In [1]:
```
# Founders: real haplotype data (ch1to10.200SNP)
# "Sample animals for sire and dam candidates" & "Dams and Sires": dam size = N of dams
# One Dam -> 1 male & 1 female (1 dam -> 2 offsprings)
# selection: increase
# 5 generation selection: increase
# heritability = 0.5
# Phenotypes : all animals in G0 to G4
# Genotypes  : all progeny in G5 and all sires in each generation
# Change muAlpha = 0.0
# 10 chromosomes; 20 loci per chromosome = > 200 Loci (50 QTL & 150 Markers)
```

In [2]:
```
include("/home/nicole/Jupyter/XSimSel.jl")
```

Out[2]: XSim

In [3]:
```
using DataFrames
```

In [4]:
```
using Distributions
```

In [5]:
```
using(Gadfly)
```

Initialize XSim

In [6]:
```
numChr    = 10
chrLength = 0.01
numLoci   = 20
nQTL      = 5
mutRate   = 0.0
locusInt  = chrLength/numLoci
mapPos    = collect(locusInt/2:locusInt:chrLength)
geneFreq  = fill(0.5,numLoci)
QTL = sample(1:numLoci,nQTL,replace=false)
qtlMarker = fill(false,numLoci)
qtlMarker[QTL] = true
Va = nQTL*numChr*0.5              # Va= nQTL*2pq*mean(alpha)^2; mean(alpha) = 0
qtlEffects= rand(Normal(0, sqrt(1/Va)),numLoci*numChr)  # Let alpha mu = 0.0
XSim.init(numChr,numLoci,chrLength,geneFreq,mapPos,qtlMarker,qtlEffects,mutRate)
```

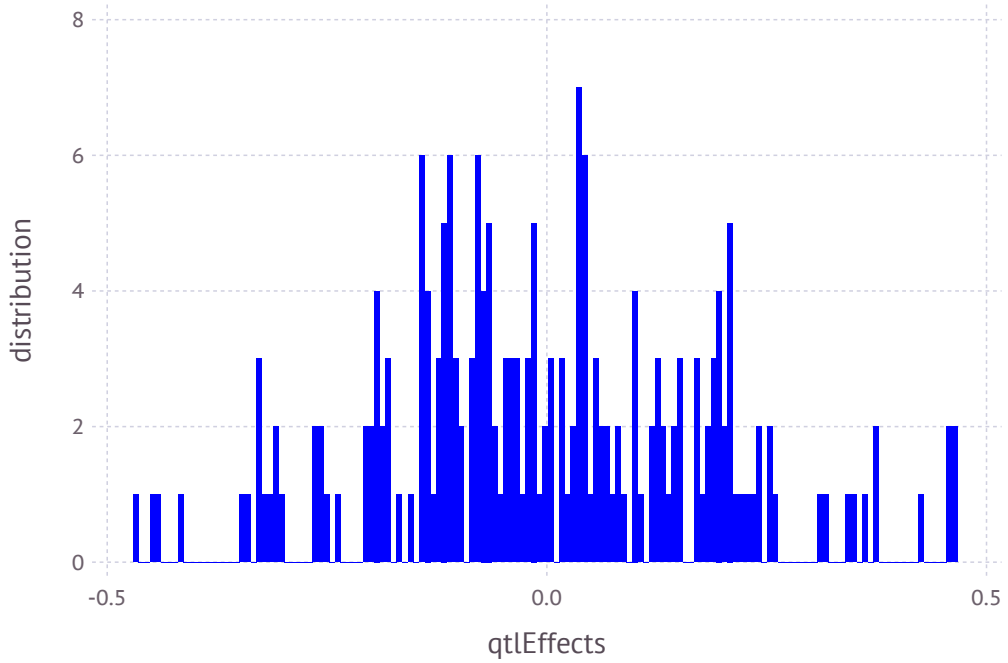
In [7]:
```
qtlEffects
```

Out[7]:
```
200-element Array{Float64,1}:
 -0.0791413
 -0.110675
 -0.0693457
  0.0442938
  0.131082
 -0.0268195
  0.376172
  0.375798
  0.0377496
  0.250978
 -0.018814
 -0.196385
 -0.0774146
  ⋮
 -0.0475644
 -0.133888
 -0.141266
  0.168196
 -0.0851228
 -0.262125
  0.0338762
  0.19275
  0.198773
 -0.307537
 -0.085281
 -0.0177556
```

In [8]:
```
writedlm("qtlEffects",qtlEffects)
```

In [9]:
```
plot(x=qtlEffects, Geom.histogram, Guide.XLabel("qtlEffects"), Guide.YLabel("distribution"), Theme(defaul
```

Out[9]:



In [10]:
```
mean(qtlEffects)
```

Out[10]:
```
-0.002846520548340204
```

In [11]:
```
var(qtlEffects)
```

Out[11]:
```
0.03436448769679758
```

In [12]:
```
# Base Population
gen=0
nGenBase    = 5
popSizeBase = 8000

# Sample 20 sire and 400 dams
popSizeSP = 8000

# Purbred Populations - mating
popSize = 8000
nGener  = 5
nSires  = 200
nDams   = 4000
npop = 1
;
```

In [13]:
```
# Animals with genotypes
posOFF0S = 1
posOFF0E = popSizeSP
posOFF1S = posOFF0E + 1
posOFF1E = posOFF0E + popSize
posOFF2S = posOFF1E + 1
posOFF2E = posOFF1E + popSize
posOFF3S = posOFF2E + 1
posOFF3E = posOFF2E + popSize
posOFF4S = posOFF3E + 1
posOFF4E = posOFF3E + popSize
posOFF5S = posOFF4E + 1
posOFF5E = posOFF4E + popSize
println("posOFF1S: ",posOFF1S,"; posOFF1E: ",posOFF1E)
println("posOFF2S: ",posOFF2S,"; posOFF2E: ",posOFF2E)
println("posOFF3S: ",posOFF3S,"; posOFF3E: ",posOFF3E)
println("posOFF4S: ",posOFF4S,"; posOFF4E: ",posOFF4E)
println("posOFF5S: ",posOFF5S,"; posOFF5E: ",posOFF5E)

# FileName :
PedAll = "PedAll.txt"           # pedigree  file with all animals
PheAll = "PheAll.txt"           # phenotype file with all animsla
GenAll = "GenAll.txt"           # genotype  file with all animals

Gen = "Gen.txt"                 # genotype file with all progeny in G5 and all sires in each generation
Phe = "Phe.txt"                 # phenotype file with all animals in G1 to G4
QTL = "QTL.txt"                 # QTL with with all progeny in G5 and all sires in each generation
Mar = "Mar.txt"                 # Marker with with all progeny in G5 and all sires in each generation
GenNF = "GenNF.txt"             # remove fixed genes from genotype file
QTLNF = "QTLNF.txt"             # remove fixed genes from QTL file
MarNF = "MarNF.txt"             # remove fixed genes from Marker file
;
```

```
posOFF1S: 8001; posOFF1E: 16000
posOFF2S: 16001; posOFF2E: 24000
posOFF3S: 24001; posOFF3E: 32000
posOFF4S: 32001; posOFF4E: 40000
posOFF5S: 40001; posOFF5E: 48000
```

In [14]:
```
fileName = "SS"
pedText = fileName * ".ped"
genText = fileName * ".gen"
pheText = fileName * ".phe"
;
```

In [15]:
```
;rm $pedText $genText $pheText
```

```
rm: cannot remove 'SS.ped': No such file or directory
rm: cannot remove 'SS.gen': No such file or directory
rm: cannot remove 'SS.phe': No such file or directory
```

Sampling Founders

In [16]:
```
sires = XSim.sampleFounders("/home/nicole/Jupyter/HERdata/data/Clean/newdata/ch1to10.200SNP.group1")
dams  = XSim.sampleFounders("/home/nicole/Jupyter/HERdata/data/Clean/newdata/ch1to10.200SNP.group2");
```

```
Sampling 360 animals into base population.
Sampling 361 animals into base population.
```

Base population

In [17]:
```
baseSires, baseDams, baseGen = XSim.sampleRan(popSizeBase, nGenBase, sires, dams, gen=gen);
```

```
Generation     1: sampling  4000 males and  4000 females
Generation     2: sampling  4000 males and  4000 females
Generation     3: sampling  4000 males and  4000 females
Generation     4: sampling  4000 males and  4000 females
Generation     5: sampling  4000 males and  4000 females
```

Sample animals for sire and dam candidates

In [18]:
```
popSP = XSim.sampleRan(popSizeSP, 1, baseSires, baseDams, gen=baseGen,fileName=fileName);
```

```
Generation     6: sampling  4000 males and  4000 females
```

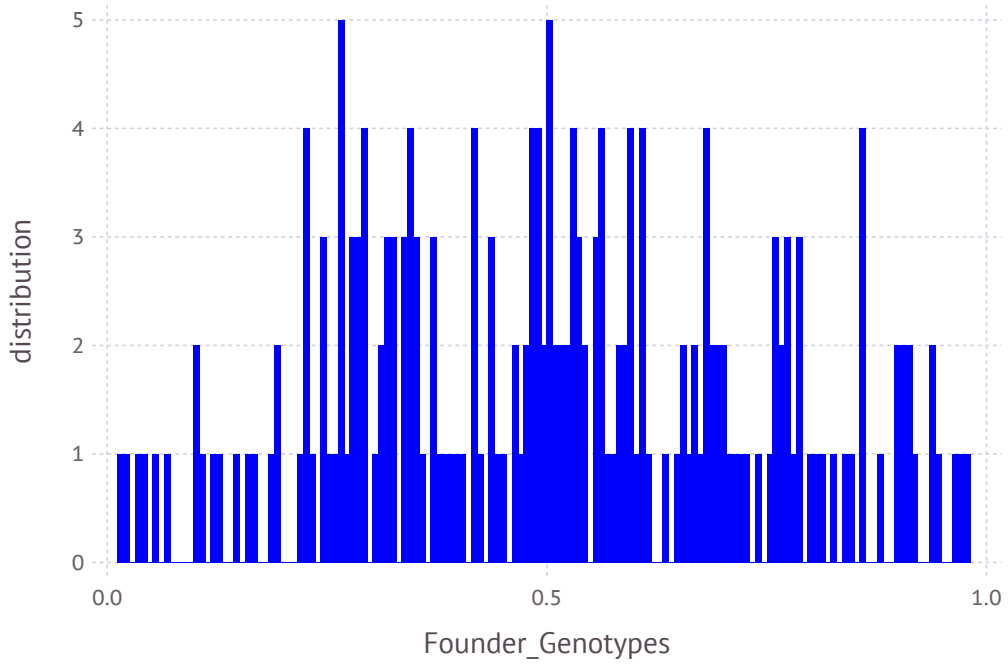
In [19]:
```
gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

In [20]:
```
FCM = mean(gSP/2,1)
```

Out[20]:
```
1x200 Array{Float64,2}:
 0.069  0.84875  0.28325  0.946625  …  0.370625  0.38975  0.907625  0.5325
```

In [21]:
```
plot(x=FCM, Geom.histogram, Guide.XLabel("Founder_Genotypes"), Guide.YLabel("distribution"), Theme(defaul
```

Out[21]:



In [22]:
```
V=var(gSP,1)
Mark=gSP[:,V.>0]
corMat=cor(Mark)
nRows =size(corMat,1)
LDMat =zeros(nRows-1,20);
```

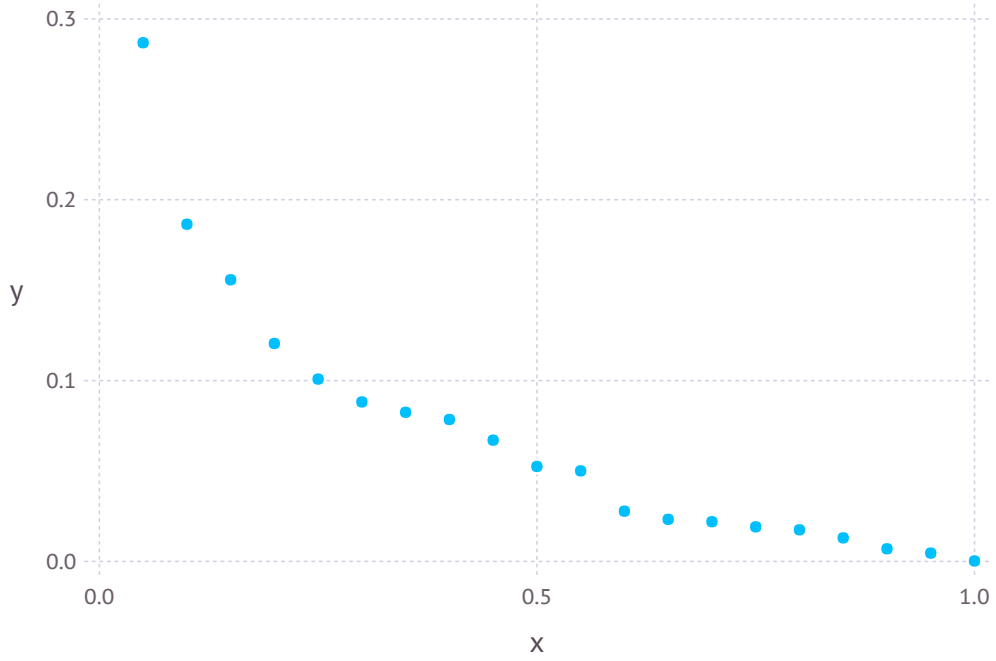
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

In [24]:
```
y=mean(LDMat,1)
sort(y,2)
```

Out[24]:
```
1x20 Array{Float64,2}:
 0.000261276  0.00461805  0.00700711  …  0.155755  0.186458  0.286837
```

In [25]:
```
plot(x=(1:20)/20*1,y=y)
```

Out[25]:



In [26]:
```
FCMstream = open("SNPCMF.txt", "w")
```

Out[26]:
```
IOStream(<file SNPCMF.txt>)
```

In [27]:
```
for i in 1:size(FCM,2)
    @printf(FCMstream, "%6.4f ", FCM[1,i])
end
```

In [28]:
```
close(FCMstream)
```

Selection - increase

In [29]:
```
aSPSire = XSim.getOurGenVals(popSP[1])
aSPDam = XSim.getOurGenVals(popSP[2])
aSP = [aSPSire;aSPDam];
```

In [30]:
```
mean(aSP)
```

Out[30]:
```
2.802077741311793
```

In [31]:
```
varGen=var(aSP)
```

Out[31]:
```
0.7411783825368791
```

In [32]:
```
XSim.common.varRes = varGen    #heritability = 0.5
```

Out[32]:
```
0.7411783825368791
```

In [33]:
```
varRes = XSim.common.varRes
```

Out[33]:
```
0.7411783825368791
```

In [34]:
```
popRMP = XSim.sampleSelNoLap(nSires, nDams, nGener,popSP[1],popSP[2],gen=popSP[3],fileName=fileName,direc
```

```
Generation     7: sampling  4000 males and  4000 females
Generation     8: sampling  4000 males and  4000 females
Generation     9: sampling  4000 males and  4000 females
Generation    10: sampling  4000 males and  4000 females
Generation    11: sampling  4000 males and  4000 females
```

In [35]:
```
ymRMP = XSim.getOurGenVals(popRMP[1])    # for males: pop[1]
mean(ymRMP)
```

Out[35]: 5.483078080046912

In [36]:
```
yfRMP = XSim.getOurGenVals(popRMP[2])    # for females: pop[2]
mean(yfRMP)
```

Out[36]: 5.482613938089123

In [37]:
```
amRMP = XSim.getOurGenVals(popRMP[1])
var(amRMP)
```

Out[37]: 0.5013847578603299

In [38]:
```
afRMP = XSim.getOurGenVals(popRMP[2])
var(afRMP)
```

Out[38]: 0.4882193283672296

Pedigree: All animals

In [39]:
```
PED = convert(Array,readtable(pedText,separator=' ',header=false))
```

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  36523  39832
 40723  36438  38529
 40724  34762  40118
 40725  34773  37940
 40726  36208  38884
 40727  33862  38603
 40728  34131  37336
 40729  36432  37177
 40730  34464  38561
 40731  33609  37005
 40732  36481  38171
 40733  34712  39675
 40734  33043  39729
     ⋮
 88710  76117  80688
 88711  75515  77996
 88712  76630  79148
 88713  75648  78637
 88714  73699  78645
 88715  75504  79064
 88716  75312  79542
 88717  73365  79221
 88718  75286  80564
 88719  74848  80402
 88720  73425  77204
 88721  76521  80643
```

In [40]:
```
PEDstream = open(PedAll, "w")
```

Out[40]:
```
IOStream(<file PedAll.txt>)
```

In [41]:
```
for i in 1:size(PED,1)
    @printf(PEDstream, "%19d%19d%19d \n", PED[i,1], PED[i,2], PED[i,3])
end
```

In [42]:
```
close(PEDstream)
```

Create matrix of `genotype" covariates for all animals

In [43]:
```
nObs = countlines(pedText)
```

Out[43]: 48000

In [44]:
```
nMarker = numChr*numLoci
```

Out[44]: 200

In [45]:
```
GT = convert(Array,readtable(genText,separator=' ',header=false))
```

Out[45]: 48000x201 Array{Int64,2}:

40722	0	2	0	2	2	0	0	0	2	0	…	2	1	0	2	0	1	1	0	0	1	2	2
40723	0	2	0	2	2	0	0	0	2	0		2	1	1	1	1	2	0	1	1	0	2	1
40724	0	1	1	2	2	0	2	2	1	1		2	2	1	1	2	2	0	1	1	0	2	1
40725	0	2	0	2	2	0	0	0	2	0		2	0	1	2	0	2	0	0	0	1	1	2
40726	0	1	1	1	1	0	1	1	1	1		2	1	1	1	2	2	0	1	1	1	2	0
40727	0	2	0	2	2	0	1	1	2	0	…	1	1	2	1	1	1	1	1	1	1	2	1
40728	0	2	0	2	2	0	1	1	2	0		2	2	1	1	1	1	0	1	1	0	1	1
40729	0	2	0	2	2	0	0	0	2	0		2	1	1	1	2	2	0	1	1	1	2	0
40730	0	2	0	2	2	0	0	0	2	0		1	1	2	1	1	1	1	1	1	1	2	1
40731	0	2	0	2	2	0	1	1	2	0		1	1	2	1	1	1	1	1	1	1	2	1
40732	0	2	0	2	2	0	0	0	2	0	…	2	1	1	1	2	2	0	1	1	1	2	0
40733	0	1	1	1	2	0	1	1	1	1		2	0	0	2	1	2	0	0	0	1	2	1
40734	0	1	2	2	1	1	1	1	1	1		1	0	1	2	0	2	1	0	0	1	1	2
⋮			⋮				⋮	⋱		⋮					⋮						⋮	
88710	0	1	1	2	2	0	1	1	1	1		2	2	2	0	2	2	0	2	2	0	2	0
88711	0	2	0	2	2	0	2	2	0	2		2	2	2	0	2	2	0	2	2	0	2	0
88712	0	2	0	2	2	0	2	2	1	1	…	2	2	2	0	2	2	0	2	2	0	2	0
88713	0	1	1	2	2	1	2	2	0	2		2	0	1	1	2	2	0	1	1	1	2	0
88714	1	1	1	2	2	1	2	2	0	2		2	1	2	0	2	2	0	2	2	0	2	0
88715	0	0	2	2	1	1	2	2	0	2		2	2	2	0	2	2	0	2	2	0	2	0
88716	0	2	0	2	2	0	2	2	2	0		2	1	1	1	1	2	0	1	1	0	2	1
88717	0	0	2	2	2	0	2	2	0	2	…	2	2	2	1	2	2	0	1	1	0	2	1
88718	1	2	0	2	2	0	1	1	2	0		1	1	2	1	2	2	1	1	1	0	1	0
88719	0	0	2	2	2	0	2	2	0	2		2	2	2	0	2	2	0	2	2	0	2	0
88720	0	2	1	2	1	0	1	1	1	1		2	2	2	0	2	2	0	2	2	0	2	0
88721	1	2	0	2	2	1	2	2	0	2		2	2	2	0	2	2	0	2	2	0	2	0

In [46]:
```
allID = GT[:,1];
```

In [47]:
```
GTM = GT[:,2:end];
```

Create marker file for all animals

In [48]:
```
M = GTM     # maker file for Julia
```

Out[48]:
```
48000x200 Array{Int64,2}:
 0  2  0  2  2  0  0  0  2  0  0  0  0  …  2  1  0  2  0  1  1  0  0  1  2  2
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  0  2  2  1  1  1  1  1     2  2  1  1  2  2  0  1  1  0  2  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  0  1  2  0  2  0  0  0  1  1  2
 0  1  1  1  1  0  1  1  1  1  1  0  1     2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  0  1  1  2  0  0  2  2  …  1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  1  1  2  0  0  1  1     2  2  1  1  1  1  0  1  1  0  1  1
 0  2  0  2  2  0  0  0  2  0  0  2  2     2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  0  0  0  2  0  0  0  0     1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  1  1  2  0  0  2  2     1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  0  0  2  0  0  0  0  …  2  1  1  1  2  2  0  1  1  1  2  0
 0  1  1  1  2  0  1  1  1  1  1  1  1     2  0  0  2  1  2  0  0  0  1  2  1
 0  1  2  2  1  1  1  1  1  1  1  1  1     1  0  1  2  0  2  1  0  0  1  1  2
 ⋮              ⋮              ⋮        ⋱        ⋮              ⋮
 0  1  1  2  2  0  1  1  1  1  1  0  0     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  0  2  2  0  2  2  0  1     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  0  2  2  1  1  1  1  2  …  2  2  2  0  2  2  0  2  2  0  2  0
 0  1  1  2  2  1  2  2  0  2  2  0  1     2  0  1  1  2  2  0  1  1  1  2  0
 1  1  1  2  2  1  2  2  0  2  2  0  1     2  1  2  0  2  2  0  2  2  0  2  0
 0  0  2  2  1  1  2  2  0  2  2  0  0     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  0  2  2  2  0  0  2  2     2  1  1  1  1  2  0  1  1  0  2  1
 0  0  2  2  2  0  2  2  0  2  2  0  2  …  2  2  2  1  2  2  0  1  1  0  2  1
 1  2  0  2  2  0  1  1  2  0  0  2  1     1  1  2  1  2  2  1  1  1  0  1  0
 0  0  2  2  2  0  2  2  0  2  2  0  0     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  1  2  1  0  1  1  1  1  1  1  1     2  2  2  0  2  2  0  2  2  0  2  0
 1  2  0  2  2  1  2  2  0  2  2  0  1     2  2  2  0  2  2  0  2  2  0  2  0
```

In [49]:
```
Mstream = open(GenAll, "w")
```

Out[49]:
```
IOStream(<file GenAll.txt>)
```

In [50]:
```
for i in 1:size(M,1)
    @printf(Mstream, "%19d", allID[i])
    for j in 1:size(M,2)
        @printf(Mstream, "%3d", M[i,j])
    end
    @printf(Mstream, "\n")
end
```

In [51]:
```
close(Mstream)
```

Genotypes - all sires and all offsprings in G5

In [52]:
```
AllSire = PED[posOFF1S:posOFF5E,2]
```

Out[52]:
```
40000-element Array{Int64,1}:
 41019
 41097
 44268
 42137
 43869
 43478
 41165
 41477
 43342
 43184
 44220
 44071
 42383
     ⋮
 76117
 75515
 76630
 75648
 73699
 75504
 75312
 73365
 75286
 74848
 73425
 76521
```

In [53]:
```
SireID = unique(AllSire)
```

Out[53]:
```
1000-element Array{Int64,1}:
 41019
 41097
 44268
 42137
 43869
 43478
 41165
 41477
 43342
 43184
 44220
 44071
 42383
     ⋮
 74122
 73365
 72781
 76117
 76694
 74706
 75517
 75784
 74870
 76336
 75159
 73741
```

In [54]:
```
OFF5 = PED[posOFF5S:posOFF5E,1]
```

Out[54]:
```
8000-element Array{Int64,1}:
 80722
 80723
 80724
 80725
 80726
 80727
 80728
 80729
 80730
 80731
 80732
 80733
 80734
     ⋮
 88710
 88711
 88712
 88713
 88714
 88715
 88716
 88717
 88718
 88719
 88720
 88721
```

In [55]:
```
SireOFF5ID = [SireID;OFF5]
```

Out[55]:
```
9000-element Array{Int64,1}:
 41019
 41097
 44268
 42137
 43869
 43478
 41165
 41477
 43342
 43184
 44220
 44071
 42383
     ⋮
 88710
 88711
 88712
 88713
 88714
 88715
 88716
 88717
 88718
 88719
 88720
 88721
```

In [56]:
```
SOFF5ID= DataFrame()
SOFF5ID[:ID] = SireOFF5ID;
```

In [57]:
```
typeof(SOFF5ID)
```

Out[57]:
```
DataFrames.DataFrame
```

In [58]:
```
MT = readtable(GenAll,separator=' ',header=false);
```

In [59]:
```
rename!(MT,:x1,:ID);
```

In [60]:
```
GSOFF5 = join(SOFF5ID, MT, on = :ID, kind = :inner);
```

In [61]:
```
size(GSOFF5)
```

Out[61]:
```
(9000,201)
```

In [62]:
```
GSOFF5Row = size(GSOFF5,1)
```

Out[62]:
```
9000
```

In [63]:
```
GSOFF5Col = size(GSOFF5,2)
```

Out[63]:
```
201
```

In [64]:
```
GSOFF5stream = open(Gen, "w")
```

Out[64]:
```
IOStream(<file Gen.txt>)
```

In [65]:
```
for i in 1:size(GSOFF5,1)
    for j in 1
        @printf(GSOFF5stream, "%19d", GSOFF5[i,j])
    end
    for k in 2:size(GSOFF5,2)
        @printf(GSOFF5stream, "%3d", GSOFF5[i,k])
    end
    @printf(GSOFF5stream, "\n")
end
```

In [66]:
```
close(GSOFF5stream)
```

Phenotypes - All animals

In [67]:
```
PBV = convert(Array,readtable(pheText,separator=' ',header=false))
```

Out[67]:
```
48000x3 Array{Real,2}:
 40722  1.958  1.146
 40723  1.093  1.996
 40724  3.911  3.195
 40725  0.141  1.81
 40726  1.603  2.46
 40727  1.665  2.993
 40728  4.293  3.456
 40729  3.584  3.121
 40730  3.39   2.867
 40731  3.666  2.858
 40732  1.364  2.047
 40733  3.669  2.281
 40734  2.28   1.882
     ⋮
 88710  5.772  6.052
 88711  7.323  6.374
 88712  6.555  6.455
 88713  6.816  6.267
 88714  5.743  6.771
 88715  5.117  6.613
 88716  5.507  6.684
 88717  6.466  6.183
 88718  6.54   6.666
 88719  6.129  6.754
 88720  5.891  6.072
 88721  7.235  7.133
```

In [68]:
```
PBVstream = open(PheAll, "w")
```

Out[68]:
```
IOStream(<file PheAll.txt>)
```

In [69]:
```
for i in 1:size(PBV,1)
    @printf(PBVstream, "%19d %10.3f %10.3f \n", PBV[i,1], PBV[i,2], PBV[i,3])
end
```

In [70]:
```
close(PBVstream )
```

Phenotypes - all animnls from G0 to G4

In [71]:
```
OFFG0toG4 = PED[posOFF0S:posOFF4E,1]
```

Out[71]:
```
40000-element Array{Int64,1}:
 40722
 40723
 40724
 40725
 40726
 40727
 40728
 40729
 40730
 40731
 40732
 40733
 40734
     ⋮
 80710
 80711
 80712
 80713
 80714
 80715
 80716
 80717
 80718
 80719
 80720
 80721
```

In [72]:
```
OFFG0toG4ID= DataFrame()
OFFG0toG4ID[:ID] = OFFG0toG4;
```

In [73]:
```
typeof(OFFG0toG4ID)
```

Out[73]:
```
DataFrames.DataFrame
```

In [74]:
```
AllPBV= readtable(pheText,separator=' ',header=false);
```

In [75]:
```
rename!(AllPBV,:x1,:ID)
head(AllPBV);
```

In [76]:
```
OFFG0toG4PBV = join(OFFG0toG4ID, AllPBV, on = :ID, kind = :inner);
```

In [77]:
```
Row = size(OFFG0toG4PBV,1)
```

Out[77]:
```
40000
```

In [78]:
```
Col = size(OFFG0toG4PBV,2)
```

Out[78]:
```
3
```

In [79]:
```
Phestream = open(Phe, "w")
```

Out[79]:
```
IOStream(<file Phe.txt>)
```

In [80]:
```
for i in 1:size(OFFG0toG4PBV,1)
    @printf(Phestream, "%19d %10.3f %10.3f \n", OFFG0toG4PBV[i,1], OFFG0toG4PBV[i,2], OFFG0toG4PBV[i,3])
end
```

In [81]:
```
close(Phestream)
```

Get files with QTL only or Markers only

QTL file and Markers file

In [82]:
```
QTLPos = XSim.common.G.qtl_index
```

Out[82]:
```
50-element Array{Int64,1}:
   2
   3
   7
  11
  16
  22
  23
  27
  31
  36
  42
  43
  47
   ⋮
 151
 156
 162
 163
 167
 171
 176
 182
 183
 187
 191
 196
```

In [83]:
```
k = size(M,2)
MarkerPos = deleteat!(collect(1:k),sort(QTLPos))
```

Out[83]:
```
150-element Array{Int64,1}:
   1
   4
   5
   6
   8
   9
  10
  12
  13
  14
  15
  17
  18
   ⋮
 186
 188
 189
 190
 192
 193
 194
 195
 197
 198
 199
 200
```

Genotype codes: 0, 1, 2

In [84]:
```
IDgen = convert(Array,readtable(Gen,separator=' ',header=false));
```

In [85]:
```
onlyID = IDgen[:,1]
QTLMarker = IDgen[:, 2:end]
```

Out[85]: 9000x200 Array{Int64,2}:

0	1	2	2	1	1	1	1	1	1	1	1	1	…	1	0	2	2	1	1	1	1	1	1	2	1
0	2	0	2	2	0	0	0	2	0	0	1	1		2	2	2	0	2	2	0	1	1	1	2	1
0	2	1	2	1	0	0	0	2	0	0	2	1		2	2	1	1	1	1	1	1	1	1	2	1
0	2	0	2	2	1	1	1	1	1	0	1	1		2	1	1	1	2	2	0	1	1	1	2	0
0	2	0	2	2	0	0	0	2	0	0	2	2		2	2	2	0	2	2	0	2	2	0	2	0
0	2	0	2	2	0	1	1	2	0	0	2	2	…	2	2	1	1	1	1	1	1	1	1	2	1
1	1	1	2	2	0	2	2	0	2	2	0	0		2	1	2	1	2	2	0	1	1	0	2	1
1	2	0	2	2	0	0	0	2	0	0	2	1		1	1	2	1	1	1	1	1	1	1	2	1
0	2	0	2	2	0	0	0	2	0	0	0	0		2	0	0	2	1	2	0	0	0	1	2	1
0	1	1	2	2	1	1	1	1	1	1	1	2		2	2	2	0	2	2	0	2	2	0	2	0
0	1	1	2	1	1	2	2	1	1	1	1	1	…	2	1	2	1	2	1	0	1	1	0	2	1
0	2	0	2	2	0	0	0	2	0	0	0	0		1	1	2	1	1	1	1	1	1	1	2	1
0	1	1	1	1	0	1	1	1	1	1	1	2		2	2	2	0	2	2	0	2	2	0	2	0
⋮				⋮					⋮				⋱			⋮					⋮				
0	1	1	2	2	0	1	1	1	1	1	0	0		2	2	2	0	2	2	0	2	2	0	2	0
0	2	0	2	2	0	2	2	0	2	2	0	1		2	2	2	0	2	2	0	2	2	0	2	0
0	2	0	2	2	0	2	2	1	1	1	1	2	…	2	2	2	0	2	2	0	2	2	0	2	0
0	1	1	2	2	1	2	2	0	2	2	0	1		2	0	1	1	2	2	0	1	1	1	2	0
1	1	1	2	2	1	2	2	0	2	2	0	1		2	1	2	0	2	2	0	2	2	0	2	0
0	0	2	2	1	1	2	2	0	2	2	0	0		2	2	2	0	2	2	0	2	2	0	2	0
0	2	0	2	2	0	2	2	2	0	0	2	2		2	1	1	1	1	2	0	1	1	0	2	1
0	0	2	2	2	0	2	2	0	2	2	0	2	…	2	2	2	1	2	2	0	1	1	0	2	1
1	2	0	2	2	0	1	1	2	0	0	2	1		1	1	2	1	2	2	1	1	1	0	1	0
0	0	2	2	2	0	2	2	0	2	2	0	0		2	2	2	0	2	2	0	2	2	0	2	0
0	2	1	2	1	0	1	1	1	1	1	1	1		2	2	2	0	2	2	0	2	2	0	2	0
1	2	0	2	2	1	2	2	0	2	2	0	1		2	2	2	0	2	2	0	2	2	0	2	0

In [86]:
```
onlyQTL = QTLMarker[:,QTLPos]
```

Out[86]:
```
9000x50 Array{Int64,2}:
 1  2  1  1  0  1  1  1  0  2  0  0  1  …  1  0  1  0  2  1  1  0  1  1  2  1
 2  0  0  0  1  1  1  2  0  2  1  1  0     2  2  0  0  0  0  0  0  2  2  2  1
 2  1  0  0  1  0  2  2  1  2  0  1  1     1  0  1  0  1  0  1  0  2  1  1  1
 2  0  1  0  1  1  1  2  0  1  0  0  0     2  1  2  2  1  0  1  1  2  2  1  1
 2  0  0  0  2  0  2  1  0  1  1  1  1     2  0  1  1  0  2  0  0  2  2  2  2
 2  0  1  0  2  1  1  0  0  1  0  2  1  …  0  0  0  0  0  0  1  0  2  1  1  1
 1  1  2  2  1  0  2  1  0  1  0  1  1     1  0  0  0  0  0  0  1  2  2  2  1
 2  0  0  0  2  1  1  2  0  2  0  0  1     1  1  0  0  1  2  1  0  1  1  2  1
 2  0  0  0  0  1  1  2  0  2  1  1  1     2  1  0  0  1  1  1  1  2  1  0  0
 1  1  1  1  1  0  2  2  0  2  0  1  2     2  1  0  0  1  1  2  0  2  2  2  2
 1  1  2  1  2  1  1  0  0  1  1  1  1  …  2  0  1  1  0  0  2  1  2  2  2  1
 2  0  0  0  0  1  1  1  1  2  1  1  1     1  0  0  0  2  2  0  0  1  1  2  1
 1  1  1  1  1  1  1  1  1  2  1  1  1     1  0  0  0  1  0  0  0  2  2  2  2
 ⋮                 ⋮                 ⋮        ⋱        ⋮                 ⋮
 1  1  1  1  2  0  2  1  0  2  0  0  1     2  0  1  0  2  1  1  0  2  2  2  2
 2  0  2  2  1  2  0  1  0  2  0  2  2     2  0  0  0  2  2  1  0  2  2  2  2
 2  0  2  1  2  1  1  2  0  2  1  0  1  …  1  0  1  0  1  0  2  0  2  2  2  2
 1  1  2  2  2  0  2  2  0  1  0  1  1     1  0  0  0  2  1  2  1  2  2  1  1
 1  1  2  2  2  1  1  1  1  2  0  1  2     1  0  0  0  2  2  0  0  2  2  2  2
 0  2  2  2  2  2  0  2  0  2  0  2  2     0  0  1  1  0  1  2  0  2  2  2  2
 2  0  2  0  2  0  2  2  0  2  0  1  2     2  0  1  0  2  0  2  1  1  2  1  1
 0  2  2  2  2  2  0  0  0  2  0  1  2  …  1  1  0  0  2  2  0  1  2  2  2  1
 2  0  1  0  2  0  2  2  1  1  0  1  2     2  0  1  1  2  1  1  0  2  2  2  1
 0  2  2  2  2  0  2  2  0  2  0  1  2     1  0  2  1  2  0  1  0  2  2  2  2
 2  1  1  1  1  0  2  2  0  2  1  0  1     2  0  1  1  1  0  2  0  2  2  2  2
 2  0  2  2  2  1  1  2  1  2  0  1  2     0  0  1  0  2  1  1  0  2  2  2  2
```

In [87]:
```
onlyMar = QTLMarker[:,MarkerPos];
```

In [88]:
```
QTLstream = open(QTL, "w")
Marstream = open(Mar, "w");
```

In [89]:
```
for i in 1:size(onlyID,1)
    @printf(QTLstream, "%19d", onlyID[i])
    for j in 1:size(onlyQTL,2)
        @printf(QTLstream, "%3d", onlyQTL[i,j])
    end
    @printf(QTLstream, "\n")
end
```

In [90]:
```
for i in 1:size(onlyID,1)
    @printf(Marstream, "%19d", onlyID[i])
    for j in 1:size(onlyMar,2)
        @printf(Marstream, "%3d", onlyMar[i,j])
    end
    @printf(Marstream, "\n")
end
```

In [91]:
```
close(QTLstream)
close(Marstream)
```

Remove Fixed Gene from the panel

In [92]:
```
VQM = var(QTLMarker,1)
QMnoFixed = QTLMarker[:,VQM .> 0]
VQ = var(onlyQTL,1)
QnoFixed = onlyQTL[:,VQ .> 0]
VM = var(onlyMar,1)
MnoFixed = onlyMar[:,VM .> 0];
```

In [93]:
```
GenNFstream = open(GenNF, "w")
QTLNFstream = open(QTLNF, "w")
MarNFstream = open(MarNF, "w");
```

In [94]:
```
for i in 1:size(onlyID,1)
    @printf(GenNFstream, "%19d", onlyID[i])
    for j in 1:size(QMnoFixed,2)
        @printf(GenNFstream, "%3d", QMnoFixed[i,j])
    end
    @printf(GenNFstream, "\n")
end
```

In [95]:
```
for i in 1:size(onlyID,1)
    @printf(QTLNFstream, "%19d", onlyID[i])
    for j in 1:size(QnoFixed,2)
        @printf(QTLNFstream, "%3d", QnoFixed[i,j])
    end
    @printf(QTLNFstream, "\n")
end
```

In [96]:
```
for i in 1:size(onlyID,1)
    @printf(MarNFstream, "%19d", onlyID[i])
    for j in 1:size(MnoFixed,2)
        @printf(MarNFstream, "%3d", MnoFixed[i,j])
    end
    @printf(MarNFstream, "\n")
end
```

In [97]:
```
close(GenNFstream)
close(QTLNFstream)
close(MarNFstream)
```

Check heritability

In [98]:
```
P = AllPBV[:,2]
BV = AllPBV[:,3];
```

In [99]:
```
VP = var(P)
VBV = var(BV)
H = VBV/VP
```

Out[99]: 0.6525280138784527

In [100]:
```
cor=cor(P,BV)
```

```
WARNING: imported binding for cor overwritten in module Main
```

Out[100]:
```
0.8074002697226894
```

In [101]:
```
QTLAll = M[:,QTLPos]
```

Out[101]:
```
48000x50 Array{Int64,2}:
 2  0  0  0  0  1  1  0  0  1  0  2  2  …  2  0  0  0  0  0  1  0  2  0  0  0
 2  0  0  0  0  1  1  0  0  1  2  0  0     2  1  0  0  0  1  0  0  2  1  1  1
 1  1  2  1  2  1  1  0  0  1  1  1  0     0  1  0  0  0  1  0  0  2  2  1  1
 2  0  0  0  0  1  1  1  1  1  0  0  1     0  0  1  1  0  2  0  1  1  0  1  0
 1  1  1  1  0  1  1  1  0  1  0  0  1     0  0  1  1  0  1  0  1  2  2  1  1
 2  0  1  0  2  0  2  2  0  2  0  2  1  …  2  0  0  0  0  1  1  0  1  1  2  1
 2  0  1  0  1  0  2  1  0  1  1  2  2     2  0  0  0  0  1  1  1  2  1  1  1
 2  0  0  0  2  1  1  1  1  1  0  2  2     1  0  1  1  1  1  0  1  2  2  1  1
 2  0  0  0  0  2  0  2  0  2  2  0  0     1  0  0  0  0  0  0  0  1  1  2  1
 2  0  1  0  2  0  2  2  1  1  1  0  0     0  0  0  0  0  0  0  0  1  1  2  1
 2  0  0  0  0  1  1  0  0  1  0  1  1  …  1  1  0  0  0  0  1  1  1  1  1  1
 1  1  1  1  1  1  1  0  0  1  1  1  1     1  0  0  0  0  1  1  1  2  1  0  0
 1  2  1  1  0  1  1  0  0  1  2  1  0     1  0  1  1  1  1  1  1  1  1  1  0
 ⋮              ⋮              ⋮        ⋱        ⋮              ⋮
 1  1  1  1  2  0  2  1  0  2  0  0  1     2  0  1  0  2  1  1  0  2  2  2  2
 2  0  2  2  1  2  0  1  0  2  0  2  2     2  0  0  0  2  2  1  0  2  2  2  2
 2  0  2  1  2  1  1  2  0  2  1  0  1  …  1  0  1  0  1  0  2  0  2  2  2  2
 1  1  2  2  2  0  2  2  0  1  0  1  1     1  0  0  0  2  1  2  1  2  2  1  1
 1  1  2  2  2  1  1  1  1  2  0  1  2     1  0  0  0  2  2  0  0  2  2  2  2
 0  2  2  2  2  2  0  2  0  2  0  2  2     0  0  1  1  0  1  2  0  2  2  2  2
 2  0  2  0  2  0  2  2  0  2  0  1  2     2  0  1  0  2  0  2  1  1  2  1  1
 0  2  2  2  2  2  0  0  0  2  0  1  2  …  1  1  0  0  2  2  0  1  2  2  2  1
 2  0  1  0  2  0  2  2  1  1  0  1  2     2  0  1  1  2  1  1  0  2  2  2  1
 0  2  2  2  2  0  2  2  0  2  0  1  2     1  0  2  1  2  0  1  0  2  2  2  2
 2  1  1  1  1  0  2  2  0  2  1  0  1     2  0  1  1  1  0  2  0  2  2  2  2
 2  0  2  2  2  1  1  2  1  2  0  1  2     0  0  1  0  2  1  1  0  2  2  2  2
```

In [102]:
```
QTLo=qtlEffects[QTLPos]
```

Out[102]:
```
50-element Array{Float64,1}:
 -0.110675
 -0.0693457
  0.376172
 -0.018814
  0.171877
  0.0371623
  0.125129
  0.240281
 -0.326052
 -0.0222132
  0.210349
  0.00472496
 -0.0382386
  ⋮
  0.350441
 -0.19659
  0.118325
 -0.0781628
 -0.107858
 -0.0674847
  0.153201
  0.175007
 -0.0646866
 -0.0313432
 -0.141266
  0.19275
```

In [103]:
```
EAlpha=QTLAll*QTLo
```

Out[103]:
```
48000-element Array{Float64,1}:
 -0.852409
  0.0057574
  0.0715596
 -0.955639
 -0.696955
  1.05663
  1.15658
  0.0205252
  0.604473
  0.62055
 -0.116476
 -0.595172
 -0.0884113
  ⋮
  1.37811
  0.756873
  1.50999
  1.32012
 -0.0717814
  0.0236421
  2.85337
 -0.701331
  1.4667
  1.13102
  2.31979
 -0.395258
```

In [104]:
```
meanEAlphaG0=mean(EAlpha[1:8000])   # our mu_g
```

Out[104]:
```
0.2842742080653621
```

In [105]:
```
meanEAlphaG1=mean(EAlpha[8001:16000])
```

Out[105]:
```
0.35080826442368973
```

In [106]:
```
meanEAlphaG2=mean(EAlpha[16001:24000])
```

Out[106]:
```
0.48494294464226323
```

In [107]:
```
meanEAlphaG3=mean(EAlpha[24001:32000])
```

Out[107]:
```
0.539142961359782
```

In [108]:
```
meanEAlphaG4=mean(EAlpha[32001:40000])
```

Out[108]:
```
0.6026749819537465
```

In [109]:
```
meanEAlphaG5=mean(EAlpha[40001:48000])
```

Out[109]:
```
0.6955507047141498
```

In [110]:
```
EAlphaG=onlyQTL*QTLo
```

Out[110]:
```
9000-element Array{Float64,1}:
  0.229271
  0.86818
  0.378603
  0.810738
  1.06823
 -0.213526
  1.35486
  0.0420416
  0.489874
  0.836708
  2.26302
  0.499493
  0.379819
  ⋮
  1.37811
  0.756873
  1.50999
  1.32012
 -0.0717814
  0.0236421
  2.85337
 -0.701331
  1.4667
  1.13102
  2.31979
 -0.395258
```

In [111]:
```
meanEAlphaG=mean(EAlphaG)
```

Out[111]: 0.6881365811474979

In [112]:
```
meanBreedingValueSelected=meanEAlphaG-meanEAlphaG0   # Legarra mu_g
```

Out[112]: 0.4038623730821358

In [113]:
```
meanEAlphaS0=mean(EAlphaG[1:200])
```

Out[113]: 0.4427996756407655

In [114]:
```
meanBreedingValueSelectedG0=meanEAlphaS0-meanEAlphaG0
```

Out[114]: 0.15852546757540342

In [115]:
```
meanEAlphaS1=mean(EAlphaG[201:400])
```

Out[115]: 0.610392314568071

In [116]:
```
meanBreedingValueSelectedG1=meanEAlphaS1-meanEAlphaG0
```

Out[116]: 0.3261181065027089

In [117]:
```
meanEAlphaS2=mean(EAlphaG[401:600])
```

Out[117]: 0.5935395984350549

In [118]:
```
meanBreedingValueSelectedG2=meanEAlphaS2-meanEAlphaG0
```

Out[118]: 0.3092653903696928

In [119]:
```
meanEAlphaS3=mean(EAlphaG[601:800])
```

Out[119]: 0.6884965776214966

In [120]:
```
meanBreedingValueSelectedG3=meanEAlphaS3-meanEAlphaG0
```

Out[120]: 0.40422236955613455

In [121]:
```
meanEAlphaS4=mean(EAlphaG[801:1000])
```

Out[121]: 0.808889796806019

In [122]:
```
meanBreedingValueSelectedG4=meanEAlphaS4-meanEAlphaG0
```

Out[122]: 0.524615588740657

In [123]:
```
meanEAlphaS5=mean(EAlphaG[1001:9000])
```

Out[123]: 0.6955507047141498

In [124]:
```
meanBreedingValueSelectedG5=meanEAlphaS5-meanEAlphaG0
```

Out[124]: 0.41127649664878774