Marine invertebrate environmental memory

Implications, mechanisms, and opportunities

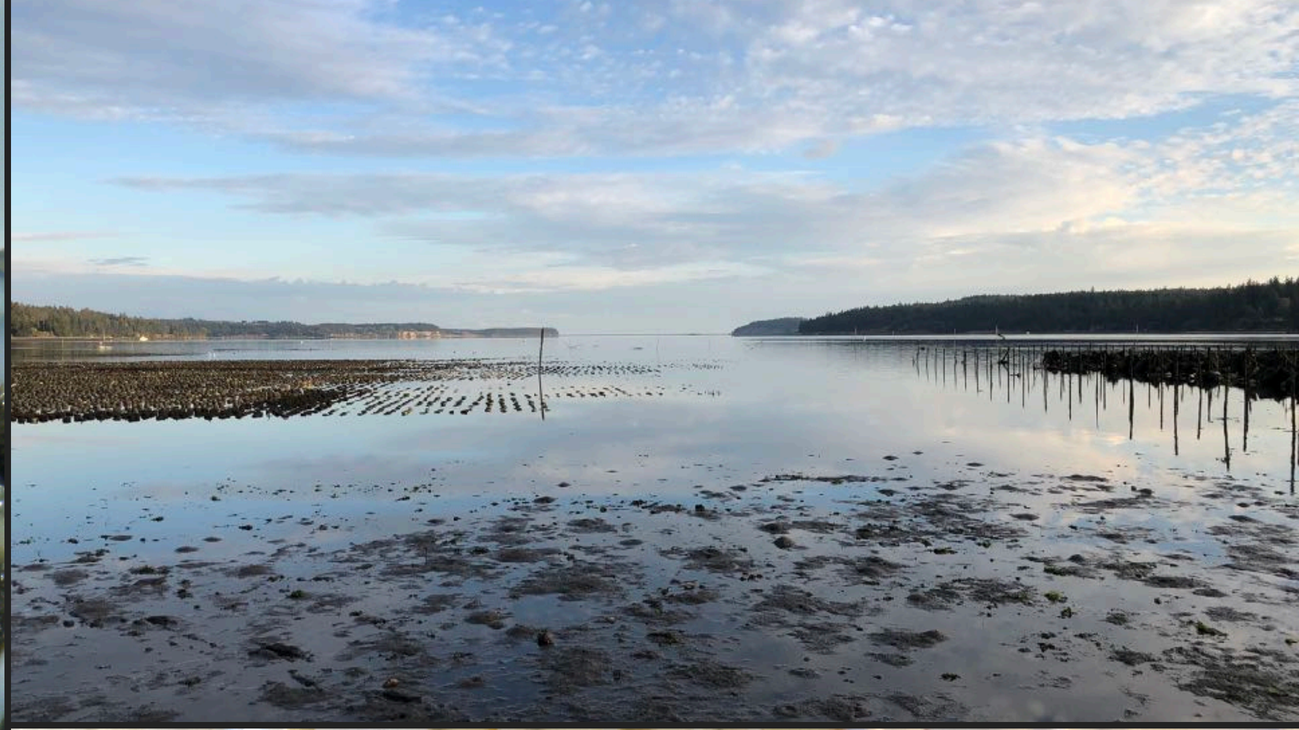
Steven Roberts - University of Washington

github.com/sr320/talk-SZAN-2024


FHL

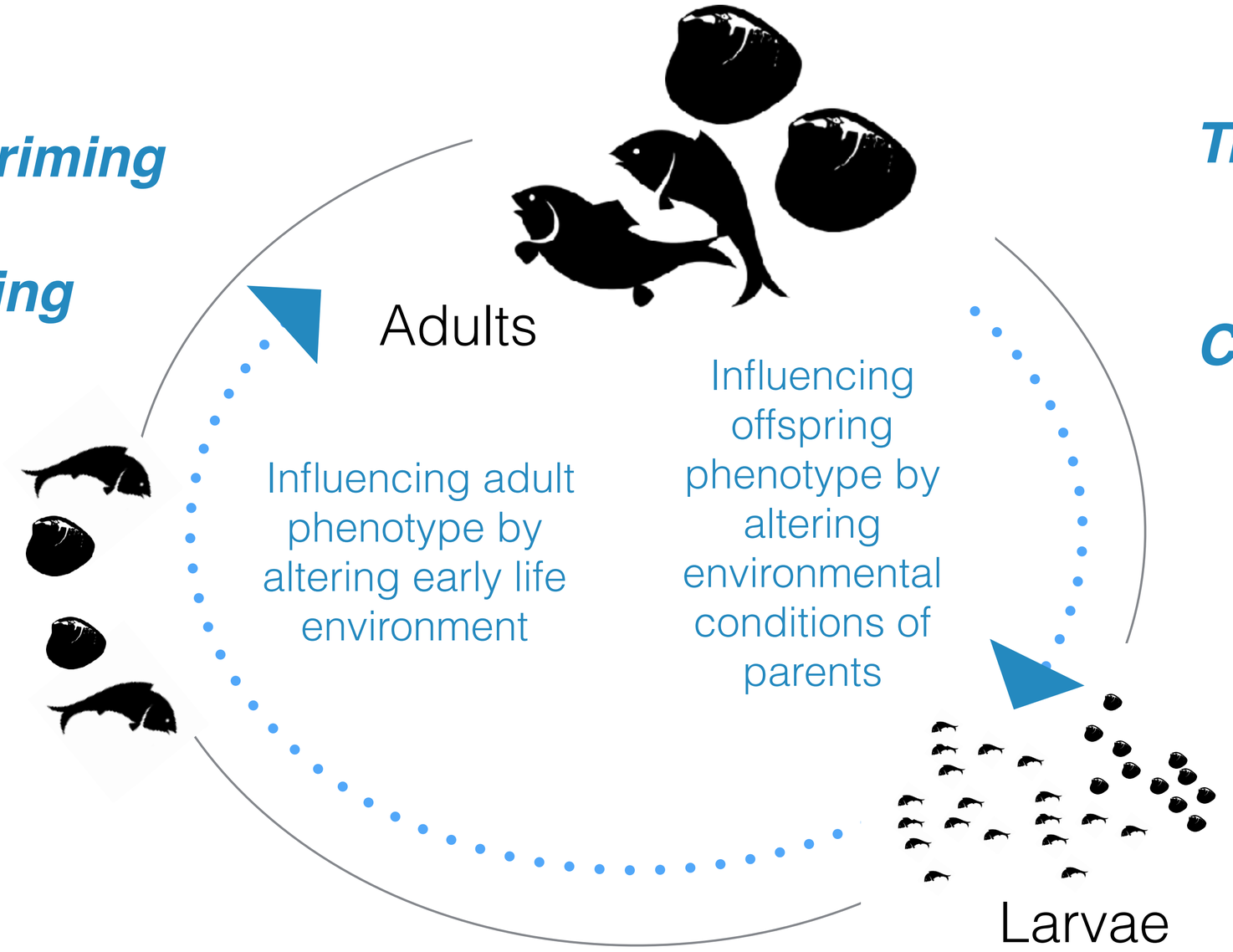

FHL


FHL



Early-life Priming

Hardening

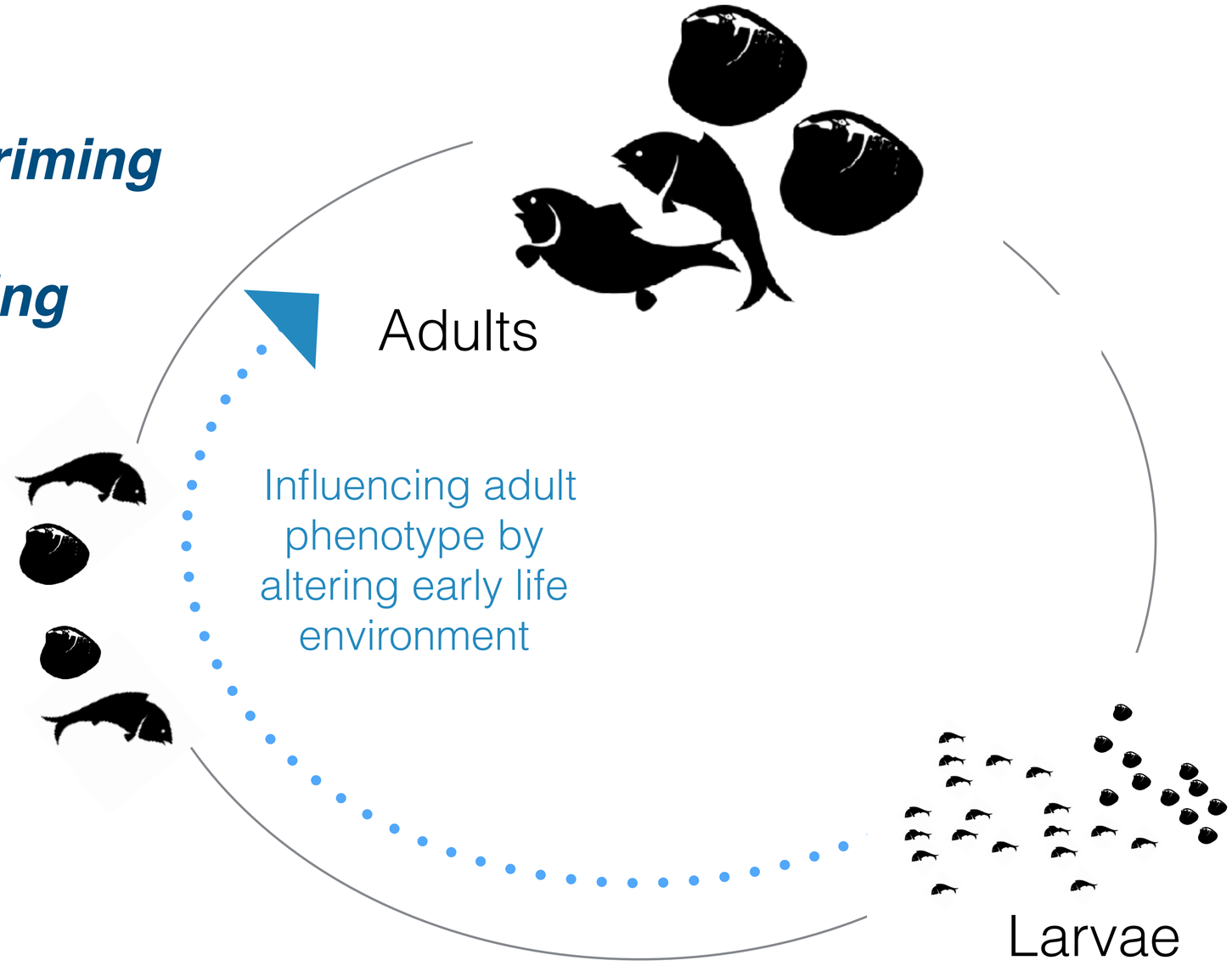


Transgenerational Plasticity

Carry-over effects

Early-life Priming

Hardening



Early-life Priming

Hardening

Trends in
Plant Science

Special issue: Climate change and sustainability I

Review

Priming crops for the future: rewiring stress memory

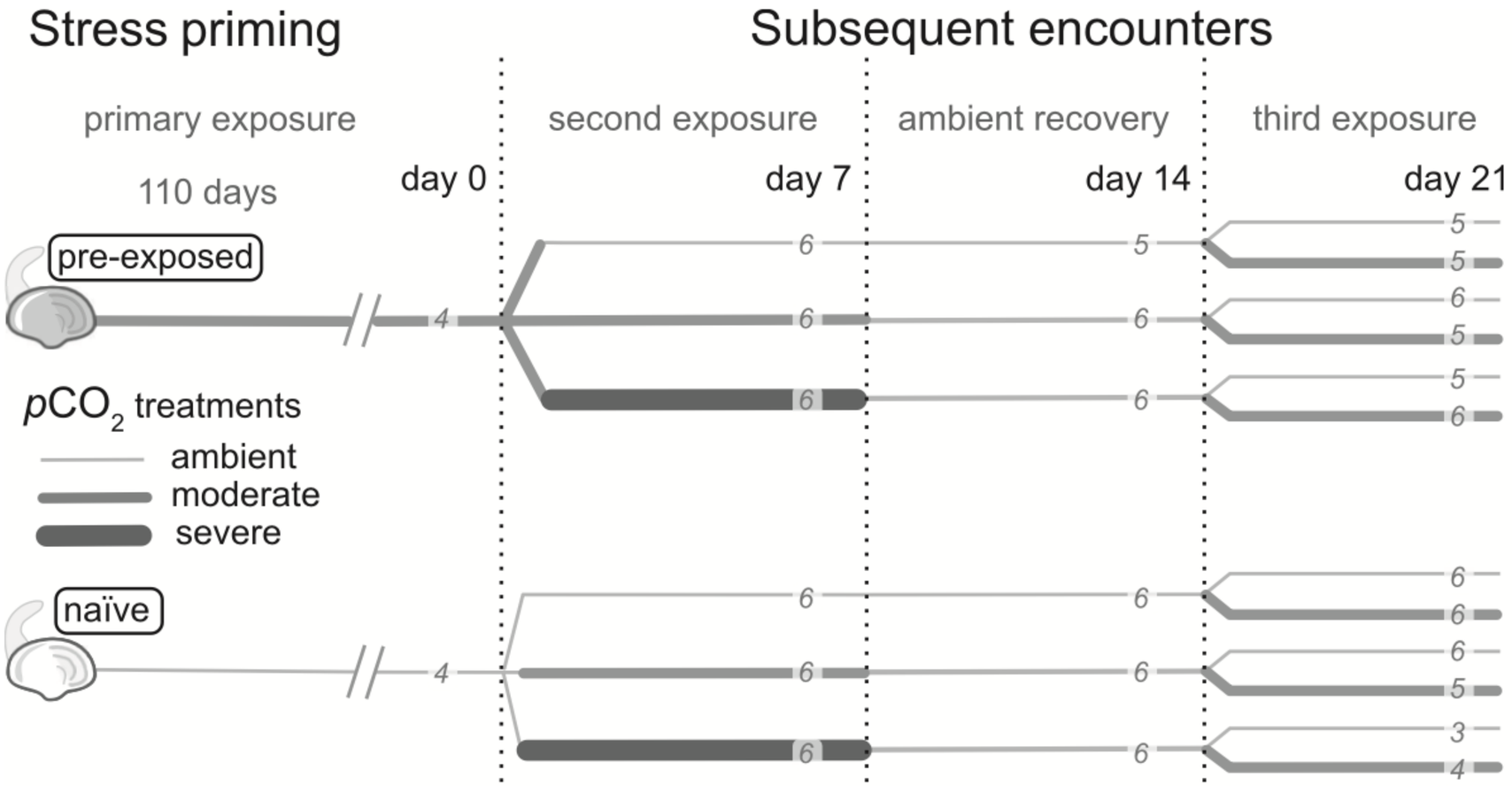
Haipei Liu [1], Amanda J. Able [1] and Jason A. Able [1,@,*]

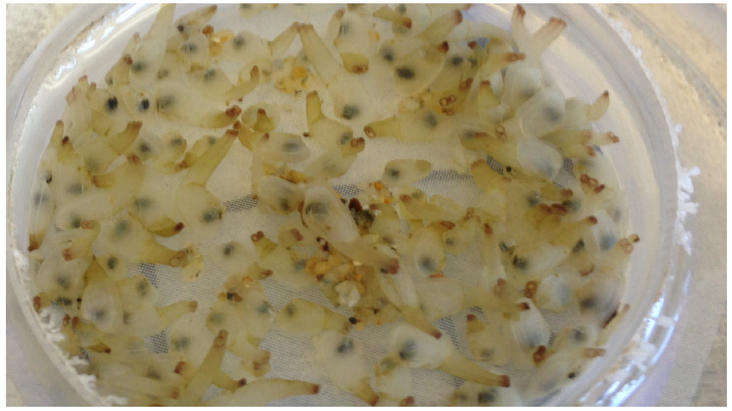
Cross-stress priming success relies on synergistic stress signaling pathways being shared across stresses varying in nature and intensity.

Geoduck Clams

Repeat exposure to hypercapnic seawater modifies growth and oxidative status in a tolerant burrowing clam

Samuel J. Gurr[1,*], Shelly A. Wanamaker[2], Brent Vadopalas[3], Steven B. Roberts[2] and Hollie M. Putnam[1]





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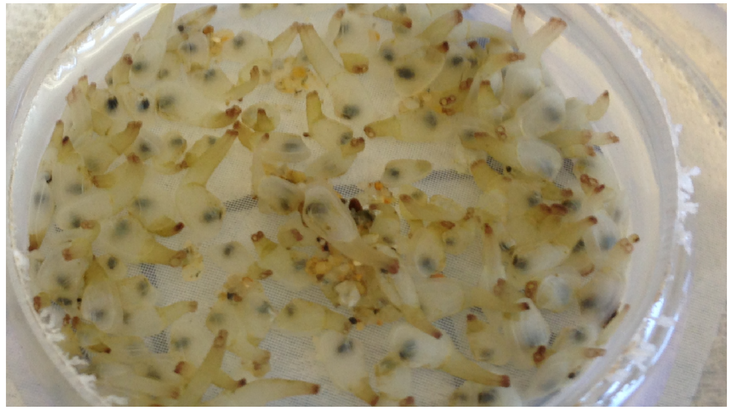
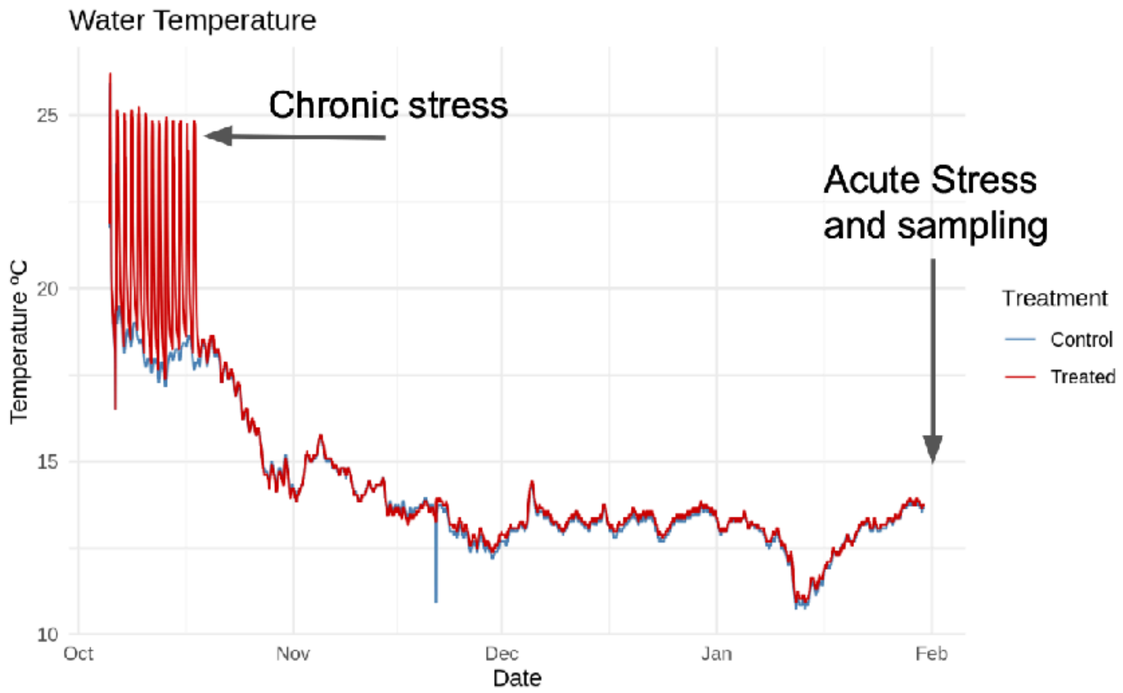
- Initial conditioning followed by second and third exposure to severe and moderate acidification stress increased respiration rate, organic biomass and shell size, suggesting a stress-intensity-dependent effect on energetics.

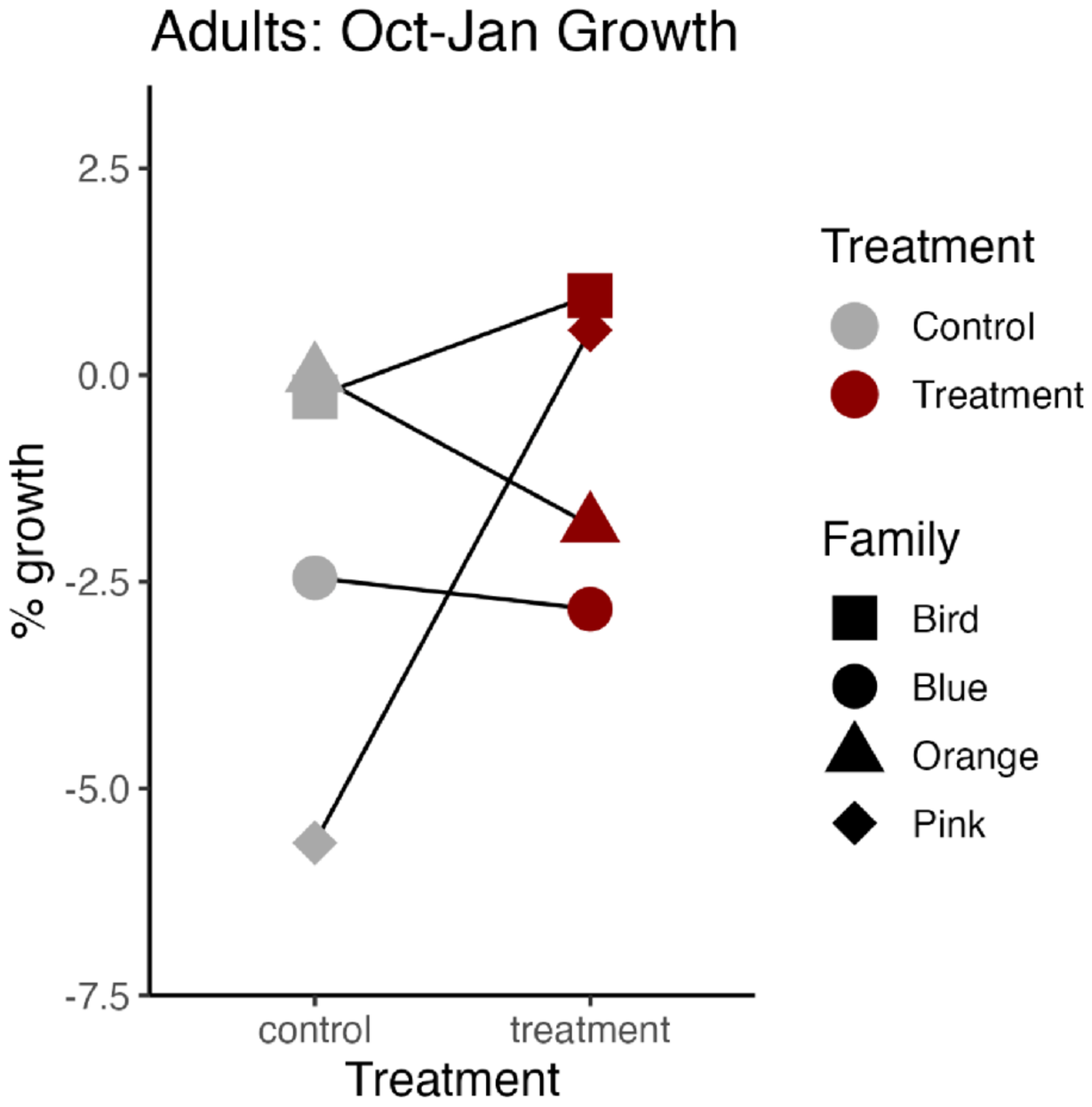
- Stress acclimated clams had lower antioxidant capacity compared with clams under ambient conditions, supporting the hypothesis that stress over postlarval-to-juvenile development affects oxidative status later in life.



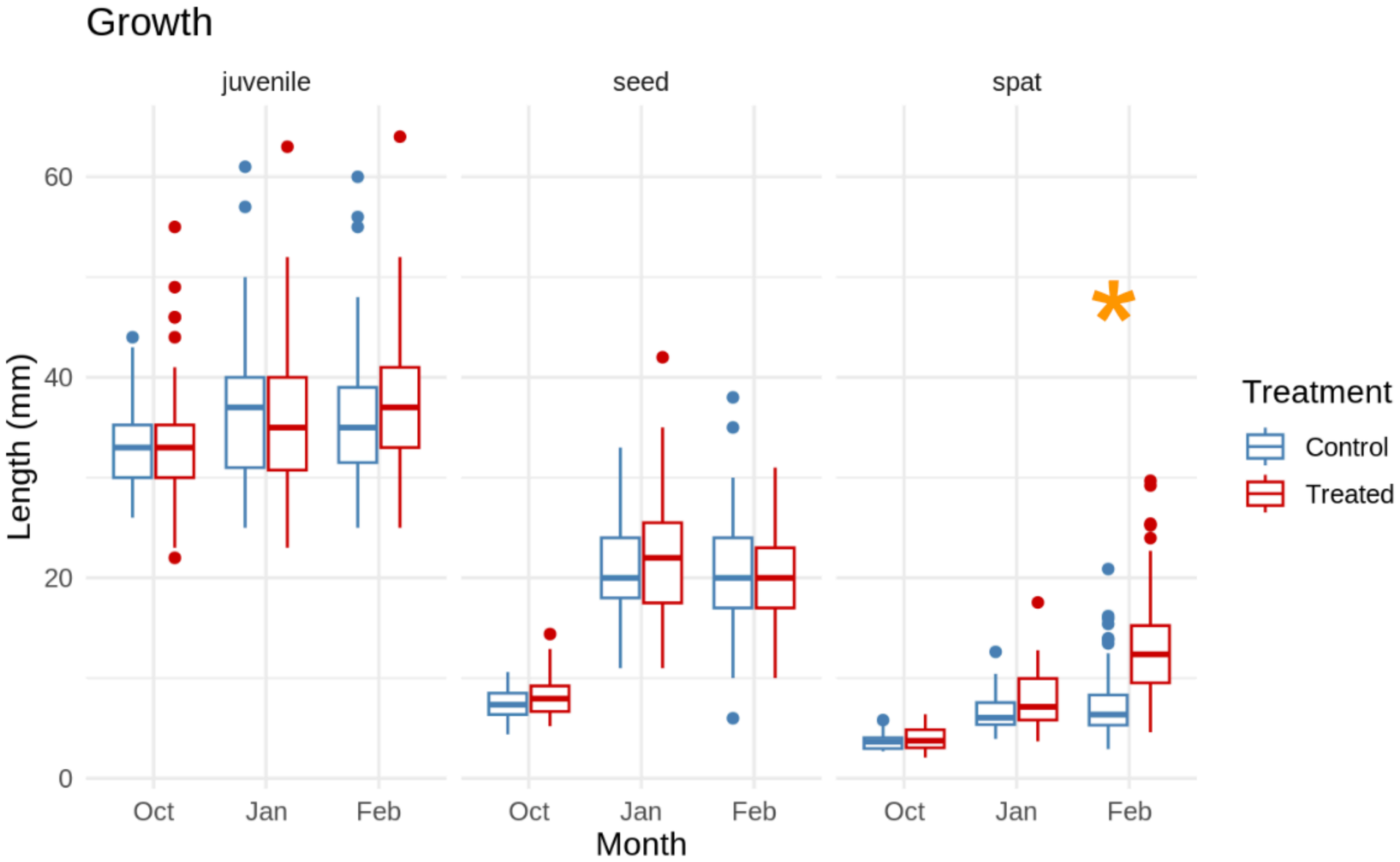
Crassostrea gigas

New data





Crassostrea gigas



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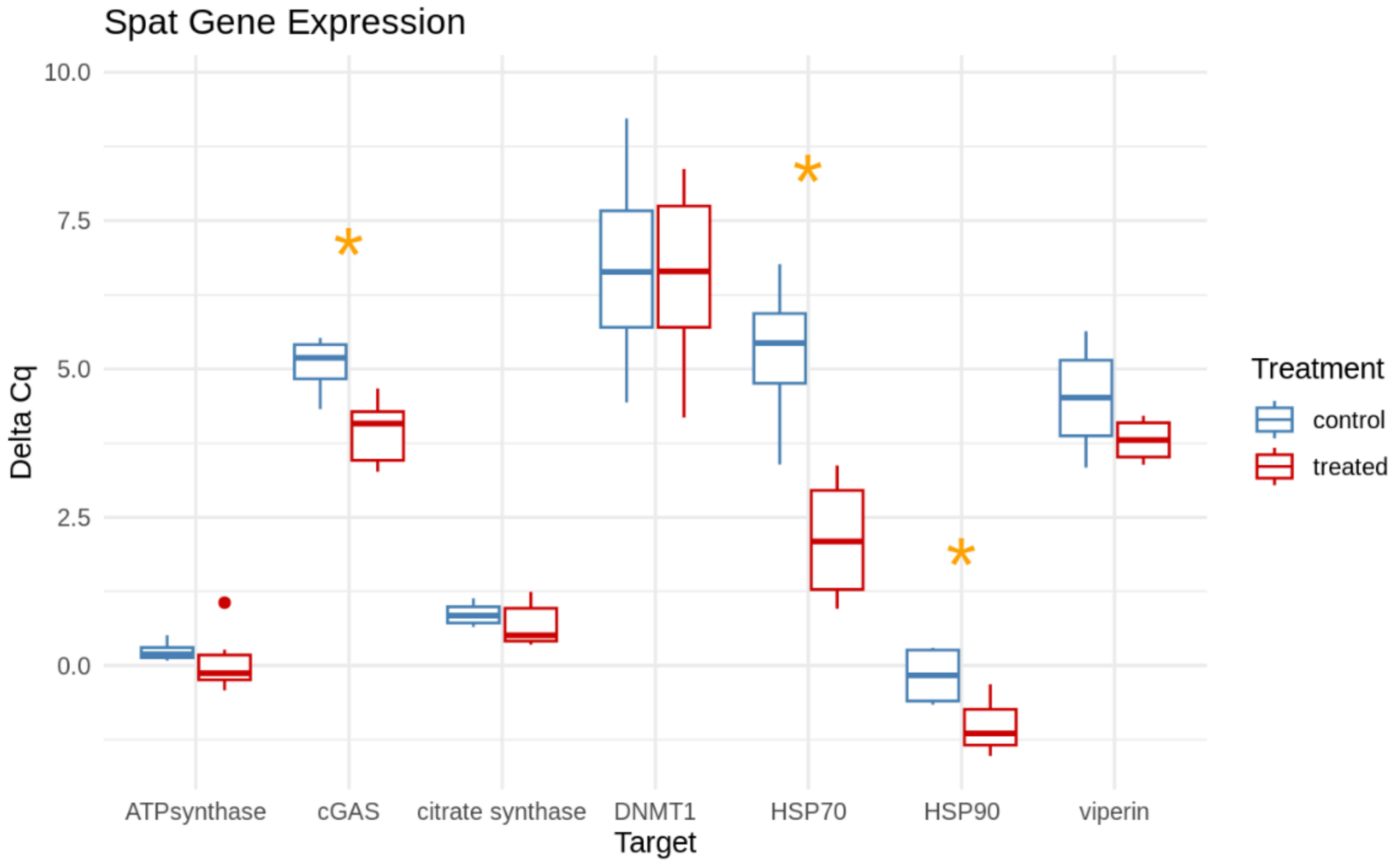

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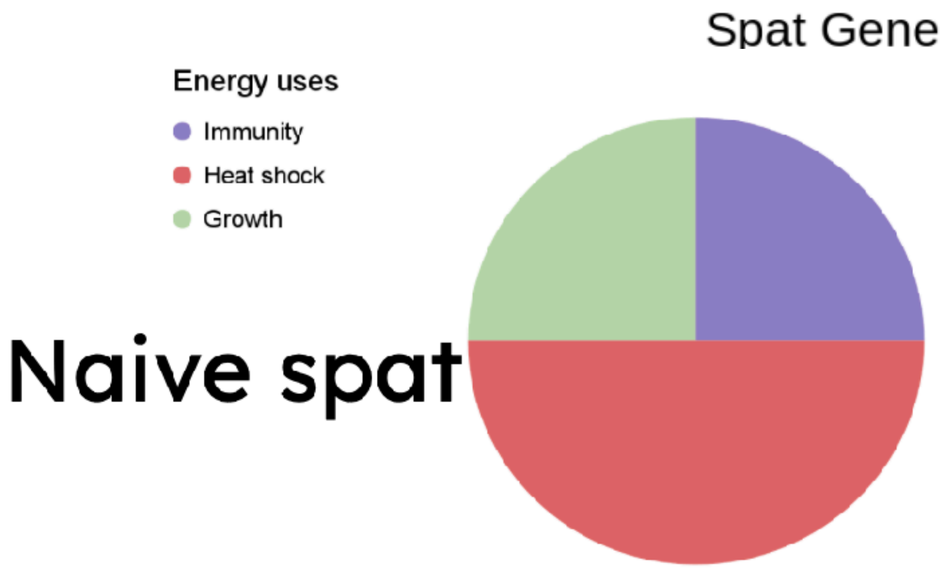
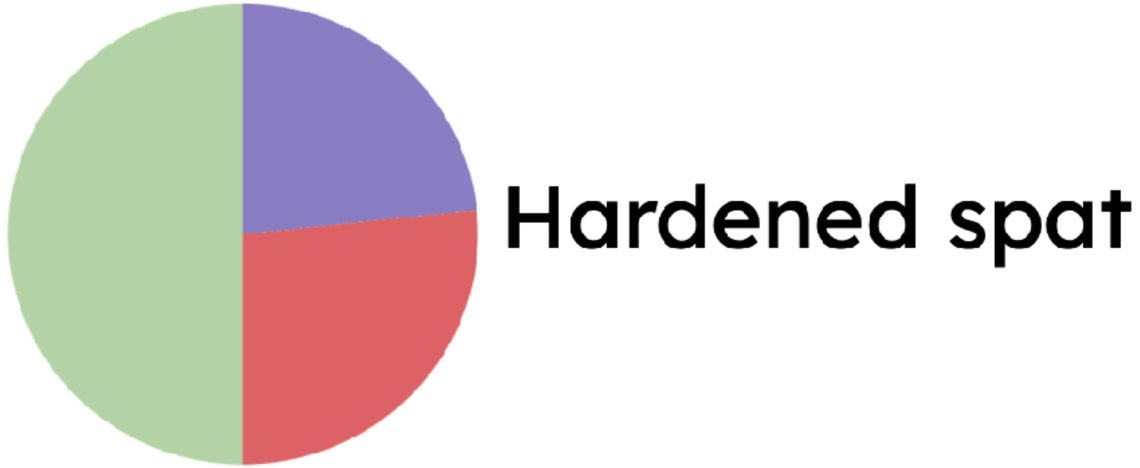
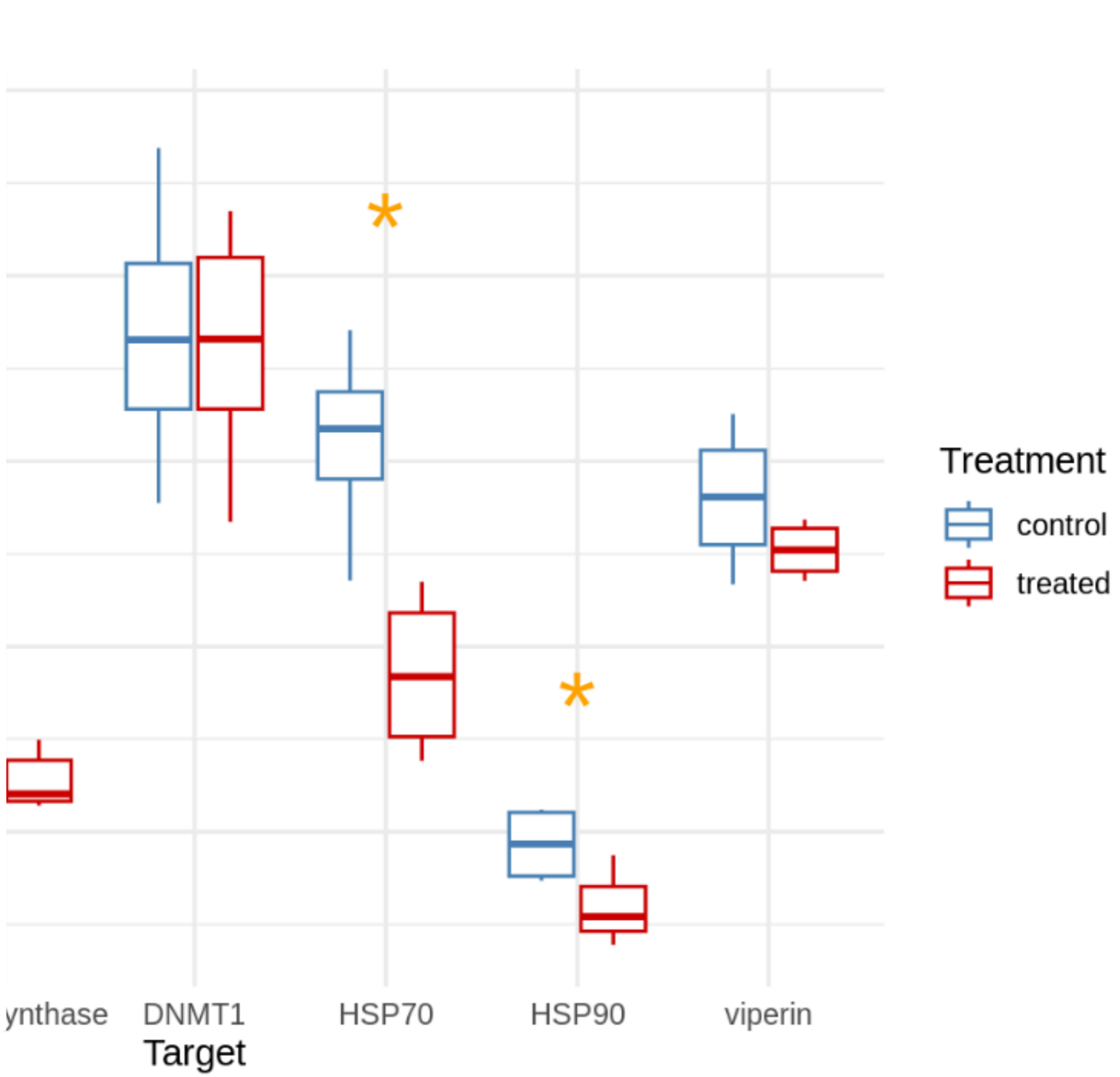
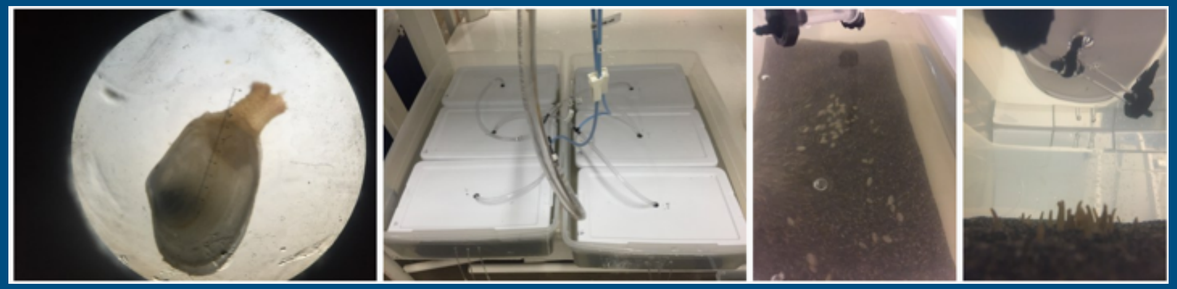


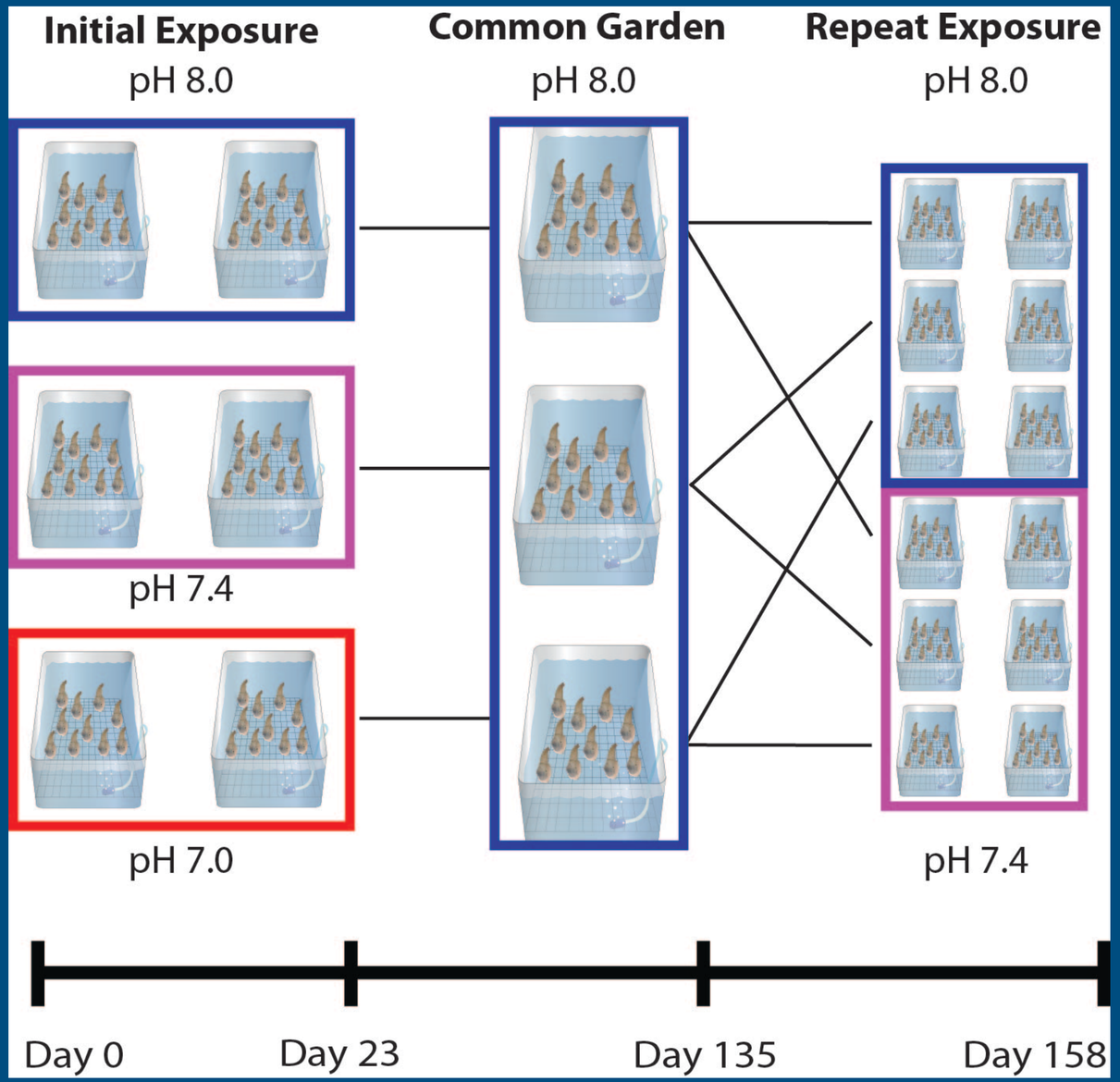




GEODUCKS CLAMS

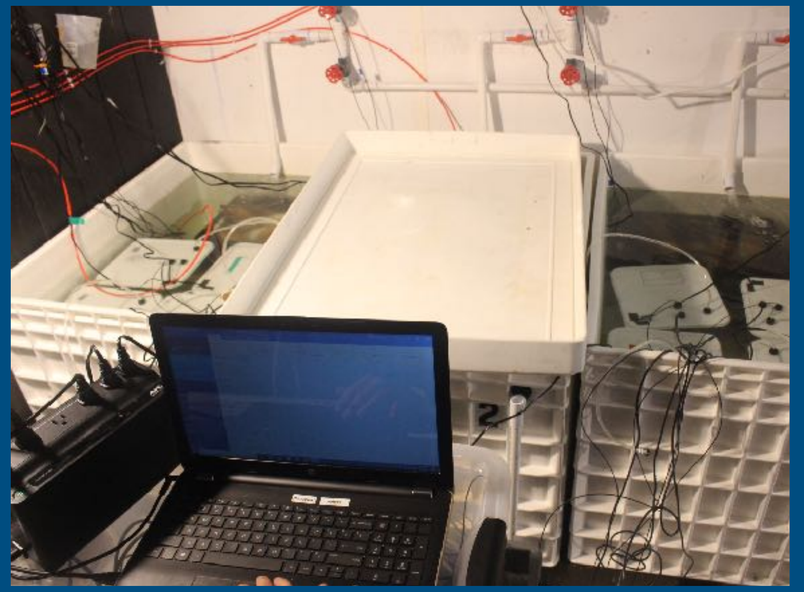


- Does conditioning to low pH confer tolerance within a generation?



HOLLIE PUTNAM, SAM GURR, BRENT VADOPALAS, SHELLY TRIGG, JAMESTOWN S'KLALLAM TRIBE

GEODUCKS CLAMS



GEODUCKS CLAMS

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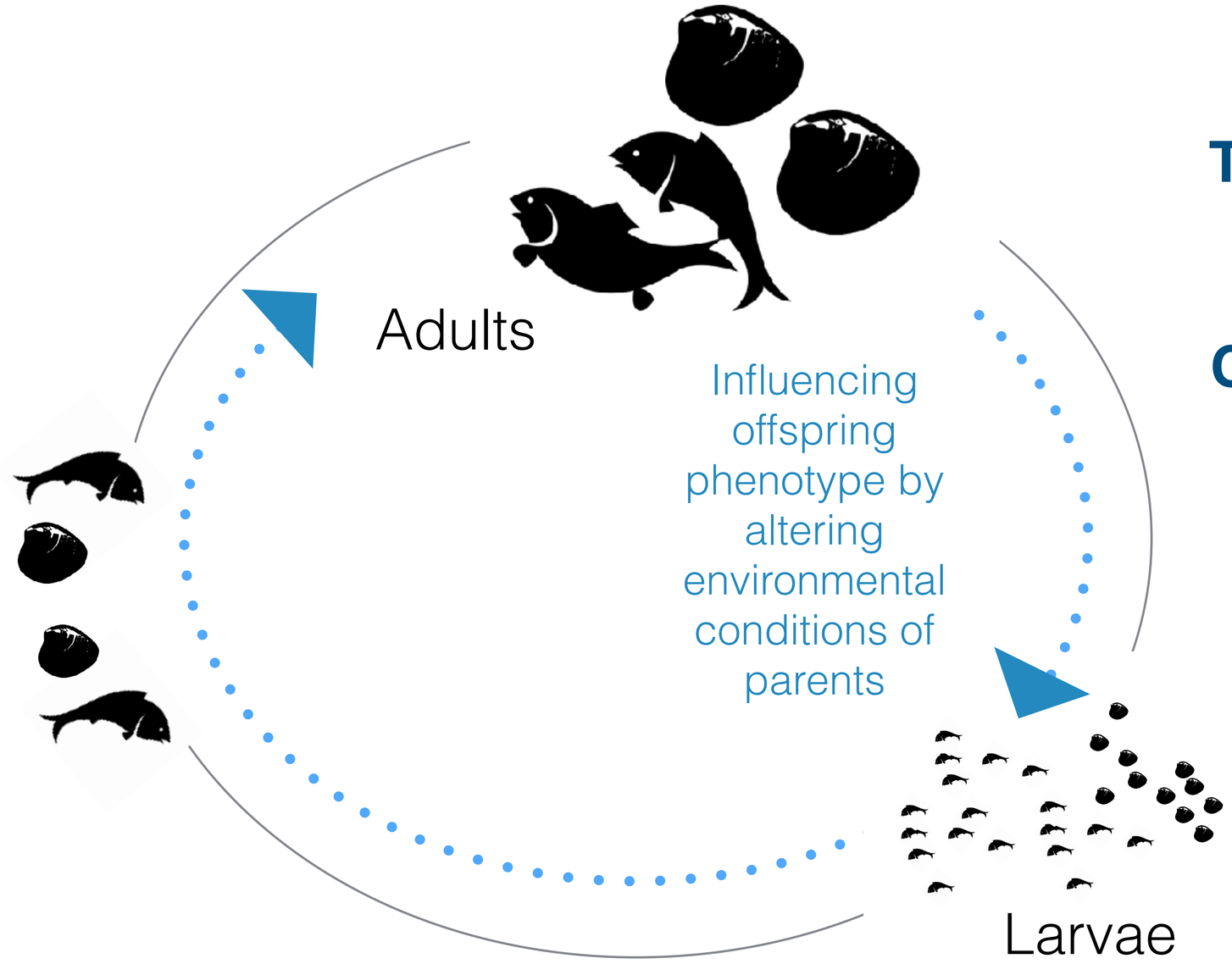
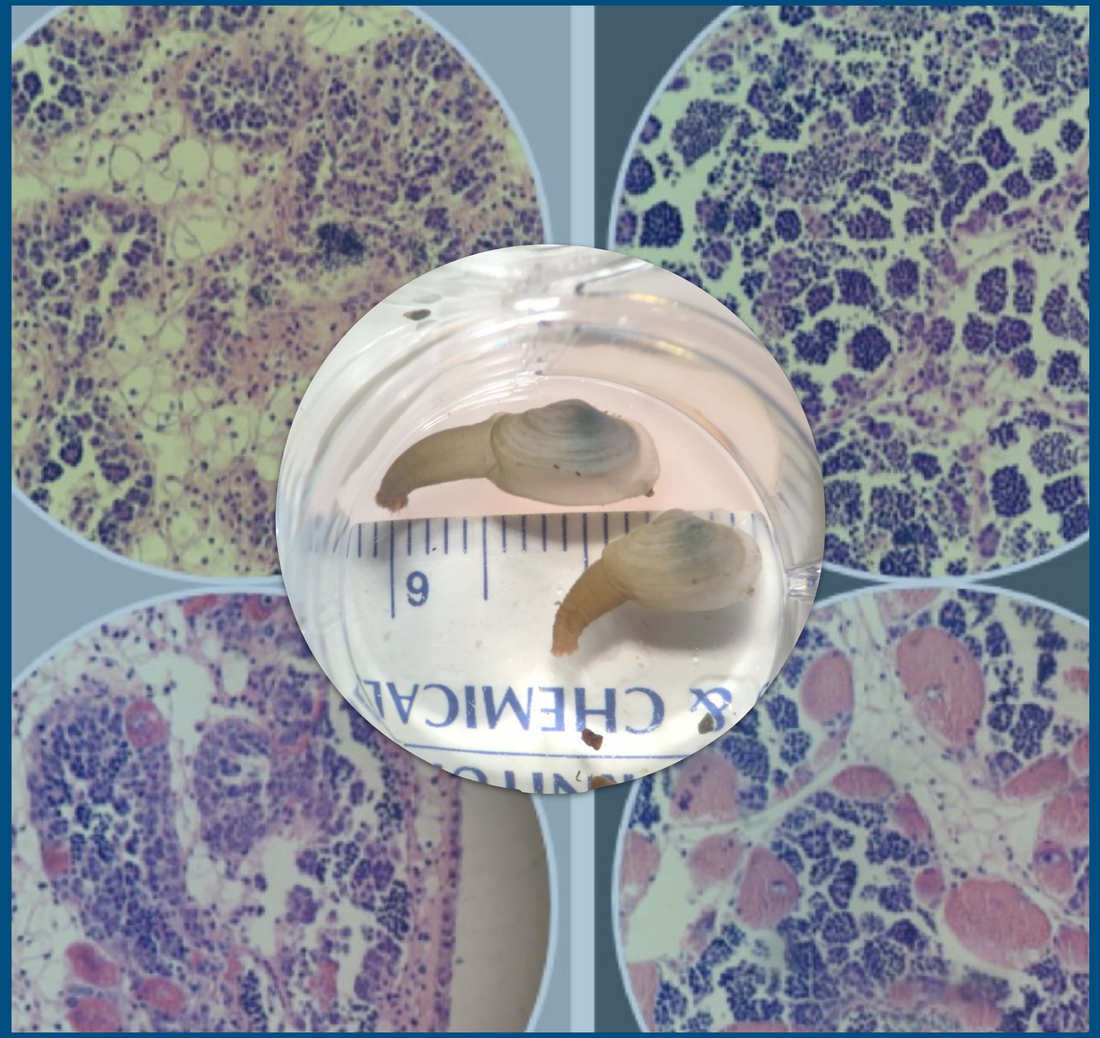


Transgenerational Plasticity

Carry-over effects

INFLUENCE OF PARENTAL CONDITIONS

- **Selection (various generations)**
- **Germ cells are present**
- **Maternal provisioning**
- **Paternal role?**
- **Beneficial** versus detrimental
- *Mechanisms at play*



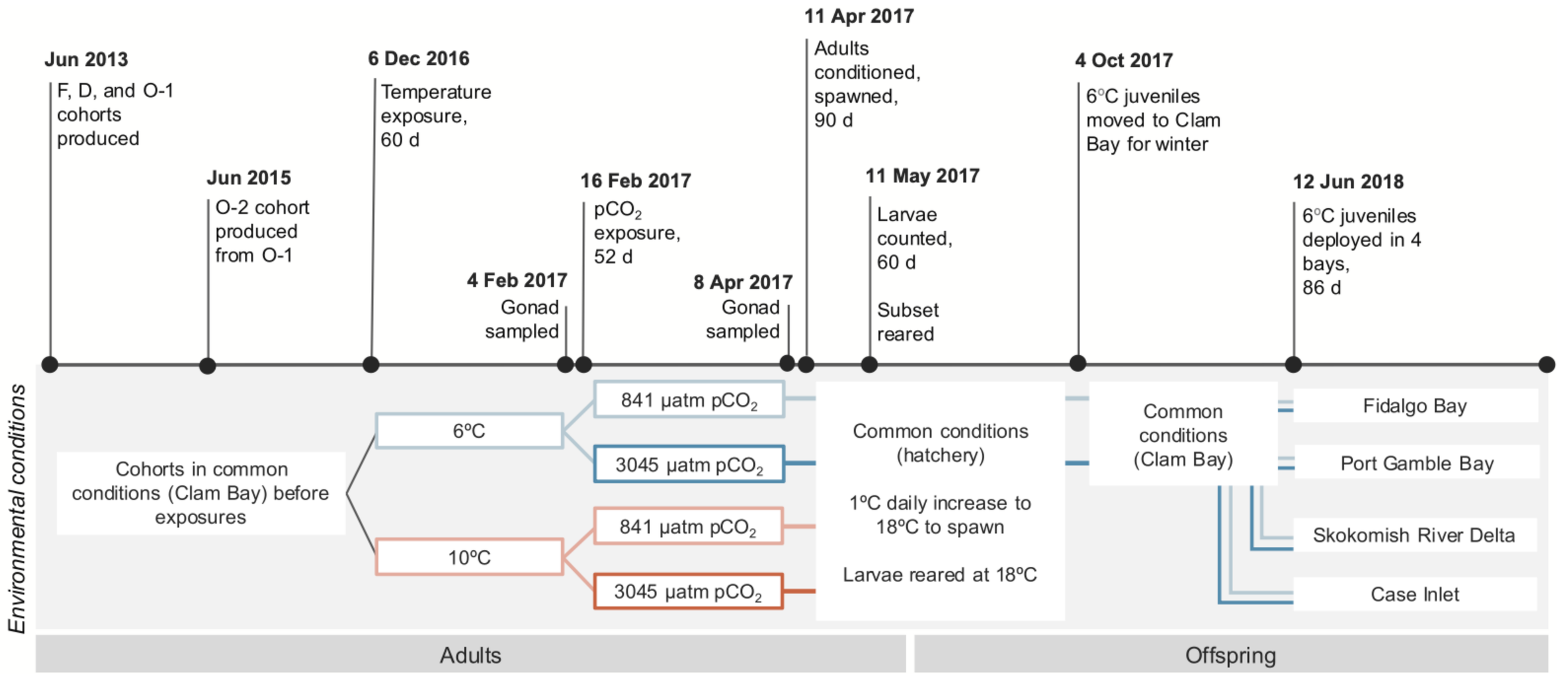
EFFECTS OF TEMPERATURE AND OA IN OLYMPIA OYSTER POPULATIONS

- Oysters were held at **two temperature regimes** (6°C and 10°C) for 60 days in December
- A differential pCO2 exposure was **carried out after the temperature treatment ended**. Held at ambient pCO2 (841 µatm) or high pCO2 (3045 µatm) for 52 days, during the Winter.

Carryover effects of temperature and pCO_2 across multiple Olympia oyster populations

Laura H. Spencer,[1] Yaamini R. Venkataraman,[1] Ryan Crim,[2] Stuart Ryan,[2] Micah J. Horwith,[3] and Steven B. Roberts[1,4]

TEXT


Jun 2013
F, D, and O-1 cohorts produced
Jun 2015
O-2 cohort produced from O-1
6 Dec 2016
Temperature exposure, 60 d
4 Feb 2017
Gonad sampled
16 Feb 2017
pCO2 exposure, 52 d
8 Apr 2017
Gonad sampled
11 Apr 2017
Adults conditioned, spawned, 90 d
11 May 2017
Larvae counted, 60 d
Subset reared
4 Oct 2017
6°C juveniles moved to Clam Bay for winter
12 Jun 2018
6°C juveniles deployed in 4 bays, 86 d
Environmental conditions
Cohorts in common conditions (Clam Bay) before exposures
6°C
10°C
841 µatm pCO2
3045 µatm pCO2
841 µatm pCO2
3045 µatm pCO2
Common conditions (hatchery)
1°C daily increase to 18°C to spawn
Larvae reared at 18°C
Common conditions (Clam Bay)
Fidalgo Bay
Port Gamble Bay
Skokomish River Delta
Case Inlet
Adults
Offspring

LAURA SPENCER

EFFECTS OF TEMPERATURE AND OA IN OLYMPIA OYSTER POPULATIONS

LAURA SPENCER

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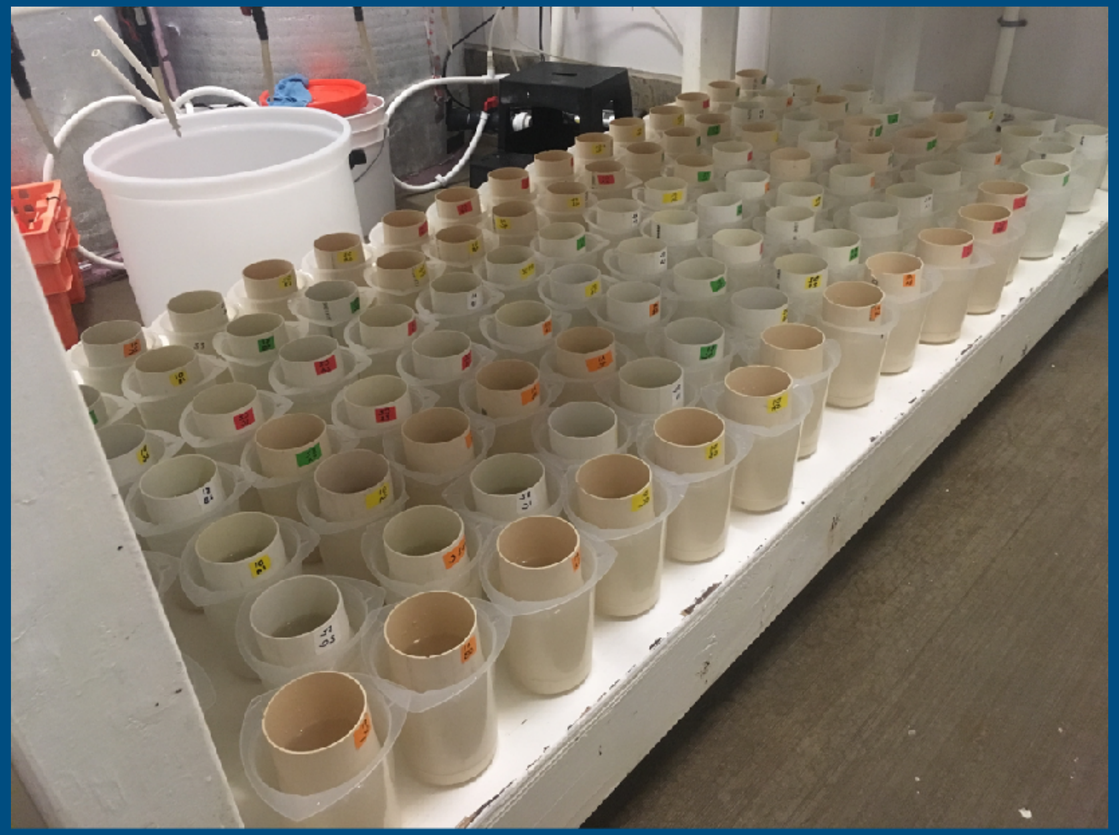
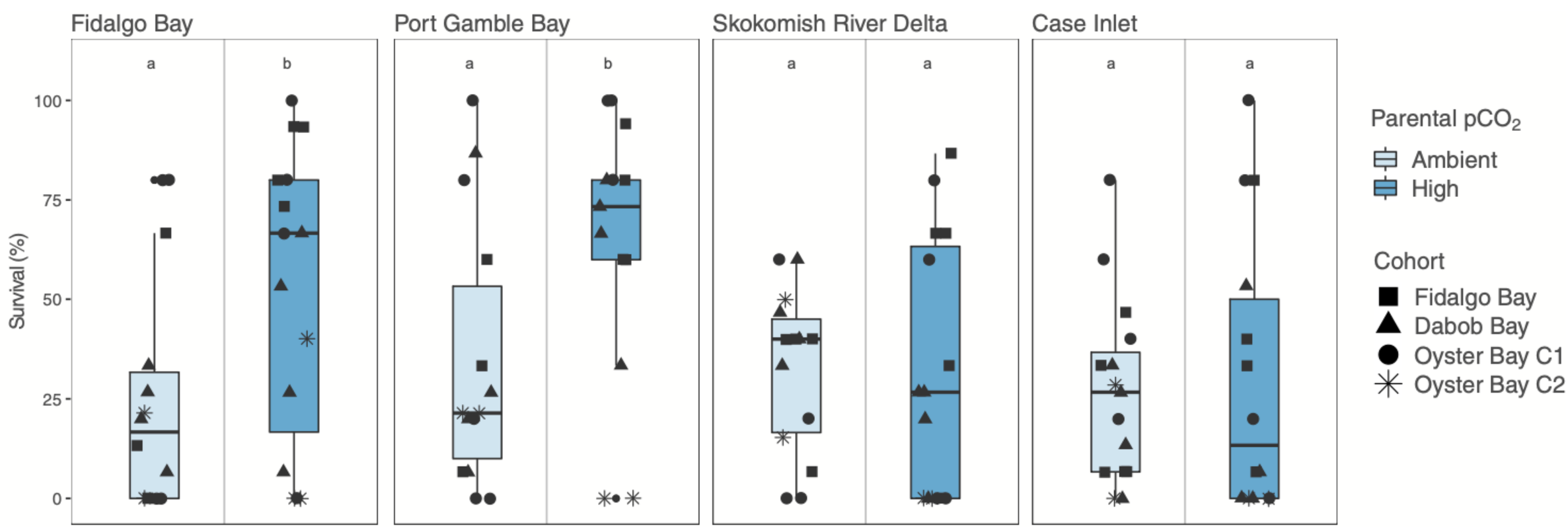


- Larval release occurred earlier in warm-exposed oysters
- Winter warming conditions increased larval production
- No effects on larval survival were detected
- **Juveniles of parents exposed to elevated pCO_2 had higher survival rates in the natural environment**

EFFECTS OF OA IN OLYMPIA OYSTER POPULATIONS



Eastern Oyster

LIMNOLOGY
and
OCEANOGRAPHY

ASLO

Limnol. Oceanogr. 67, 2022, 1732–1745

doi: 10.1002/lno.12162

Parental exposure of Eastern oysters (*Crassostrea virginica*) to elevated pCO_2 mitigates its negative effects on early larval shell growth and morphology

Elise M. McNally, * Alan M. Downey-Wall, F. Dylan Titmuss, Camila Cortina, Kathleen Lotterhos, Justin B. Ries

Department of Marine and Environmental Sciences, Marine Science Center, Northeastern University, Nahant, Massachusetts

Transgenerational plasticity in early larval shell growth and morphology, but not in survival, in response to the parental pCO2 exposure. Larvae from parents exposed to elevated pCO2 exhibited faster shell growth rates than larvae from control parents, with this effect being signicantly larger when larvae were grown under elevated pCO2

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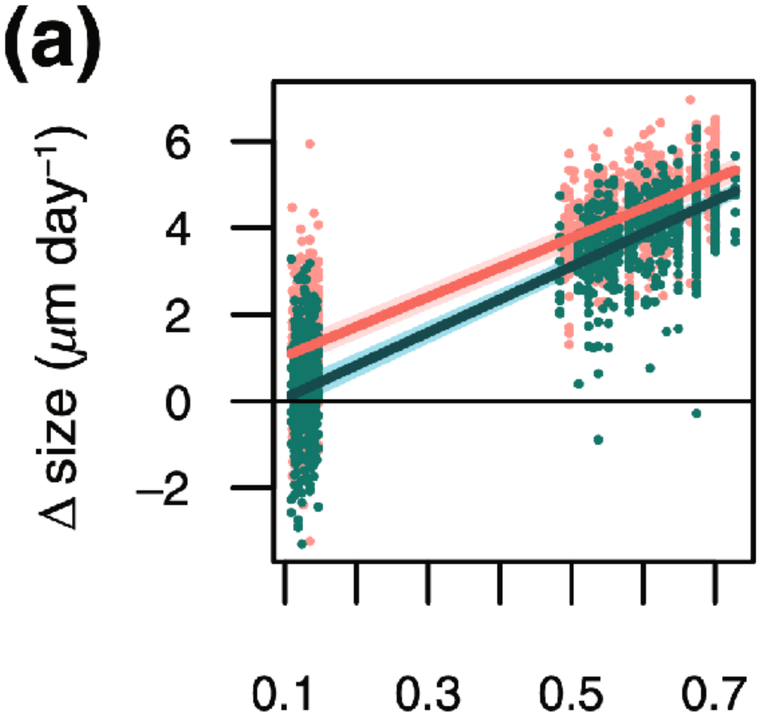

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Environmental Memory

CAN BE BENEFICIAL
STAGE DEPENDENT
ACROSS GENERATION
IMPLICATIONS . . .

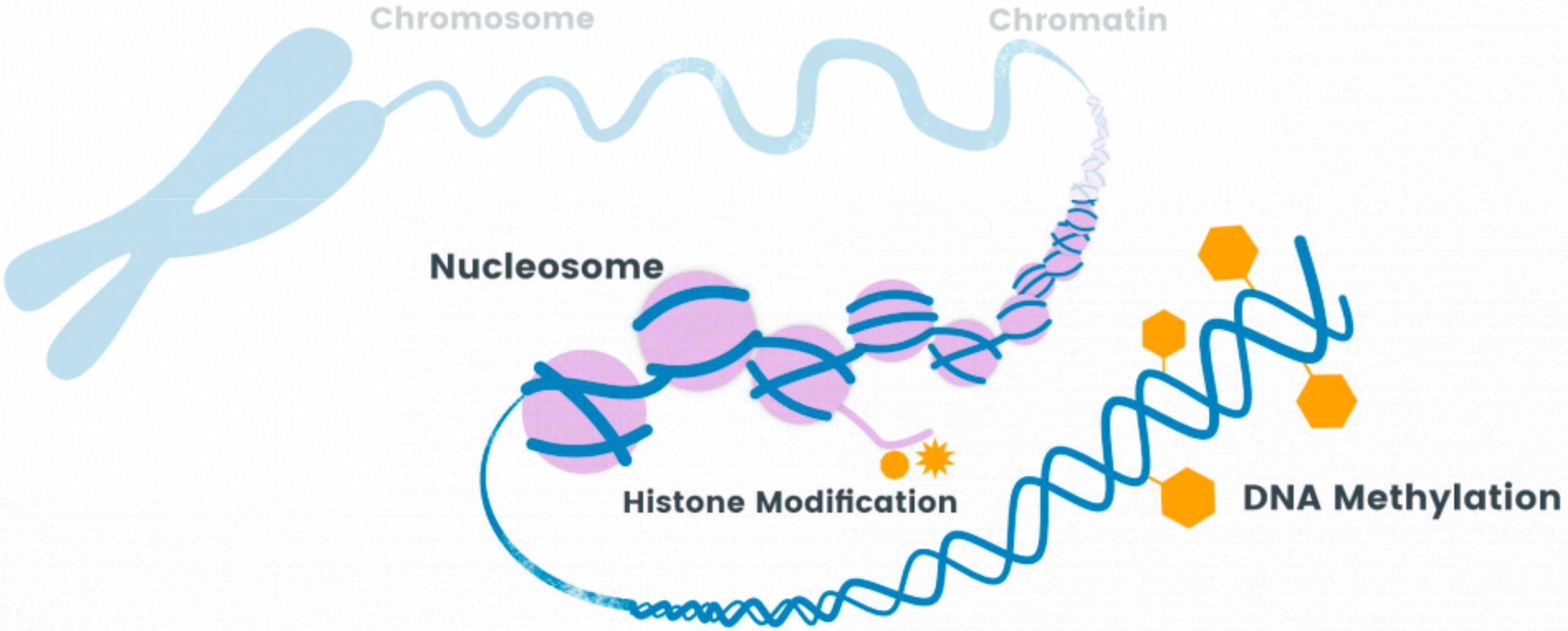
Environmental Memory

CAN BE BENEFICIAL STAGE DEPENDENT ACROSS GENERATION IMPLICATIONS . . .

Epigenetic Mechanisms

Epigenetics

ALTERS THE PHENOTYPE (WITHOUT CHANGING DNA CODE); HERITABLE



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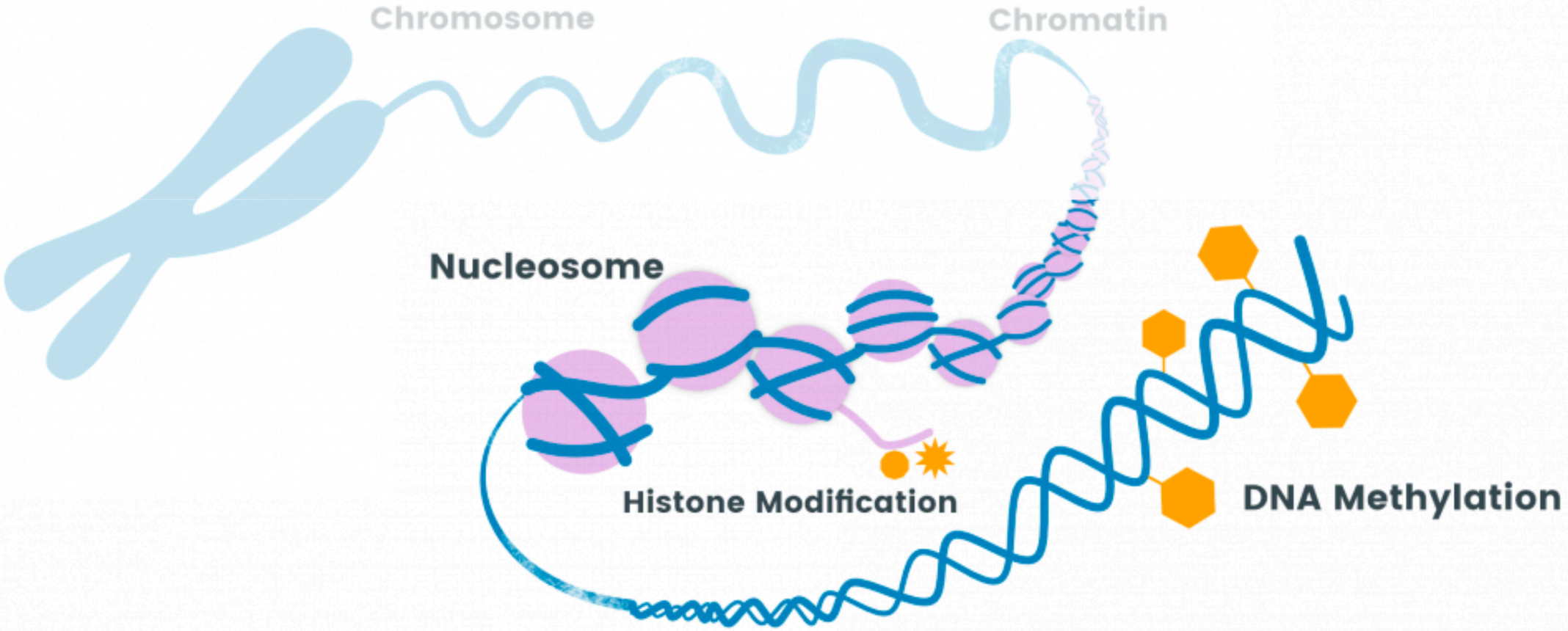
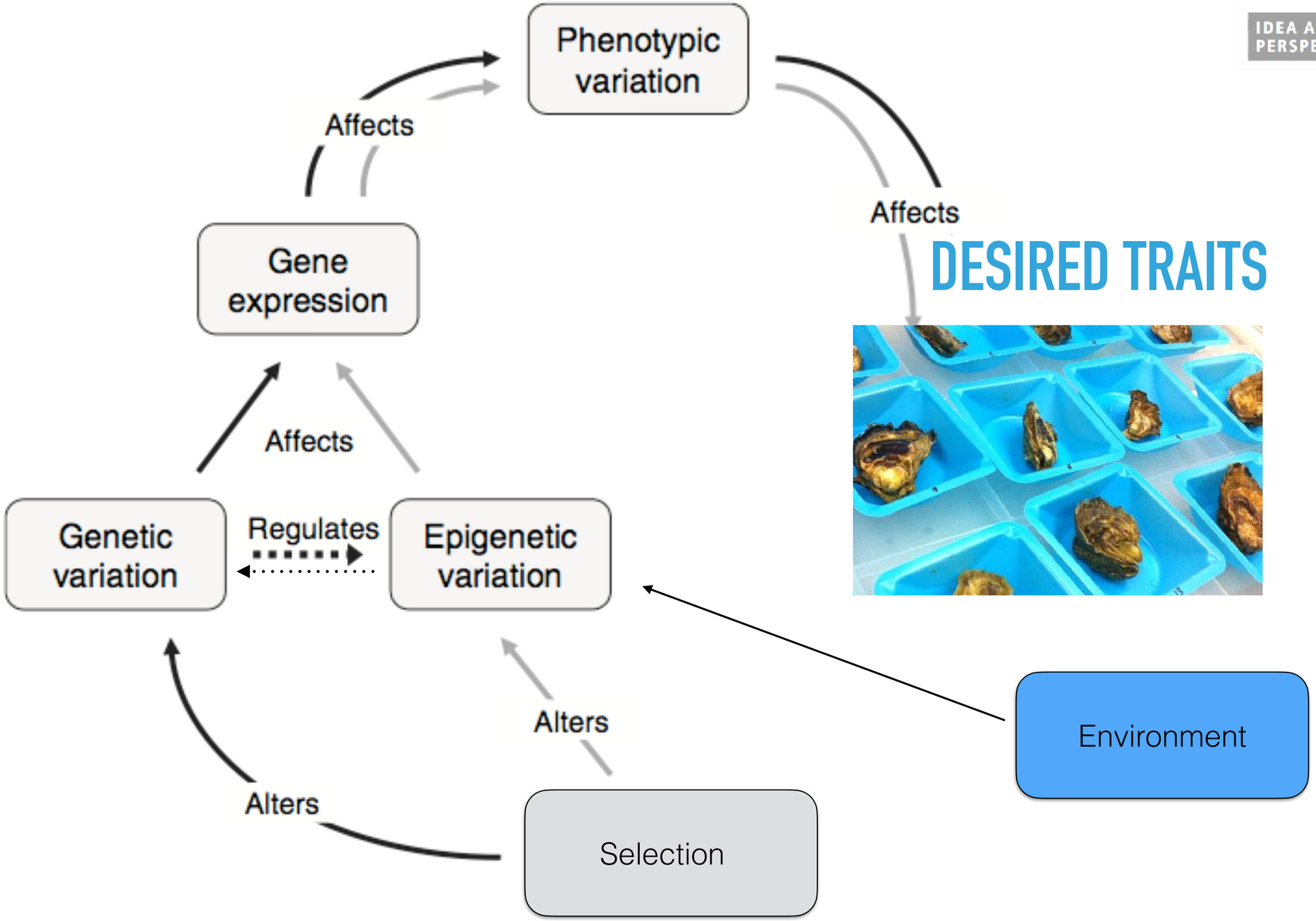


CAN BE INDUCED WITH ENVIRONMENTAL MANIPULATION

ECOLOGICAL EPIGENETICS

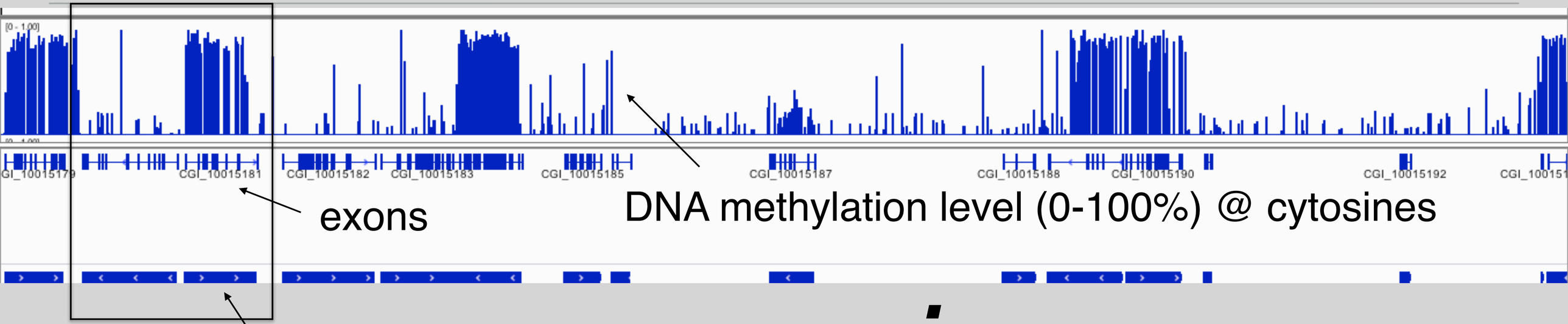


Ecology Letters, (2008) **11**: 106–115 doi: 10.1111/j.1461-0248.2007.01130.x

IDEA AND PERSPECTIVE

Epigenetics for ecologists

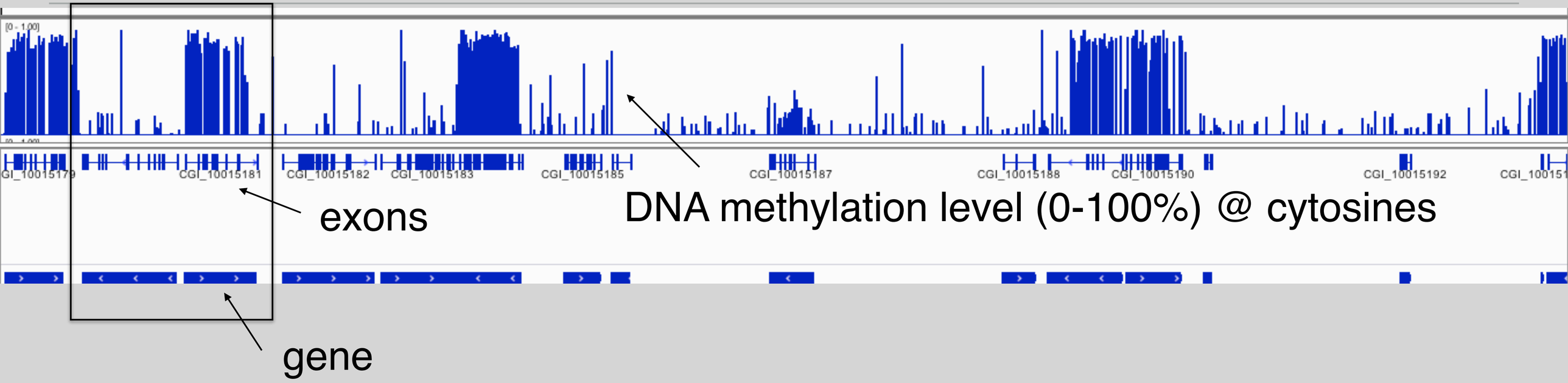
DESIRED TRAITS

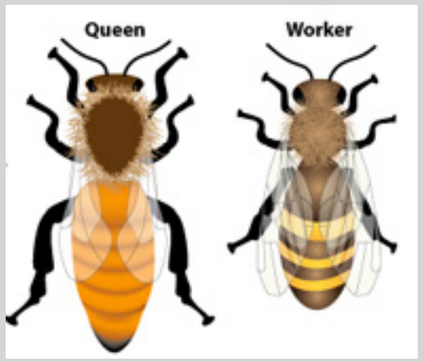


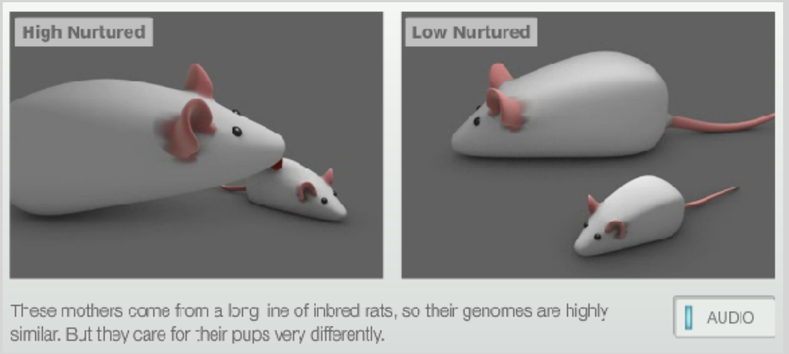
mosaic

associated with gene bodies

METHYLATION LANDSCAPE IN MARINE INVERTEBRATES







Four Dimensionalities

Targeted Regulation

Stochastic Regulation

Reliable Transcription

Spurious Transcription

Four Dimensionalities

- Evolutionary
- Life History Driven
- Constitutive

Four Dimensionalities

- Distinct Lineage
- Experiential
- Inducible

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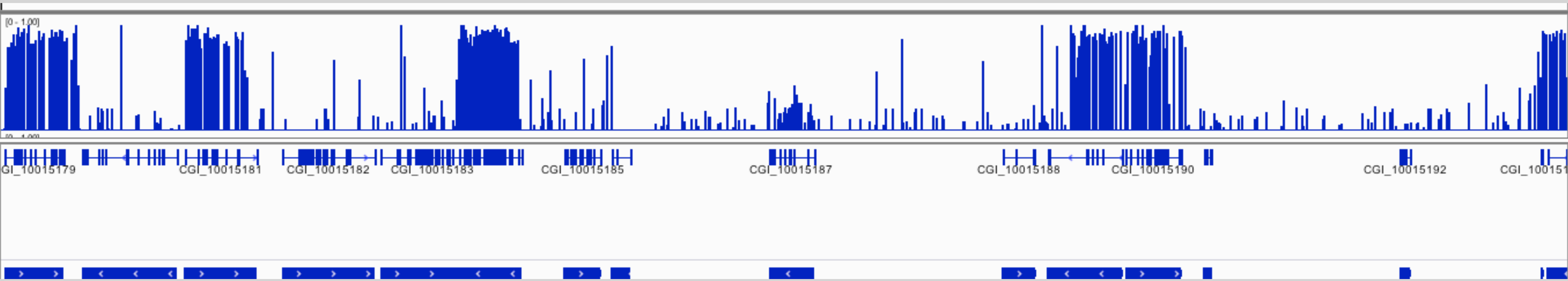

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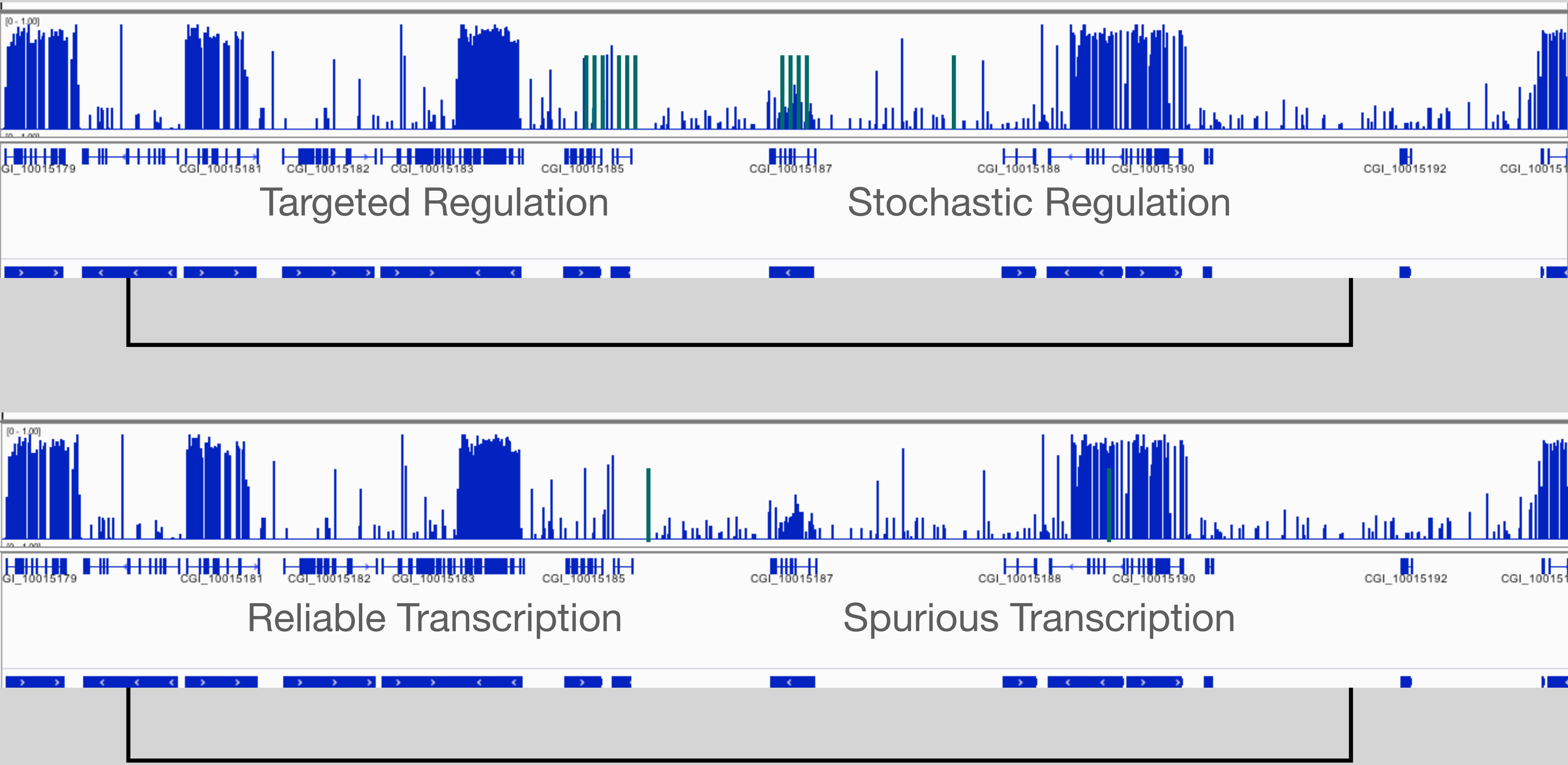

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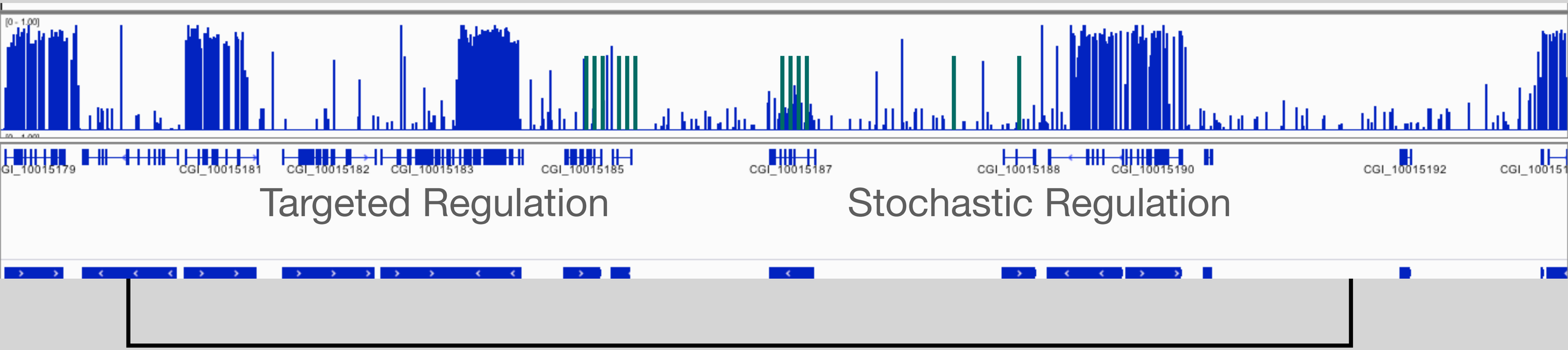

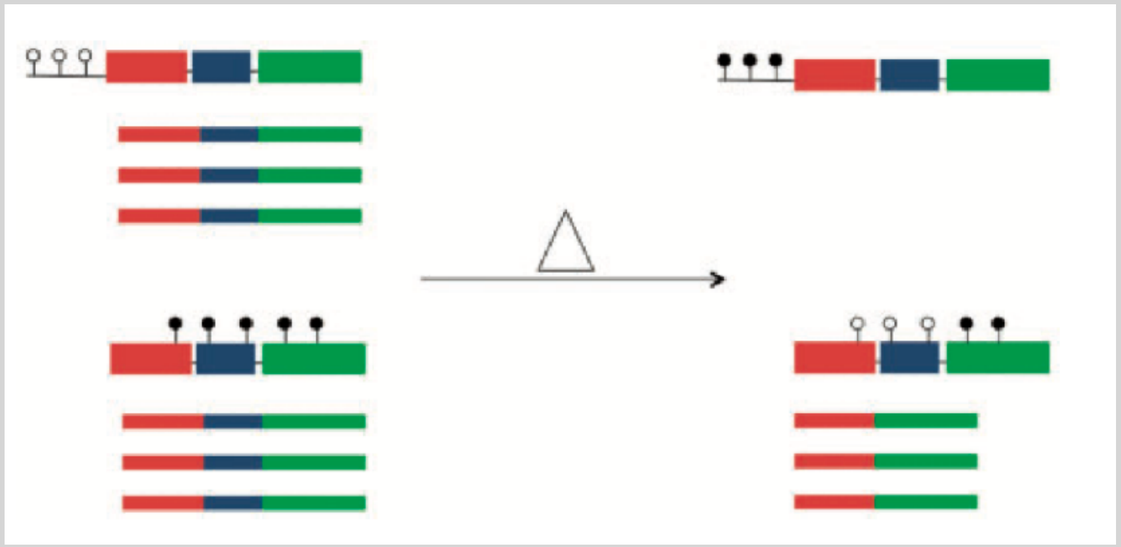

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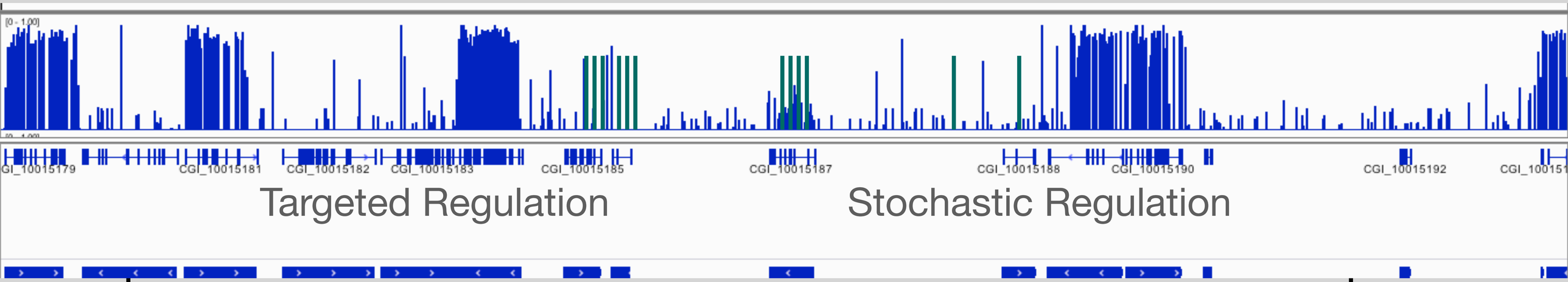

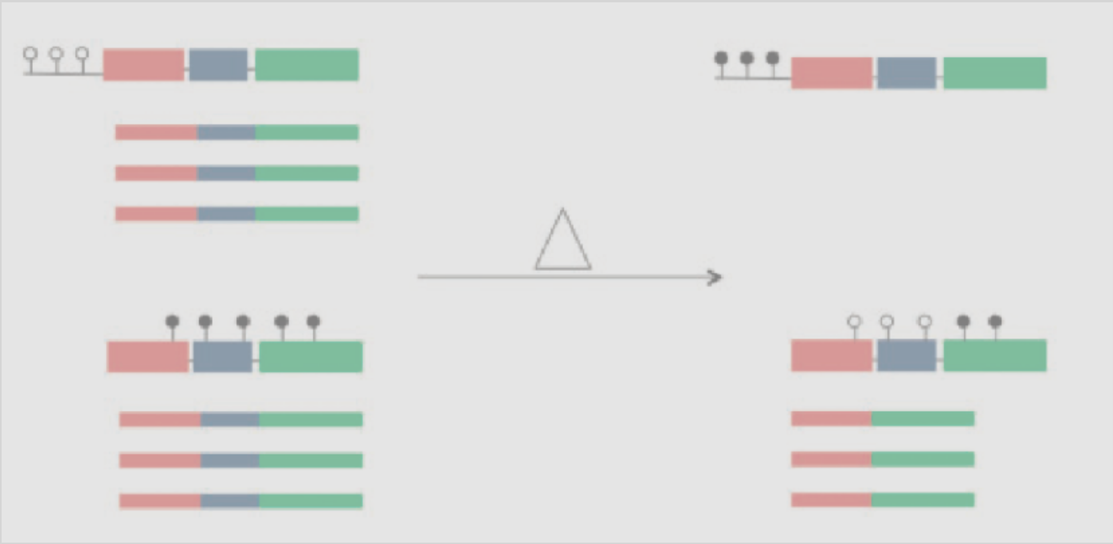

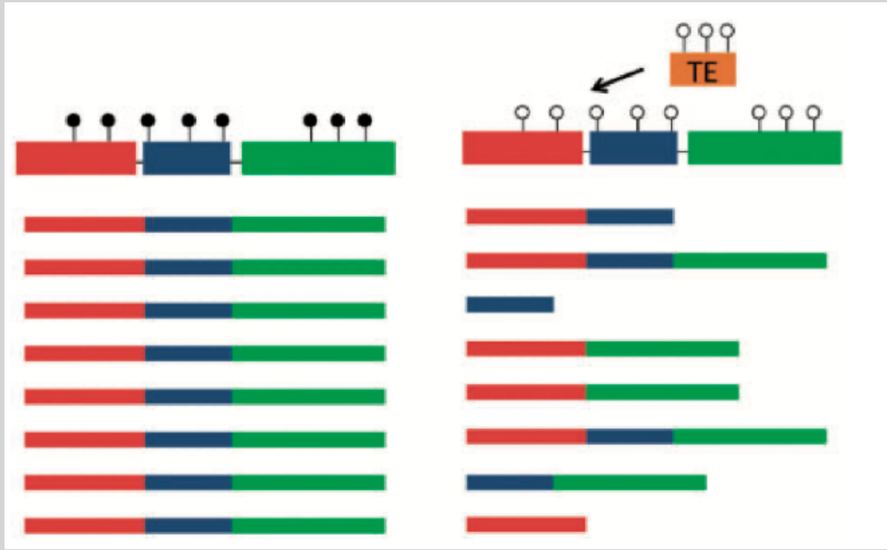

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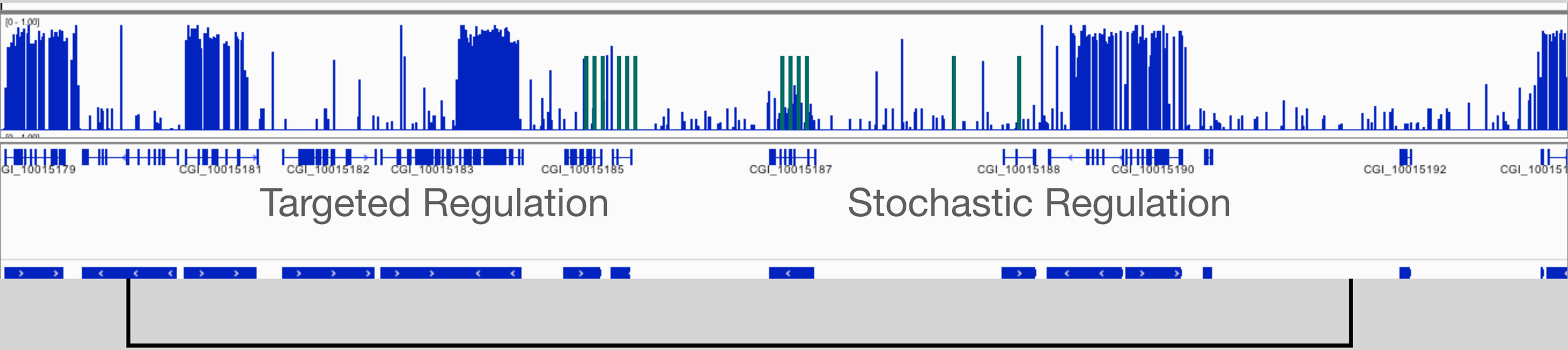
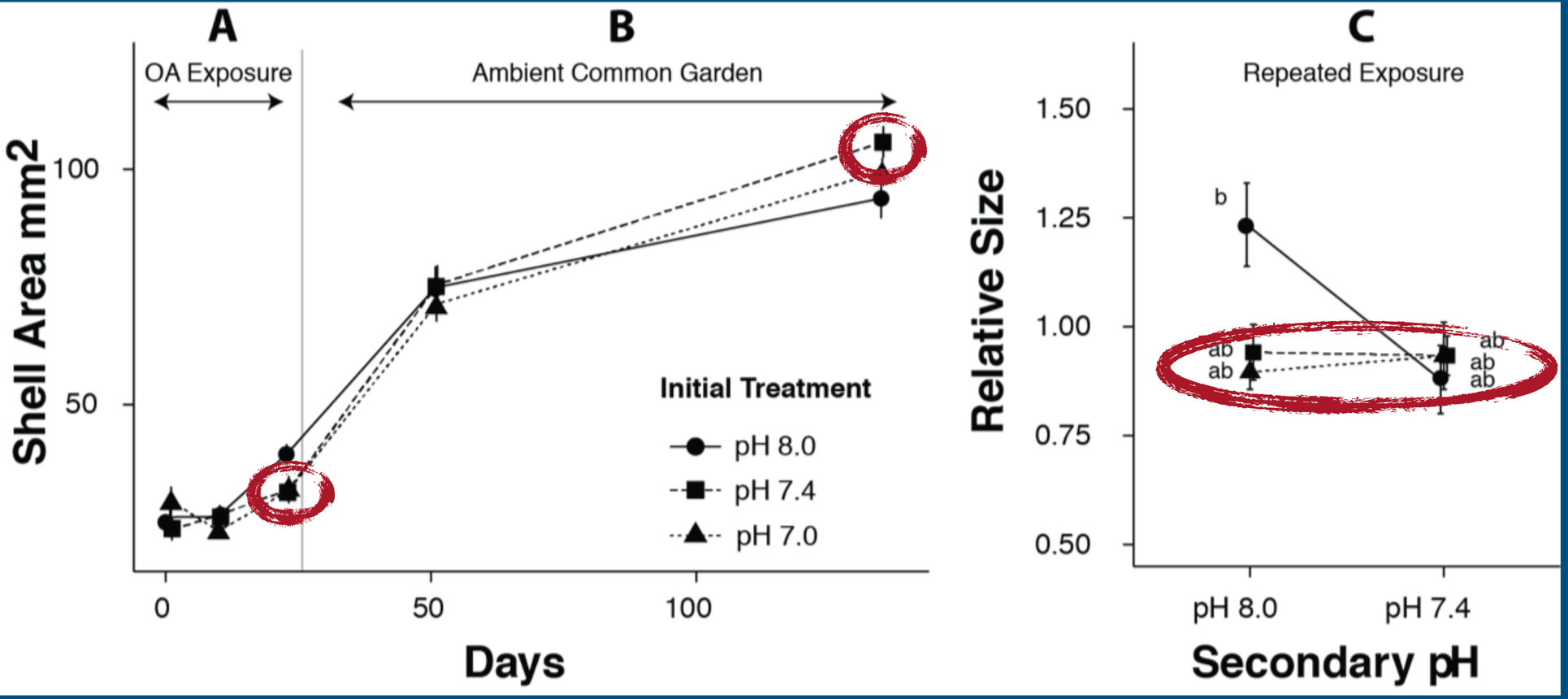


We ***do not*** see correlation of differential expressed genes and differential methylation patterns

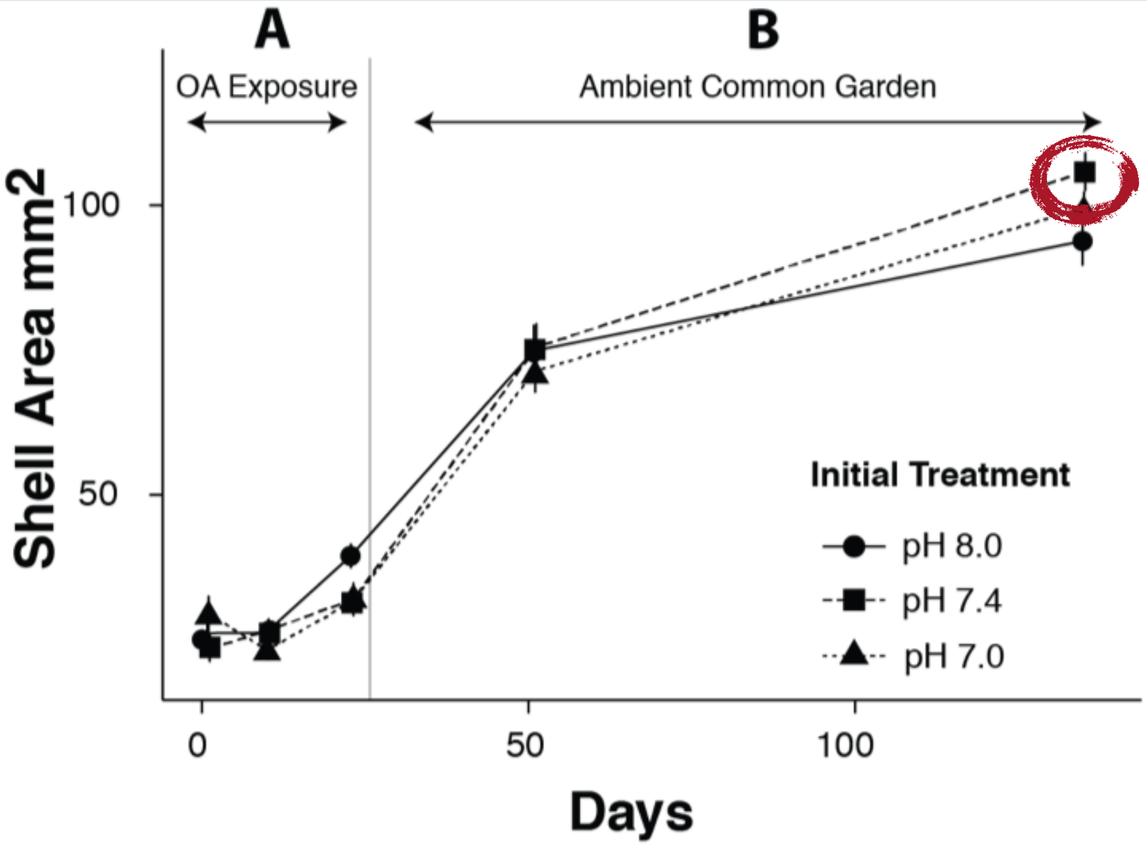
GEODUCKS AND OA

- Does conditioning to low pH confer tolerance within a generation?

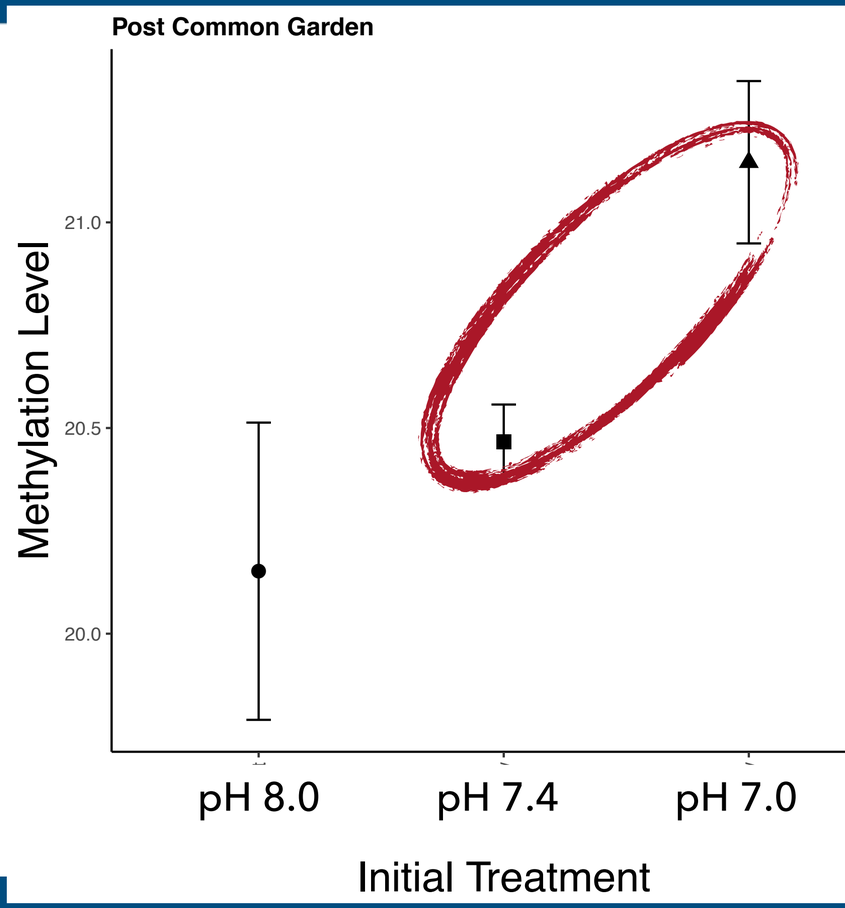


HOLLIE PUTNAM AND RICK GOETZ

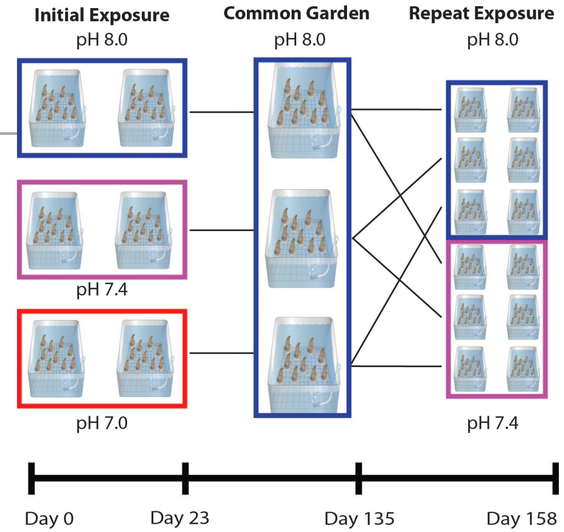
GEODUCKS AND OA

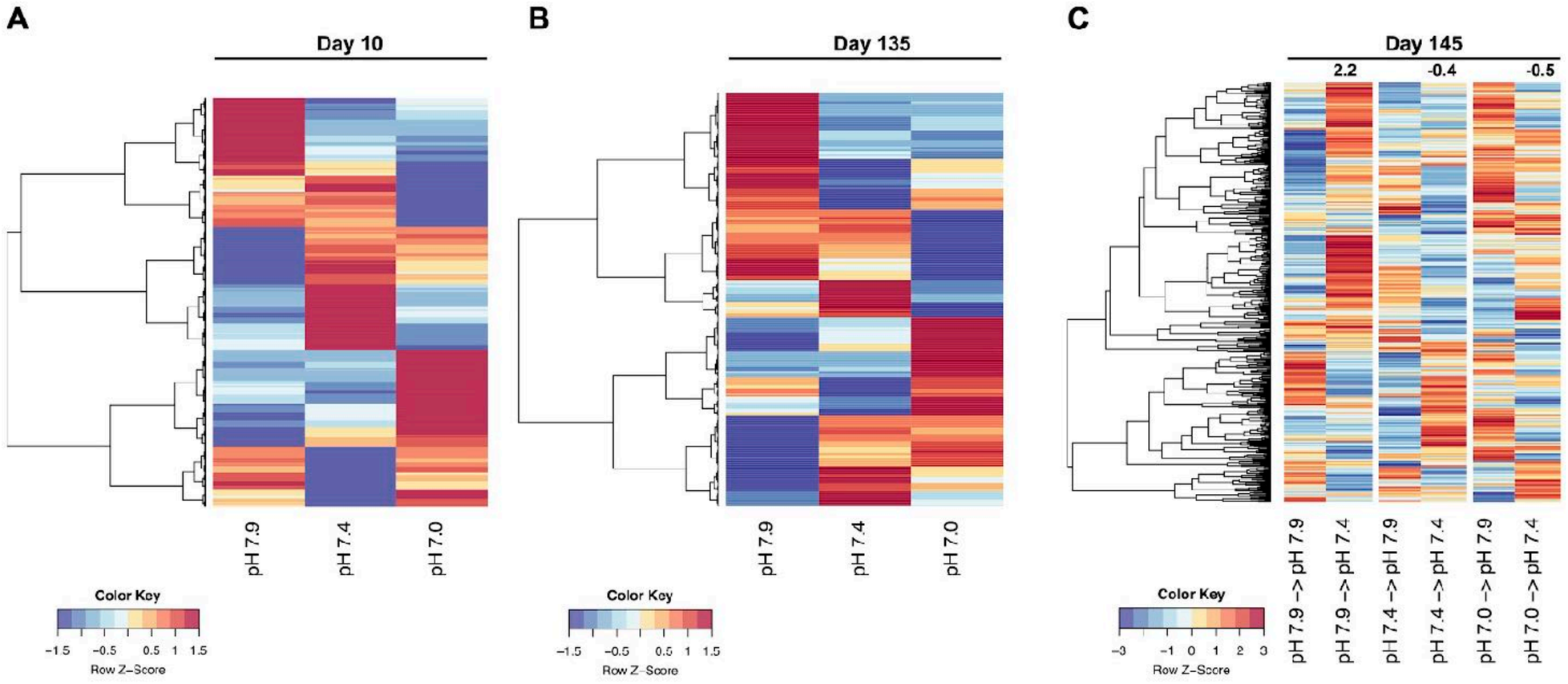


DNA METHYLATION



GEODUCKS AND OA





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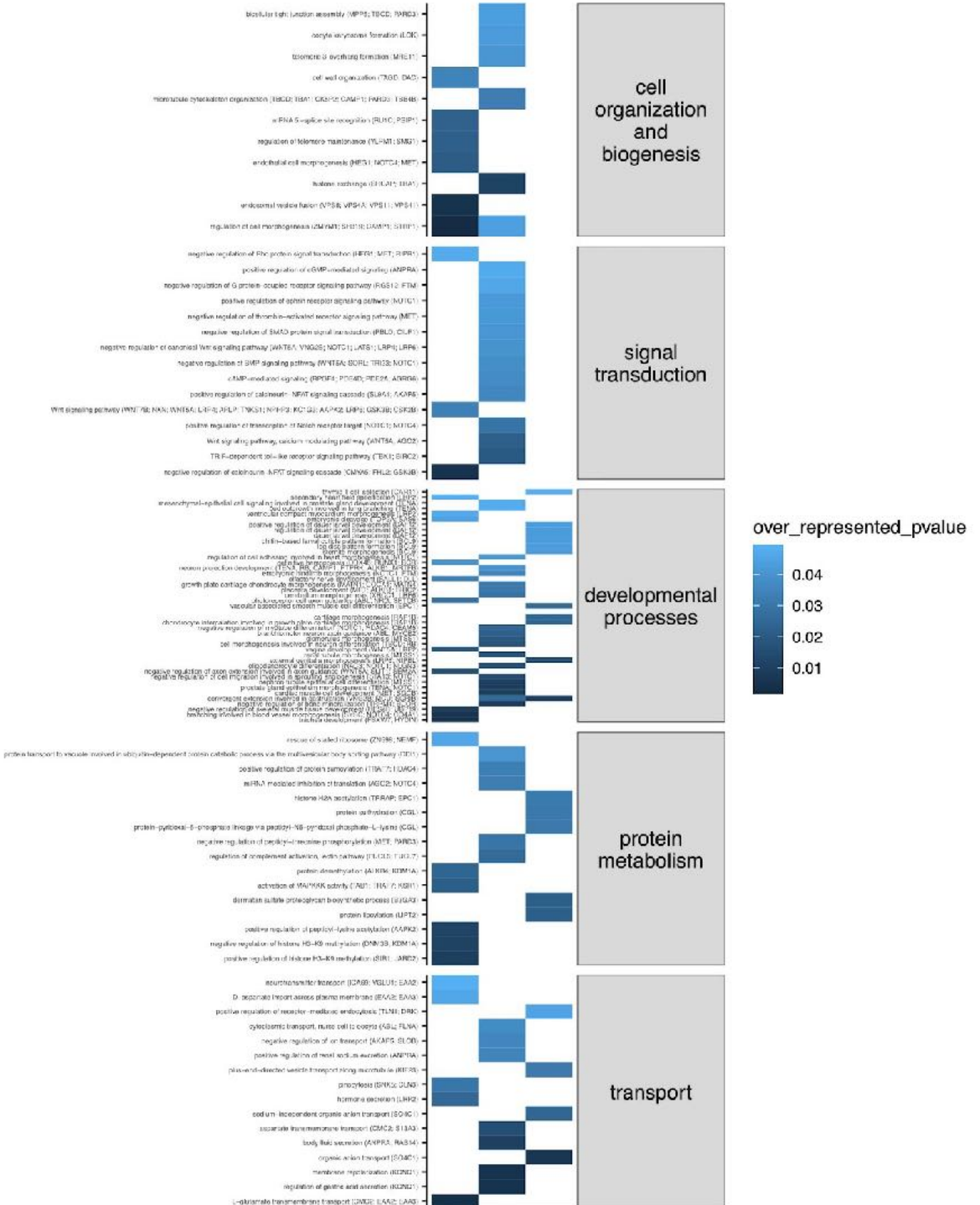

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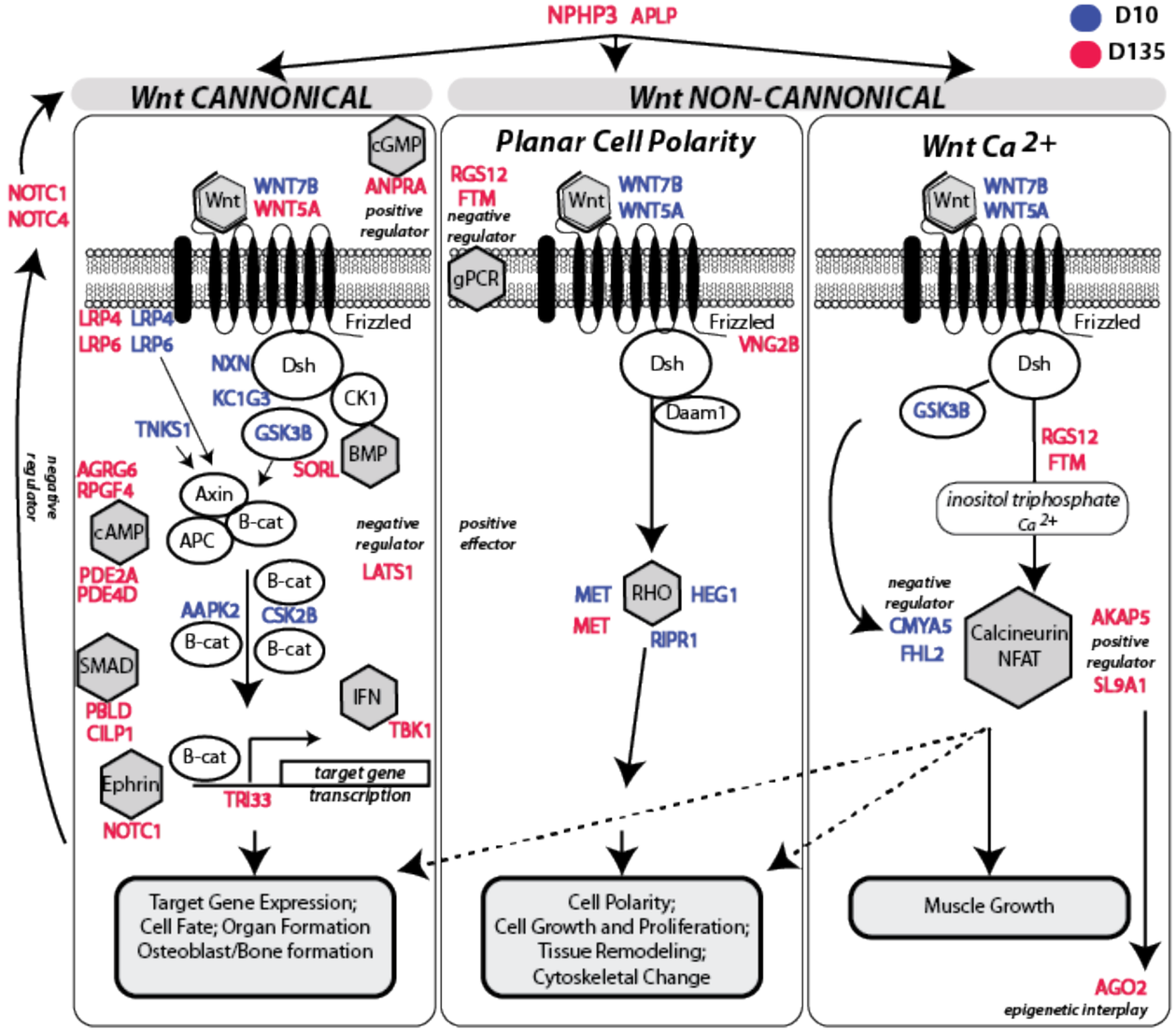
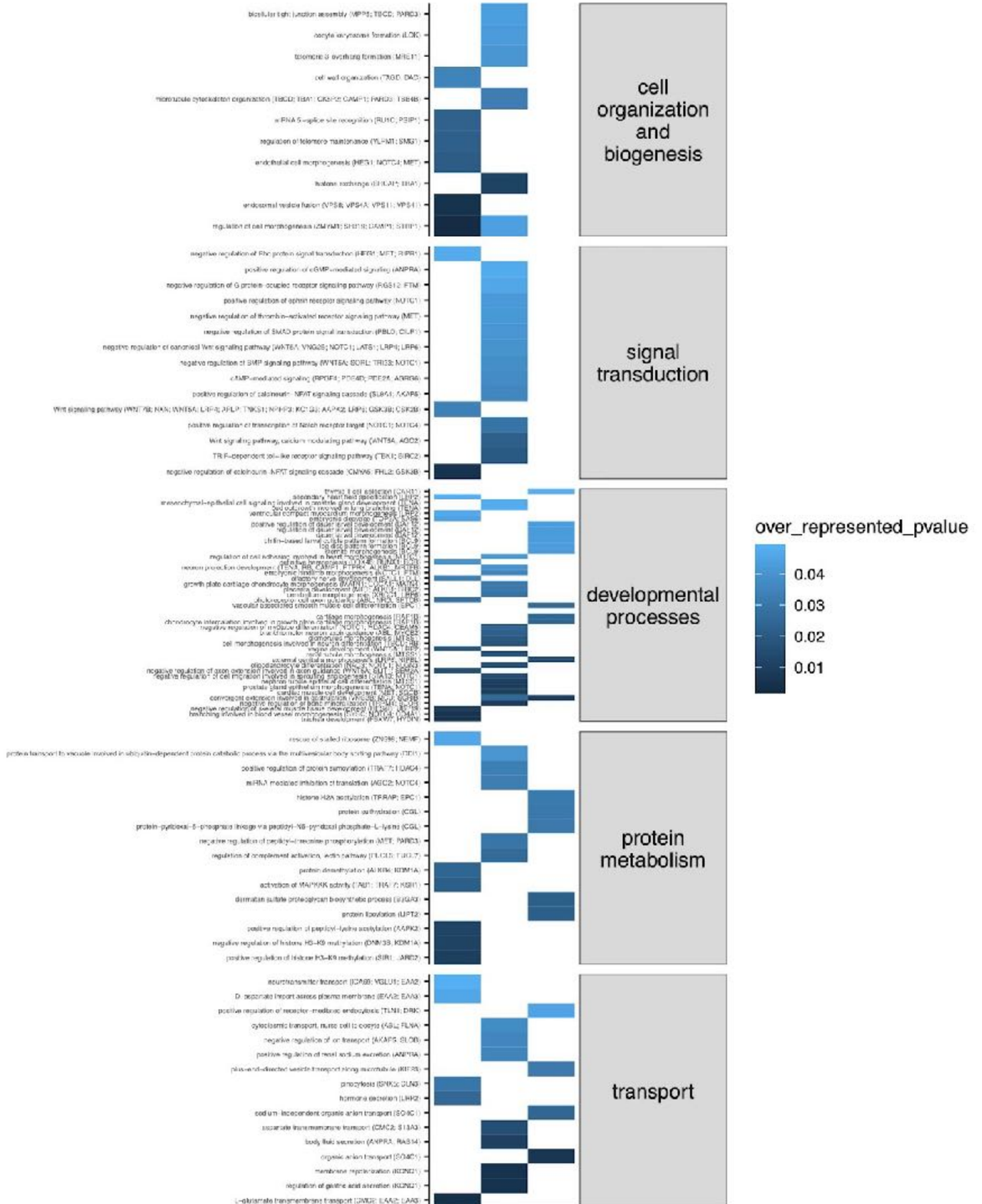
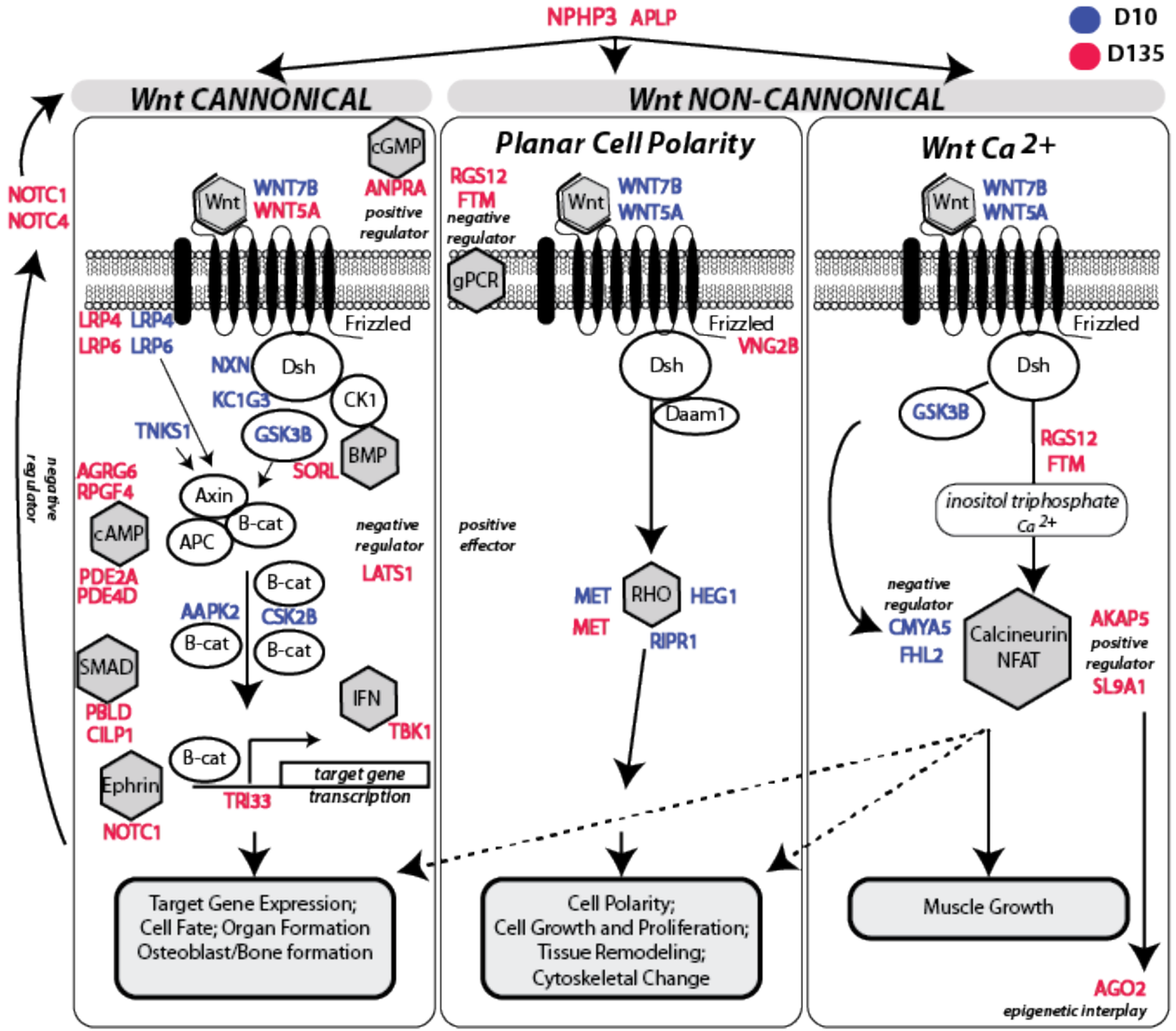




GEODUCKS AND OA



New Results

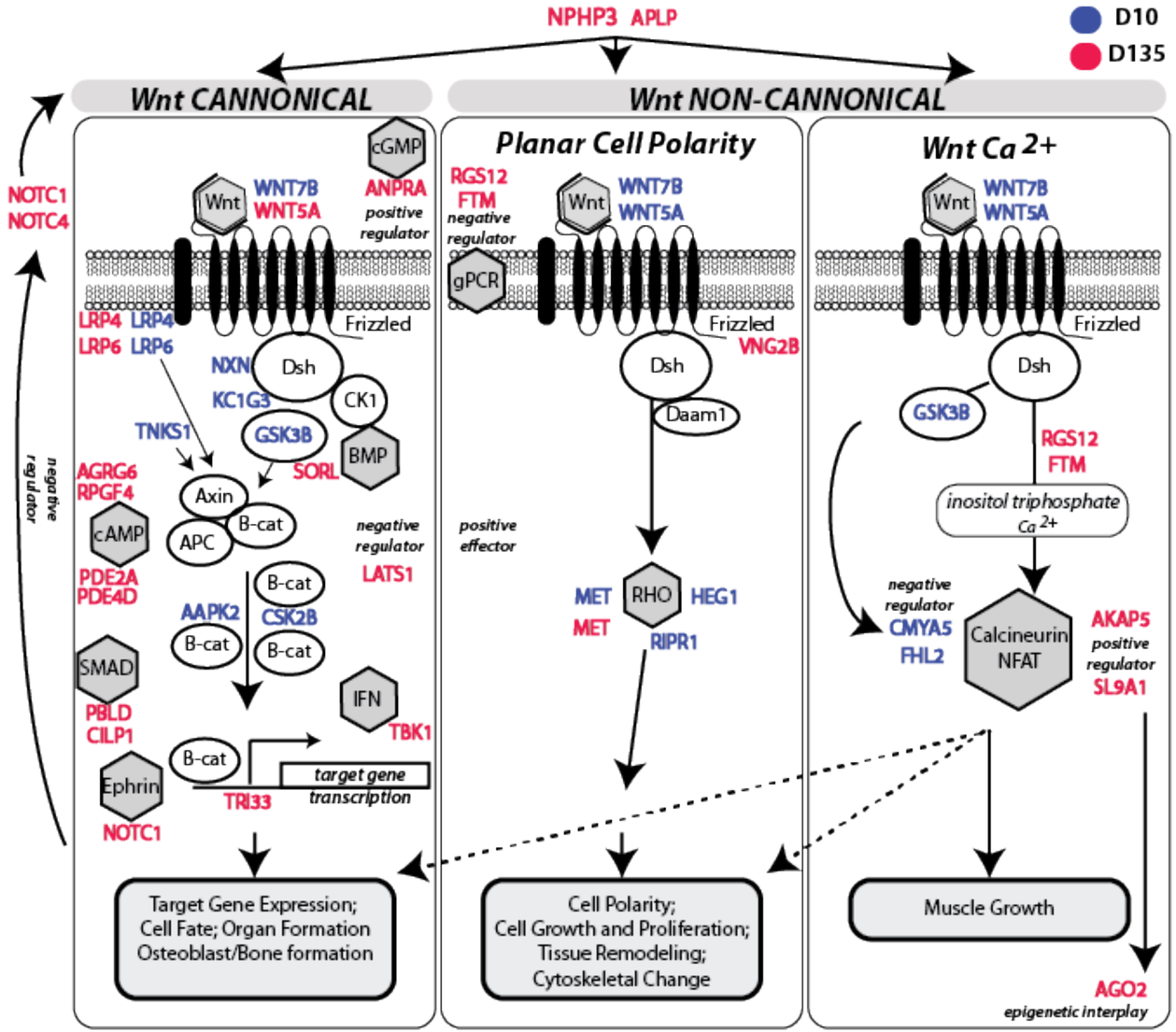
Follow this preprint

Dynamic DNA methylation contributes to carryover effects and beneficial acclimatization in geoduck clams

Hollie M. Putnam, Shelly A. Trigg, Samuel J. White, Laura H. Spencer, Brent Vadopalas, Aparna Natarajan, Jonathan Hetzel, Erich Jaeger, Jonathan Soohoo, Cristian Gallardo-Escárate, Frederick W. Goetz, Steven B. Roberts

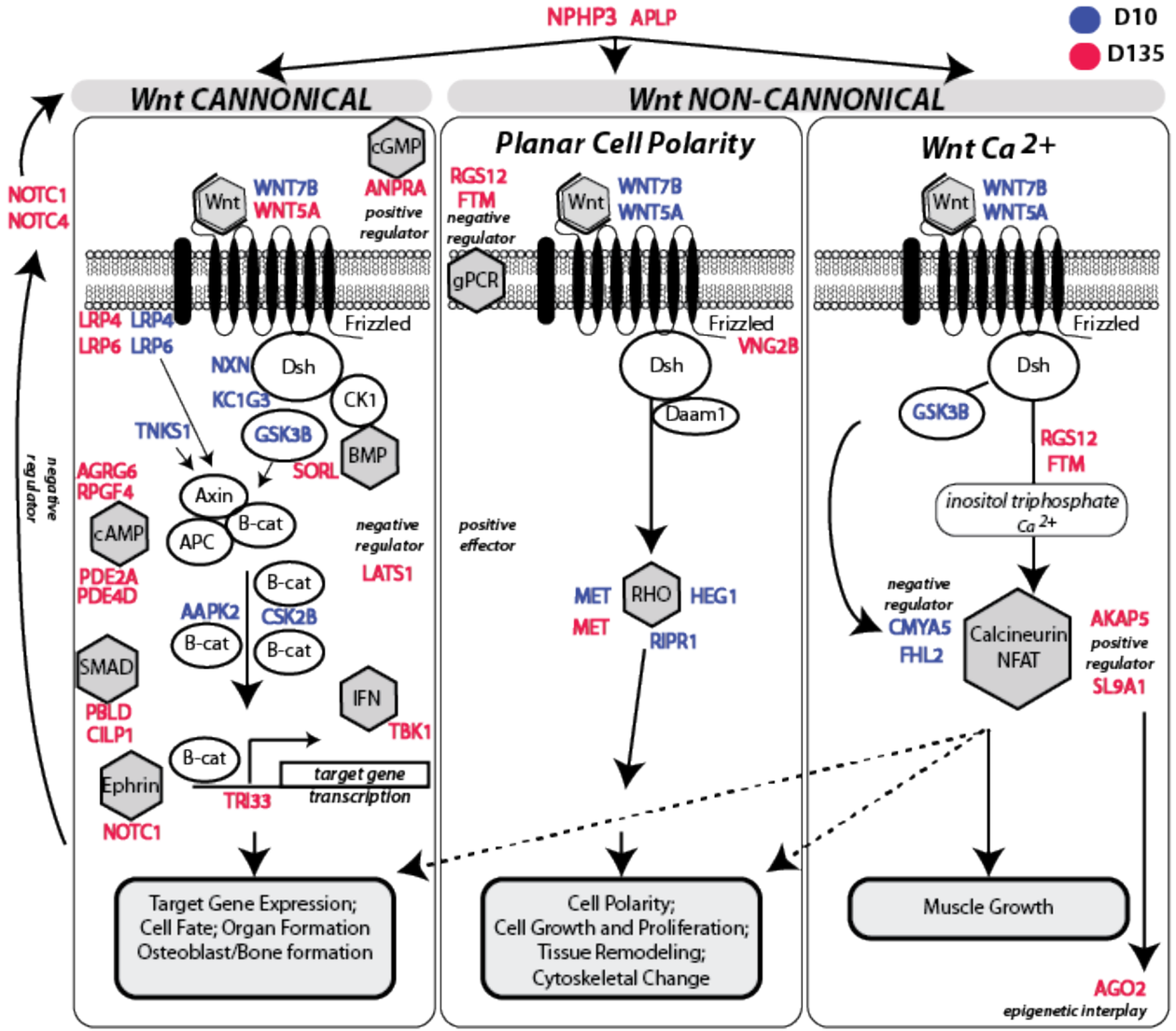
doi: https://doi.org/10.1101/2022.06.24.497506

GEODUCKS AND OA



Following four months of ambient common-garden conditions, **juveniles initially exposed to low pH compensatorily grew larger**, with DNA methylation indicative of these phenotypic differences, demonstrating epigenetic carryover effects persisted months after initial exposure.

GEODUCKS AND OA



Functional enrichment analysis of differentially methylated genes revealed regulation of signal transduction through widespread changes in the **Wnt signaling pathways that influence cell growth, proliferation, tissue and skeletal formation, and cytoskeletal change.**

EPIGENETIC MECHANISM INVOLVED?

LIMNOLOGY and OCEANOGRAPHY

ASLO

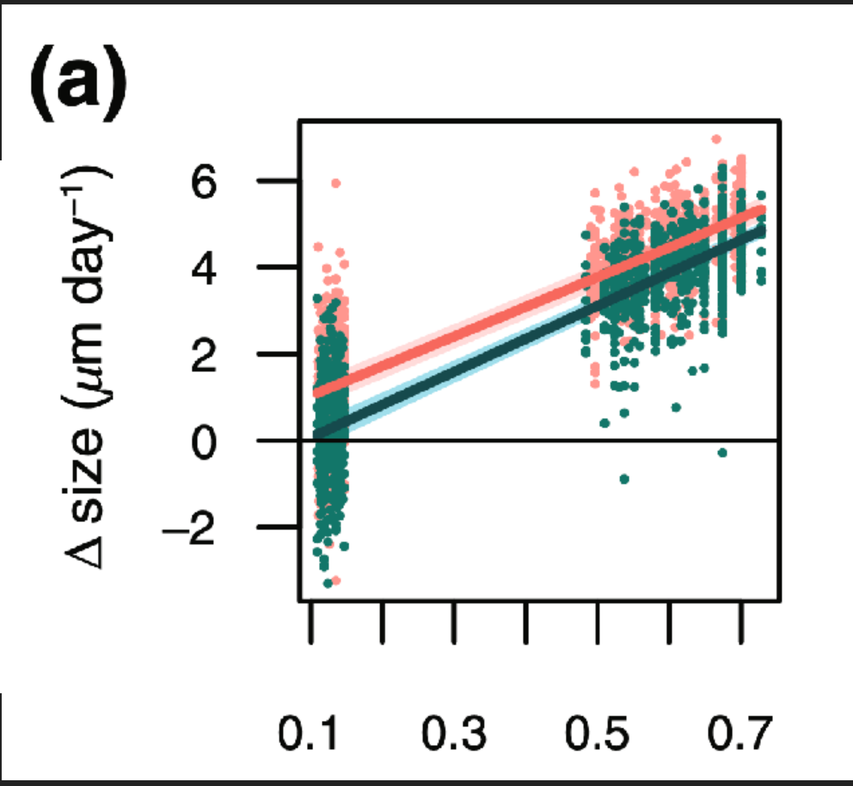
Limnol. Oceanogr. 67, 2022, 1732–1745

doi: 10.1002/lno.12162

Parental exposure of Eastern oysters (*Crassostrea virginica*) to elevated pCO_2 mitigates its negative effects on early larval shell growth and morphology

Elise M. McNally,* Alan M. Downey-Wall, F. Dylan Titmuss, Camila Cortina, Kathleen Lotterhos, Justin B. Ries

Department of Marine and Environmental Sciences, Marine Science Center, Northeastern University, Nahant, Massachusetts



EPIGENETIC MECHANISM INVOLVED?

DNA methylation correlates with transcriptional noise in response to elevated pCO_2 in the eastern oyster (*Crassostrea virginica*)

Yaamini R. Venkataraman[1]*, Ariana S. Huffmyer[2,3], Samuel J. White[2], Alan Downey-Wall[4], Jill Ashey[3], Danielle M. Becker[3], Zachary Bengtsson[2], Hollie M. Putnam[3], Emma Strand[3,5], Javier A. Rodríguez-Casariego[6], Shelly A. Wanamaker[5], Kathleen E. Lotterhos[7], Steven B. Roberts[2]

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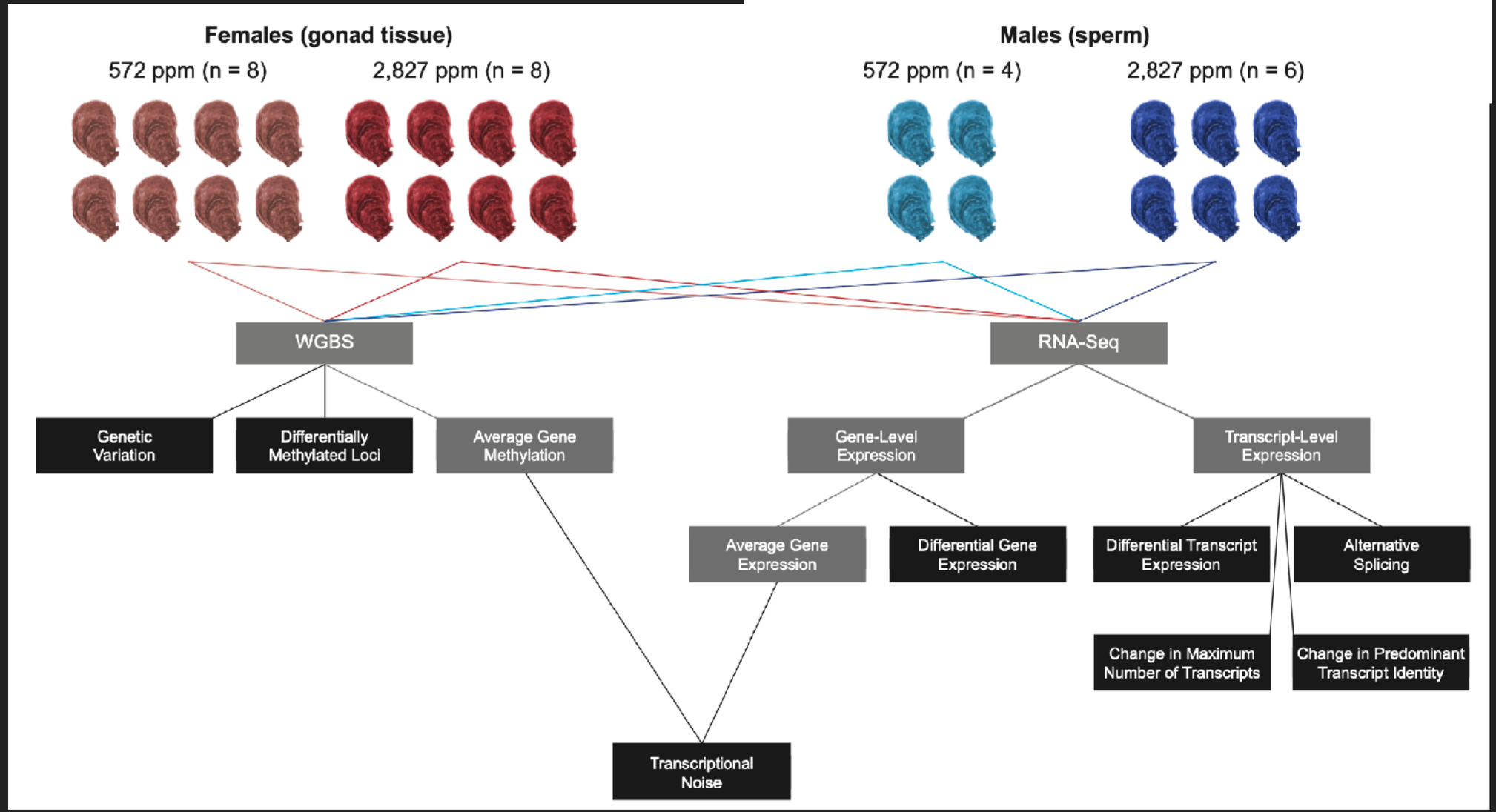

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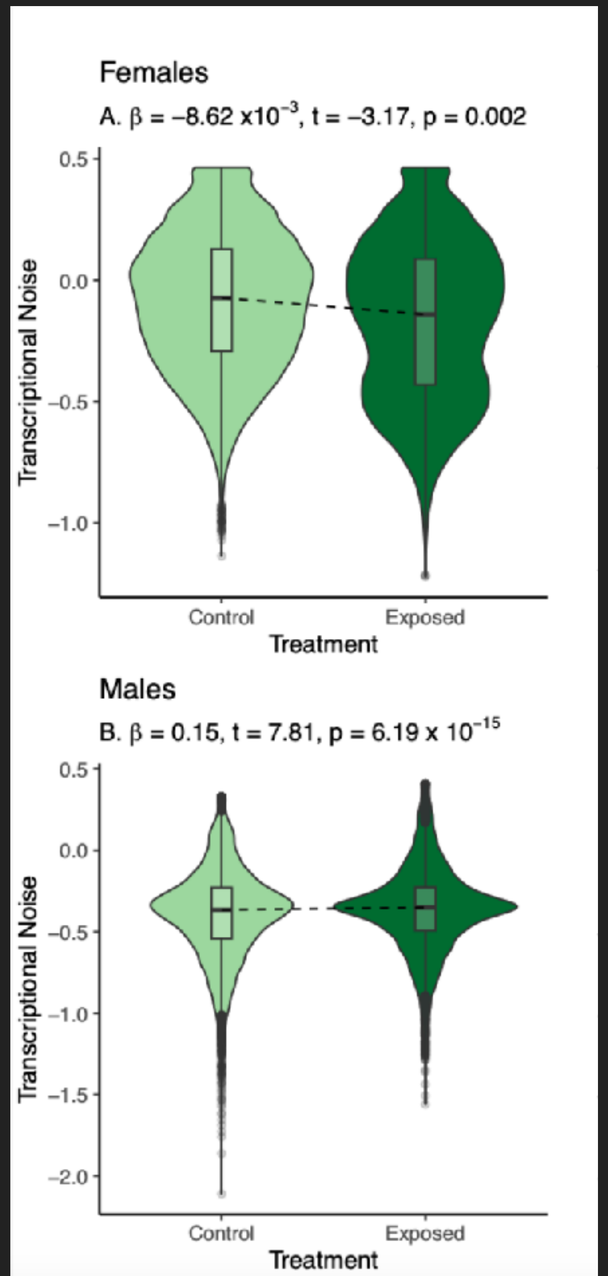
Gene body methylation impacts maximum number of transcripts expressed per gene and changes in the predominant transcript expressed. Elevated pCO2 exposure increased gene expression variability (transcriptional noise) in males but decreased noise in females, suggesting a sex-specific role of methylation in gene expression regulation.

VENKATARAMAN: DNA METHYLATION CORRELATES WITH TRANSCRIPTIONAL NOISE



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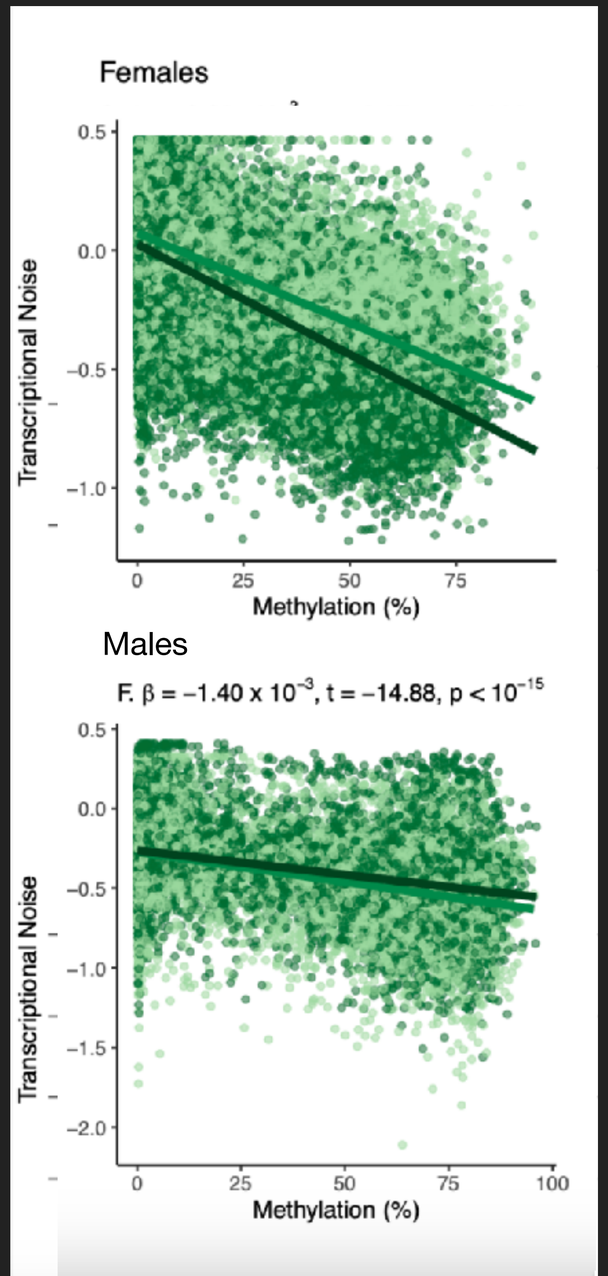

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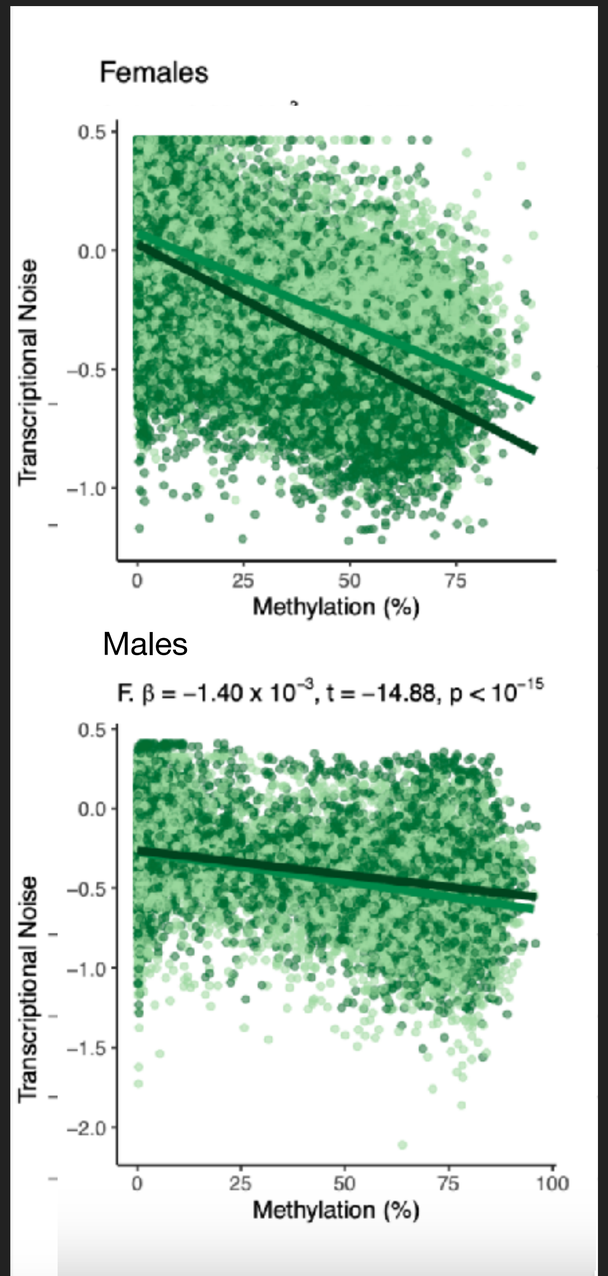

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Methylation has a genome-wide regulatory role, effectively maintaining gene expression homeostasis in reproductive tissues under elevated pCO2 by reducing transcriptional noise.

The relationship between methylation and transcriptional noise was different between female reproductive tissue and sperm: male oysters required higher levels of methylation to achieve similar reductions in transcriptional noise when compared to female oysters.

Epigenetic maintenance of reproduction could confer intergenerational resilience to environmental perturbations.

VENKATARAMAN: DNA METHYLATION CORRELATES WITH TRANSCRIPTIONAL NOISE

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Males

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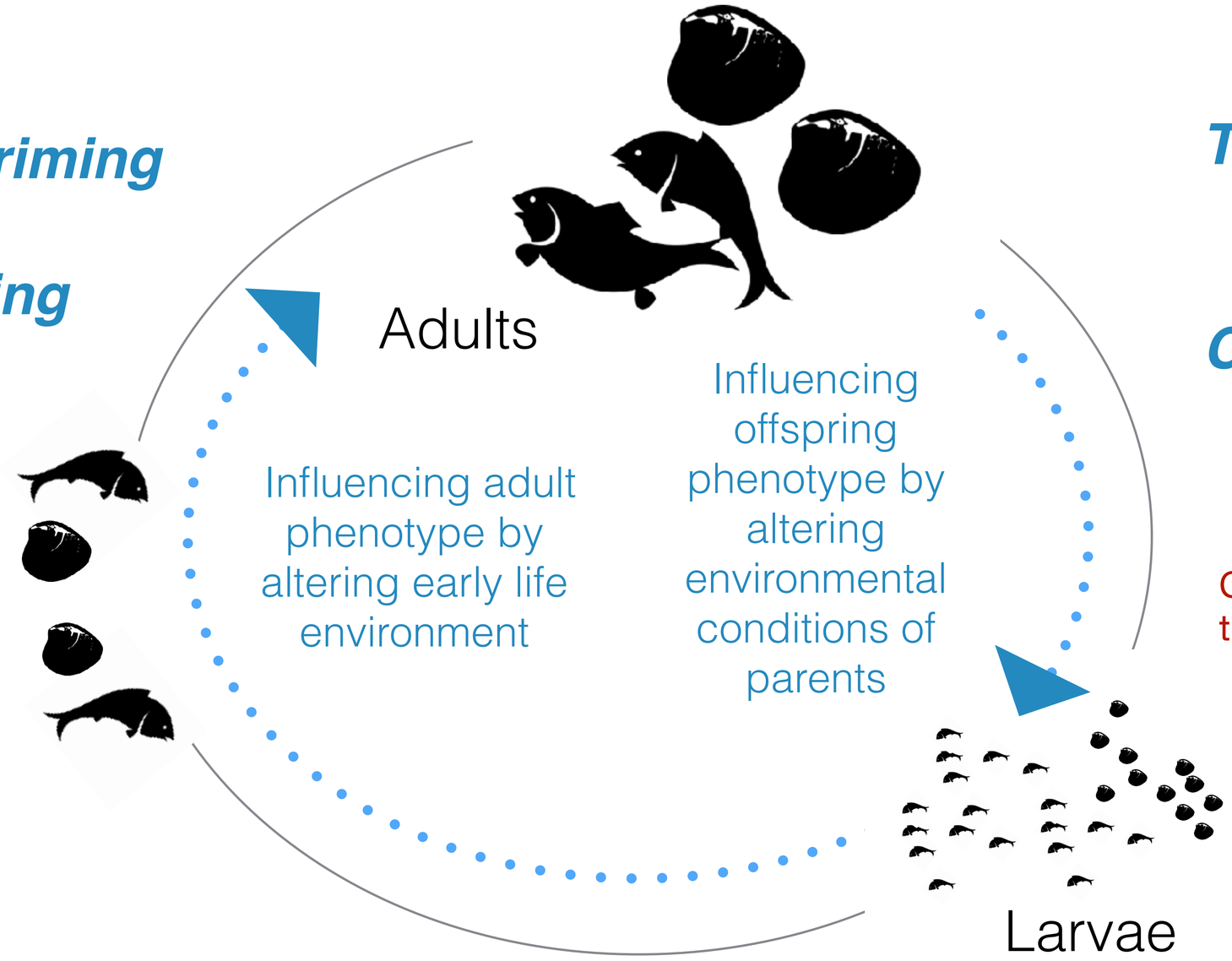
Early-life Priming

Hardening



Transgenerational Plasticity

Carry-over effects

Can we see an imprint in parents transmitted to the offspring?

Early-life Priming

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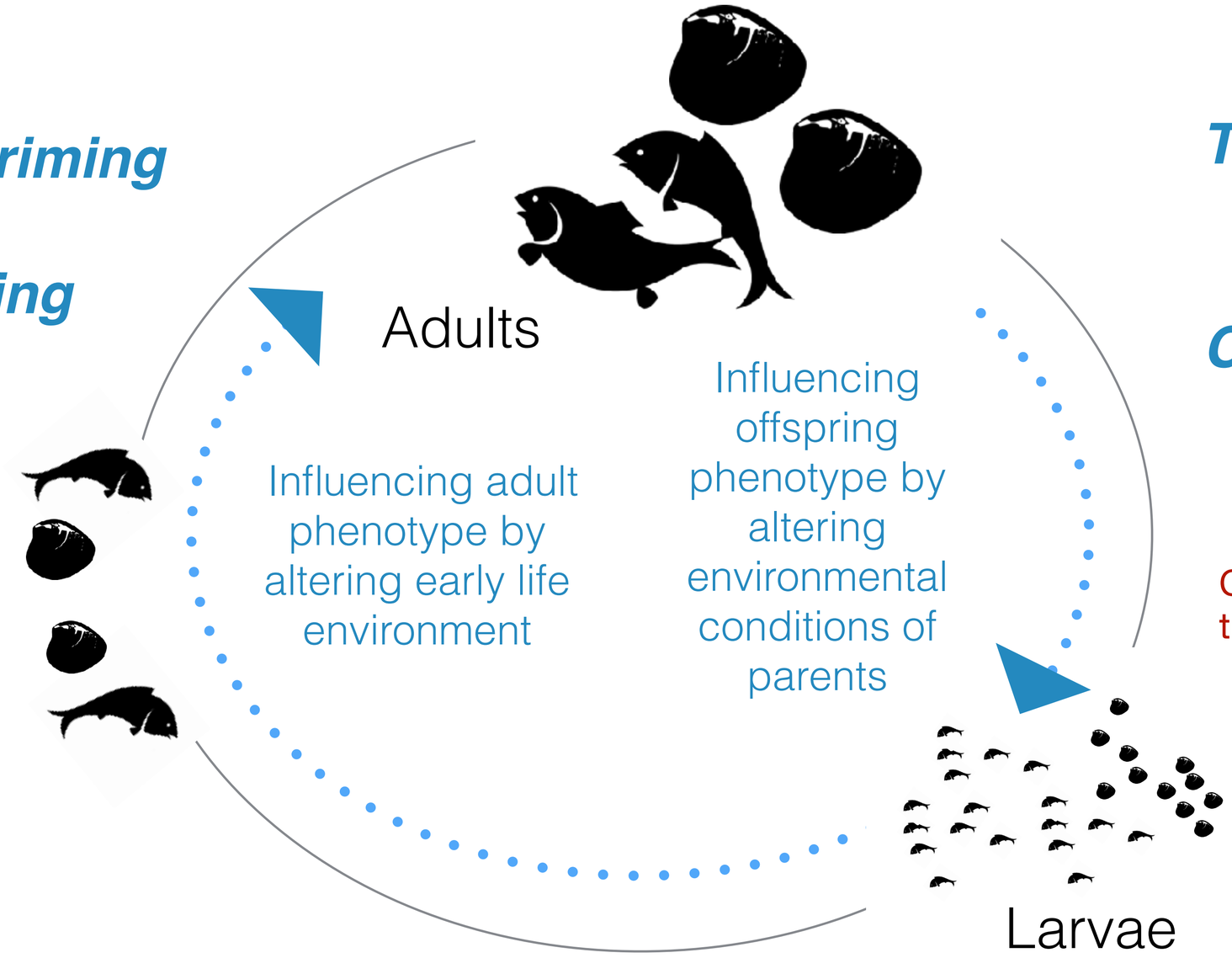

Transgenerational Plasticity

Carry-over effects

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NO

EXCITING?
COMPLEX
‘LAYER’ OF RESILIENCE

EXCITING?
COMPLEX
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Genetic Linkage

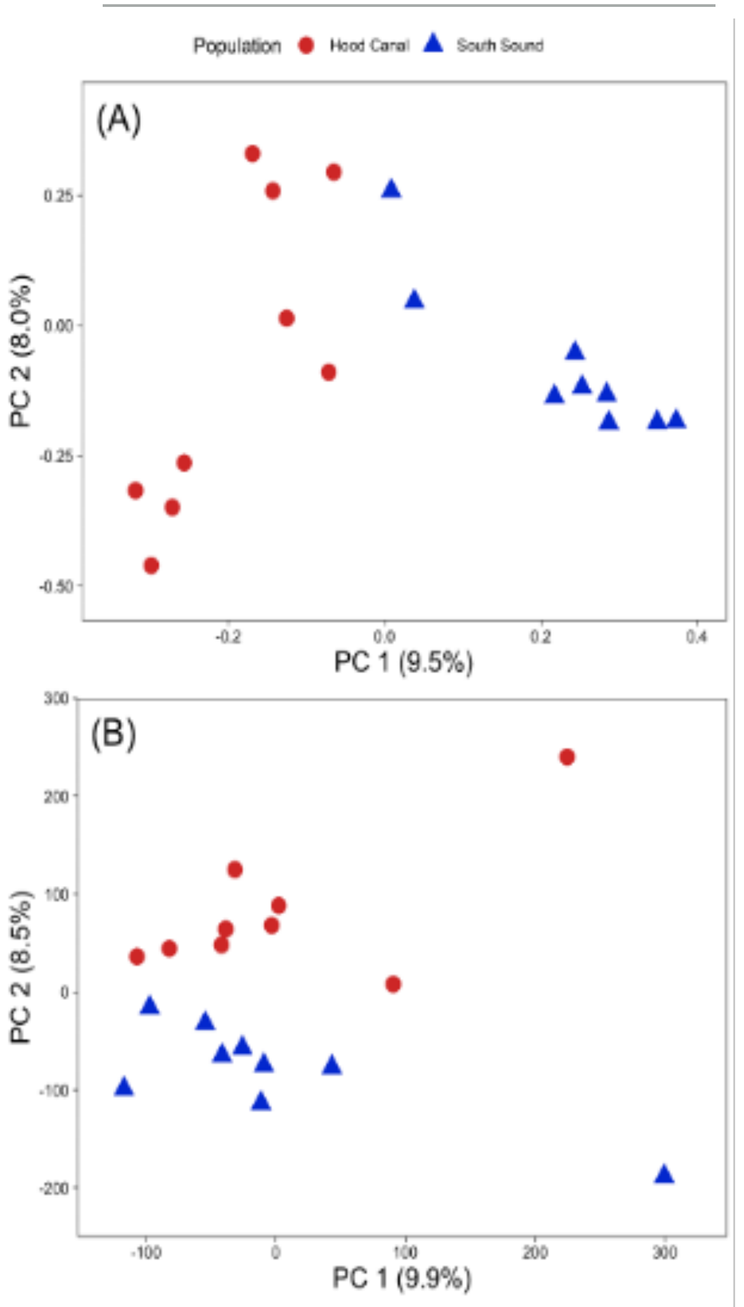
Epigenetic and Genetic Population Structure is Coupled in a Marine Invertebrate

Katherine Silliman [1,†], Laura H. Spencer [2,†], Samuel J. White[2], and Steven B. Roberts [2,*]

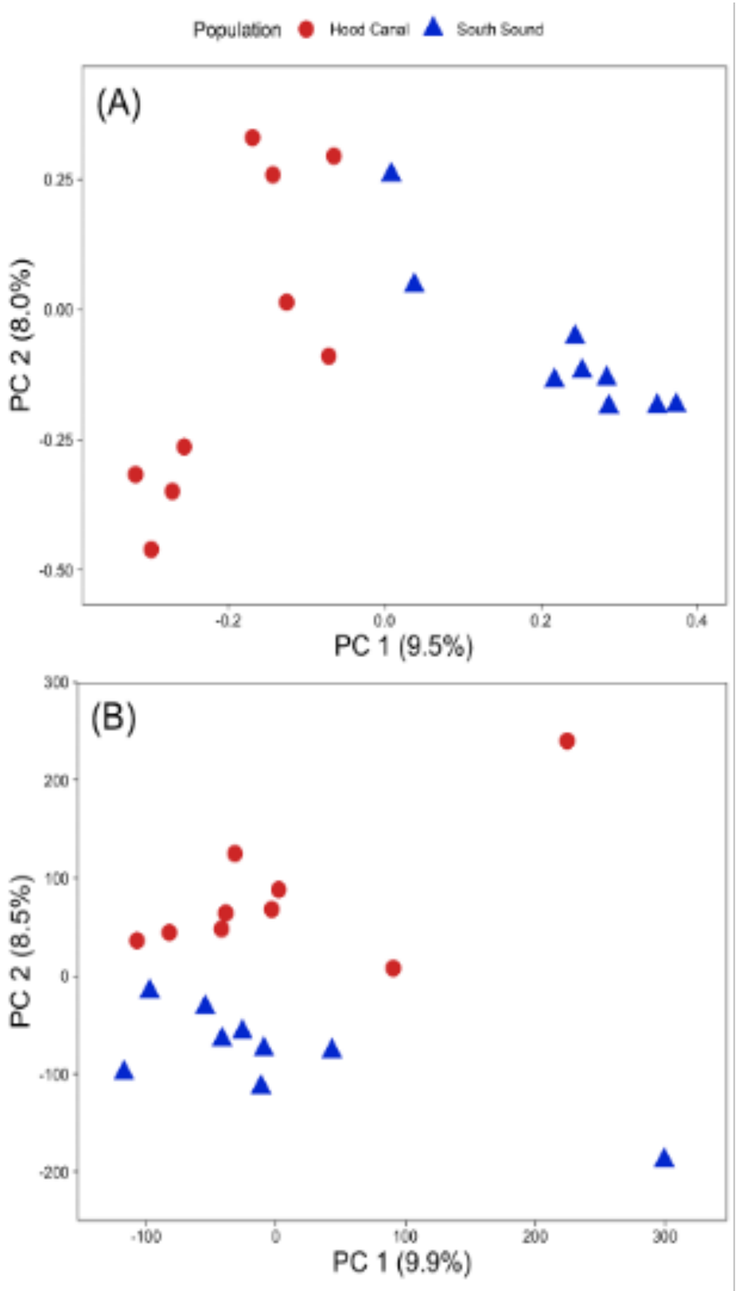
First characterization of genome-wide DNA methylation patterns in the oyster genus *Ostrea*

Identified 3,963 differentially methylated loci between populations. Clear coupling between genetic and epigenetic patterns of variation, **with 27% of variation in inter-individual methylation differences explained by genotype**.

Underlying this association are both direct genetic changes in CpGs (CpG-SNPs) and genetic variation with indirect influence on methylation (mQTLs).



EPIGENETIC AND GENETIC POPULATION STRUCTURE



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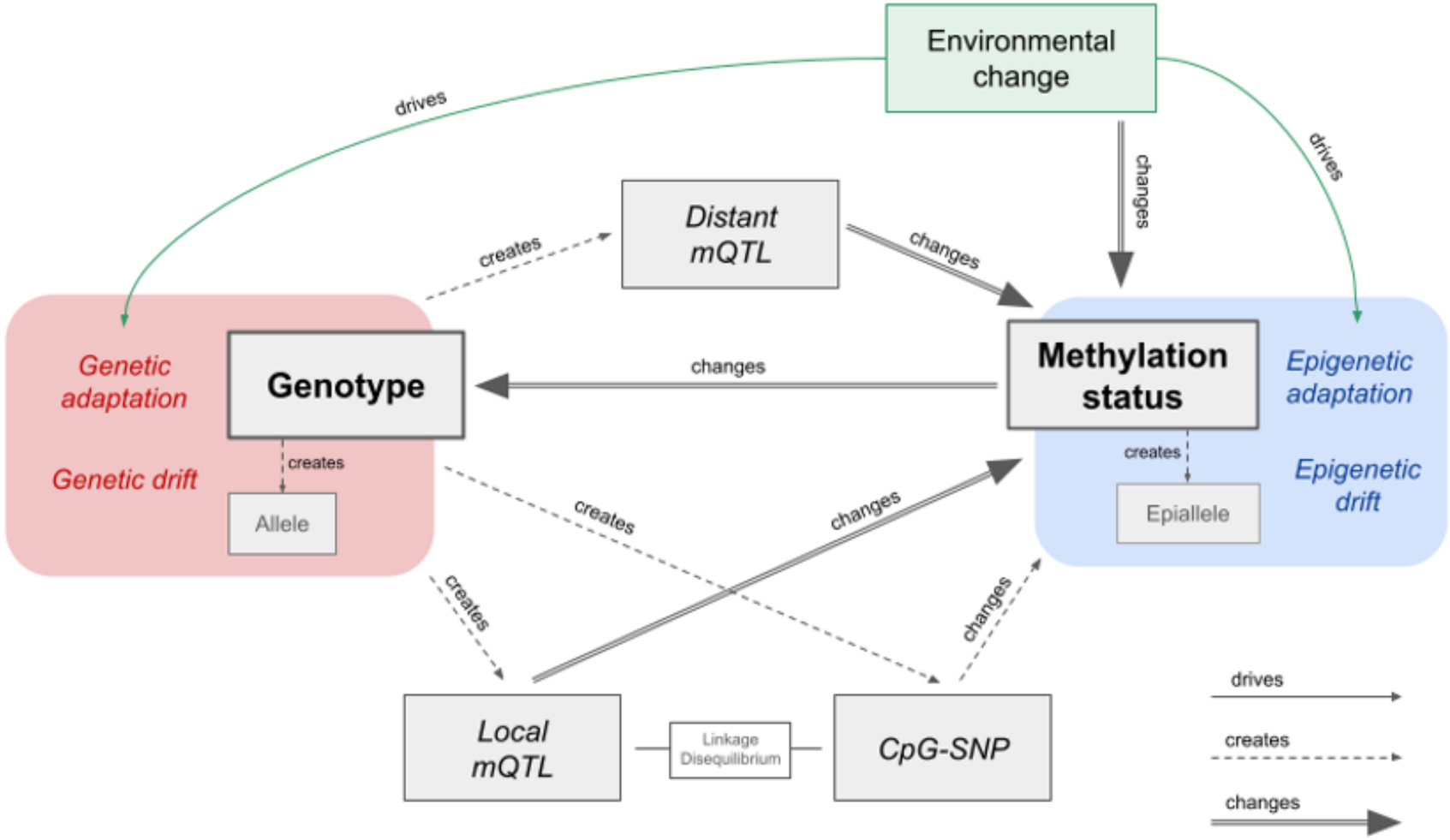

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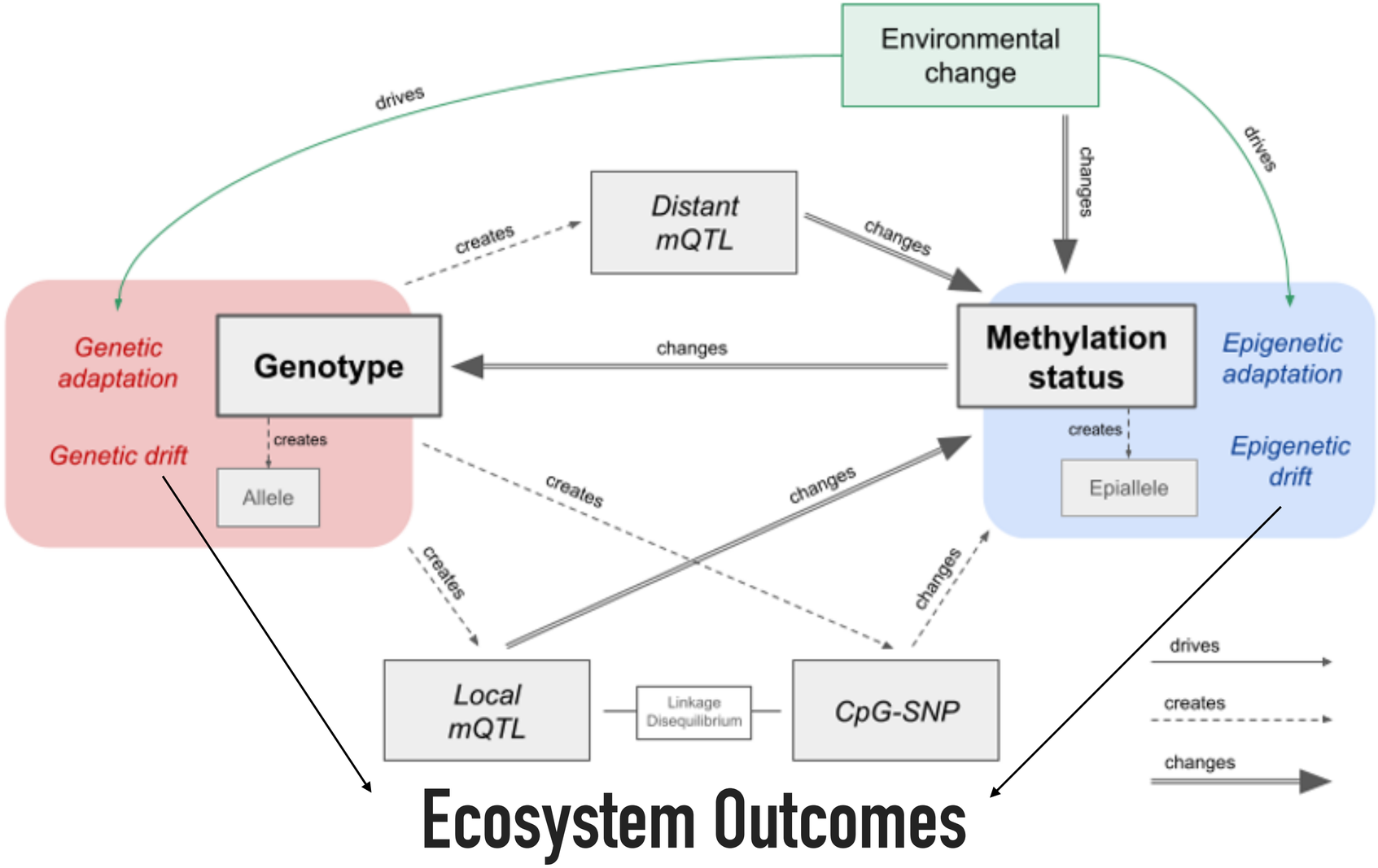

Open Science

Bioinformatic Approaches in non-model species

marineomics.io

Received: 29 March 2023 | Accepted: 11 September 2023
DOI: 10.1111/2041-210X.14219

Methods in Ecology and Evolution

APPLICATION

A dynamic web resource for robust and reproducible genomics in nonmodel species: marineomics.io

Samuel N. Bogan[1] | Jason Johns[1] | Joanna S. Griffiths[2] | Danielle Davenport[3] | Sara J. Smith[4,5,6] | Sara M. Schaal[7] | Alan Downey-Wall[8] | Runyang Nicolas Lou[9,10] | Katie Lotterhos[11] | Megan E. Guidry[12] | Hanny E. Rivera[13] | Joseph A. McGirr[14] | Jonathan B. Puritz[12] | Steven B. Roberts[15] | Katherine Silliman[16,17]

Tabs for website topics

MarineOmics

Best Principles | Contributions | Population Genomics | Functional Genomics | Genome-Phenome | Panel Seminars | Discussion Forum

Topics covered within RADSeq tutorial

- Setup for running code
- Reduced Representation Sequencing (RADseq/GBS)
- Considerations During Lab Work
- Principles for Analyzing Your Data
  - Steps for a robust RAD analysis
  - First, look at the raw data!
  - Run an assembly pipeline
  - Evaluate potential sources of error
    - "Bad" samples
    - The power of PCA
    - Batch effects
    - Cryptic species/contamination/clones
  - Test a range of key parameters
    - Clustering threshold
    - Mapping parameters

RADseq

Katherine Silliman, Danielle Davenport

Description of tutorial steps

Setup for running code

If you would like to run the R code examples that are scattered throughout the guide (recommended but not required!), you will need to install some R packages. Only need to run this code once:

```
install.packages("tidyverse")
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")

BiocManager::install("SeqArray")
BiocManager::install("SNPRelate")
```

Example code to run using real data

Now load those packages, if using:

```
library(SeqArray) # efficient storage and filtering of genomic data
```

```
## Loading required package: gdsfmt
```

ACKNOWLEDGEMENTS

- Mackenzie Gavery (NOAA), Sam White (UW), Brent Vadopalas (UW), Shelly Wanamaker (GMGI), Sam Gurr (NOAA), Hollie Putnam (URI), Laura Spencer (UW), Katherine Silliman (NOAA), Yaamini Venkataraman (WHOI), Katie Lotterhos (NEU)

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