Electronic Supplementary Material

Tissue-specific Nrf2 signaling protects against methylmercury toxicity in *Drosophila* development.

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Online Resource 2. Table S1. Drosophila strains, purpose, and source. Stocks obtained from the Bloomington Drosophila Stock Center (BDSC) includes the corresponding catalog number.

Strain Name	Purpose	Source
Canton S (CS)	Wild-type strain	BDSC #1
w[1118]	Genotype control for UAS lines	BDSC #5905
Mef2-GAL4	Pan-muscle (Myocyte enhancer factor 2 (Mef2) promoter) expression of GAL4	BDSC #27390
MHC-RFP-GAL4	Differentiated muscle (Myosin Heavy Chain (MHC) promoter) expression of GAL4 recombined with a UAS-RFP reporter	BDSC #38464
Elav(I)-GAL4	Pan-neural expression of GAL4 (X chromosome)	BDSC #458
Elav(III)-GAL4	Pan-neural expression of GAL4 (III chromosome)	BDSC #8760
OK371-GAL4	Glutamatergic neuron expression of GAL4. All Drosophila motor neurons are glutamatergic neurons.	BDSC #26160
OK371mCherry-GAL4, MHC-GFP	Glutamatergic neuron GAL4 expression together with GFP reporter under control of MHC promoter	BDSC #79600
UAS-RFP-NLS	RFP reporter with nuclear localization signal (NLS) under control of GAL4 responsive upstream activating sequence (UAS)	BDSC #38424
UAS-GFP-CD8	GFP reporter (membrane localized) with cytosolic expression under control of GAL4 responsive upstream activating sequence (UAS)	BDSC #5130
ARE-GFP-NLS	Reporter for Antioxidant Response Element (ARE) expressing GFP with a nuclear localization signal (NLS)	Gifted from Dirk Bohmann (Chatterjee and Bohmann 2012)
ARE-GFP; Mef2-GAL4, Tub-GAL80^{TS}	Temperature sensitive GAL80 controlled pan-muscle GAL4 expression combined with ARE-GFP reporter	Gifted from Dirk Bohmann
UAS-CncC	CncC expression under control of GAL4 responsive upstream activating sequence (UAS)	Gifted from Dirk Bohmann (Sykiotis and Bohmann 2008)
UAS-CncC^{RNAi}	Hairpin RNAi knockdown of CncC expression under control of GAL4 responsive upstream activating sequence (UAS)	Gifted from Dirk Bohmann

		(Sykiotis and Bohmann 2008)
UAS-Keap1	Keap1 under control of GAL4 responsive upstream activating sequence (UAS)	Gifted from Dirk Bohmann (Sykiotis and Bohmann 2008)
UAS-Keap1[RNAi]	Hairpin RNAi knockdown of Keap1 expression under control of GAL4 responsive upstream activating sequence (UAS)	Gifted from Dirk Bohmann (Sykiotis and Bohmann 2008)
Cnc-T2A-GAL4	GAL4 expression under control of endogenous Cnc gene promoter/enhancer. Abbreviated Cnc-GAL4 in the text.	Gifted from Dirk Bohmann Created in Hugo Bellen lab
Mef2-RFP-GAL4	Pan-muscle GAL4 expression together with UAS-RFP reporter expression	This study
Cnc-RFP-GAL4	GAL4 expression under control of endogenous Cnc gene promoter/enhancer together with UAS-RFP reporter expression	This study

Online Resource 3. RT-qPCR forward and reverse primer sequences.

Gene	Forward (5' → 3')	Reverse (5' → 3')
RP49	AGT ATC TGA TGC CCA ACA TCG	TTC CGA CCA GGT TAC AAG AAC
CncC	GAT ACC GCC TCG CTG GAC CC	GAT CCT GCA GCG CAT GTG GC
Keap1	TGG CCA GCG TGG AGT GCT AC	TTG CAG CAA CAC CCG CTC CA
Ho	ACC ATT TGC CCG CCG GGA TG	AGT GCG ACG GCC AGC TTC CT
Gclc	ATG ACG AGG AGA ATG AGC TG	CCA TGG ACT GCA AAT AGC TG
dMRP	CCA GTC GCA TCA AGA CCT ATC	GCG TAC AAT TTG AGC ACC TTA AT

Online Resource 4. Representative images of ARE-GFP-NLS DIOMs used for quantification of nuclei fluorescence intensity upon MeHg exposure. A single region of interest containing at least 100 nuclei primarily from A1-A5 most medial DIOMs (indicated by white asterisks in 0 μM MeHg abdomen) was used for quantification purposes.
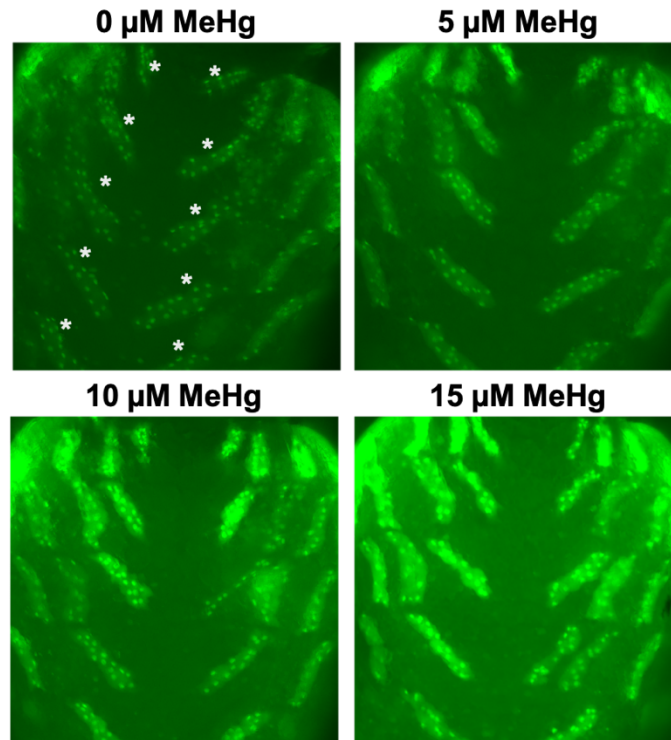
Online Resource 5. Keap1 expression level influences DIOMs remodeling success upon MeHg treatment. **a** Representative images of p7 DIOMs morphology with either no change, knockdown, or overexpression of Keap1 in conjunction with larval exposure to MeHg. Number of myospheres originating from the most medial DIOMs in the A2-A5 abdominal segments (indicated by white asterisks) were quantified to assess the influence of Keap1 expression on DIOMs remodeling upon exposure to various MeHg concentrations: **(b)** 0 µM, **(c)** 5 µM, and **(d)** 10 µM. **b-d** n ≥ 10 abdomens/genotype/treatment, mean ± s.d.m., Kruskal-Wallis test with Dunn's post-hoc for multiple comparisons, p<0.05, data not connected by the same letter are significantly different.