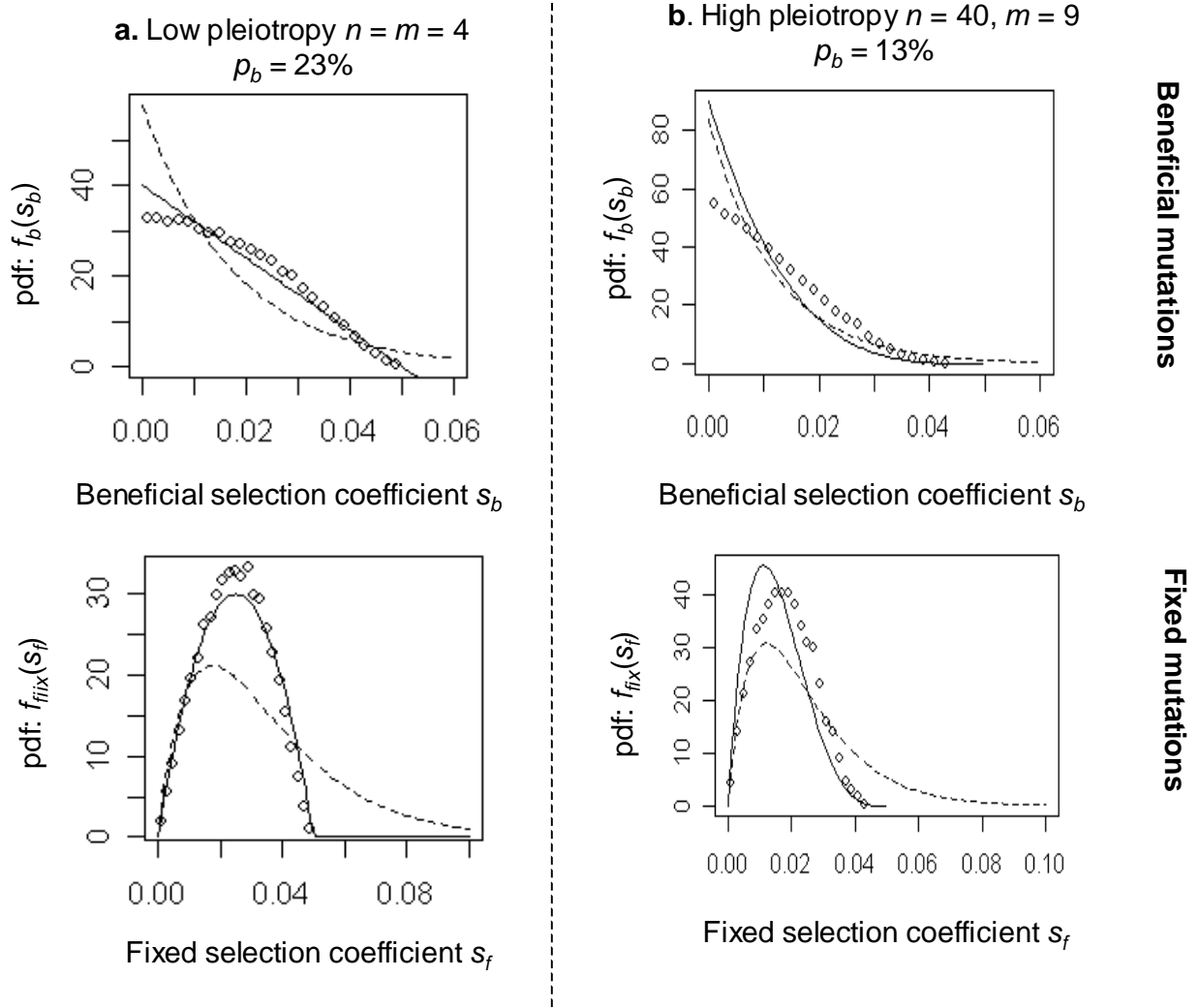


Supplementary Figure 1. Displaced gamma approximation for the whole distribution of mutation effects. $f(s)$ is given for the same parameters as in **Figure 1** ($s_0 = 0.2\bar{s}$, left panel) and **Supplementary Figure 2** ($s_0 = \bar{s}$, right panel). Dots show the distribution obtained with simulations (400,000 random mutations). The plain line gives the displaced gamma distribution fitted to the simulated s values and the dashed line gives the displaced gamma distribution predicted from Eq. (A.1.4). In each case, the total number of traits n affected by mutation, the dimensionality m and the corresponding proportion p_b of beneficial mutations is indicated directly on the figure. The displaced gamma always provides a fairly good approximation of $f(s)$ over its whole range, although it is not the best approximation for its tail behaviour when s gets close to s_0 . This figure also shows that the best - fitting displaced gamma (plain lines) is not exactly the one predicted theoretically by eq. (A.1.4) (dashed lines), which is only an approximation, although both are usually fairly similar.



Supplementary Figure 2: Fitness effect distribution among beneficial and fixed mutations for a less well-adapted genotype

Same as **Figure 1** (top panels: beneficial effects distribution) and **Figure 3** (bottom panels: fixed effect distribution) except that the wild-type is less well-adapted to the environment, i.e. the distance to the optimum is larger: $s_o = 0.05 = \bar{s}$ (as in **Supplementary Figure 1**, right column). The tail behaviour is still fairly accurately captured by the Beta approximation, for beneficial effects (Eq.(1), top panels) and particularly for fixed effects (eq. (3), bottom panels), although the proportion of beneficial mutations p_b is substantial in this case as indicated on the graph. As a comparison, the dashed lines show the best fitting exponential approximation (on top panels) and the corresponding fixed effects distribution (on bottom panels): the exponential gives less accurate results, at least in the low pleiotropy case (left column), and for fixed effects (bottom panels).