

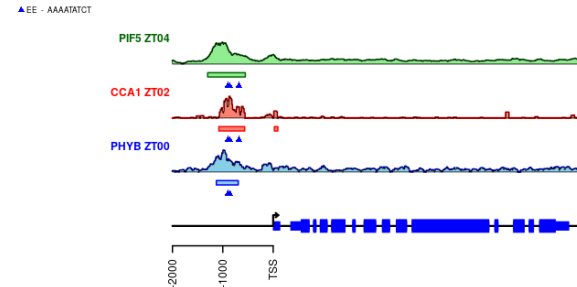
# ATTRACTOR, a circadian clock transcriptional network based on ChIP-seq data unveils potential gene modules for crop improvement

**Fran Romero-Campero**  
@fran\_rom\_cam

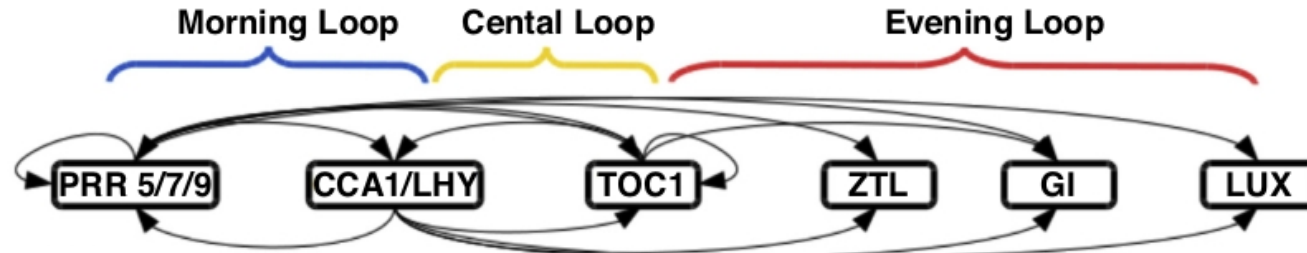
Plant Development Unit  
Dpt. Computer Science and Artificial Intelligence  
Institute for Plant Biochemistry and Photosynthesis  
University of Sevilla - CSIC



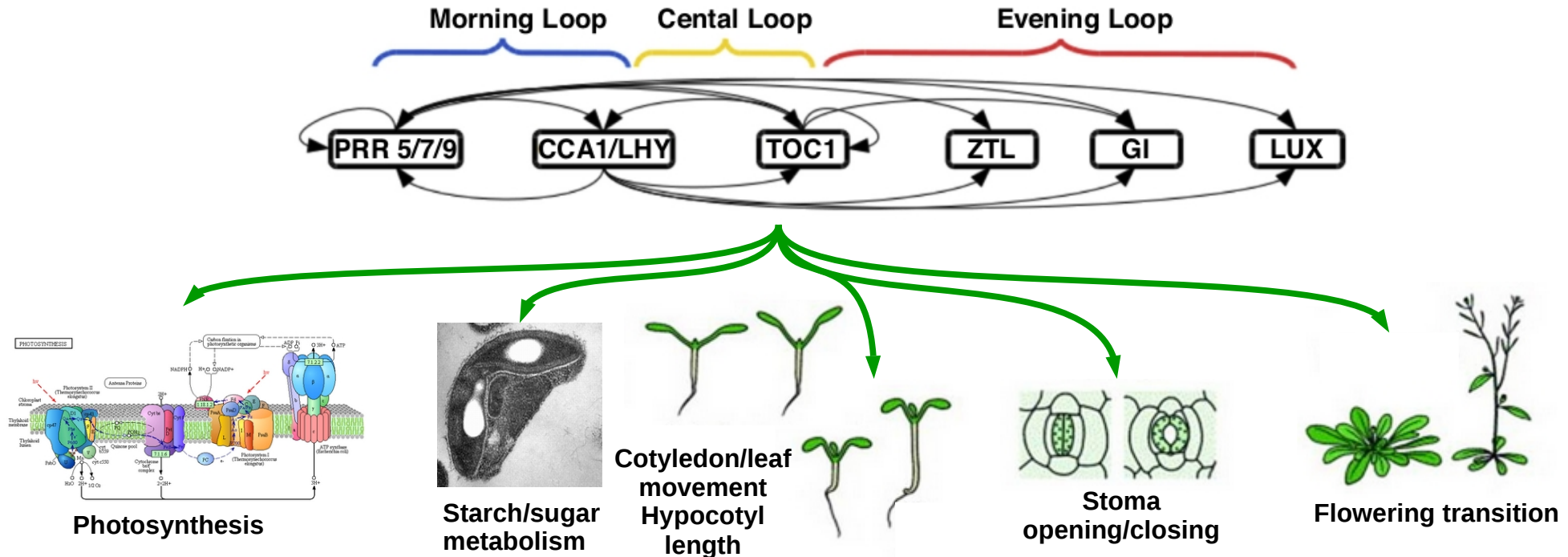
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@PlantDevelUnit



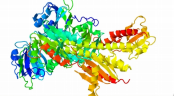
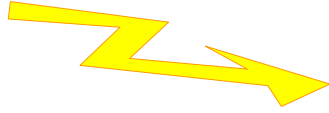
# Circadian Clock is central to Plant Development and Physiology



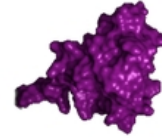
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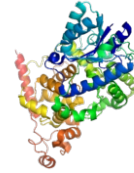
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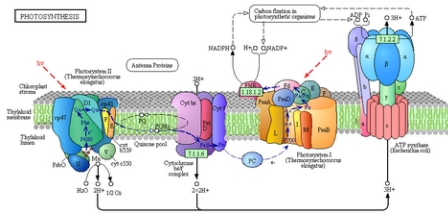
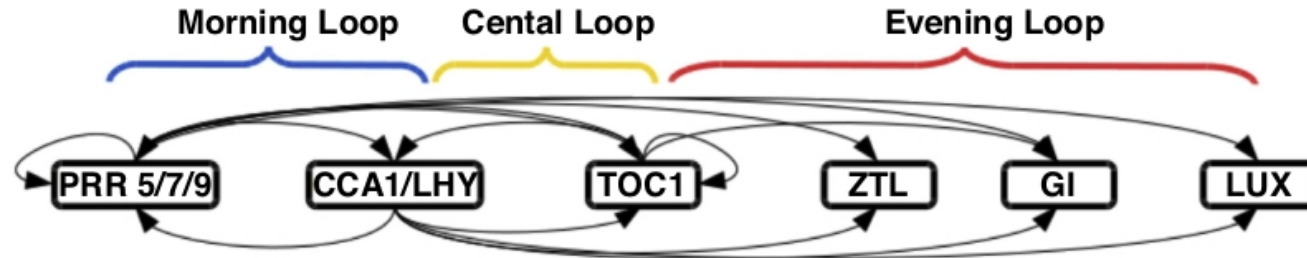
Phytochromes



Phytochrome  
Interacting Factors



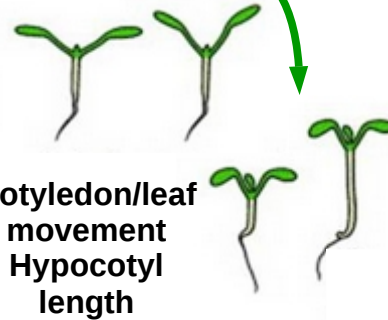
Cryptochromes



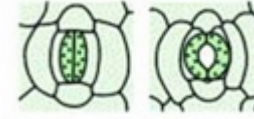
Photosynthesis



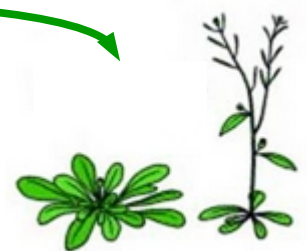
Starch/sugar  
metabolism



Cotyledon/leaf  
movement  
Hypocotyl  
length



Stoma  
opening/closing



Flowering transition

# Transcriptomics and Cistromics data accumulate in Data Bases for key regulators in the Circadian Clock

The Plant Cell, Vol. 17, 3257–3281, December 2005, www.plantcell.org © 2005 American Society of Plant Biologists



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Science 06 Apr 2012:  
Vol. 336, Issue 6077, pp. 75-79  
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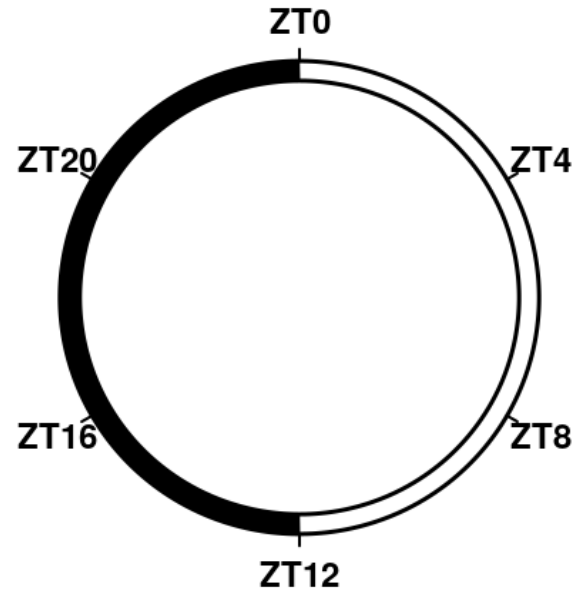
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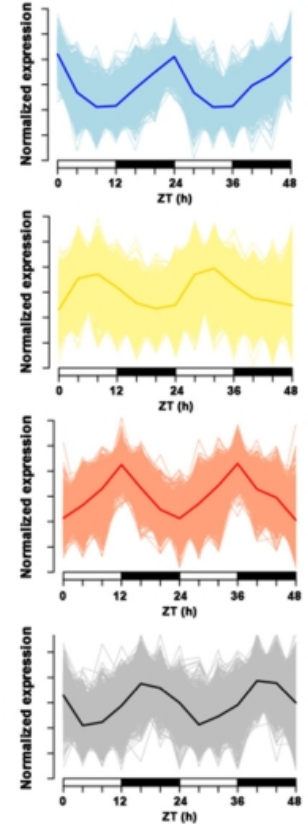
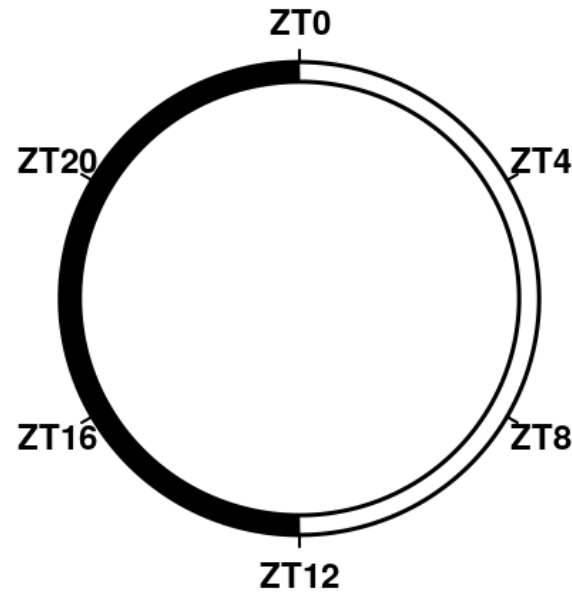
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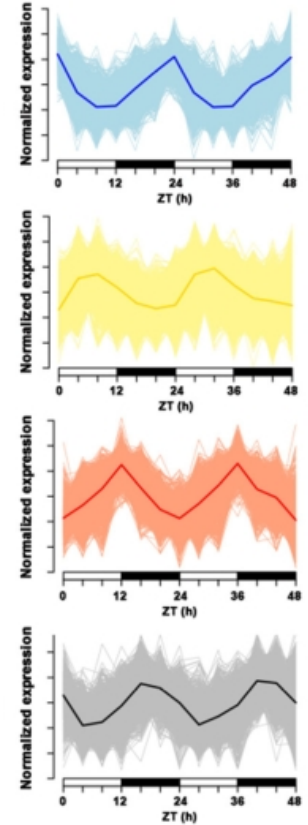
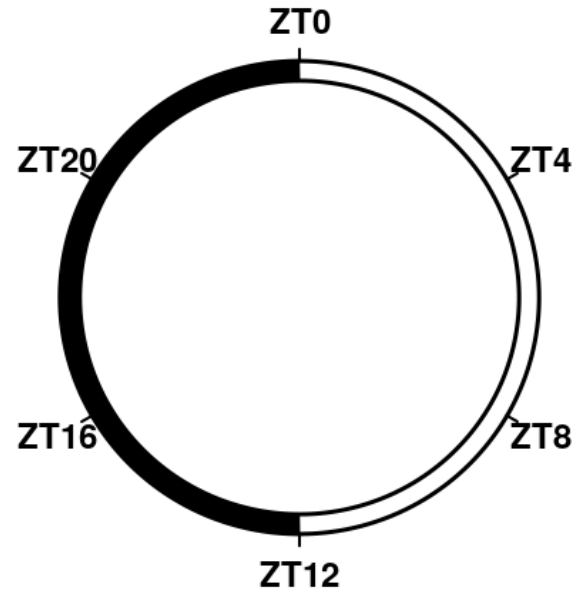
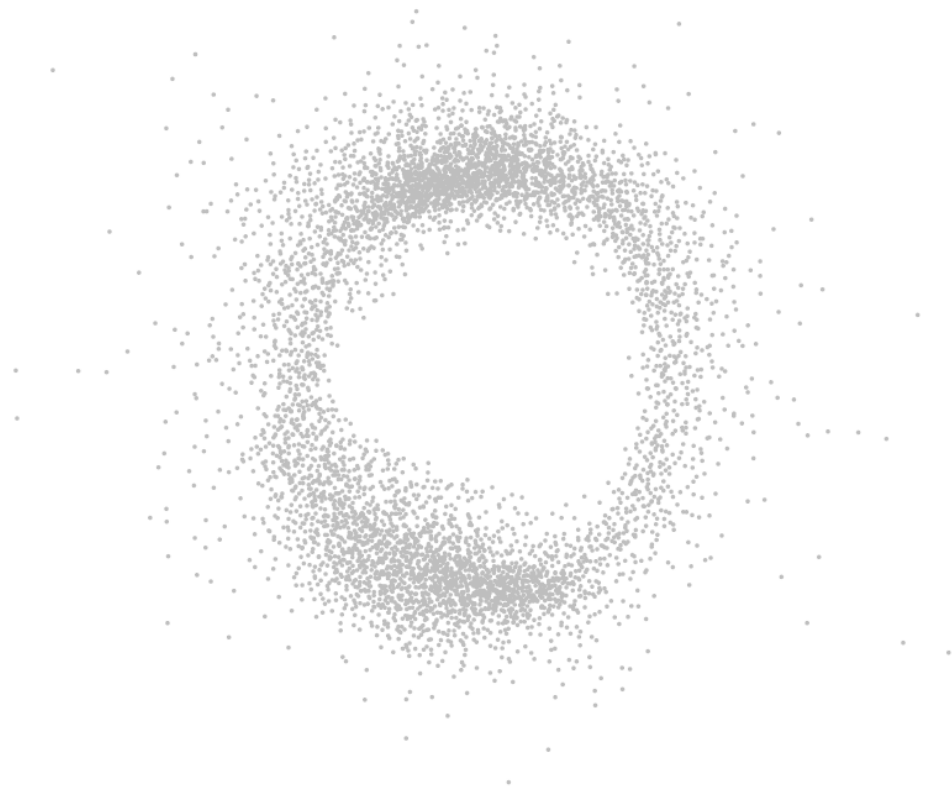




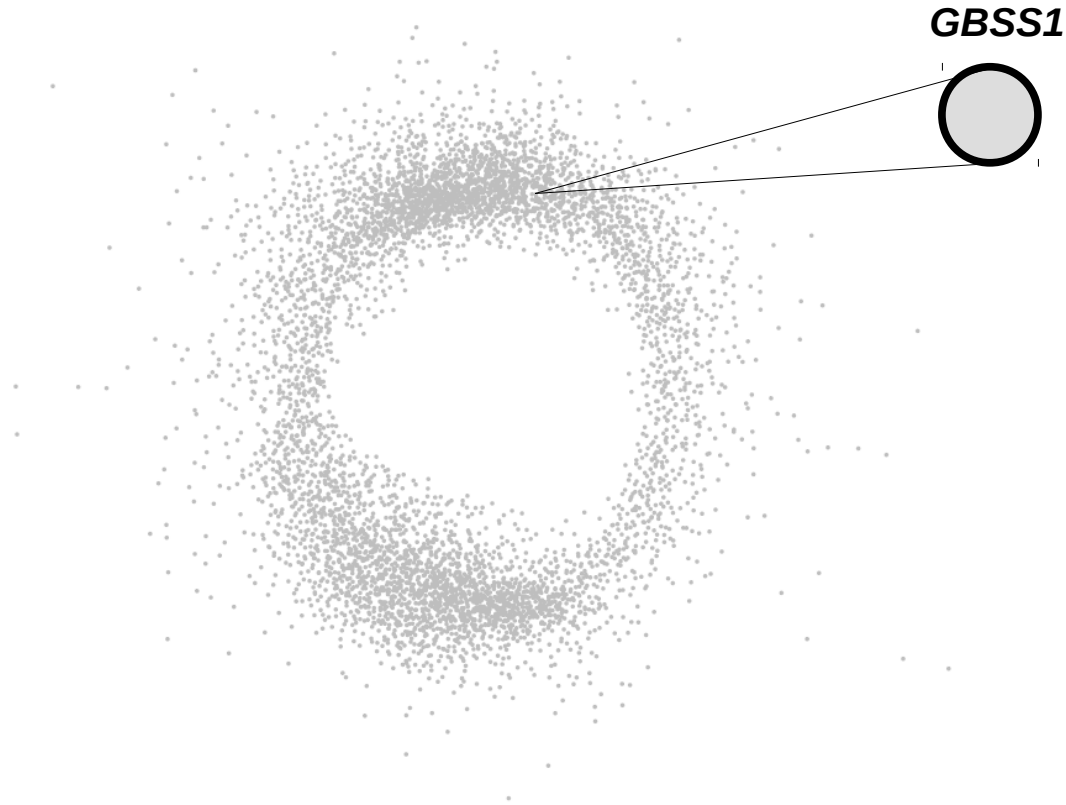
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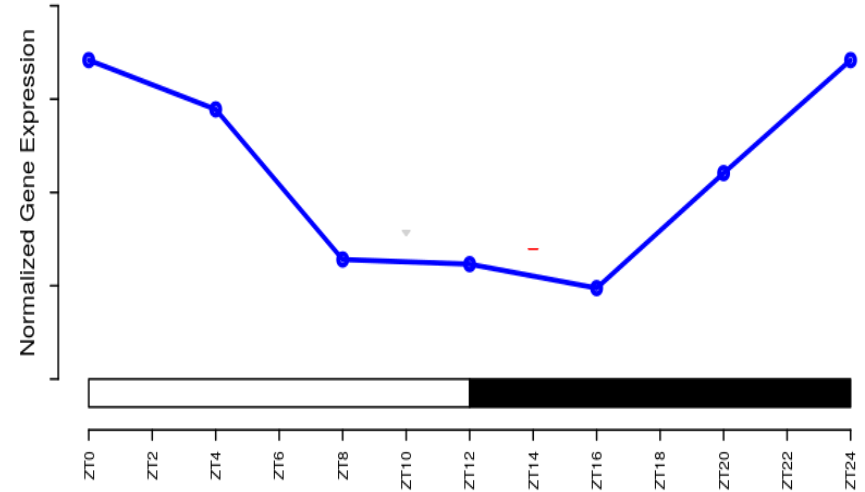
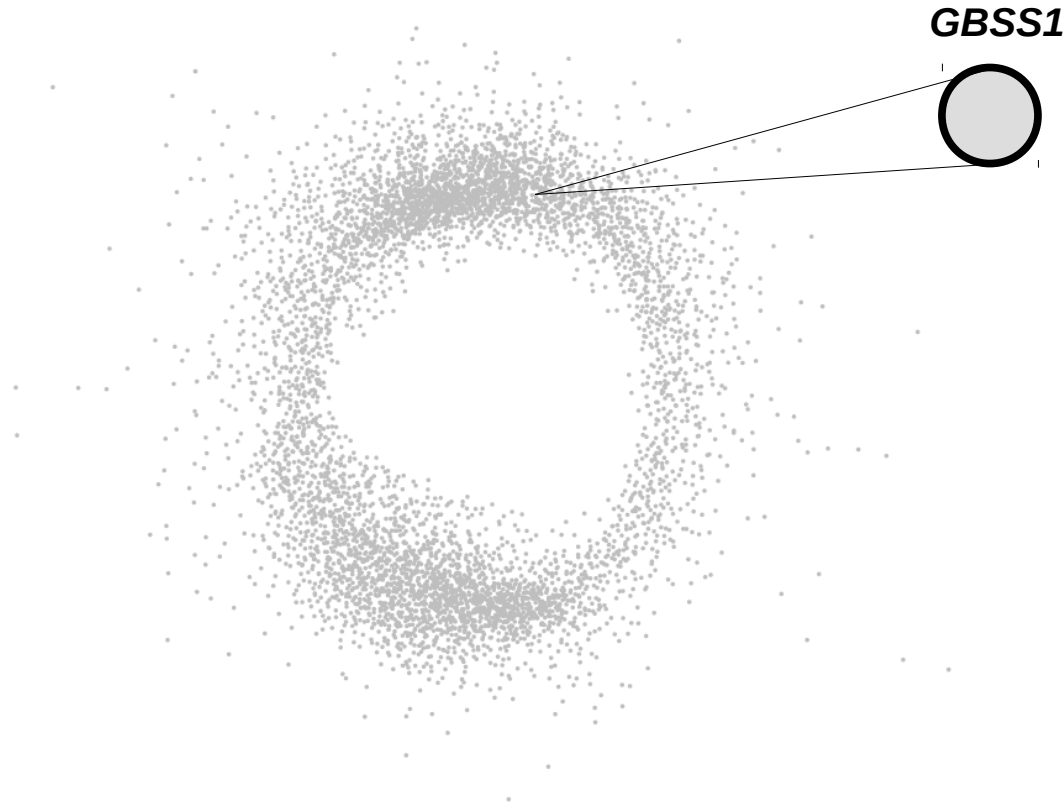
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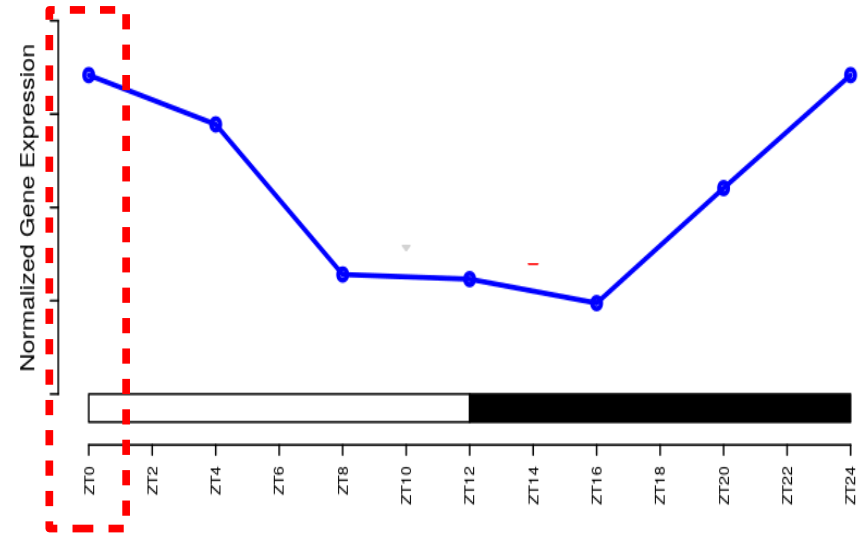
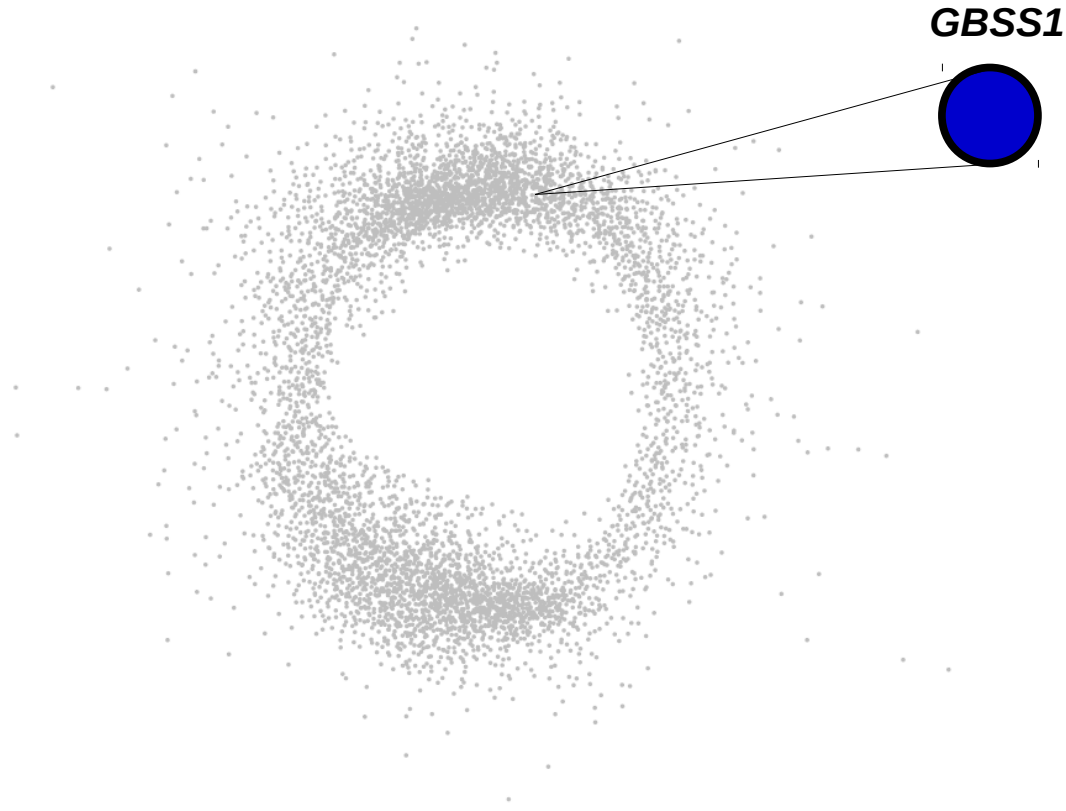
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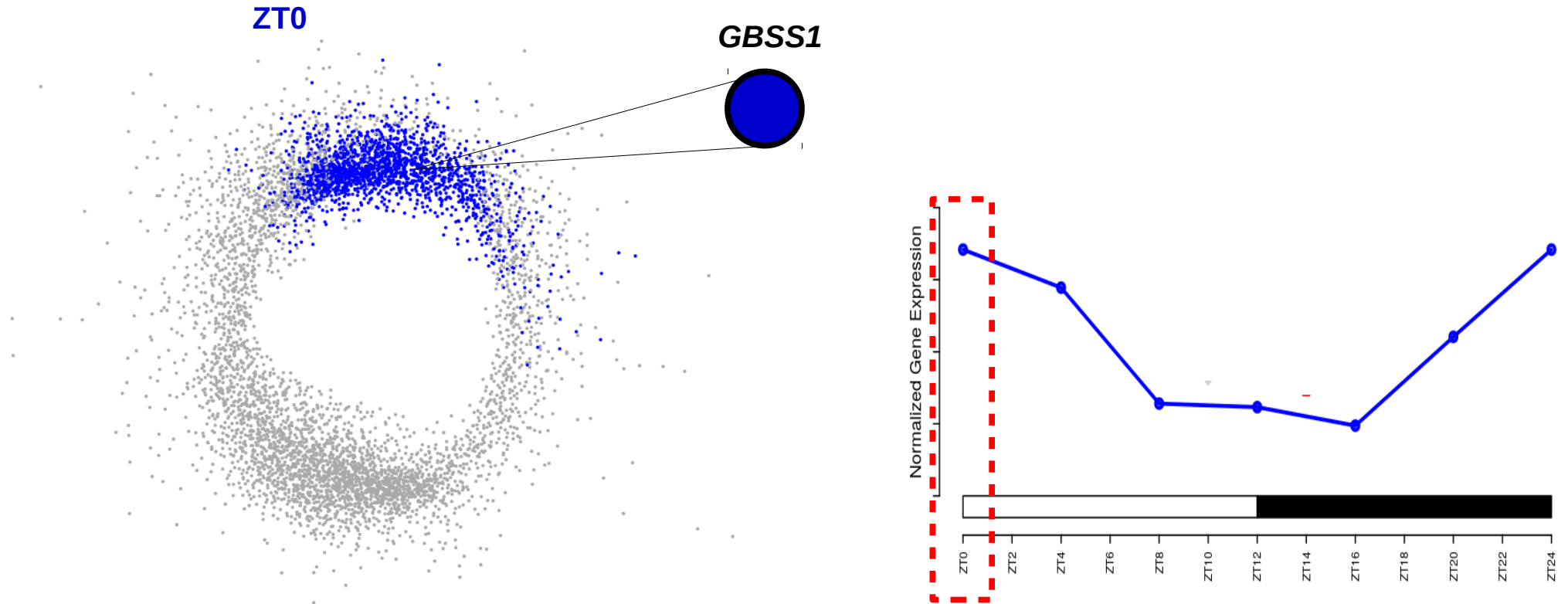
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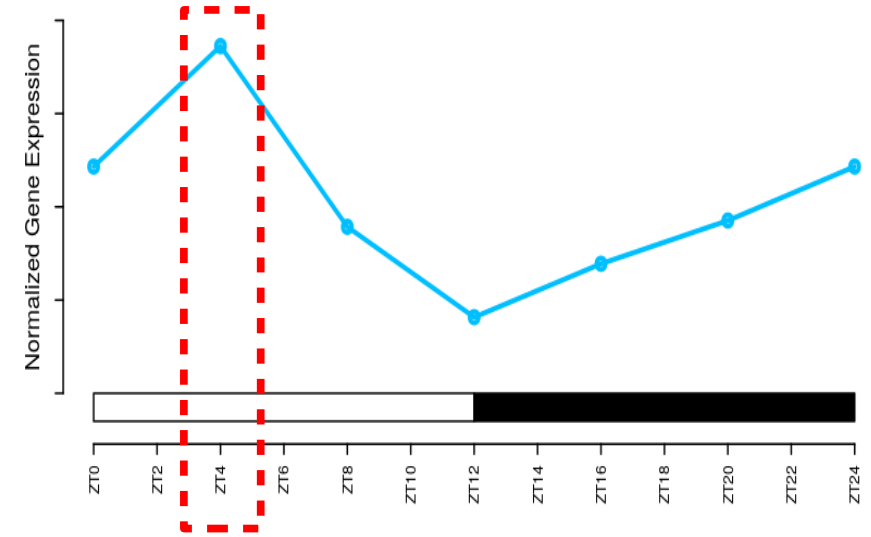
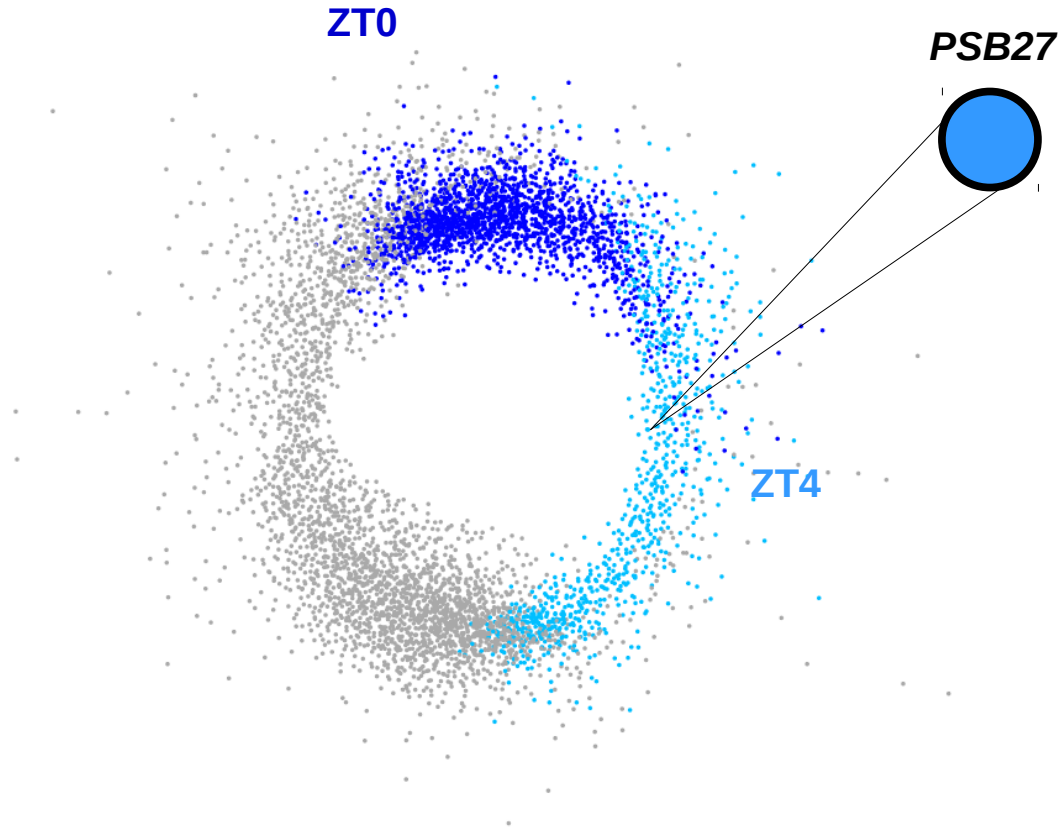
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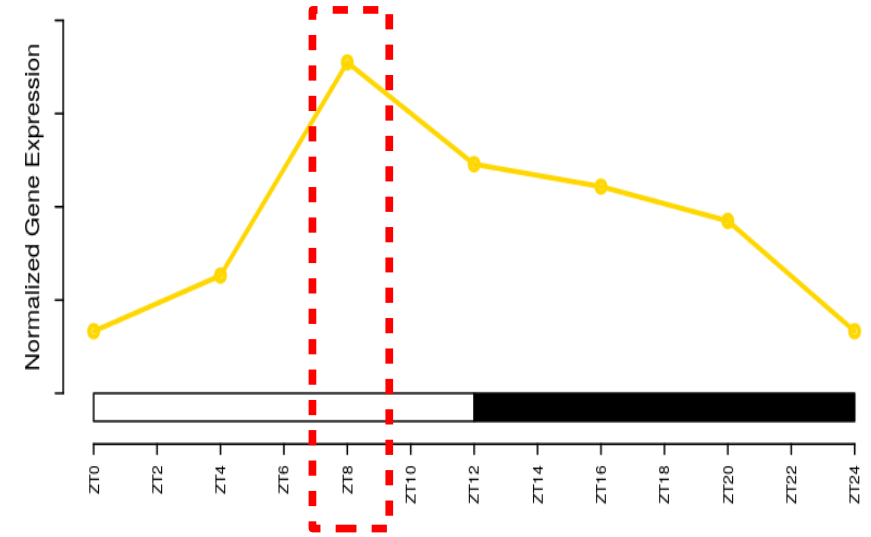
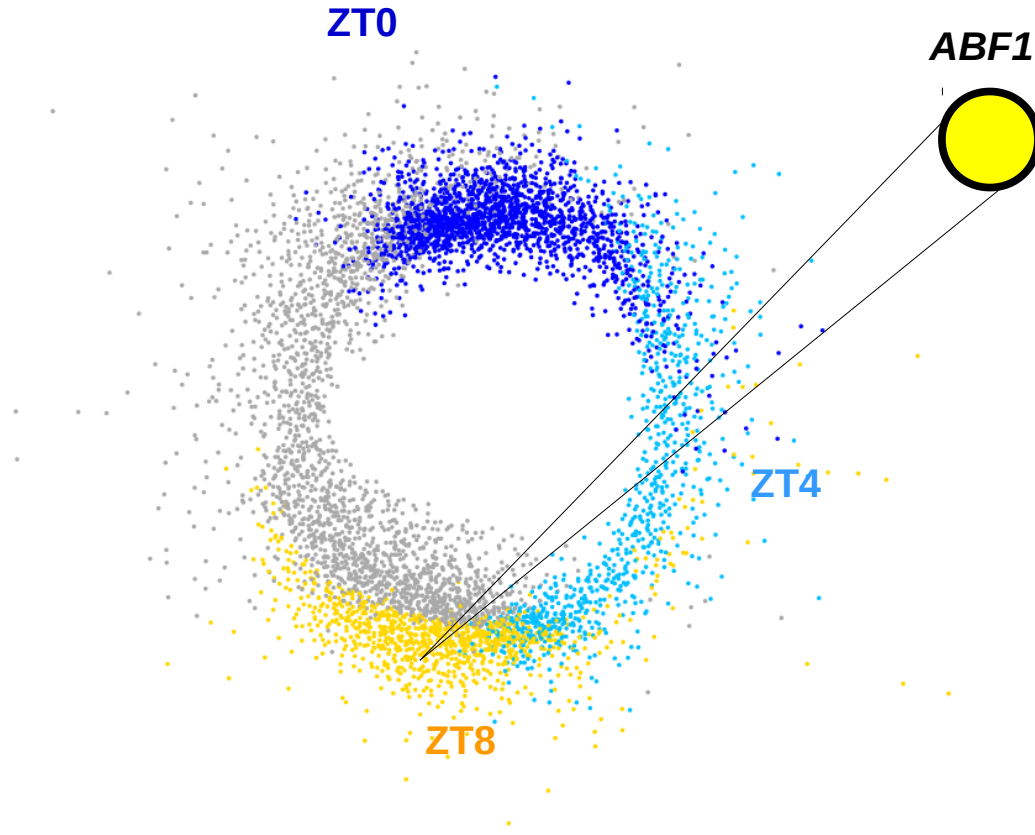


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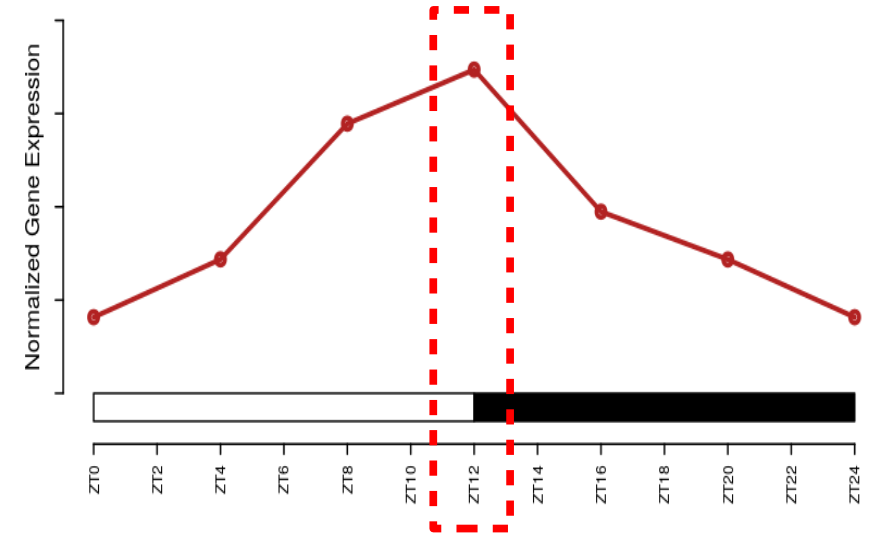
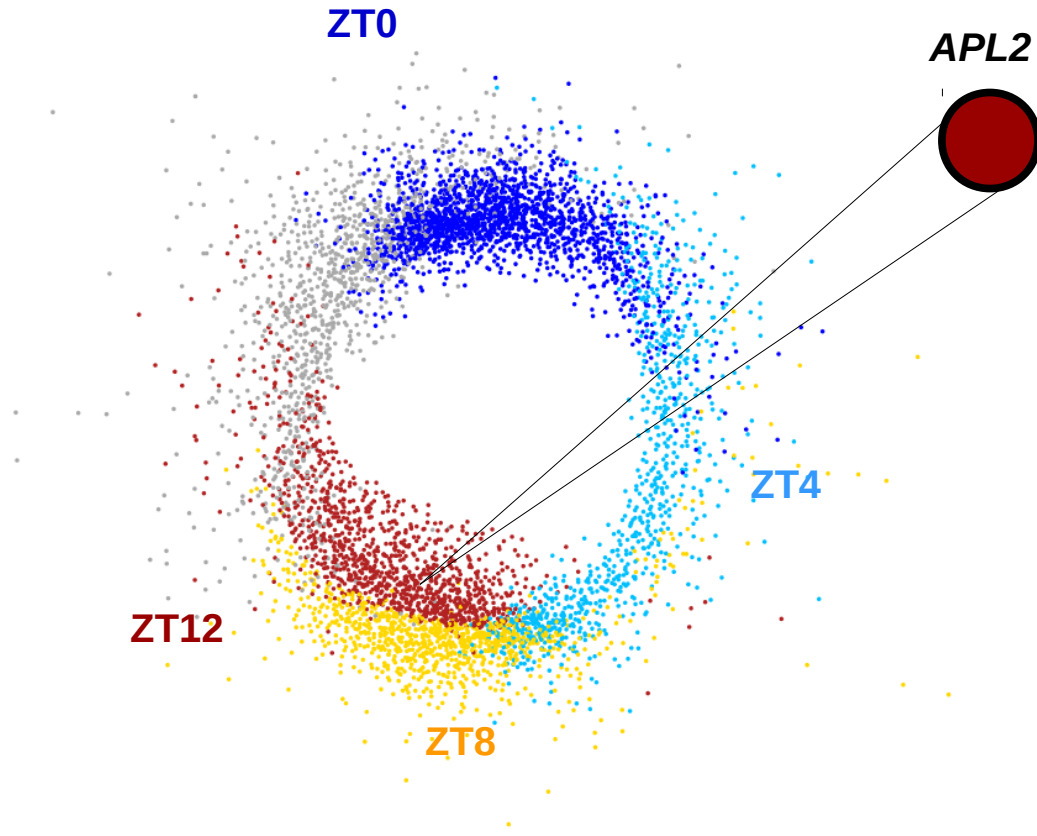




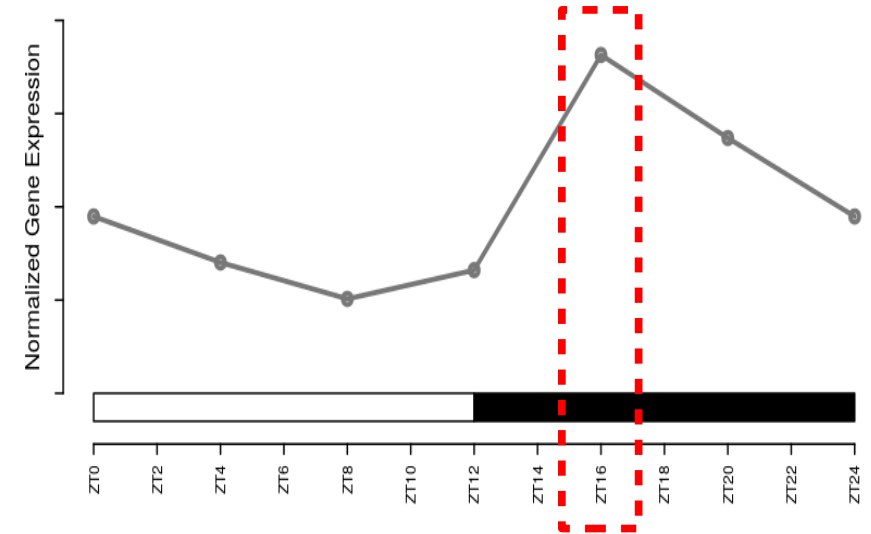
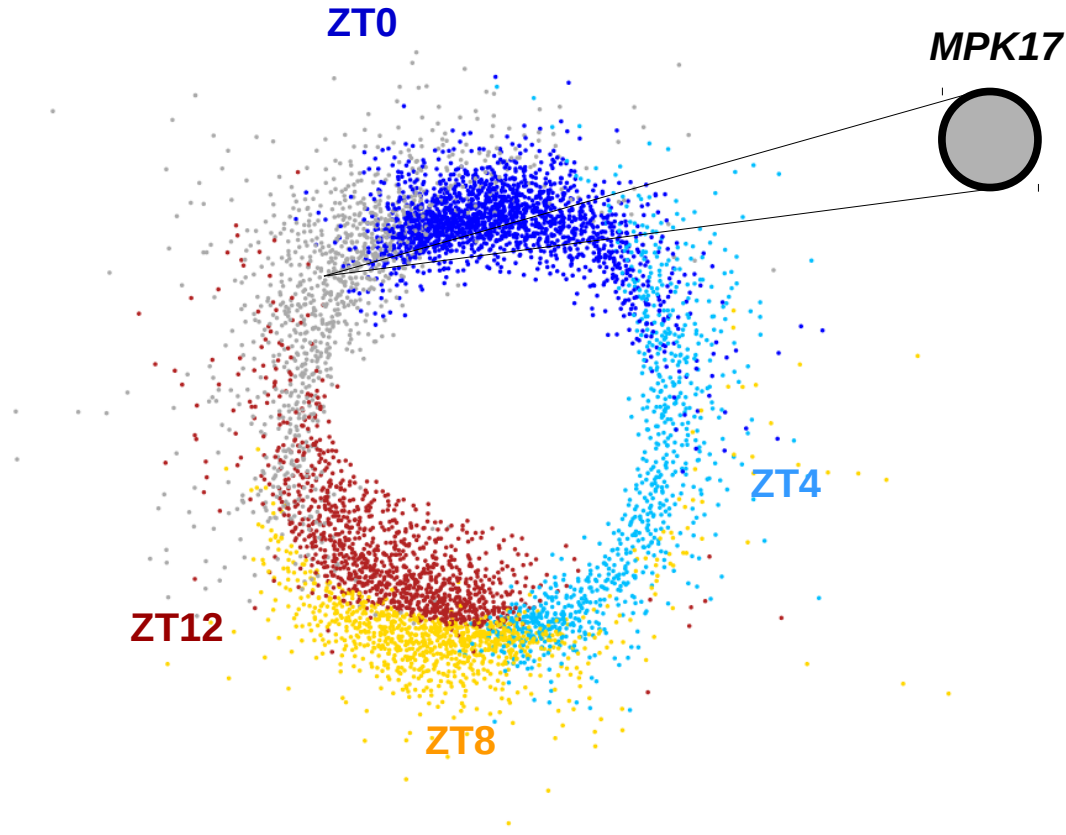
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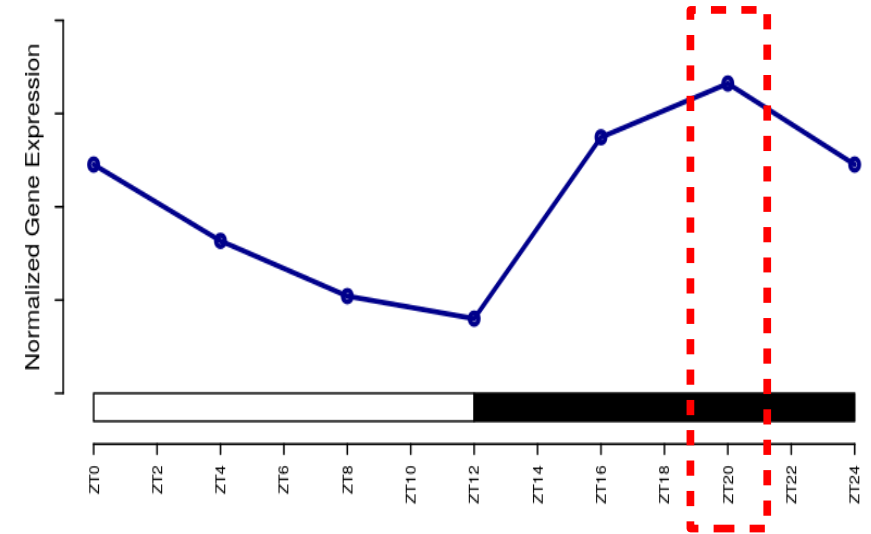
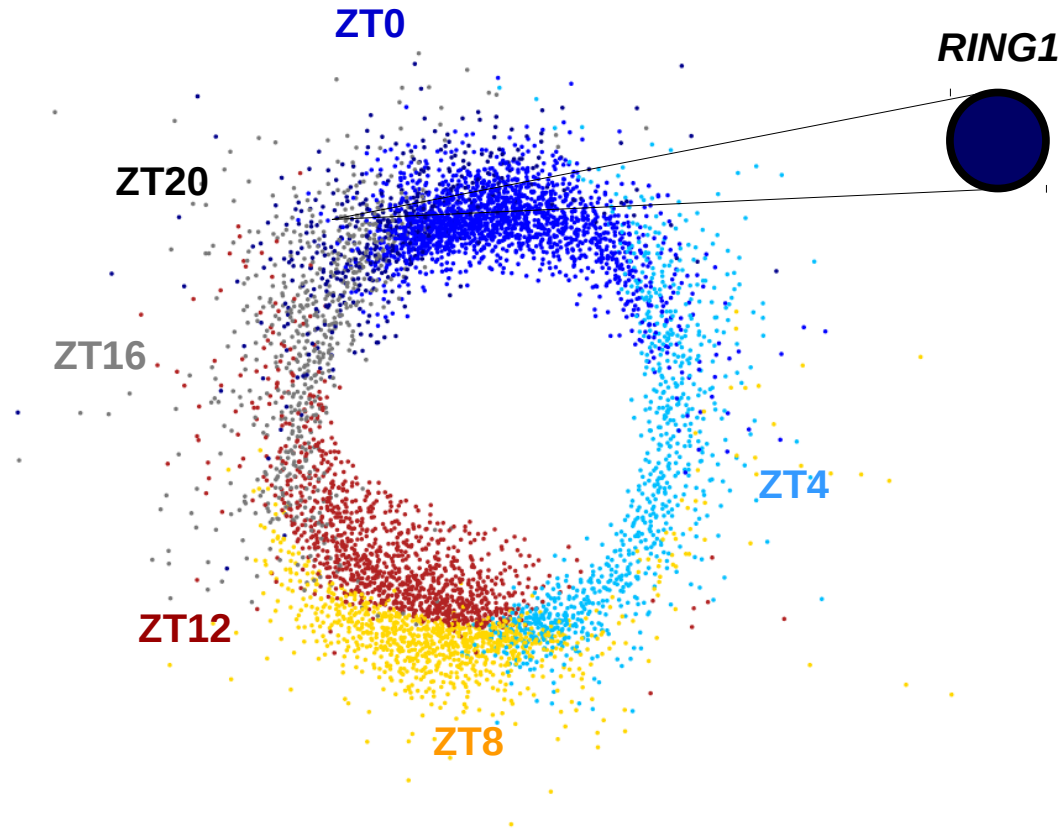
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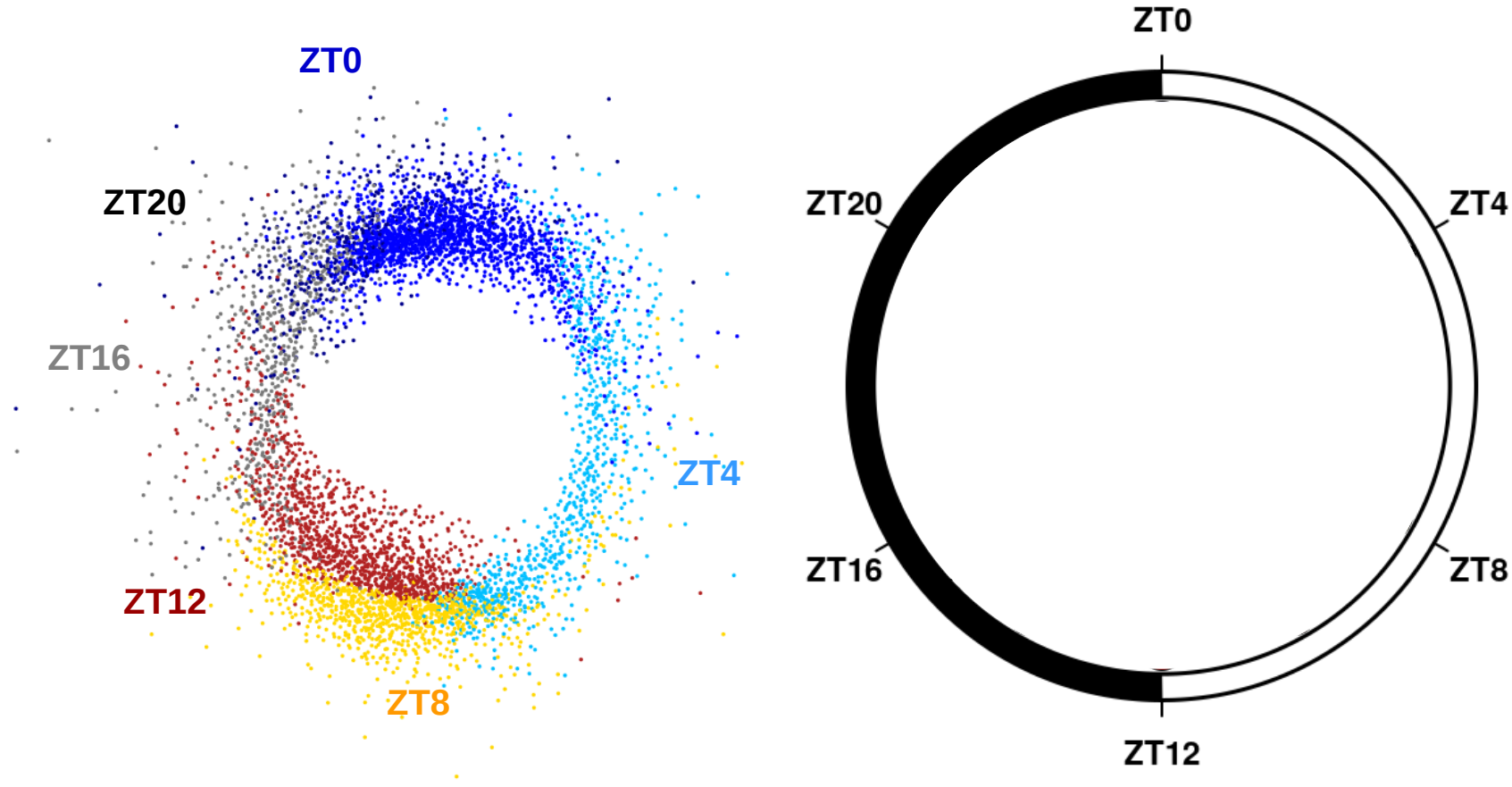
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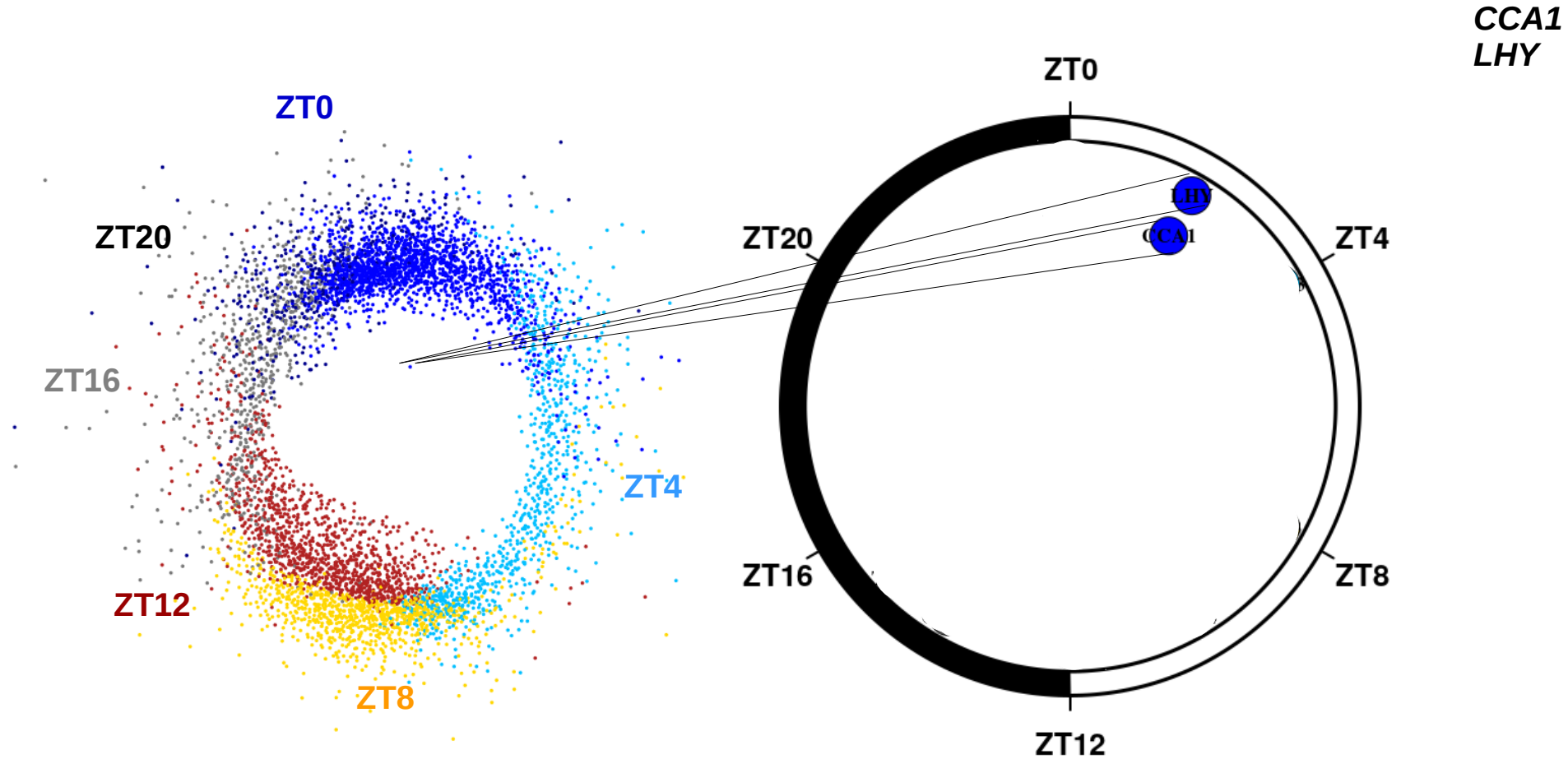
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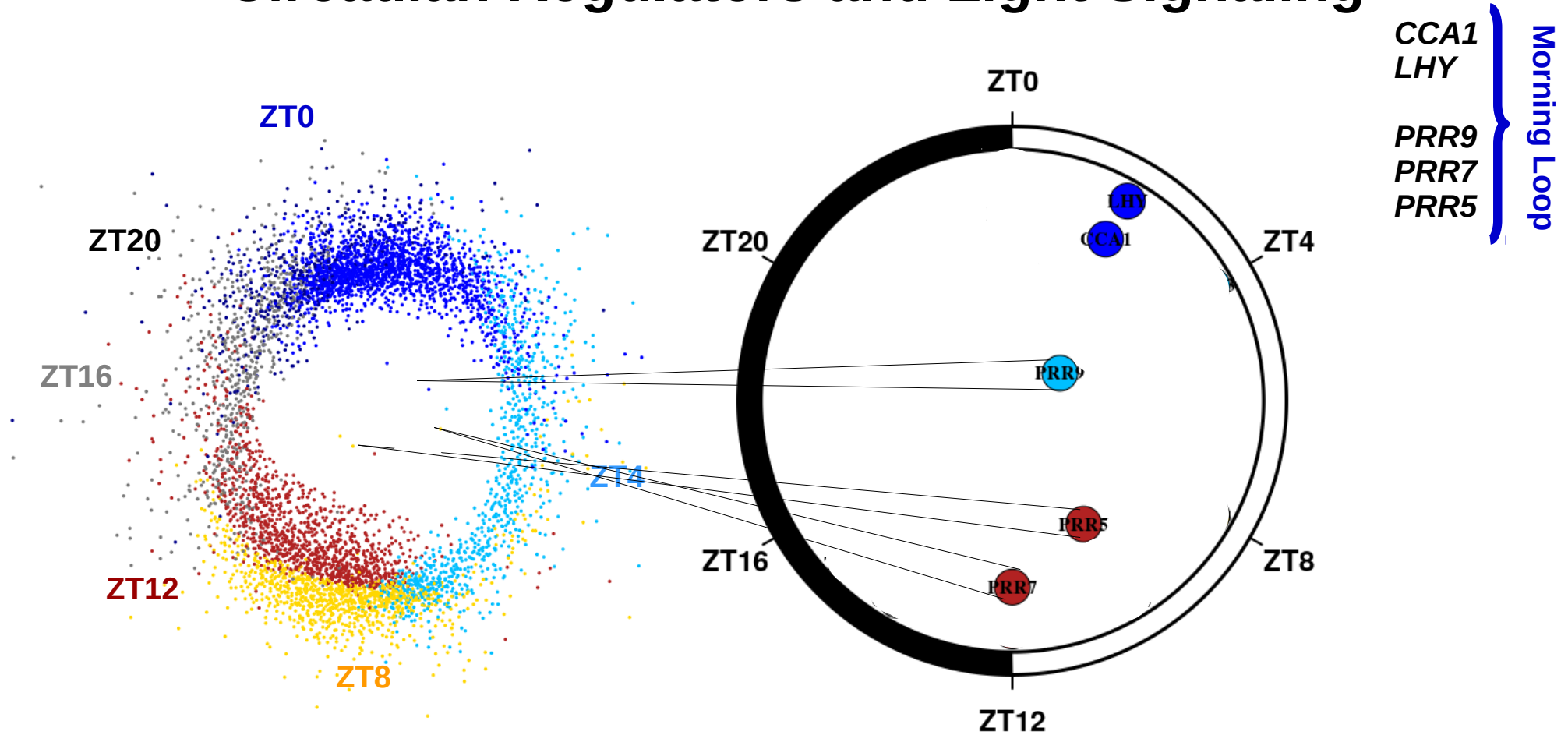


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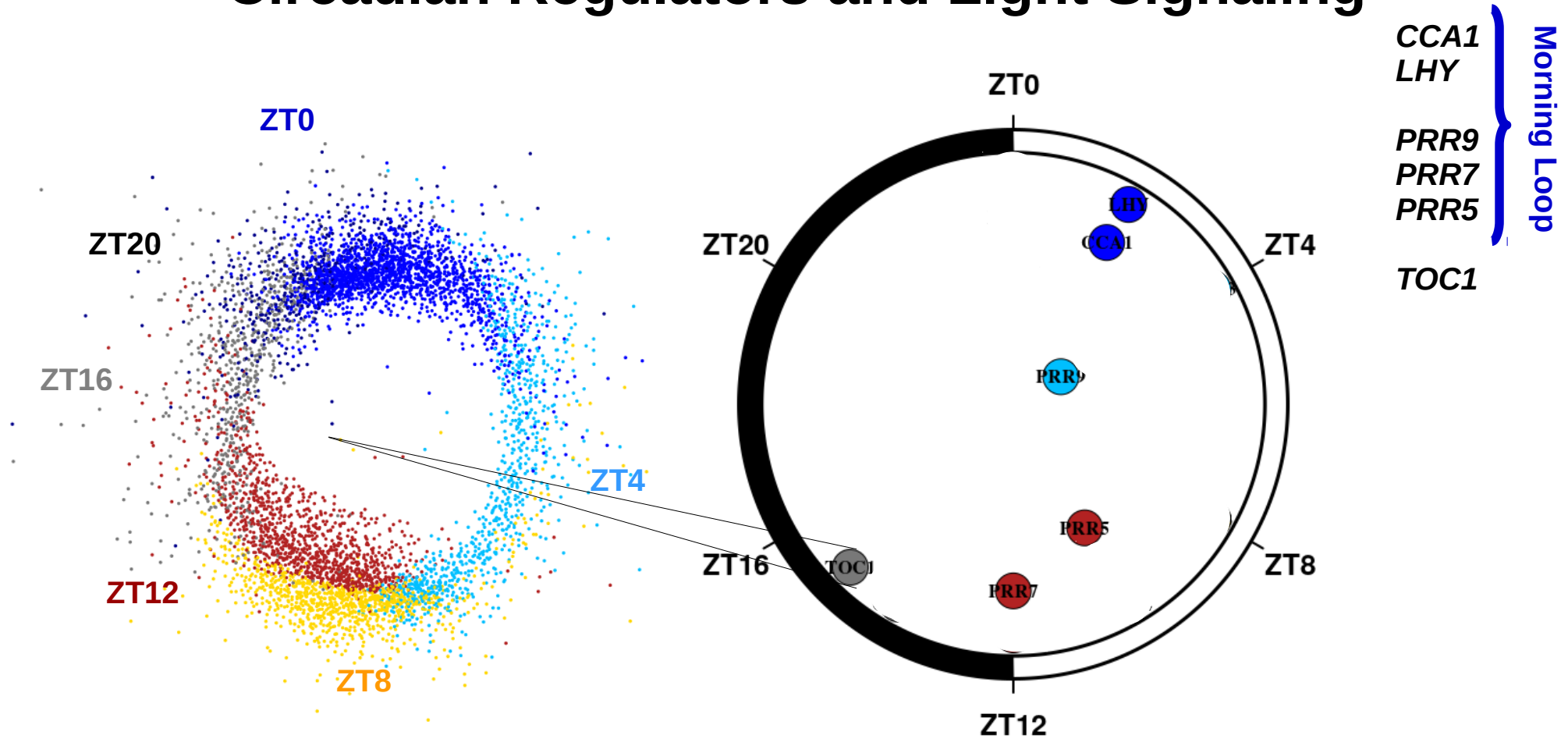




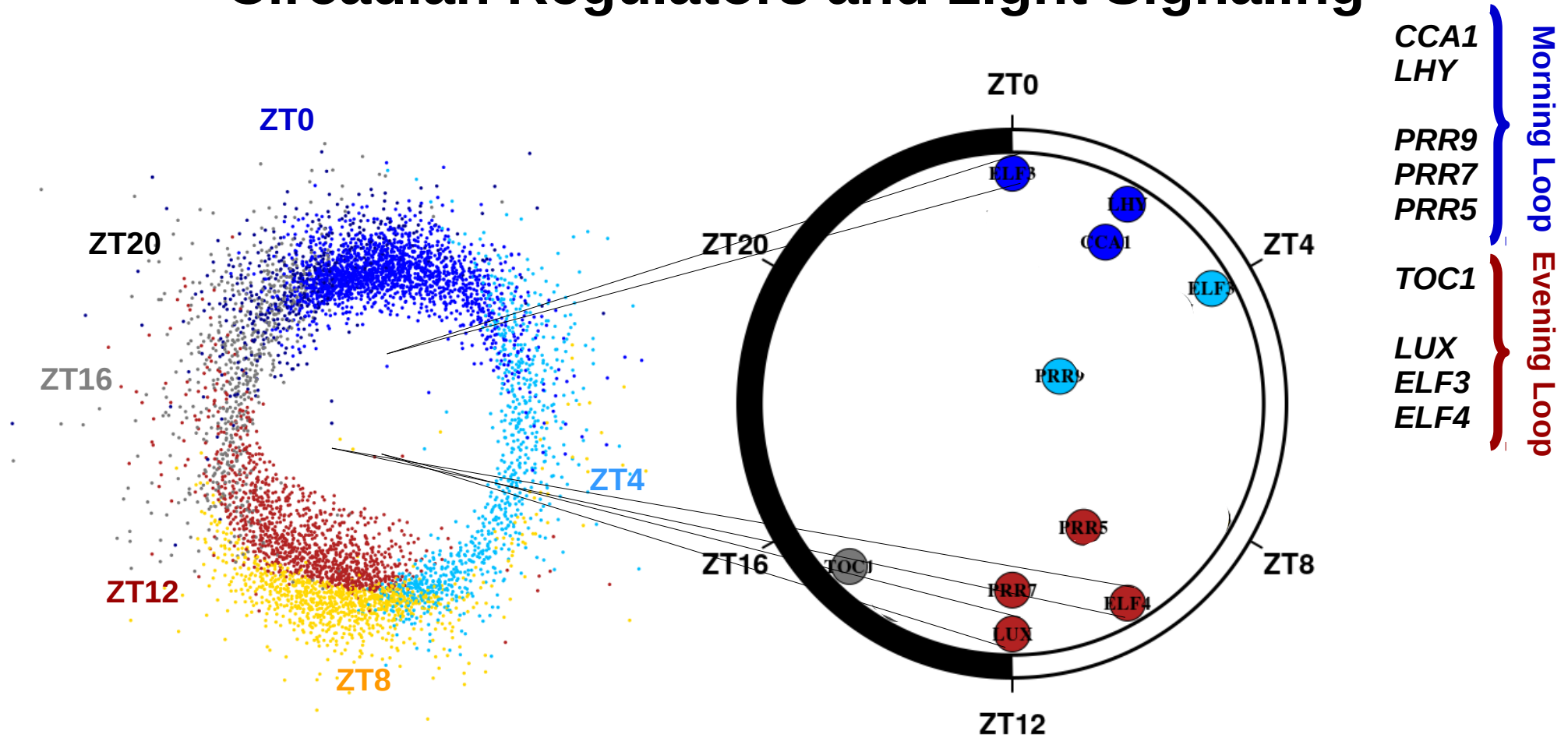
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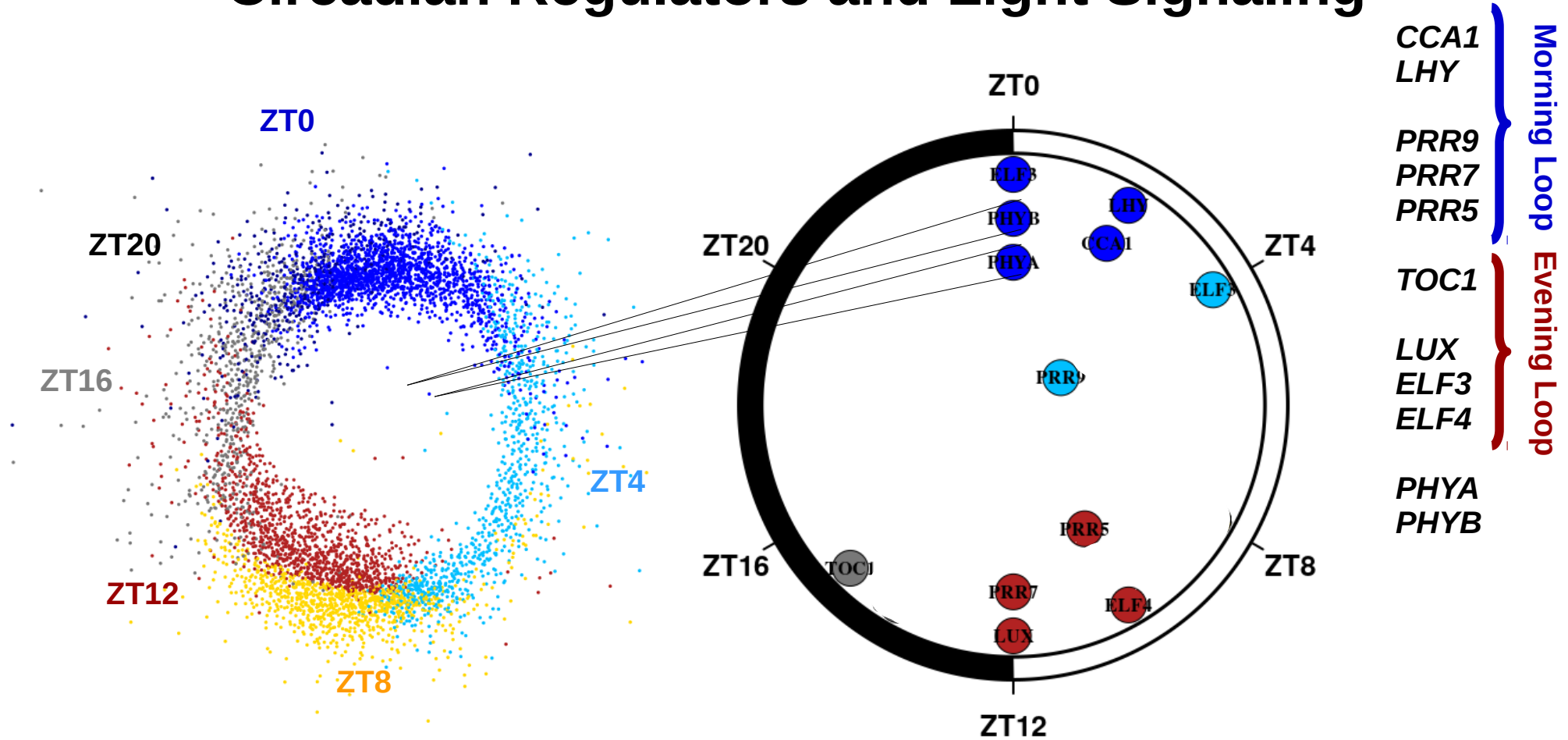
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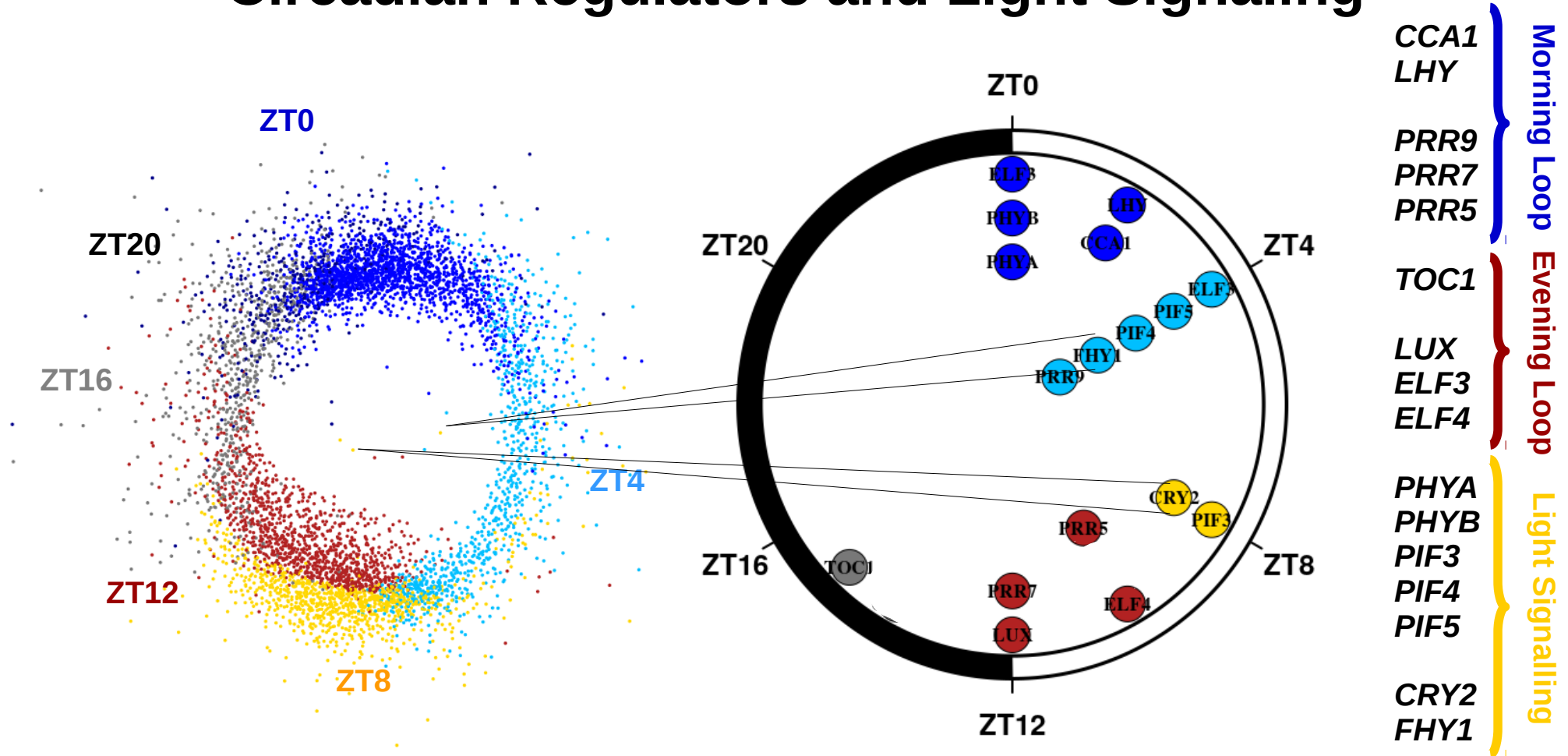


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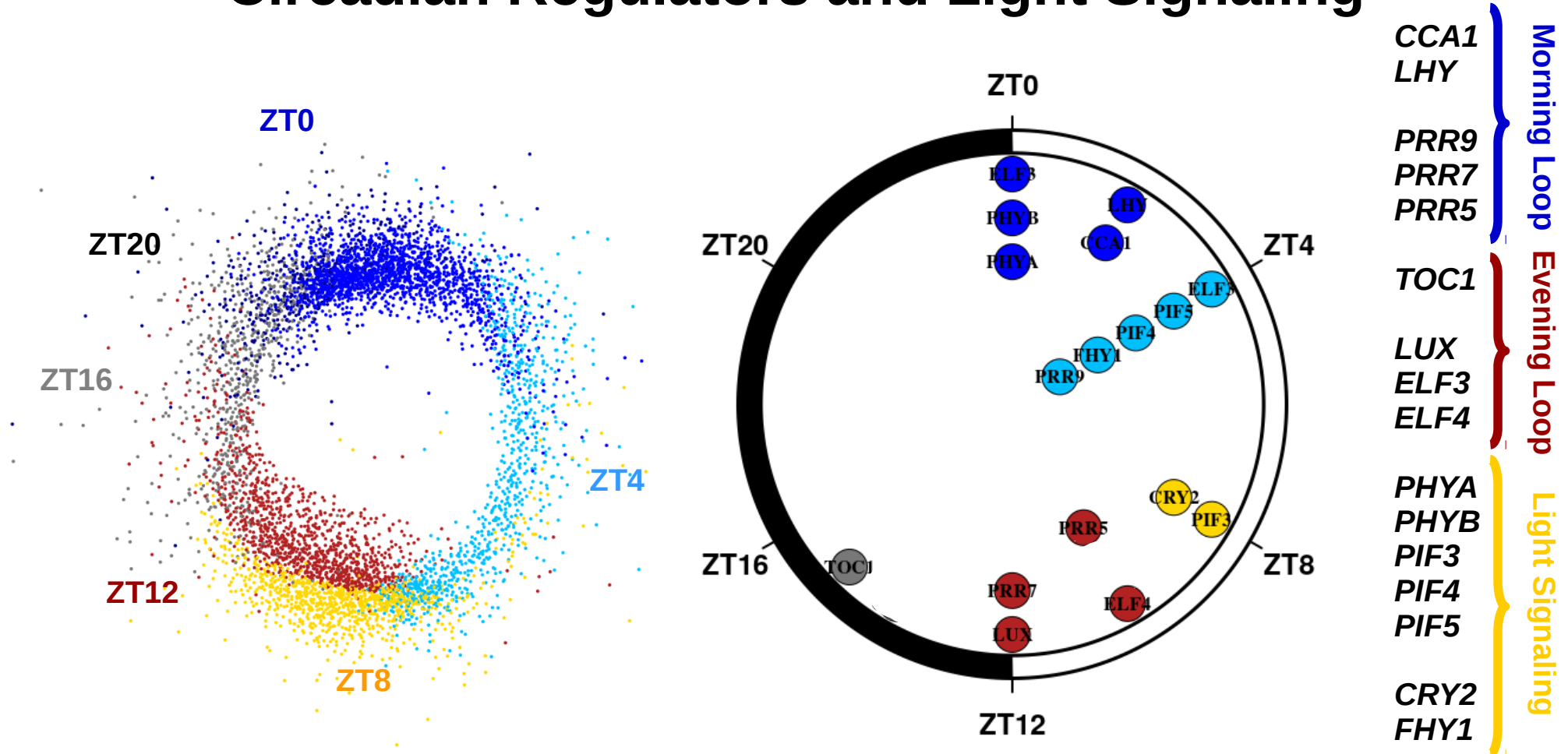




# ATTRACTOR, a Transcriptional Network integrating key Circadian Regulators and Light Signaling

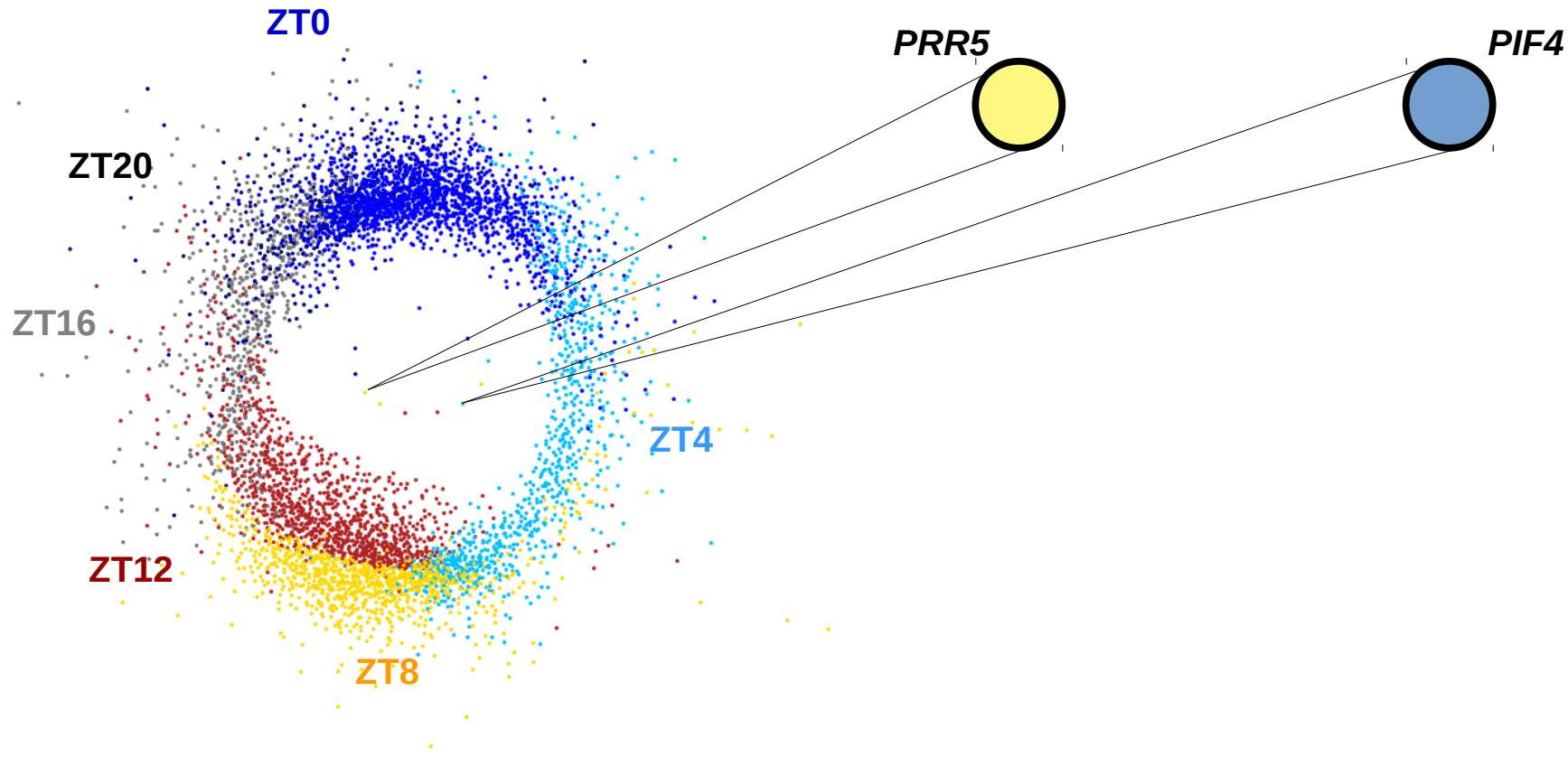


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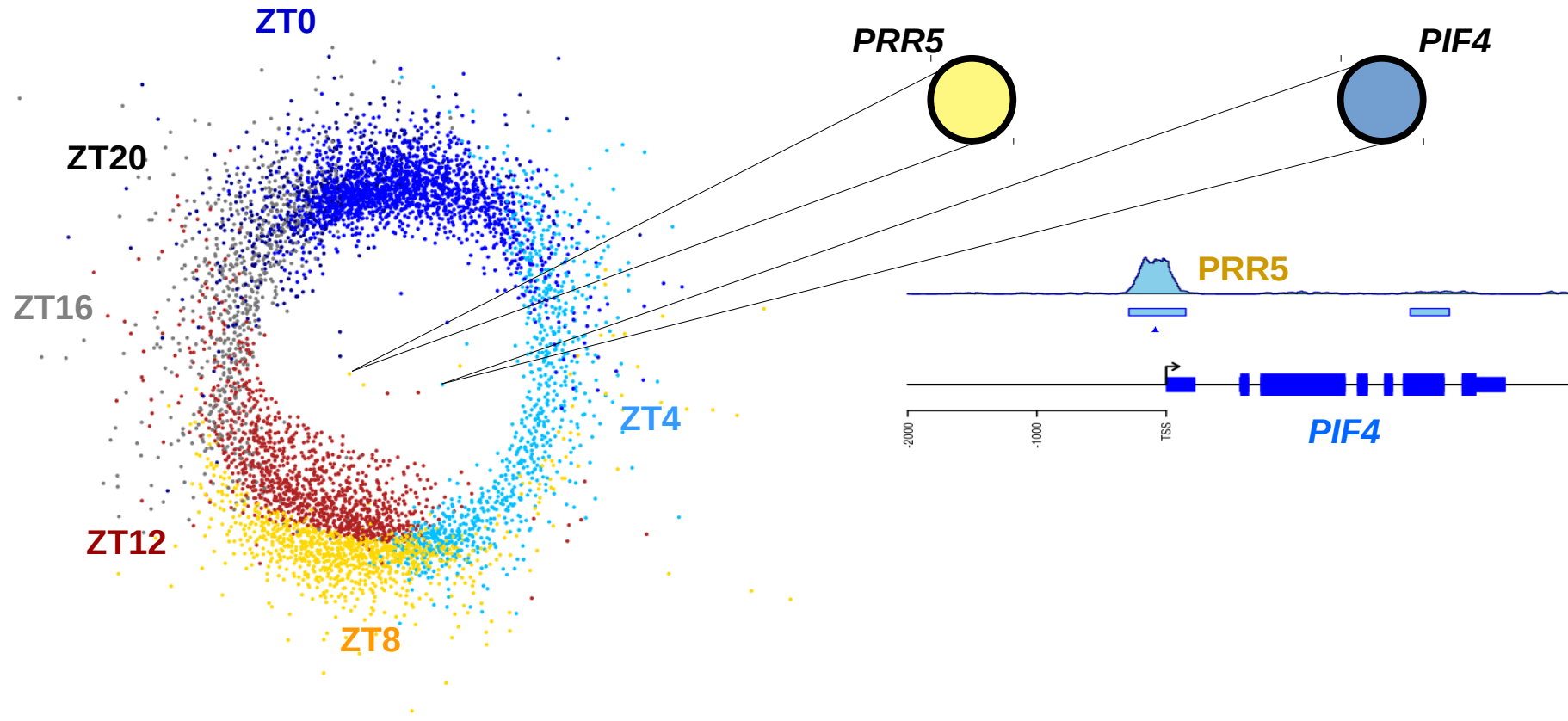




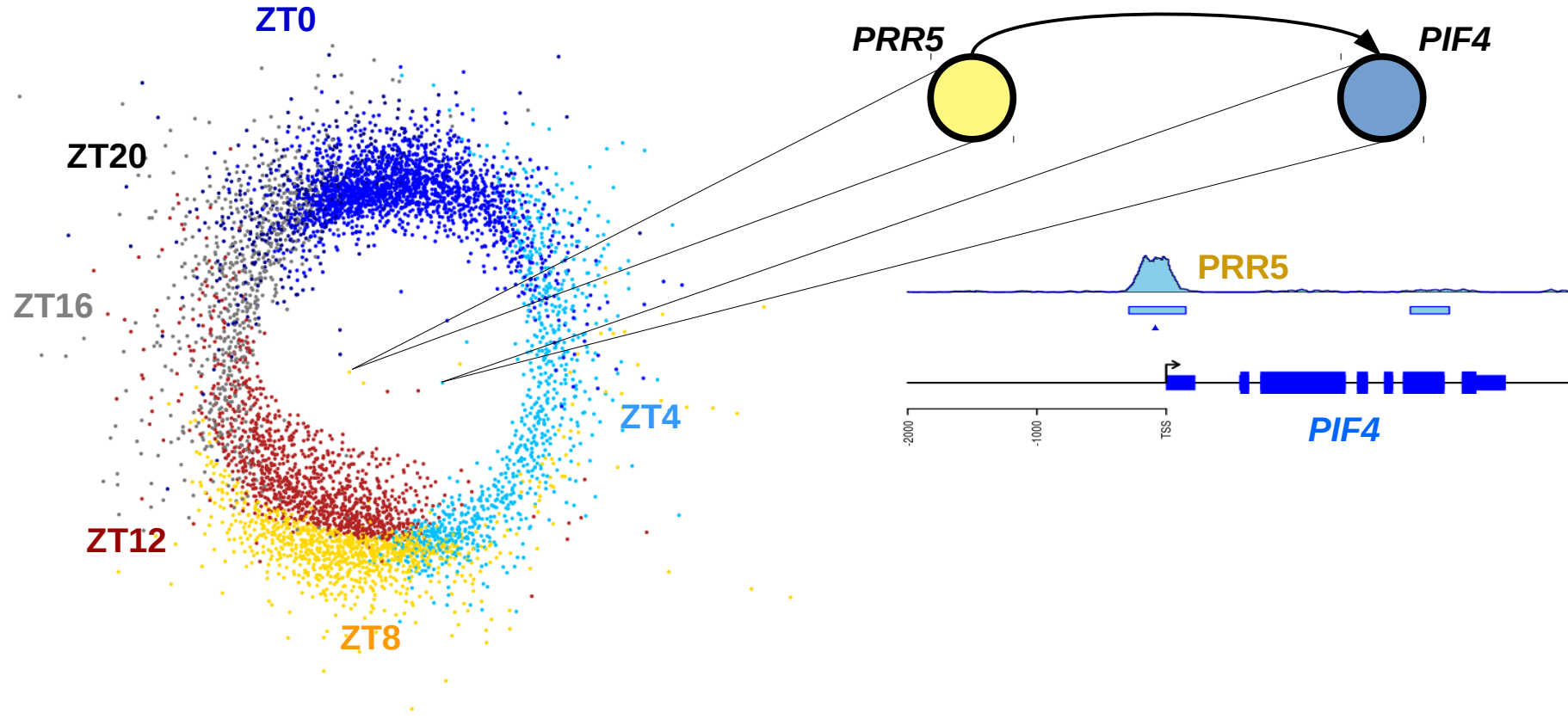
Transcriptional regulations are assigned a positive/negative/neutral effect depending on the target expression profile



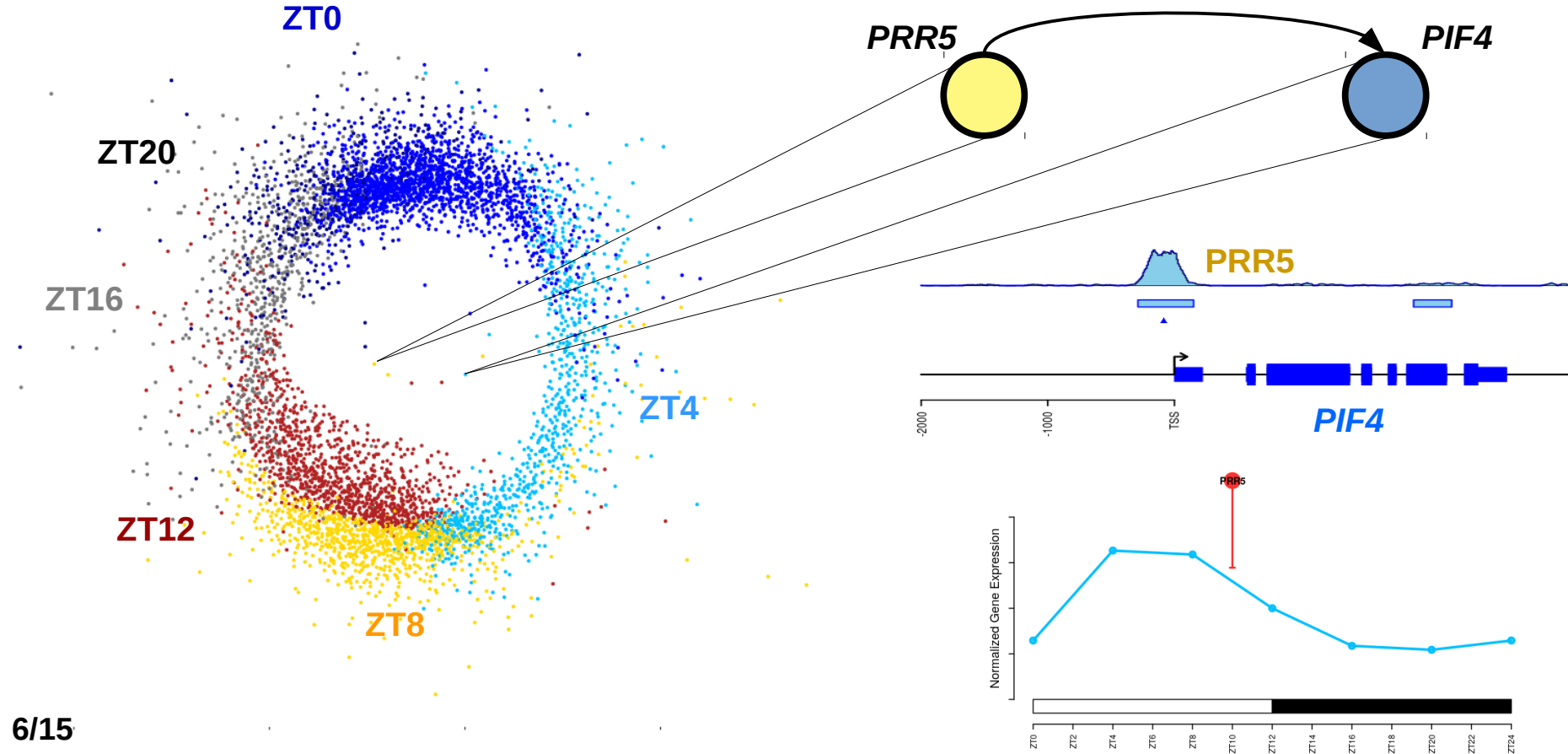
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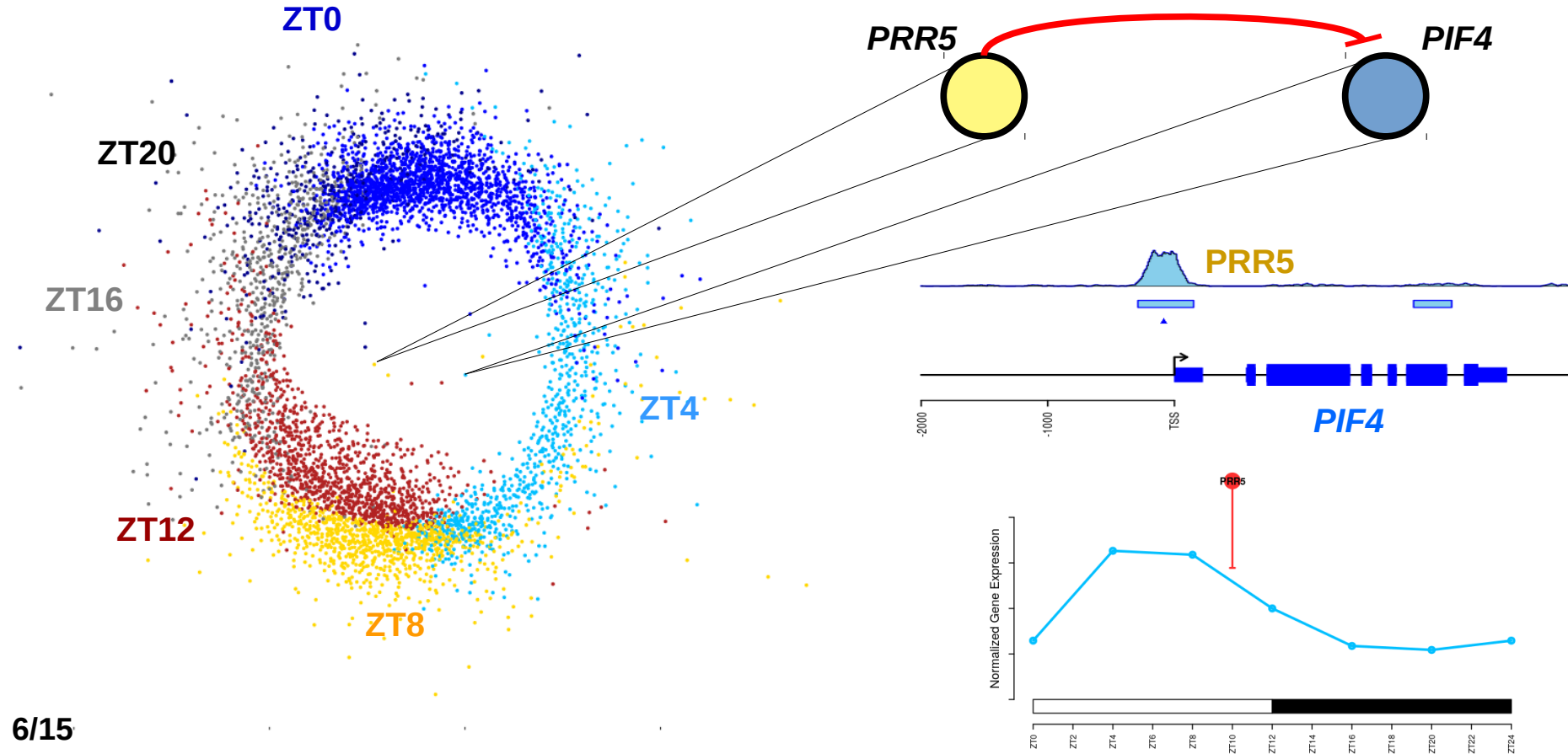
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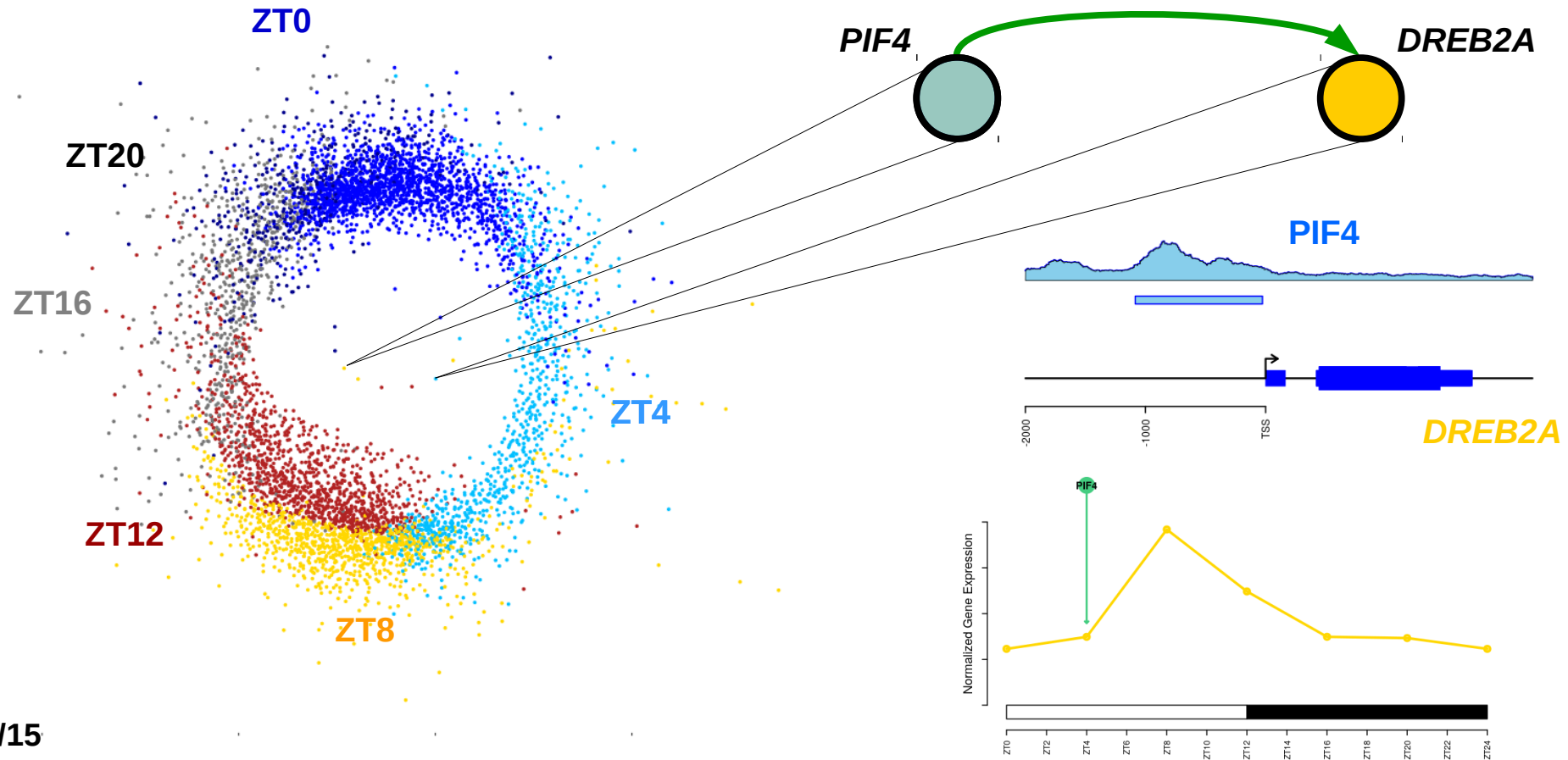
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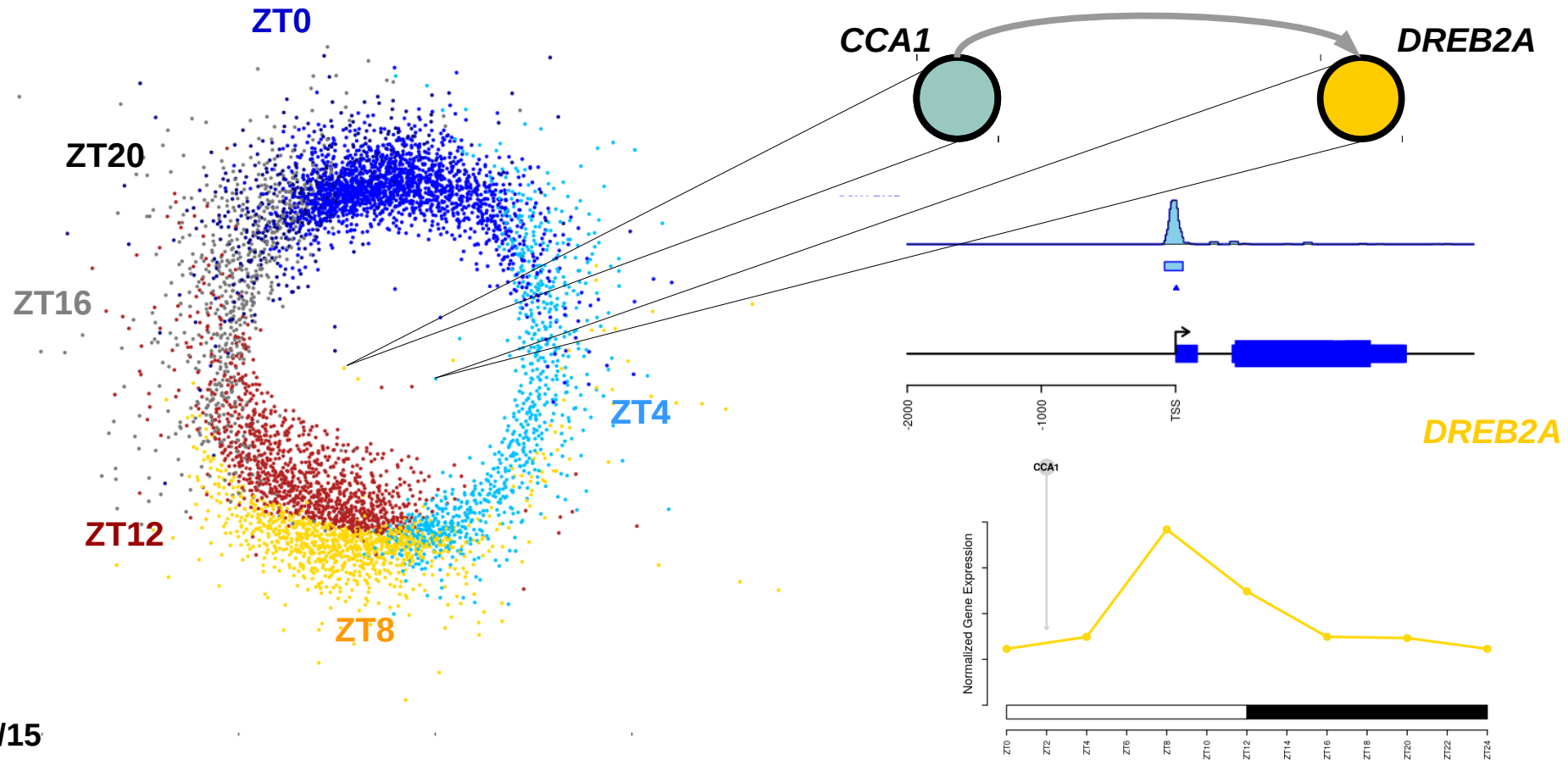
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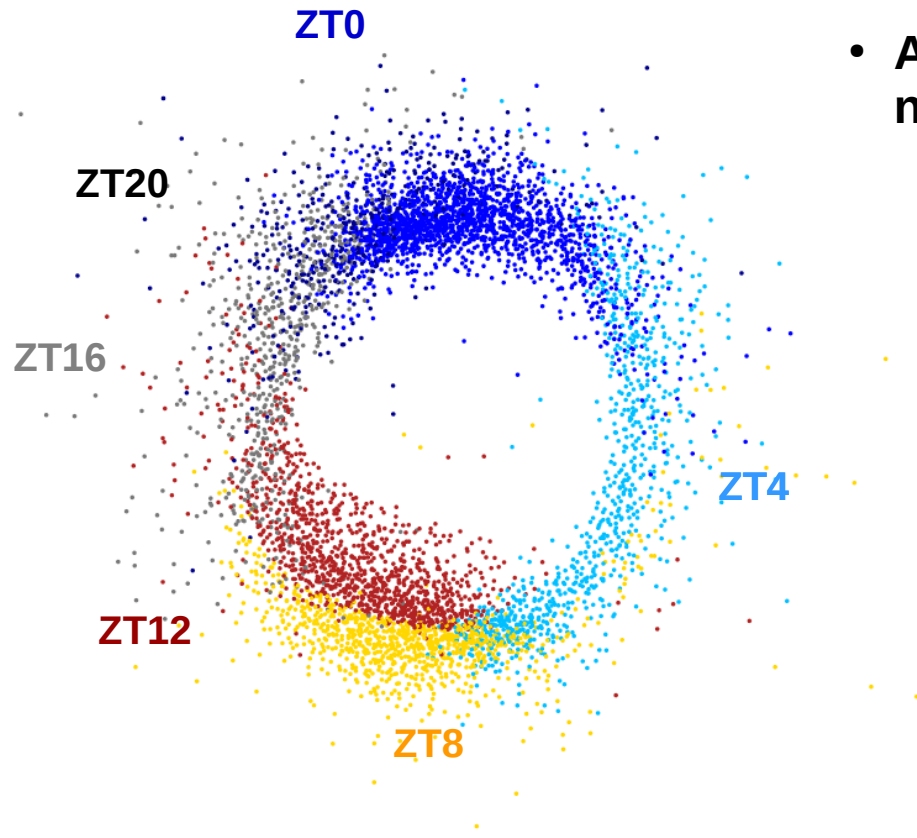


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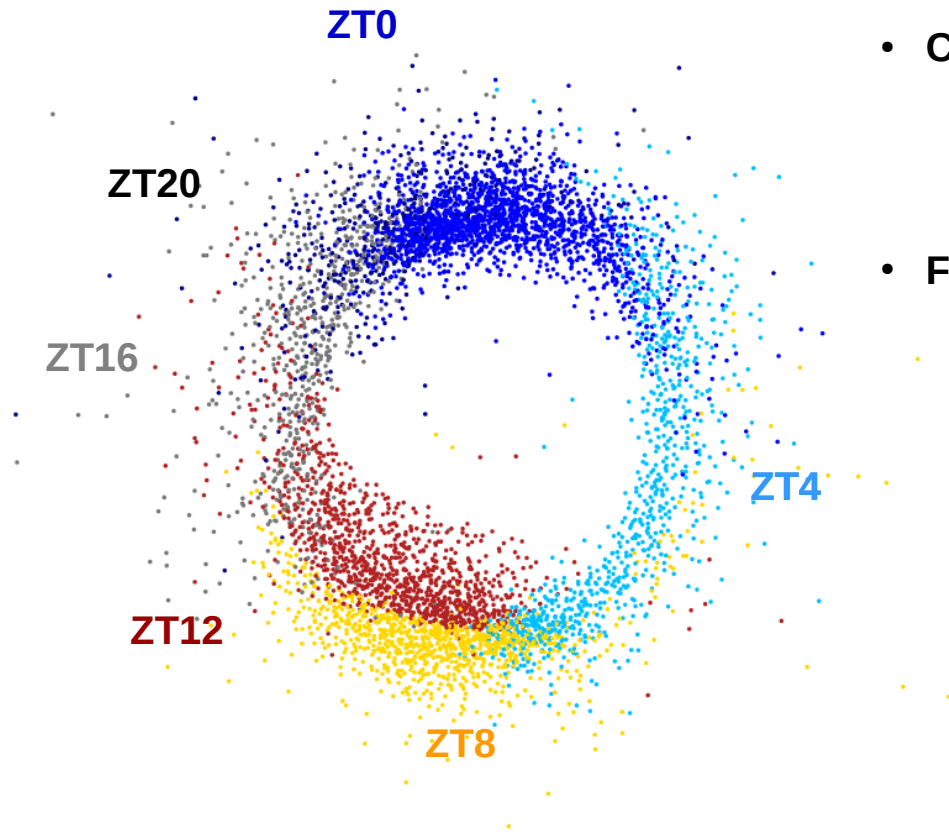


# Transcriptional regulations are assigned a positive/negative/neutral effect depending on the target expression profile



- ATTRACTOR is a gene transcriptional network comprising:
  - 5778 nodes or genes with rhythmic expression profiles
  - 14529 edges or transcriptional regulations

# ATTRACTOR, a web based tool for the exploration of a transcriptional network integrating key regulators of the circadian clock and light signalling



- Completely developed using R packages.

Shiny

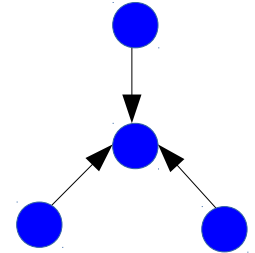
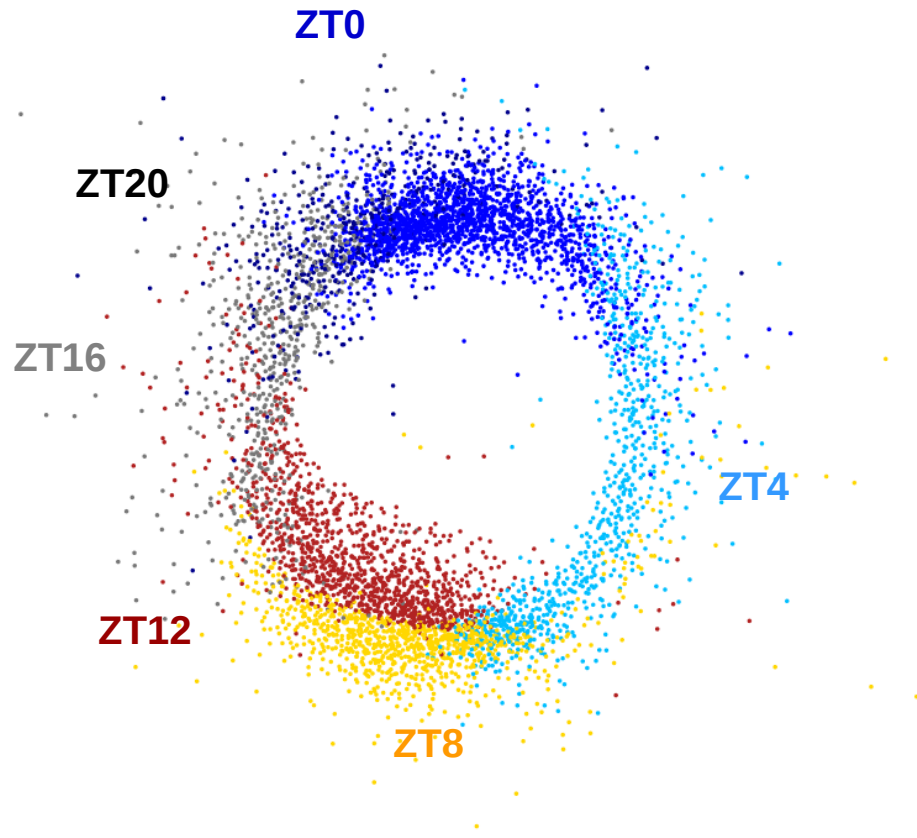
from R Studio

Bioconductor  
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS



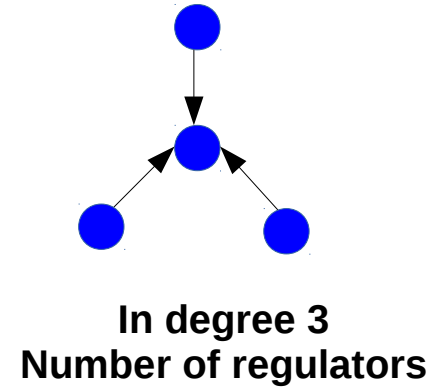
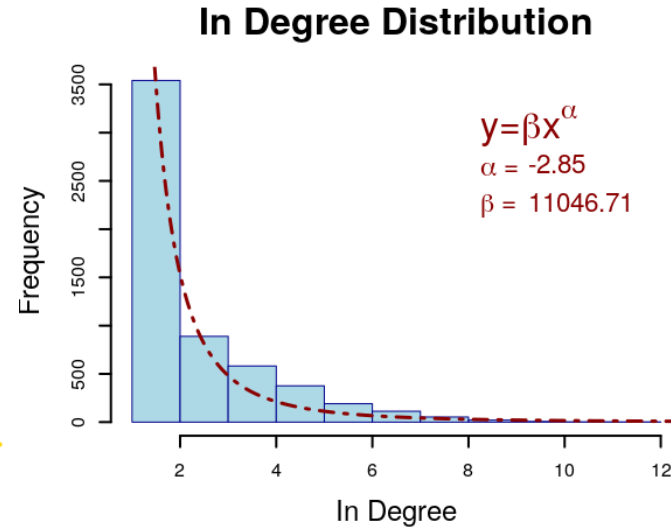
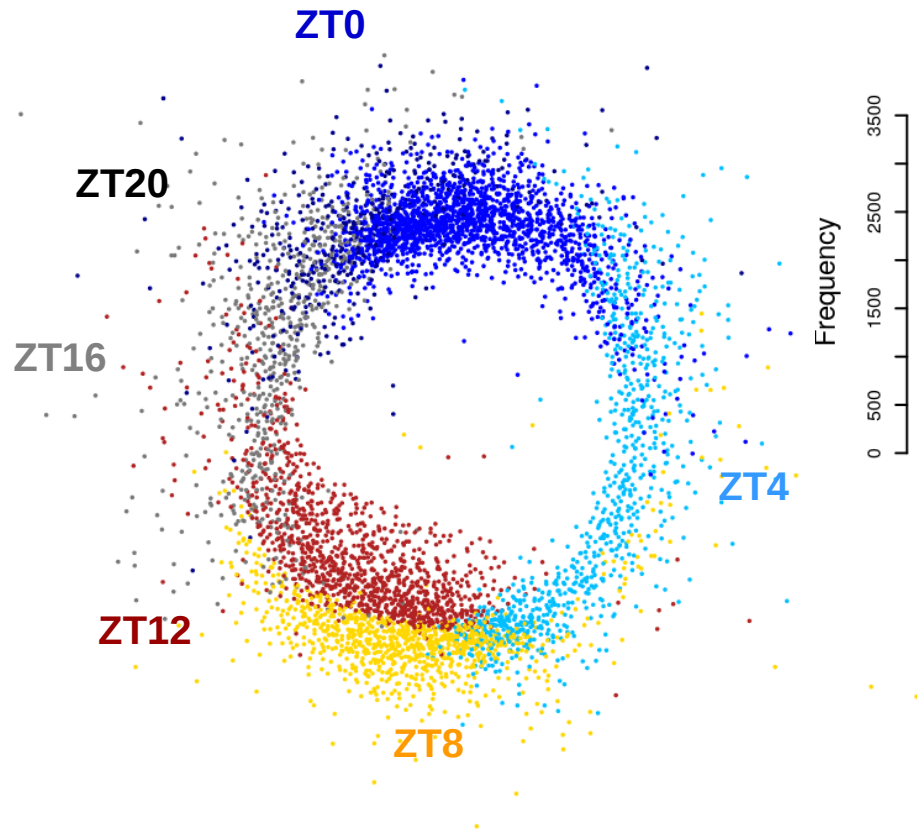
- Functionalities:
  - Global properties analysis and visualization
  - Analysis of the regulation of individual genes
  - Analysis of coordinated regulation over set of genes including:
    - Significance enrichment in specific expression patterns
    - GO enrichment and TFBS overrepresentation
    - Significance of binding sites overlaps between different transcription factors

# ATTRACTOR suggests that the Circadian Clock Transcriptional Program is simultaneously robust to random perturbations and sensitive to directed tuning

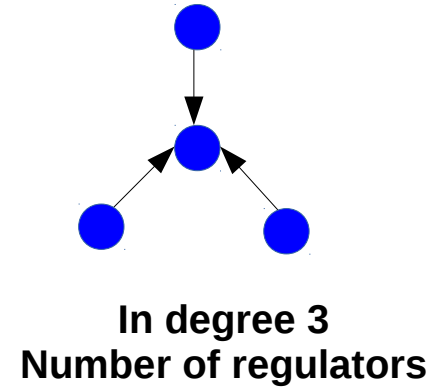
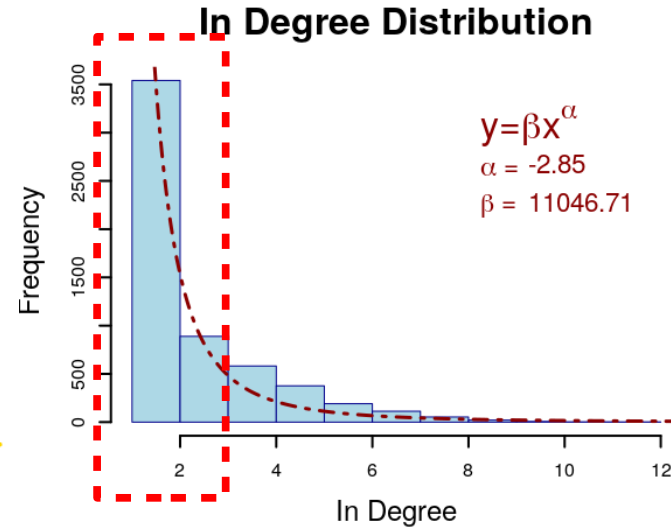
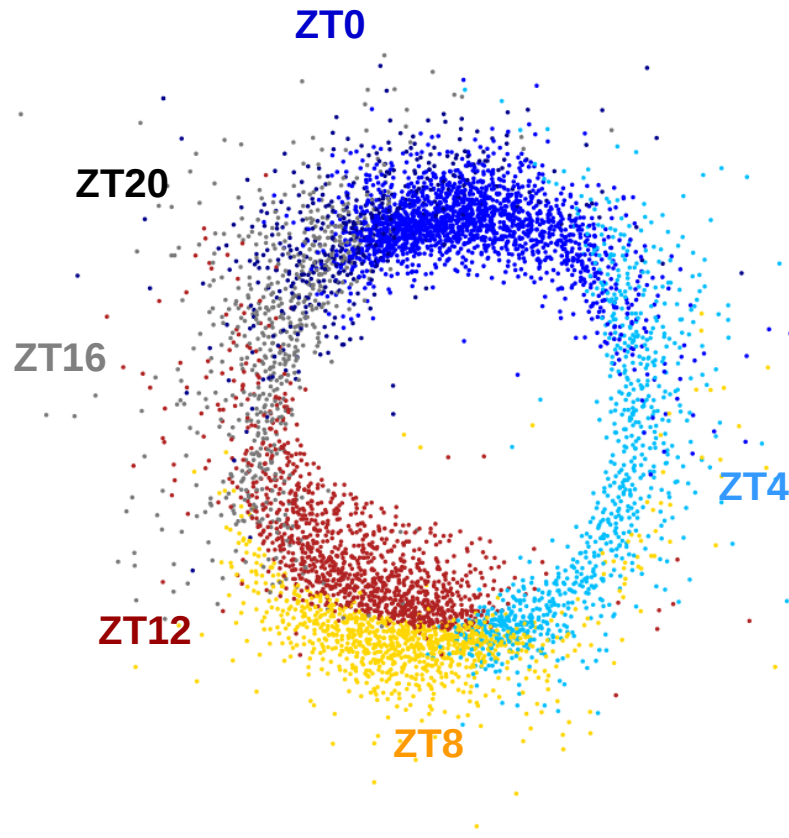


In degree 3  
Number of regulators

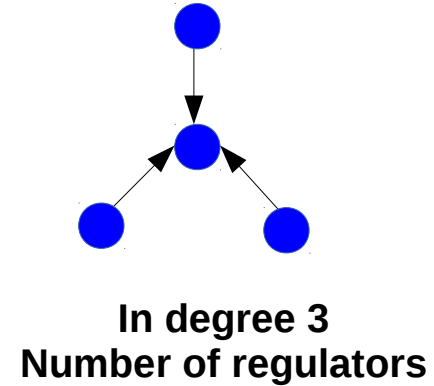
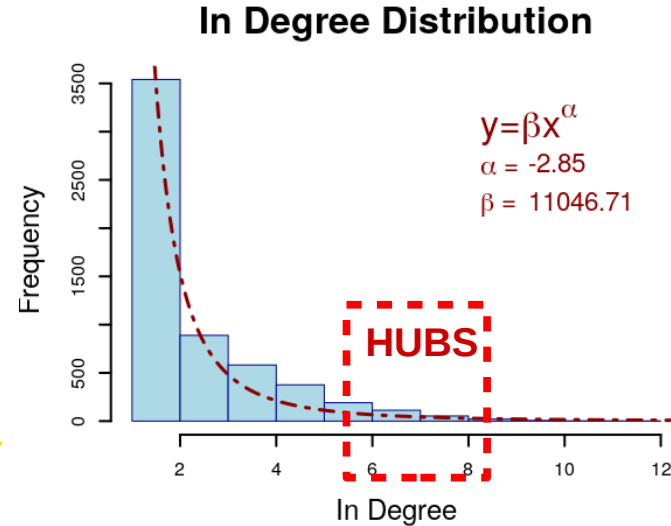
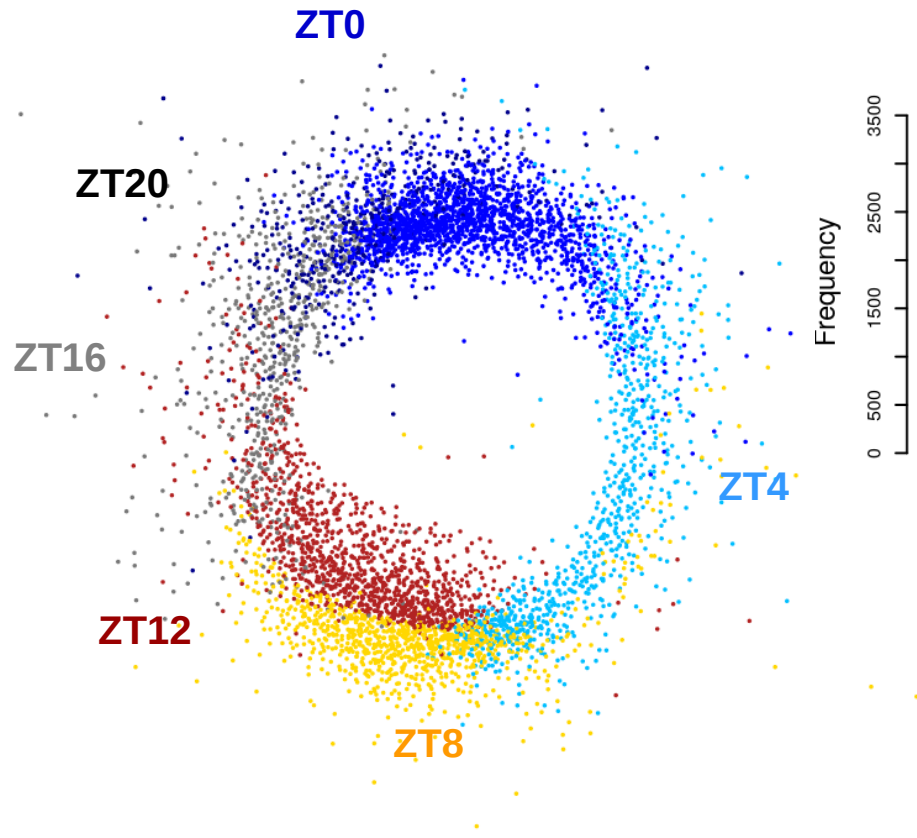
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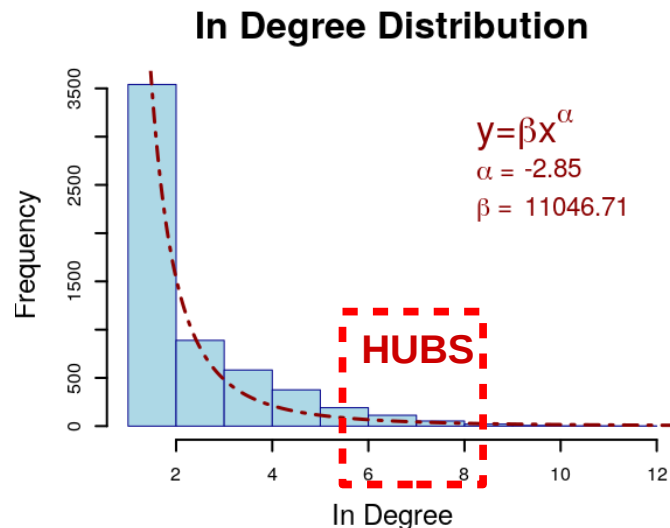
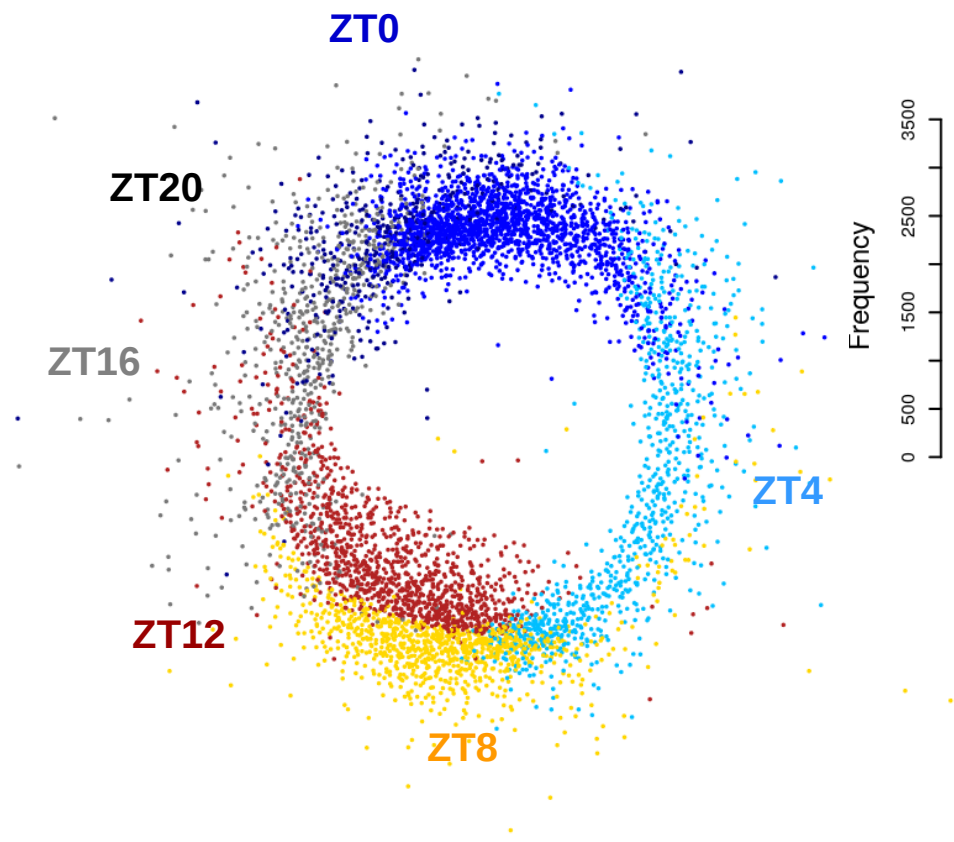
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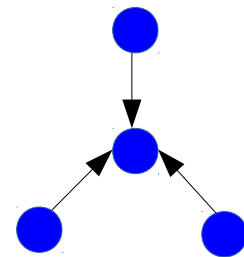
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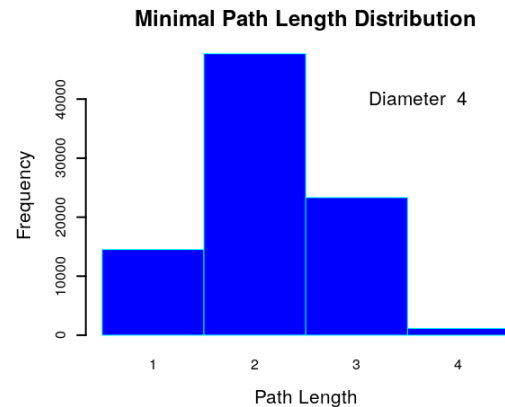
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An ultra-small world network

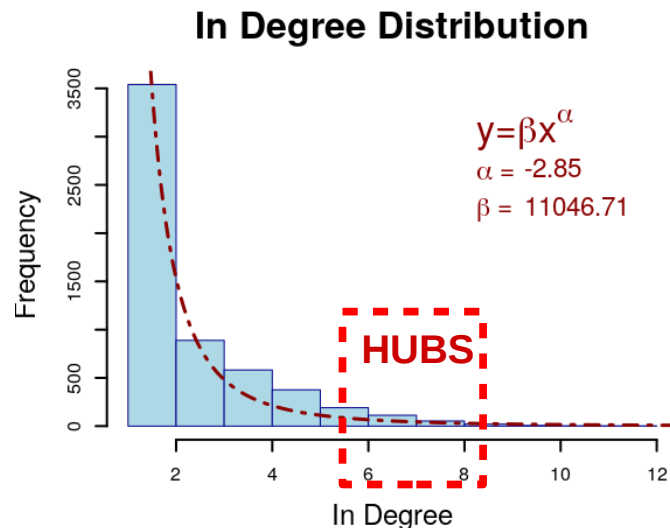
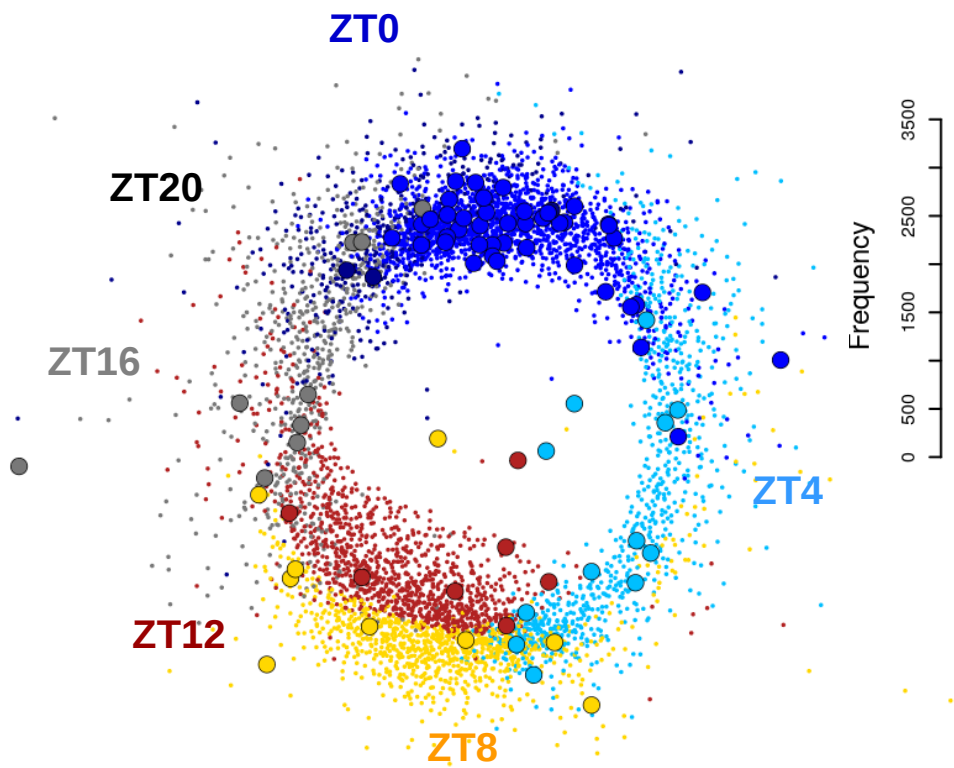


**In degree 3  
Number of regulators**

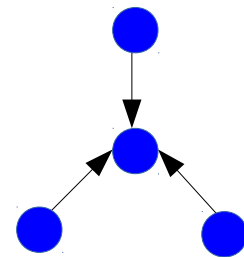




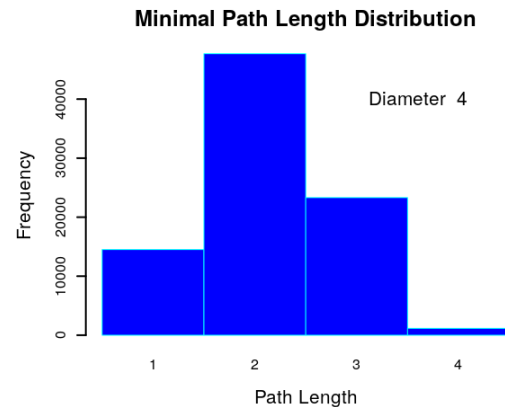
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An ultra-small world network



**In degree 3  
Number of regulators**



Hubs genes significantly enriched in genes peaking at the dark/light transition (p-value =  $1.16 \times 10^{-8}$ )



# ATTRACTOR enables researchers to explore the expression profile, potential regulators and their binding sites of individual genes

**Target gene**

AT1G22770 - GI

**Select Transcription Factors:**

☐ CCA1 ☐ LHY ☐ TOC1

☐ PRR5 ☐ PRR7 ☐ PRR9

☐ PHYA ☐ PHYB ☐ CRY2

☐ FHY1 ☐ LUX ☐ PIF3

☐ PIF4 ☐ PIF5 ☐ ELF4

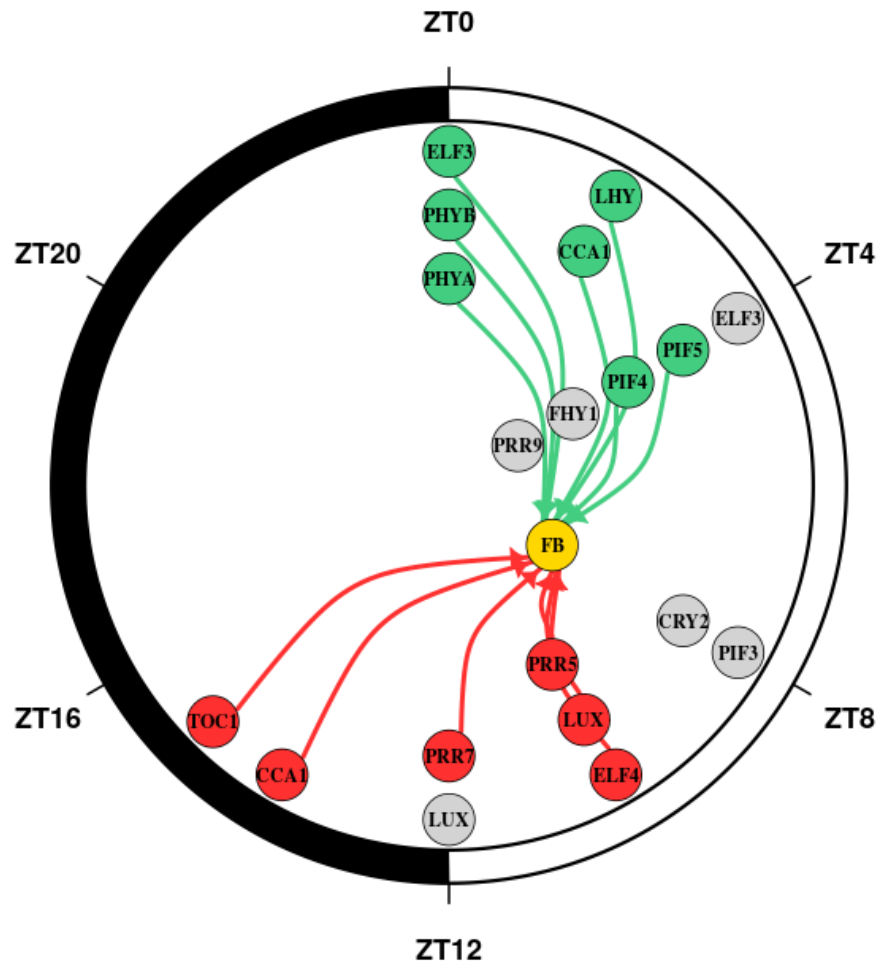
☐ ELF3

☒ Select All

**Show interactions between TFs?**

No

GO



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Target gene

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☐ CCA1 ☐ LHY ☐ TOC1

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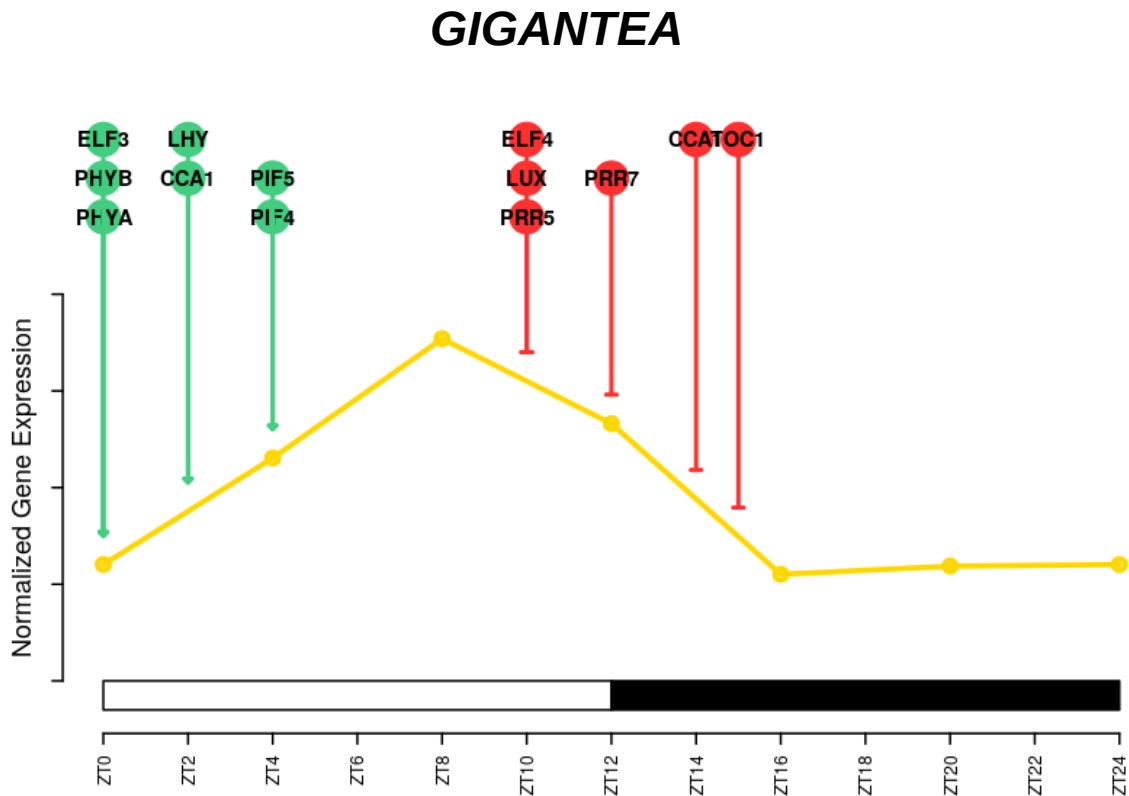
☐ ELF3

☒ Select All

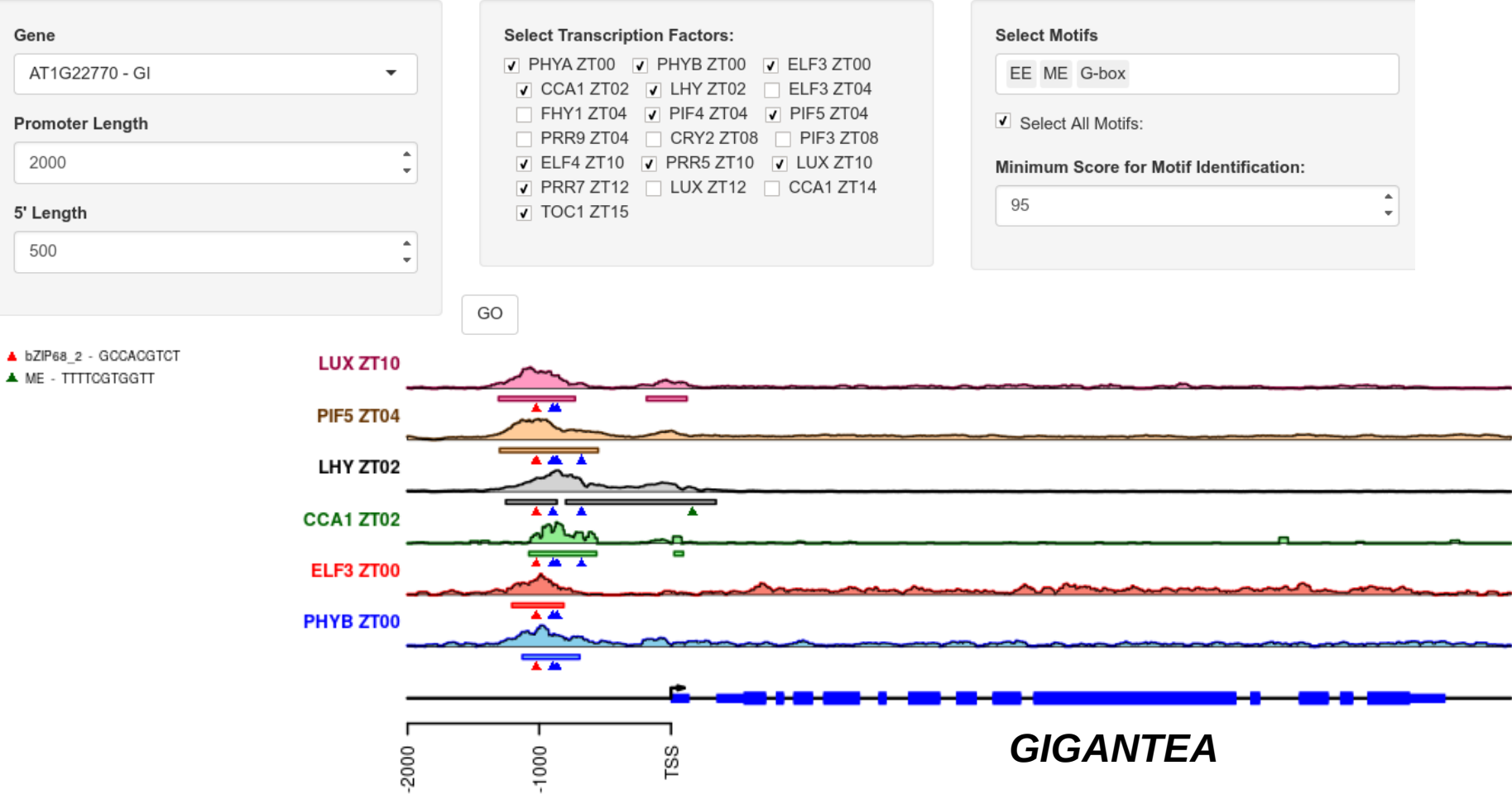
Show interactions between TFs?

No

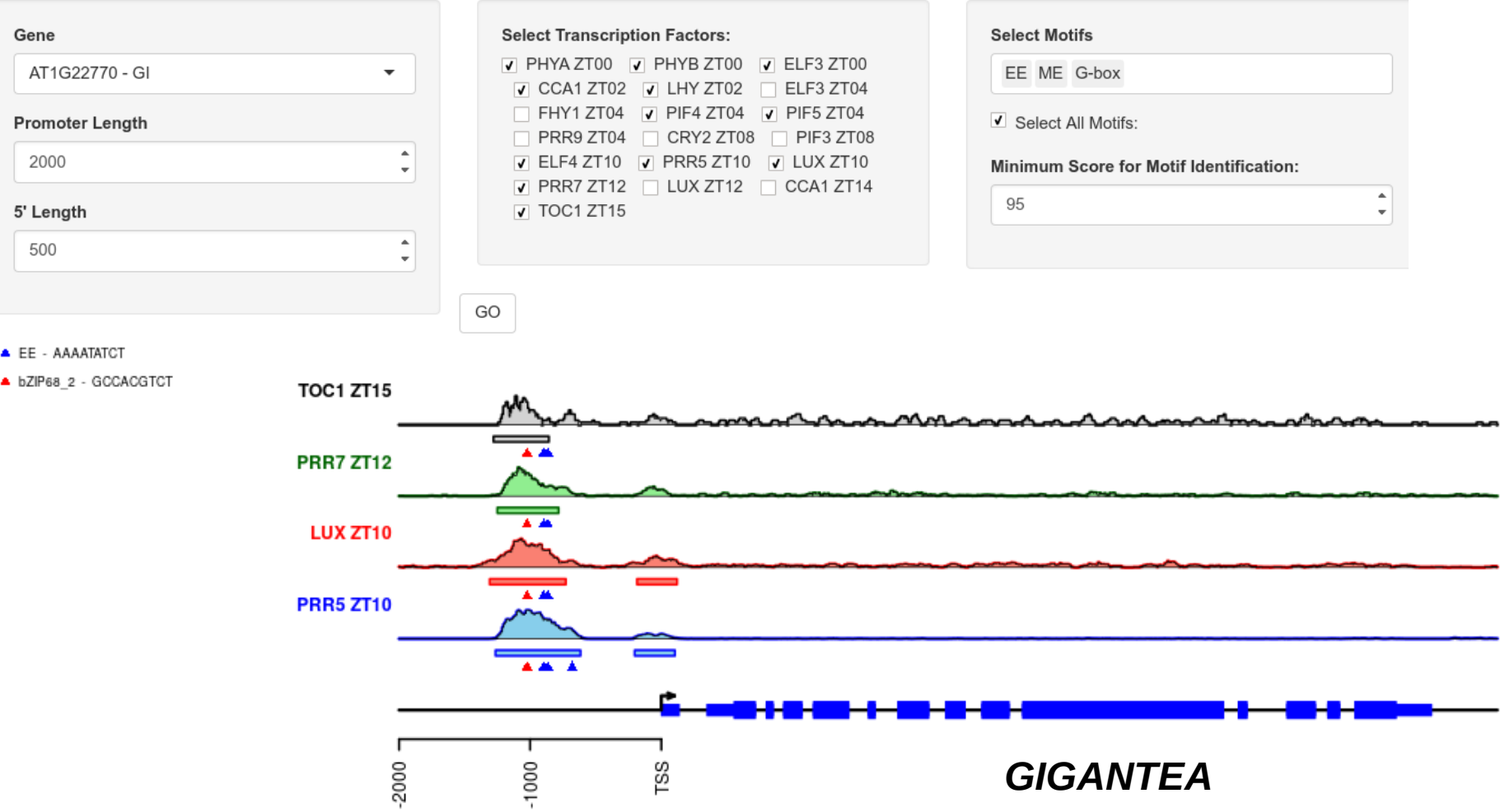
GO



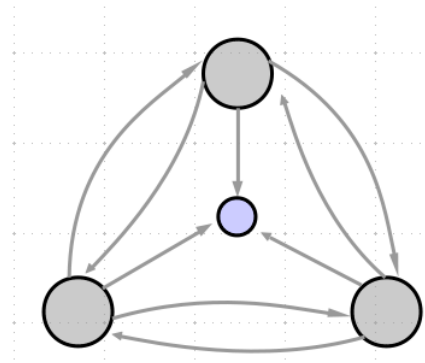
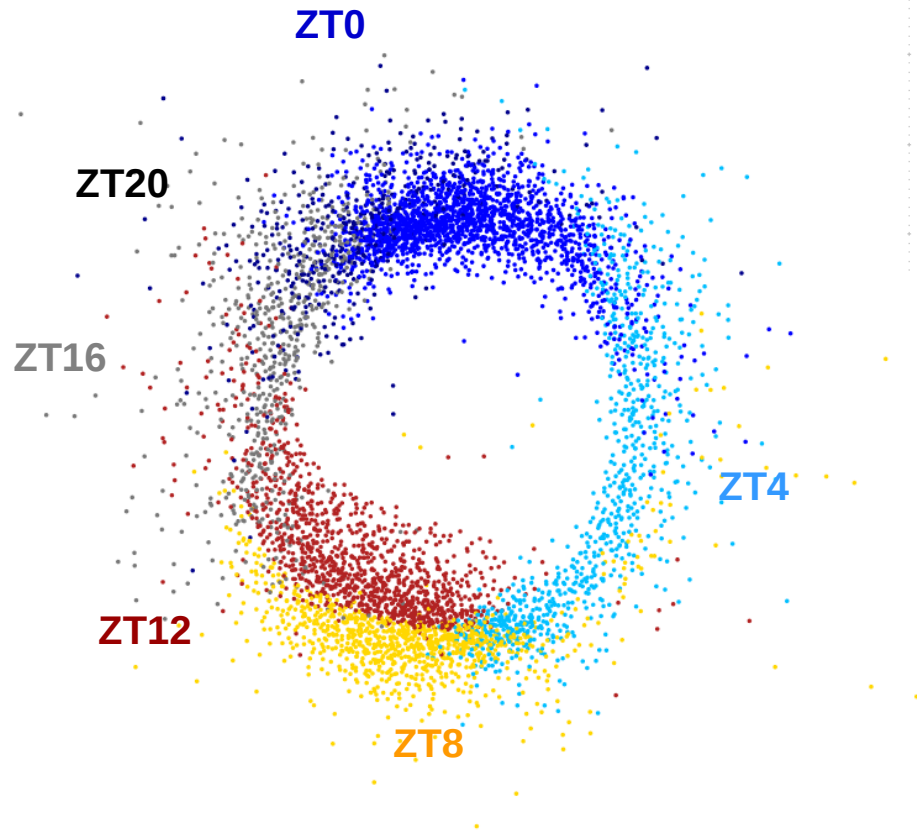
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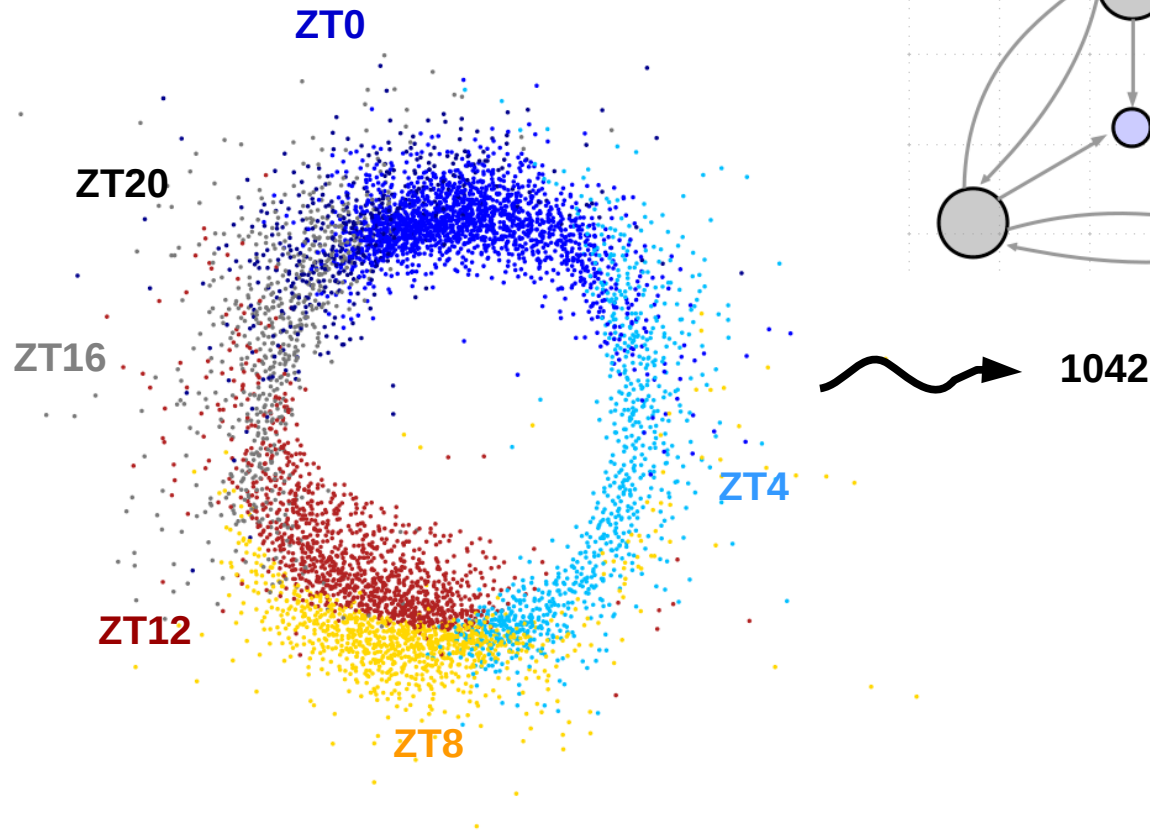
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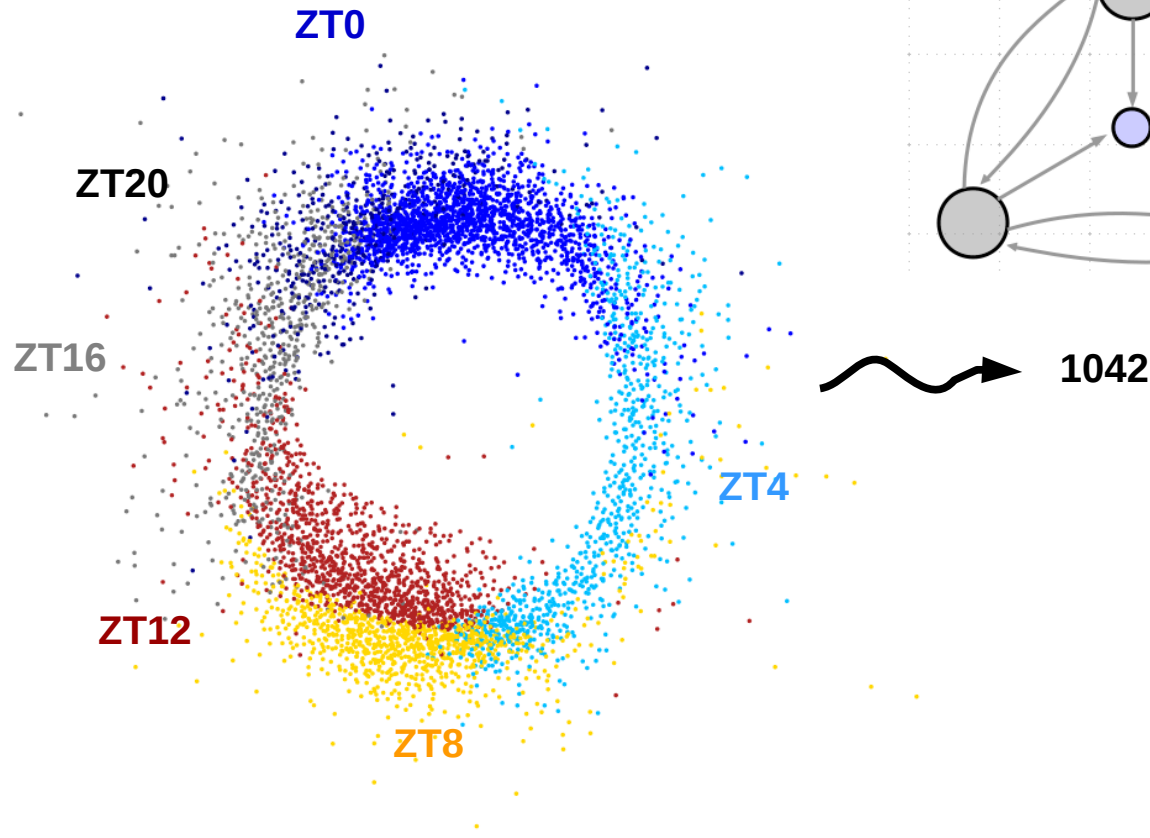
# ATTRACTOR is constituted by non-random subgraphs called network motives



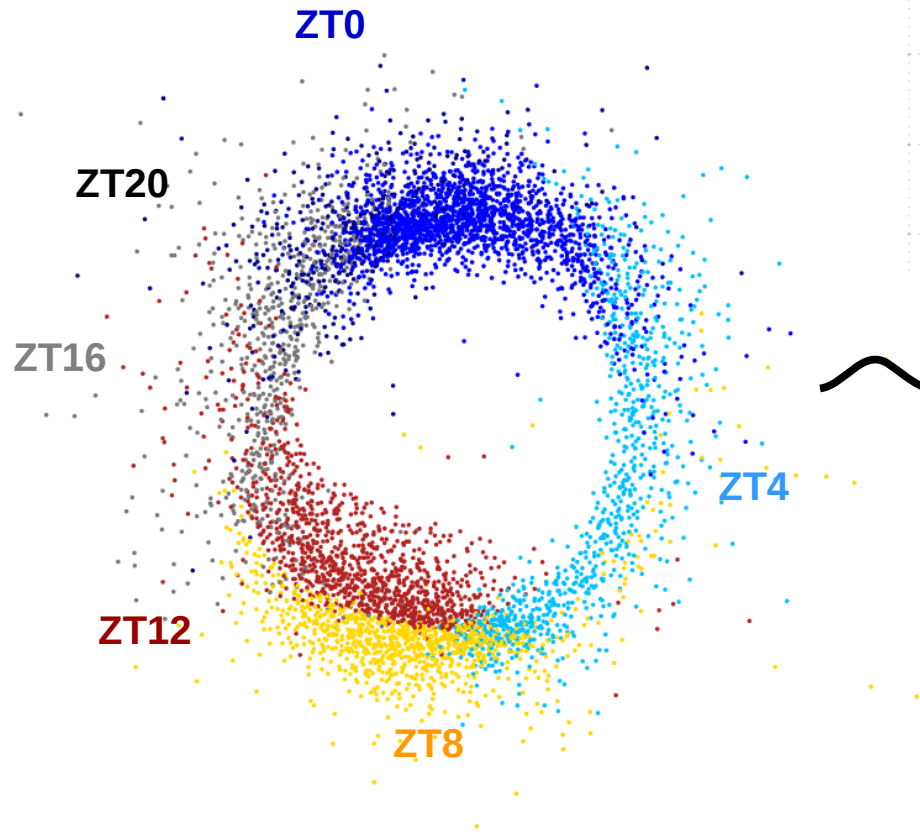
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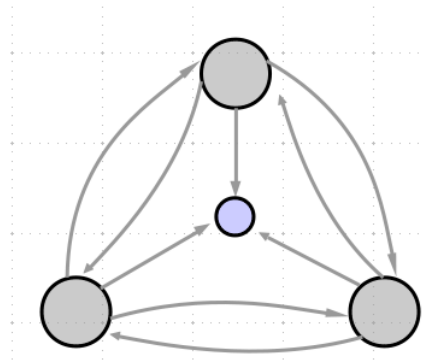
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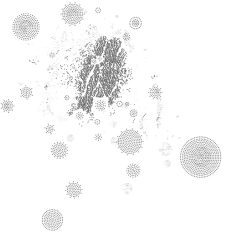
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1042

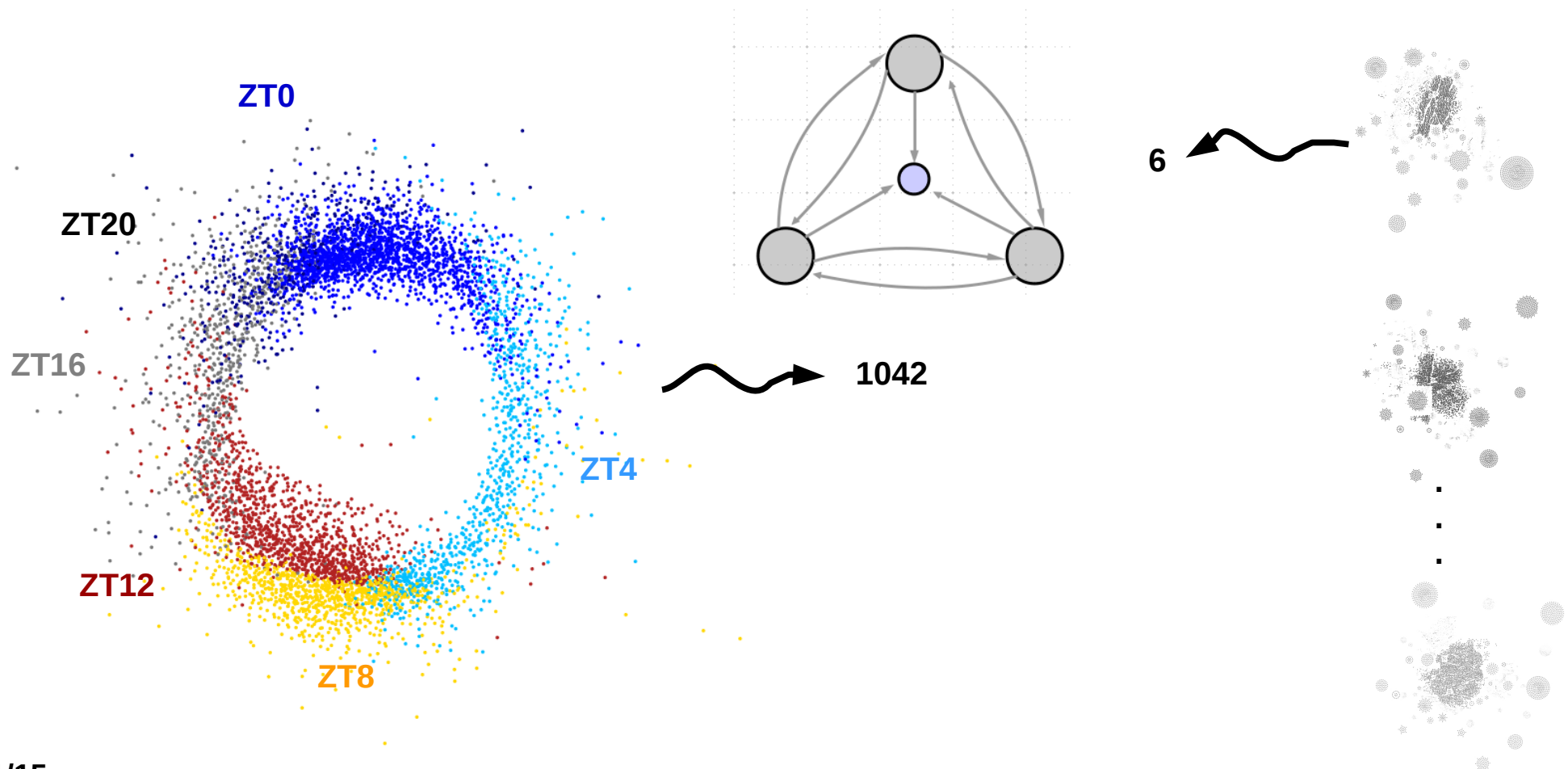


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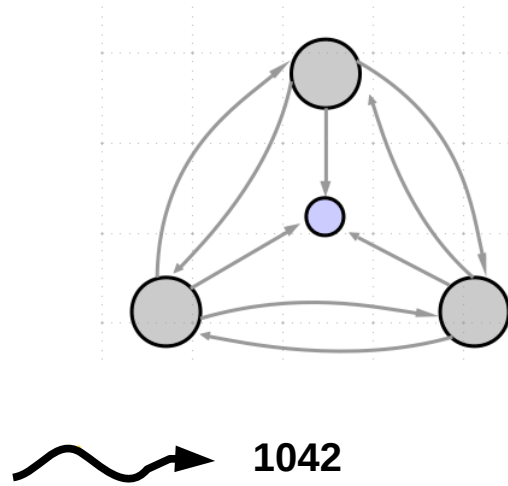
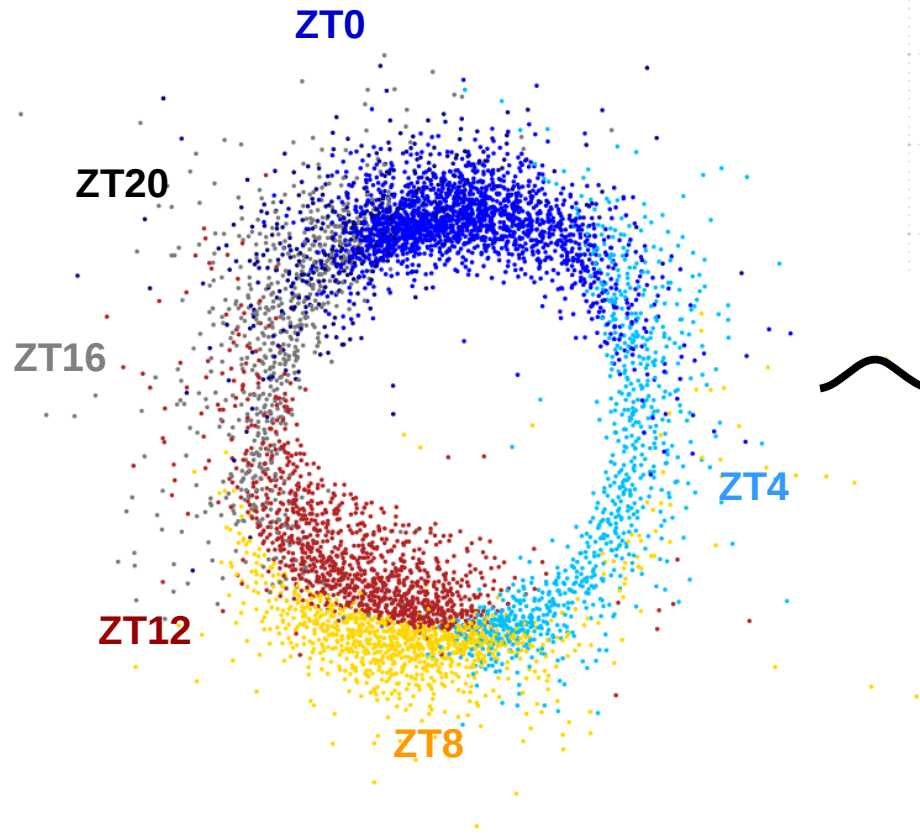




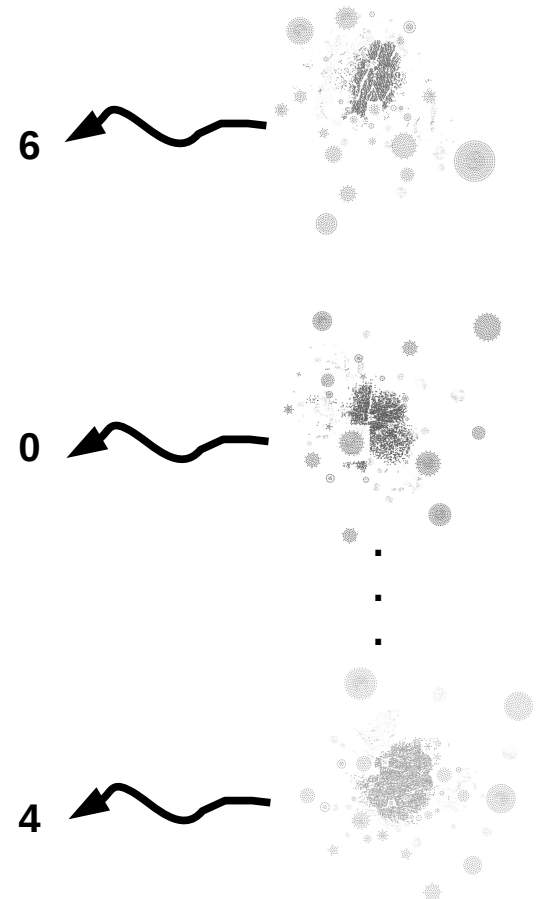
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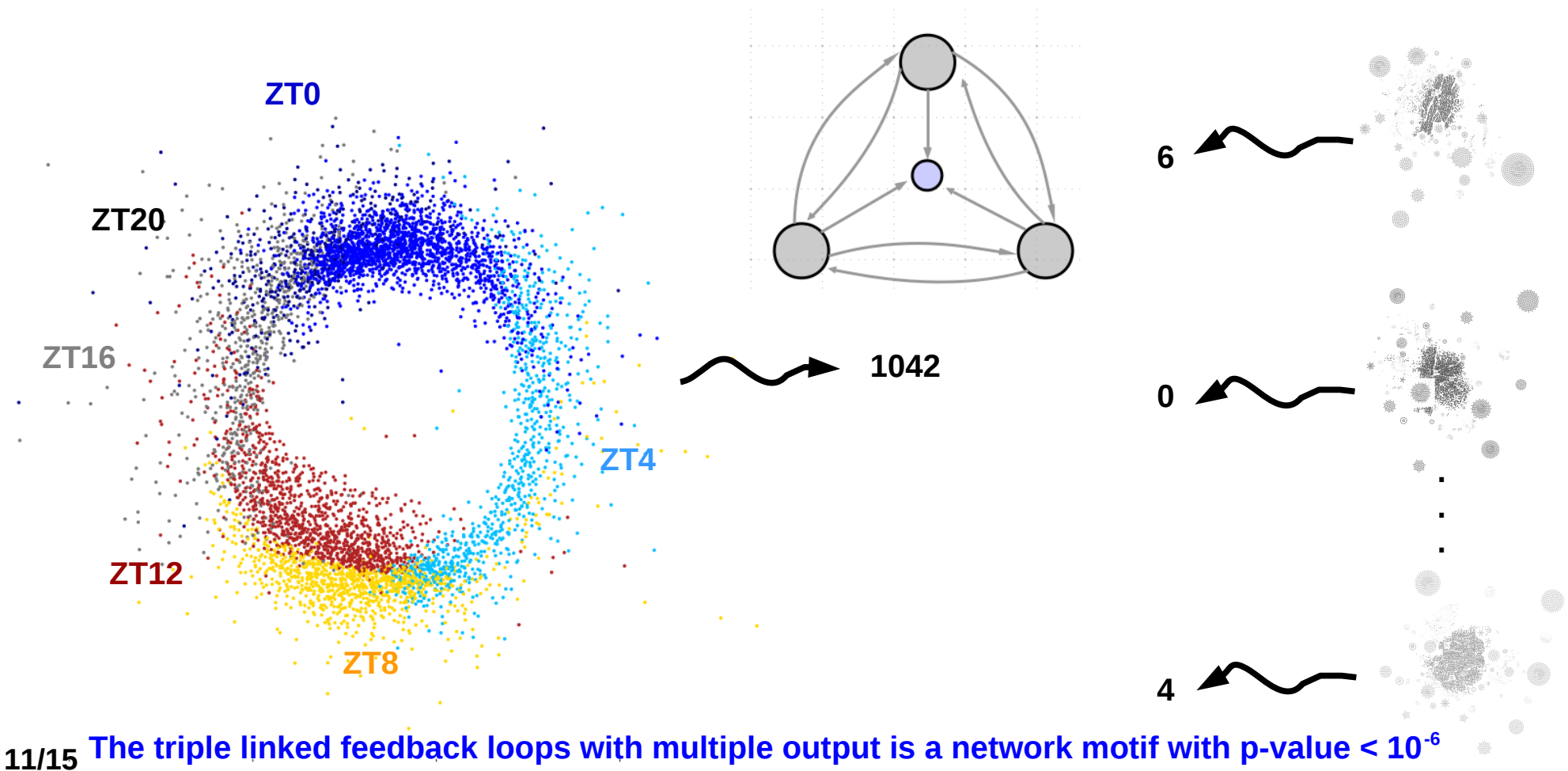
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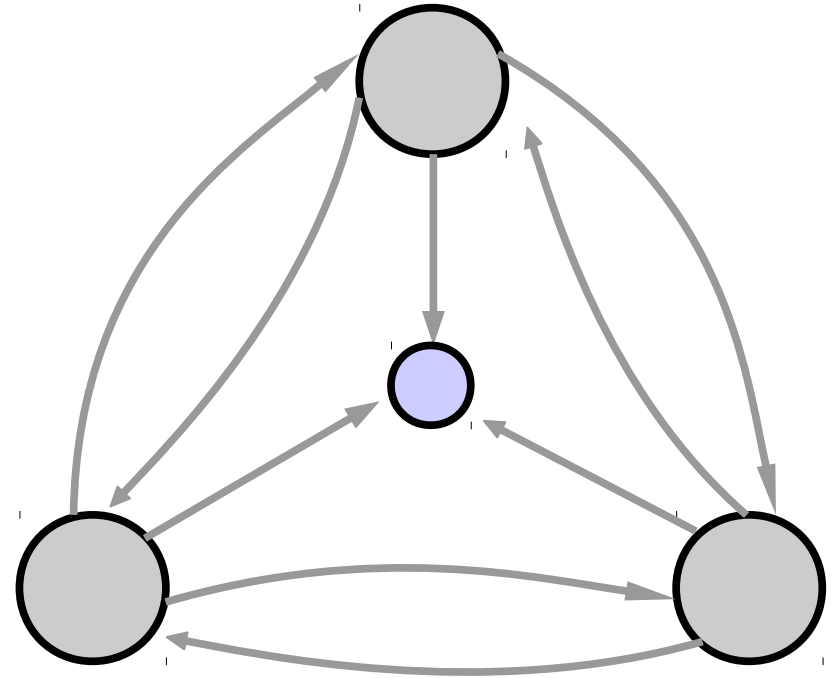
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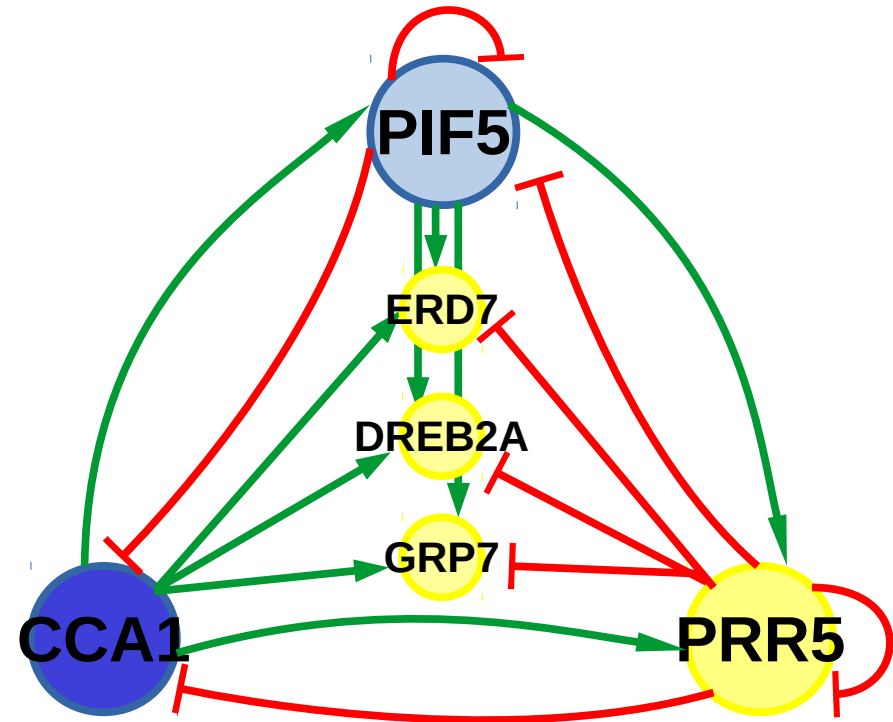
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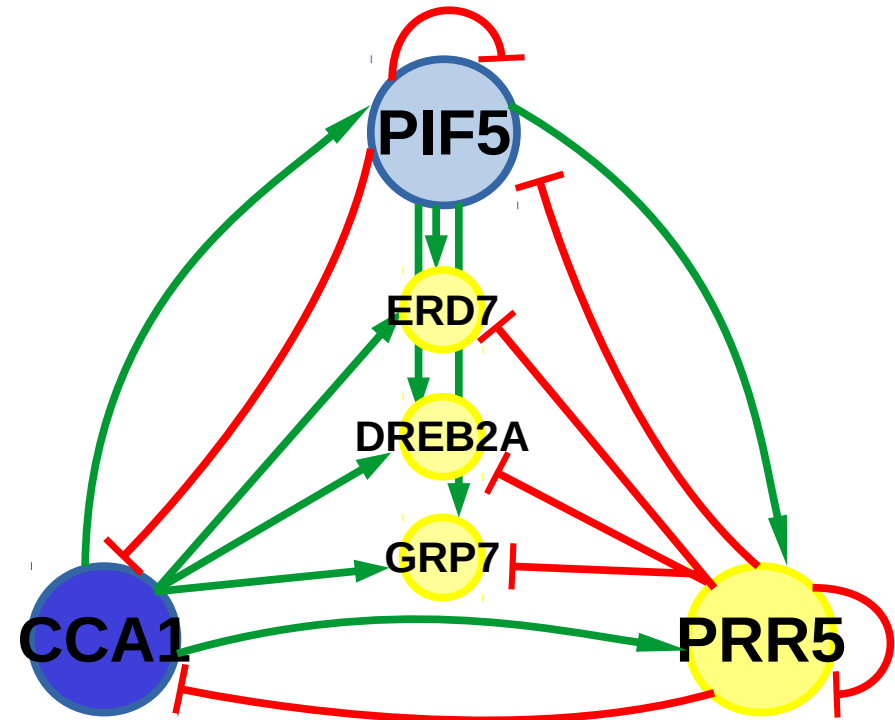
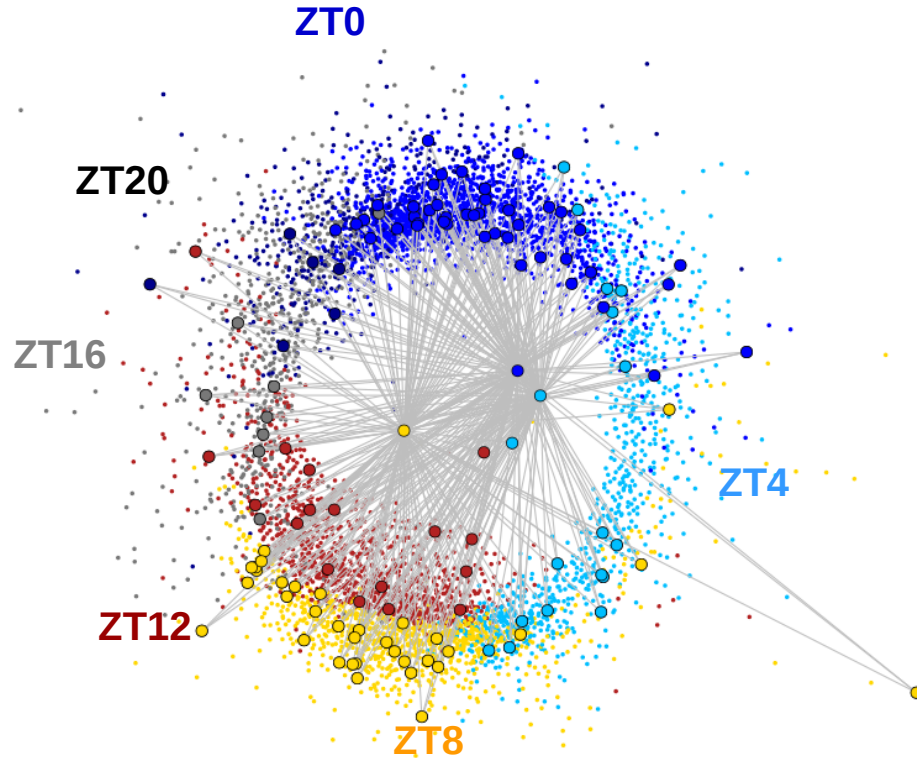
**PIFs establish multiple output linked feedback loops with PRRs and CCA1/LHY producing specific expression patterns involved in drought response**



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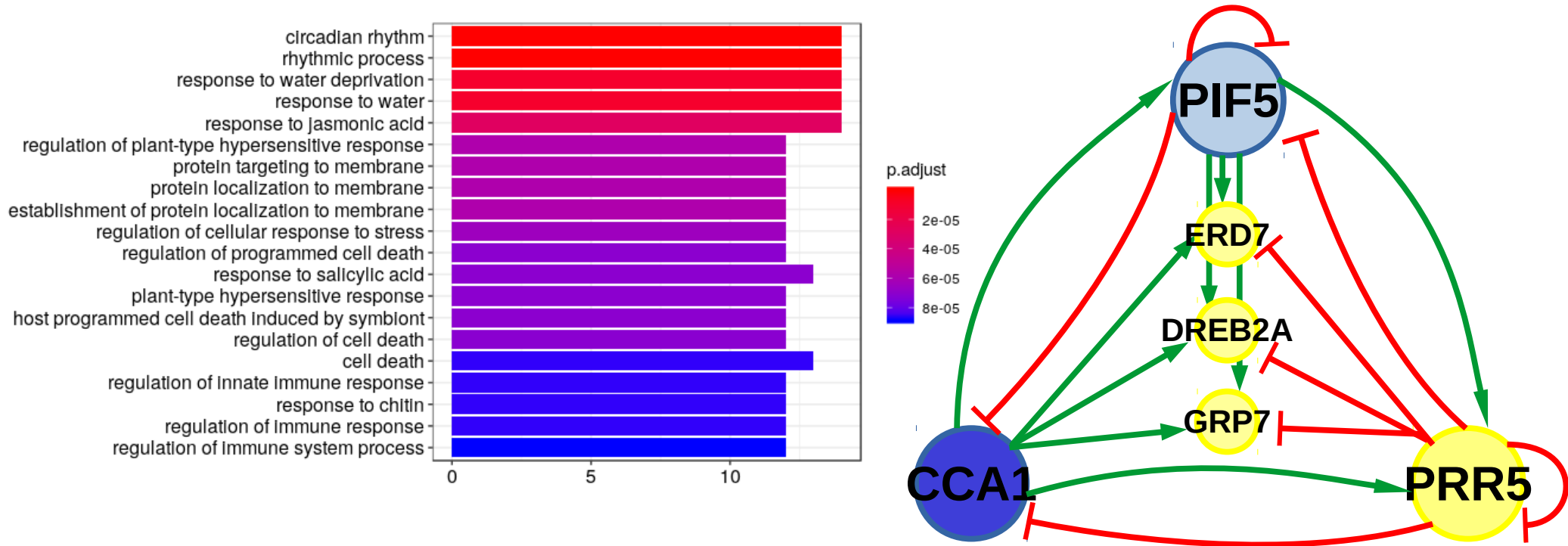


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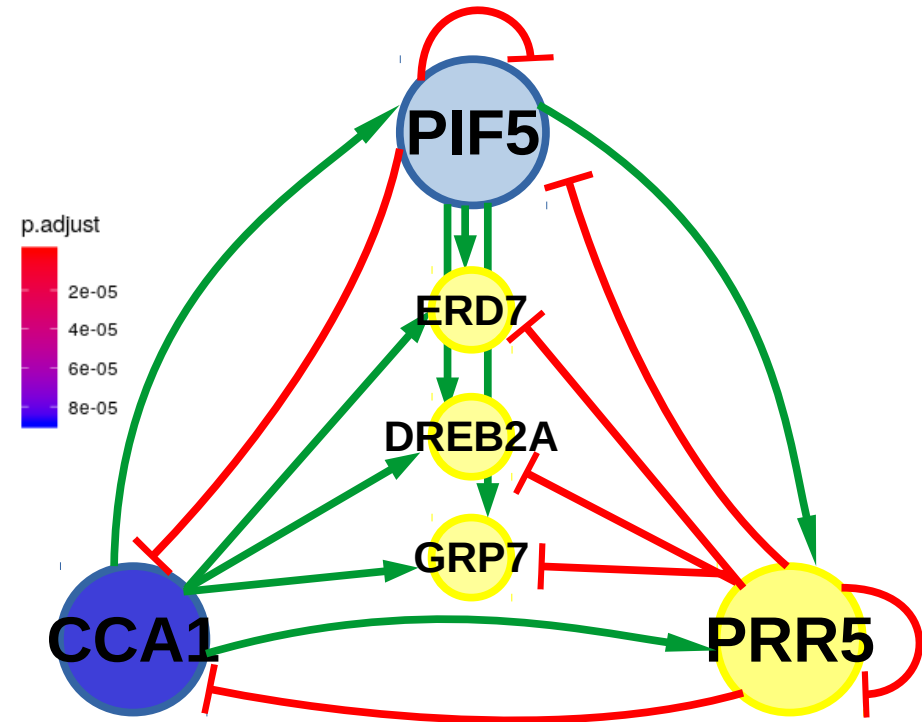
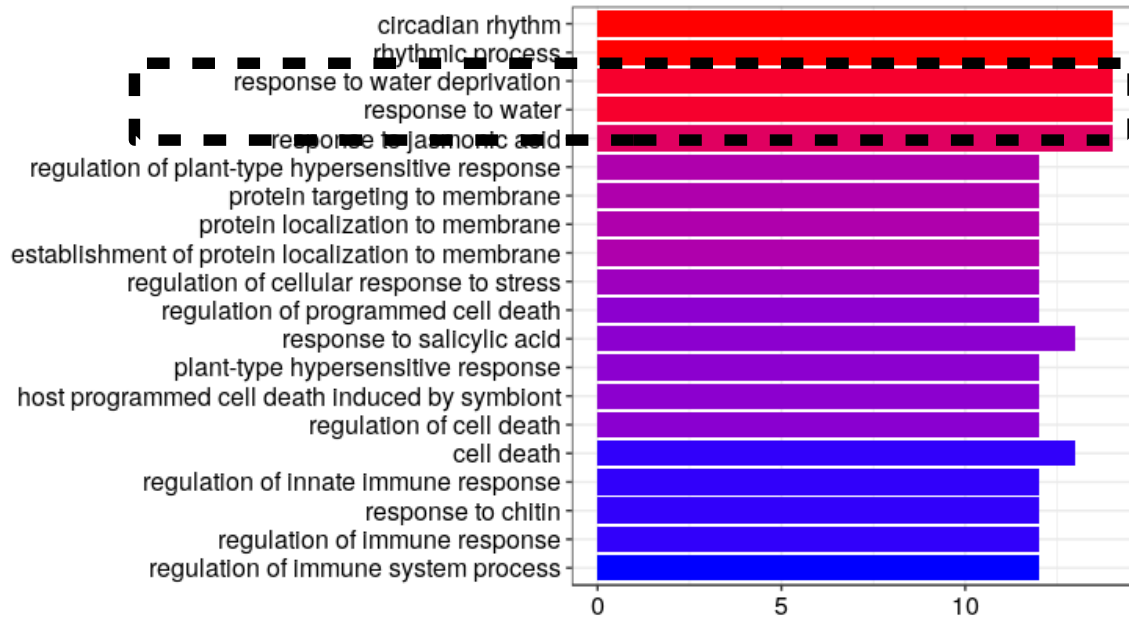


The common targets are not uniformly distributed but they are enriched in genes peaking at ZT8.

# PIFs establish multiple output linked feedback loops with PRRs and CCA1/LHY producing specific expression patterns involved in drought response

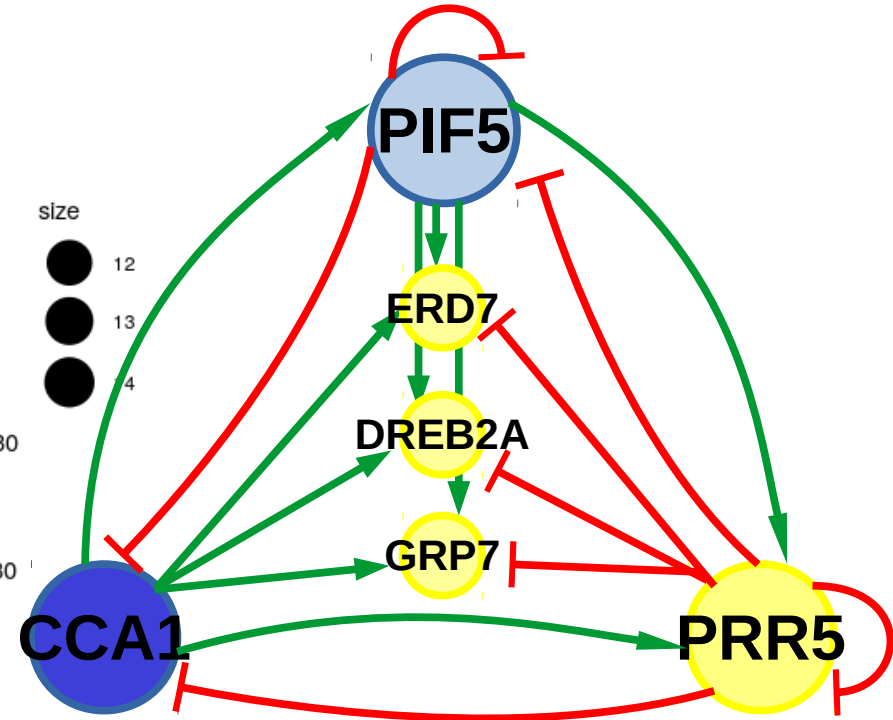
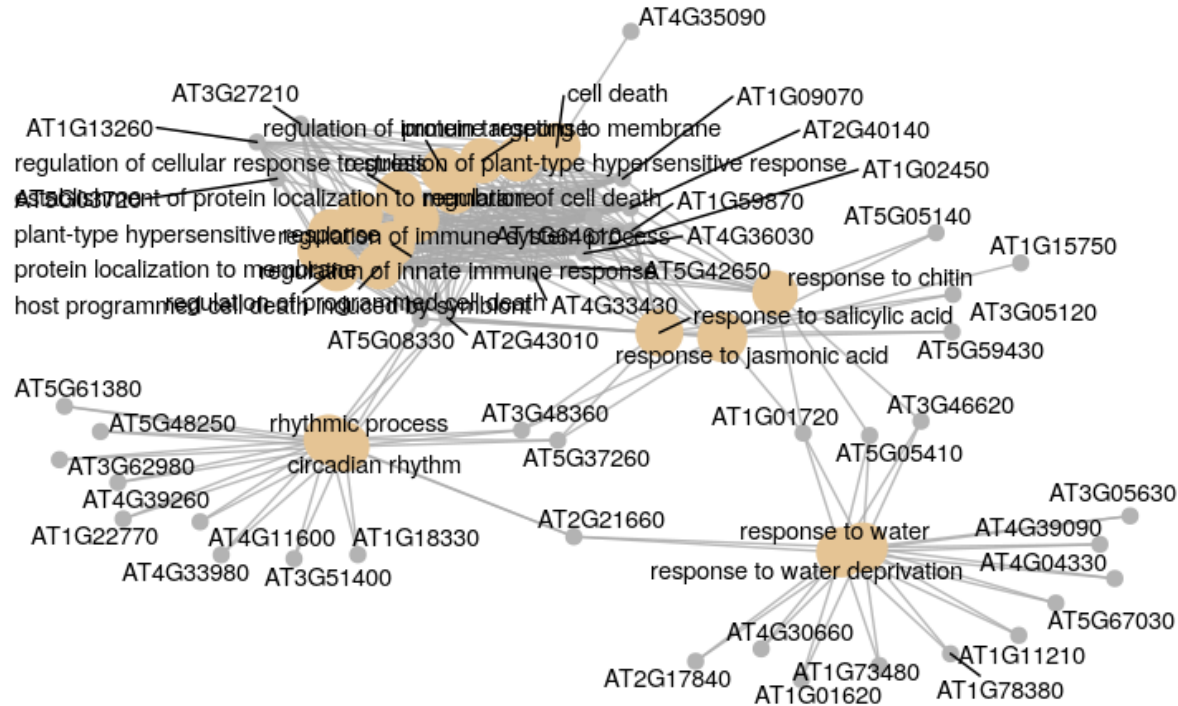


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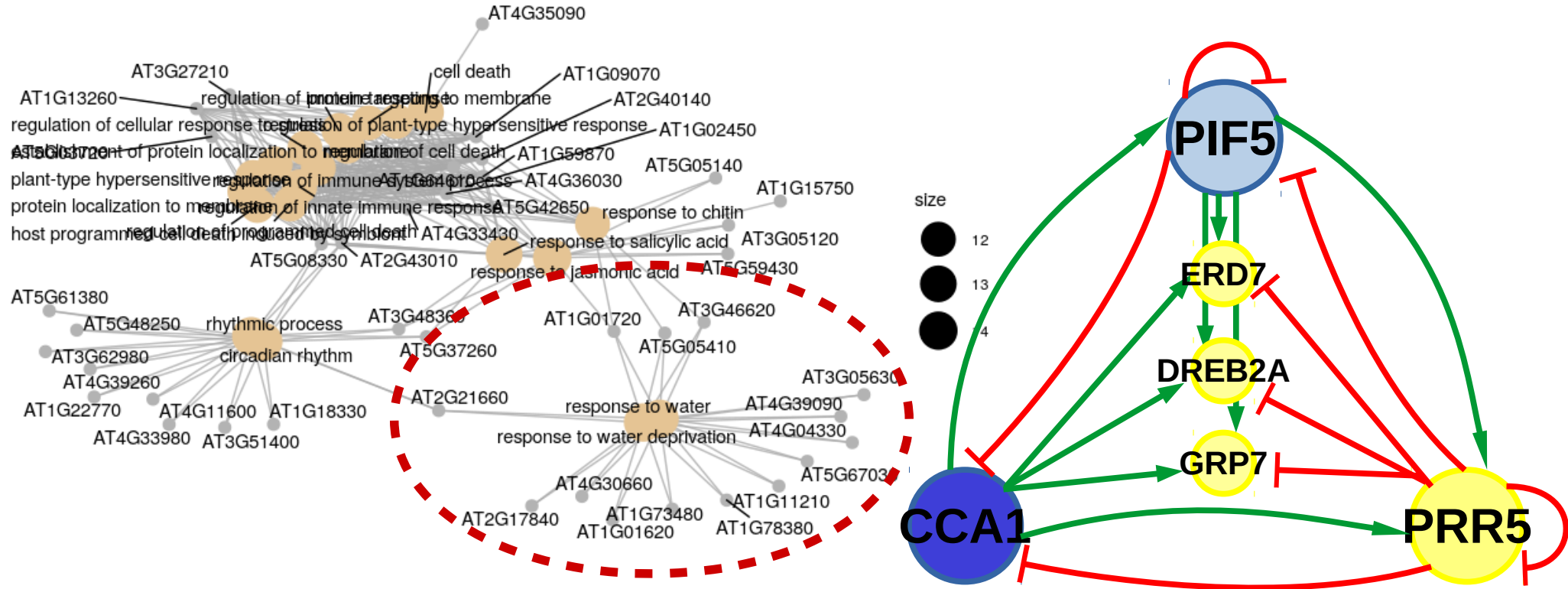




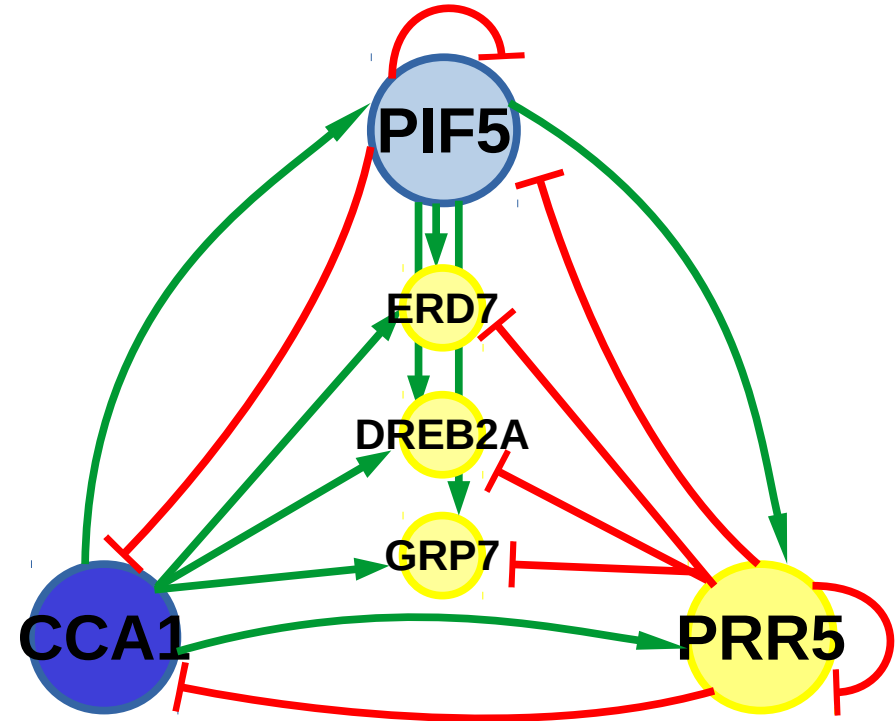
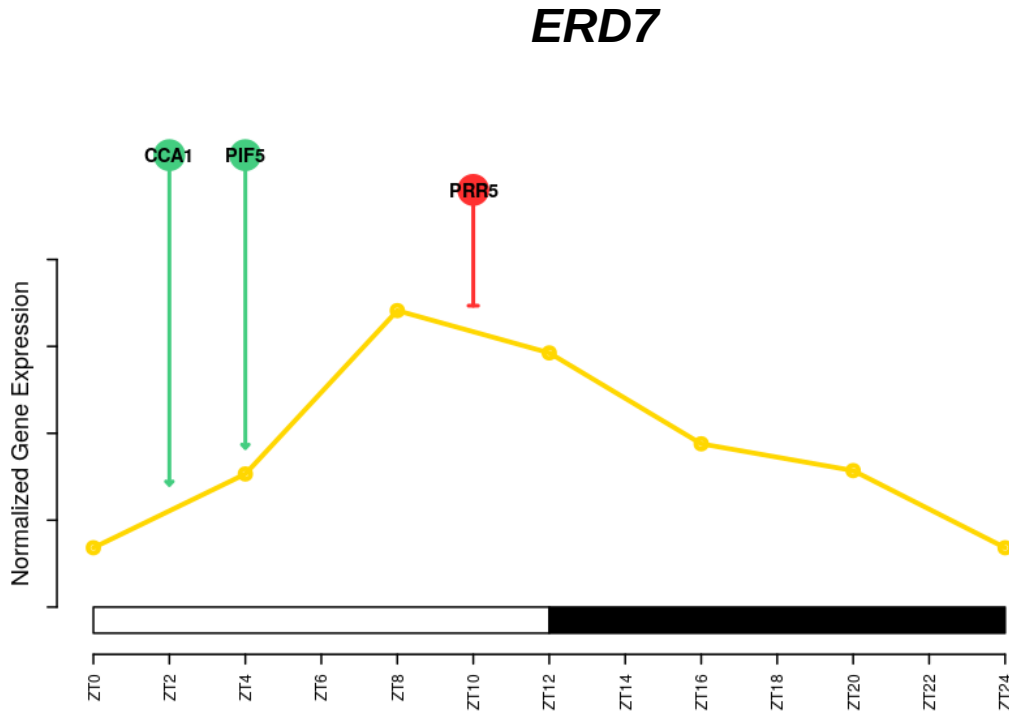
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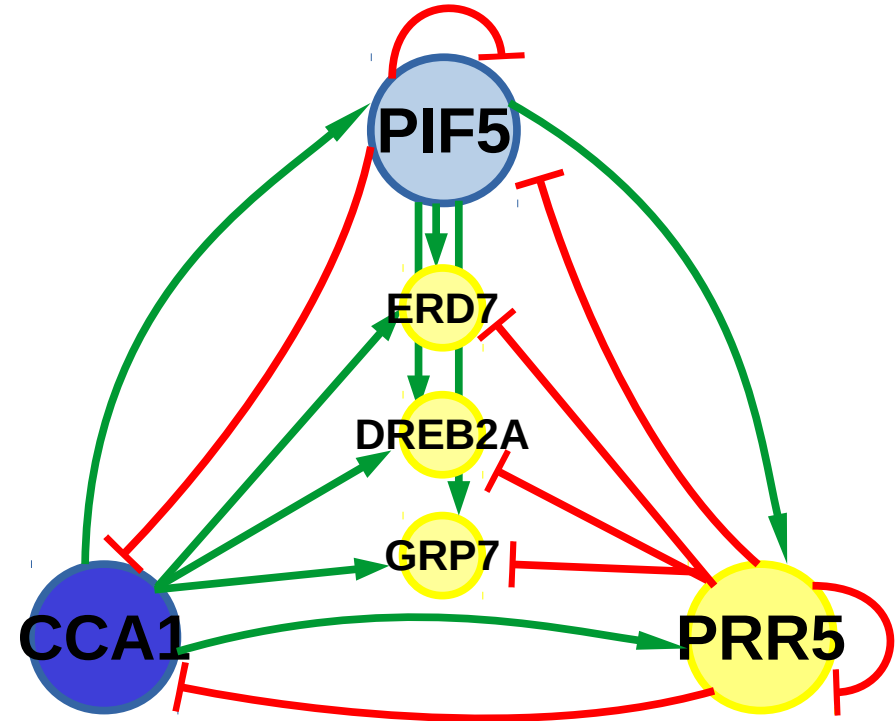
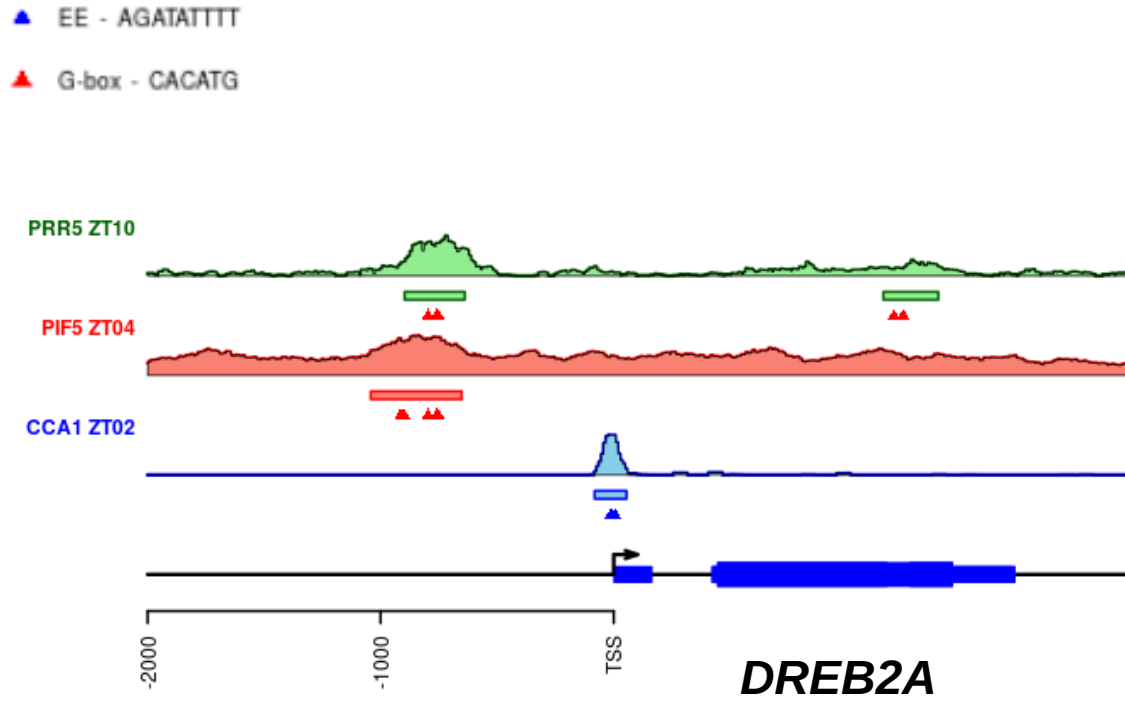
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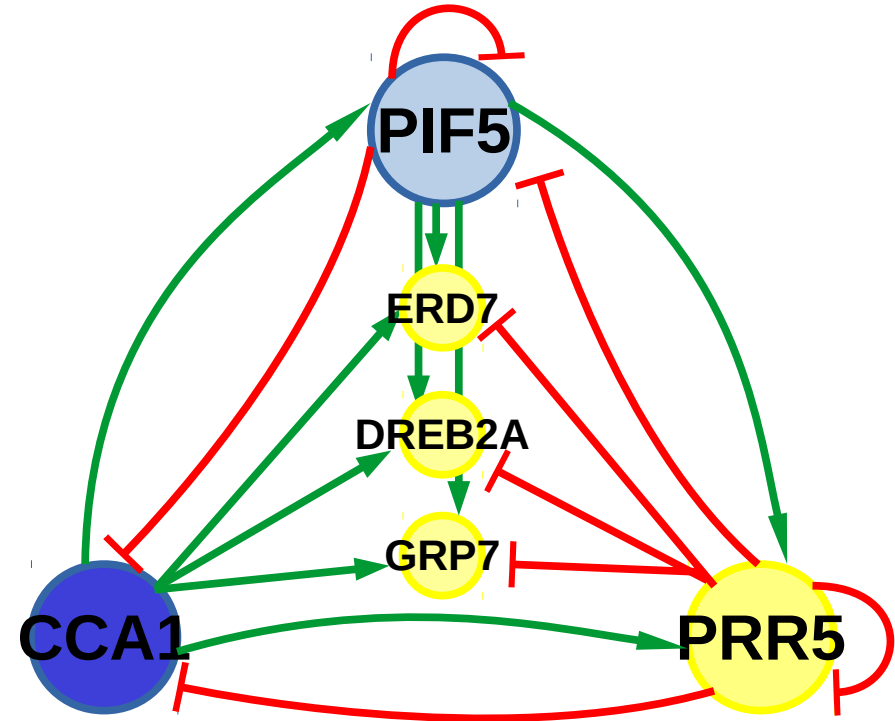
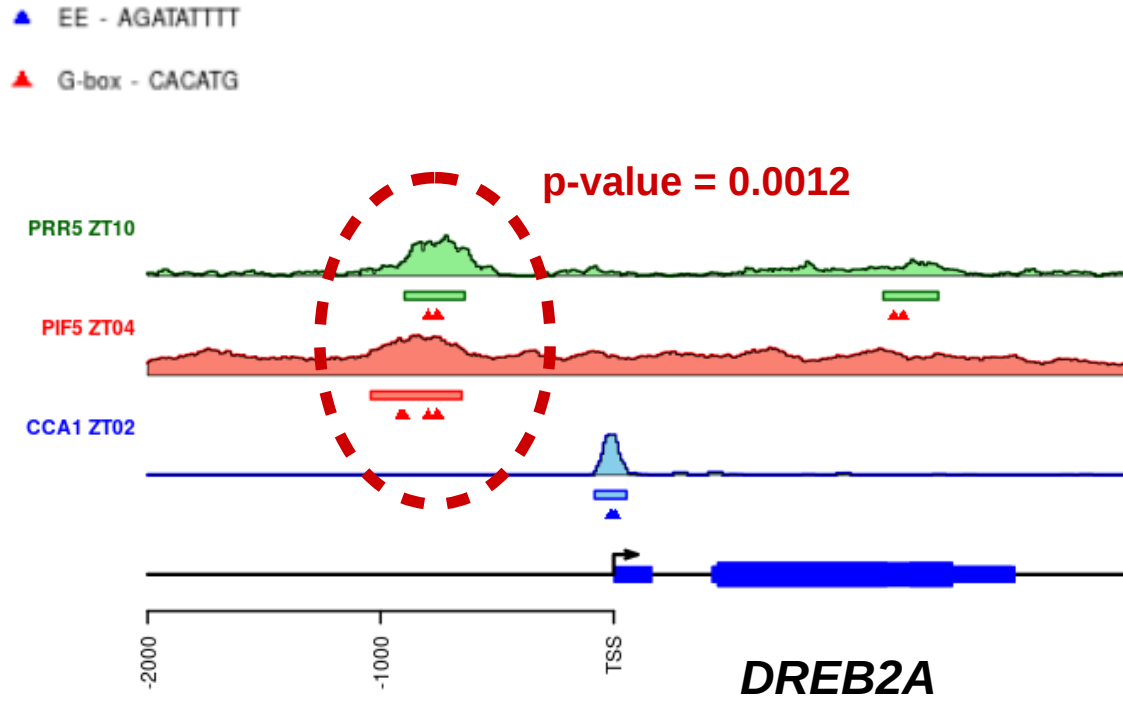
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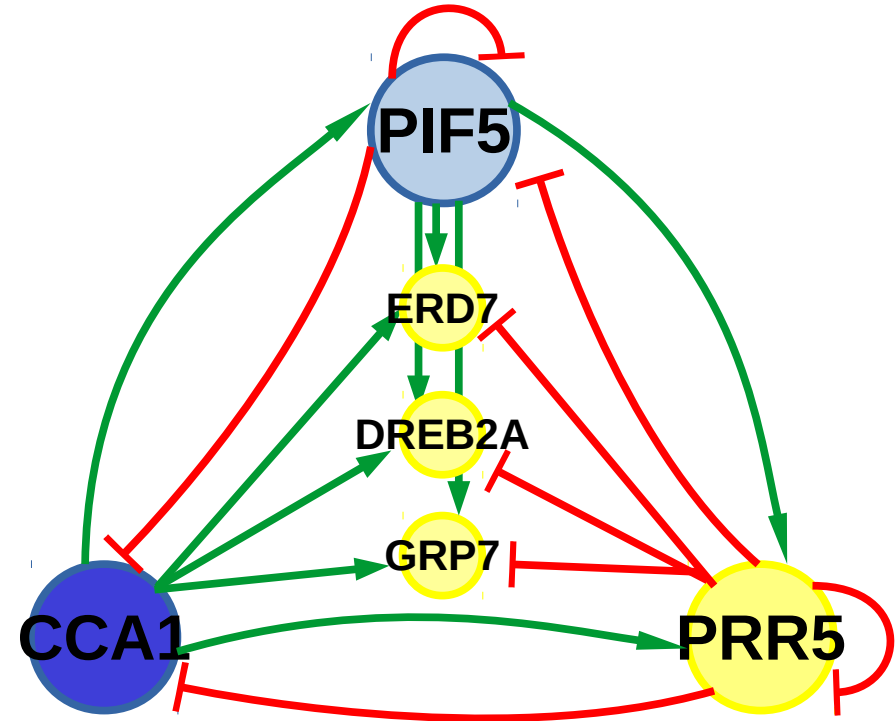
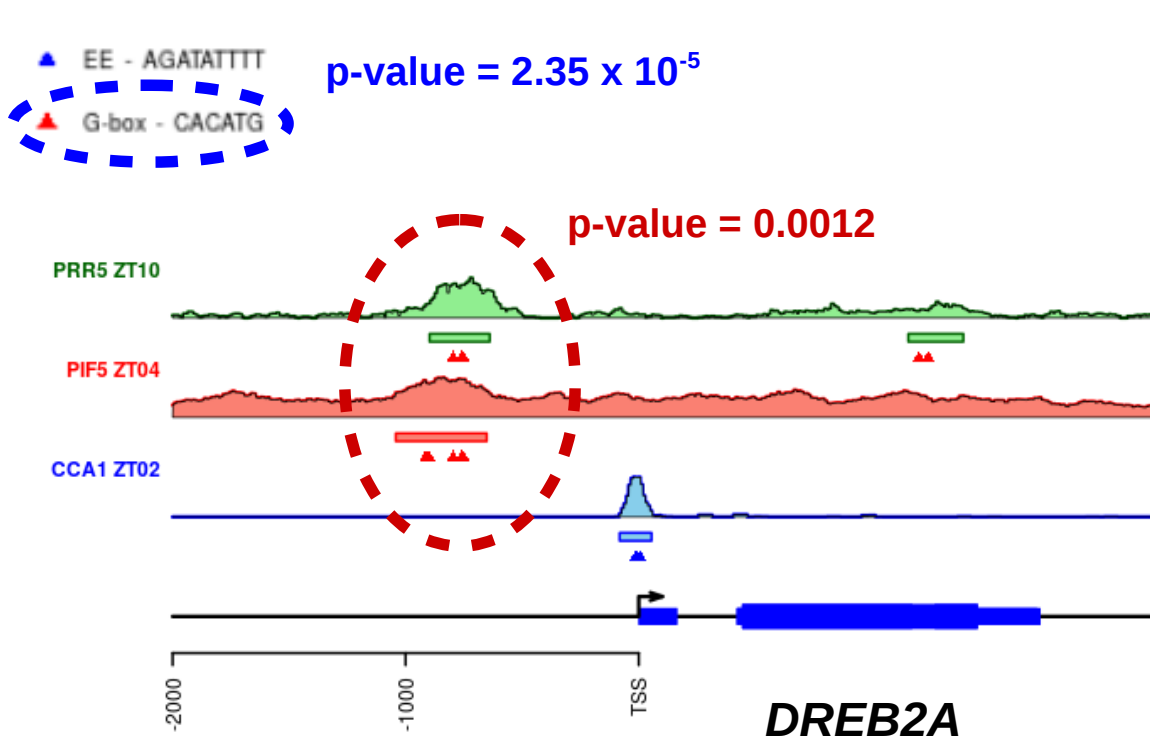
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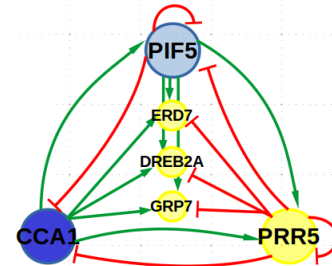
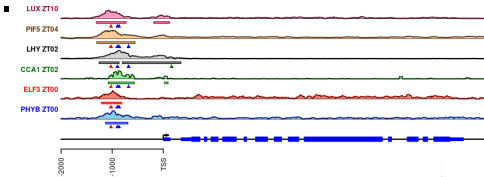
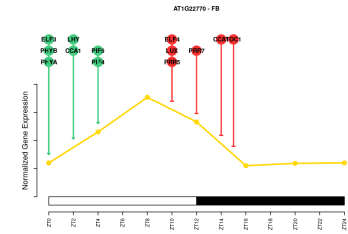
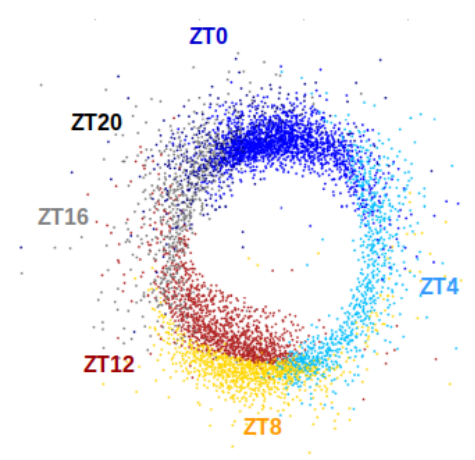


# PIFs establish multiple output linked feedback loops with PRRs and CCA1/LHY producing specific expression patterns involved in drought response



# Summary

- **ATTRACTOR** is a **transcriptional network** capturing the synergistic regulation exerted by the circadian clock and light signaling that unveils a system simultaneously **robust to random perturbations** and **sensitive to directed tuning**.
- **ATTRACTOR** is a web based tool that **enables researchers to explore** the expression profile, regulators and their binding sites of **individual genes** as well as the **coordinated regulation** of multiple transcription factors over common target genes.
- **Network motive** analysis reveals that PIFs, PRRs and CCA1/LHY form linked **controlling response to drought**.





# Acknowledgments



**Plant Development Unit - IBVF**  
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## Members:

**Myriam Calonje**  
**Federico Valverde**  
**Jose M. Romero**  
**Teresa Ruiz**  
**Gloria Serrano**  
**Isabel Jiménez**

**Pedro de los Reyes**  
**Ana Belén Romero**

