## Supporting Figures and Tables

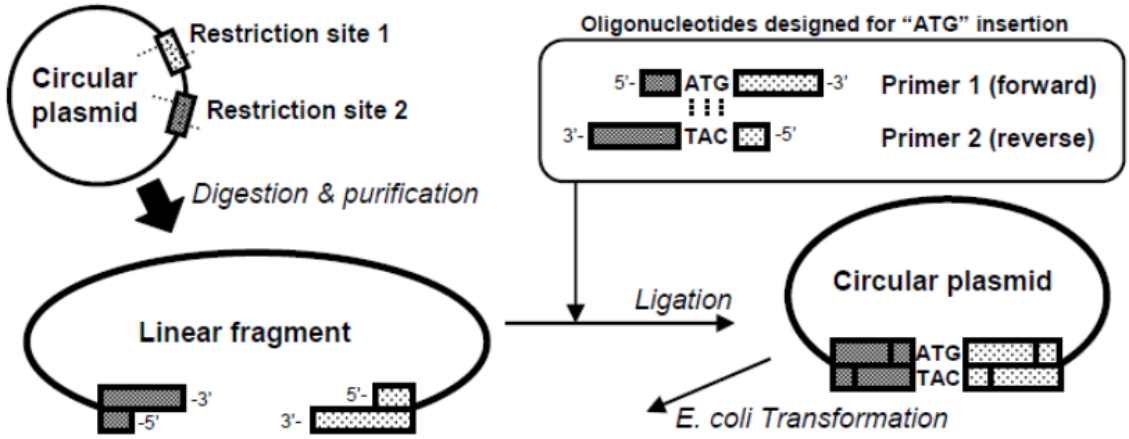


**Figure S1. Schematic illustration of the one-step construction method for plasmids (OSCoM-P).** The digested linear fragments of the plasmids were ligated with the designed primers at a dry weight ratio of 1:1–1:10 (linear plasmid:each primer). The reaction solution was directly transformed into *E. coli* DH5α competent cells (Toyobo). The purchased oligonucleotides were dissolved in $dH_2O$ at 10 ng/μL before use. TE buffer was not used because OSCoM-P was severely inhibited by the presence of TE buffer (data not shown). Maximum length of fragments to be inserted into plasmids using OSCoM-P is 45 bp (data not shown).

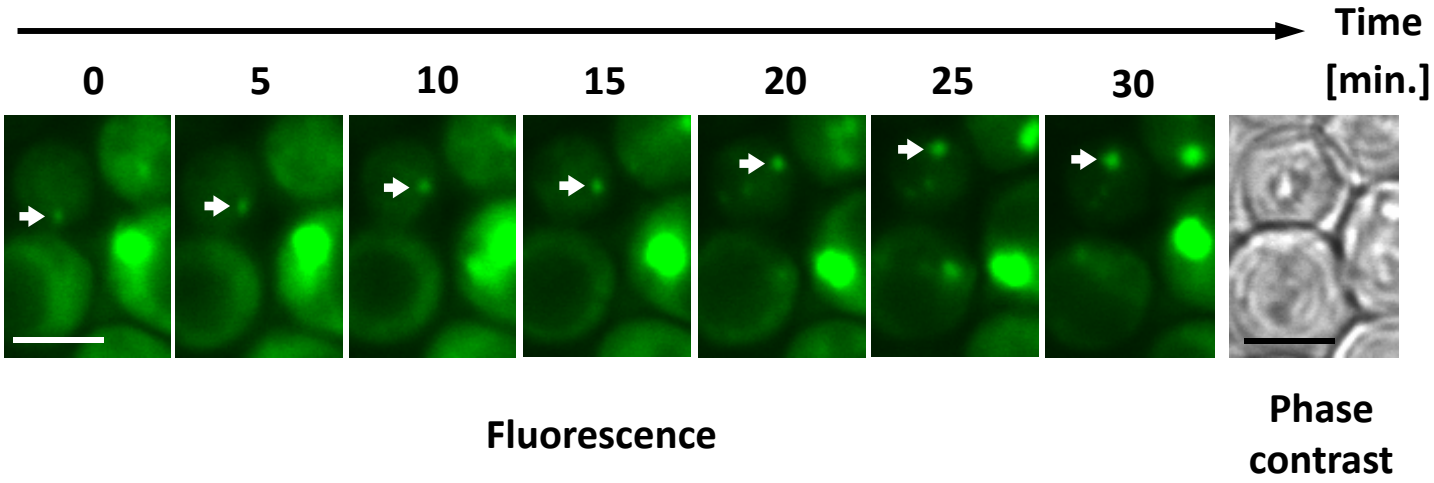


**Figure S2. Time-dependent localization change of the eno(1–28) fragment fused to EGFP.**
Scale bar: 5 μm.

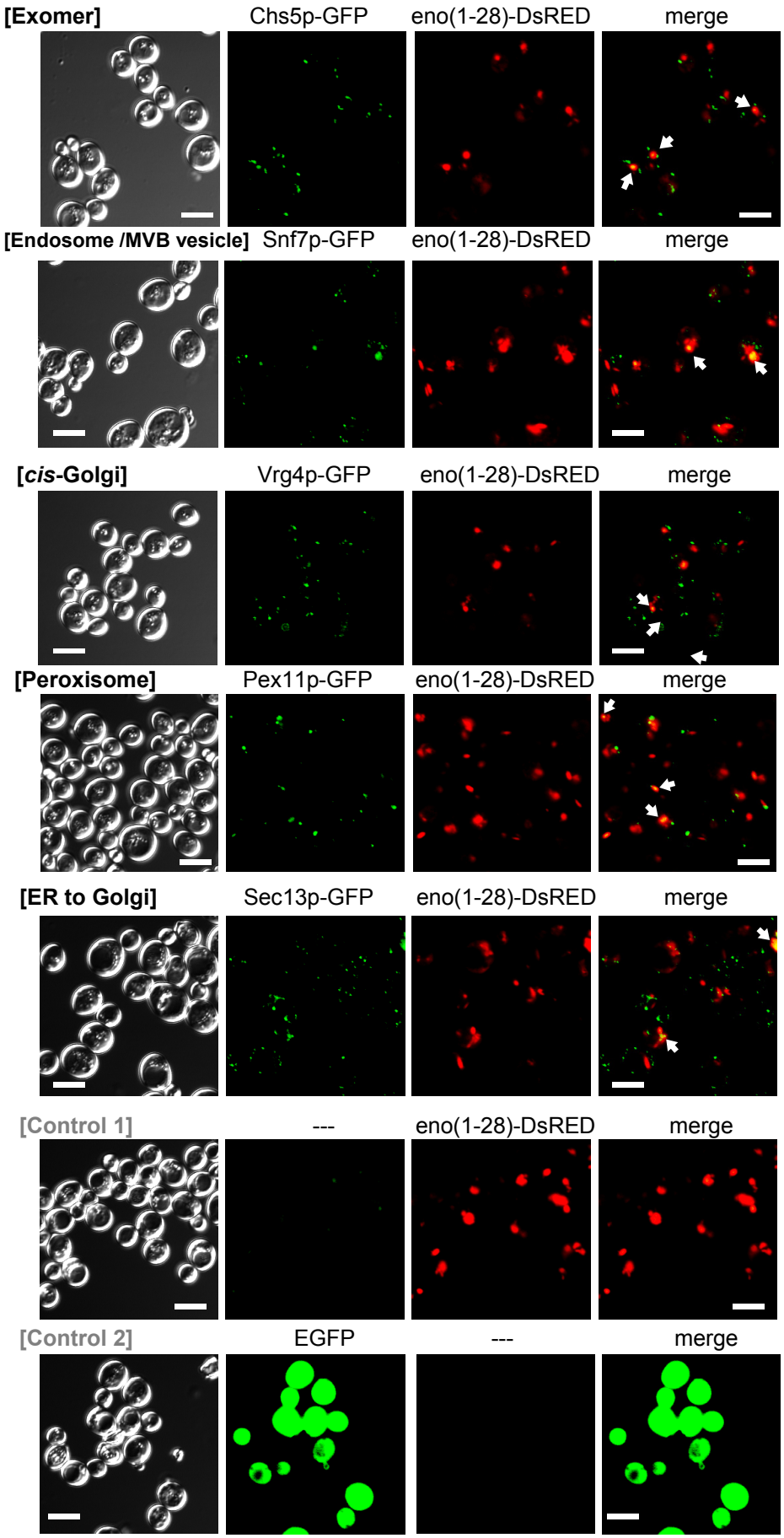


**Figure S3. Co-localization of the enolase fragment conjugated to DsRED and the organelle markers conjugated to GFP (continued from Fig. 3).** Control 1, wild-type cells transformed with pULR-eno(1–28); control 2, wild-type cells transformed with pUL-ATG-EGFP. Scale bar: 5 μm.

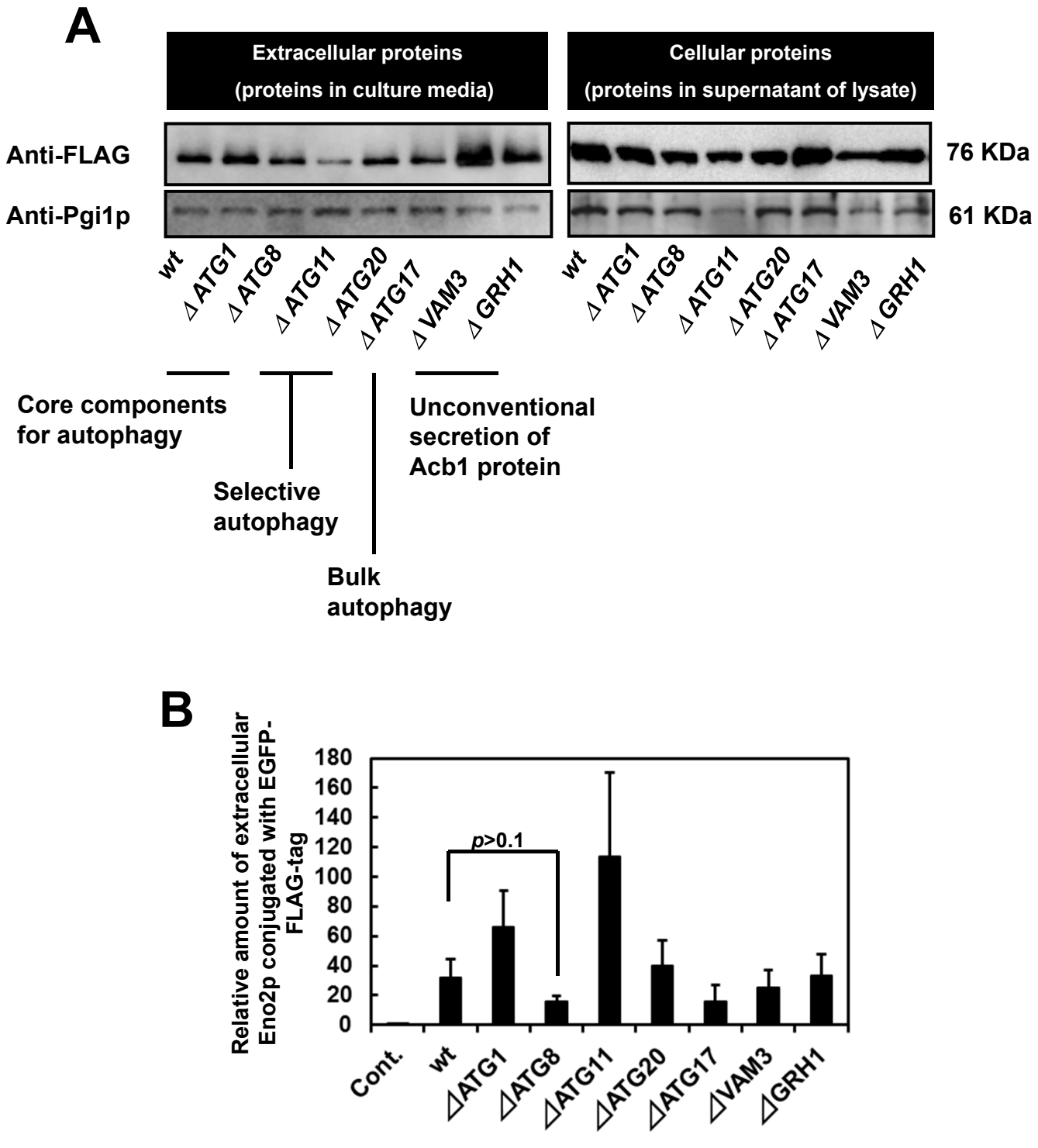


**Figure S4. Autophagy independency of Eno2p and Pgi1p secretion.** A: Western blots. B: Calculated amounts of secreted Eno2p by comparison to the Pgi1p secreted. Values are the mean ± SEM of 3 independent experiments.

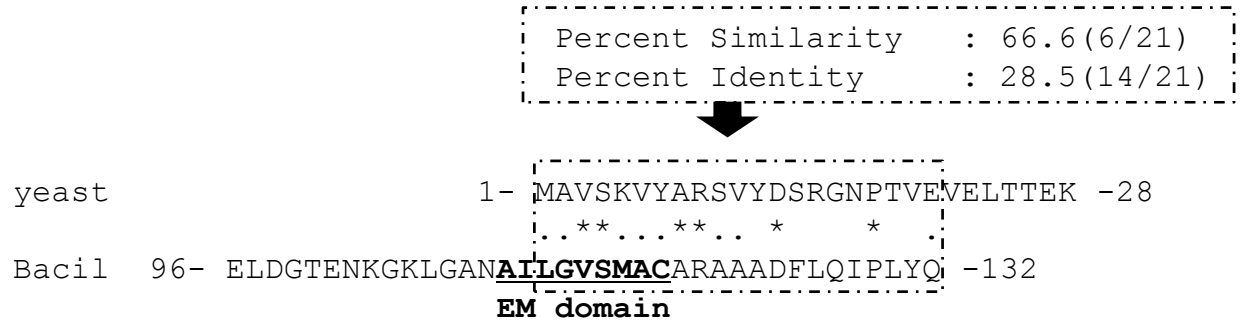


**Figure S5. Similarity of eno(1-28) region with EM domain.** Percent similarity and percent identity between the two sequences in the box with dotted line are shown. Yeast, *S. cerevisiae* enolase (1-28) aa sequence; Bacil, *Bacillus subtilis* enolase (96-132) aa sequence including EM domain (56); underline, EM domain; asterisk, identical amino acid residues; dot, similar amino acid residues.

## Table S1. List of identified noncovalently-bound cell surface proteins

The data is available in the PRIDE database (57, www.ebi.ac.uk/pride) under accession number 26880. The data was converted using PRIDE Converter (58, http://pride-converter.googlecode.com).

| Cellular process | | | Accession | SGDID | Name | Description | # AAs | MW [kDa] | calc. pI | ΣCoverage | Σ# PSMs | Σ# Peptides |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Metabolism*** | Glycolysis | | YHR174W | S000001217 | ENO2 | Enolase II, a phosphopyruvate hydratase | 437 | 46.9 | 6.0 | 31 | 41 | 9 |
| | | | YGR192C | S000003424 | TDH3 | Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3 | 332 | 35.7 | 7.0 | 40 | 53 | 8 |
| | | | YCR012W | S000000605 | PGK1 | 3-phosphoglycerate kinase | 416 | 44.7 | 7.6 | 32 | 28 | 8 |
| | | | YJL052W | S000003588 | TDH1 | Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1 | 332 | 35.7 | 8.3 | 32 | 32 | 7 |
| | | | YDR050C | S000002457 | TPI1 | Triose phosphate isomerase | 248 | 26.8 | 6.0 | 35 | 38 | 6 |
| | | | YJR009C | S000003769 | TDH2 | Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2 | 332 | 35.8 | 7.0 | 26 | 33 | 6 |
| | | | YGR254W | S000003486 | ENO1 | Enolase I, a phosphopyruvate hydratase | 437 | 46.8 | 6.6 | 20 | 32 | 6 |
| | | | YKL152C | S000001635 | GPM1 | Tetrameric phosphoglycerate mutase | 247 | 27.6 | 8.8 | 26 | 21 | 5 |
| | | | YAL038W | S000000036 | CDC19 | Pyruvate kinase | 500 | 54.5 | 7.7 | 13 | 10 | 5 |
| | | | YBR196C | S000000400 | PGI1 | Phosphoglucose isomerase | 554 | 61.3 | 6.5 | 10 | 6 | 4 |
| | | | YKL060C | S000001543 | FBA1 | Fructose 1,6-bisphosphate aldolase | 359 | 39.6 | 5.8 | 13 | 5 | 3 |
| | Amino acid biosynthesis | Methionine biosynthesis | YER091C | S000000893 | MET6 | Cobalamin-independent methionine synthase | 767 | 85.8 | 6.5 | 17 | 21 | 10 |
| | | Isoleucine biosynthesis | YIL051C | S000001313 | MMF1 | Mitochondrial protein required for transamination of isoleucine | 145 | 15.9 | 9.3 | 49 | 15 | 5 |
| | | Methionine and threonine biosynthesis | YDR158W | S000002565 | HOM2 | Aspartic beta semi-aldehyde dehydrogenase | 365 | 39.5 | 6.7 | 19 | 13 | 5 |
| | | Glycine catabolic process | YAL044C | S000000042 | GCV3 | H subunit of the mitochondrial glycine decarboxylase complex | 170 | 18.8 | 4.7 | 30 | 12 | 4 |
| | | Lysine biosynthesis | YIL094C | S000001356 | LYS12 | Homo-isocitrate dehydrogenase | 371 | 40.0 | 8.0 | 15 | 7 | 4 |
| | | Histidine biosynthesis | YOR202W | S000005728 | HIS3 | Imidazoleglycerol-phosphate dehydratase | 220 | 23.8 | 6.4 | 15 | 5 | 2 |
| | TCA cycle | | YKL085W | S000001568 | MDH1 | Mitochondrial malate dehydrogenase | 334 | 35.6 | 8.5 | 10 | 3 | 2 |
| | Pentose phosphate pathway | | YPR074C | S000006278 | TKL1 | Transketolase | 680 | 73.8 | 7.0 | 4 | 3 | 2 |
| | Alcoholic fermentation | | YLR044C | S000004034 | PDC1 | Pyruvate decarboxylase | 563 | 61.5 | 6.2 | 33 | 36 | 13 |
| | Fatty acid metabolism | | YGR037C | S000003269 | ACB1 | Acyl-CoA-binding protein | 87 | 10.1 | 4.9 | 59 | 7 | 3 |
| ***Protein binding*** | | | YAL005C | S000000004 | SSA1 | ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport | 642 | 69.6 | 5.1 | 5 | 5 | 3 |
| | | | YMR186W | S000004798 | HSC82 | Cytoplasmic chaperone of the Hsp90 family | 705 | 80.8 | 4.8 | 4 | 8 | 2 |
| | | | YDR155C | S000002562 | CPR1 | Cytoplasmic peptidyl-prolyl cis-trans isomerase | 162 | 17.4 | 7.4 | 17 | 6 | 2 |
| | | | YLL050C | S000003973 | COF1 | Cofilin (Actin binfing) | 143 | 15.9 | 5.2 | 22 | 4 | 2 |
| | | | YBR109C | S000000313 | CMD1 | Calmodulin | 147 | 16.1 | 4.3 | 21 | 3 | 2 |
| | | | YJL034W | S000003571 | KAR2 | ATPase involved in protein import into the ER | 682 | 74.4 | 4.9 | 3 | 2 | 2 |
| ***Homeostasis*** | | | YML028W | S000004490 | TSA1 | Thioredoxin peroxidase | 196 | 21.6 | 5.1 | 31 | 10 | 4 |
| | | | YLR043C | S000004033 | TRX1 | Cytoplasmic thioredoxin isoenzyme | 103 | 11.2 | 4.9 | 49 | 8 | 4 |
| | | | YGR209C | S000003441 | TRX2 | Cytoplasmic thioredoxin isoenzyme | 104 | 11.2 | 4.9 | 49 | 8 | 4 |
| | | | YFL014W | S000001880 | HSP12 | Heat Shock Protein | 109 | 11.7 | 5.4 | 23 | 4 | 3 |
| | | | YHR008C | S000001050 | SOD2 | Mitochondrial manganese superoxide dismutase | 233 | 25.8 | 8.5 | 17 | 2 | 2 |
| ***Translation*** | | | YJL138C | S000003674 | TIF2 | Translation initiation factor eIF4A | 395 | 44.7 | 5.1 | 10 | 8 | 3 |
| | | | YEL034W | S000000760 | HYP2 | Translation elongation factor eIF-5A | 157 | 17.1 | 5.0 | 19 | 12 | 2 |
| | | | YDR385W | S000002793 | EFT2 | Elongation factor 2 | 842 | 93.2 | 6.3 | 3 | 2 | 2 |
| | | | YDR382W | S000002790 | RPP2B | Ribosomal protein P2 beta | 110 | 11.0 | 4.1 | 24 | 2 | 2 |
| ***Folding*** | | | YCL043C | S000000548 | PDI1 | Protein disulfide isomerase | 522 | 58.2 | 4.5 | 27 | 28 | 10 |
| ***Signaling*** | | | YMR116C | S000004722 | ASC1 | G-protein beta subunit and guanine nucleotide dissociation inhibitor for Gpa2p | 319 | 34.8 | 6.2 | 34 | 28 | 8 |
| ***Traffic*** | Endocytosis | | YIL041W | S000001303 | GVP36 | BAR domain-containing protein | 326 | 36.6 | 5.0 | 20 | 6 | 4 |
| ***Unknown*** | | | YOL154W | S000005514 | ZPS1 | Zinc- and pH-regulated surface protein | 249 | 27.5 | 5.0 | 27 | 17 | 5 |
| | | | YDR519W | S000002927 | FPR2 | Membrane-bound peptidyl-prolyl cis-trans isomerase (PPIase), | 135 | 14.5 | 5.5 | 34 | 8 | 3 |
| | | | YPL225W | S0000061 | YPL225W | Unknown | 146 | 17.4 | 5.3 | 16 | 4 | 2 |

# Table S2. Primers used in this research (continuing)

| Plasmid | Oligo name | Description | Sequence (5'-3') |
|---|---|---|---|
| pULI1 | GAP-Pro-F | Primer for amplification of MCS-t*GAPDH* (forward) | CTTAAACTTCTTAAATTCTACTTTTATAGTTAGTC |
| | *Kpn*I-TGAP-R | Primer for amplification of MCS-t*GAPDH* (reverse) | ATGCTGGTACCTCAATCAATGAATCGAAAATGTCATTAAAATAG |
| pUL-ATG-EGFP | *Ec*ATG*Xh*OSCoM_F | Oligonucleotide for OSCoM (forward) | AATTCATGC |
| | *Ec*ATG*Xh*OSCoM_R | Oligonucleotide for OSCoM (reverse) | TCGAGCATG |
| pRS423-ATG-EGFP | *GAPDH* promoter -F | Primer for amplification of p*GAPDH-EGFP*-FLAGtag-t*GAPDH* (forward) | GGTACGGGATTCACCAGTTCTCACACGGAACACCAC |
| | *GAPDH* terminator -R | Primer for amplification of p*GAPDH-EGFP*-FLAGtag-t*GAPDH* (forward) | ATAAGAATGCGGCCGCTCAATCAATGAATCGAAAATGTCAT |
| pUL-ATG-DsRED | *DsRed-EcoR1*ATG*Xho1* F | Primer for amplification of *DsRED* from pKRD4 (forward) | TAAACAGAATTCATGCTCGAGGGTGGATCTGGTGGCGACAACACCGA |
| | *DsRed-Sal1* R | Primer for amplification of *DsRED* from pKRD4 (reverse) | GTTCAACCAAGTCGACTTACTGGGAGCCGGAGTGGCGGGCCTCG |
| | seq*DsRED*(27-34) | Primer for sequencing *DsRED* | CGAGTTCATGCGCTTCAAGG |
| pULGI2 | pULSG1mcskaiF | Oligonucleotide for OSCoM (forward) | AATTCGGATCCCGGCTCGAGCGGAGATCTCGGGAGCTCCCGG |
| | pULSG2mcskaiR | Oligonucleotide for OSCoM (reverse) | TCGACCGGGAGCTCCCGAGATCTCCGCTCGAGCCGGGATCCG |
| pULGI2-ATG-HA | ATG-HAtagF (pULIG2) | Oligonucleotide for OSCoM (forward) | AATTCATGTACCCATACGATGTTCCAGATTACGCTG |
| | ATG-HAtagR (pULIG2) | Oligonucleotide for OSCoM (reverse) | GATCCAGCGTAATCTGGAACATCGTATGGGTACATG |
| pULGI2-ENO2/ pULGI2-HA-ENO2 | pULIG-eno2 F (*BamH1*) | Primer for amplification of *ENO2* (forward) | GAATTCGGATCCATGGCTGTCTCTAAAGTTTACGCT |
| | pULIG-eno2all R (*Sac1*) | Primer for amplification of *ENO2* (reverse) | CGACCGGGAGCTCCAACTTGTCACCGTGGTGGAAGT |
| | eno2-1 F | Primers for cloning *ENO2* from genome and for sequencing | ATACCAAGTCAGCATACACC |
| | eno2-2 F | | TTATCTTCCTACCAGAGTTG |
| | eno2-3 F | | AAGTCGAATTAACCACCGAA |
| | eno2-4 F | | TCTTGTTGTCTTTGGATGGT |
| | eno2-5 F | | GTTCCGAAGTTTACCACAAC |
| | eno2-6 F | | TTCAAGGACGGTAAGTACGA |
| | eno2-7 F | | ACTGGGAAGCTTGGTCTCAC |
| | eno2-8 F | | CTGGTGAAACTGAAGACACT |
| | eno2-9 F | | TTTTCAAAGACTCGTGCTGT |
| | eno2-10 R | | ACACGTATTCTTGTATGACC |
| pULGI2-CDC19 | *CDC19-BamH1* F | Primer for amplification of *CDC19* (forward) | AACAGAATTCGGATCCATGTCTAGATTAGAAAGATTGACCTCATTA |
| | *CDC19-Xho1* R | Primer for amplification of *CDC19* (reverse) | GAGATCTCCGCTCGAGAACGGTAGAGACTTGCAAAGTGTTGGAGTG |
| | *CDC19* (291-310) seqF | Primers for sequencing *CDC19* | CGATGTTGACTACCCAATCC |
| | *CDC19* (681-700) seqF | | CTTGGGTGAACAAGGTAAGG |
| | *CDC19* (1078-1097) seqF | | GCTTACTTGCCAAACTACGA |
| | *CDC19* (1306-1325) seqF | | TACAGAGGTGTCTTCCCATT |
| pULGI2-PYK2 | *PYK2-BamH1* F | Primer for amplification of *PYK2* (forward) | AACAGAATTCGGATCCATGCCAGAGTCCAGATTGCAGAGACTAGCT |
| | *PYK2-Xho1* R | Primer for amplification of *PYK2* (reverse) | GAGATCTCCGCTCGAGGAATTCTTGACCAACAGTAGAAATGCGTAA |
| | *PYK2* (211-230) seqF | Primers for sequencing *PYK2* | AAATCGGAACAGCAATTCCC |
| | *PYK2* (592-611) seqF | | ATGAAGGACTTGCAATTCGG |
| | *PYK2* (993-1012) seqF | | TATGCTTTCTGGAGAAACGG |
| | *PYK2* (1336-1355) seqF | | TATGAACCGAAACGCCTAGA |
| pULGI2-GPM1 | *GPM1-BamH1* F | Primer for amplification of *GPM1* (forward) | AACAGAATTCGGATCCATGCCAAAGTTAGTTTTAGTTAGACACGGT |
| | *GPM1-Xho1* R | Primer for amplification of *GPM1* (reverse) | GAGATCTCCGCTCGAGTTTCTTACCTTGGTTGGCAACAGCAGCGGC |
| | *GPM1* (281-300) seqF | Primer for sequencing *GPM1* | AAGGTAAGGACAAGGCTGAA |
| pULGI2-TPI1 | *TPI1-BamH1* F | Primer for amplification of *TPI1* (forward) | AACAGAATTCGGATCCATGGCTAGAACTTTCTTTGTCGGTGGTAAC |
| | *TPI1-Xho1* R | Primer for amplification of *TPI1* (reverse) | GAGATCTCCGCTCGAGGTTTCTAGAGTTGATGATATCAACAAATTC |
| | *TPI1* (243-262) seqF | Primer for sequencing *TPI1* | CCAAATCAAGGATGTTGGTG |
| pULGI2-PGI1 | *PGI1-BamH1* F | Primer for amplification of *PGI1* (forward) | AACAGAATTCGGATCCATGTCCAATAACTCATTCACTAACTTCAAA |
| | *PGI1-Xho1* R | Primer for amplification of *PGI1* (reverse) | AACAGAATTCGGATCCATGACTGTTACTACTCCTTTTGTGAATGGT |
| | *PGI1* (252-271) seqF | Primers for sequencing *PGI1* | TAACGTCACCGGTTTGAGAG |
| | *PGI1* (697-716) seqF | | GCCAAGAACTGGTTCTTGTC |
| | *PGI1* (1178-1197) seqF | | CTACCAACGCTCAACACTCT |
| pULGI2-PGK1 | *PGK1-BamH1* F | Primer for amplification of *PGK1* (forward) | AACAGAATTCGGATCCATGTCTTTATCTTCAAAGTTGTCTGTCCAA |
| | *PGK1-Xho1* R | Primer for amplification of *PGK1* (reverse) | GAGATCTCCGCTCGAGTTTCTTTTCGGATAAGAAAGCAACACCTGG |
| | *PGK1* (221-240) seqF | Primers for sequencing *PGK1* | AATACTCTTTGGCTCCAGTT |
| | *PGK1* (510-529) seqF | | TCACTCTTCTATGGTCGGTT |
| | *PGK1* (848-867) seqF | | ACTTCATCATTGCTGATGCT |
| pULGI2-FBA1 | *FBA1-BamH1* F | Primer for amplification of *FBA1* (forward) | AACAGAATTCGGATCCATGGGTGTTGAACAAATCTTAAAGAGAAAG |
| | *FBA1-Xho1* R | Primer for amplification of *FBA1* (reverse) | GAGATCTCCGCTCGAGTAAAGTGTTAGTGGTACGGAAAGTTTCCAA |
| | *FBA1* (296-315) seqF | Primers for sequencing *FBA1* | CAGCTTACGGTATCCCAGTT |
| | *FBA1* (627-646) seqF | | TTTGCACCCAATCTCTCCAA |
| pUL-eno(1-17) | *Eno2*(-17)_*Xho1*R | Primers for cloning *ENO2* fragments | CACCAGATCCACCCTCGAGGTTACCACGGGAGTCGTAGACGGATCTAGC |
| pUL-eno(1-28)/ pULR-eno(1-28) | *Eno2*(-28)_*Xho1*R | | CAGATCCACCCTCGAGCTTTTCGGTGGTTAATTCGACTT |
| pUL-eno(1-30) | *Eno2*(-30)_*Xho1*R | | CACCAGATCCACCCTCGAGAACACCCTTTTCGGTGGTTAATTCGACTTC |
| pUL-eno(1-50) | *Eno2*(-50)_*Xho1*R | | CACCAGATCCACCCTCGAGTCTCATTTCCAAAGCTTCGT |
| pUL-eno(1-110) | *Eno2*(-110)_*Xho1*R | | CACCAGATCCACCCTCGAGAGCGTTAGCACCCAACTTGG |
| pUL-eno(1-169) | *Eno2*(-169)_*Xho1*R | | AGATCCACCCTCGAGTTCTTGCAAAGCCAAAGCACC |
| GAPDH promotor | pGAP_F | Primer for sequencing | AGACGGTAGGTATTGATTGTAATTCTG |

## Table S2. Primers used in this research (continued)

| Plasmid | Oligo name | Description | Sequence (5'-3') |
|---|---|---|---|
| p413-ADH-TLG2 | *BamH1-TLG2* F | Primer for amplification of *TLG2* (forward) | AGAACTAGTGAATTCATGTTTAGAGATAGAACTAATTTAT |
| | *Xho1-TLG2* R | Primer for amplification of *TLG2* (reverse) | ACATGACTCGAGTCAAAGTAGGTCATCCAAAGCATCATTC |
| | ADH pro F | Primer for sequencing p413-ADH plasmid | ATGAGCAACGGTATACGG |
| | *TLG2* (140-164) seqF | Primers for sequencing *TLG2* | ACGATATATCGGCCAGATTGACAGA |
| | *TLG2* (444-466) seqF | | GCAATTAAGTCGAGAAGAGCTGA |
| | *TLG2* (786-807) seqF | | AGAAGTGAGCACTATTTTCAGG |
| *ΔTLG2* (genome) | *TLG2* (coloP) F | Primers for checking the sizes of cording regions | GCAAGACAGGAAAGTCTCCAA |
| | *TLG2* (coloP) R | | GCAACAGGTCATATGAACGCT |
| *KanMX4* (gene) | *KanB*-R | Primers for checking genotypes | CTGCAGCGAGGAGCCGTAAT |
| *ΔSEC22* (genome) | *SEC22* (coloP) F | | AATTTTCAACCAAACGTGTTGTACT |
| *ΔGOS1* (genome) | *GOS1* (coloP) F | | AAAGATGCTTATGAAAAATCTCACG |
| *ΔPEP12* (genome) | *PEP12* (coloP) F | | TGCCTTAGCTGGAAAATTGTATTTA |
| *ΔVPS51* (genome) | *VPS51* (coloP) F | | AATCTACCCAGGCCTTAAAAGTATG |
| *ΔBTN2* (genome) | *BTN2* (coloP) F | | CGAGAGTTGTATCCAGTTTTCTTGT |
| *ΔSNC2* (genome) | *SNC2* (coloP) F | | AGTGATCTTGGTCACATGATATACG |
| *ΔSNX4* (genome) | *SNX4* (coloP) F | | AATAACAGTTCAAAAATCTATGCCG |
| *ΔSSO1* (genome) | *SSO1* (coloP) F | | CACACTAACGACAAAAGACGATATG |
| *ΔSSO2* (genome) | *SSO2* (coloP) F | | TACCCATAAGAGAGCTGGAATAGTG |
| *ΔATG1* (genome) | *ATG1* (coloP) F | | AAGTTAAGTACCAAGGCCATCTTTT |
| *ΔATG20* (genome) | *ATG20* (coloP) F | | ATAAGGCTTGGCTTATTTGCTTACT |
| *ΔATG17* (genome) | *ATG17* (coloP) F | | CTTGAATTATTATCTTCCTCATCGC |

## Table S3. List of genes and proteins used in this research.

| Category | Accession | Name | Description |
|---|---|---|---|
| ***Organelle marker proteins*** | YGL008C | PMA1 | Plasma membrane H+-ATPase, pumps protons out of the cell |
| | TDL116W | NUP84 | Subunit of the nuclear pore complex (NPC) |
| | YKL029C | MAE1 | Mitochondrial malic enzyme |
| | YLR330W | CHS5 | Component of the exomer complex |
| | YLR025W | SNF7 | One of four subunits of the endosomal sorting complex required for transport III (ESCRT-III) |
| | YGL225W | VRG4 | Golgi GDP-mannose transporter; regulates Golgi function and glycosylation in Golgi |
| | YOL147C | PEX11 | Peroxisomal membrane protein required for medium-chain fatty acid oxidation and peroxisome proliferation |
| | YLR208W | SEC13 | Component of the Nup84 nuclear pore sub-complex, the Sec13p-Sec31p complex of the COPII vesicle coat, and the SEA (Seh1-associated) complex; required for vesicle formation in ER to Golgi transport and nuclear pore complex organization |
| ***SNAREs*** | YPL232W | SSO1 | Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane and in vesicle fusion during sporulation |
| | YMR183C | SSO2 | Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane |
| | YLR268W | SEC22 | R-SNARE protein; assembles into SNARE complex with Bet1p, Bos1p and Sed5p; cycles between the ER and Golgi complex; involved in anterograde and retrograde transport between the ER and Golgi |
| | YOR327C | SNC2 | Vesicle membrane receptor protein (v-SNARE) involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane |
| | YOL018C | TLG2 | Syntaxin-like t-SNARE that forms a complex with Tlg1p and Vti1p and mediates fusion of endosome-derived vesicles with the late Golgi |
| | YGR142W | BTN2 | v-SNARE binding protein that facilitates specific protein retrieval from a late endosome to the Golgi |
| | YOR036W | PEP12 | Target membrane receptor (t-SNARE) for vesicular intermediates traveling between the Golgi apparatus and the vacuole |
| | YKR020W | VPS51 | Component of the GARP (Golgi-associated retrograde protein) complex,which is required for the recycling of proteins from endosomes to the late Golgi |
| | YHL031C | GOS1 | v-SNARE protein involved in Golgi transport, homolog of the mammalian protein GOS-28/GS28 |
| | YOR106W | VAM3 | Syntaxin-like vacuolar t-SNARE that functions with Vam7p in vacuolar protein trafficking; mediates docking/fusion of late transport intermediates with the vacuole |
| ***Transport*** | YDR517W | GRH1 | Acetylated, cis-golgi localized protein involved in ER to Golgi transport; homolog of human GRASP65; forms a complex with the coiled-coil protein Bug1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes |
| ***Autohagy-related proteins*** | YGL180W | ATG1 | Protein ser/thr kinase required for vesicle formation in autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway |
| | YBL078C | ATG8 | Component of autophagosomes and Cvt vesicles; undergoes conjugation to phosphatidylethanolamine (PE) |
| | YPR049C | ATG11 | Adapter protein for pexophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway |
| | YLR423C | ATG17 | Scaffold protein responsible for phagophore assembly site organization; regulatory subunit of an autophagy-specific complex that includes Atg1p and Atg13p |
| | YDL113C | ATG20 | Sorting nexin family member required for the cytoplasm-to-vacuole targeting (Cvt) pathway and for endosomal sorting |
| ***Cell wall protein*** | YDR077W | SED1 | Major stress-induced structural GPI-cell wall glycoprotein in stationary-phase cells |

## Supporting References


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58. **Barsnes H, Vizcaíno JA, Eidhammer I, Martens L.** 2009. PRIDE Converter: making proteomics data-sharing easy. Nat. Biotechnol. **27:** 598-599.