

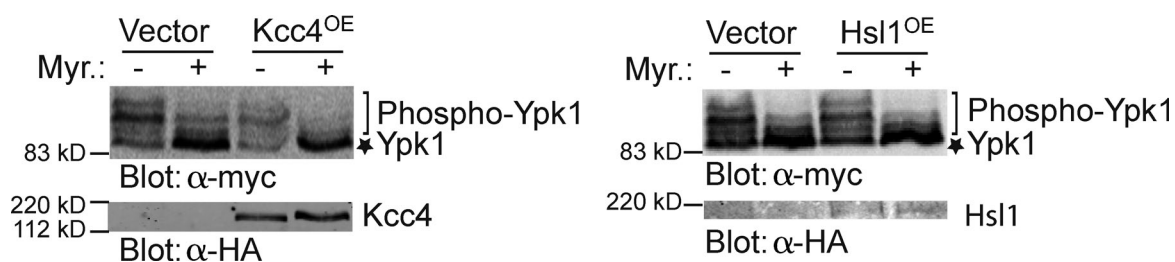
Roelants et al., <http://www.jcb.org/cgi/content/full/jcb.201410076/DC1>

Figure S1. **Kcc4 and Hsl1 do not affect Fpk1-dependent phosphorylation of Ypk1.** Wild-type cells (Y258) carrying a plasmid expressing Ypk1-myc from the *GAL1* promoter (pAM54) and either an empty vector (BG1805) or the same vector expressing Kcc4 (pKcc4-zz; left) or Hsl1-(HA)<sub>3</sub> (pMJS109; right) from the *GAL1* promoter were lysed, and the resulting extracts were resolved by SDS-PAGE and analyzed by immunoblotting with anti-c-myc mAb 9E10 and anti-HA antibodies, as indicated.

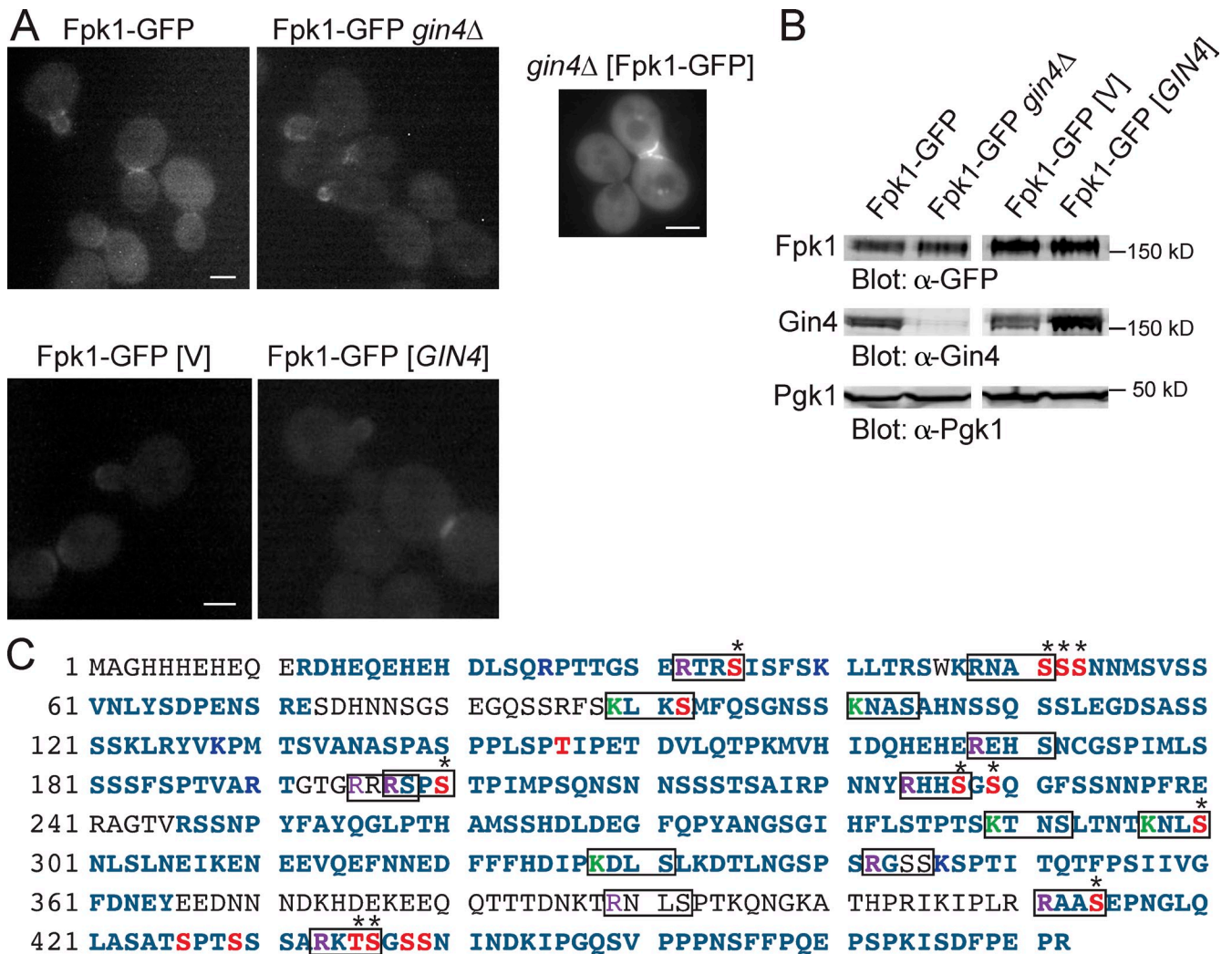


Figure S2. **Gin4 does not affect Fpk1 localization or level.** (A) Wild-type cells (YFR221) or isogenic *gin4* $\Delta$  cells (YFR224) expressing Fpk1-GFP (top left) from its chromosomal locus, as well as *gin4* $\Delta$  cells (YAT100) expressing Fpk1-GFP from the *TPI1* promoter on a *CEN* plasmid [pFR150; top right], and wild-type cells (YFR221) expressing Fpk1-GFP from its endogenous promoter and carrying an empty vector [V] (YCpUG) or the same vector overexpressing *GIN4* (pMVB115) from the *GAL1* promoter (bottom) were grown to mid-exponential phase and viewed with fluorescence microscopy. Bars, 2  $\mu$ m. (B) The same cells as in A were lysed and the resulting extracts were resolved by SDS-PAGE and analyzed by immunoblotting with anti-GFP and anti-Gin4 antibodies. (C) Sites in the N-terminal regulatory domain of Fpk1 phosphorylated by Gin4 were determined by mass spectrometry, as described in the Materials and methods. Sequence coverage is indicated by bold blue letters. Ser and Thr residues phosphorylated in the presence of Gin4 are indicated in red. Occurrences of the apparent Gin4 consensus sequence (-R/K-x-x-S-) derived from this work and from analysis of synthetic peptide arrays (Mok et al., 2010), with Arg (purple) and Lys (green) highlighted, are boxed. Asterisks indicate the 10 Ser and 1 Thr mutated to Ala in Fpk1<sup>11A</sup>.

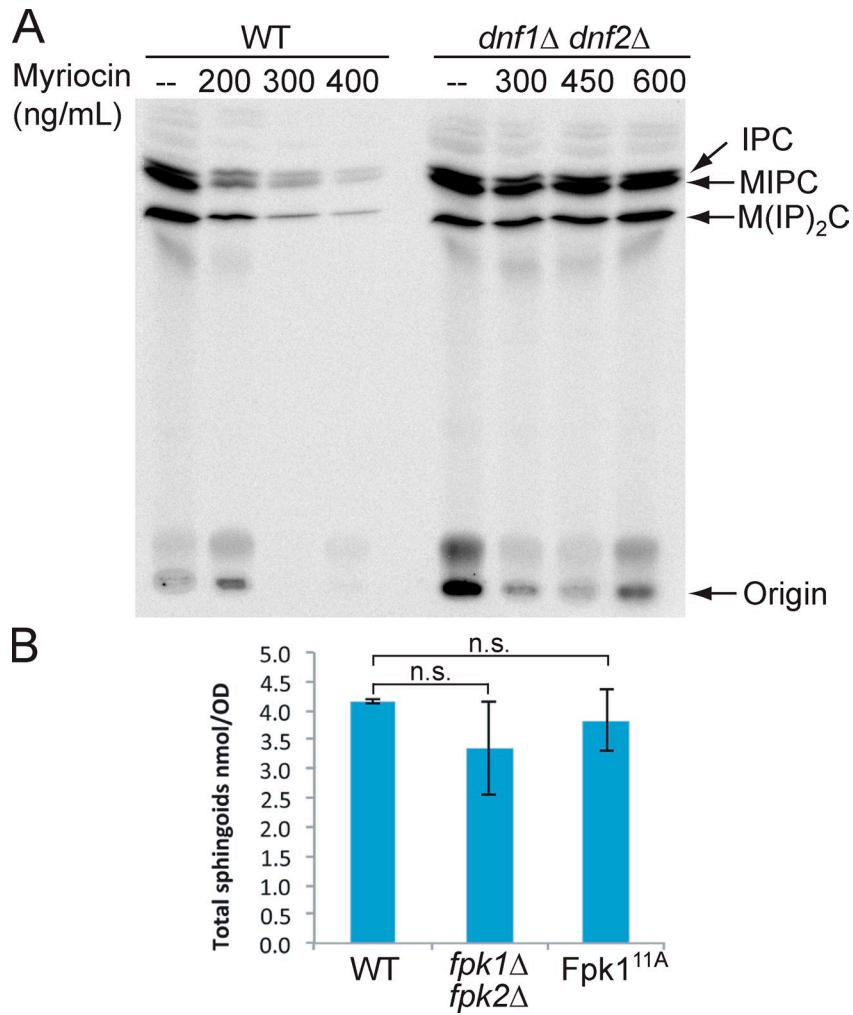


Figure S3. **PM flippase activity is required for susceptibility to Myr, but does not affect sphingolipid levels.** (A) Wild-type (BY4741, WT) and isogenic *dnf1Δ dnf2Δ* (YFR313) cells were grown at 30°C to mid-exponential phase, then treated with the indicated amount of Myr and cultivated for an additional 8 h. An equivalent number of cells from each culture (2 ml of  $A_{600nm} = 1.0$ ) were then labeled with 100  $\mu$ Ci of [<sup>32</sup>P]H<sub>2</sub>PO<sub>4</sub> for 3 h. Complex (inositol-P-containing) sphingolipids were then extracted and analyzed by ascending TLC and autoradiography as described in the Materials and methods. The identity of the indicated complex sphingolipid species was assigned on the basis of either pharmacological inhibition or mutational ablation of the enzymes responsible for the production of IPC (Aur1), MIPC (Sur1-Csg2 and Csh1-Csg2), and M(IP)<sub>2</sub>C (Ipt1) in control cultures (not depicted). (B) Total sphingoid base (PHS) was generated from equivalent numbers of wild-type (BY4741, WT), isogenic *fpk1Δ fpk2Δ* (YFR205), and Fpk1<sup>11A</sup> (YJW2) cells and quantified by HPLC, as described in the Materials and methods. Values represent the mean and SD (error bars) of five independent experiments. n.s., not statistically significant.

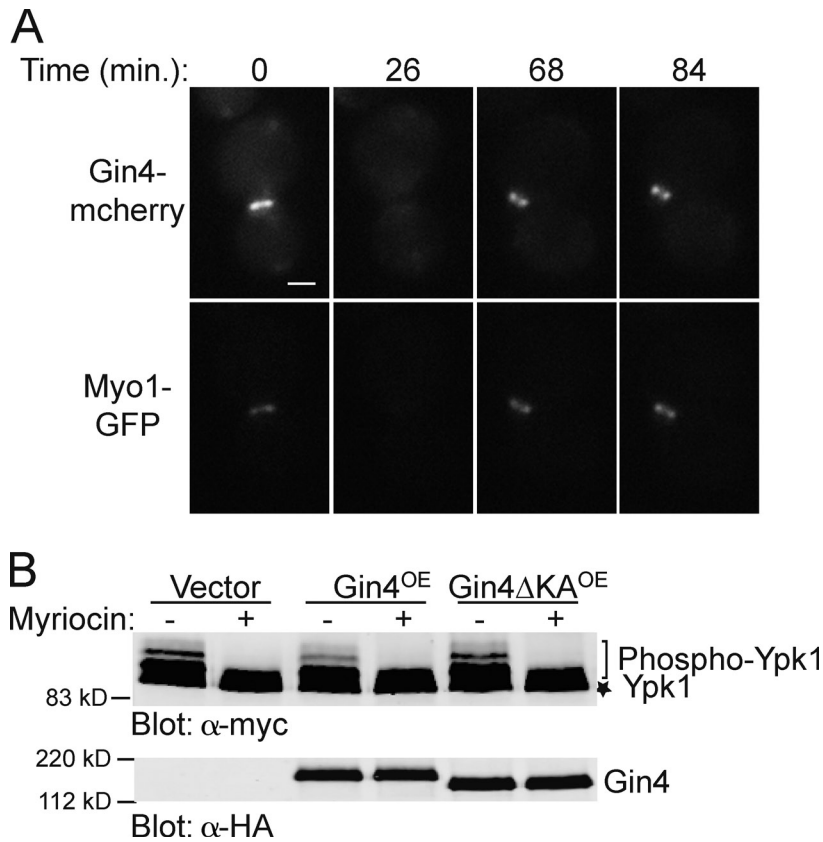


Figure S4. **KA1 domain-mediated PM targeting of Gin4 is required for its negative regulation of Fpk1 activity.** (A) Cells coexpressing Gin4-mCherry and Myo1-GFP (YFR388) were observed by time-lapse microscopy at the indicated times. Bar, 2  $\mu$ m. (B) Wild-type strain (Y258) expressing Ypk1-myc from the *GAL1* promoter (pAM54) and also carrying either an empty vector (BG1805) or the same vector expressing Gin4 (pGin4-zz) or Gin4 $\Delta$ KA-zz (pFR305) from the *GAL1* promoter, were grown to mid-exponential phase, not treated or treated with Myr (1.25  $\mu$ M), and lysed. The resulting extracts were resolved by SDS-PAGE and analyzed by immunoblotting with anti-c-myc mAb 9E10 and anti-HA antibodies.

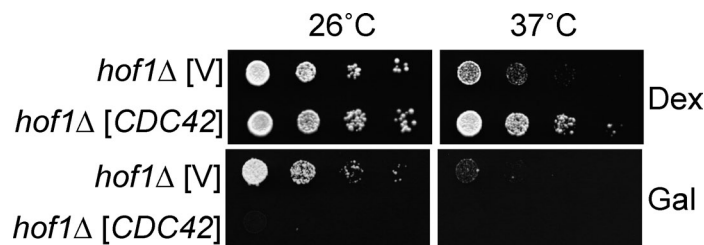


Figure S5. **Modest elevation of Cdc42 rescues *hof1* $\Delta$  cells, whereas galactose-driven overexpression is toxic.** Cultures of *hof1* $\Delta$  cells (YFR386) carrying both an empty vector (YCpLG, V), or the same vector expressing *CDC42* (PB3050) and pRS316-*HOF1*, were streaked onto plates containing 5-FOA medium to select against the presence of the *URA3*-marked pRS316-*HOF1* vector. Freshly appearing colonies were then streaked on a second set of 5-FOA plates. The resulting colonies were grown to mid-exponential phase in SCD-L and serial 10-fold dilutions were spotted on SCD-L (Dex, low/leaky expression of *GAL*<sub>prom</sub>-*CDC42*) or SCG-L (Gal, high expression of *GAL*<sub>prom</sub>-*CDC42*) plates. After incubation for 2 d (Dex) or 5 d (Gal) at either 26°C or 37°C, as indicated, the plates were photographed.

Table S1. **S. cerevisiae strains used in this study**

Strain	Genotype <sup>a</sup>	Source/reference
BY4741	<i>MATa his3-Δ 1<sup>b</sup> leu2Δ0 met15Δ0 ura3Δ0</i>	Research Genetics, Inc.
YAT100	<i>BY4741 gin4Δ::KanMX4</i>	This study
YFR326	<i>BY4741 gin4Δ::KanMX4 sap190Δ::KanMX4 lys2Δ0</i>	This study
YFR313	<i>BY4741 dnf1Δ::KanMX4 dnf2Δ::KanMX4 lys2Δ0</i>	This study
YFR191	<i>BY4741 fpk1Δ::KanMX4</i>	This study
YFR205	<i>BY4741 fpk1Δ::KanMX4 fpk2Δ::KanMX4 lys2Δ0</i>	Roelants et al., 2010
YFR221	<i>BY4741 FPK1-GFP(S65T)::HIS3MX6</i>	Roelants et al., 2010
YFR224	<i>BY4741 FPK1-GFP(S65T)::HIS3MX6 gin4Δ::KanMX4</i>	This study
YFR328	<i>BY4741 FPK1-GFP(S65T)::HIS3MX6 sap190Δ::KanMX4</i>	This study
YJW2	<i>BY4741 FPK1<sup>11A</sup>::HIS3<sup>c</sup></i>	This study
YFR320	<i>BY4741 sap190Δ::KanMX4</i>	This study
YFR323	<i>BY4741 FPK1<sup>11A</sup>::HIS3 sap190Δ::KanMX4</i>	This study
YFR355	<i>BY4741 GIN4-mCherry::caURA3 lys2Δ0</i>	This study
YFR385	<i>BY4741 MYO1-mCherry::caURA3</i>	This study
YFR388	<i>BY4741 GIN4-mCherry::caURA3 MYO1-GFP(S65T)::HIS3MX6</i>	This study
YFR386	<i>BY4741 hof1Δ::KanMX4 [pRS316-HOF1]</i>	This study
YFR396	<i>BY4741 FPK1<sup>11A</sup>::HIS3 hof1Δ::KanMX4 [pRS316-HOF1]</i>	This study
YFR398	<i>BY4741 fpk1Δ::KanMX4 fpk2Δ::HIS3 hof1Δ::KanMX4 [pRS316-HOF1]</i>	This study
YFR425	<i>BY4741 fpk1Δ::KanMX4 fpk2Δ::KanMX4 cyk3Δ::KanMX4 hof1Δ::KanMX4 [pRS316-HOF1]</i>	This study
BY4742	<i>MATα his3-Δ 1 leu2Δ0 lys2Δ0 ura3Δ0</i>	Research Genetics, Inc.
YFR307	<i>BY4742 FPK1<sup>11A</sup>::HIS3</i>	This study
YFR308	<i>BY4742 FPK1<sup>11A</sup>::HIS3 dnf1Δ::KanMX4</i>	This study
YFR312	<i>BY4742 FPK1<sup>11A</sup>::HIS3 dnf1Δ::KanMX4 dnf2Δ::KanMX4</i>	This study
JTY6581	<i>BY4742 fpk1Δ::KanMX4</i>	Research Genetics, Inc.
YFR278	<i>BY4742 fpk1Δ::KanMX4 fpk2Δ::HIS3 gin4Δ::KanMX4 LYS2 met15Δ0</i>	This study
sap190Δ	<i>BY4742 sap190Δ::KanMX4</i>	Research Genetics, Inc.
YFR387	<i>BY4742 hof1Δ::KanMX4 [pRS316-HOF1]</i>	This study
YFR422	<i>BY4742 cyk3Δ::KanMX4 hof1Δ::KanMX4 [pRS316-HOF1]</i>	This study
YFR424	<i>BY4742 fpk1Δ::KanMX4 fpk2Δ::KanMX4 hof1Δ::KanMX4 [pRS316-HOF1]</i>	This study
YFR438	<i>BY4742 myo1Δ::LEU2 [pRS316-MYO1] LYS2 met15Δ0</i>	This study
YFR439	<i>BY4742 myo1Δ::LEU2 FPK1<sup>11A</sup>::HIS3 [pRS316-MYO1] LYS2</i>	This study
YFR440	<i>BY4742 myo1Δ::LEU2 fpk1Δ::KanMX4 fpk2Δ::KanMX4 [pRS316-MYO1] met15Δ0</i>	This study
YFR448	<i>BY4742 myo1Δ::leu2::KanMX FPK1<sup>11A</sup>::HIS3 [pRS316-MYO1] [YCpLG] MATα</i>	This study
YFR449	<i>BY4742 myo1Δ::leu2::KanMX FPK1<sup>11A</sup>::HIS3 [pRS316-MYO1] [YCpLG-CDC42] LYS2 met15Δ0</i>	This study
YFR451	<i>BY4742 myo1Δ::leu2::KanMX FPK1<sup>11A</sup>::HIS3 [pRS316-MYO1] [pRS315]</i>	This study
YFR452	<i>BY4742 myo1Δ::leu2::KanMX FPK1<sup>11A</sup>::HIS3 [pRS316-MYO1] [pMETprom-CDC24] LYS2</i>	This study
Y258	<i>MATα his4-580 ura3-52 leu2-3,112 pep4-3<sup>d</sup></i>	GE Healthcare
BY4743	<i>his3-Δ 1/his3-Δ 1 leu2Δ0/leu2Δ0 ura3Δ0/ura3Δ0 met15Δ0/MET15 lys2Δ0/LYS2</i>	Research Genetics, Inc.
YFR420	<i>BY4743 myo1Δ::LEU2/MYO1</i>	This study
YFR412	<i>BY4743 myo1Δ::LEU2/MYO1 FPK1<sup>11A</sup>::HIS3/FPK1<sup>11A</sup>::HIS3</i>	This study
YFR443	<i>BY4743 myo1Δ::leu2::KanMX/MYO1 FPK1<sup>11A</sup>::HIS3/FPK1<sup>11A</sup>::HIS3</i>	This study
YFR413	<i>BY4743 myo1Δ::LEU2/MYO1 fpk1Δ::KanMX4/fpk1Δ::KanMX4 fpk2Δ::KanMX4/fpk2Δ::KanMX4</i>	This study
YFR421	<i>BY4743 inn1Δ::LEU2/INN1</i>	This study
YFR419	<i>BY4743 inn1Δ::LEU2/INN1 FPK1<sup>11A</sup>::HIS3/FPK1<sup>11A</sup>::HIS3</i>	This study
YFR414	<i>BY4743 inn1Δ::LEU2/INN1 fpk1Δ::KanMX4/fpk1Δ::KanMX4 fpk2Δ::KanMX4/fpk2Δ::KanMX4</i>	This study
YFR433	<i>BY4743 dnf1Δ::KanMX4/dnf1Δ::KanMX4 dnf2Δ::KanMX4/dnf2Δ::KanMX4</i>	This study
YFR434	<i>BY4743 inn1Δ::LEU2/INN1 dnf1Δ::KanMX4/dnf1Δ::KanMX4 dnf2Δ::KanMX4/dnf2Δ::KanMX4</i>	This study

<sup>a</sup>All null alleles indicated with a Δ symbol are complete deletions of the ORF, unless otherwise indicated.

<sup>b</sup>This null allele is an internal deletion of a 187-bp HindIII–HindIII fragment (nucleotides 305–492) from the *HIS3* ORF (Scherer and Davis, 1979).

<sup>c</sup>The *FPK1<sup>11A</sup>* allele carries the following substitution mutations of *FPK1* (S35A S51A S52A S53A S200A S227A S229A S300A S414A T435A S436A), as described in this study.

<sup>d</sup>The mutations carried by this strain represent: *his4-580*, a strongly polar mutation that drastically reduces all three activities (phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase) encoded in the *HIS4* gene product (Fink and Styles, 1974), but whose molecular identity has not yet been characterized (Fink, G.R., personal communication); *ura3-52*, an insertion of the endogenous yeast retrotransposon Ty1 at codon 121 in the *URA3* ORF (and transcribed in the same orientation as would the *URA3* mRNA; Rose and Winston, 1984); *leu2-3,112*, containing two frameshift mutations that destroy the *LEU2* ORF, a G insertion at nucleotide 249, and a G insertion at nucleotide 792, as well as a GTC-to-GTT silent change at codon 56, a GTT-to-GCT missense change at codon 69, a GTT-to-GTC silent change at codon 299, and a GAC-to-AAC missense change at codon 300 (Hinnen et al., 1978); and *pep4-3* (Hemmings et al., 1981), a nonsense mutation converting TGG (Trp) at codon 39 of the *PEP4* ORF to TGA (stop; Woolford et al., 1993).

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

Plasmid	Description	Source/reference
pGEX4T-1	GST tag, bacterial expression vector	GE Healthcare
pAB1	pGEX4T-1 <i>GIN4</i>	This study
pAT103	pGEX4T-1 <i>Gin4(K48A)</i>	This study
pFR143	pGEX4T-1 <i>FPK1</i>	Roelants et al., 2010
pFR144	pGEX4T-1 <i>fpk1(D621A)</i>	Roelants et al., 2010
pBS1	pGEX4T-1 <i>fpk1(1-472)</i>	This study
pBS2	pGEX4T-1 <i>fpk1(473-893) D621A</i>	This study
pJW2	pGEX4T-1 <i>fpk1(1-472) S35A S51A S52A S53A S200A S227A S229A S300A S414A T435A S436A</i>	This study
pRS303	<i>HIS3</i> ; an integrative [YIp] vector	Sikorski and Hieter, 1989
pJW4	pRS303 <i>FPK1(S35A S51A S52A S53A S200A S227A S229A S300A S414A T435A S436A)</i>	This study
YEp352GAL	2 $\mu$ m, <i>URA3</i> , <i>GAL1<sub>prom</sub></i> vector	Benton et al., 1994
pAM76	YEp352GAL <i>YPK1-myc</i>	Roelants et al., 2002
YEp351GAL	2 $\mu$ m, <i>LEU2</i> , <i>GAL1<sub>prom</sub></i> vector	Benton et al., 1994
pAM54	YEp351GAL <i>YPK1-myc</i>	Casamayor et al., 1999
BG1805	2 $\mu$ m, <i>URA3</i> , <i>GAL1<sub>prom</sub></i> , C-terminal tandem affinity (TAP) tag vector	GE Healthcare
pGin4-zz	BG1805 <i>GIN4-zz</i>	GE Healthcare
pFR305	BG1805 <i>gin4(<math>\Delta</math>1026-1125)-zz</i>	This study
pKcc4-zz	BG1805 <i>KCC4</i>	GE Healthcare
YCpUG	<i>CEN</i> , <i>URA3</i> , <i>GAL1<sub>prom</sub></i> vector	Bardwell et al., 1998
pMVB115	YCpUG <i>GIN4</i>	Versele and Thorner, 2004
YCpLG	<i>CEN</i> , <i>LEU2</i> , <i>GAL1<sub>prom</sub></i> vector	Bardwell et al., 1998
pMJS109	YCpLG <i>HSL1-HA<sub>3</sub></i>	Shulewitz et al., 1999
pJT5241	YCpLG <i>GIN4-eGFP<sup>a</sup></i>	G. Finnigan, Thorner laboratory
pRS415	<i>CEN</i> , <i>LEU2</i> , <i>GAL1<sub>prom</sub></i> vector	New England Biolabs, Inc.
PB3050	pRS415 <i>HA-CDC42</i>	Atkins et al., 2013
pJT4350	pRS415 <i>MET15<sub>prom</sub> GFP(S65T)-A<math>\beta</math>-CDC24</i>	Toenjes et al., 1999
pRS315	<i>CEN</i> , <i>LEU2</i>	Sikorski and Hieter, 1989
pRC181	pRS315- <i>TPI1<sub>prom</sub></i> vector	R.E. Chen, Thorner laboratory
pFR150	pRC181- <i>FPK1-eGFP</i>	Roelants et al., 2010
pRS316	<i>CEN</i> , <i>URA3</i>	Sikorski and Hieter, 1989
pRS316- <i>HOF1</i>	pRS316 <i>HOF1</i>	Vallen et al., 2000
pRS316- <i>MYO1</i>	pRS316 <i>MYO1</i>	G. Finnigan, Thorner laboratory
pTS408	<i>CEN</i> , <i>URA3</i> , <i>GAL1<sub>prom</sub></i> GFP vector	Carminati and Stearns, 1997
pES10	pTS408 <i>dnf1(1403-1571)-myc</i>	This study

<sup>a</sup>eGFP is GFP(F64L S65T).

## References

- Atkins, B.D., S. Yoshida, K. Saito, C.F. Wu, D.J. Lew, and D. Pellman. 2013. Inhibition of Cdc42 during mitotic exit is required for cytokinesis. *J. Cell Biol.* 202:231–240. <http://dx.doi.org/10.1083/jcb.201301090>
- Bardwell, L., J.G. Cook, J.X. Zhu-Shimoni, D. Voora, and J. Thorner. 1998. Differential regulation of transcription: repression by unactivated mitogen-activated protein kinase Kss1 requires the Dig1 and Dig2 proteins. *Proc. Natl. Acad. Sci. USA.* 95:15400–15405. <http://dx.doi.org/10.1073/pnas.95.26.15400>
- Benton, B.M., J.H. Zang, and J. Thorner. 1994. A novel FK506- and rapamycin-binding protein (FPR3 gene product) in the yeast *Saccharomyces cerevisiae* is a proline rotamase localized to the nucleolus. *J. Cell Biol.* 127:623–639. <http://dx.doi.org/10.1083/jcb.127.3.623>
- Carminati, J.L., and T. Stearns. 1997. Microtubules orient the mitotic spindle in yeast through dynein-dependent interactions with the cell cortex. *J. Cell Biol.* 138:629–641. <http://dx.doi.org/10.1083/jcb.138.3.629>
- Casamayor, A., P.D. Torrance, T. Kobayashi, J. Thorner, and D.R. Alessi. 1999. Functional counterparts of mammalian protein kinases PDK1 and SGK in budding yeast. *Curr. Biol.* 9:186–197. [http://dx.doi.org/10.1016/S0960-9822\(99\)80088-8](http://dx.doi.org/10.1016/S0960-9822(99)80088-8)
- Fink, G.R., and C.A. Styles. 1974. Gene conversion of deletions in the *his4* region of yeast. *Genetics.* 77:231–244.
- Hemmings, B.A., G.S. Zubenko, A. Hasilik, and E.W. Jones. 1981. Mutant defective in processing of an enzyme located in the lysosome-like vacuole of *Saccharomyces cerevisiae*. *Proc. Natl. Acad. Sci. USA.* 78:435–439. <http://dx.doi.org/10.1073/pnas.78.1.435>
- Hinnen, A., J.B. Hicks, and G.R. Fink. 1978. Transformation of yeast. *Proc. Natl. Acad. Sci. USA.* 75:1929–1933. <http://dx.doi.org/10.1073/pnas.75.4.1929>
- Mok, J., P.M. Kim, H.Y. Lam, S. Piccirillo, X. Zhou, G.R. Jeschke, D.L. Sheridan, S.A. Parker, V. Desai, M. Jwa, et al. 2010. Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. *Sci. Signal.* 3:ra12. <http://dx.doi.org/10.1126/scisignal.2000482>
- Roelants, F.M., P.D. Torrance, N. Bezman, and J. Thorner. 2002. Pkh1 and Pkh2 differentially phosphorylate and activate Ypk1 and Ykr2 and define protein kinase modules required for maintenance of cell wall integrity. *Mol. Biol. Cell.* 13:3005–3028. <http://dx.doi.org/10.1091/mbc.E02-04-0201>
- Roelants, F.M., A.G. Baltz, A.E. Trott, S. Fereres, and J. Thorner. 2010. A protein kinase network regulates the function of aminophospholipid flippases. *Proc. Natl. Acad. Sci. USA.* 107:34–39. <http://dx.doi.org/10.1073/pnas.0912497106>
- Rose, M., and F. Winston. 1984. Identification of a Ty insertion within the coding sequence of the *S. cerevisiae* *URA3* gene. *Mol. Gen. Genet.* 193:557–560. <http://dx.doi.org/10.1007/BF00382100>
- Scherer, S., and R.W. Davis. 1979. Replacement of chromosome segments with altered DNA sequences constructed *in vitro*. *Proc. Natl. Acad. Sci. USA.* 76:4951–4955. <http://dx.doi.org/10.1073/pnas.76.10.4951>
- Shulewitz, M.J., C.J. Inouye, and J. Thorner. 1999. Hsl7 localizes to a septin ring and serves as an adapter in a regulatory pathway that relieves tyrosine phosphorylation of Cdc28 protein kinase in *Saccharomyces cerevisiae*. *Mol. Cell. Biol.* 19:7123–7137.
- Sikorski, R.S., and P. Hieter. 1989. A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in *Saccharomyces cerevisiae*. *Genetics.* 122:19–27.
- Toenjes, K.A., M.M. Sawyer, and D.I. Johnson. 1999. The guanine-nucleotide-exchange factor Cdc24p is targeted to the nucleus and polarized growth sites. *Curr. Biol.* 9:1183–1186. [http://dx.doi.org/10.1016/S0960-9822\(00\)80022-6](http://dx.doi.org/10.1016/S0960-9822(00)80022-6)
- Vallen, E.A., J. Caviston, and E. Bi. 2000. Roles of Hof1p, Bni1p, Bnr1p, and myo1p in cytokinesis in *Saccharomyces cerevisiae*. *Mol. Biol. Cell.* 11:593–611. <http://dx.doi.org/10.1091/mbc.11.2.593>
- Verselle, M., and J. Thorner. 2004. Septin collar formation in budding yeast requires GTP binding and direct phosphorylation by the PAK, Cla4. *J. Cell Biol.* 164:701–715. <http://dx.doi.org/10.1083/jcb.200312070>
- Woolford, C.A., J.A. Noble, J.D. Garman, M.F. Tam, M.A. Innis, and E.W. Jones. 1993. Phenotypic analysis of proteinase A mutants. Implications for autoactivation and the maturation pathway of the vacuolar hydrolases of *Saccharomyces cerevisiae*. *J. Biol. Chem.* 268:8990–8998.