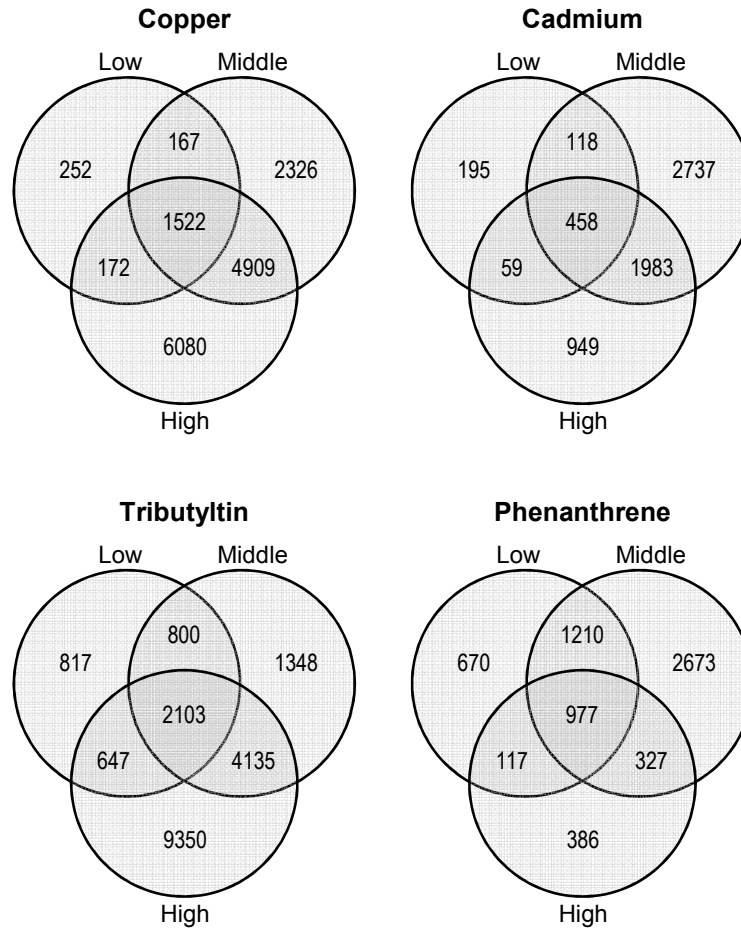
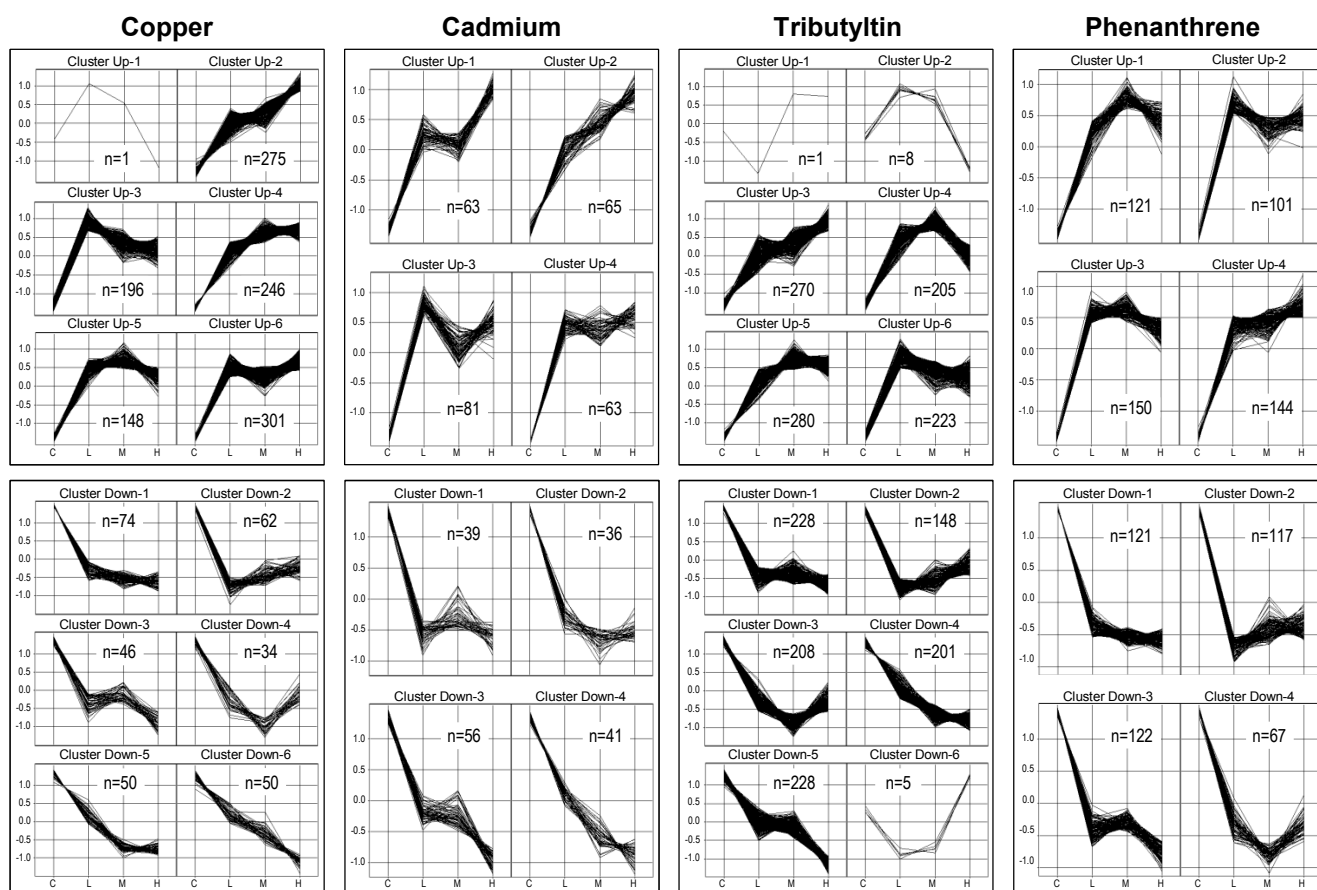


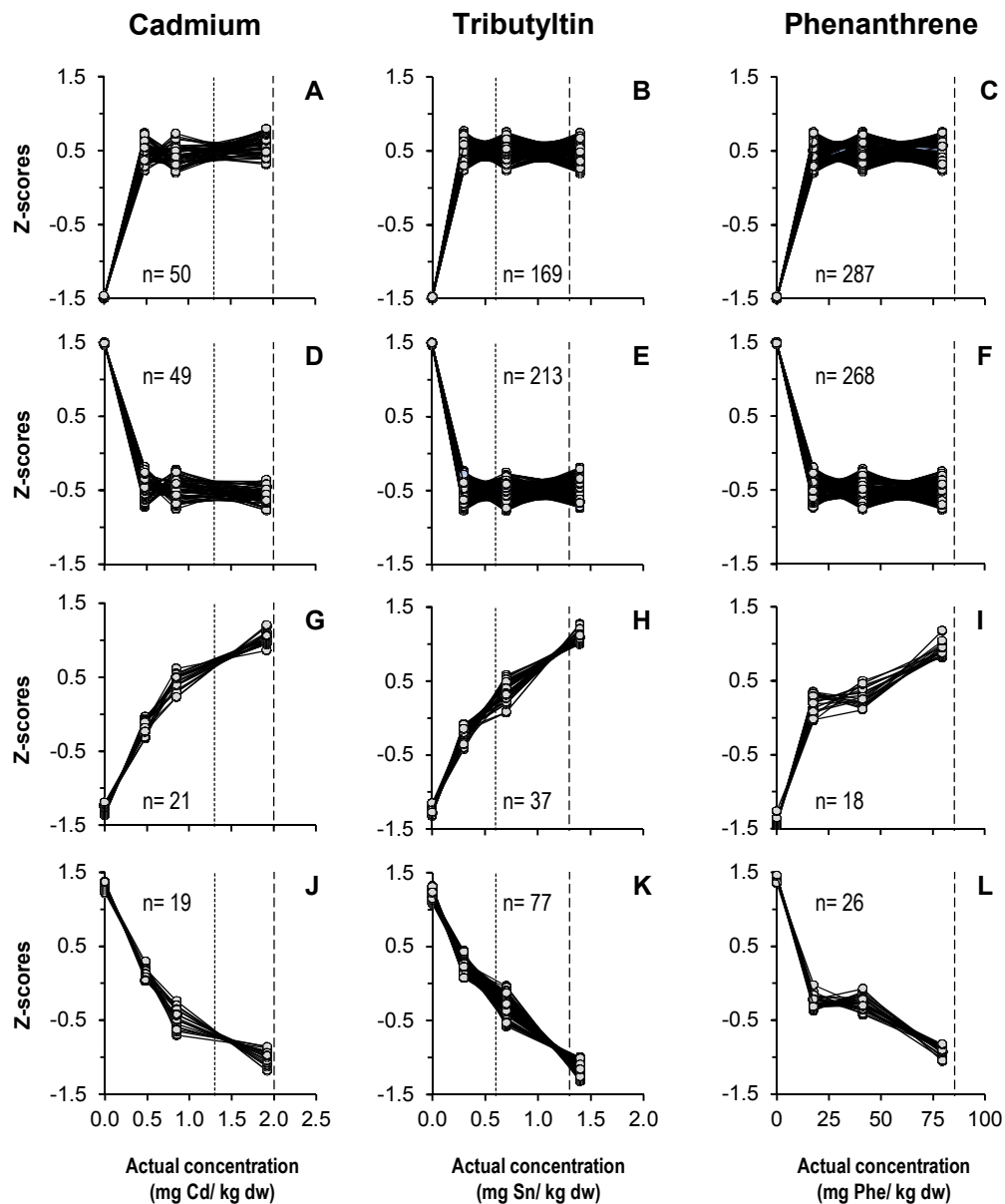
Supplemental figure S1: Principal component analysis (PCA) using the gene expression measurements obtained for all 37,368 *C. riparius* transcripts after exposure to, respectively, copper (panel A), cadmium (panel B), tributyltin (panel C) and phenanthrene (panel D). In each PCA plot, the symbols represent individual larvae, with the white circles indicating the (solvent) control treatment, the light grey squares the low toxicant concentration, the dark grey triangles the intermediate toxicant concentration and the black squares the high toxicant concentration. The two arrows indicate outliers that were technically sound but nevertheless did not group with the other replicates, and which were therefore excluded from further analysis. In panel B the cadmium high treatment consisted of two subgroups that could not be explained by technical artifacts or biological variables, and which were therefore treated as separate subgroups in the subsequent analyses. The differentially expressed transcripts in response to the cadmium high test concentration were defined as the transcripts that were differentially expressed in both cadmium high subgroups.



Supplemental figure S2: Venn diagrams showing for each toxicant the overlap in differentially expressed transcripts between the three test concentrations.



Supplemental figure S3: K-means clustering of transcripts that were differentially expressed at all three test concentrations per toxicant. A two-step clustering procedure, where the transcripts were first separated into two clusters (typically up- and down-regulated), and subsequently further separated into four to six clusters, showed many different gene expression dose response profiles per toxicant. For each cluster the number of transcripts belonging to the respective group is indicated. The x-axis represents the four treatments per toxicant (C= control, L = Low, M = Medium, H = High), while the y-axis is a relative measure for the change in gene expression (z-score). It should be noted that not all DEGs were included in the clustering, i.e. 32 out of 1522 for copper, 14 out of 458 DEGs for cadmium, 89 DEGs out of 2103 for tributyltin, 28 out of 977 DEGs for phenanthrene, as the probes that were differentially expressed over the three test concentrations did not correspond.



Supplemental figure S4: Gene expression profiles obtained for cadmium, tributyltin and phenanthrene. The transcripts that have a *low dose responsive* profile are shown for in panels A to F, while the transcripts matching a *dose range responsive* profile are shown in panels G to L. In each panel the number of transcripts belonging to the respective group is indicated.