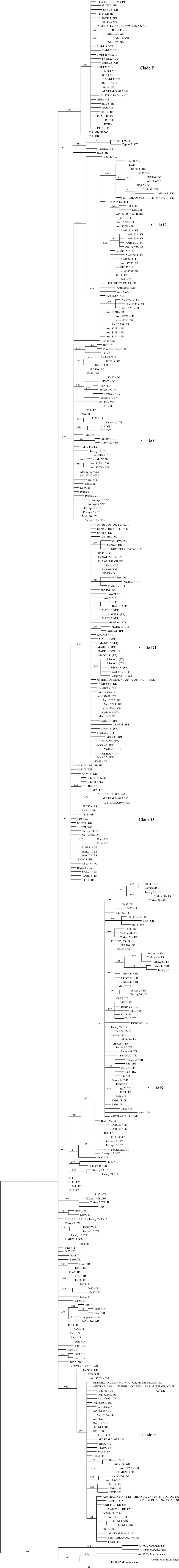


Figure S1 Detailed phylogenetic tree of *Mus musculus domesticus*. This is the detailed 50% majority rule consensus tree after Bayesian inference that is summarized in Figure 1 in the paper (based on a total of 378 *Mus musculus domesticus* D-loop haplotypes, derived from this study and all previous data available at the time of analysis) (Prager *et al.* 1993, 1996, 1998; Nachman *et al.* 1994; Gündüz *et al.* 2000, 2001, 2005; Ihle *et al.* 2006; Rajabi-Maham *et al.* 2008; Förster *et al.* 2009; Searle *et al.* 2009a, b; Jones *et al.* 2011). Posterior probabilities of 0.50 and above are shown on branch nodes. All haplotypes detected in this study are highlighted with an asterisk in the tree (details of samples can be found in Table S1). Codes indicate GenBank number or code used in the publication where the sequence was first reported, followed by a list of all the countries (country codes) where the haplotype has been recorded: AR, Argentina; AU, Australia, BG, Bulgaria; CH, Switzerland; CM, Cameroon; CY, Cyprus; DE, Germany; DK, Denmark; EG, Egypt; ES, Spain; (ES), Canary Islands (Spanish dependency); FI, Finland; FR, France; GB, Great Britain; GE, Georgia; GR, Greece; HR, Croatia; IE, Ireland; IL, Israel; IR, Iran; IT, Italy; LU, Luxembourg; MA, Morocco; MR, Mauritania; NE, Niger; NO, Norway; NL, Netherlands; NZ, New Zealand; PE, Peru; PT, Portugal; (PT), Madeiran Archipelago (Portuguese dependency); SE, Sweden; TR, Turkey; US, United States.



Clade F

Clade C1

Clade C

Clade D1

Clade D

Clade B

Clade E

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