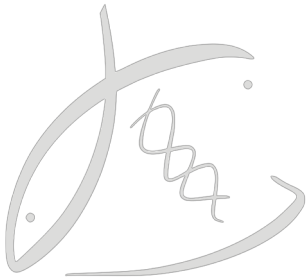


DNA METHYLATION ASSOCIATIONS WITH GROWTH RATE IN OLYMPIA OYSTER POPULATIONS

Laura H Spencer, Katherine Silliman, Sam White, Steven Roberts
Roberts Lab

School of Aquatic and Fishery Sciences
University of Washington
Aquaculture America in Honolulu, HI

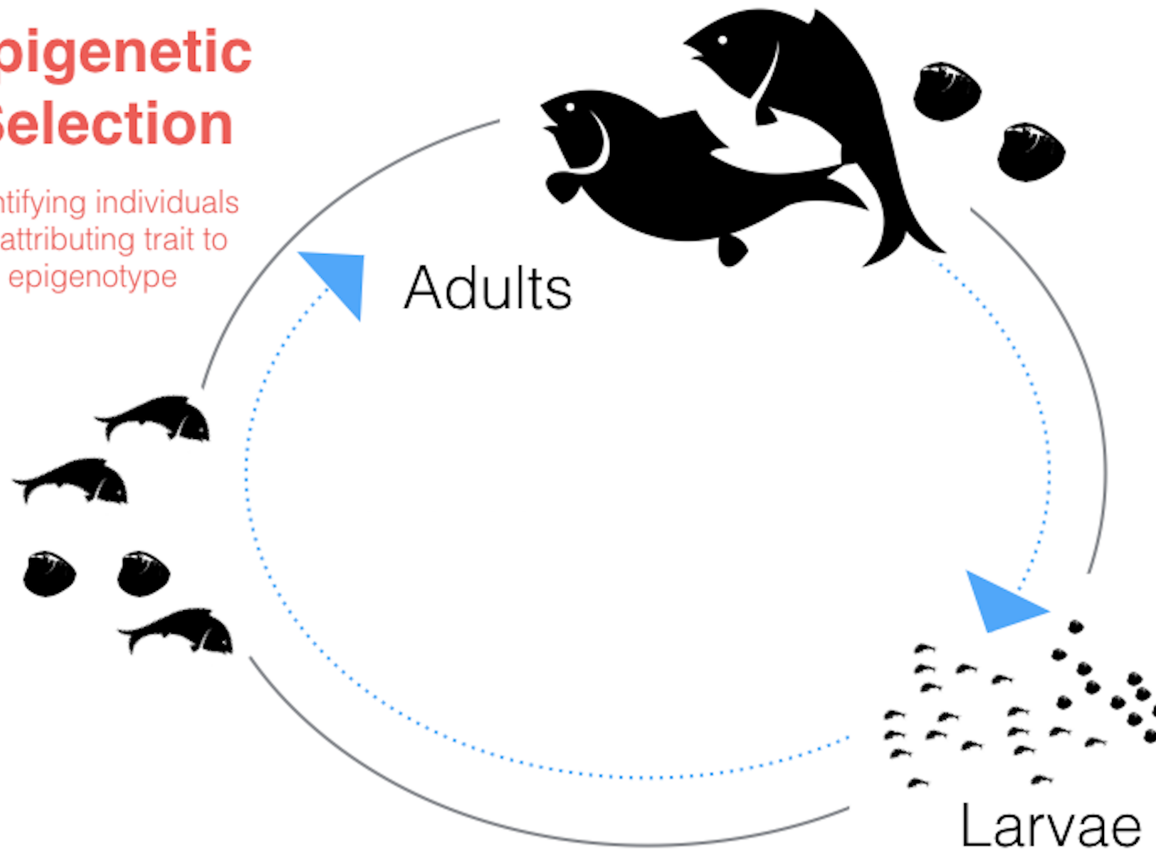
<https://laurahspencer.github.io/LabNotebook/>



EPIGENETIC SELECTION & AQUACULTURE

Epigenetic Selection

Identifying individuals
by attributing trait to
epigenotype



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Epigenetic considerations in aquaculture

Literature review Aquaculture, Fisheries and Fish Science Molecular Biology

Mackenzie R. Gavary, Steven B. Roberts

Published December 7, 2017 PubMed 29230373

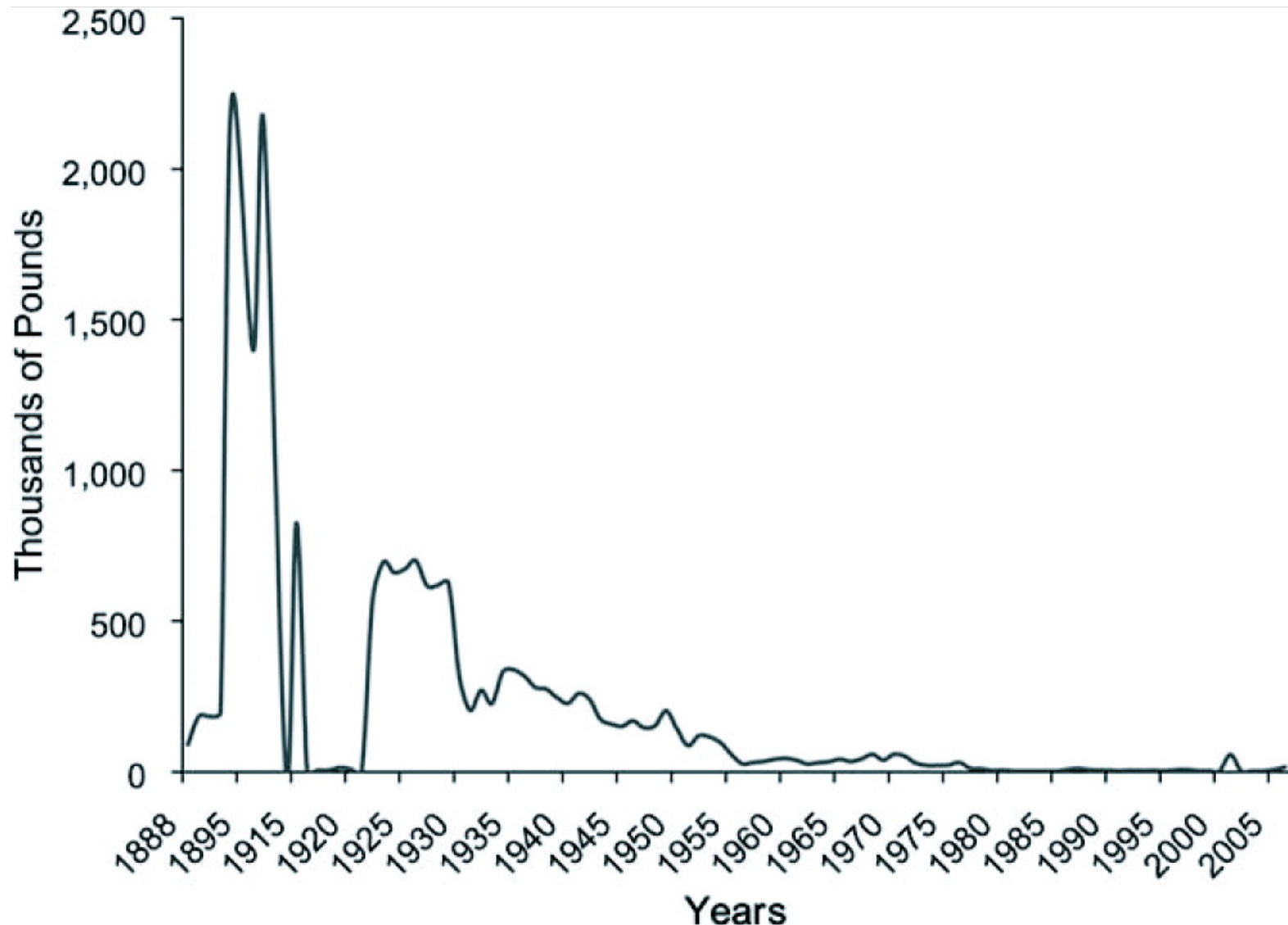


Olympia oyster
Ostrea lurida

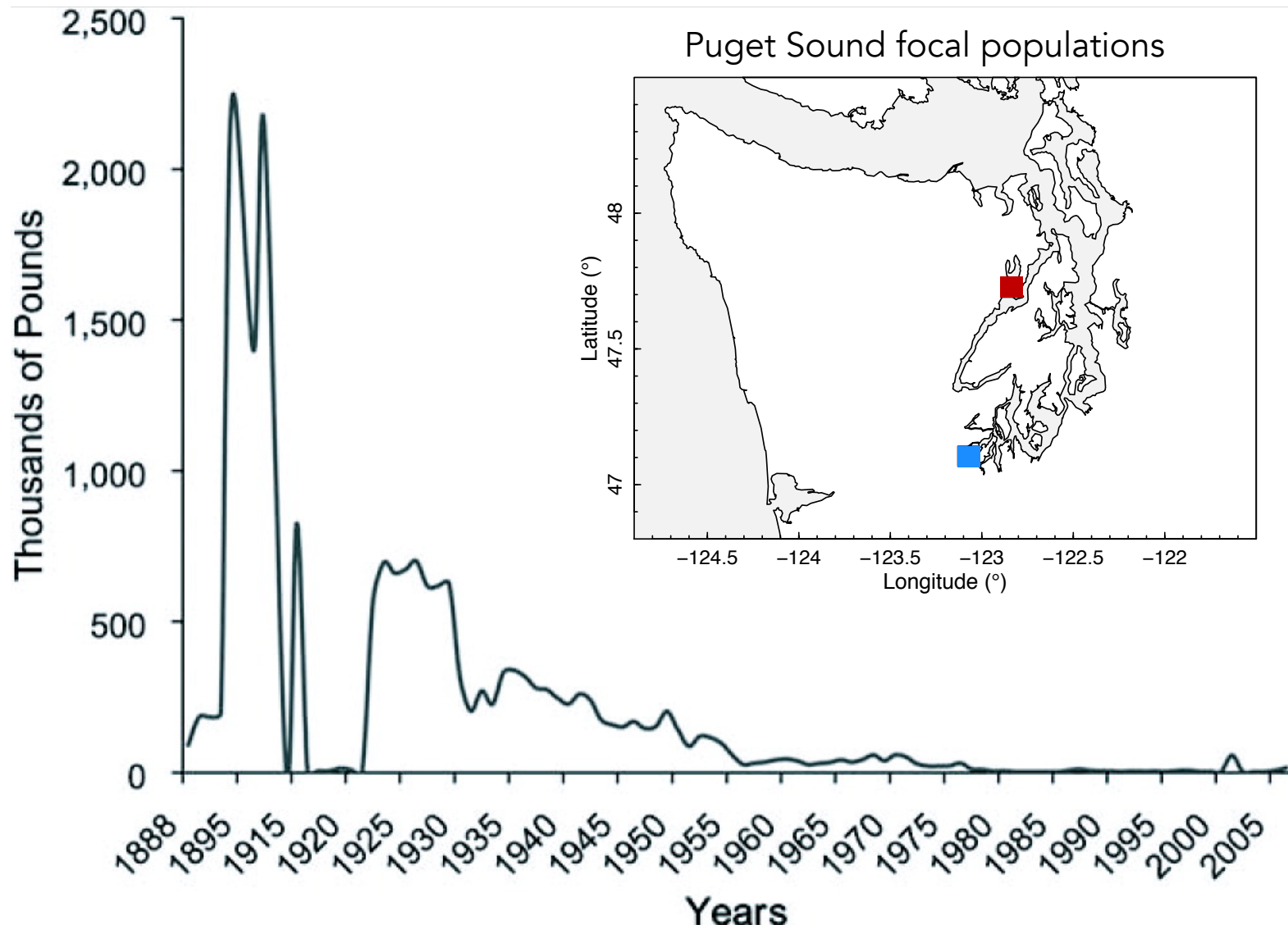


September, 1910, Brenner Oyster Company in Totten Inlet

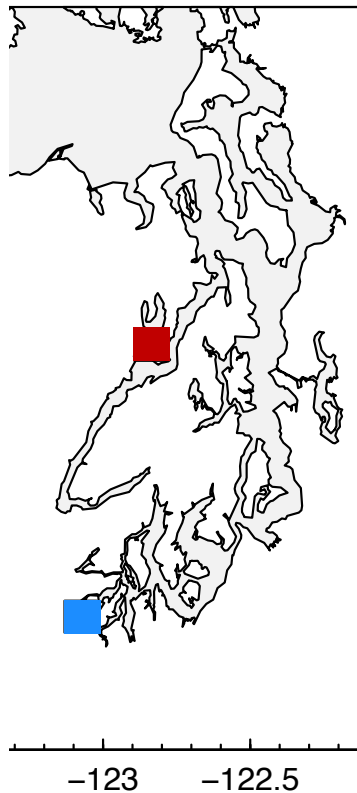
Olympia oyster populations declined rapidly in early 1900's



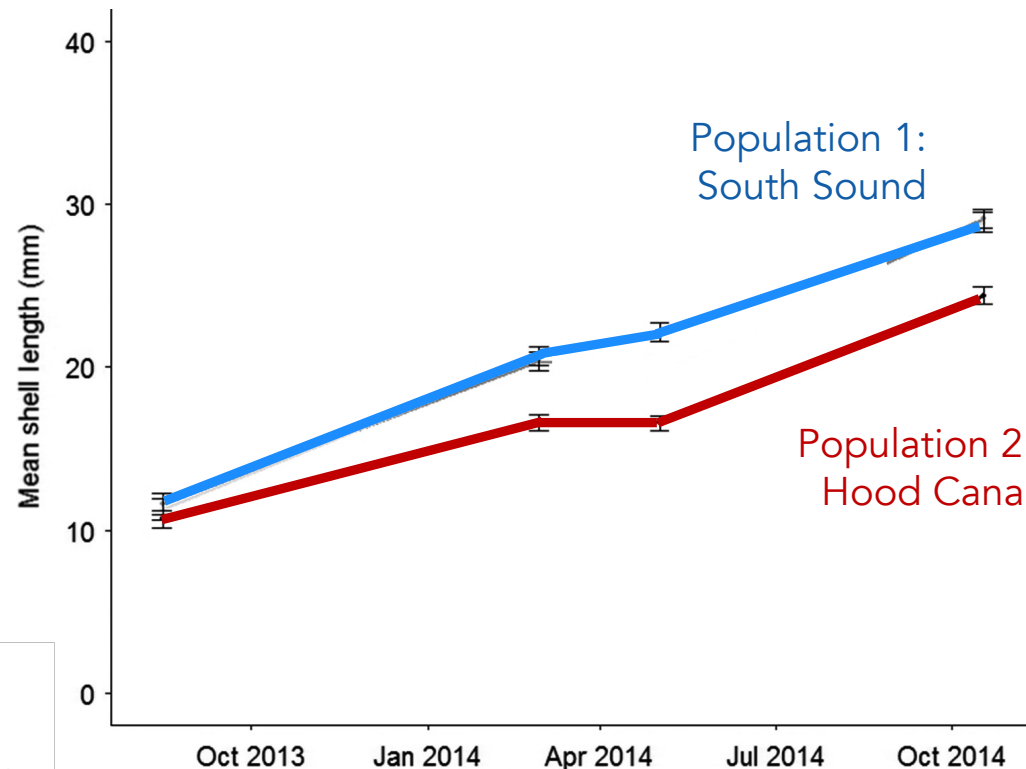
Olympia oyster populations declined rapidly in early 1900's



OLYMPIA OYSTER POPULATIONS EXHIBIT VARYING GROWTH RATES



FASTER GROWTH in Population 1



marine ecology

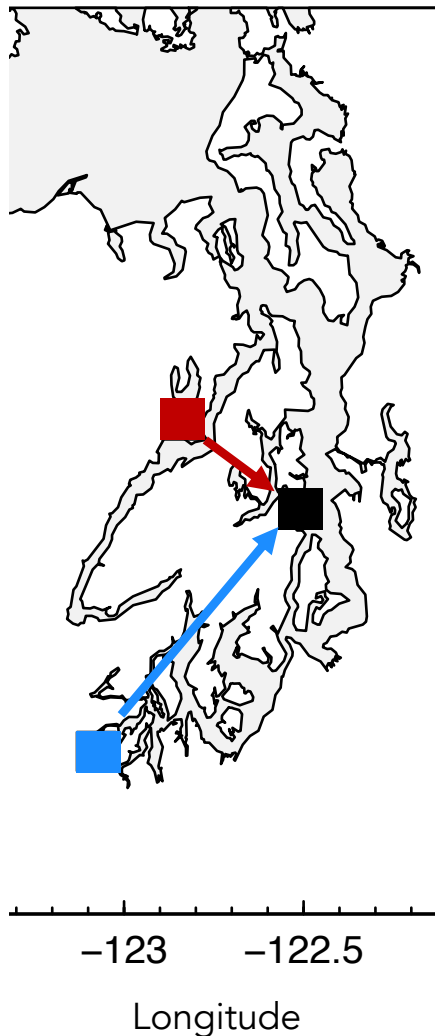
ORIGINAL ARTICLE | [Full Access](#)

Evidence of *Ostrea lurida* Carpenter, 1864, population structure in Puget Sound, WA, USA

Jake E. Heare, Brady Blake, Jonathan P. Davis, Brent Vadopalas, Steven B. Roberts

First published: 21 October 2017

Is inherited DNA methylation associated with different phenotypes?



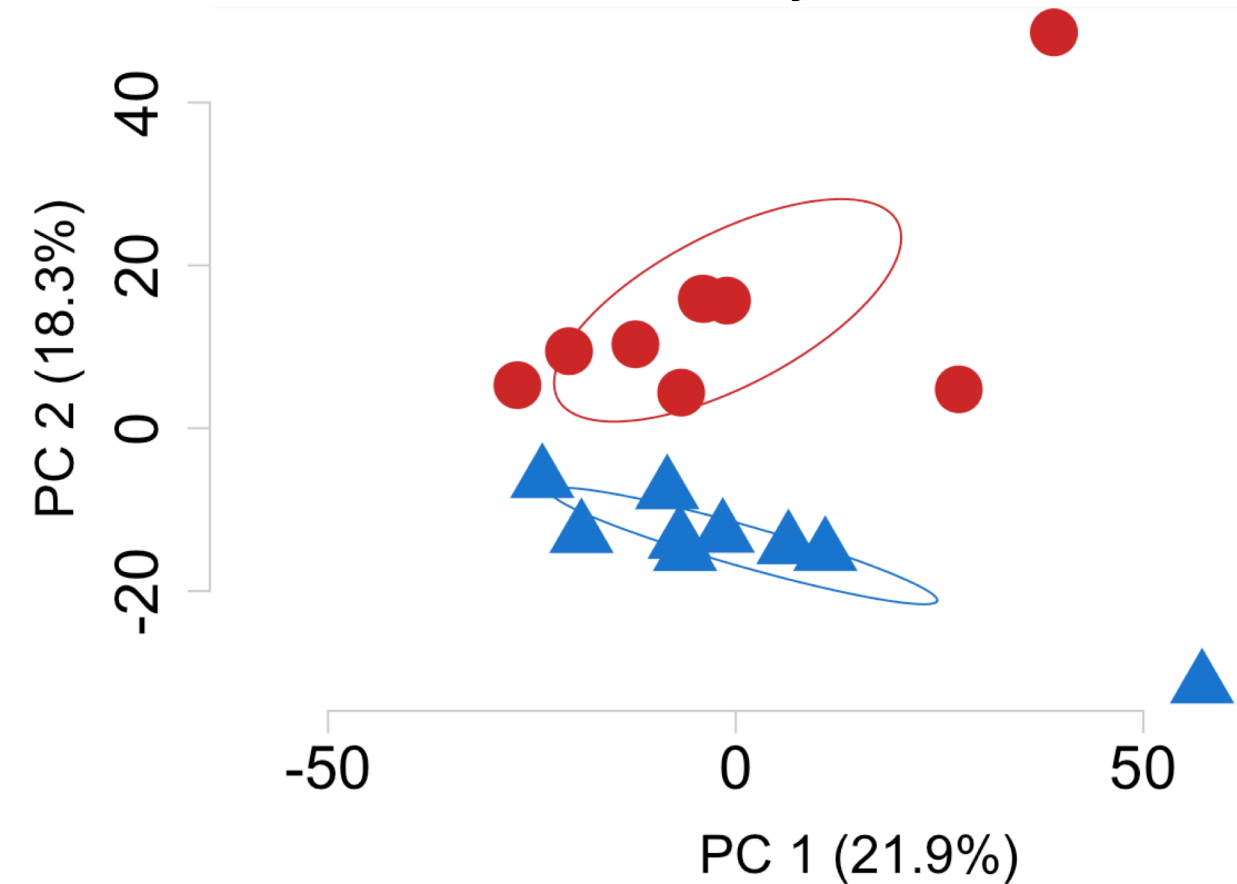
Design

- Wild adults collected from Hood Canal (■) and South Sound (■), and spawned in hatchery
- Offspring reared in common conditions (■) to adulthood
- DNA from offspring gill tissue sampled, bisulfite-treated and sequenced using methyl-binding domain (MBD-seq)
- Simultaneously examining genetic patterns using 2B Rad

DNA METHYLATION LEVELS (%) DIFFER BETWEEN POPULATIONS



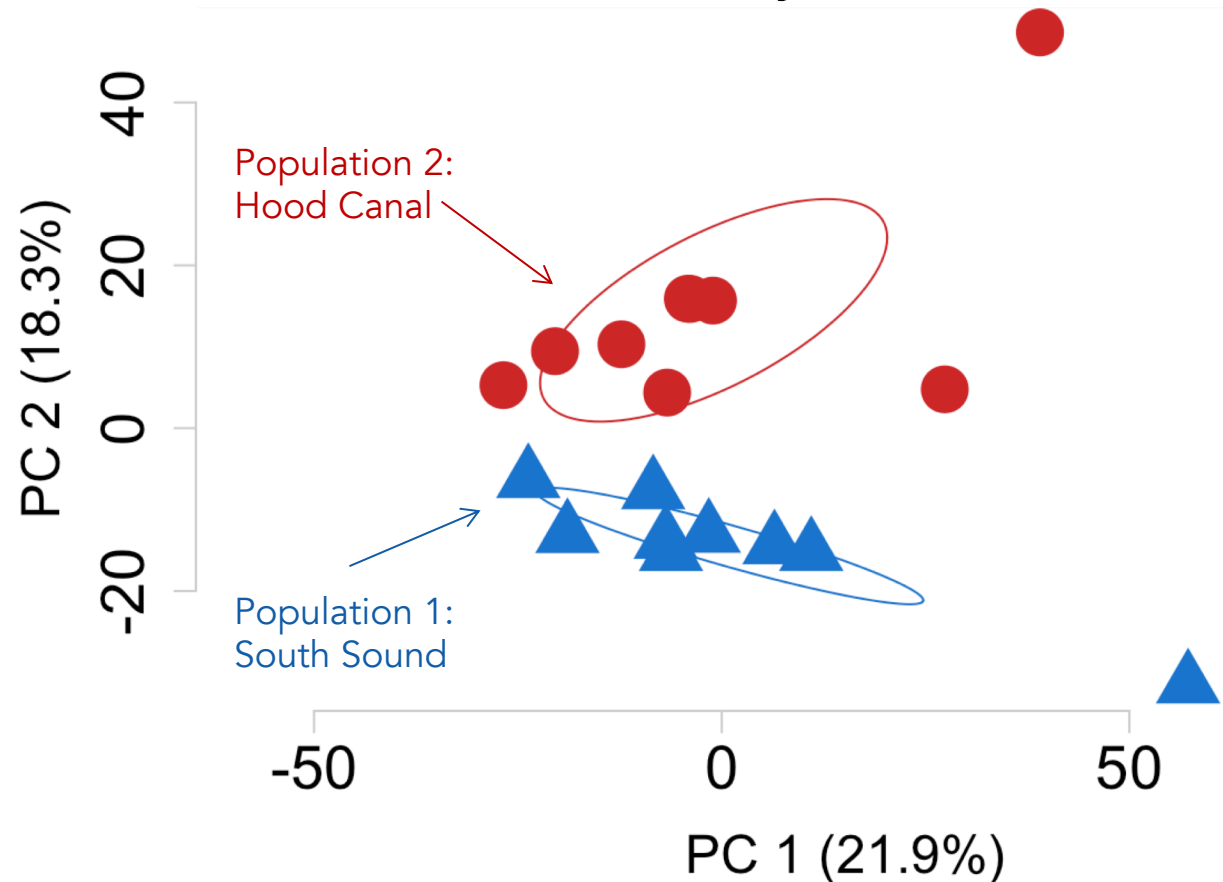
PCA of % Methylation



DNA METHYLATION LEVELS (%) DIFFER BETWEEN POPULATIONS



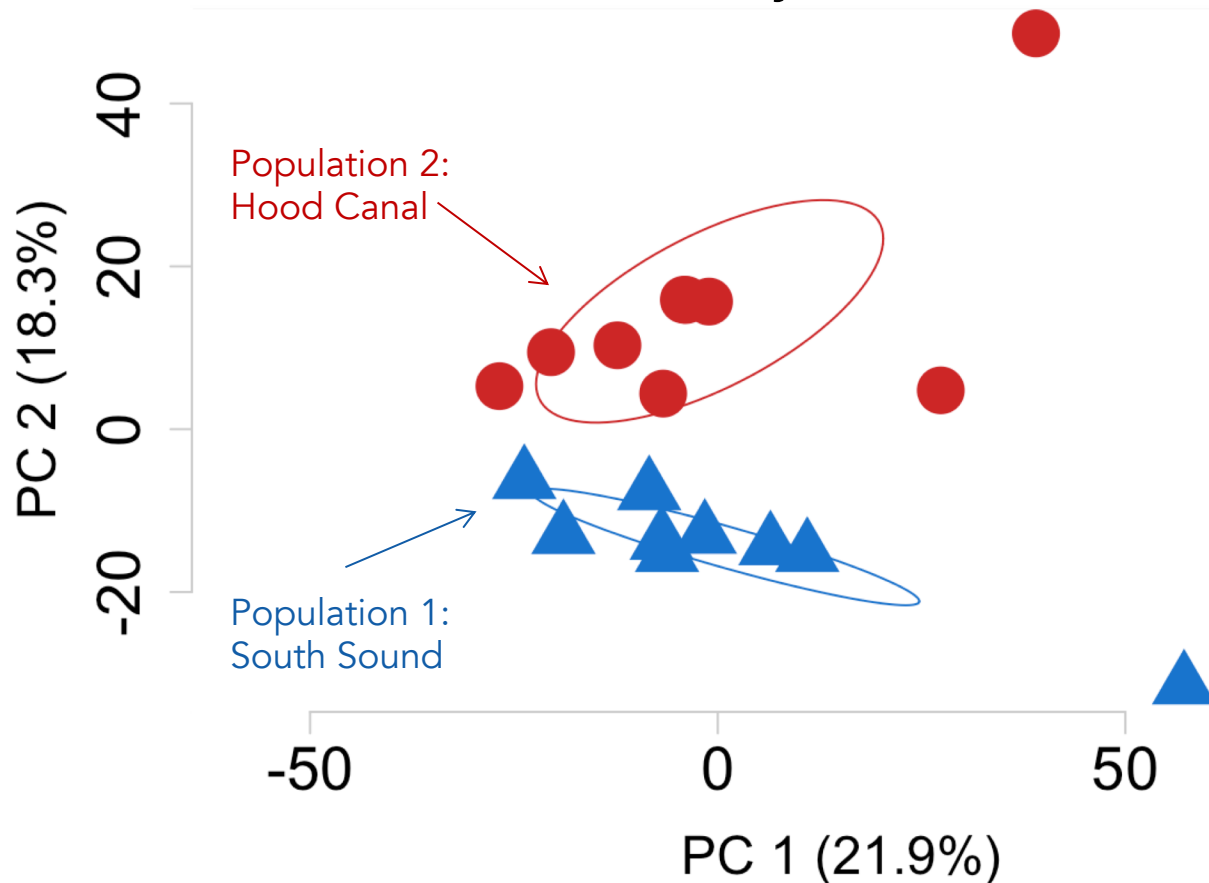
PCA of % Methylation



DNA METHYLATION LEVELS (%) DIFFER BETWEEN POPULATIONS



PCA of % Methylation



HOWEVER other traits differ too: *reproduction, stress response, larval vigor*

Are there size-specific methylation differences?

Analysis to find associations between size and methylation

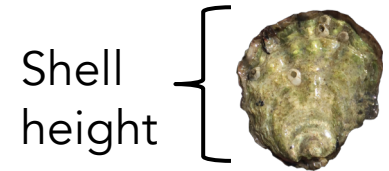


Inputs:

1. **Methylation & coverage data** (counts) for each locus
2. **Shell size data** (shell height)
3. **Genetic data** for relatedness matrix, controls for genetic covariance

Test associations with binomial mixed model

Analysis to find associations between size and methylation

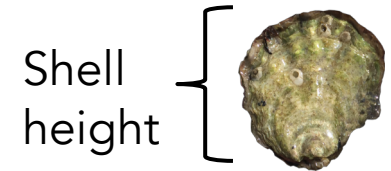


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Test associations with binomial mixed model

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Inputs:

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2. **Shell size data** (shell height)
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Test associations with binomial mixed model

Program used:

MACAU, *Mixed model Association for Count data via data Augmentation*



A Flexible, Efficient Binomial Mixed Model for Identifying Differential DNA Methylation in Bisulfite Sequencing Data

Amanda J. Lea¹, Jenny Tung^{1,2,3,4}*, Xiang Zhou^{5,6}* 2015

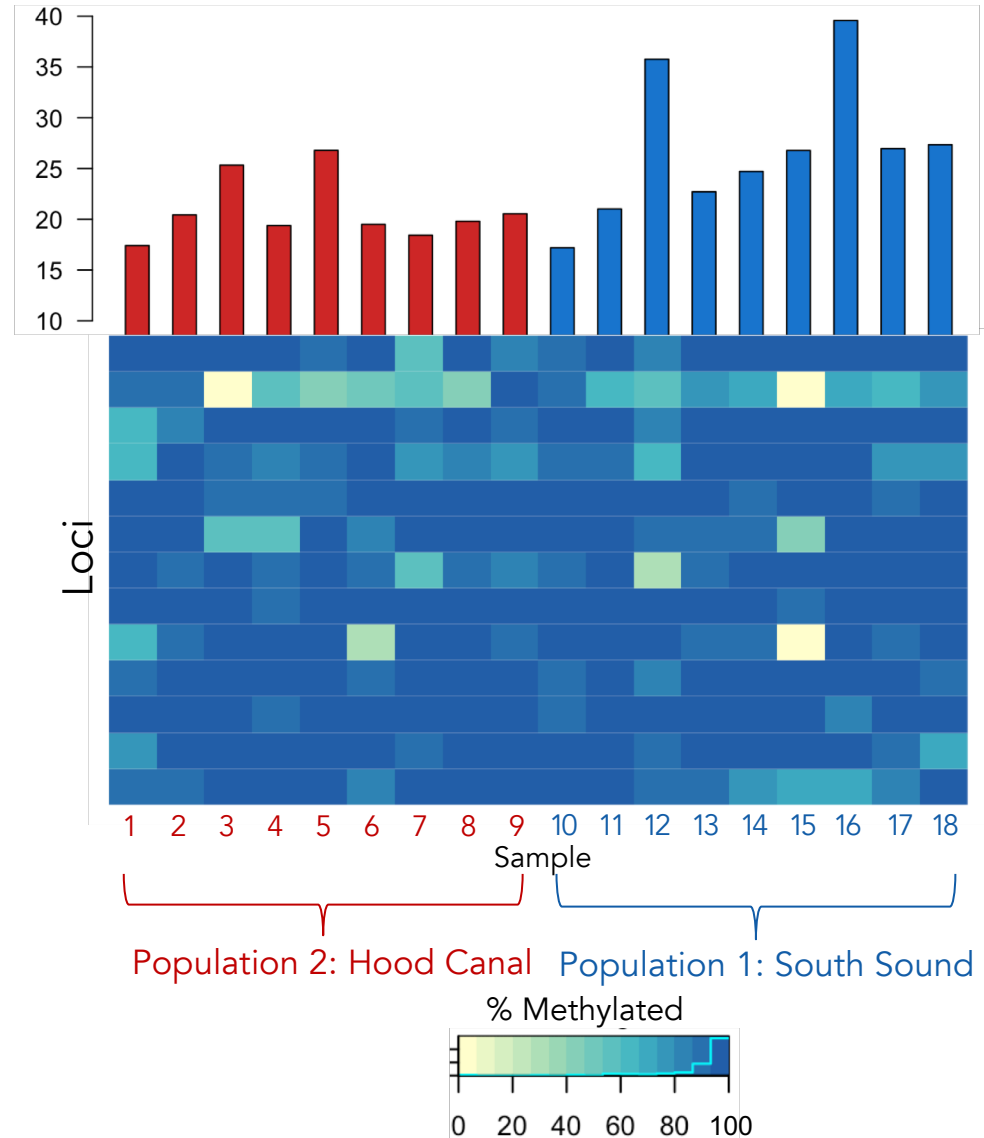
13 methylated loci associated with size



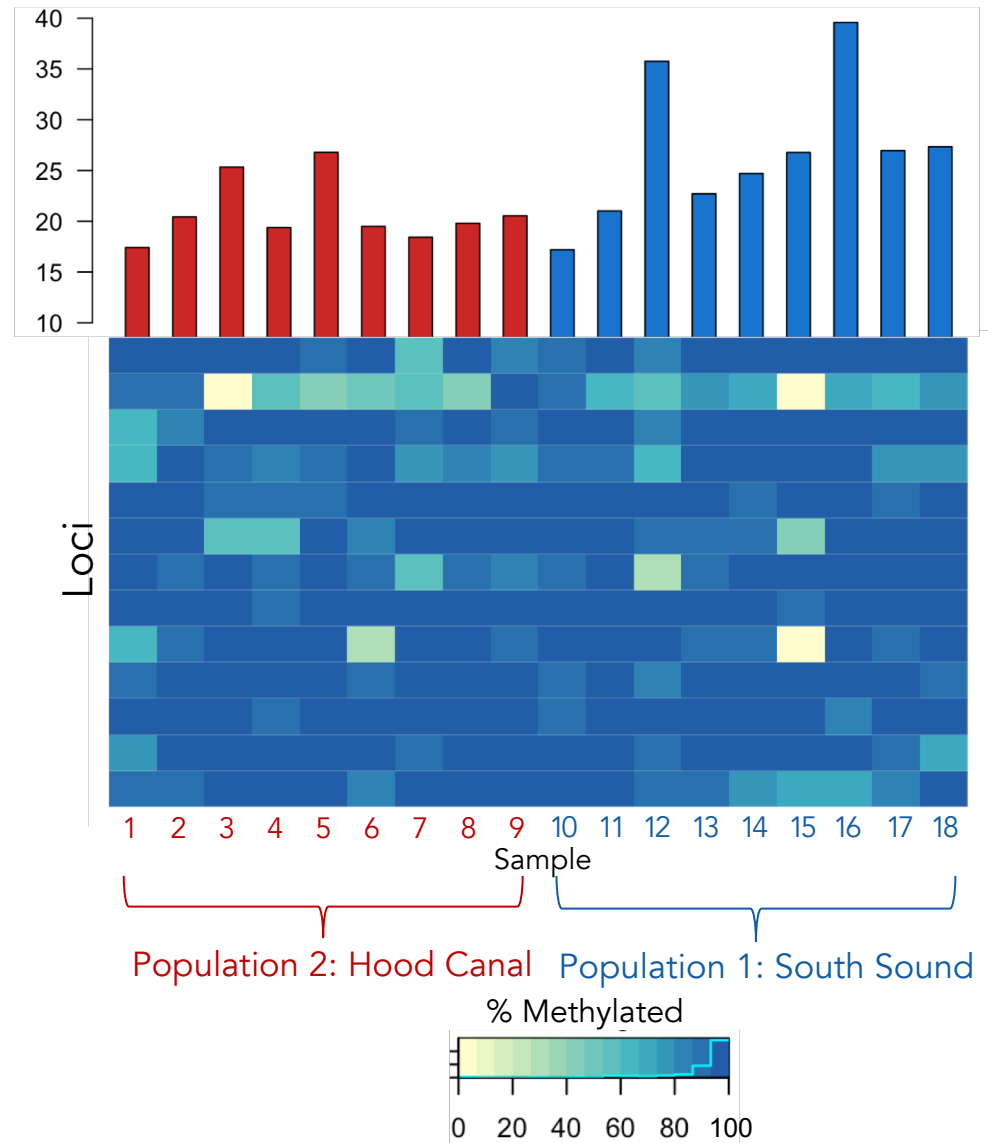
*9 loci located in genes
6 with known functions*

Shell Height (mm)

% Methylated



13 methylated loci associated with size

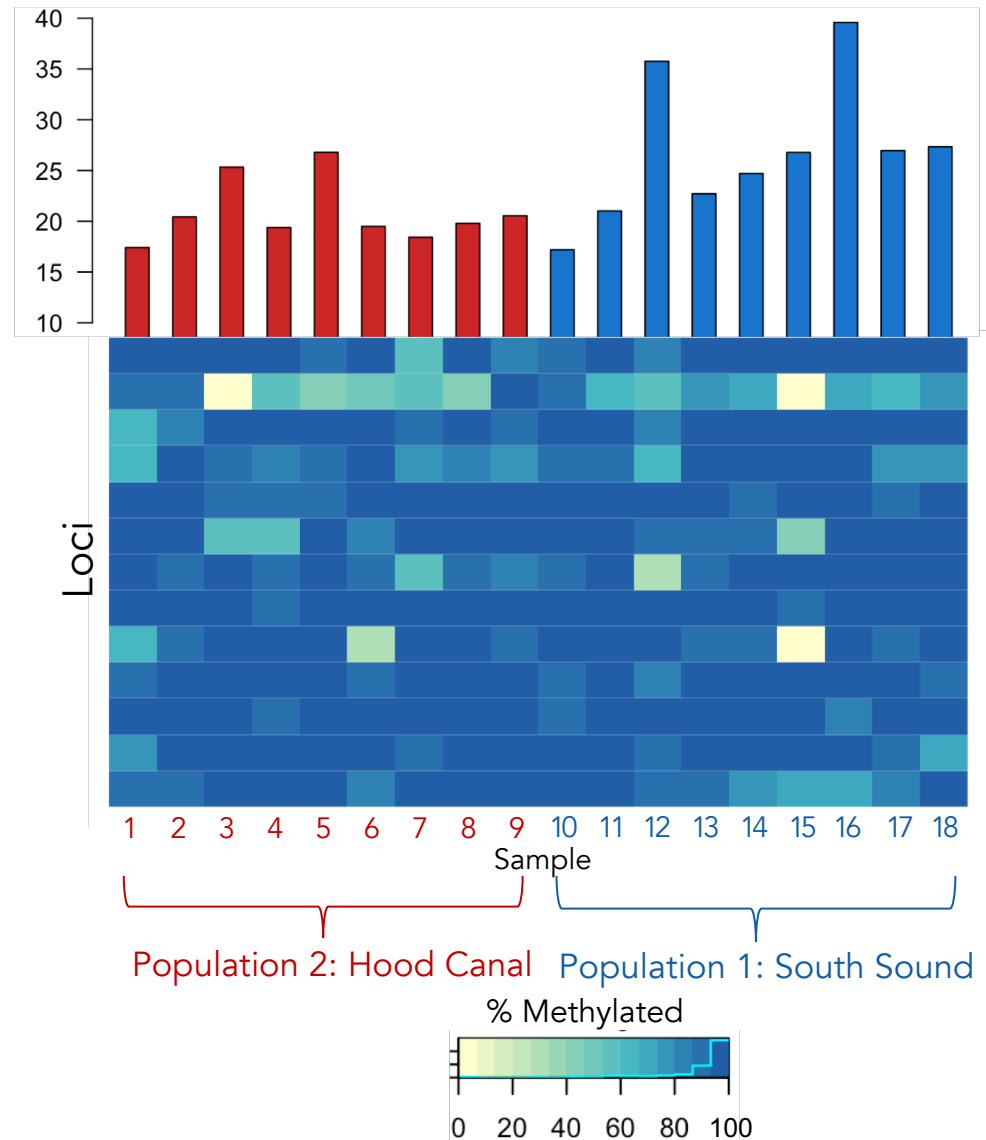


13 methylated loci associated with size



Gene functions

- Wnt/calcium signaling, cell growth/division, cilium activity
Polycystin-1

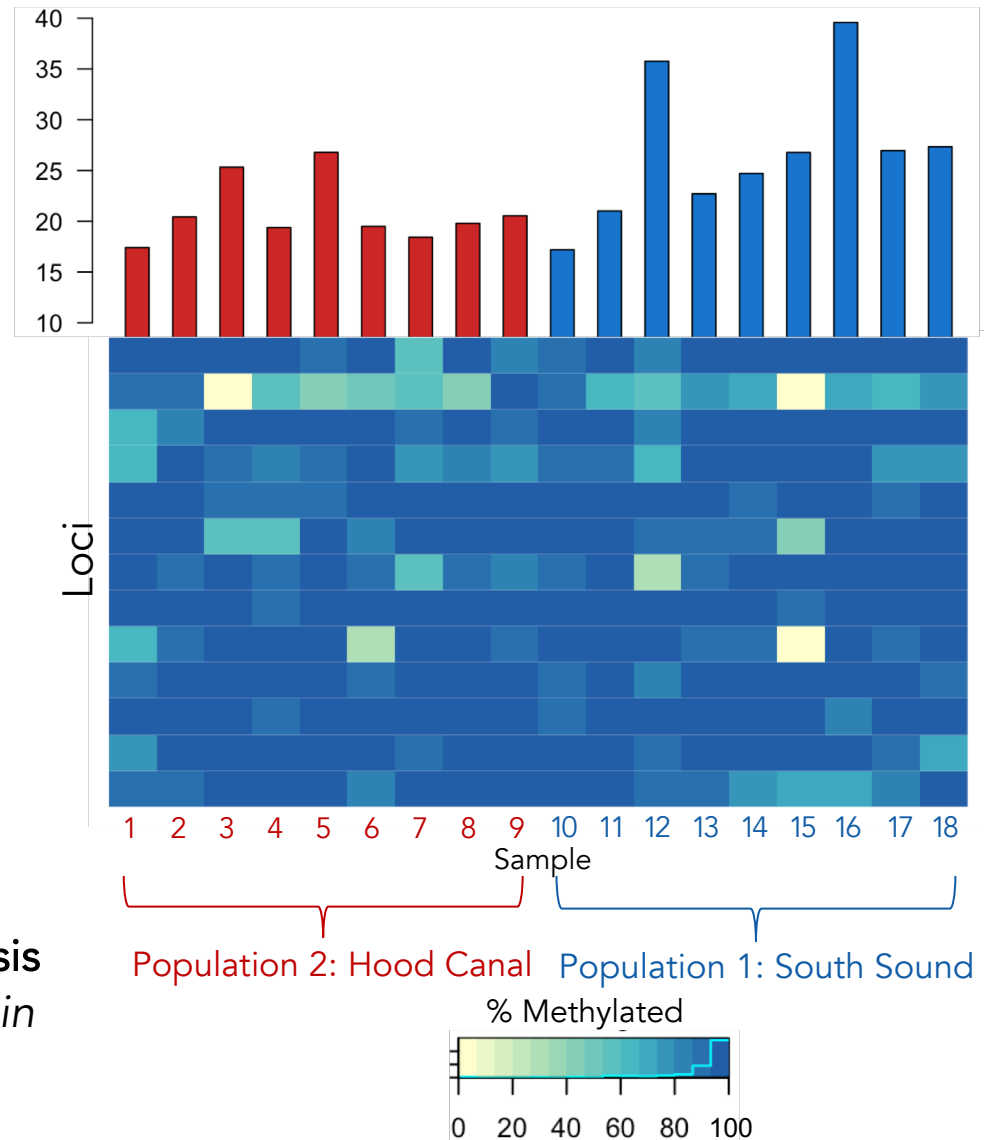


13 methylated loci associated with size



Gene functions

- Wnt/calcium signaling, cell growth/division, cilium activity
Polycystin-1
- Mitochondrial activity
ADP, ATP Carrier Protein
- Unfolded protein response in endoplasmic reticulum
Ubiquitin thioesterase & Ubiquitin carboxyl-terminal hydrolase
- Transcriptional regulator influencing chromatin structure & spermatogenesis
Protein kinase C-binding protein

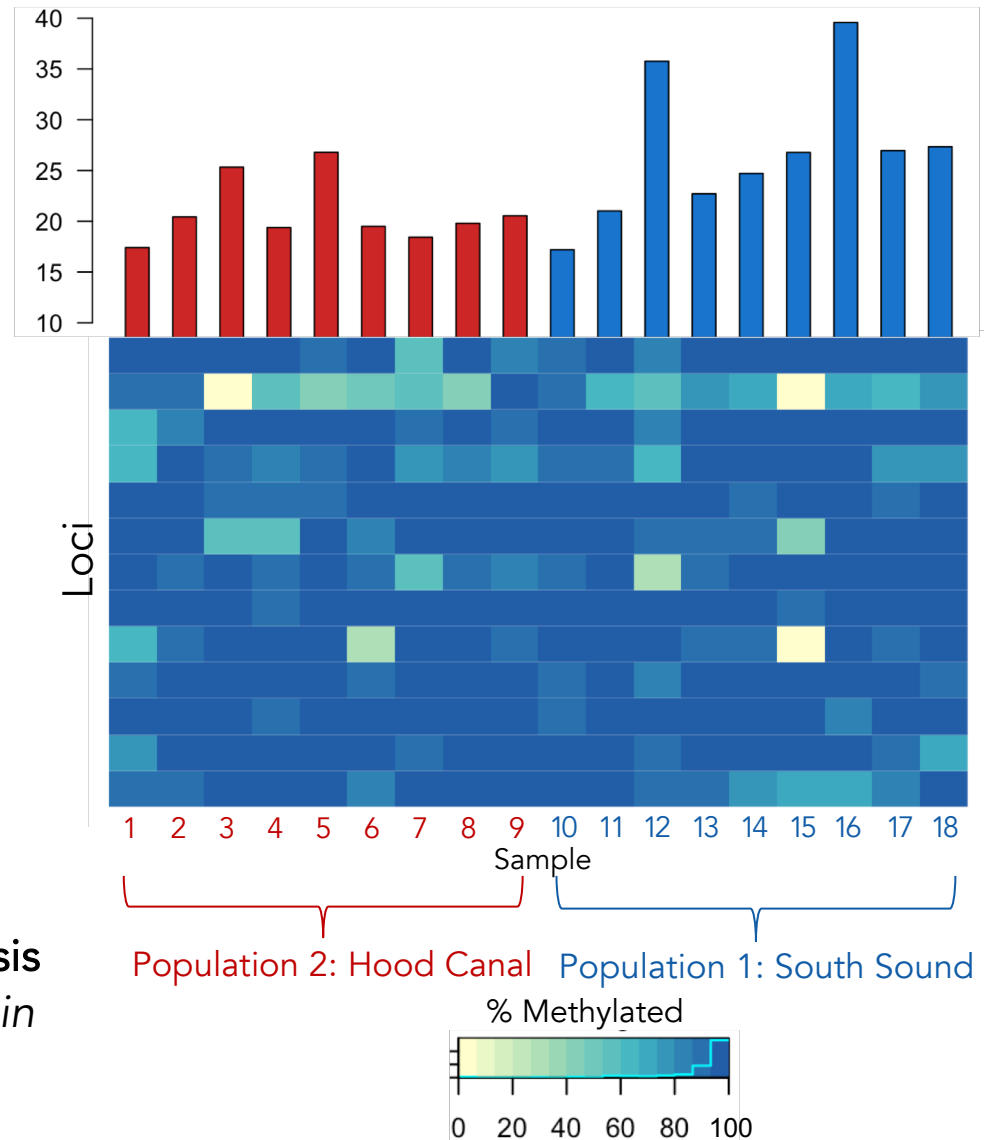


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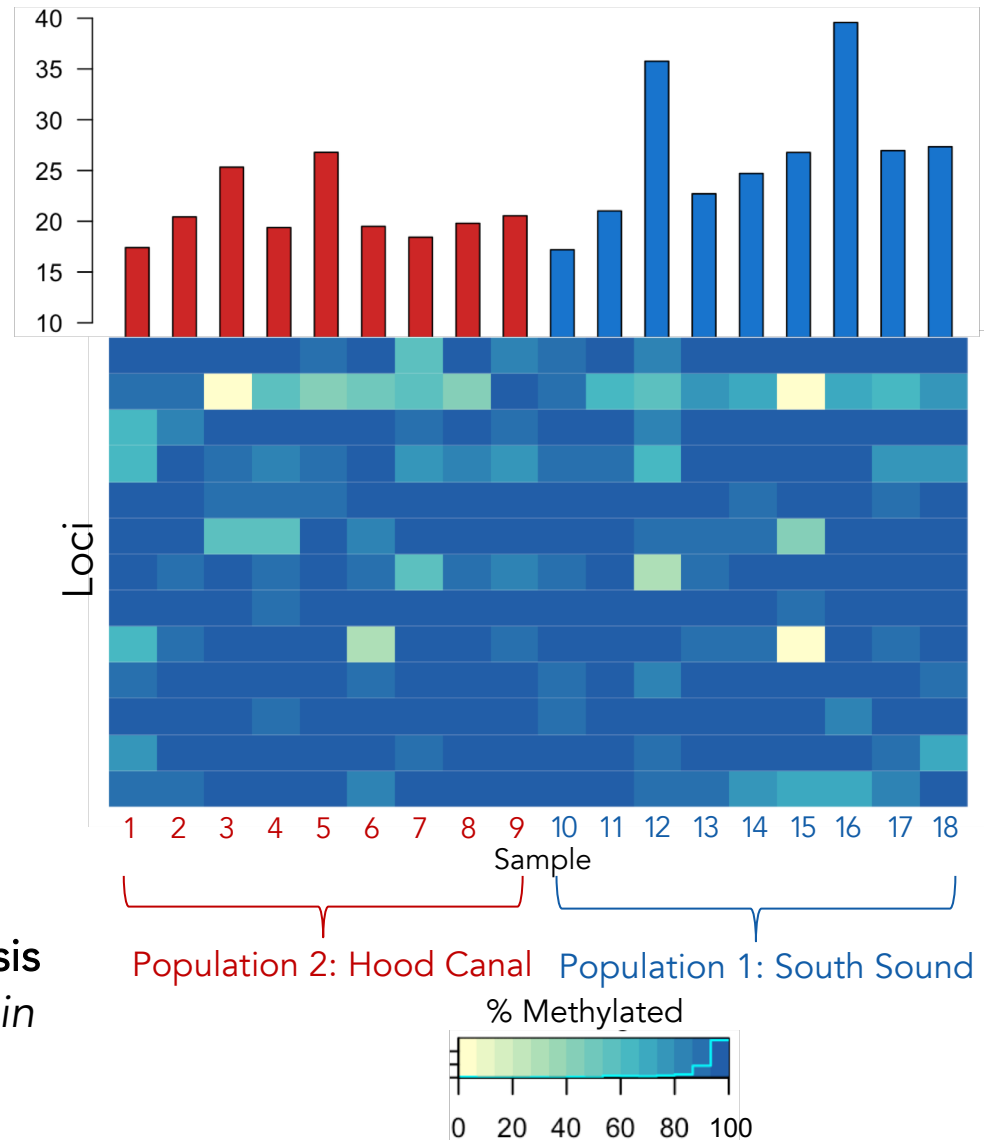


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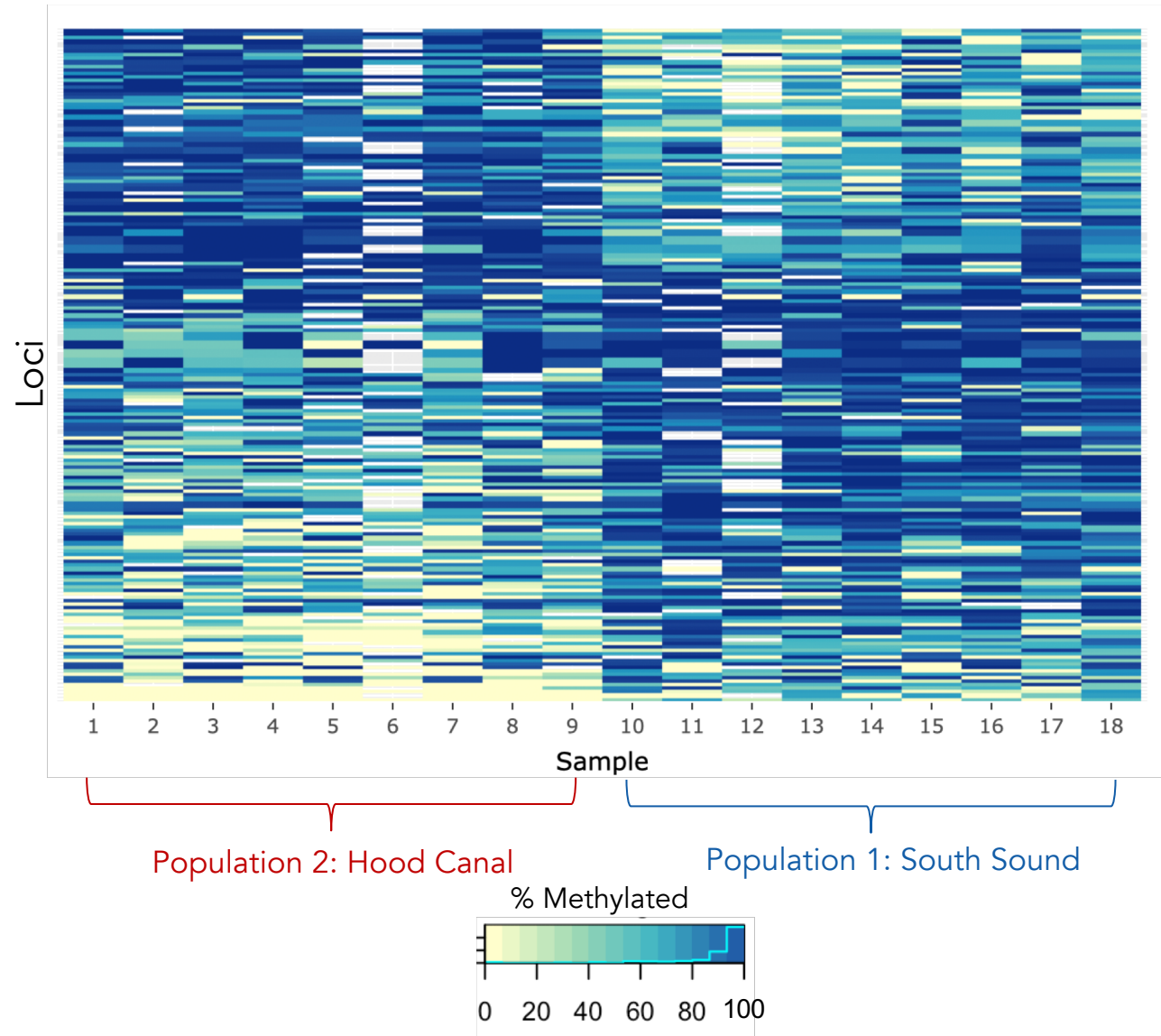


Gene functions

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180 DIFFERENTIALLY METHYLATED LOCI BETWEEN POPULATIONS

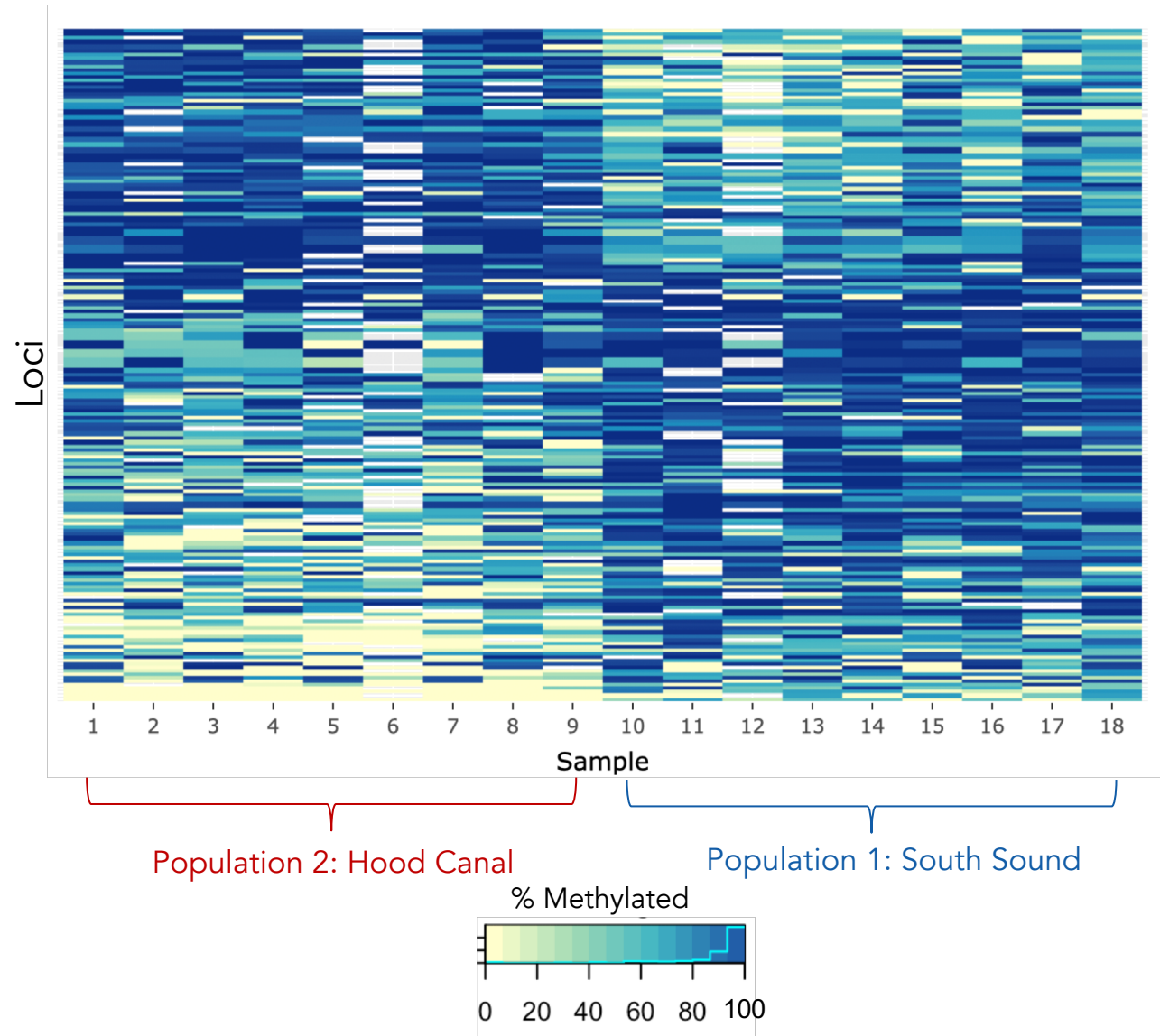


180 DIFFERENTIALLY METHYLATED LOCI BETWEEN POPULATIONS



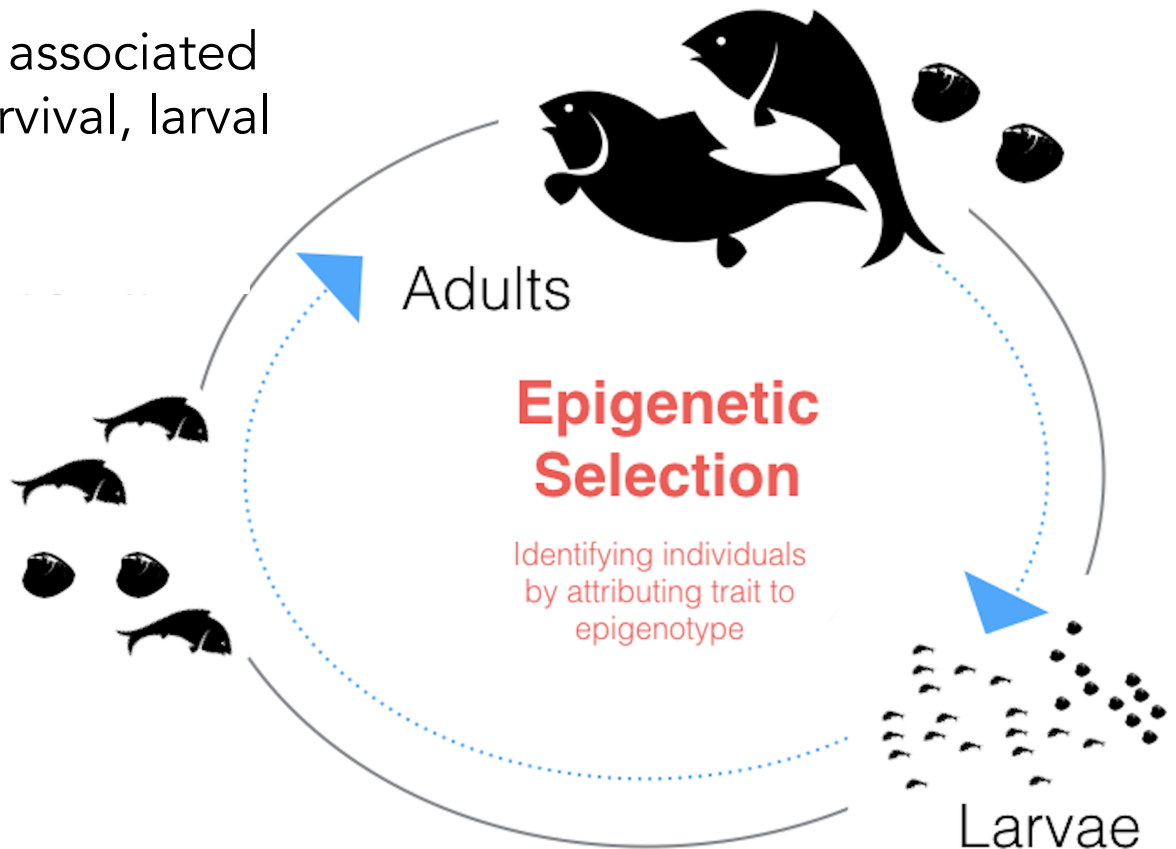
Enriched gene functions

- Cell morphogenesis
- Regulation of cell proliferation
- Cellular response to DNA damage
- Endosomal transport
- Protein monoubiquitination



WHAT COULD THIS MEAN?

- Breeding programs could select individuals with growth-associated methylation patterns
- Other desirable traits associated with methylation? Survival, larval vigor, fecundity/sex



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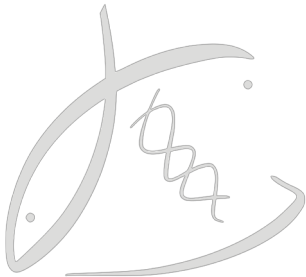
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THANK YOU

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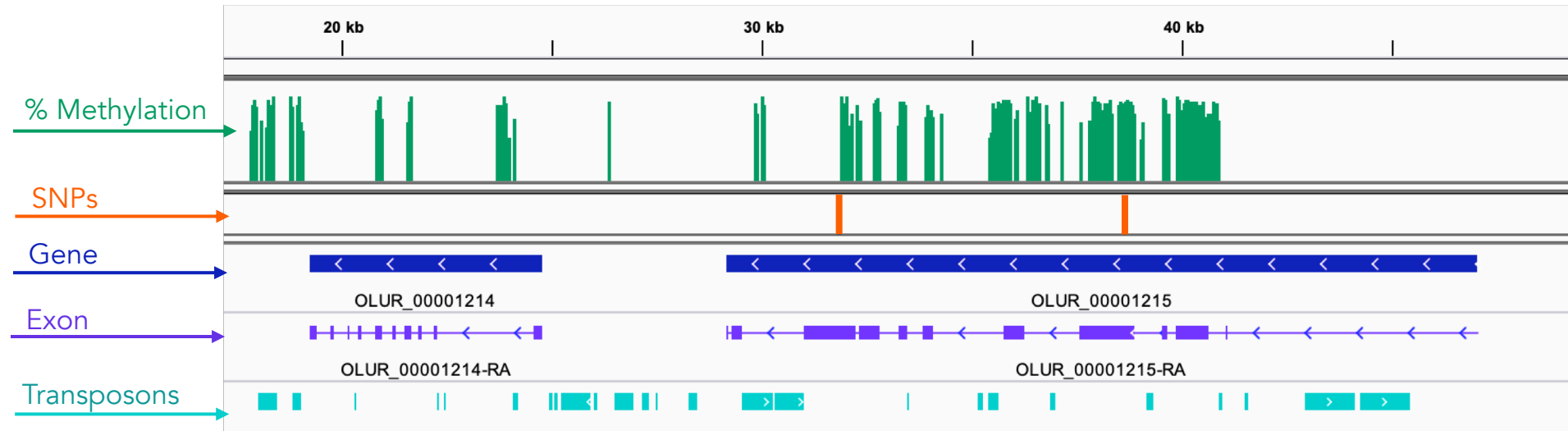
School of Aquatic and Fishery Sciences
University of Washington
Aquaculture America in Honolulu, HI

<https://laurahspencer.github.io/LabNotebook/>



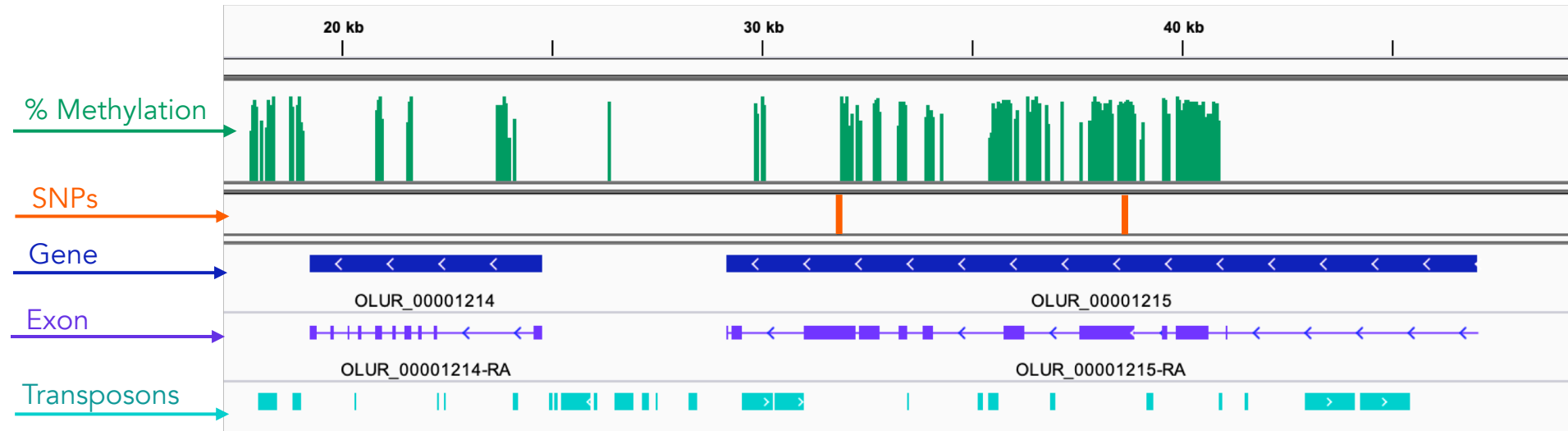
EXTRA SLIDES

DNA METHYLATION LANDSCAPE IN OLYMPIA OYSTERS

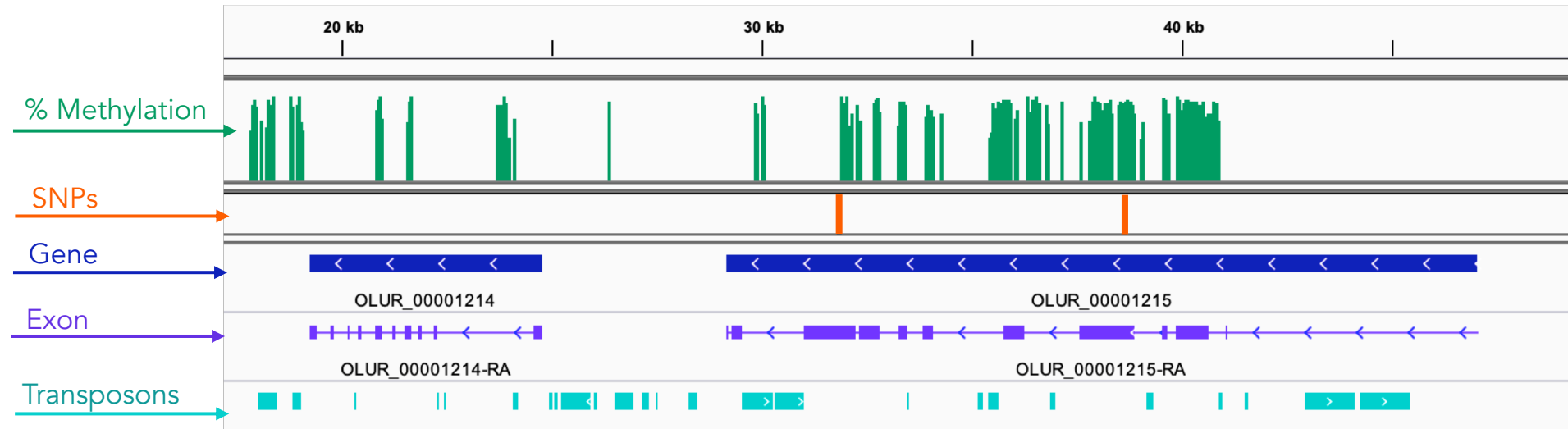


Methylation in/near genes, mosaic pattern

DNA METHYLATION LANDSCAPE IN OLYMPIA OYSTERS



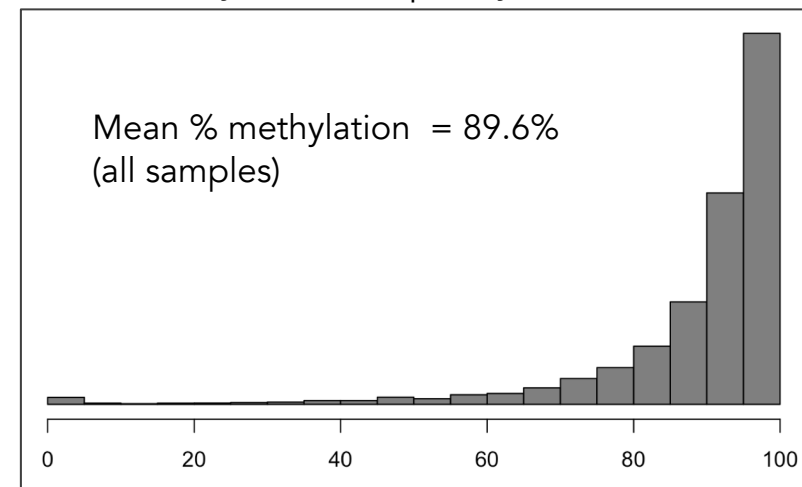
DNA METHYLATION LANDSCAPE IN OLYMPIA OYSTERS



19,752 total CpG loci (after filtering)

- Majority have *some* methylation (99.2%)
- 10,345 in genes
- 8,889 in exons
- 1,029 in transposable elements
- 3,000 intragenic

% Methylation Frequency Distribution



PUGET SOUND OLYMPIA OYSTER POPULATIONS

EXHIBIT VARYING TRAITS



Population 1 is more fecund than Population 2

