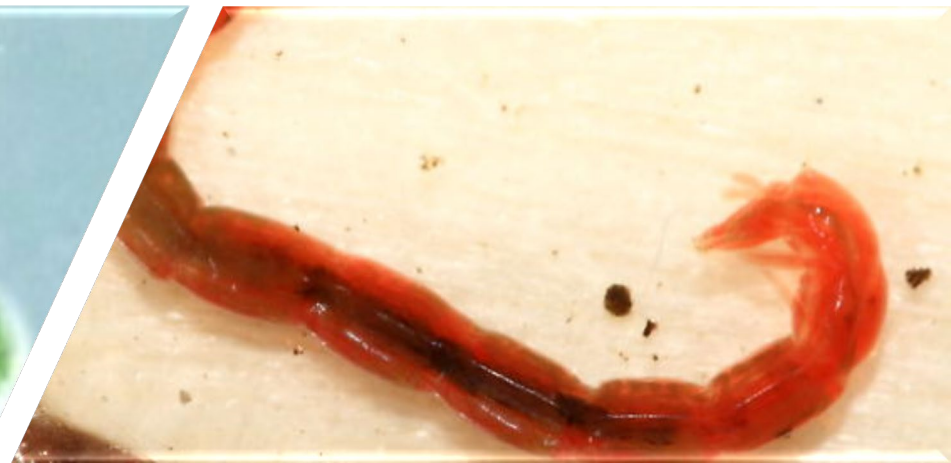
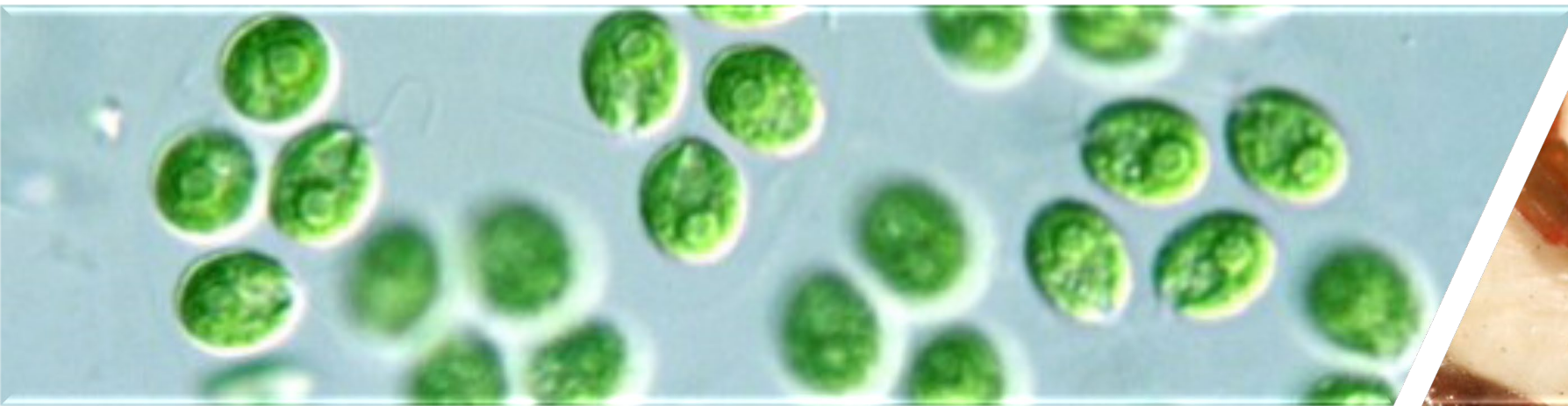


Transcriptomics-based points of departure for ecotoxicology – an update





APCRA

ACCELERATING THE PACE OF
CHEMICAL RISK ASSESSMENT

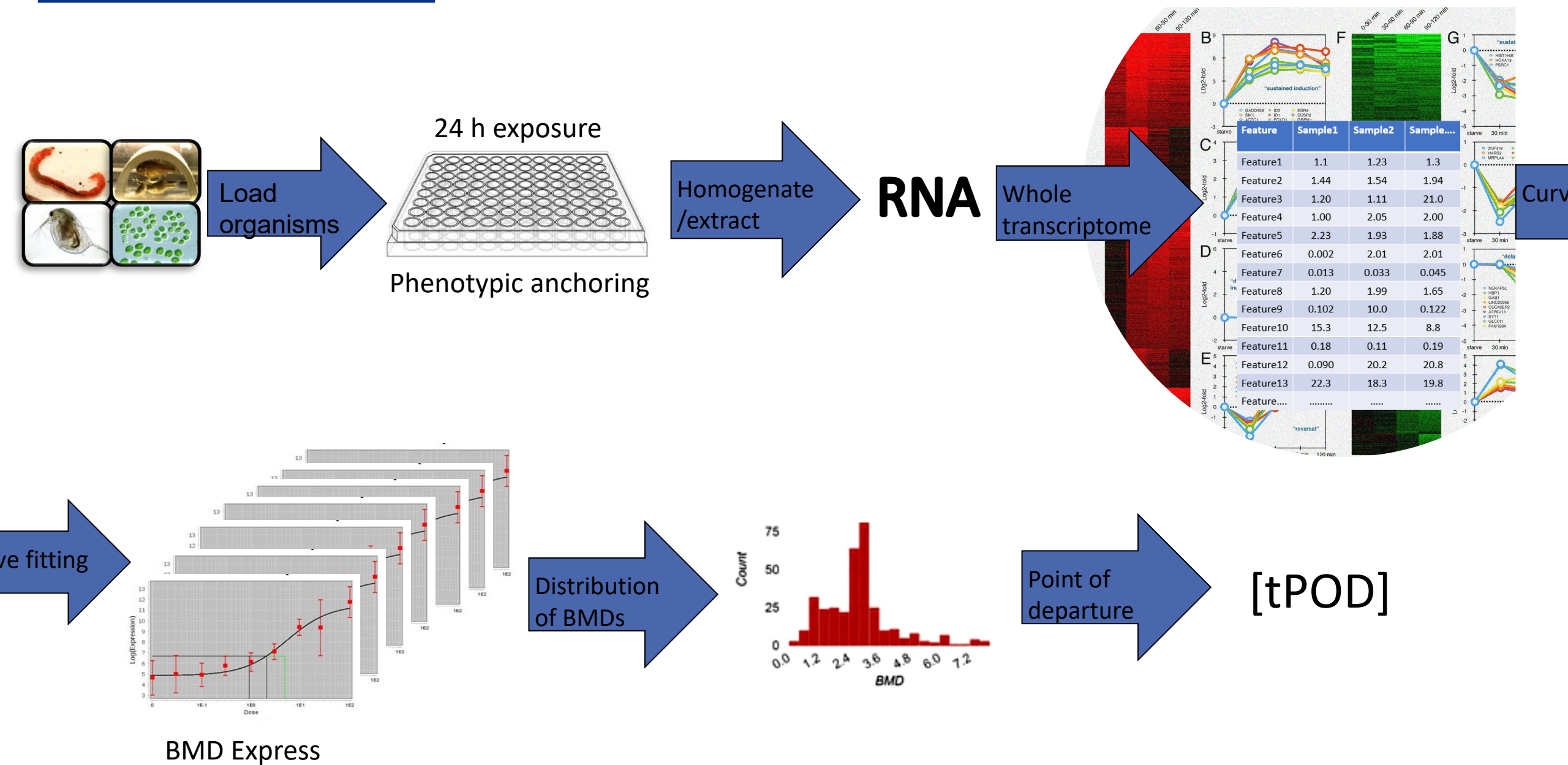
APCRA Case study: Transcriptomics-based PODs for Ecotoxicology

Hypothesis: 24 h whole body transcriptomics can provide a protective, but not overly protective, point of departure for ecological toxicity.

Approach:

1. Generate transcriptomic PODs for ≈ 20 chemicals
 - Initial focus on fathead minnow
2. Compare tPODs with available acute and chronic toxic toxicity data
3. Compare tPODs with in vitro-derived PODs

Method Overview



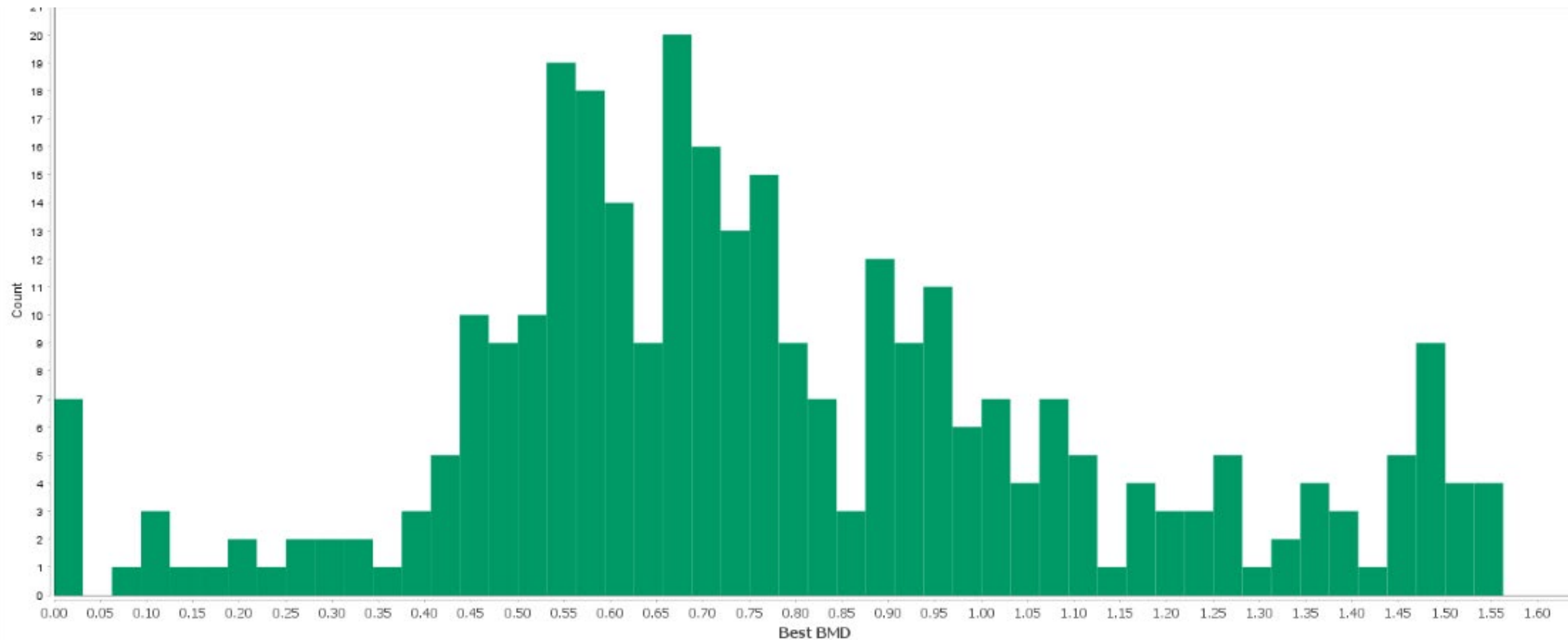
Case study Progress

- Exposures have been completed for 22 chemicals.
 - 7 mode of action groupings
 - 3-4 chemicals per MoA group
- Sequencing complete and tPOD generated for 10 chemicals to date
 - 3 metals
 - 3 SSRIs
 - 4 neonicotinoid / related
- Contracts and funds in place to generate data for next 12.

Pre-covid

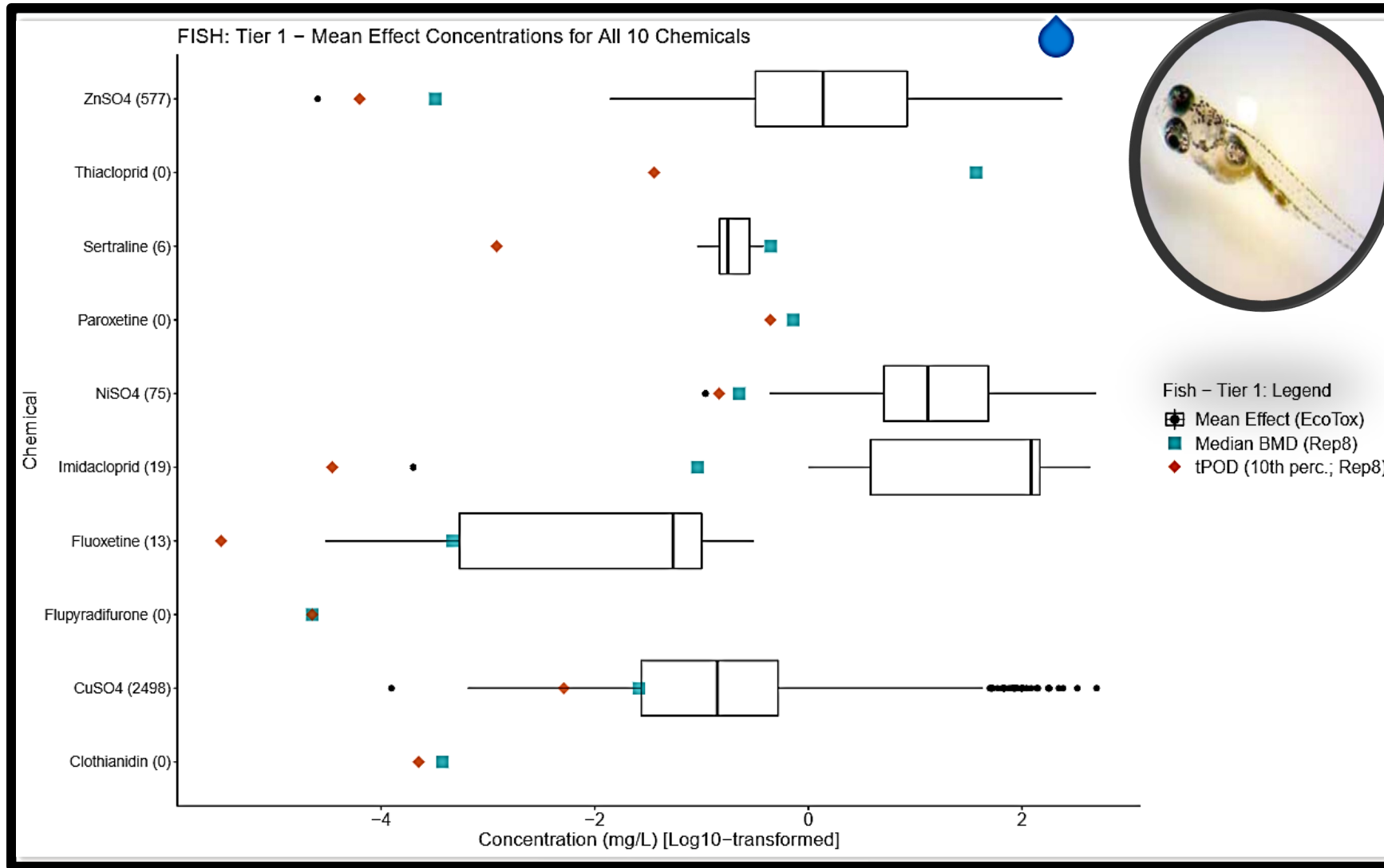
Covid

	Test Chemical	Assay Completed	Library Prep	tPOD	
1	CuSO ₄	X	X	X	Nominal concentrations only
2	ZnSO ₄	X	X	X	
3	NiSO ₄	X	X	X	
4	Clothidin	X	X	X	
5	Flupyradifurone	X	X	X	
6	Imidacloprid	X	X	X	
7	Thiacloprid	X	X	X	
8	Sertraline	X	X	X	Analytical exposure verification
9	Fluoxetine	X	X	X	
10	Paroxetine	X	X	X	
11	Dibutyl phthalate	X			
12	DEHP	X			
13	Benzyl butyl phthalate	X			
14	Parathion	X	X		
15	Fenthion	X	X		
16	Methidathion	X	X		
17	Bisphenol A	X	X		
18	4-nonyl phenol	X			
19	Estrone	X	X		
20	Methoxyfenozide	X	X		
21	Tebufofenozide	X			
22	Halofenozide	X			



Preliminary Results:
First 10 chemicals

Comparison with In vivo, **Adverse Effect** Concentrations (Fish)

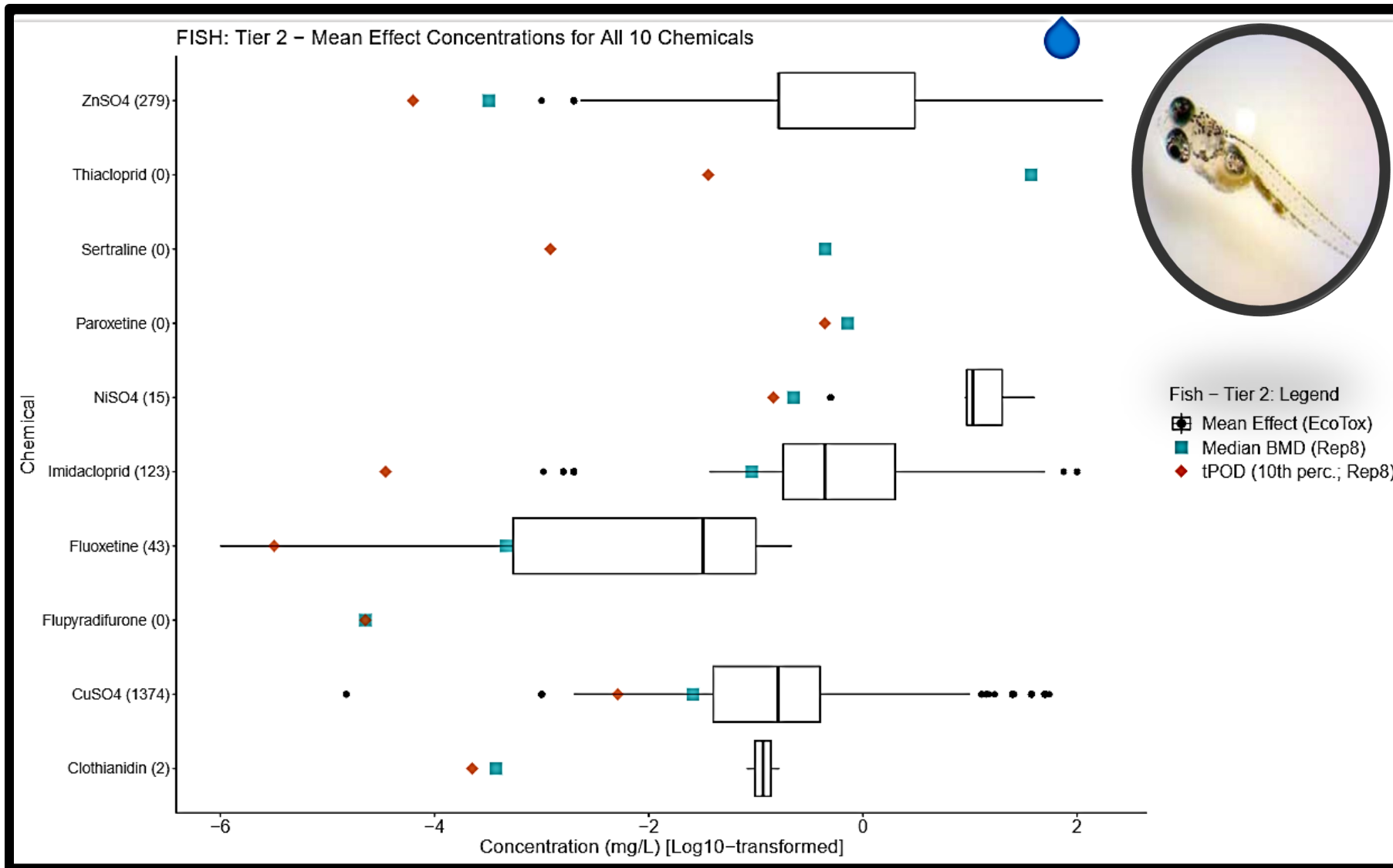


tPODs (10th centile BMD) were generally more sensitive than apical adverse effect concentrations.

tPOD based on median BMD were less protective

Up to 4 orders of magnitude more protective

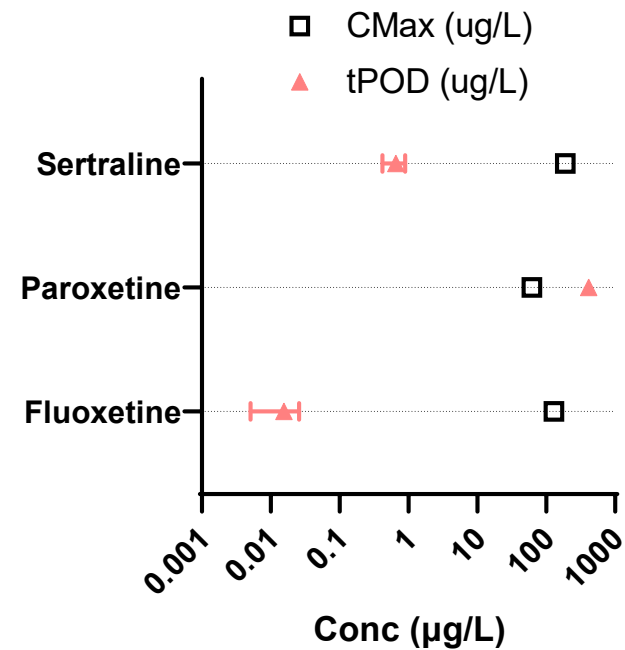
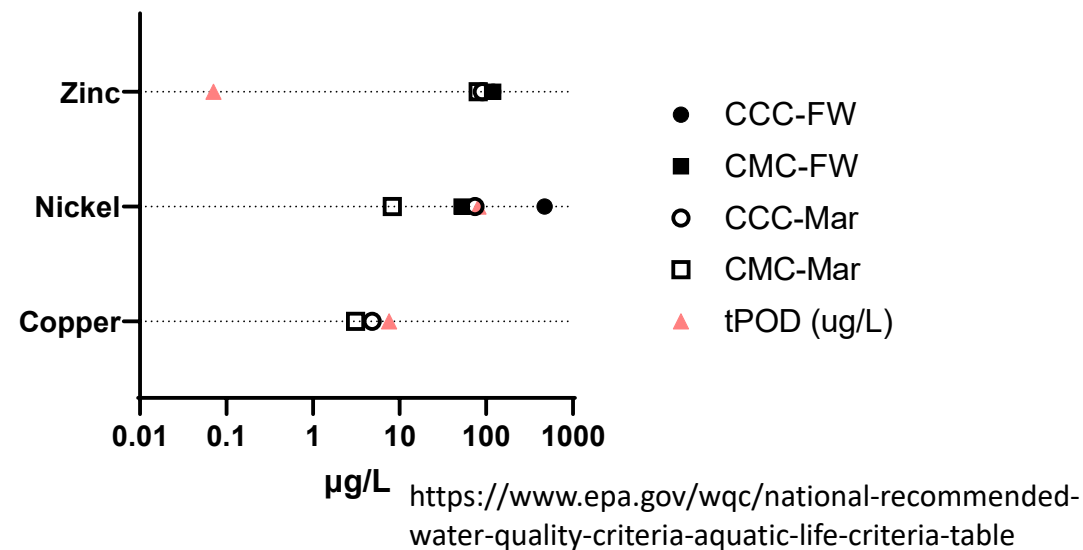
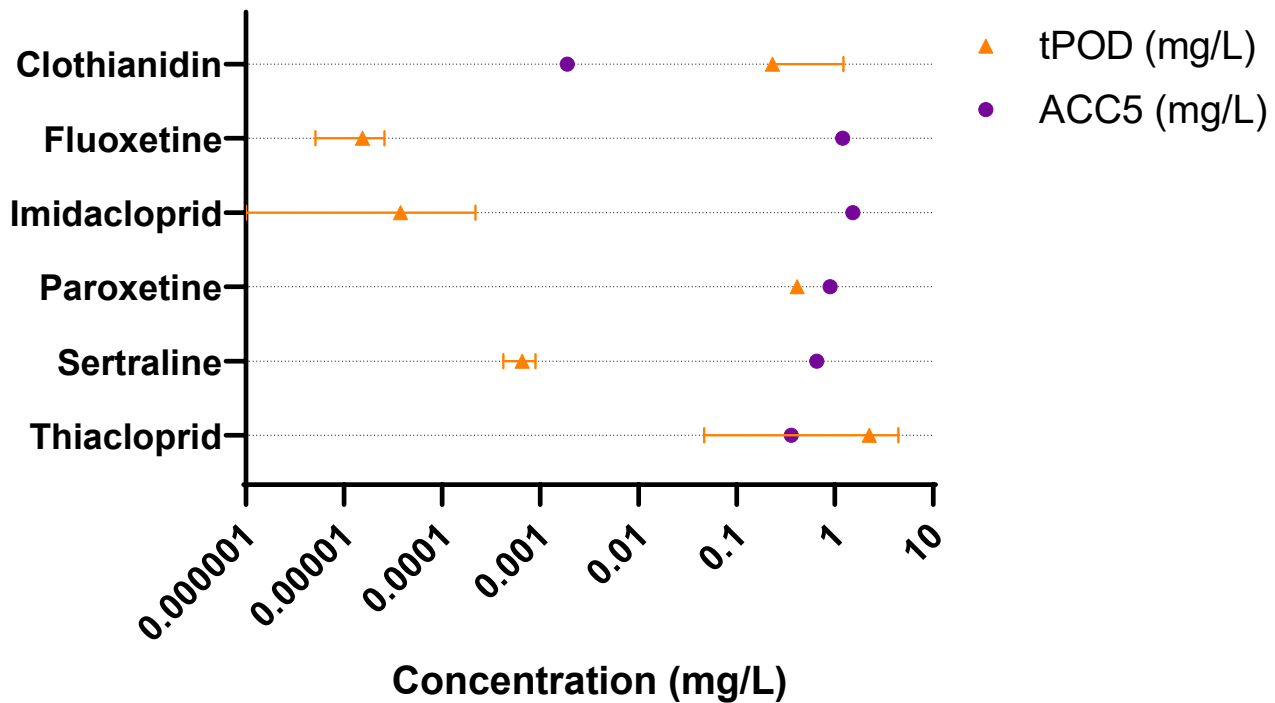
Comparison with In vivo, **Biological Effect** Concentrations (Fish)



tPODs still generally more sensitive in vivo biological effect concentrations.

Up to 2 order of magnitude lower to overlapping lower quartile

ToxCast-ACC5 vs tPOD



Optimization and Assay Acceptance



Concentration range based on in vivo LC50 as upper bound

Concentration range based on in vivo LC50 as upper bound

8 biological replicates (1 fish/well)

- 96 samples
Whole genome RNAseq
Approx. \$8500 per chemical

Phenotypic observations: Survival, swimming behavior, deformities/abnormalities

Optimization



How much can we reduce gene set size, but still determine tPOD?



How much can we reduce samples size per treatment, maintain power?



Can we estimate biological uncertainty in tPOD estimate?



Performance criteria for an acceptable assay?

In silico Subsampling

Transcript ID

Sample ID

Dose

	A	B	C	D	E	F	G	H	I
1		Cu_P1_A1	Cu_P1_A10	Cu_P1_A2	Cu_P1_A3	Cu_P1_A4	Cu_P1_A5	Cu_P1_A6	Cu_P1_A7
2	Dose	0	0.2	0.00002	0.00006	0.0002	0.0006	0.002	0.006
3	FMt000003	6.396698281	7.165080955	6.139417185	5.625463693	5.936491943	5.984797836	6.526667329	6.526667329
4	FMt000004	2.727597133	2.819530386	2.476866196	2.260722943	2.072535549	2.408035192	2.829599109	2.829599109
5	FMt000005	2.666574282	2.757823089	2.957500498	3.294229757	3.698358555	3.209724111	2.681578019	2.681578019
6	FMt000006	4.675333003	4.768559009	4.858302489	5.139450164	4.551132645	4.819989912	4.829061001	4.829061001
7	FMt000008	5.816765605	5.550398239	5.373006159	5.467031575	5.756057101	5.692205772	5.572099115	5.572099115
8	FMt000009	1.921778265	1.337509659	1.842399017	1.364723466	1.820179855	2.227968209	1.720804988	1.720804988
9	FMt000010	0.400578876	1.02468777	0.580341068	1.428654949	1.048759955	1.133331622	0.796197253	0.796197253
10	FMt000011	1.036715489	1.337509659	1.179840942	1.762168511	2.033423943	1.907113212	1.682372652	1.682372652
11	FMt000013	4.339705191	4.231422779	4.457041355	4.158758634	4.390170142	4.287434091	4.354221981	4.354221981
12	FMt000014	0.753428738	1.497088068	1.179840942	1.227677204	0.694880669	1.737858491	1.117537912	1.117537912
13	FMt000016	4.685621982	4.677065189	4.791080697	4.988545119	4.631905782	4.902412506	5.063939077	5.063939077
14	FMt000017	1.15990699	1.392687117	1.548825352	2.575114318	1.623516583	2.058579857	2.227306515	2.227306515
15	FMt000019	2.982521854	1.092914161	1.969452091	3.276966231	2.985273802	2.37954184	2.472248844	2.472248844
16	FMt000020	4.326615646	3.729709358	4.659064377	3.978274305	3.280771887	3.922966112	3.700540563	3.700540563
17	FMt000022	0.753428738	0.427434191	0.350624657	0.608894253	0.224966545	0.332838013	0.997448031	0.997448031
18	FMt000026	2.536192677	2.859249401	3.166436765	3.031435449	2.856737829	2.90442897	2.963836436	2.963836436
19	FMt000031	1.886534004	2.036875017	2.086216064	2.709867426	2.474112535	2.463387273	2.898278494	2.898278494
20	FMt000032	4.210281411	3.872414951	4.088442997	3.934904526	3.907492756	4.116679066	3.631612409	3.631612409
21	FMt000034	3.641040659	3.975408278	3.930816133	3.425369888	3.928963604	4.116679066	4.285372312	4.285372312
22	FMt000035	3.20831699	4.413005717	4.267645049	4.435879765	4.332726221	4.354221981	4.354221981	4.354221981
23	FMt000036	0.025579454	3.364405188	3.409614619	2.5591869	2.982290068	3.505201762	3.505201762	3.505201762
24	FMt000037	0.220389325	0.470050181	0.081807702	0.59096166	0.072994421	0.796197253	0.796197253	0.796197253

BMD
Express2.2

10th percentile(BMD) = tPOD

In silico Subsampling



How much can we reduce gene set size, but still determine tPOD?

LEGEND	
-----	Transition to next replicate set
<div style="border: 1px solid red; width: 20px; height: 10px; display: inline-block;"></div>	Sampled data

Fluoxetine	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	B01	B02	B03	B04	B06	B07	B08	B09	B10	B11
Dose	0	1.5E-05	0.00005	0.00015	0.0005	0.0015	0.005	0.015	0.05	0.15	0.5	0	1.5E-05	0.00005	0.00015	0.0015	0.005	0.015	0.05	0.15	0.5
FMT000003	5.69	5.66	5.67	5.98	5.63	5.88	5.46	5.56	5.43	5.69	5.49	6.01	6.01	5.69	5.48	5.53	5.54	5.15	5.61	5.48	5.45
FMT000004	1.85	1.93	1.97	2.01	2.10	1.33	2.12	1.83	1.47	1.71	2.03	2.23	2.13	1.58	1.37	2.15	1.81	2.09	1.51	1.05	1.50
FMT000005	2.78	2.22	2.22	2.36	2.91	3.21	1.92	2.48	2.28	3.24	2.83	3.20	2.30	2.62	1.93	2.62	2.34	3.16	2.90	2.16	2.79
FMT000006	4.63	4.45	4.49	4.45	4.16	4.39	4.88	4.21	4.25	4.35	4.52	3.90	4.06	4.20	4.53	4.09	4.24	4.10	4.12	4.01	4.38
FMT000008	5.21	5.40	5.41	5.15	5.49	5.48	5.37	5.43	5.49	5.37	5.28	5.41	5.38	5.40	5.43	5.40	5.44	5.62	5.61	5.38	5.27
FMT000009	1.72	1.49	1.63	1.66	1.96	1.54	1.30	1.69	1.21	1.32	1.07	1.91	1.44	1.67	1.87	1.75	2.10	1.72	1.58	1.35	1.36
FMT000010	1.14	1.23	1.05	1.30	1.89	1.72	2.30	1.95	1.73	1.66	1.36	1.63	1.35	1.44	1.33	1.47	1.39	1.18	1.86	1.64	1.33
FMT000011	1.75	1.67	1.54	1.30	1.89	1.72	2.30	1.95	1.73	1.66	1.36	2.11	2.26	1.94	2.02	1.78	1.91	2.12	1.58	1.78	1.46
FMT000013	4.32	4.63	4.69	5.39	4.74	4.83	5.06	4.80	4.89	4.69	4.46	4.90	4.77	4.97	4.71	5.05	4.99	4.74	4.84	5.01	4.61
FMT000014	0.97	1.04	1.49	1.65	1.02	1.33	1.18	1.07	1.16	1.37	1.51	1.40	0.74	0.84	1.37	0.70	1.29	1.33	0.98	1.00	1.29
FMT000016	5.14	5.38	5.13	5.42	4.99	4.82	5.09	4.63	4.90	5.03	4.94	4.96	5.02	4.98	5.04	4.96	4.86	4.80	5.13	5.11	5.27
FMT000017	2.51	2.57	2.56	2.61	2.65	2.16	2.40	1.73	2.08	2.26	2.31	2.44	2.10	2.49	2.31	1.98	2.18	2.09	2.44	2.39	2.61
FMT000019	1.60	1.28	1.87	2.01	2.26	1.59	3.13	1.73	3.39	1.14	2.03	0.30	0.74	1.67	2.53	2.74	2.69	2.54	2.98	1.48	1.70
FMT000020	3.29	3.58	3.42	3.64	3.32	3.79	3.86	3.30	3.67	3.50	3.76	3.48	3.82	3.68	3.65	3.81	3.43	3.26	3.85	3.34	3.21

Original expression matrix

Full dataset:

- 31,158 transcripts
- 12 doses, 8 reps per dose
- 96 samples total

Transcript(m), m=100 - 30,000 at random intervals

"Transcript(100) example"

Fluoxetine	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	B01	B02	B03	B04
Dose	0	1.5E-05	0.00005	0.00015	0.0005	0.0015	0.005	0.015	0.05	0.15	0.5	0	1.5E-05	0.00005	0.00015
FMT000003	5.69	5.66	5.67	5.98	5.63	5.88	5.46	5.56	5.43	5.69	5.49	6.01	6.01	5.69	5.48
FMT000004	1.85	1.93	1.97	2.01	2.10	1.33	2.12	1.83	1.47	1.71	2.03	2.23	2.13	1.58	1.37
FMT000005	2.78	2.22	2.22	2.36	2.91	3.21	1.92	2.48	2.28	3.24	2.83	3.20	2.30	2.62	1.93
FMT000006	4.63	4.45	4.49	4.45	4.16	4.39	4.88	4.21	4.25	4.35	4.52	3.90	4.06	4.20	4.53
FMT000008	5.21	5.40	5.41	5.15	5.49	5.48	5.37	5.43	5.49	5.37	5.28	5.41	5.38	5.40	5.43
FMT000009	1.72	1.49	1.63	1.65	1.96	1.54	1.30	1.69	1.21	1.32	1.07	1.91	1.44	1.67	1.87
FMT000010	1.14	1.23	1.05	0.53	1.59	1.39	0.51	1.22	1.42	1.57	1.41	1.63	1.35	1.44	1.33
FMT000011	1.75	1.67	1.54	1.50	1.89	1.72	2.30	1.95	1.73	1.66	1.56	2.11	2.26	1.94	2.02
FMT000013	4.32	4.63	4.69	5.39	4.74	4.83	5.06	4.80	4.89	4.69	4.46	4.90	4.77	4.97	4.71
FMT000014	0.97	1.04	1.49	1.65	1.02	1.33	1.18	1.07	1.16	1.37	1.51	1.40	0.74	0.84	1.37
FMT000016	5.14	5.38	5.13	5.42	4.99	4.82	5.09	4.63	4.90	5.03	4.94	4.96	5.02	4.98	5.04
FMT000017	2.51	2.57	2.56	2.61	2.65	2.16	2.40	1.73	2.08	2.26	2.31	2.44	2.10	2.49	2.31
FMT000019	1.60	1.28	1.87	2.01	2.26	1.59	3.13	1.73	3.39	1.14	2.03	0.30	0.74	1.67	2.53
FMT000020	3.29	3.58	3.42	3.64	3.32	3.79	3.86	3.30	3.67	3.50	3.76	3.48	3.82	3.68	3.65

Transcript 100 dataset:

- 100 transcripts
- 12 doses, 8 reps per dose
- 96 samples total

Variable Transcript Set Sizes: tPOD

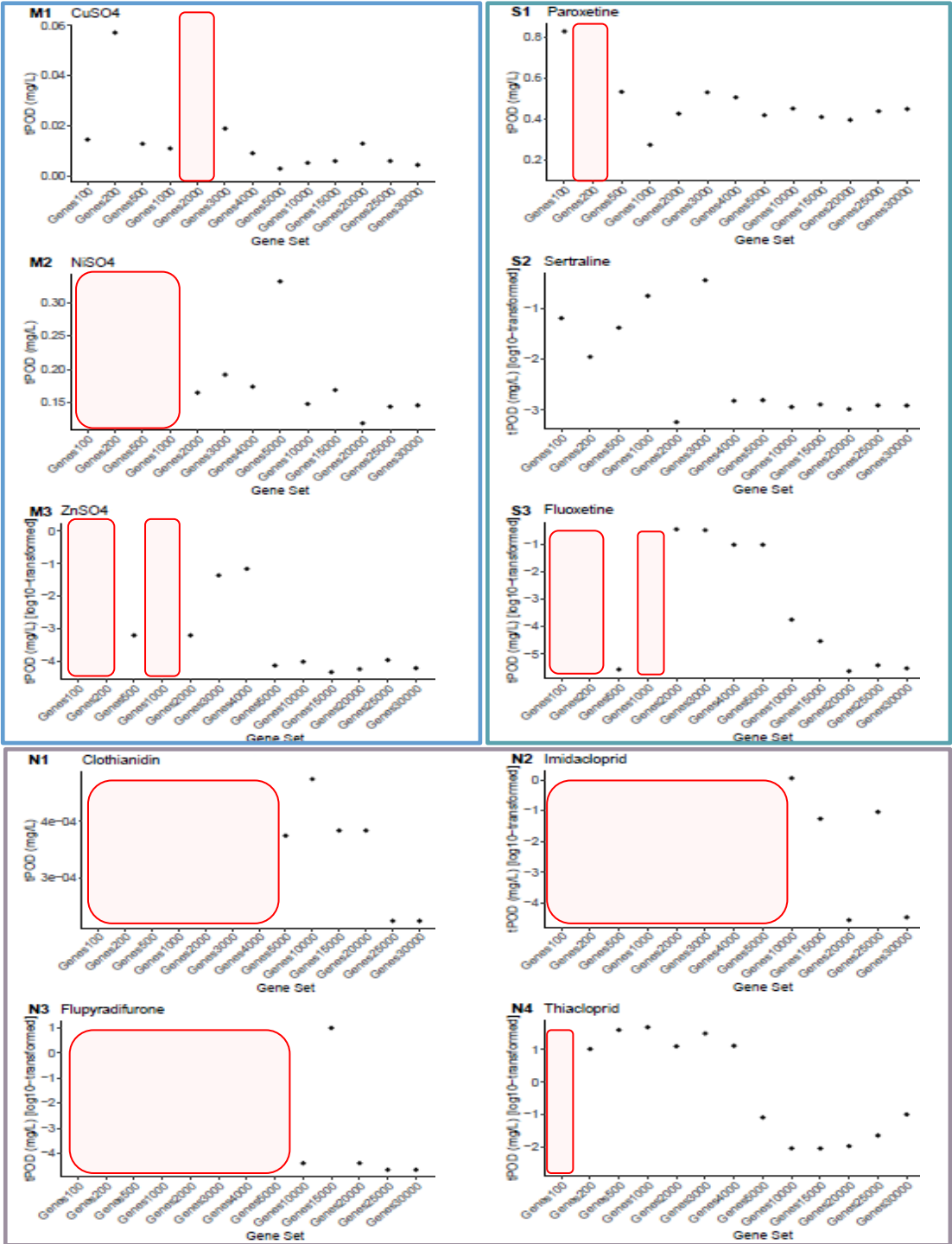
Metals

Pharms

Neonics

No tPOD could be estimated

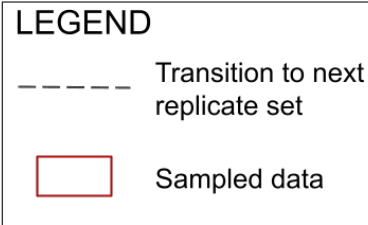
- tPOD could always be estimated when $\geq 10,000$ transcripts were analyzed
- $\geq 1,000$ was sufficient for 6/10 chemicals



Methods – *In silico* Subsampling

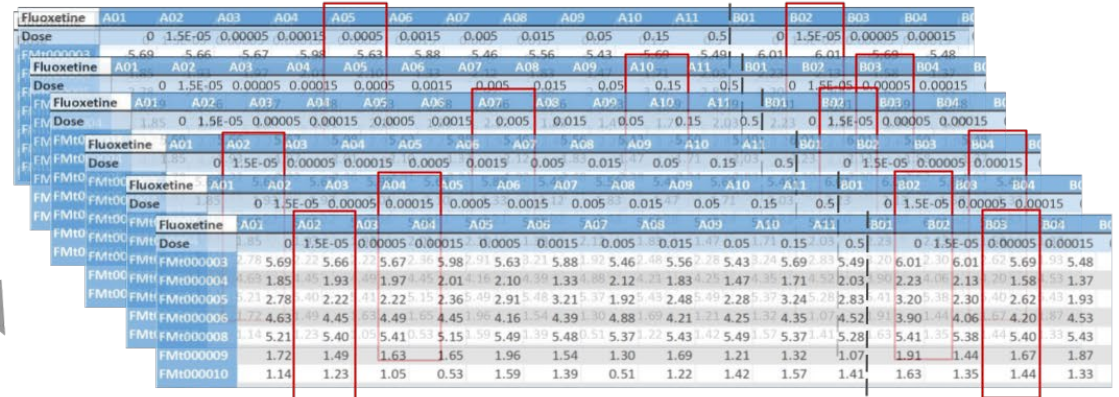
Replicate 3, 12x dataset:

- 31,158 transcripts
- 12 doses, **3 reps per dose**
- 96 samples total
- **12 iterations of each dataset**



Replicate(n,12x), n=3 - 7

"Replicate(3,12x) example"



Iterations 6 - 12

Iteration 5

Iteration 4

Iteration 3

Iteration 2

Iteration 1

Fluoxetine	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	B01	B02	B03	B04	B06	B07	B08	B09	B10	B11	
Dose	0	1.5E-05	0.00005	0.00015	0.0005	0.0015	0.005	0.015	0.05	0.15	0.5	0	1.5E-05	0.00005	0.00015	0.0005	0.0015	0.005	0.015	0.05	0.15	0.5
FMT000003	5.69	5.66	5.67	5.98	5.63	5.88	5.46	5.56	5.43	5.69	5.49	6.01	6.01	5.69	5.48	5.53	5.54	5.15	5.61	5.48	5.45	
FMT000004	1.85	1.93	1.97	2.01	2.10	1.33	2.12	1.83	1.47	1.71	2.03	2.23	2.13	1.58	1.37	2.15	1.81	2.09	1.51	1.05	1.50	
FMT000005	2.78	2.22	2.22	2.36	2.91	3.21	1.92	2.48	2.28	3.24	2.83	3.20	2.30	2.62	1.93	2.62	2.34	3.16	2.90	2.16	2.79	
FMT000006	4.63	4.45	4.49	4.45	4.16	4.39	4.88	4.21	4.25	4.35	4.52	3.90	4.06	4.20	4.53	4.09	4.24	4.10	4.12	4.01	4.38	
FMT000008	5.21	5.40	5.41	5.15	5.49	5.48	5.37	5.43	5.49	5.37	5.28	5.41	5.38	5.40	5.43	5.40	5.44	5.62	5.61	5.38	5.27	
FMT000009	1.72	1.49	1.63	1.66	1.96	1.54	1.30	1.69	1.21	1.32	1.07	1.91	1.44	1.67	1.87	1.75	2.10	1.72	1.58	1.35	1.36	
FMT000010	1.14	1.23	1.05	Original expression matrix								1.44	1.63	1.35	1.44	1.33	1.47	1.39	1.18	1.86	1.64	1.33
FMT000011	1.75	1.67	1.54	1.30	1.89	1.72	2.30	1.95	1.73	1.66	1.36	2.11	2.26	1.94	2.02	1.78	1.91	2.12	1.58	1.78	1.46	
FMT000013	4.32	4.63	4.69	5.39	4.74	4.83	5.06	4.80	4.89	4.69	4.46	4.90	4.77	4.97	4.71	5.05	4.99	4.74	4.84	5.01	4.61	
FMT000014	0.97	1.04	1.49	1.65	1.02	1.33	1.18	1.07	1.16	1.37	1.51	1.40	0.74	0.84	1.37	0.70	1.29	1.33	0.98	1.00	1.29	
FMT000016	5.14	5.38	5.13	5.42	4.99	4.82	5.09	4.63	4.90	5.03	4.94	4.96	5.02	4.98	5.04	4.96	4.86	4.80	5.13	5.11	5.27	
FMT000017	2.51	2.57	2.56	2.61	2.65	2.16	2.40	1.73	2.08	2.26	2.31	2.44	2.10	2.49	2.31	1.98	2.18	2.09	2.44	2.39	2.61	
FMT000019	1.60	1.28	1.87	2.01	2.26	1.59	3.13	1.73	3.39	1.14	2.03	0.30	0.74	1.67	2.53	2.74	2.69	2.54	2.98	1.48	1.70	
FMT000020	3.29	3.58	3.42	3.64	3.32	3.79	3.86	3.30	3.67	3.50	3.76	3.48	3.82	3.68	3.65	3.81	3.43	3.26	3.85	3.34	3.21	

Original expression matrix

Full dataset:

- 31,158 transcripts
- 12 doses, 8 reps per dose
- 96 samples total



How much can we reduce samples size per treatment, maintain power?



Can we estimate biological uncertainty in tPOD estimate?

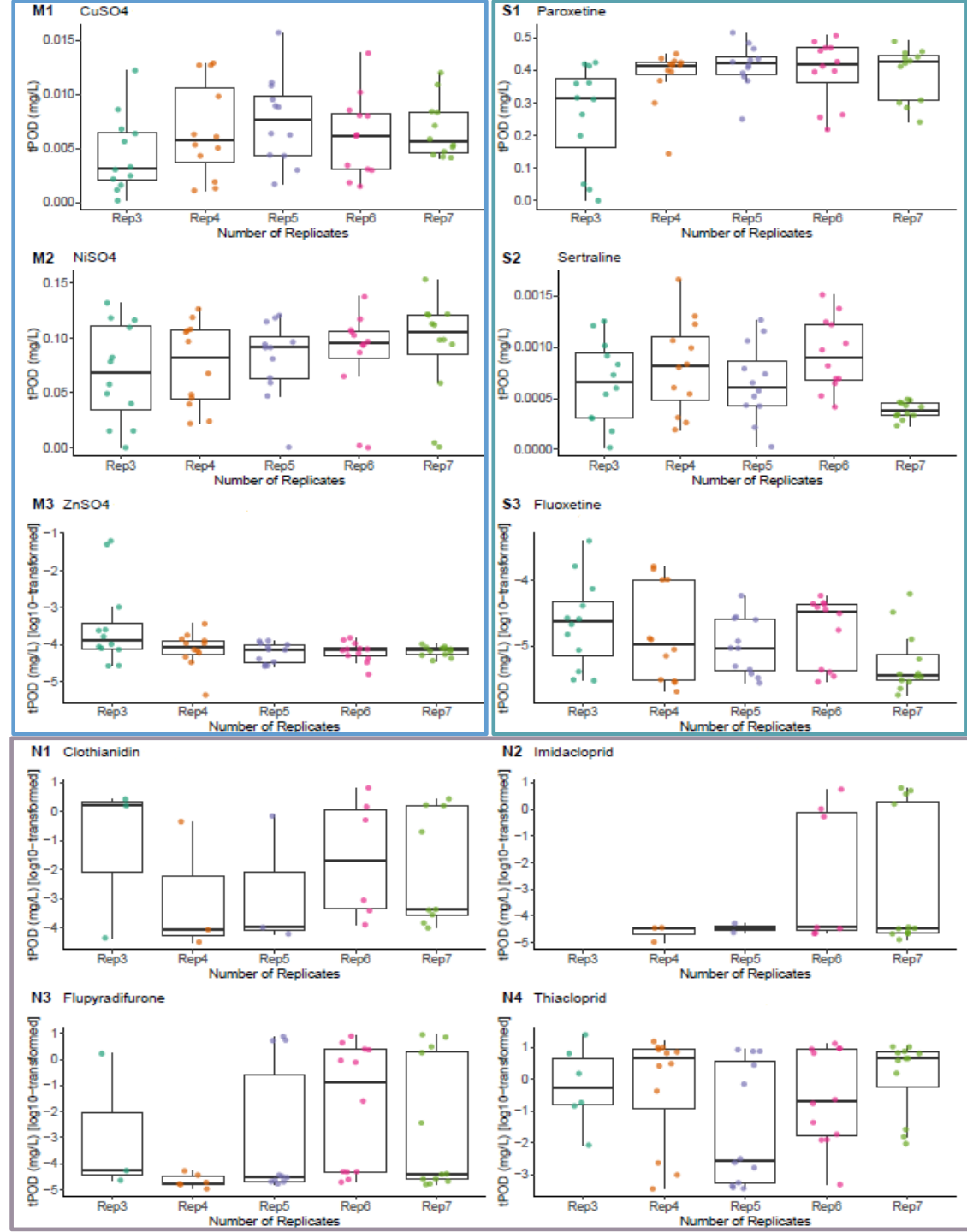
Variable Replicate (12x) Sizes: tPOD

Metals

Pharms

Neonics

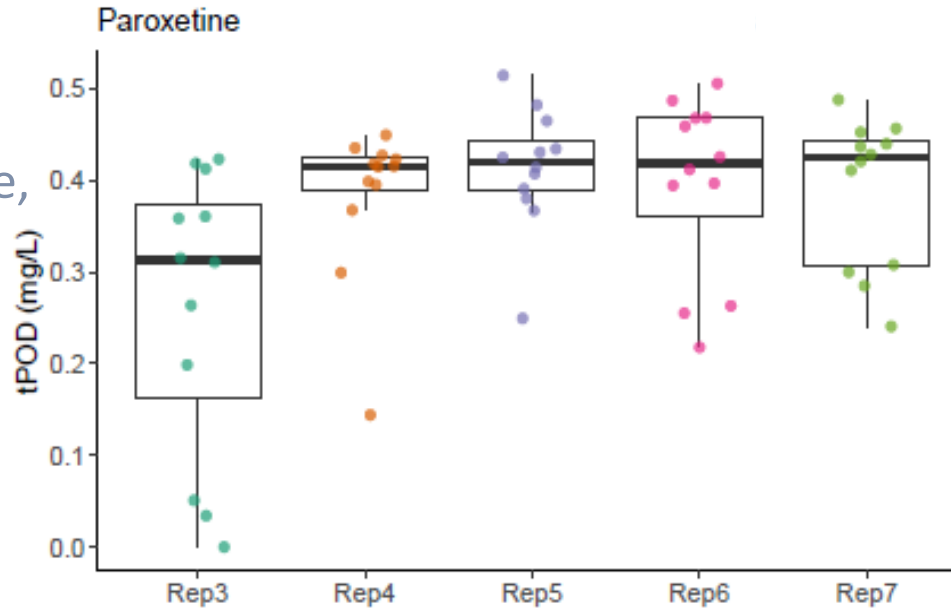
- In silico sub-sampling approach provided a means to estimate the biological variability/uncertainty in the tPOD determination.
- tPODs based on n=4 individuals were, on average, no more variable than those based on >4.
- Uncertainty around tPOD ranged from just 2-3 fold (paroxetine) to up to 6 orders of magnitude (flupyradifone)



tPOD Variability

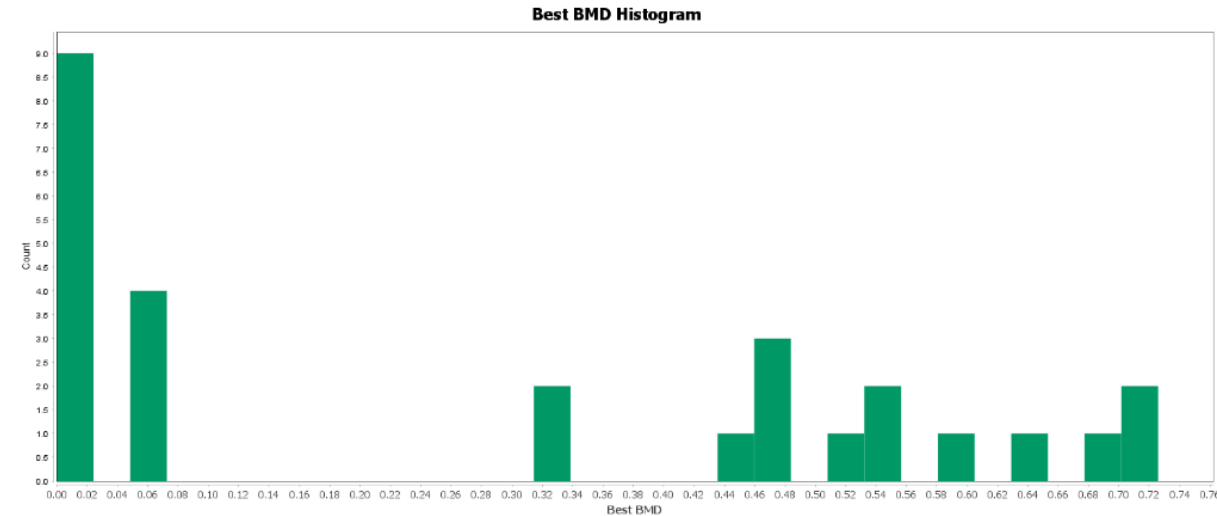
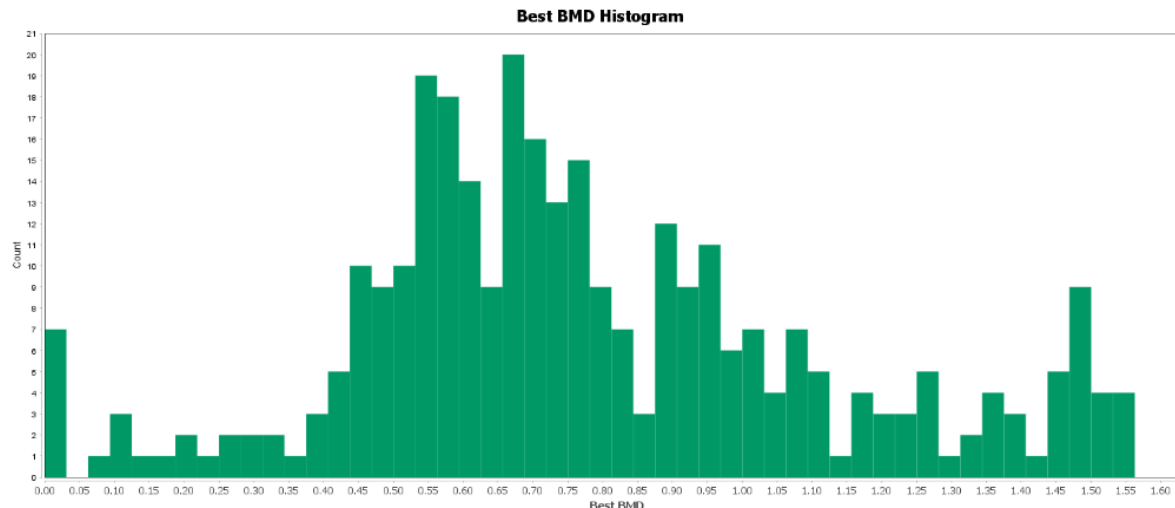
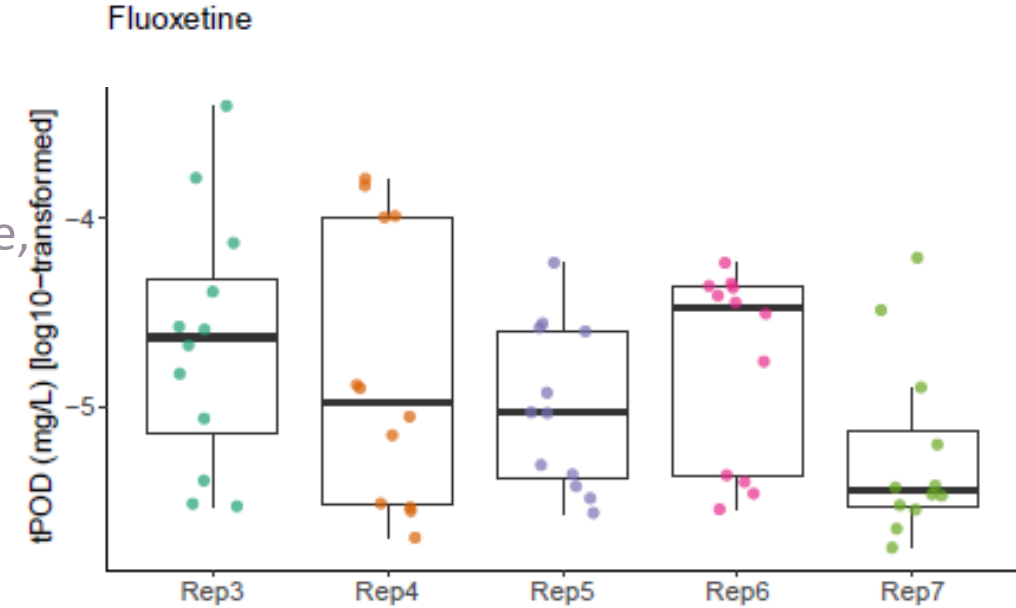
Paroxetine (500-600 DEGs)

Linear scale,
2-3 fold
variability



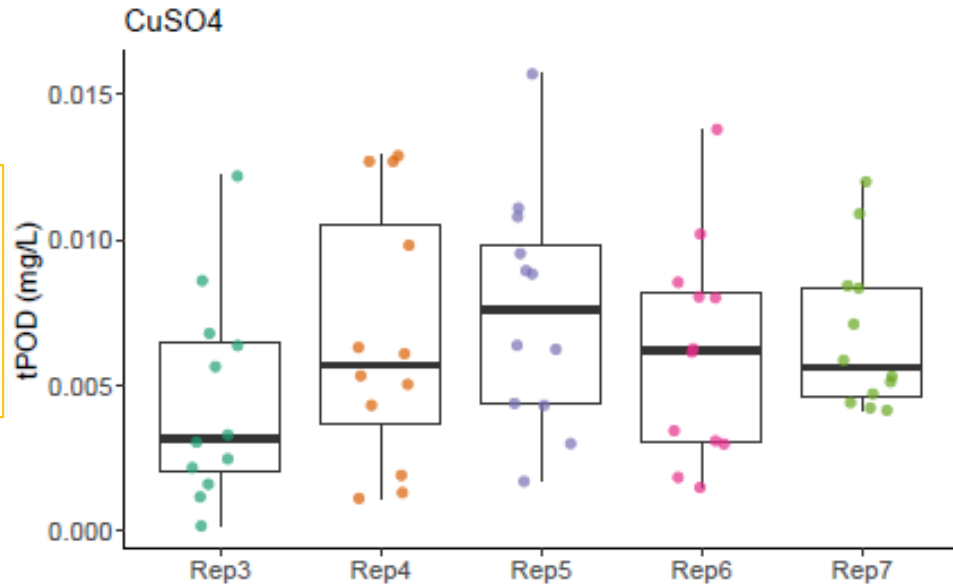
Fluoxetine (25-60 DEGs)

Log 10 scale,
1-1.5 log
variability



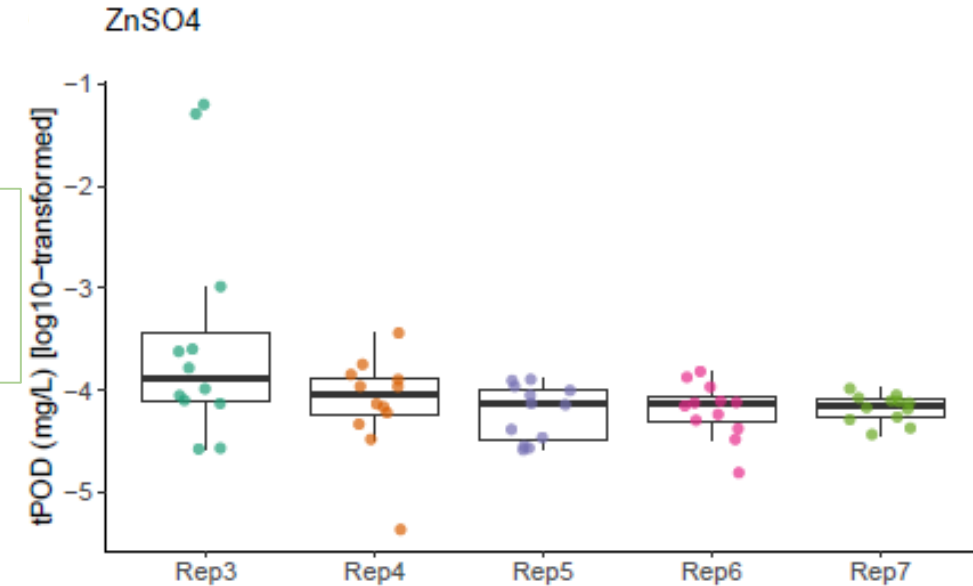
tPOD Variability

Copper sulfate (100-150 DEGs)

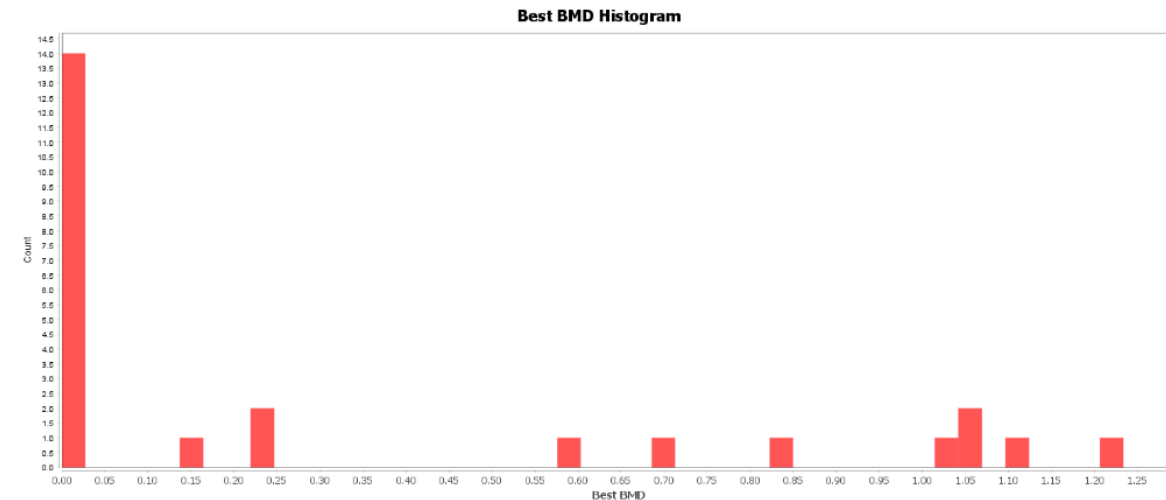
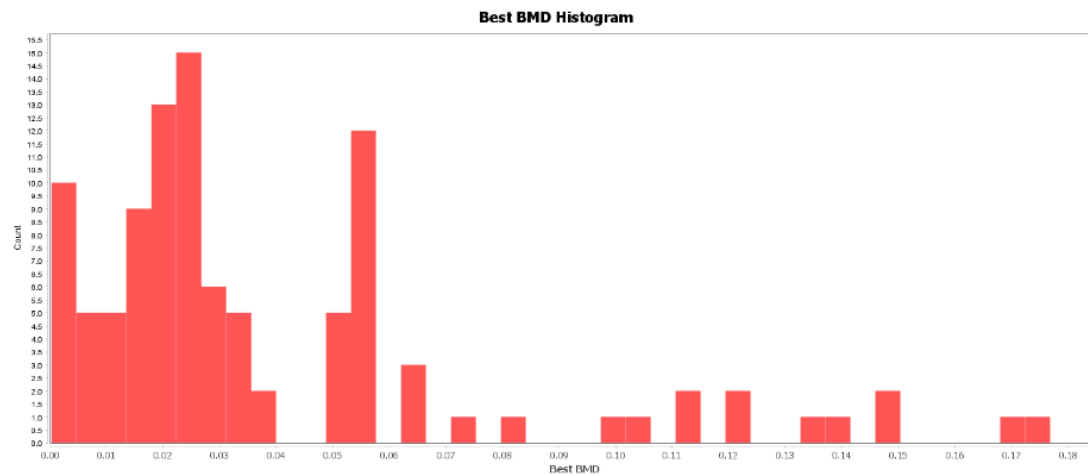


Linear
scale, 3-4
fold
variability

Zinc sulfate (20-60 DEGs)

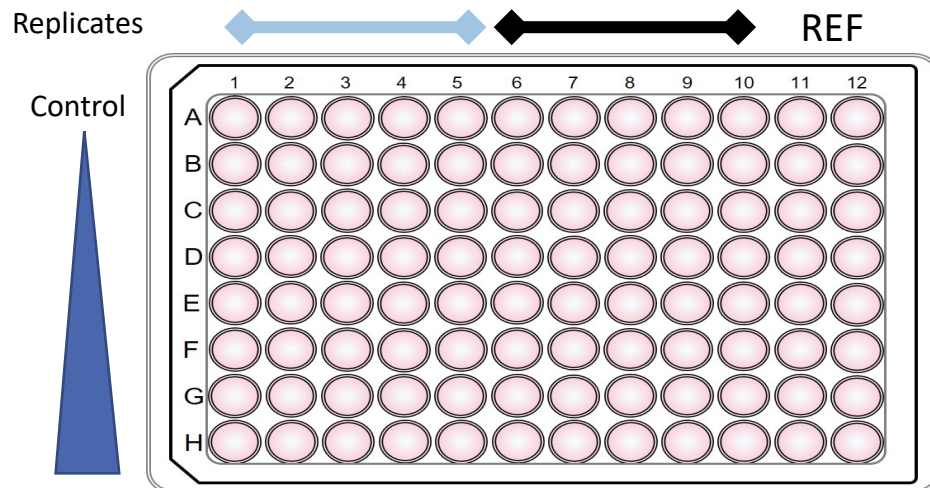


Log 10 scale,
≈ 1 log
variability



Assay optimization – tentative conclusions

- Minimum gene set size $\approx 10,000$
- Minimum biological replication $n=4$; include $n=5$ to allow in silico sub-sampling
- Minimum number of DEGs **[TBD]**
- BMD distribution **[TBD]**



Conceptual illustration – actual layout will be randomized

Revised Design:

- $n= 5$ biological replicates
- $n= 8$ concentrations
- Reference samples included on each plate
- Currently testing with 3 other species

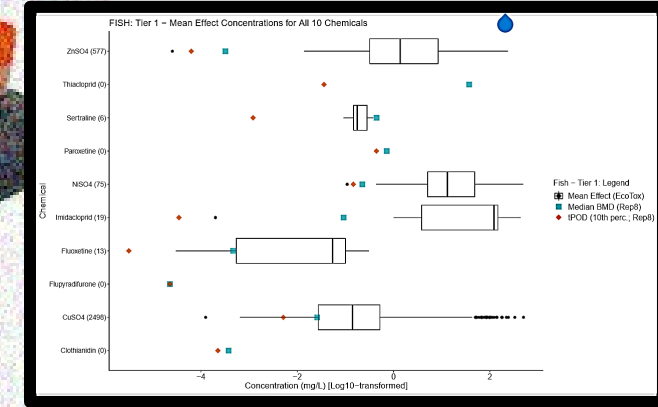


ALGAE

AQUATIC
VERTEBRATE

CRUSTACEAN

INSECT



Expand the tPOD to traditional Ecotox benchmark comparisons:

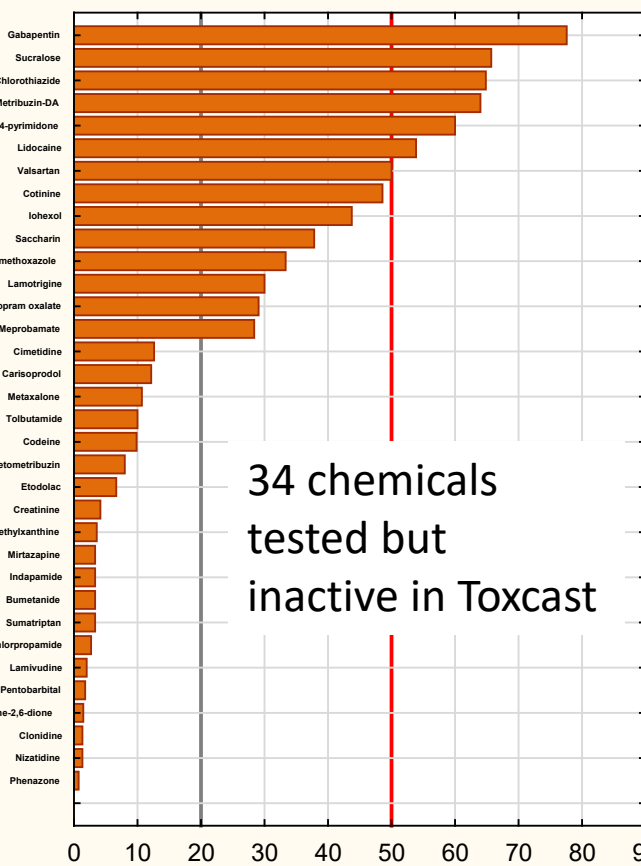
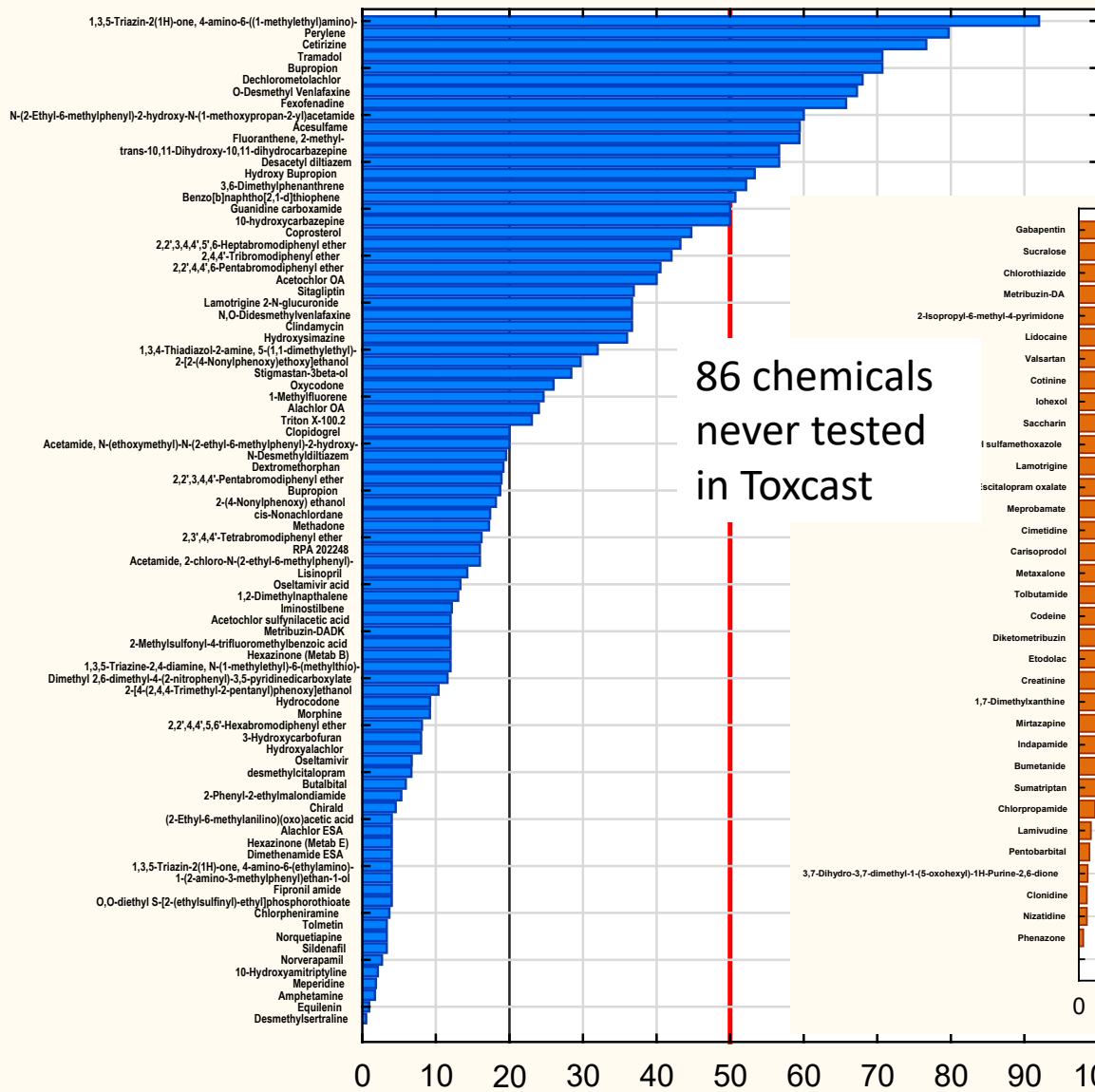
- 50ish chemicals
- Four species
- Testing model prediction of free chemical concentration in plate
- Reduced cost (optimized design; lower cost sequencing)

10 years monitoring emerging contaminants in the Great Lakes

NO EMPIRICAL BENCHMARKS for $\approx 30\%$
of Contaminants Detected in Water

Prioritize for tPOD
derivation based on
detection frequencies

Pilot for $n \approx 12$
chemicals



% of sites detected

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