Table S10 Demographic parameters used in ms (Hudson 2002) simulations. Population size estimates are based on averages of estimates from Geraldes *et al.* (2011) and assume a generation length of 1 year. Gene flow was increased until the proportion of simulated loci with low average values of differentiation matched observed proportions.

Subspecies 1	Subspecies 2	$N_{e\ species\ 1}$	$N_{e\ species\ 2}$	$N_{e\ Ancestral}$	t	2Nm (species1)[a]	2Nm (species2)[b]
M. m. castaneus	*M. m. domesticus*	366,700	82,600	277,800	325,000	1.930	0.000
M. m. castaneus	*M. m. musculus*	366,700	36,600	277,800	325,000	1.330	0.406
M. m. domesticus	*M. m. musculus*	82,600	36,600	277,800	325,000	0.045	0.855

[a] The effective rate at which genes enter subspecies 1 from subspecies 2

[b] The effective rate at which genes enter subspecies 2 from subspecies 1