SUPPLEMENTAL MATERIAL

for

TORC2-dependent Ypk1-mediated phosphorylation of Lam2/Ltc4 disrupts its association with the β -propeller protein Laf1 **at endoplasmic reticulum-plasma membrane contact sites in the yeast** *Saccharomyces cerevisiae*

Magdalena Topolska,^{1,2} Françoise M. Roelants,¹ Edward P. Si,^{1,3} and Jeremy Thorner^{1*}

1 Division of Biochemistry, Biophysics and Structural Biology, Department of Molecular and Cell Biology, University of California, Berkeley, CA 94720-3202 USA

2 Present address: Department of Biochemistry and Molecular Biology, Villum Center for Bioanalytical Sciences University of Southern Denmark, 5000 Odense, Denmark

3 Present address: Eastern Virginia Medical School, P.O. Box 1980, Norfolk, VA 23501-1980

USA

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*To whom correspondence should be addressed:

Professor Emeritus Jeremy Thorner Division of Biochemistry, Biophysics and Structural Biology Department of Molecular and Cell Biology University of California at Berkeley Room 526, Barker Hall Berkeley, CA 94720-3202 USA Phone: (510) 642-2558 FAX: (510) 642-6420 e-mail: jthorner@berkeley.edu

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Fig. S1. Laf1 and Dgr2 are predicted ten-bladed β -propeller proteins.

The paralogous *S. cerevisiae* proteins Laf1/Ymr102c and Dgr2/Ykl121w, first identified as components of ER-PM CSs using mass spectrometry (Murley *et al*., 2017), were aligned by NCBI-BLAST (Johnson *et al*., 2008) with identities (white letters on a black box), standard conservative substitutions (bold letters in a gray box), and one-residue gaps (-) to maximize the alignment. The ten apparent WD40 repeats (#1-#10) predicted by the WD40-repeat protein Structure Predictor algorithm (WDSP) (Wang et al., 2013; Wang et. al, 2015), which constitute the ten blades of their predicted b-propeller fold, are indicated and the corresponding sequences highlighted in green shading and boxed in red.

Fig. S2, Panel A. Localization of Laf1 to ER-PM CSs requires Lam2 and Lam4. Same as in Fig. 1C, except that the strains, wild-type (YFR651-A), *lam2∆* single mutant (YFR652-B), *lam4∆* single mutant (YFR653-B), or *lam2∆ lam4∆* double mutant (YFR654-B), as indicated, expressed Laf1-mKate (instead of Laf1-mNG).

Fig. S2, Panel B. Level of Laf1-mKate unaffected by absence of Lam2 and/or Lam4. Extracts of the same cells as in (A) above were resolved by SDS-PAGE and analyzed by immuno-blotting, as described in Materials and Methods. Note that the level of Laf1-mKate remains stable, but is not phosphorylated, when cells lack Lam2 and/or Lam4.

Fig. S2, Panel C. Demonstration that Laf1 is a phospho-protein and only phosphorylated when Lam2 and Lam4 are present. Extracts of either a *lam2∆ lam4∆* double mutant expressing Laf1 mKate (YFR654) or otherwise isogenic WT cells expressing Laf1-mKate (YFR651) were either treated (+) or not (-) with calf intestinal phosphatase, as indicated, and then resolved by SDS-PAGE and analyzed by immuno-blotting, all as described in Materials and Methods.

Fig. S2, Panel D. Phosphorylation of Laf1 is dependent on Ypk1 and Ypk2. Extracts of cells of the indicated genotypes, W (YFR651), *lam2∆ lam4∆* (YFR654), and *ypk1-as ypk2∆* (YFR660), each expressing Laf1-mKate, were grown to mid-exponential phase and then treated with vehicle (DMSO) (-) or with 3MB-PP1 (10 µM final concentration) in the same solvent (+) for 1 h, as indicated, harvested, extracts prepared, and analyzed by SDS-PAGE (6.5% gel) and immunoblotting. (To stimulate TORC2-mediated activation of Ypk1-as, the *ypk1-as ypk2∆* strain expressing Laf-mKate (YFR660) cells were pre-treated with 1.25 µM myriocin for 2 h before exposure to the Ypk1-as inhibitor 3MB-PP1).

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Fig. S2, Panel E. Phosphorylation of Laf1 and Dgr2 occurs at their predicted Ypk1 consensus sites. GST-Laf1(684-834) (pFR398), GST-Laf1(684-834) S709A S710A (pFR402), GST-Dgr2(1- 128) (pFR399), GST-Dgr2(1-128) S48A S49A (pFR403), and GST-Orm1(1-85) (pFR203) were purified from *E. coli* and incubated, in the absence $(-)$ or presence $(+)$ of 3MB-PP1, with $[y-$ 32P]ATP and Ypk1-as-His6-HA that was purified from *S. cerevisiae* strain yAM135-A (*ypk1-as ypk2∆*) containing plasmid BG1805 expressing Ypk1-as-His6-HA-3C-ZZ, as described in detail elsewhere (Muir et al. 2014; Muir, 2015). The products were resolved by SDS-PAGE and analyzed, as indicated. Unlike the control (Orm1), a known Ypk1 substrate (Muir et al., 2014), incorporation into the Laf1 and Dgr2 fragments was not prevented by the Ypk1-as inhibitor 3MB-PP1, even though incorporation was abrogated by Ser-to-Ala mutations at the same sites. Thus,

an as yet unidentified protein kinase in the Ypk1-as-His6-HA preparation is responsible for the observed incorporation into Laf1 and Dgr2 in this *in vitro* context.

REFERENCES

Johnson, M., Zaretskaya, I., Raytselis, Y., Merezhuk, Y., McGinnis, S., and Madden, T.L. (2008) NCBI BLAST: a better web interface. Nucleic Acids Res. 36: W5-9.

Muir, A. (2015) Systematic identification of proteins regulated by the TOR Complex 2-dependent kinase Ypk1 in *Saccharomyces cerevisiae*. Ph.D. Thesis, University of California, Berkeley, 123pp.

Muir, A., Ramachandran, S., Roelants, F. M., Timmons, G. and Thorner, J. (2014) TORC2 dependent protein kinase Ypk1 phosphorylates ceramide synthase to stimulate synthesis of complex sphingolipids. *Elife* 3, pp. e.03779.

Murley, A., Yamada, J., Niles, B. J., Toulmay, A., Prinz, W. A., Powers, T. and Nunnari, J. (2017) 'Sterol transporters at membrane contact sites regulate TORC1 and TORC2 signaling', *J Cell Biol,* 216(9), pp. 2679-2689.

Roelants, F. M., Breslow, D. K., Muir, A., Weissman, J. S. and Thorner, J. (2011) Protein kinase Ypk1 phosphorylates regulatory proteins Orm1 and Orm2 to control sphingolipid homeostasis in Saccharomyces cerevisiae. *Proc. Natl. Acad. Sci. USA* 108, pp. 19222-19227.

Wang, Y., Jiang, F., Zhuo, Z., Wu, X.-H., and Wu, Y.-D. (2013) A method for WD40 repeat detection and secondary structure prediction. *PLoS One* 8, pp. e65705.

Wang, Y., Hu, X.-J., Zou, X.-D., Wu, X.-H., Ye, Z.Q., and Wu, Y.-D. (2015) WDSPdb: a database for WD40-repeat proteins. *Nucleic Acids Res*. 43, pp. D339-D344.