**Supplementary**

**Table S1** Variance components1, heritabilities and dominant variance proportions across 10 repetitions

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Scenarios | Type2 | $$σ\_{u}^{2}$$ | $$σ\_{v}^{2}$$ | $$σ\_{u,v}$$ | $$σ\_{(u+v)}^{2}$$ | $$σ\_{e}^{2}$$ | $$σ\_{p}^{2}$$ | $$h\_{u}^{2}$$ | $$h\_{v}^{2}$$ | $$H^{2}$$ |  |
| *SelYBD3* | True | 0.40 (0.06) | 0.14 (0.03) | -0.10 (0.02) | 0.34 (0.07) | 0.90 (0.02) | 1.24 (0.07) | 0.33 (0.03) | 0.11 (0.02) | 0.28 (0.04) |  |
| M1-MAC | 0.35 (0.09) | 0.10 (0.04) | -0.05 (0.03) | 0.34 (0.08) | 0.88 (0.03) | 1.23 (0.07) | 0.28 (0.06) | 0.08 (0.03) | 0.28 (0.05) |  |
| M2-MAC | 0.26 (0.05) | 0.08 (0.03) | 0.00 (0.00) | 0.34 (0.08) | 0.90 (0.04) | 1.24 (0.07) | 0.21 (0.03) | 0.06 (0.02) | 0.27 (0.05) |  |
| M3 | 0.29 (0.07) | 0.07 (0.03) | 0.00 (0.00) | 0.35 (0.09) | 0.91 (0.04) | 1.27 (0.09) | 0.23 (0.03) | 0.05 (0.02) | 0.28 (0.05) |  |
| Others | 0.30 (0.06) | 0.08 (0.03) | 0.00 (0.00) | 0.38 (0.09) | 0.90 (0.04) | 1.28 (0.08) | 0.24 (0.04) | 0.06 (0.02) | 0.30 (0.05) |  |
|  |  |  |  |  |  |  |  |  |  |  |  |
| *SelYBD2* | True | 0.37 (0.05) | 0.15 (0.03) | -0.08 (0.02) | 0.36 (0.05) | 0.90 (0.02) | 1.26 (0.06) | 0.29 (0.03) | 0.12 (0.02) | 0.29 (0.03) |  |
| M1-MAC | 0.33 (0.09) | 0.12 (0.04) | -0.05 (0.03) | 0.36 (0.08) | 0.89 (0.02) | 1.25 (0.08) | 0.26 (0.06) | 0.09 (0.03) | 0.29 (0.05) |  |
| M2-MAC | 0.26 (0.06) | 0.10 (0.03) | 0.00 (0.00) | 0.36 (0.08) | 0.91 (0.03) | 1.27 (0.08) | 0.20 (0.03) | 0.08 (0.02) | 0.28 (0.05) |  |
| M3 | 0.30 (0.05) | 0.08 (0.03) | 0.00 (0.00) | 0.37 (0.07) | 0.92 (0.04) | 1.30 (0.08) | 0.23 (0.03) | 0.06 (0.02) | 0.29 (0.04) |  |
| Others | 0.29 (0.06) | 0.10 (0.03) | 0.00 (0.00) | 0.39 (0.08) | 0.90 (0.03) | 1.29 (0.09) | 0.23 (0.03) | 0.08 (0.02) | 0.30 (0.05) |  |
|  |  |  |  |  |  |  |  |  |  |  |  |
| *SelNBD3* | True | 0.68 (0.06) | 0.16 (0.01) | 0.00 (0.03) | 0.84 (0.08) | 0.90 (0.02) | 1.73 (0.10) | 0.39 (0.03) | 0.09 (0.01) | 0.48 (0.02) |  |
| M1-MAC | 0.74 (0.09) | 0.16 (0.04) | -0.02 (0.05) | 0.85 (0.12) | 0.83 (0.04) | 1.68 (0.13) | 0.44 (0.05) | 0.09 (0.03) | 0.50 (0.03) |  |
| M2-MAC | 0.70 (0.10) | 0.15 (0.04) | 0.00 (0.00) | 0.85 (0.11) | 0.83 (0.03) | 1.68 (0.12) | 0.42 (0.04) | 0.09 (0.02) | 0.50 (0.03) |  |
| Others | 0.70 (0.10) | 0.15 (0.04) | 0.00 (0.00) | 0.85 (0.11) | 0.83 (0.03) | 1.68 (0.12) | 0.42 (0.04) | 0.09 (0.02) | 0.50 (0.03) |  |
|  |  |  |  |  |  |  |  |  |  |  |  |
| *SelNBD2* | True | 0.67 (0.06) | 0.16 (0.01) | 0.00 (0.03) | 0.85 (0.07) | 0.90 (0.02) | 1.74 (0.08) | 0.39 (0.03) | 0.09 (0.01) | 0.49 (0.02) |  |
| M1-MAC | 0.73 (0.09) | 0.17 (0.05) | -0.02 (0.04) | 0.87 (0.10) | 0.83 (0.04) | 1.69 (0.10) | 0.43 (0.05) | 0.10 (0.03) | 0.51 (0.03) |  |
| M2-MAC | 0.71 (0.09) | 0.16 (0.03) | 0.00 (0.00) | 0.87 (0.10) | 0.83 (0.03) | 1.70 (0.10) | 0.42 (0.03) | 0.09 (0.02) | 0.51 (0.03) |  |
| Others | 0.71 (0.09) | 0.16 (0.03) | 0.00 (0.00) | 0.87 (0.10) | 0.83 (0.03) | 1.70 (0.10) | 0.42 (0.03) | 0.09 (0.02) | 0.51 (0.03) |  |

1Variance components:$σ\_{u}^{2}$ is the variance of genotypic additive effects;$ σ\_{v}^{2}$ is variance of genotypic dominance effects; $σ\_{u,v}$ is the covariance between genotypic additive and dominance effects; $σ\_{(u+v)}^{2}$is the variance of total genotypic effects, $σ\_{(u+v)}^{2}=σ\_{u}^{2}+σ\_{v}^{2}+2σ\_{u,v}$; $σ\_{e}^{2}$ is the residual variance; $σ\_{p}^{2}$ is the phenotypic variance, $σ\_{p}^{2}=σ\_{(u+v)}^{2}+σ\_{e}^{2}$; $h\_{u}^{2}$ is the narrow sense of heritability, $h\_{u}^{2}=σ\_{u}^{2}/σ\_{p}^{2}$; $h\_{v}^{2}$ is the dominant variance proportion, $h\_{v}^{2}=σ\_{v}^{2}/σ\_{p}^{2}$; $H^{2}$ is the broad sense of heritability, $H^{2}=σ\_{(u+v)}^{2}/σ\_{p}^{2}$. Numbers in the parentheses are the corresponding standard errors across 10 repeats.

2Type: True represents the variance components that were calculated based on the QTL loci in the last generation; “M1-MAC” indicates the estimated variance components when the major allele coding in combination with model 1 (M1) was applied; “M2-MAC” indicates the estimated variance components when the major allele coding in combination with model 2 (M2) was applied; “Others” indicates the estimated variance components when one of the two following combinations was applied in the respective scenario: random allele coding (RAC) in combination with model 1 (M1): M1-RAC, and random allele coding (RAC) in combination with model 2 (M2): M2-RAC.



**Figure S1** Bivariate plots between additive and dominance QTL effects for the *BayesD2* in the 10 simulated datasets.



 **Figure S2** Bivariate plots between additive and dominance QTL effects for the *BayesD3* in the 10 simulated datasets.

**S4: Parameter file for running software QMSim**

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

 \*\* Global parameters \*\*

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

title = "this is a .prm file for QMsim";

seed="seed2.prv";

nrep = 1; //Number of replicates

h2 = 0.38; //Heritability

qtlh2 = 0.38; //QTL heritability

phvar = 1.74; //Phenotypic variance

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

 \*\* Historical population \*\*

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

begin\_hp;

 hg\_size = 500[0] //Size of the historical generations

 500[2500]

 65 [2501]

 65 [2530]

 220[2535];

 nmlhg = 20;

end\_hp;

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

 \*\* Populations \*\*

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

begin\_pop = "p0";

 begin\_founder;

 male [n = 20, pop = "hp"];

 female [n = 200, pop = "hp"];

 end\_founder;

 ls = 10; //Litter size

 pmp = 0.5 /fix; //Proportion of male progeny

 ng = 1; //Number of generations

 md = rnd; //Mating design

 sr = 1; //Replacement ratio for sires

 dr = 1; //Replacement ratio for dams

 sd = rnd; //Selection design

 cd = rnd; //Culling design

 ebv\_est = blup;

 begin\_popoutput;

 ld /maft 0.01 /max\_distance 10 /chr 1;

 data;

 stat;

 allele\_freq;

 genotype /snp\_code;

 end\_popoutput;

end\_pop;

begin\_pop = "p2";

 begin\_founder;

 male [n = 100, pop = "p0",gen=1,select=ebv /h];

 female [n = 500, pop = "p0",gen=1,select=ebv /h];

 end\_founder;

 ls = 7 8[0.005] 9[0.03] 10[0.04] 11[0.06] 12[0.08] 13[0.1] 14[0.13] 15[0.18] 16[0.13] 17[0.08] 18[0.06] 19[0.04] 20[0.03] 21[0.02] 22[0.005]; //Litter size

 pmp = 0.5 /fix; //Proportion of male progeny

 ng = 13; //Number of generations

 md = rnd; //Mating design

 sr = 1; //Replacement ratio for sires

 dr = 1; //Replacement ratio for dams

 sd = rnd; //Selection design

 cd = rnd; //Culling design

 ebv\_est = external\_bv "R CMD BATCH solver\_bv.R";

 begin\_popoutput;

 data;

 stat;

 allele\_freq;

 genotype /snp\_code;

 end\_popoutput;

end\_pop;

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

 \*\* Genome \*\*

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

begin\_genome;

 begin\_chr = 18;

 chrlen = 120; //Chromosome length

 nmloci = 18200; //Number of markers

 mpos = rnd; //Marker positions

 nma = all 2; //Number of marker alleles

 maf = eql; //Marker allele frequencies

 nqloci = 200; //Number of QTL was 25

 qpos = rnd; //QTL positions

 nqa = all 2; //Number of QTL alleles

 qaf = eql; //QTL allele frequencies

 qae = rndg 0.4; //QTL allele effects

 end\_chr;

 mmutr = 2.5e-5 /recurrent; //Marker mutation rate

 qmutr = 2.5e-5 /recurrent; //QTL mutation rate

 r\_mpos\_g; // Randomize marker positions across genome

 r\_qpos\_g; // Randomize QTL positions across genome

end\_genome;

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

 \*\* Output options \*\*

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

begin\_output;

 allele\_effect;

 monitor\_hp\_homo;

 linkage\_map;

 hp\_stat;

end\_output;

**S5: R file for calculating the external breeding values:**

#The name of this file is solver\_bv.R

unlink(".RData")

Z=read.table(pipe("perl getZ.pl"),header=F) # the getZ.pl can be found in S3.

id=Z[,1]

Z=as.matrix(Z[,-1])

popsize=length(id)

noqtl=ncol(Z)

set.seed(1000)

a=rt(noqtl,2.5) #this is addtive genetic values for each qtl

aabs=abs(a)

delta=aabs/(4+aabs)+0.3\*rnorm(noqtl)

#delta=rnorm(noqtl,mean=0.193,sd=0.312)

d=delta\*aabs

#d=rt(noqtl,2.5)

add=Z %\*% a

sd1=sd(add[1:600])

sda=sqrt(0.38\*1.74)/sd1

add=add\*sda

add=add-mean(add[1:600])

Z[Z!=0]=2

Z[Z==0]=1

Z[Z==2]=0

dom=t(Z)\*d

dom=Z %\*% d

sd2=sd(dom[1:600])

sdd=sqrt(0.1\*1.74)/sd2

dom=dom\*sdd

err=rnorm(popsize)\*sqrt(1.74\*(1-0.38-0.1))

gvalue=add+dom+err

ebv=matrix(NA,popsize,2)

for (i in 1:popsize){

 ebv[i,1]=id[i]

 ebv[i,2]=gvalue[i]

}

colnames(ebv)=c('ID',"EBV")

write.table(ebv,'my\_bv.txt',quote=F,row.names=F,col.names=T)

com=matrix(NA,popsize,5)

for(i in 1:nrow(com)){

 com[i,1]=id[i]

 com[i,2]=add[i]

 com[i,3]=dom[i]

 com[i,4]=err[i]

 com[i,5]=gvalue[i]

}

write.table(com,'my\_phe.txt',quote=F,row.names=F,col.names=T)