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Supplementary Material

Assessing plant translocation success: common metrics mask high levels of inbreeding in a recently established *Banksia brownii* (Proteaceae) population

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Supplementary Table S1. Genetic diversity of a translocated population of *Banksia brownii* and its four source populations (CE, WY, HH and CB). *N*, number of sampled plants; *Na*, mean number of alleles per locus; *Nar*, allelic richness (mean number of alleles per locus) estimated using rarefaction; *Ho*, observed heterozygosity; *He*, unbiased expected heterozygosity; *Fis*, inbreeding coefficient (SE shown in parentheses).

Population	<i>N</i>	<i>Na</i>	<i>Nar</i>	<i>Ho</i>	<i>He</i>	<i>Fis</i>
Translocated	116	6.5	3.49 (0.22)	0.451 (0.03)	0.668 (0.04)	0.316 (0.04)
CE	34	4.0	2.92 (0.26)	0.366 (0.05)	0.588 (0.06)	0.368 (0.06)
WY	31	4.25	2.78 (0.28)	0.461 (0.07)	0.545 (0.05)	0.151 (0.13)
HH	27	4.88	3.43 (0.27)	0.543 (0.06)	0.670 (0.04)	0.200 (0.06)
CB	24	4.75	2.84 (0.27)	0.434 (0.06)	0.522 (0.06)	0.170 (0.05)

Supplementary Table S2. Pairwise F_{ST} (below diagonal) and D_{ST} (above the diagonal) values for translocated and wild populations of *Banksia brownii*.

	Translocated	Hassell	Millbrook	Waychincup	Yungemere
Translocated	-	0.478	0.118	0.142	0.486
Hassell	0.118	-	0.563	0.406	0.278
Millbrook	0.028	0.125	-	0.188	0.497
Waychincup	0.043	0.118	0.051	-	0.378
Yungemere	0.124	0.081	0.118	0.116	-



Figure S1: Inflorescence of *Banksia brownii*

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