Environmental influence on the Atlantic salmon epigenome during sea lice infestation

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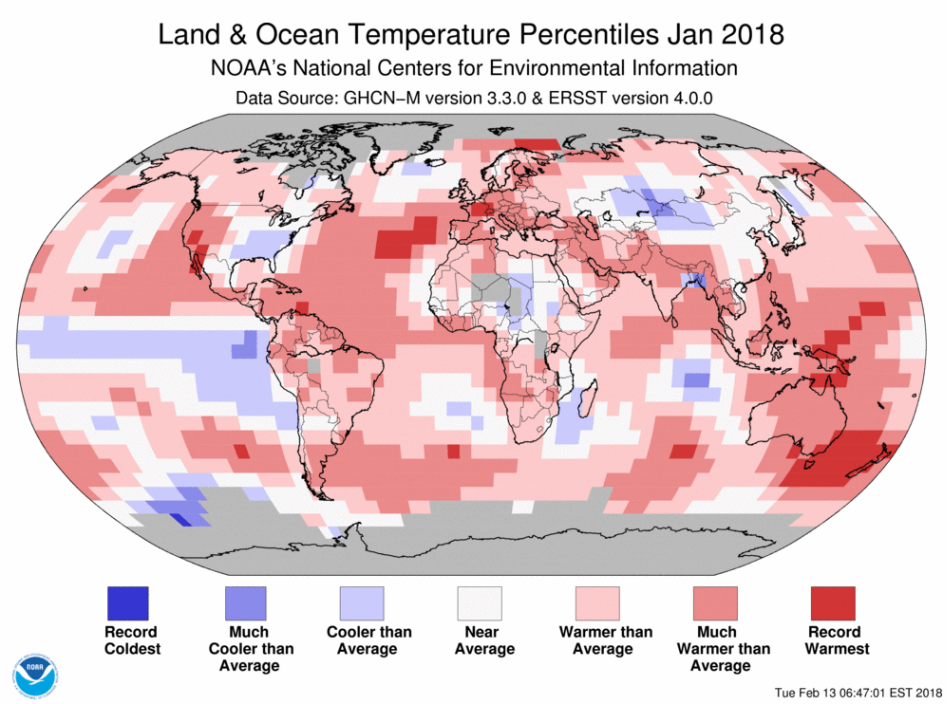
Environmental threats to Salmon

- Ocean change
  - temperature impacts salmon physiology
    - Some studies show heat tolerance BUT at a cost
      - Anttila et al (2014) *Nat Comm,* Tromp et al. (2018) *Aquaculture*, Nuez-Ortin et al. (2018) *BMC Genomics*



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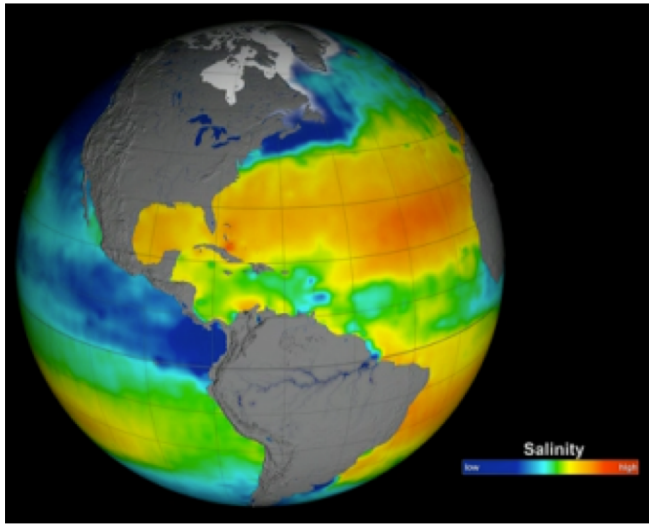
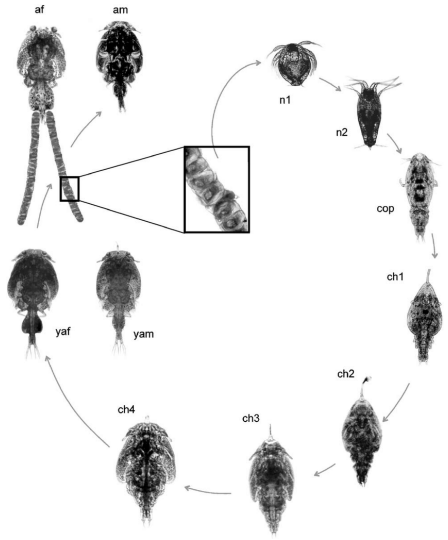
  - salinity
    - Brown et al. (2018) *J. Fish Biol.,* Duston (1994) *Aquaculture,* Vargas-Chacoff et al (2018) *J. Fish Biol.*

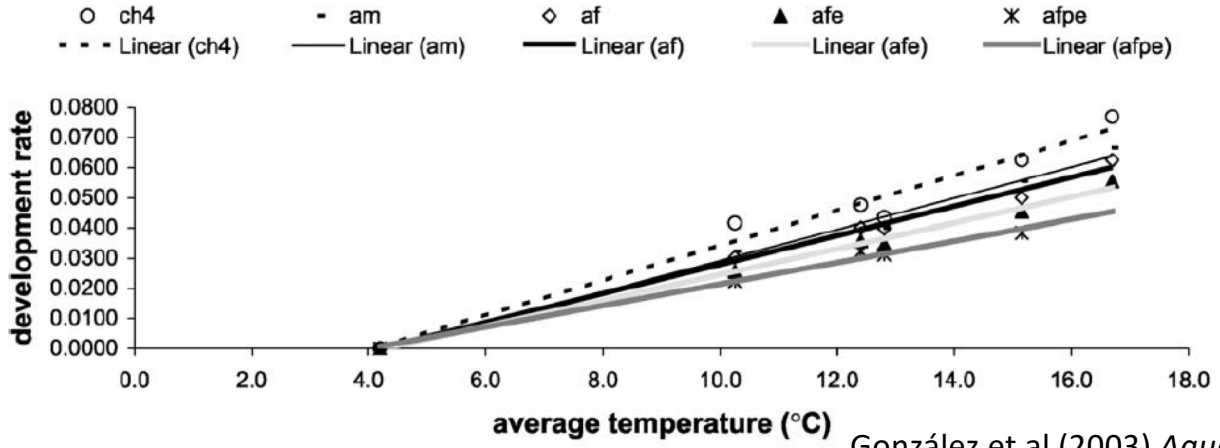


https://science.nasa.gov/earth-science/oceanography/physical-ocean/salinity

Environmental conditions can exacerbate sea lice infestation



Temperature affects development



González et al (2003) *Aquaculture*

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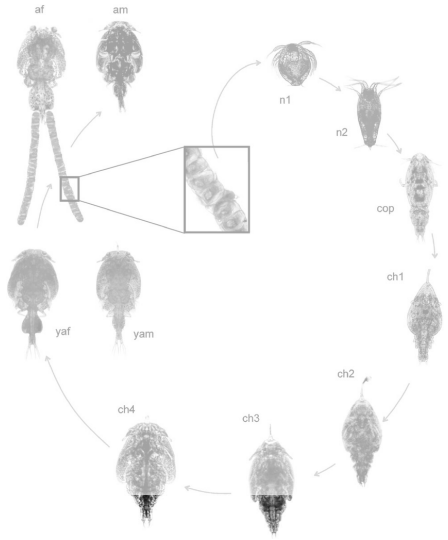

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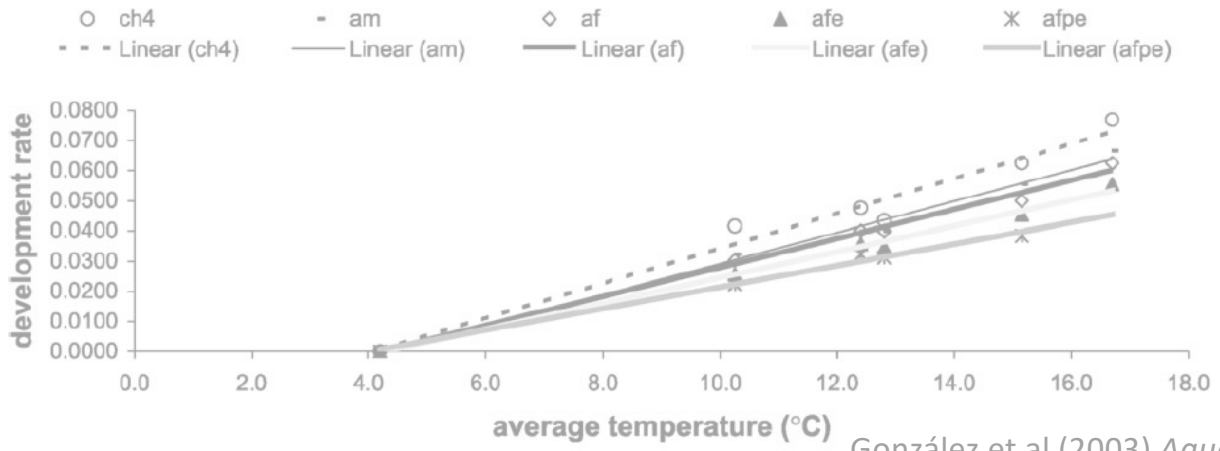

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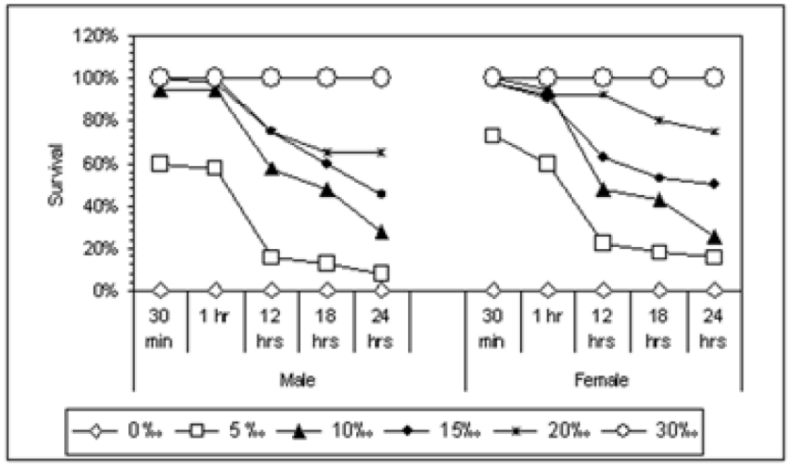
Salinity affects survival



Bravo et al (2008) *Bulletin of the European Association of Fish Pathologists*

How do temperature and salinity affect salmon response to sea lice?

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- Methylation is a good way to measure wide-spread change
  - Epigenetic marks can be directly influenced by the environment
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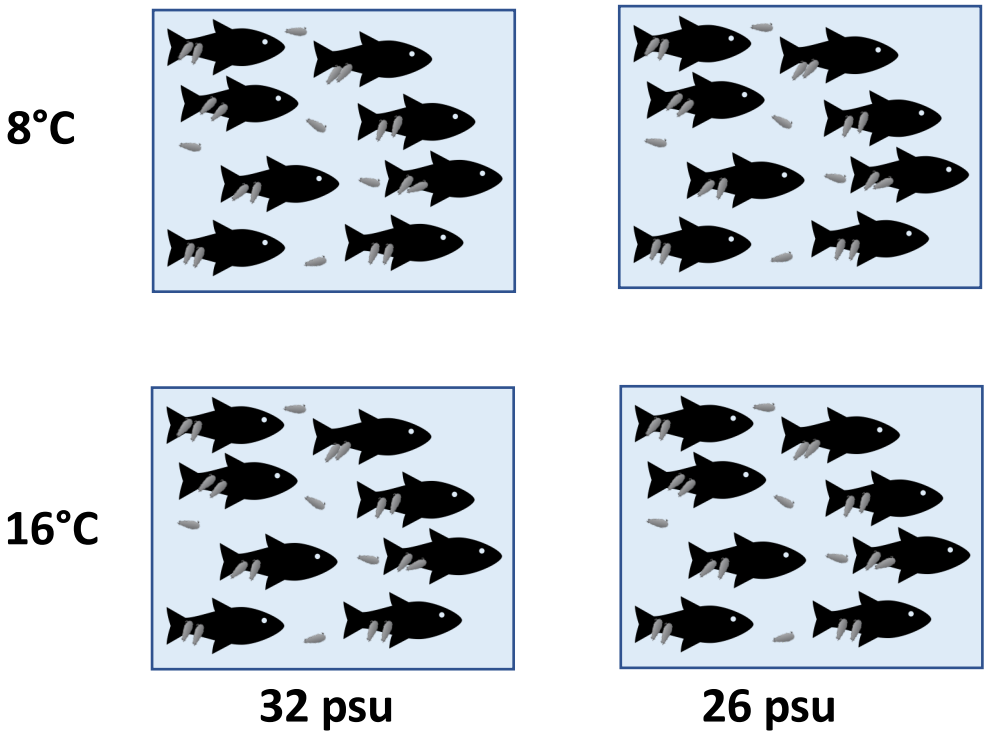
- Do salmon methylomes change in response to environment during sea lice infestation?
  - How might these methylation changes influence physiology?
  - Are specific regulatory pathways affected by one factor more than another?

Temperature x salinity experimental set-up

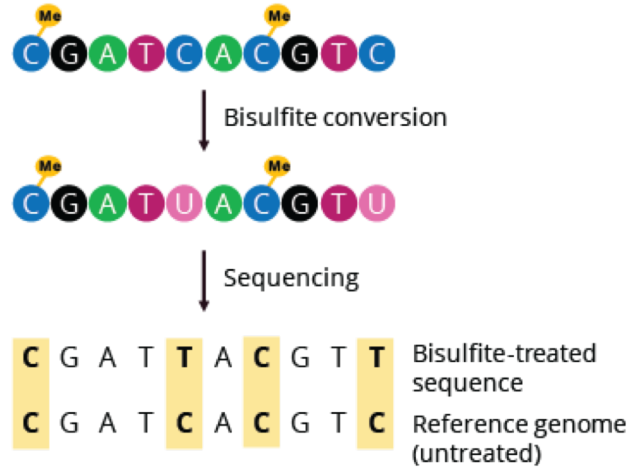
- 8 fish (*S. salar*) per tank
- 4 tanks/treatment
- Initial load: 35 sea lice (*C. rogercresseyi*) per fish
- 30 days



skin sections

4 fish/ treatment

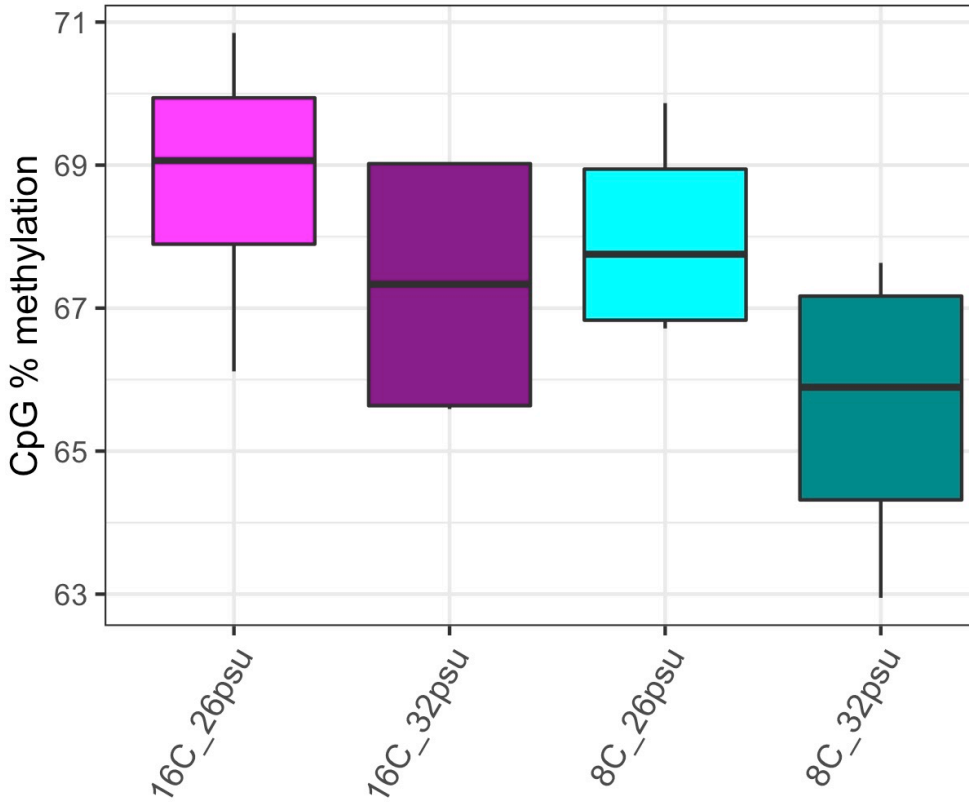
Reduced-Representation Bisulfite Sequencing



Normal conditions in Chile = 12 °C and 32 psu

CpG methylation across groups

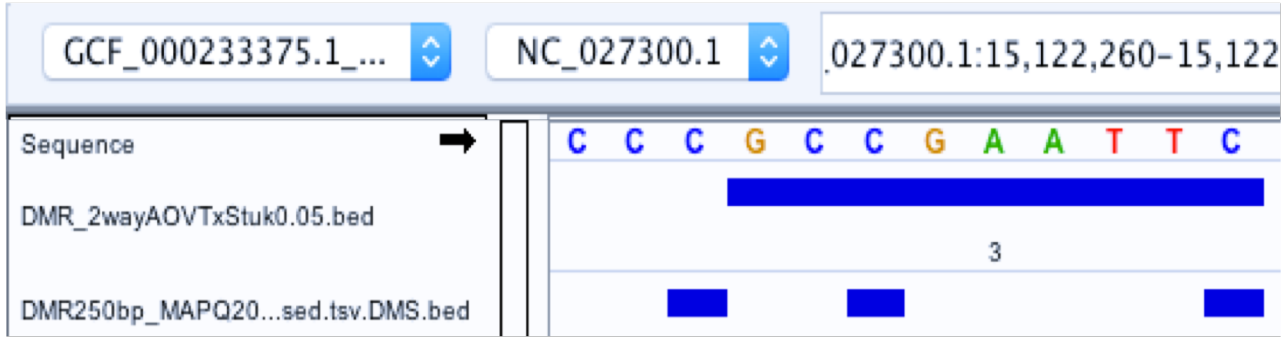
Total CpGs analyzed: 34,478,010



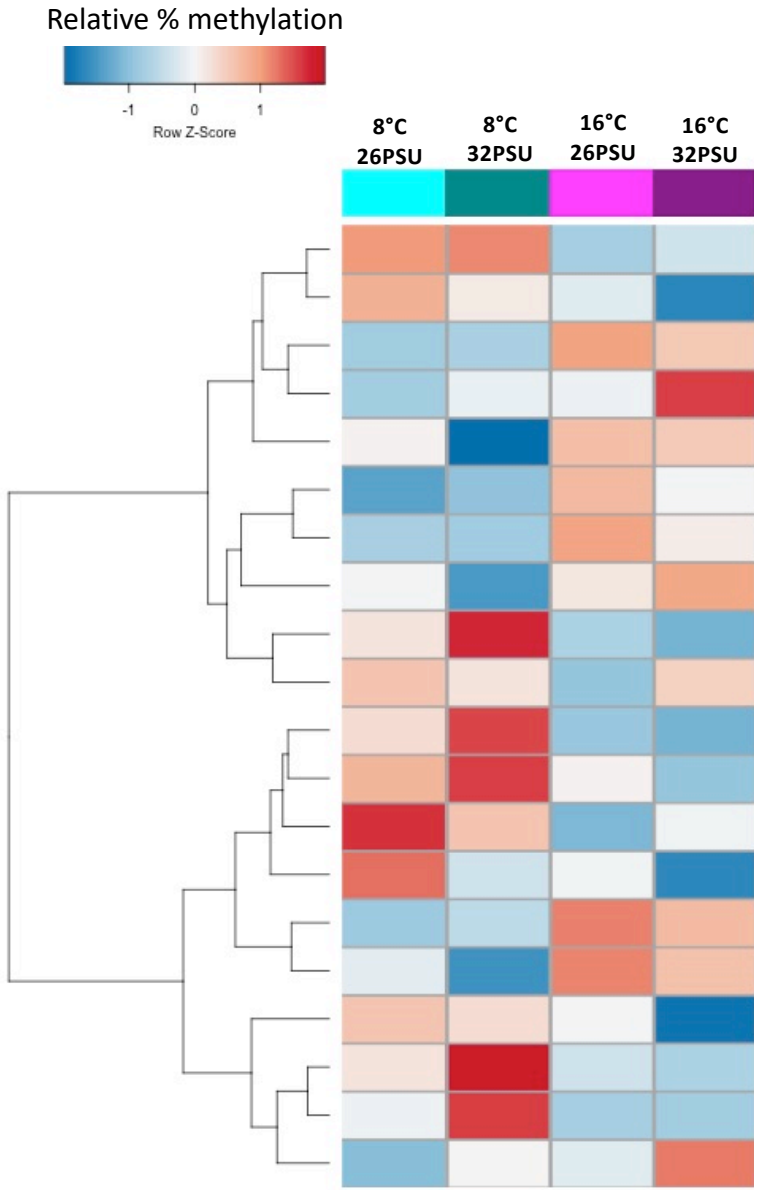
High salinity groups show a general decrease in overall methylation and greater variance

DMR: Differentially methylated region

A 10 - 300bp region containing at least 3 CpGs that are significantly differentially methylated



Influence of temperature on methylation



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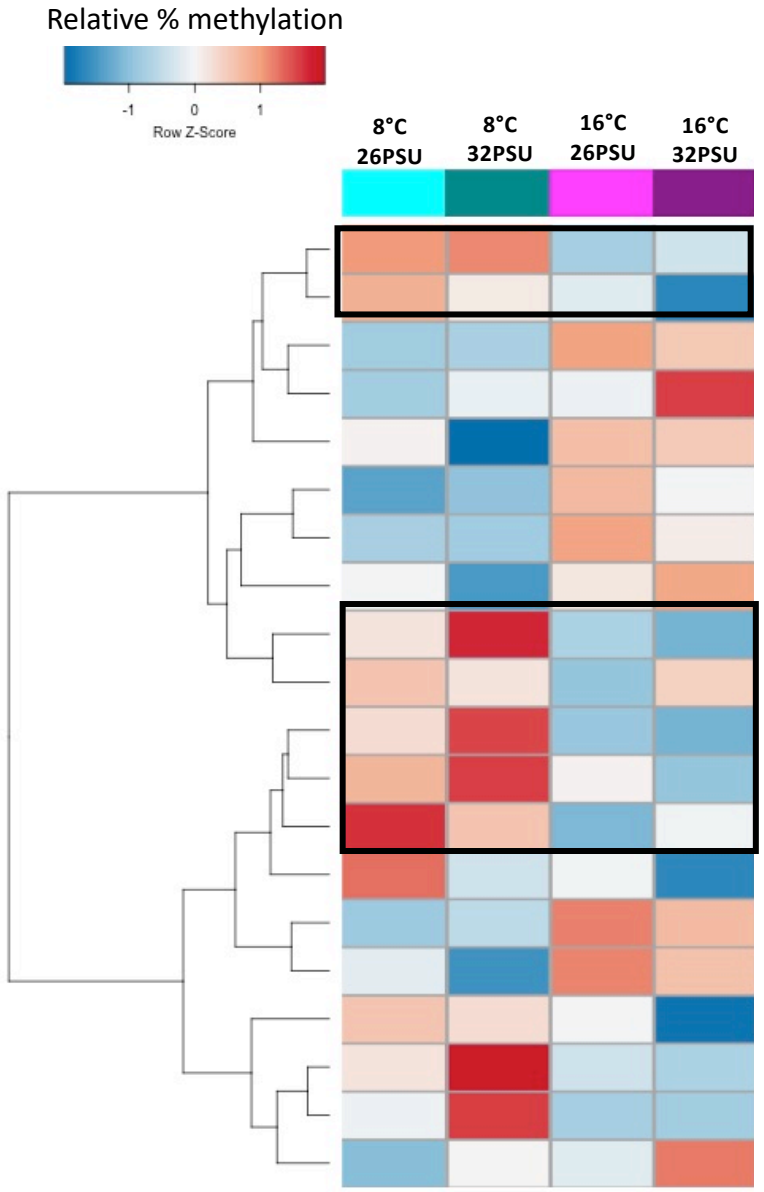
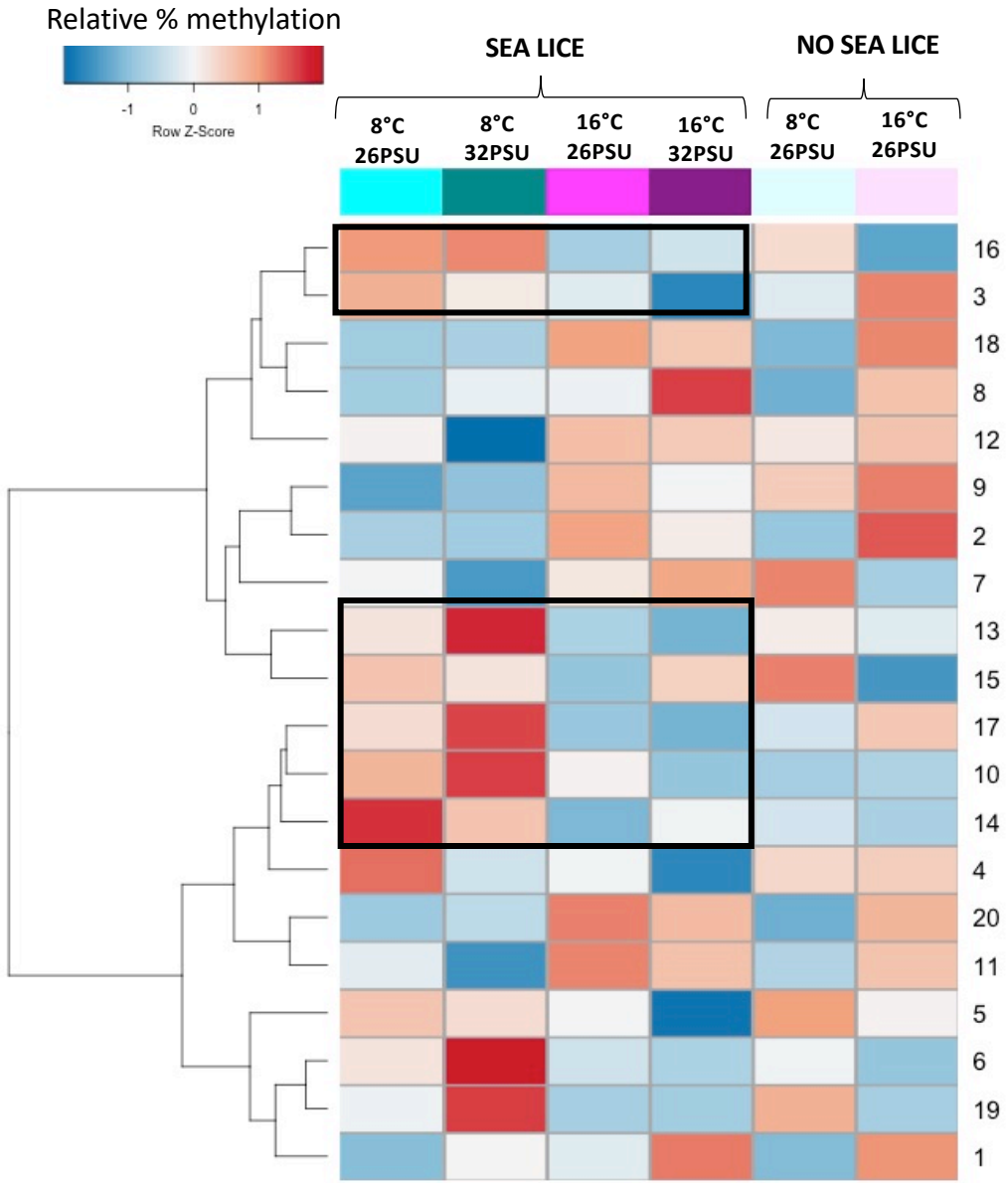


Increase in methylation under low temperature (8°C)

Influence of temperature on methylation



Sea lice-dependent **increase** in methylation under low temperature (8°C)

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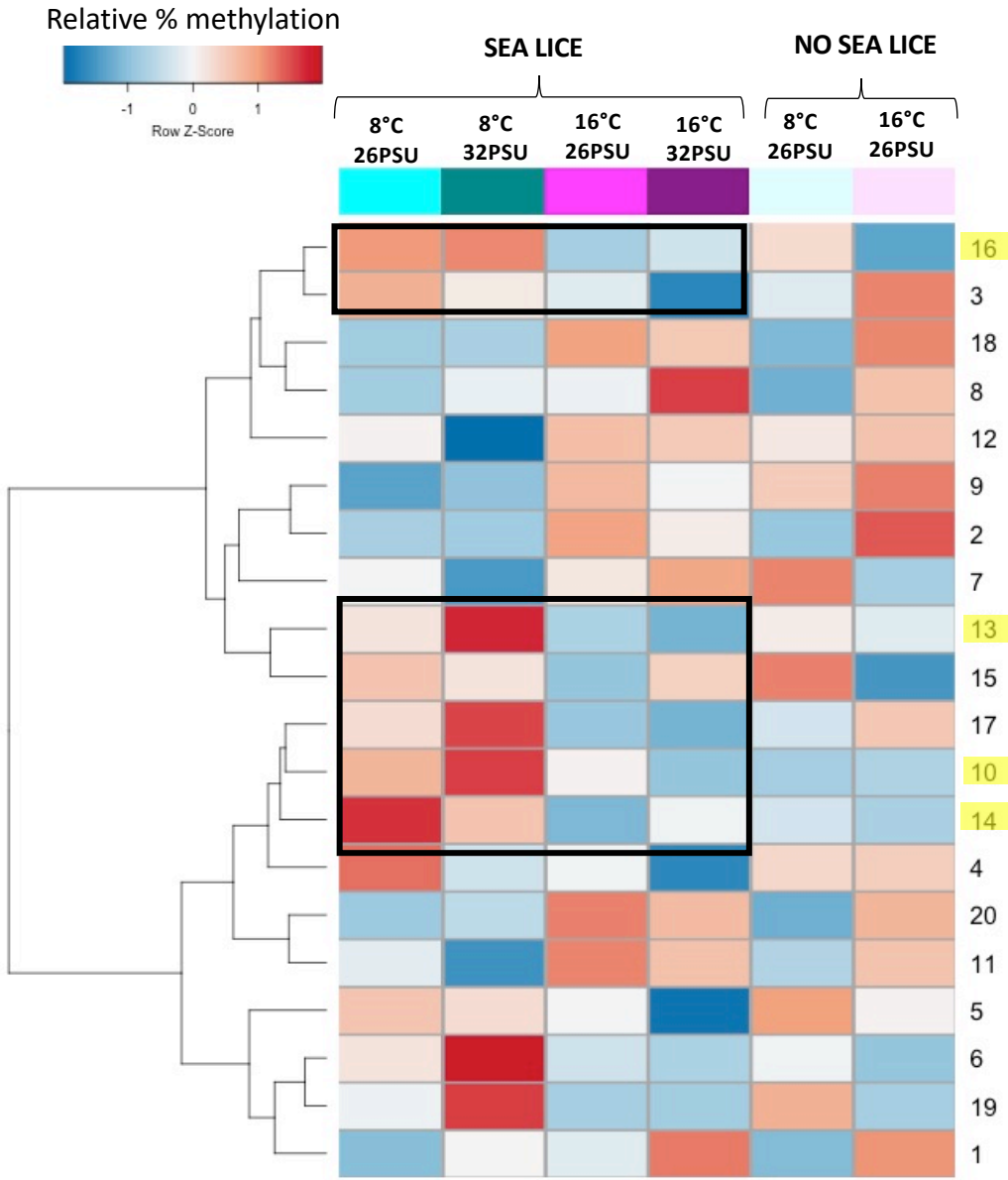

Sea lice-dependent **increase** in methylation under low temperature (8°C)

RARA (intron)

HOX activator complex

HOX: **specify spatial plan in organ development**

Agrin-like (intron) **modulates growth (favors aggregation)**

Uncharacterized lncRNA

EGR1

zinc finger that **regulates inflammatory response** and **cell proliferation**

Influence of salinity on methylation

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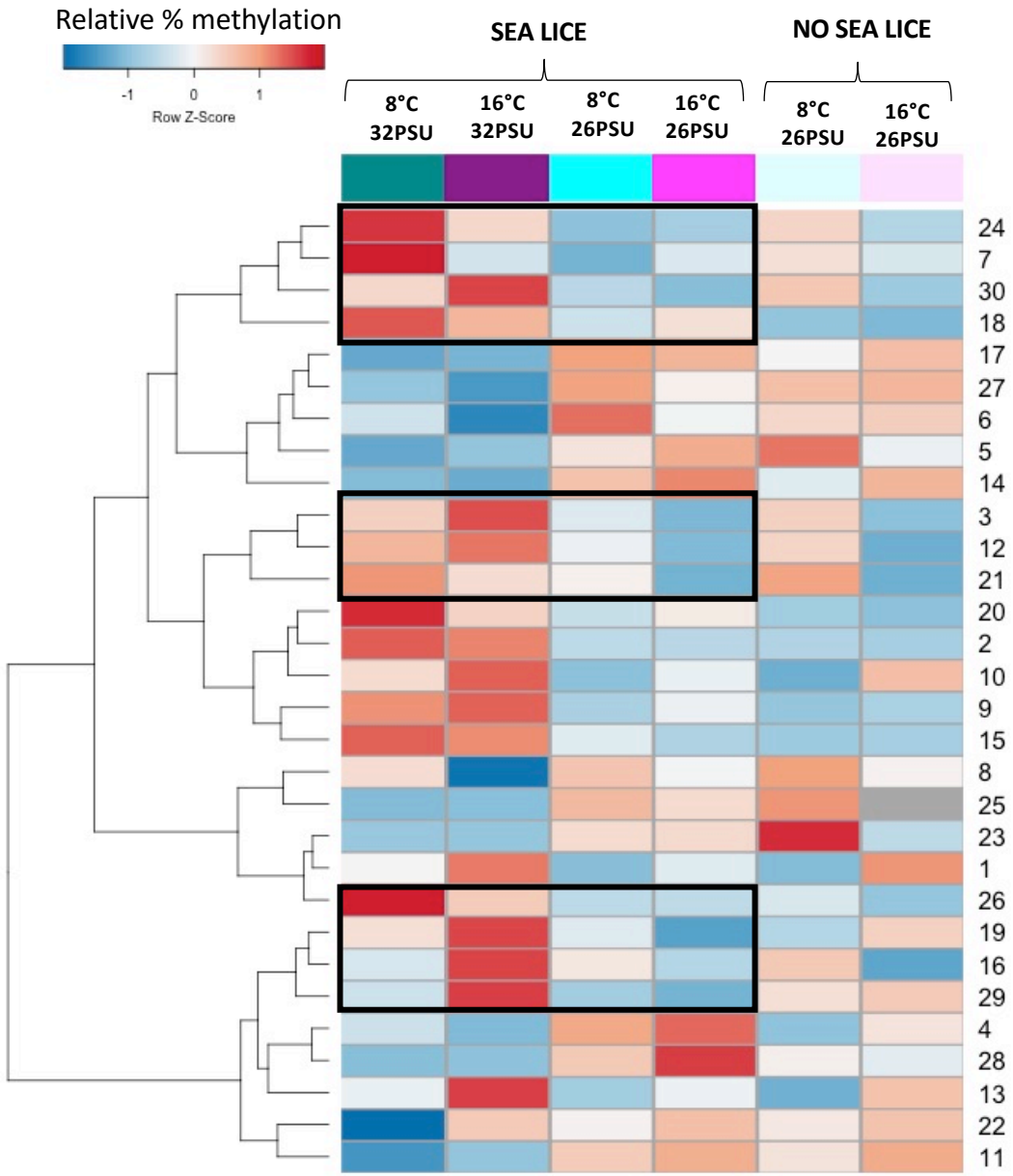
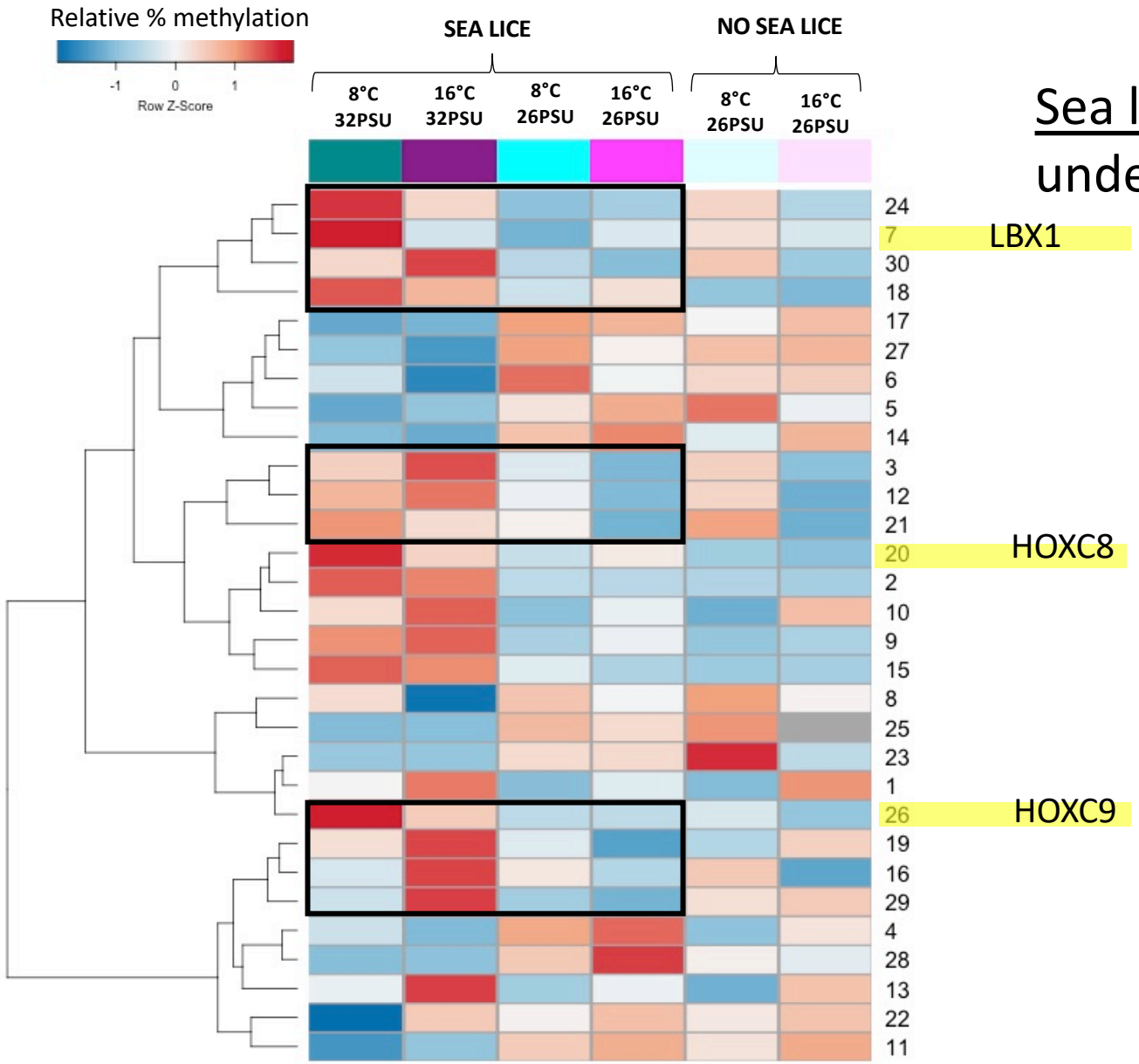


Sea lice-dependent **decrease** in methylation under low salinity (26psu) and low temp (8°C)

Influence of salinity on methylation



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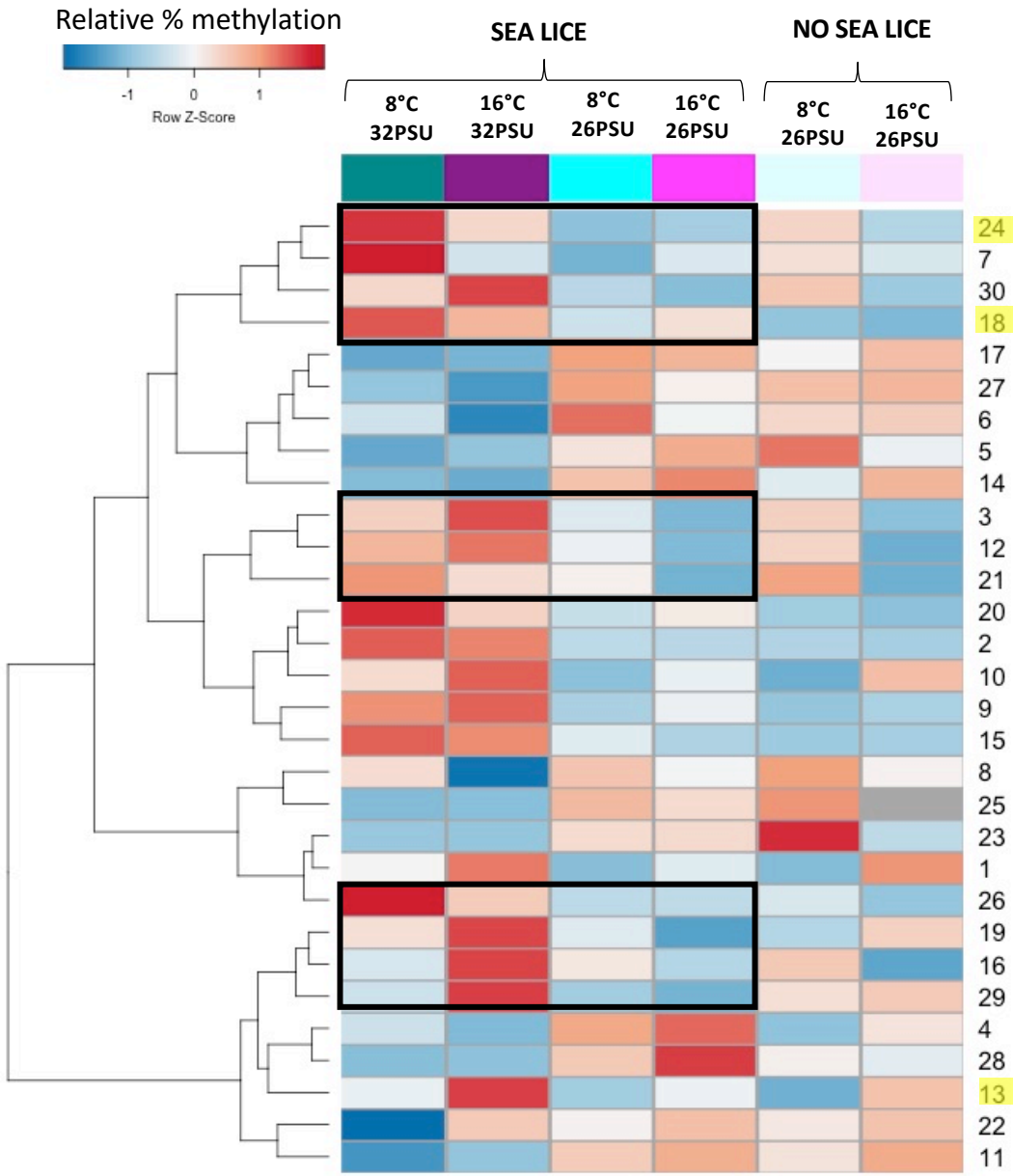
HOX transcription factors

- **Cell differentiation, spatial specificity**

Influence of salinity on methylation



RAPGEF6 (intron)

HCCA2 (intron)

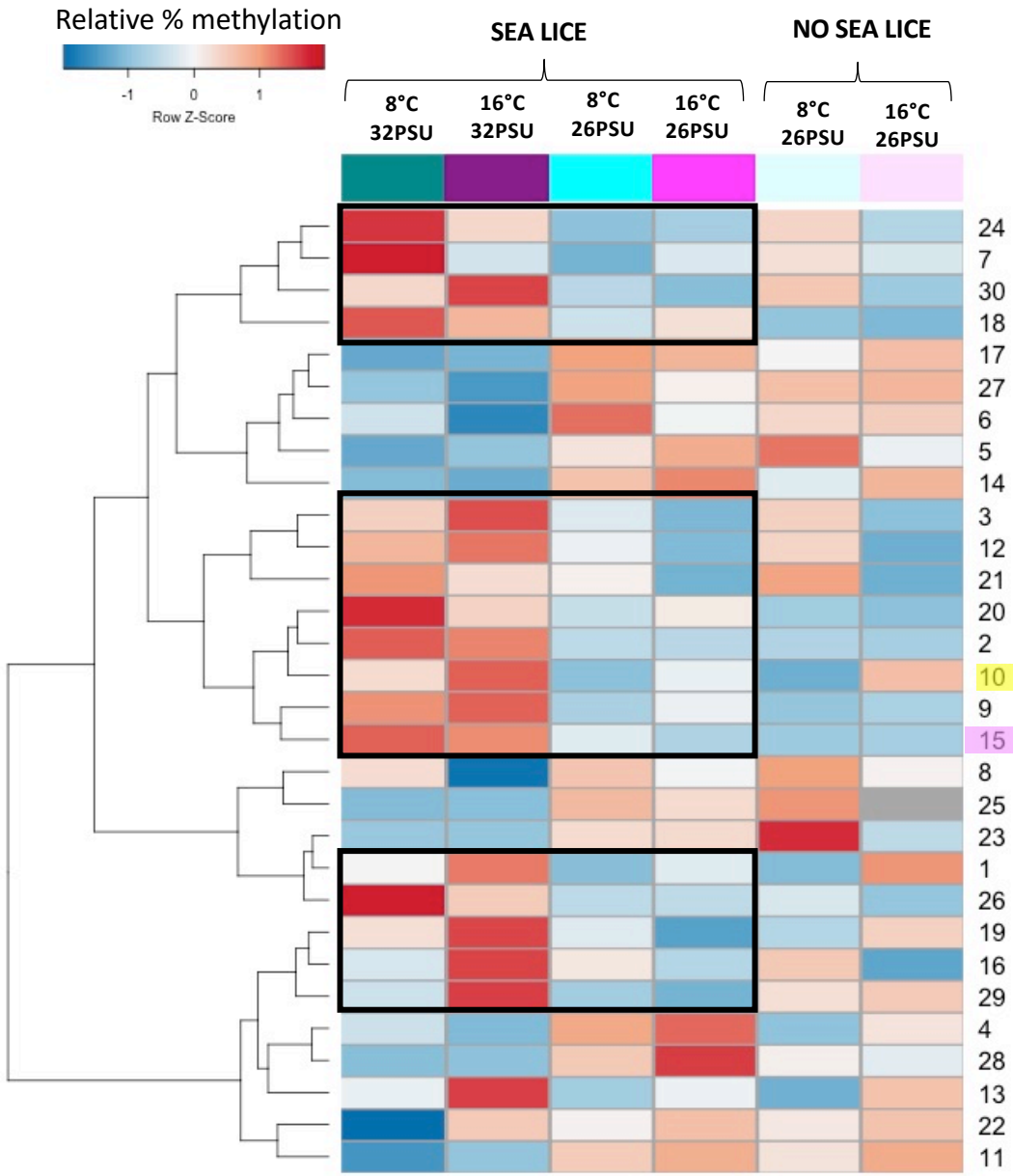
UNC5D (intron)

Sea lice-dependent **decrease** in methylation under low salinity (26psu) and low temp (8°C)

genes associated with

- **apoptosis**
- **inhibition of cell proliferation**
- **response to damage**

Influence of salinity on methylation



increase in methylation under high salinity (32psu)

Cell aggregation

ALS10

lncRNA

Associated with FAM1142a

(**MAPK signaling/cell proliferation**)

Conclusions

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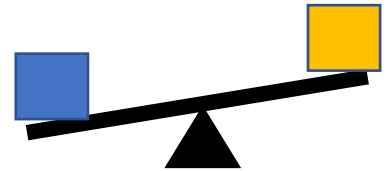

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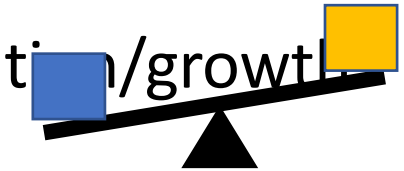

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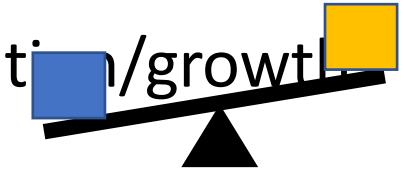

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Next steps

- Compare with expression data (check for targets of regulators)