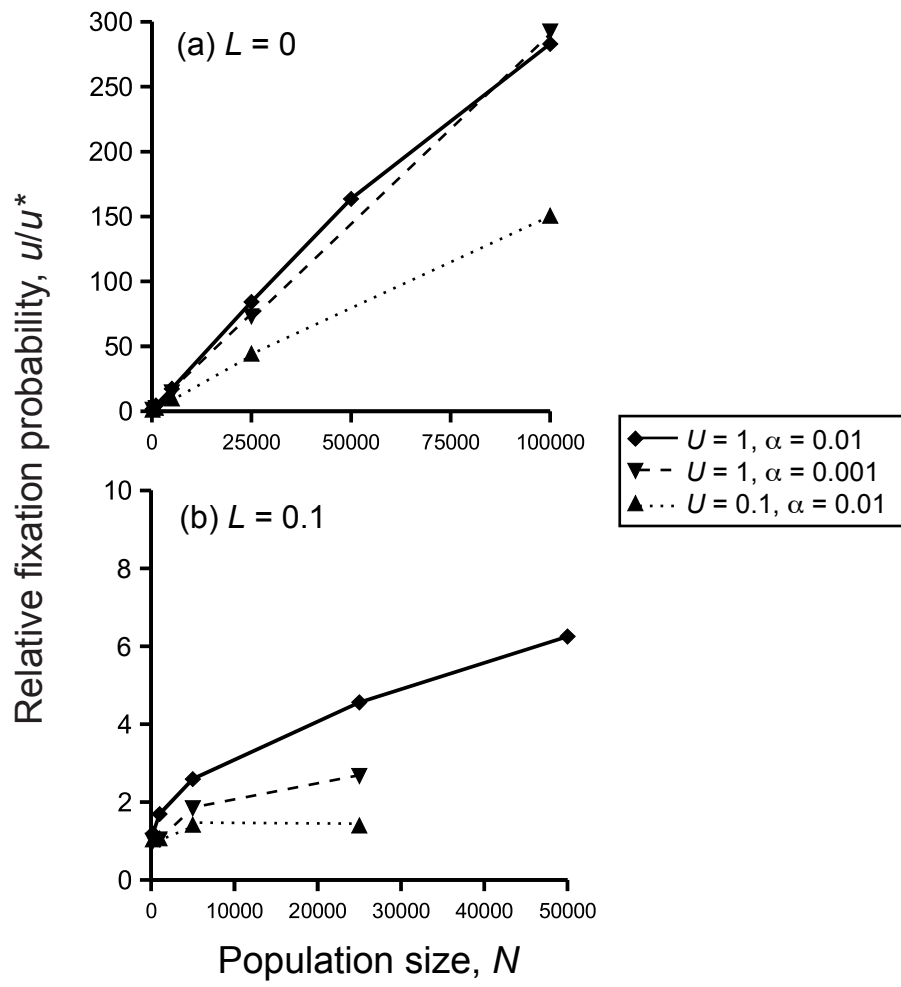


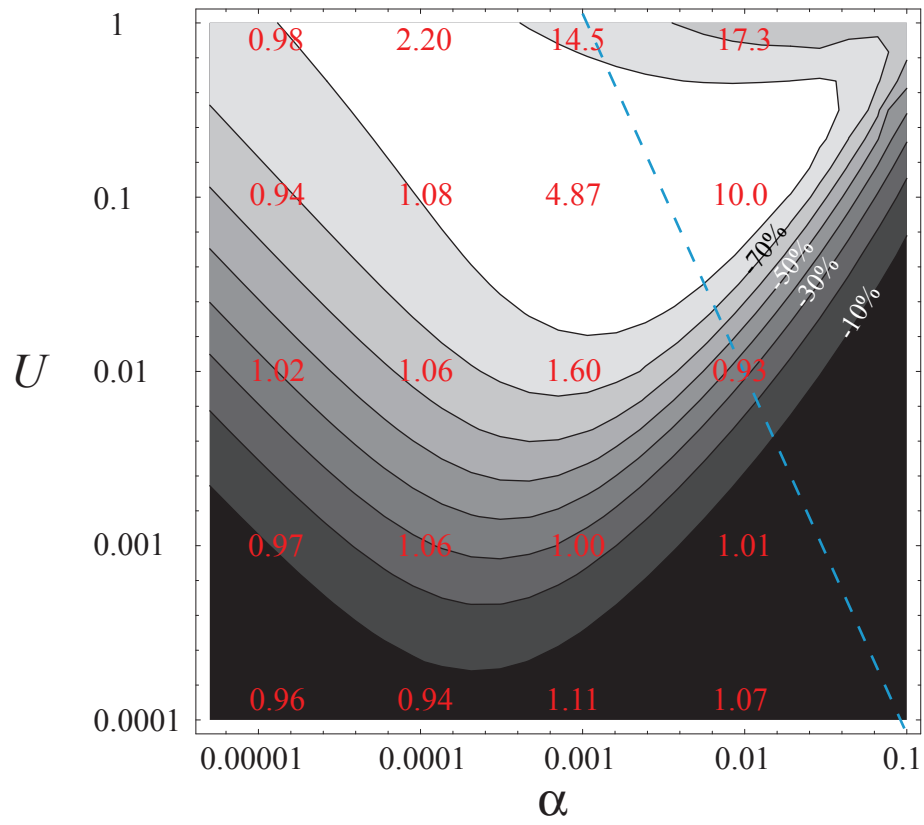
Supplementary Information – *Nature* 2006-05-05402B

Supplementary Figure 1: Relative fixation probability of a modifier of recombination that increases recombination uniformly across a chromosome by 0.1 M plotted against population size.. The flux of modifier alleles (a) increases approximately linearly with population size with initial map length $L = 0M$ and (b) shows a concave downward relationship with initial map length $L = 0.1M$. Mutant effects on fitness were independent (i.e., $\beta = 0$); in this case and with recurrent mutation, the relative fixation probability is predicted to return to $u/u^* = 1$ for populations of infinite size (Barton 1995; ref. 17). However, the reduction in N_e brought about by multi-locus selection may imply that this theoretical prediction is never reached.



Supplementary Figure 2. Contour plot illustrating the effect of recombination on the strength of the Hill-Robertson effect. Based on the theory of Santiago and Caballero (1998) (ref. 29), we calculated the strength of drift, $1/N_e$, when recombination was present ($L = 0.1M$) and compared this to $1/N_e$ when recombination was absent ($L = 0M$). The -50% contour, for example, describes cases where recombination halved the amount of drift (i.e., doubled N_e).

Superimposed upon the contour plot is the relative fixation probability of a modifier allele that increased the map length from $0M$ to $0.1M$ from simulations (red). Although the correspondence is not perfect, the figure indicates that the change to the amount of drift is a good predictor of the fate of the modifier (t -test of the significance of the slope: $p = 0.057$; coefficient of determination: $R^2 = 0.19$). Data from metazoans (Caballero and Keightley 1994; ref. 28) suggest that the mutational variance, V_m , for fitness is greater than $\approx 10^{-6}$, suggesting that realistic parameter combinations fall to the right of the dashed blue line. The population size was 5,000, epistasis was absent, and N_e was calculated as in Supplementary Table 3 (the focal locus was placed at each of the 100 possible loci, and the average of these N_e values was used). The standard error of each fixation probability was less than or equal to 10% of the fixation probability.



Supplementary Table 1. Relative fixation probabilities of a modifier of recombination with an effect of +0.1M on a chromosome that was initially 1M in length. We excluded cases in which antagonistic epistasis led to individuals with fitness > 1 , implying that advantageous mutations were present.

N	$U/\text{chromosome}$	α	β	$u/u^* (SE)$
200	1	0.01	0.000001	1.00 (0.033)
			0.000000	1.04 (0.030)
			-0.000001	1.03 (0.033)
			-0.000100	1.01 (0.031)
			-0.010000	1.07 (0.037)
1,000	1	0.01	0.000001	1.01 (0.029)
			0.000000	1.03 (0.031)
			-0.000001	0.97 (0.029)
			-0.000100	1.10 (0.036)
			-0.010000	1.24 (0.036)
5,000	1	0.01	0.000001	1.06 (0.057)
			0.000000	1.04 (0.043)
			-0.000001	1.03 (0.059)
			-0.000100	1.03 (0.052)
			-0.010000	1.90 (0.074)
200	0.1	0.01	0.000001	0.97 (0.028)
			0.000000	1.05 (0.032)
			-0.000001	0.95 (0.029)
			-0.000100	1.04 (0.032)
			-0.010000	0.99 (0.028)
1,000	0.1	0.01	0.000001	1.01 (0.034)
			0.000000	1.01 (0.034)
			-0.000001	1.01 (0.028)
			-0.000100	1.03 (0.032)
			-0.010000	1.00 (0.031)
5,000	0.1	0.01	0.000001	0.97 (0.056)
			0.000000	1.04 (0.062)
			-0.000001	1.08 (0.053)
			-0.000100	0.96 (0.047)
			-0.010000	1.11 (0.057)

<i>N</i>	<i>U</i> / chromosome	α	β	<i>u/u*</i> (<i>SE</i>)
200	1	0.001	0.000001	Adv. mutants
			0.000000	0.96 (0.032)
			-0.000001	1.03 (0.033)
			-0.000100	1.03 (0.033)
			-0.010000	1.06 (0.036)
1,000	1	0.001	0.000001	Adv. mutants
			0.000000	0.99 (0.032)
			-0.000001	1.09 (0.037)
			-0.000100	1.09 (0.036)
			-0.010000	1.21 (0.034)
5,000	1	0.001	0.000001	Adv. mutants
			0.000000	1.01 (0.062)
			-0.000001	1.12 (0.053)
			-0.000100	1.27 (0.053)
			-0.010000	2.00 (0.075)

Supplementary Table 2. Relative fixation probabilities of a modifier of recombination arising at a random locus in a genome containing either 1 or 5 chromosomes, each with initial length 0 or 0.1M. The population size was 5,000, and there were 100 loci affecting fitness per genome. The genomic mutation rate was 1 (*i.e.*, for the case of 5 chromosomes, the chromosomal mutation rate was 0.2), and α was 0.01.

β	L	u/u^* (SE)	
		1 chromosome	5 chromosomes
0.000001	0	18.5 (0.99)	12.7 (0.49)
	0.1	2.5 (0.17)	1.8 (0.10)
0.000000	0	17.3 (0.76)	15.5 (1.0)
	0.1	2.6 (0.071)	1.7 (0.17)
-0.000001	0	15.5 (0.90)	14.8 (0.59)
	0.1	2.7 (0.16)	1.6 (0.12)
-0.000100	0	10.4 (1.2)	6.6 (0.37)
	0.1	2.3 (0.14)	2.0 (0.092)
-0.010000	0	6.4 (0.48)	2.5 (0.16)
	0.1	2.6 (0.14)	2.1 (0.14)

Supplementary Table 3. The effective population size estimated in our simulations (Sim) is compared to the theoretical results of Santiago and Caballero (1998; Theory). A numerical evaluation of N_e was obtained from the first part of their equation (4a) using equation (1), modified for haploids (details available upon request). In the simulations and theoretical evaluations, N_e was estimated at one telomeric (T) or centrally (C) located neutral locus, assuming one chromosome carrying 100 equidistant loci subject to deleterious mutations. The order of magnitude of N_e , but not the exact value, is accurately predicted by the theory; discrepancies arise, in part, because the theory does not account for disequilibria among the selected loci. (“na”: Not available due to length of simulation runs.)

(a) $U = 1, \alpha = 0.01, \beta = 0$

N	<i>Location</i>	<i>Map Length</i>					
		0 M		0.1 M		1 M	
		Sim	Theory	Sim	Theory	Sim	Theory
1,000	T	94	35	165	105	333	538
1,000	C			126	67	261	421
5,000	T	119	45	246	224	862	2,435
5,000	C			181	111	600	1,815
25,000	T	131	55	348	547	4,223	11,858
25,000	C			244	187	2,068	8,700
50,000	T	148	59	389	868	5,568	23,633
50,000	C			368	238	3,654	17,298
100,000	T	na	64	na	1,459	na	47,182
100,000	C			na	309	na	34,494
1,000,000	T	na	79	na	11,432	na	471,055
1,000,000	C			na	923	na	344,015

Supplementary Table 3. (cont)**(b) $U = 0.1, \alpha = 0.01, \beta = 0$**

<i>N</i>	<i>Location</i>	<i>Map Length</i>					
		0 M		0.1 M		1 M	
		Sim	Theory	Sim	Theory	Sim	Theory
1,000	T	192	156	452	659	911	929
1,000	C			338	505	656	902
5,000	T	277	303	1,952	3,125	4,434	4,606
5,000	C			1,130	2,249	3,583	4,462
25,000	T	366	635	8,361	15,422	18,503	22,987
25,000	C			3,994	10,895	19,352	22,258
50,000	T	395	920	13,409	30,791	na	45,963
50,000	C			7,371	21,697	na	44,503
100,000	T	na	1,400	na	61,529	na	91,915
100,000	C			na	43,300	na	88,993
1,000,000	T	na	8,483	na	614,808	na	919,045
1,000,000	C			na	432,150	na	889,806