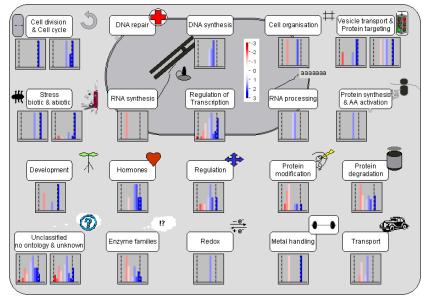
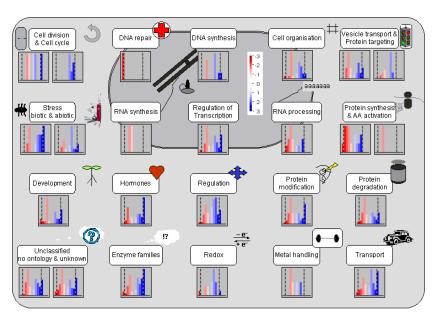
### **Pollen Germination**

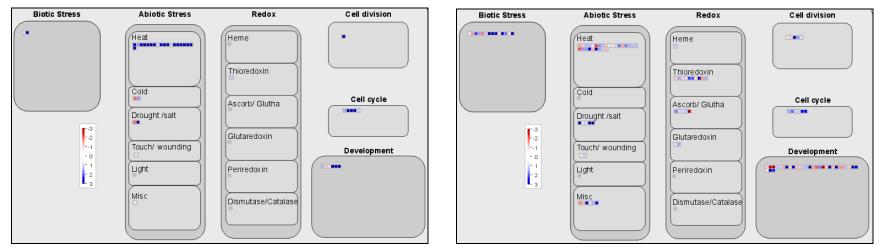
## **Pollen Tube Growth**





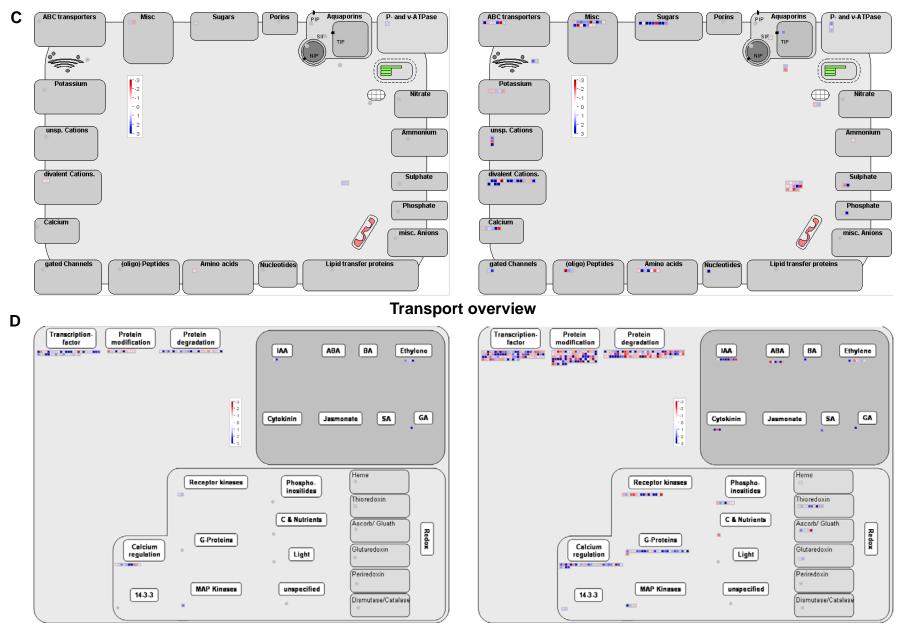
В

## **Cell function overview**



Cellular response overview

Α



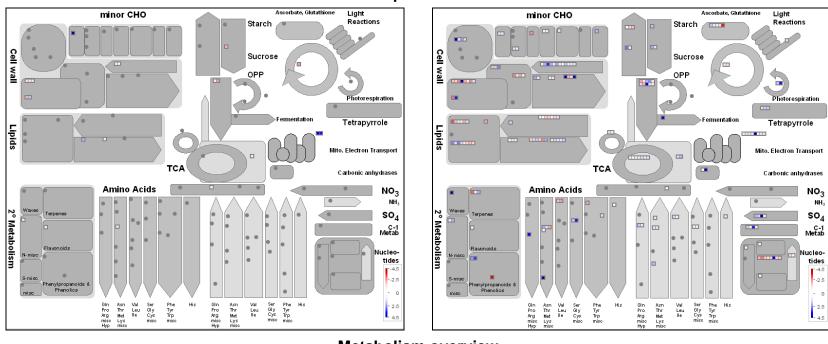
**Regulation overview** 

Ε

ABI3VP1	Alfin-like	CCAAT-HAP2	CPP	SBP	⊜ ТСР	Global High	mobility
AP2-EREBP		E2F-DP	EIL	Trihelix	TUB	Histone DAase Hist	one ATse
ARF	ARR-B	G2-like	GRAS	WRKY		Histone	
DHLH			GRF	Argonaute	AS2	JUMONJI	
		нв	HSF	AT-rich	AtSR	LUG	Methyl BD
bZIP			•	AuxIAA	B3	NIN-like	NPR1
C2C2-CO-like	C2C2-Dof	MADS2			Bromodomain BZR nucleosome assembly		embly
C2C2-Gata	C2C2-YABBY	MYB	- 0 - 1	Chromatin n	emodeling	PHD finger	PHOR1
C2H2		MYB-related	23	Dicer-Like	DNA MT	Polycomb	Psudo ARR
СЗН		NAC		ELF	FHA	PWWP domain	SET-domain
CCAAT-DR1		ORPHAN		GeBP	General	Silencing	SNF7
•		•			•	0 0	
putative DNA-binding		unspec	ified		TAZ	ССНС	

ABI3VP1	Alfin-like	CCAAT-HAP2	• СРР	SBP	<sub>☉</sub> TCP	Global	High mobility
AP2-EREBP	ARR-B	E2F-DP	EL	Trihelix	UB	Histone DAa	se Histone ATse
ARF		G2-like	GRAS	WRKY		Histone	
ьнгн			GRF	Argonaute	as2	JUMONJI	
		нв	HSF	AT-rich	AtSR	LUG	Methyl BD
bZIP			-	AuxAAA	B3	NIN-like	NPR1
C2C2-CO-like	C2C2-Dof	MADS	3 2	Bromodomain	BZR	nucleoso	me assembly
C2C2-Gata	C2C2-YABBY	MYB	- 0	Chromatin remodeling		PHD finge	er PHOR1
C2H2		MYB-related	- 2	Dicer-Like	DNA MT	Polycomb	Psudo ARR
СЗН		NAC		ELF	FHA	PWWP do	
CCAAT-DR1		ORPHAN		GeBP	General	Silencing	SNF7
putative DN	A-binding	•	unspecifie	■ d	•	• TAZ	ССНС
						•	0





# **Transcription overview**

Metabolism overview

#### Figure S2. The difference analysis of changed genes between pollen germination and pollen tube growth using MAPMAN software.

The distinctions of changed genes between pollen germination (left panel) and pollen tube growth (right panel) were shown on the diagrams. The overview display of genes assigned to cell function (A), cellular response (B), transport (C), regulation (D), transcription (E) and metabolism (F) were represented respectively. In diagram A, the distributions of changed genes according to their degrees in main cell functional categories were displayed by using histogram. The color of the bars indicated the change degree of gene expression level; red and blue represented a decrease (a series red bars on the left side) and increase (a series blue bars on the right side) respectively. The scale value of the color was set to 3. In diagrams B to F, all the changed genes were shown in their corresponding functional categories. A pane in the diagram represented one gene, the color of which indicated the change degree of expression level. The detailed definition of MAPMAN software is provided at <a href="http://gabi.rzpd.de/projects/MapMan/">http://gabi.rzpd.de/projects/MapMan/</a>.