## Supplemental material

JCB

Miyata et al., http://www.jcb.org/cgi/content/full/jcb.201601082/DC1



HE JOURNAL OF CELL BIOLOGY

Figure S1. **Ups2 enhances PE accumulation in the post-log phase in a synthetic medium.** (A) 4m and  $4m ups2\Delta$  cells (OD<sub>600</sub>, 0.05) were cultured in SCD supplemented with 3 mM choline for the indicated periods. At each time point, the cell density was analyzed by measuring OD<sub>600</sub>. Closed circle, 4m cells; open circle,  $4m ups2\Delta$  cells. (B and C) 4m and  $4m ups2\Delta$  cells (OD<sub>600</sub>, 0.05) were cultured in SCD supplemented with 3 mM choline in the presence of [<sup>32</sup>P]Pi for the indicated periods. At each time point, total cellular phospholipids were extracted, separated by TLC, and then analyzed by an imaging analyzer. (C) The percentages of PE relative to total phospholipids. The mean values for two independent experiments and deviations are shown. Closed circle, 4m cells; open circle,  $4m ups2\Delta$  cells.



Figure S2. **Ups2** is involved in PS conversion to PE in wild-type and 2m cells under nonfermentable conditions. (A) PS conversion to PE and PC in wild-type and  $ups2\Delta$  cells growing in YPD was analyzed as in Fig. 5. The mean values for two independent experiments and deviations are shown. (B) PS conversion to PE and PC in wild-type and  $ups2\Delta$  cells growing in YPLac was analyzed as in Fig. 5. The mean values for two independent experiments and deviations are shown. (C) PS conversion to PE and PC in 2m and 2m  $ups2\Delta$  cells growing in YPD was analyzed as in Fig. 5. The mean values for two independent experiments and deviation are shown. (D) PS conversion to PE and PC in 2m and 2m  $ups2\Delta$  cells growing in YPLac was analyzed as in Fig. 5. The mean values for two independent experiments and deviations are shown.



Figure S3. **Mass spectrometry-based phospholipid transfer assay.** (A and B) SC Ups2-Mdm35 was incubated with heavy donor liposomes (200  $\mu$ M; DOPC/DOPE/DOPS/18:1 Liss-Rhod-PE = 50/29.9/20/0.1) or (200  $\mu$ M; DOPC/DOPE/DOPA/18:1 Liss-Rhod-PE = 50/29.9/20/0.1) containing 10% sucrose and light acceptor liposomes (200  $\mu$ M; DOPC/DOPE/18:1 CL = 50/40/10) at 25°C for 10 min. Liposomes were separated by sucrose density-gradient ultracentrifugation. Phospholipids in the acceptor liposomes were analyzed by mass spectrometry. DOPE, DOPS, and DOPA in acceptor liposomes were detected as singly charged ions and indicated in the charts. DOPC in acceptor liposomes was detected as a formate adduct ion and indicated in the charts.

## Table S1. Yeast strains used in this study

| Genetic background | Mating type  | Genotype  | Source   |
|--------------------|--|---|--|
| W303               | a  | ura3-52 trp1∆2 leu2-3_112 his3-11 ade2-1 CAN1   | Kuroda et al.,<br>2011   |
| W303               | a  | TKY705, ups2∆::CgLEU2   | This study   |
| W303               | a  | TKY705, psd1∆::natMX4 can1-100  | This study   |
| W303               | a  | TKY705, psd1∆::natMX4 ups2∆::hphNT1 can1-100  | This study   |
| W303               | a  | TKY705, psd2 <i>∆::CgURA3 dpl1</i> ∆::CgTRP1  | This study   |
| W303               | a  | TKY705, psd2∆::CgURA3 dpl1∆::CgTRP1 ups2∆::CgLEU2   | This study   |
| W303               | a  | TKY705, psd24::CgURA3 dpl14::CgTRP1 cho24::hphNT1 opi34::natNT2   | This study   |
| W303               | a  | TKY705, psd24::CgURA3 dpl14::CgTRP1 cho24::hphNT1 opi34::natNT2<br>ups24::CgLEU2  | This study   |
| W303               | a  | TKY705, psd2∆::CgURA3 dpl1∆::CgTRP1 cho2∆::hphNT1 opi3∆::natNT2<br>mdm35∆::CgLEU2   | This study   |
| W303               | a  | TKY705, psd22::CgURA3 dpl12::CgTRP1 cho22::hphNT1 opi32::CgHIS3<br>GPDpr-UPS2::kanMX4 GPDpr-MDM35::natNT2   | This study   |
| W303               | a  | TKY705, psd2Δ::CgURA3 dpl1Δ::CgTRP1 cho2Δ::hphNT1 opi3Δ::natNT2<br>ups1Δ::CgHIS3  | This study   |
| W303               | a  | TKY705, psd2∆::CgURA3 dpl1∆::CgTRP1 cho2∆::hphNT1 opi3∆::natNT2<br>ups1∆::CgHIS3 ups2∆::CgLEU2  | This study   |
| W303               | a  | TKY705, UPS1-HA::kanMx4   | This study   |
| W303               | a  | TKY705, UPS2-HA::kanMx4   | This study   |
|                    | Genetic background   \W303   \W303 | Genetic background   Mating type     N303   a     N303   a | Cenetic backgroudMating typeCenotypeW303aura3-52 trp 1/2 lev2-3_112 his3-11 ade2-1 CAN1W303aTKY705, ups2.:: CgLU2W303aTKY705, psd14::nat/W4 can1-100W303aTKY705, psd14::nat/W4 ups2.: hphNT1 can1-100W303aTKY705, psd24:: CgURA3 dpl14:: CgTRP1W303aTKY705, psd24:: CgURA3 dpl14:: CgTRP1 ups24:: cgLU2W303aTKY705, psd24:: CgURA3 dpl14:: CgTRP1 ups24:: cgLU2W303aTKY705, psd24:: CgURA3 dpl14:: CgTRP1 cho24:: hphNT1 opi34:: nat/NT2W303aTKY705, psd24:: CgURA3 dpl14:: CgTRP1 cho24:: hphNT1 opi34:: |

GPD, glyceraldehyde-3-phosphate dehydrogenase.

## Table S2. PCR templates and primers used for gene manipulation

| Gene                | Template<br>plasmid    | Source                 | Primers (5' to 3')  |
|---------------------|------------------------|------------------------|---|
| ups24::CgLEU2       | pCgLEU2-NT1            | This study             | 1: TCAGACTAAGATAAAATAATCGAGAATAATTAAAAGACGATAATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: AAGTAGTATGCAGTGCCATGCGGGATCAAGGAATTTGTATCTCTAATCGATGAATTCGAGCTCG       |
| ups24::hphNT1       | pFA6a-hphNT1ª          | EUROSCARF              | 1: TCAGACTAAGATAAAATAATCGAGAATAATTAAAAGACGATAATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: AAGTAGTATGCAGTGCCATGCGGGATCAAGGAATTTGTATCTCTAATCGATGAATTCGAGCTCG       |
| psd1∆∷natMX4        | р4339 <sup>ь</sup>     | Gift from<br>C. Boone∘ | 1: TTGGTCGTTATTTTTGAAGAAGAAGGAAAAGCAAAGCCAGGATGACATGGAGGCCCAGAATA<br>CCCT |
|                     |                        |                        | 2: TATATACAGCAAAATAAATGCTAACTTTACATATGATTGCTTTCACAGTATAGCGACCAGCATTCAC    |
| psd2∆::CgURA3       | pCgURA3-NT2            | This study             | 1: TGGTAAAGAATCCTCGATTTTCAGGAGCATCCAACGACGAAGATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: TTTTTCCATTTTGGTAACCACTAACTACAGCCAATTTTTCGGCGGCTTCAATCGATGAATTCGAGCTCG  |
| dpl1∆::CgTRP1       | pCg <i>TRP1-</i> TB    | This study             | 1: AAGTAGGCTAGCTTCTGTAAAGGGATTTTTCCATCTAATACAATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: CTCTCGTTCTTTAAATTATGTATGAGATTTGATTCTATATAGCTAATCGATGAATTCGAGCTCG       |
| cho2∆::hphNT1       | pFA6a-hphNT1°          | EUROSCARF              | 1: CGAGTGATTTTCTTAGTGACAAAGCTTTTTCTTCATCTGTAGATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: ATCCTAGTACTTTTTAAATATATATATACTCAAAAAAAAA                               |
| opi3∆::natNT2       | pFA6a- <i>natNT2</i> ª | EUROSCARF              | 1: TAAACAGCAATTGAAGACAACAAGAATAGCGCAAGTCAAGCGATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: GCATAGGCTTCTAACATTATAGAATATAGAAATAGAGCACTTAATCGATGAATTCGAGCTCG         |
| opi3∆::CgHIS3       | р <i>СgHIS3</i> -ТВ    | This study             | 1: TAAACAGCAATTGAAGACAACAAGAATAGCGCAAGTCAAGCGATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: GCATAGGCTTCTAACATTATAGAATATAGAAATAGAGCACTTAATCGATGAATTCGAGCTCG         |
| mdm35∆::CgLEU2      | pCgLEU2-NT1            | This study             | 1: GTGTTTTAACTTGAATTACAATAACAATAATACCAGTTTTATATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: TTACATGTTGAATAATGCACATTCTGTGCTAAAATATATACTTCAATCGATGAATTCGAGCTCG       |
| UPS1∆::CgHIS3       | р <i>СgHIS3-</i> ТВ    | This study             | 1: TCTGGCTTCTGAGACGGCGGTAAGATATCCTTAAGAGTTGCAATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: CTCGCCCATGGTGATATCTTTAAAGATCTTTAAATGGGAACATCAATCGATGAATTCGAGCTCG       |
| GPDpr-UPS2::kanMx4  | pYM-N14ª               | EUROSCARF              | 1: TCAGACTAAGATAAAATAATCGAGAATAATTAAAAGACGATAATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: CTGGTCCCATGGATAGTTGAAATCGTAACTGTTTTGAAACAATTTCATCGATGAATTCTCTGTCG      |
| GPDpr-MDM35::natNT2 | pYM-N15°               | EUROSCARF              | 1: GTGTTTTAACTTGAATTACAATAACAATAATACCAGTTTTATATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: CAGGTCAGTGCATTCAGGCGCAAAACTAGCTGACATTATATTCCCCATCGATGAATTCTCTGTCG      |
| UPS1-HA::kanMX4     | pYM45°                 | EUROSCARF              | 1: TCTGGCTTCTGAGACGGCGGTAAGATATCCTTAAGAGTTGCAATGCGTACGCTGCAGGTCGAC        |
|                     |                        |                        | 2: GCATTIGTTATCCAAAAACTCGAAGAGGCGAGAAATCCTCAGTTTCGTACGCTGCAGGTCGAC        |
| UPS2-HA::kanMX4     | pYM45°                 | EUROSCARF              | 1: AAGTAGTATGCAGTGCCATGCGGGATCAAGGAATTTGTATCTCTAATCGATGAATTCGAGCTCG       |
|                     |                        |                        | 2: CAGCAAAATATTGACTTGTTTAGAGACGCATACAACCACGAAAATCGTACGCTGCAGGTCGAC        |

<sup>o</sup>Janke et al., 2004. <sup>b</sup>Tong and Boone, 2006. <sup>c</sup>University of Toronto, Toronto, Ontario, Canada.

## References

- Janke, C., M.M. Magiera, N. Rathfelder, C. Taxis, S. Reber, H. Maekawa, A. Moreno-Borchart, G. Doenges, E. Schwob, E. Schiebel, and M. Knop. 2004. A versatile toolbox for PCR-based tagging of yeast genes: new fluorescent proteins, more markers and promoter substitution cassettes. Yeast. 21:947–962. http://dx.doi.org /10.1002/yea.1142
- Kuroda, T., M. Tani, A. Moriguchi, S. Tokunaga, T. Higuchi, S. Kitada, and O. Kuge. 2011. FMP30 is required for the maintenance of a normal cardiolipin level and mitochondrial morphology in the absence of mitochondrial phosphatidylethanolamine synthesis. *Mol. Microbiol.* 80:248–265. http://dx.doi.org/10.1111/j.1365 -2958.2011.07569.x
- Tong, A.H., and C. Boone. 2006. Synthetic genetic array analysis in Saccharomyces cerevisiae. Methods Mol. Biol. 313:171–192. http://dx.doi.org/10.1385/1-59259 -958-3:171