Appendix S1:
Diversity-stability relationships across organism groups and ecosystem types become decoupled across spatial scales

Ecology

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Section S1: Data sets used in this research

Below, we list all the data sets used to perform the analysis. We include the name of the dataset (matching Table 1 in the main text), the location of the publicly available data on Environmental Data Initiative (EDI) or Ecological Archives and its package ID or accession number, and the citations to the data, which include the DOI of the data package.

1. and-birds, EDI knb-lter-and.4781.2, Hadley (2017)
2. and-plants-mtStHelens, Ecological Archives E091-152, del Moral (2010)
3. bes-birds, EDI knb-lter-bes.543.170, Nilon and Brodsky (2017)
4. cap-birds, EDI knb-lter-cap.46.15, Bateman et al. (2017)
5. cap-herps, EDI knb-lter-cap.627.3, Bateman and Childers (2018)
6. cdr-grasshopper, EDI knb-lter-cdr.106.8, Knops (2018)
7. cdr-plantsABC, EDI knb-lter-cdr.14.8, Tilman (2018)
8. cdr-plantsD, EDI knb-lter-cdr.14.8, Tilman (2018)
9. fce-diatoms, EDI knb-lter-fce.1211.3, Gaiser (2021)
10. fce-fishDry, EDI knb-lter-fce.1164.7, Rehage (2017)
11. fce-fishWet, EDI knb-lter-fce.1164.7, Rehage (2017)
12. gce-mollusc, EDI, Pennings (2014); Alber (2014d,c,a); Bishop (2014i,h,e,f,d,c,a,b); Alber (2014b); Bishop (2014g)
13. hays-plants, Ecological Archives E088-161, Adler et al. (2007)
14. jrn-lizards, EDI knb-lter-jrn.2100007001.13, Lightfoot and Whitford (2022)
15. jrn-plants, EDI knb-lter-jrn.210351002.75, Chapline (2017)
16. knz-grasshopper, EDI knb-lter-knz.29.12, Joern (2018)

17. luq-snails, EDI knb-lter-luq.107.9996736, Willig (2010)

18. mcr-algae, EDI knb-lter-mcr.8.28, Carpenter (2015)

19. mcr-coral, EDI knb-lter-mcr.4.35, Edmunds (2018)

20. mcr-inverts, EDI knb-lter-mcr.7.33, Carpenter (2022)

21. sbc-algae, EDI knb-lter-sbc.50.7, Reed (2018)

22. sbc-fish, EDI knb-lter-sbc.50.7, Reed (2018)

23. sbc-mobileInverts, EDI knb-lter-sbc.50.7, Reed (2018)

24. sbc-sessileInverts, EDI knb-lter-sbc.50.7, Reed (2018)

25. sev-arthropods, EDI knb-lter-sev.29.175390, Lightfoot (2013)

26. sev-grasshopper, EDI knb-lter-sev.106.214968, Lightfoot (2010)

27. sev-plants, EDI knb-lter-sev.278.245672, Muldavin (2015)

28. sgs-plants1, EDI knb-lter-sgs.140.17, Stapp (2013)

29. sgs-plants2, EDI knb-lter-sgs.527.1, Milchunas (2014)

Section S2: Data overview

This document describes the data cleaning, subsetting, and aggregation methods specific to each dataset. We plot species accumulation curves, spatio-temporal variation in the number of taxa observed, the spatio-temporal sampling effort, and the number of taxa shared by each pairwise combination of plots within the study.

Section S3: Marine datasets

Section S3.1: SBC all taxa

We downloaded from the Environmental Data Initiative (EDI) annual taxon-specific estimates of the biomass density (g dry/m^2) of kelp forest macroalgae, sessile invertebrates, mobile invertebrates, and fishes in the Santa Barbara Channel (Reed, 2018). Briefly, between 2000-2004 and 2022, divers estimated the summer taxon-specific density or percentage cover of 225 taxa within 2–8 permanent transects (2 m wide x 40 m long) at each of 11 sites (44 total transects). Abundance and size were converted to dry biomass using taxon-specific relationships developed for the study region. Detailed methods are available in (Harrer et al., 2013; Reed et al., 2016; Reed, 2018). Data are shown in Figures S1, S2, S3, and S4.

Section S3.2: MCR all taxa

We downloaded from EDI annual taxon-specific estimates of the percentage cover of stony corals (Edmunds, 2018), benthic algae (Carpenter, 2015), and invertebrates (Carpenter, 2022). Briefly, between 2005 and 2021, divers surveyed corals using photoquadrats (0.5 m x 0.5 m) along a permanent 40-m transect in each of 4 habitats at 6 sites surrounding the island of Moorea (24 total transects): fringing reef, lagoon (backreef), shallow outer reef (10 m depth on forereef), and deep outer reef (17 m depth on forereef) (Edmunds, 2018). Benthic algae were estimated in a similar way, except that 0.5 m x 0.5 m photoquadrats were recorded at 5 permanent 10-m transects per site-habitat combination (Carpenter, 2015). Invertebrate herbivores and corallivores were counted in 1 m^2 quadrats along the same transects (Carpenter, 2022). Detailed methods are available in Edmunds (2018); Carpenter (2015, 2022).

Section S3.3: mcr-inverts

Data were downloaded from EDI (knb-lter-mcr.7.33). Non-relevant taxa and taxa observed outside the quadrat were removed from the dataset. Abundance was averaged across subplots, transects, and habitats for each species at each site in each year. Data are in Figure S5.

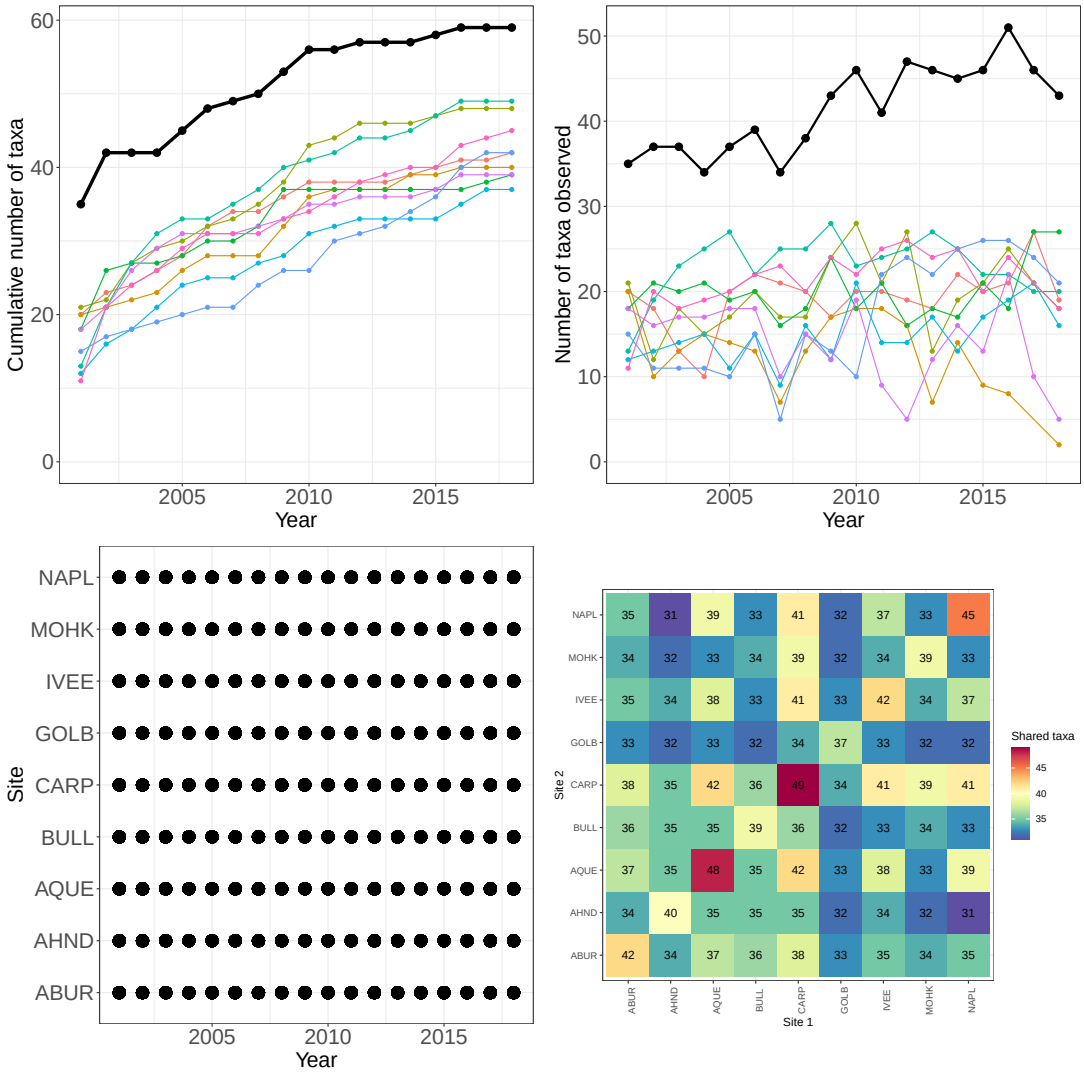

Figure S1: **SBC-algae:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for algae observed in the Santa Barbara Coastal LTER (2001-2016). The black lines represent total site-level values across all plots.

Section S3.4: mcr-coral

Data were downloaded from EDI (Edmunds, 2018). The corals are identified to the genus level. Non-relevant taxa were removed from the dataset. Abundance was averaged across subplots, transects, and habitats for each species at each site in each year. Data are in Figure S6.

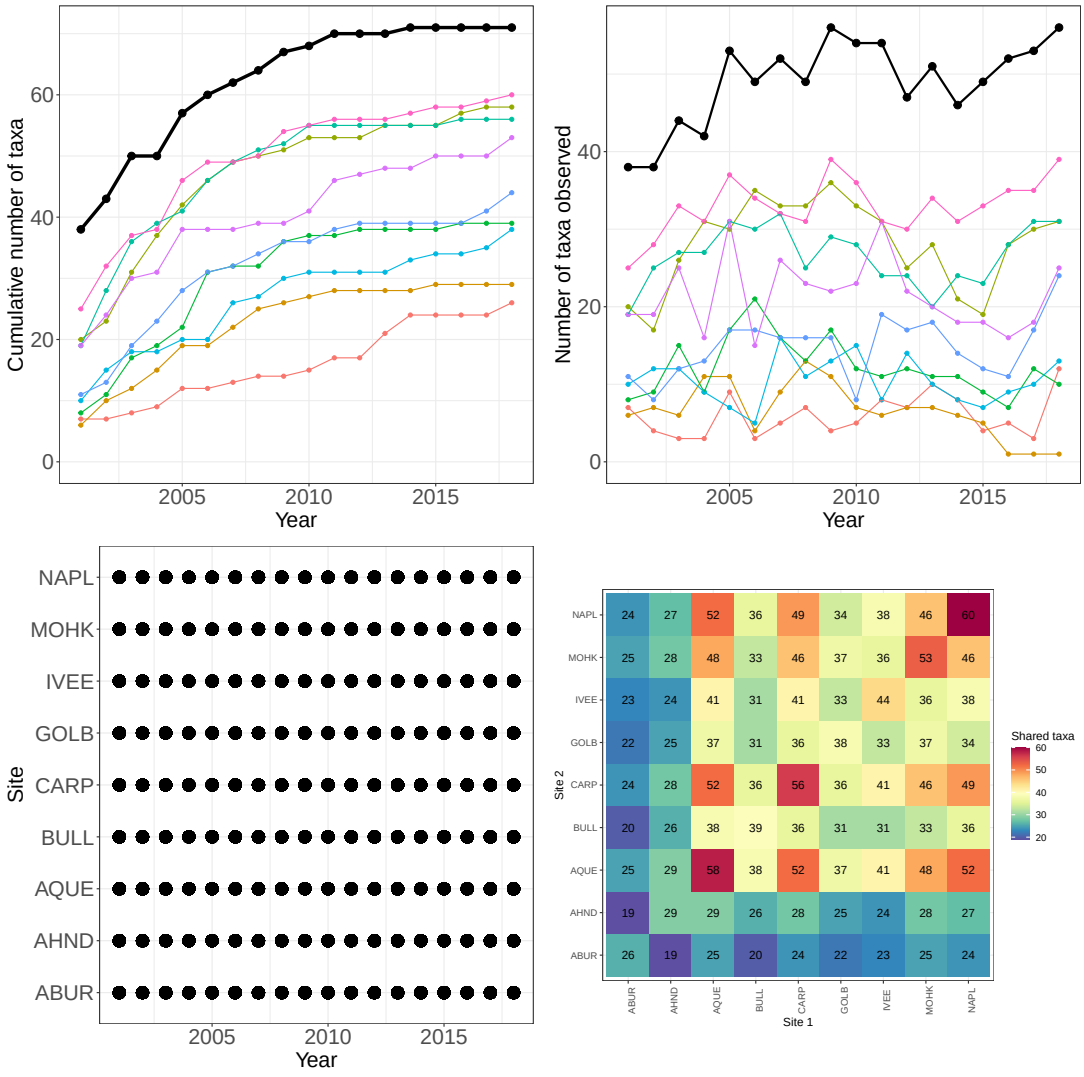

Figure S2: **SBC-sessile invertebrates:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and number of shared species (bottom right) for sessile invertebrate taxa observed in the Santa Barbara Coastal LTER (2001-2018). The black lines represent total site-level values across all plots.

Section S3.5: mcr-algae

Data were downloaded from EDI (Carpenter, 2015). Non-relevant taxa were removed from the dataset. Abundance was averaged across subplots, transects, and habitats for each species at each site in each year. Data are in Figure S7. The cumulative number of taxa was still increasing at the end of the time series.

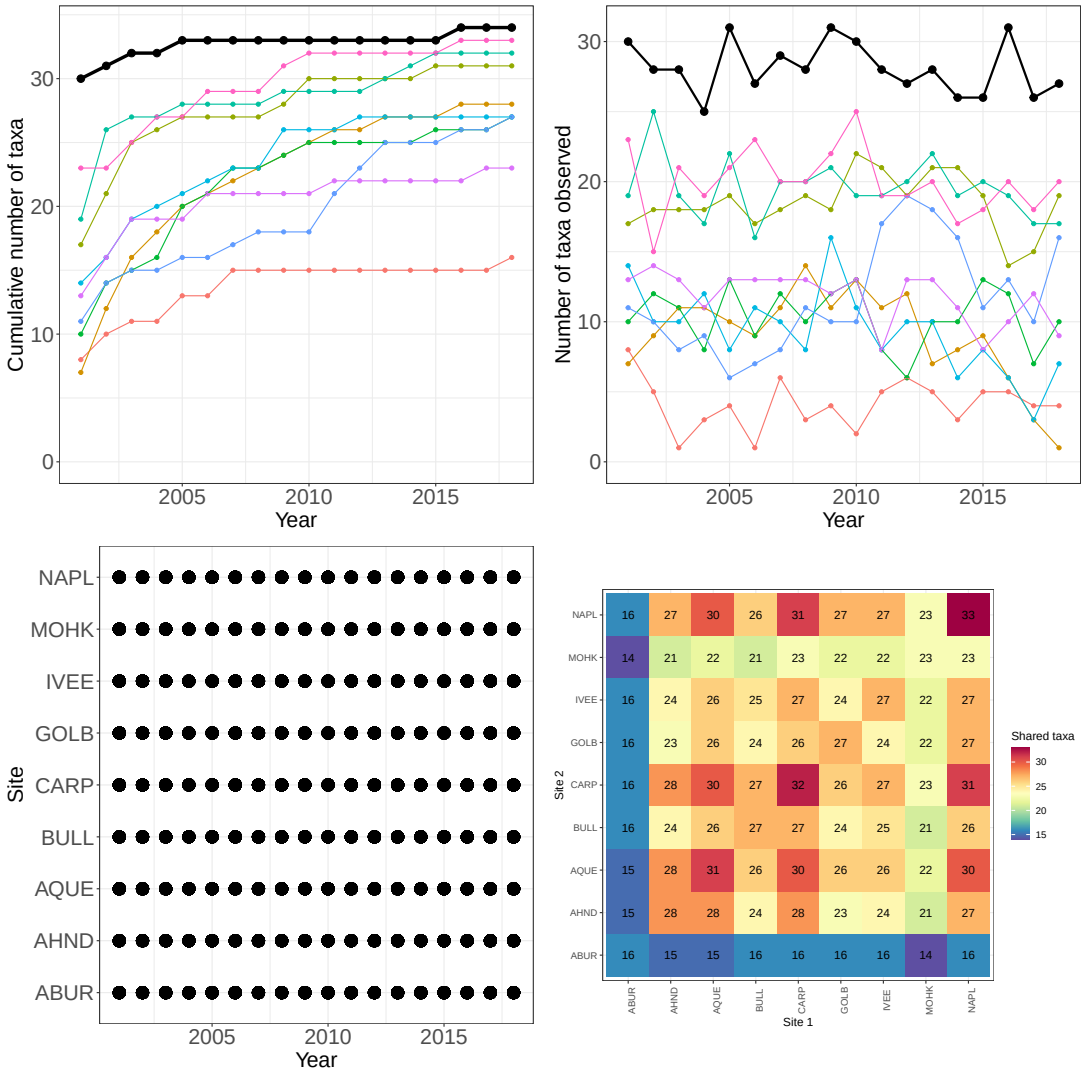

Figure S3: **SBC-mobile invertebrates:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for mobile invertebrate taxa observed at the Santa Barbara Coastal LTER (2001-2018). The black lines represent total site-level values across all plots.

Section S3.6: gce-mollusc

We downloaded 14 mollusc datasets (2000-2013) from EDI (Pennings, 2014; Alber, 2014a,b,c,d; Bishop, 2014i,h,e,f,d,c,a,b,g). We combined these datsets, and removed all missing or unclear data points; specifically, we removed all NAs, all data points categorized as "slug" or unidentified hybrid, and sites which were not sampled in every single year. Finally, we took averages of density data by plot. Data are in Figure S8.

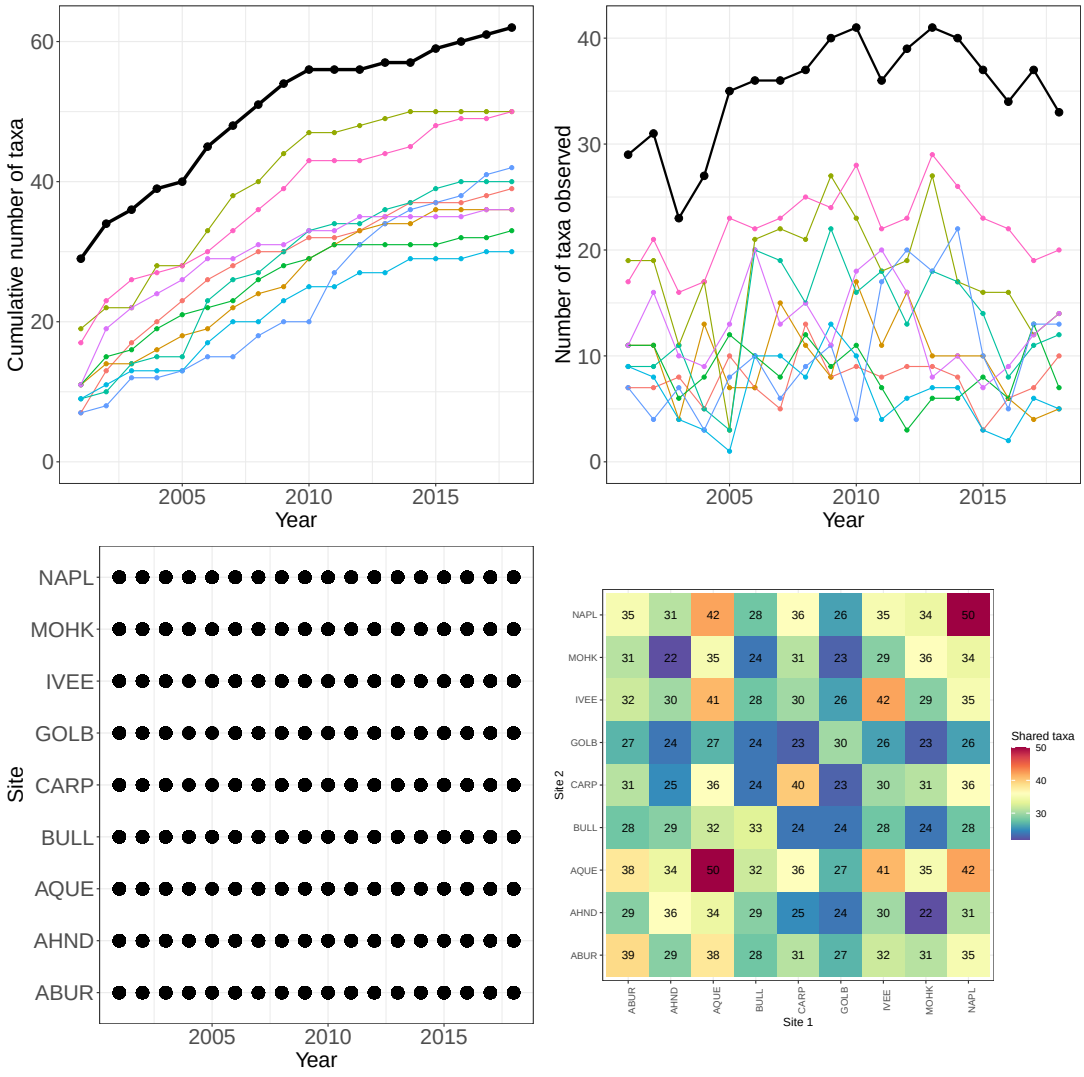

Figure S4: **SBC-fish:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) observed at the Santa Barbara Coastal LTER (2001-2018). The black lines represent total site-level values across all plots.

Section S4: Freshwater datasets

Section S4.1: fce-diatoms

Data were obtained from EDI. Metadata and citation can be found on EDI (Gaiser, 2021). Diatom abundance collected from 800m x 800m Principal Sampling Units (hereafter called 'sites') distributed across the Florida Everglades. Full data set included 367 diatom taxa and 171 sites; however, not all sites were sampled every year. We retained sites from Shark River Slough (SRS)

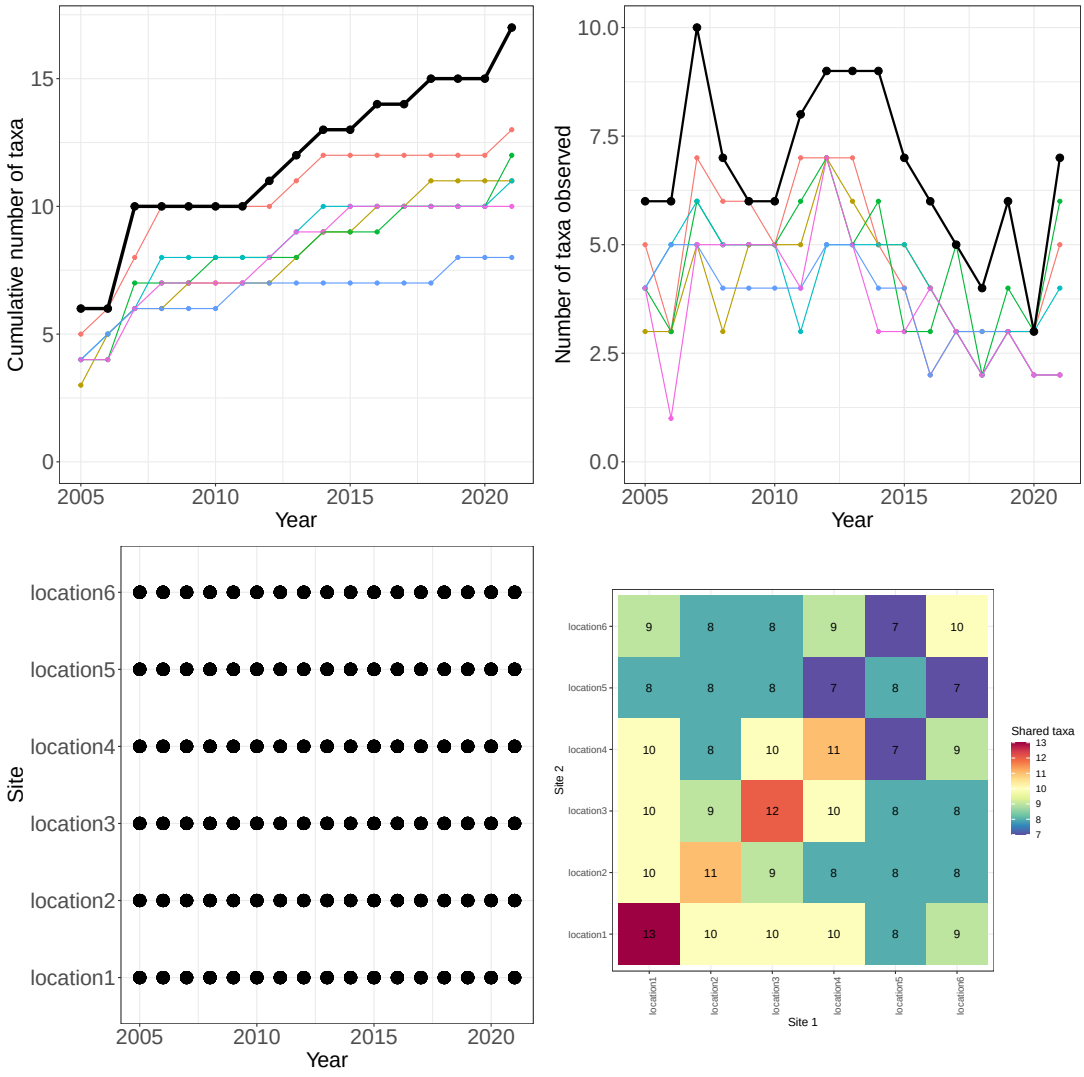

Figure S5: **MCR-inverts:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for invertebrate taxa observed on Moorea coral reef LTER (2006-2021). The black lines represent total site-level values across all plots.

and Taylor Slough (TSL) of Everglades National Park that were sampled in 7 consecutive years. Diatom abundance was aggregated as yearly mean of four samples collected per year (three samples for 2006). Data are shown in Figure S9

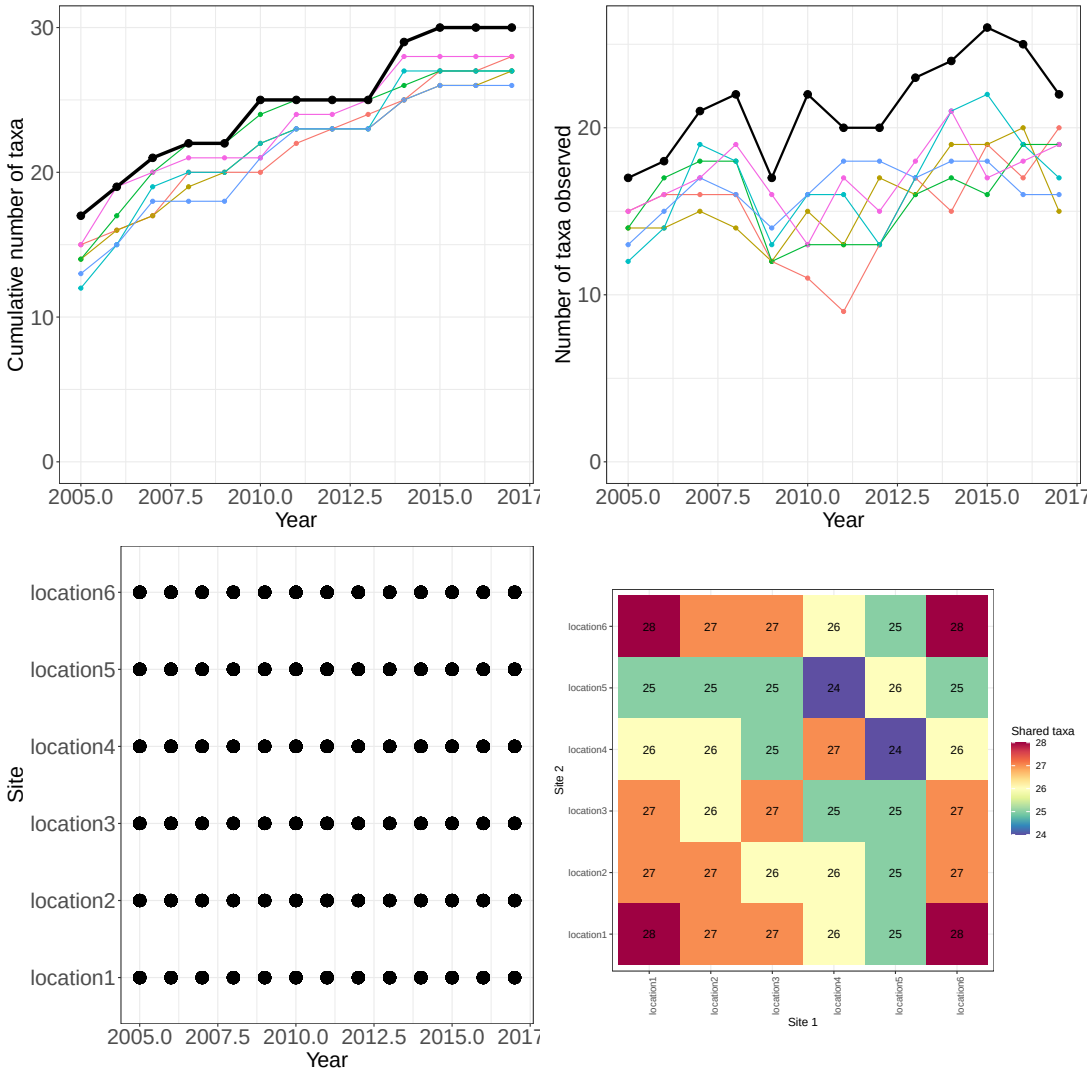

Figure S6: **MCR-coral:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for 31 coral taxa observed at six sites on Moorea coral reef LTER (2006-2017). The black lines represent total site-level values across all plots.

Section S4.2: fce-fish

Data were obtained from the PI, and are cataloged on EDI (Rehage, 2017). Catch per unit effort (CPUE) was calculated as (count/distance)*100 For each species, the CPUE was aggregated by summing the CPUE measured in each bout (i.e., replicate) within each Creek Number | River | YEAR | Season combination. The format was re-arranged to reflect the aggregated CPUE ('total CPUE') per season as columns and mean CPUE column was created by averaging the CPUE across

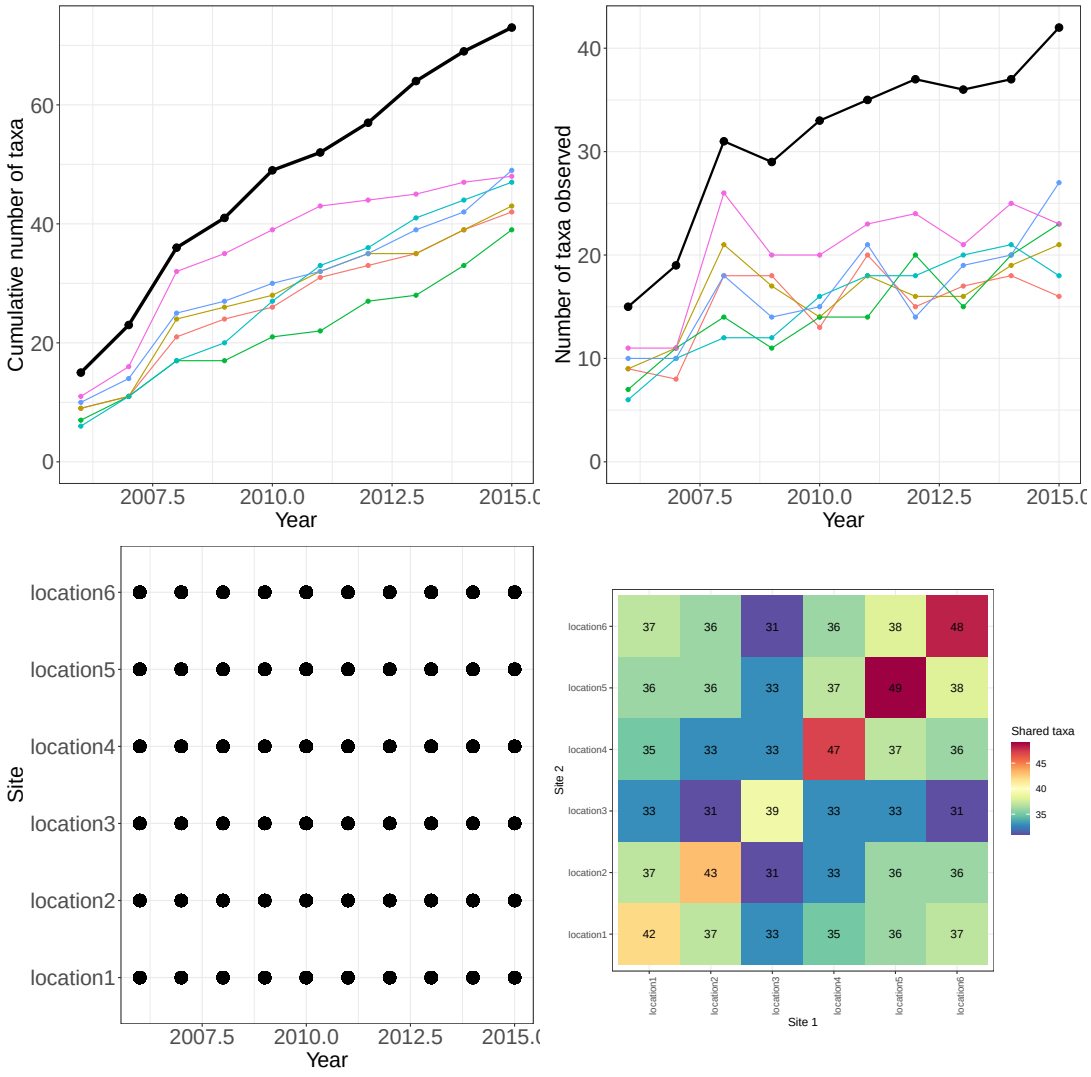

Figure S7: **MCR-algae:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for 73 algae taxa observed at six sites on Moorea coral reef LTER (2006-2015). The black lines represent total site-level values across all plots.

the three seasons. NOTE: After the first preliminary examination of the aggregated CPUE values the mean CPUE was ignored due to the unbalanced observations across the years and seasons. So, only the observations in the Wet and Dry season were considered. Dry season: In this set, only the sites within RB were considered to create a balanced design for the analysis. Thus, this set encompassed a longer temporal range with a cost of less spatial replication. NOTE: Also, YEAR 2004-2005 and 2011 were eliminated due to incomplete representation across the sites Wet season:

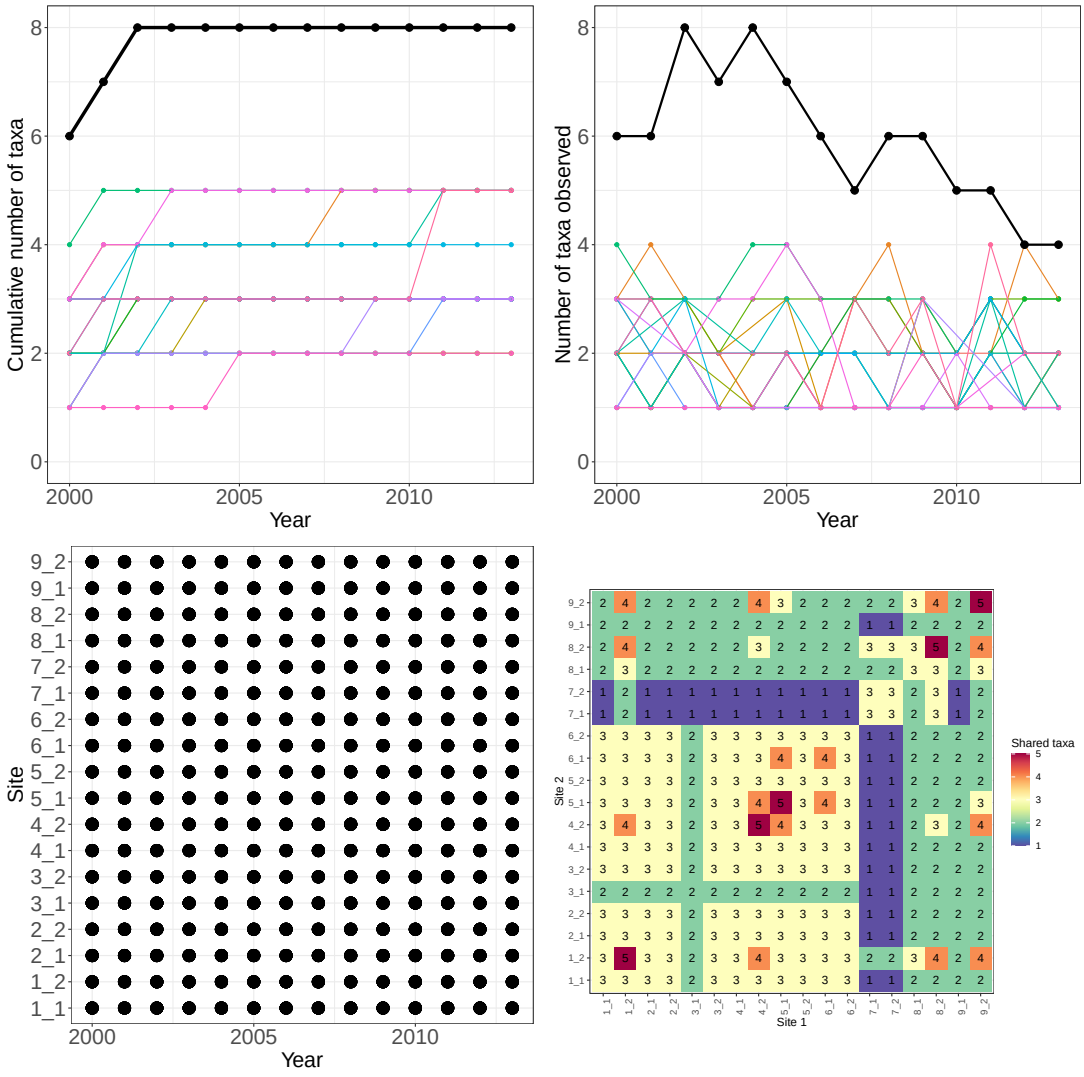

Figure S8: **GCE-mollusc:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for mollusc taxa observed at Georgia Coastal Ecosystems LTER. The black lines represent total site-level values across all plots.

In this set both RB and TB were considered but only after 2010. Thus, this set has a wider spatial replication but a shorter temporal range. NOTE: The difference in the spatial replication between seasons is related to the limitation of the sampling approach (electrofishing) which is limited to low salinity conditions. Salinity threshold for electrofishing is often reached in TB during the Dry season (i.e., TB is considered the estuarine portion of the Shark River System). Data from the dry season are shown in Figure S10. Data from the wet season are shown in Figure S11.

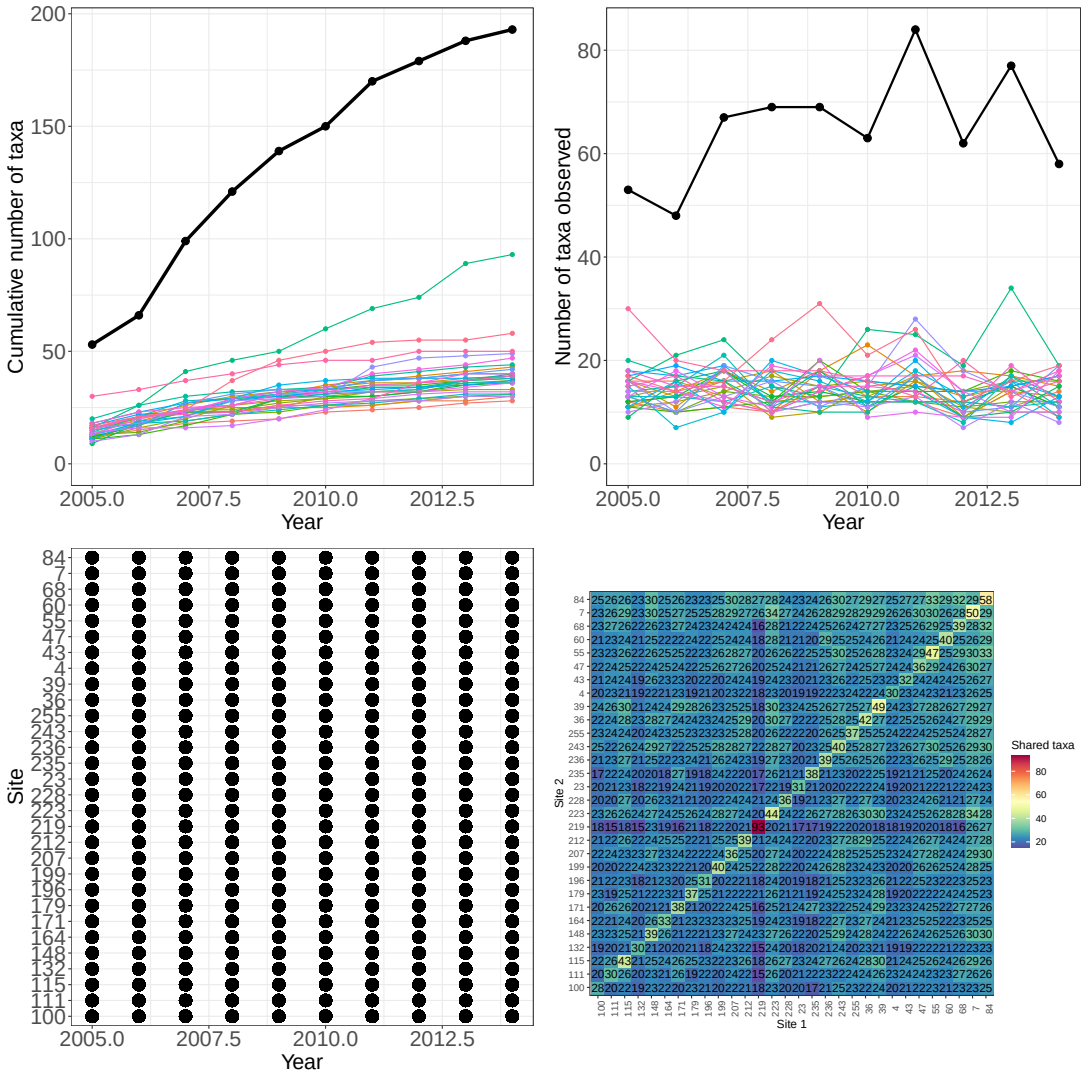

Figure S9: **FCE-diatoms:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for diatom taxa observed at Florida Coastal Everglades LTER. The black lines represent total site-level values across all plots.

Section S5: Terrestrial datasets

Section S5.1: and-plants-mtStHelens

We downloaded the data from ecological archives (del Moral, 2010). We retained data from 12 100 m^2 plots at a single site, Abraham Plain, which provides annual data on a primary succession on pumice, with no gaps, from 1989 to 2009. All individuals of this dataset were identified to the species level. Data are shown in Figure S12.

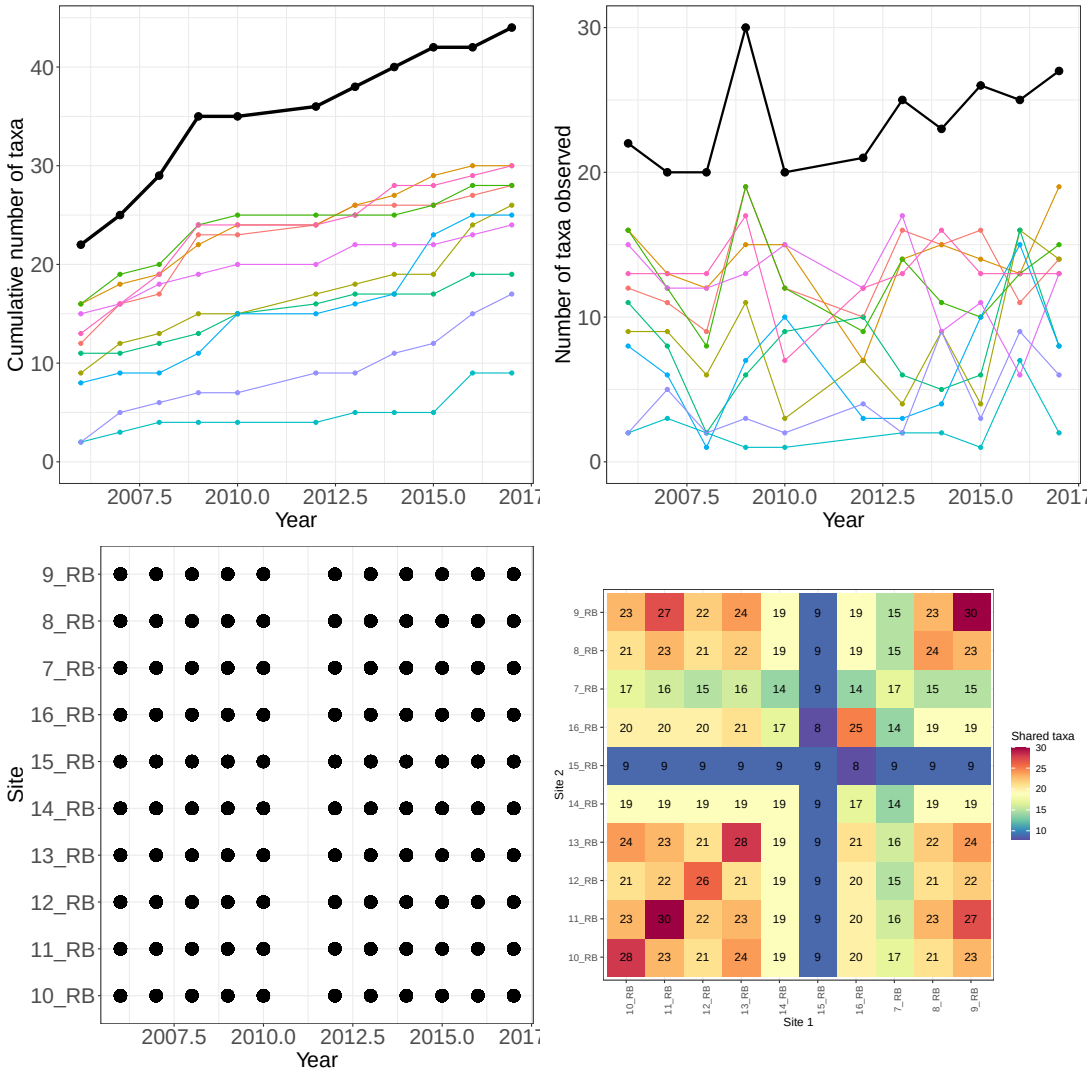

Figure S10: **FCE-fish dry season:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for fish taxa observed at the Florida Coastal Everglades. The black lines represent total site-level values across all plots.

Section S5.2: cdr-plants

Data were downloaded from EDI (Tilman, 2018). Annual censuses are incomplete after 2004, so we only consider data from 1982 until 2004. We used data from control plots only, from all four sites (A, B, C, and D). Fields A, B, and C contain 4x4 m plots and were considered together as a single dataset, while D contained 2x4 m plots and was considered a separate dataset because of its unique fire history. We prepared taxonomic data by cleaning clear mistakes (such as 'carex sp.' instead of

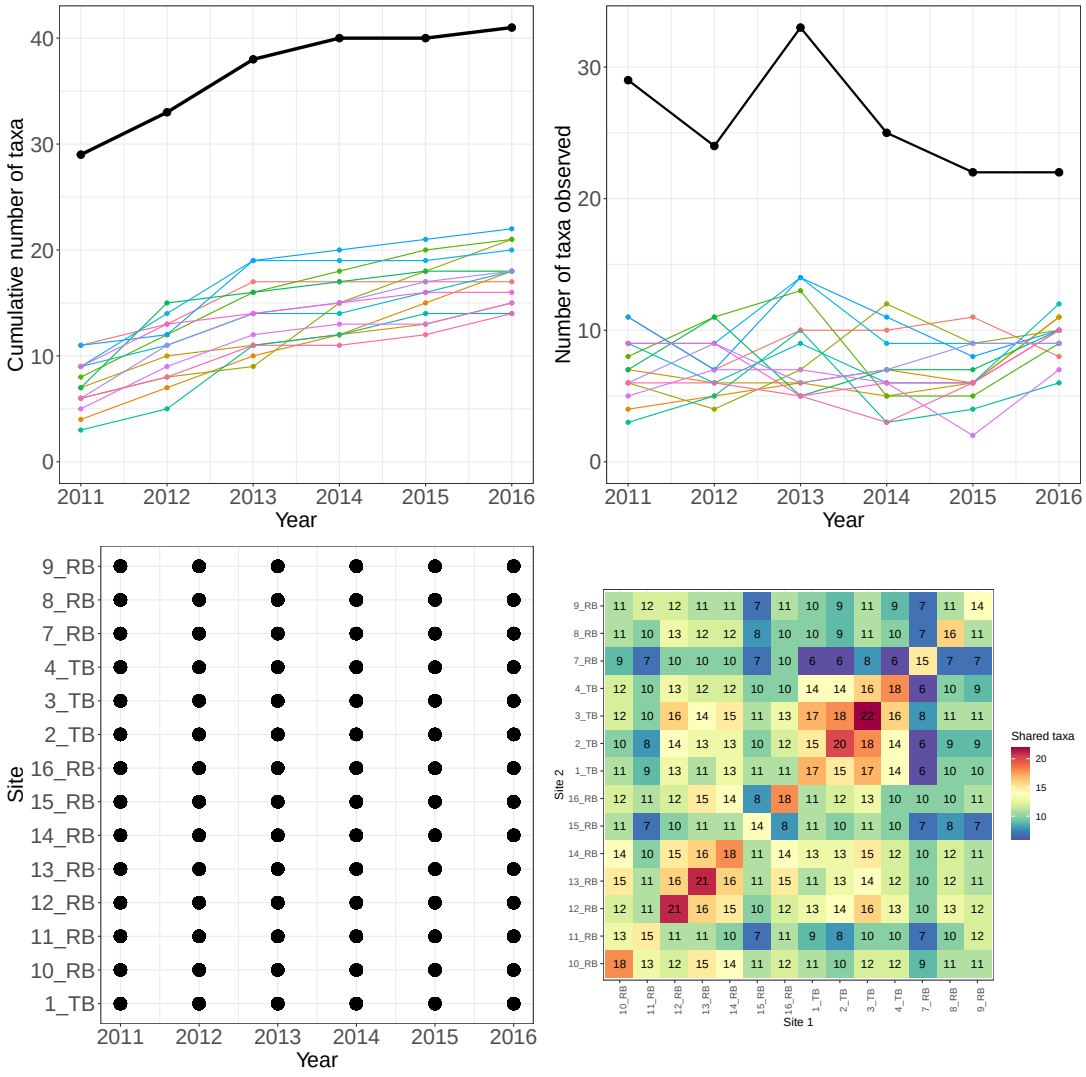

Figure S11: **FCE-fish wet season:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for fish taxa observed at the Florida Coastal Everglades. The black lines represent total site-level values across all plots.

'Carex sp.'), removed non-taxonomic entities ("Miscellaneous litter") and non-plant taxa ('Fungi', and 'Mosses & lichens'). We also lumped or dropped certain taxonomic information. Specifically, we lumped taxonomic information to the genus level when more than 1% of the biomass of a genus was not identified to the species level. For example, *Cyperus* species are usually identified to the genus level ("Cyperus sp.") rather than species level ("*Cyperus schweinitzii*"), with a minority of the biomass (less than 10%) identified at the specific level. We therefore consider only genus

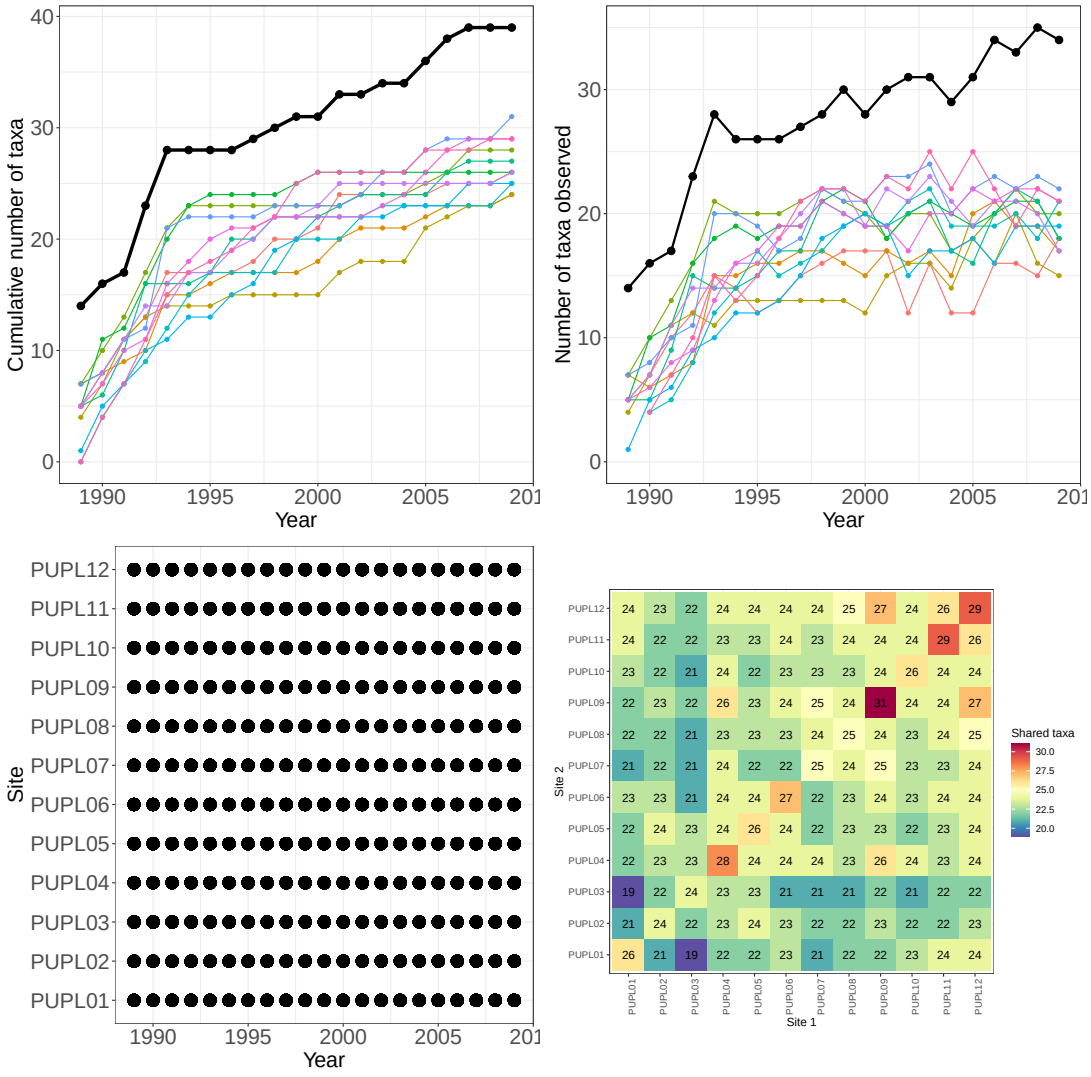

Figure S12: **and-plants:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and species shared across sites (bottom right) for the plant species observed at the Mount Saint Helens long-term monitoring plots located at Abraham Plain. The black lines represent total site-level values across all plots.

information for *Cyperus*. We dropped taxonomic information when within a certain genus, biomass is identified to the genus level. For example, in the genus *Viola*, more than 99.8% of biomass was determined to the species level. We therefore dropped from the dataset the instances when biomass is assigned to 'Viola sp.'. Data are shown in figures S13 and S14.

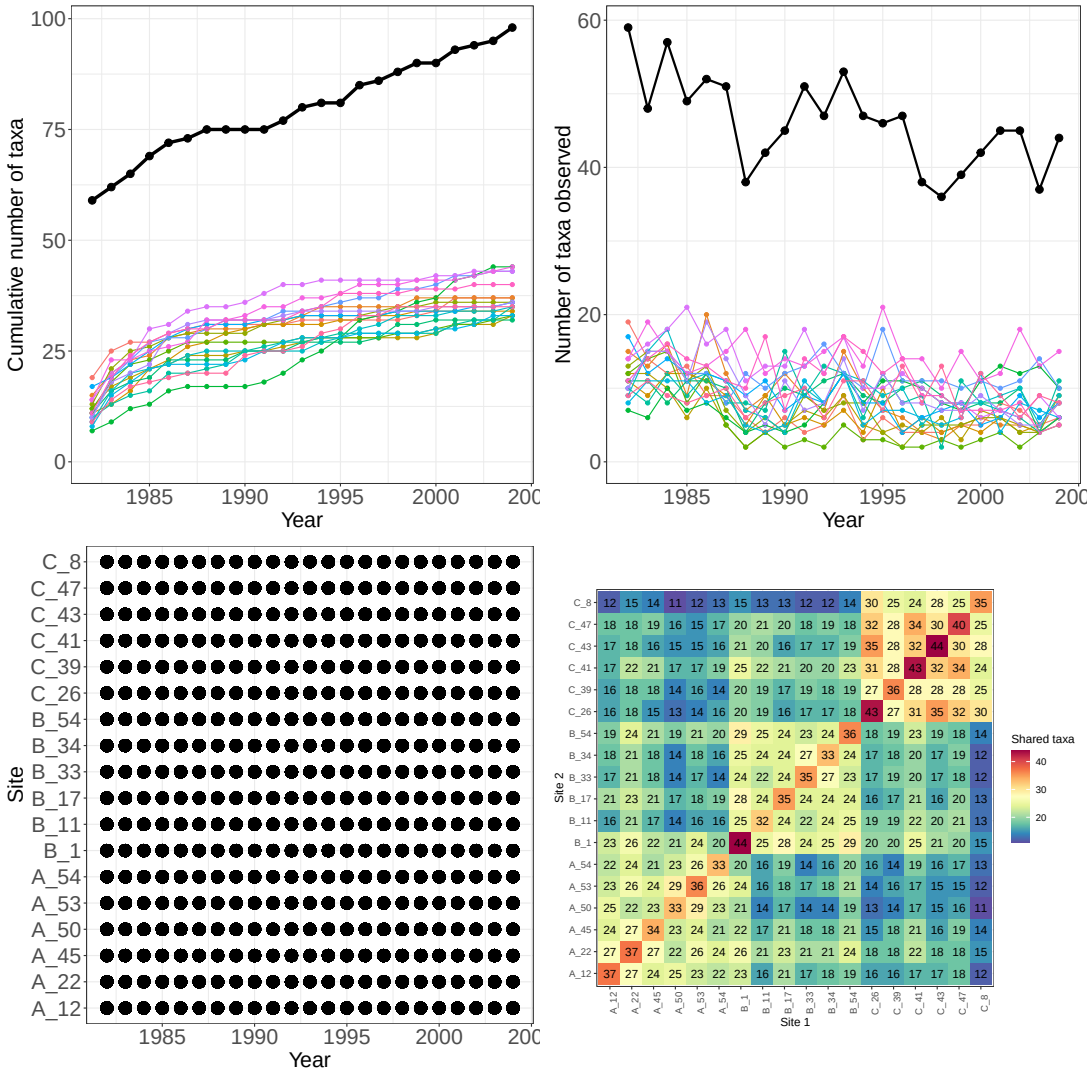

Figure S13: **CDR-plants, A, B, and C fields:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for plant species observed in the A, B, and C fields at Cedar Creek. The black lines represent total site-level values across all plots.

Section S5.3: hays-plants

Data were downloaded from Ecological Archives (Adler et al., 2007). We removed unknown species, and data points categorized as 'short grass', 'Fragment', and 'Bare ground'. Moreover, we identified seven issues with species identification. First, we removed individuals identified a the genus level for *Ambrosia*, *Oxalis*, and *Solidago*. In these genera more than 95% of individuals were identified at the species level. Second, we 'lumped' to genus level, species belonging to the general *Allium*,

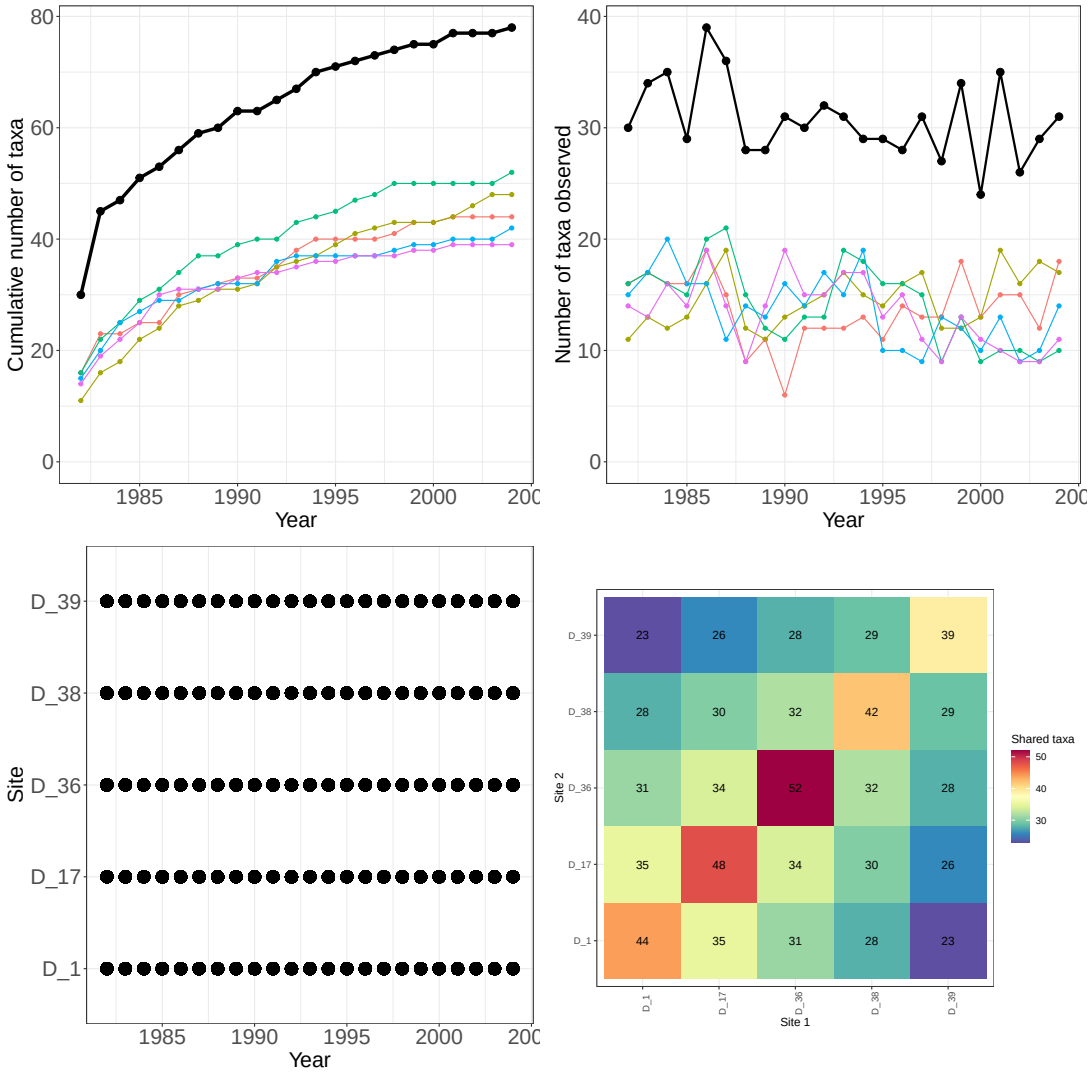

Figure S14: **CDR-plants, D field:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for plant species observed in the D field at Cedar Creek. The black lines represent total site-level values across all plots.

Chamaesyce, *Opuntia*, *Polygala*. In these genera, more than 5% of counts were identified at the genus level. Finally, we only retained the 14 plots (1 m^2 quadrats) with continuous replication between 1938 and 1973. Data are shown in Figure S15.

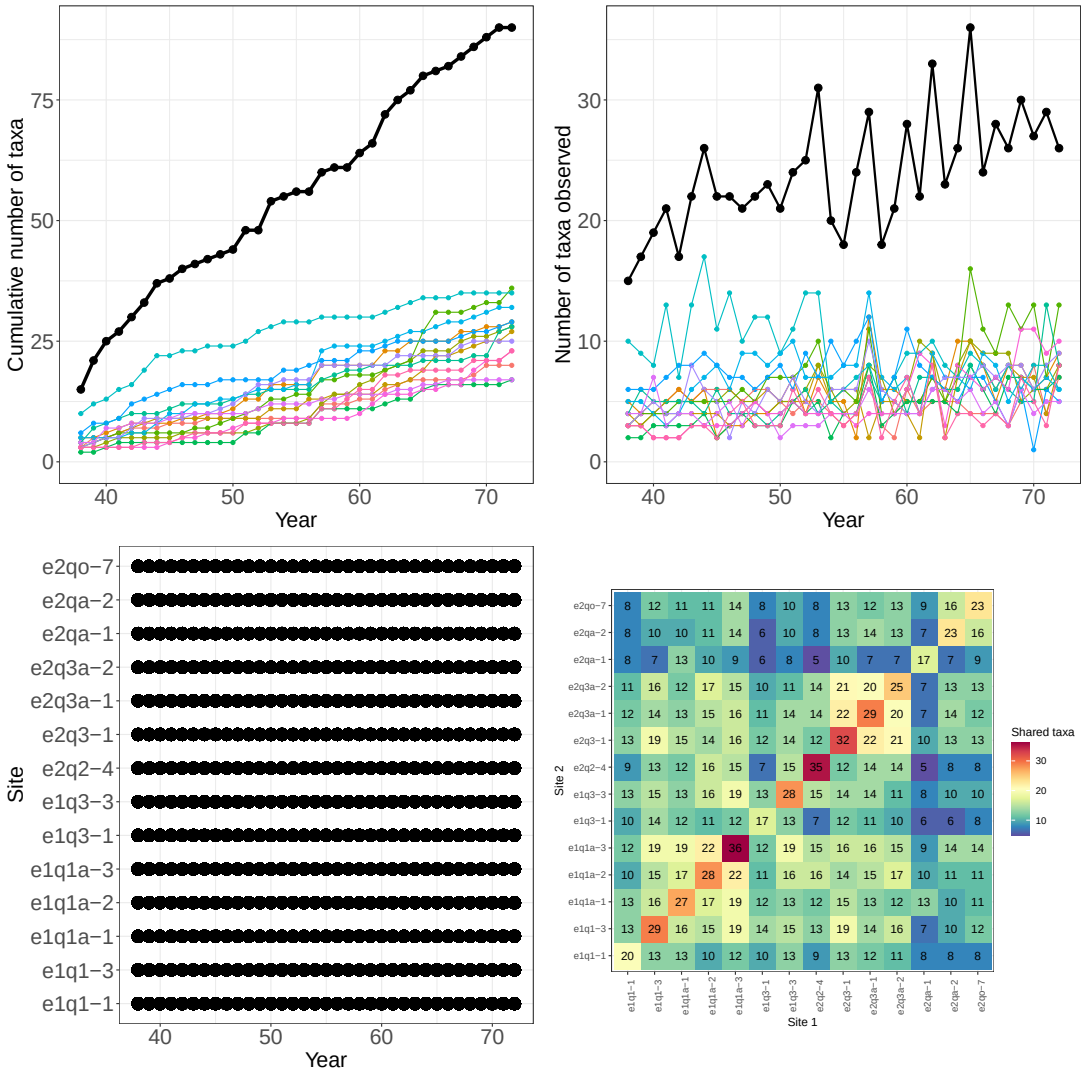

Figure S15: **hays-plants:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for mixed-grass prarie plant species observed at long-term monitoring plots in Hays, Kansas. The black lines represent total site-level values across all plots.

Section S5.4: jrn-plants

We downloaded the data from ecological archives (Chapline, 2017). We retained data from 10 plots (quadrats) sampled 19 years: from 1915 to 1938 with five gaps (1918, 1922, 1926, 1929-1930, and 1934). We removed data from individuals not identified to genus or species. Finally, we lumped taxonomic data at the genus level in case over 5% of individual data points were identified at the genus level; conversely, if this percentage was lower than 5%, we discarded data identified at the

genus level. Data are shown in Figure S16.

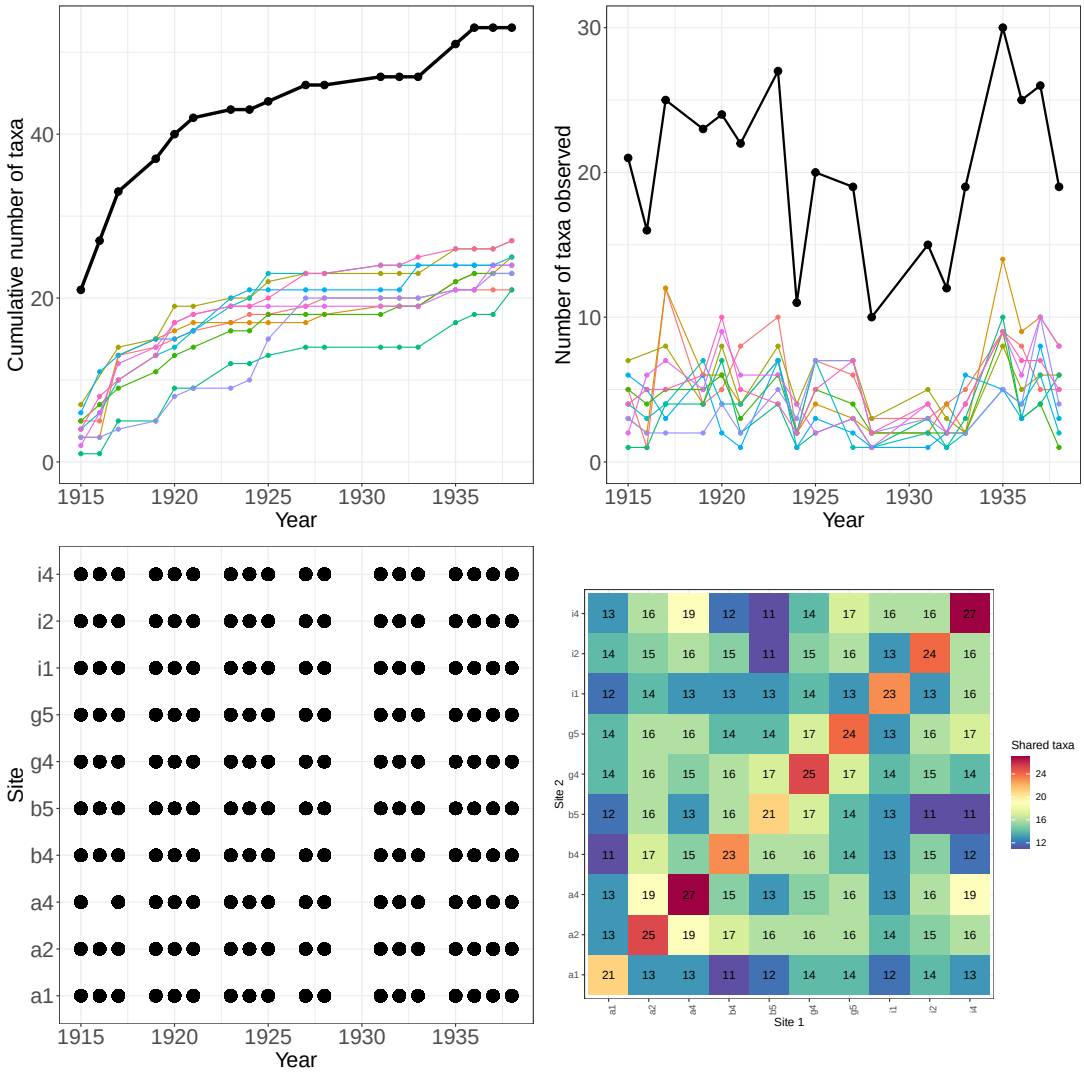

Figure S16: **jrn-plants:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and species shared across replicates (bottom right) for the plant species observed across the 10 plots we retained from the Jornada Experimental Range. The black lines represent total site-level values across all plots.

Section S5.5: sev-plants

Data were downloaded from EDI (Muldavin, 2015). This dataset has a consistent spatio-temporal sampling: quadrats, within four transects (N,S,R,V) within two plots, all at one site, sampled twice a year (spring and fall). There is, however, a third plot (plot number 3) that contains four new

transects (A,B,C,D), which contain 5 - rather than 10 - quadrats each. Moreover, the replicates have been occasionally censused in winter, but not consistently through the years. Therefore, we removed plot 3 and winter censuses. We then removed NAs in species counts and species identity, and summed species counts across the 10 quadrats contained in each transect. Finally, the "DATE" variable is defined as "year.month" (hence, 2000.5 refers to year 2000 in May). We chose to have season 2 (spring) correspond to May, and season 3 (Fall) correspond to September. Data are shown in Figure S17.

Section S5.6: sgs-plants

Data were downloaded from EDI (Stapp, 2013). Plant community composition on the three grassland and three shrubland small mammal trapping webs (hereafter called 'sites'; n = 6). Vegetation measurements were made once per year, usually in mid-July. Percent canopy cover of each plant species was estimated visually in 30 0.10-m^2 Daubenmire quadrats on each web. We aggregated plant species percent cover data at the site scale because each year, transects and plot locations were determined based on a randomization procedure (3 trap stations were chosen randomly within each site from a list of 12 permanent points, where transects with random orientations were centered on each trap station location). Trapping web '31W' was removed because it was sampled in only 2 years (2006 and 2007). Samples for year 2007 were removed because not all sites were sampled in 2007. Species codes that did not identify plant species were removed (litter, bare ground, etc.). Species codes that were otherwise inconsistent (different cases, naming conventions, etc.) were reconciled so that all species were identified by unique 4 letter codes. Observations for codes that did not represent plants, or plants were unknown or not resolved to species were removed prior to analysis. Data are shown in Figure S18.

Section S5.7: sgs-plants

We downloaded the dataset from EDI (Milchunas, 2014). We kept data from 1995 to 2008, discarding data from 1992 and 1993 because of a gap in 1994. We only retained sites that were always grazed, which is the natural condition in this ecosystem. Daubenmire plots were established in

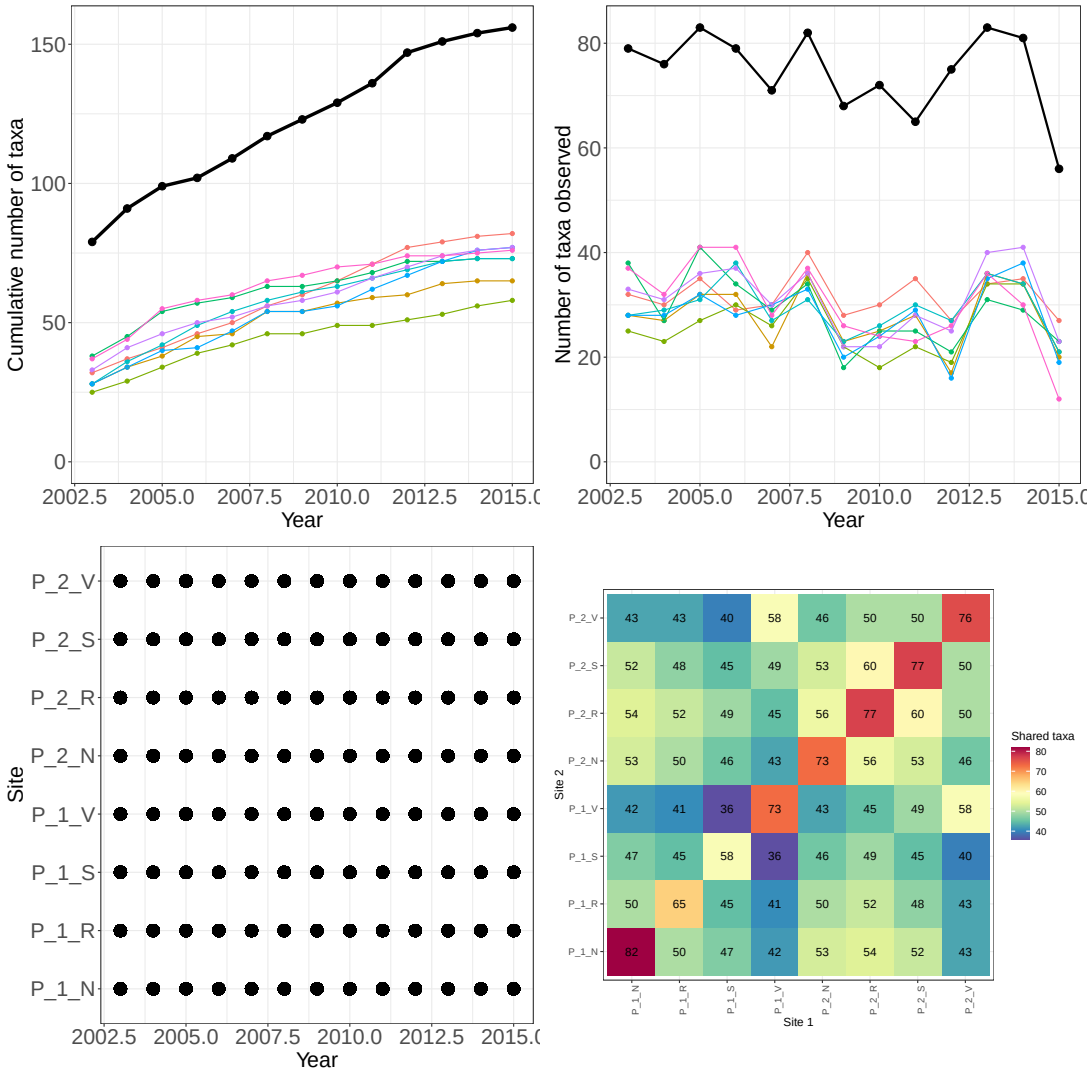

Figure S17: **SEV-plants:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for plant species observed in the Pinon-Juniper habitat at the Sevilleta (SEV) LTER. The black lines represent total site-level values across all plots.

each treatment site. We took the mean of basal cover across plots. Finally, we removed data points not identified at the species level.

Data are shown in Figure S19.

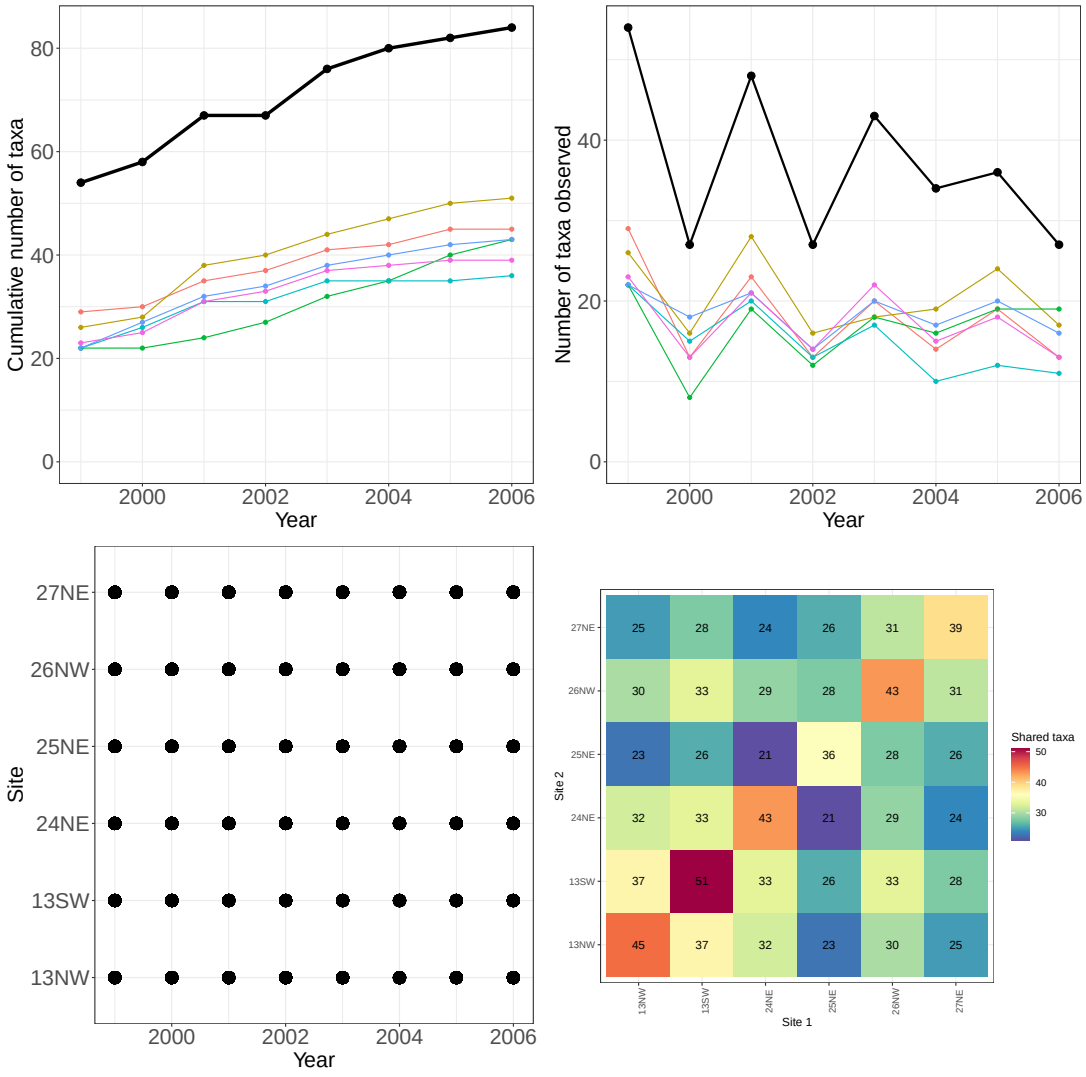

Figure S18: **SGS-plants:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for plant species observed at the Shortgrass Steppe (SGS) LTER. The black lines represent total site-level values across all plots.

Section S5.8: sev-arthropods

We downloaded this arthropod data (1992-2004) from EDI (Lightfoot, 2013). To prepare this dataset, we first removed unreliable data points: data from unidentified sites, from sites with inconsistent sampling (sites "P" and "B"), from lines reporting "pooled" data, and from all taxa not identified to the species level. Second, we took means of traps within each trap line. We took means because sampling frequency is not homogeneously 6 times a year. Data are shown in Figure

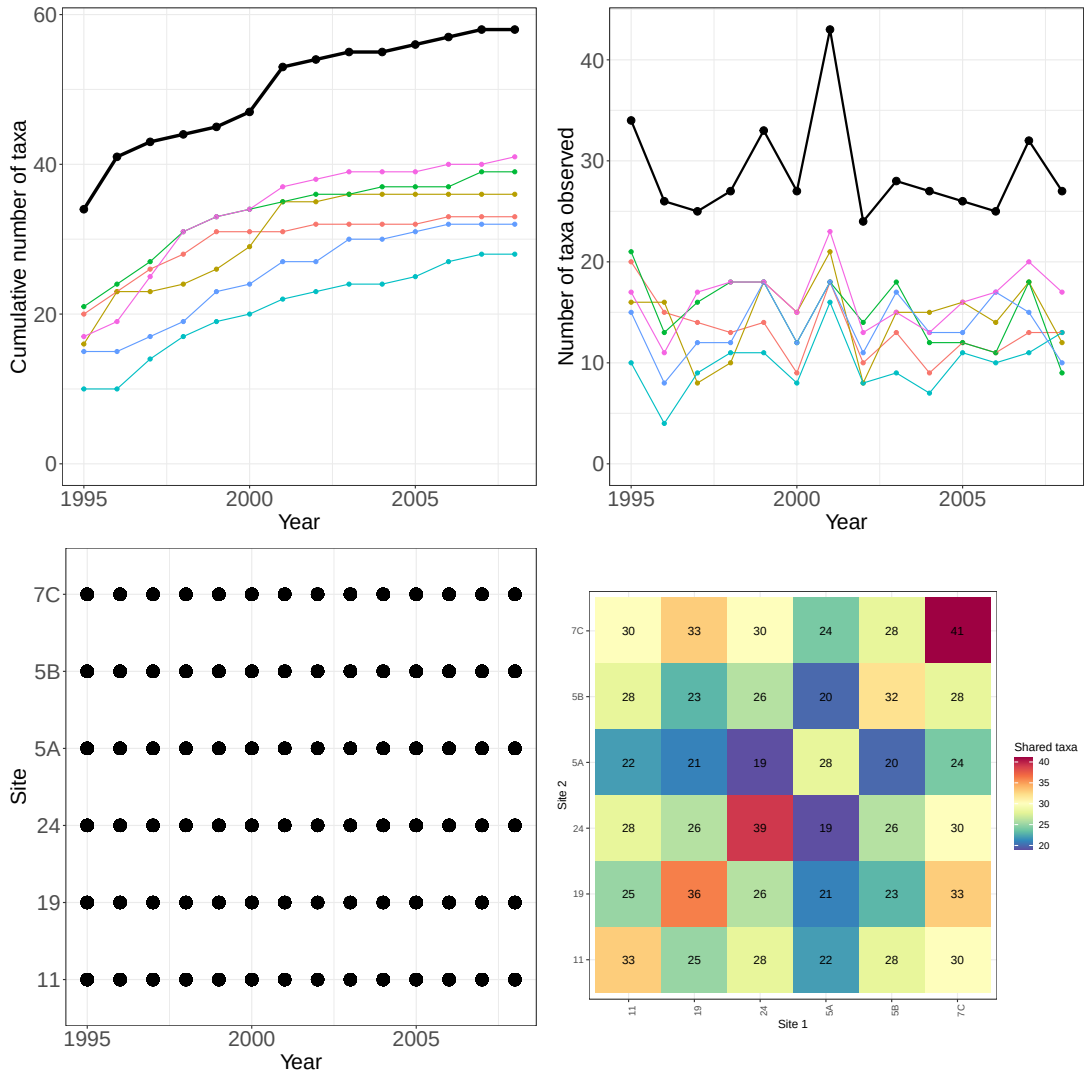

Figure S19: **SGS-plants:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for plant species observed at the Shortgrass Steppe (SGS) LTER. The black lines represent total site-level values across all plots.

S20.

Section S5.9: sev-grasshoppers

The data (1992-2013) were downloaded from the EDI Data Portal (Lightfoot, 2010). We retained data from only two habitats (Black grama and Creosotebush) that shared many species, and presented 20 years of temporal replication. These data were collected twice a year, and spatial replica-

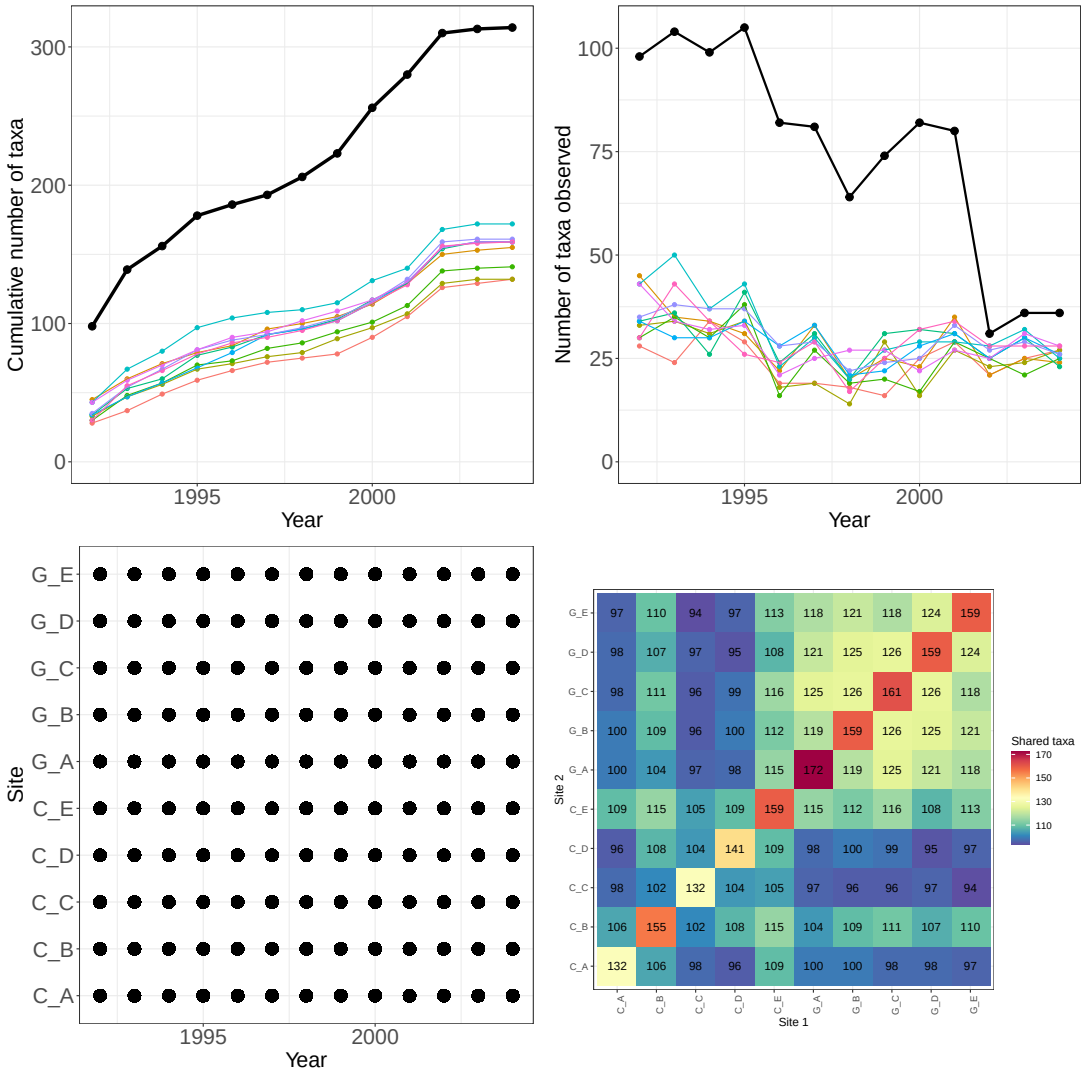

Figure S20: **SEV-arthropods:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for arthropod species observed in the Sevilleta LTER. The black lines represent total site-level values across all plots.

tion included site, transect, and web. Population (count) data is structured, being collected across sex, age, and substrate. We summed numbers across webs, sex, age, and substrate. Data are shown in Figure S21.

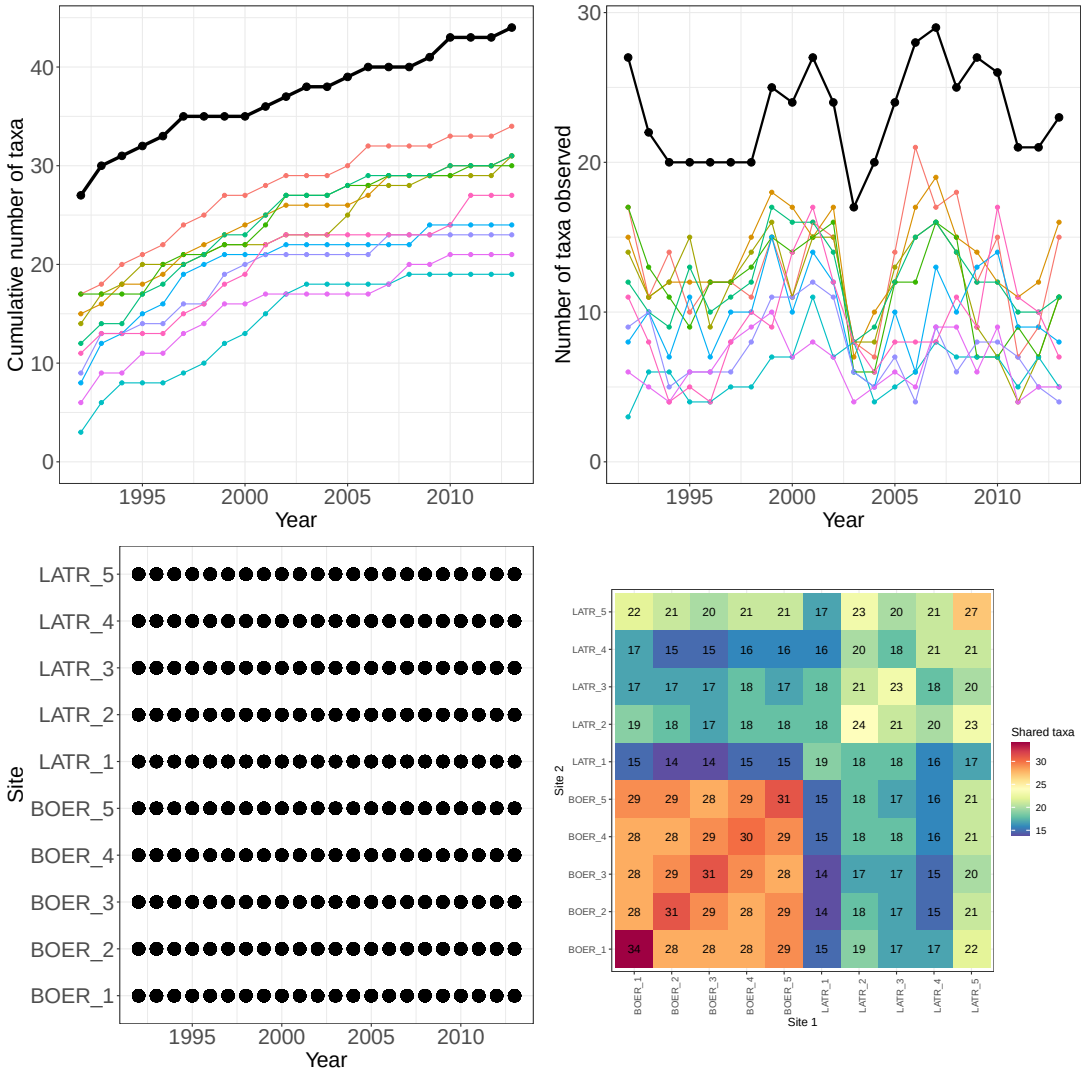

Figure S21: **SEV-grasshoppers:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for grasshopper species observed in Black grama (BOER) and Creosotebush (LATR) habitats the Sevilleta LTER (1992-2013). The black lines represent total site-level values across all plots.

Section S5.10: cdr-grasshoppers

Data (1989-2006) were accessed on EDI (Knops, 2018). Counts were sampled from 1x0.5 m quadrats. We removed sites '28' and '11', which were added to the sampling after 1989. Then, we summed the number of individuals across all life stages and all months. We summed across months even in 2003, when June and August samples were lost for some fields. However, as the documen-

tation reports, "The total counts for these fields were augmented by proportional additions from remaining samples by John Haarstad and crew". Taxonomic information is available for only for the *Acrididae* family before 1994. We lumped taxonomic identifications to genus level for *Conocephalus*, *Scudderia*, and *Tetrix*, as over 5% of individuals from these genera were not identified at the species level. 6% of individuals belonging to the *Melanoplus* genus were identified at the genus level: however, we did not lump this data to the genus level, because *Melanoplus* contains 12 out of the 50 species of this dataset. We removed the individuals identified as belonging to *Melanoplus* without being identified to species. Data are shown in Figure S22.

Section S5.11: knz-grasshoppers

Data on grasshopper abundance (1996-2015) were downloaded from EDI (Joern, 2018). Counts were obtained via 20 sweep samples. We retained 13 spatial replicates which provide continuous temporal replicates from 1995 to 2013 (2012 is missing). We lumped taxonomic information level whenever the counts at the genus level made up more than 5% of the total individuals counted. We did not do this lumping for *Melanopus* spp. because it is a hyperdiverse genus. In this case, we dropped all *Melanopus* records identified at the genus level. Finally, we averaged count data across a year, because some spatial replicates could occasionally contain more observations within a year. Data are shown in Figure S23.

Section S5.12: luq-snails

We downloaded these data on snail abundance (1991-2017) from EDI (Willig, 2010). We averaged number of snails across runs ("Run.ID" in dataset) and seasons ("Seasons" in dataset). There were no codes for unknown or non-living taxa. The 16 ha plot is 500 x 320 m, divided into 20 x 20 m quadrats, with each quadrat further subdivided into 5 x 5 m sub-quadrats. We only retained sites which were present in every year of the dataset. Data are shown in Figure S24.

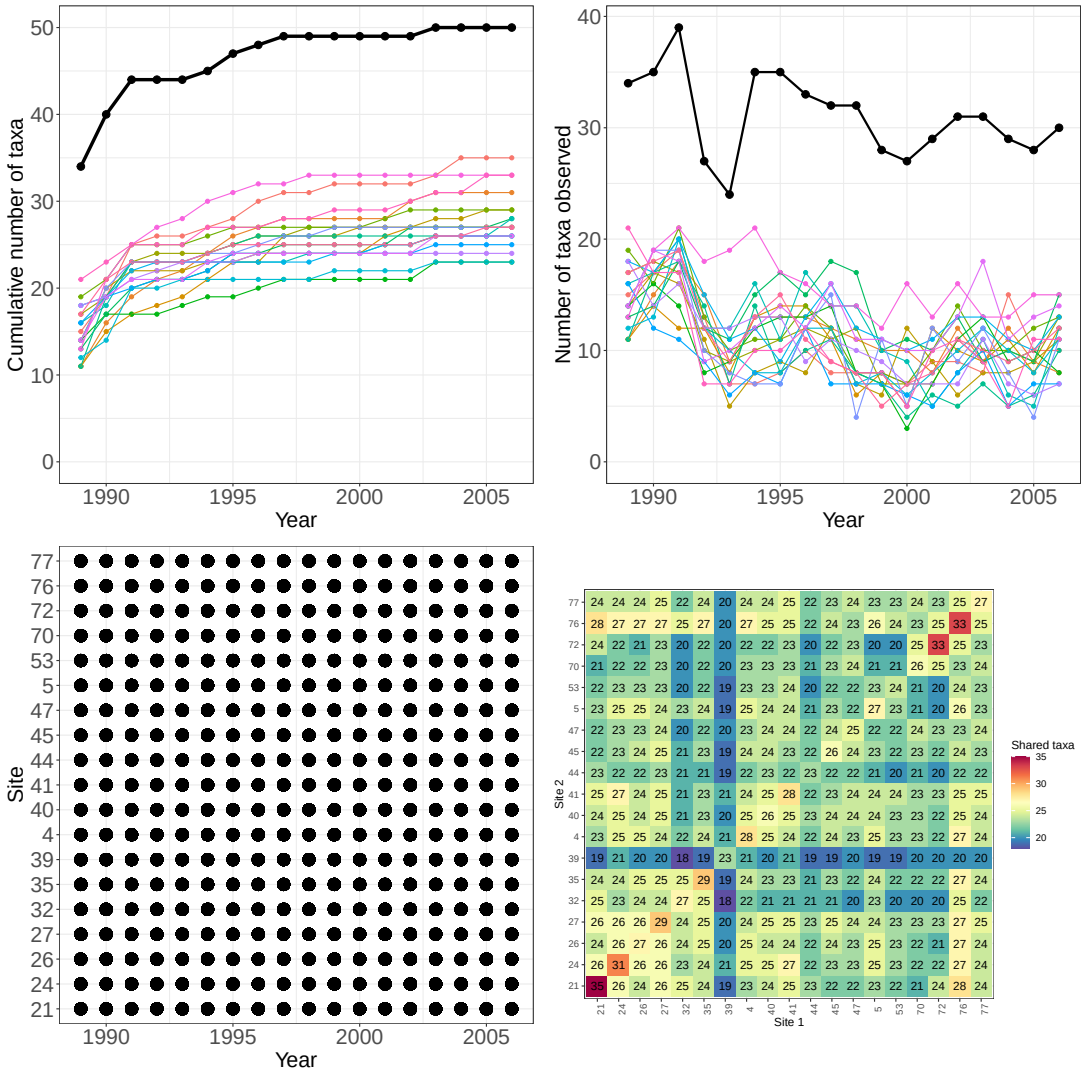

Figure S22: **CDR-grasshoppers:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for grasshopper species observed at the Cedar Creek LTER. The black lines represent total site-level values across all plots.

Section S5.13: jrn-lizards

The data were downloaded from the EDI Data Portal (Lightfoot and Whitford, 2022). Data were gathered in a mark-recapture study. Pitfall traps were opened for two weeks four times per year (quarterly). The monthly samples from 1990 and 1991 were removed. Individual lizards were identified and the number of unique individuals per site per year were summed. Two sites that were established five years after the start of the study (SUMM and NORT) were excluded. Data

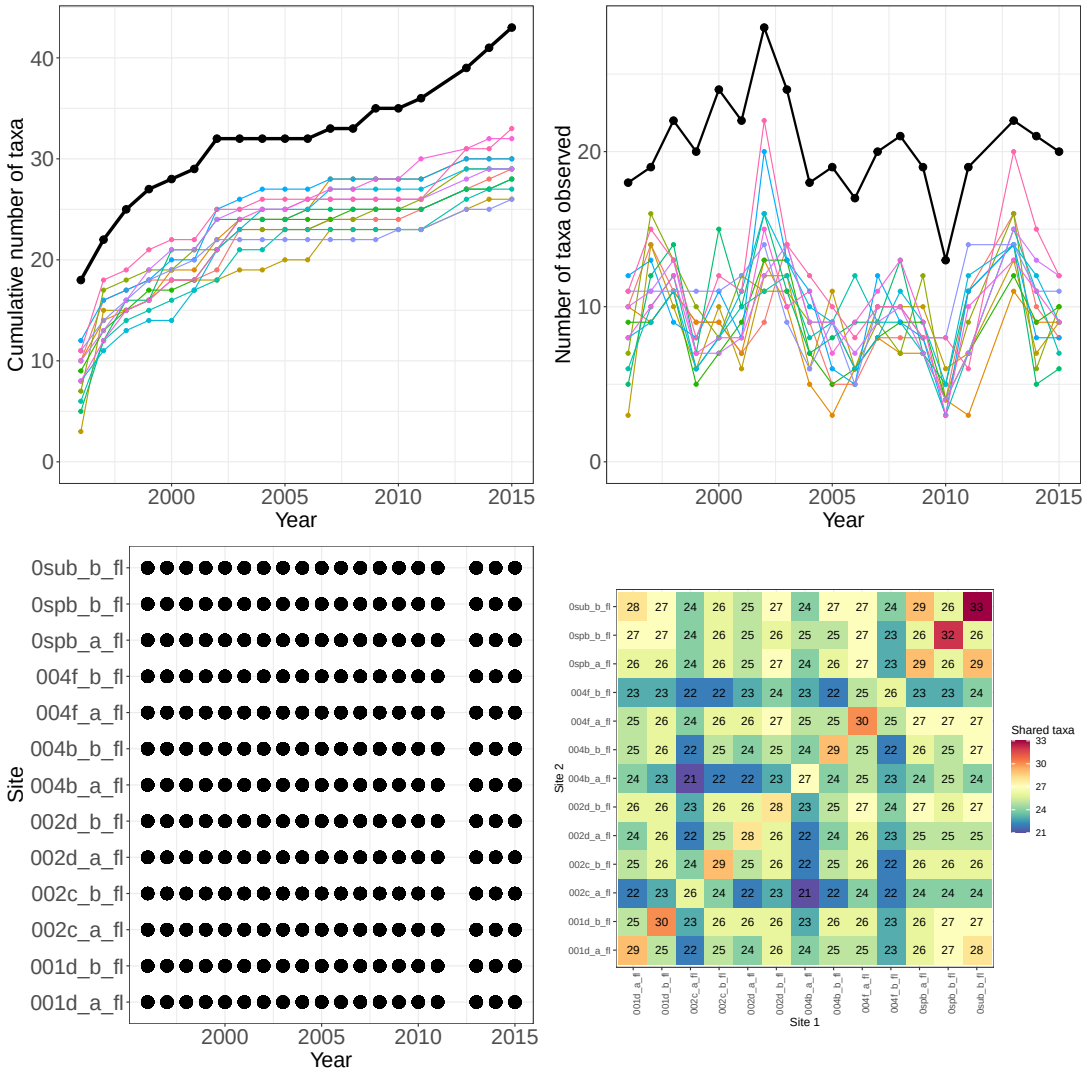

Figure S23: **KNZ-grasshoppers:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for grasshopper species observed in the Konza Prairie. The black lines represent total site-level values across all plots.

are shown in Figure S25.

Section S5.14: cap-herps

The data were downloaded from the EDI Data Portal (Bateman and Childers, 2018). Herpetofauna occurrence data were gathered in a visual encounter survey. Observations were nested by 3 10 x 20 m plots within 3 transects per site. Each site represents the reach level (each reach level

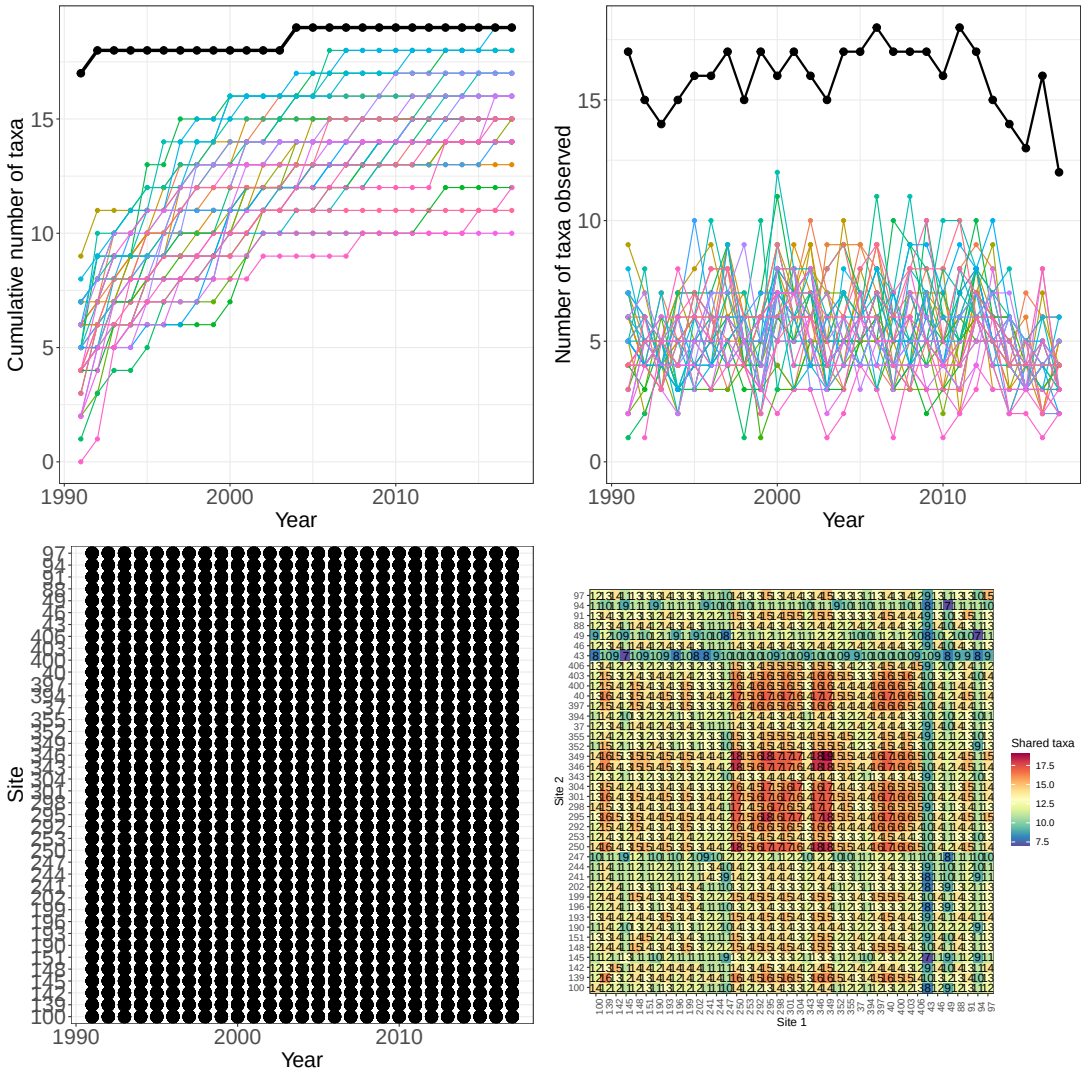

Figure S24: **LUQ-snails:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for snail species observed in Luquillo LTER. The black lines represent total site-level values across all plots.

site is composed of 3 transects with equal area sampling efforts). Surveys from 2012 and March were dropped to standardize sampling efforts temporally. Taxon count was calculated as the maximum abundance per year in any one of the sampling events (with 3 sampling events per reach in April/May, June/July, and September/October). Data are shown in Figure S26.

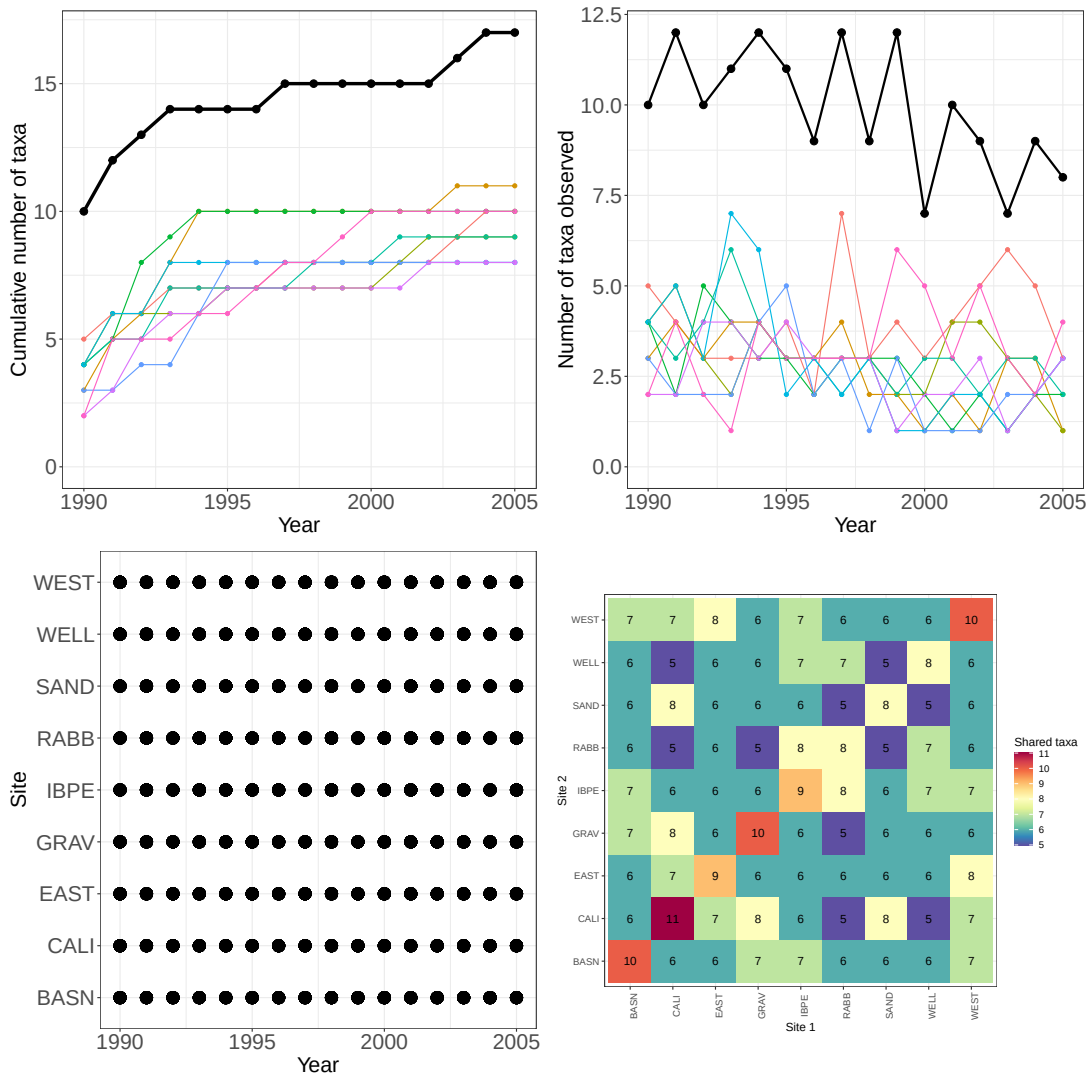

Figure S25: **JRN-lizards:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for 20 lizard species observed at 9 plots in the Jornada LTER (1990-2005). The black lines represent total site-level values across all plots.

Section S5.15: and-birds

The data were downloaded from the EDI Data Portal (Hadley, 2017). We used data from the first five years of study (2009 - 2013) because six counts per season were conducted in those years. We summed the counts of new individuals observed within the closest distance radius (< 50 m) of the points during the 10-minute interval for on each sampling occasion, and used the maximum number of individuals of each species recorded at each point as the abundance value for that year. Data

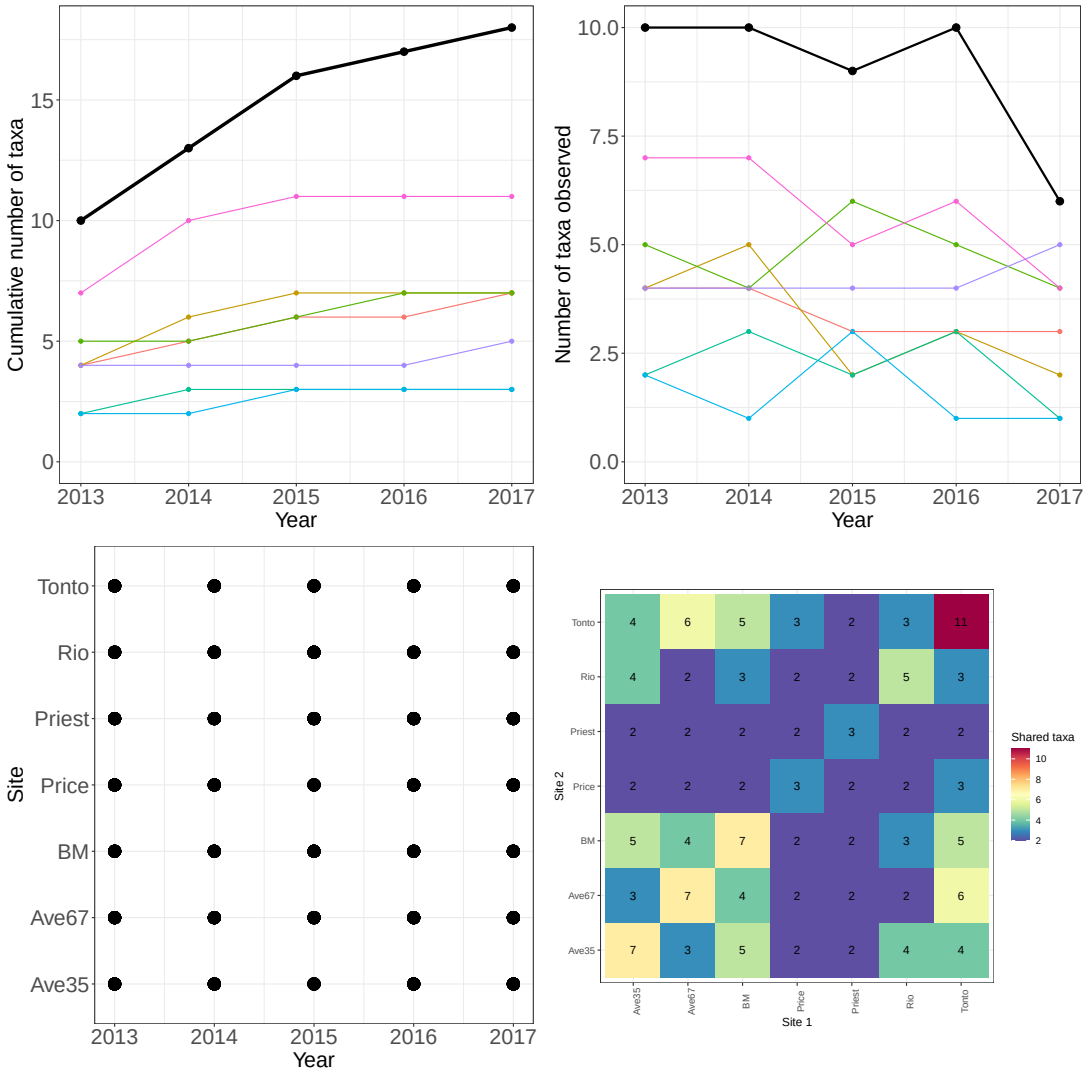

Figure S26: **CAP-herps:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for species observed in the Central Area Phoenix LTER (1990-2005). The black lines represent total site-level values across all plots.

are shown in Figure S27.

Section S5.16: cap-birds

Data were obtained from EDI (Bateman et al., 2017). This is a point count study where birds were observed (seen or heard) for 15 minutes within a 40 m fixed radius. Each site represents one point count. Only ESCA point counts are included. Data from 2017 were dropped because not

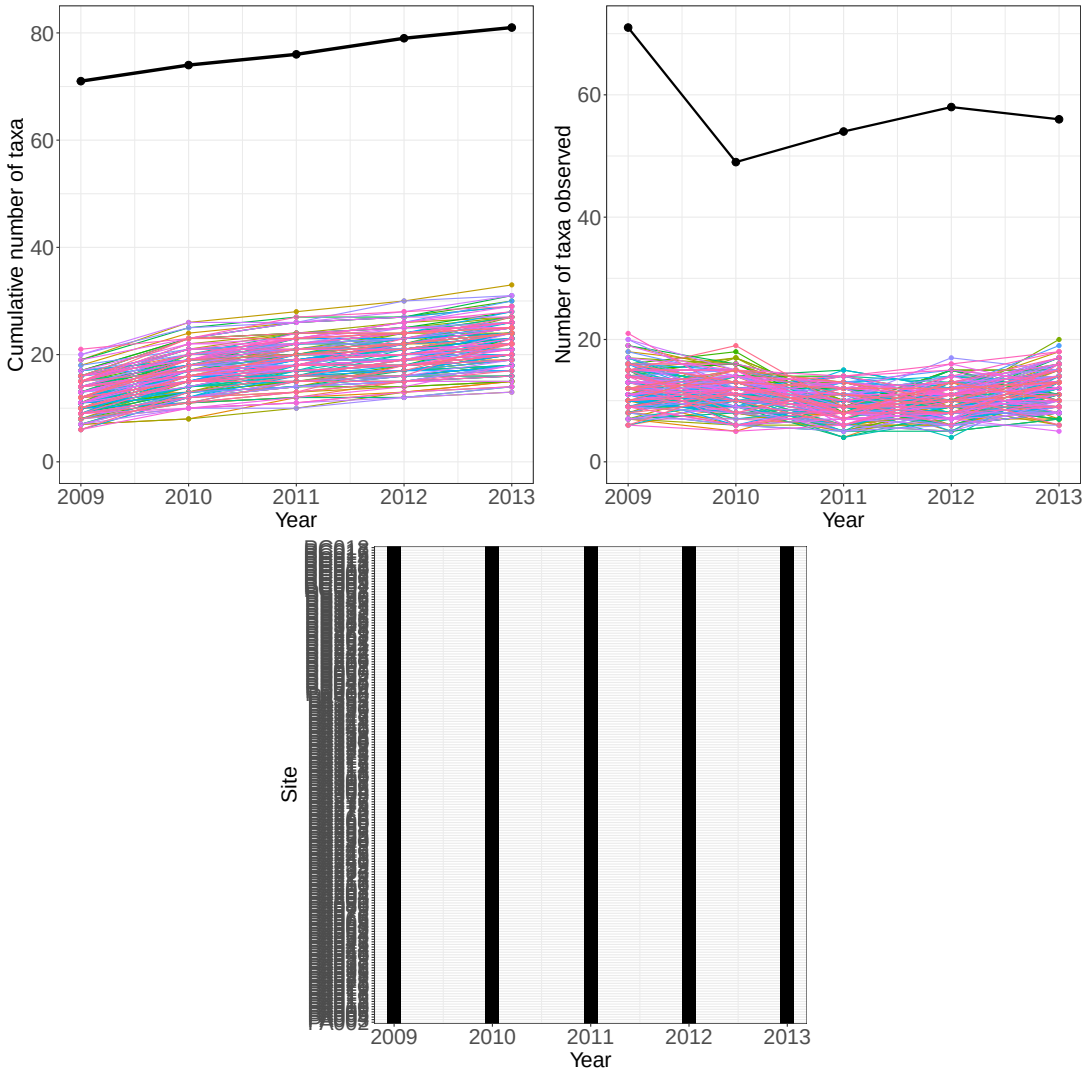

Figure S27: **AND-birds:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for bird species in the Andrews Forest. The black lines represent total site-level values across all plots.

all sites were sampled. Four point count sites (M-9, V-18, X-8, and V-16) were dropped due to uneven sampling across years. Unidentified species accounted for less then 2% of the total data and were dropped. Taxon count was calculated as the maximum abundance per year during the spring month's sampling events (with 3 sampling events per site between March, April, and May). Data are shown in Figure S28.

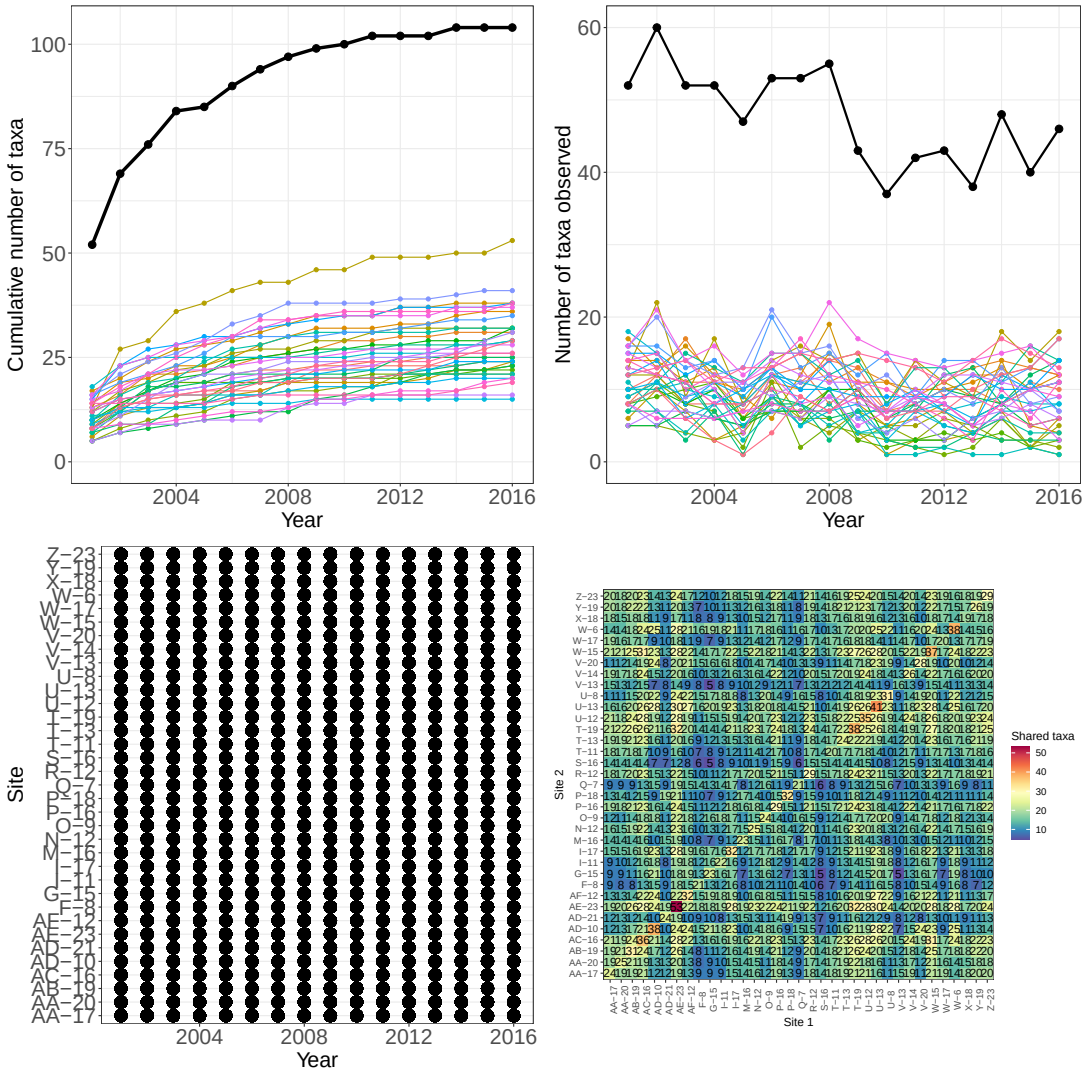

Figure S28: **CAP-birds:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for birds in the Phoenix urban LTER site. The black lines represent total site-level values across all plots.

Section S5.17: bes-birds

Data were downloaded from EDI (Nilon and Brodsky, 2017). We dropped all observations in the distance catagory "FT" and all observations not identified to species. We only used sites with surveys every year from 2005-2009. When there was multiple surveys per year for a single site, the abundance counts were aggregated to the maximum observed count from any survey for each species at the respective site. We only included plots in which at least one bird was observed in

each year of study. Sampling was conducted with a 5 min point-count method. Data are shown in (Figure S29).

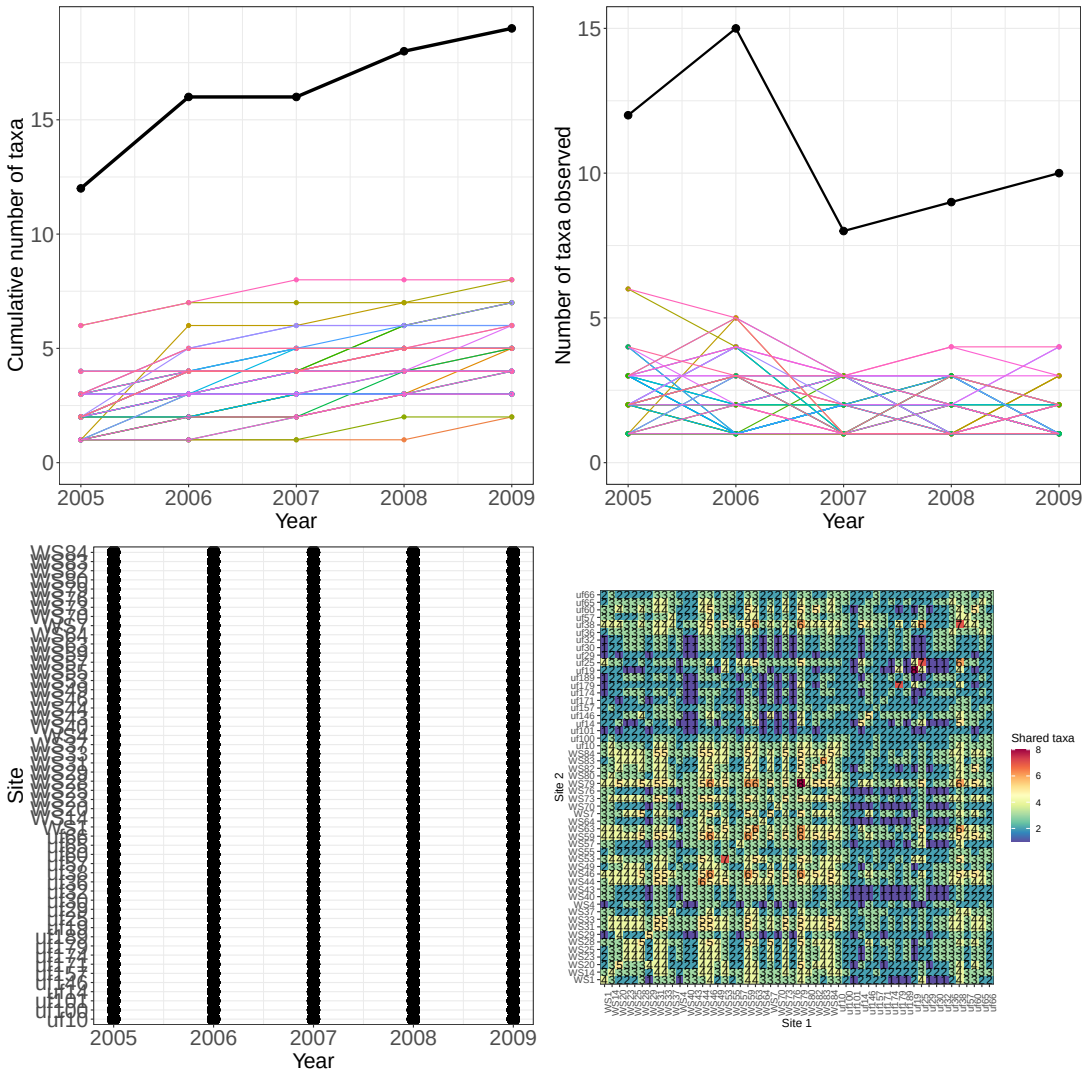

Figure S29: **BES-birds:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and shared taxa between sites (bottom right) for birds in the Baltimore urban LTER site. The black lines represent total site-level values across all plots.

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