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Table S1. Plasmid list.

Plasmid	Construct	Reference
pQF86	*hph-URA3-hph* cassette containing *pBluescript II KS*(+)	[2]
pQF181	*hph-URA3-hph* cassette containing *pUC18*	This work
pQGD1-1	5′-*GST2*(1-87bp)inpQF181	This work
pQGD1-2	3′-*GST2*(556-660bp)inpQGD1-1	This work
pQGD2-1	5′-*GST2*(40-120bp)inpQF181	This work
pQGD2-2	3′-*GST2*(283-551bp)inpQGD2-1	This work
pYPB1-ADHpt	*CaADH1* promoter *URA3Ca.*ARS, *Sc.* 2 μm plasmid	[1]
pADH-*GST2*	pYPB1-ADHpt-*CaGST2*	This work
pADH-*CPH1*	pYPB1-ADHpt-*CaCPH1*	This work
pADH-*CST20*	pYPB1-ADHpt-*CaCST20*	This work
pADH-*EFG1*	pYPB1-ADHpt-*CaEFG1*	This work
pADH-*RAS1*	pYPB1-ADHpt-*CaRAS1*	This work
pADH-*RAS1*^{G13V}	pYPB1-ADHpt-*CaRAS1*^{G13V}	This work
pADH-*GPA2*	pYPB1-ADHpt-*CaGPA2*	This work
pADH-*GPA2*^{Q354L}	pYPB1-ADHpt-*CaGPA2*^{Q354L}	This work
pMEP2pt-*MEP2*	pYPB1-MEP2pt-*CaMEP2*	This work
pMEP2pt-*MEP2*$^{\Delta C440}$	pYPB1- MEP2pt-*CaMEP2*$^{\Delta C440}$	This work
pET21-*GST2*	pET-21a-*CaGST2*	This work
pET21-*GST2*^{L41S}	pET-21a-*CaGST2*^{L41S}	This work
pET21-*GTT11*	pET-21a-*CaGTT11*	This work

Table S2. Primers used in this study.

Primer	Gene	Sequence (5′-3′)[a]
For RACE		
5′-GSP1	*GST2*	CATACGGAACTCCAAACG GTTTCAA
3′-GSP1	*GST2*	TTGGACCGTTTTCTGAAACTTGGA A
For gene disruption		
pQGD1-1F	*GST2*	TAGTCGACATGACTAAACCAATTCAATTCTACACATAC(*Sal*I)
pQGD1-1R	*GST2*	TACTCGAGGTAAGCCAATCCTAAAACTTCTAAGAA(*Ava*I)
pQGD1-2F	*GST2*	TACCCGGGGTTGGTATTGATATTCATGATTGGCC(*Sma*I)
pQGD1-2R	*GST2*	TTGAGCTCCTTTTATTTTTTCTCTGGGACATTGACA(*Sac*I)
pQGD2-1F	*GST2*	TTGAGCTCACGGTTTCAAAGTAAGCATTTTCTTAG(*Sac*I)
pQGD2-1R	*GST2*	TACCCGGGCTCGTTTTTAGTGATATCAACAGAAATG(*Sma*I)
pQGD2-2F	*GST2*	TACTCGAGGGAACAGAAGAATATTACAAGACTTTAG(*Ava*I)
pQGD2-2R	*GST2*	TAGTCGACTGCAAACTGTAGGCCCATCCAA (*Sal*I)
For Southern blot anaylsis		
pQF62	*hph*	GGATCGATCTATTCCTTTGCCCTCGG
GST2probe-R	*GST2*	ATCCAGGTACTGTTTCTGGTGGTGATTC
For GST assay		
GST2-F	*GST2*	CAGGATCCATGACTAAACCAATTCAATTCTACACA
GST2-R	*GST2*	AACTCGAGTTTTTTCTCTGGGACATTGACAC
GTT11-F	*GTT11*	CAGGATCCATGTCTGACACCAAAATTATTGTTC
GTT11-R	*GTT11*	GCCTCGAGAATGTTAGGCTTAACAGTTTC

[a]The created restriction sites are underlined.

Table S2. Continued.

Primer	Gene	Sequence (5′-3′)[b]
For mutagenesis		
GST2^{L41S}-F	GST2	CATTTCTGTTGATATCACTAAAAACGAG**TCT**AAATCTGATTGGTTTGTTAAATTGAATCC
GST2^{L41S}-R	GST2	GGATTCAATTTAACAAACCAATCAGATTT**AGA**CTCGTTTTTAGTGATATCAACAGAAATG
RAS1^{G13V}-F	RAS1	GTTGTTGTTGGAGGA**GTT**GGTGTTGGTAAATCCGC
RAS1^{G13V}-R	RAS1	GCGGATTTACCAACACC**AAC**TCCTCCAACAACAAC
GPA2^{Q354L}-F	GPA2	GATGTTGGTGGT**TTA**AGGTCAGAAAG
GPA2^{Q354L}-R	GPA2	CTTTCTGA CCTT**AAA**CCACCAACATC
For overexpression		
ADH-GST2-F	GST2	GCAGATCTAGCAGCAACAATGACTAAACCA(*Bgl*II)
ADH- GST2-R	GST2	GCCTCGAGTTTATTTTTTCTCTGGGACATTG(*Xho*I)
ADH-CPH1-F	CPH1	GGCAGATCTCTTTCGCCATGTCAATTACTAAAAC(*Bgl*II)
ADH-CPH1-R	CPH1	GACTCGAGCTATGTTTGTGACTGTTTTACTTC(*Xho*I)
ADH-EFG1-F	EFG1	CCGGATCCATGTCAACGTATTCTATACC(*Bam*HI)
ADH-EFG1-R	EFG1	CCACGCGTCAATGACTGAACTTGGG(*Mlu*I)
ADH-RAS1-F	RAS1	GAAAGATCTATGTTGAGAGAATATAAATTAG(*Bgl*II)
ADH-RAS1-R	RAS1	GAAGATATCTCAAACAATAACACAACATCC(*Eco*RV)
ADH-GPA2-F	GPA2	AACTTTAGATCTATGGGTTCTTGTGCTTC(*Bgl*Ⅱ)
ADH-GPA2-R	GPA2	TGCCTCGAGCTATAAAATACCACTATCTT(*Xho*I)
MEP2pt-MEP2-F	MEP2	TAAATACTCGAGCCAAACGATTGGCTTGAATGTC(*Xho*I)
MEP2pt-MEP2-R	MEP2	AGAAGATCTTTAATTTTTAGCTTCTCCTGAGTCG(*Bgl*Ⅱ)
MEP2pt-MEP2$^{\Delta C440}$-R	MEP2	GGTTGGAGATCTAATCGTCATCAGCATAATAGG(*Bgl*Ⅱ)
For northern blot analysis		
RAS1-F	RAS1	GAAAGATCTATGTTGAGAGAATATAAATTAG
RAS1-R	RAS1	GAAGATATCTCAAACAATAACACAACATCC

[b]The created restriction sites are underlined and the mutated codons are in boldface.

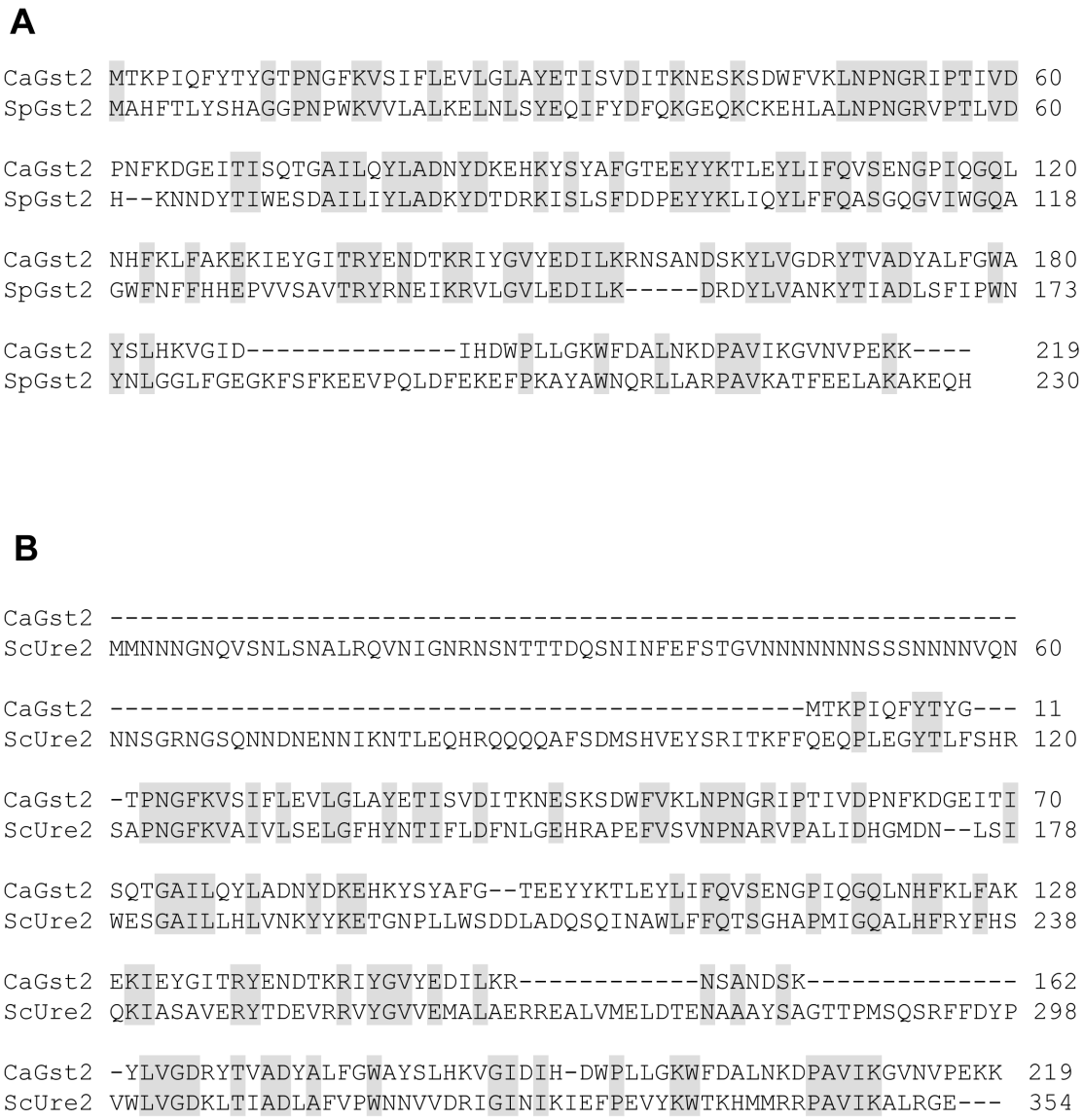

Fig. S1. Amino acid sequence alignment of *C. albicans* GST2.

(**A**) Alignment of *C. albicans* Gst2p and *S. pomb* Gst2p was performed using CLUSTALW. Identities are highlighted. (**B**) Alignment of *C. albicans* Gst2p and *S. cerevisiae* Ure2p was performed using CLUSTALW. Identities are highlighted.

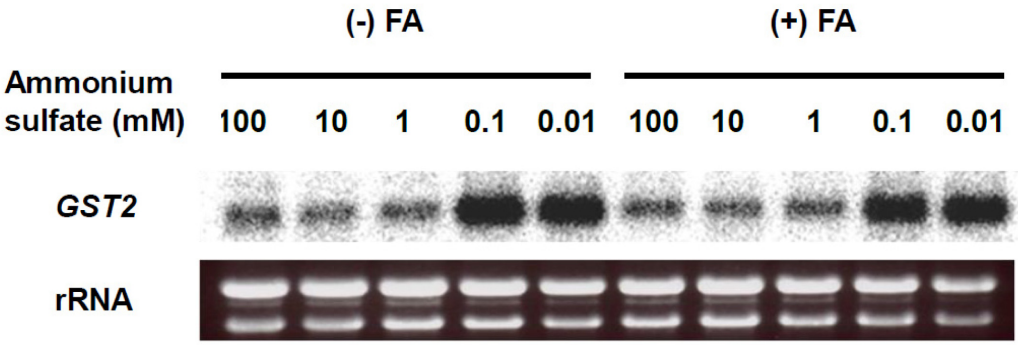

Fig. S2. Effects of farnesoic acid (FA) on *GST2* expression.
Cells were grown at 28°C for 2 h in SD liquid medium containing the indicated concentrations of ammonium sulfate with (+) or without (–) 40 μg/ml FA.

References

1. Bertram G, Swoboda RK, Gooday GW, Gow NAR, Brown AJP. 1996. Structure and regulation of the *Candida albicans* ADH1 gene encoding an immunogenic alcohol dehydrogenase. *Yeast* **12:** 115-127.
2. Feng QH, Summers E, Guo B, Fink G. 1999. Ras signaling is required for serum-induced hyphal differentiation in *Candida albicans*. *J. Bacteriol*. **181:** 6339-6346.