

## Supplemental Information

### **Subcellular distribution of dietary methyl-mercury in *Gammarus fossarum* and its impact on the amphipod proteome**

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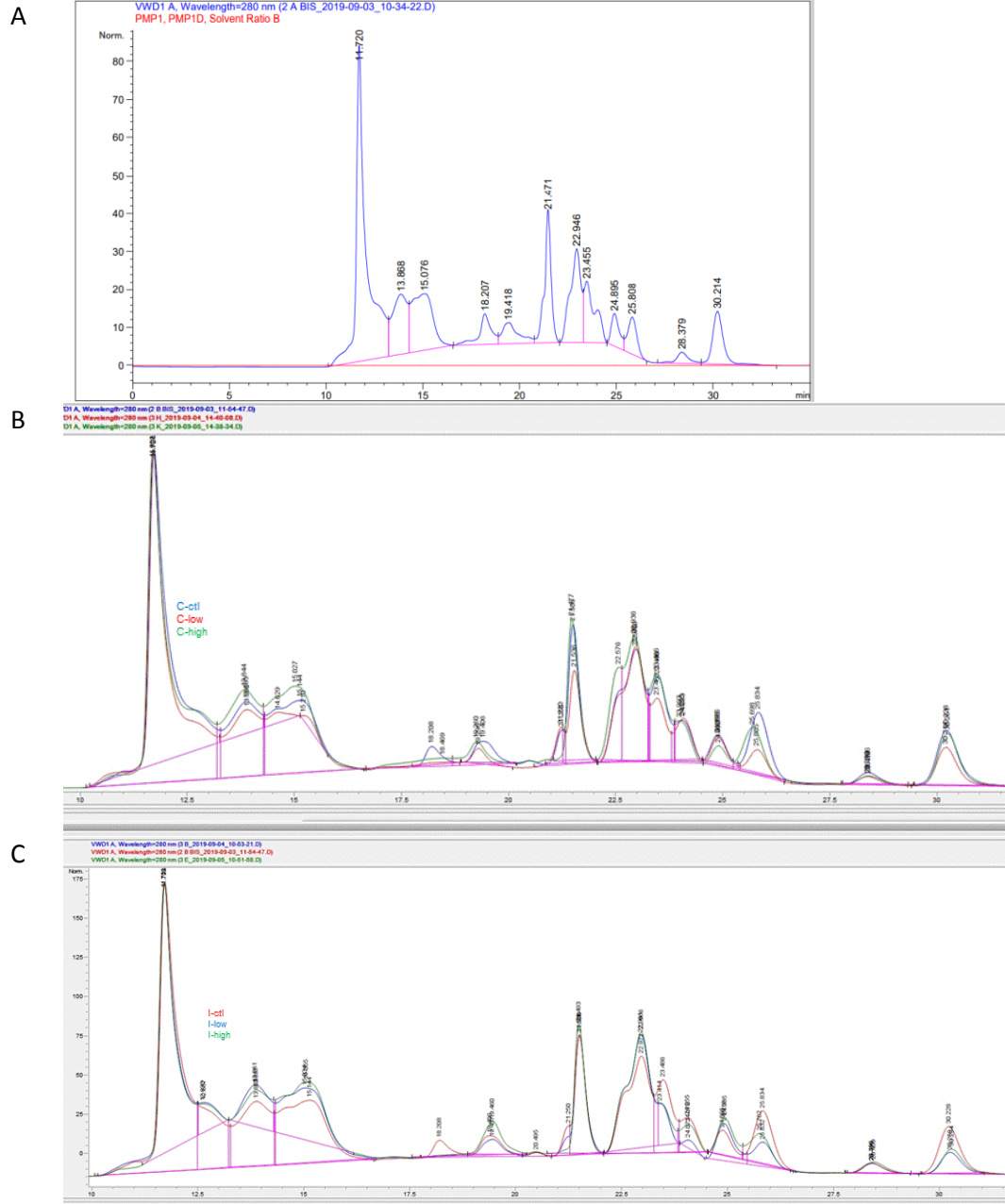
**Table S1:** Concentrations (mean  $\pm$  SD) of THg measured in water at the beginning of *E. nuttallii* exposure (n=3) and THg and MeHg concentrations measured in shoots of *E. nuttallii* at the beginning of feeding of *G. fossarum*, and in *G. fossarum* after 7 days of feeding.

Treatment	Water			
	THg ( $\mu\text{g}\cdot\text{L}^{-1}$ )			
Control	0.05 $\pm$ 0.001			
4 $\mu\text{g}\cdot\text{L}^{-1}$	4.30 $\pm$ 0.02			
20 $\mu\text{g}\cdot\text{L}^{-1}$	16.99 $\pm$ 0.20			
<i>Elodea nuttallii</i>				
	Intracellular	Cell wall	Intracellular	Cell wall
	THg ( $\mu\text{g}\cdot\text{g}^{-1}$ dw)		MeHg ( $\mu\text{g}\cdot\text{g}^{-1}$ dw)	
Control	0.05 $\pm$ 0.01	0.04 $\pm$ 0.001	0.04 $\pm$ 0.02	0.07 $\pm$ 0.02
4 $\mu\text{g}\cdot\text{L}^{-1}$	0.41 $\pm$ 0.02	0.76 $\pm$ 0.07	0.51 $\pm$ 0.21	0.76 $\pm$ 0.11
20 $\mu\text{g}\cdot\text{L}^{-1}$	4.18 $\pm$ 0.48	6.98 $\pm$ 0.52	7.06 $\pm$ 1.32	8.22 $\pm$ 4.60
<i>Gammarus fossarum</i>				
Control	0.07 $\pm$ 0.01	0.06 $\pm$ 0.01	0.01 $\pm$ 0.00	0.00 $\pm$ 0.00
4 $\mu\text{g}\cdot\text{L}^{-1}$	0.23 $\pm$ 0.07	0.42 $\pm$ 0.02	0.03 $\pm$ 0.02	0.06 $\pm$ 0.02
20 $\mu\text{g}\cdot\text{L}^{-1}$	1.04 $\pm$ 0.14	2.60 $\pm$ 0.13	0.82 $\pm$ 0.05	1.22 $\pm$ 0.24

**Table S2:** THg and MeHg concentrations measured (mean  $\pm$ SD) in subcellular fractions *G. fossarum* ( $\text{ng}\cdot\text{g}^{-1}$  dw) fed with the MeHg contaminated intracellular or cell wall compartment of *E. nuttallii*.

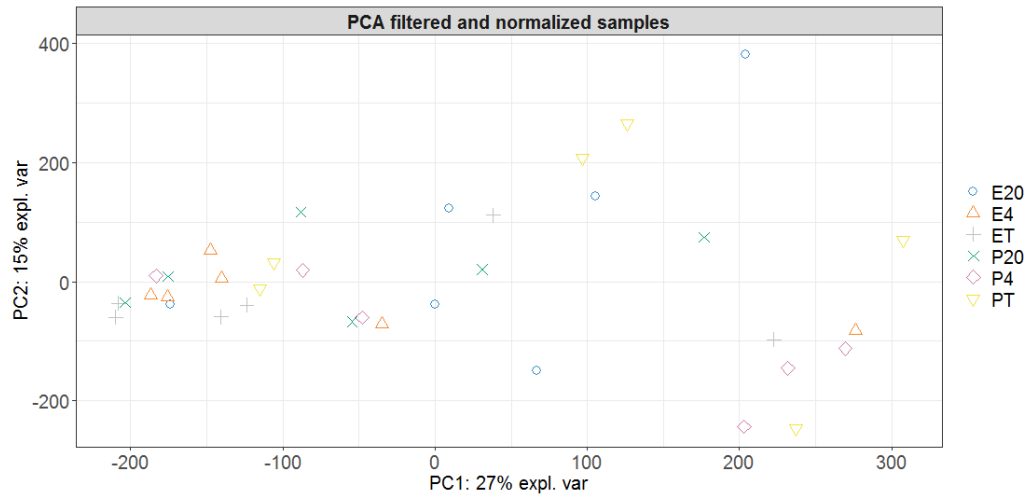
Treatment	THg						MeHg					
	Intracellular			Cell wall			Intracellular			Cell wall		
	MSF	BDM	S2	MSF	BDM	S2	MSF	BDM	S2	MSF	BDM	S2
<b>control</b>	2.7 $\pm$	2.8 $\pm$	4.2 $\pm$	2.9 $\pm$	2.6 $\pm$	4.1 $\pm$	1.9 $\pm$	1.9 $\pm$	4.2 $\pm$	2.0 $\pm$	1.8 $\pm$	4.1 $\pm$
	0.5	0.3	0.8	0.6	0.9	0.8	0.3	0.2	0.8	0.4	0.6	0.8
<b>low MeHg</b>	4.2 $\pm$	4.5 $\pm$	5.7 $\pm$	8.4 $\pm$	10.2 $\pm$	10.0 $\pm$	3.3 $\pm$	3.6 $\pm$	5.7 $\pm$	7.3 $\pm$	9.1 $\pm$	10.0 $\pm$
	0.6	1.5	0.8	1.0	2.0	1.2	0.5	1.2	0.8	0.9	1.8	1.2
<b>high MeHg</b>	24.0 $\pm$	21.0 $\pm$	15.3 $\pm$	70.6 $\pm$	121.3 $\pm$	54.3 $\pm$	21.9 $\pm$	18.8 $\pm$	15.3 $\pm$	65.3 $\pm$	116.0 $\pm$	54.3 $\pm$
	3.4	3.8	2.1	13.1	6.7	10.1	3.1	3.4	2.1	12.2	6.4	10.1

Table S3-S6: associated excel files

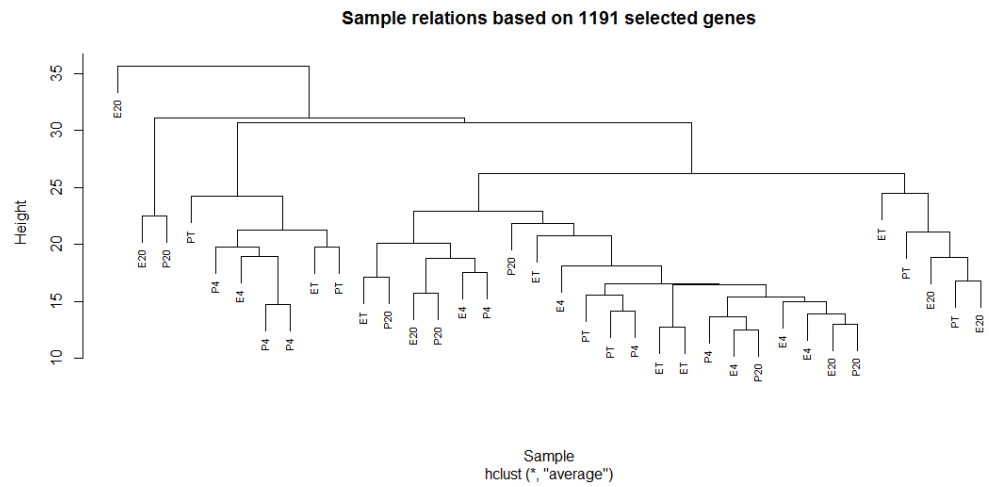


**Figure S1:** A typical chromatogram (A), superposition of cell wall (B) and intracellular treatments (C).

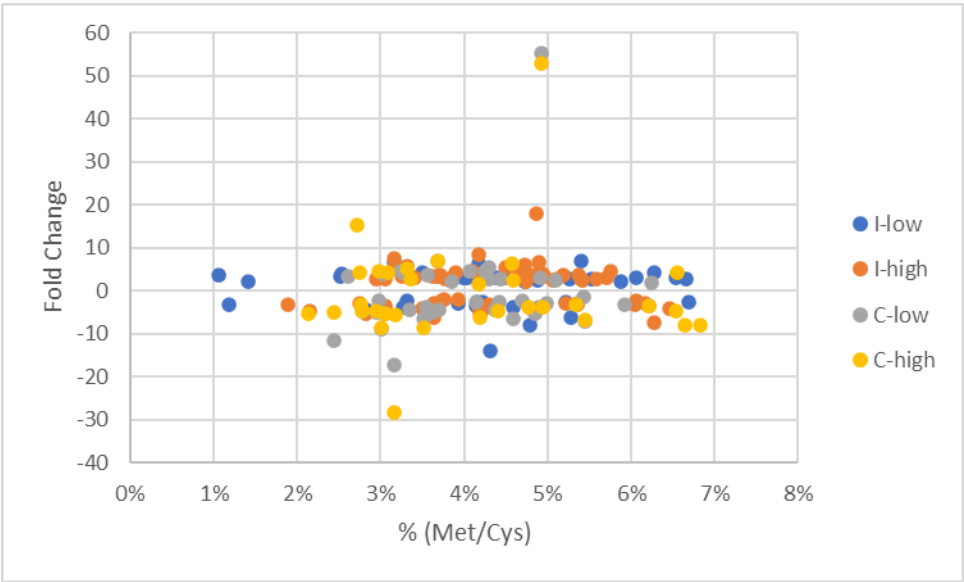
A



B



**Figure S2:** A) Principal Component Analysis showing the distribution of the organisms based on the abundance of 1191 detected proteins, after filtering the low-abundant proteins (< 3 spectral counts) and sample normalization. B) Hierarchical clustering of the same samples in intracellular (E) and cell wall (P) non-treated (T) or treated with low (4) and high (20) MeHg.



**Figure S3:** proportion of Cysteine and Methionine residues in modulated proteins against the level of regulation (Fold change)