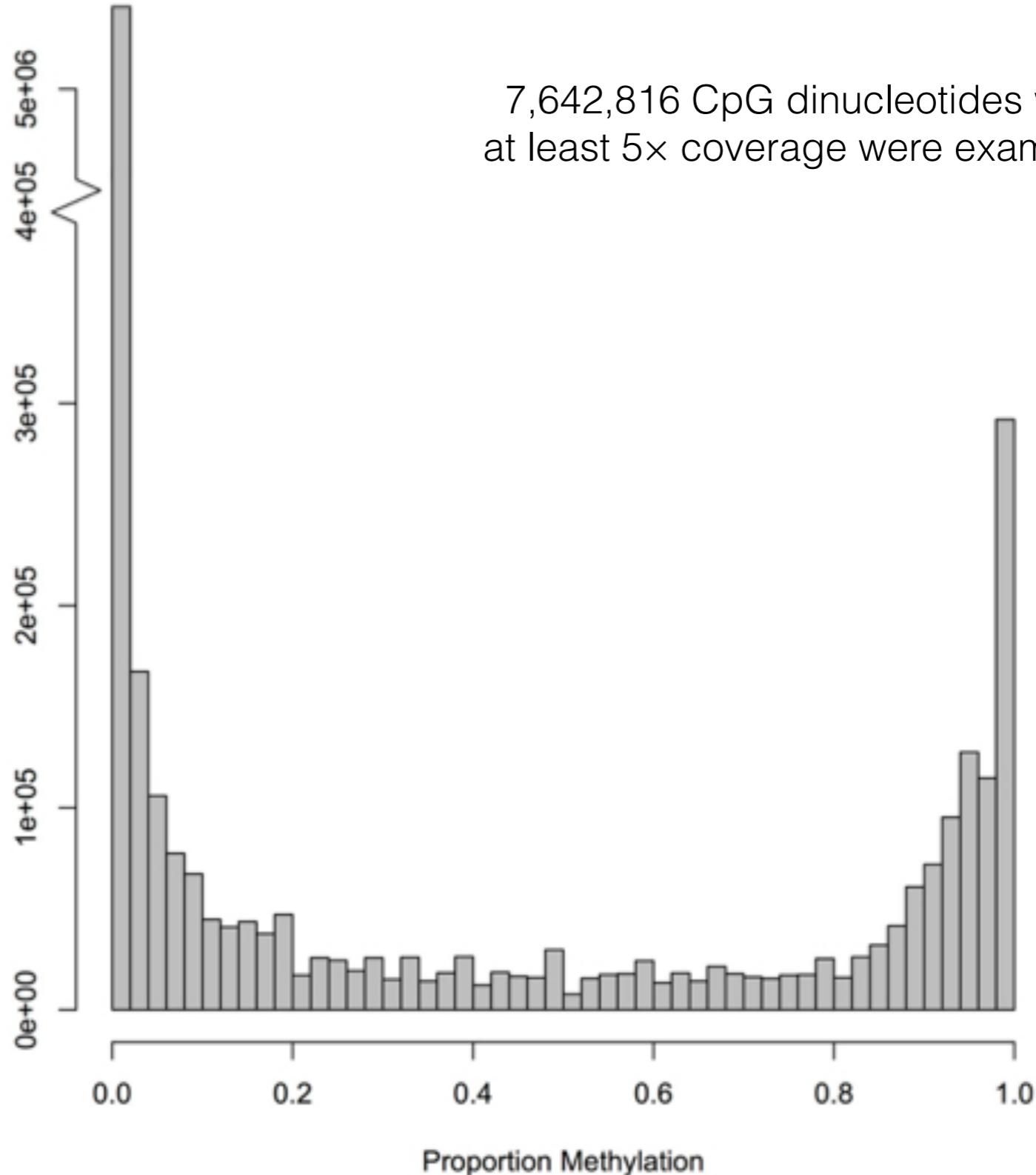
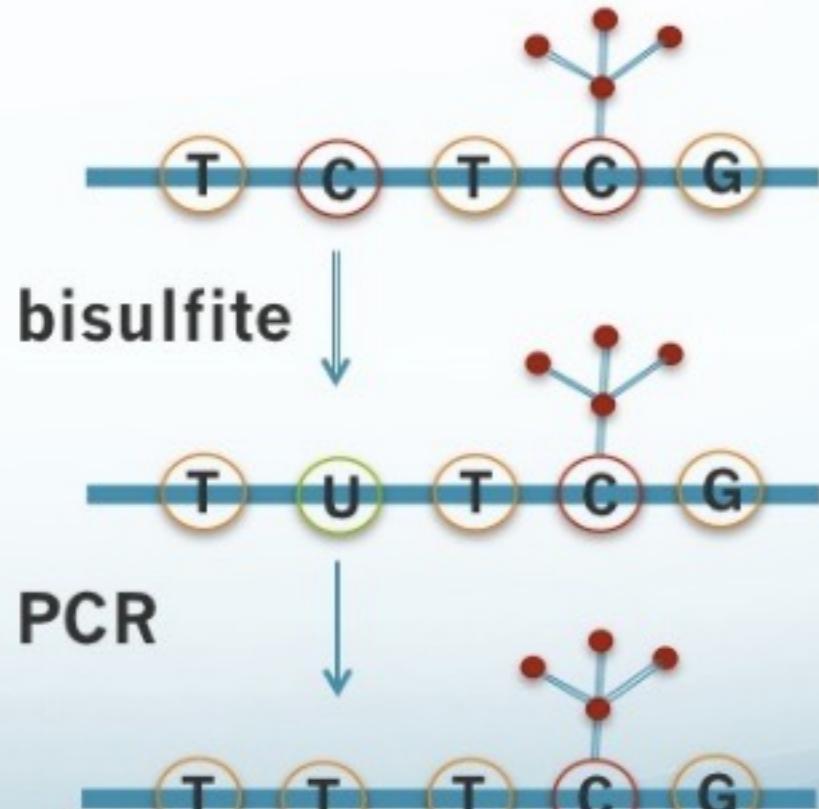
Epigenetic variation **1**



**Figure 1** Frequency distribution of methylation ratios for CpG dinucleotides in oyster gill tissue. A total of 2,625,745 CpG dinucleotides with  $\geq 5 \times$  coverage are represented.

Epigenetic variation **1**

- Bisulfite conversion

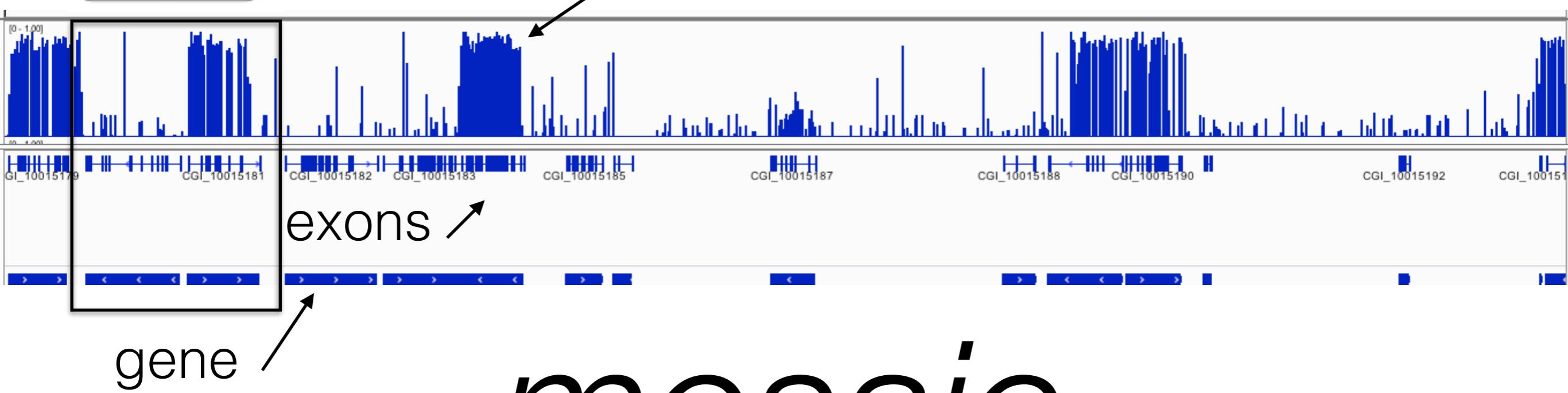


7,642,816 CpG dinucleotides with at least 5x coverage were examined



Epigenetic variation **1**

DNA methylation level (0-100%) @ cytosines

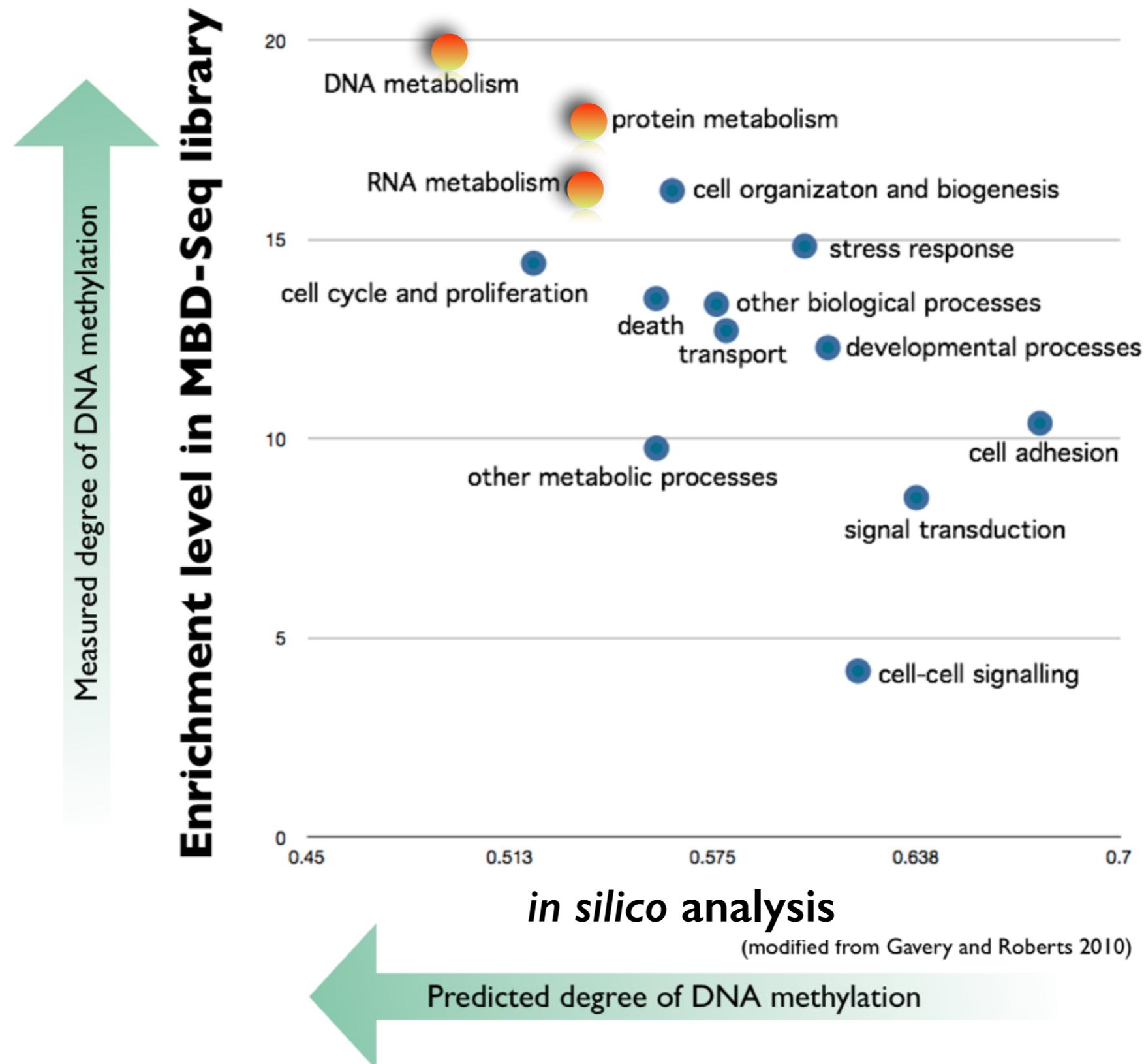


*mosaic*

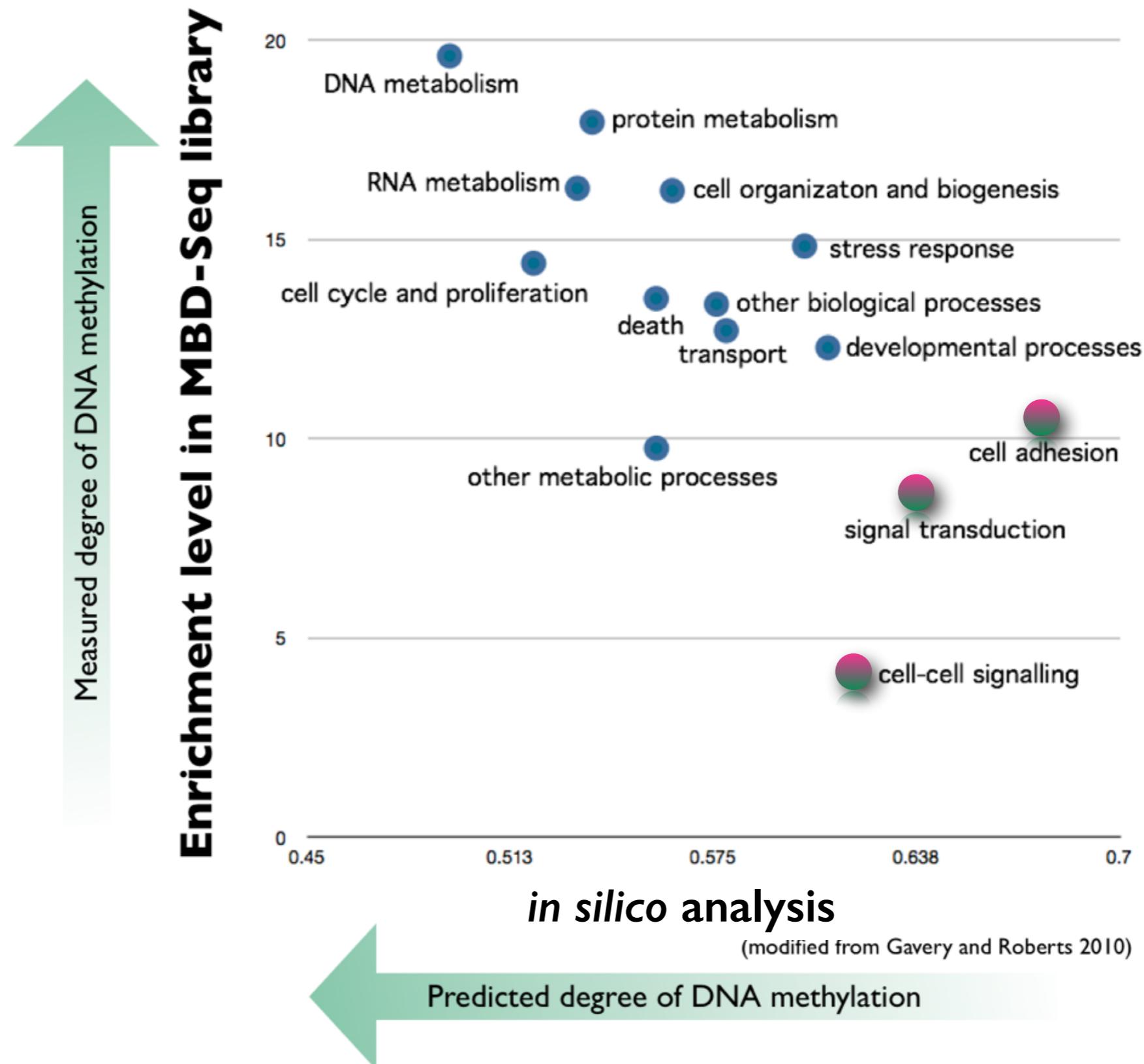
**Why are only a subset of genes methylated?**

associated with gene bodies

Epigenetic variation **1**



Epigenetic variation **1**



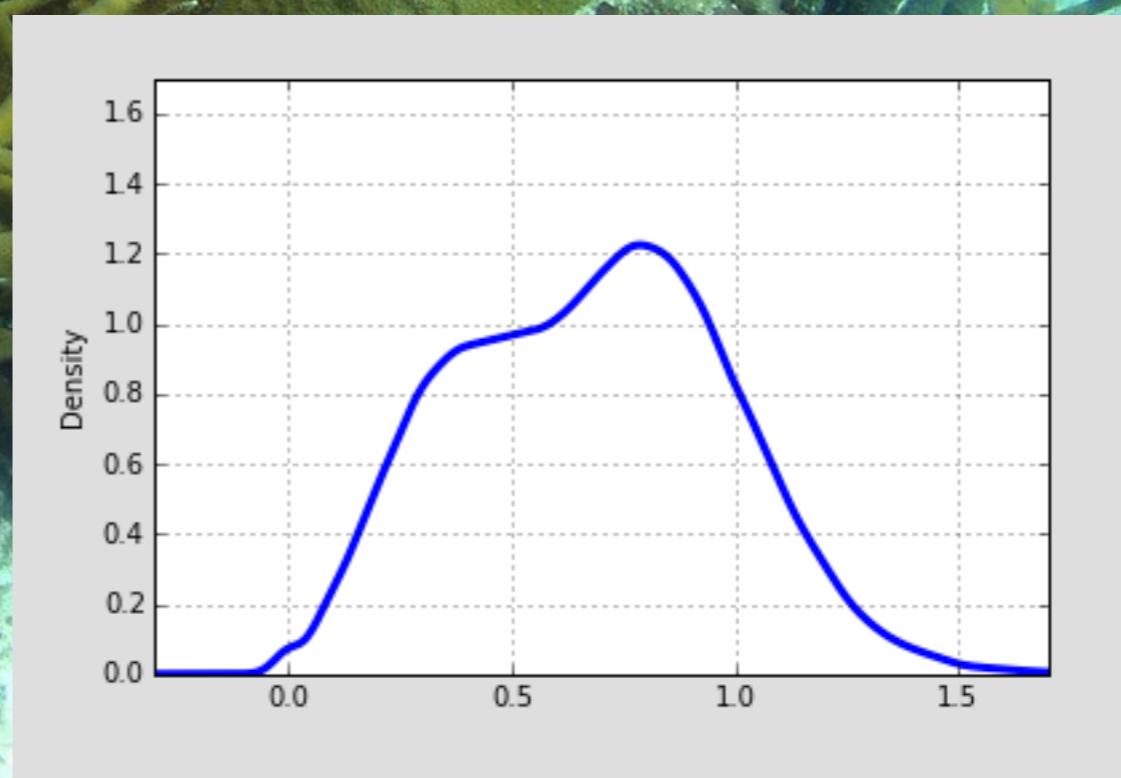
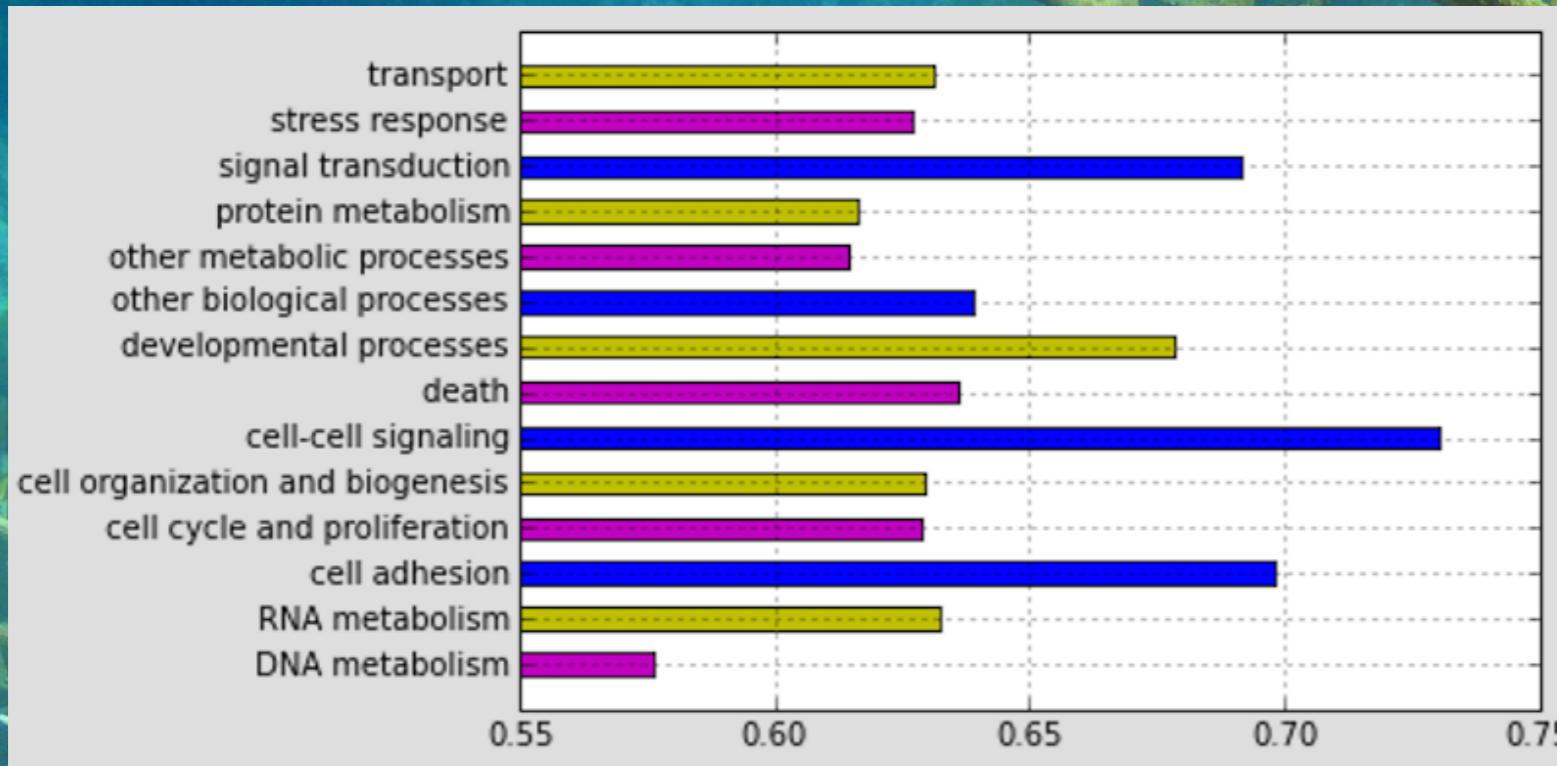
Jay Dimond

*Acropora palmata*

*Acropora cervicornis*

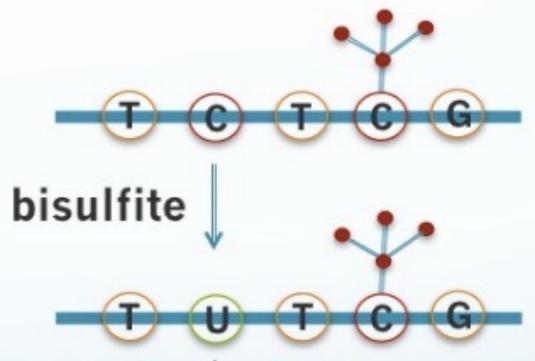
# Jay Dimond

*Acropora palmata*



Epigenetic variation **1**

# Family and Developmental Variation



Sperm &  
Larvae  
(72h & 120h)



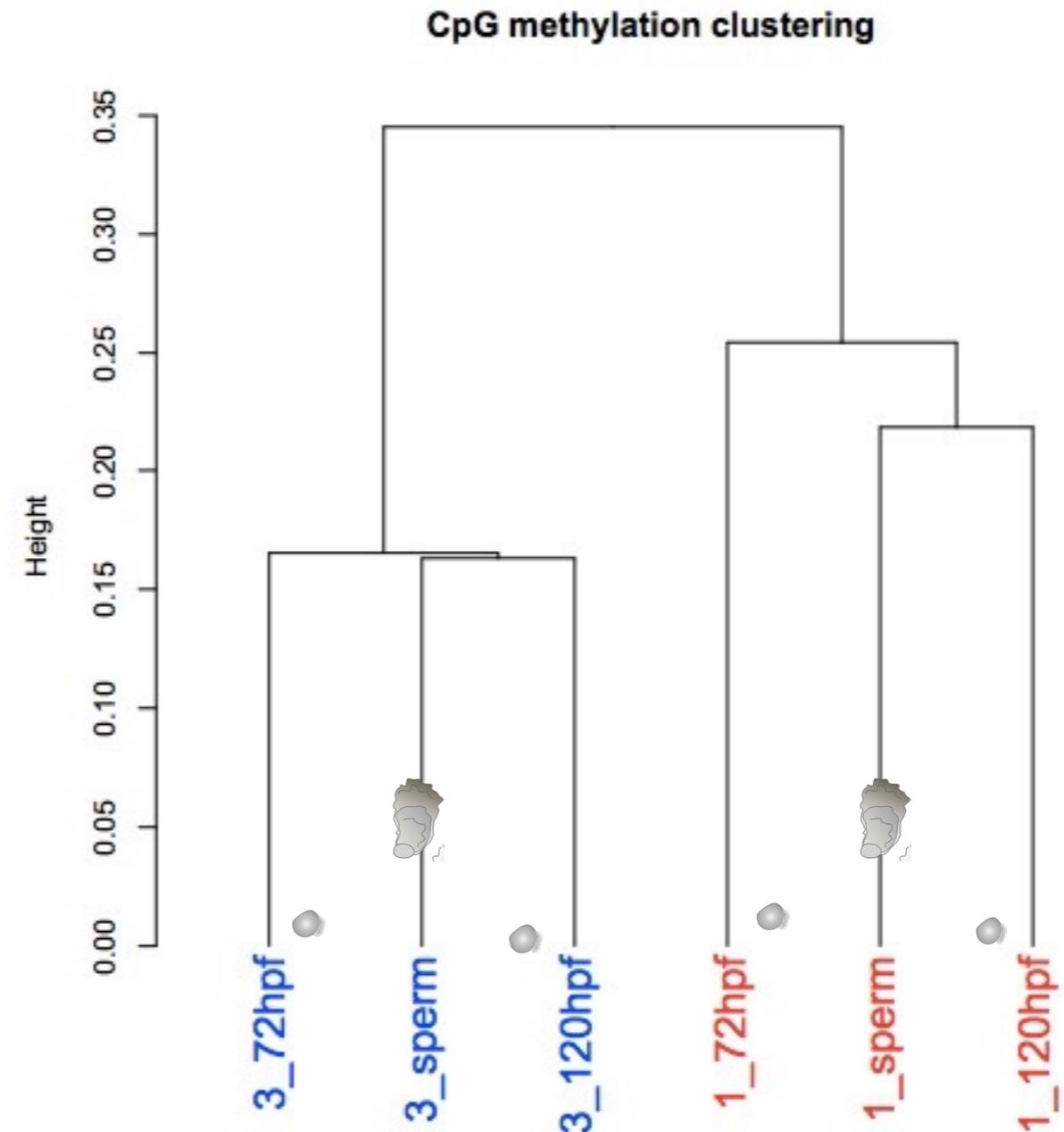
**bioRxiv**  
beta  
THE PREPRINT SERVER FOR BIOLOGY

New Results

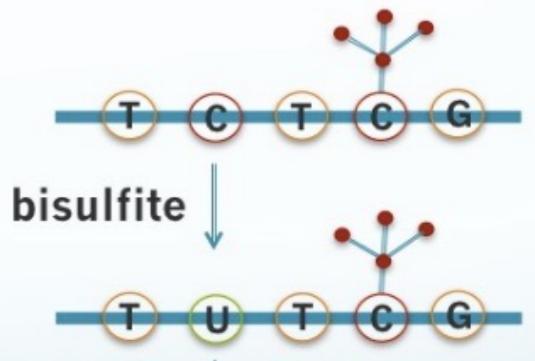
**Indication of family-specific DNA methylation patterns in developing oysters**

Claire E. Olson , Steven B. Roberts

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



# Family and Developmental Variation



## Inheritance



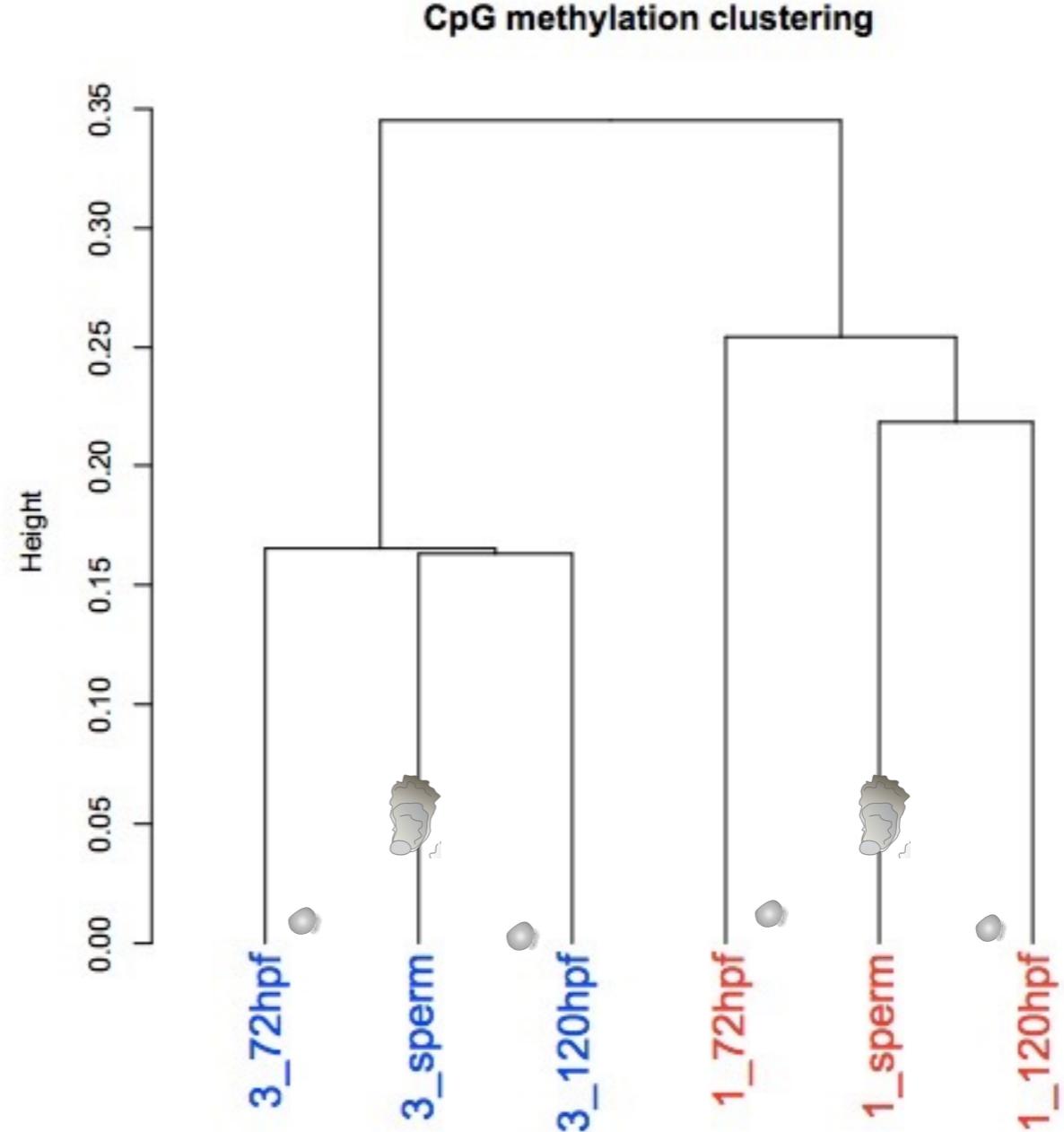
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THE PREPRINT SERVER FOR BIOLOGY

New Results

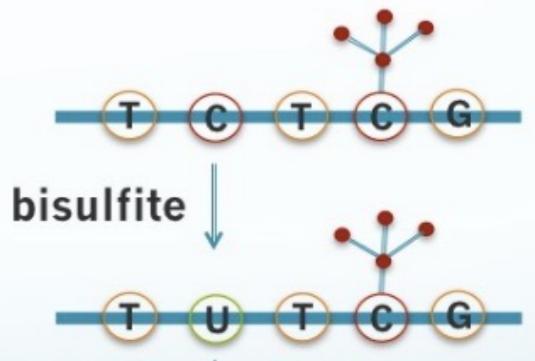
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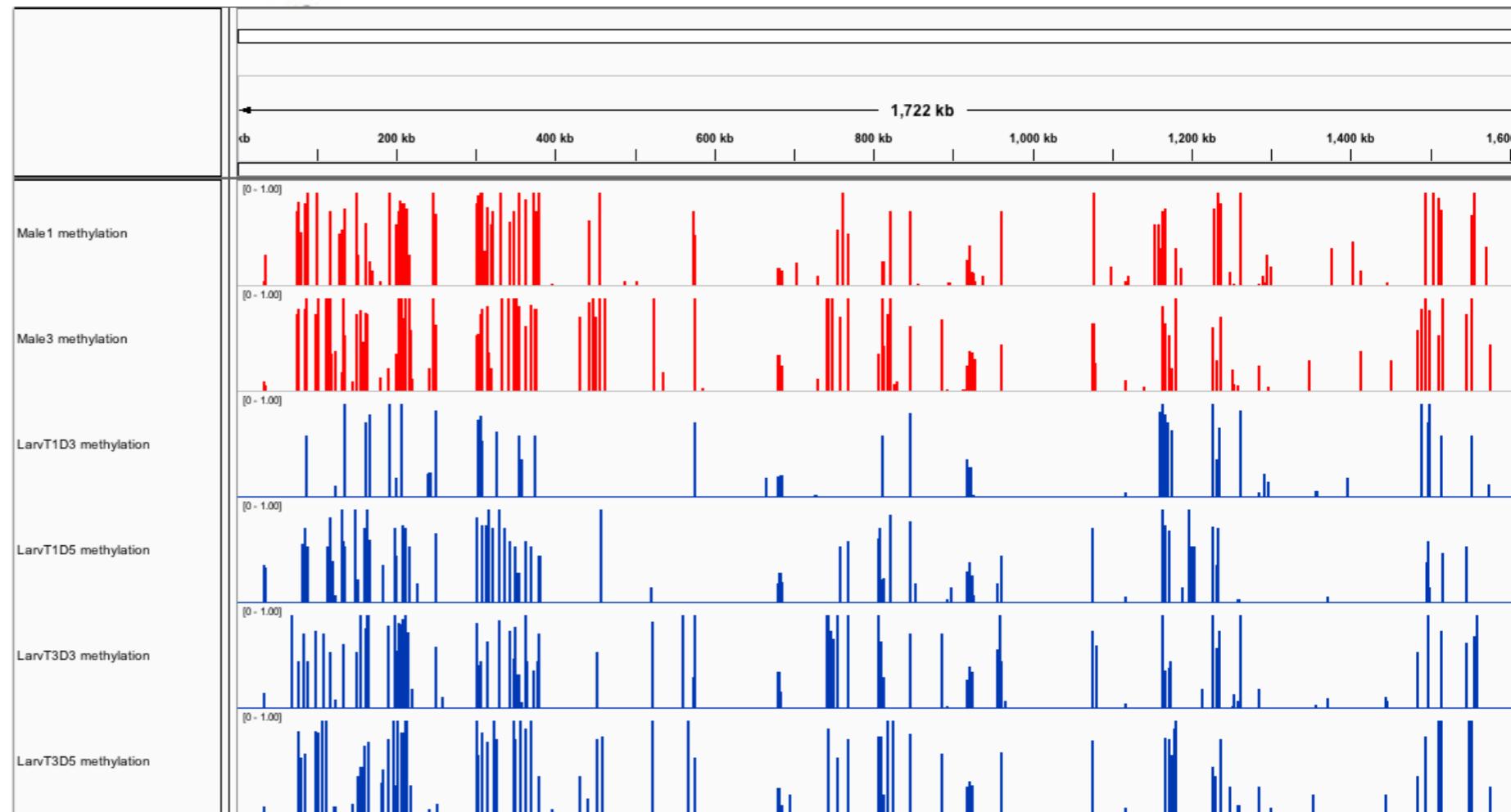
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# Family and Developmental Variation



Sperm &  
Larvae  
(72h & 120h)



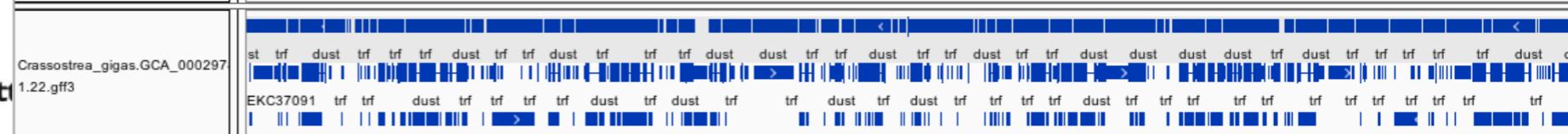
**bioRxiv**  
beta

THE PREPRINT SERVER FOR BIOLOGY

DNA methylation level (0-100%) @ cytosines

New Results

**Indication of family-specific DNA methylation patterns in developing oysters**



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

Gene  
expression



Epigenetic  
variation

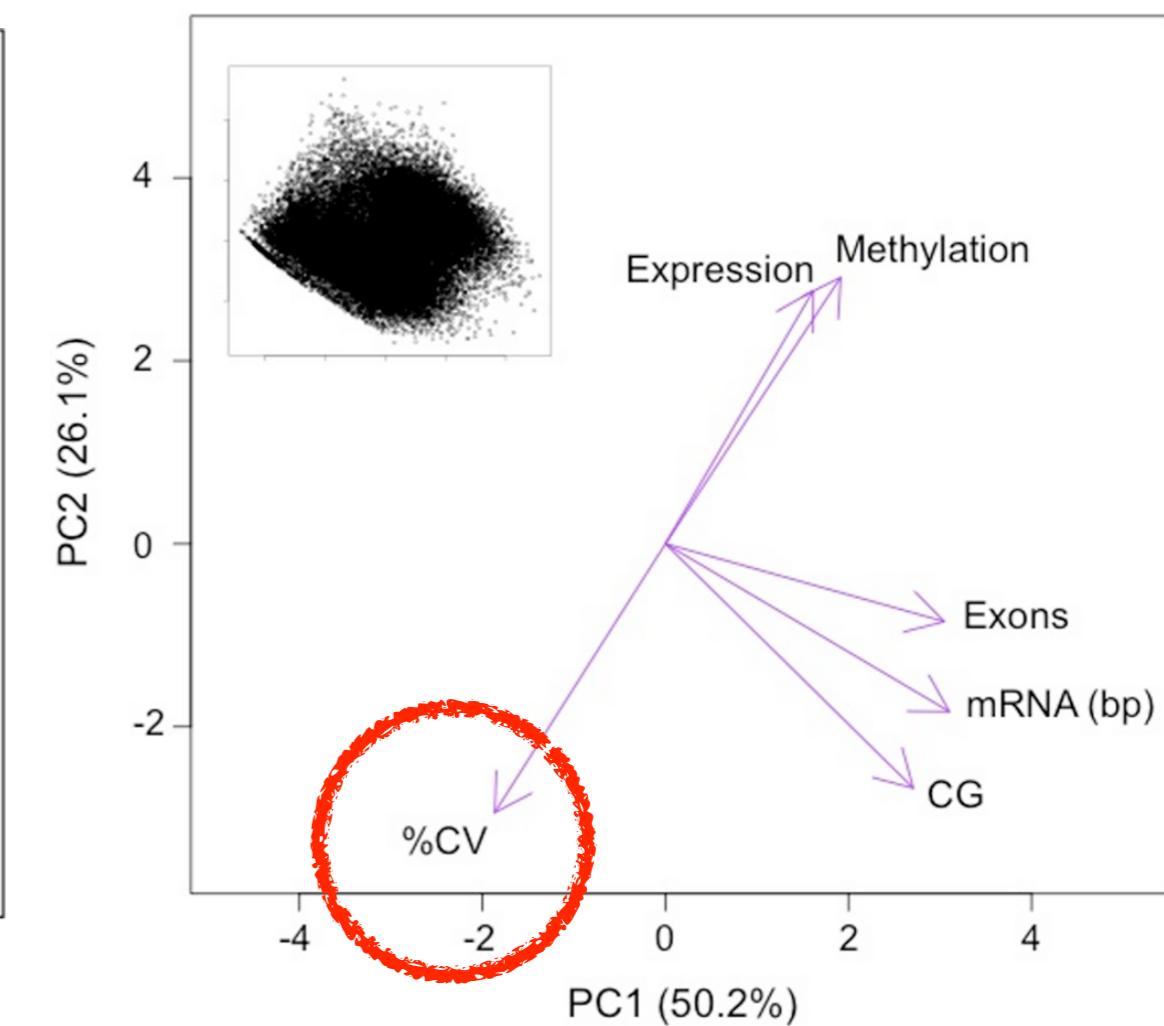
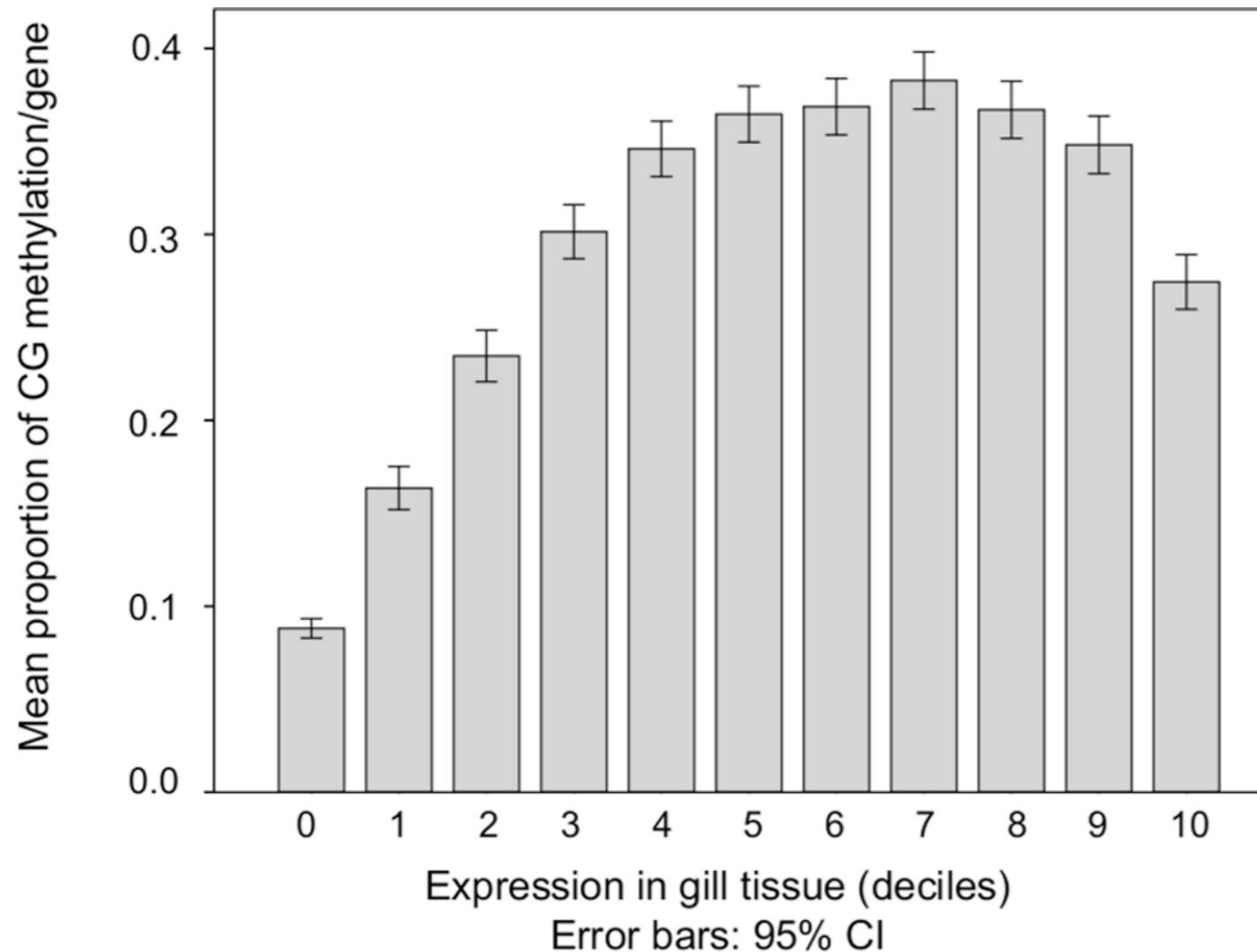
# Function?

Gene expression

2

Epigenetic variation

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

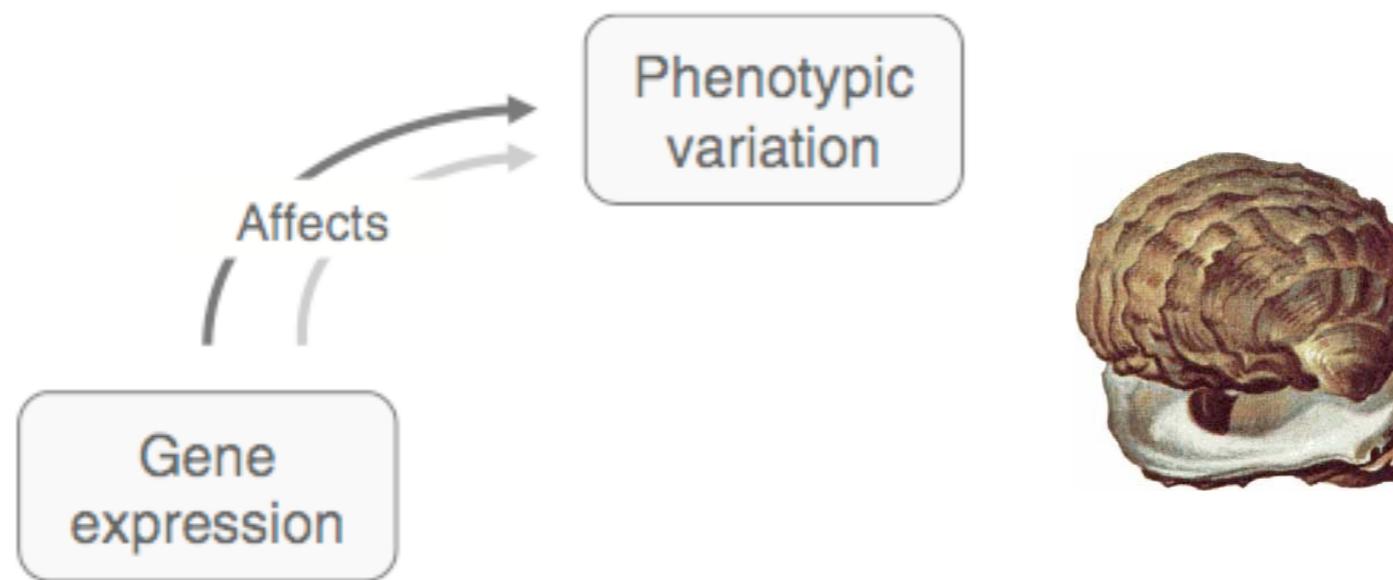




In species that experience a diverse range of environmental conditions, processes have evolved to increase the number of potential phenotypes in a population in order to improve the chances for an individual's survival.



# Conceptual Models for a functional role of DNA methylation



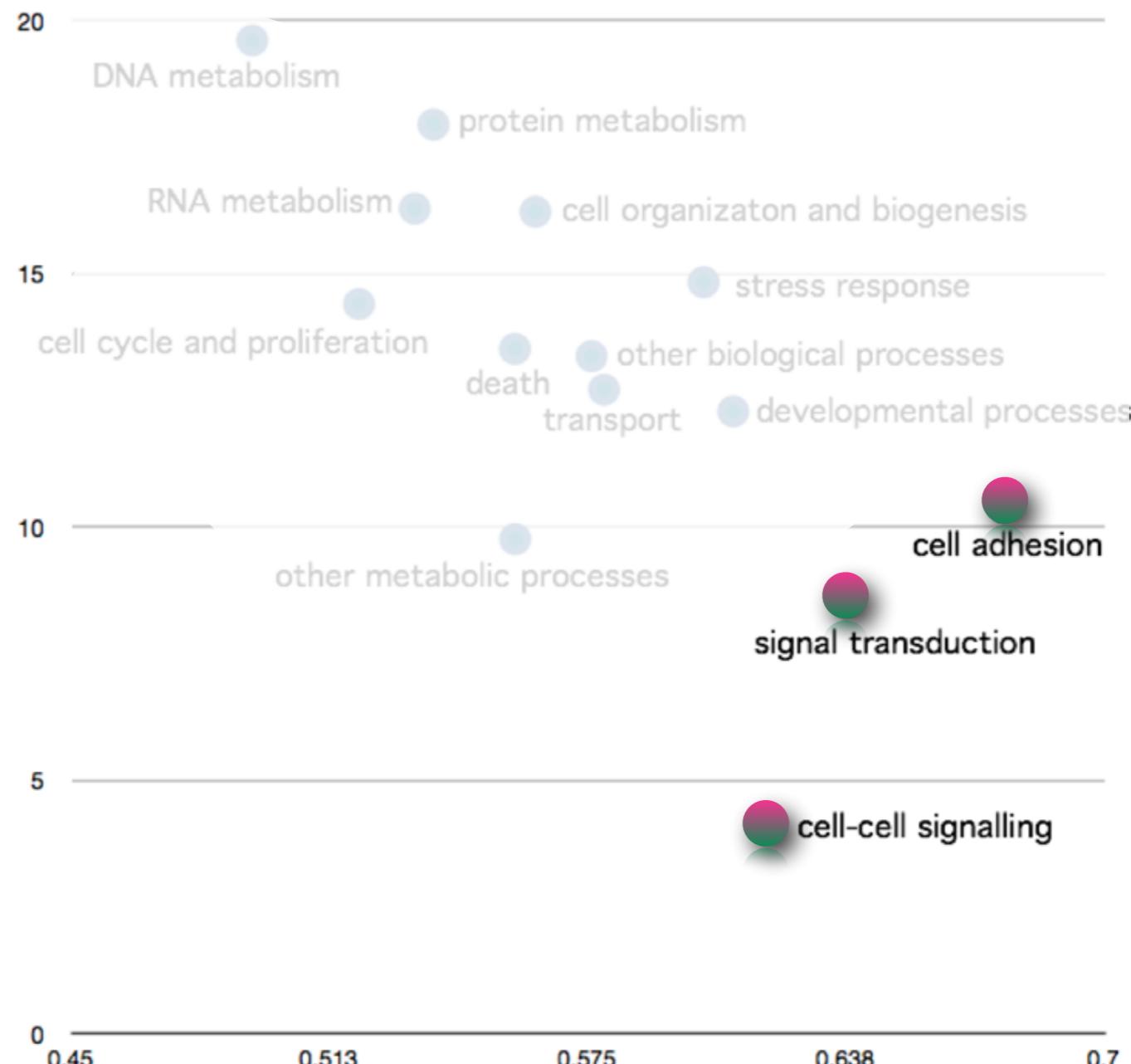
## Stochastic Variation

increased transcriptional opportunities  
increased likelihood of suitable phenotype



Gene expression

Epigenetic variation  
2

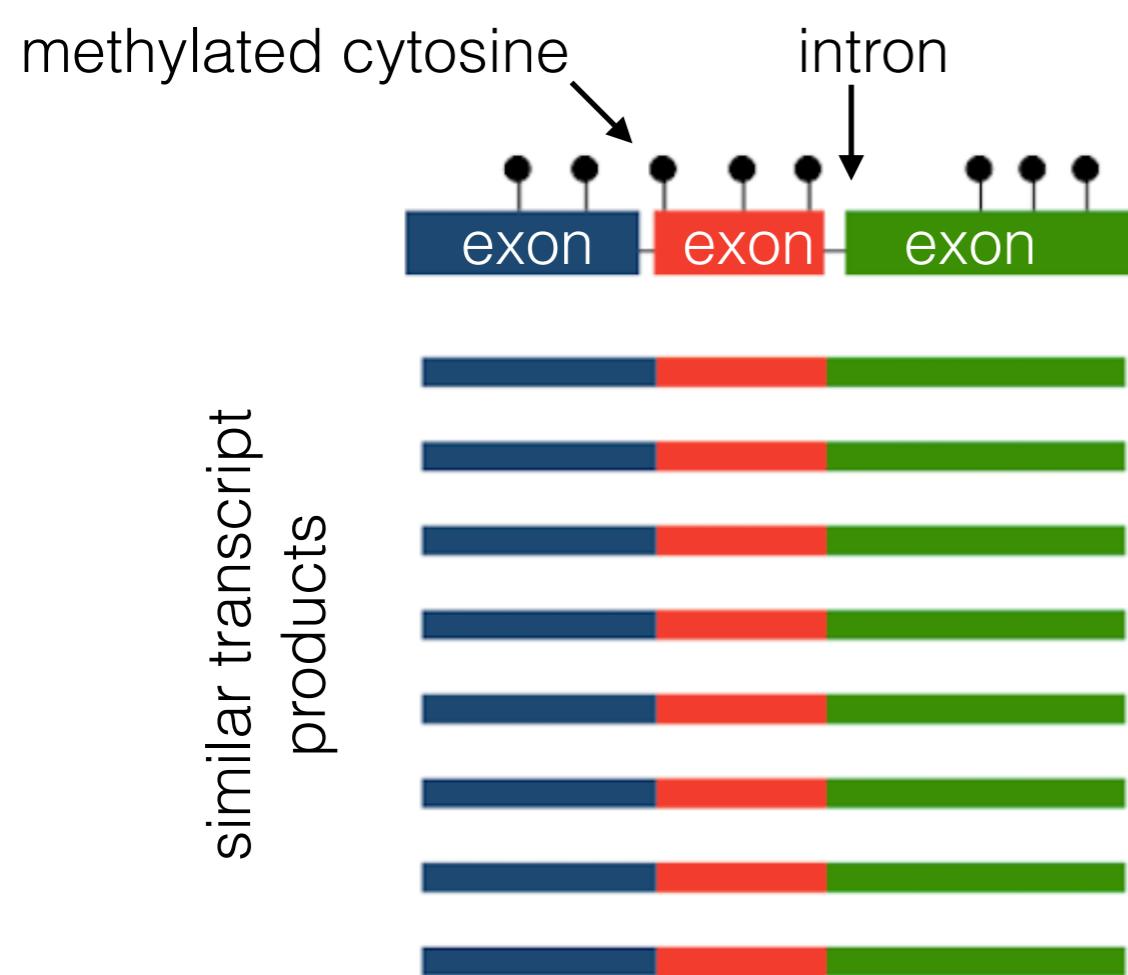


*in silico analysis*

(modified from Gavery and Roberts 2010)

Predicted degree of DNA methylation

Roberts and Gavery 2012

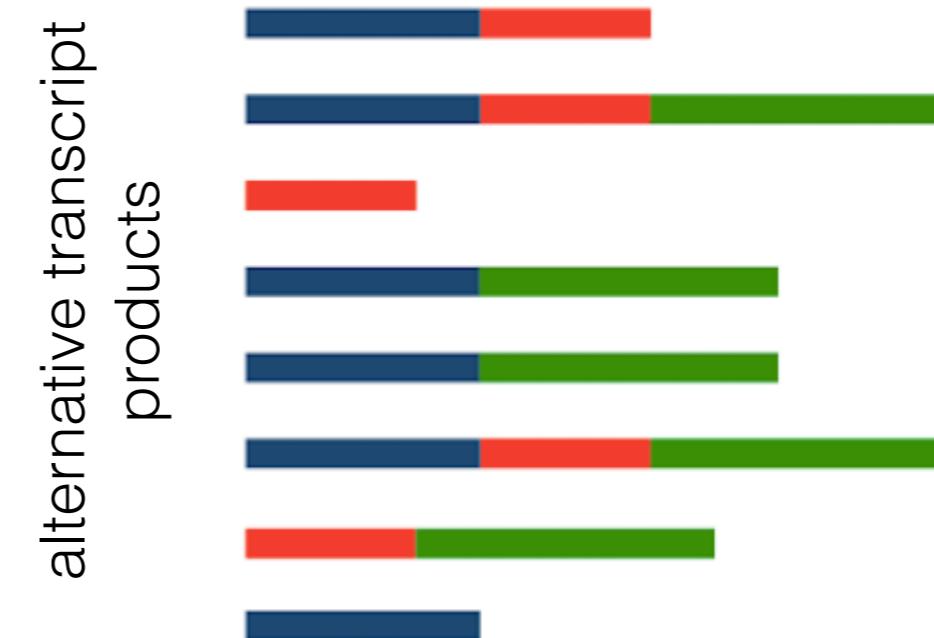


housekeeping

# Stochastic Variation

## A context dependent role for DNA methylation in bivalves

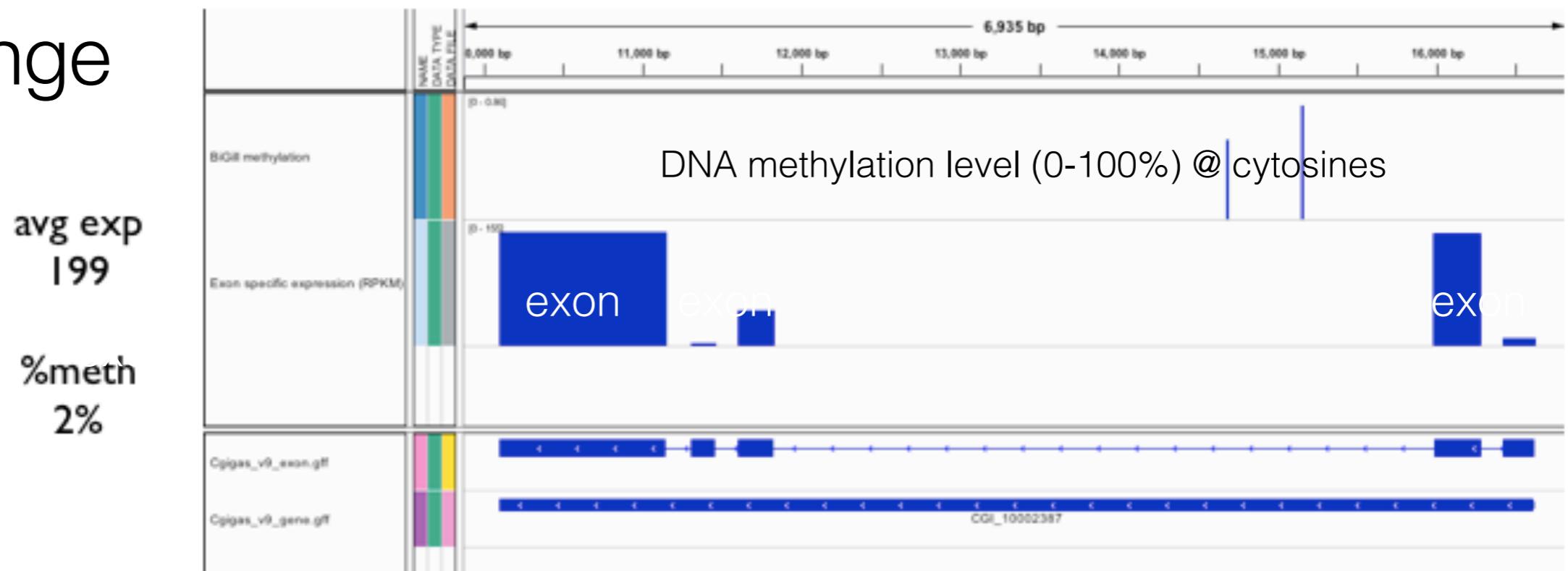
Mackenzie R. Gavery and Steven B. Roberts  
Advance Access publication date 7 January 2014



response to  
change

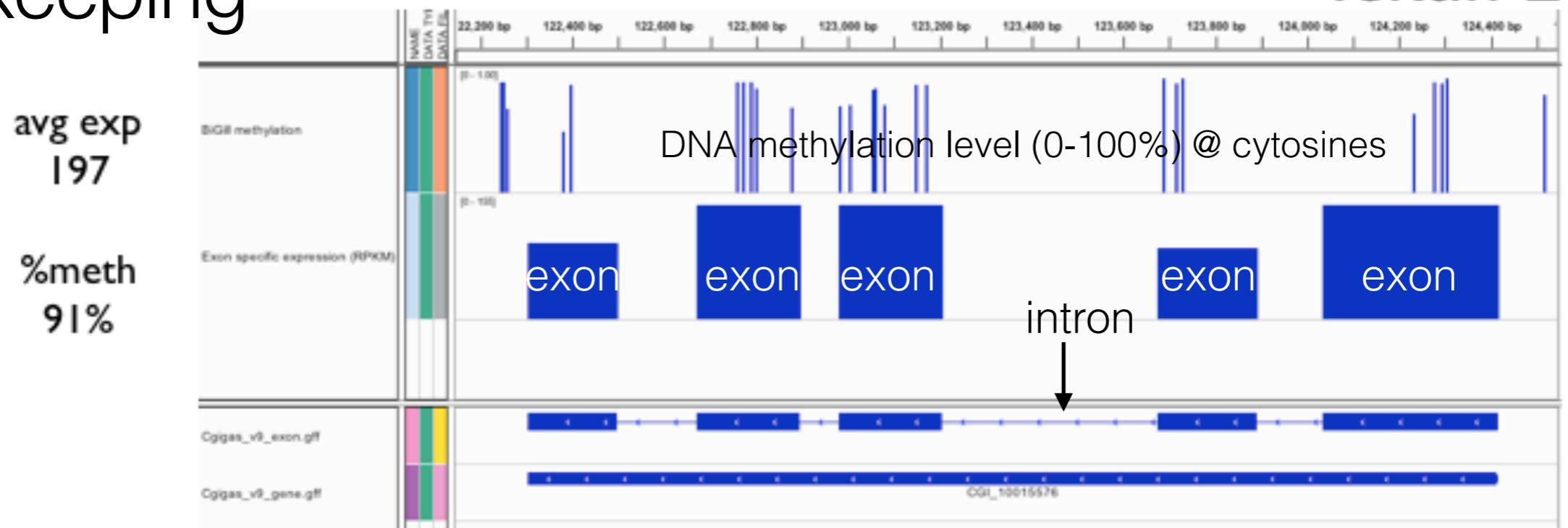
response to  
change

# Heat shock 70 kDa protein 12A



housekeeping

# Tektin-2



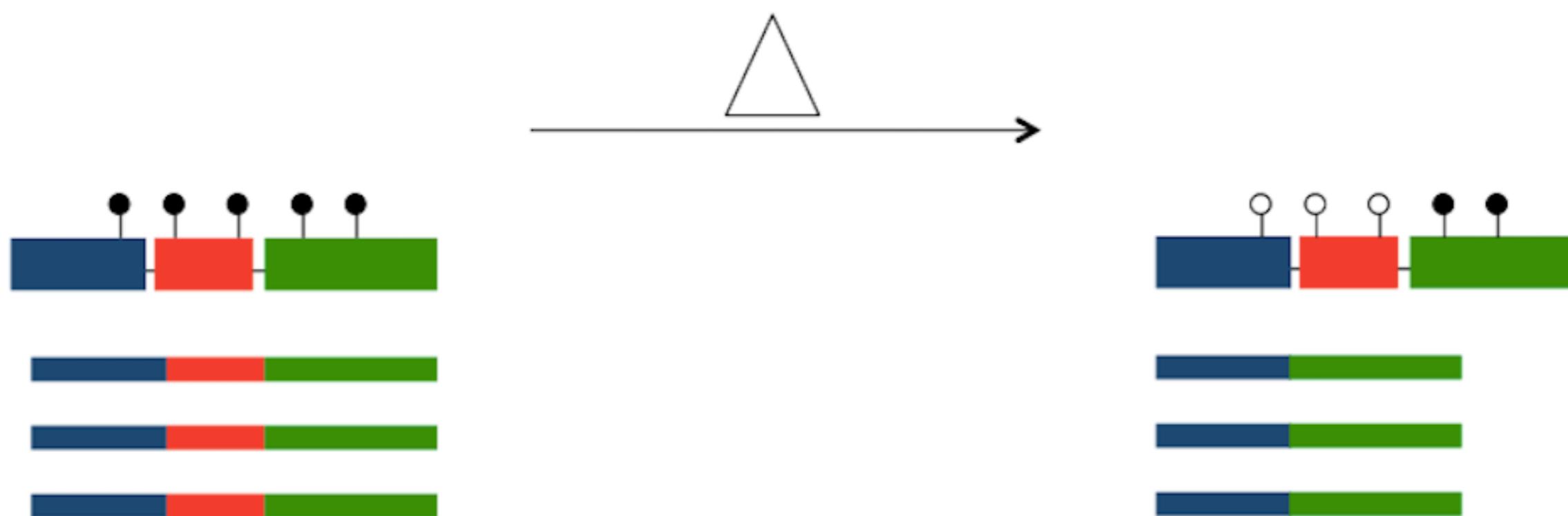


# Targeted Regulation

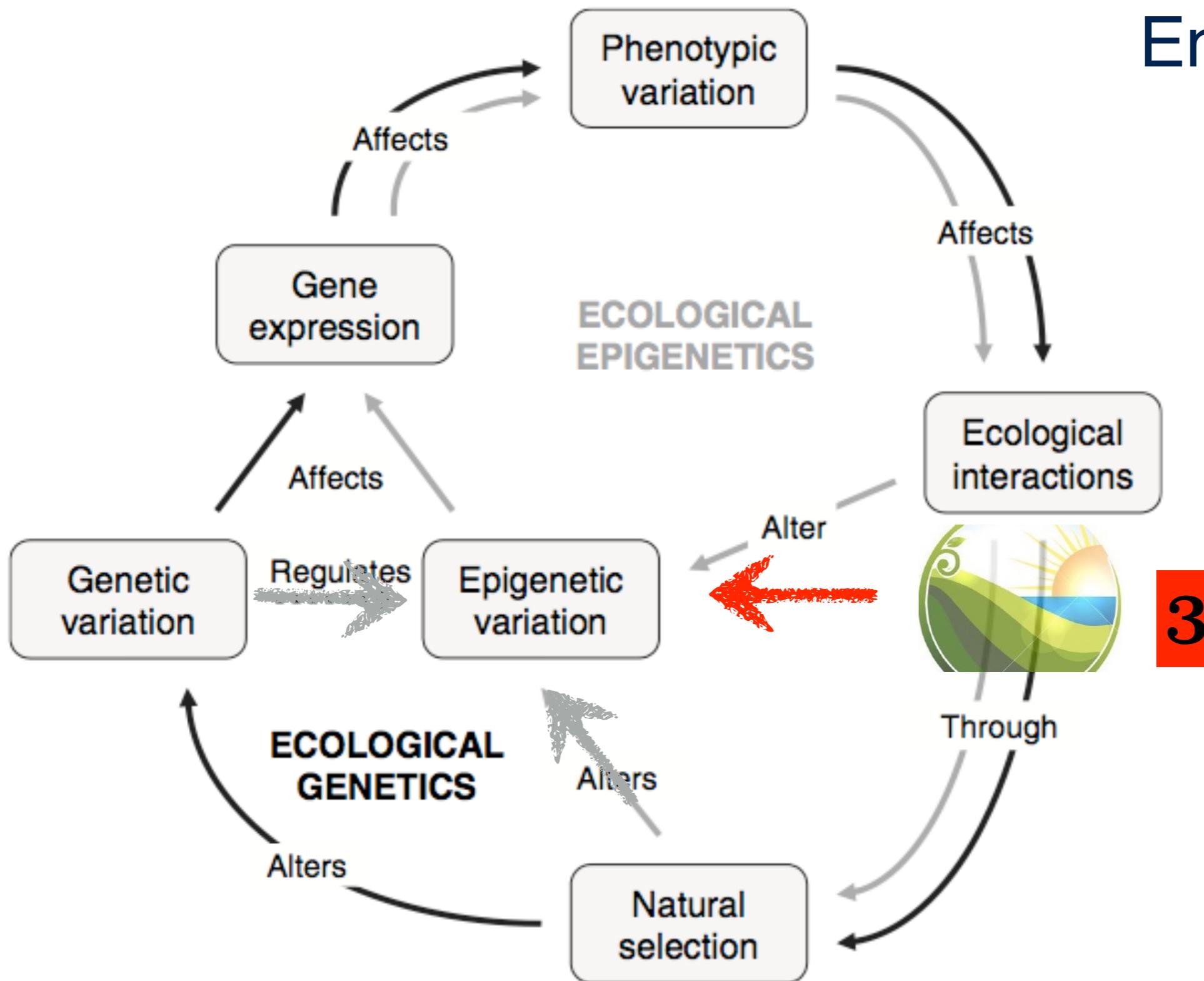
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Mackenzie R. Gavery and Steven B. Roberts

Advance Access publication date 7 January 2014



# Environmental Influence



*Ecology Letters*, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

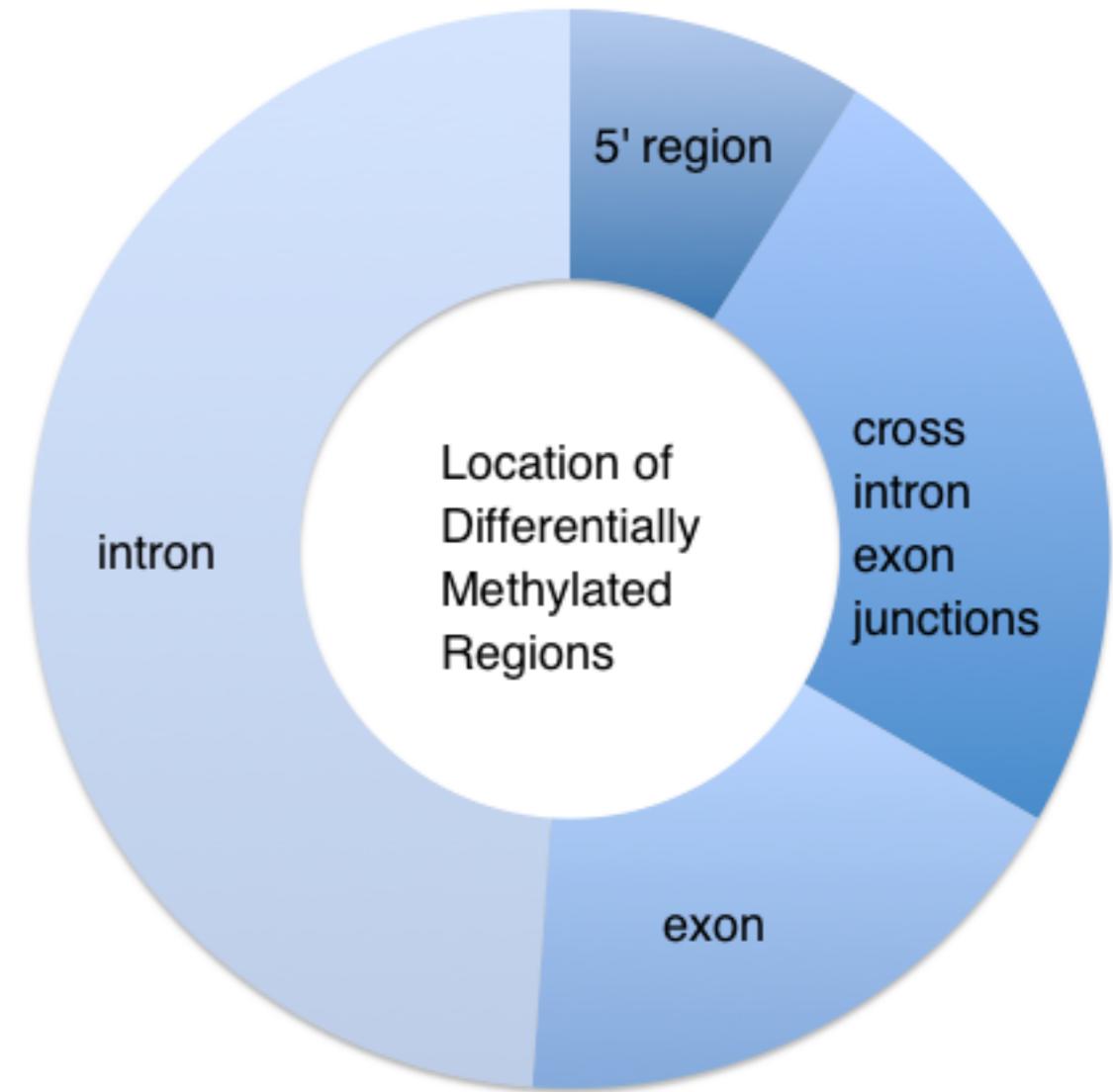
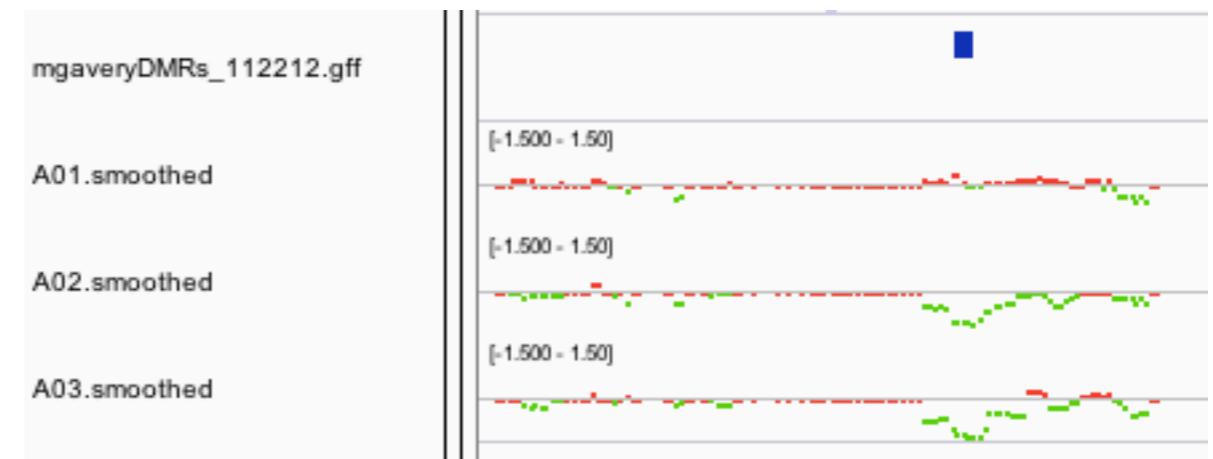
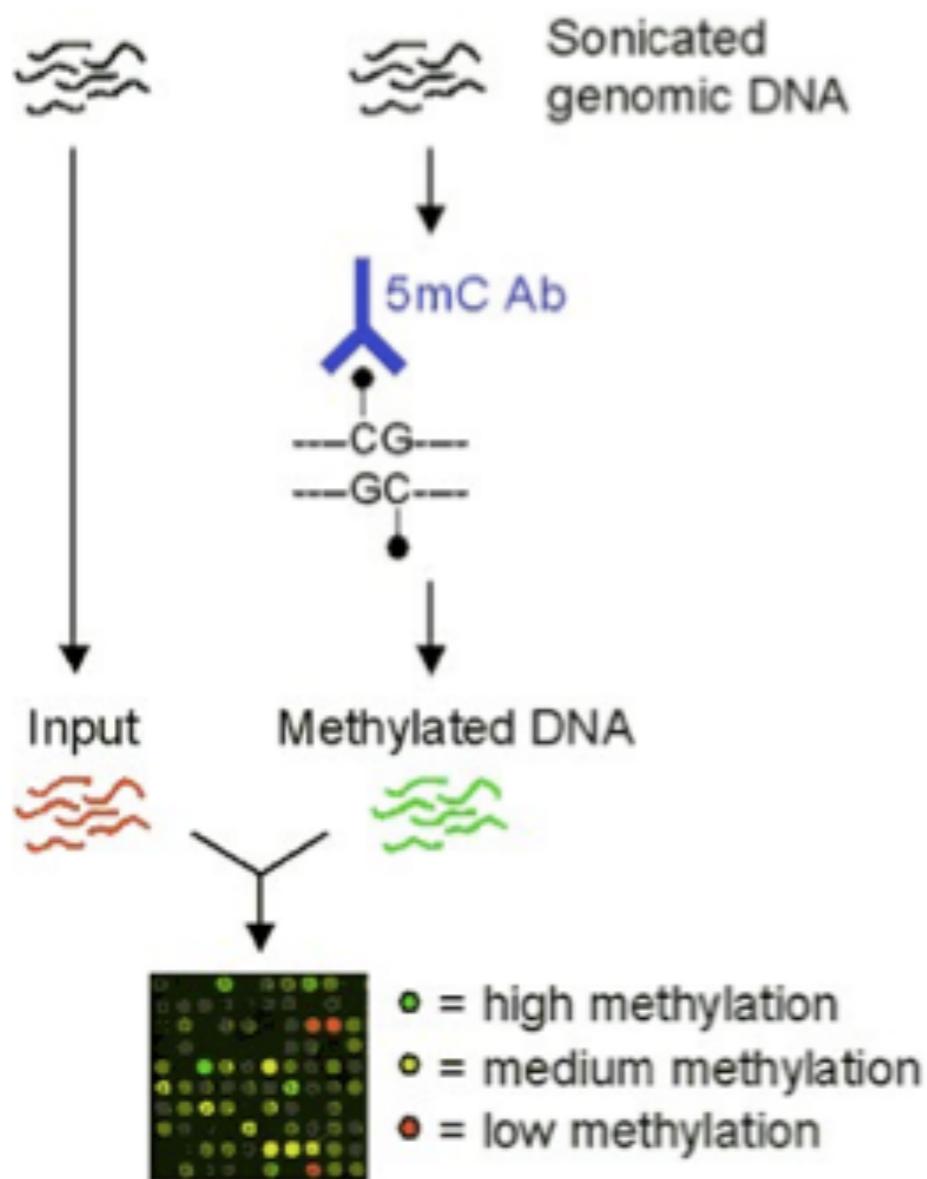
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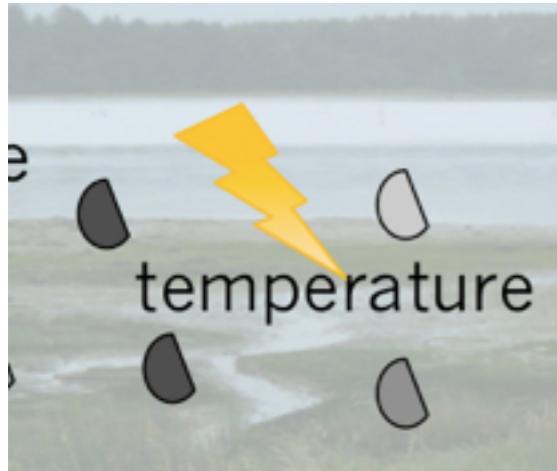
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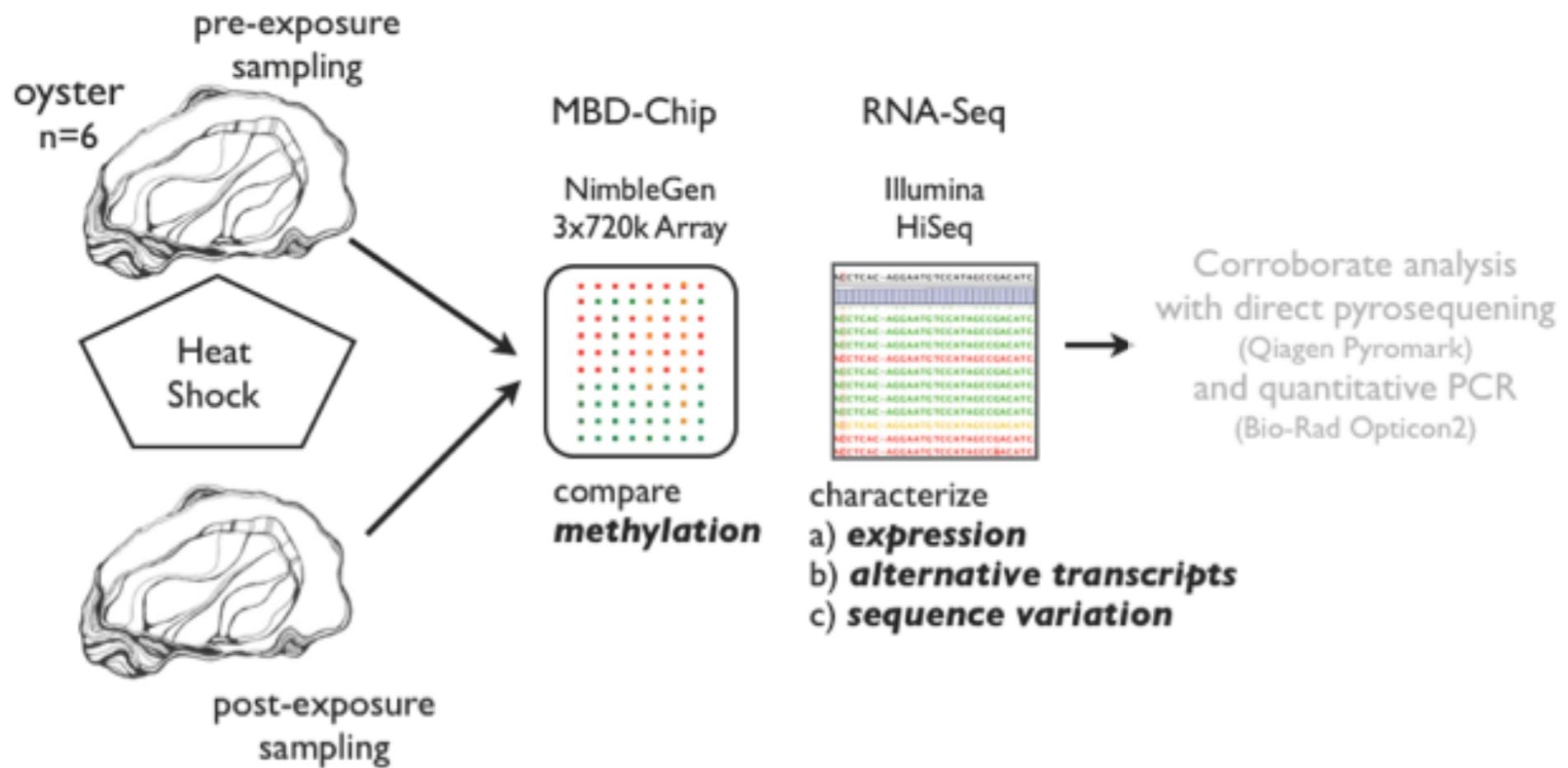
# Environmental impact (Estrogens)



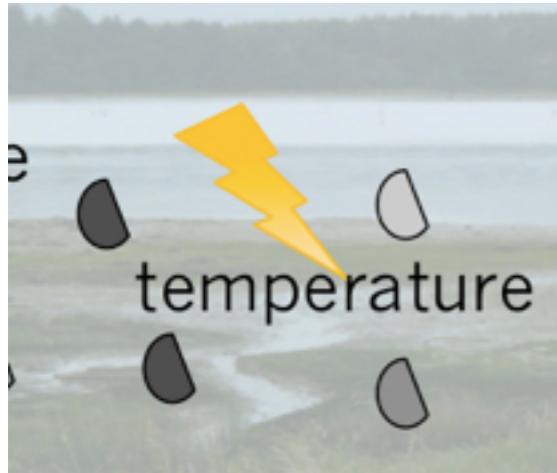
# Environment and gene expression



*stochastic or targeted?*



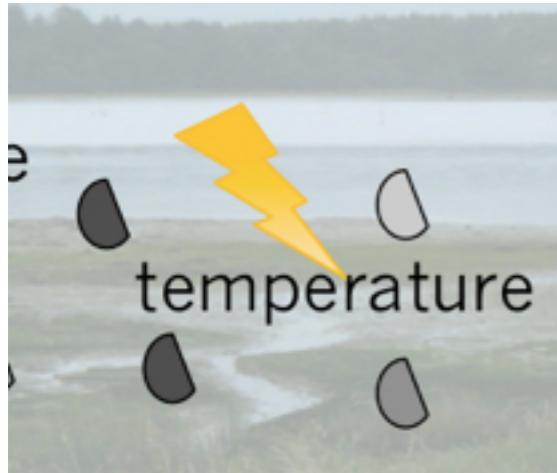
# Environment and gene expression



*stochastic or targeted?*

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

# Environment and gene expression

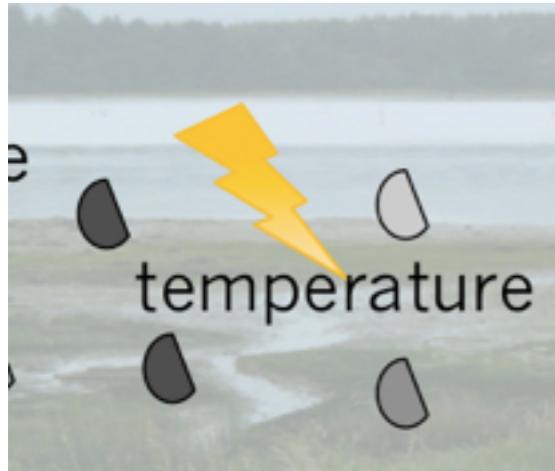


*stochastic or targeted?*

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

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

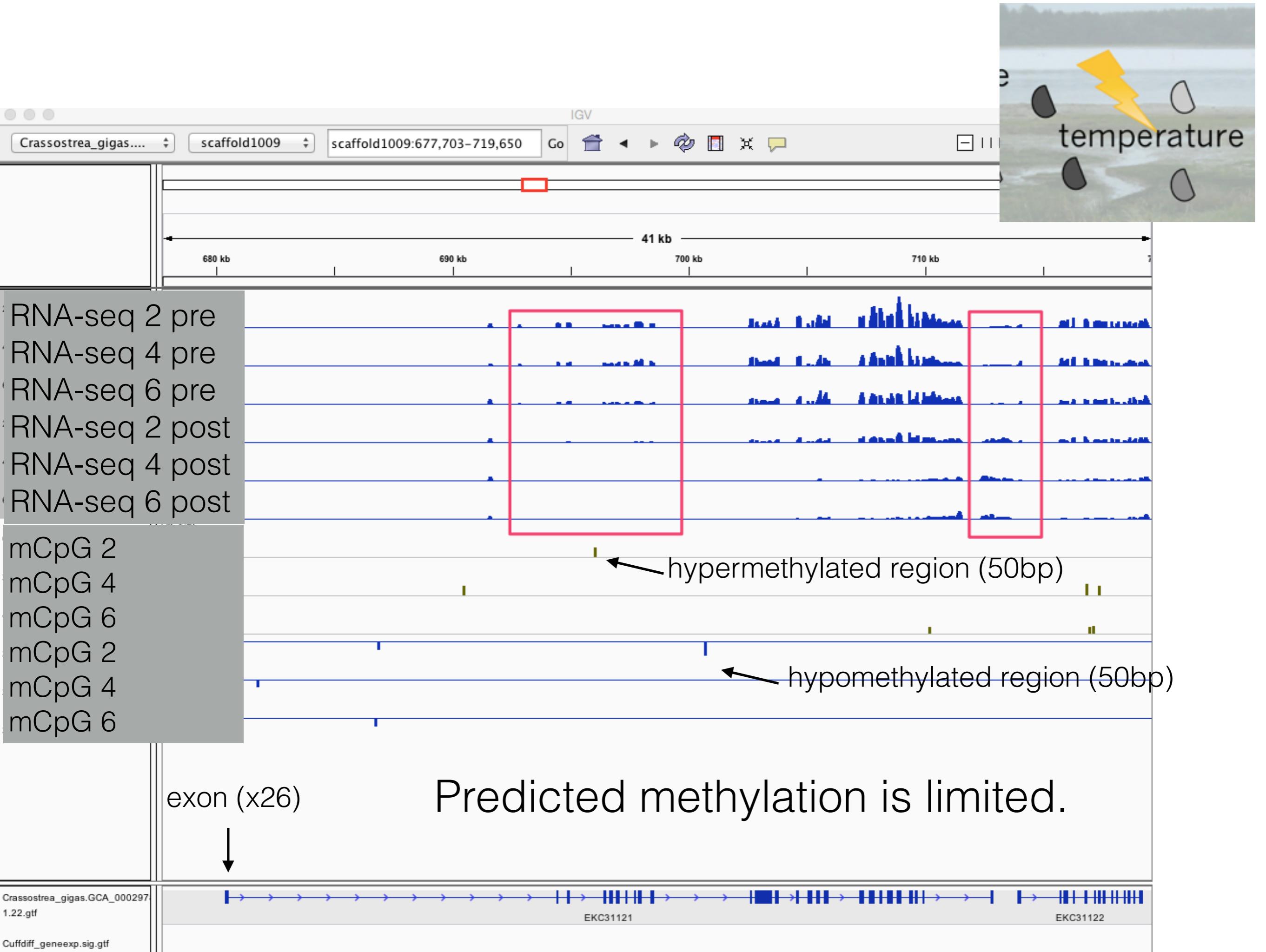
# Environment and gene expression



*stochastic or targeted  
or ..?*

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

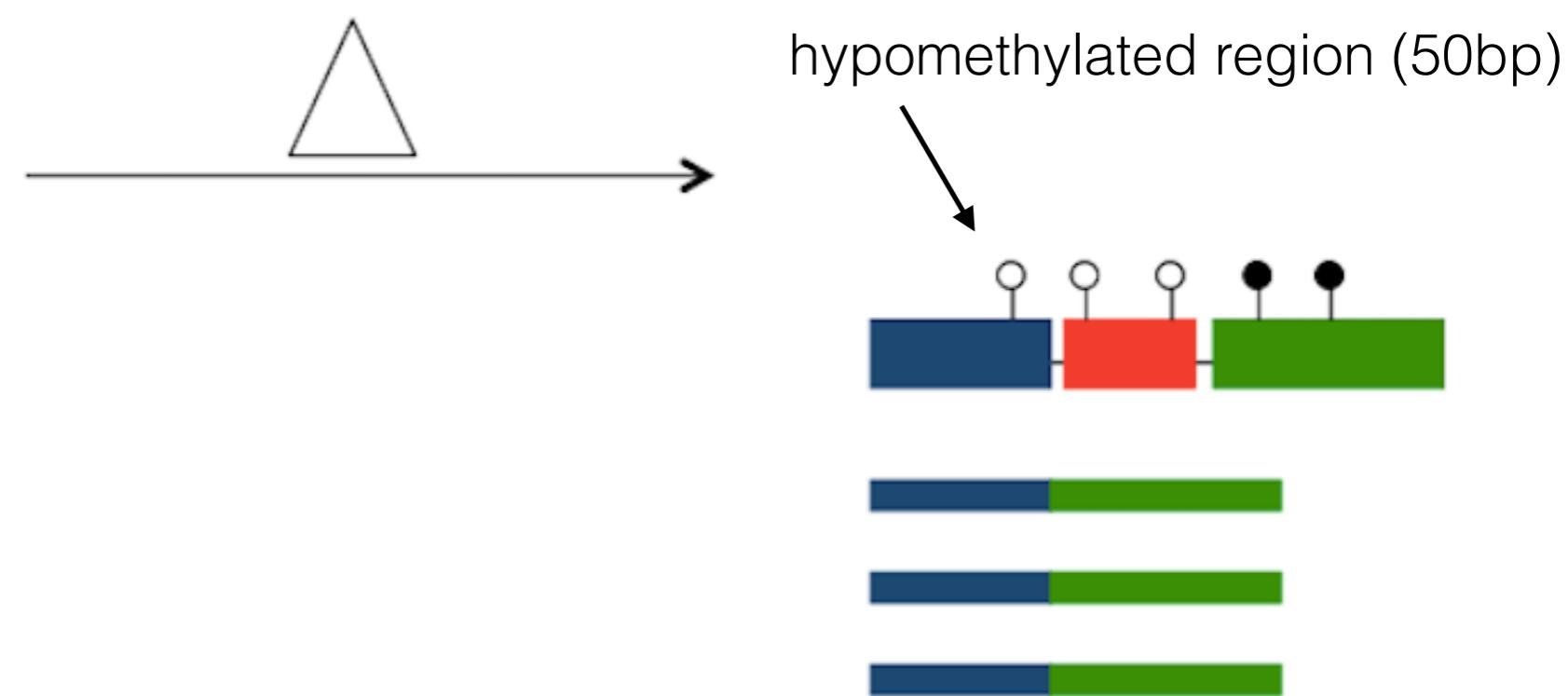
Changes in methylation (either direction) are more prevalent in introns, repeats, and transposable elements.



Gene  
expression

2

Epigenetic  
variation



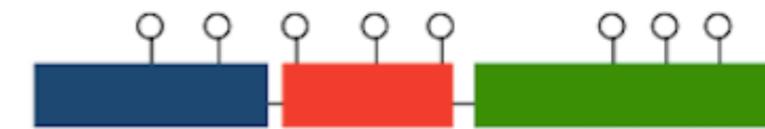
**not** in this experiment

not even consistent methylation changes at loci level

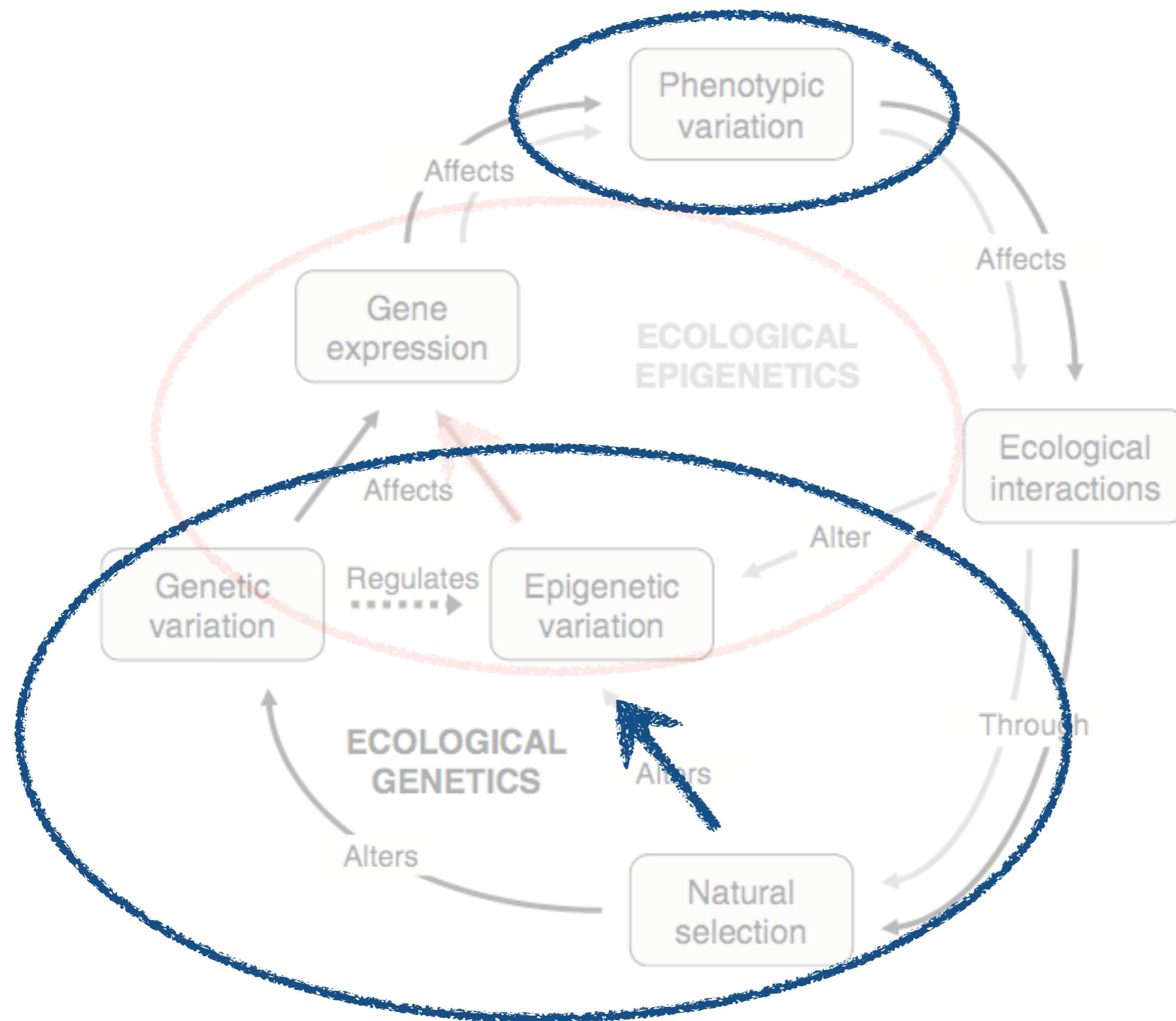
Gene  
expression

2

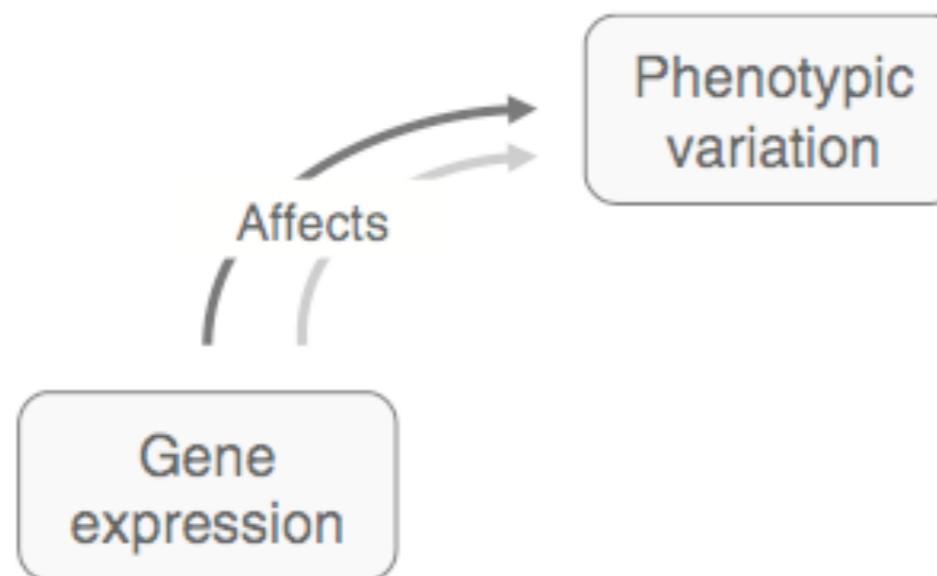
Epigenetic  
variation



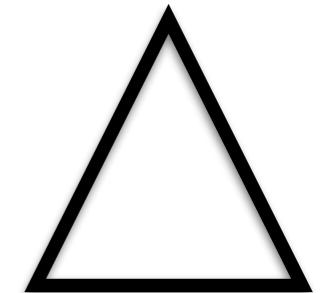
more questions....  
interesting but what is controlling?

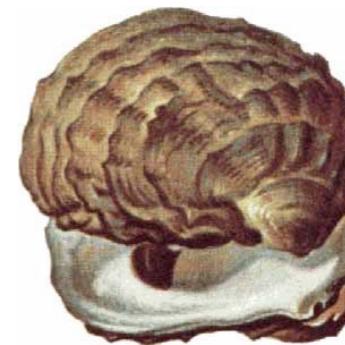
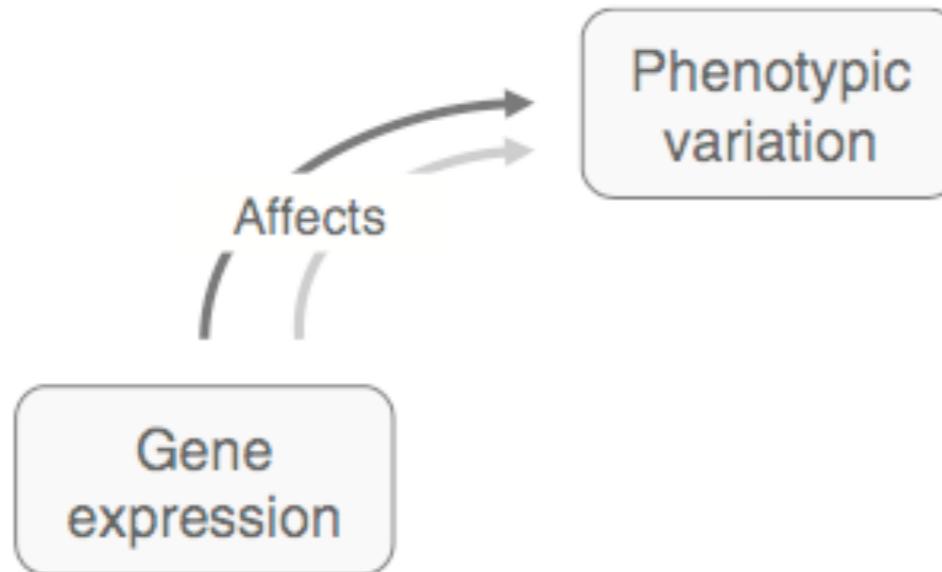


# Conceptual Models for a functional role of DNA methylation



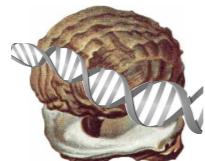
## Mystery - Natural Epigenetic Variation Exists



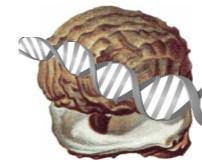


# Conceptual Models for a functional role of DNA methylation

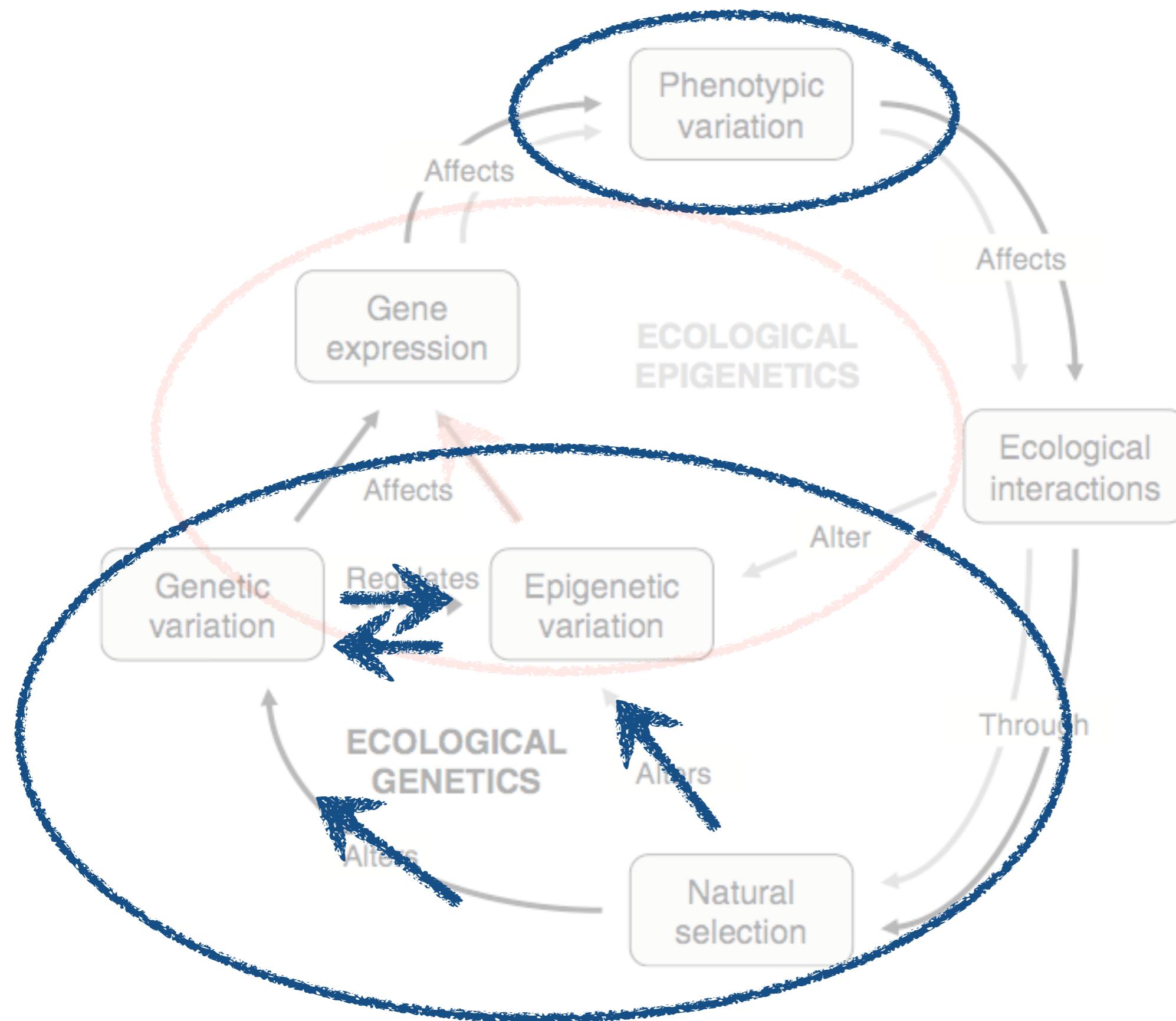
**Mystery - Natural Epigenetic Variation Exists**



Biological Scale?  
Population



\*



# Population studies

*Ostrea lurida*



# Population studies

*Ostrea lurida*



## Reciprocal Transplant Experiment



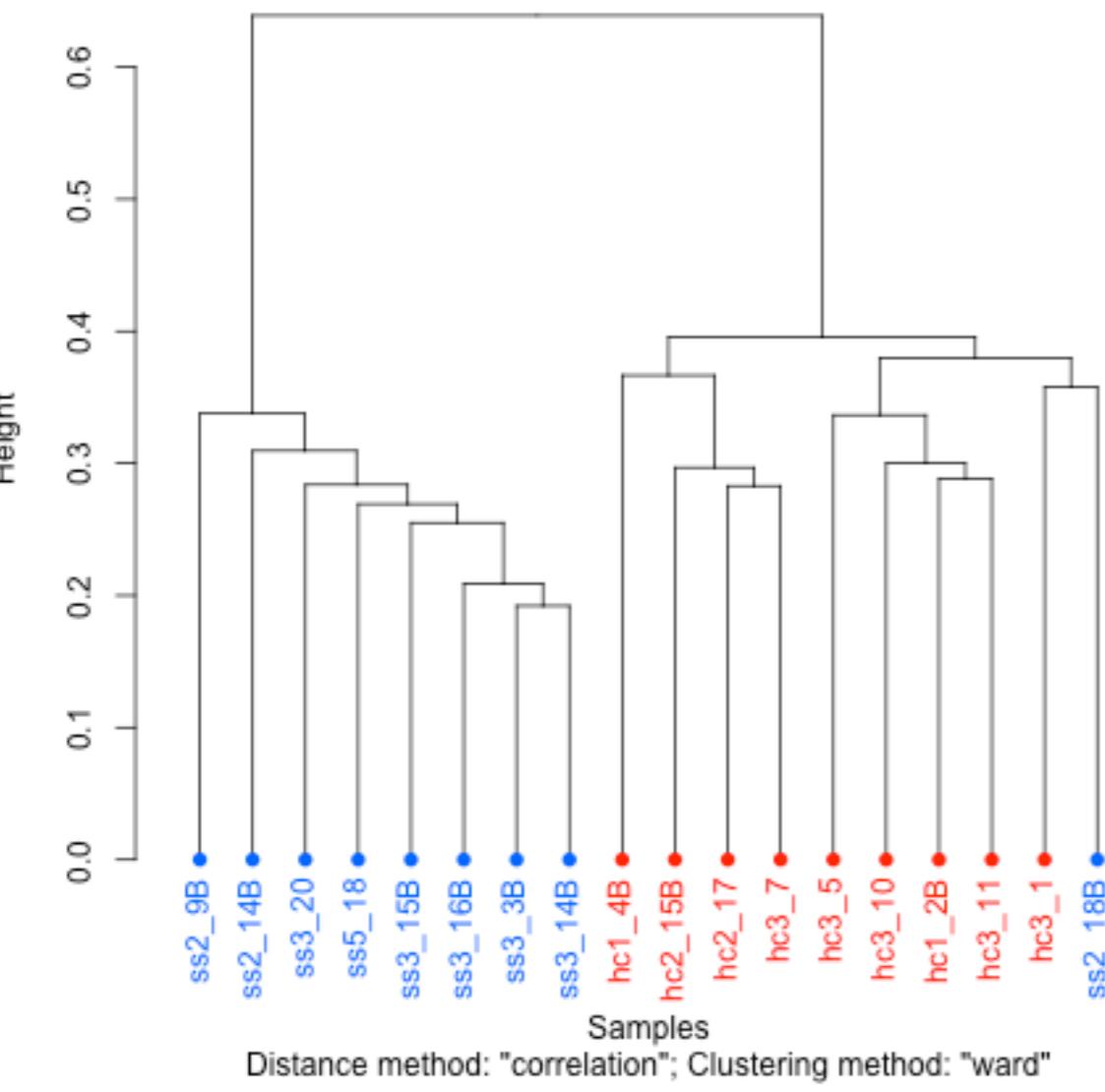
Manchester

# Population studies



## Reciprocal Transplant Experiment

CpG methylation clustering



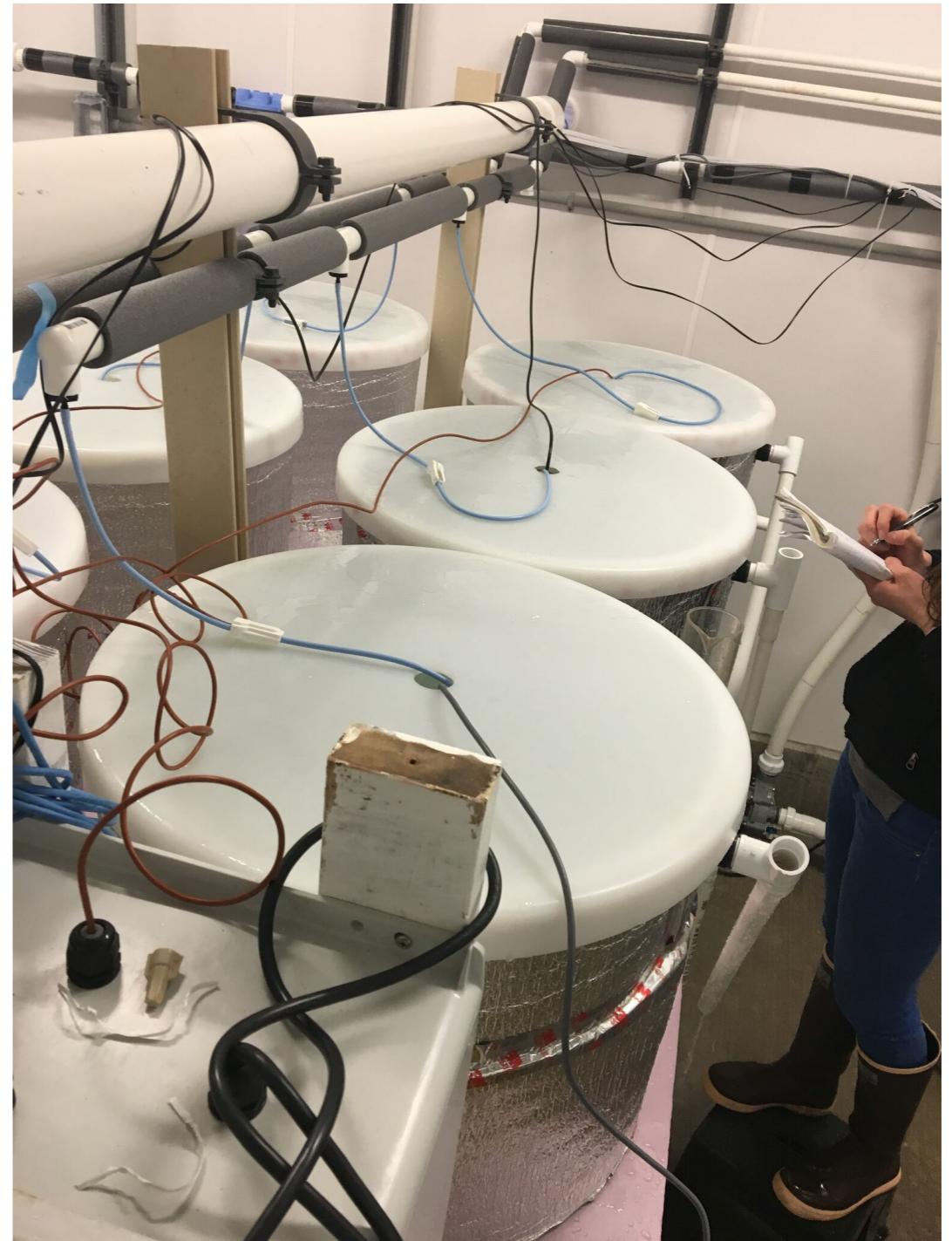
Manchester

# Very new data

## Selection

## Ocean Acidification

*Panopea generosa*



# Very new data

## Selection

### Ocean Acidification

Day 10

Control: Random Mortality

~42% ACGCTGATCGT  
~38% ACGCTAATCGT

Day 1

Proportion of sequences in pooled  
larvae sample with given allele (G vs A)

~42% ACGCTGATCGT  
~38% ACGCTAATCGT

Day 10

High  $p\text{CO}_2$ : Non-random  
Mortality

~80% ACGCTGATCGT  
~20% ACGCTAATCGT

Day 1

Ambient  $p\text{CO}_2$   
Ambient temperature

High  $p\text{CO}_2$   
Ambient temperature

High  $p\text{CO}_2$   
High temperature

Ambient  $p\text{CO}_2$   
High temperature

Ambient  $p\text{CO}_2$   
Ambient temperature

Evidence of allele beneficial (G) to survival  
under High  $p\text{CO}_2$  conditions

→

# Very new data

## Selection

### Ocean Acidification

Day 10

Control: Random Mortality

~42% ACGCTGATCGT  
~38% ACGCTAATCGT

Day 1

Proportion of sequences in pooled  
larvae sample with given allele (G vs A)

~42% ACGCTGATCGT  
~38% ACGCTAATCGT

Day 10

High  $p\text{CO}_2$   
Ambient temperature

High  $p\text{CO}_2$   
High temperature

Day 1

Ambient  $p\text{CO}_2$   
Ambient temperature

Ambient  $p\text{CO}_2$   
High temperature

Ambient  $p\text{CO}_2$   
Ambient temperature

Evidence of allele beneficial (G) to survival  
under High  $p\text{CO}_2$  conditions

High  $p\text{CO}_2$ : Non-random  
Mortality

~80% ACGCTGATCGT  
~20% ACGCTAATCGT

Day 10

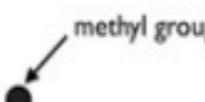
Control: Random Mortality

~44% ACGCTGATCGT  
~56% ACGCTAATCGT

Day 1

Proportion of sequences in pooled  
larvae sample with given allele (methylated  
cytosine vs unmethylated cytosine)

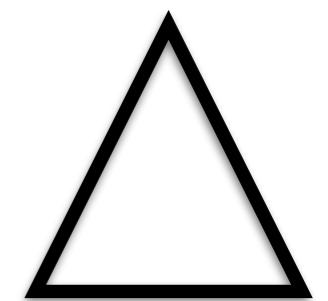
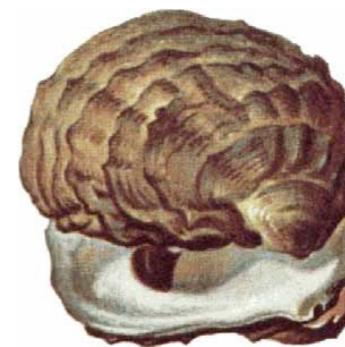
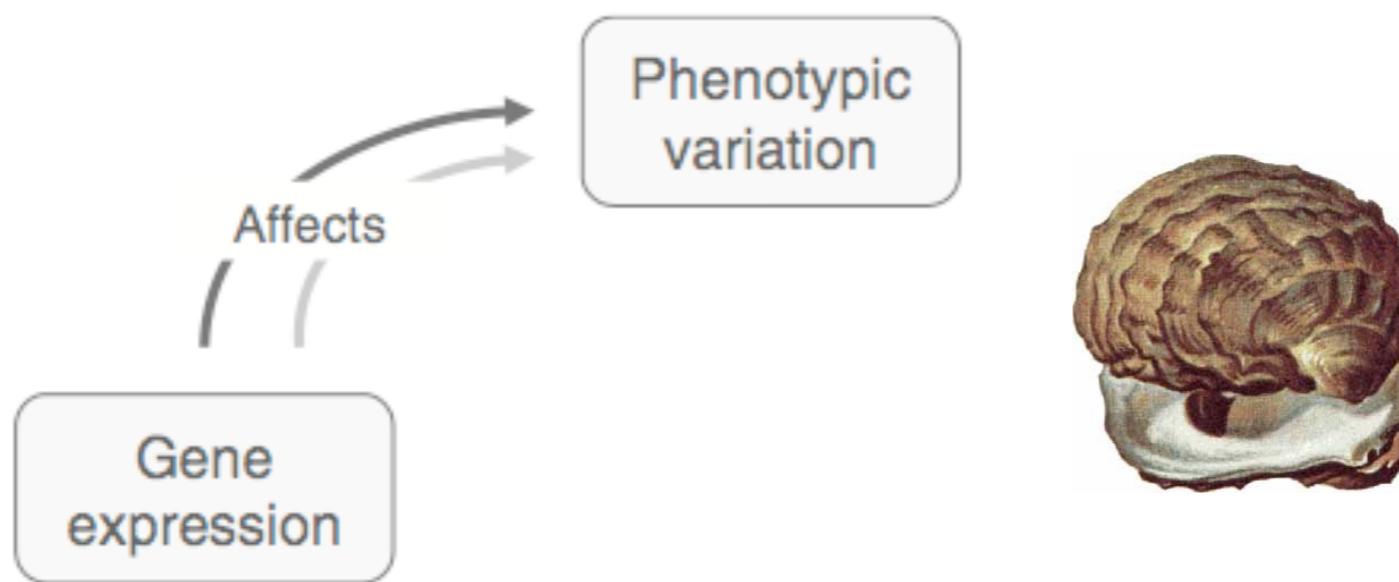
~44% ACGCTGATCGT  
~56% ACGCTAATCGT



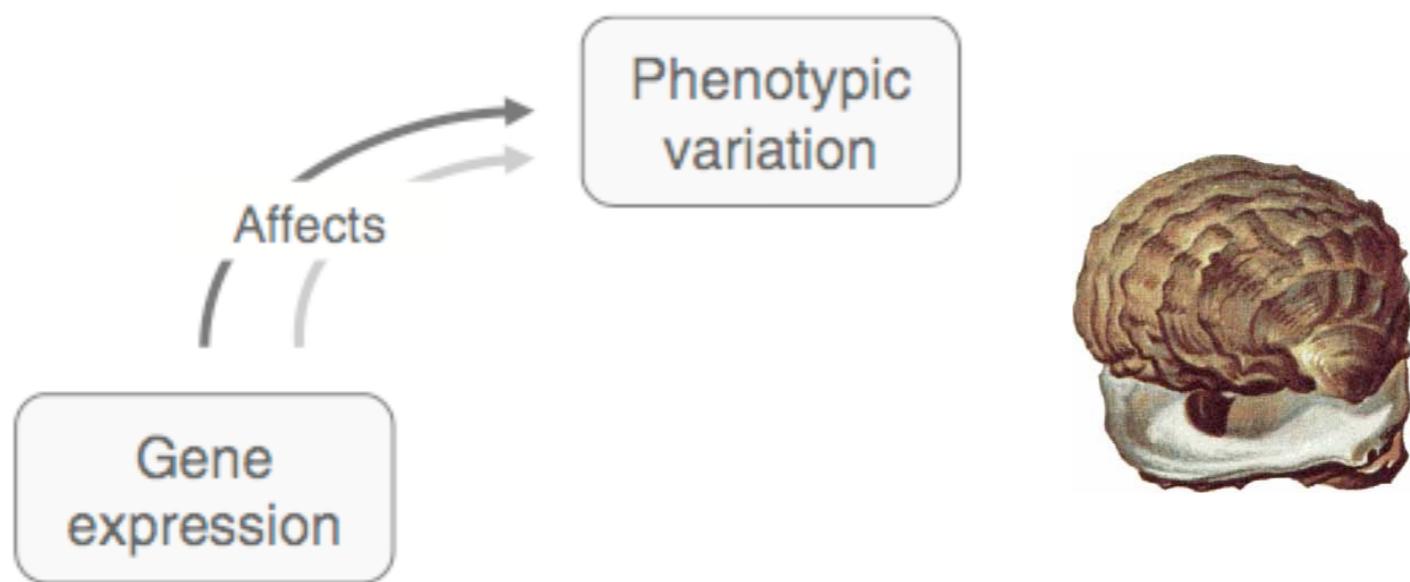
Evidence of epiallele (methylated cytosine)  
beneficial to survival  
under High  $p\text{CO}_2$  conditions

High  $p\text{CO}_2$ : Non-random  
Mortality

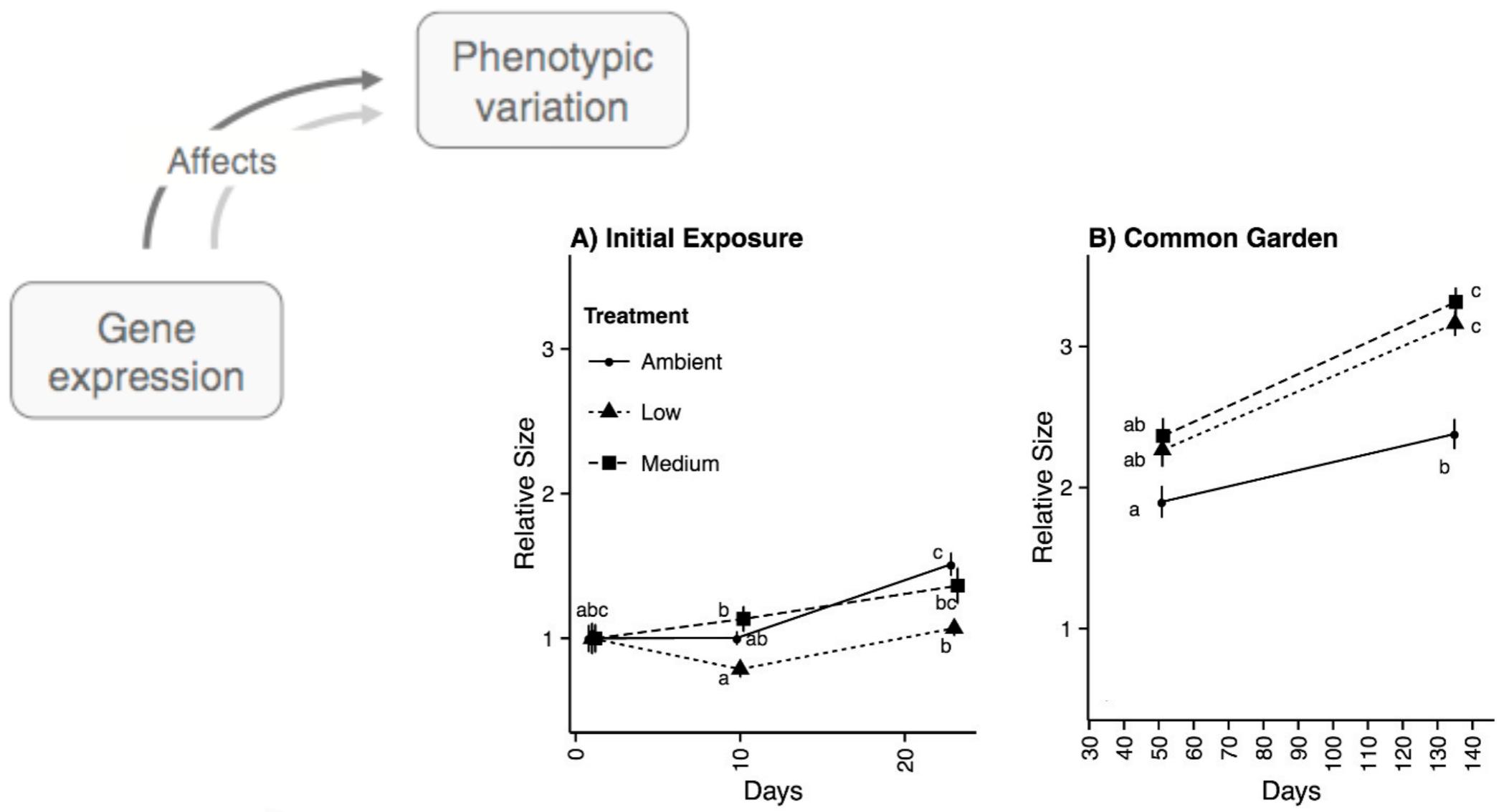
~81% ACGCTGATCGT  
~19% ACGCTAATCGT

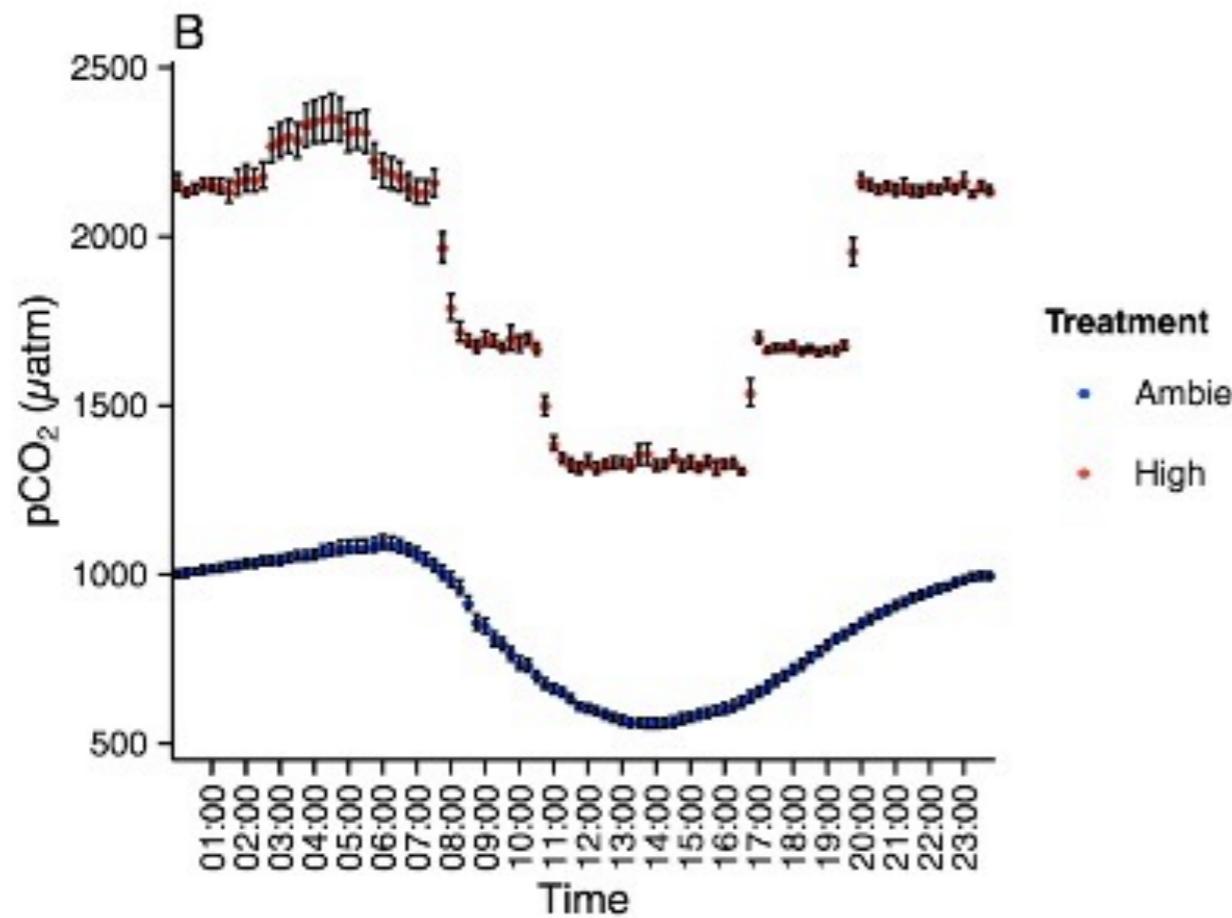


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\*

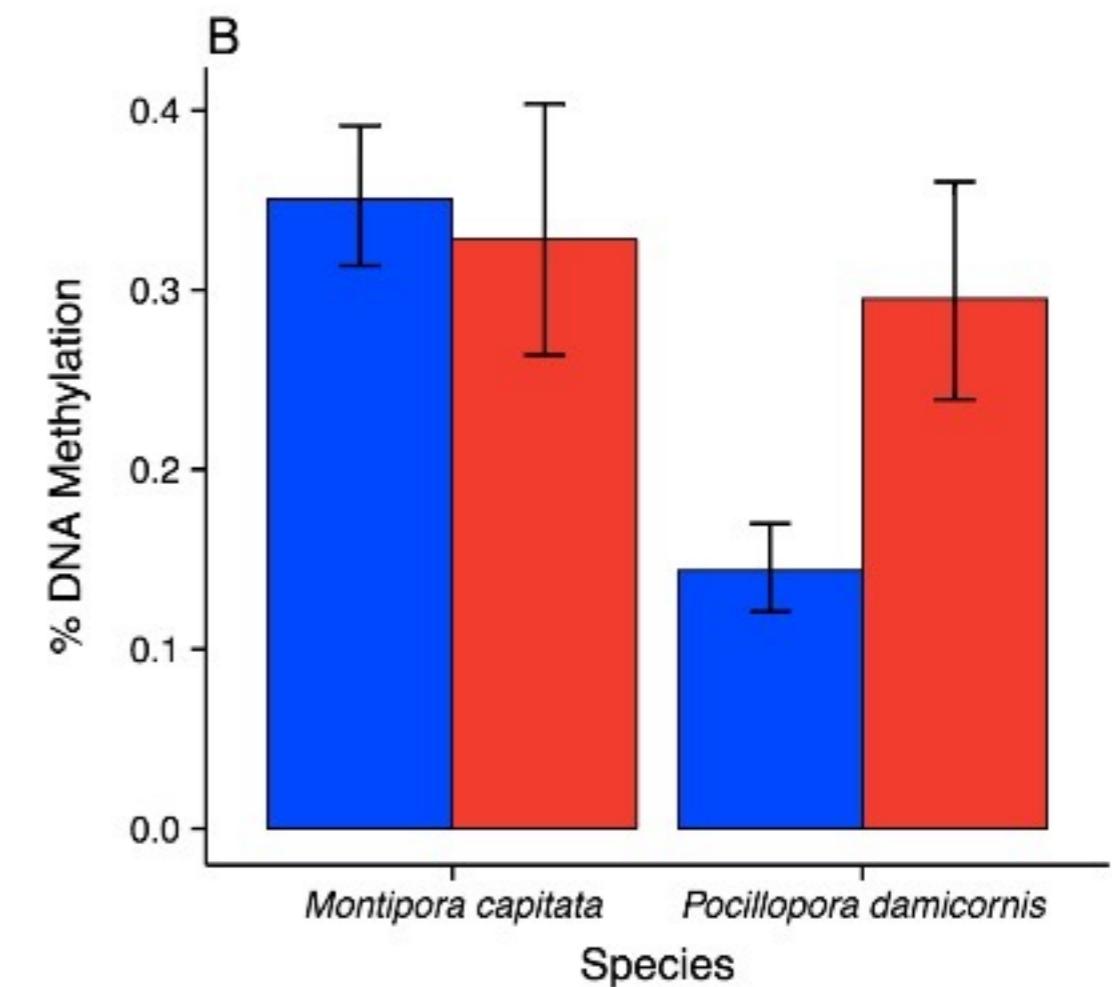




Treatment

• Ambient

• High

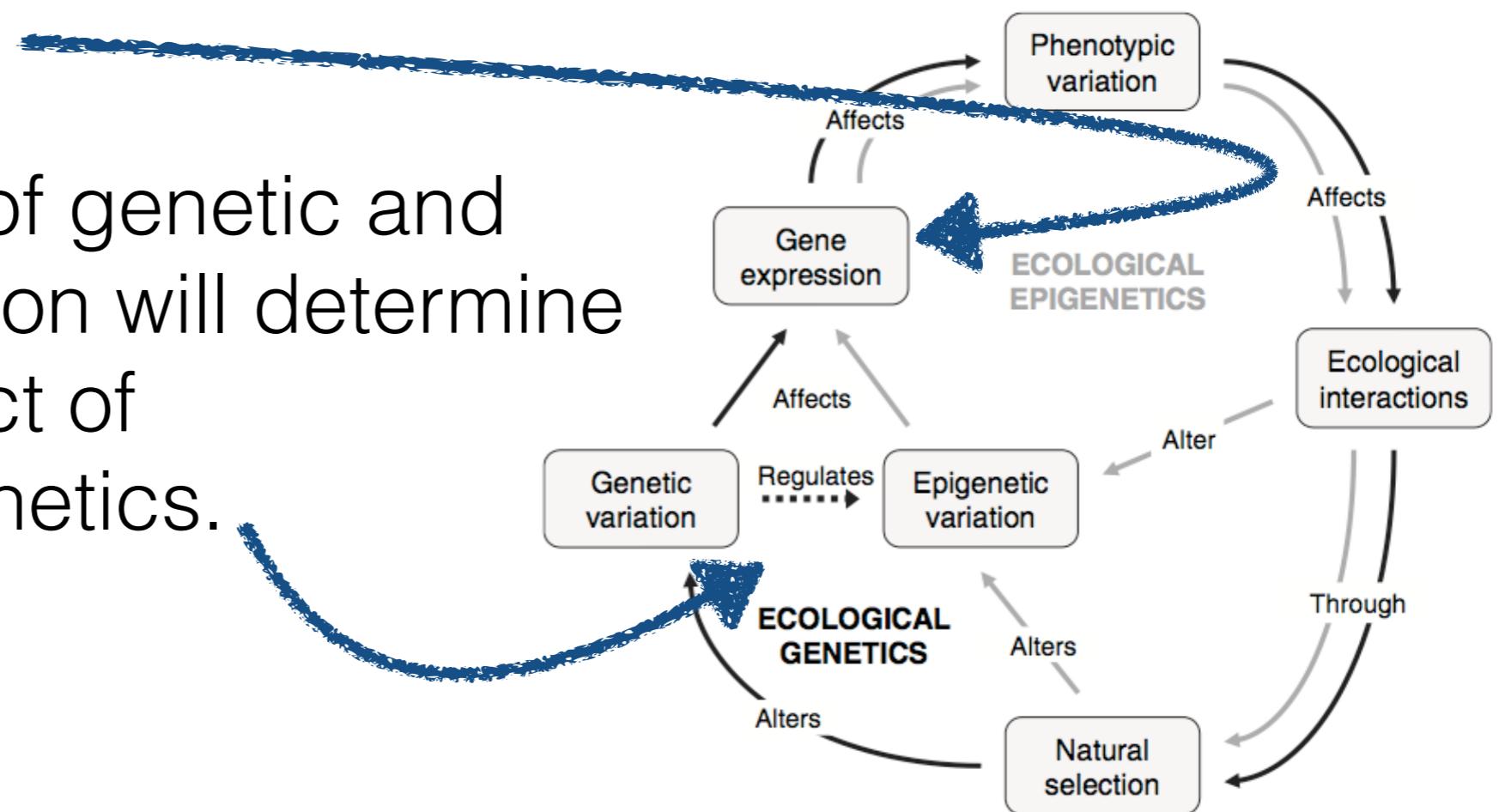


Evolutionary Applications.

**Putnam HM**, Davidson JM, and Gates RD. Ocean acidification influences host DNA methylation and phenotypic plasticity in environmentally susceptible corals

# Summary

- The role of DNA methylation is complicated... *on many levels.*
- In terms of gene regulation, numerous epigenetic phenomenon are likely at play.
- The relationship of genetic and epigenetic variation will determine the relative impact of ecological epigenetics.



# Acknowledgements

Mackenzie Gavery

Claire Olson

Sam White

Brent Vadopalas

Jake Heare

Jay Dimond

Katherine Silliman



Hollie Putnam  
Laura Spencer

slides, data & more @  
[github.com/sr320/talk-Chicago-eed-2016](https://github.com/sr320/talk-Chicago-eed-2016)