

Supplementary Tables

Table S1: Gene ontology terms used for identifying transcripts with immune, MHC, growth or metabolism functions.

Function	Search Terms
Immune	"immune system process", "innate immune response", "antigen", "chemokine", "T cell", "Antibody", "Interleukin", "leukocyte", "Lymphocyte", "B cell", "response to fungus", "bacterium"
MHC	"MHC", "major histocompatibility", "histocompatibility"
Growth	"GO:005126", "regulation of growth", "growth factor activity"
Metabolism	"oxidative stress", "carbohydrate metabolic process", "metabolic response", "energy homeostasis", "metabolic process", "gluconeogenesis", "glucose transport", "energy homeostasis"

Table S2: Inference criteria derived in Manichaikul *et al.* (2010) and used here to assign relatedness categories. Estimated PLINK Z scores were combined to generate the kinship coefficient = $\frac{Z1}{4} + \frac{Z2}{2}$. Z0 reflects the proportion of the genome where a pair of individuals share zero alleles identical by descent.

Relationship	Kinship coefficient	Inference criteria	Z0	Inference criteria
Monozygotic twin	$\frac{1}{2}$	$> \frac{1}{2^{3/2}}$	0	< 0.1
Parent-offspring	$\frac{1}{4}$	$\frac{1}{2^{5/2}} < \frac{1}{2^{3/2}}$	0	< 0.1
Full-sibling	$\frac{1}{2}$	$\frac{1}{2^{5/2}}, \frac{1}{2^{3/2}}$	$\frac{1}{4}$	0.1, 0.365
Second-degree	$\frac{1}{8}$	$\frac{1}{2^{7/2}}, \frac{1}{2^{5/2}}$	$\frac{1}{2}$	0.365, $\frac{1}{2^{3/2}}$
Third-degree	$\frac{1}{16}$	$\frac{1}{2^{9/2}}, \frac{1}{2^{7/2}}$	$\frac{3}{4}$	$1 - \frac{1}{2^{3/2}}, 1 - \frac{1}{2^{5/2}}$
Unrelated	0	$< \frac{1}{2^{9/2}}$	1	$1 - \frac{1}{2^{5/2}}$

Supplementary Figures

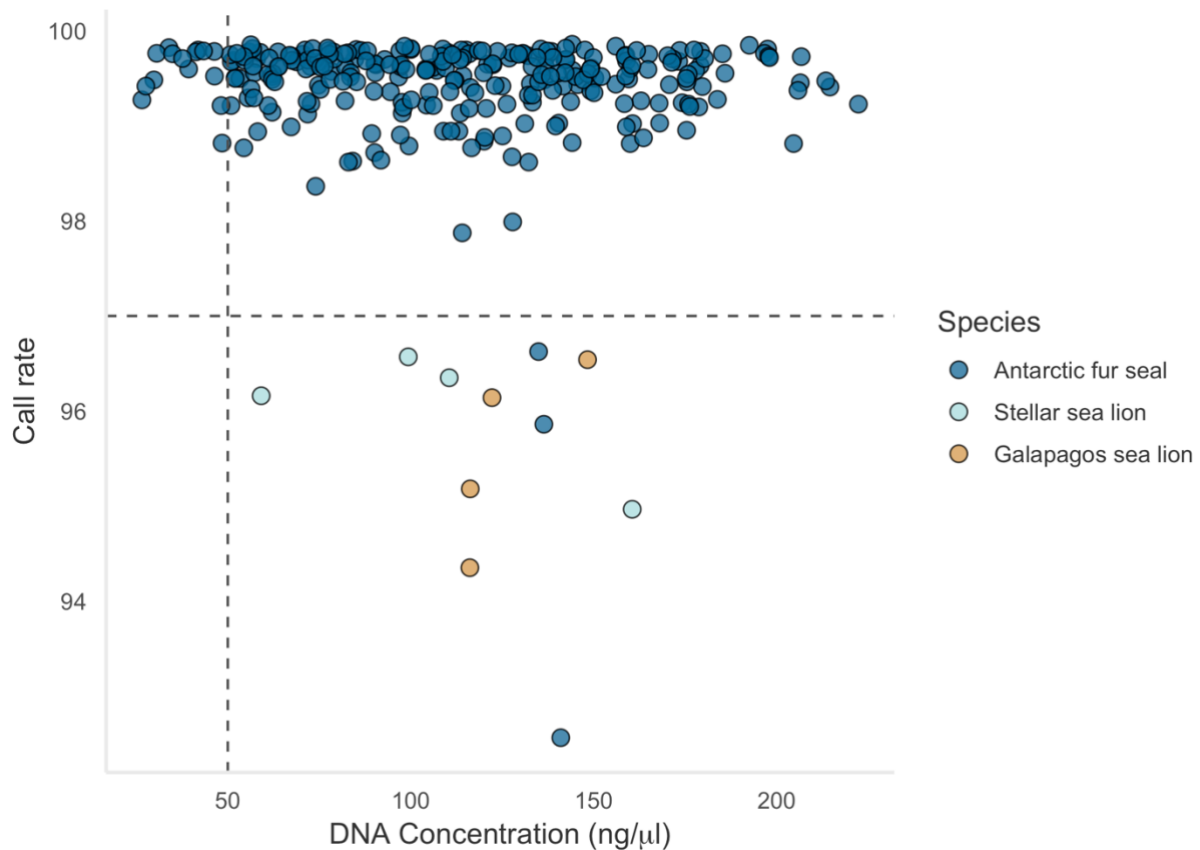


Figure S1. Relationship between DNA concentration and call rate for samples that were genotyped on the Antarctic fur seal genotyping array and that passed dish QC quality control filtering. DNA concentration was not available for one sample leaving a total of 282 data points. The dashed vertical line represents the array manufacturer's recommended sample quality and the dashed horizontal line represents the call rate threshold applied to the data for downstream analysis. Samples are colour coded by species. No relationship was found between call rate and DNA concentration (slope = -3.4, $t = -1.10$, $n = 282$, $df = 280$, $P = 0.27$). This relationship also holds when outliers with a call rate below 97% were removed (slope = -7.03, $t = -0.86$, $n = 271$, $df = 269$, $P = 0.39$).

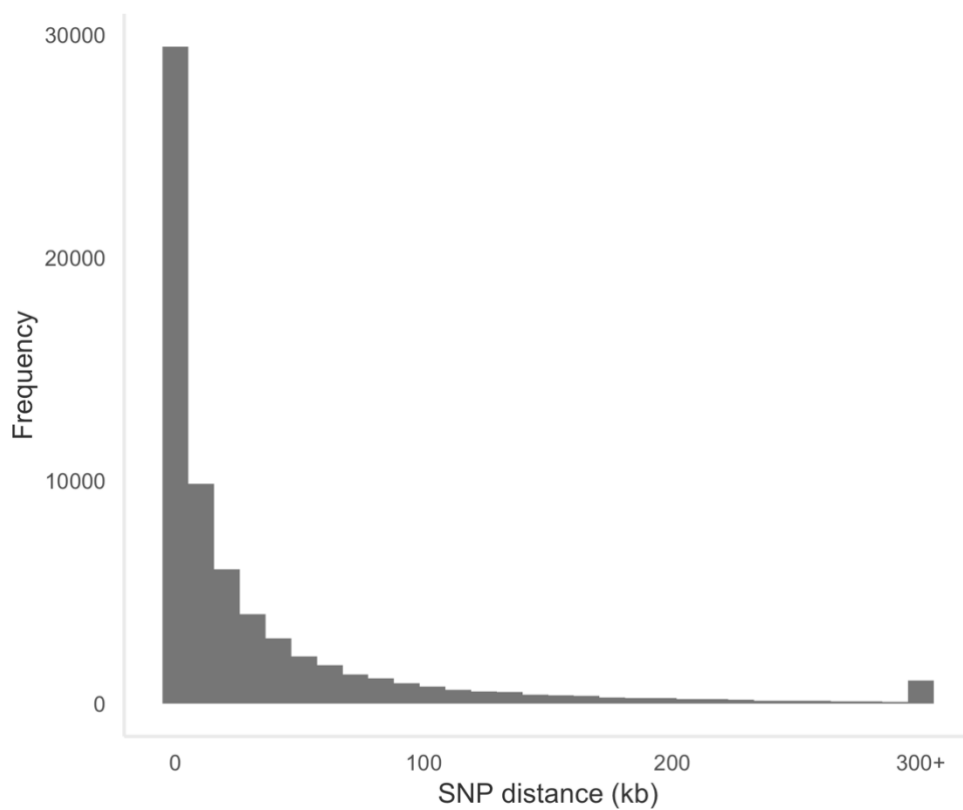


Figure S2. Distribution of the distance between adjacent RAD derived SNPs that were successfully typed on the Antarctic fur seal genotyping array.

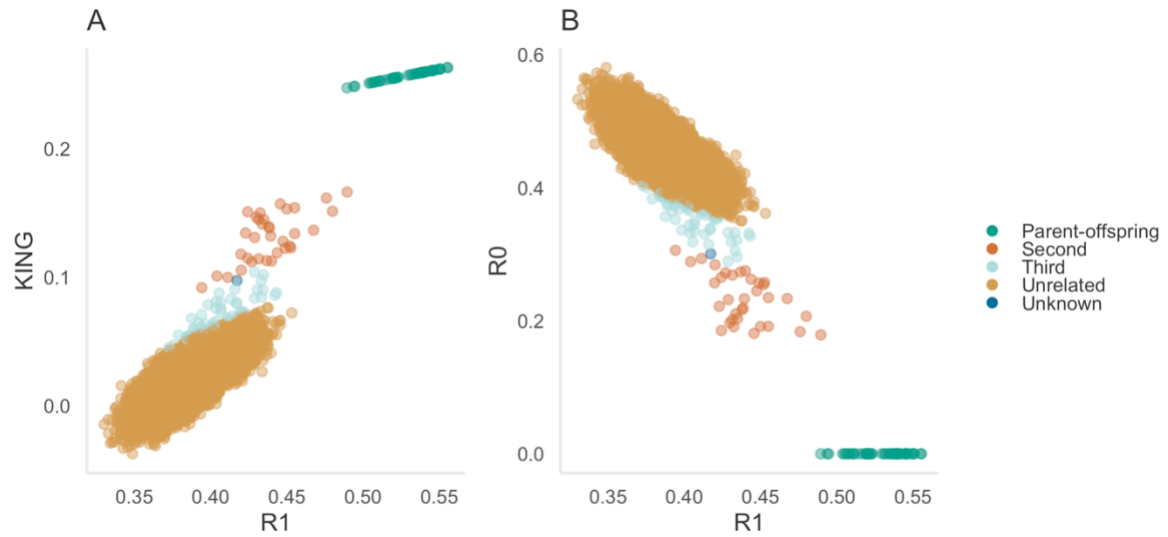


Figure S3. R1 coefficients plotted against (A) KING-robust kinship coefficients; and (B) R0 coefficients for all individual pairwise comparisons. Points are coloured according to the relationship categories inferred by comparing PLINK Z scores with the inference criteria derived in Manichaikul *et al.* (2010) and provided in Table S2.

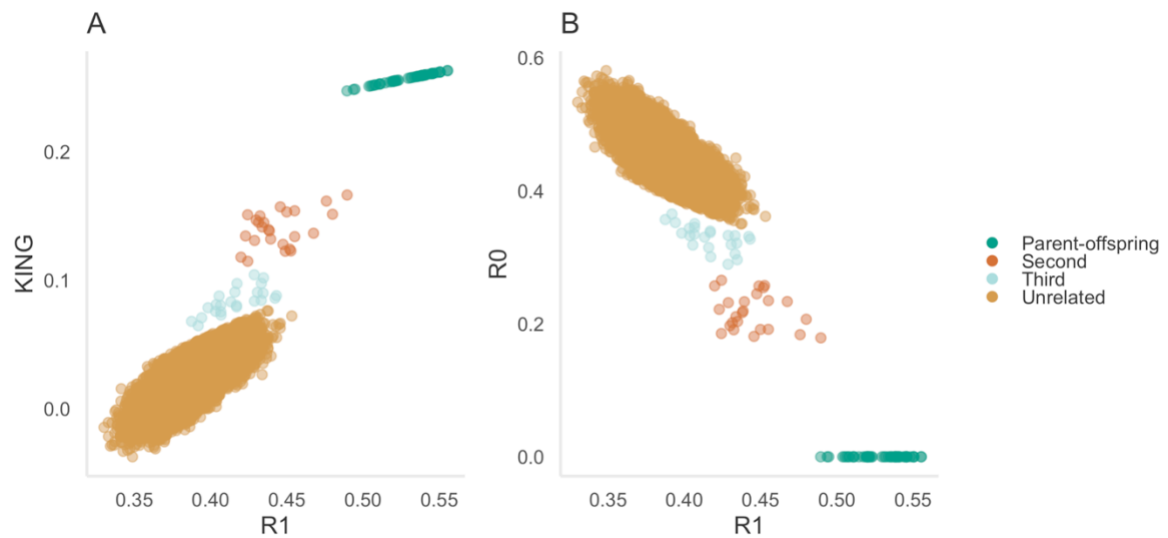


Figure S4. R1 coefficients plotted against (A) KING-robust kinship coefficients; and (B) R0 coefficients for individual pairwise comparisons. Difficult to call relationships, i.e. those within 0.01 of the inference thresholds, have been excluded. Points are coloured according to the relationship categories inferred by comparing PLINK Z scores with the inference criteria derived in Manichaikul *et al.* (2010) and provided in Table S2.

References

Manichaikul, A., J. C. Mychaleckyj, S. S. Rich, K. Daly, M. Sale *et al.*, 2010 Robust relationship inference in genome-wide association studies. *Bioinformatics* 26: 2867–2873.