Table S9 Demographic parameters used in ms (Hudson 2002) simulations intended to more closely match the number of SNPs surveyed in the observed data.

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*	167,000	101,000	280,000	325,000	0.193	0.000	2.61 (2.39)	3.34 (1.93)
M. m. castaneus	*M. m. musculus*	167,000	89,000	280,000	325,000	0.190	0.058	2.59 (2.36)	3.28 (1.90)
M. m. domesticus	*M. m. musculus*	101,000	89,000	280,000	325,000	0.003	0.057	2.38 (2.08)	2.65 (1.52)

[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.