

Supplemental information

**The Myo2 adaptor Ldm1
and its receptor Ldo16 mediate actin-dependent
lipid droplet motility**

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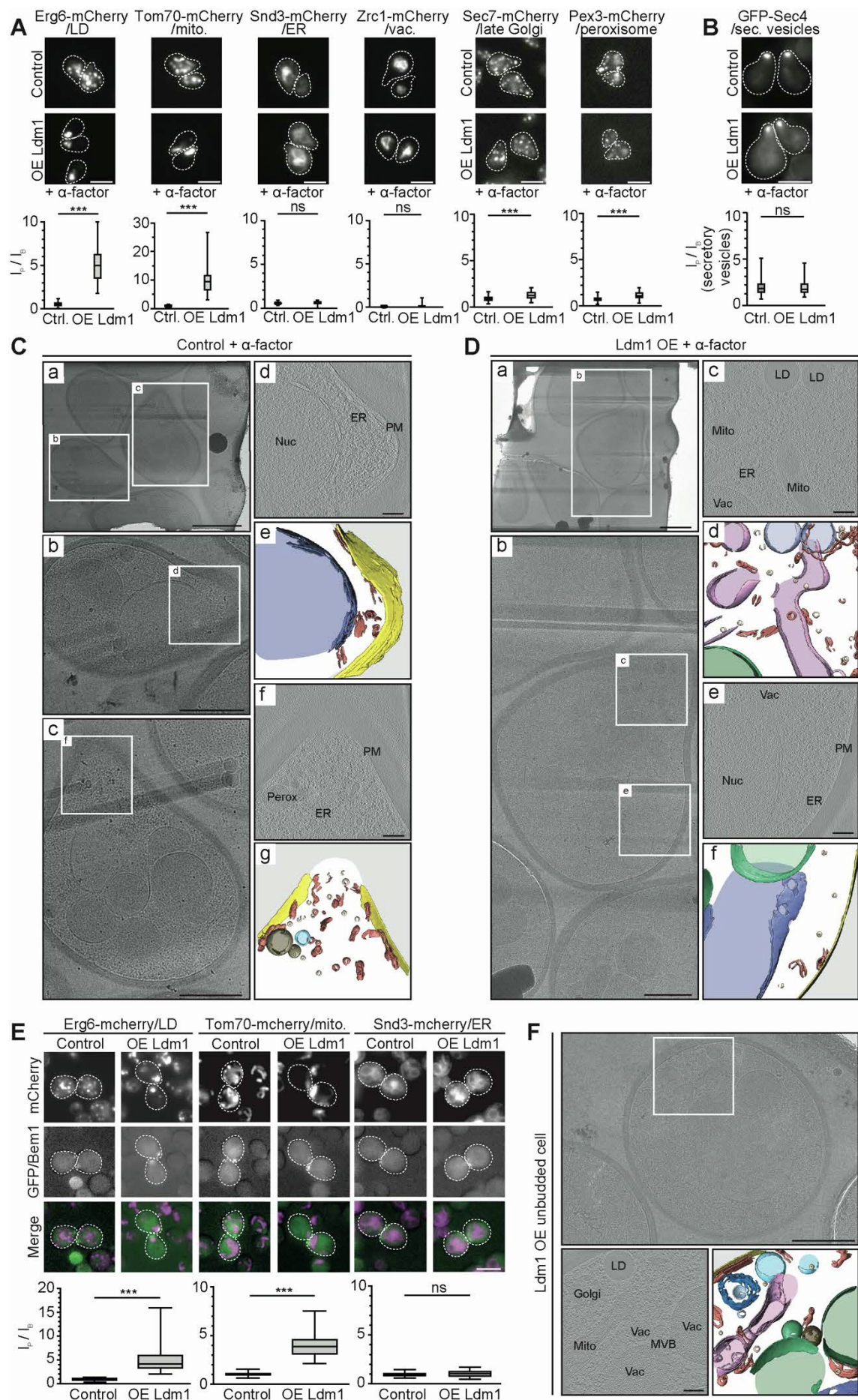


Figure S1. Characterization of Ldm1 overexpression strains. Related to Figure 2.

(A) Ldm1 overexpressing (*TEF2* promoter) and control cells expressing mCherry-fused organelle markers were treated for 2 hours with the mating pheromone α -factor and analyzed by microscopy. Mean intensity ratio of fluorescent organelle marker signals in cell protrusions over cell bodies (I_P/I_B) is depicted as boxplots (5-95 percentile). ns, not significant; ***, $p < 0.001$. Scale bars, 5 μ m. N=60 cells, n=3.

(B) Secretory vesicles were labeled by plasmid-derived GFP-Sec4 in control and p*TEF2*-Ldm1 cells and analyzed as in (A). The ratio of the mean fluorescent signal of the vesicular structure in the cell protrusion to the mean fluorescent signal of the cell body is shown as a boxplot (5-95 percentile). ns, not significant. Scale bar, 5 μ m. N=60 cells, n=3.

(C) a: transmission electron microscopy image of a FIB-milled lamella of control cells treated for 2 hours with the mating pheromone α -factor to induce a uniform polarization of the cell population and formation of mating protrusions. Scale bar: 2 μ m. b and c: zoom-ins on the cells from which the tomograms were collected. Scale bars: 1 μ m. d-g: tomographic slices and corresponding segmentations. Scale bars: 200 nm. Yellow, plasma membrane (PM); red, ER; purple, nucleus (Nuc); brown, peroxisomes (Perox); light blue, lipid droplets; beige, vesicles.

(D) a: transmission electron microscopy image of a FIB-milled lamella of p*TEF2*-Ldm1 cells treated for 2 hours with the mating pheromone α -factor to induce a uniform polarization of the cell population and formation of mating protrusions. Scale bar: 2 μ m. b: zoom-in on the cell from which the tomogram was collected. Scale bar: 1 μ m. c-f: tomographic slices and corresponding segmentations. Scale bars: 200 nm. Red, ER; pink, mitochondria (Mito); green, vacuole (Vac); light blue, lipid droplets (LD); beige, vesicles.

(E) Ldm1 overexpressing (*TEF2* promoter) and control cells expressing mCherry-fused organelle markers were transformed with a plasmid for expression of the polarization marker Bem1-GFP and analyzed by microscopy. Mean intensity ratio of fluorescent organelle marker signals in polarized cell areas over the rest of the cell (I_P/I_B) is depicted as boxplots (5-95 percentile). ns, not significant; ***, $p < 0.001$. Scale bar, 5 μ m. N=60 cells, n=3.

(F) Top: transmission electron microscopy image of a FIB-milled lamella of a p*TEF2*-Ldm1 unbudded cell. Scale bar: 2 μ m. Bottom: tomographic slice and corresponding segmentation. White square indicates the region where the tomogram was collected. Scale bar: 200 nm. Dark blue, Golgi; pink, mitochondria (Mito); green, vacuole (Vac); red, ER; light blue, lipid droplets (LD); brown, multivesicular body (MVB); beige, vesicles.

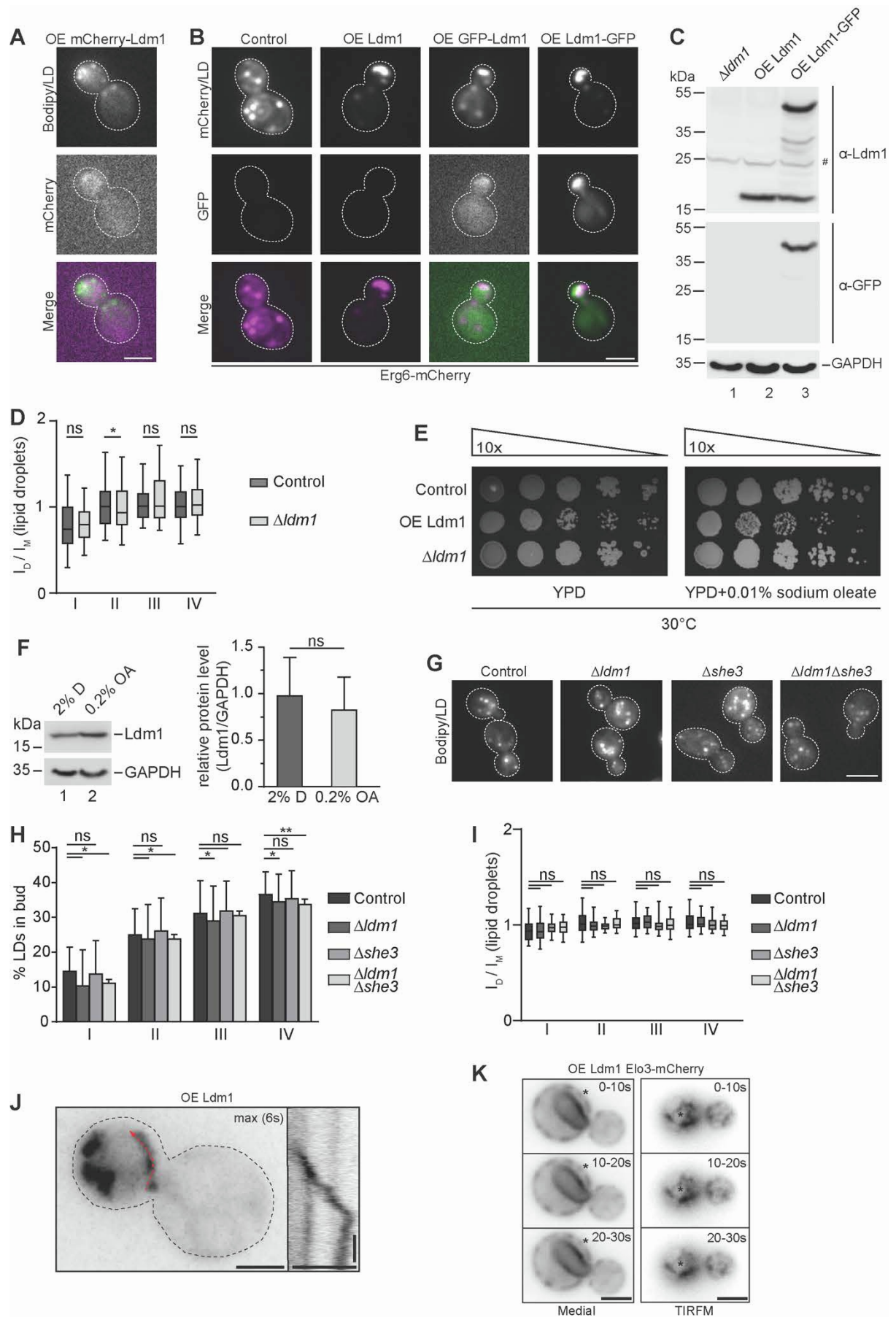


Figure S2. Analysis of Ldm1-dependent LD motility. Related to Figure 3.

(A) pTEF2-mCherry-Ldm1 cells were stained with BODIPY493/503. Scale bar, 5 μ m.

(B) Control, pTEF2-Ldm1, pTEF2-GFP-Ldm1, and pTEF2-Ldm1-GFP cells expressing Erg6-mCherry were analyzed by microscopy. Scale bar, 5 μ m.

(C) Proteins from Δ ldm1, pTEF2-Ldm1 and pTEF2-Ldm1-GFP cells were extracted and subjected to SDS-PAGE and western blotting using α -Ldm1, α -GFP and α -GAPDH antibodies. #, unspecific band.

(D) Control and Δ ldm1 cells were stained with BODIPY493/503 and imaged. Mean intensity ratio of BODIPY493/503 signal in daughter over mother cells (I_D/I_M) is depicted as boxplots (5-95 percentile). Cells were categorized by bud size: I, 0-24%, II, >24-39%, III, >39-50%, IV, >50-61%. ns, not significant; *, $p < 0.05$. N=60 cells, n=3.

(E) Control, pTEF2-Ldm1, and Δ ldm1 cells were grown overnight at 30°C, adjusted to an OD₆₀₀ of 0.05, serially 10-fold diluted, spotted on YPD and YPD+0.01% sodium oleate agar plates and incubated at 30°C for 3 days.

(F) pTEF2-Ldm1 cells were cultured on synthetic media supplemented with glucose (2% D) or oleic acid (0.2% OA). Proteins were extracted and subjected to SDS-PAGE and western blotting using α -Ldm1 and α -GAPDH antibodies. For quantifications, Ldm1 signal was normalized to GAPDH, and the resulting values were further normalized to the 2% D value (set to 1). Data represented as \pm SD. ns, not significant. n=3.

(G) Control, Δ ldm1, Δ she3 and Δ ldm1 Δ she3 cells were stained with BODIPY493/503 and analyzed by fluorescence microscopy. Scale bar, 5 μ m.

(H) Quantification of phenotype in (G). Bar graph shows the percentage of the number of LDs in the daughter to the total number of LDs in the whole cell. Cells were categorized by bud size: I, 0-24%, II, >24-39%, III, >39-50%, IV, >50-61%. Data represented as mean \pm SD. ns, not significant; *, $p < 0.05$; **, $p < 0.01$. N=60 cells, n=3.

(I) Quantification of phenotype in (G). Mean intensity ratio of fluorescent LD marker signal in daughter over mother cells (I_D/I_M) is depicted as boxplots (5-95 percentile). Cells were categorized by bud size: I, 0-24%, II, >24-39%, III, >39-50%, IV, >50-61%. ns, not significant. N=60 cells, n=3.

(J) pTEF2-Ldm1 (OE-Ldm1) cells were labeled with BODIPY493/503 and analyzed by time-resolved microscopy at 33 frames per second. Maximal projection of 6 s and kymograph are shown. Scale bar, 2 μ m. Time bar, 1 s.

(K) Medial and surface (TIRFM) distribution of Elo3-mCherry was monitored to follow nuclear and peripheral ER dynamics. We found no rapid motility of ER fragments within a sub-minute time frame. Asterisks indicate stable peripheral ER elements that are immotile over 30 s. Images represent average projections of 10 s periods. Scale bars, 2 μ m.

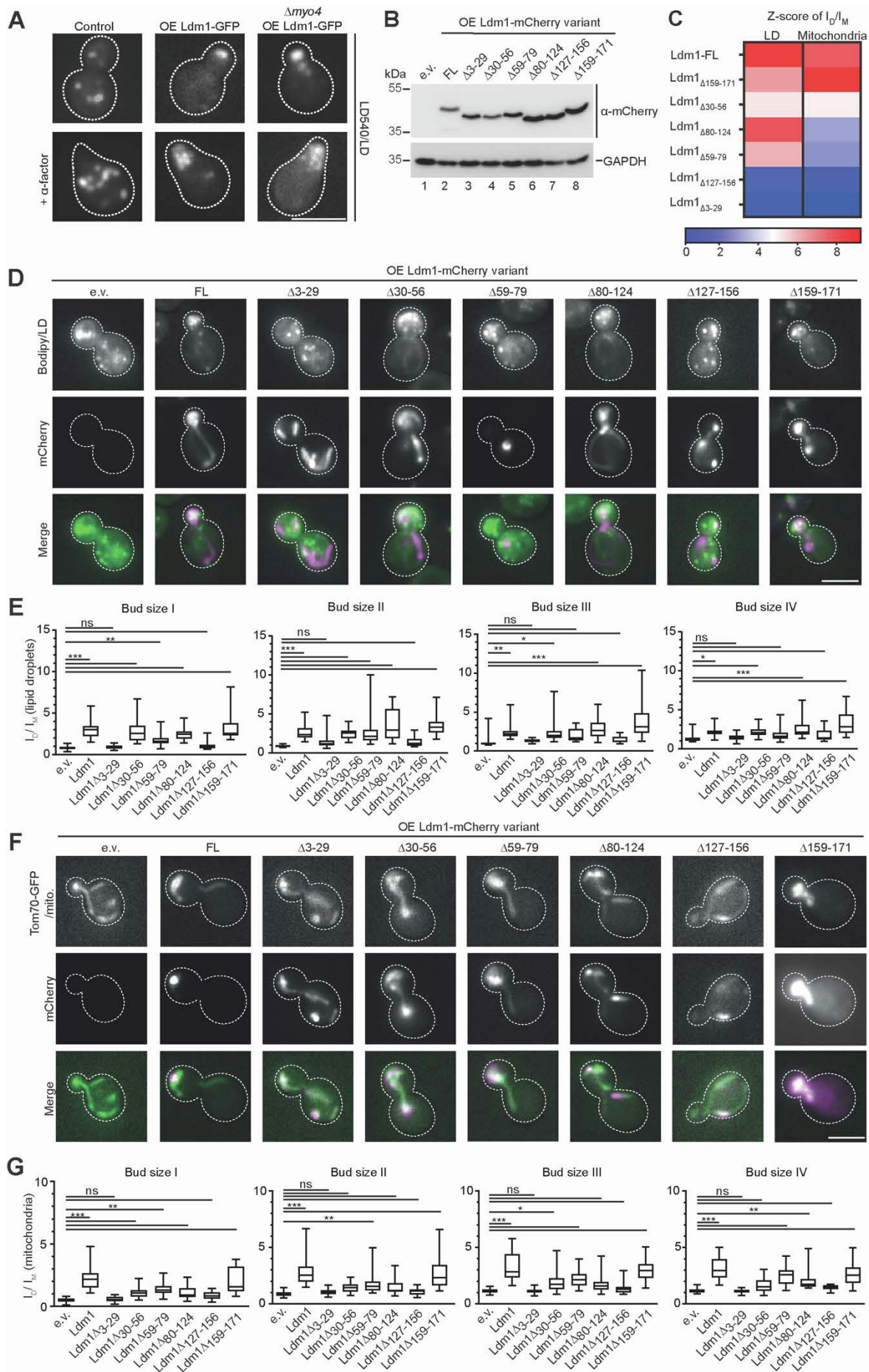


Figure S3. Structure function analysis of Ldm1. Related to Figure 5.

(A) Control, pTEF2-Ldm1-GFP and pTEF2-Ldm1-GFP $\Delta myo4$ cells were treated for 2 hours with the mating pheromone α -factor and were stained with the red neutral lipid dye LD540. Scale bar, 5 μ m.

(B) Proteins from control cells transformed with plasmids for expression (TEF2 promoter) of indicated Ldm1-mCherry variants (FL, full length; and variants with indicated deletions) were extracted and subjected to SDS-PAGE and western blotting using α -mCherry and α -GAPDH antibodies.

(C) Heatmap of organellar distribution, related to (E) and (G). Z-score of I_D/I_M (mitochondria) and I_D/I_M (LDs) in reference to the empty vector control was calculated over all bud sizes.

(D) Control cells transformed with plasmids for expression of indicated Ldm1-mCherry variants (TEF2 promoter) were stained with BODIPY493/503 and analyzed by microscopy. e.v., empty vector. Scale bar, 5 μ m.

(E) Mean intensity ratio of fluorescent LD marker signal in daughter over mother cells (I_D/I_M) from cells analyzed in (D) is depicted as boxplots (5-95 percentile). Cells were categorized by bud size: I, 0-24%, II, >24-39%, III, >39-50%, IV, >50-61%. e.v., empty vector. ns, not significant; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. N=60 cells, n=3.

(F) Tom70-GFP cells transformed with plasmids for expression of indicated Ldm1-mCherry variants (TEF2 promoter) were analyzed by microscopy. e.v., empty vector. Scale bar, 5 μ m.

(G) Tom70-GFP cells were analyzed as in (E) to assess mitochondrial I_D/I_M . e.v., empty vector. ns, not significant; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. N=60 cells, n=3.

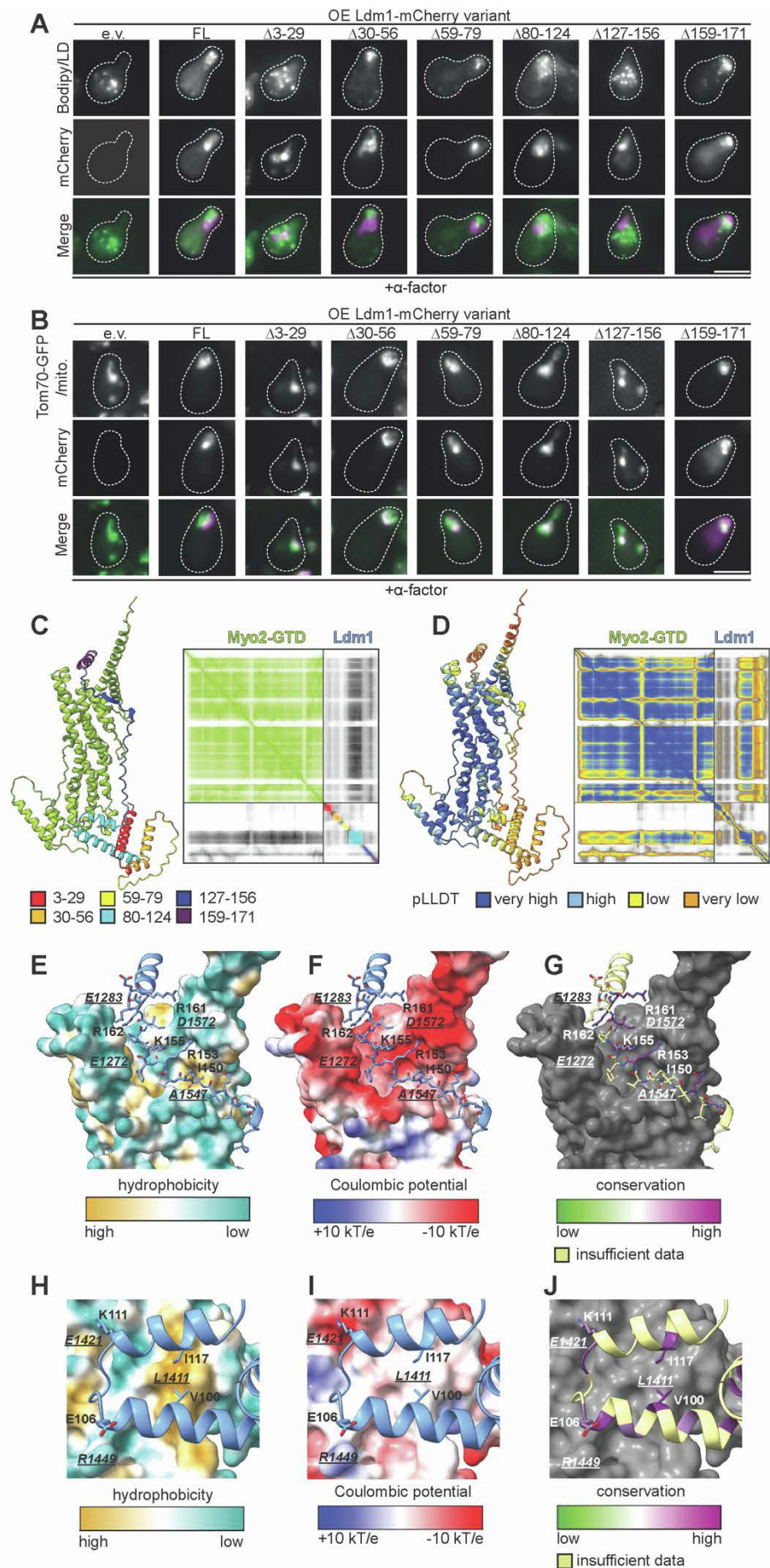


Figure S4. Interplay between Ldm1 and Myo2. Related to Figure 5.

(A) Control cells transformed with plasmids for expression of indicated Ldm1-mCherry variants (*TEF2* promoter) were treated for 2 hours with α -factor, stained with BODIPY493/503 and analyzed by microscopy. e.v., empty vector. Scale bar, 5 μ m.

(B) Tom70-GFP cells transformed with plasmids for expression of indicated Ldm1-mCherry variants (*TEF2* promoter) were treated for 2 hours with α -factor and were analyzed by microscopy. e.v., empty vector. Scale bar, 5 μ m.

(C) AlphaFold 3 structure prediction of Myo2-GTD (green) in complex with Ldm1 (color coded according to truncations used in Figures S3B-G and S4A and B) with corresponding PAE (predicted aligned error) plot colored by chain (pTM = 0.75, ipTM = 0.71). Domain boundaries chosen for interaction site mapping are labelled.

(D) Same as (C) but colored by predicted local distance difference test (pLDDT) scores.

(E-G) Close ups of interface A between Myo2-GTD (surface representation) and Ldm1 (cartoon). Myo2 interface residues mutated in Figure S5 are labeled in bold, underlined, Ldm1 interface residues mutated in Figures 5 and S5 are labeled in regular font.

(H-J) Close ups of interface B between Myo2-GTD (surface representation) and Ldm1 (cartoon). Myo2 interface residues mutated in Figure S5 are labeled in bold, underlined, Ldm1 interface residues mutated in Figure S5 are labeled in regular font.

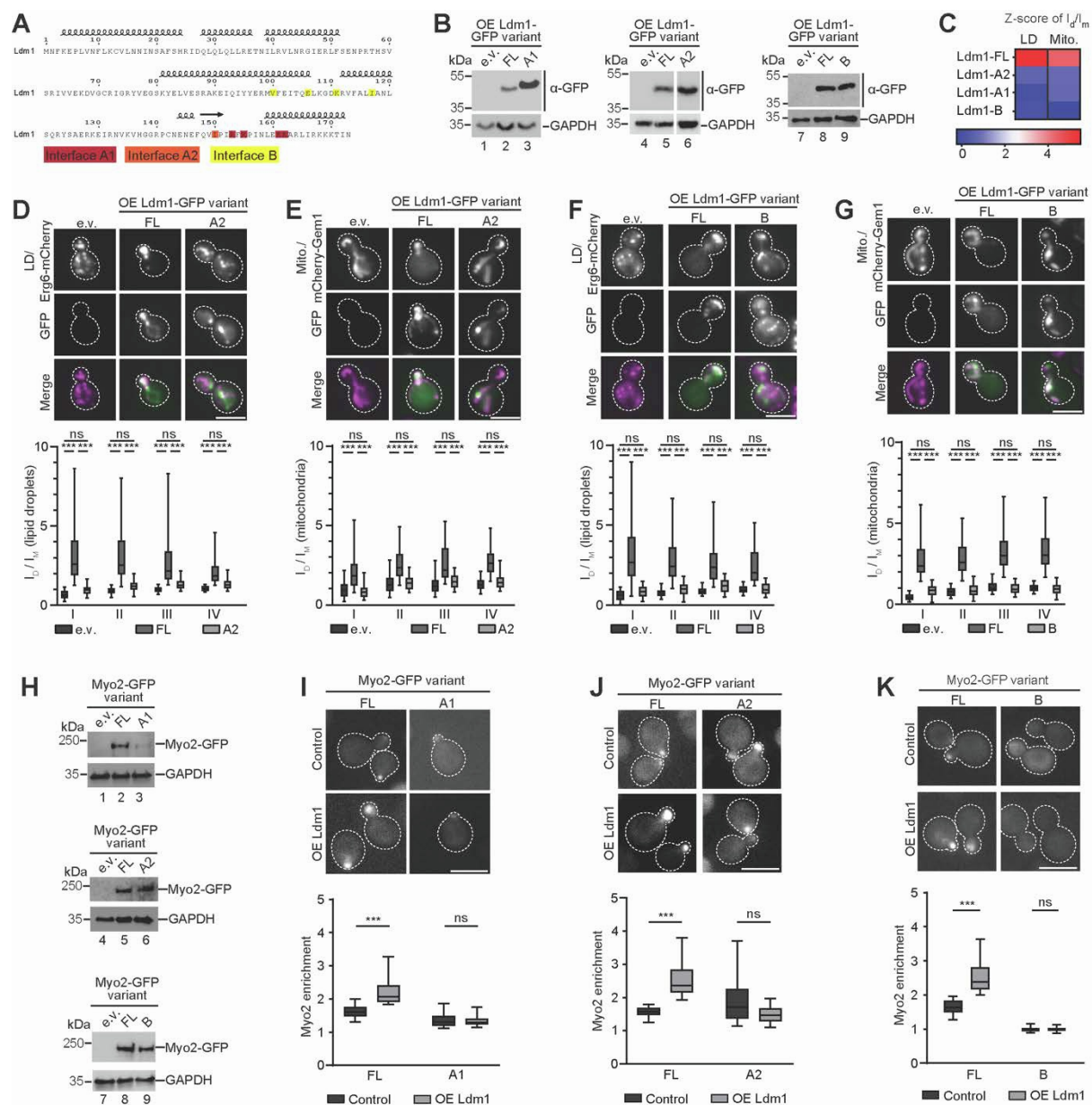


Figure S5. Analysis of the Ldm1-Myo2 interfaces. Related to Figure 5.

(A) Amino acid sequence of Ldm1 with annotated secondary structure and interface regions. α -helices and β -strand from the AlphaFold 3 prediction in complex with the Myo2-GTD are shown above the sequence as coils and arrows, respectively. Residues mutated to disrupt interface A1 (red), A2 (orange), and B (yellow) are highlighted.

(B) Proteins from control cells transformed with plasmids for expression of indicated Ldm1-GFP variants (*TEF2* promoter) were extracted and subjected to SDS-PAGE and western blotting using α -GFP and α -GAPDH antibodies.

(C) Heatmap of organellar distribution, related to (D-G) and Figure 5F and G. Z-score of I_D/I_M (mitochondria) and I_D/I_M (LDs) in reference to the empty vector control was calculated over all bud sizes.

(D-G) Erg6-mCherry (D and F) and mCherry-Gem1 (E and G) cells transformed with plasmids for expression of indicated Ldm1-GFP variants (*TEF2* promoter) were analyzed by microscopy. Mean intensity ratio of fluorescent organelle marker signal in daughter over mother cells (I_D/I_M) is depicted as boxplots (5-95 percentile). Cells were categorized by bud size: I, 0-24%, II, >24-39%, III, >39-50%, IV, >50-61%. e.v., empty vector. ns, not significant; ***, $p < 0.001$. Scale bars, 5 μ m. N=60 cells, n=3.

(H) Proteins from control cells transformed with plasmids for expression of indicated Myo2-GFP variants (*MYO2* promoter) were extracted and subjected to SDS-PAGE and western blotting using α -GFP and α -GAPDH antibodies.

(I-K) Control and p*TEF2*-Ldm1 cells transformed with plasmids for expression of indicated Myo2-GFP variants (*MYO2* promoter) were analyzed by microscopy. The ratio of the max fluorescent Myo2 signal intensity in the bud to the max fluorescent signal of the cytoplasm in the mother cell (Myo2 enrichment) is shown as boxplots (5-95 percentile). ns, not significant; ***, $p < 0.001$. Scale bars, 5 μ m. N=60 cells, n=3.

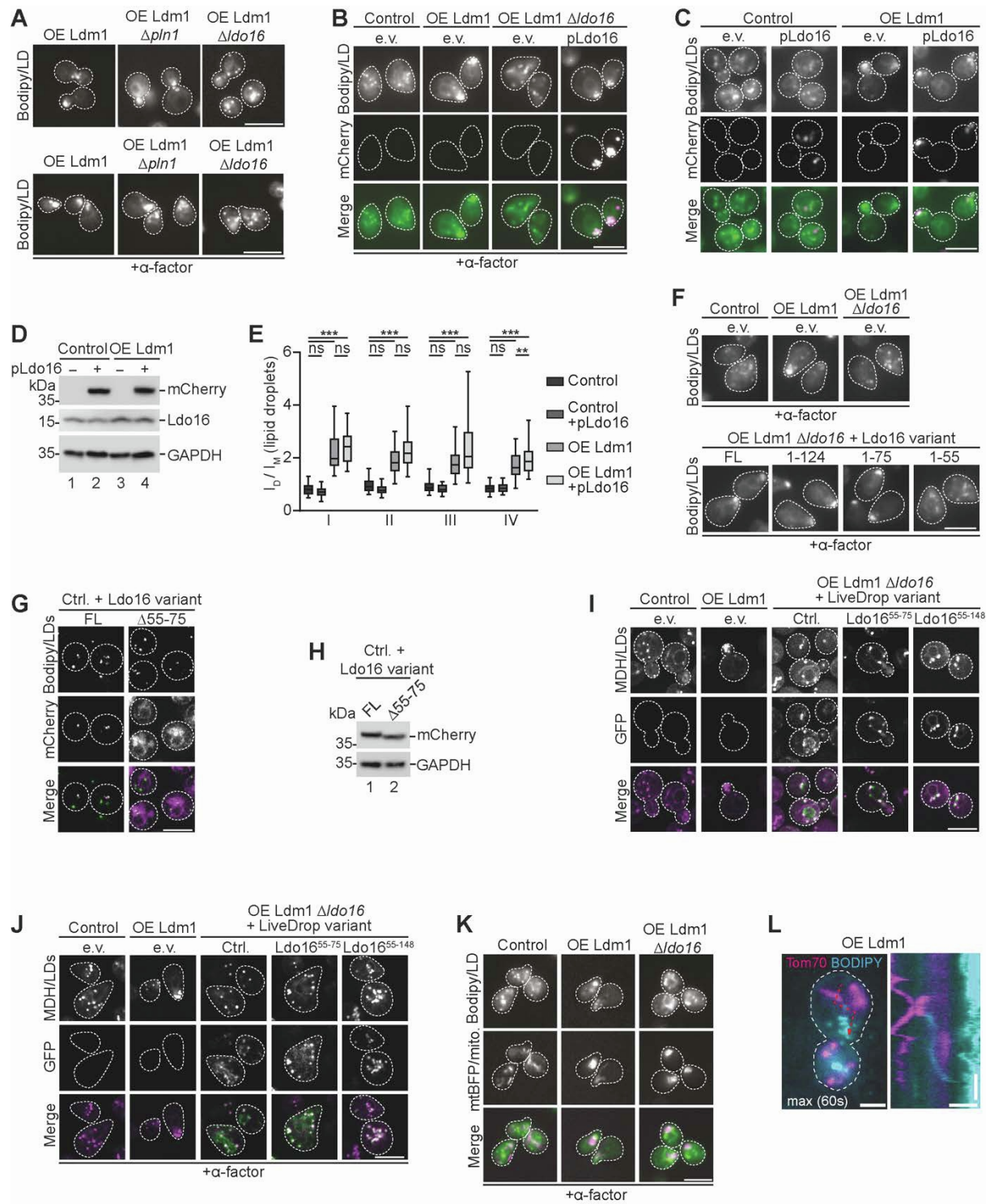


Figure S6. Ldo16 is an Ldm1 partner protein. Related to Figure 6.

(A) pTEF2-Ldm1-GFP, pTEF2-Ldm1-GFP $\Delta pln1$ and pTEF2-Ldm1-GFP $\Delta ldo16$ cells were treated for 2 hours with α -factor or left untreated, stained with BODIPY493/503 and analyzed by microscopy. Scale bars, 5 μ m.

(B) Control, pTEF2-Ldm1, and pTEF2-Ldm1 $\Delta ldo16$ cells were transformed with a centromeric plasmid for expression of Ldo16-mCherry from its own promoter (pLdo16) or an empty vector (e.v.), treated for 2 hours with α -factor and stained with BODIPY493/503. Scale bar, 5 μ m.

(C) Control and pTEF2-Ldm1 cells were transformed with a centromeric plasmid for expression of Ldo16-mCherry from its own promoter (pLdo16) or an empty vector (e.v.) and stained with BODIPY493/503. Scale bar, 5 μ m.

(D) Proteins from indicated cells in (C) were extracted and subjected to SDS-PAGE and western blotting using α -Ldo16, α -mCherry and α -GAPDH antibodies.

(E) Quantification of phenotype in (C). Mean intensity ratio of fluorescent LD marker signal in daughter over mother cells (I_D/I_M) is depicted as boxplots (5-95 percentile). Cells were categorized by bud size: I, 0-24%, II, >24-39%, III, >39-50%, IV, >50-61%. e.v., empty vector. ns, not significant; **, $p < 0.01$; ***, $p < 0.001$. N=60 cells, n=3.

(F) Control, pTEF2-Ldm1, and pTEF2-Ldm1 $\Delta ldo16$ cells were transformed with indicated plasmids, treated for 2 hours with α -factor and stained with BODIPY493/503. FL, centromeric plasmid for expression of full length Ldo16 from the pLDO16 promoter. 1-124, 1-75, 1-55, centromeric plasmids for expression of truncated Ldo16 variants comprising amino acids 1-124, 1-75 or 1-55 from the pLDO16 promoter. e.v., empty vector. Scale bar, 5 μ m.

(G) Control cells were transformed with indicated plasmids and stained with BODIPY493/503. FL, centromeric plasmid for expression of full length Ldo16-mCherry from the pLDO16 promoter. $\Delta 55-75$, centromeric plasmid for expression of truncated Ldo16 variants lacking amino acids 55-75 from the pLDO16 promoter. Scale bar, 5 μ m.

(H) Proteins from indicated cells in (G) were extracted and subjected to SDS-PAGE and western blotting using α -mCherry and α -GAPDH antibodies.

(I) Control, pTEF2-Ldm1, and pTEF2-Ldm1 $\Delta ldo16$ cells were transformed with indicated plasmids and stained with MDH. Ctrl., centromeric plasmid for expression of control GFP-LiveDrop from the TEF2 promoter. Ldo16⁵⁵⁻⁷⁵ and Ldo16⁵⁵⁻¹⁴⁸, centromeric plasmids for expression of GFP-LiveDrop-Ldo16⁵⁵⁻⁷⁵ or GFP-LiveDrop-Ldo16⁵⁵⁻¹⁴⁸ from the TEF2 promoter. e.v., empty vector. Scale bar, 5 μ m.

(J) Same as (I), with the difference that cells were treated for 2 hours with α -factor.

(K) Control, pTEF2-Ldm1, and pTEF2-Ldm1 $\Delta ldo16$ cells were transformed with a plasmid for expression of mtBFP to label mitochondria (mito.), treated for 2 hours with α -factor and stained with BODIPY493/503. Scale bar, 5 μ m.

(L) Representative pTEF2-Ldm1 (OE-Ldm1) cell (n>20) expressing Tom70-mCherry labeled with BODIPY493/503 was analyzed by time-resolved microscopy at 2 frames per second. Maximal projection of 60 s and kymograph are shown. Scale bars, 2 μ m. Time bar, 10 s.

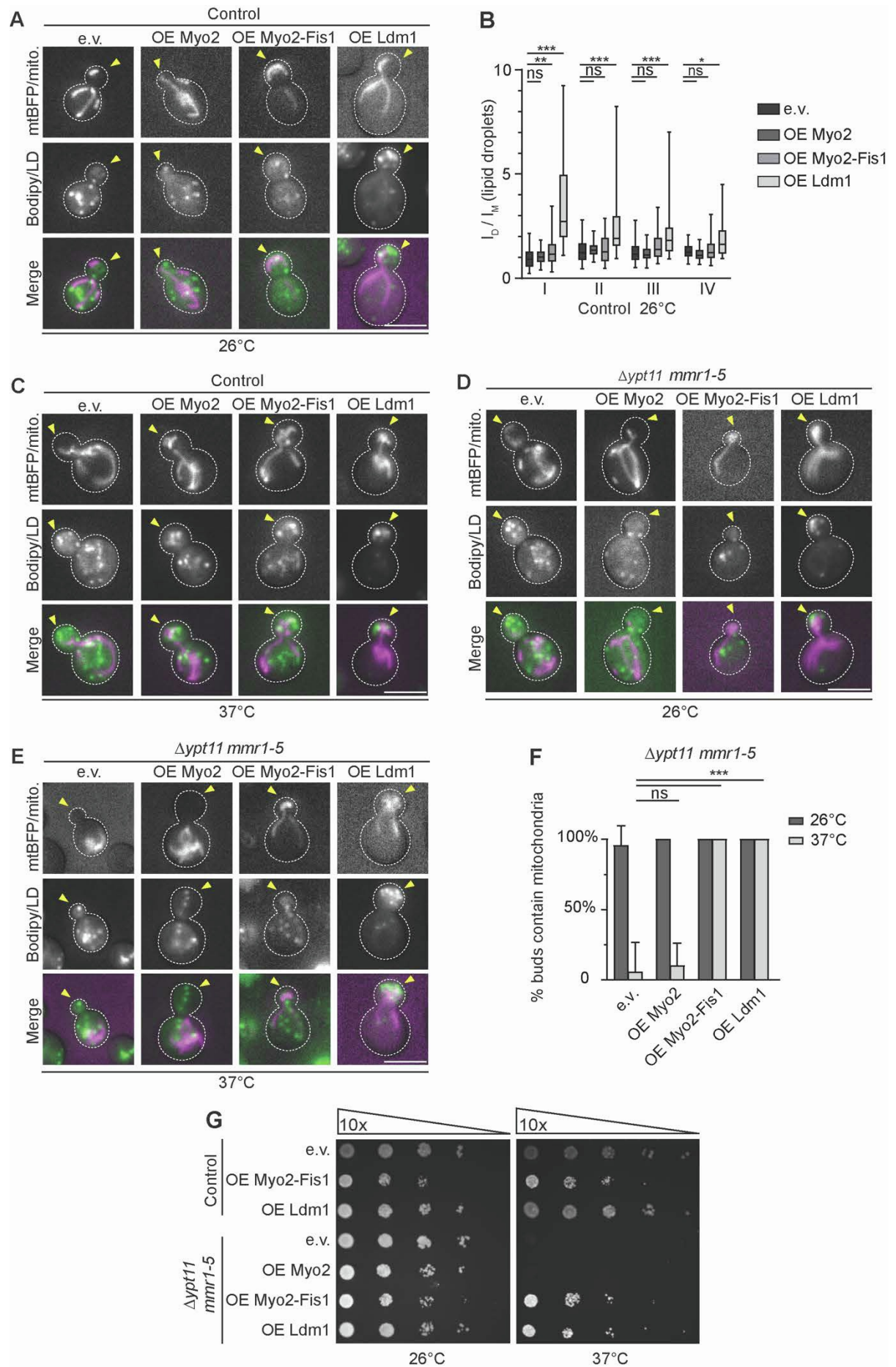


Figure S7. Ldm1 function is independent of Ypt11 and Mmr1. Related to Figure 7.

(A) Control cells expressing mtBFP for labeling of mitochondria (mito.) were transformed with plasmids for overexpression of Myo2, a Myo2 variant fused to the outer mitochondrial membrane protein Fis1 (Myo2-Fis1) for attachment of the motor protein to mitochondria independent of Myo2-adaptor proteins, or Ldm1. Cells were cultured at 26°C, stained with BODIPY493/503, and analyzed by microscopy. e.v., empty vector. Scale bar, 5 μ m.

(B) Control cells were analyzed as in (A) and lipid droplet distribution was quantified. Mean intensity ratio of fluorescent LD marker signal in daughter over mother cells (I_D/I_M) is depicted as boxplots (5-95 percentile). Cells were categorized by bud size: I, 0-24%, II, >24-39%, III, >39-50%, IV, >50-61%. ns, not significant; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. N=60 cells, n=3.

(C) Same as in (A), with the difference that cells were incubated at 37°C for 1.5 hours prior to and during imaging.

(D) $\Delta ypt11 mmr1-5$ cells expressing mtBFP for labeling of mitochondria (mito.) were transformed with plasmids described in (A). Cells were cultured at 26°C, stained with BODIPY493/503, and analyzed by microscopy. e.v., empty vector. Scale bar, 5 μ m.

(E) Same as in (D), with the difference that cells were incubated at 37°C for 1.5 hours prior to and during imaging.

(F) The percentage of dividing cells with mitochondria present in the bud was determined. Data represented as mean \pm SD. ns, not significant; ***, $p < 0.001$. N \geq 60 cells, n=3.

(G) Control and $\Delta ypt11 mmr1-5$ cells transformed with plasmids described in (A) were grown overnight at 26°C, adjusted to an OD₆₀₀ of 0.05, serially 10-fold diluted, spotted on SC-Leu-Ura agar plates and grown at 26°C or 37°C for 3 days. e.v., empty vector.

Table S1. Hits of microscopy-based screens for factors involved in LD motility. Top, list of genes overexpression of which results in altered abundance, morphology and distribution of LDs. Bottom, list of genes deletion of which results in loss of Ldm1-dependent LD accumulation at sites of polarized growth. Related to Figures 1 and 4.

| | Phenotype | Name | ORF | Description |
|---|-------------------------|--|--|--|
| Overexpression library, BODIPY | Polarized LDs | <i>LDM1</i> <i>RCY1</i> | <i>YER085C</i> <i>YJL204C</i> | Putative protein of unknown function F-box protein involved in recycling endocytosed proteins |
| | Less LDs | <i>BCK2</i> <i>DGK1</i> <i>IZH4</i> <i>SET4</i> <i>SFP1</i> <i>UGX2</i> | <i>YER167W</i> <i>YOR311C</i> <i>YOL101C</i> <i>YJL105W</i> <i>YLR403W</i> <i>YDL169C</i> | Serine-threonine-rich protein involved in PKC1 signaling Diacylglycerol kinase localized to the ER Membrane protein involved in zinc ion homeostasis Chromatin-associated protein regulating stress response Regulator of ribosomal protein gene expression Protein of unknown function |
| | More LDs | <i>AEP1</i> <i>BOI1</i> <i>CSE4</i> <i>HPT1</i> <i>NGR1</i> <i>NUP1</i> <i>PIF1</i> <i>RAD27</i> <i>SET1</i> <i>SPO11</i> <i>TIM11</i> <i>VIK1</i> <i>YDL129W</i> <i>YOR019W</i> <i>YOR072W-B</i> <i>ZDS1</i> | <i>YMR064W</i> <i>YBL085W</i> <i>YKL049C</i> <i>YDR399W</i> <i>YBR212W</i> <i>YOR098C</i> <i>YML061C</i> <i>YKL113C</i> <i>YHR119W</i> <i>YHL022C</i> <i>YDR322C-A</i> <i>YPL253C</i> <i>YDL129W</i> <i>YOR019W</i> <i>YOR072W-B</i> <i>YMR273C</i> | Protein required for expression of F1F0 ATPase subunit 9 Protein involved in polar growth Centromeric histone H3-like protein Dimeric hypoxanthine-guanine phosphoribosyltransferase RNA binding protein that negatively regulates growth rate FG-nucleoporin component of the nuclear pore complex DNA helicase 5' to 3' exonuclease, 5' flap endonuclease Histone methyltransferase, subunit of the COMPASS Meiosis-specific protein that initiates meiotic recombination Subunit e of mitochondrial F1F0-ATPase Subunit of a kinesin-14 heterodimeric motor with Kar3 Protein of unknown function Protein of unknown function Putative protein of unknown function Regulator of Swe1-dependent polarized growth |
| | Strong clustering | <i>CSF1</i> <i>FMP27</i> <i>LDO16</i> <i>MTC4</i> <i>PUL4</i> | <i>YLR087C</i> <i>YLR454W</i> <i>YMR148W</i> <i>YBR255W</i> <i>YNR063W</i> | Protein with similarity to lipid transfer protein Vps13 Protein with similarity to lipid transfer protein Vps13 Seipin partner, LD-vacuole tether together with Vac8 Protein of unknown function Putative zinc-cluster protein |
| | Partial clustering | <i>ACE2</i> <i>FAA1</i> <i>ICY1</i> <i>MEX67</i> <i>NIP100</i> <i>OLE1</i> <i>RGD1</i> <i>RTC4</i> <i>SCT1</i> <i>SLD2</i> <i>SPO77</i> <i>SPT23</i> <i>STP4</i> <i>TLD1</i> | <i>YLR131C</i> <i>YOR317W</i> <i>YMR195W</i> <i>YPL169C</i> <i>YPL174C</i> <i>YGL055W</i> <i>YBR260C</i> <i>YNL254C</i> <i>YBL011W</i> <i>YKL108W</i> <i>YLR341W</i> <i>YKL020C</i> <i>YDL048C</i> <i>YDR275W</i> | Transcription factor required for septum destruction Long chain fatty acyl-CoA synthetase Protein of unknown function Poly(A)RNA binding protein for nuclear mRNA export Large subunit of the dynactin complex Delta(9) fatty acid desaturase RhoGAP for Rho3 and Rho4 Protein of unknown function Acyltransferase for glycerolipid synthesis Replication initiation protein Protein required for spore wall formation Regulator of <i>OLE1</i> transcription Predicted transcription factor Protein that regulates lipolysis |
| Deletion/DAmP library x Ldm1-OE, BODIPY | Loss of LD polarization | <i>ARF1</i> <i>AVO2</i> <i>BNI1</i> <i>BRE5</i> <i>CAF16</i> <i>CDC50</i> <i>CHO2</i> <i>CIK1</i> <i>DRS2</i> <i>FAT1</i> <i>FOX2</i> <i>INO4</i> <i>KCS1</i> <i>LDB18</i> <i>LDO16</i> <i>MRPS12</i> <i>NCA3</i> <i>OPI9</i> <i>PUB1</i> <i>RAD51</i> <i>RAD52</i> <i>RPS27B</i> <i>SEC26</i> <i>TEC1</i> <i>VAM3</i> <i>VMA4</i> <i>VPS4</i> <i>VPS52</i> <i>VPS53</i> <i>VPS61</i> <i>VPS63</i> <i>YKR073C</i> <i>YPT6</i> <i>YPT7</i> | <i>YDL192W</i> <i>YMR068W</i> <i>YNL271C</i> <i>YNR051C</i> <i>YFL028C</i> <i>YCR094W</i> <i>YGR157W</i> <i>YMR198W</i> <i>YAL026C</i> <i>YBR041W</i> <i>YKR009C</i> <i>YOL108C</i> <i>YDR017C</i> <i>YLL049W</i> <i>YMR148W</i> <i>YNR036C</i> <i>YJL116C</i> <i>YLR338W</i> <i>YNL016W</i> <i>YER095W</i> <i>YML032C</i> <i>YHR021C</i> <i>YDR238C</i> <i>YBR083W</i> <i>YOR106W</i> <i>YOR332W</i> <i>YPR173C</i> <i>YDR484W</i> <i>YJL029C</i> <i>YDR136C</i> <i>YLR261C</i> <i>YKR073C</i> <i>YLR262C</i> <i>YML001W</i> | GTPase of the Ras superfamily TORC2 subunit Formin that nucleates formation of linear actin filaments Ubiquitin protease cofactor Part of CCR4-NOT regulatory complex Endosomal partner of phospholipid flippase Drs2p Phosphatidylethanolamine methyltransferase (PEMT) Kinesin-associated protein Trans-Golgi network phospholipid flippase Very long chain fatty acyl-CoA synthetase Multifunctional enzyme of peroxisomal beta-oxidation Transcription factor involved in phospholipid synthesis IP6 and IP7 kinase Component of the dynactin complex Seipin partner, LD-vacuole tether together with Vac8 Mitochondrial ribosomal protein Regulator of expression of F1F0 ATPase subunits 6 and 8 Dubious open reading frame, overlaps with <i>VRP1</i> Poly (A)+ RNA-binding protein Strand exchange protein involved in DNA DSB breaks Protein involved in homologous recombination Protein component of the small ribosomal subunit Essential beta-coat protein of the COPI coatomer Transcription factor Syntaxin-like vacuolar t-SNARE V-ATPase subunit E AAA-ATPase involved in MVB protein sorting Component of the GARP complex Component of the GARP complex Dubious open reading frame, overlaps with <i>RGP1</i> Putative protein of unknown function, overlaps with <i>YPT6</i> Putative protein of unknown function Rab family GTPase Rab family GTPase |