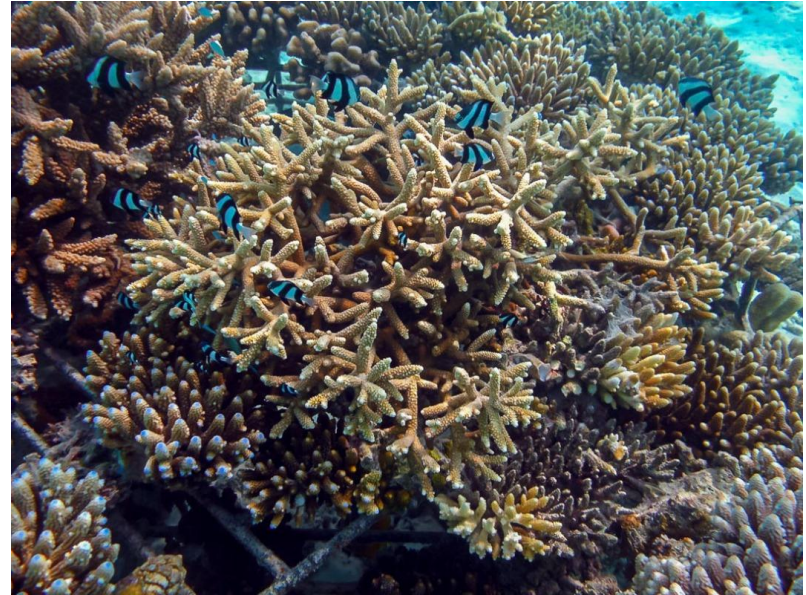


# **Comparative analyses of long non-coding RNA activity in three coral species**

**Zach Bengtsson, Hollie Putnam, Sam White, Danielle  
Becker, and Steven Roberts**

# Transcriptomics and Coral Reef Resilience

- Coral reefs are under imminent threat due to climate change
- Transcriptomics has emerged as a useful tool to **measure stress response and mechanisms of resilience at the molecular level**
- This analysis typically focuses on messenger RNA (mRNA), **leaving non-coding RNAs out of the picture.**

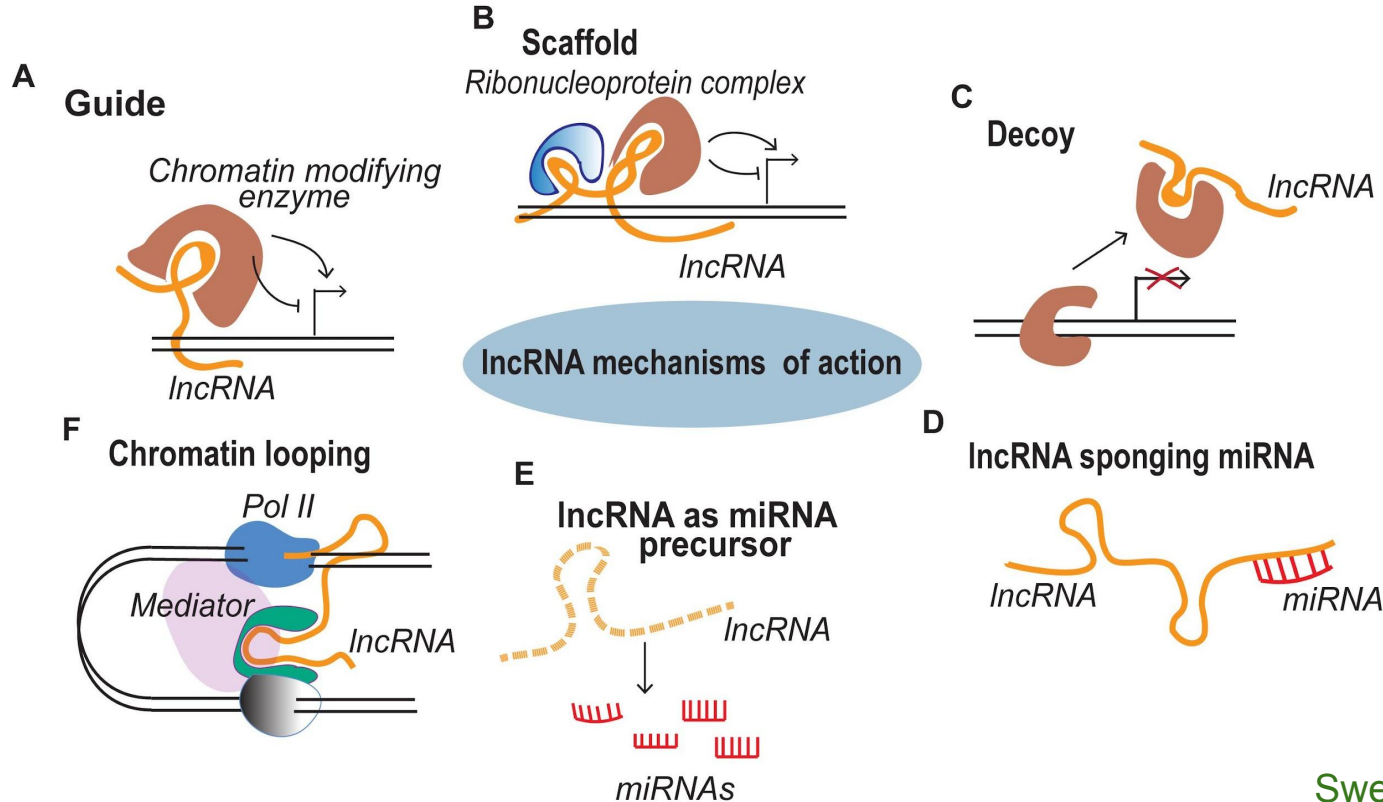


# Understanding Non-Coding RNAs (ncRNAs)

- Constitute a significant portion of the transcriptome
- **DO NOT code for a protein**
- microRNAs, small interfering RNAs, **long non-coding RNAs (lncRNAs)**, etc.
- Roles in **gene regulation** other essential biological processes
- **lncRNAs 200nt or greater**



# Diverse Functions of lncRNAs



# lncRNA work in marine invertebrates

## Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity

Federico Gaiti, Selene L. Fernandez-Valverde, Nagayasu Nakanishi, Andrew D. Calcino, Itai Yanai, Milos Tanurdzic, Bernard M. Degnan  [Author Notes](#)

## Identification of long non-coding RNAs in two anthozoan species and their possible implications for coral bleaching

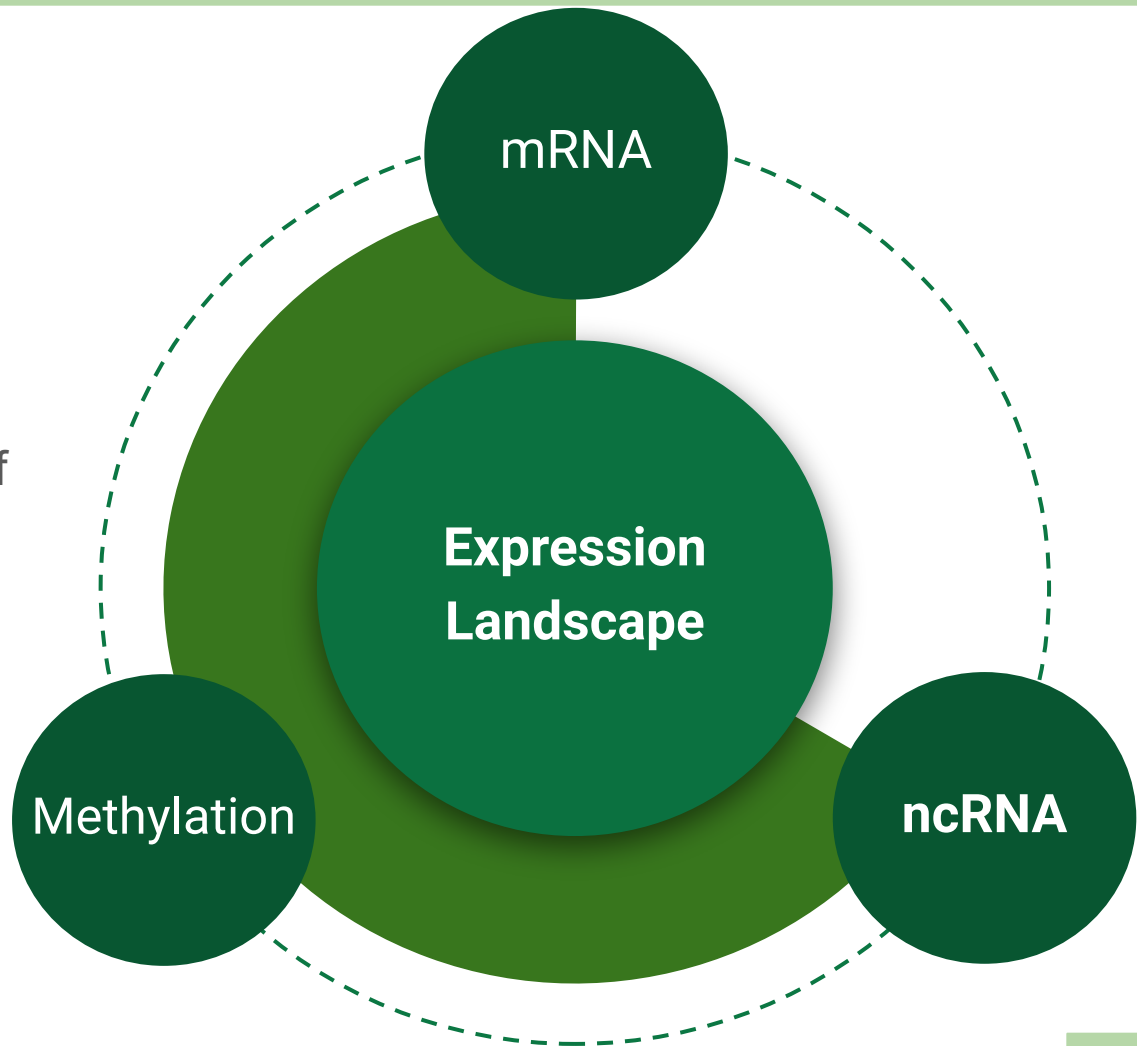
[Chen Huang](#), [Jean-Étienne R. L. Morlighem](#), [Jing Cai](#) , [Qiwen Liao](#), [Carlos Daniel Perez](#), [Paula Braga Gomes](#), [Min Guo](#), [Gandhi Rádis-Baptista](#)  & [Simon Ming-Yuen Lee](#) 

## Re-analysis of the coral *Acropora digitifera* transcriptome reveals a complex lncRNAs-mRNAs interaction network implicated in *Symbiodinium* infection

[Chen Huang](#), [Dongliang Leng](#), [Shixue Sun](#) & [Xiaohua Douglas Zhang](#) 

# Gene Expression

- Contribution of **lncRNAs** to complex expression landscape
- **Comparative analysis** of lncRNAs across reef building species



# Objectives

1. Identify lncRNAs in RNA-seq data
2. Characterize size distribution of lncRNAs
3. Compare lncRNA sequences across 3 species



*Acropora pulchra*



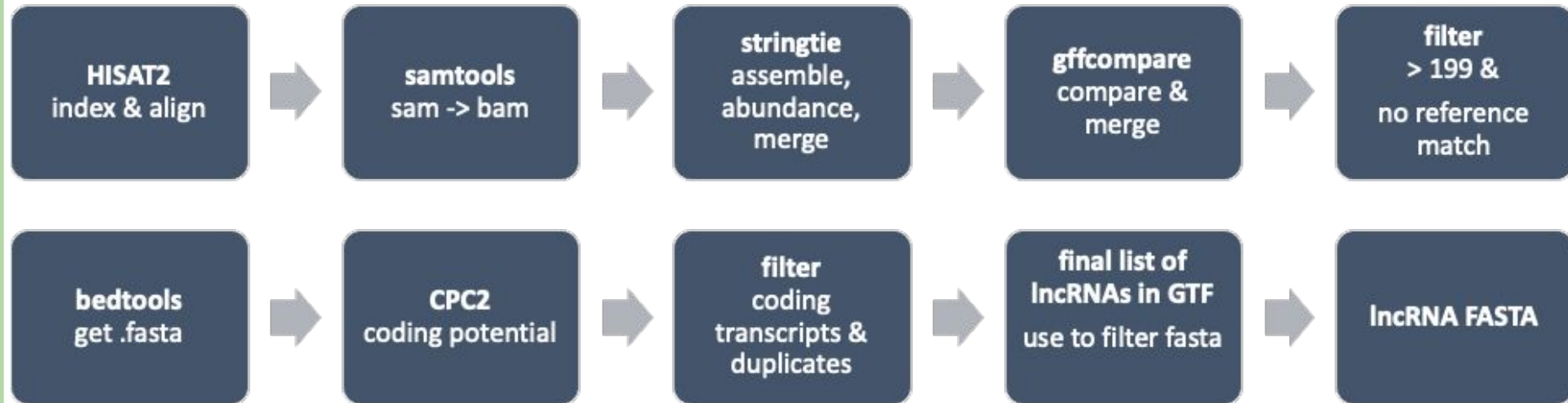
*Pocillopora meandrina*



*Porites evermanni*



# lncRNA identification workflow





# lncRNA Discovery

**Filter for size**

>199 nt

**Filter for known  
coding genes**

Remove previously  
annotated genes

**Filter for  
predicted coding  
potential**

Remove those  
transcripts with  
coding potential



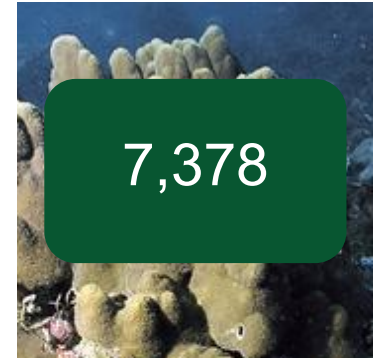
## Number of identified lncRNAs in each species



*Acropora pulchra*



*Pocillopora meandrina*

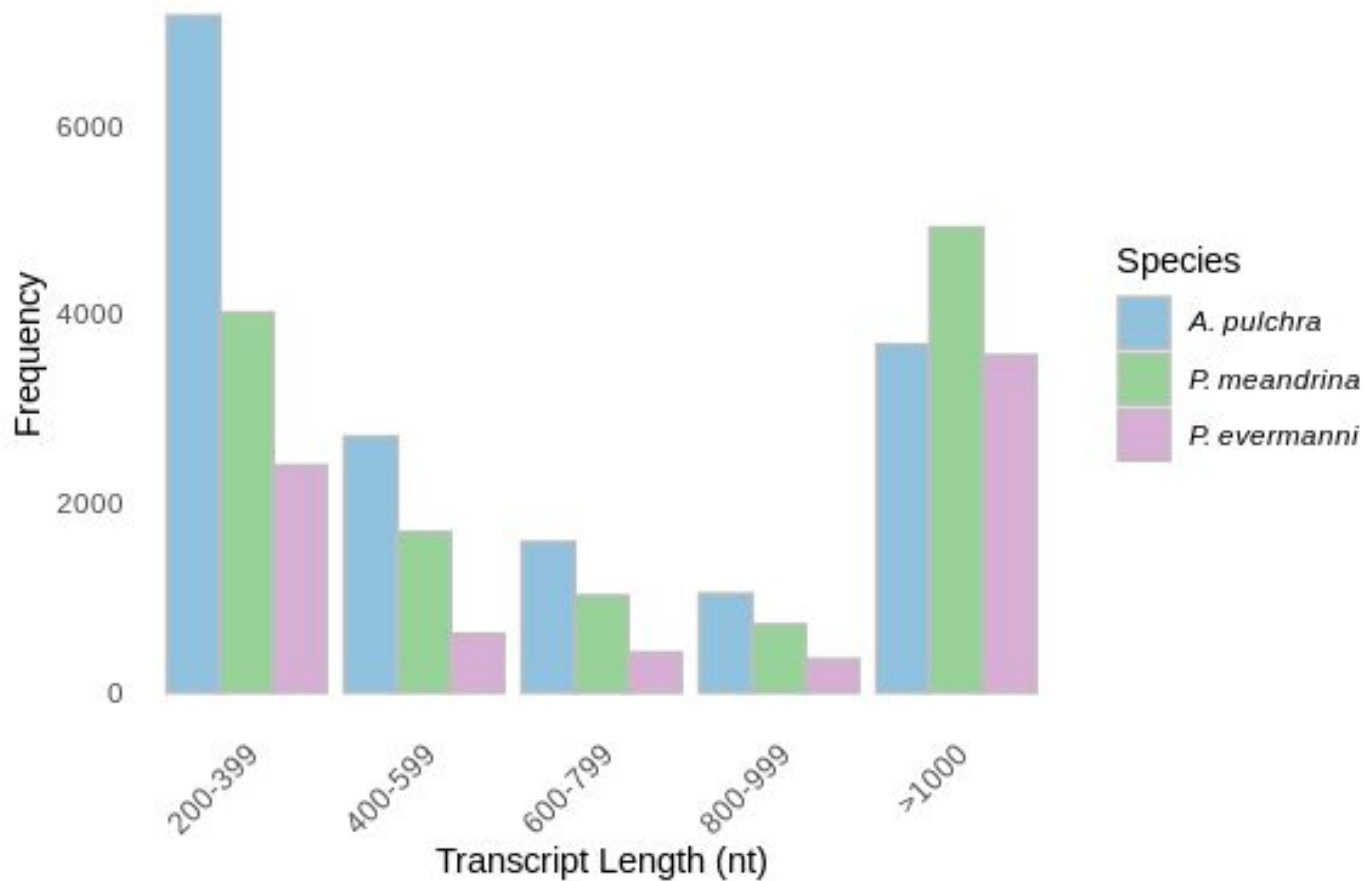


*Porites evermanni*

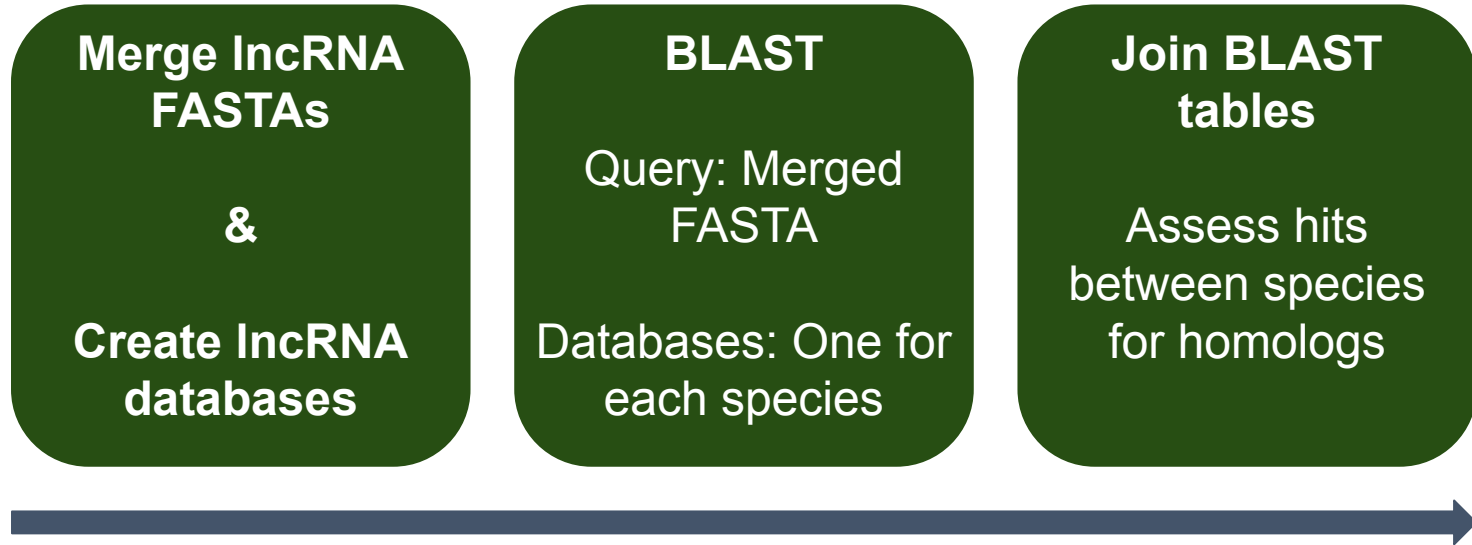
## Comparison to other species

- Conservative estimates of lncRNAs in humans place are around 30,000 to 60,000
- Other model organisms are similar
- General consensus that at least thousands of lncRNAs in marine invertebrates is common

## Size distribution



# BLAST sequence comparison



# BLAST lncRNA comparison

- Approximately 5% of transcripts are found in three species and 14% of sequences are present in two species.
- *P. evermanni* and *P. meandrina* had the least number of similar transcripts

Number of Hits	
2 Species	3 Species
14%	5%

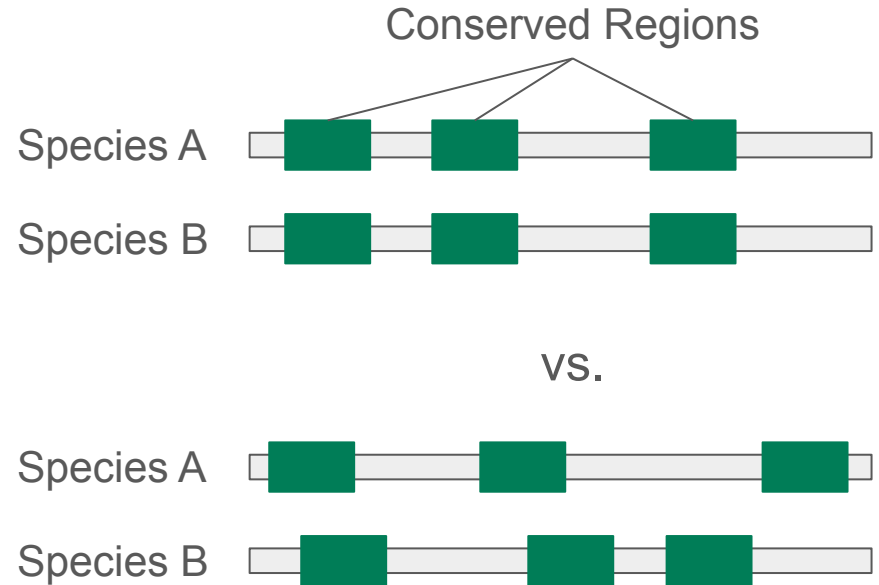
# Conclusions

- Even under stringent filtering criteria, thousands of lncRNAs can be identified in corals from RNA-seq data
- Size distributions of lncRNAs follow similar trends across species
- A small number of homologs exist across all 3 species



# Future work: conserved regions & function

- lncRNAs are poorly conserved across even closely related species
  - Sequence vs. functional conservation
  - Conserved regions
- Weighted gene co-expression network analysis



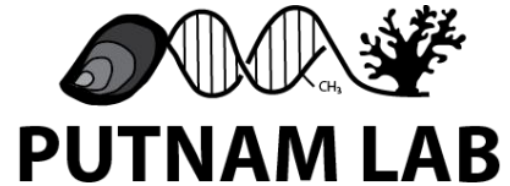
## A better understanding of functionality

Narrowing down which lncRNAs may be most important to cellular function and stress response, **gives us another metric to assess coral health and molecular mechanisms of stress response.**



# Acknowledgements

- Ariana Huffmyer
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- Jose Eirin-Lopez



# Thank you!

Questions?