SI Appendix part 1. Supplemental methods

Search terms

We searched Web of Science core collection for all records through 12/31/2016 using the following keywords (TS = topic):

TS = ("alien species" OR "alien organism*" OR "invasive species" OR "invasive organism*" OR "species invasion" OR "introduced species" OR "introduced organism*" OR "species introduced" OR "species introduction" OR "allochthonous species" OR "nonindigenous species" OR "non-indigenous species" OR "nonindigenous organism*" OR "non-indigenous organism*" OR "non native species" OR "non-native species" OR "non-native organism*" OR "exotic species" OR bioinvasion OR "bioinvasive species" OR "bioinvasive organism*" OR "naturalized species" OR "naturalized organism" OR "naturalised species" OR "naturalised organism") AND TS = (abundance OR density OR cover OR count OR occupancy OR number OR "population size") AND TS = (impact* OR effect* OR respons*)

Meta-analysis methods

The following text provides extended methodological detail and justification of the methods given in the main body of the manuscript. Definition of variables and equation terms are as given in the body text.

Prior to fitting Equation 1, we mean centered the IAS data (x) by subtracting the mean x value associated with the study from each raw data value. Mean centering minimized any dependence between linear and polynomial effect size estimates within studies (1) and was performed for both the partial-r and slopes meta-analyses. This repositioning of the x-axis to a mean of zero has no impact on invasive abundance–native response shape. This method for effect size estimation allowed us to estimate linear and polynomial partial-r effect sizes for studies where the underlying raw data were on different scales, a key strength of formal meta-analysis (2, 3). Analysis of these effect sizes yielded separate estimates of the

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direction and strength of the linear and polynomial (curvature) components of the IAS abundance–native response relationship. However, these effect sizes could not be used to reconstruct the expected shape of the IAS–native relationship, because of the way in which the regression *t*-value used to compute effect sizes (Eqn 2) combined information on regression term magnitude and precision, and because there was no obvious IAS abundance prediction interval for plotting results (IAS values in different studies had different units and scales, despite being centered).

The slopes meta-analysis used the three regression terms of Equation 1 as effect size estimates, with the goal of determining the shape of the IAS–native response relationship. This direct meta-analysis of regression parameters assumed (i) that a consistent regression model was used across studies to analyze raw data and generate effect sizes and (ii) that IAS abundance and native response variates (*x* and *y*) were comparably distributed among studies (since regression term estimates are scale dependent; 4, 5). We were able to use a common regression equation (Eqn 1) to generate all regression parameter effect sizes because we extracted and had access to raw data from component studies. We transformed the raw data within each study (both invasive abundance, *x* and native responses, *y*) to the unit scale (0, 1), satisfying the assumption for comparably distributed raw data. We then mean-centered the rescaled IAS abundance values, as before, prior to analysis using Equation 1 to generate three regression-term effect sizes (β_0, β_{linear}, β_{poly}). Transformation to the unit scale was chosen because our raw data (abundance measures, diversity metrics) were bounded within each study by a minimum of zero, and extended to some maximum (depending on the variable in question).

We used Bayesian mixed-effects meta-analyses (MCMCglmm in R version 3.5.1; 6, 7) to analyze the two effect size datasets in order to assess the IAS–native response relationship. We examined the distributions of effect sizes and *mev* and excluded one study because its polynomial regression term was an extreme outlier. The *mev*, assumed to be known without error, were fitted as a set of within-effect-size variance estimates, to weight the meta-analyses. Paper identity was included as a set of random effects to account for the non-independence of studies in the same paper (sharing common methodology, location, time period and taxonomic scope). Paper-level and residual random effects were normally distributed. Prior distributions for random effects were non-informative uniform distributions on the standard deviation of the random effects (8). We accepted default settings for the priors for fixed effects (7). Posterior distributions for model parameters were extracted from models as MCMC samples of size 1000. MCMC chain parameters (number of iterations, burnin and thin interval) were chosen to maintain effective sample sizes or posterior distributions close to 1000 and to limit chain autocorrelation. Parameter estimates (posterior mean values) were statistically supported (significant) when their posterior 95% credible interval did not include zero. All p-values presented represent the probability that parameters differ from zero, or from each other.

To reconstruct the shape of the relationship between IAS abundance and native responses, posterior mean values for β_0, β_{linear}, and β_{poly} were substituted into Equation 1 and model predictions were made in the rescaled range of the invasive abundance raw data (0, 1). An approximate 95% credible zone was established around the expected regression line using the posterior distributions for β_0, β_{linear}, and β_{poly}. These posteriors (each with sample size 1000) were used to define 1000 alternative regression equations, which were used to calculate 95% credible bounds on the native response (*y*) axis over the (0, 1) prediction interval of the invasive abundance (*x*) axis. This credible zone therefore takes into account uncertainty in all three posterior distributions. Our method for reconstructing the expected invasive abundance–native response relationship does not take into account the covariance of regression terms within studies. These covariance estimates are often non-zero for polynomial models fitted using a raw, non-scaled polynomial model matrix, such as we applied to generate effect sizes in Eqn 1. Analysis using the raw polynomial model matrix was, however, desirable as it led to the generation of consistently scaled regression terms (and therefore effect sizes) between studies, which was essential for meta-analysis. The predicted regression equation and its 95% credible zone represent the expected shape of the IAS–native species relationship for the typical range in raw response variables reported in the literature.

Bayesian mixed-effects meta-analyses were fitted with either partial-r or slopes effect sizes as the response variable and the predictors of interest as fixed effects (response level [population or community]; trophic category [above, the same, below]; response type [for community-level studies only; richness, diversity, evenness]; invader taxon [plant, animal]; habitat [terrestrial, fresh water, marine]; study type [spatial, temporal, experimental]). Up to two fixed effects were fitted at one time in each meta-analysis, and no fixed effects interactions were fitted (**Table S1.1**).

TABLE S1.1: Meta-analyses fitted to effect size datasets. All models were fitted to both partial-r and slopes effect size datasets. Only the fixed effects specifications are shown. All models contained paper-level random effects and *mev* as described above.

Model	Figures
ES ~ Response_level	2
ES ~ Trophic_category + Response_level	3
ES ~ Response_type	4; S3.2
ES ~ Habitat + Trophic_category	S3.3
ES ~ Taxon + Trophic_category	S3.4
ES ~ Study_type	S3.5

Sensitivity analyses were carried out to determine how our data rescaling decisions and how the design of studies that we meta-analyzed (spatial, temporal, experimental) influenced our findings (**SI Appendix, part 3**), and to check for publication bias within the effect size datasets (**Figure S1.1**). Finally, we checked a subset of our meta-analysis results by comparing average effect size estimates with plots of the raw data. In all cases, we detected no biases in the analysis that would influence the main conclusions presented in the paper.

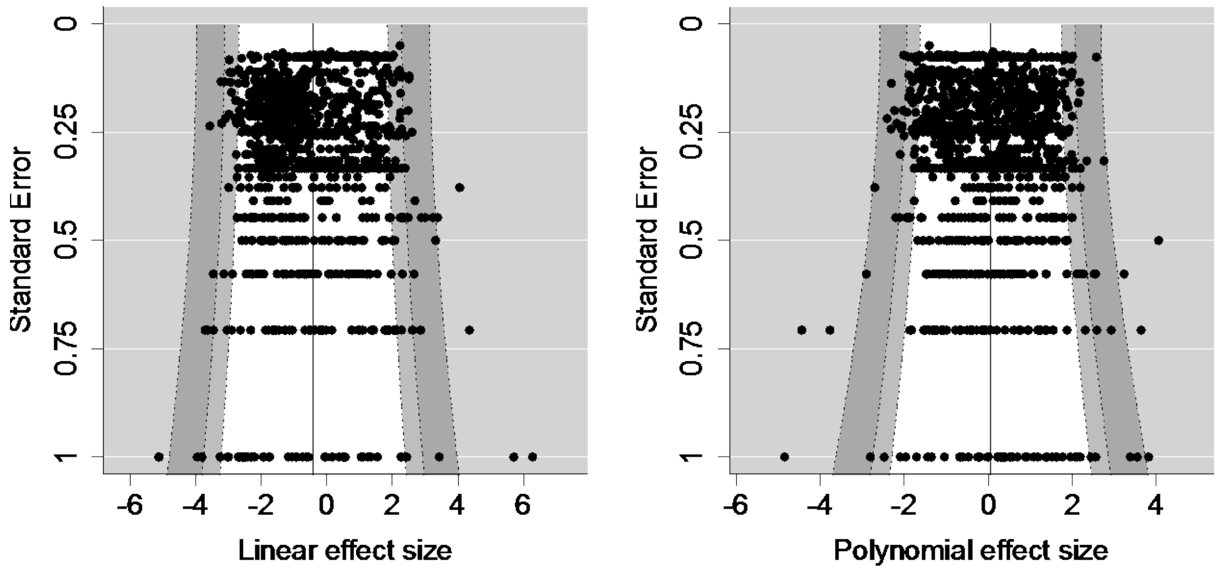

Figure S1.1 Funnel plots for study-level (mean) invasive abundance–native response effect sizes (partial-r analysis; n = 1258). Study-level error variance was taken to be the median measurement error variance within studies. Effect size data are plotted against their standard error (square root of measurement error variance). (a) Funnel plot for linear effect size (b) Funnel plot for polynomial effect size. The vertical line indicates the pooled effect size for a random-effects model with an intercept as the only fixed effect (this model was fitted using the R package metaphor; 9). Shaded areas of the funnel give pseudo-confidence interval regions: grey shading, 95% pseudo-confidence interval region; dark grey shading, 99% pseudo-confidence interval region. The pseudo-confidence regions incorporate between-effect size variation. Studies with smaller sample sizes are towards the bottom of the Y-axis and studies with larger sample sizes are towards the top. The funnel plots give no suggestion of publication bias, which would be visible as bias in the distribution of effect sizes with the greatest standard errors.

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SI Appendix, part 3. Supplemental Tables & Figures

Table S3.1. Distribution of IAS and habitats included in this meta-analysis. Numbers are total number of papers with studies in parentheses.

	Freshwater	Marine	Terrestrial	Total
Animal	43 (295)	27 (235)	37 (262)	107 (792)
Plant	8 (21)	8 (77)	78 (358)	94 (456)

Table S3.2. Summary of model parameters and pMCMC values for comparisons between groups for each meta-analysis and regression term. Effect sizes (ES) are differences between groups within each model. pMCMC values are given in parentheses. Differences with pMCMC < 0.05 are indicated in bold font.

Model	Comparison	Partial-r, linear term	Partial-r, polynomial term	Slopes, linear term	Slopes, polynomial term	Number of studies[#]
ES ~ Response_level	Population vs. community	+0.121 (0.316)	+ 0.190 (0.054)	+0.045 (0.282)	**+0.172** (0.026)	443 vs.812
ES ~ Trophic_category + Response_level	Above vs. same	**−0.479** (0.010)	**+0.427** (0.006)	**−0.244** (0.002)	**+0.292** (0.018)	176 vs. 541
	Above vs. below	**−1.049** (<0.001)	**+0.517** (0.004)	**−0.438** (<0.001)	**+0.340** (0.026)	176 vs. 251
	Same vs. below	**−0.569** (<0.001)	+0.085 (0.400)	**−0.198** (<0.001)	+0.055 (0.586)	541 vs. 251
ES ~ Response_type	Richness vs. diversity	+0.295 (0.066)	−0.078 (0.564)	**+0.128** (0.036)	−0.122 (0.188)	218 vs. 92
	Richness vs. evenness	**+0.602** (0.002)	−0.304 (0.060)	**+0.189** (0.004)	**−0.261** (0.012)	218 vs. 52
	Diversity vs. evenness	+0.293 (0.308)	−0.243 (0.184)	+0.063 (0.278)	−0.143 (0.200)	92 vs. 52
ES ~ Habitat + Trophic_category	Terrestrial vs. freshwater	−0.318 (0.152)	−0.277 (0.074)	−0.090 (0.328)	−0.227 (0.112)	566 vs. 210
	Terrestrial vs. marine	−0.408 (0.086)	−0.040 (0.826)	**−0.199** (0.024)	+0.008 (0.878)	566 vs. 192
	Freshwater vs. marine	−0.092 (0.812)	+0.253 (0.250)	−0.107 (0.376)	+0.236 (0.152)	210 vs. 192
ES ~ Taxon + Trophic_category	Animal vs. plant	**+0.461** (0.010)	+0.220 (0.104)	+0.103 (0.190)	**+0.246** (0.036)	792 vs. 456
ES ~ Study_type[§]	Spatial vs. temporal	−0.235 (0.346)	−0.238 (0.174)	−0.001 (1.000)	−0.233 (0.164)	553 vs. 146
	Spatial vs. experimental	−0.121 (0.608)	+0.021 (0.892)	−0.109 (0.180)	+0.055 (0.678)	553 vs. 217
	Experimental vs. temporal	−0.122 (0.668)	−0.269 (0.170)	+0.104 (0.372)	**−0.421** (0.018)	217 vs. 146

[#]Number of studies associated with each group listed in the Comparison column

[§]For a dataset in which trophic category was known and was not "multiple"

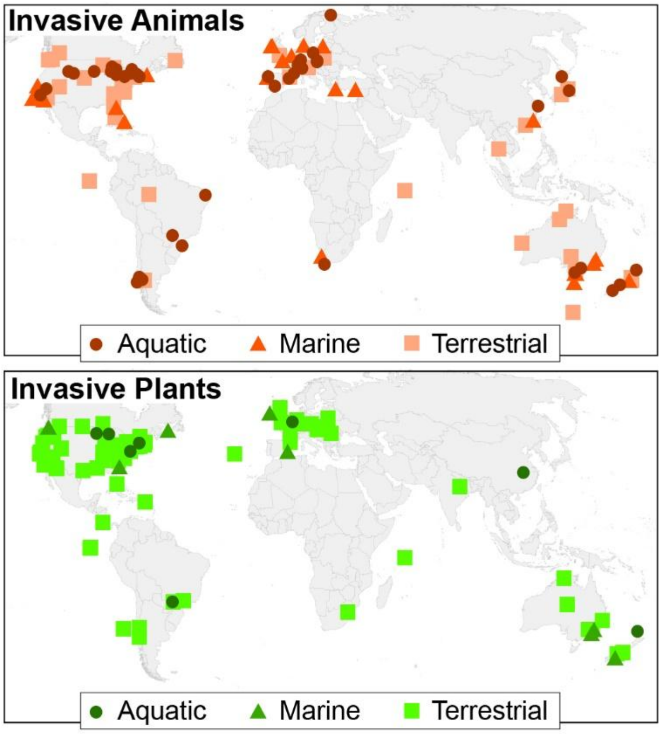

Figure S3.1. Spatial distribution of papers reporting the impact of invasive animal (top panel) and invasive plant (bottom panel) abundance on native species or communities.

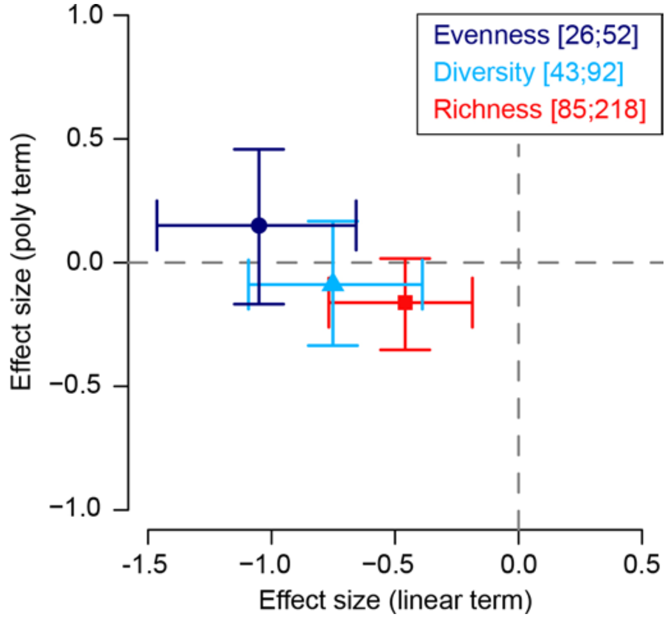

Figure S3.2 Partial-r analysis for community diversity metrics (richness, diversity, and evenness). All community diversity metrics had significant, negative linear responses to IAS abundance ($p<0.001$). The linear response of richness was significantly less negative than evenness ($p=0.002$) and marginally less negative than diversity ($p=0.07$). None of the community response metrics had a significant polynomial term in the partial-r analysis. However, richness had a marginally more negative polynomial term than evenness ($p=0.06$). Slopes analyses are consistent with these results and are presented in Figure 4.

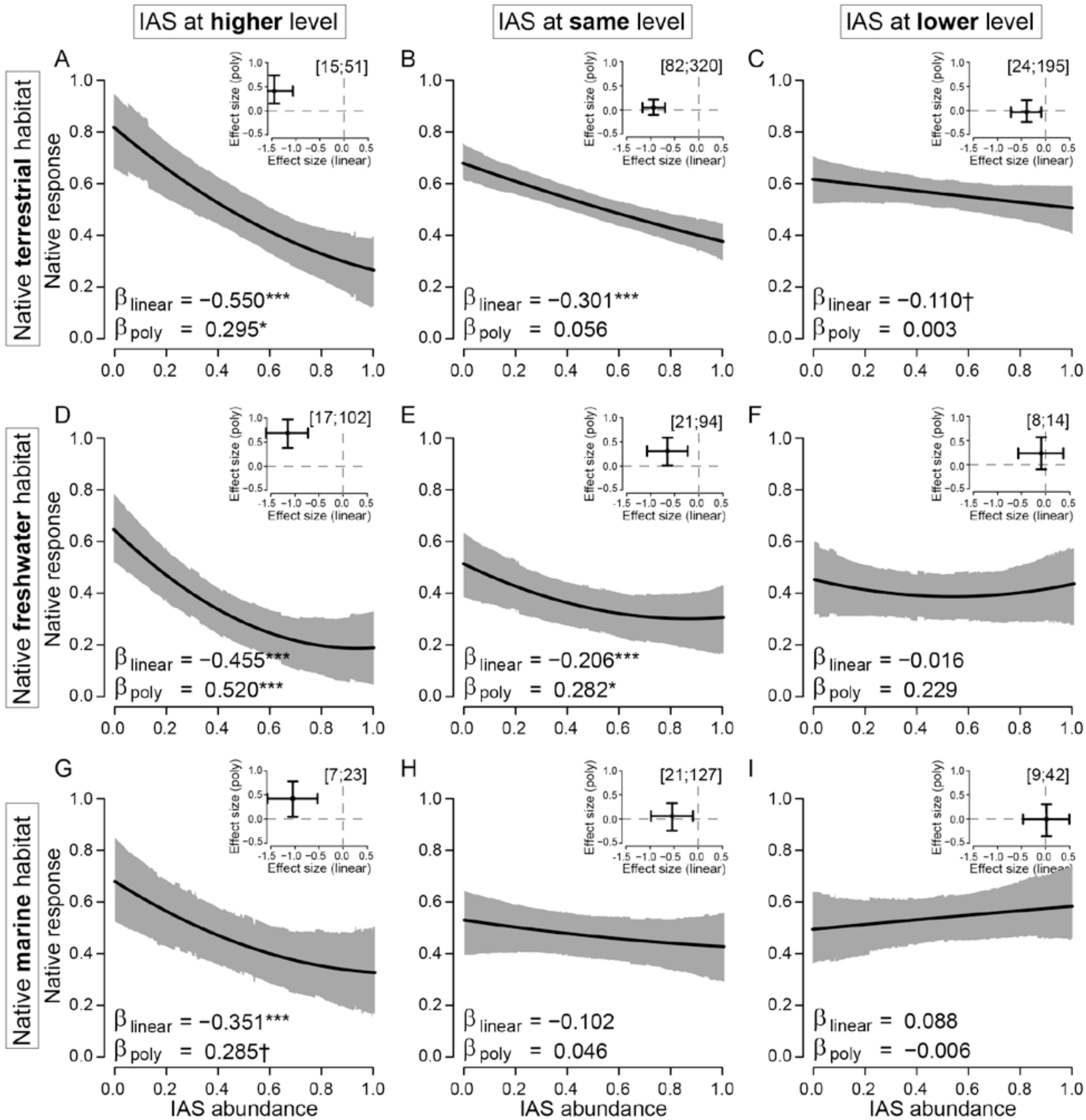

Figure S3.3. IAS impacts varied more by trophic level than by recipient habitat. Main panels show slopes analyses; insets show partial-r analyses on the same scale for comparability. A-C) Terrestrial IAS had significant non-linear impacts on native species populations and communities when invaders were at higher trophic levels. Terrestrial IAS had significant negative linear impacts when they were at the same and marginally negative linear impacts at lower trophic levels. D-F) Freshwater IAS had significant non-linear impacts when they were at higher or the same trophic levels. G-I) Marine IAS had significant negative linear and marginally positive polynomial impacts when they were at a higher trophic level. Numbers in brackets are total papers and studies analyzed, respectively. Significant partial-r effect sizes are indicated by 95% credible interval bars not crossing the zero lines. Gray shading in slopes analyses indicates the 95% credible interval. Significant linear (β_{linear}) or polynomial (β_{poly}) terms are indicated as follows: † p<0.10; * p<0.05; *** p<0.001).

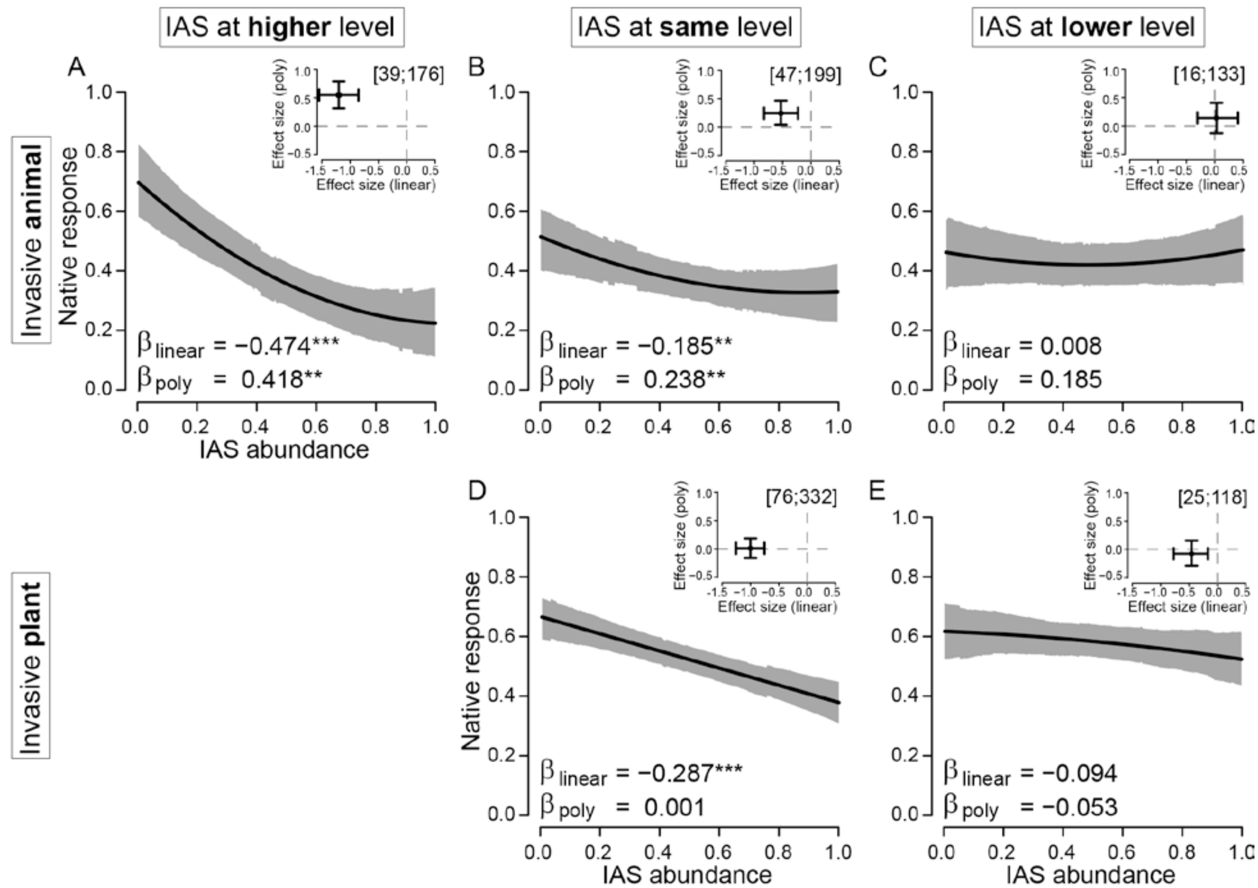

Figure S3.4. Both invasive plants and animals had negative impacts on native populations and communities. Main panels show slopes analyses; insets show partial-r analyses on the same scale for comparability. A-C) Invasive animals had significant negative, non-linear impacts on native species populations and communities when invaders were at the same or higher trophic levels. D-E) Invasive plants had significant negative linear impacts when they were at the same or lower trophic levels (no plants were at a higher trophic level). Numbers in brackets are total papers and studies analyzed, respectively. Significant partial-r effect sizes are indicated by 95% credible interval bars not crossing the zero lines. Gray shading in slopes analyses indicates the 95% credible interval. Significant linear (β_{linear}) or polynomial (β_{poly}) terms are indicated by asterisks (** $p<0.01$; *** $p<0.001$).

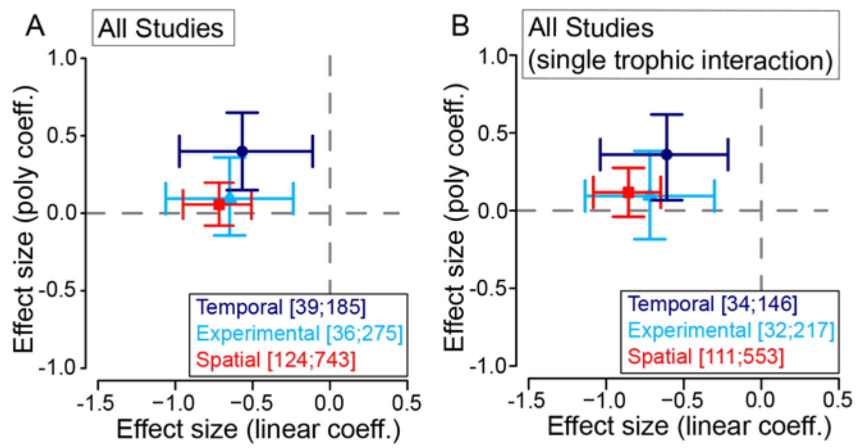

Figure S3.5. Results did not differ with study type. Plots show partial-r meta-analysis results. A) All study types showed a significant negative linear impact on native species and communities. There were not significant differences in the linear term between study types ($p>0.40$). There was a significant different in the polynomial term between spatial and temporal studies ($p=0.02$). B) When only studies with a single trophic interaction were included (i.e. excluding studies with unknown or multiple trophic interactions to be comparable to the data analyzed in Figure 3, Figure S3.3, and Figure S3.4), there remained no significant differences in the linear term between study types ($p>0.35$) and there were also no significant differences in the polynomial term between study types ($p>0.17$).