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4 1 **Predictability of species diversity by family diversity across global**
5 2 **terrestrial animal taxa**

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8 3 **Running title:** *Higher taxa diversity surrogacy for animals*

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11 4 **Abstract**

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14 5 **Aim:** While biodiversity is in sharp decline around the globe, collecting precise
15 6 information on changes in overall species richness remains extremely
16 7 challenging. Efficient and reliable proxy methods are therefore needed, with
17 8 the diversity of higher taxa representing one such potential proxy for
18 9 species-level diversity. Nonetheless, the stability of using this measure across
19 10 different regions and animal taxa at the global scale has never been
20 11 thoroughly investigated.

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23 12 **Location:** Global

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26 13 **Time period:** Up to 2016

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29 14 **Major taxa studied:** Animalia

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32 15 **Methods:** We use a large global dataset containing published studies on
33 16 diversity in the terrestrial Animalia to analyse the relationship between diversity
34 17 at family, **genus** and species level across different orders.

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37 18 **Results:** Family- and species-diversity are positively correlated, with the
38 19 strongest correlations **in** Diptera, Hemiptera and Coleoptera. Correlations are
39 20 **slightly** weaker in family-species than genus-species relationships. **These**
40 21 differences are stronger in observed richness than in diversity indices. Across
41 22 all taxa, family-species-correlations of Shannon diversity **index values** were
42 23 independent of sample size, and they showed limited variation across biomes
43 24 for the three orders containing sufficient case studies for this analysis. Based
44 25 on **the Shannon diversity index, the species diversity** per site increases linearly
45 26 with the increase **in family diversity**, with an average species / family diversity
46 27 **index ratio of 2.5, slightly lower than the ratio of 2.7 for observed species and**

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4 28 family richness values.
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6 29 **Main conclusions:** Our study confirms that recording family-level diversity
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8 30 can be a meaningful proxy to determine species-level diversity patterns in
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10 31 biodiversity studies, while trade-offs between identification costs and retained
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12 32 information content need to be considered when using higher taxon surrogacy.
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16 17 34 **Key words**

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20 35 **Arthropods**, bio-geographical distribution, biodiversity conservation, higher
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22 36 taxa surrogate, meta-analyses, PREDICTS, Shannon diversity
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25 37 **Introduction**

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28 38 The decrease in biodiversity has led to dramatic declines in the provision of
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30 39 ecosystem services (Díaz *et al.*, 2015). To address these declines and devise
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32 40 effective conservation measures, we need a thorough understanding of the
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34 41 specific quantitative changes in biodiversity, with species diversity
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36 42 representing the most commonly used currency (Myers *et al.*, 2000; Kreft &
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38 43 Jetz, 2007; Jenkins *et al.*, 2013). Collecting and recording species diversity
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40 44 information, however, is challenging, since this work requires enormous
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42 45 resources in time, money and expert knowledge, but also because only a
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44 46 fraction of the global species pool is currently known to science, which makes
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46 47 this task extremely difficult (Scheffers *et al.*, 2012; Stork, 2018). A potential
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48 48 alternative approach in biodiversity assessments is to focus on the diversity
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49 49 patterns at higher taxonomic levels. The relative ease of identification at higher
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50 50 taxonomic levels makes working on this scale significantly cheaper and
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51 51 quicker, and it also allows for the efficient training of staff and volunteers with
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52 52 limited taxonomic knowledge to contribute towards biodiversity assessments
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53 53 (Lovell *et al.*, 2009).
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54 54 The application of higher taxa surrogacy for species diversity needs to
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55 55 consider trade-offs between retaining information content and identification
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4 56 costs (Balmford *et al.*, 1996b; Balmford *et al.*, 1996a; Perez-Fuertes *et al.*,
5 57 2016). Identification work at high taxonomic ranks (e.g. order) is easy and fast,
6 58 but resulting information may poorly reflect species diversity (Terlizzi *et al.*,
7 59 2009; Driessen & Kirkpatrick, 2019). The number of lower taxonomic ranks
8 60 (e.g. genera) may strongly indicate underlying species diversity, but
9 61 identification of large numbers of specimens to that level is often
10 62 time-consuming and challenging, particularly in mega-diverse arthropod taxa
11 63 (Balmford *et al.*, 2000; Cardoso *et al.*, 2004; Perez-Fuertes *et al.*, 2016).
12 64 Family-level data in this context might represent a sensible compromise, both
13 65 requiring limited identification effort and still potentially serving as a good proxy
14 66 of species diversity. A further general concern relating to higher taxon
15 67 surrogacy for species diversity is that higher taxa are not natural units, but
16 68 represent rather arbitrary classifications to facilitate the organization of
17 69 taxonomic information (see Gaston, 2000) (Williams & Gaston, 1994;
18 70 Bevilacqua *et al.*, 2012). A key rationale in conserving species diversity across
19 71 taxonomic groups is the maintenance of functionally diverse ecosystems, with
20 72 species diversity often directly linked to the complexity of ecosystem properties
21 73 that in turn affect the strength and resilience of ecological functions (Naeem *et al.*,
22 74 1999; Hooper *et al.*, 2005; Kremen, 2005; Zavaleta *et al.*, 2010). Linkages
23 75 between functional properties and morphological characteristics, meanwhile,
24 76 are already strongly associated with family-level differentiations (Warwick,
25 77 1993), with a high family-level diversity commonly associated with a high
26 78 structural or trait diversity (Terlizzi *et al.*, 2009). While higher taxonomic ranks
27 79 are not as clearly defined as species (Sepkoski, 1992), family level diversity
28 80 cannot therefore be regarded only as an arbitrary functional unit with limited
29 81 ecological meaning. On the contrary, family level diversity in itself provides
30 82 ecologically relevant information (Gaston, 2000).

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52 83 The crucial step for the use of family diversity as a proxy for species diversity
53 84 in biodiversity assessments is to establish the strength of links between
54 85 richness patterns at species level and family level (Gaston & Williams, 1993).
55 86 In particular, we need to know: i) whether a consistent relationship between
56 87 family diversity and species diversity exists across different geographic

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4 88 regions, and ii) whether the relative species richness per family is stable
5 89 across different geographic regions. The first question has been studied
6 90 already on regional scales for a variety of taxa and geographic regions. For
7 91 example, family richness can be used successfully to predict species richness
8 92 on a regional scale in higher plants (Negi & Gadgil, 2002; Villasenor *et al.*,
9 93 2005), amphibians (Mazaris *et al.*, 2008), birds (Williams & Gaston, 1994;
10 94 Mazaris *et al.*, 2008), mammals (Mazaris *et al.*, 2008) and arthropods
11 95 (Williams & Gaston, 1994; Báldi, 2003; Heino & Soininen, 2007). Nonetheless,
12 96 several studies also reported that species diversity is only poorly predicted by
13 97 family diversity (Prance, 1994; Balmford *et al.*, 2000; Grelle, 2002). All these
14 98 studies have generally focused on one region or a small set of regions, with
15 99 regional or local inventories across the respective taxonomic groups. On their
16 100 own, the results of these individual inventories, however, cannot be used to
17 101 fully guide specific biodiversity studies. This relates to the fact that these
18 102 detailed inventories generally used a much more comprehensive sampling
19 103 effort than 'normal' ecological studies, while higher taxa surrogacy might be
20 104 influenced by sampling effort per se (Larsen & Rahbek, 2005; Vieira *et al.*,
21 105 2012; Neeson *et al.*, 2013). Results from these inventory studies therefore
22 106 represent a compromise between the immense effort required in
23 107 species-specific studies covering a range of families, and the very limited
24 108 regional coverage possible when using such an approach. These studies
25 109 therefore need to balance the spatial and taxonomic resolutions they can
26 110 achieve. To understand the general patterns and links between the richness
27 111 recorded at species levels and that at higher taxonomic levels across taxa and
28 112 regions, it is therefore necessary to combine the existing approaches into a
29 113 common analytical framework.

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51 114 The second question, i.e. are the relative number of species per family across
52 115 different geographic regions similar, to some extent relates to the theory of
53 116 species' bio-geographical distributions. One of the most widely observed
54 117 bio-geographical rules in species distributions is the increase of species
55 118 richness from the poles to the equator (Williams *et al.*, 1997; Willig *et al.*, 2003;
56 119 Hillebrand, 2004). A variety of hypotheses has been proposed to explain the

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4 120 latitudinal gradients of biodiversity, among which the diversification rate -
5 121 hypothesis argues generational turnover and speciation rate in low latitude
6 122 regions is higher than at high latitudes due to the higher temperature and, at
7 123 least in the case of tropical rainforests, also high levels of humidity (Rohde,
8 124 1992; Mittelbach *et al.*, 2007; Condamine *et al.*, 2012). These conditions
9 125 resulted in ample opportunities for isolation, paratactic and sympatric
10 126 speciation, and genetic drift due to spatial-temporal heterogeneity (Rohde,
11 127 1992; Mittelbach *et al.*, 2007; Condamine *et al.*, 2012). According to this
12 128 hypothesis, we can expect that the number of species per higher taxa in
13 129 random samples increases from the poles to the equator, as well as potentially
14 130 from mountain tops to mountain bases. Although the diversification rate
15 131 hypothesis has not been supported by recent studies of ants (Economo *et al.*,
16 132 2018) and marine fishes (Rabosky *et al.*, 2018), an increasing trend in the
17 133 species / family ratio from high to low latitude has been observed already for
18 134 eastern Pacific marine molluscs (Roy *et al.*, 1996). The high heterogeneity of
19 135 environmental conditions linked for example to mountainous environments and
20 136 precipitation gradients in many terrestrial systems might limit the strength of
21 137 this trend in terrestrial taxa (McClain *et al.*, 2007; Rundell & Price, 2009).
22 138 Nonetheless, establishing existing trends in terrestrial species-family ratios
23 139 across different geographic regions is seen as important to provide guidance
24 140 for the use of family-level surrogacy.

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41 141 Here we examined the relationship between diversity at family and species
42 142 level across terrestrial animal taxa using data from the PREDICTS database
43 143 (Projecting Responses of Ecological Diversity in Changing Terrestrial
44 144 Systems) (Hudson *et al.*, 2017). This database contains site-level terrestrial
45 145 biodiversity data from hundreds of published studies of over 26,000 study sites
46 146 around the world. This database can be used to investigate a variety of core
47 147 ecological and biogeographic questions related to biodiversity and
48 148 conservation (Newbold *et al.*, 2015; Gray *et al.*, 2016; Newbold *et al.*, 2016;
49 149 Hudson *et al.*, 2017). We used the PREDICTS database to investigate the
50 150 following research questions at a global level and across a wide range of taxa:
51 151 i) What is the predictability of family-level surrogacy for species diversity, i.e.

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4 152 the correlation between the diversity at family and species level? ii) How does
5 153 the predictability of family surrogacy differ from genus-level surrogacy, and
6 154 how does it differ when using diversity indices rather than observed richness?
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9 155 iii) If significant correlations between family and species diversity occur, how
10 156 do these correlations differ between different biomes, and how are they linked
11 157 to sample size? iv) What is the influence of latitude, elevation and sample size
12 158 on the ratio between species number and family number?

159 **Method**

160 *Data selection*

161 The PREDICTS dataset (Hudson *et al.*, 2016), containing more than 3 million
162 records, was downloaded in January 2018. Unpublished sources and
163 non-English articles were excluded. We selected source studies containing
164 orders of both arthropods and vertebrates (Arthropoda and Chordata) with
165 abundance recording (presence and absence recordings were excluded),
166 which resulted in 215 source articles containing data for 281 studies

167 From these 281 studies, we selected those that have a full coverage within a
168 certain order, i.e. excluding source studies that only selected a subset of
169 families within an order. This resulted in a total of 160 source articles
170 representing 201 studies and 401 order \times study data-sets (a study could
171 contain multiple orders). In the next step of our analysis, we retained only the
172 studies that identified samples to species or morpho-species level with family
173 information. For the calculation of genus-level diversity surrogacy, species
174 without genus information were excluded. This resulted in 154 source articles
175 describing 191 source studies (see Appendix S1 for the flow chart of data
176 selection procedure and Appendix S2 for the respective selected study codes
177 from the PREDICT data source, with bibliographic references to these studies
178 included in list Appendix 1), 366 order \times studies, 13183 order \times sites, and
179 147,003 species records with a recorded abundance >0 . Sample sites
180 (hereafter referred to as "site"), considered as independent observations with
181 coordinate records, for which a list of taxa were sampled using the same

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3 182 method, represent our lowest unit of measurement. In some studies, different
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5 183 blocks were distinguished, e.g. according to biome or level of human
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7 184 disturbance. We treated such "blocks" as separate studies in the context of
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9 185 this analysis.

10 11 186 *Data Analysis*

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14 187 We calculated the Shannon diversity index for each site for the species, genus
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16 188 and family level, respectively. Shannon diversity is the most frequently used
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18 189 biodiversity index and has been considered to be a reasonably good measure
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20 190 of diversity for taxa that are incompletely sampled (Fiedler & Truxa, 2012).
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22 191 Shannon entropy (H , Appendix S3: Equation 1) describes the degree of chaos
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24 192 in a species assemblage. Exponentiation of the Shannon entropy results in the
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26 193 Shannon diversity (D , Appendix S3: Equation 2), a measure reflecting the
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28 194 effective richness (Jost, 2006). In addition, we also calculated Simpson's
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30 195 diversity index and the observed richness to check how robust the results
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32 196 generated for Shannon's diversity index are in comparison with these
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34 197 alternative diversity measures.

35 198 Pearson correlation coefficients (Pearson's r) between family and species
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37 199 diversities, and between genus and species diversities, were calculated for
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39 200 each study. Calculations and analysis were performed for each different order,
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41 201 respectively. We excluded sites where less than 20 individuals were recorded
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43 202 to ensure that diversity index values were robust (Appendix S1). Studies
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45 203 reporting from less than 5 sites were also excluded, resulting in a final pool of
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47 204 79 source articles, 101 source studies and 232 order \times studies (Appendix S1).

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49 205 A random effect meta-analysis was then conducted using Fisher's z ,
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51 206 calculated from Pearson's r (Appendix S3: Equation 3) (Field, 1999) as the
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53 207 effect size, based on restricted maximum likelihood (REML) methods to
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55 208 estimate the between-study variance, with the study included as a random
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57 209 factor (Schwarzer *et al.*, 2015). Funnel plots (for the Shannon diversity index)
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59 210 were made of Fisher's z and its standard error (Appendix S3: Equation 4) to
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211 assess publication bias. Results were converted back to Pearson's r for easier

212 interpretation.

213 To investigate the correlation across different regions, biome-specific
 214 correlations (Pearson's r) were calculated according to the Terrestrial
 215 Ecoregions of the World dataset (The Nature Conservancy, 2009), as used by
 216 PREDICTS (Hudson *et al.*, 2017). Of the 14 biomes represented by the
 217 selected source-studies in the PREDICTS dataset, six contained sufficient
 218 numbers of studies to allow for comparisons of species-family structures within
 219 the same order with other biomes. These six biomes are 'Temperate Broadleaf
 220 & Mixed Forests' (TBMF), 'Temperate Grasslands, Savanna & Shrublands'
 221 (TGSS), 'Tropical & Subtropical Moist Broadleaf Forests' (TSMBF), 'Tropical &
 222 Subtropical Grasslands, Savanna & Shrublands' (TSGSS), 'Montane
 223 Grasslands & Shrublands' (MGS) and 'Boreal Forests/Taiga' (BFT).

224 To investigate how sample size affects the correlation between species and
 225 family diversity, linear models were used to establish the relationship between
 226 Pearson's r (response variable) and sampling effort (explanatory variable),
 227 expressed as the median value for the log number of individuals per study. For
 228 the modelling analysis exploring the relationship between the response
 229 variable and explanatory variable, orders that were presented in the dataset by
 230 less than 5 studies (block-studies) were excluded to avoid model over-fit.

231 Linear regression based on Shannon entropy was applied to investigate the
 232 relationship between Shannon Entropy at species (H_S) and family level (H_F)
 233 (Equation 1):

$$234 \quad H_{S_{m,j}} = b * H_{F_{m,j}} + a \quad (1),$$

235 where a is the intercept and b is the slope of the model. Coefficients a and b
 236 were estimated by meta-analysis (random effects model, REML to estimate
 237 between-study variance). Left- and right-hand sides of the above equation are
 238 then exponentiated to convert Shannon entropy to Shannon diversity
 239 (Equation 2):

$$240 \quad D_{S_{m,j}} = \exp(a) * D_{F_{m,j}}^b \quad (2).$$

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4 241 If the value of $b=1$, the equation represents a linear relationship (without
5 242 intercept) between the number of species and the number of families. Since
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7 243 this was the case for our data, linear models were used to establish the
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9 244 species / family ratio for the Shannon diversity index (D , Equation 3), allowing
10 245 a direct comparison between taxa. The model can be expressed as:

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$$D_{S_{m,j}} = \beta * D_{F_{m,j}} + C \quad (3),$$

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16 247 where D_S and D_F are the Shannon diversity indices at species and family level
17 248 in site j for a study m ; β is the slope, and C is the intercept in the linear model.
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19 249 By setting the intercept to 0, the slope (β) therefore corresponds to the number
20 250 of species per family. The mean value of β was estimated by meta-analysis
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22 251 (random effects model, REML to estimate between-study variance). Species /
23 252 family ratios were also calculated for the observed richness in each taxon, in
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25 253 addition to the species / genus ratios calculated for both the Shannon diversity
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27 254 index and observed richness. All these measures were used to study the
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29 255 correlations in diversity patterns between these higher taxonomic levels and
30 256 species diversity in models constructed in the same way as described for the
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32 257 Shannon diversity index values in a meta-analysis.

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37 258 Finally, multiple linear regression was used to investigate how the species /
38 259 family ratio for each study (i.e. β_j) was related to sample size (log transformed
39 260 number of individuals), latitude (absolute value for UTM system, reflecting
40 261 kilo-meters from the equator) and elevation (Appendix S3: Equation 5), with
41 262 elevations obtained from Google Maps based on the coordinates given for
42 263 each site in the dataset.

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48 264 All analysis and calculations were performed in R (V.3.5.2) (R Core Team,
49 265 2018). Package “vegan” (Oksanen *et al.*, 2014) was used to calculate diversity
50 266 indices, “meta” (Schwarzer, 2015) for meta-analysis and “rgbif” (Chamberlain
51 267 *et al.*, 2015) to obtain elevation information.

52 268 **Results**

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59 269 The total 401 ‘order x studies’ cases that covered all families within an order

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4 270 included 10 classes (Aves, Amphibia, Arachnida, Mammalia, Insecta,
5 271 Chilopoda, Diplopoda, Reptilia, Malacostraca, Entognatha) and 46 orders.
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7 272 Apart from 33 studies out of 132 in Insecta, and 2 out of 36 in Arachnida that
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9 273 identified taxa only to family levels, the remaining 366 cases identified taxa to
10 274 (morpho-) species level (Figure 1a). Across Terrestrial Ecoregions of the
11 275 World, most of these 366 cases were located in the biomes Tropical &
12 276 Subtropical Moist Broadleaf Forests (TSMBF, 129), Temperate Broadleaf &
13 277 Mixed Forests (TBMF, 84) and Tropical & Subtropical Grasslands, Savanna &
14 278 Shrublands (TSGSS, 51) (Figure 1b).

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20 279 Valid studies meeting all our selection criteria covered nine orders in 5 classes.
21 280 The estimated mean correlation coefficients (Pearson's r) were higher than 0.5
22 281 for all diversity metrics in all orders, and for both, family-species correlation
23 282 and genus-species correlation (Figure 2). With regards to the performance of
24 283 the Shannon diversity index in family-level surrogacy, the highest correlations
25 284 were observed in Diptera (mean, 95% CI and number of samples: 0.88,
26 285 0.71-0.95, $n=6$), following by Hemiptera (0.87, 0.75-0.93, $n=9$) and Coleoptera
27 286 (0.86, 0.82-0.90, $n=33$), Passeriformes (0.80, 0.75-0.84, $n=61$), Hymenoptera
28 287 (0.73, 0.66-0.79, $n=36$) and Araneae (0.73, 0.67-0.78, $n=45$). Weaker
29 288 correlations were observed in Squamata (0.64, 0.21-0.87, $n=4$) and Anura
30 289 0.60, 0.32-0.78, $n=9$), while the lowest correlation coefficients were recorded
31 290 for Lepidoptera (0.57, 0.44-0.68, $n=17$). The funnel plots indicate an absence
32 291 of publication bias across all orders (Appendix S4), while scatter plots showing
33 292 family-level versus species-level Shannon entropy highlight distinct linear
34 293 relationships (Appendix S5).

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48 295 Comparing different taxonomic ranks, Shannon index correlations were similar
49 296 for family-level and genus-level surrogacy in Diptera, Hemiptera and
50 297 Hymenoptera, while correlations were slightly stronger in family-species
51 298 relationships than genus-species relationship for Coleoptera. In
52 299 Passeriformes, Araneae, Squamata and Lepidoptera, this trend was reversed
53 300 (Figure 2a). The patterns for the Simpson diversity index were very similar to
54 301 results obtained for the Shannon diversity index (Figure 2b). When using

302 observed taxon richness, genus-species correlations generally performed
303 better than family-species correlations across all taxa (Figure 2c).

304 Only three orders, Araneae, Coleoptera and Passeriformes, were recorded in
305 at least 2 biomes with more than 3 studies in each biome. In these taxa,
306 species– family diversity correlations did not differ between biomes with the
307 exception of Passeriformes, where assemblages in temperate forests (TBMF
308 biome) showed a higher correlation than assemblages in the two tropical
309 biomes TSMBF and TSGSS (Figure 3a). Sample size (log-transformed
310 number of individuals) did not have a significant influence on Pearson's r for
311 any of the orders (Figure 3b).

312 Exponential models (Equation 1) showed that the number of species increases
313 linearly with the number of families (b in Equation 1 reaches values ~ 1 across
314 all orders, Figure 4). The species / family ratio based on the Shannon diversity
315 index was very similar to the ratio based on species richness. The average
316 value of β (Equation 3) was 2.5 for the Shannon diversity indices, in
317 comparison to a ratio of 2.7 for species versus family richness. The minimum
318 species / family Shannon diversity ratio was 1.6 for Anura (95% CI: 1.4 - 1.8),
319 and the maximum was 4.6 in Lepidoptera (3.9 - 5.3, Table 1). In contrast, the
320 species / genus ratio was 1.5 and 1.6 based on the Shannon diversity index
321 and observed richness, with 7 out of 9 orders showing values ≤ 1.5 . The ratio
322 for Lepidoptera based on Shannon diversity index values was only 1.3 (1.20
323 – 1.35, Table 1).

324 Species / family Shannon diversity ratios were positively correlated with
325 sample size across all taxa, but the increase rate was low, with an average
326 increase in the ratio of 0.51 (range: 0.2 to 0.81) for an exponential increase in
327 the overall sample size (Table 1). This positive correlation was furthermore
328 only significant in Araneae ($\beta=0.72 \pm 0.18$, $P<0.001$), Passeriformes
329 ($\beta=0.42 \pm 0.1$, $P<0.001$) and Hymenoptera ($\beta=0.7 \pm 0.27$, $P=0.047$)
330 (Table 1, Appendix S6). Effects of elevation and latitude on species / family
331 Shannon diversity ratio among taxa differed strongly. For example, elevation
332 had a negative relationship with the species / family ratio for Araneae

333 (beta=-0.09 ± 0.03, $P=0.003$), but a positive one for Coleoptera (beta=0.16 ±
334 0.08, $P=0.025$); latitude had a significant negative relationship with the species
335 / family ratio only in Passeriformes (beta=-0.06 ± 0.03, $P=0.025$), whereas no
336 significant links were observed in any of the other taxa (Table 1).

337 Discussion

338 Family-species diversity correlation is generally high across a wide range of
339 different taxonomic groups, with particularly high correlations observed across
340 the majority of arthropod taxa. For other taxa such as mammals, patterns
341 remain somewhat inconclusive due to an insufficient number of studies
342 available for a robust investigation. While family-level diversity surrogacy was
343 weaker than genus-level surrogacy, the cost of using genera as surrogates
344 needs to be considered. Genus-species ratios for most orders were less than
345 1.5, indicating that limited identification effort has been saved when using
346 genus diversity as a surrogate for species diversity. Particularly in some
347 mega-diverse arthropod taxa, identification of specimens to genus level might
348 already pose significant challenges, resulting in low trade-offs between
349 cost-effectiveness and information retainment (Cardoso *et al.*, 2004;
350 Perez-Fuertes *et al.*, 2016). The weaker trend for family-level surrogacy in
351 comparison to genus-level surrogacy was furthermore reversed for Shannon
352 diversity index values in Coleoptera, which might reflect the particularly strong
353 difficulties in identifying all specimens in this mega-diverse order reliably to
354 genus level. In addition, the differences between family-species diversity links
355 and genus-species diversity links are stronger in observed richness than for
356 diversity indices in many taxa, suggesting that diversity indices represent the
357 preferred means when using family-level surrogacy.

358 Our results furthermore showed that sample size had no influence on the
359 correlations between Shannon diversity at family- and species-levels
360 (Pearson's r). This suggests that the potential requirement to collect very large
361 samples can be negated when using higher taxa surrogacy particularly in
362 regional investigations and when between-site variance of sample sizes is
363 relatively small (Villasenor *et al.*, 2005; Wolters *et al.*, 2006). While species /

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4 364 family ratios were positively correlated with the sample size for all taxa on a
5 365 global scale, the underlying trend (k_1 in Equation 5, Appendix S3) was
6 366 relatively low. Overall, these results suggest that sample size only needs to be
7 367 considered in evaluations of diversity changes at species level based on
8 368 diversity changes at families level in cases where the variance in sample sizes
9 369 within a study is very high (e.g. at exponential scales) (Larsen & Rahbek,
10 370 2005; Terlizzi *et al.*, 2009; Vieira *et al.*, 2012). In addition, it needs to be
11 371 considered that different sample sizes in studies might be related to different
12 372 sampling methods used, while they could also relate to differences in sampling
13 373 effort, such as the number of traps used or of sampling days (Chao *et al.*,
14 374 2014), which may distort family- and species diversity correlations (Vieira *et al.*,
15 375 2012). We were unfortunately unable to comprehensively investigate the
16 376 overall influence of sampling effort in this study, since standardized sampling
17 377 effort information was not available for all studies, and reducing the dataset
18 378 exclusively to studies with available information would have resulted in a
19 379 strong reduction in overall statistical power of the analysis.

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33 380 The consistency of species-family Shannon diversity correlations across
34 381 different biomes, while needing further verification through the inclusion of
35 382 more taxonomic groups, confirms the potential of higher-taxon survey
36 383 approaches for biodiversity assessments. We nonetheless need to
37 384 acknowledge that cross-biome transferability cannot generally be assumed
38 385 across the different taxonomic levels, as shown by a higher family-species
39 386 correlation performance in temperate than tropical regions for Passeriformes.
40 387 Likewise, van Rijn *et al.* (2015) reported, based on both genus- and
41 388 subfamily-level surrogacy, that the performance of higher taxa surrogate
42 389 approaches for bees differed between biomes. Overall, the transferability of
43 390 higher taxa surrogacy across regions requires significant future attention,
44 391 testing and additional research.

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55 392 The mean species / family ratio across our studies is relatively low for both the
56 393 Shannon diversity index (~2.5) and observed richness (~2.7), with all taxa
57 394 showing values on a similar scale and with a low variance. Such low values

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4 395 are in strong contrast to the much greater, and highly variable, number of
5 396 globally described species per family among different taxa, for example
6 397 varying between 40 and 60 for birds (Reddy, 2015), but being about 160 for
7 398 frogs (Pough *et al.*, 2015), about 400 for spiders (World Spider Catalog, 2018)
8 399 and >1400 for Leiodoptera (Capinera, 2008). Nonetheless, this low species /
9 400 family ratio is consistent with previous higher-taxa surrogate studies. For
10 401 example Li *et al.* (2006) reported a linear relationship of about 2 species per
11 402 family in a variety of aquatic plant groups within a grid survey on a 9 X 9 km²
12 403 area in China's northwest arid zone. Williams and Gaston (1994) also
13 404 recorded between 2 and 5 species per family for ferns, butterflies and birds in
14 405 their regional study in Britain, Australia and America when the recorded
15 406 species count is low (i.e. <20 species). This implies that, while species are
16 407 distributed asymmetrically within higher taxa (i.e. some taxa contain many
17 408 species and some contain few) (Gaston, 2000), the species-family ratio is
18 409 relatively low in general ecological studies where spatial resolutions of
19 410 individual study plots are commonly small. Nonetheless, although we found
20 411 the species / family ratio to be similar for many taxa (e.g. 2.7 for Araneae, 2.3
21 412 for Coleoptera and 2.1 for Hemiptera), we suggest a prediction of species
22 413 numbers by observed families should be order-specific, as variance is still
23 414 existent (e.g. 1.6 for Anura and 4.6 for Lepidoptera). In taxa with low ratios, the
24 415 predictability of species diversity by family diversity is greatly enhanced, with a
25 416 high ratio often linked to a high variability due to stochastic factors (Rosser,
26 417 2017; Driessen & Kirkpatrick, 2019). For example, among arthropods,
27 418 Lepidoptera show the highest species-family ratios, but also the lowest
28 419 correlation coefficients between taxonomic levels. Here, we only applied linear
29 420 models to obtain species-family relationship, but considering the relatively low
30 421 observed species in each site for most studies, a linear model usually works
31 422 well (Cardoso *et al.*, 2004). Therefore, we consider the relatively low number of
32 423 species per family that we found to be consistent with previous ecological
33 424 studies, done at much smaller spatial extent than the current global
34 425 meta-analysis.

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59 426 In contrast to our expectation, we did not find a uniform decrease in the
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4 427 species / family ratio with higher latitude or elevation across taxa. As local
5 428 species richness is determined not only by speciation, but also by dispersal
6 429 and extinction (Mittelbach *et al.*, 2007; Condamine *et al.*, 2012), inconformity in
7 430 species / family ratios across different taxa may have a number of reasons.
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9 431 First, it might be related to the limited statistical power for observing a
10 432 significant geographical trend, due to the relatively low number of species and
11 433 families observed in each study, and the lack of sufficient studies that cover a
12 434 wide range of regions. Second, species might not be randomly distributed
13 435 across their geographical range (McClain *et al.*, 2007). Species diversification
14 436 resulting from ecological processes such as regional and local environmental
15 437 heterogeneity (e.g. isolation) in terrestrial systems may influence their global
16 438 geographical pattern, and such effects might vary between different taxa
17 439 (McClain *et al.*, 2007; Rundell & Price, 2009). Furthermore, separation of
18 440 specimens into species (let alone morpho-species) might be biased due to
19 441 differing ease of separation / identification, and such bias might differ between
20 442 regions and taxa. Overall, species / family ratios in ecological studies are
21 443 therefore ill suited to directly test the latitudinal change of speciation
22 444 hypothesis (Roy *et al.*, 1996).

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36 445 Despite criticism of the higher taxonomic surrogacy approaches raised for
37 446 example suggesting that higher taxa are unlikely to reflect intricate
38 447 species-level responses to environmental disturbances (Bevilacqua *et al.*,
39 448 2012), our results demonstrate that family diversity is generally closely related
40 449 to species-level diversity, which means family-level taxon diversity can provide
41 450 a useful proxies measure for species-level diversity particularly for taxa with
42 451 low species-family ratios in individual samples. Although genus-level diversity
43 452 might perform better in indicating species diversity, family-level proxies are
44 453 applicable much more widely, particularly in studies of mega-diverse
45 454 arthropods, where the trade-off between cost-effectiveness and information
46 455 retained in the recorded data structure is low. However, in studies containing
47 456 data for multiple high-rank taxa (e.g. orders), comparisons between taxa may
48 457 also reflect differences in speciation and taxonomic resolution (Purvis &
49 458 Hector, 2000). Family surrogacy can enrich insights generated by biodiversity-

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4 459 and conservation-related studies, offering an additional measure to
5 460 molecular-based technologies such as DNA barcoding and eDNA (Bush *et al.*,
6 461 2017; Lopes *et al.*, 2017), and provide complementary information to the
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8 462 current well-established measures that focus on vertebrates and plants. The
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10 463 use of family diversity proxies could address the problems associated with the
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12 464 current focus in biodiversity conservation on a minute fraction of the global
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14 465 species pool, **facilitating much-needed rapid biodiversity assessments to**
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16 466 **inform conservation-related evaluation and planning.**

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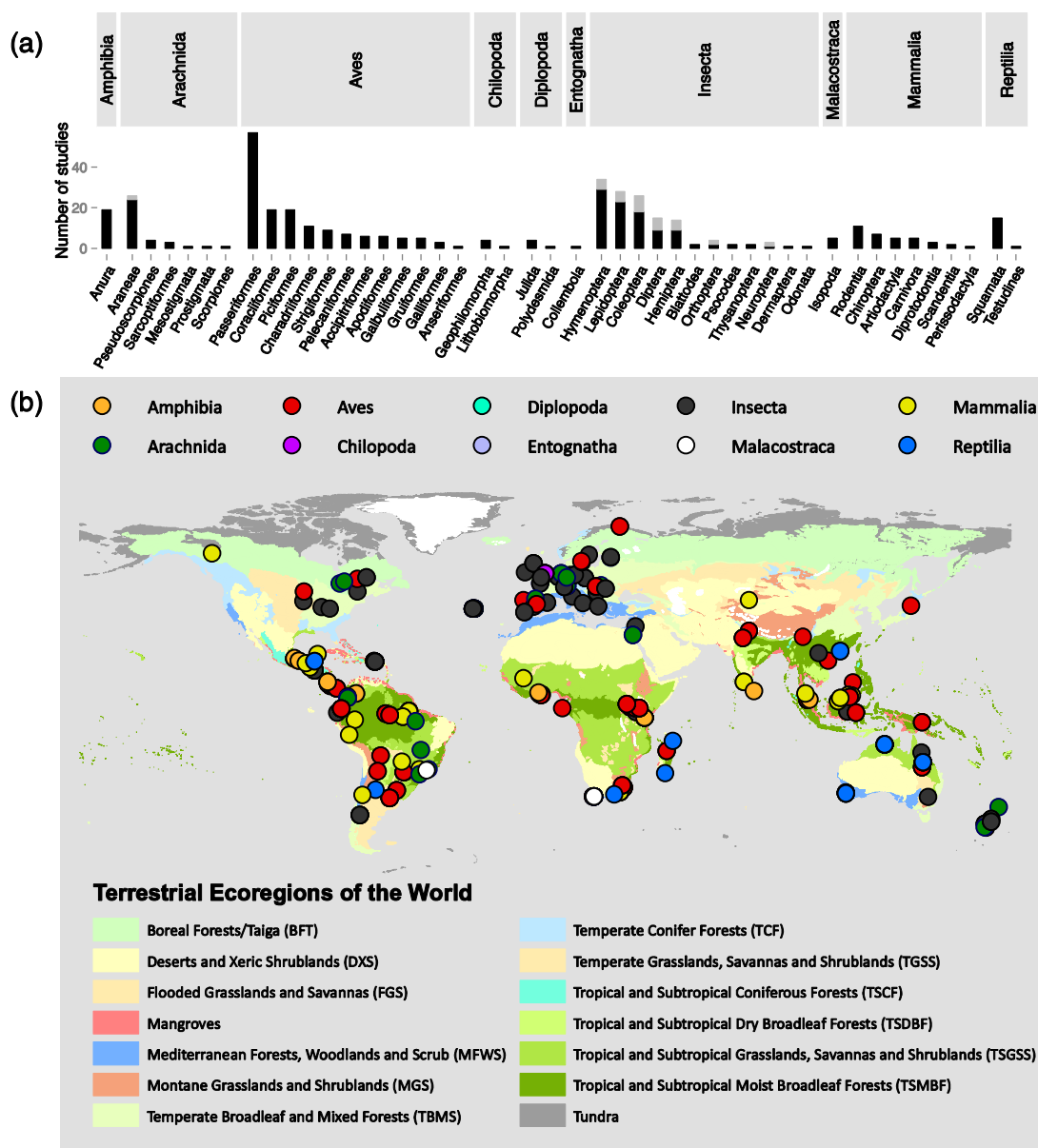
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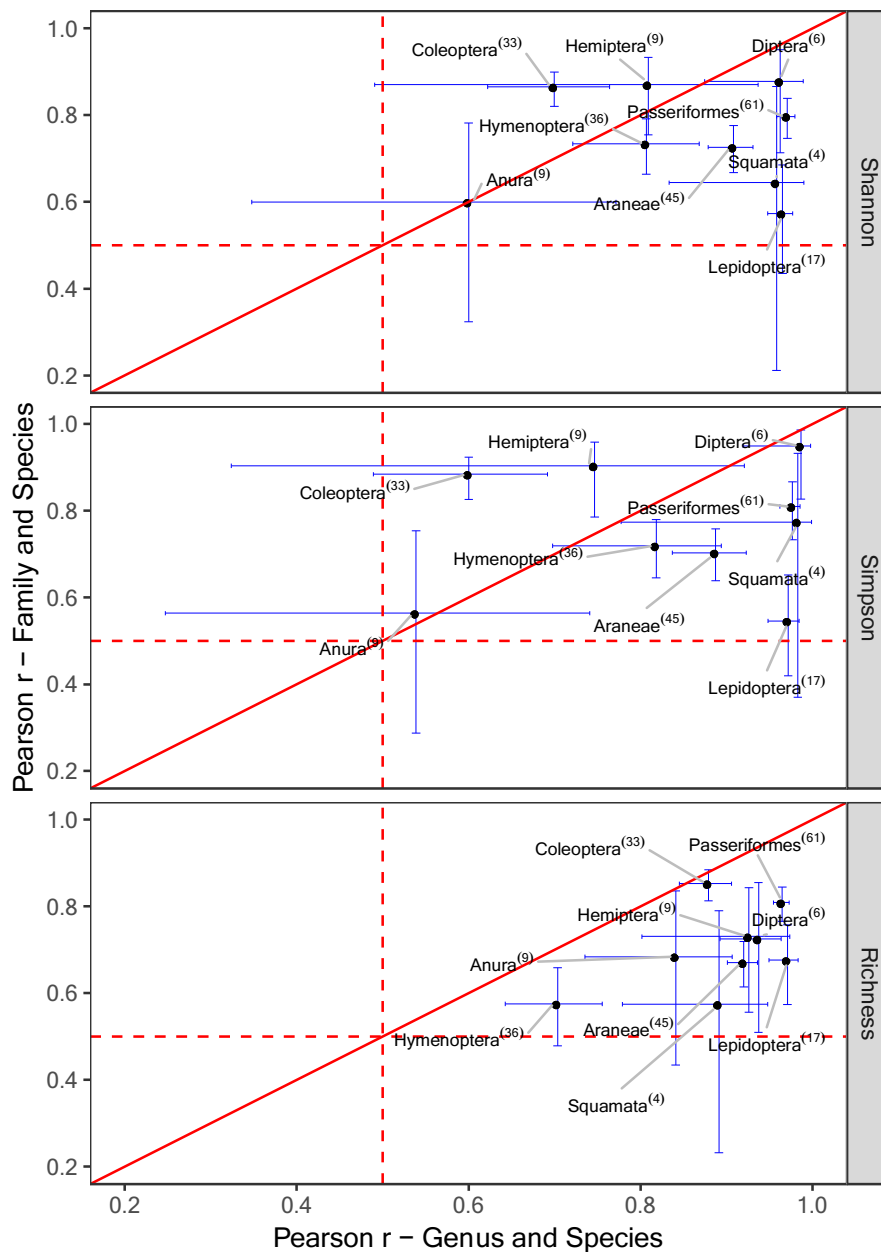
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678 **Figures**



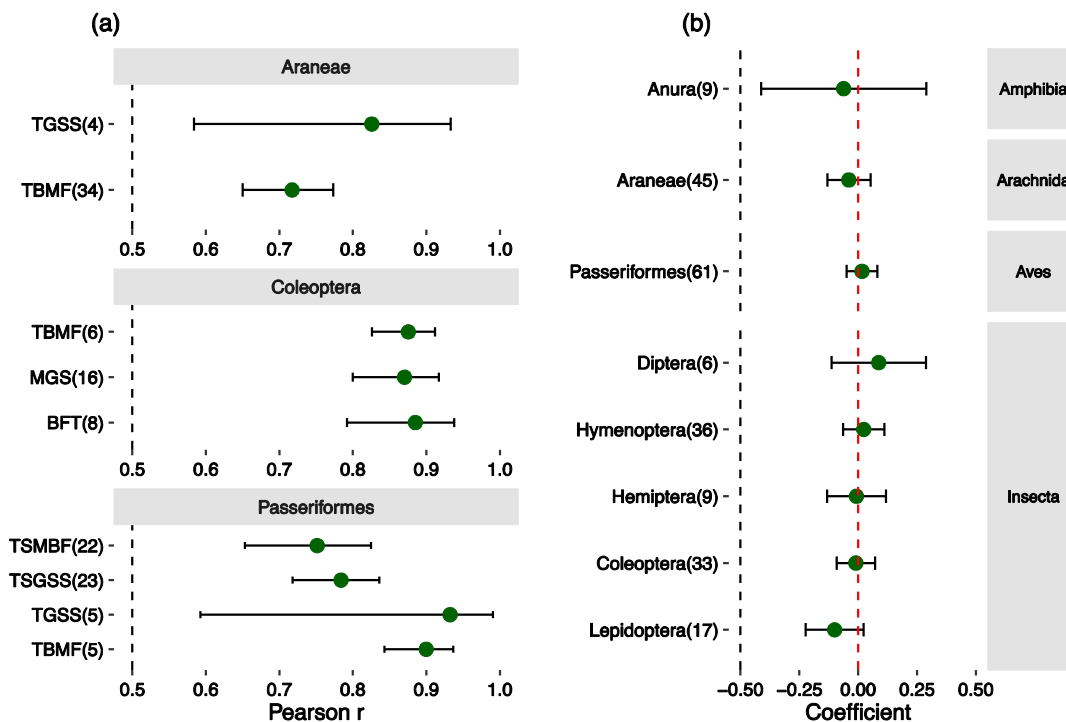
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680 Figure 1. World map of biodiversity studies covering all families with an order
 681 of terrestrial animals in the PREDICTS database (Hudson et al., 2017). Panel
 682 a: grey bars represent studies that identify taxa to family level only, while black
 683 bars represent studies that identify taxa in addition to (morpho-)species-level.
 684 Panel b: locations of species-level identified studies across the Terrestrial
 685 Ecoregions of the World.



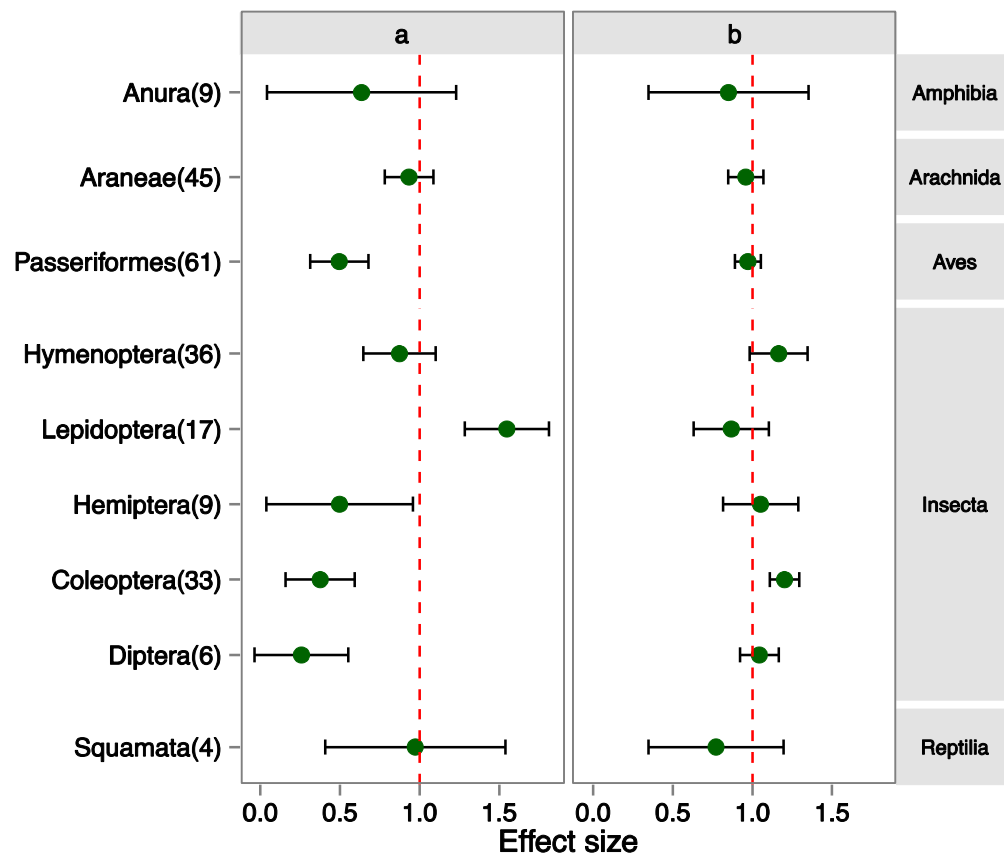
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687 Figure 2. Meta-analysis results from random effects models showing
 688 Pearson's r of family-species relationships and genus-species relationships for
 689 the Shannon diversity index, the Simpson's diversity index and observed
 690 richness in nine different orders of terrestrial animals. Numbers in brackets
 691 refer to the number of studies, and error bars show 95% CI; dashed lines refer
 692 to values of $r = 0.5$; solid lines refer to a 1:1 relationship between x and y axis;
 693 points below the 1:1 diagonal line represent cases where r values for
 694 family-species relationship are lower than for genus-species relationship and
 695 vice versa. Orders represented in less than three studies were not included.



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697 Figure 3 Meta-analysis results (a) for Pearson's r (based on the Shannon
 698 diversity index) in different biomes (only orders that cover at least 2 biomes
 699 with at least 3 studies from each biome were included); TBMF: Temperate
 700 Broadleaf & Mixed Forests, TGSS: Temperate Grasslands, Savannas &
 701 Shrublands, TSMF: Tropical & Subtropical Moist Broadleaf Forests, TSGSS:
 702 Tropical & Subtropical Grasslands, Savannas & Shrublands, MGS: Montane
 703 Grasslands & Shrublands, BFT: Boreal Forests/Taiga; and slope of the
 704 relationship between Pearson's r and sample size (b), showing the median log
 705 number of individuals per site in each study



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707 Figure 4. Meta-analysis results from random effects models showing the
 708 intercept (a) and slope (b) of order-specific regression models of species-level
 709 versus family-level values for Shannon entropy (H)

Table 1. Median value of the number of species, genera and families per site, meta-analysis results from random effects models showing estimated species / family, and species / genus ratios based on Shannon diversity and observed richness (orders represented by <3 studies were excluded), and coefficients of the species / family ratio based on the Shannon diversity index, in response to the change of sample size (log-transformed number of individuals), elevation and latitude for different taxa (Equation 5 in Appendix S4, orders more than six studies were included in the regression); Asterisks show significance levels (* ≤ 0.05 ; ** ≤ 0.01 ; *** ≤ 0.001)

Class	Order	Number of studies	Number of species	Number of Genus	Number of families	Species / family (Shannon)			Species / genus (Shannon)			Species / genus (Richness)			Regression coefficients		
						family (Shannon)	family (Richness)	genus (Shannon)	genus (Shannon)	genus (Richness)	Sample Size	Latitude	Altitude				
Amphibia	Anura	9	9.3	5.0	4.3	1.6 (1.4-1.8)	1.8 (1.6-2)	1.5 (1.3-1.7)	1.6 (1.5-1.8)	0.29 ± 0.17	-0.14 ± 0.25	0.36 ± 0.18					
Arachnida	Araneae	45	18.1	13.7	6.0	2.7 (2.4-3.0)	2.7 (2.4-2.9)	1.3 (1.2-1.3)	1.3 (1.3-1.4)	0.72 ± 0.18	0.19 ± 0.1	-1.76 ± 0.45	***		***		
Aves	Passeriformes	61	11.3	10.7	7.5	1.7 (1.6-1.9)	1.7 (1.5-1.8)	1.1 (1.08-1.14)	1.1 (1.08-1.13)	0.42 ± 0.1	-0.11 ± 0.05 *	-0.05 ± 0.1	***				
Insecta	Hymenoptera	36	11.4	4.8	3.3	3.1 (2.7-3.6)	3.7 (3.1-4.3)	2.4 (2.1-2.7)	2.5 (2.2-2.8)	0.7 ± 0.27 *	0.63 ± 0.2 **	-0.75 ± 0.86	0.2 ± 0.16	0.2 ± 0.11	1.23 ± 0.37 **		
	Coleoptera	33	34.7	12.1	15.9	2.3 (2.1-2.5)	2.4 (2.2-2.5)	2.1 (1.8-2.5)	2.7 (2.3-3.1)	0.81 ± 0.41	-0.49 ± 0.3	0.38 ± 2.02	0.81 ± 0.41	-0.49 ± 0.3	0.38 ± 2.02		
	Lepidoptera	17	55.8	43.1	5.8	4.6 (3.9-5.3)	5.3 (3.8-6.8)	1.3 (1.20-1.35)	1.3 (1.2-1.4)	0.42 ± 0.27	0.15 ± 0.2	-4.02 ± 1.72	0.42 ± 0.27	0.15 ± 0.2	-4.02 ± 1.72		
	Hemiptera	9	6.8	5.9	4.1	2.2 (1.5-2.9)	2.2 (1.6-2.9)	1.4 (1.1-1.6)	1.6 (1.2-2)	/	/	/	/	/	/		
	Diptera	6	13.2	10.9	6.5	1.8 (1.2-2.5)	2.6 (1.0-4.3)	1.1 (1-1.3)	1.3 (1-1.6)	/	/	/	/	/	/		
Reptilia	Squamata	4	6.8	6.5	4.1	2.1 (1.2-3.0)	2 (1.3-2.7)	1.1 (1-1.3)	1.1 (1-1.2)	/	/	/	/	/	/		

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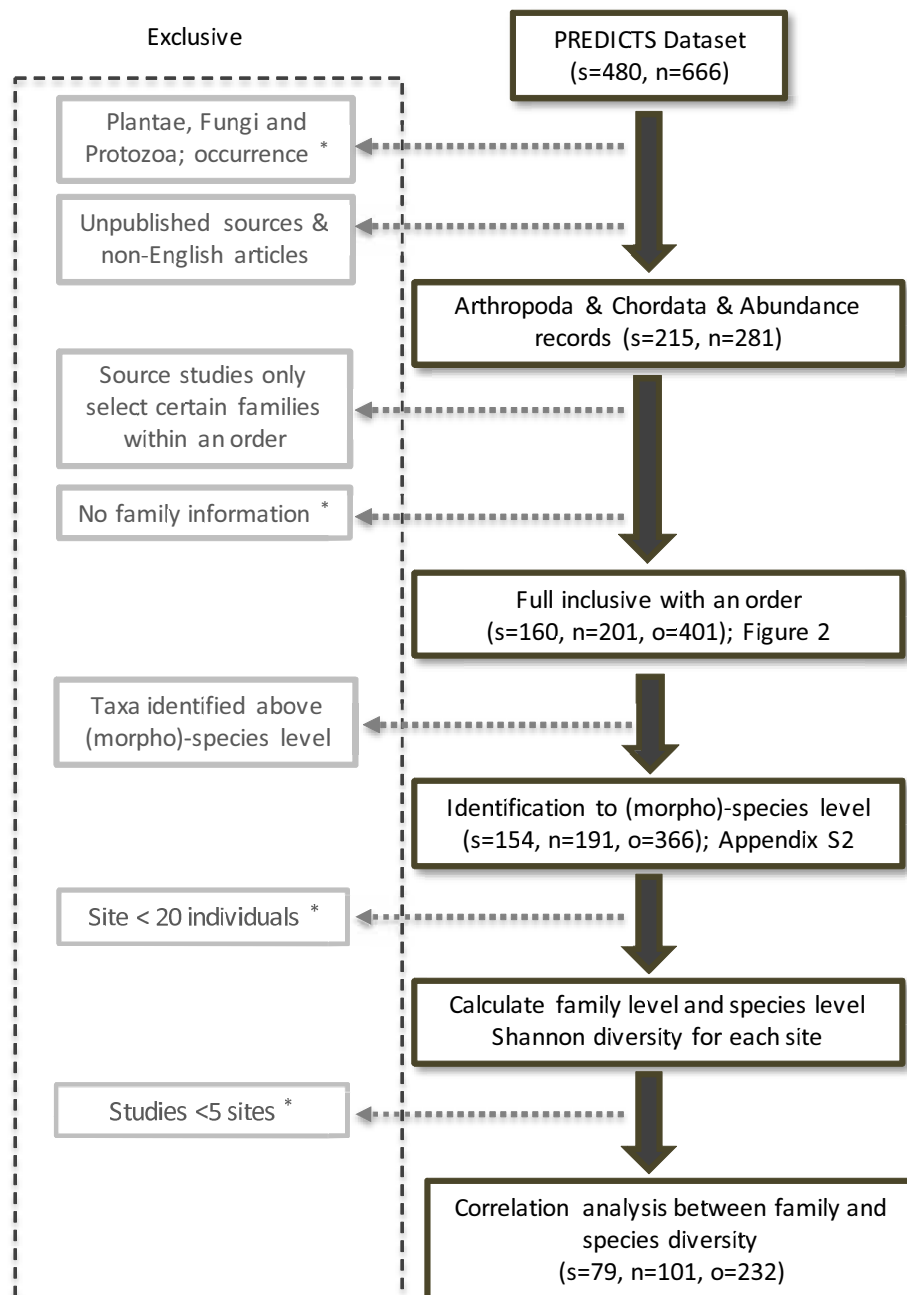
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Electronic Supplementary Materials

Appendix S1. Flow chart of the data selection, s: number of source articles, n: number of studies, o: number of order x studies; * refers to the selection criteria was applied at dataset records



Appendix S2. List of selected studies from the PREDICTS database (<https://doi.org/10.5519/0066354>) dataset. “Source_ID” and “SS” are indices for the PREDICTS data source, referring to the ID of the Data Source and the code combination of “Source_ID” and “Study_number”.

No.	Source_ID	SS	Class	Order
1	MJ1_2013__Adum	MJ1_2013__Adum 1	Amphibia	Anura
2	SE2_2012__Craig	SE2_2012__Craig 1	Amphibia	Anura
3	SE2_2014a__Craig	SE2_2014a__Craig 1	Amphibia	Anura
4	SE2_2014b__Craig	SE2_2014b__Craig 1	Amphibia	Anura
5	SC1_2008__Eigenbrod	SC1_2008__Eigenbrod 1	Amphibia	Anura
6	DI1_2013__Faruk	DI1_2013__Faruk 1	Amphibia	Anura
7	SE1_2004__Gutierrez	SE1_2004__Gutierrez 1	Amphibia	Anura
8	SE1_2004__Gutierrez	SE1_2004__Gutierrez 2	Amphibia	Anura
9	CM1_2012__Hilje	CM1_2012__Hilje 1	Amphibia	Anura
10	SE1_2011__Isaacs	SE1_2011__Isaacs 1	Amphibia	Anura
11	SC1_2014__Kurz	SC1_2014__Kurz 1	Amphibia	Anura
12	HZ1_2012__Kutt	HZ1_2012__Kutt 1	Amphibia	Anura
13	MJ1_2012__Malonza	MJ1_2012__Malonza 1	Amphibia	Anura
14	DL1_2013__OforiBoateng	DL1_2013__OforiBoateng 1	Amphibia	Anura

15	KS1_2012__Pethiyagoda	KS1_2012__Pethiyagoda 1	Amphibia	Anura
16	HP1_2004__Pineda	HP1_2004__Pineda 1	Amphibia	Anura
17	YP1_2012__Sung	YP1_2012__Sung 1	Amphibia	Anura
18	SC1_2006__UrbinaCardona	SC1_2006__UrbinaCardona 1	Amphibia	Anura
19	DL1_2009__Woinarski	DL1_2009__Woinarski 2	Amphibia	Anura
20	AD1_2008__Billeter	AD1_2008__Billeter 15	Arachnida	Araneae
21	AD1_2008__Billeter	AD1_2008__Billeter 16	Arachnida	Araneae
22	AD1_2008__Billeter	AD1_2008__Billeter 17	Arachnida	Araneae
23	AD1_2008__Billeter	AD1_2008__Billeter 18	Arachnida	Araneae
24	AD1_2008__Billeter	AD1_2008__Billeter 19	Arachnida	Araneae
25	AD1_2008__Billeter	AD1_2008__Billeter 20	Arachnida	Araneae
26	AD1_2008__Billeter	AD1_2008__Billeter 21	Arachnida	Araneae
27	KS1_2006__Borges	KS1_2006__Borges 1	Arachnida	Araneae
28	VK1_2008__Buddle	VK1_2008__Buddle 1	Arachnida	Araneae
29	SE1_2012__Cabra	SE1_2012__Cabra 1	Arachnida	Araneae
30	SC1_2011__Meijer	SC1_2011__Meijer 1	Arachnida	Araneae
31	CC1_2004__Clark	CC1_2004__Clark 1	Arachnida	Araneae
32	GP1_2011__Freire	GP1_2011__Freire 1	Arachnida	Araneae
33	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Arachnida	Araneae

34	HP1_2008__Kapoor	HP1_2008__Kapoor 1	Arachnida	Araneae
35	CM1_2008__LoManHung	CM1_2008__LoManHung 1	Arachnida	Araneae
36	VB1_2011__LoManHung	VB1_2011__LoManHung 1	Arachnida	Araneae
37	DB1_2010__Magura	DB1_2010__Magura 1	Arachnida	Araneae
38	CC1_2014__MalumbresOlarte	CC1_2014__MalumbresOlarte 1	Arachnida	Araneae
39	SH1_2012__Norfolk	SH1_2012__Norfolk 1	Arachnida	Araneae
40	VK1_2011__Paradis	VK1_2011__Paradis 1	Arachnida	Araneae
41	SC1_2014__Raub	SC1_2014__Raub 1	Arachnida	Araneae
42	SC1_2005__Richardson	SC1_2005__Richardson 1	Arachnida	Araneae
43	VB1_2009__UeharaPrado	VB1_2009__UeharaPrado 1	Arachnida	Araneae
44	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Arachnida	Mesostigmata
45	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Arachnida	Prostigmata
46	SE1_2012__Cabra	SE1_2012__Cabra 1	Arachnida	Pseudoscorpiones
47	SC1_2011__Meijer	SC1_2011__Meijer 1	Arachnida	Pseudoscorpiones
48	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Arachnida	Pseudoscorpiones
49	SC1_2005__Richardson	SC1_2005__Richardson 1	Arachnida	Pseudoscorpiones
50	MG1_2005__Arroyo	MG1_2005__Arroyo 1	Arachnida	Sarcoptiformes
51	SE1_2012__Cabra	SE1_2012__Cabra 1	Arachnida	Sarcoptiformes

52	MG1_2006__Zaitsev	MG1_2006__Zaitsev 1	Arachnida	Sarcoptiformes
53	CM1_2008__LoManHung	CM1_2008__LoManHung 1	Arachnida	Scorpiones
54	DL1_2005__Cockle	DL1_2005__Cockle 1	Aves	Accipitriformes
55	HP1_2008__Gomes	HP1_2008__Gomes 1	Aves	Accipitriformes
56	HP1_2010__Lasky	HP1_2010__Lasky 1	Aves	Accipitriformes
57	HP1_2010__Lasky	HP1_2010__Lasky 2	Aves	Accipitriformes
58	DI1_2010__Milder	DI1_2010__Milder 2	Aves	Accipitriformes
59	TN1_2007__ODea	TN1_2007__ODea 1	Aves	Accipitriformes
60	HW1_2011__Cerezo	HW1_2011__Cerezo 1	Aves	Anseriformes
61	DL1_2005__Cockle	DL1_2005__Cockle 1	Aves	Apodiformes
62	HP1_2008__Gomes	HP1_2008__Gomes 1	Aves	Apodiformes
63	DI1_2010__Milder	DI1_2010__Milder 2	Aves	Apodiformes
64	TN1_2007__ODea	TN1_2007__ODea 1	Aves	Apodiformes
65	MH1_2010__Sheldon	MH1_2010__Sheldon 1	Aves	Apodiformes
66	KS1_2009__SuarezRubio	KS1_2009__SuarezRubio 1	Aves	Apodiformes
67	DI1_2013__Azhar	DI1_2013__Azhar 1	Aves	Charadriiformes
68	DL1_2009__Azpiroz	DL1_2009__Azpiroz 1	Aves	Charadriiformes
69	HW1_2005__Baldi	HW1_2005__Baldi 1	Aves	Charadriiformes
70	HW1_2011__Cerezo	HW1_2011__Cerezo 1	Aves	Charadriiformes

71	HW1_2007__Chapman	HW1_2007__Chapman 1	Aves	Charadriiformes
72	DB1_2010__Dures	DB1_2010__Dures 1	Aves	Charadriiformes
73	SH1_2012__Ims	SH1_2012__Ims 1	Aves	Charadriiformes
74	DI1_2010__Milder	DI1_2010__Milder 2	Aves	Charadriiformes
75	MJ1_2013__Reynolds	MJ1_2013__Reynolds 1	Aves	Charadriiformes
76	HP1_2007__Shahabuddin	HP1_2007__Shahabuddin 1	Aves	Charadriiformes
77	DL1_2009__Woinarski	DL1_2009__Woinarski 1	Aves	Charadriiformes
78	DI1_2013__Azhar	DI1_2013__Azhar 1	Aves	Coraciiformes
79	HW1_2005__Baldi	HW1_2005__Baldi 1	Aves	Coraciiformes
80	HP1_2008__Farwig	HP1_2008__Farwig 1	Aves	Coraciiformes
81	HP1_2009__Kessler	HP1_2009__Kessler 5	Aves	Coraciiformes
82	GP1_2007__Kutt	GP1_2007__Kutt 2	Aves	Coraciiformes
83	HZ1_2012__Kutt	HZ1_2012__Kutt 1	Aves	Coraciiformes
84	DI1_2010__Milder	DI1_2010__Milder 2	Aves	Coraciiformes
85	BS1_2012__Naithani	BS1_2012__Naithani 1	Aves	Coraciiformes
86	DI1_2011__Neuschulz	DI1_2011__Neuschulz 1	Aves	Coraciiformes
87	TN1_2007__ODea	TN1_2007__ODea 1	Aves	Coraciiformes
88	TN1_1998__Owiunji	TN1_1998__Owiunji 1	Aves	Coraciiformes
89	MH1_2011__Phalan	MH1_2011__Phalan 1	Aves	Coraciiformes

90	KS1_2005__Pons	KS1_2005__Pons 1	Aves	Coraciiformes
91	SC1_2014__Sam	SC1_2014__Sam 1	Aves	Coraciiformes
92	HP1_2007__Shahabuddin	HP1_2007__Shahabuddin 1	Aves	Coraciiformes
93	MH1_2010__Sheldon	MH1_2010__Sheldon 1	Aves	Coraciiformes
94	SC1_2011__Stouffer	SC1_2011__Stouffer 1	Aves	Coraciiformes
95	KS1_2009__SuarezRubio	KS1_2009__SuarezRubio 1	Aves	Coraciiformes
96	DL1_2009__Woinarski	DL1_2009__Woinarski 1	Aves	Coraciiformes
97	FB1_2007a__Barlow	FB1_2007a__Barlow 1	Aves	Galbuliformes
98	FB1_2007a__Barlow	FB1_2007a__Barlow 2	Aves	Galbuliformes
99	HP1_2007__Borges	HP1_2007__Borges 1	Aves	Galbuliformes
100	SC1_2011__Stouffer	SC1_2011__Stouffer 1	Aves	Galbuliformes
101	HP1_2006__Wunderle	HP1_2006__Wunderle 1	Aves	Galbuliformes
102	HP1_2008__Farwig	HP1_2008__Farwig 1	Aves	Galliformes
103	TN1_1998__Owiunji	TN1_1998__Owiunji 1	Aves	Galliformes
104	KS1_2005__Pons	KS1_2005__Pons 1	Aves	Galliformes
105	HW1_2005__Baldi	HW1_2005__Baldi 1	Aves	Gruiformes
106	FB1_2007a__Barlow	FB1_2007a__Barlow 1	Aves	Gruiformes
107	HW1_2011__Cerezo	HW1_2011__Cerezo 1	Aves	Gruiformes
108	HZ1_2012__Kutt	HZ1_2012__Kutt 1	Aves	Gruiformes

109	MJ1_2013_Reynolds	MJ1_2013_Reynolds 1	Aves	Gruiformes
110	DL1_2008_Aben	DL1_2008_Aben 1	Aves	Passeriformes
111	DI1_2013_Azhar	DI1_2013_Azhar 1	Aves	Passeriformes
112	DL1_2009_Azpiroz	DL1_2009_Azpiroz 1	Aves	Passeriformes
113	HW1_2005_Baldi	HW1_2005_Baldi 1	Aves	Passeriformes
114	FB1_2007a_Barlow	FB1_2007a_Barlow 1	Aves	Passeriformes
115	FB1_2007a_Barlow	FB1_2007a_Barlow 2	Aves	Passeriformes
116	HP1_2007_Borges	HP1_2007_Borges 1	Aves	Passeriformes
117	SE2_2013_Brandt	SE2_2013_Brandt 1	Aves	Passeriformes
118	HW1_2011_Cerezo	HW1_2011_Cerezo 1	Aves	Passeriformes
119	HW1_2007_Chapman	HW1_2007_Chapman 1	Aves	Passeriformes
120	DL1_2005_Cockle	DL1_2005_Cockle 1	Aves	Passeriformes
121	DI1_2013_deLima	DI1_2013_deLima 1	Aves	Passeriformes
122	DB1_2010_Dures	DB1_2010_Dures 1	Aves	Passeriformes
123	VK1_2011_Edenius	VK1_2011_Edenius 1	Aves	Passeriformes
124	HP1_2008_Farwig	HP1_2008_Farwig 1	Aves	Passeriformes
125	HP1_2008_Gomes	HP1_2008_Gomes 1	Aves	Passeriformes
126	SH1_2012_Ims	SH1_2012_Ims 1	Aves	Passeriformes
127	HP1_2009_Kessler	HP1_2009_Kessler 5	Aves	Passeriformes

128	GP1_2007__Kutt	GP1_2007__Kutt 2	Aves	Passeriformes
129	HZ1_2012__Kutt	HZ1_2012__Kutt 1	Aves	Passeriformes
130	HP1_2010__Lasky	HP1_2010__Lasky 1	Aves	Passeriformes
131	HP1_2010__Lasky	HP1_2010__Lasky 2	Aves	Passeriformes
132	MJ1_2009__Lehouck	MJ1_2009__Lehouck 1	Aves	Passeriformes
133	MJ1_2009__Lehouck	MJ1_2009__Lehouck 2	Aves	Passeriformes
134	MJ1_2009__Lehouck	MJ1_2009__Lehouck 3	Aves	Passeriformes
135	MJ1_2009__Lehouck	MJ1_2009__Lehouck 4	Aves	Passeriformes
136	MJ1_2009__Lehouck	MJ1_2009__Lehouck 5	Aves	Passeriformes
137	DG1_2013__Zou	DG1_2013__Zou 1	Aves	Passeriformes
138	DL1_2011__Mallari	DL1_2011__Mallari 1	Aves	Passeriformes
139	DI1_2010__Milder	DI1_2010__Milder 2	Aves	Passeriformes
140	MJ1_2008__Munyekenye	MJ1_2008__Munyekenye 1	Aves	Passeriformes
141	DI1_2004__Naidoo	DI1_2004__Naidoo 1	Aves	Passeriformes
142	BS1_2012__Naithani	BS1_2012__Naithani 1	Aves	Passeriformes
143	MJ1_2013__Ndanganga	MJ1_2013__Ndanganga 1	Aves	Passeriformes
144	MJ1_2013__Ndanganga	MJ1_2013__Ndanganga 2	Aves	Passeriformes
145	DI1_2011__Neuschulz	DI1_2011__Neuschulz 1	Aves	Passeriformes
146	TN1_2007__ODea	TN1_2007__ODea 1	Aves	Passeriformes

147	TN1_1998__Owiunji	TN1_1998__Owiunji 1	Aves	Passeriformes
148	MH1_2011__Phalan	MH1_2011__Phalan 1	Aves	Passeriformes
149	DL1_2012__Politi	DL1_2012__Politi 1	Aves	Passeriformes
150	KS1_2005__Pons	KS1_2005__Pons 1	Aves	Passeriformes
151	DL1_2010__Proenca	DL1_2010__Proenca 2	Aves	Passeriformes
152	DI1_2012__Reid	DI1_2012__Reid 1	Aves	Passeriformes
153	SC1_2010__ReyBenayas	SC1_2010__ReyBenayas 1	Aves	Passeriformes
154	MJ1_2013__Reynolds	MJ1_2013__Reynolds 1	Aves	Passeriformes
155	SC1_2014__Sam	SC1_2014__Sam 1	Aves	Passeriformes
156	SC1_2014__Sam	SC1_2014__Sam 2	Aves	Passeriformes
157	SC2_2012__Santana	SC2_2012__Santana 1	Aves	Passeriformes
158	HP1_2007__Shahabuddin	HP1_2007__Shahabuddin 1	Aves	Passeriformes
159	MH1_2010__Sheldon	MH1_2010__Sheldon 1	Aves	Passeriformes
160	VK1_2007__StLaurent	VK1_2007__StLaurent 3	Aves	Passeriformes
161	SC1_2011__Stouffer	SC1_2011__Stouffer 1	Aves	Passeriformes
162	KS1_2009__SuarezRubio	KS1_2009__SuarezRubio 1	Aves	Passeriformes
163	CC1_2013__Waite	CC1_2013__Waite 1	Aves	Passeriformes
164	DL1_2009__Woinarski	DL1_2009__Woinarski 1	Aves	Passeriformes
165	HP1_2006__Wunderle	HP1_2006__Wunderle 1	Aves	Passeriformes

166	AD1_2012__Yamaura	AD1_2012__Yamaura 1	Aves	Passeriformes
167	HW1_2011__Cerezo	HW1_2011__Cerezo 1	Aves	Pelecaniformes
168	DB1_2010__Dures	DB1_2010__Dures 1	Aves	Pelecaniformes
169	LK1_2009__Hayward	LK1_2009__Hayward 1	Aves	Pelecaniformes
170	MJ1_2013__Ndanganga	MJ1_2013__Ndanganga 1	Aves	Pelecaniformes
171	MJ1_2013__Ndanganga	MJ1_2013__Ndanganga 2	Aves	Pelecaniformes
172	MJ1_2013__Reynolds	MJ1_2013__Reynolds 1	Aves	Pelecaniformes
173	DL1_2009__Woinarski	DL1_2009__Woinarski 1	Aves	Pelecaniformes
174	DL1_2008__Aben	DL1_2008__Aben 1	Aves	Piciformes
175	DI1_2013__Azhar	DI1_2013__Azhar 1	Aves	Piciformes
176	FB1_2007a__Barlow	FB1_2007a__Barlow 1	Aves	Piciformes
177	HP1_2007__Borges	HP1_2007__Borges 1	Aves	Piciformes
178	DL1_2005__Cockle	DL1_2005__Cockle 1	Aves	Piciformes
179	HP1_2008__Farwig	HP1_2008__Farwig 1	Aves	Piciformes
180	HP1_2008__Gomes	HP1_2008__Gomes 1	Aves	Piciformes
181	MJ1_2009__Lehouck	MJ1_2009__Lehouck 1	Aves	Piciformes
182	MJ1_2009__Lehouck	MJ1_2009__Lehouck 4	Aves	Piciformes
183	DI1_2010__Milder	DI1_2010__Milder 2	Aves	Piciformes
184	MJ1_2008__Munyekenye	MJ1_2008__Munyekenye 1	Aves	Piciformes

185	BS1_2012__Naithani	BS1_2012__Naithani 1	Aves	Piciformes
186	DI1_2011__Neuschulz	DI1_2011__Neuschulz 1	Aves	Piciformes
187	TN1_2007__ODea	TN1_2007__ODea 1	Aves	Piciformes
188	TN1_1998__Owiunji	TN1_1998__Owiunji 1	Aves	Piciformes
189	MH1_2011__Phalan	MH1_2011__Phalan 1	Aves	Piciformes
190	DL1_2012__Politi	DL1_2012__Politi 1	Aves	Piciformes
191	DI1_2012__Reid	DI1_2012__Reid 1	Aves	Piciformes
192	MH1_2010__Sheldon	MH1_2010__Sheldon 1	Aves	Piciformes
193	DI1_2013__Azhar	DI1_2013__Azhar 1	Aves	Strigiformes
194	DL1_2009__Azpiroz	DL1_2009__Azpiroz 1	Aves	Strigiformes
195	DL1_2005__Cockle	DL1_2005__Cockle 1	Aves	Strigiformes
196	HP1_2009__Kessler	HP1_2009__Kessler 5	Aves	Strigiformes
197	GP1_2007__Kutt	GP1_2007__Kutt 2	Aves	Strigiformes
198	HZ1_2012__Kutt	HZ1_2012__Kutt 1	Aves	Strigiformes
199	DI1_2010__Milder	DI1_2010__Milder 2	Aves	Strigiformes
200	TN1_2007__ODea	TN1_2007__ODea 1	Aves	Strigiformes
201	DL1_2009__Woinarski	DL1_2009__Woinarski 1	Aves	Strigiformes
202	KS1_2006__Borges	KS1_2006__Borges 1	Chilopoda	Geophilomorpha
203	SC1_2011__Meijer	SC1_2011__Meijer 1	Chilopoda	Geophilomorpha

204	VB1_2008__Smith	VB1_2008__Smith 1	Chilopoda	Geophilomorpha
205	VB1_2008a_Smith	VB1_2008a_Smith 1	Chilopoda	Geophilomorpha
206	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Chilopoda	Lithobiomorpha
207	KS1_2006__Borges	KS1_2006__Borges 1	Diplopoda	Julida
208	SC1_2011__Meijer	SC1_2011__Meijer 1	Diplopoda	Julida
209	VB1_2008__Smith	VB1_2008__Smith 1	Diplopoda	Julida
210	VB1_2008a_Smith	VB1_2008a_Smith 1	Diplopoda	Julida
211	SC1_2011__Meijer	SC1_2011__Meijer 1	Diplopoda	Polydesmida
212	SC1_2005__Richardson	SC1_2005__Richardson 1	Entognatha	Collembola
213	SC1_2011__Meijer	SC1_2011__Meijer 1	Insecta	Blattodea
214	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Insecta	Blattodea
215	KS1_2006__Borges	KS1_2006__Borges 1	Insecta	Coleoptera
216	SC1_2011__Meijer	SC1_2011__Meijer 1	Insecta	Coleoptera
217	VB1_2012__Carpenter	VB1_2012__Carpenter 5	Insecta	Coleoptera
218	CC1_2007__Ewers	CC1_2007__Ewers 1	Insecta	Coleoptera
219	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Insecta	Coleoptera
220	AD1_2013__Grass	AD1_2013__Grass 1	Insecta	Coleoptera
221	HW1_2012__Jonsell	HW1_2012__Jonsell 1	Insecta	Coleoptera
222	HP1_2009__Kessler	HP1_2009__Kessler 3	Insecta	Coleoptera

223	VK1_2011__Legare	VK1_2011__Legare 1	Insecta	Coleoptera
224	VK1_2011__Legare	VK1_2011__Legare 2	Insecta	Coleoptera
225	CC1_2013__Litchwark	CC1_2013__Litchwark 1	Insecta	Coleoptera
226	HP1_2013__Mico	HP1_2013__Mico 1	Insecta	Coleoptera
227	DI1_2012__Muchane	DI1_2012__Muchane 1	Insecta	Coleoptera
228	SH1_2012__Norfolk	SH1_2012__Norfolk 1	Insecta	Coleoptera
229	MG1_2008__Paritsis	MG1_2008__Paritsis 1	Insecta	Coleoptera
230	AD1_2010__Quintero	AD1_2010__Quintero 1	Insecta	Coleoptera
231	SC1_2005__Richardson	SC1_2005__Richardson 1	Insecta	Coleoptera
232	AD1_2011__Schuepp	AD1_2011__Schuepp 1	Insecta	Coleoptera
233	SC1_2011__Meijer	SC1_2011__Meijer 1	Insecta	Dermaptera
234	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Insecta	Diptera
235	AD1_2013__Grass	AD1_2013__Grass 1	Insecta	Diptera
236	CC1_2013__Litchwark	CC1_2013__Litchwark 1	Insecta	Diptera
237	AD1_2010__Quintero	AD1_2010__Quintero 1	Insecta	Diptera
238	CC1_2014__Rader	CC1_2014__Rader 1	Insecta	Diptera
239	SC1_2005__Richardson	SC1_2005__Richardson 1	Insecta	Diptera
240	HW1_2011__Savage	HW1_2011__Savage 1	Insecta	Diptera
241	AD1_2011__Schuepp	AD1_2011__Schuepp 1	Insecta	Diptera

242	AD1_2009__Vergara	AD1_2009__Vergara 1	Insecta	Diptera
243	KS1_2006__Borges	KS1_2006__Borges 1	Insecta	Hemiptera
244	SC1_2011__Meijer	SC1_2011__Meijer 1	Insecta	Hemiptera
245	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Insecta	Hemiptera
246	DB1_2004__Helden	DB1_2004__Helden 1	Insecta	Hemiptera
247	DB1_2004__Helden	DB1_2004__Helden 2	Insecta	Hemiptera
248	MG1_2012__Littlewood	MG1_2012__Littlewood 1	Insecta	Hemiptera
249	MG1_2012__Littlewood	MG1_2012__Littlewood 2	Insecta	Hemiptera
250	SE2_2005__Moir	SE2_2005__Moir 1	Insecta	Hemiptera
251	SC1_2005__Richardson	SC1_2005__Richardson 1	Insecta	Hemiptera
252	AD1_2011__Bates	AD1_2011__Bates 1	Insecta	Hymenoptera
253	AD1_2008__Billeter	AD1_2008__Billeter 1	Insecta	Hymenoptera
254	AD1_2008__Billeter	AD1_2008__Billeter 2	Insecta	Hymenoptera
255	AD1_2008__Billeter	AD1_2008__Billeter 3	Insecta	Hymenoptera
256	AD1_2008__Billeter	AD1_2008__Billeter 4	Insecta	Hymenoptera
257	AD1_2008__Billeter	AD1_2008__Billeter 5	Insecta	Hymenoptera
258	AD1_2008__Billeter	AD1_2008__Billeter 6	Insecta	Hymenoptera
259	AD1_2008__Billeter	AD1_2008__Billeter 8	Insecta	Hymenoptera
260	AD1_2008__Billeter	AD1_2008__Billeter 9	Insecta	Hymenoptera

261	AD1_2008__Billeter	AD1_2008__Billeter 10	Insecta	Hymenoptera
262	AD1_2008__Billeter	AD1_2008__Billeter 11	Insecta	Hymenoptera
263	AD1_2008__Billeter	AD1_2008__Billeter 12	Insecta	Hymenoptera
264	AD1_2008__Billeter	AD1_2008__Billeter 13	Insecta	Hymenoptera
265	AD1_2008__Billeter	AD1_2008__Billeter 14	Insecta	Hymenoptera
266	AD1_2006__Blanche	AD1_2006__Blanche 1	Insecta	Hymenoptera
267	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Insecta	Hymenoptera
268	AD1_2013__Grass	AD1_2013__Grass 1	Insecta	Hymenoptera
269	AD1_2012__Lentini	AD1_2012__Lentini 1	Insecta	Hymenoptera
270	CC1_2013__Litchwark	CC1_2013__Litchwark 1	Insecta	Hymenoptera
271	AD1_2007__Meyer	AD1_2007__Meyer 1	Insecta	Hymenoptera
272	AD1_2007__Meyer	AD1_2007__Meyer 2	Insecta	Hymenoptera
273	AD1_2012__MudriStojnic	AD1_2012__MudriStojnic 1	Insecta	Hymenoptera
274	AD1_2004__Quaranta	AD1_2004__Quaranta 1	Insecta	Hymenoptera
275	AD1_2010__Quintero	AD1_2010__Quintero 1	Insecta	Hymenoptera
276	CC1_2014__Rader	CC1_2014__Rader 1	Insecta	Hymenoptera
277	SC1_2005__Richardson	SC1_2005__Richardson 1	Insecta	Hymenoptera
278	AD1_2011__Schuepp	AD1_2011__Schuepp 1	Insecta	Hymenoptera
279	DI1_2005__Tyllianakis	DI1_2005__Tyllianakis 1	Insecta	Hymenoptera

280	AD1_2009__Vergara	AD1_2009__Vergara 1	Insecta	Hymenoptera
281	MG1_2006__Baur	MG1_2006__Baur 2	Insecta	Lepidoptera
282	MG1_2006__Baur	MG1_2006__Baur 3	Insecta	Lepidoptera
283	KS1_2006__Borges	KS1_2006__Borges 1	Insecta	Lepidoptera
284	SC1_2011__Meijer	SC1_2011__Meijer 1	Insecta	Lepidoptera
285	HP1_2004__Cleary	HP1_2004__Cleary 1	Insecta	Lepidoptera
286	SC2_2011__Daniello	SC2_2011__Daniello 1	Insecta	Lepidoptera
287	CC1_2012__deSassi	CC1_2012__deSassi 1	Insecta	Lepidoptera
288	AD1_2013__Grass	AD1_2013__Grass 1	Insecta	Lepidoptera
289	SC2_2012__Kati	SC2_2012__Kati 1	Insecta	Lepidoptera
290	HP1_2010__Krauss	HP1_2010__Krauss 3	Insecta	Lepidoptera
291	CC1_2013__Litchwark	CC1_2013__Litchwark 1	Insecta	Lepidoptera
292	LH1_2008__Littlewood	LH1_2008__Littlewood 1	Insecta	Lepidoptera
293	DI1_2010__Milder	DI1_2010__Milder 3	Insecta	Lepidoptera
294	AD1_2011__Peer	AD1_2011__Peer 1	Insecta	Lepidoptera
295	AD1_2011__Power	AD1_2011__Power 1	Insecta	Lepidoptera
296	SC1_2005__Richardson	SC1_2005__Richardson 1	Insecta	Lepidoptera
297	CM1_2011__Safian	CM1_2011__Safian 1	Insecta	Lepidoptera
298	HW1_2011__Summerville	HW1_2011__Summerville 1	Insecta	Lepidoptera

299	SC1_2002__Summerville	SC1_2002__Summerville 1	Insecta	Lepidoptera
300	HW1_2006__Summerville	HW1_2006__Summerville 1	Insecta	Lepidoptera
301	SC2_2012__Verdasca	SC2_2012__Verdasca 1	Insecta	Lepidoptera
302	HB1_2009__Vu	HB1_2009__Vu 1	Insecta	Lepidoptera
303	AD1_2008__Franzen	AD1_2008__Franzen 1	Insecta	Lepidoptera
304	SC1_2005__Richardson	SC1_2005__Richardson 1	Insecta	Neuroptera
305	HP1_2004__Cleary	HP1_2004__Cleary 1	Insecta	Odonata
306	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Insecta	Orthoptera
307	SC1_2005__Richardson	SC1_2005__Richardson 1	Insecta	Orthoptera
308	KS1_2006__Borges	KS1_2006__Borges 1	Insecta	Psocodea
309	SC1_2011__Meijer	SC1_2011__Meijer 1	Insecta	Psocodea
310	KS1_2006__Borges	KS1_2006__Borges 1	Insecta	Thysanoptera
311	SC1_2011__Meijer	SC1_2011__Meijer 1	Insecta	Thysanoptera
312	SE2_2010__Gaigher	SE2_2010__Gaigher 1	Malacostraca	Isopoda
313	VB1_2011__Magrini	VB1_2011__Magrini 1	Malacostraca	Isopoda
314	SC1_2005__Richardson	SC1_2005__Richardson 1	Malacostraca	Isopoda
315	VB1_2008__Smith	VB1_2008__Smith 1	Malacostraca	Isopoda
316	VB1_2008a__Smith	VB1_2008a__Smith 1	Malacostraca	Isopoda
317	HZ1_2013__Garmendia	HZ1_2013__Garmendia 1	Mammalia	Artiodactyla

318	LK1_2009__Hayward	LK1_2009__Hayward 1	Mammalia	Artiodactyla
319	HZ1_2009__McShea	HZ1_2009__McShea 1	Mammalia	Artiodactyla
320	DI1_2008__Sridhar	DI1_2008__Sridhar 1	Mammalia	Artiodactyla
321	DL1_2009__Woinarski	DL1_2009__Woinarski 2	Mammalia	Artiodactyla
322	HZ1_2013__Garmendia	HZ1_2013__Garmendia 1	Mammalia	Carnivora
323	LK1_2009__Hayward	LK1_2009__Hayward 1	Mammalia	Carnivora
324	SE2_2010__McCarthy	SE2_2010__McCarthy 1	Mammalia	Carnivora
325	HZ1_2009__McShea	HZ1_2009__McShea 1	Mammalia	Carnivora
326	DI1_2008__Sridhar	DI1_2008__Sridhar 1	Mammalia	Carnivora
327	HP1_2007c__Barlow	HP1_2007c__Barlow 1	Mammalia	Chiroptera
328	TN1_2007__CastroLuna	TN1_2007__CastroLuna 1	Mammalia	Chiroptera
329	HP1_2007__MacSwiney	HP1_2007__MacSwiney 1	Mammalia	Chiroptera
330	HP1_2008__Presley	HP1_2008__Presley 1	Mammalia	Chiroptera
331	LH1_2011__Shafie	LH1_2011__Shafie 1	Mammalia	Chiroptera
332	HP1_2007__Willig	HP1_2007__Willig 1	Mammalia	Chiroptera
333	DL1_2009__Woinarski	DL1_2009__Woinarski 2	Mammalia	Chiroptera
334	SE2_2012__Craig	SE2_2012__Craig 1	Mammalia	Dipterodontia
335	HZ1_2012__Kutt	HZ1_2012__Kutt 1	Mammalia	Dipterodontia
336	DL1_2009__Woinarski	DL1_2009__Woinarski 2	Mammalia	Dipterodontia

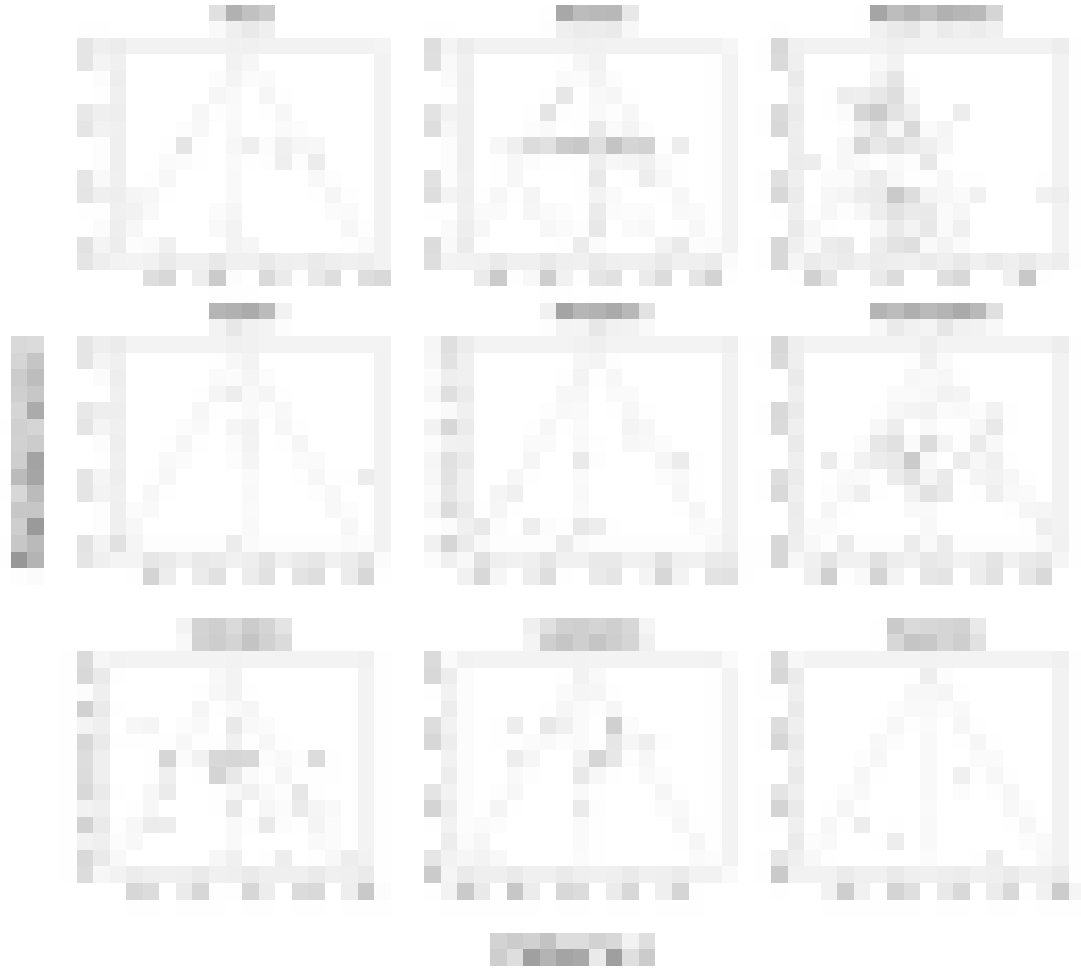
337	LK1_2009__Hayward	LK1_2009__Hayward 1	Mammalia	Perissodactyla
338	FB1_2009__Bernard	FB1_2009__Bernard 1	Mammalia	Rodentia
339	JD1_2010__Caceres	JD1_2010__Caceres 2	Mammalia	Rodentia
340	SC1_2013__Fernandez	SC1_2013__Fernandez 1	Mammalia	Rodentia
341	MJ1_2011__Granjon	MJ1_2011__Granjon 1	Mammalia	Rodentia
342	LK1_2009__Hayward	LK1_2009__Hayward 1	Mammalia	Rodentia
343	VK1_2011__Jung	VK1_2011__Jung 1	Mammalia	Rodentia
344	DI1_2012__Martin	DI1_2012__Martin 1	Mammalia	Rodentia
345	HZ1_2009__McShea	HZ1_2009__McShea 1	Mammalia	Rodentia
346	JD1_2010__Mena	JD1_2010__Mena 1	Mammalia	Rodentia
347	TN1_2006__Nakagawa	TN1_2006__Nakagawa 1	Mammalia	Rodentia
348	HP1_2007__Wells	HP1_2007__Wells 1	Mammalia	Rodentia
349	TN1_2006__Nakagawa	TN1_2006__Nakagawa 1	Mammalia	Scandentia
350	HP1_2007__Wells	HP1_2007__Wells 1	Mammalia	Scandentia
351	SE2_2009__Craig	SE2_2009__Craig 1	Reptilia	Squamata
352	SE2_2012__Craig	SE2_2012__Craig 1	Reptilia	Squamata
353	SE2_2014a__Craig	SE2_2014a__Craig 1	Reptilia	Squamata
354	SE2_2014b__Craig	SE2_2014b__Craig 1	Reptilia	Squamata
355	SC1_2011__DCruze	SC1_2011__DCruze 1	Reptilia	Squamata

356	TN1_2003__Fabricius	TN1_2003__Fabricius 1	Reptilia	Squamata
357	SC1_2014__Kurz	SC1_2014__Kurz 1	Reptilia	Squamata
358	GP1_2007__Kutt	GP1_2007__Kutt 1	Reptilia	Squamata
359	HZ1_2012__Kutt	HZ1_2012__Kutt 1	Reptilia	Squamata
360	TN1_2008__Luja	TN1_2008__Luja 1	Reptilia	Squamata
361	HW1_2012__Pelegrin	HW1_2012__Pelegrin 1	Reptilia	Squamata
362	YP1_2012__Sung	YP1_2012__Sung 1	Reptilia	Squamata
363	SC1_2006__UrbinaCardona	SC1_2006__UrbinaCardona 1	Reptilia	Squamata
364	DL1_2009__Woinarski	DL1_2009__Woinarski 2	Reptilia	Squamata
365	DI1_2006__Scott	DI1_2006__Scott 1	Reptilia	Squamata
366	TN1_2008__Luja	TN1_2008__Luja 1	Reptilia	Testudines

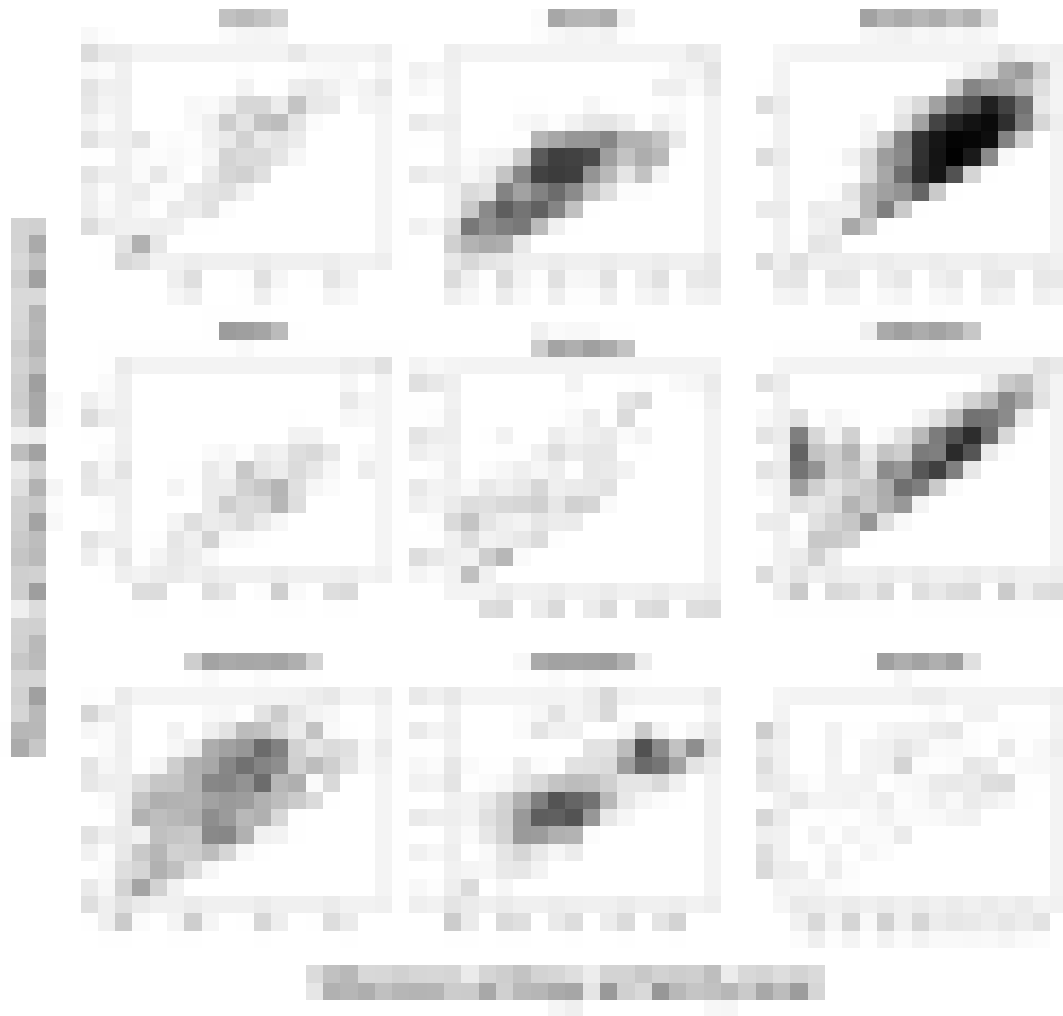
Appendix S3. Equations used in our analysis

Equation No.	Equation Name	Equation Expression	Explanation
1	Shannon entropy	$H_{m,j} = - \sum_{i=1}^{S_{m,j}} P_i \ln P_i$	For site j in study m , H is the Shannon entropy, D is the Shannon diversity, and S represents the number of species, while P_i is the relative abundance (proportion) of species i in the sample from the respective study site.
2	Shannon diversity	$D_{m,j} = \exp(H_{m,j})$	
3	Fisher's z	$z = 0.5 * \ln\left(\frac{1+r}{1-r}\right)$	" r " refers to the Pearson correlation coefficient and n represents the sample size.
4	Standard Error of Fisher's z	$SE_z = \sqrt{\frac{1}{n-3}}$	
5	Multiple linear regression	$\beta_j = k_1 * \log_e(N_j) + k_2 * Lat_{j_e} + k_3 * Alt_j + T$	Multiple linear regression reflects the species / family ratio for each study (β_j) in relation to the sample size, latitude and elevation. N_j , Lat_j and Alt_j are mean values for the number of individuals, latitude and elevation for the j^{th} study; k_1 , k_2 and k_3 are estimated coefficients, and T is the intercept.

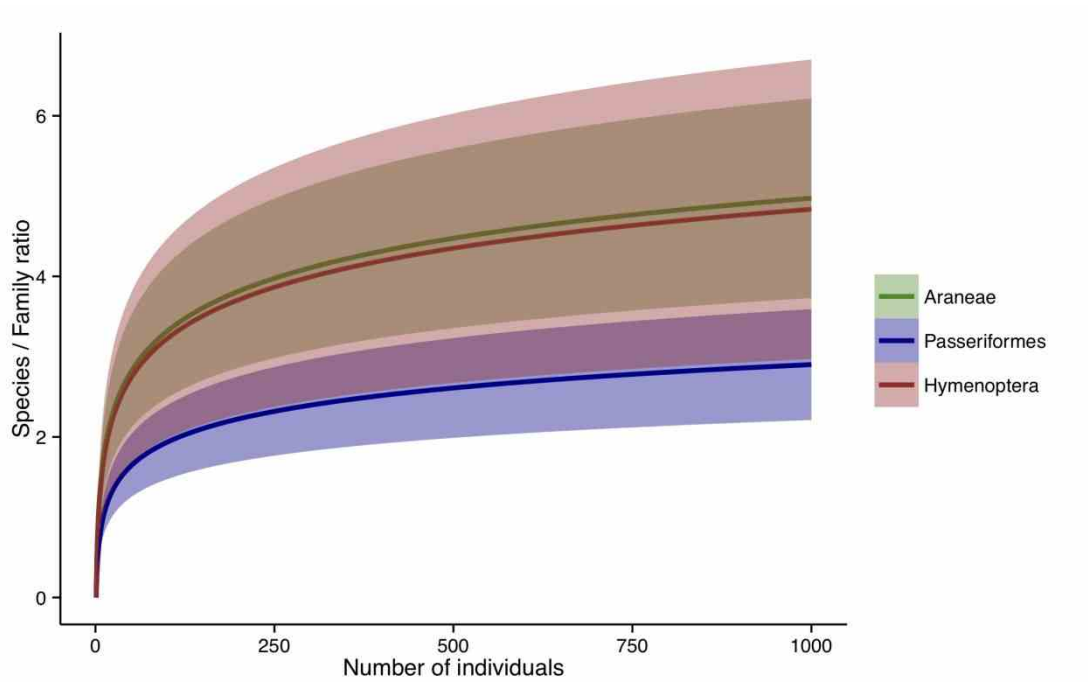
Appendix S4. Funnel plots showing the relationship between Fisher's z (based on the correlation between Species and Family Shannon entropy index values) and its's standard error for different orders.



1
2
3 **Appendix S5.** Relationship between species- and family-level Shannon
4 entropy indices for different orders.
5
6



1 **Appendix S6.** Influence of sample size (number of individuals) on the species
2 / family ratio for Araneae, Passeriformes and Lepidoptera; lines and shadings
3 refer to mean and SE of the estimates. Models estimated using Equation 5 in
4 **Appendix S3.**



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