Supplemental Materials

Molecular Biology of the Cell

Nair et al.

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 acid potassium salt	8
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

Supplementary Table 2

Primer sequences used

Primer name	5’ – 3’ Sequence
ABETA-F	TTTCTCTAGGGATCCATGGATGCAGAATTC
ABETA-R	AGACATGTTGTCGACCGCTATGACAACACC
ABETA-R-S	AGACATGTTGTCGACTTACGCTATGACAACACC
ABETA-R-MUT	AGACATGTTGTCGACTGGTTCGACAACACC
ABETA-40-R	GTTTAGATCGTCGACGACAACACCGCCCAC
ABETA-40-R-S	GTTTAGGTCGACTTAGACAACACCGCCCAC
ESC-URA-F	TCATTGCTAGAGCTCAGTACGGATTAGAAG
ESC-URA-R	CGTATTACGTCTAGAGGGTTTTTTCTCCTT

Supplementary Table 3

Mutants exhibiting weak/faint Aβ_{42}EGFP-associated fluorescence

ORF	Gene name	Description
YDL243C	*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 aminoimidazole ribotide synthetase and glycinamide ribotide synthetase activities
YDR408C	*ADE8*	Phosphoribosyl-glycinamide 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
YJL180C	*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 pseudohyphal 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: polyprenyl 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-A	*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 co-repressor, acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters
YDL117W	*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
YPR023C	*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

YJR040W	*GEF1*	Chloride channel localized to late- or post-Golgi vesicles, involved in iron metabolism; highly homologous to voltage-gated chloride channels in vertebrates
YDL198C	*GGC1*	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
YML094W	*GIM5*	Subunit of the heterohexameric co-chaperone prefoldin complex which binds specifically to cytosolic chaperonin and transfers target proteins to it
YJL184W	*GON7*	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
YKL109W	*HAP4*	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
YCR065W	*HCM1*	Forkhead transcription factor involved in cell cycle specific transcription of SPC110; dosage-dependent suppressor of calmodulin mutants with specific defects in SPB assembly; involved in telomere maintenance
YLR192C	*HCR1*	Dual function protein involved in translation initiation as a substoichiometric component of eukaryotic translation initiation factor 3 (eIF3) and required for processing of 20S pre-rRNA; binds to eIF3 subunits Rpg1p and Prt1p and 18S rRNA
YDR317W	*HIM1*	Protein of unknown function involved in DNA repair
YMR172W	*HOT1*	Transcription factor required for the transient induction of glycerol biosynthetic genes GPD1 and GPP2 in response to high osmolarity; targets Hog1p to osmostress responsive promoters; has similarity to Msn1p and Gcr1p
YKL138C-A	*HSK3*	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
YBR272C	*HSM3*	Protein of unknown function, involved in DNA mismatch repair during slow growth; has weak similarity to Msh1p
YCR046C	*IMG1*	Mitochondrial ribosomal protein of the small subunit, required for respiration and for maintenance of the mitochondrial genome
YBR107C	*IML3*	Protein with a role in kinetochore function, localizes to the outer kinetochore in a Ctf19p-dependent manner, interacts with Chl4p and Ctf19p
YIR005W	*IST3*	Component of the U2 snRNP, required for the first catalytic step of splicing and for spliceosomal assembly; interacts with Rds3p and is required for Mer1p-activated splicing
YJR097W	*JJJ3*	Protein of unknown function, contains a J-domain, which is a region with homology to the E. coli DnaJ protein
YNL104C	*LEU4*	Alpha-isopropylmalate synthase (2-isopropylmalate synthase); the main isozyme responsible for the first step in the leucine biosynthesis pathway
YJR070C	*LIA1*	Deoxyhypusine hydroxylase, a HEAT-repeat containing metalloenzyme that catalyses hypusine formation; binds to and is required for the modification of Hyp2p (eIF5A); complements S. pombe mmd1 mutants defective in mitochondrial positioning
YFL018C	*LPD1*	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes
YCL051W	*LRE1*	Protein involved in control of cell wall structure and stress response; inhibits Cbk1p protein kinase activity; overproduction confers resistance to cell-wall degrading enzymes
YAL024C	*LTE1*	Putative GDP/GTP exchange factor required for mitotic exit at low temperatures; acts as a guanine nucleotide exchange factor (GEF) for Tem1p, which is a key regulator of mitotic exit; physically associates with Ras2p-GTP
YDL182W	*LYS20*	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p
YMR021C	*MAC1*	Copper-sensing transcription factor involved in regulation of genes required for high affinity copper transport
YDR318W	*MCM21*	Protein involved in minichromosome maintenance; component of the COMA complex (Ctf19p, Okp1p, Mcm21p, Ame1p) that bridges kinetochore subunits that are in contact with centromeric DNA and the subunits bound to microtubules

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
YLL006W	*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
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	*MRP1*	Mitochondrial ribosomal protein of the small subunit; MRP1 exhibits genetic interactions with PET122, encoding a COX3-specific translational activator, and with PET123, encoding a small subunit mitochondrial ribosomal protein
YPL118W	*MRP51*	Mitochondrial ribosomal protein of the large subunit; MRP51 exhibits genetic interactions with mutations in the COX2 and COX3 mRNA 5'-untranslated leader sequences
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
YDL107W	*MSS2*	Peripherally 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 Msl1p 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 deadenylation-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	*RIP1*	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	*SCS3*	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 Myo2p; 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*	General repressor of transcription, forms complex with Cyc8p, involved in the establishment of repressive chromatin structure through interactions with histones H3 and H4, appears to enhance expression of some genes
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
YJL029C	*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

YIL173W	*VTH1*	Putative membrane glycoprotein with strong similarity to Vth2p and Pep1p/Vps10p, may be involved in vacuolar protein sorting
YDR369C	*XRS2*	Protein required for DNA repair; component of the Mre11 complex, which is involved in double strand breaks, meiotic recombination, telomere maintenance, and checkpoint signaling
YNL107W	*YAF9*	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
YPR024W	*YME1*	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
YGL259W	*YPS5*	Protein with similarity to GPI-anchored aspartic proteases such as Yap1p and Yap3p
YGR285C	*ZUO1*	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
YCR016W	-	Unknown function
YDL218W	-	Unknown function
YDR262W	-	Unknown function
YAL056C-A	-	Unknown function
YCL075W	-	Unknown function
YCL076W	-	Unknown function
YJR098C	-	Unknown function
YJR100C	-	Unknown function
YJR107W	-	Unknown function
YJR119C	-	Unknown function
YDL133W	-	Unknown function
YJL007C	-	Unknown function
YJL016W	-	Unknown function
YJR054W	-	Unknown function
YNR025C	-	Unknown function
YNR029C	-	Unknown function
YBR053C	-	Unknown function
YBR062C	-	Unknown function
YIL100W	-	Unknown function
YIL110W	-	Unknown function
YIL166C	-	Unknown function
YIL168W	-	Unknown function
YKL202W	-	Unknown function
YKR040C	-	Unknown function
YKR041W	-	Unknown function
YBR090C	-	Unknown function
YBR280C	-	Unknown function
YCR061W	-	Unknown function

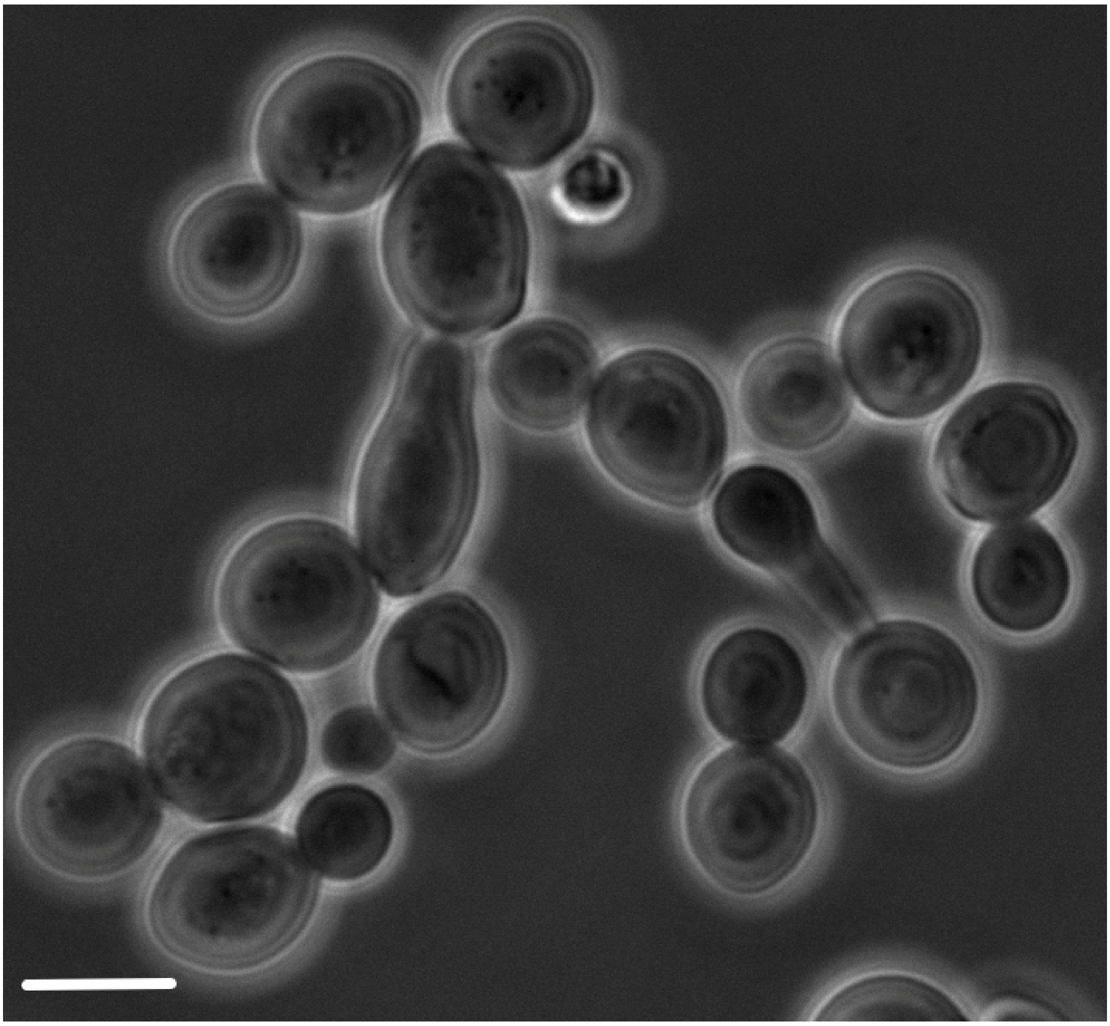
YER137C	-	Unknown function
YER185W	-	Unknown function
YER186C	-	Unknown function
YER187W	-	Unknown function
YGL101W	-	Unknown function
YPL183W-A	-	Unknown function
YBR099C	-	Unknown function
YBR108W	-	Unknown function
YGR012W	-	Unknown function
YGR015C	-	Unknown function
YGR016W	-	Unknown function
YGR017W	-	Unknown function
YGR021W	-	Unknown function
YGL262W	-	Unknown function
YGR001C	-	Unknown function
YGR153W	-	Unknown function
YGR206W	-	Unknown function
YIL039W	-	Unknown function
YBR284W	-	Unknown function
YBR300C	-	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
YJL022W	-	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
YJL136W-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)	*DPP1* *PAH1* *PLC1*	Wild-type Δ*opi3* Δ*ice2*	Δ*cho2* Δ*psd1* Δ*psd2*	Δ*lro1* Δ*dga1*
1-acyl-Dihydroxyacetone-Phosphate (1-acyl-DHAP) and lyso-phosphatidic-acid (lysoPA)	*GAT1* *GAT2*	Wild-type Δ*opi3* Δ*ice2* Δ*fum1*	Δ*cho2* Δ*psd1* Δ*psd2*	Δ*ayr1* Δ*slc1* Δ*slc4*
Cystidine-Diphosphate-DAG (CDP-DAG)	*CDS1*	Wild-type Δ*opi3* Δ*ice2*	Δ*cho2* Δ*psd1*	Δ*psd2* Δ*cho1*
Dihydroxyacetone phosphate (DHAP)	*DAK1* *DAK2*	Wild-type Δ*opi3* Δ*ice2* Δ*cho2*	Δ*psd1* Δ*psd2* Δ*gpd1* Δ*gpd2*	Δ*gpt2* Δ*sct1* Δ*fum1*
Phosphatidic acid (PA)	*SLC1* *SPO14*	Wild-type Δ*opi3* Δ*ice2*	Δ*cho2* Δ*psd1* Δ*psd2*	Δ*fum1* Δ*lpp1* Δ*dpp1*
Phosphatidylserine (PS)	*CHO1*	Wild-type Δ*ice2*	Δ*opi3* Δ*cho2*	Δ*psd1* Δ*psd2*
Phosphatidylethanolamine (PE)	*PSD1* *PSD2*	Wild-type Δ*ice2*	Δ*opi3* Δ*cho2*	Δ*psd1* Δ*psd2*
Phosphatidylcholine (PC) and phosphatidyl-dimethyl-ethanolamine (PDME)	*OPI3*	Wild-type Δ*ice2* Δ*cho2*	Δ*psd1* Δ*psd2* Δ*plb1*	Δ*spo14* Δ*nte1*



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