

Sean M. Murphy, Ben C. Augustine, Jennifer R. Adams, Lisette P. Waits, and John J. Cox. 2018. Integrating multiple genetic detection methods to estimate population density of social, territorial carnivores. *Ecosphere*.

Appendix S1. Results from sex-specific spatial capture-recapture models and the expected distributions of Bayesian p -values relative to observed Bayesian p -values.

Table S1. Parameter estimates and their 95% credible intervals from sex-specific spatial capture-recapture models using only the scat transect detection data (i.e., SO model).

Parameter	Males		Females	
	Estimate	95% CI	Estimate	95% CI
λ_0	0.015	0.006–0.038	0.019	0.010–0.040
σ^s	1560	1112–2582	1525	1158–2416
N	132	59–276	97	41–178
D	3.54	1.58–7.39	2.60	1.10–4.77

Notes: Parameters are baseline detection rate (λ_0), spatial scale of the detection function (σ), population size (N), and population density (D). Estimates of σ and D are in meters and individuals per 100 km², respectively. The posterior mode for the probability an individual was male (sex ratio) was 0.58 (95% CI: 0.36–0.81).

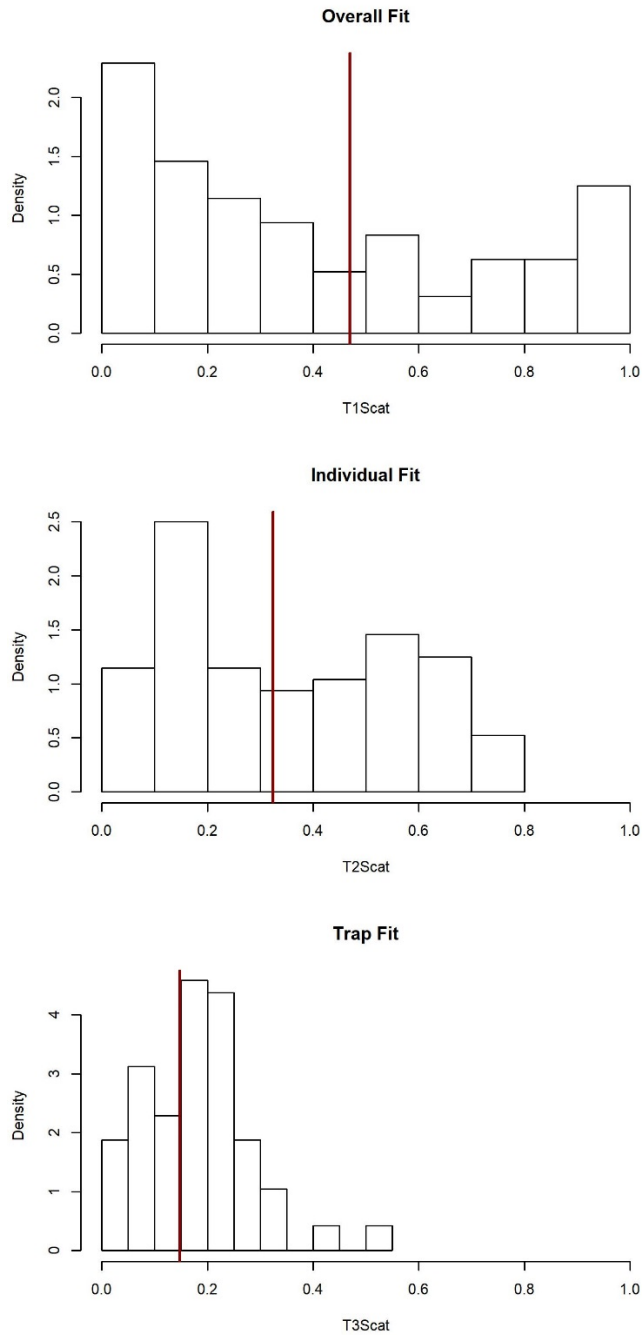


Fig. S1. Expected distribution of Bayesian p -values from model SO (histogram), with the observed Bayesian p -values indicated by red lines. The three histograms depict the expected distributions of T1, T2, and T3, which quantified overall, individual, and trap-level fit, respectively.

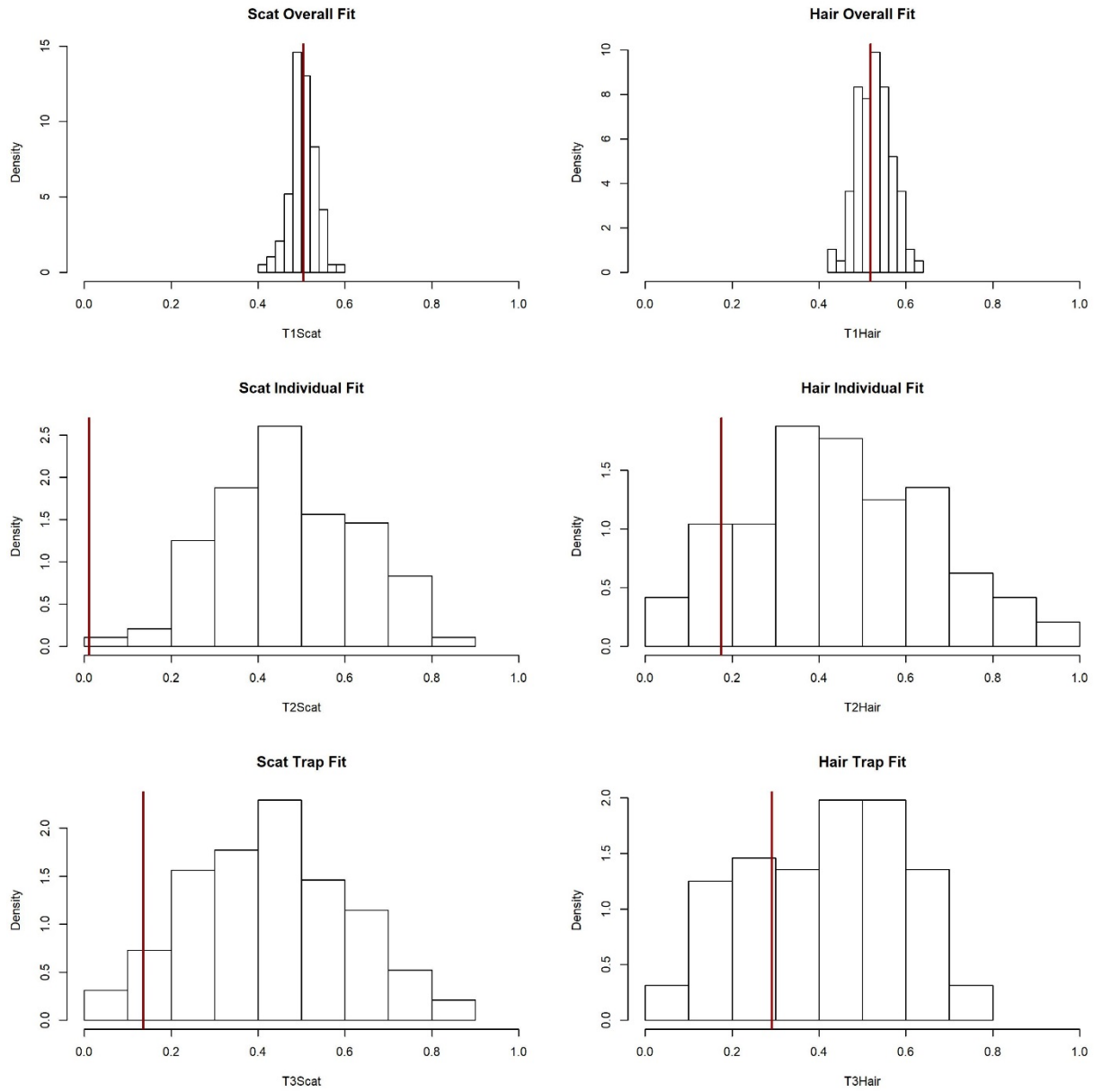


Fig. S2. Expected distribution of Bayesian p -values from model SH1 (histogram), with the observed Bayesian p -values indicated by red lines. The three histograms depict the expected distributions of T1, T2, and T3, which quantified overall, individual, and trap-level fit, respectively.

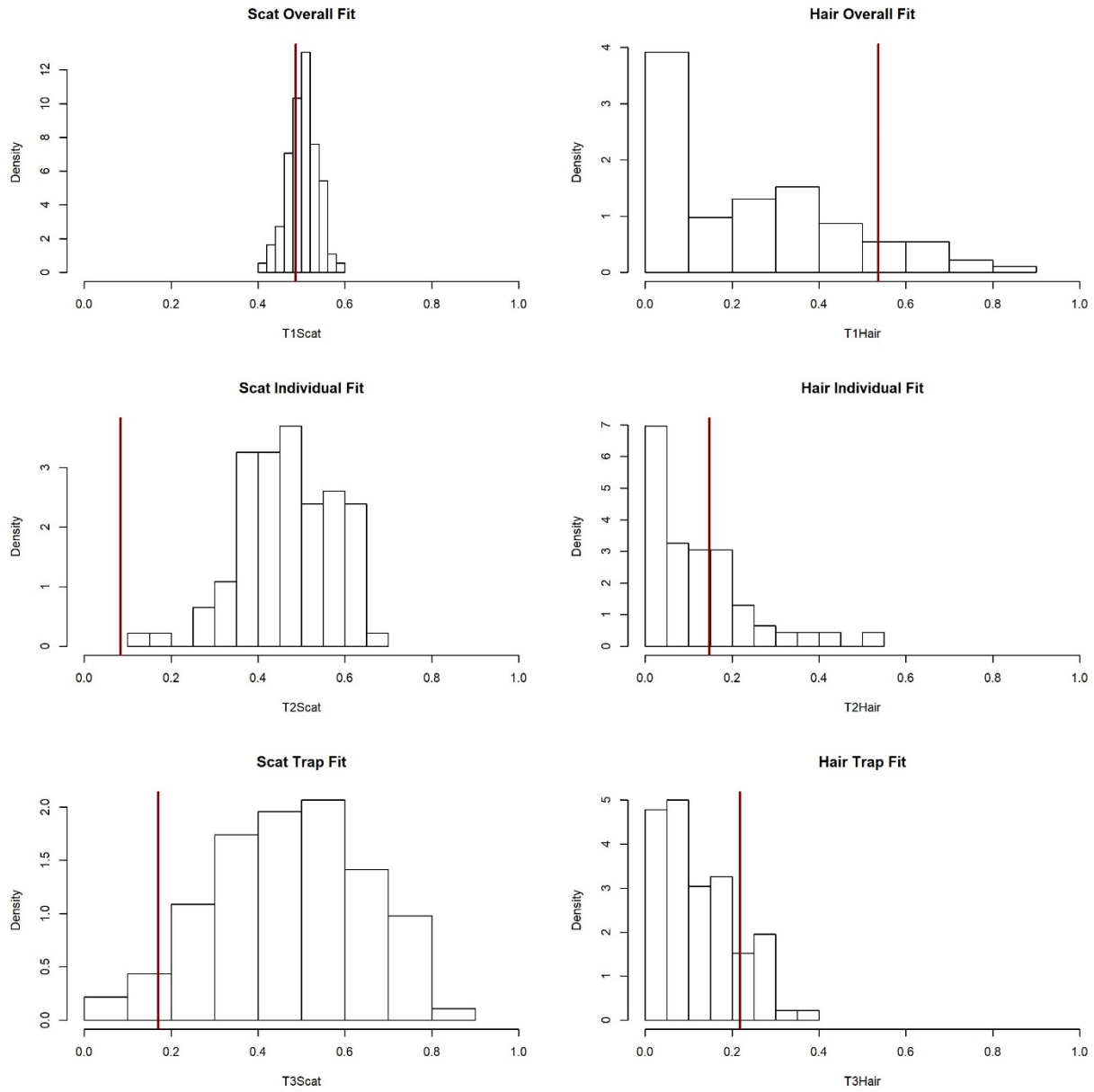


Fig. S3. Expected distribution of Bayesian p -values from model SH2 (histogram), with the observed Bayesian p -values indicated by red lines. The three histograms depict the expected distributions of T1, T2, and T3, which quantified overall, individual, and trap-level fit, respectively.

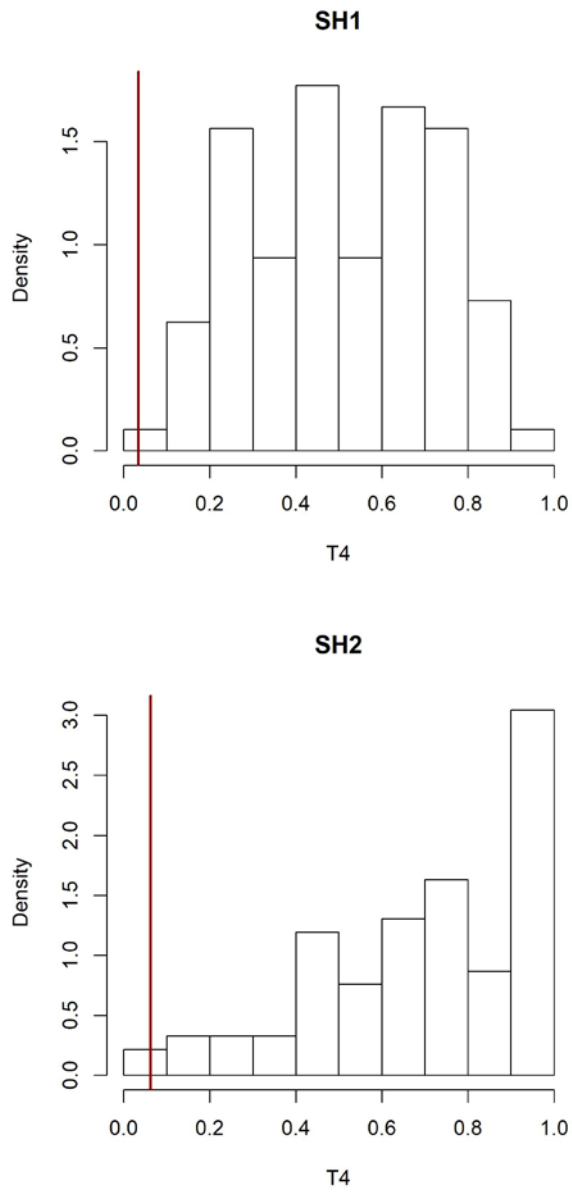


Fig. S4. Expected distribution of Bayesian p -values for T4, the number of individuals detected by both hair and scat sampling, from models SH1 and SH2. The observed Bayesian p -values are denoted by red lines.