Supporting information

Supplementary figure legends

Figure S1. mRNA abundance of *STREP-ATG8* gene in wild-type cells (WT) and cells expressing P_{CYC6}-driven ATG8 (STREP-ATG8) treated with different concentrations of Ni^{2+} for 8 hours. mRNA levels were compared and normalized to control cells (expression = 1). The data are represented as mean ± standard deviation from three independent experiments.

Figure S2. Immunolocalization of ATG8 in *cw15* cells grown to log phase in TAP medium and treated with 100 µM Ni^{2+}, 150 µM Co^{2+}, 150 µM Cu^{2+}, 150 µM Cd^{2+} or 2 µM Hg^{2+} for 8 hours. Control refers to untreated cells.

Figure S3. (a) mRNA abundance (FPKM) of selected genes taken from Ni^{2+} and H_2O_2 transcriptome data sets. (b) Expression analysis of *GSTS1* and *GPXH* genes by qPCR in *cw15* cells treated with 100 µM Ni^{2+} for 8 hours. C refers to untreated control cells. mRNA levels were compared and normalized to control cells (expression = 1). The data are represented as mean ± standard deviation from three independent experiments.

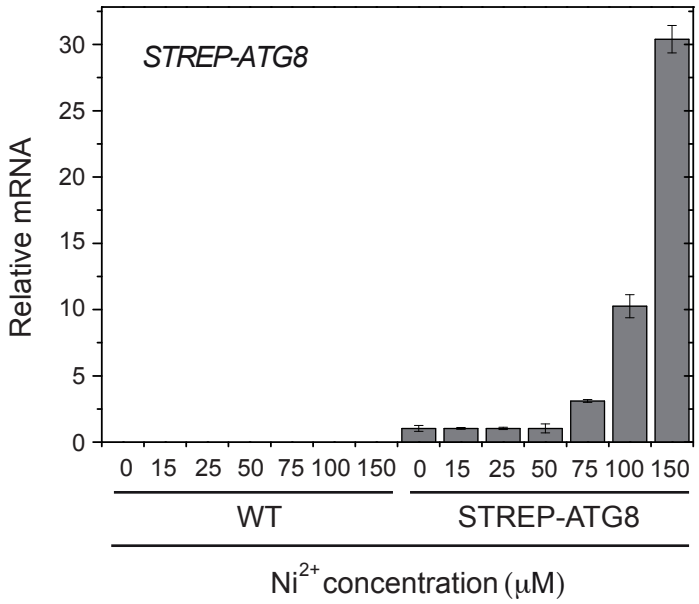
STREP-ATG8
Relative mRNA
30
25
20
15
10
5
0
0 15 25 50 75 100 150 0 15 25 50 75 100 150
WT
STREP-ATG8
Ni2+ concentration (μM)

Fig. S1

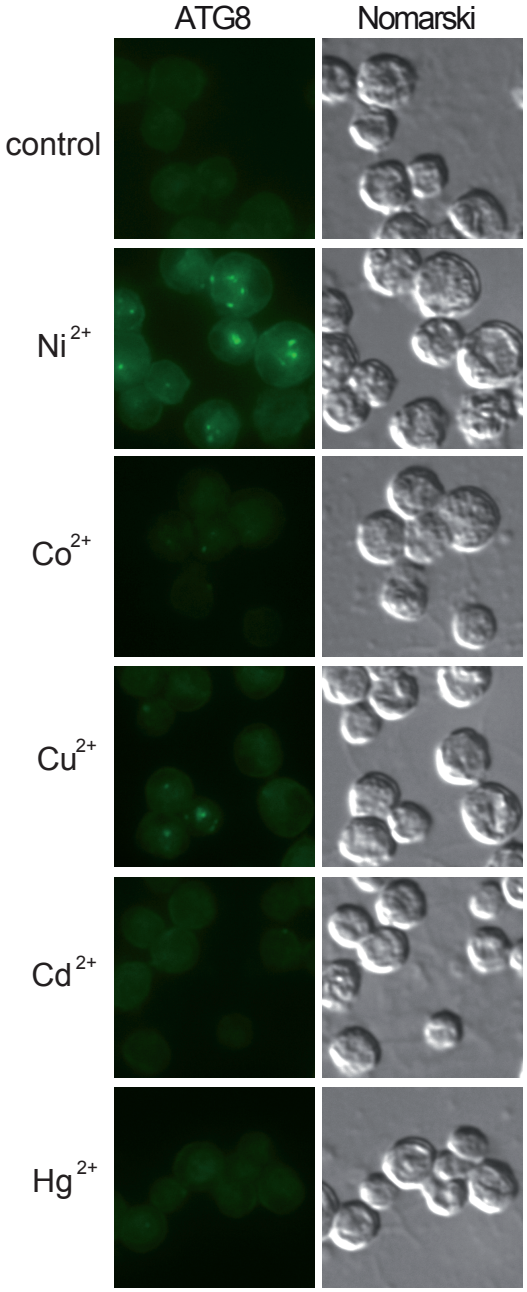

Fig. S2

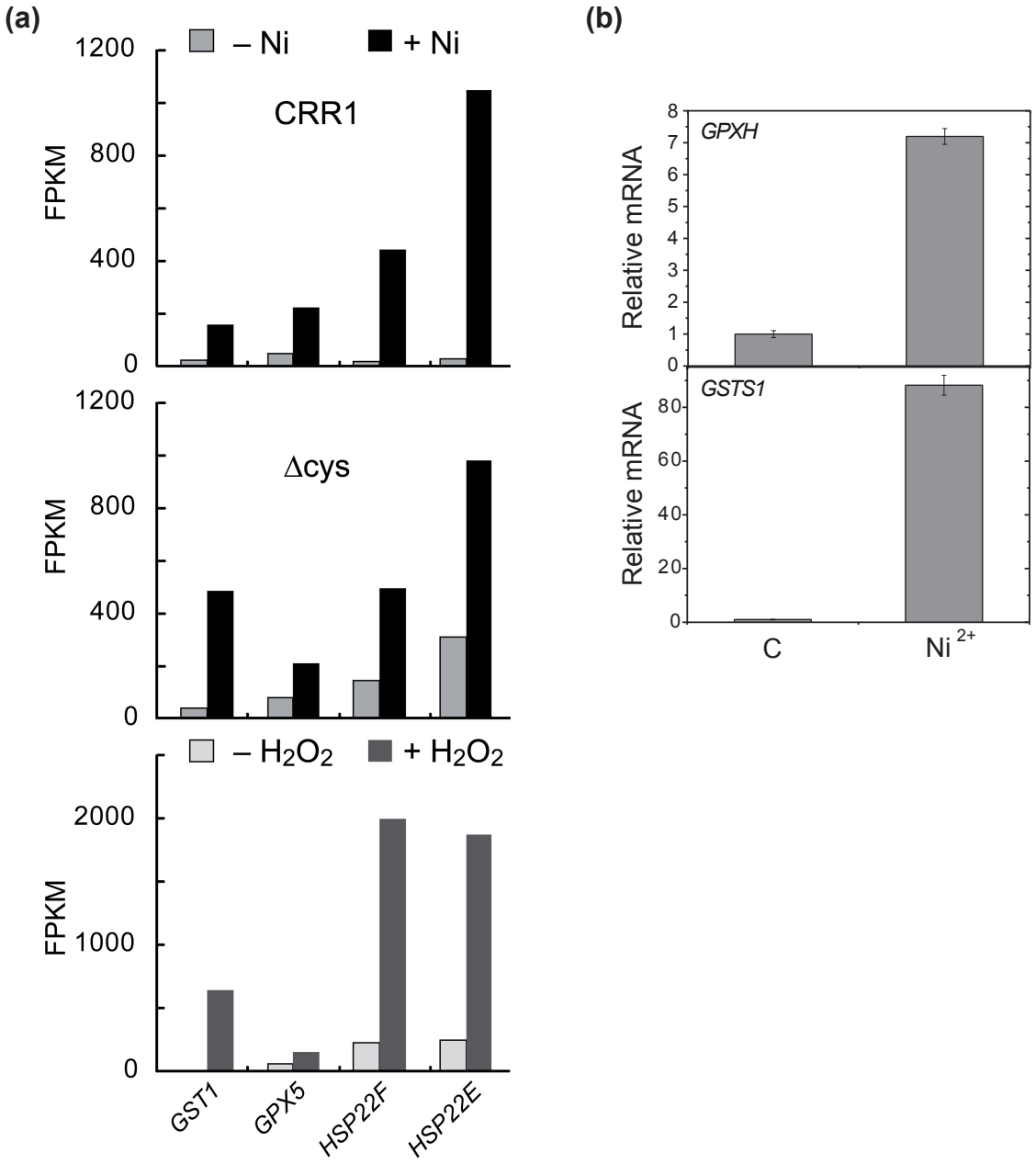
(a)
– Ni
+ Ni
CRR1
Δcys
FPKM
1200
800
400
0
– H2O2
+ H2O2
2000
1000
GST1
GPX5
HSP22F
HSP22E
(b)
GPXH
GSTS1
Relative mRNA
C
Ni 2+

Fig. S3