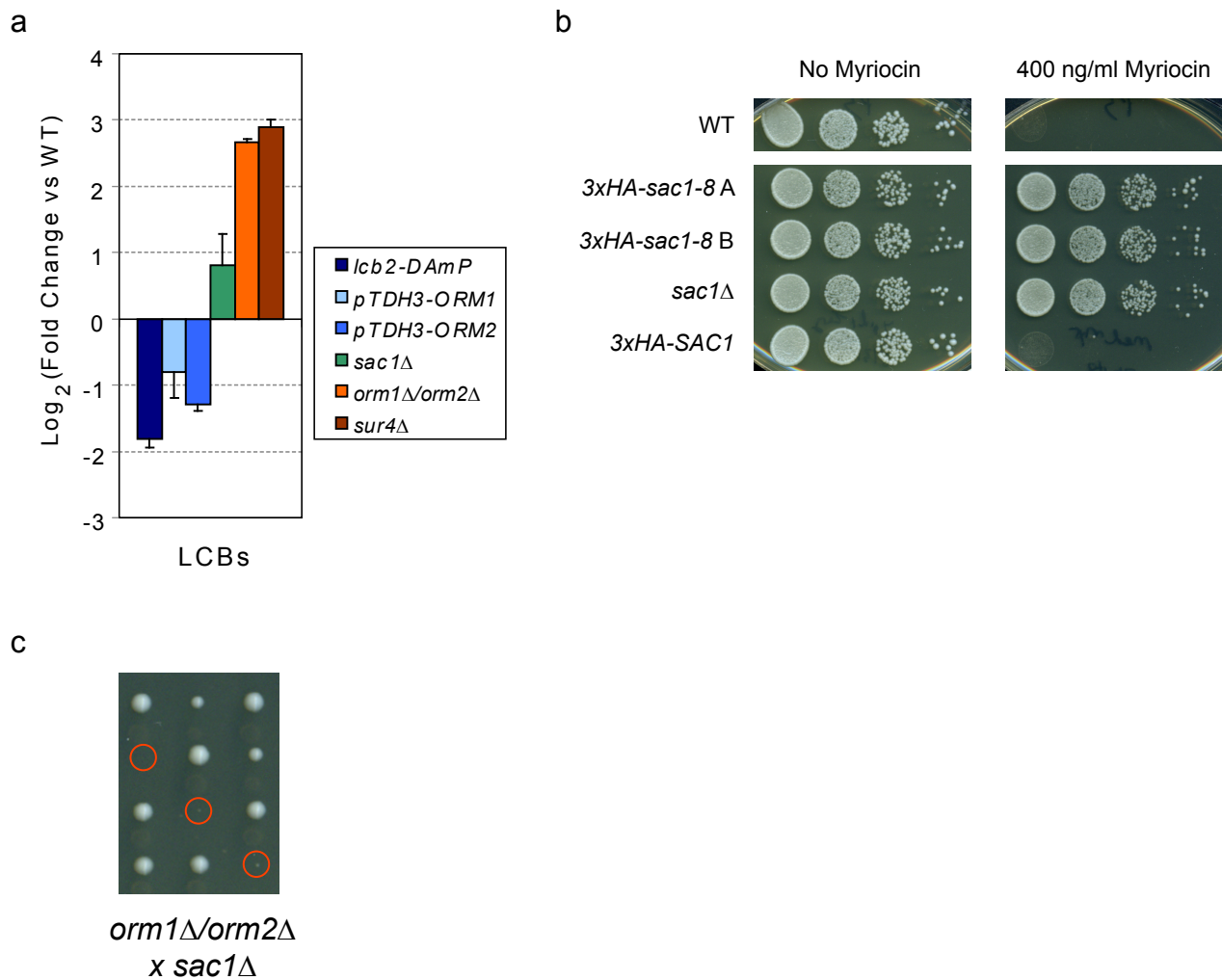


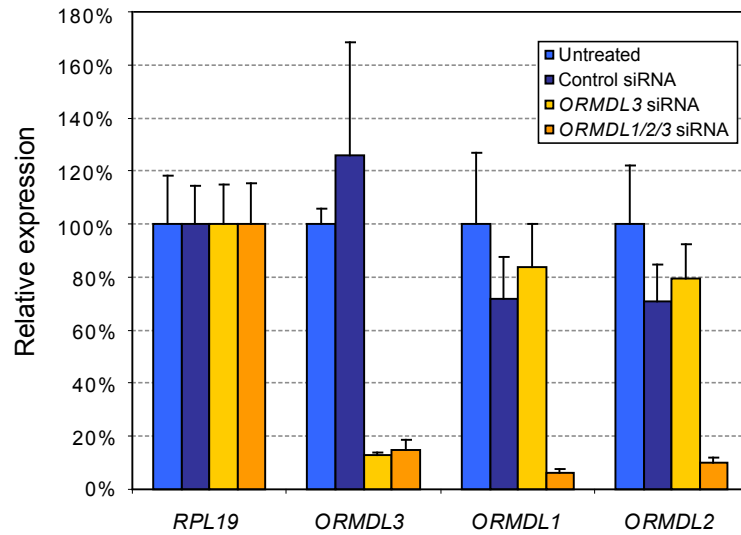
SUPPLEMENTARY INFORMATION

**Supplementary Figure 1. A functional role for Sac1 in sphingolipid metabolism.**

a, Lipidomic analysis of LCB levels in the indicated strains are shown (average \pm s.d., $n = 3$).

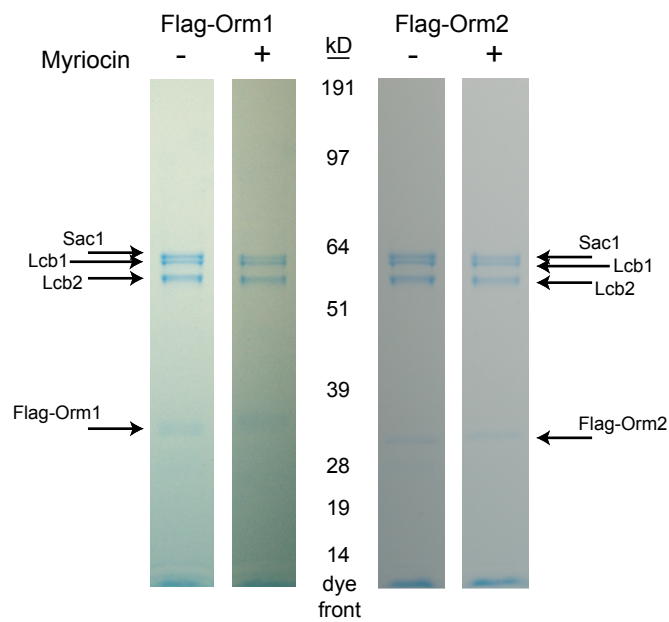
b, Serial ten-fold dilutions of the indicated strains were spotted on plates with 0 or 400 ng/ml myriocin and imaged after 24–48 hr of growth. The *sac1-8* allele of *SAC1* is a catalytically inactive *SAC1* mutant described previously (ref. 1).

c, *ORM1/ORM2* and *SAC1* deletion mutants exhibit synthetic lethality. Representative tetrads from a *orm1Δ/orm2Δ x sac1Δ* cross are shown, with circles indicating spores with the *orm1Δ/orm2Δ/sac1Δ* genotype that fail to grow.

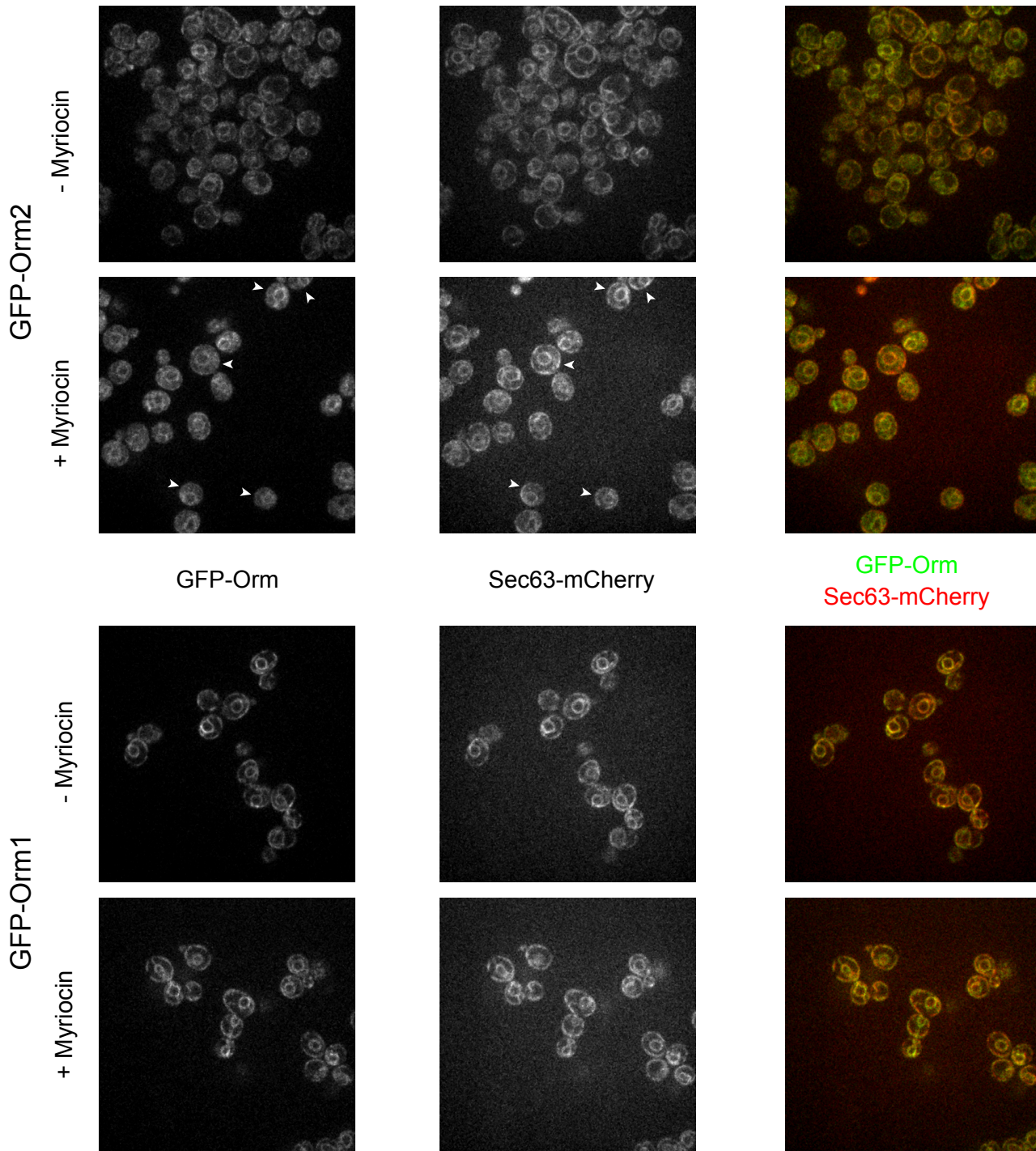


Supplementary Figure 2. *ORMDL* gene expression after RNAi treatment

Gene expression was quantified for the indicated genes after transfection of HeLa cells with indicated siRNAs. RT-PCR was performed with primers for the indicated genes using *RPL19* as a reference. Data are normalized to expression levels in untreated cells (average \pm s.d., $n = 3$).



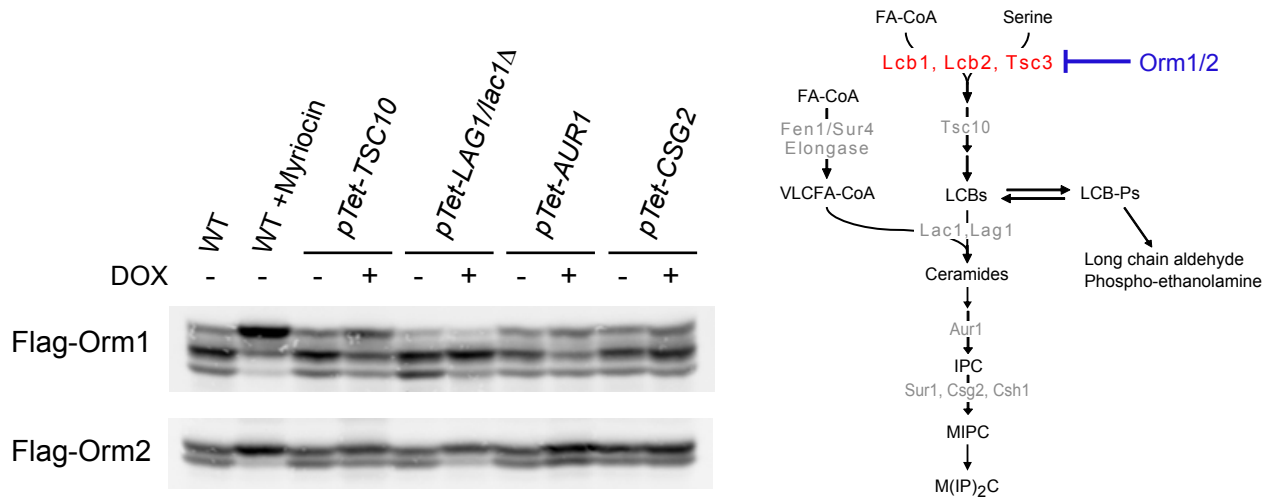
Supplementary Figure 3. Myriocin treatment does not prevent formation of the Orm1/2-Lcb1/2-Sac1 complex. Colloidal-stained SDS/PAGE gels are shown for native affinity purifications from strains expressing 3xFlag-Orm1 or 3xFlag-Orm2. Prior to harvest, the indicated strains were grown for 12-16 hr in standard rich media or media supplemented with 150 ng/ml myriocin.



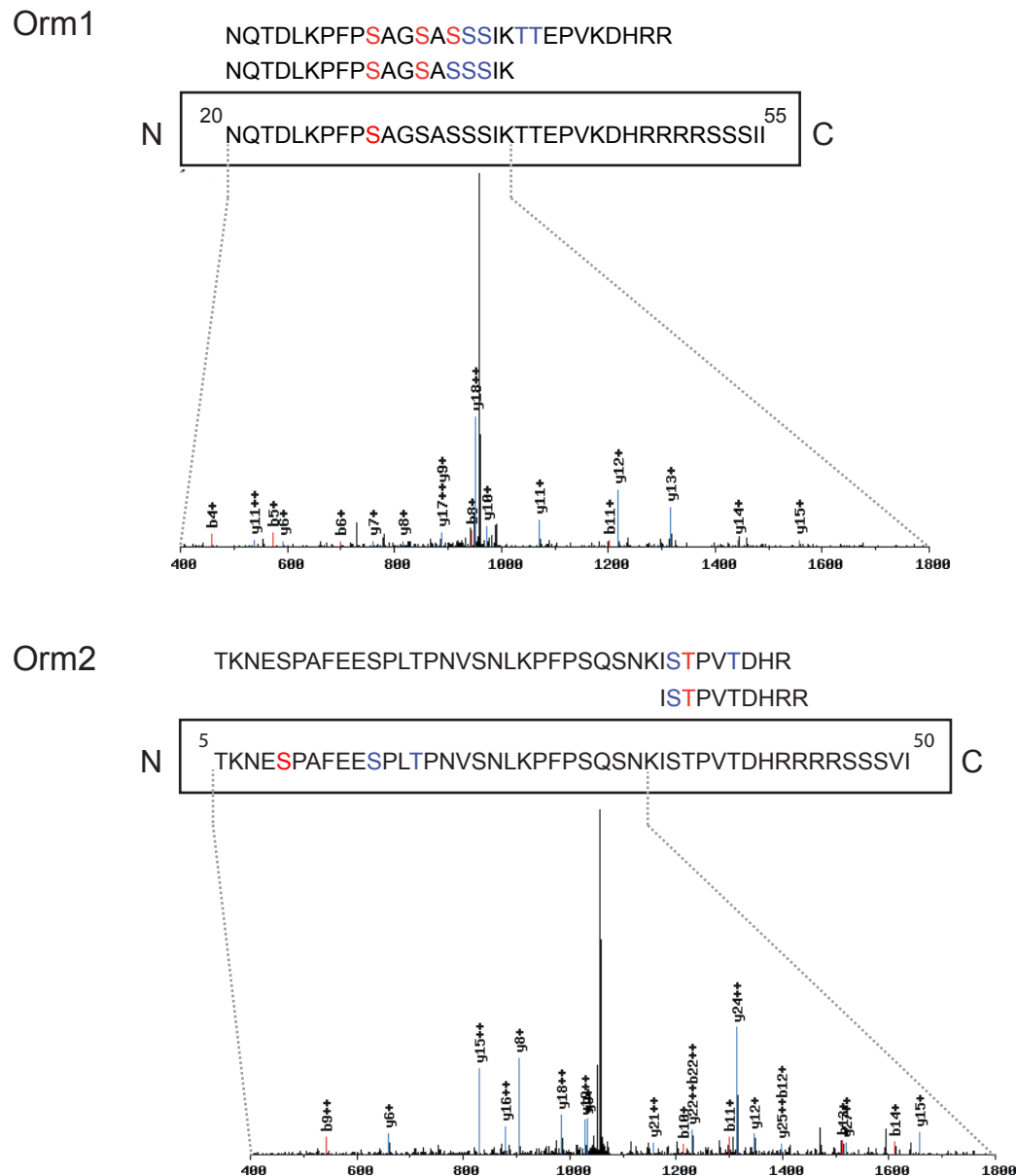
Supplementary Figure 4. Orm2 localization changes in response to myriocin treatment.

GFP-Orm2 and GFP-Orm1 were visualized in strains grown in rich media with or without myriocin. Sec63-mCherry was used as a marker for ER localization. Arrowheads in images of GFP-Orm2 indicate a reduction in cortical ER localization in response to myriocin treatment. Median filtering was applied to reduce image noise.

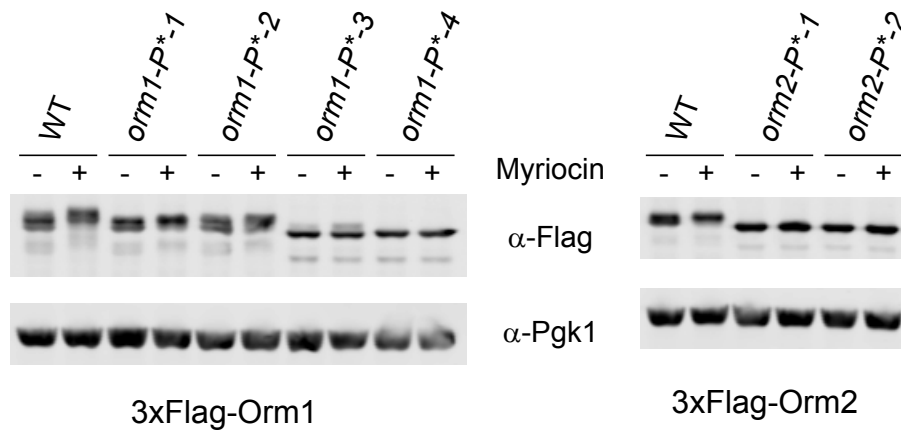
Breslow et al. Supplementary Figure 5



Supplementary Figure 5. Disruptions to sphingolipid synthesis that act downstream of Lcb1/2 but upstream of Aur1 induce Orm1/2 phosphorylation. Tetracycline-repressible promoters were inserted in front of the indicated genes in strains expressing 3xFlag-Orm1 or 3xFlag-Orm2 (note: *pTet-LAG1* was combined with deletion of *LAC1*). Lysates were prepared before and after gene expression shut-off (treatment with 5 μ g/ml doxycycline for 14-16 hr) and analyzed by Western blot against the Flag epitope after separation on phosphate-affinity SDS/PAGE gels. Note: gel-to-gel differences in banding pattern are due to variability in phosphate-affinity gel resolution.



Supplementary Figure 6. Mass spectrometry identifies phosphorylated residues on Orm1 and Orm2. Phospho-peptides from immuno-precipitated 3xFlag-Orm1 and 3xFlag-Orm2 proteins were analyzed using an orbitrap mass spectrometer. For both Orm1 and Orm2, three phospho-peptides were identified. All Orm2 phospho-peptides were singly phosphorylated, whereas singly, doubly and triply phosphorylated peptides were identified for Orm1. The most probable phosphorylation site assignments are highlighted in red, and alternative assignments (with a lower probability) are highlighted in blue. For the boxed peptides NQTDLKPFP**S***AG**S**ASS**S**IK (Orm1) and TKNES**P**AF**E**ESPLTPN**V**SNLKPFP**S**QSN**K** (Orm2), annotated tandem mass spectra are shown, where *S** indicates the site of phosphorylation.



Supplementary Figure 7. Wild type and phospho-mutant forms of Orm1 and Orm2 show similar expression levels. Lysates from strains expressing 3xFlag-tagged wildtype (WT) or phospho-mutant alleles of *ORM1* and *ORM2* were prepared after growth for 12-16 hr in 0 or 150 ng/ml myriocin. Western blots of these lysates were probed against the Flag epitope and against Pgk1 as a loading control.

Supplementary Methods

Plasmid sequences below are derived in part from published constructs described in Gari et al.² and Shaner et al.³

pFA6a-NATMX4_pTEF2_eGFP_Adh1-tm-AG

Primer annealing sequences used for PCR are underlined. TEF2 promoter sequence is in bold font.

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pFA6a-NATMX4_pTDH3_eGFP_Adh1-tm-AG

Primer annealing sequences used for PCR are underlined. TDH3 promoter sequence is in bold font.

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 ACTATA

pFA6a-NAT-MX4-Tet-Act-pTet

A fusion PCR product of the pFA6a-NATMX4 marker, Tet-Activator, and 4XTet-Operator promoter was generated and cloned into the pCR2.1-TOPO vector

(Invitrogen). The sequence of the cloned PCR product is given below (NAT marker is underlined, TetO sites are in bold font):

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 agtcaaacgctatccacgcccattgatgtactgcaaaacccgcatcccatggtaatagcgaatgactaatacgtag
 atgtactgccaagtaggaaagtcccataaggctcatgtactgggcataatgccaggcggggccatttacggctcattgac
 gtcaatagggggcgtacttggcatatgatacacttgatgtactgccaagtgggcagtttagcgtaaatactccacc
 attgacgtcaatggaaagtcctattggcgcttactatgggaacatacgtcattattgacgtcaatggggcgggggctcg
 ttgggcggtcagccaggcggggccatttacggtaagttatgtaacgcggaactccatataatgggctatgaactaatga
 cccgtaattgattactattaataactagtcaataatcaatgtcaacatggcggtaatgttggacatgagccaatat
 aatgtacataattatgatatggatacaacgtatgcaatgggccaagctcctcgagtaattcgcgccacttctaaata
 agcgaatttcttatgatttttattattaataaagttataaaaaaataagtgatatacaaaattttaaagtg
 actcttaggtttttaaagcaaaattcttattcttgagtaactcttctctgtaggtcagggttgccttctcaggatag
 tatgaggtcgtcttattgaccacacctctaccggcAGATCCGCTAGGGATAACAGGGTAATATagatcaattcctc
 gatcgagtttaccact**ccctatcagtgatagagaaaagtgaaagtcgagtttaccactccctatcagtgatagagaa**
aagtgaaagtcgagtttaccactccctatcagtgatagagaaaagtgaaagtcgagtttaccactccctatcagtgat
tagagaaaagtgaaagtcgagctcggtaccctatggcagtcagtgctctgtatgtatataaaactcttggtttctt
 cttttctctaaatattcttcttatacattaggtcctttgtagcataaataactatacttctatagacacgcaaac
 acaatacacacactaaattaccggatcaattcggg**ATG**

pNT18_mCherry_URA

Primer annealing sequences used for PCR are underlined. mCherry sequence used for C-terminal tagging is in bold font.

ATATCAGATCCACTAGTGGCCTATGCGGCCGCGGATCTGCCGGTCTCCCTATAGTGAGTCGTATTAATTTTCGATAAG
 CCAGGTTAACCTGCATTAATGAATCGGCCAACCGCGGGGAGAGGCGGTTTTCGCTATTGGGCGCTCTTCCGCTTCCT
 CGCTCACTGACTCGCTGCGCTCGGTTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTA
 TCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGC
 CGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC
 GAAACCCGACAGGACTATAAAGATAACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTG
 CCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCT
 CAGTTCCGGTGTAGGTTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTAT
 CCGGTAACCTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT
 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGT
 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA
 CCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTG
 ATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAG
 GATCTTACCTAGATCCTTTTTAAATTAATAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG
 ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTC
 CCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCACG
 CTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTAT
 CCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCACAACGTT
 GTTGGCATTGCTACAGGCATCGTGGTGTACGCTCGTTCGTTTGGTAGTGGCTTCACTTCCAGTCCGGTTCCCAACGATC
 AAGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAGTA
 AGTTGGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTTACTGTTCATGCCATCCGTAAGATGC
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 TAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGCTCTCGCGCGTTTTCGG
 TGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTACAGCTTGTCTGTAAGCGGATGCCGGGAGCA
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 GTACTGAGAGTGCACCATATGGACATATTGTGCTTAGAACGCGGGCTACAATTAATACATAACCTTATGTATCATACA
 CATACGATTTAGGTGACACTATAGAACGCGGCCAGCTGAAGCTTCGTACGCTGCAGGTGCGACGGATCGGTGACG
 GTGCTGGTTTTAATTAACATG**GTGAGCAAGGGCGAGGAGGATAACATGGCCATCATCAAGGAGTTCATGAGATTCAAG**
GTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCAGACCCTACGAGGGCAC
CCAGACCGCAAGCTGAAGGTGACCAAGGGTGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATGT
ACGGCTCCAAGGCCTACGTGAAGCACCCCGCGACATCCCCGACTACTTGAAGCTGTCTTCCCCGAGGGCTTCAAG
TGGGAGAGAGTGAAGTTCGAGGACGGCGCGTGGTACCGTACCCAGGACTCCTCCCTGCAGGACGGCGAGTT
CATCTACAAGGTGAAGTTGAGAGGCACCAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACCATGGGCTGGG
AGGCCTCCTCCGAGAGAATGTACCCCGAGGACGGCGCCCTGAAGGGCGAGATCAAGCAGAGGCTGAAGCTGAAGGAC
GGCGGCCACTACGACGCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAACGT
CAACATCAAGTTGGACATCACCTCCCACAACGAGGACTACACCATTGTGGAACAATATGAAAAGAGCTGAAGGTAGAC
ATTCTACTGGTGGTATGGATGAATTGTACAAATAA**GGCGCGCCACTTCTAAATAAGCGAATTTCTTATGATTTATGA**
 TTTTTATTATTAATAAGTTATAAAAAAATAAGTGATAACAAATTTTAAAGTGACTCTTAGGTTTTTAAACGAAAA
 TTCTTATTCTTGAGTAACTCTTTCCTGTAGGTTCAGGTTGCTTTCTCAGGTATAGTATGAGGTGCTCTTATTGACCA
 CACCTTACCAGGACATCCGCTAGGGATAACAGGGTAATATAGATCTGTTTAGCTTGCCTCGTCCCCGCGGGTTCAC
 CCGGCCAGCGACATGGAGGCCAGAAATACCCTCCTTGACAGTCTTGACGTGCGCAGCTCAGGGGCATGATGTGACTG
 TCGCCCCGTACATTTAGCCCATACATCCCCATGTATAATCATTTGCATCCATACATTTTGTGAGGCGCACGGCGCGAA
 GCAAAAATTACGGCTCCTCGCTGCAGACCTGCGAGCAGGGAAACGCTCCCCTCACAGACGCGTTGAATTGTCCCCAC
 GCCGCGCCCCCTGTAGAGAAATATAAAAAGGTTAGGATTTGCCACTGAGGTTCTTCTTTCATATACTTCTTTTTAAAT
 CTTGCTAGGATACAGTTCTCACATCACATCCGAACATAAACAACCATGACAGTCAACACTAAGACCTATAGTGAGAG
 AGCAGAAACTCATGCCTCACCAGTAGCACAGCGATTATTTTCGATTAATGGAAGTGAAGAAAACCAATTTATGTGCAT
 CAATTGACGTTGATACCACTAAGGAATTCCTTGAATTAATTGATAAATTAGGTCCTTATGTATGCTTAATCAAGACT
 CATATTGATATAATCAATGATTTTTCTTATGAATCCACTATTGAACCATTATTAGAATTTTACGTAACATCAATT

TATGATTTTTGAAGATAGAAAATTTGCTGATATTGGTAATACCGTAAAGAAACAATATATTGGTGGAGTTTATAAAA
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AAAGAAACCACCACCAACCAAGAGCCAAGAGGGTTATTGATGTTAGCTGAATTATCATCAGTGGGATCATTAGCATA
TGGAGAATATTCTCAAAAAACTGTTGAAATTGCTAAATCCGATAAGGAATTTGTTATTGGATTTATTGCCAACGTG
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TTAGGACAACAATATAGAACTGTTGATGAAGTTGTTAGCACTGGAAGTATGATATTATCATTGTTGGTAGAGGATTGTT
TGGTAAAGGAAGAGATCCAGATATTGAAGGTAAAAGGTATAGAAATGCTGGTTGGAATGCTTATTTGAAAAAGACTG
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TTAAGTGCGCAGAAAGTAATATCATGCGTCAATCGTATGTGAATGCTGGTCGCTATACTGCTGTTCGATTTCGATACTA
ACGCCGCCATCCAGTGTCGAAAACGAGCTCGAATTCATCGATG

Supplementary Notes

References for Supplementary Information

1. Kearns, B. G. et al. Essential role for diacylglycerol in protein transport from the yeast Golgi complex. *Nature* 387, 101-5 (1997).
2. Gari, E., Piedrafita, L., Aldea, M. & Herrero, E. A set of vectors with a tetracycline-regulatable promoter system for modulated gene expression in *Saccharomyces cerevisiae*. *Yeast* 13, 837-48 (1997).
3. Shaner, N. C. et al. Improved monomeric red, orange and yellow fluorescent proteins derived from *Discosoma* sp. red fluorescent protein. *Nat Biotechnol* 22, 1567-72 (2004).

Protein ID	IP 3xFlag-Orm1		IP 3xFlag-Orm2	
	# of peptides	% Sequence Coverage	# of peptides	% Sequence Coverage
Sac1	42	74.6	33	62.1
Lcb1	23	40.9	26	43.5
Lcb2	23	41.0	22	37.1
Orm1	10	49.1	4	19.4
Orm2	6	25.0	8	31.9
Tsc3	3	30.0	1	17.5

Supplementary Table 1. Orm-associated proteins identified by mass spectrometry. Proteins found in immunoprecipitations of 3xFlag-Orm1 and 3xFlag-Orm2 were analyzed by mass spectrometry. Peptide coverage information for identified proteins corresponding to the bands indicated in **Fig. 2a** are shown above.

Supplementary Notes

References for Supplementary Information

1. Kearns, B. G. et al. Essential role for diacylglycerol in protein transport from the yeast Golgi complex. *Nature* 387, 101-5 (1997).
2. Gari, E., Piedrafita, L., Aldea, M. & Herrero, E. A set of vectors with a tetracycline-regulatable promoter system for modulated gene expression in *Saccharomyces cerevisiae*. *Yeast* 13, 837-48 (1997).
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