Genomic Applications in Sustainable Aquaculture

Steven Roberts - University of Washington

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Genomic Applications in Sustainable Aquaculture

Steven Roberts - University of Washington
Mackenzie Gavery - NOAA
Hollie Putnam - University of Rhode Island
Shelly Wanamaker - GMGI

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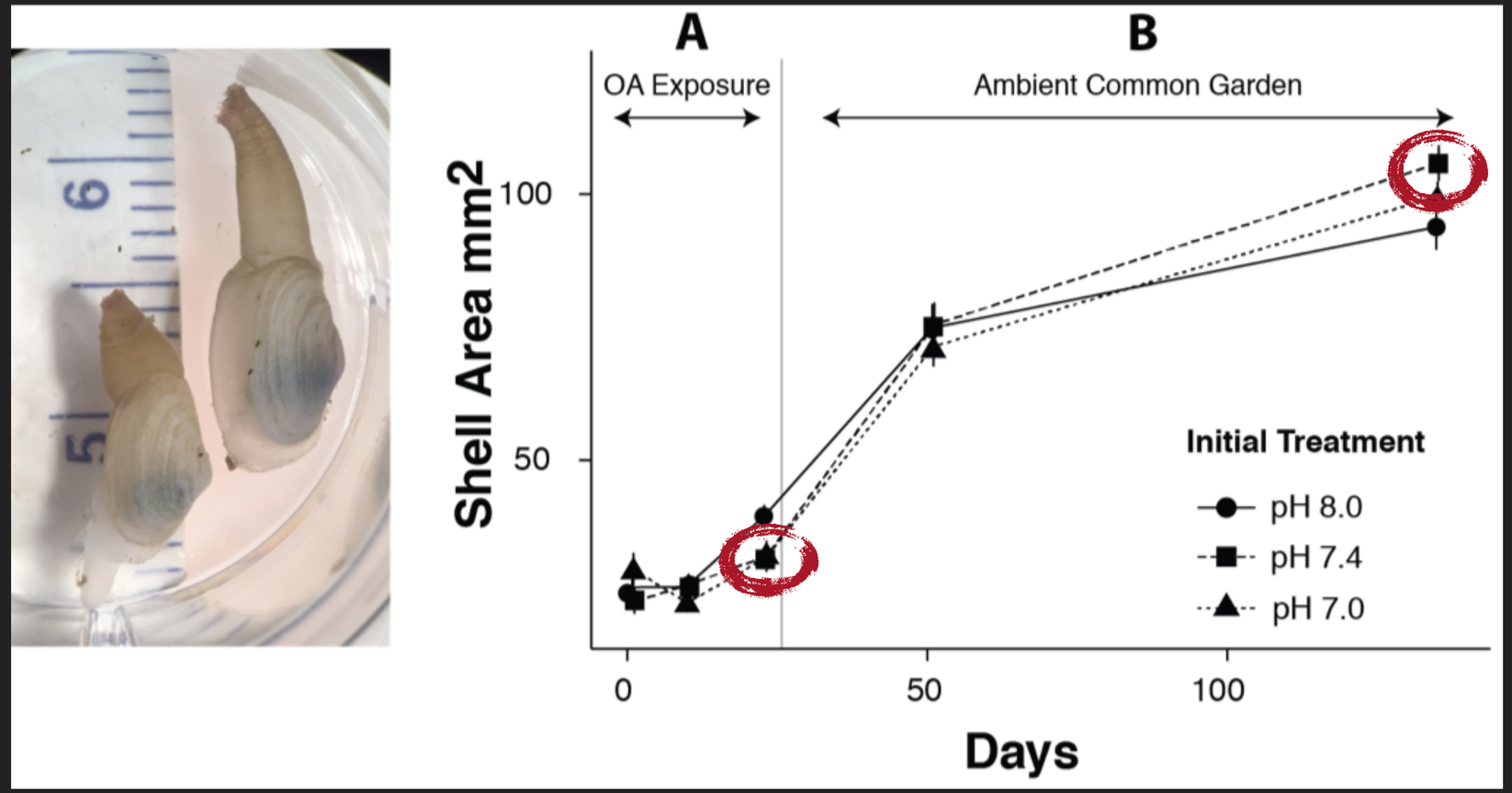
Aquaculture
is key for global food production

GEODUCKS AND OA

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



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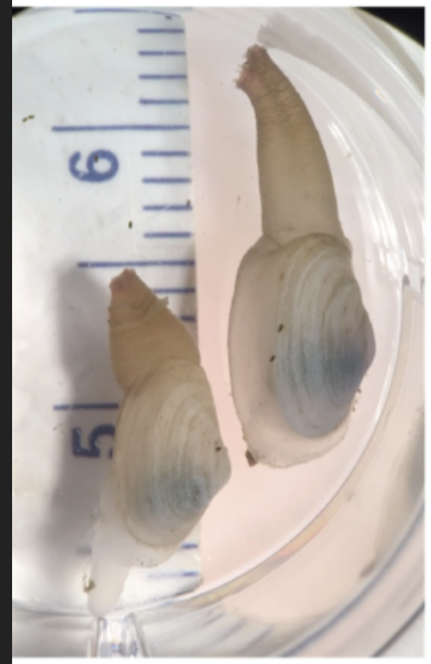

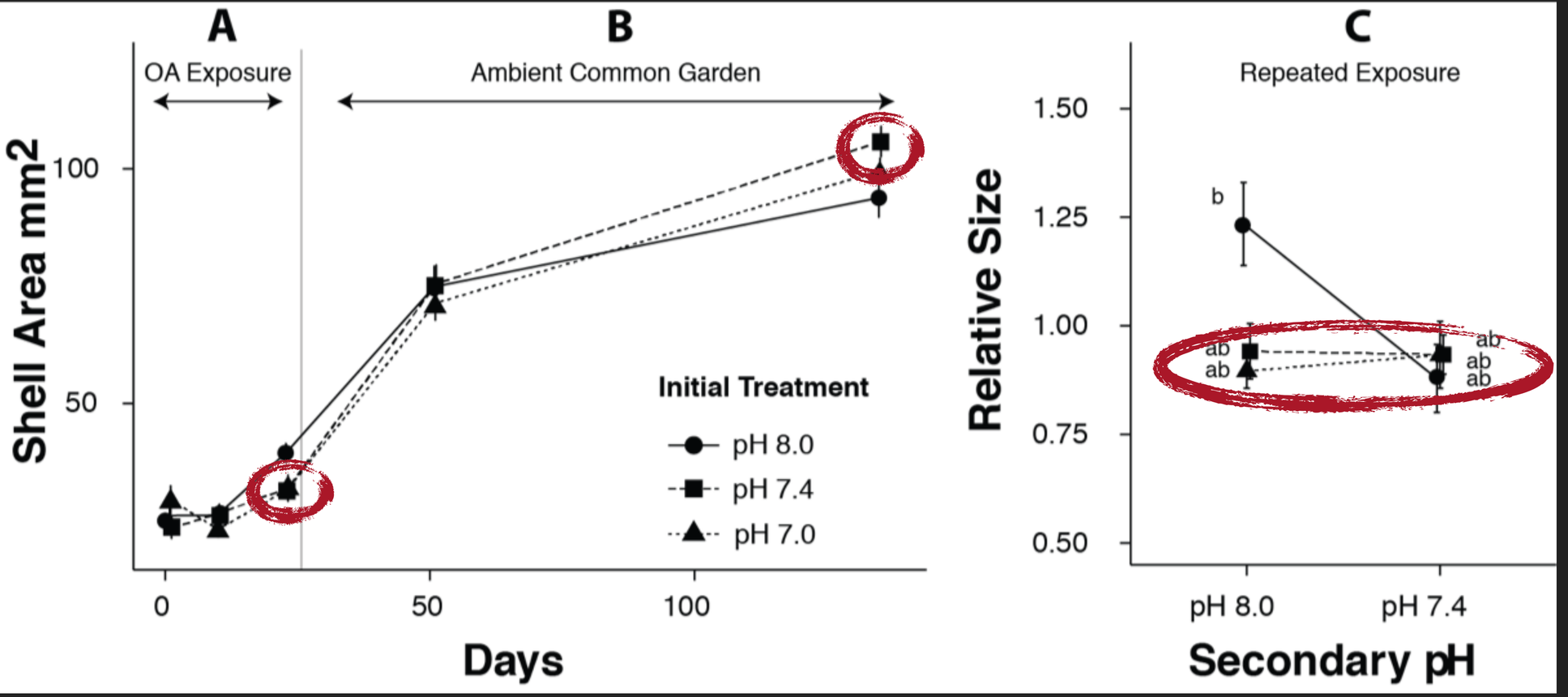

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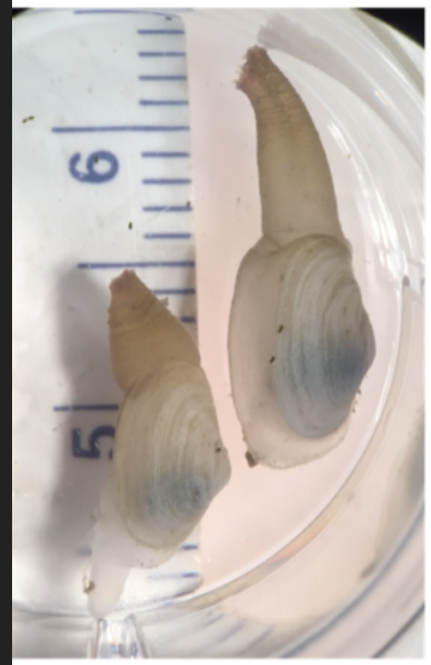
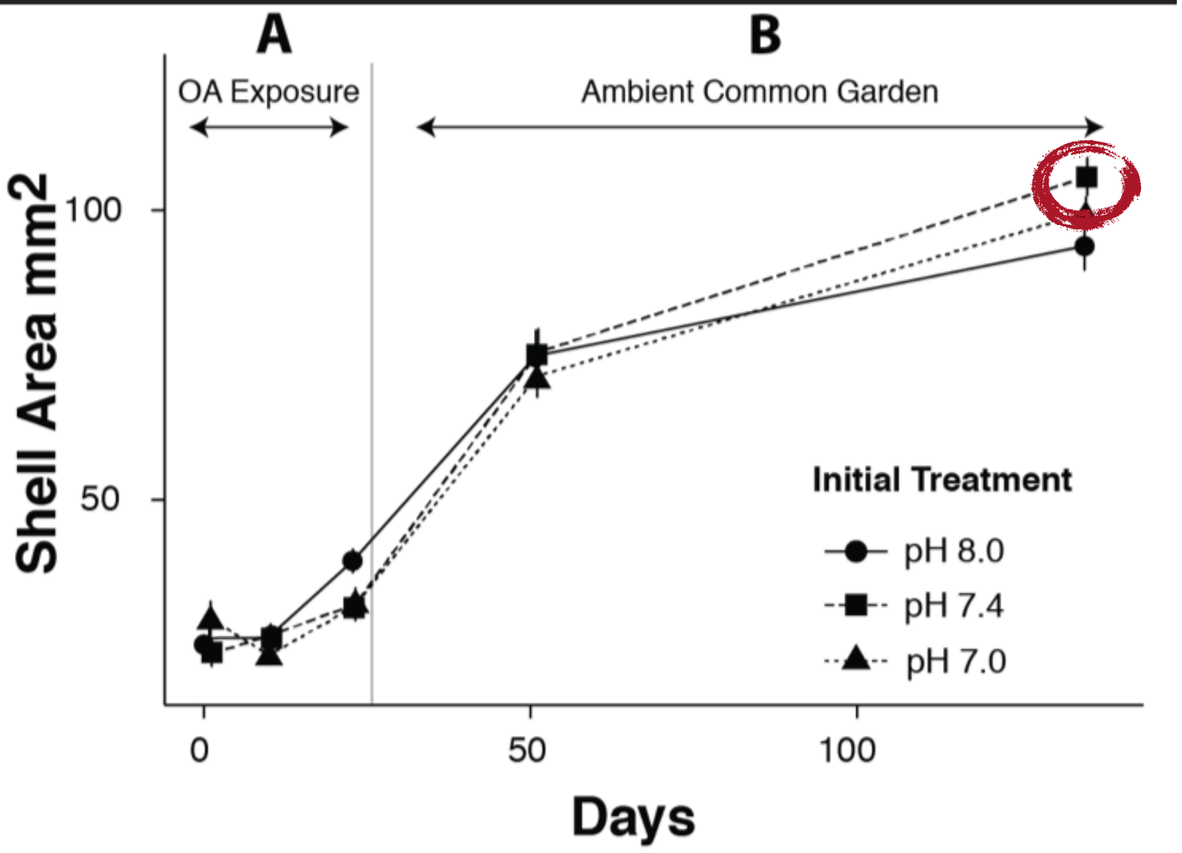
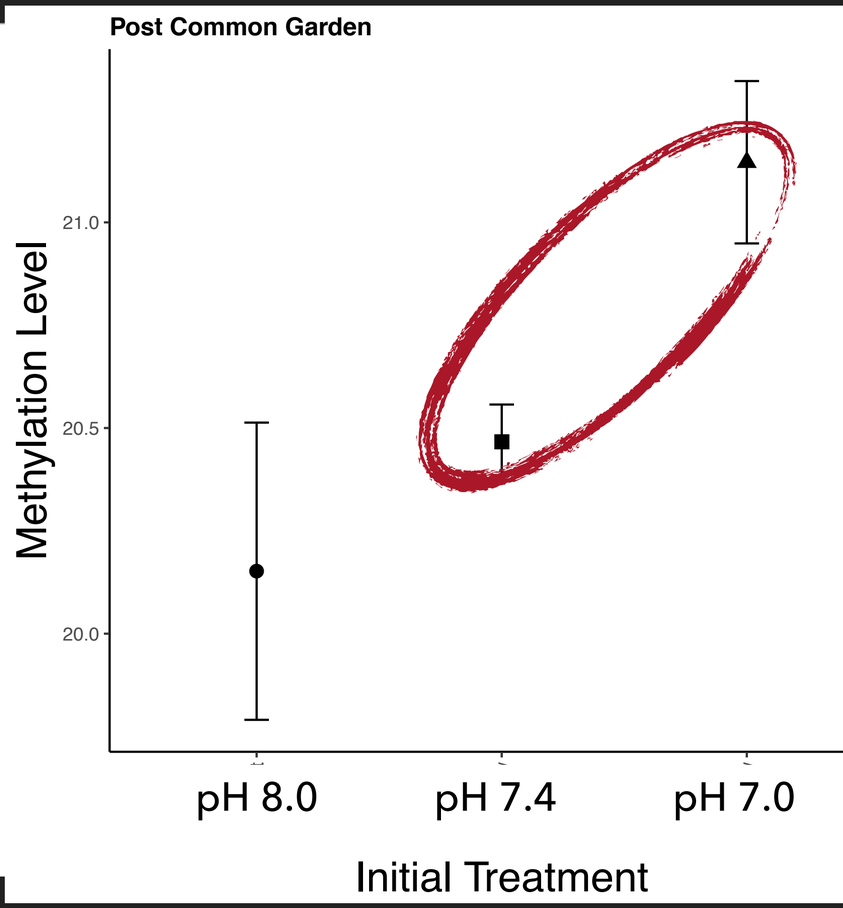




DNA METHYLATION



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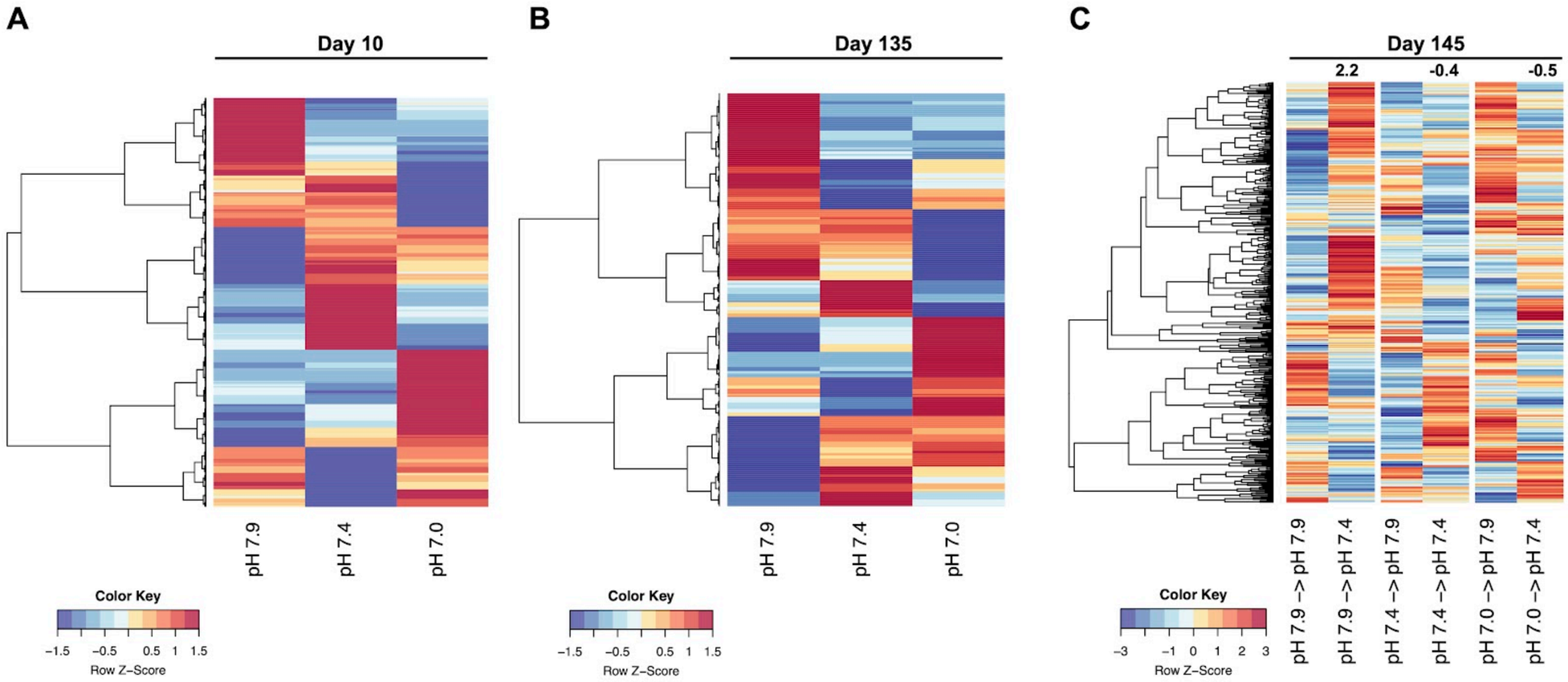

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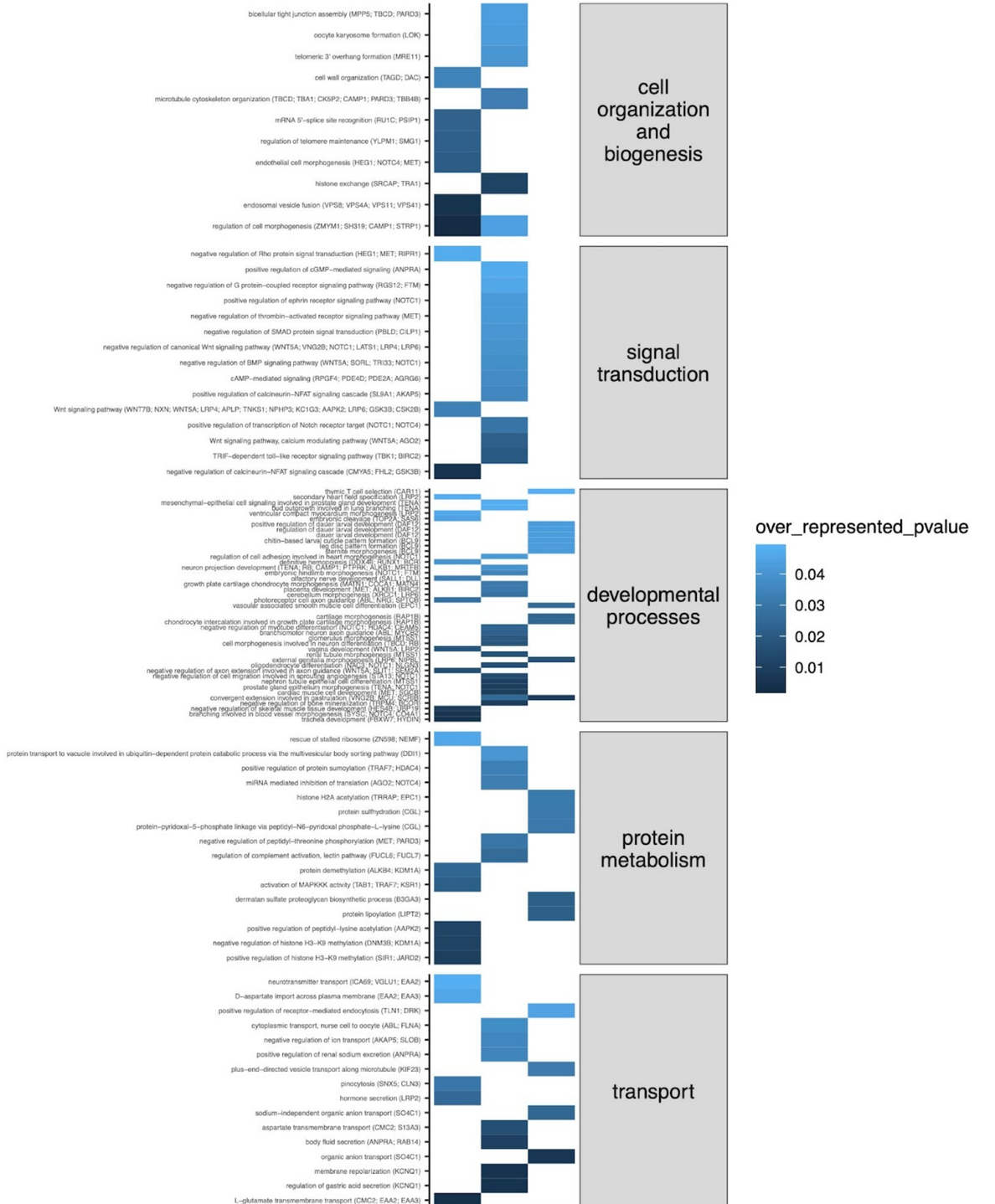

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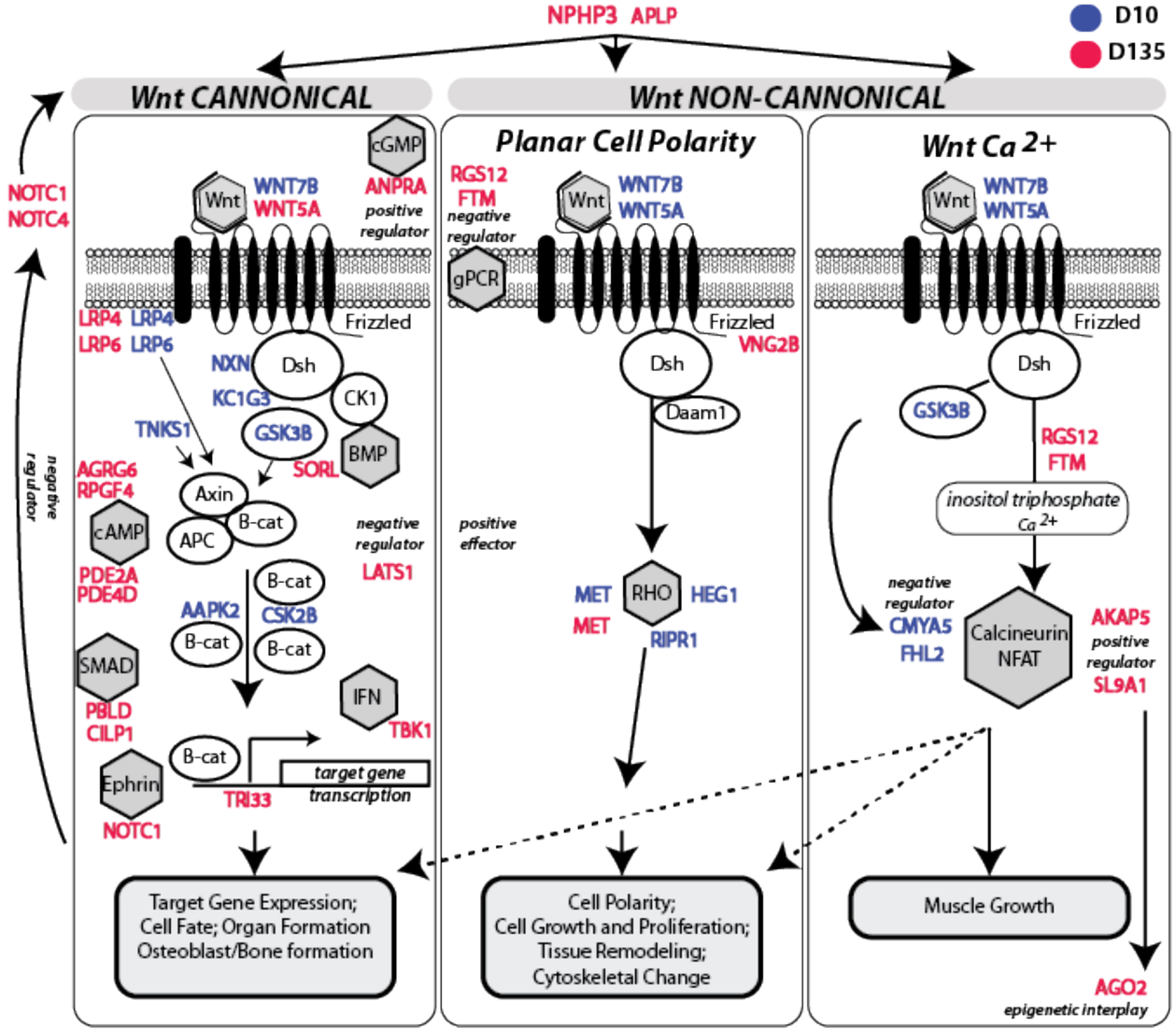

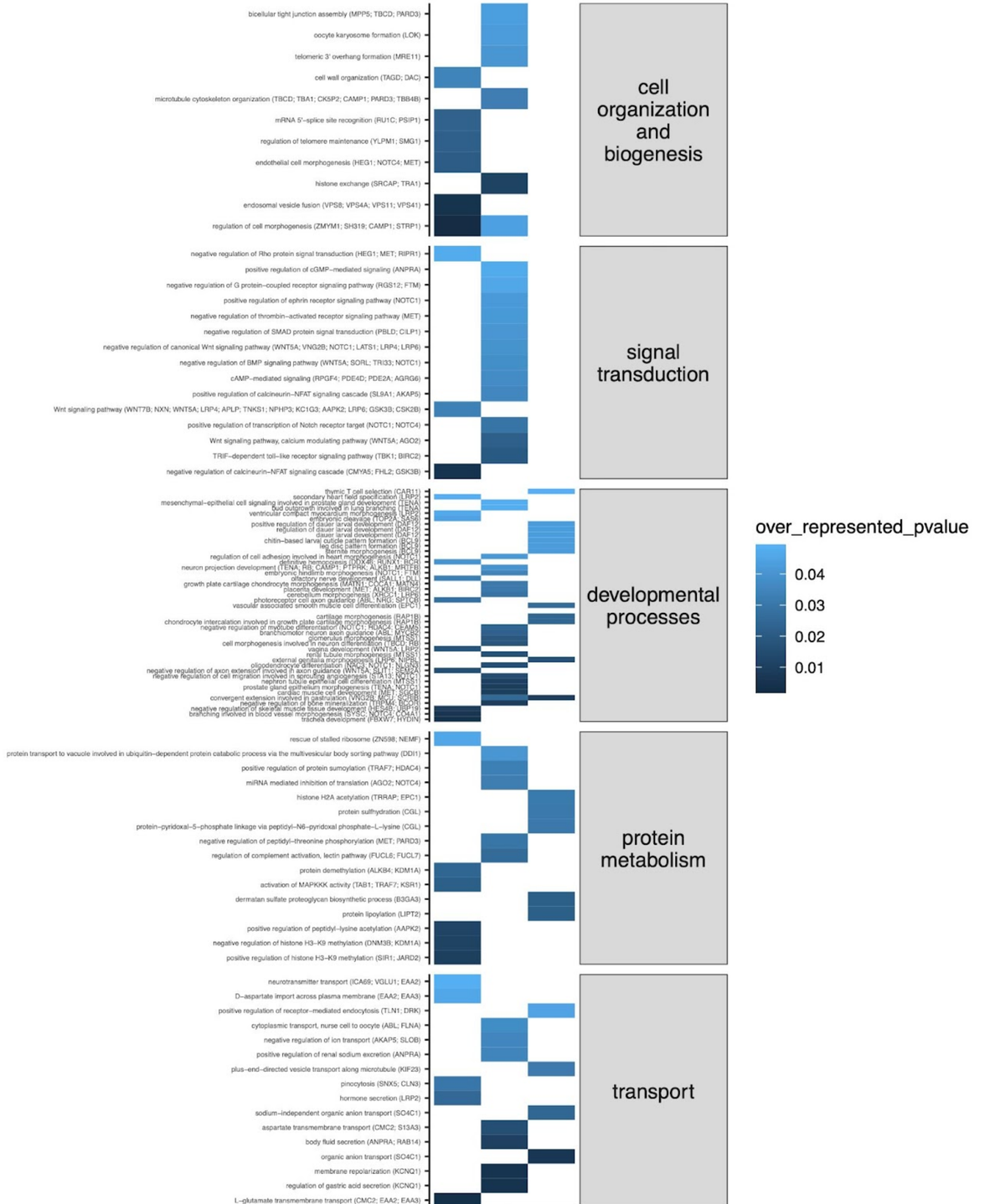

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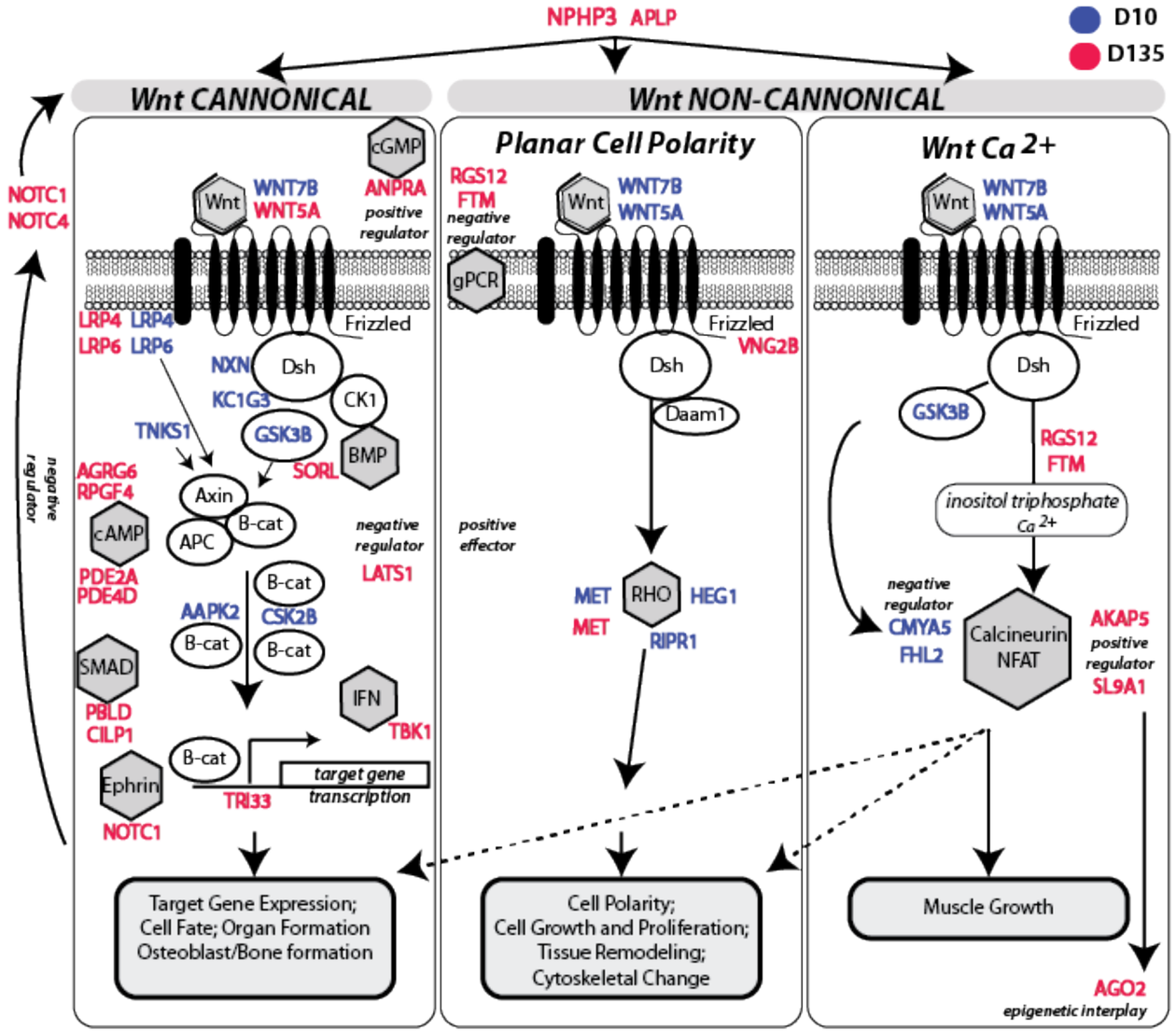


New Results

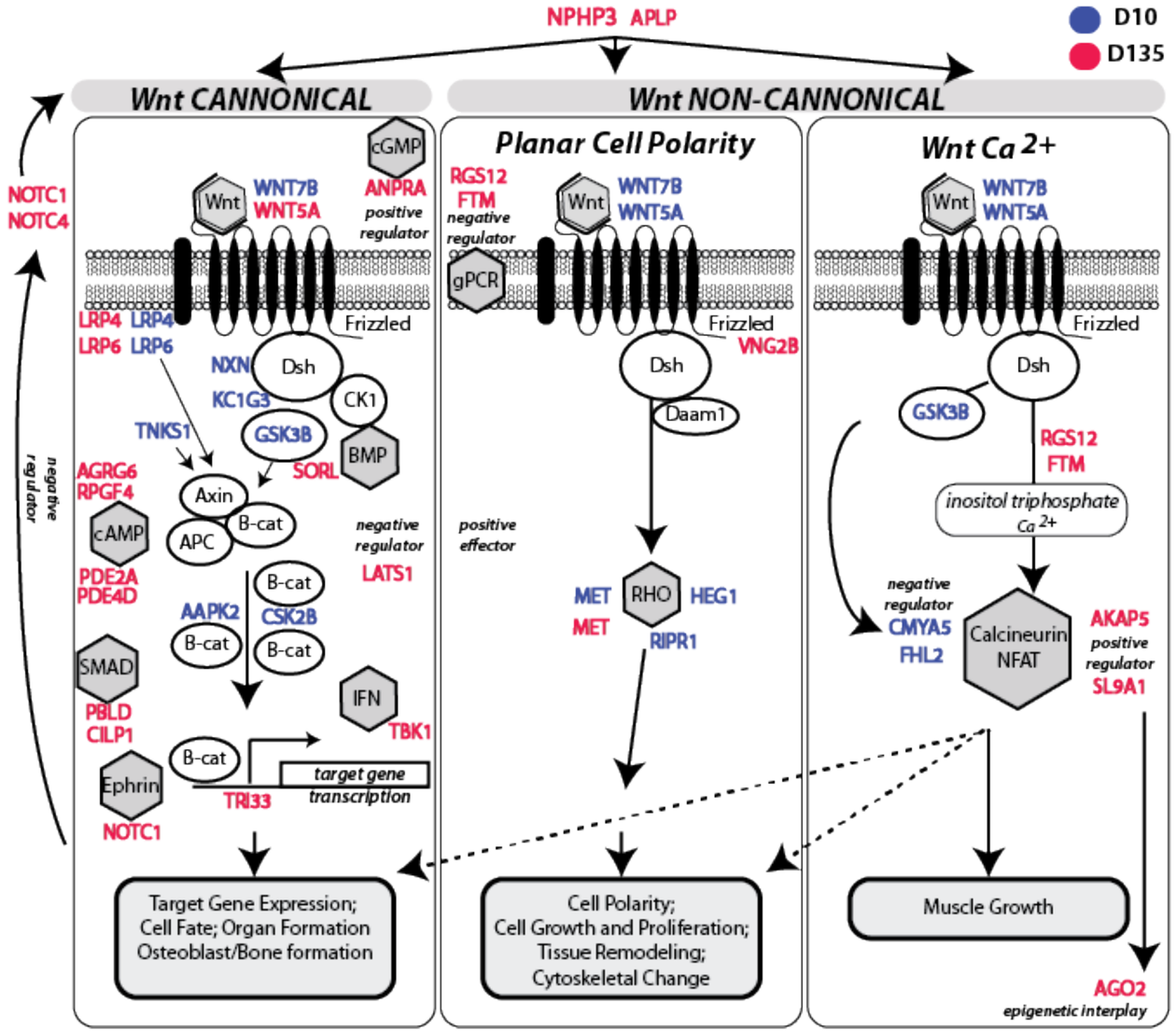
Follow this preprint

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

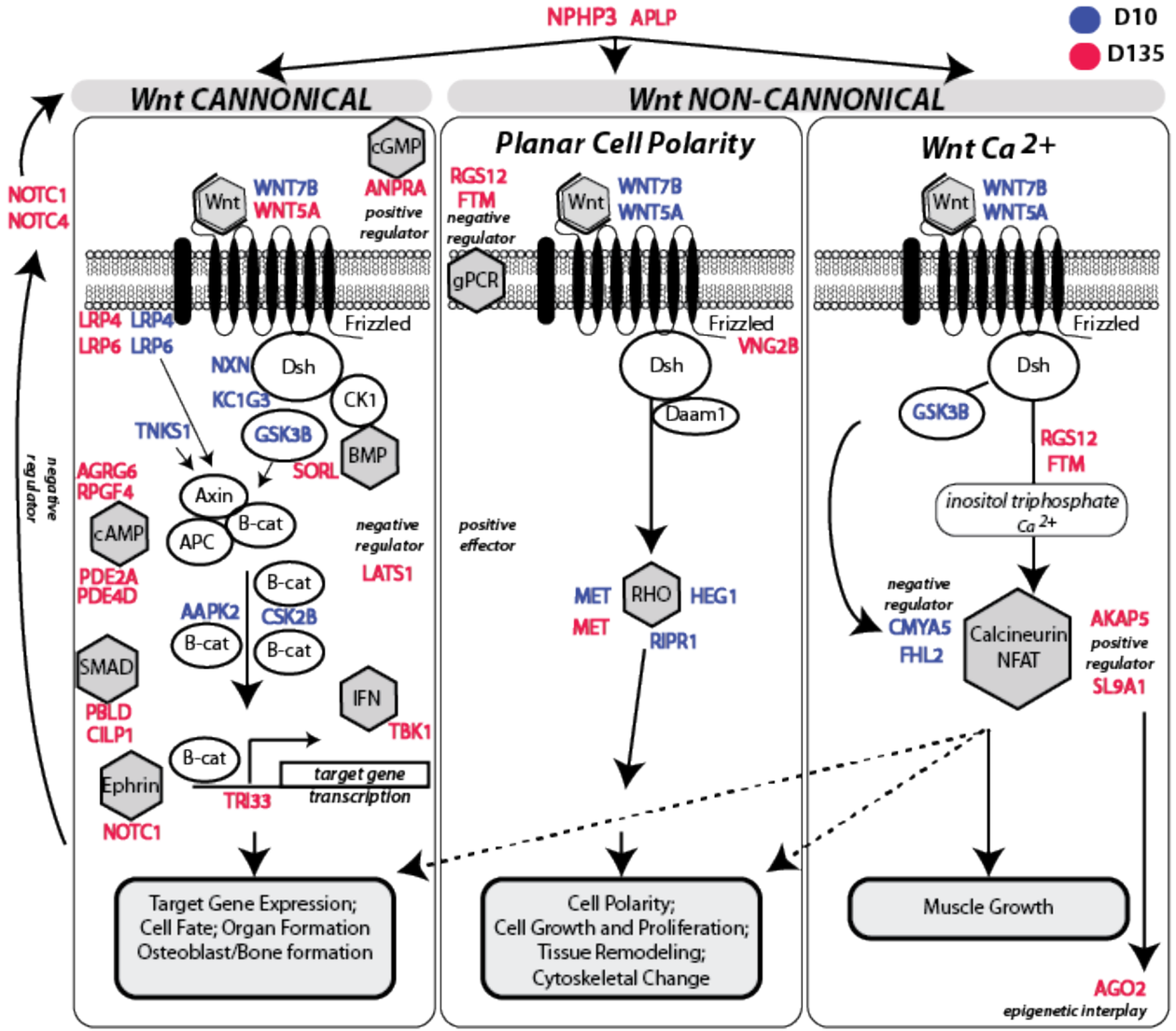
doi: https://doi.org/10.1101/2022.06.24.497506

GEODUCKS AND OA



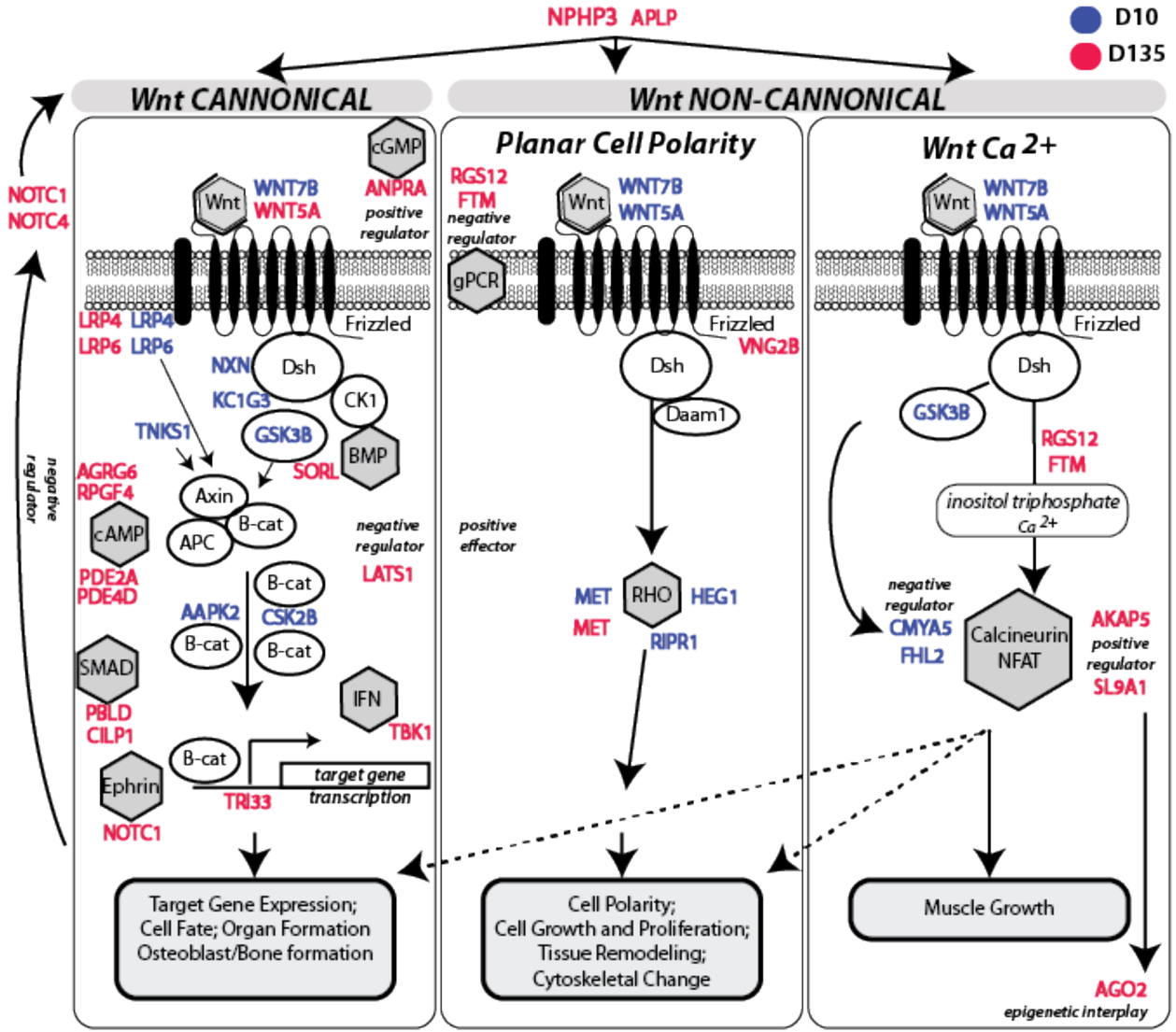
Following four months of ambient common-garden conditions, **juveniles initially exposed to low pH compensatorily grew larger**, with DNA methylation indicative of these phenotypic differences, demonstrating epigenetic carryover effects persisted months after initial exposure.

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.**

GEODUCKS AND OA



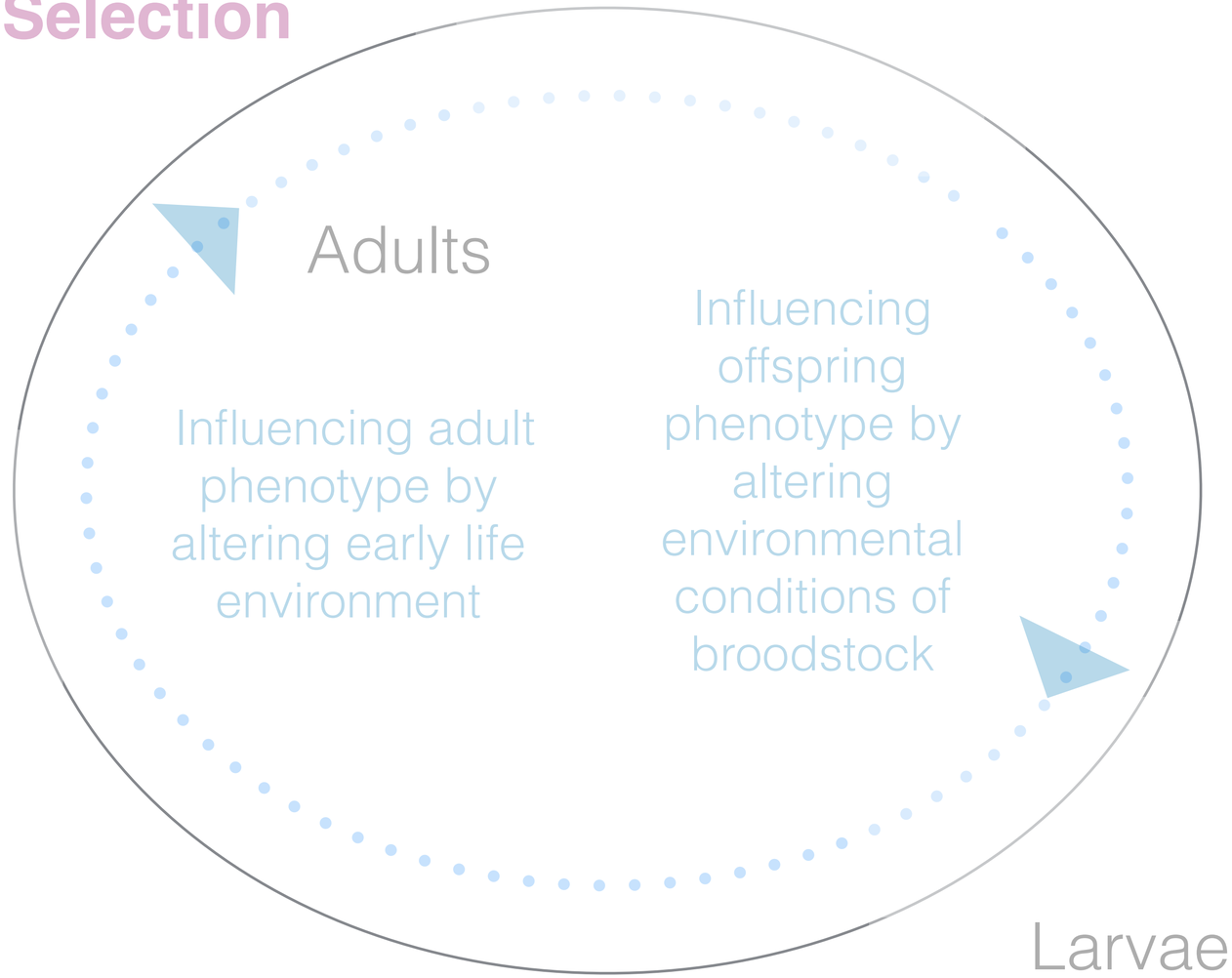
After 10 days of secondary exposure to pH 7.4, naive juvenile clams were more sensitive to low pH compared to those initially exposed, showing reduced growth and having nearly a 2-fold greater change in DNA methylation.

DNA Methylation in Bivalves

- Early-life Environment
- **Epigenetic Selection**
- Future Perspectives

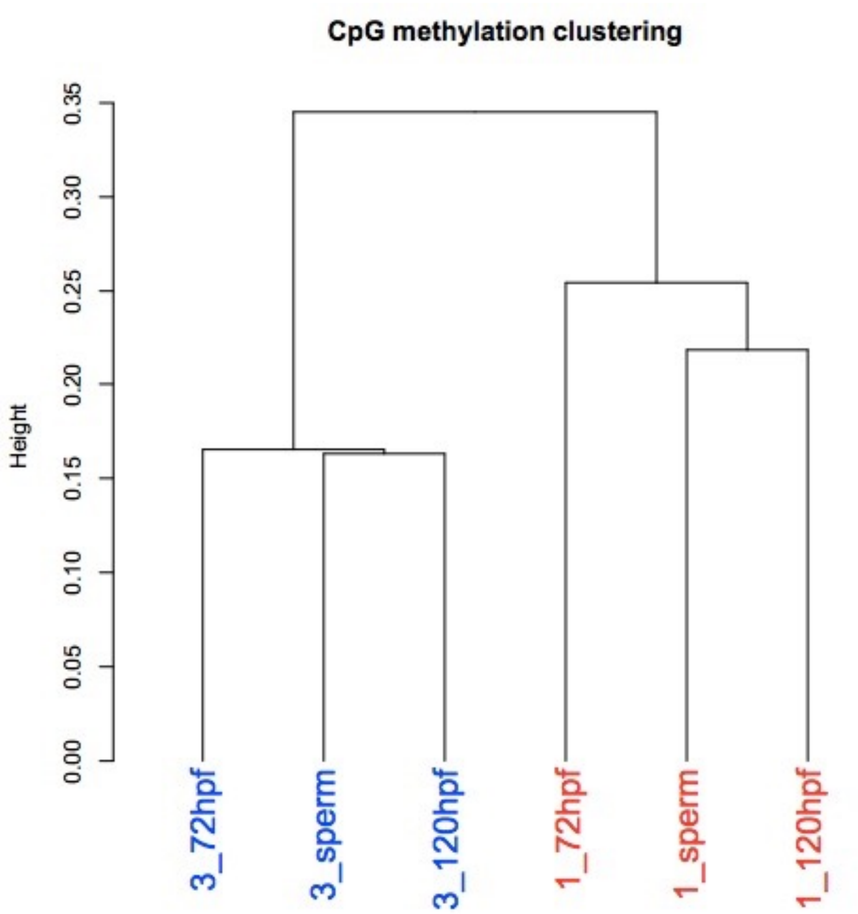
Epigenetic Selection

Identifying individuals by attributing trait to epigenotype



Environmental Manipulation

SELECTION POTENTIAL



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

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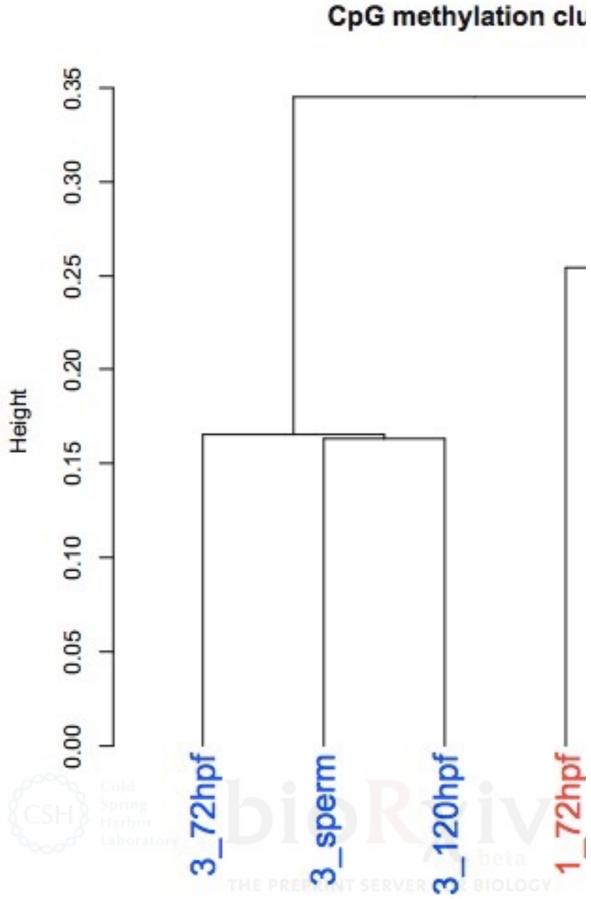

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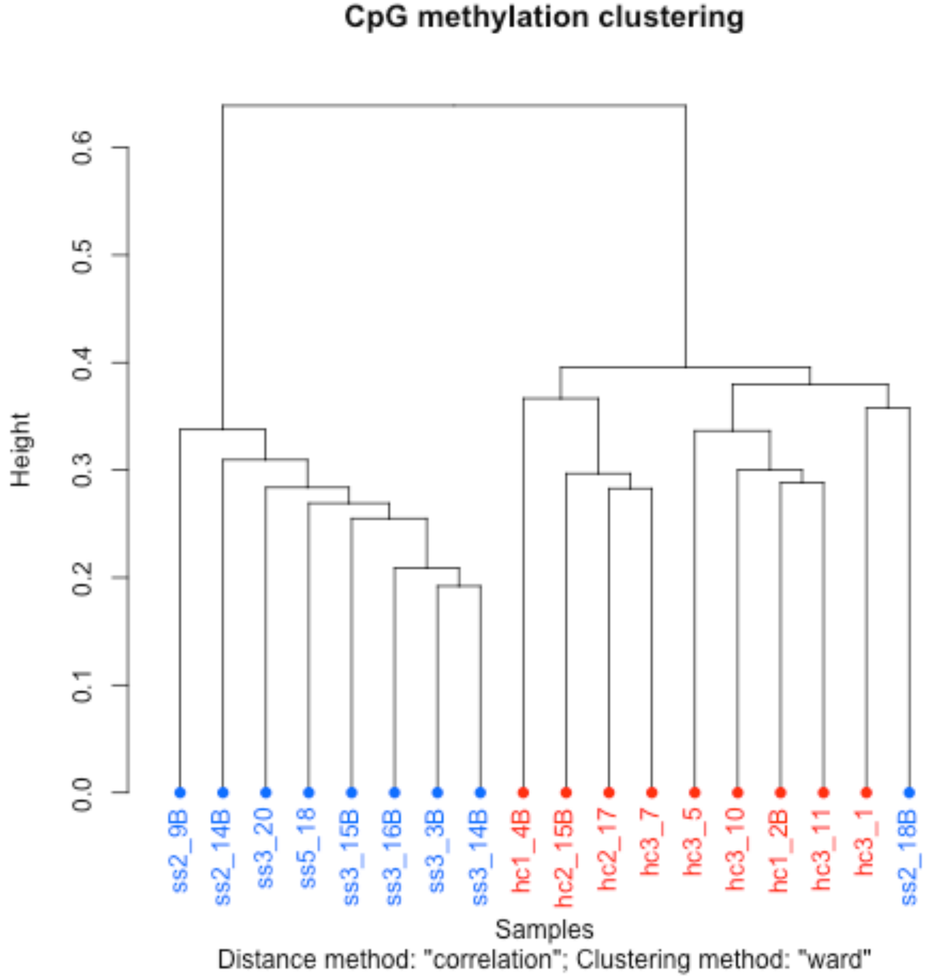


Epigenetic and genetic population structure is coupled in a marine invertebrate

Katherine Silliman, Laura H. Spencer, Samuel J. White, Steven B. Roberts

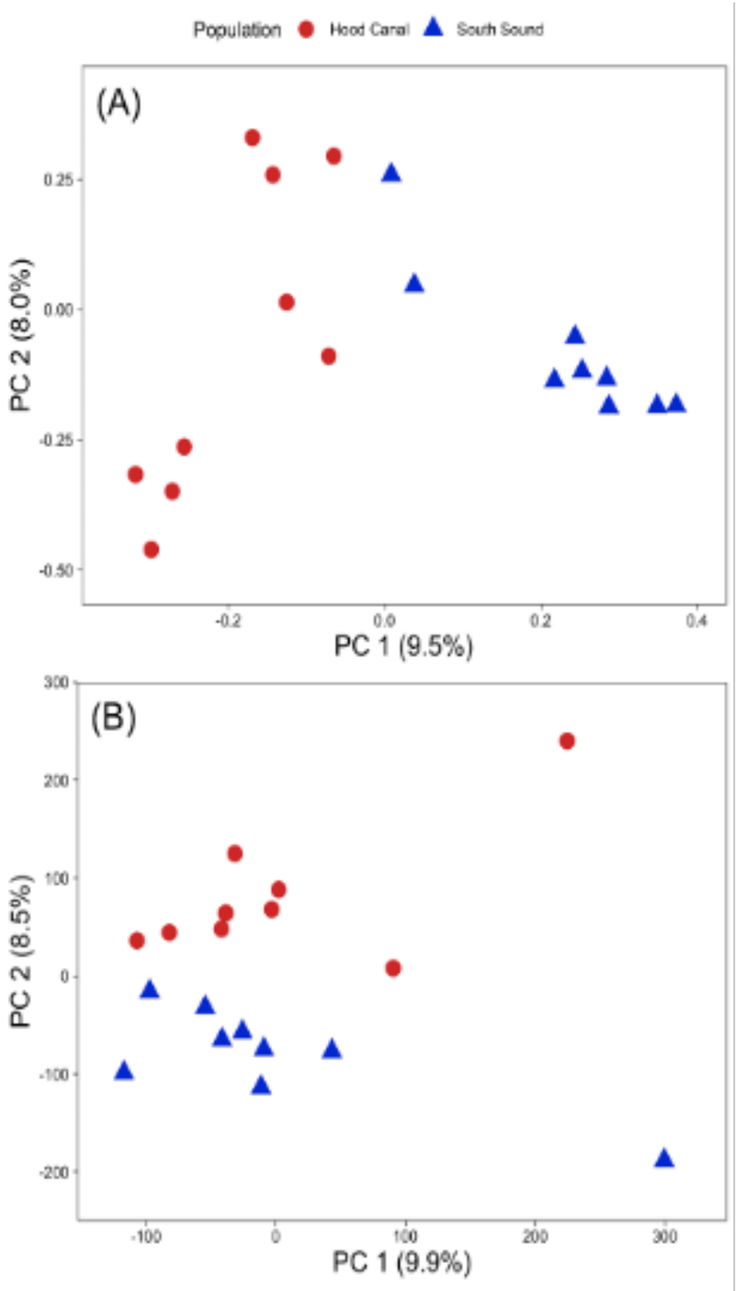
doi: https://doi.org/10.1101/2022.03.23.485415

EPIGENETIC AND GENETIC POPULATION STRUCTURE

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).



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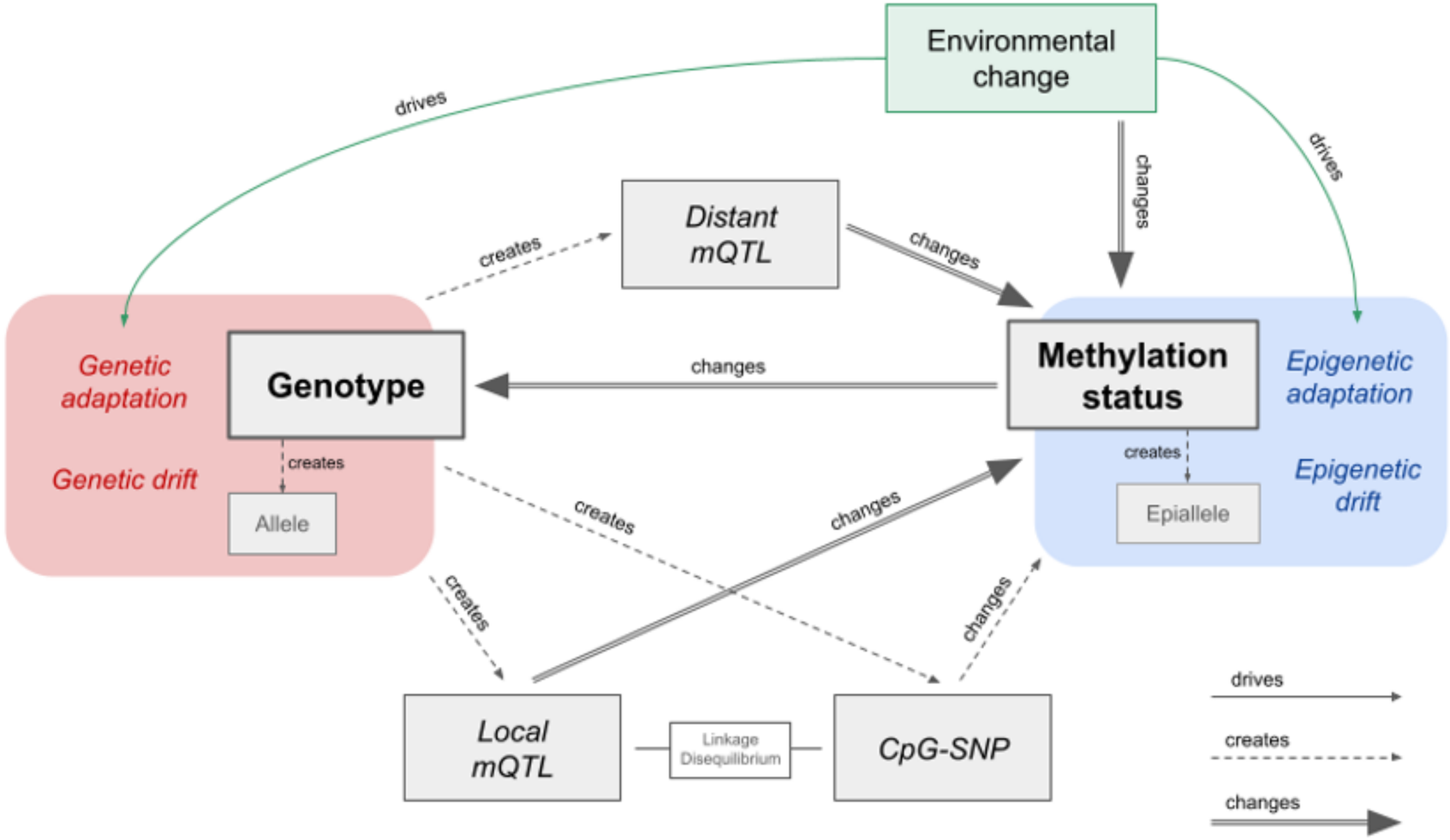
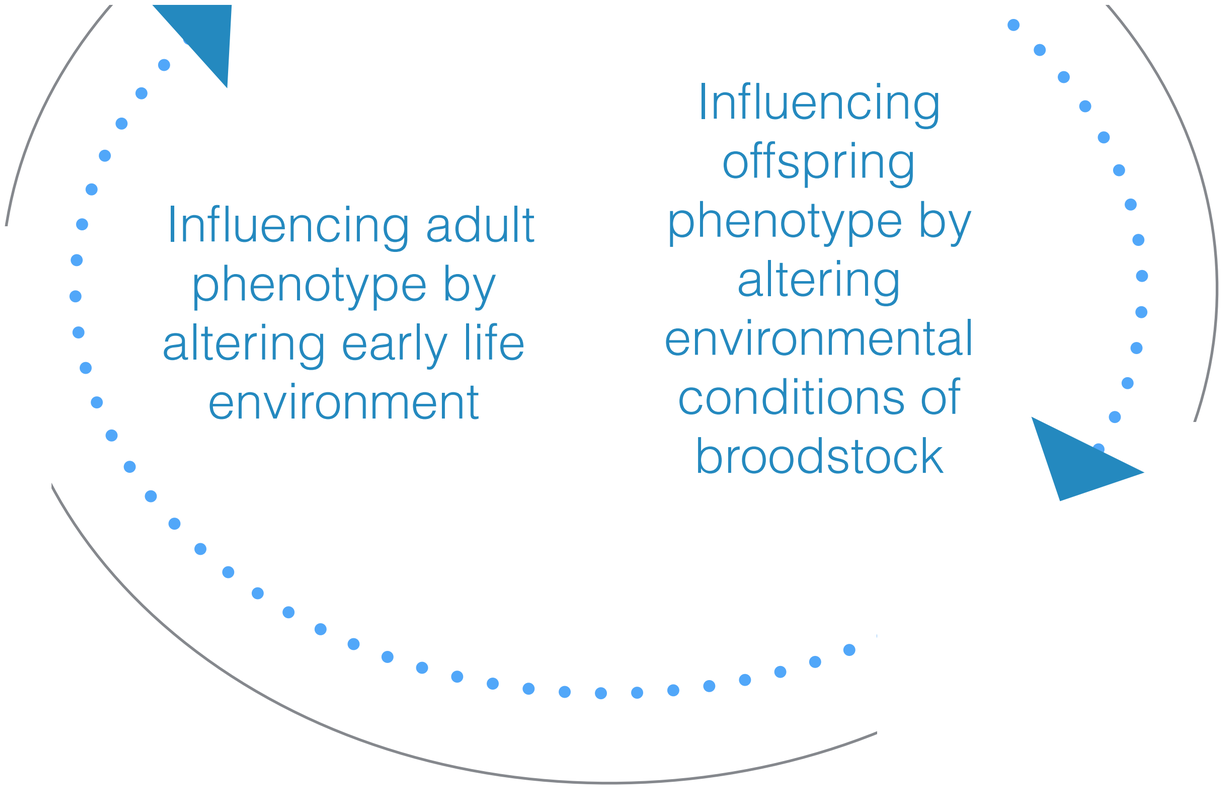


Epigenetics is an attractive lens through which to consider manipulation of traits through environmental memory or selection.



Genomic Applications

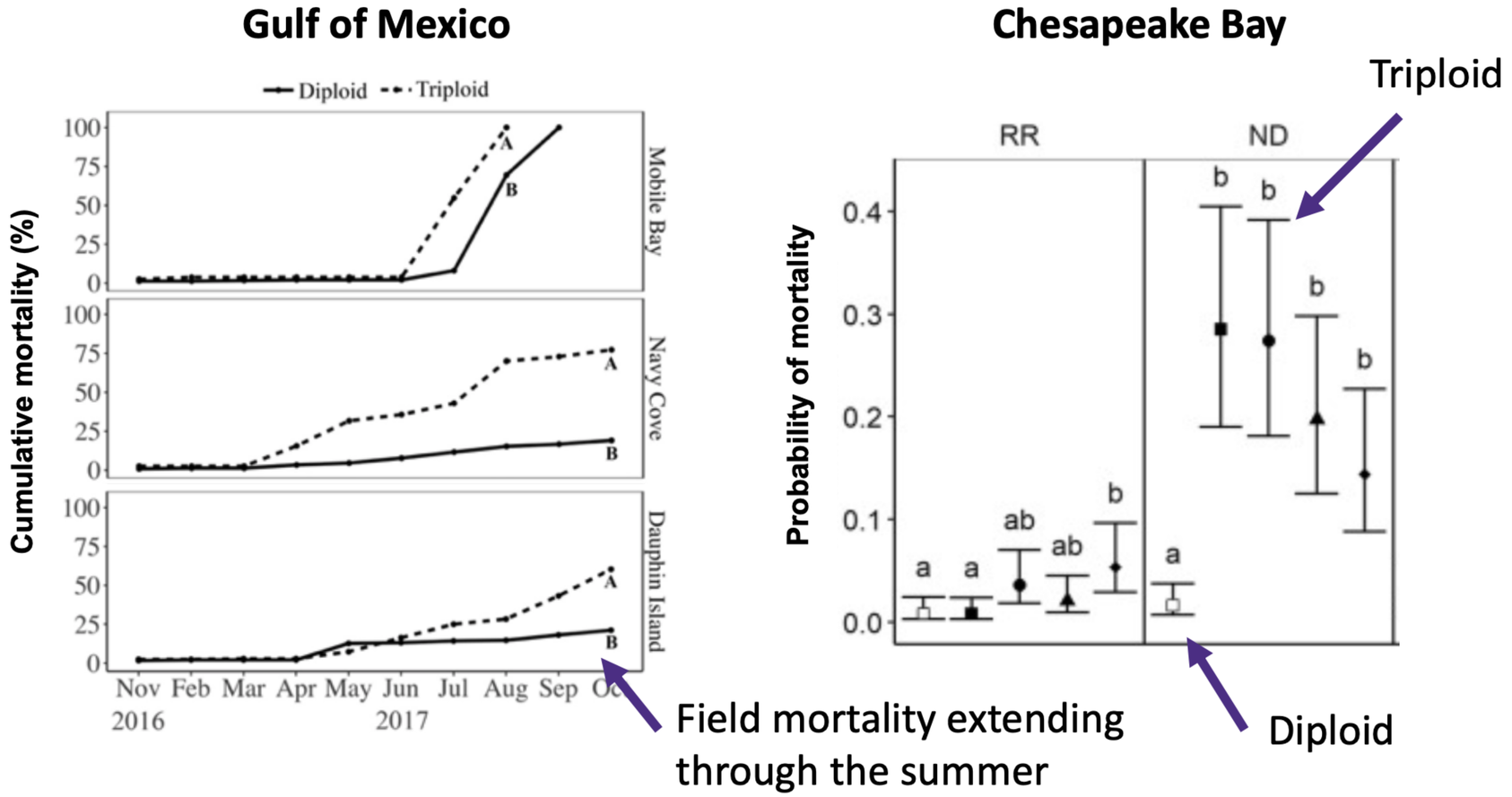
Epigenetics — scRNAseq

- Leveraging environmental memory mechanisms to improve phenotypes
- Developing alternatives to sterility (Gavery)

Environmental Challenges

Triploid Oysters are more susceptible

Summer Mortality Syndrome



Wadsworth 2018; http://hdl.handle.net/10415/6074

Matt et al. 2020; doi: 10.1016/j.aquaculture.2020.735375

Matt George - UW

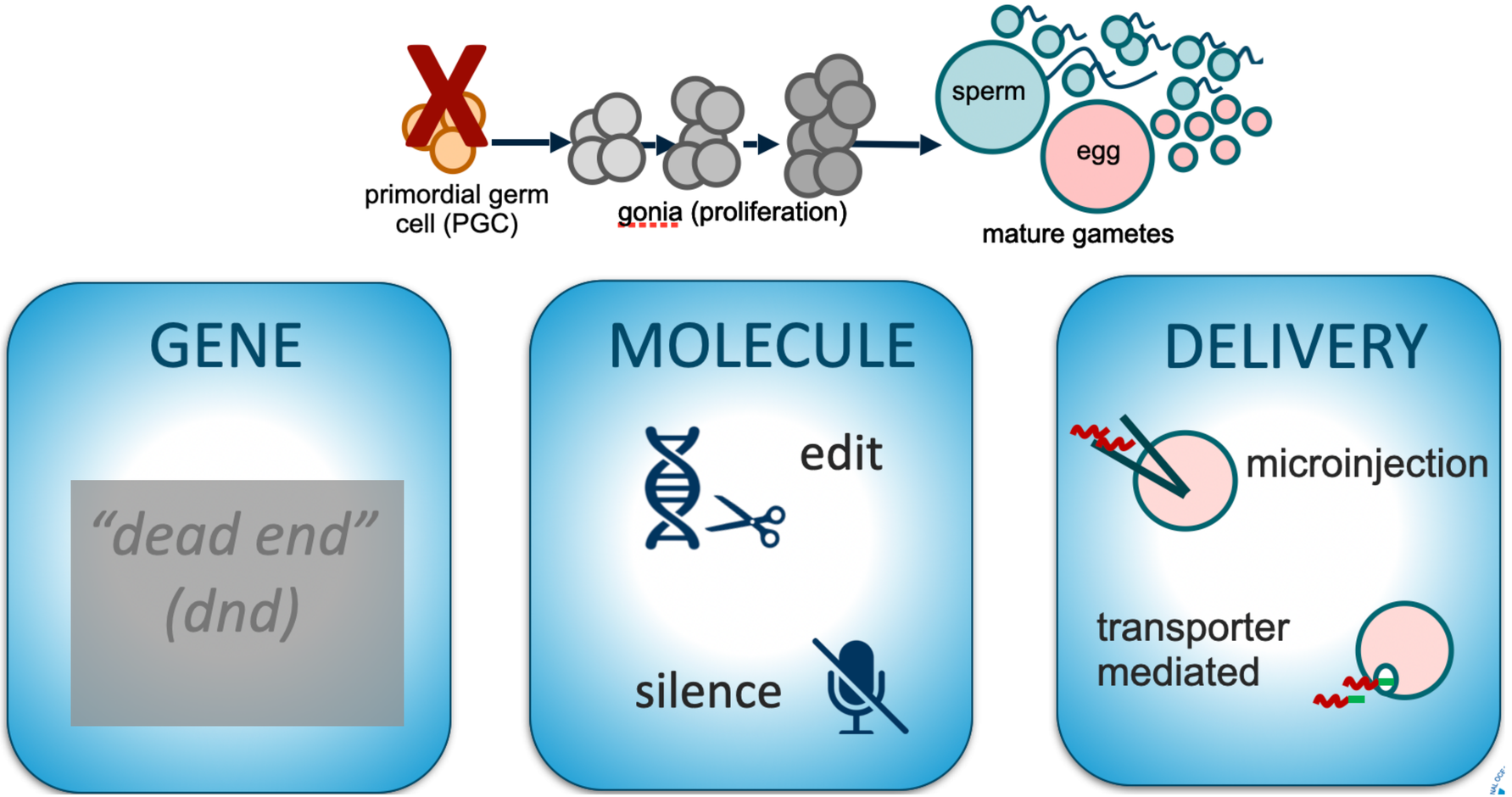
Benefits of Sterility

Improved Growth

Prevents genetic contamination

Year-round Marketability

Germ Cell Elimination



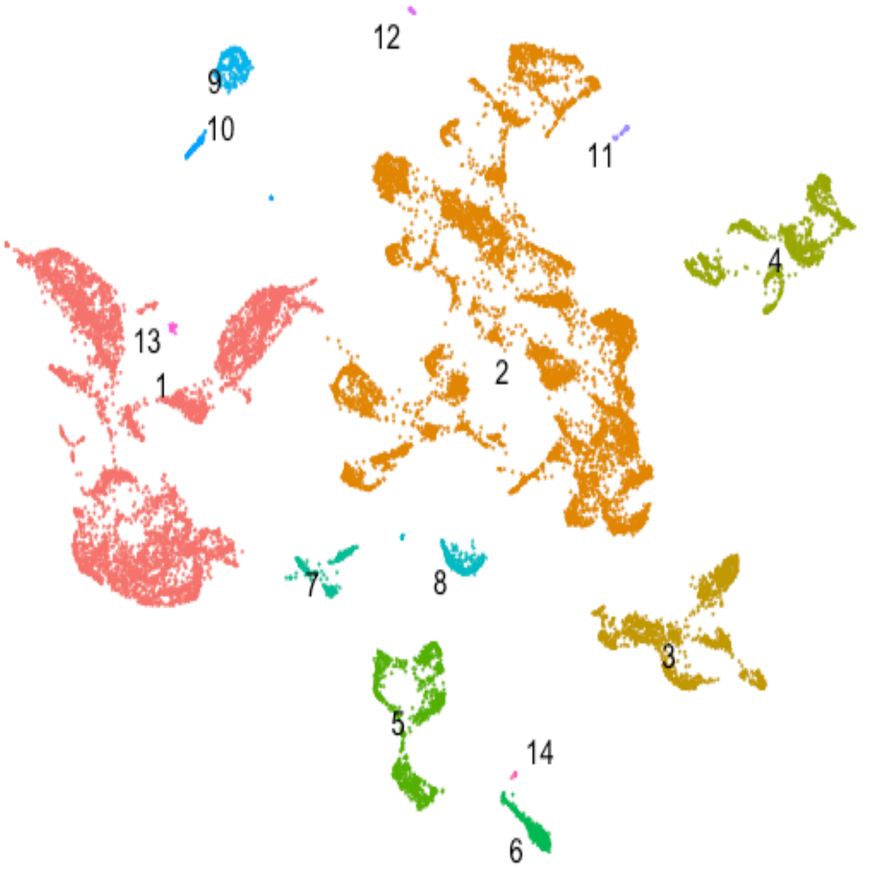
Single Cell RNA Sequencing

1. Fertilize, monitor development, sample: cleavage through gastrula stage

2. Dissociate the embryos into a single cell suspension

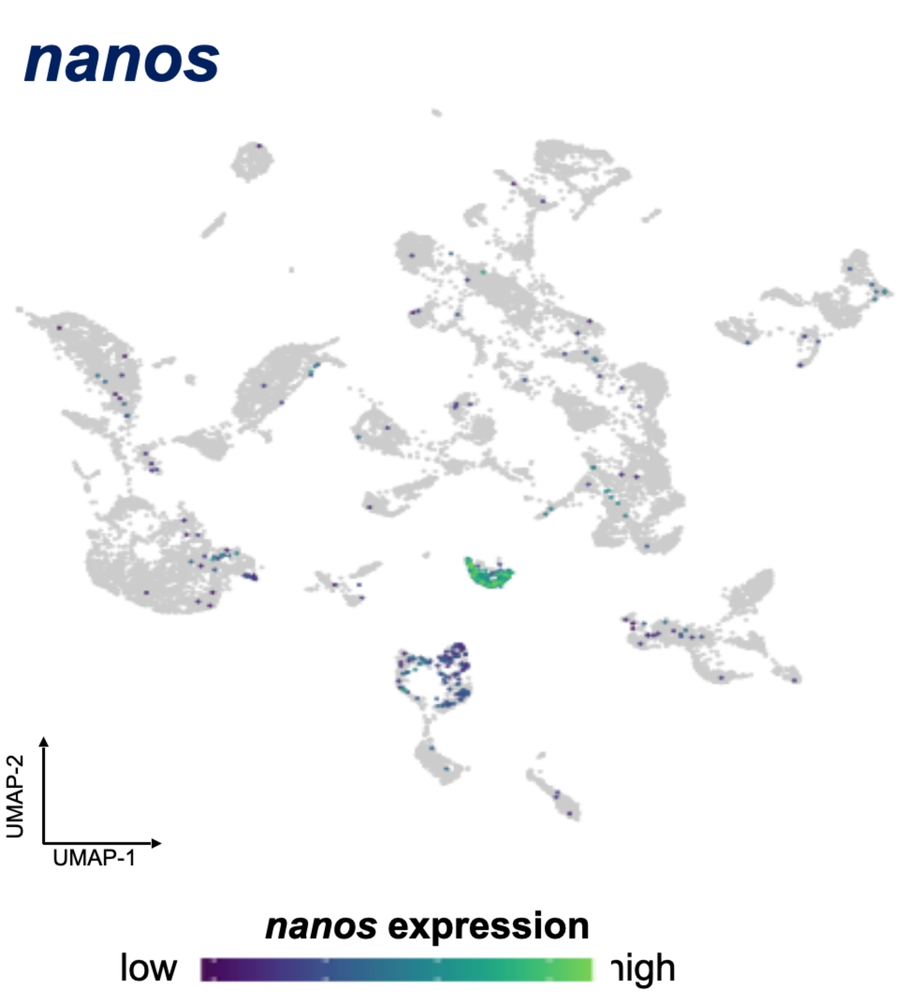
3. Prepare the single-cell RNA-Seq libraries and sequence the expressed genes in each cell

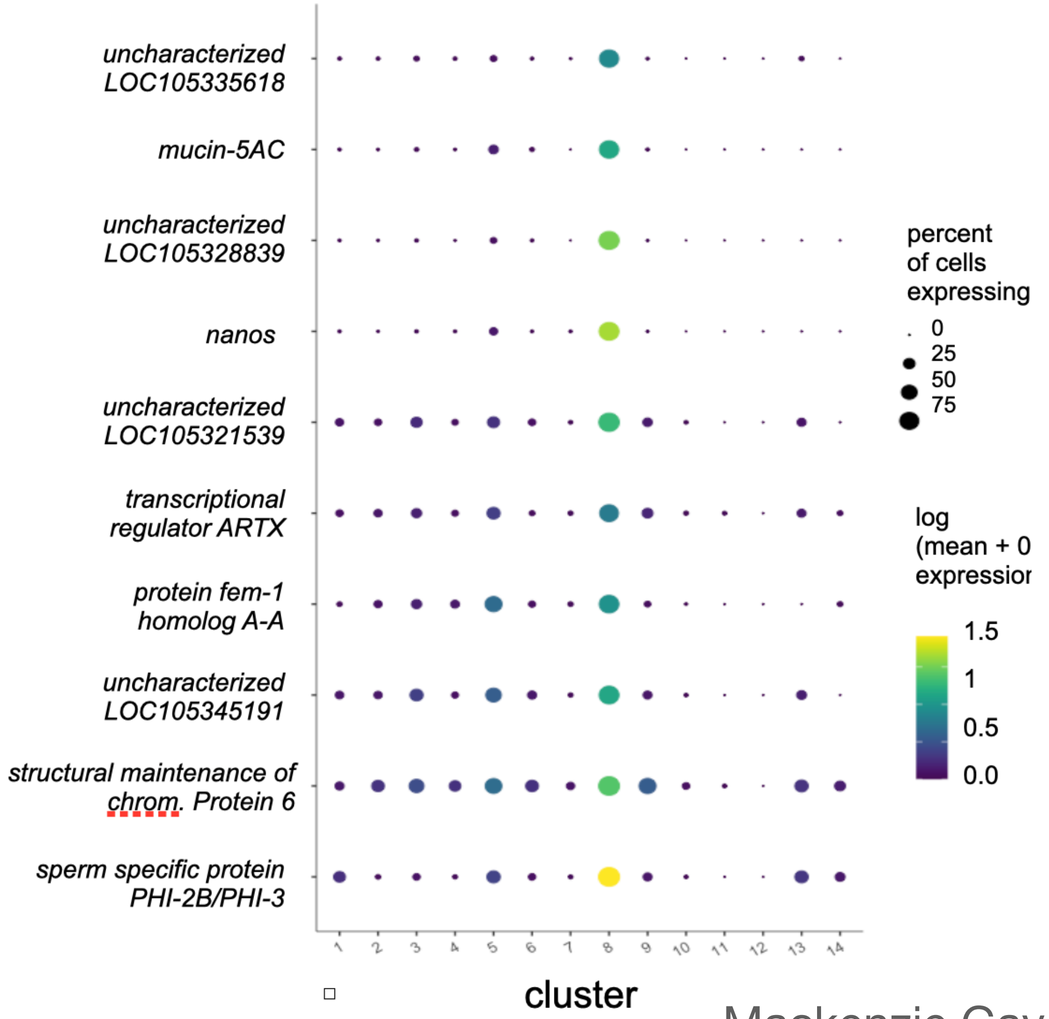
4. Group the cells according to gene expression patterns (“clustering”)



Mackenzie Gavery - NOAA

Candidates uniquely expressed in PGC





Mackenzie Gavery - NOAA

Next Step

- We have identified candidate genes involved in primordial germ cell development in Pacific oysters
- Next Steps:
    - Develop methods to deliver gene silencing molecules to (small) bivalve embryos
    - Evaluate the effect of silencing candidate genes on reproductive phenotypes
- Long-term Goal: work collaboratively to develop protocols to induce sterility via germ cell elimination at a hatchery-scale

Bioinformatic Approaches in non-model species

marineomics.io

Received: 29 March 2023 | Accepted: 11 September 2023

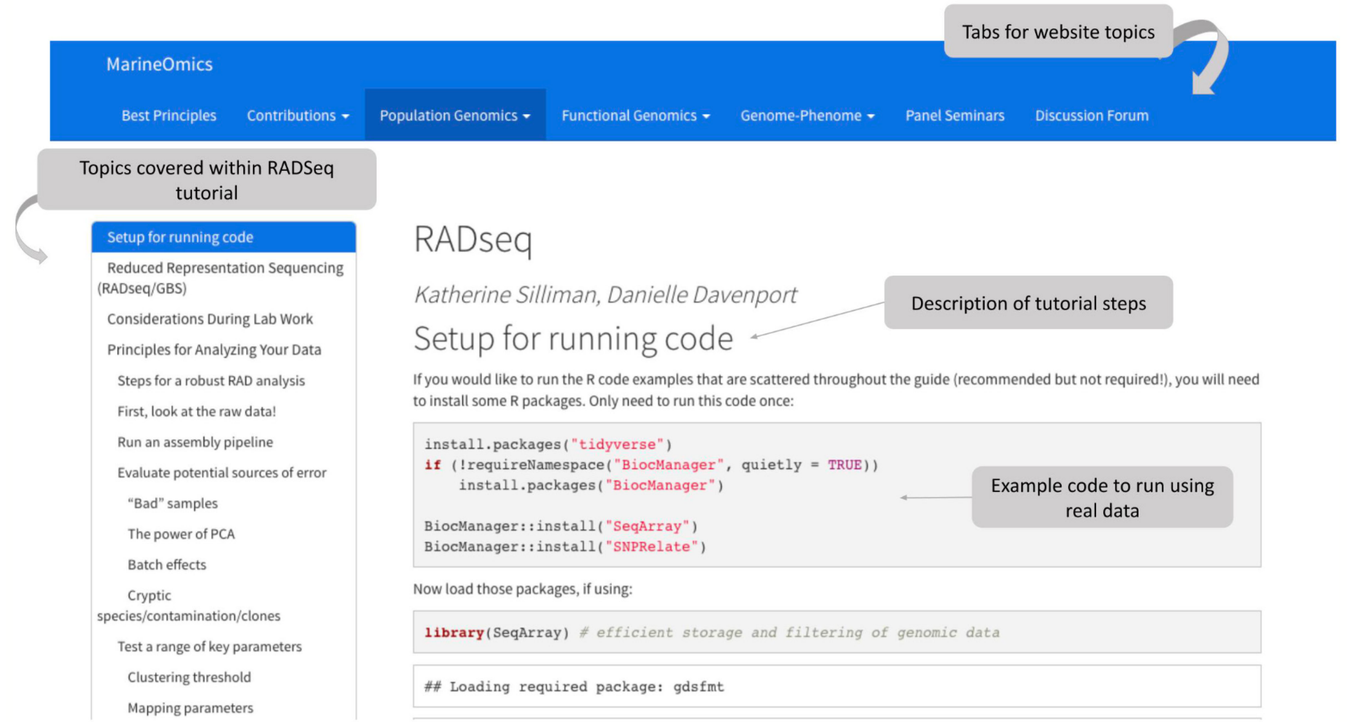
DOI: 10.1111/2041-210X.14219

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]



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See also our Lab Handbook

robertslab.github.io/resources

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
```

GITHUB.COM/SR320/TALK-DBEA-2023

ACKNOWLEDGEMENTS

USDA

1er Congreso de Biología Experimental y Aplicada
LA CIENCIAS DE LA VIDA A TRAVÉS DE LAS ESCALAS

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