

Insoluble solids at high concentrations repress yeast's response against stress and increase intracellular ROS levels

Antonio D. Moreno^{1*}, Cristina González-Fernández², Mercedes Ballesteros^{1,2}, Elia Tomás-Pejó²

¹ CIEMAT, Department of Energy, Biofuels Unit, 28040 Madrid, Spain

² IMDEA Energy Institute, Biotechnological Processes for Energy Production Unit, 28935 Móstoles, Spain.

*Correspondence to: Antonio D. Moreno, CIEMAT, Department of Energy, Biofuels Unit, Avda. Complutense 40, 28040 Madrid, Spain. Phone: +34 91 346 6054. E-mail: david.moreno@ciemat.es

Supplementary Table S1

Table S1. Upregulated and downregulated genes with molecular function unknown

Gene (Systematic name)	Brief description	Log2-fold change
Upregulated genes:		
ECM1	Pre-ribosomal factor involved in 60S ribosomal protein subunit export	0.9
SEO1	Putative permease	1.5
YBL028C	Protein of unknown function that may interact with ribosomes	0.7
PAU9	Protein of unknown function	1.9
MIC10	Conserved component of the MICOS complex	0.8
YCR051W	Putative protein of unknown function; non-essential gene	1.0
YDL012C	Tail-anchored plasma membrane protein with a conserved CYSTM module; possibly involved in response to stress	0.7
KNH1	Protein with similarity to Kre9p; required for propionic acid resistance	1.1
RAD59	Protein involved DNA double-strand break repair; repairs breaks in DNA during vegetative growth via recombination and single-strand annealing	1.1
YDL121C	Putative protein of unknown function; non-essential gene	0.8
YDR034C-A	Putative protein of unknown function	1.9
BCP1	Essential protein involved in nuclear export of Mss4p, which plays a role in actin cytoskeleton organization and vesicular transport	1.2
IRC22	Protein of unknown function; non-essential gene	0.7
GTT3	Protein of unknown function may be involved in glutathione metabolism	0.6
SCC4	Subunit of cohesin loading factor (Scc2p-Scc4p); involved in establishing sister chromatid cohesion during double-strand break repair via phosphorylated histone H2AX	1.1
YER156C	Putative protein of unknown function; expression is copper responsive and downregulated in strains deleted for MAC1, a copper-responsive transcription factor	0.9
FMP10	Putative protein of unknown function	0.8
YER186C	Putative protein of unknown function	1.0
YFR035C	Putative protein of unknown function	1.1
YGL101W	Protein of unknown function; non-essential gene	0.9
MTO1	Mitochondrial protein	1.0

VHT1	High-affinity plasma membrane H ⁺ -biotin (vitamin H) symporter	0.8
YGR125W	Putative protein of unknown function	0.6
BNS1	Protein of unknown function	1.2
YGR266W	Protein of unknown function; protein abundance increases in response to DNA replication stress	1.2
CIA2	Component of cytosolic iron-sulfur protein assembly (CIA) machinery; forms the CIA targeting complex with Cia1p and Met18p that directs Fe-S cluster incorporation into a subset of proteins involved in methionine biosynthesis, DNA replication and repair, transcription, and telomere maintenance	1.1
AXL2	Integral plasma membrane protein; required for axial budding in haploid cells	0.8
AIM20	Protein of unknown function; overexpression causes cell cycle delay or arrest	0.9
YJL047C-A	Putative protein of unknown function	1.1
ALB1	Shuttling pre-60S factor; involved in the biogenesis of ribosomal large subunit	0.8
CYC1	Cytochrome c, isoform 1; electron carrier of mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c oxidoreductase to cytochrome c oxidase during cellular respiration	2.7
YKL068W-A	Putative protein of unknown function	1.8
DPH2	Protein required for synthesis of diphthamide	1.1
SRP40	Nucleolar serine-rich protein; role in preribosome assembly or transport; may function as a chaperone of small nucleolar ribonucleoprotein particles (snoRNPs)	1.0
PTR2	Integral membrane peptide transporter; mediates transport of di- and tri-peptides	1.6
MIM2	Mitochondrial protein required for outer membrane protein import	1.1
YML018C	Protein of unknown function; non-essential gene	0.9
SUR7	Plasma membrane protein, component of eisosomes	1.5
MIX17	Mitochondrial intermembrane space protein; required for normal oxygen consumption; protein abundance increases in response to DNA replication stress	0.8
AIM34	Protein of unknown function	1.5
FMP42	Putative protein of unknown function	1.0
YNL095C	Putative protein of unknown function; non-essential gene	1.6
CWC25	Splicing factor required for the first step of pre-mRNA splicing; heat-stable protein	0.8
YOL014W	Putative protein of unknown function	1.3
YOL019W	Protein of unknown function	0.8

ZEO1	Peripheral membrane protein of the plasma membrane; regulates the cell integrity pathway mediated by Pkc1p and Slp2p	0.8
CYT1	Cytochrome c1; component of the mitochondrial respiratory chain	1.4
YOR072W-B	Putative protein of unknown function	1.7
YTM1	Constituent of 66S pre-ribosomal particles; required for maturation of the large ribosomal subunit	1.0
SFG1	Nuclear protein putative transcription factor; required for growth of superficial pseudohyphae but not for invasive pseudohyphal growth	1.1
CIR2	Putative ortholog of human ETF-dH; may have a role in oxidative stress response	1.9
TYW1	Iron-sulfur protein required for synthesis of Wybutosine modified tRNA; induction by Yap5p in response to iron provides protection from high iron toxicity; overexpression results in increased cellular iron	0.8
NIP7	Nucleolar protein required for 60S ribosome subunit biogenesis	1.0
Downregulated genes:		
MAK16	Essential nuclear protein; maintenance of killer	-1.0
FRT2	Tail-anchored ER membrane protein of unknown function; functionally related to TCP1	-2.0
FUN19	Non-essential protein of unknown function; expression induced in response to heat stress	-1.1
YAR023C	Putative integral membrane protein	-1.1
YAR029W	Member of DUP240 gene family but contains no transmembrane domains (protein localized to the cytoplasm)	-1.0
MOH1	Protein of unknown function, essential for stationary phase survival	-1.6
YBL111C	Helicase-like protein encoded within the telomeric Y' element; relocalizes from mitochondrion to cytoplasm upon DNA replication stress	-1.3
YRO2	Protein with a putative role in response to acid stress (protein localized to the mitochondrion and detected in plasma membrane in the presence of acetic acid)	-2.6
YBR085C-A	Protein of unknown function	-1.0
VID24	GID Complex regulatory subunit; vacuolar import and degradation	-0.8
AIM3	Protein that inhibits barbed-end actin filament elongation; altered inheritance rate of mitochondria	-1.8
YBR138C	Cytoplasmic protein of unknown function	-2.2
YSW1	Protein required for normal prospore membrane formation	-1.3
SDS24	Protein involved in cell separation during budding	-2.2
MTC4	Cytoplasmic protein of unknown function	-1.7
YBR285W	Putative protein of unknown function	-1.2

FUS1	Membrane protein localized to the shmoo tip that regulates the termination of mating projection growth; has a role in cortical protein anchoring	-1.0
GID7	Subunit of GID Complex that binds directly to central component Vid30p	-0.9
HSP30	Negative regulator of the H(+)-ATPase Pma1p involved in the response to various stresses such as heat, osmotic stress, and DNA damage; also involved in negative regulation of ATPase activity	-2.0
GPM2	Homolog of Gpm1p phosphoglycerate mutase; may be non-functional	-2.3
USO1	Essential protein involved in vesicle-mediated ER to Golgi transport; binds membranes and functions during vesicle docking to the Golgi; required for assembly of the ER-to-Golgi SNARE complex	-2.5
PEX19	Chaperone and import receptor for newly-synthesized class I PMPs; binds peroxisomal membrane proteins (PMPs) in the cytoplasm and delivers them to the peroxisome for subsequent insertion into the peroxisomal membrane	-1.2
BUG1	Cis-golgi localized protein involved in ER to Golgi transport; forms a complex with the mammalian GRASP65 homolog, Grh1p	-1.2
MSS2	Peripherally bound inner membrane protein of the mitochondrial matrix; involved in membrane insertion of C-terminus of Cox2p	-1.9
YDL109C	Putative lipase; involved in lipid metabolism; non-essential gene	-1.4
IWR1	RNA polymerase II transport factor, conserved from yeast to humans; also has a role in transporting RNA polymerase III into the nucleus	-1.1
SAS10	Subunit of U3-containing Small Subunit (SSU) processome complex; involved in production of 18S rRNA and assembly of small ribosomal subunit; disrupts silencing when overproduced	-1.5
MSH5	Protein of the MutS family; forms a dimer with Msh4p that facilitates crossovers between homologs during meiosis	-1.1
RTN2	Reticulon protein; involved in nuclear pore assembly and maintenance of tubular ER morphology; promotes membrane curvature; regulates the ER asymmetry-induced inheritance block during ER stress; role in ER-derived peroxisomal biogenesis	-1.5
FMP45	Integral membrane protein localized to mitochondria; required for sporulation and maintaining sphingolipid content	-1.6
HBT1	Shmoo tip protein, substrate of Hub1p ubiquitin-like protein	-1.2
ADY3	Protein required for spore wall formation; mediates assembly of the LEP complex, formation of the ring-like structure via interaction with spindle pole body components and prospore membrane maturation	-1.6
GAL3	Transcriptional regulator; involved in activation of the GAL genes in response to galactose	-1.1
RAD61	Subunit of a complex that inhibits sister chromatid cohesion; also negatively regulates chromosome condensation	-1.5
PST1	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; upregulated by cell wall damage via disruption of FKS1	-1.1
YOS9	ER quality-control lectin; participates in efficient ER retention of misfolded proteins by recognizing them and delivering them to Hrd1p	-1.2

RRG1	Protein of unknown function; required for vacuolar acidification and mitochondrial genome maintenance	-1.3
DOS2	Protein of unknown function	-1.7
SLU7	RNA splicing factor; required for ATP-independent portion of 2nd catalytic step of spliceosomal RNA splicing	-2.0
DOP1	Golgi-localized, leucine-zipper domain containing protein; involved in endosome to Golgi transport, organization of the ER, establishing cell polarity, and morphogenesis	-0.6
VPS64	Protein required for cytoplasm to vacuole targeting of proteins	-1.6
RAV2	Subunit of RAVE complex (Rav1p, Rav2p, Skp1p)	-0.9
DON1	Meiosis-specific component of the spindle pole body	-1.0
MTH1	Negative regulator of the glucose-sensing signal transduction pathway	-1.5
RAD34	Protein involved in nucleotide excision repair (NER)	-1.8
ESC2	Sumo-like domain protein; prevents accumulation of toxic intermediates during replication-associated recombinational repair; roles in silencing, lifespan, chromatid cohesion and the intra-S-phase DNA damage checkpoint	-1.9
YDR391C	Putative protein of unknown function; possibly involved in zinc homeostasis; Bdf1p-dependent transcription induced by salt stress	-1.1
HEH2	Inner nuclear membrane (INM) protein	-1.1
PRP3	Splicing factor; component of the U4/U6-U5 snRNP complex	-2.2
EMI2	Non-essential protein of unknown function implicated in sporulation and transcription regulation; required for transcriptional induction of the early meiotic-specific transcription factor IME1; required for sporulation	-1.1
KRE28	Subunit of a kinetochore-microtubule binding complex; required for sister chromatid bi-orientation and kinetochore binding of SAC components	-2.4
FIT1	Mannoprotein that is incorporated into the cell wall	-2.0
IRC4	Protein of unknown function	-1.3
RGH1	Protein of unknown function; involved in energy metabolism under respiratory conditions; protein abundance is increased upon intracellular iron depletion or in response to DNA replication stress	-1.7
SPI1	GPI-anchored cell wall protein involved in weak acid resistance	-1.1
YER158C	Protein of unknown function; potentially phosphorylated by Cdc28p	-0.8
SLO1	Protein interacting with Arl3p	-1.2
IES1	Subunit of the INO80 chromatin remodeling complex; relocalizes to the cytosol in response to hypoxia	-0.8
LAM5	Putative sterol transfer protein with a role in intracellular sterol transport, by similarity with Lam6p	-0.9

COS4	Endosomal protein involved in turnover of plasma membrane proteins; predicted to have a role in the multivesicular body sorting pathway	-0.9
YFL065C	Putative protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA irradiation	-1.4
FAR7	Protein involved in recovery from pheromone-induced cell cycle arrest	-1.4
YFR016C	Protein of unknown function	-1.5
ERJ5	Type I membrane protein with a J domain; required to preserve the folding capacity of the endoplasmic reticulum; loss of the non-essential ERJ5 gene leads to a constitutively induced unfolded protein response	-0.9
RIM8	Protein involved in proteolytic activation of Rim101p; part of response to alkaline pH	-1.0
YGL081W	Putative protein of unknown function; non-essential gene; interacts genetically with CHS5, a gene involved in chitin biosynthesis	-1.1
RRT6	Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription	-1.1
NUT1	Component of the RNA polymerase II mediator complex; mediator is required for transcriptional activation and also has a role in basal transcription	-1.0
VID30	Central component of GID Complex, involved in FBPase degradation; required for association of Vid vesicles and actin patches in vacuole import and degradation pathway; shifts the balance of nitrogen metabolism toward glutamate production	-1.2
YGL262W	Putative protein of unknown function	-1.1
STF2	Protein involved in resistance to desiccation stress; exhibits antioxidant properties, and its overexpression prevents ROS accumulation and apoptosis	-1.1
SEC9	t-SNARE protein required for secretory vesicle-plasma membrane fusion	-1.7
MTL1	Putative plasma membrane sensor; involved in cell integrity signaling and stress response during glucose starvation and oxidative stress	-0.9
MCO32	Putative protein of unknown function	-1.6
YGR066C	Putative protein of unknown function	-1.8
YGR130C	Component of the eisosome with unknown function	-1.6
ECL1	Protein of unknown function; overexpression increases oxygen consumption and respiratory activity while deletion results in reduced oxygen consumption under conditions of caloric restriction	-0.9
YHR022C	Putative protein of unknown function; non-essential gene	-1.4
NMD2	Protein involved in the nonsense-mediated mRNA decay (NMD) pathway	-1.6
RTC3	Protein of unknown function involved in RNA metabolism	-1.2
YHR140W	Putative integral membrane protein of unknown function	-1.2
LIN1	Non-essential component of U5 snRNP	-2.6

KEL1	Protein required for proper cell fusion and cell morphology	-1.3
PEX18	Peroxin; peroxisomal protein involved in the import of proteins into the peroxisomal matrix	-1.3
VID28	GID Complex subunit, serves as adaptor for regulatory subunit Vid24p; vacuolar import and degradation	-0.9
YIL055C	Putative protein of unknown function	-1.8
YRB2	Protein of unknown function; involved in nuclear processes of the Ran-GTPase cycle; involved in nuclear protein export; contains Ran Binding Domain and FxFG repeats	-1.2
PCI8	Possible shared subunit of Cop9 signalosome (CSN) and eIF3	-1.5
SPO22	Meiosis-specific protein essential for chromosome synapsis; involved in synaptonemal complex assembly and protein sumoylation	-1.1
YIL108W	Putative metalloendopeptidase; forms cytoplasmic foci upon DNA replication stress	-0.8
OM45	Mitochondrial outer membrane protein of unknown function	-1.3
FLO11	GPI-anchored cell surface glycoprotein (flocculin); Protein involved in flocculation, coflocculation, cell adhesion during biofilm formation, and in pseudohyphal and invasive growth	-1.5
INA22	F1F0 ATP synthase peripheral stalk assembly factor; mitochondrial inner membrane protein and subunit of the INA complex (INAC) with a role in assembly of mitochondrial F1F0 ATP synthase	-1.2
MGA2	ER membrane protein involved in regulation of OLE1 transcription; inactive ER form dimerizes and one subunit is then activated by ubiquitin/proteasome-dependent processing followed by nuclear targeting	-0.9
TPH3	Putative protein of unknown function	-1.1
PET130	Protein required for respiratory growth	-1.4
CHM7	Yeast homolog of human CHMP7, localizes to the endoplasmic reticulum	-1.8
NCA3	Protein involved in mitochondrion organization	-1.3
MTC1	Protein of unknown function that may interact with ribosomes	-0.7
YJL132W	Putative protein of unknown function	-1.0
YJL144W	Cytoplasmic hydrophilin essential in desiccation-rehydration process; expression induced by osmotic stress, starvation and during stationary phase	-1.2
FMP33	Putative protein of unknown function	-1.2
JJJ2	Protein of unknown function	-1.6
RCY1	F-box protein involved in recycling endocytosed proteins; involved in recycling plasma membrane proteins internalized by endocytosis	-1.0
LSO1	Protein with a potential role in response to iron deprivation	-1.0

MHO1	Protein of unknown function	-1.1
MNN14	Putative protein of unknown function; non-essential gene	-0.9
BIR1	Subunit of chromosomal passenger complex (CPC); required for chromosome bi-orientation and for spindle assembly checkpoint activation upon reduced sister kinetochore tension; relative distribution to shortened microtubules increases upon DNA replication stress	-1.5
SGM1	Protein of unknown function; required for wild-type growth rate on galactose and mannose	-2.3
YJR149W	Putative protein of unknown function	-1.5
YJR154W	Putative protein of unknown function	-1.1
DID4	Class E Vps protein of the ESCRT-III complex; required for sorting of integral membrane proteins into luminal vesicles of multivesicular bodies, and for delivery of newly synthesized vacuolar enzymes to the vacuole, involved in endocytosis	-0.6
VPS24	One of four subunits of the ESCRT-III complex; forms an endosomal sorting complex required for transport III (ESCRT-III) subcomplex with Did4p; involved in the sorting of transmembrane proteins into the multivesicular body (MVB) pathway	-0.9
BLI1	Subunit of the BLOC-1 complex involved in endosomal maturation	-1.1
STB6	Protein that binds Sin3p in a two-hybrid assay	-1.4
RRP14	Essential protein, constituent of 66S pre-ribosomal particles; interacts with proteins involved in ribosomal biogenesis and cell polarity	-2.3
YJU2	Essential protein required for pre-mRNA splicing	-1.3
YKL107W	Putative short-chain dehydrogenase/reductase	-1.2
SBA1	Co-chaperone that binds and regulates Hsp90 family chaperones; involved in protein folding, positive regulation of telomere maintenance via telomerase, negative regulation of DNA binding, and regulation of telomerase activity	-0.4
RCI50	Putative protein of unknown function; not required for growth of cells lacking the mitochondrial genome; SWAT-GFP and mCherry fusion proteins localize to the mitochondria	-1.1
COY1	Golgi membrane protein with similarity to mammalian CASP; genetic interactions with GOS1 (encoding a Golgi snare protein) suggest a role in Golgi function	-1.4
YKR011C	Protein of unknown function; protein abundance increases in response to DNA replication stress	-1.0
YKR015C	Putative protein of unknown function	-1.1
MIC60	Component of the MICOS complex; involved in mitochondrial cristae formation and the import of proteins into the mitochondrial intermembrane space	-0.7
YKR023W	Putative protein of unknown function; is detected in highly purified mitochondria in high-throughput studies	-1.6
YKR041W	Protein of unknown function; localizes to the mitotic spindle; its overexpression affects endocytic protein trafficking	-1.3

THI73	Putative plasma membrane permease; proposed to be involved in carboxylic acid uptake and repressed by thiamine	-1.9
SNF7	One of four subunits of the ESCRT-III complex; involved in ubiquitin-dependent protein catabolism via the multivesicular body sorting pathway, late endosome to vacuole transport, intraluminal vesicle formation, ATP export, and the cellular response to anoxia	-1.0
YLR046C	Putative membrane protein	-0.8
OSW2	Protein of unknown function reputedly involved in spore wall assembly	-1.0
EMP46	Integral membrane component of ER-derived COPII-coated vesicles	-2.5
GIS3	Protein of unknown function	-1.3
AVL9	Conserved protein involved in exocytic transport from the Golgi	-1.5
YLR149C	Protein of unknown function; non-essential gene; null mutation results in a decrease in plasma membrane electron transport; protein abundance increases in response to DNA replication stress	-1.1
YLR179C	Protein of unknown function with similarity to Tfs1p	-0.7
YLR225C	Putative protein of unknown function; non-essential gene	-1.0
CMG1	Putative protein of unknown function	-2.0
IMH1	Protein involved in vesicular transport	-1.5
ATG23	Peripheral membrane protein required for autophagy and CVT; involved in upregulation of macroautophagy, protein localization to pre-autophagosomal structure, late nucleophagy, cytoplasm-to-vacuole targeting (CVT) pathway	-1.5
YML003W	Putative protein of unknown function	-1.2
ITT1	Protein that modulates the efficiency of translation termination	-1.1
COG8	Component of the conserved oligomeric Golgi complex; involved in vesicle-mediated transport within the Golgi and CVT pathway	-1.0
MSC1	Protein of unknown function	-1.3
YML131W	Protein of unknown function	-1.4
BUD22	Protein required for rRNA maturation and ribosomal subunit biogenesis	-1.2
TAP42	Essential protein involved in the TOR signaling pathway	-1.4
EIS1	Component of the eisosome required for proper eisosome assembly; protein increases in abundance and relocates from plasma membrane to cytoplasm upon DNA replication stress	-1.4
KAR5	Protein required for nuclear membrane fusion during karyogamy	-1.0
SOV1	Mitochondrial protein of unknown function	-1.1
YMR111C	Protein of unknown function	-1.0

SHH3	Putative mitochondrial inner membrane protein of unknown function	-1.0
YMR122W-A	Protein of unknown function	-0.5
YMR158C-A	Putative protein of unknown function	-2.0
YMR181C	Protein of unknown function; non-essential gene	-0.8
MIN3	Putative protein of unknown function	-1.3
VTI1	Protein involved in cis-Golgi membrane traffic; SNAP receptor subunit of SNARE complex that mediates membrane fusion; integral component of Golgi membrane involved in vesicle-mediated transport and fusion, Golgi to vacuole transport, non-autophagic vacuole fusion, and macroautophagy	-0.7
YMR253C	Putative protein of unknown function; non-essential gene	-1.2
VAC7	Integral vacuolar membrane protein	-1.2
YNL115C	Putative protein of unknown function	-0.9
FYV6	Protein of unknown function; required for survival upon exposure to K1 killer toxin; proposed to regulate double-strand break repair via non-homologous end-joining	-0.9
EAF7	Subunit of the NuA4 histone acetyltransferase complex	-1.5
YNL144C	Putative protein of unknown function	-1.3
YGP1	Cell wall-related secretory glycoprotein; may be involved in adaptation prior to stationary phase entry	-2.1
KAR1	Protein involved in karyogamy during mating and spindle pole body duplication during mitosis	-1.9
SQS1	Protein that stimulates the ATPase and helicase activities of Prp43p	-1.2
PDR16	Phosphatidylinositol transfer protein (PITP); controls levels of various lipids, may regulate lipid synthesis	-0.7
YTP1	Probable type-III integral membrane protein of unknown function	-1.0
KRI1	Essential nucleolar protein required for 40S ribosome biogenesis	-1.3
EGO4	Protein of unknown function	-3.1
YNR068C	Putative protein of unknown function	-1.3
TLG2	Syntaxin-like t-SNARE; required along with VPS45 for an early step of the constitutive CVT pathway; interactions with Vps45 prevents Tlg2p degradation, and facilitates t-SNARE complex formation	-1.6
DDR2	Multi-stress response protein; expression is activated by a variety of xenobiotic agents and environmental or physiological stresses	-1.0
IZH4	Membrane protein involved in zinc ion homeostasis; possible role in sterol metabolism; protein increases in abundance and relocalizes from nucleus to ER upon DNA replication stress	-1.0

PEP12	Target membrane receptor (t-SNARE); for vesicular intermediates traveling between the Golgi apparatus and the vacuole; controls entry of biosynthetic, endocytic, and retrograde traffic into the prevacuolar compartment; syntaxin	-0.9
TMC1	AN1-type zinc finger protein, effector of proteotoxic stress response	-0.6
SLD7	Protein with a role in chromosomal DNA replication	-1.5
RTS2	Basic zinc-finger protein	-1.5
YOR097C	Putative protein of unknown function; non-essential gene	-1.1
SIA1	Protein of unassigned function; involved in activation of the Pma1p plasma membrane H ⁺ -ATPase by glucose	-1.1
SLK19	Kinetochores-associated protein; required for chromosome segregation and kinetochores clustering; required for normal segregation of chromosomes in meiosis and mitosis	-2.2
RRP36	Component of 90S preribosomes	-1.1
SNU66	Component of the U4/U6.U5 snRNP complex	-1.0
FIT2	Mannoprotein that is incorporated into the cell wall; involved in the retention of siderophore-iron in the cell wall	-0.6
FIT3	Mannoprotein that is incorporated into the cell wall; involved in the retention of siderophore-iron in the cell wall	-1.0
YOR389W	Putative protein of unknown function; expression regulated by copper levels	-1.5
ATG29	Autophagy-specific protein; involved in macroautophagy, late nucleophagy, mitochondrion degradation and piecemeal microautophagy of nucleus; required for recruiting other ATG proteins to the pre-autophagosomal structure (PAS)	-1.3
UIP4	Protein that interacts with Ulp1p	-1.8
YPL191C	Protein of unknown function	-1.2
APL5	Delta adaptin-like subunit of the clathrin associated protein complex	-1.1
YPL247C	Putative protein of unknown function	-1.1
YPL277C	Putative protein of unknown function; gene expression regulated by copper levels	-1.5
YPL278C	Putative protein of unknown function; gene expression regulated by copper levels	-1.1
THP3	Protein that may have a role in transcription elongation; possibly involved in splicing based on pre-mRNA accumulation defect for many intron-containing genes	-1.1
YPR127W	Putative pyridoxine 4-dehydrogenase	-0.9

Data obtained from Saccharomyces Genome Database (<https://www.yeastgenome.org>)

Supplementary Figure S1

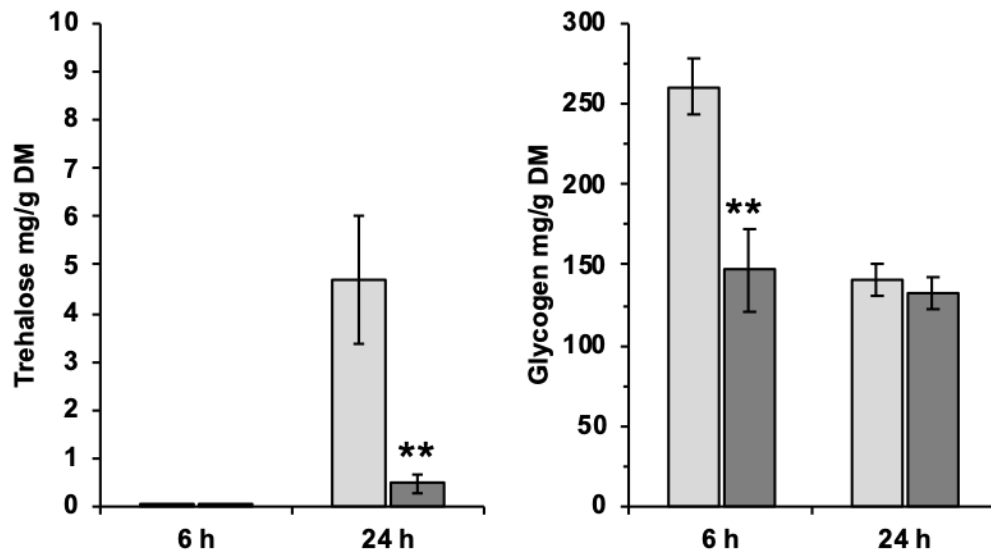


Figure S1. Intracellular trehalose and glycogen concentration after 6 and 24 h of fermentation in the presence of 0% (light grey) and 40% (dark grey) IS (w/w). Significant differences: ** $P < 0.01$