

Supplemental Materials

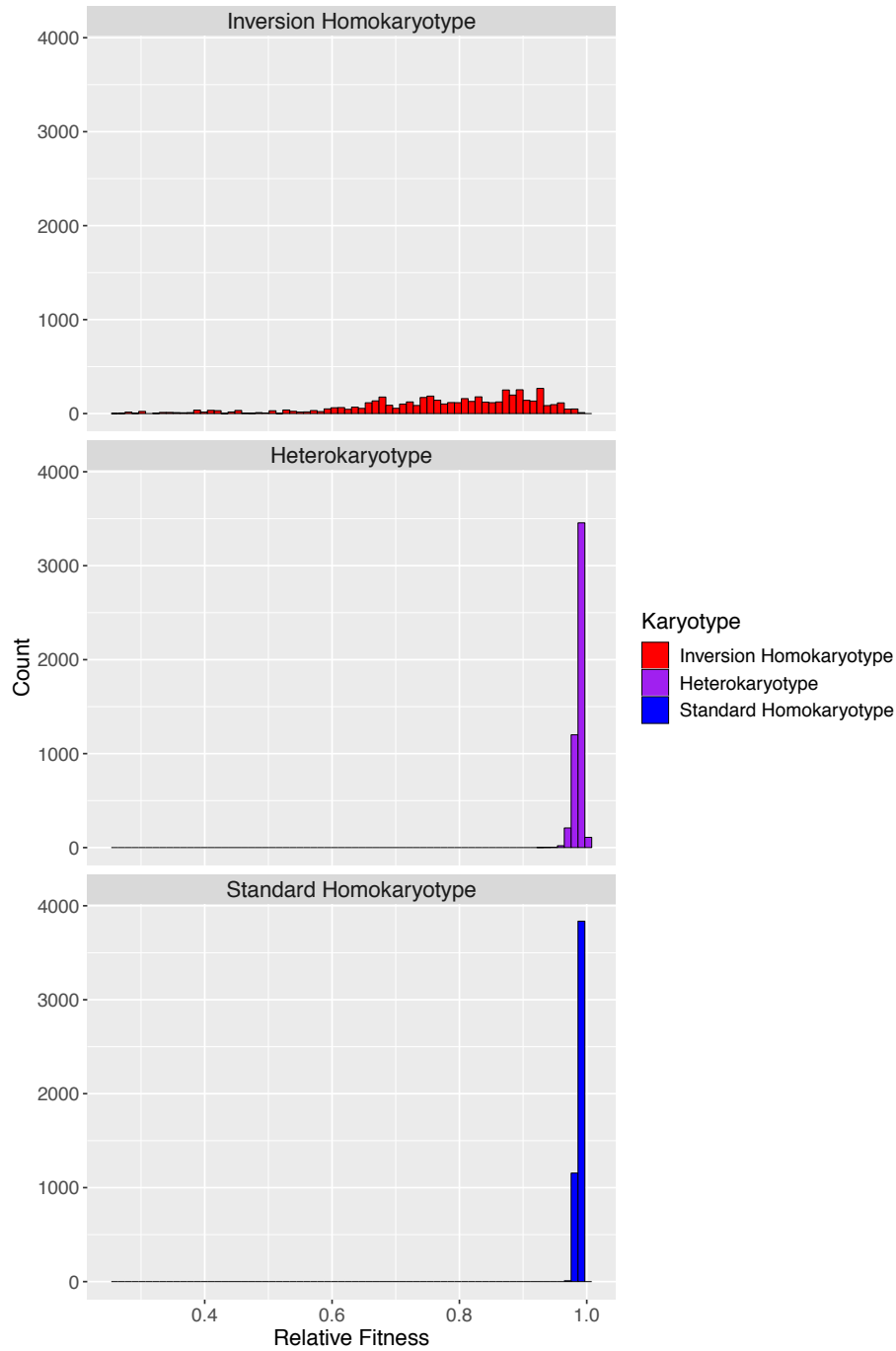


Fig. S1

Distribution of the initial relative fitnesses of all 3 karyotypes when an inversion occurs in any haplotype in a population.

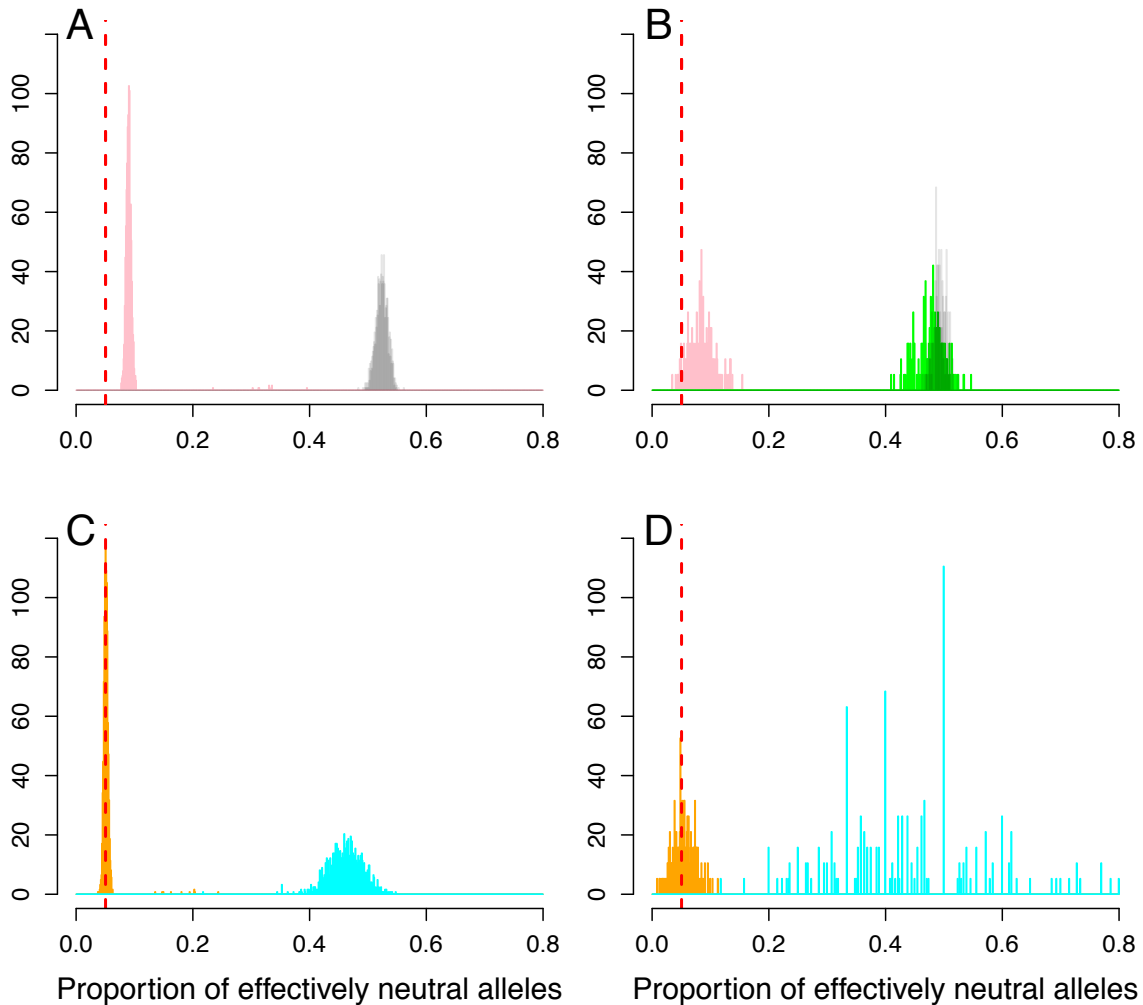


Fig. S2

Distribution of proportion of effectively neutral alleles among fixed mutations with (A,C) and without (B,D) gene conversion. Orange corresponds to mutations fixed in minor arrangement, cyan to mutations fixed in the major arrangement, pink to the average of mutations fixed in either the major or minor arrangement (i.e. alleles with an F_{ST} of 1), green to mutations that have fixed in the inverted region (i.e. fixed in both arrangements), and black to mutations that have fixed in the collinear region (chromosomes 2 and 3). The dashed black line indicate the proportion of new mutations that are effectively neutral, and the red dashed line corresponds to the proportion of effectively neutral mutations that fixed during the burn-in.

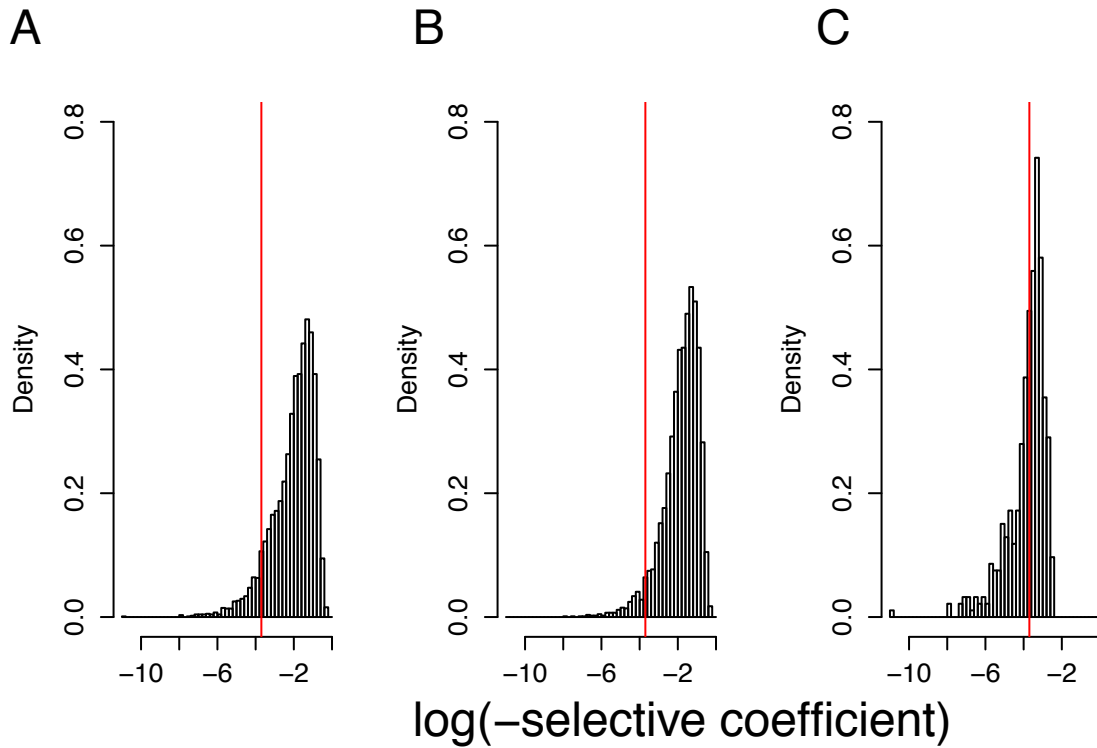


Fig. S3

Density distribution of selective coefficient (log scale) of deleterious mutation with a F_{st} of 1 between the two arrangements. The red line indicates $s=1/N$; to the left mutation are effectively neutral. A) All deleterious mutations within the inverted region, B) all deleterious mutations private to and fixed in the minority arrangement and C) all deleterious mutations private to and fixed in the majority arrangement.

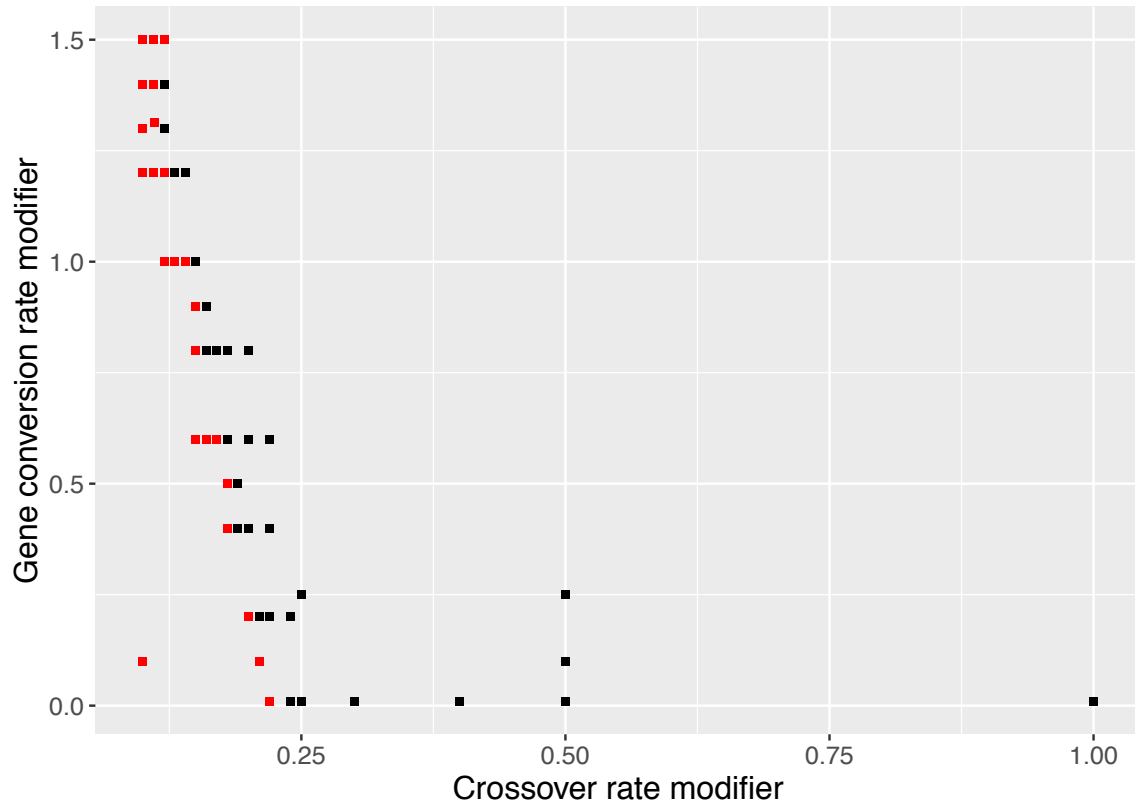


Fig. S4

Formation of haplotype structuring in a model without an inversion. We consider a chromosome without an inversion but sharing the same properties than our inversion model (see methods for details) and determine the combination of crossing over and gene conversion rate where we observe haplotype structuring in at least 1 of 10 replicates (in red; black indicates that haplotype structuring was not observed). The X and Y axis corresponds to the relative values of crossing over and gene conversion rate compared to the main simulations.

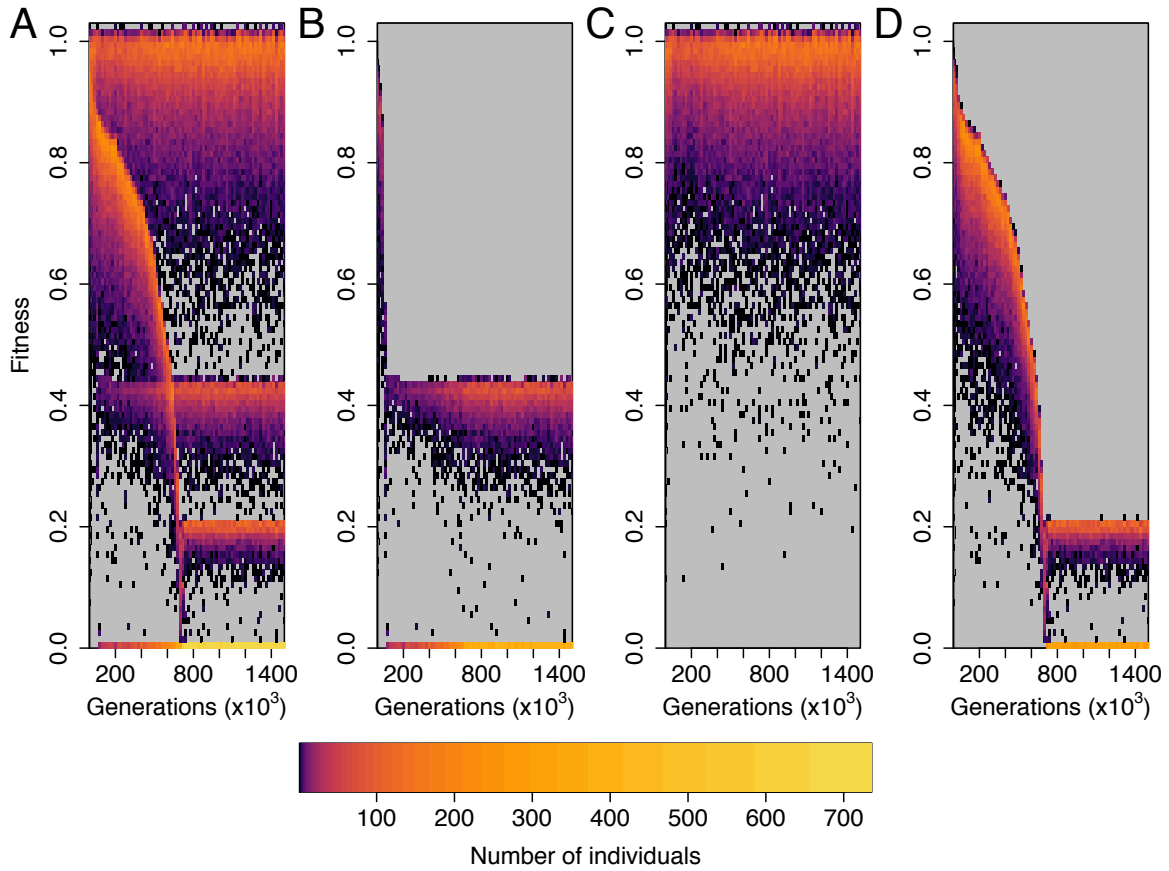


Fig. S5

Fitness distributions as a function of time reveal bimodality of the fitness. The different panels correspond to the fitness distribution of A) the whole population, B) the inversion homokaryotype, C) the heterokaryotype and D) the standard homokaryotype. The color indicates how many individuals share a given fitness values (on a log scale).

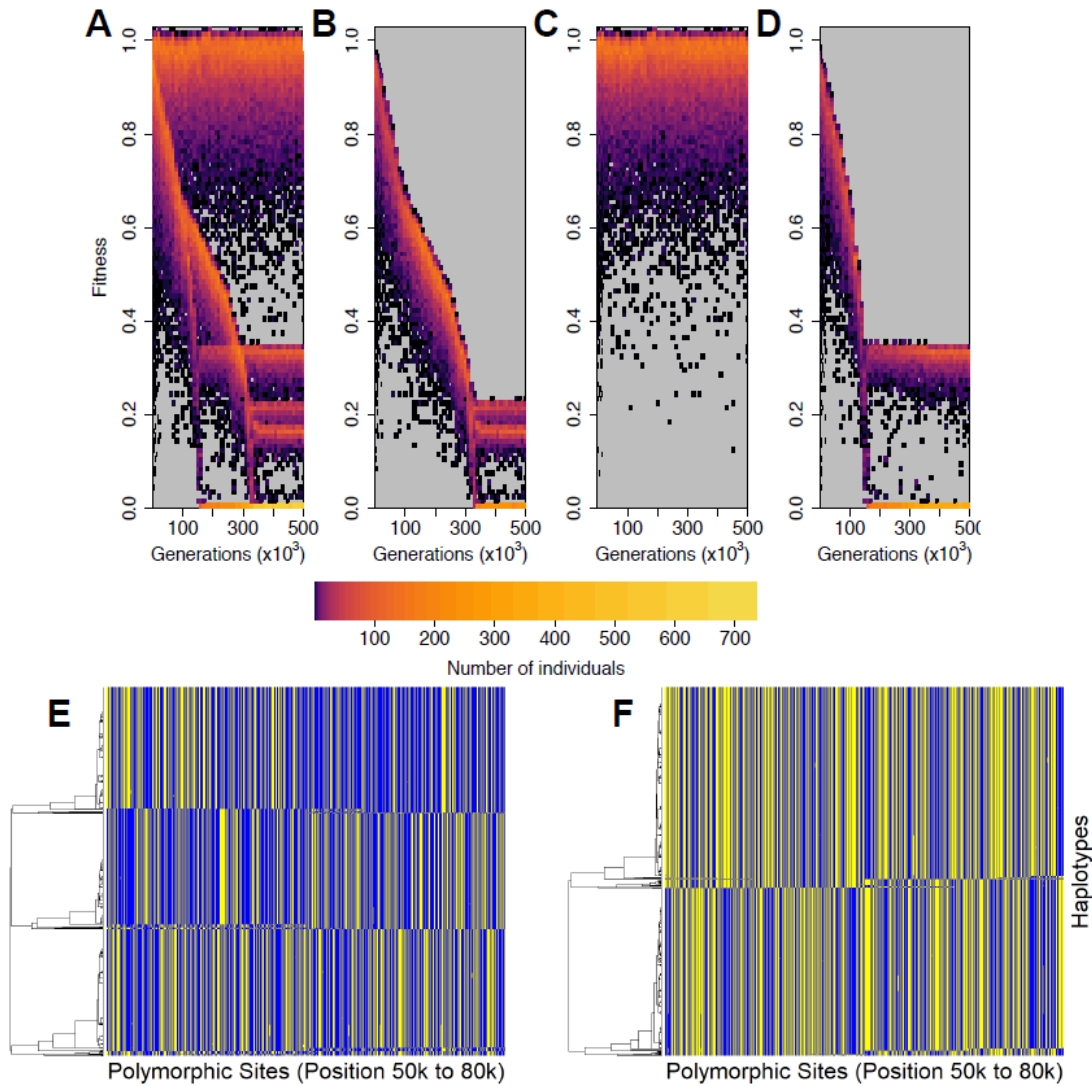


Fig S6

Haplotype structuring when more than two haplotype clusters emerge in an arrangement. Panels A to D display the fitness distributions of A/ the whole population, B/ the homokaryotype for the inverted arrangement, C/ the heterokaryotype and D/ the homokaryotype for the standard arrangement. Panels A to D are similar to Figure S5 but for a different simulation run. Panel E/ and F/ corresponds to the allelic content of the inverted (E) and standard arrangement (F) at generation 500,000. Each horizontal line represents a haplotype in the population and each vertical line represents a genomic locus. Yellow denotes that an individual possesses the derived allele and blue the ancestral one.

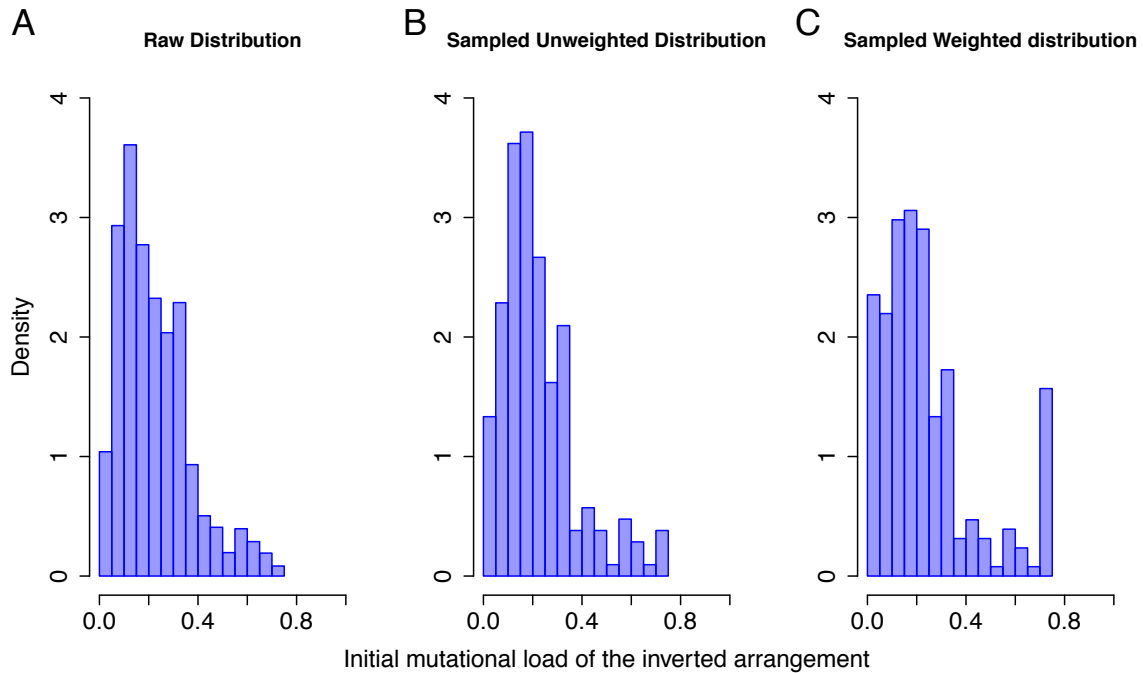


Fig. S7

Density distribution of the initial mutational load. A) the mutational load in the whole population at the end of the burn-in. B) the mutational load of the inverted arrangement in the haplotypes we selected (200 random plus the 4 best and the 4 worst and one close to the median). C) the mutational load of the inverted arrangement after correcting for the number of simulations done per haplotype. This figure illustrates that we do not always have the same number of simulations for each datapoint in Figure 1.