

TABLE S1**Deletion strains that confer an Ino- phenotype**

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YJR083C	<i>ACF4</i>	+	+	S	Protein of unknown function	This study
YDL203C	<i>ACK1</i>	+	+	S	Protein that functions upstream of the PKC-CWI signaling pathway	This study
YDR448W	<i>ADA2</i>	S	W	W	Transcription coactivator, component of the ADA and SAGA transcriptional adaptor/HAT (histone acetyltransferase) complexes	This study
YDR226W	<i>ADK1</i>	S	S	S	Adenylate kinase, required for purine metabolism	This study
YIL044C	<i>AGE2</i>	+	+	S	ADP-ribosylation factor (ARF) GTPase activating protein (GAP) effector, involved in Trans-Golgi-Network (TGN) transport	This study
YMR092C	<i>AIP1</i>	+	+	W	Actin cortical patch component, interacts with the actin depolymerizing factor cofilin	This study
YNL148C	<i>ALF1</i>	W	W	S	Alpha-tubulin folding protein, similar to mammalian cofactor B	This study
YOR002W	<i>ALG6</i>	+	W	S	Glycosyltransferase of the ER, involved in N-linked protein glycosylation	This study
YOR067C	<i>ALG8</i>	+	W	S	Glycosyltransferase of the ER, involved in N-linked protein glycosylation	This study
YNL219C	<i>ALG9</i>	+	+	W	Mannosyltransferase of the ER, involved in N-linked glycosylation	This study
YLR089C	<i>ALT1</i>	VW	VW	W	Putative alanine transaminase (glutamic pyruvic transaminase)	This study
YML022W	<i>APT1</i>	+	+	S	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate	This study
YHR013C	<i>ARD1</i>	W	S	S	Subunit of the N-terminal acetyltransferase NatA (Nat1p, Ard1p, Nat5p)	This study
YDL192W	<i>ARF1</i>	+	W	S	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of vesicles in intracellular trafficking within the Golgi	This study
YDR173C	<i>ARG82</i>	S	S	NG	Inositol polyphosphate multikinase (IPMK), sequentially phosphorylates I(1,4,5)P ₃ to I(1,3,4,5,6)P ₅	This study
YPR201W	<i>ARR3</i>	+	VW	S	Arsenite transporter of the plasma membrane, required for resistance to arsenic compounds	This study
YLR242C	<i>ARV1</i>	W	W	S	Protein functioning in transport of glycosylphosphatidylinositol intermediates into the ER lumen; required for sterol distribution	This study
YJL115W	<i>ASF1</i>	+	+	W	Nucleosome assembly factor, involved in chromatin assembly after DNA replication	This study
YER101C	<i>AST2</i>	+	+	W	Protein that may have a role in targeting of plasma membrane [H ⁺]ATPase (Pma1p) to the plasma membrane	This study
YGL180W	<i>ATG1</i>	+	+	W	Protein serine/threonine kinase, required for autophagy and for the cytoplasm-to-vacuole targeting (Cvt) pathway	This study
YDR384C	<i>ATO3</i>	+	+	W	Plasma membrane protein, regulation pattern suggests a possible role in export of ammonia from the cell	This study
YMR068W	<i>AVO2</i>	+	+	S	Component of the TORC2 complex containing the Tor2p kinase	This study
YER167W	<i>BCK2</i>	+	+	W	Protein involved in the PKC-CWI signaling pathway	This study

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TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YER177W	<i>BMH1</i>	+	VW	S	14-3-3 protein, major isoform involved in regulation of many processes such as exocytosis, vesicle transport, Ras/MAPK signaling	This study
YLL015W	<i>BPT1</i>	+	+	S	ABC type transmembrane transporter of MRP/CFTR family	This study
YDL074C	<i>BRE1</i>	W	W	S	E3 ubiquitin ligase for Rad6p, required for the ubiquitination of histone H2B, and subsequent methylation of histone H3	This study
YLR015W	<i>BRE2</i>	+	+	VW	Subunit of the COMPASS (Set1C) complex, which methylates histone H3 on lysine 4	This study
YEL029C	<i>BUD16</i>	VW	W	S	Protein involved in bud-site selection and telomere maintenance	This study
YLR074C	<i>BUD20</i>	+	+	S	Protein involved in bud-site selection	This study
YOR078W	<i>BUD21</i>	+	VW	VW	Component of small ribosomal subunit (SSU) processosome that contains U3 snoRNA	This study
YMR014W	<i>BUD22</i>	+	+	W	Protein involved in bud-site selection	This study
YCR047C	<i>BUD23</i>	+	+	S	Methyltransferase, methylates residue G1575 of 18S rRNA; required for rRNA processing and nuclear export of 40S ribosomal subunits	This study
YKR036C	<i>CAF4</i>	+	VW	W	WD40 repeat-containing protein associated with the CCR4-NOT complex	This study
YDL069C	<i>CBS1</i>	+	+	W	Mitochondrial translational activator of the COB mRNA	This study
YCR094W	<i>CDC50</i>	+	+	W	Endosomal and TGN protein that regulates cell polarity; associates with DRS2; similar to Crf1p and Lem3p	This study
YLR418C	<i>CDC73</i>	S	S	S	Constituent of Pafl complex	This study
YHR142W	<i>CHS7</i>	+	VW	S	Protein of unknown function, involved in chitin biosynthesis	This study
YPL241C	<i>CIN2</i>	VW	W	W	Tubulin folding factor C (putative) involved in Tub2p folding	This study
YJL158C	<i>CIS3</i>	+	+	W	Mannose-containing glycoprotein constituent of the cell wall	This study
YGR108W	<i>CLB1</i>	+	+	W	B-type cyclin that activates Cdc28p and is involved in transition from G2 to M phase of the cell cycle progression	This study
YAL040C	<i>CLN3</i>	+	+	W	G1 cyclin that activates Cdc28p kinase to promote G1 to S phase transition	This study
YKL190W	<i>CNBI</i>	VW	VW	W	Calcineurin B; the regulatory subunit of calcineurin, a Ca ⁺⁺ /calmodulin-regulated protein phosphatase	This study
YAL058W	<i>CNE1</i>	W	W	S	Calnexin; integral membrane ER chaperone involved in folding and quality control of glycoproteins	This study
YNL051W	<i>COG5</i>	VW	VW	VW	Component of the conserved oligomeric Golgi complex (COG)	This study
YNL041C	<i>COG6</i>	W	W	W	Component of the conserved oligomeric Golgi complex (COG)	This study
YML071C	<i>COG8</i>	W	W	W	Component of the conserved oligomeric Golgi complex (COG)	This study
YER130C	<i>COM2</i>	+	VW	S	Protein of unknown function	This study
YLR087C	<i>CSF1</i>	W	W	W	Protein required for fermentation at low temperature	This study
YIL036W	<i>CST6</i>	VW	VW	S	Transcription factor of the ATF/CREB family, activates transcription of genes involved in utilization of non-optimal carbon sources	This study

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TABLE S1
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ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YEL027W	<i>CUP5</i>	S	S	S	Proteolipid subunit of the vacuolar H(+)-ATPase V0 sector (subunit c)	This study
YPL177C	<i>CUP9</i>	+	VW	W	Transcriptional repressor of PTR2, which encodes a major peptide transporter	This study
YDR482C	<i>CWC21</i>	+	+	S	Component of a complex containing Cef1p, putatively involved in pre-mRNA splicing	This study
YGR092W	<i>DBF2</i>	W	S	S	Ser/Thr kinase involved in transcription and stress response; functions in exit from mitosis; Component of the CCR4-NOT complex	This study
YDR411C	<i>DFM1</i>	+	+	W	Protein of unknown function, localizes to the ER	This study
YKL121W	<i>DGR2</i>	+	+	S	Protein of unknown function; null mutant is resistant to 2-deoxy-D-glucose	This study
YGR227W	<i>DIE2</i>	+	+	S	Glucosyl transferase of the ER, involved in N-linked protein glycosylation, has a role in regulation of ITR1 and INO1	This study
YDR403W	<i>DIT1</i>	+	+	S	Sporulation-specific enzyme required for spore wall maturation	This study
YKL213C	<i>DOA1</i>	W	W	S	WD repeat protein required for ubiquitin-mediated protein degradation, forms complex with Cdc48p	This study
YDR294C	<i>DPL1</i>	+	+	W	Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs)	This study
YAL026C	<i>DRS2</i>	+	+	S	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation (flipase)	This study
YMR276W	<i>DSK2</i>	+	VW	S	Ubiquitin-like polyubiquitin-binding protein, involved in proteolysis, interacts with the proteasome	This study
YLR436C	<i>ECM30</i>	+	+	W	Non-essential protein of unknown function	This study
YBL047C	<i>EDE1</i>	+	+	W	Endocytic protein that binds membranes in a ubiquitin-dependent manner	This study
YDR385W	<i>EFT2</i>	+	+	S	Elongation factor 2 (EF-2), also encoded by EFT1	This study
YKL160W	<i>ELF1</i>	VW	W	S	Transcription elongation factor implicated in the maintenance of proper chromatin structure	This study
YKL048C	<i>ELM1</i>	+	+	S	Ser/Thr kinase that regulates cellular morphogenesis, septin behavior, and cytokinesis	This study
YMR312W	<i>ELP6</i>	+	VW	VW	Subunit of Elongator complex	This study
YCL045C	<i>EMC1</i>	+	+	W	Member of a transmembrane complex required for efficient folding of proteins in the ER	This study
YNL080C	<i>EOS1</i>	W	S	S	Putative protein of unknown function predicted to contain transmembrane domains	This study
YMR202W	<i>ERG2</i>	W	W	S	C-8 sterol isomerase, at an intermediate step in ergosterol biosynthesis	This study
YLR056W	<i>ERG3</i>	W	W	S	C-5 sterol desaturase, in ergosterol biosynthesis	This study
YGL012W	<i>ERG4</i>	+	W	S	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis	This study
YMR015C	<i>ERG5</i>	+	+	S	C-22 sterol desaturase, catalyzes the formation of the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis	This study
YML008C	<i>ERG6</i>	W	W	S	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway	This study
YGL054C	<i>ERV14</i>	W	W	S	Protein localized to COPII-coated vesicles, involved in vesicle formation	This study

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TABLE S1
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ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YDR363W	<i>ESC2</i>	VW	VW	S	Protein involved in mating-type locus silencing, interacts with Sir2p	This study
YBR026C	<i>ETR1</i>	+	W	W	2-enoyl thioester reductase localized to in mitochondria	This study
YFR019W	<i>FAB1</i>	S	S	NG	1-phosphatidylinositol-3-phosphate 5-kinase that generates PI(3,5)P ₂ ,	This study
YNL127W	<i>FAR11</i>	+	+	W	Protein involved in G1 cell cycle arrest in response to pheromone, in a Far1p-independent pathway	This study
YMR052W	<i>FAR3</i>	+	+	W	Protein involved in G1 cell cycle arrest in response to pheromone, in a Far1p-independent pathway	This study
YMR029C	<i>FAR8</i>	+	+	S	Protein involved in G1 cell cycle arrest in response to pheromone, in a Far1p-independent pathway	This study
YJL155C	<i>FBP26</i>	VW	VW	S	Fructose-2,6-bisphosphatase, required for glucose metabolism	This study
YCR089W	<i>FIG2</i>	+	+	W	Cell wall adhesin containing a GPI anchor, expressed specifically during mating	This study
YLR342W	<i>FKS1</i>	VW	VW	S	Catalytic subunit of 1,3-beta-D-glucan synthase, alternate catalytic subunit Gsc2p; binds to Rho1p	This study
YHR199C	<i>FMP34</i>	W	VW	S	The authentic, non-tagged protein was localized to the mitochondria	This study
YLL043W	<i>FPS1</i>	+	VW	NG	Plasma membrane glycerol channel, involved in efflux of glycerol and in uptake of the trivalent metalloid arsenite and acetic acid	This study
YNL133C	<i>FYV6</i>	VW	W	NG	Protein of unknown function, required for survival to K1 killer toxin	This study
YER027C	<i>GAL83</i>	+	+	S	One of three beta-subunits of the Snf1 kinase complex	This study
YMR307W	<i>GAS1</i>	+	VW	S	Beta-1.3-glucanosyltransferase with a GPI anchor, required for cell wall assembly	This study
YDR283C	<i>GCN2</i>	+	+	S	Protein kinase, phosphorylates the alpha-subunit of translation initiation factor eIF2 (Sui2p) in response to starvation	This study
YKR026C	<i>GCN3</i>	W	W	S	Alpha subunit of the translation initiation factor eIF2B	This study
YGR252W	<i>GCN5</i>	VW	VW	VW	Histone acetyltransferase; catalytic subunit of the ADA and SAGA histone acetyltransferase complexes	This study
YGL020C	<i>GET1</i>	+	W	S	Subunit of the GET complex; involved in Golgi to ER retrieval	This study
YER083C	<i>GET2</i>	W	W	NG	Subunit of the GET complex; involved in Golgi to ER retrieval	This study
YDR358W	<i>GGA1</i>	+	+	VW	Golgi-localized protein with homology to gamma-adaptin	This study
YCR098C	<i>GIT1</i>	+	VW	W	Plasma membrane permease, of glycerophosphoinositol and glycerophosphocholine as sources of inositol and phosphate	This study
YER122C	<i>GLO3</i>	W	VW	W	ADP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport	This study
YOR320C	<i>GNT1</i>	+	W	S	N-acetylglucosaminyltransferase capable of modification of N-linked glycans in the Golgi apparatus	This study
YOR371C	<i>GPB1</i>	+	+	W	Multistep regulator of cAMP-PKA signaling; inhibits Ras activity through direct interactions with Ira1p/2p	This study
YAL056W	<i>GPB2</i>	+	+	S	Multistep regulator of cAMP-PKA signaling; inhibits Ras activity through direct interactions with Ira1p/2p	This study

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TABLE S1
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ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YDL022W	<i>GPD1</i>	+	+	W	NAD ⁺ -dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress	This study
YOL059W	<i>GPD2</i>	W	W	W	NAD ⁺ -dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, located in cytosol and mitochondria	This study
YDL021W	<i>GPM2</i>	+	+	W	Homolog of Gpm1p phosphoglycerate mutase which converts 3-phosphoglycerate to 2-phosphoglycerate	This study
YHR104W	<i>GRE3</i>	VW	W	S	NADP ⁺ -dependant glycerol dehydrogenase; regulated by the HOG pathway	This study
YER174C	<i>GRX4</i>	+	W	S	Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase	This study
YDL010W	<i>GRY6</i>	+	+	W	Cis-golgi localized monothiol glutaredoxin that binds an iron-sulfur cluster; involved in the oxidative stress response	This study
YGL181W	<i>GTS1</i>	+	+	W	Arf3p GTPase Activating Protein (GAP) that localizes to endocytic patches	This study
YOR070C	<i>GYP1</i>	S	S	S	Cis-golgi GTPase-activating protein (GAP) for the Ypt1p (in vivo) and for Ypt1p, Sec4p, Ypt7p, and Ypt51p (in vitro)	This study
YLR192C	<i>HCRI</i>	+	+	S	Protein involved in translation initiation as a component of eukaryotic eIF3 and required for processing of 20S pre-rRNA	This study
YPR179C	<i>HDA3</i>	+	+	S	Subunit of a histone deacetylase (HDA1) complex that contains an Hda1p homodimer and an Hda2p-Hda3p heterodimer	This study
YDR174W	<i>HMO1</i>	+	+	W	Chromatin associated high mobility group (HMG) member involved in genome maintenance	This study
YJR075W	<i>HOC1</i>	+	+	W	Alpha-1,6-mannosyltransferase subunit of a Golgi-localized complex that also contains Anp1p, Mnn9p, Mnn11p, and Mnn10p	This study
YLR113W	<i>HOG1</i>	W	W	W	Mitogen-activated protein kinase involved in osmoregulation; yeast homolog of the mammalian p38 MAPK.	This study
YIL072W	<i>HOP1</i>	+	VW	S	Meiosis-specific DNA binding protein required for homologous chromosome synapsis and chiasma formation	This study
YDR399W	<i>HPT1</i>	+	+	W	Dimeric hypoxanthine-guanine phosphoribosyltransferase; yeast homolog of the human HPRT1p	This study
YBR133C	<i>HSL7</i>	+	+	S	Protein arginine N-methyltransferase; required along with Hsl1p for bud neck recruitment, phosphorylation, and degradation of Swe1p	This study
YBR272C	<i>HSM3</i>	+	+	S	Protein of unknown function, involved in DNA mismatch repair during slow growth	This study
YCR021C	<i>HSP30</i>	+	+	W	Hydrophobic plasma membrane localized, stress-responsive protein that negatively regulates the H(+)-ATPase Pma1p	This study
YOL068C	<i>HST1</i>	VW	VW	VW	Histone deacetylase; essential subunit of the Sum1p/Rfm1p/Hst1p complex; non-essential subunit of the Set3C complex	This study
YGR223C	<i>HSV2</i>	+	+	VW	Phosphatidylinositol 3,5-bisphosphate-binding protein, predicted to fold as a seven-bladed beta-propeller	This study

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TABLE S1
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ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YGL168W	<i>HUR1</i>	W	W	S	Protein required for hydroxyurea resistance	This study
YJL214W	<i>HXT8</i>	+	+	W	Protein of unknown function with similarity to hexose transporters	This study
YDL066W	<i>IDP1</i>	+	VW	S	Mitochondrial NADP-specific isocitrate dehydrogenase	This study
YFL013C	<i>IES1</i>	+	+	S	Subunit of the Ino80 chromatin remodeling complex	This study
YNL215W	<i>IES2</i>	W	W	NG	Protein that associates with the Ino80 chromatin remodeling complex under low-salt conditions	This study
YOR189W	<i>IES4</i>	VW	W	S	Protein that associates with the Ino80 chromatin remodeling complex under low-salt conditions	This study
YER092W	<i>IES5</i>	+	+	S	Protein that associates with the Ino80 chromatin remodeling complex under low-salt conditions	This study
YBR107C	<i>IML3</i>	W	W	S	Protein with a role in kinetochore function	This study
YLR021W	<i>IRC25</i>	+	+	S	Component of a heterodimeric Poc4p-Irc25p chaperone involved in assembly of alpha subunits into the 20S proteasome	This study
YDR540C	<i>IRC4</i>	+	W	S	Putative protein of unknown function	This study
YKL032C	<i>IXR1</i>	+	+	S	Protein that binds DNA containing intrastrand cross-links formed by cisplatin	This study
YDR017C	<i>KCS1</i>	W	W	S	Inositol hexaphosphate kinase, phosphorylates inositol hexakisphosphate (IP ₆) to diphosphoinositol polyphosphates	This study
YGL203C	<i>KEX1</i>	+	+	S	Protease involved in the processing of killer toxin and alpha factor precursor	This study
YLL019C	<i>KNS1</i>	+	+	W	Nonessential putative protein kinase of unknown cellular role	This study
YNL322C	<i>KRE1</i>	+	+	S	Cell wall GPI-anchored glycoprotein involved in beta-glucan assembly; serves as a K1 killer toxin membrane receptor	This study
YGR166W	<i>KRE11</i>	+	+	S	Subunit of the TRAPP (transport protein particle) complex; involved in the late steps of endoplasmic reticulum to Golgi transport	This study
YIL027C	<i>KRE27</i>	+	VW	W	Protein of unknown function; null mutant shows K1 killer toxin resistance	This study
YJL134W	<i>LCB3</i>	VW	W	S	Long-chain base-1-phosphate phosphatase, regulates ceramide and long-chain base phosphates levels	This study
YOR322C	<i>LDB19</i>	+	VW	NG	Protein involved in regulating the endocytosis of plasma membrane proteins by recruiting the ubiquitin ligase Rsp5p to its target	This study
YNL323W	<i>LEM3</i>	+	VW	W	Plasma membrane and ER protein, involved in translocation of phospholipids and lyso-PE and lyso-PC across the plasma membrane	This study
YOR123C	<i>LEO1</i>	W	W	S	Component of the Paf1 complex	This study
YPL055C	<i>LGE1</i>	+	W	S	Protein of unknown function; null mutant forms abnormally large cells	This study
YDR439W	<i>LRS4</i>	+	VW	W	Protein involved in rDNA silencing	This study
YKL176C	<i>LST4</i>	+	+	W	Protein possibly involved in a post-Golgi secretory pathway; required for the transport of Gap1p from the Golgi to the cell surface	This study
YGR057C	<i>LST7</i>	+	VW	S	Protein possibly involved in a post-Golgi secretory pathway; required for the transport of Gap1p from the Golgi to the cell surface	This study

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TABLE S1
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ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YAL024C	<i>LTE1</i>	W	W	W	Putative GDP/GTP exchange factor (GEF) for Tem1p, required for mitotic exit at low temperatures; physically associates with Ras2p-GTP	This study
YNL307C	<i>MCK1</i>	+	VW	W	Ser/Thr /Tyr (dual-specificity) kinase involved in control of chromosome segregation and in regulating entry into meiosis	This study
YGL219C	<i>MDM34</i>	W	S	S	Mitochondrial outer membrane protein, required for normal mitochondrial morphology and inheritance	This study
YKL053C-A	<i>MDM35</i>	W	W	NG	Protein of unknown function; mutation affects mitochondrial distribution and morphology	This study
YOL111C	<i>MDY2</i>	+	+	S	Protein required for efficient mating; involved in shmoo formation and nuclear migration in the pre-zygote	This study
YKR007W	<i>MEH1</i>	+	+	S	Component of the EGO complex; involved with the TORC1 complex in the regulation of microautophagy, and amino acid signaling	This study
YPR167C	<i>MET16</i>	+	+	S	3'-phosphoadenylylsulfate reductase; involved in sulfate assimilation and methionine metabolism	This study
YLR332W	<i>MID2</i>	+	VW	W	O-glycosylated plasma membrane sensor to activate the PKC-CWI signaling pathway; interacts with Rom2p and Zeo1p	This study
YPL140C	<i>MKK2</i>	+	+	W	Mitogen-activated kinase kinase involved in protein kinase C signaling pathway; functionally redundant with Mkk1p	This study
YLR320W	<i>MMS22</i>	W	W	S	Protein involved in resistance to ionizing radiation	This study
YBR015C	<i>MNN2</i>	+	+	W	Alpha-1,2-mannosyltransferase, involved in branched glycosylation in an early Golgi compartment	This study
YKL064W	<i>MNR2</i>	+	+	W	Putative magnesium transporter; has similarity to Alr1p and Alr2p, which mediate influx of Mg ²⁺ and other divalent cations	This study
YGR014W	<i>MSB2</i>	+	VW	W	Mucin family member involved in the filamentous growth signaling pathway; also functions as an osmosensor in parallel with Sho1p	This study
YOL090W	<i>MSH2</i>	W	VW	S	Protein that forms heterodimers with Msh3p and Msh6p that bind to DNA mismatches to initiate the mismatch repair process	This study
YOL116W	<i>MSN1</i>	+	+	W	Transcriptional activator involved in regulation of invertase and glucoamylase expression, invasive and pseudohyphal growth	This study
YDR335W	<i>MSN5</i>	+	+	S	Karyopherin involved in nuclear import and export; responsible for nuclear import of protein A and proteins Swi6p, Far1p, and Pho4p	This study
YDR277C	<i>MTH1</i>	+	+	W	Negative regulator of the glucose-sensing signal transduction pathway	This study
YML117W	<i>NAB6</i>	+	+	S	Putative RNA-binding protein, based on computational analysis	This study
YDL040C	<i>NAT1</i>	VW	W	S	Subunit of the N-terminal acetyltransferase NatA (Nat1p, Ard1p, Nat5p)	This study
YDR162C	<i>NBP2</i>	+	+	S	Protein involved in the HOG pathway, negatively regulates Hog1p by recruitment of phosphatase Ptc1p to the Pbs2p-Hog1p complex	This study
YNL119W	<i>NCS2</i>	VW	VW	VW	Protein with a role in urmylation and in invasive and pseudohyphal growth	This study

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TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YGL211W	<i>NCS6</i>	+	VW	S	Protein with a role in urmylation and in invasive and pseudohyphal growth	This study
YPL226W	<i>NEW1</i>	W	S	S	ATP binding cassette protein that cosediments with polysomes and is required for biogenesis of the small ribosomal subunit	This study
YDR176W	<i>NGG1</i>	VW	W	W	Transcriptional regulator involved in glucose repression of Gal4p-regulated genes; component of the SAGA complex	This study
YDL002C	<i>NHP10</i>	+	+	S	Protein related to mammalian high mobility group proteins; likely component of the INO80 complex	This study
YPL174C	<i>NIP100</i>	VW	W	W	Large subunit of the dyactin complex; putative ortholog of mammalian p150(glued)	This study
YLR315W	<i>NKP2</i>	W	S	NG	Non-essential kinetochore protein, subunit of the Ctf19 central kinetochore complex	This study
YDR432W	<i>NPL3</i>	S	S	NG	RNA-binding protein that carries poly(A)+ mRNA from the nucleus into the cytoplasm	This study
YDR043C	<i>NRG1</i>	+	+	S	Transcriptional repressor that recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and regulates filamentous growth and alkaline pH response	This study
YJL208C	<i>NUC1</i>	+	+	S	Major mitochondrial nuclease, has RNase and DNA endo- and exonucleolytic activities; has a role in mitochondrial recombination	This study
YML103C	<i>NUP188</i>	W	W	S	Subunit of the nuclear pore complex (NPC), involved in the structural organization of the complex and of the nuclear envelope	This study
YAL051W	<i>OAF1</i>	+	+	W	Oleate-activated transcription factor, acts alone and as a heterodimer with Pip2p	This study
YJL212C	<i>OPT1</i>	+	+	W	Plasma membrane transporter that transports tetra- and pentapeptides and glutathione; member of the OPT family	This study
YHR179W	<i>OYE2</i>	VW	W	S	Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN)	This study
YDR071C	<i>PAA1</i>	+	+	S	Polyamine acetyltransferase; acetylates polyamines such as putrescine, spermidine and spermine	This study
YDL173W	<i>PAR32</i>	+	VW	W	Putative protein of unknown function; hyperphosphorylated upon rapamycin treatment in a Tap42p-dependent manner	This study
YJL128C	<i>PBS2</i>	W	W	S	MAP kinase kinase that plays a pivotal role in the osmosensing signal-transduction pathway, activated under severe osmotic stress	This study
YER059W	<i>PCL6</i>	+	+	W	Pho85p cyclin of the Pho80p subfamily; forms the major Glc8p kinase together with Pcl7p and Pho85p	This study
YBR221C	<i>PDB1</i>	VW	+	W	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex	This study
YLR134W	<i>PDC5</i>	VW	W	S	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde	This study
YER149C	<i>PEA2</i>	+	+	S	Polarisome protein required for polarized morphogenesis, cell fusion; forms polarisome complex with Bni1p, Bud6p, and Spa2p	This study

(continued)

TABLE S1**(Continued)**

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YPL159C	<i>PET20</i>	VW	VW	W	Mitochondrial protein, required for respiratory growth and for stability of the mitochondrial genome	This study
YLR324W	<i>PEX30</i>	+	+	W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number	This study
YGL025C	<i>PGD1</i>	S	S	S	Subunit of the SRB/Mediator global transcriptional cofactor complex, which is part of the RNA polymerase II holoenzyme	This study
YJL117W	<i>PHO86</i>	+	+	W	Endoplasmic reticulum (ER) resident protein required for ER exit of Pho84p in COPII vesicles	This study
YBR106W	<i>PHO88</i>	W	W	S	Probable membrane protein, involved in phosphate transport	This study
YMR123W	<i>PKR1</i>	+	VW	W	V-ATPase assembly factor, functions with other V-ATPase assembly factors in the ER	This study
YLR016C	<i>PML1</i>	+	+	VW	Subunit of the RES complex, which is required for nuclear retention of unspliced pre-mRNAs	This study
YDR276C	<i>PMP3</i>	+	+	W	Plasma membrane protein related to a family of plant polypeptides that are overexpressed under high salt or low temperature	This study
YGL167C	<i>PMR1</i>	W	W	S	High affinity Ca ²⁺ /Mn ²⁺ P-type ATPase required for Ca ²⁺ and Mn ²⁺ transport into Golgi	This study
YDL095W	<i>PMT1</i>	+	VW	S	Protein O-mannosyltransferase in the ER, transfers mannose residues to protein Ser/Thr residues; in a complex with Pmt2p	This study
YAL023C	<i>PMT2</i>	W	W	S	Protein O-mannosyltransferase in the ER, transfers mannose residues to protein Ser/Thr residues; in a complex with Pmt1p	This study
YPL144W	<i>POC4</i>	VW	VW	S	Component of a heterodimeric Poc4p-Irc25p chaperone involved in assembly of alpha subunits into the 20S proteasome	This study
YHR026W	<i>PPA1</i>	S	S	S	Subunit c" of the vacuolar ATPase, which functions in acidification of the vacuole; subunit of the V0 domain	This study
YGR135W	<i>PRE9</i>	+	+	S	20S proteasome beta-type subunit; the only nonessential 20S subunit	This study
YDR300C	<i>PRO1</i>	+	+	W	Gamma-glutamyl kinase, catalyzes the first step in proline biosynthesis	This study
YDL006W	<i>PTC1</i>	W	W	NG	Type 2C protein phosphatase (PP2C); inactivates the osmosensing MAPK cascade by dephosphorylating Hog1p	This study
YGL062W	<i>PYC1</i>	W	W	S	Pyruvate carboxylase isoform, cytoplasmic enzyme that converts pyruvate to oxaloacetate	This study
YEL037C	<i>RAD23</i>	+	+	W	Protein with ubiquitin-like N terminus, recognizes and binds damaged DNA (with Rad4p) during nucleotide excision repair	This study
YER095W	<i>RAD51</i>	+	+	W	Strand exchange protein, forms a helical filament with DNA that searches for homology	This study
YGL058W	<i>RAD6</i>	VW	W	S	Ubiquitin-conjugating enzyme (E2), part of H2B ubiquitination complex	This study
YJL204C	<i>RCY1</i>	+	VW	S	F-box protein involved in recycling plasma membrane proteins internalized by endocytosis; localized to sites of polarized growth	This study
YDR379W	<i>RGA2</i>	+	+	W	GTPase-activating protein for the polarity-establishment protein Cdc42p	This study

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YPL089C	<i>RLM1</i>	+	VW	S	Transcription factor, component of the protein kinase C-mediated MAP kinase pathway; activated by the MAP-kinase Slt2p	This study
YDL001W	<i>RMD1</i>	+	+	S	Cytoplasmic protein required for sporulation	This study
YFR048W	<i>RMD8</i>	+	+	S	Cytosolic protein required for sporulation	This study
YLR371W	<i>ROM2</i>	VW	W	S	GDP/GTP exchange protein (GEP) for Rho1p and Rho2p	This study
YJL121C	<i>RPE1</i>	VW	W	S	D-ribulose-5-phosphate 3-epimerase, catalyzes a reaction in the non-oxidative part of the pentose-phosphate pathway	This study
YER169W	<i>RPH1</i>	+	W	S	Transcriptional repressor of PHR1, which is a photolyase induced by DNA damage	This study
YIL119C	<i>RPI1</i>	+	+	W	Putative transcriptional regulator; overexpression suppresses the heat shock sensitivity of wild-type RAS2	This study
YKL006W	<i>RPL14A</i>	VW	W	S	Protein component of the large (60S) ribosomal subunit	This study
YBL027W	<i>RPL19B</i>	+	VW	W	Protein component of the large (60S) ribosomal subunit	This study
YMR242C	<i>RPL20A</i>	+	VW	W	Protein component of the large (60S) ribosomal subunit	This study
YBR191W	<i>RPL21A</i>	+	VW	W	Protein component of the large (60S) ribosomal subunit	This study
YLR061W	<i>RPL22A</i>	W	W	VW	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl22Bp	This study
YGL031C	<i>RPL24A</i>	+	+	VW	Ribosomal protein L30 of the large (60S) ribosomal subunit	This study
YHR010W	<i>RPL27A</i>	W	S	S	Protein component of the large (60S) ribosomal subunit	This study
YDL191W	<i>RPL35A</i>	W	W	S	Protein component of the large (60S) ribosomal subunit	This study
YPR043W	<i>RPL43A</i>	VW	VW	VW	Protein component of the large (60S) ribosomal subunit	This study
YDL020C	<i>RPN4</i>	+	VW	VW	Transcription factor that stimulates expression of proteasome genes	This study
YDL081C	<i>RPP1A</i>	+	+	S	Ribosomal protein P1 alpha, a component of the ribosomal stalk	This study
YDL130W	<i>RPP1B</i>	+	+	S	Ribosomal protein P1 beta, component of the ribosomal stalk	This study
YLR048W	<i>RPS0B</i>	W	W	W	Protein component of the small (40S) ribosomal subunit	This study
YDL083C	<i>RPS16B</i>	+	+	S	Protein component of the small (40S) ribosomal subunit	This study
YOL121C	<i>RPS19A</i>	+	+	S	Protein component of the small (40S) ribosomal subunit	This study
YOR096W	<i>RPS7A</i>	VW	VW	W	Protein component of the small (40S) ribosomal subunit	This study
YBR189W	<i>RPS9B</i>	+	W	W	Protein component of the small (40S) ribosomal subunit	This study
YIL153W	<i>RRD1</i>	+	+	W	Peptidyl-prolyl cis/trans-isomerase, activator of the phosphotyrosyl phosphatase activity of PP2A	This study

(continued)

TABLE S1**(Continued)**

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YHR038W	<i>RRF1</i>	+	W	S	Mitochondrial ribosome recycling factor, essential for mitochondrial protein synthesis and respiratory function of mitochondria	This study
YGR056W	<i>RSC1</i>	VW	VW	S	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex	This study
YLR357W	<i>RSC2</i>	VW	W	S	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex	This study
YOL067C	<i>RTG1</i>	W	W	S	Transcription factor (bHLH) involved in interorganellar communication between mitochondria, peroxisomes, and nucleus	This study
YDR289C	<i>RTT103</i>	+	+	S	Protein that interacts with exonuclease Rat1p and Rai1p and plays a role in transcription termination by RNA polymerase II	This study
YOR216C	<i>RUD3</i>	VW	W	W	Golgi matrix protein involved in the structural organization of the cis-Golgi; interacts genetically with COG3 and USO1	This study
YDR389W	<i>SAC7</i>	W	W	S	GTPase activating protein (GAP) for Rho1p, involved in signaling to the actin cytoskeleton	This study
YGL175C	<i>SAE2</i>	+	VW	S	Endonuclease that processes hairpin DNA structures with the MRX complex; involved in meiotic and mitotic double-strand break repair	This study
YER129W	<i>SAK1</i>	+	+	S	Upstream kinase for the SNF1 complex	This study
YFR040W	<i>SAP155</i>	+	+	S	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function	This study
YDR351W	<i>SBE2</i>	+	+	W	Protein involved in the transport of cell wall components from the Golgi to the cell surface	This study
YMR214W	<i>SC71</i>	+	+	S	One of several homologs of bacterial chaperone DnaJ	This study
YBL091C-A	<i>SCS22</i>	+	+	W	Protein involved in regulation of phospholipid metabolism; homolog of Scs2p	This study
YMR272C	<i>SCS7</i>	VW	W	VW	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids	This study
YBL011W	<i>SCT1</i>	VW	W	S	Glycerol 3-phosphate/dihydroxyacetone phosphate dual substrate-specific sn-1 acyltransferase of the glycerolipid biosynthesis pathway	This study
YDR469W	<i>SDC1</i>	VW	VW	W	Subunit of the COMPASS (Set1C) complex	This study
YLR268W	<i>SEC22</i>	W	W	S	R-SNARE protein; assembles into SNARE complex with Bet1p, Bos1p and Sed5p; cycles between the ER and Golgi complex	This study
YLR292C	<i>SEC72</i>	+	+	S	Non-essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p)	This study
YER081W	<i>SER3</i>	+	+	S	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser33p	This study
YBL102W	<i>SFT2</i>	+	W	VW	Non-essential tetra-spanning membrane protein found mostly in the late Golgi, can suppress some sed5 alleles	This study
YGL066W	<i>SGF73</i>	W	W	S	Subunit of SAGA histone acetyltransferase complex	This study
YMR190C	<i>SGS1</i>	+	VW	W	Nucleolar DNA helicase of the RecQ family involved in maintenance of genome integrity	This study
YER118C	<i>SHO1</i>	+	+	W	Transmembrane osmosensor, participates in activation of both the filamentous growth pathway and the HOG pathway	This study

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YBL058W	<i>SHP1</i>	+	+	W	UBX (ubiquitin regulatory X) domain-containing protein that regulates Glc7p phosphatase activity and interacts with Cdc48p	This study
YOL110W	<i>SHR5</i>	+	+	S	Subunit of a palmitoyltransferase, composed of Shr5p and Erf2p, that adds a palmitoyl lipid moiety to Ras2p	This study
YLR079W	<i>SIC1</i>	+	W	S	Inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase	This study
YNL236W	<i>SLN4</i>	S	S	NG	Subunit of the Mediator complex; interacts with the RNA polymerase II holoenzyme	This study
YDR422C	<i>SIP1</i>	+	+	W	Alternate beta-subunit of the Snf1p kinase complex, may confer substrate specificity	This study
YHR206W	<i>SKN7</i>	+	+	S	Transcription factor required for induction of heat-shock genes; involved in osmoregulation; associates with and stabilizes Crz1p	This study
YBL061C	<i>SKT5</i>	+	+	W	Activator of Chs3p (chitin synthase III), recruits Chs3p to the bud neck via interaction with Bni4p	This study
YOR008C	<i>SLG1</i>	VW	W	S	Sensor-transducer to activate the PKC-CWI signaling pathway	This study
YIL105C	<i>SLM1</i>	+	+	S	Phosphoinositide PI(4,5)P ₂ binding protein, forms a complex with Slm2p; acts downstream of Mss4p; effector of the TORC2 complex	This study
YDL033C	<i>SLM3</i>	+	+	W	tRNA-specific 2-thiouridylyase, responsible for 2-thiolation of the wobble base of mitochondrial tRNAs	This study
YBR077C	<i>SLM4</i>	+	+	W	Component of the EGO complex, which is involved in the regulation of microautophagy; required for sorting of Gap1p	This study
YER116C	<i>SLX8</i>	W	W	S	Protein that forms a complex with Hex3p; possible role in resolving recombination intermediates during DNA replication or repair	This study
YOL122C	<i>SMF1</i>	+	+	W	Divalent metal ion transporter with a broad specificity for di-valent and tri-valent metals	This study
YGR229C	<i>SMI1</i>	+	+	S	Protein involved in the regulation of cell wall synthesis; proposed to be involved in coordinating cell cycle progression with cell wall integrity	This study
YKL079W	<i>SMY1</i>	+	+	S	Protein that interacts with Myo2p, proposed to be involved in exocytosis	This study
YJL151C	<i>SN43</i>	+	+	S	Integral membrane protein localized to vacuolar intraluminal vesicles	This study
YDL194W	<i>SNF3</i>	+	+	W	Plasma membrane glucose sensor that regulates glucose transport; required for low glucose induction of Hxt2p and Hxt4p	This study
YGL127C	<i>SOH1</i>	VW	W	S	Subunit of the RNA polymerase II mediator complex	This study
YMR016C	<i>SOK2</i>	+	+	S	Nuclear protein that plays a regulatory role in the cyclic AMP (cAMP)-PKA signal transduction pathway	This study
YJL192C	<i>SOP4</i>	+	+	S	ER-membrane protein; suppressor of pma1-7, deletion of SOP4 slows down the export of wild-type Pma1p and Pma1-7 from the ER	This study
YLL021W	<i>SPA2</i>	+	+	S	Component of the polarisome; acts as a scaffold for Mkk1p and Mpk1p cell wall integrity signaling components	This study

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YML055W	<i>SPC2</i>	+	+	W	Subunit of signal peptidase complex (Spc1p, Spc2p, Spc3p, Sec11p), which cleavage of proteins targeted to the secretory pathway	This study
YKL184W	<i>SPE1</i>	+	VW	S	Ornithine decarboxylase, catalyzes the first step in polyamine biosynthesis	This study
YOL052C	<i>SPE2</i>	W	VW	VW	S-adenosylmethionine decarboxylase, required for the biosynthesis of spermidine and spermine	This study
YEL031W	<i>SPF1</i>	W	W	S	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca ²⁺ homeostasis	This study
YER150W	<i>SPI1</i>	+	+	W	GPI-anchored, serine/threonine rich cell wall protein of unknown function; basal expression requires Msn2p/Msn4p	This study
YPL138C	<i>SPP1</i>	+	+	S	Subunit of COMPASS (Set1C), complex	This study
YDR392W	<i>SPT3</i>	VW	W	S	Subunit of the SAGA and SAGA-like transcriptional regulatory complexes, interacts with Spt15p	This study
YGR063C	<i>SPT4</i>	W	W	S	Protein that forms a complex with Spt5p and mediates both activation and inhibition of transcription elongation	This study
YLR055C	<i>SPT8</i>	+	+	S	Subunit of the SAGA transcriptional regulatory complex but not present in SAGA-like complex SLIK/SALSA	This study
YML034W	<i>SRC1</i>	W	W	S	Inner nuclear membrane protein with a putative role in sister chromatid segregation	This study
YHR178W	<i>STB5</i>	S	S	S	Activator of multidrug resistance genes, forms a heterodimer with Pdr1p	This study
YCL032W	<i>STE50</i>	+	+	S	Protein involved in invasive/filamentous growth, and osmotolerance, acts as an adaptor linking Cdc42p-Ste20p complex to Ste11p	This study
YLR150W	<i>STM1</i>	+	+	S	Protein that binds G4 quadruplex and purine motif triplex nucleic acid	This study
YDL048C	<i>STP4</i>	+	+	S	Protein containing a Kruppel-type zinc-finger domain	This study
YDR297W	<i>SUR2</i>	+	+	W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosynthesis	This study
YDR346C	<i>SVF1</i>	+	+	S	Protein with a potential role in cell survival pathways, required for the diauxic growth shift	This study
YAR003W	<i>SWD1</i>	+	+	S	Subunit of the COMPASS (Set1C) complex	This study
YBR175W	<i>SWD3</i>	VW	+	S	Subunit of the COMPASS (Set1C) complex	This study
YDR260C	<i>SWM1</i>	+	+	S	Subunit of the anaphase-promoting complex, which is an E3 ubiquitin ligase that regulates exit from mitosis	This study
YDR395W	<i>SXM1</i>	+	+	S	Nuclear transport factor (karyopherin) involved in protein transport between the cytoplasm and nucleoplasm	This study
YLR354C	<i>TAL1</i>	+	+	W	Transaldolase, enzyme in the non-oxidative pentose phosphate pathway	This study
YEL048C	<i>TCA17</i>	+	+	S	TRAPP Complex Associated protein 17 kDa	This study
YDL185W	<i>TFP1</i>	W	S	S	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites	This study
YPL157W	<i>TGS1</i>	+	+	W	Trimethyl guanosine synthase, responsible for conversion of the m(7)G cap structure of snRNAs and snoRNAs to m(2,2,7)G	This study

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YLR237W	<i>THI7</i>	+	+	W	Plasma membrane transporter responsible for the uptake of thiamine, member of the major facilitator superfamily of transporters	This study
YGR162W	<i>TIF4631</i>	W	W	W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p)	This study
YGL049C	<i>TIF4632</i>	+	+	S	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p)	This study
YOL018C	<i>TLG2</i>	VW	VW	VW	Syntaxin-like t-SNARE that forms a complex with Tlg1p and Vti1p and mediates fusion of endosome-derived vesicles with the late Golgi	This study
YKL056C	<i>TMA19</i>	+	+	S	Protein that associates with ribosomes; homolog of translationally controlled tumor protein	This study
YER007C-A	<i>TMA20</i>	VW	VW	W	Protein of unknown function that associates with ribosomes and has a putative RNA binding domain	This study
YJR066W	<i>TOR1</i>	+	+	S	PIK-related protein kinase and rapamycin target; subunit of TORC1, a complex that controls growth in response to nutrients	This study
YGL179C	<i>TOS3</i>	+	+	S	Protein kinase, related to and functionally redundant with Elm1p and Sak1p for the phosphorylation and activation of Snf1p	This study
YNL079C	<i>TPM1</i>	W	W	S	Major isoform of tropomyosin; acetylated by the NatB complex	This study
YBR126C	<i>TPS1</i>	W	W	NG	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose	This study
YDR074W	<i>TPS2</i>	+	+	S	Phosphatase subunit of the trehalose-6-phosphate synthase/phosphatase complex, which synthesizes trehalose	This study
YOL093W	<i>TRM10</i>	+	+	S	tRNA methyltransferase, methylates the N-1 position of guanosine in tRNAs	This study
YOL124C	<i>TRM11</i>	+	+	W	Catalytic subunit of an adoMet-dependent tRNA methyltransferase complex (Trm11p-Trm112p)	This study
YDL201W	<i>TRM8</i>	+	+	S	Subunit of a tRNA methyltransferase complex composed of Trm8p and Trm82p that catalyzes 7-methylguanosine modification of tRNA	This study
YML014W	<i>TRM9</i>	VW	VW	S	tRNA methyltransferase, catalyzes the esterification of modified uridine nucleotides in tRNAs	This study
YDR354W	<i>TRP4</i>	+	+	W	Anthranilate phosphoribosyl transferase of the tryptophan biosynthetic pathway	This study
YML028W	<i>TSA1</i>	+	+	S	Ubiquitous housekeeping thioredoxin peroxidase	This study
YHR111W	<i>UBA4</i>	S	S	S	Protein that activates Urm1p before its conjugation to proteins (urmylation)	This study
YLL039C	<i>UBI4</i>	+	+	S	Ubiquitin, becomes conjugated to proteins, marking them for selective degradation via the ubiquitin-26S proteasome system	This study
YBR058C	<i>UBP14</i>	+	VW	S	Ubiquitin-specific protease that specifically disassembles unanchored ubiquitin chains	This study
YMR304W	<i>UBP15</i>	+	+	W	Ubiquitin-specific protease that may play a role in ubiquitin precursor processing	This study

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YFR010W	<i>UBP6</i>	W	W	S	Ubiquitin-specific protease in the subcomplex of the 26S proteasome, releases free ubiquitin from branched polyubiquitin chains	This study
YML013W	<i>UBX2</i>	VW	VW	S	Protein involved in ER-associated protein degradation; proposed to coordinate the assembly of proteins involved in ERAD	This study
YMR067C	<i>UBX4</i>	+	+	S	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p	This study
YDL190C	<i>UFD2</i>	+	+	S	Ubiquitin chain assembly factor (E4) that cooperates with enzymes (E1), (E2), (E3) to conjugate ubiquitin to substrates	This study
YNL229C	<i>URE2</i>	W	W	S	Nitrogen catabolite repression regulator that acts by inhibition of GLN3 transcription in good nitrogen source	This study
YDR400W	<i>URH1</i>	+	+	VW	Uridine nucleosidase (uridine-cytidine N-ribohydrolase), cleaves N-glycosidic bonds in nucleosides	This study
YEL040W	<i>UTR2</i>	+	+	W	Cell wall protein that functions in the transfer of chitin to beta(1-6)glucan; GPI-anchored protein localized to the bud neck	This study
YEL013W	<i>VAC8</i>	+	+	S	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway	This study
YOR106W	<i>VAM3</i>	+	+	S	Protein required for vacuolar assembly; functions with Vam7p in vacuolar protein trafficking	This study
YDL077C	<i>VAM6</i>	+	+	W	Vacuolar protein; plays a role in vacuolar membrane fusion as GEF of the Ypt7p and it is also a GEF of Gtr1p in the EGO complex	This study
YML115C	<i>VAN1</i>	W	W	W	Component of the mannan polymerase I; forms a complex with Mnn9p, which is involved in mannan synthesis	This study
YLR373C	<i>VID22</i>	VW	VW	VW	Glycosylated membrane protein; plays a role in fructose-1,6-bisphosphatase (FBPase) degradation and transport	This study
YIL017C	<i>VID28</i>	+	+	S	Protein involved in proteasome-dependent degradation of fructose-1,6-bisphosphatase (FBPase)	This study
YPR036W	<i>VMA13</i>	S	S	S	Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase)	This study
YBR127C	<i>VMA2</i>	S	S	S	Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase)	This study
YGR105W	<i>VMA21</i>	VW	W	S	Integral membrane protein that is required for vacuolar H ⁺ -ATPase (V-ATPase) function; not a component of the V-ATPase complex	This study
YHR060W	<i>VMA22</i>	W	W	S	Integral membrane protein that is required for vacuolar H ⁺ -ATPase (V-ATPase) function; not a component of the V-ATPase complex	This study
YGR020C	<i>VMA7</i>	VW	W	S	Subunit F of the eight-subunit V1 peripheral membrane domain of vacuolar H ⁺ -ATPase (V-ATPase)	This study

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YEL051W	<i>VMA8</i>	S	S	S	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase)	This study
YOR270C	<i>VPH1</i>	+	+	W	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole	This study
YKL119C	<i>VPH2</i>	W	S	S	Integral membrane protein that is required for vacuolar H ⁺ -ATPase (V-ATPase) function; not a component of the V-ATPase complex	This study
YPL065W	<i>VPS28</i>	+	+	S	Component of the ESCRT-I complex, which is involved in ubiquitin-dependent sorting of proteins into the endosome	This study
YDR080W	<i>VPS41</i>	+	VW	W	Vacuolar membrane protein that is a subunit of the homotypic vacuole fusion and vacuole protein sorting (HOPS) complex	This study
YDR486C	<i>VPS60</i>	+	+	S	Cytoplasmic and vacuolar membrane protein involved in late endosome to vacuole transport	This study
YDR200C	<i>VPS64</i>	+	+	S	Cytoplasmic protein required for cytoplasm to vacuole targeting of proteins	This study
YPR139C	<i>VPS66</i>	+	W	S	Cytoplasmic protein of unknown function involved in vacuolar protein sorting.	This study
YOR359W	<i>VTS1</i>	VW	VW	S	Protein of unknown function, shows genetic interactions with Vti1p, which is a v-SNARE involved in cis-Golgi membrane traffic	This study
YGR241C	<i>YAP1802</i>	+	+	W	Protein involved in clathrin cage assembly	This study
YGL060W	<i>YBP2</i>	+	+	W	Protein with a role in resistance to oxidative stress	This study
YEL004W	<i>YEA4</i>	+	+	W	Uridine diphosphate-N-acetylglucosamine (UDP-GlcNAc) transporter required for cell wall chitin synthesis	This study
YEL041W	<i>YEF1</i>	+	+	S	ATP-NADH kinase; phosphorylates both NAD and NADH;	This study
YDR057W	<i>YOS9</i>	+	+	W	Lectin; soluble luminal ER protein; serves as a receptor that recognizes misfolded N-glycosylated proteins targeted to ERAD	This study
YBR183W	<i>YPC1</i>	VW	+	W	Alkaline ceramidase that also has reverse (CoA-independent) ceramide synthase activity	This study
YMR104C	<i>YPK2</i>	W	W	W	Protein kinase with similarity to Ser/Thr protein kinase Ypk1p; functionally redundant with YPK1	This study
YDR368W	<i>YPR1</i>	+	+	W	NADP ⁺ -dependant glycerol dehydrogenase	This study
YLR262C	<i>YPT6</i>	+	+	VW	GTPase, Ras-like GTP binding protein, required for fusion of endosome-derived vesicles with the late Golgi	This study
YOL109W	<i>ZE01</i>	+	+	S	Peripheral membrane protein of the plasma membrane that interacts with Mid2p and mediates the PKC-CWI signaling pathway	This study
YCL033C	<i>YCL033C</i>	+	+	S	Putative protein-methionine-R-oxide reductase; involved in response to oxidative stress	This study
YCR045C	<i>YCR045C</i>	+	+	W	Putative protein of unknown function	This study
YCR076C	<i>YCR076C</i>	+	+	W	Putative protein of unknown function; is not an essential gene	This study
YDL073W	<i>YDL073W</i>	+	+	S	Putative protein of unknown function; is not an essential gene	This study

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YDR049W	<i>YDR049W</i>	VW	W	S	Zinc finger protein; putative transcription factor that may interact with proteins involved in histone acetylation or deacetylation	This study
YDR266C	<i>YDR266C</i>	+	+	W	Protein of unknown function that may interact with ribosomes, based on co-purification experiments	This study
YDR348C	<i>YDR348C</i>	+	+	S	Protein of unknown function	This study
YER152C	<i>YER152C</i>	+	VW	S	Putative protein of unknown function; is not an essential gene	This study
YGR250C	<i>YGR250C</i>	+	+	W	Putative protein of unknown function	This study
YHR162W	<i>YHR162W</i>	+	VW	W	Putative protein of unknown function	This study
YIL029C	<i>YIL029C</i>	+	+	S	Putative protein of unknown function	This study
YIL077C	<i>YIL077C</i>	+	+	W	Putative protein of unknown function	This study
YJL193W	<i>YJL193W</i>	+	+	S	Putative protein of unknown function; deletion mutant has a respiratory growth defect	This study
YKL027W	<i>YKL027W</i>	+	+	S	Protein of unknown function	This study
YKL077W	<i>YKL077W</i>	VW	W	S	Putative protein of unknown function	This study
YKR070W	<i>YKR070W</i>	+	+	W	Putative protein of unknown function	This study
YLR199C	<i>YLR199C</i>	+	+	S	Putative protein of unknown function	This study
YLR426W	<i>YLR426W</i>	+	W	S	Putative protein of unknown	This study
YMR010W	<i>YMR010W</i>	+	W	S	Putative protein of unknown function	This study
YMR099C	<i>YMR099C</i>	+	+	W	Protein of unknown function with similarity to aldose 1-epimerase	This study
YOL087C	<i>YOL087C</i>	+	+	S	Putative protein of unknown function	This study
YOL098C	<i>YOL098C</i>	+	+	W	Putative metalloprotease	This study
YOL107W	<i>YOL107W</i>	+	+	S	Putative protein of unknown function; colocalizes with COPI-coated vesicles	This study
YOR012W	<i>YOR012W</i>	+	+	W	Putative protein of unknown function	This study
YOR246C	<i>YOR246C</i>	+	+	W	Protein with similarity to oxidoreductases, found in lipid particles	This study
YPL264C	<i>YPL264C</i>	W	VW	W	Putative membrane protein of unknown function	This study
YOR141C	<i>ARP8</i>	W	S	NG	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes INO80	(Shen et al. 2003a)
YJL095W	<i>BCK1</i>	S	S	S	Mitogen-activated protein (MAP) kinase kinase kinase acting in the protein kinase C signaling pathway	(Nunez et al. 2008)
YAL021C	<i>CCR4</i>	+	+	W	Component of the CCR4-NOT transcriptional complex	(Betz et al. 2002)
YDR069C	<i>DOA4</i>	S	S	NG	Ubiquitin hydrolase, required for recycling ubiquitin; acts at the proteasome, late endosome/prevacuolar compartment	(Henry and Patton-Vogt 1998)
YFL031W	<i>HAC1</i>	S	S	S	Transcription factor that regulates the unfolded protein response, via UPRE binding; spliced by Ire1p upon ER stress	(Nikawa et al. 1996)
YGL194C	<i>HOS2</i>	W	W	S	Histone deacetylase; subunit of the Set3 complex, a meiotic-specific repressor of sporulation specific genes	(Cohen et al. 2008)

(continued)

TABLE S1**(Continued)**

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YEL044W	<i>IES6</i>	S	S	NG	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions	(Fernandez-Murray et al. 2009)
YJL153C	<i>INO1</i>	S	S	S	Inositol 1-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids	(Culbertson and Henry 1975)
YDR123C	<i>INO2</i>	S	S	S	Component of the Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements (ICREs)	(Donahue and Henry 1981)
YOL108C	<i>INO4</i>	S	S	S	Component of the Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements (ICREs)	(Donahue and Henry 1981)
YHR079C	<i>IRE1</i>	S	S	S	Ser/Thr kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response mediates HAC1 mRNA splicing	(Nikawa and Yamashita 1992)
YML059C	<i>NTE1</i>	+	W	S	Serine esterase that deacylates exogenous lysophospholipids, homolog of human neuropathy target esterase (NTE)	(Nunez et al. 2008)
YBR279W	<i>PAF1</i>	S	S	NG	RNA polymerase II-associated protein, defines the Paf1 complex that is biochemically and functionally distinct from the Srb-Mediator	(Betz et al. 2002)
YLR039C	<i>RIC1</i>	VW	W	NG	Protein involved in retrograde transport to TGN; forms heterodimer with Rgp1p that acts as a GTP exchange factor for Ypt6p	(Kodaki et al. 1995)
YJL140W	<i>RPB4</i>	S	S	NG	RNA polymerase II subunit B32; forms two subunit dissociable complex with Rpb7p	(Woychik and Young 1989)
YGL244W	<i>RTF1</i>	VW	W	S	Subunit of the RNA polymerase II-associated Paf1 complex	(Betz et al. 2002)
YKL212W	<i>SAC1</i>	S	S	S	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein trafficking and secretion	(Whitters et al. 1993)
YER120W	<i>SCS2</i>	W	W	S	Integral ER membrane protein; regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p	(Kagiwada et al. 1998)
YGL126W	<i>SCS3</i>	VW	S	S	Protein required for inositol prototrophy, appears to be involved in the synthesis of inositol phospholipids from inositol	(Hosaka et al. 1994)
YKR029C	<i>SET3</i>	+	W	S	Defining member of the SET3 histone deacetylase complex which is a meiosis-specific repressor of sporulation genes	(Cohen et al. 2008)
YBR103W	<i>SIF2</i>	W	W	S	WD40 repeat-containing subunit of the Set3C histone deacetylase complex, which represses early/middle sporulation genes	(Cohen et al. 2008)
YHR030C	<i>SLT2</i>	VW	S	S	Ser/Thr MAP kinase involved in cell wall integrity and progression through the cell cycle; part of the protein kinase C signaling pathway	(Nunez et al. 2008)
YDR477W	<i>SNF1</i>	W	W	S	AMP-activated Ser/Thr kinase; forms a complex with Snf4p and members of the Sip1p/Sip2p/Gal83p family	(Hirschhorn et al. 1992)
YOR290C	<i>SNF2</i>	+	VW	VW	Catalytic subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation	(Peterson and Herskowitz 1992)

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YGL115W	<i>SNF4</i>	W	W	S	Protein kinase activator found in a complex containing Snf1p and its beta subunits; activates the Snf1p protein kinase	(Fernandez-Murray et al. 2009)
YBR289W	<i>SNF5</i>	S	S	S	Subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation	(Peterson and Herskowitz 1992)
YHL025W	<i>SNF6</i>	S	S	S	Subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation	(Peterson and Herskowitz 1992)
YCR033W	<i>SNT1</i>	W	S	S	Subunit of the Set3C deacetylase complex; putative DNA-binding protein	(Cohen et al. 2008)
YHR041C	<i>SRB2</i>	S	S	S	Transcription factor, subunit of the RNA polymerase II mediator complex	(Koleske et al. 1992)
YGR104C	<i>SRB5</i>	VW	VW	NG	Subunit of the RNA polymerase II mediator complex	(Betz et al. 2002)
YMR039C	<i>SUB1</i>	W	W	S	Transcriptional coactivator, facilitates elongation, acts in a peroxide resistance pathway involving Rad2p	(Knaus et al. 1996)
YJL176C	<i>SWI3</i>	W	S	S	Subunit of the SWI/SNF chromatin remodeling complex; required for transcription of many genes such as <i>HO</i> and <i>INO1</i>	(Peterson and Herskowitz 1992)
YKL065C	<i>YET1</i>	W	S	S	Endoplasmic reticulum transmembrane protein, form a complex with the ER translocation machinery; homolog of human BAP31 protein	(Wilson and Barlowe 2010)
YDL072C	<i>YET3</i>	S	S	S	Endoplasmic reticulum transmembrane protein, form a complex with the ER translocation machinery; homolog of human BAP31 protein	(Wilson and Barlowe 2010)
YNL059C	<i>ARP5^a</i>	NG	NG	NG	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes	(Shen et al. 2003a)
YLR226W	<i>BUR2^a</i>	+	+	+	Cyclin for the Sgv1p (Bur1p) protein kinase	(Prelich and Winston 1993)
YBR135W	<i>CKS1^a</i>	NS	NS	NS	Subunit of the Cdc28 protein kinase, required for mitotic proteolysis, may also be involved in the proteolysis of the G1 cyclins	(Yu and Reed 2004)
YOL145C	<i>CTR9^a</i>	NS	NS	NS	Component of the Paf1p complex	(Betz et al. 2002)
YPL254W	<i>HFI1^a</i>	NG	NG	NG	Adaptor protein required for integrity of the SAGA complex	(Horiuchi et al. 1997)
YDR138W	<i>HPR1^a</i>	NG	NG	NG	Subunit of THO/TREX complexes	(Betz et al. 2002)
YGL070C	<i>RPB9^a</i>	NG	NG	NG	RNA polymerase II subunit B12.6	(Furter-Graves et al. 1994)
YOL148C	<i>SPT20^a</i>	NG	NG	NG	Subunit of the SAGA transcriptional regulatory complex	(Roberts and Winston 1996)
YBR081C	<i>SPT7^a</i>	NS	NS	NS	Subunit of the SAGA transcriptional regulatory complex	(Gansheroff et al. 1995)
YGL150C	<i>INO80^a</i>	NS	NS	NS	ATPase that forms a large complex Ino80, containing actin and several actin-related proteins, that has chromatin remodeling activity	(Ebbert et al. 1999)
YNL267W	<i>PIK1^a</i>	NS	NS	NS	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate	(Walch-Solimena and Novick 1999)
YPR113W	<i>PLS1^a</i>	NS	NS	NS	Phosphatidylinositol synthase	(Nikawa et al. 1987)
YBL105C	<i>PKC1^a</i>	NS	NS	NS	Protein serine/threonine kinase essential for cell wall remodeling during growth	(Nunez et al. 2008)

(continued)

TABLE S1
(Continued)

ORF	Gene	I-C- 30°	I-C+ 30°	I-C+ 37°	Description	Reference
YOR210W	<u><i>RPB10^a</i></u>	NS	NS	NS	RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III	(Shpakovski et al. 1995)
YOR151C	<u><i>RPB2^a</i></u>	NS	NS	NS	RNA polymerase II second largest subunit B150, part of central core; similar to bacterial beta subunit	(Scafe et al. 1990b)
YOR224C	<u><i>RPB8^a</i></u>	NS	NS	NS	RNA polymerase subunit ABC14.5, common to RNA polymerases I, II, and III	(Shpakovski et al. 1995)
YHR143W-A	<u><i>RPC10^a</i></u>	NS	NS	NS	RNA polymerase subunit, found in RNA polymerase complexes I, II, and III	(Shpakovski et al. 1995)
YDL140C	<u><i>RPO21^a</i></u>	NS	NS	NS	RNA polymerase II largest subunit B220, part of central core	(Nonet and Young 1989)
YPR187W	<u><i>RPO26^a</i></u>	NS	NS	NS	RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III; part of central core	(Shpakovski et al. 1995)
YLR208W	<u><i>SEC13^a</i></u>	NS	NS	NS	Component of both the Nup84 nuclear pore sub-complex and of the COPII complex (Sar1p, Sec13p, Sec16p, Sec23p, Sec24p, Sec31p, Sfb2p, and Sfb3p)	(Gilstring et al. 1999)
YMR079W	<u><i>SEC14^a</i></u>	NS	NS	NS	Phosphatidylinositol/phosphatidylcholine transfer protein; involved in regulating PtdIns, PtdCho, and ceramide metabolism, products of which regulate intracellular transport and UPR	(Kearns et al. 1997)
YPR161C	<u><i>SGV1^a</i></u>	NS	NS	NS	Cyclin (Bur2p)-dependent protein kinase that functions in transcriptional regulation	(Prelich and Winston 1993)
YER148W	<u><i>SPT15^a</i></u>	NS	NS	NS	TATA-binding protein, general transcription factor that interacts with other factors to form the preinitiation complex at promoters	(Shirra and Arndt 1999)
YPR086W	<u><i>SUA7^a</i></u>	NS	NS	NS	Transcription factor TFIIIB, a general transcription factor required for transcription initiation and start site selection by RNA polymerase II	(Berroteran et al. 1994)
YPL016W	<u><i>SWI1^a</i></u>	NS	NS	NS	Subunit of the SWI/SNF chromatin remodeling complex; required for transcription of many genes such as <i>HO</i> and <i>INO1</i>	(Peterson and Herskowitz 1992)
YPR056W	<u><i>TFB4^a</i></u>	NS	NS	NS	Subunit of TFIIH complex, involved in transcription initiation	(Feaver et al. 1999)
YDR050C	<u><i>TPI1^a</i></u>	NS	NS	NS	Triose phosphate isomerase	(Shi et al. 2005)
YHR099W	<u><i>TRA1^a</i></u>	NS	NS	NS	Subunit of SAGA and NuA4 histone acetyltransferase complexes	(Mutiu et al. 2007)
YJL087C	<u><i>TRL1^a</i></u>	NS	NS	NS	tRNA ligase, required for tRNA splicing	(Sidrauski et al. 1996)

Phenotypes were scored as follows: mutants that grew well on I⁺C⁻ medium at a given temperature, but whose growth was visibly weaker on either I⁻C⁻ or I⁻C⁺ media, were scored as very weak (VW). Mutants exhibiting very reduced but still detectable growth in I⁻C⁻ or I⁻C⁺ media were scored as weak (W). Mutants exhibiting no visible growth on I⁻C⁻ or I⁻C⁺ media were scored as strong (S) (See Figure 1). A score of “+” indicates no growth reduction in any inositol lacking media, and compared to growth on I⁺C⁻ and I⁺C⁺ medium at the corresponding temperature. A score of “NS” (Not Screened) indicates that the mutant conferring the Ino⁻ phenotype was not present in the homozygous diploid strain collection. A score of “NG” (No Growth) indicates that the deletion mutant from the homozygous diploid collection failed to grow in either synthetic I⁺C⁺, I⁺C⁻, and/or YPD medium at a given temperature. Underlined gene names indicate deletions of essential genes for which conditional alleles have been reported to confer an Ino⁻ phenotype. References are provided for those mutations previously shown to confer an Ino⁻ phenotype.

^a Mutations previously shown to confer an Ino⁻ phenotype that were not confirmed in this study.

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