*Figure S 1 Mean genotypic value across generations for different genetic models and magnitudes. In each subplot, the additive scenario (A) was included for reference (i.e. magnitude “none”).*

*Figure S 2 Loss of additive genetic variance over time under different genetic models and magnitudes. The dotted line represents the additive genetic variance under an additive model.*

*Figure S 3 Relationship between the fraction of inital non-additive variance (i.e. sum of dominance and epistatic variance divided by the total genetic variance in generation 1) and in generation 50, for all scenarios.*

*Figure S 4 Effect of difference in allele frequency between two populations at locus 2 (x-axis) on the difference in average effects at locus 1 (left column) and at locus 2 (right column). Colours of lines indicate the epistatic interaction model.*

*Figure S 5 Effect of magnitude of non-additive effects on across generations, using non-additive effects that were 100 times larger than in the original simulations. The left plot is for genetic model D and the right plot for genetic model EAA. Colours of lines indicate the magnitude of non-additive effects.*

*Figure S 6 Effect of magnitude of epistatic effects () on the average effect of locus 2 (red), the difference in average effects at locus 2 between populations (green), and the ratio between them­ (yellow).*

*Figure S 7 Effect of genetic model (indicated by coloured lines) on the rate of fixation of favourable (left plot) and unfavourable (right plot) alleles across generations (x-axis).*