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Supplementary

**Supplementary Table 1**

Nutrient supplements for SC medium

| Supplement       | Final conc. (mg L\(^{-1}\)) | Supplement       | Final conc. (mg L\(^{-1}\)) |
|------------------|------------------------------|------------------|------------------------------|
| Adenine          | 18                           | Leucine          | 260                          |
| Alanine          | 76                           | Lysine           | 76                           |
| Arginine         | 76                           | Methionine       | 76                           |
| Asparagine       | 76                           | p-aminobenzoic   | 8                            |
|                  |                              | acid potassium   |                              |
|                  |                              | salt             |                              |
| Aspartic acid    | 76                           | Phenylalanine    | 76                           |
| Cysteine         | 76                           | Proline          | 76                           |
| Glutamic acid    | 76                           | Serine           | 76                           |
| Glutamine        | 76                           | Threonine        | 76                           |
| Glycine          | 76                           | Tryptophan       | 76                           |
| Histidine        | 211                          | Tyrosine         | 76                           |
| Myo-inositol     | 76                           | Uracil           | 22                           |
| Isoleucine       | 76                           | Valine           | 76                           |
| Primer name   | 5’ – 3’ Sequence                                      |
|--------------|------------------------------------------------------|
| ABETA-F      | TTTCTCTAGGGATCCATGGATGCAGAATTC                       |
| ABETA-R      | AGACATGTGGTCGACCGCTATGACAACACC                       |
| ABETA-R-S    | AGACATGTGGTCGACTTACGCTATGACAACACC                    |
| ABETA-R-MUT  | AGACATGTGGTCGACTTACGCTATGACAACACC                    |
| ABETA-40-R   | GTTTAGTGTCGACCGACACACCCCGACCCAC                     |
| ABETA-40-R-S | GTTTAGTGTCGACCGACACACCCCGACCCAC                     |
| ESC-URA-F    | TCATGGCTAGCAGTCAGTGACGGATTAGAAG                    |
| ESC-URA-R    | CGTATTACGTCTAGAGGTTTTTCTCCTT                       |
## Supplementary Table 3

Mutants exhibiting weak/faint Aβ42EGFP-associated fluorescence

| ORF     | Gene Name | Description                                                                                                                                                                                                 |
|---------|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| YDL234C | AAD4      | Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response                                                                 |
| YGL234W | ADE5,7    | Bifunctional enzyme of the 'de novo' purine nucleotide biosynthetic pathway, contains aninomimidazole ribotide synthetase and glycinamide ribotide synthetase activities |
| YDR408C | ADE8      | Phosphoribosylglycinamide transformylase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway                                                                                           |
| YDR226W | ADK1      | Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence                                                                              |
| YBR288C | APM3      | Mu3-like subunit of the clathrin associated protein complex (AP-3); functions in transport of alkaline phosphatase to the vacuole via the alternate pathway                                                                 |
| YMR119W | ASI1      | Putative integral membrane E3 ubiquitin ligase; genetic interactions suggest a role in negative regulation of amino acid uptake                                                                                  |
| YCR068W | ATG15     | Lipase, required for intravacuolar lysis of autophagic bodies; located in the endoplasmic reticulum membrane and targeted to intravacuolar vesicles during autophagy via the multivesicular body (MVB) pathway |
| YIL180C | ATP12     | Molecular chaperone, required for the assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase                                                                               |
| YML081C-A| ATP18     | Subunit of the mitochondrial F1F0 ATP synthase, which is a large enzyme complex required for ATP synthesis; termed subunit I or subunit j; does not correspond to known ATP synthase subunits in other organisms |
| YDR298C | ATP5      | Subunit 5 of the stator stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; homologous to bovine subunit OSCP (oligomycin sensitivity-conferring protein) |
| YER177W | BMH1      | 14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes including exocytosis and vesicle transport, Ras/MAPK signaling during pseudohypal development, rapamycin-sensitive signaling, and others |
| YNR027W | BUD17     | Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern                                                                             |
| YDR241W | BUD26     | Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 1% of ORF overlaps the verified gene SNU56; diploid mutant displays a weak budding pattern phenotype in a systematic assay |
| YCR063W | BUD31     | Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern                                                                             |
| YKL005C | BYE1      | Negative regulator of transcription elongation, contains a TFIIS-like domain and a PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably binds RNA polymerase II large subunit |
| YER061C | CEM1      | Mitochondrial beta-keto-acyl synthase with possible role in fatty acid synthesis; required for mitochondrial respiration                                                                                        |
| YBR003W | COQ1      | Hexaprenyl pyrophosphate synthetase, catalyzes the first step in ubiquinone (coenzyme Q) biosynthesis                                                                                                         |
| YNR041C | COQ2      | Para hydroxybenzoate: polyphenol transferase, catalyzes the second step in ubiquinone (coenzyme Q) biosynthesis                                                                                             |
| YLR201C | COQ9      | Mitochondrial inner membrane protein required for ubiquinone (coenzyme Q) biosynthesis, which in turn is required for respiratory growth; exhibits genetic interaction with ABC1, suggesting a possible common function |
| YGL263W | COS12     | Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomERICally-encoded proteins                                                                                        |
| YPL132W | COX11     | Mitochondrial inner membrane protein required for delivery of copper to the Cox1p subunit of cytochrome c oxidase; association with mitochondrial ribosomes suggests that copper delivery may occur during translation of Cox1p |
YLl018C  COX19  Protein required for cytochrome c oxidase assembly, located in the cytosol and mitochondrial intermembrane space; putative copper metallochaperone that delivers copper to cytochrome c oxidase

YHR051W  COX6  Subunit VI of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; expression is regulated by oxygen levels

YBR036C  CSG2  Endoplasmic reticulum membrane protein, required for mannosylation of inositolphosphorylceramide and for growth at high calcium concentrations

YJR048W  CYC1  Cytochrome c, isoform 1; electron carrier of the mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c oxidoreductase to cytochrome c oxidase during cellular respiration

YBR112C  CYC8  General transcriptional corepressor, acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters

YDL17W  CYK3  SH3-domain protein located in the mother-bud neck and the cytokinetic actin ring; mutant phenotype and genetic interactions suggest a role in cytokinesis

YOR065W  CYT1  Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex

YDR320C-A  DAD4  Essential subunit of the DASH microtubule ring complex, couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; is transferred to the kinetochore prior to mitosis

YKR034W  DAL80  Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-binding family, forms homodimers and heterodimers with Deh1p

YDL101C  DUN1  Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and Sml1p, and transient G2/M arrest after DNA damage; also regulates postreplicative DNA repair

YPJ023C  EAF3  Esa1p-associated factor, nonessential component of the NuA4 acetyltransferase complex, homologous to Drosophila dosage compensation protein MSL3

YNL136W  EAF7  Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-terminal tails of histones H4 and H2A

YKL204W  EAP1  eIF4E-associated protein, binds eIF4E and inhibits cap-dependent translation, also functions independently of eIF4E to maintain genetic stability; plays a role in cell growth, implicated in the TOR signaling cascade

YBR078W  ECM33  GPI-anchored protein of unknown function, has a possible role in apical bud growth; GPI-anchoring on the plasma membrane crucial to function; similar to Sps2p and Pst1p

YDR512C  EMI1  Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation

YNL280C  ERG24  C-14 sterol reductase, acts in ergosterol biosynthesis; mutants accumulate the abnormal sterol ignosterol (ergosta-8,14 dienol), and are viable under anaerobic growth conditions but inviable on rich medium under aerobic conditions

YBR026C  ETR1  2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase family; localized to in mitochondria, where it has a probable role in fatty acid synthesis

YFR019W  FAB1  1-phosphatidylinositol-3-phosphate 5-kinase; vacuolar membrane kinase that generates phosphatidylinositol (3,5)P2, which is involved in vacuolar sorting and homeostasis

YBR040W  FIG1  Integral membrane protein required for efficient mating; may participate in or regulate the low affinity Ca2+ influx system, which affects intracellular signalling and cell-cell fusion during mating

YER109C  FLO8  Transcription factor required for flocculation, diploid filamentous growth, and haploid invasive growth; genome reference strain S288C and most laboratory strains have a mutation in this gene

YER145C  FTR1  High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron
Chloride channel localized to late- or post-Golgi vesicles, involved in iron metabolism; highly homologous to voltage-gated chloride channels in vertebrates.

Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein.

Subunit of the heterohexameric co-chaperone prefoldin complex which binds specifically to cytosolic chaperonin and transfers target proteins to it.

Protein of unknown function, proposed to be involved in the transfer of mannosylphosphate groups onto N-linked oligosaccharides; also proposed to be involved in responding to osmotic stress.

Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; provides the principal activation function of the complex.

Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein.

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Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein.
| Yeast Gene ID | Gene Symbol | Function and Description |
|--------------|-------------|-------------------------|
| YJR010W      | MET3       | ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for assimilatory reduction of sulfate to sulfide, involved in methionine metabolism |
| YOR211C      | MGM1       | Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; homolog of human OPA1 involved in autosomal dominant optic atrophy |
| YBR084W      | MIS1       | Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase |
| YLI006W      | MMM1       | Mitochondrial outer membrane protein required for normal mitochondrial morphology and mtDNA stability; involved in tethering mitochondria to the actin cytoskeleton and in anchoring mtDNA nucleoids |
| YBR098W      | MMS4       | Subunit of the structure-specific Mms4p-Mus81p endonuclease that cleaves branched DNA; involved in recombination and DNA repair |
| YGL257C      | MNT2       | Mannosyltransferase involved in adding the 4th and 5th mannose residues of O-linked glycans |
| YDR347W      | MRPL1      | Mitochondrial ribosomal protein of the small subunit; MRPL1 exhibits genetic interactions with PET122, encoding a COX3-specific translational activator, and with PET123, encoding a small subunit mitochondrial ribosomal protein |
| YBL038W      | MRPL16     | Mitochondrial ribosomal protein of the large subunit |
| YNL252C      | MRPL17     | Mitochondrial ribosomal protein of the large subunit |
| YKR085C      | MRPL20     | Mitochondrial ribosomal protein of the large subunit |
| YOR150W      | MRPL23     | Mitochondrial ribosomal protein of the large subunit |
| YCR003W      | MRPL32     | Mitochondrial ribosomal protein of the large subunit |
| YBR268W      | MRPL37     | Mitochondrial ribosomal protein of the large subunit |
| YLR439W      | MRPL4      | Mitochondrial ribosomal protein of the large subunit |
| YPR100W      | MRPL51     | Mitochondrial ribosomal protein of the large subunit |
| YHR091C      | MSR1       | Mitochondrial arginyl-tRNA synthetase |
| YDL177W      | MRPL16     | Peripheral bound inner membrane protein of the mitochondrial matrix, required for export of C-terminal tail of Cox2p through the inner membrane |
| YMR287C      | MSU1       | RNase, component of the mitochondrial degradosome along with the ATP-dependent RNA helicase Suv3p; the degradosome associates with the ribosome and mediates turnover of aberrant or unprocessed RNAs |
| YNL119W      | NCS2       | Protein with a role in urmylation and in invasive and pseudohyphal growth; inhibits replication of Brome mosaic virus in *S. cerevisiae*, which is a model system for studying replication of positive-strand RNA viruses in their natural hosts |
| YPR072W      | NOT5       | Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation |
| YNL091W      | NST1       | Protein of unknown function, mediates sensitivity to salt stress; interacts physically with the splicing factor Ms1p and also displays genetic interaction with MSL1 |
| YER154W      | OXA1       | Translocase of the mitochondrial inner membrane, mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner membrane, interacts with mitochondrial ribosomes; null is respiratory deficient |
| YCR077C      | PAT1       | Topoisomerase II-associated deamidation-dependent mRNA-decapping factor; also required for faithful chromosome transmission, maintenance of rDNA locus stability, and protection of mRNA 3’-UTRs from trimming; functionally linked to Pab1p |
| YDL179W      | PCL9       | Cyclin, forms a functional kinase complex with Pho85p cyclin-dependent kinase (Cdk), expressed in late M/early G1 phase, activated by Swi5p |
YGR004W  PEX31  Peroxisomal integral membrane protein, involved in negative regulation of peroxisome size; partially functionally redundant with Pex30p and Pex32p; probably acts at a step downstream of steps mediated by Pex28p and Pex29p
YBR168W  PEX32  Peroxisomal integral membrane protein, involved in negative regulation of peroxisome size; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p
YDL236W  PHO13  Alkaline phosphatase specific for p-nitrophenyl phosphate, involved in dephosphorylation of histone II-A and casein
YNL082W  PMS1  ATP-binding protein required for mismatch repair in mitosis and meiosis; functions as a heterodimer with Mlh1p, binds double- and single-stranded DNA via its N-terminal domain, similar to E. coli MutL
YDR300C  PRO1  Gamma-glutamyl kinase, catalyzes the first step in proline biosynthesis
YDL214C  PRR2  Protein kinase with a possible role in MAP kinase signaling in the pheromone response pathway
YDL230W  PTP1  Phosphotyrosine-specific protein phosphatase that dephosphorylates a broad range of substrates in vivo, including Fpr3p; localized to the cytoplasm and the mitochondria
YPR191W  QCR2  Subunit 2 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; transcription is regulated by Hap1p, Hap2p/Hap3p, and Heme
YDR529C  QCR7  Subunit 7 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; oriented facing the mitochondrial matrix; N-terminus appears to play a role in complex assembly
YDL104C  QRI7  Putative metalloprotease, similar to O-sialoglycoprotein metallopeptidase from P. haemolytica
YER173W  RAD24  Checkpoint protein, involved in the activation of the DNA damage and meiotic pachytene checkpoints; subunit of a clamp loader that loads Rad17p-Mec3p-Ddc1p onto DNA; homolog of human and S. pombe Rad17 protein
YJR035W  RAD26  Protein involved in transcription-coupled repair nucleotide excision repair of UV-induced DNA lesions; homolog of human CSB protein
YJR052W  RAD7  Protein that recognizes and binds damaged DNA in an ATP-dependent manner (with Rad16p) during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 4 (NEF4)
YGL246C  RAI1  Nuclear protein that binds to and stabilizes the exoribonuclease Rat1p, required for pre-rRNA processing
YJR033C  RAV1  Subunit of the RAVE complex (Rav1p, Rav2p, Skp1p), which promotes assembly of the V-ATPase holoenzyme; required for transport between the early and late endosome/PVC and for localization of TGN membrane proteins; potential Cdc28p substrate
YBR073W  RDH54  DNA-dependent ATPase, stimulates strand exchange by modifying the topology of double-stranded DNA; involved in the recombinational repair of double-strand breaks in DNA during mitosis and meiosis; proposed to be involved in crossover interference
YNL090W  RHO2  Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, involved in the establishment of cell polarity and in microtubule assembly
YFL033C  RIM15  Glucose-repressible protein kinase involved in signal transduction during cell proliferation in response to nutrients, specifically the establishment of stationary phase; originally identified as a regulator of IME2
YEL024W  RPI1  Ubiquinol-cytochrome-c reductase, a Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex; transfers electrons from ubiquinol to cytochrome c1 during respiration
YGL107C  RMD9  Mitochondrial protein required for sporulation
YNL072W  RNH201  Ribonuclease H2 catalytic subunit, removes RNA primers during Okazaki fragment synthesis; cooperates with Rad27p nuclease
YIL119C  RPI1  Putative transcriptional regulator; overexpression suppresses the heat shock sensitivity of wild-type RAS2 overexpression and also suppresses the cell lysis defect of an mpk1 mutation
YGL135W  RPL1B  N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal
YDR289C  RTT103  Protein that interacts with exonuclease Rat1p and Rai1p and plays a role in transcription termination by RNA polymerase II, has an RPR domain (carboxy-terminal domain interacting domain); also involved in regulation of Ty1 transposition
YJR004C  SAG1  Alpha-agglutinin of alpha-cells, binds to Aga1p during agglutination, N-terminal half is homologous to the immunoglobulin superfamily and contains binding site for a-agglutinin, C-terminal half is highly glycosylated and contains GPI anchor

YGL126W  SCS1  Protein required for inositol prototrophy, appears to be involved in the synthesis of inositol phospholipids from inositol but not in the control of inositol synthesis

YKR029C  SET3  Defining member of the SET3 histone deacetylase complex which is a meiosis-specific repressor of sporulation genes; necessary for efficient transcription by RNAPII; one of two yeast proteins that contains both SET and PHD domains

YIR001C  SGN1  Cytoplasmic RNA-binding protein, contains an RNA recognition motif (RRM); may have a role in mRNA translation, as suggested by genetic interactions with genes encoding proteins involved in translational initiation

YNL032W  SIW14  Tyrosine phosphatase that plays a role in actin filament organization and endocytosis; localized to the cytoplasm

YBR172C  SMY2  Protein of unknown function that interacts with Mio2p; has similarity to S. pombe Mpd2

YDR477W  SNF1  AMP-activated serine/threonine protein kinase found in a complex containing Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis

YBR169C  SSE2  Member of the heat shock protein 70 (HSP70) family; may be involved in protein folding; localized to the cytoplasm; highly homologous to the heat shock protein Sse1p

YCR030C  SYP1  Protein with a potential role in actin cytoskeletal organization; overexpression suppresses a pfy1 (profilin) null mutation

YJL004C  SYS1  Integral membrane protein of the Golgi required for targeting of the Arf-like GTPase Arl3p to the Golgi; multicopy suppressor of ypt6 null mutation

YPL129W  TAF14  Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain

YBR150C  TBS1  Probable Zn-finger protein

YGL049C  TIF4632  Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4631p

YBR162C  TOs1  Covalently-bound cell wall protein of unknown function; identified as a cell cycle regulated SBF target gene; deletion mutants are highly resistant to treatment with beta-1,3-glucanase; has sequence similarity to YJL171C

YNL079C  TPM1  Major isoform of tropomyosin; binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; acetylated by the NatB complex and acetylated form binds actin most efficiently

YLR435W  TSR2  Protein with a potential role in pre-rRNA processing

YCR084C  TUP1  Integral membrane protein of the Golgi required for targeting of the Arf-like GTPase Arl3p to the Golgi; multicopy suppressor of ypt6 null mutation

YGR019W  UGA1  Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase) involved in the 4-aminobutyrate and glutamate degradation pathways; required for normal oxidative stress tolerance and nitrogen utilization

YPL045W  VPS16  Subunit of the homotypic vacuole fusion and vacuole protein sorting (HOPS) complex; part of the Class C Vps complex essential for membrane docking and fusion at both the Golgi-to-endosome and endosome-to-vacuole stages of protein transport

YJR029C  VPS53  Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting

YJR044C  VPS55  Late endosomal protein involved in late endosome to vacuole trafficking; functional homolog of human obesity receptor gene-related protein (OB-RGRP)

YJR126C  VPS70  Protein of unknown function involved in vacuolar protein sorting

YGL104C  VPS73  Mitochondrial protein of unknown function involved in vacuolar protein sorting
Putative membrane glycoprotein with strong similarity to Vth2p and Pep1p/Vps10p, may be involved in vacuolar protein sorting.

Protein required for DNA repair; component of the Mre11 complex, which is involved in double strand breaks, meiotic recombination, telomere maintenance, and checkpoint signaling.

Subunit of both the NuA4 histone H4 acetyltransferase complex and the SWR1 complex, may function to antagonize silencing near telomeres; interacts directly with Swc4p, has homology to human leukemogenic protein AF9, contains a YEATS domain.

Subunit, with Mgr1p, of the mitochondrial inner membrane i-AAA protease complex, which is responsible for degradation of unfolded or misfolded mitochondrial gene products; mutation causes an elevated rate of mitochondrial turnover.

Protein with similarity to GPI-anchored aspartic proteases such as Yap1p and Yap3p.

Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain and functions as a J-protein partner for Ssb17p and Ssb2p.

Unknown function.
| Gene ID    | Function          |
|-----------|-------------------|
| YER137C   | Unknown function  |
| YER185W   | Unknown function  |
| YER186C   | Unknown function  |
| YER187W   | Unknown function  |
| YGL101W   | Unknown function  |
| YPL183W-A | Unknown function  |
| YBR099C   | Unknown function  |
| YBR108W   | Unknown function  |
| YGR012W   | Unknown function  |
| YGR015C   | Unknown function  |
| YGR016W   | Unknown function  |
| YGR017W   | Unknown function  |
| YGR021W   | Unknown function  |
| YGL262W   | Unknown function  |
| YGR001C   | Unknown function  |
| YGR153W   | Unknown function  |
| YGR206W   | Unknown function  |
| YIL039W   | Unknown function  |
| YBK284W   | Unknown function  |
| YBK300C   | Unknown function  |
| YCL001W-A | Unknown function  |
| YDR537C   | Unknown function  |
| YDR271C   | Unknown function  |
| YOR331C   | Unknown function  |
| YOR333C   | Unknown function  |
| YJR039W   | Unknown function  |
| YMR118C   | Unknown function  |
| YER087W   | Unknown function  |
| YGR150C   | Unknown function  |
| YJR120W   | Unknown function  |
| YIL022W   | Unknown function  |
| YNR020C   | Unknown function  |
| YML090W   | Unknown function  |
| YLR149C   | Unknown function  |
| YLR235C   | Unknown function  |
| YMR293C   | Unknown function  |
| YOR199W   | Unknown function  |
| YPR123C   | Unknown function  |
YDL068W - Unknown function
YDR532C - Unknown function
YDL062W - Unknown function
YDR442W - Unknown function
YDR458C - Unknown function
YDR048C - Unknown function
YDR307W - Unknown function
YDR319C - Unknown function
YDR336W - Unknown function
YDR348C - Unknown function
YDR370C - Unknown function
YAL016C-B - Unknown function
YCR075W-A - Unknown function
YER053C-A - Unknown function
YHR050W-A - Unknown function
YIL002W-A - Unknown function
YIL136W-A - Unknown function
YBR287W - Protein of unknown function; mutation results in a zinc sensitive phenotype
YJR080C - The authentic, non-tagged protein was localized to the mitochondria
**Supplementary Table 4**

List of genes encoding enzymes of the phospholipid intermediates that were over-expressed in wild-type cells and relevant phospholipid mutants

| Accumulation of metabolite-of-interest | Gene over-expressed | Strains |
|---------------------------------------|---------------------|---------|
| Diacylglycerol (DAG)                  | PP1                 | Wild-type | Δcho2 | Δtro1 |
|                                       | PAH1                | Δopi3    | Δpsd1 | Δdga1 |
|                                       | PLC1                | Δice2    | Δpsd2 |       |
| 1-acyl-Dihydroxyacetone-Phosphate (1-| GAT1                | Wild-type | Δcho2 | Δayr1 |
| acyl-DHAP) and lyso-phosphatidic-acid | GAT2                | Δopi3    | Δpsd1 | Δscl1 |
| (lysoPA)                              |                     | Δice2    | Δpsd2 | Δscl4 |
|                                       |                     | Δfum1    |       |       |
| Cystidine-Diphosphate-DAG (CDP-DAG)   | CDS1                | Wild-type | Δcho2 | Δpsd2 |
|                                       |                     | Δopi3    | Δpsd1 | Δcho1 |
|                                       |                     | Δice2    |       |       |
| Dihydroxyacetone phosphate (DHAP)     | DAK1                | Wild-type | Δpsd1 | Δgpi2 |
|                                       | DAK2                | Δopi3    | Δpsd2 | Δsct1 |
|                                       |                     | Δice2    | Δgpd1 | Δfum1 |
|                                       |                     | Δcho2    | Δgpd2 |       |
| Phosphatidic acid (PA)                | SLC1                | Wild-type | Δcho2 | Δfum1 |
|                                       | SPO14               | Δopi3    | Δpsd1 | Δlpp1 |
|                                       |                     | Δice2    | Δpsd2 | Δdpp1 |
| Phosphatidylserine (PS)               | CHO1                | Wild-type | Δopi3 | Δpsd1 |
|                                       |                     | Δice2    | Δcho2 | Δpsd2 |
| Phosphatidylethanolamine (PE)         | PSD1                | Wild-type | Δpsd1 | Δspo14|
|                                       | PSD2                | Δopi3    | Δpsd2 | Δnte1 |
|                                       |                     | Δice2    | Δpsd2 |       |
| Phosphatidyldcholine (PC) and         | OPI3                | Wild-type | Δpsd1 |       |
| phosphatidyl-dimethyl-ethanolamine    |                     | Δopi3    | Δpsd2 |       |
| (PDME)                                |                     | Δice2    | Δpsd2 |       |
|                                       |                     | Δcho2    |       |       |
|                                       |                     | Δplb1    |       |       |
Supplementary Figure 1. The Δopi3 mutant expressing pUG35GAL1 (empty vector) were grown in SC galactose medium and cell morphology observed using light microscopy. The image indicates that a sub-population of Δopi3 cells exhibit an elongated morphology when grown under the conditions tested. Bar, 5 μm