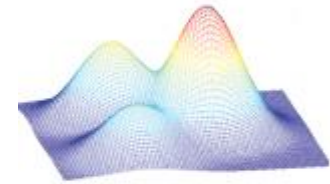
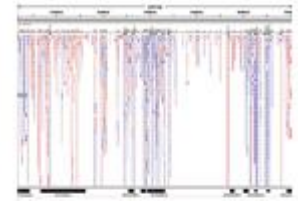


De l'expression des gènes aux réseaux

Ecole-chercheur de mai à décembre 2017



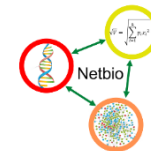
Le projet
Formation



Paris-Saclay
Computational Biology



Réseaux NETBIO
du département MIA



Premières impressions



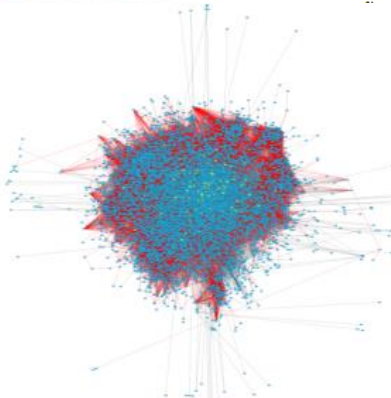
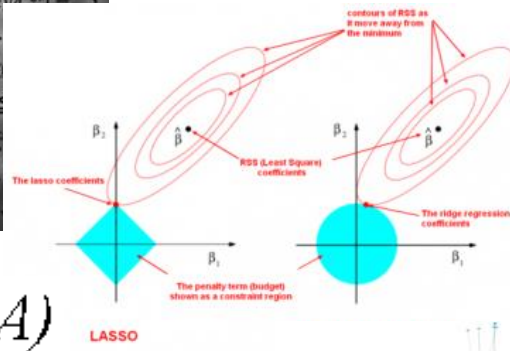
$$\rho(x) = -G(-x^2)/[xH(-x^2)]$$

$$\mu > \sum_{j=0, j \neq p} A_j \rho^j$$

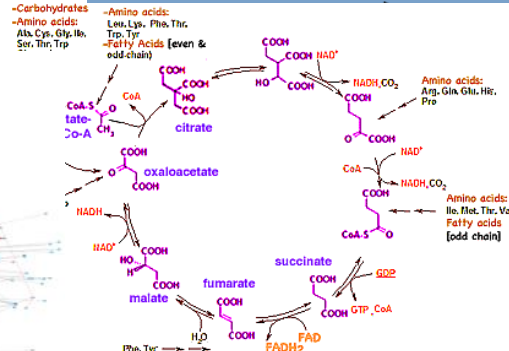
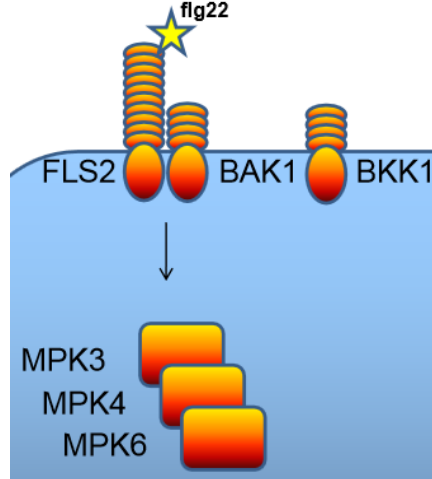
$$\Delta_L \arg f(z) = (\pi/2)(S_1 + S_2)$$

$$G(u) = \prod_{k=1}^n (u + u_k) G_0(u)$$

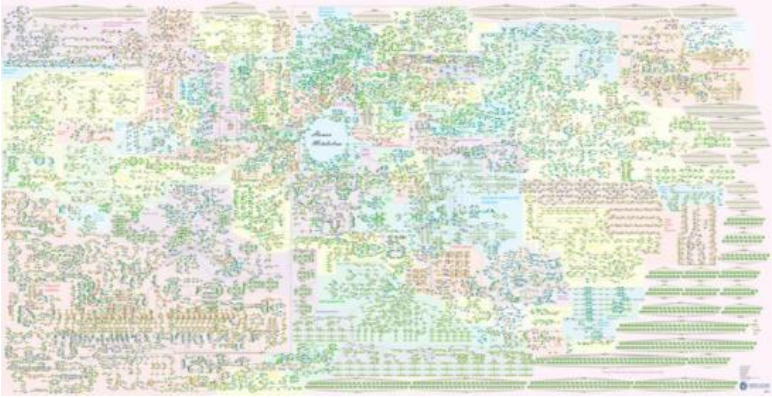
$$G(u) = \prod_{k=1}^n (u + u_k) G_0(u)$$



probability density prior given example case Section likelihood function independent observations parameter q known model log posterior variance results data methods found rule one parameters may sample uniform



$P(B|A)$



Objectifs de l'école chercheurs

- Comprendre les spécificités des données omiques, en particulier de transcriptomique
- Comprendre les objectifs des analyses bio-informatiques et statistiques
- Connaître les méthodes proposées
- Savoir interpréter a minima les résultats

- Se familiariser avec les concepts et partager un vocabulaire technique commun
- Etre capable d'interagir avec les plateformes de omiques et les modélisateurs
- Savoir faire des choix méthodologiques avisés

6 modules de formation indépendants

Matin > Cours en amphithéâtre

2 fois 90 minutes avec une pause de 15 minutes

Après-midi > 2 TP de 90 minutes pour un groupe
de 20 personnes

6 modules de formation indépendants

Organisés selon les différentes étapes de l'analyse

Les technologies de séquençage actuelles et futures et leurs protocoles associés (30 mai)

La bioinformatique du RNAseq (29 juin)

Normalisation et analyse différentielle des données RNAseq (28 septembre)

Analyse de la coexpression de données RNAseq (12 octobre)

Les réseaux de régulation (30 novembre)

Les intégrations de données omiques (14 décembre)

Gene co-expression analysis

MORNING TALKS

- Co-expression analysis: what for? Examples of co-expression studies
- Co-expression analysis: How?

AFTERNOON PRACTICAL SESSIONS

- coseq R package for RNA-seq co-expression analysis
- Using the Gem2Net database

Co-expression analysis: what for?

Examples of co-expression studies

Co-expressed genes =
Groups of genes that have **similar expression patterns** over a range of different experiments

Co-expression analysis: what for?

Examples of co-expression studies

Co-expressed genes =
Groups of genes that have similar expression patterns over a range of different experiments

Groups of genes sharing regulatory inputs, functional pathways, and biological process(es)

Functional modules/pathways

Gene annotation using guilt-by-association

Networks

Co-expression analysis: what for?

Examples of co-expression studies

Co-expressed genes =
Groups of genes that have similar expression
patterns over a **range of different experiments**

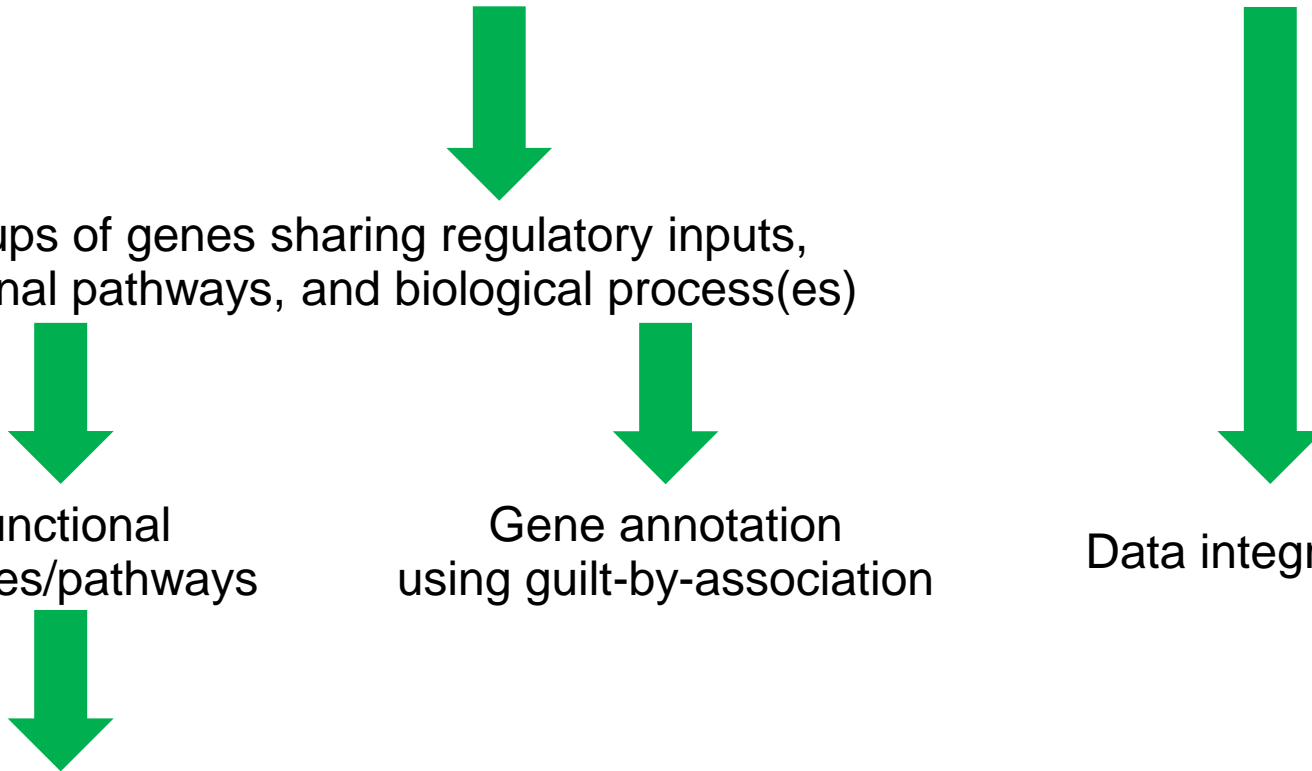
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Co-expression analysis: what for?

Examples of co-expression studies



RESEARCH ARTICLE



Temporal network analysis identifies early physiological and transcriptomic indicators of mild drought in *Brassica rapa*

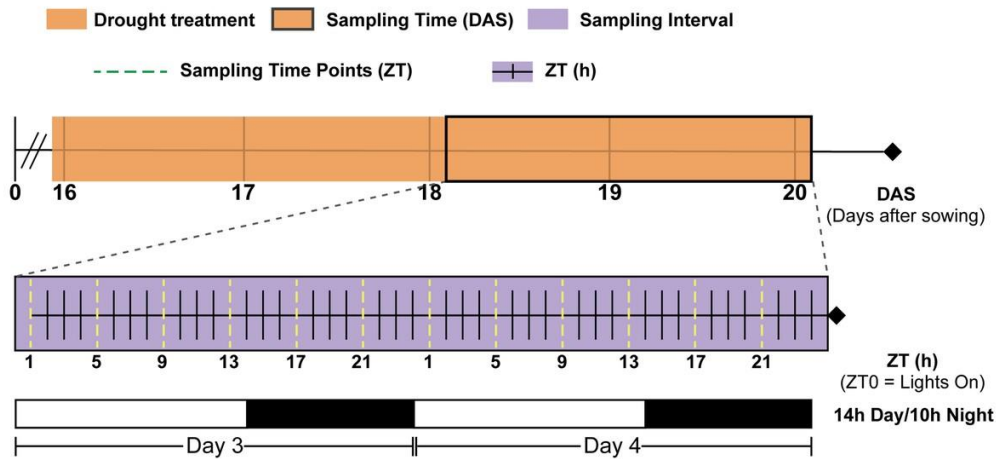
Kathleen Greenham^{1†}, Carmela Rosaria Guadagno^{2†}, Malia A Gehan³,
Todd C Mockler³, Cynthia Weinig^{2,4,5}, Brent E Ewers^{2,5}, C Robertson McClung^{1*}

October, 4th 2017

Co-expression analysis: what for?

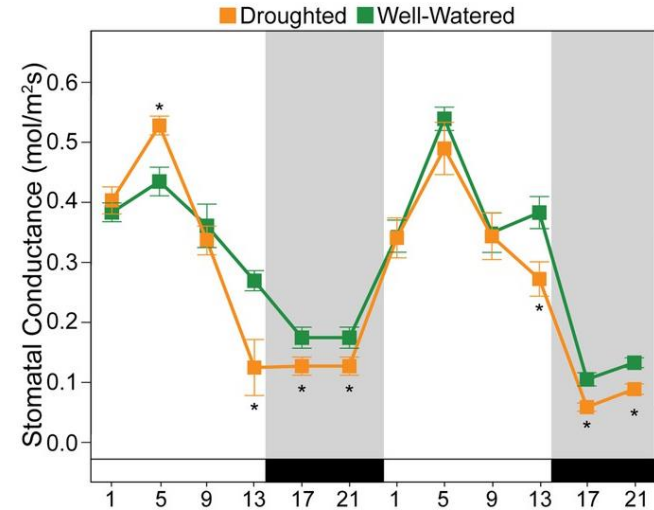
Examples of co-expression studies

A



Mild drought, sampling every 4h for 48h

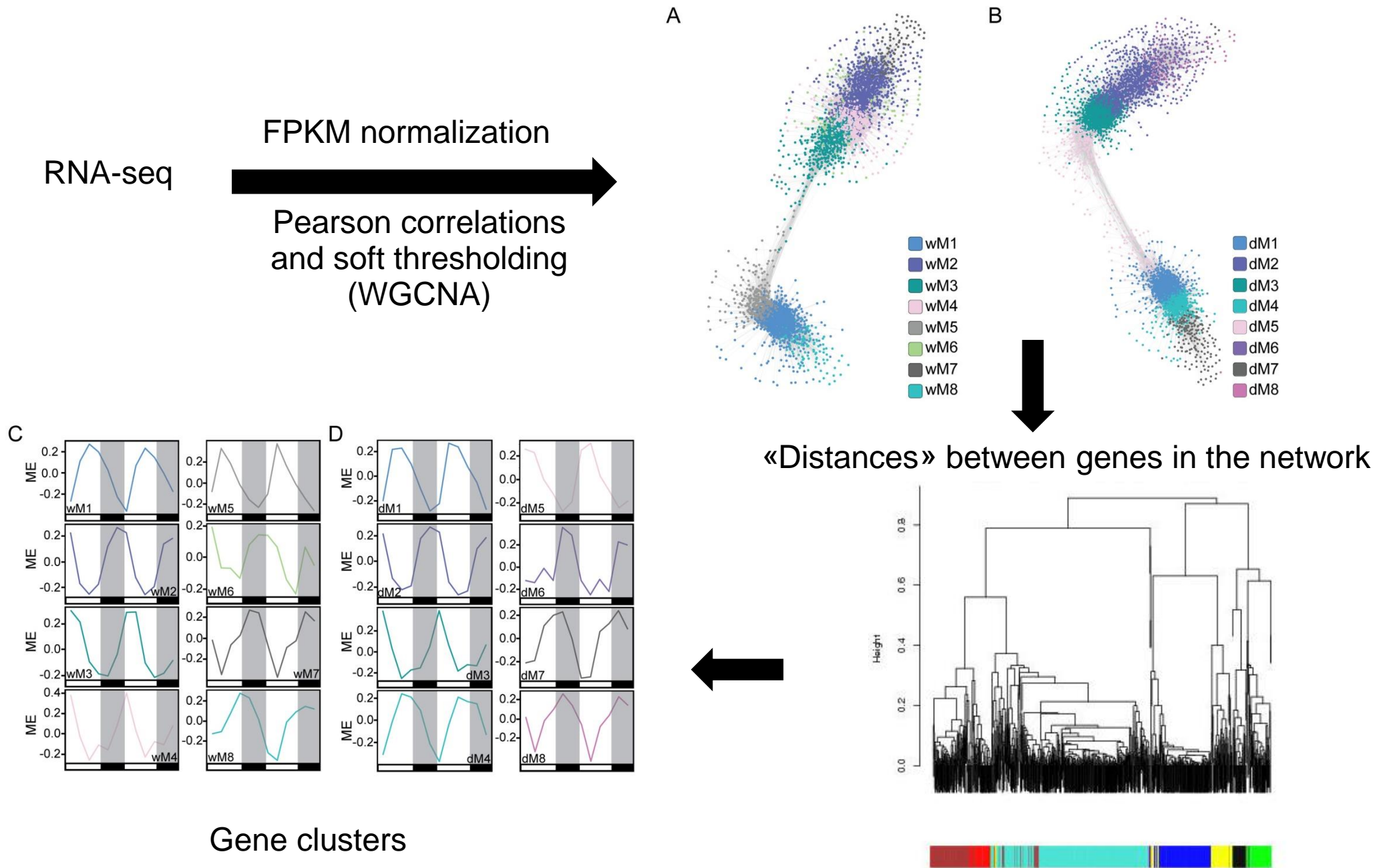
Physiological measures



Fv'/Fm', gs and NSC are impacted by drought

Co-expression analysis: what for?

Examples of co-expression studies

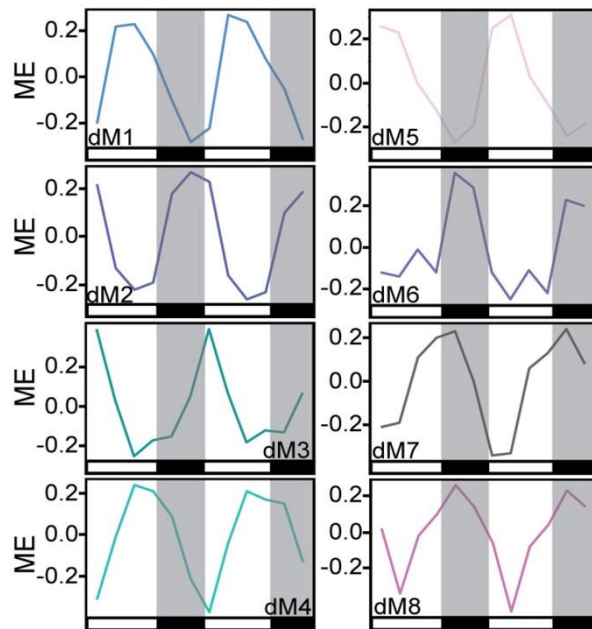


Co-expression analysis: what for?

Examples of co-expression studies

Selection of the clusters of interest

clusters

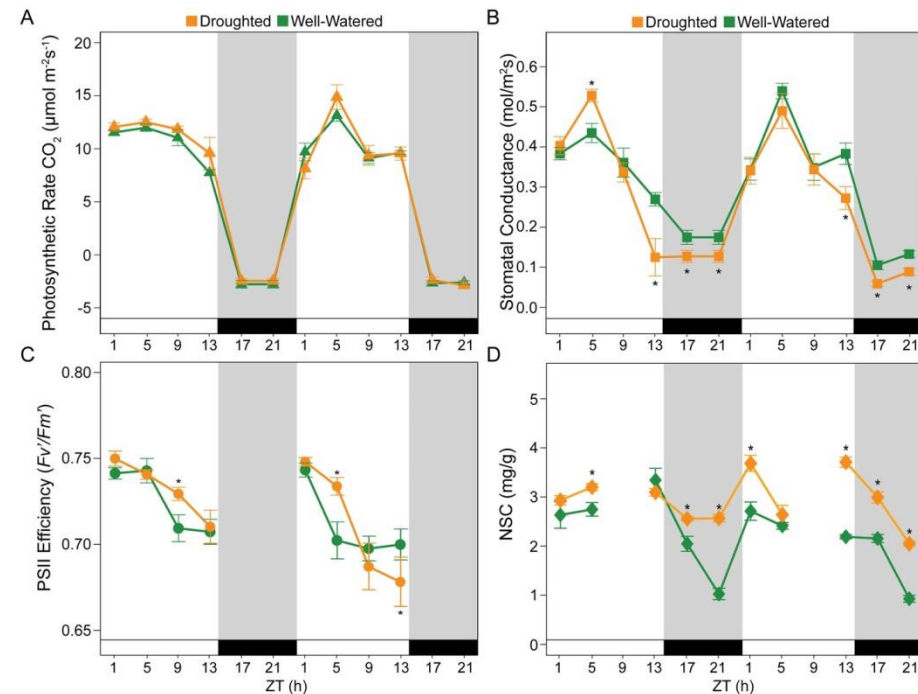


Pearson
correlation

+

changes in expression rhythm between drought and control

physiology



Co-expression analysis: what for?

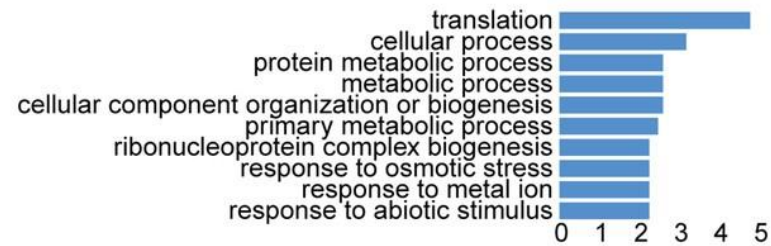
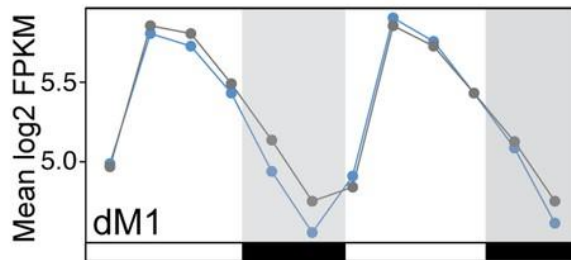
Examples of co-expression studies

Correlated to

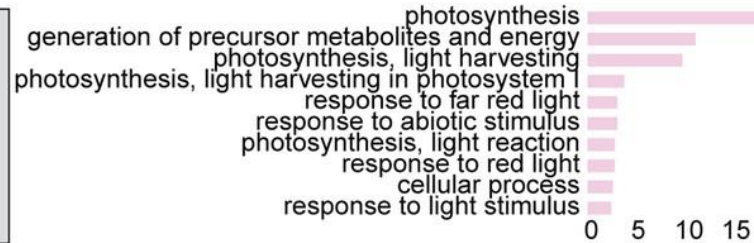
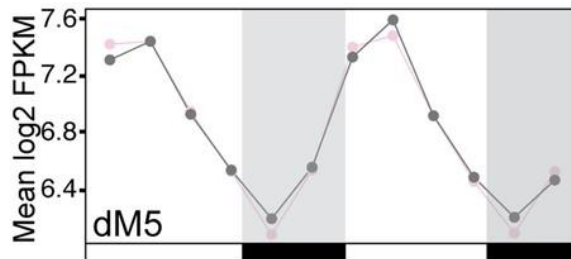
Cluster expression profile

GO enrichments

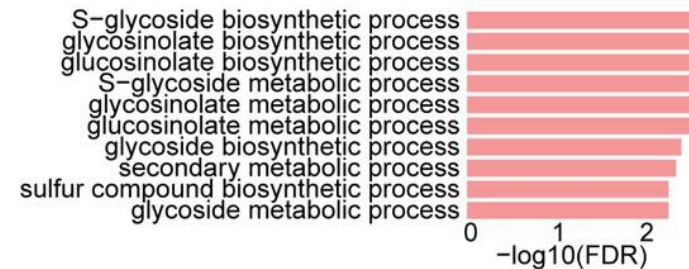
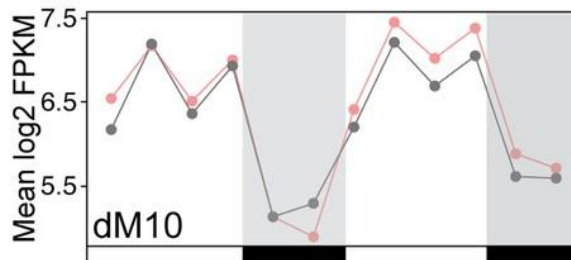
gs



gs



Fv'/Fm'



Identification of functional modules (pathways) associated with the early onset of drought

Co-expression analysis: what for?

Examples of co-expression studies

The Plant Cell, Vol. 29: 2086–2105, September 2017, www.plantcell.org © 2017 ASPB.



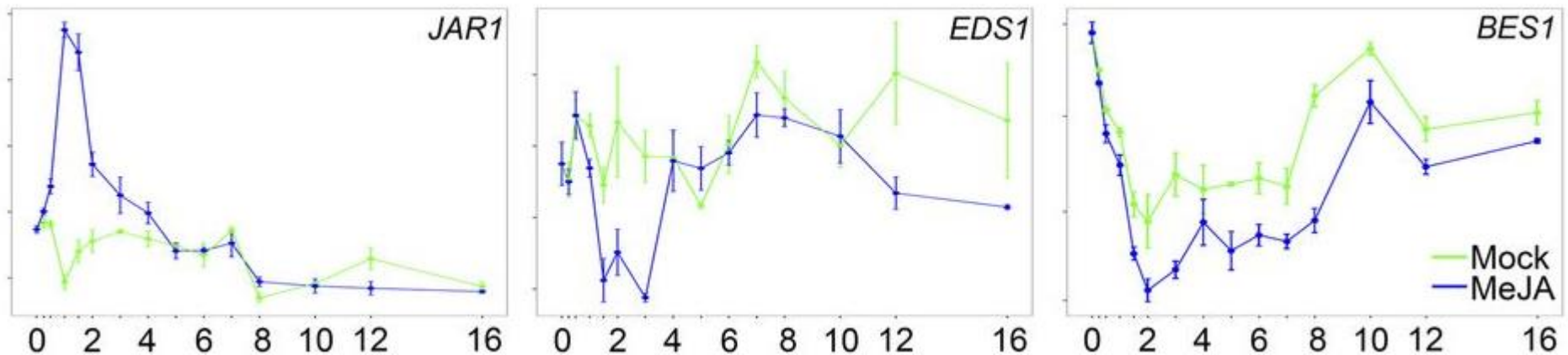
LARGE-SCALE BIOLOGY ARTICLE

Architecture and Dynamics of the Jasmonic Acid Gene Regulatory Network ^{OPEN}

Richard Hickman,^{a,1} Marcel C. Van Verk,^{a,b,1} Anja J.H. Van Dijken,^a Marciel Pereira Mendes,^a Irene A. Vroegop-Vos,^a Lotte Caarls,^a Merel Steenbergen,^a Ivo Van der Nagel,^a Gert Jan Wesselink,^a Aleksey Jironkin,^c Adam Talbot,^{d,e} Johanna Rhodes,^c Michel De Vries,^f Robert C. Schuurink,^f Katherine Denby,^{c,d,e} Corné M.J. Pieterse,^a and Saskia C.M. Van Wees^{a,2}

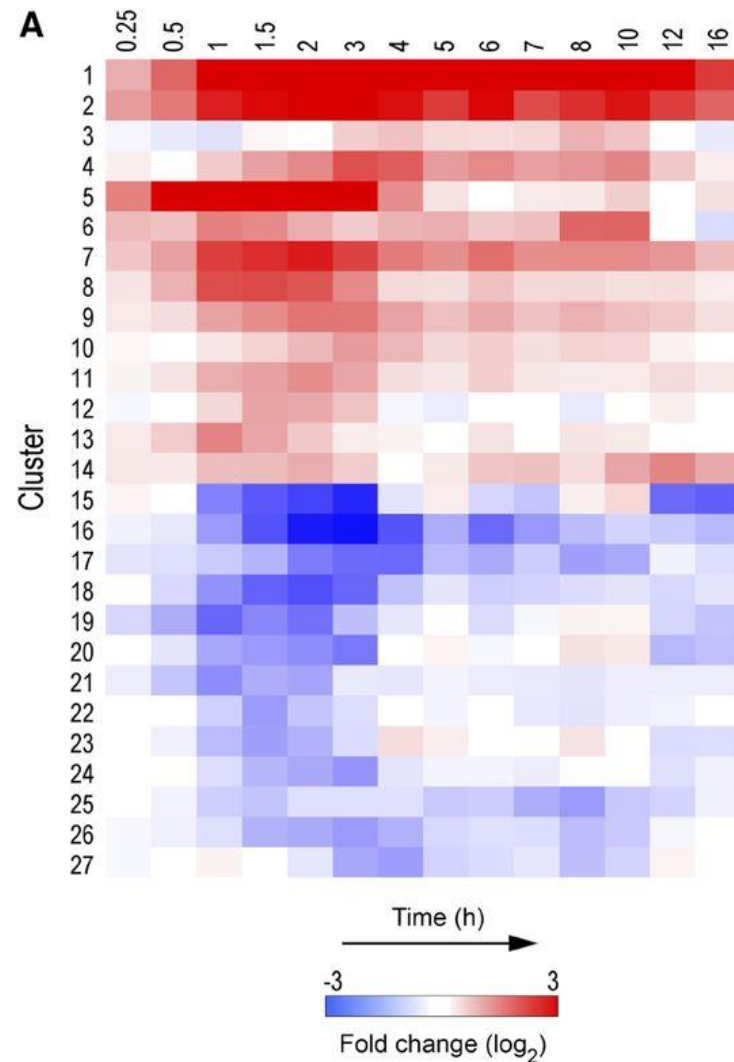
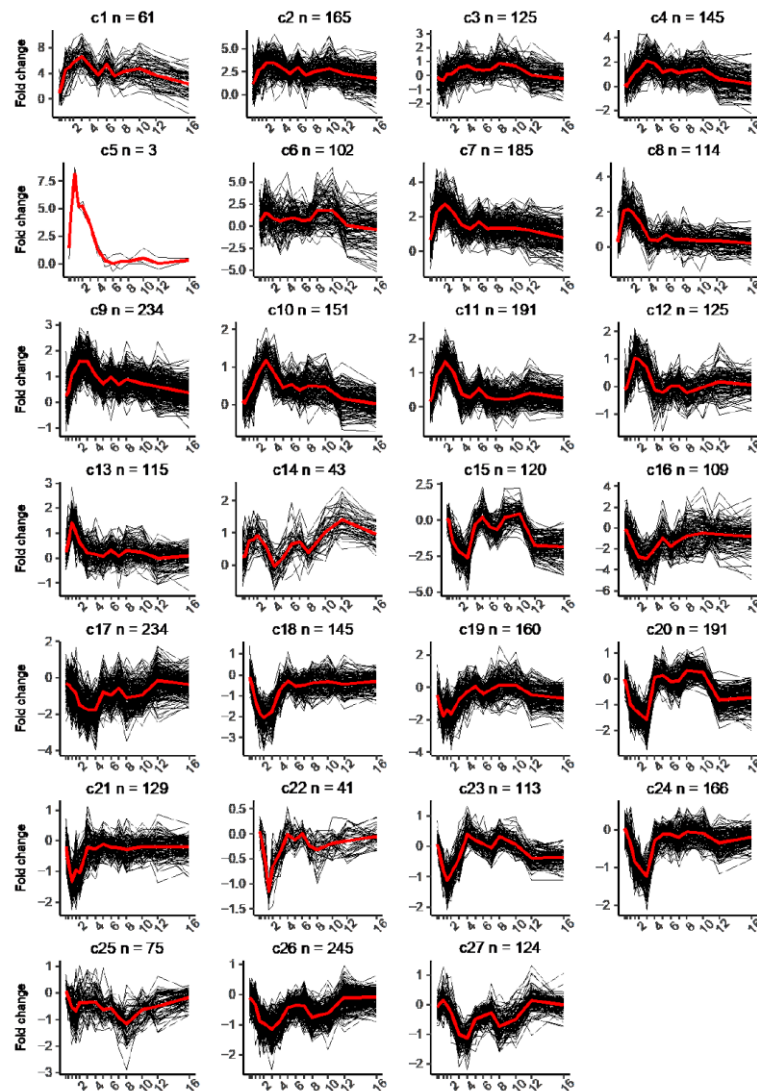
MeJA treatment of *Arabidopsis thaliana* leaf 6 (+mock).

Kinetic over 16h with 15 time points followed by RNA-seq analysis



Co-expression analysis: what for?

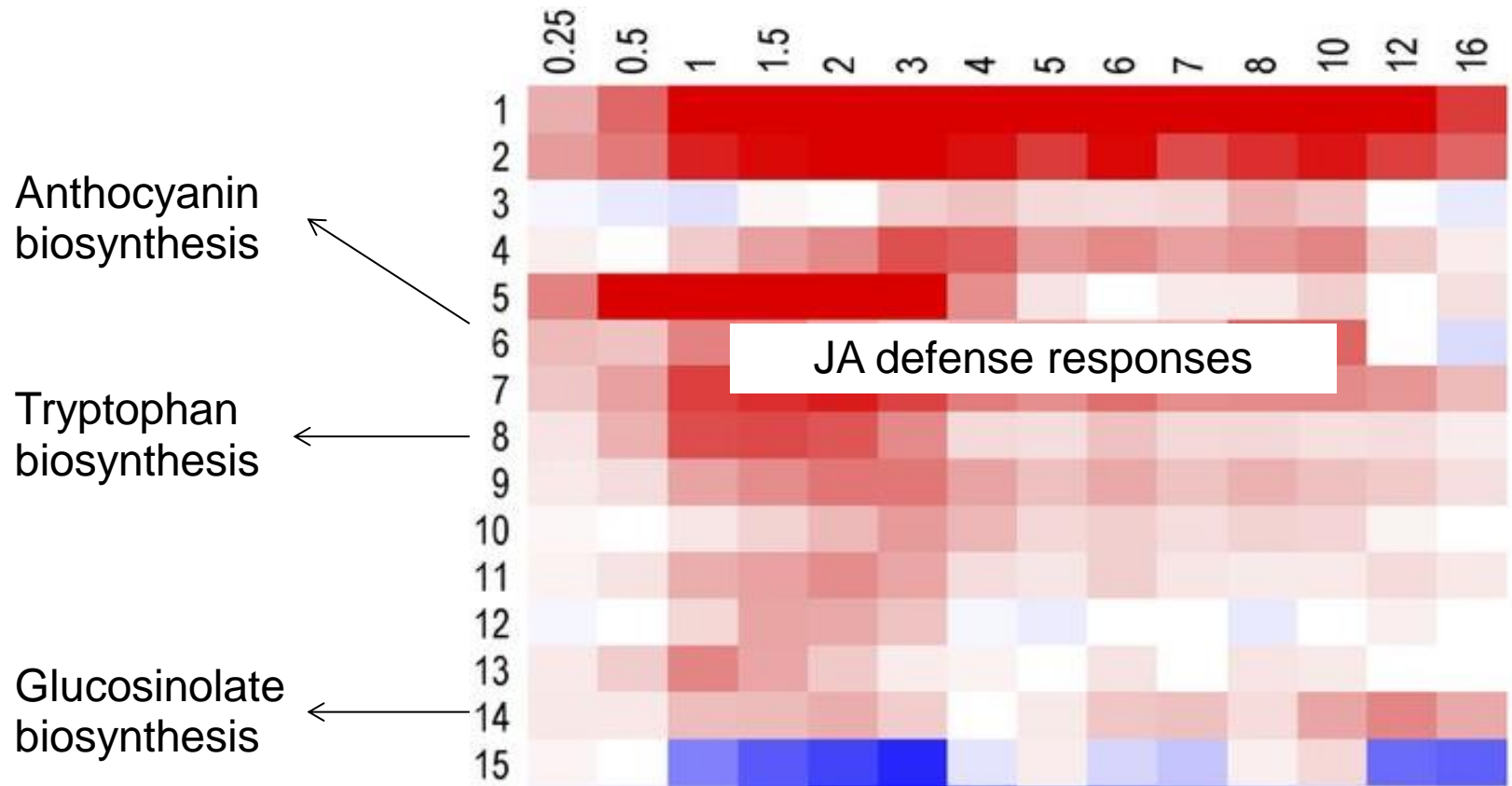
Examples of co-expression studies



Co-expression analysis: what for?

Examples of co-expression studies

Functional modules: GO enrichments



Identification of discrete sectors of the JA-controlled gene network

Co-expression analysis: what for?

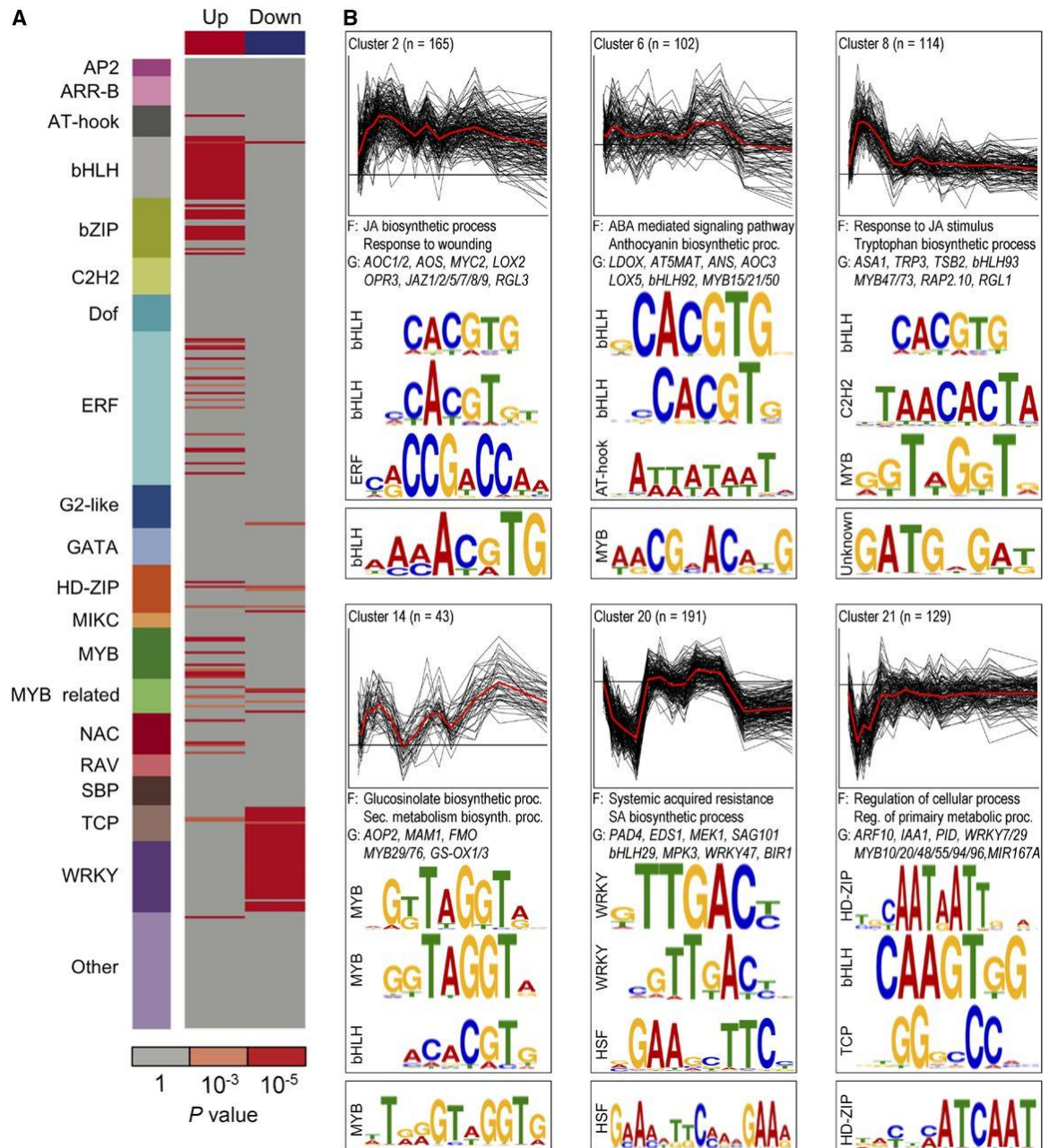
Examples of co-expression studies

Gene regulation:
DNA binding motif analysis

bHLH binding motifs enriched in most up-regulated clusters



bHLH TFs are essential components of MeJA induction



Co-expression analysis: what for?

Examples of co-expression studies

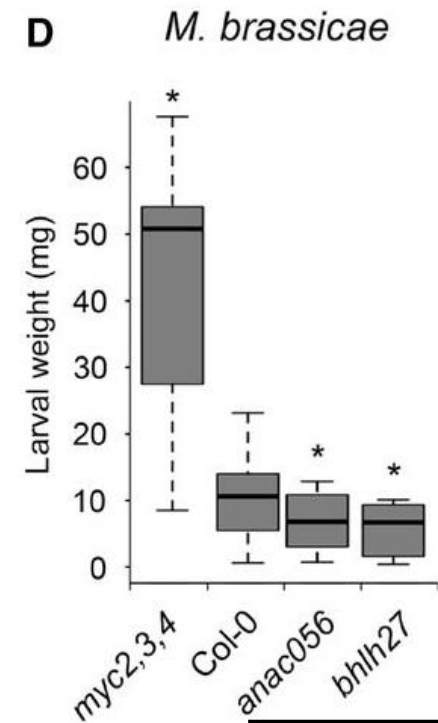
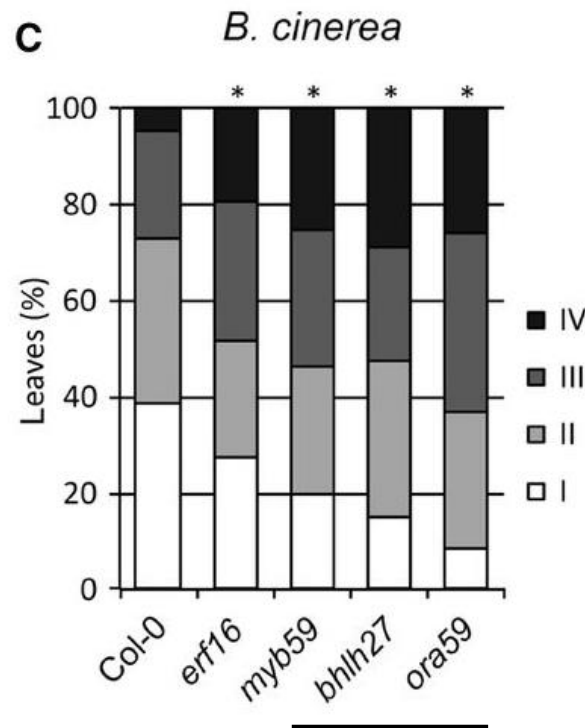
Gene annotation: New regulators of JA defense responses

Enriched in known JA-related genes including regulators



Testing of 12 uncharacterised TF from these clusters

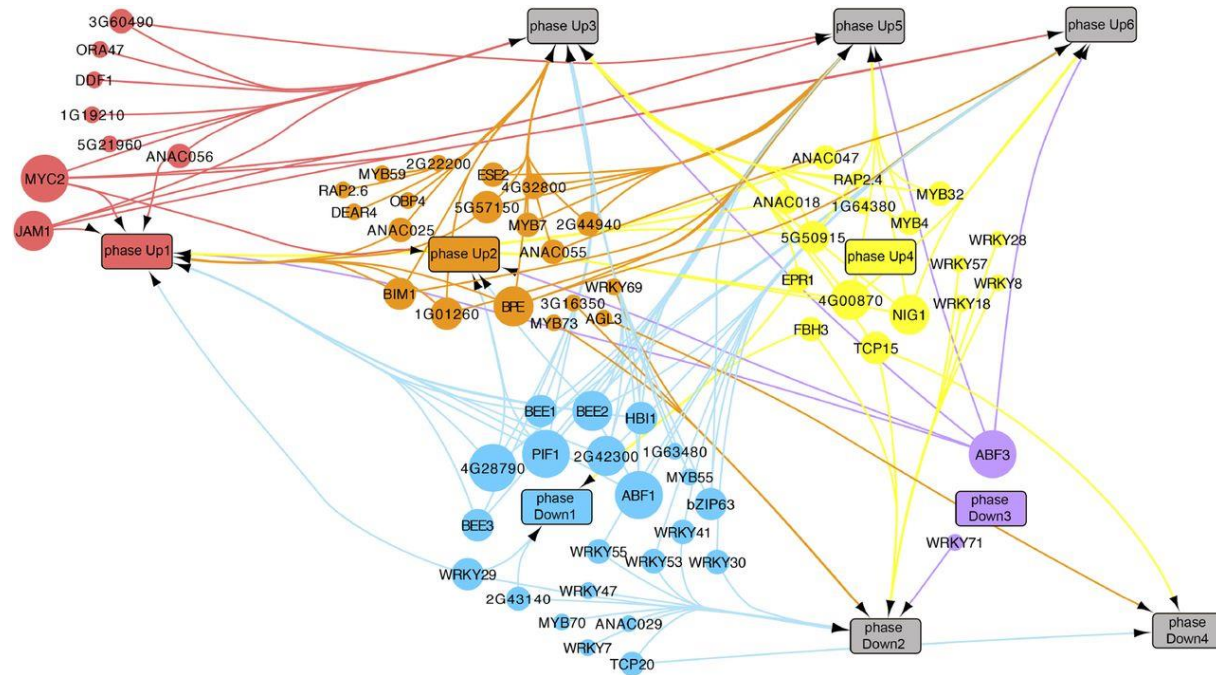
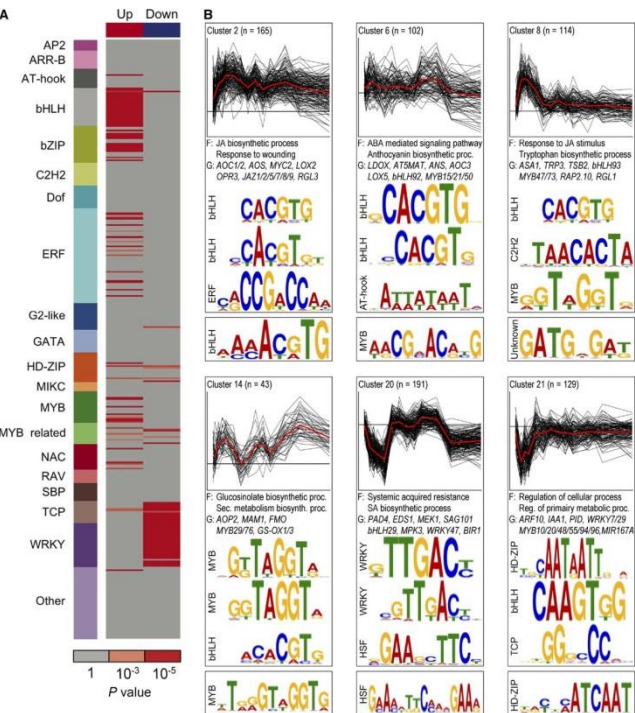
4/12 tested TF are involved in JA defense responses



Co-expression analysis: what for?

Examples of co-expression studies

Data integration and gene clustering for network inference



Gene clusters, gene annotation and promoter analysis

JA gene regulatory network

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