

Supplementary material

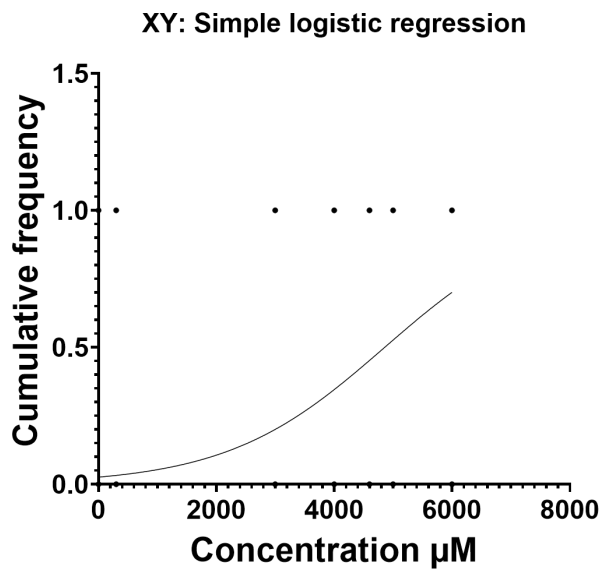
Table S1. Characterization of *C. elegans* wildtype and mutant strains.

Strain name and WB ID	Genotype	Description	Ref
N2	Wild type	<i>C. elegans</i> was isolated in 1951 by W. L. Nicholas in Bristol from mushroom compost from a garden. Only a tiny part of the population is male; most are hermaphrodites. Its development has been described as lasting 3 days with a lifespan of 3 weeks. During their fertile stage, they can have an average of 300 eggs.	[32]
VC128	<i>mtl-2(gk125) V</i>	The metallothionein 2 enables Cd ion binding activity and zinc ion binding activity. Involved in response to Cd ion and response to heat. Mutant strain. T08G5.10. Superficially wild type. Made by Mark Edgley.	[33]
RB1623	<i>cdr-2(ok1996) V</i>	A gene involved in regulating protein deneddylation and stress response to cadmium ion. Predicted to be located in the cytoplasm. Mutant strain. C54D10.1. Homozygous. Outer Left sequence: GTTGGTGGCGTGAAGAATTT. Outer right Sequence: ATTCCGCTGCAAAATTAACG. Inner Left sequence: TGTCCTGGACAGCAACACA. Inner right sequence: AGCGTGTTCGCAAAGAGATT. Inner primer PCR Length: 2727 bp. Deletion Size: 1109 bp. Deletion left flank: ATTTTGGAATACCAATGCTTCTGACAAGAA. Deletion right flank: AAAAAAATCAAGAAGAGTTTACAAATTTT. Made by OMRF Knockout Group.	[33]
TK22	<i>mev-1(kn1) III</i>	<i>mev-1</i> encodes the <i>C. elegans</i> ortholog for human mitochondrial succinate dehydrogenase cytochrome b560 subunit, the mutation of which is associated with a significantly decreased life span, increased reactive oxygen species, and severely impaired reproduction. Methylviologen (paraquat) sensitive. Made by Naoaki Ishii.	[34,35]
TJ1052	<i>age-1(hx546) II.</i>	Mutant strain. Long life. Normal fertility. Not temperature sensitive. Stress tolerant. Made by Hutchinson and Johnson.	[36]

QV225	<i>skn-1(zj15) IV</i>	SKN-1/Nrf2 proteins are members of the cap 'n' collar (CNC) family of transcription factors that are master regulators of oxidative stress resistance and longevity. <i>skn-1(zj15)</i> is a point mutation in an intron that causes mis-splicing of a fraction of mRNA and strongly reduces wildtype mRNA levels of the two long <i>skn-1a/c</i> variants. Hypomorphic allele of <i>skn-1</i> that may be propagated as a homozygote. High rate of embryonic lethality and slightly lower brood size compared to N2. Made by Keith Choe.	[37]
GR2245	<i>skn-1(mg570) IV</i>	<i>skn-1(mg570)</i> mutants lack SKN-1a but retain other SKN-1 isoforms. SKN-1a/Nrf1 is an unusual transcription factor associated with the endoplasmic reticulum via an N-terminal transmembrane domain. Mutant strain. Superficially wild type. Made by Nicholas Lehrbach.	[38,39]
GR1307	<i>daf-16(mgDf50)I</i>	The <i>daf-16</i> gene produces the sole <i>C. elegans</i> equivalent of the Forkhead box O (FOXO) transcription factor. Deficiency completely eliminates the <i>daf-16</i> coding region. Makes partial dauers on pheromone. Made by Shoshanna Gottlieb	[35]
SJ4143	<i>zcls17 [ges-1::GFP(mit)]</i>	Stable transgenic line expressing GFP in mitochondria of intestinal cells. Made by Cristina Benedetti.	[40,41]]
QQ202	<i>daf-2(cv20[daf-2::GFP]) III</i>	Superficially wildtype. Made by Jeff Simske.	---
OH16024	<i>daf-16(ot971[daf-16: GFP]) I</i>	The CRISPR allele of <i>daf-16</i> is tagged at the C-terminus with GFP. Made by Ulkar Aghayeva.	[42]

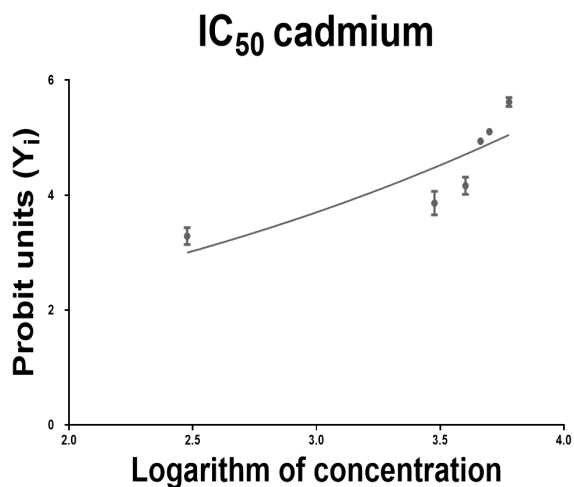
Cd: cadmium, CNC: cap 'n' collar, CRISPR: clustered regularly interspaced short palindromic repeats, FOXO4: forkhead box O4, GFP: green fluorescent protein, Mit: mitochondria, mRNA: messenger RNA, Mtl-2: metallothionein 2, Nrf2: nuclear factor erythroid 2-related factor 2, PCR: polymerase chain reaction.

a) Graphpad prism 5



Std. Error	
X at 50%	79.14
95% Confidence Intervals	
X at 50%	4707 to 5019
Goodness of Fit	
Tjur's R squared	43
Cox-Snell's R squared	0.8208
Model deviance, G squared	3966
Data summary	
Rows in table	1960
Rows skipped (missing data)	0
Rows analyzed (#observations)	1960
Number of 1	642
Number of 0	1318
Number of parameter estimates	2
$LC_{50} = 4\ 858\ \mu\text{M}$	

b) Probit analysis



R^2	0.7204	
Slope	6.1334	
Intercept	-17.61	
Lethal concentration 16	3344.333	μM
Lethal concentration 84	7054.016	μM
Standard deviation (S)	18.54.841	
Population size ($Y_i = 0.07-0.93$) N'	1377	
Standard error of measurement (SEM)	70.689	μM
$t(\alpha=0.05, \text{gl}=N-2)$	1.96	
$t_{0.05} \cdot \text{SEM}$	138.5514	
Lower Control Limit (LCL)	4719	μM
Upper Control Limit (UCL)	4996	μM
$LC_{50} = 4\ 857 \pm 138.6\ \mu\text{M}$		

Figure S1: Calculation of the mean lethal concentration (LC_{50}). A) LC_{50} was calculated using the GraphPad prism 10, and B) LC_{50} was calculated using Probit analysis.