

SUPPLEMENTARY MATERIAL 6. Sample sizes, observed heterozygosity (H_o), expected heterozygosity (H_e), and inbreeding coefficients (F_{IS}) for camas pocket gophers (*Thomomys bulbivorus*) at the 16 sampling sites with at least 7 individuals collected, treating sample site as population. Two sets of averaged estimates are presented, including Set 1 (all 6 variable microsatellite loci) and Set 2 (4 variable microsatellite loci, loci TM5 and TM6 excluded because they showed evidence of potential null alleles).

Site	Sample size	Set 1 (6 loci)			Set 2 (4 loci)		
		H_o	H_e	F_{IS}	H_o	H_e	F_{IS}
G1	10	0.42	0.51	0.18	0.38	0.45	0.17
G2	10	0.43	0.61	0.29	0.48	0.49	0.04
G3	10	0.43	0.65	0.34	0.53	0.65	0.19
G16	7	0.26	0.50	0.47	0.29	0.43	0.33
G21	10	0.47	0.61	0.24	0.50	0.58	0.14
G23	7	0.57	0.64	0.11	0.54	0.57	0.06
LC01	10	0.28	0.46	0.38	0.33	0.48	0.33
LC02	10	0.29	0.36	0.20	0.30	0.31	0.01
LC03	10	0.34	0.57	0.39	0.37	0.56	0.34
LC04	8	0.11	0.27	0.58	0.11	0.13	0.20
LC05	10	0.35	0.62	0.44	0.33	0.53	0.39
LC06	10	0.47	0.56	0.16	0.43	0.43	0.02
LC07	10	0.40	0.43	0.07	0.35	0.37	0.05
LC08	10	0.57	0.62	0.09	0.60	0.55	-0.09
LC09	8	0.40	0.55	0.28	0.53	0.64	0.17
LC10	10	0.31	0.37	0.17	0.36	0.35	-0.02