

## Supplementary Information

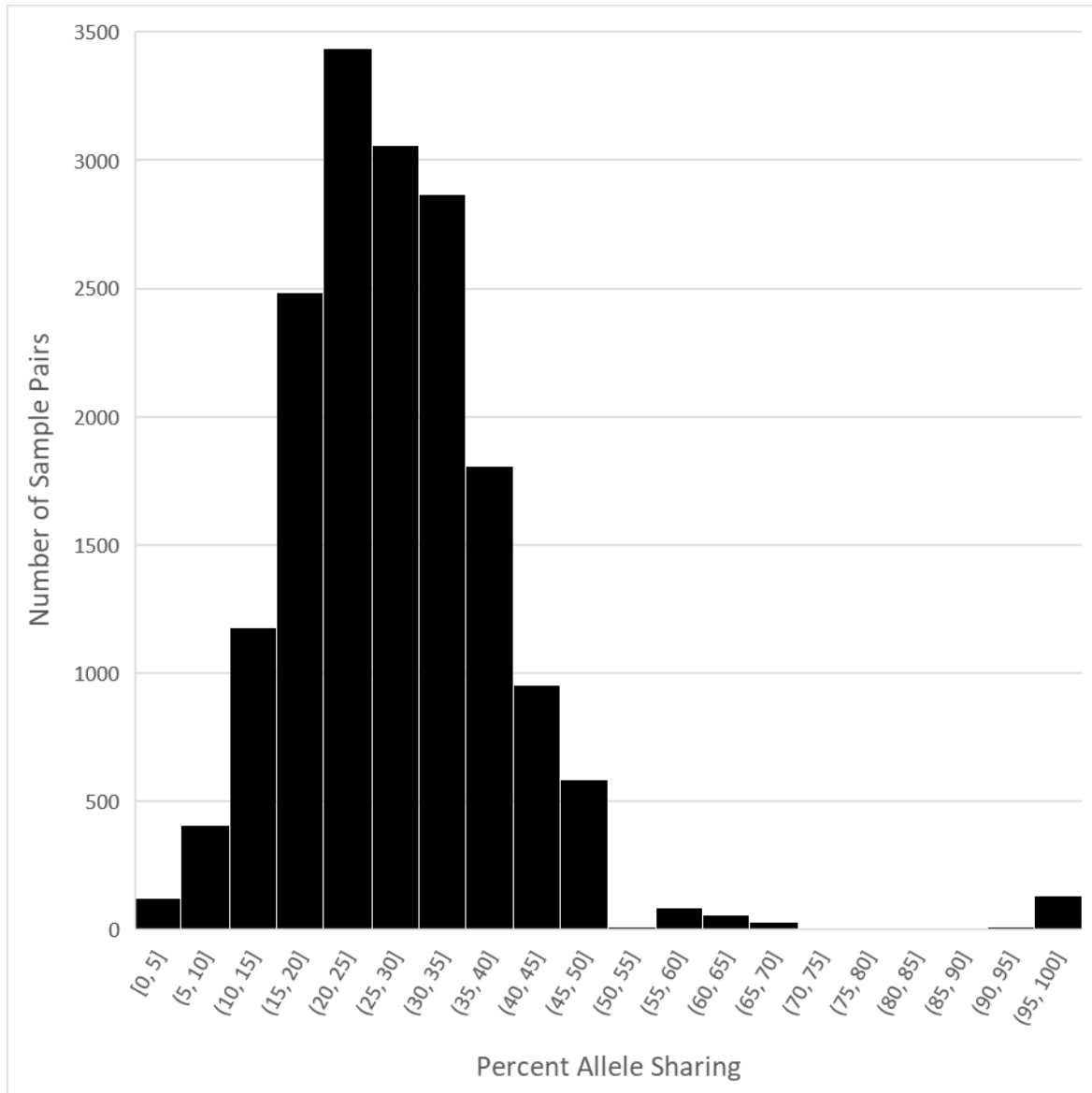
**Supplemental Table 1.** Diversity and resolving power information for the 11 microsatellite loci used in this study. The multilocus PID is  $3.5 \times 10^{-15}$  and PIDsibs is  $1.9 \times 10^{-5}$

Locus <sup>a</sup>	Multiplex	No. Alleles	Repeat Size (bp)	Allele size range (bp)	PID <sup>b</sup>	PIDsibs <sup>c</sup>
dst119	1	6	4	277-309	0.767	0.881
dst1318	1	16	4	360-420	0.016	0.306
dst168	1	11	4	142-186	0.043	0.343
dst2601	1	16	4	155-223	0.020	0.312
dst2793	1	16	2	195-249	0.028	0.324
dst2887	1	14	4	161-221	0.035	0.342
dst1210	2	10	4	253-289	0.052	0.354
dst1230	2	12	2	190-260	0.055	0.363
dst1567	2	11	4	302-358	0.031	0.327
dst3268	2	5	4	416-464	0.134	0.438
dst3315	2	15	4	238-298	0.027	0.323

<sup>a</sup> Shier et al. (2021)

<sup>b</sup> PID stands for probability of identity

<sup>c</sup> PIDsibs stands for the probability of identity of siblings



**Supplemental Figure 1.** Percent allele sharing among genotypes recovered from giant kangaroo rat fecal pellets 2020–2021. The bimodal spread of the data allowed us to differentiate genotypes originating from the same individual animal (89–100% of alleles) versus genotypes from distinct individuals (0–70% of alleles).