Supplementary Material

# Supplementary Figures and Tables

## Supplementary Figures

**Figure S1** Comparison of expression profiles among 6 selected genes as determined by qRT-PC and RNA-Seq analyses, respectively. The description of *acat2*, *pla2g1b*, *gpx3*, *gclc*, *kyat*1 and *aldh9a1* are acetyl-CoA acetyltransferase 2, phospholopase A2 group 1B, glutathione peroxidase 3, glutamate-cysteine ligase catalytic subunit, kynurenine aminotransferase 1 and aldehyde dehydrogenase 9 family member A1a, respectively.

**Figure S2.** Glutathione metabolism regulatory pathway.

**Figure S3.** Thyroid hormone synthesis regulatory pathway.

**Figure S4.** Linoleic acid metabolism regulatory pathway.

**Figure S5.** Biosynthesis of unsaturated fatty acids regulatory pathway.

**Figure S6.** Thyptophan metabolism regulatory pathway.

**Figure S7.** Serotonergic synapse regulatory pathway.

## Supplementary Tables

**Table S1.** GO enrichment of transcriptomic analyses.

**Table S2.** KEGG enrichment of transcriptomic analyses.

**Table S3.** Primary metabolites of metabolomic analyses.

**Table S4.** The list of identified secondary metabolites showing significant difference between the control group and MeHg treatment group in the liver tissues of juvenile flounder in ESI+ and ESI-. The determination of metabolites exerting significant difference among the MeHg treatment and the control groups should simultaneously meet the following requirements: fold-change ≥ 2 or ≤ 0.5, *p* value ≤ 0.05 and VIP ≥ 1.

**Table S5.** The significantly enriched pathways analyzed by multi-omic analyses.

**Table S6.** The information from current (last decade) toxicological studies of waterborne MeHg exposure for fish individuals, including exposure dose, fish species as well as their life stages, exposure periods and the literature sources.