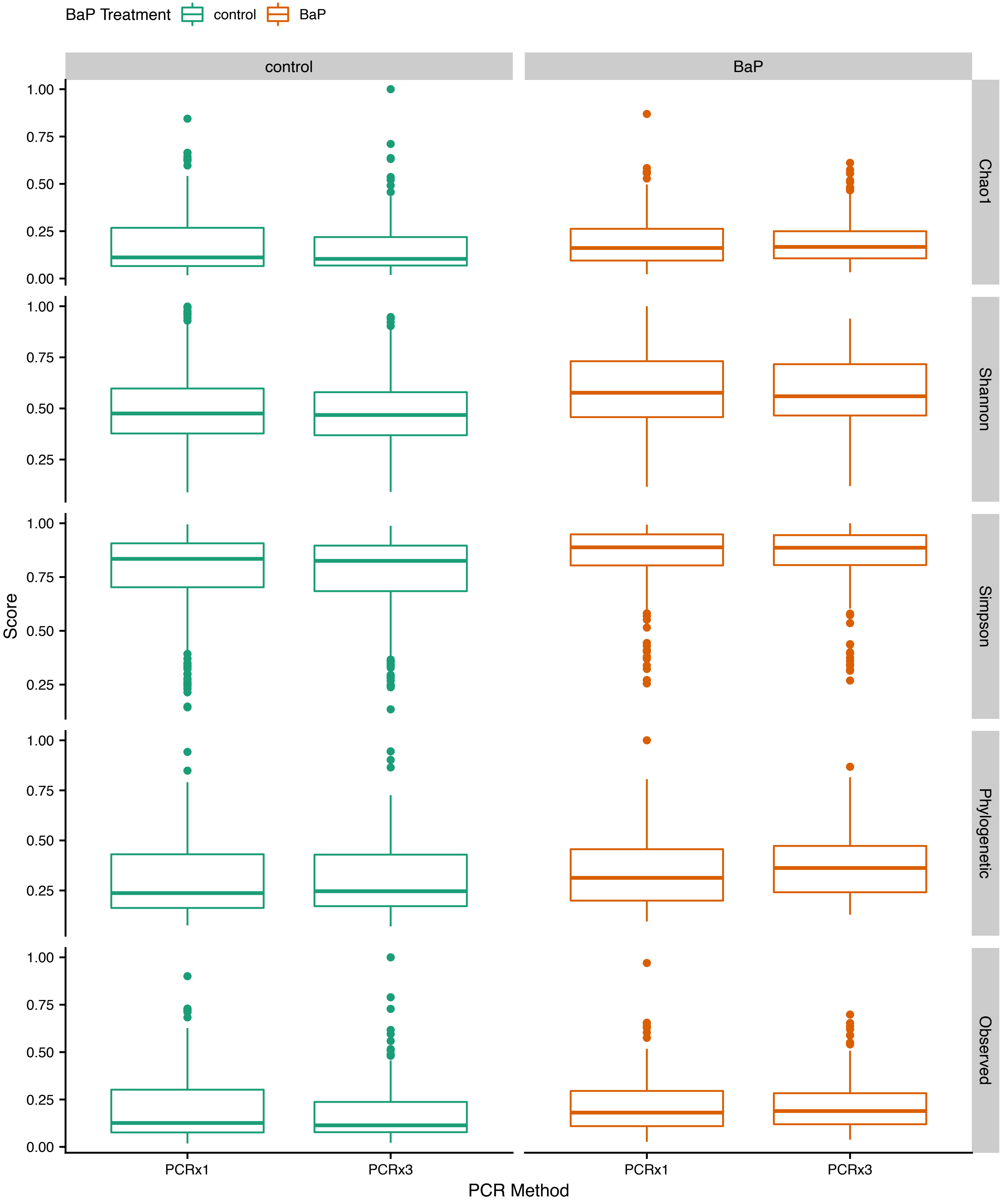
BaP Treatment
control
BaP
control
BaP
Chao1
Shannon
Simpson
Phylogenetic
Observed
Score
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0.75
0.50
0.25
0.00
PCRx1
PCRx3
PCR Method


Increased in controls
Increased in BaP-exposed
LDA Effect Size
−5.0
−2.5
0.0
2.5
5.0
Taxon
Dissection Methods
Extraction Kits
Bacteria.Actinobacteriota
Bacteria.Bacteroidota
Bacteria.Cyanobacteria
Bacteria.Firmicutes
Bacteria.Fusobacteriota
Bacteria.Proteobacteria
Bacteria.Spirochaetota
Bacteria.Verrucomicrobiota
Bacteria.Actinobacteriota.Actinobacteria
Bacteria.Actinobacteriota.Coriobacteriia
Bacteria.Bacteroidota.Bacteroidia
Bacteria.Cyanobacteria.Cyanobacteriia
Bacteria.Cyanobacteria.Vampirivibrionia
Bacteria.Firmicutes.Bacilli
Bacteria.Firmicutes.Clostridia
Bacteria.Firmicutes.Desulfitobacteriia
Bacteria.Firmicutes.Negativicutes
Bacteria.Fusobacteriota.Fusobacteriia
Bacteria.Proteobacteria.Gammaproteobacteria
Bacteria.Verrucomicrobiota.Chlamydiae
Bacteria.Verrucomicrobiota.Verrucomicrobiae
Bacteria.Actinobacteriota.Actinobacteria.Bifidobacteriales
Bacteria.Actinobacteriota.Actinobacteria.Micrococcales
Bacteria.Actinobacteriota.Actinobacteria.Propionibacteriales
Bacteria.Actinobacteriota.Coriobacteriia.Coriobacteriales
Bacteria.Bacteroidota.Bacteroidia.Bacteroidales
Bacteria.Bacteroidota.Bacteroidia.Chitinophagales
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Bacteria.Bdellovibrionota.Oligoflexia.Oligoflexales
Bacteria.Cyanobacteria.Cyanobacteriia.Cyanobacteriales
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Bacteria.Deinococcota.Deinococci.Thermales
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Bacteria.Firmicutes.Bacilli.Erysipelotrichales
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Bacteria.Firmicutes.Bacilli.Staphylococcales
Bacteria.Firmicutes.Clostridia.Christensenellales
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Bacteria.Proteobacteria.Gammaproteobacteria.Burkholderiales
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Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales
Bacteria.Proteobacteria.Gammaproteobacteria.Salinisphaerales
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Bacteria.Cyanobacteria.Vampirivibrionia.Obscuribacterales.Obscuribacteraceae
Bacteria.Deinococcota.Deinococci.Thermales.Thermaceae
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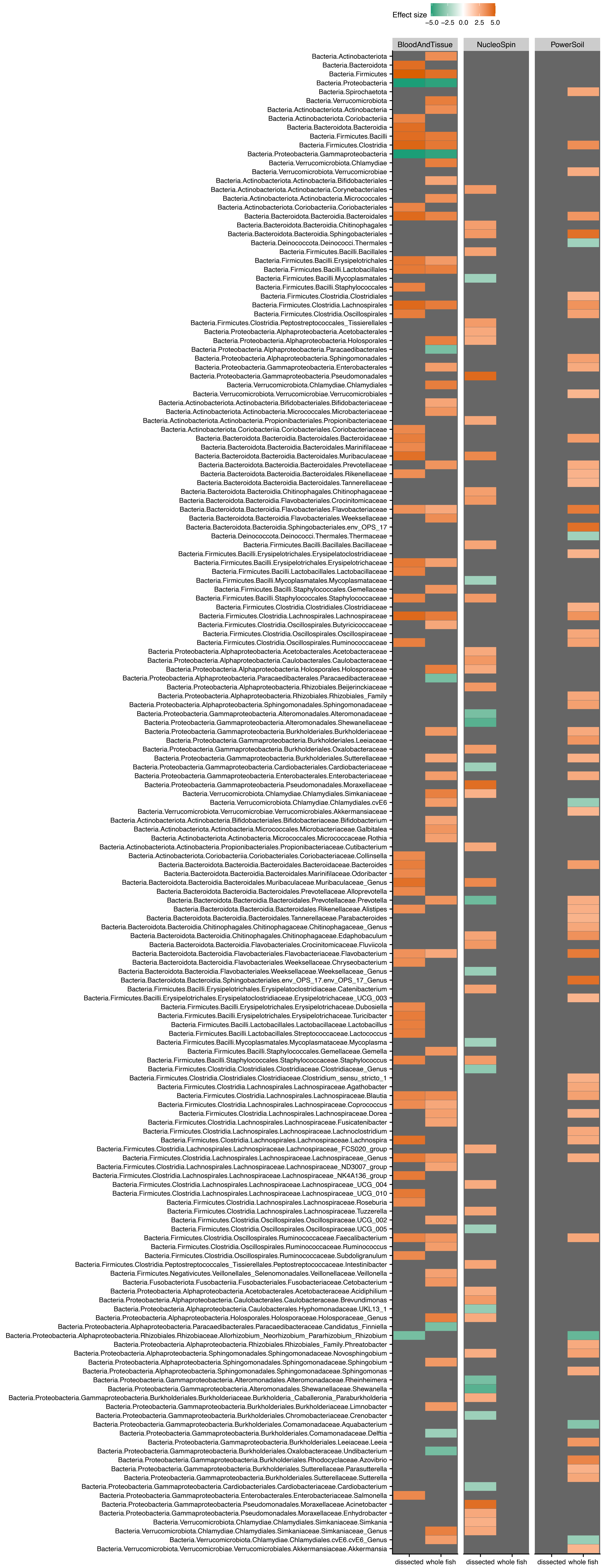
dissected
whole fish
Blood & Tissue
NucleoSpin
PowerSoil


Effect size
−5.0 −2.5 0.0 2.5 5.0
BloodAndTissue
NucleoSpin
PowerSoil
Bacteria.Actinobacteriota
Bacteria.Bacteroidota
Bacteria.Firmicutes
Bacteria.Proteobacteria
Bacteria.Spirochaetota
Bacteria.Verrucomicrobiota
Bacteria.Actinobacteriota.Actinobacteria
Bacteria.Actinobacteriota.Coriobacteriia
Bacteria.Bacteroidota.Bacteroidia
Bacteria.Firmicutes.Bacilli
Bacteria.Firmicutes.Clostridia
Bacteria.Proteobacteria.Gammaproteobacteria
Bacteria.Verrucomicrobiota.Chlamydiae
Bacteria.Verrucomicrobiota.Verrucomicrobiae
Bacteria.Actinobacteriota.Actinobacteria.Bifidobacteriales
Bacteria.Actinobacteriota.Actinobacteria.Corynebacteriales
Bacteria.Actinobacteriota.Actinobacteria.Micrococcales
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Bacteria.Bacteroidota.Bacteroidia.Bacteroidales
Bacteria.Bacteroidota.Bacteroidia.Chitinophagales
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Bacteria.Deinococcota.Deinococci.Thermales
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Bacteria.Verrucomicrobiota.Verrucomicrobiae.Verrucomicrobiales.Akkermansiaceae.Akkermansia
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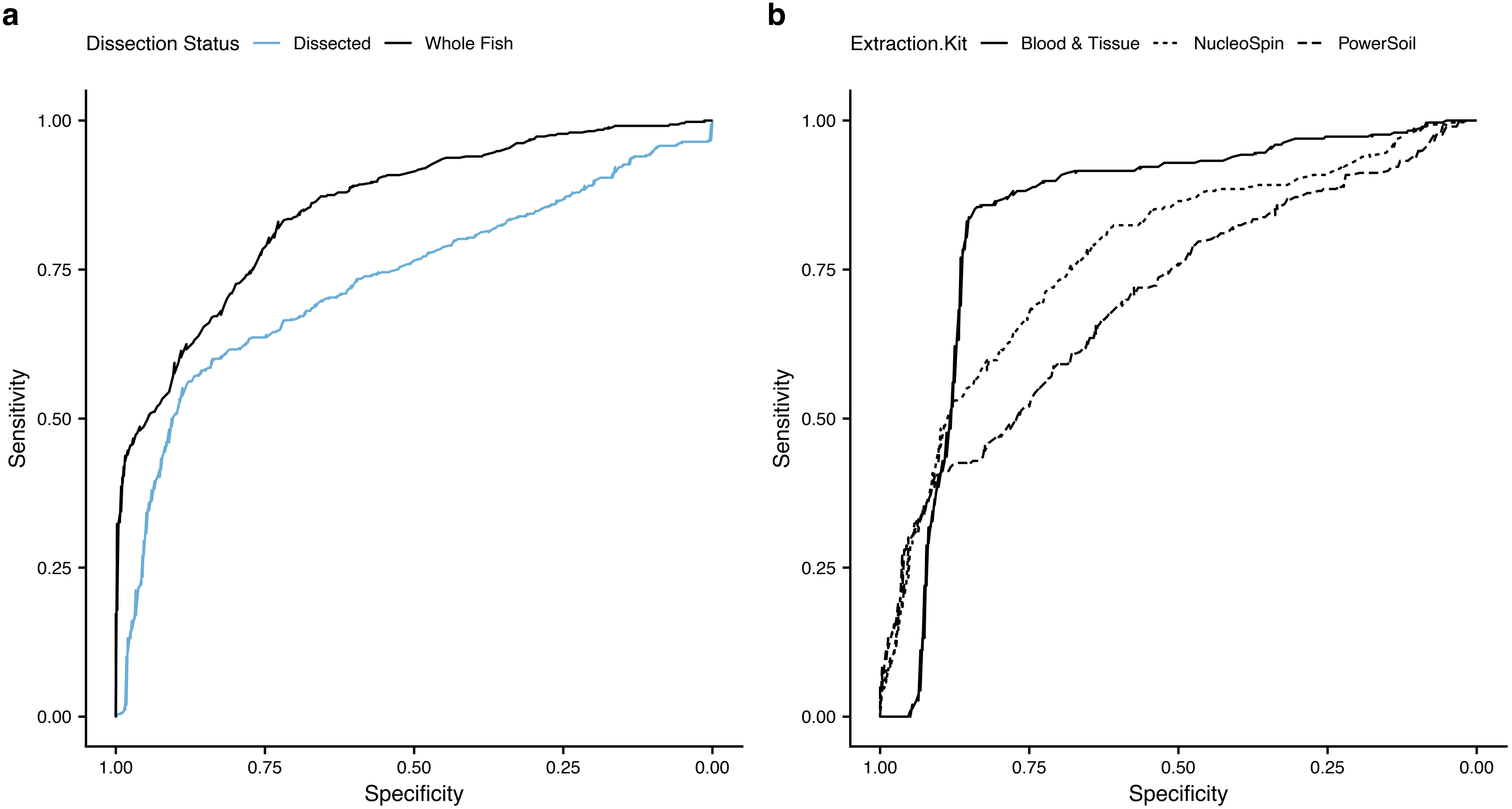
dissected
whole fish
dissected
whole fish



Dissection Method	AUC
Dissected	0.730
Whole Fish	0.854

Extraction Kit	AUC
Blood & Tissue	0.838
NucleoSpin	0.773
PowerSoil	0.701


Candidatus_Finniella|ASV00038
Simkaniaceae_Genus|ASV00032
Pseudomonas|ASV00117
env.OPS_17_Genus|ASV00004
Turicibacter|ASV00049
Brevundimonas|ASV00019
Faecalibacterium|ASV00046
Escherichia/Shigella|ASV00103
Shewanella|ASV00017
Zoogloea|ASV00182
Hydrogenophaga|ASV00002
Holosporaceae_Genus|ASV00024
dissected
whole fish
BaP
control
BaP
control
0 250 500 750
0 200 400 600
0 100 200
0 2000 4000 6000
0 250 500 750 1000
0 200 400 600 800
0 50 100 150
0 50 100 150 200
0 1000 2000 3000 4000
0 10 20
0 500 1000
0 250 500 750 1000
Chitinophagaceae_Genus|ASV00239
Bifidobacterium|ASV00098
Galbitalea|ASV00078
Limnobacter|ASV00138
Bacteroides|ASV00092
Staphylococcus|ASV00087
Coprococcus|ASV00219
Streptococcus|ASV00110
Lachnospiraceae_Genus|ASV00240
Lachnospiraceae_ND3007_group|ASV00225
Acidovorax|ASV00099
Porphyromonas|ASV00131
dissected
whole fish
Treatment
BaP
control
BaP
control
0 10 20 30
0 25 50 75 100
0 100 200 300
0 50 100
0 10 20 30 40 50
0 300 600 900
0 30 60 90
0 10 20 30 40 50
0 5 10 15 20
0 10 20 30
0 30 60 90 120
0 25 50 75
Azovibrio|ASV00014
UKL13−1|ASV00075
Akkermansia|ASV00095
Reyranella|ASV00324
Staphylococcus|ASV00266
Shinella|ASV00007
Solimonadaceae_Genus|ASV00093
Micrococcus|ASV00298
Chryseobacterium|ASV00029
Neisseria|ASV00109
Klebsiella|ASV00140
dissected
whole fish
BaP
control
BaP
control
0 500 1000 1500
0 50 100
0 25 50 75 100
0 10 20
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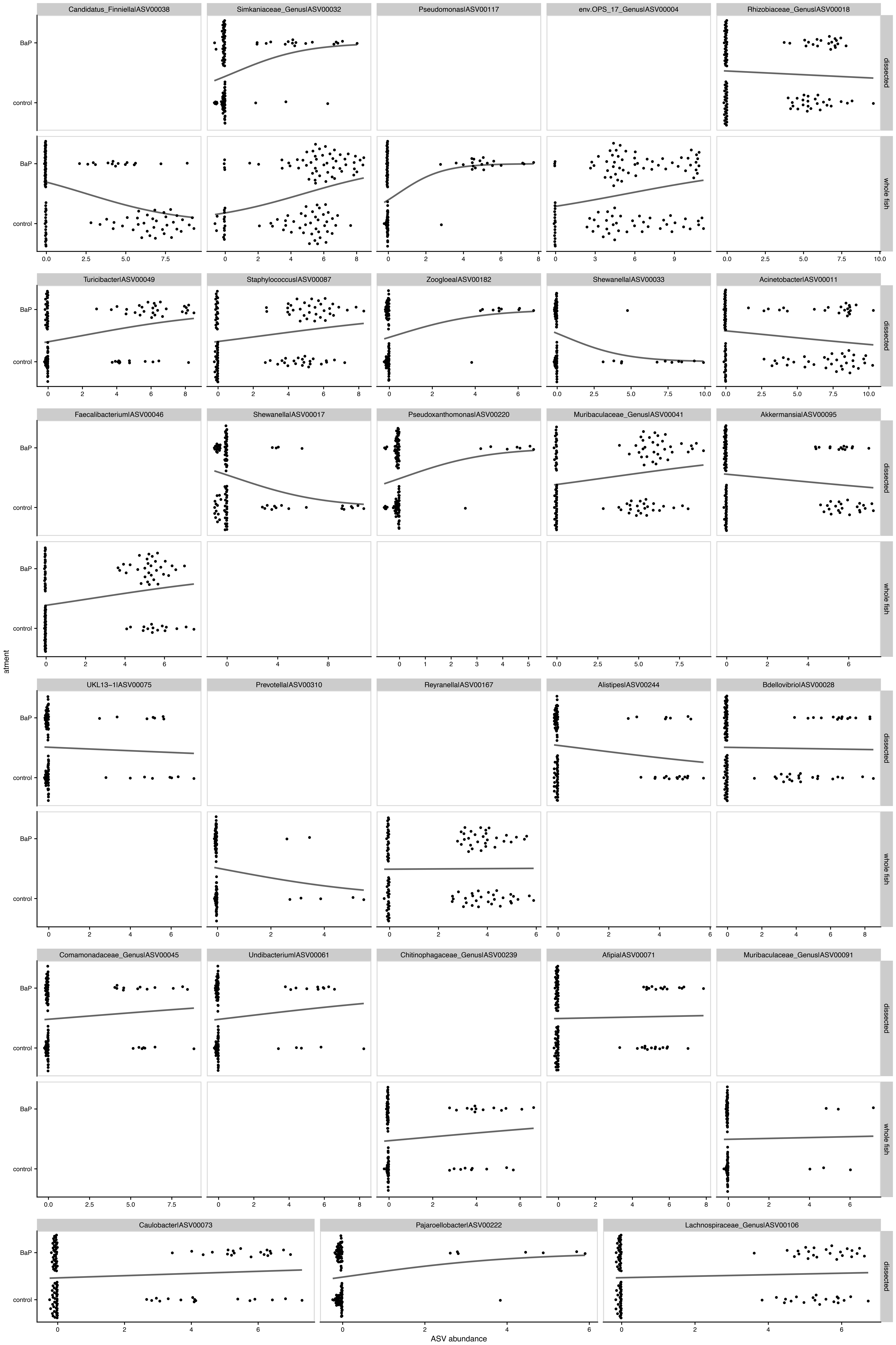
0 30 60 90
0 200 400
ASV abundance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Pseudomonas|ASV00117
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Turicibacter|ASV00049
Staphylococcus|ASV00087
Zoogloea|ASV00182
Shewanella|ASV00033
Acinetobacter|ASV00011
Faecalibacterium|ASV00046
Shewanella|ASV00017
Pseudoxanthomonas|ASV00220
Muribaculaceae_Genus|ASV00041
Akkermansia|ASV00095
UKL13-1|ASV00075
Prevotella|ASV00310
Reyranella|ASV00167
Alistipes|ASV00244
Bdellovibrio|ASV00028
Comamonadaceae_Genus|ASV00045
Undibacterium|ASV00061
Chitinophagaceae_Genus|ASV00239
Afipia|ASV00071
Muribaculaceae_Genus|ASV00091
Caulobacter|ASV00073
Pajaroellobacter|ASV00222
Lachnospiraceae_Genus|ASV00106
dissected
whole fish
BaP
control
atment
ASV abundance
0.0
2.5
5.0
7.5
10.0
0
2
4
6
8
3
9
1
5


Fusobacterium|ASV00443
Candidatus_Finniella|ASV00038
Rhizobiaceae_Genus|ASV00018
Lachnospiraceae_Genus|ASV00133
Simkaniaceae_Genus|ASV00032
Blood & Tissue
NucleoSpin
PowerSoil
BaP
control
0 10 20 30 40
0 300 600 900 1200
0 500 1000 1500
0 50 100 150
0 200 400 600
obium–Neorhizobium–Pararhizobium–Rhizobium|ASV
Edaphobaculum|ASV00015
Bosea|ASV00025
Dechloromonas|ASV00039
Faecalibacterium|ASV00046
0 200 400 600
0 1000 2000 3000
0 50 100 150 200
0 200 400 600
0 100 200 300
Turicibacter|ASV00049
Blautia|ASV00040
Lactobacillus|ASV00060
Rhizobiaceae_Genus|ASV00021
Acinetobacter|ASV00035
Treatment
0 500 1000
0 100 200
0 250 500 750
0 400 800 1200
0 200 400 600
Bdellovibrio|ASV00101
Comamonadaceae_Genus|ASV00045
Aeromonas|ASV00013
Chitinophagaceae_Genus|ASV00239
Muribaculaceae_Genus|ASV00041
0 20 40
0 50 100 150
0 400 800 1200
0 5 10 15 20 25
0 500 1000
Salmonella|ASV00388
Escherichia/Shigella|ASV00103
Hydrogenophaga|ASV00139
Novosphingobium|ASV00084
Aeromonas|ASV00001
0 40 80 120
0 30 60 90 120
0 10 20 30 40
0 10 20 30 40 50
0 2500 5000 7500
ASV abundance


Fusobacterium|ASV00443
Candidatus_Finniella|ASV00038
Simkaniaceae_Genus|ASV00032
Blautia|ASV00040
Muribaculaceae_Genus|ASV00041
Bosea|ASV00025
Staphylococcus|ASV00087
Acinetobacter|ASV00035
Chitinophagaceae_Genus|ASV00239
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0 300 600 900 1200
0 200 400 600
0 100 200 300
0 500 1000
0 50 100 150 200
0 300 600 900
0 200 400 600
0 10 20 30
Lachnospiraceae_Genus|ASV00133
Comamonadaceae_Genus|ASV00045
Lachnospiraceae_Genus|ASV00106
Odoribacter|ASV00339
Sediminibacterium|ASV00008
Pseudomonas|ASV00043
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Blautia|ASV00126
Comamonadaceae_Genus|ASV00208
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0 20 40 60
0 2 4 6 8
0 500 1000
0 500 1000
0 200 400 600
0 20 40 60 80
0 10 20
Pseudoduganella|ASV00096
Shinella|ASV00166
Elstera|ASV00076
Dechloromonas|ASV00039
Chryseobacterium|ASV00029
Shinella|ASV00007
Klebsiella|ASV00140
0 20 40 60 80
0 25 50 75 100 125
0 40 80 120
0 200 400 600
0 1000 2000 3000 4000 5000
0 1000 2000 3000
0 5 10 15 20 25
BaP
control
Blood & Tissue
NucleoSpin
PowerSoil
Treatment
ASV abundance

Supplemental Figure 1. Box plots of alpha-diversity metric scores by B*a*P exposure and PCR method (triplicate vs single reactions).

Supplemental Figure 2. Heatmap of statistically significant effect sizes estimated by LEfSe. This plot shows all phylotypes that were identified as indicators across any data set. The color of the square indicates the effect size with green meaning a phylotype is indicative of the control (no BaP exposure) while orange means a phylotype is indicative of BaP exposure.

Supplemental Figure 3. Receiver operating characteristic (ROC) curve plots for random forest models predicting BaP exposure from various data subsets, indicated by line color or line type, of rarefied ASV counts. (a) ROC curves for dissected gut versus whole fish, with the areas under the curve (AUCs) listed in the table below. (b) Similar data as in panel a, but for subsets by DNA extraction kit.

Supplemental Figure 4. Swarm plots of logistic regressions predicting BaP exposure from individual ASV abundances (rarefied) using data subsets partititioned by dissection method. ASVs are orded by importance from the preceding random forest analysis. Points indicate an ASV's abundance per each dissection method. Black lines indicate the predicted relationship taken directly from the logistic regression models.

Supplemental Figure 5. Swarm plots of logistic regressions predicting BaP exposure from individual ASV abundances (CLR-transformed) using data subsets partititioned by dissection method. ASVs are orded by importance from the preceding random forest analysis. (This first 8 ASVs in this figure comprised Figure 6). Points indicate an ASV's abundance per each dissection method. Black lines indicate the predicted relationship taken directly from the logistic regression models.

Supplemental Figure 6. Swarm plots of logistic regressions predicting BaP exposure from individual ASV abundances (rarefied) using data subsets partititioned by DNA extraction kit. ASVs are orded by importance from the preceding random forest analysis. Points indicate an ASV's abundance per each dissection method. Black lines indicate the predicted relationship taken directly from the logistic regression models.

Supplemental Figure 7. Swarm plots of logistic regressions predicting BaP exposure from individual ASV abundances (CLR-transformed) using data subsets partititioned by DNA extraction kit. ASVs are orded by importance from the preceding random forest analysis. (This first 8 ASVs in this figure comprised Figure 7). Points indicate an ASV's abundance per each dissection method. Black lines indicate the predicted relationship taken directly from the logistic regression models.

Supplemental Table 1. Counts of biological samples (so not including x3 and x1 PCR as separate samples) in each treatment set. We started with 384 (4 x 96) zebrafish embryos, and after dada2 processing (which include rejecting reads based on low quality) and rarefaction, we ended with 277 biological replicates. For analyses in which we tested the effects of dissection method and extraction kit together, we used the samples subsetted by extraction kit.

BaP Treatment	Dissection Method	Extraction Kit	Count after QC	Count after subsampling
-	-	-	277	-
Unexposed	-	-	123	-
Exposed	-	-	154	-
-	Dissected	-	127	112
-	Whole fish	-	150	112
-	-	PowerSoil	92	74
-	-	NucleoSpin	96	74
-	-	Blood & Tissue	89	74
Unexposed	Dissected	-	56	56
Unexposed	Whole fish	-	67	56
Exposed	Dissected	-	71	56
Exposed	Whole fish	-	83	56
Unexposed	-	PowerSoil	43	37
Unexposed	-	NucleoSpin	43	37
Unexposed	-	Blood & Tissue	37	37
Exposed	-	PowerSoil	49	37
Exposed	-	NucleoSpin	53	37
Exposed	-	Blood & Tissue	52	37
Unexposed	Dissected	PowerSoil	18	16
Unexposed	Dissected	NucleoSpin	22	20
Unexposed	Dissected	Blood & Tissue	16	16
Unexposed	Whole fish	PowerSoil	25	21
Unexposed	Whole fish	NucleoSpin	21	17
Unexposed	Whole fish	Blood & Tissue	21	21
Exposed	Dissected	PowerSoil	21	16
Exposed	Dissected	NucleoSpin	26	18
Exposed	Dissected	Blood & Tissue	24	18
Exposed	Whole fish	PowerSoil	28	21
Exposed	Whole fish	NucleoSpin	27	19
Exposed	Whole fish	Blood & Tissue	28	19

Supplemental Table 2. Alpha-diversity by PCR method MM-GLM results (n = 277)

metric	term	statistic	df	p.value	sig
Chao1	BaP Treatment	0.59	1	0.444	
	PCR Method	0.08	1	0.783	
	BaP Treatment:PCR Method	0.13	1	0.717	
Shannon	BaP Treatment	2.45	1	0.117	
	PCR Method	0.07	1	0.796	
	BaP Treatment:PCR Method	0.01	1	0.909	
Simpson	BaP Treatment	1.98	1	0.159	
	PCR Method	0.01	1	0.907	
	BaP Treatment:PCR Method	0	1	0.973	
Phylogenetic	BaP Treatment	1.36	1	0.244	
	PCR Method	0.14	1	0.704	
	BaP Treatment:PCR Method	0.03	1	0.869	
Observed	BaP Treatment	0.87	1	0.35	
	PCR Method	0.13	1	0.716	
	BaP Treatment:PCR Method	0.25	1	0.616	

Supplemental Table 3. Alpha-diversity by extraction kit and dissection method GLM results (n = 222)

metric	term	statistic	df	p.value	sig
Chao1	BaP Treatment	4.73	1	0.03	*
	Extraction Kit	173.76	2	0	*
	Dissection Method	22.06	1	0	*
	BaP Treatment:Extraction Kit	6.94	2	0.031	*
	BaP Treatment:Dissection Method	0.16	1	0.692	
Shannon	BaP Treatment	15.5	1	0	*
	Extraction Kit	78.42	2	0	*
	Dissection Method	16.09	1	0	*
	BaP Treatment:Extraction Kit	4.5	2	0.105	
	BaP Treatment:Dissection Method	2.3	1	0.129	
Simpson	BaP Treatment	11.28	1	0.001	*
	Extraction Kit	38.17	2	0	*
	Dissection Method	1.22	1	0.27	
	BaP Treatment:Extraction Kit	2.5	2	0.286	
	BaP Treatment:Dissection Method	2.06	1	0.151	
Phylogenetic	BaP Treatment	12.45	1	0	*
	Extraction Kit	233.9	2	0	*
	Dissection Method	13.36	1	0	*
	BaP Treatment:Extraction Kit	4.13	2	0.127	
	BaP Treatment:Dissection Method	0.03	1	0.867	
Observed	BaP Treatment	5.82	1	0.016	*
	Extraction Kit	177.55	2	0	*
	Dissection Method	26.18	1	0	*
	BaP Treatment:Extraction Kit	6.36	2	0.042	*
	BaP Treatment:Dissection Method	0.12	1	0.726	

Supplemental Table 4. PCR methods PERMANOVA results (n = 277)

metric	term	df	SumOfSqs/Variance	statistic	p.value	sig
Bray-Curtis	BaP Treatment	1	2.81	7.35	0.002	*
	PCR Method	1	0.08	0.21	0.002	*
	BaP Treatment:PCR Method	1	0.04	0.11	0.581	
	Residual	623	238.27			
Canberra	BaP Treatment	1	1.4	3.18	0.001	*
	PCR Method	1	0.4	0.9	0.001	*
	BaP Treatment:PCR Method	1	0.24	0.55	0.304	
	Residual	623	275.08			
Sørensen	BaP Treatment	1	1.98	6.09	0.001	*
	PCR Method	1	0.34	1.05	0.001	*
	BaP Treatment:PCR Method	1	0.16	0.48	0.054	
	Residual	623	202.77			
Aitchison	BaP Treatment	1	15.2	4.58	0.001	*
	PCR Method	1	2.78	0.84	0.001	*
	BaP Treatment:PCR Method	1	1.51	0.46	0.089	
	Residual	622	2,065.26			
W Unifrac	BaP Treatment	1	0.39	20.03	0.001	*
	PCR Method	1	0	0.19	0.001	*
	BaP Treatment:PCR Method	1	0	0.07	0.326	
	Residual	623	12			
0.5 Unifrac	BaP Treatment	1	1.41	13.52	0.001	*
	PCR Method	1	0.04	0.39	0.001	*
	BaP Treatment:PCR Method	1	0.02	0.18	0.071	
	Residual	623	64.87			
U Unifrac	BaP Treatment	1	2.11	6.13	0.001	*
	PCR Method	1	0.34	0.98	0.001	*
	BaP Treatment:PCR Method	1	0.16	0.47	0.083	
	Residual	623	214.18			

Supplemental Table 5. Extraction kit and dissection methods PERMANOVA results (n = 222)

metric	term	df	SumOfSqs/Variance	statistic	p.value	sig
Bray-Curtis	BaP Treatment	1	0.83	2.54	0.005	*
	Extraction Kit	2	6.13	9.4	0.001	*
	Dissection Method	1	6.65	20.38	0.001	*
	BaP Treatment:Extraction Kit	2	0.76	1.16	0.239	
	BaP Treatment:Dissection Method	1	0.38	1.15	0.277	
	Residual	214	69.81			
Canberra	BaP Treatment	1	0.65	1.54	0.001	*
	Extraction Kit	2	4.13	4.94	0.001	*
	Dissection Method	1	2.68	6.4	0.001	*
	BaP Treatment:Extraction Kit	2	0.91	1.09	0.098	
	BaP Treatment:Dissection Method	1	0.49	1.18	0.053	
	Residual	214	89.58			
Sørensen	BaP Treatment	1	0.81	3.12	0.001	*
	Extraction Kit	2	8.48	16.28	0.001	*
	Dissection Method	1	4.09	15.7	0.001	*
	BaP Treatment:Extraction Kit	2	0.67	1.28	0.085	
	BaP Treatment:Dissection Method	1	0.34	1.3	0.113	
	Residual	214	55.74			
Aitchison	BaP Treatment	1	17.79	2.17	0.003	*
	Extraction Kit	2	212.71	12.95	0.001	*
	Dissection Method	1	129.6	15.78	0.001	*
	BaP Treatment:Extraction Kit	2	20.43	1.24	0.099	
	BaP Treatment:Dissection Method	1	11.22	1.37	0.078	
	Residual	213	1,749.26			
W Unifrac	BaP Treatment	1	0.12	7.39	0.001	*
	Extraction Kit	2	0.36	11.05	0.001	*
	Dissection Method	1	0.42	25.82	0.001	*
	BaP Treatment:Extraction Kit	2	0.04	1.37	0.151	
	BaP Treatment:Dissection Method	1	0.02	0.95	0.409	
	Residual	214	3.5			
0.5 Unifrac	BaP Treatment	1	0.46	5.63	0.001	*
	Extraction Kit	2	2.96	18.23	0.001	*
	Dissection Method	1	2.23	27.45	0.001	*
	BaP Treatment:Extraction Kit	2	0.22	1.38	0.101	
	BaP Treatment:Dissection Method	1	0.13	1.57	0.09	
	Residual	214	17.37			
U Unifrac	BaP Treatment	1	0.84	2.77	0.001	*
	Extraction Kit	2	6.73	11.13	0.001	*
	Dissection Method	1	3.43	11.34	0.001	*
	BaP Treatment:Extraction Kit	2	0.71	1.17	0.113	
	BaP Treatment:Dissection Method	1	0.43	1.43	0.038	*
	Residual	214	64.68			

Supplemental Table 6. Results of two binomial GLM models (one for each dissection method), built in a serial, forward stepwise manner predicting BaP treatment from individual ASV abundances.

data.set	term	statistic	df	p.value	sig
dissected	ASV00002	1,335.57	1	0	*
	ASV00007	1,912.27	1	0	*
	ASV00017	18.23	1	0	*
	ASV00019	42.08	1	0	*
	ASV00049	13.03	1	0	*
	ASV00067	2.2	1	0.138	
	ASV00075	11.98	1	0.001	*
	ASV00078	21.8	1	0	*
	ASV00087	1,263.48	1	0	*
	ASV00095	4.31	1	0.038	*
	ASV00098	22.48	1	0	*
	ASV00103	27.09	1	0	*
	ASV00109	5.52	1	0.019	*
	ASV00131	1,191.39	1	0	*
	ASV00138	7.45	1	0.006	*
	ASV00140	10.56	1	0.001	*
	ASV00219	11.08	1	0.001	*
	ASV00225	7.96	1	0.005	*
	ASV00266	12.65	1	0	*
	ASV00298	8.21	1	0.004	*
whole fish	ASV00004	32.04	1	0	*
	ASV00014	25.03	1	0	*
	ASV00024	34.19	1	0	*
	ASV00029	20.91	1	0	*
	ASV00032	57.77	1	0	*
	ASV00038	32.7	1	0	*
	ASV00046	37.83	1	0	*
	ASV00092	14.92	1	0	*
	ASV00093	11.56	1	0.001	*
	ASV00099	24.96	1	0	*
	ASV00110	30.36	1	0	*
	ASV00117	34.72	1	0	*
	ASV00182	31.43	1	0	*
	ASV00239	22.82	1	0	*
	ASV00240	20.57	1	0	*
	ASV00324	15.75	1	0	*

Supplemental Table 7. Results of two binomial GLM models (one for each dissection method), built in a serial, forward stepwise manner predicting BaP treatment from individual ASV abundances.

data.set	term	statistic	df	p.value	sig
dissected	ASV00011	39.2	1	0	*
	ASV00017	33.78	1	0	*
	ASV00018	42.81	1	0	*
	ASV00028	58.23	1	0	*
	ASV00032	70.57	1	0	*
	ASV00033	72.52	1	0	*
	ASV00041	34.75	1	0	*
	ASV00045	38.52	1	0	*
	ASV00049	28.05	1	0	*
	ASV00061	43.83	1	0	*
	ASV00071	22.74	1	0	*
	ASV00073	50.89	1	0	*
	ASV00075	47.71	1	0	*
	ASV00087	34.96	1	0	*
	ASV00095	23.97	1	0	*
	ASV00106	29.8	1	0	*
	ASV00182	73.23	1	0	*
	ASV00220	1,946.36	1	0	*
	ASV00222	36.8	1	0	*
	ASV00244	27.22	1	0	*
whole fish	ASV00003	0.75	1	0.386	
	ASV00004	16.9	1	0	*
	ASV00032	34.04	1	0	*
	ASV00038	31.38	1	0	*
	ASV00046	7.26	1	0.007	*
	ASV00091	7.03	1	0.008	*
	ASV00117	21.6	1	0	*
	ASV00167	4.16	1	0.041	*
	ASV00239	13.28	1	0	*
	ASV00310	4.84	1	0.028	*
	ASV00324	3.48	1	0.062	

Supplemental Table 8. Results of three binomial GLM models (one for each extraction kit), built in a serial, forward stepwise manner predicting BaP treatment from individual ASV abundances.

data.set	term	statistic	df	p.value	sig
Blood & Tissue	ASV00011	0	1	0.999	
	ASV00022	10.89	1	0.001	*
	ASV00024	0	1	1	
	ASV00032	19.06	1	0	*
	ASV00038	25.86	1	0	*
	ASV00041	21.02	1	0	*
	ASV00046	0	1	0.999	
	ASV00076	792.96	1	0	*
	ASV00087	27.98	1	0	*
	ASV00106	8.69	1	0.003	*
	ASV00145	0	1	1	
	ASV00208	21.03	1	0	*
NucleoSpin	ASV00008	21.29	1	0	*
	ASV00025	14.98	1	0	*
	ASV00032	17.94	1	0	*
	ASV00035	21.86	1	0	*
	ASV00038	39.93	1	0	*
	ASV00040	30.59	1	0	*
	ASV00041	432.52	1	0	*
	ASV00096	14.78	1	0	*
	ASV00239	18.77	1	0	*
	ASV00339	9.98	1	0.002	*
	ASV00443	28.48	1	0	*
PowerSoil	ASV00005	3.79	1	0.052	
	ASV00007	15.62	1	0	*
	ASV00029	5.13	1	0.023	*
	ASV00039	5.62	1	0.018	*
	ASV00043	17.61	1	0	*
	ASV00045	18.34	1	0	*
	ASV00062	1.57	1	0.211	
	ASV00126	4.24	1	0.039	*
	ASV00133	8.52	1	0.004	*
	ASV00140	4.8	1	0.028	*
	ASV00166	13.61	1	0	*
	ASV00239	8.77	1	0.003	*

Supplemental Table 9. Results of three binomial GLM models (one for each extraction kit), built in a serial, forward stepwise manner predicting BaP treatment from individual ASV abundances.

data.set	term	statistic	df	p.value	sig
Blood & Tissue	ASV00001	26.43	1	0	*
	ASV00013	25.29	1	0	*
	ASV00018	28.59	1	0	*
	ASV00022	21.33	1	0	*
	ASV00032	59.8	1	0	*
	ASV00038	45.04	1	0	*
	ASV00041	23.68	1	0	*
	ASV00046	30.82	1	0	*
	ASV00049	30.16	1	0	*
	ASV00103	28.6	1	0	*
	ASV00239	29.57	1	0	*
	ASV00388	26.83	1	0	*
NucleoSpin	ASV00015	20.18	1	0	*
	ASV00024	0	1	0.999	
	ASV00025	18.74	1	0	*
	ASV00032	12.21	1	0	*
	ASV00035	17.68	1	0	*
	ASV00038	44.9	1	0	*
	ASV00041	0	1	1	
	ASV00046	22.33	1	0	*
	ASV00049	0	1	0.984	
	ASV00093	0	1	0.999	
	ASV00133	18.63	1	0	*
	ASV00443	29.36	1	0	*
PowerSoil	ASV00021	6.24	1	0.013	*
	ASV00038	0	1	1	
	ASV00039	17.48	1	0	*
	ASV00040	4.48	1	0.034	*
	ASV00045	19.26	1	0	*
	ASV00046	15.95	1	0	*
	ASV00058	0.98	1	0.323	
	ASV00060	20.36	1	0	*
	ASV00084	27.18	1	0	*
	ASV00099	1.16	1	0.282	
	ASV00101	21.69	1	0	*
	ASV00133	15.84	1	0	*
	ASV00139	12.74	1	0	*