Regulatory response of maize to water deficit mediated by cis-regulatory elements

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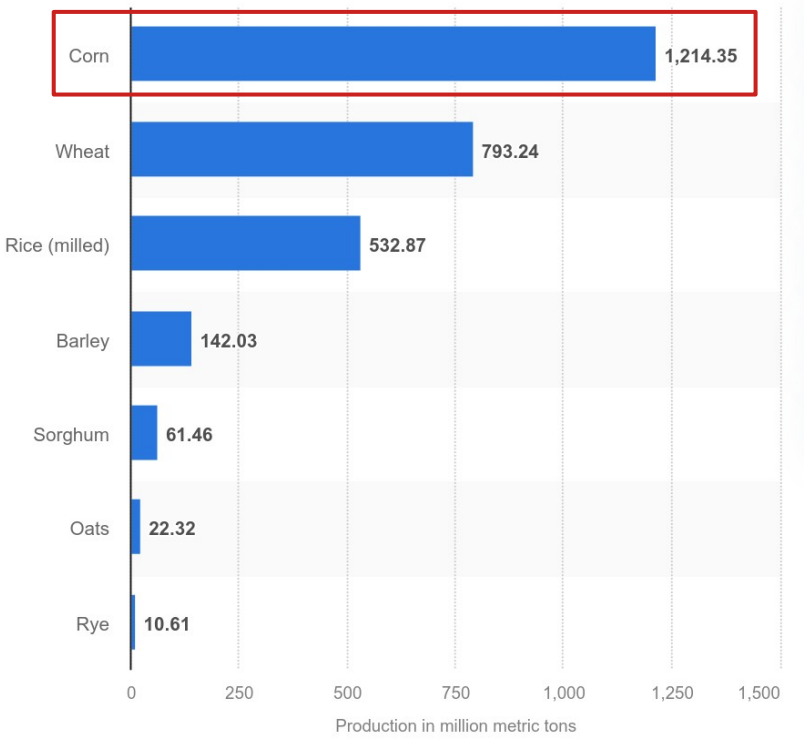
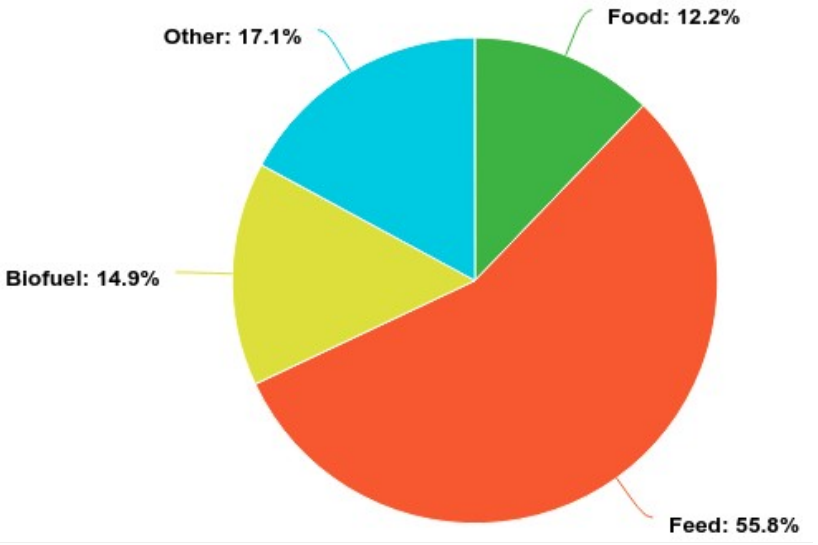
Maize, a widely cultivated crop

Worldwide production of grain in 2024/25



Statista 2025

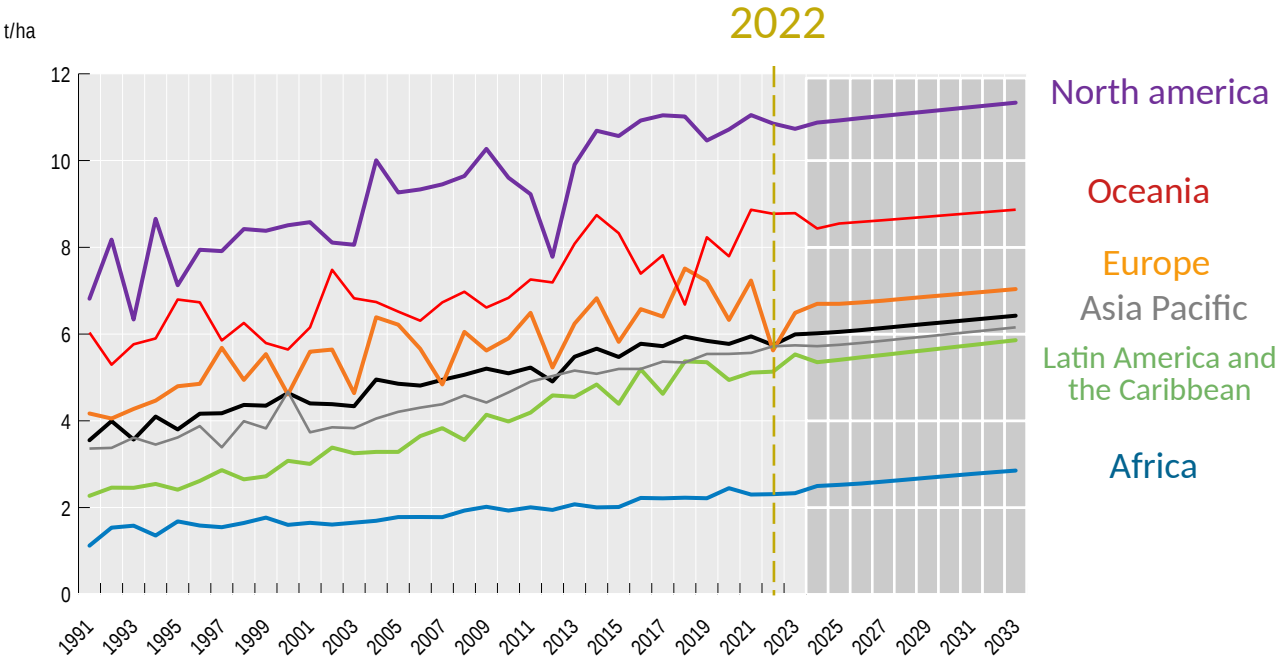
Global use of maize in 2023



OECD/FAO (2024), "OECD-FAO Agricultural Outlook"

Drought impact on yield

Worldwide maize production

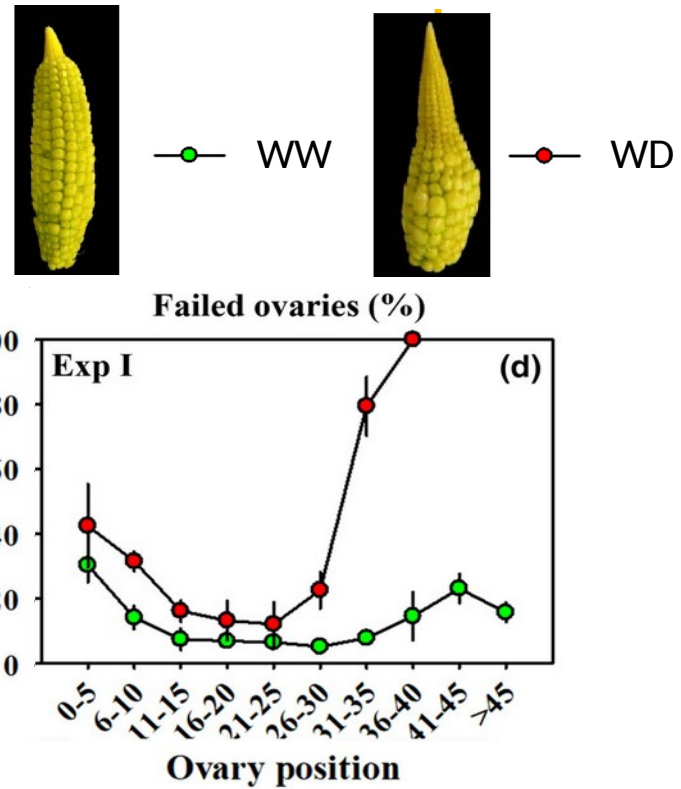


OECD/FAO (2024), "OECD-FAO Agricultural Outlook"

Maize field mid-August 2022

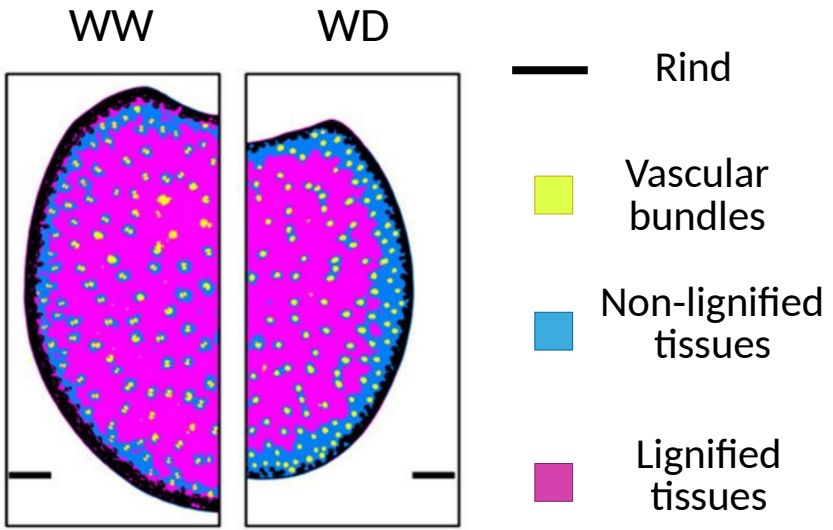
Various effects of the water deficit

Kernel abortion



Adapted from Li Y et al. Plant-Environment Interactions. 2024

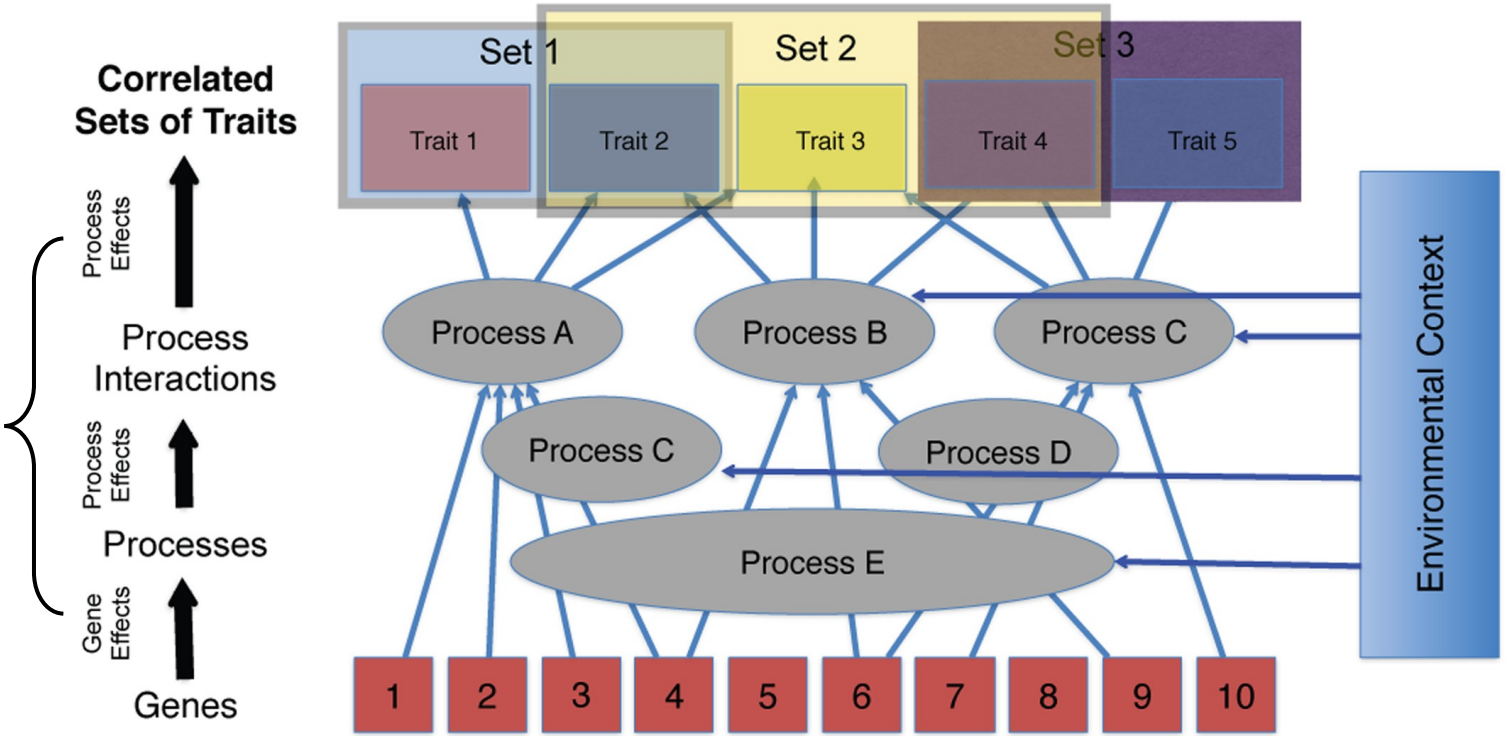
Changes in stalk composition



Extract from Legland D et al. Plant Methods. 2017

Regulation of traits

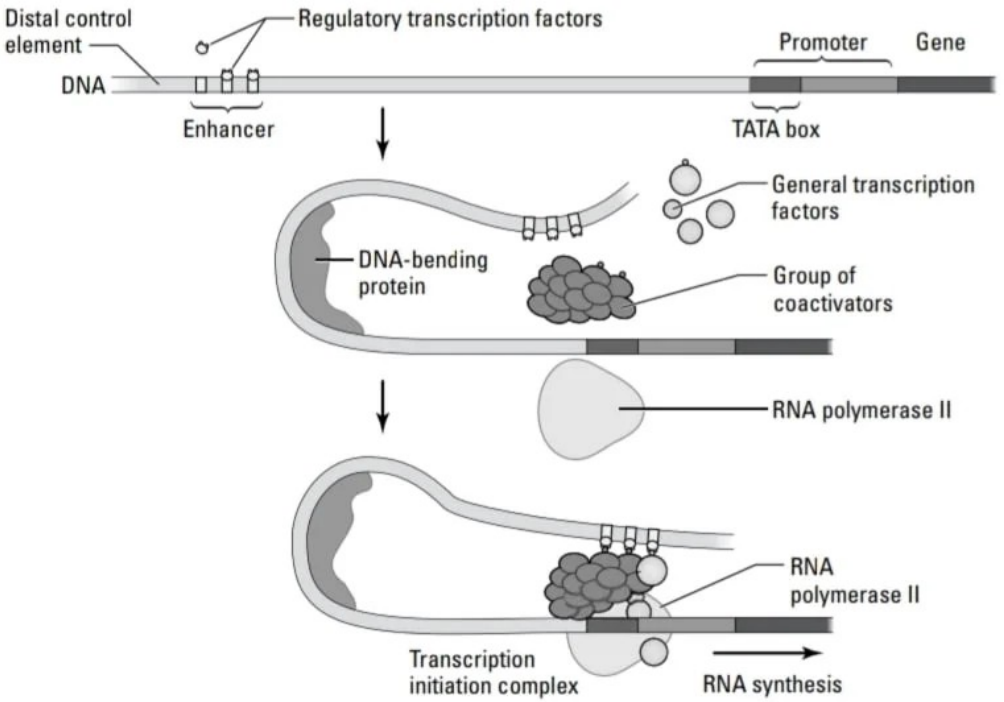
Regulation of gene expression



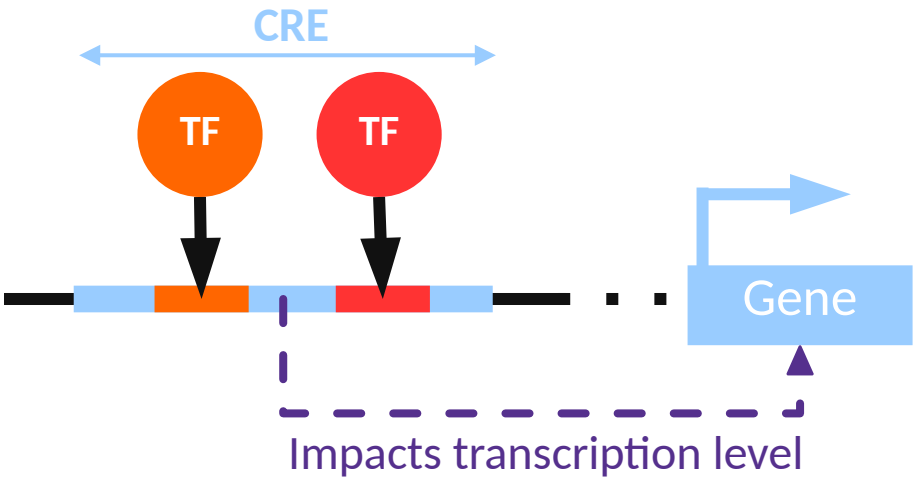
Adapted from Hallgrimsson *et al.*, *PLoS Genetics*, 2014

Cis-regulatory elements

Regulation of gene expression



Schematic interaction between a gene and a CRE



Distal CRE (dCRE) :

- Integrate environmental factors
- Regulate developmental genes

How to assess the effect of cis-regulatory elements in a co-regulatory network ?

- Building cis-regulatory elements based network

- Analysis of the regulatory variations in response to water deficit

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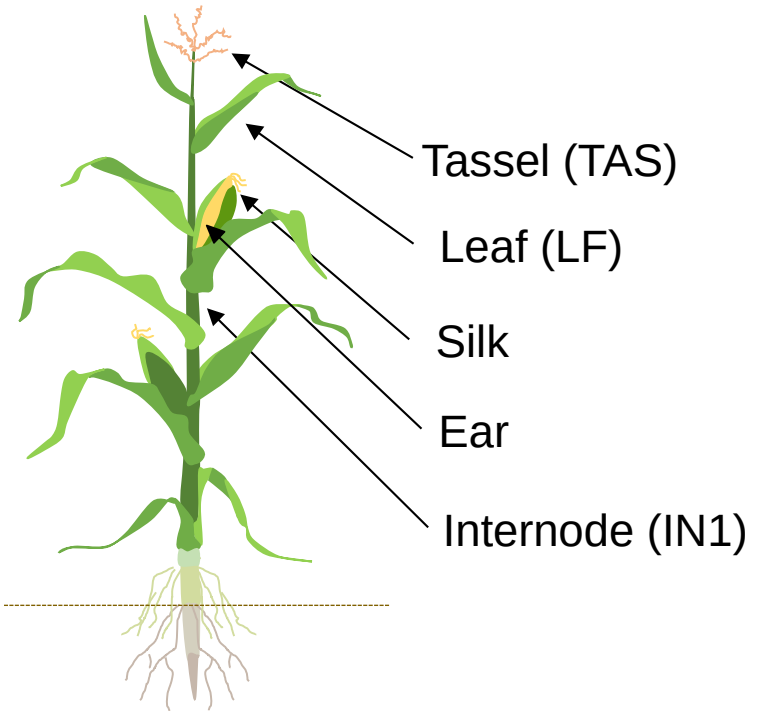
Expression data

5 Tissues



×

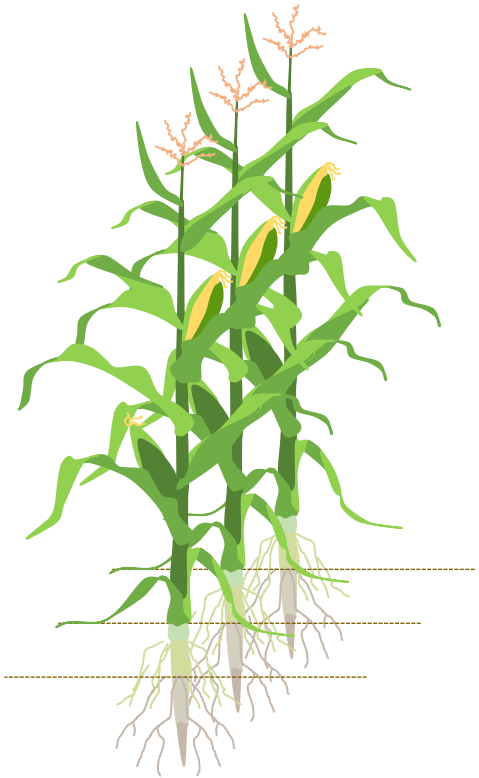
2 Watering conditions

Well Watered (WW)

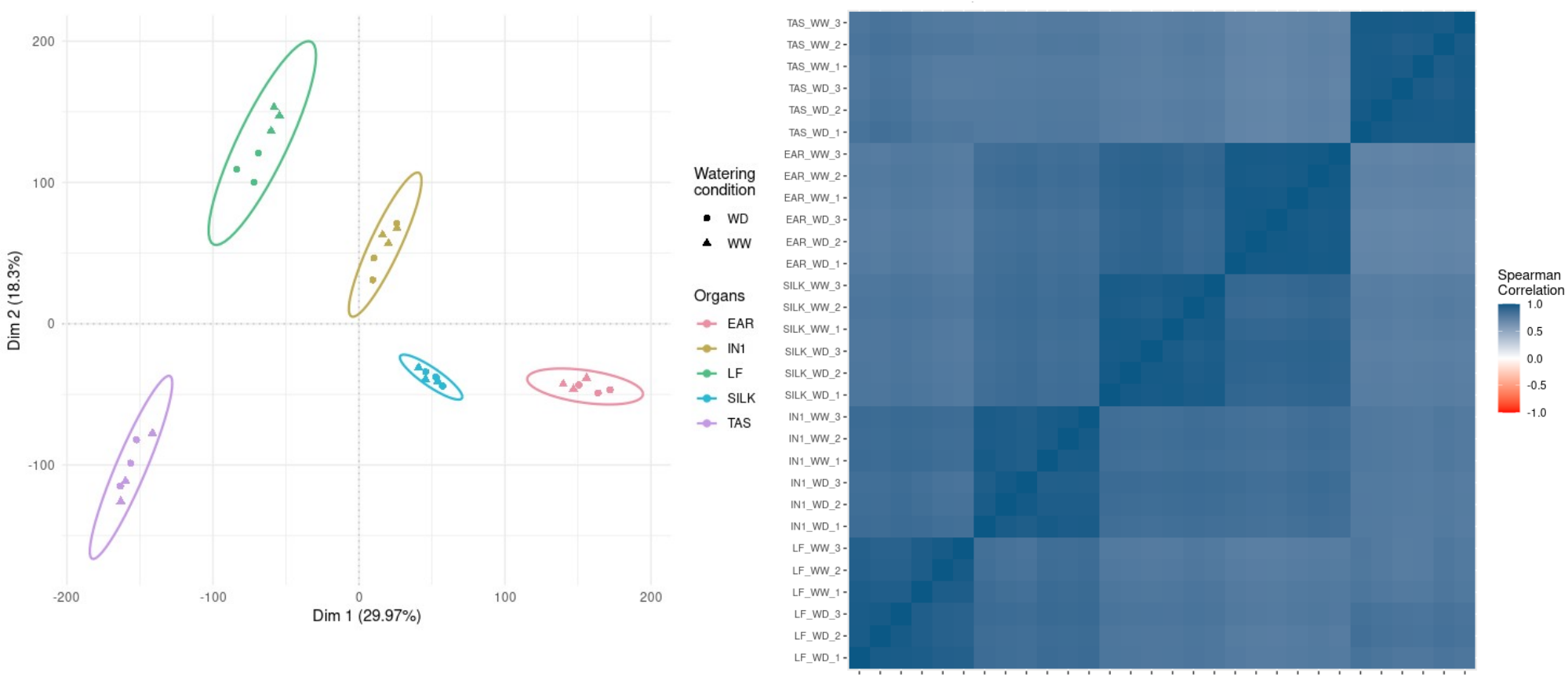
Water Deficit (WD)

×

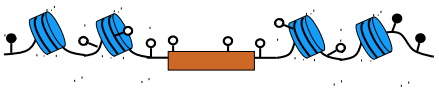
3 Replicates



Expression data



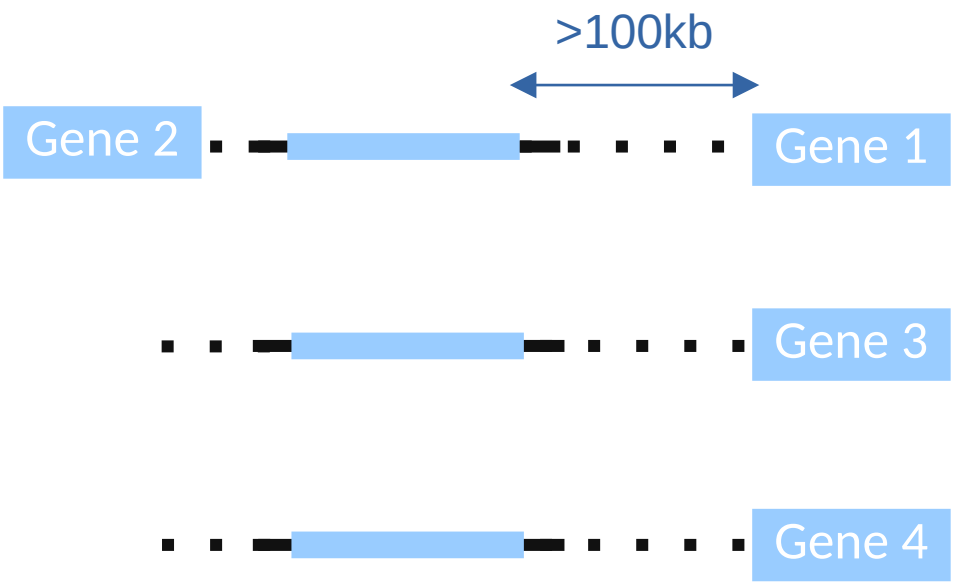
UMRs as potential dCRE



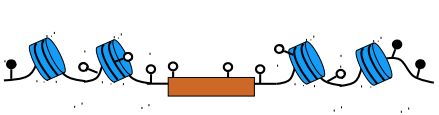
Bisulfite sequencing

Unmethylated region (UMR) are potential dCRE

Possible interactions



UMRs as potential dCRE



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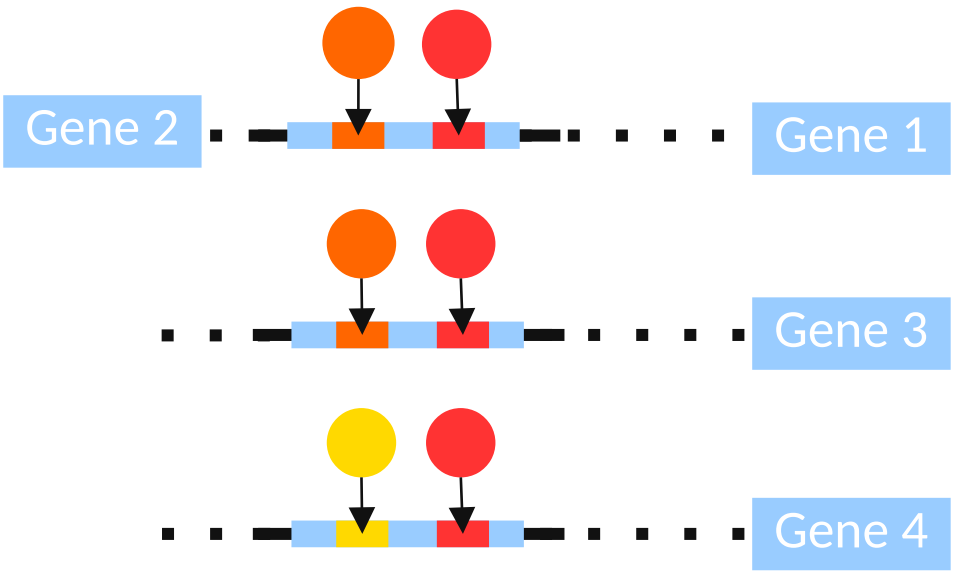
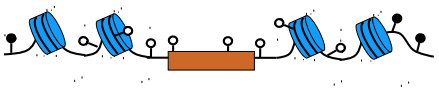


UMRs as potential dCRE



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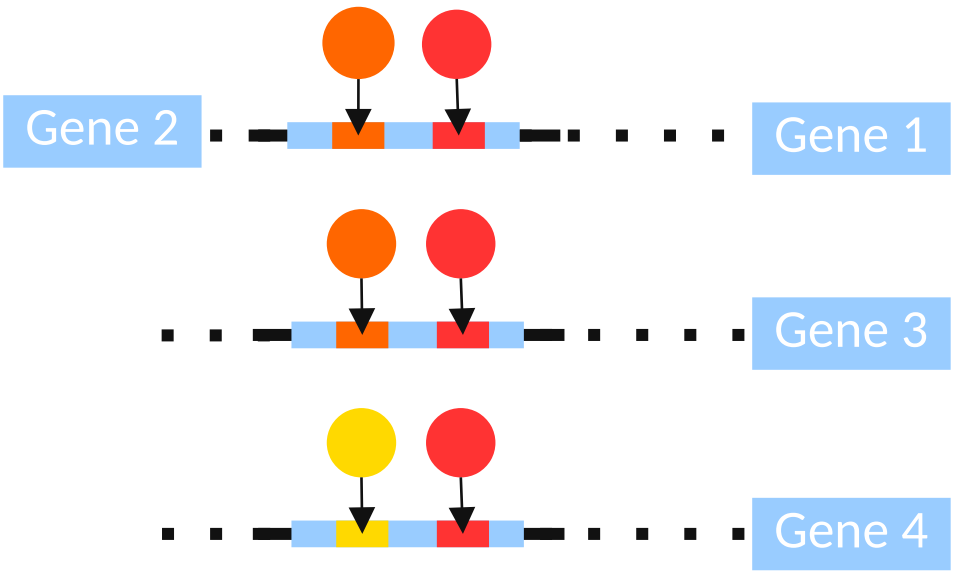
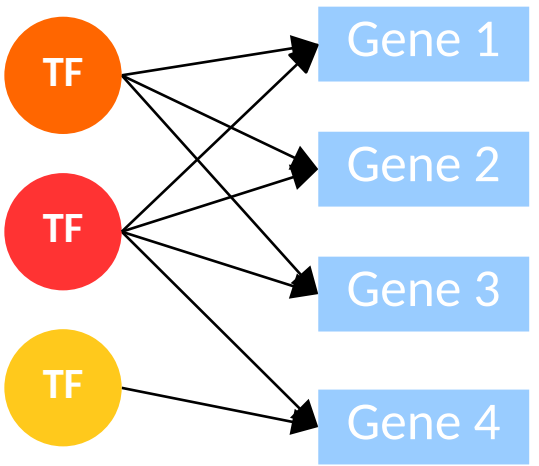
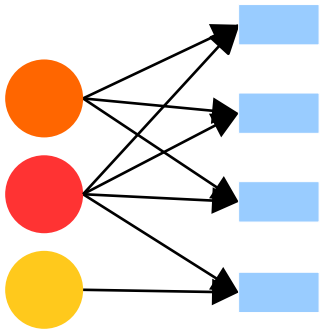


Prior network

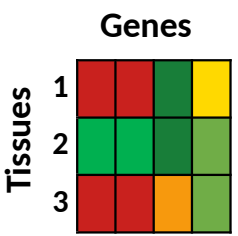


Global regulatory networks

Prior network

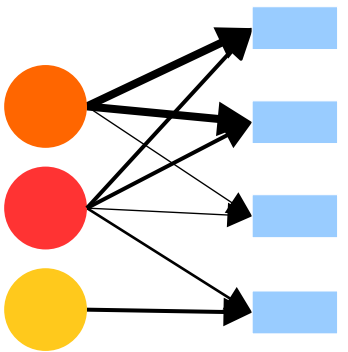


Expression data



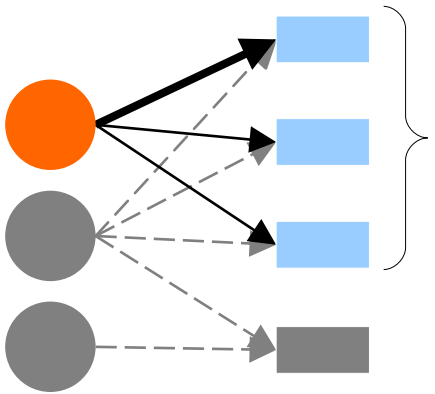
PANDA

Global network



Notions behind PANDA

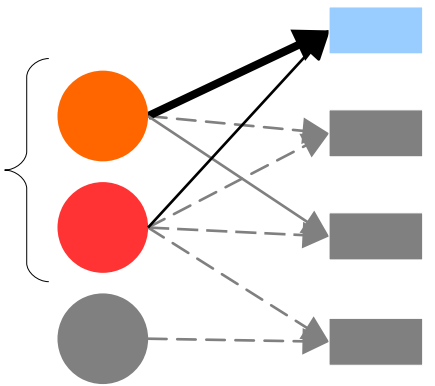
Availability



Coexpressed ?

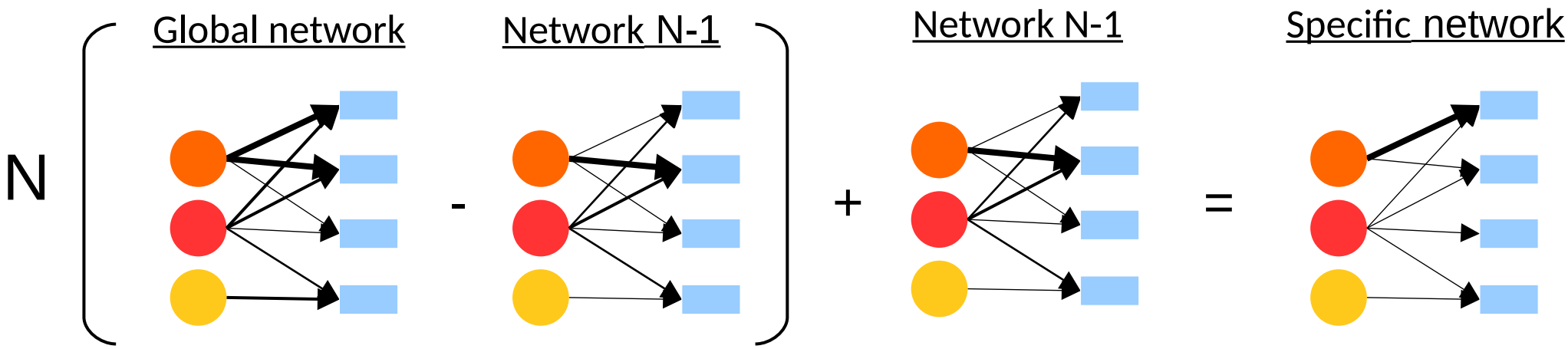
Responsability

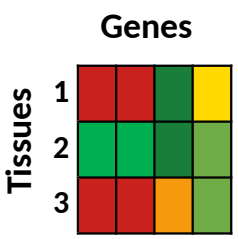
Interacting ?

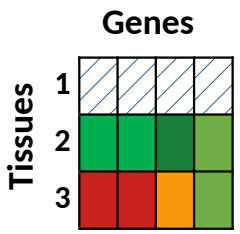


Increase agreeing edges, reduces them otherwise.

Sample specific networks







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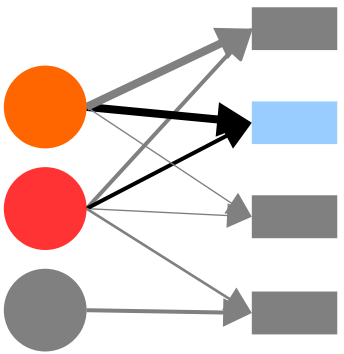
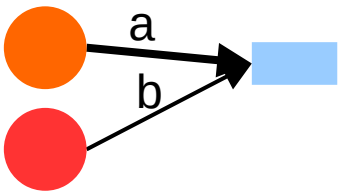
Targeting score

Regulatory network



Regulation at gene level

In the network :

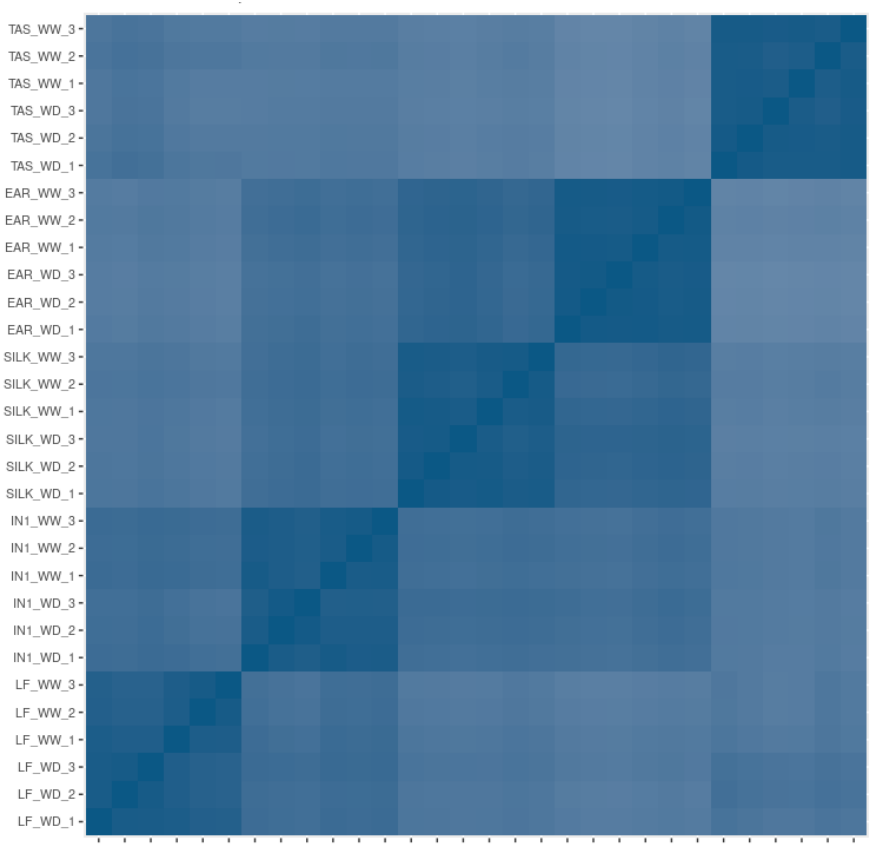


Indegree :

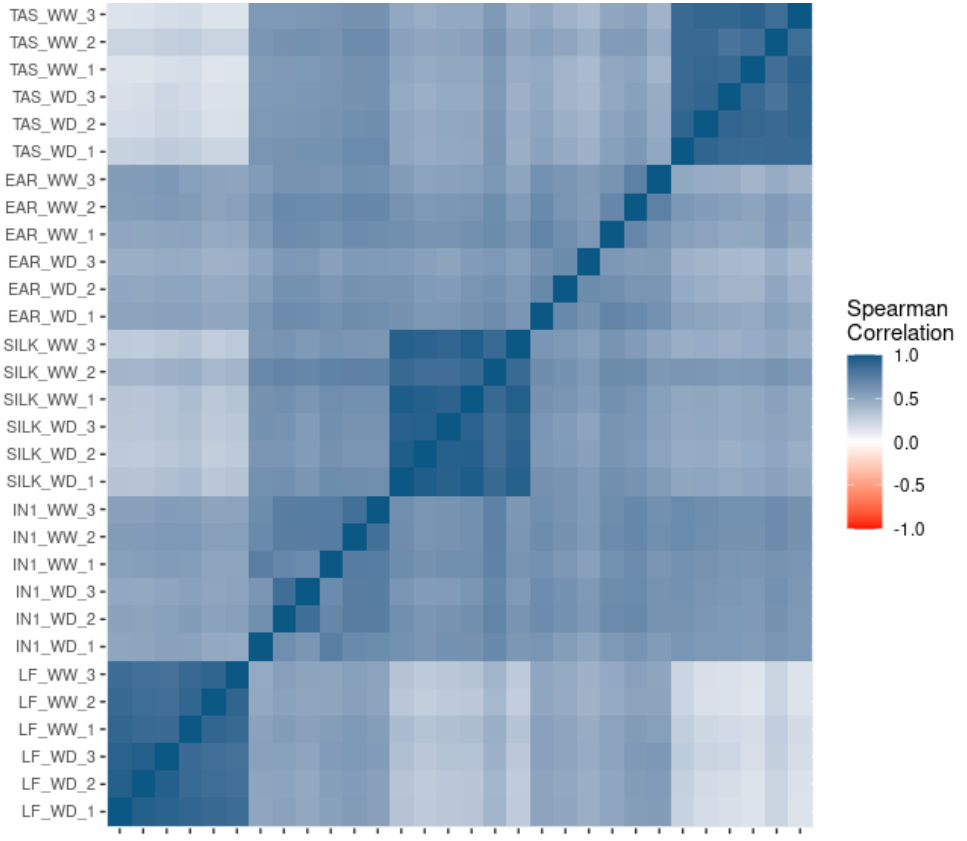
Sum the effects of every TFs on a gene

Gene indegree (targeting score)

Gene expression

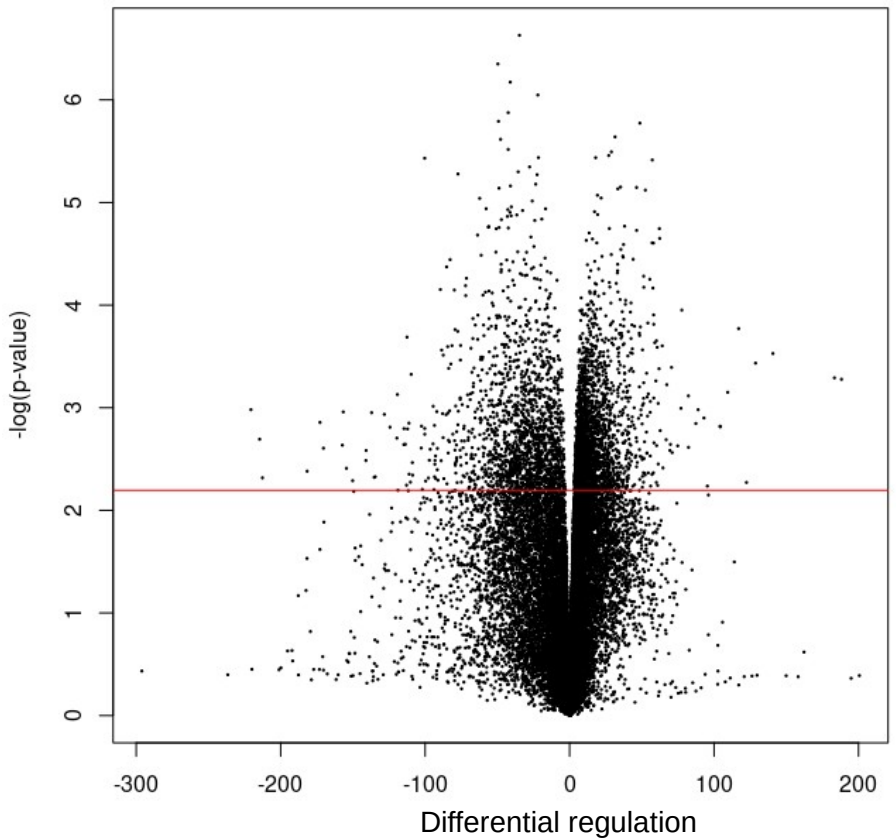


Gene indegree

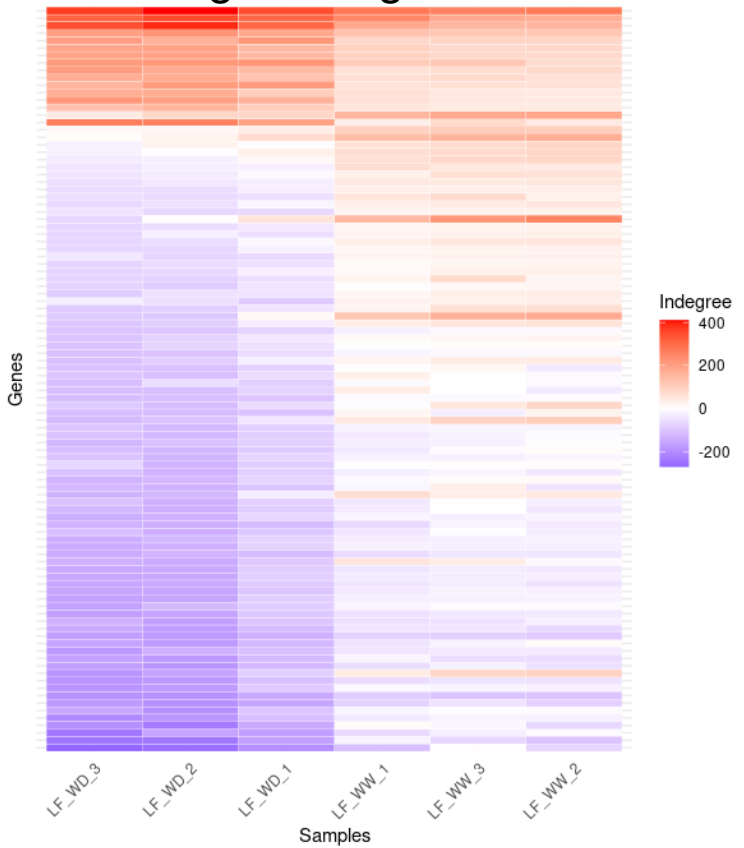


Differential analysis of genes degree, Leaves

Volcano plot of differential indegree

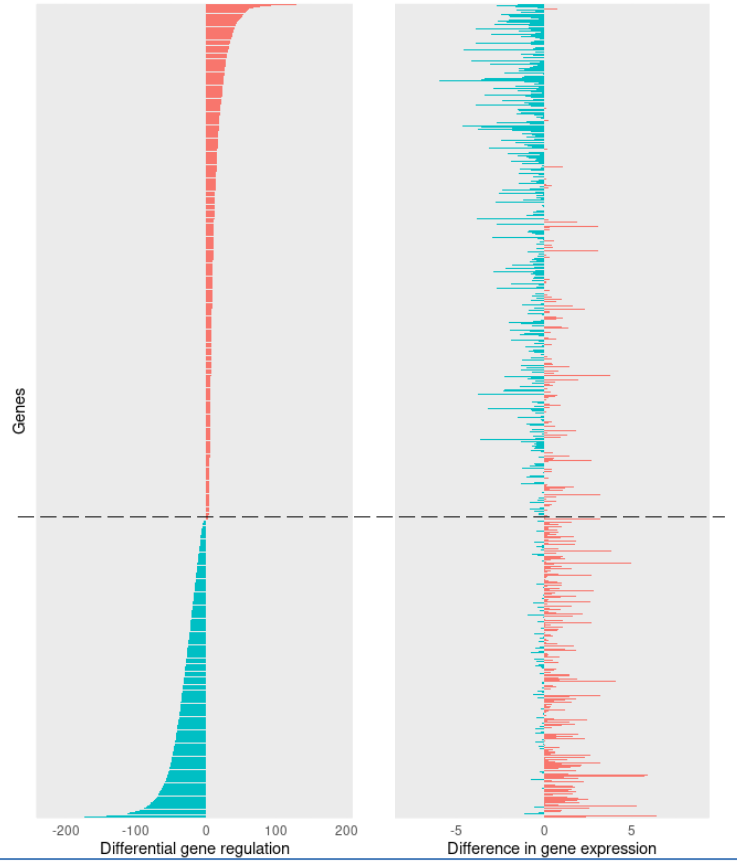


Top 100 most differentially regulated genes

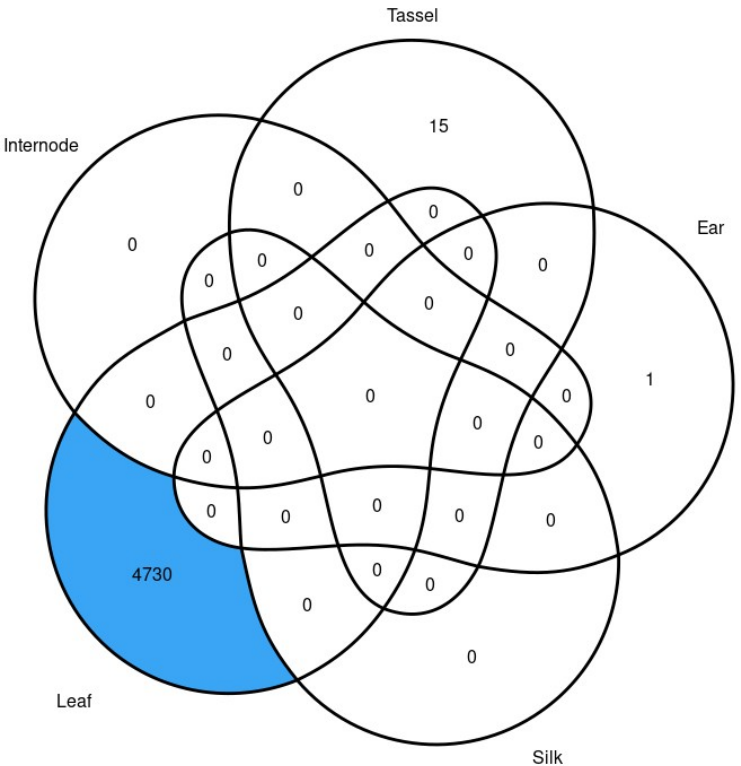


Differential gene regulation

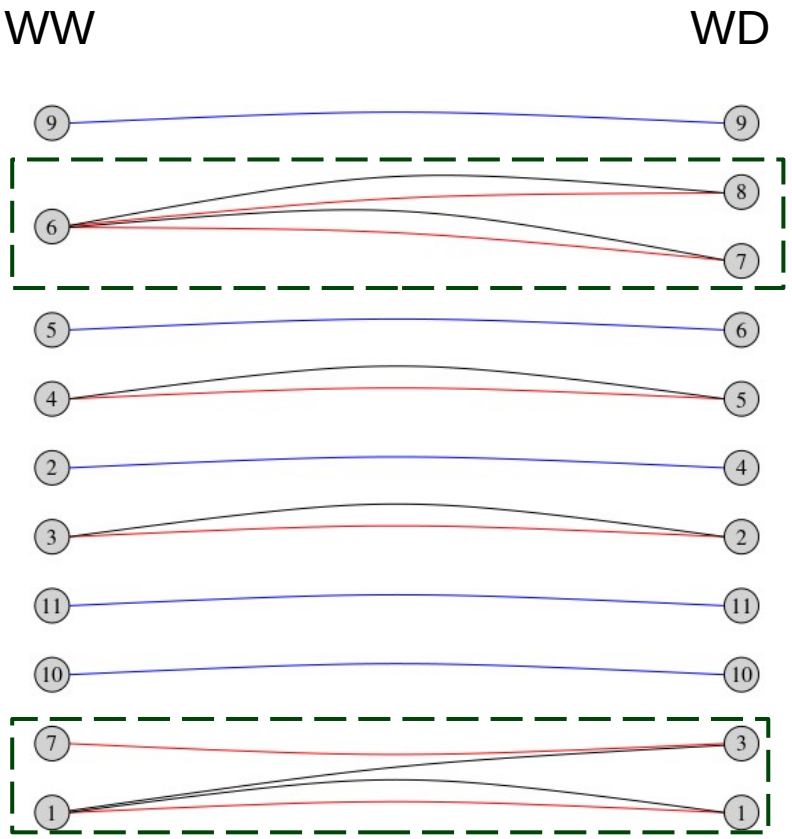
Comparaison between differential regulation and gene expression, Leaves



Differentialy regulated genes in water deficit, across 5 organs



Water condition effects on the regulatory network structure of leaves



Jacquard index > 0.8 (well preserved)

Inclusion of «WW» module > 0.3

Inclusion of «WD» module > 0.3

Lower preservation

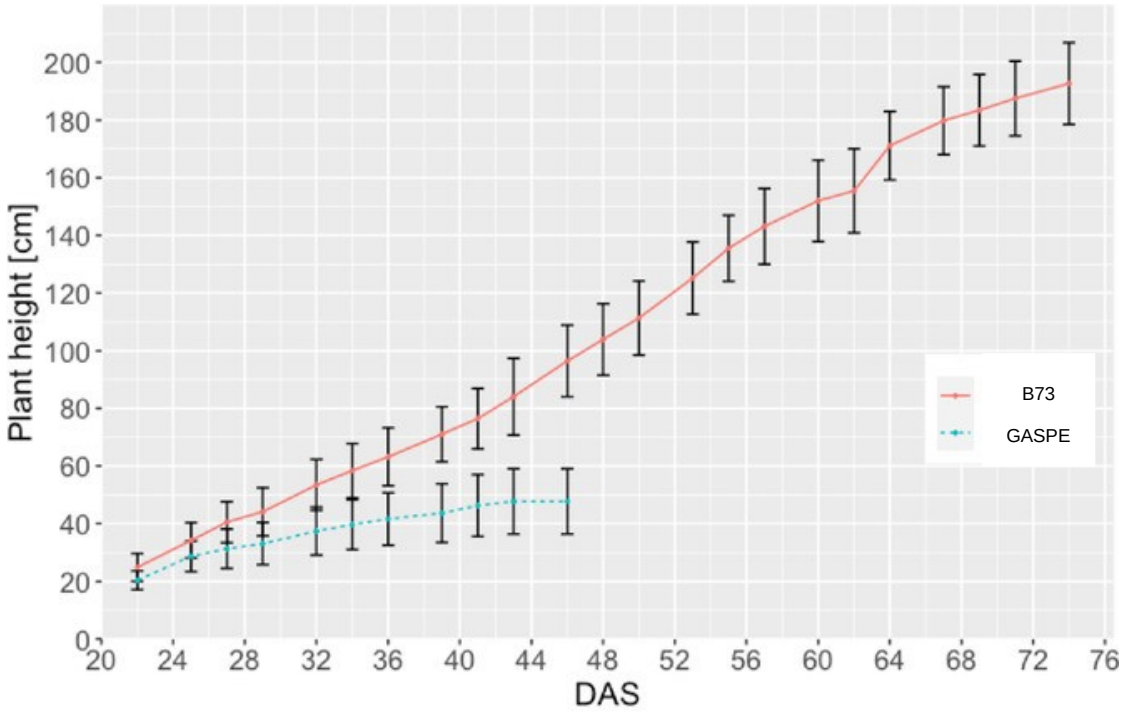
Regulation changes

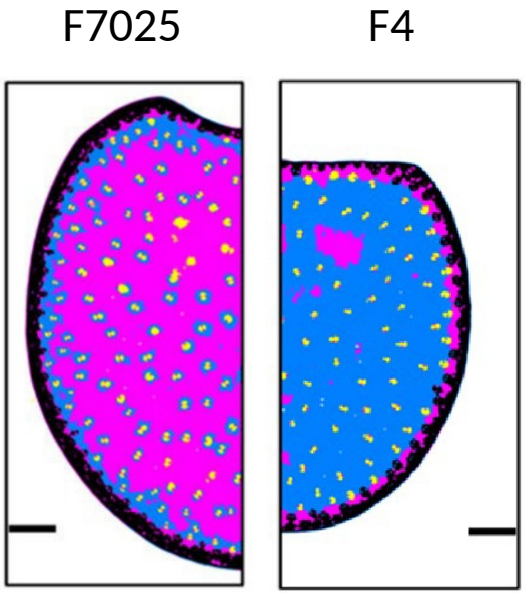
Conclusion

Coregulatory network based on cis-regulatory elements :

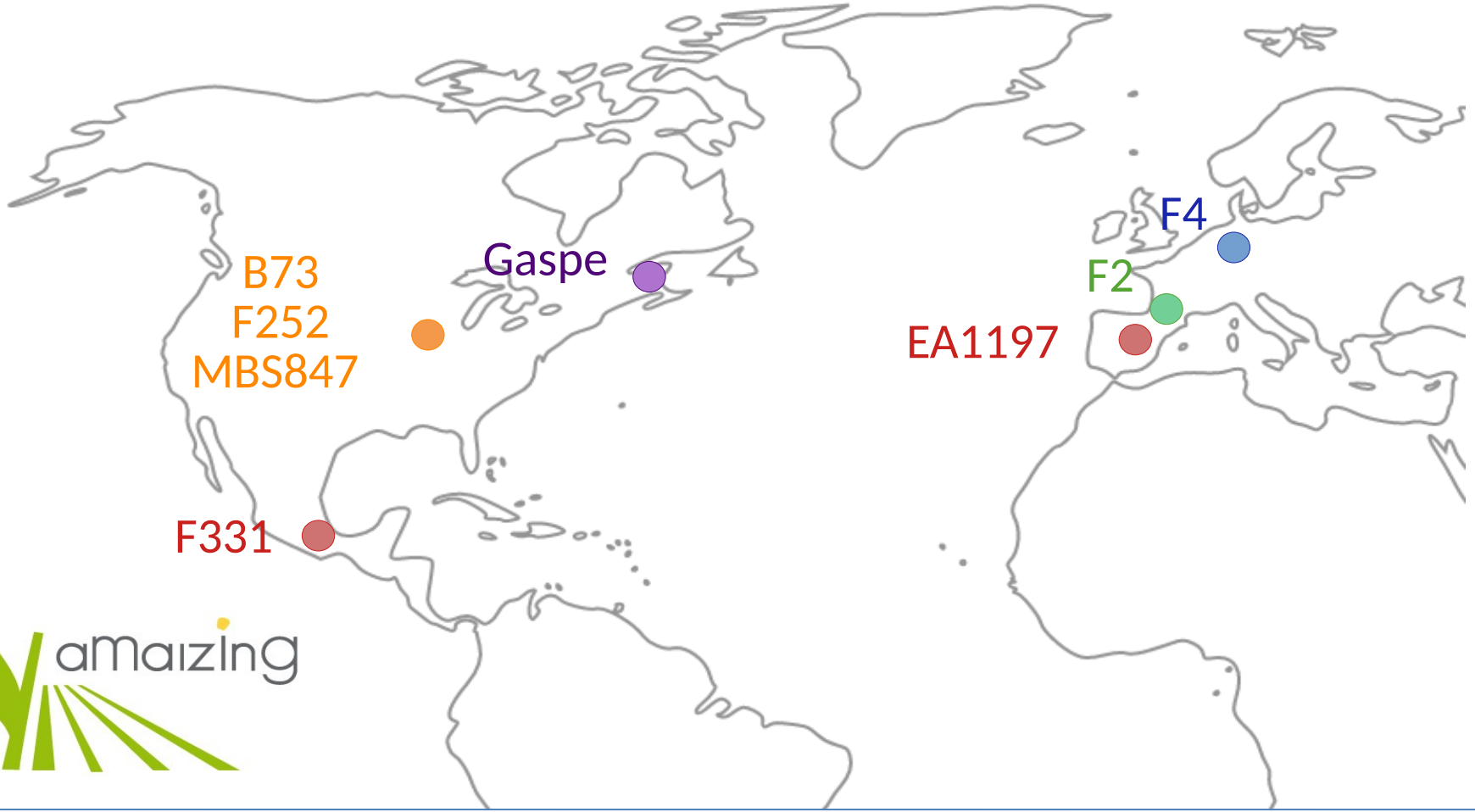
- Based on epigenetic marks, across the whole genome
- Possible interactions between transcription factors and gene
- Shows tissue-specificity : genes and functions regulated

Future work



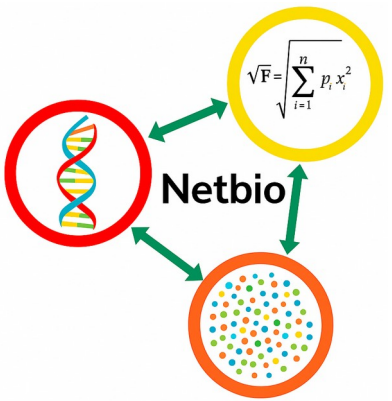


Future work



Aknowledgements

- Marieke Kuijjer's team



Thank you for your attention