

**Table S1.** Plasmid list.

Plasmid	Construct	Reference
pQF86	<i>hph</i> -URA3- <i>hph</i> cassette containing <i>pBluescript II KS(+)</i>	[2]
pQF181	<i>hph</i> -URA3- <i>hph</i> cassette containing <i>pUC18</i>	This work
pQGD1-1	5'- <i>GST2</i> (1-87bp)inpQF181	This work
pQGD1-2	3'- <i>GST2</i> (556-660bp)inpQGD1-1	This work
pQGD2-1	5'- <i>GST2</i> (40-120bp)inpQF181	This work
pQGD2-2	3'- <i>GST2</i> (283-551bp)inpQGD2-1	This work
pYPB1-ADHpt	<i>CaADH1</i> promoter URA3 <i>Ca</i> .ARS, <i>Sc</i> . 2 $\mu$ m plasmid	[1]
pADH- <i>GST2</i>	pYPB1-ADHpt- <i>CaGST2</i>	This work
pADH- <i>CPH1</i>	pYPB1-ADHpt- <i>CaCPH1</i>	This work
pADH- <i>CST20</i>	pYPB1-ADHpt- <i>CaCST20</i>	This work
pADH- <i>EFG1</i>	pYPB1-ADHpt- <i>CaEFG1</i>	This work
pADH- <i>RAS1</i>	pYPB1-ADHpt- <i>CaRAS1</i>	This work
pADH- <i>RAS1</i> <sup>G13V</sup>	pYPB1-ADHpt- <i>CaRAS1</i> <sup>G13V</sup>	This work
pADH- <i>GPA2</i>	pYPB1-ADHpt- <i>CaGPA2</i>	This work
pADH- <i>GPA2</i> <sup>Q354L</sup>	pYPB1-ADHpt- <i>CaGPA2</i> <sup>Q354L</sup>	This work
pMEP2pt- <i>MEP2</i>	pYPB1-MEP2pt- <i>CaMEP2</i>	This work
pMEP2pt- <i>MEP2</i> <sup>AC440</sup>	pYPB1- MEP2pt- <i>CaMEP2</i> <sup>AC440</sup>	This work
pET21- <i>GST2</i>	pET-21a- <i>CaGST2</i>	This work
pET21- <i>GST2</i> <sup>L415</sup>	pET-21a- <i>CaGST2</i> <sup>L415</sup>	This work
pET21- <i>GTT11</i>	pET-21a- <i>CaGTT11</i>	This work

**Table S2.** Primers used in this study.

Primer	Gene	Sequence (5'-3') <sup>a</sup>
For RACE		
5'-GSP1	<i>GST2</i>	CATACGGAACCTCCAAACG GTTTCAA
3'-GSP1	<i>GST2</i>	TTGGACCGTTTTCTGAAACTTGGAA A
For gene disruption		
pQGD1-1F	<i>GST2</i>	<u>TAGTCGAC</u> ATGACTAAACCAATTCAATTCTACACATAC( <i>Sall</i> )
pQGD1-1R	<i>GST2</i>	TAC <u>CTCGAG</u> GTAAGCCAATCCTAAAACTTCTAAGAA( <i>AvaI</i> )
pQGD1-2F	<i>GST2</i>	TAC <u>CCCGGG</u> GTTGGTATTGATATTCATGATTGGCC( <i>SmaI</i> )
pQGD1-2R	<i>GST2</i>	TT <u>GAGCTC</u> CCTTTTATTTTTTCTCTGGGACATTGACA( <i>SacI</i> )
pQGD2-1F	<i>GST2</i>	TT <u>GAGCTC</u> ACGGTTTCAAAGTAAGCATTTCCTTAG( <i>SacI</i> )
pQGD2-1R	<i>GST2</i>	TAC <u>CCCGGG</u> CTCGTTTTTAGTGATATCAACAGAAATG( <i>SmaI</i> )
pQGD2-2F	<i>GST2</i>	TAC <u>CTCGAG</u> GGGAACAGAAGAATATTACAAGACTTTAG( <i>AvaI</i> )
pQGD2-2R	<i>GST2</i>	TAG <u>TCGACT</u> GCAAACTGTAGGCCATCCAA ( <i>Sall</i> )
For Southern blot analysis		
pQF62	<i>hph</i>	GGATCGATCTATTCCTTTGCCCTCGG
GST2probe-R	<i>GST2</i>	ATCCAGGTACTGTTTCTGGTGGTGATTC
For GST assay		
GST2-F	<i>GST2</i>	CAGGATCCATGACTAAACCAATTCAATTCTACACA
GST2-R	<i>GST2</i>	AACTCGAGTTTTTCTCTGGGACATTGACAC
GTT11-F	<i>GTT11</i>	CAGGATCCATGCTGACACCAAAATTATTGTTC
GTT11-R	<i>GTT11</i>	GCCTCGAGAAATGTTAGGCTTAACAGTTTC

<sup>a</sup>The created restriction sites are underlined.

**Table S2.** Continued.

Primer	Gene	Sequence (5'-3') <sup>b</sup>
For mutagenesis		
GST2 <sup>L41S</sup> -F	GST2	CATTCTGTGATATCACTAAAAACGAGTCTAAATCTGATTGGTTTGTAAATTGAATCC
GST2 <sup>L41S</sup> -R	GST2	GGATTCAATTTAACAAACCAATCAGATTTAGACTCGTTTTTAGTGATATCAACAGAAATG
RAS1 <sup>G13V</sup> -F	RAS1	GTTGTTGTTGGAGGAG <b>TTGGT</b> GTTGGTAAATCCGC
RAS1 <sup>G13V</sup> -R	RAS1	GCGGATTTACCAACACCA <b>AACTCCT</b> CCAACAACAAC
GPA2 <sup>Q354L</sup> -F	GPA2	GATGTTGGTGGTTTAAGGTCAGAAAG
GPA2 <sup>Q354L</sup> -R	GPA2	CTTCTGA CCTTAAACCACCAACATC
For overexpression		
ADH-GST2-F	GST2	GCAGATCTAGCAGCAACAATGACTAAACCA( <i>Bgl</i> II)
ADH-GST2-R	GST2	GCCTCGAGTTTATTTTTTCTCTGGGACATTG( <i>Xho</i> I)
ADH-CPH1-F	CPH1	GGCAGATCTCTTCGCCATGTCAATTACTAAAAC( <i>Bgl</i> II)
ADH-CPH1-R	CPH1	GACTCGAGCTATGTTTGACTGTTTACTTC( <i>Xho</i> I)
ADH-EFG1-F	EFG1	CCGGATCCATGTCAACGTATTCTATAACC( <i>Bam</i> HI)
ADH-EFG1-R	EFG1	CCACGCGTCAATGACTGAACTGGG( <i>Mlu</i> I)
ADH-RAS1-F	RAS1	GAAAGATCTATGTTGAGAGAATATAAATTAG( <i>Bgl</i> II)
ADH-RAS1-R	RAS1	GAAGATATCTCAAACAATAACACAACATCC( <i>Eco</i> RV)
ADH-GPA2-F	GPA2	AACTTTAGATCTATGGGTTCTTGCTTC( <i>Bgl</i> II)
ADH-GPA2-R	GPA2	TGCCTCGAGCTATAAAATACCACTATCTT( <i>Xho</i> I)
MEP2 <sup>pt</sup> -MEP2-F	MEP2	TAAATACTCGAGCCAAACGATTGGCTTGAATGTC( <i>Xho</i> I)
MEP2 <sup>pt</sup> -MEP2-R	MEP2	AGAAGATCTTAAATTTTAGCTTCTCCTGAGTCG( <i>Bgl</i> II)
MEP2 <sup>pt</sup> -MEP2 <sup>Ac440</sup> -R	MEP2	GGTTGGAGATCTAATCGTCATCAGCATAATAGG( <i>Bgl</i> II)
For northern blot analysis		
RAS1-F	RAS1	GAAAGATCTATGTTGAGAGAATATAAATTAG
RAS1-R	RAS1	GAAGATATCTCAAACAATAACACAACATCC

<sup>b</sup>The created restriction sites are underlined and the mutated codons are in boldface.

## A

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CaGst2 MTKPIQFYTYGTPNGFKVSI FLEVLGLAYETISVDITKNESKSDWVFKLNPNGRIPTIVD 60
SpGst2 MAHFTLYSHAGGPNPWKVVLALKELNLSYEQIFYDFQKGEQKKEHLALNPNGRVPTLVD 60

CaGst2 PNFKDGEITISQTGAILQYLADNYDKEHKYSYAFGTEEYKTYLYLIFQVSENGPIQGQL 120
SpGst2 H--KNNDYTIWESDAILIYLADKYDTRKISLSFDDPEYKLIQYLFQASGQGVWGWQA 118

CaGst2 NHFKLFAKEKIEYGITRYENDTKRIYGVYEDILKRNSANDSKYLVGDRYTVADYALFGWA 180
SpGst2 GWFNFFHHEPVVSAVTRYRNEIKRVLGVLEDILK-----DRDYLVANKYTIADLSFIPWN 173

CaGst2 YSLHKVGID-----IHDWPLLGKWF DALNKDPAVIKGVNVPEKK----- 219
SpGst2 YNLGGLFGEKGF SFKEEVPQLDFEKEFPKAYAWNQRLLARPAVKATFEELAKAKEQH 230
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## B

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CaGst2 -----
ScUre2 MMNNNGNQVSNLSNALRQVNI GNRNSNTTTDQSNINFEFSTGVNNNNNNSSSNNNNVQN 60

CaGst2 -----MTKPIQFYTYG--- 11
ScUre2 NNSGRNGSQNNDNENNIKNTLEQHRQQQAFSDMSHVEYSRITKFFQEQLLEGYTLFSHR 120

CaGst2 -TPNGFKVSI FLEVLGLAYETISVDITKNESKSDWVFKLNPNGRIPTIVDPNFKDGEITI 70
ScUre2 SAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNARVPALIDHGMDN--LSI 178

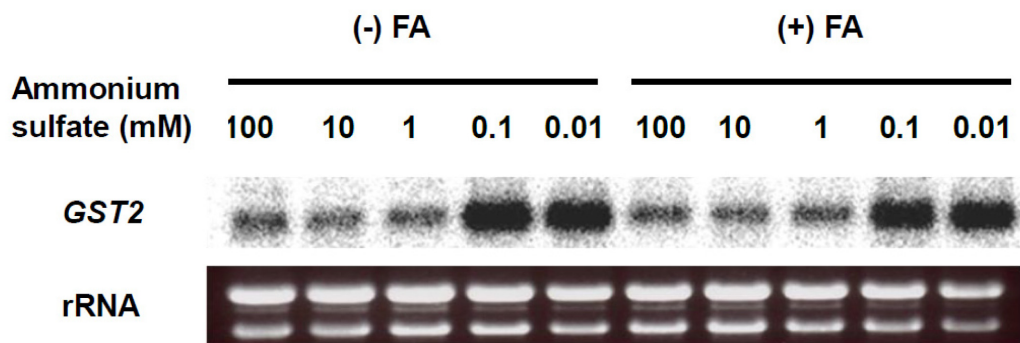
CaGst2 SQTGAILQYLADNYDKEHKYSYAFG--TEEYKTYLYLIFQVSENGPIQGQLNHFKLFAK 128
ScUre2 WESGAILLHLVKNKYYKETGNPLLWSDDLADQSQINAWLFFQTSGHAPMIGQALHFRYFHS 238

CaGst2 EKIEYGITRYENDTKRIYGVYEDILKR-----NSANDSK----- 162
ScUre2 QKIASAVERYTDEVRVYGVVEMALAEERREALVMELDTENAAAAYSAGTTPMSQSRFFDYP 298

CaGst2 -YLVGDRYTVADYALFGWAYSLHKVGIDIH-DWPLLGKWF DALNKDPAVIKGVNVPEKK 219
ScUre2 VWLVGDKLTIADLAFVPPNNDVDRIGINIKIEFPEVYKWKHMMRRPAVIKALRGE--- 354
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**Fig. S1.** Amino acid sequence alignment of *C. albicans* GST2.

(A) Alignment of *C. albicans* Gst2p and *S. pombe* 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

- 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.
- 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.