Supplementary material

Table S1: Source of *Isoodon* samples for mitochondrial DNA (mtDNA) sequences and microsatellite genotypes

	Western Australia	South Australia	Victoria	Total
mtDNA				218
This study	146			
Li et al. [1]		20	29	
Cooper et al. [2]	13	1	9	
Microsatellite				731
This study	56			
Ottewell et al. [3]	77			
Ottewell et al. [4]	39			
Li et al. [1]		372	186	

Table S2: Pairwise F_{ST} based on microsatellite data (above diagonal) and p-distance values of mitochondrial data (below diagonal) between populations of *Isoodon* bandicoots. Significant F_{ST} values after correction for multiple comparisons and p-distance values are denoted with bold font.

| | | WA | | | | | | SA | | | VIC | | |
		Barrow Island	Kimberley islands	Kimberley mainland	Perth	SW WA coast	SW WA inland	Kangaroo Island	Fleurieu Peninsula	Mount Lofty Ranges	The Grampians	Lower Glenelg	Mount Burr
WA	Barrow Island	-	**0.195**	**0.150**	**0.234**	**0.237**	**0.232**	**0.405**	**0.359**	**0.356**	**0.387**	**0.391**	**0.318**
	Kimberley islands	0.020	-	0.097	**0.243**	**0.252**	**0.248**	**0.421**	0.380	**0.356**	**0.410**	0.413	**0.315**
	Kimberley mainland	0.017	0.020	-	**0.137**	**0.123**	**0.122**	**0.287**	0.247	**0.24**	**0.294**	0.301	**0.228**
	Perth	0.028	0.030	0.030	-	0.015	**0.052**	**0.258**	**0.228**	0.176	**0.331**	**0.338**	**0.280**
	SW WA coast	0.031	0.034	0.033	0.025	-	0.047	0.306	0.212	**0.165**	**0.366**	0.394	**0.292**
	SW WA inland	0.025	0.027	0.026	0.024	0.021	-	**0.266**	**0.194**	**0.156**	**0.321**	0.346	**0.271**
SA	Kangaroo Island	0.031	0.031	0.032	0.025	0.027	0.026	-	0.453	**0.318**	**0.510**	0.565	**0.416**
	Fleurieu Peninsula	0.019	0.023	0.024	0.026	0.030	0.022	0.034	-	0.077	**0.490**	**0.544**	**0.398**
	Mount Lofty Ranges	0.020	0.021	0.019	0.029	0.033	0.026	0.034	0.020	-	**0.434**	**0.455**	**0.367**
VIC	Grampians	0.043	0.048	0.045	0.050	0.047	0.044	0.049	0.050	0.045	-	0.253	**0.186**
	Lower Glenelg	0.041	0.047	0.043	0.051	0.049	0.044	0.050	0.048	0.046	0.007	-	**0.114**
	Mount Burr	0.039	0.045	0.041	0.049	0.047	0.042	0.050	0.046	0.044	0.012	0.005	-
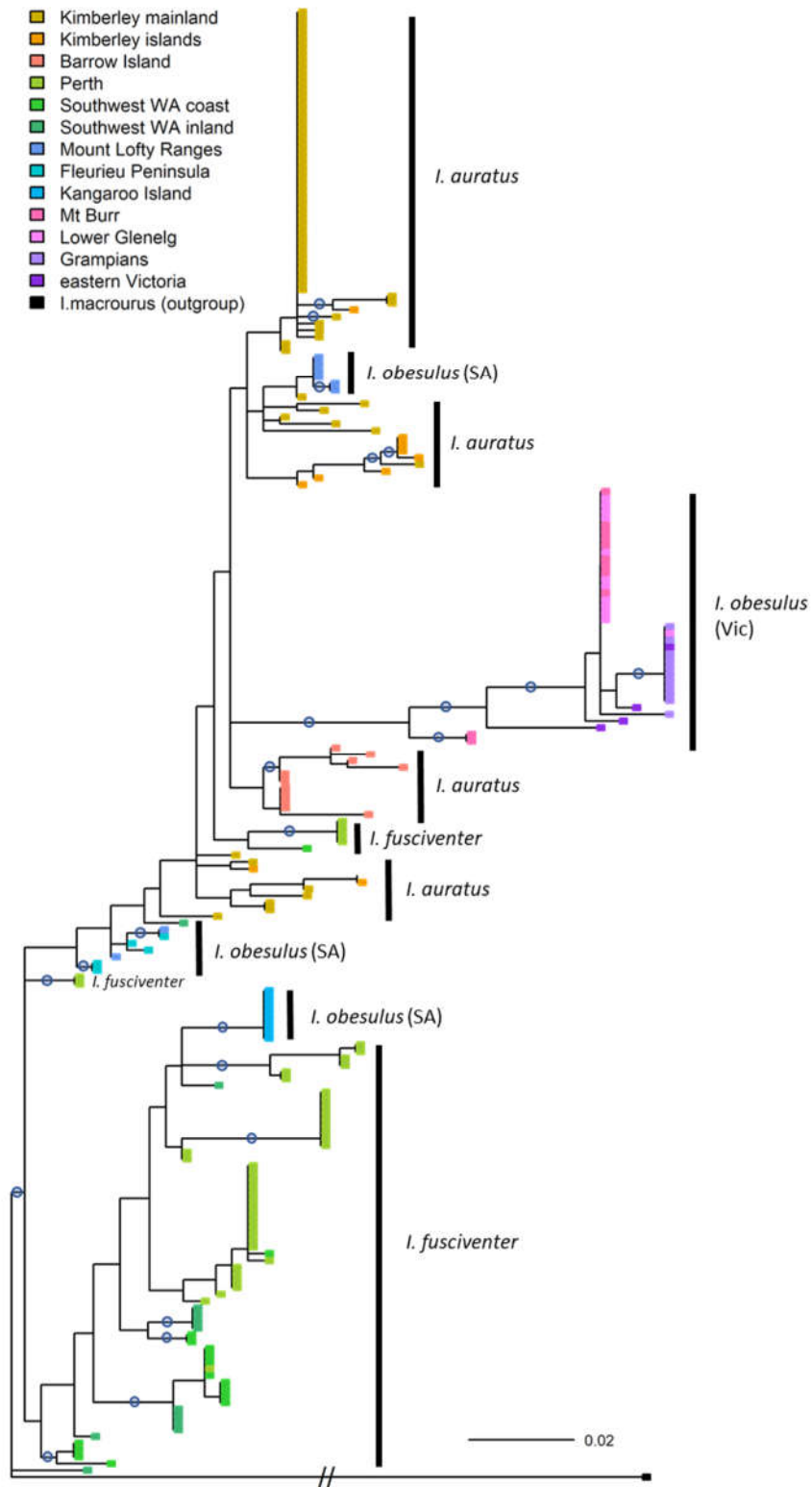
Figure S1: Maximum likelihood analysis of mitochondrial D-Loop sequences analysed using RAxML. Bootstrap values >80% are indicated on branches as grey circles.
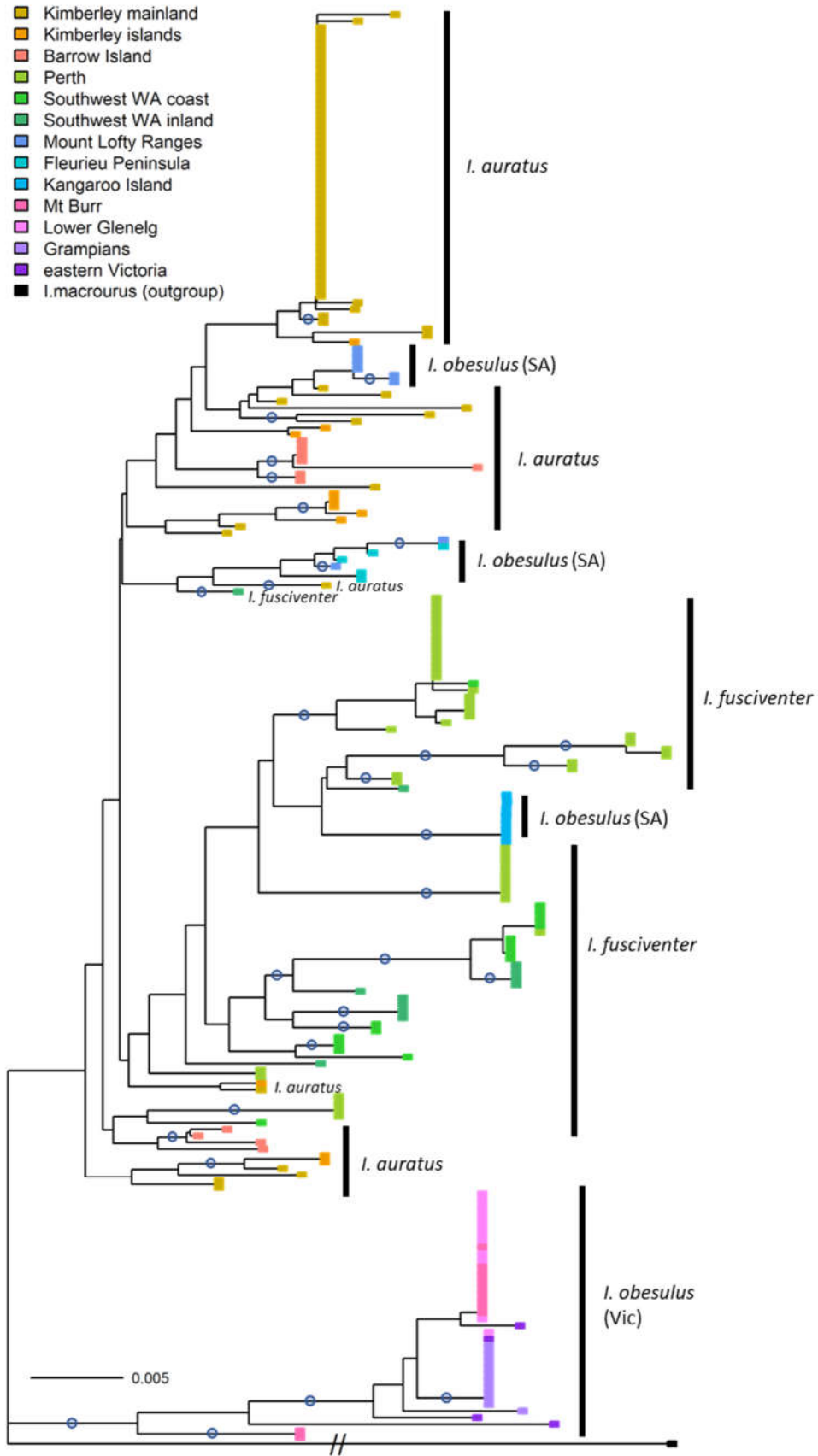
Figure S2: Neighbour joining analysis of Isoodon D-Loop sequences using MEGA. Bootstrap values >80% are indicated on branches as grey circles.
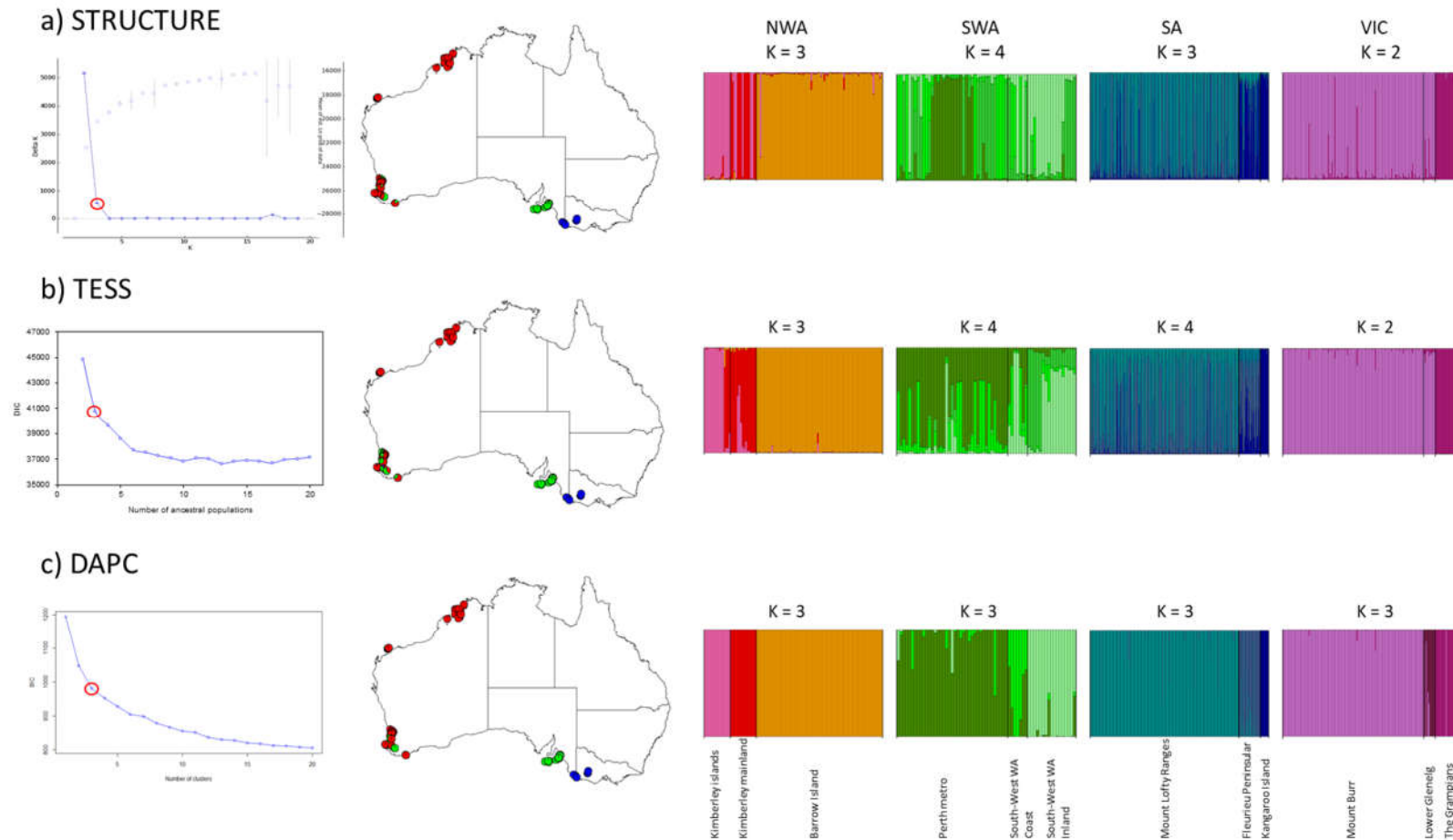
Figure S3: Summary of the clustering analyses based on 10 microsatellite loci obtained from STRUCTURE (a), TESS (b) and DAPC (c). Different colours reflect estimated membership to particular clusters. Insert graphs on the left show the modal value of $K = 3$ which is circled in red colour for each analysis when all samples were analysed. Australia map illustrated individuals' estimated membership to three genetic clusters relative to their geographic locations. Bar graphs on the right show individuals' estimated membership when each region is analysed separately. These regions include North Western Australia, South Western Australia, South Australia and Victoria. Black lines separate samples from different sampling locations. Each coloured bar represents each individual.
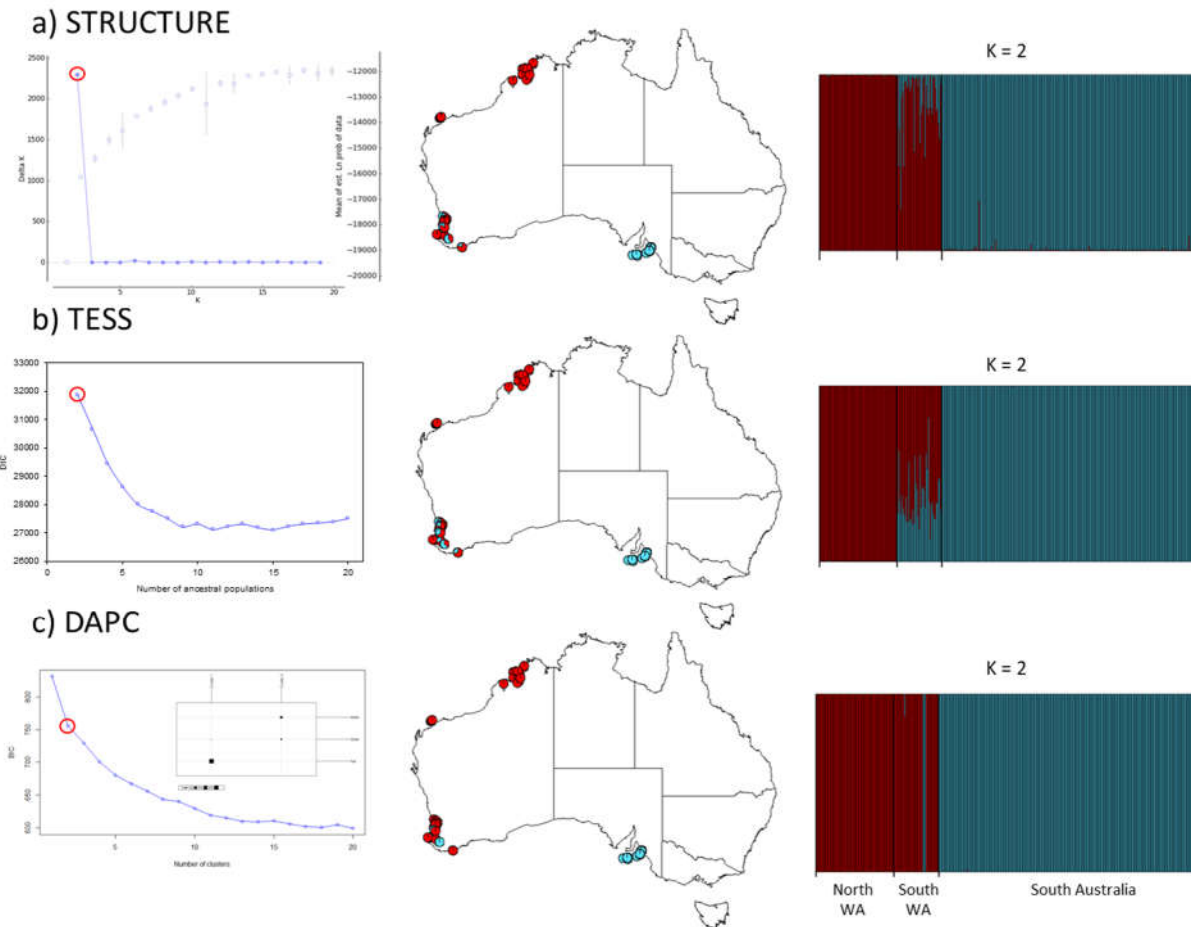
Figure S4: Summary of the clustering analyses based on 10 microsatellite loci obtained from STRUCTURE (a), TESS (b) and DAPC (c). Different colours reflect estimated membership to particular clusters. Insert graphs on the left show the modal value of $K = 2$ which is circled in red colour for each analysis when all samples were analysed. Australia map illustrated individuals' estimated membership to two genetic clusters relative to their geographic locations. Bar graphs on the right show individuals' estimated membership when each region is analysed separately. These regions include North Western Australia, South Western Australia, and South Australia. Black lines separate samples from different sampling locations. Each coloured bar represents each individual.
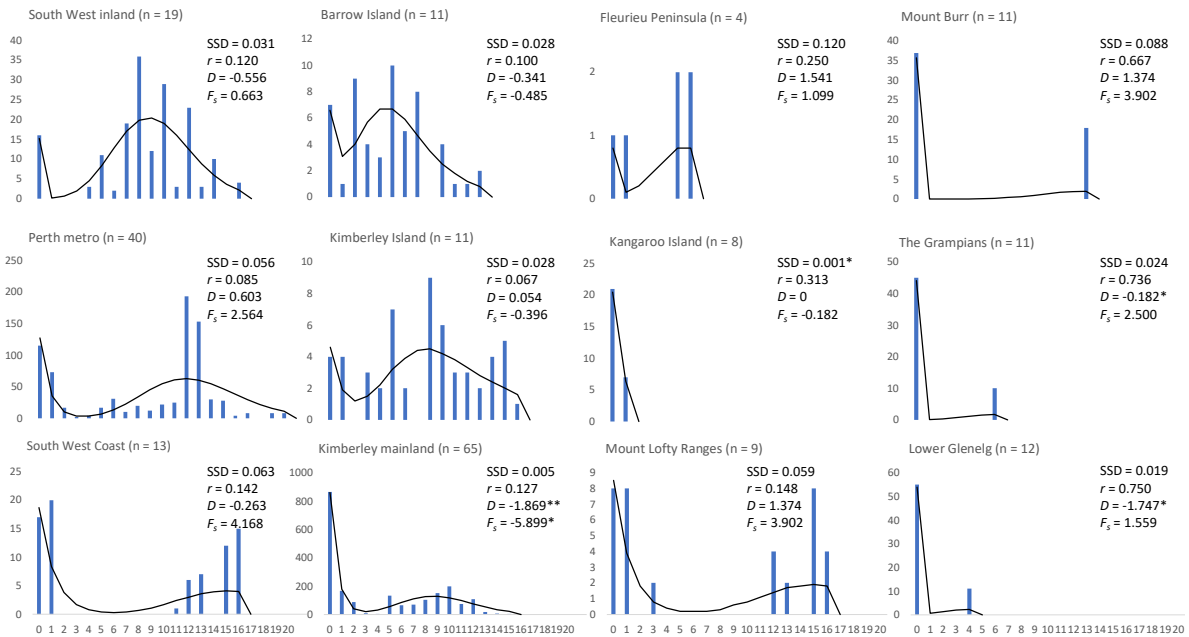
Figure S5: Mismatch distribution of mtDNA sequences in *Isoodon* species from North Western Australia, South Western Australia, East South Australia, West South Australia and Victoria. Black line represents the expected distribution for the spatial expansion model. SSD, associated sums of squares; *r*, Raggedness index; *D*, Tajima's D and F_S, Fu's F_S. Significant level *P < 0.05, **P < 0.01, ***P < 0.001.

References

1. Li, Y.; Lancaster, M.L.; Carthew, S.M.; Packer, J.G.; Cooper, S.J.B. Delineation of conservation units in an endangered marsupial, the southern brown bandicoot (*isoodon obesulus obesulus*), in south australia/western victoria, australia. *Australian Journal of Zoology* **2014**, *62*, 345-359.
2. Cooper, S.J.B.; Ottewell, K.; MacDonald, A.J.; Adams, M.; Byrne, M.; Carthew, S.M.; Eldridge, M.D.B.; Li, Y.; Pope, L.C.; Saint, K.M*., et al.* Phylogeography of southern brown and golden bandicoots: Implications for the taxonomy and distribution of endangered subspecies and species. *Australian Journal of Zoology* **2020**, *66*, 379-393.
3. Ottewell, K.; Dunlop, J.; Thomas, N.; Morris, K.; Coates, D.; Byrne, M. Evaluating success of translocations in maintaining genetic diversity in a threatened mammal. *Biological Conservation* **2014**, *171*, 209-219.
4. Ottewell, K.; Pitt, G.; Pellegrino, B.; Van Dongen, R.; Kinloch, J.; Willers, N.; Byrne, M. Remnant vegetation provides genetic connectivity for a critical weight range mammal in a rapidly urbanising landscape. *Landscape and Urban Planning* **2019**, *190*, 103587.