

## Supplementary Figure

The 88 *Saccharomyces cerevisiae* deletion strains that were shown to be sensitive to 4-(*N*-(*S*-glutathionylacetyl)amino) phenylarsenoxide (GSAO). The 50% inhibitory concentration (IC<sub>50</sub>) for inhibition of growth and function of the gene product is indicated. **Green**, **yellow**, **pink**, **blue**, **black**, and **red** indicate genes that are involved in drug transport, cysteine and glutathione biosynthesis, oxidative stress, cytoskeleton function, DNA repair, and general defense mechanisms, respectively.

Deleted gene	Process	IC <sub>50</sub> , mM	Function of gene product
YCF1		0.027	Homologue of mammalian multidrug-resistance proteins
CYS4		0.032	Enzyme that converts homocysteine to cystathionine
CYS3		0.043	Enzyme that converts cystathionine to cysteine
PEP3		0.045	Vacuolar membrane protein involved in protein trafficking
SOD1		0.049	Cu/Zn superoxide dismutase
GSH1		0.054	Enzyme that converts cysteine to $\gamma$ -glutamylcysteine
YDL041W		0.062	Unknown
MET8		0.070	Transcriptional activator regulating expression of 3' phosphoadenylylsulfate reductase and SO <sub>3</sub> reductase
MET14		0.073	Enzyme that converts adenylylsulfate to 3' phosphoadenylylsulfate
ECM17		0.080	$\beta$ subunit of enzyme that converts SO <sub>3</sub> to H <sub>2</sub> S
MET16		0.080	Enzyme that converts 3' phosphoadenylylsulfate to SO <sub>3</sub>
YML094C-A		0.080	Unknown
MET10		0.083	$\alpha$ subunit of enzyme that converts SO <sub>3</sub> to H <sub>2</sub> S
KCS1		0.096	Inositol hexaphosphate kinase required for vacuole morphology
MET28		0.100	Transcriptional activator that participates in the regulation of sulfur metabolism
PHO85		0.108	Cyclin-dependent kinase involved in stress response
PRM7		0.110	Unknown
MET22		0.120	Enzyme that dephosphorylates 3'-phosphoadenosine-5'-phosphosulfate
YDJ1		0.125	Heat shock protein involved in mitochondrial protein import
CCR4		0.130	Transcriptional regulator for some glucose-repressed genes
BRE1		0.135	E3 ubiquitin ligase for Rad6p; required for the ubiquitination of histone H2B
YDL023C		0.135	Unknown
RHR2		0.140	DL-glycerol-3-phosphatase
RSM23		0.150	Mitochondrial ribosome small subunit component
HOM3		0.180	Enzyme that converts aspartate to aspartate-4-P
VID28		0.188	Involved in vacuole import and degradation
HOM2		0.190	Enzyme that converts aspartate-4-P to aspartate-semialdehyde
MET17		0.200	Enzyme that converts <i>o</i> -acetylhomoserine and H <sub>2</sub> S to homocysteine
CSM1		>0.2	Molecular function unknown. May be involved in premeiotic DNA replication
UME6		>0.2	Regulator of both repression and induction of early meiotic genes
YIL029C		>0.2	Unknown
YOR305W		>0.2	Unknown
YIL077C		>0.2	Unknown
RIB1		>0.2	Cyclohydrolase that catalyzes the first step in the riboflavin biosynthesis pathway
PGD1		>0.2	Probable transcription factor; RNA polymerase II transcription mediator activity
NGG1		>0.2	Transcription cofactor involved in glucose repression
FMC1		>0.2	Required for assembly of the F1 sector of mitochondrial F1F0 ATP synthase

PPA1		>0.2	Vacuolar ATPase subunit c
PHM6		>0.2	Unknown
TOS1		>0.2	Unknown
VPS60		>0.2	Unknown; putative vacuolar protein sorting
CBF1		>0.2	Centromere binding factor required for mitotic segregation
ECM25		>0.2	Unknown function; involved in cell wall organization
YNL046W		>0.3	Unknown
YAP1		>0.3	bZip transcription factor required for oxidative stress tolerance
FIS1		>0.3	Mitochondrial outer membrane protein of unknown function; involved in mitochondrial fission
RPL2B		>0.3	Protein component of the large (60S) ribosomal subunit
HOM6		>0.5	Enzyme that converts L-aspartate-semialdehyde to homoserine
STB5		>0.5	Transcription factor potentially involved in response to xenobiotic stimulus
EAP1		>0.5	Translation initiation factor
YDL038C		>0.5	Unknown
YPL208W		>0.5	Unknown
LTE1		>0.5	GDP/GTP exchange factor essential for low-temperature growth
ADE1		>0.5	SAICAR synthetase; required for de novo purine nucleotide biosynthesis
ARG82		>0.5	Inositol/phosphatidylinositol kinase involved in arginine metabolism
UBP3		>0.5	Ubiquitin-specific protease; involved in transport between endoplasmic reticulum and Golgi compartments
GPA1		>0.5	G-protein $\alpha$ subunit; involved in the mating pheromone signal transduction pathway
SWC1		>0.5	Unknown
YIL039W		>0.5	Unknown
YGL211W		>0.5	Unknown
EMI2		>0.5	Nonessential protein of unknown function
MAM33		>0.5	Unknown; mitochondrial acidic matrix protein
SSD1		>0.5	Product of gene unknown; involved in RNA binding
URM1		>0.5	Ubiquitin-like protein
GTR2		>0.5	Cytoplasmic GTP binding protein; putative GTPase activity
MTO1		>0.5	Unknown
ACO1		>0.5	Mitochondrial aconitase; part of TCA cycle
YPR044C		>0.5	Unknown
YOL050C		>0.5	Unknown
UBP14		>0.5	Ubiquitin-specific protease involved in ubiquitin-dependent degradation of proteins
VPS65		>0.5	Unknown; possible role in vacuolar protein sorting
TPS1		>0.5	$\alpha$ , $\alpha$ -trehalose-phosphate synthase; probable regulator of glucose influx
CSG2		>0.5	Required for mannosylation of inositolphosphorylceramide and for growth at high $\text{Ca}^{2+}$ concentrations
SHP1		>0.5	Unknown
YBR077C		>0.5	Unknown
RPB9		>0.5	RNA polymerase II core subunit
MAC1		>0.5	Metal binding transcriptional activator
YJL120W		>0.5	Unknown
SFK1		>0.5	Unknown
FPS1		>0.5	Transmembrane channel potentially involved in glycerol efflux and in uptake of trivalent metalloids
YIL110W		>0.5	Putative S-adenosylmethionine-dependent methyltransferase
ELM1		>1	Serine/threonine protein kinase that regulates cellular morphogenesis
YLR455W		>1	Unknown
GOS1		>1	Anchored membrane protein involved in Golgi transport
RPL23B		>1	Protein component of the large (60S) ribosomal subunit

RMD8		>1	Unknown; required for sporulation
ISA2		>1	Mitochondrial protein involved in iron–sulfur complex assembly/transport
SCP160		>1	Protein involved in control of mitotic chromosome transmission
MMS22		>1	Unknown; involved in double-strand break repair