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)
```

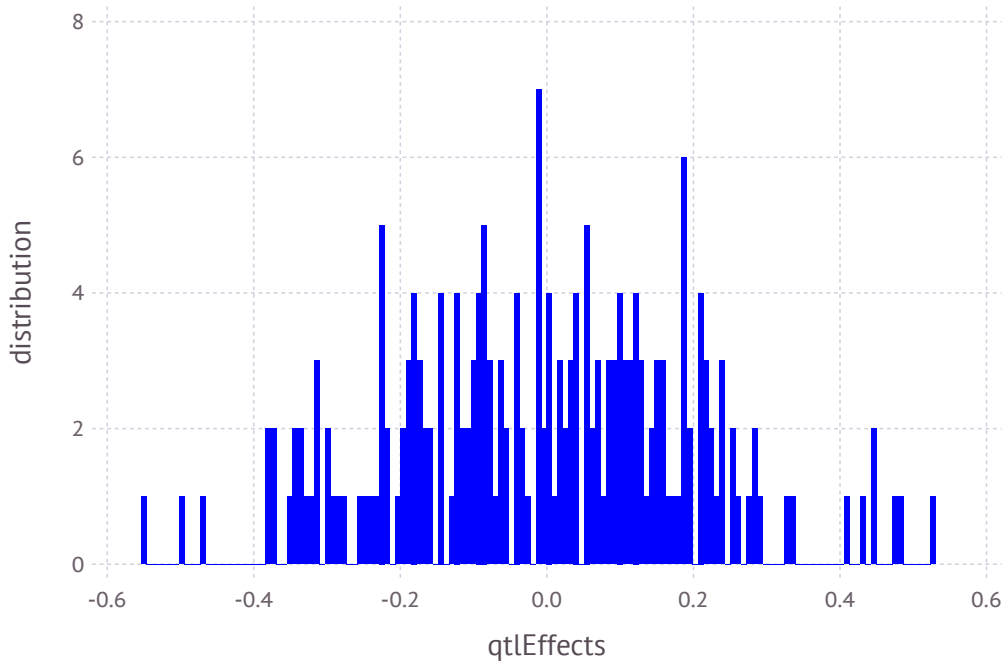
In [7]:
```
qtlEffects
```

Out[7]:
```
200-element Array{Float64,1}:
 -0.216211
 -0.222238
 -0.324808
  0.18648
  0.0915788
  0.118382
 -0.553589
  0.273582
 -0.0783824
  0.096736
  0.207391
  0.188817
  0.150082
  ⋮
 -0.0892829
  0.189936
  0.235835
 -0.175264
  0.0813265
 -0.0324184
 -0.0844959
 -0.223786
  0.0886406
 -0.310722
  0.212269
 -0.125657
```

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]:
```
-0.007237082835571364
```

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

Out[11]:
```
0.040828918934020374
```

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
```

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}:
 0.06825  0.840875  0.275125  0.950125  …  0.384375  0.90425  0.540375
```

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);
```

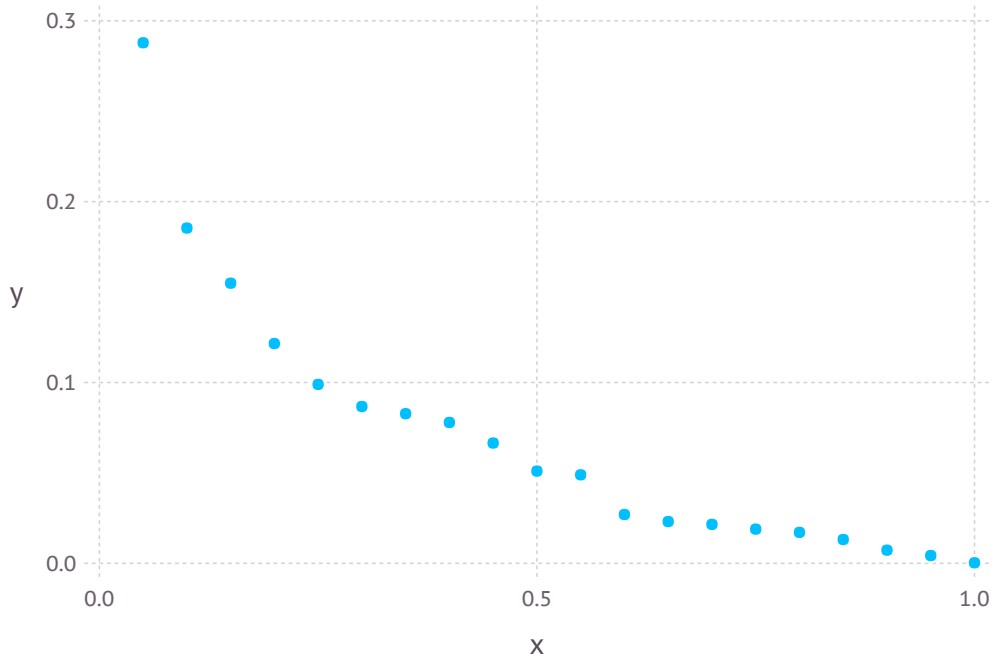
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.000315148  0.00434901  0.00731404  …  0.154919  0.18541  0.287888
```

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]:
```
0.8388578780141539
```

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

Out[31]:
```
1.408398085269593
```

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

Out[32]:
```
1.408398085269593
```

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

Out[33]:
```
1.408398085269593
```

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]:
```
4.164682823420736
```

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

Out[36]:
```
4.16227407686104
```

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

Out[37]: 0.7361581122759424

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

Out[38]: 0.7060292434872438

Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  33535  40197
 40723  35657  38246
 40724  33368  39183
 40725  34443  38777
 40726  34501  37384
 40727  34664  37568
 40728  34235  38283
 40729  33517  40086
 40730  34166  37396
 40731  35522  37133
 40732  35753  38743
 40733  33959  38867
 40734  33873  39529
     ⋮
 88710  76498  79416
 88711  74494  80156
 88712  74860  78296
 88713  73447  78940
 88714  75788  77757
 88715  75944  78714
 88716  74372  78064
 88717  73084  79716
 88718  76311  79888
 88719  74915  80227
 88720  76198  77725
 88721  76184  79555
```

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

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

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}:
 43735
 41074
 43137
 41523
 43960
 43538
 43636
 43564
 41252
 43835
 42100
 43312
 42244
     ⋮
 76498
 74494
 74860
 73447
 75788
 75944
 74372
 73084
 76311
 74915
 76198
 76184
```

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

Out[53]:
```
1000-element Array{Int64,1}:
 43735
 41074
 43137
 41523
 43960
 43538
 43636
 43564
 41252
 43835
 42100
 43312
 42244
    ⋮
 75635
 76286
 73685
 76612
 75121
 76720
 74824
 75788
 75270
 73846
 76301
 72951
```

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}:
 43735
 41074
 43137
 41523
 43960
 43538
 43636
 43564
 41252
 43835
 42100
 43312
 42244
     ⋮
 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  -0.012   0.223
 40723  -1.313   0.423
 40724   0.22    0.319
 40725   2.372   0.405
 40726   0.364   0.699
 40727   1.635   2.172
 40728   0.533  -0.234
 40729   1.239   1.172
 40730   1.17    1.462
 40731  -0.407  -0.551
 40732   0.974   1.17
 40733   0.808   0.716
 40734   1.055   1.554
     ⋮
 88710   6.615   4.884
 88711   4.92    5.035
 88712   7.187   6.219
 88713   4.678   5.201
 88714   6.33    5.097
 88715   4.811   4.527
 88716   5.262   5.047
 88717   2.958   3.981
 88718   5.777   4.85
 88719   4.113   4.172
 88720   4.219   4.514
 88721   6.558   5.668
```

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}:
   5
   7
  11
  15
  17
  25
  27
  31
  35
  37
  45
  47
  51
   ⋮
 155
 157
 165
 167
 171
 175
 177
 185
 187
 191
 195
 197
```

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

Out[83]:
```
150-element Array{Int64,1}:
   1
   2
   3
   4
   6
   8
   9
  10
  12
  13
  14
  16
  18
   ⋮
 184
 186
 188
 189
 190
 192
 193
 194
 196
 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	2	0	2	2	0	0	0	2	0	0	1	1	…	1	0	1	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	2	1	2	0	0	0	0	2	1
0	1	1	2	2	0	1	1	1	1	1	1	2		2	1	1	1	2	2	0	1	1	1	2	0
0	2	1	2	1	0	0	0	2	0	0	2	1		1	0	2	2	1	0	2	0	0	2	2	2
0	2	0	2	2	0	0	0	2	0	0	1	1		2	2	2	0	2	2	0	2	2	0	2	0
0	2	1	2	1	0	0	0	2	0	0	2	1	…	2	1	2	1	1	2	0	1	1	0	1	1
0	2	1	2	1	0	0	0	2	0	0	1	0		1	0	1	2	1	0	1	0	0	1	2	2
0	1	2	1	1	0	1	1	1	1	1	1	0		0	0	2	2	0	0	2	0	0	2	2	2
2	2	0	2	2	0	1	1	1	1	1	1	0		1	1	2	1	1	1	1	1	1	1	2	1
0	2	1	2	1	0	0	0	2	0	0	2	1		1	0	1	2	1	1	1	0	0	2	2	1
0	1	1	2	2	1	2	2	0	2	2	0	2	…	1	0	2	2	0	0	1	0	0	1	2	2
0	2	0	2	2	0	0	0	2	0	0	2	2		1	0	1	2	1	2	0	0	0	1	2	1
0	2	0	2	2	0	0	0	2	0	0	2	2		1	0	1	2	0	1	1	0	0	1	2	2
⋮				⋮					⋮				⋱			⋮				⋮					
0	2	1	2	1	0	0	0	2	0	0	1	0		1	1	2	2	2	2	0	1	1	1	2	1
0	2	0	2	2	0	0	0	2	0	0	1	1		0	0	2	2	0	0	2	0	0	2	2	2
0	2	0	2	2	0	0	0	2	0	0	0	0	…	1	1	2	2	2	2	0	1	1	1	2	1
0	2	0	2	2	0	0	0	2	0	0	1	1		1	1	2	2	1	1	1	0	0	2	2	2
0	2	0	2	2	0	0	0	2	0	0	1	1		0	0	2	2	0	0	2	0	0	2	2	2
0	2	0	2	2	0	0	0	2	0	0	0	0		2	2	2	0	2	2	0	2	2	0	2	0
0	2	0	2	2	0	0	0	2	0	0	2	2		0	0	2	2	0	0	2	0	0	2	2	2
0	2	0	2	2	0	0	0	2	0	0	1	1	…	1	1	1	2	1	1	1	0	0	1	2	2
0	2	0	2	2	0	0	0	2	0	0	0	0		2	2	1	1	1	1	1	1	1	1	2	1
0	2	0	2	2	0	0	0	2	0	0	0	0		1	1	2	2	2	2	0	1	1	1	2	1
0	2	0	2	2	0	0	0	2	0	0	0	0		2	1	2	1	2	2	1	2	2	0	2	1
0	2	0	2	2	0	0	0	2	0	0	1	1		1	0	1	2	1	1	1	1	1	1	2	1

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

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

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]: 0.6314929915948931

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

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

Out[100]:
```
0.7947742281675249
```

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

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

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

Out[102]:
```
50-element Array{Float64,1}:
  0.0915788
 -0.553589
  0.207391
  0.0924915
  0.155066
  0.480991
 -0.0393481
  0.107069
 -0.281392
  0.189348
  0.224629
 -0.0405346
  0.05887
  ⋮
 -0.0410931
  0.00216645
  0.530803
  0.0535231
  0.143752
  0.0966926
 -0.22537
  0.151077
 -0.351851
  0.235835
 -0.0844959
  0.0886406
```

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

Out[103]:
```
48000-element Array{Float64,1}:
  0.249436
  0.440239
 -0.501499
  0.852404
 -0.280216
 -0.226631
  0.440782
  0.146922
  1.78584
  1.25073
  2.46665
  1.38379
 -0.326311
  ⋮
  1.56209
  2.34894
  3.66854
  1.7227
  2.25899
  2.64222
  0.816917
  0.850019
  2.00154
  2.42427
  2.01461
  2.12901
```

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

Out[104]:
```
0.8847065485394396
```

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

Out[105]:
```
1.0686274617992173
```

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

Out[106]:
```
1.2797618022614676
```

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

Out[107]:
```
1.4313298954287743
```

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

Out[108]:
```
1.590004235795422
```

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

Out[109]:
```
1.6784011360545674
```

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

Out[110]:
```
9000-element Array{Float64,1}:
 1.07985
 1.62111
 0.465143
 2.34264
 2.22404
 2.04965
 0.573047
 2.14709
 1.39161
 0.53625
 1.68004
 1.17079
 1.38114
 ⋮
 1.56209
 2.34894
 3.66854
 1.7227
 2.25899
 2.64222
 0.816917
 0.850019
 2.00154
 2.42427
 2.01461
 2.12901
```

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

Out[111]: 1.6659982792661965

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

Out[112]: 0.7812917307267568

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

Out[113]: 1.2535170037461942

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

Out[114]: 0.3688104552067546

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

Out[115]: 1.461473551832738

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

Out[116]: 0.5767670032932983

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

Out[117]: 1.6277581291187564

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

Out[118]: 0.7430515805793168

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

Out[119]: 1.7186187156177053

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

Out[120]: 0.8339121670782657

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

Out[121]: 1.7725097244807448

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

Out[122]: 0.8878031759413052

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

Out[123]: 1.6784011360545674

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

Out[124]: 0.7936945875151278