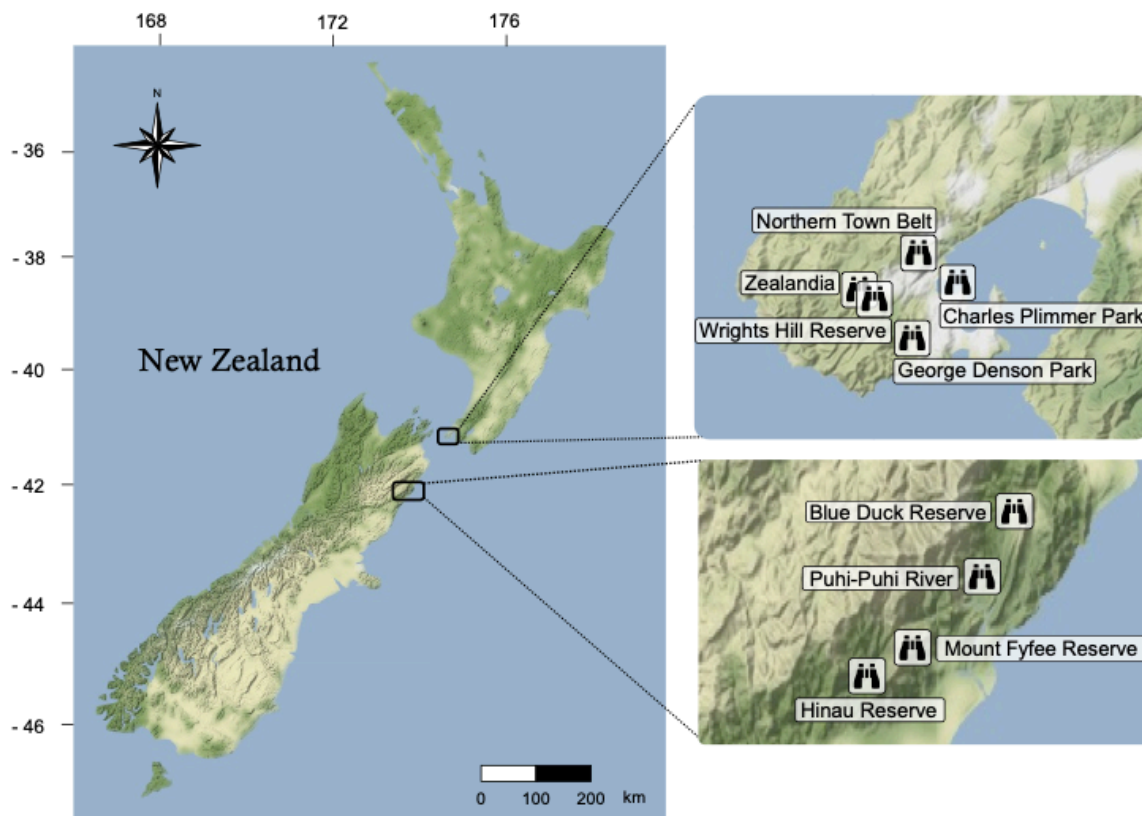


Supporting Information. Coux, C., I. Donoso, J.M. Tylianakis, D. García, D. Martínez, D.M. Dehling, and D.B. Stouffer. 2020. Tricky partners: native plants show stronger interaction preferences than their exotic counterparts. *Ecology*.

APPENDIX S1

Figure S1. Map of New Zealand with close-ups of the sampled sites. The sites from the North Island were more urbanised and were in the vicinity of Wellington, whereas the South Island sites were much more isolated.



Section S2 : Calculation of the deviance residuals d_{ij} and global deviance D_{model}

For each interaction between species i and j , the deviance residuals are calculated as:

$$d_{ij} = 2 \cdot F_{ij} \left[\log \left(\frac{F_{ijmin1}}{\hat{F}_{ij}} \right) \right] - \left[(F_{ij} + \theta_k) \left(\log \left(\frac{F_{ij} + \theta_k}{\hat{F}_{ij} + \theta_k} \right) \right) \right], \quad (S1)$$

such that:

F_{ij} corresponds to the frequencies of observed, realized frugivory events between pairs of species i and j ;

F_{ijmin1} corresponds to the observed frequencies but with zeros replaced by ones;

θ_k is the clumping parameter for the negative binomial distribution for a given site k ;

\hat{F}_{ij} to the estimated interaction frequencies between pairs of species i and j , which in turn are defined by:

$$\hat{F}_{ij} = e^{\log(C_{nb}) + \log(A_i) + \log(A_j)},$$

with \hat{F}_{ij} following a negative binomial distribution.

They can be easily extracted from the *negative.binomial()* function in R (see code in Data S2).

The global deviance D_{model} was calculated as the sum of the deviance residuals d_{ij} for each site k :

$$D_{model} = \sum d_{ij} = \sum 2 \cdot F_{ij} \left[\log \left(\frac{F_{ijmin1}}{\hat{F}_{ij}} \right) \right] - \left[(F_{ij} + \theta_k) \left(\log \left(\frac{F_{ij} + \theta_k}{\hat{F}_{ij} + \theta_k} \right) \right) \right],$$

with F_{ij} and \hat{F}_{ij} defined as above.

Figure S2. Observed interaction frequencies versus the fitted values of the ZINB model after a $\log(x+1)$ transformation for the Wrights Hill Reserve site.

The dotted line indicates the exact neutrality limit (i.e. when interaction frequencies are perfectly predicted by relative abundances), such that interactions that had low deviances (yellow points) appear closest to it, and high deviances (purple points) are further based on an orthogonal projection from this line. Points located on the top side of the dotted line correspond to avoidances, whereas those on the bottom side are preferences. Note that all of the zero values on the observed frequencies axis correspond to avoidances: the darker points correspond to higher predicted frequencies, which suggests that these high deviances were generated from the lack of interaction between two abundant species, and are more likely to be “true” zeros. Conversely, the lighter points indicate zeroes more likely to be related to the rarity of one or both of the species involved in the interaction (“false” zeroes).

