

**Supplemental Methods.** Details of genetic analysis.

Fourteen polymorphic microsatellite loci were amplified by PCR using fluorescently labelled primers and conditions optimized from protocols developed for other sciurids (May *et al.*, 1997, Stevens 1997, Goossens *et al.*, 1998, Hanslik & Kruckenhauser, 2000, Da Silva *et al.*, 2003, Kyle *et al.*, 2004; See Table S2). A Qiagen Multiplex PCR Kit was used to amplify 2g2, GS22, IGS-6, and MA018, following kit specifications for a 10µl reaction and using 0.5µl of template DNA. Multiplexed primers were run following Qiagen kit suggestions: starting with 95°C for 15 minutes, 20 cycles at 95°C for 30 seconds, at the  $T_m$  (decreasing temperature by 0.5°C every cycle) for 1:30 minutes, 72°C for 1 minute, then 18 cycles at 94°C for 30 seconds,  $T_m$  for 1:30 minutes, 72°C for 1 minute, and finishing with 60°C for 30 minutes. The remaining primers were carried out in 12.5µl reactions using 1µl of template DNA using the following reagents: 1.25µl 10X PCR buffer, 1mM MgCl<sub>2</sub>, 0.2µM forward and reverse primer, 0.25mM dNTP, and 0.2U Ampli *Taq* DNA polymerase (Roche), with the exception that 0.15µM of forward primer was used for GS17 and GS25. With the exception of GS17, non-multiplexed primer reactions were run with the following thermal cycler conditions: denaturation at 94°C for 3 minutes; 34 cycles to anneal primers starting at 94°C for 1 minute, annealing temperature ( $T_m$ ) for 30 seconds, 72°C for 30 seconds, and finishing with 72°C for 5 minutes. The multiplex PCR thermal cycler conditions were used for GS17 with a few modifications: the initial denaturation step was changed to 95°C for 3 minutes and the final elongation step was changed to 72°C for 10 minutes. An ABI 3730 DNA Analyzer (Applied Biosystems, Inc.) was used to size PCR products and alleles were manually scored in Genemapper 4.0 (Applied Biosystems, Inc.).

The dataset was checked for errors using Micro-Checker 2.2.3 [44] and adjusted for null alleles using FREENA [45]. We tested for Hardy-Weinberg equilibrium (HWE) and linkage

disequilibrium for each population in Genepop 4.2 [46]. Four loci were eliminated due to indications of a high frequency of null alleles. There were no significant deviations from HWE in the remaining loci. Genotypic disequilibrium tests detected linkage disequilibrium for locus ST 10 with IGS-6 ( $\chi^2 = 32.3$ ,  $P = 0.04$ ) and GS 22 ( $\chi^2 = 46.7$ ,  $P = 0.004$ ). After a Bonferroni correction for multiple comparisons linkage disequilibrium was no longer significant ( $\alpha = 0.05$ ,  $k = 45$ ,  $P_{\text{corr}} = 0.001$ ), so the loci can be considered independent.

Fifty-seven *U. beldingi* were considered juveniles (weight less than 200 g and/or classified by expert examination of physical characteristics) and excluded from analysis to avoid sampling highly related individuals.