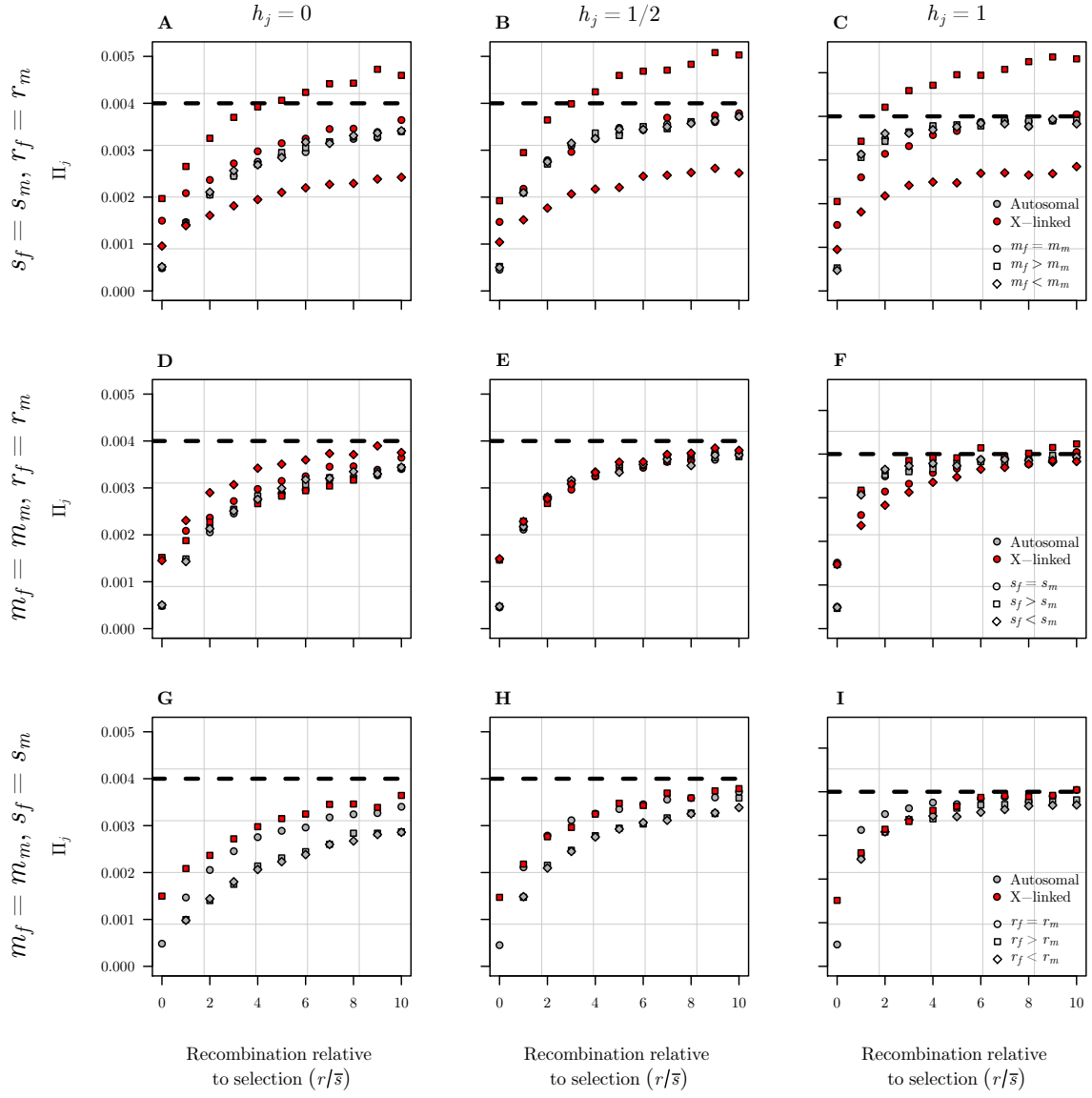
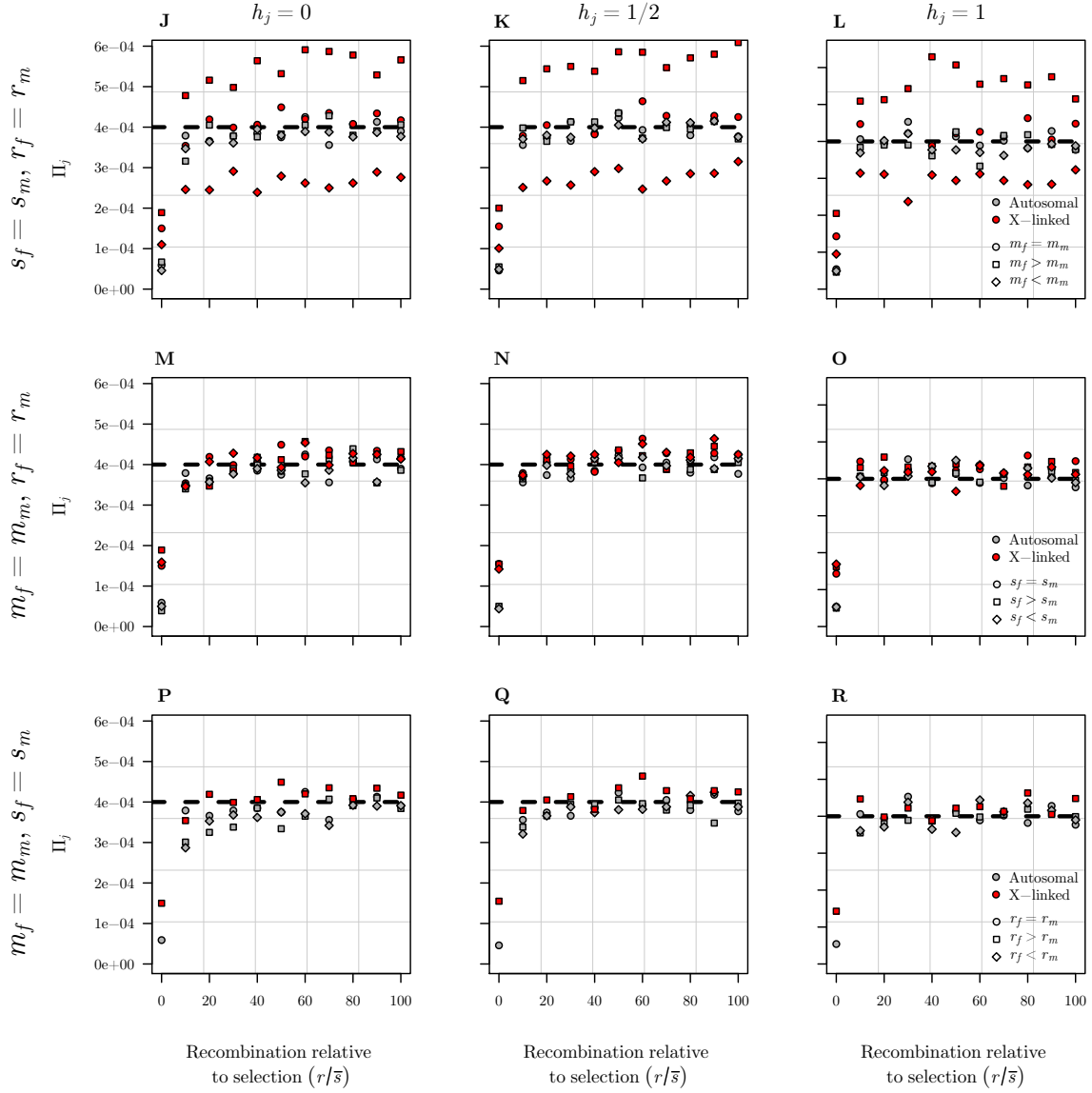


$$N = 3 \times 10^4$$

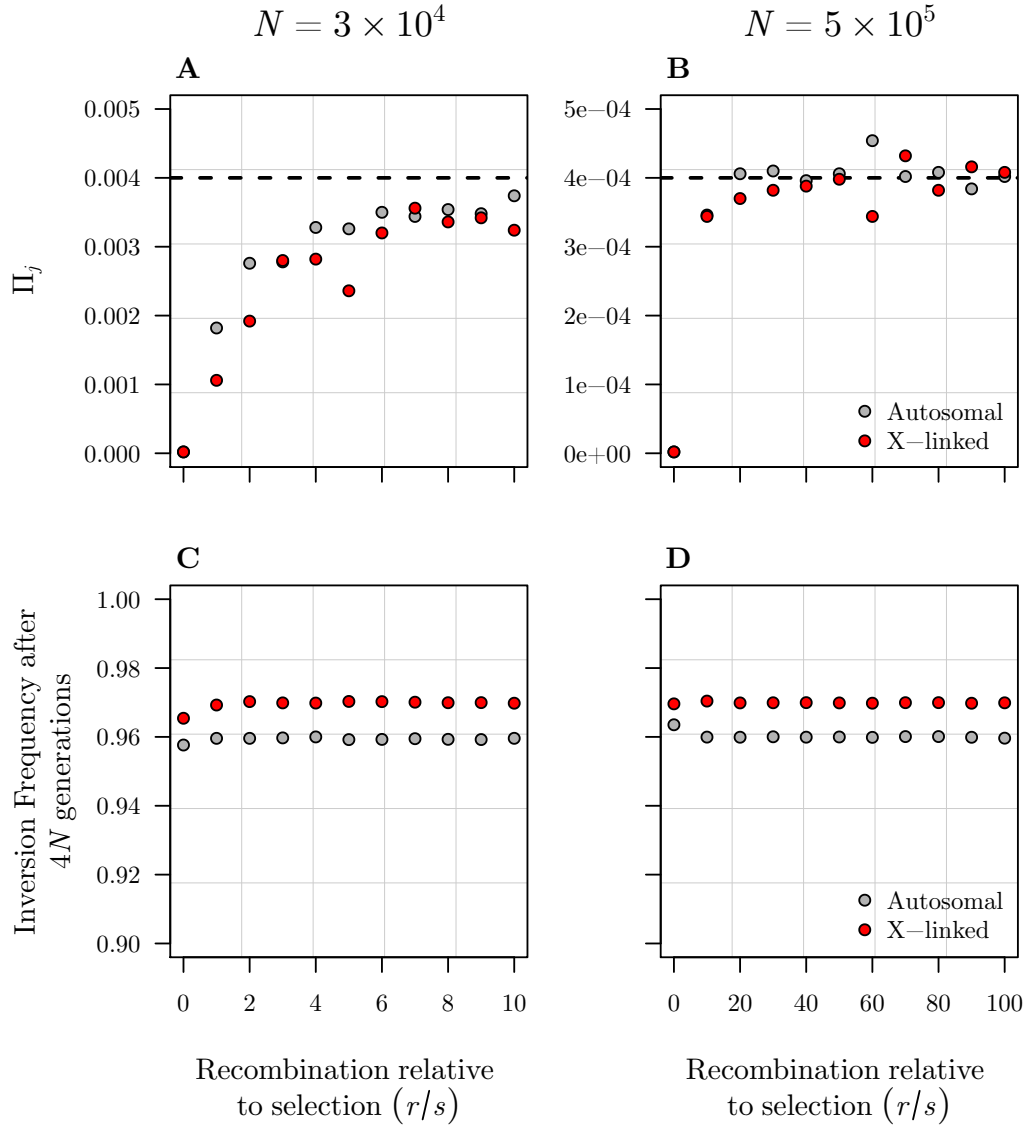


$$N = 5 \times 10^5$$



**Figure S1.** Effects of recombination on the establishment of inversions that capture two locally adapted alleles: additional simulation results. See the Fig. 1 legend for additional details. Here we present additional results comparing analytic approximations of establishment probabilities (dashed line, based on eqs. (5a-5b), with  $m_f = m_m$ ) and stochastic simulations for inversion establishment on the X (red symbols) and autosomes (grey symbols). Simulations were carried out in a Wright-Fisher population with effective population size of  $N = 30,000$  (panels A-I) and  $N$

= 500,000 (panels J-R), and for three dominance scenarios for the locally adaptive alleles ( $h = 0$  in the left-hand column;  $h = 1/2$  for the middle column;  $h = 1$  for the right-hand column). For each combination of  $h$  and  $N$ , we performed simulations corresponding to equal (circles), female-limited (squares), and male-limited (diamonds) parameterizations of migration rate ( $m_f, m_m$ ), selection ( $s_f, s_m$ ), and recombination rate ( $r_f, r_m$ , with no X-linked recombination in males). The sex-averaged rate of migration and strength of selection were held constant across simulations. For simplicity, we present results in which we explore the effects of sex-bias in only one of the three parameters at a time. For simulations using  $N = 30,000$ , we set  $\bar{m} = (m_f + m_m)/2 = 0.002$  and  $\bar{s} = (s_f + s_m)/2 = 0.05$ . For simulations using  $N = 500,000$ , we set  $\bar{m} = (m_f + m_m)/2 = 0.0002$  and  $\bar{s} = (s_f + s_m)/2 = 0.005$ . Hence, panels A–C and J–L explore effects of equal migration (where  $m_f = m_m = \bar{m}$ ), female-limited migration ( $m_m = 0; m_f = 2\bar{m}$ ), and male-limited migration ( $m_f = 0; m_m = 2\bar{m}$ ), with equal selection and recombination between sexes ( $s_f = s_m = \bar{s}; r_f = r_m = r$ ). Panels D–F and M–O show results explore effects of equal selection ( $s_f = s_m = \bar{s}$ ), female-limited selection ( $s_m = 0; s_f = 2\bar{s}$ ), and male-limited selection ( $s_f = 0; s_m = 2\bar{s}$ ), with equal migration and recombination between sexes ( $m_f = m_m = \bar{m}; r_f = r_m = r$ ). Panels G–I and P–R explore effects of equal recombination ( $r_f = r_m = r$ ), female-limited recombination ( $r_m = 0; r_f = r$ ), and male-limited recombination ( $r_f = 0; r_m = r$ ), with equal migration and selection between sexes ( $m_f = m_m = \bar{m}; s_f = s_m = \bar{s}$ ). The  $j$  in the establishment probability,  $\Pi_j$ , refers to the mode of inheritance ( $j = \{A, X\}$ ). Each data point shows the fraction of  $10^6$  single-copy inversions that eventually become established in the population. Analytical, numerical and simulation results are based on the two-locus model of local adaptation in which inversions capture locally adaptive alleles at both loci.



**Figure S2.** Long-run evolutionary dynamics of inversions. Instead of using frequency thresholds to delineate inversions that successfully invade the population, we ran forward simulations for  $4N$  generations – a sufficient number of generations for the population to reach migration-selection-drift equilibrium. Data points show the results for  $5 \times 10^4$  replicate simulations, each of which was run until a new inversion was lost or  $4N$  generations had passed. Panels A and B show the proportion of inversions that are not lost from the population. Panels C and D show the mean frequency, at generation  $4N$ , of inversions that became established in the population. We present

results for Wright-Fisher populations of size  $N = 30,000$  with  $s = s_f = s_m = 0.05$ ,  $m_f = m_m = 0.002$  (panels A, C) and  $N = 500,000$  with  $s = s_f = s_m = 0.005$ ,  $m_f = m_m = 0.0002$  (panels B, D), with recombination rates between the sexes ( $r = r_f = r_m$ , and no X-linked recombination in males). Fitness effects of locally adaptive alleles are additive ( $h = h_f = h_m = 0.5$ ). The dashed line in Panels A and B show the analytic approximation for inversion establishment probability, based on eqs. (5a-5b), with  $m_f = m_m$ . Note, in Panels C-D, that the simulation results show that the average frequency of established X-linked inversions is slightly higher than the average frequency for autosomal inversions, though inversions are nearly fixed under both modes of inheritance.