**Text S1  Complete recombination**

We checked the effect of fitness variance in the absence of linkage disequilibrium by simulating a large number of concurrent selective sweeps. The population is represented by two lists: the numbers of copies of rare favorable alleles, $n$, and the frequencies of common alleles, $p$. Whenever an allele rises above 100 copies, it is assumed to increase deterministically: therefore, it is deleted from the first list, and its frequency added to the second list. In each generation, a Poisson number of new mutations is added, with expectation $NU$, and each in a single copy. The common allele frequencies $p$ evolve deterministically, so that $p_i \rightarrow \frac{1+sp}{1+sp_i}p_i$ every generation. The key step is to draw the number of copies of each rare allele. For each locus, the distribution of frequencies of genetic backgrounds is calculated. for example, a gene at locus 1 will find itself on background 000...0 with probability $q_2 \ldots q_k$; with $k$ loci, there are $2^{k-1}$ possible backgrounds for each locus. However, we only need to track the numbers of each fitness class, defined by the number of favorable alleles it carries. The $n_i$ copies at locus $i$ are distributed over the possible fitness classes with multinomial probability, and for each fitness class, a Poisson number of offspring is drawn with the appropriate expectation. The rate of sweeps is measured after 200 generations. Figure S1 shows a close match between the simulated and predicted rate of accumulation of favorable alleles.