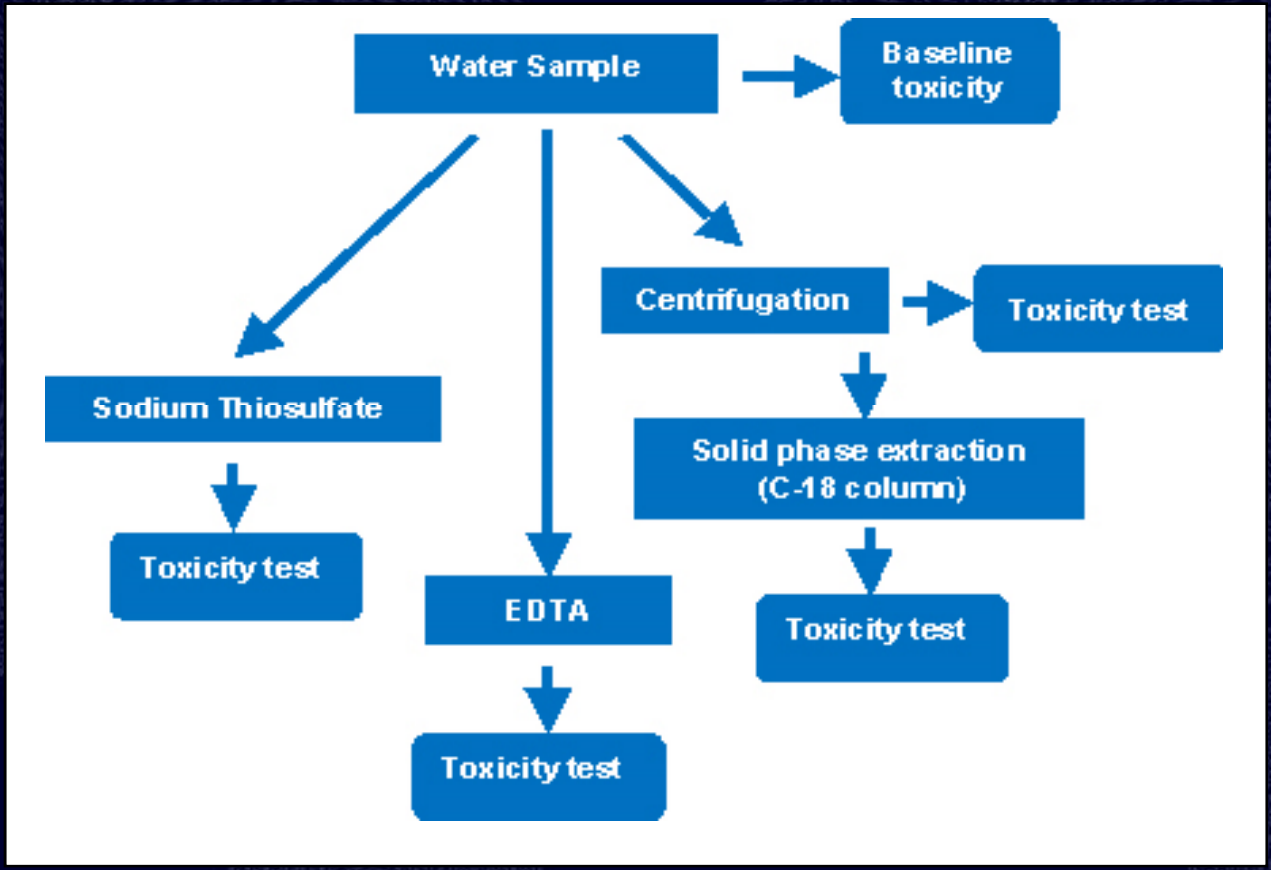
Aquatic Toxicology Laboratory
School of Veterinary Medicine - UC Davis

Refining tools to distinguish pyrethroid toxicity from other contaminants: a TIE approach utilizing transcriptomics.

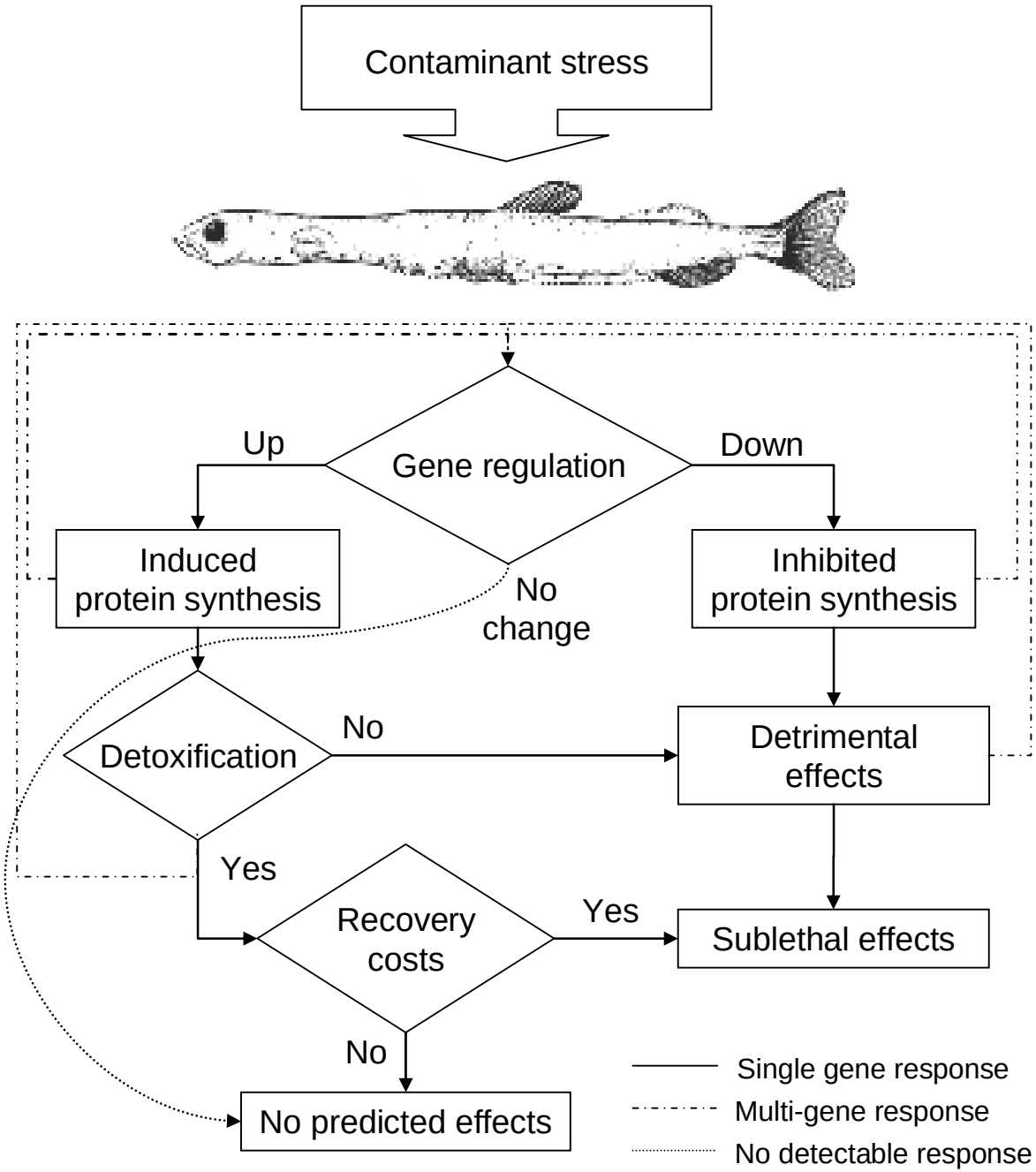
Richard Connon, Linda Deanovic, Sebastian Beggel and Inge Werner

Toxicity Identification and Evaluation



Stolen from: http://www.sccwrp.org/ResearchAreas/Contaminants

Biomarker criticism



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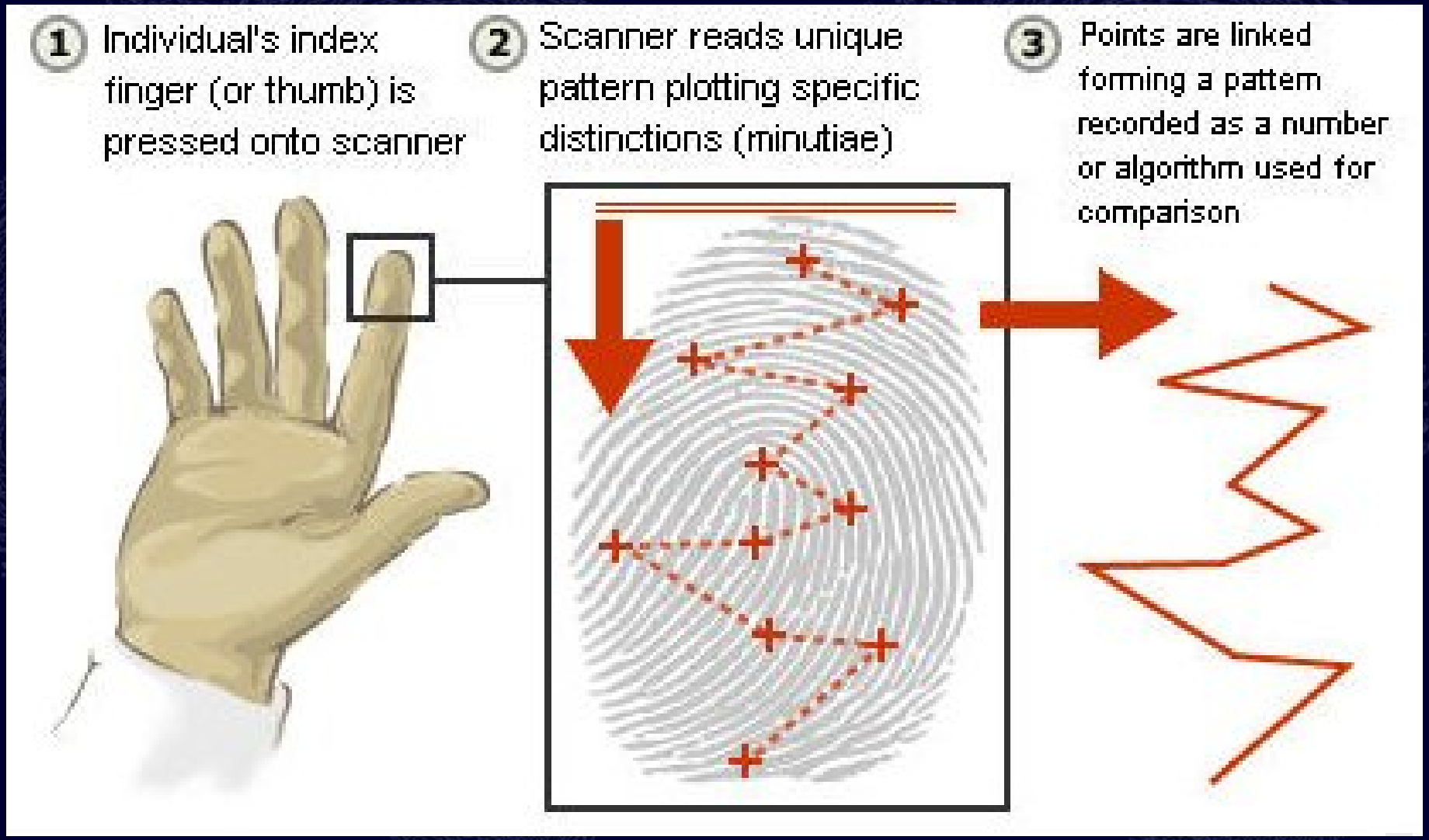
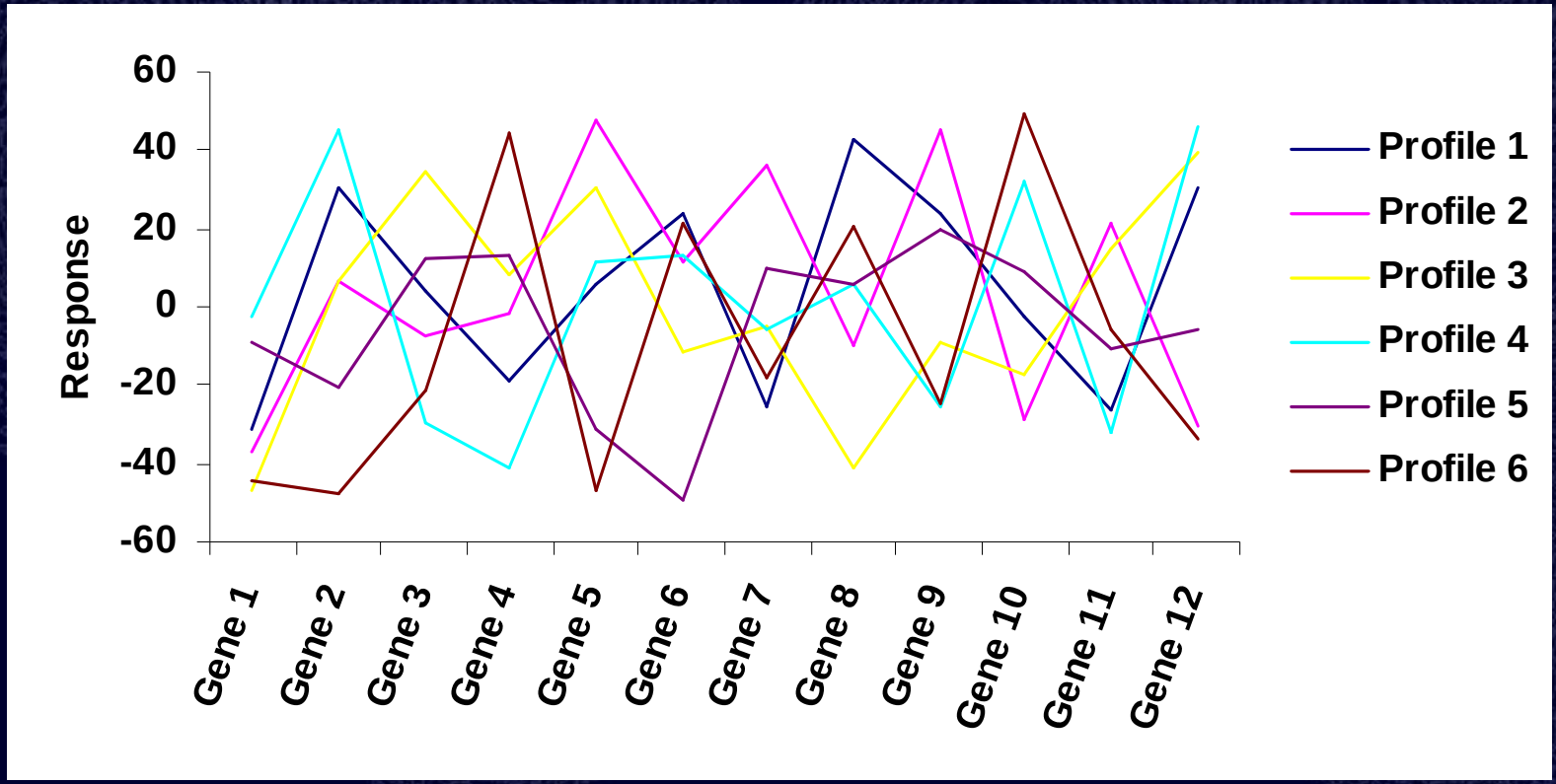
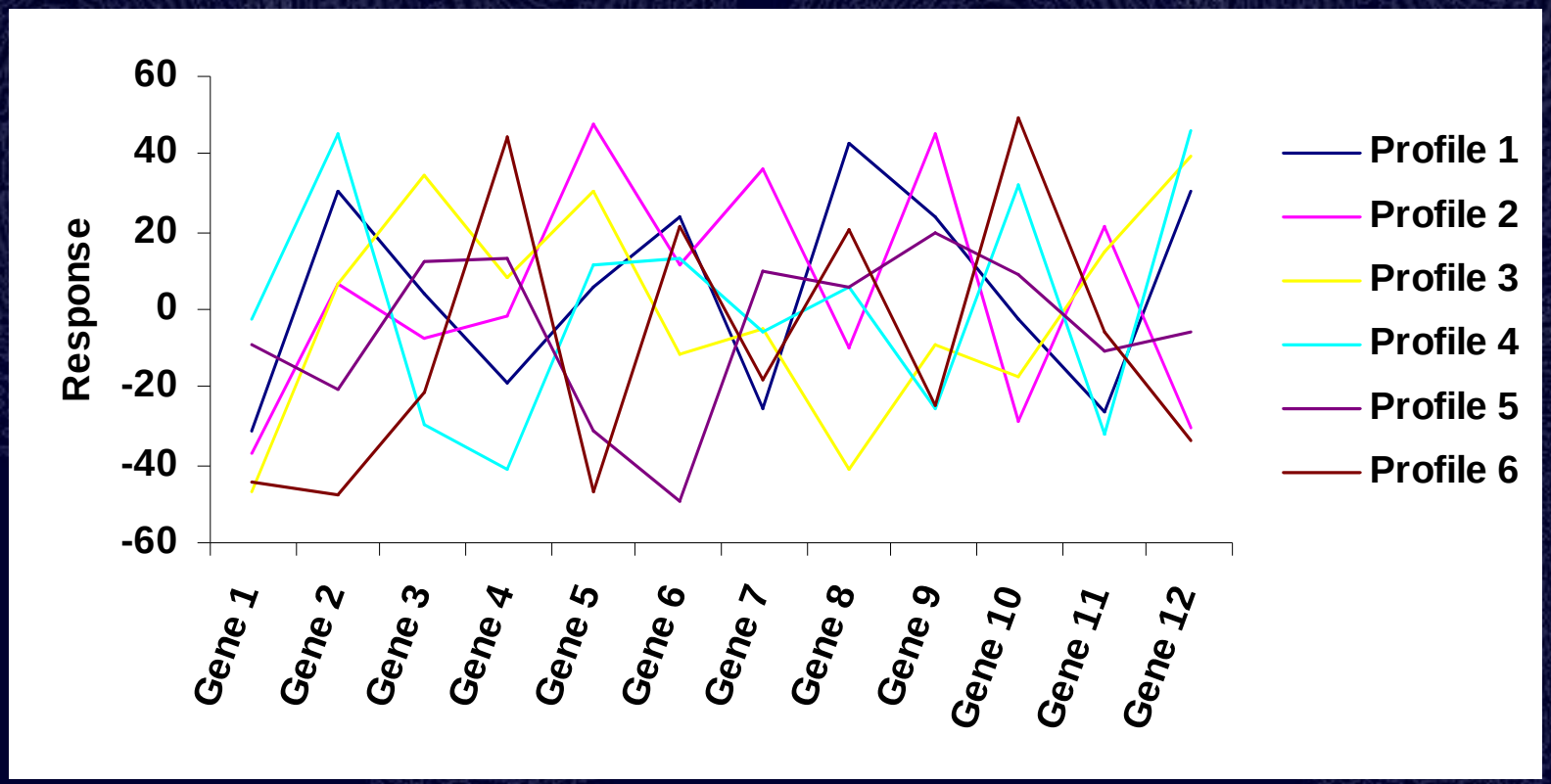


Stolen from: http://www.leavethemkidsalone.com


60
40
20
0
-20
-40
-60
Response
Gene 1
Gene 2
Gene 3
Gene 4
Gene 5
Gene 6
Gene 7
Gene 8
Gene 9
Gene 10
Gene 11
Gene 12
Profile 1
Profile 2
Profile 3
Profile 4
Profile 5
Profile 6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Response
Gene 1
Gene 2
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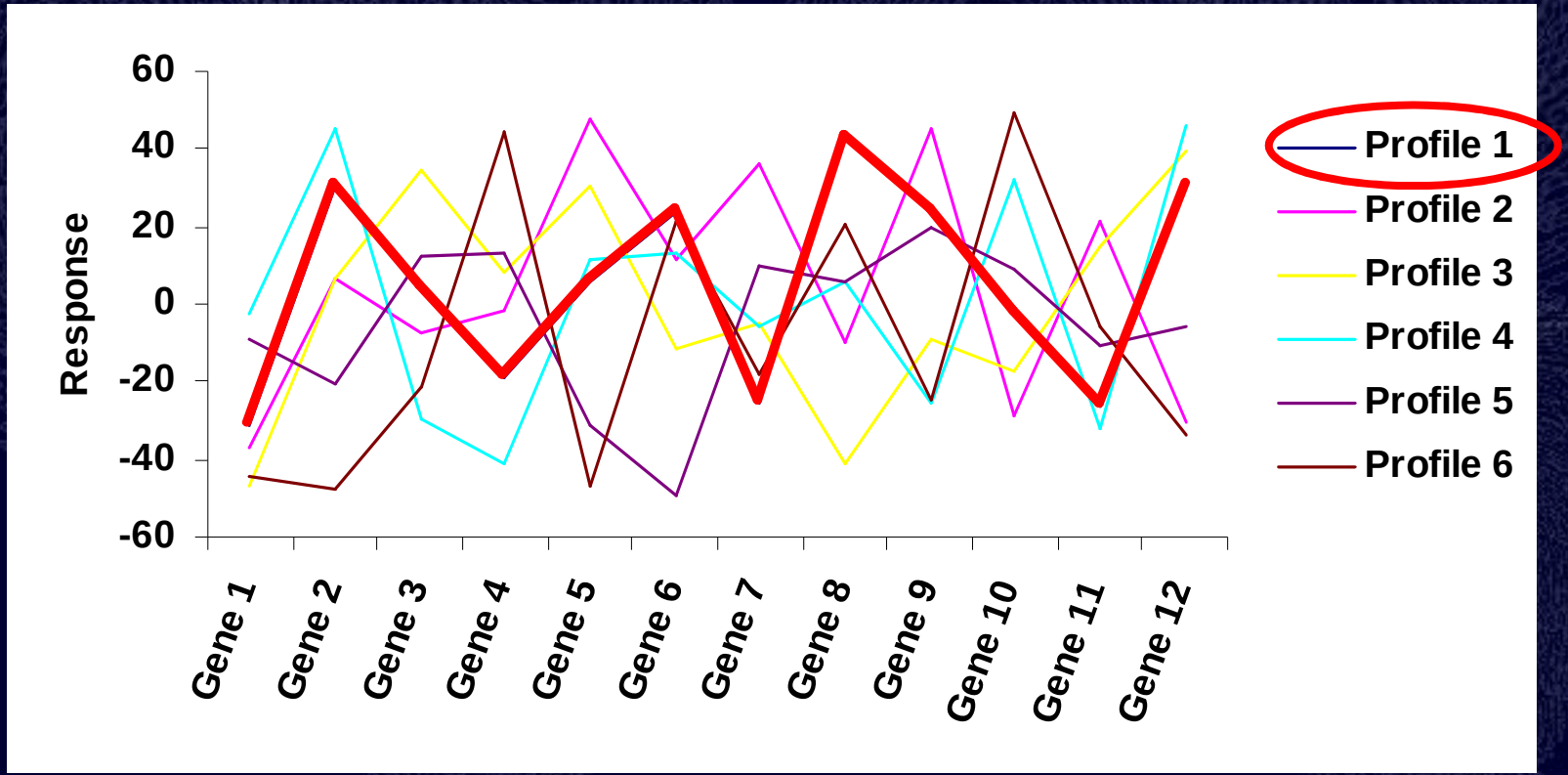
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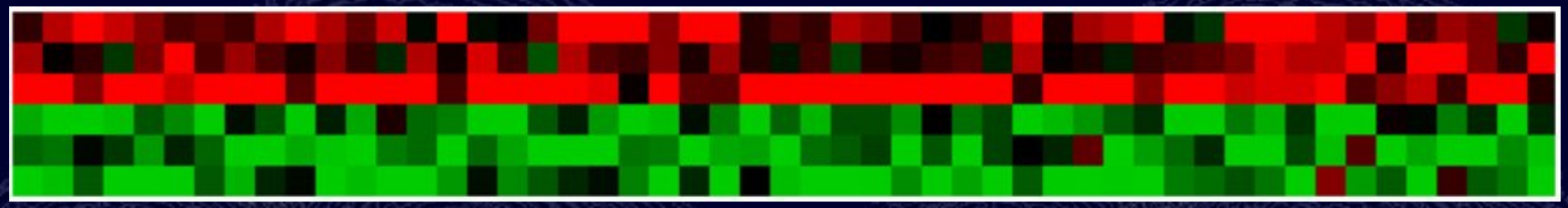
-60
Response
Gene 1
Gene 2
Gene 3
Gene 4
Gene 5
Gene 6
Gene 7
Gene 8
Gene 9
Gene 10
Gene 11
Gene 12
Profile 1
Profile 2
Profile 3
Profile 4
Profile 5
Profile 6

Heatmaps



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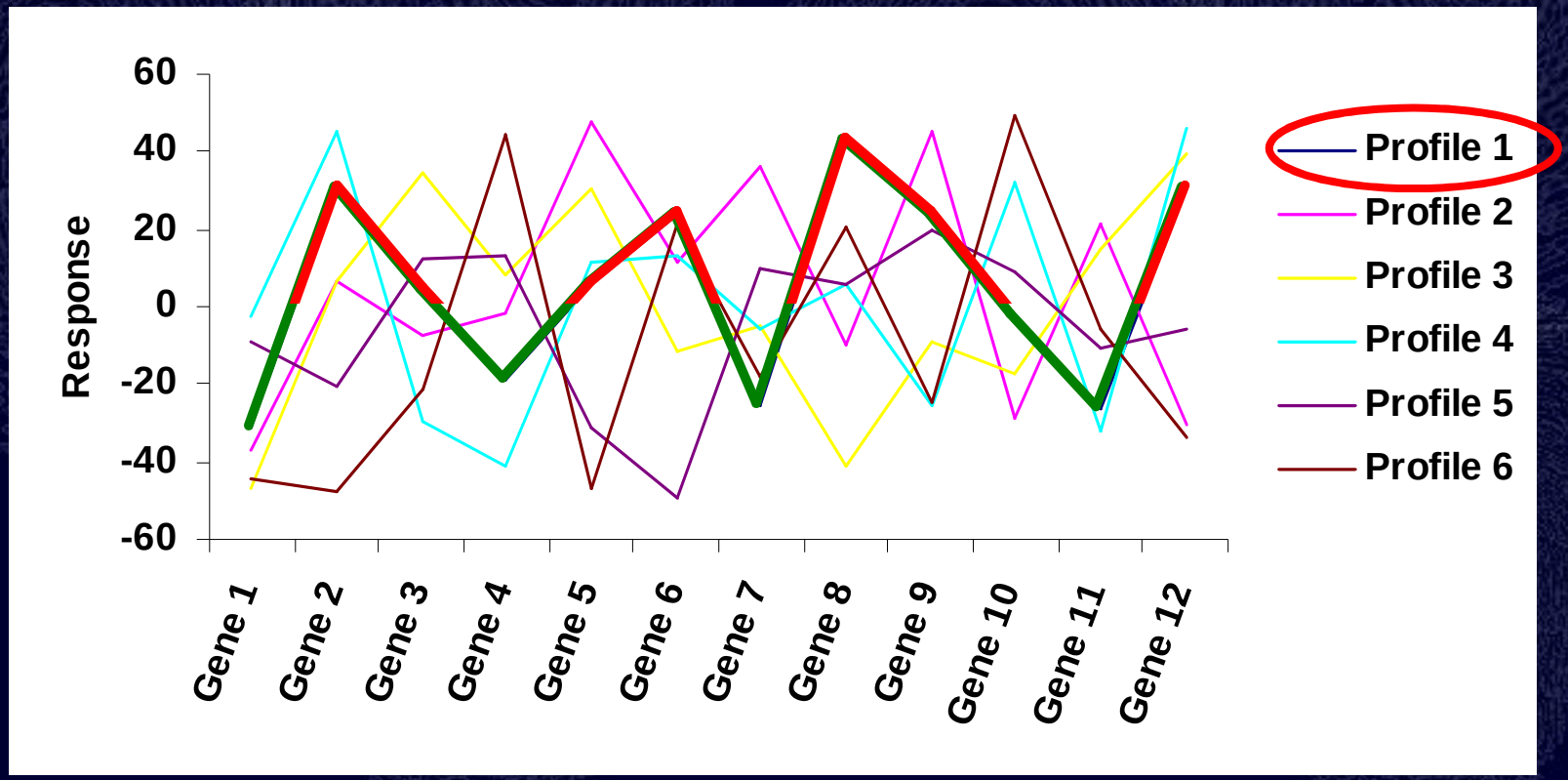
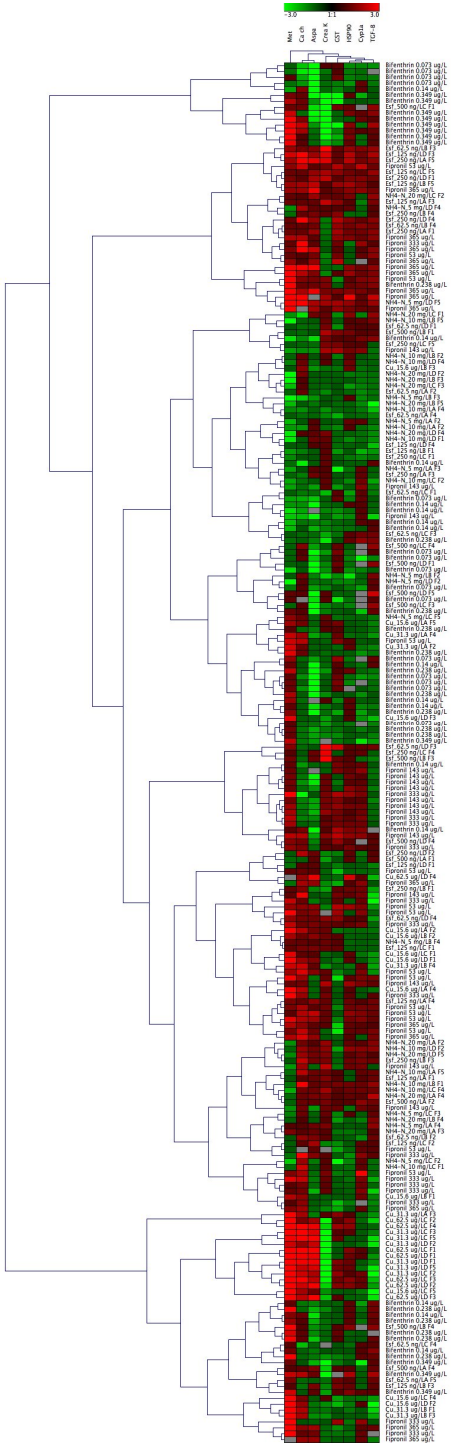
3.0


Response
60
40
20
0
-20
-40
-60
Gene 1
Gene 2
Gene 3
Gene 4
Gene 5
Gene 6
Gene 7
Gene 8
Gene 9
Gene 10
Gene 11
Gene 12
Profile 1
Profile 2
Profile 3
Profile 4
Profile 5
Profile 6



Fathead minnows

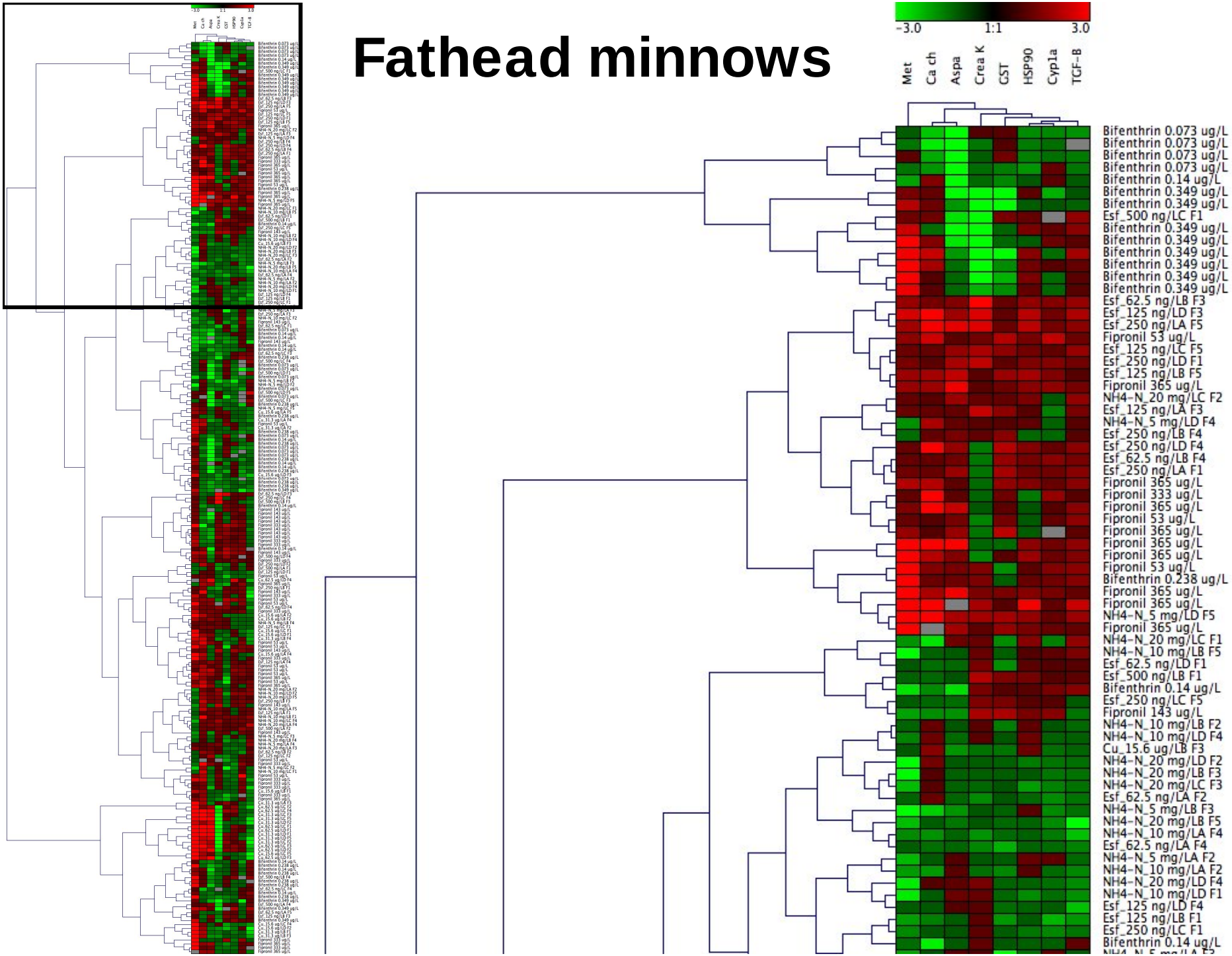
Eight genes

Metallothionein (Mt)
Calcium channel (Ca Ch)
Aspartoacylase (ASPA)
Creatine Kinase (CK)
Glutathione *S*-transferase (GST)
Heat Shock Protein 90 (HSP90)
Cytochrome P4501A (Cyp1a)
Transforming Growth Factor beta (TGF-b)

Five Contaminants

Bifenthrin } Pyrethroids
Esfenvalerate } Pyrethroids
Fipronil — Phenylpyrazole
Ammonia
Copper

Fathead minnows



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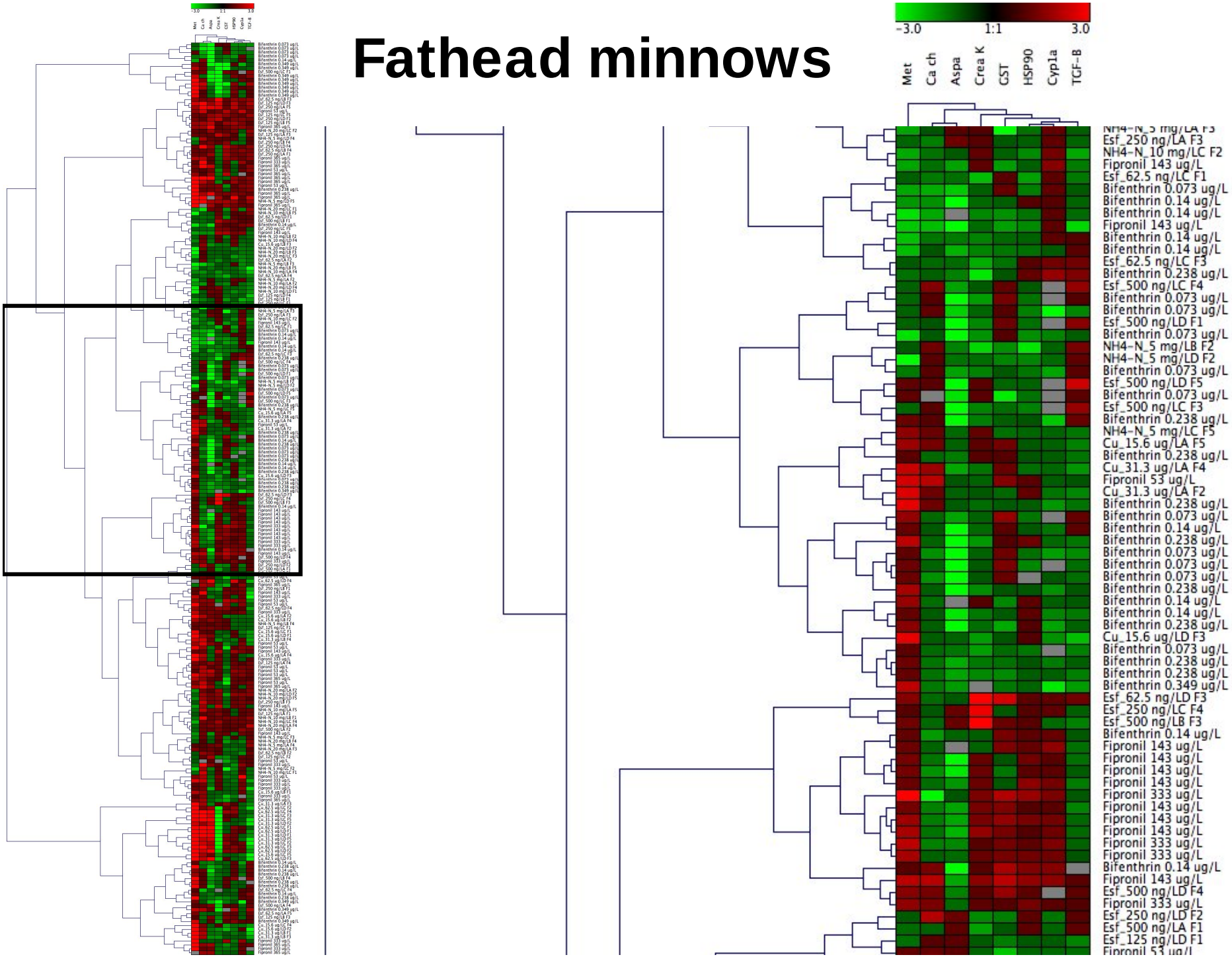

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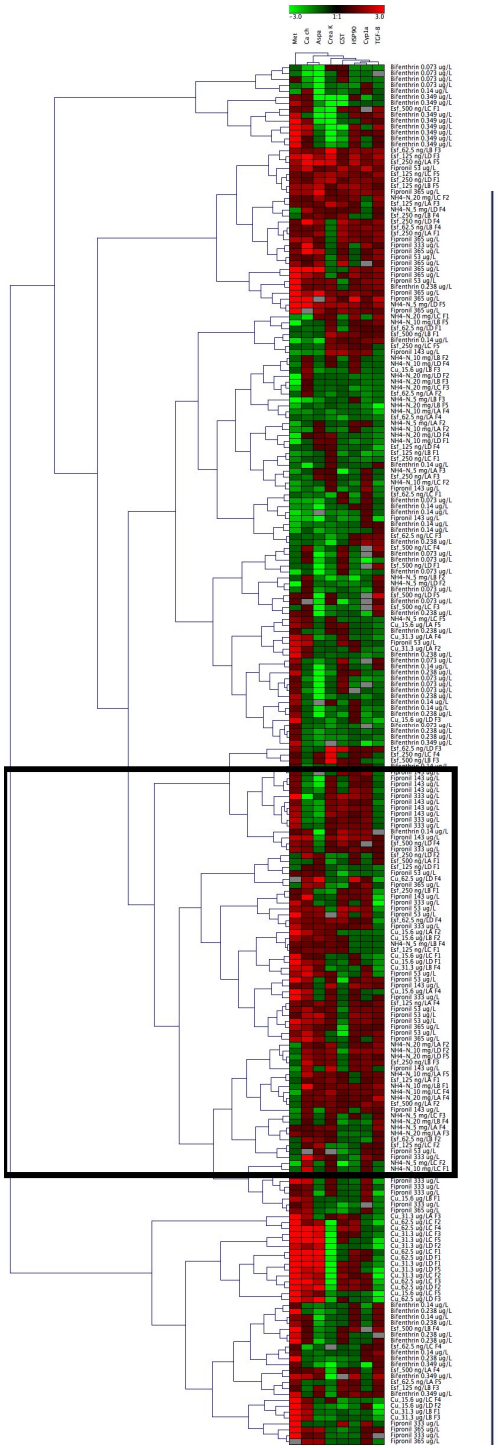
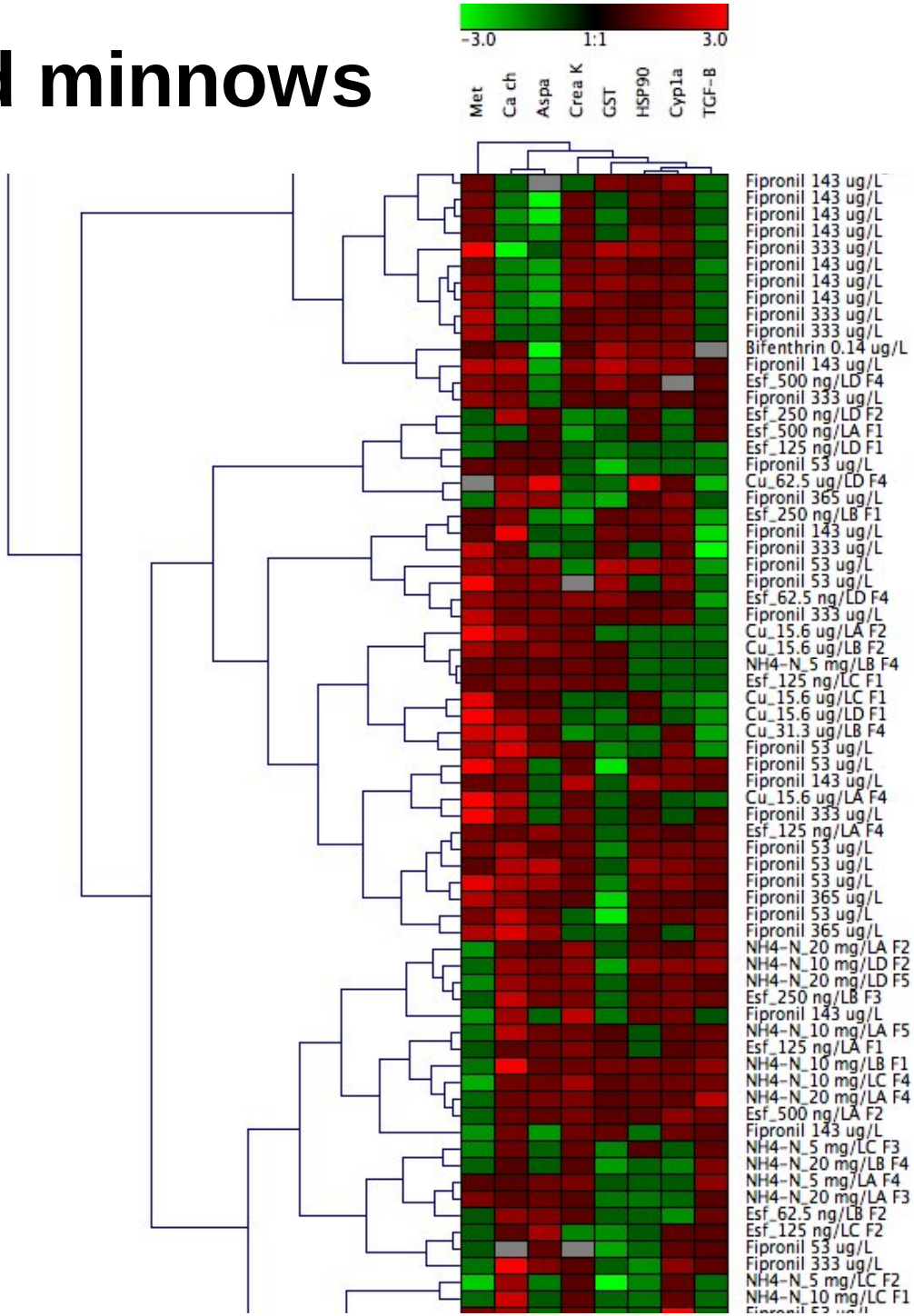
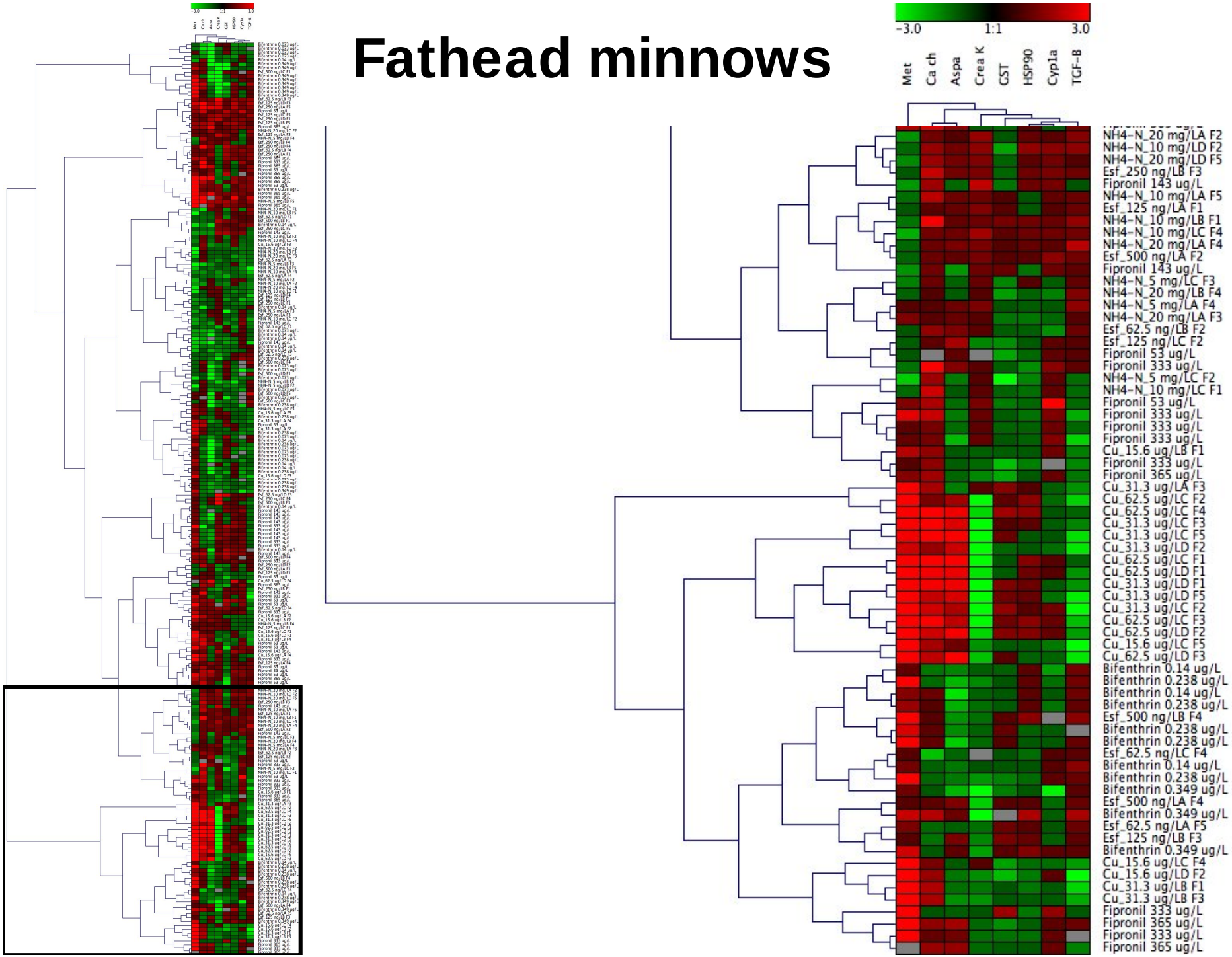
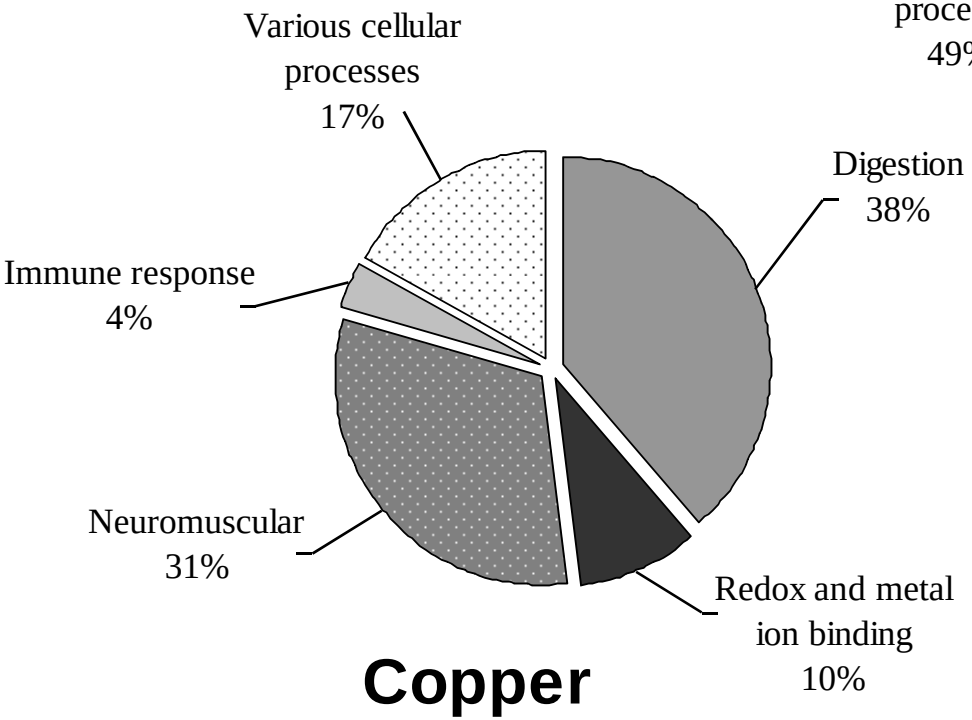


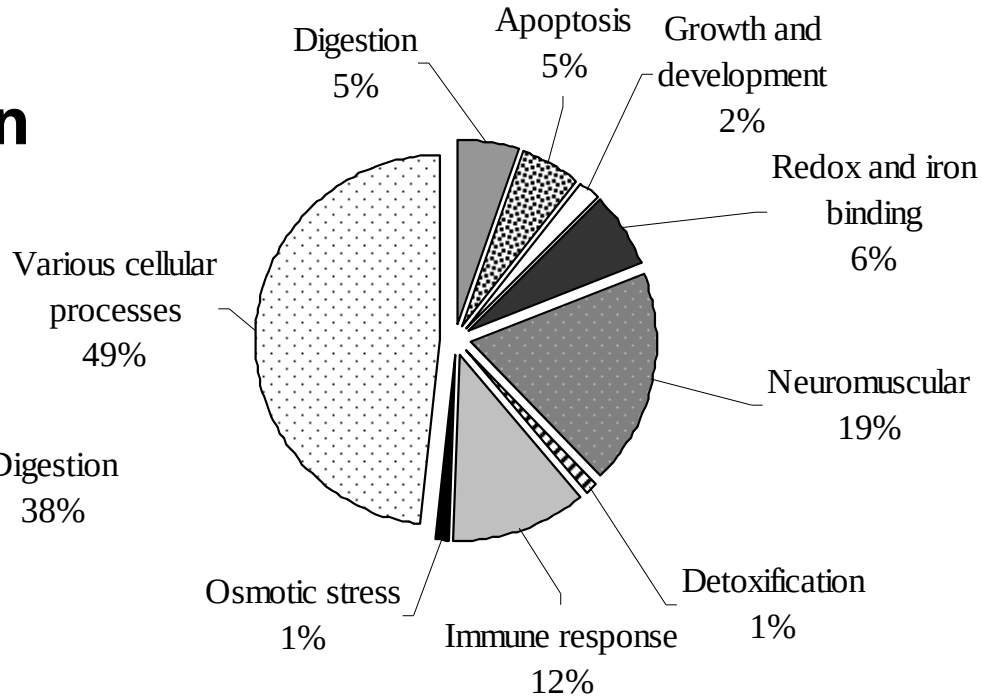


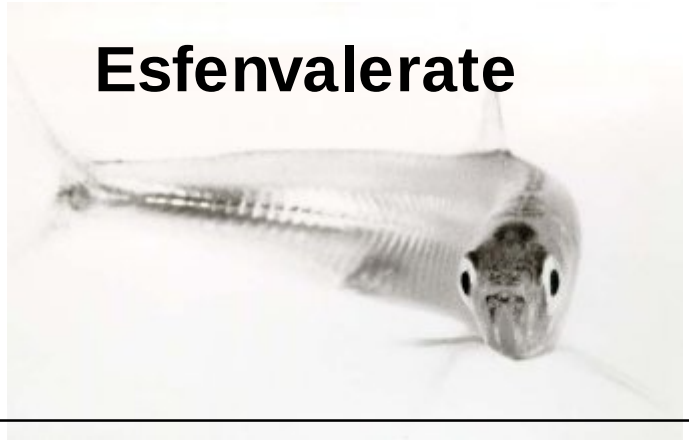
Fathead minnows



Functional classification of genes responding contaminant exposures in juvenile delta smelt



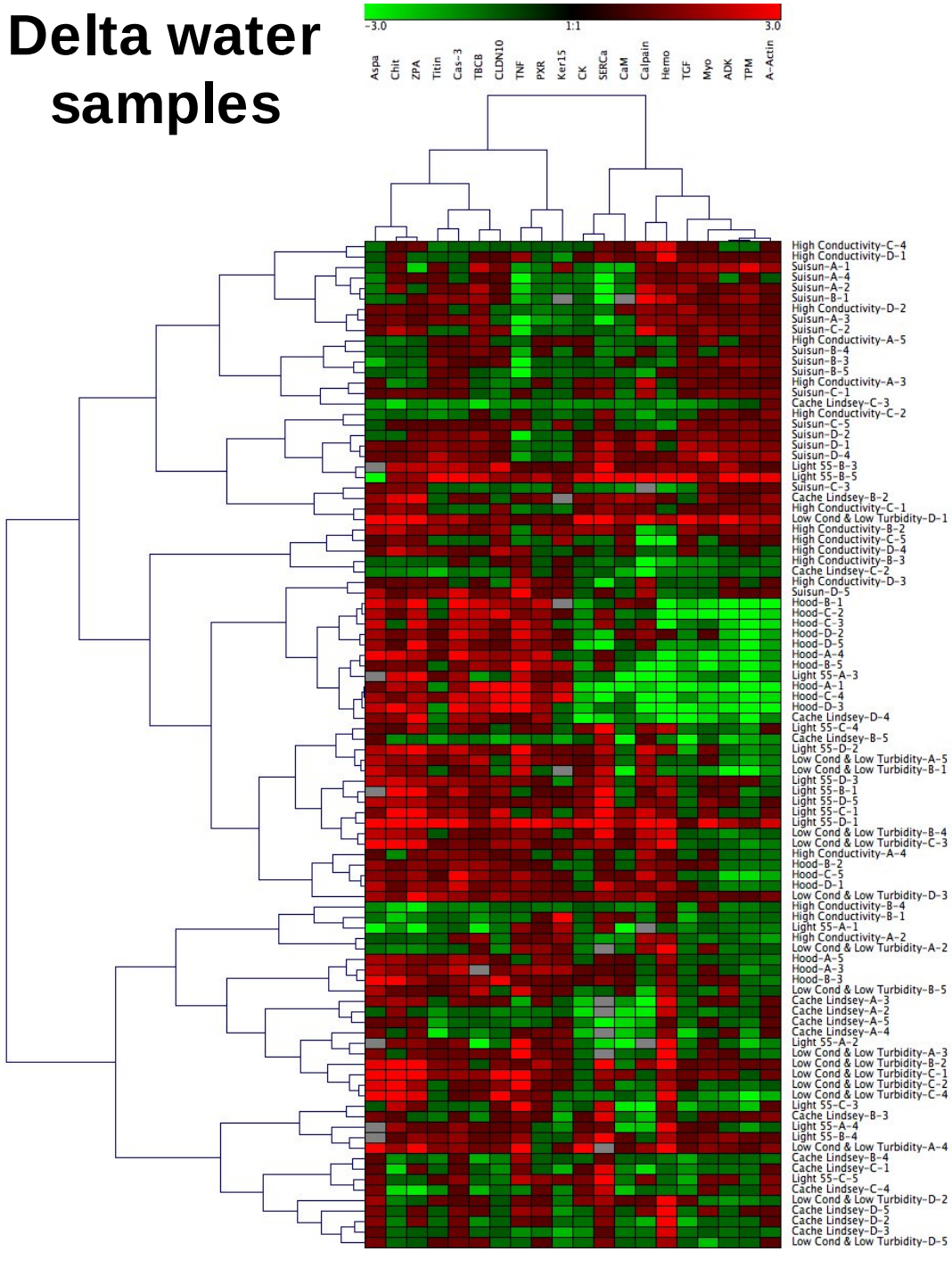




Also available:

Ammonia, Chlorpyrifos, Permethrin, High and Low EC,

Delta water samples



Delta smelt

High Cond.

Suisun

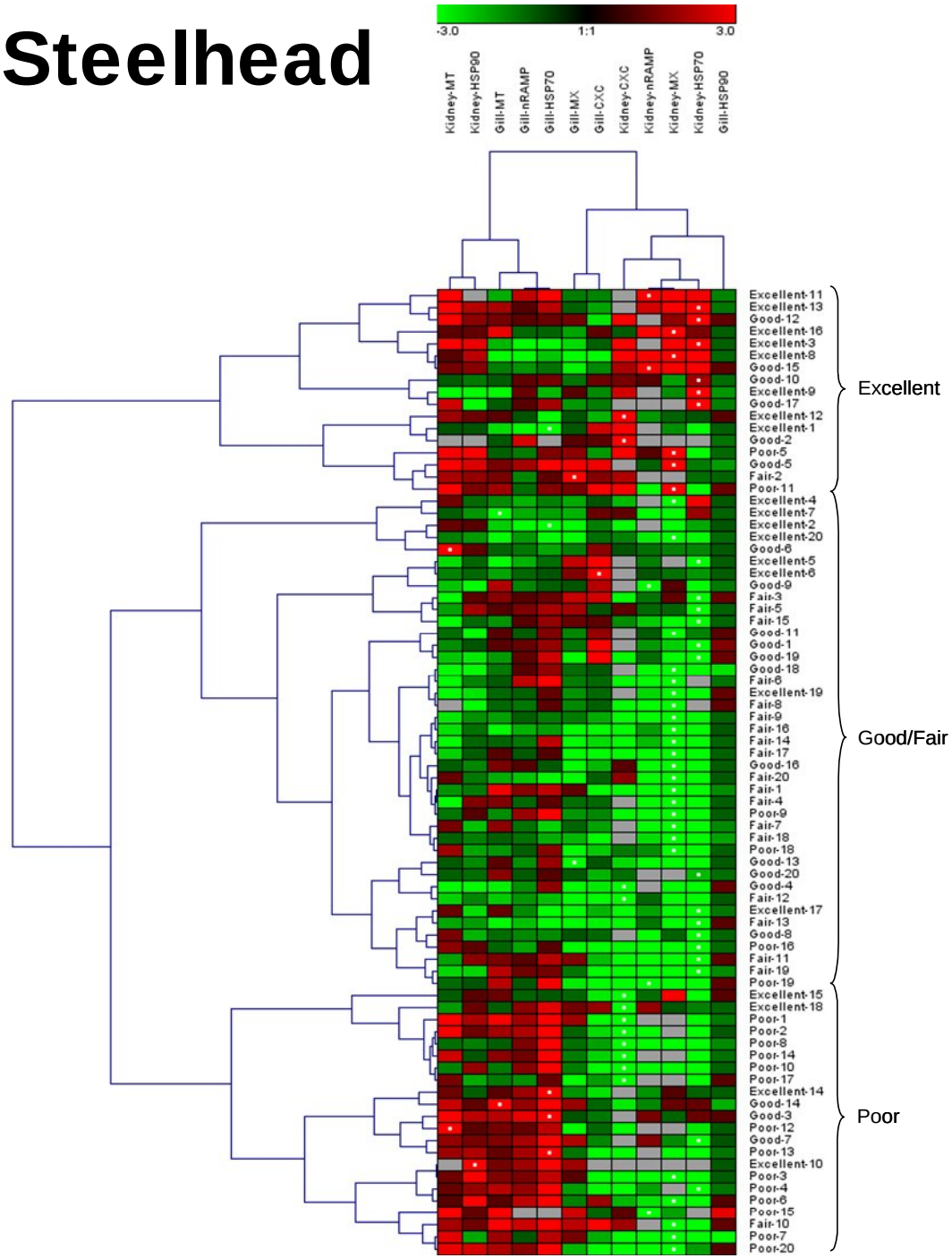
Hood

Light 55

Low Cond.

Cache Lindsay

Steelhead


-3.0
1:1
3.0
Kidney-MT
Kidney-HSP90
Gill-MT
Gill-nRAMP
Gill-HSP70
Gill-MX
Gill-CXC
Kidney-CXC
Kidney-nRAMP
Kidney-MX
Kidney-HSP70
Gill-HSP90
Excellent-11
Excellent-13
Good-12
Excellent-16
Excellent-3
Excellent-8
Good-15
Good-10
Excellent-9
Good-17
Excellent-12
Excellent-1
Good-2
Poor-5
Good-5
Fair-2
Poor-11
Excellent-4
Excellent-7
Excellent-2
Excellent-20
Good-6
Excellent-5
Excellent-6
Good-9
Fair-3
Fair-5
Fair-15
Good-11
Good-1
Good-19
Good-18
Fair-6
Excellent-19
Fair-8
Fair-9
Fair-16
Fair-14
Fair-17
Good-16
Fair-20
Fair-1
Fair-4
Poor-9
Fair-7
Fair-18
Poor-18
Good-13
Good-20
Good-4
Fair-12
Excellent-17
Fair-13
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Fair-11
Fair-19
Poor-19
Excellent-15
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Poor-1
Poor-2
Poor-8
Poor-14
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Poor-17
Excellent-14
Good-14
Good-3
Poor-12
Good-7
Poor-13
Excellent-10
Poor-3
Poor-4
Poor-6
Poor-15
Fair-10
Poor-7
Poor-20
Excellent
Good/Fair
Poor

Summary

- The mode of action of chemicals will elicit specific genomic responses.
- Contaminant specific profiles can be generated using gene expression.
- Gene expression profiling (heatmaps) can be a useful tool to aid TIE approaches.
- Genomic profiling can be applied to field samples, offering valuable information as to possible contaminants through their mode of action.

Future Work

- Generate contaminant-specific genomic profile database, using microarray and qPCR technology
- Assay field based exposures
- Use profiling system to aid TIE investigations based on chemical modes of action
- Conduct species comparison studies.

Thank you!

- To the staff of the UC Davis Aquatic Toxicology Laboratory for conducting exposure experiments and assisting with everything they can.
- To the UC Davis Fish Conservation and Culture Laboratory, Byron, CA, for providing plenty of Delta smelt and advice.
- To the Interagency Ecological Program – Pelagic Organism Decline (IEP-POD) for funding.
- To the Bavarian Research Foundation for a Ph.D. scholarship to S. Beggel.