**SUPPLEMENTARY**

**S1. Localization of Gor1p.** Mitochondrial isolation and extracts prepared from the *met15Δgor1Δ* strain, transformed with a plasmid bearing the GOR1 expressed from its native promoter. Immunoblots were carried out with control antibodies to determine the localization.

**Table No. 1**

**List of all mitochondrial gene deletions bearing a *gsh1****∆* **that show improved growth compared to *gsh1****∆* **on low level of glutathione**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene Name |  Function | Key genotype of deleted strain | Phenotype | Sources |
| YJL101C | γ- glutamylcysteine synthetase | *gsh1∆* | + | This study |
| YOR384W/FRE5 | Putative ferric reductase  | *fre5∆gsh1∆* | +++ | This study |
| YNL274C/ GOR1 | Glyoxylate reductase | *gor1∆gsh1∆* | +++ | This study |
| YPL222W/FMP40 | Pseudokinase involved in AMPylarion | *fmp40∆gsh1∆* | +++ | This study |
| YHL021C/AIM17 | Protein of unknown function | *aim17∆gsh1∆* | +++ | This study |
| YBR054W/YRO2  | Protein with a putative role in response to acid stress | *yro2∆gsh1∆* | +++ | This study |
| YKR052C/ MRS4 | Iron transporter of the mitochondrial carrier family | *mrs4∆gsh1∆* | ++ | This study |
| YBL030C/ AAC2 | Major ADP/ATP carrier of the mitochondrial inner membrane | *aac2∆gsh1∆* | ++ | This study |
| YML120C/ NDI1 | NADH: ubiquinone oxidoreductase | *ndi1∆gsh1∆* | ++ | This study |
| YNL305C/BXI1 | Protein involved in apoptosis | *bxi1∆gsh1∆* | ++ | This study |
| YEL047C/ FRD1 | Soluble fumarate reductase | *frd1∆gsh1∆* | ++ | This study |
| YAL010C/ MDM10 | Subunit of both the ERMES and the SAM complex | *mdm10∆gsh1∆* | ++ | This study |
| YKR066C/ CCP1 | Mitochondrial cytochrome-c peroxidase | *ccp1∆gsh1∆* | ++ | This study |
| YPR049C/ ATG11 | Adapter protein for pexophagy and the Cvt targeting pathway | *atg11∆gsh1∆* | ++ | This study |
| YMR031C/ EIS1 | Component of the eisosome required for proper eisosome assembly | *eis1∆gsh1∆* | ++ | This study |
| YOR022C | Putative carboxylic ester hydrolase | *yor022c∆gsh1∆* | ++ | This study |
| YHR076W/ PTC7 | Type 2C serine/threonine protein phosphatase (PP2C | *ptc7∆gsh1∆* | ++ | This study |
| YLR087C/ CSF1 | Protein required for fermentation at low temperature | *csf1∆gsh1∆* | ++ | This study |
| YDL230W/ PTP1 | Phosphotyrosine-specific protein phosphatase | *ptp1∆gsh1∆* | ++ | This study |
| YLR368W/MDM30 | F-box component of an SCF ubiquitin protein ligase complex;  | *mdm30∆ gsh1∆* | ++ | This study |
| YER033C/ ZRG8 | Protein of unknown function | *zrg8∆gsh1∆* | ++ | This study |
| YNL077W/ APJ1 | Chaperone with a role in SUMO-mediated protein degradation;  | *apj1∆gsh1∆* | ++ | This study |
| YKL132C/RMA1 | Putative dihydrofolatesynthetase | *rma1∆gsh1∆* | ++ | This study |
| YER140W/EMP65  | Integral membrane protein of the ER | *emp65∆gsh1∆* | ++ | This study |
| YPR001W/ CIT3 | Citrate synthase | *cit3∆gsh1∆*  | ++ | This study |
| YJL200C/ ACO2 | Aconitase |  *aco2∆gsh1∆*  | ++ | This study |
| YOR136W/ IDH2 | NAD(+)-dependent-isocitrate dehydrogenase |  *idh2∆gsh1∆*  | ++ | This study |
| YIL125W/ KGD1 | alpha-Keto Glutarate Dehydrogenase | *kgd1∆gsh1∆*  | ++ | This study |
| YDR148C/ KGD2 | alpha-Keto Glutarate Dehydrogenase  |  *kgd2∆gsh1∆*  | ++ | This study |
| YGR244C/ LSC2 | Beta subunit of succinyl-CoA ligase |  *lsc2∆gsh1∆*  | ++ | This study |
| YER073W/ ALD5  | Mitochondrial aldehyde dehydrogenase |  *ald5∆gsh1∆*  | ++ | This study |
| YMR145C/ NDE1 | Mitochondrial-external NADH dehydrogenase | *nde1∆gsh1∆* | ++ | This study |
| YHR106W/ TRR2 |  Mitochondrial thioredoxin reductase | *trr2∆gsh1∆* | ++ | This study |
| YPL262W/ FUM1 | Fumarase | *fum1∆gsh1∆* | ++ | This study |
| YIL065C/ FIS1 | Protein has a role in mitochondrial fission and peroxisome abundance | *fis1∆gsh1∆* | ++ | This study |

**Table No. 2**

**List of all mitochondrial gene deletions bearing a *gsh1****∆* **that show decreased growth compared to *gsh1****∆* **on low level of glutathione**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene Name | Function | Key genotype of deleted strain | Phenotype | Sources |
| YJL101C | ϒ- glutamylcysteine synthetase | *gsh1∆* | + | This study |
| YNL307C/ MCK1 | Dual-specificity ser/thr and tyrosine protein kinase | *mck1∆gsh1∆* | --- | This study |
| YGR257C/ MTM1 | The mitochondrial protein of the mitochondrial carrier family | *mtm1∆gsh1∆* | --- | This study |
| YKL040C/ NFU1 | Protein involved in iron metabolism in mitochondria | *nfu1∆gsh1∆* | --- | This study |
| YPL271W/ ATP15 | Epsilon subunit of the F1 sector of mitochondrial F1F0 ATP synthase | *atp15∆gsh1∆* | --- | This study |
| YBL099W/ ATP1 | The alpha subunit of the F1 sector of mitochondrial F1F0 ATP synthase | *atp1∆gsh1∆* | --- | This study |
| YPL170W/ DAP1 | Heme-binding protein; involved in regulation of cytochrome P450 protein Erg11p | *dap1∆gsh1∆* | --- | This study |
| YPL091W/ GLR1 | Cytosolic and mitochondrial glutathione oxidoreductase | *glr1∆gsh1∆*  | --- | This study |
| YHR030C/ SLT2 | Serine/threonine MAP kinase | *slt2∆gsh1∆* | -- | This study |
| YHR038W/ RRF1 | Mitochondrial ribosome recycling factor | *rrf1∆gsh1∆* | -- | This study |
| YBR026C/ ETR1 | 2-enoyl thioester reductase | *etr1∆gsh1∆* | -- | This study |
| YPR083W/ MDM36 | Mitochondrial protein; required for normal mitochondrial morphology  | *mdm36∆gsh1∆* | -- | This study |
| YNL076W/ MKS1 | Pleiotropic negative transcriptional regulator;  | *mks1∆gsh1∆* | -- | This study |
| YMR021C/ MAC1∆ | Copper-sensing transcription factor | *mac1∆gsh1∆* | -- | This study |
| YCL009C/ ILV6 | Regulatory subunit of acetolactate synthase | *ilv6∆gsh1∆* | -- | This study |
| YNL241C/ ZWF1 | Glucose-6-phosphate dehydrogenase (G6PD)  | *zwf1∆gsh1∆*  | - | This study |
| YDL045W-A/ MRP10 | The mitochondrial ribosomal protein of the small subunit | *mrp10∆gsh1∆* | - | This study |
| YPL188W/POS5 | Mitochondrial NADH kinase  | *pos5∆gsh1∆*  | - | This study |
| YLR426W/ TDA5 | Putative protein of unknown function | *tda5∆gsh1∆* | - | This study |