

Figure S1. Mutational response as a function of generation for mass, BLUP_OP and GBLUP_no_OP selection when having 2 DNMs per animal (panel A) or when $V_m=0.004V_e$ (panel B) (default parameters, see Table 1).

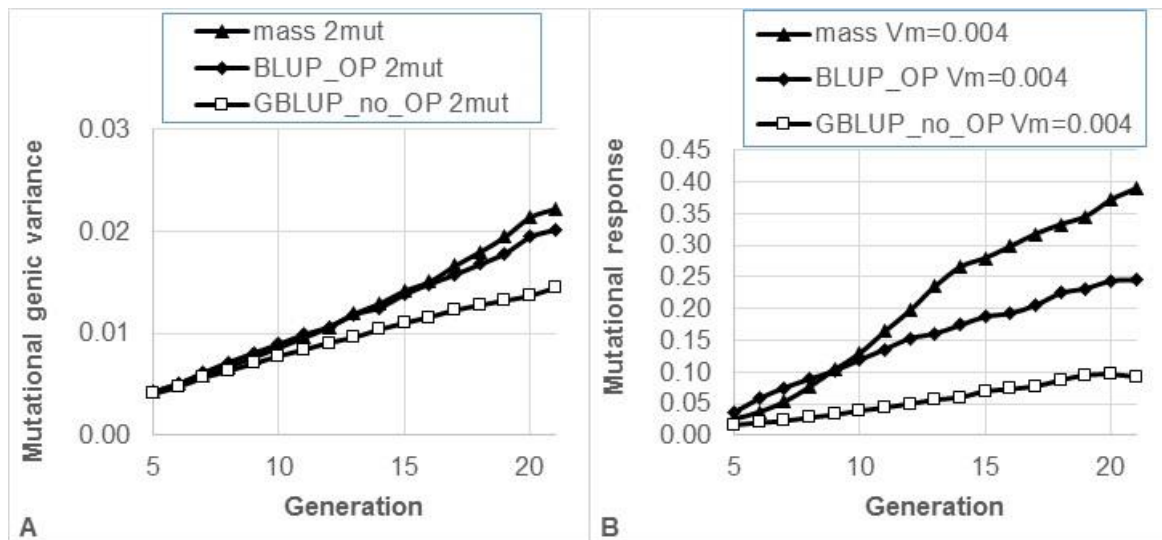


Figure S2. Mutational genetic variance as a function of generation for mass, BLUP_OP and GBLUP_no_OP selection when having 2 DNM per animal (panel A) or when $V_m=0.004V_e$ (panel B) (default parameters, see Table 1).

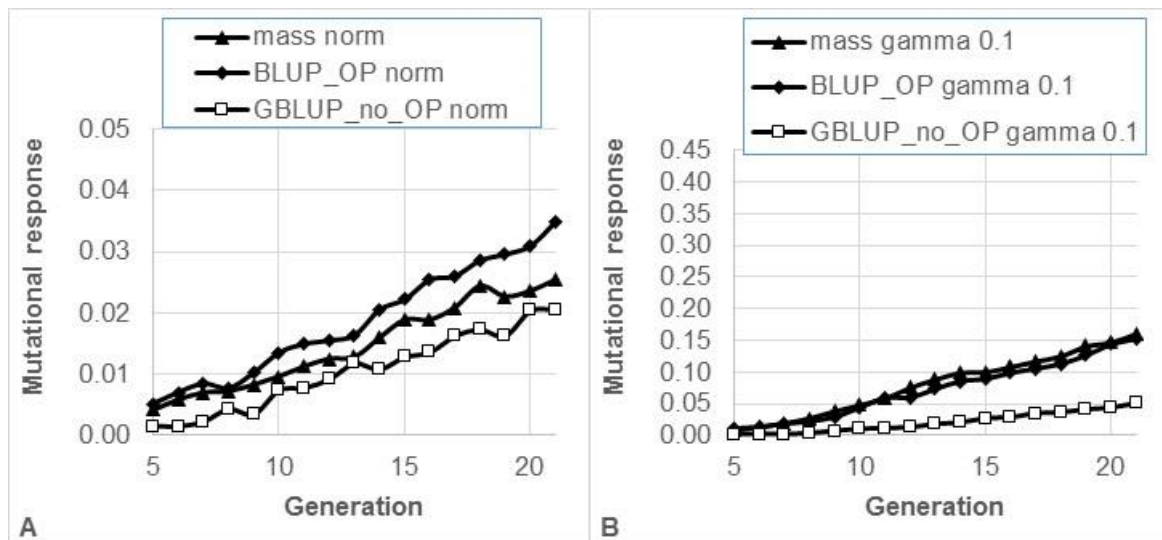


Figure S3. Mutational response as a function of generation for mass, BLUP_OP and GBLUP_no_OP selection when effects of QTL and DNM are normally distributed (panel A) or gamma distributed with shape parameter 0.1 (panel B) (default parameters, see Table 1).

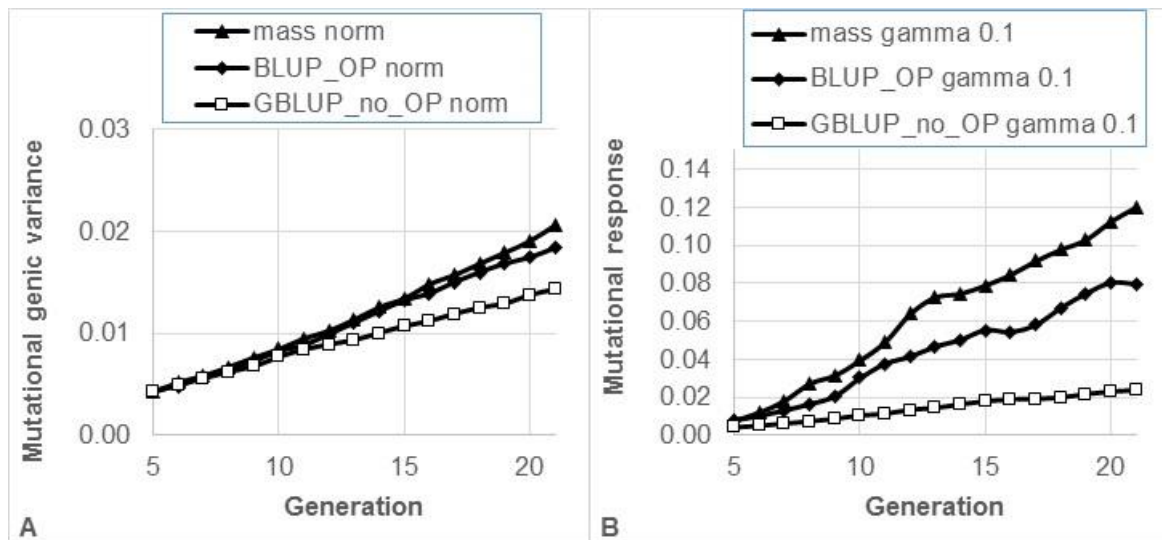


Figure S4. Mutational genetic variance as a function of generation for mass, BLUP_OP and GBLUP_no_OP selection when effects of QTL and DNM are normally distributed (panel A) or gamma distributed with shape parameter 0.1 (panel B) (default parameters, see Table 1).

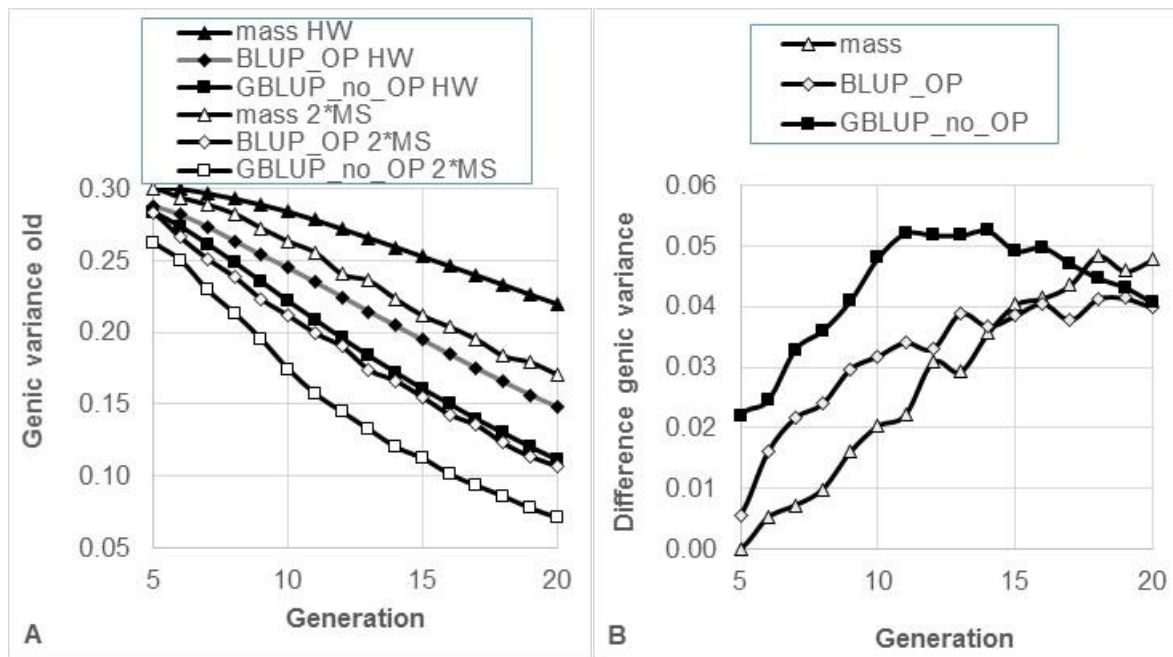


Figure S5. Standing genic variance as a function of generation for mass, BLUP_OP and GBLUP_no_OP selection either based on twice the segregation variance (2*MS) or on Hardy-Weinberg equilibrium (HW) and no linkage disequilibrium between loci (panel A) or the difference between the two measures of genic variance (panel B) (default parameters, see Table 1).

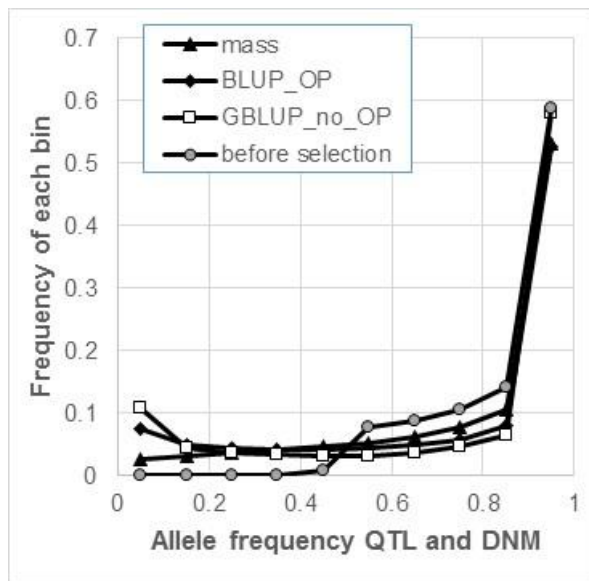


Figure S6. Frequency of 10 bins according to allele frequency of the 2-allele of segregating QTL and DNM before selection and after 20 generations of mass, BLUP_OP or GBLUP_no_OP selection. The minor allele was coded as 1 in the base population, which results in that all initial frequencies are 0.5 in the base population (default parameters, see Table 1).

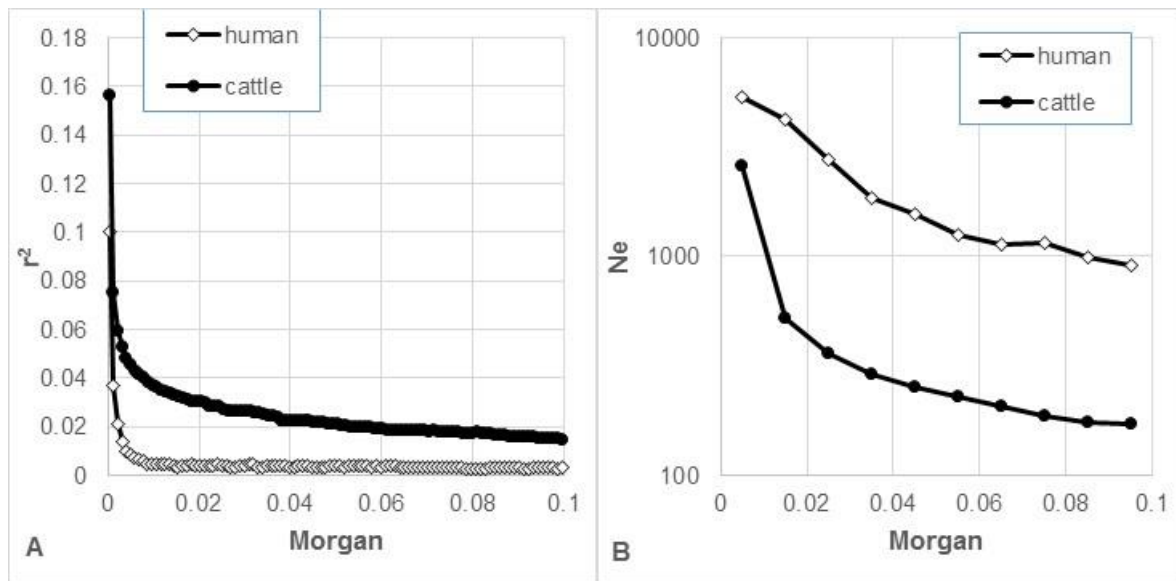


Figure S7. The decay in linkage disequilibrium r^2 as a function of the distance between SNP on chromosome 1 for human and cattle (panel A) and the estimated effective population size N_e for each bin of 0.01 Morgan using the equation $E(r^2) = \frac{1}{4N_e c + 1}$, where c is the distance in Morgans (Hayes *et al.* 2003).

Literature Cited

Hayes, B. J., P. M. Visscher, H. C. McPartlan and M. E. Goddard, 2003 Novel multilocus measure of linkage disequilibrium to estimate past effective population size. *Genome Res.* 13: 635-643.