Supplementary Material

Kinship analysis reveals low dispersal in a hog deer (*Axis porcinus*) population in Wilsons Promontory National Park, Australia

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Supplementary material Table S1 Filtering steps implemented in *dartR* to filter hog deer SNP loci, the number of SNPs pre- and post-filtering step, and the number of loci removed at each step
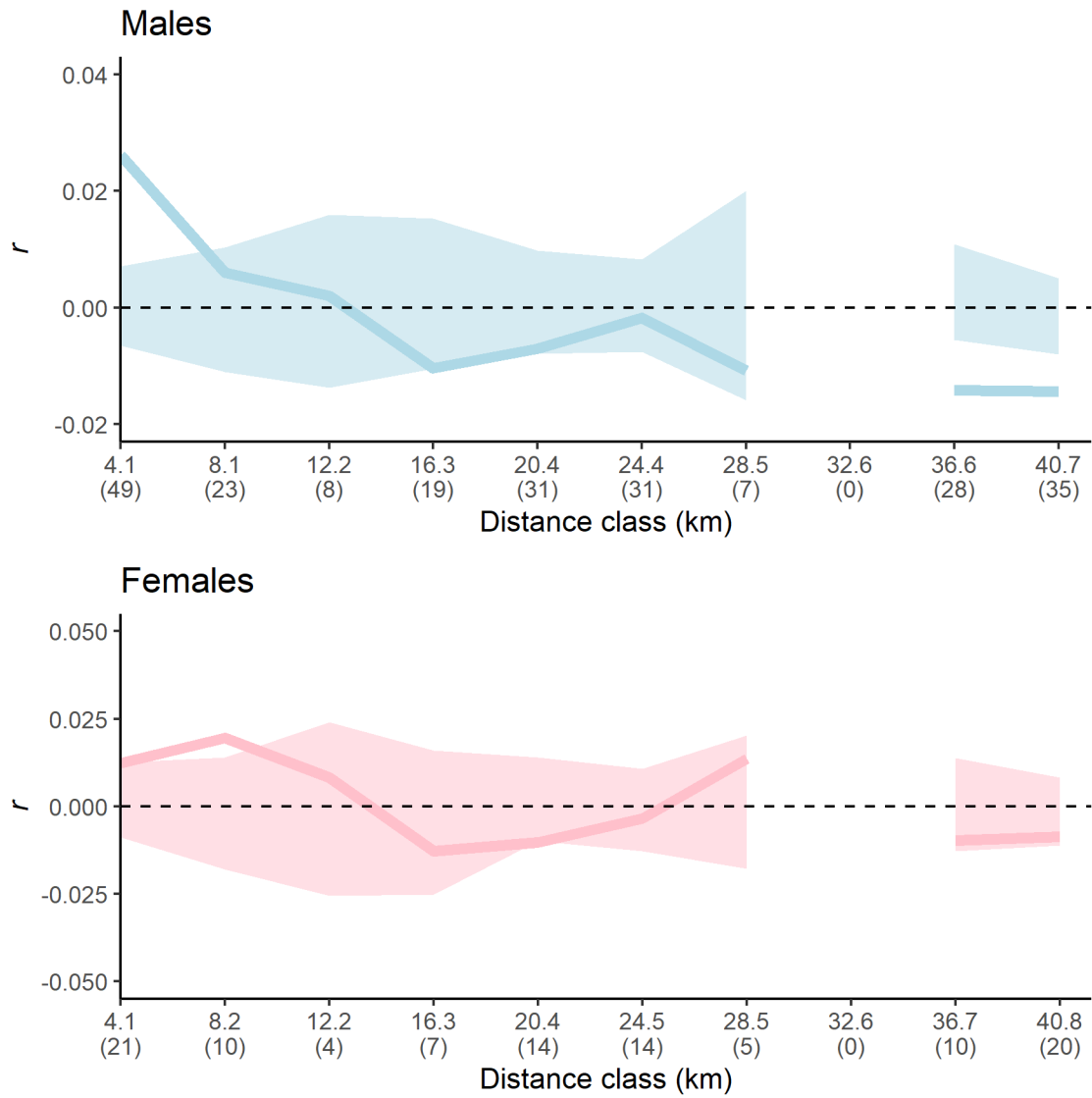
Filter	dartR function	Threshold	Pre-filter loci no.	Post-filter loci no.	*n* loci removed
X/Y Chromosome	NA	NA	12881	12584	297
DArT reproducibility	Gl.filter.reproducibility	1	12584	9821	2763
Call rate (loci)	Gl.filter.callrate	0.9	9821	9137	684
Linkage	Gl.filter.secondaries	Retain 'best' SNP (based on average PIC)	9137	8959	178
Minor allele frequency	Gl.filter.maf	0.05	8959	8366	593
Hardy Weinberg equilibrium	Gl.filter.hwe	$\geq$2 pops out of HWE for locus (where all WPNP sites are considered one pop)	8366	8328	38
Read depth	Gl.filter.rdepth	<5, >75	8328	8295	33
Heterozygote excess (loci)	Gl.basic.stats Gl.drop.loc	$\geq$2 pops with heterozygote values above 0.7 for locus (where all WPNP sites are considered one pop)	8295	8275	20
Sex linkage	Gl.filter.sexlinked	Heterogametic sex = 0.1 Homogametic sex = 1 Presence = 0.1	8275	8275	0
Monomorphs	Gl.filter.monomorphs	NA	8275	8275	0
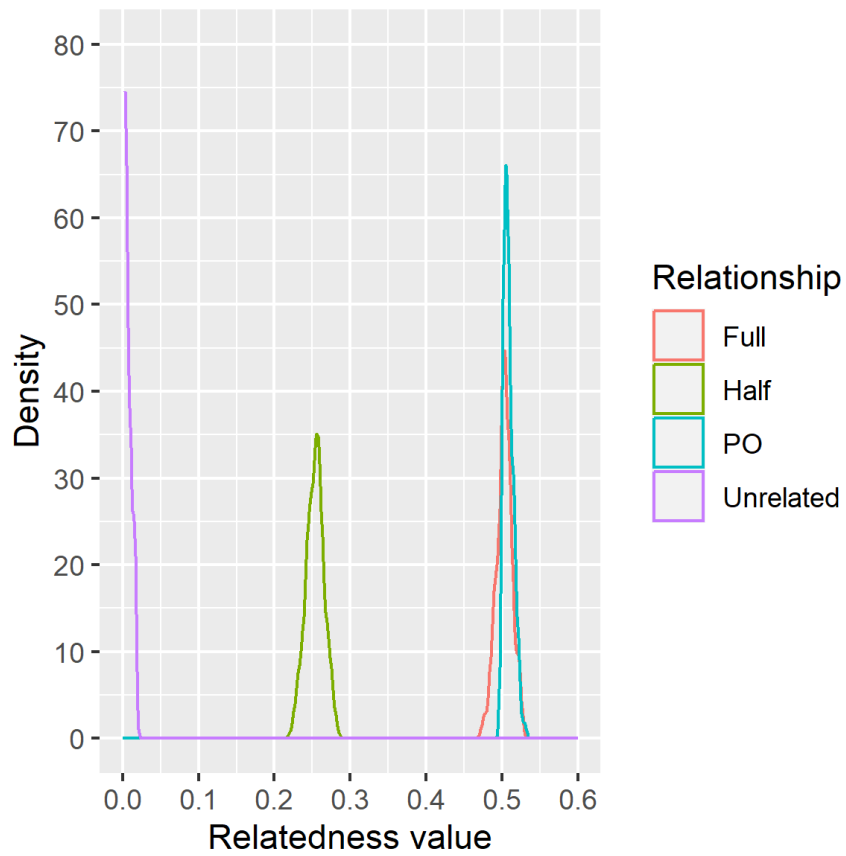
Supplementary material Fig. S1 Density plot of relatedness values from simulated pairs of known relationship. Full = full siblings, Half = half siblings, PO = parent-offspring

Supplementary material Table S2 Diversity indices calculated for each hog deer site sampled, as well as combined Wilsons Promontory National Park (WPNP) sites, and combined WPNP and Yanakie sites. Standard errors are in parentheses. g_2 values in bold represent statistically significant variance in inbreeding (null hypothesis $g_2 = 0$) at a p-value of 0.001. n = sample size; H_O = observed heterozygosity; H_S = observed gene diversities; F_{IS} = inbreeding coefficient; g_2 = identity disequilibrium; $sMLH$ = standardised multi-locus heterozygosity

Site	n	H_O	H_S	F_{IS}	g_2	$sMLH$
Boole Poole	13	0.3121	0.3321	0.0500	**0.0082**	1 (0.0255)
		(0.0021)	(0.0019)	(0.0034)	**(0.0048)**	
Sunday Island	12	0.3292 (0.002)	0.3566	0.0684	**0.0166**	0.9999
			(0.0017)	(0.0034)	**(0.0071)**	(0.0372)
Snake Island	14	0.3729	0.3908	0.0384	**0.0024**	1 (0.0136)
		(0.0019)	(0.0015)	(0.0031)	**(0.0010)**	
Yanakie	13	0.3330	0.3535	0.0478	**0.0018**	1 (0.0126)
		(0.0018)	(0.0018)	(0.0032)	**(0.0005)**	
Kangaroo Valley	14	0.3329	0.3537	0.0453	**0.0037**	1 (0.0167)
		(0.0018)	(0.0018)	(0.0031)	**(0.0013)**	
Tidal River	14	0.3366	0.3460	0.0244	**0.0048**	1 (0.019)
		(0.0018)	(0.0018)	(0.0030)	**(0.0014)**	
Oberon Bay	11	0.3361	0.3485	0.0264	**0.0069**	0.9998
		(0.0019)	(0.0019)	(0.0035)	**(0.0022)**	(0.0244)
WPNP	39	0.3352	0.3601	0.0692	**0.0047**	0.9999
		(0.0016)	(0.0016)	(0.0021)	**(0.0009)**	(0.0111)
WPNP/Yanakie	52	0.3347	0.3618	0.0750	**0.0040**	0.9999
		(0.0016)	(0.0015)	(0.0019)	**(0.0007)**	(0.0089)

Supplementary material Fig. S2 Correlogram showing genetic similarity (*r*) at different distance classes for male samples and female samples across WPNP and Yanakie, with kin pairs identified in *Colony* removed. Solid lines show genetic similarity across distances, shaded areas show 95% confidence intervals, with values falling between these confidence intervals representing a random distribution of genotypes and therefore no correlation. Values falling outside of confidence intervals indicate a significant correlation. Numbers in parentheses are sample sizes