Table S3. Threshold indicator taxa analysis of individual taxa in response to PO$_4$-P concentration. Taxa are listed alphabetically. Indicator taxa that passed the

screening criteria ($P < 0.05$, purity ≥ 0.95, reliability ≥ 0.95) are shown in boldface.

Taxa	ienv.cp	zenv.cp	freq	IndVal	zscore	5%	95%	purity	reliability	z.median	filter
Baetidae	135	47.5	48	62.59	6.02	12	135	1	1	6.58	1
Bithyniidae	102.5	102.5	9	21.62	2.54	21	102.5	0.83	0.73	2.92	0
Caenidae	54.5	67	62	55.63	3.46	51	135.2	0.88	0.95	3.53	0
Ceratopogonidae	9.5	11	10	49.9	8.11	8	37	0.97	0.99	9.07	1
Chironomidae	93.5	93.5	69	52.95	1.72	4.5	152	0.72	0.77	0.72	0
Ecnomidae	47.5	47.5	14	36.26	5.55	44	93.5	1	0.99	5.97	1
Elmidae	62.5	62.5	21	53.74	8.5	51	67	1	1	8.47	1
Erpobdellidae	110	90	7	22.1	4.7	54.5	110	0.99	0.93	5.15	0
Euphaeidae	7.5	8	6	69.81	13.33	7	11	1	0.99	12.91	1
Gecarcinucidae	7	106	14	19.43	0.85	7.5	121	0.46	0.7	2.65	0
Glossiphoniidae	67	67	6	17.14	3.8	58	135	0.99	0.82	3.76	0
Heptageniidae	12	47.5	14	46.51	8.35	11	51	0.99	0.99	9.11	1
Hydropsychidae	7.5	11	36	51.36	2.98	7	121	0.87	0.94	4.02	0
Hydroptilidae	138	138	8	53.09	5.45	8	152	0.52	0.98	7.51	0
Leptophlebiidae	54	58	33	71.36	11.42	47	67	1	1	11.16	1
Oligochaeta	81	58	53	67.41	7.92	58	93.5	0.98	1	8.32	2
Palaemonidae	67.0	67.0	8	21.05	3.80	51.0	72.0	0.92	0.92	4.13	0
Perlidae	7	72	8	19.51	2.95	4.5	90	0.98	0.87	4.93	0
Podocopida	121	99	13	38.97	6.5	97	152	0.99	0.99	6.88	2
Psychodidae	7	8	6	13.91	1.12	7.5	102.5	0.64	0.6	2.52	0
Psychomyiidae	44	44	11	39.83	8.64	44	54.5	1	0.99	8.11	1
Pyralidae	8	8	6	25.4	3.09	8	149	0.7	0.69	3.97	0
Thiaridae	11	11	31	56.36	4.39	9.5	99	0.99	0.99	5.03	2
Tipulidae	93.5	93.5	22	33.77	2.94	51	149	0.83	0.9	3.79	0
Veliidae	81	81	8	19.05	3.2	43.3	90	0.85	0.84	3.56	0
Viviparidae	21	21	8	15.69	1.48	12	106	0.59	0.44	1.99	0

Ienv.cp is the environmental change point for each taxon based on the IndVal maximum; zenv.cp is the environmental change point for each taxon based on the z maximum; freq is the number of times each taxon occurred in the data set; IndVal is the Indval statistics, scaled from 0–100, with 100 indicating a taxon that occurred in all of the samples above or below a change point value and in none of the samples on the other side of the change point; zscore is scaled to reflect how different the IndVal was from values that were obtained by random reshuffling of the data (1000 permutations); 5% and 95% are change point quantiles among bootstrap replicates; purity is the proportion of the bootstrap replicates that correctly assigned the taxon as an increase or decrease; reliability is the proportion of the bootstrap replicates that resulted in a p-value of < 0.05; z.median is the median score magnitude across all bootstrap replicates; filter is logical (if >0) indicating whether each taxa met purity and reliability criteria and 1 if z- (negative response) or 2 if z+ (positive response) (Nguyen et al. 2017).