Supplementary Figure S1: Differences in primary producer and animal biomass. Bars indicate treatment means ±1SE, stage structure indicates what stage of a predator species is present: S = small stage, L = large stage, S+L = both stages co-occur. Solid lines indicate the mean observed in controls. Dashed lines indicate expected values for the respective response variable when both stages of a species co-occur based on additive effects model assuming independent effects of each stage (see Supplementary Methods for details). (a) and (b) indicate proportional change in respective primary producer biomass over the course of the experiment based on chlorophyll-a concentrations. (c) Dry biomass of all macro-invertebrates and amphibians at the end of the experiment.
Supplementary Figure S2: Differences in ecosystem processes. Bars indicate treatment means ±1SE, size structure indicates what stage of a predator species is present (see Fig. 2). Solid lines indicate the mean observed in controls. Dashed lines indicate expected values for the respective response variable when both stages of a species co-occur based on additive effects model assuming independent effects of each stage (see Supplementary Table S2 for analysis details).

(a) Leaf litter decomposition rate (k) (see Supplementary Methods for details). (b) and (c) indicate proportional change in net primary productivity (NPP) and respiration (R) based on diurnal cycles of dissolved oxygen over the duration of the experiment (see Supplementary Table S1 for details).
**Supplementary Table S1: Effects of stages and species on ecosystem processes**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Periphyton</th>
<th>Phytoplankton</th>
<th>Animal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species</td>
<td>$\chi^2_{1,29}$ 0.0</td>
<td>$\chi^2_{1,29}$ 0.1</td>
<td>$\chi^2_{1,30}$ 3.0$^\dagger$</td>
</tr>
<tr>
<td>Stage</td>
<td>$\chi^2_{2,29}$ 2.4</td>
<td>$\chi^2_{2,29}$ 2.2</td>
<td>$\chi^2_{2,30}$ 9.5$^{**}$</td>
</tr>
<tr>
<td>Species*Stage</td>
<td>$\chi^2_{2,29}$ 0.3</td>
<td>$\chi^2_{2,29}$ 6.9$^*$</td>
<td>$\chi^2_{2,30}$ 1.6</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>NPP</th>
<th>R</th>
<th>Decomposition (k)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species</td>
<td>$F_{1,29}$ 41.9$^{****}$</td>
<td>$F_{1,29}$ 31.7$^{****}$</td>
<td>$\chi^2_{1,22}$ 0.4</td>
</tr>
<tr>
<td>Stage</td>
<td>$F_{2,29}$ 0.9</td>
<td>$F_{2,29}$ 0.6</td>
<td>$\chi^2_{2,22}$ 10.5$^{**}$</td>
</tr>
<tr>
<td>Species*Stage</td>
<td>$F_{2,29}$ 22.8$^{****}$</td>
<td>$F_{2,29}$ 24.0$^{****}$</td>
<td>$\chi^2_{1,22}$ 6.7$^*$</td>
</tr>
</tbody>
</table>

All analyses are based on raw data without correcting for potential differences in biomass across predator treatments. See Table 1 in main text for analyses of per-unit biomass effects of predators. Degrees of freedom were adjusted for block effects and missing replicates because of removal of significant outliers. (Note that removal of outliers did not alter general patterns). P-values are based on general linear models (with corresponding F- or likelihood-ratio $\chi^2$-statistics), and corrected for missing replicates (see Analysis for details). $^\dagger P<0.1$, $^\ddagger P<0.06$, $^* P<0.05$, $^{**} P<0.01$, $^{***} P<0.001$, $^{****} P<0.0001$. 
**Supplementary Table S2:** Differences in expected vs. observed effects on ecosystem responses for treatments where small and large stages co-occur.

<table>
<thead>
<tr>
<th>Model</th>
<th>Anax</th>
<th>Cybister</th>
<th>Anax</th>
<th>Cybister</th>
<th>Anax</th>
<th>Cybister</th>
</tr>
</thead>
<tbody>
<tr>
<td>Multiplicative model*</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Anax</td>
<td>t_5=0.80,</td>
<td>t_5=1.86,</td>
<td>t_5=0.66,</td>
<td>P = 0.458</td>
<td>P = 0.120</td>
<td>0.539</td>
</tr>
<tr>
<td>Cybister</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Additive model*</td>
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<tr>
<td>Anax</td>
<td>t_5=0.66,</td>
<td>P = 2.61,</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cybister</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Biomass corrected model*</td>
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<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Anax</td>
<td>t_5=0.85,</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cybister</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Ecosystem properties & functions**

- **Animal biomass**
  - Anax: t_5=0.80, P = 0.458
  - Cybister: t_5=1.86, P = 0.120
- **Change in periphyton**
  - Anax: t_5=1.15, P = 0.300
  - Cybister: t_5=0.24, P = 0.815
- **Change in phytoplankton**
  - Anax: t_5=3.25, P = 0.023
  - Cybister: t_5=7.25, P = 0.0008
- **Decomposition rate**
  - Anax: t_4=4.90, P = 0.004
  - Cybister: t_4=1.57, P = 0.191
- **Change in respiration rate**
  - Anax: t_5=1.78, P = 0.292
  - Cybister: t_5=1.61, P = 0.168
- **Change in net primary productivity**
  - Anax: t_5=0.92, P = 0.401
  - Cybister: t_5=0.993, P = 0.366

<table>
<thead>
<tr>
<th>Anax</th>
<th>P</th>
<th>Cybister</th>
<th>P</th>
<th>Anax</th>
<th>P</th>
<th>Cybister</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.047</td>
<td></td>
<td>0.714</td>
<td></td>
<td>0.0002</td>
<td>P &lt; 0.0001</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.003</td>
<td></td>
<td></td>
<td>0.017</td>
<td></td>
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</tr>
</tbody>
</table>
* type of models used for estimating expected values (see Supplementary Methods “Intraspecific diversity effects” for details).

Statistics are based on two-tailed t-tests; differences in df are due to removal of significant outliers.
Supplementary Methods

Focal organisms

Larvae of the dragonfly *Anax junius* and the diving beetle *Cybister fimbriolatus* are wide-spread species in North America. We chose both species for several reasons. Final instars of both species are top predators in fishless ponds, and both species are known to strongly determine the structure of these pond communities\(^{41-46}\). Both species increase by more than 15 fold in length (mass) during their development. Depending on the season, a population can consist of a single cohort composed entirely of either small- or large-bodied larvae (beginning vs. end of reproductive season), or it can be strongly size-structured when multiple cohorts overlap (e.g., middle of breeding season)\(^{39,46}\). In south east Texas, similar differences in stage structure can also occur within a season across populations (ponds) because of differences in the onset of reproduction across populations. In addition, our preliminary stable isotope analysis indicates that both species show significant changes in trophic position (measured with relative differences in \(\delta^{15}\)N) with size during their ontogeny. However, although both species occupy a seemingly similar ecological role, they differ substantially in key aspects of their morphology (e.g. gills vs. breathing air, chewing mouth parts vs. piercing mouth parts and poison), development, and changes in gape width over ontogeny (*Anax*: 11-13 instars with different gape width vs. *Cybister*: 3 instars with different gape width), and ecology (e.g. habitat use, hunting mode). Given these differences both species are expected to show some differences in their functional role and the relative importance of size and strength of ontogenetic niche shifts (i.e. functional differences among stages).

Experimental design
Detecting functional differences among predators is challenging when predators differ substantially in their biomass. Traditional designs typically standardize either predator biomass or density among treatments using additive or substitutive designs. While such designs may be appropriate for systems where predators differ little in size, it leads to dramatic differences in density or biomass when predators differ in size. As a consequence, conclusions about identity effects are inevitably confounded by biomass or density. Recent studies indicate that density-dependent effects cause population effects to differ from that expected based on allometric (or biomass) scaling relationships. Consequently, the null models underlying traditional designs that keep density or biomass constant are likely to be incorrect. For systems in which the functional role of individuals largely depends on body size (mass), there is a high risk of misinterpreting results when using traditional additive or substitutive designs. Furthermore, neither biomass nor density are ever constant across stages/size classes in natural populations of our study species, and keeping total biomass constant would lead to unrealistically high densities and experimental artifacts with little relevance to natural systems. Thus, we refrained from keeping biomass or density constant. Instead, we followed suggestions from previous studies and used natural mass-abundance relationships based on field densities. This approach allowed us to estimate the actual impact of each size class in natural populations and the relative impact of each size class by separating quantitative from qualitative differences among size classes. Future studies that adjust densities based on metabolic demands could provide additional mechanistic insight into how potential stage specific differences in metabolic rates influence a species functional role, but this was outside of the scope of this study.

The experiment consisted of seven treatments each replicated six times (N = 42 ponds) that manipulated the presence/absence of two size classes of either *A. junius* or *C. fimbriolatus*.
Mesocosms either received 18 small *A. junius* (head width (HW): 2.85-3.3 mm, body length (BL): 8.9-11.7 mm, dry mass (DM): 0.026-0.05 mg), or 3 large *A. junius* (HW: ~6.9 mm, BL: ~32 mm, DM: ~0.61 mg) or both, or 18 small *C. fimbriolatus* (HW: 1.9-2.1 mm, DM: 0.027-0.06 mg) or 3 large *C. fimbriolatus* (HW: ~5.2, DM: ~0.64 mg) or both, or none of these stages (control). Such differences in stage-structure (one or two stages present) reflect natural differences among populations (ponds) within a time period or seasonal changes within a population. Size classes were chosen based on the size structure of the natural population and to keep total predator biomass (larvae of *A. junius* or *C. fimbriolatus*) within a size class treatment constant across species, while reducing the risk of early metamorphosis of the largest size class. We collected all *A. junius* and *C. fimbriolatus* larvae from two local ponds.

**Experimental communities**

The experiment was carried out in mesocosms that closely mimicked the structure and complexity of local fishless ponds that are dominated by invertebrate predators. Mesocosms were established in 1200 L plastic stock tanks set up in a randomized complete block design at Rice University’s South Campus experimental facility, Houston, TX. All tanks were filled with water March 16th, 2009, three months before the start of the experiment. All tanks were covered with 50% shade cloth lids which provided natural shading levels and allowed a variety of small to medium-sized invertebrates to colonize the tanks while keeping large predators out of and metamorphs (insects and amphibians) in the tanks. After one month (April 23) we added 2.5 kg (air dried) of mixed leaf litter to each pond. Leaf litter represented a random mixture of leaves (mostly pine and oak) that were collected from the border of two local ponds. The next day, each tank received 500 ml of concentrated zooplankton and phytoplankton collected from two local fishless ponds. We fertilized tanks once seven weeks before experiment initiation with nitrogen.
(10.4 g NaNO₃ per tank) and phosphorus (0.33 g NaH₂PO₄ per tank) to increase initial primary productivity. On May 14th, we added to each tank 220 g (wet mass) of macrophytes collected from one local pond (mostly *Potamogeton sp.* and *Najas sp.*). To establish a natural complex community, one week before the start of the experiment we added to each tank a total of 1 L of highly concentrated and diverse mix of small invertebrates (benthic and pelagic organisms) sifted from the vegetation and sediment of two local fishless ponds. This approach also inevitably resulted in the random addition of a few recently hatched (1st instar) *A. junius* to tanks that were too small to be detected during our screening process. In addition we collected a diverse range of larger invertebrates (including other predatory insects, see Supplementary Table S3) from several local ponds, which were added in equal numbers to all tanks (from May 22nd – June 1st). Each tank also received an equal number of tadpoles (mix of hatchlings and medium-sized tadpoles) from five anuran species collected from four local ponds (299 *Bufo nebulifer*, 75 *Rana clamitans*, 157 *Hyla (versicolor & cinerea)* per tank). Together with natural colonization of tanks (mostly beetles and chironomids) this created a highly diverse community with >60 morpho-species of vertebrates and invertebrates across all tanks (Supplementary Table S3). The experiment started on June 3rd when the different *Anax* and *Cybister* stages were added to the tanks. The experiment was terminated after three weeks when the first *Anax* started to emerge.

**Ecosystem functions and properties**

**Decomposition**

We estimated decomposition rates within a pond from a mixture (mostly oak) of dried leaves over the entire duration of the experiment. Each pond received two leaf litter bags (15 x 20 mm, mesh size: 3.5 mm²) each filled with 2500 mg of oven-dried leaves (48 h at 60°C) from the same
random mixture of leaf litter added to the ponds. Decomposition rates \((k)\) were calculated from the exponential decomposition decay curve model with \(M_t = M_0 \exp(-k t)\), where \(M_0\) indicates the initial mass of leaf litter bags, \(M_t\) the average final leaf litter mass, and \(t\) is duration of the experiment.

*Ecosystem productivity and respiration*

We took weekly measurements to estimate net primary productivity (NPP) and respiration (R) calculated from diurnal oxygen cycles \(^{47, 48}\). We measured Dissolved Oxygen (DO) with an oxygen probe (YSI, Professional Plus) three times a day: at sunrise \((t_0)\), sunset \((t_1)\), and the following sunrise \((t_2)\). NPP is given by the increase in DO\(_{t1-t0}\), and R by the decrease in DO\(_{t1-t2}\).

*Primary producer biomass*

We estimated standing biomass of two dominant forms of primary producer in our ponds, periphyton (benthic algae) and phytoplankton (pelagic algae). Standing biomass of periphyton was estimated weekly from three glass microscope slides per tank \((0.74\text{ cm x }0.25\text{ cm})\) that were propped at an angle against the side of the tank above the leaf litter layer for seven days. After seven days, glass slides were removed for processing and replaced with a set of new slides. Periphyton from both sides of all three slides from the respective sample period was combined for the analysis. Biomass of Phytoplankton was estimated from 250-ml water samples collected at mid water level weekly from each tank. Periphyton and phytoplankton concentrations were then determined fluorometrically (AquaFluor, Turner Designs) through chlorophyll-a extraction in 95% Ethanol following standard protocols \(^{49}\). The first sample was taken one week after the start of the experiment and then every week for three consecutive weeks.

*Community structure*
Sampling - We quantified the structure of the zooplankton, amphibian, and macro-invertebrate (benthic, vegetation, and total) community by counting, measuring, and weighing over 35,500 individuals from >65 species (see Supplementary Table S3). We monitored tanks daily for emerging insects and amphibians during the experiment. Amphibian metamorphs were weighed after tail absorption and released at the origin of capture. We converted metamorph wet mass into dry mass using our previously established, species-specific wet to dry mass conversion relationships for amphibians, and a subset of emerged invertebrates were used to calculate species specific averages for dry mass. At the end of the experiment we first took six zooplankton samples per tank (total 2.5 L) using a depth integrated tube sampler. The samples were filtered through an 80-µm Nytex mesh, combined and preserved in 75% ethanol. We then sub-sampled the floating vegetation and benthos community with a fine mesh (500-micron mesh Nytex) D-net (30.5 cm wide). Vegetation samples included several sweeps that removed the entire floating vegetation. Benthos samples were taken with two perpendicular sweeps across the full diagonal of the tank through the leaf litter layer. Vegetation and benthos sample were then carefully rinsed, filtered, and the contents preserved in 75% ethanol. Finally, we destructively sampled mesocosms and collected all macro-invertebrates (≥ 4 mm long) and amphibians until no individuals were left in the tank (hereafter referred to as "final samples"). All animals were initially preserved in 75% ethanol and stored at -25°C until further analysis.

We calculated benthos, vegetation, and total (vegetation + benthos + final samples) dry biomass of invertebrates, and dry mass of tadpoles grouped by species after drying samples at 60°C for 48 h. Species specific invertebrate and amphibian dry masses (including emerged individuals) were calculated by measuring body length and/or head width of individuals using image analysis (Image J) and converting them into dry mass using our own and published length-mass.
regressions. The obtained invertebrate dry mass estimates closely followed the pattern of actual
weighed dry mass without treatment bias, although it consistently underestimated total dry mass.
Zooplankton community structure was determined by counting all individuals within a sample.
Larvae and adults of invertebrate species with complete metamorphosis were analyzed separately
because of their functional differences (e.g., beetle larvae vs. adults).

Quantifying community structure - Community structure was analyzed for both the abundances
and total biomass of species. The goal of this analysis was to detect whether species and stages
of A. junius and C. fimbriolatus have different effects on the community structure rather than the
total abundance of species (which was analyzed separately). Thus analyses were carried out
using relative biomass or density of each species (i.e. proportion of total community biomass or
density of an experimental pond) as response variable to test for differences in community
structure across treatments. For the biomass analysis we scaled zooplankton samples up to the
volume of the whole tanks. We did not scale the densities of zooplankton up to whole tank
volume since this would have resulted in zooplankton species being up to 10,000 times more
abundant than any other species. While the scaling also resulted in significant differences in
whole community structure among size treatments, the differences were completely dominated
by zooplankton species (accounting for 80-90% of differences among tanks even after fourth
root transformation). Thus, we used densities from our actual zooplankton subsamples instead
which were within the range of all other vertebrate and invertebrate densities (results are reported
in Table 1 in main text). A separate analysis on only macro-invertebrates without zooplankton
species showed a very similar pattern (PERMANOVA Size*Species: P = 0.045, Size: P = 0.603,
Species: P =0.112, Block: P<0.001). In conclusion, regardless of how and whether zooplankton
densities were included in the density-based analysis of community structure, statistical analyses
always indicated a significant species\* size interaction. Consequently we only show the analysis that includes the rescaled zooplankton densities in the main text as this includes the most information (i.e. species). A full species list with corresponding average densities and biomass for each treatment are given in Supplementary Table S3. Finally, we analyzed changes in the size-structure of the macro-invertebrate community (not including Zooplankton species) by comparing square-root transformed abundance of individuals within log_{10} size classes based on dry mass. The two focal predator species were never included in any of the analyses on community structure or animal biomass.

**Statistical analyses**

The goals of this experiment were to determine whether changes in the population (stage) alters i) the functional role of a species at the ecosystem level, and ii) functional differences among species, and iii) whether stages had independent effects (see “Interspecific diversity effects” below for details). To answer i) and ii) we used a 2 (species) x 3 (stage) factorial design to test how changes in stage-structure and species identity influence the respective response variables and whether these effects were independent. A significant interaction (species\*stage) indicates that functional differences among species are not constant, but instead change depending on the specific stage-structure of the species. A significant stage effect indicates that the population structure of a species determines its functional role in the ecosystem. To account for any potential differences in biomass effects among treatments, we estimated the per-capita biomass effect (= effect_{B}) for each predator treatment on all ecosystem processes (see details in section: “Biomass corrected analysis”) except for community structure because the latter analyses already account for potential biomass differences among predator treatments. Results of the biomass corrected analyses (see Table 1, Fig. 2, 3) are qualitatively similar to the full analyses of
predator effects on the untransformed data which are given in Supplementary Table S1 and Figures S1, S2.

Ecosystem responses

To account for natural variation in initial conditions among tanks we used proportional change [(final sample-first sample)/first sample] in NPP, Respiration and periphyton and phytoplankton biomass. NPP and Respiration, periphyton, phytoplankton, animal biomass, and decomposition rates were analyzed with a general linear mixed model with normal or gamma distributed error terms (depending on the variable) and species, size and their interaction (species*size) as fixed effects and block as a random effect using SAS 51. When block effects were not significant, block degrees of freedom were pooled with the error term degrees of freedom for the final analysis 51. One tank was a significant outlier (based on studentized residual outlier test with Bonferroni adjustments and interquartile range detection of outliers), likely because of dramatic differences in community structure (see below), and thus removed from these analyses. To account for differences in sample size all reported test statistics and P values are based on likelihood estimates and type III sums of squares.

Community structure

We analyzed differences in the structure of communities among treatments using non-parametric, permutational multivariate statistics based on Bray-Curtis similarity metrics using PRIMER 52. First, we tested whether the variability in community structure (i.e. dispersion) differed among treatments using PERMDISP 53. Secondly, if treatments met the assumption of similar variances (in general we found no significant differences in dispersion among treatments) we tested whether communities differed significantly among treatments using permutational
multivariate analysis (PERMANOVA)\textsuperscript{54,55}. When block effects were not significant, block
degrees of freedom were pooled with the error term degrees of freedom for the final analysis.
Both permutation analyses were carried out using 999 permutations and based on centroids.
Community structures were visualized using non-metric Multi-Dimensional Scaling plots
(nMDs) using the packages “Vegan”, “Ecodist”, “BiodiversityR”, and “Ellipse” implemented in
the R-software. One tank was a significant outlier (based on ordered squared robust Mahalanobis
distances) and thus removed from the analysis. This was largely driven by the 19-61 times lower
biomass of \textit{Hyla} and \textit{Rana} tadpoles compared to the average across all other 41 tanks and
corresponding dramatic increase in some zooplankton (in particular Ostracods). It is possible that
this was mediated by a disease outbreak in the tadpoles or low water quality with associated
bacterial bloom but the exact reasons remained unclear.

\textit{Relationships among variables}

To identify whether the changes in animal community composition were at least partly
responsible for changes in other ecosystem properties, we analyzed the partial correlations
among ecosystem properties. Due to the complexity of the pond communities, we used two non-
metric multi-dimensional scaling metrics to represent community structure in this analysis. In
general, the qualitative relationship between community structure and other ecosystem response
variables were similar regardless of whether community structure was based on relative or total
biomass or density indices. Because we were most interested in how community composition
was related to ecosystem processes we only represent here one example with community
structure based on proportional biomass which also provided the best model fit.

\textit{Results}: Table 1 (in main text) summarizes the partial correlation coefficients. Overall,
we found that community composition (based on relative biomass of species) was indeed strongly correlated with all other ecosystem processes. Interestingly, community structure was more strongly correlated with NPP and respiration than periphyton or phytoplankton. Furthermore, one community composition score was typically associated with NPP and respiration, while the other was strongly correlated with primary producer biomass. In general this is consistent with the hypothesis that predator mediated effects on primary producer and ecosystem rates were indirectly driven by changes in community composition. Since the analyses were based on proportional biomass of species, this suggests that changes in predator stage structure or species identity lead to functional shifts in community composition.

**Biomass corrected analyses & results**

In our experiment we used natural densities of each stage. While this is the recommended design when predators differ substantially in size to avoid many experimental artifacts that would be caused by using traditional designs that keep biomass or densities of predators constant, it inevitably also results in differences in biomass among stages within predator treatments. To test whether these potential differences among predator stages were important in explaining the observed results, we first tested whether and how average predator (*Anax* or *Cybister*) biomass differed among stage treatments and then tested whether the per-unit biomass effect size (= \( \text{effect}_B \)) differed among predator size treatments.

*Predator biomass across treatments:* We calculated the average of the total dry biomass of *Anax* and *Cybister* populations within a pond in a given treatment over the duration of the experiment assuming an exponential model, where the biomass at time, \( B_t \), is given by \( B_t = B_0 e^{(g^t)} \), with \( B_0 \)
indicating the initial biomass within a tank, \( g = \) biomass growth rate, and \( t = \) time. \( g \) was calculated by setting \( B_t \) equal to the final biomass, \( t \) equal to the duration of the experiment, and solving the equation for \( g \). While the average size of individuals remained significantly different between stage treatments for the duration of the experiment, the average total (population) biomass of *Anax* was not significantly different between treatments with large stages (mean = 264.3 mg, s.e.m. = ±22.2) and small stages (mean = 226.8 mg, s.e.m. = ±15.4) (unequal variance t-test: \( P= 0.29 \)). Biomass in treatments with both stages (S+L) was significantly lower than expected from the sum of both S and L treatments (expected: 508 mg vs. observed: mean= 341.0 mg, s.e.m. = ±35.8)(\( P=0.006 \)). Average *Cybister* biomass was significantly higher in treatments with large stages (mean = 217.1 mg, s.e.m. = ±4.4) than in treatments with small stages (mean = 135.7 mg, s.e.m. = ±11.4) (unequal variance t-test: \( P<0.001 \)). Biomass in treatments with both stages (S+L) was not significantly (\( P = 0.286 \)) different from biomass expected from the sum of S and L treatments (expected: 352 mg; observed: mean= 320.8 mg, s.e.m. = ±26.8). While this exponential model is the most biologically realistic scenario, we also estimated biomass assuming a linear increase to test how robust our analysis was to specific model assumptions. Different model assumptions led to qualitatively similar results as the relative differences in biomass among treatments remained largely constant regardless of model specifications. Consequently we only present analyses based on the most realistic (exponential) model here.

*Per unit biomass effect of predators:* We calculated the biomass corrected effect (\( \text{effect}_{B} \)) of different predator treatments on a given ecosystem response variables (X) as \( X_B = (X_{JP} - X_C)/B_{J} \), where \( X_{JP} \) indicates the value of a given response variable for pond P in predator treatment J (AS, AL, ASL, CS, CL, CSL), \( X_C \) indicates the average of the respective response variable in the control, and \( B_{J} \) is the average biomass in predator treatment J. Positive values of
X_B indicate that the respective mesocosms had larger values than the control and negative values the opposite. Results of these analyses are given in Table 1 and Figures 1 & 2 in the main text.

**Intraspecific diversity effects – Additive vs. non-additive effects of multiple stages**

When both stages of a species are present in the same pond this allows for indirect interactions that can lead to non-additive (diversity) effects. If such non-additive interactions are present, the observed effects in treatments with both stages should be different from expectations calculated from the average effects of individual stage treatments and the control. The biomass corrected effect (effect_B) on ecosystem processes (Table 1, Fig. 2-3) already accounts for potential non-additive effects that may stem from predation among functional groups (i.e. cannibalism). Thus, we first used the raw data to calculate the expected effect for S+L treatments on the different ecosystem traits. Given the complexity of the system, it is not clear whether expected effects of both stages should be additive or multiplicative. Therefore, we calculated both types of effects. Given our additive design, multiplicative effects are given by: \( x_S \cdot x_L / x_C \), while the additive model is given by: \( (x_S - x_C) + (x_L - x_C) + x_C \) (21), where \( x_S, x_L, \) and \( x_C \) indicate the respective response variable (NPP, R, decomposition rate, periphyton, phytoplankton) of mesocosms with only the small, or large stage, or control respectively. This was done for each species separately. We then compared predictions to observed values of the respective response variables in mesocosms with both stages present using two-tailed t-test since we had no a priori expectations about the directional differences. Because additive and multiplicative models showed similar qualitative results we only present expected values for S+L treatments from additive models (in Supplementary Fig. S1, S2) which were generally more conservative.

*Results & Discussion* – Supplementary Table S2, Figures S1 and S2 summarize the
expected values for six different ecosystem properties and whether they differ significantly from observed values of the respective ecosystem property. At least one null model (additive or multiplicative) indicated “non-additive” (diversity) effects for phytoplankton biomass in dragonfly and beetle treatments. In addition, both models indicated non-additive effects of dragonfly stages on decomposition rates, and there was some support indicating non-additive effects on animal biomass in beetle treatments (Supplementary Table S2). Observed values were lower than expected values for phytoplankton and decomposition rates, while the opposite was true for animal biomass. Combined effects of stages in both species were not significantly different from null models assuming additive effects for NPP, respiration, and periphyton biomass (Supplementary Fig. S1, S1, Table S2). While it may seem somewhat surprising that we observed non-additive effects on phytoplankton biomass but not on NPP and respiration, this can be explained by the fact that phytoplankton biomass was only weakly correlated with NPP and respiration. Instead NPP and respiration were more strongly correlated with the animal community composition (see Table 1). Given the substantial variation in community structure within treatments and the potential for “functional redundancy” (with regards to their impact on NPP and respiration) among individuals and species within the community, this could explain why we did not detect non-additive effects for NPP and respiration.

These non-additive effects indicate the presence of indirect interactions. Given the complexity of our pond communities it is difficult to infer the exact nature of these indirect interactions. However, both of our species are highly cannibalistic, and previous studies suggest that cannibalism in a predator can often alter the combined effect of different predator stages on prey survival through consumptive and non-consumptive (behavioral) mediated indirect interactions that could explain the observed non-additive effects of stages. For instance, the
presence of large cannibals can reduce the density or foraging rate of small conspecific victims and thereby indirectly increase prey survival. We found that survival of small *Anax* was generally lower (~50%) in the presence of larger conspecifics (unequal variance t-test: P = 0.011). We did not find significant differences in survival of *Cybister* larvae among treatments (t-test: P > 0.55), but survival was generally lower in these treatments than in *Anax* treatments. Although we cannot directly identify the cause of mortality, we did occasionally observe large larvae of both species (*Cybister* and *Anax*) consume smaller conspecifics during our daily monitoring, suggesting that cannibalism may indeed be responsible for the reduced survival of small *Anax* and *Cybister*. The reduced survival of small stages (at least in *Anax* treatments) in the presence of cannibalistic conspecifics should reduce the combined effect of both stages on their prey and thereby indirectly also ecosystem processes. Indeed, the combined effects of both beetle stages were lower than expected on animal (i.e. their prey) biomass, and decomposition rates were reduced as well, consistent with the presence of a trophic cascade. However, it cannot explain why a similar pattern was observed in beetles, where survival of small stages was not significantly lower in the presence of large stages or why phytoplankton decreased less than expected when both stages were present in both predator treatments.

Cannibalism mediated behavioral interactions among predator stages (i.e. small individuals often alter their foraging behavior or habitat in the presence of large cannibalistic conspecifics) and/or prey (e.g. prey respond differentially to predator stages) could potentially explain some of these patterns. Indeed, previous studies indicate that the indirect effects of behavioral responses can have equal or even larger effects than the consumption (cannibalism) of small predators in some cannibalistic species. To test whether the observed diversity effects were largely driven by the reduction in predator density due to cannibalism, we adjusted our null
models to account for the potential reduction in predator biomass in treatments where both stages are present. In particular, we calculated the expected per-unit biomass effect for S+L treatments as: $(X_S B_S) + (X_L B_L)/(B_S + B_L)$, where $X_S$ and $X_L$ represent the per-unit biomass effect for small and large predator stages respectively (for calculation details see section: “Biomass corrected analysis” above) and $B_S$ and $B_L$ $B_{S+L}$ the corresponding average biomass of for a given stage structure treatment. While the non-additive effect for decomposition rates disappeared after accounting for the reduction in predator biomass, we still found non-additive “diversity effects” on primary producer biomass. Thus, the differences between observed and expected effects on ecosystem properties likely was driven by a combination of both consumptive and non-consumptive mediated indirect interactions in our system.
Supplementary References


