

Classification		Structure	<i>H. minnesotensis</i>		
Order	Superfamily		Number of Consensus Sequences	Number of Occurrences	% Assembly Coverage
<b>Class I (retrotransposons)</b>					
LTR	Copia		70	2,035	4.60%
	Gypsy		93	2,880	7.18%
	Others LTR		15	590	2.22%
LINE	I		47	2,260	4.50%
	R2		1	7	0.03%
	Others LINE		3	86	0.14%
SINE			2	15	0.01%
Elements confused			102	2,789	4.93%
<b>Class II (DNA transposons)- Subclass 1</b>					
TIR	Tc1-Mariner		62	1,720	3.03%
	hAT		54	2,012	2.57%
	MuDR		27	1,048	1.72%
	PiggyBac		14	272	0.51%
	P		3	41	0.07%
	Others TIR		7	184	0.20%
<b>Class II (DNA transposons)- Subclass 2</b>					
Helitron	Helitron		9	430	1.45%
Elements confused			12	191	0.26%
<b>Elements not categorized</b>			<b>14</b>	<b>594</b>	<b>1.23%</b>
<b>Total</b>			<b>535</b>	<b>17,154</b>	<b>34.67%</b>

Fig. S1

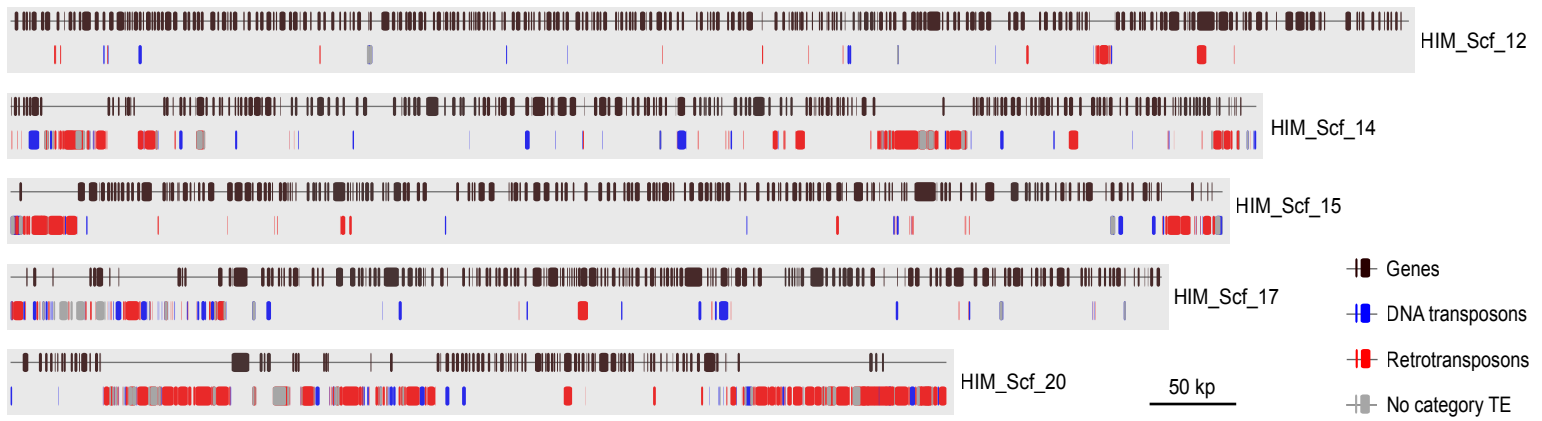


Fig. S2

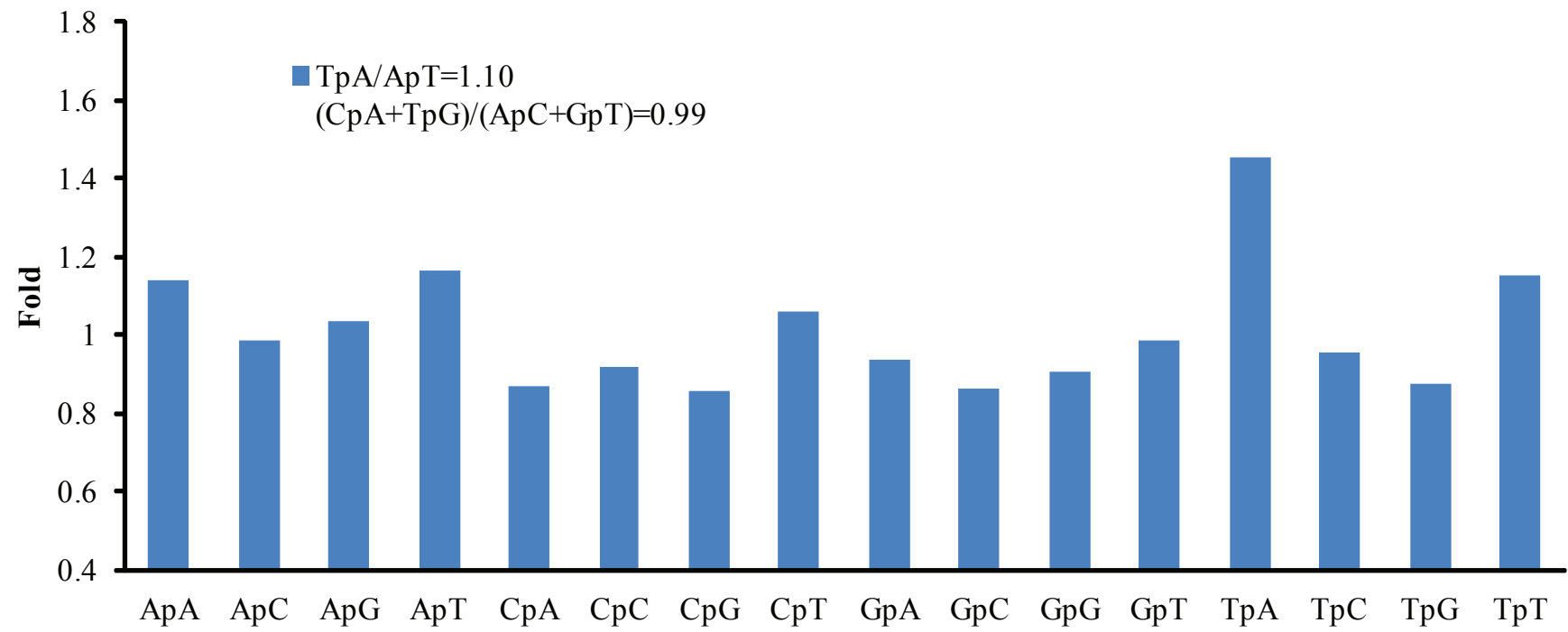


Fig. S3

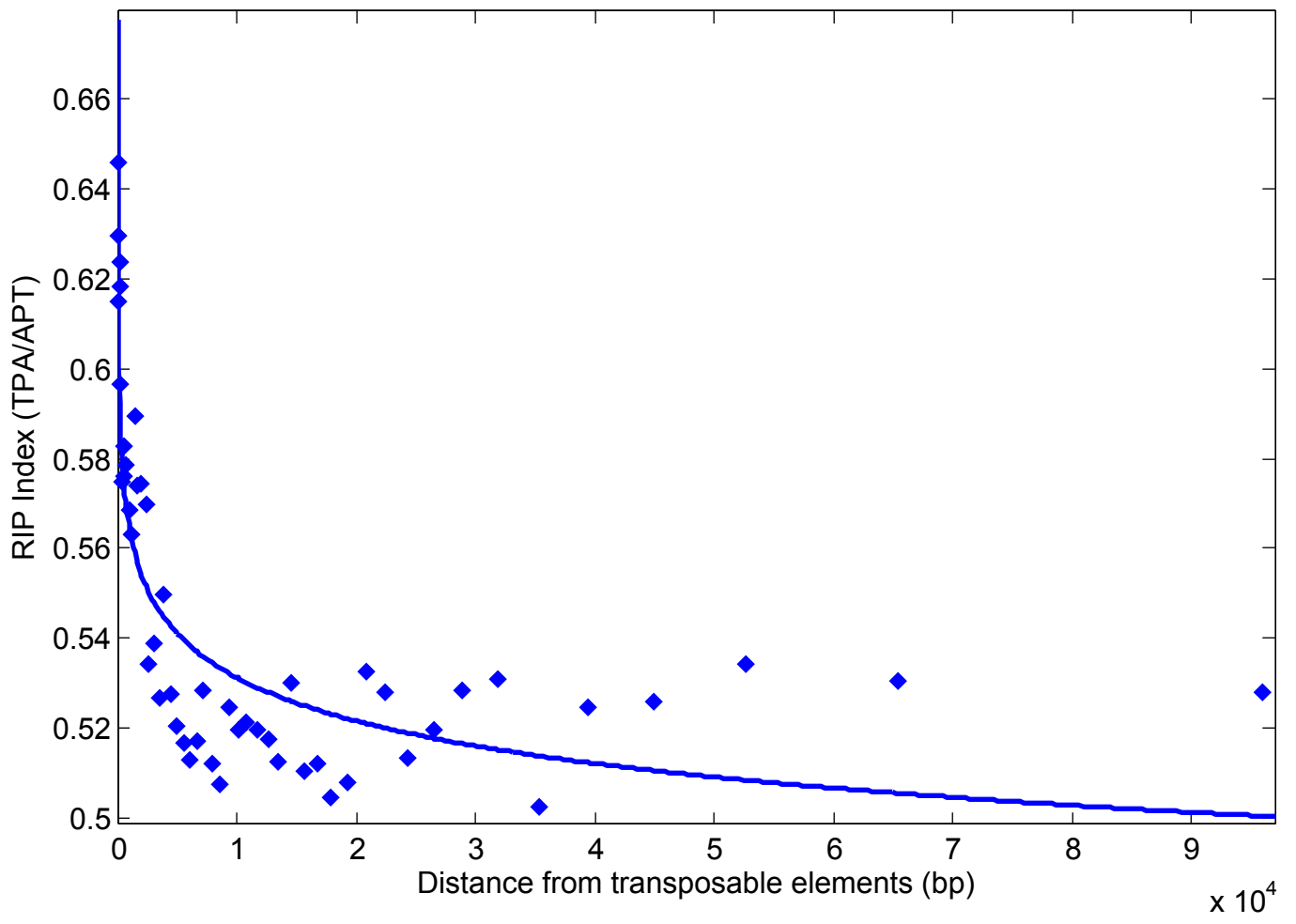
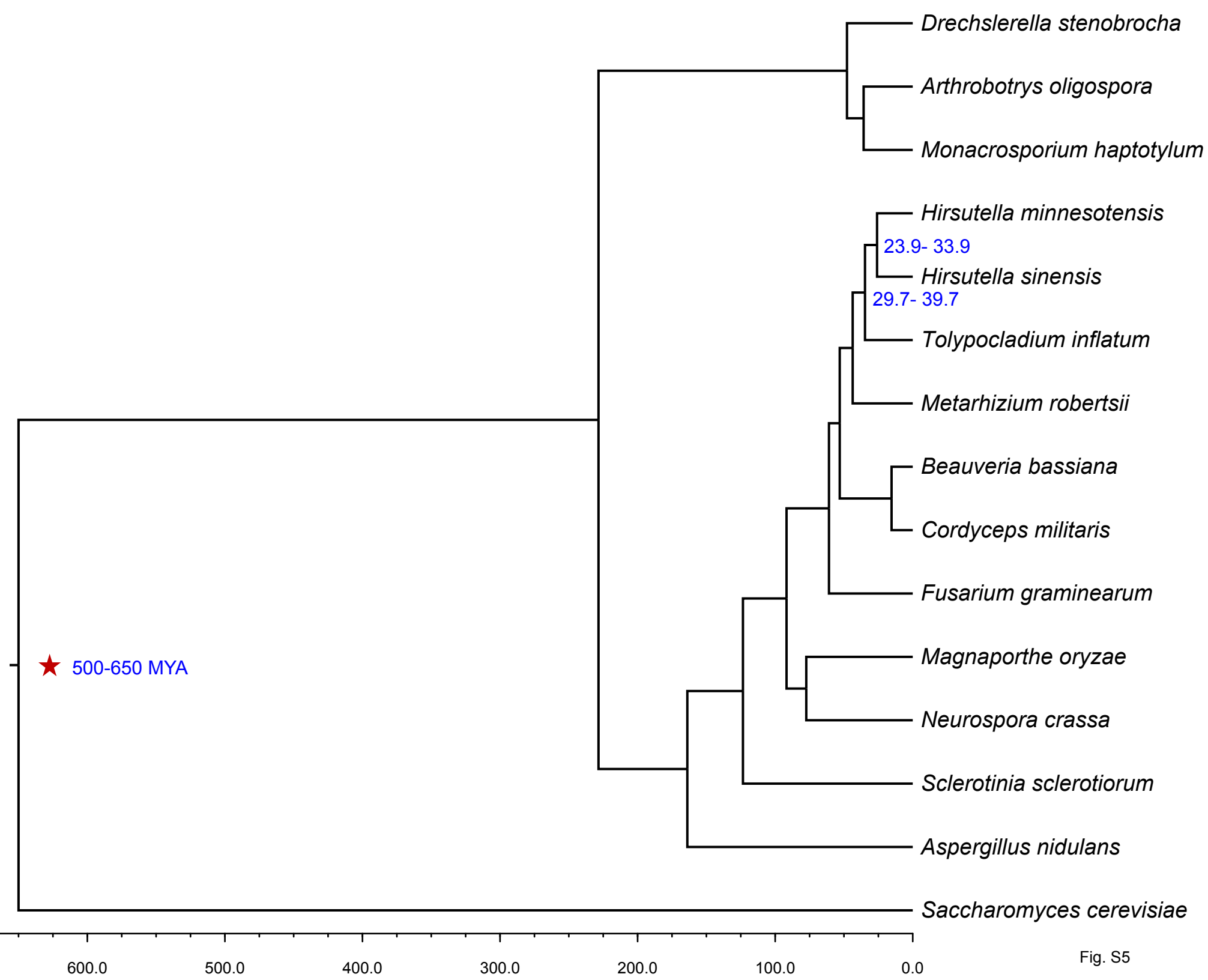
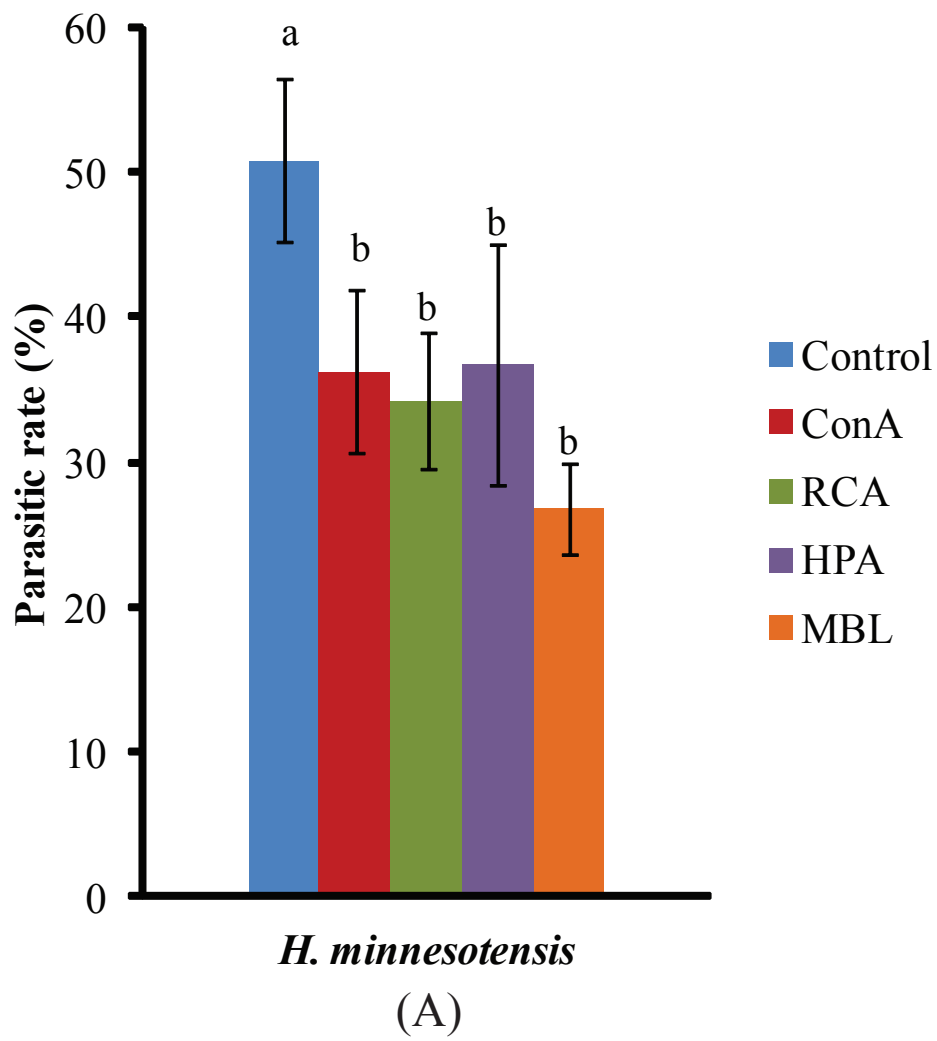
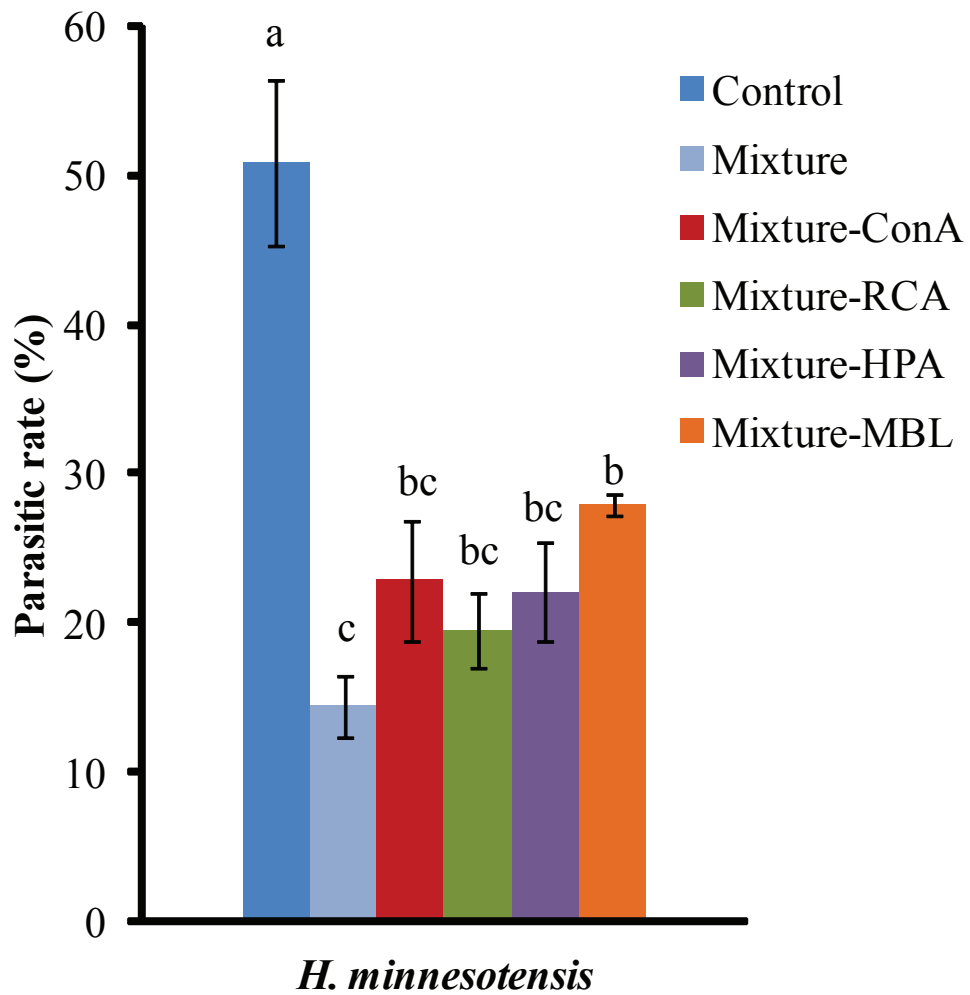


Fig. S4





(A)



(B)

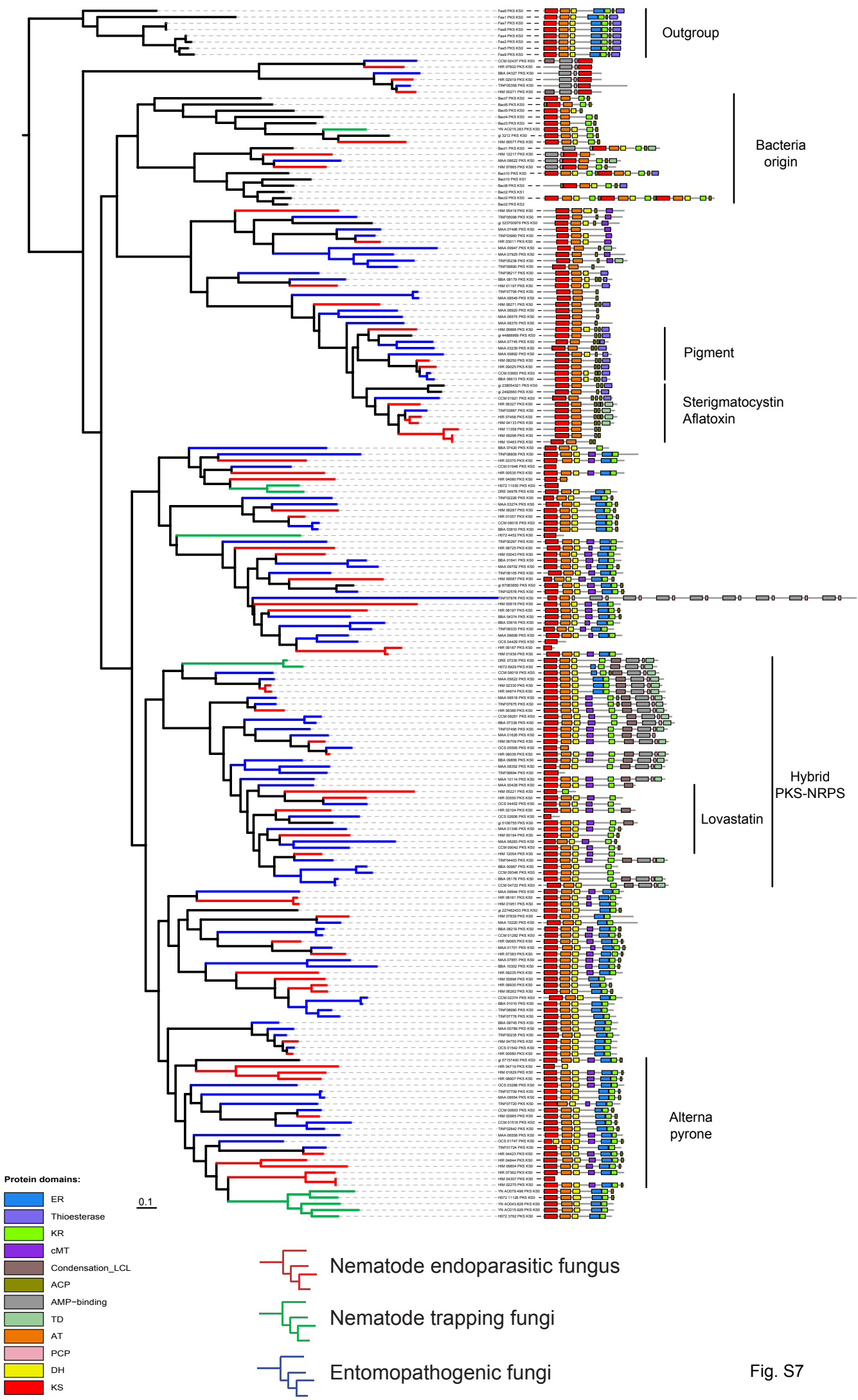


Fig. S7

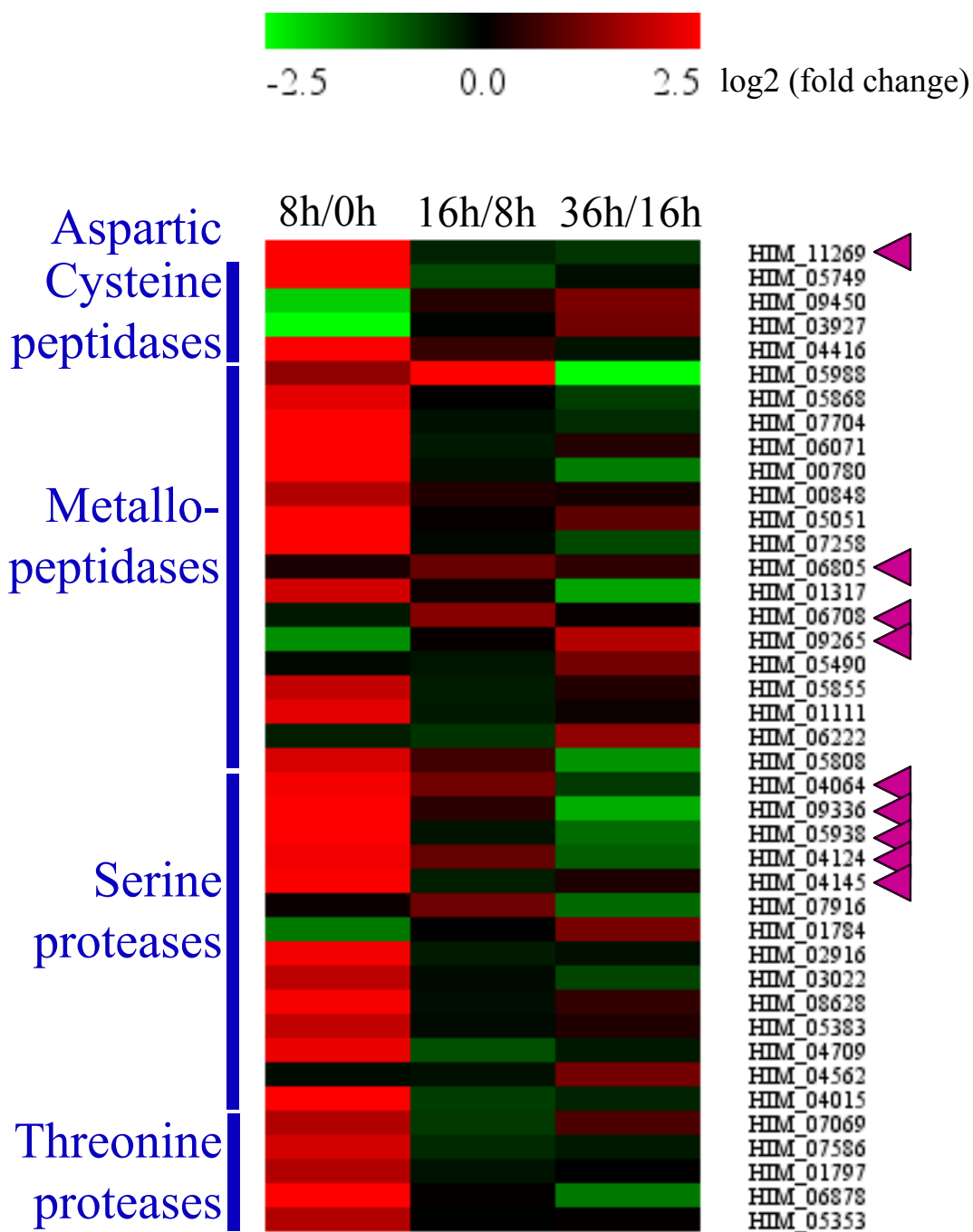


Fig. S8



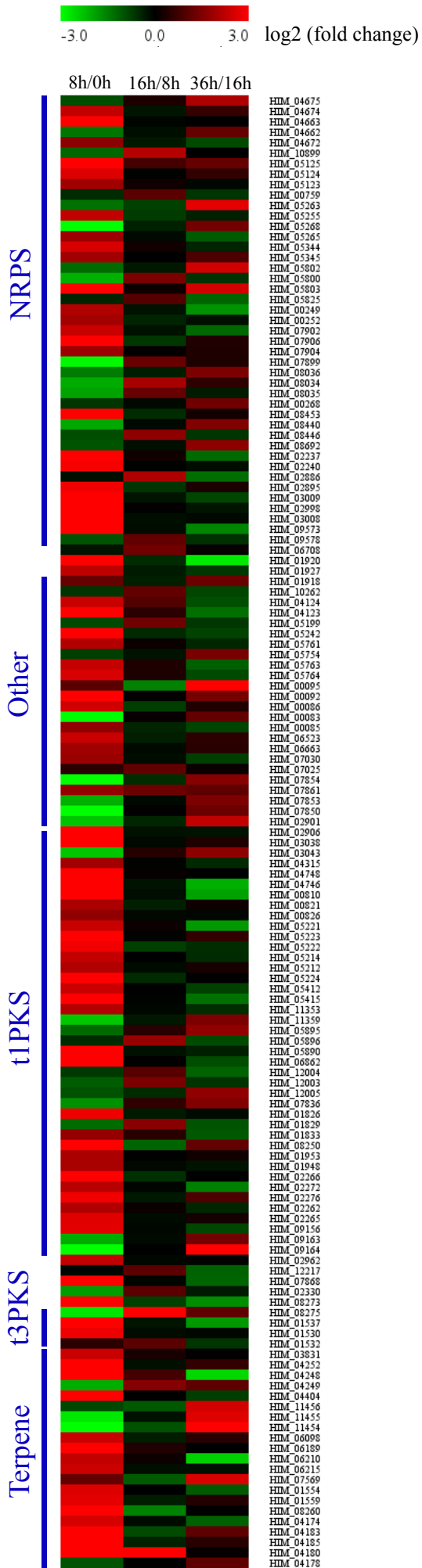


Fig. S9

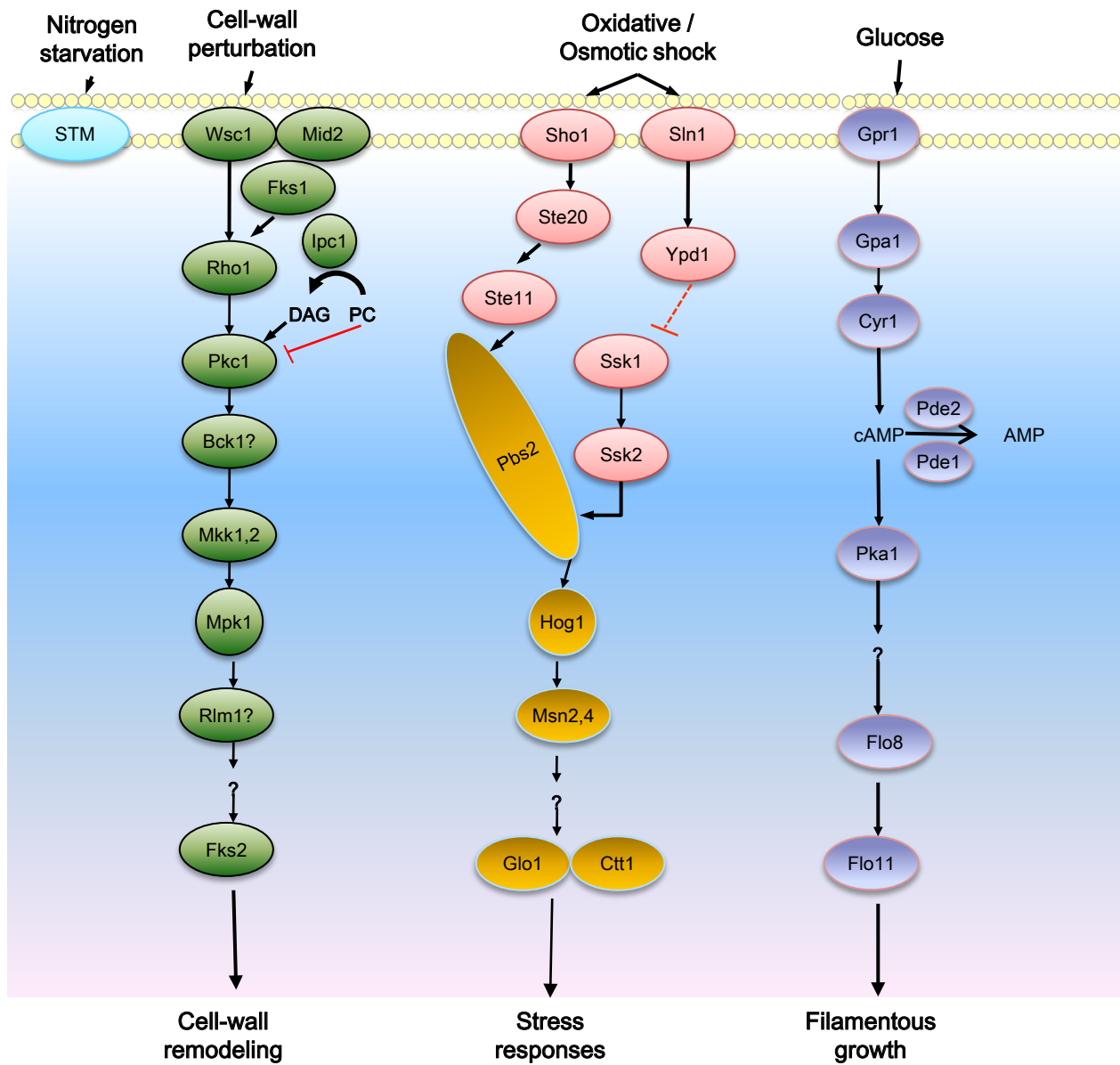


Fig. S10