



Fig.S1 Real-time PCR analysis of select genes from different metabolic pathways

*S. cerevisiae* transformants expressing TEF-YCT1 were either exposed to 500µM cysteine or no cysteine for 5 hours (Control samples). Total RNA was extracted followed by cDNA synthesis. RT-PCR analysis was done using SYBR green dye-based method. The experiment was carried out twice and the figure represents expression levels of the above mentioned genes in treated samples relative to the corresponding untreated control samples. The data above are means  $\pm$  SD from technical replicates (n=3) of the biological duplicates. [ARG8, ARG5,6 and RTC2 belong to the arginine biosynthetic pathway, SSU1 is a part of sulphur metabolism and TIS11 is a gene involved in maintaining iron homeostasis in the cells.]

**Table S1: List of strains used in this study**

Strain	Genotype	Source
ABC 1738 ( <i>yct1</i> Δ)	<i>MATa his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 YLL055W::kanMX4</i>	Euroscarf (Y01543)
ABC3612( <i>arg3</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YJL088w::kanMX4</i>	Euroscarf (Y11335)
ABC4812( <i>arg5,6</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YER069w::kanMX4</i>	Euroscarf (Y10209)
ABC4811( <i>arg8</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YOL140w::kanMX4</i>	Euroscarf (Y17711)
ABC4814( <i>spe1</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YKL184w::kanMX4</i>	Euroscarf (Y15034)
ABC4815( <i>spe2</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YOL052c::kanMX4</i>	Euroscarf (Y11743)
ABC4816( <i>spe3</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YPR069c::kanMX4</i>	Euroscarf (Y15488)
ABC4817( <i>spe4</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YLR146c::kanMX4</i>	Euroscarf (Y16945)
ABC3604( <i>ssu1</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YPL092w::kanMX4</i>	Euroscarf (Y12160)
ABC1486( <i>str2</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YJR130c::kanMX4</i>	Euroscarf (Y12608)
ABC4818( <i>str3</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YGL184c::kanMX4</i>	Euroscarf (Y17556)
ABC3610( <i>aft1</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YGL071w::kanMX4</i>	Euroscarf (Y14438)
ABC3611( <i>aft2</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YPL202c::kanMX4</i>	Euroscarf (Y11090)
ABC4820( <i>tis11</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YLR136c::kanMX4</i>	Euroscarf (Y14093)
ABC4821( <i>fit2</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YOR382w::kanMX4</i>	Euroscarf (Y11679)
ABC4822( <i>sit1</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YEL065w::kanMX4</i>	Euroscarf (Y10307)
ABC3609( <i>fmp23</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YBR047w::kanMX4</i>	Euroscarf (Y13184)
ABC4824( <i>tmt1</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YER175c::kanMX4</i>	Euroscarf (Y16171)
ABC1092( <i>zrt1</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YGL255w::kanMX4</i>	Euroscarf (Y14622)
ABC4827( <i>srl4</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 YPL033c::kanMX4</i>	Euroscarf (Y12795)
ABC4742( <i>arg5,6</i> Δ)	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YER069w::kanMX4</i>	Euroscarf (Y00209)

ABC4741( <i>arg8Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YOL140w::kanMX4</i>	Euroscarf (Y07711)
ABC4744( <i>spe1Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YKL184w::kanMX4</i>	Euroscarf (Y05034)
ABC4745( <i>spe2Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YOL052c::kanMX4</i>	Euroscarf (Y01743)
ABC4746( <i>spe3Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YPR069c::kanMX4</i>	Euroscarf (Y05488)
ABC4747( <i>spe4Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YLR146c::kanMX4</i>	Euroscarf (Y06945)
ABC4106( <i>str3Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YGL184c::kanMX4</i>	Euroscarf (Y07556)
ABC4752( <i>fit2Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YOR382w::kanMX4</i>	Euroscarf (Y01679)
ABC4751( <i>sit1Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YEL065w::kanMX4</i>	Euroscarf (Y00307)
ABC4754( <i>tmt1Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YER175c::kanMX4</i>	Euroscarf (Y06171)
ABC4761( <i>icy2Δ</i> )	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YPL250c::kanMX4</i>	Euroscarf (Y01042)
ABC4756	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YGL117w::kanMX4</i>	Euroscarf (Y04484)
ABC4757	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YLR152c::kanMX4</i>	Euroscarf (Y04109)
ABC4758	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YDL199c::kanMX4</i>	Euroscarf (Y03897)
ABC4759	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YEL057c::kanMX4</i>	Euroscarf (Y00298)
ABC4760	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YJL160c::kanMX4</i>	Euroscarf (Y07009)
ABC4762	<i>MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 YHR138c::kanMX4</i>	Euroscarf (Y01966)

**Table S2: List of genes found to be up regulated in presence of cysteine**

Gene Name	GmeanF	Fold change	Pathway	Description
<i>ARG3</i>	4.18	18.13	Arginine biosynthesis	Ornithine carbamoyltransferase
<i>FMP23</i>	4.17	18.00	Iron homeostasis	Putative protein of unknown function
<i>TIS11</i>	3.83	14.22	Iron homeostasis	mRNA-binding protein expressed during iron starvation
<i>SRL4</i>	3.44	10.85	Unknown	unknown function; regulation of dNTP

				production
<i>YJL160C</i>	3.37	10.34	Unknown	Putative protein of unknown function;
<i>TMT1</i>	3.24	9.45	Leucine biosynthesis	Trans-aconitate methyltransferase
<i>ANB1</i>	3.19	9.13	Translation	Translation elongation factor eIF-5A
<i>RTC2</i>	3.18	9.06	Arginine biosynthesis	YPQ3 vacuolar cationic amino acid transporter
<i>ARG8</i>	3.18	9.06	Arginine biosynthesis	Acetylornithine aminotransferase,
<i>ZRT1</i>	3.13	8.75	Zinc Homeostasis	High-affinity zinc transporter of the plasma membrane
<i>PKP2</i>	3.04	8.22	Pyruvate metabolism	Mitochondrial protein kinase
<i>CPA1</i>	3.04	8.22	Arginine biosynthesis	Small subunit of carbamoyl phosphate synthetase
<i>SSU1</i>	3.01	8.06	Sulfur metabolism	Plasma membrane sulfite pump
<i>CRF1</i>	3.00	8.00	Transcriptional regulation	Transcriptional corepressor;
<i>FIT2</i>	2.96	7.78	Iron homeostasis	Mannoprotein that is incorporated into the cell wall
<i>ARG5,6</i>	2.88	7.36	Arginine biosynthesis	Acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase
<i>NCA3</i>	2.76	6.77	ATP synthesis	Regulates mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p ) of the Fo-F1 ATP synthase
<i>YEL057C</i>	2.72	6.59	Telomere maintenance	Protein of unknown function
<i>YLR152C</i>	2.71	6.54	Unknown	Putative protein of unknown function
<i>ICY2</i>	2.67	6.36	Unknown	Putative protein of unknown function
<i>YGL117W</i>	2.63	6.19	Unknown	Putative protein of unknown function
<i>ADH5</i>	2.63	6.19	Amino acid degradation	Alcohol dehydrogenase isoenzyme
<i>BSC5</i>	2.58	5.98	Unknown	Putative protein of unknown function
<i>GCY1</i>	2.53	5.78	Glycerol metabolism	Putative NADP(+) coupled glycerol dehydrogenase,
<i>SIT1</i>	2.42	5.35	Iron homeostasis	Ferrioxamine B transporter
<i>GLG1</i>	2.40	5.28	Glycogen biosynthesis	Self-glucosylating initiator of glycogen synthesis

<i>STR2</i>	2.39	5.24	Sulfur metabolism	Cystathionine gamma-synthase,
<i>ENB1</i>	2.35	5.10	Iron homeostasis	Endosomal ferric enterobactin transporter
<i>LYS20</i>	2.34	5.06	Lysine biosynthesis	Homocitrate synthase isozyme
<i>YDL199C</i>	2.32	4.99	Unknown	Putative transporter, member of the sugar porter family
<i>YSWI</i>	2.31	4.96	Unknown	required for normal prospore membrane formation
<i>YMR317W</i>	2.28	4.86	Unknown	Putative protein of unknown function
<i>AAD10</i>	2.25	4.76	Amino acid metabolism	Putative aryl-alcohol dehydrogenase
<i>ORT1</i>	2.19	4.56	Arginine biosynthesis	Mitochondrial Ornithine transporter,
<i>LYS1</i>	2.19	4.56	Lysine biosynthesis	Saccharopine dehydrogenase
<i>ARN1</i>	2.19	4.56	Iron homeostasis	ARN family transporter for siderophore-iron chelates
<i>NCE103</i>	2.18	4.53	Non-classical protein export pathway	Carbonic anhydrase;
<i>VMR1</i>	2.17	4.50	Multidrug Resistance	Vacuolar membrane protein
<i>YOR186W</i>	2.17	4.50	Unknown	Putative protein of unknown function
<i>FIG2</i>	2.15	4.44	Cell wall maintenance	Cell wall adhesion
<i>ECM13</i>	2.14	4.41	Cell wall organization	Protein of unknown function
<i>PEX21</i>	2.10	4.29	Peroxisome biogenesis	Required for targeting of peroxisomal matrix proteins
<i>YGP1</i>	2.08	4.23	Unknown	Cell wall-related secretory glycoprotein;
<i>YHI9</i>	2.07	4.20	Unknown	Protein of unknown function
<i>ARG4</i>	2.07	4.20	Arginine biosynthesis	Argininosuccinate lyase
<i>BOP2</i>	2.07	4.20	Unknown	Protein of unknown function
<i>YPL113C</i>	2.05	4.14	Unknown	Glyoxylate reductase
<i>BAP2</i>	2.01	4.03	Leucine uptake	High-affinity leucine permease
<i>RTS3</i>	2.00	4.00	unknown	Put. component of protein phosphatase type 2A complex

**Table S3: List of genes found to be up regulated in presence of cystine**

Gene Name	GmeanF	Fold change	Pathway	Description
<i>TIS11</i>	3.57	11.88	Iron homeostasis	mRNA-binding protein expressed in iron starvation
<i>FMP23</i>	3.14	8.82	Iron homeostasis	Putative protein of unknown function
<i>ARG3</i>	2.85	7.21	Arginine biosynthesis	Ornithine carbamoyltransferase
<i>FIT2</i>	2.38	5.21	Iron homeostasis	Mannoprotein that is incorporated into the cell wall
<i>TMT1</i>	2.25	4.76	Leucine biosynthesis	Trans-aconitate methyltransferase
<i>SFC1</i>	2.22	4.66	Gluconeogenesis	Mitochondrial succinate-fumarate transporter,
<i>RTC2</i>	2.10	4.29	Arginine biosynthesis	YPQ3 vacuolar cationic amino acid transporter
<i>ARG5,6</i>	2.07	4.20	Arginine biosynthesis	Acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase
<i>YGL117W</i>	1.94	3.84	Unknown	Putative protein of unknown function
<i>YLR152C</i>	1.87	3.66	Unknown	Putative protein of unknown function
<i>ARN1</i>	1.86	3.63	Iron homeostasis	Arn1p specifically recognize siderophore-iron chelates
<i>SRL4</i>	1.80	3.48	Iron homeostasis	Unknown function; regulation of dNTP production
<i>ARG8</i>	1.77	3.41	Arginine biosynthesis	Acetylornithine aminotransferase,
<i>ANB1</i>	1.73	3.32	Translation	Translation elongation factor eIF-5A
<i>TMA10</i>	1.71	3.27	Unknown	Protein of unknown function, associates with ribosomes
<i>ICY2</i>	1.70	3.25	Unknown	Protein of unknown function
<i>PKP2</i>	1.68	3.20	Pyruvate metabolism	Mitochondrial protein kinase
<i>CPA1</i>	1.67	3.18	Arginine biosynthesis	Small subunit of carbamoyl phosphate synthetase
<i>ORT1</i>	1.64	3.12	Arginine biosynthesis	Exports ornithine from mitochondria
<i>YLR194C</i>	1.63	3.10	Cell wall protein	Structural constituent of the cell wall
<i>ZRT1</i>	1.62	3.07	Zinc Homeostasis	High-affinity zinc transporter of the plasma membrane,
<i>STR3</i>	1.62	3.07	Sulfur metabolism	Cystathionine beta-lyase, converts cystathionine into homocysteine
<i>EST1</i>	1.56	2.95	Telomere maintenance	TLC1 RNA-associated factor involved in telomere length regulation
<i>SIT1</i>	1.49	2.81	Iron homeostasis	Ferrioxamine B transporter,
<i>SSU1</i>	1.48	2.79	Sulphur metabolism	Plasma membrane sulfite efflux pump
<i>YDR034W-B</i>	1.46	2.75	Unknown	Protein of unknown function
<i>SOL4</i>	1.43	2.69	Pentose phosphate	6-phosphogluconolactonase with similarity to

			pathway	Sol3p
<i>YHR138C</i>	1.43	2.69	Unknown	Putative protein of unknown function
<i>SNO4</i>	1.42	2.68	Unknown	Possible chaperone and cysteine protease
<i>GOT1</i>	1.41	2.66	Secretory trafficking	Homodimeric protein packaged into COPII vesicles
<i>NQM1</i>	1.41	2.66	Unknown	Transaldolase of unknown function
<i>ARG4</i>	1.40	2.64	Arginine biosynthesis	Argininosuccinate lyase
<i>YNR034W-A</i>	1.38	2.60	Unknown	Putative protein of unknown function
<i>YGL024W</i>	1.35	2.55	Unknown	Dubious open reading frame
<i>DDI2</i>	1.35	2.55	Unknown	Protein of unknown function
<i>HSP32</i>	1.34	2.53	Unknown	Possible chaperone and cysteine protease
<i>YGR109W-A</i>	1.34	2.53	Transposable element	Retrotransposon TYA Gag gene

**Table S4: List of genes found to be down regulated in presence of cysteine**

Gene Name	GmeanF	Fold change	Pathway	Description
<i>MET14</i>	-4.59	24.08	Sulfur metabolism	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism
<i>MET3</i>	-3.81	14.03	Sulfur metabolism	ATP sulfurylase,
<i>SUL1</i>	-3.39	10.48	Sulfur metabolism	High affinity sulfate permease;
<i>SPL2</i>	-3.20	9.19	Unknown	Protein with similarity to cyclin-dependent kinase
<i>MET5</i>	-3.19	9.13	Sulfur metabolism	Sulfite reductase beta subunit
<i>MET2</i>	-3.13	8.75	Sulfur metabolism	L-homoserine-O-acetyltransferase,
<i>MHT1</i>	-3.06	8.34	Sulfur metabolism	S-methylmethionine-homocysteine methyltransferase
<i>SPS4</i>	-2.92	7.57	Unknown	Protein whose expression is induced during sporulation
<i>SUL2</i>	-2.90	7.46	Sulfur metabolism	High affinity sulfate permease
<i>MMP1</i>	-2.74	6.68	Sulfur metabolism	High-affinity S-methylmethionine permease,
<i>YDR379C-A</i>	-2.62	6.15	Unknown	Putative protein of unknown function
<i>YLR053C</i>	-2.57	5.94	Unknown	Putative protein of unknown function

<i>PHO89</i>	-2.52	5.74	Phosphate transport	Na <sup>+</sup> /Pi cotransporter,
<i>MET32</i>	-2.52	5.74	Sulfur metabolism	Zinc-finger DNA-binding transcription factor
<i>COX7</i>	-2.52	5.74	Electron transport chain	Subunit VII of cytochrome c oxidase
<i>YFL051C</i>	-2.44	5.43	Unknown	Putative protein of unknown function;
<i>CYC1</i>	-2.42	5.35	Electron transport chain	Cytochrome c, isoform 1
<i>YGR153W</i>	-2.38	5.21	Unknown	Putative protein of unknown function
<i>EMC6</i>	-2.26	4.79	Protein folding	Member of conserved ER transmembrane complex
<i>MET10</i>	-2.21	4.63	Sulfur metabolism	Subunit alpha of assimilatory sulfite reductase
<i>HPF1</i>	-2.21	4.63	cell wall organization and biosynthesis	Haze-protective mannoprotein
<i>YLR460C</i>	-2.19	4.56	Unknown	Member of the quinone oxidoreductase family,
<i>CSN9</i>	-2.16	4.47	mating pheromone response	Subunit of the Cop9 signalosome
<i>PHM6</i>	-2.15	4.44	Unknown	Protein of unknown function
<i>MXR1</i>	-2.12	4.35	Oxidative stress response	Methionine-S-sulfoxide reductase,
<i>DAD4</i>	-2.09	4.26	Chromosome segregation	Component of the DASH complex, a microtubule-binding subcomplex
<i>GRX8</i>	-2.09	4.26	Sulfur metabolism	Glutaredoxin that employs a dithiol mechanism of catalysis;
<i>MIC14</i>	-2.06	4.17	Unknown	Mitochondrial protein of unknown function
<i>RAD59</i>	-2.02	4.06	DNA amplification	Repair of double-strand breaks in DNA
<i>MNN4</i>	-1.98	3.94	Protein glycosylation	Putative regulator of mannosylphosphate transferase Mnn6p
<i>LSM2</i>	-1.87	3.66	mRNA splicing	Lsm protein; involved in mRNA decay
<i>YGL230C</i>	-1.87	3.66	Unknown	Putative protein of unknown function
<i>EFG1</i>	-1.83	3.56	RNA processing	Required for maturation of 18S rRNA
<i>YDL085C-A</i>	-1.83	3.56	Unknown	Putative protein of unknown function
<i>MET17</i>	-1.82	3.53	Sulfur metabolism	O-acetyl homoserine-O-acetyl serine sulfhydrylase
<i>RSB1</i>	-1.81	3.51	Fatty acid transport	Putative integral membrane transporter



<i>CAR2</i>	-1.77	3.41	Arginine catabolism	L-ornithine transaminase
<i>AIM34</i>	-1.75	3.36	Unknown	Protein of unknown function
<i>CNL1</i>	-1.75	3.36	Endosome organization	Component of the biogenesis of lysosome-related organelles complex-1 (BLOC-1)
<i>DTD1</i>	-1.74	3.34	tRNA metabolism	D-tyrosyl-tRNA(Tyr) deacylase
<i>DYN2</i>	-1.74	3.34	Cargo trafficking	Cytoplasmic light chain dynein
<i>CMC2</i>	-1.73	3.32	Mitochondrial respiration	Respiratory chain complex assembly or maintenance
<i>AZR1</i>	-1.71	3.27	Azole transport	Plasma membrane transporter of the MFS superfamily
<i>YJR011C</i>	-1.68	3.20	Unknown	Putative protein of unknown function
<i>YNL122C</i>	-1.68	3.20	Translation	Putative mitochondrial ribosomal protein
<i>QCR10</i>	-1.65	3.14	Mitochondrial electron transport	Cytochrome b-c1 complex subunit 10
<i>SDC1</i>	-1.64	3.12	Chromatin silencing at telomeres	Subunit of the COMPASS (Set1C) complex
<i>CHZ1</i>	-1.64	3.12	Chromatin remodeling	Histone chaperone for Htz1p/H2A-H2B dimer
<i>YPL225W</i>	-1.62	3.07	Unknown function	May interact with ribosomes,
<i>IES5</i>	-1.62	3.07	Telomere maintenance	Non-essential INO80 chromatin remodeling complex subunit
<i>ALG13</i>	-1.56	2.95	Oligosaccharide biosynthesis	Catalytic component of UDP-GlcNAc transferase
<i>SPO16</i>	-1.55	2.93	Meiotic recombination	Synaptonemal complex assembly
<i>BLS1</i>	-1.55	2.93	Endosome organization and transport	Biogenesis of lysosome-related organelles complex 1 subunit
<i>YCR102C</i>	-1.53	2.89	Unknown	Putative protein of unknown function
<i>YLR456W</i>	-1.52	2.87	Vitamin B6 metabolism	Pyridoxamine 5'-phosphate oxidase
<i>YLR346C</i>	-1.51	2.85	Unknown	Mitochondrial putative protein of unknown function
<i>COX12</i>	-1.50	2.83	Oxidative phosphorylation	Subunit VIb of cytochrome c oxidase
<i>TFB5</i>	-1.50	2.83	Transcriptional regulation	Component of the RNA polymerase II general transcription and DNA repair factor TFIIF

**Table S5: list of genes found to be down regulated in presence of cystine**

Gene Name	GmeanF	Fold Change	Pathway	Description
<i>YOL079W</i>	-1.87	3.66	Unknown	Dubious open reading frame
<i>HAC1</i>	-1.46	2.75	Unfolded protein response	Basic leucine zipper (bZIP) transcription factor
<i>COX4</i>	-1.39	2.62	Electron transport chain	Subunit IV of cytochrome c oxidase
<i>OPT1</i>	-1.16	2.23	Glutathione and phytochelatin transport	Proton-coupled oligopeptide transporter of the plasma membrane
<i>LRO1</i>	-1.14	2.20	Triglyceride biosynthesis	Acyltransferase that catalyzes diacylglycerol esterification
<i>MET3</i>	-1.10	2.14	Sulfur metabolism	ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation
<i>RSB1</i>	-1.10	2.14	Unknown	Suppressor of sphingoid LCB sensitivity
<i>MNN4</i>	-1.04	2.06	Protein glycosylation	Putative positive regulator of mannosylphosphate transferase Mnn6p
<i>NDE1</i>	-1.04	2.06	Mitochondrial respiratory chain	Mitochondrial external NADH dehydrogenase,
<i>MET2</i>	-1.04	2.06	Sulfur metabolism	L-homoserine-O-acetyltransferase
<i>CAR2</i>	-0.99	1.99	Arginine biosynthesis	L-ornithine transaminase
<i>SUL1</i>	-0.99	1.99	Sulfur metabolism	High affinity sulfate permease
<i>ERC1</i>	-0.97	1.96	Unknown	Putative protein of unknown function
<i>MET10</i>	-0.96	1.95	Sulfur metabolism	Subunit alpha of assimilatory sulfite reductase
<i>YPR089W</i>	-0.96	1.95	Unknown	Protein of unknown function
<i>SPS4</i>	-0.96	1.95	Unknown	Protein whose expression is induced during sporulation
<i>SUL2</i>	-0.96	1.95	Sulfur metabolism	High affinity sulfate permease
<i>SCT1</i>	-0.95	1.93	Glycerolipid biosynthesis	Glycerol 3-phosphate/dihydroxyacetone phosphate
<i>SPT5</i>	-0.93	1.91	Transcriptional elongation	Protein involved in regulating Pol I and Pol II transcription
<i>YMR086C-A</i>	-0.92	1.89	Unknown	Dubious open reading frame
<i>LSB6</i>	-0.92	1.89	Actin polymerization	Type II phosphatidylinositol 4-kinase
<i>YFR018C</i>	-0.91	1.88	Unknown	Putative protein of unknown function
<i>FET4</i>	-0.91	1.88	Iron homeostasis	Low-affinity Fe(II) transporter of the

plasma membrane				
<i>YGR054W</i>	-0.89	1.85	Translation	Eukaryotic initiation factor (eIF) 2A
<i>YVC1</i>	-0.87	1.83	Cation homeostasis	Vacuolar cation channel
<i>YBL070C</i>	-0.86	1.82	Unknown	Dubious open reading frame
<i>NOP58</i>	-0.85	1.80	Pre RNA processing	involved in producing mature rRNAs and snoRNAs
<i>YAL004W</i>	-0.85	1.80	Unknown	Dubious open reading frame
<i>YOR282W</i>	-0.83	1.78	Unknown	Dubious open reading frame
<i>YPR142C</i>	-0.83	1.78	Unknown	Dubious open reading frame
<i>MET6</i>	-0.82	1.77	Sulfur metabolism	Cobalamin-independent methionine synthase
<i>SSN2</i>	-0.82	1.77	Transcriptional regulation	Subunit of the RNA polymerase II mediator complex
<i>SSA2</i>	-0.81	1.75	Protein folding	ATP binding protein involved in protein folding and vacuolar import of proteins
<i>NCE102</i>	-0.81	1.75	Unknown	Protein of unknown function
<i>SYH1</i>	-0.81	1.75	Unknown	unknown function
<i>ATM1</i>	-0.80	1.74	Iron sulfur biogenesis	Mitochondrial inner membrane ATP-binding cassette (ABC) transporter

**Table S6 Common list of genes found to be up regulated in presence of cystine/cysteine.**

<b>Gene Name</b>	<b>Fold change cysteine</b>	<b>Fold change cystine</b>	<b>Description</b>
<i>ARG3</i>	18.13	7.21	Ornithine carbamoyltransferase
<i>FMP23</i>	18	8.82	Putative protein of unknown function
<i>TIS11</i>	14.22	11.88	mRNA-binding protein : iron starvation
<i>SRL4</i>	10.85	3.48	Protein of unknown function
<i>TMT1</i>	9.45	4.76	Trans-aconitate methyltransferase
<i>RTC2</i>	9.06	4.29	YPQ3 vacuolar cationic amino acid transporter
<i>ARG8</i>	9.06	3.41	Acetylornithine aminotransferase,
<i>ZRT1</i>	8.75	3.07	High-affinity zinc transporter (Plasma membrane)
<i>PKP2</i>	8.22	3.2	Mitochondrial protein kinase
<i>CPA1</i>	8.22	3.18	Small subunit of carbamoyl phosphate synthetase
<i>SSU1</i>	8.06	2.79	Plasma membrane sulfite pump
<i>FIT2</i>	7.78	5.21	Mannoprotein : incorporated into the cell wall
<i>ARG5,6</i>	7.36	4.2	Acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase

<i>YLR152C</i>	6.54	3.66	Putative protein of unknown function
<i>YGL117W</i>	6.19	3.84	Putative protein of unknown function
<i>SIT1</i>	5.35	2.81	Ferrioxamine B transporter,
<i>ARN1</i>	4.56	3.63	recognizes siderophore-iron chelates
<i>ORT1</i>	4.56	3.12	Arginine biosynthesis
<i>ARG4</i>	4.2	2.64	Argininosuccinate lyase
<i>NQMI</i>	2.41	2.66	Transaldolase of unknown function

**Table S7: Common list of genes found to be down regulated in presence of cystine/cysteine**

Gene Name	Fold change cysteine	Fold change cystine	Description
<i>MET3</i>	14.03	2.14	ATP sulfurylase
<i>SUL1</i>	10.48	1.99	High affinity sulfate permease
<i>MET2</i>	8.75	2.06	L-homoserine-O-acetyltransferase
<i>SPS4</i>	7.57	1.95	Protein whose expression is induced during sporulation
<i>SUL2</i>	7.46	1.95	High affinity sulfate permease
<i>MET10</i>	4.63	1.95	Subunit alpha of assimilatory sulfite reductase
<i>RSB1</i>	3.51	2.14	Suppressor of sphingoid LCB sensitivity of an LCB-lyase mutation
<i>CAR2</i>	3.41	1.99	L-ornithine transaminase
<i>OPT1</i>	2.69	2.23	Proton-coupled oligopeptide transporter
<i>NDE1</i>	1.99	2.06	Mitochondrial external NADH dehydrogenase,
<i>MNN4</i>	1.82	2.06	Putative positive regulator of mannosylphosphate transferase Mnn6p

**Table S8: list of primers used for the RT-PCR analysis**

Primer Name	Sequence
ARG8_F	GGCCAGAGAATTGGGACTTT
ARG8_R	GCATCCATCCCCTTCTTCGATTA
ARG5,6_F	GACGTAGCTGCTGGTGAATTAG
ARG5,6_R	CCCGTGGAGCCATTGATAATAC
RTC2_F	CTTGAGCTTGGCAGAACAATAG
RTC2_R	CGGCAATAAGTACACCTGAAAC
SSU1_F	TGGCTGCATGCCATTATCT
SSU1_R	CCTGTGTCATTGGTGGTATCT
TIS11_F	TCGGCAGTTTCATTCTCTCC
TIS11_R	GTAGTAGGTGCCGTGCTATTC