

Parameter	Value
Number of chromosomes	10
Number of SNP markers per chromosome	1000
Genome length	1000 cM
Number of QTL per chromosome	50
Mutation rate per QTL	2.5×10^{-5}
Distribution of additive QTL effects	Normal
Distribution of QTL allele frequency	Constant, uniform, L-shaped, U-shaped, lowMAF
Base population size:	
– male	100
– female	100
Number of historical generations	500
Reference set	All individuals of generation 502 (1000 individuals – 500 males and 500 females)
Validation set	All individuals of generation 503 to 505 (3000 – including 1500 males and 1500 females)
Heritability	0.5