Supplementary Material for "Do rare species matter for ecosystem multifunctioning?"

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Table S1. Details of the sampling procedure for each trophic group. Note that for belowground groups the taxonomic unit was either operational taxonomic units (OTU: fungi and protists) or families (bacteria and belowground insect larvae). Abundance measures were: % cover (plants, bryophytes), number of individuals captured (arthropods) and relative proportion of sequence reads assigned to each family among all reads within each plot (protists, soil bacteria and mycorrhiza).

<table>
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<tr>
<th>Trophic group</th>
<th>Subgroup</th>
<th>Sampling method</th>
<th>Author</th>
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<tr>
<td>Autotrophs</td>
<td>Plants, bryophytes</td>
<td>Measurement of % cover in a 4×4 m subplot, done in 2009</td>
<td>Boch, Heinze, Hölzel, Klaus, Kleinebecker, Müller, Prati, Socher, Fischer</td>
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<td>Aboveground herbivores</td>
<td>Herbivorous insects</td>
<td>Sweep netting (Hemiptera: Heteroptera/Auchenorrhyncha, Hymenoptera, Neuroptera and Orthoptera). Transects of 150m with 60 double sweeps, done twice per plot in 2008-2010.</td>
<td>Lange, Pašalić, Türke, Gossner, Weisser</td>
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<tr>
<td>Aboveground predators</td>
<td>Carnivorous insects</td>
<td>Sweep netting (Hemiptera: Heteroptera/Auchenorrhyncha, Hymenoptera, Neuroptera and Orthoptera). Transects of 150m with 60 double sweeps done twice per plot in 2008-2010.</td>
<td>Lange, Pašalić, Türke, Gossner, Weisser</td>
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<td>Sweep netting. Transects of 150m with 60 double sweeps, done twice per plot in 2008-2010.</td>
<td>Lange, Pašalić, Türke, Gossner, Weisser</td>
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<td>Chilopoda</td>
<td>Kempson extraction from one soil core of 20 ×5 cm per plot, done in 2008</td>
<td>Birkhofer, Diekötter, Wolters</td>
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<td>Annelids</td>
<td>Hand sorting from two soil cores of 20 ×10 cm per plot, done in 2008</td>
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<td>Detritivorous insects</td>
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<td>Lange, Pašalić, Türke, Gossner, Weisser</td>
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<td>Microbial decomposers</td>
<td>Soil bacteria</td>
<td>cDNA amplicon sequencing of partial (V3) 16S rRNA gene transcripts, done in 2011</td>
<td>Baumgartner, Sikorski, Overmann</td>
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<td>Bacterivores</td>
<td>Bacterivorous protists</td>
<td>18S rDNA gene PCR and amplicon sequencing (454) filtering for rhizarians, alveolates, stramenopiles and opisthokonts, done in 2011</td>
<td>Venter, Arndt</td>
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<td>Symbionts</td>
<td>Arbuscular mycorrhizal fungi</td>
<td>Pyrotag sequencing of the NS31 - AM1 fragment of the 18S rDNA genes, done in 2011</td>
<td>Klemmer, Wubet, Buscot</td>
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<td>Belowground herbivores</td>
<td>Insect larvae</td>
<td>Extracted from a heat/moisture gradient in one soil core of 20 x 5 cm per site, done in 2011 over a period of eight days.</td>
<td>Sonnemann, Wurst</td>
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<td>Belowground predators</td>
<td>Insect larvae</td>
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### Table S2. Details of the sampling procedure for each ecosystem function.

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<td>Aboveground plant biomass</td>
<td>Harvested in four 0.5 m × 0.5 m quadrats per plot, done in May-June in 2008-2012.</td>
<td>Schmitt, Prati, Fischer, Klaus, Kleinebecker, Hözel</td>
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<td>Belowground plant biomass</td>
<td>Measured in 14 soil cores (10 × 5 cm). Fine roots were sorted according to a diameter size class of &lt; 2 mm and weighted after drying in the oven, done in May 2011.</td>
<td>Solly, Schöning, Schrumpf</td>
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<td>Root decomposition rate</td>
<td>Measured as the mass loss from root litter bags after 6 months, done in March 2012.</td>
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<td>Potential nitrification</td>
<td>10 mM ammonium sulphate solution was added as substrate to 2.5g of soil composite samples (i.e. the same samples as for soil carbon; see below).</td>
<td>Stempfhuber, Schloter</td>
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<td>Phosphorus uptake and retention</td>
<td>Proportion of ( P ) in plants and microbes (shoot P stock + microbial P stock) / (shoot P stock + microbial P stock + soil extractable P ([\text{NaHCO}_3])).</td>
<td>Alt, Sorkau, Oelman, Wilcke</td>
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<td>Arbuscular mycorrhizal fungal root colonization</td>
<td>Cultured in sterile soil in the field from April to October 2011 and then extracted with sodium hexametaphosphate (35 g l(^{-1})). Hyphal length was quantified after staining with trypan blue.</td>
<td>Morris, Rillig</td>
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<td>Stability of soil aggregates</td>
<td>A subsample of the same soil than above (AMF colonization) was passed through a 250 μm sieve under water to determine the percentage of water stable macroaggregates.</td>
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<td>Soil organic Carbon</td>
<td>Measured in 14 soil cores (40 × 5 cm). Calculated as the difference between total carbon (measured with a CN analyzer “Vario Max” ([\text{Elementar Analysensysteme GmbH, Hanau, Germany}])) and inorganic carbon (determined after combustion of organic carbon in a muffle furnace; 450°C for 16 h), done in October 2011</td>
<td>Schöning, Solly, Schrumpf</td>
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<td>Forage quality</td>
<td>Was calculated as a function of mean of scaled crude protein concentration and scaled relative forage value, done in May-June in 2008-2012.</td>
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<td>Resistance to plant pathogens</td>
<td>Calculated as the inverse of the total cover of foliar fungal pathogens. The cover of pathogens was measured in four 25 × 1 m transects per plot, were proportion of plants infected, and leaf area infected of these individuals was measured; done in October 2011.</td>
<td>Blaser, Prati, Fischer</td>
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<td>Pest control</td>
<td>Number of trap nesting wasps known to feed on pest insects, done between April and October 2008.</td>
<td>Steckel, Westphal, Steffan-Dewenter</td>
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<td>Pollinator abundance</td>
<td>Estimated as the total abundance of flower visitors, measured in one 200 × 3 m transect per plot, done in May 2008.</td>
<td>Krauss, Klein, Weiner, Werner, Blüthgen</td>
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<td>Bird diversity</td>
<td>Measured as the cumulative species richness estimated by audio-visual point-counts, done in May-June 2008-2010</td>
<td>Renner, Böhm, Tschapka</td>
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<td>Flower cover</td>
<td>Measured as the number of inflorescences in four 50 × 3 m transects per plot. Flower area for each species was obtained from the literature.</td>
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Table S3. Model selection summary. Results for each multifunctionality scenario are shown with the best model highlighted in grey. Results for each multifunctionality scenario are shown with the best model highlighted in dark grey. Those models with ΔAICc < 2 (and therefore equally plausible than the best one) are shown in light grey. For each of the models performed, an identification number (model #), the number of variables (n.var), AICc, ΔAICc and AIC weight (AICw) are shown. Env = environmental variables (region+soil ph+soil depth+land-use intensity+topographic wetness index).
Table S4. Model selection summary for the analyses performed with the 50% least abundance species as rare species. Results for each multifunctionality scenario are shown with the best model highlighted in dark grey. Those models with $\Delta$AICc < 2 (and therefore equally plausible than the best one) are shown in light grey. For each of the models performed, an identification number (model #), the number of variables (n.var), AICc, $\Delta$AICc and AIC weight (AICw) are shown. Env = environmental variables (region+soil ph+soil depth+land-use intensity+ topographic wetness index).
Table S5. Model selection summary for the analyses performed with abundance instead of species richness. Results for each multifunctionality scenario are shown with the best model highlighted in dark grey. Those models with ΔAICc < 2 (and therefore equally plausible than the best one) are shown in light grey. For each of the models performed, an identification number (model #), the number of variables (n.var), AICc, ΔAICc and AIC weight (AICw) are shown. Env = environmental variables (region+soil ph+soil depth+land-use intensity+ topographic wetness index).

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<td>7.4</td>
<td>0</td>
</tr>
<tr>
<td>34</td>
<td>env + (EUI * region) * aboveare90 + beloware90</td>
<td>11</td>
<td>445.5</td>
<td>11.5</td>
<td>0</td>
<td>434.3</td>
<td>10.4</td>
<td>0</td>
<td>427.5</td>
<td>9.9</td>
<td>0</td>
</tr>
<tr>
<td>35</td>
<td>env + (EUI * region) * aboveare90</td>
<td>11</td>
<td>443.4</td>
<td>9.3</td>
<td>0</td>
<td>433.2</td>
<td>9.3</td>
<td>0</td>
<td>425.5</td>
<td>8.9</td>
<td>0</td>
</tr>
<tr>
<td>36</td>
<td>env + (EUI * region) * beloware90</td>
<td>11</td>
<td>449.2</td>
<td>15.1</td>
<td>0</td>
<td>434.9</td>
<td>11.0</td>
<td>0</td>
<td>425.8</td>
<td>8.2</td>
<td>0</td>
</tr>
<tr>
<td>37</td>
<td>env + (EUI * region) * aboveare90 + beloware90</td>
<td>17</td>
<td>459.2</td>
<td>25.1</td>
<td>0</td>
<td>448.6</td>
<td>19.7</td>
<td>0</td>
<td>448.7</td>
<td>21.1</td>
<td>0</td>
</tr>
</tbody>
</table>
Table S6. Summary of the database used to test species-specific effects on multifunctionality. Number of species (n.species) and average abundance are given for each trophic group and category (common vs- rare species). Average positive (black) and negative (red) effects (measured as the standardized effect size) are shown (averages obtained only from those Standardized effect sizes > 2).

<table>
<thead>
<tr>
<th>Species Type</th>
<th>n.species</th>
<th>Average abundance</th>
<th>50% Average.effects</th>
<th>75% Average.effects</th>
<th>90% Average.effects</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td><strong>Autotrophs</strong></td>
<td>common</td>
<td>25</td>
<td>6.59</td>
<td>-2.31</td>
<td>6.59</td>
</tr>
<tr>
<td></td>
<td>rare</td>
<td>25</td>
<td>1.64</td>
<td>2.37</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Herbivores</strong></td>
<td>common</td>
<td>25</td>
<td>19.96</td>
<td>0.00</td>
<td>2.62</td>
</tr>
<tr>
<td></td>
<td>rare</td>
<td>25</td>
<td>2.61</td>
<td>3.12</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Microbe.decomposer</strong></td>
<td>common</td>
<td>16</td>
<td>0.58</td>
<td>2.84</td>
<td>0.00</td>
</tr>
<tr>
<td></td>
<td>rare</td>
<td>34</td>
<td>0.01</td>
<td>2.52</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Predators</strong></td>
<td>common</td>
<td>13</td>
<td>2.65</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td></td>
<td>rare</td>
<td>7</td>
<td>1.30</td>
<td>2.19</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Bacterivores</strong></td>
<td>common</td>
<td>22</td>
<td>8.30</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td></td>
<td>rare</td>
<td>28</td>
<td>1.54</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Symbionts</strong></td>
<td>common</td>
<td>23</td>
<td>13.66</td>
<td>0.00</td>
<td>2.20</td>
</tr>
<tr>
<td></td>
<td>rare</td>
<td>27</td>
<td>3.77</td>
<td>0.00</td>
<td>2.72</td>
</tr>
</tbody>
</table>
Table S7. Summary of the null-model approach applied to test the functional effects of individual species. The number of significant positive (black) and negative (red) effects are shown as the percentage of significant effects regarding the number of species tested (shown in parenthesis). The averaged results across the three multifunctionality scenarios is shown in grey.

<table>
<thead>
<tr>
<th>Trophic group</th>
<th>50%</th>
<th>75%</th>
<th>90%</th>
<th>Average</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALL (270)</td>
<td>7/5</td>
<td>6/4</td>
<td>5/3</td>
<td>6/4</td>
</tr>
<tr>
<td>Autotrophs (50)</td>
<td>6/8</td>
<td>4/0</td>
<td>4/4</td>
<td>5/4</td>
</tr>
<tr>
<td>Herbivores (50)</td>
<td>8/0</td>
<td>4/6</td>
<td>4/4</td>
<td>5/3</td>
</tr>
<tr>
<td>Microbe.decomp (50)</td>
<td>14/0</td>
<td>8/2</td>
<td>10/2</td>
<td>11/1</td>
</tr>
<tr>
<td>Predators (20)</td>
<td>5/0</td>
<td>5/10</td>
<td>0/0</td>
<td>3/3</td>
</tr>
<tr>
<td>Bacterivores (50)</td>
<td>4/2</td>
<td>8/2</td>
<td>4/2</td>
<td>5/2</td>
</tr>
<tr>
<td>Symbiont (50)</td>
<td>4/16</td>
<td>4/10</td>
<td>4/4</td>
<td>4/10</td>
</tr>
</tbody>
</table>
Table S8. Standardized estimated coefficients from the multiple regressions including the functional effect of each individual species (response variable), and its average abundance (Abundance) and response to land-use intensity (Resp. land-use) as predictors. Response to land-use intensity was measured as the standardized coefficient between the abundance of each species across every plot where it occurred and the land-use intensity index of the same plot. Coefficients were corrected by number of data points available to estimate the functional effect for each species. Main effects are reported for the model containing all functional groups together (All), in which the interactions of functional group by abundance and response to land-use were considered. Significant coefficients are highlighted in bold.

<table>
<thead>
<tr>
<th>Group</th>
<th>Resp. land-use</th>
<th>Abundance</th>
<th>Height</th>
<th>SLA</th>
<th>Resp. land-use</th>
<th>Abundance</th>
<th>Body size</th>
<th>Resp. land-use</th>
<th>Abundance</th>
<th>Body size</th>
<th>Resp. land-use</th>
<th>Abundance</th>
<th>Body size</th>
</tr>
</thead>
<tbody>
<tr>
<td>Autotrophs</td>
<td>0.20</td>
<td>-0.35</td>
<td>-0.41</td>
<td></td>
<td>0.12</td>
<td>0.07</td>
<td>0.23</td>
<td>0.18</td>
<td>0.01</td>
<td>0.04</td>
<td>0.17</td>
<td>-0.08</td>
<td>-0.08</td>
</tr>
<tr>
<td>Herbivores</td>
<td>0.12</td>
<td>-0.21</td>
<td>-0.43</td>
<td></td>
<td>0.12</td>
<td>0.03</td>
<td>0.11</td>
<td>-0.33</td>
<td>-0.08</td>
<td>0.18</td>
<td>0.16</td>
<td>-0.16</td>
<td>-0.16</td>
</tr>
<tr>
<td>Predators</td>
<td>0.51</td>
<td>0.25</td>
<td>-0.14</td>
<td></td>
<td>0.27</td>
<td>-0.37</td>
<td>-0.27</td>
<td>-0.21</td>
<td>-0.08</td>
<td>0.01</td>
<td>0.27</td>
<td>-0.27</td>
<td>-0.27</td>
</tr>
<tr>
<td>Microb.decomp</td>
<td>0.40</td>
<td>-0.09</td>
<td>-0.33</td>
<td></td>
<td>-0.13</td>
<td>0.06</td>
<td>-0.02</td>
<td>0.13</td>
<td>0.22</td>
<td>0.30</td>
<td>0.40</td>
<td>-0.27</td>
<td>-0.32</td>
</tr>
<tr>
<td>Bacterivores</td>
<td>-0.27</td>
<td>-0.29</td>
<td>-0.32</td>
<td></td>
<td>0.13</td>
<td>0.22</td>
<td>0.30</td>
<td>-0.27</td>
<td>-0.28</td>
<td>-0.10</td>
<td>0.00</td>
<td>-0.10</td>
<td>-0.10</td>
</tr>
<tr>
<td>Symbionts</td>
<td>-0.22</td>
<td>-0.28</td>
<td>-0.14</td>
<td></td>
<td>-0.22</td>
<td>-0.00</td>
<td>-0.08</td>
<td>-0.00</td>
<td>-0.10</td>
<td>-0.08</td>
<td>-0.00</td>
<td>-0.10</td>
<td>-0.08</td>
</tr>
<tr>
<td>All</td>
<td>0.06</td>
<td>-0.29</td>
<td>-0.46</td>
<td></td>
<td>0.19</td>
<td>0.21</td>
<td>0.62</td>
<td>0.06</td>
<td>-0.29</td>
<td>-0.08</td>
<td>0.06</td>
<td>-0.08</td>
<td>-0.08</td>
</tr>
</tbody>
</table>
**Figure S1.** Abundance distribution of common and rare species within each trophic group.

Different colors show those species considered common (the top 10%, in red), or rare (bottom 90% in blue and green, or bottom 50%, in green).
Figure S2. Standardized coefficients (with 95% confidence intervals) of the different terms related to biodiversity in our models obtained from model averaging using those models with $\Delta$AICc < 2. These include interactions between multidiversity and region and LUI as drivers of multifunctionality. Regions are: Schwäbische Alb, Hainich-Dün (CR) and Schorfheide-Chorin (NR). Multidiversity of common species aboveground, and interactions between rare species multidiversity per region, and multidiversity of aboveground organisms per LUI were not included in any of the best models and therefore are not presented. If a given predictor was not included in the best models, the effect was considered to be 0.