**Example input file simulation**

1 # Numrep

21 # Numgen

0.3 # vara

0.7 # vare

0.001 # varm

30000 # NSNP ! we may specify here the SNP chip

5000 #NQTL

2 0.4 #QTLdistri ! 1 Normal distribution; 2 Gamma distribution with shape parameter; 3 dominance all QTL effects normally distributed, second value amount of variance explained by dominance; 4 all QTL effects normally distributed, second value amount of variance explained by dominance, 90% of DNM have negative additive effects, 5 epistasis second value amount of variance explained by epistasis

0.5 #mutation rate ! probability per animal

1.0E6 # number of base pairs/centimorgan

50 # NS

200 # ND

8 # noffdam

1 1.0 0.0 #sel\_type ! 1 is mass selection, 2 is BLUP selection, 3 is GBLUP selection, 5 is GBLUP with own phenotype

3 # number of chromosomes

map1.map # mapfiles for each chromosome

map2.map # mapfiles for each chromosome

map3.map # mapfiles for each chromosome

maf1dat # maf-file for each chromosome

maf2.dat # maf-file for each chromosome

maf3.dat # maf-file for each chromosome

SNP1.dat # SNP files for each chromosome

SNP2.dat # SNP files for each chromosome

SNP3.dat # SNP files for each chromosome

ped.fam #pedigree file