

41st TBI Winter seminar in Bled 2026

Evolutionary origin of the lncRNA RMST

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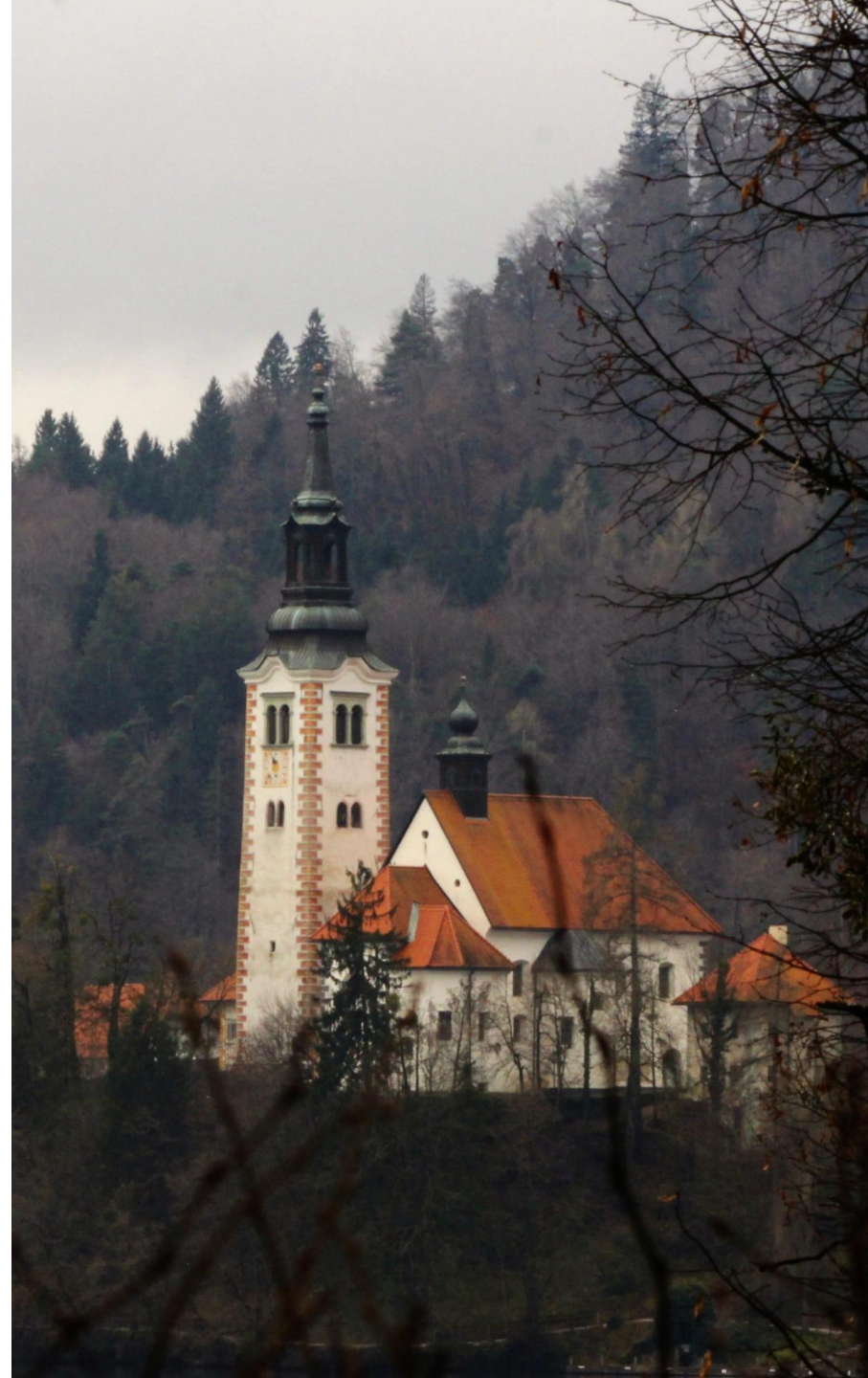
Federico D. Brown



universität
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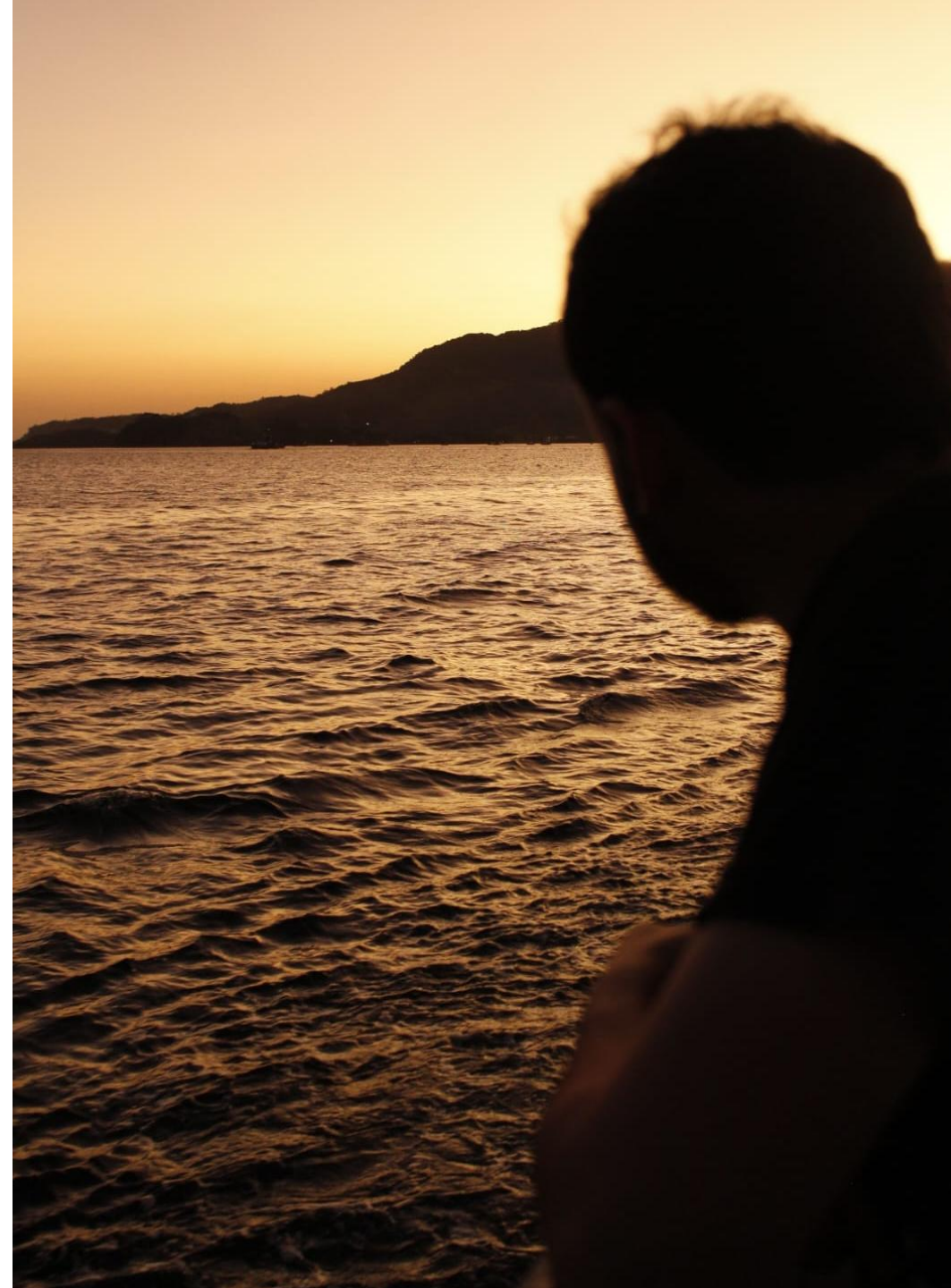


Universidade de São Paulo
Brasil



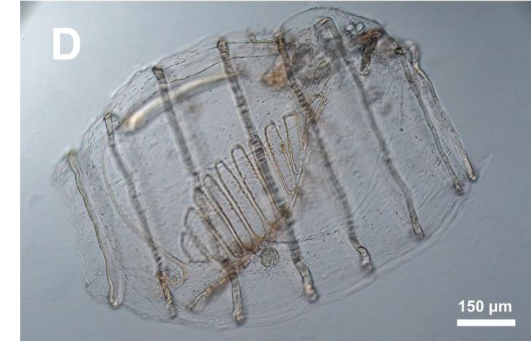
About me

- Undergraduate in Biology
- Master's student at the University of São Paulo – Brazil
- Stem cells and regeneration in tunicates
- Marine Biology laboratory
- Internship at TBI – Vienna
- First approach to bioinformatics



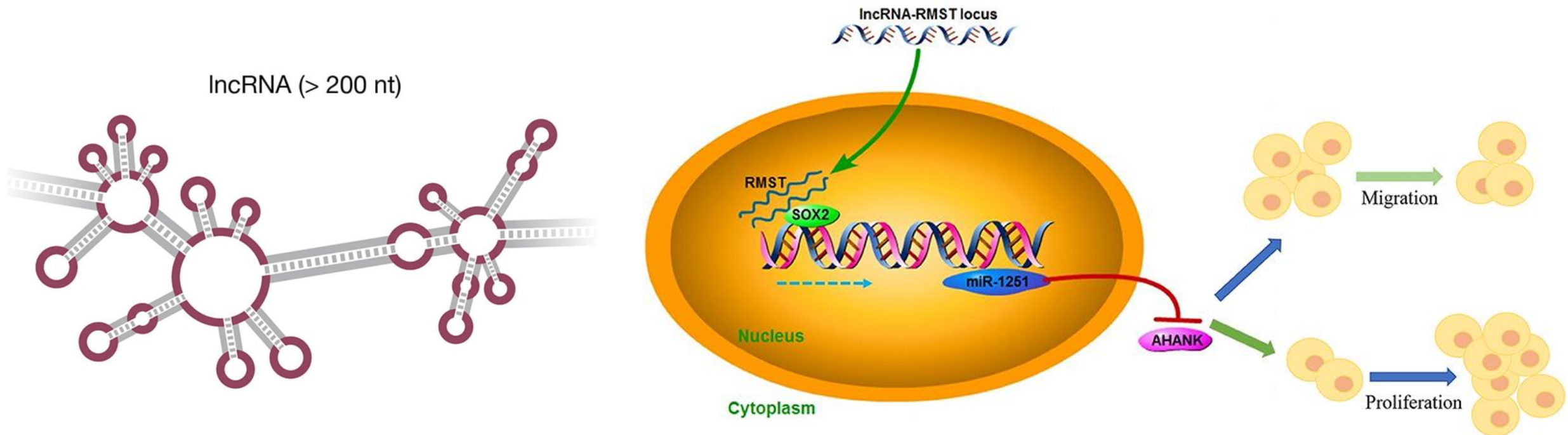
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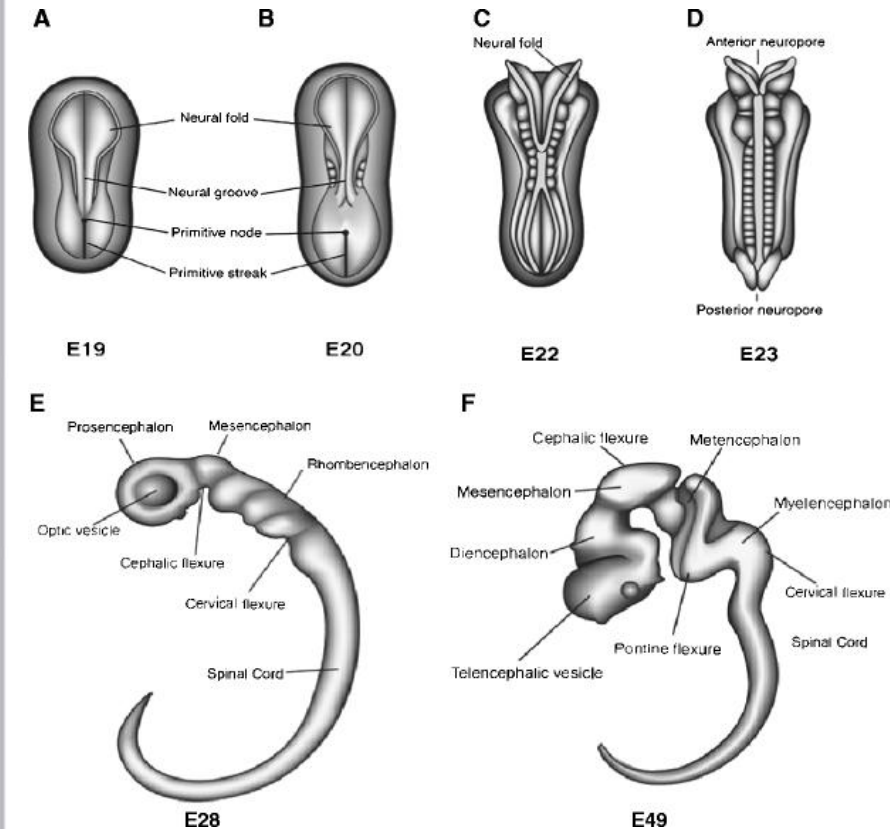
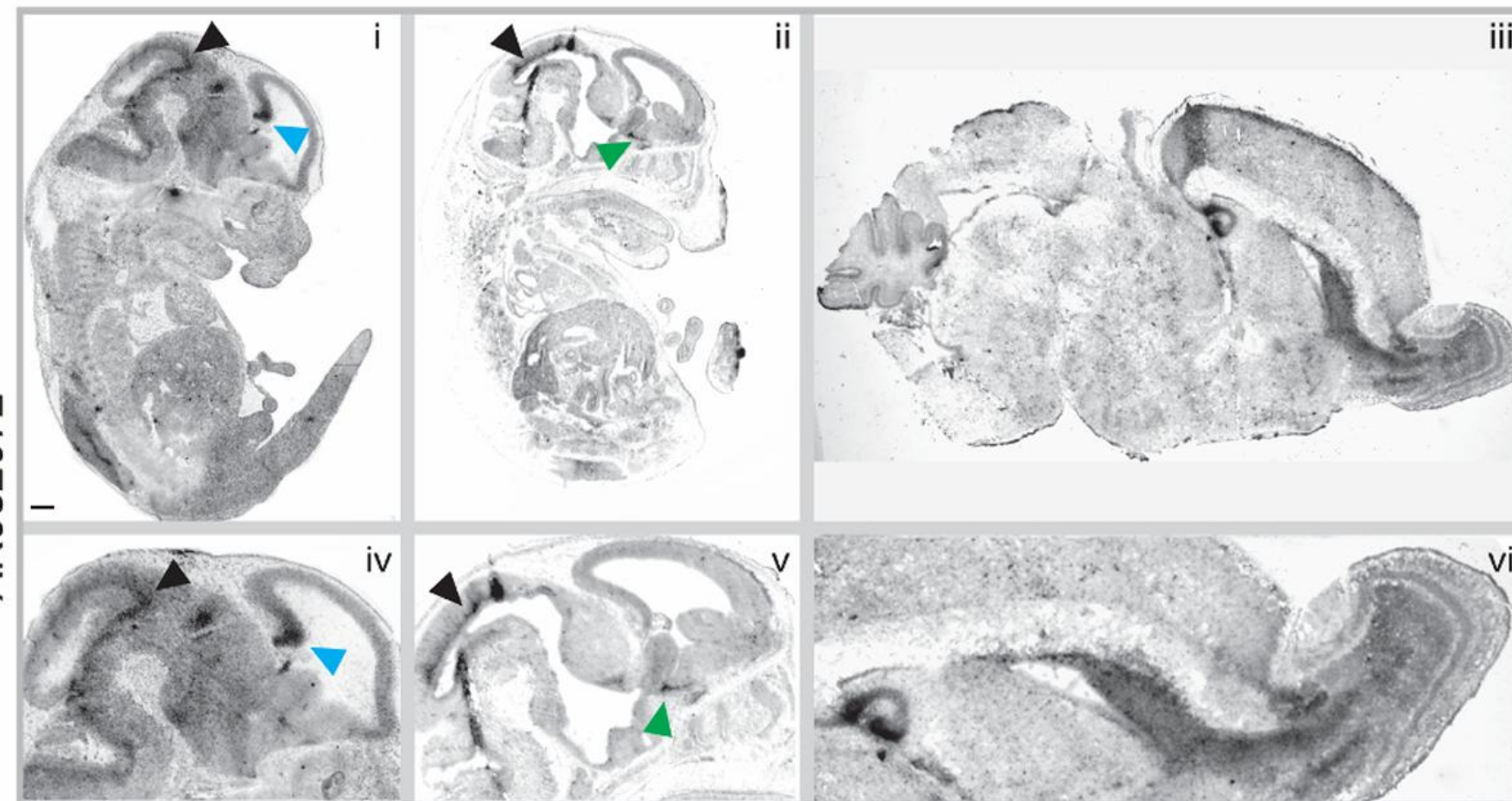
lncRNA RMST

- Essential during embryonic development
- Rhabdomyosarcoma 2-associated transcript
- RMST is involved in neuronal development in mammals



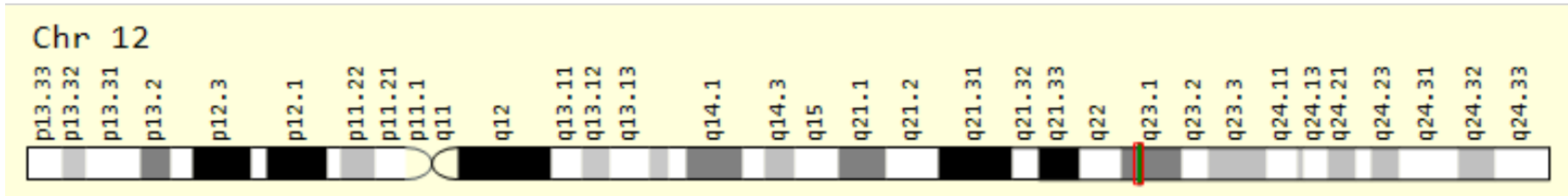
Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes

Rebecca A Chodroff^{1,2}, Leo Goodstadt³, Tamara M Sirey¹, Peter L Oliver³, Kay E Davies^{1,3}, Eric D Green², Zoltán Molnár^{1*}, Chris P Ponting^{1,3*}



RMST – Annotation in Human

- Assembly reference from human **GRCh38**
- Genomic Locations
- Chromosome **12**
 - 96,985,650-97,843,832
 - Latest Assembly Size: **858,183 base pairs (bp)**



RMST conserved families in vertebrates

RMST 1

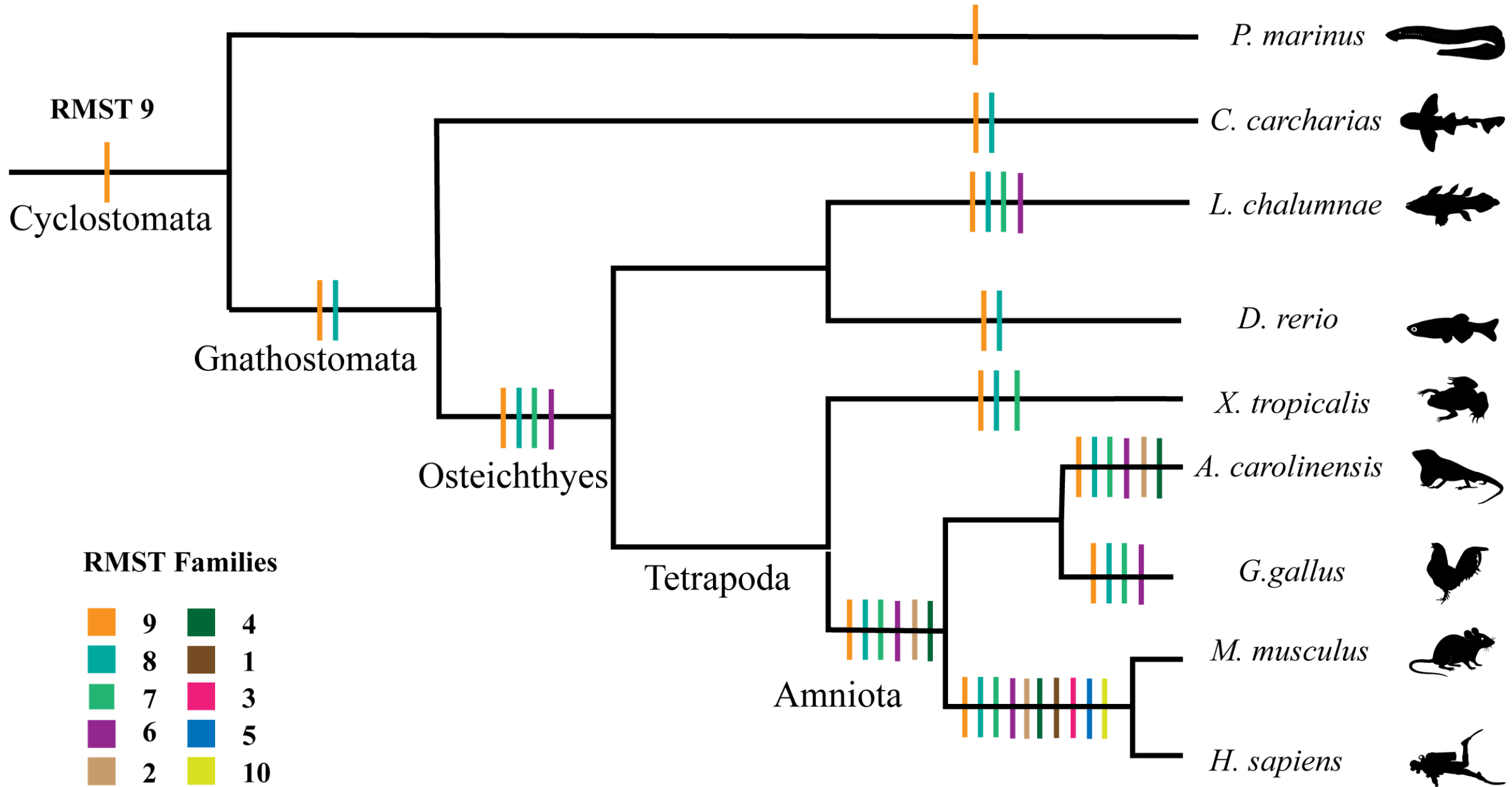
RMST 2,3,4 5

RMST 6, 7

RMST 8,9,10

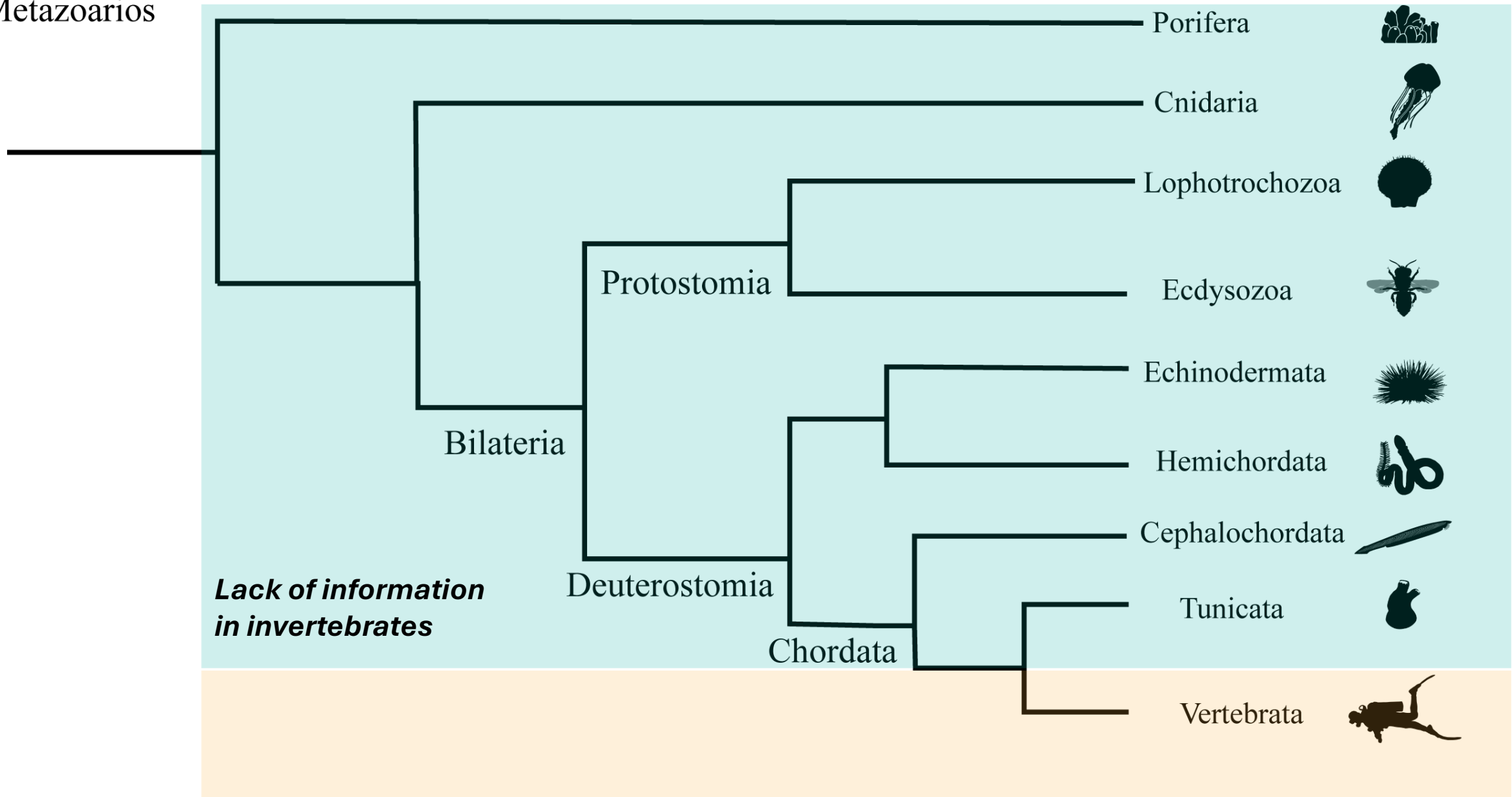


RMST families in vertebrates

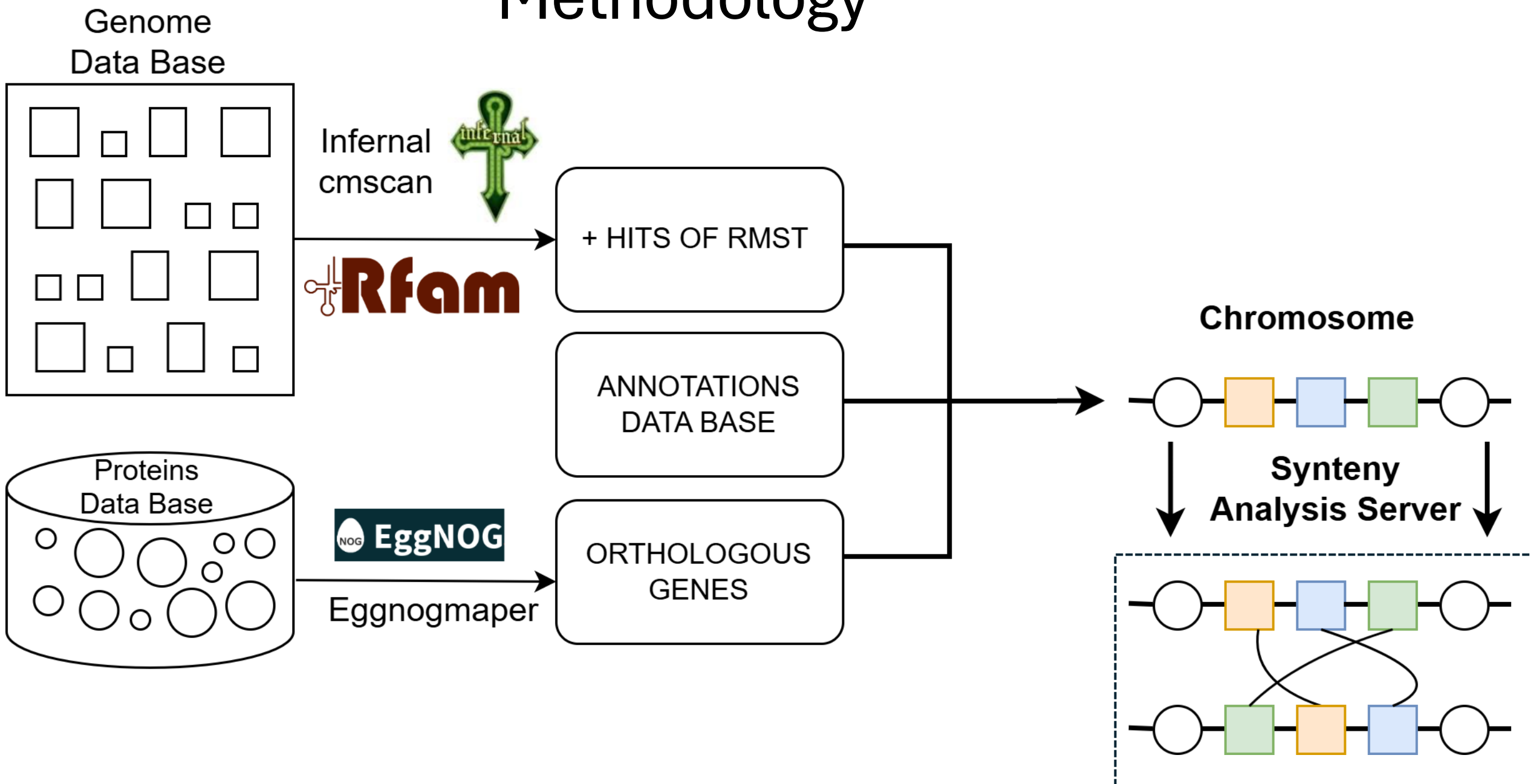


Objective: Determine the evolutionary origin of the *RMST lncRNA*

Metazoarios



Methodology



Family-defined cutoff

RMST_Family	Gathering cutoff
RMST_1	40
RMST_2	45
RMST_3	55
RMST_4	40
RMST_5	58
RMST_6	90
RMST_7	100
RMST_8	80
RMST_9	65
RMST_10	55

cmscan + hits :

- E-value ≤ 0.001
- Hit Score



[HOME](#) [SEARCH](#) [PROJECTS](#) [FTP](#) [BLOG](#)

Family: **RMST_9 (RF01970)**

Description: *Rhabdomyosarcoma 2 associated transcript conserved region 9*

[Summary](#)
[Sequences](#)
[Alignment](#)
[Secondary structure](#)
[Species](#)
[Trees](#)
[Structures](#)
[Motif matches](#)
[Database references](#)

Curation

[Publications](#)

Curation and family details

This section shows the detailed information about the Rfam family. We're happy to receive updated or improved information.

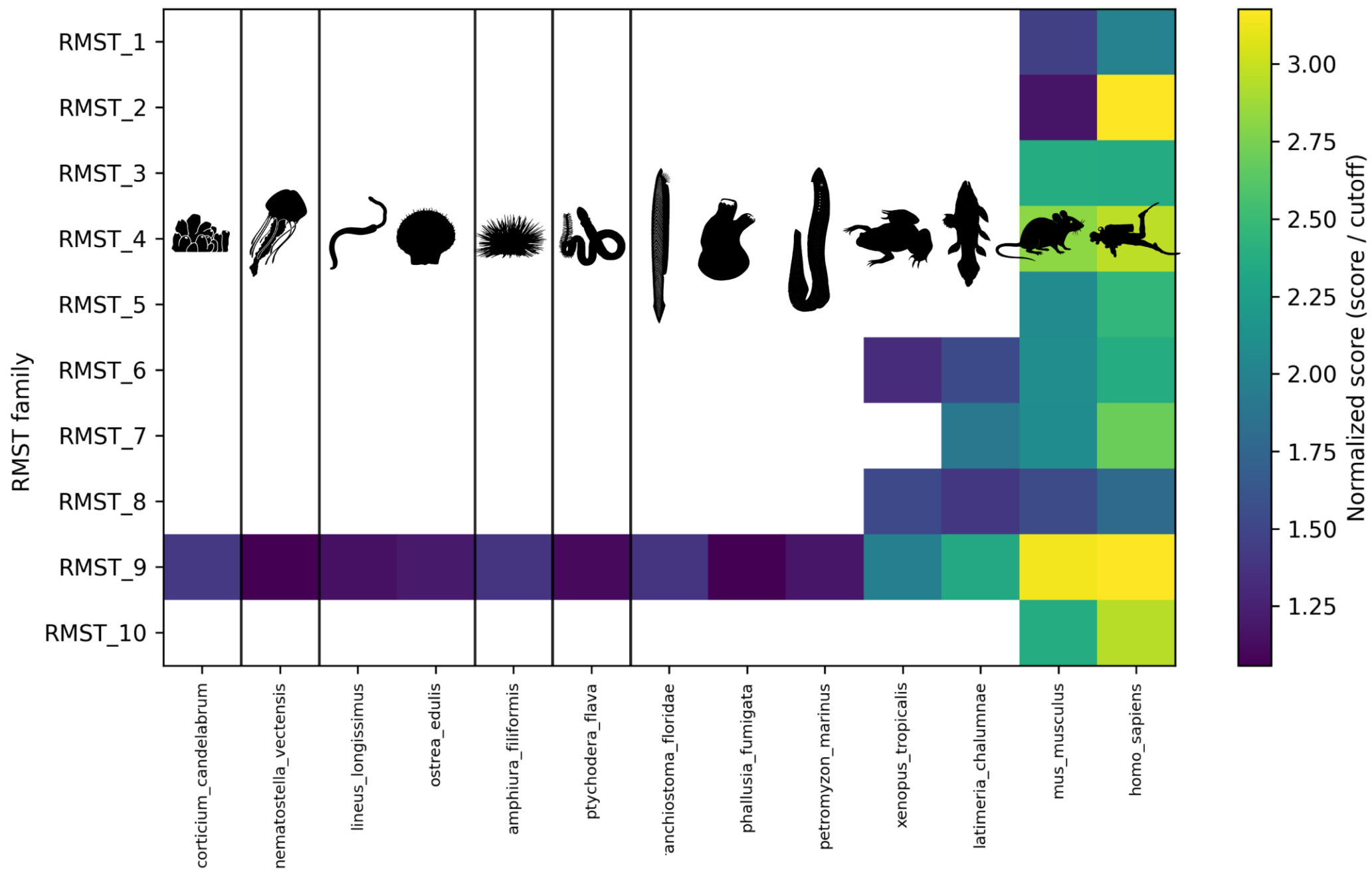
Curation

Seed source	Predicted; CMfinder; Eberhardt R	
Structure source	Predicted; CMfinder;	
Type	Gene; lncRNA;	
Author	Eberhardt R	
Alignment details	Alignment	Number of sequences
	full	558
	seed	28

Model information

Build commands	cmbuild -F CM SEED cmcalibrate --mpi CM
Search command	cmsearch --cpu 4 --verbose --nohmmonly -T 27.38 -Z 2958934 CM SEQDB
Gathering cutoff	65.0
Trusted cutoff	66.0
Noise cutoff	64.9
Covariance model	Download

Default parameters



Covariance models of RFAM based

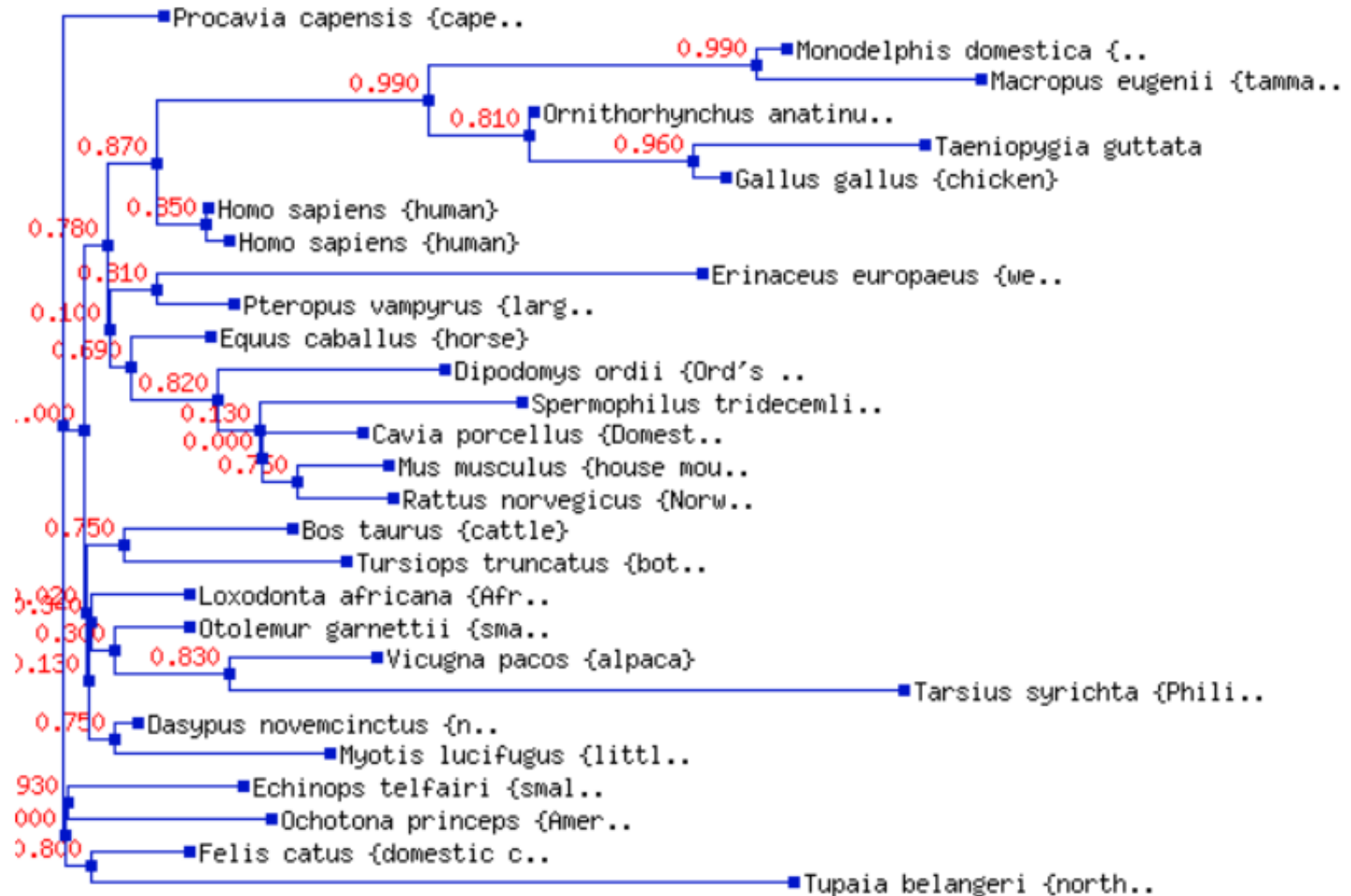
- In sequences of vertebrates
- Guttering Cutoff ?
- The problem:
 - We **do not** have **representatives** of invertebrates

Trees

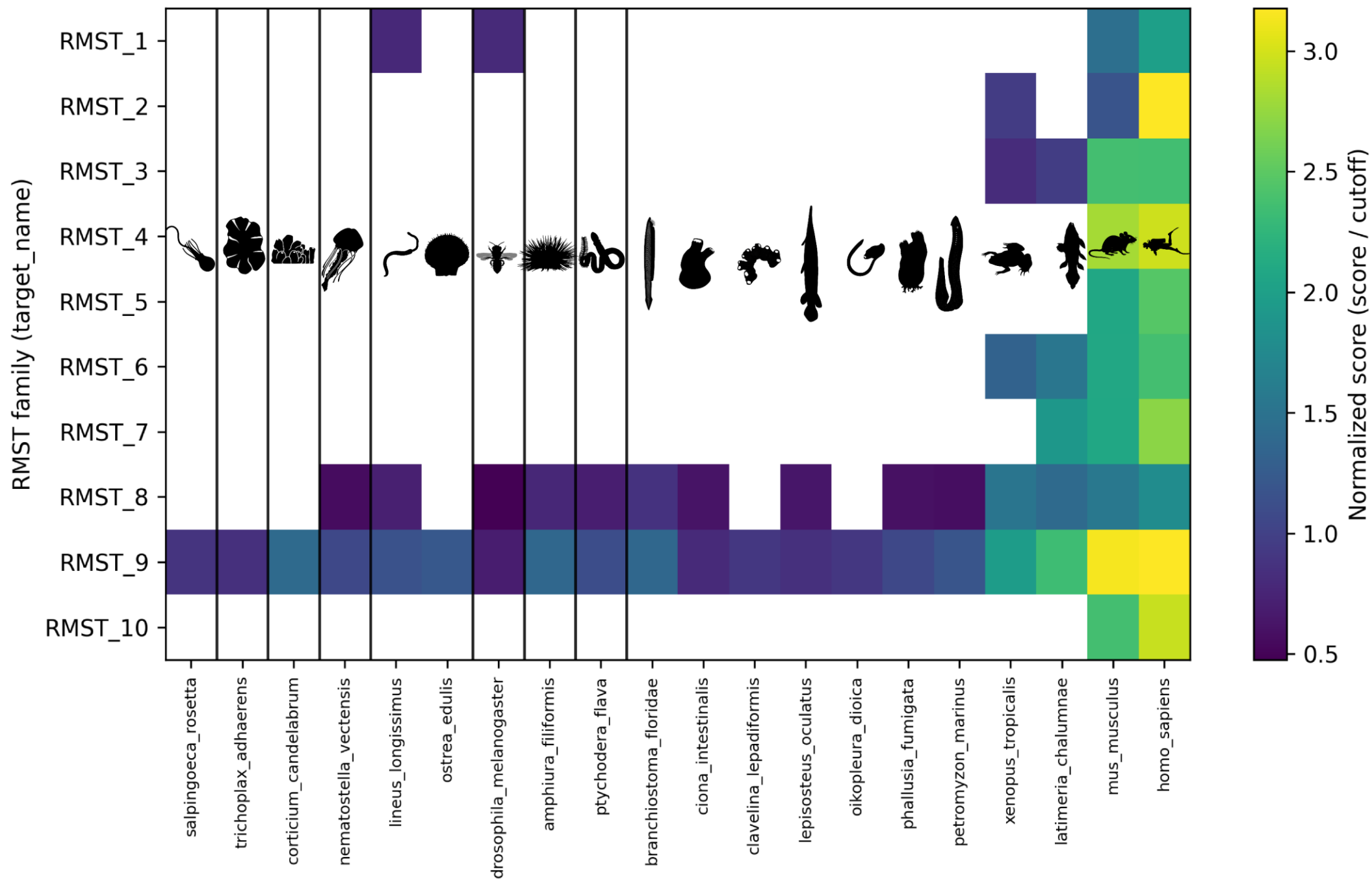
This page displays the predicted phylogenetic tree for the alignment. [More...](#)

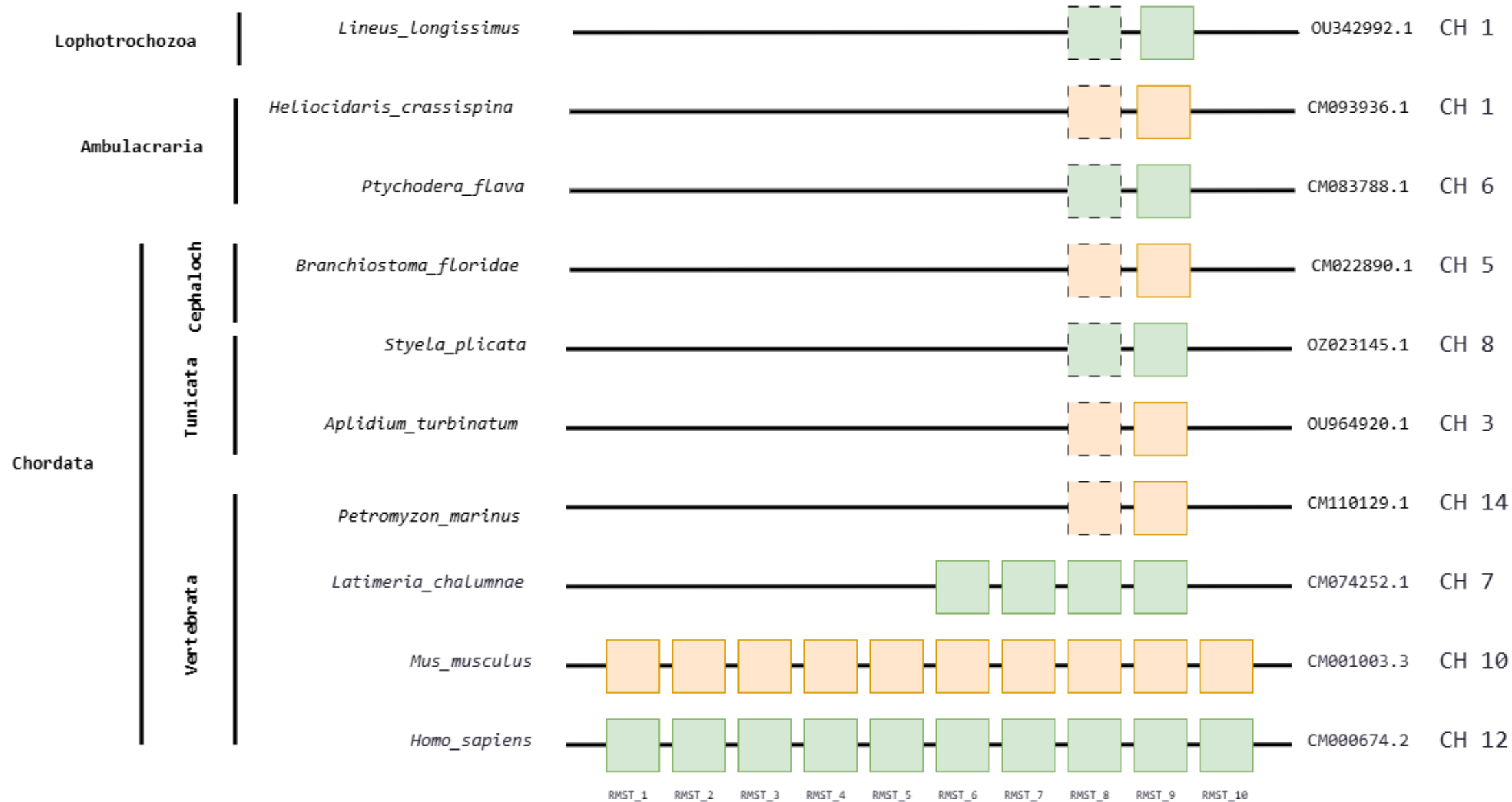
This tree was built using the *fasttree* method.

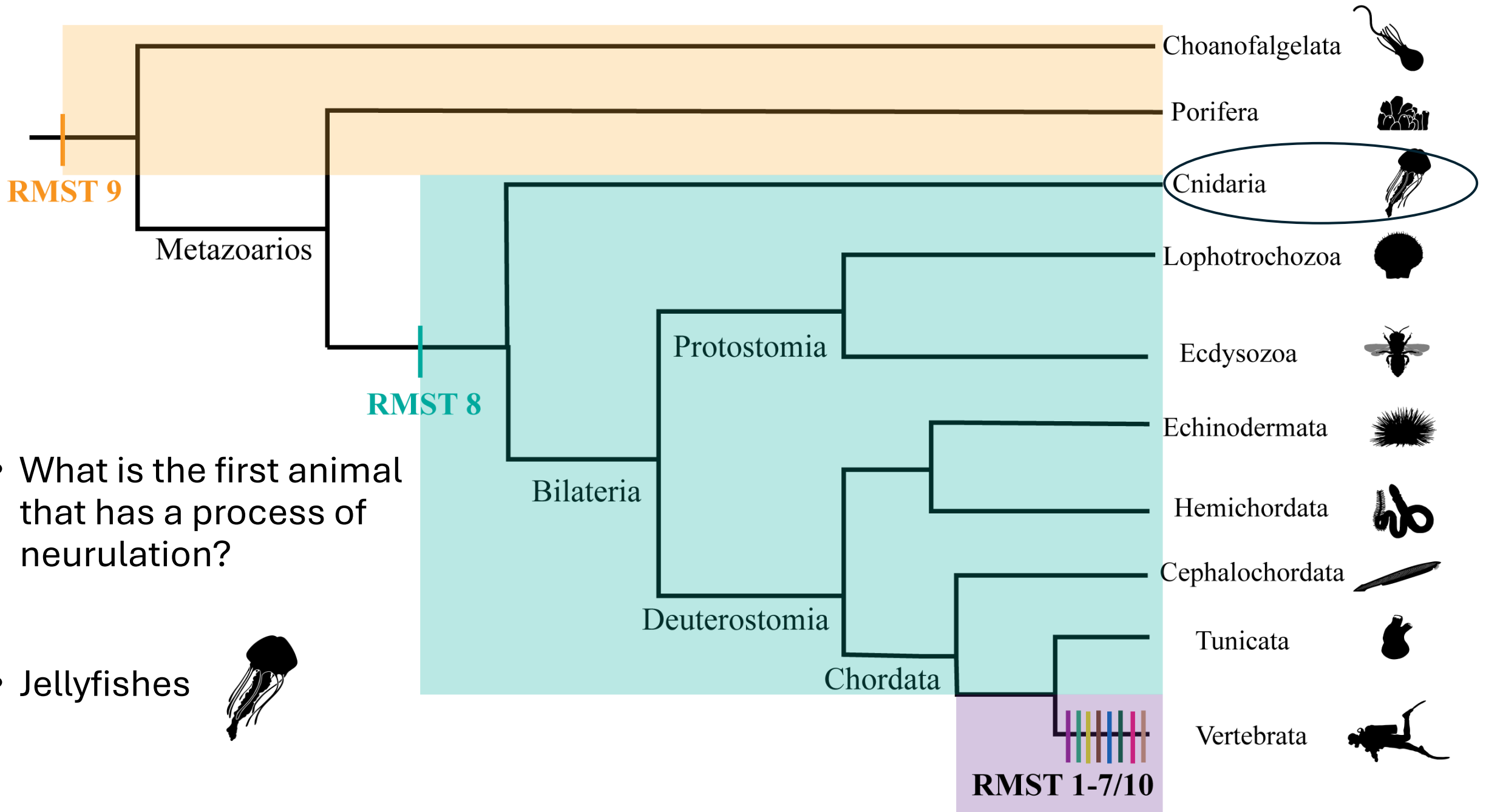
Label the trees using ☒ species names or ☐ accessions.



Relax parameters



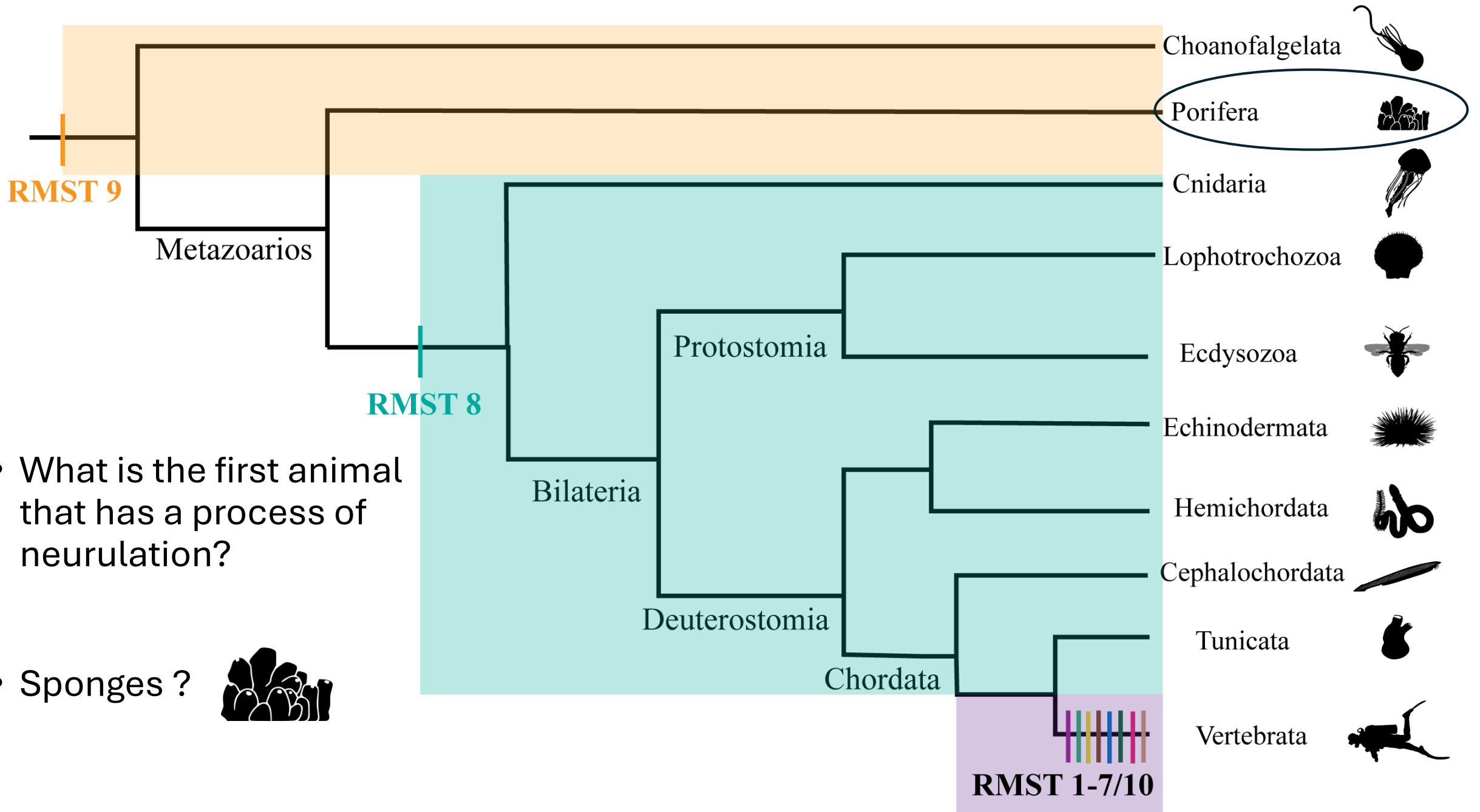




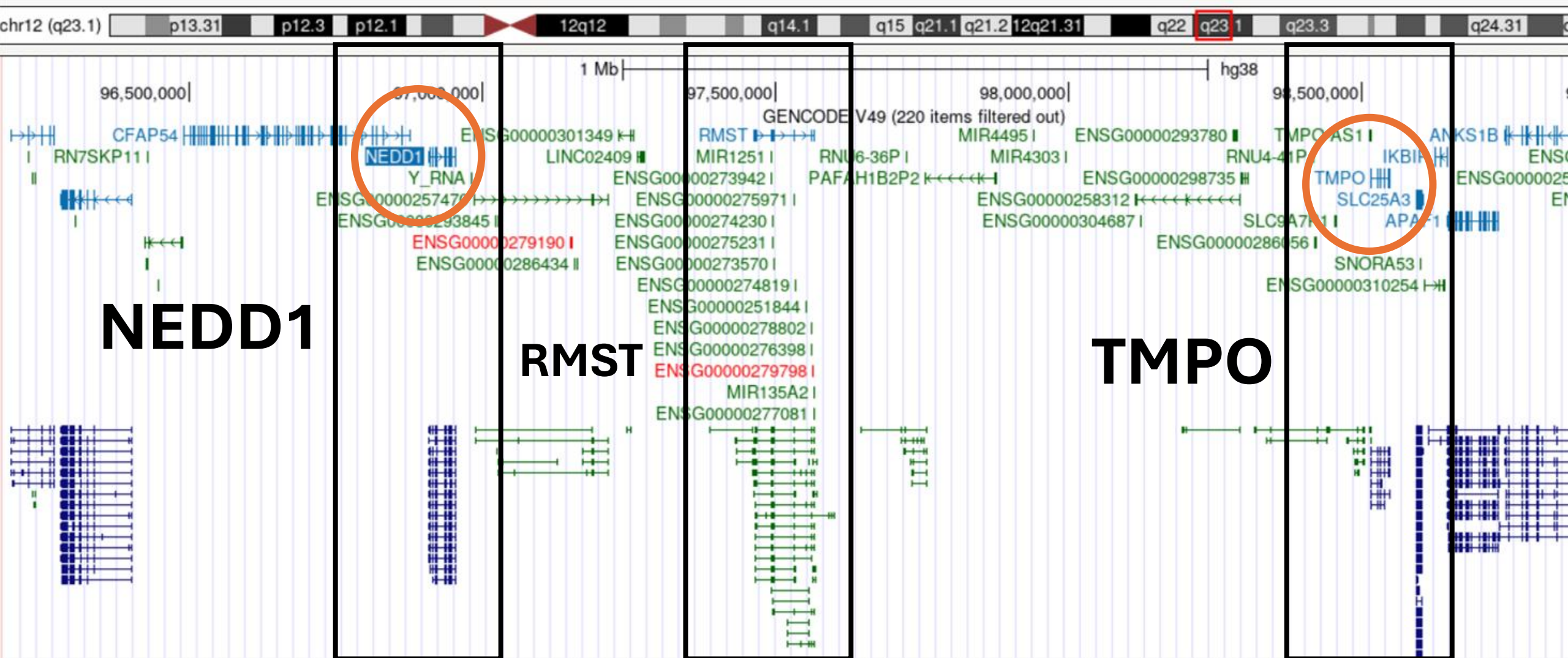
• What is the first animal that has a process of neurulation?

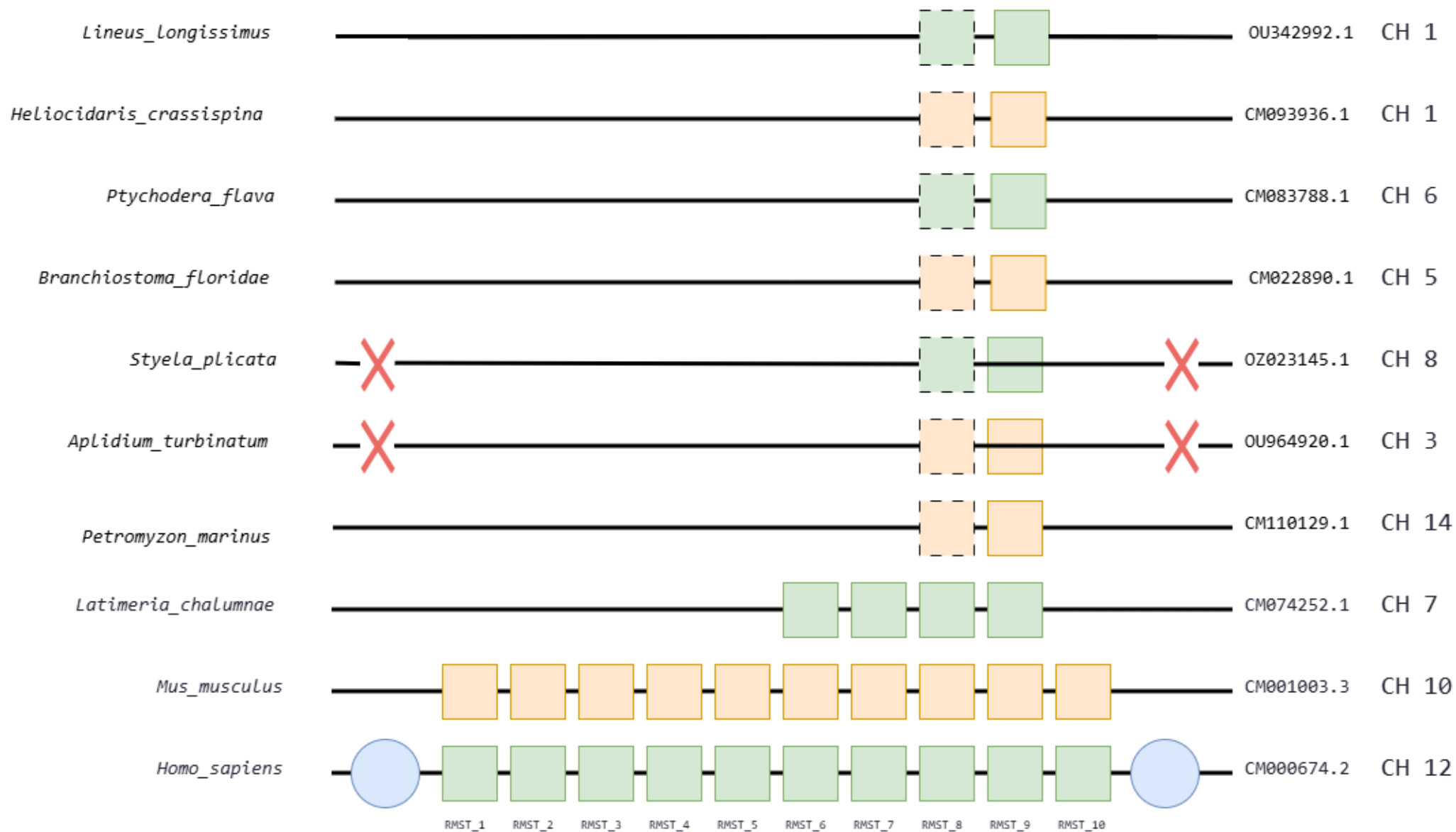
• Jellyfishes



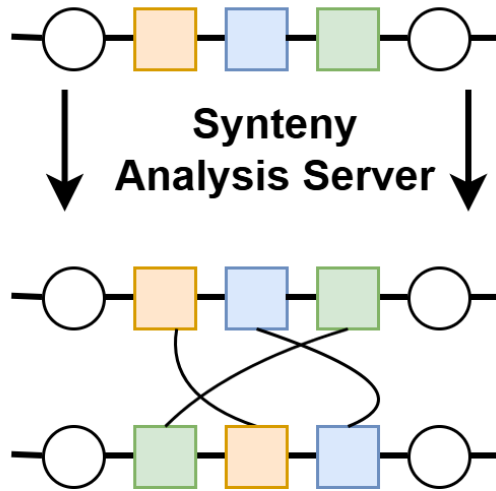


Searching for orthologous genes





Future analyses



To take home

- RMST 9 is well conserved in metazoans
- RMST 8 may represent a family that is also well conserved in metazoans
- Most of the models are only based on vertebrates
- We need to increase the information on invertebrates

Acknowledgements

- Cristian Velandia
- Federico D. Brown
- Ivo Hofacker
- EvoDevo Lab
- TBI members
- **Thank you for your attention !!**
- **Do you have questions?**

