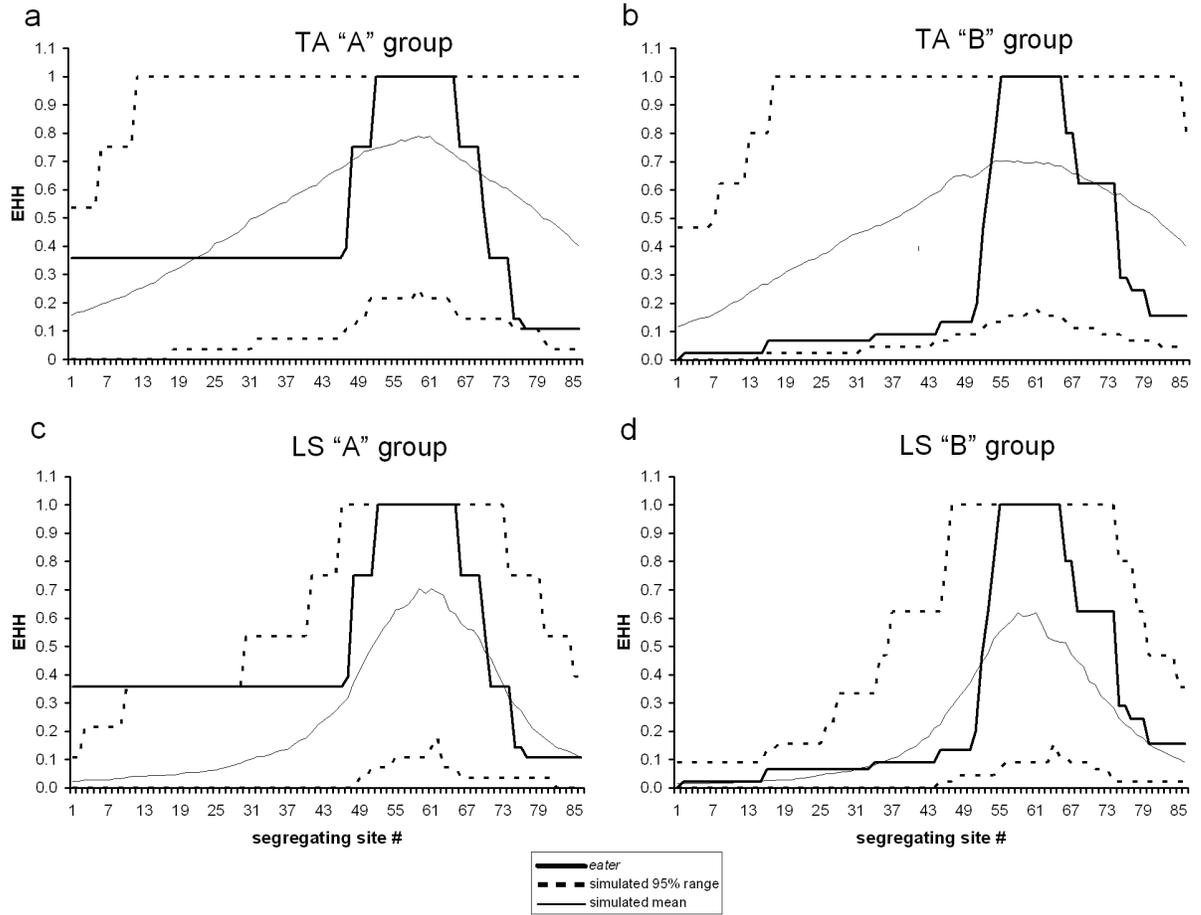


Supplementary Figure 1: Extended haplotype homozygosity. EHH at the *eater* locus is compared with values obtained from simulations under various demographic scenarios. The mean and the 2.5% and 97.5% tails of the simulated distributions are shown. a, b) EHH at *eater* and simulated EHH values obtained from the TA demographic scenario for the “A” and “B” haplotypes respectively based upon Thornton and Andolfatto (2006) c, d) EHH at *eater* and simulated EHH values obtained from the LS demographic scenario for the “A” and “B” haplotypes respectively based upon Li and Stephan (2006). EHH at the *eater* locus is not consistent with distributions of EHH obtained from simulations of the locus under the LS demographic scenario

Supplementary Figure 1



Supplementary Table 1: Evolutionary patterns of independently evolving NIM repeat units.

NIM #	Microbial binding? ^a	K_A^b K_S^b	K_A/K_S	$\pi_{zimbabwe}^c$ π_{US}^c	Tree structure ^d
1	yes	0.0602 0.2326	0.259	0.00947 0.00769	yak ₈₃ (mel ₆₄ sim)
2	yes	0 0.1073	0	0 0	yak ₉₁ (mel ₉₂ sim)
3	yes	0 0.0632	0	0.00697 0.00310	sim ₄₀ (mel ₂₇ yak) ^e
4	yes	0.0475 0.1145	0.415	0.01111 0.00739	mel ₉₃ (yak ₅₃ sim)
5	unknown	0 0	NA	0.00539 0.00354	mel/sim/yak
6	unknown	0.0347 0	NA	0.01594 0.00673	sim ₈₇ (mel ₄₈ yak)
7	unknown	0.0170 0.0556	0.306	0.00208 0.00110	yak ₇₇ (mel ₆₃ sim)
8	unknown	0 0.0589	0	0.00920 0.00780	yak ₄₂ (mel/sim)
9	unknown	0.0167 0.1253	0.133	0.01047 0.00449	yak ₅₀ (mel ₈₁ sim)
10	unknown	0.0360 0.0690	0.522	0.01047 0.00449	yak ₉₈ (mel ₆₃ sim) ^e
11	unknown	0 0.1337	0	0.00359 0	yak ₉₉ (mel/sim)

^a Kocks et al. 2005

^b K_A and K_S are the rates of amino acid or silent substitution respectively polarized along the *D. melanogaster* branch using *D. yakuba* and *D. simulans* as outgroups.

^c π indicates nucleotide diversity calculated as the average pairwise differences between sequences per base pair.

^d Neighbor joining trees were constructed for all NIM repeat units. Subscript numbers indicate bootstrap support for each node based on 500 replicates.

^e One *D. melanogaster* allele was an outlier from the pattern indicated here.