**Simulations**

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Simulations start with a random mating historical population to establish pre-breeding equilibrium genotypes. Then, breeding commences and simulations proceed with more control over each generation. Truncation selection was performed based on high phenotype. Drift simulations were always identical to selection simulations in terms of genome layout and even genetic basis of the trait, but individuals were selected randomly. Below is a table of parameters that were used for the simulations. For parameters that varied with simulations, all options used are shown. Simulations were performed with QMSim (http://www.aps.uoguelph.ca/~msargol/qmsim/).

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| Parameter | Value(s) |
| Genetic basis of the trait |  |
| Heritability | 0.5 |
| QTL Heritability | 0.5 (all heritability attributable to QTL) |
| Phenotypic variance | 1 |
| Historical Population |  |
| Population size | 10000 |
| Number of generations | 10000 |
| Marker mutation rate (only historical gens) | 2.5e-5 |
| QTL mutation rate (only historical gens) | 2.5e-5 |
| Breeding (selected) Population |  |
| Number of selected males/generation | 500 |
| Number of selected females/generation | 500 |
| Litter size | 50 (total pop size = 500\*50 = 25,000) |
| Number of generations | 20 |
| Mating design | Random union of gametes, discrete generations |
| Genome |  |
| Number of chromosomes | 10 |
| Chromosome size | 100 cM |
| Markers/chromosome | 10,000 |
| Marker spacing | Even |
| Alleles/marker | 2 |
| Marker allele frequencies | Random (uniformly distributed) |
| Number of QTL | 10, 50, 100, 200 |
| QTL spacing | Even |
| Alleles/QTL | 2 |
| QTL allele frequencies (in first gen) | Equal (0.5) |
| QTL allele effects | Random (uniformly distributed) |
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