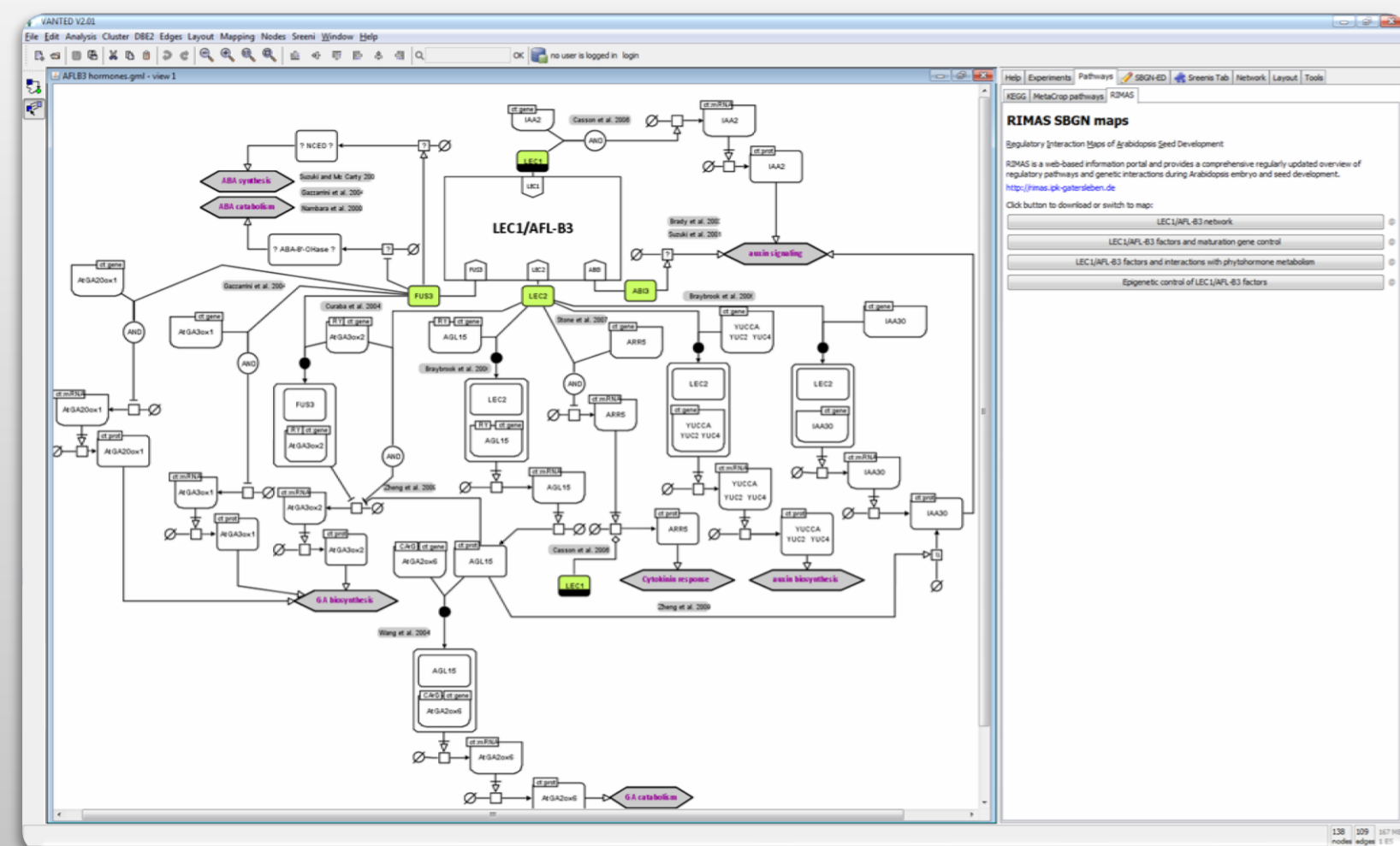


PLANT BIOINFORMATICS

Applications

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RIMAS



<http://rimas.ipk-gatersleben.de>

BIOLOGICAL NETWORK RESOURCES

VANTED provides direct database access

Regulatory Interaction Maps of Arabidopsis Seed Development

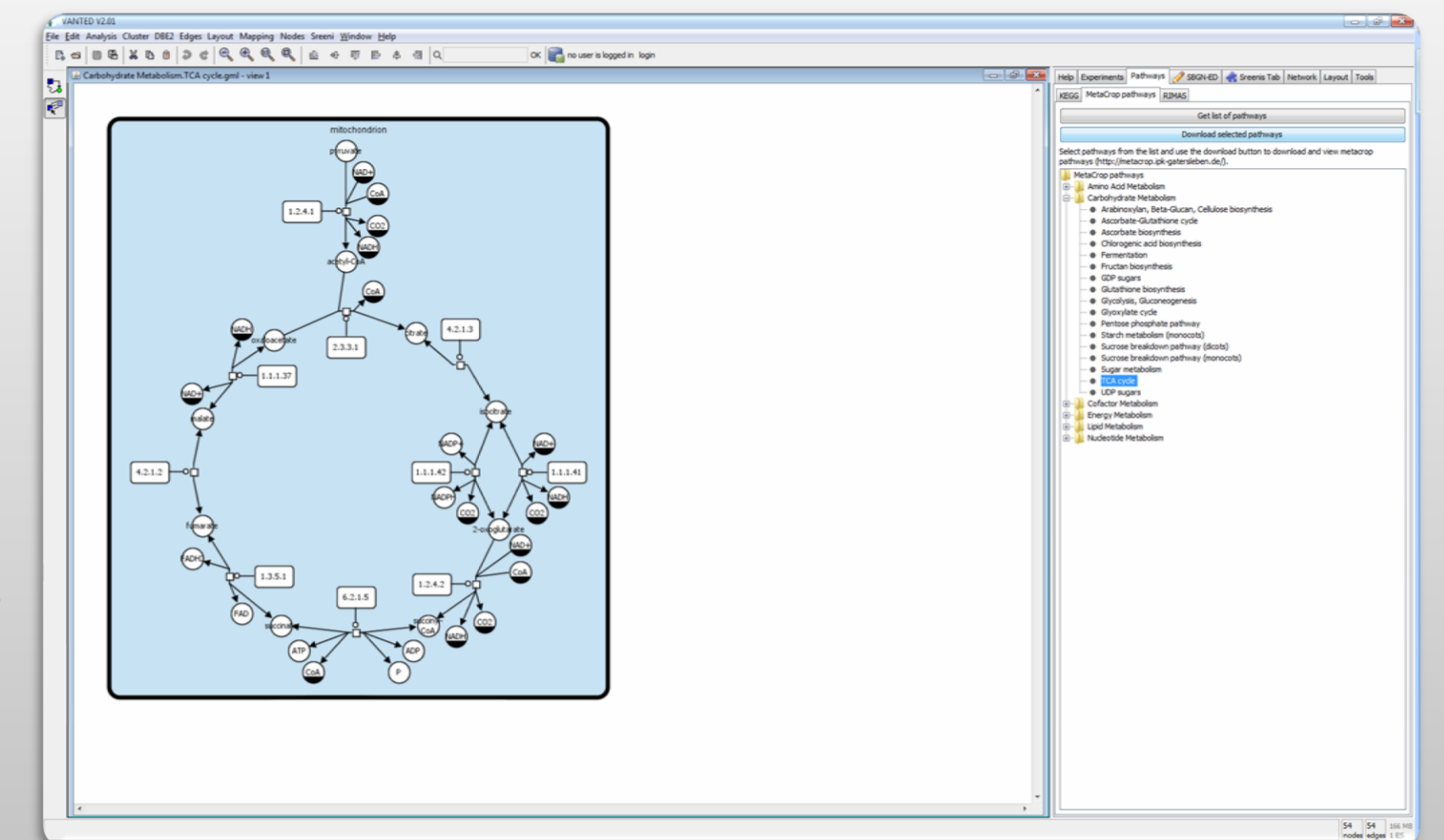
RIMAS is a web-based information portal and provides a comprehensive regularly updated overview of regulatory pathways and genetic interactions during Arabidopsis embryo and seed development.

Metabolic pathway database for crop plant metabolism

MetaCrop is a database that summarizes diverse information about metabolic pathways in crop plants and allows automatic export of information for the creation of detailed metabolic models.

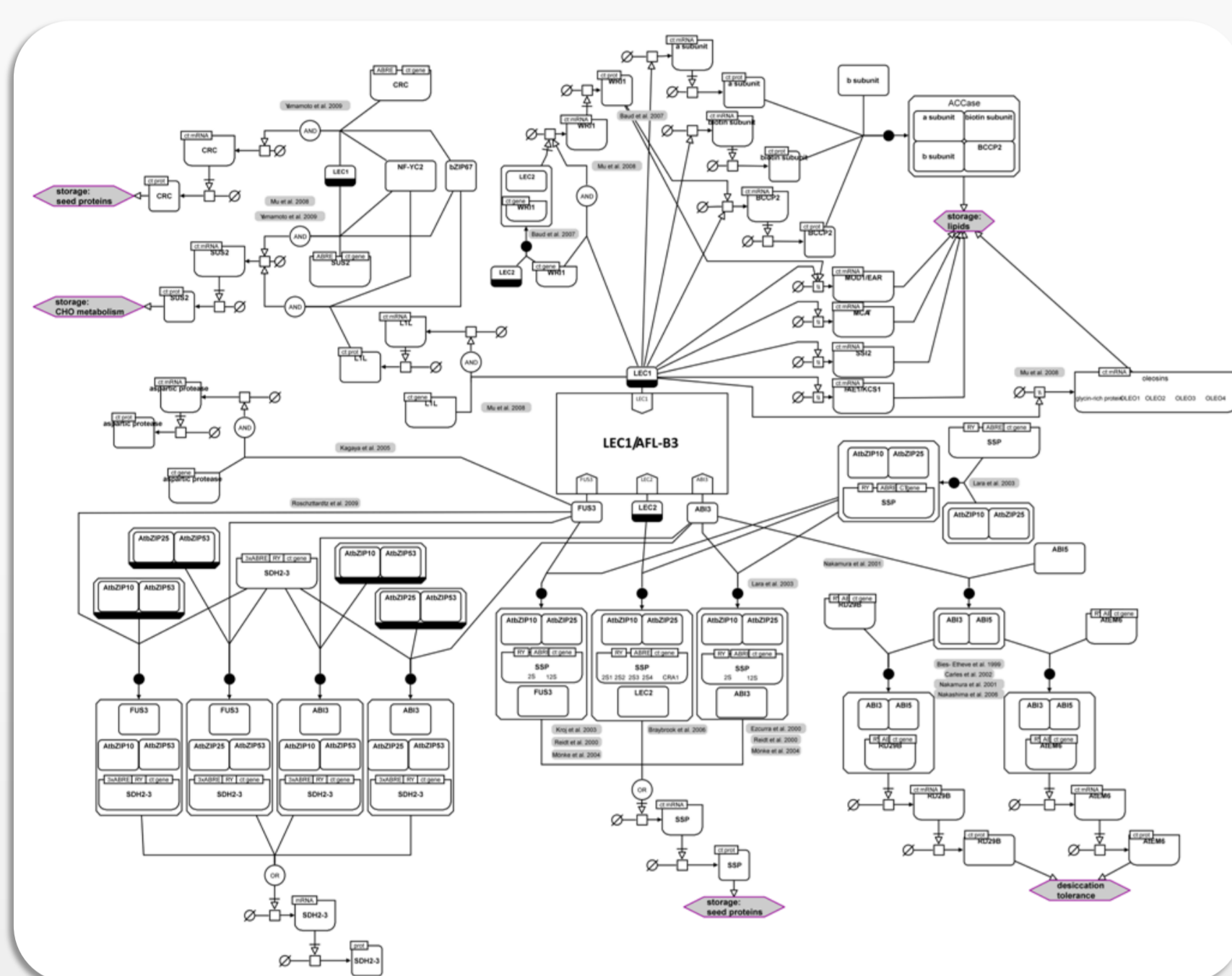


MetaCrop



<http://metacrop.ipk-gatersleben.de>

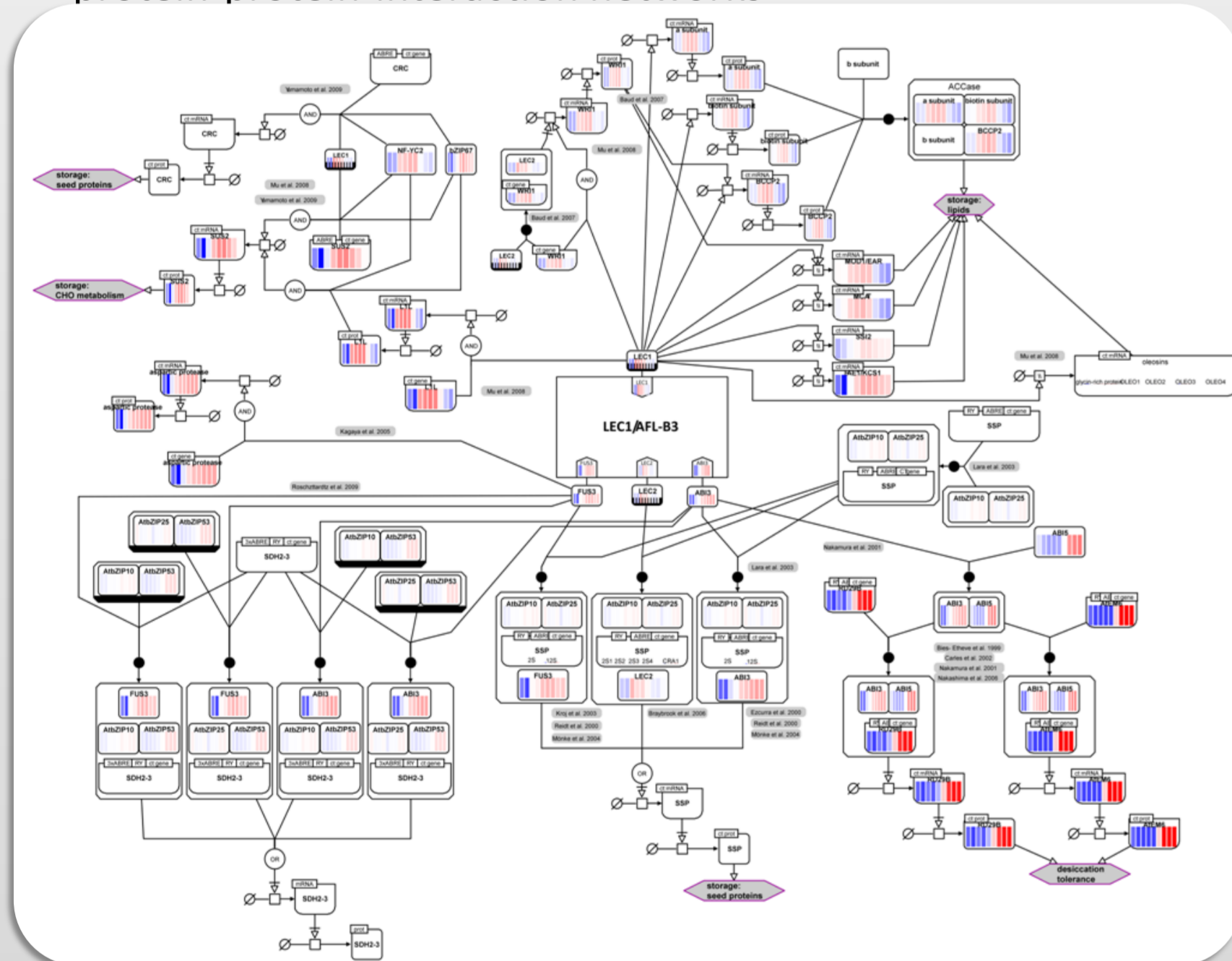
NETWORK-BASED ANALYSIS OF EXPERIMENTAL DATA



Transcriptional control of Arabidopsis seed storage compound accumulation

LEC1/AFL-B3 transcription factors are involved in the regulation of several aspects of seed maturation, including the synthesis of storage compounds (seed storage proteins, lipids) as well as the acquisition of dormancy and desiccation tolerance.

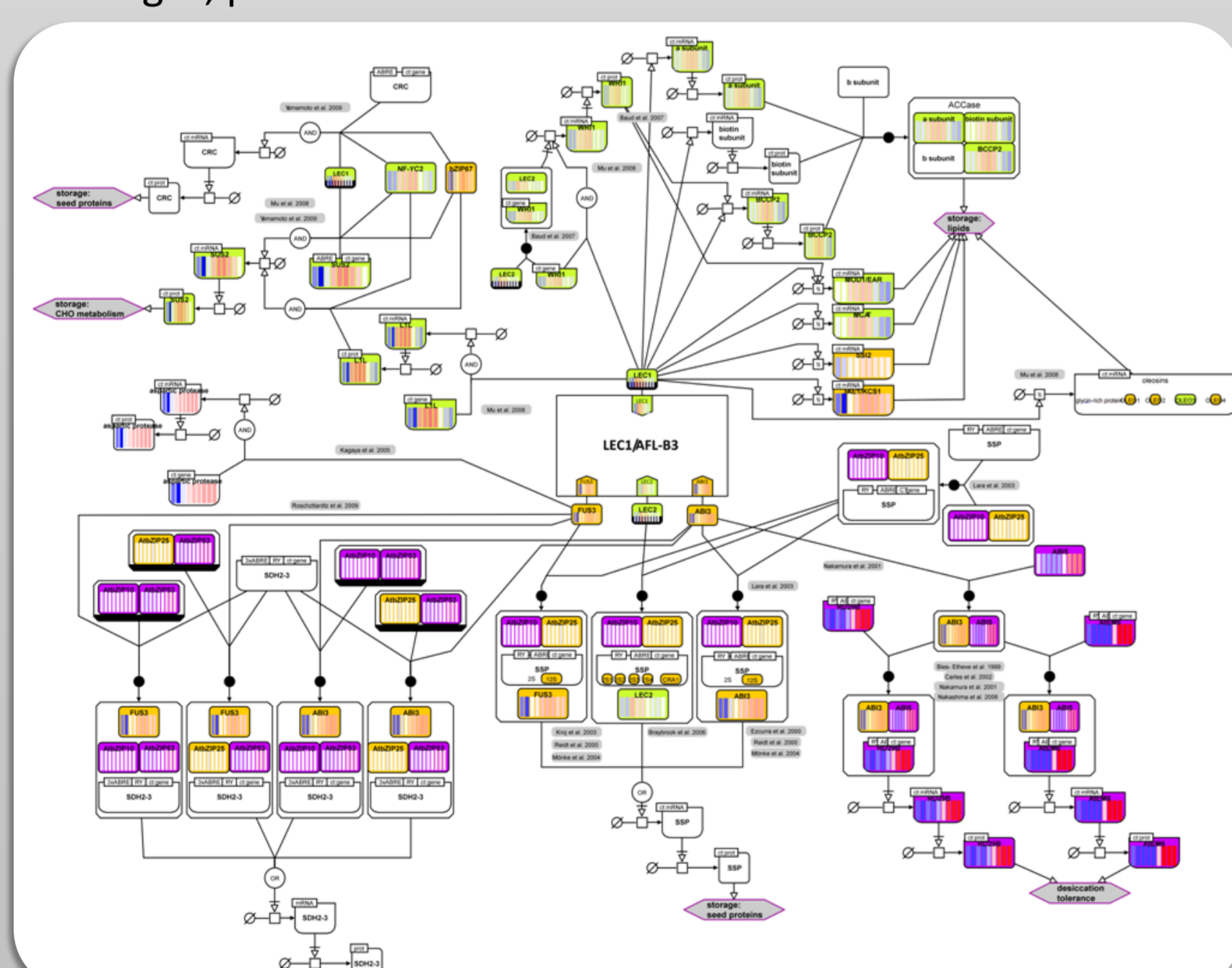
Other network types: metabolic network, signaling networks, networks of functional genomics, protein-protein-interaction networks



Integration of expression data into the gene regulatory context

The regulatory network was enriched by time-resolved expression data with the single bar representing the color-coded expression value of the respective gene at one of nine seed developmental stages. This allows for global analysis of transcription patterns in the context of the network, especially in frame of further mapping-based analyses.

Integration of other data domains: metabolite concentrations, enzyme activities, flux values, images, proteomics data



SOM-based clustering of expression profiles

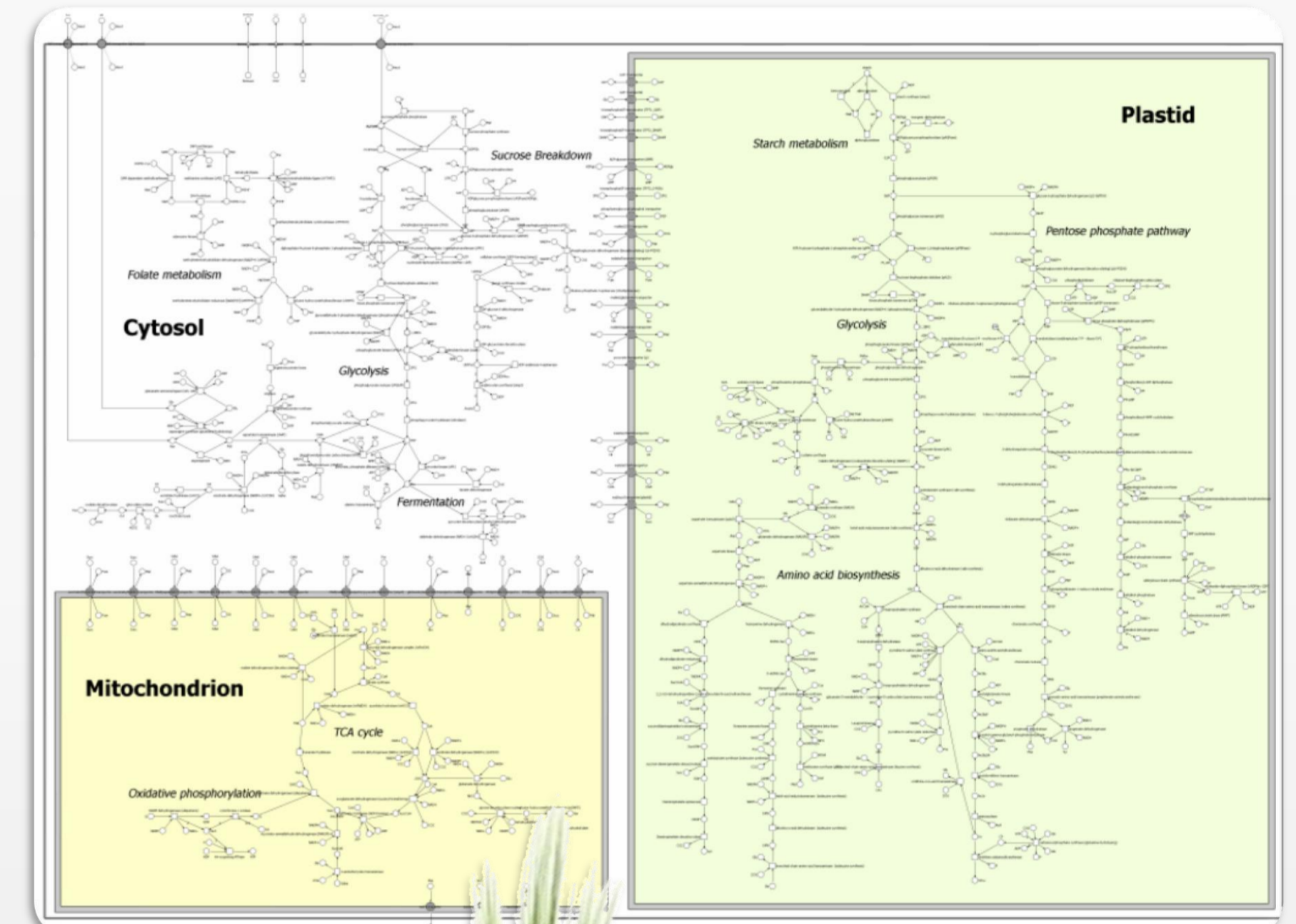
Gene regulation is dependent on overlapping expression domains of transcription factor and target gene. LEC1 is expressed during early stages of embryogenesis as most of its targets (green cluster). ABI3 and FUS3 are regulators of seed maturation and cluster together with their targets such as seed storage protein and desiccation-related genes (orange and purple clusters).

Other types of mapping-based statistical analyses: correlations (1:n; n:n)

METABOLIC MODELING

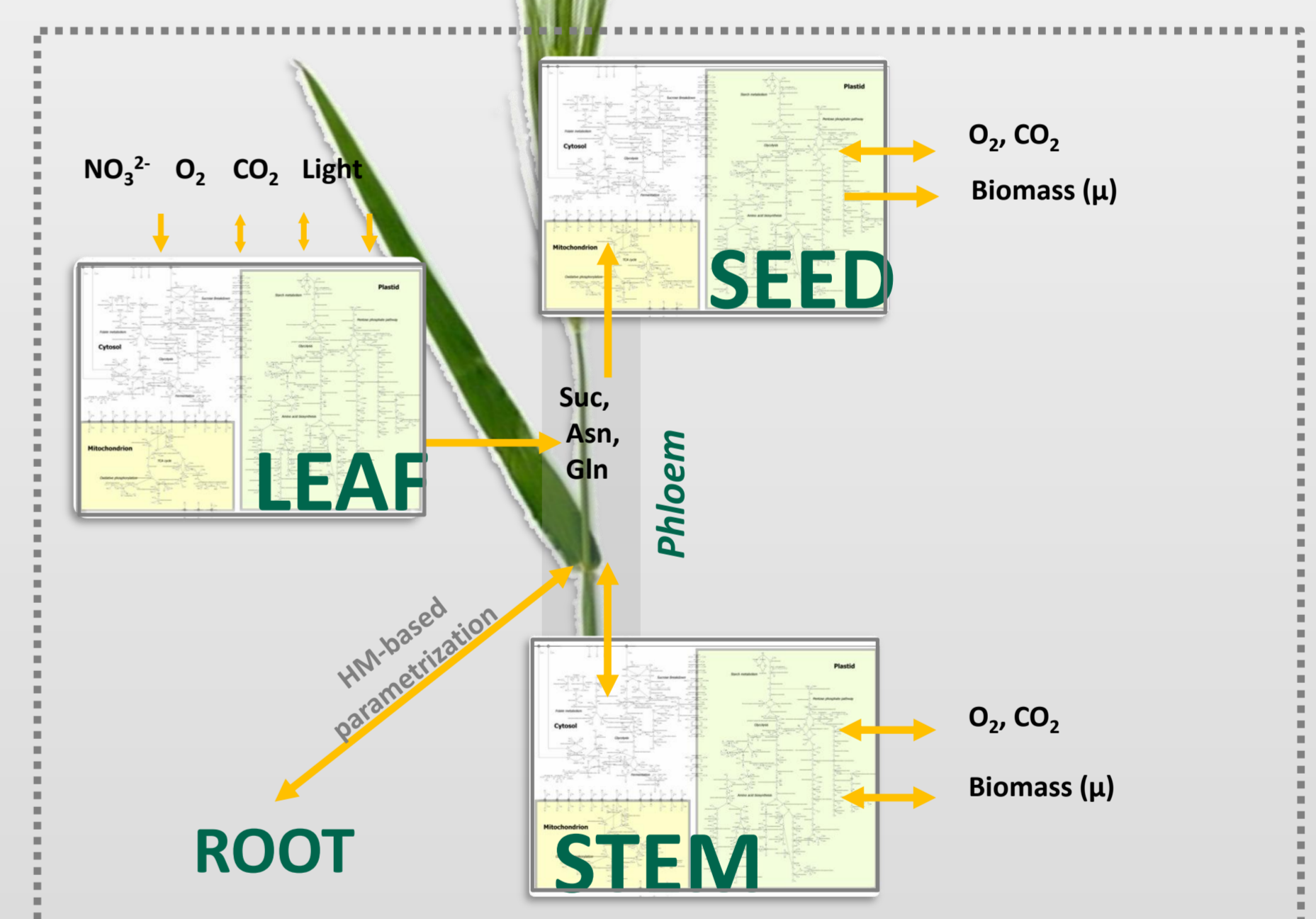
Reconstruction of barley organ-specific stoichiometric models

Based on the pathway collection in the MetaCrop database, stoichiometric models have been generated for the barley leaf, stem and seed comprising between 335 and 355 biochemical and transport reactions each.



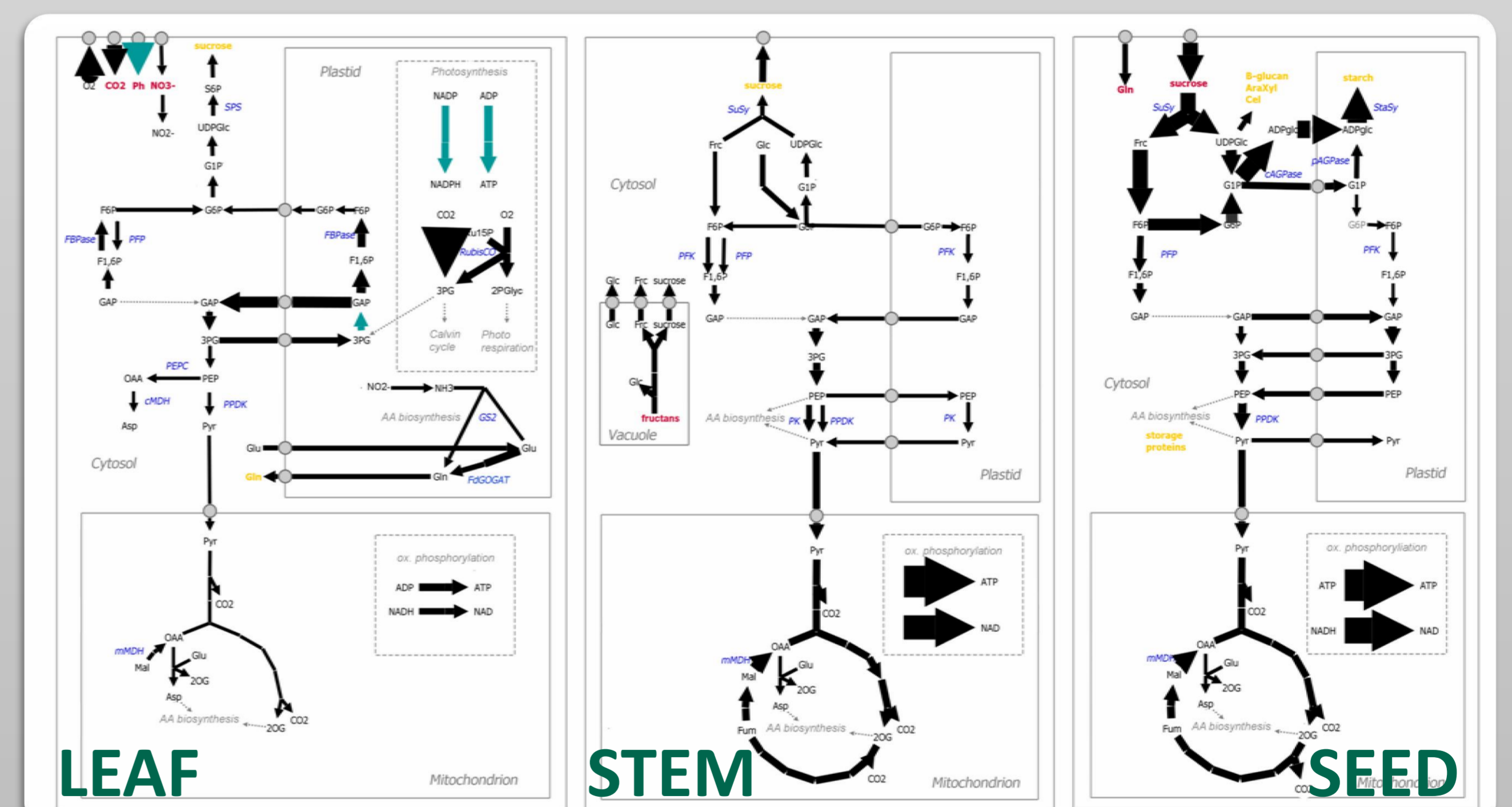
Multilevel metabolic modeling (MMM)

This approach integrates highly detailed, compartmentalized static metabolic models on the organ-scale (seed, leaf, stem) with a dynamic functional-structural model (household model, HM) on the whole plant scale, resulting into a quasi-dynamic multi-organ model.



Analysis and visualization of source-sink interactions during barley seed development

In order to find efficient flux distributions across the whole plant metabolism, Flux Balance Analysis (FBA) was applied to the quasi-dynamic, whole-plant model. This method enabled us to analyse the relations of source and sink organs during plant development, focussing on the seed developmental phase of barley. The model is capable of representing the sink-to-source shift of the barley stem in a quantitative and time-resolved manner and it provides evidence for significant contributions of the stem to seed filling.



Network

Data mapping

Mapping-based analysis

Model reconstruction

Model coupling

Simulation/Analysis

References

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