



MAX-PLANCK-GESELLSCHAFT

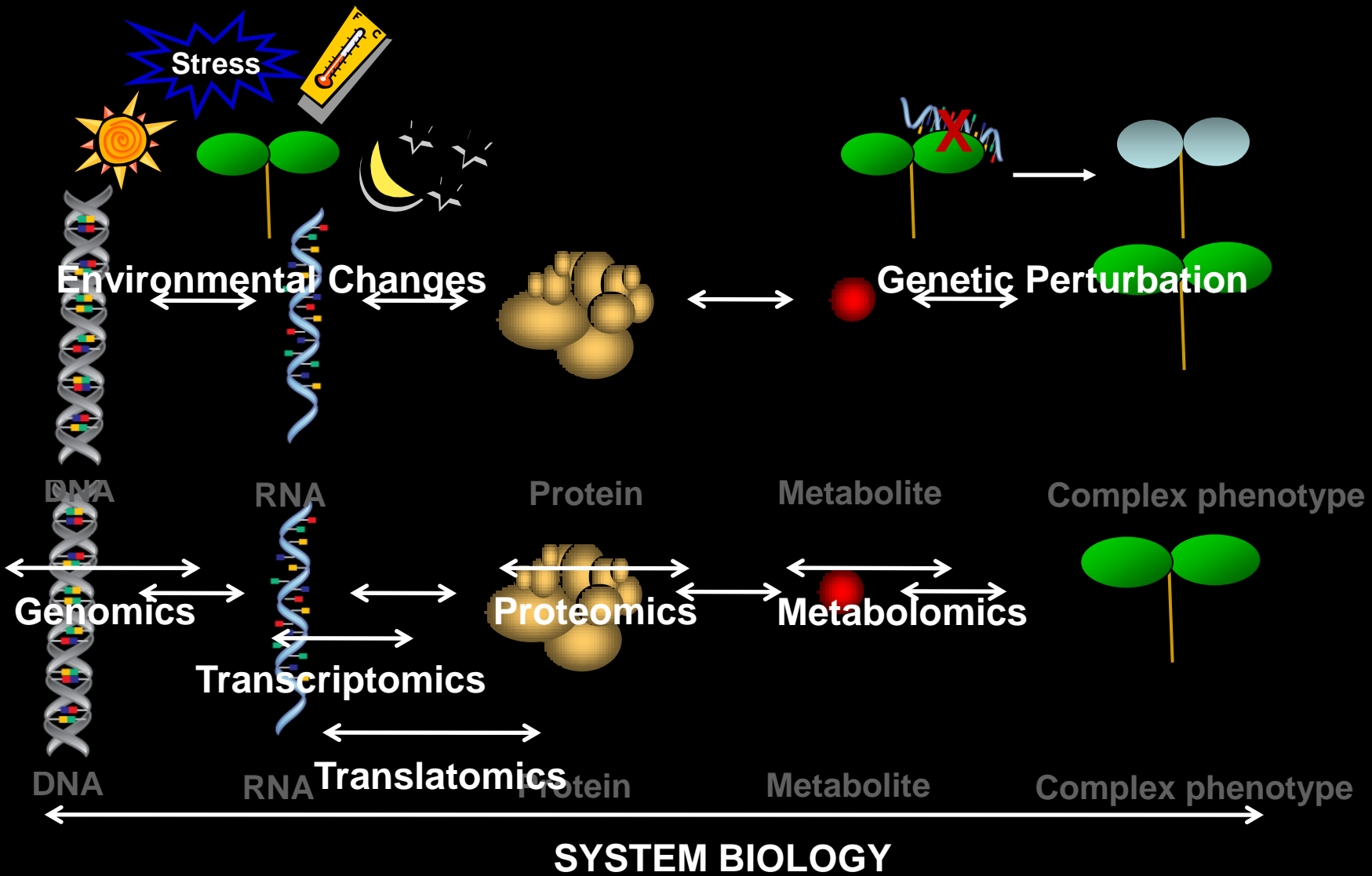


Max-Planck-Institut  
für Molekulare Pflanzenphysiologie

# Metabolite and transcript interactions in response to the environment

Camila Caldana

# Systems Biology



# Outline

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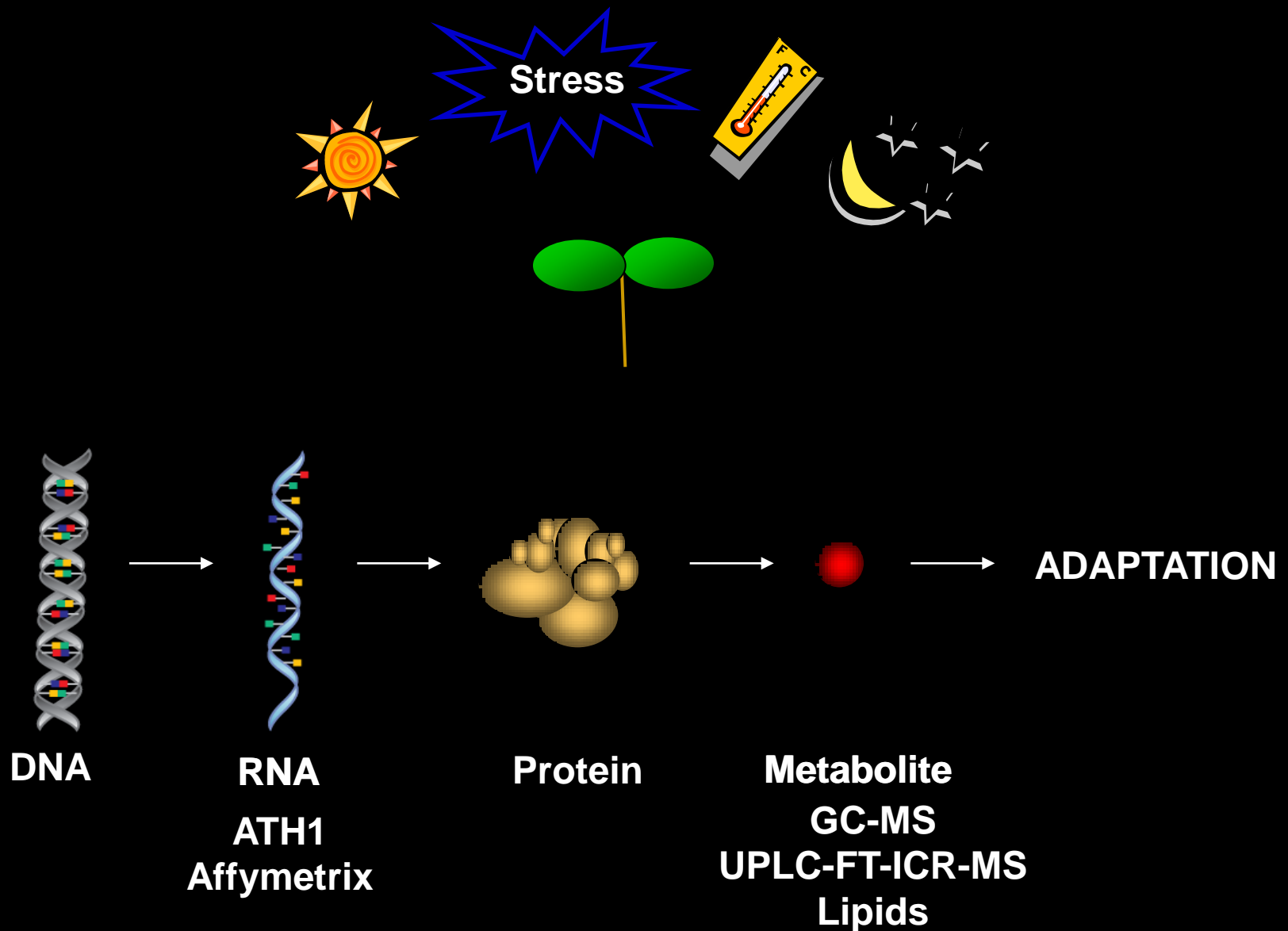
## I. Environmental Changes

Metabolomic and transcriptomic high-density kinetic response analysis of *A. thaliana* to eight environmental conditions.

## II. Genetic Perturbation

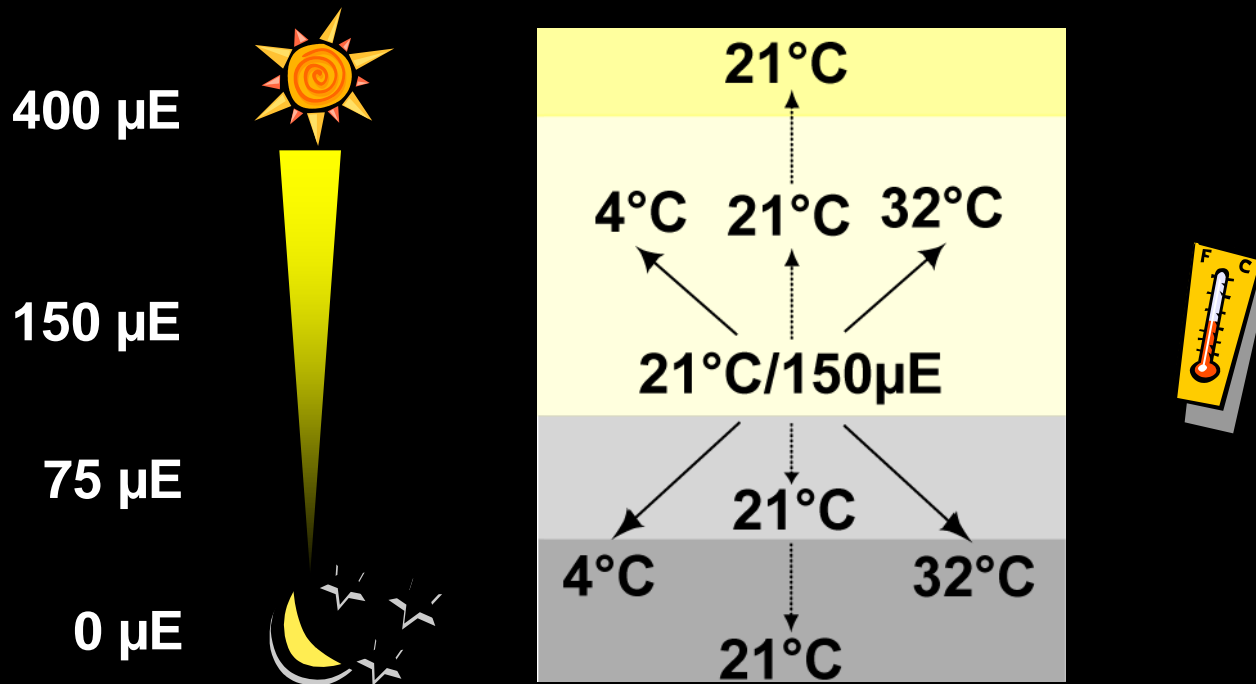
Functional characterization of Target of Rapamycin (TOR) complex and its link with growth.

# Systems-level analysis: Environmental Changes



# Dynamic environmental response networks

## Experimental design



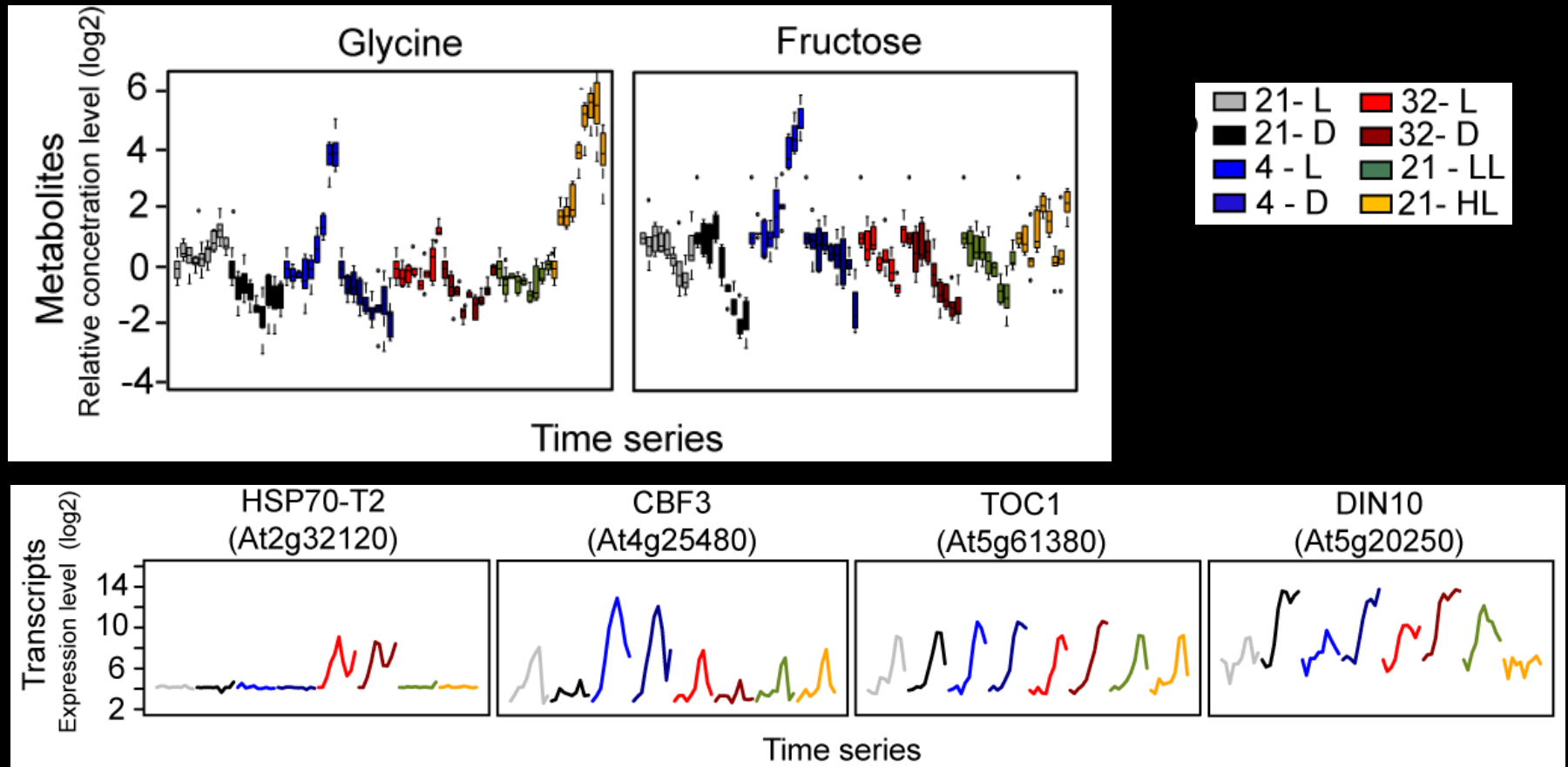
Linear: 0, 20... 360 min = 19 times

Log: 0, 5, 10min... 21.3h = 10 times



# Dynamic environmental responses

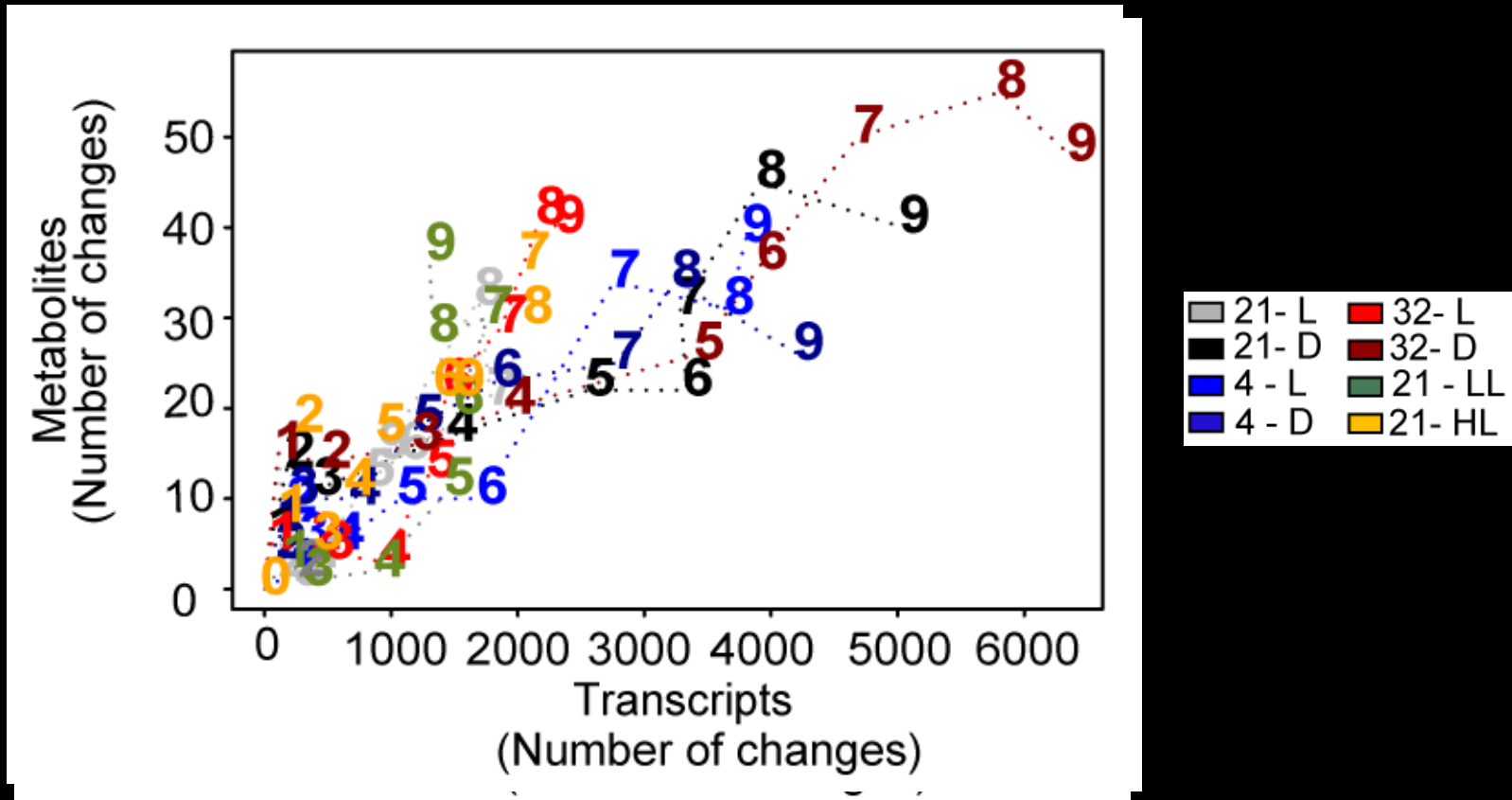
## Analysis overview



- Reproducibility of data: 6 biological replicates
- Condition-dependent response in time-dependent manner

# Global coordination of the responses

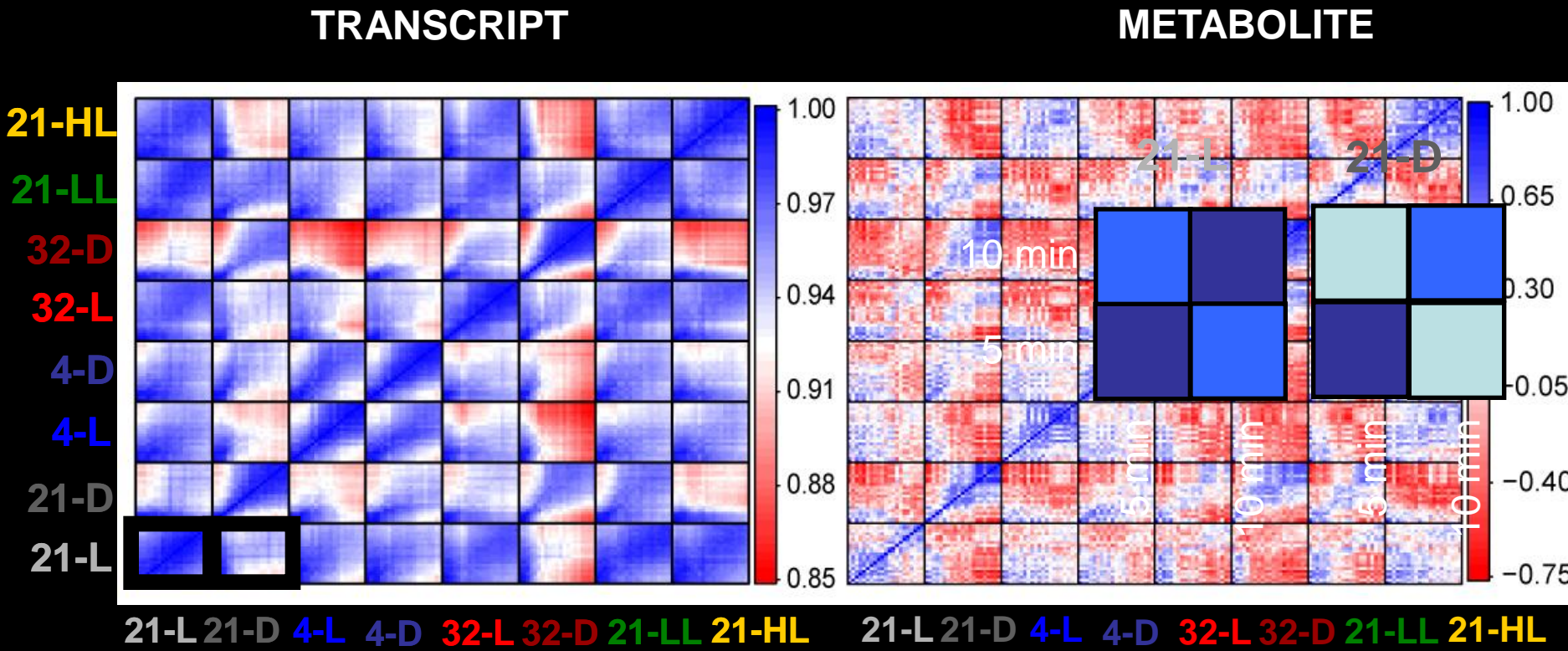
## Number of changes



- Coordination of the responses is condition-dependent

# Metabolite response is more diverse

## Spearman correlation

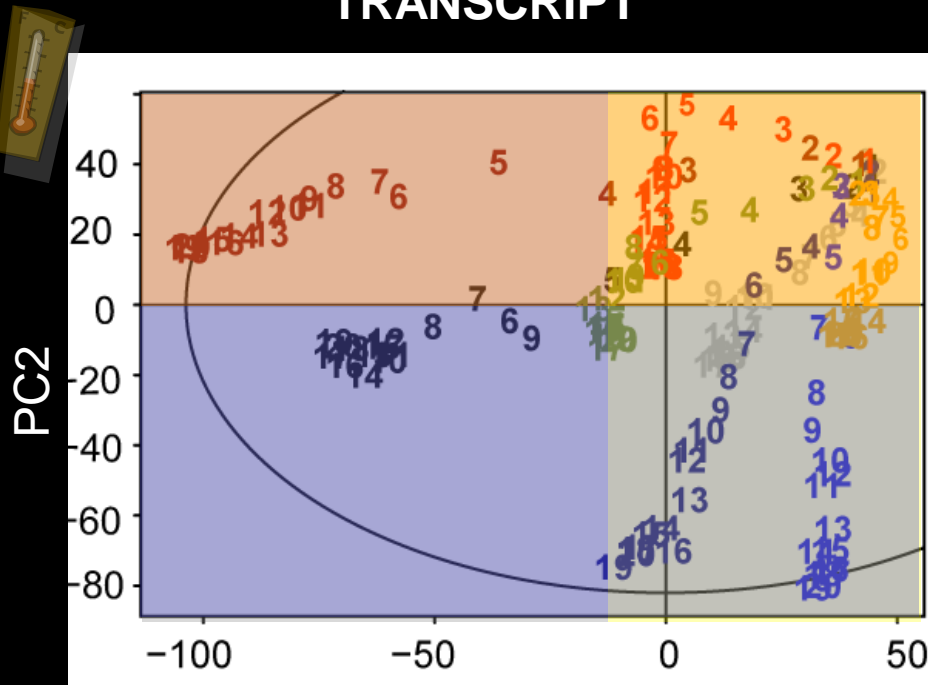




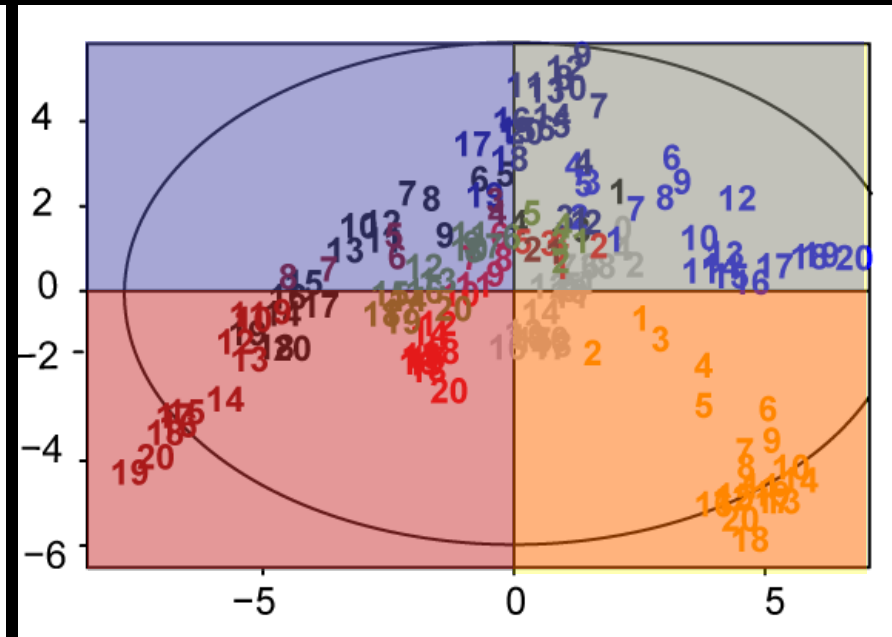
# Light and temperature interactions

## Principal Component Analysis (PCA)

### TRANSCRIPT



### METABOLITE



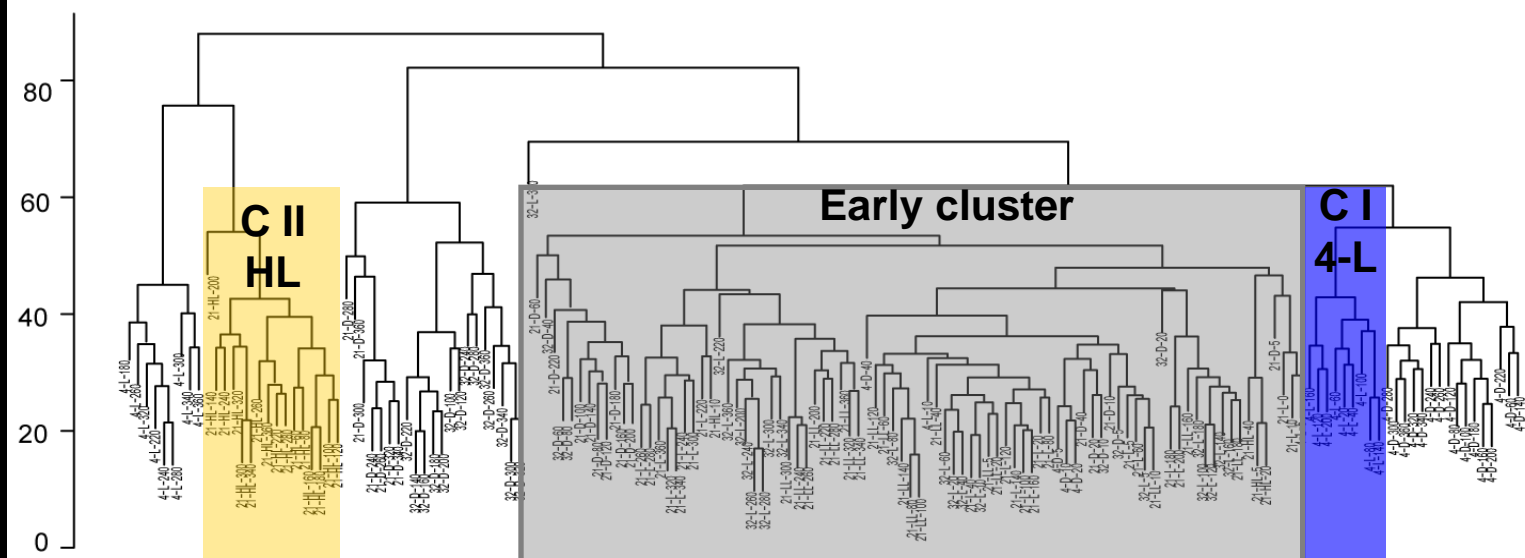
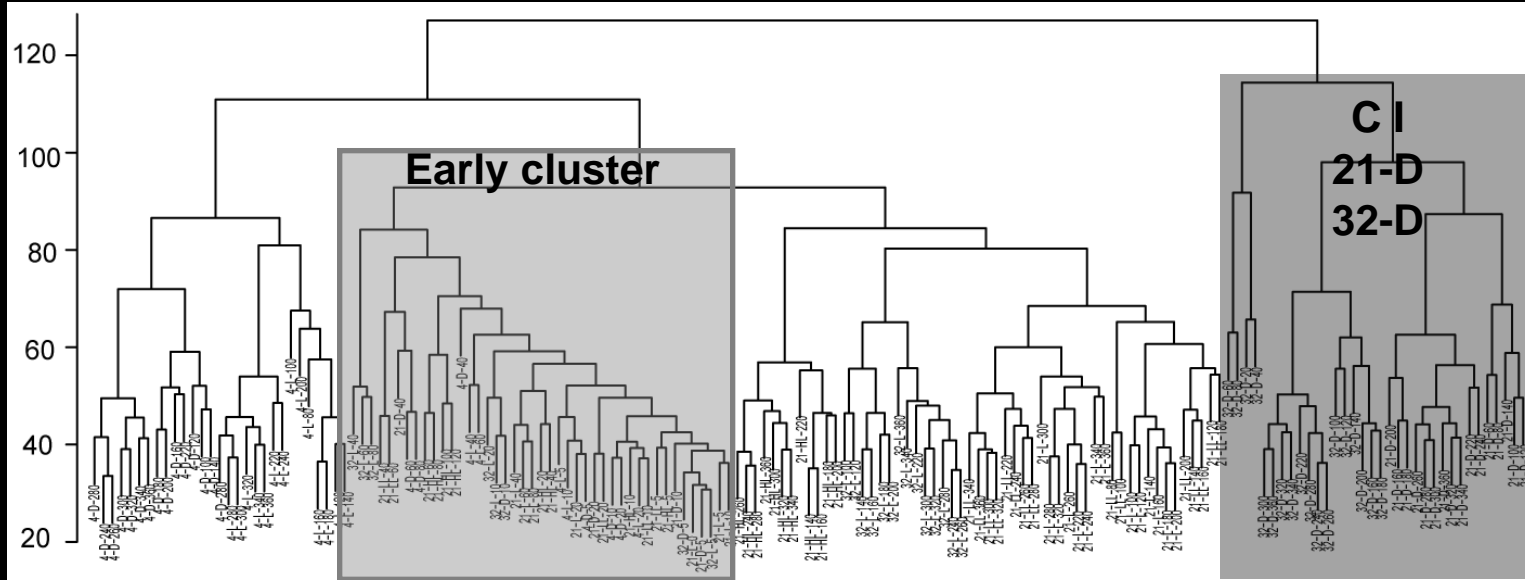
PC1



- Dark response is made more strong by combination with heat
- Cold response has an additive effect in combination with light

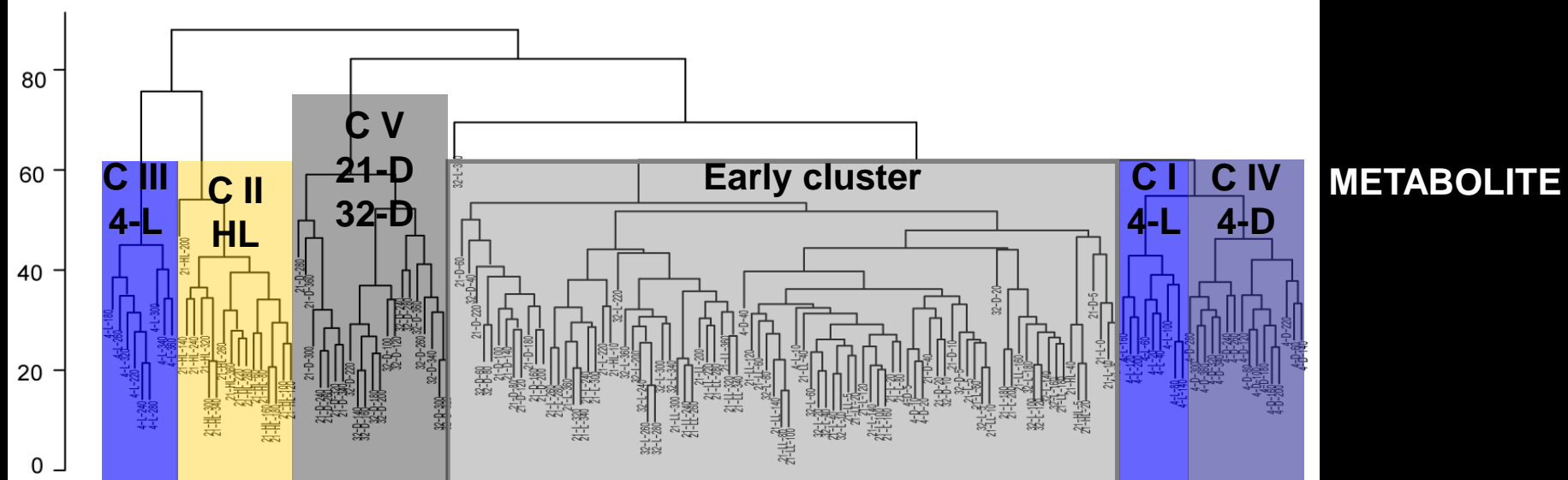
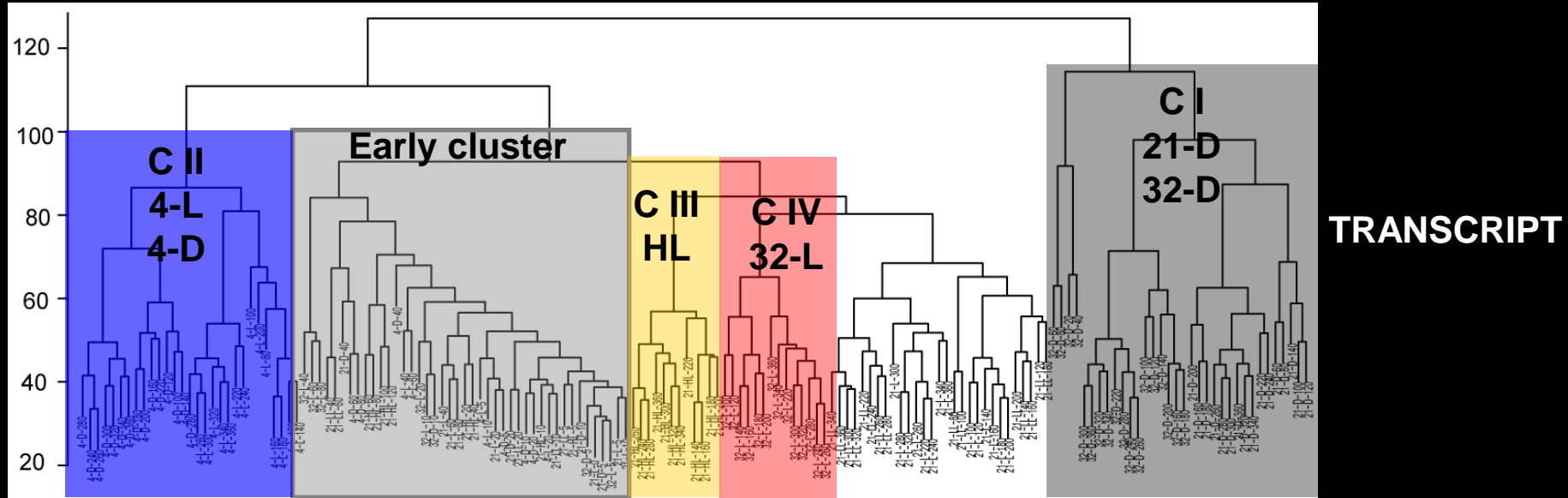
# Condition-dependent kinetics

## Hierarchical clustering analysis (HCA)



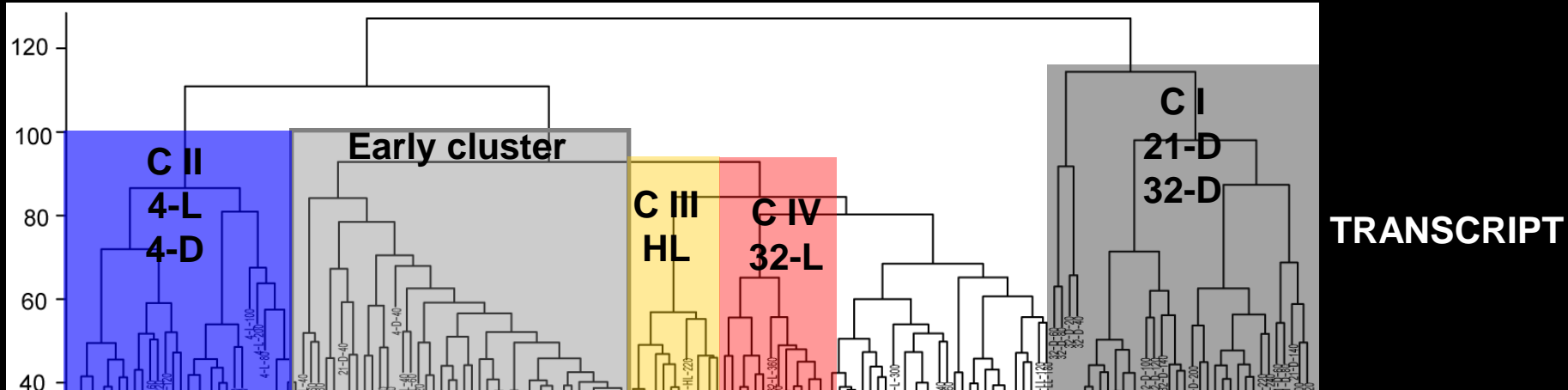
# Condition-dependent kinetics

## Hierarchical clustering analysis (HCA)

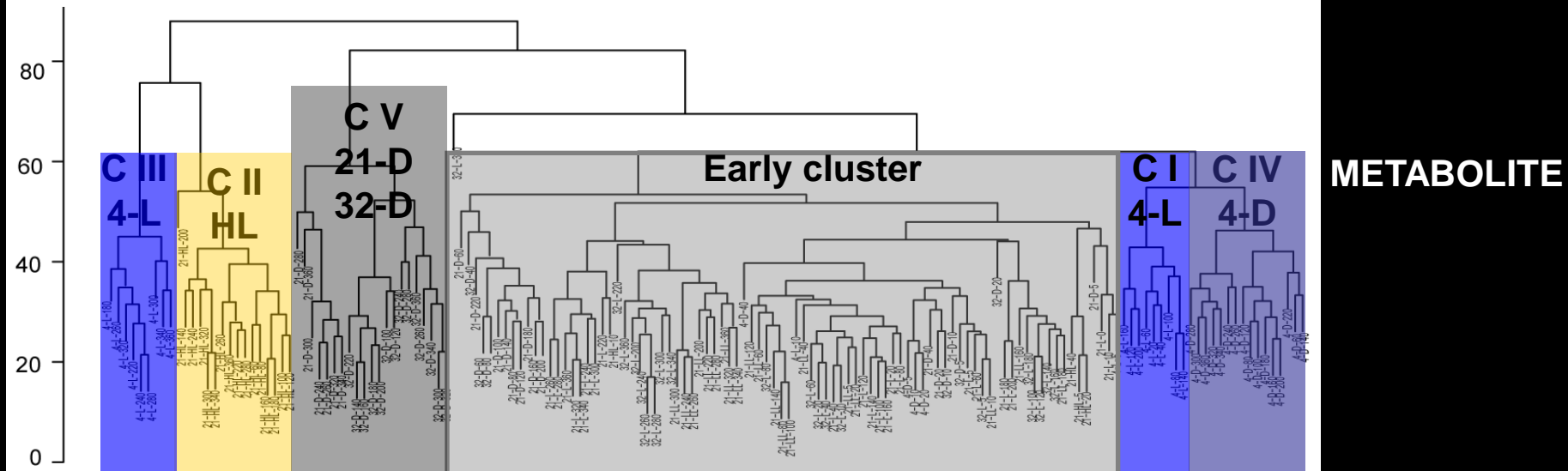


# Condition-dependent kinetics

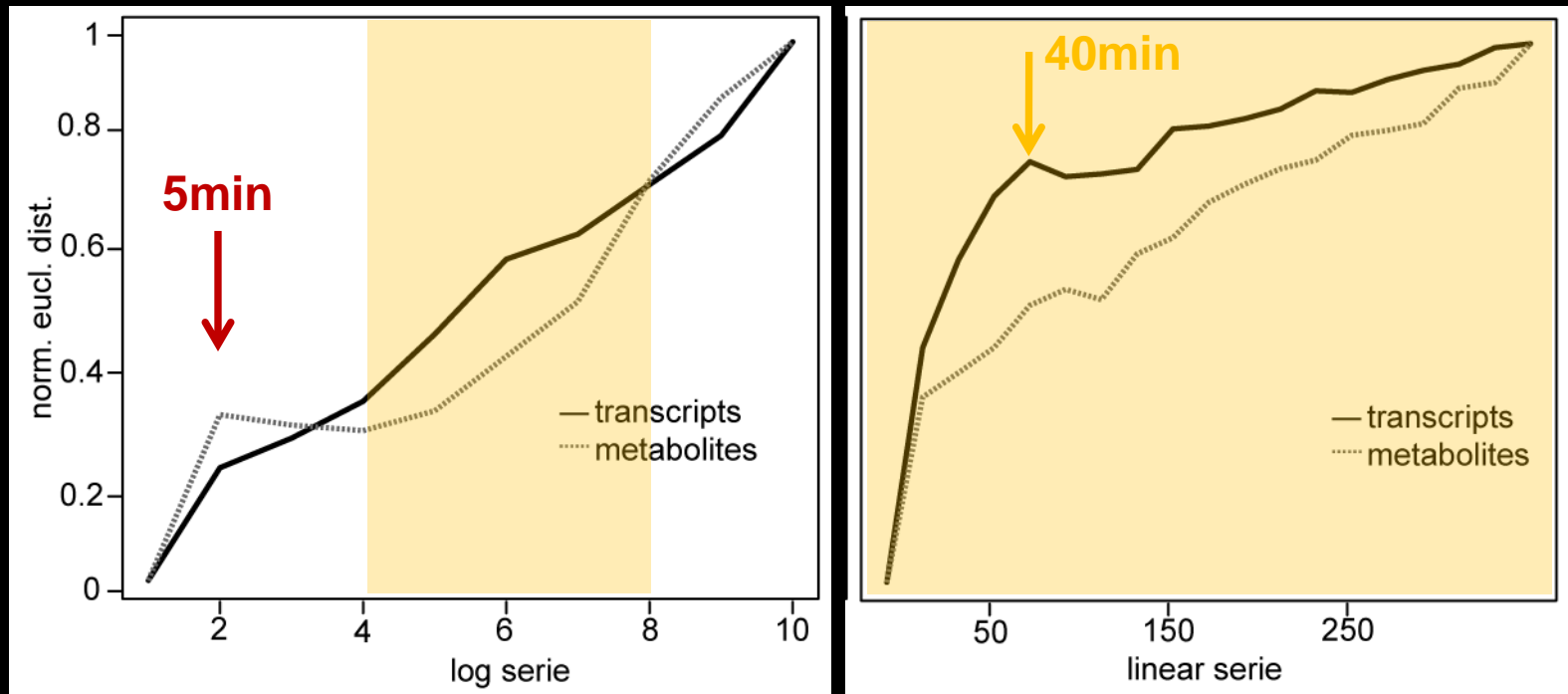
## Hierarchical clustering analysis (HCA)



**-Response kinetics of the system on the transcript and the metabolite level is different**



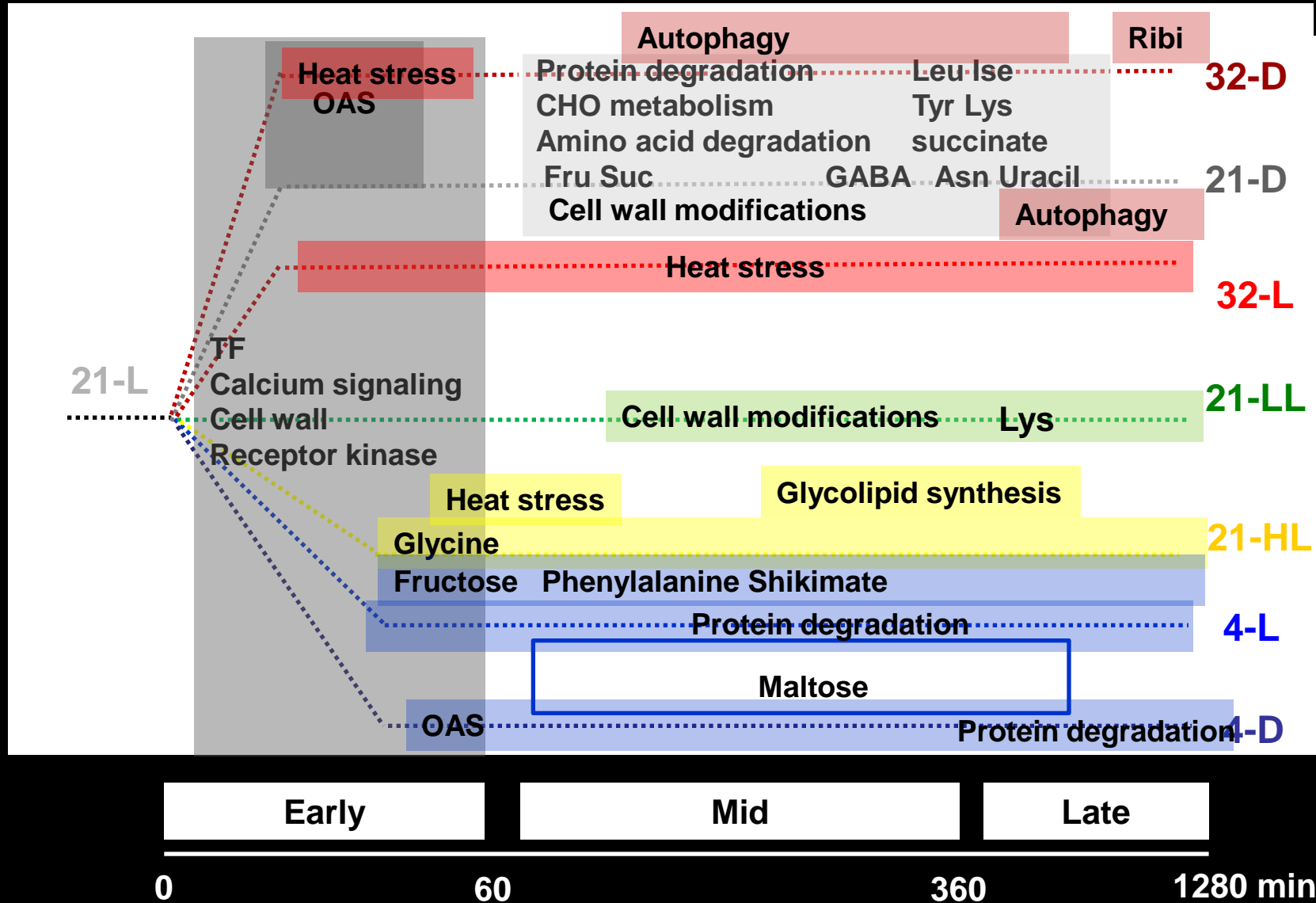
# Metabolites respond by initial burst of changes



- Response on the metabolite level is initially faster (5min)
- After 40 minutes, the relative separation on the transcript level exceeds that of the metabolite level

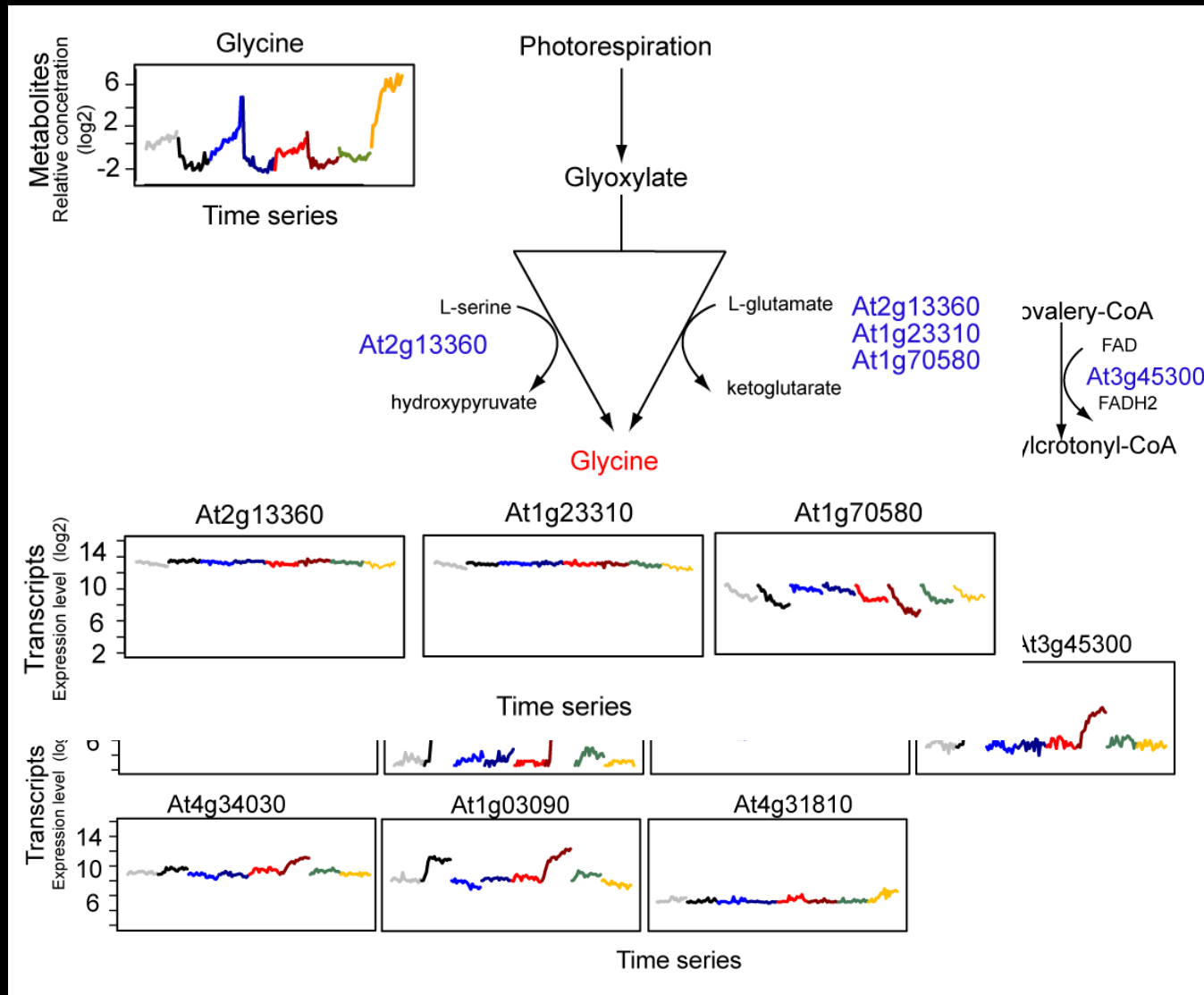
# Overall conserved response is transcript-restricted

## GO terms over-representation analysis



# Correlation between metabolic and gene expression changes

## Photorespiration



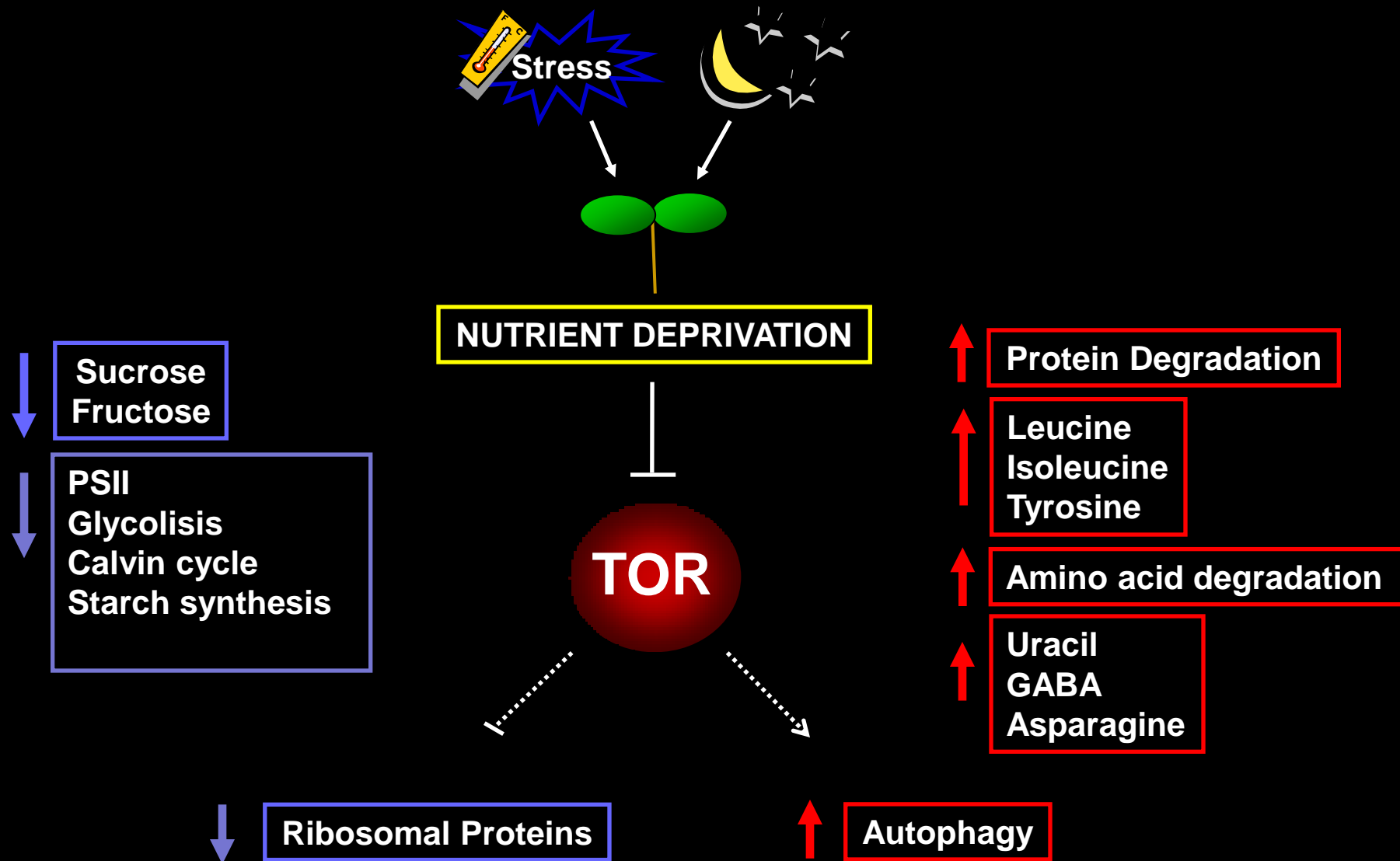
# I. Conclusions: Environmental Changes

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- **System-wide reprogramming is driven by interacting temperature and light gradients leading to distinct states over time.**
- **Response on the metabolite level is initially faster and displays a higher level of specificity than transcript response.**
- **Overall conserved system response is restricted to the transcriptome.**
- **Coordination of global metabolite and transcriptional responses is condition-dependent.**
- **Starvation dominates the dark response.**



# Starvation dominates the system response to darkness



# Outline

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## I. Environmental Changes

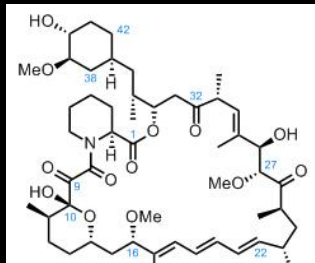
Metabolomic and transcriptomic high-density kinetic response analysis of *A. thaliana* to eight environmental conditions.

## II. Genetic Perturbation

Functional characterization of Target of Rapamycin (TOR) complex and its link with growth.

# Target of rapamycin (TOR) function

## RAPAMYCIN

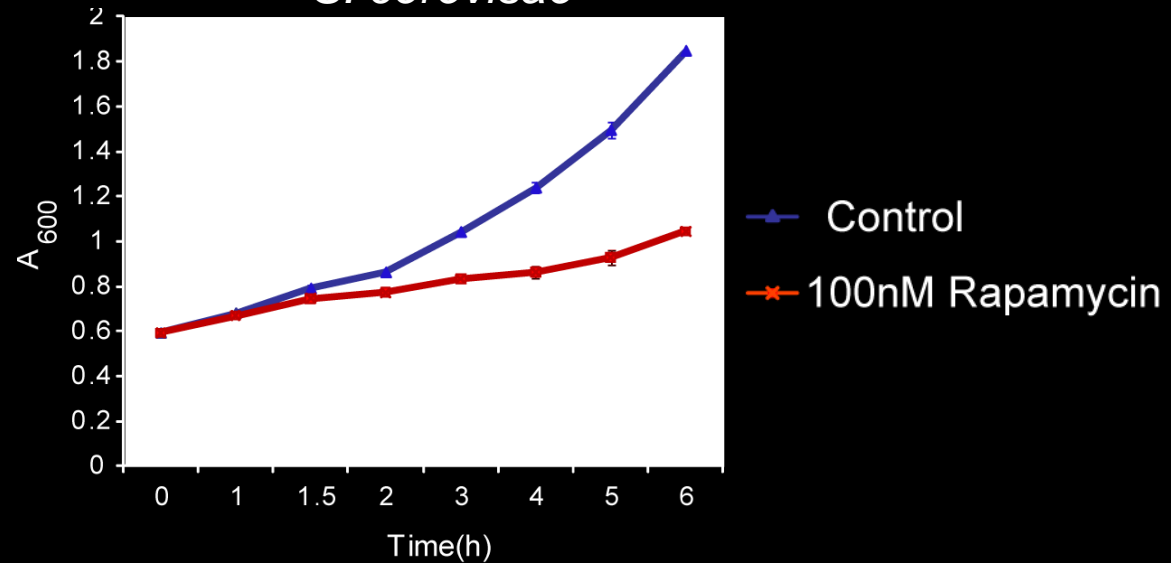


FKBP12

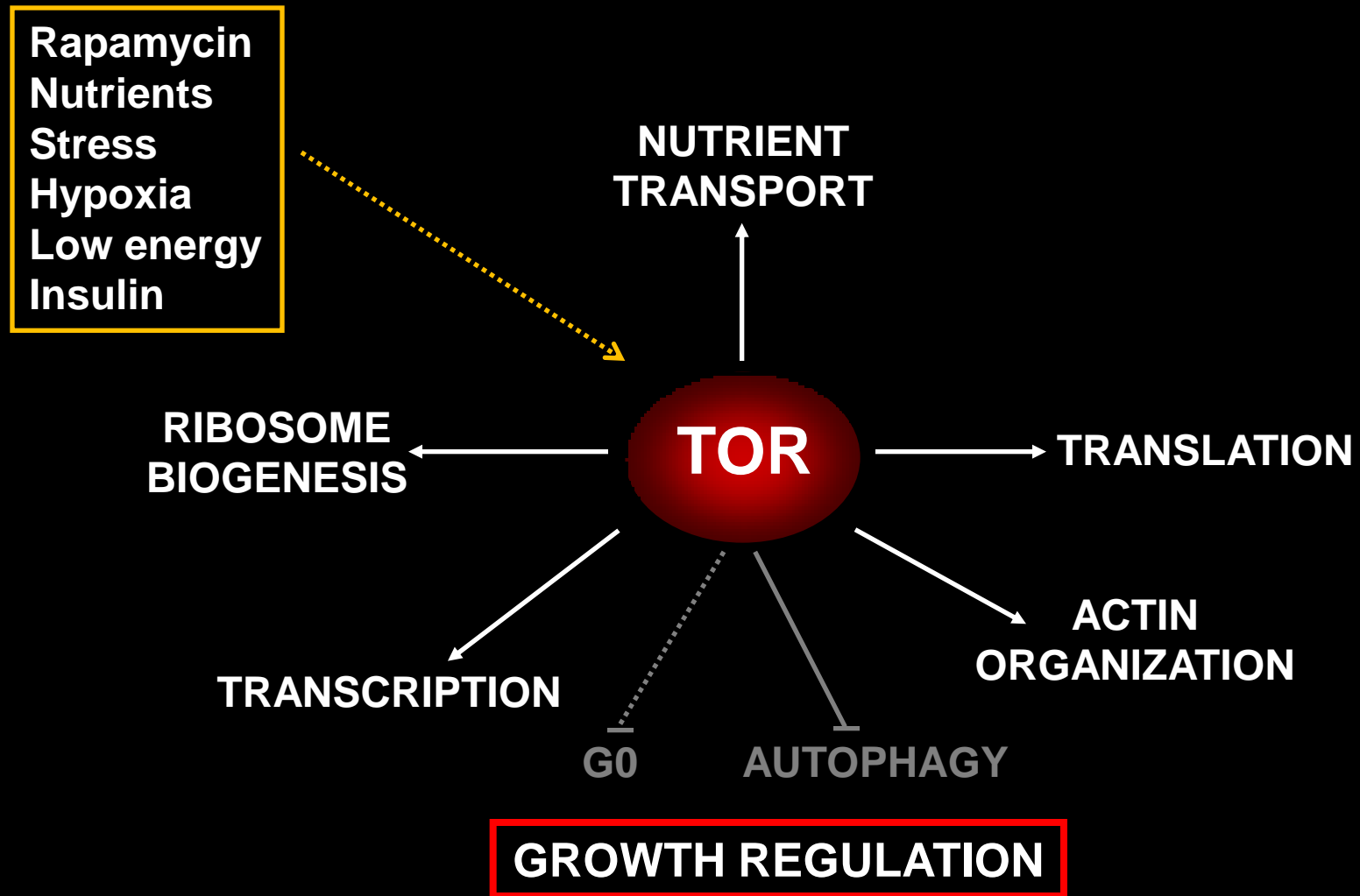
TOR

GROWTH

*S. cerevisiae*

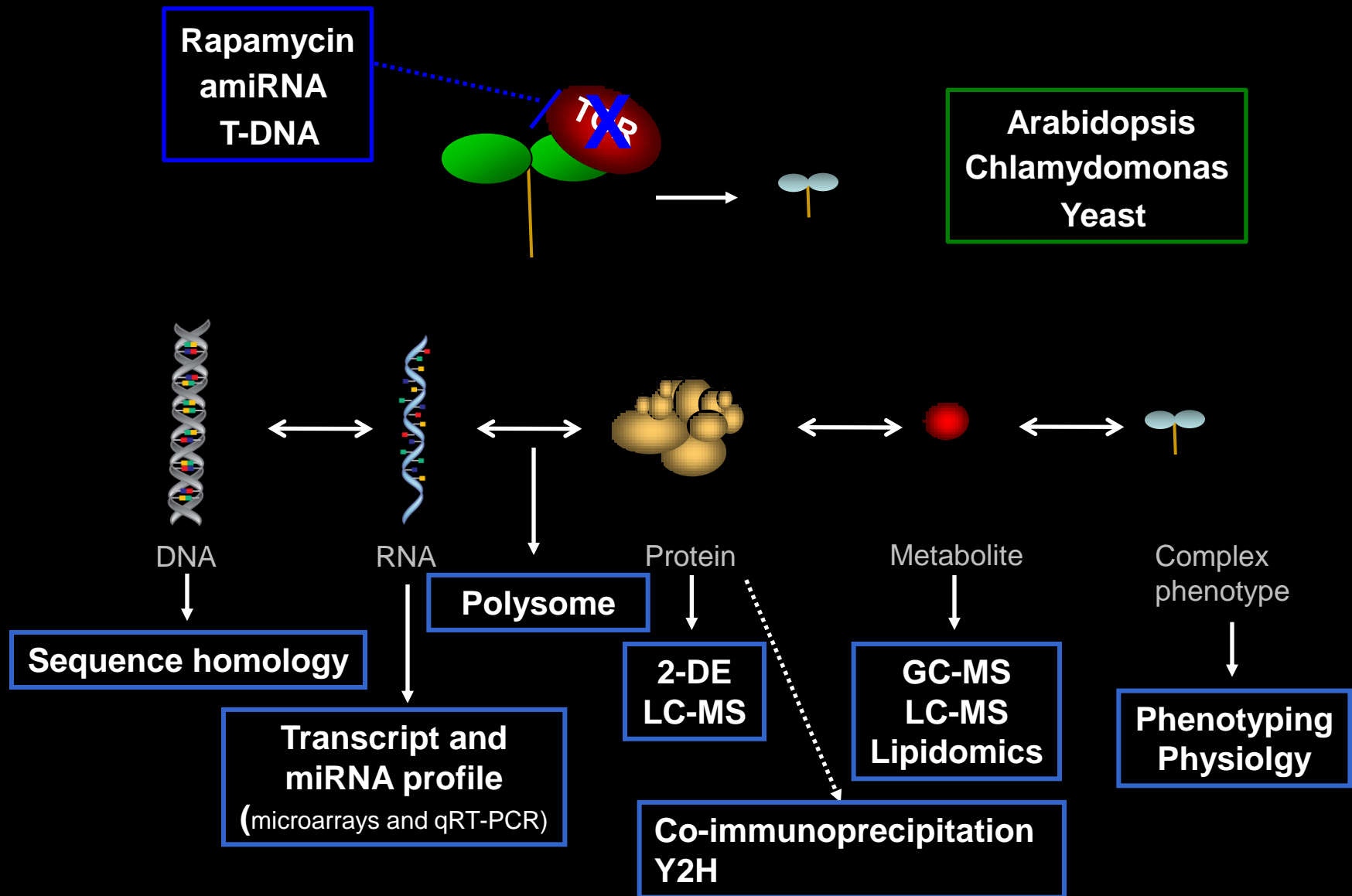


# Target of rapamycin (TOR) functions

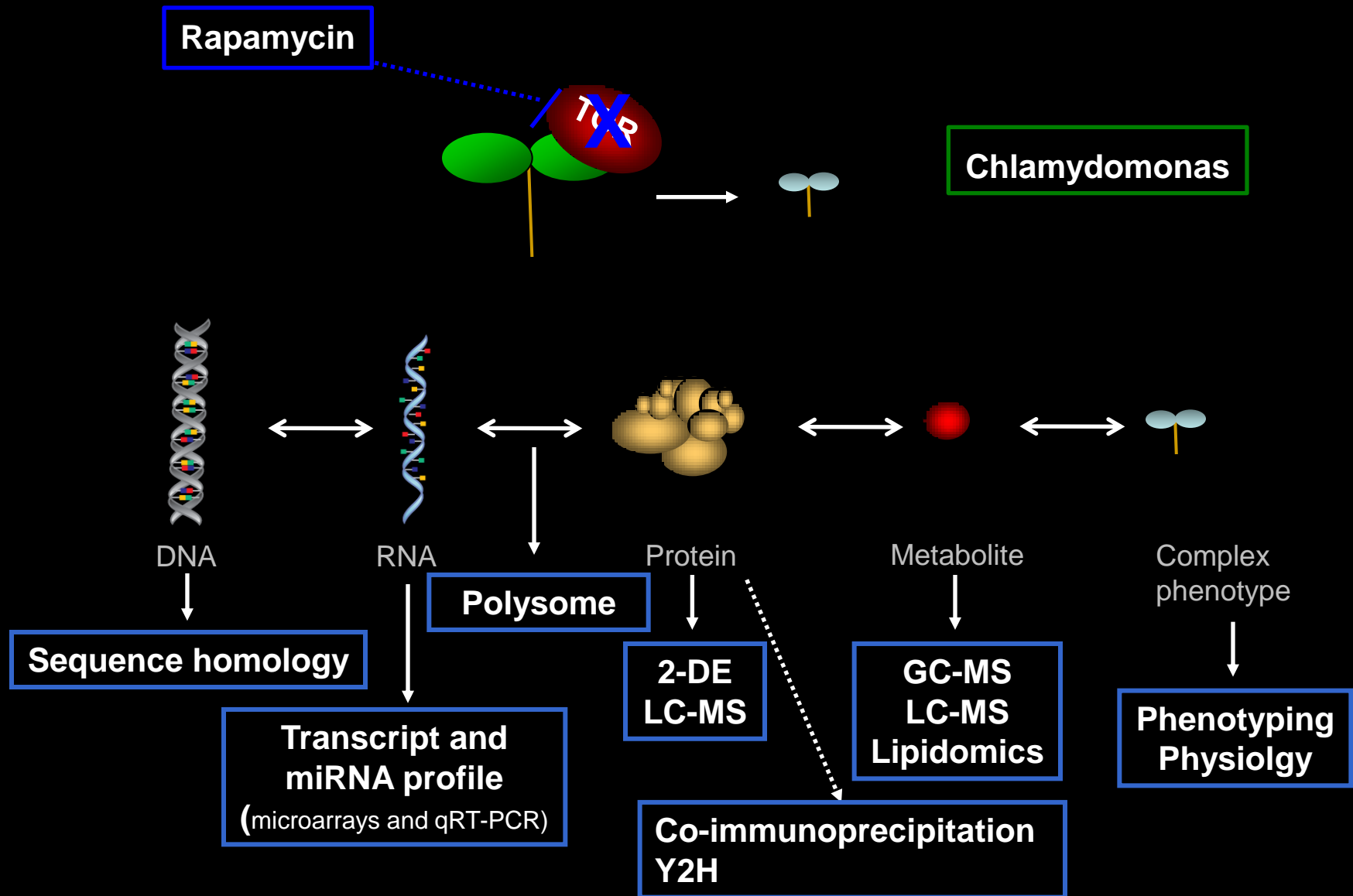


- TOR present in all eukaryotic genome

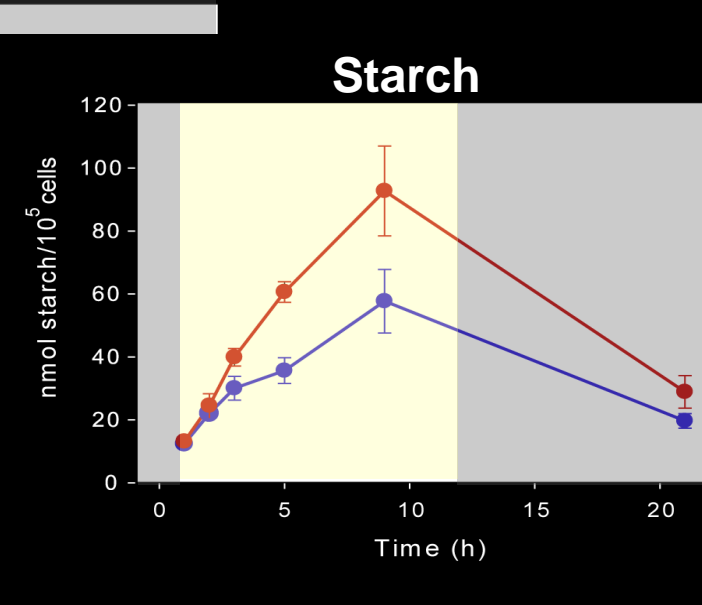
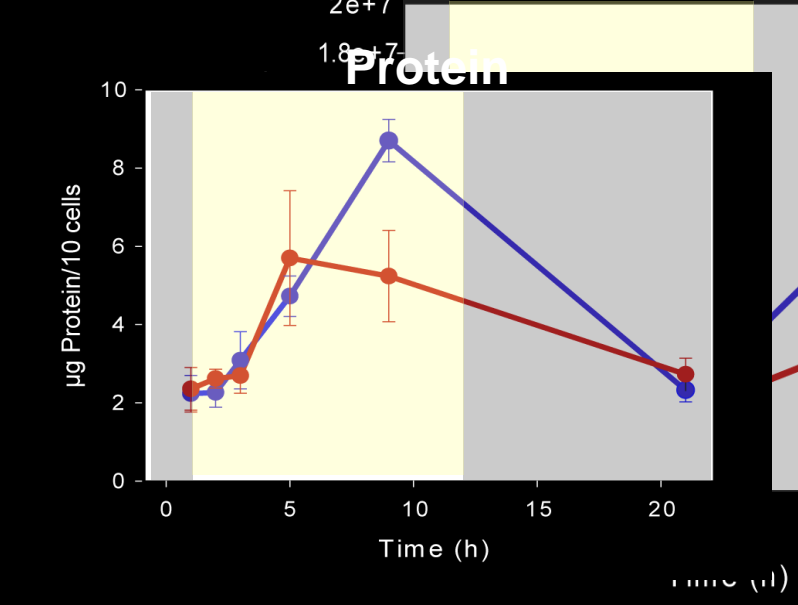
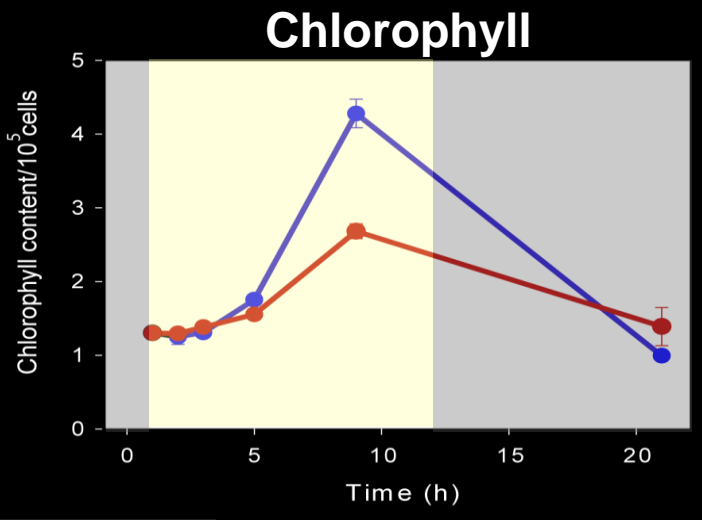
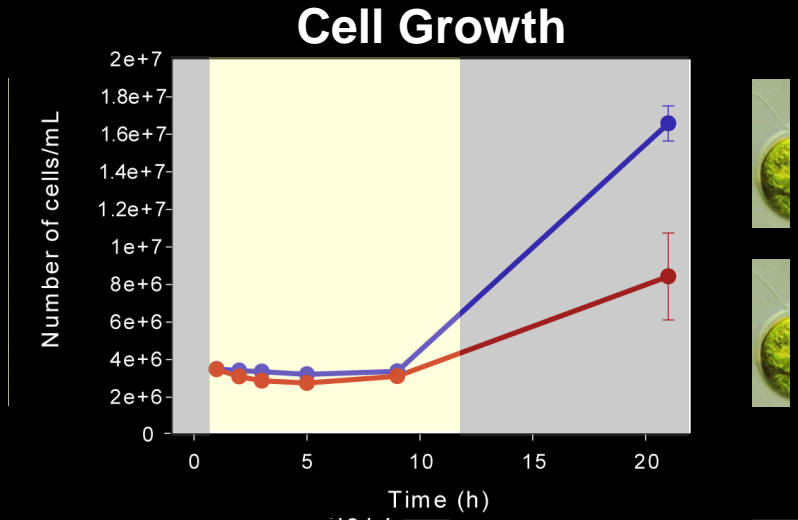
# Systems-level analysis: Genetic Perturbation



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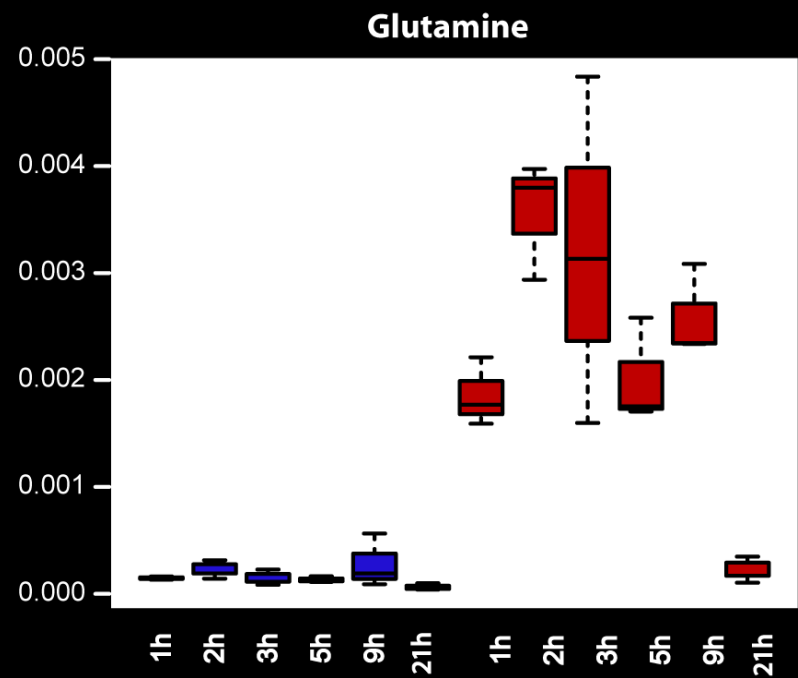
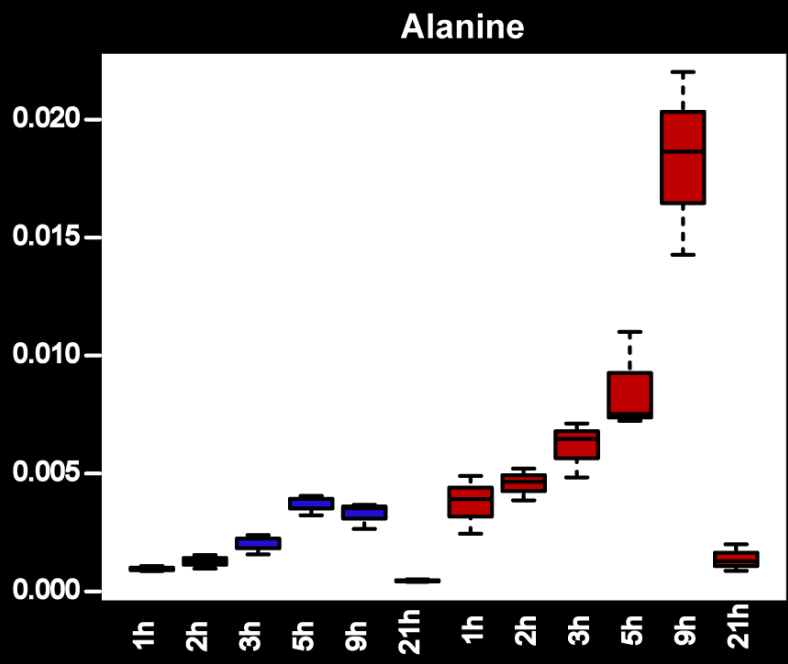
# Chlamydomonas growth and TOR



— 500nM Rapamycin      — Control

# Chlamydomonas metabolism and TOR

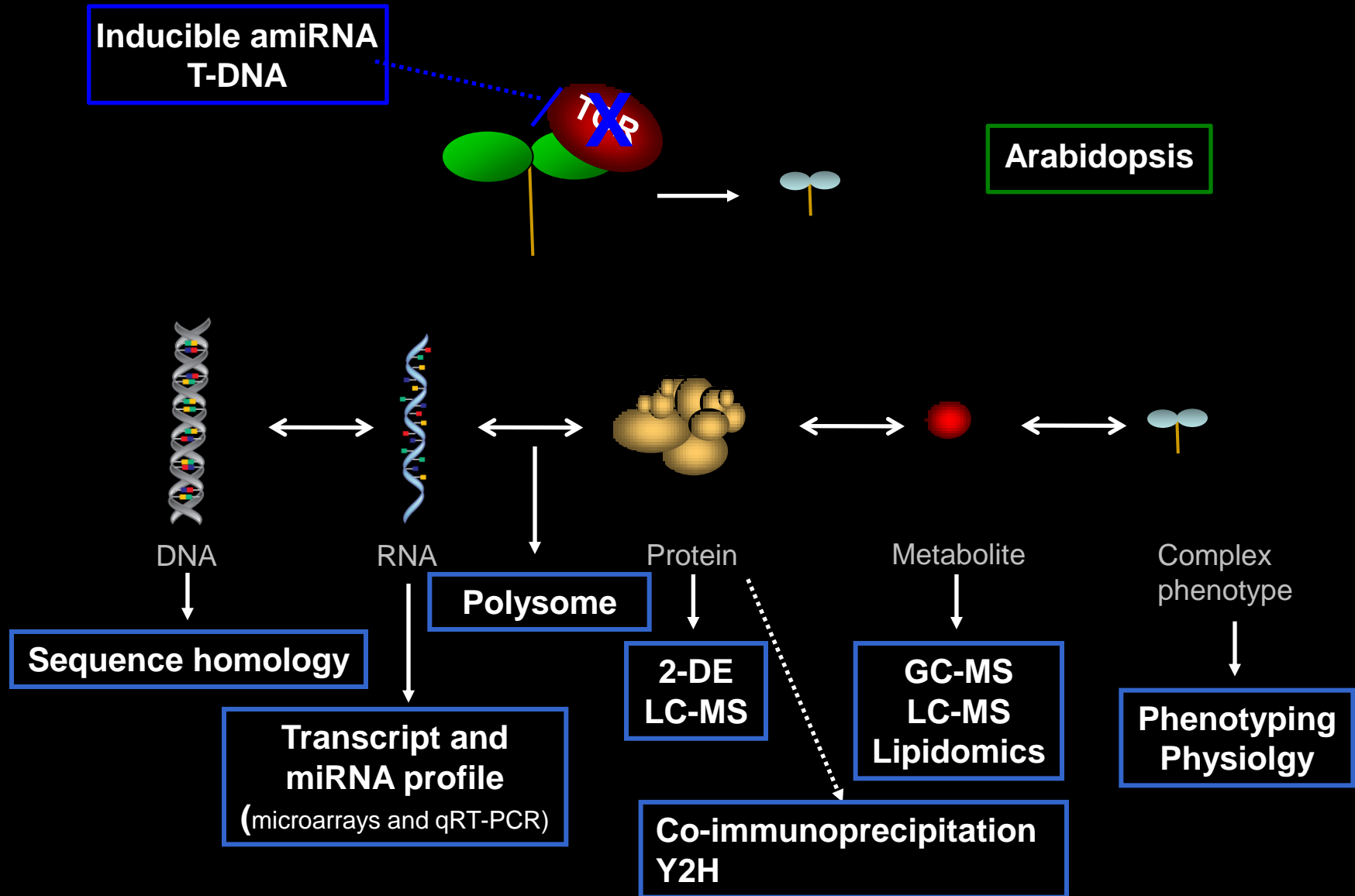
- Out of 51 identified metabolites, 27 show significant changes
- Amino acids



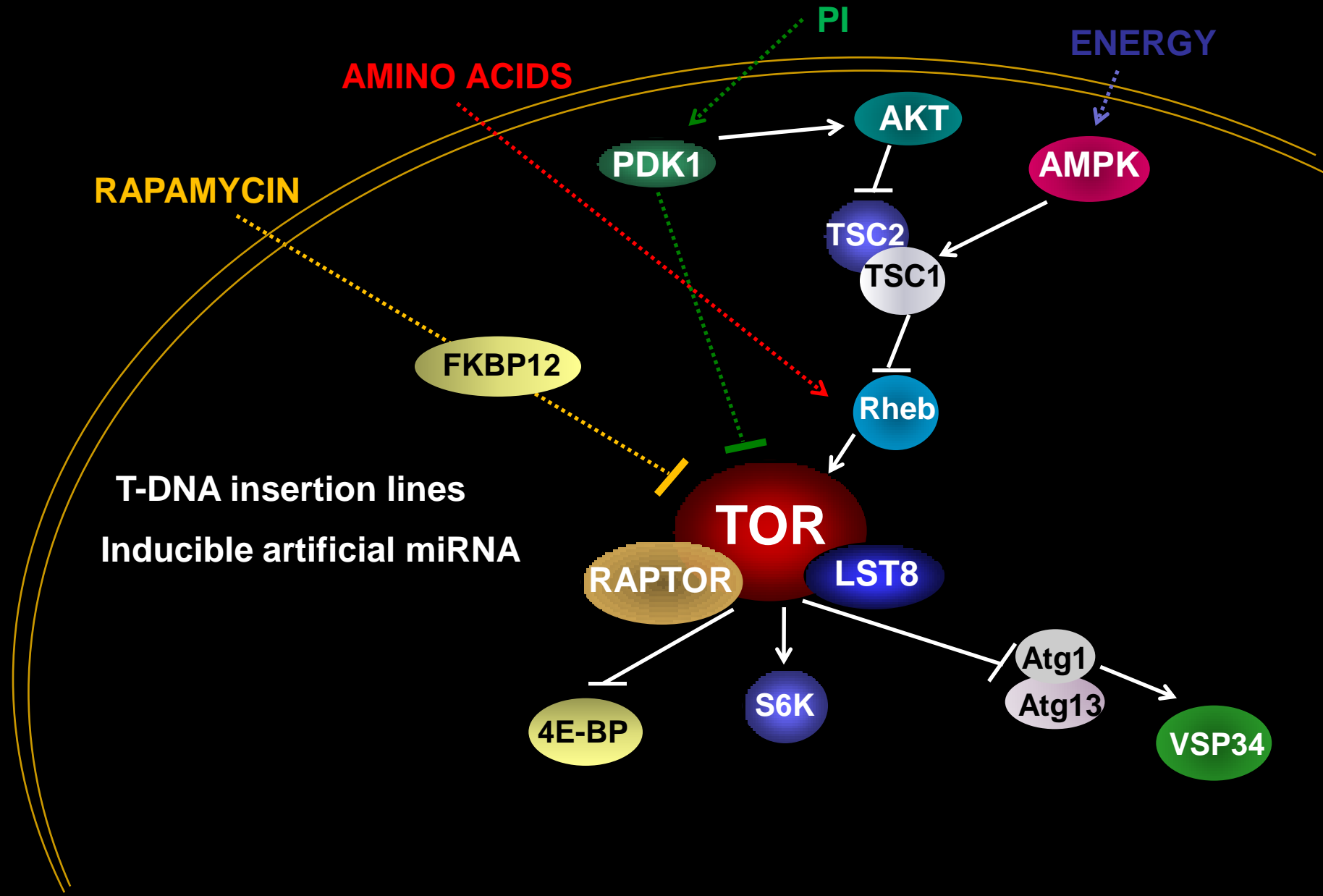
— 500nM Rapamycin      — Control



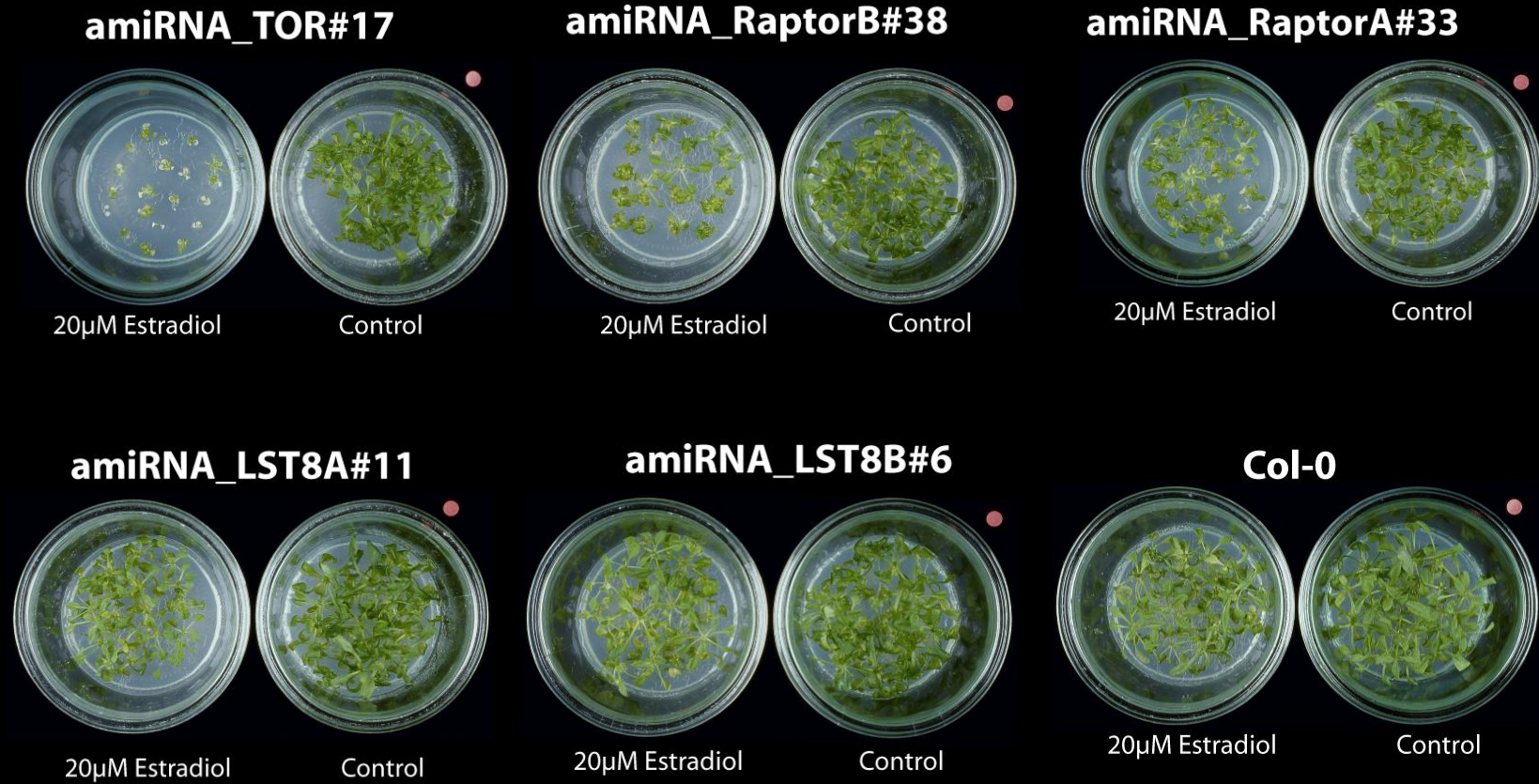
# Systems-level analysis: Genetic Perturbation



# TOR complex in Arabidopsis



# Arabidopsis TOR complex: first results...



~20 DAG

Reduction expression of AtTOR and other genes of the complex arrest plant growth

# Ongoing

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## TOR and Chlamydomonas

- Transcript profiling
- Lipids/ LC-MS

## TOR and Arabidopsis

- Kinetics responses of TOR repression ( and other genes in the complex)

## TOR and yeast

- Metabolite profiling

# Acknowledgements

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**Antjie Bolze**

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**Yan Li**

**Susan Irgang**

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MAX-PLANCK-GESellschaft



# TOR in photosynthetic organisms

- Chlamydomonas is sensitive to rapamycin (Crespo et al, 2005).
- Plants might **NOT** be sensitive to rapamycin (Menand et al, 2002).
- Growth is positively correlated with TOR (Deprost et al, 2007).



Col-0

iRNA

OX

- TOR Homozygous T-DNA lines are embryo lethal (Menand et al., 2002).

# Overall conserved response is transcript-restricted

## GO terms over-representation analysis

