Updating MCI tolerance values for freshwater invertebrate taxa

Prepared for Environment Southland and Hawkes Bay Regional Council

September 2015

Prepared by:
Michelle Greenwood[1]
Doug Booker[1]
John Stark[2]
Alastair Suren[3]
Joanne Clapcott[4]

[1]National Institute of Water & Atmospheric Research Ltd
PO Box 8602
Riccarton
Christchurch 8011
Phone +64 3 348 8987

[2]Stark Environmental Limited
PO Box 1831
Nelson 7040

[3]Environment Bay of Plenty
PO Box 364
Whakatane 3158

[4]Cawthron Institute
Private Bag 2
Nelson 7042

For any information regarding this report please contact:

Michelle Greenwood
Scientist
Freshwater Ecology
+64-3-343 8061
Michelle.Greenwood@niwa.co.nz

R scripts are available to run the method described in this report. Please contact Michelle for further information.

NIWA CLIENT REPORT No:	CHC2015-008
Report date:	September 2015
NIWA Project:	ELF15201

Quality Assurance Statement		
	Reviewed by:	R. G. Storey Richard Storey
	Approved for release by:	Charles Pearson

Contents

Tables

Figures

Summary

The Macroinvertebrate Community Index (MCI) is used by Regional Councils and other organisations in New Zealand for a range of purposes including State of Environment and consent monitoring in freshwaters. The index is designed to reflect human impacts on waterways, particularly organic pollution, and is calculated from tolerance values (TVs) assigned to freshwater invertebrate taxa. For streams with hard bed substrate, published TVs exist for 180 freshwater invertebrate taxa, with many other taxa not having TVs assigned. Regional Councils currently treat taxa that do not have assigned TVs in different ways; some councils exclude these taxa from their MCI calculations while others have developed TVs using professional judgement. Developing standard TVs for all freshwater invertebrate taxa is a key step towards ensuring national consistency in calculation and reporting of the MCI.

The objectives of this study were to:

1. use an objective computational process to produce TVs for as many freshwater invertebrate taxa as possible at a range of taxonomic levels,
2. compare existing and revised MCI TVs and resultant site scores, and
3. develop R scripts that can be used to develop TVs using other datasets.

Extensive testing of the revised TVs and resulting MCI site scores was beyond the scope of this study.

We compiled a national-scale dataset of macroinvertebrate community data from over 1300 freshwater monitoring sites. There were insufficient data from streams with soft bed substrate to revise the version of the MCI used in soft-bottomed streams (MCI-sb) therefore these 122 sites were excluded. A total of 10548 samples were collected at the remaining 1266 hard-bottomed sites. Data were divided into two datasets; the full dataset with all sampling occasions per site and a reduced dataset, consisting of 50 random sub-samples of the full dataset, each sub-sample consisting of one sampling occasion per site. Data were further grouped into eight classes based on Climate and Source of Flow categories from the River Environment Classification (REC).

To revise the MCI TVs we applied an iterative computational process developed by Chessman (2003), which has been previously applied to develop two other indices in New Zealand (MCI-sb and a wetland MCI). The Chessman method was run on all eight environmental classes on both the full and reduced datasets. Tolerance values were compared across the environmental classes and two different approaches to assigning singular TVs to taxa across the environmental classes were compared.

This resulted in revised MCI TVs for 234 taxa. There were 12 taxa with insufficient data to generate revised TVs. All of the revised TVs reported here were assigned using an objective computational approach, whereas of the 180 original published scores, 133 were assigned by professional judgement. Further testing is required to determine whether the revised TVs are more or less sensitive to gradients of human impacts than the original TVs. Our preliminary analyses show that the revised TVs and resulting MCI site scores were correlated with existing TVs and MCI site scores, and also with catchment-scale measures of land use. Revised MCI site scores were generally, but not always, higher than original MCI scores. This was caused in part by increased revised TVs for many of the most common taxa in the full dataset (7 of the most common 10 taxa had a higher revised TV than their original TV). As such, while revised TVs and MCI site scores are likely to provide a sensitive indicator of human impacts on rivers and streams it may be necessary to also revise water quality

categories. For example, the original values place 15% of sites in the ‘excellent’ water quality category (MCI > 120) while the revised values place 57% of sites in this category.

We provide revised TVs for 234 taxa but note the following caveats:

1) Original and revised TVs must be used separately; they are not interchangeable or directly comparable. Back calculation of MCI site scores would be required for historical comparisons using the revised TVs. We recommend that revised MCIs are reported as MCI-2-hb.

2) How taxa without revised TVs are included or excluded from analyses should be reported to ensure transparency, especially when comparing between sites or over time.

3) A new water quality categorical scale may be required as MCI site scores based on revised MCI TVs are generally higher than those created using the original TVs.

4) Further testing is required to validate the sensitivity (in relation to human impacts on waterways) of the MCI scores developed using the revised TVs and to inform the need for development of a new water quality categorical scale.

1 Background

Regional councils routinely collect freshwater invertebrate samples as part of State of Environment and consent monitoring to assess the ecological condition of rivers throughout New Zealand. A key part of this monitoring involves the calculation of biotic indices, such as the Macroinvertebrate Community Index (MCI) and its quantitative variant (QMCI). These indices rely on the assumption that different aquatic invertebrates respond to human stressors in a consistent manner and that the environmental conditions at a site are reflected by the aquatic invertebrate community present. The MCI is designed to respond to human impacts on rivers and is calculated from taxon-specific tolerance values (TVs) considered to reflect sensitivity to organic pollution.

The MCI was first developed by Stark (1985) based on data obtained from gravel-bed streams on the Taranaki ring plain by Yvonne Stark in 1981-2 (Taranaki Catchment Commission 1984) and a user guide published in 2007 (Stark and Maxted 2007b). A version of the index for use in streams dominated by fine sediment (silt or sand) has also been created (MCI-sb: Stark and Maxted (2007a)). During the development of the original MCI for application in hard-bottomed streams (MCI-hb), individual taxa were assigned TVs using a weighting procedure based on the relative occurrence of taxa across three groups of sites differing in organic enrichment levels. The groups were assigned according to the degree of nutrient input they were likely to receive from local or upstream agricultural activities. TVs for rare taxa (and those added subsequently) were assigned by professional judgement. The MCI-sb was developed using an iterative computational process developed by Chessman (2003).

While MCI-hb and MCI-sb scores are commonly used to indicate state and trends in freshwater health throughout New Zealand, published TVs are not available for all taxa present. The most recently published MCI TVs (Stark and Maxted 2007) include a total of 190 taxa, of which hard-bottomed TVs are available for 180 taxa and soft-bottomed TVs for 159 taxa. However, there are currently 240 taxa identified (to genus) in the NIWA Freshwater Biodata Information System (FBIS). Although some groups such as Trichoptera have published TVs for all 38 taxa, other groups such as Diptera are missing published TVs for 22 of the 47 taxa in the FBIS master list.

This situation has resulted in MCI values being generated in inconsistent ways between and within regions. Some councils omit taxa without published TVs from their MCI calculations, while others assign TVs to these taxa based on their professional judgement. Thus, the identity of the taxa included in MCI calculations, and the tolerance values for taxa without published values may vary between regions, or even within the same region over time. Generating TVs for taxa that are currently missing them is an important step towards achieving regional and national consistency in MCI calculations.

Our objectives for this study were to use a national-scale aquatic invertebrate dataset to:

1. Develop an efficient R script which uses an objective computational process to produce TVs for as many taxa as possible, at a range of taxonomic levels, for both hard-bottomed and soft-bottomed streams.
2. Compare the newly generated TVs and resultant site MCI scores with the original TVs and MCI scores.

2 Methods and Results

2.1 Data sources

Benthic macroinvertebrate community composition data were obtained from regional council monitoring databases and from 66 sites of the National River Water Quality Network (NRWQN) operated by NIWA. The data were collected between 1990 and 2012 from 1388 sites distributed nationally (Figure 2-1).

2.1.1 Hard-bottomed and soft-bottomed streams

There are two MCI tolerance values assigned to many invertebrate taxa currently, the original MCI-hb TVs (Stark 1985) for use in streams with hard bed substrate and the MCI-sb variant (Stark and Maxted 2007a) for use in streams with soft bed substrate. As our goal was to generate tolerance values for taxa for both soft- and hard-bottomed streams we created two datasets by assigning sample data to one of the two bed substrate categories.

Sixty-eight percent of sites were classified as 'hard-bottomed' (HB) or 'soft-bottomed' (SB) a priori by regional councils. For the remaining 32% of the sites, we assigned bed substrate status using the 'segSubstrate' variable in the Freshwater Ecosystems of New Zealand database (FENZ; Leathwick et al. (2008)). SegSubstrate is the weighted average of proportional bed substrate, in categories of: 1 = mud, 2 = sand, 3 = fine gravel, 4 = coarse gravel, 5 = cobble, 6 = boulder, 7 = bedrock, predicted from a model fitted to field data from 8600 sites in the New Zealand Freshwater Fish Database (Leathwick et al. 2007). FENZ contains predicted values of this index for all stream segments (i.e. river length between tributary confluences) in New Zealand. Sites that were in a segment assigned a segSubstrate value <2 were classified as SB following the Stark et al. (2001) definition of soft-bottomed streams being greater than half the bed covered in sand/silt. We checked this classification of sites using the sites for which the regional councils had assigned the substrate categories. Of the 939 sites for which substrate type had been provided, 839 or 91% matched the SB/HB classification assigned using the segSubstrate variable.

Only 122 sites (8.8%) were classified as SB and they were relatively geographically restricted (Figure 2-1). We determined that these data were insufficient to enable the derivation of TVs for taxa from SB streams. Consequently, we limited our analyses to sites classified as HB, and thus can only generate MCI-hb TVs. The HB dataset comprised 10548 samples from 1266 sites. Individual sites had data from between 1 and 33 visits, with 205 sites visited once.

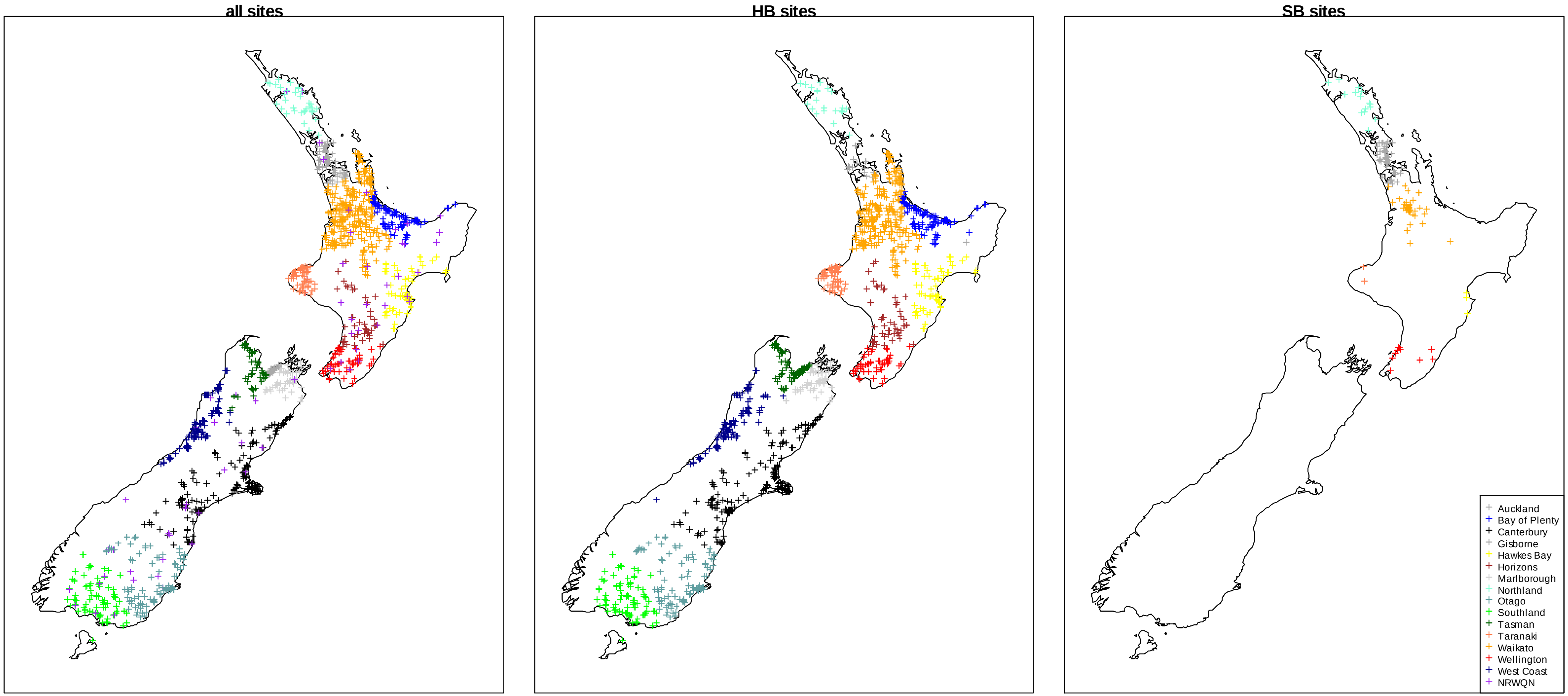


Figure 2-1: Distribution of invertebrate sampling sites showing all sites and those with hard (HB sites) and soft (SB sites) bed substrate. Sites are colour coded by their regional council or NRWQN source. Due to the limited number and restricted geographic distribution of SB sites these were excluded from further analyses.

2.1.2 Macroinvertebrate sample data processing

The macroinvertebrate samples from regional council monitoring sites were mainly, but not exclusively, collected using semi-quantitative kick-net sampling of a run or riffle habitat (Stark et al. 2001). At the 66 NRWQN sites seven quantitative Surber samples were collected from a riffle or run habitat and pooled into one sample (Scarsbrook et al. 2000). For all sites, samples were preserved in the field and invertebrates identified in the lab, generally to a level consistent with that of Stark and Maxted (2007b) for calculating the MCI.

Invertebrate abundances were recorded as either full counts of all individuals (65.9% of samples) or in coded abundance at 5 levels (34.1% of samples).The five-level scale had categories of 1-4, 5-19, 20-99, 100-499 and 500+ individuals (Stark 1998). For these sites, the lowest number of each category bracket was entered into the datasheet as the taxa abundance. To retain the greatest number of sites possible we included samples that were processed using either coded abundance or full count methods.

We removed any differences in taxonomic resolution across the dataset by collapsing all samples to one common taxon list. This collapsed the original list of 443 taxa to 348 taxa. The remaining taxa were identified to multiple taxonomic levels, for example the family Chironomidae, subfamily Chironominae, genus *Chironomus* and species *Chironomus zealandica.* These multiple taxonomic levels were collapsed so that all lower taxonomic levels were included in the relevant identified higher levels. Due to the relatively low number of samples with identifications to the species level the lowest taxonomic level that we provide TVs for is genus, giving a total of 234 taxa included in our analyses. To allow comparisons with historic MCI calculations we include tolerance values for *Aoteapsyche* and *Orthopsyche* individually, although these taxa have been collectively re-named *Hydropsyche.* By persisting with mainly generic TVs as for the existing MCI (rather than species-level) we also maintain overall compatibility with existing datasets.

2.2 Statistical process

2.2.1 Defining datasets

Individual sites in our dataset were sampled different numbers of times, with the potential for more impacted sites having been visited more often than sites less affected by human activities. In order to remove this bias, and create TVs based on a dataset representative of national aquatic invertebrate communities while still retaining information about as many taxa as possible, we created two datasets from the original dataset. Subsequent analyses were conducted on both of these datasets:

1. The full dataset with multiple and varying numbers of visits per site (10548 rows, 348 taxa) (full dataset).
2. A reduced dataset consisting of one randomly selected site visit selected for each site (1266 rows, ~310 taxa). This reduced dataset was generated 50 times, each time with a random sampling date selected for each site. For the 16% of sites that were only visited once, this sampling date was included in all 50 reduced datasets. For the remaining sites, a single date was randomly selected to be part of each of the 50 reduced datasets. Subsequent analyses were run on all 50 reduced datasets.

2.2.2 Classifying natural environmental gradients

As the desired outcome of the index was sensitivity to anthropogenic impacts, particularly organic pollution, we required datasets in which the predominant gradient in aquatic invertebrate community composition was related to human activities rather than natural spatial variation associated with geographic, climatic or hydrological differences between locations. In order to reduce natural environmental variation we classified sites by climatic and topographic parameters and generated TVs for taxa within each of these smaller datasets. Sites were categorised using the Climate and Source of Flow categories from the River Environment Classification (REC) database (Snelder et al. 2010). Within this database all stream segments in New Zealand have been categorised into six Climate and eight Source of Flow categories. We combined several of these categories to have sufficient sites within each class for analysis (Table 2-1). Both the full and reduced datasets were retained and also divided into the resulting eight Climate-Source of Flow classes, giving nine different sub-datasets for subsequent analysis (Table 2-1).

We did not group samples by season and considered the influence of temporal variation to be relatively minor. Evidence of this is in Stark & Phillips (2009) who showed that, for individual sampling sites, seasonal mean MCI values tended to be within ±3% of annual means. In addition, the majority of samples were collected in spring or summer (72%) and less than 1% of the samples were collected in winter, indicating that seasonal differences in aquatic invertebrate community composition should not be overly large.

Table 2-1: Sites were categorised by combined REC Climate and Source of Flow classes. The environmental categories used in the analysis (first column) were created from a combination of compiled REC Source of Flow categories (second column) and Climate categories (third column). The number of samples in the full and reduced datasets are indicated in the last two columns.

Class name	Compiled categories		Number of data rows (full dataset)	Number of sites (reduced dataset)
	Source of Flow	Climate		
H_D	Hill	Warm-dry, cool-dry	707	79
H_W	Hill	Warm-wet, cool-wet	2052	245
H_X	Hill	Warm-extremely wet, cool-extremely wet	940	87
L_D	Lowland	Warm-dry, cool-dry	1783	188
L_W	Lowland	Warm-wet, cool-wet	3501	473
L_X	Lowland	Warm-extremely wet, cool-extremely wet	752	120
Lk	Lake	All categories	288	29
M	Mountain, glacial mountain	All categories	525	45
All	All categories	All categories	10548	1266

2.2.3 Generating new taxa tolerance values

We followed the method of Chessman (2003), as it was previously applied to create the MCI-sb index (Stark and Maxted 2007a) and a wetland MCI (Suren et al. 2010). Analyses were run on all nine environmental categories (Table 2-1) for both the full dataset and for the 50 datasets within the reduced dataset group.

For each dataset, rank correlation coefficients were calculated between original MCI site scores and abundances of each taxon across all samples. To adjust for rare taxa, all correlation coefficients were expressed as a proportion of the maximum mathematically possible. Correlation coefficients adjusted in this way were then used to assign tolerance values. The original Chessman method describes that taxon with the highest positive adjusted correlation coefficient are assigned a 10 and the taxon with the most negative coefficient was assigned a 1. The remaining taxa are then assigned intermediate TVs (to the nearest integer) in proportion to their adjusted coefficients. From these new TVs a revised MCI score for each site was calculated. This process was then repeated up to 15 times until the TVs stabilised.

This process resulted in TVs for each taxon generated for the eight environmental classes separately and combined, for both the full and reduced datasets. The analysis on the full dataset resulted in one set of numbers, while the reduced dataset group resulted in 50 TVs generated for each taxon for each environmental class.

In general, we followed the Chessman method, as it was applied to generate the MCI-sb. We did, however, make one modification to this method. Within each iteration the new TVs values (between 1 and 10) are created from the adjusted correlation coefficients (ranging from 0 to 1). The original method of rescaling the correlation coefficients to TVs was found to assign a value of 10 only to the individual taxon with the highest correlation coefficient. Values of 1 to 9 had equal probability of being assigned to taxa, depending on their correlation coefficient. This resulted in no TVs of 10 being assigned to taxa once we had accounted for differences across REC classes. We adjusted this scaling process so that TVs of 1 to 10 had an equal probability of being assigned given an even distribution of correlation coefficients. This was achieved by first re-scaling the correlation coefficients such that they ranged between 0 and 10, and then rounding up to the next whole number. This alteration to the rescaling method used in the generation of the MCI-sb TVs led to slight changes in taxa tolerance values (Figure 2-2). However, the TVs generated using the two methods were highly correlated (r_s = 0.89, $p < 0.001$) and the new method had the benefit of generating final TVs of 10 (Figure 2-2). The results from the revised method are presented from here. See section 2.3.4 for details about development of the final TVs from the full and reduced datasets.

All analyses were conducted in R (R Development Core Team 2011), using scripts we have specifically created to efficiently implement the Chessman method. The script could be applied to other suitable datasets in the future and is available on request.

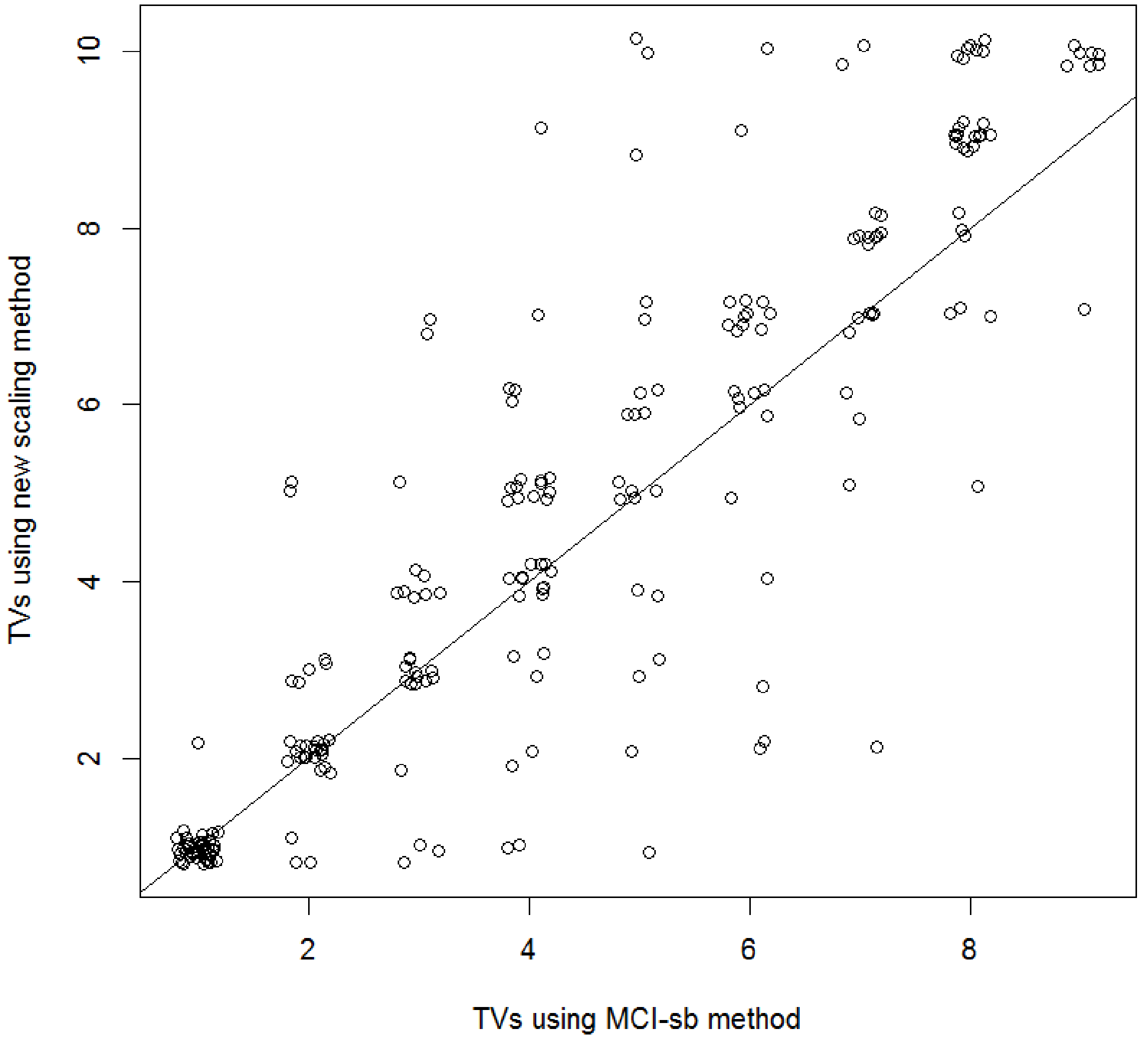


Figure 2-2: Comparison of taxa TVs generated using the MCI-sb method of assigning TVs from correlation coefficients and a revised scaling method. Points have been jittered (given a small random perturbation to prevent overplotting) for clarity.

2.3 Defining revised MCI-hb tolerance values

We investigated several methodological questions when determining how to assign the revised TVs to taxa:

2.3.1 Do different methods for analysing tied values produce different tolerance values?

The presence of some coded abundance data within our dataset (~ 34% of the full dataset) means that there are likely to be common taxon abundances between samples, which causes values to have duplicate rank orders (also known as 'ties') in the rank correlation procedure. The manner in which these tied values are dealt with by different rank correlation methods can lead to differences in reported correlation strengths. Kendall's rank correlation uses a tau-b statistic that accounts for tied values, but is computationally more intensive and takes longer to process than Spearman rank correlation. To explore the potential effects of using these two different rank correlation methods we ran a subset of the analyses using both Spearman rank (R_s) and Kendall tau-b correlation within the Chessman method.

Spearman rank correlation methods provided very similar TVs to Kendall tau-b rank methods when trialled with the Chessman method on one of the 50 reduced datasets. Over 91% of the taxa (210 taxa) had the same TV, while the TVs of the remaining 9% of taxa varied by 1 unit. As the Spearman rank correlation is computationally faster than Kendall tau-b, and because the majority of our dataset is full count, we used Spearman rank correlations in all further analyses.

2.3.2 Do taxon TVs vary across environmental classes, i.e., are we justified in assigning one national-scale TV to a taxon?

The differences in tolerance values from different environmental classes within the reduced datasets were examined graphically and statistically. Kruskal-Wallis rank sum tests were used to investigate the effect of environmental class on the generated tolerance values for each taxon across the 50 datasets.

Tolerance values generated for each taxon from the 50 reduced datasets varied between the 8 environmental classes (Appendix C). Of the 214 taxa that occurred in multiple environmental classes only 11 (5%) did not show a significant effect of environmental class on the resulting taxon TVs (Appendices C and E). While this supports the use of separate TVs for different environmental classes for taxa, it would make use of the MCI complex and difficult to implement. The graphs in Appendix C show that there is some overlap between many of the taxon TVs between environmental classes. Similarly, many of the density plots of taxon TVs generated across environmental classes show a relatively unimodal pattern (Appendix D). Based on this, and considering the difficulty of applying an MCI score if taxon TVs varied across environmental classes, we decided to assign one TV per taxon, while taking into account some of the variability across environmental classes. We generated these singular taxon TVs using the All-Sample-Mode and Mode-Iteration-Mode methods described below (see Section 2.3.3). Confidence limits are provided in Appendix A for TVs as a measure of the variability of TVs across environmental classes.

2.3.3 Does the method of assigning national-scale TVs across environmental classes affect the taxon TVs and resulting site MCI scores?

In the full dataset we calculated the average TV for each taxon across the eight environmental classes. In the reduced dataset the TV for each taxon was assigned in two different ways. Firstly, taxon TVs were assigned as the mode (the value that appears most often) of all TVs from across all 50 datasets and environmental classes (All-Sample-Mode). Secondly, because not all taxa occurred equally often in all environmental classes, we assigned taxon TVs as the overall mode of modes calculated for each environmental class across the 50 reduced datasets (Mode-Iteration-Mode). We compared TVs and resulting MCI site scores created using these two methods using rank correlations and mixed-effects regression models (MEMs) with random intercept (site) terms. Model simplification and Likelihood Ratio Test (LRTs) were used to test the significance of these models. LRTs measure the trade-off between explanatory power and model complexity. MEMs were fitted using the lme4 package (Bates et al. 2013) in R with Gaussian errors.

Taxon TVs generated from the 50 reduced datasets as the mode of all generated TVs (All-Sample-Mode) were very similar to those generated as the overall mode of modes within each environmental class (Mode-Iteration-Mode) when tested with rank correlation (Rs: 0.91, $p < 0.001$).

Site MCI-hb values generated using TVs from the All-Sample-Mode were also very similar to those generated using the Mode-Iteration-Mode method when tested with either rank correlation (Rs: 0.99, $p<0.001$) or with mixed effects models with a random intercept term to account for differences between sites (MEM: LRT: 33525, $p <0.001$). We used the All-Sample-Mode method to generate final revised taxa TVs across environmental classes.

2.3.4 Final assignment of revised TVs from the full and reduced datasets

The distribution of MCI-hb site scores in the full dataset had the potential to be biased towards lower values, as impacted sites are often monitored more often than less impacted sites. To more accurately reflect the environmental gradient present spatially across New Zealand we preferentially used TVs for taxa generated from the fifty reduced datasets. Tolerance values for taxa that had few samples in the reduced datasets were taken from the analyses applied to the full dataset (marked with an asterisk in Appendix A).

2.4 Comparing original and revised TVs for MCI taxa

2.4.1 Approach

We compared the original and revised TVs (and MCI-hb site scores; see following section) visually via frequency histograms. For statistical analysis, we used rank correlations, similar to Stark and Maxted (2007a) and Suren et al. (2010). We also used linear regression and mixed-effects regression models (MEMs) with random intercept (site) terms. Model simplification and Likelihood Ratio Test (LRTs) were used to test the significance of these models. LRTs measure the trade-off between explanatory power and model complexity. MEMs were fitted using the lme4 package (Bates et al. 2013) in R with Gaussian errors.

2.4.2 Output

We developed revised MCI-hb scores for 234 taxa, of which 161 had previous MCI-hb TVs (Appendix A). There were eighteen taxa that had existing MCI-hb TVs for which we did not generate revised TVs (Appendix B). There were no data to generate new scores for 12 of these taxa, two taxa are now synonymous with existing taxa, three taxa are semi-terrestrial taxa and unlikely to be affected by water quality (Collembola, *Dolomedes* and Staphylinidae), and one taxon (Diptera) we determined was too broad taxonomically to be assigned a meaningful TV (Appendix B).

Invertebrate TVs range from 1-10, to match the original range of MCI TVs. The original MCI-hb TVs were dominated by values of 3 and 5 (Figure 2-3). A value of 5 was assigned to taxa that were lacking information regarding their pollution tolerances when the MCI was originally developed. The revised MCI-hb TVs had a relatively uniform distribution, apart from a higher frequency of low values (1s; Figure 2-3).

The original TVs were significantly correlated with the revised TVs but the variance explained was not overly high (linear model, $F_{1, 159} = 60$, $p <0.001$, $R^2 = 0.27$; Figure 2-4). Of the 161 taxa that had original TVs, 23 taxa (14%) had the same value in the revised version , 41 taxa (25%) varied by ± 1 , 32 taxa (20%) varied by ± 2 , and 65 taxa (41%) varied by ± 3 or more (Appendix A). Thus, 59% of taxa were assigned revised MCI TVs ±2 from the original values. The largest difference between original and revised scores was a drop of 7 units for the mayflies *Isothralus* and *Siphlaenigma* from TVs of 8 and 9 to 1 and 2, respectively. Other taxa that showed relatively large changes (-5) between the original and revised TVs were *Tepakia, Zelandoptila, Taraperla, Scatella, Procordulia, Polyplectropus,* *Philorheithrus,* Pelecorhynchidae, *Austronella, Austrolestes, Antipodocholora, Nesoperla,* Tabanidae and *Triplectidina* (Appendix A).

While just under half of the 234 taxa (101 taxa, 43%) were found in more than 10% of the 1266 sites, many taxa were also relatively rare in the dataset (Appendix A). Almost a quarter of the taxa (57 taxa, 24%) were present at fewer than 10 sites. Several of the taxa that had the largest changes in revised TVs were these rarer taxa. For example, *Triplectidina, Scatella, Procordulia, Siphlaenigma, Nesoperla, Zelandoptila* and Pelecorhynchidae had TVs that altered by ≥5 from their original TVs and were found at only 3, 4, 8, 8, 9, 14 and 14 sites, respectively. Ten of the 43 taxa (23%) that had revised tolerance values that changed by four or more units were found in fewer than 10 sites. However, only 15 of the 118 taxa (13%) whose revised score changed by <4 units were found in 10 or fewer sites (Appendix A). The confidence intervals surrounding TVs for such rare taxa were often relatively large (Appendix A), indicating that our confidence in the assigned TVs for these taxa is lower than for taxa that are either more common, or may have more defined habitat preferences.

Many of the taxa that were assigned revised TVs of 1 were those commonly associated with slow flowing or standing waters e.g., mosquitoes and odonates and some mollusc and beetle taxa (Appendix A).

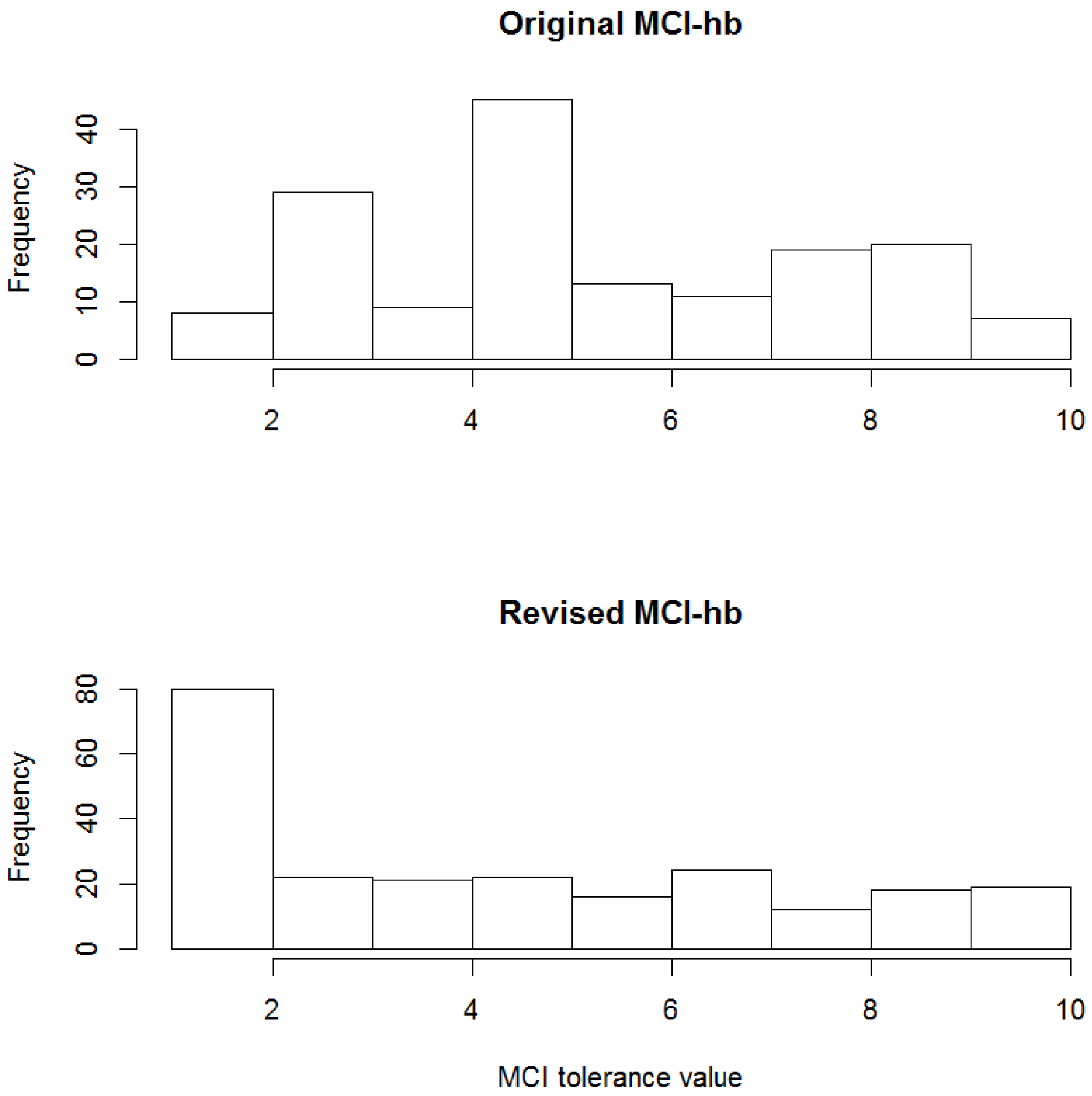


Figure 2-3: Histograms of MCI-hb tolerance values for taxa a) as originally reported by Stark and Maxted (2007b) and b) the revised MCI-hb. Revised MCI-hb TVs were generated for 234 taxa, while 161 of these had existing MCI-hb TVs.

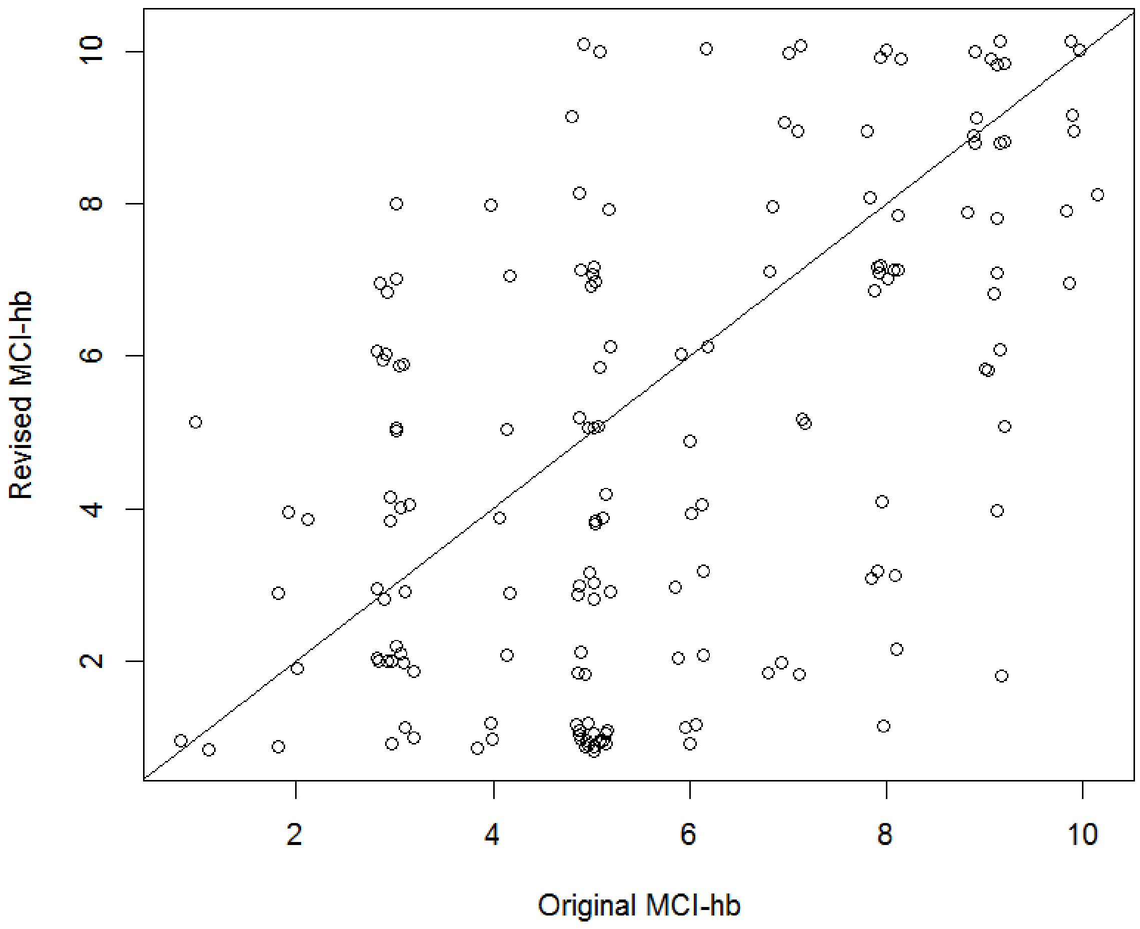


Figure 2-4: Original MCI-hb tolerance values (as reported in Stark and Maxted 2007b) and revised MCI-hb tolerance values for 161 taxa for which both values exist. Solid line is 1:1. Points have been jittered (given a small random perturbation to prevent overplotting) for clarity.

2.5 Comparing site MCI-hb scores calculated using original and revised TVs

2.5.1 Approach

We used correlation and MEMs analysis to compare original and revised MCI-hb site scores, as outlined in section 2.4.1.

2.5.2 Output

When tested across the full dataset MCI site scores generated using the original and revised taxon TVs were significantly correlated (R_s: 0.83, p <0.001; MEM random site (intercept) LRT: 7232, p <0.001). However, revised MCI-hb site scores generally were higher than original MCI-hb site scores (Figure 2-5). This resulted in more samples being classified as ‘excellent’ or ‘good’ water quality using the water quality categories provided by Stark and Maxted (2007b)(Figure 2-6, Table 2-2). More than half of the samples were classified as ‘excellent’ (i.e., >119) using the revised MCI-hb TVs compared to only 15% using the original TVs.

Table 2-2: Number and percentage of samples with MCI-hb site scores within the four water quality classes for MCI-hb as identified in Stark and Maxted (2007b) . MCI-hb site scores were calculated using both the original and revised MCI-hb tolerance values.

Current MCI Categories	Original MCI TVs		Revised MCI TVs	
	No. samples	Percentage	No. samples	Percentage
<80	1279	12%	552	5%
80-99	3973	38%	1205	11%
100-119	3725	35%	2816	27%
>119	1571	15%	5975	57%

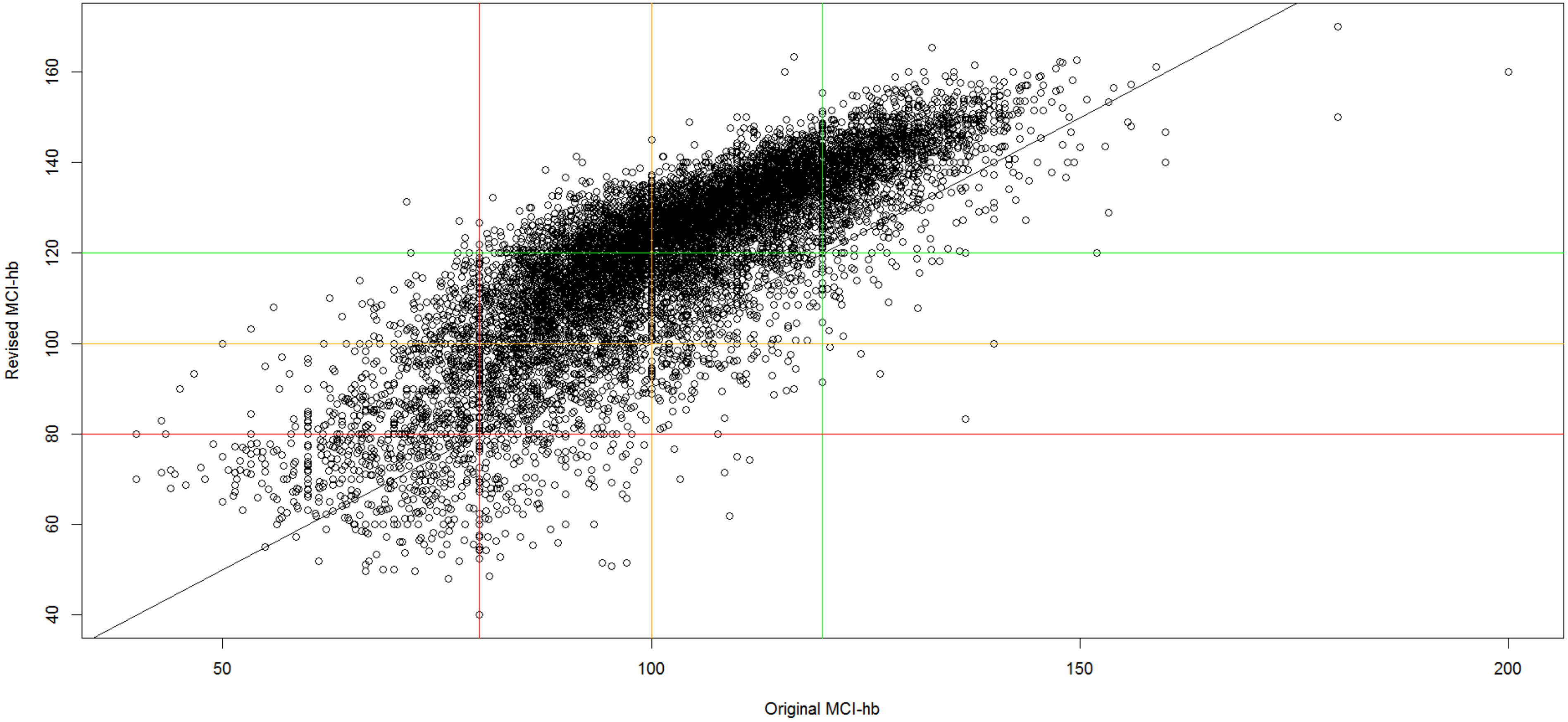


Figure 2-5: MCI-hb for all site visits (n = 10548) calculated from the original and revised MCI-hb taxa tolerance values. Horizontal and vertical lines delineate the water quality categories reported in Stark and Maxted (2007b): >120 = excellent, 100-120 = good, 80-100 = fair, < 80 = poor.

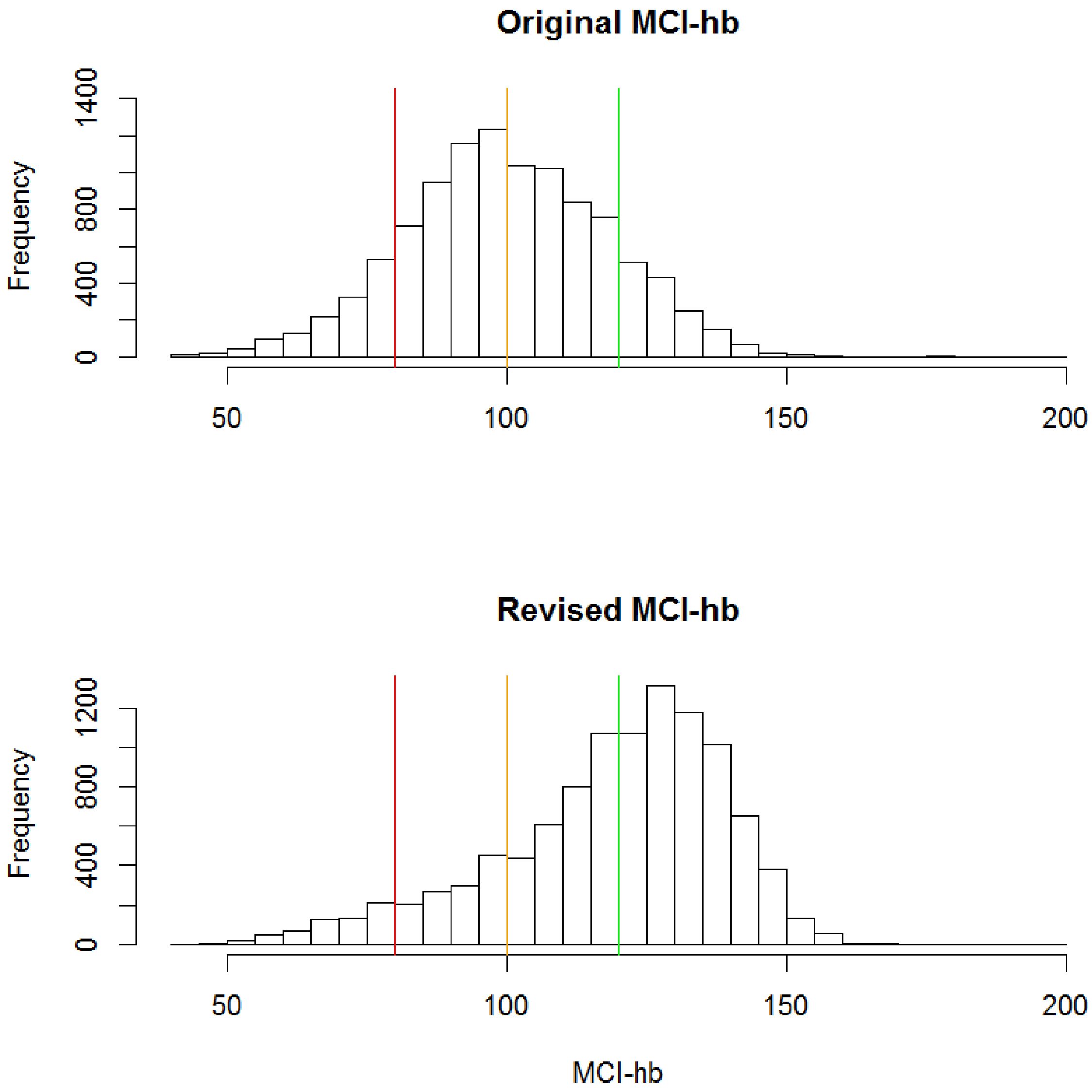


Figure 2-6: Frequency histograms for MCI site scores calculated using the original MCI-hb tolerance values in Stark and Maxted (2007b) and the revised values. Values were calculated for 10548 samples collected from a total of 1266 sites. Vertical lines delineate the water quality categories reported in Stark and Maxted (2007b): >120 = excellent, 100-120 = good, 80-100 = fair, < 80 = poor.

2.6 Comparing original and revised MCI-hb site scores with catchment land use

2.6.1 Approach

For each river segment containing a sampling site, catchment land use parameters such as the proportion of upstream land use in urban, pastoral and exotic forest were extracted from the REC database. The proportion of native land use in a catchment was calculated as the sum of scrub, tussock, wetland, bare ground and indigenous forest. MCI-hb sites scores generated using the original and revised TVs were calculated for one of the reduced datasets (one sample per site) and tested against the environmental parameters using Spearman rank correlation.

2.6.2 Output

The MCI-hb site scores calculated using original and revised MCI-hb TVs were both significantly related to the proportion of native, urban and pastoral land use in the upstream catchment, but not to exotic forest (Table 2-3, Figure 2-7).

Table 2-3: Spearman rank correlations (R_s) between upstream land use type and MCI-hb site scores generated using the original and revised TVs.

	Revised MCI-hb		Original MCI-hb	
	R_s	p	R_s	p
Native	0.54	<0.001	0.49	<0.001
Urban	-0.25	<0.001	-0.34	<0.001
Exotic forest	0.04	NS	0.01	NS
Pastoral	-0.53	<0.001	-0.52	<0.001

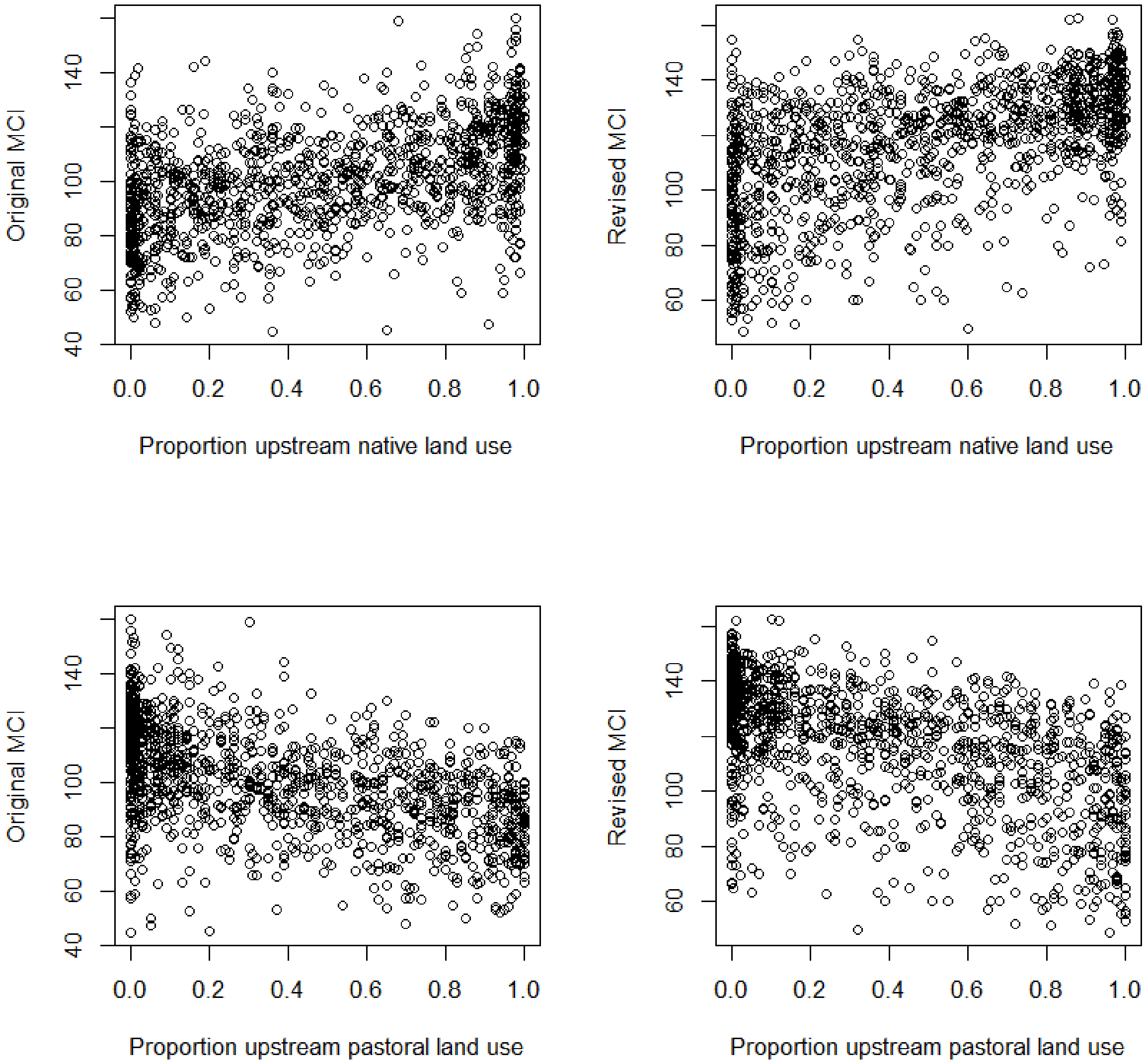


Figure 2-7: Scatterplots of MCI-hb site scores calculated from revised and original MCI TVs and the proportion of upstream land in pastoral and native land use.

3 Discussion

The goal of this report was to generate revised MCI TVs for as many freshwater invertebrate taxa as possible. Due to a limited dataset from soft-bottomed sites we could only generate revised values for the MCI-hb and not the MCI-sb. The newly generated TVs were not tested in detail here, as it was beyond the scope of this project. Although we did find correlation between the revised and existing MCI-hb TVs and resulting site scores, and similar correlations with land-use descriptors, the revised values require greater in-depth testing before we would recommend that they could routinely replace existing MCI-hb TVs. Also, the trend for higher site scores generated by the revised MCI TVs means that the two sets of TVs must be used independently and that current water quality indicator bands may need to be adjusted for use with the revised values.

Stark (1985) derived TVs for 69 macroinvertebrate taxa of which 47 were calculated based on data from organic enrichment gradients in Taranaki ring-plain streams. Original TVs for the other 22 taxa were not considered reliable (mostly because they were not well-represented in the data set) so TVs were assigned by professional judgment or adjusted by ±1 from the numerically derived TVs. Stark & Maxted (2007b) provided MCI-hb TVs for 180 taxa with, effectively, 133 of these having been assigned by professional judgment. In this report we document the derivation of revised MCI-hb TVs for 234 taxa, improving on the 180 taxa which had original TVs (Stark & Maxted 2007b), and using an efficient objective numerical process based on the distributions and abundances of taxa within real-world datasets from throughout New Zealand. Further testing against measures of human impacts will be required in order to confirm whether or not the objective numerical process has produced biotic indices that perform better than the existing MCI-hb which was derived much more subjectively.

Revised MCI-hb TVs generally, but not always, resulted in higher MCI site scores than the original TVs. This was caused by generally higher average taxa TVs for samples within the dataset. When we examined the number of occurrences of taxa with different TVs across the full dataset there were proportionally more occurrences of taxa with TVs of 4, 6, 7, 8 and 9 when the new TVs were used. There were proportionally more occurrences of taxa with TVs of 1, 2, 3, 5 and 10 when the original TVs were used. At least part of the general trend for higher revised than original MCI-hb scores in many sites was caused by an increase in revised TVs for some relatively common taxa. Of the ten most common taxa in the full dataset (present in most number of samples), seven taxa had revised TVs that were higher than their original values (Chironomidae, Orthocladiinae, *Potamopyrgus, Hydrobiosis, Aoteapsyche,* Tipulidae and Oligochaeta). One taxon had a lower revised TV (*Deleatidium*) and TVs remained the same for two taxa (Elmidae and Eriopterini). The number of samples from our dataset in the ‘excellent’ water quality category of Stark and Maxted (2007b) increased from 15% to 50% when the new TVs were used. This will have large implications for how sites are categorised and highlights the fact that the two sets of TVs must be used independently. Back calculations of MCI using the revised TVs will be required for historical comparisons, otherwise there is potential for historically ‘fair’ water quality sites to appear to suddenly have ‘excellent’ simply because a different set of TVs were used. However, while the overall value of the MCI site scores has increased in many sites with use of the revised TVs the rank order of sites remains generally similar. Thus, the change in MCI site scores with the revised TVs may not necessarily be a problem for water managers. This is because their focus, we believe, should remain on raising the standard of rivers that are in relatively poor condition and protecting the rivers that are in relatively good condition.

One solution to the general shift upwards in MCI site scores with the revised TVs is to redistribute the water quality categories. For example, Taranaki Regional Council has adapted the existing stream health assessment categories to six by sub-dividing the best and worst categories (Table 4-1). Such a revised water quality scale could be used with the revised MCI-hb TVs. Under this grading only 12% of samples from our dataset are now in the highest water quality class, however 83 % are still classified as between 'Good' and 'Excellent' (Table 4-1). Using the original MCI TVs 50% of samples were classified in this range (Table 3-1).

Table 3-1: Taranaki Regional Councils MCI categories of biological water quality conditions adapted for Taranaki streams. The number and percentage of samples in our dataset occurring in each category using the revised MCI-hb TVs are indicated.

Grading	MCI	No. samples	% samples
Excellent	140+	1232	12
Very Good	120 – 139	4562	43
Good	100 – 119	2923	28
Fair	80 – 99	1222	11
Poor	60 – 79	536	5
Very Poor	<60	73	1

Our results suggested that there was some justification for each taxon to have different TVs for separate environmental classes of river. However, we decided that the use of an index with multiple taxon values would be difficult to implement consistently. In developing the singular taxon TVs we attempted to account for environmental variation in TVs by taking the most commonly occurring value for each taxa across the environmental classes. It should also be noted that taxa that were only rarely found in our samples, or those with general habitat requirements, often showed more variation in their TVs across and within environmental classes. Less confidence can be associated with the final TVs for these taxa (marked with an asterisk in Appendix A). While we used the largest and most up to date dataset available, we could not generate revised TVs for all taxa. The creation of R code to run the scripts means that this analysis could be repeated in the future if more detailed and expansive datasets become available. In the meantime, we recommend that existing MCI-hb TVs are used for the 12 taxa with insufficient data to revise values. Taxa that have neither existing nor revised values could be omitted from MCI calculations or TVs could be assigned by professional judgement. Whatever the case, it is important that the list of TVs used is documented by reference to a published list and that any additions or alterations are noted.

Many taxa that are more commonly associated with slow flowing or standing water (such as some odonates, beetles and diptera) were assigned revised TVs of 1. This value may reflect their preference for such habitats, rather than their organic pollution tolerance, per se. These taxa, being comparatively rare in stony streams, are unlikely to have a marked influence on health assessments for hard-bottomed streams. However, if the resulting MCI (or QMCI etc.) was applied to a still water habitat, where these taxa may predominate, then the resulting index could under-estimate the 'true' health of that system. For this reason we recommend that this version of the MCI is used only in hard-bottomed streams. However, if biotic indices are used for detecting trends in river health (where the absolute value of the indices are of lesser importance) then the new indices may prove useful for detecting trends in weedy or slow-flowing streams.

In our current analysis we have resisted the temptation to manually alter any of the TVs because we wanted the TV derivation process to be as objective as possible. Furthermore, without specific ‘rules’ to guide any manual TV changes it would be difficult to know where to stop and we could end up with many TVs effectively being assigned by professional judgment.

4 Closing remarks

In deriving new TVs for calculation of MCI, SQMCI, and QMCI values we have retained the (mainly) genus level of identification used previously. This was due to a lack of species-level data but also enables existing datasets to be used with the new indices and retains the cost-effectiveness of MCI-based stream-health assessments.

The new version of the MCI (or SQMCI and QMCI) calculated using the new TVs is intended primarily for hard-bottomed streams. It is likely to under-estimate the health of weedy, soft-bottomed, or slow-flowing waterways.

Taxa that we have been unable to provide revised TVs for may be encountered. These can be omitted from the MCI calculation, TVs from the existing indices can be substituted, or, in the absence of existing TVs, they could be assigned by professional judgment. Any report using the MCI should make it very clear what list of TVs has been used and highlight any additions or alterations.

In light of this, we suggest that MCI site scores calculated using the revised TVs should be labelled MCI-hb-2 in all reports and databases. This would help clarify differences with the original Stark (1985) MCI.

The two hydropsychid caddisfly genera, *Aoteapsyche* and *Orthopsyche*, are now considered to belong to the genus *Hydropsyche* (Geraci, 2007). Since the new TVs for these taxa are both 7, data for these taxa should be combined before calculating MCI values from historic datasets.

If trends testing of stream health based on the MCI (or related indices) is to be undertaken, the TVs used for index calculation must be the same throughout the entire time-series. This also applies to comparisons of MCI values between sites. MCI values calculated using the new TVs are not directly comparable with existing MCI values.

An expanded six-level scale of interpretation is recommended: Excellent (140+), Very Good (120-139), Good 100-119), Fair (80-99), Poor (60-79), Very Poor (<60). This is expected to apply to hard-bottomed streams only (although the indices can be applied to other stream types if trends testing is the aim (rather than evaluation of stream health).

There is still a need to undertake further testing of the performance of the indices based on the new TVs before we can recommend widespread adoption.

5 Acknowledgements

Our thanks to all the people that collected, processed and collated the Regional Council and NRWQN dataset.

6 References

Bates, D., B. M. Bolker, M. Maechler, and S. Walker. 2013. lme4: linear mixed effects models using Eigan and S4 R package version 1.0-4.

Chessman, B. C. 2003. New senstivity grades for Australian river macroinvertebrates. Marine and Freshwater Research **54**:95-103.

Leathwick, J. R., K. Julian, J. Elith, W. L. Chadderton, S. Ferrier, and T. H. Snelder. 2008. A biologically-optimised environmental classification of New Zealand rivers and streams: reanalysis excluding human impact variables. Prepared for the Department of Conservation, NIWA, Hamilton, NIWA client report HAM2008-027.

Leathwick, J. R., K. Julian, J. Elith, S. Ferrier, and T. H. Snelder. 2007. A biologically-optimised environmental classification of New Zealand rivers and streams Prepared for the Department of Conservation, NIWA client report: HAM2007-043.

R Development Core Team. 2011. R: A language and environment for statistical computing. R Foundation for Statistical Computing, URL http://www.R-project.org, Vienna, Austria.

Scarsbrook, M. R., I. K. G. Boothroyd, and J. M. Quinn. 2000. New Zealand's National River Water Quality Network: long-term trends in macroinvertebrate communities. New Zealand Journal of Marine and Freshwater Research **34**:289-302.

Snelder, T. H., B. Biggs, and M. Weatherhead. 2010. New Zealand River Environment Classification User guide. Prepared for the Ministry for the Environment.

Stark, J. D. 1985. A Macroinvertebrate Community Index of water quality for stony streams.

Stark, J. D. 1998. SQMCI: a biotic index for freshwater macroinvertebrate coded-abundance data. New Zealand Journal of Marine and Freshwater Research **32**:55-66.

Stark, J. D., I. K. G. Boothroyd, J. S. Harding, J. R. Maxted, and M. R. Scarsbrook. 2001. Protocols for sampling macroinvertebrates in wadeable streams. New Zealand Macroinvertebrate Working Group Report No. 1, Prepared for the Ministry for the Environment.

Stark, J. D., and J. R. Maxted. 2007a. A biotic index for New Zealand's soft-bottomed streams. New Zealand Journal of Marine and Freshwater Research **41**:43-61.

Stark, J. D., and J. R. Maxted. 2007b. A user guide for the Macroinvertebrate Community Index. Prepared for the Ministry for the Environment.

Stark, J. D., and Phillips, N. 2009. Seasonal variability in the Macroinvertebrate Community Index: are seasonal correction factors required? New Zealand Journal of Marine and Freshwater Research **43**: 867-882.

Suren, A. M., J. Stark, J. A. Wech, and P. Lambert. 2010. Development of a South Island Wetland Macroinvertebrate Community Index Score. NIWA report no:CHC2010-0, Prepared for Department of Conservation, West Coast Regional Council and Environment Southland.

Taranaki Catchment Commission. 1984. Taranaki Ring Plain Water Resources: Freshwater Biology. Taranaki Catchment Commission. 196p.

Taranaki Regional Council. 2014. Fresh water macroinvertebrate fauna biological monitoring programme annual State of Environment Monitoring report 2012-2013. Taranaki Regional Council Technical Report No. 2013-48: 247p.

Appendix A Revised MCI-hb tolerance values for freshwater invertebrate taxa.

The revised MCI-hb tolerance value for each taxon is the mode of values generated following the method of (Chessman 2003) across eight environmental classes and 50 reduced datasets with one sample per site. Five and 95 percent confidence intervals are reported, as well as the number of environmental classes each taxon occurred in. The original MCI-hb tolerance values are as reported in Stark and Maxted (2007b). *tolerance values were generated from the full dataset including all site visits for poorly-represented taxa in the dataset. **Note that values for *Aoteapsyche* and *Orthopsyche* are provided separately in this table. They are now both renamed *Hydropsyche*, however the larvae have different habitat requirements and could be kept separate as *Hydropysche* (*Aoteapsyche* group) and *Hydropsyche* (*Orthopsyche* group; B. Smith, pers comm.). Bold, and underlined text indicates where a taxa at a higher taxonomic level includes those listed below.

Taxa	Original MCI-hb value	Revised MCI-hb value	5% CI	95% CI	No. REC categories	No. sites
COELENTERATA						
Cnidaria/*Hydra*	3	2	1.0	4.0	6	76
PLATYHELMINTHES	3	4	3.0	8.0	8	643
Temnocephala	-	5	5.0	9.0	2	3
Cura	-	1	1.0	7.0	4	33
Neppia	-	9	7.0	10.0	2	4
NEMATODA	3	5	1.0	6.0	8	376
NEMATOMORPHA	3	6	1.0	10.0	8	111
NEMERTEA	3	2	1.0	5.0	8	299
OLIGOCHAETA	1	5	2.0	5.0	8	1073
Lumbricidae	-	2	1.0	7.0	4	49
POLYCHAETA	-	6	2.0	10.0	5	31
*Scolecolepides**	-	4	2.0	5.7	1	1
HIRUDINEA	3	2	1.0	7.0	8	217
Alboglossiphonia	-	1	1.0	6.0	2	7
Barbronia	-	1	1.0	2.0	2	2
Placobdelloides	-	1	1.0	2.0	2	3
CRUSTACEA	-					
Amphipoda	5	4	1.0	5.0	8	694
Chiltonia	-	5	1.1	10.0	2	11
Gammaridae*	-	2	2.0	5.9	1	1
Orchestia	-	9	3.4	9.0	3	8
Paracalliope	5	5	1.0	7.0	8	389
Paracorophium	-	1	1.0	10.0	3	3
Paraleptamphopidae	-	6	1.0	8.0	8	98
Paraleptamphopus	5	7	2.0	8.0	6	84
Phreatogammarus	-	4	2.0	7.0	6	58

Talitridae	-	3	2.0	8.0	7	66
Isopoda	5	4	1.0	9.0	8	133
Austridotea	-	7	1.0	9.0	2	3
Phreatoicidae	-	3	1.2	7.0	3	11
Phreatoicus	-	2	1.0	7.6	3	9
Cladocera	5	1	1.0	6.0	7	109
Daphnia	-	1	1.0	10.0	3	4
*Simocephalus**	-	1	1.0	1.0	1	1
Copepoda	5	1	1.0	5.0	7	128
Cyclopoida	-	1	1.0	8.0	2	2
Ostracoda	3	3	1.0	6.0	8	662
Herpetocypris	-	5	2.0	6.0	3	8
Tanaidacea	4	1	1.0	8.0	5	11
Decapoda						
*Amarinus**	-	2	1.0	3.0	1	7
*Helice**	-	4	1.0	4.0	1	1
*Hemigrapsus**	-	2	2.0	2.0	1	1
Paranephrops	5	1	1.0	5.0	7	177
Paratya	5	4	1.0	6.0	8	296
Mysidae	-	1	1.0	9.2	2	5
*Tenagomysis**	-	3	1.0	2.0	1	1
INSECTA						
Ephemeroptera						
Acanthophlebia	7	9	3.4	10.0	6	121
Ameletopsis	10	10	4.6	10.0	8	189
Arachnocolus	8	4	1.5	7.5	4	48
Atalophlebioides	9	6	2.0	8.0	8	48
Austroclima	9	6	3.0	8.0	8	698
Austronella	7	2	1.0	6.0	5	35
Coloburiscus	9	9	6.0	10.0	8	811
Deleatidium	8	7	6.0	10.0	8	1078
Ichthybotus	8	9	4.0	10.0	7	144
*Isothraulus**	8	1	1.0	9.0	1	2
Mauiulus	5	3	1.8	9.0	8	124
Neozephlebia	7	7	3.0	10.0	8	346
Nesameletus	9	8	7.0	10.0	8	618
Oniscigaster	10	7	2.0	10.0	7	76
Rallidens	9	7	2.0	10.0	7	137
Siphlaenigma	9	2	2.0	3.0	3	8
Tepakia	8	2	1.0	3.0	3	23

Zephlebia	7	5	2.0	8.0	8	601
Plecoptera						
Acroperla	5	7	4.0	10.0	6	203
Austroperla	9	9	5.0	10.0	8	370
Cristaperla	8	10	3.0	10.0	4	8
Megaleptoperla	9	7	3.0	10.0	8	339
Nesoperla	5	10	4.0	10.0	3	9
Spaniocerca	8	7	2.0	9.1	7	168
Spaniocercoides	8	10	5.0	10.0	3	7
Stenoperla	10	9	8.0	10.0	8	438
Taraperla	7	2	2.0	10.0	6	50
Zelandobius	5	7	4.0	9.0	8	625
Zelandoperla	10	8	6.0	10.0	8	567
Megaloptera						
Archichauliodes	7	8	6.0	9.0	8	903
Odonata						
*Aeshna**	5	1	1.0	1.0	1	6
Anisoptera	5	1	1.0	3.5	6	91
Antipodochlora	6	1	1.0	4.0	5	57
Austrolestes	6	1	1.0	8.0	4	32
Hemicordulia	5	1	1.0	5.2	4	22
Ischnura	-	1	1.0	2.6	2	10
Procordulia	6	1	1.0	7.0	3	8
Xanthocnemis	5	1	1.0	2.0	8	216
Hemiptera						
Anisops	5	1	1.0	3.5	8	54
Diaprepocoris	5	1	1.0	1.0	4	7
Hydrometra	-	1	1.0	2.0	2	396
Mesovelia	-	1	1.0	2.0	3	4
Mesoveliidae	-	1	1.0	4.0	4	7
Microvelia	5	1	1.0	6.0	8	208
Saldidae	5	3	1.0	8.2	6	45
Saldula	-	4	1.0	8.0	6	34
Sigara	5	2	1.0	8.0	8	248
Coleoptera						
Dytiscidae	5	1	1.0	6.0	8	134
Antiporus	5	1	1.0	4.0	5	26
*Huxelhydrus**	-	1	1.0	2.8	1	1
Lancetes	-	3	1.0	3.0	3	3
Liodessus	5	1	1.0	5.0	5	27

Rhantus	5	1	1.0	1.0	4	21
Elmidae	6	6	5.0	9.0	8	1117
Gyrinidae*	-	5	4.4	7.3	1	1
Hydraenidae	8	8	4.0	10.0	8	241
*Homalaena**	-	8	9.0	9.9	1	1
Orchymontia	-	9	4.0	10.0	4	14
Hydrophilidae	5	3	2.0	8.0	8	1058
Berosus	5	4	1.0	9.0	8	159
Enochrus	5	1	1.0	4.0	2	3
Ptilodactylidae	8	8	2.0	10.0	8	271
Scirtidae	8	7	2.4	10.0	8	158
Neuroptera						
Kempynus	5	2	1.0	8.0	4	12
*Sisyra**	-	2	2.0	2.0	1	1
Diptera						
Austrosimulium	3	6	4.0	8.0	8	1064
Blephariceridae	-	10	5.0	10.0	7	92
Neocurupira	7	10	5.0	10.0	7	80
Peritheates	7	10	3.0	10.0	3	6
Ceratopogonidae	3	6	2.0	9.0	8	275
Ceratopogoninae	-	5	1.0	9.0	3	5
Chironomidae	2	4	3.0	6.0	8	1240
Chironominae	-	4	2.0	6.0	8	1108
Chironomini	-	4	1.0	7.0	8	684
Chironomus	1	1	1.0	3.0	8	268
Harrisius	6	2	1.0	7.0	6	98
Paucispinigera	6	3	2.5	9.5	5	6
Polypedilum	3	2	1.0	10.0	8	524
Tanytarsini	3	5	2.0	7.0	8	779
Tanytarsus	3	7	2.0	9.0	8	277
Diamesinae	-	7	3.0	8.0	8	815
Lobodiamesa	5	3	1.0	8.0	4	22
Maoridiamesa	3	7	3.0	9.0	8	589
Orthocladiinae	2	4	3.0	6.0	8	1205
Corynoneura	2	2	1.0	5.0	5	40
Cricotopus	-	10	2.0	10.0	5	28
Naonella	-	1	1.0	10.0	6	35
Pirara	-	10	2.0	10.0	5	18
Stictocladius	-	7	3.0	10.0	8	65
Podonominae	8	7	1.0	10.0	7	163

Parochlus	8	10	3.9	10.0	5	64
Tanypodinae	5	5	3.0	6.0	8	860
Culicidae	3	1	1.0	2.0	7	57
Culex	3	1	1.0	1.0	4	29
Dixidae	4	3	1.0	10.0	8	294
Nothodixa	4	7	2.0	10.0	7	84
Paradixa	4	2	1.0	7.0	7	235
Dolichopodidae*	3	6	4.0	7.0	1	5
Empididae	3	6	3.0	8.0	8	523
Ephydridae	4	4	1.0	6.0	8	194
*Brachydeutera**	-	6	5.0	6.7	1	1
Ephydrella	-	1	1.0	7.0	6	10
Scatella	7	2	1.0	4.2	3	4
Muscidae	3	4	2.0	6.0	8	765
Limnophora	3	4	4.0	5.0	2	2
Pelecorhynchidae	9	4	4.0	9.0	4	14
Psychodidae	1	1	1.0	8.0	7	154
Sciomyzidae	3	2	1.0	5.0	6	36
Neolimnia	3	2	2.0	10.0	2	6
Stratiomyidae	5	2	1.0	4.1	8	94
Tabanidae	3	8	3.0	9.0	8	226
Tanyderidae	-	6	2.0	10.0	8	246
Thaumaleidae	9	6	2.0	8.0	2	3
Tipulidae	5	8	5.0	9.0	8	1101
Aphrophila	5	9	5.0	10.0	8	879
Eriopterini	9	9	5.0	9.0	8	1038
Hexatomini	5	5	3.0	10.0	8	420
Limoniinae	-	8	5.0	9.0	8	1097
Limonia	6	5	1.0	10.0	7	102
Molophilus	5	6	2.0	9.0	8	209
Paralimnophila	6	3	2.0	10.0	8	228
Zelandotipula	6	2	1.0	5.0	8	93
Trichoptera						
Alloecentrella	9	10	2.0	10.0	6	29
Beraeoptera	8	7	5.0	10.0	8	336
Confluens	5	7	3.0	10.0	8	133
Diplectrona	9	10	9.5	10.0	2	3
Oecetis	6	4	1.0	8.0	7	92
Olinga	9	9	6.0	10.0	8	793
Philorheithrus	8	3	2.0	10.0	7	74

Pycnocentrella	9	10	3.0	10.0	7	28
Pycnocentria	7	5	5.0	9.0	8	879
Pycnocentrodes	5	6	4.0	9.0	8	978
Rakiura	10	8	5.0	9.1	3	7
Triplectides	5	3	1.0	10.0	8	480
Triplectidina	5	10	4.0	10.0	2	3
Zelandoptila	8	3	2.0	6.5	6	14
Zelolessica	10	10	2.0	10.0	6	94
Ecnomidae	-	2	1.0	8.6	5	37
Helicopsyche	10	9	7.0	10.0	8	484
Hudsonema	6	4	2.0	7.0	8	686
Hydrobiosella	9	10	6.0	10.0	8	1176
Hydrobiosidae	-	5	5.0	9.0	8	1109
Costachorema	7	9	5.0	9.0	8	730
Edpercivalia	9	10	4.0	10.0	6	15
Hydrobiosis	5	8	5.0	9.0	8	122
Hydrochorema	9	9	5.0	10.0	8	2
Neurochorema	6	6	4.0	9.0	8	611
Psilochorema	8	7	5.0	9.0	8	974
Tiphobiosis	6	10	1.0	10.0	8	49
Hydropsychidae	-	9	4.0	9.0	8	929
*Aoteapsyche***	4	8	4.0	9.0	8	1003
*Orthopsyche***	9	8	2.0	10.0	8	229
Hydroptilidae	-	3	1.0	4.0	8	95
Oxyethira	2	3	1.0	5.0	8	925
Paroxyethira	2	1	1.0	3.0	8	183
Oeconesidae	9	5	1.0	10.0	8	154
Oeconesus	-	1	1.0	10.0	8	101
*Zelandopsyche**	-	8	8.0	10.0	1	1
Polycentropodidae	-	4	3.0	9.0	8	520
Plectrocnemia	8	7	4.0	10.0	8	241
Polyplectropus	8	3	2.0	9.0	8	363
Lepidoptera						
Hygraula	4	1	1.0	8.0	7	95
Mecoptera						
Nannochorista	5	7	2.0	9.0	4	10
ACARINA	5	3	1.0	7.0	8	711
*Arrenurus**	-	1	2.0	2.0	1	1
*Hydrachna**	-	1	1.0	1.0	1	528
Limnesiidae*	-	4	4.0	5.0	1	1

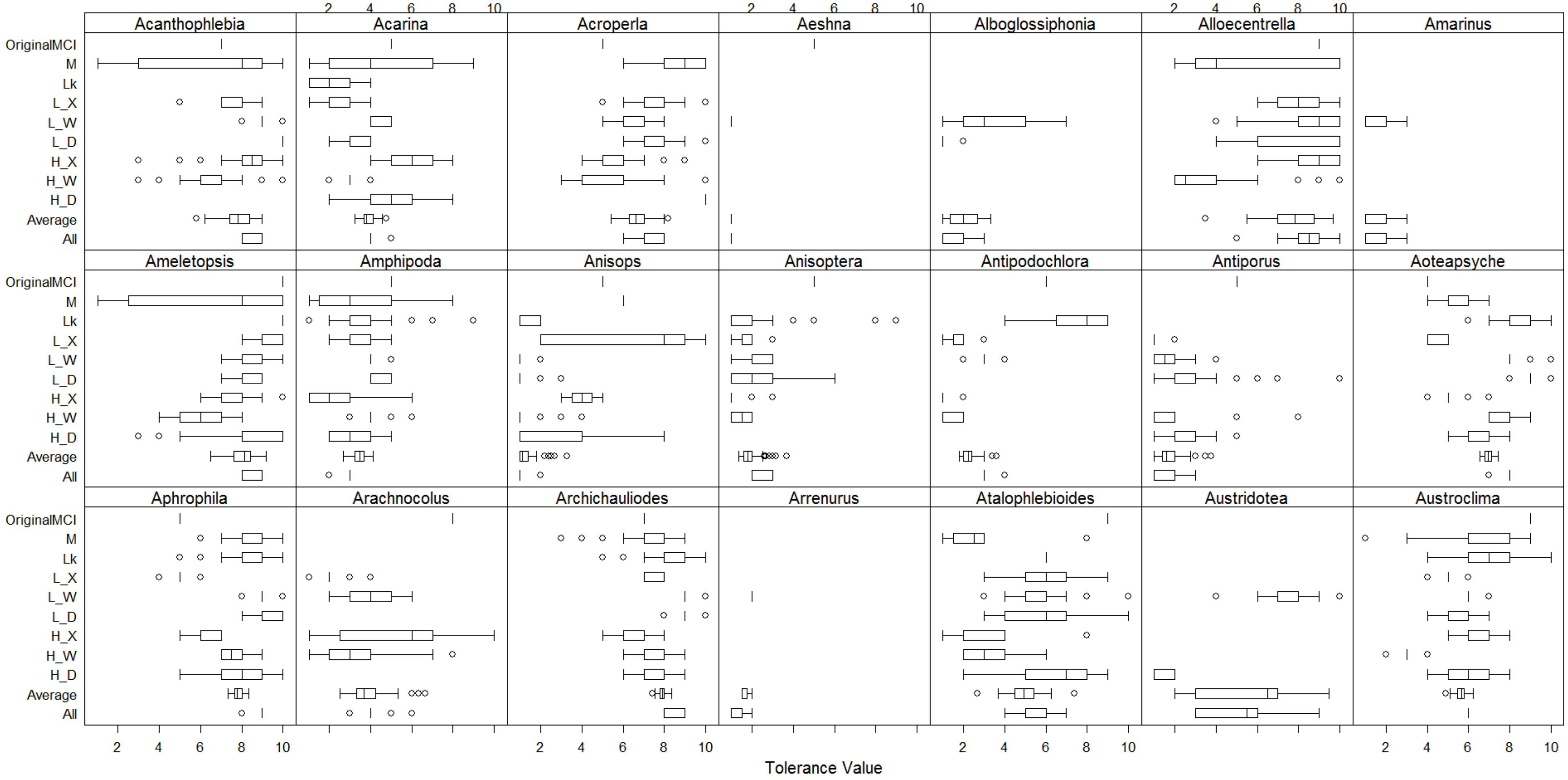
Oribatida	-	1	1.0	8.0	5	34
Piona	5	1	1.0	5.0	2	2
*Zelandobates**	-	7	4.0	6.0	1	22
MOLLUSCA						
Ferrissia	3	4	1.0	6.0	7	160
Glyptophysa	5	1	1.0	4.8	4	9
Gyraulus	3	3	1.0	5.0	8	287
Hyridella	3	5	3.0	10.0	3	10
Latia	3	7	2.0	7.0	8	175
Melanopsis	3	3	1.0	9.0	5	20
*Nucula**	-	7	5.0	7.0	1	1
Physella	3	2	1.0	8.0	8	524
Potamopyrgus	4	5	3.0	6.0	8	1152
Lymnaeidae	3	1	1.0	6.0	7	138
Austropeplea	3	7	1.0	9.0	4	9
Pseudosuccinea	4	1	1.0	8.0	2	4
Sphaeriidae	3	2	1.0	5.9	8	367
Sphaerium	-	3	1.0	6.0	6	140

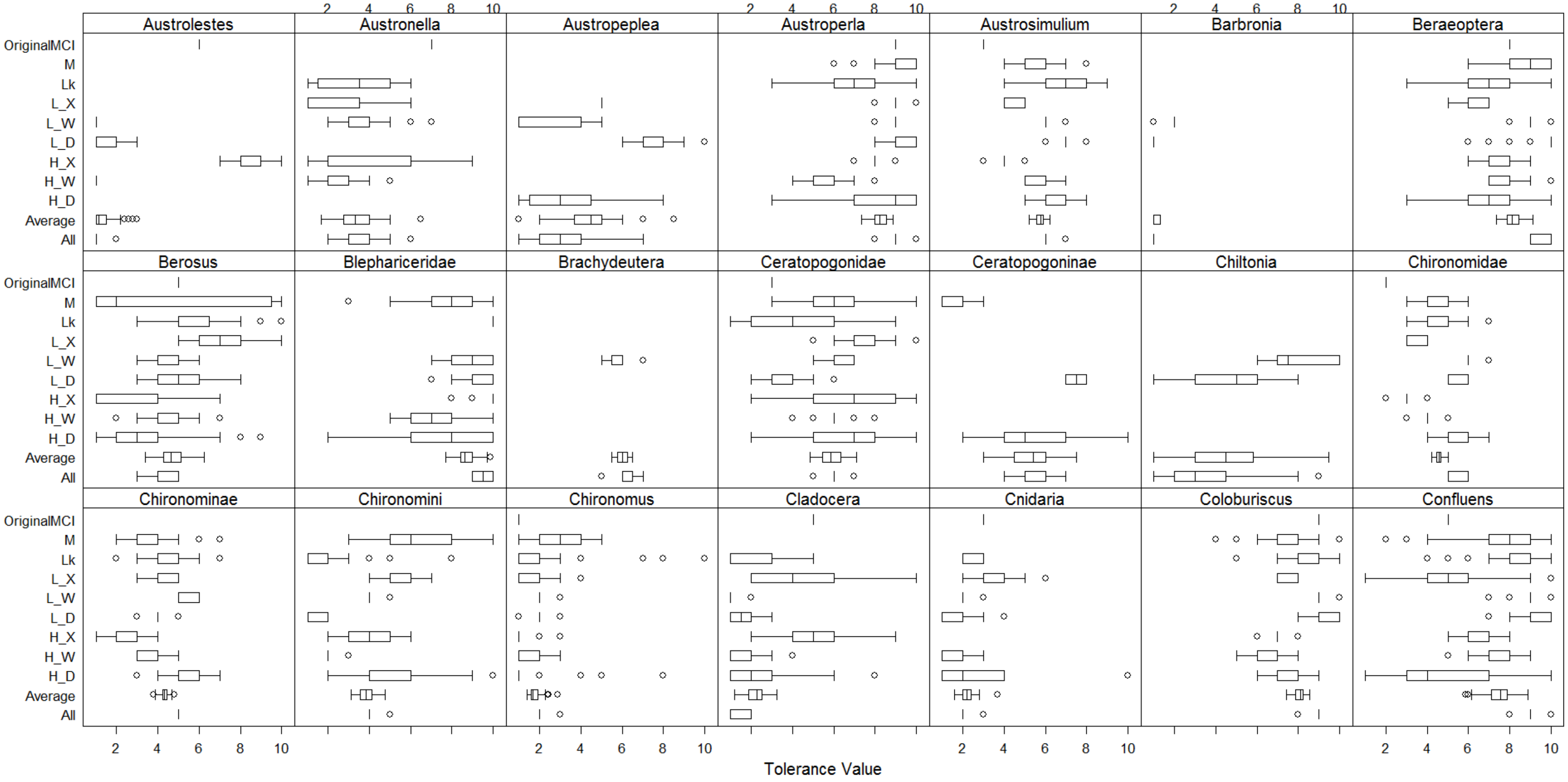
Appendix B Taxa with existing MCI-hb tolerance values for which revised scores were not generated

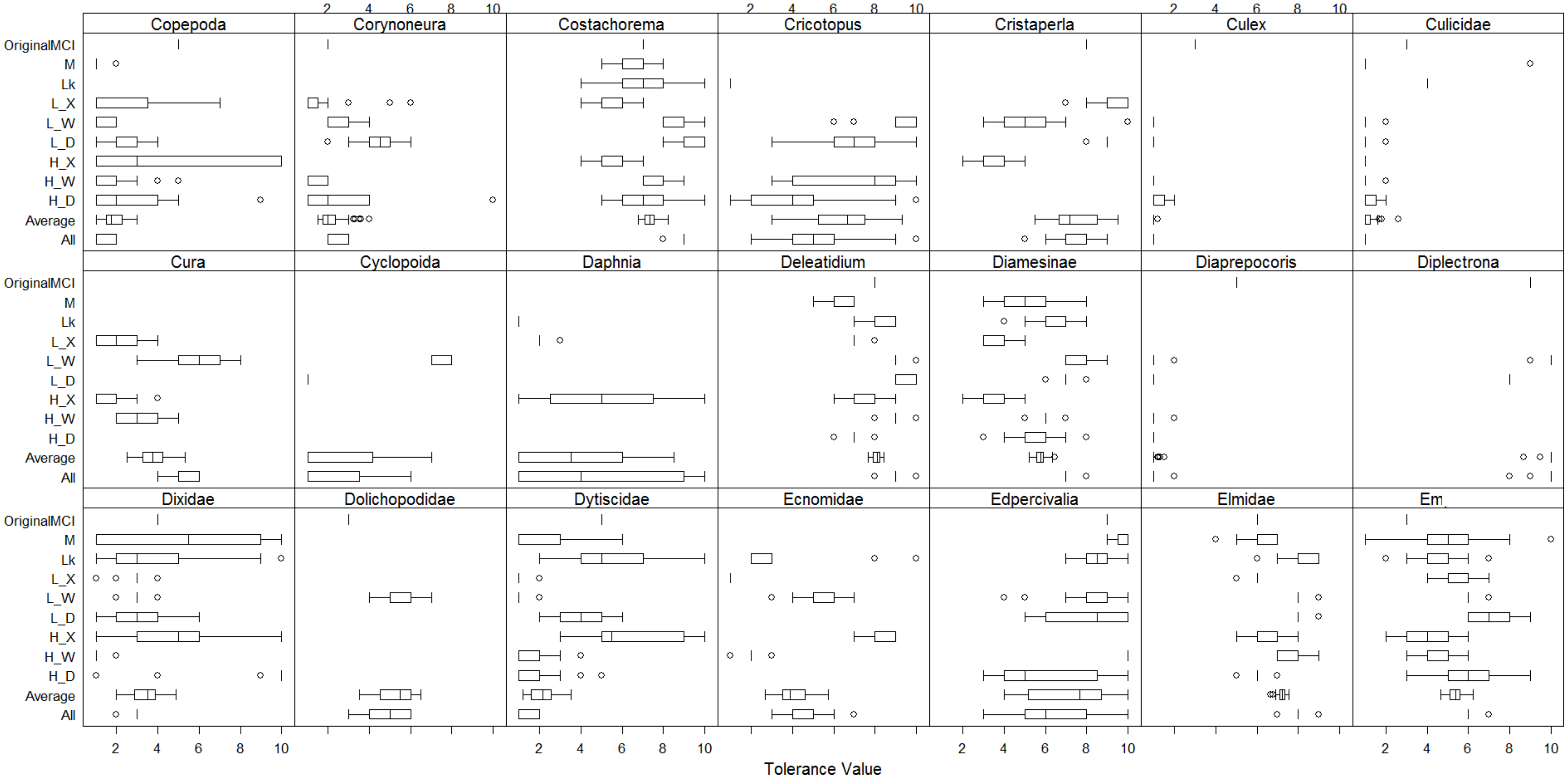
Taxa	original MCI-hb	reason for exclusion
Diptera	3	Category too broad
Halticoperla	8	Data deficient
Uropetala	5	Data deficient
Copelatus	5	Data deficient
Onychohydrus	5	Data deficient
Podaena	8	Data deficient
Calopsectra	4	Data deficient
Cryptochironomus	3	Data deficient
Mischoderus	4	Data deficient
Syrphidae	1	Data deficient
Synchorema	9	Data deficient
Kokiria	9	Data deficient
Ecnomina	8	Data deficient
Conuxia	8	Synonymous with *Pycnocentria*
Anthomyiidae	3	Synonymous with Muscidae
Dolomedes	5	Relatively unaffected by water quality
Collembola	6	Relatively unaffected by water quality
Staphylinidae	5	Relatively unaffected by water quality

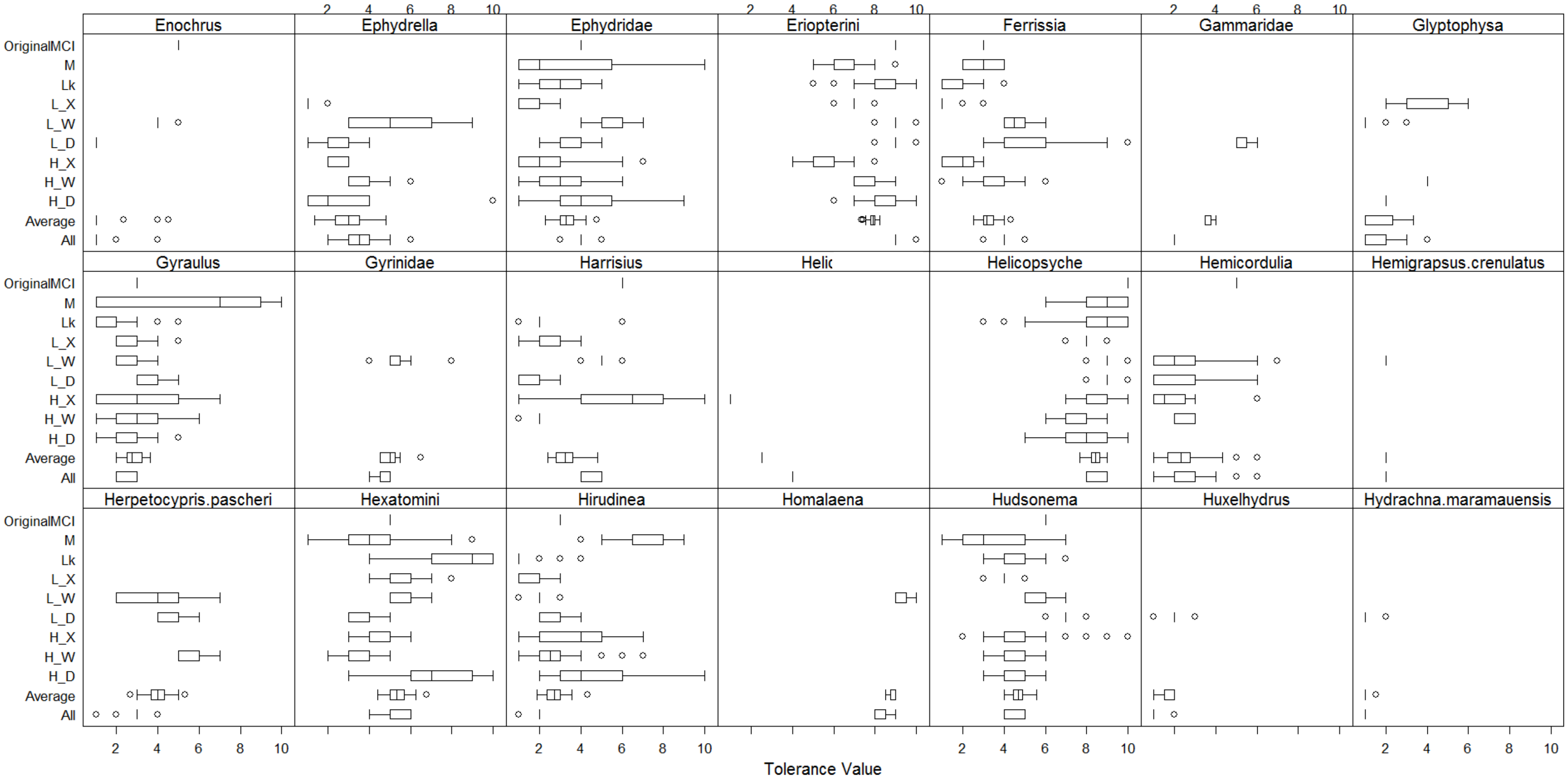
Appendix C Original and revised taxa tolerance values across environmental classes

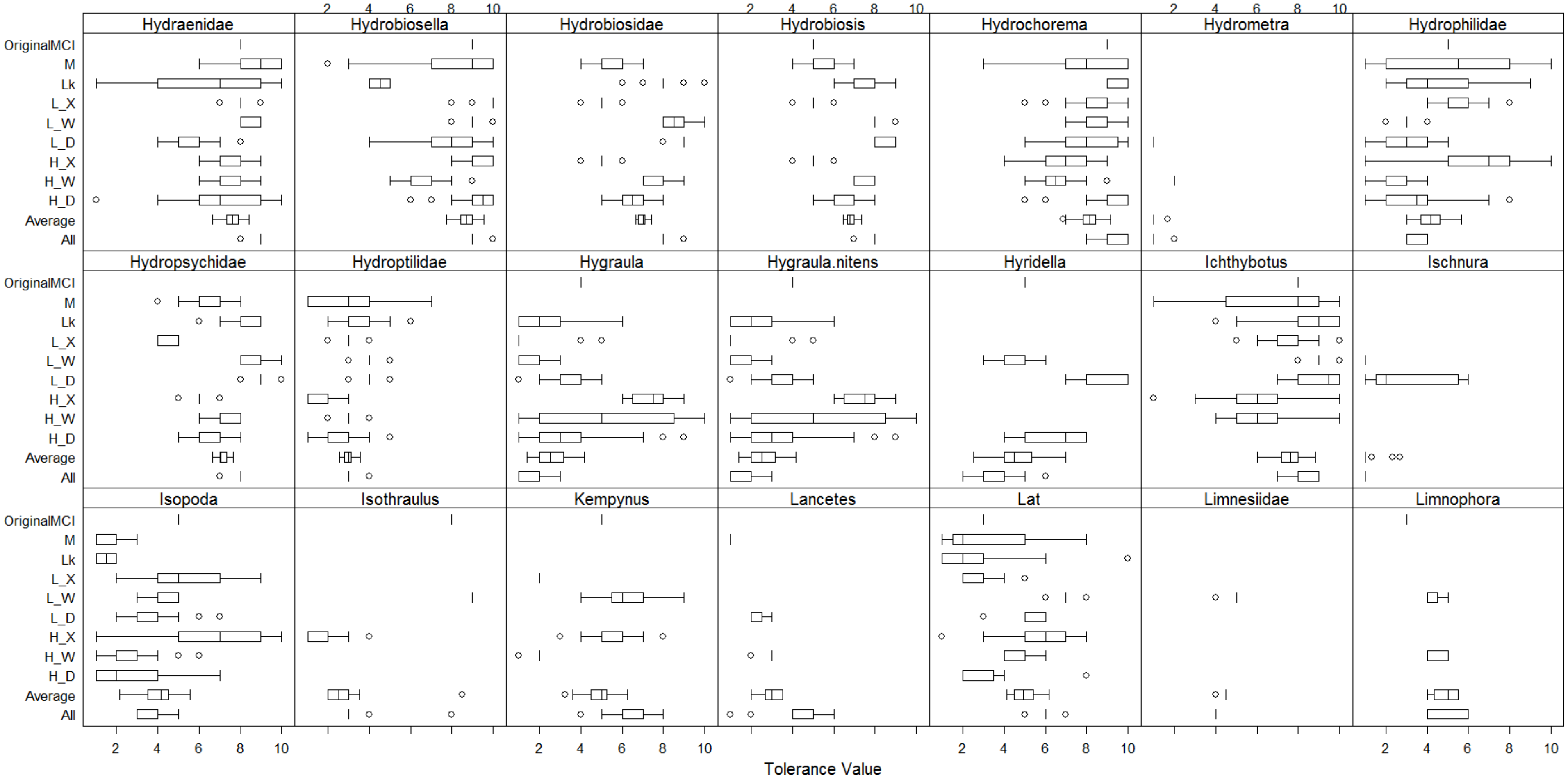
Tolerance values are provided for the original published MCI TV (OriginalMCI), for 8 environmental classes (M to H_D), for the average of TVs across the environmental classes (average) and for all sites run at once (all). Values are generated from 50 datasets created by randomly selecting one visit per site each time, note that 205 sites were only visited once. We include the old taxonomic names for *Aoteapsyche* and *Orthopsyche* to allow comparisons with historical datasets. These are taxa now *Hydropsyche.* See Table 2-1 for definitions of environmental classes. Centre bars of boxes are medians.

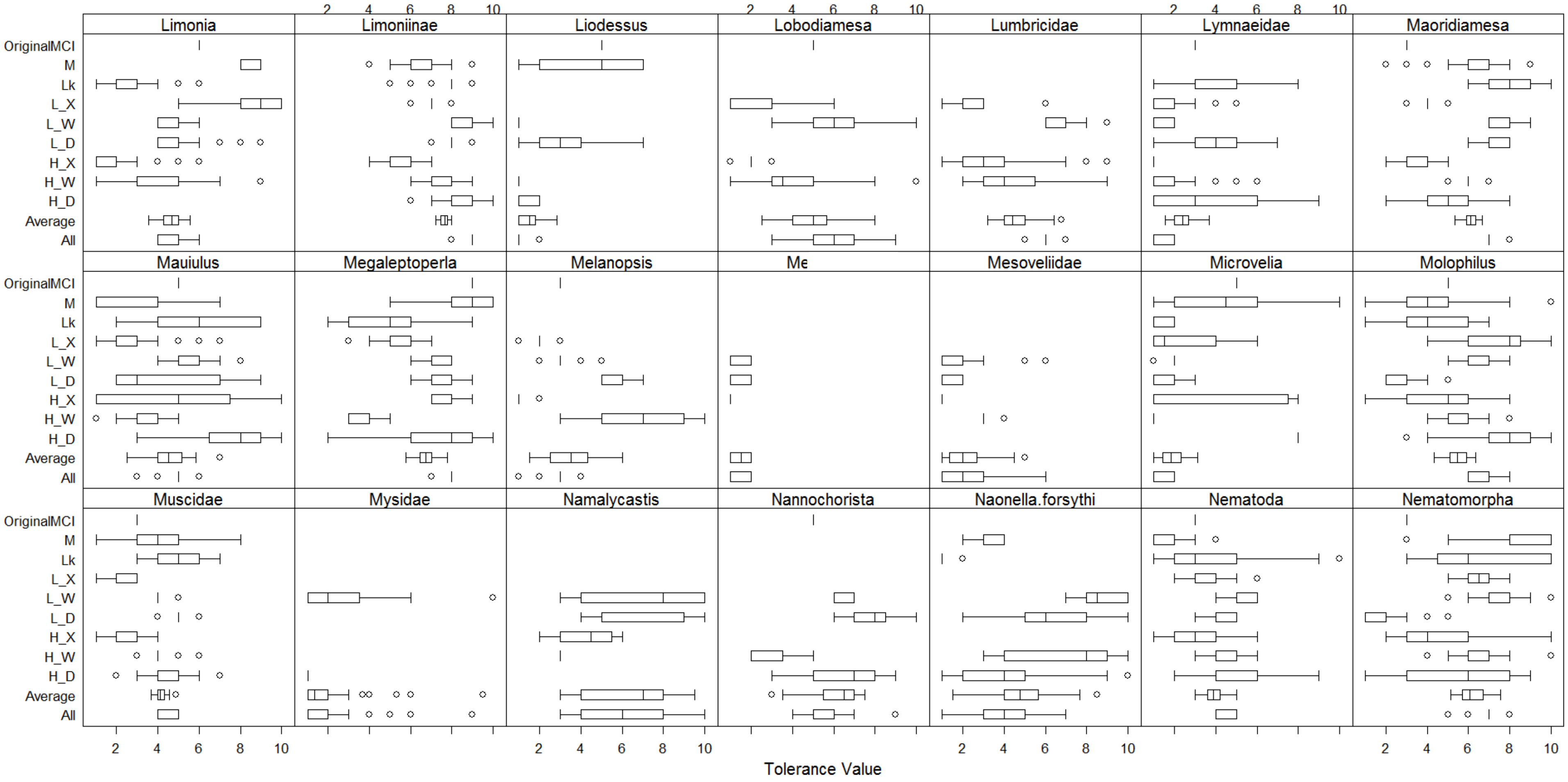


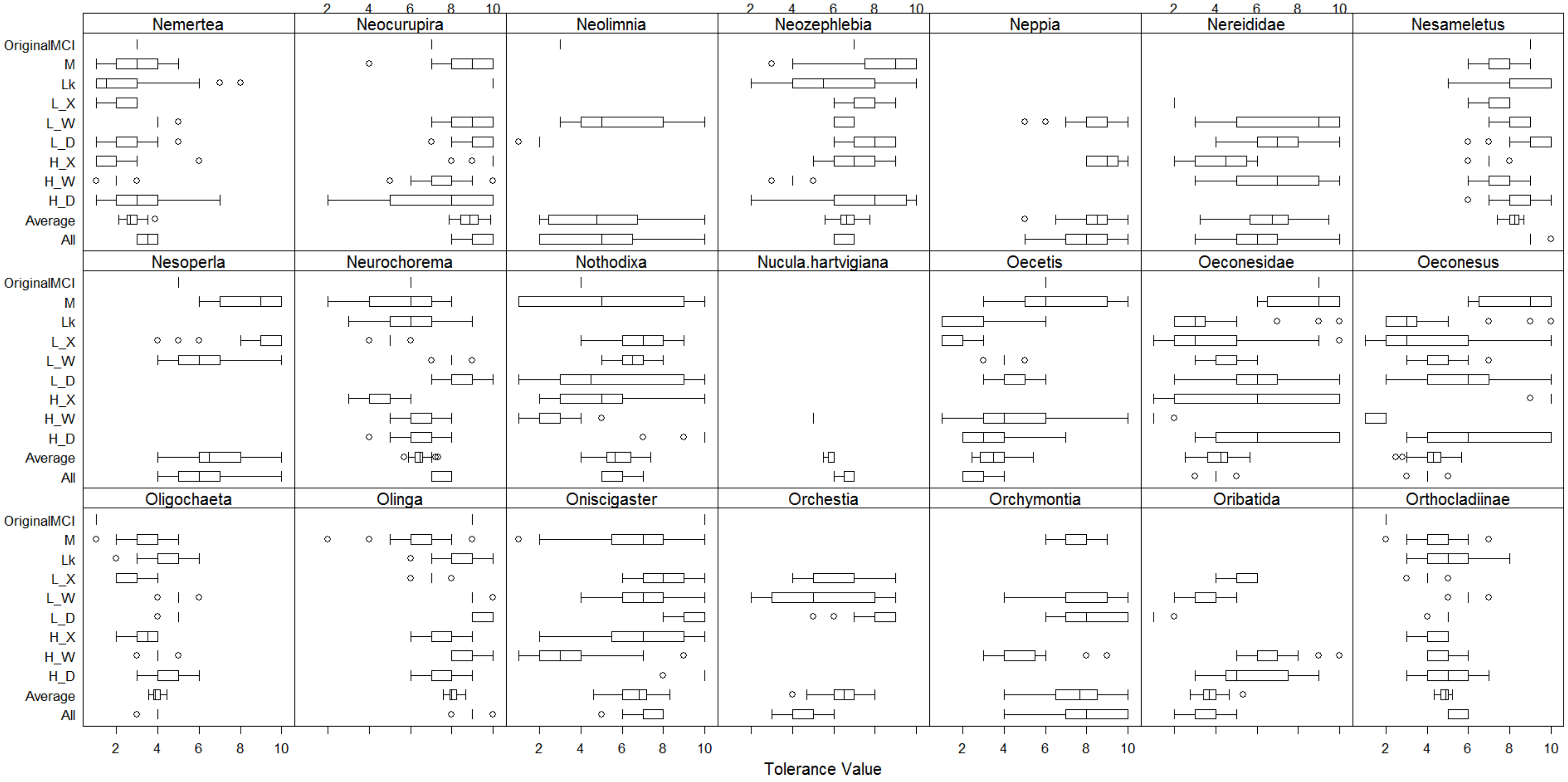

Austrolestes
Austronella
Austropeplea
Austroperla
Austrosimulium
Barbronia
Beraeoptera
Berosus
Blephariceridae
Brachydeutera
Ceratopogonidae
Ceratopogoninae
Chiltonia
Chironomidae
Chironominae
Chironomini
Chironomus
Cladocera
Cnidaria
Coloburiscus
Confluens
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

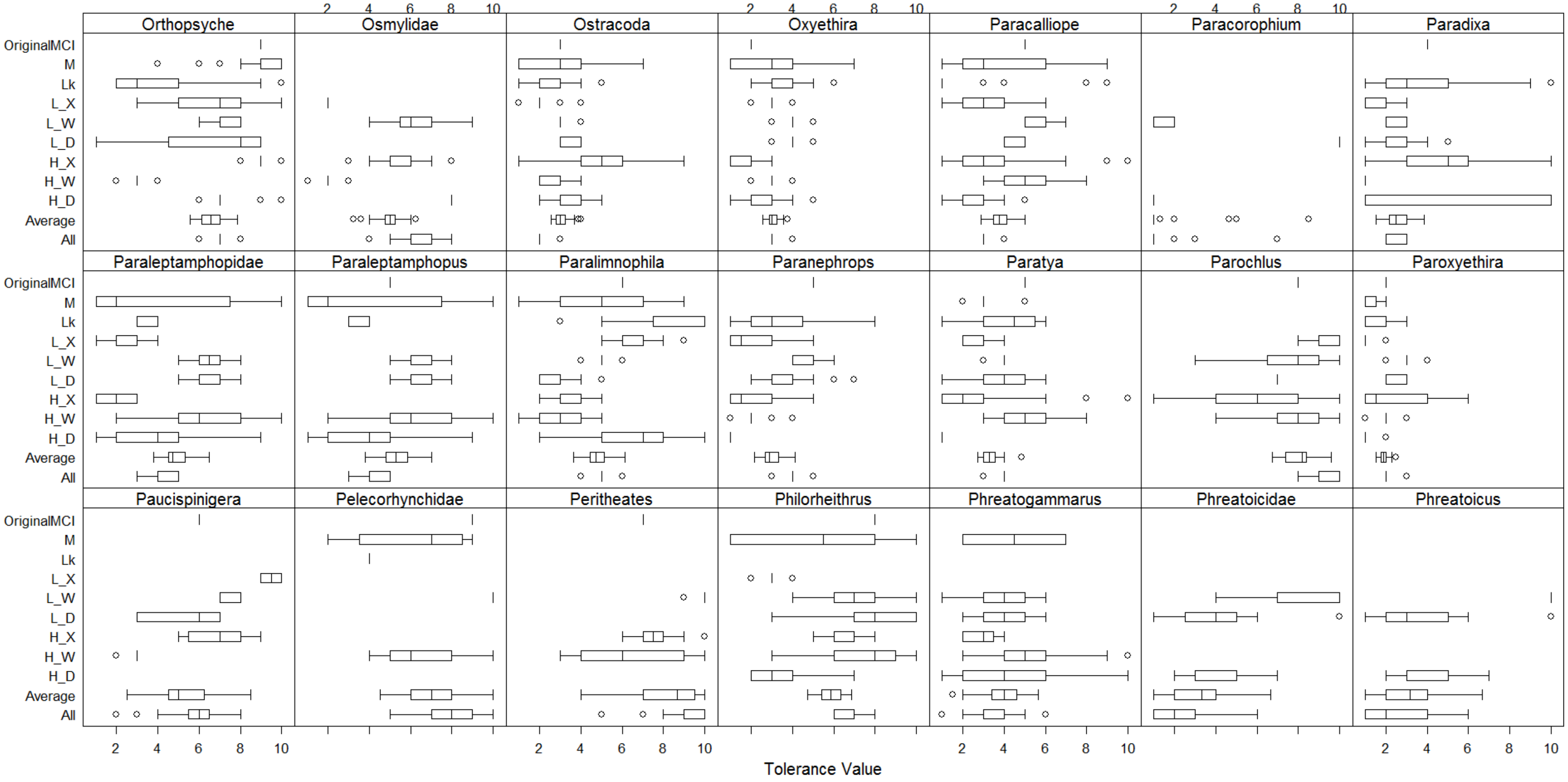

Copepoda
Corynoneura
Costachorema
Cricotopus
Cristaperla
Culex
Culicidae
Cura
Cyclopoida
Daphnia
Deleatidium
Diamesinae
Diaprepocoris
Diplectrona
Dixidae
Dolichopodidae
Dytiscidae
Ecnomidae
Edpercivalia
Elmidae
Em
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

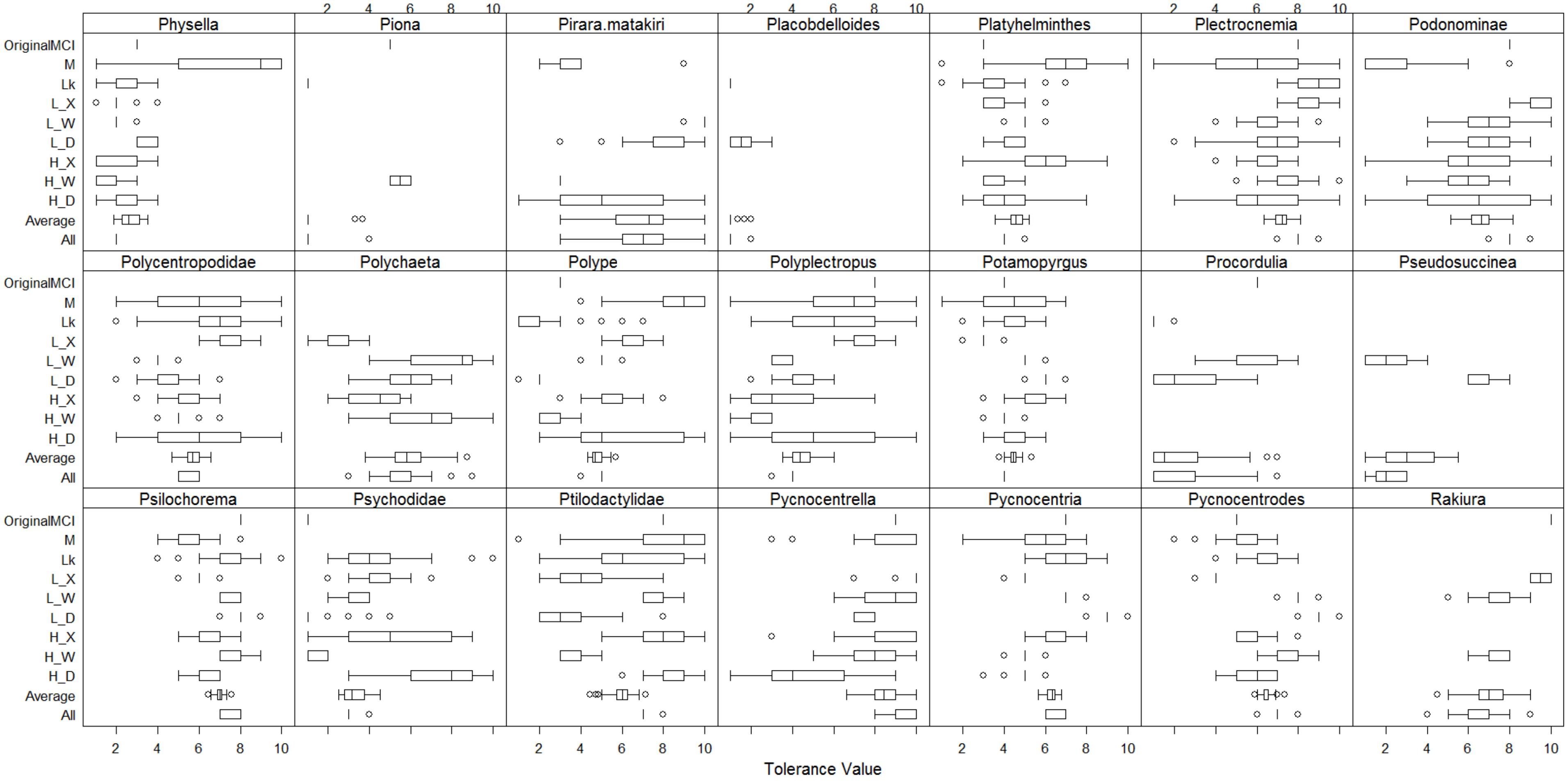

Enochrus
Ephydrella
Ephydridae
Eriopterini
Ferrissia
Gammaridae
Glyptophysa
Gyraulus
Gyrinidae
Harrisius
Helic
Helicopsyche
Hemicordulia
Hemigrapsus.crenulatus
Herpetocypris.pascheri
Hexatomini
Hirudinea
Homalaena
Hudsonema
Huxelhydrus
Hydrachna.maramauensis
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

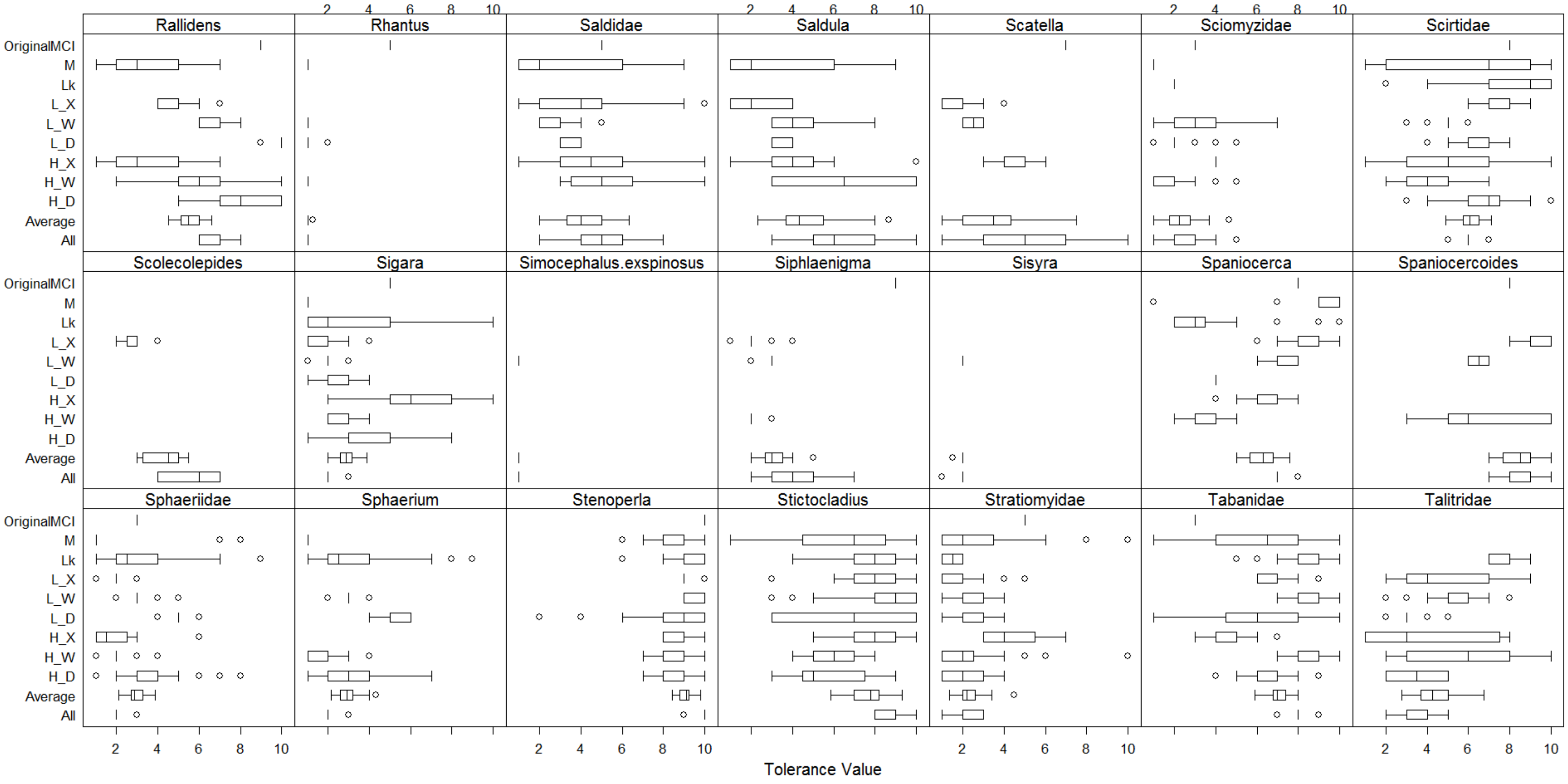

Hydraenidae
Hydrobiosella
Hydrobiosidae
Hydrobiosis
Hydrochorema
Hydrometra
Hydrophilidae
Hydropsychidae
Hydroptilidae
Hygraula
Hygraula.nitens
Hyridella
Ichthybotus
Ischnura
Isopoda
Isothraulus
Kempynus
Lancetes
Lat
Limnesiidae
Limnophora
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

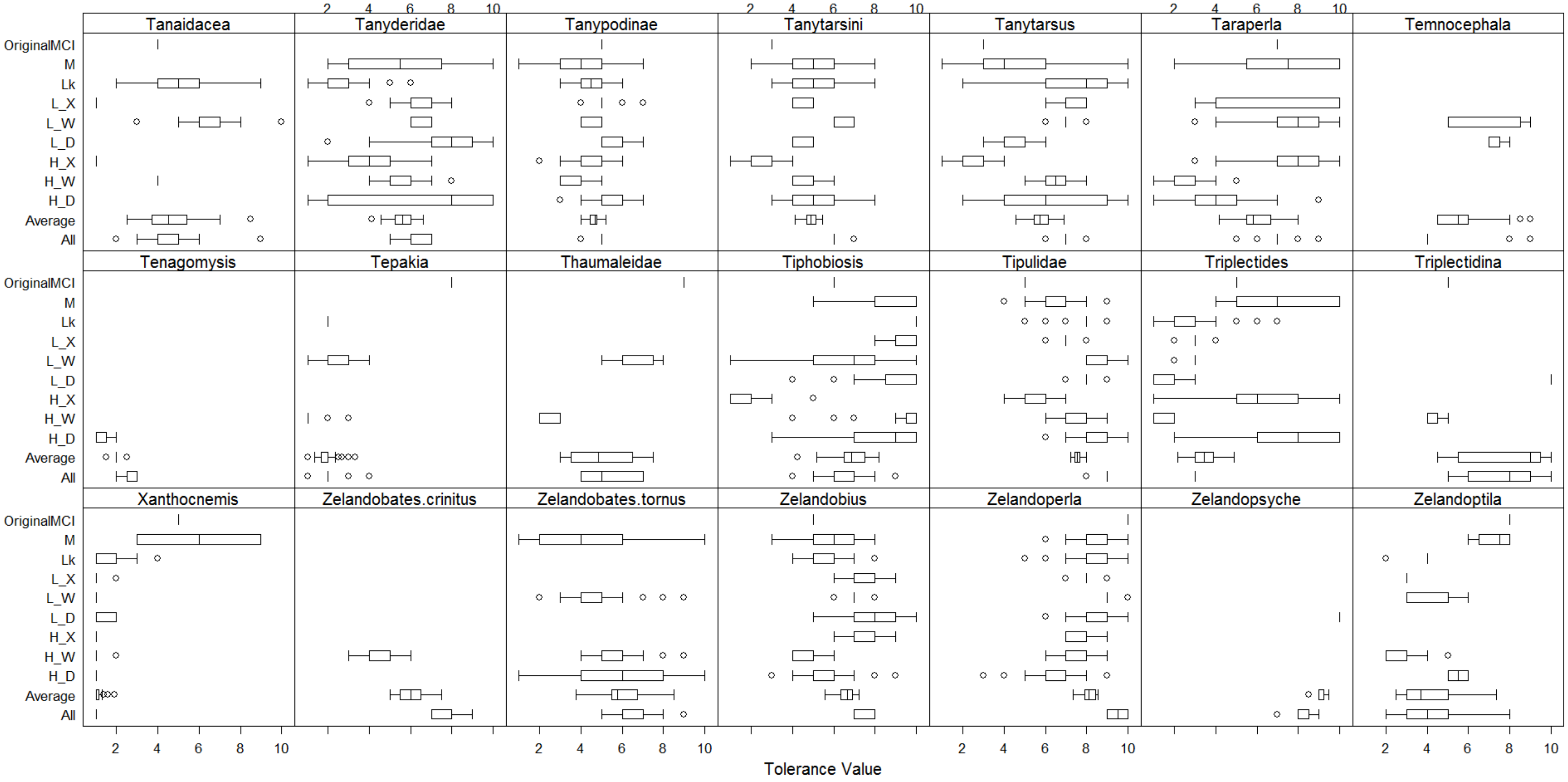

Limonia
Limoniinae
Liodessus
Lobodiamesa
Lumbricidae
Lymnaeidae
Maoridiamesa
Mauiulus
Megaleptoperla
Melanopsis
Mε
Mesoveliidae
Microvelia
Molophilus
Muscidae
Mysidae
Namalycastis
Nannochorista
Naonella.forsythi
Nematoda
Nematomorpha
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

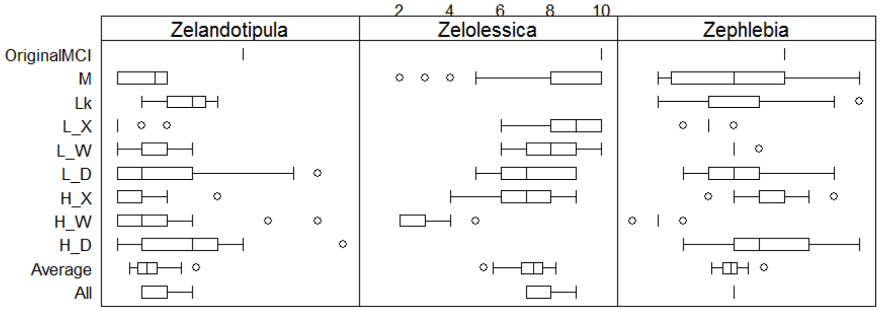

Nemertea
Neocurupira
Neolimnia
Neozephlebia
Neppia
Nereididae
Nesameletus
Nesoperla
Neurochorema
Nothodixa
Nucula.hartvigiana
Oecetis
Oeconesidae
Oeconesus
Oligochaeta
Olinga
Oniscigaster
Orchestia
Orchymontia
Oribatida
Orthocladiinae
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value


Orthopsyche
Osmylidae
Ostracoda
Oxyethira
Paracalliope
Paracorophium
Paradixa
Paraleptamphopidae
Paraleptamphopus
Paralimnophila
Paranephrops
Paratya
Parochlus
Paroxyethira
Paucispinigera
Pelecorhynchidae
Peritheates
Philorheithrus
Phreatogammarus
Phreatoicidae
Phreatoicus
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

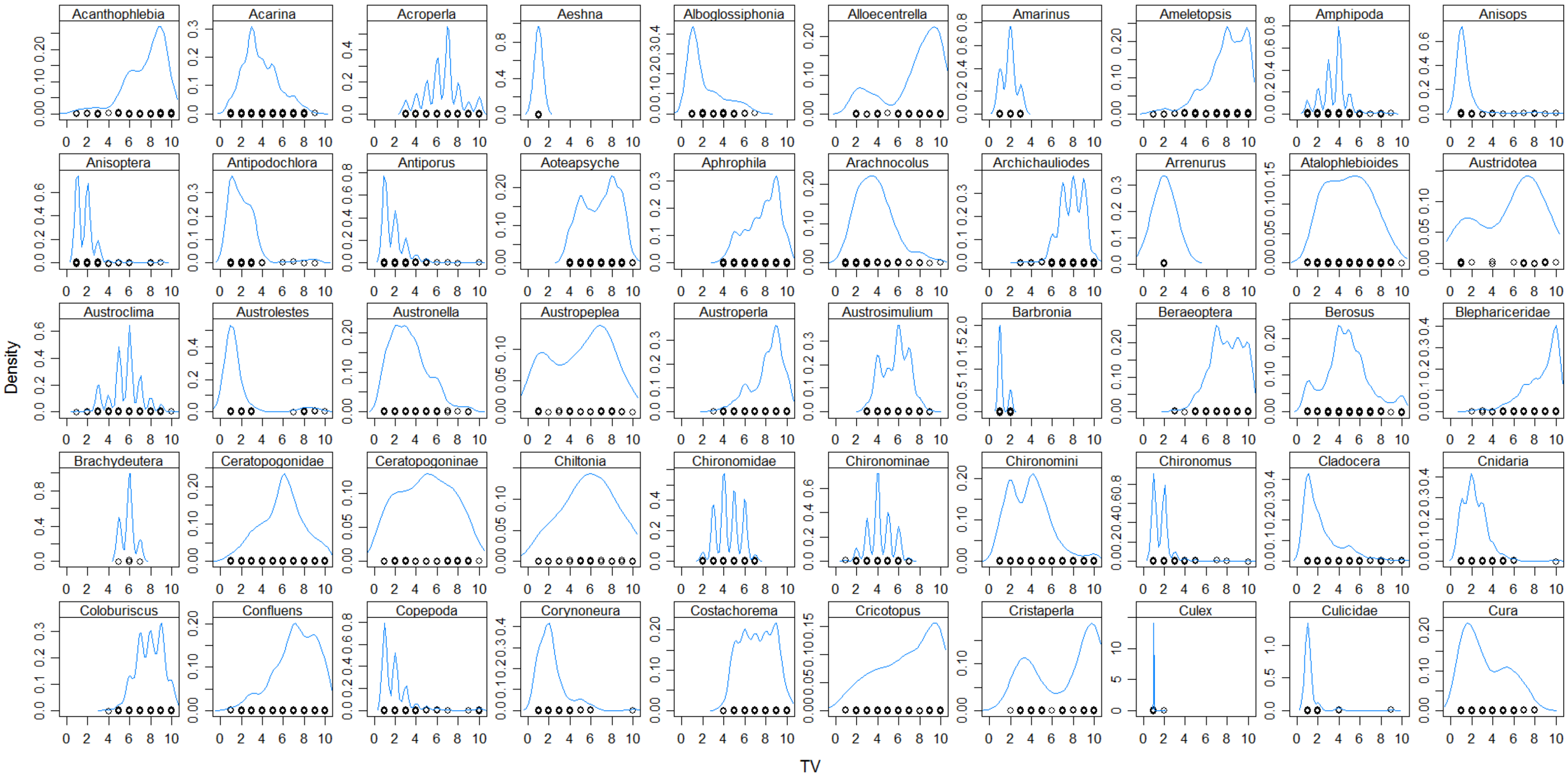

Physella
Piona
Pirara.matakiri
Placobdelloides
Platyhelminthes
Plectrocnemia
Podonominae
Polycentropodidae
Polychaeta
Polype
Polyplectropus
Potamopyrgus
Procordulia
Pseudosuccinea
Psilochorema
Psychodidae
Ptilodactylidae
Pycnocentrella
Pycnocentria
Pycnocentrodes
Rakiura
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

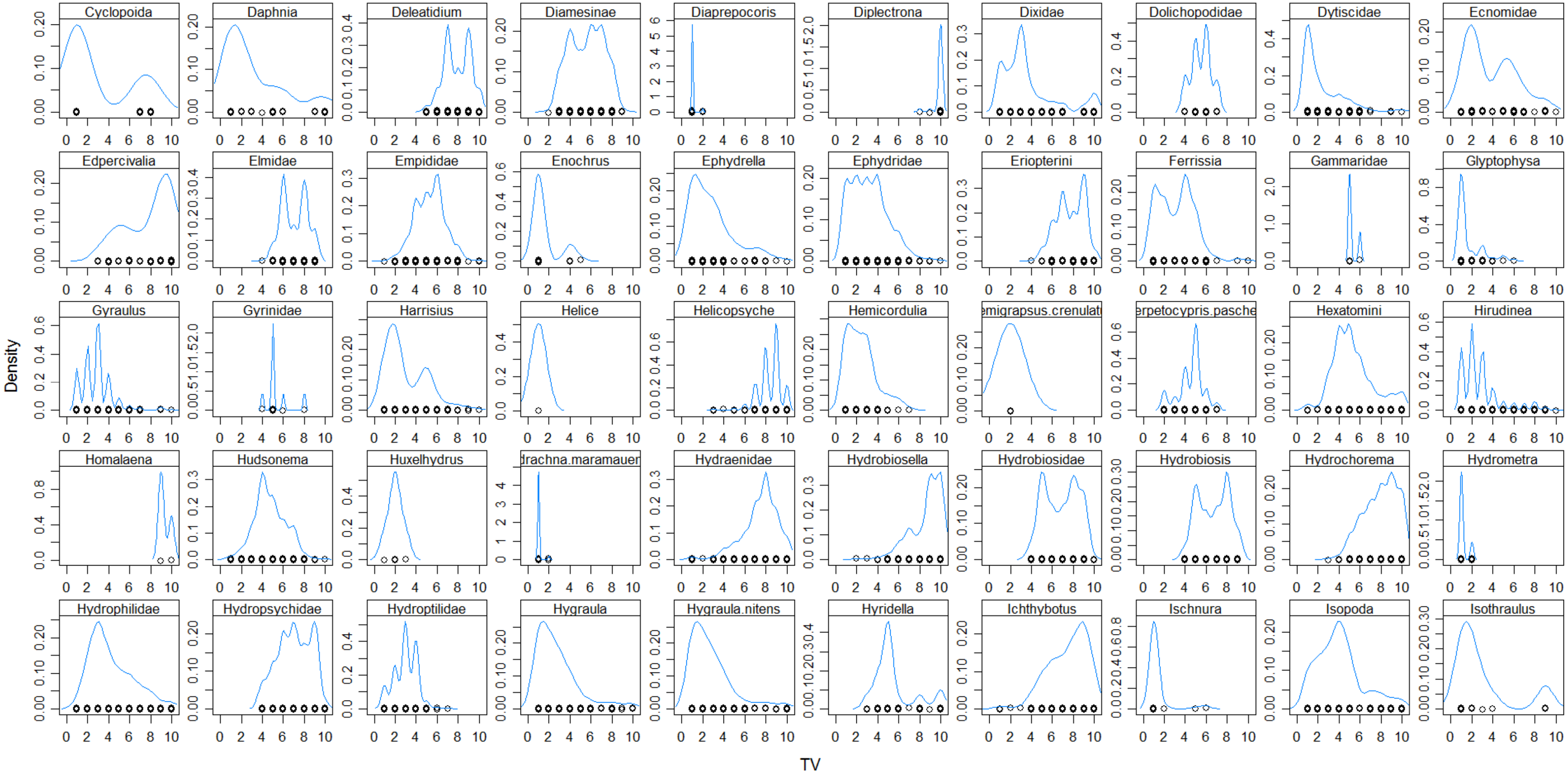

Rallidens
Rhantus
Saldidae
Saldula
Scatella
Sciomyzidae
Scirtidae
Scolecolepides
Sigara
Simocephalus.exspinosus
Siphlaenigma
Sisyra
Spaniocerca
Spaniocercoides
Sphaeriidae
Sphaerium
Stenoperla
Stictocladius
Stratiomyidae
Tabanidae
Talitridae
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

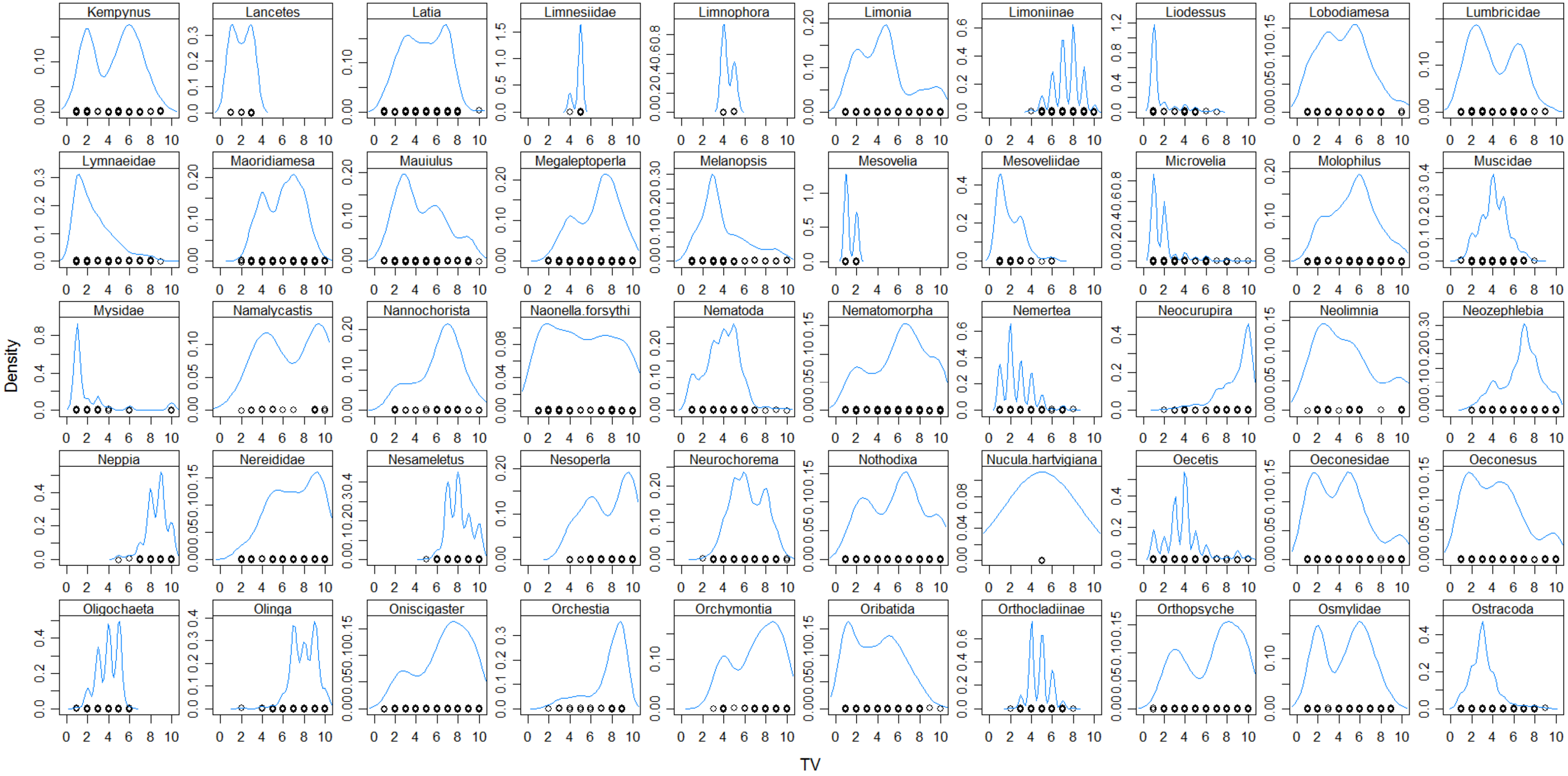

Tanaidacea
Tanyderidae
Tanypodinae
Tanytarsini
Tanytarsus
Taraperla
Temnocephala
Tenagomysis
Tepakia
Thaumaleidae
Tiphobiosis
Tipulidae
Triplectides
Triplectidina
Xanthocnemis
Zelandobates.crinitus
Zelandobates.tornus
Zelandobius
Zelandoperla
Zelandopsyche
Zelandoptila
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
2
4
6
8
10
Tolerance Value

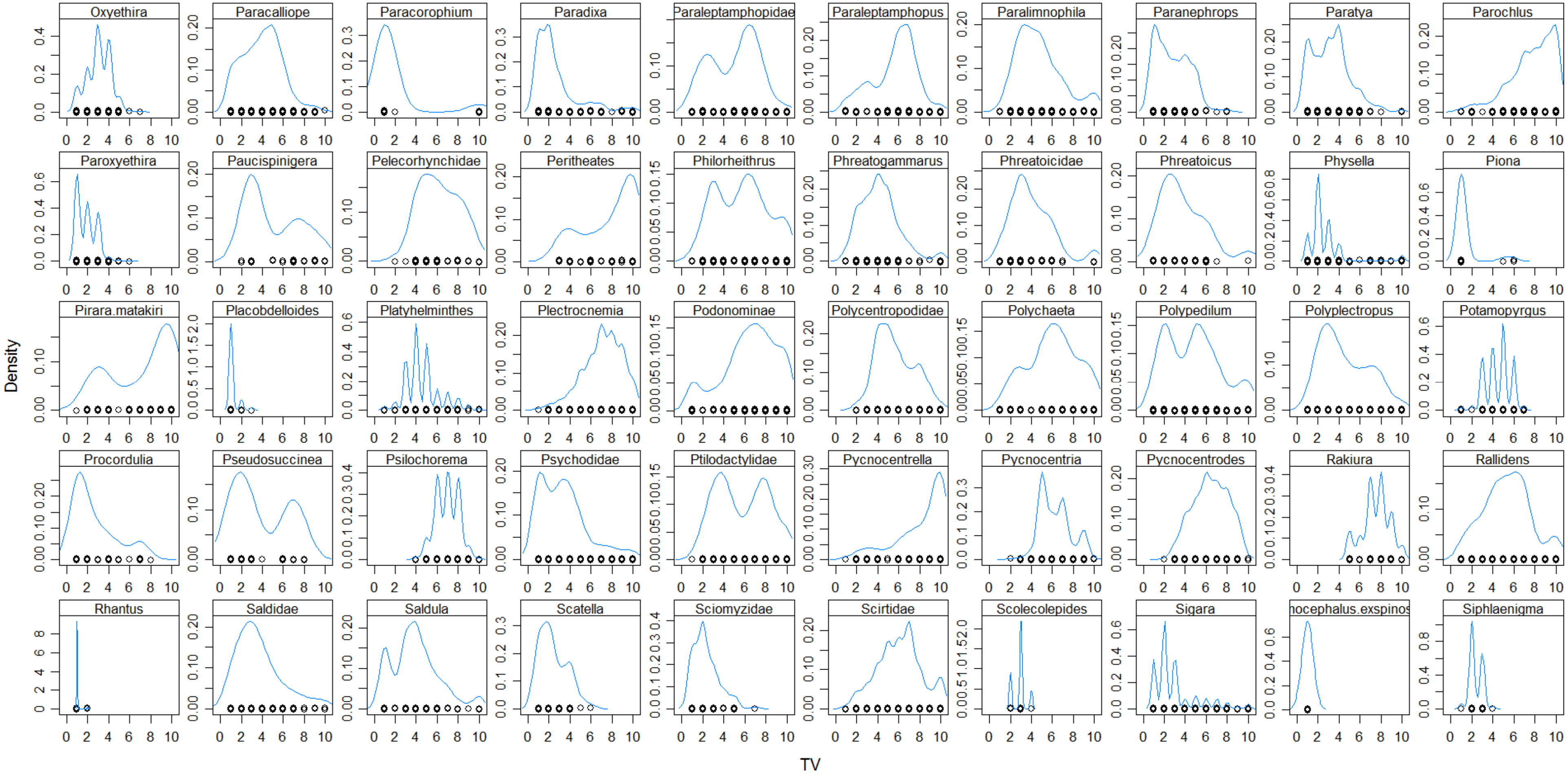

2
4
6
8
10
Zelandotipula
Zelolessica
Zephlebia
OriginalMCI
M
Lk
L_X
L_W
L_D
H_X
H_W
H_D
Average
All
Tolerance Value

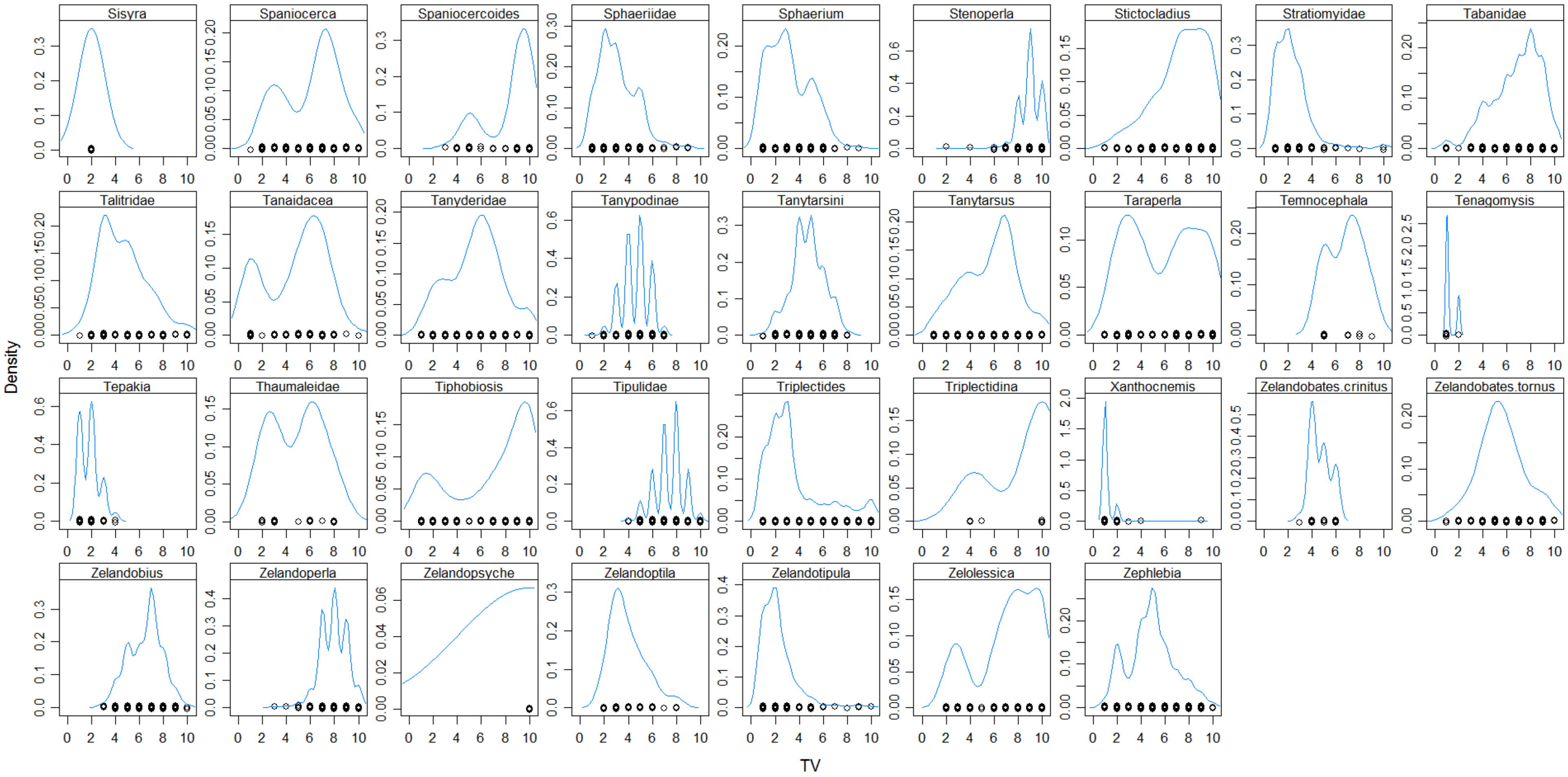
Appendix D Distributions of tolerance values across eight environmental class for individual taxa from 50 datasets each generated with one random visit per site.




Cyclopoida
Daphnia
Deleatidium
Diamesinae
Diaprepocoris
Diplectrona
Dixidae
Dolichopodidae
Dytiscidae
Ecnomidae
Edpercivalia
Elmidae
Empididae
Enochrus
Ephydrella
Ephydridae
Eriopterini
Ferrissia
Gammaridae
Glyptophysa
Gyraulus
Gyrinidae
Harrisius
Helice
Helicopsyche
Hemicordulia
emigrapsus.crenulati
erpetocypris.pasche
Hexatomini
Hirudinea
Homalaena
Hudsonema
Huxelhydrus
drachna.maramauer
Hydraenidae
Hydrobiosella
Hydrobiosidae
Hydrobiosis
Hydrochorema
Hydrometra
Hydrophilidae
Hydropsychidae
Hydroptilidae
Hygraula
Hygraula.nitens
Hyridella
Ichthybotus
Ischnura
Isopoda
Isothraulus
Density
TV


Kempynus
Lancetes
Latia
Limnesiidae
Limnophora
Limonia
Limoniinae
Liodessus
Lobodiamesa
Lumbricidae
Lymnaeidae
Maoridiamesa
Mauiulus
Megaleptoperla
Melanopsis
Mesovelia
Mesoveliidae
Microvelia
Molophilus
Muscidae
Mysidae
Namalycastis
Nannochorista
Naonella.forsythi
Nematoda
Nematomorpha
Nemertea
Neocurupira
Neolimnia
Neozephlebia
Neppia
Nereididae
Nesameletus
Nesoperla
Neurochorema
Nothodixa
Nucula.hartvigiana
Oecetis
Oeconesidae
Oeconesus
Oligochaeta
Olinga
Oniscigaster
Orchestia
Orchymontia
Oribatida
Orthocladiinae
Orthopsyche
Osmylidae
Ostracoda
Density
TV
0 2 4 6 8 10


Oxyethira
Paracalliope
Paracorophium
Paradixa
Paraleptamphopidae
Paraleptamphopus
Paralimnophila
Paranephrops
Paratya
Parochlus
Paroxyethira
Paucispinigera
Pelecorhynchidae
Peritheates
Philorheithrus
Phreatogammarus
Phreatoicidae
Phreatoicus
Physella
Piona
Pirara.matakiri
Placobdelloides
Platyhelminthes
Plectrocnemia
Podonominae
Polycentropodidae
Polychaeta
Polypedilum
Polyplectropus
Potamopyrgus
Procordulia
Pseudosuccinea
Psilochorema
Psychodidae
Ptilodactylidae
Pycnocentrella
Pycnocentria
Pycnocentrodes
Rakiura
Rallidens
Rhantus
Saldidae
Saldula
Scatella
Sciomyzidae
Scirtidae
Scolecolepides
Sigara
hocephalus.exspinos
Siphlaenigma
Density
TV
0 2 4 6 8 10


Sisyra
Spaniocerca
Spaniocercoides
Sphaeriidae
Sphaerium
Stenoperla
Stictocladius
Stratiomyidae
Tabanidae
Talitridae
Tanaidacea
Tanyderidae
Tanypodinae
Tanytarsini
Tanytarsus
Taraperla
Temnocephala
Tenagomysis
Tepakia
Thaumaleidae
Tiphobiosis
Tipulidae
Triplectides
Triplectidina
Xanthocnemis
Zelandobates.crinitus
Zelandobates.tornus
Zelandobius
Zelandoperla
Zelandopsyche
Zelandoptila
Zelandotipula
Zelolessica
Zephlebia
Density
TV
0 2 4 6 8 10

Appendix E Testing the influence of environmental class on generated TV's.

Separate Kruskal-Wallis rank sum tests were performed for each taxon with environmental class as the predictor and generated tolerance values from 50 reduced datasets. Not all taxa were found in all environmental classes. * indicates that the taxon was found only in one environmental class. d.f. = degrees of freedom. A significant test statistic (p<0.05) means that a significant difference in TV value among environmental classes was found.

Taxa	Statistic	d.f.	P
Acanthophlebia	75.7	5	<0.001
Acarina	236.3	7	<0.001
Acroperla	113.8	6	<0.001
*Aeshna**	NA	NA	NA
Alboglossiphonia	64.8	1	<0.001
Alloecentrella	49.6	5	<0.001
*Amarinus**	NA	NA	NA
Ameletopsis	139.8	7	<0.001
Amphipoda	135.8	7	<0.001
Anisops	65.2	7	<0.001
Anisoptera	56.7	5	<0.001
Antipodochlora	128.4	4	<0.001
Antiporus	69.6	4	<0.001
Aoteapsyche	340.3	7	<0.001
Aphrophila	281.2	7	<0.001
Arachnocolus	27.5	3	<0.001
Archichauliodes	266.6	7	<0.001
*Arrenurus**	NA	NA	NA
Atalophlebioides	83.9	7	<0.001
Austridotea	13.2	1	<0.001
Austroclima	232.9	7	<0.001
Austrolestes	93.4	3	<0.001
Austronella	35.6	4	<0.001
Austropeplea	44.9	3	<0.001
Austroperla	198.6	7	<0.001
Austrosimulium	299.2	7	<0.001
Barbronia	57.4	1	<0.001
Beraeoptera	237.9	7	<0.001
Berosus	121.9	7	<0.001
Blephariceridae	138.6	6	<0.001
*Brachydeutera**	NA	NA	NA

Taxa	**Statistic**	**d.f.**	**P**
Ceratopogonidae	151.5	7	<0.001
Ceratopogoninae	40.3	2	<0.001
Chiltonia	19.0	1	<0.001
Chironomidae	300.0	7	<0.001
Chironominae	227.7	7	<0.001
Chironomini	282.2	7	<0.001
Chironomus	95.1	7	<0.001
Cladocera	145.8	6	<0.001
Cnidaria / *Hydra*	77.0	5	<0.001
Coloburiscus	273.4	7	<0.001
Confluens	162.4	7	<0.001
Copepoda	55.0	6	<0.001
Corynoneura	58.1	4	<0.001
Costachorema	280.5	7	<0.001
Cricotopus	68.3	4	<0.001
Cristaperla	72.8	3	<0.001
Culex	50.0	3	<0.001
Culicidae	54.3	6	<0.001
Cura	107.3	3	<0.001
Cyclopoida	32.8	1	<0.001
Daphnia	40.6	2	<0.001
Deleatidium	327.5	7	<0.001
Diamesinae	299.7	7	<0.001
Diaprepocoris	3.7	3	NS
Diplectrona	15.0	1	<0.001
Dixidae	170.7	7	<0.001
Dolichopodidae*	NA	NA	NA
Dytiscidae	182.9	7	<0.001
Ecnomidae	104.1	4	<0.001
Edpercivalia	23.0	5	<0.001
Elmidae	316.3	7	<0.001
Empididae	206.4	7	<0.001
Enochrus	31.8	1	<0.001
Ephydrella	96.9	5	<0.001
Ephydridae	169.9	7	<0.001
Eriopterini	287.6	7	<0.001
Ferrissia	202.5	6	<0.001
Gammaridae*	NA	NA	NA
Glyptophysa	46.5	3	<0.001

Taxa	Statistic	d.f.	P
Gyraulus	100.0	7	<0.001
Gyrinidae*	NA	NA	NA
Harrisius	140.9	5	<0.001
*Helice**	NA	NA	NA
Helicopsyche	140.3	7	<0.001
Hemicordulia	5.4	3	NS
*Hemigrapsus**	NA	NA	NA
Herpetocypris	22.1	2	<0.001
Hexatomini	222.0	7	<0.001
Hirudinea	172.2	7	<0.001
*Homolaena**	NA	NA	NA
Hudsonema	208.8	7	<0.001
*Huxelhydrus**	NA	NA	NA
*Hydrachna**	NA	NA	NA
Hydraenidae	153.4	7	<0.001
Hydrobiosella	144.1	7	<0.001
Hydrobiosidae	342.1	7	<0.001
Hydrobiosis	338.1	7	<0.001
Hydrochorema	127.5	7	<0.001
Hydrometra	59.0	1	<0.001
Hydrophilidae	176.7	7	<0.001
Hydropsychidae	338.9	7	<0.001
Hydroptilidae	204.3	7	<0.001
Hygraula	106.5	6	<0.001
Hyridella	35.5	2	<0.001
Ichthybotus	112.5	6	<0.001
Ischnura	38.4	1	<0.001
Isopoda	127.6	7	<0.001
Isothraulus	5.2	1	0.02
Kempynus	106.5	3	<0.001
Lancetes	10.2	2	0.006
Latia	163.7	7	<0.001
Limnesiidae*	NA	NA	NA
Limnophora	0.3	1	NS
Limonia	206.9	6	<0.001
Limoniinae	262.0	7	<0.001
Liodessus	105.6	4	<0.001
Lobodiamesa	48.7	3	<0.001
Lumbricidae	101.4	3	<0.001

Taxa	Statistic	d.f.	P
Lymnaeidae	104.9	6	<0.001
Maoridiamesa	287.8	7	<0.001
Mauiulus	99.1	7	<0.001
Megaleptoperla	236.5	7	<0.001
Melanopsis	88.4	4	<0.001
Mesovelia	5.3	2	0.07
Mesoveliidae	44.1	3	<0.001
Microvelia	85.9	7	<0.001
Molophilus	205.2	7	<0.001
Muscidae	227.5	7	<0.001
Mysidae	30.1	1	<0.001
Namalycastis	5.7	3	NS
Nannochorista	34.5	3	<0.001
Naonella	89.3	5	<0.001
Nematoda	184.8	7	<0.001
Nematomorpha	177.9	7	<0.001
Nemertea	161.4	7	<0.001
Neocurupira	111.5	6	<0.001
Neolimnia	30.1	1	<0.001
Neozephlebia	149.3	7	<0.001
Neppia	0.6	1	NS
Nereididae	17.1	4	0.002
Nesameletus	188.2	7	<0.001
Nesoperla	24.6	2	<0.001
Neurochorema	281.7	7	<0.001
Nothodixa	136.7	6	<0.001
*Nucula**	NA	NA	NA
Oecetis	72.1	6	<0.001
Oeconesidae	149.0	7	<0.001
Oeconesus	149.2	7	<0.001
Oligochaeta	268.3	7	<0.001
Olinga	278.0	7	<0.001
Oniscigaster	124.4	6	<0.001
Orchestia	19.1	2	<0.001
Orchymontia	20.7	3	<0.001
Oribatida	153.4	4	<0.001
Orthocladiinae	163.0	7	<0.001
Orthopsyche (now *Hydropsyche*)	212.0	7	<0.001
Osmylidae	107.6	4	<0.001

Taxa	**Statistic**	**d.f.**	**P**
Ostracoda	148.5	7	<0.001
Oxyethira	216.4	7	<0.001
Paracalliope	162.2	7	<0.001
Paracorophium	27.1	2	<0.001
Paradixa	153.4	6	<0.001
Paraleptamphopidae	133.1	7	<0.001
Paraleptamphopus	58.6	5	<0.001
Paralimnophila	200.5	7	<0.001
Paranephrops	179.4	6	<0.001
Paratya	197.6	7	<0.001
Parochlus	71.2	4	<0.001
Paroxyethira	207.8	7	<0.001
Paucispinigera	41.1	4	<0.001
Pelecorhynchidae	7.9	3	0.05
Peritheates	35.0	2	<0.001
Philorheithrus	180.9	6	<0.001
Phreatogammarus	30.9	5	<0.001
Phreatoicidae	4.6	2	NS
Phreatoicus	6.8	2	0.03
Physella	170.4	7	<0.001
Piona	52.9	1	<0.001
Pirara	60.0	4	<0.001
Placobdelloides	28.3	1	<0.001
Platyhelminthes	161.6	7	<0.001
Plectrocnemia	157.4	7	<0.001
Podonominae	157.7	6	<0.001
Polycentropodidae	166.7	7	<0.001
Polychaeta	77.9	4	<0.001
Polypedilum	313.4	7	<0.001
Polyplectropus	175.8	7	<0.001
Potamopyrgus	241.0	7	<0.001
Procordulia	41.1	2	<0.001
Pseudosuccinea	41.6	1	<0.001
Psilochorema	261.2	7	<0.001
Psychodidae	195.5	6	<0.001
Ptilodactylidae	186.5	7	<0.001
Pycnocentrella	96.0	6	<0.001
Pycnocentria	302.8	7	<0.001
Pycnocentrodes	324.4	7	<0.001

Taxa	Statistic	d.f.	P
Rakiura	14.9	2	<0.001
Rallidens	163.3	6	<0.001
Rhantus	7.7	3	0.05
Saldidae	24.0	5	<0.001
Saldula	9.4	5	NS
Scatella	16.8	2	<0.001
Sciomyzidae	20.3	5	0.001
Scirtidae	162.9	7	<0.001
*Scolecolepides**	NA	NA	NA
Sigara	175.8	7	<0.001
*Simocephalus**	NA	NA	NA
Siphlaenigma	17.2	2	<0.001
*Sisyra**	NA	NA	NA
Spaniocerca	175.8	6	<0.001
Spaniocercoides	17.9	2	<0.001
Sphaeriidae	167.1	7	<0.001
Sphaerium	139.4	5	<0.001
Stenoperla	85.9	7	<0.001
Stictocladius	64.5	7	<0.001
Stratiomyidae	55.7	7	<0.001
Tabanidae	191.1	7	<0.001
Talitridae	62.6	6	<0.001
Tanaidacea	59.3	4	<0.001
Tanyderidae	181.5	7	<0.001
Tanypodinae	190.6	7	<0.001
Tanytarsini	210.9	7	<0.001
Tanytarsus	229.6	7	<0.001
Taraperla	134.4	5	<0.001
Temnocephala	0.9	1	NS
*Tenagomysis**	NA	NA	NA
Tepakia	51.1	2	<0.001
Thaumaleidae	15.6	1	<0.001
Tiphobiosis	155.8	7	<0.001
Tipulidae	258.6	7	<0.001
Triplectides	233.2	7	<0.001
Triplectidina	8.8	1	0.003
Xanthocnemis	91.7	7	<0.001
*Zelandobates**	NA	NA	NA
Zelandobius	235.5	7	<0.001

Taxa	Statistic	d.f.	P
Zelandoperla	177.9	7	<0.001
*Zelandopsyche**	NA	NA	NA
Zelandoptila	21.7	5	<0.001
Zelandotipula	62.3	7	<0.001
Zelolessica	145.1	5	<0.001
Zephlebia	193.7	7	<0.001