

**Supporting Information.** Neff, F., M.C. Resch, A. Marty, J.D. Rolley, M. Schütz, A.C. Risch, and M.M. Gossner. 2020. Long-term restoration success of insect herbivore communities in semi-natural grasslands: a functional approach. *Ecological Applications*.

**APPENDIX S1.** Supporting information

**Table of contents**

Study site description.....	2
Arthropod sampling and identification .....	6
Determination of traits .....	11
Confounding factors, nested structure and spatial autocorrelation.....	17
Effect pathways .....	24
Additional tables and figures.....	32
Results for Auchenorrhyncha only .....	38
Literature .....	48

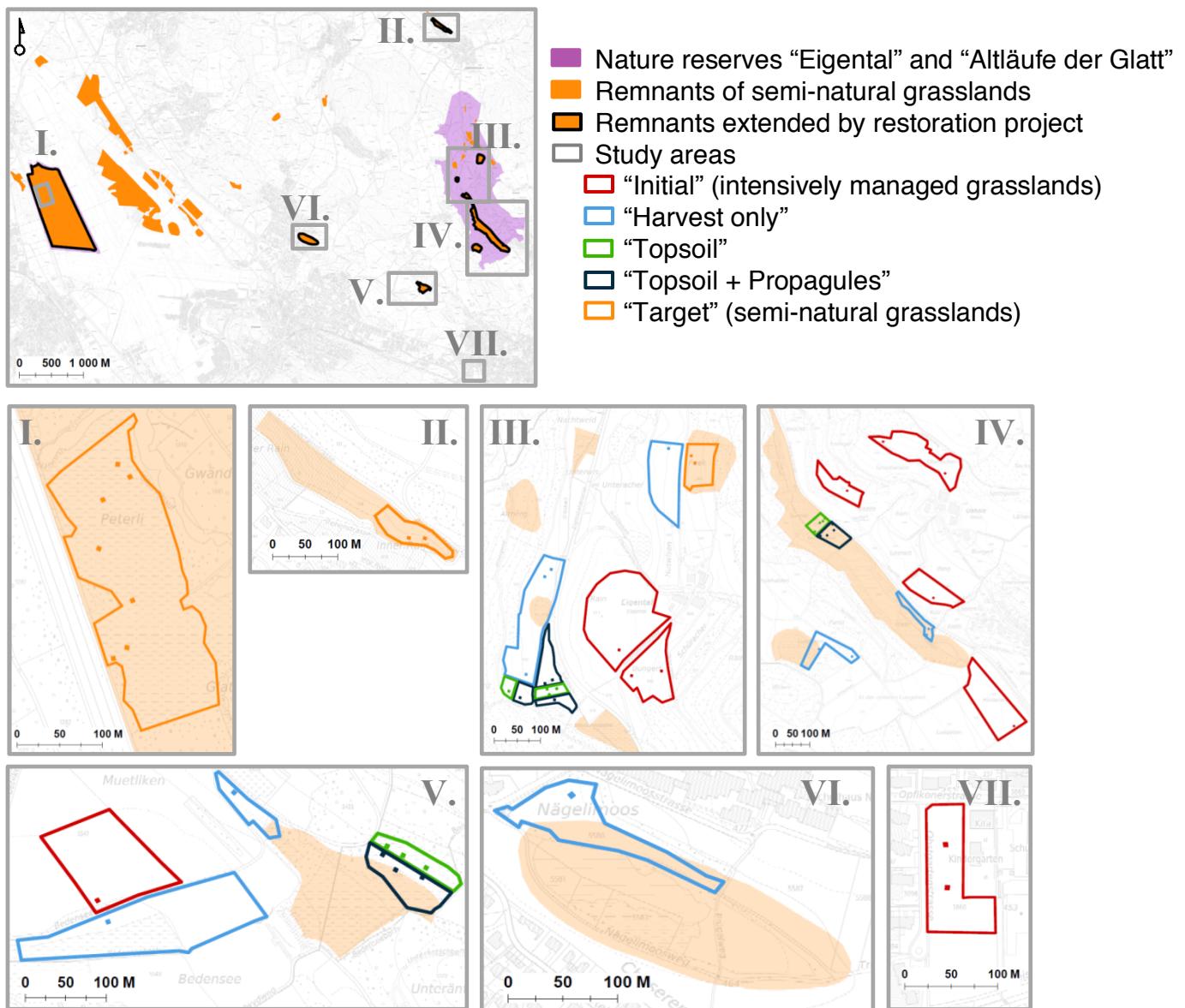
## Study site description

**Table S1.** Detailed description of the study plots. Land-use history: recent agricultural use for *Initial*; agricultural use before restoration for all restored sites; temporary grasslands were re-sown every sixth year. Last tillage: Last time the site was tilled. Earliest mowing: Earliest date of biomass harvest based on contracts between farmers and the Nature Protection Agency of Zurich (excluding *Initial*). Exact yearly dates depended on local and seasonal weather conditions.

Management: Frequency and intensity of mowing and manuring (intensity1 = mowing once and no manure; intensity2 = 2-3 times mowing and no manure; intensity3 = 2-3 times mowing and manuring; intensity4 = 4-5 times mowing and manuring). Slope: slope gradient according to classes defined by FAO (1990).

Plot	Treatment	Coordinates	Land-use history	Last tillage	Earliest mowing	Management	Slope [%]
I1	<i>Initial</i>	47°28'08.3"N 8°37'12.8"E	temporary grassland	<5 years	~ 01.05.	intensity4	2-5
I2	<i>Initial</i>	47°28'06.7"N 8°37'17.2"E	permanent grassland	>50years	~ 01.05.	intensity3	5-10
I3	<i>Initial</i>	47°27'51.2"N 8°37'26.3"E	permanent grassland	>50years	~ 01.05.	intensity3	15-30
I4	<i>Initial</i>	47°27'52.7"N 8°37'39.9"E	permanent grassland	>50years	~ 01.05.	intensity3	10-15
I5	<i>Initial</i>	47°27'55.8"N 8°37'31.4"E	permanent grassland	>50years	~ 01.05.	intensity3	5-10
I6	<i>Initial</i>	47°27'41.0"N 8°37'38.1"E	permanent grassland	>50years	~ 01.05.	intensity3	5-10
I7	<i>Initial</i>	47°28'06.4"N 8°37'14.1"E	permanent grassland	>50years	~ 01.05.	intensity3	10-15
I8	<i>Initial</i>	47°27'28.7"N 8°37'49.0"E	temporary grassland	<5 years	~ 01.05.	intensity4	2-5
I9	<i>Initial</i>	47°27'16.5"N 8°36'23.7"E	temporary grassland	<5 years	~ 01.05.	intensity4	1-2
I10	<i>Initial</i>	47°26'34.7"N 8°37'15.6"E	temporary grassland	<5 years	~ 01.05.	intensity4	1-2
I11	<i>Initial</i>	47°26'33.2"N 8°37'15.6"E	temporary grassland	<5 years	~ 01.05.	intensity4	1-2
H1	<i>Harvest only</i>	47°28'22.3"N 8°37'18.3"E	permanent grassland	>50years	15.06.	intensity2	15-30
H2	<i>Harvest only</i>	47°28'14.0"N 8°37'06.0"E	permanent grassland	>50years	01.06.	intensity2	1-2
H3	<i>Harvest only</i>	47°28'13.5"N 8°37'05.3"E	permanent grassland	>50years	01.06.	intensity2	1-2
H4	<i>Harvest only</i>	47°28'06.7"N 8°37'03.2"E	permanent grassland	>50years	15.06.	intensity2	10-15
H5	<i>Harvest only</i>	47°27'38.0"N 8°37'37.4"E	permanent grassland	>50years	15.07.	intensity2	5-10
H6	<i>Harvest only</i>	47°27'37.5"N 8°37'37.1"E	permanent grassland	>50years	15.07.	intensity2	2-5
H7	<i>Harvest only</i>	47°27'36.3"N 8°37'22.1"E	permanent grassland	>50years	01.09.	intensity1	1-2
H8	<i>Harvest only</i>	47°27'35.5"N 8°37'26.6"E	temporary grassland	>20years	15.06.	intensity2	1-2
H9	<i>Harvest only</i>	47°27'20.8"N 8°36'31.8"E	permanent grassland	>50years	15.06.	intensity2	5-10
H10	<i>Harvest only</i>	47°27'15.7"N 8°36'24.3"E	temporary grassland	>20years	15.06.	intensity2	1-2
H11	<i>Harvest only</i>	47°27'45.7"N 8°35'08.3"E	permanent grassland	>50years	15.06.	intensity2	5-10
Ts12	<i>Topsoil</i>	47°28'05.5"N 8°37'01.4"E	temporary grassland	>20years	01.10.	intensity1	15-30
Ts13	<i>Topsoil</i>	47°28'05.6"N 8°37'05.4"E	temporary grassland	>20years	01.10.	intensity1	5-10

Ts14	<i>Topsoil</i>	47°28'05.6"N 8°37'06.4"E	temporary grassland	>20years	01.10.	intensity1	2-5
Ts15	<i>Topsoil</i>	47°28'05.2"N 8°37'05.6"E	temporary grassland	>20years	01.10.	intensity1	5-10
Ts16	<i>Topsoil</i>	47°27'48.6"N 8°37'23.1"E	permanent grassland	>50years	15.07.	intensity2	15-30
Ts17	<i>Topsoil</i>	47°27'48.4"N 8°37'22.8"E	permanent grassland	>50years	01.10.	intensity1	1-2
Ts18	<i>Topsoil</i>	47°27'48.2"N 8°37'22.4"E	permanent grassland	>50years	01.10.	intensity1	1-2
Ts19	<i>Topsoil</i>	47°27'47.4"N 8°37'21.7"E	permanent grassland	>50years	01.10.	intensity1	1-2
Ts20	<i>Topsoil</i>	47°27'18.5"N 8°36'40.8"E	temporary grassland	>20years	01.09.	intensity1	10-15
Ts21	<i>Topsoil</i>	47°27'18.2"N 8°36'41.7"E	temporary grassland	>20years	01.09.	intensity1	10-15
Ts22	<i>Topsoil</i>	47°27'17.6"N 8°36'43.1"E	temporary grassland	>20years	01.09.	intensity1	10-15
TsP23	<i>Topsoil+Propagules</i>	47°28'05.0"N 8°37'02.5"E	temporary grassland	>20years	01.10.	intensity1	15-30
TsP24	<i>Topsoil+Propagules</i>	47°28'06.0"N 8°37'05.1"E	permanent grassland	>50years	01.10.	intensity1	2-5
TsP25	<i>Topsoil+Propagules</i>	47°28'06.2"N 8°37'05.9"E	permanent grassland	>50years	01.10.	intensity1	2-5
TsP26	<i>Topsoil+Propagules</i>	47°28'04.8"N 8°37'06.1"E	temporary grassland	>20years	01.10.	intensity1	10-15
TsP27	<i>Topsoil+Propagules</i>	47°27'48.1"N 8°37'24.2"E	permanent grassland	>50years	15.07.	intensity2	15-30
TsP28	<i>Topsoil+Propagules</i>	47°27'47.5"N 8°37'24.4"E	permanent grassland	>50years	01.10.	intensity1	1-2
TsP29	<i>Topsoil+Propagules</i>	47°27'47.0"N 8°37'23.4"E	permanent grassland	>50years	01.10.	intensity1	1-2
TsP30	<i>Topsoil+Propagules</i>	47°27'47.0"N 8°37'22.5"E	permanent grassland	>50years	01.10.	intensity1	1-2
TsP31	<i>Topsoil+Propagules</i>	47°27'18.2"N 8°36'40.5"E	temporary grassland	>20years	01.09.	intensity1	10-15
TsP32	<i>Topsoil+Propagules</i>	47°27'17.6"N 8°36'41.3"E	temporary grassland	>20years	01.09.	intensity1	10-15
TsP33	<i>Topsoil+Propagules</i>	47°27'17.3"N 8°36'42.9"E	temporary grassland	>20years	01.09.	intensity1	10-15
T1	<i>Target</i>	47°28'21.2"N 8°37'21.0"E	permanent grassland	>50years	01.10.	intensity1	15-30
T2	<i>Target</i>	47°28'21.8"N 8°37'20.6"E	permanent grassland	>50years	01.10.	intensity1	15-30
T3	<i>Target</i>	47°29'26.3"N 8°36'58.6"E	permanent grassland	>50years	01.07.	intensity1	30-60
T4	<i>Target</i>	47°29'26.3"N 8°36'59.8"E	permanent grassland	>50years	01.07.	intensity1	30-60
T5	<i>Target</i>	47°28'00.9"N 8°31'52.7"E	permanent grassland	>50years	01.09.	intensity1	1-2
T6	<i>Target</i>	47°28'07.9"N 8°31'52.3"E	permanent grassland	>50years	01.09.	intensity1	1-2
T7	<i>Target</i>	47°28'07.4"N 8°31'53.0"E	permanent grassland	>50years	01.09.	intensity1	1-2
T8	<i>Target</i>	47°28'06.5"N 8°31'51.5"E	permanent grassland	>50years	01.09.	intensity1	1-2
T9	<i>Target</i>	47°28'04.7"N 8°31'51.2"E	permanent grassland	>50years	01.09.	intensity1	2-5
T10	<i>Target</i>	47°28'02.7"N 8°31'53.1"E	permanent grassland	>50years	01.09.	intensity1	2-5
T11	<i>Target</i>	47°28'00.5"N 8°31'51.9"E	permanent grassland	>50years	01.09.	intensity1	5-10



**Fig. S1.** Detailed description of the study area. The main map shows the two nature reserves, 'Eigental' (right; III. & IV.) and 'Altläufe der Glatt' (left; I.), as well as the fragmented and isolated remnants of the surrounding, legally protected semi-natural grasslands as of 1980. Patches of targeted semi-natural grasslands chosen to be improved in quality, extended and reconnected in 1990 are indicated by black borders. Single study areas are magnified to show the detailed design of the treatment arrangement in the field (I.-VII.). Filled, colored squares within treatment sites represent the  $5\text{ m} \times 5\text{ m}$  plots sampled for aboveground arthropods and plant community.



<b>1992:</b>	First restoration measure - cessation of fertilization - biomass harvest 3 times a year
<b>1995:</b>	Implementation of large-scale experiment - Harvest only (continued biomass harvest 2-3 times a year) - Topsoil removal (removal of top 10-20 cm of A horizon)
<b>1995-1997:</b>	Application of targeted plant species from semi-dry and semi-wet grasslands - fresh seed-containing hay from semi-natural grasslands of local provenance (within radius of 7 km) - hand-collected propagules from semi-natural grasslands of regional provenance (within radius of 30 km)
<b>2000:</b>	Start of management for both topsoil treatments - biomass harvest once a year
<b>2016:</b>	Establishment of <i>Initial</i> and <i>Target</i> sites
<b>2017:</b>	Sampling event

**Fig. S2.** Timeline of the experiment from the implementation of the first restoration measures until the sampling of the insect communities.

## **Arthropod sampling and identification**

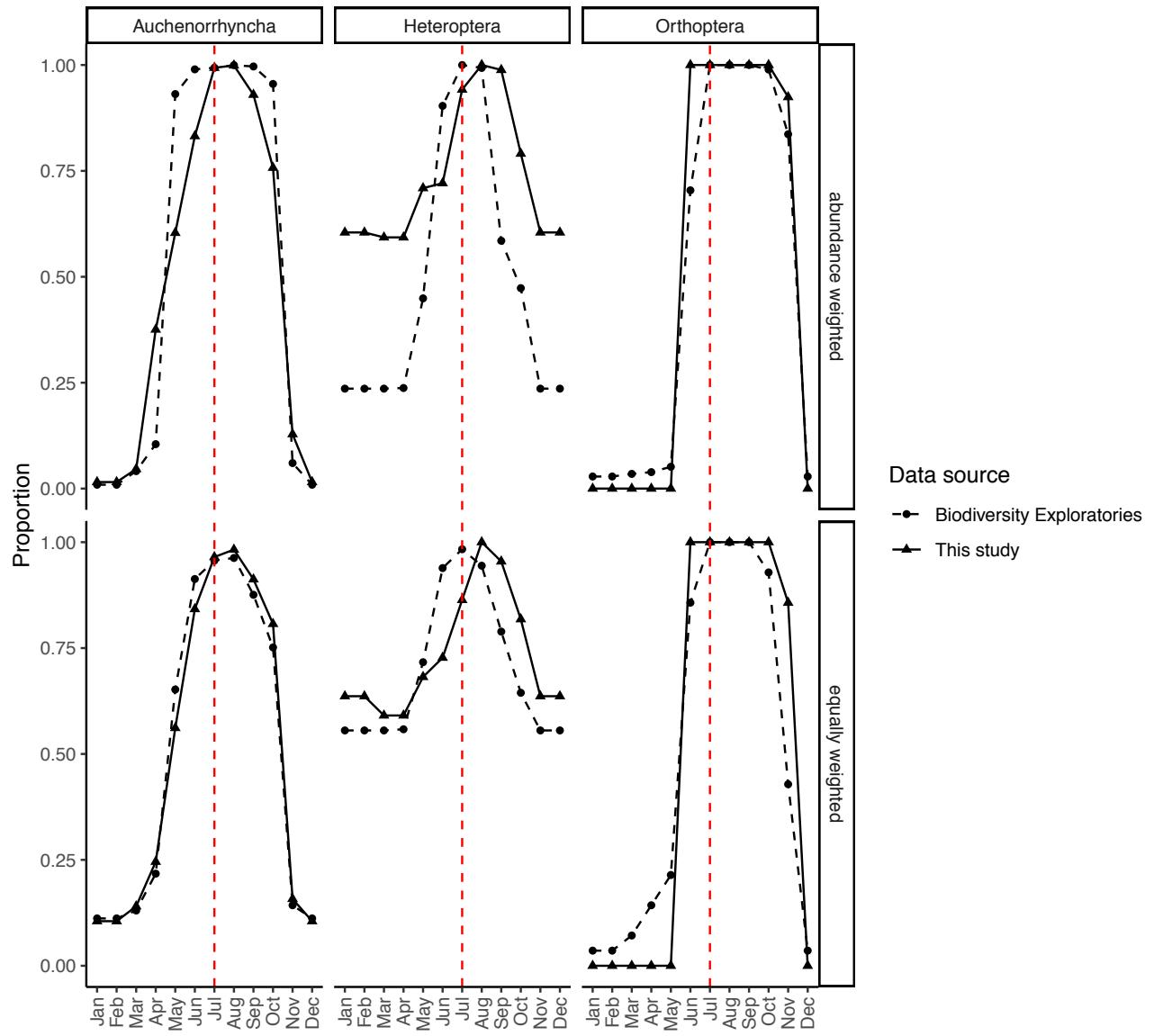
We used existing data to determine the best time for sampling the highest proportion of species in the adult stage in a single sampling event. We determined the proportion of all herbivorous Auchenorrhyncha, Heteroptera and Orthoptera species occurring in grasslands in adult stage per month. We therefore used data from the large-scale and long-term Biodiversity Exploratories Project (Fischer et al. 2010), where Auchenorrhyncha, Heteroptera and Orthoptera were sampled by sweep netting (cf. Simons et al. 2014, 2015, 2016, Neff et al. 2019) in grasslands of different land-use intensity (comparable to our study sites) between 2008 and 2017. It showed that in July most of the species occurred in the adult stage (Fig. S3) and thus we set our sampling time to the beginning of July before mowing. To assess a potential bias imposed by this single sampling point, we conducted some additional analyses. First, we compared the phenology of the species sampled in this study to the phenology of the species sampled in the large-scale and long-term Biodiversity Exploratories Project (Fig. S3). We found that the species sampled in this study are a good representation of species phenologies, because our data were well aligned with the data from the Biodiversity Exploratories, although we might have slightly under-sampled earlier species in our study. Second, we looked at potential changes in functional community composition throughout the season, because we were mainly interested in effects of restoration on the functional composition of our study communities. We again used the data set from the Biodiversity Exploratories mentioned above. For each month, we subsampled those species potentially occurring at the adult stage based on their known phenology and calculated monthly community weighted means with the package ‘FD’ (Laliberté et al. 2014). The results show that little change in functional community composition occurred over time, in which most species are present as adults (June to October), and that samples taken in July are a good representation of the mean functional community composition (Fig. S4).

In our current study, arthropods were sampled with two cylindrical baskets (50 cm diameter, 67 cm height; woven fabric) that were thrown simultaneously from outside the plot into the two corners to avoid disturbance and to achieve a random position of the sampling subplots. A closable mosquito mesh sleeve was mounted on top of the baskets to prevent arthropods from escaping. At the bottom, an integrated metal ring was fixed to the ground with metal stakes to seal the construction. After placing the baskets, they were sampled by suction sampling (Vortis, Burkhard Manufacturing Co. Ltd., Hertfordshire, England). The enclosed volume was sampled

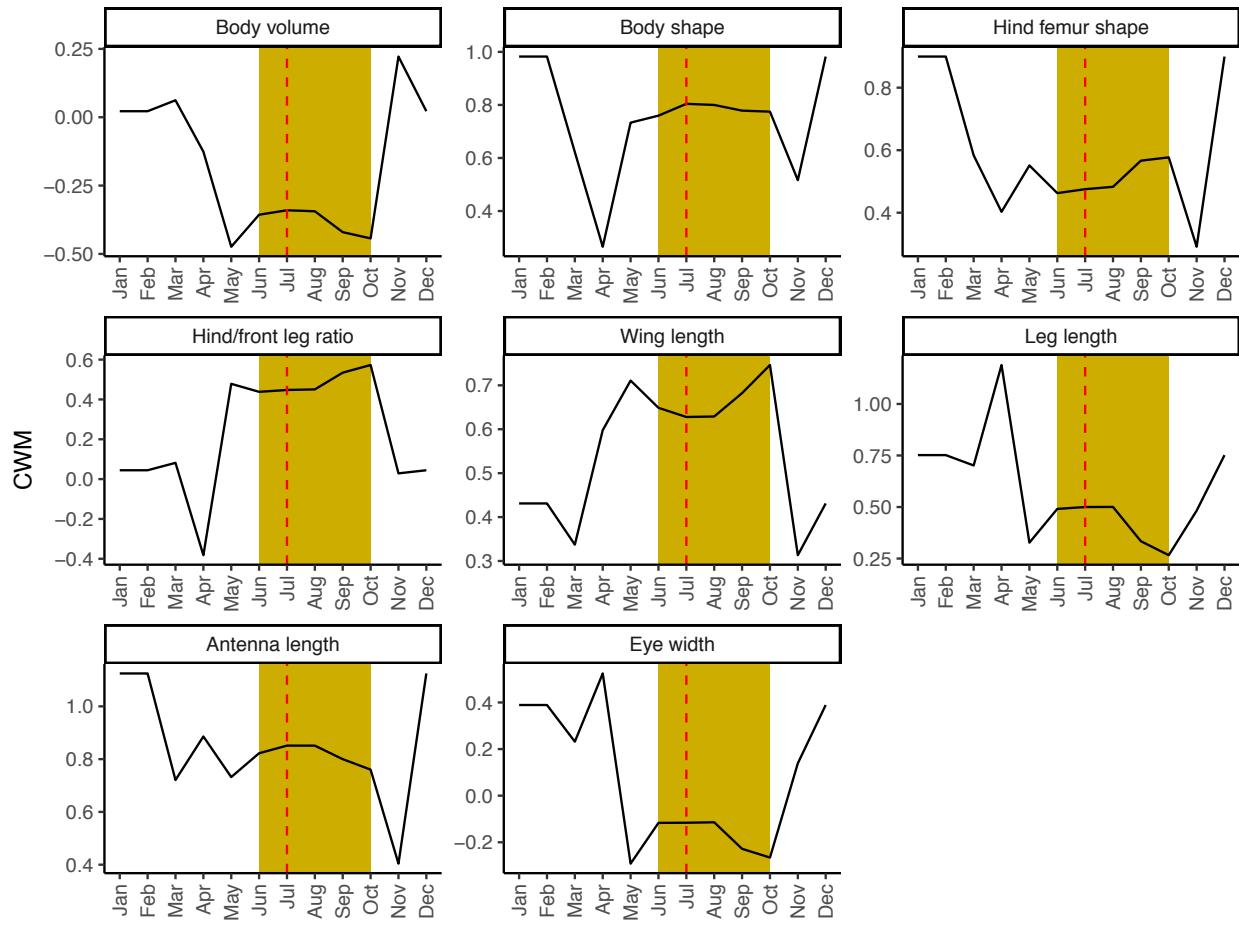
for two sessions of 105 seconds with a 30-seconds break to allow hiding arthropods to become active. The collected arthropods were immediately transferred into 70% ethanol.

First, all collected arthropods were sorted to order or lower taxonomic level. The two subsamples per plot were pooled to increase the number of insect individuals per sample. Next, three of the main herbivorous taxa (Hemiptera: Heteroptera, Hemiptera: Auchenorrhyncha, Orthoptera) were identified to species level using common identification keys and verified by taxonomic specialists (Heteroptera: MMG, Auchenorrhyncha: Roland Mühlethaler, Orthoptera: Tobias Maier). We excluded juveniles (1898 Auchenorrhyncha, 234 Heteroptera and 18 Orthoptera individuals), specimens not identifiable to genus or lower (7 Auchenorrhyncha individuals), and purely predatory species (17 Heteroptera individuals). In addition, identification to species level was not possible for female specimen of several Auchenorrhyncha genera. We assigned these to a species in a three-step procedure to avoid a bias and to prevent overestimation of diversity measures. First, genus-level specimens were assigned to the species of the same genus that were found in the respective plots based on their relative abundances (145 specimens / 13.6 % of the total abundance). Second, if no species of that genus were recorded on the plots, we assigned the genus-level specimens to the most abundant species of the same genus recorded across all plots of the same treatment (32 / 3.0 %). Finally, if no species of that genus was recorded on plots of the same treatment, those genus-level specimens were assigned to the most abundant species of that genus in the whole data set (11 / 1.0 %). The remaining genus-level specimens were kept with genus-level attribution (6 / 0.56 %). A complete species list is given in Table S4 (Section ‘Determination of traits’).

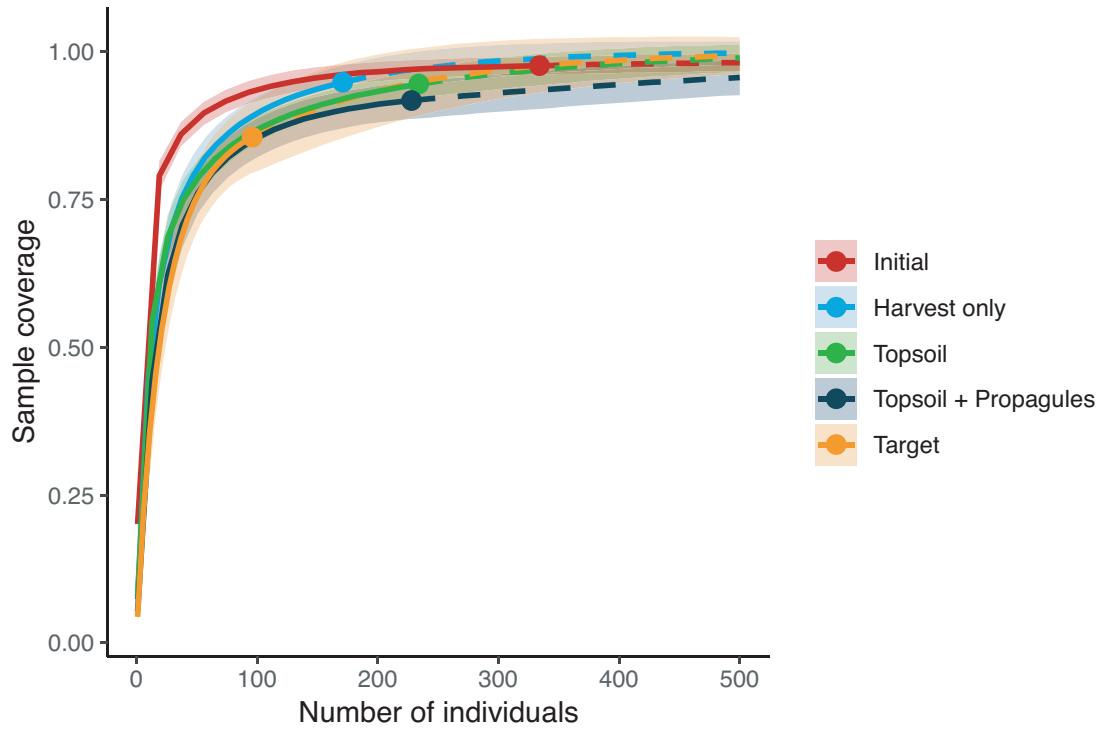
To test for sample completeness, we used coverage-based rarefaction and extrapolation methods for Hill numbers (Chao and Jost 2012, Chao et al. 2014). We determined sample completeness curves for all five restoration treatments based on species abundances in the pooled data set per treatment using the package ‘iNext’ (Hsieh et al. 2019). Results showed that sample coverage was high in all treatments, ranging from 85.5 % in *Target* to 97.6 % in *Initial* (Fig. S5).



**Fig. S3.** Phenology of the herbivorous insect species of the three studied groups represented by the proportion of species potentially being present in the adult stage at a particular month. Solid lines indicate proportions based on data from the current study, whereas dashed lines are based on data from the Biodiversity Exploratories Project (Fischer et al. 2010, Simons et al. 2014, 2015, 2016, Neff et al. 2019). The lower panels weigh all species equally, the upper panel correct for differences in total species abundance in samplings. The red line indicates the month of sampling for our current study.



**Fig. S4.** Change in community weighted means (CWMs) of eight standardized morphometric traits in potential communities of Auchenorrhyncha, Heteroptera and Orthoptera for different months. Shaded areas indicate months with high amounts of species present in the adult stage (cf. Fig. S3), the dashed red line indicates the month of sampling in our current study. Data originates from 10 years of sweep-netting sampling in the large-scale and long-term Biodiversity Exploratories Project (Fischer et al. 2010, Simons et al. 2014, 2015, 2016, Neff et al. 2019).



**Fig. S5.** Sample completeness curves for the different restoration treatment showing the sample coverage for different numbers of sampled individuals. Solid lines show interpolations based on rarefaction, dashed lines show extrapolations. Different colors stand for the different treatments. Points indicate observed number of individuals. Shaded areas show 95% confidence limits based on 50 bootstraps.

## Determination of traits

We used trait measurements from Simons et al. (2016) and Neff et al. (2019) and complemented them with measurements on study specimens. These measurements were conducted using a high-resolution measuring stereo microscope (Leica DVM6, Leica Microsystems) including automated high-resolution photo stacking with the software Leica Application Suite X (LAS X, © 2018 Leica Microsystems CMS GmbH) and Leica Map Premium (Leica Microsystems, © 1996-2017 Digital Surf) at WSL Birmensdorf.

The eight morphometric traits were calculated from direct measurements of body parts on specimens of all identified species (see Table S2 for details). From each species, we measured at least one female and one male specimen. For two species (2.3 %; *Anoscopus albifrons* and *Kelisia ribauti*), only one sex was available for measurement and traits were estimated from congeneric species for the missing sex. Additionally, for species that show wing dimorphism, we included the different wing morphs and weighted them by their prevalence reported in literature. For few species, of which not all wing morphs were available for measurements (10 cases), we estimated relative wing length from congeneric species or from the literature. Body volume was log-transformed prior to analyses. Because of differences in trait value ranges between the three insect groups studied (Heteroptera, Auchenorrhyncha, Orthoptera), trait values were scaled to a mean of 0 and standard deviation of 1 within each group's study species pool prior to merging the data sets.

**Table S2.** Calculation of the eight morphometric traits, their related functions and hypotheses for the effects of restoration measures on these traits in the respective communities (based on functions and previous research).

Trait	Calculation	Sources	Functions	Hypotheses
Body volume	$\text{body length} \times \text{body width} \times \text{body height}$	(Siemann et al. 1999)	Dispersal (+) (e.g. Peters 1983) Disturbance tolerance (−) (e.g. Cole et al. 2002) Microhabitat use (e.g. Fountain-Jones et al. 2015) Resource consumption (+) (e.g. Fountain-Jones et al. 2015)	↑ (e.g., less disturbances) (e.g., Cole et al. 2002, Simons et al. 2016, Neff et al. 2019)
Body shape	$\frac{\text{body length}}{\text{body width}}$	(Simons et al. 2016)	Microhabitat use (e.g. Barton et al. 2011)	↓ (Simons et al. 2016, Neff et al. 2019)
Hind femur shape	$\frac{\text{hind-femur length}}{\text{hind-femur width}}$	(Simons et al. 2016)	Disturbance avoidance (−) through jumping ability in Heteroptera (e.g. Schuh and Slater 1995) and Orthoptera (e.g. Chapman 2013)	↑ (less disturbances) ↓ (Simons et al. 2016, Neff et al. 2019)
Hind/front leg ratio	$\frac{\text{hind-leg length}}{\text{front-leg length}}$	(Burrows and Sutton 2008)	Disturbance avoidance (+) through jumping ability in Auchenorrhyncha (e.g. Burrows and Sutton 2008)	↓ (less disturbances)
Wing length	$\frac{\text{fore-wing length}}{\text{body length}}$	(Simons et al. 2016)	Dispersal (+) (e.g. Rose 1972) and consequently disturbance avoidance (+)	↓ (less disturbances) (e.g., Ribera et al. 2001, Börschig et al. 2013, Birkhofer et al. 2017, Neff et al. 2019)
Leg length	$\frac{\text{front-leg length}}{\text{body length}}$	(Simons et al. 2016)	Dispersal (+) (e.g. Barton et al. 2011) Microhabitat use (e.g. Kaspari and Weiser 1999)	↓ (longer time for colonisation) (e.g., Simons et al. 2016)
Antenna length	$\frac{\text{antenna length}}{\text{body length}}$	(Simons et al. 2016)	Microhabitat use (e.g. Bauer and Kredler 1993)	↓ (more open habitat, thus less tactile orientation) (e.g., Simons et al. 2016, Neff et al. 2016)

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Eye width	$\frac{\text{eye width}}{\text{head width}}$ (Auchenorrhyncha, Heteroptera)	(Defaut 2012, Simons et al. 2016)	Microhabitat use (e.g. Bauer and Kredler 1993)	↑ (more open habitat, thus more visual orientation)
	$\frac{\text{eye width}}{\text{head height}}$ (Orthoptera)			

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Leg length is calculated from the sum of femur and tibia length.

Signs (+) and (-) next to functions indicate the direction of the relation where possible

**Table S3.** Determination of the six life-history traits, their related functions and hypotheses (when justified) for the effects of restoration measures on these traits in the respective communities (based on functions and previous research).

Trait	Levels and definitions	Encoding	Sources	Functions	Hypotheses
Feeding specialization	<ul style="list-style-type: none"> <li><u>Monophagous</u>: Feeding on one plant genus</li> <li><u>Oligophagous</u>: Feeding on one higher plant lineage</li> <li><u>Polyphagous</u>: Feeding on more than one higher plant lineage</li> </ul>	Ordinal	(Gossner et al. 2015 and sources therein)	Vulnerability to changes in the plant community (e.g., Weiner et al. 2011)	More monophagous (higher plant diversity) (e.g., Rader et al. 2014, Simons et al. 2016)
Feeding tissue	<ul style="list-style-type: none"> <li><u>Chewing</u>: Chewing on leaves (all Orthoptera)</li> <li><u>Xylem</u>: Sucking on xylem</li> <li><u>Phloem</u>: Sucking on phloem</li> <li><u>Mesophyll</u>: Sucking on mesophyll</li> <li><u>Mesophyll and phloem and/or reproductive organs</u>: Sucking on Mesophyll, but also on phloem and/or reproductive organs</li> <li><u>Reproductive organs</u>: Sucking on flowers and unripe seeds</li> <li><u>Ripe seeds</u>: Sucking on ripe seeds</li> </ul>	Nominal	(Gossner et al. 2015 and sources therein)	Microhabitat use	?
Hibernation stage	<ul style="list-style-type: none"> <li><u>Egg</u>: Overwintering as egg</li> <li><u>Egg and nymph</u>: Overwintering both as egg and as nymph possible</li> <li><u>Nymph</u>: Overwintering as nymph</li> <li><u>Adults</u>: Overwintering as adult</li> </ul>	Nominal	A: (Nickel 2003) H: (Wachmann et al. 2004, 2006, 2007, 2008, 2012) O: (Schlumprecht and Waeber 2003)	Disturbance tolerance through time of emergence (e.g., Börschig et al. 2013)	More overwintering in early stages (less disturbances) (e.g., Börschig et al. 2013)
Number of generations per year	<ul style="list-style-type: none"> <li><u>1</u>: Univoltine</li> <li><u>1–2</u>: Uni- and bivoltine</li> <li><u>2</u>: Bivoltine</li> </ul>	Ordinal	A: (Nickel 2003) H: (Wachmann et al. 2004, 2006, 2007, 2008, 2012) O: (Schlumprecht and Waeber 2003)	Disturbance tolerance (e.g. Börschig et al. 2013)	More univoltine (less disturbances) (e.g., Börschig et al. 2013)
Moisture preference & Moisture range	<p>The range of preferred habitat moistures was reported for all species based on the following ordered categories:</p> <ul style="list-style-type: none"> <li>Xerophilous (1)</li> <li>Moderately xerophilous (2)</li> <li>Moderately mesohygrophilous (3)</li> <li>Mesohygrophilous (4)</li> <li>Moderately hygrophilous (5)</li> <li>Hygrophilous (6)</li> <li>Moderately hydrophilous (7)</li> <li>Hydrophilous (8)</li> </ul> <p>From this, we determined moisture preference as the weighted mean of all reported habitat moistures (suboptimal but rarely reported habitats were weighted half) and moisture range as the range of all encountered habitat moistures</p>	Numeric	A: (Nickel 2003) H: (Wachmann et al. 2004, 2006, 2007, 2008, 2012) O: (Schlumprecht and Waeber 2003, Baur et al. 2006)	Moisture preference	Increasing moisture preference (moister habitats when intensive use is ceased) Consequently, larger moisture range

A = Auchenorrhyncha; H = Heteroptera; O = Orthoptera

**Table S4.** List of all study species, their total abundance in the five study treatments and their morphometric and life-history traits

Group	Species	Abundance in treatments					Morphometric traits								Life-history traits					
		Initial	Harvest only	Topsoil	Topsoil + Propagules	Target	Body volume	Body shape	Hind femur shape	Hind/femur leg ratio	Wing length	Leg length	Antenna length	Eye width	Moisture preference	Moisture range	Feeding tissue	Feeding specialization	Hibernation stage	Number of generations
Auchenorrhyncha	<i>Acanthodelphe spinosus</i>	0	8	0	2	7	1.618	2.59	3.72	1.49	0.529	0.352	0.291	0.290	2.8	2.5	p	m	n	2
	<i>Anaceratagallia ribauti</i>	3	0	0	0	0	3.342	2.53	4.22	1.89	0.765	0.358	0.264	0.189	2.5	4.0	p	p	a	1
	<i>Anaceratagallia venosa</i>	0	4	6	12	0	3.334	2.72	4.94	1.99	0.925	0.400	0.308	0.129	2.0	3.0	p	p	e	1
	<i>Anoscopus alibrons</i>	0	0	0	0	1	6.625	2.48	4.94	2.24	0.730	0.366	0.147	0.144	3.0	3.0	p	o	e	1
	<i>Anoscopus serratalae</i>	0	0	0	1	0	6.557	2.68	4.45	2.22	0.679	0.324	0.215	0.154	3.6	4.0	p	o	e	1
	<i>Aphrodes bicinctus</i>	0	2	0	1	3	16.782	2.84	5.04	2.34	0.697	0.358	0.127	0.168	2.5	4.0	p	o	e	1
	<i>Aphrophora alni</i>	0	0	4	0	0	73.431	2.20	3.19	1.56	0.860	0.298	0.135	0.135	3.5	6.0	x	p	e	1
	<i>Aphrophora major</i>	0	0	2	4	0	81.321	2.88	3.03	1.26	0.971	0.309	0.162	0.125	5.0	3.0	x	p	e	1
	<i>Arboridula ribauti</i>	0	0	1	0	0	0.756	3.86	5.75	2.10	1.004	0.389	0.335	0.163	3.0	3.0	m	p	a	1
	<i>Arthaldeus pascuellus</i>	0	1	2	4	3	2.025	2.91	5.46	1.95	0.896	0.409	0.368	0.244	4.0	1.0	p	o	e	2
	<i>Athyrsanus argentarius</i>	0	0	1	0	0	33.196	2.84	4.81	2.12	0.774	0.352	0.152	0.153	4.0	5.0	p	o	e	1
	<i>Athyrsanus quadrum</i>	0	0	1	2	1	13.554	2.42	4.76	1.82	0.895	0.520	0.255	0.191	5.0	3.0	p	p	e	1
	<i>Batrachomorpha allionii</i>	0	0	1	0	0	25.025	2.48	4.86	2.26	0.945	0.397	0.131	0.090	3.0	3.0	p	o	e	1
	<i>Cicadella viridis</i>	0	2	23	10	1	22.437	3.16	5.84	2.17	0.847	0.382	0.205	0.171	4.4	4.0	x	p	e	1-2
	<i>Cicadula spec.</i>	0	3	0	0	0	3.602	3.05	5.76	2.19	0.949	0.403	0.252	0.194	4.5	6.0	p	m	e	1-2
	<i>Conomelus anceps</i>	0	1	2	29	1	2.935	2.30	2.71	1.24	0.531	0.409	0.287	0.256	5.5	4.0	p	m	e	1
	<i>Conosanus obscurus</i>	1	0	42	21	2	13.798	2.50	4.42	2.24	0.675	0.315	0.175	0.190	5.0	3.0	p	o	e	1
	<i>Deltotettix pulicaris</i>	6	0	0	0	1	1.654	3.20	4.35	1.94	0.708	0.389	0.300	0.227	4.0	5.0	p	o	e	1-2
	<i>Dicranotropis hamata</i>	2	2	0	0	0	4.117	2.32	4.42	1.49	0.823	0.440	0.285	0.259	3.6	4.0	p	o	n	1-2
	<i>Dikraneura spec.</i>	0	1	0	0	0	1.393	3.82	5.75	2.48	0.962	0.322	0.191	0.156	3.0	3.0	m	o	e	2
	<i>Diplocolenus bohemani</i>	0	0	0	0	1	8.235	2.95	4.55	2.01	0.618	0.318	0.188	0.166	2.0	3.0	p	o	e	1
	<i>Ditropis flavipes</i>	0	0	0	1	0	2.702	1.98	4.32	1.43	0.505	0.479	0.324	0.243	2.0	1.0	p	m	n	2
	<i>Dolotettix lunulatus</i>	0	0	0	0	3	6.580	2.65	4.54	2.21	0.887	0.383	0.183	0.194	4.5	4.0	p	m	n	1
	<i>Emelyanoviana mollicula</i>	0	4	0	0	0	1.416	2.83	6.37	2.24	1.011	0.406	0.281	0.156	2.5	4.0	m	p	e	2
	<i>Eupteryx notata</i>	0	10	1	0	0	0.703	2.65	5.90	2.11	0.961	0.441	0.270	0.181	2.5	4.0	m	o	e	2
	<i>Euscelis incisus</i>	20	3	2	1	0	5.688	2.35	4.07	2.02	0.786	0.406	0.155	0.192	4.5	4.0	p	p	e/n	1-2
	<i>Evacanthus interruptus</i>	0	3	1	5	1	14.315	3.00	5.29	2.00	0.688	0.390	0.155	0.188	5.0	3.0	x	p	e	1
	<i>Javesella dubia</i>	62	5	0	0	0	2.468	2.01	3.78	1.38	0.649	0.448	0.314	0.278	4.5	2.0	p	o	n	2
	<i>Javesella obscurella</i>	127	0	0	0	0	1.962	1.84	4.05	1.38	0.719	0.532	0.316	0.230	5.0	1.0	p	o	n	2
	<i>Kelsia ribauti</i>	0	0	0	1	0	1.378	2.90	4.50	1.44	1.076	0.416	0.343	0.290	4.5	2.0	p	m	e	1
	<i>Kelsia sima</i>	0	0	5	4	5	1.358	2.84	4.58	1.49	1.100	0.413	0.369	0.274	5.5	2.0	p	m	e	1
	<i>Kosswigianella exigua</i>	0	0	0	0	2	1.447	2.25	3.77	1.40	0.759	0.374	0.245	0.223	2.2	3.0	p	m	n	2
	<i>Laodelphax striatellus</i>	40	15	7	5	0	1.982	2.33	4.29	1.28	1.064	0.545	0.327	0.270	2.5	4.0	p	o	n	2
	<i>Lepyrinia coleoptrata</i>	0	0	0	0	2	49.536	1.87	2.28	1.26	0.735	0.317	0.124	0.147	3.1	5.0	x	p	e	1
	<i>Macropsis spec.</i>	0	0	0	0	1	6.098	2.20	4.09	1.66	0.967	0.500	0.141	0.103	5.0	5.0	p	m	e	1
	<i>Macrostelus laevis</i>	17	2	0	1	0	2.004	2.94	5.11	2.32	1.052	0.372	0.264	0.141	2.5	2.0	p	p	e	2
	<i>Megamelodes quadrifaculatus</i>	0	1	0	3	0	2.652	2.03	4.20	1.37	0.423	0.545	0.171	0.261	5.5	2.0	p	o	a	1
	<i>Megamelus notulus</i>	0	33	0	0	0	3.486	2.47	4.35	1.43	0.515	0.417	0.251	0.326	6.0	3.0	p	m	e	1
	<i>Megophthalmus scanicus</i>	0	0	0	1	0	3.382	2.14	4.06	1.72	0.827	0.356	0.250	0.131	4.0	5.0	p	o	e	1
	<i>Muellerianella brevipennis</i>	4	0	13	8	5	2.062	2.44	4.25	1.37	0.712	0.451	0.358	0.262	4.5	4.0	p	m	e	1-2
	<i>Muellerianella extrusa</i>	0	20	2	0	0	2.032	2.32	3.63	1.52	0.808	0.398	0.210	0.283	3.5	2.0	p	m	e	1
	<i>Neophilaenus lineatus</i>	0	0	4	23	0	12.856	2.73	3.54	1.48	0.800	0.328	0.167	0.128	4.0	5.0	x	o	e	1
	<i>Paradelphacodes paludosus</i>	1	11	4	4	1	1.901	2.71	4.55	1.38	0.565	0.477	0.419	0.255	6.0	1.0	p	m	n	1-2
	<i>Philaenus spumarius</i>	1	5	28	13	3	18.399	2.27	3.33	1.45	0.854	0.385	0.163	0.140	2.5	4.0	x	p	e	1
	<i>Psammotettix alienus</i>	1	0	0	0	0	3.425	3.04	5.36	2.24	0.910	0.352	0.252	0.170	3.5	6.0	p	o	e	2
	<i>Psammotettix confinis</i>	1	0	0	0	0	2.991	3.23	5.35	2.53	0.750	0.280	0.149	0.219	3.0	5.0	p	o	e	2
	<i>Psammotettix helvolus</i>	5	10	4	3	7	2.289	3.21	4.99	2.14	0.855	0.336	0.216	0.213	2.5	4.0	p	o	e	1-2
	<i>Recilia conifer</i>	6	4	0	1	5	2.281	3.42	5.69	2.13	0.793	0.402	0.318	0.223	5.0	3.0	p	o	e	1
	<i>Ribautodelphax collinus</i>	0	0	0	1	0	2.268	2.54	3.50	1.27	0.892	0.403	0.202	0.254	2.5	4.0	p	m	n	2
	<i>Ribautodelphax imitans</i>	0	1	29	15	13	2.691	2.57	3.79	1.26	0.781	0.406	0.234	0.235	4.0	3.0	p	m	n	2
	<i>Sorhoanus assimilis</i>	0	0	9	9	1	3.325	3.69	5.58	2.15	0.861	0.364	0.301	0.204	5.0	3.0	p	m	e	1
	<i>Stenocranus fuscovittatus</i>	0	2	0	0	0	3.847	2.65	4.38	1.25	1.204	0.453	0.186	0.290	6.0	3.0	p	m	a	1
	<i>Stictoma bicarinata</i>	0	1	0	0	0	4.930	2.34	4.25	1.38	0.785	0.422	0.177	0.205	4.5	4.0	p	o	n	1
	<i>Strogyllocephalus agrestis</i>	0	1	2	0	0	24.815	2.63	4.72	2.02	0.705	0.364	0.145	0.128	6.0	1.0	p	m	e	1
	<i>Turritus socialis</i>	0	0	0	0	4	4.195	2.71	6.09	2.70	0.517	0.272	0.166	0.206	3.0	3.0	p	o	e	2
	<i>Xanthodelphax spec.</i>	0	0	1	0	0	1.659	2.43	3.43	1.42	0.792	0.364	0.210	0.251	4.0	5.0	p	m	n	1-2
	<i>Zygindia scutellaris</i>	3	0	0	0	0	0.914	2.47	6.96	2.18	1.020	0.395	0.257	0.242	2.0	3.0	m	o	a	1
Heteroptera	<i>Acalyptia marginata</i>	0	0	1	0	0	0.914	2.31	7.25	1.20	0.835	0.400	0.446	0.328	3.5	6.0	m	o	e/n	1-2
	<i>Adelphocoris lineolatus</i>	0	2	0	1	1	25.477	4.17	6.60	1.95	1.032	0.649	1.181	0.341	2.2	2.5	r	p	e	1
	<i>Adelphocoris seticornis</i>	0	0	1	1	0	19.004	3.02	6.76	1.84	1.082	0.680	0.974	0.270	3.5	6.0	r	o	e	1
	<i>Carpocoris purpureipennis</i>	0	0	0	0	1	287.692	1.63	7.59	1.65	0.778									

	<i>Lygus rugulipennis</i>	1	0	0	0	0	11.550	2.57	4.92	1.45	0.912	0.557	0.729	0.311	3.5	6.0	m-p/r	p	a	2
	<i>Notostira elongata</i>	2	0	0	0	0	8.851	5.71	12.23	1.62	0.793	0.682	1.258	0.271	2.0	3.0	m-p/r	o	a	2
	<i>Peritrechus geniculatus</i>	0	1	0	0	0	11.112	2.80	5.14	1.36	0.665	0.450	0.524	0.255	2.0	3.0	se	p	a	1
	<i>Polymerus microphthalmus</i>	0	0	0	1	0	9.856	2.91	4.83	1.98	1.049	0.551	0.908	0.249	2.5	4.0	m-p/r	m	e	1
	<i>Stenodema calcarata</i>	0	0	5	0	1	4.991	5.41	8.88	1.56	1.126	0.716	1.106	0.261	4.5	4.0	r	o	a	2
	<i>Stenodema laevigata</i>	1	0	0	1	0	13.224	5.85	7.59	1.91	0.799	0.470	0.851	0.253	4.0	5.0	r	o	a	1
	<i>Stenotus binotatus</i>	0	0	0	1	1	11.236	3.60	6.24	1.95	0.964	0.552	1.052	0.286	4.5	4.0	r	o	e	1
	<i>Tingis reticulata</i>	0	0	0	2	0	4.010	2.94	6.48	1.34	0.719	0.380	0.380	0.210	2.0	3.0	m	o	a	1
	<i>Trigonotylus caelestialium</i>	7	2	0	0	0	1.962	7.73	10.43	1.78	0.976	0.662	1.084	0.267	3.5	6.0	r	o	e	2
Orthoptera	<i>Chorthippus montanus</i>	0	0	3	2	0	217.967	5.52	5.43	3.88	0.736	0.342	0.524	0.555	5.0	3.0	c	o	e	1
	<i>Chorthippus parallelus</i>	7	7	11	10	5	284.309	6.05	4.60	3.71	0.517	0.284	0.397	0.529	3.5	6.0	c	p	e	1
	<i>Conocephalus fuscus</i>	0	0	1	1	0	312.296	4.36	6.01	3.71	0.904	0.358	2.871	0.364	5.0	3.0	c	p	e	1
	<i>Metrioptera roeselii</i>	0	0	2	3	0	440.231	4.19	5.56	4.07	0.603	0.389	1.099	0.309	4.0	5.0	c	p	e	1
	<i>Parapleurus alliaceus</i>	4	0	2	2	2	429.928	6.43	5.75	3.62	0.738	0.268	0.451	0.490	3.0	3.0	c	p	e	1
	<i>Pholidoptera griseoaptera</i>	0	0	2	1	0	787.368	4.39	5.19	3.56	0.184	0.428	1.310	0.323	4.5	4.0	c	p	e	1
	<i>Tettigoniaviridissima</i>	0	0	0	1	0	2199.266	4.69	7.21	2.97	1.404	0.512	1.772	0.322	2.5	4.0	c	p	e	1

Calculation of morphometric traits is given in Table S2.

Definition of life-history traits is given in Table S3.

Feeding tissue: c = chewing; x = xylem; p = phloem; m = mesophyll, m-p/r = mesophyll and phloem and/or reproductive organs; r = reproductive organs; se = ripe seeds

Feeding specialisation: m = monophagous; o = oligophagous; p = polyphagous

Hibernation stage: e = egg; e/n = egg and nymph; n = nymph; a = adult

### **Confounding factors, nested structure and spatial autocorrelation**

We tested for effects of confounding factors, the nested structure of the plot arrangement and for spatial autocorrelation in the data by using a set of linear mixed-effect models (LMM) and linear models (LM). We performed two sets of analyses, one for diversity and another for community composition. For diversity, we calculated for each plot the attribute diversity for all possible combinations of three levels of  $q$  (0, 1, 2) and three levels of  $\tau$  ( $d_{min}$ ,  $d_{mean}$ ,  $d_{max}$ ) for both data sets (morphometric, life history), resulting in 18 different diversity measures. For community composition, we used the values of the first two ordination axes from the principal coordinate analyses (PCoA) performed on taxonomic, morphometric and life-history dissimilarities, resulting in 6 different composition measures. As explanatory variables, we used restoration treatment and two potential confounding environmental variables (see Table S1): land-use history (temporary or permanent grassland) and slope (6 levels, converted to numeric variable). A third potential confounding factor (time since last tillage) was highly dependent on land-use history (Fisher's exact test:  $P = 3.6 \times 10^{-15}$ ) and thus excluded from the models. To test for the effect of the nested structure, we defined six clusters of plots laying in close proximity (I, II, III-IV, V, VI, VII in Fig. S1) and included them as random intercept in our LMM, which were run with the package 'lmerTest' (Kuznetsova et al. 2019). The same data was then analysed with LM not including the random intercept. Results were very similar for LMM and LM, showing that the nested structure is not influencing our results (Tables S5-S6). At the same time, they showed little influence of the confounding factor (Tables S5-S6). Thus, we did not further account for the nested structure and the confounding factors in the main analyses of this study.

Additionally, to test for further spatial autocorrelation in the data, we plotted standardized residuals from all LMM along the plot coordinates (Figs. S6-S8). As no spatial autocorrelation was visually detected, corrections of analyses were not considered in this study.

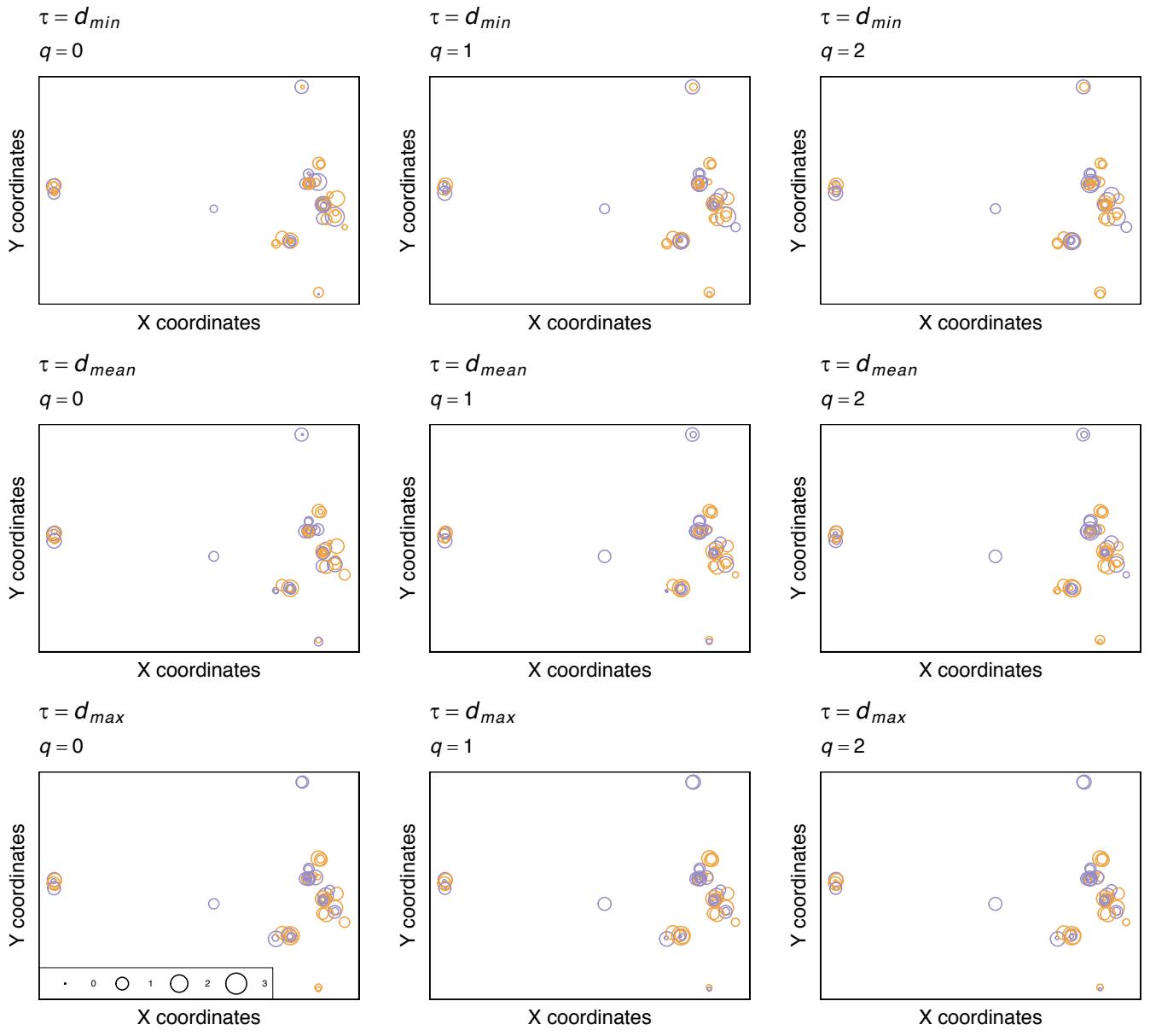
**Table S5.** Results from linear mixed-effects models including a random intercept for cluster (LMM) and linear models (LM) for the effect of restoration treatment, land-use history and slope on attribute diversity. Attribute diversity values for all possible combinations of three levels of  $q$  (0, 1, 2) and three levels of  $\tau$  ( $d_{min}$ ,  $d_{mean}$ ,  $d_{max}$ ) for both data sets (morphometric, life history) were used as response variables. Satterthwaite's method was used to estimate denominator degrees of freedom and  $F$ -statistics for linear mixed-effects models.

Data	q	Variable	LMM									LM								
			$\tau = d_{min}$			$\tau = d_{mean}$			$\tau = d_{max}$			$\tau = d_{min}$			$\tau = d_{mean}$			$\tau = d_{max}$		
			df	F	P val.	df	F	p value	df	F	P val.	df	F	P val.	df	F	P val.	df	F	P val.
Morphometric	0	Restoration Treatment	4, 19	2.9	0.050	4, 33	4.5	<b>0.005</b>	4, 18	1.9	0.15	4, 48	3.3	<b>0.017</b>	4, 48	3.9	<b>0.008</b>	4, 48	1.5	0.207
		Land-use history	1, 32	2.1	0.161	1, 48	0.7	0.422	1, 48	0.8	0.366	1, 48	4.0	0.051	1, 48	2.4	0.128	1, 48	0.3	0.578
		Slope	1, 23	3.5	0.073	1, 20	6.3	<b>0.021</b>	1, 9	1.5	0.254	1, 48	3.4	0.072	1, 48	5.9	<b>0.019</b>	1, 48	0.6	0.451
	1	Restoration Treatment	4, 15	3.0	0.052	4, 8	3.8	<b>0.049</b>	4, 48	1.7	0.167	4, 48	3.1	<b>0.025</b>	4, 48	3.6	<b>0.012</b>	4, 48	1.7	0.167
		Land-use history	1, 18	0.1	0.728	1, 27	0.0	0.966	1, 48	0.3	0.588	1, 48	0.3	0.592	1, 48	0.2	0.643	1, 48	0.3	0.588
		Slope	1, 25	1.9	0.177	1, 11	2.6	0.134	1, 48	0.5	0.495	1, 48	1.9	0.175	1, 48	2.6	0.113	1, 48	0.5	0.495
	2	Restoration Treatment	4, 48	2.2	0.083	4, 48	3.1	<b>0.025</b>	4, 48	1.8	0.140	4, 48	2.2	0.083	4, 48	3.1	<b>0.025</b>	4, 48	1.8	0.140
		Land-use history	1, 48	0.1	0.726	1, 48	0.0	0.955	1, 48	0.3	0.594	1, 48	0.1	0.726	1, 48	0.0	0.955	1, 48	0.3	0.594
		Slope	1, 48	0.5	0.497	1, 48	1.1	0.304	1, 48	0.4	0.536	1, 48	0.5	0.497	1, 48	1.1	0.304	1, 48	0.4	0.536
Life history	0	Restoration Treatment	4, 20	3.0	<b>0.045</b>	4, 48	1.8	0.136	4, 48	0.8	0.511	4, 48	3.5	<b>0.014</b>	4, 48	1.8	0.136	4, 48	0.8	0.511
		Land-use history	1, 34	1.8	0.186	1, 48	0.7	0.395	1, 48	0.1	0.759	1, 48	3.9	0.056	1, 48	0.7	0.395	1, 48	0.1	0.759
		Slope	1, 22	3.4	0.078	1, 48	0.3	0.580	1, 48	2.7	0.109	1, 48	3.2	0.079	1, 48	0.3	0.580	1, 48	2.7	0.109
	1	Restoration Treatment	4, 15	3.0	0.054	4, 48	0.7	0.628	4, 48	0.7	0.579	4, 48	3.0	<b>0.027</b>	4, 48	0.7	0.628	4, 48	0.7	0.579
		Land-use history	1, 18	0.1	0.758	1, 48	0.0	0.887	1, 48	0.0	0.877	1, 48	0.3	0.618	1, 48	0.0	0.887	1, 48	0.0	0.877

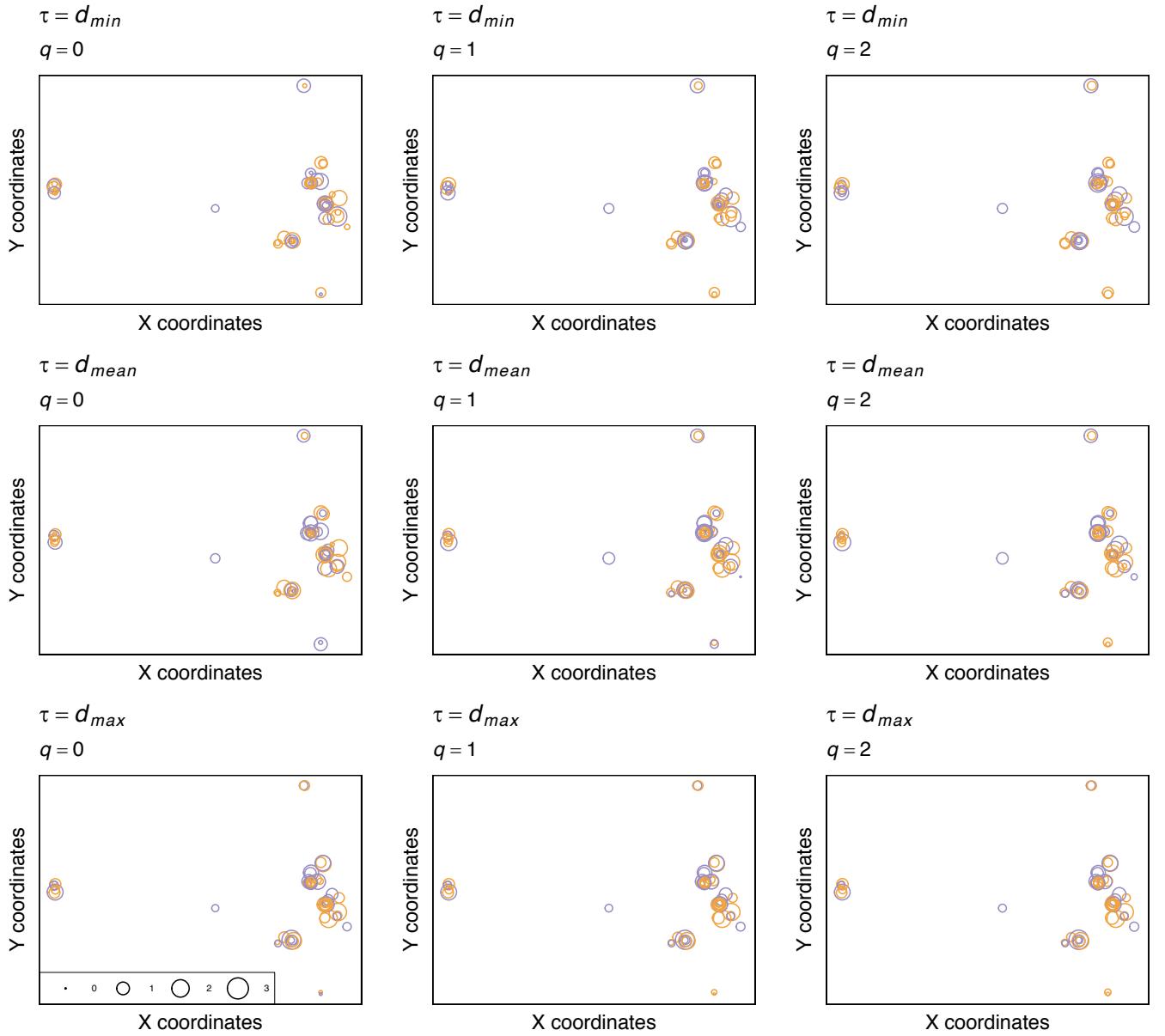
	Slope	1, 25	1.8	0.196	1, 48	0.0	0.928	1, 48	2.7	0.104	1, 48	1.7	0.194	1, 48	0.0	0.928	1, 48	2.7	0.104
2	Restoration Treatment	4, 48	2.2	0.086	4, 48	0.6	0.697	4, 48	0.7	0.603	4, 48	2.2	0.086	4, 48	0.6	0.697	4, 48	0.7	0.603
	Land-use history	1, 48	0.1	0.720	1, 48	0.0	0.994	1, 48	0.0	0.936	1, 48	0.1	0.720	1, 48	0.0	0.994	1, 48	0.0	0.936
	Slope	1, 48	0.4	0.508	1, 48	0.1	0.704	1, 48	2.8	0.100	1, 48	0.4	0.508	1, 48	0.1	0.704	1, 48	2.8	0.100

**Table S6.** Results from linear mixed-effects models including a random intercept for cluster (LMM) and linear models (LM) for the effect of restoration treatment, land-use history and slope on community composition. Values of the first two ordination axes from the principal coordinate analyses performed on taxonomic, morphometric and life-history dissimilarities were used as response variables. Satterthwaite's method was used to estimate denominator degrees of freedom and *F*-statistics for linear mixed-effects models.

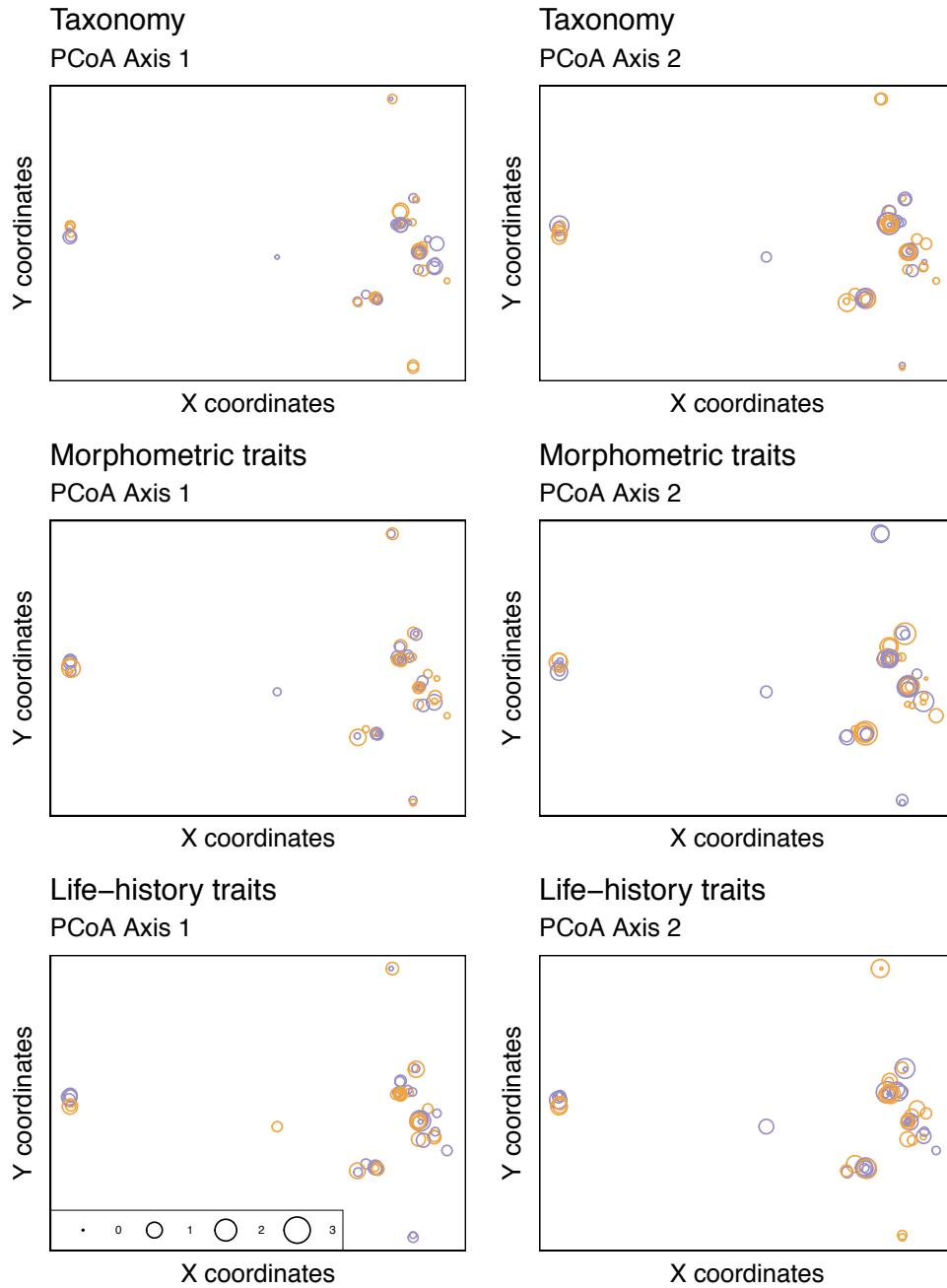
Data	Variable	LMM						LM					
		Axis 1			Axis 2			Axis 1			Axis 2		
		df	F	P val.	df	F	P val.	df	F	P val.	df	F	P val.
Taxonomy	Restoration treatment	4, 48	51.7	<b>8.3E-17</b>	4, 44	0.9	0.452	4, 48	51.7	<b>8.3E-17</b>	4, 48	1.2	0.327
	Land-use history	1, 48	8.7	<b>0.005</b>	1, 46	1.8	0.187	1, 48	8.7	<b>0.005</b>	1, 48	0.1	0.789
	Slope	1, 48	1.5	0.233	1, 40	4.8	<b>0.034</b>	1, 48	1.5	0.233	1, 48	3.1	0.087
Morphometric	Restoration Treatment	4, 45	29.1	<b>6.3E-12</b>	4, 48	1.4	0.261	4, 48	18.2	<b>3.8E-09</b>	4, 48	1.4	0.261
	Land-use history	1, 44	11.8	<b>0.001</b>	1, 48	0.0	0.853	1, 48	2.0	0.161	1, 48	0.0	0.853
	Slope	1, 48	0.3	0.615	1, 48	0.0	0.878	1, 48	0.7	0.401	1, 48	0.0	0.878
Life history	Restoration Treatment	4, 48	18.8	<b>2.3E-09</b>	4, 21	2.0	0.129	4, 48	18.8	<b>2.3E-09</b>	4, 48	1.8	0.140
	Land-use history	1, 48	0.0	0.835	1, 46	2.5	0.118	1, 48	0.0	0.835	1, 48	1.1	0.306
	Slope	1, 48	0.0	0.985	1, 13	4.2	<b>0.060</b>	1, 48	0.0	0.985	1, 48	4.7	<b>0.036</b>



**Fig. S6.** Standardized residuals of linear mixed-effects models for attribute diversity based on morphometric traits with different order  $q$  and different threshold distinctiveness value  $\tau$ , plotted along the plot coordinates. The size of the circles indicates the size of residuals, the colors indicate the signs of the residuals (orange: negative; purple: positive).



**Fig. S7.** Standardized residuals of linear mixed-effects models for attribute diversity based on life-history traits with different order  $q$  and different threshold distinctiveness value  $\tau$ , plotted along the plot coordinates. The size of the circles indicates the size of residuals, the colors indicate the signs of the residuals (orange: negative; purple: positive).



**Fig. S8.** Standardized residuals of linear models for the first two PCoA axes against treatments, plotted along the plot coordinates. PCoA axes originate from taxonomic dissimilarities as well as trait-based dissimilarities (morphometric traits, life-history traits; see Materials and methods section of the main manuscript). The size of the circles indicates the size of residuals, the colors indicate the signs of the residuals (orange: negative; purple: positive).

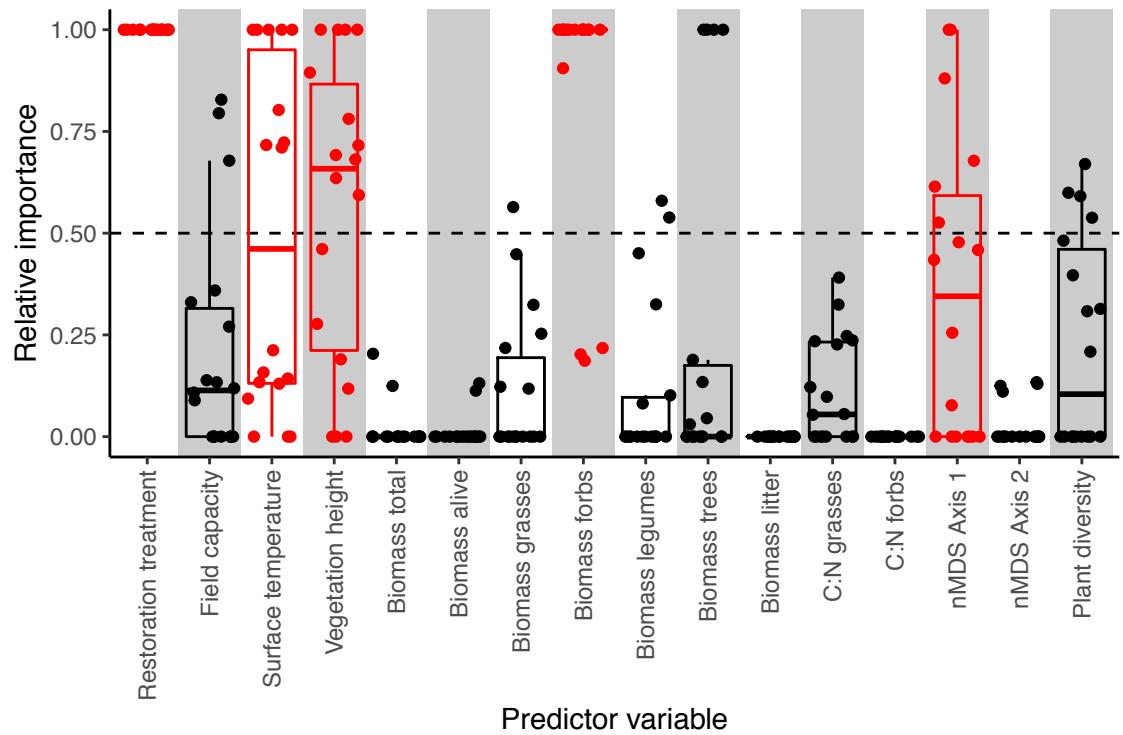
## **Effect pathways**

To test for the pathways through which the restoration treatments were affecting diversity and composition of the insect communities, we used piecewise structural equation models (SEM) (Lefcheck 2016a) for a set of 16 variables describing the treatment, the environmental conditions as well as the vegetation (Table S7). We performed two sets of analyses, one for diversity and another for community composition. As response variable, we used the same set of 18 diversity variables and 6 composition variables, which were used to test for confounding factors and the effects of the nested structure. To reduce the number of variables included in the SEMs, we performed multi-model averaging with the package ‘MuMIn’ (Bartón 2018) for all diversity and composition measures. We used linear models including all 16 predictor variables (Table S7). Restoration treatment was kept in all models as a fixed factor. Additionally, we excluded models combining total (alive) plant biomass and biomass of single groups to reduce correlation among predictors. On these sets of models for the different combinations of predictor variables, we then performed model averaging based on the Akaike’s Information Criterion (AICc). Finally, we selected variables that reached a relative importance of 0.5 (i.e., present in 50% of the models with a  $\Delta\text{AIC} \leq 2$  (Burnham and Anderson 2004)) for at least one third of the diversity/composition measures (Figs. S9-S10). This procedure was performed separately for the diversity and the composition measures, resulting in two different sets of variables, which were then used for SEMs.

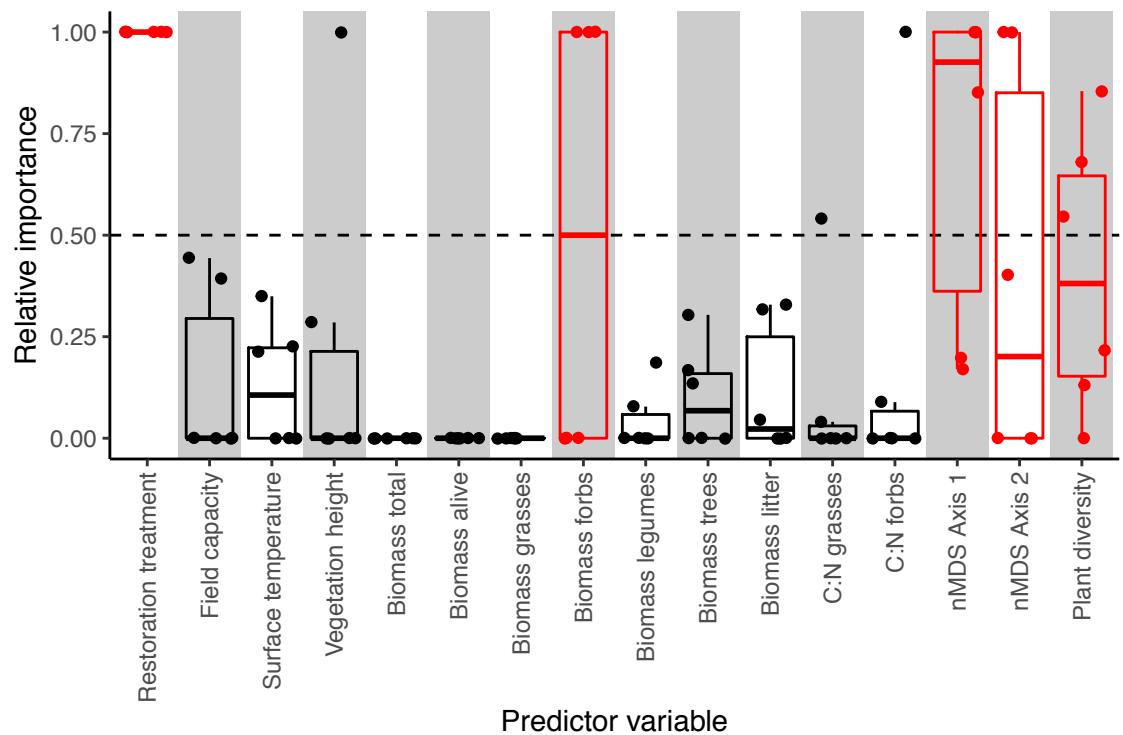
For the selected sets of predictor variables, we built hypothetical pathways linking the different predictors and the response variables (diversity/composition measures) based on our expectations, which were slightly adjusted to ensure a set of non-significant *d*-separation claims (Fig. S11). All pathways were modelled using linear regression. From these models, we calculated piecewise SEMs for all response variables using the package ‘piecewiseSEM’ (Lefcheck 2016b) (Figs. S12-S13).

**Table S7.** Variables describing the environment and the plant community, which were used for analysis of effect pathways. All variables were sampled within the 5 m × 5 m plots, except field capacity and surface temperature, where measurements were done at 2 m × 2 m subplots randomly established at least 2 m away from the 5 m × 5 m plots (further details see Resch et al. 2019).

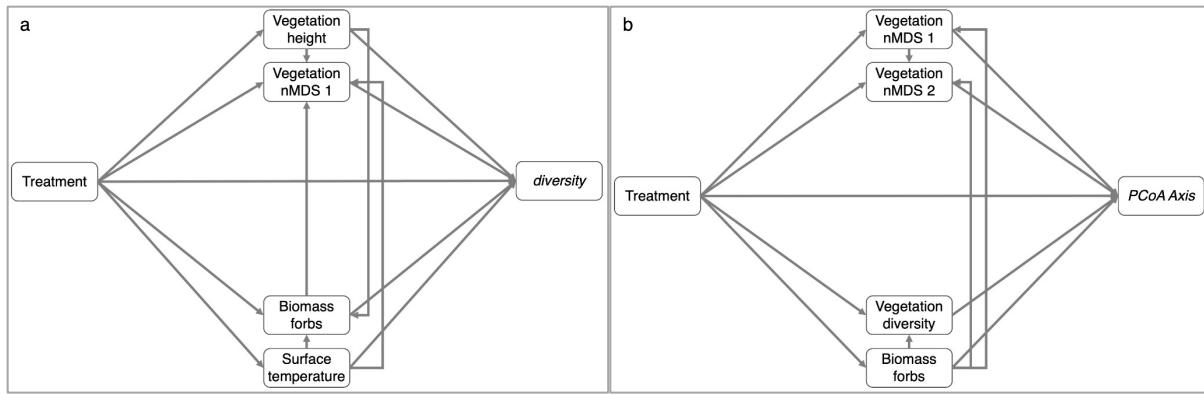
Variable(s)	Description / Method
Restoration treatment	Factorial variable for the five restoration treatments ( <i>Initial, Harvest only, Topsoil, Topsoil + Propagules, Target</i> )
Field capacity	Measure for soil humidity. One undisturbed soil core (5 cm diameter, 12 cm depth) was collected per subplot with a slide hammer corer (AMS Samplers, American Falls, Idaho, USA). Field capacity was measured in the lab. Soils remaining in the cylinder were saturated in a water bath and then drained on a sand/silt-bed with suction corresponding to 60 cm hydrostatic head. Field capacity was calculated by dividing the mass of water by the total mass of wet soil contained at 60 cm hydrostatic head (Klute 1986).
Surface temperature	Climatic measure. Surface temperature was measured with a water-resistant digital pocket thermometer (IP65, H-B Instrument, Trappe, Pennsylvania, USA) at five random locations within the subplots every month from beginning of June to beginning of September.
Vegetation height	Measure for habitat configuration. Vegetation height was assessed along the diagonal of each plot. We measured the mean height at three sampling locations along the plot diagonal.
Biomass total, Biomass alive, Biomass grasses, Biomass forbs, Biomass legumes, Biomass trees, Biomass litter	Measure for available plant biomass. Total plant biomass was collected along a 2 m × 0.1 m strip on the diagonal transect. Plant biomass was sorted into functional groups (grasses, forbs, legumes, trees, litter), dried for 48 h at 60 °C, and weighted (Meyer et al. 2015). <i>Biomass total</i> was calculated as the sum of all functional groups, while <i>biomass alive</i> was calculated by summarizing weights of functional groups excluding litter.
C:N grasses, C:N forbs	Measure for plant nutrient contents. Plant C:N ratios were assessed for the two main functional groups (grasses, forbs). The dried plant biomass was ground (Pulverisette 16, Fritsch, Idar-Oberstein, Germany) to pass a 0.5-mm sieve and shoot C and N content were measured (Leco TruSpec Analyzer, Leco, St. Joseph, MI, USA).
nMDS Axis 1, nMDS Axis 2	Measure for plant community composition. Cover of each plant species was visually assessed according to the semi-quantitative cover-abundance scale of Braun-Blanquet (1964, nomenclature: Lauber and Wagner 1996) and thereafter transformed according to van der Maarel (1979) for subsequent analyses. Based on these vegetation surveys, we performed nonmetric Multi-Dimensional Scaling (nMDS) analysis based on Bray-Curtis dissimilarities using the package ‘vegan’ (Oksanen et al. 2018) to quantify the differences between communities. We used two nMDS axes as predictor variables.
Plant diversity	Measure for the taxonomic diversity of the plant community. Based on the vegetation surveys (see above), we calculated Shannon diversity for each plot with the package ‘vegan’ (Oksanen et al. 2018).



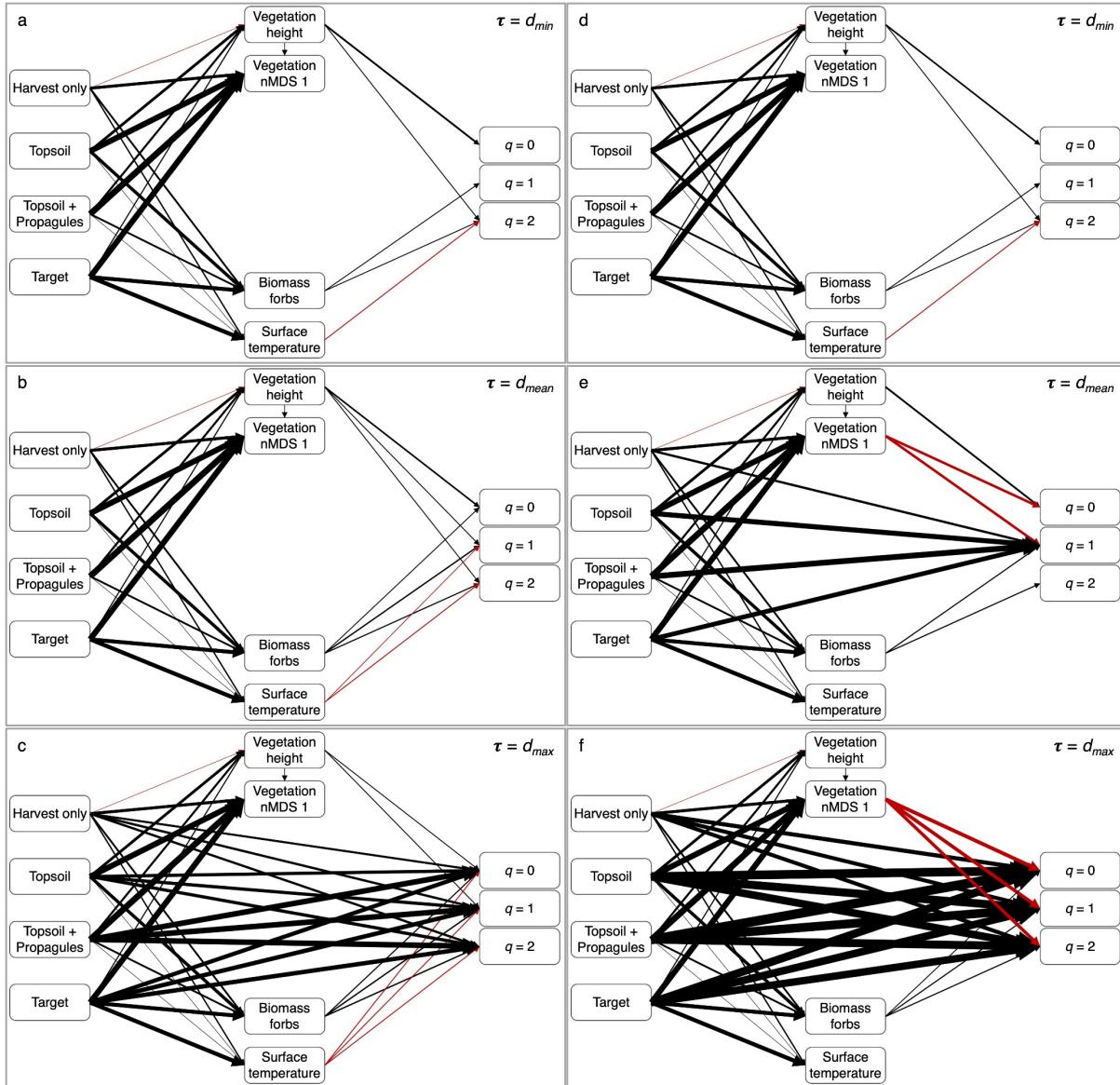
**Fig. S9.** Relative importance of different predictor variables in model averaging for the different diversity measures ( $\Delta\text{AIC} \leq 2$ ,  $n = 18$ ). Variables which reached an importance of 0.5 for at least one third of the measures were selected for SEMs (highlighted in red). Restoration treatment was a fixed factor.



**Fig. S10.** Relative importance of different predictor variables in model averaging for the different composition measures ( $\Delta\text{AIC} \leq 2$ ,  $n = 6$ ). Variables which reached an importance of 0.5 for at least one third of the measures were selected for SEMs (highlighted in red). Restoration treatment was a fixed factor.

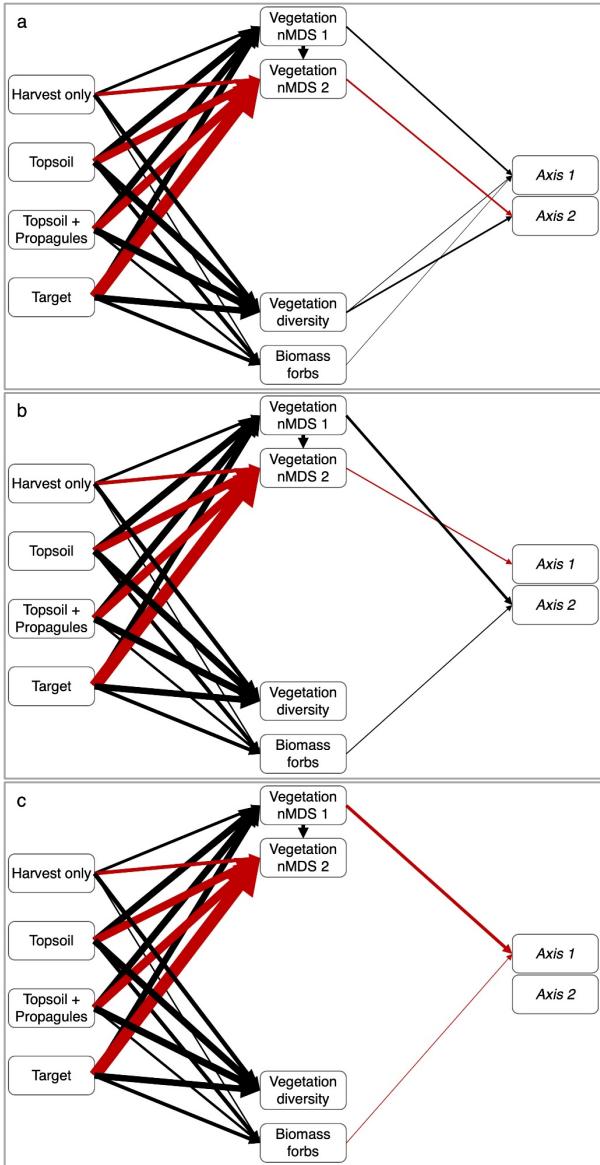


**Fig. S11.** Hypothetical pathways which were used for piecewise SEMs for (a) the different diversity measures and (b) the different composition measures.



**Fig. S12.** Results from piecewise SEMs for attribute diversity with different order  $q$  and different threshold distinctiveness value  $\tau$  (a-c: morphometric traits; d-f: life-history traits). Positive effects in black, negative effects in red. Arrow thickness corresponds to scaled effect size. Effects of treatments are in reference to the *Initial* treatment. Only significant relationships are shown. Restoration measures are indirectly affecting attribute diversity through changes in vegetation height, biomass of forbs and plant community composition for several levels of the distinctiveness value and for both data sets. Additionally, for high distinctiveness values, there are direct effects of restoration measures on attribute diversity. Generally, effects and effect pathways are positive for all measures compared to the *Initial* treatment (except for indirect

pathways through plant community composition). *Topsoil*, *Topsoil + Propagules* and *Target* have stronger effects compared to *Harvest only*.



**Fig. S13.** Results from piecewise SEMs for community composition, i.e. PCoA Axes 1 and 2 (a: taxonomic; b: morphometric; c: life-history). Positive effects in black, negative effects in red. Arrow thickness corresponds to scaled effect size. Effects of treatments are in reference to the *Initial* treatment. Only significant relationships are shown. Restoration measures are only indirectly affecting community composition for all measures of composition. The indirect pathways involve plant community composition (and diversity) as well as biomass of forbs. Effects of *Topsoil*, *Topsoil + Propagules* and *Target* in comparison to *Initial* are stronger than effects of *Harvest only*.

## Additional tables and figures

**Table S8.** Results from pairwise permutational multivariate analysis of variance (PerMANOVA) between all treatment pairs for taxonomic dissimilarities between plots as well as functional dissimilarities between plots based on morphometric traits and life-history traits. Adjusted P values from Bonferroni corrections. Bold numbers indicate significant P values ( $P < 0.05$ ). I = *Initial*; H = *Harvest only*; Ts = *Topsoil*; TsP = *Topsoil + Propagules*; T = *Target*.

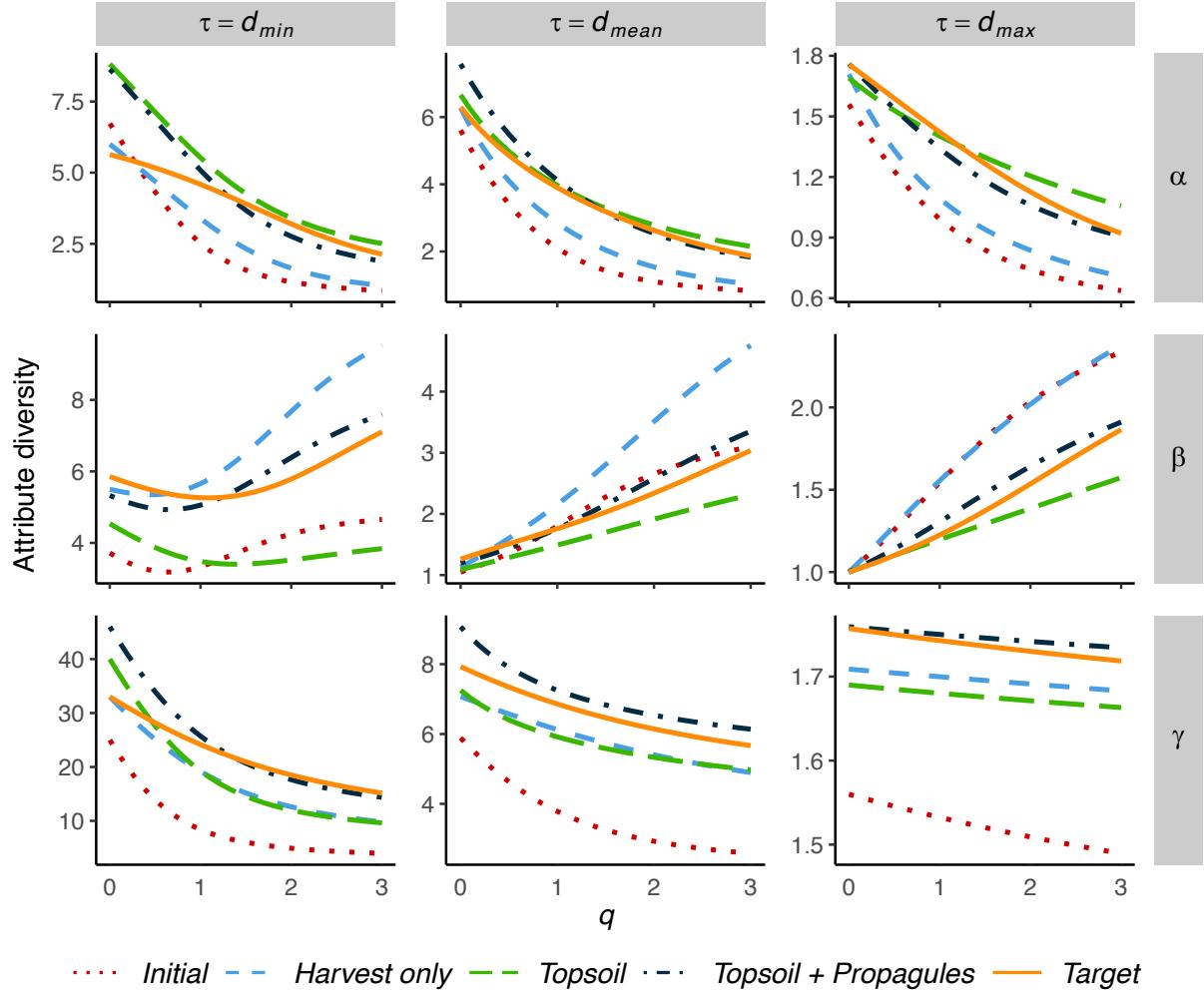
	Pairs	F <sub>1,20</sub>	R <sup>2</sup>	P value	adj. P value
Taxonomic	I vs. H	2.59	0.11	<b>0.001</b>	<b>0.01</b>
	I vs. Ts	4.92	0.20	<b>0.001</b>	<b>0.01</b>
	I vs. TsP	3.81	0.16	<b>0.001</b>	<b>0.01</b>
	I vs. T	3.89	0.16	<b>0.001</b>	<b>0.01</b>
	H vs. Ts	2.71	0.12	<b>0.001</b>	<b>0.01</b>
	H vs. TsP	1.77	0.08	<b>0.003</b>	<b>0.03</b>
	H vs. T	1.64	0.08	<b>0.021</b>	0.21
	Ts vs. TsP	0.54	0.03	0.936	1.00
	Ts vs. T	2.14	0.10	<b>0.005</b>	0.05
	TsP vs. T	1.21	0.06	0.194	1.00
Morphometric	I vs. H	3.17	0.14	<b>0.001</b>	<b>0.01</b>
	I vs. Ts	5.71	0.22	<b>0.001</b>	<b>0.01</b>
	I vs. TsP	4.51	0.18	<b>0.001</b>	<b>0.01</b>
	I vs. T	4.24	0.17	<b>0.001</b>	<b>0.01</b>
	H vs. Ts	2.48	0.11	<b>0.003</b>	<b>0.03</b>
	H vs. TsP	1.80	0.08	<b>0.019</b>	0.19
	H vs. T	1.42	0.07	0.135	1.00
	Ts vs. TsP	0.74	0.04	0.734	1.00
	Ts vs. T	1.55	0.07	0.109	1.00
	TsP vs. T	0.90	0.04	0.571	1.00
Life history	I vs. H	3.65	0.15	<b>0.001</b>	<b>0.01</b>
	I vs. Ts	8.71	0.30	<b>0.001</b>	<b>0.01</b>
	I vs. TsP	8.18	0.29	<b>0.001</b>	<b>0.01</b>
	I vs. T	6.01	0.23	<b>0.001</b>	<b>0.01</b>
	H vs. Ts	2.71	0.12	<b>0.002</b>	<b>0.02</b>
	H vs. TsP	1.98	0.09	<b>0.012</b>	0.12
	H vs. T	1.36	0.06	0.186	1.00
	Ts vs. TsP	0.53	0.03	0.885	1.00
	Ts vs. T	1.32	0.06	0.214	1.00
	TsP vs. T	1.11	0.05	0.325	1.00

Results based on 999 permutations

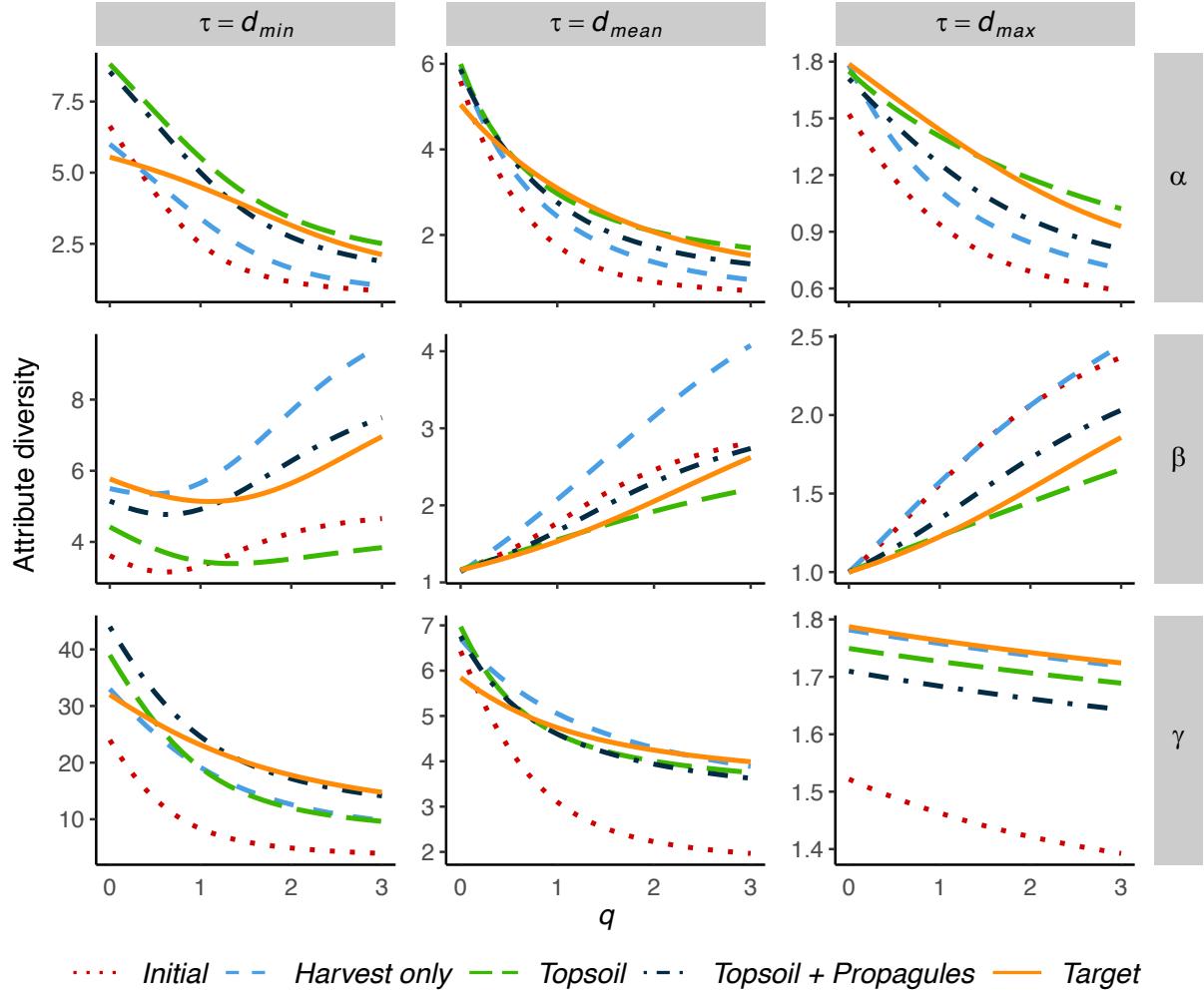
**Table S9.** Overview of all study species of the three study groups (Auchenorrhyncha, Heteroptera, Orthoptera) and the clusters they were assigned to in RLQ analyses (also indicated by the colors). The column “Morphometric” denotes the cluster from RLQ analysis on morphometric traits, the column “Life history” denotes the cluster from RLQ analysis on life-history traits.

Group	Suborder	Species	Morphometric	Life history
Auchenorrhyncha	Cicadomorpha	<i>Anaceratagallia ribauti</i>	1	2
Auchenorrhyncha	Cicadomorpha	<i>Anaceratagallia venosa</i>	1	2
Auchenorrhyncha	Cicadomorpha	<i>Anoscopus albifrons</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Anoscopus serratulae</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Aphrodes bicinctus</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Aphrophora alni</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Aphrophora major</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Arboridia ribauti</i>	3	3
Auchenorrhyncha	Cicadomorpha	<i>Arthaldeus pascuellus</i>	3	1
Auchenorrhyncha	Cicadomorpha	<i>Athysanus argentarius</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Athysanus quadrum</i>	1	2
Auchenorrhyncha	Cicadomorpha	<i>Batracomorphus allionii</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Cicadella viridis</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Cicadula spec.</i>	3	2
Auchenorrhyncha	Cicadomorpha	<i>Conosanus obsoletus</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Deltoccephalus pulicaris</i>	3	2
Auchenorrhyncha	Cicadomorpha	<i>Dikraneura spec.</i>	2	3
Auchenorrhyncha	Cicadomorpha	<i>Diplocolenus bohemani</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Doliotettix lunulatus</i>	1	2
Auchenorrhyncha	Cicadomorpha	<i>Emelyanoviana mollicula</i>	3	3
Auchenorrhyncha	Cicadomorpha	<i>Eupteryx notata</i>	3	3
Auchenorrhyncha	Cicadomorpha	<i>Euscelis incisus</i>	1	1
Auchenorrhyncha	Cicadomorpha	<i>Evacanthus interruptus</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Lepyronia coleoptrata</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Macropsis spec.</i>	1	2
Auchenorrhyncha	Cicadomorpha	<i>Macrosteles laevis</i>	1	1
Auchenorrhyncha	Cicadomorpha	<i>Megophthalmus scanicus</i>	1	2
Auchenorrhyncha	Cicadomorpha	<i>Neophilaenus lineatus</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Philaenus spumarius</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Psammotettix alienus</i>	1	1
Auchenorrhyncha	Cicadomorpha	<i>Psammotettix confinis</i>	2	1
Auchenorrhyncha	Cicadomorpha	<i>Psammotettix helvolus</i>	2	1
Auchenorrhyncha	Cicadomorpha	<i>Recilia coronifer</i>	3	2
Auchenorrhyncha	Cicadomorpha	<i>Sorhoanus assimilis</i>	2	2
Auchenorrhyncha	Cicadomorpha	<i>Stroggylocephalus agrestis</i>	4	2
Auchenorrhyncha	Cicadomorpha	<i>Turrtus socialis</i>	2	1
Auchenorrhyncha	Cicadomorpha	<i>Zygindia scutellaris</i>	3	3
Auchenorrhyncha	Fulgoromorpha	<i>Acanthodelphax spinosus</i>	3	1
Auchenorrhyncha	Fulgoromorpha	<i>Conomelus anceps</i>	3	2
Auchenorrhyncha	Fulgoromorpha	<i>Dicranotropis hamata</i>	1	1
Auchenorrhyncha	Fulgoromorpha	<i>Ditropis flavipes</i>	3	1
Auchenorrhyncha	Fulgoromorpha	<i>Javesella dubia</i>	3	1
Auchenorrhyncha	Fulgoromorpha	<i>Javesella obscurella</i>	1	1

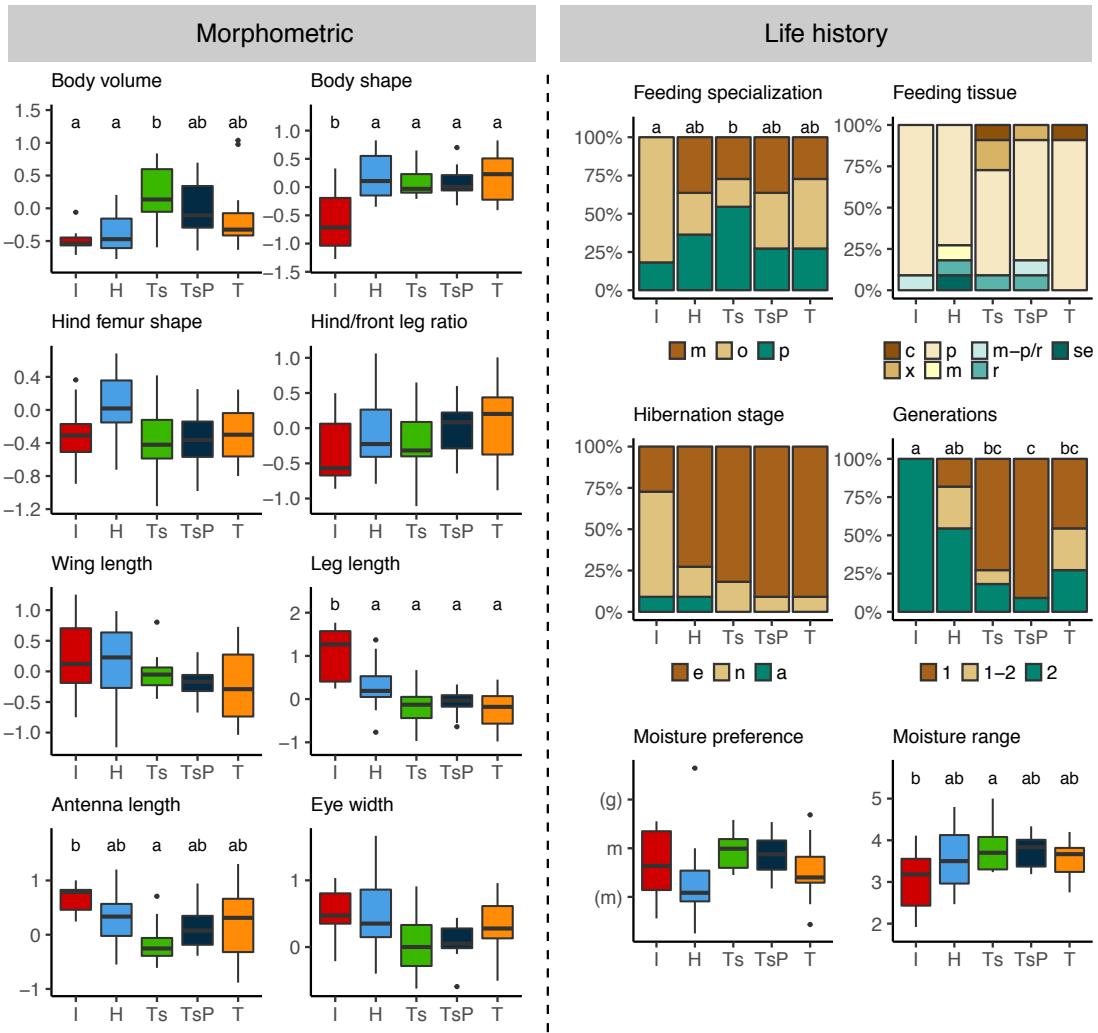
Auchenorrhyncha	Fulgoromorpha	<i>Kelisia ribauti</i>	3	2
Auchenorrhyncha	Fulgoromorpha	<i>Kelisia sima</i>	3	2
Auchenorrhyncha	Fulgoromorpha	<i>Kosswigianella exigua</i>	3	1
Auchenorrhyncha	Fulgoromorpha	<i>Laodelphax striatellus</i>	1	1
Auchenorrhyncha	Fulgoromorpha	<i>Megamelodes quadrimaculatus</i>	3	2
Auchenorrhyncha	Fulgoromorpha	<i>Megamelus notulus</i>	3	2
Auchenorrhyncha	Fulgoromorpha	<i>Muellerianella brevipennis</i>	3	2
Auchenorrhyncha	Fulgoromorpha	<i>Muellerianella extrusa</i>	3	2
Auchenorrhyncha	Fulgoromorpha	<i>Paradelphacodes paludosus</i>	3	1
Auchenorrhyncha	Fulgoromorpha	<i>Ribautodelphax collinus</i>	1	1
Auchenorrhyncha	Fulgoromorpha	<i>Ribautodelphax imitans</i>	1	1
Auchenorrhyncha	Fulgoromorpha	<i>Stenocranus fuscovittatus</i>	1	2
Auchenorrhyncha	Fulgoromorpha	<i>Stiroma bicarinata</i>	1	2
Auchenorrhyncha	Fulgoromorpha	<i>Xanthodelphax spec.</i>	3	1
Heteroptera	Heteroptera	<i>Acalypta marginata</i>	3	1
Heteroptera	Heteroptera	<i>Adelphocoris lineolatus</i>	3	2
Heteroptera	Heteroptera	<i>Adelphocoris seticornis</i>	1	2
Heteroptera	Heteroptera	<i>Carpocoris purpureipennis</i>	4	2
Heteroptera	Heteroptera	<i>Catoplatus fabricii</i>	2	2
Heteroptera	Heteroptera	<i>Compsidolon salicellum</i>	3	2
Heteroptera	Heteroptera	<i>Cymus glandicolor</i>	2	2
Heteroptera	Heteroptera	<i>Dolycoris baccarum</i>	4	2
Heteroptera	Heteroptera	<i>Eurygaster maura</i>	4	1
Heteroptera	Heteroptera	<i>Globiceps fulvicollis</i>	3	2
Heteroptera	Heteroptera	<i>Halticus apterus</i>	3	2
Heteroptera	Heteroptera	<i>Lygus pratensis</i>	1	1
Heteroptera	Heteroptera	<i>Lygus punctatus</i>	1	2
Heteroptera	Heteroptera	<i>Lygus rugulipennis</i>	1	1
Heteroptera	Heteroptera	<i>Notostira elongata</i>	3	1
Heteroptera	Heteroptera	<i>Peritrechus geniculatus</i>	2	3
Heteroptera	Heteroptera	<i>Polymerus microphthalmus</i>	1	2
Heteroptera	Heteroptera	<i>Stenodema calcarata</i>	1	1
Heteroptera	Heteroptera	<i>Stenodema laevigata</i>	2	2
Heteroptera	Heteroptera	<i>Stenotus binotatus</i>	3	2
Heteroptera	Heteroptera	<i>Tingis reticulata</i>	2	3
Heteroptera	Heteroptera	<i>Trigonotylus caelestialium</i>	3	1
Orthoptera	Caelifera	<i>Chorthippus montanus</i>	3	2
Orthoptera	Caelifera	<i>Chorthippus parallelus</i>	2	2
Orthoptera	Caelifera	<i>Parapleurus alliaceus</i>	2	2
Orthoptera	Ensifera	<i>Conocephalus fuscus</i>	3	2
Orthoptera	Ensifera	<i>Metrioptera roeselii</i>	1	2
Orthoptera	Ensifera	<i>Pholidoptera griseoaptera</i>	1	2
Orthoptera	Ensifera	<i>Tettigonia viridissima</i>	1	2



**Fig. S14.** Diversity profiles of attribute diversity for different threshold distinctiveness levels ( $\tau$ ) and different diversity levels ( $\alpha$ - $\beta$ - and  $\gamma$ -diversity) on the basis of morphometric traits for each of the five treatments (indicated by different line colors). Each plot shows the attribute diversity along increasing levels of order  $q$ , reflecting increasing weighting of common species ( $q = 0$  corresponds to richness). The threshold distinctiveness level  $\tau$  varies between  $d_{min}$  (attribute diversity corresponds to taxonomic diversity, except species pairs with exactly the same traits, which are counted as one species),  $d_{mean}$  (dissimilarity values greater than the mean pairwise dissimilarity value  $d_{mean}$  are truncated), and  $d_{max}$  (pairwise functional dissimilarities are not truncated and thus considered along the whole range of functional dissimilarity values).



**Fig. S15.** Diversity profiles of attribute diversity for different threshold distinctiveness levels ( $\tau$ ) and different diversity levels ( $\alpha$ - $\beta$ - and  $\gamma$ -diversity) on the basis of life-history traits for each of the five treatments (indicated by different line colors). Each plot shows the attribute diversity along increasing levels of order  $q$ , reflecting increasing weighting of common species ( $q = 0$  corresponds to richness). The threshold distinctiveness level  $\tau$  varies between  $d_{min}$  (attribute diversity corresponds to taxonomic diversity, except species pairs with exactly the same traits, which are counted as one species),  $d_{mean}$  (dissimilarity values greater than the mean pairwise dissimilarity value  $d_{mean}$  are truncated), and  $d_{max}$  (pairwise functional dissimilarities are not truncated and thus considered along the whole range of functional dissimilarity values).



**Fig. S16.** Community weighted means (CWMs) of all morphometric and life-history traits and their distribution among the five treatments (I: *Initial*; H: *Harvest only*; Ts: *Topsoil*; TsP: *Topsoil + Propagules*; T: *Target*). For traits measured on a continuous scale, boxplots show the distribution of traits. The y-axis for moisture preference denotes the underlying moisture preference classification (m: mesohygrophilous; g: hygrophilous; brackets denote transition states). For discrete traits, the graphs show the distribution of trait values within each treatment. Feeding specialization (m: monophagous; o: oligophagous; p: polyphagous), feeding tissue (c: chewers, x: xylem, p: phloem, m: mesophyll, m-p/r: mesophyll as well as phloem and/or reproductive organs; r: reproductive organs; se: ripe seeds), hibernation stage (e: egg; e/n: egg and nymph; n: nymph; a: adult) and number of generations per year are shown. Significant differences in community weighted means between treatments are indicated with letters (Anova with Tukey-HSD for continuous trait values, pairwise Chi-squared tests for discrete trait values).

## Results for Auchenorrhyncha only

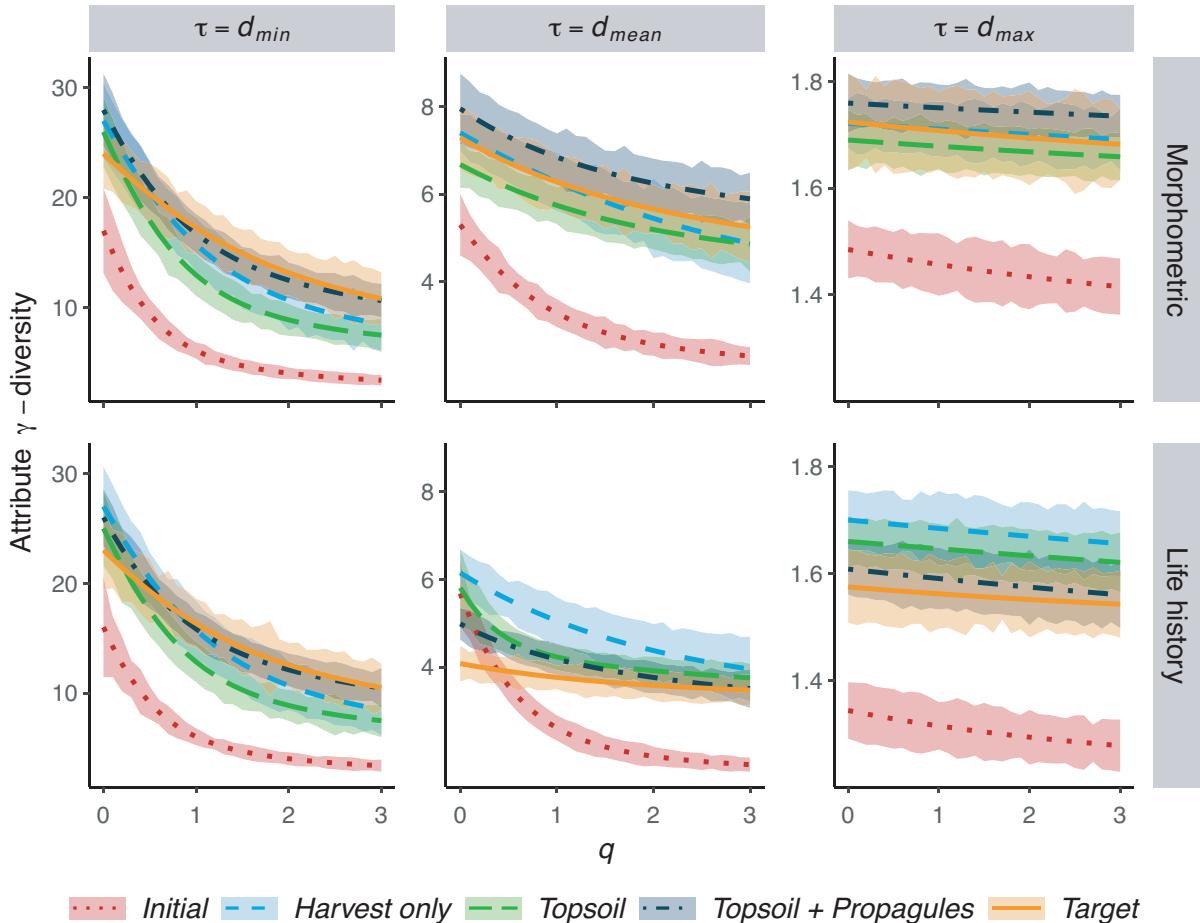
**Table S10.** Results from pairwise permutational multivariate analysis of variance (PerMANOVA) between all treatment pairs for taxonomic dissimilarities between plots as well as functional dissimilarities between plots based on morphometric traits and life-history traits for Auchenorrhyncha only. Adjusted P values from Bonferroni corrections. Bold numbers indicate significant P values ( $P < 0.05$ ). I = Initial; H = Harvest only; Ts = Topsoil; TsP = Topsoil + Propagules; T = Target.

	Pairs	F <sub>Model</sub>	R <sup>2</sup>	P value	adj. P value
taxonomy	I vs. H	2.64	0.12	<b>0.001</b>	<b>0.01</b>
	I vs. Ts	5.08	0.20	<b>0.001</b>	<b>0.01</b>
	I vs. TsP	3.87	0.16	<b>0.001</b>	<b>0.01</b>
	I vs. T	4.09	0.17	<b>0.001</b>	<b>0.01</b>
	H vs. Ts	2.82	0.12	<b>0.001</b>	<b>0.01</b>
	H vs. TsP	1.72	0.08	<b>0.010</b>	0.10
	H vs. T	1.79	0.08	<b>0.014</b>	0.14
	Ts vs. TsP	0.66	0.03	0.832	1.00
	Ts vs. T	2.31	0.10	<b>0.004</b>	<b>0.04</b>
	TsP vs. T	1.29	0.06	0.174	1.00
morphometric	I vs. H	3.10	0.13	<b>0.002</b>	<b>0.02</b>
	I vs. Ts	6.87	0.26	<b>0.001</b>	<b>0.01</b>
	I vs. TsP	4.76	0.19	<b>0.001</b>	<b>0.01</b>
	I vs. T	5.04	0.20	<b>0.001</b>	<b>0.01</b>
	H vs. Ts	2.86	0.13	<b>0.001</b>	<b>0.01</b>
	H vs. TsP	1.62	0.07	<b>0.042</b>	0.42
	H vs. T	1.78	0.08	<b>0.040</b>	0.40
	Ts vs. TsP	0.68	0.03	0.723	1.00
	Ts vs. T	1.69	0.08	0.091	0.91
	TsP vs. T	0.82	0.04	0.665	1.00
life history	I vs. H	3.45	0.15	<b>0.001</b>	<b>0.01</b>
	I vs. Ts	7.30	0.27	<b>0.001</b>	<b>0.01</b>
	I vs. TsP	7.04	0.26	<b>0.001</b>	<b>0.01</b>
	I vs. T	4.87	0.20	<b>0.001</b>	<b>0.01</b>
	H vs. Ts	2.66	0.12	<b>0.010</b>	0.10
	H vs. TsP	1.92	0.09	<b>0.027</b>	0.27
	H vs. T	1.62	0.07	0.099	0.99
	Ts vs. TsP	0.66	0.03	0.710	1.00
	Ts vs. T	1.40	0.07	0.203	1.00
	TsP vs. T	1.11	0.05	0.328	1.00

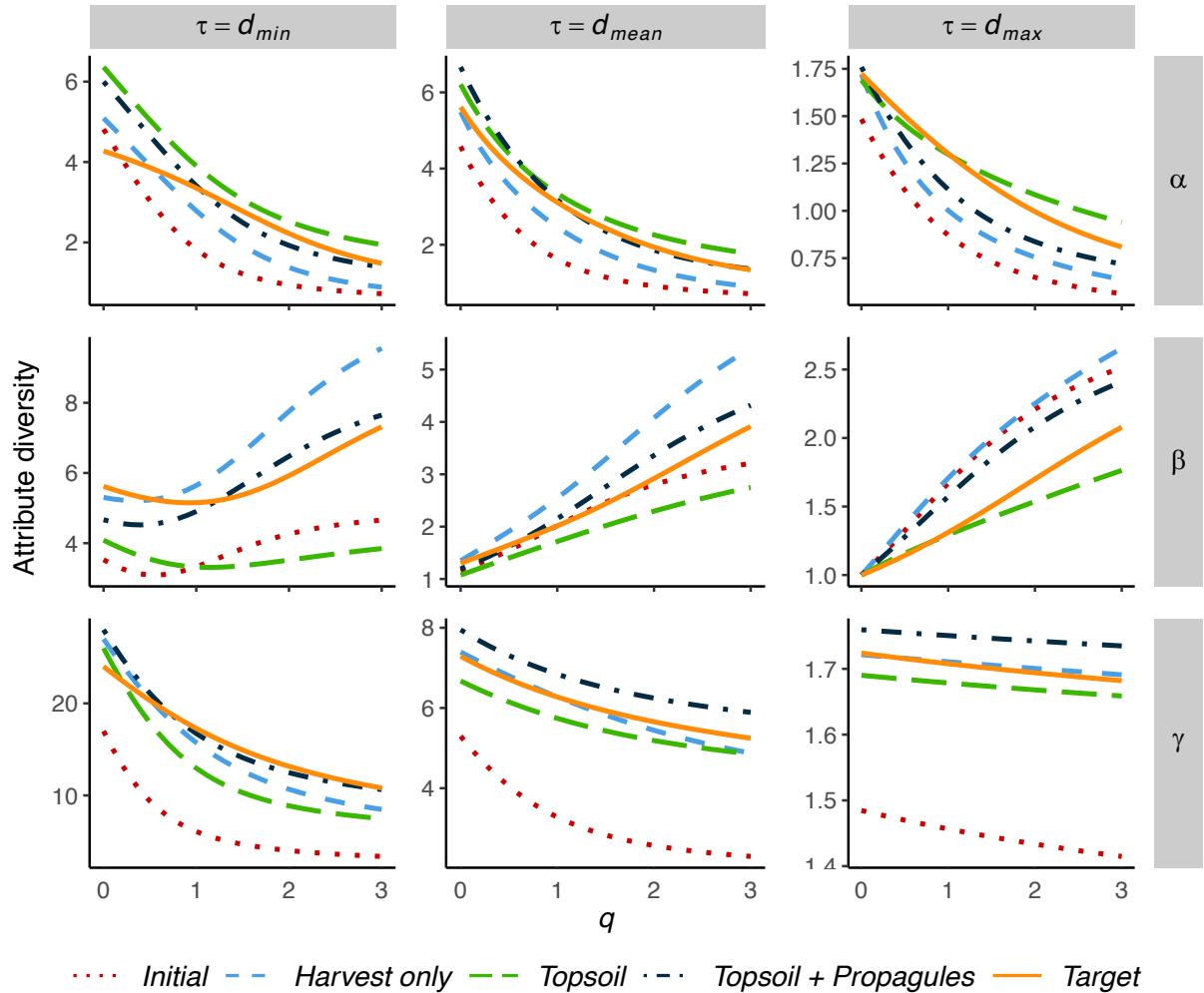
**Table S11.** Overview of all Auchenorrhyncha study species and the clusters they were assigned to in RLQ analyses for Auchenorrhyncha only (also indicated by the colors). The column “Morphometric” denotes the cluster from RLQ analysis on morphometric traits, the column “Life history” denotes the cluster from RLQ analysis on life-history traits.

Suborder	Species	Morphometric	Life history
Cicadomorpha	<i>Anaceratagallia ribauti</i>	1	1
Cicadomorpha	<i>Anaceratagallia venosa</i>	1	2
Cicadomorpha	<i>Anoscopus albifrons</i>	2	2
Cicadomorpha	<i>Anoscopus serratulae</i>	2	2
Cicadomorpha	<i>Aphrodes bicinctus</i>	2	2
Cicadomorpha	<i>Aphrophora alni</i>	3	2
Cicadomorpha	<i>Aphrophora major</i>	3	2
Cicadomorpha	<i>Arboridia ribauti</i>	2	3
Cicadomorpha	<i>Arthaldeus pascuellus</i>	1	1
Cicadomorpha	<i>Athysanus argentarius</i>	3	2
Cicadomorpha	<i>Athysanus quadrum</i>	1	2
Cicadomorpha	<i>Batracomorphus allionii</i>	3	2
Cicadomorpha	<i>Cicadella viridis</i>	2	2
Cicadomorpha	<i>Cicadula spec.</i>	1	2
Cicadomorpha	<i>Conosanus obsoletus</i>	2	2
Cicadomorpha	<i>Deltoccephalus pulicaris</i>	2	2
Cicadomorpha	<i>Dikraneura spec.</i>	2	3
Cicadomorpha	<i>Diplocolenus bohemani</i>	2	2
Cicadomorpha	<i>Doliotettix lunulatus</i>	1	2
Cicadomorpha	<i>Emelyanoviana mollicula</i>	1	3
Cicadomorpha	<i>Eupteryx notata</i>	1	3
Cicadomorpha	<i>Euscelis incisus</i>	1	1
Cicadomorpha	<i>Evacanthus interruptus</i>	2	2
Cicadomorpha	<i>Lepyronia coleoptrata</i>	3	2
Cicadomorpha	<i>Macropsis spec.</i>	1	2
Cicadomorpha	<i>Macrosteles laevis</i>	1	1
Cicadomorpha	<i>Megophthalmus scanicus</i>	1	2
Cicadomorpha	<i>Neophilaenus lineatus</i>	3	2
Cicadomorpha	<i>Philaenus spumarius</i>	1	2
Cicadomorpha	<i>Psammotettix alienus</i>	2	2
Cicadomorpha	<i>Psammotettix confinis</i>	2	2
Cicadomorpha	<i>Psammotettix helvolus</i>	2	2
Cicadomorpha	<i>Recilia coronifer</i>	2	2
Cicadomorpha	<i>Sorhoanus assimilis</i>	2	2

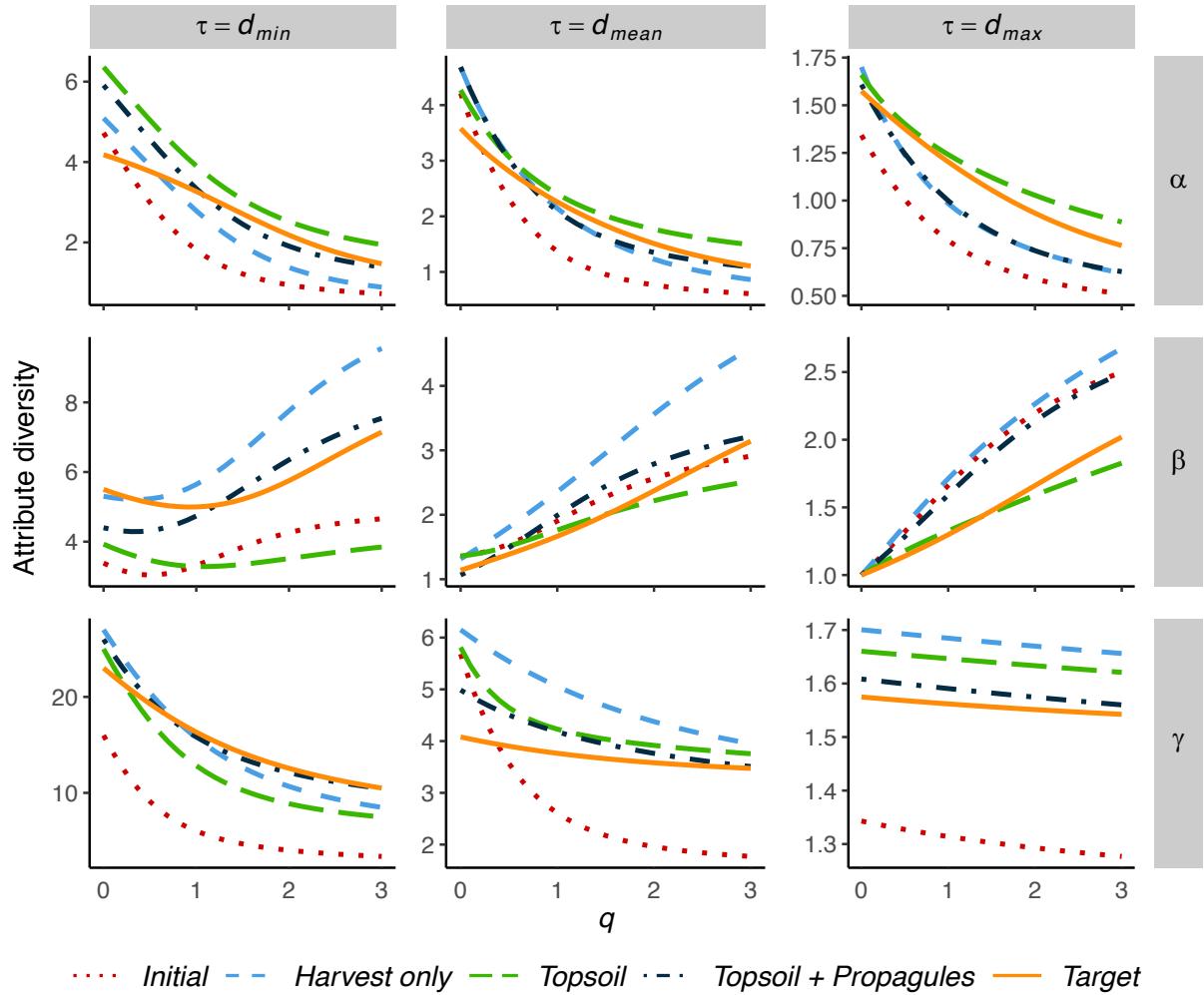
Cicadomorpha	<i>Stroggylocephalus agrestis</i>	3	2
Cicadomorpha	<i>Turrutus socialis</i>	2	2
Cicadomorpha	<i>Zyginidia scutellaris</i>	1	3
Fulgoromorpha	<i>Acanthodelphax spinosus</i>	1	1
Fulgoromorpha	<i>Conomelus anceps</i>	1	2
Fulgoromorpha	<i>Dicranotropis hamata</i>	1	1
Fulgoromorpha	<i>Ditropsis flavipes</i>	1	1
Fulgoromorpha	<i>Javesella dubia</i>	1	1
Fulgoromorpha	<i>Javesella obscurella</i>	1	1
Fulgoromorpha	<i>Kelisia ribauti</i>	1	2
Fulgoromorpha	<i>Kelisia sima</i>	1	2
Fulgoromorpha	<i>Kosswigianella exigua</i>	1	1
Fulgoromorpha	<i>Laodelphax striatellus</i>	1	1
Fulgoromorpha	<i>Megamelodes quadrimaculatus</i>	1	1
Fulgoromorpha	<i>Megamelus notulus</i>	1	2
Fulgoromorpha	<i>Muellerianella brevipennis</i>	1	2
Fulgoromorpha	<i>Muellerianella extrusa</i>	1	2
Fulgoromorpha	<i>Paradelphacodes paludosus</i>	1	1
Fulgoromorpha	<i>Ribautodelphax collinus</i>	1	1
Fulgoromorpha	<i>Ribautodelphax imitans</i>	1	1
Fulgoromorpha	<i>Stenocranus fuscovittatus</i>	1	1
Fulgoromorpha	<i>Stiroma bicarinata</i>	1	2
Fulgoromorpha	<i>Xanthodelphax spec.</i>	1	2



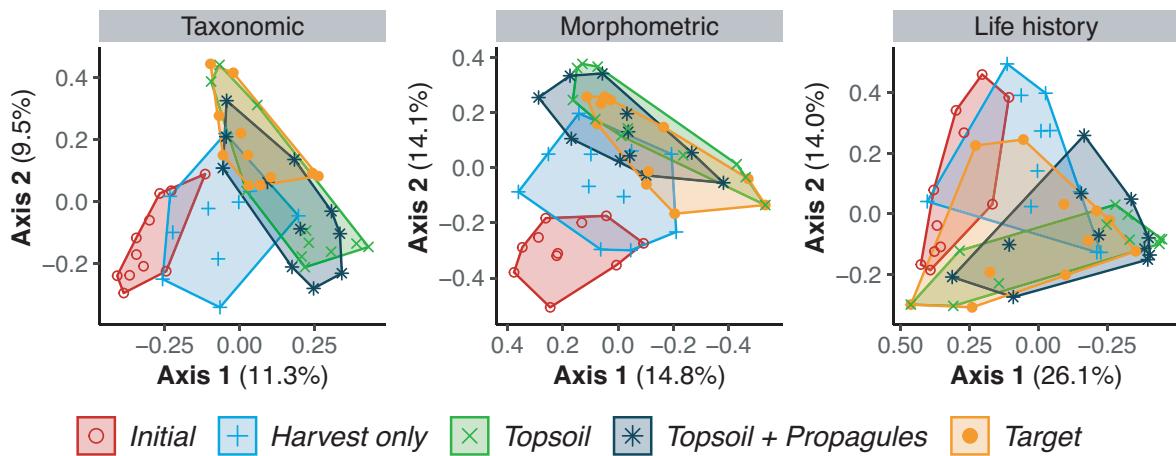
**Fig. S17.** Diversity profiles of attribute  $\gamma$ -diversity for different threshold distinctiveness levels ( $\tau$ ) and different trait data sets (morphometric, life-history) for each of the five treatments (indicated by different line colors) for Auchenorrhyncha only. Each plot shows the attribute diversity along increasing levels of order  $q$ , reflecting increasing weighting of common species ( $q = 0$  corresponds to richness). The threshold distinctiveness level  $\tau$  varies between  $d_{min}$  (attribute diversity corresponds to taxonomic diversity, except species pairs with exactly the same traits, which are counted as one species),  $d_{mean}$  (dissimilarity values greater than the mean pairwise dissimilarity value  $d_{mean}$  are truncated), and  $d_{max}$  (pairwise functional dissimilarities are not truncated and thus considered along the whole range of functional dissimilarity values). The uncertainty is calculated based on 50 bootstraps.



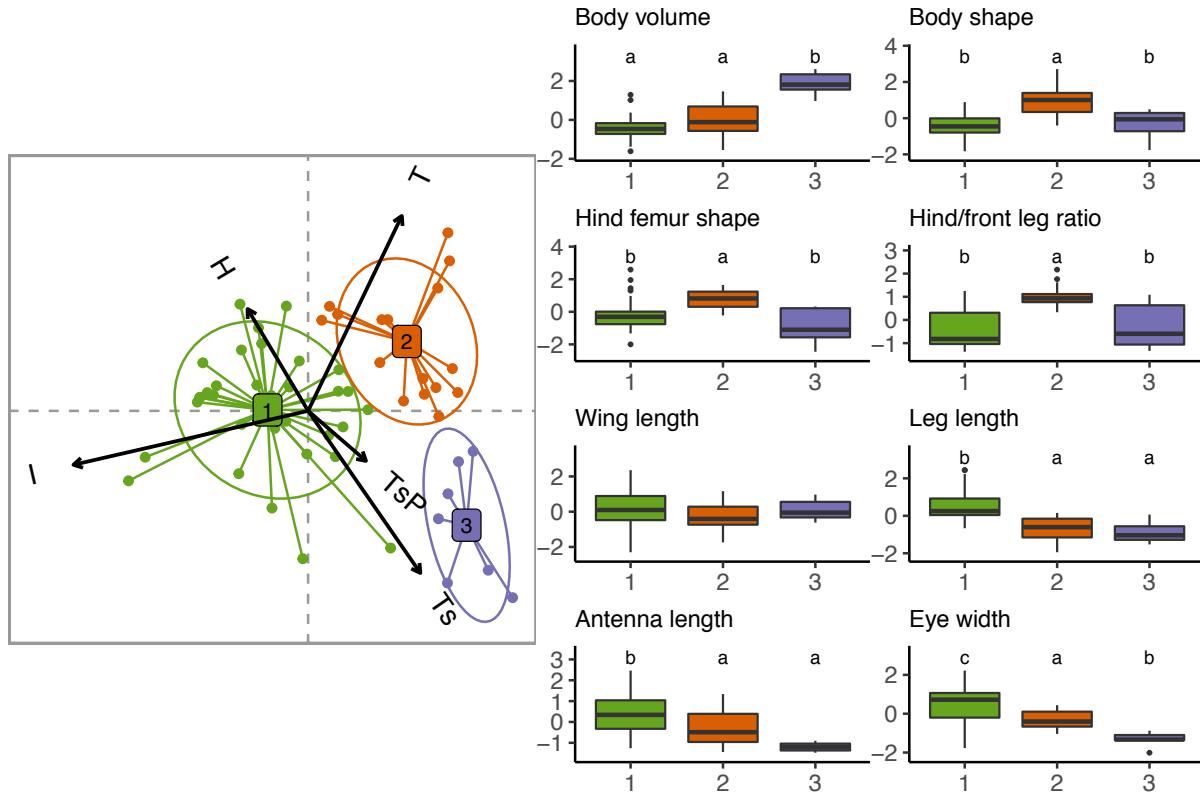
**Fig. S18.** Diversity profiles of attribute diversity for different threshold distinctiveness levels ( $\tau$ ) and different diversity levels ( $\alpha$ -,  $\beta$ - and  $\gamma$ -diversity) on the basis of morphometric traits for each of the five treatments (indicated by different line colors) for Auchenorrhyncha only. Each plot shows the attribute diversity along increasing levels of order  $q$ , reflecting increasing weighting of common species ( $q = 0$  corresponds to richness). The threshold distinctiveness level  $\tau$  varies between  $d_{min}$  (attribute diversity corresponds to taxonomic diversity, except species pairs with exactly the same traits, which are counted as one species),  $d_{mean}$  (dissimilarity values greater than the mean pairwise dissimilarity value  $d_{mean}$  are truncated), and  $d_{max}$  (pairwise functional dissimilarities are not truncated and thus considered along the whole range of functional dissimilarity values).



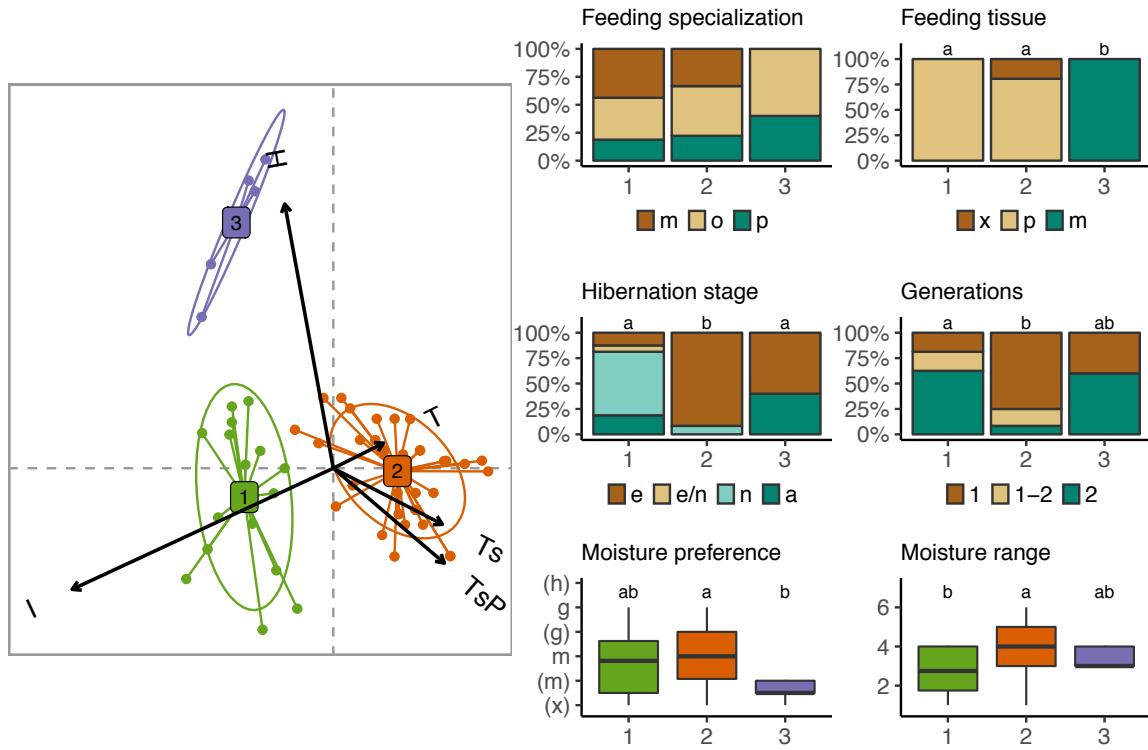
**Fig. S19.** Diversity profiles of attribute diversity for different threshold distinctiveness levels ( $\tau$ ) and different diversity levels ( $\alpha$ -,  $\beta$ - and  $\gamma$ -diversity) on the basis of life-history traits for each of the five treatments (indicated by different line colors) for Auchenorrhyncha only. Each plot shows the attribute diversity along increasing levels of order  $q$ , reflecting increasing weighting of common species ( $q = 0$  corresponds to richness). The threshold distinctiveness level  $\tau$  varies between  $d_{min}$  (attribute diversity corresponds to taxonomic diversity, except species pairs with exactly the same traits, which are counted as one species),  $d_{mean}$  (dissimilarity values greater than the mean pairwise dissimilarity value  $d_{mean}$  are truncated), and  $d_{max}$  (pairwise functional dissimilarities are not truncated and thus considered along the whole range of functional dissimilarity values).



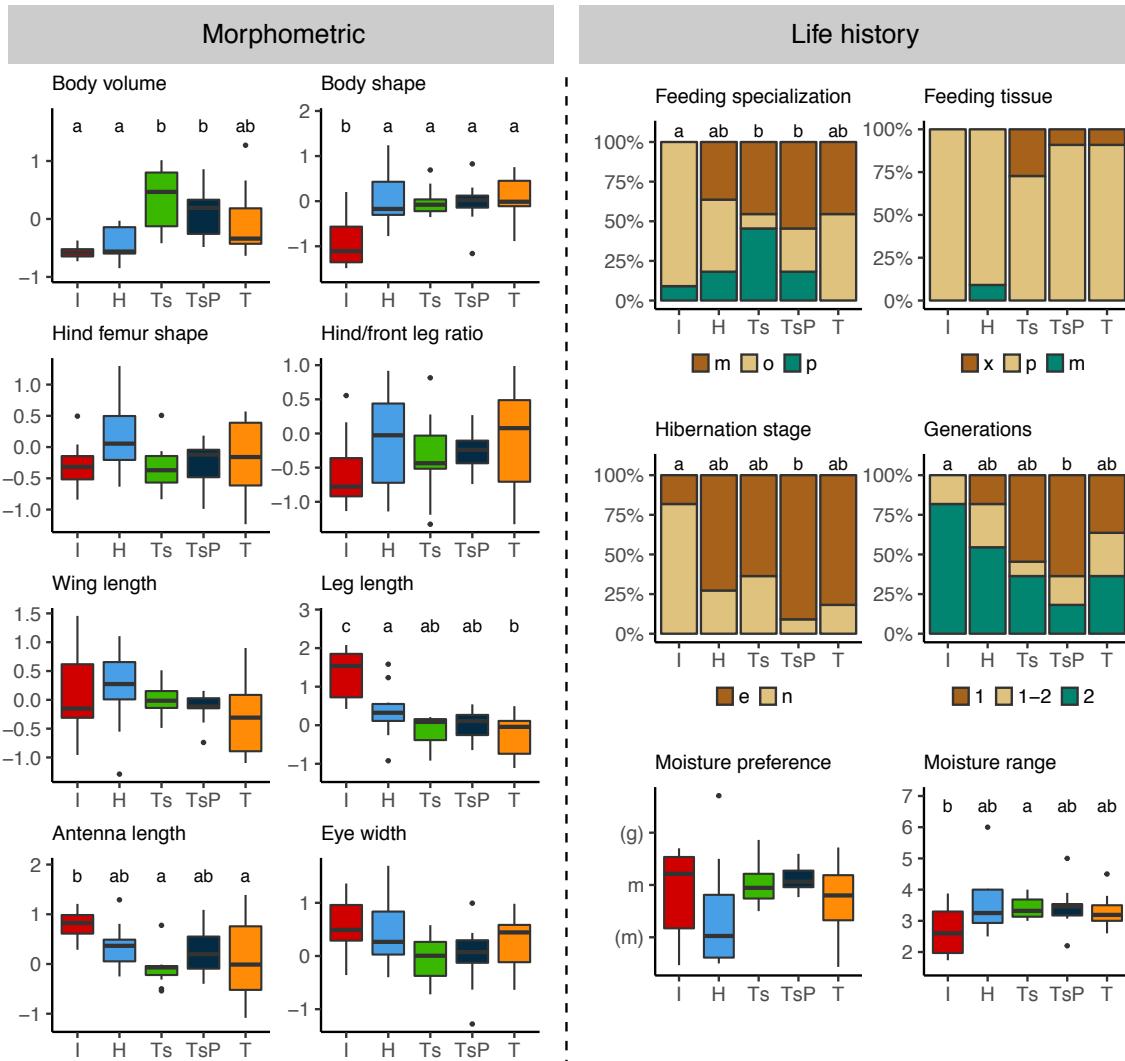
**Fig. S20.** Biplots of the first two axes from principal coordinate analyses (PCoA) for different sets of pairwise dissimilarities between Auchenorrhyncha-only communities. Each point represents a community, colors and shapes denote the five treatments. The enclosing shapes are convex hulls. Taxonomic dissimilarities are Bray-Curtis distances calculated from species abundances, whereas functional dissimilarities for morphometric and life-history traits were calculated based on the trait probability density (TPD) framework.



**Fig. S21.** RLQ analysis for morphometric traits for Auchenorrhyncha only. Graph on the left: Ordination biplot with each point representing a species. The colors refer to the four clusters, which were derived from hierarchical cluster analysis. The cluster ellipses were calculated based on a multivariate normal distribution with a confidence level of 0.66. Arrows were rescaled for illustration purposes, and show both strength and direction of treatment effects (I: *Initial*; H: *Harvest only*; Ts: *Topsoil*; TsP: *Topsoil + Propagules*; T: *Target*). Boxplots on the right: Scaled trait values for the four clusters for all eight morphometric traits. Significant differences (Anova, Tukey-HSD) in trait values between clusters are indicated with letters.



**Fig. S22.** RLQ analysis for life-history traits for Auchenorrhyncha only. Graph on the left: Ordination biplot with each point representing a species. The colors refer to the three clusters, which were derived from hierarchical cluster analysis. The cluster ellipses were calculated based on a multivariate normal distribution with a confidence level of 0.66. Arrows were rescaled for illustration purposes and show both strength and direction of treatment effects (I: *Initial*; H: *Harvest only*; Ts: *Topsoil*; TsP: *Topsoil + Propagules*; T: *Target*). Graphs on the right: For continuous traits (moisture preference, moisture range) the boxplots show the scaled trait values for the three clusters. The y-axis for moisture preference denotes the underlying moisture preference classification (x: xerophilous; m: mesohygrophilous; g: hygrophilous; brackets denote transition states). Moisture range indicates the specialization for a certain habitat moisture, with high values indicating moisture generalists. For discrete traits, the graphs show the distribution of trait values within each cluster. Feeding tissue (c: chewers, x: xylem, p: phloem, m: mesophyll, m-p/r: mesophyll as well as phloem and/or reproductive organs; r: reproductive organs; se: ripe seeds), feeding specialization (m: monophagous; o: oligophagous; p: polyphagous), hibernation stage (e: egg; e/n: egg and nymph; n: nymph; a: adult) and number of generations per year are shown. Significant differences in trait values between clusters are indicated with letters (Anova with Tukey-HSD for continuous trait values, pairwise Chi-squared tests for discrete trait values).



**Fig. S23.** Community weighted means (CWMs) of all morphometric and life-history traits and their distribution among the five treatments (I: *Initial*; H: *Harvest only*; Ts: *Topsoil*; TsP: *Topsoil + Propagules*; T: *Target*) for Auchenorrhyncha only. For traits measured on a continuous scale, boxplots show the distribution of traits. The y-axis for moisture preference denotes the underlying moisture preference classification (m: mesohygrophilous; g: hygrophilous; brackets denote transition states). For discrete traits, the graphs show the distribution of trait values within each treatment. Feeding specialization (m: monophagous; o: oligophagous; p: polyphagous), feeding tissue (x: xylem, p: phloem, m: mesophyll), hibernation stage (e: egg; n: nymph) and number of generations per year are shown. Significant differences in community weighted means between treatments are indicated with letters (Anova with Tukey-HSD for continuous trait values, pairwise Chi-squared tests for discrete trait values).

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