Appendix S1

April 21, 2023

1 Data overview

This document describes the data cleaning, subsetting, and aggregation methods specific to each dataset. Table S1 lists the datasets included in the meta-analysis. 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.

2 Marine datasets

2.1 sbc-allTaxa

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.

2.2 mcr-inverts

Need to get updated data. Need to separate by habitat. Needs data package citation. Data were downloaded from EDI (knb-lter-mcr.7.28). Data were aggregated across habitats and transects. Thus each of the six sites contains data from very different habitats lumped together (back, fringing, outer reefs) and there is likely very little overlap in the species found in each habitat. This is different than the other datasets, and it would be good to discuss whether or not to separate by habitat. 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. It's unclear whether these are mobile inverts, sessile inverts, or both (need to know for comparison with SBC).

2.3 mcr-fish

Updated data in ecocomdp format on EDI. Need to prepare it for this analysis. Need to separate by habitat. Needs data package citation. Data were downloaded from EDI (knb-lter-mcr.6.54). Data were aggregated across habitats and transects. Thus each of the six sites contains data from very different habitats lumped together (backreef, forereef, fringing) and there is likely very little overlap in the species found in each habitat. This is different than the other datasets, and it would be good to discuss whether or not to separate by habitat. Non-relevant taxa codes (e.g. "No fish present") were removed from the dataset. Abundance was recorded as dry biomass per 250 m^2, averaged across subplots, transects, and habitats for each species at each site in each year. Data are in Figure S6. Six extra locations in forereef habitats were sampled in 2015. These appear to be in addition to the four transects per habitat per site performed as part of the long term data collections, and thus they were removed from the dataset prior to analysis.

2.4 mcr-coral

Need to get updated data. Need to separate by habitat. Needs data package citation. Data were downloaded from EDI (Edmunds, 2018). The corals are identified to the genus level. Data were aggregated across habitats and transects. Thus each of the six sites contains data from very different habitats lumped together (back, fringing, outer reefs) and there is likely very little overlap in the species found in each habitat. This is different than the other datasets, and it would be good to discuss whether or not to separate by habitat. 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.

2.5 mcr-algae

Need to get updated data. Need to separate by habitat. Needs data package citation. Data were downloaded from EDI (Carpenter, 2015). Data were aggregated across habitats and transects. Thus each of the six sites contains data from very different habitats lumped together (back, fringing, outer reefs) and there is likely very little overlap in the species found in each habitat. This is different than the other datasets, and it would be good to discuss whether or not to separate by habitat. 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 S8. The cumulative number of taxa was still increasing at the end of the time series.

2.6 gce-mollusc

Data were downloaded from several EDI packages (approx. one per year of study). Data are in Figure S9.

3 Freshwater datasets

3.1 fce-diatoms

Data were obtained from the PI. Metadata and citation can be found on EDI (Gaiser, 2017). 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) 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 S10

3.2 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 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: 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 S11. Data from the wet season are shown in Figure S12.

3.3 ntl-zooplankton

The data were downloaded from the EDI Data Portal (Center for Limnology, 1983). Samples were taken via vertical tows at fortnightly intervals on a minimum of five occasions per year (range = 5 - 18 occasions per year). Density was recorded as number of individuals per liter for each taxa, integrated volumetrically over the water column. Many taxa are identified to species level, but some are identified to genus level. Lake 'Tr' was only sampled in one year and was assumed to be the same as lake 'TR'. The initial year (1981) was removed from analysis because only five of the seven sites were sampled. We additionally removed 165 records with missing or unknown taxa designations. Data were aggregated annually for each taxa in each lake by taking the maximum density observed in a tow sampling occasion. Data are shown in Figure S13.

3.4 ntl-fish

Data on fish abundance were downloaded from the EDI Data Portal (Magnuson et al., 2010). Seine net data from five northern lakes (Allequash, Big Muskellunge, Crystal, Sparkling, and Trout Lakes) were included (1981 - 2017). Data from the two bog lakes (Crystal Bog and Trout Bog) were not included. Catch per unit effort (CPUE) was calculated for each species in each lake per year as the total catch divided by the total effort. Data are shown in Figure S14.

4 Terrestrial datasets

4.1 cdr-plants

Data were downloaded from EDI (Tilman, 2018). Annual censuses are incomplete after 2004, so we only consider data until 2004. We used data from control plots only, from all four sites (A, B, C, and D). Fields A, B, and C were considered together as a single dataset, while D was considered a separate datasets because of its unique fire history. We cleaned taxonomic data by cleaning clear mistakes (such as 'carex sp.' instead of 'Carex sp.'), removed non-taxonomic entities ("Miscellaneous litter") and non-plant taxa ('Fungi', and 'Mosses & lichens'). We lumped taxonomic information to the genus level when more than 1% (more than a proportion of 0.01) 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 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 S15 and S16.

4.2 hays-plants

Data were downloaded from Ecological Archives (Adler et al., 2007). We removed unknown species, species categorized as 'short grass' and '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 the genera more than 95% of individuals were identified at the species level. Second, we 'lumped' to genus level, species belonging to the general *Allium*, *Chamaesyce*, *Opuntia*, *Polygala*. In these genera, more than 5% of counts were identified at the genus level. Finally, we only retained the 14 plots with continuous replication between 1938 and 1973. Data are shown in Figure S17.

4.3 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 plots (plot number 3) that contains four new transect (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 S18.

4.4 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 S19.

4.5 sgs-plants

Data were downloaded from EDI knb-lter-sgs.527.1. Data are shown in Figure S20.

4.6 sev-arthropods

Data provenance needed. Data could be could from: Lightfoot, D. 2013. Ground Arthropod Community Survey in Grassland, Shrubland, and Woodland at the Sevilleta National Wildlife Refuge, New Mexico (1992-2004) ver 175390. Environmental Data Initiative. https://doi.org/10.6073/pasta/9e7e6dc9c9d8f (Accessed 2023-04-19). Data are shown in Figure S21.

4.7 sev-grasshoppers

The data 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 replication 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 S22.

4.8 cdr-grasshoppers

Data were accessed on EDI (Knops, 2018). 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 documentation 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 it Tetrix, as too high a proportion of individuals from these genera were not identified at the species level. Similarly, some individuals belonging to the *Melanoplus* genus were identified at the genus level only. We removed these records, as they comprised only 6% of the entire counts in the *Melanoplus* genus. Data are shown in Figure S23.

4.9 knz-grasshoppers

Data on grasshopper abundance (1996-2015) were downloaded from EDI (Joern, 2018). 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 average count data across a year, because some spatial replicates could occasionally contain more observations within a year. Data are shown in Figure S24.

4.10 luq-snails

Data were downloaded 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. Data are shown in Figure S25.

4.11 jrn-lizards

The data were downloaded from the EDI Data Portal (Whitford et al., 1991). 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 are shown in Figure S26.

4.12 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 plots within 3 transects per site. Each site represents the reach level (each reach level 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 S27.

4.13 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 are shown in Figure S28.

4.14 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 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 S29.

4.15 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. Data are shown in (Figure S30).

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Table S1: Data sets.

	dataset	initial.year	study.length	n.years	n.plots	n.taxa	organism
1	and-birds-wisnoski	2009	5	5	184	81	birds
3	bes-birds-nilon	2005	5	5	52	33	birds
4	cap-birds-banville	2001	16	16	35	104	birds
5	cap-herps-banville	2013	5	5	7	18	herps
6	cdr-grasshopper-compagnoni	1989	18	18	19	51	grasshopper
7	cdr-plantsABC-compagnoni	1982	23	23	18	128	plantsABC
8	cdr-plantsD-compagnoni	1982	23	23	5	128	plantsD
9	fce-diatoms-catano	2005	7	7	30	192	diatoms
10	fce-fish-rehageDry	2006	12	11	10	56	fish
11	fce-fish-rehageWet	2011	6	6	14	56	fish
12	gce-mollusc-compagnoni	2000	14	14	18	13	mollusc
13	hays-plants-compagnoni	1938	35	35	14	140	plants
14	jrn-lizards-hope	1990	16	16	9	18	lizards
16	knz-grasshopper-compagnoni	1996	20	19	13	43	grasshopper
17	luq-snails-compagnoni	1991	27	27	40	19	snails
18	mcr-algae-castorani	2006	10	10	6	73	algae
19	mcr-coral-castorani	2005	11	11	6	31	coral
20	mcr-fish-castorani	2006	10	10	6	376	fish
21	mcr-inverts-castorani	2005	11	11	6	13	inverts
22	ntl-fish-stanleyLottig	1981	37	37	5	47	fish
23	ntl-zooplankton-stanleyLottig	1982	34	34	7	143	zooplankton
24	sbc-algae-castorani	2001	18	18	9	59	algae
25	sbc-fish-castorani	2001	18	18	9	64	fish
26	sbc-mobileInverts-castorani	2001	18	18	9	34	mobileInverts
27	sbc-sessileInverts-castorani	2001	18	18	9	71	sessileInverts
28	sev-arthropods-compagnoni	1992	13	13	10	316	arthropods
29	sev-grasshopper-compagnoni	1992	22	22	10	54	grasshopper
30	sev-plants-compagnoni	2003	13	13	8	157	plants
31	sgs-plants-catano	1999	8	8	6	84	plants
32	sgs-plants-compagnoni	1995	14	14	6	58	plants
33	usvi-coral-castorani	1992	24	24	6	34	coral

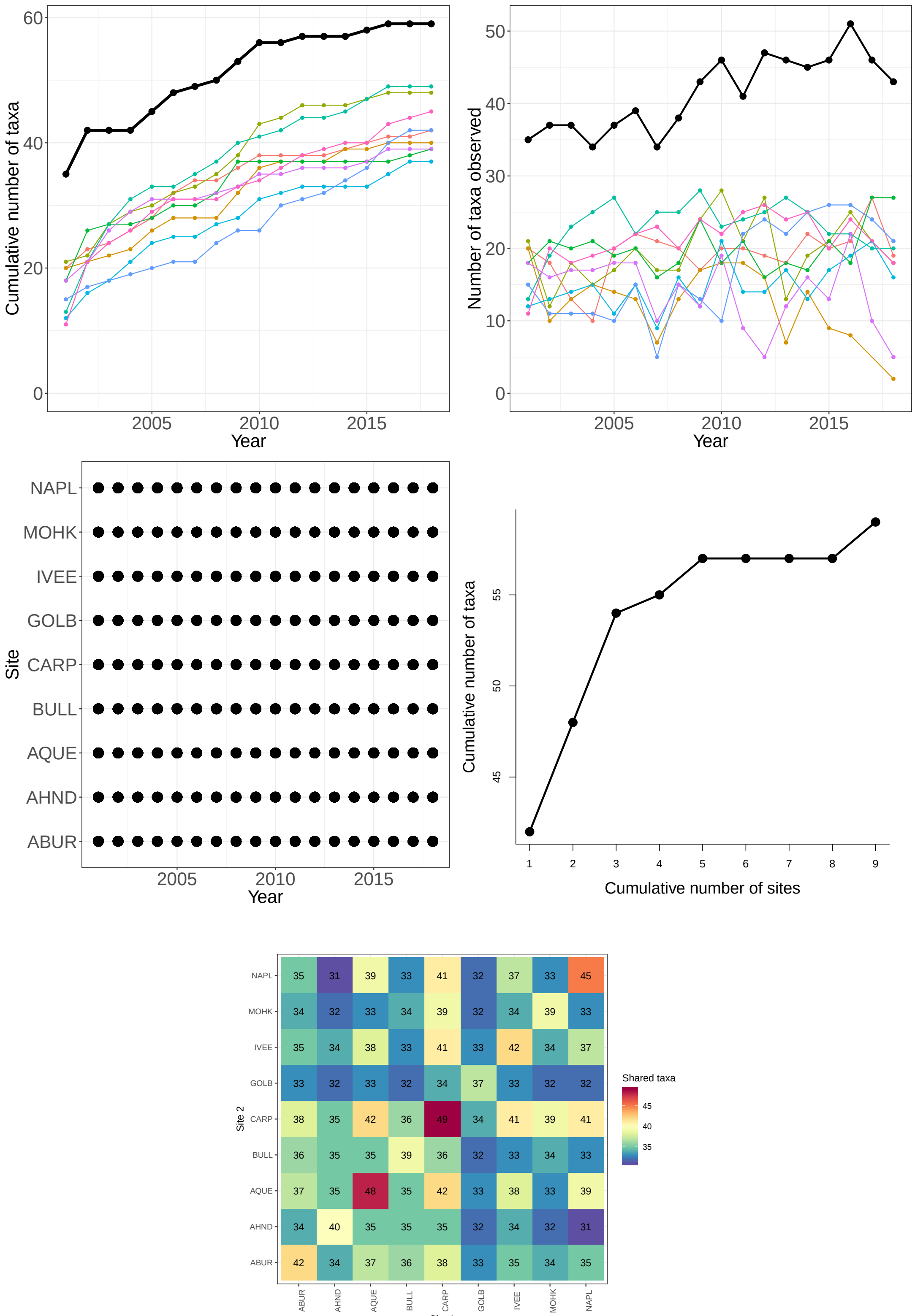

Figure S1: **SBC-algae:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for algae taxa observed in the Santa Barbara Channel LTER (2001-2016). The black lines represent total site-level values across all plots.

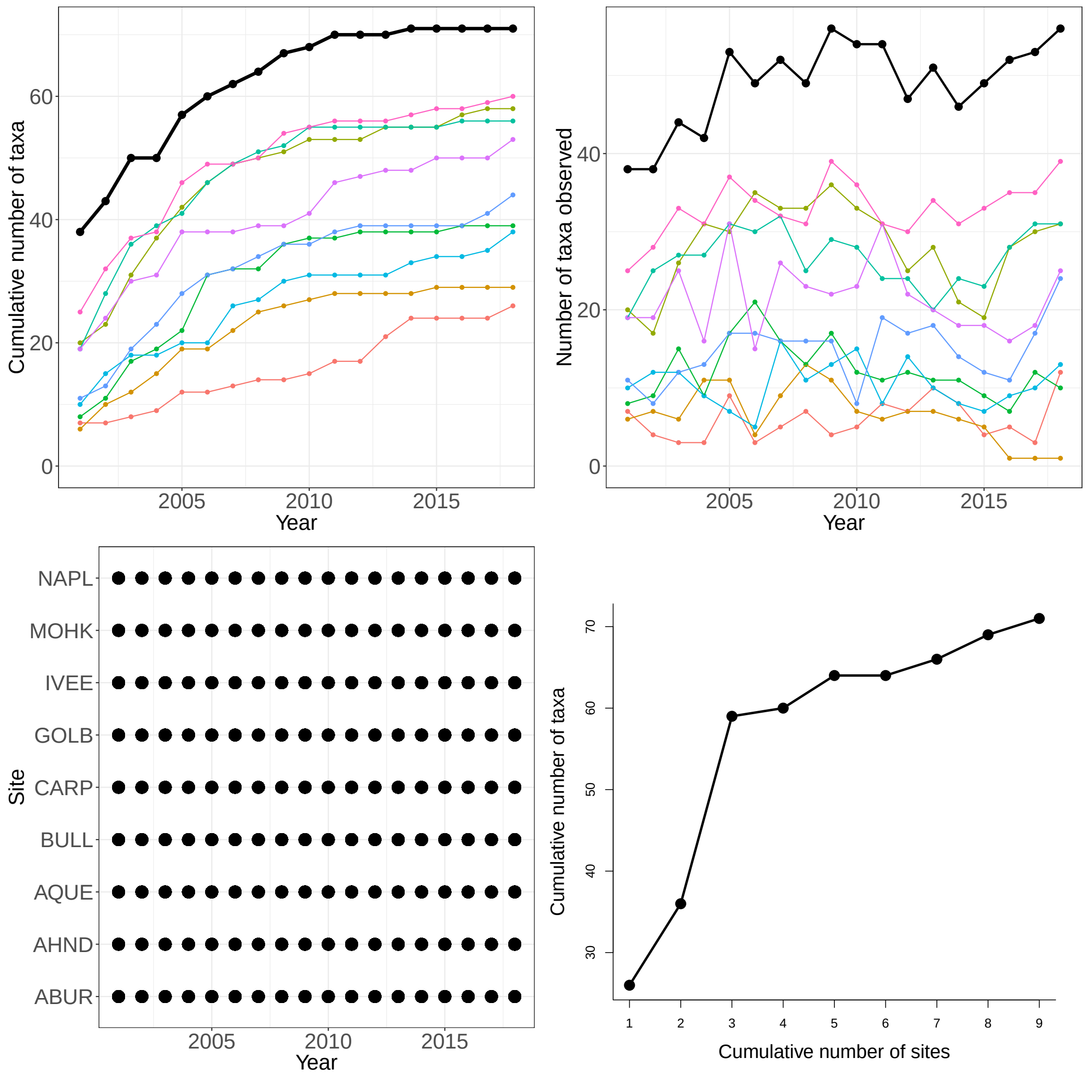

Figure S2: **SBC-sessile invertebrates:** Species accumulation curves (top left), annual richness (top right), sampling effort (bottom left), and number of shared species (bottom right) for sessile invertebrate taxa observed in the Santa Barbara Channel LTER (2001-2016). The black lines represent total site-level values across all plots.

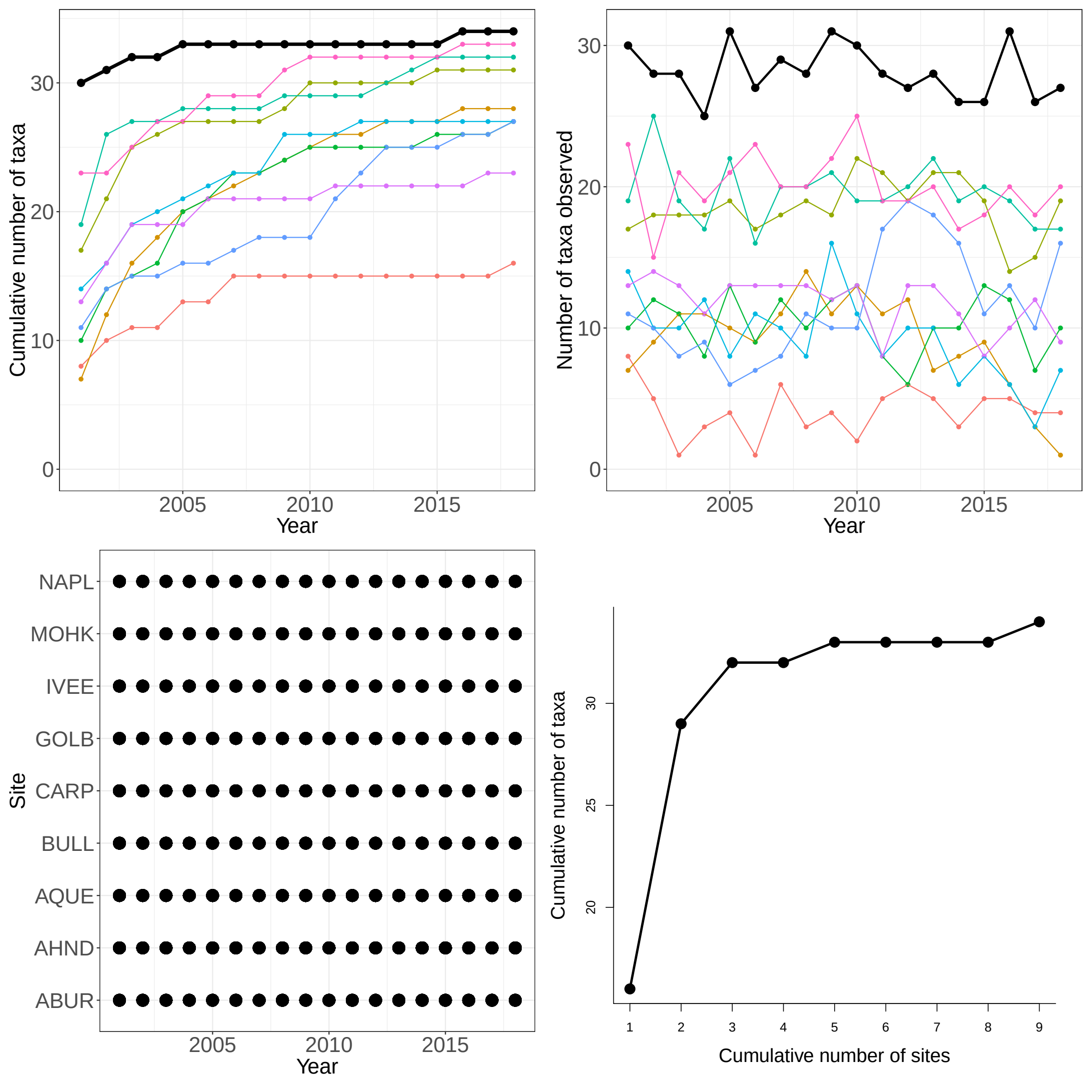

Figure S3: **SBC-mobile invertebrates:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for mobile invertebrate taxa observed at the Santa Barbara Channel LTER (2001-2016). The black lines represent total site-level values across all plots.

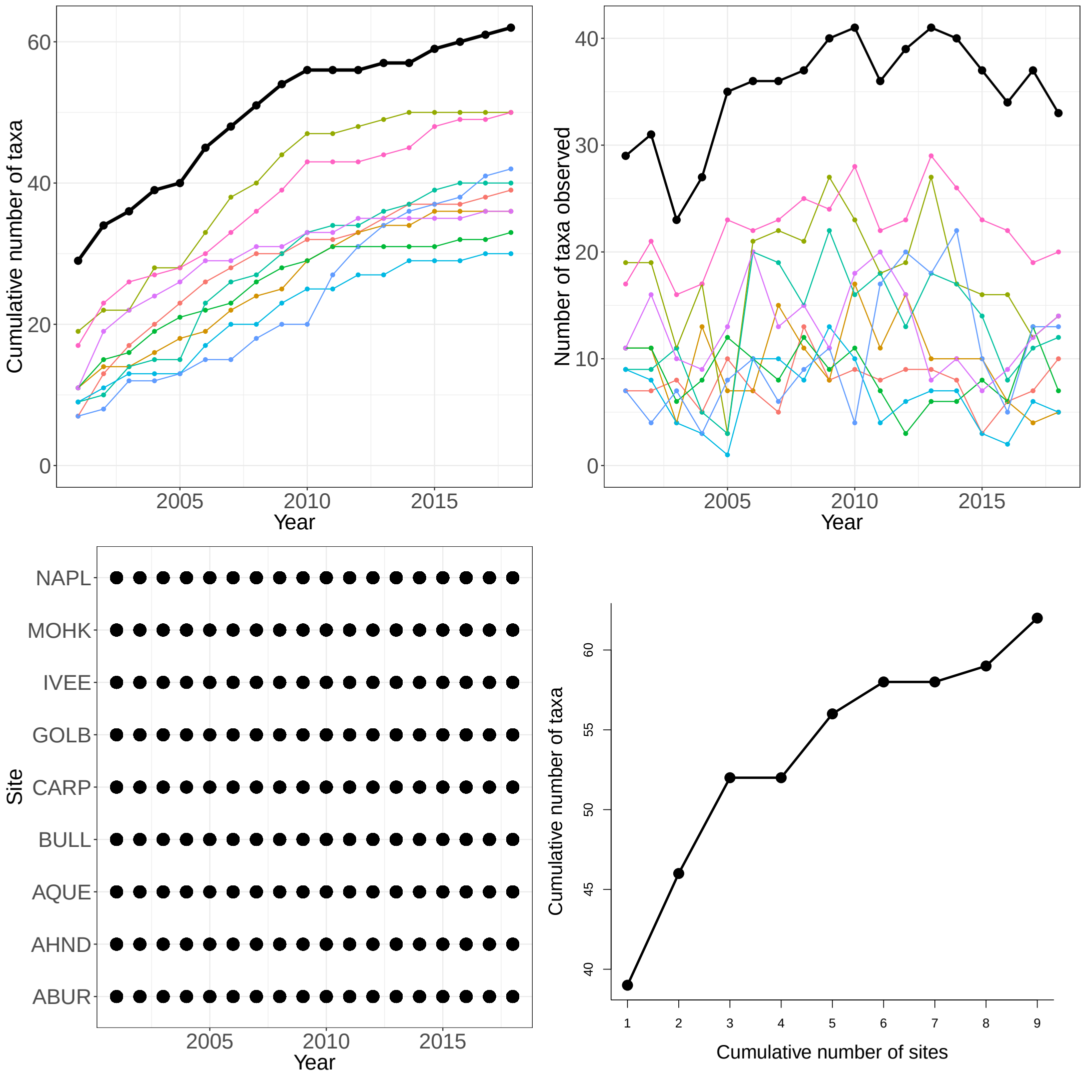

Figure S4: **SBC-fish:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) observed at the Santa Barbara Channel LTER (2001-2016). The black lines represent total site-level values across all plots.

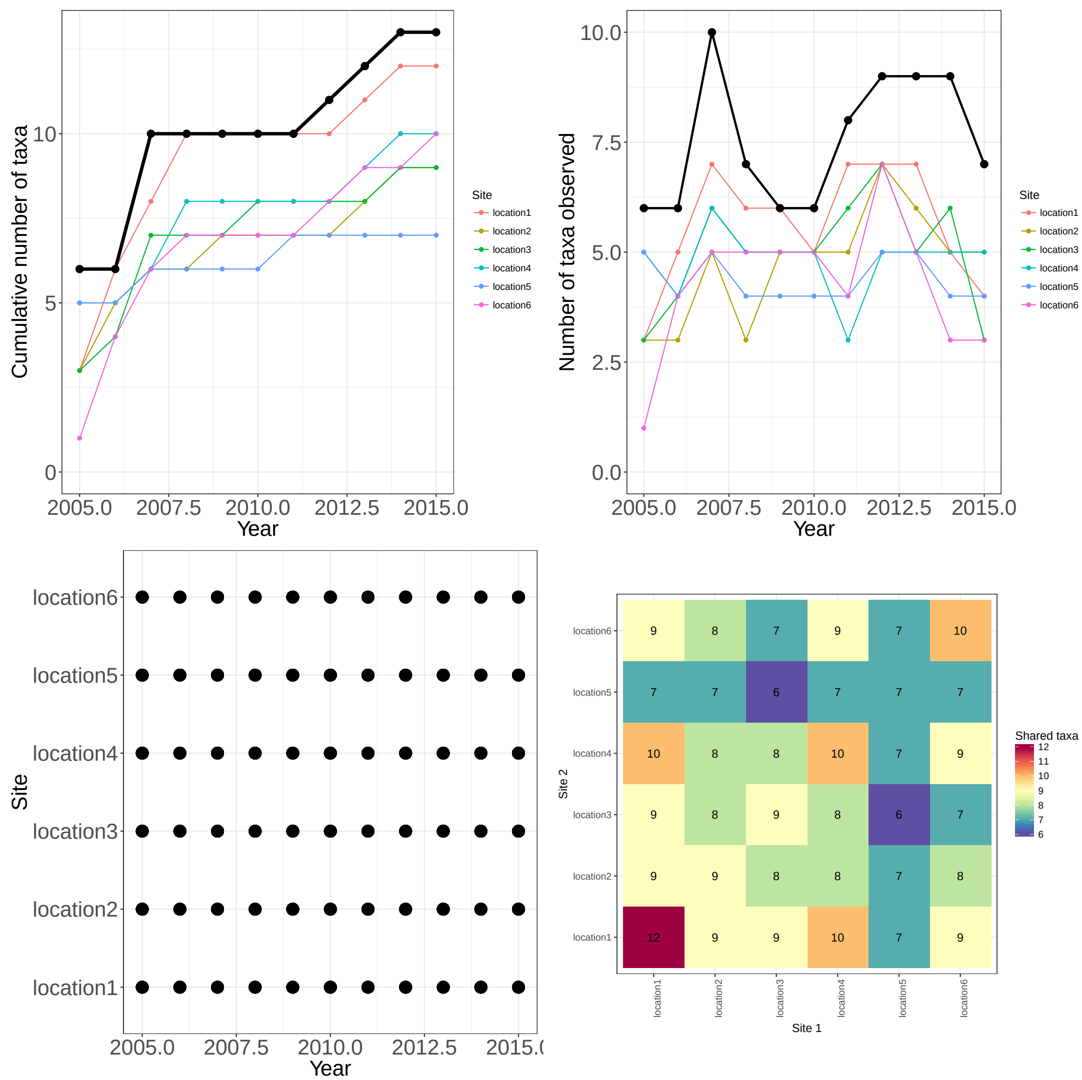

Figure S5: **MCR-inverts:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for invertebrate taxa observed on Moorea coral reef LTER (2006-2015). The black lines represent total site-level values across all plots.

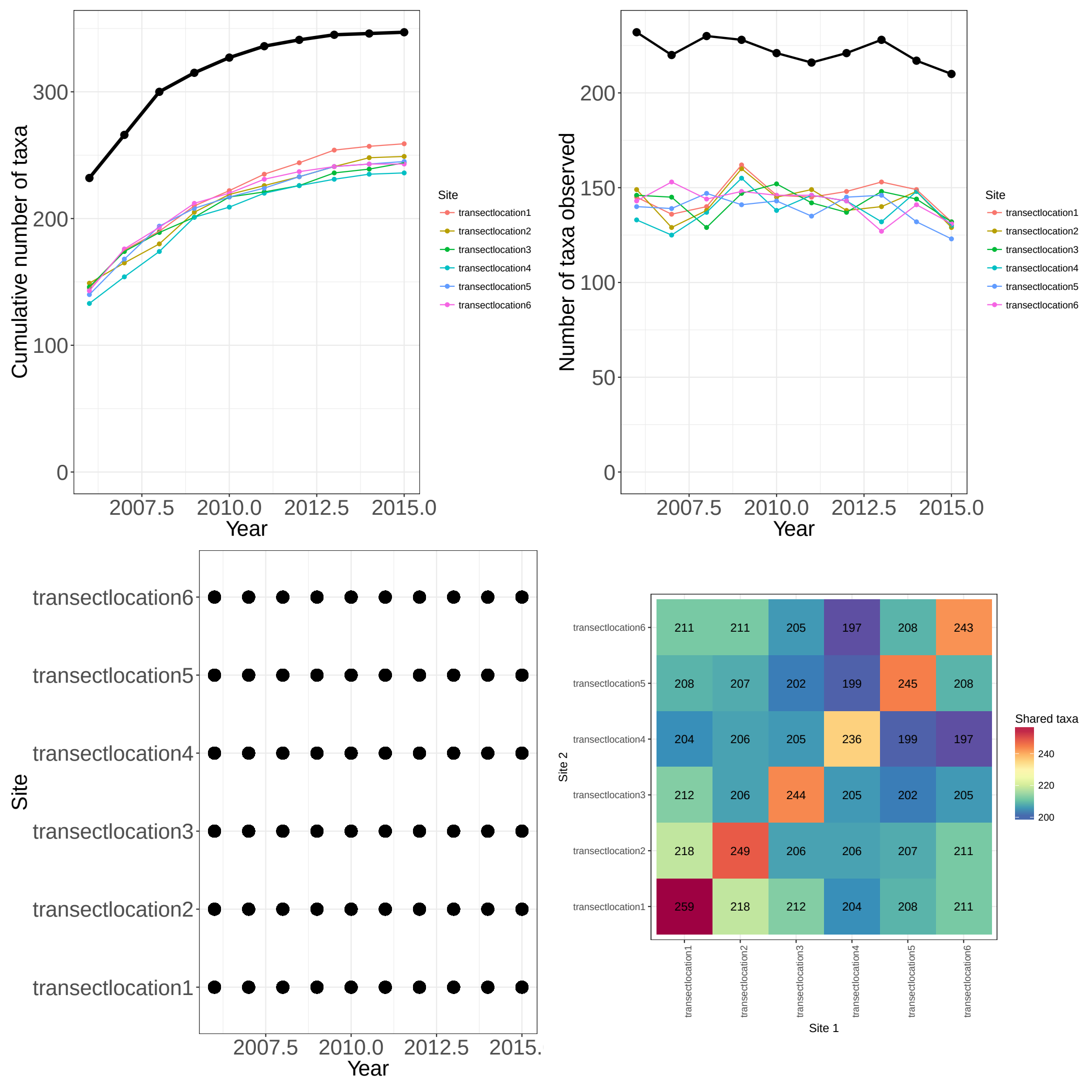

Figure S6: **MCR-fish:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for fish taxa observed on Moorea coral reef LTER (2006-2015). The black lines represent total site-level values across all plots.

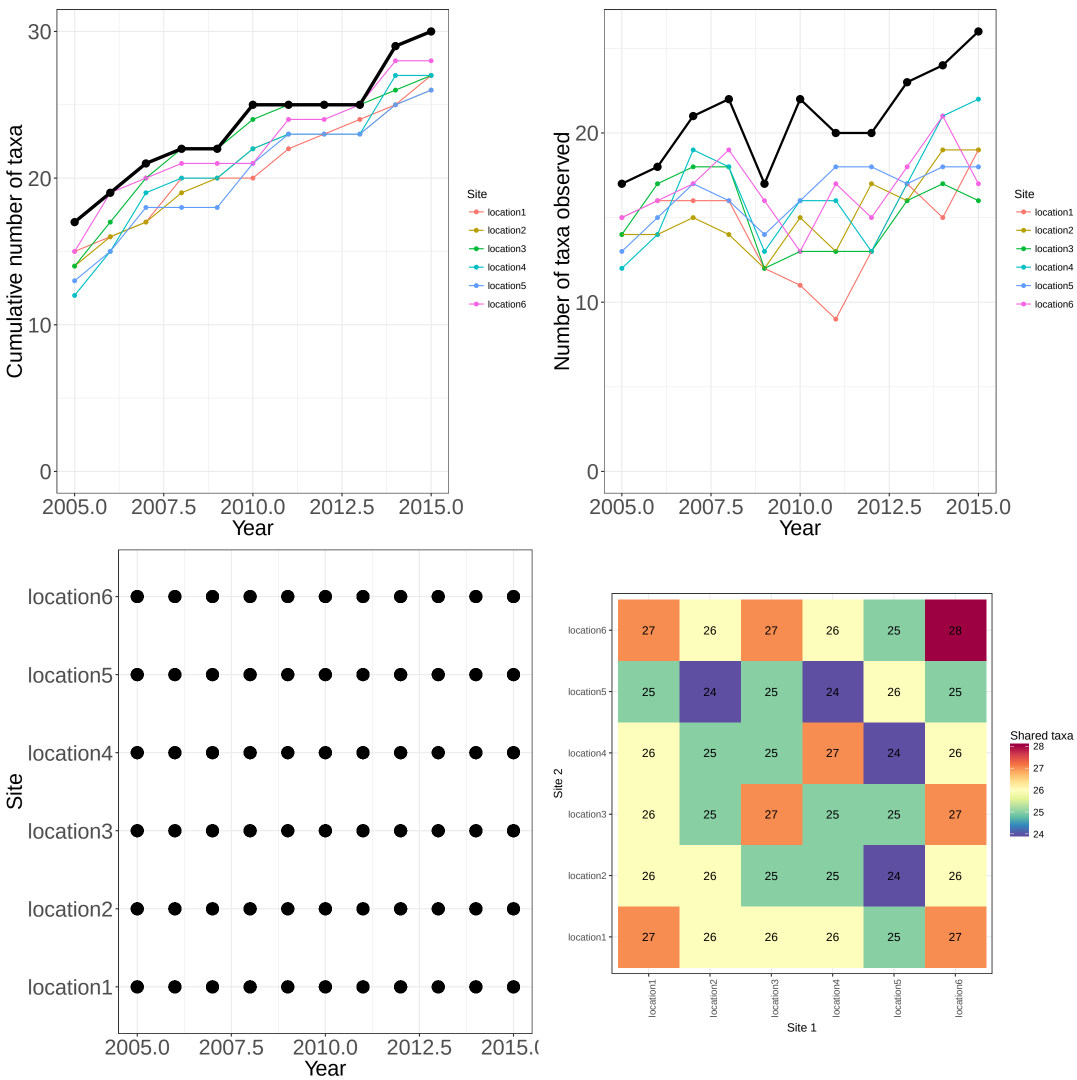

Figure S7: **MCR-coral:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for 31 coral taxa observed at six sites on Moorea coral reef LTER (2006-2015). The black lines represent total site-level values across all plots.

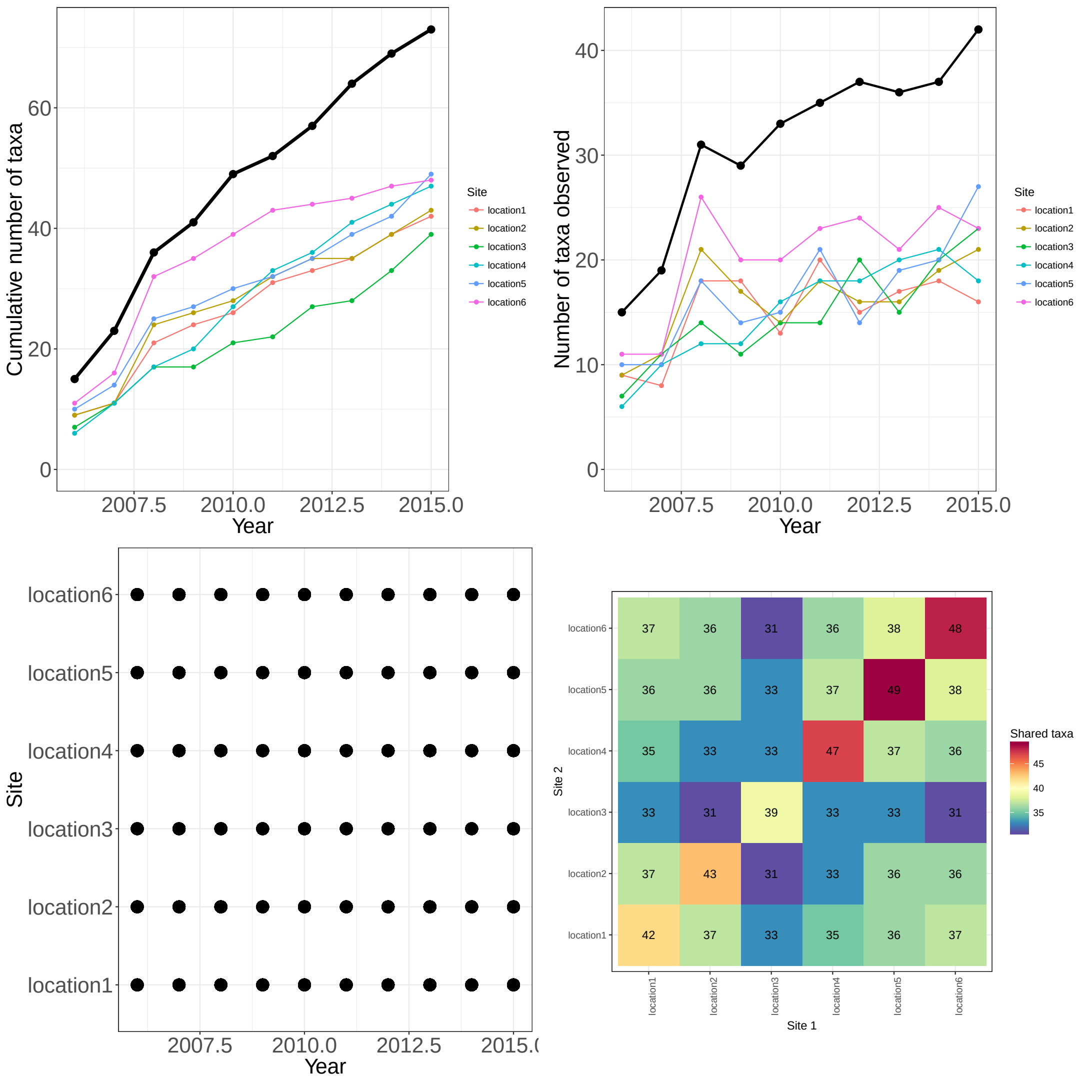

Figure S8: **MCR-algae:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for 73 algae taxa observed at six sites on Moorea coral reef LTER (2006-2015). The black lines represent total site-level values across all plots.

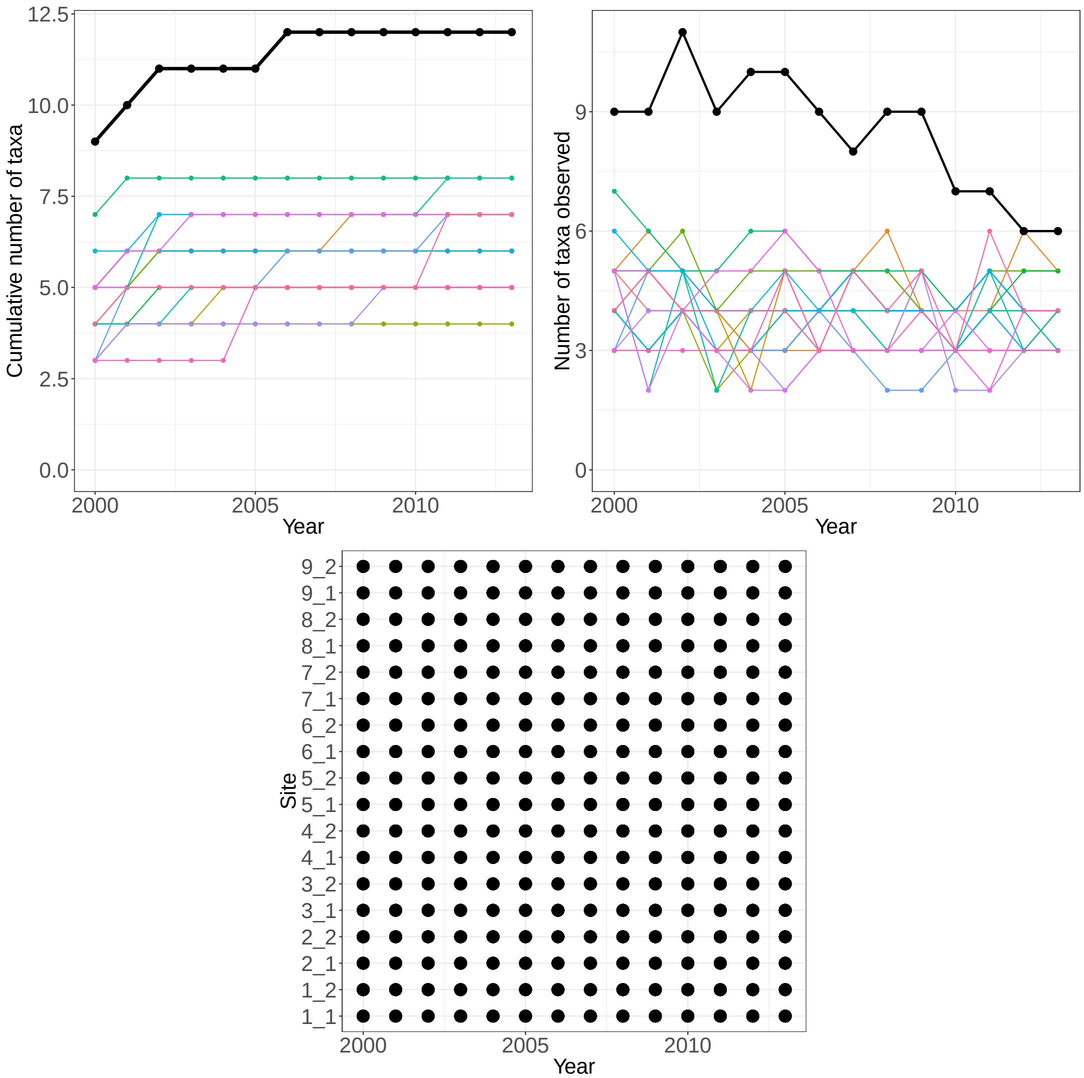

Figure S9: **GCE-mollusc:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for mollusc taxa observed at Georgia Coastal Ecosystems LTER. The black lines represent total site-level values across all plots.

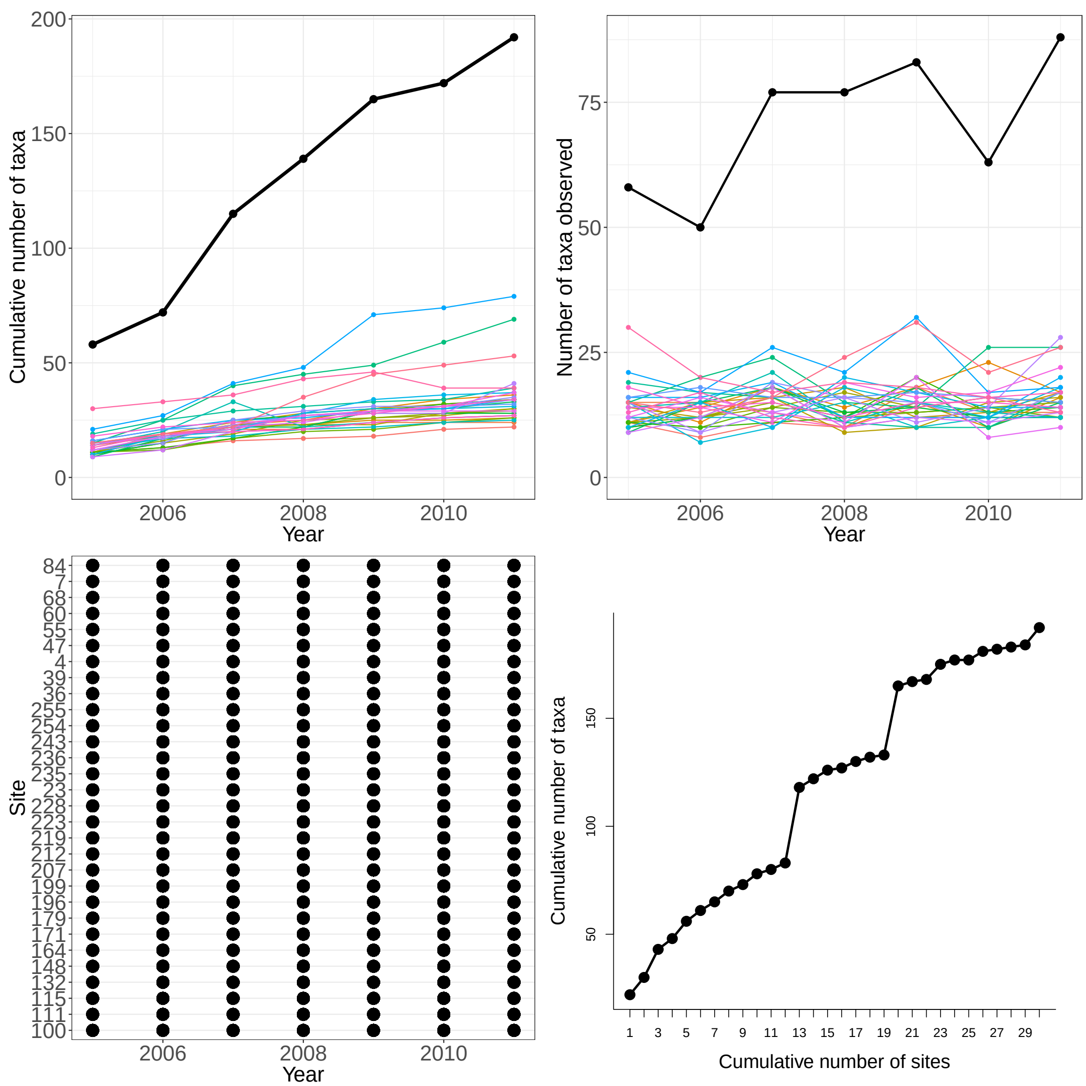

Figure S10: **FCE-diatoms:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for diatom taxa observed at Florida Coastal Everglades LTER. The black lines represent total site-level values across all plots.

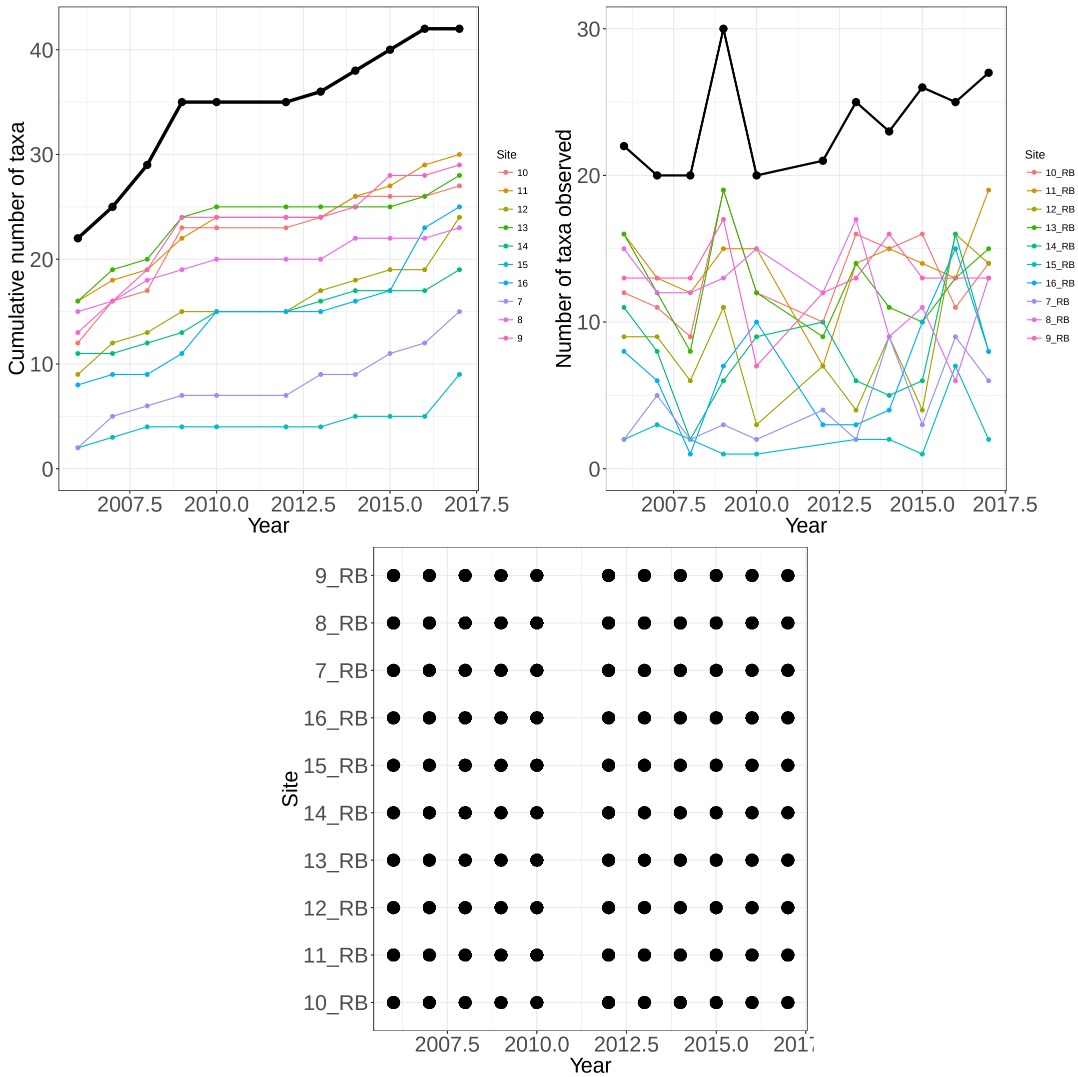

Figure S11: **FCE-fish dry season:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for fish taxa observed at the Florida Coastal Everglades . The black lines represent total site-level values across all plots.

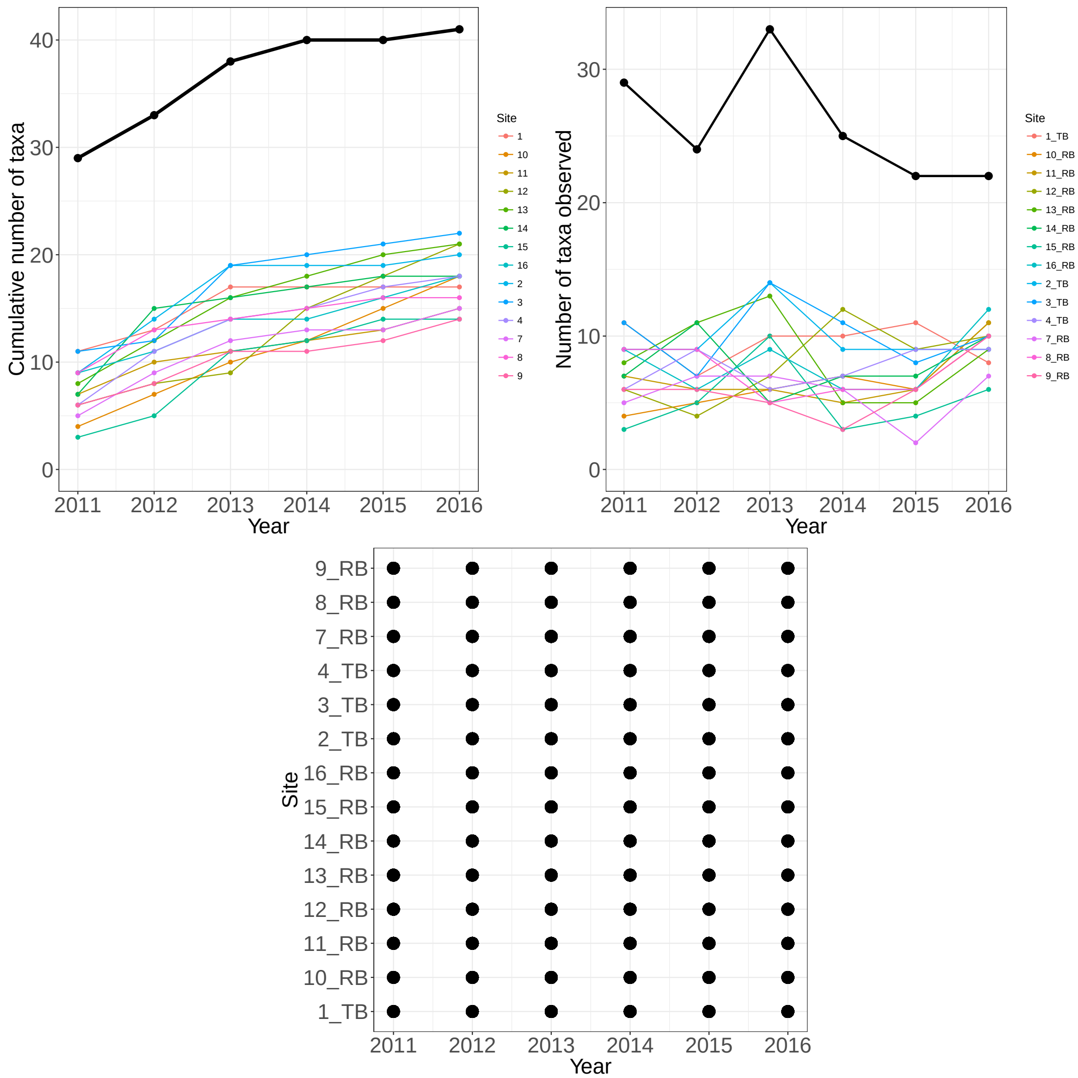

Figure S12: **FCE-fish wet season:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for fish taxa observed at the Florida Coastal Everglades . The black lines represent total site-level values across all plots.

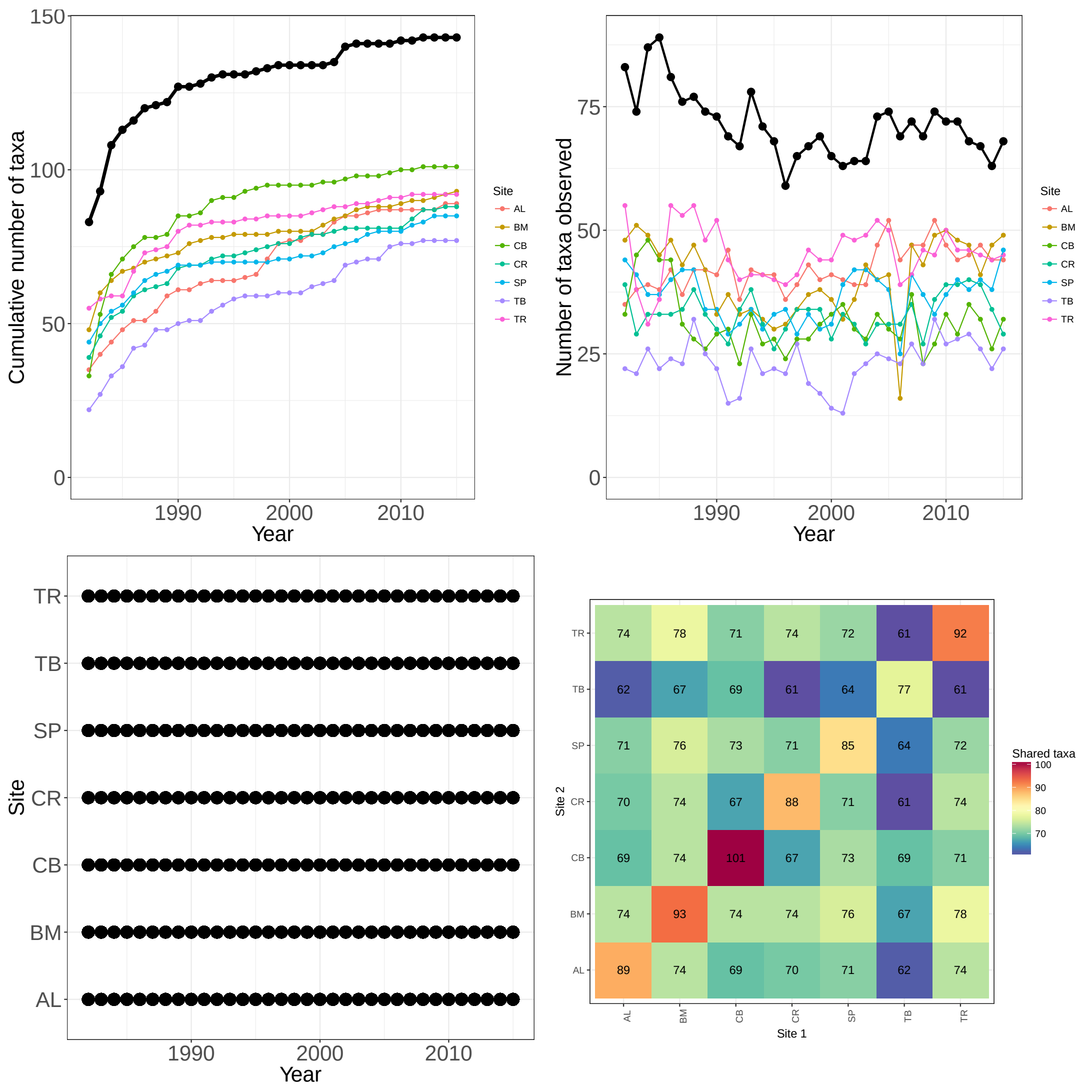

Figure S13: **NTL-zooplankton:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for 143 zooplankton taxa observed at 7 sites North Temperate Lakes LTER . The black lines represent total site-level values across all plots. The plot of the species accumulation curve failed because one site was sampled in only one year, and will be fixed once that site is removed.

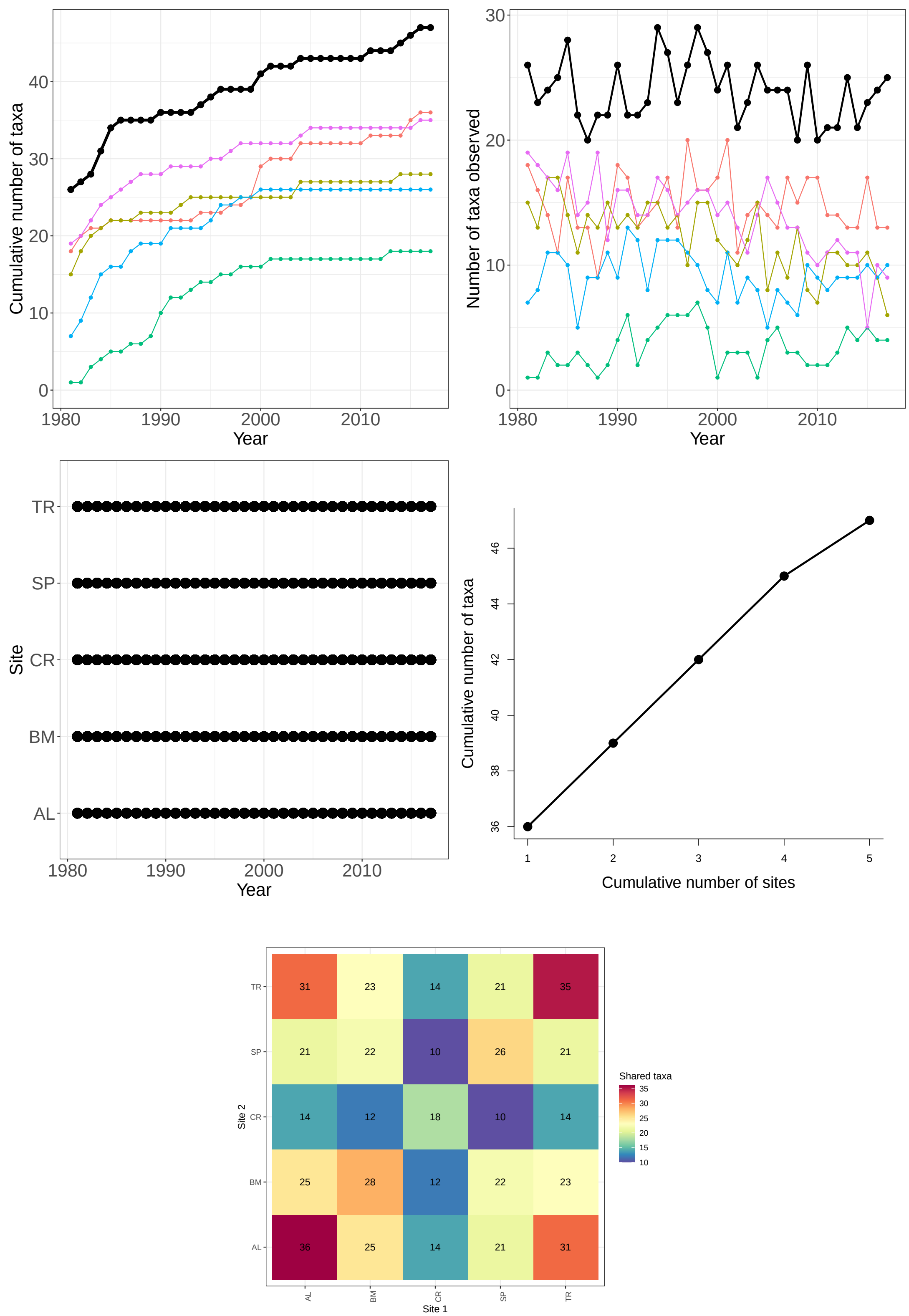

Figure S14: **NTL-fish:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for fish taxa observed at 5 lakes in the North Temperate Lakes LTER (1981 - 2017). The black lines represent total site-level values across all plots.

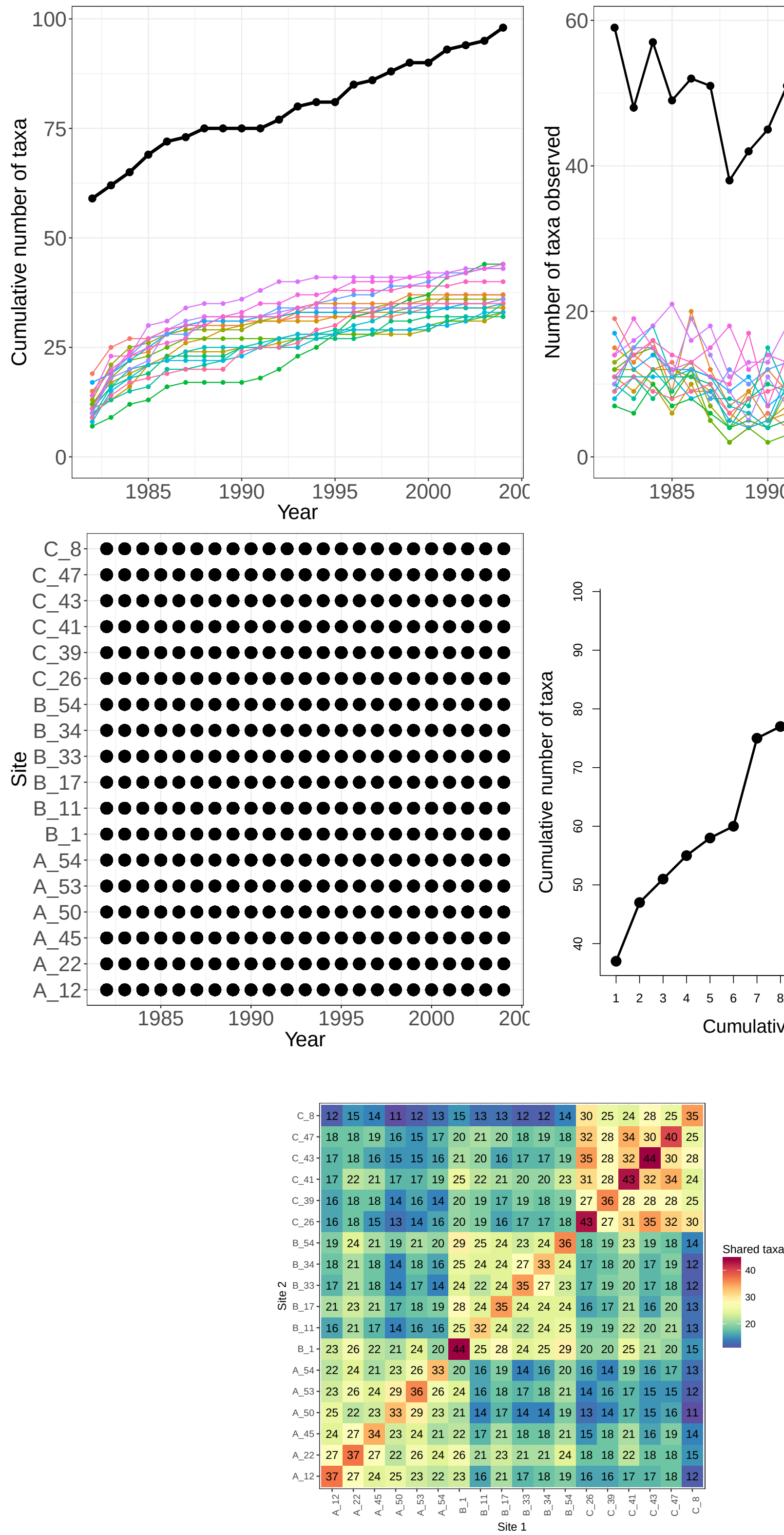

Figure S15: **CDR-plants, A, B, and C fields:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for plant species observed in the A, B, and C fields at Cedar Creek. The black lines represent total site-level values across all plots.

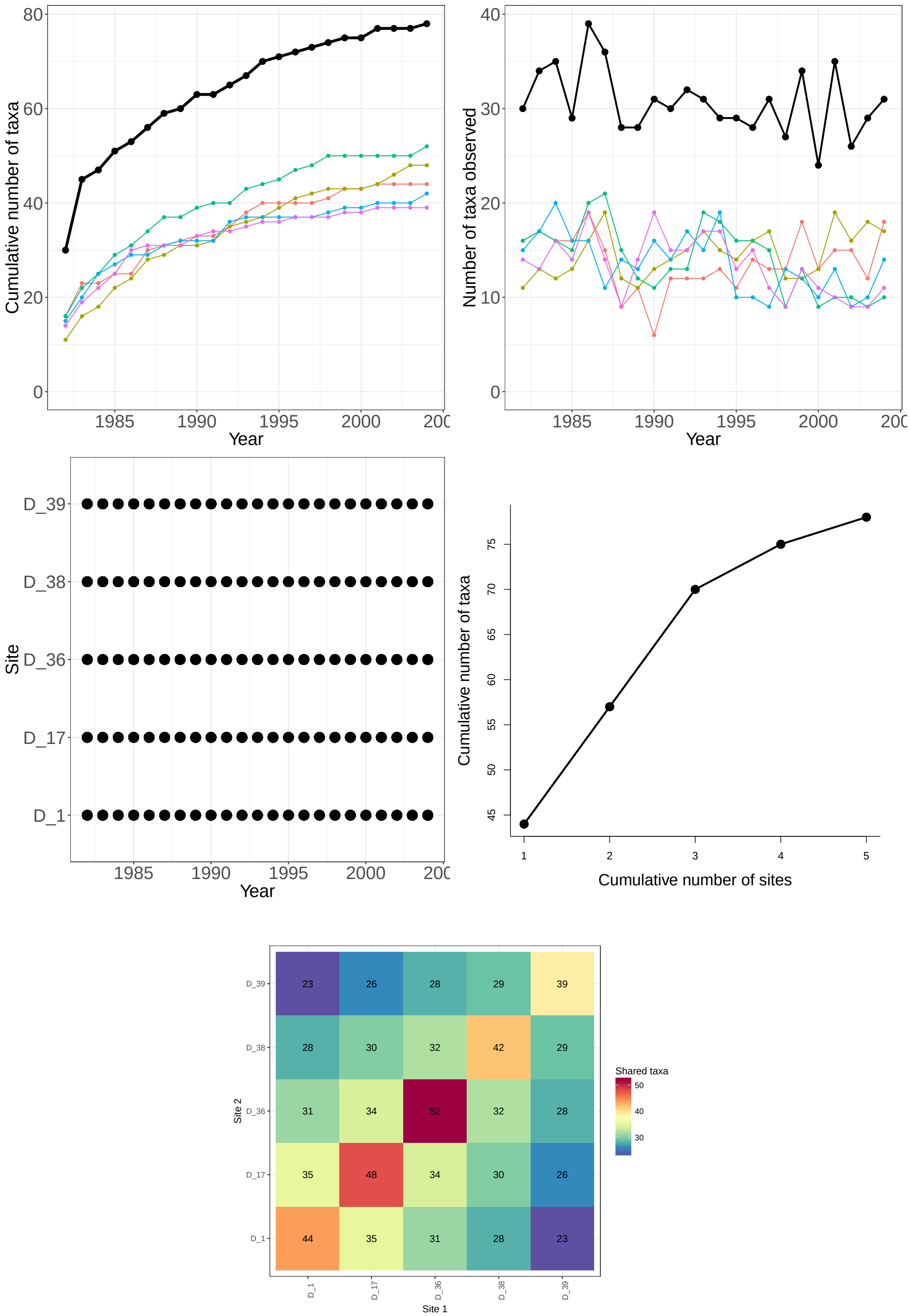

Figure S16: **CDR-plants, D field:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for plant species observed in the D field at Cedar Creek. The black lines represent total site-level values across all plots.

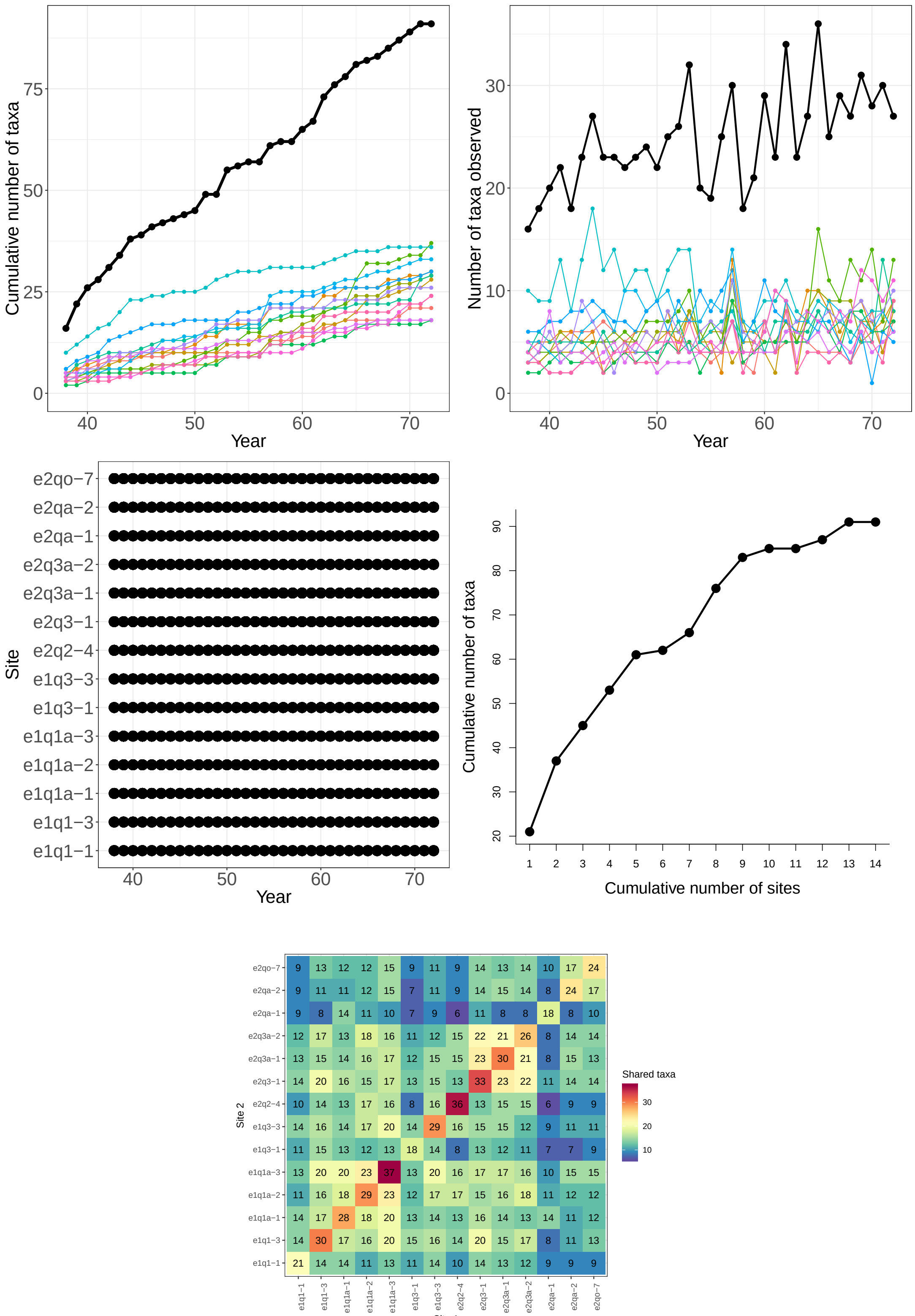

Figure S17: **hays-plants:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for mixed-grass prarie plant species observed at long-term monitoring plots in Hays, Kansas. The black lines represent total site-level values across all plots.

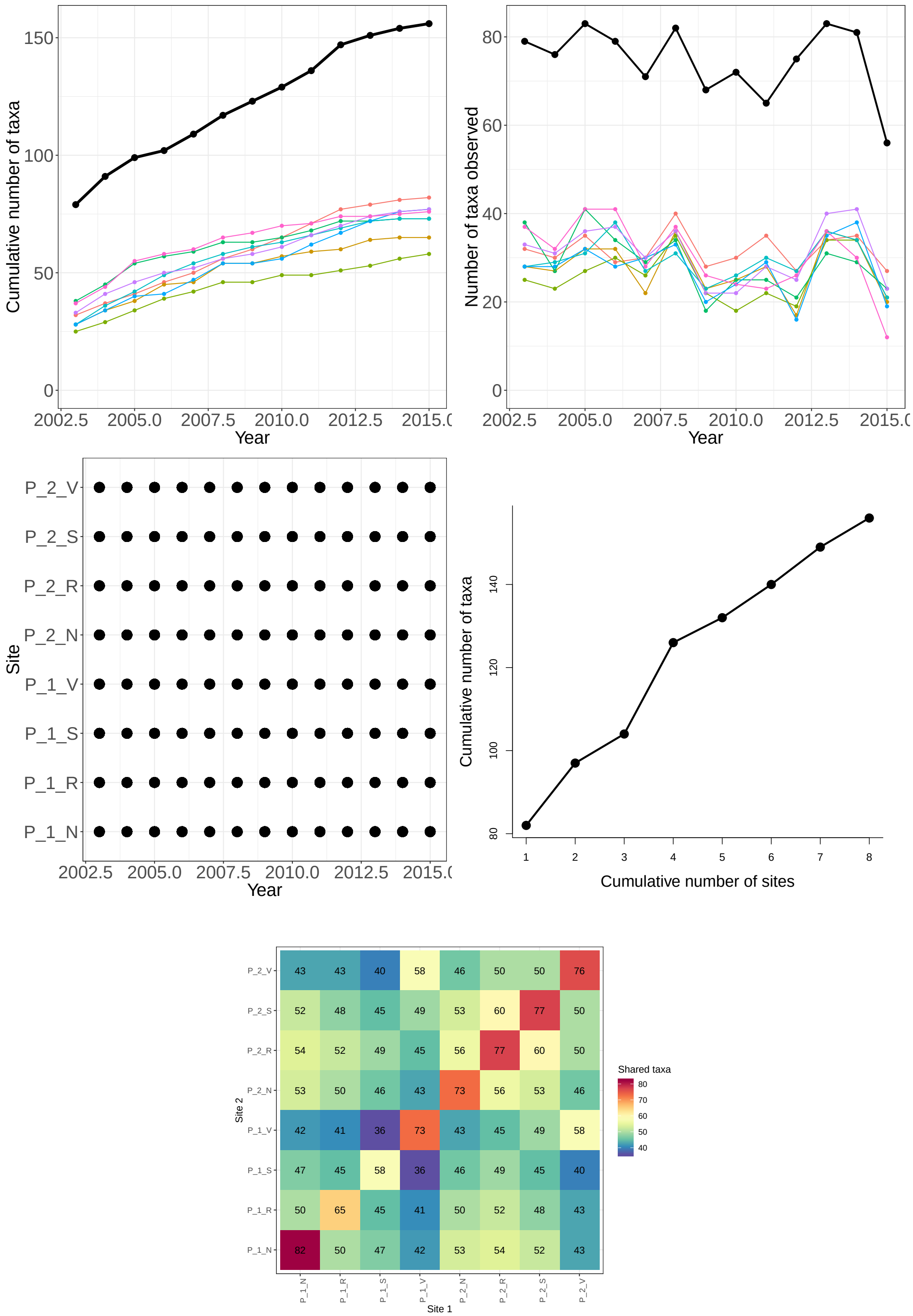

Figure S18: **SEV-plants:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for plant species observed in the Pinon-Juniper habitat at the Sevilleta (SEV) LTER. The black lines represent total site-level values across all plots.

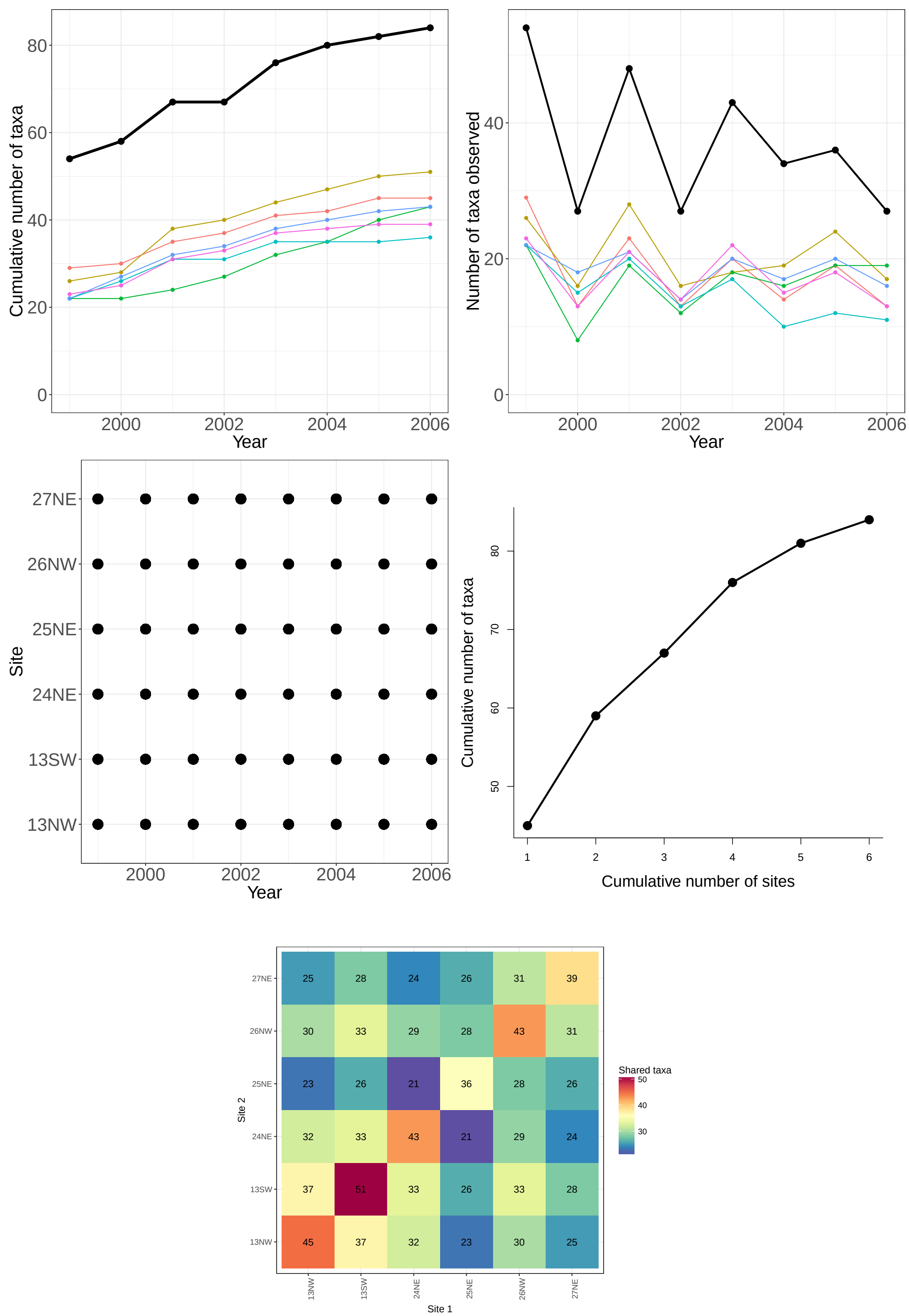

Figure S19: **SGS-plants:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for plant species observed at the Shortgrass Steppe (SGS) LTER. The black lines represent total site-level values across all plots.

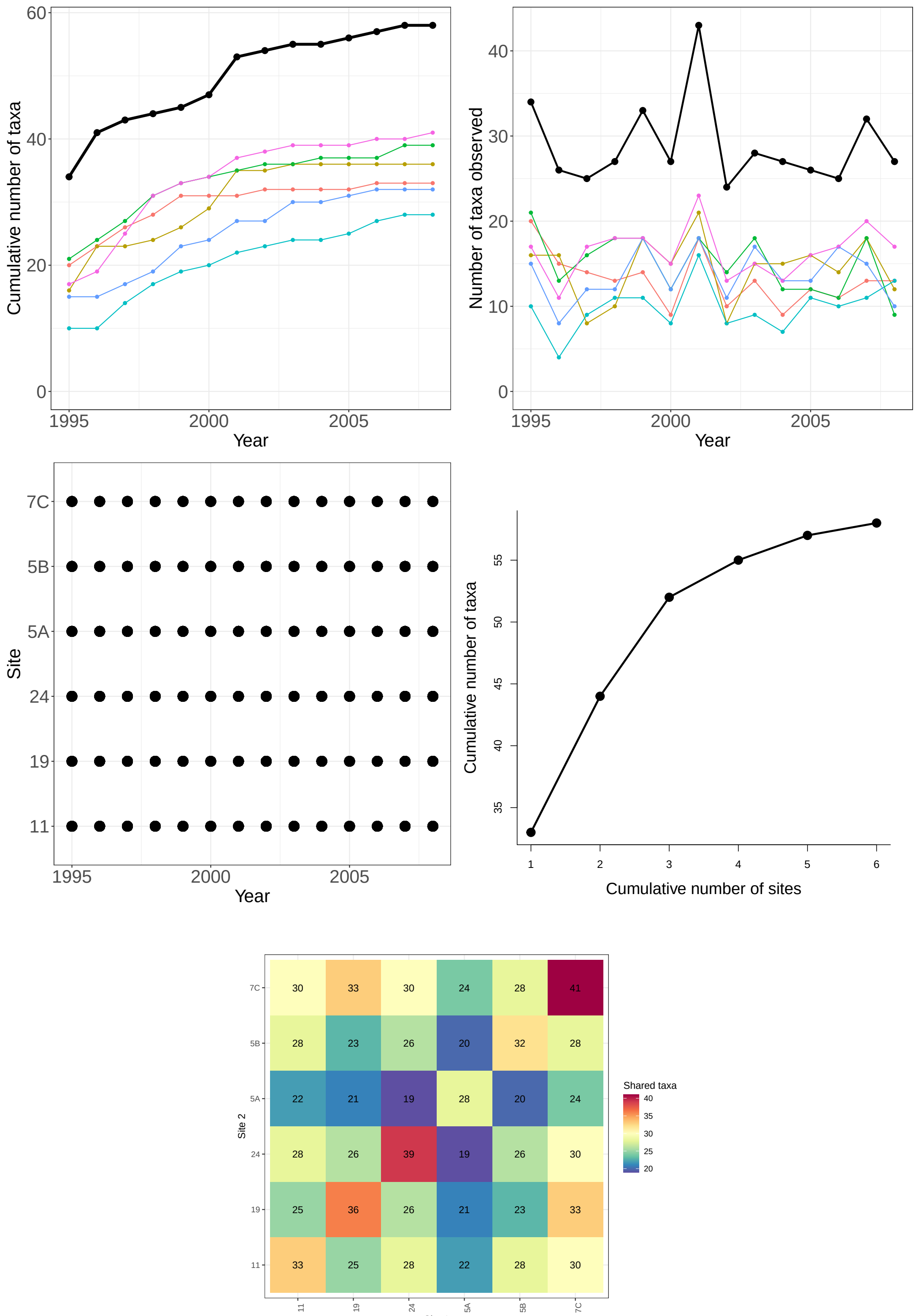

Figure S20: **SGS-plants:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for plant species observed at the Shortgrass Steppe (SGS) LTER. The black lines represent total site-level values across all plots.

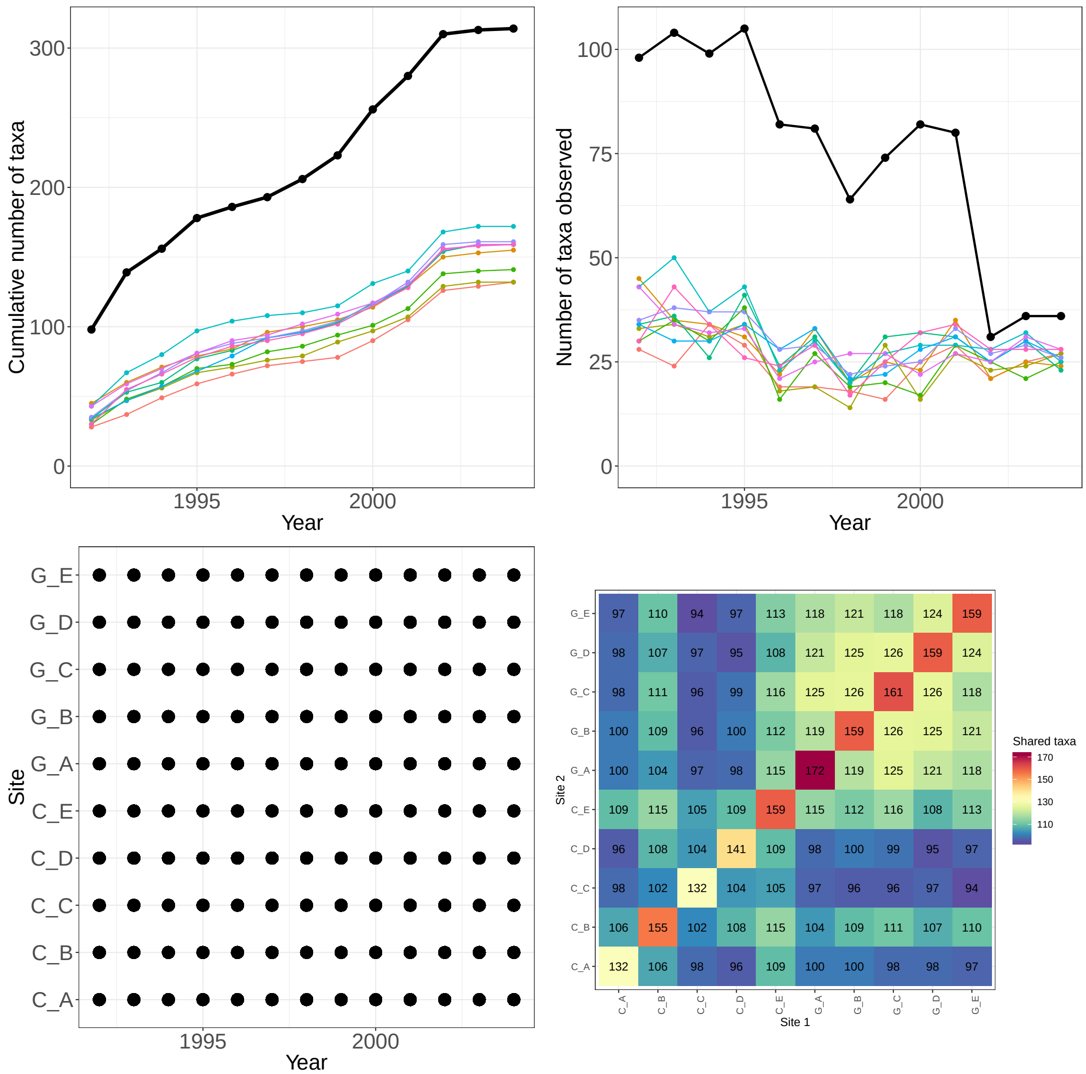

Figure S21: **SEV-arthropods:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for arthropod species observed in the Sevilleta LTER. The black lines represent total site-level values across all plots.

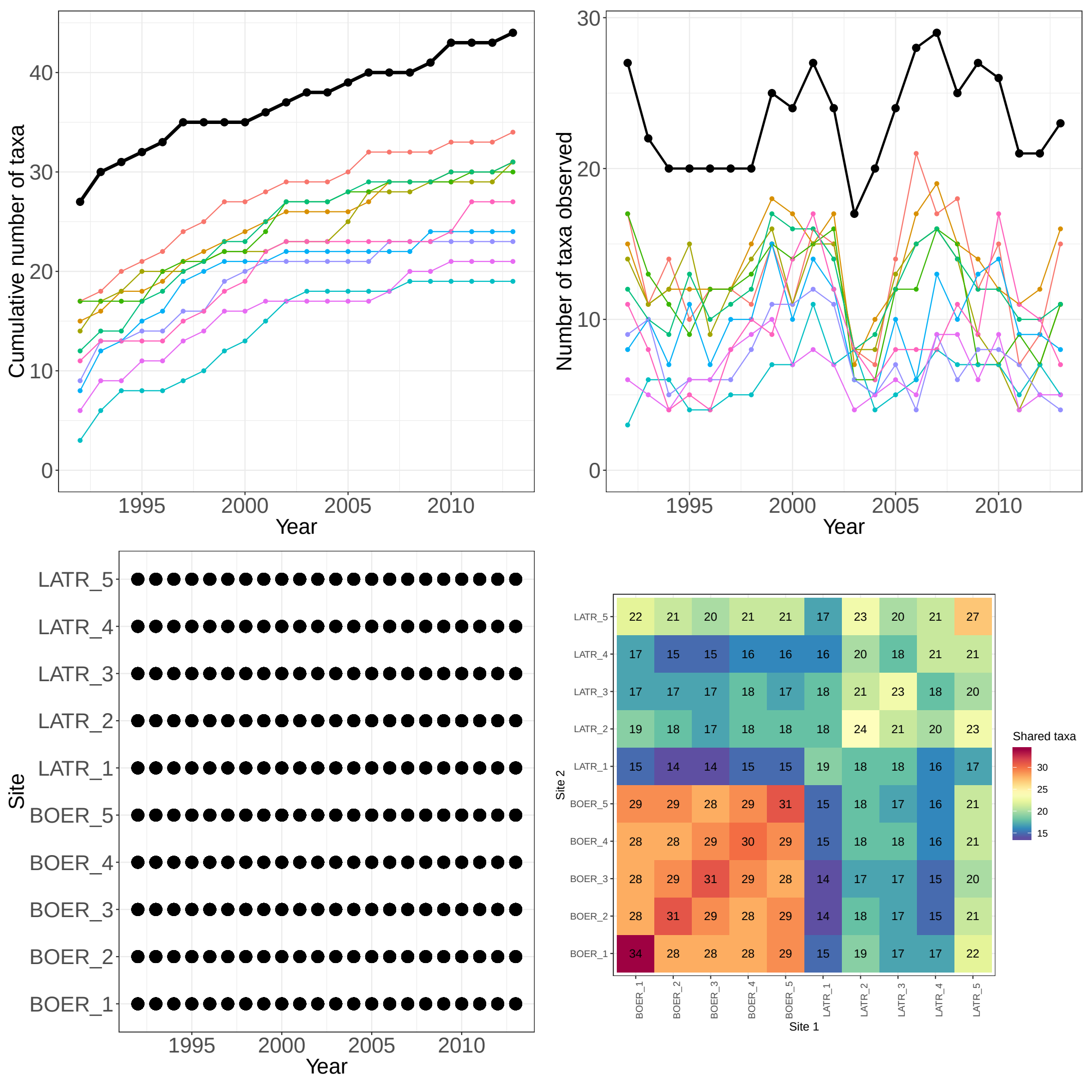

Figure S22: **SEV-grasshoppers:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for grasshopper species observed in Black grama (BOER) and Creosotebush (LATR) habitats the Sevilleta LTER (1992-2013). The black lines represent total site-level values across all plots.

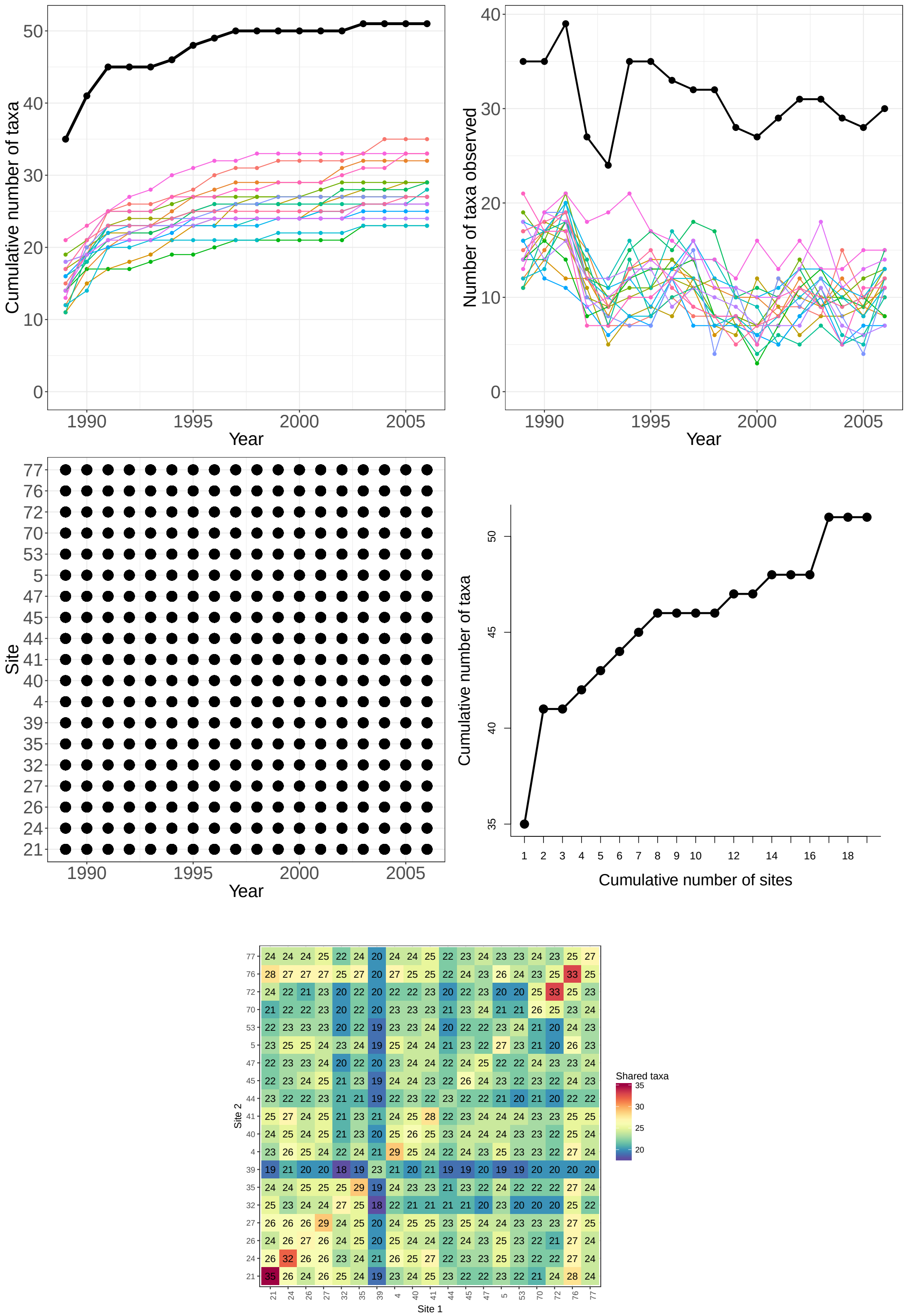

Figure S23: **CDR-grasshoppers:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for grasshopper species observed at the Cedar Creek LTER. The black lines represent total site-level values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

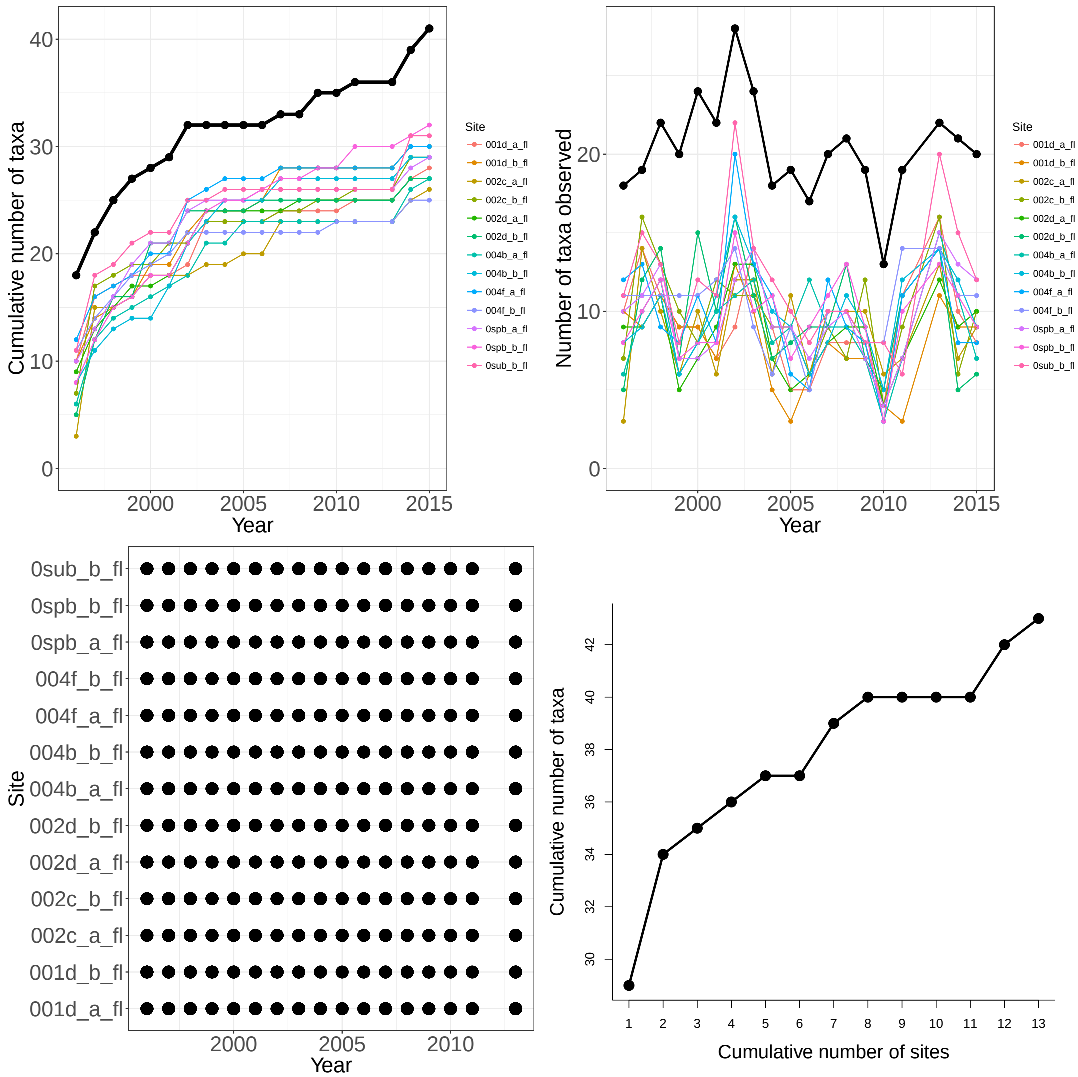

Figure S24: **KNZ-grasshoppers:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for grasshopper species observed in ... The black lines represent total site-level values across all plots.

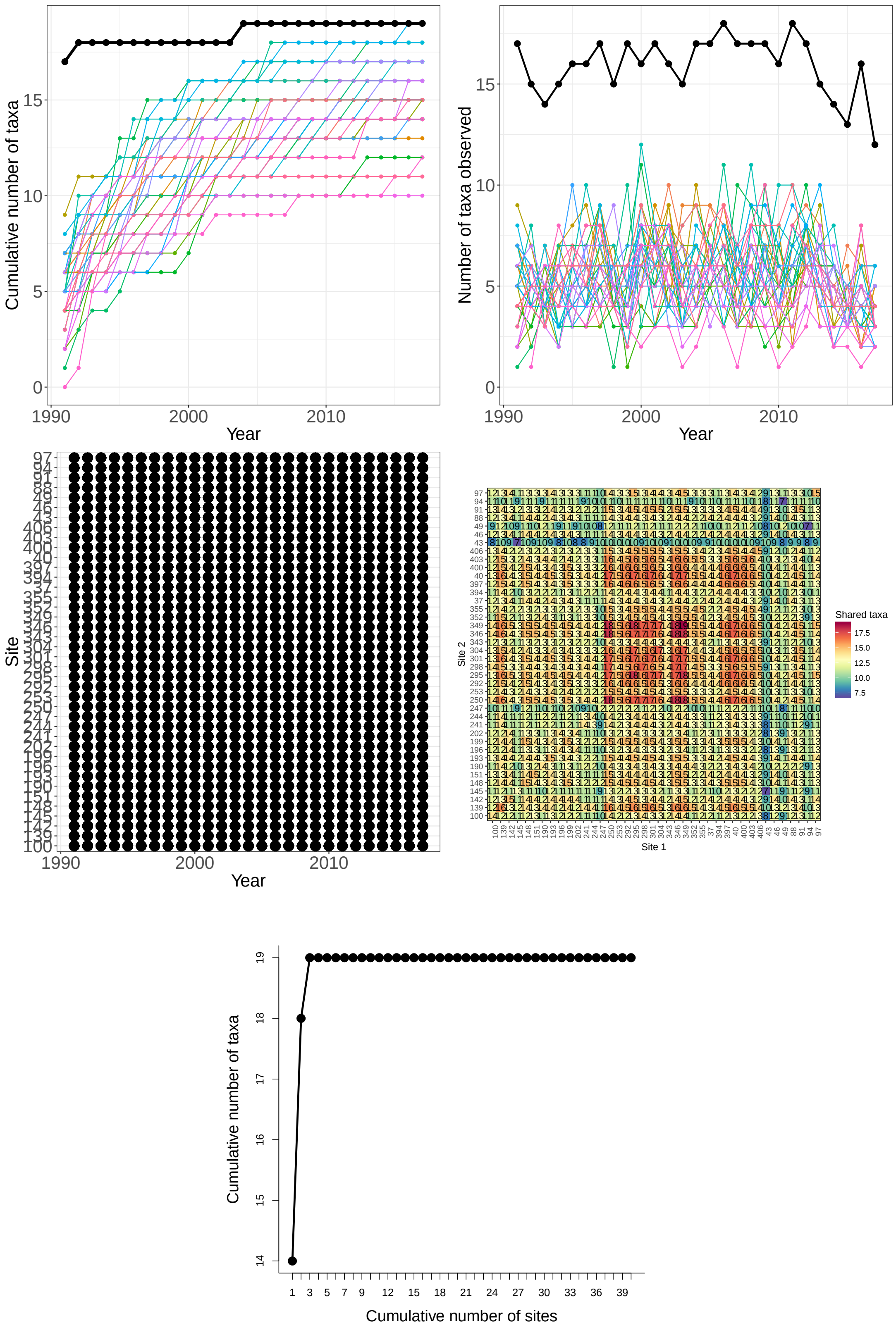

Figure S25: **LUQ-snails:** Species accumulation curves (top left), annual richness (top right), spatio-temporal sampling effort (bottom left), and number of shared species (bottom right) for snail species observed in Luquillo LTER. The black lines represent total site-level values across all plots.

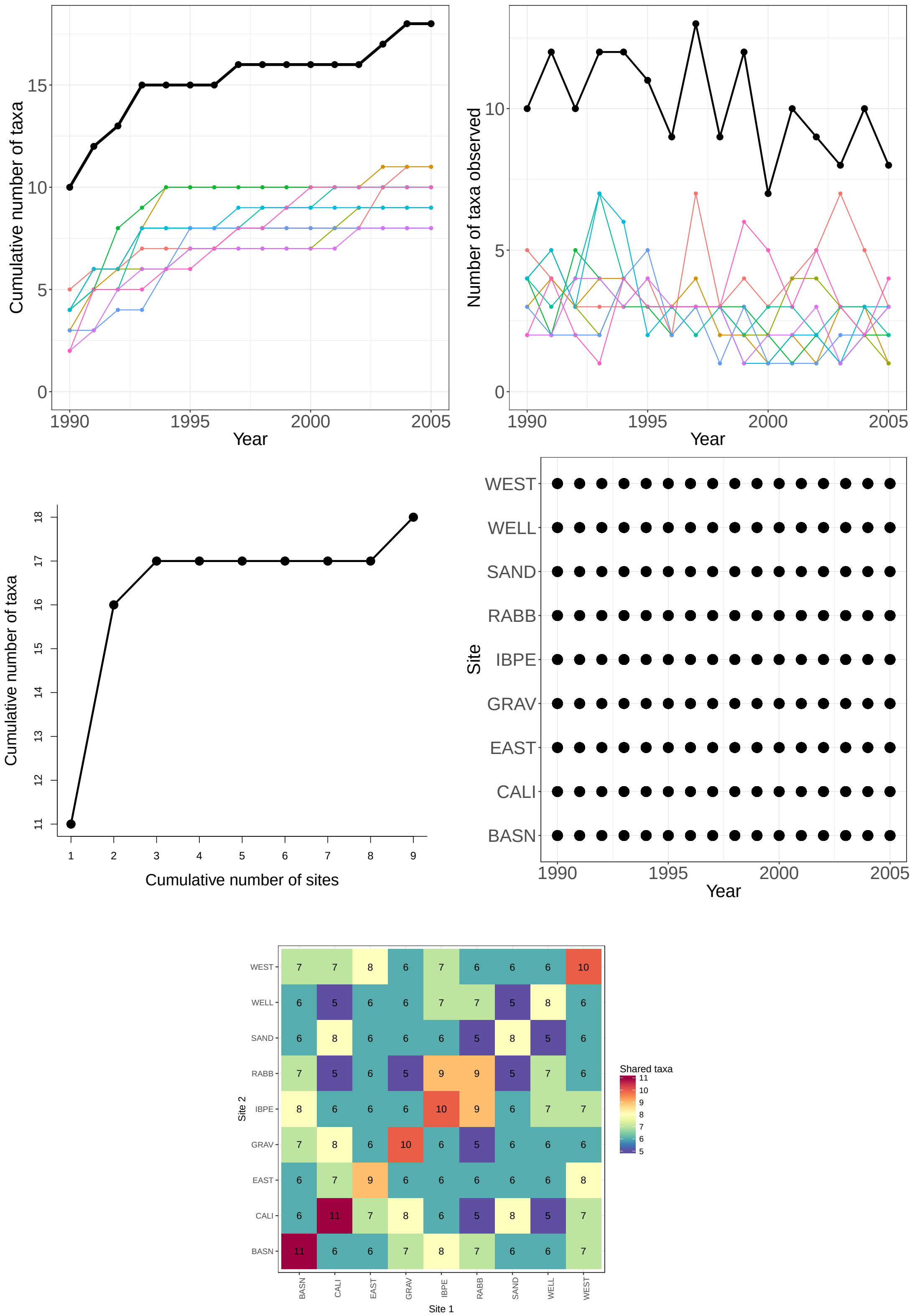

Figure S26: **JRN-lizards:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for 20 lizard species observed at 9 plots in the Jornada LTER (1990-2005). The black lines represent total site-level values across all plots.

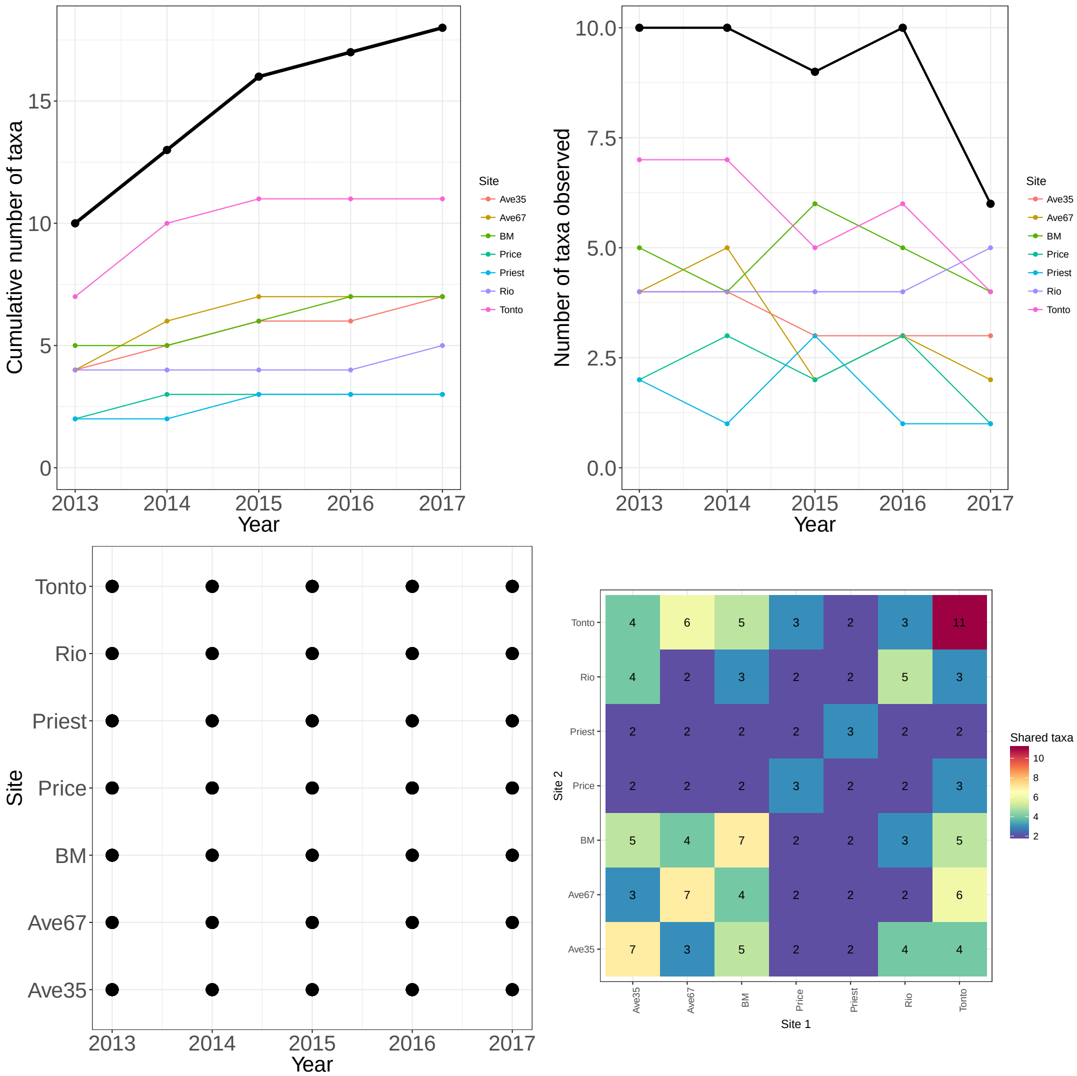

Figure S27: **CAP-herps:** Species accumulation curves (top left), annual richness (top right), and sampling effort (bottom) for species observed in the Central Area Phoenix LTER (1990-2005). The black lines represent total site-level values across all plots.

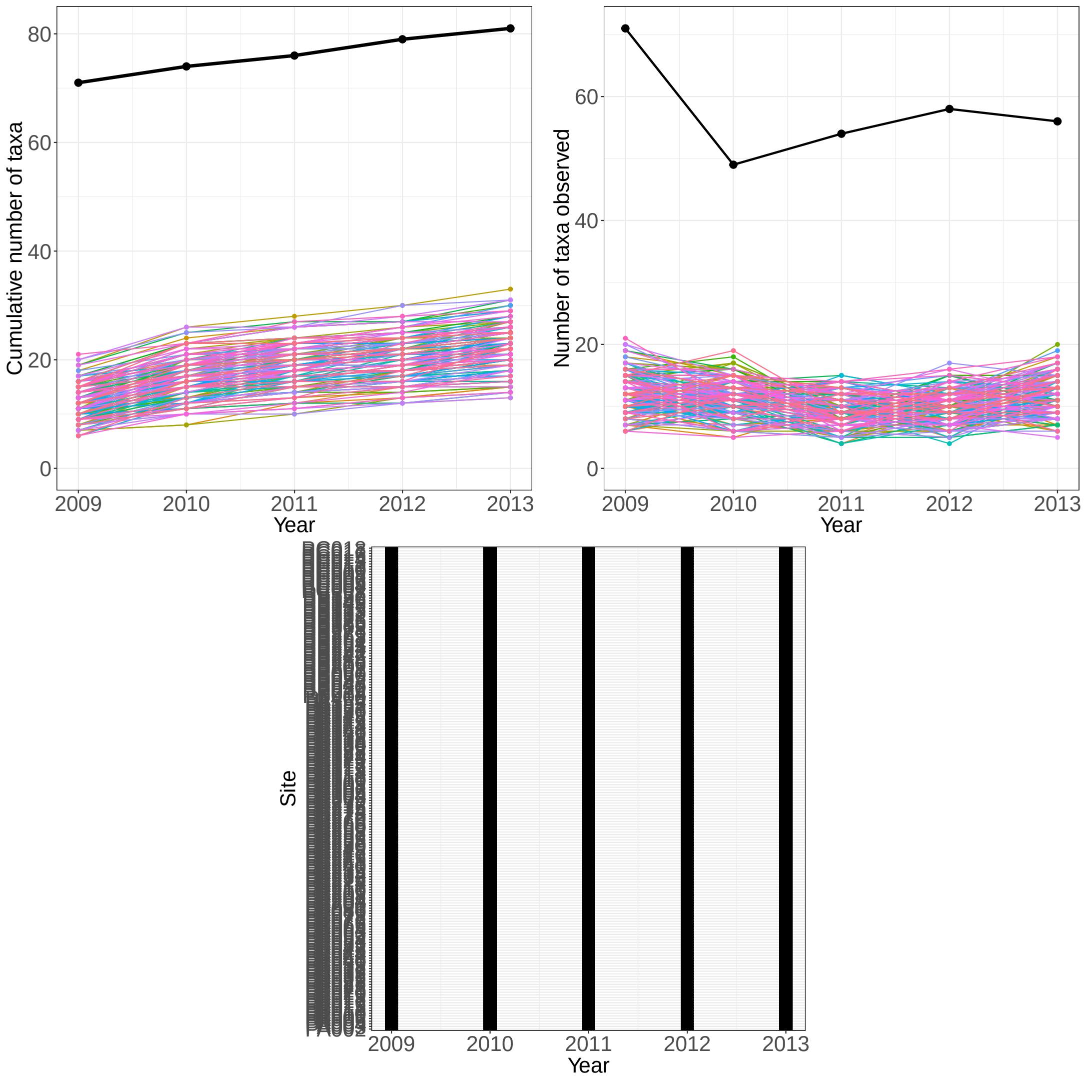

Figure S28: **AND-birds:**

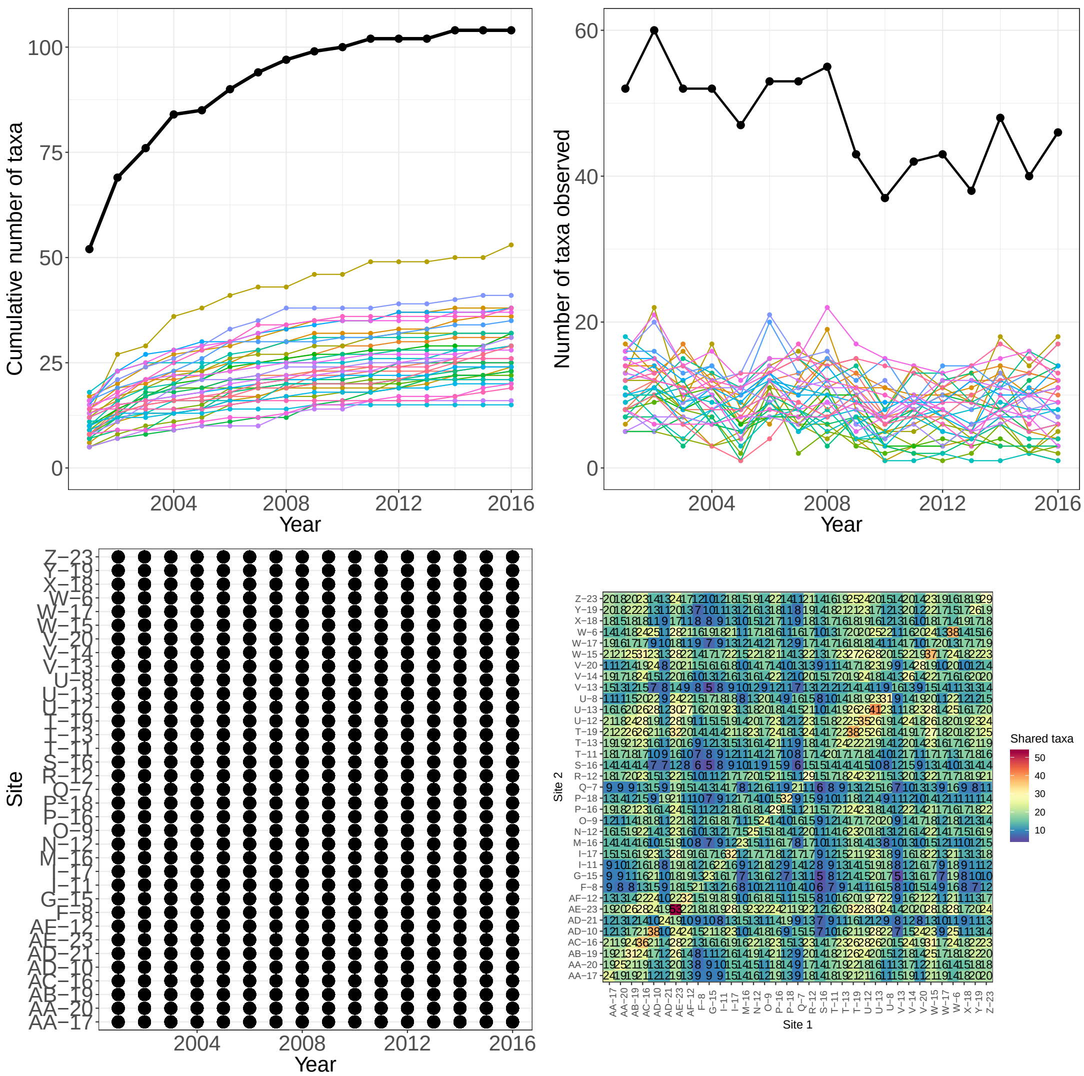

Figure S29: **CAP-birds:**

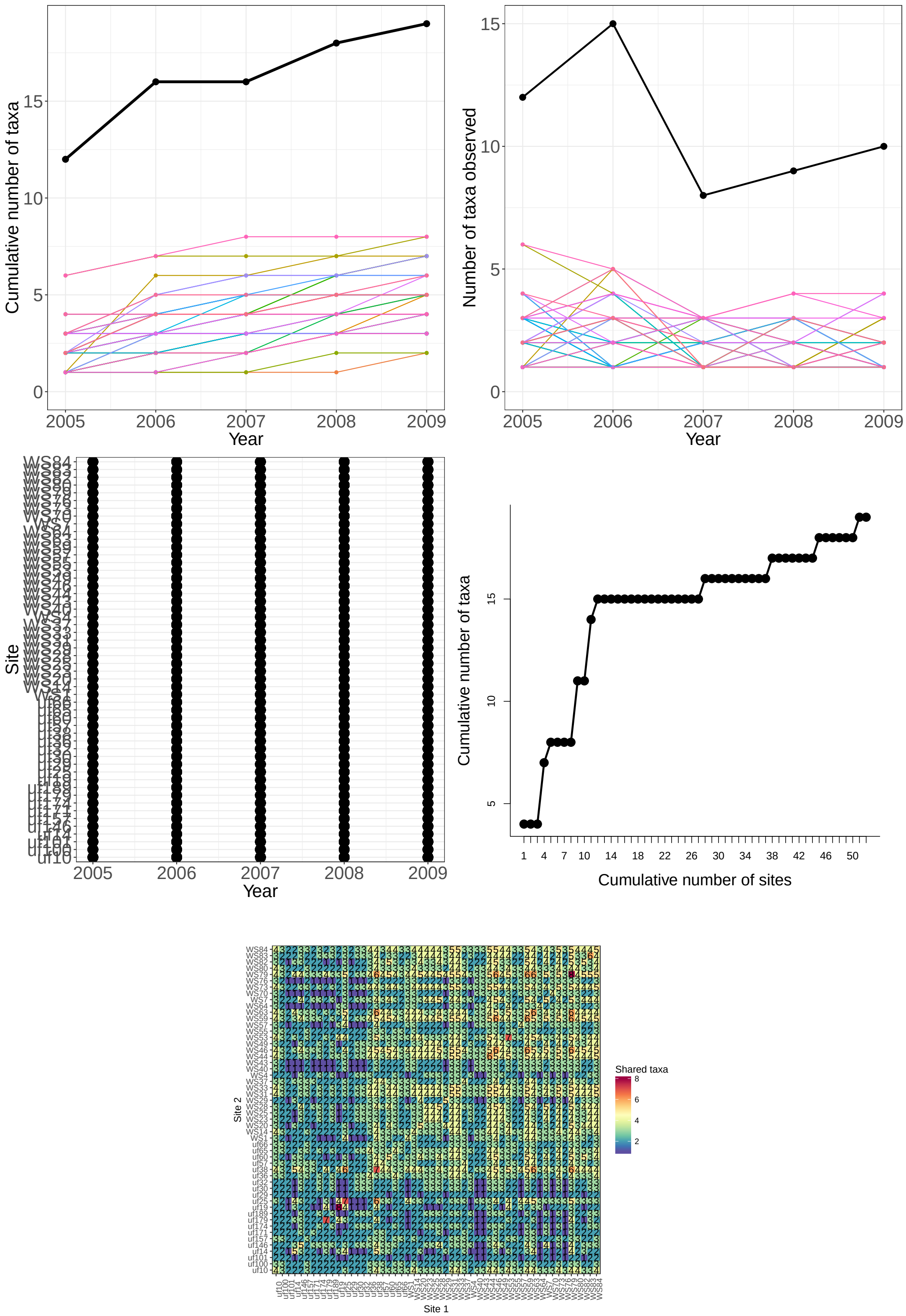

Figure S30: **BES-birds:**