

## SUPPLEMENTARY FIGURE 2

Sampling effect. The genotype-phenotype map was evaluated from a finite  $F_2$  population, and the estimates of genotypic values are necessarily subject to sampling effects. The most sensitive genotypes are likely to be the fully homozygous ones, because they are less frequent in the  $F_2$ .

To check if this sampling effect may have an impact on the results of our simulations, we computed “noised”  $F_2$  populations, similar to the real one, but in which the phenotype of the 538 individuals is changed (the phenotype  $P_i$  of individual  $i$  will be replaced by  $P_i' = P_i + \varepsilon_i$ , where  $\varepsilon_i$  is sampled in a Gaussian distribution of variance  $\sigma^2_R$ , *i.e.* the estimate of the residual variance in the  $F_2$ ). The genotype-phenotype map was then computed in the same way as for the real dataset, and the figures below represent the results of the corresponding simulations for 5 independent sampling repetitions (same parameters as Fig 4).

The shape of the response to selection is really similar for each of the sampled genotype-phenotype map (A), but their amplitude (and therefore the ending point) is highly sensitive to the value of the “best” genotype (H allele fixed at each locus). However, the evolutionary dynamics of the system is not disturbed by sampling effects, *e.g.* the evolution of allelic frequencies in the course of time (B) remain very similar to the results presented in Fig 4, and the conclusions are not affected by potential sampling errors in the original dataset.

