A case study: gene network beyond flagellin and MAPK signaling

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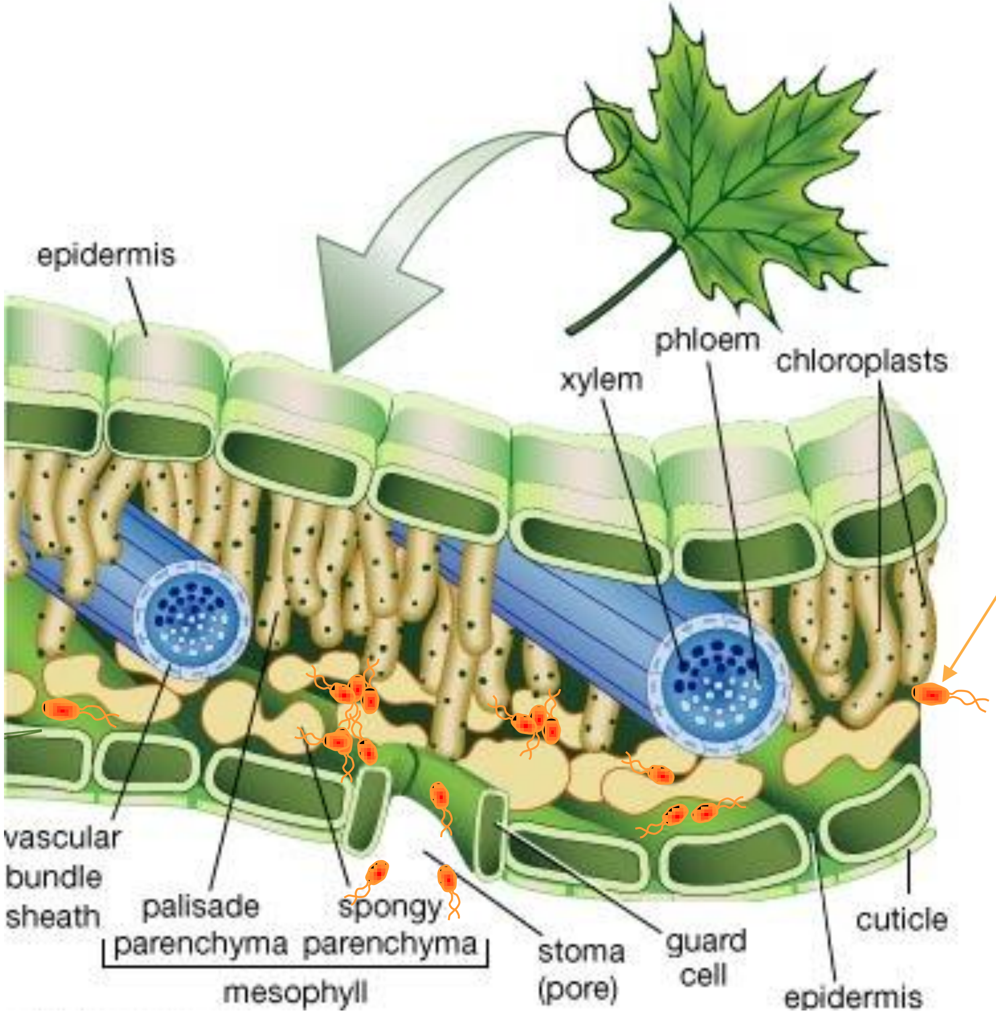
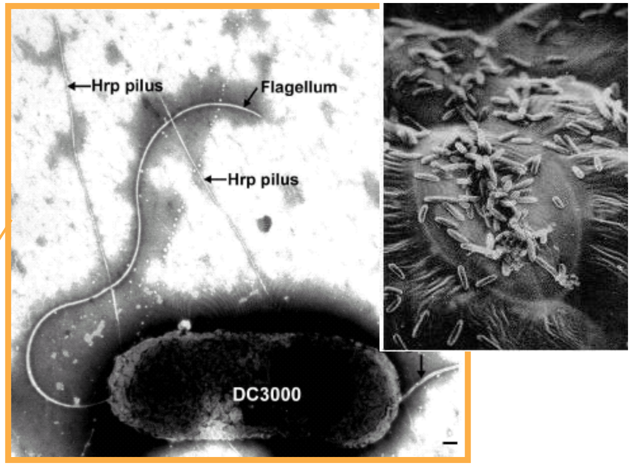
URGV, Evry

Journée « Inférence de réseaux chez les plantes »
6 Septembre 2011

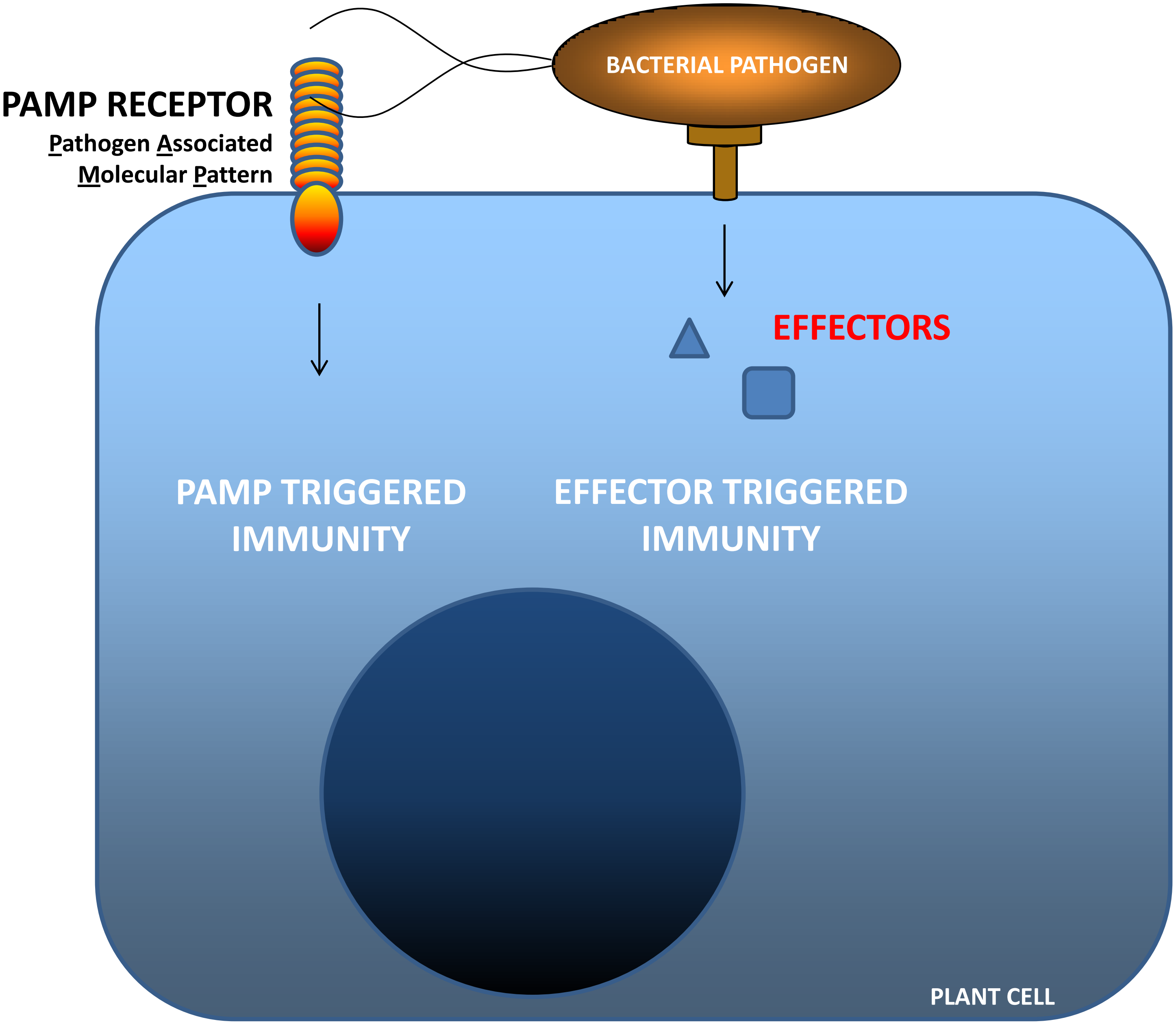
Bacterial infection in plants



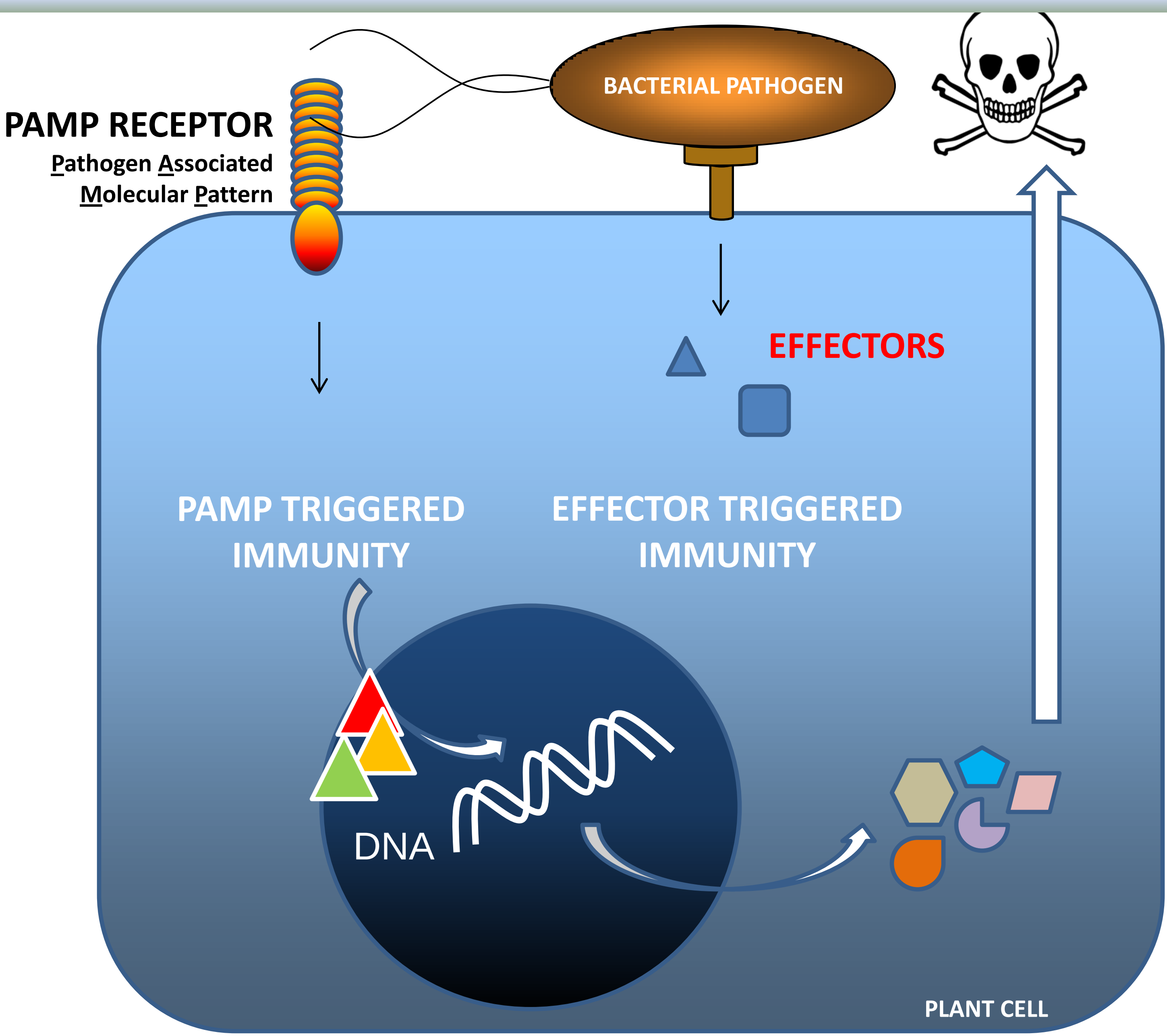
Pseudomonas syringae



Plant resistance to pathogens : two layers of defense



Plant resistance to pathogens : two layers of defense



PAMP RECEPTOR

Pathogen Associated Molecular Pattern

BACTERIAL PATHOGEN

EFFECTORS

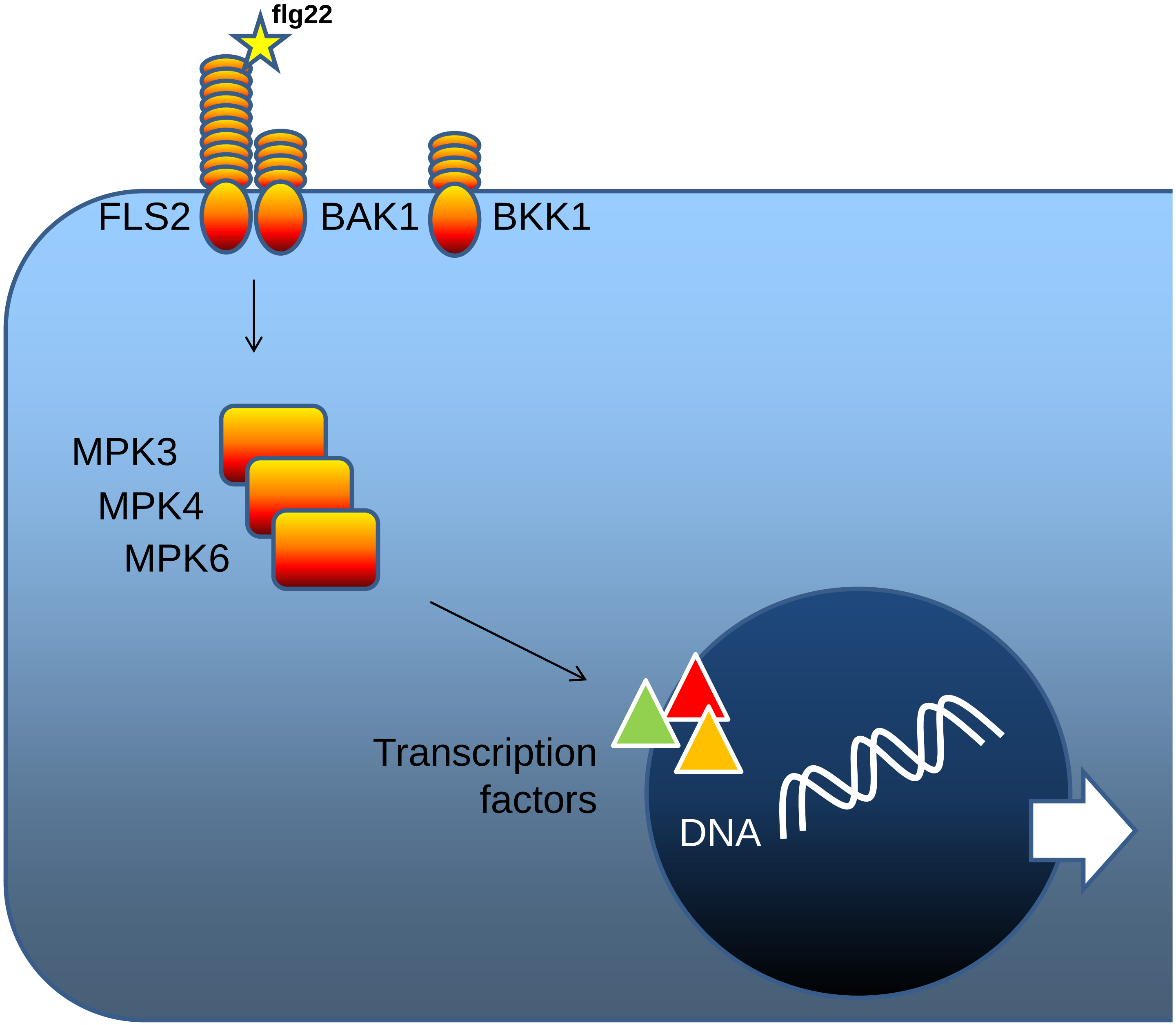
PAMP TRIGGERED IMMUNITY

EFFECTOR TRIGGERED IMMUNITY

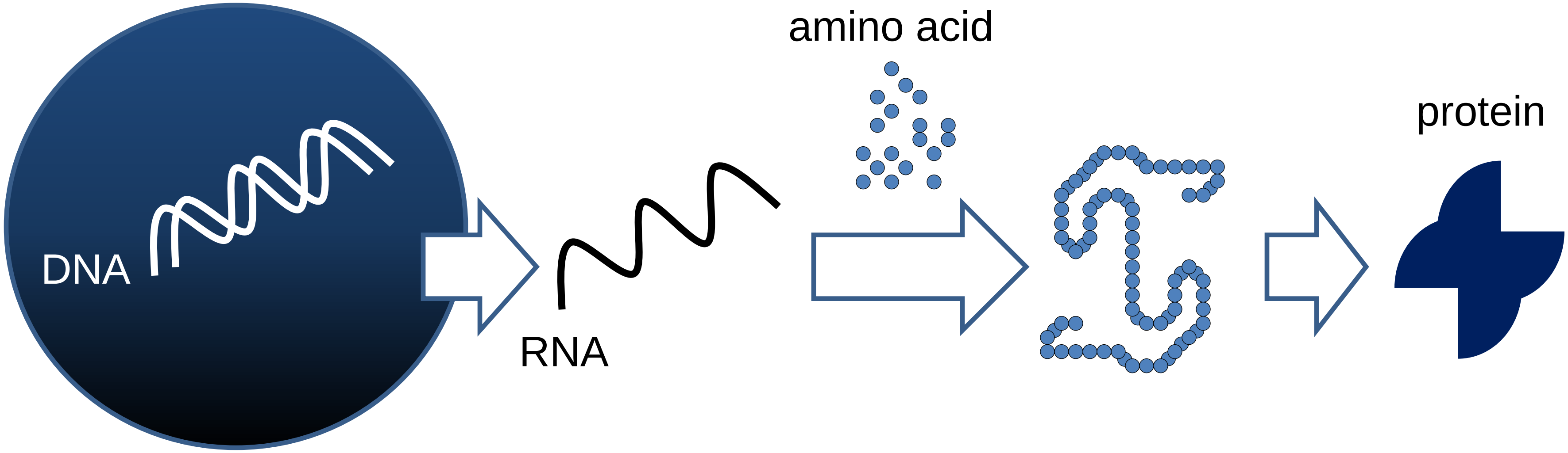
DNA

PLANT CELL

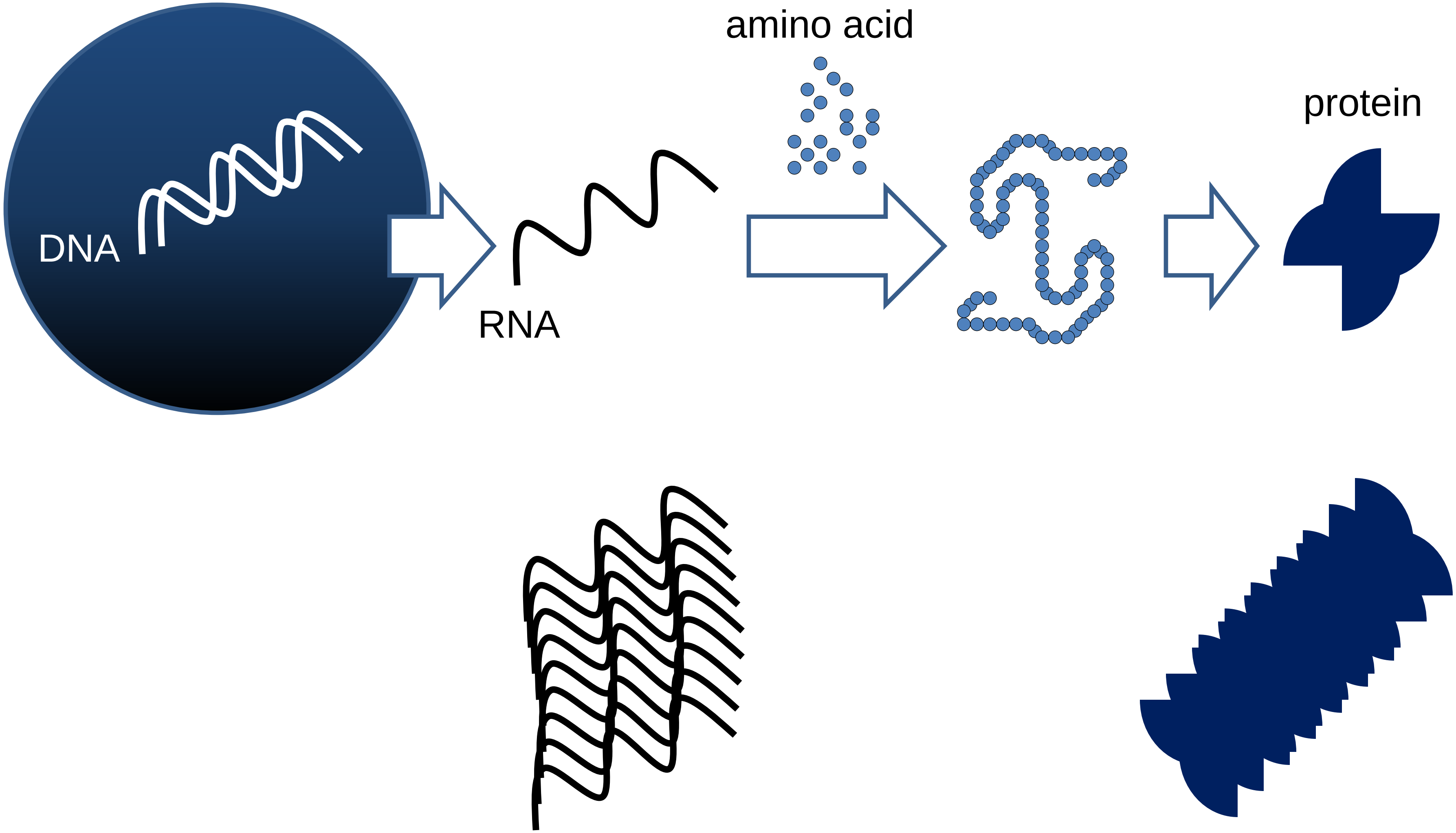
Gene regulation downstream of flagellin and MAPK signaling



Quantifying transcript abundance as a read-out for gene regulation



Quantifying transcript abundance as a read-out for gene regulation



DNA

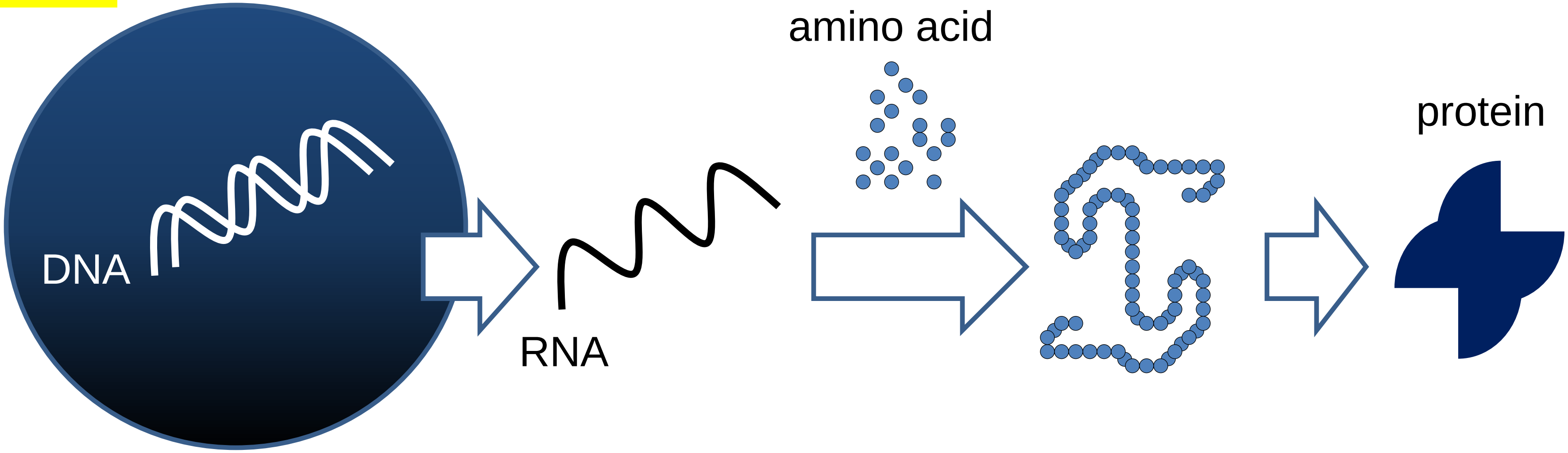
RNA

amino acid

protein

Quantifying transcript abundance as a read-out for gene regulation

- flg22


amino acid

protein

DNA

RNA

+ flg22

From transcriptome analysis to gene clustering

Transcriptome analysis
~25.000 gene products

bak1 bkk1	vs	Col
mpk3	vs	Col
mpk4	vs	Col
mpk6	vs	Col
bak1 bkk1 + flg22	vs	*bak1 bkk1*
mpk3 + flg22	vs	*mpk3*
mpk4 + flg22	vs	*mpk4*
mpk6 + flg22	vs	*mpk6*
Col + flg22	vs	Col

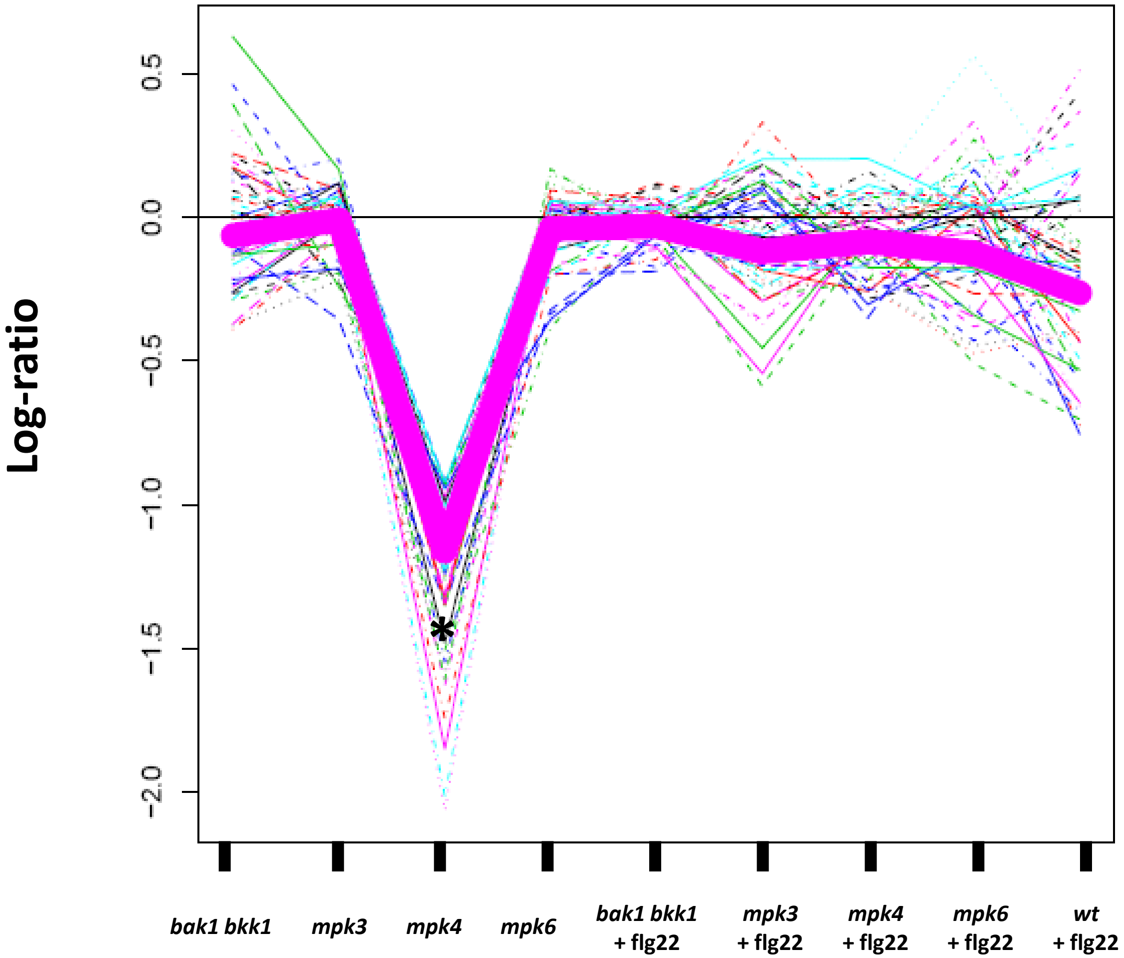
4406 genes found to be differentially expressed at least once among the comparisons

⇩

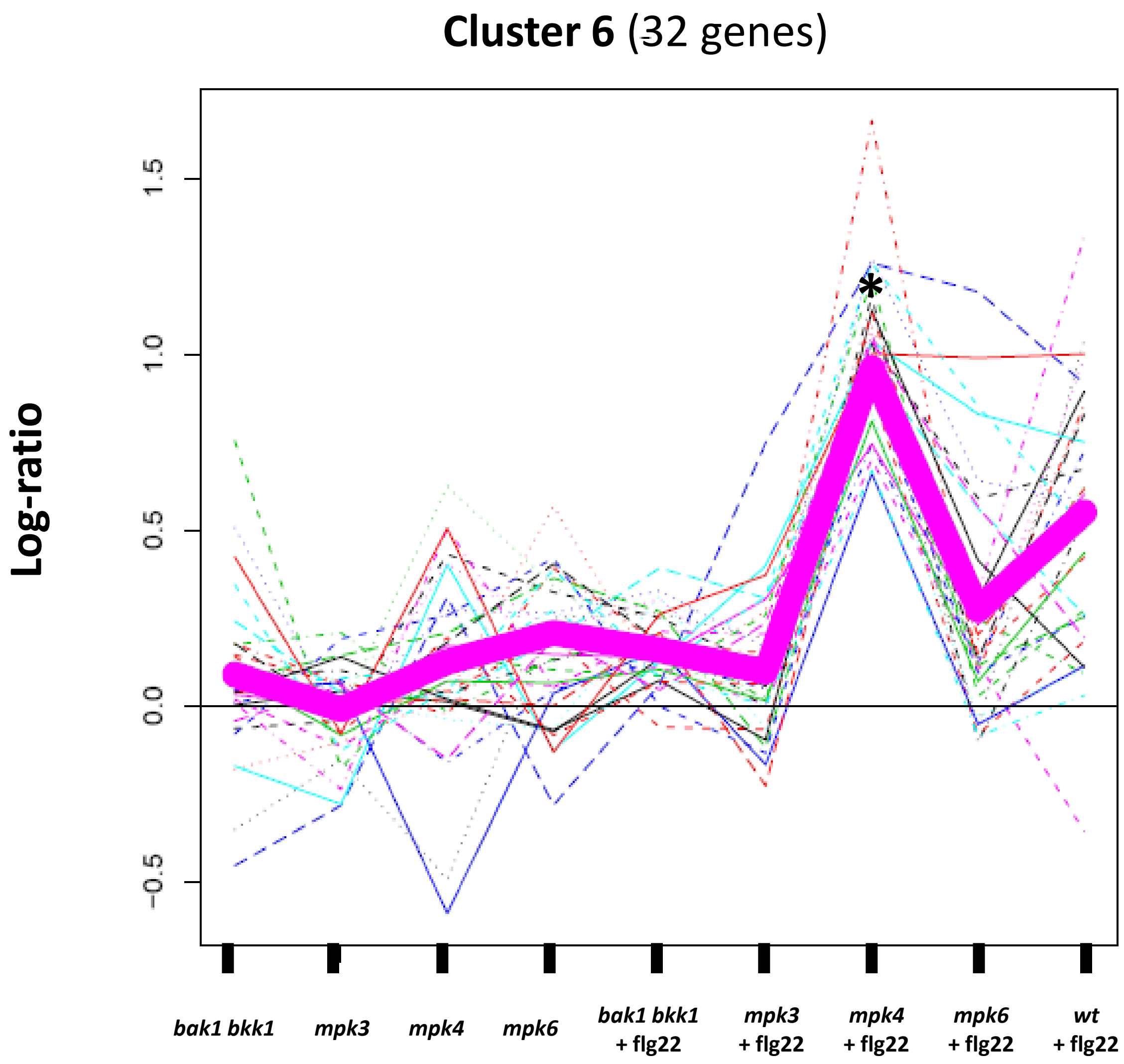
31 clusters

Cluster example (1/4)

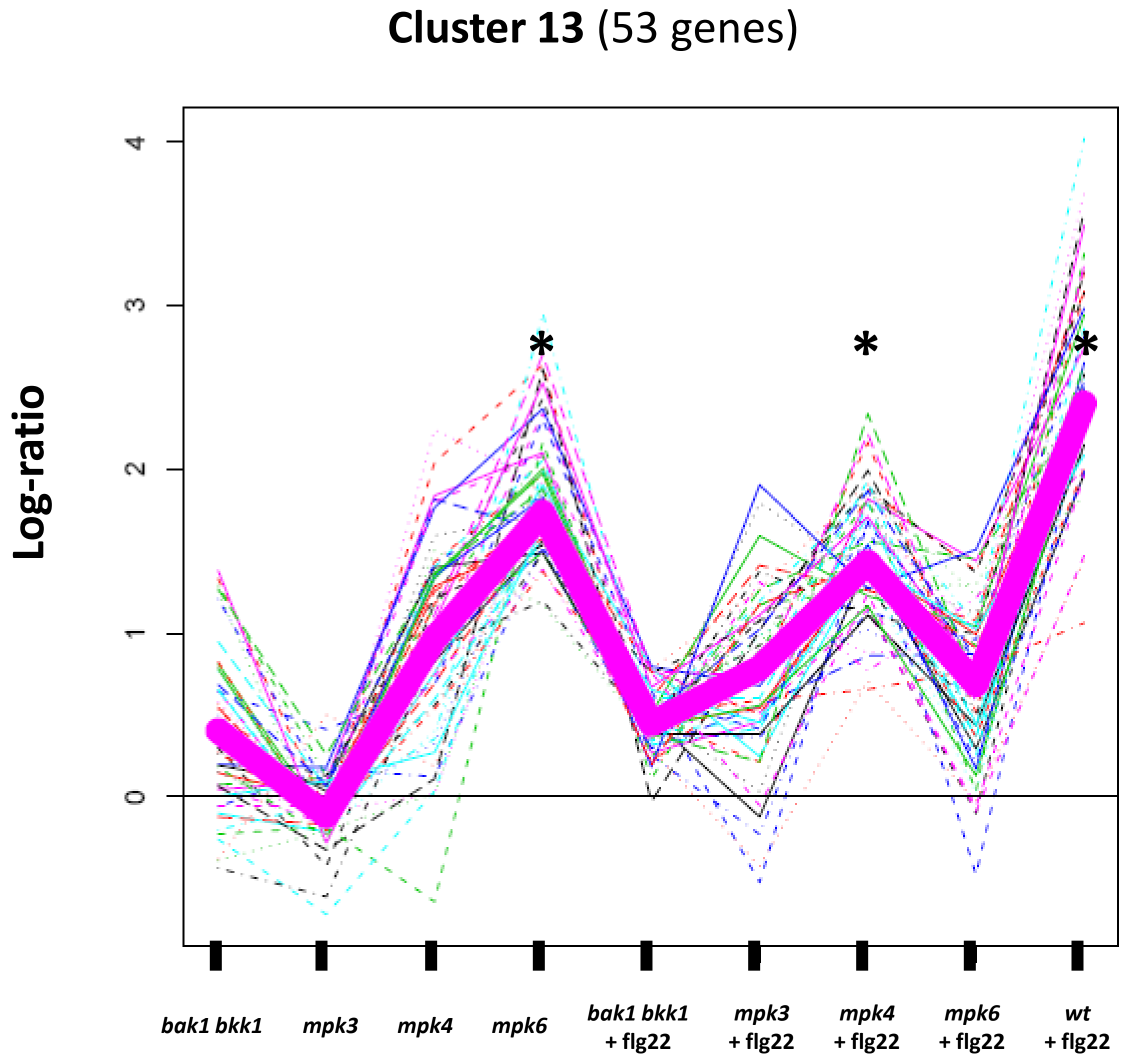
Cluster 2 (54 genes)



Cluster example (2/4)

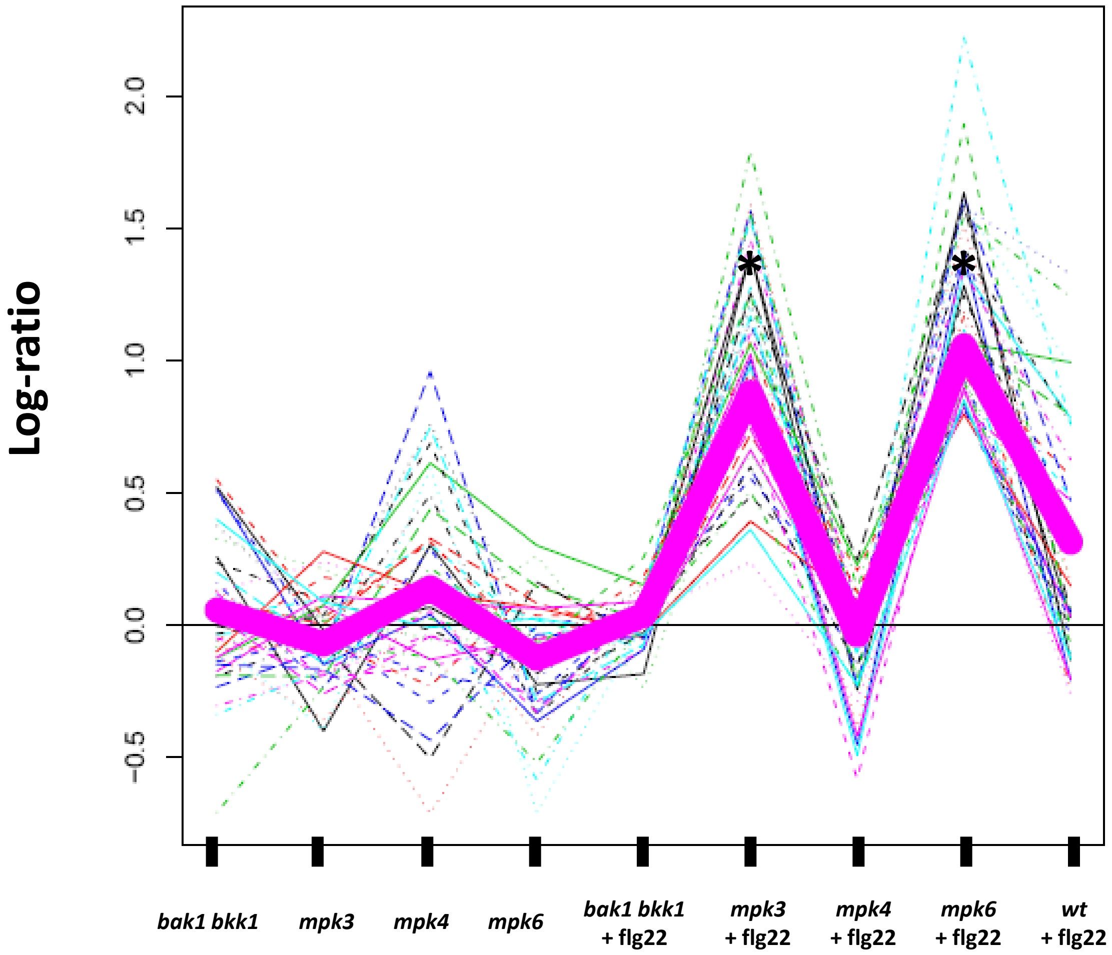


Cluster example (3/4)



Cluster example (4/4)

Cluster 16 (42 genes)



What biological information to extract from different clusters ?

Which of the mutants are similar ?
Which mutant is the most severely impaired in the flg22 response ?

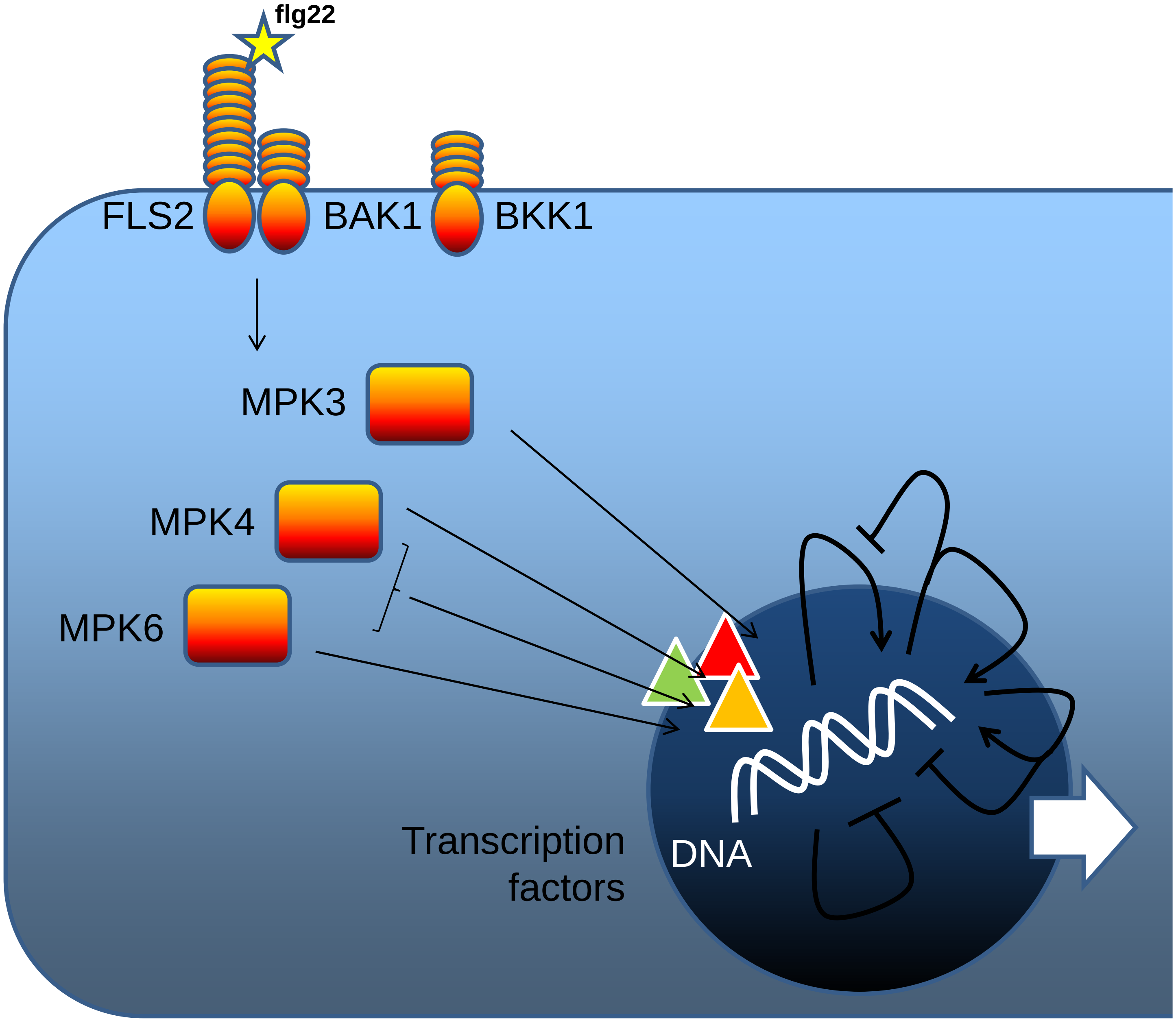
Analysis of each cluster :
    Protein subcellular localisation
    **Membrane ? Nucleus ? Organelles ? Etc…*
    Protein function
    **Gene regulation ? Metabolic Pathway ? Etc…*

Is a mutant more affected in a specific response / pathway ?

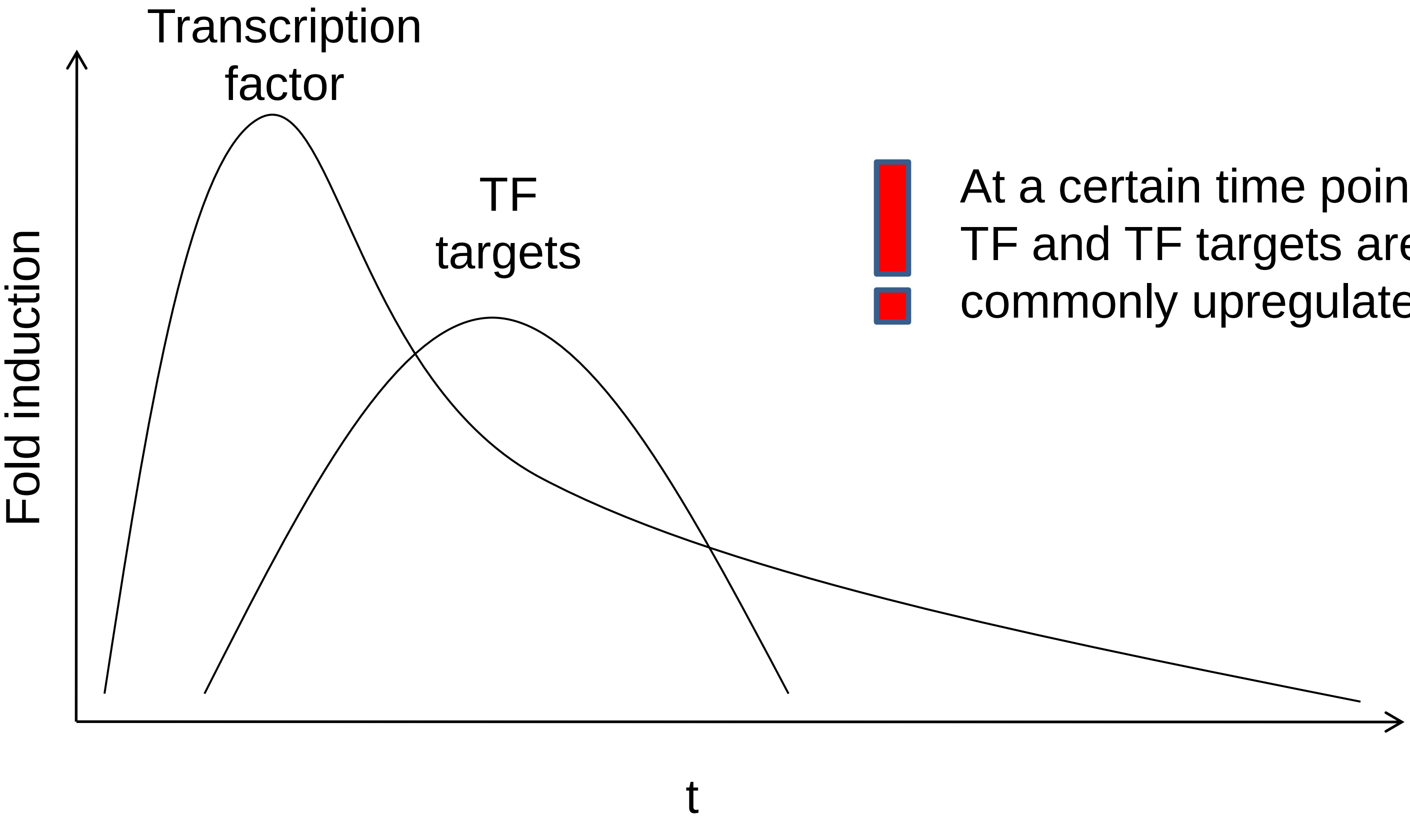
…

… but how to identify MAPK targets ? Downstream regulators ?

No time serie available… How to identify primary regulators ?



Common regulation in TF and TF targets

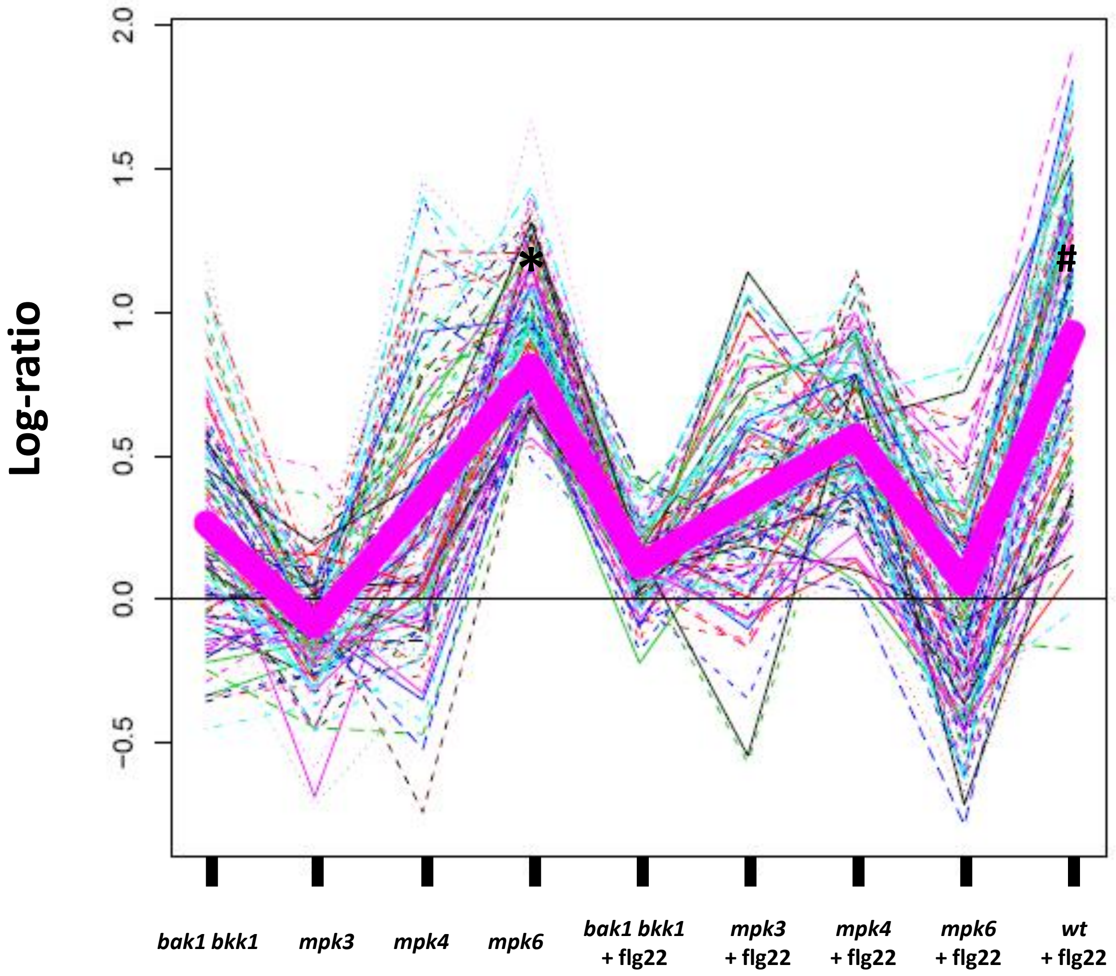


❗ At a certain time point, TF and TF targets are commonly upregulated

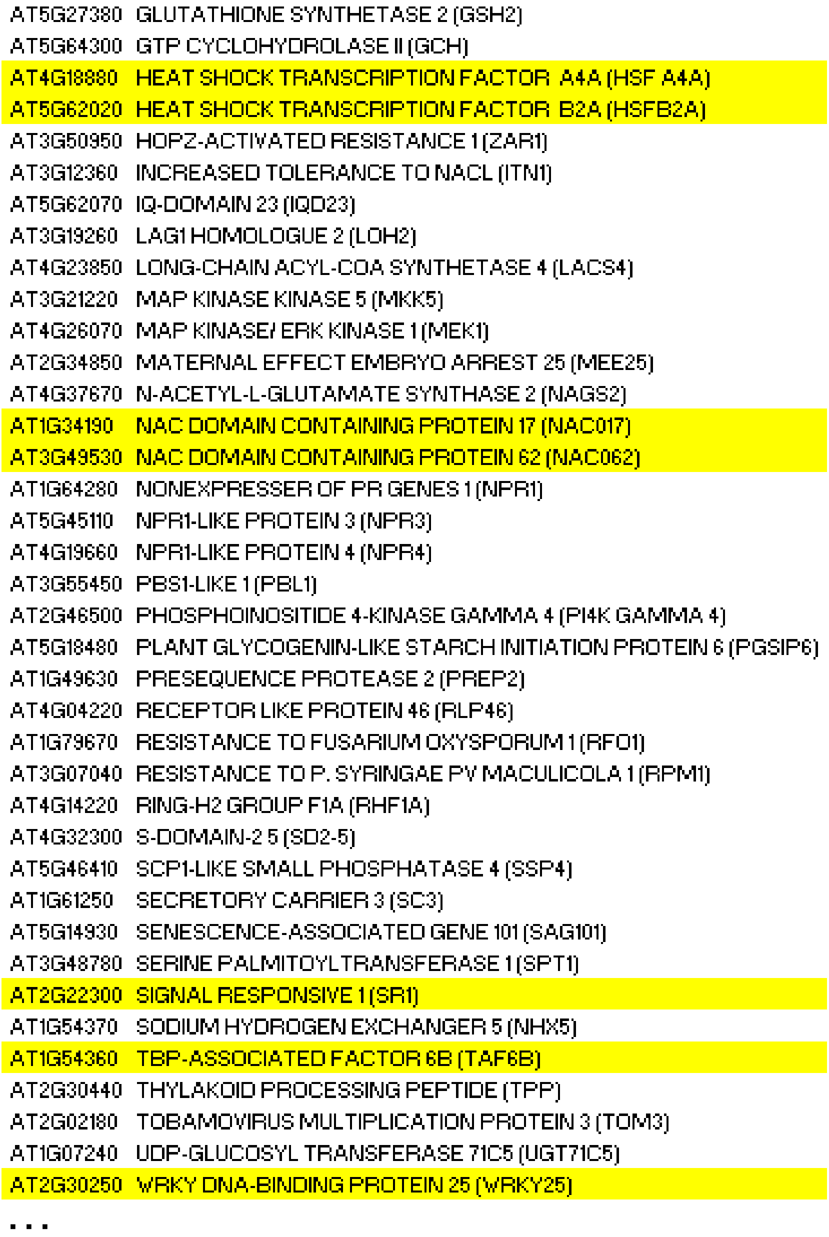
⇨ **TF and their targets can be identified in the same cluster**

Practical case study: cluster 17

Cluster 17 (132 genes)



Practical case study: cluster 17



AT5G27380	GLUTATHIONE SYNTHETASE 2 (GSH2)
AT5G64300	GTP CYCLOHYDROLASE II (GCH)
AT4G18880	HEAT SHOCK TRANSCRIPTION FACTOR A4A (HSF A4A)
AT5G62020	HEAT SHOCK TRANSCRIPTION FACTOR B2A (HSFB2A)
AT3G50950	HOPZ-ACTIVATED RESISTANCE 1 (ZAR1)
AT3G12360	INCREASED TOLERANCE TO NACL (ITN1)
AT5G62070	IQ-DOMAIN 23 (IQD23)
AT3G19260	LAG1 HOMOLOGUE 2 (LOH2)
AT4G23850	LONG-CHAIN ACYL-COA SYNTHETASE 4 (LACS4)
AT3G21220	MAP KINASE KINASE 5 (MKK5)
AT4G26070	MAP KINASE/ ERK KINASE 1 (MEK1)
AT2G34850	MATERNAL EFFECT EMBRYO ARREST 25 (MEE25)
AT4G37670	N-ACETYL-L-GLUTAMATE SYNTHASE 2 (NAGS2)
AT1G34190	NAC DOMAIN CONTAINING PROTEIN 17 (NAC017)
AT3G49530	NAC DOMAIN CONTAINING PROTEIN 62 (NAC062)
AT1G64280	NONEXPRESSER OF PR GENES 1 (NPR1)
AT5G45110	NPR1-LIKE PROTEIN 3 (NPR3)
AT4G19660	NPR1-LIKE PROTEIN 4 (NPR4)
AT3G55450	PBS1-LIKE 1 (PBL1)
AT2G46500	PHOSPHOINOSITIDE 4-KINASE GAMMA 4 (PI4K GAMMA 4)
AT5G18480	PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6 (PGSIP6)
AT1G49630	PRESEQUENCE PROTEASE 2 (PREP2)
AT4G04220	RECEPTOR LIKE PROTEIN 46 (RLP46)
AT1G79670	RESISTANCE TO FUSARIUM OXYSPORUM 1 (RFO1)
AT3G07040	RESISTANCE TO P. SYRINGAE PV MACULICOLA 1 (RPM1)
AT4G14220	RING-H2 GROUP F1A (RHF1A)
AT4G32300	S-DOMAIN-2 5 (SD2-5)
AT5G46410	SCP1-LIKE SMALL PHOSPHATASE 4 (SSP4)
AT1G61250	SECRETORY CARRIER 3 (SC3)
AT5G14930	SENESCENCE-ASSOCIATED GENE 101 (SAG101)
AT3G48780	SERINE PALMITOYLTRANSFERASE 1 (SPT1)
AT2G22300	SIGNAL RESPONSIVE 1 (SR1)
AT1G54370	SODIUM HYDROGEN EXCHANGER 5 (NHX5)
AT1G54360	TBP-ASSOCIATED FACTOR 6B (TAF6B)
AT2G30440	THYLAKOID PROCESSING PEPTIDE (TPP)
AT2G02180	TOBAMOVIRUS MULTIPLICATION PROTEIN 3 (TOM3)
AT1G07240	UDP-GLUCOSYL TRANSFERASE 71C5 (UGT71C5)
AT2G30250	WRKY DNA-BINDING PROTEIN 25 (WRKY25)

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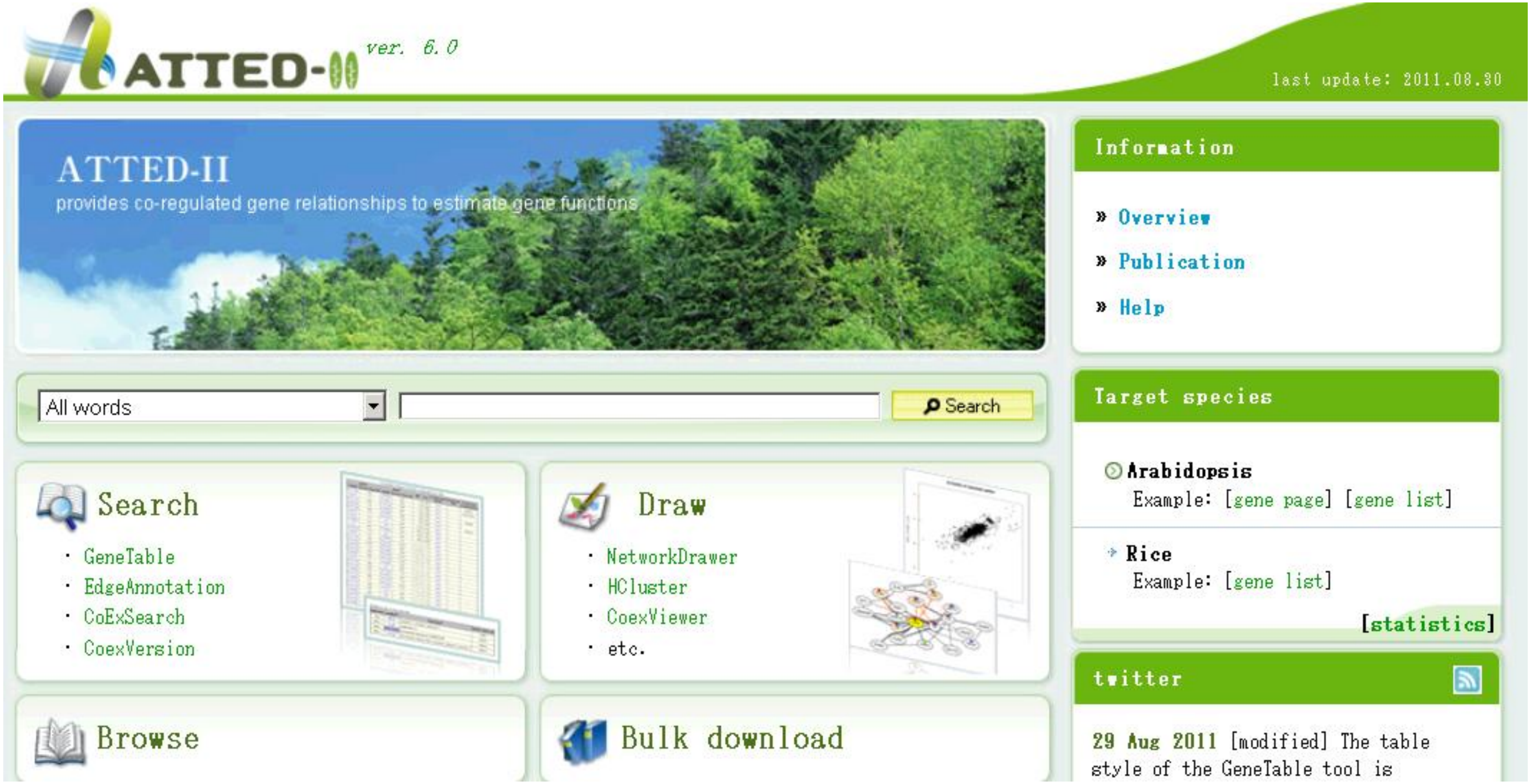
Use ATTED-II as a sub-clustering tool



ATTED-II ver. 6.0

last update: 2011.08.30

ATTED-II

provides co-regulated gene relationships to estimate gene functions

Information

- Overview
- Publication
- Help

Search

- GeneTable
- EdgeAnnotation
- CoExSearch
- CoexVersion

Draw

- NetworkDrawer
- HCluster
- CoexViewer
- etc.

Target species

Arabidopsis
Example: [gene page] [gene list]

Rice
Example: [gene list]

[statistics]

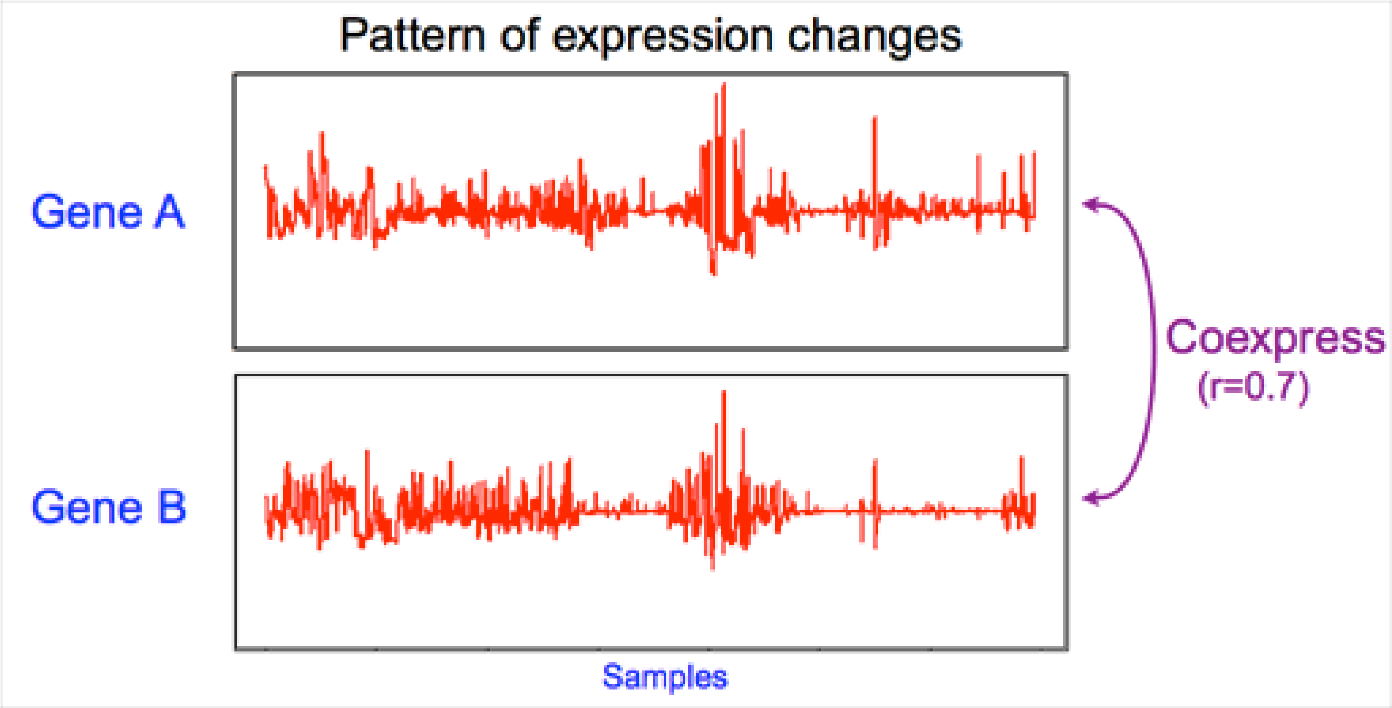
Browse

Bulk download

twitter

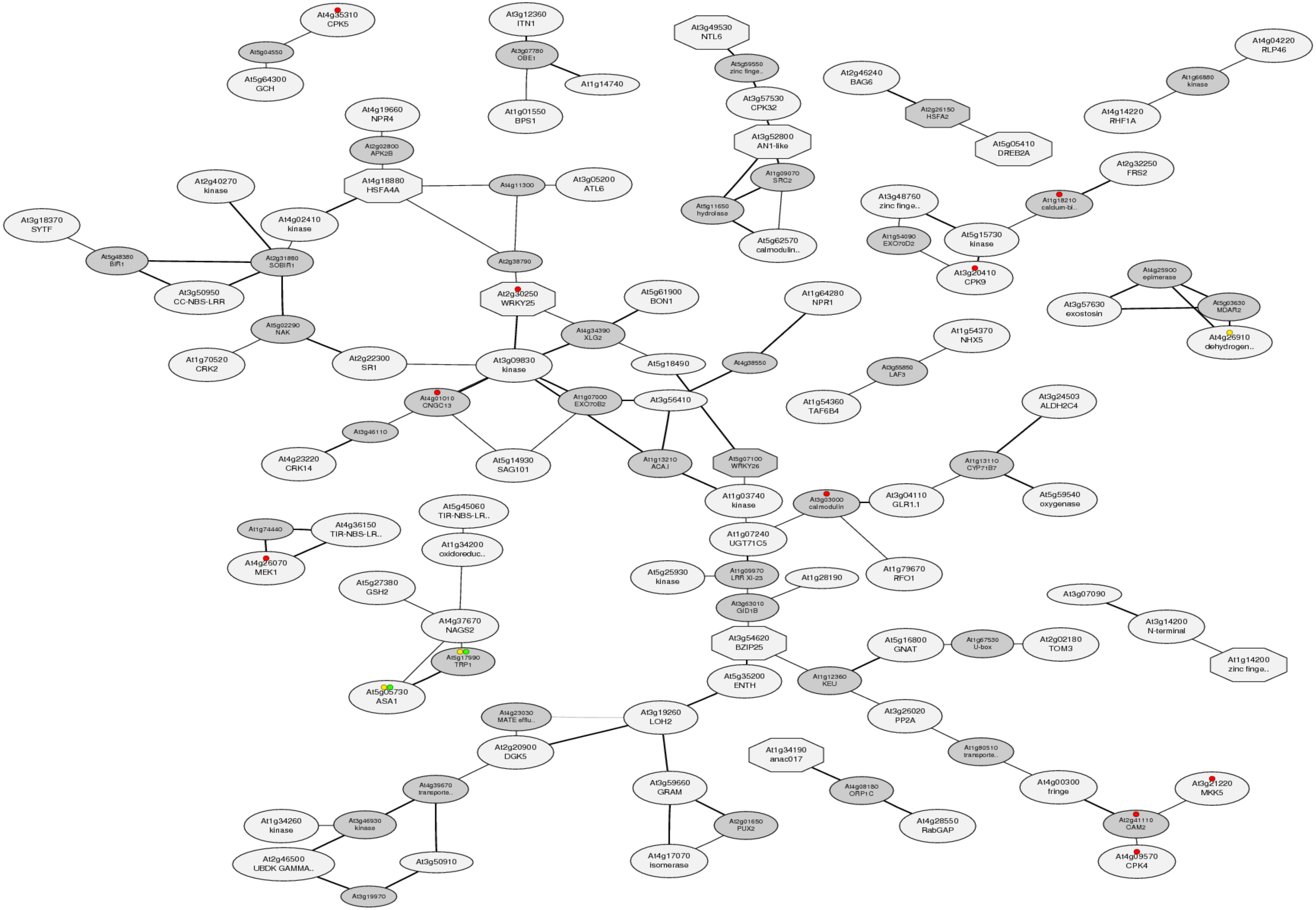
29 Aug 2011 [modified] The table style of the GeneTable tool is

Use ATTED-II as a sub-clustering tool

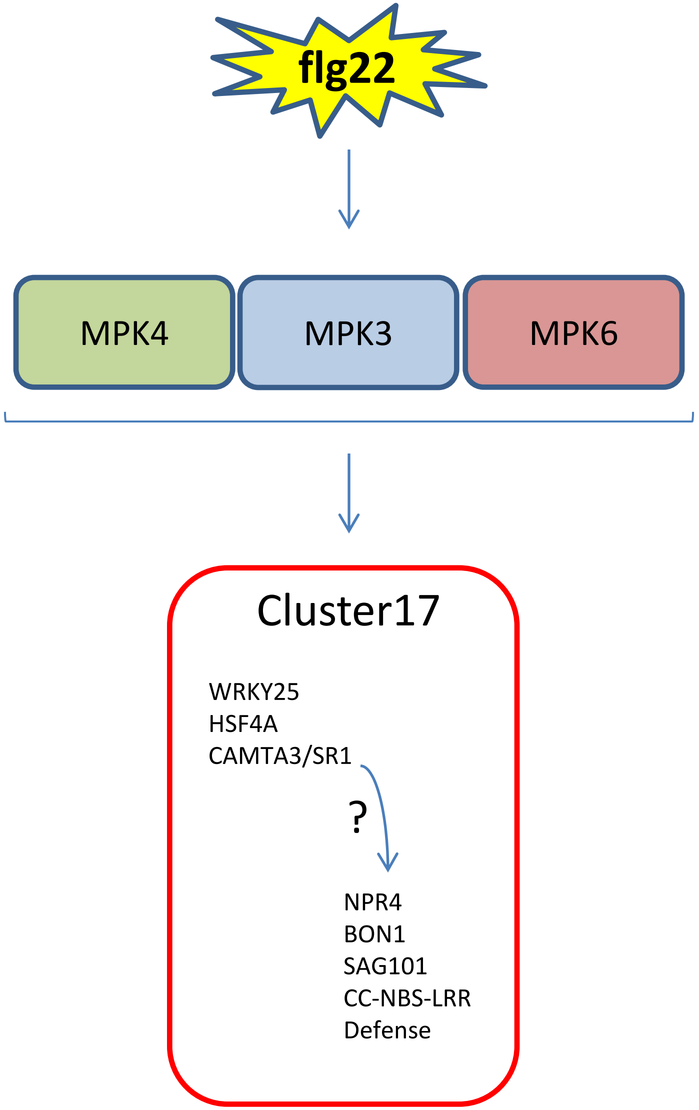


Matrix : 1388 transcritpomes in Arabidopsis
For every 25.000 genes, identification of the 300 most co-regulated

ATTED output using the cluster 17 (132 genes)



Prediction from cluster 17 analysis



flg22

MPK4

MPK3

MPK6

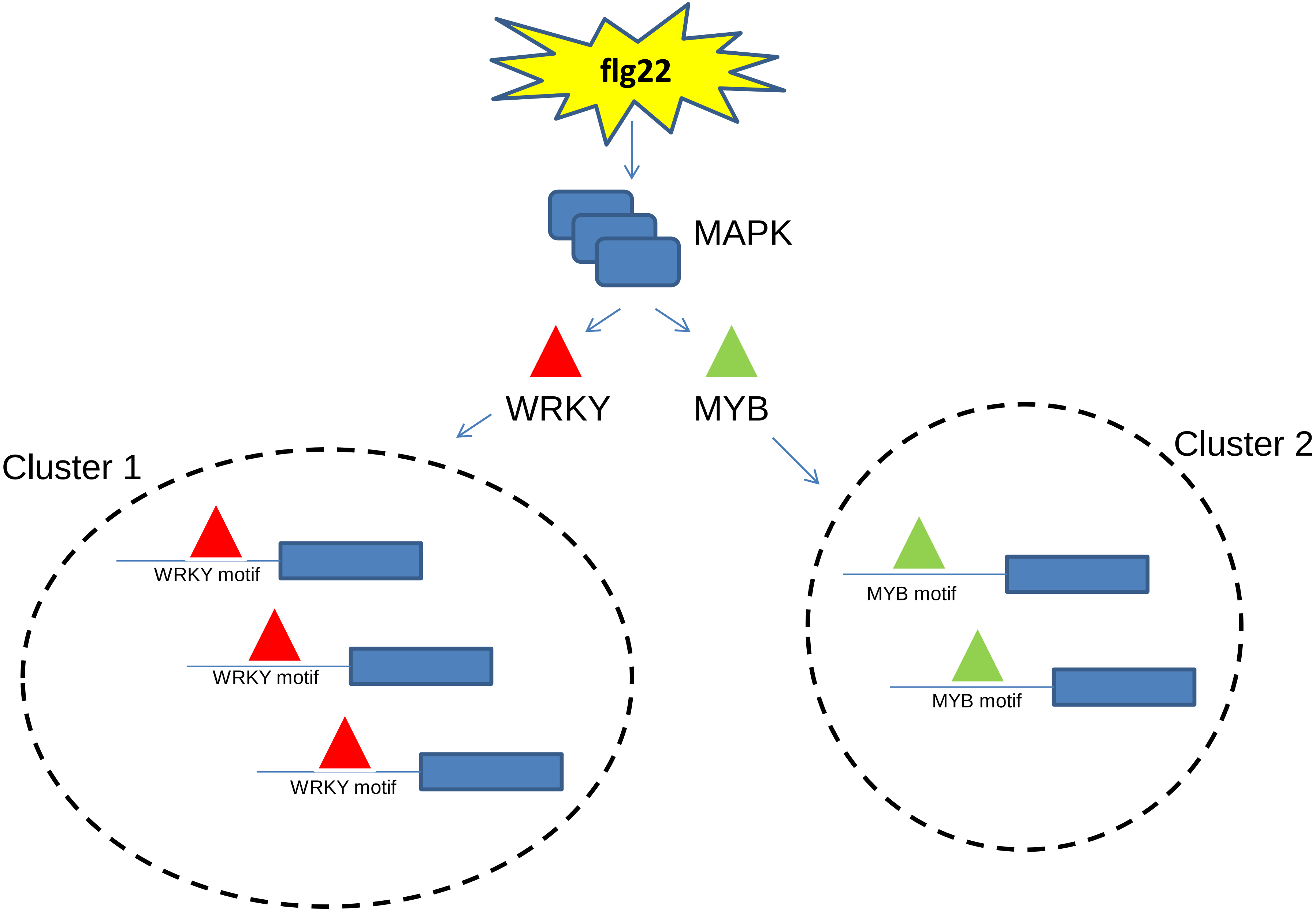
Cluster17

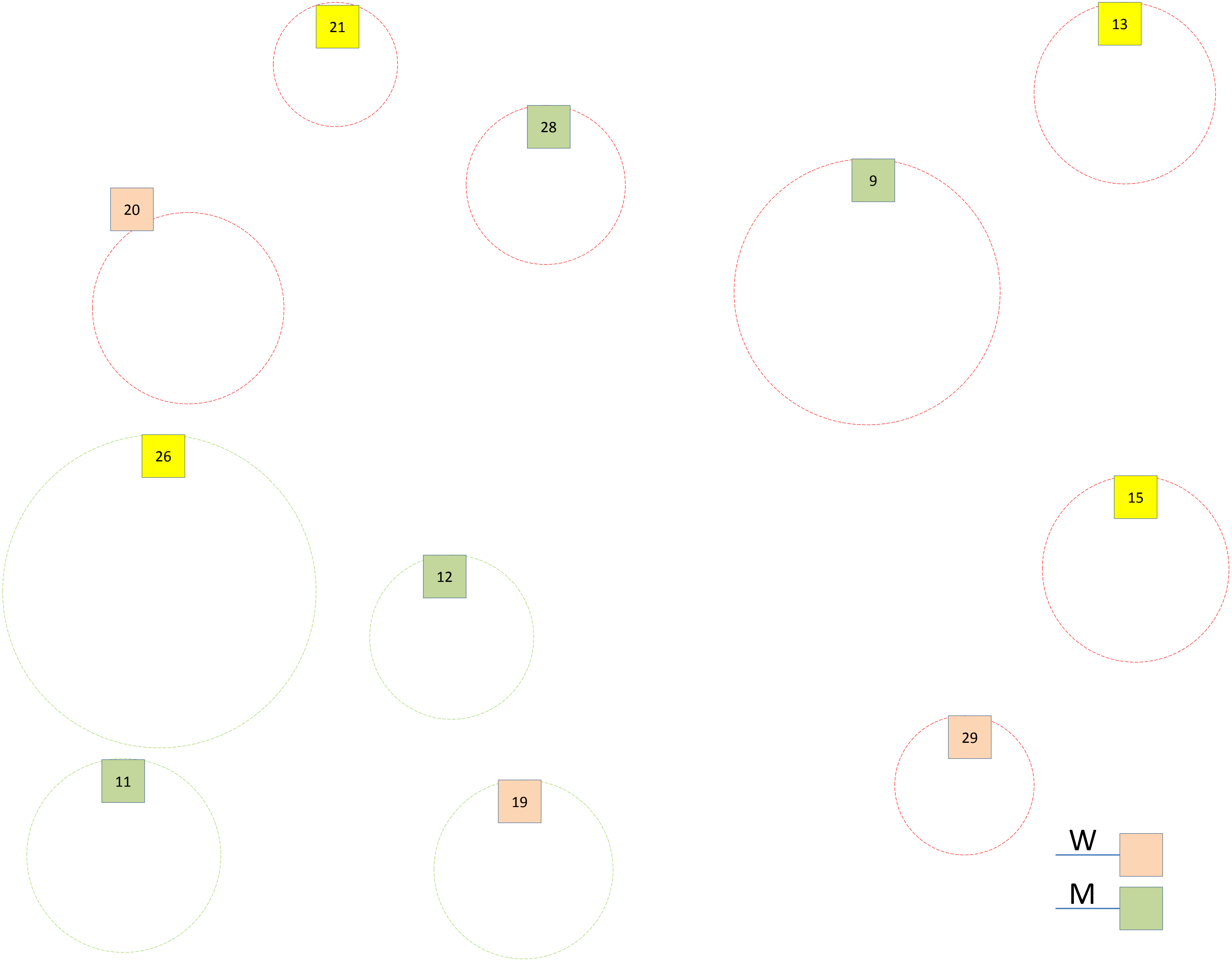
WRKY25
HSF4A
CAMTA3/SR1

?

NPR4
BON1
SAG101
CC-NBS-LRR
Defense

Prediction from promoter analysis

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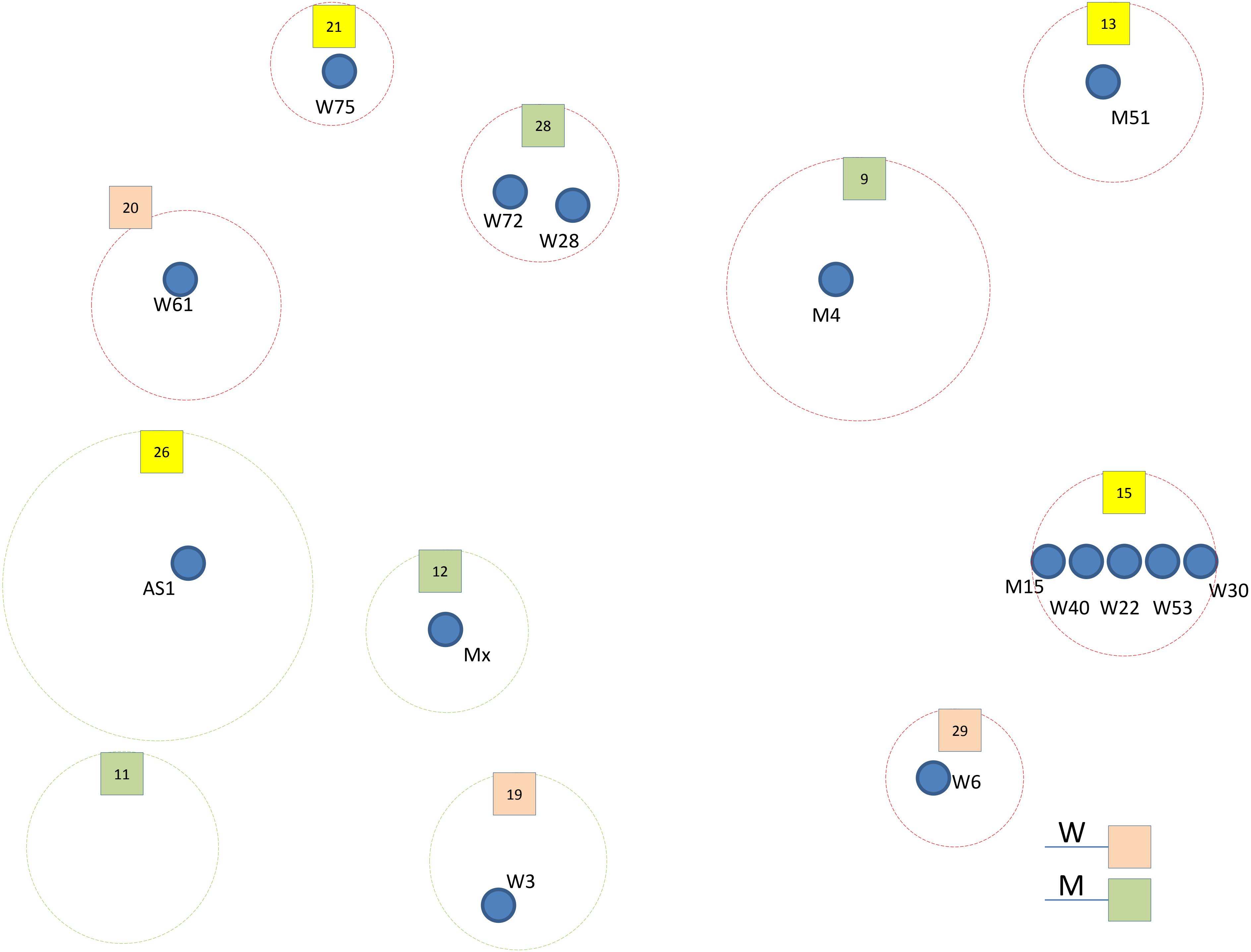
21
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W72
W28
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W61
M4
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AS1
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M15
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W22
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W30
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Mx
29
W6
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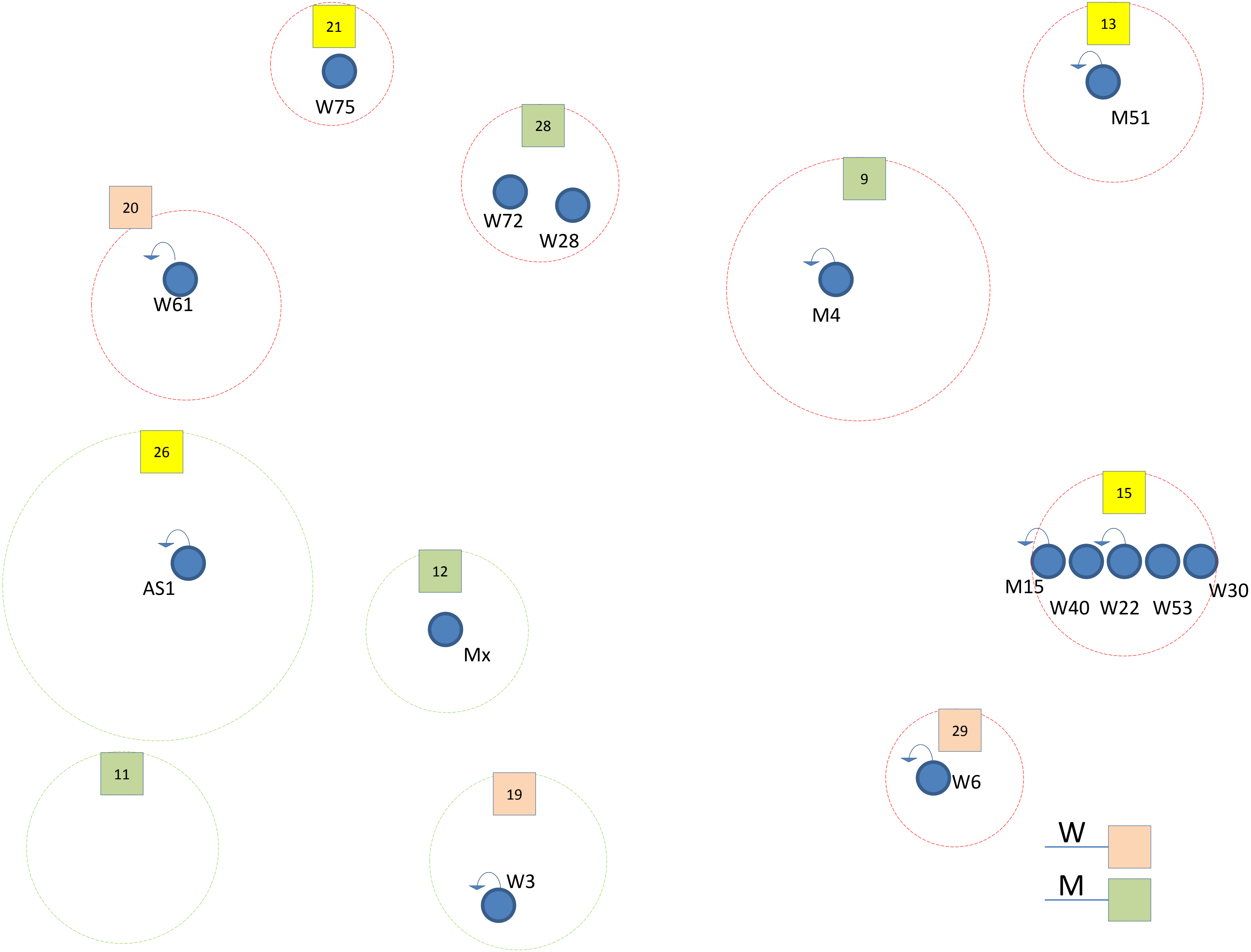
W3
W
M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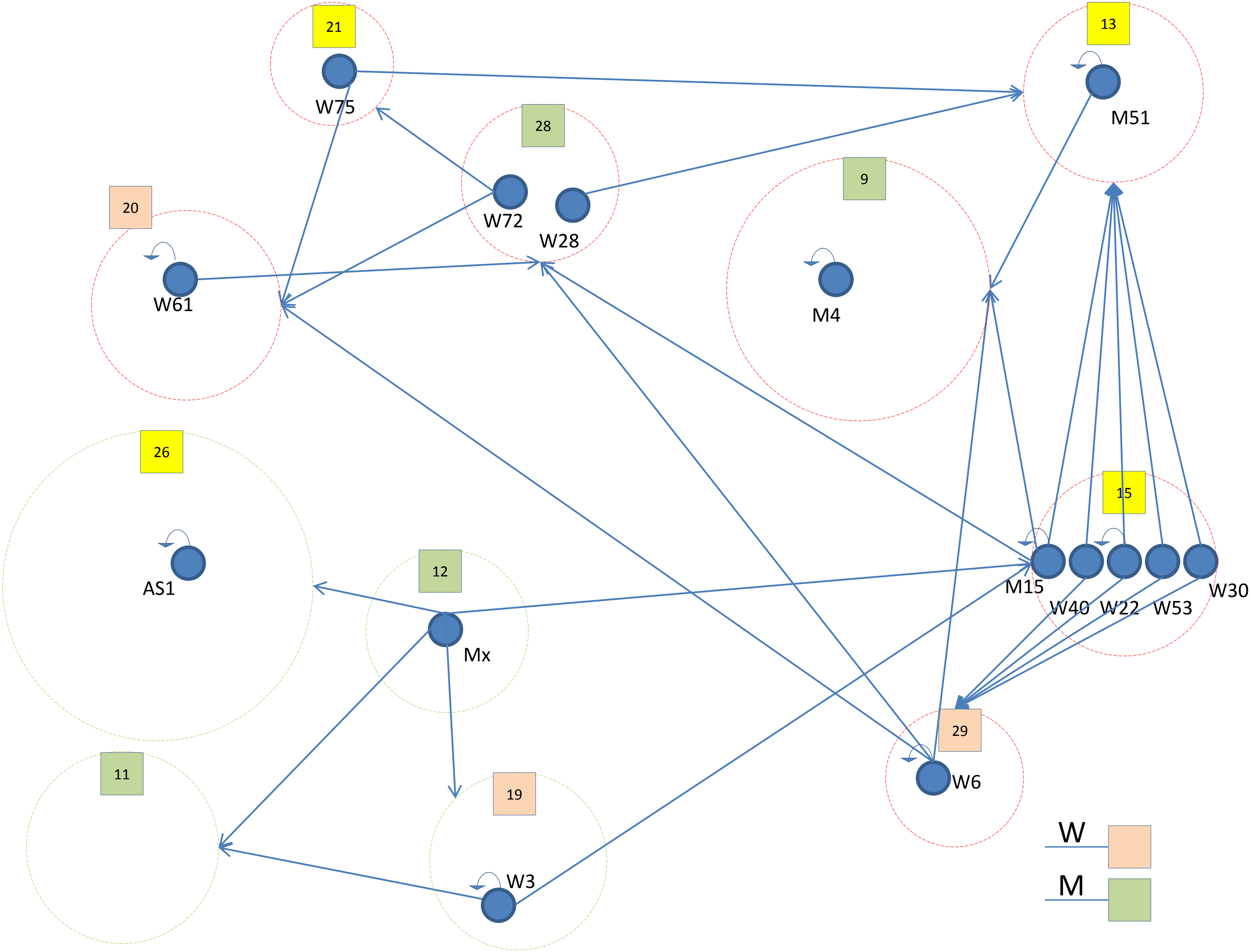
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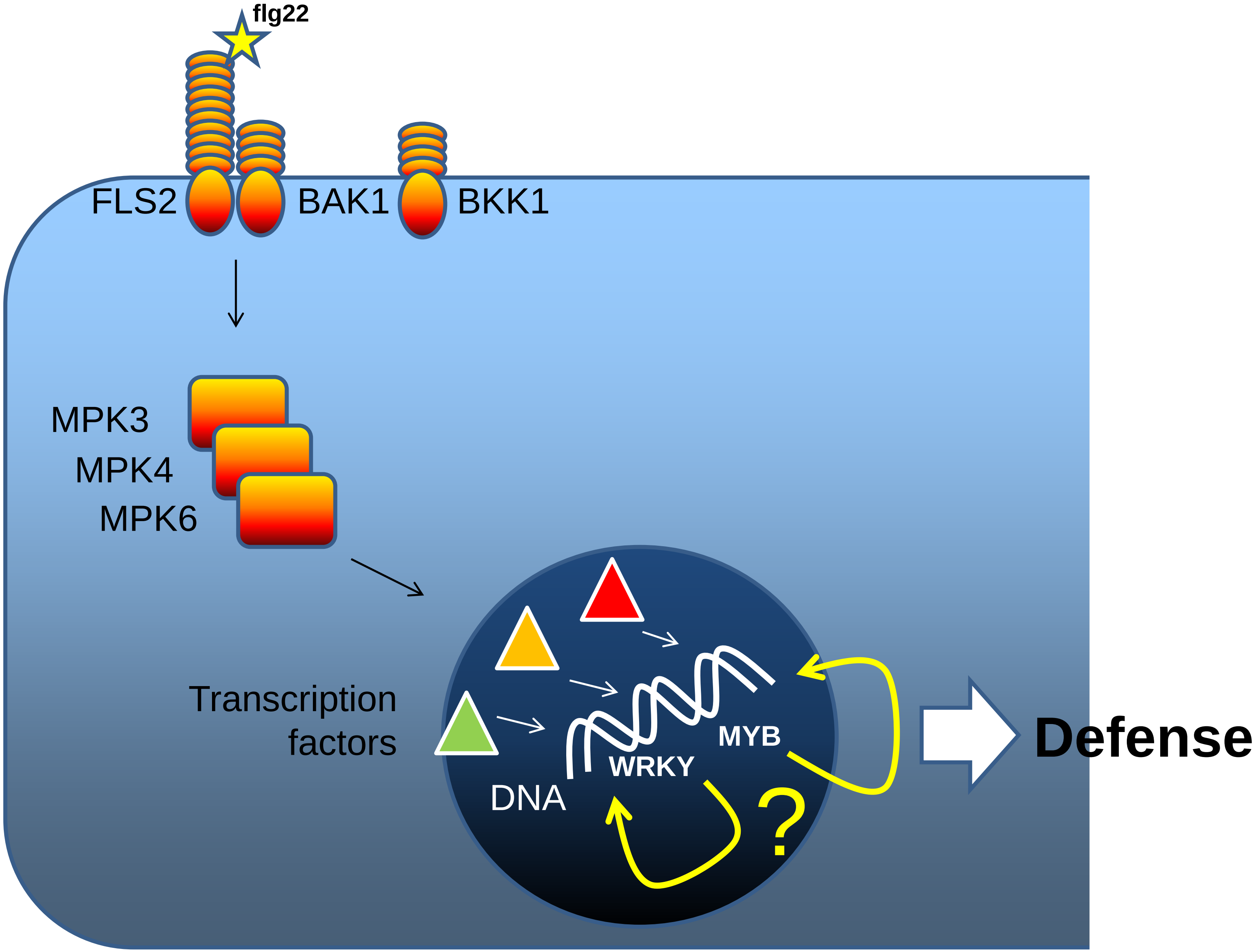
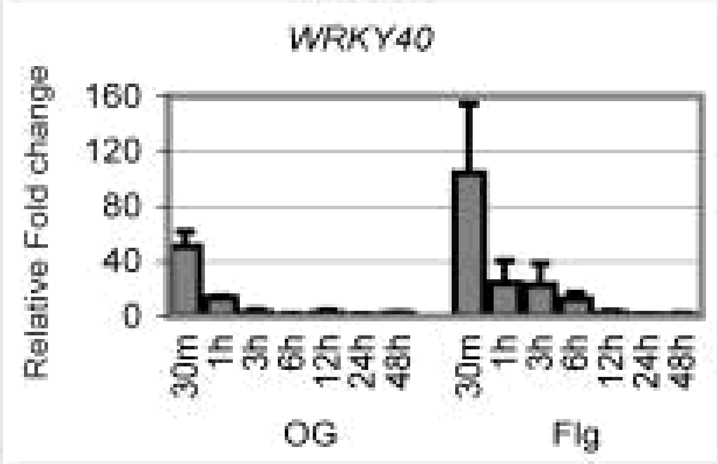
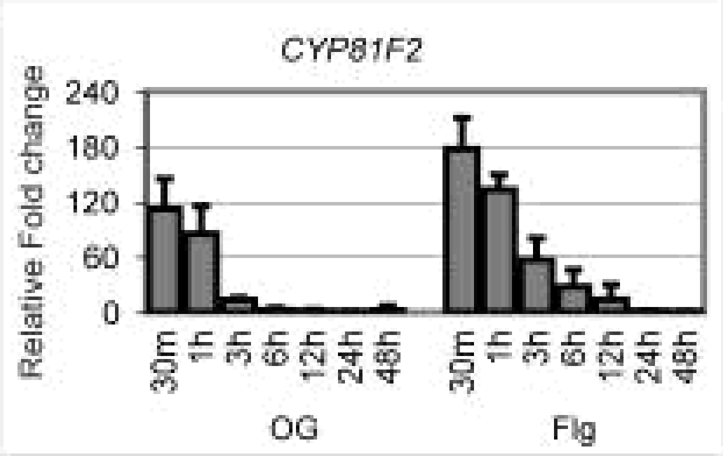
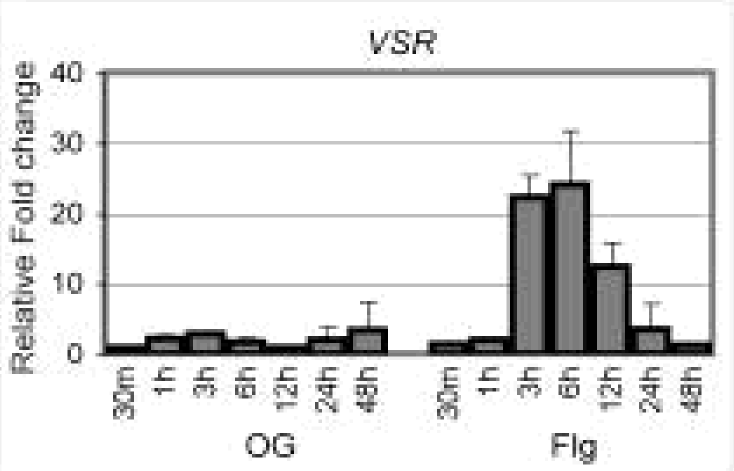
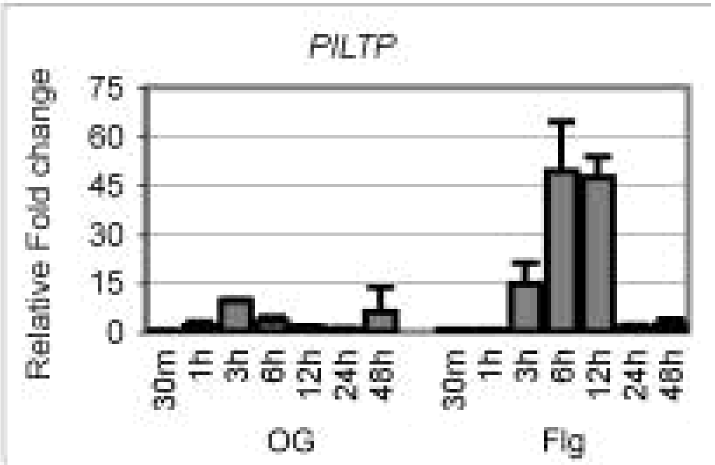
What‘s next ? Go beyond the prediction and test the model(s)…











Denoux et al., 2008 Mol. Plant