Table S7 Demographic parameters used in ms (Hudson 2002) simulations. All values are based on averages of estimates from Geraldes *et al.* (2011) and assume a generation length of 1 year.

Subspecies 1	Subspecies 2	$N_{e\ species\ 1}$	$N_{e\ species\ 2}$	$N_{e\ Ancestral}$	t	2Nm (species1)[a]	2Nm (species2)[b]	Avg. # SNPs surveyed in observed loci (SD)	Avg. # SNPs in simulated loci (SD)
M. m. castaneus	*M. m. domesticus*	366,700	82,600	277,800	313,800	0.193	0.000	2.61 (2.39)	5.28 (3.05)
M. m. castaneus	*M. m. musculus*	366,700	36,600	277,800	345,800	0.190	0.058	2.59 (2.36)	4.90 (2.93)
M. m. domesticus	*M. m. musculus*	82,600	36,600	277,800	320,800	0.003	0.057	2.38 (2.08)	2.24 (1.29)

[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.