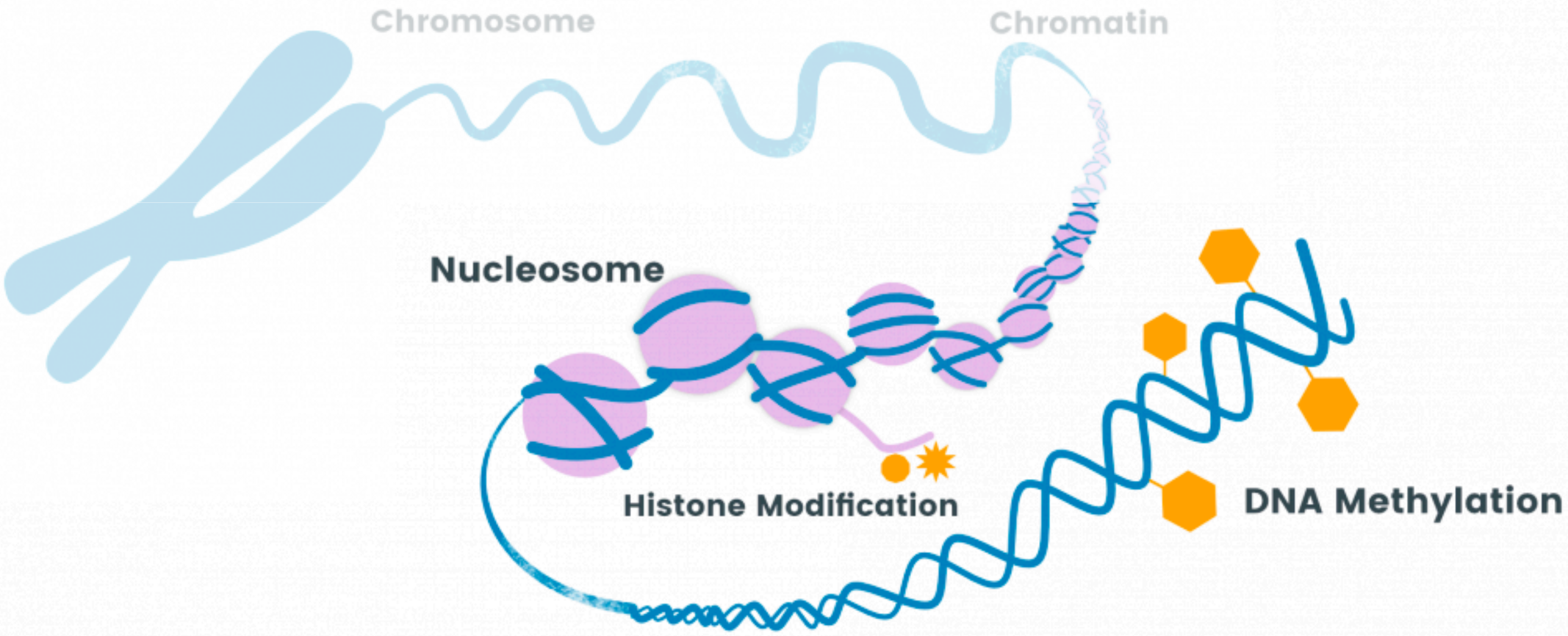
DNA Methylation in Bivalves

IMPLICATIONS FOR AQUACULTURE

Epigenomics in Aquaculture (EpiAqua)
Understanding the effects of Climate Change on farmed species
25-27th, January 2023. University of Concepción, Chile

Steven Roberts - University of Washington

ALTERS THE PHENOTYPE (WITHOUT CHANGING DNA CODE); HERITABLE



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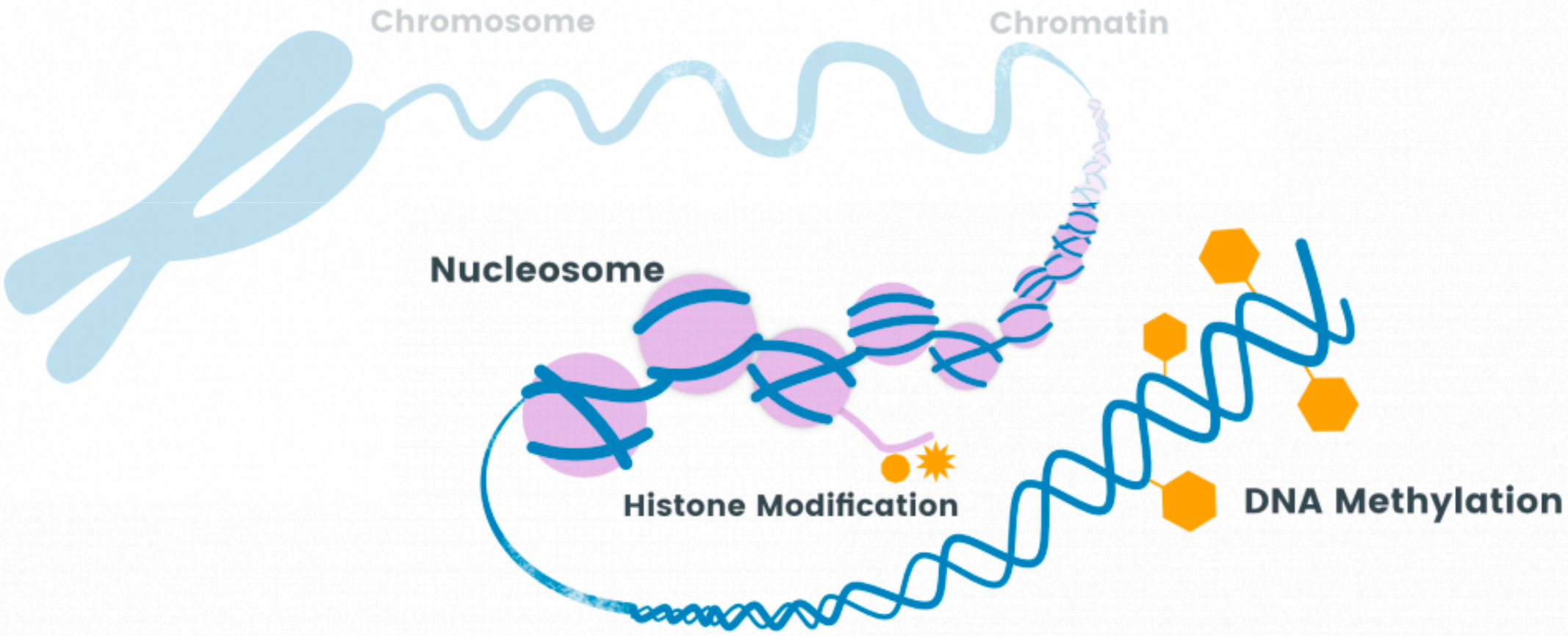
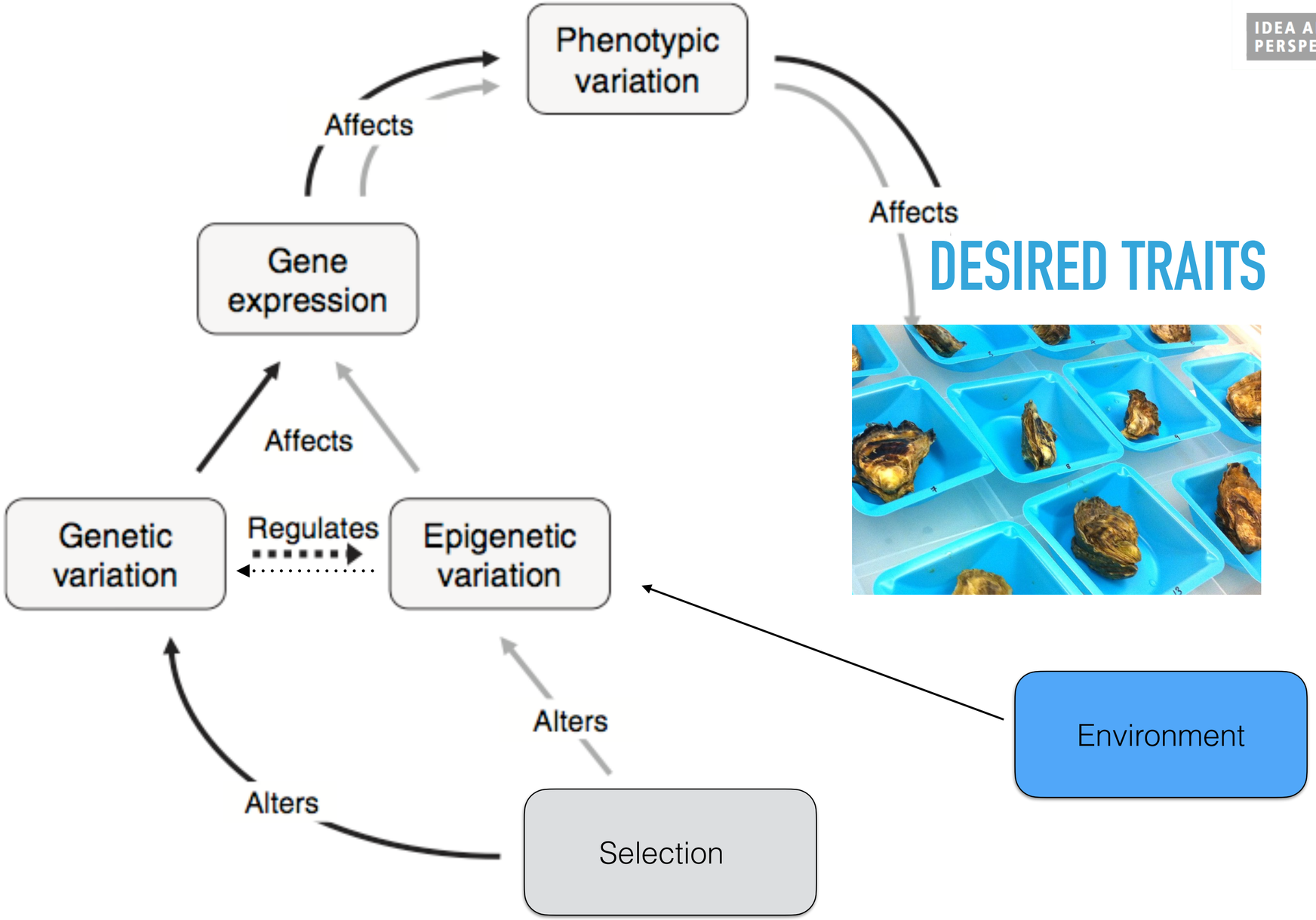


CAN BE INDUCED WITH ENVIRONMENTAL MANIPULATION

ECOLOGICAL EPIGENETICS



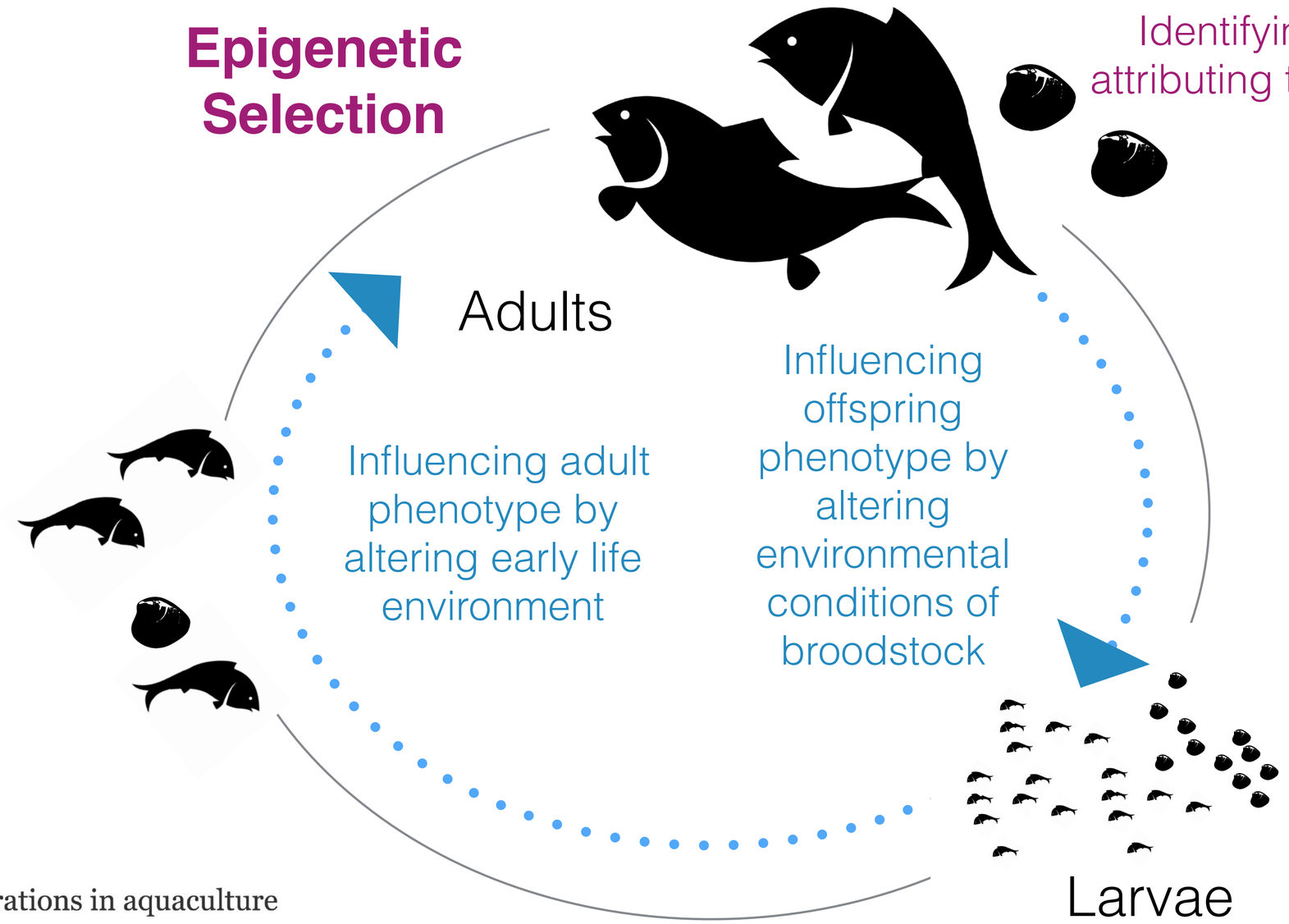
Ecology Letters, (2008) **11**: 106–115 doi: 10.1111/j.1461-0248.2007.01130.x

IDEA AND PERSPECTIVE

Epigenetics for ecologists

Affects

DESIRED TRAITS



PEER-REVIEWED Aquatic Biology section ›

Epigenetic considerations in aquaculture

Literature review | Aquaculture, Fisheries and Fish Science | Molecular Biology

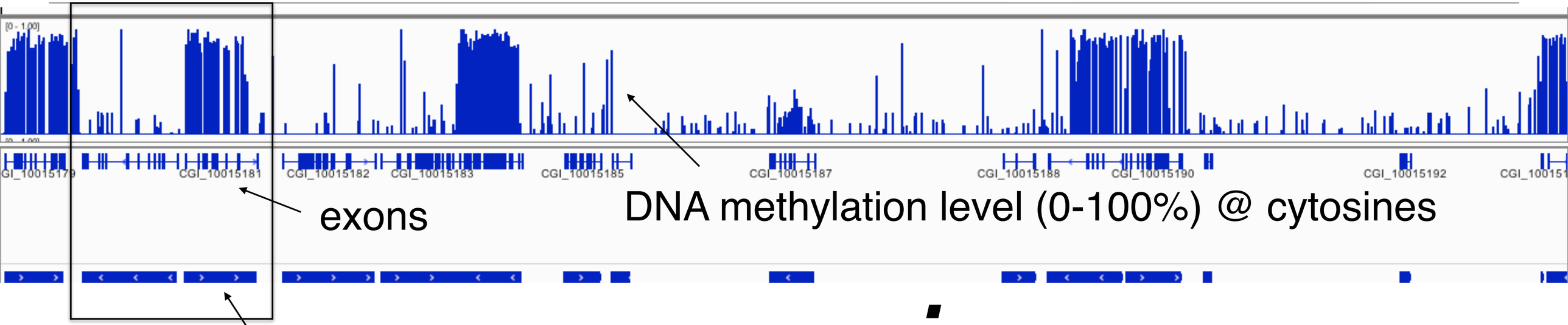
Mackenzie R. Gavery, Steven B. Roberts

Outline

DNA Methylation in Bivalves

- General Aspects *including* Methods and Approaches
- Influencing Offspring
- Early-life Environment
- Epigenetic Selection
- Future Perspectives

METHYLATION LANDSCAPE IN SHELLFISH

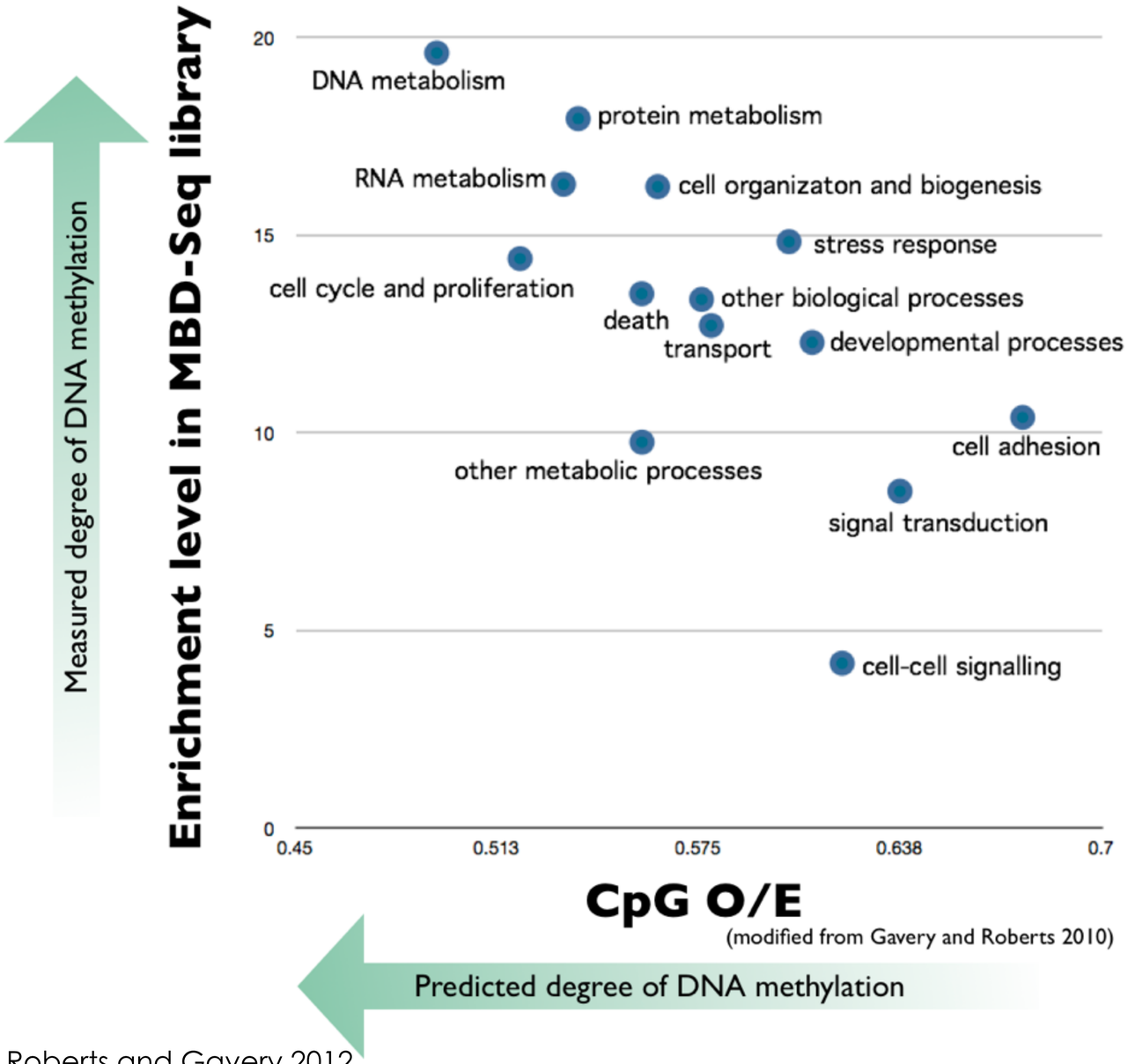


mosaic

associated with gene bodies

Why are only a subset of genes methylated?

METHYLATION LANDSCAPE IN SHELLFISH



Roberts and Gavery 2012

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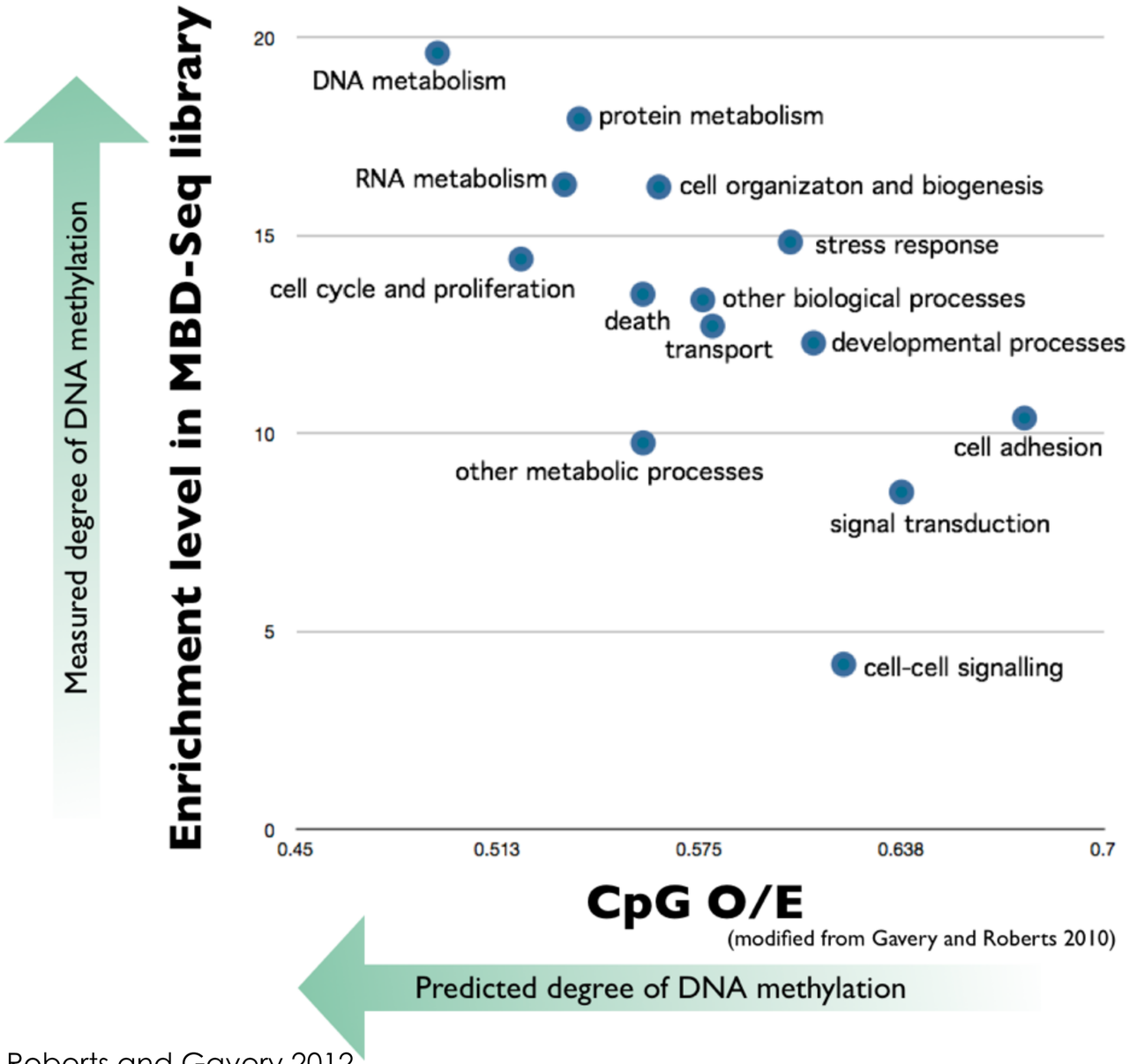

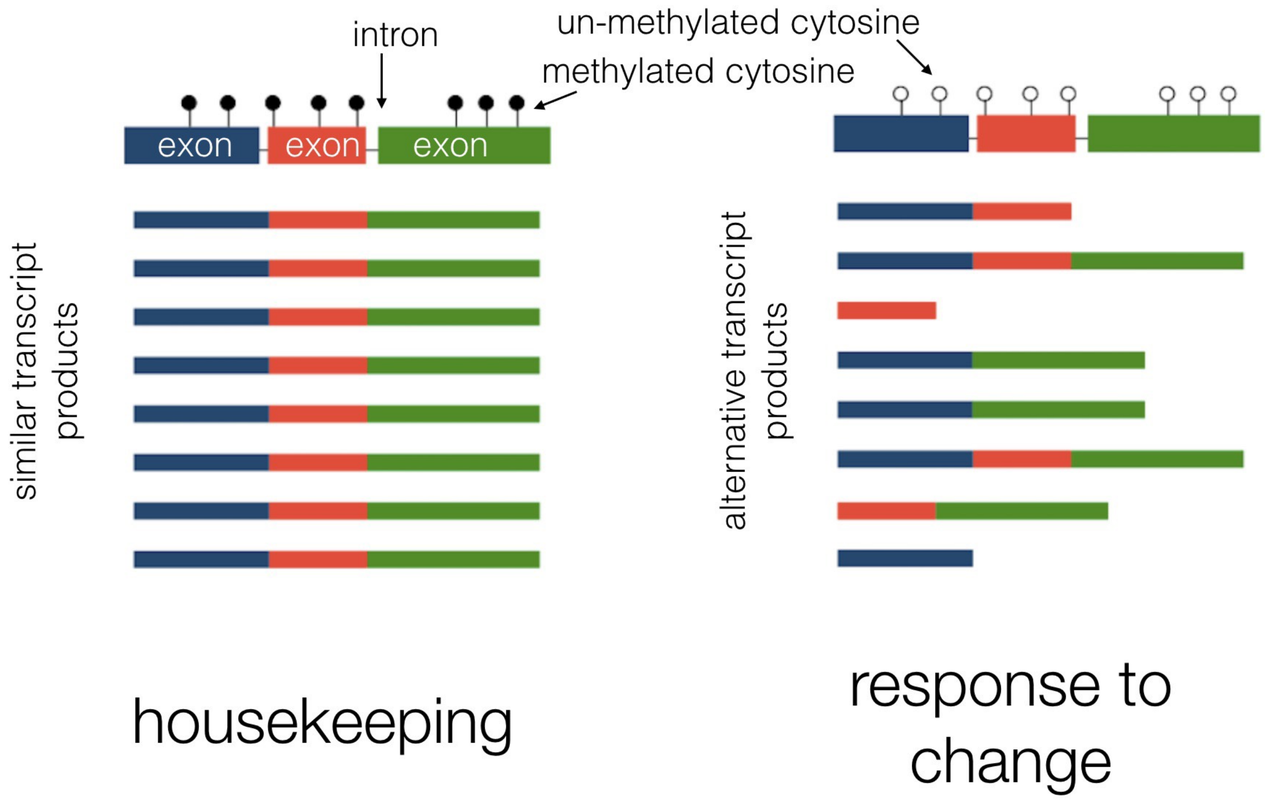

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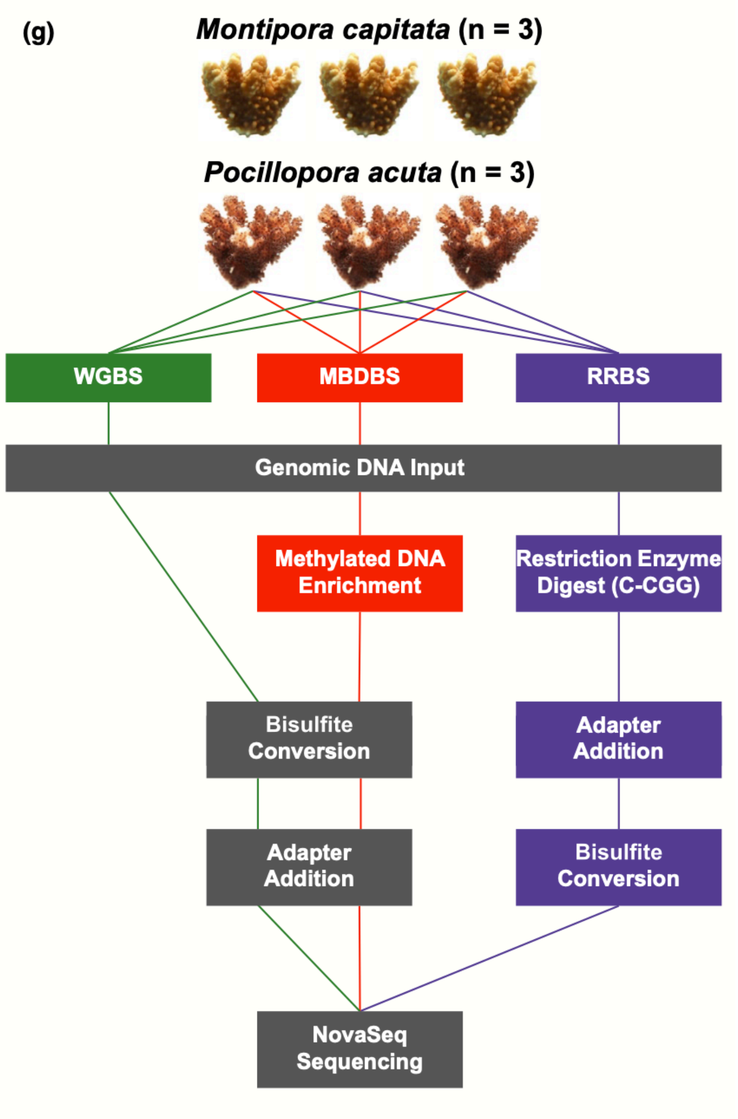
HIGH THROUGHPUT SEQUENCING TO ASSESS DNA METHYLATION



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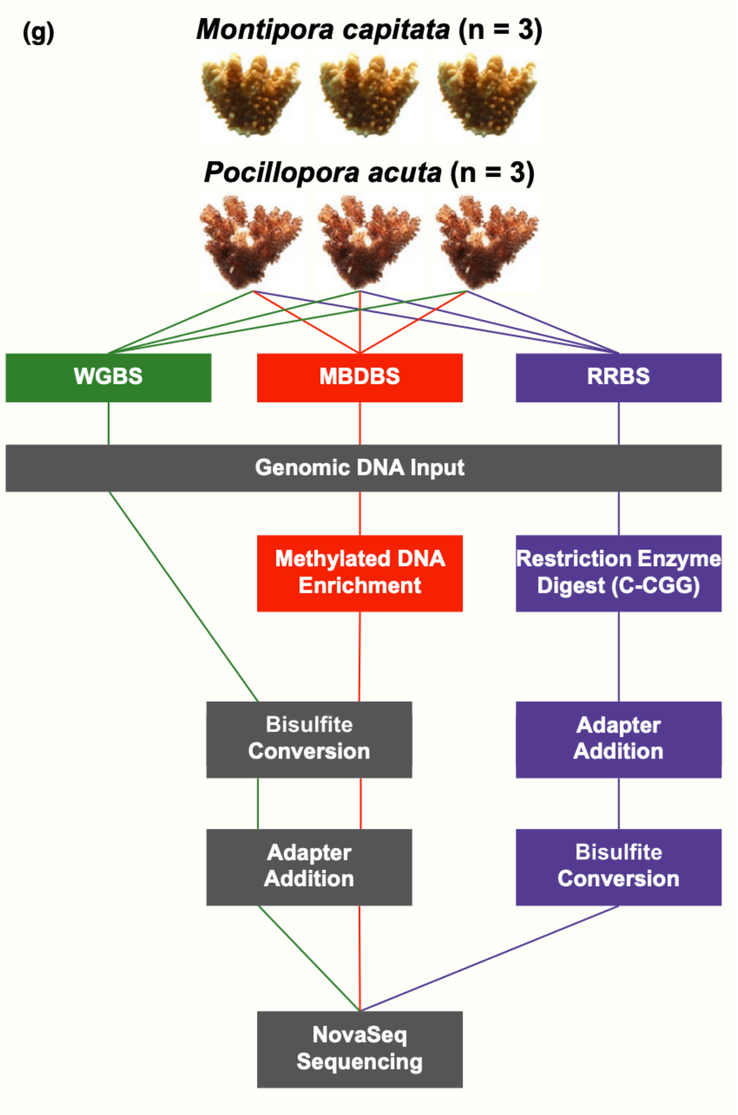

DOI: 10.1111/1755-0998.13542

MOLECULAR ECOLOGY RESOURCES WILEY

RESOURCE ARTICLE

Invertebrate methylomes provide insight into mechanisms of environmental tolerance and reveal methodological biases

Shelly A. Trigg[1] | Yaamini R. Venkataraman[1,2] | Mackenzie R. Gavery[3] | Steven B. Roberts[1] | Debashish Bhattacharya[4] | Alan Downey-Wall[5] | Jose M. Eirin-Lopez[6] | Kevin M. Johnson[7,8] | Katie E. Lotterhos[5] | Jonathan B. Puritz[9] | Hollie M. Putnam[9]

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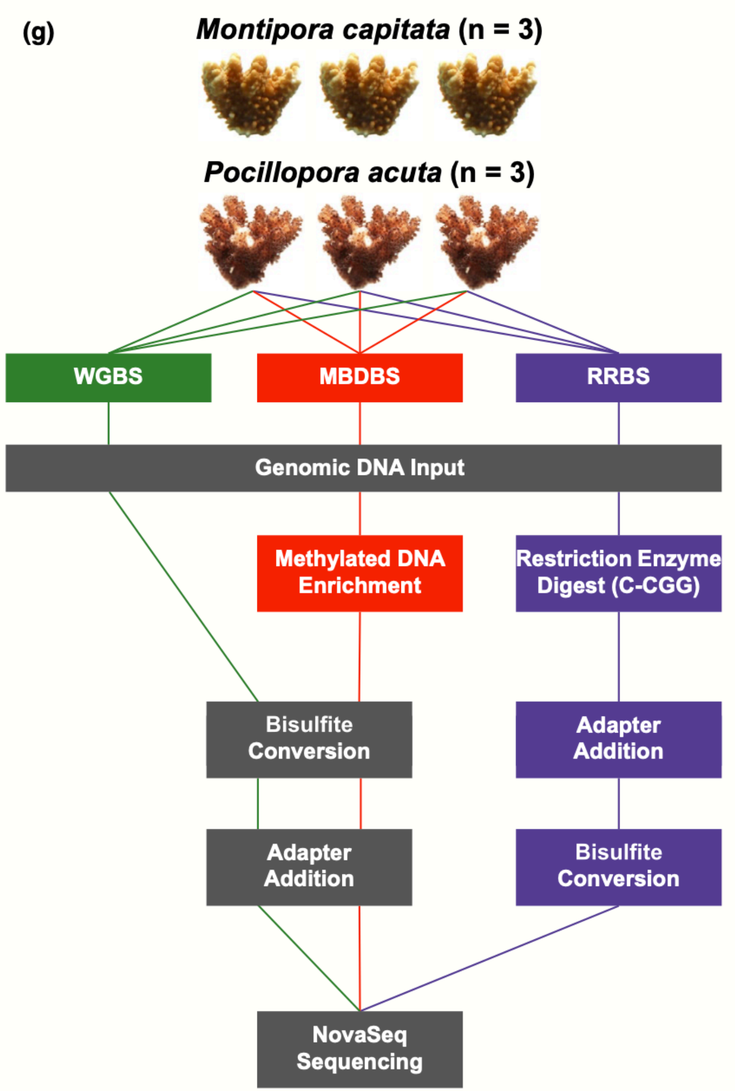
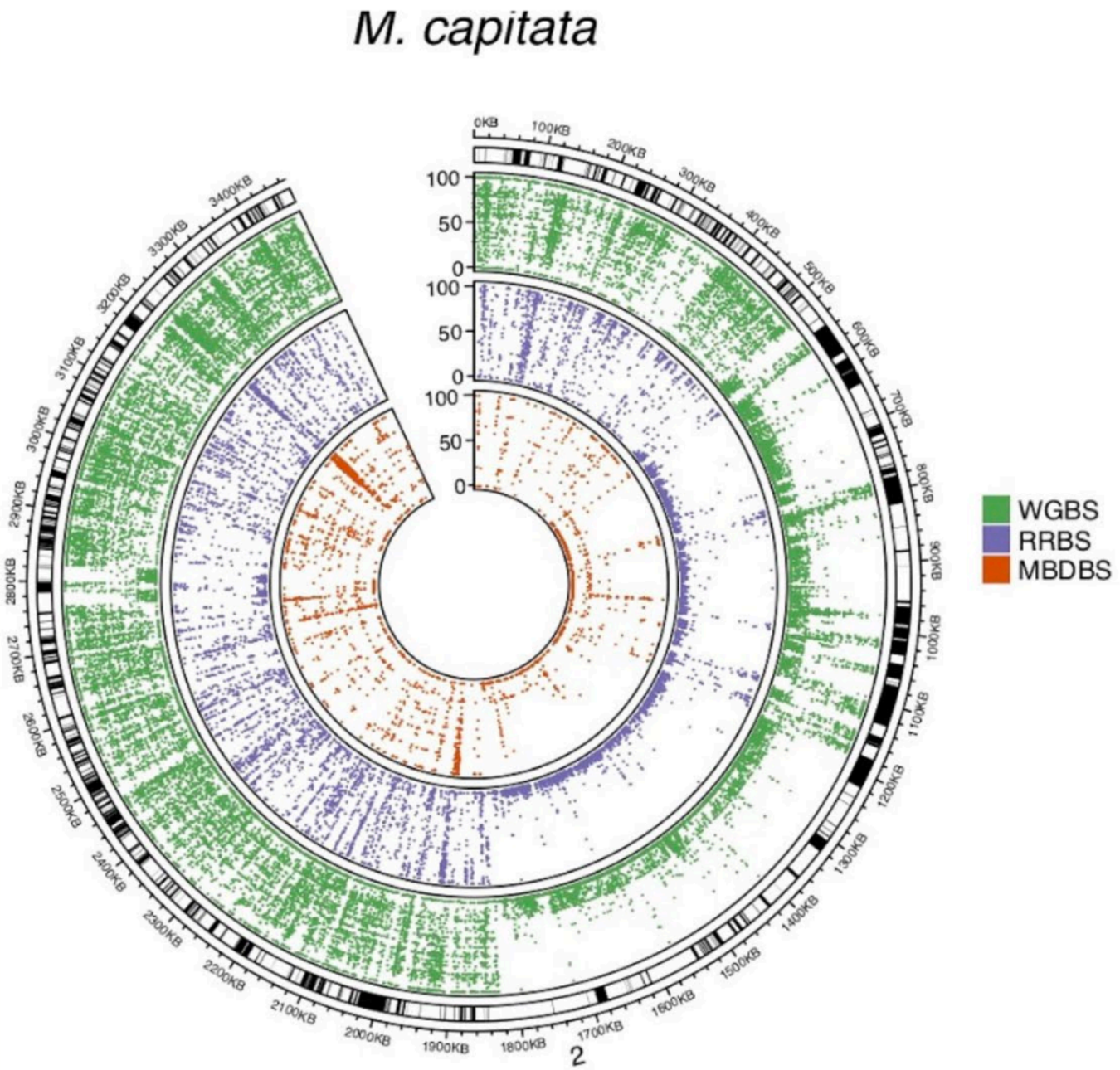
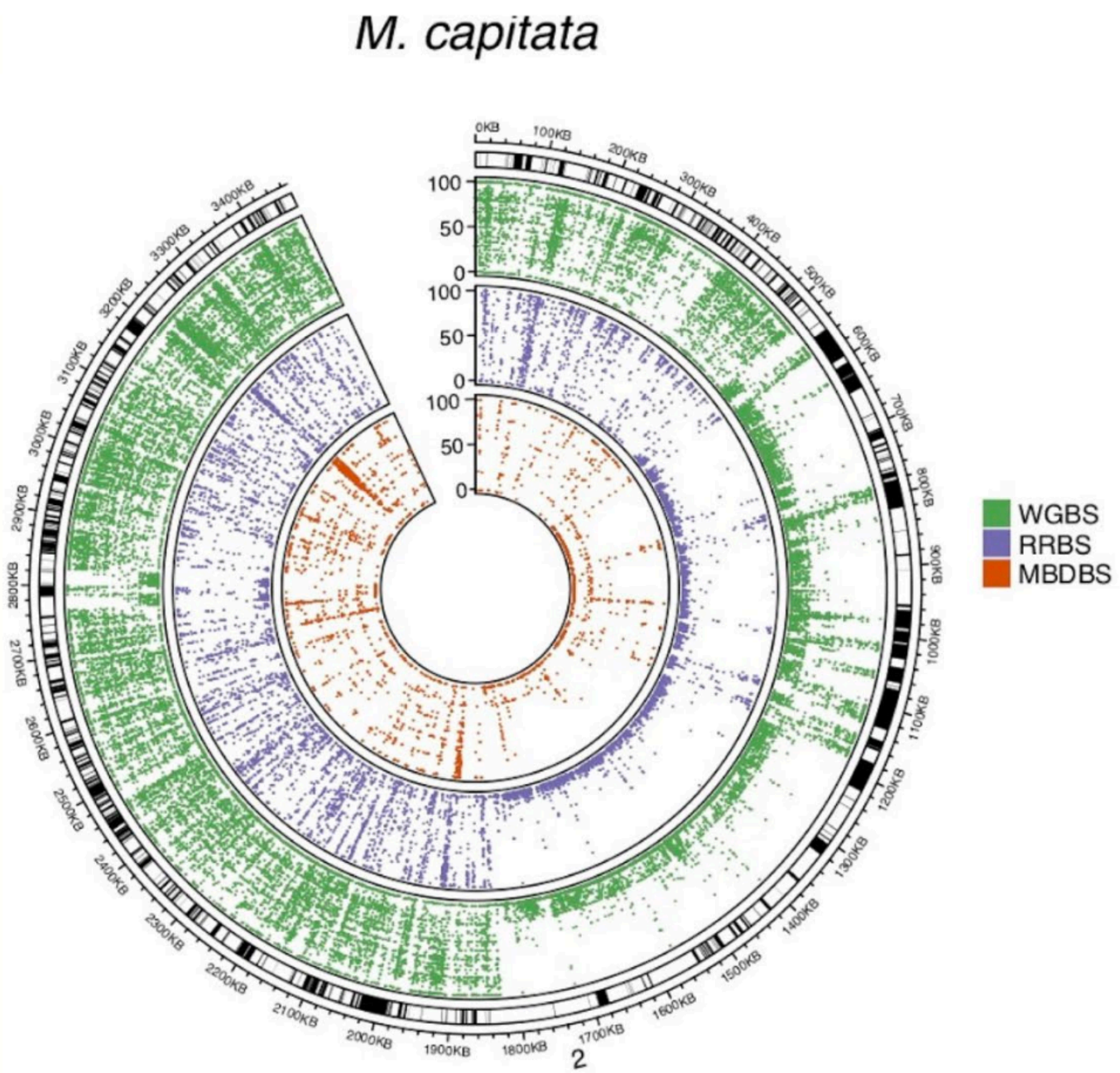




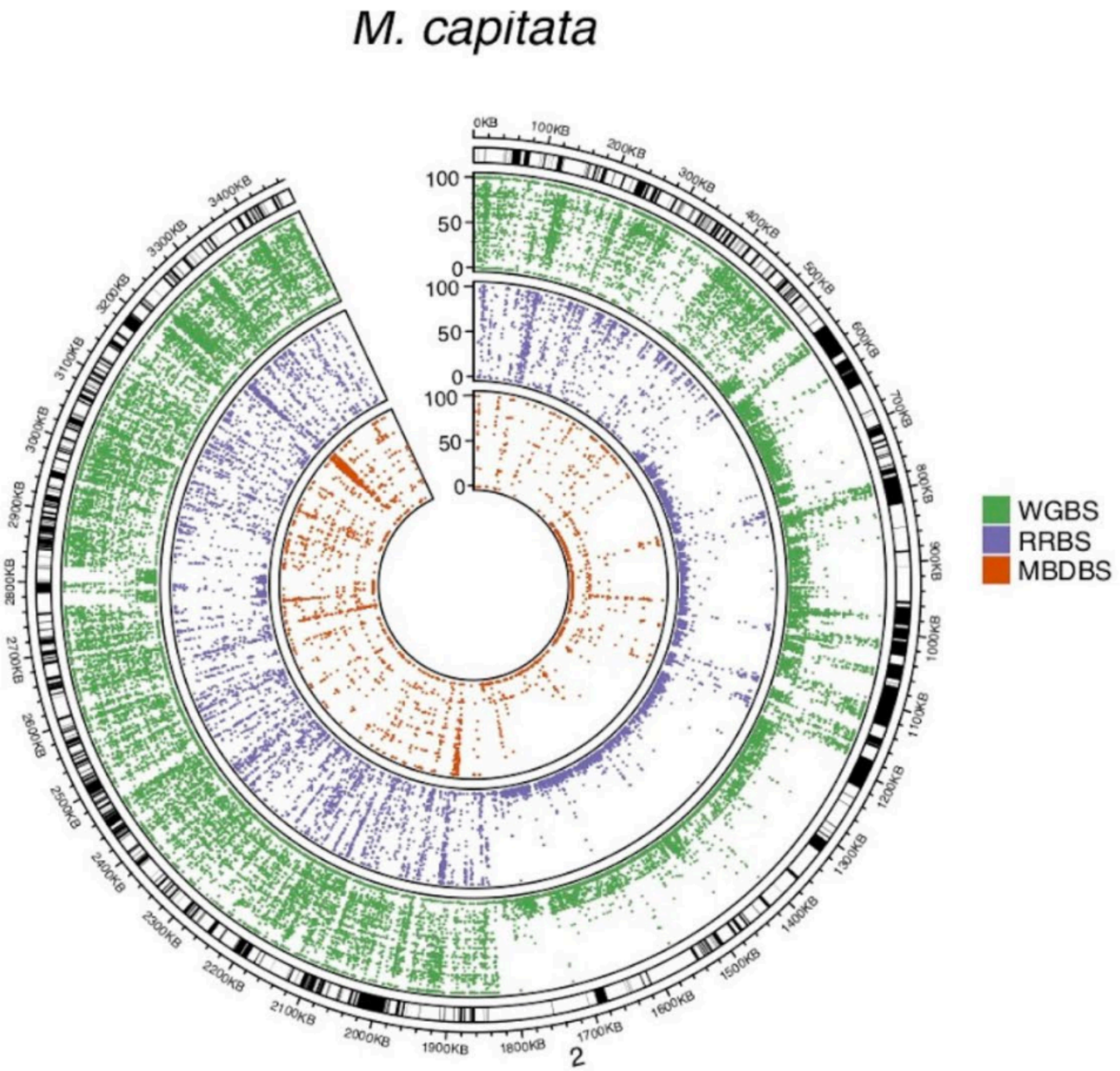
HIGH THROUGHPUT SEQUENCING

MBDBS has the greatest capacity for detecting CpGs in coding regions at our sequencing depth, but MBDBS may be influenced by intrasample methylation heterogeneity.

RRBS yields robust information for specific loci albeit without enrichment of any particular genome feature and with significantly reduced genome coverage.



CONSIDERATION GOING FORWARD



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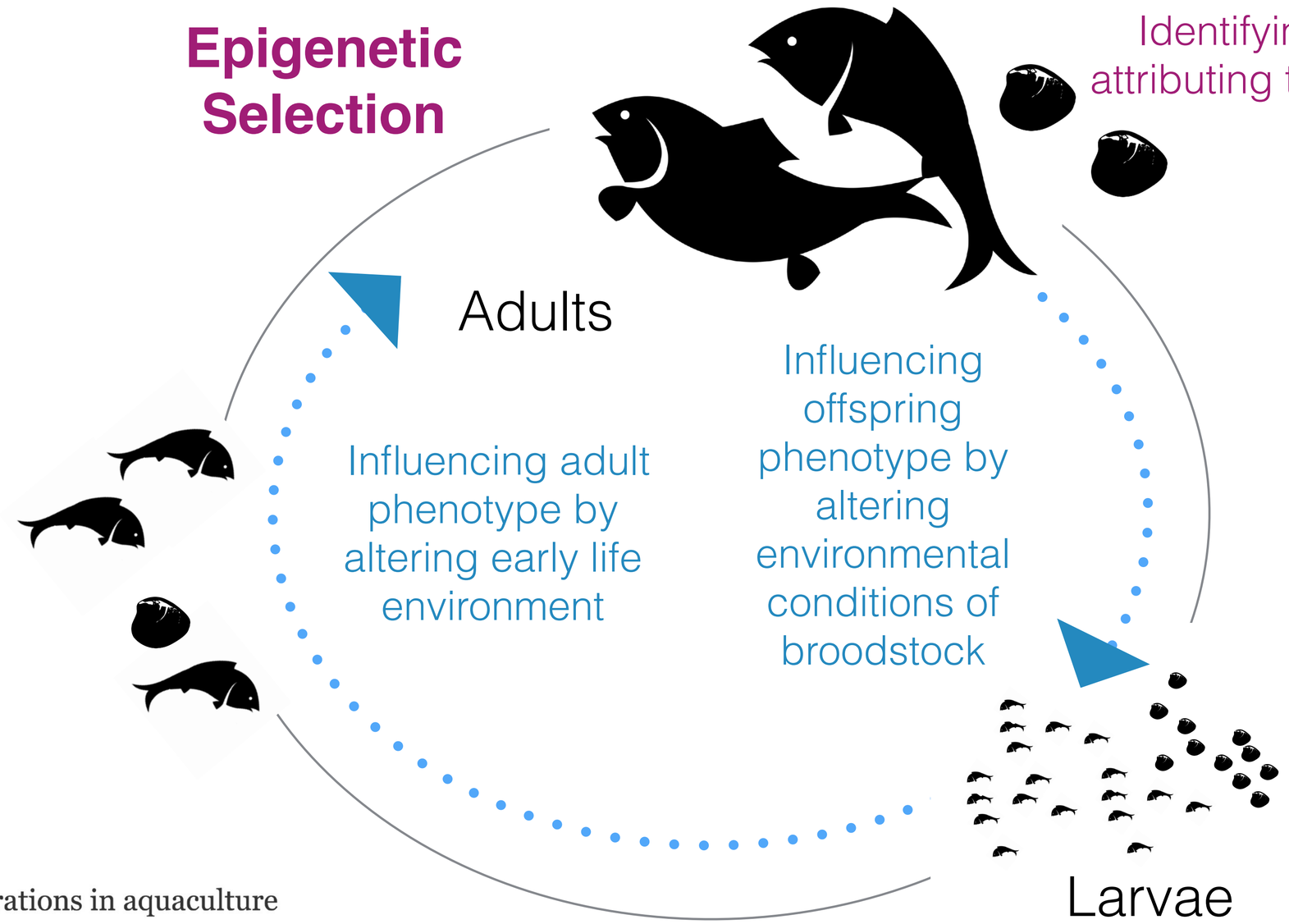

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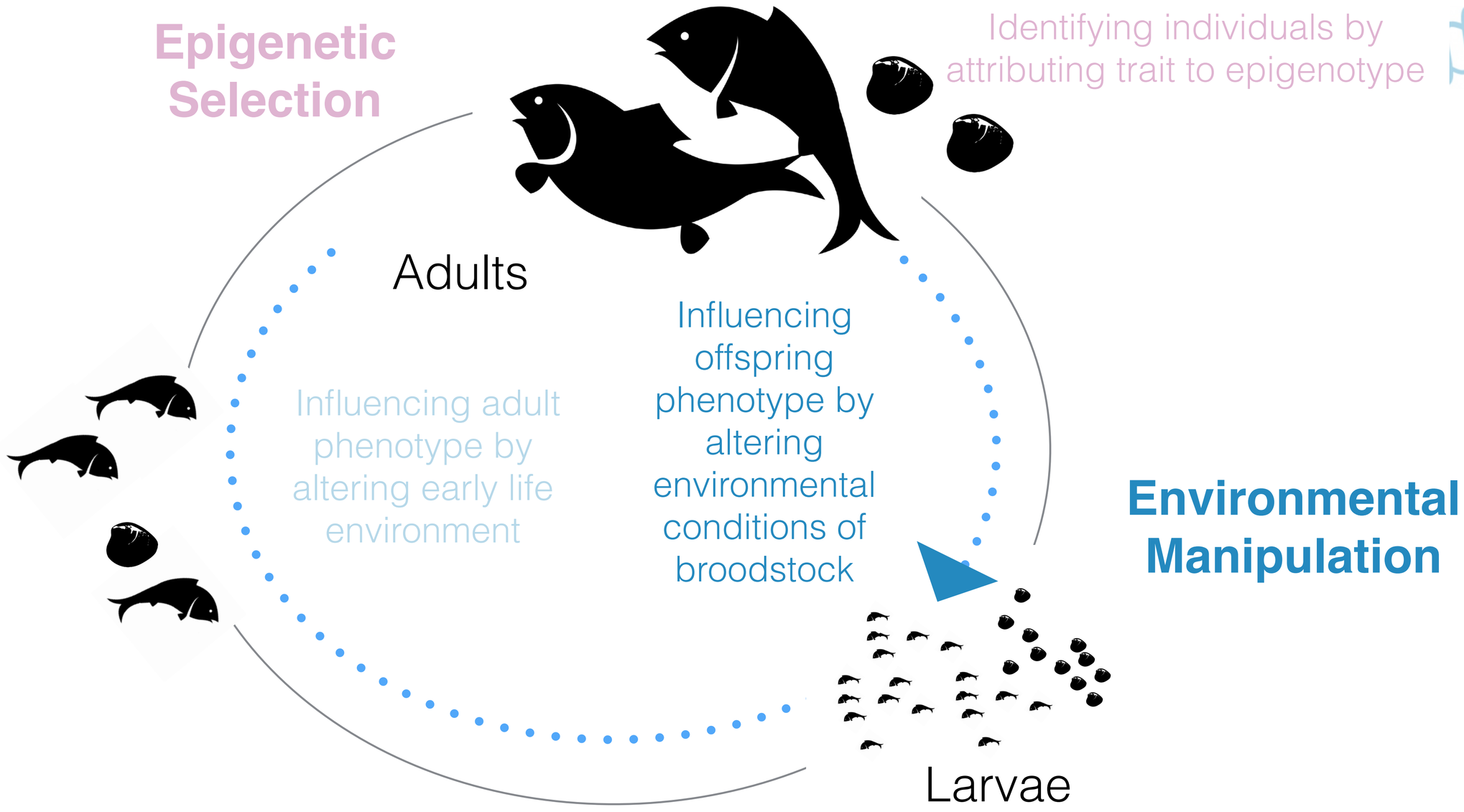
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EFFECTS OF TEMPERATURE AND OA IN OLYMPIA OYSTER POPULATIONS

- Broodstock were held at ambient pCO2 (841 µatm) or high pCO2 (3045 µatm) for 52 days, during the Winter.
- **Juveniles of parents exposed to elevated pCO_2 had higher survival rates in the natural environment**

EFFECTS OF TEMPERATURE AND OA IN OLYMPIA OYSTER POPULATIONS

EFFECTS OF OA IN OLYMPIA OYSTER POPULATIONS

Parental pCO_2 Ambient High

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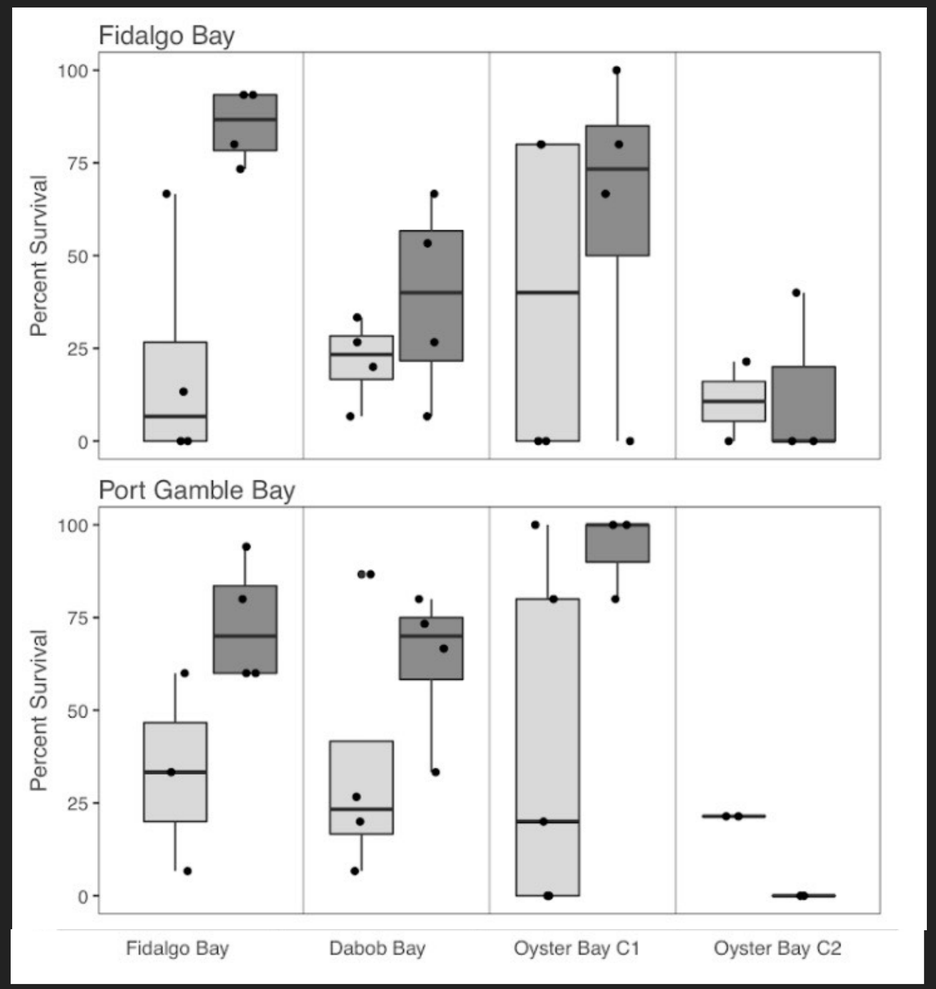

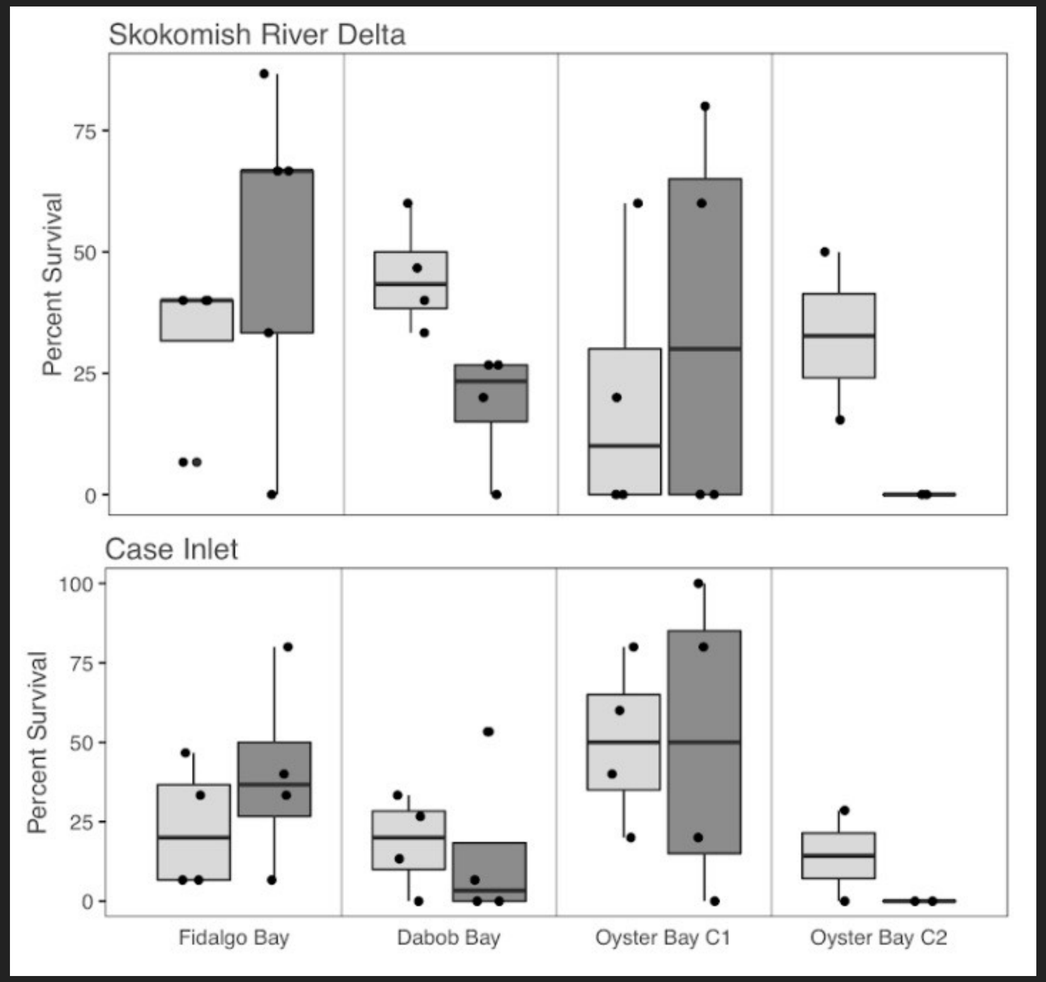

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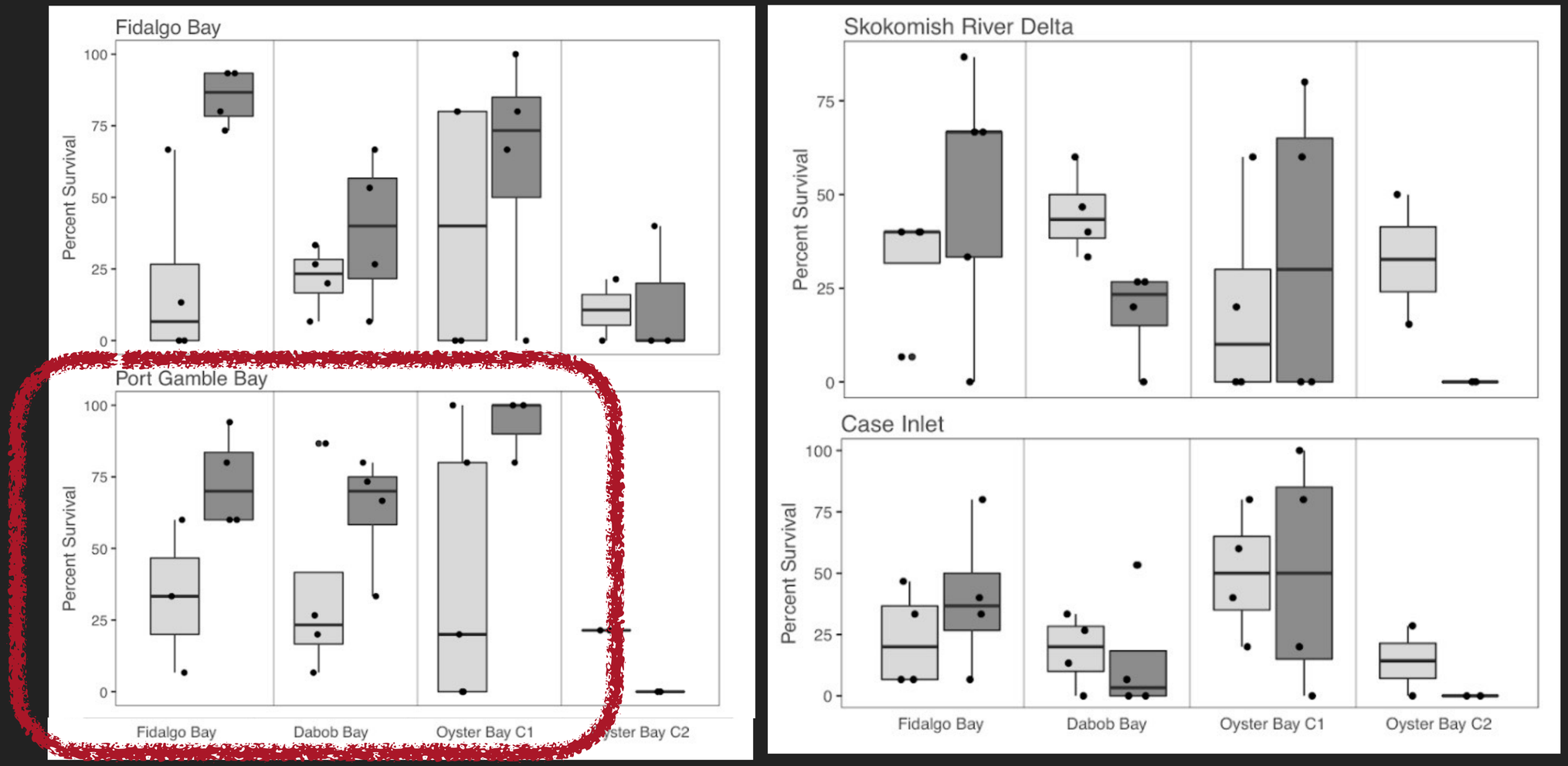

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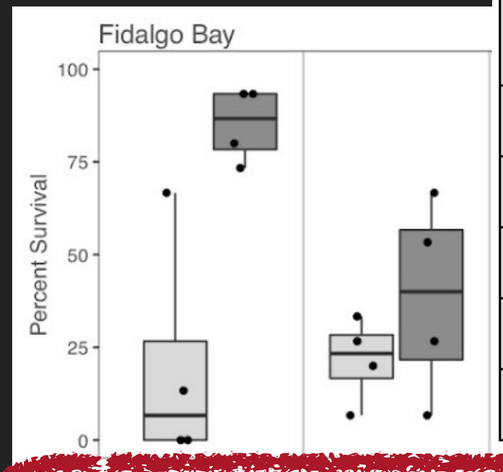
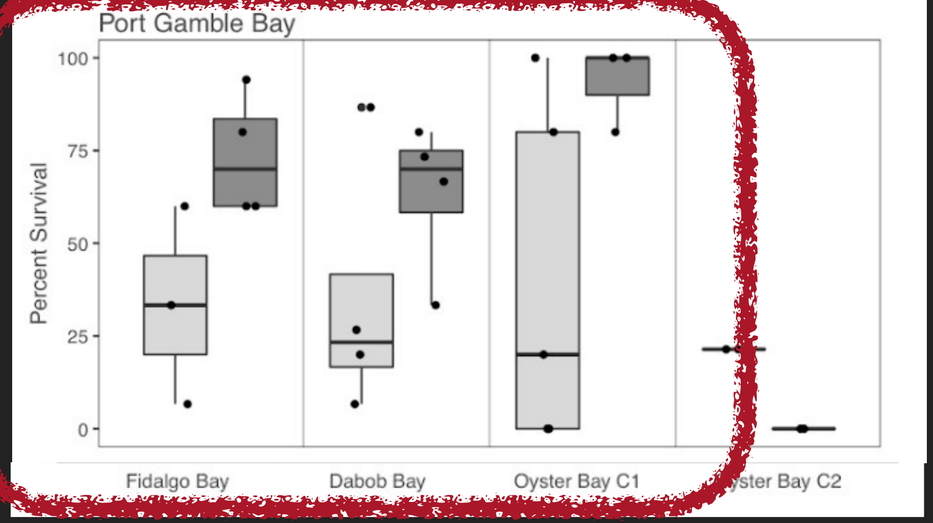


	Fidalgo Bay	*Port Gamble Bay*	*Skokomish River Delta*	*Case Inlet*
Temperature (°C)	**15.4±1.5**	**15.0±1.0**	**16.2±2.7**	**16.8±1.7**
DO (mg/L)	**10.6±2.4**	**10.5±1.9**	**10.2±3.9**	**11.2±2.8**
Salinity (PSU)	**28.5±3.9**	**31.9±2.0**	**29.6±1.3**	**24.6±1.7**
pH	**8.07±0.15**	**7.86±0.17**	**8.01±0.20**	**8.01.±0.16**
chlorophyll	**227±409**	**225±145**	**572±1536**	**331±613**



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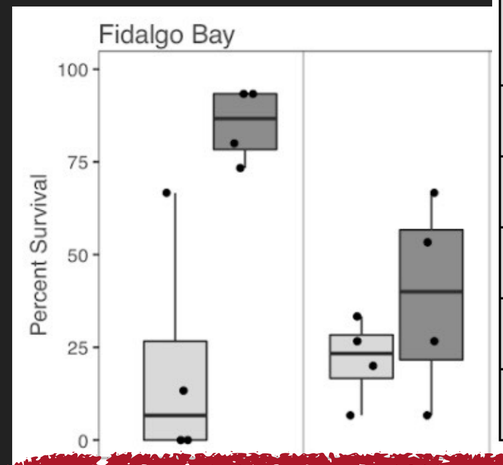

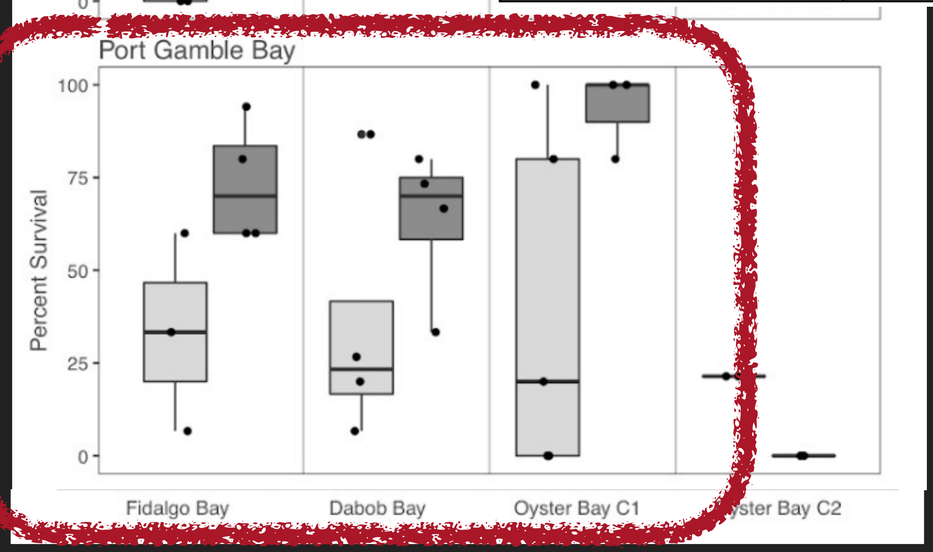

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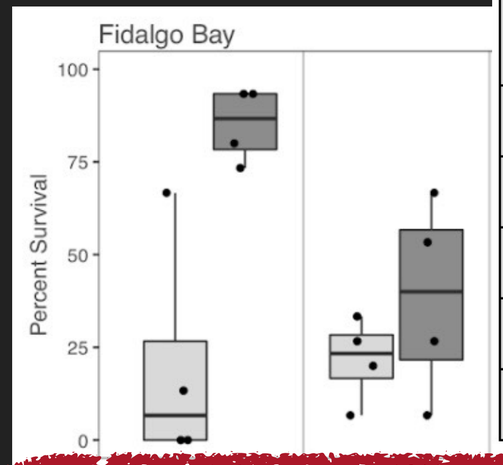

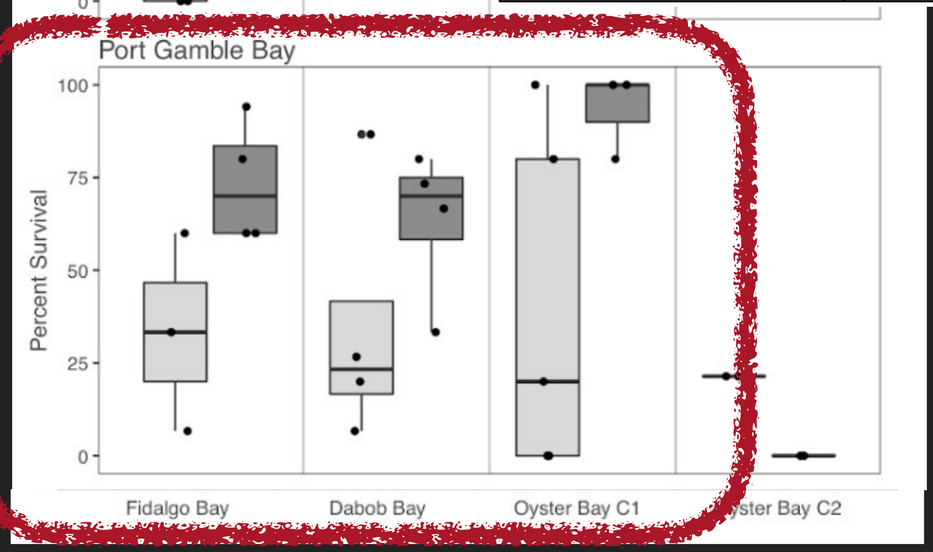

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- ENVIRONMENTAL MEMORY

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]

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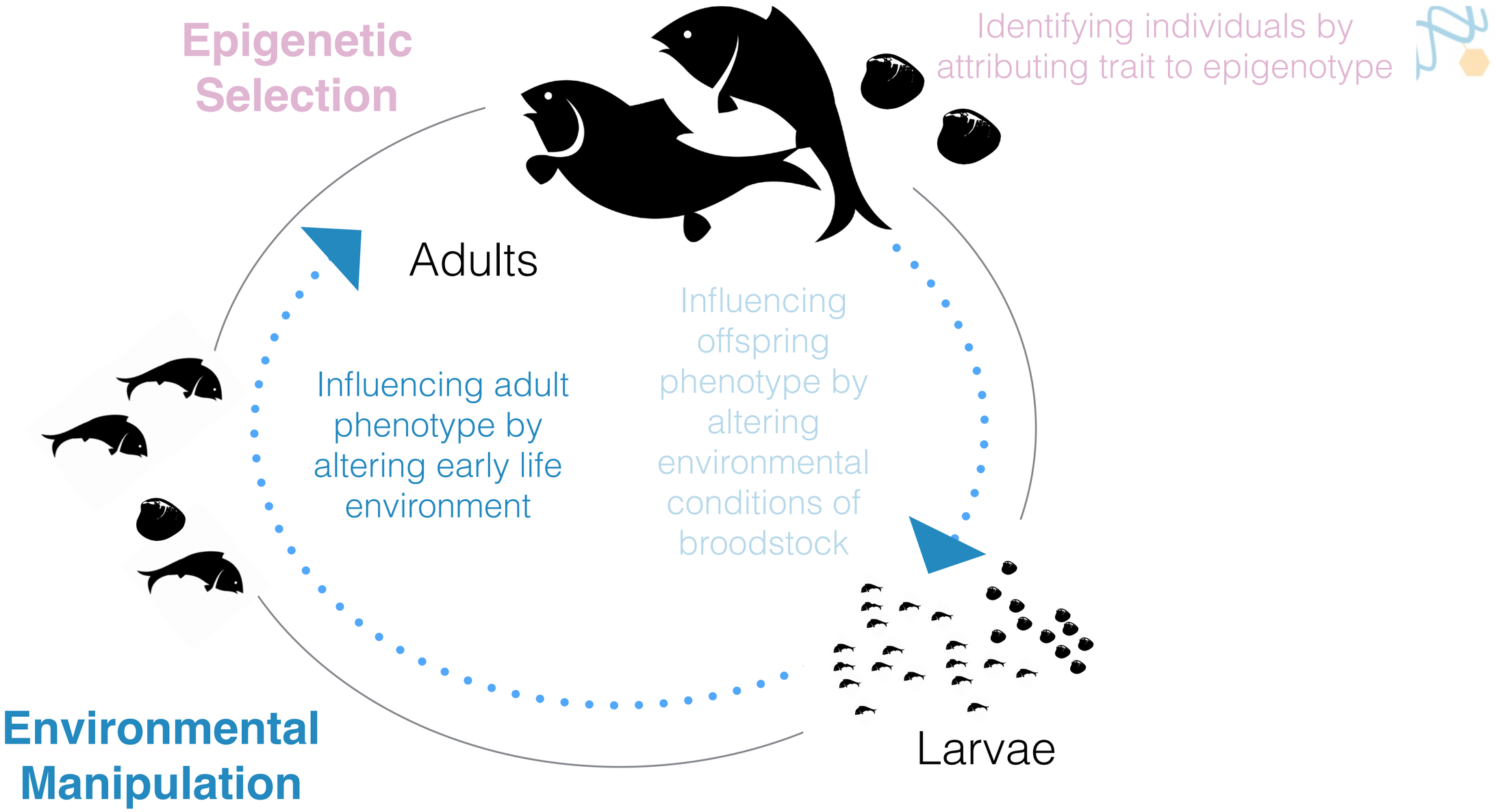
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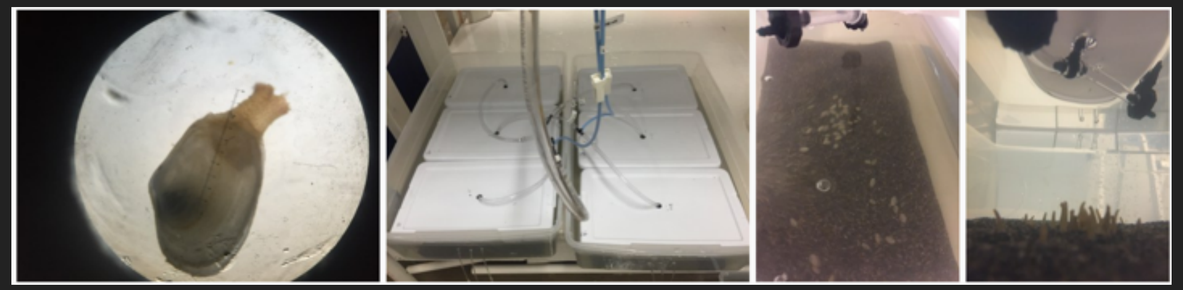
GEODUCKS AND OA



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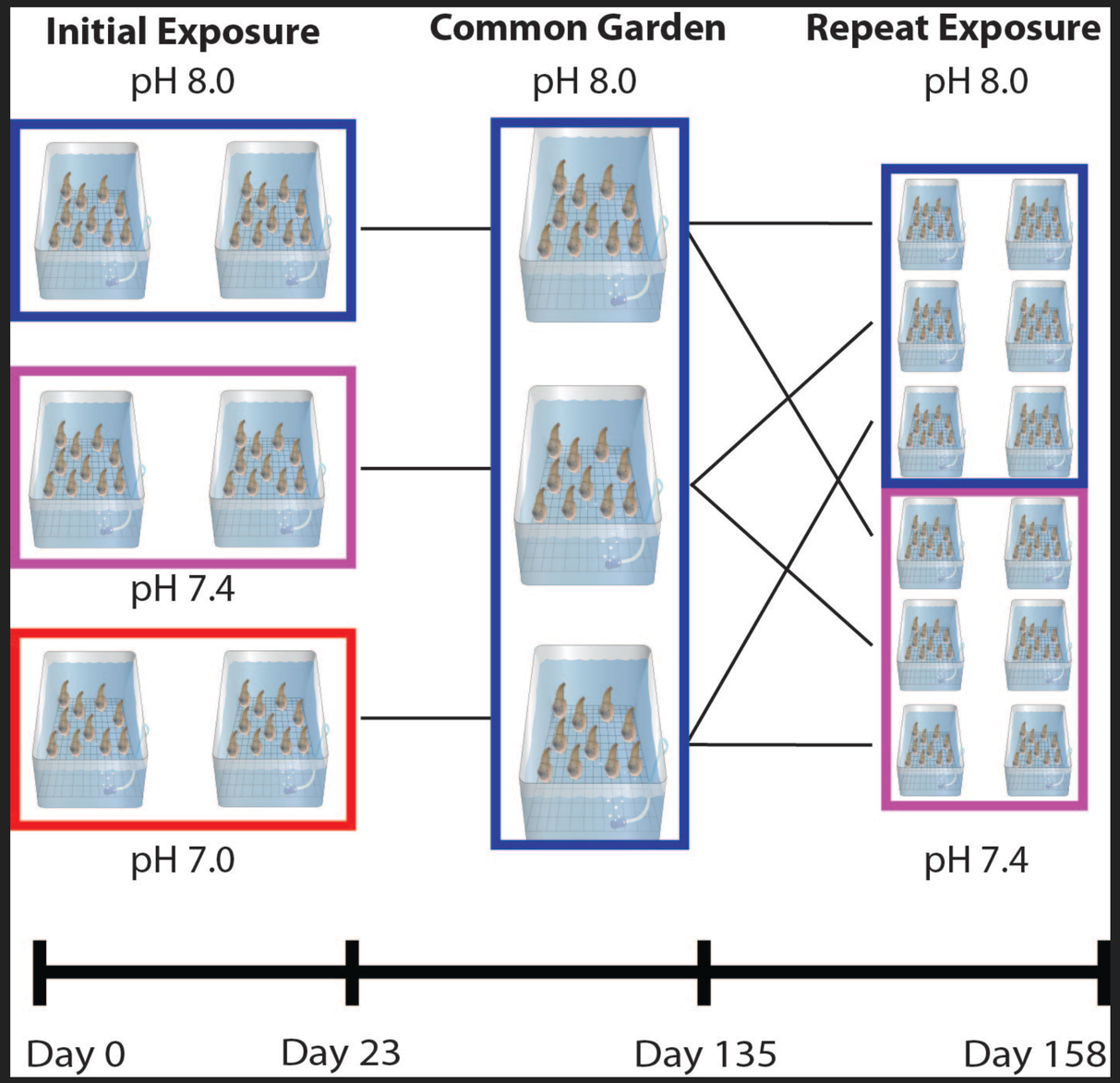

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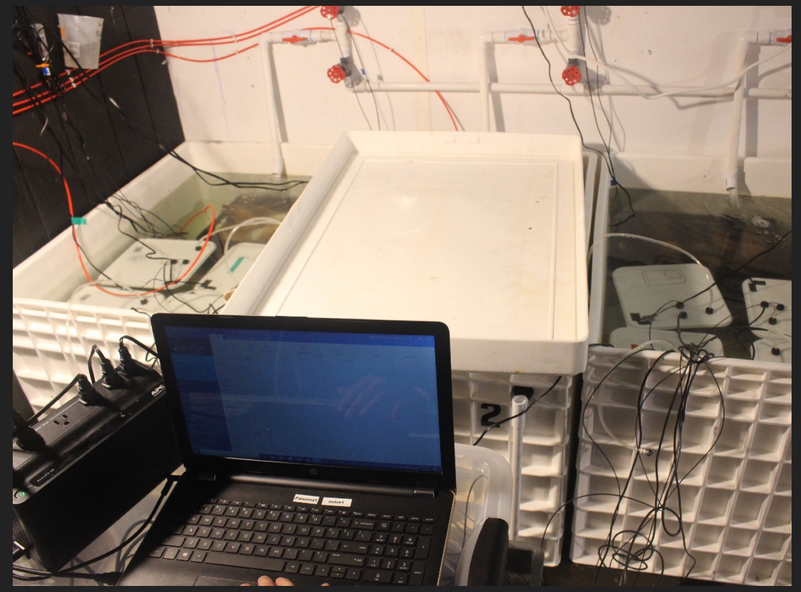

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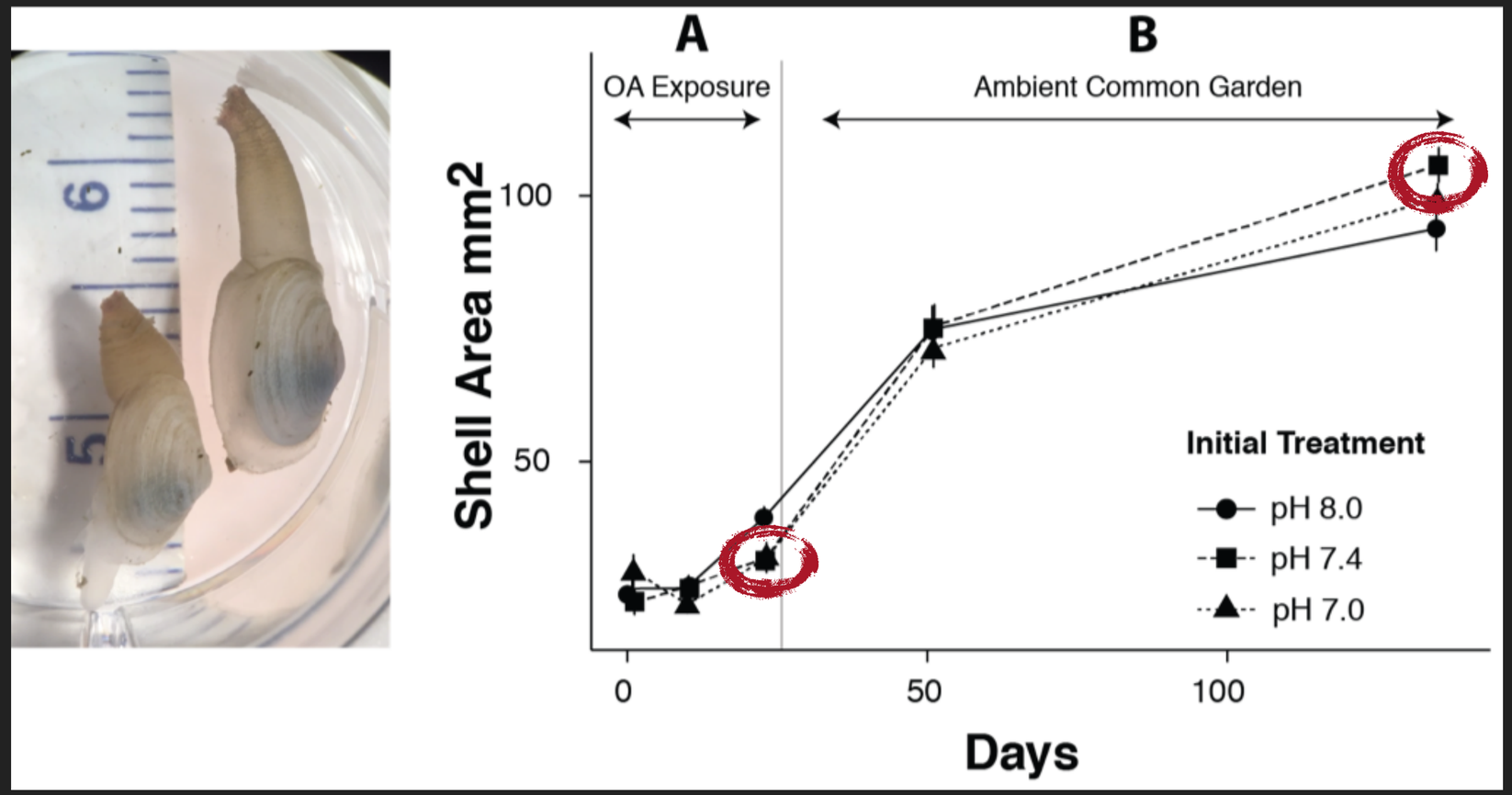

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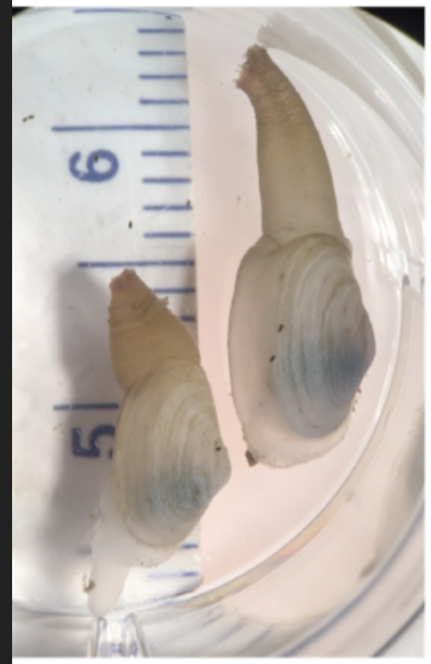

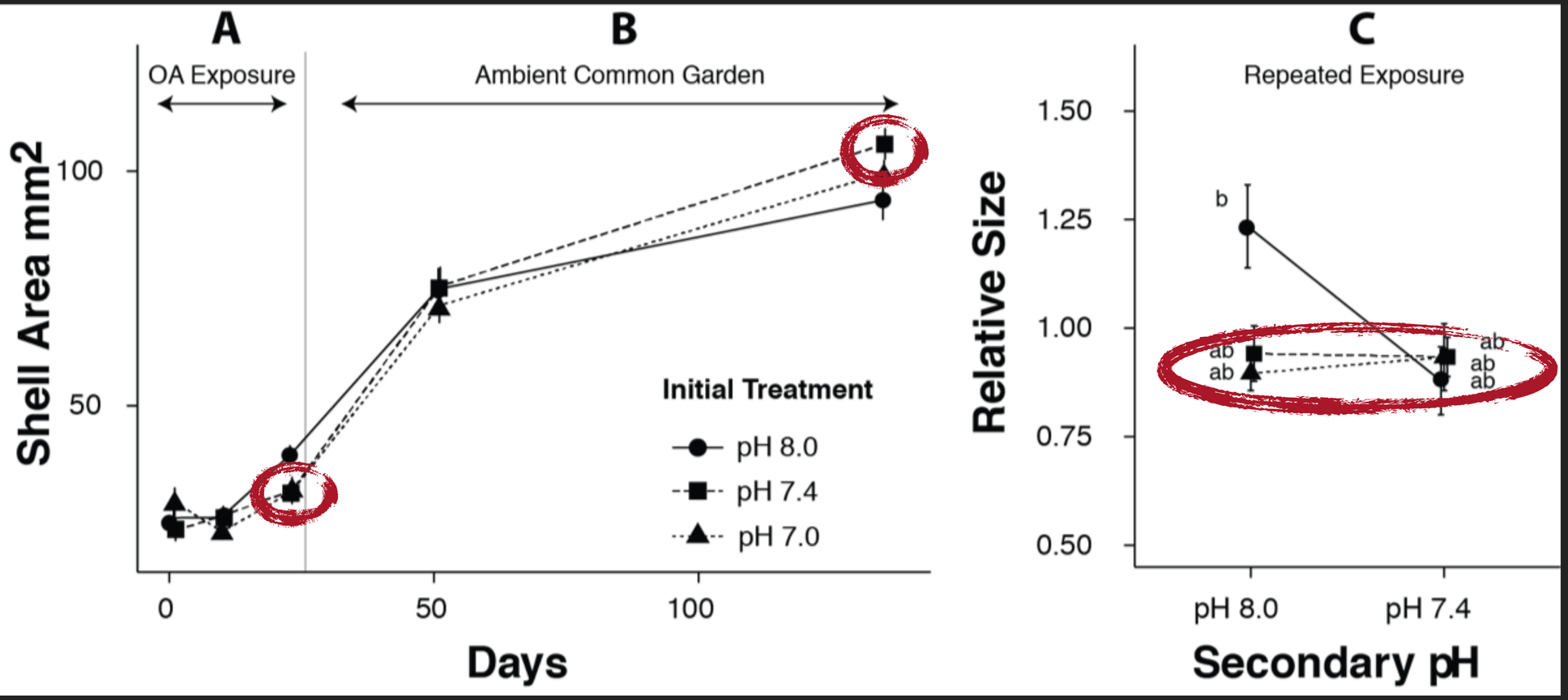

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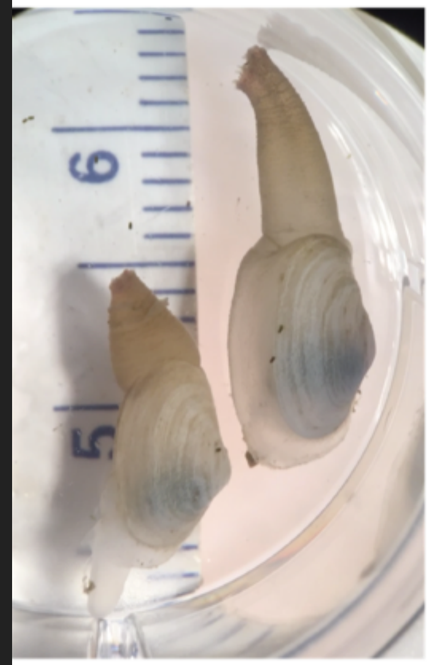

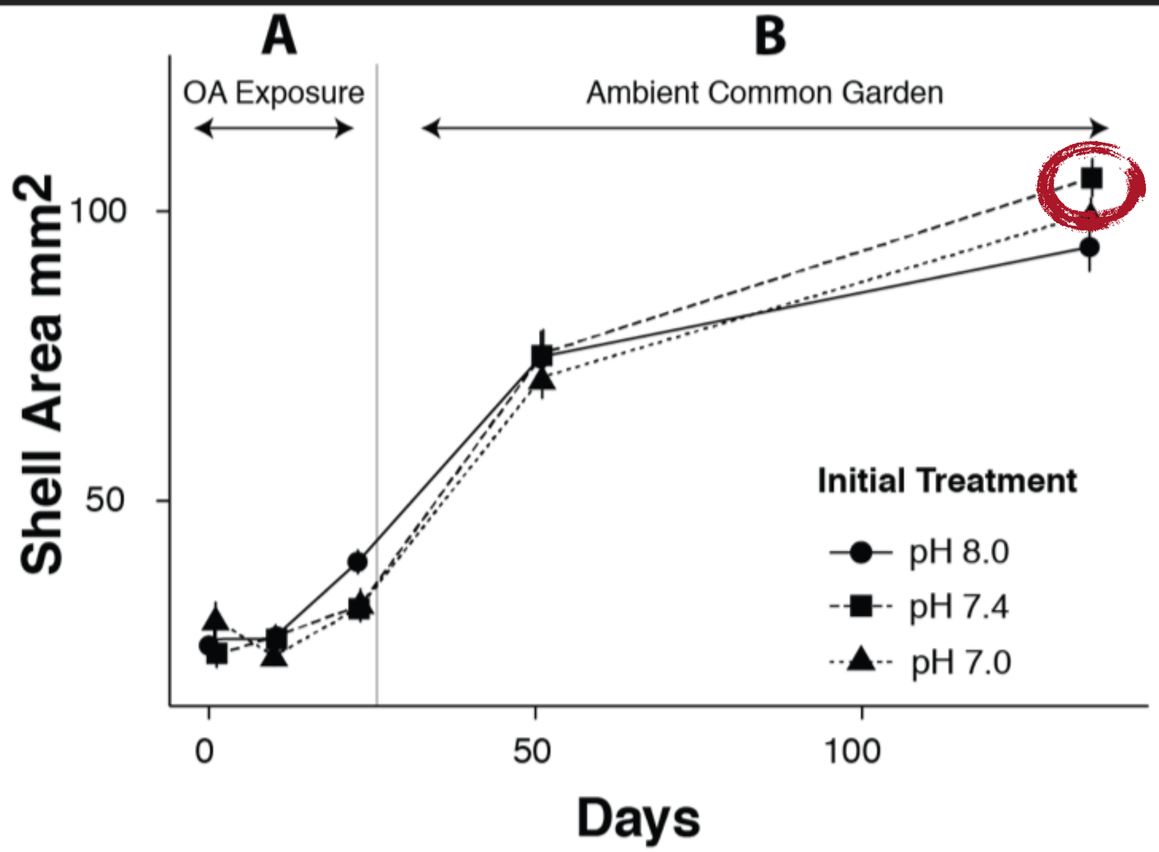

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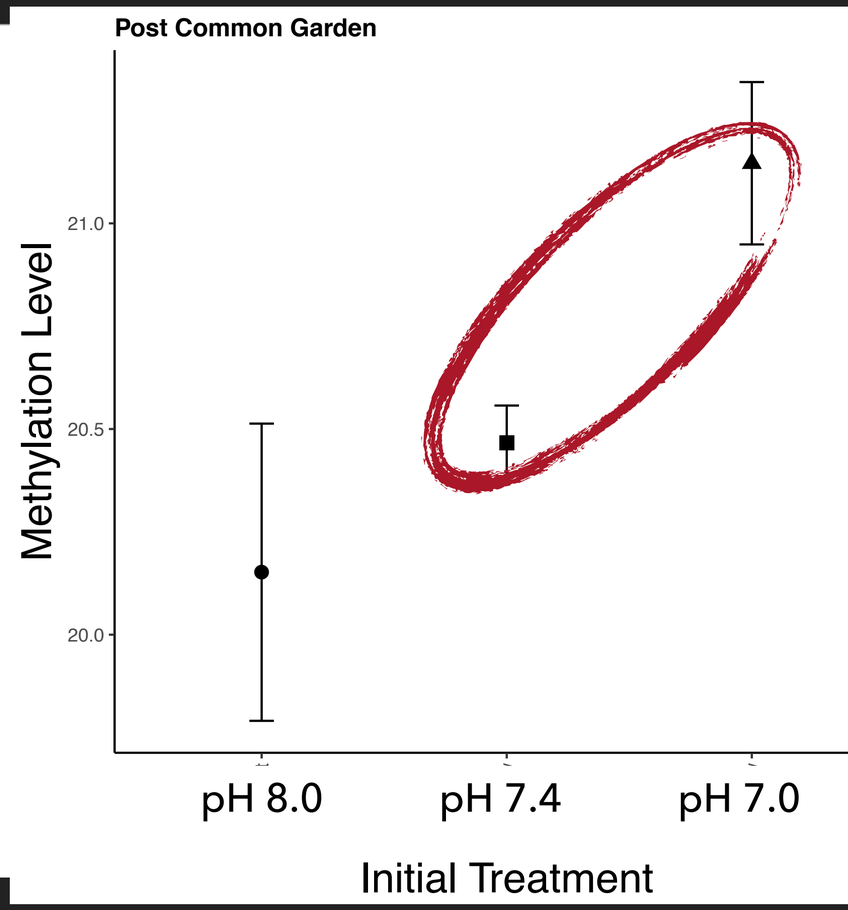

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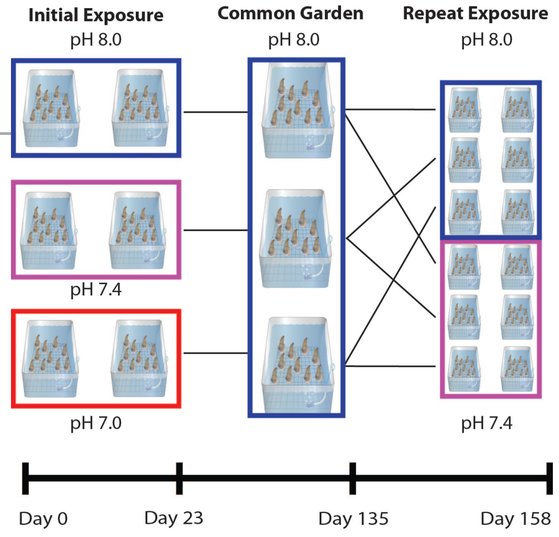

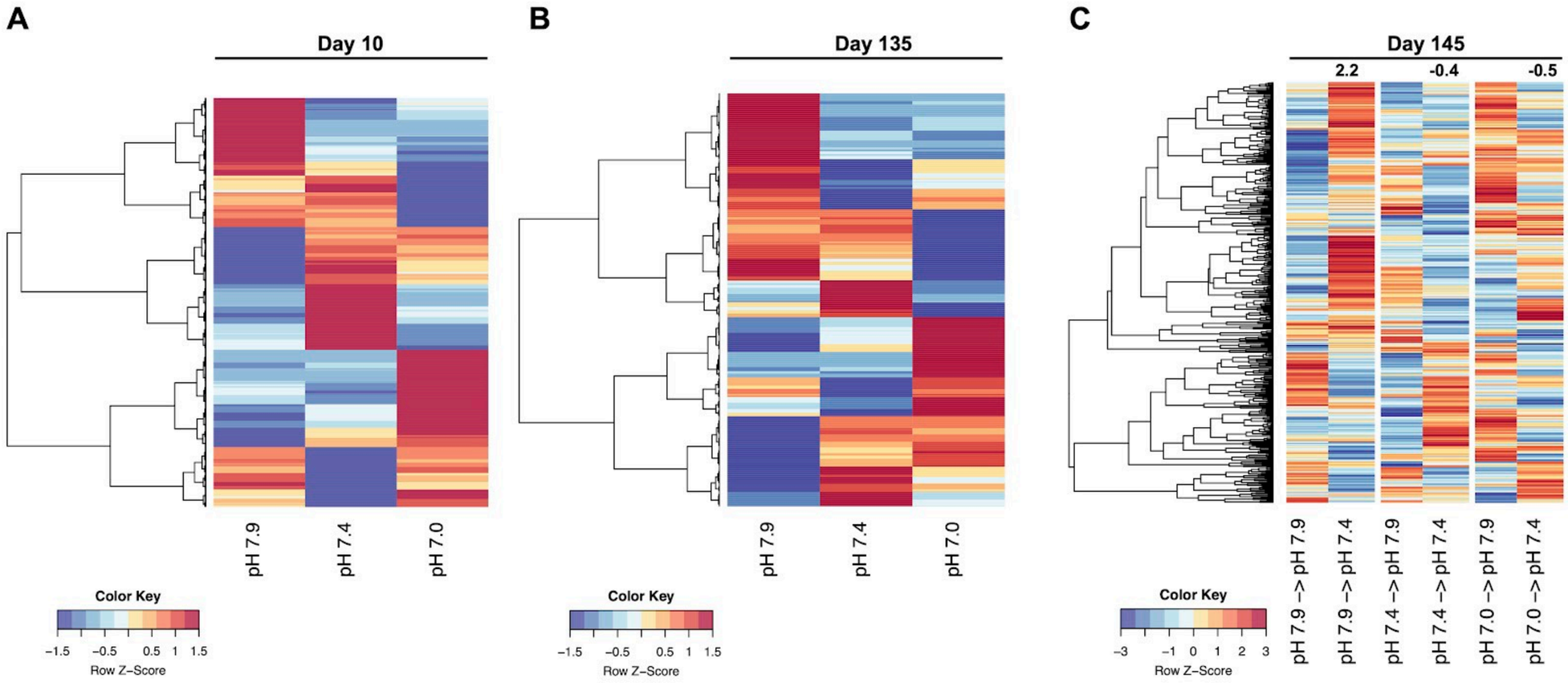

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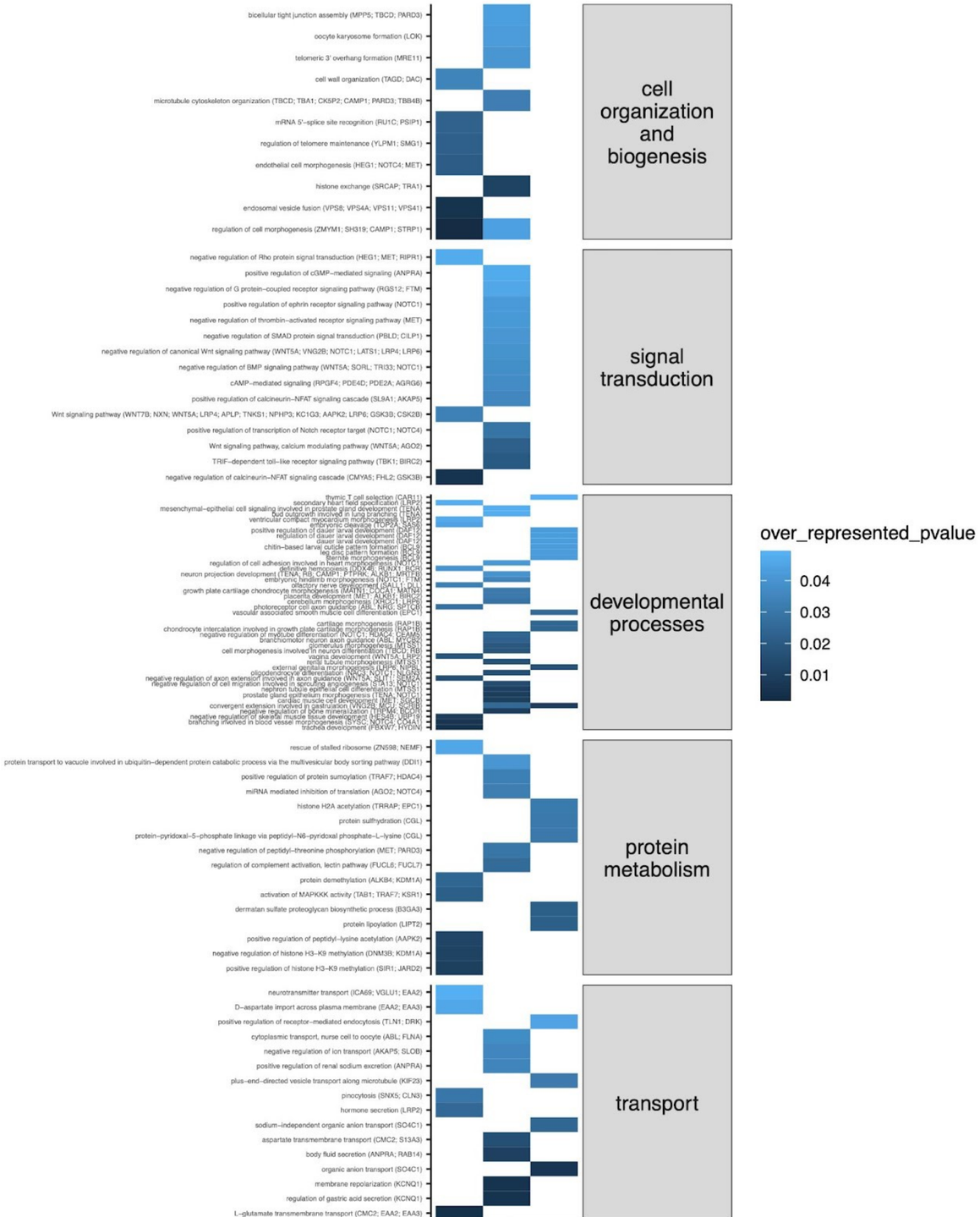

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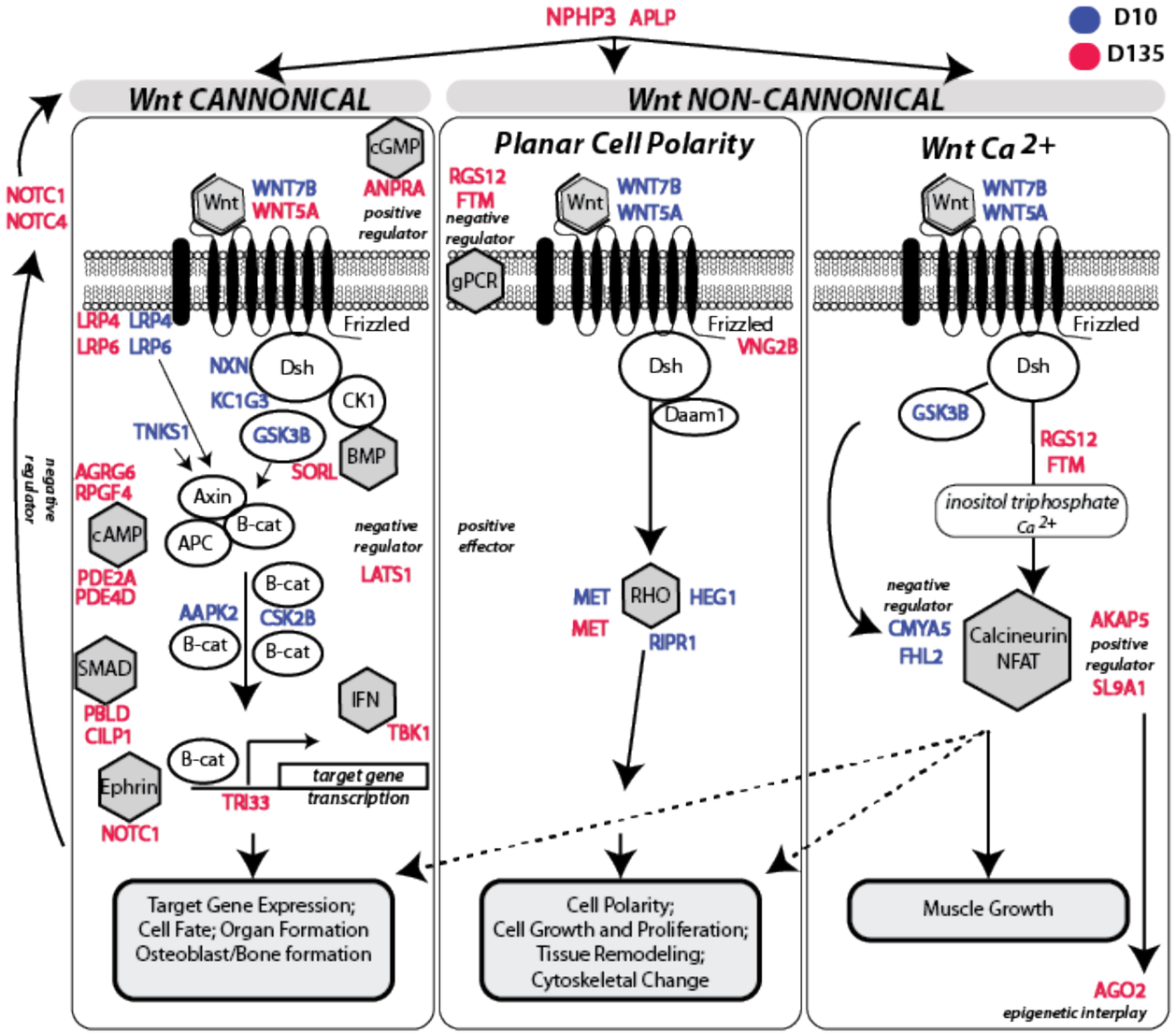

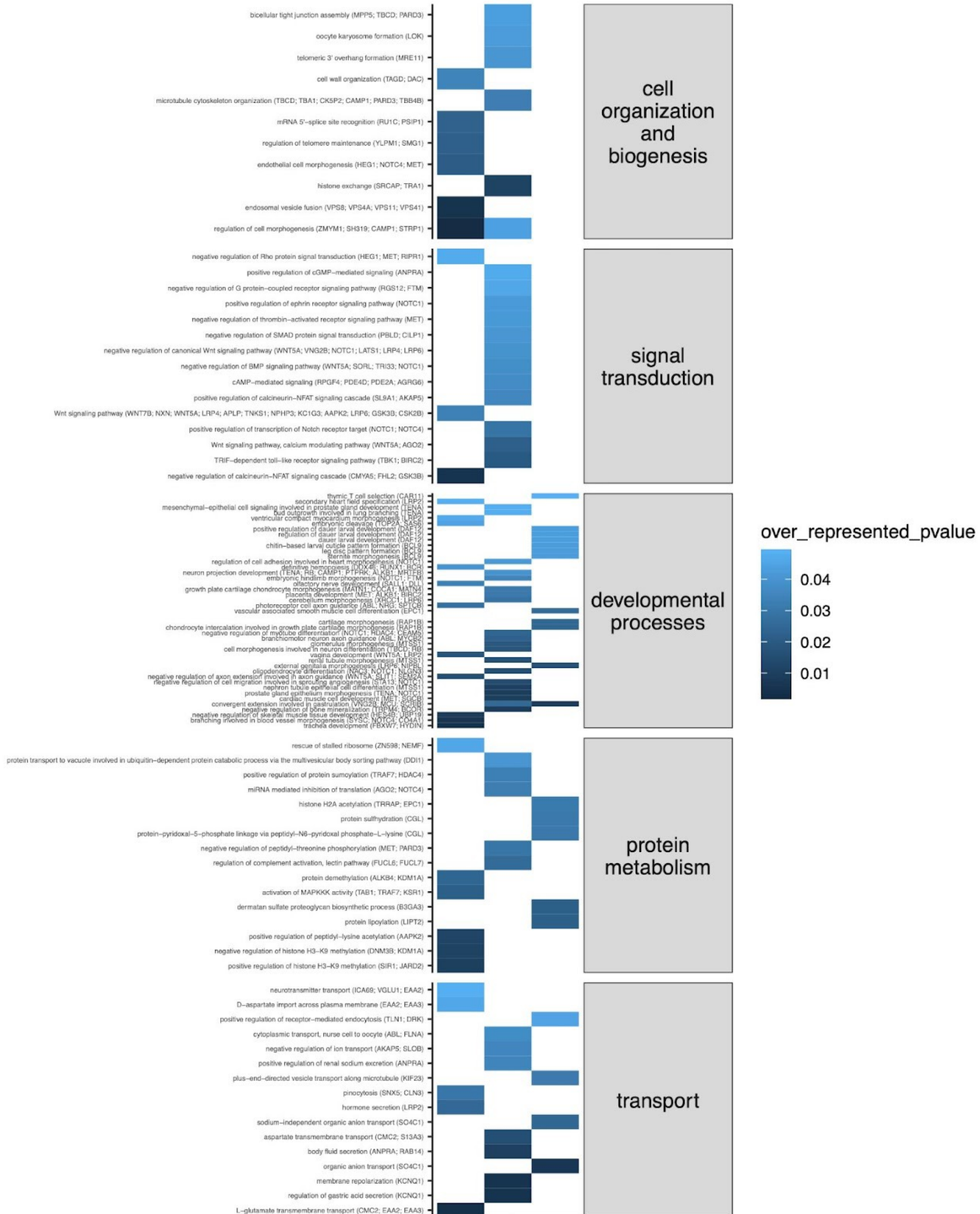

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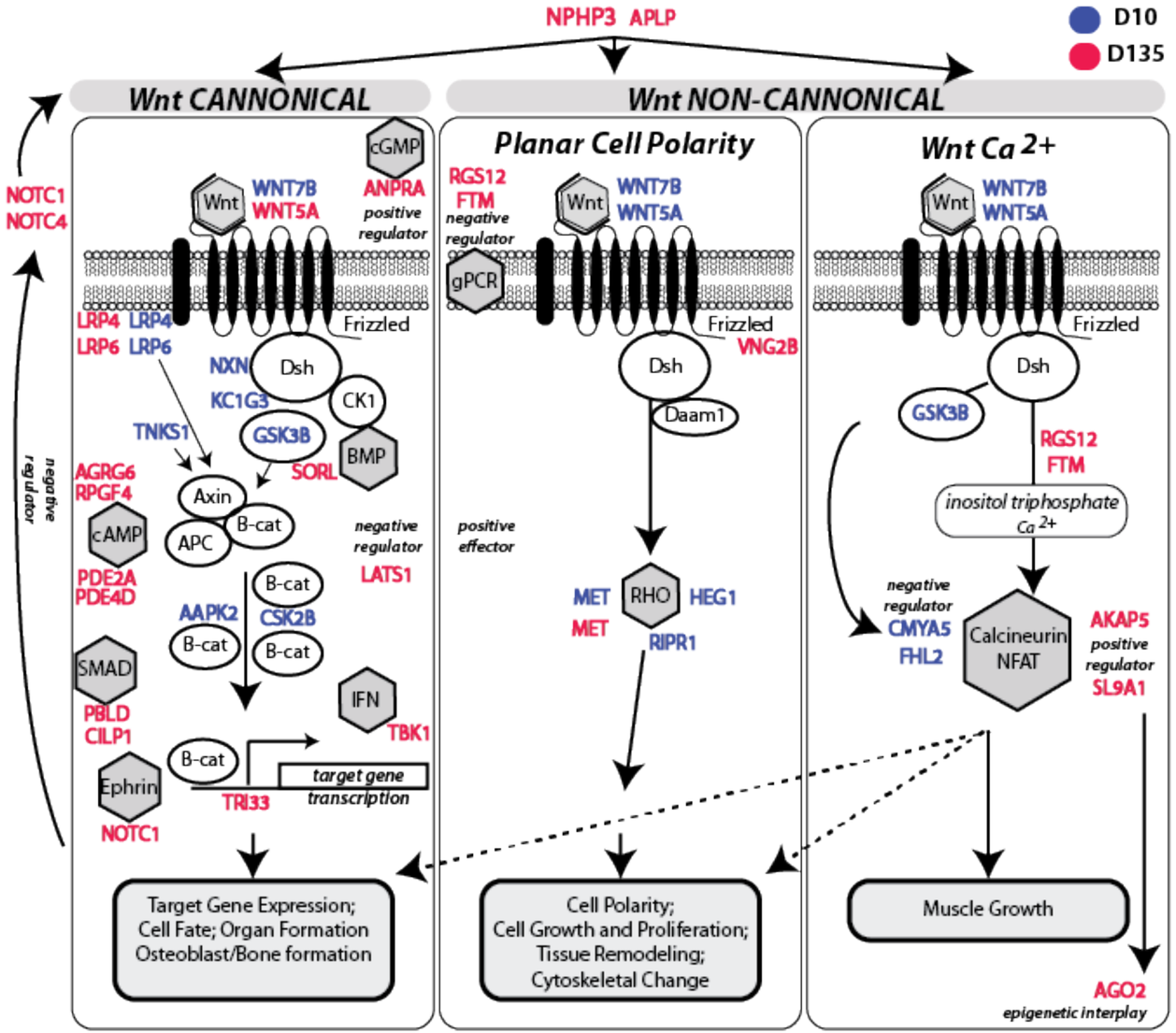

New Results

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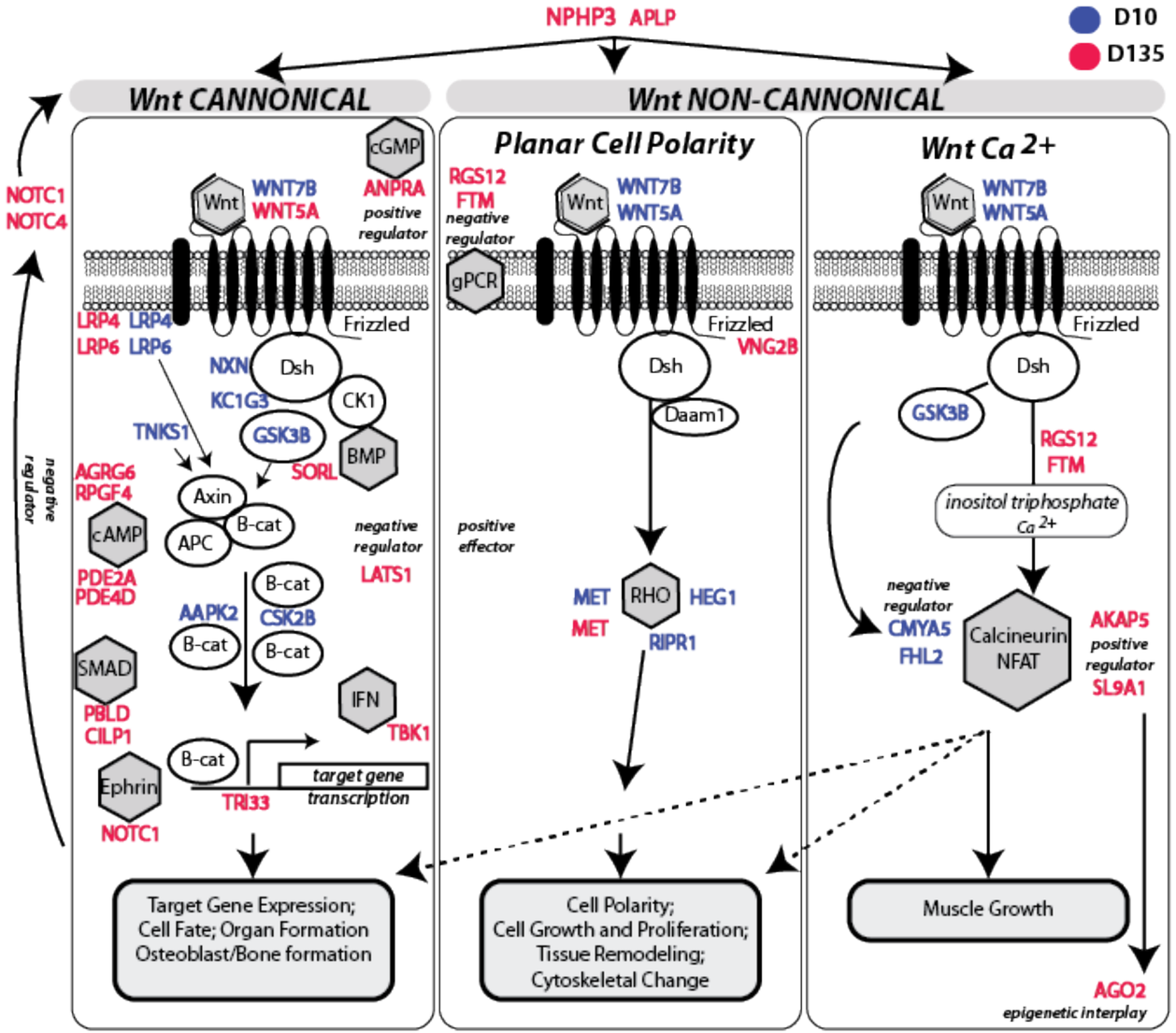
Dynamic DNA methylation contributes to carryover effects and beneficial acclimatization in geoduck clams

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

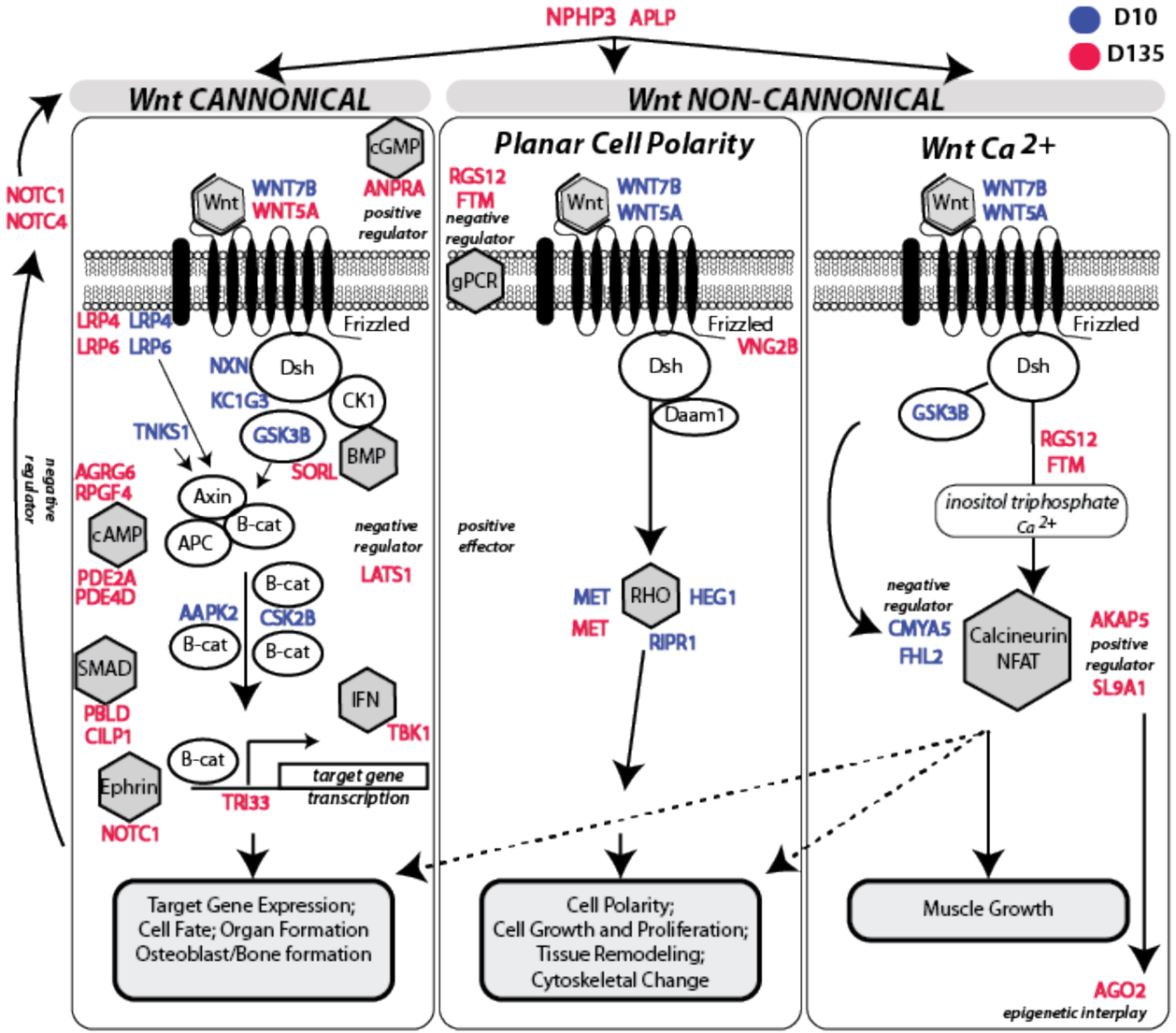
doi: https://doi.org/10.1101/2022.06.24.497506

GEODUCKS AND OA



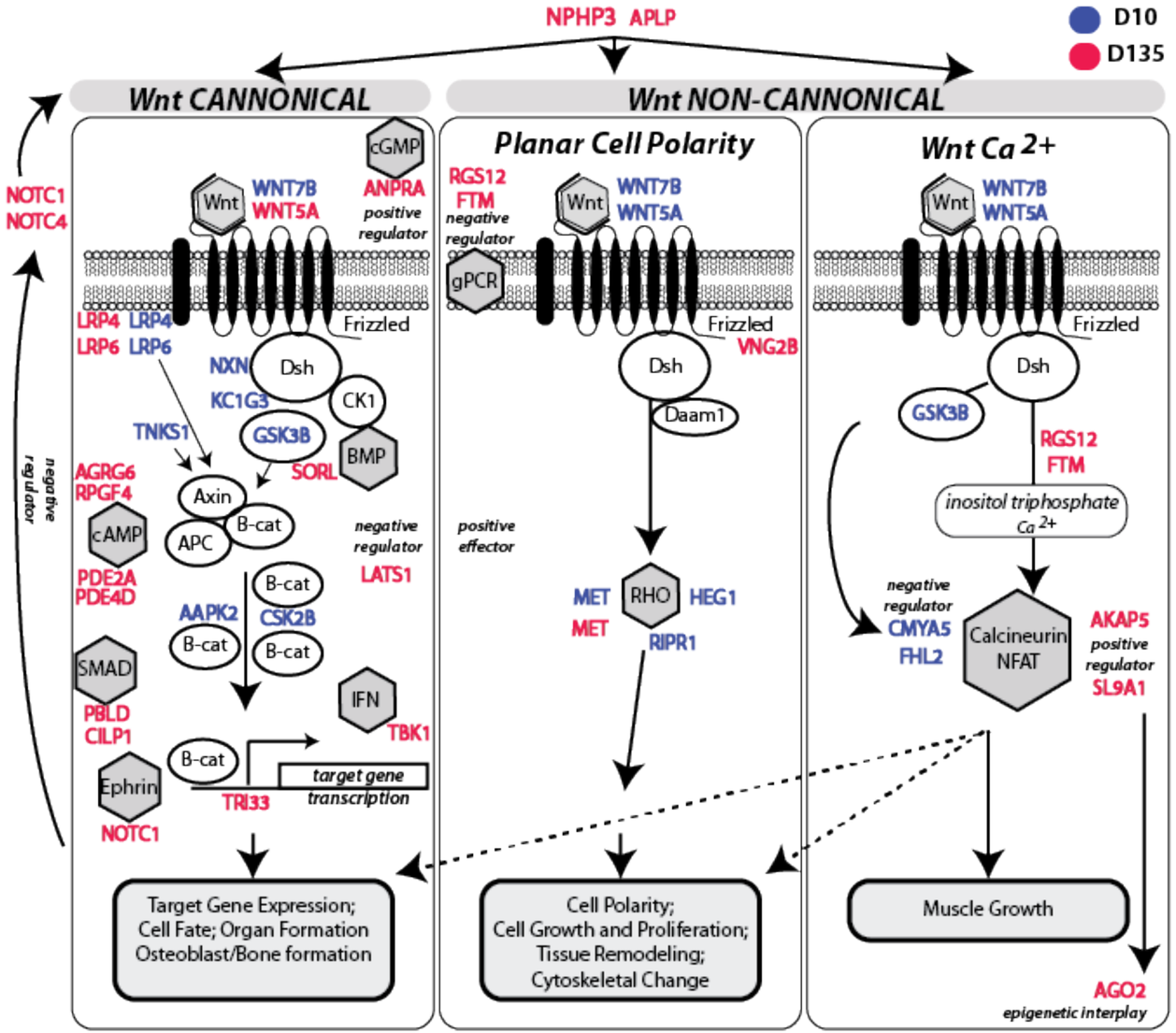
Following four months of ambient common-garden conditions, **juveniles initially exposed to low pH compensatorily grew larger**, with DNA methylation indicative of these phenotypic differences, demonstrating epigenetic carryover effects persisted months after initial exposure.

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

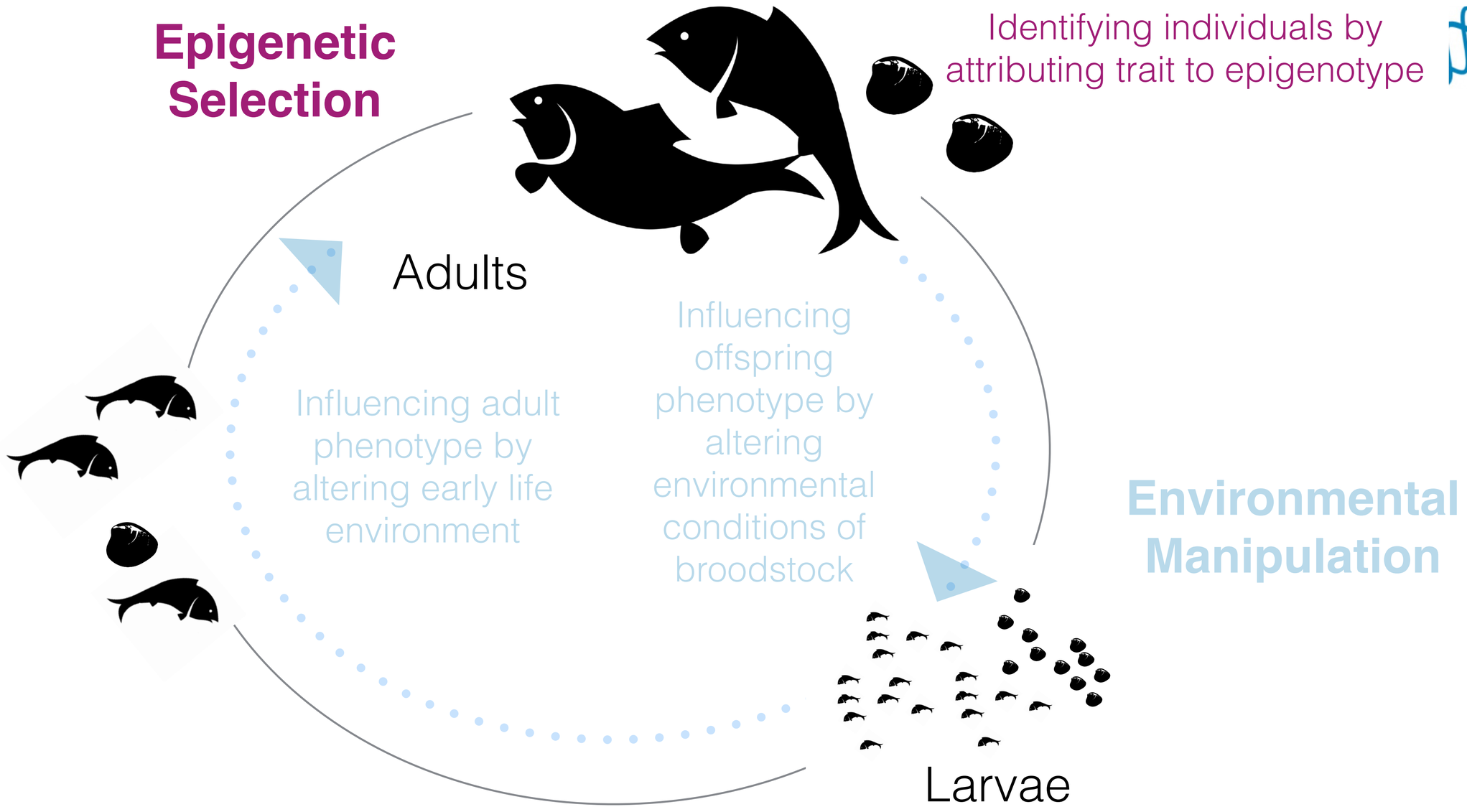


After 10 days of secondary exposure to pH 7.4, naive juvenile clams were more sensitive to low pH compared to those initially exposed, showing reduced growth and having nearly a 2-fold greater change in DNA methylation.

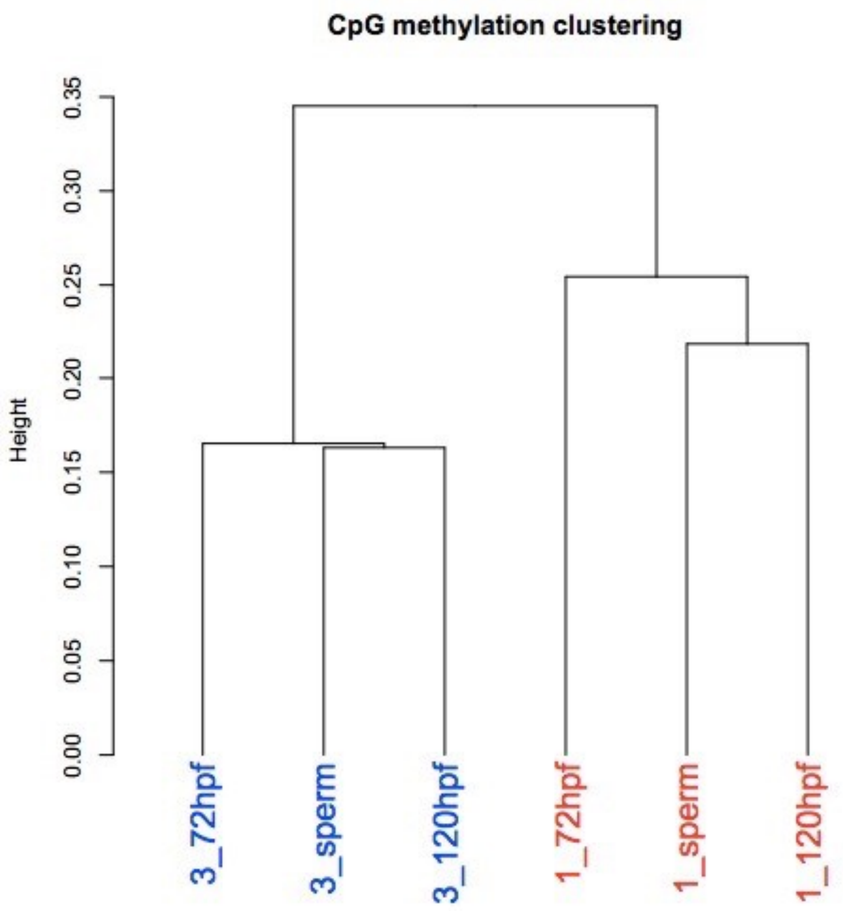
Outline

DNA Methylation in Bivalves

- General Aspects *including* Methods and Approaches
- Influencing Offspring
- Early-life Environment
- **Epigenetic Selection**
- Future Perspectives


Epigenetic Selection
Identifying individuals by attributing trait to epigenotype
Adults
Influencing offspring phenotype by altering environmental conditions of broodstock
Influencing adult phenotype by altering early life environment
Environmental Manipulation
Larvae

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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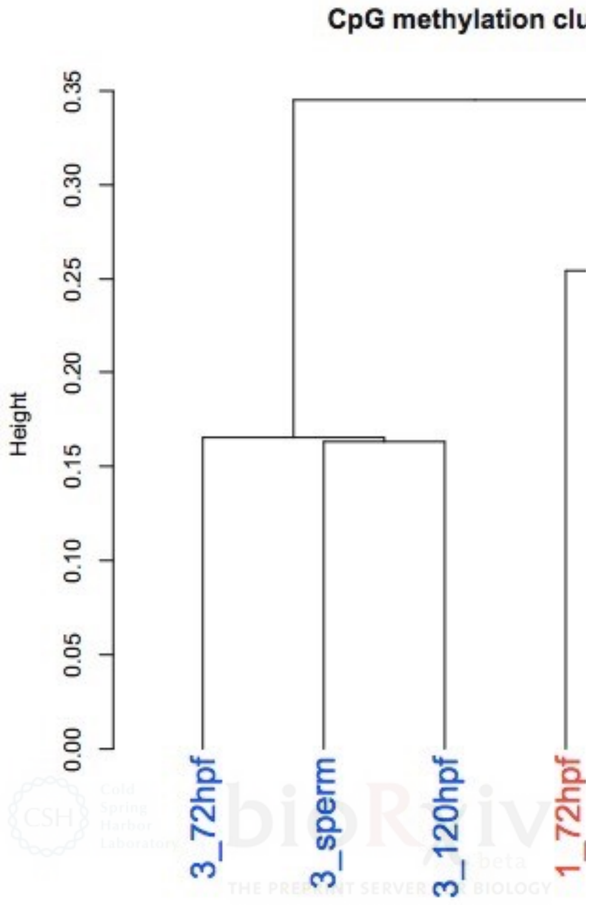

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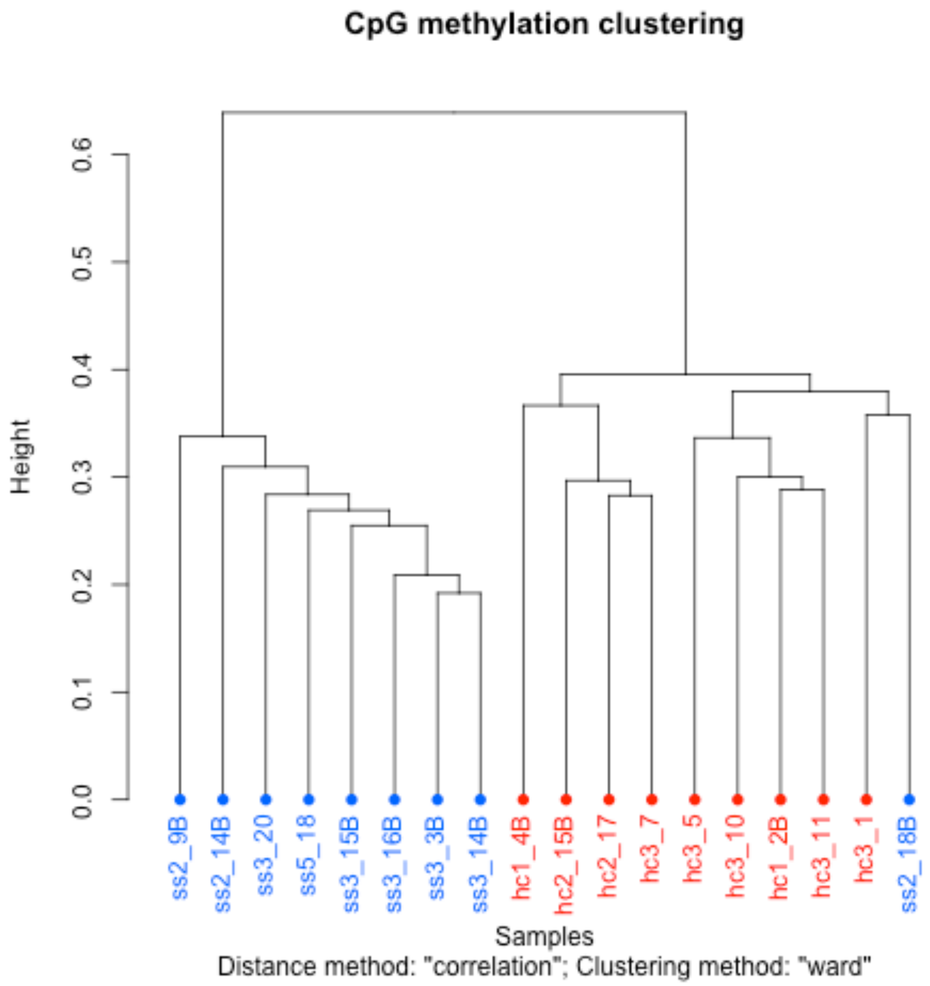


Epigenetic and genetic population structure is coupled in a marine invertebrate

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

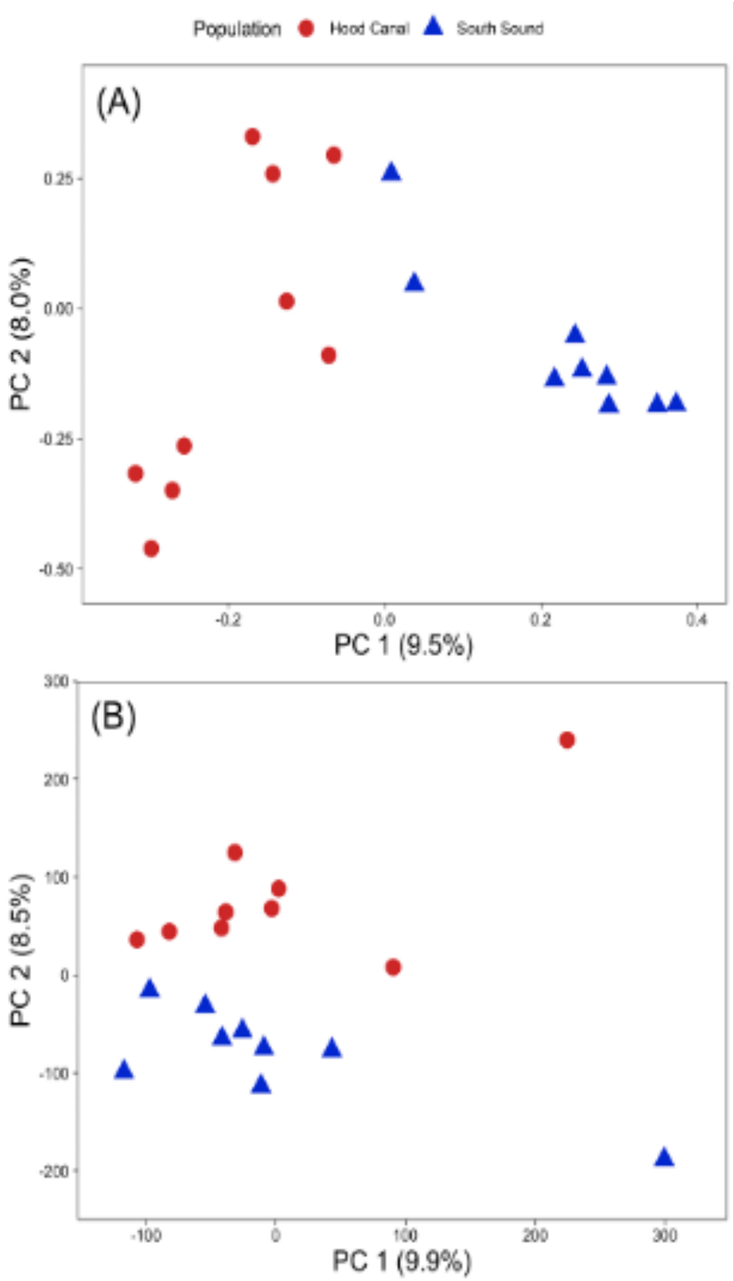
doi: https://doi.org/10.1101/2022.03.23.485415

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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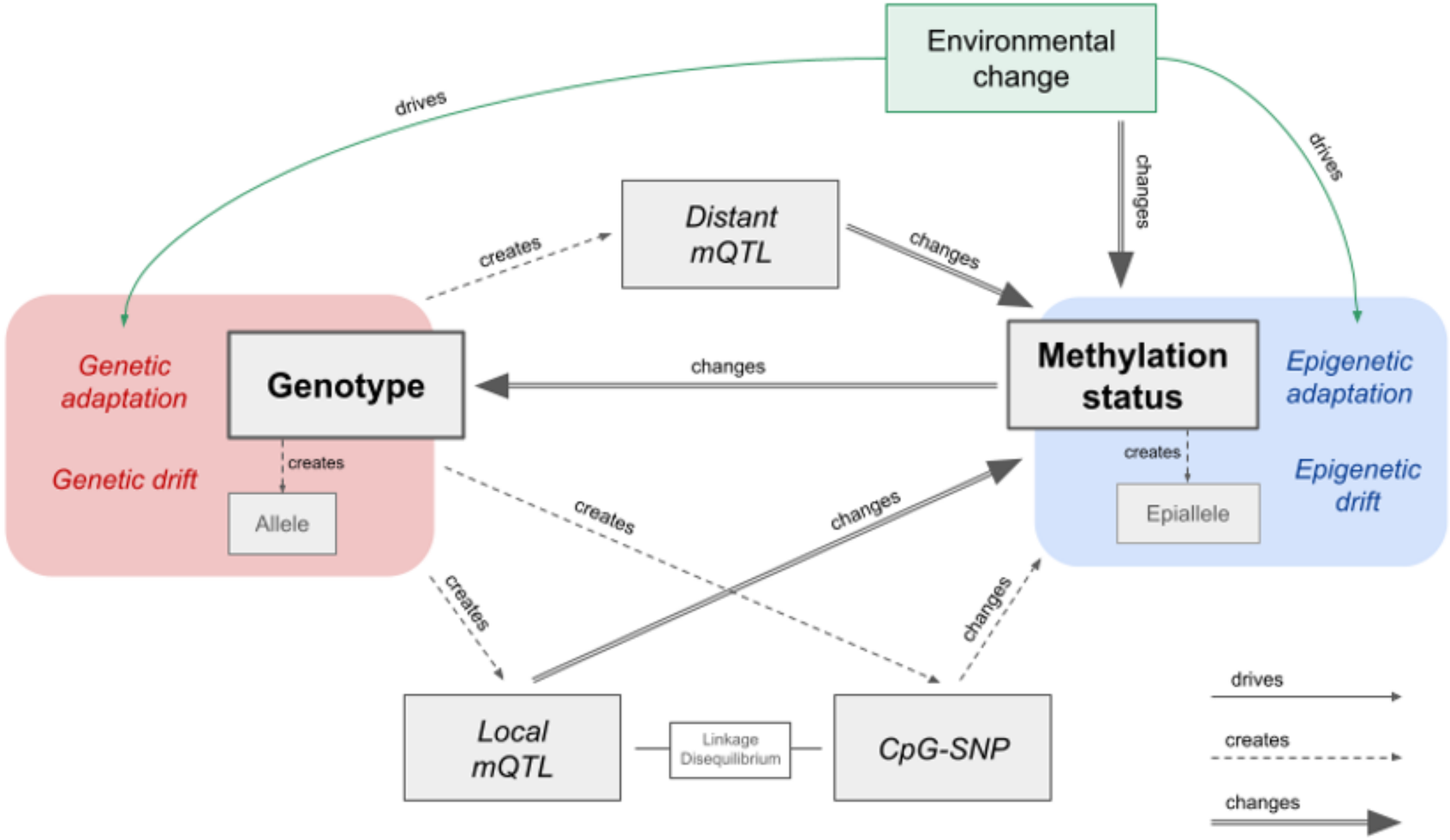

Outline

DNA Methylation in Bivalves

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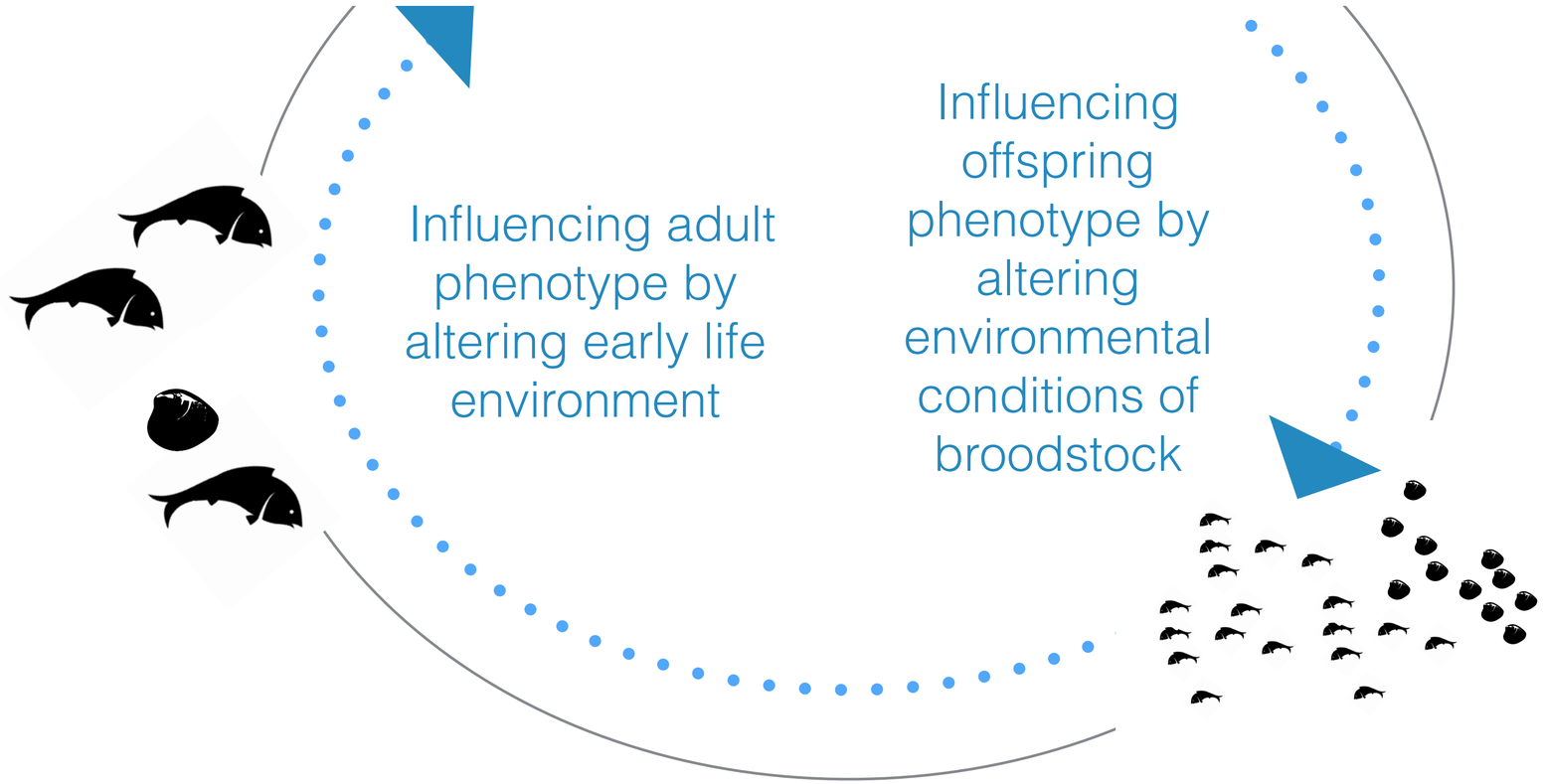
Epigenetics is an attractive lens through which to consider manipulation of traits through environmental memory or selection.



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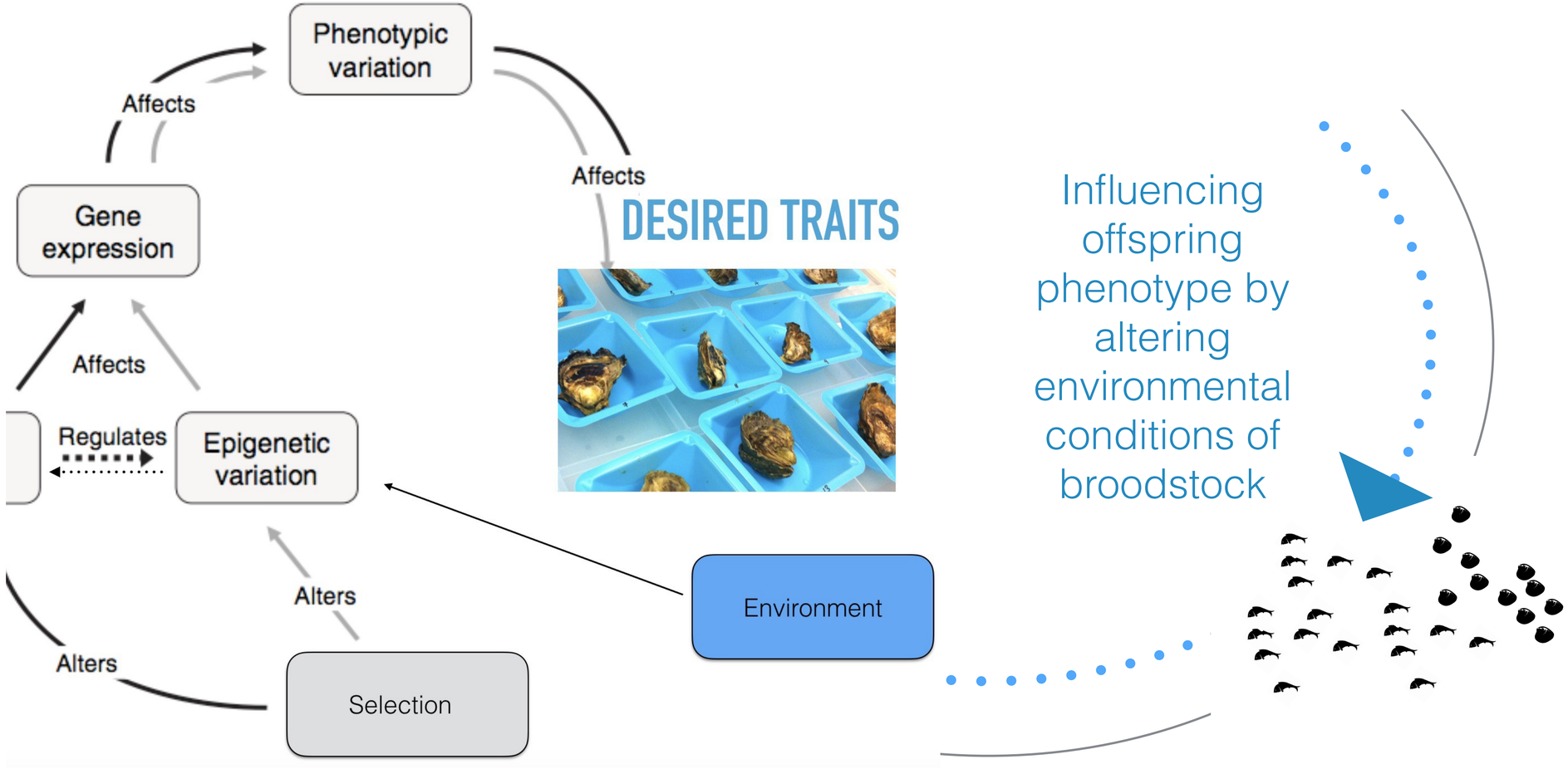

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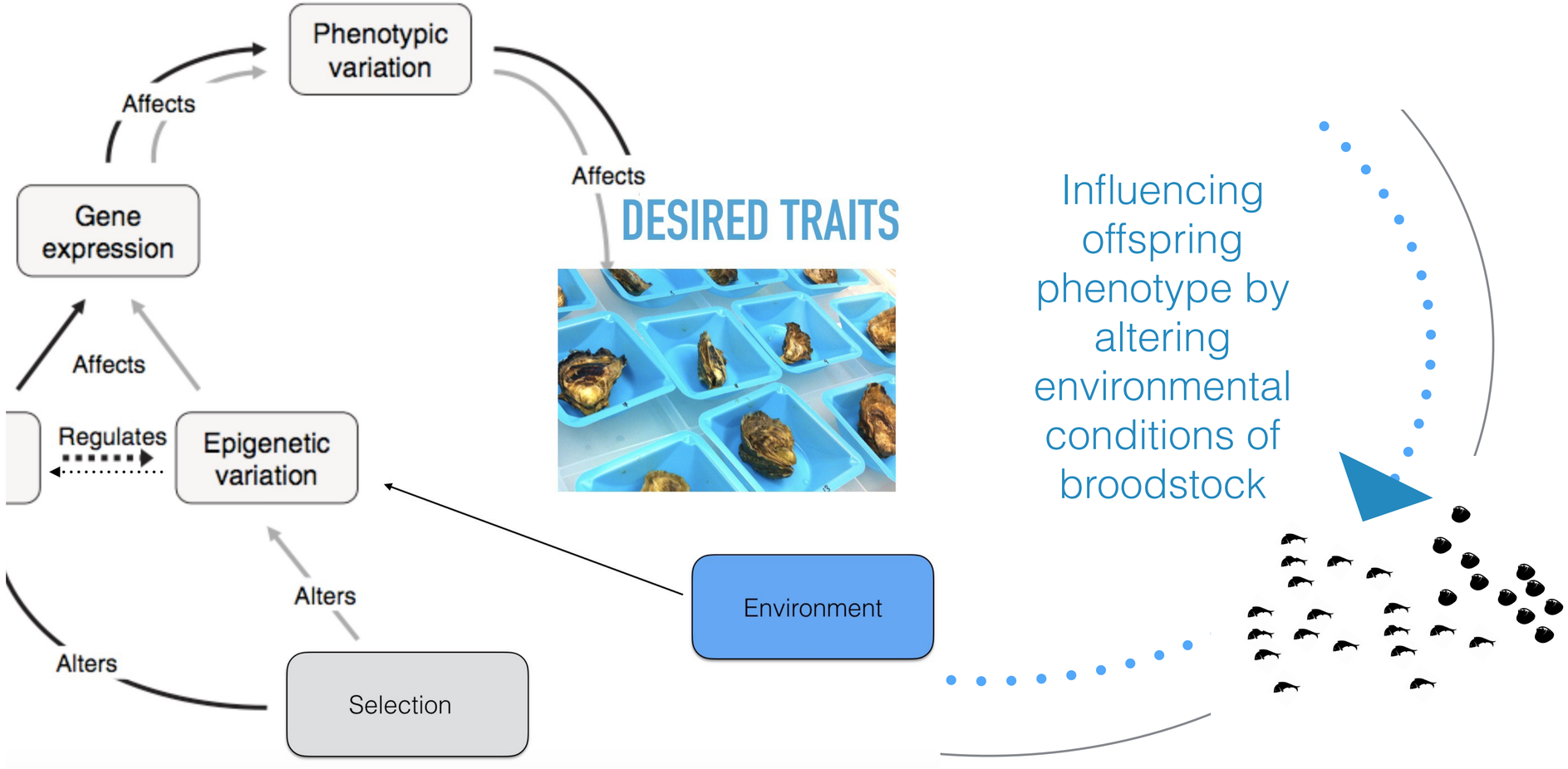

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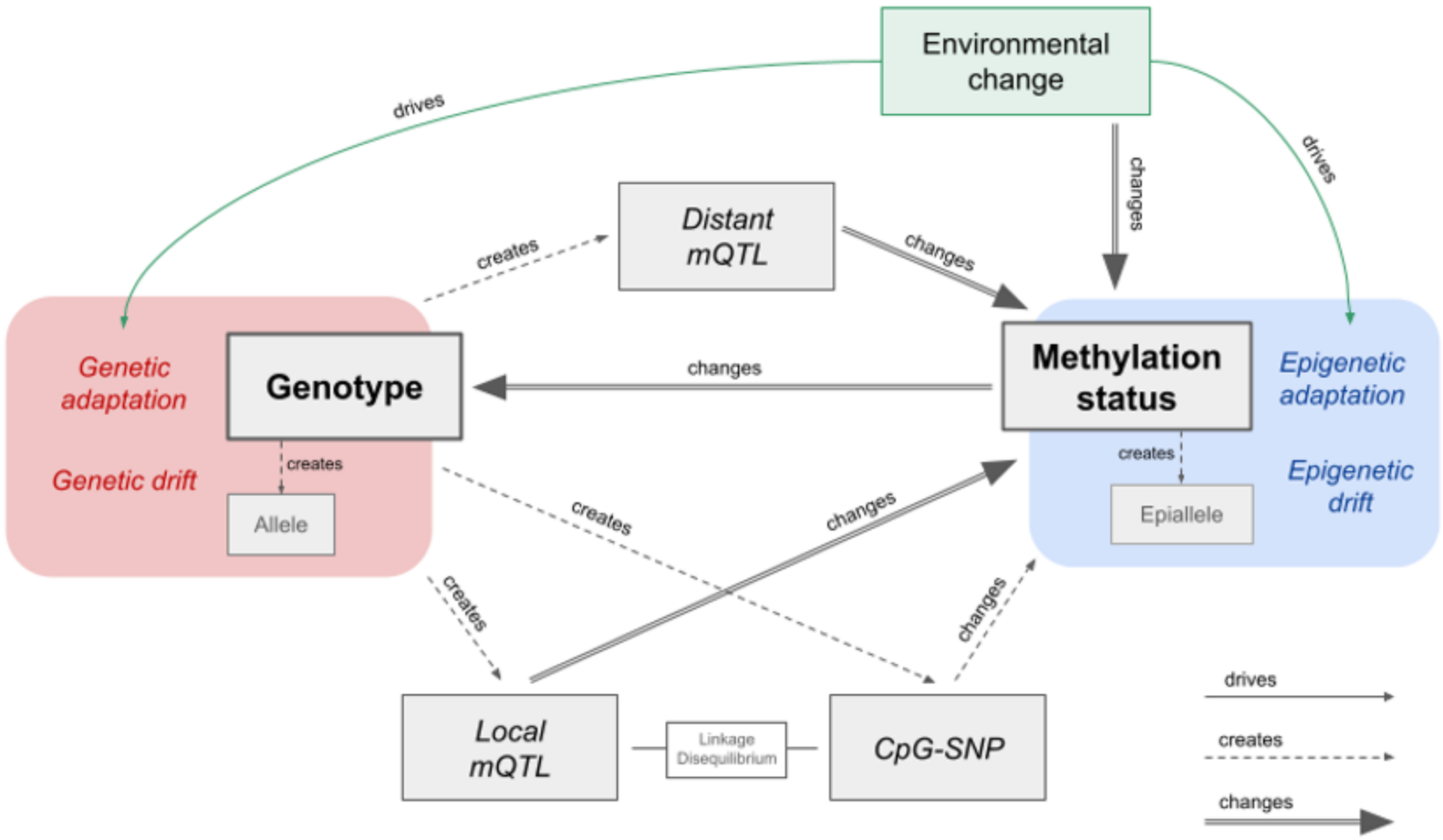

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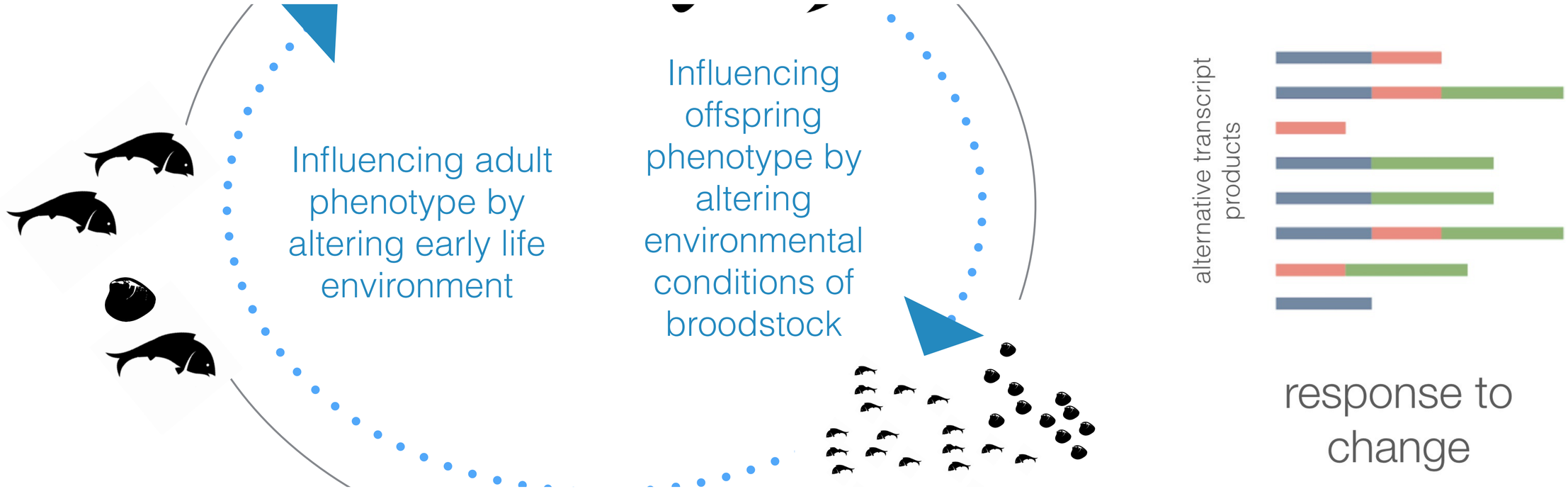

Epigenetics may also function to disrupt predictable phenotypes through the creation of unexpected variation

GITHUB.COM/SR320/TALK-EPIAQUA-2023

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NSF

FFAR

NOAA

Epigenomics in Aquaculture (EpiAqua)

Understanding the effects of Climate Change on farmed species

25-27th, January 2023. University of Concepción, Chile