Α	FarA group				
,	A.nidulans _	<u> </u>	$\nabla \nabla$	$\nabla\nabla$	$\blacksquare$
	fumigatus_			$\nabla\nabla$	▼
S	S.nodorum _	<b>***</b>			
F.gra	minearum _	<b>***</b>			
	M.grisea_	<b>***</b>			
C.	globosum _	<b>***</b>			
	N.crassa_	<b>***</b>			
	B.cineria_	<b>***</b>			$\blacksquare$
Y	Y.lipolytica _	lacktriangledown			
В		3 group			
В		_	<b>V</b>		
В	FarE		<b>V</b>	_	
<b>B</b> A.	FarE A.nidulans _	▼ □ ▼	<b>V</b>		
<b>B</b> A.	FarE A.nidulans _ fumigatus _	\ \ \ \ \	<b>V</b>		
<b>B</b> A.	FarE  A.nidulans _ fumigatus _ S.nodorum _	V V	<b>V</b>		
A. S. F.gra	FarE A.nidulans _ fumigatus _ S.nodorum _ minearum _	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	▼ ▼		
A. S. F.gra	FarE A.nidulans _ fumigatus _ G.nodorum _ minearum _ M.grisea _ globosum _	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	▼	-	

Supplementary Figure S 4. Intron positions predicted in *farA* and *farB* genes. Conserved introns are indicated as black and non-conserved as white triangles. The sequence encoding the Zn(2)-Cys(6) DNA binding domain is represented by a white box and the fungal specific transcription domain as a black box. (A) *farA* genes contain five highly conserved introns. *Y.lipolytica* contains one of the conserved introns and one extra non-conserved intron. Both *C.albicans* and *D.hansenii* do not contain any introns. (B) All *farB* genes contain two conserved introns except the *N. crassa* gene. Both *B. cineria* and *F. graminearum* genes have introns in the Cys6 finger coding region.