Supplementary materials

Method S1 List of published studies from which data were extracted

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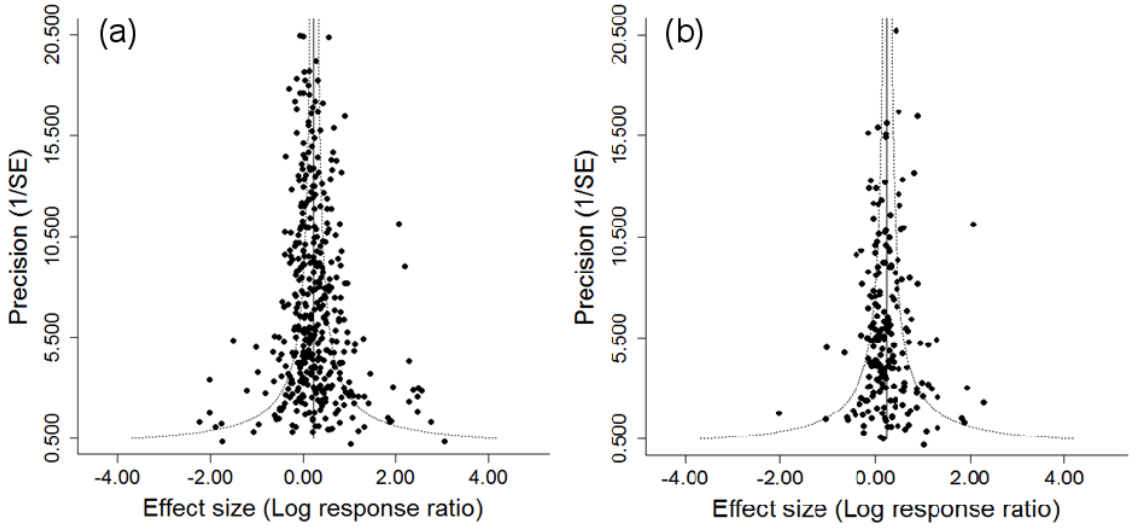
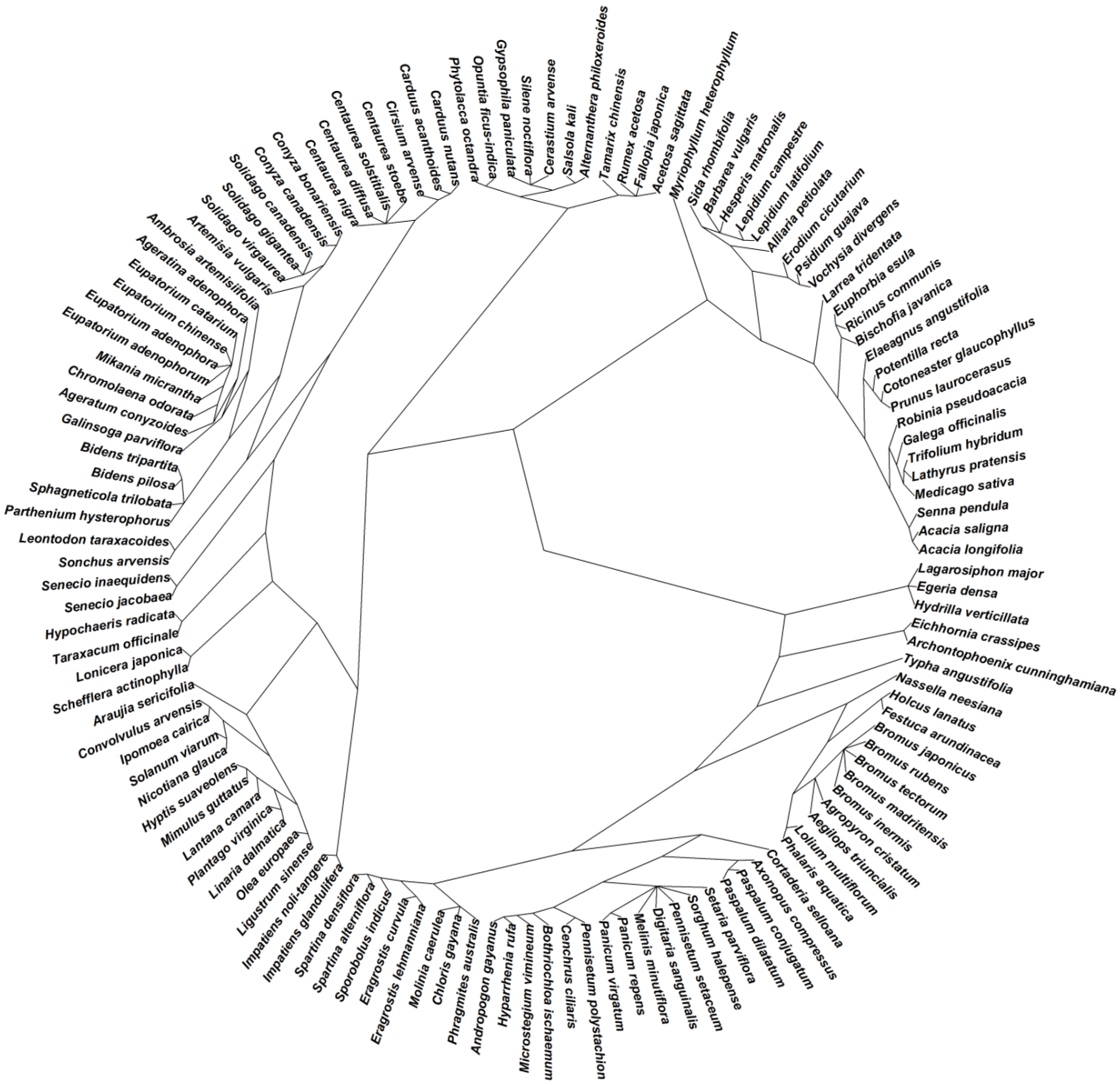
Method S2 Publication bias



Funnel plot showing the relationship between effect size (ln *R*) and inverse of the standard error. (a) Funnel plot for Data-I. (b) Funnel plot for Data-II.

Method S3 Phylogenetic tree used in this study and list of published studies employed for resolving polytomies within the initial base tree.



We included phylogenetic relatedness among the study species in models as a random factor by including the variance-covariance matrix of species relatedness. First, a super tree was constructed using the online program, Phylomatic42. Next, we solved polytomies within the base tree using the published molecular phylogenies below. Subsequently, the phylogenetic tree was

transformed to an ultrametric tree using the compute.brlen function in the package ape v 3.2. Finally, we calculated a variance-covariance matrix from the ultrametric tree using the vcv function in the package ape v 3.2, which represents phylogenetic relatedness among species.

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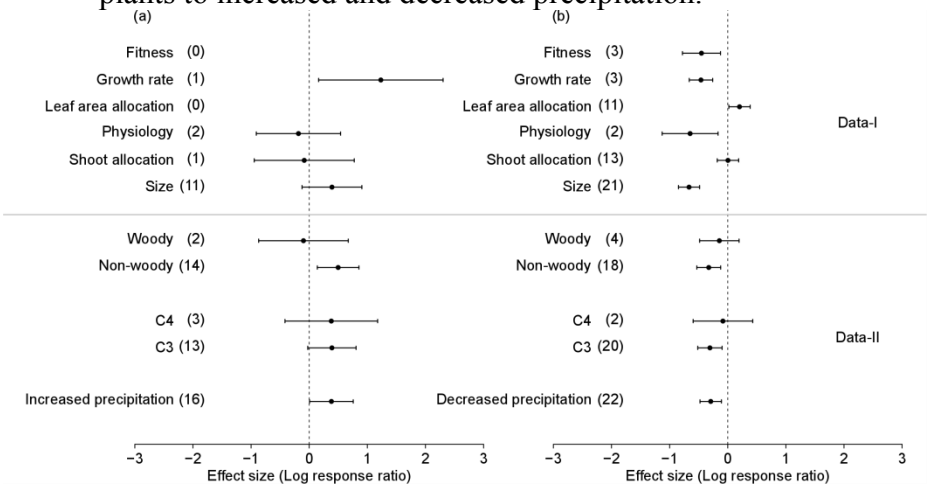
Figure S1. Performance response (indicated by log response ratio mean effect sizes) of alien plants to increased and decreased precipitation.



Performance response (indicated by log response ratio of mean effect sizes) of alien plants to increased (a) and decreased precipitation (b). Error bars represent 95% confidence intervals around the mean effect size estimates derived from the phylogenetically informed meta-analytic model. For drought studies, we calculated the effect size by dividing values obtained with drought treatment by those obtained under ambient conditions, whereas for elevated precipitation studies, the effect size was calculated by dividing values obtained with elevated precipitation treatment by those obtained under ambient conditions.