

Does DNA methylation facilitate phenotypic plasticity in marine invertebrates?

Steven Roberts
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@sr320

Ecology of Infectious Marine Diseases [course]

ABOUT NOTEBOOKS COURSE DISCUSSION SYLLABUS SCHEDULE GENOMICS LINKS

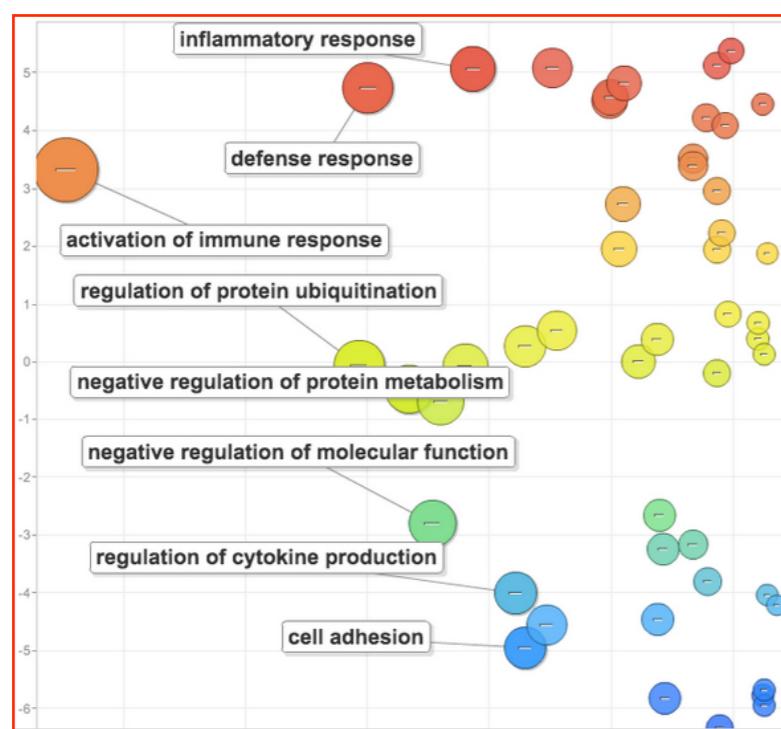


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Does DNA methylation facilitate phenotypic plasticity in marine invertebrates?

Mackenzie Gavery
Claire Olson

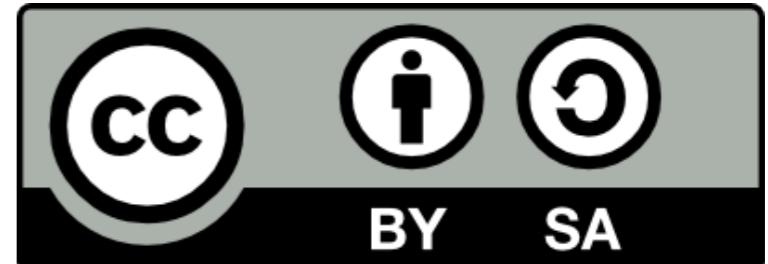


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Open Science

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



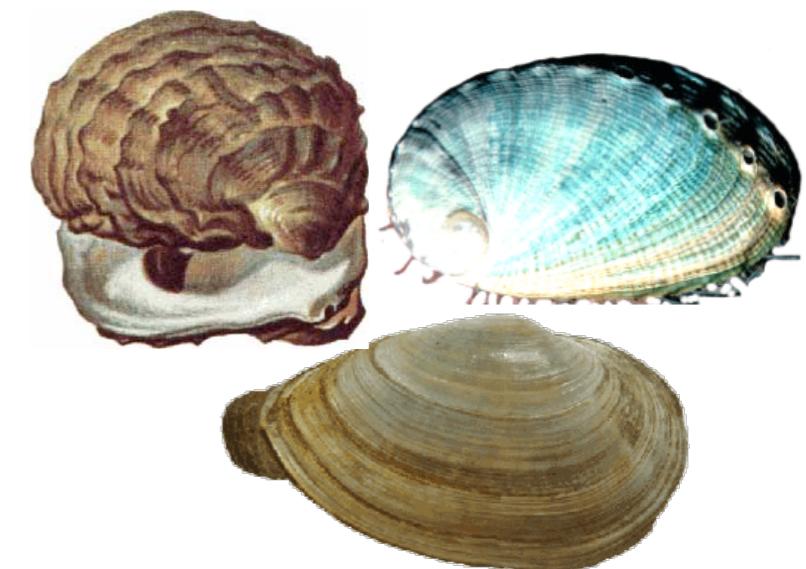
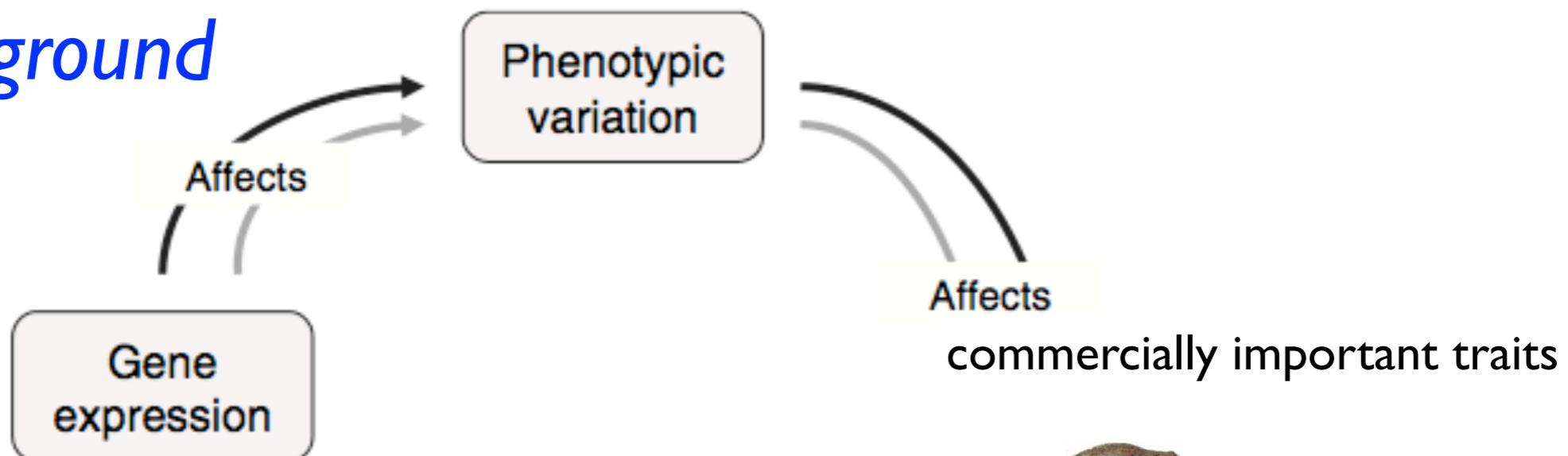
IP[y]: IPython
Interactive Computing



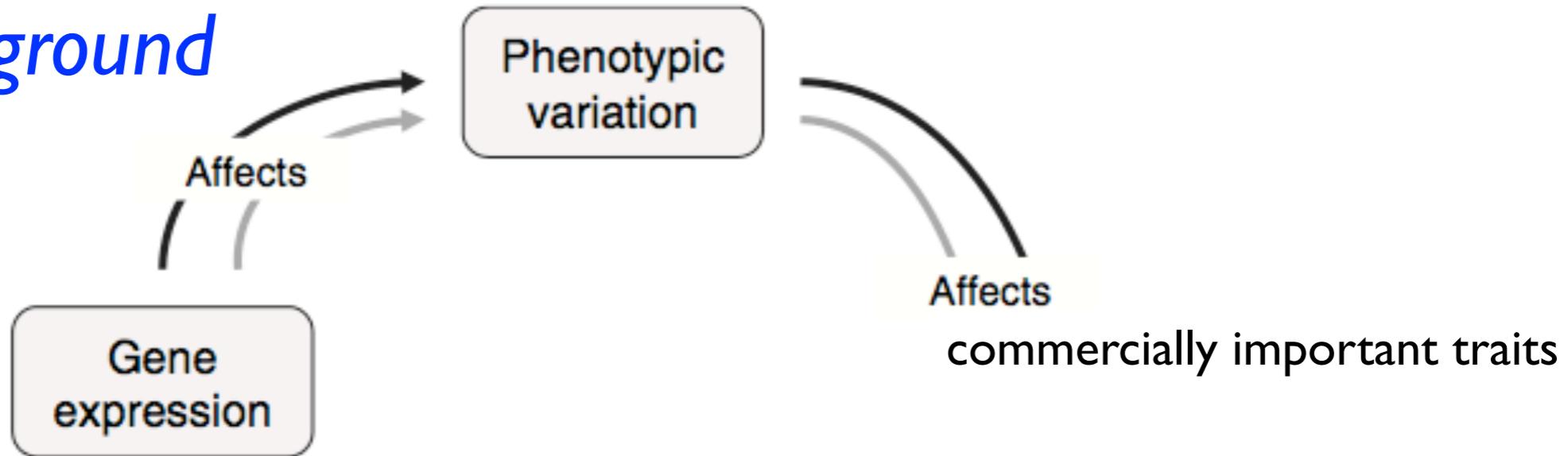
- Data, Preprints, Proposals, Slidedecks available
FigShare, GitHub, and lab website (robertslab.info)

These slides plus links @ robertslab.info

Lab Background



Lab Background



modified from

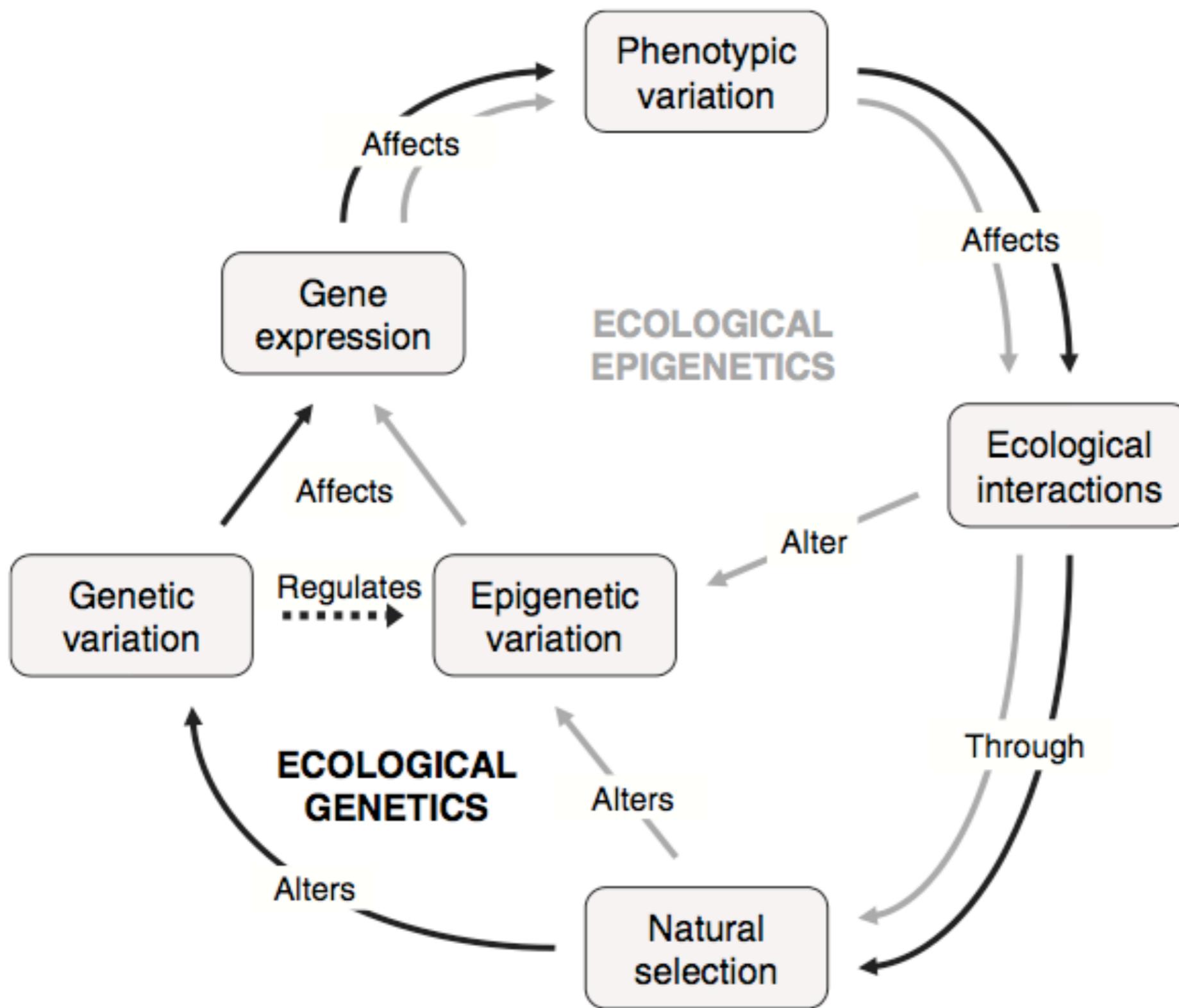
IDEA AND
PERSPECTIVE

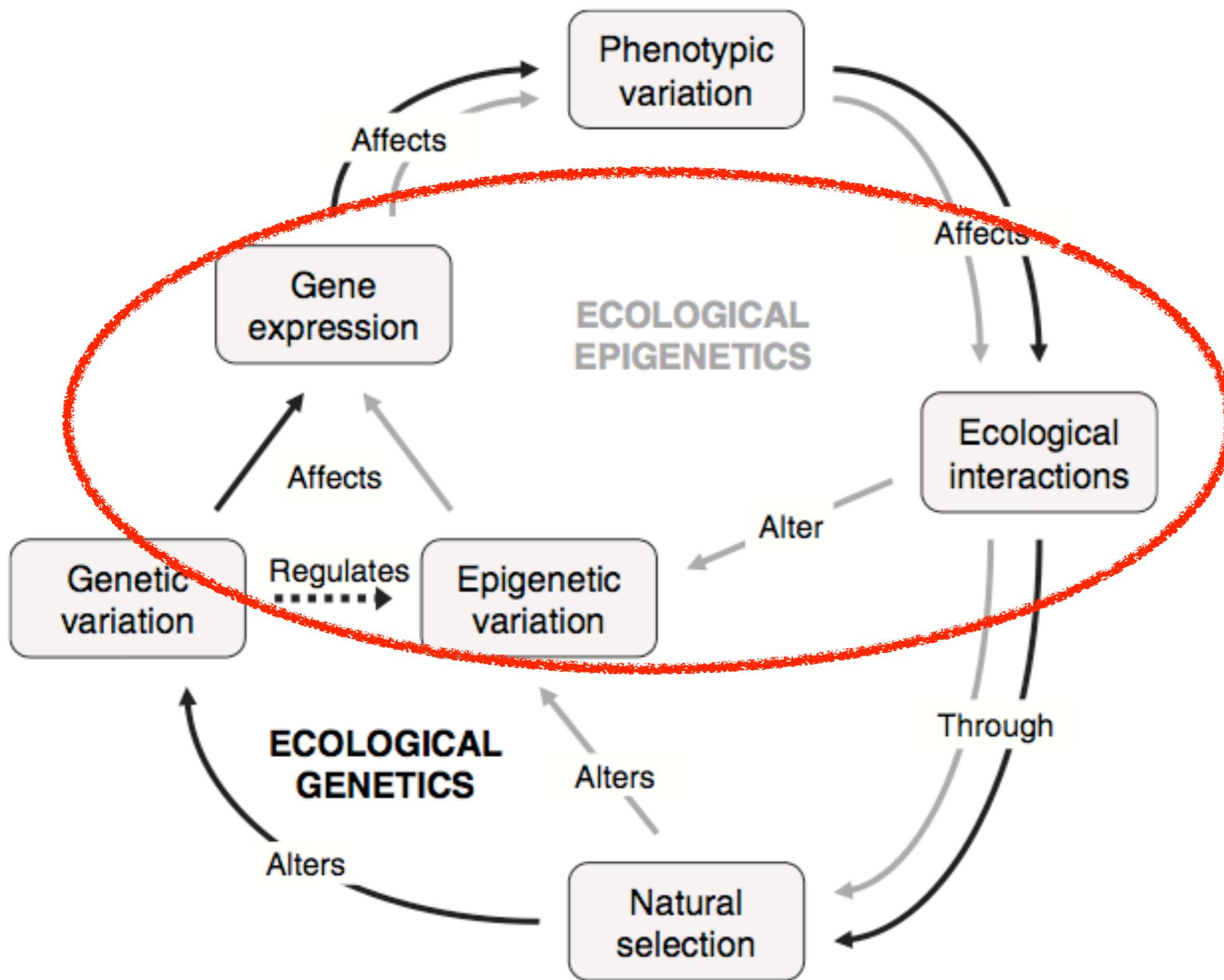
Epigenetics for ecologists

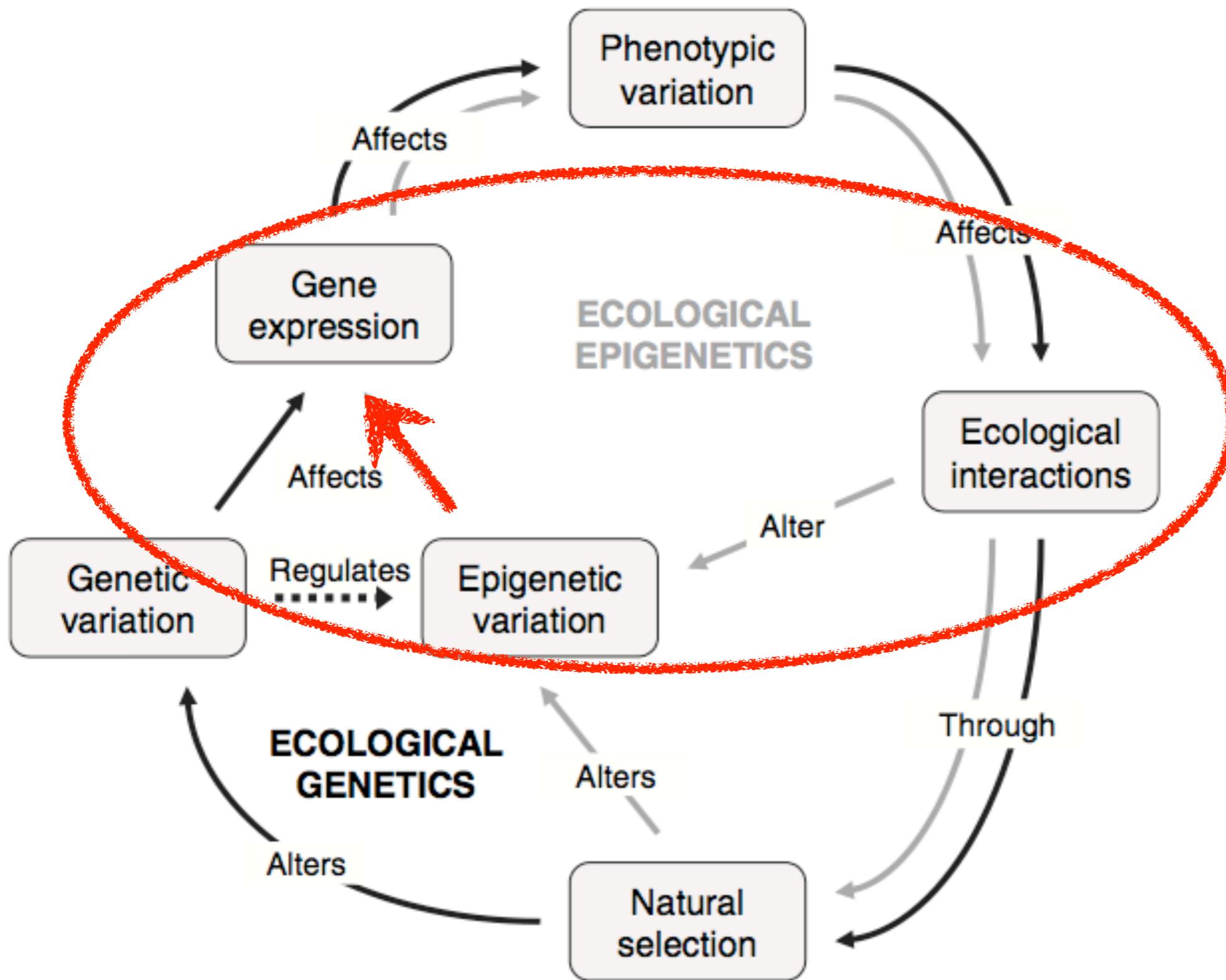
Ecology Letters, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

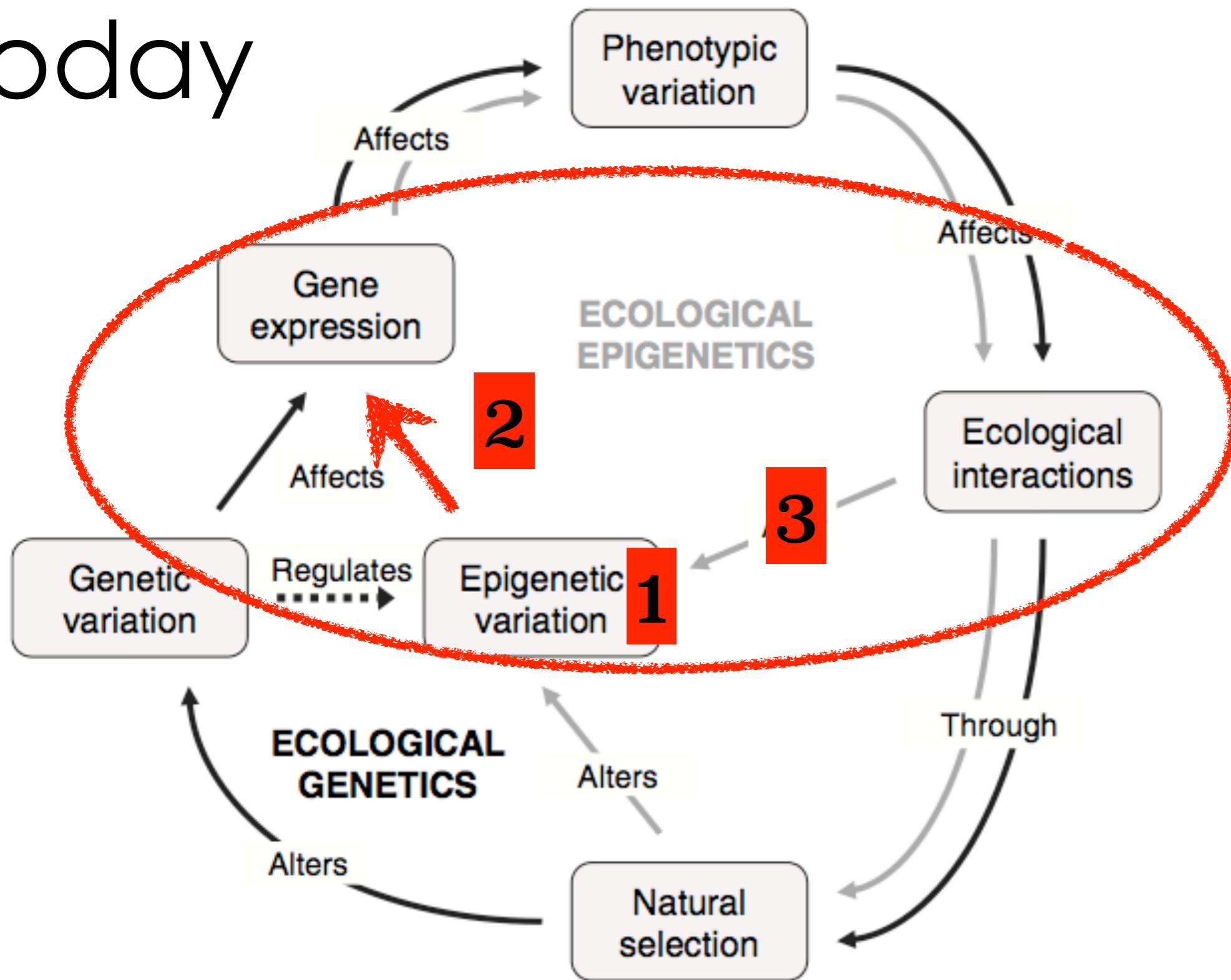
Oliver Bossdorf,^{1,*} Christina L.
Richards² and Massimo Pigliucci³







Today



Ecology Letters, (2008) 11: 106–115

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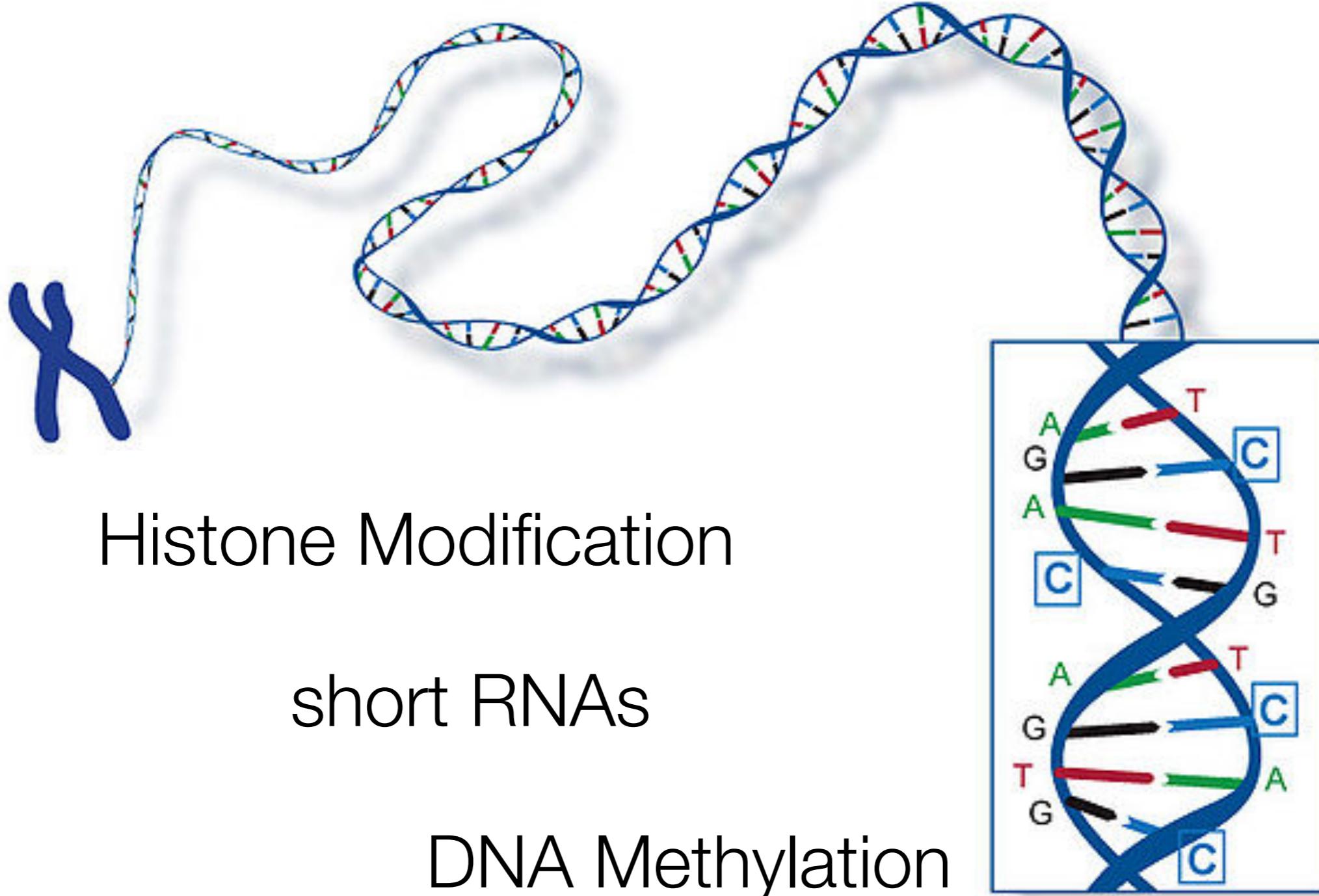
IDEA AND
PERSPECTIVE

Epigenetics for ecologists

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



Epigenetics



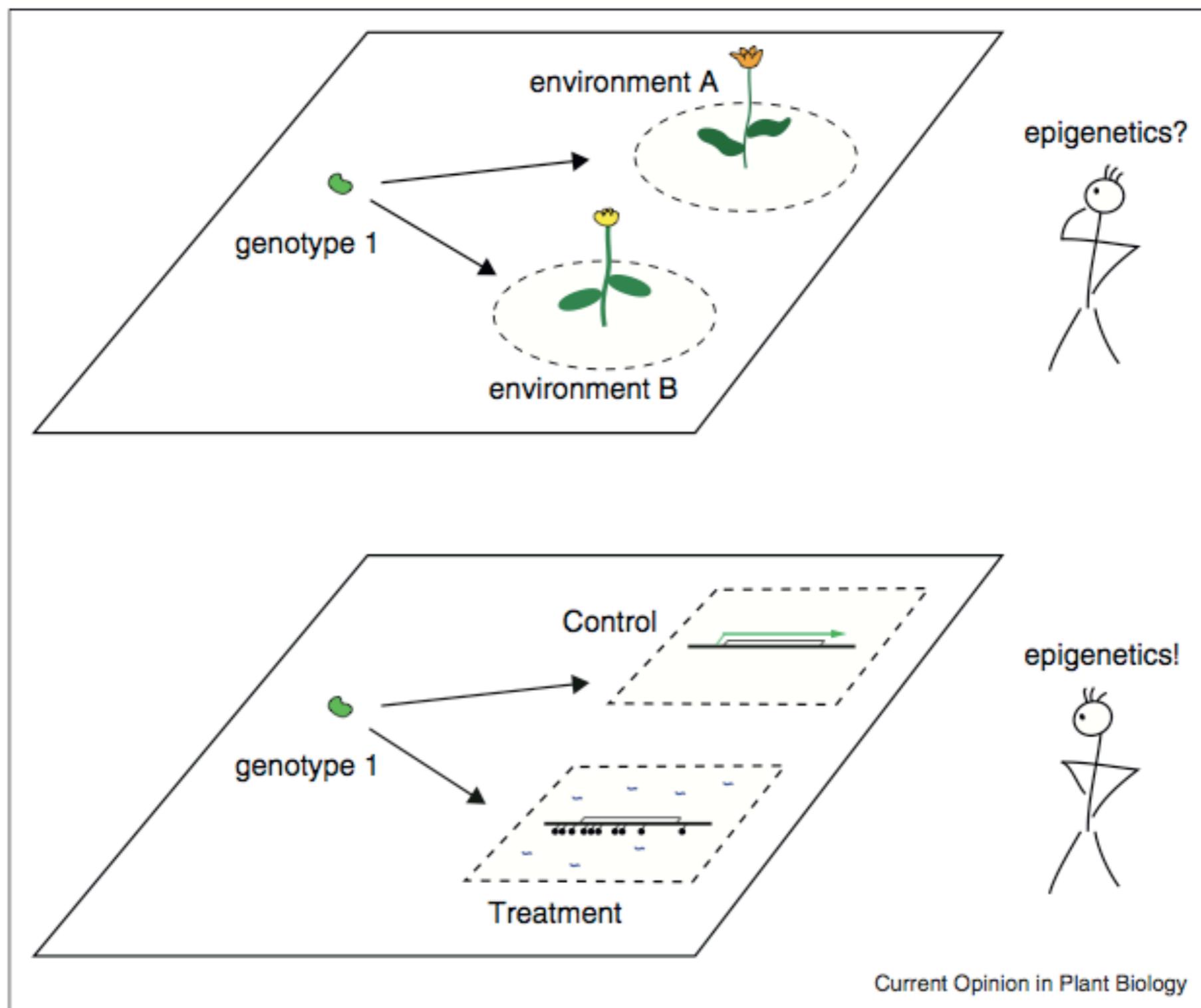
Epigenetics



Photo credit: Flickr, Creative Commons, he-boden

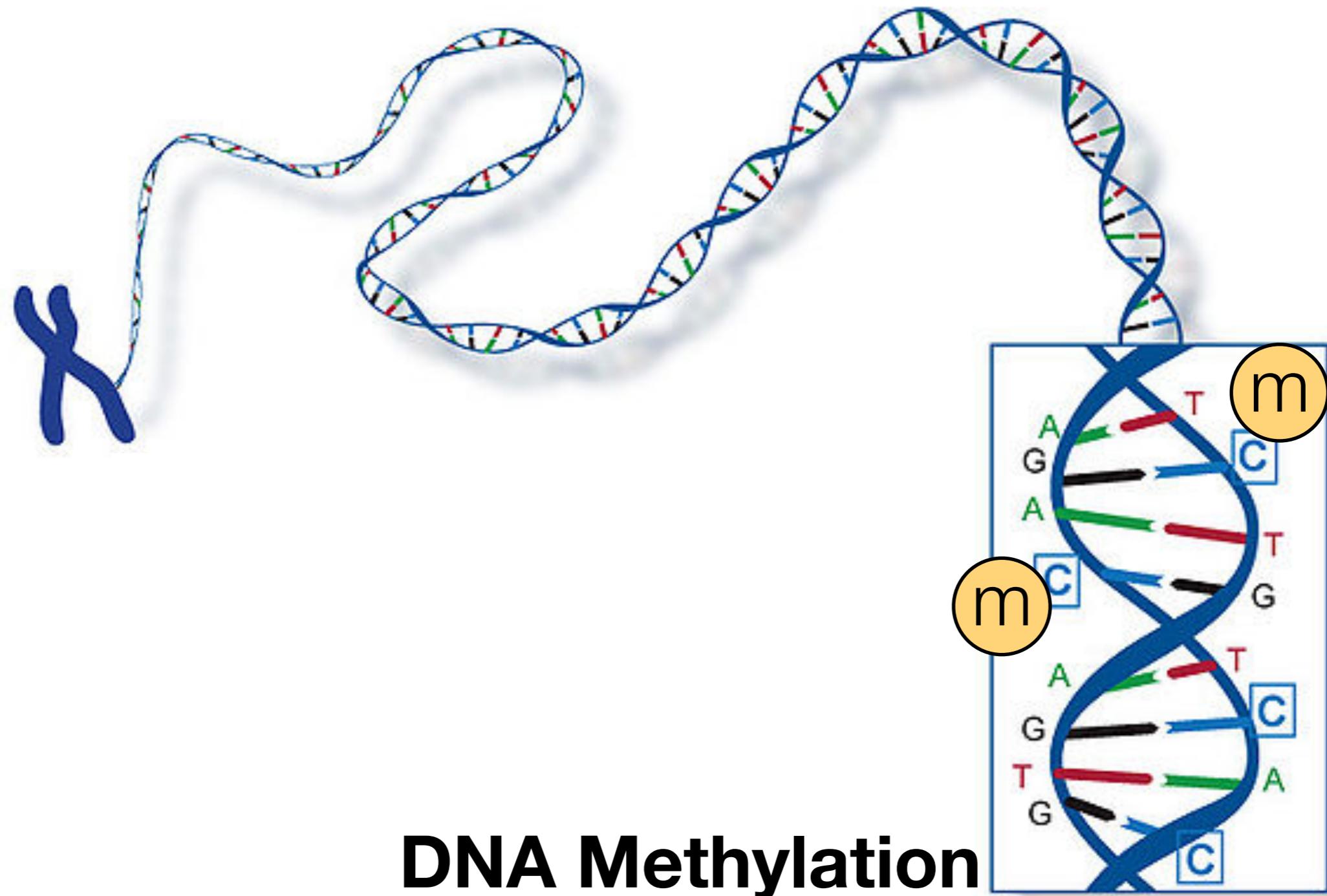


Epigenetics



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

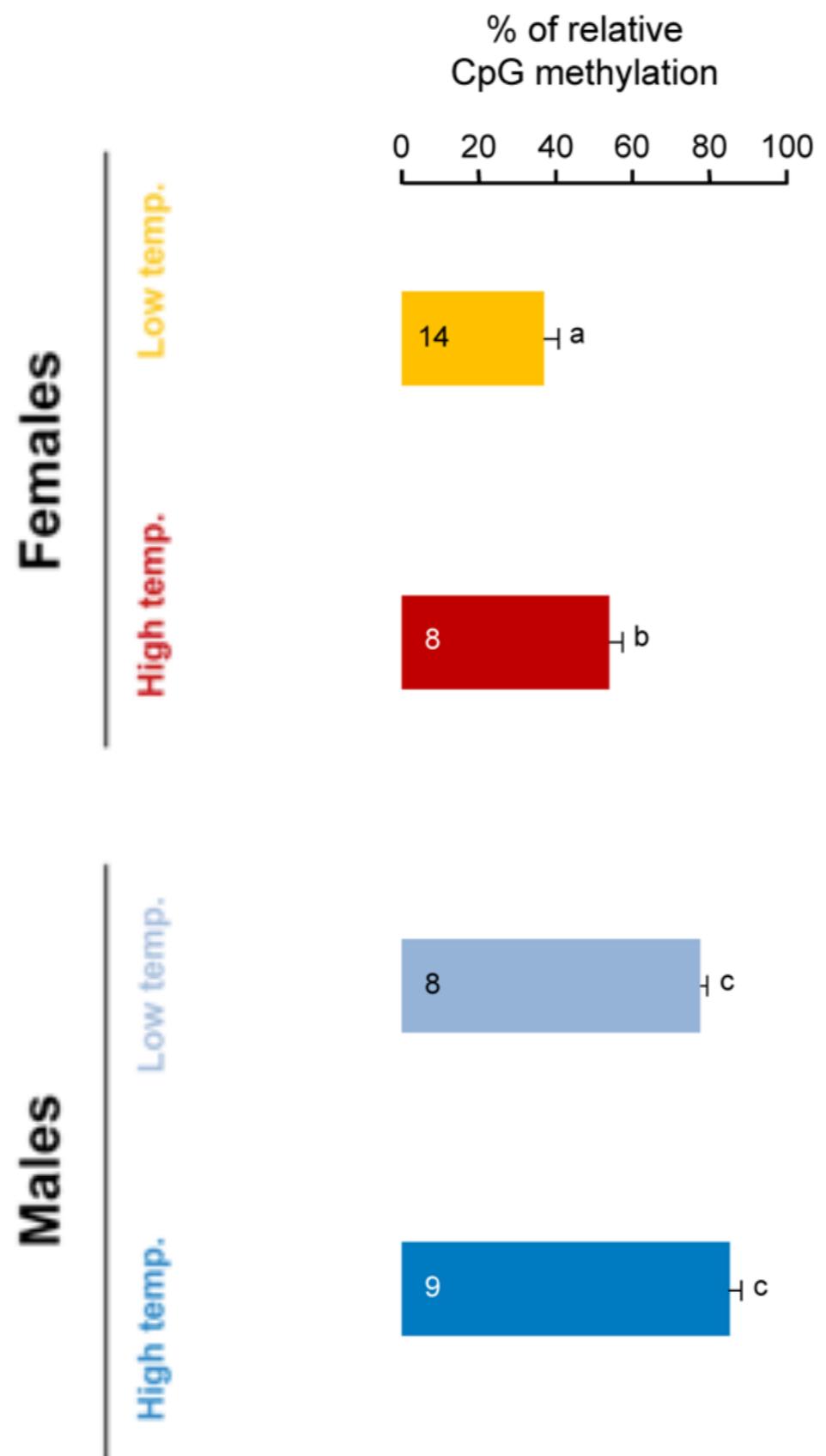
Eric J Richards



Function?

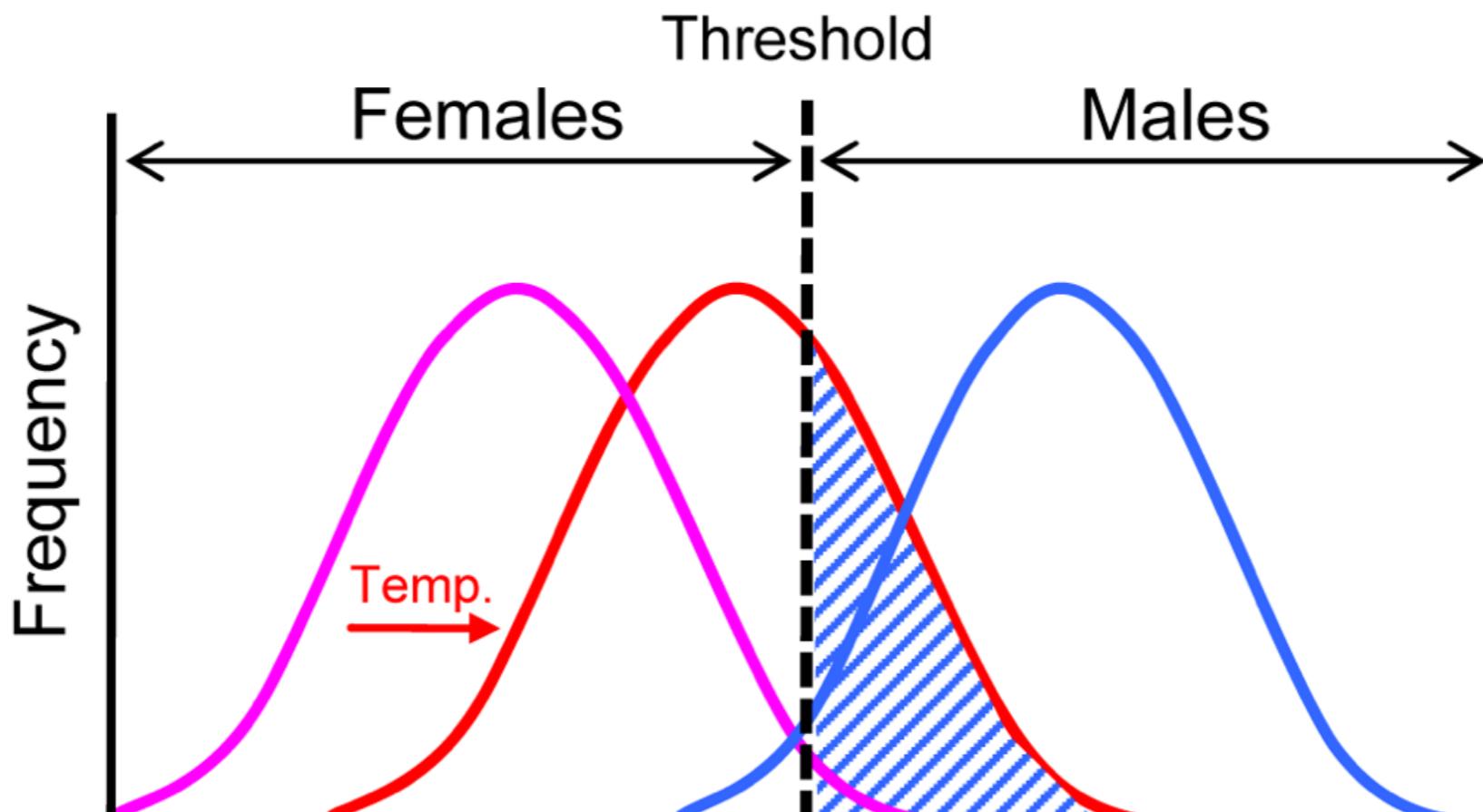
DNA Methylation of the Gonadal Aromatase (*cyp19a*) Promoter Is Involved in Temperature-Dependent Sex Ratio Shifts in the European Sea Bass

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



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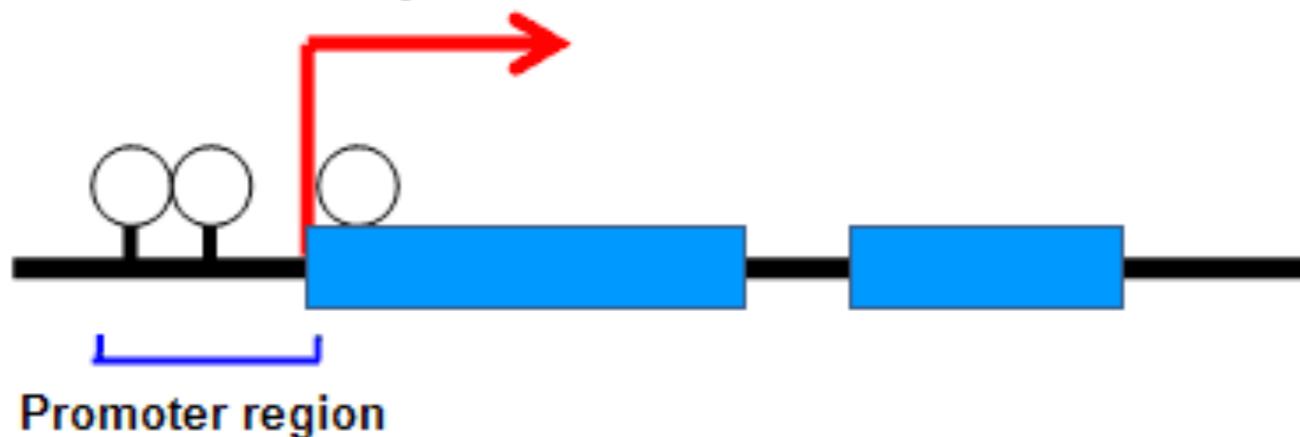
cyp19a promoter methylation level

- Low temperature females
- High temperature females
- Males

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

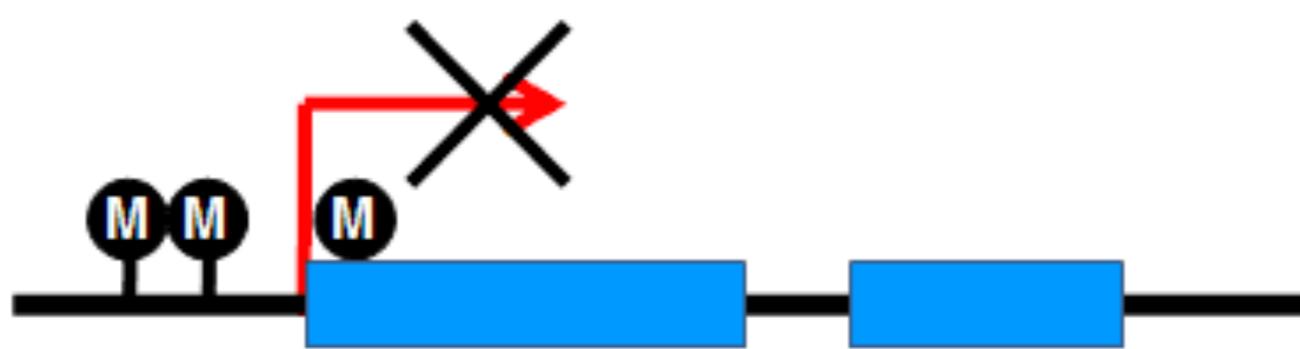
Low temp.

Genes that can be expressed



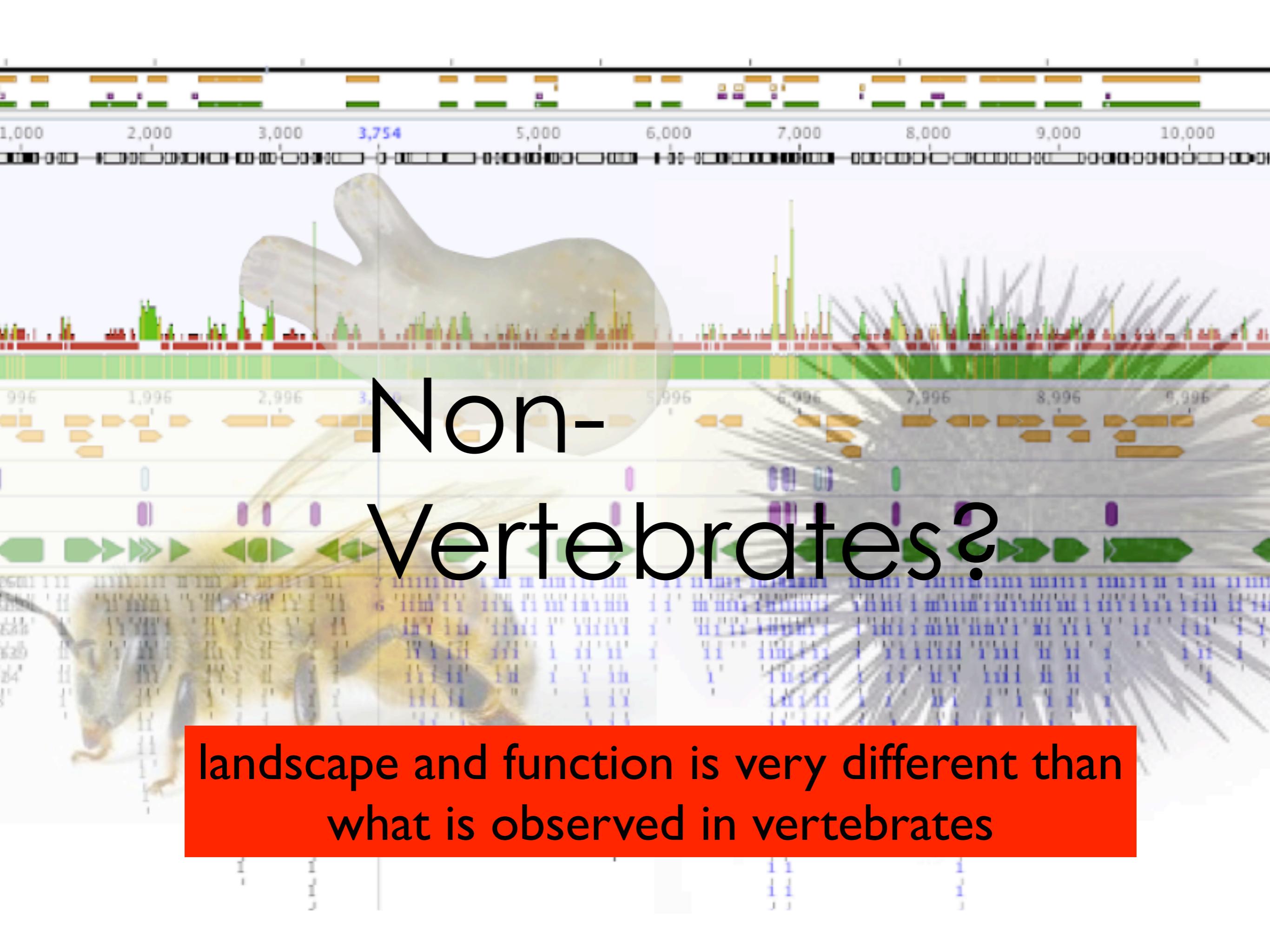
High temp.

Genes inactivated by DNA methylation



Methylated

Unmethylated

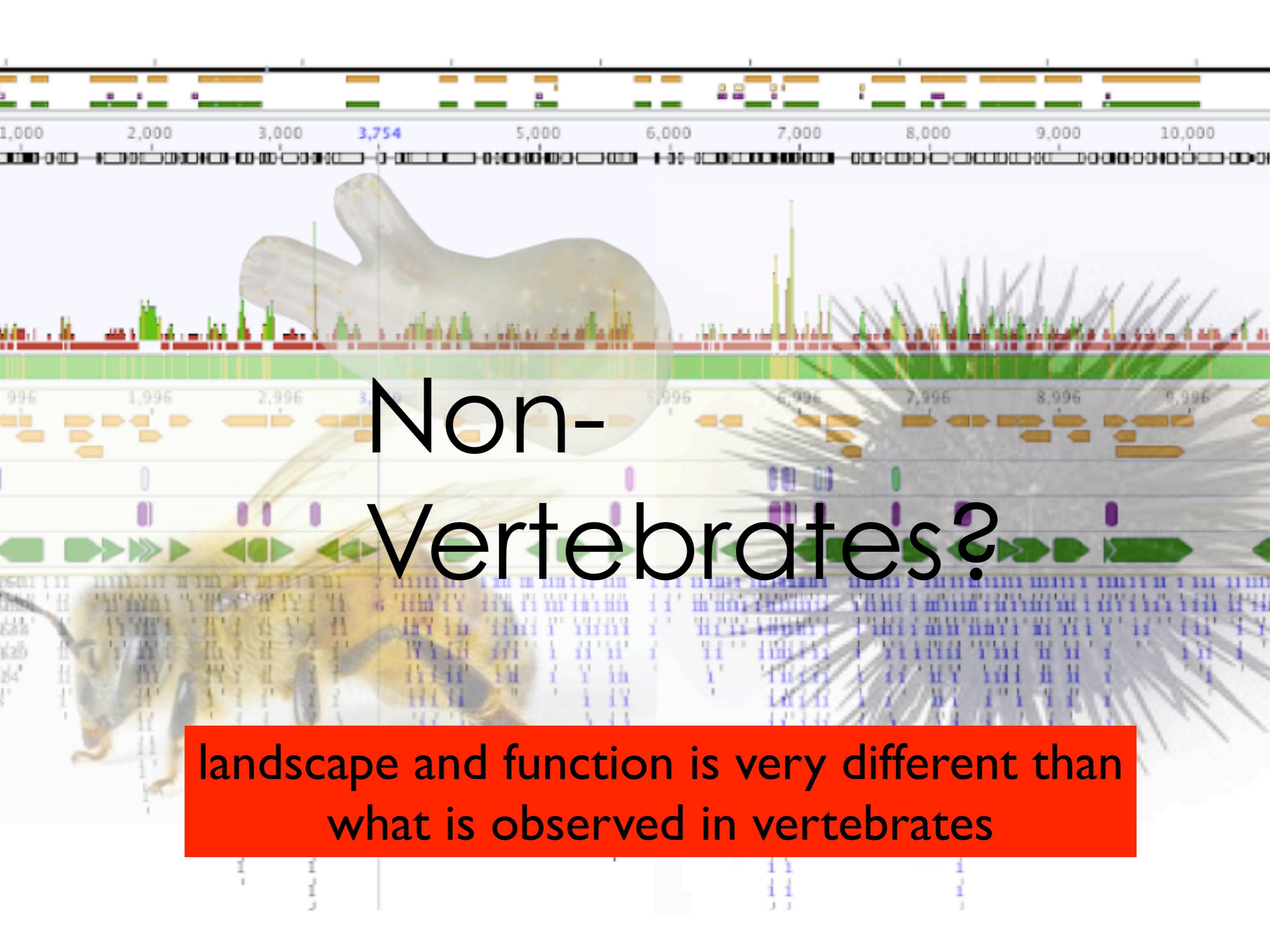


Non- Vertebrates?

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

Non-Vertebrates?

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Non- Vertebrates?

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

*Absent in
several
model
organisms*



Oysters?

Epigenetic variation **1**

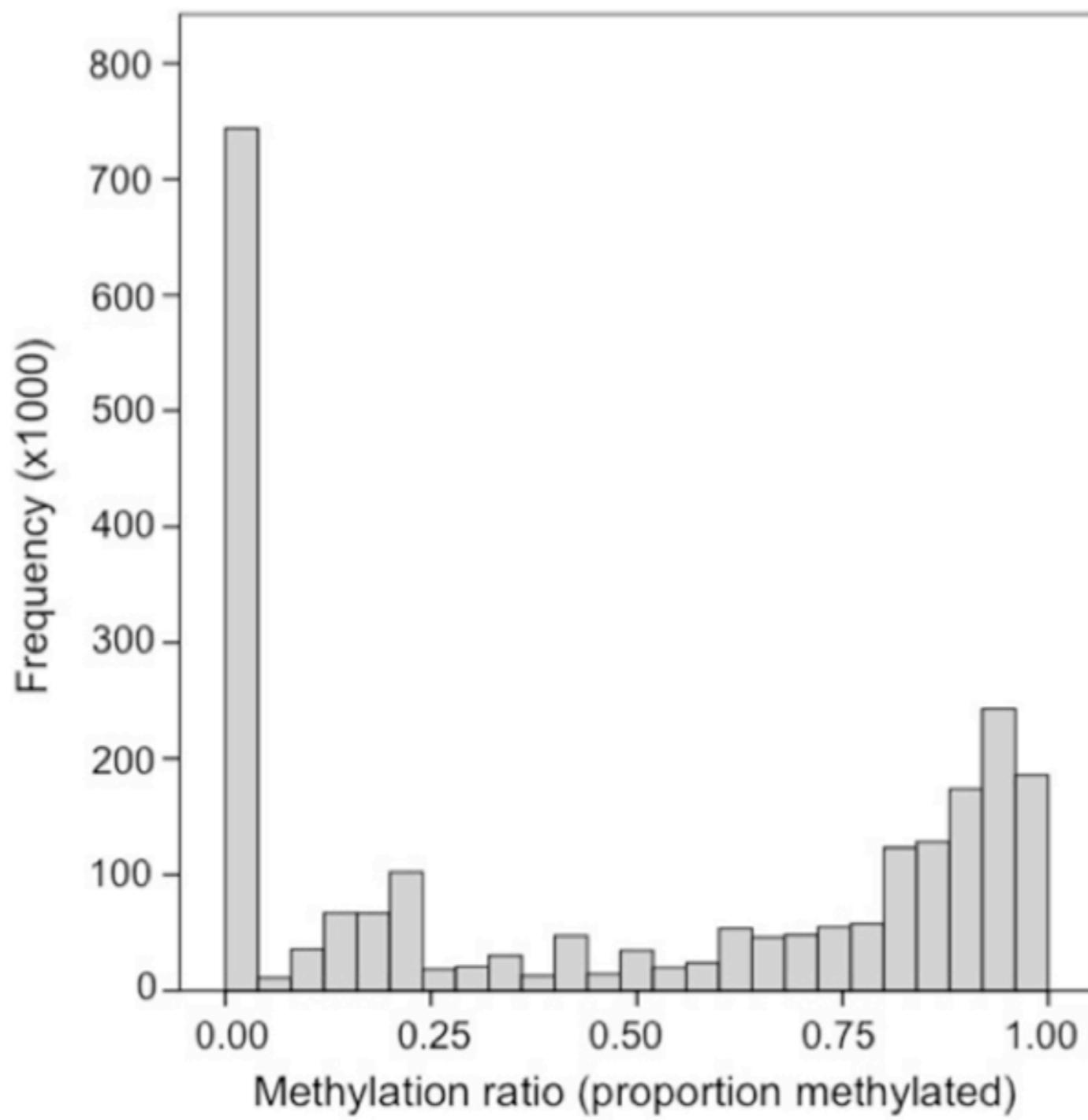
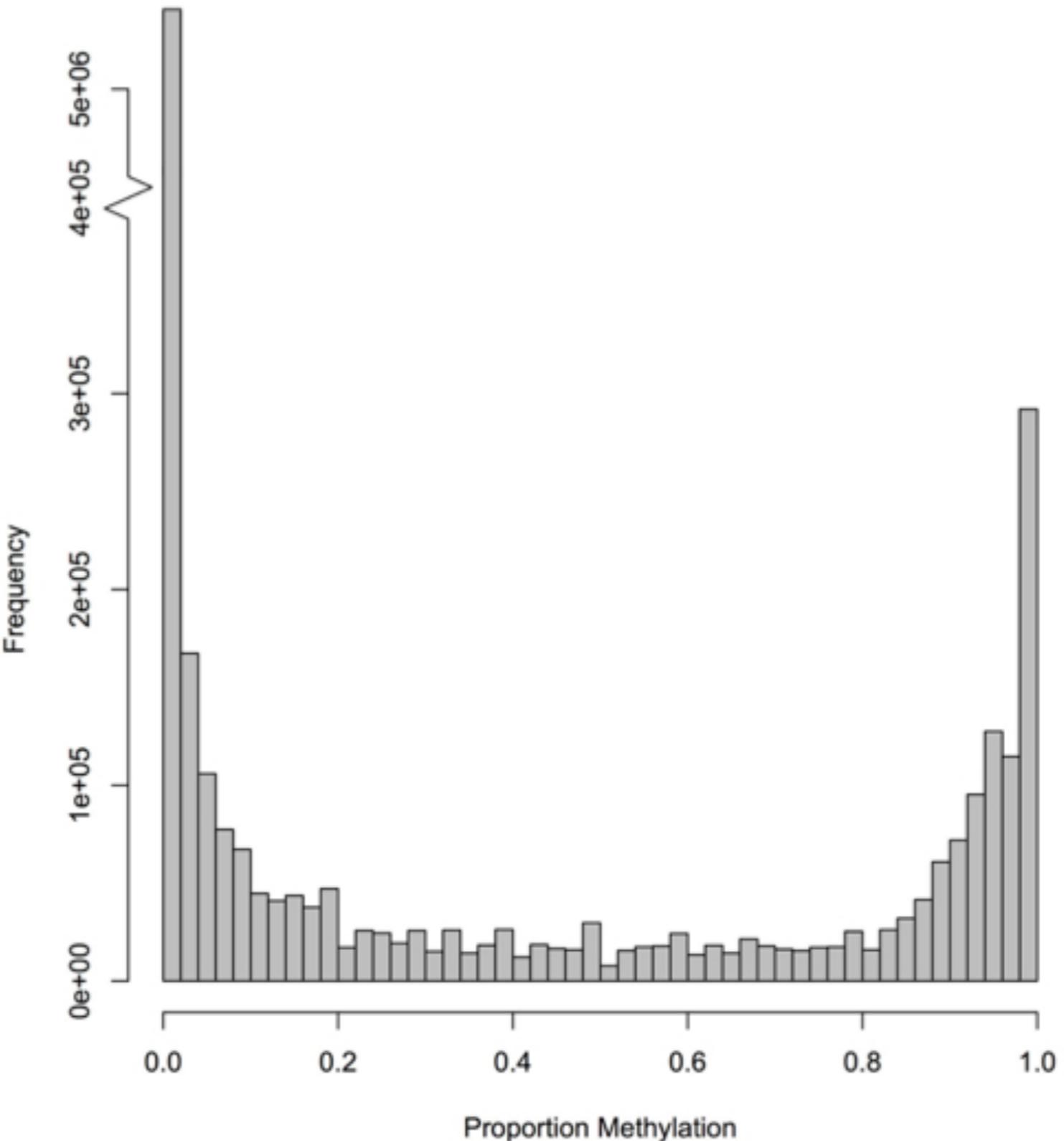
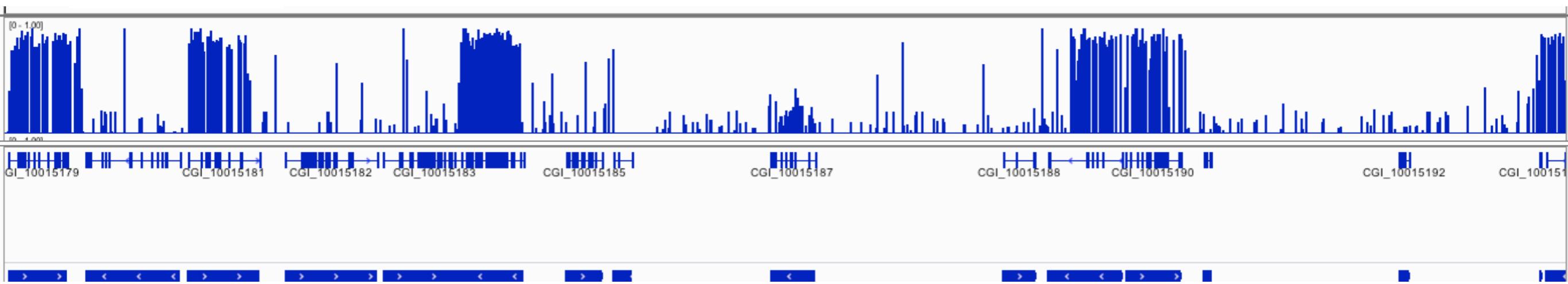


Figure 1 Frequency distribution of methylation ratios for CpG dinucleotides in oyster gill tissue. A total of 2,625,745 CpG dinucleotides with $\geq 5 \times$ coverage are represented.

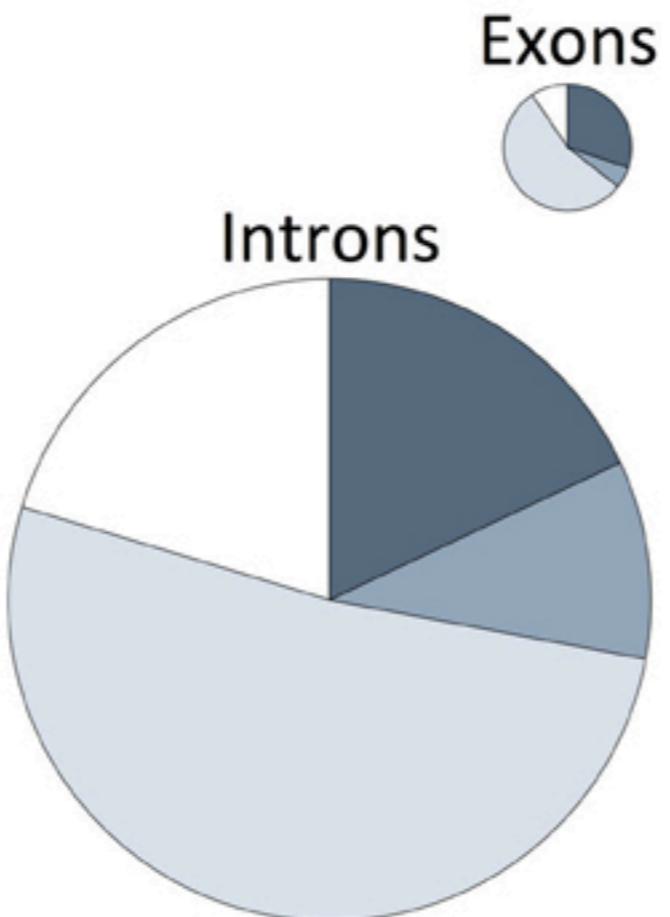


Epigenetic variation **1**



mosaic

associated with gene bodies



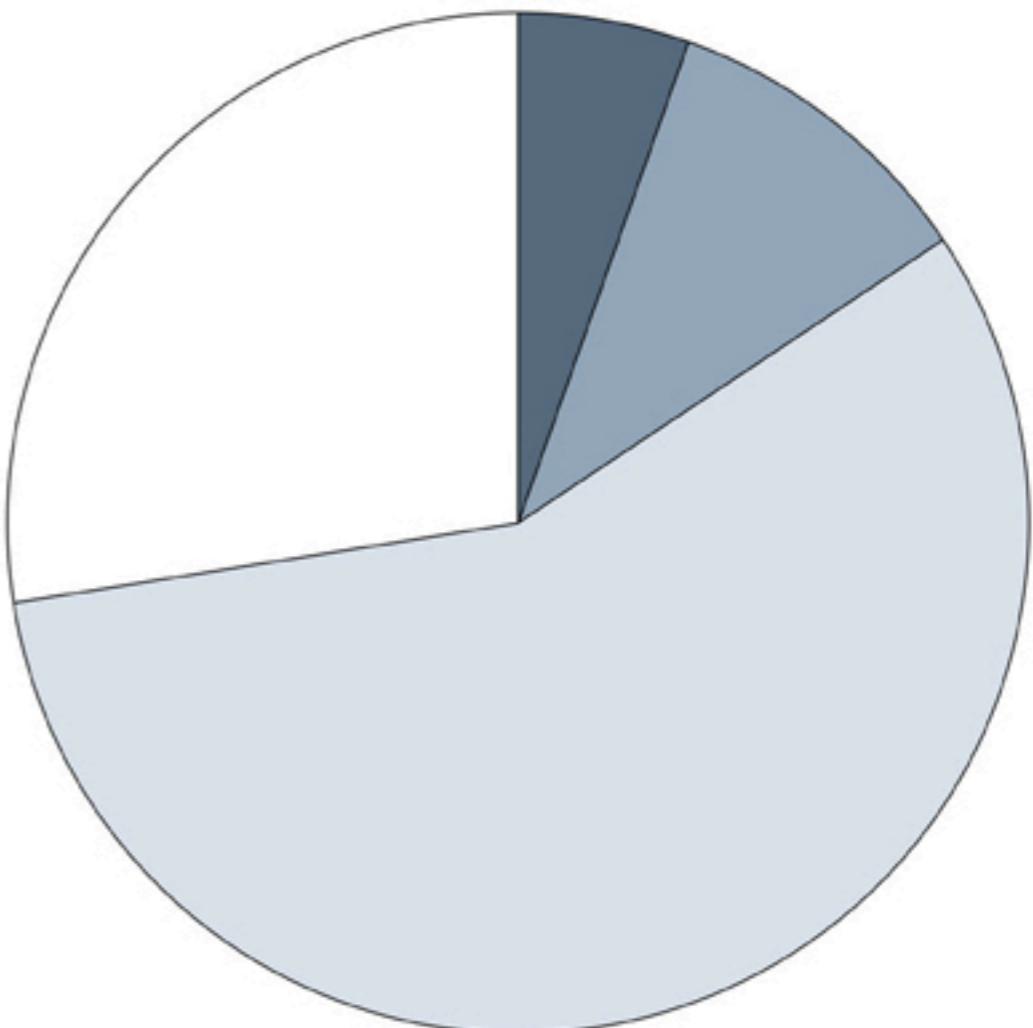
Transposable Elements



Promoter Regions



Other



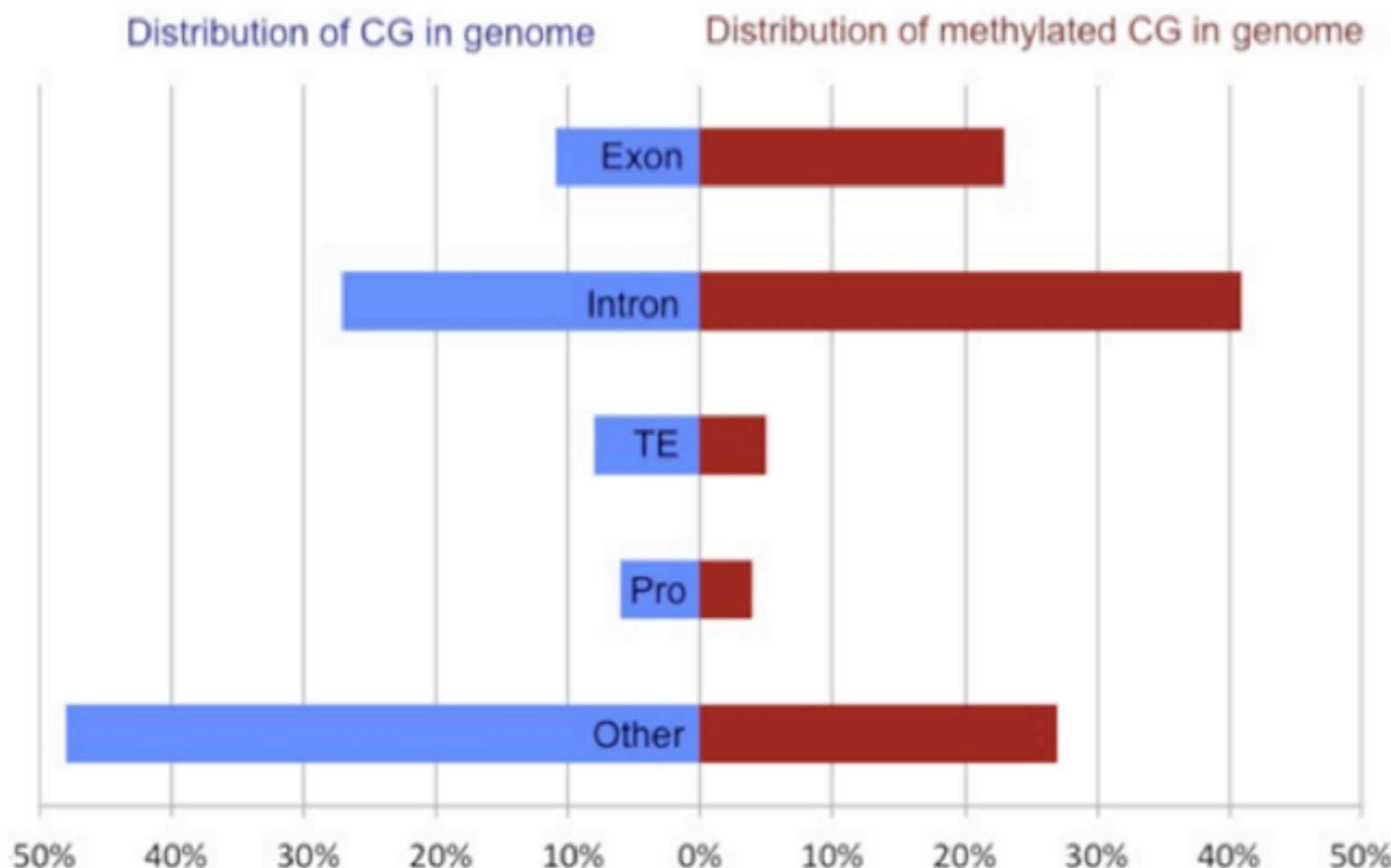
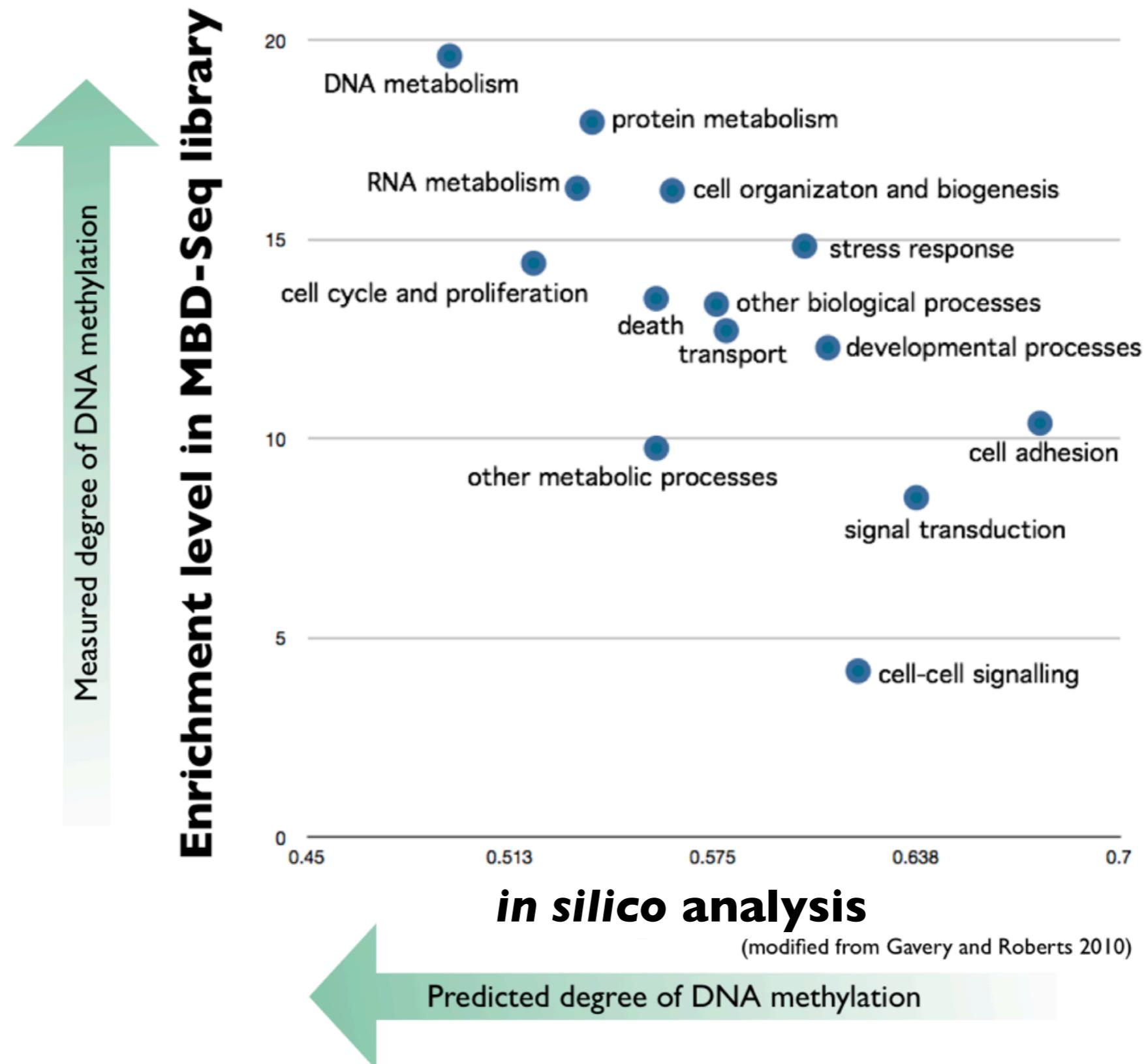
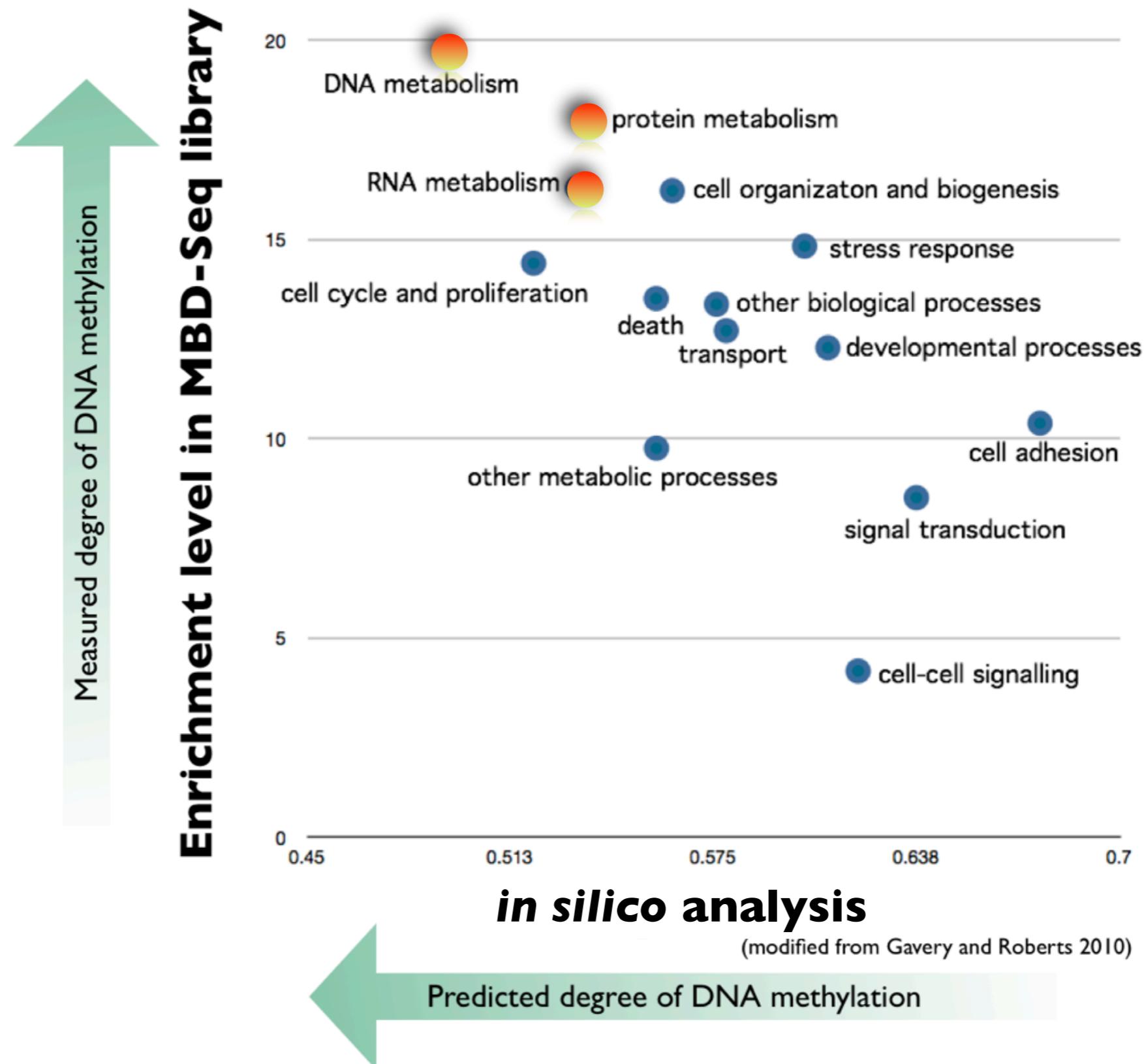


Figure 2 Comparison of the total CpG versus methylated CpG in oyster gill tissue by genomic feature. Proportion of all CpG (blue) and methylated CpG (red) in gill tissue across genomic features of *C. gigas*. Percent of CpG dinucleotides in Exons, Introns, Transposable Elements (TE), promoters (Pro)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

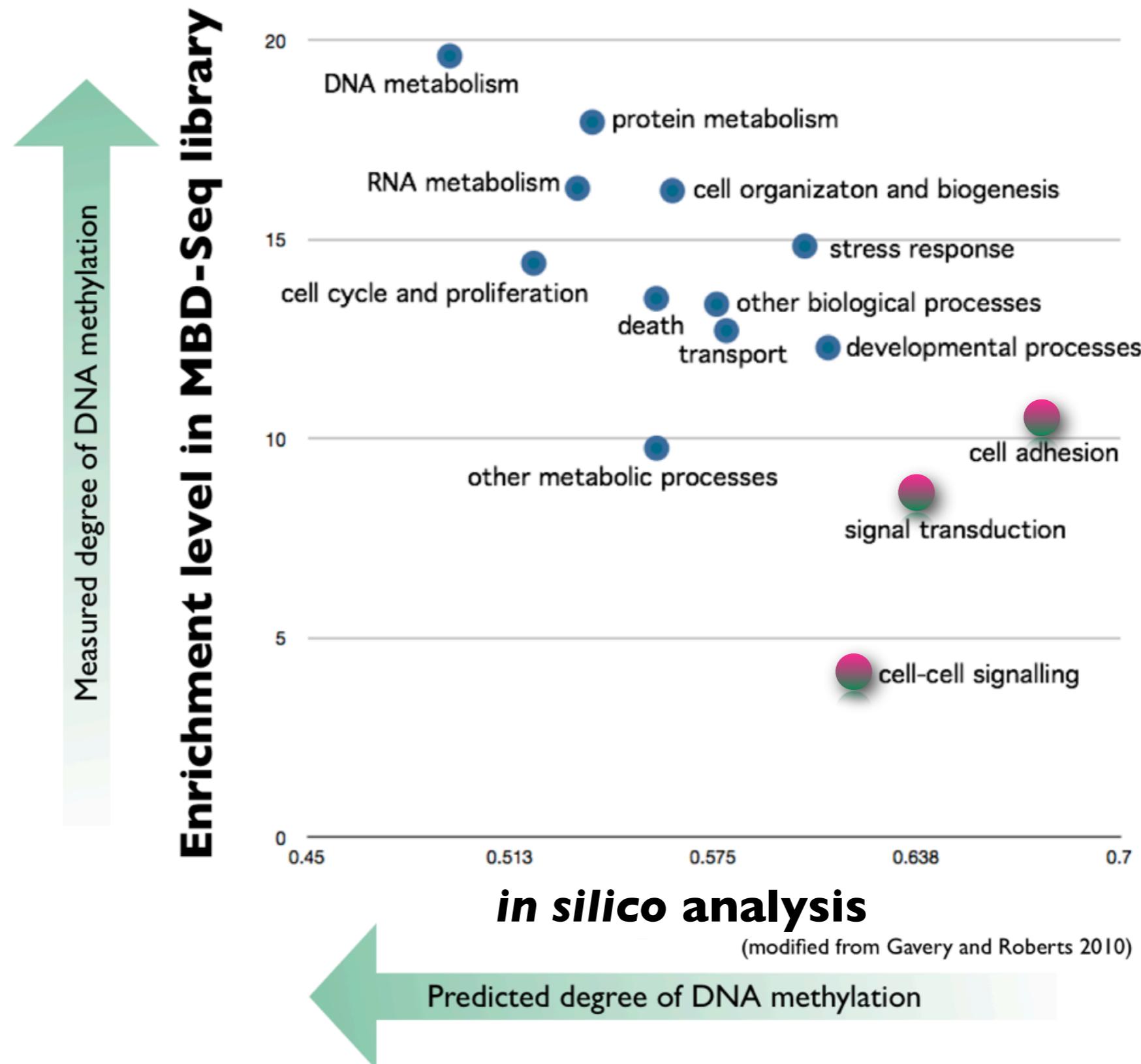
Epigenetic variation **1**



Epigenetic variation **1**

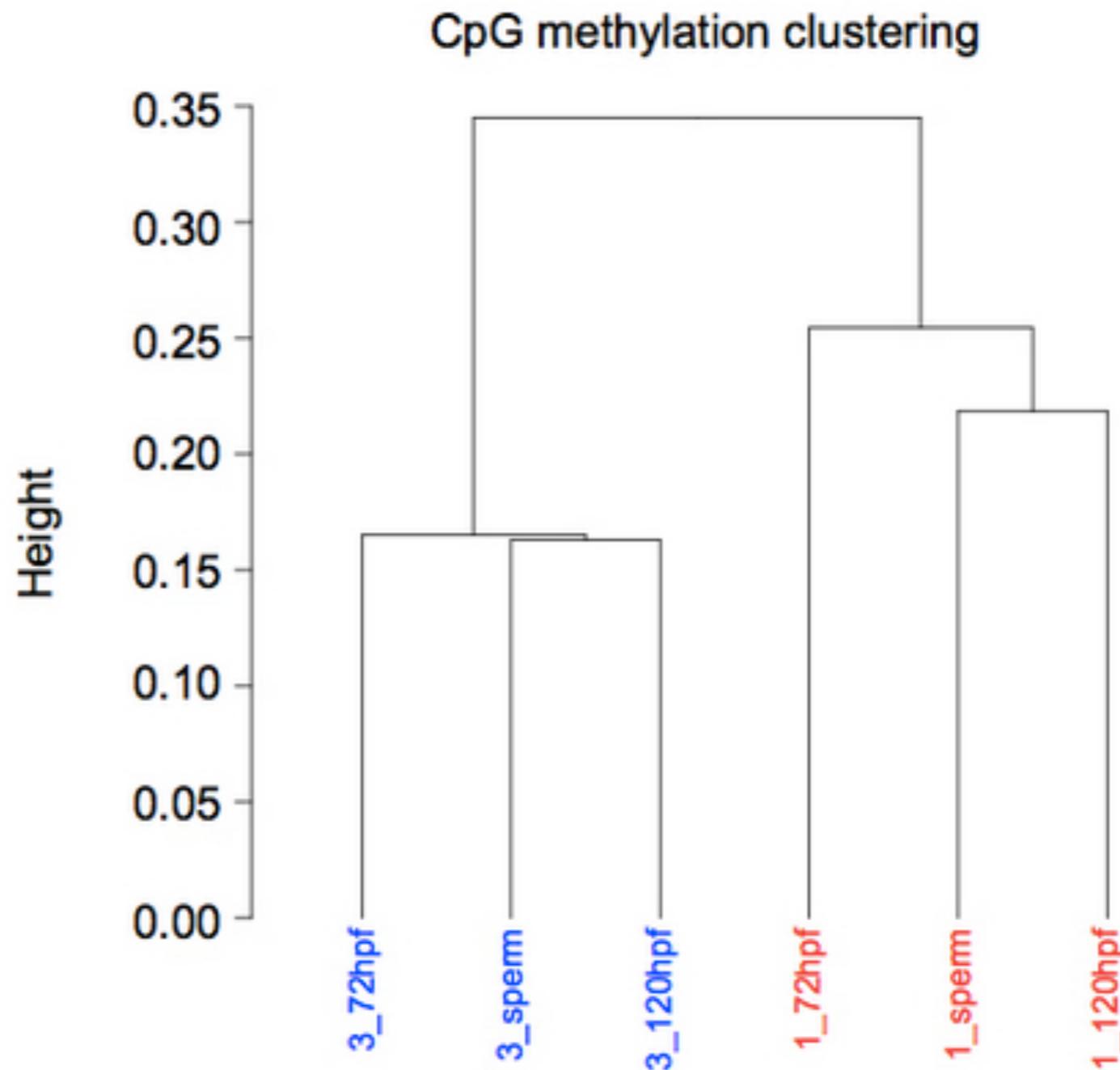


Epigenetic variation **1**

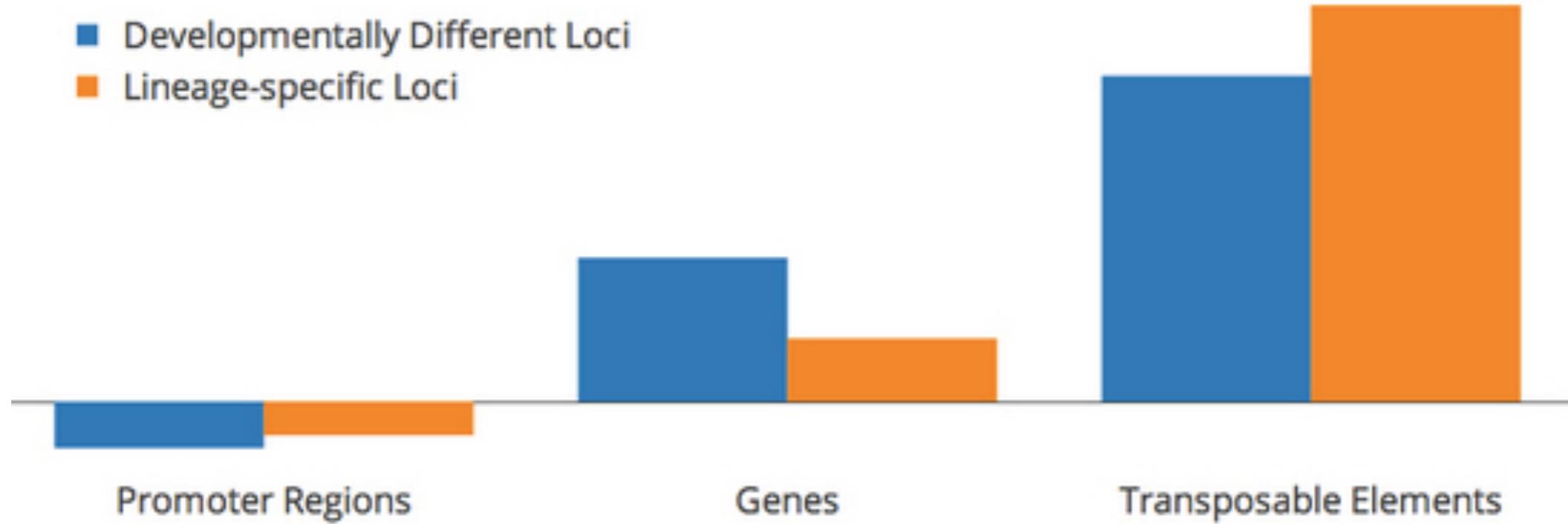


Whole Genome BS-Seq

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

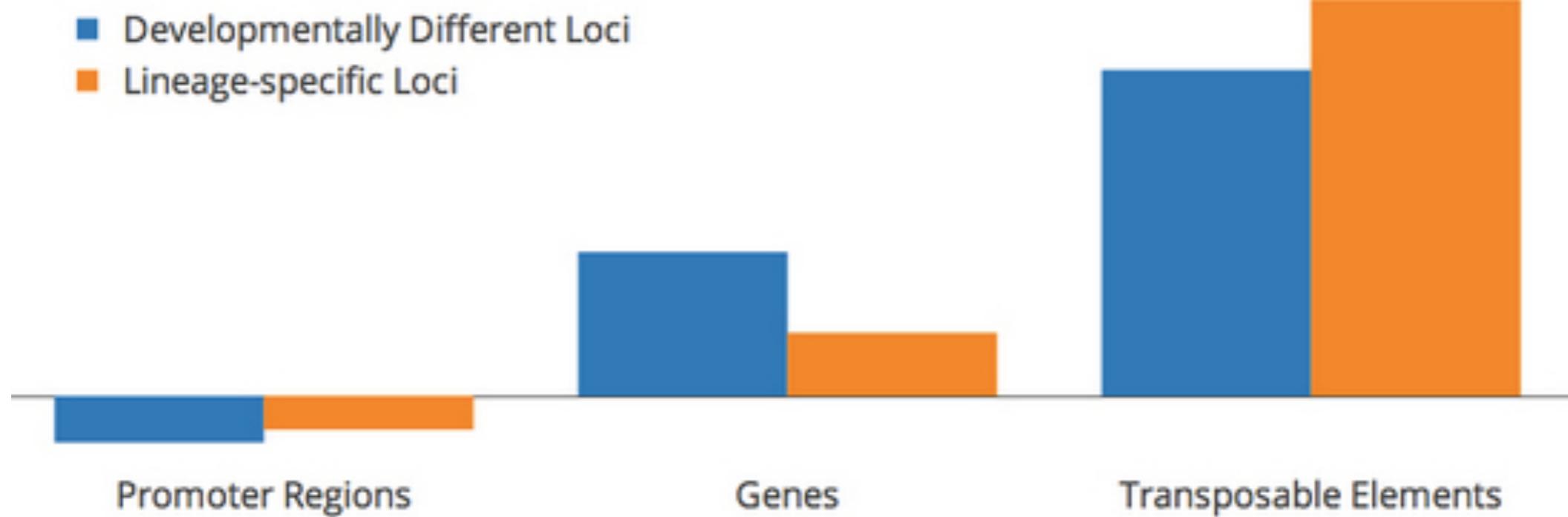


Claire Olson



*Differentially Methylated Loci predominant in
Transposable Elements*

Epigenetic variation **1**



branch: master ➔ [olson-dev](#) / +

File	Edit	View	Insert	Cell	Kernel	Help

IP[y]: Notebook

fix this
sr320 authored 4 days ago

.ipynb_checkpoints added .. for

img init

scripts cleaned up

wd added file to

BiGo_dev_manu.html updated html with cd correction

BiGo_dev_manu.ipynb fix this

README.md sm

github.com/sr320/olson-dev

Claire Olson

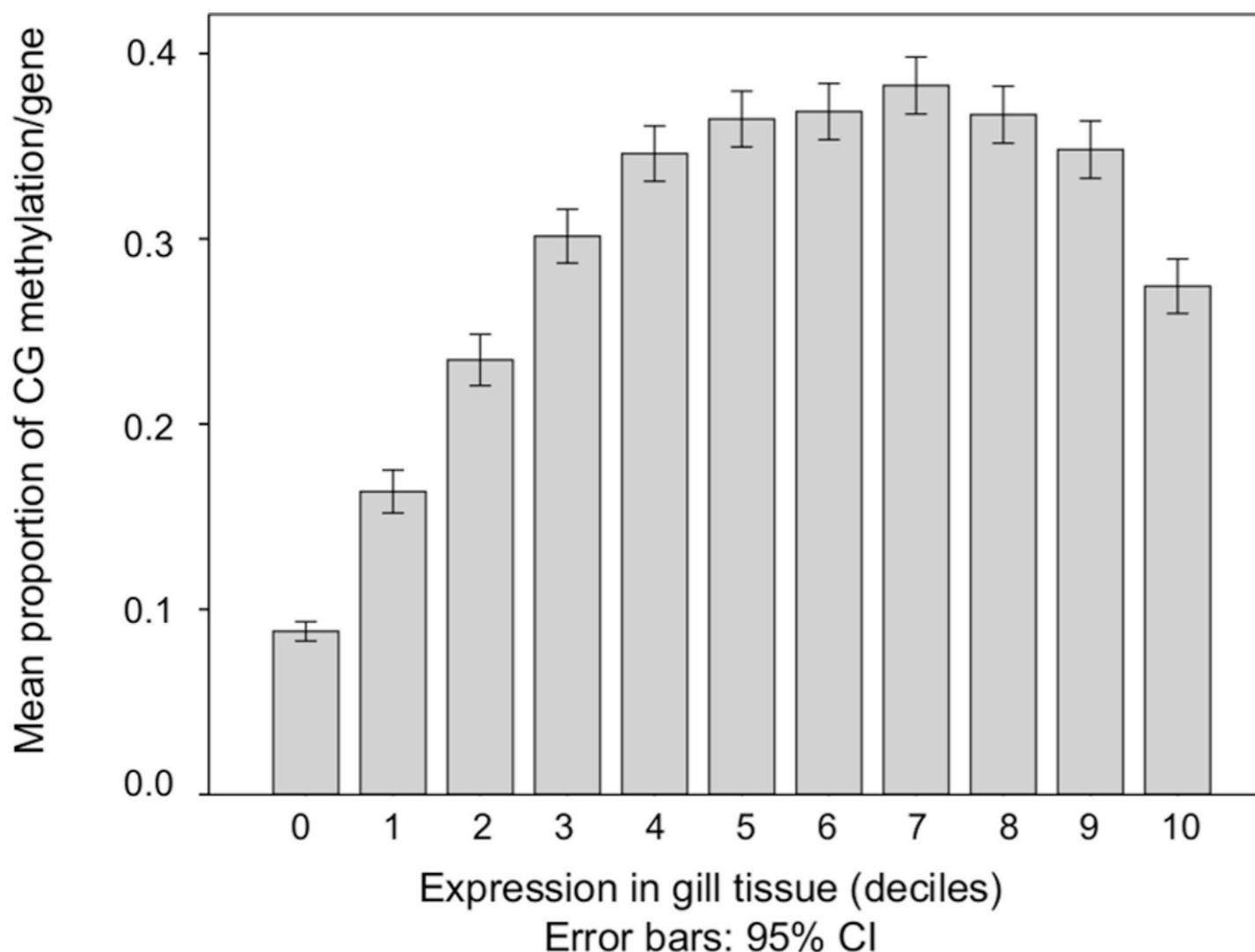
Summary

- 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



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

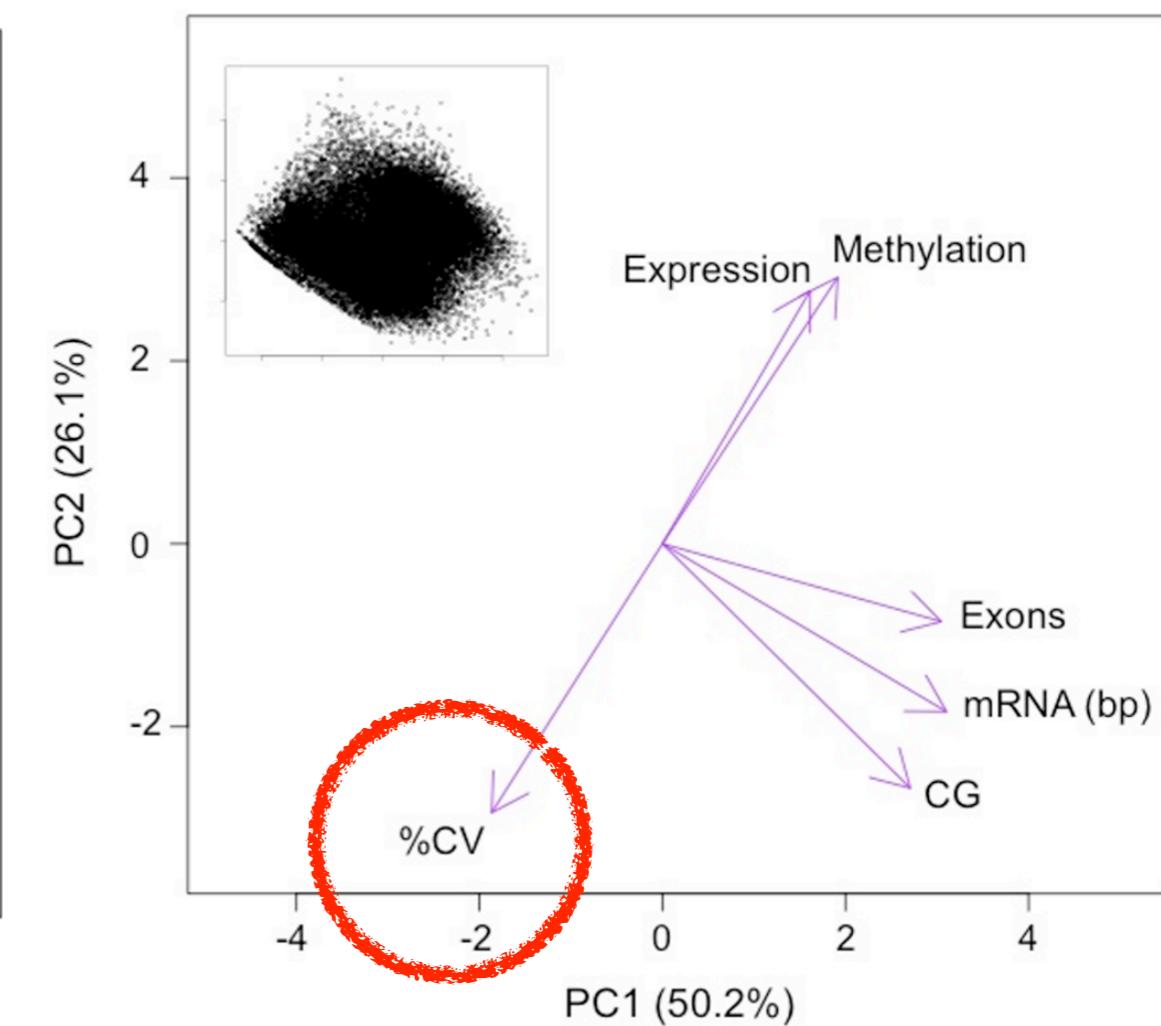
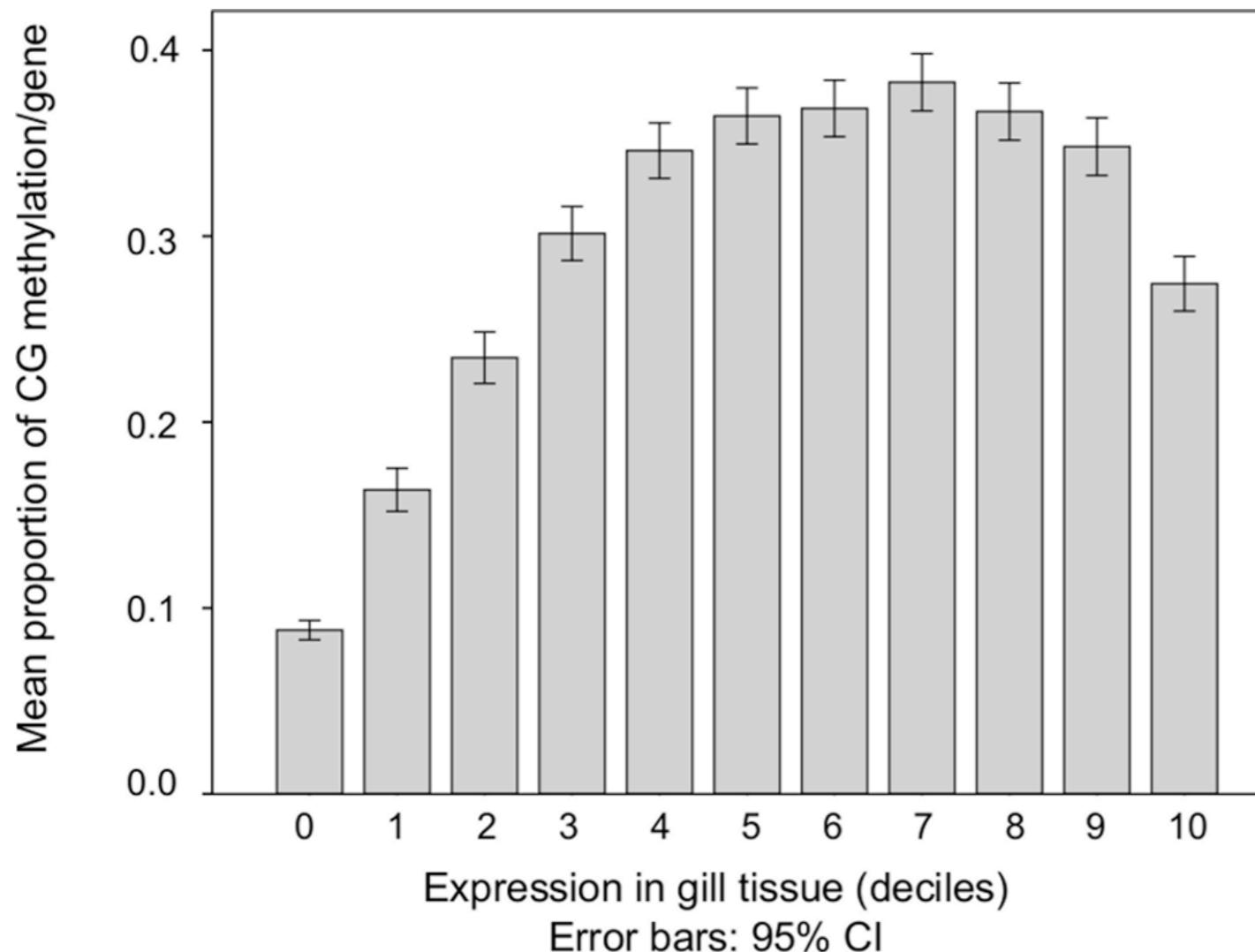
Mackenzie R. Gavery and Steven B. Roberts

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

Gene expression

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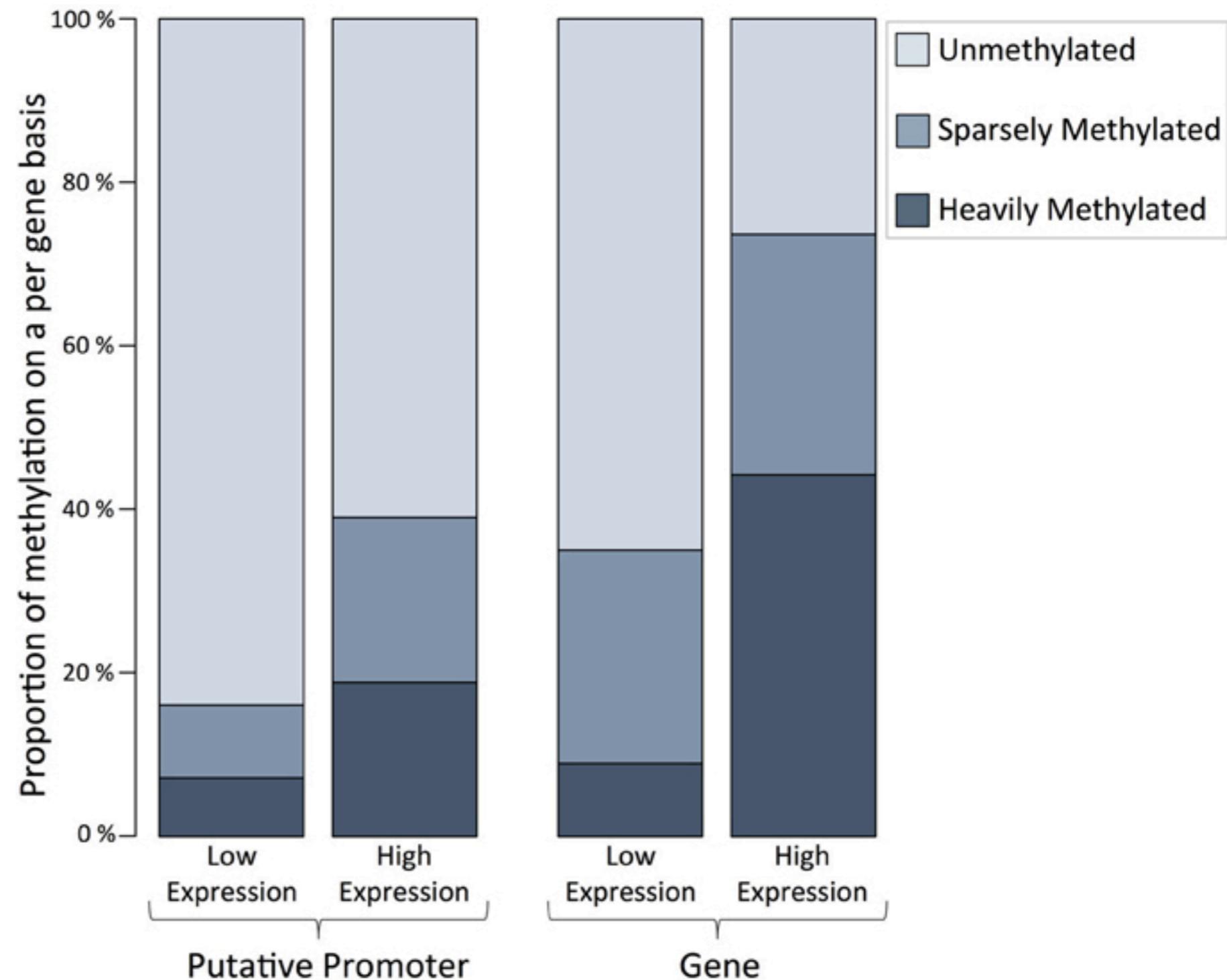
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Gene expression

2

Epigenetic variation



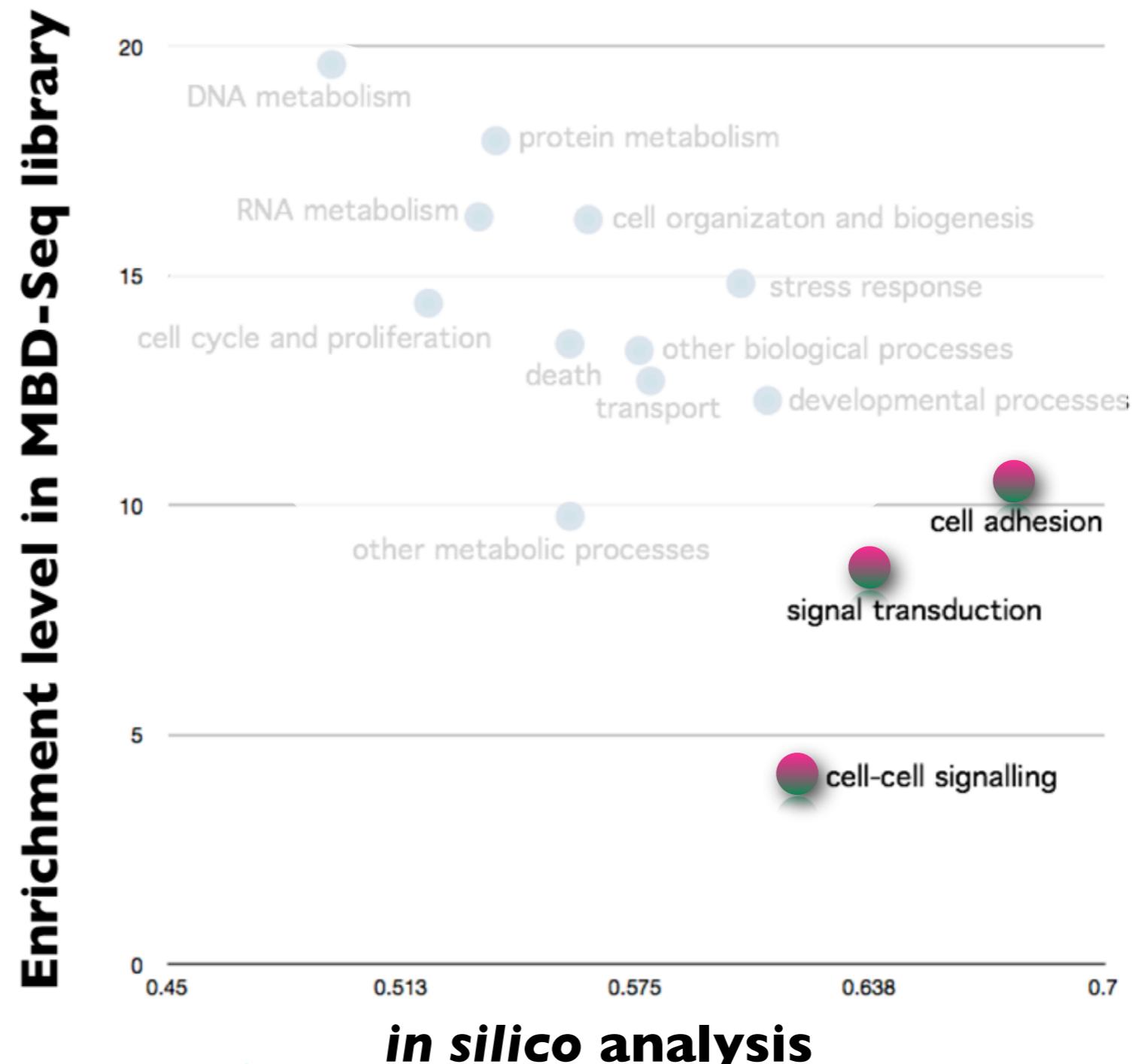
Role?

A context dependent role for DNA methylation in bivalves

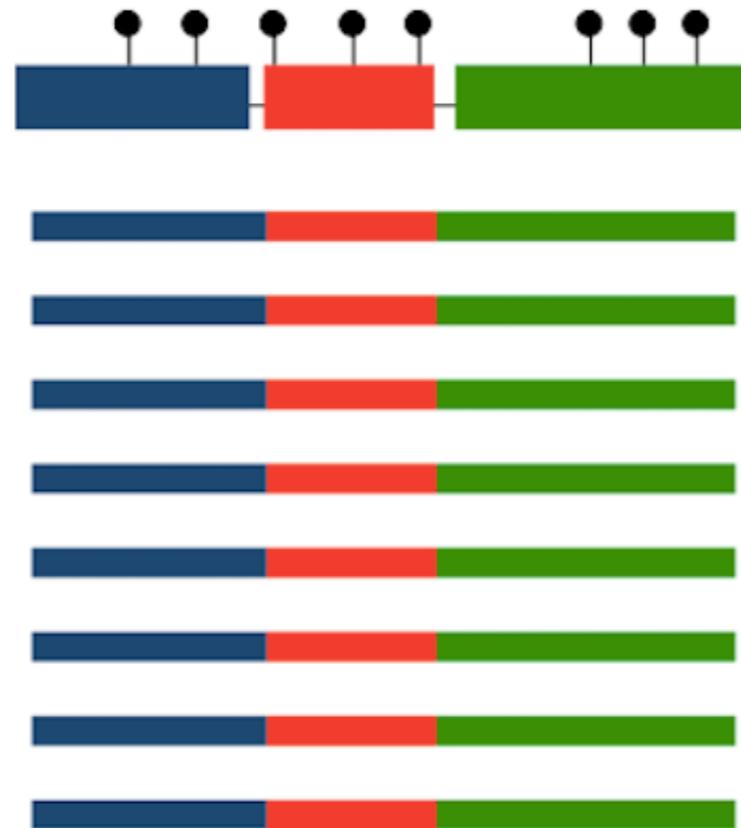
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Advance Access publication date 7 January 2014

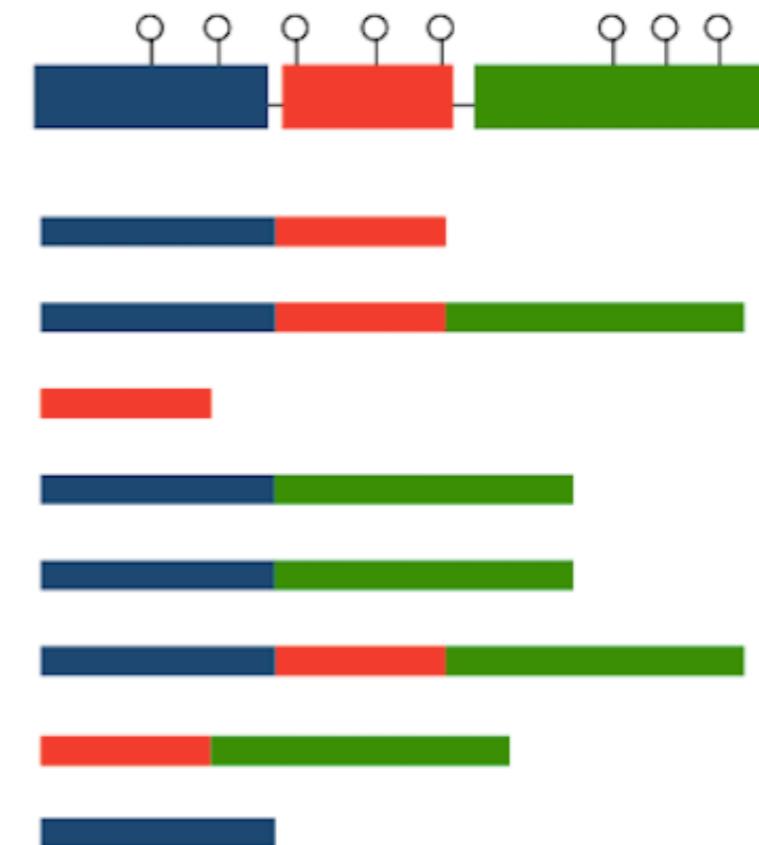
In species that experience a diverse range of environmental conditions, processes have evolved to increase the number of potential phenotypes in a population in order to improve the chances for an individual's survival.



Roberts and Gavery 2012



housekeeping



response to
change

A context dependent role for DNA methylation in bivalves

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Gene
expression

2

Epigenetic
variation

unmethylated



inducible



disease

temperature

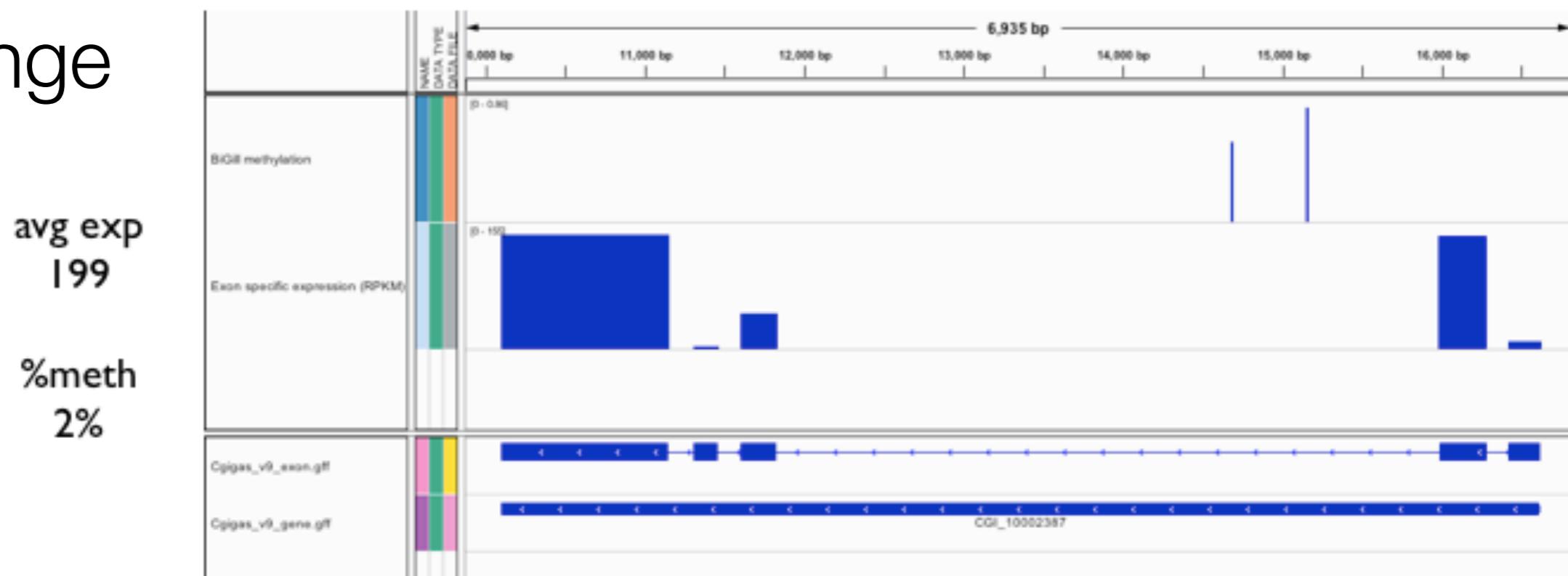
desiccation

salinity

Mackenzie Gavery

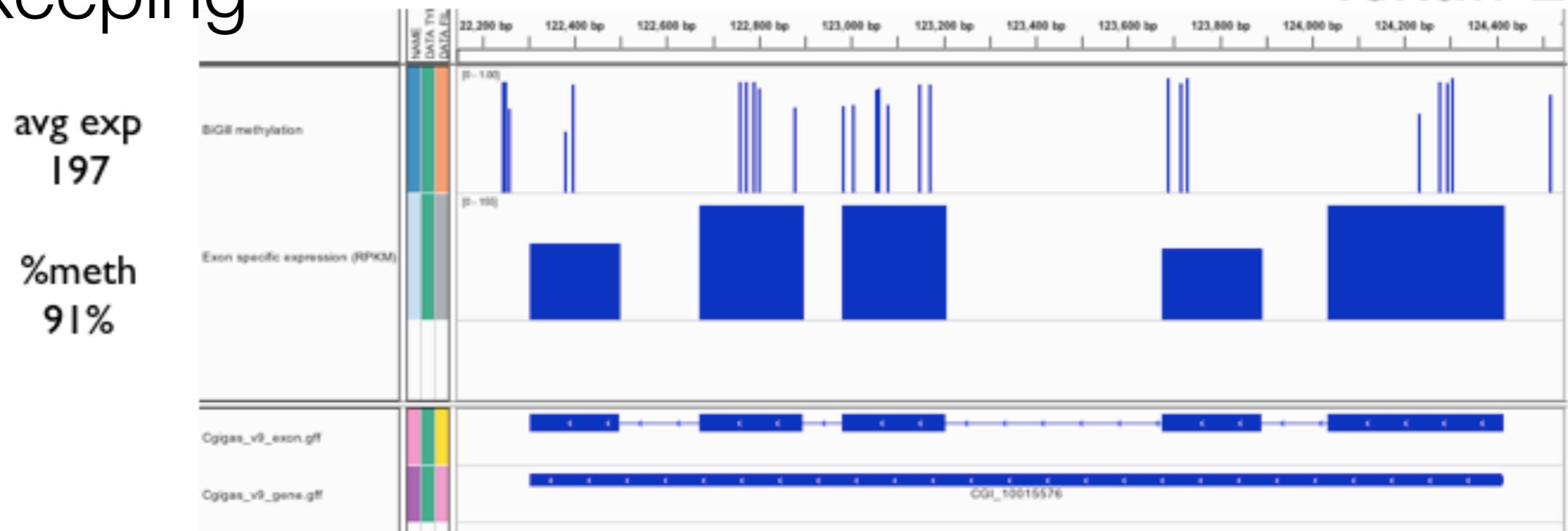
response to
change

Heat shock 70 kDa protein 12A



housekeeping

Tektin-2



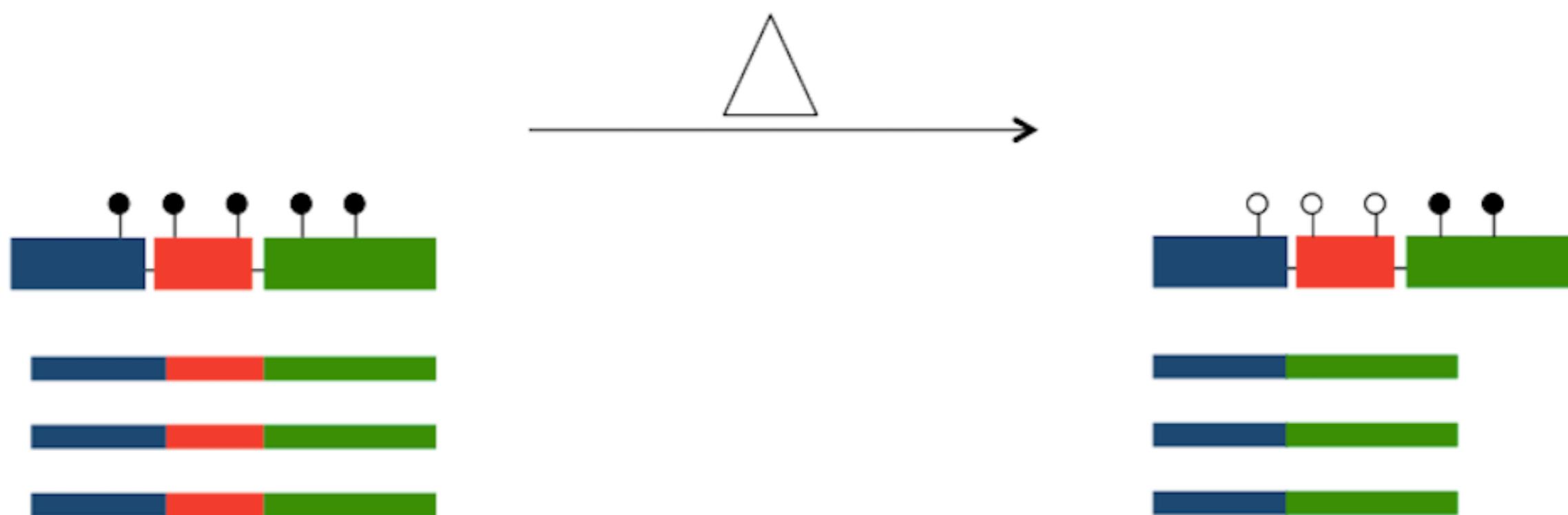


Targeted Regulation

A context dependent role for DNA methylation in bivalves

Mackenzie R. Gavery and Steven B. Roberts

Advance Access publication date 7 January 2014



Gene expression

2

Epigenetic variation

unmethylated



inducible



disease

temperature

desiccation

salinity

Mackenzie Gavery

Gene expression



Epigenetic variation

unmethylated



inducible



disease

temperature

desiccation

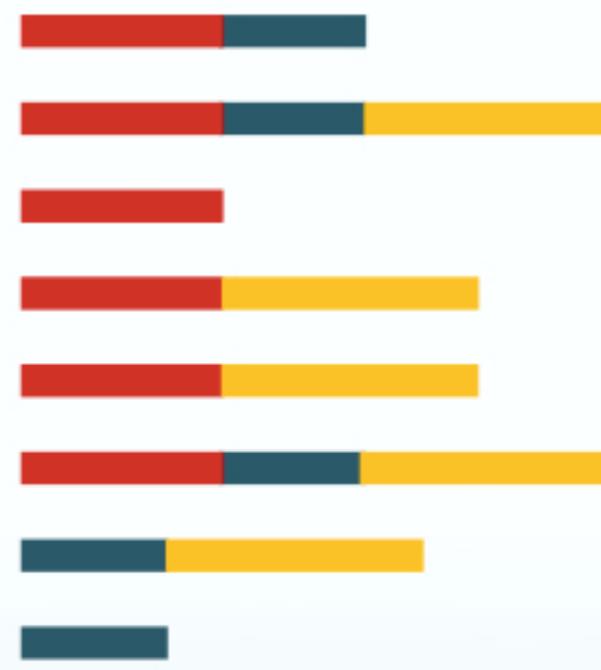
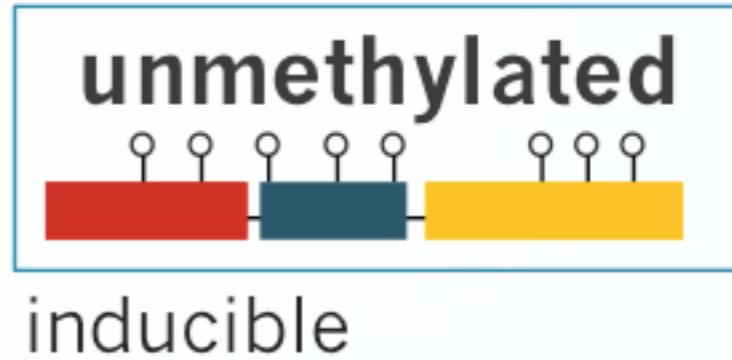
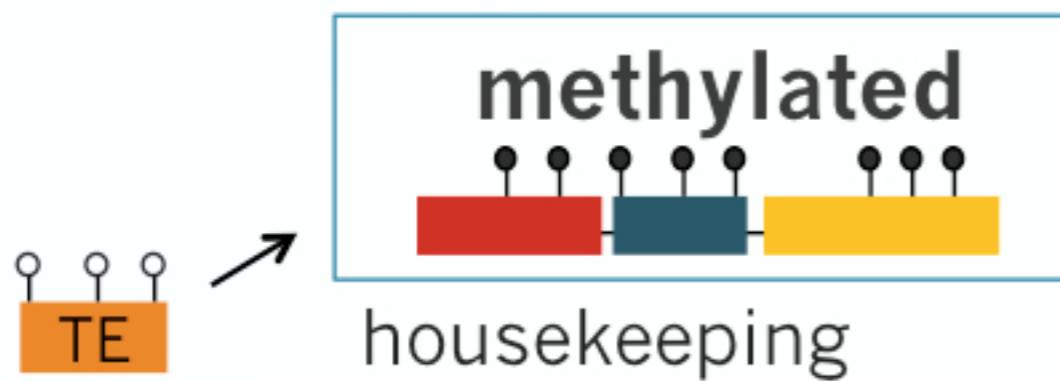
salinity

Mackenzie Gavery

Genetic variation

Regulates
.....
Epigenetic variation

Epigenetic variation





disease



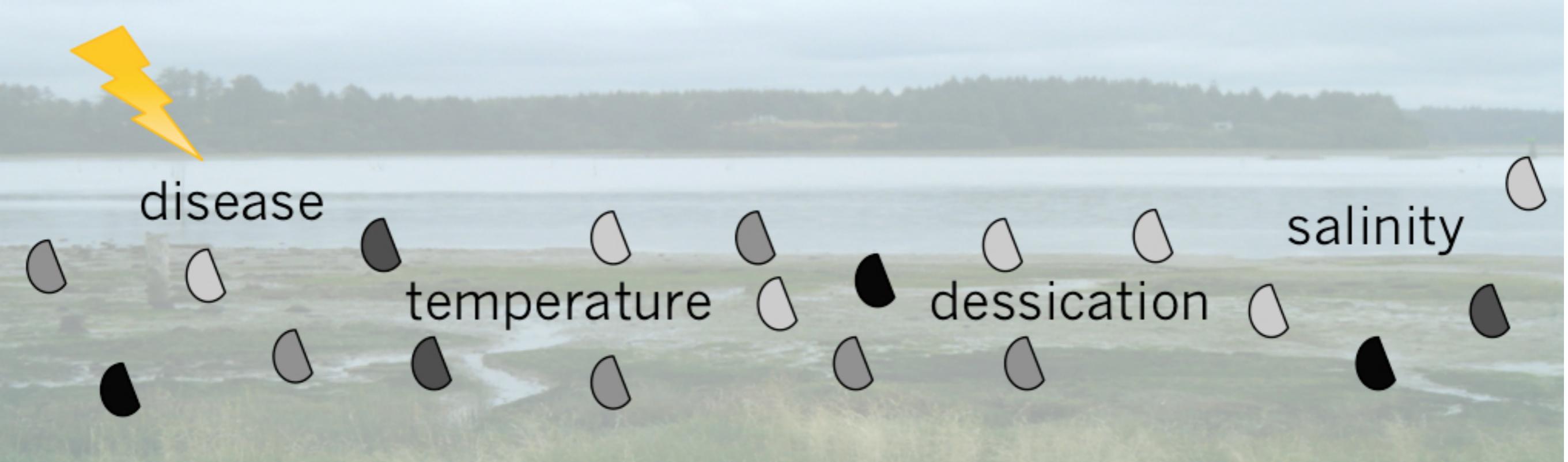
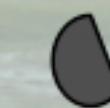
temperature



desiccation



salinity





disease



temperature



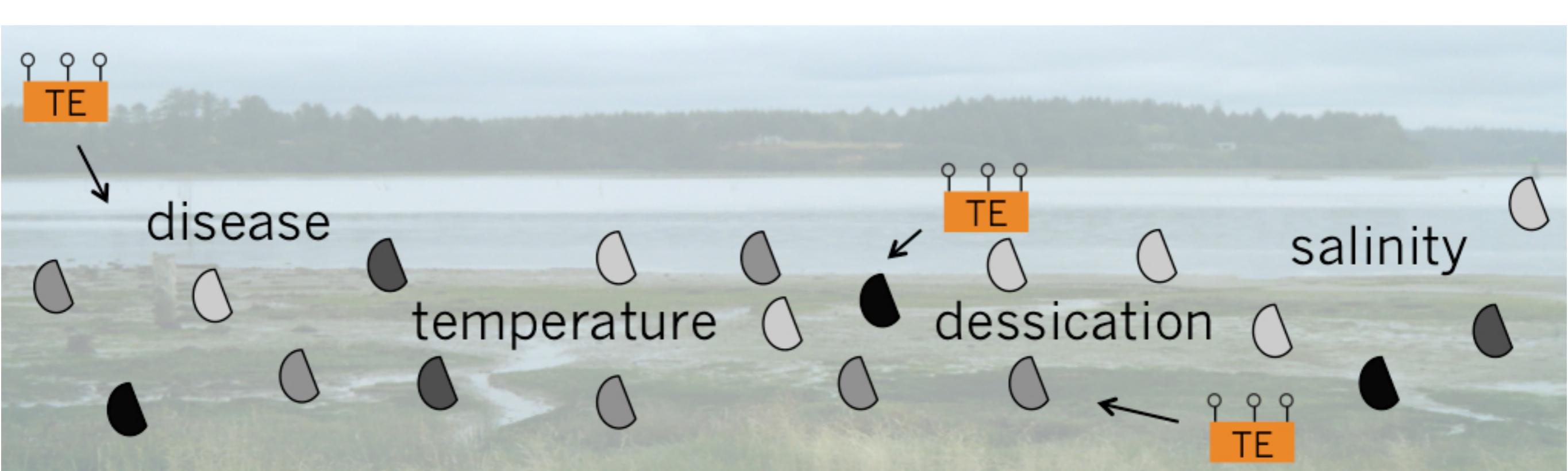
desiccation



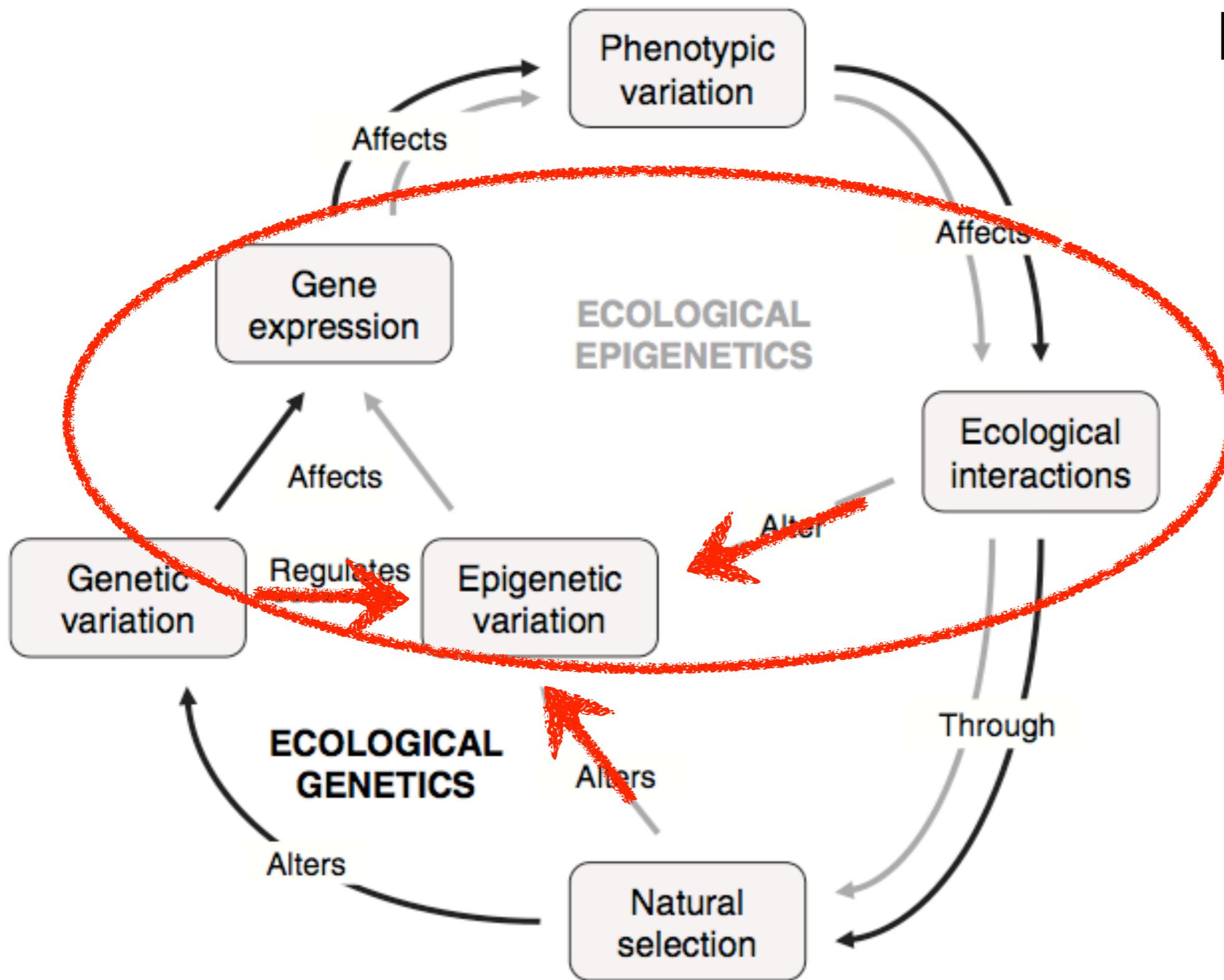
salinity



Transposable Elements providing increased diversity?



Beginning to test these Hypotheses



Ecology Letters, (2008) 11: 106–115

doi: 10.1111/j.1461-0248.2007.01130.x

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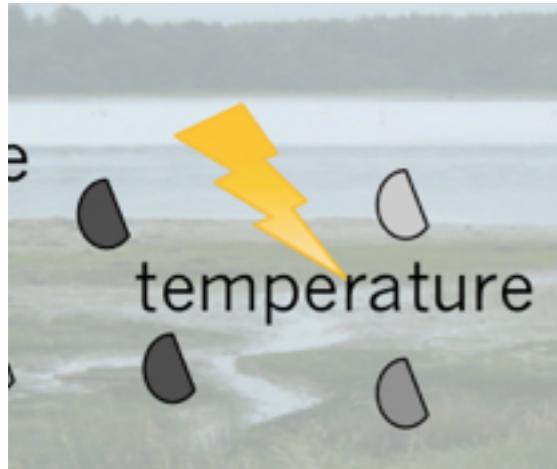
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Epigenetics for ecologists

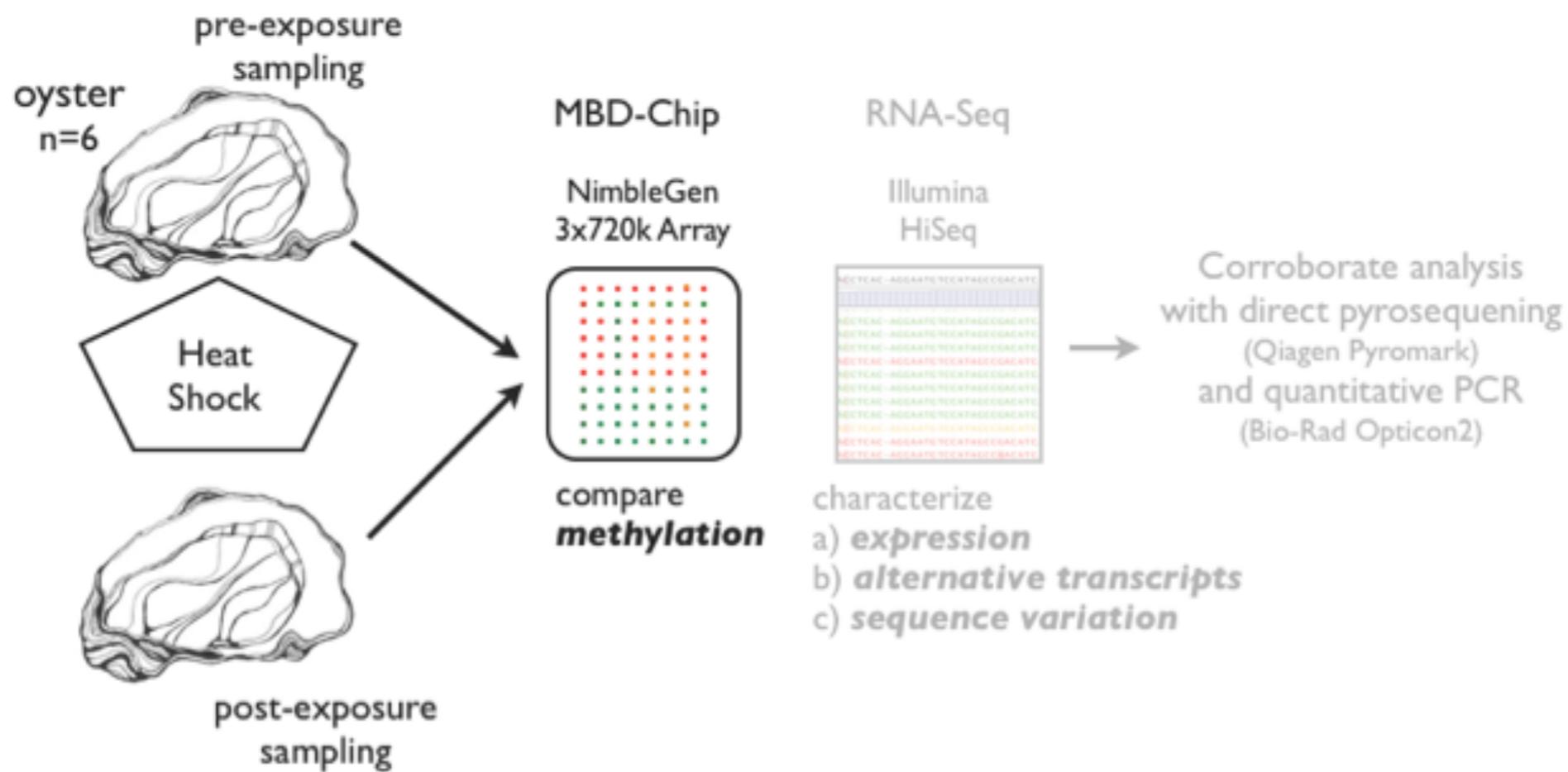
Oliver Bossdorf,^{1,*} Christina L.
Richards² and Massimo Pigliucci³

Very new data

Environment and gene expression

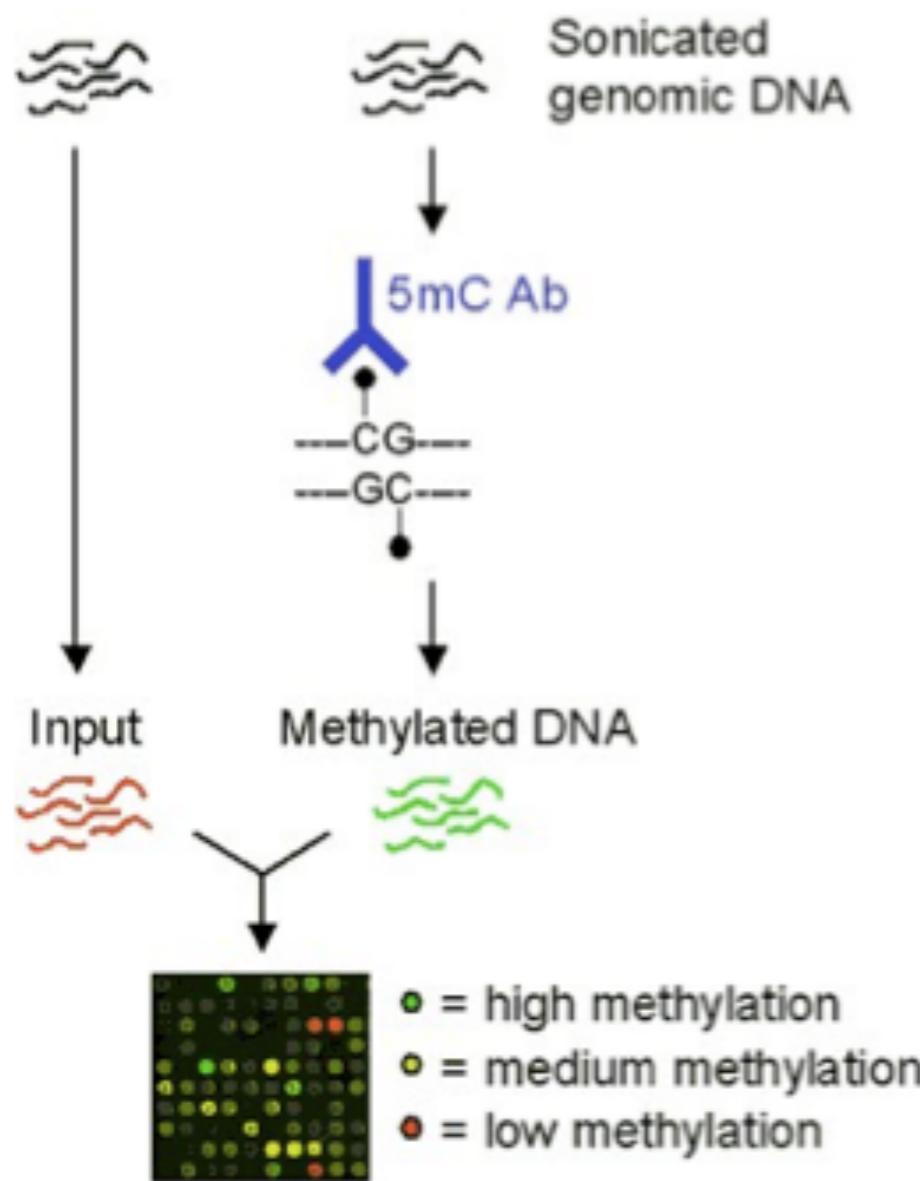


stochastic or targeted?



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

Day 10

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

Day 1

~44% ACGCTGATCGT
~56% ACGCTAATCGT

methyl group

Control: Random Mortality

~44% ACGCTGATCGT
~56% ACGCTAATCGT

**High pCO₂: Non-random
Mortality**

~81% ACGCTGATCGT
~19% ACGCTAATCGT

Katie Lotterhos

Evidence of epiallele (methylated cytosine)
beneficial to survival
under High pCO₂ conditions

~~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

Sam White

Bill Howe

Dan Halperin



EPA
STAR



slides, data & more @ robertslab.info

