**Table S1:** Number of bluegill used in RNAseq analyses broken down by treatment group (control, niclosamide, or a TFM:niclosamide mixture) and by exposure duration (6, 12, or 24 h).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Exposure series** | **Tissue** | **Control** | | | **Treatment** | | |
|  |  | *6 h* | *12 h* | *24 h* | *6 h* | *12 h* | *24 h* |
| *Niclosamide* | *Gill* | **5** | **7** | **6** | **6** | **4** | **3** |
|  | *Liver* | **8** | **8** | **8** | **6** | **6** | **5** |
| *TFM:niclosamide* | *Gill* | **5** | **7** | **6** | **5** | **4** | **5** |
|  | *Liver* | **8** | **8** | **8** | **6** | **5** | **6** |

**Table S2:** Total sequencing reads counts by treatment and tissue.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Exposure series** | **Tissue** | **Total reads** | | |
|  |  |  |  |  |
| *Niclosamide* | *Gill* | **1.13x109** | | |
|  | *Liver* | **1.47x109** | | |
| *TFM:niclosamide* | *Gill* | **1.15x109** | | |
|  | *Liver* | **1.39x109** | | |



**Figure S1:** Summary of enriched gene ontology (GO) terms associated with Biological Processes (green) and Molecular Functions (blue) in transcripts that were upregulated following 12 h of niclosamide (0.068 mg L-1 nominal) exposure in the gills of juvenile bluegill (*Lepomis macrochirus*). Transcripts were considered differentially regulated at a false discovery rate < 0.05. Only GO terms from the functional analysis with an adjusted p < 0.05 and at least four transcripts were considered significantly enriched. REVIGO was used to summarize GO terms to reduce redundancy and group according to similarity (right labels).



**Figure S2:** Summary of enriched gene ontology (GO) terms associated with Biological Processes in transcripts that were upregulated following 24 h of niclosamide (0.068 mg L-1 nominal) exposure in the gills of juvenile bluegill (*Lepomis macrochirus*). Transcripts were considered differentially regulated at a false discovery rate < 0.05. Only GO terms from the functional analysis with an adjusted p < 0.05 and at least four transcripts were considered significantly enriched. REVIGO was used to summarize GO terms to reduce redundancy and group according to similarity (right labels).



**Figure S3:** Summary of enriched gene ontology (GO) terms associated with Biological Processes (green) or Molecular Functions (blue) in transcripts that were upregulated following 12 h of TFM:niclosamide (1.5%) mixture (3-trifluoromethyl-4'-nitrophenol; TFM = 4.5 mg L-1 & niclosamide = 0.068 mg L-1; Nominal doses) exposure in the gills of juvenile bluegill (*Lepomis macrochirus*). Transcripts were considered differentially regulated at a false discovery rate < 0.05. Only GO terms from the functional analysis with an adjusted p < 0.05 and at least four transcripts were considered significantly enriched. REVIGO was used to summarize GO terms to reduce redundancy and group according to similarity (right labels).



**Figure S4:** Summary of enriched gene ontology (GO) terms associated with Molecular Functions in transcripts that were downregulated following 12 h of TFM:niclosamide (1.5%) mixture (3-trifluoromethyl-4'-nitrophenol; TFM = 4.5 mg L-1 & niclosamide = 0.068 mg L-1; Nominal doses) exposure in the gills of juvenile bluegill (*Lepomis macrochirus*). Transcripts were considered differentially regulated at a false discovery rate < 0.05. Only GO terms from the functional analysis with an adjusted p < 0.05 and at least four transcripts were considered significantly enriched. REVIGO was used to summarize GO terms to reduce redundancy and group according to similarity (right labels).



**Figure S5:** Summary of enriched gene ontology (GO) terms associated with Biological Processes (green) or Molecular Functions (blue) in transcripts that were downregulated following 24 h of TFM:niclosamide (1.5%) mixture (3-trifluoromethyl-4'-nitrophenol; TFM = 4.5 mg L-1 & niclosamide = 0.068 mg L-1; Nominal doses) exposure in the gills of juvenile bluegill (*Lepomis macrochirus*). Transcripts were considered differentially regulated at a false discovery rate < 0.05. Only GO terms from the functional analysis with an adjusted p < 0.05 and at least four transcripts were considered significantly enriched. REVIGO was used to summarize GO terms to reduce redundancy and group according to similarity (right labels).



**Figure S6:** Principal component analysis (PCA) of bluegill (*Lepomis macrochirus*) gene expression in the gills of fish exposed to control (blue, purple, cyan) or niclosamide 0.068 mg L-1 nominal; red, yellow, brown) being sampled at 6 h (circles), 12 h (squares), or 24 h (triangles).



**Figure S7:** Principal component analysis (PCA) of bluegill (*Lepomis macrochirus*) gene expression in the livers of fish exposed to control (blue, purple, cyan) or niclosamide 0.068 mg L-1 nominal; red, yellow, brown) being sampled at 6 h (circles), 12 h (squares), or 24 h (triangles).



**Figure S8:** Principal component analysis (PCA) of bluegill (*Lepomis macrochirus*) gene expression in the gills of fish exposed to control (blue, purple, cyan) or a TFM:niclosamide (1.5%) mixture (3-trifluoromethyl-4'-nitrophenol; TFM = 4.5 mg L-1 & niclosamide = 0.068 mg L-1; Nominal doses; red, yellow, brown) being sampled at 6 h (circles), 12 h (squares), or 24 h (triangles).



**Figure S9:** Principal component analysis (PCA) of bluegill (*Lepomis macrochirus*) gene expression in the livers of fish exposed to control (blue, purple, cyan) or a TFM:niclosamide (1.5%) mixture (3-trifluoromethyl-4'-nitrophenol; TFM = 4.5 mg L-1 & niclosamide = 0.068 mg L-1; Nominal doses; red, yellow, brown) being sampled at 6 h (circles), 12 h (squares), or 24 h (triangles).