

Does DNA methylation facilitate phenotypic plasticity in marine invertebrates?

Steven Roberts

School of Aquatic and Fishery Sciences

robertslab.info

@sr320

Ecology of Infectious Marine Diseases [course]

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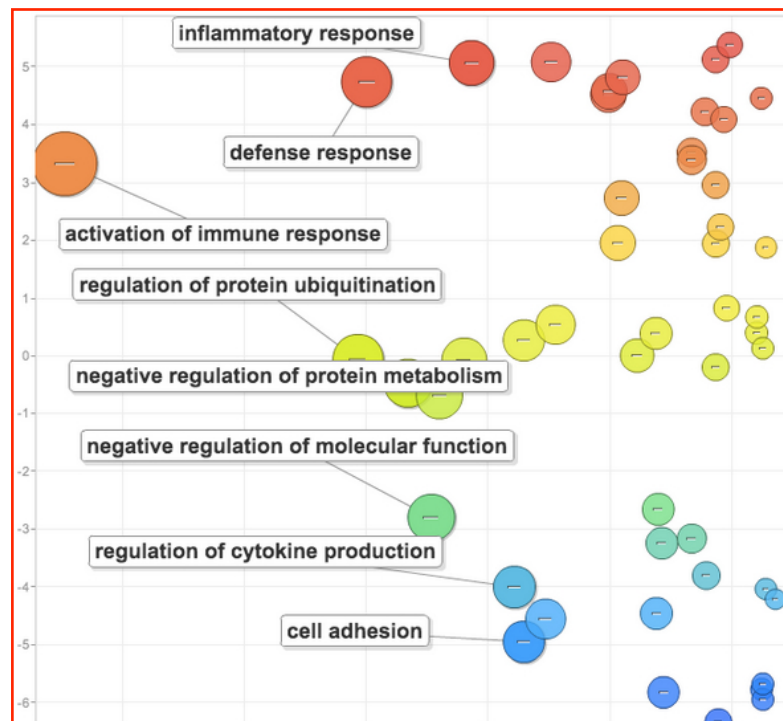


onsnetwork.org/eimd

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Ecology of Infectious Marine Diseases [course]

ABOUT NOTEBOOKS COURSE DISCUSSION SYLLABUS SCHEDULE GENOMICS LINKS



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Does DNA methylation facilitate phenotypic plasticity in marine invertebrates?

Mackenzie Gavery
Claire Olson

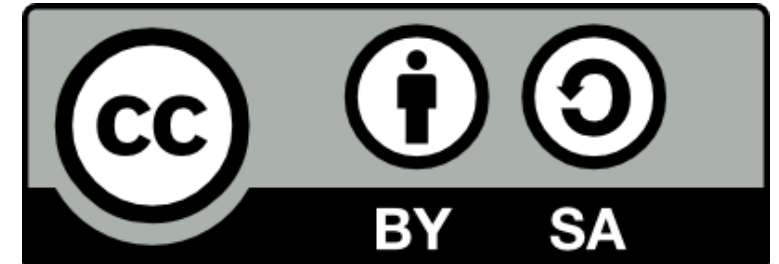


EPA
STAR



Open Science

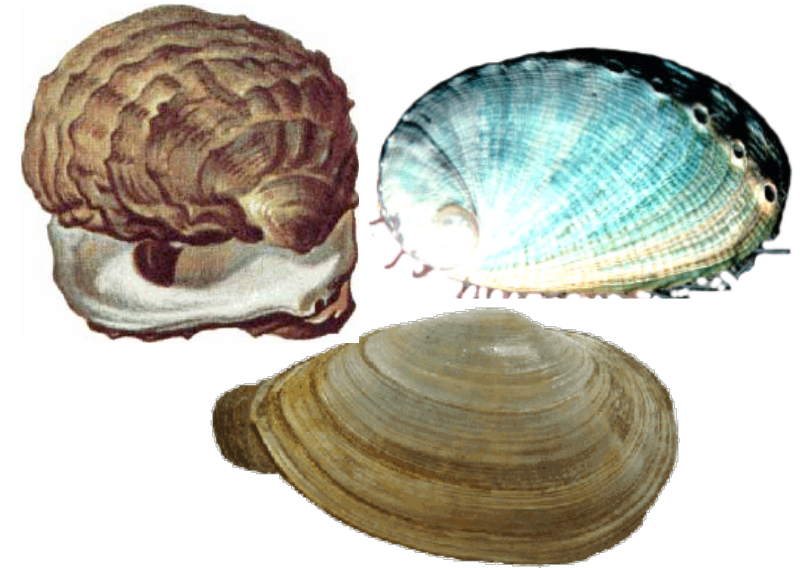
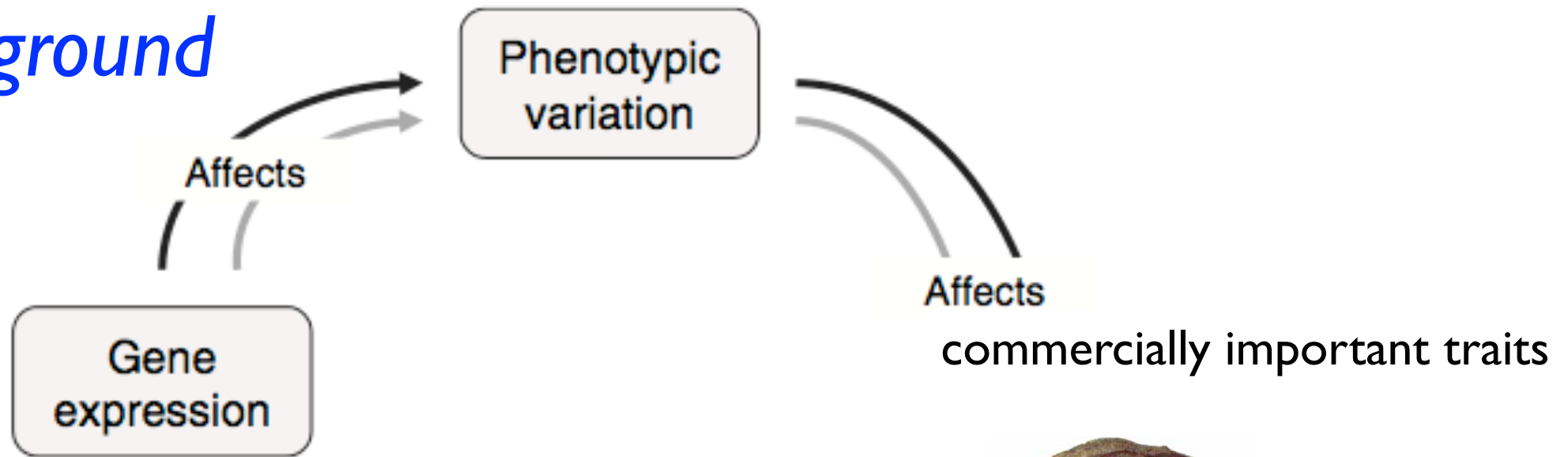
- You are free to Share!
- Our lab practices open notebook science



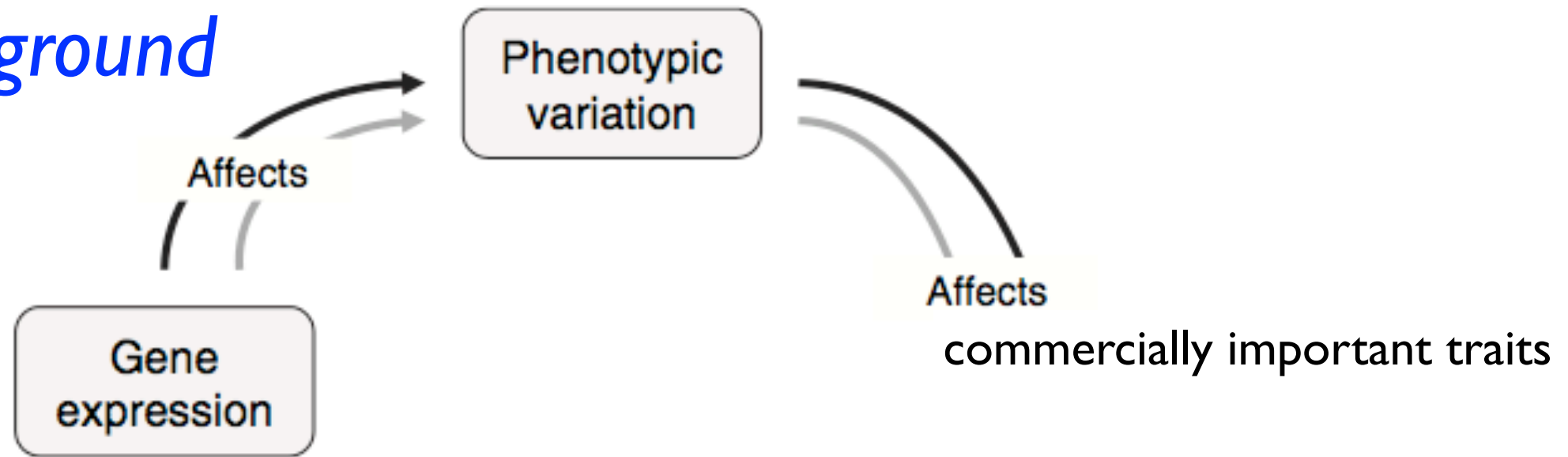
- Data, Preprints, Proposals, Slidedecks available FigShare, GitHub, and lab website (robertslab.info)

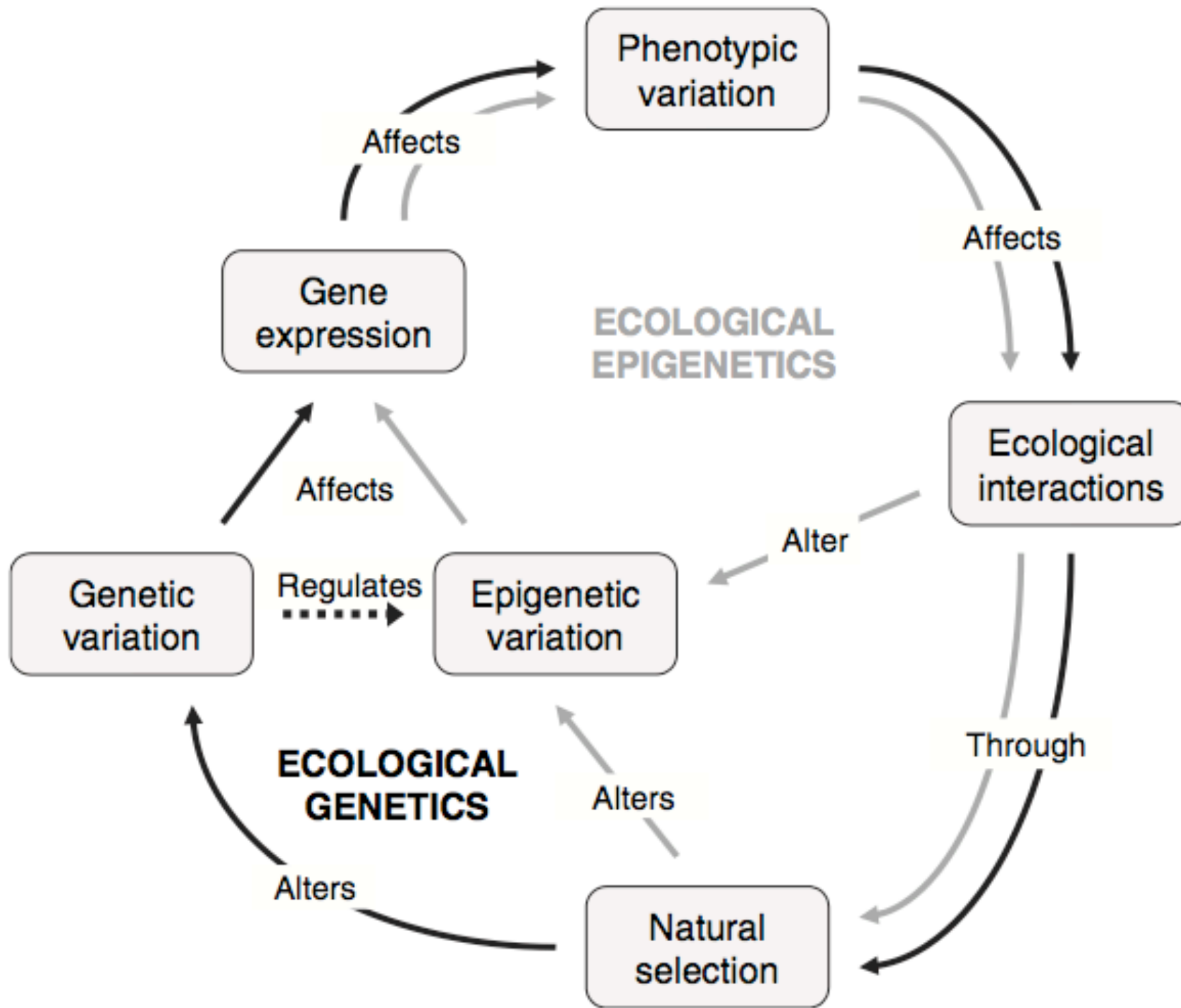
These slides plus links @ robertslab.info

Lab Background



Lab Background



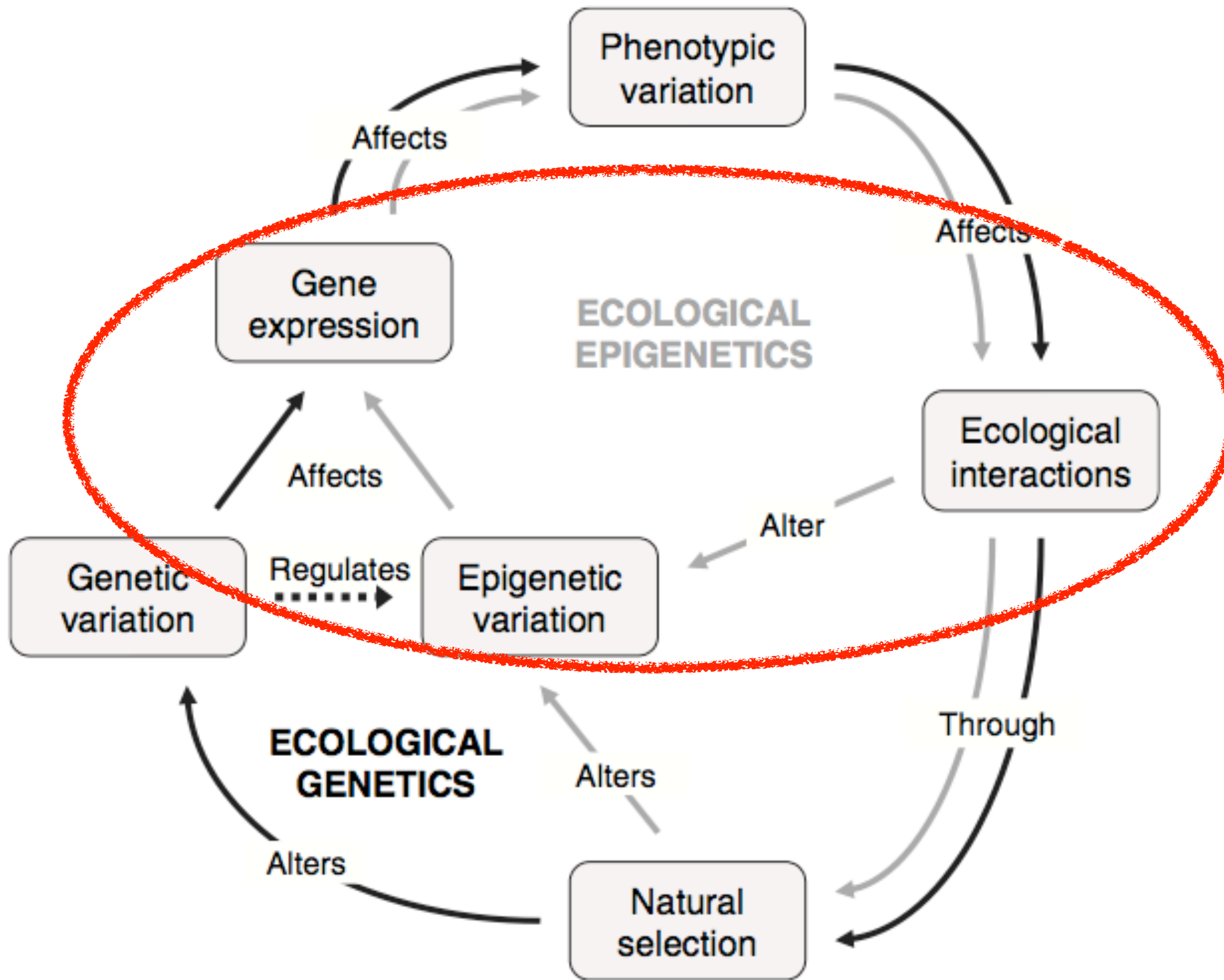


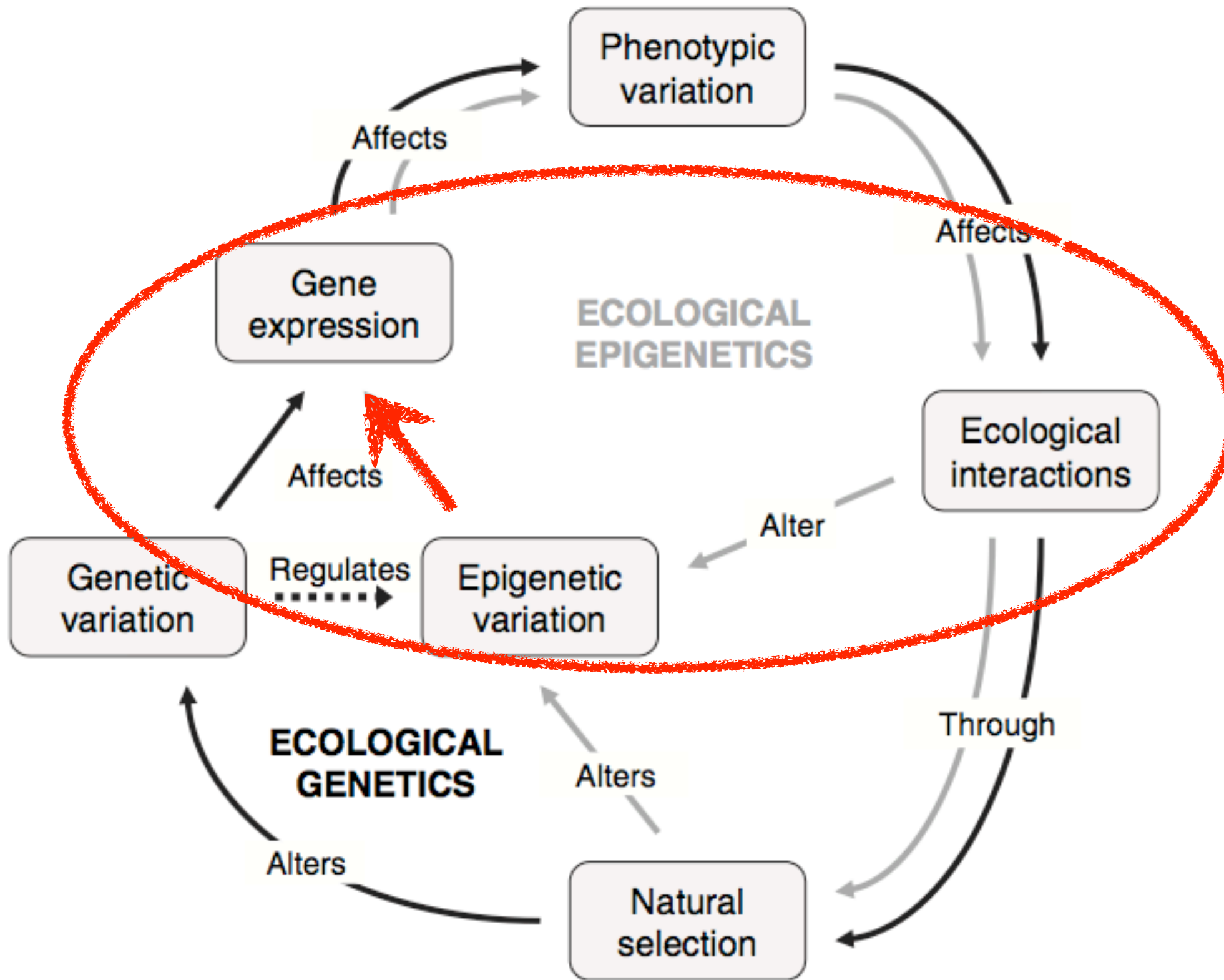
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IDEA AND PERSPECTIVE

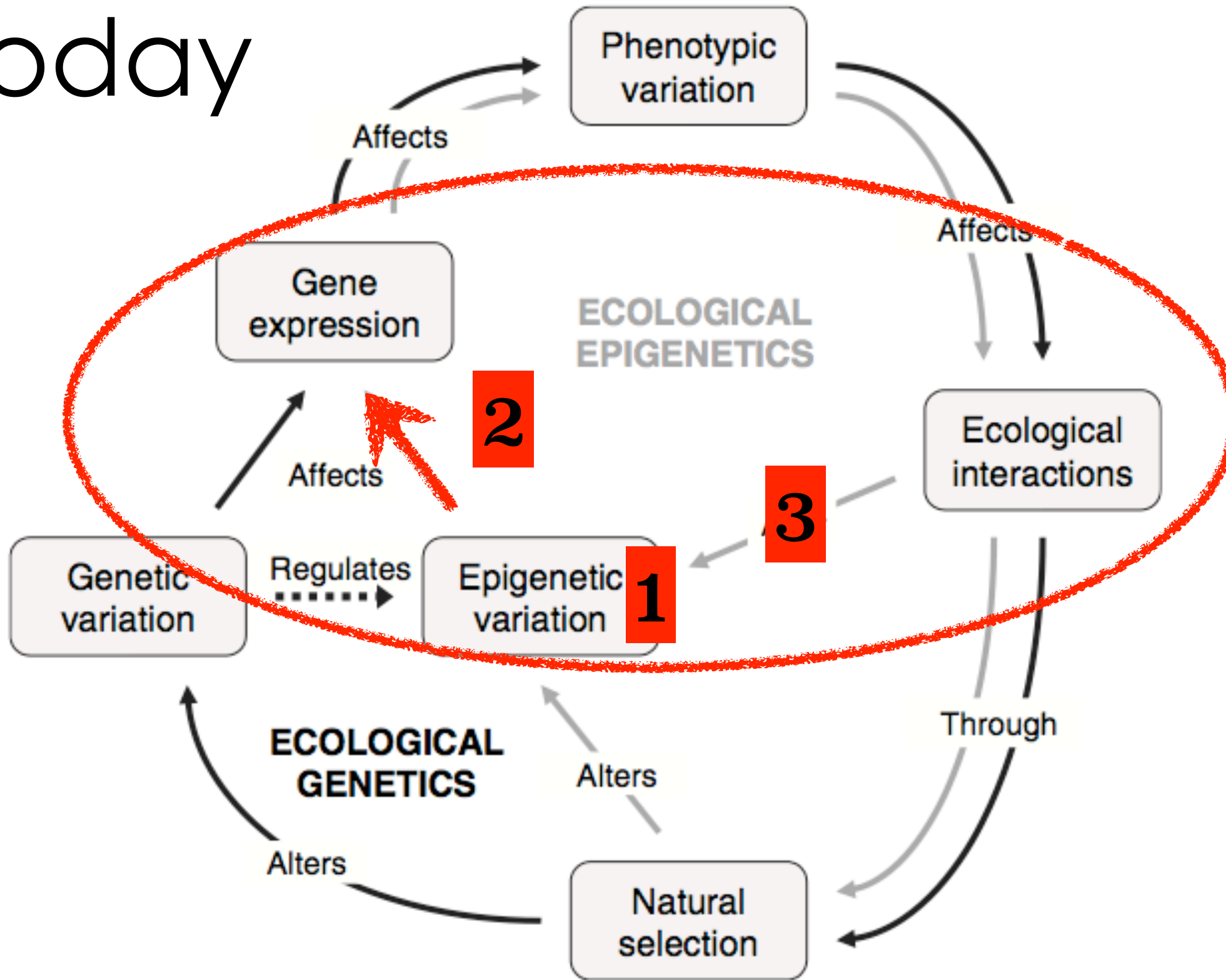
Epigenetics for ecologists

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





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



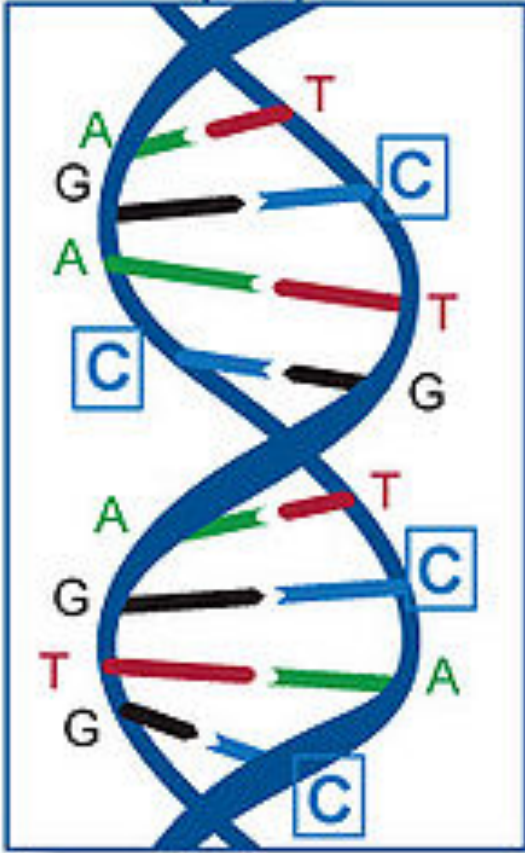
Epigenetics



Histone Modification

short RNAs

DNA Methylation



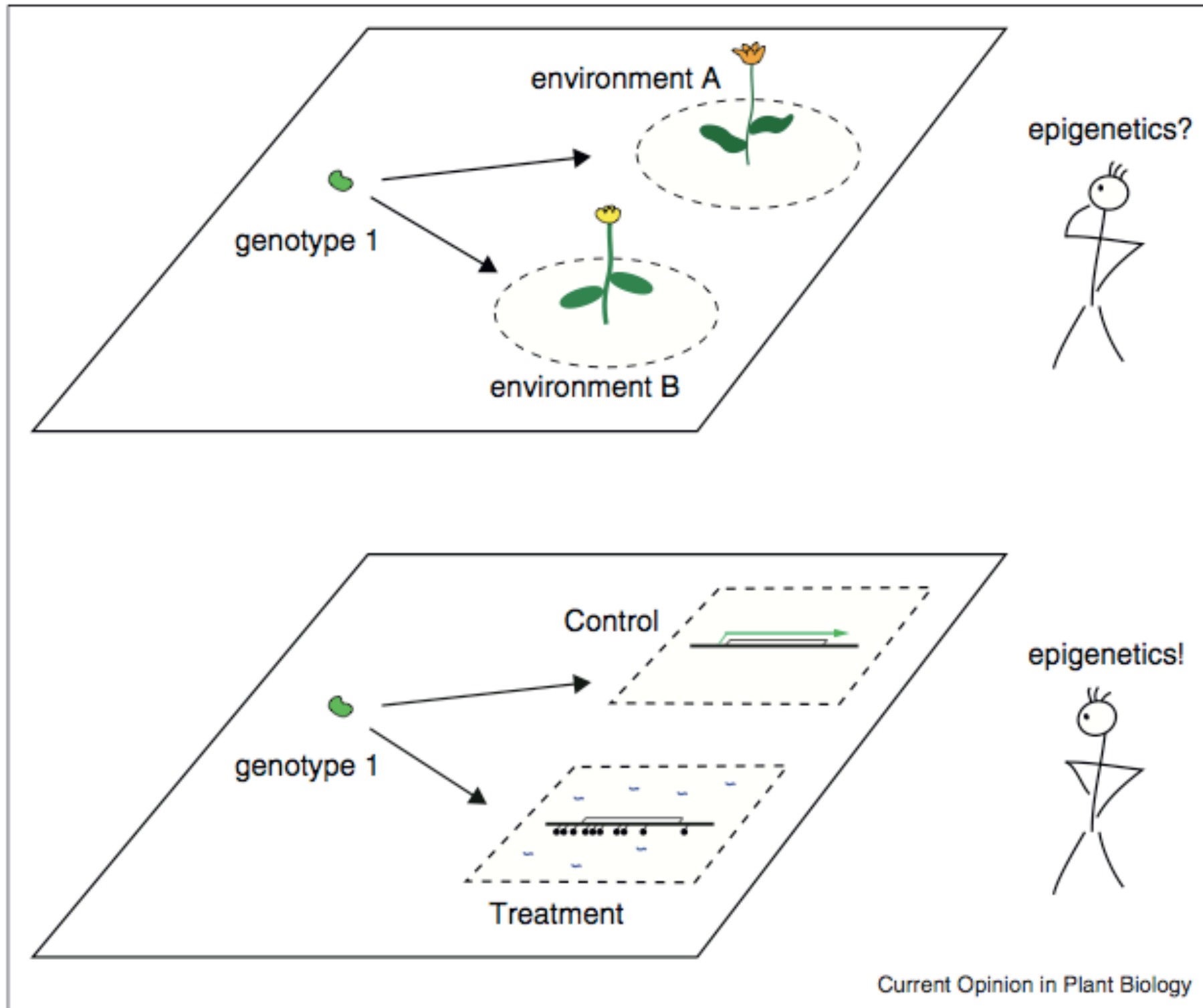
Epigenetics



Photo credit: Flickr, Creative Commons, he-boden

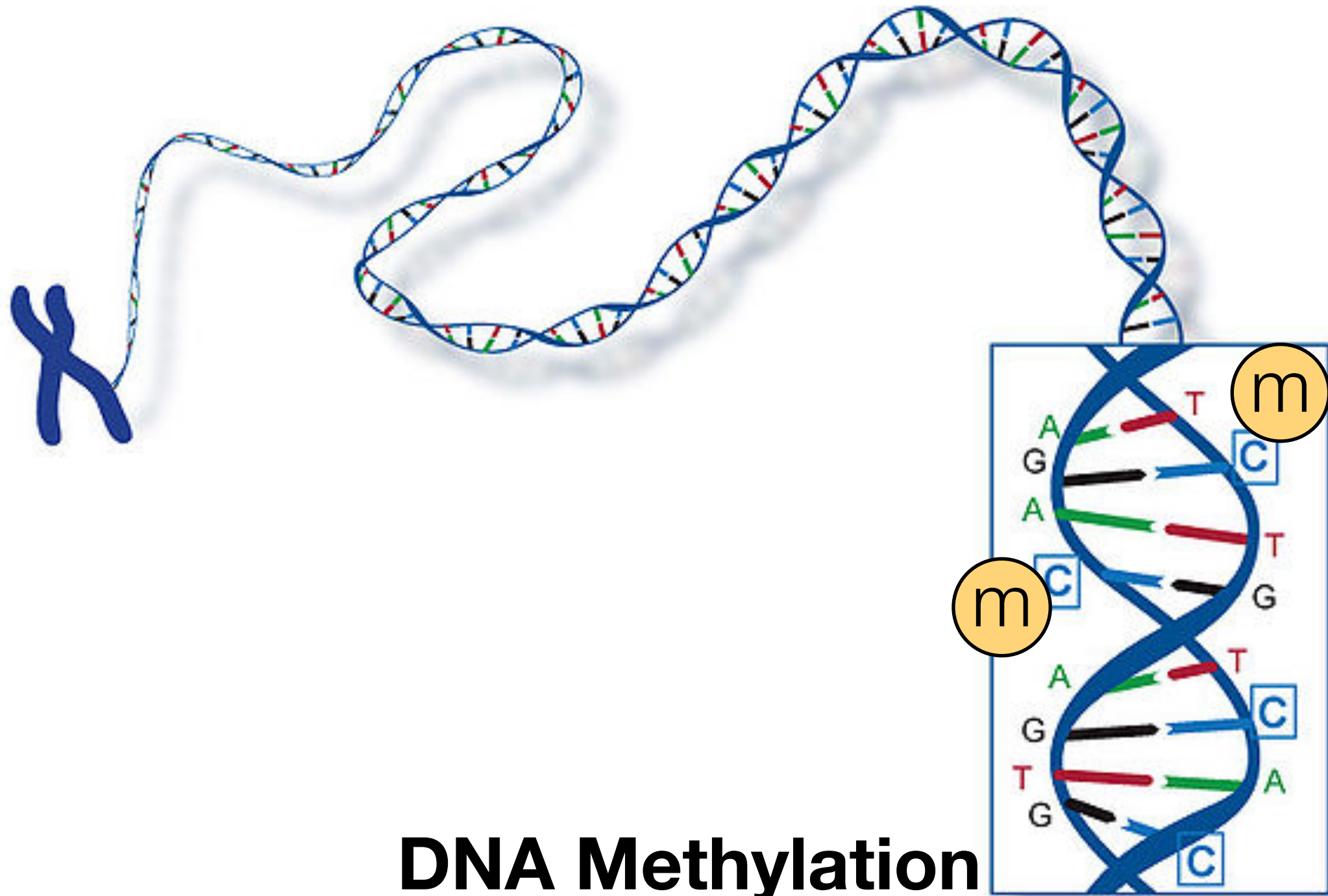


Epigenetics



Natural epigenetic variation in plant species: a view from the field


Eric J Richards

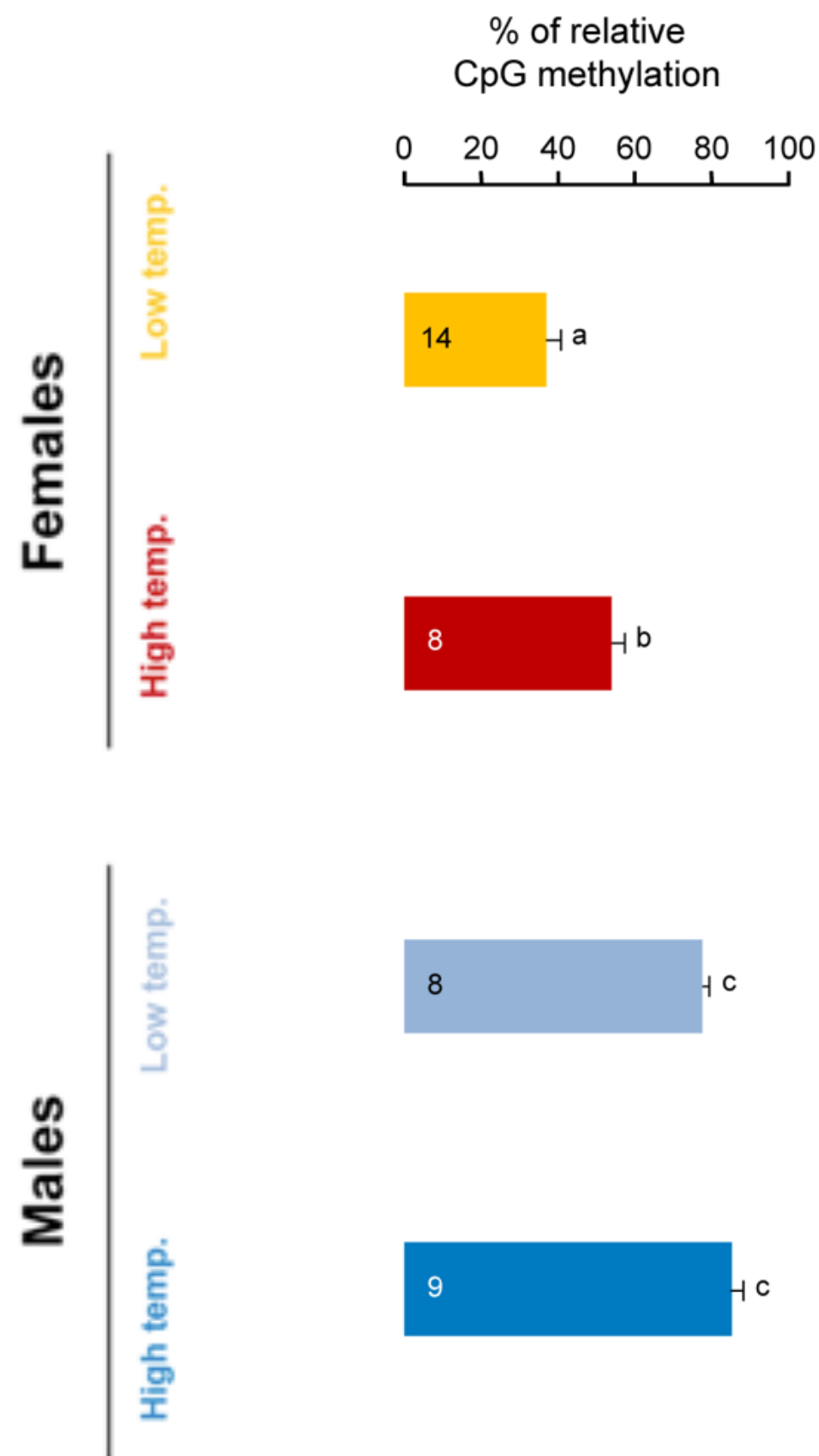


DNA Methylation


Function?

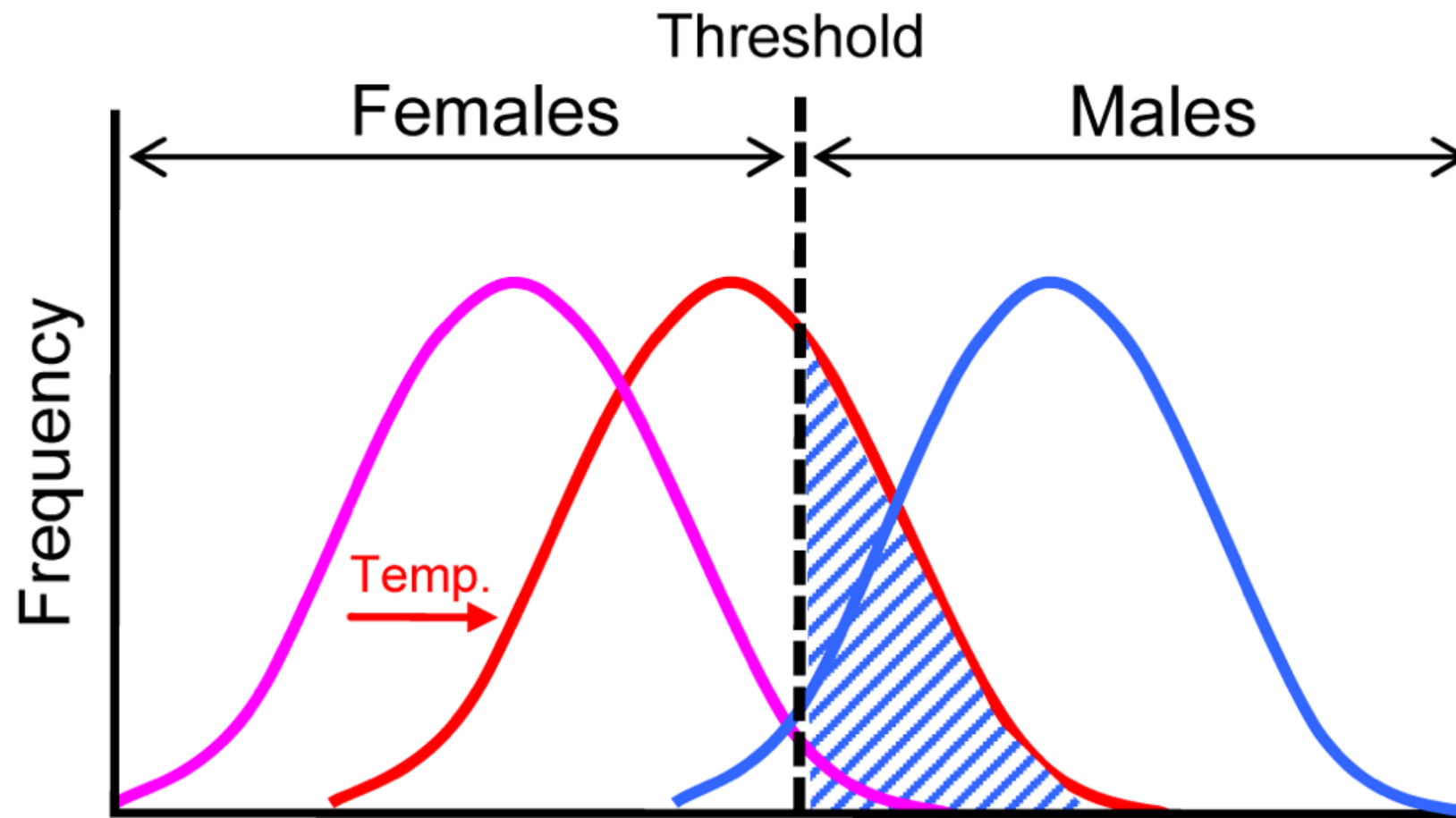
DNA Methylation of the Gonadal Aromatase (*cyp19a*) Promoter Is Involved in Temperature-Dependent Sex Ratio Shifts in the European Sea Bass

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



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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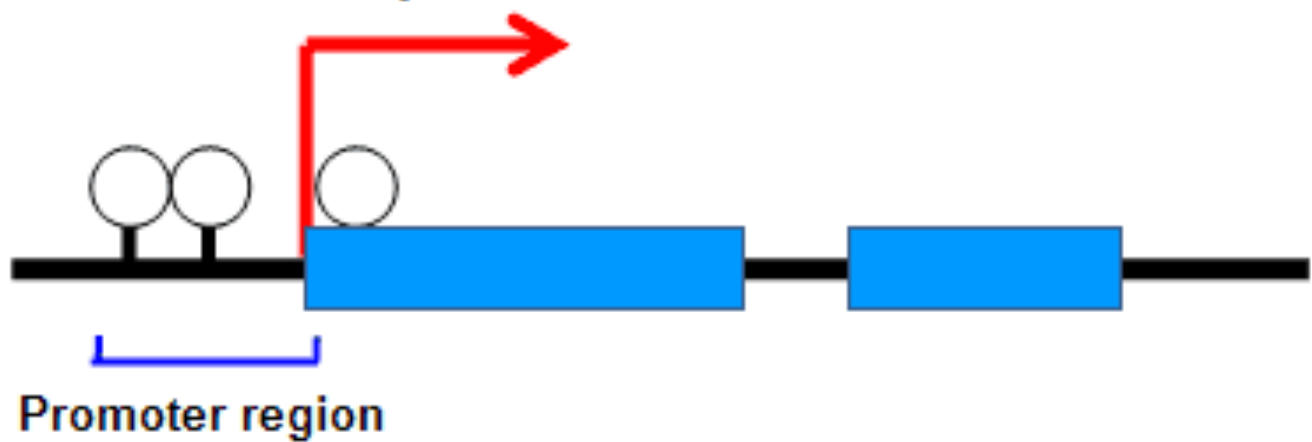


cyp19a promoter methylation level

- Low temperature females
- High temperature females
- Males

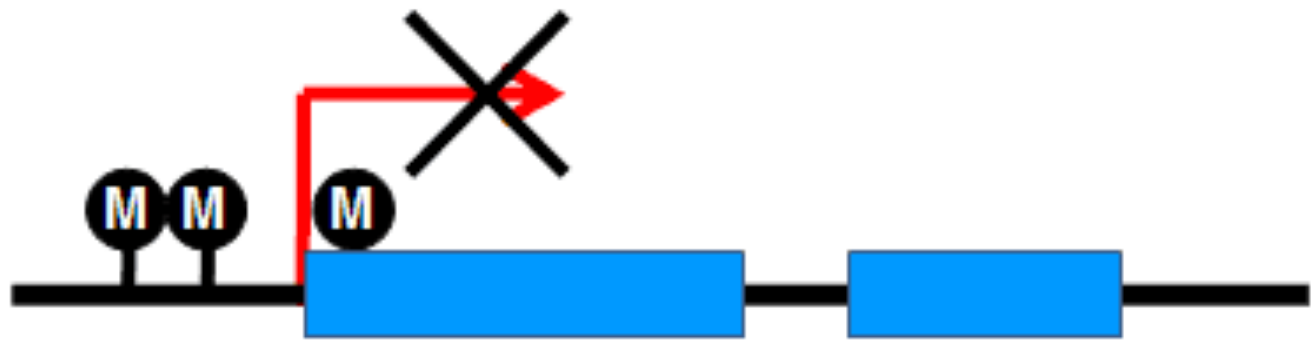
Genes that can be expressed

Low temp.



Genes inactivated by DNA methylation

High temp.



- M** Methylated
- Unmethylated

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 arrows, likely representing regulatory elements or expression patterns. A vertical line is drawn at the 3,754 position on the top track. In the center, there are two semi-transparent images: a grey seal-like animal at the top and a lizard at the bottom. The text 'Non-Vertebrates?' is overlaid in the center. At the bottom, a red box contains text comparing the genomic landscape of non-vertebrates to that of vertebrates.

Non-Vertebrates?

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

The background of the slide features 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 green arrows. A vertical line is drawn at the 3,754 position. In the center, a semi-transparent image of a hand is overlaid. At the bottom, a semi-transparent image of a lizard is overlaid. The text 'Non-Vertebrates?' is centered in a large black 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 arrows, likely representing regulatory elements or expression patterns. A vertical line is drawn at the 3,754 position on the top track. In the center, there are two semi-transparent images of animals: a grey seal-like creature at the top and a lizard at the bottom. The text 'Non-Vertebrates?' is overlaid in the center. At the bottom, a red box contains text comparing the genomic landscape of non-vertebrates to that of vertebrates.

Non-Vertebrates?

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

Absent in
several
model
organisms

Oysters?



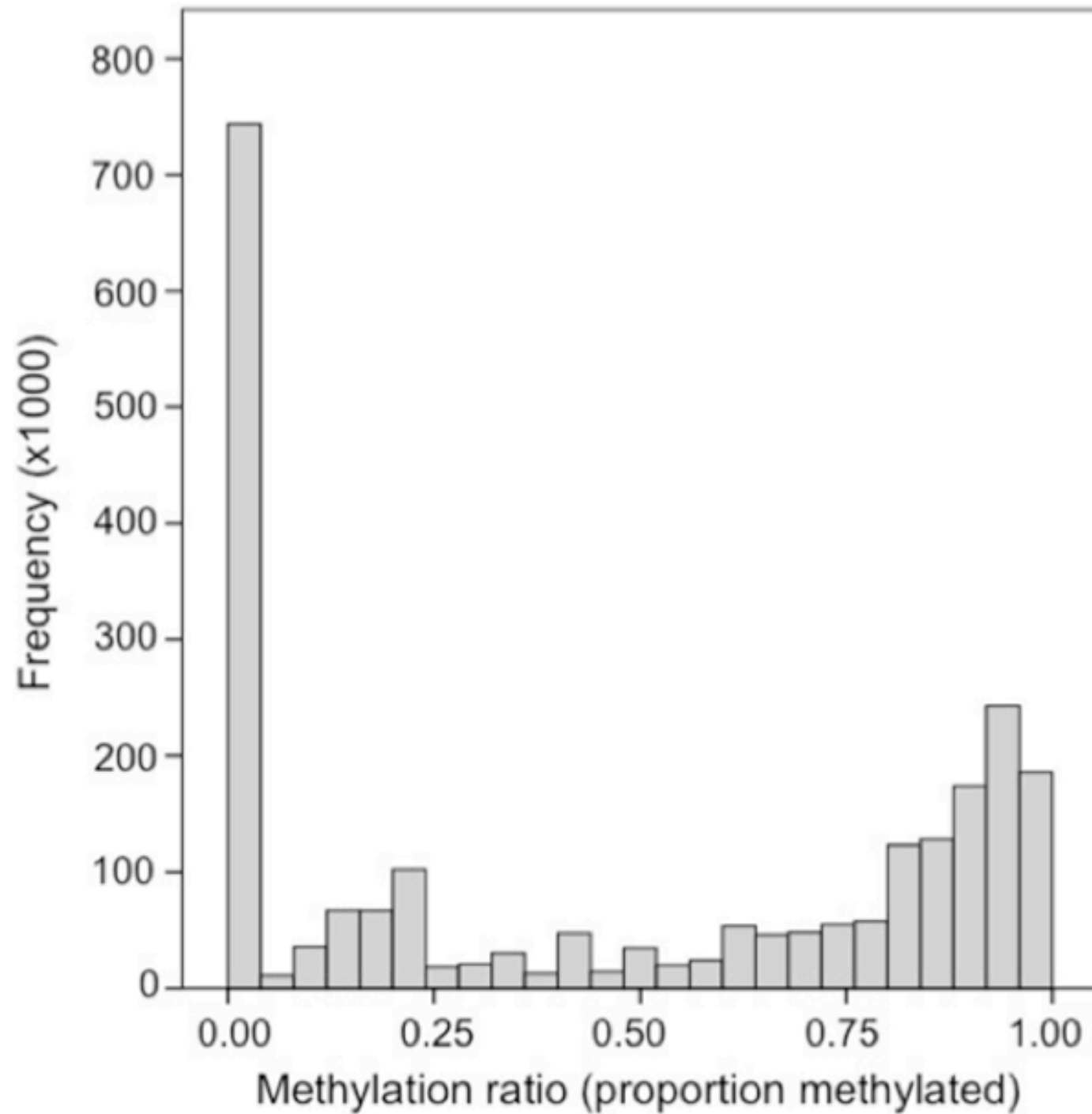
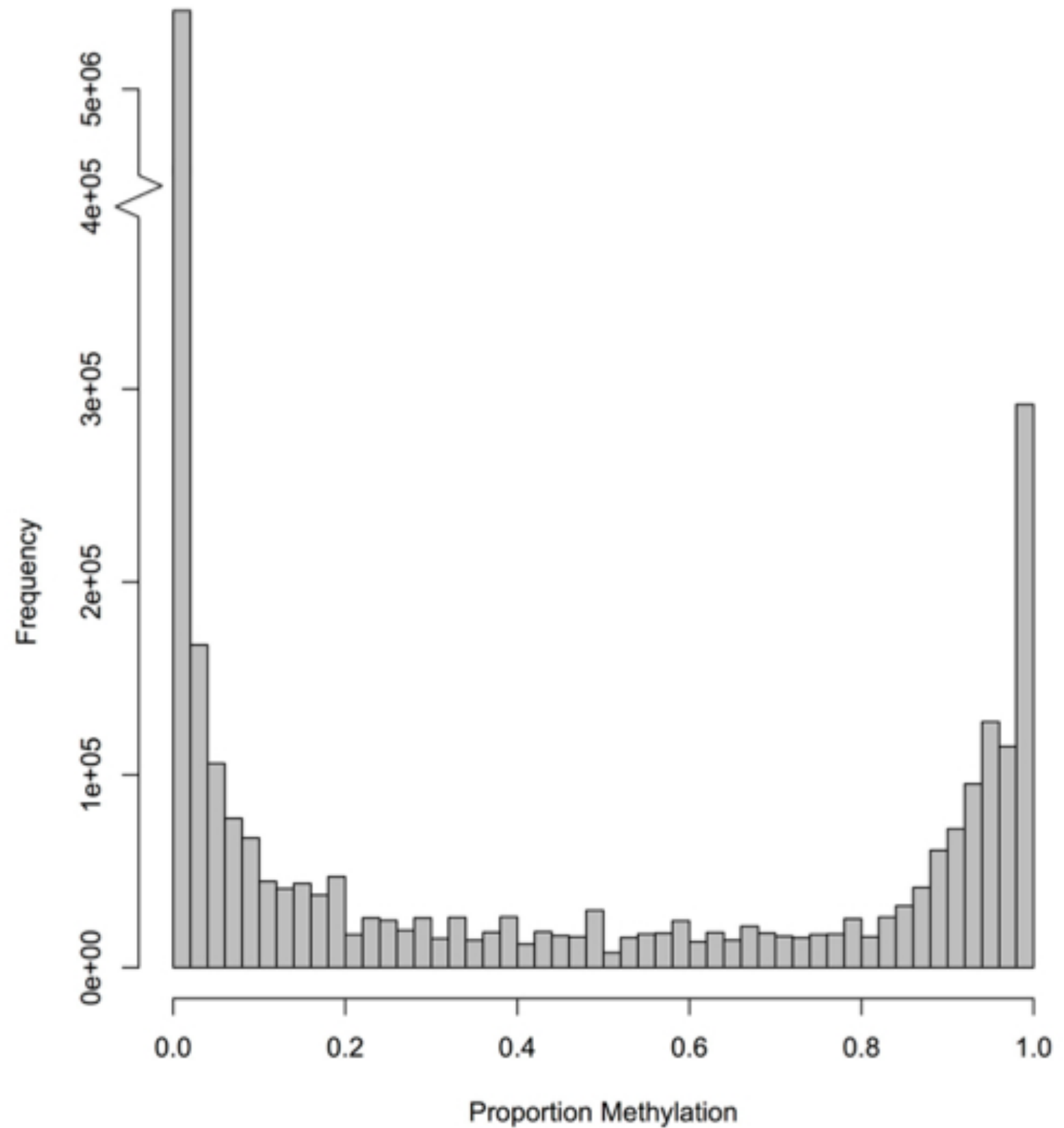


Figure 1 Frequency distribution of methylation ratios for CpG dinucleotides in oyster gill tissue. A total of 2,625,745 CpG dinucleotides with $\geq 5\times$ coverage are represented.

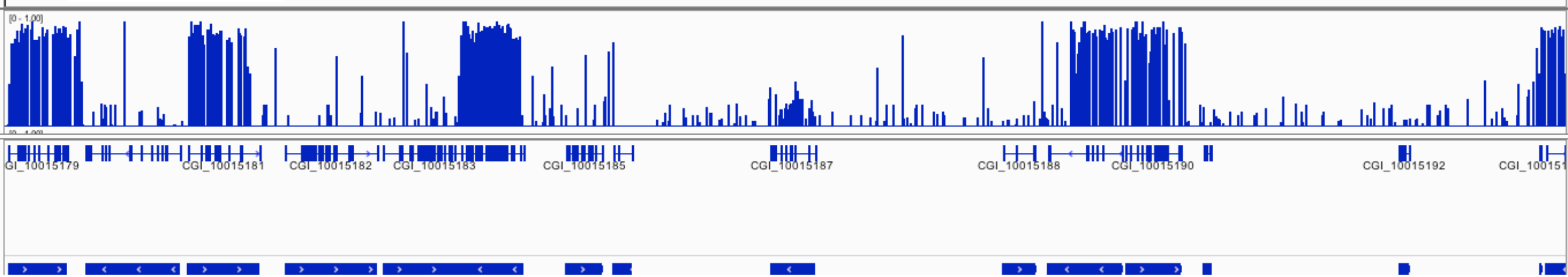


Genome-wide profiling of DNA methylation and gene expression in *Crassostrea gigas* male gametes

Claire E. Olson and Steven B. Roberts*

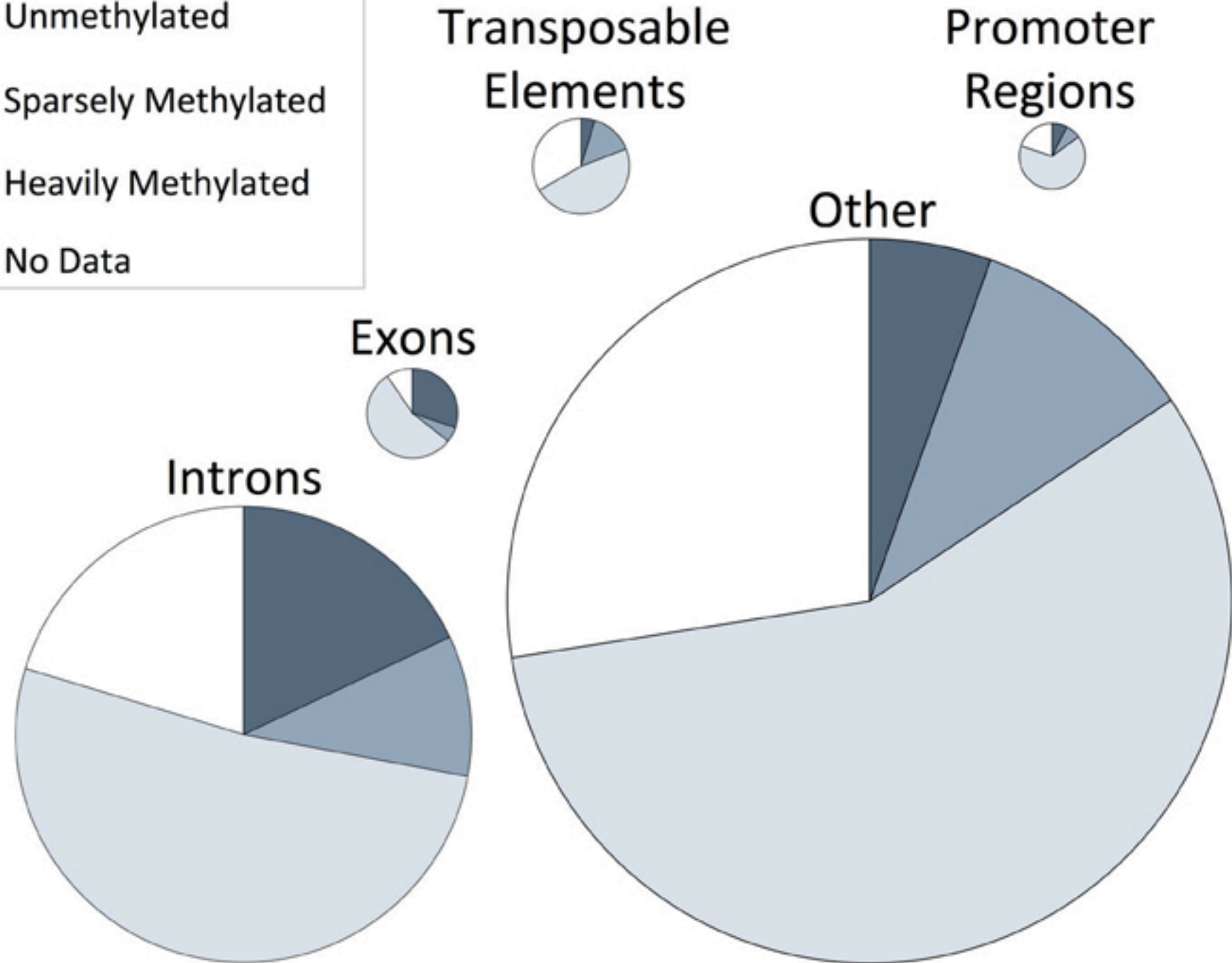
School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA

Epigenetic variation **1**



mosaic

associated with gene bodies



Genome-wide profiling of DNA methylation and gene expression in *Crassostrea gigas* male gametes

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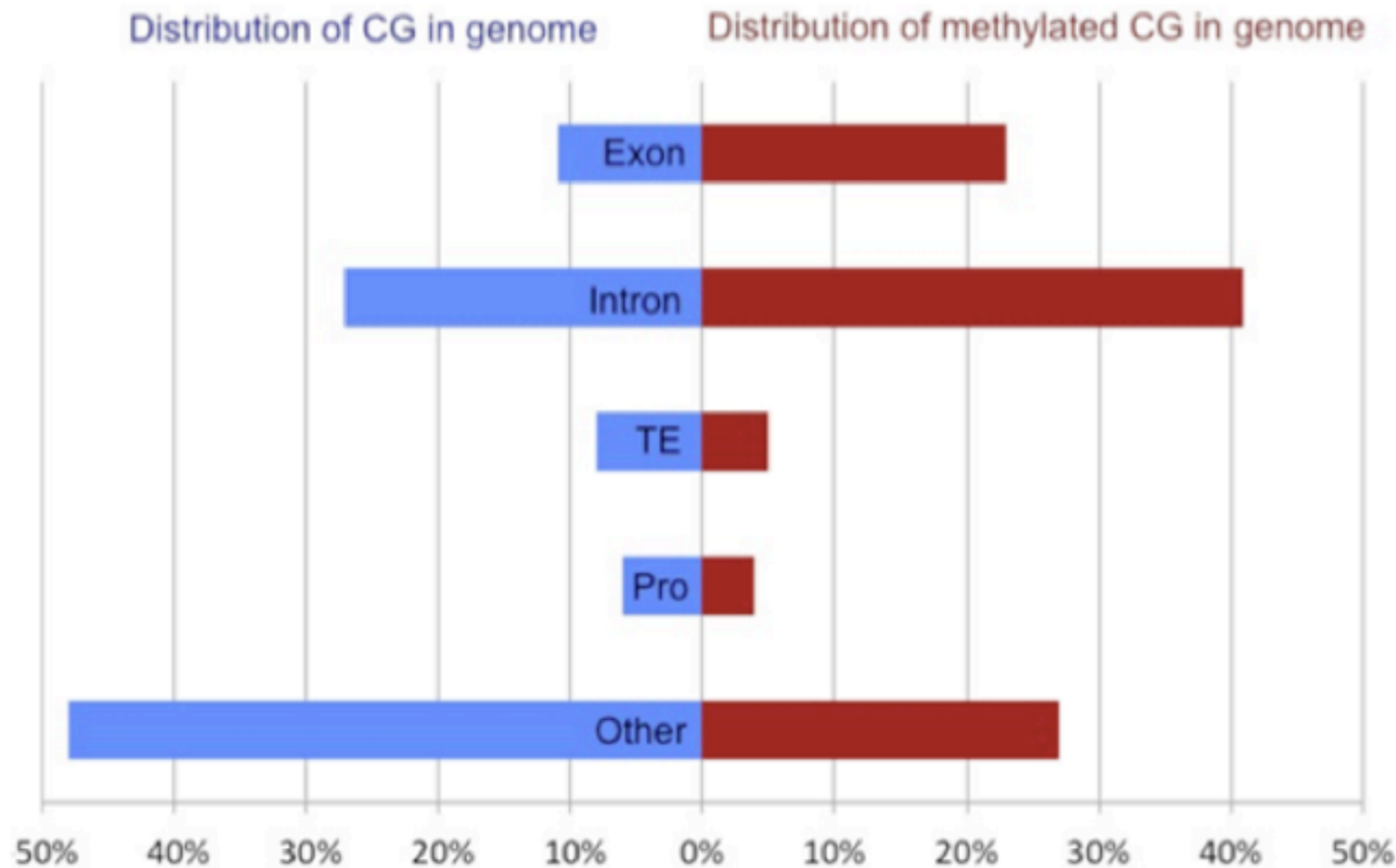
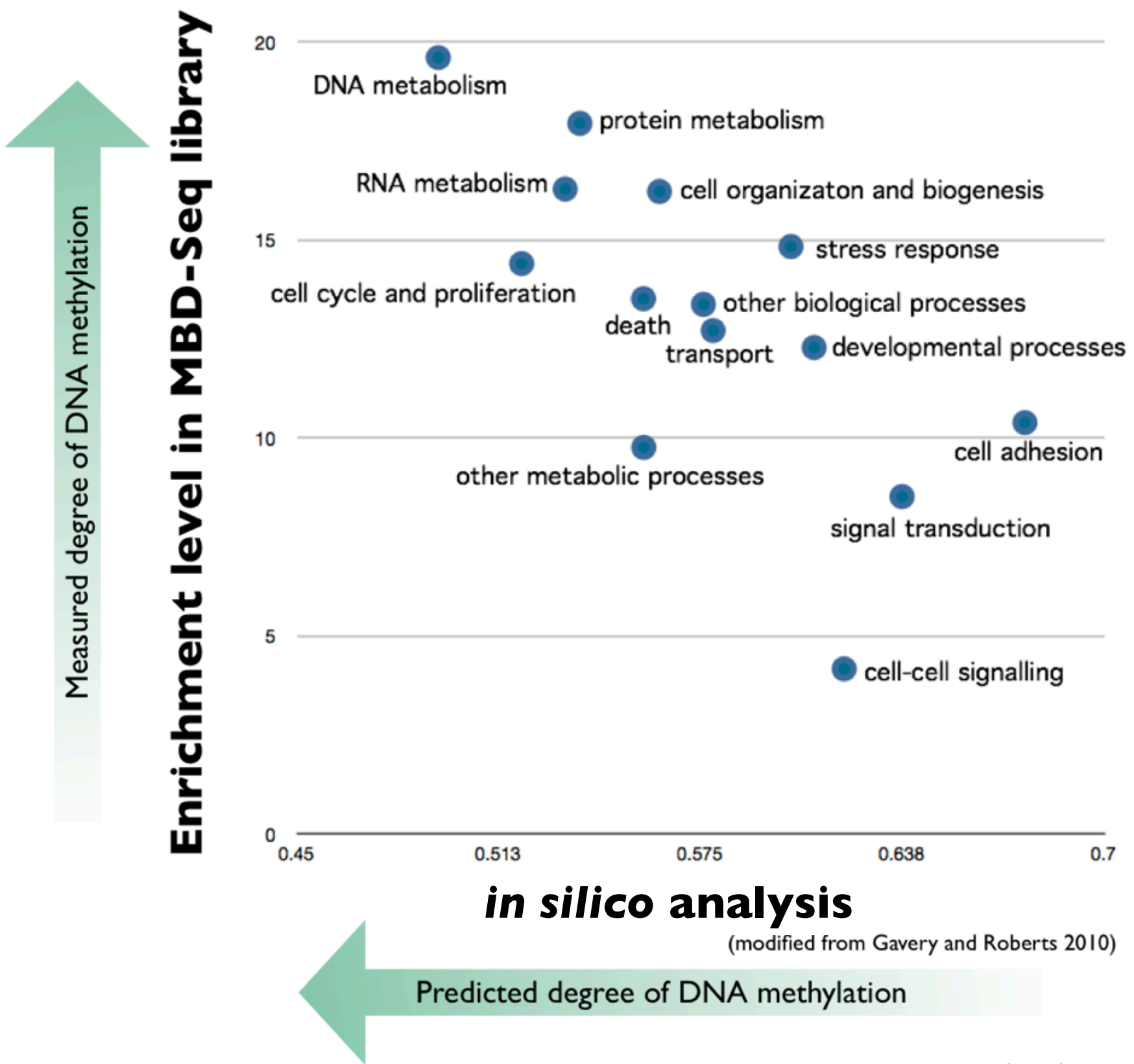
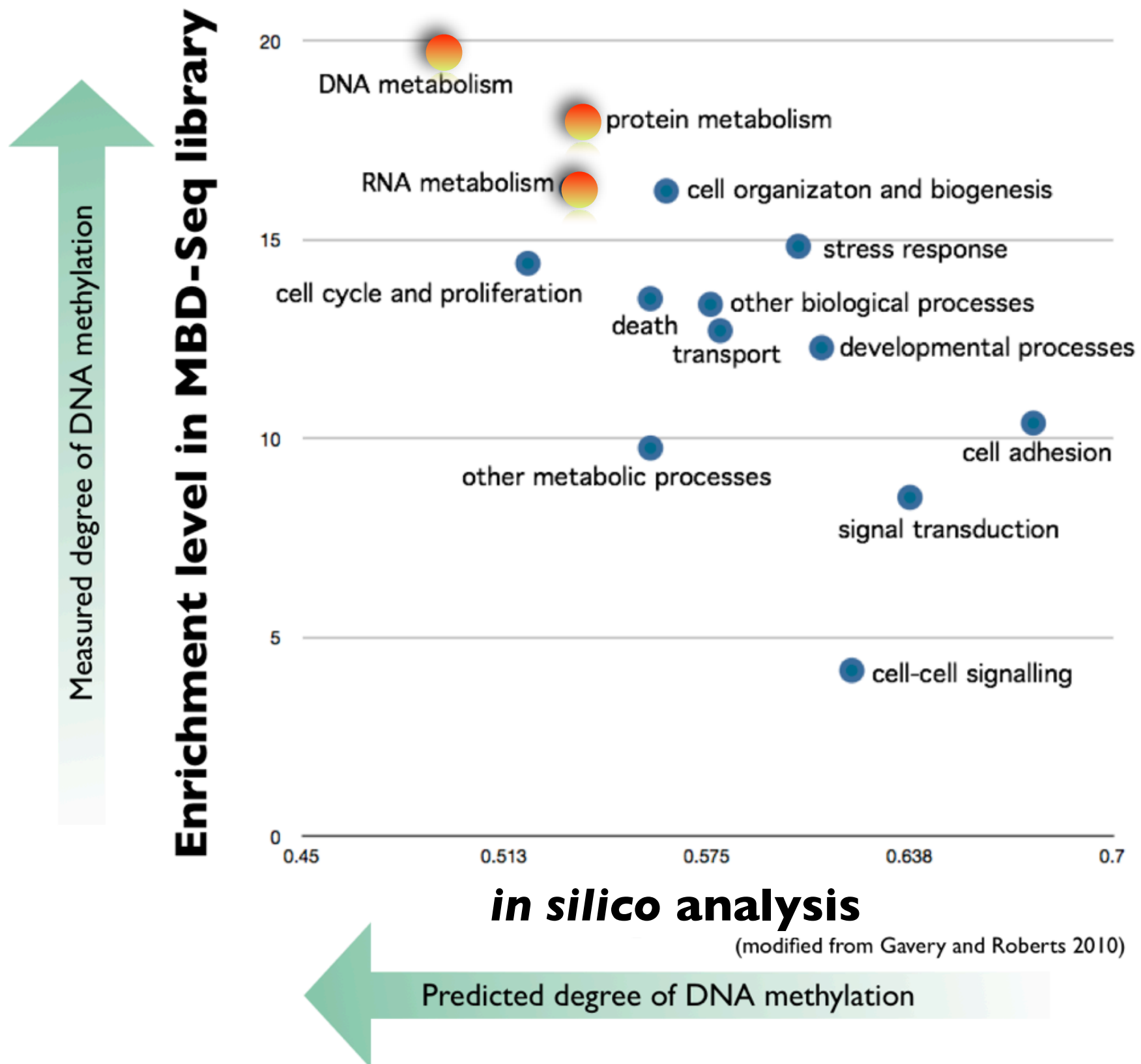
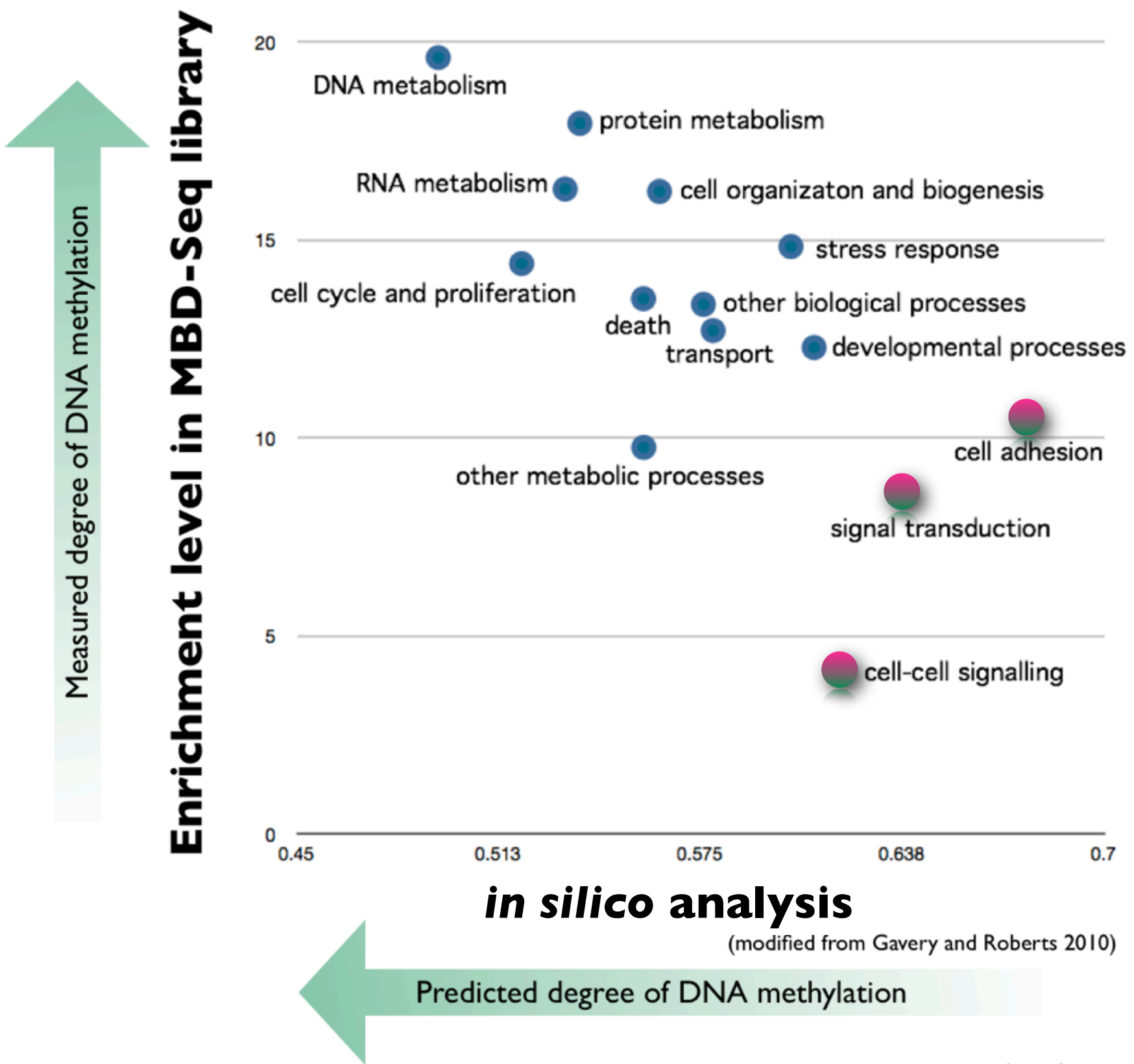


Figure 2 Comparison of the total CpG versus methylated CpG in oyster gill tissue by genomic feature. Proportion of all CpG (blue) and methylated CpG (red) in gill tissue across genomic features of *C. gigas*. Percent of CpG dinucleotides in Exons, Introns, Transposable Elements (TE), promoters (Pro) and unannotated intergenic regions (Other) are reported.

Epigenetic variation **1**

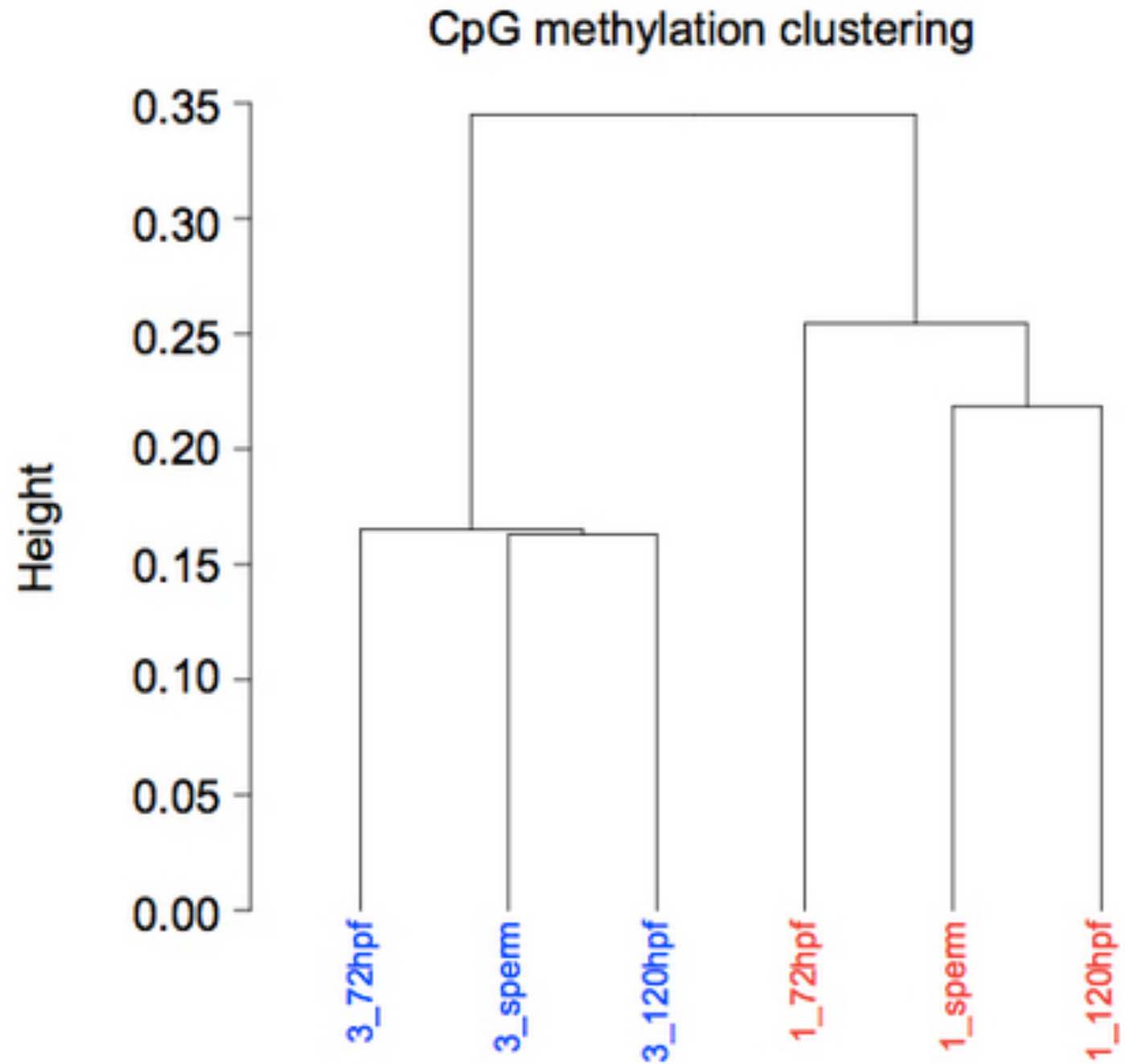


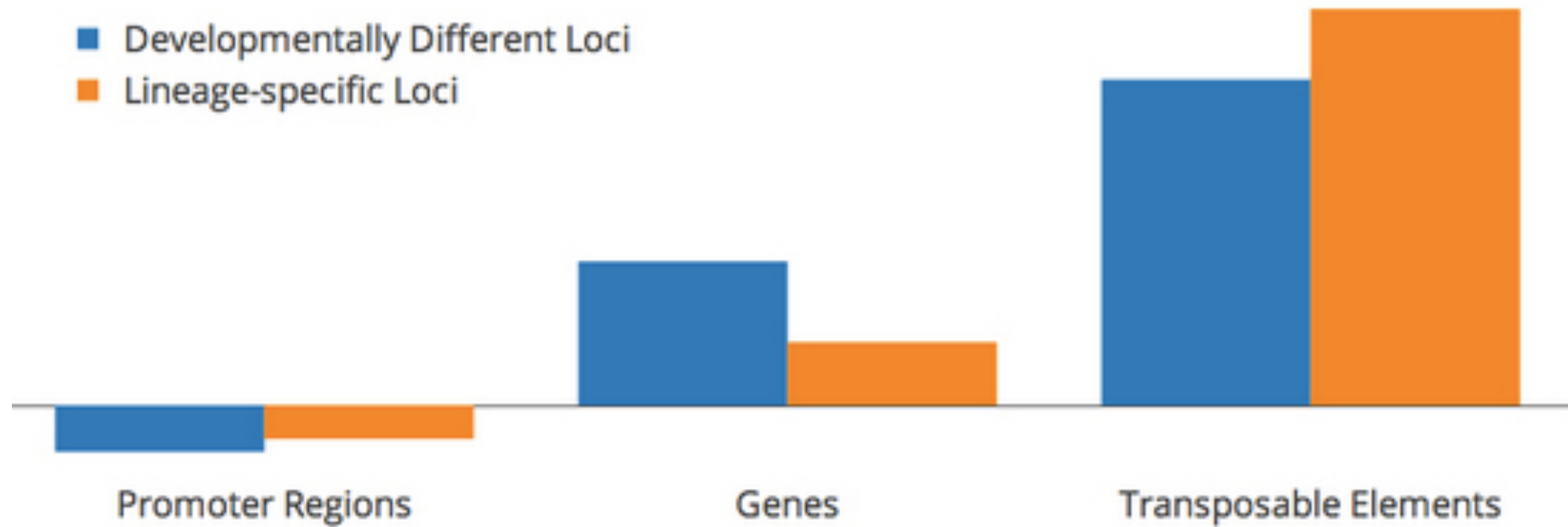




Whole Genome BS-Seq

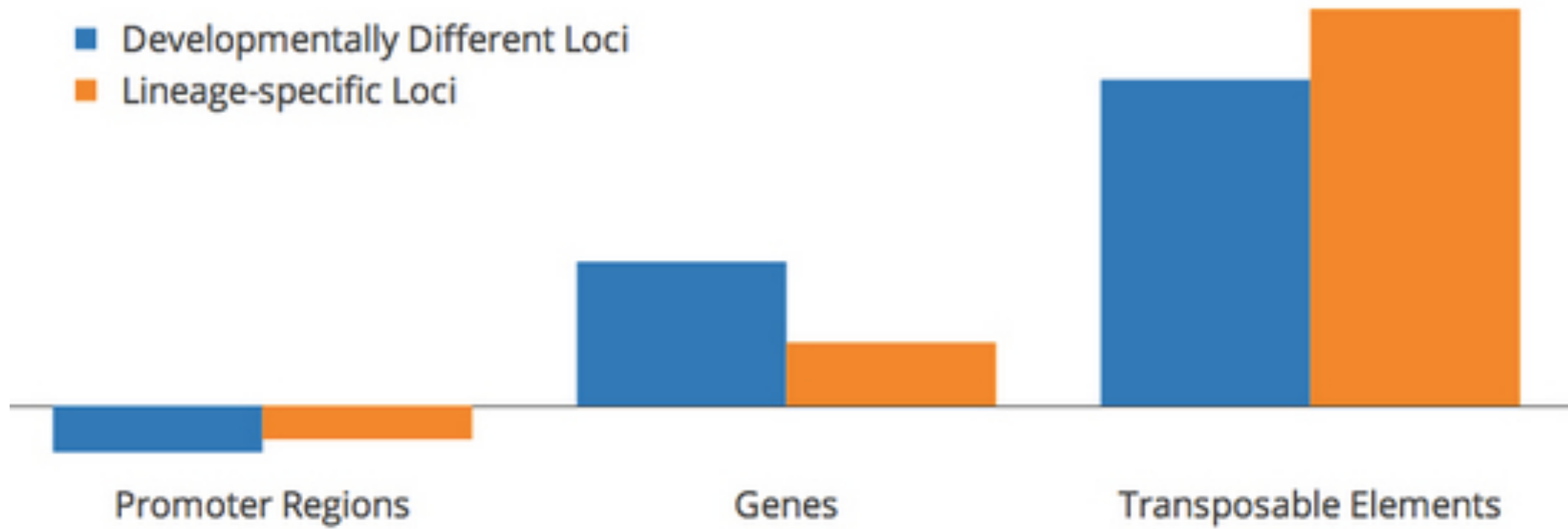
Two Lineages
-
Sperm +
Larvae
(72h & 120h)





Differentially Methylated Loci predominant in Transposable Elements

Epigenetic variation **1**



branch: master olson-dev / +

fix this

sr320 authored 4 days ago

- .ipynb_checkpoints
- img
- scripts
- wd
- BiGo_dev_manu.html
- BiGo_dev_manu.ipynb
- README.md

IP[y]: Notebook

File Edit View Insert Cell Kernel Help

Code

github.com/sr320/olson-dev

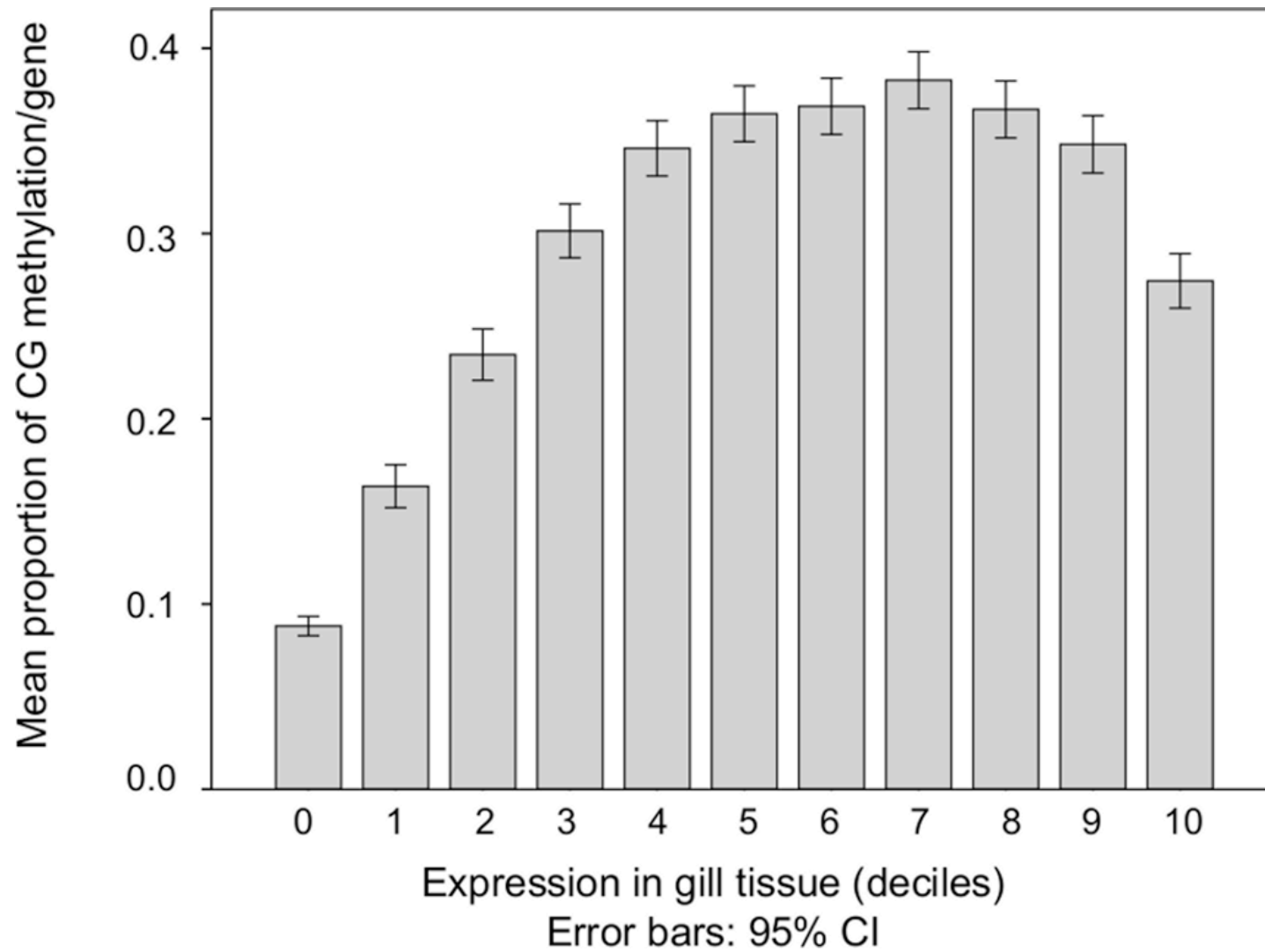
Claire Olson

- Sparsely (~16 %) methylated genome
- Gene body methylation
 - Function specific
- TEs are *not* hypermethylated across genome
 - Preliminary evidence indicates DMRs are predominant in TEs

Gene
expression

2

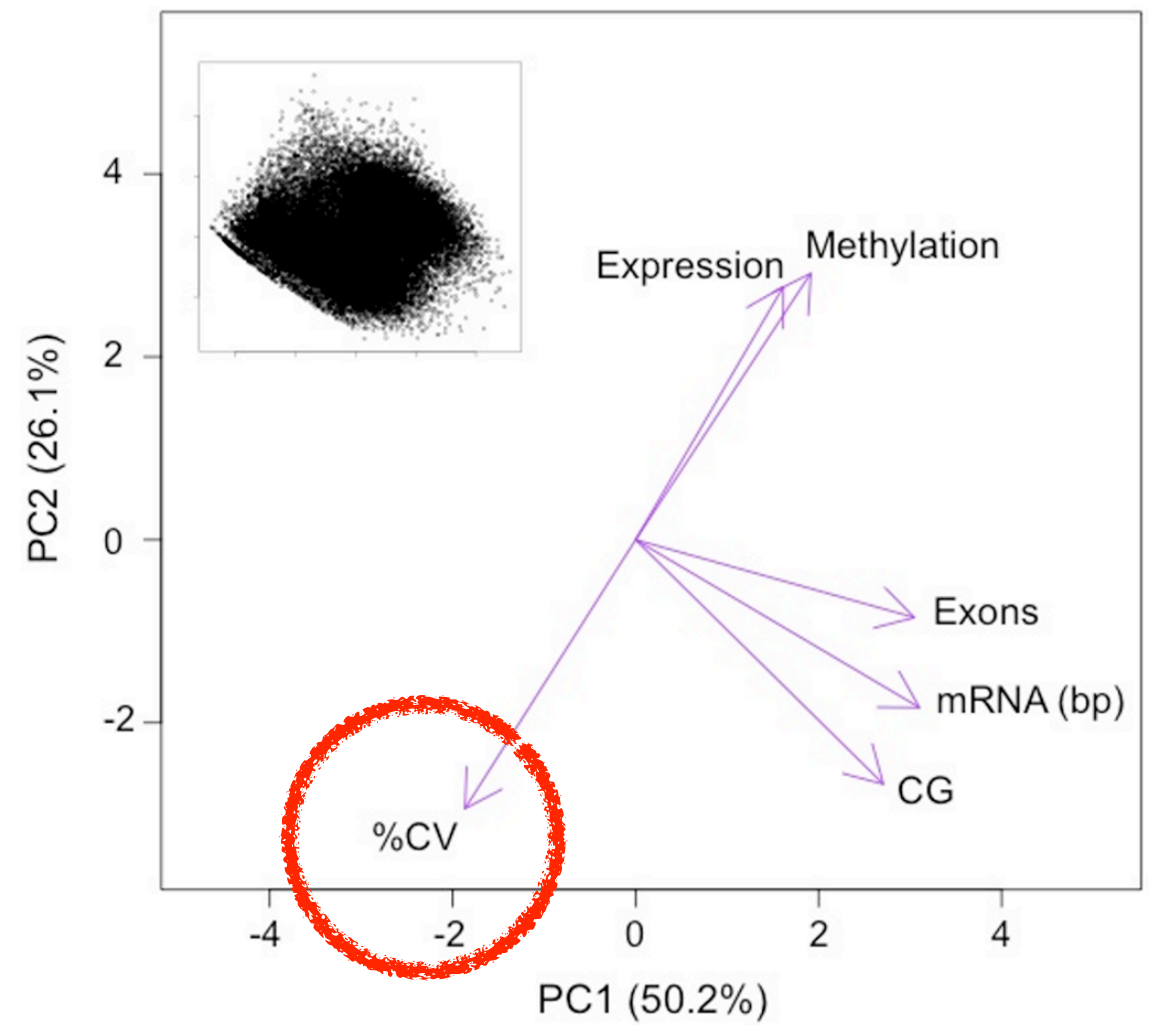
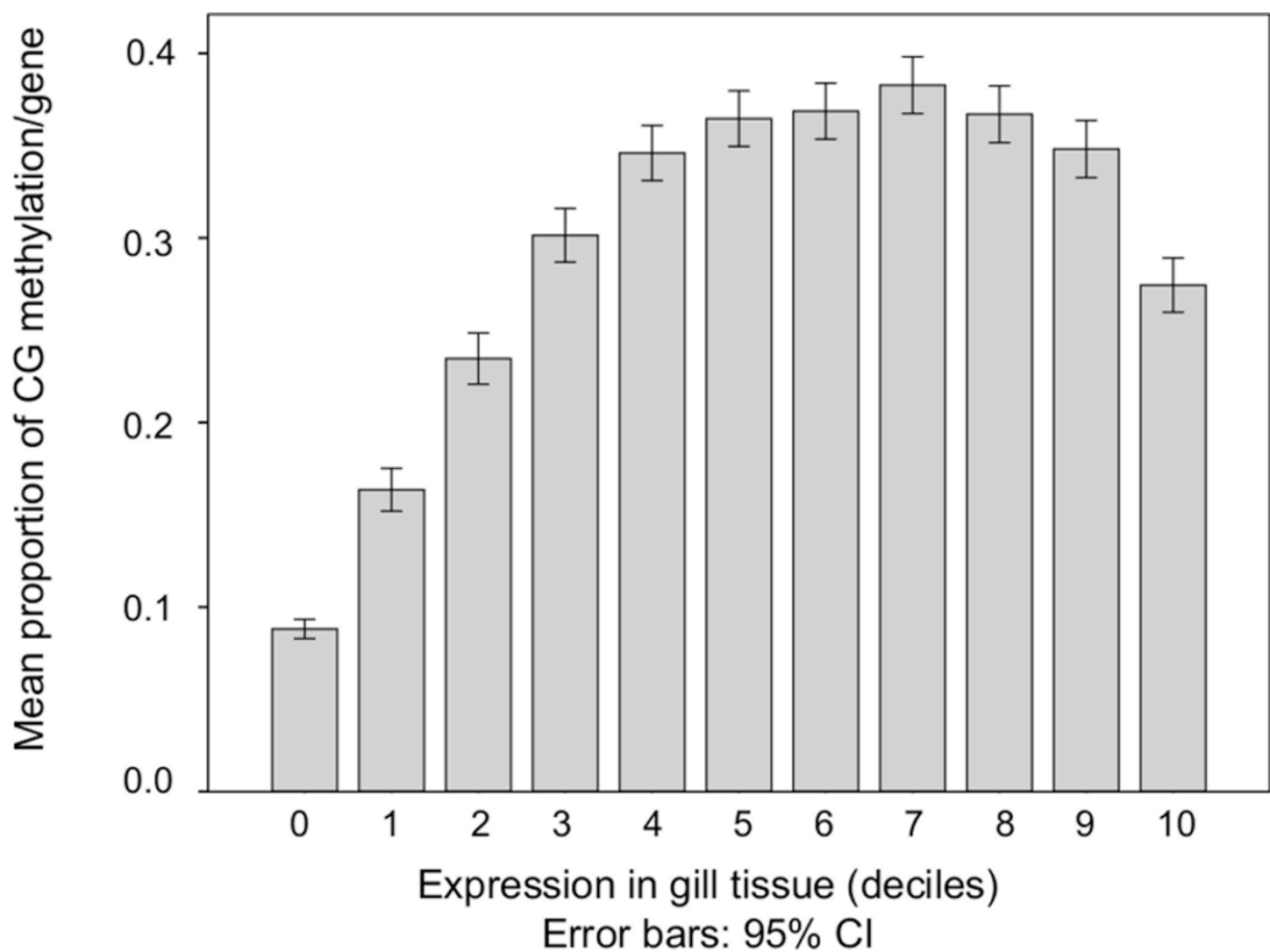
Epigenetic
variation



Gene expression

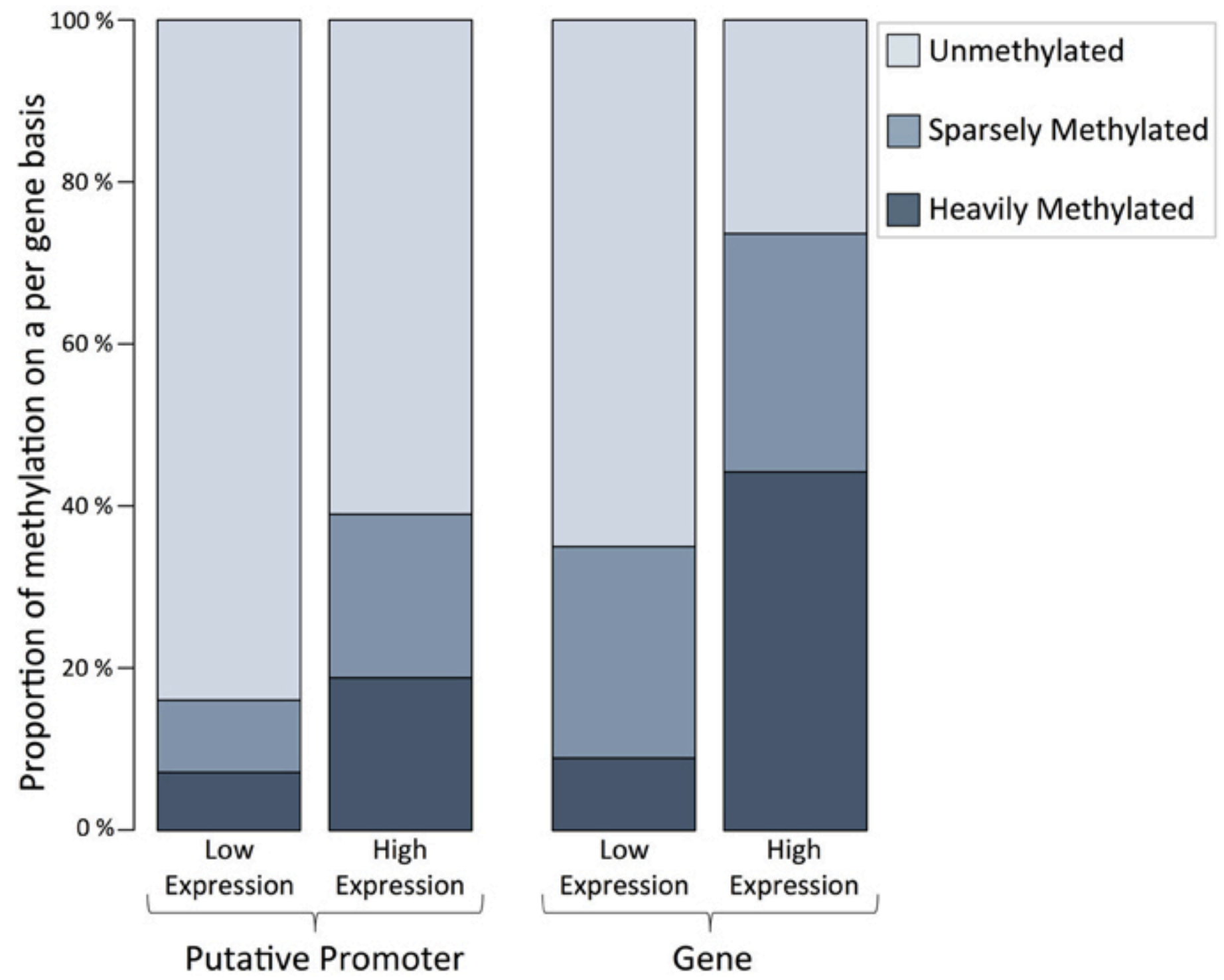
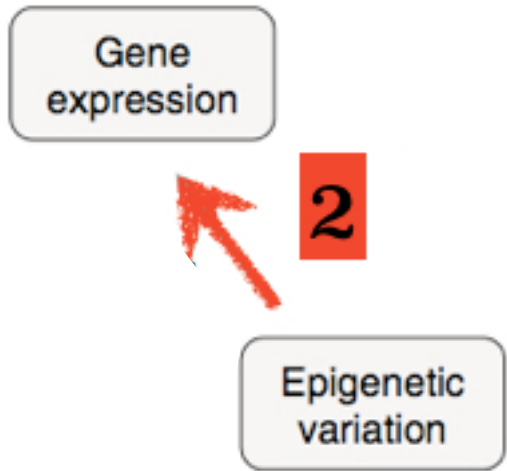
2

Epigenetic variation



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

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



Genome-wide profiling of DNA methylation and gene expression in *Crassostrea gigas* male gametes

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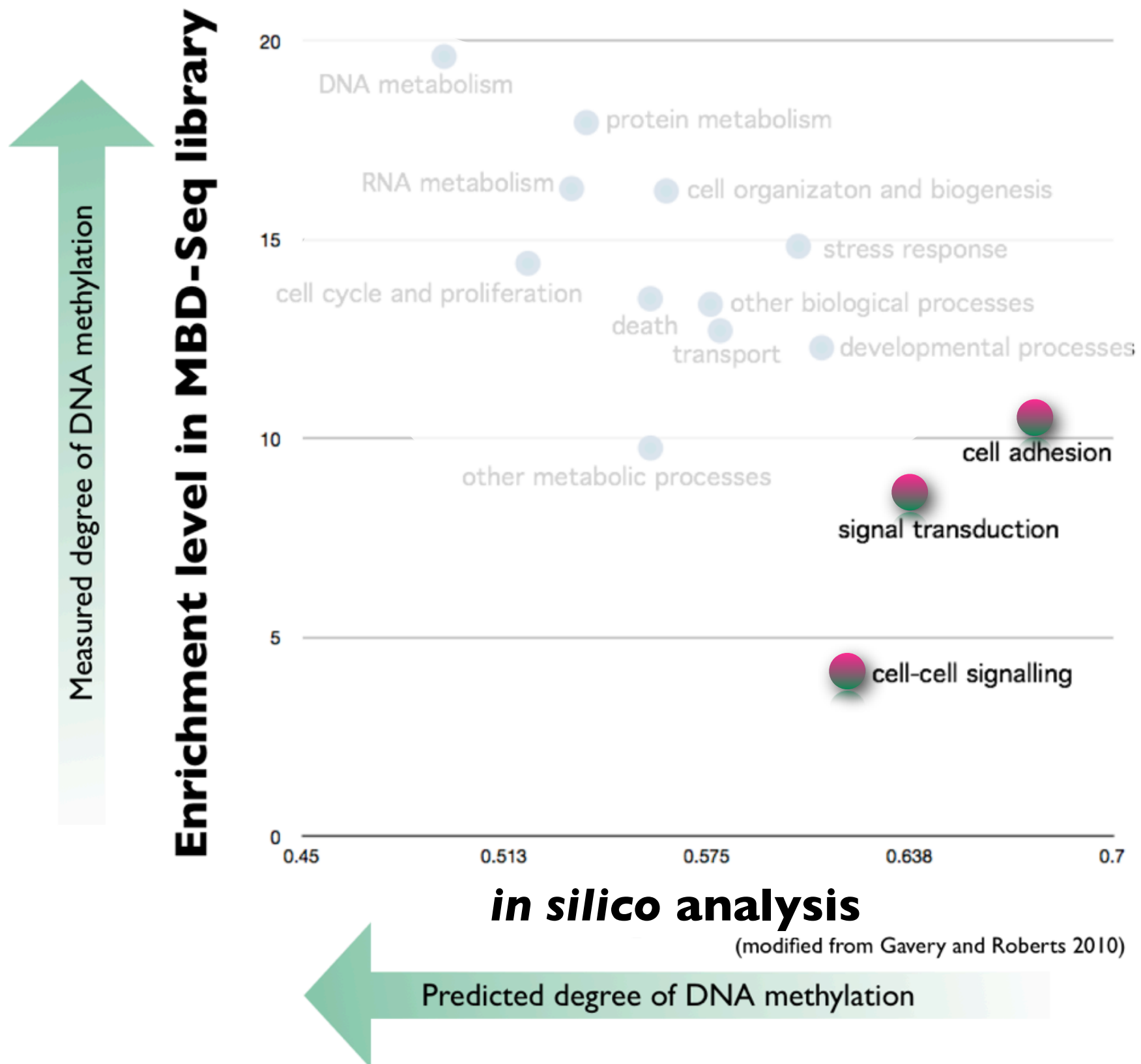
Role?

A context dependent role for DNA methylation in bivalves

Mackenzie R. Gavery and Steven B. Roberts

Advance Access publication date 7 January 2014

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.



A context dependent role for DNA methylation in bivalves

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Advance Access publication date 7 January 2014

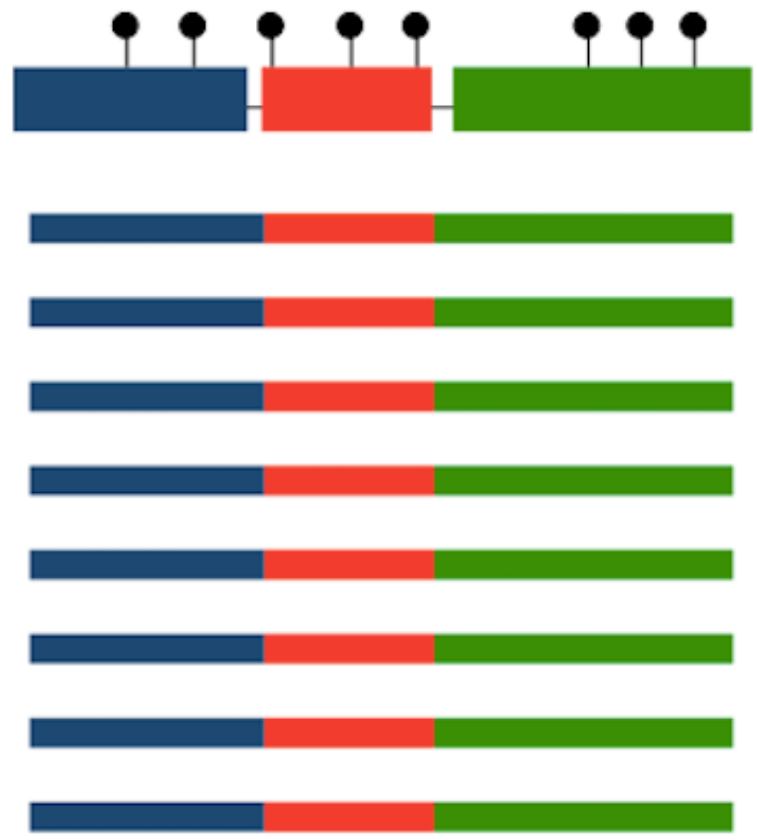
Stochastic Variation

Gene expression

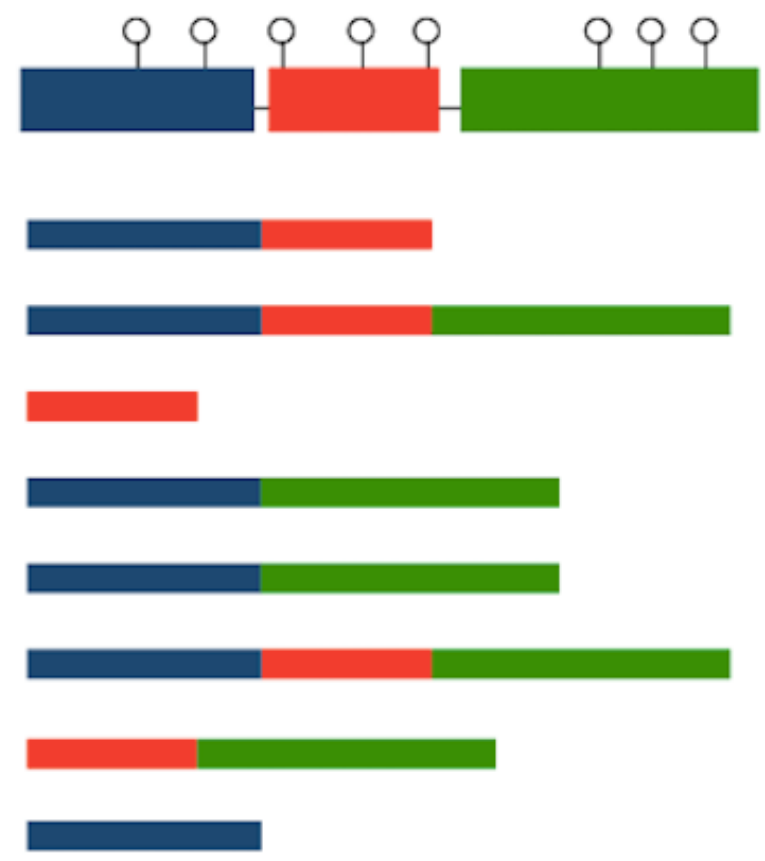
2



Epigenetic variation



housekeeping

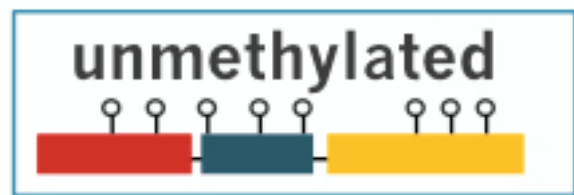


response to change

Gene expression

2

Epigenetic variation



inducible



disease

temperature

dessication

salinity

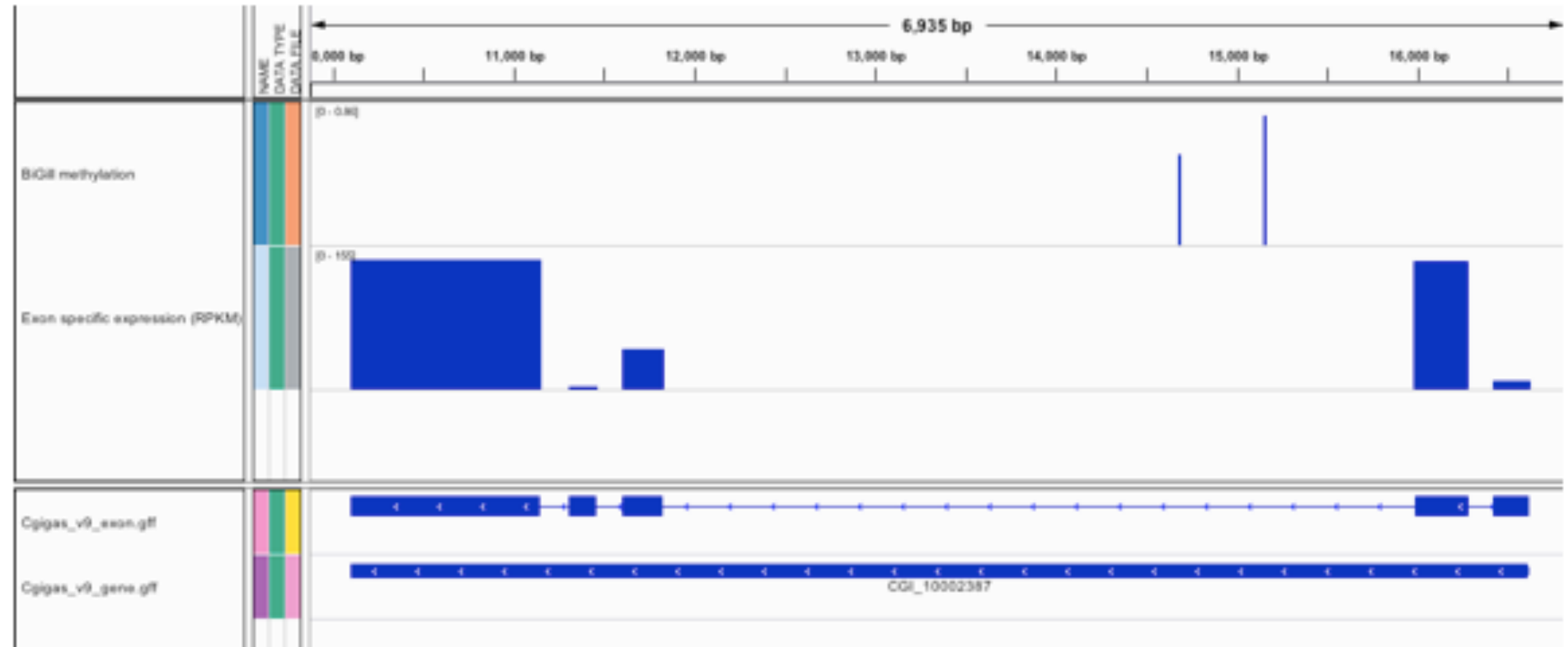
Mackenzie Gavery

response to
change

Heat shock 70 kDa protein 12A

avg exp
199

%meth
2%

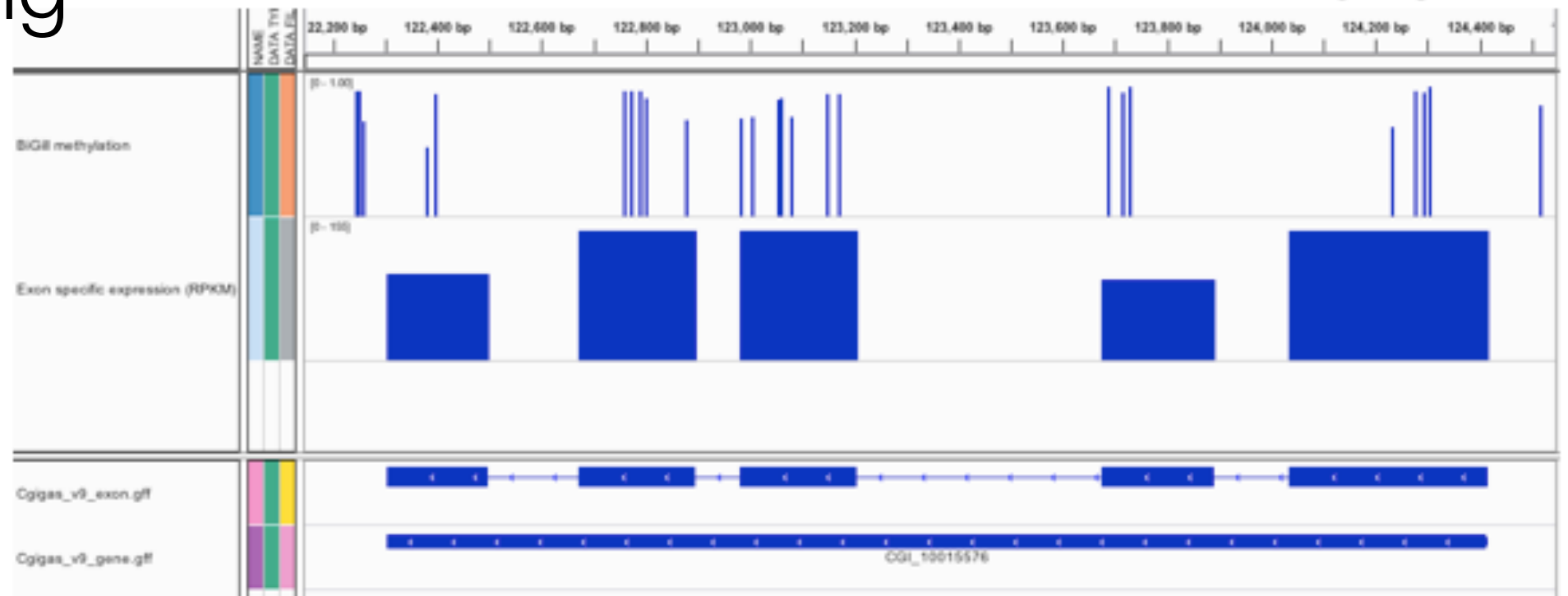


housekeeping

Tektin-2

avg exp
197

%meth
91%

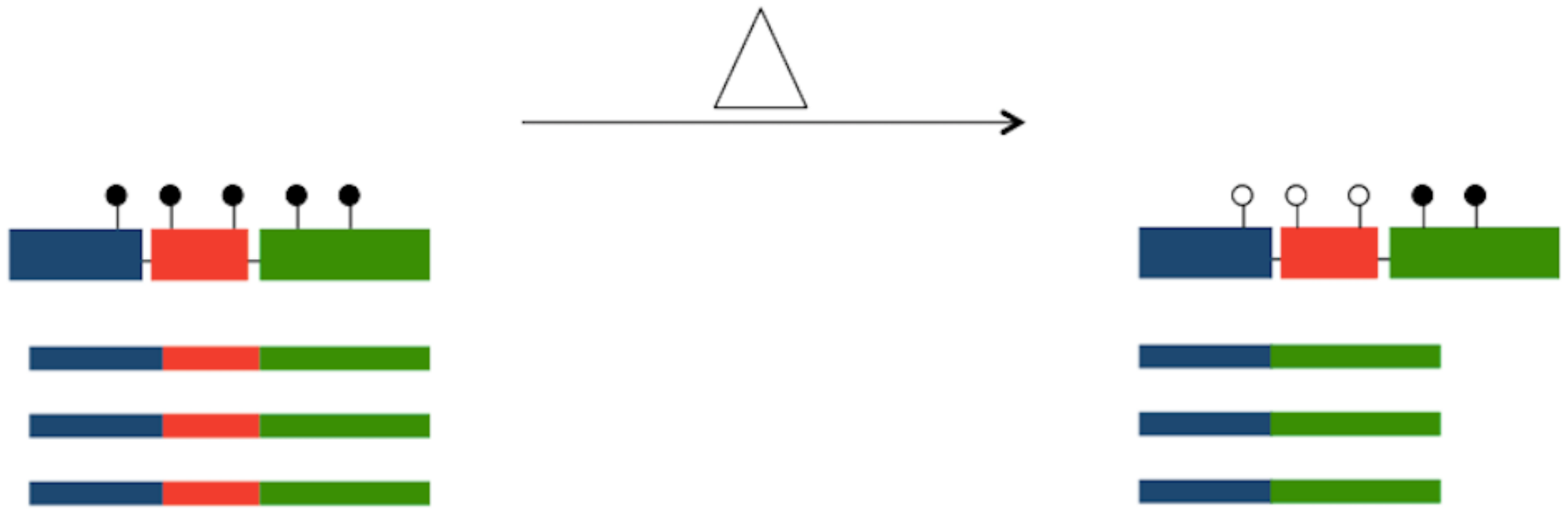
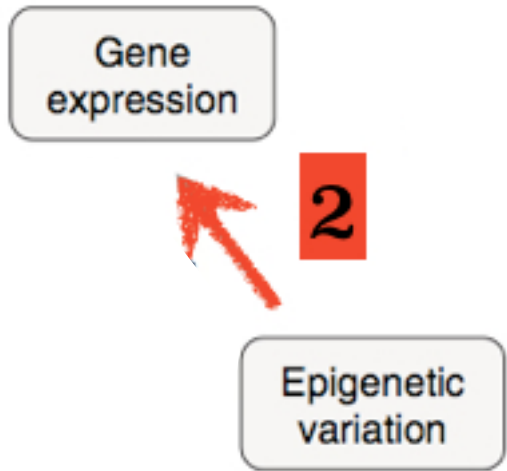


A context dependent role for DNA methylation in bivalves

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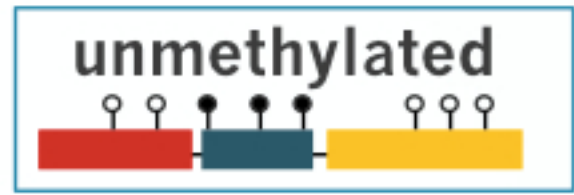
Targeted Regulation



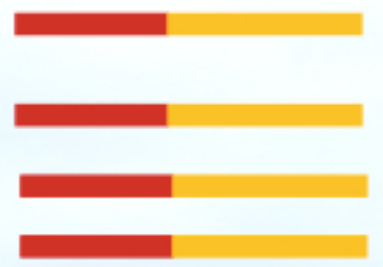
Gene expression

2

Epigenetic variation



inducible



disease

temperature

dessication

salinity

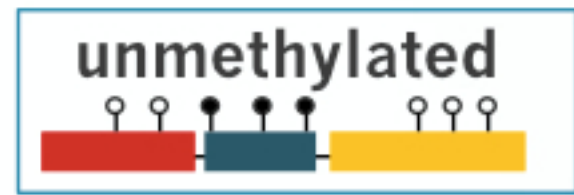


Mackenzie Gavery

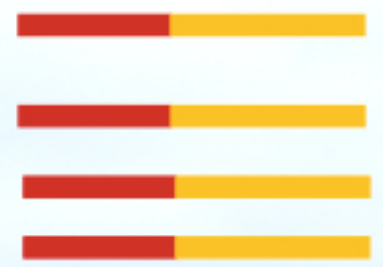
Gene expression

2

Epigenetic variation



inducible



disease

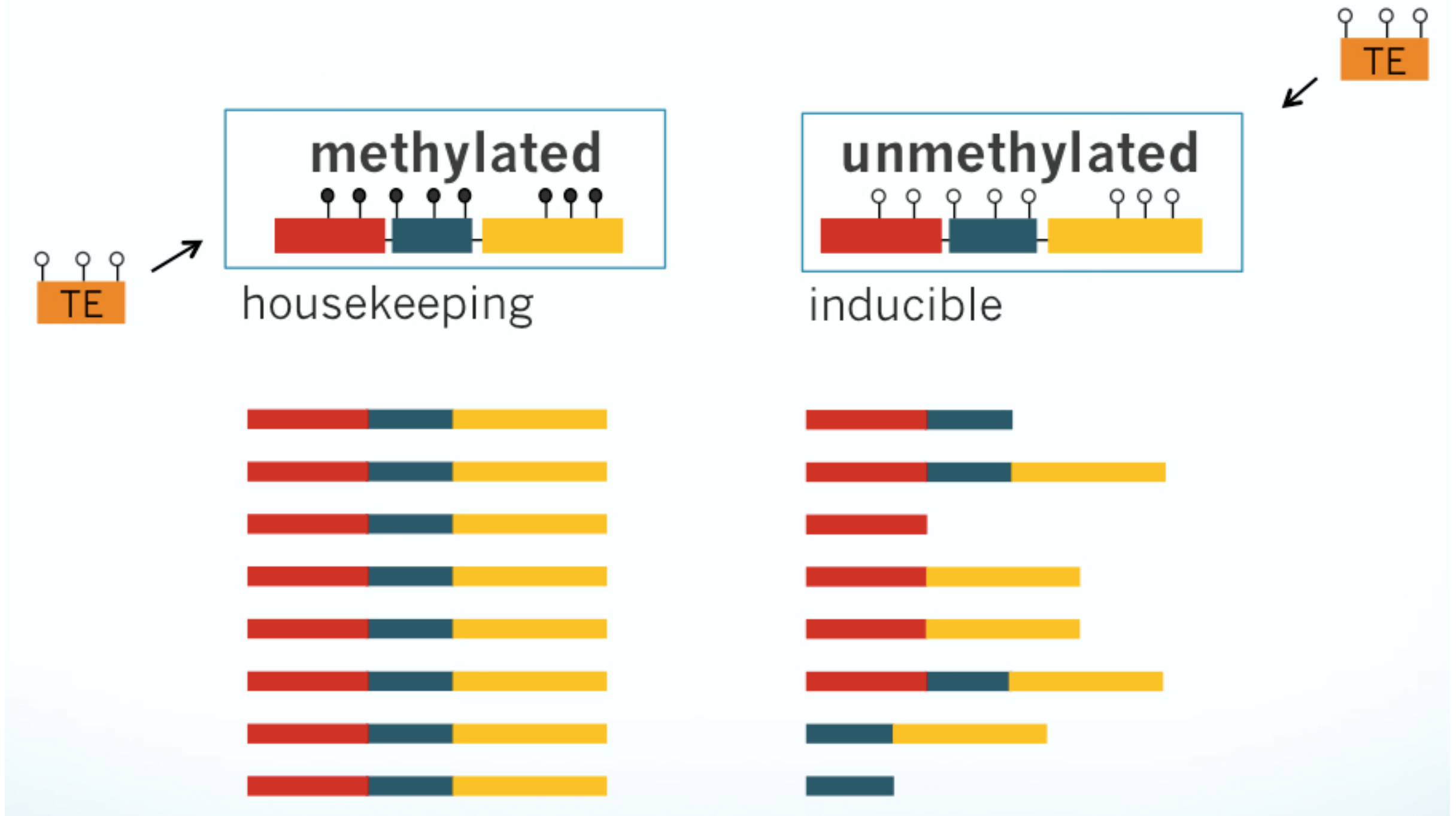
temperature

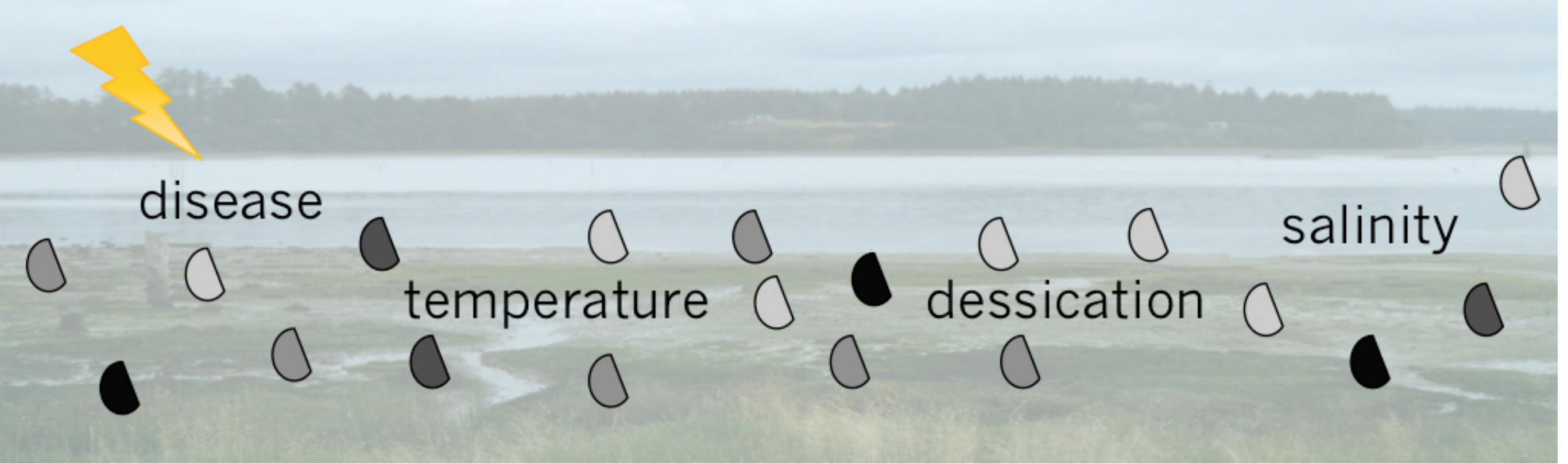
dessication

salinity



Mackenzie Gavery



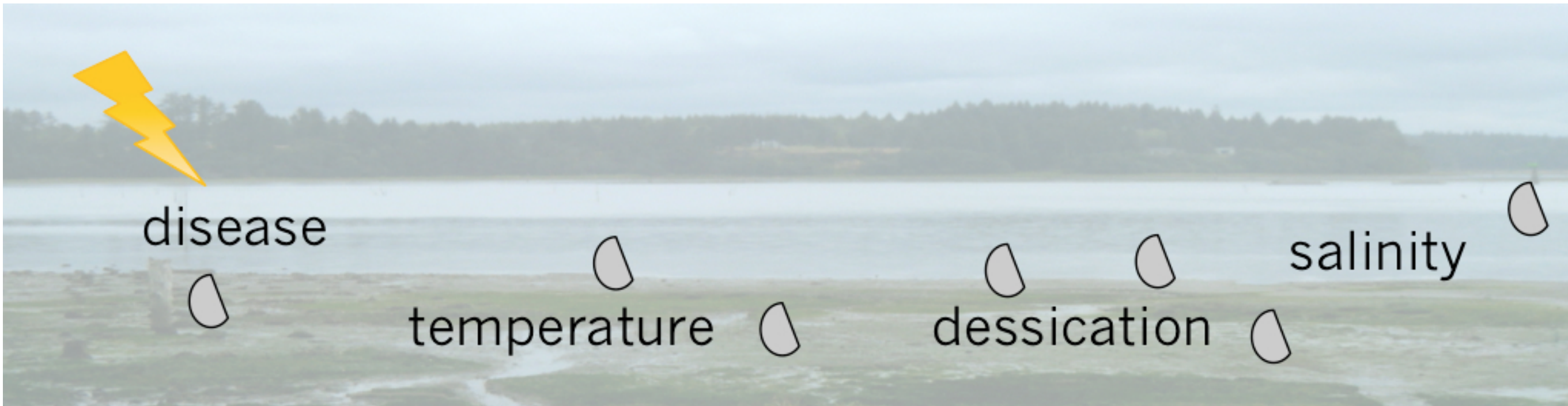


disease

temperature

dessication

salinity



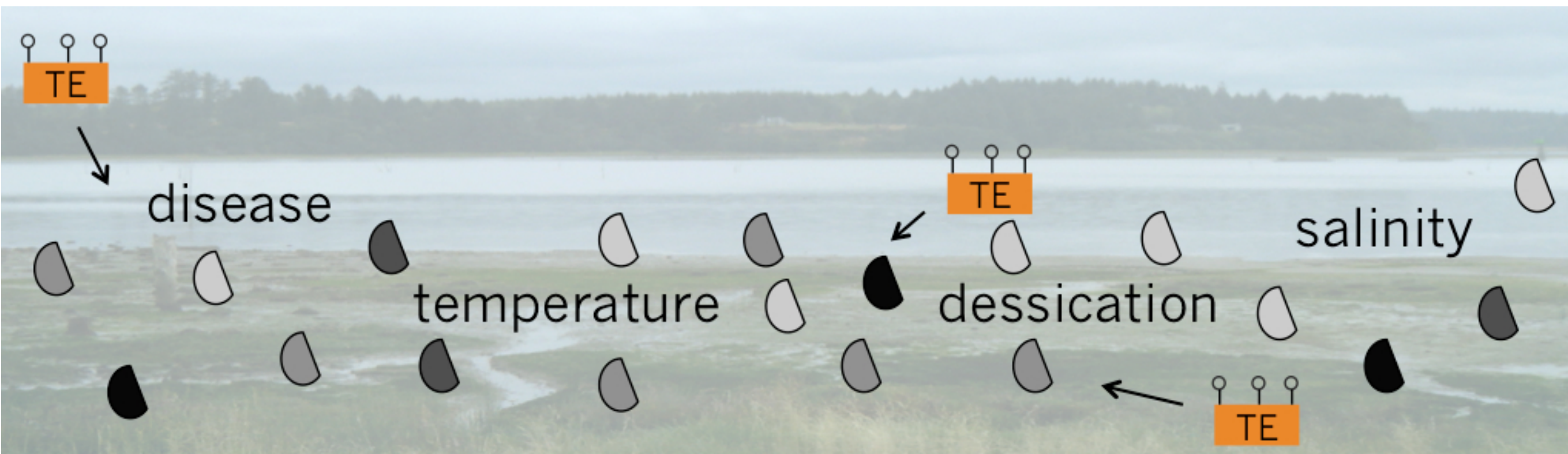
disease

temperature

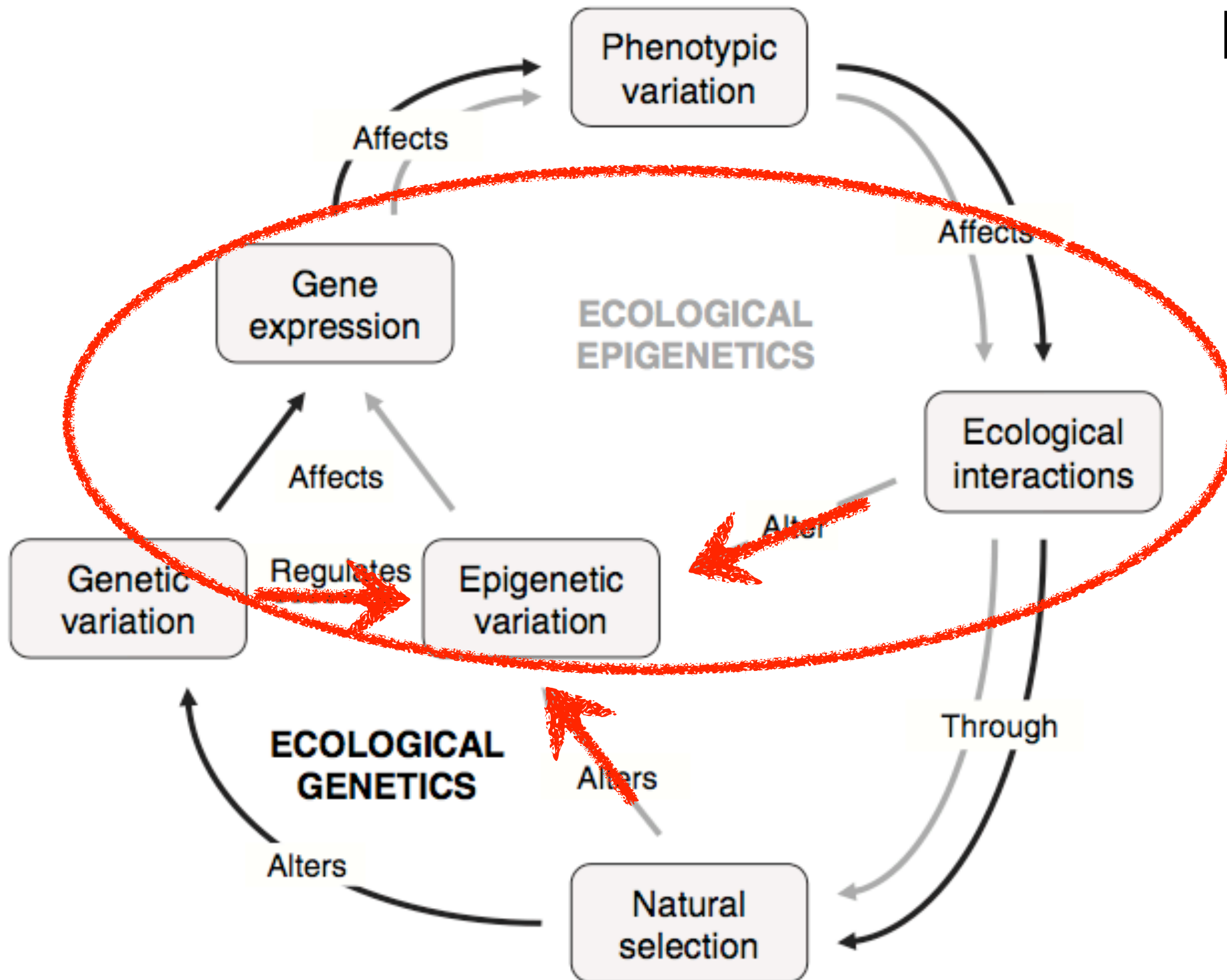
deseccation

salinity

Transposable Elements providing increased diversity?

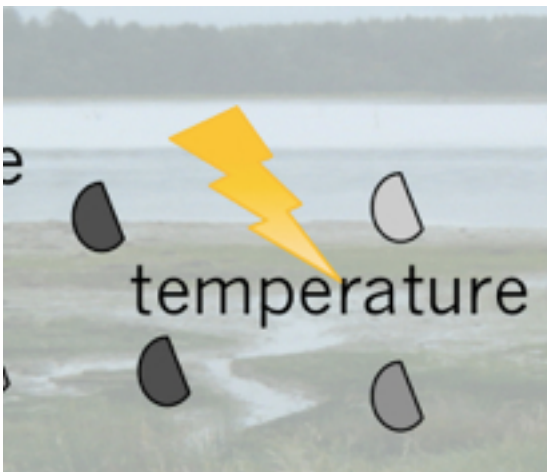


Beginning to
test these
Hypotheses

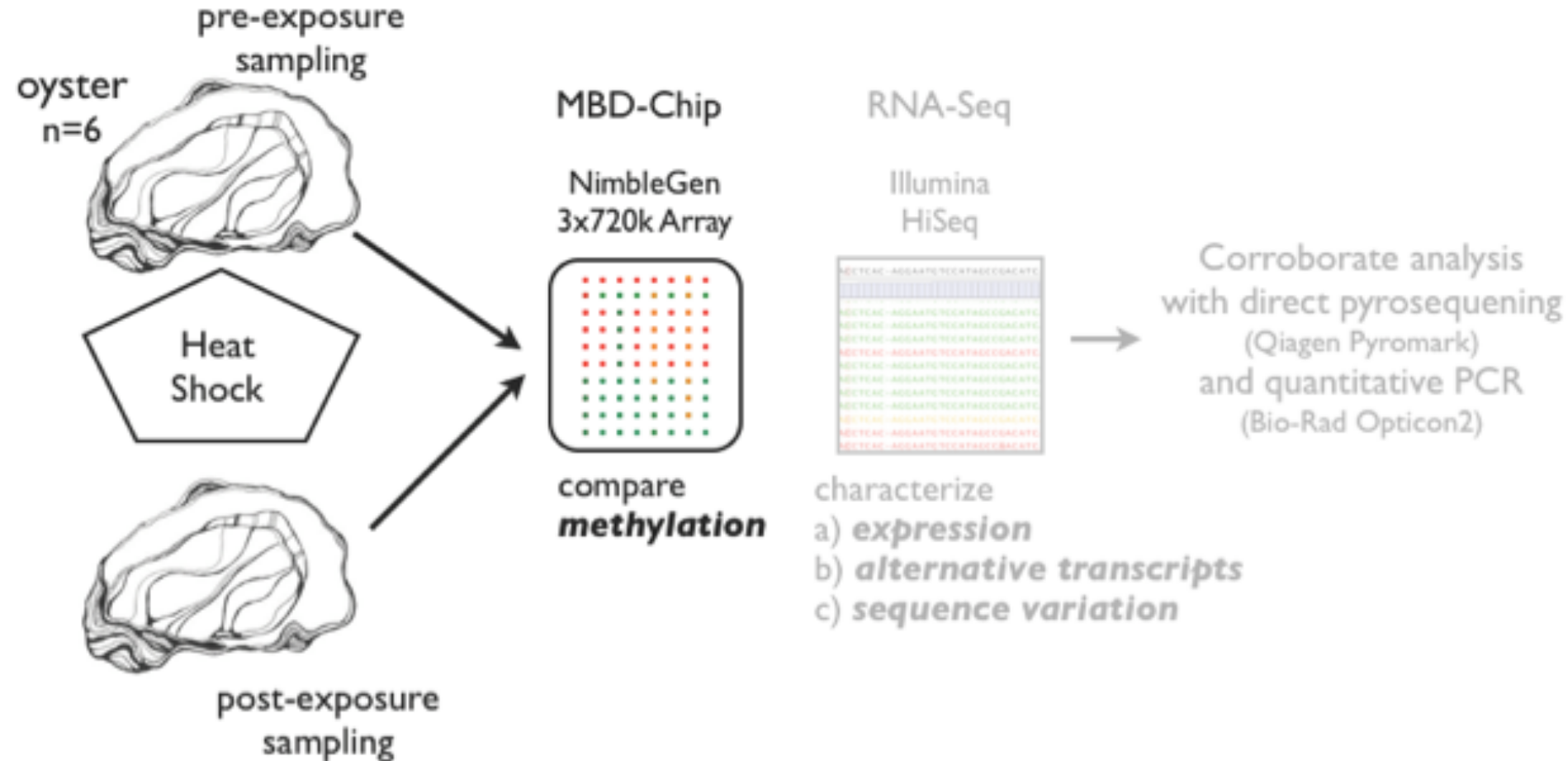


Very new data

Environment and gene expression

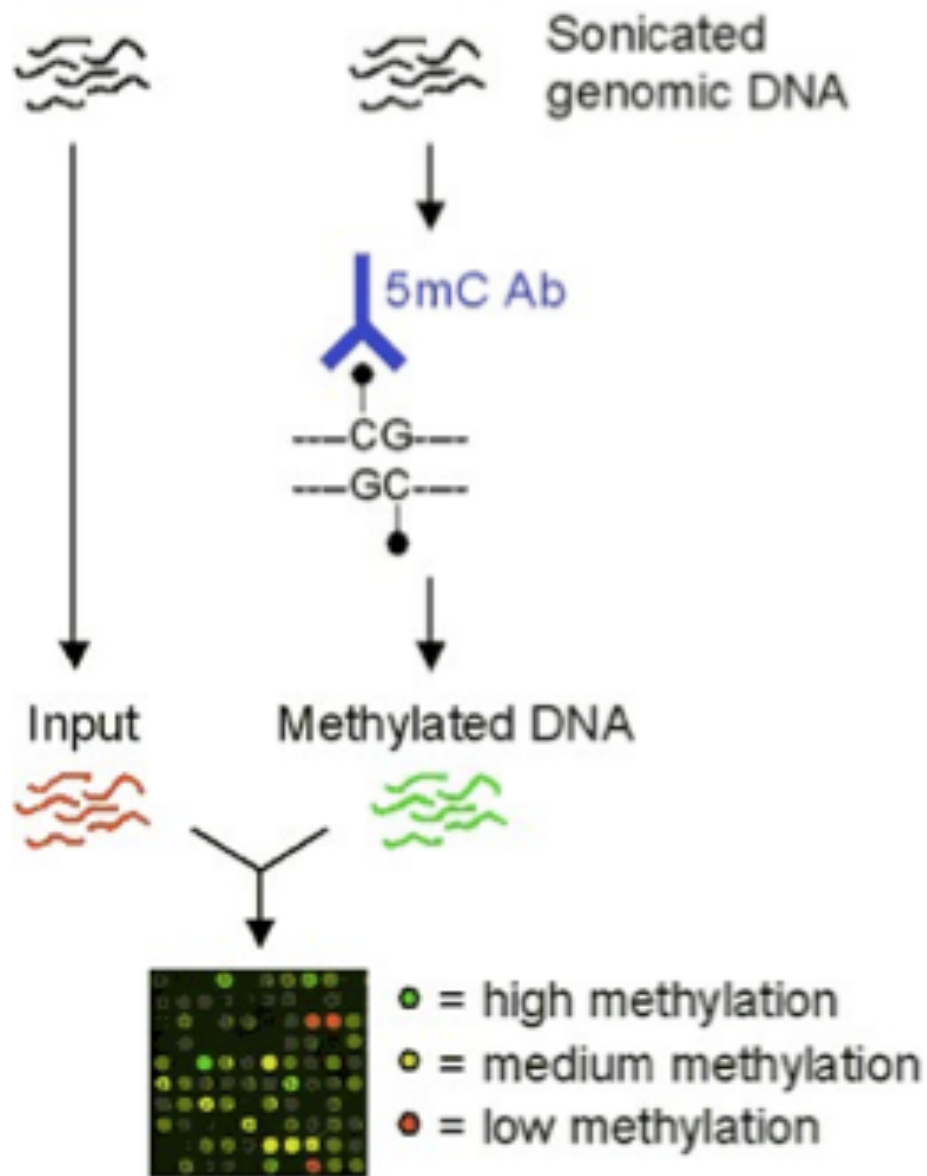


stochastic or targeted?



Very new data

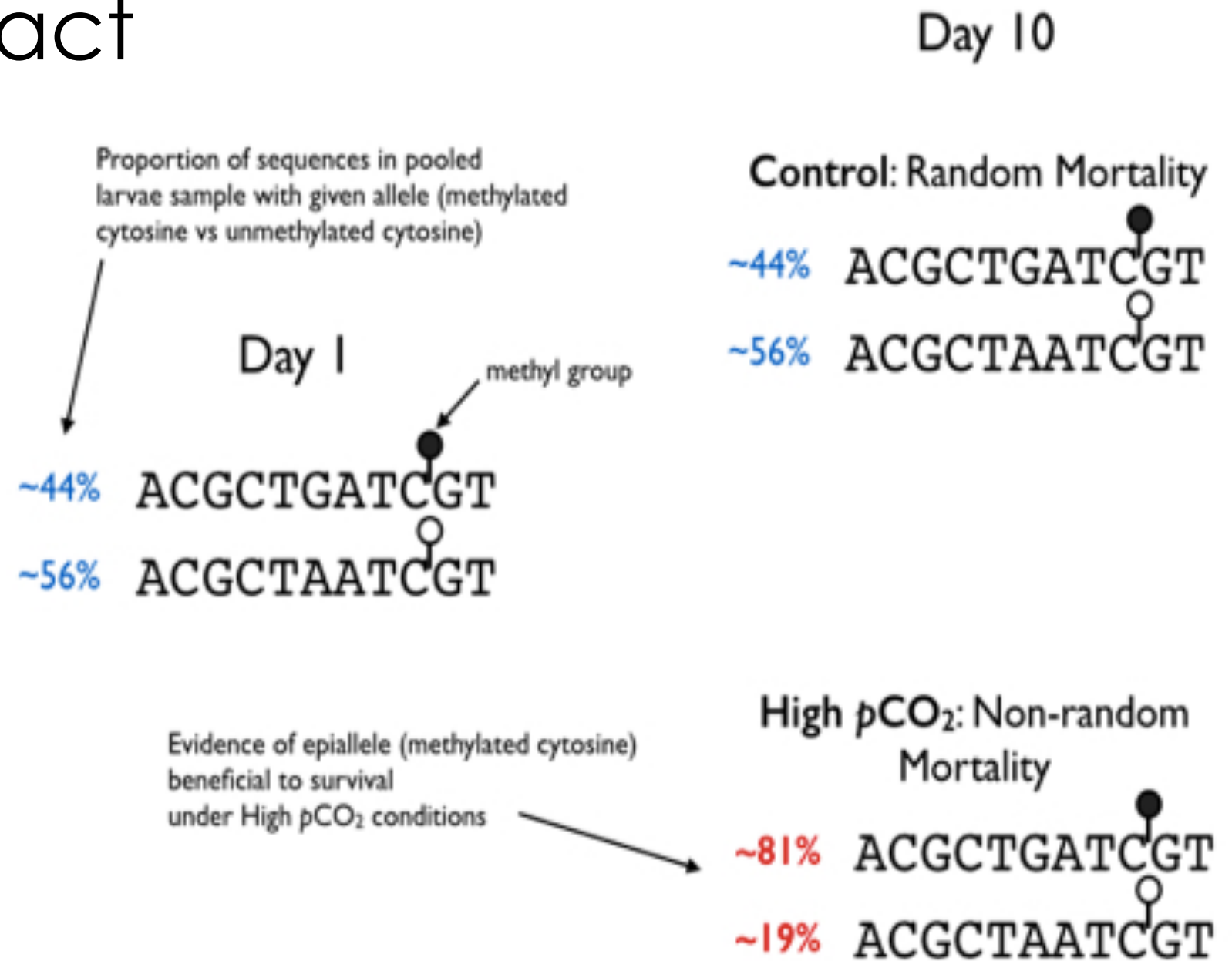
Environmental impact (Estrogens)



- 96 regions that were hypermethylated in EE2
 - 90 are in genes
 - 52 of these cross exon/intron boundary another
 - 32 are in introns
 - 6 are just in exons
- 287 regions that were hypomethylated in EE2
 - 256 are in genes
 - 138 cross exon/intron boundary
 - 114 are in introns only and
 - 4 are just in exons

Very new ~~data~~

Ocean Acidification Selection Environmental Impact



Katie Lotterhos

~~Very new data~~
Heritability
Plasticity
Local Adaptation

*Genetics
versus
Epigenetics*

Common Garden Experiment



Figure 3. Map indicating three sites where Olympia oysters will be characterized for both phenotypic and molecular traits following a reciprocal transplant experiment. Mean annual temperature - °C (T) and mean salinity - PSU (S)

Acknowledgements

Mackenzie Gavery
Claire Ellis

DNA methylation



EPA
STAR



Sam White



Bill Howe
Dan Halperin



slides, data & more @ robertslab.info

