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 = 0.1
# Phenotypes : all animals in G0 to G4
# Genotypes  : all progeny in G5 and all sires in each generation
# Change muAlpha = 0.2
# 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
mu = 100                                  #  alpha ~ N(100,1)
Va = nQTL*numChr*0.5*mu*mu                # Va= nQTL*2pq*mean(alpha)^2
qtlEffects= rand(Normal(mu/sqrt(Va), sqrt(1/Va)),numLoci*numChr)  # Let alpha mu = 0.115
XSim.init(numChr,numLoci,chrLength,geneFreq,mapPos,qtlMarker,qtlEffects,mutRate)
```

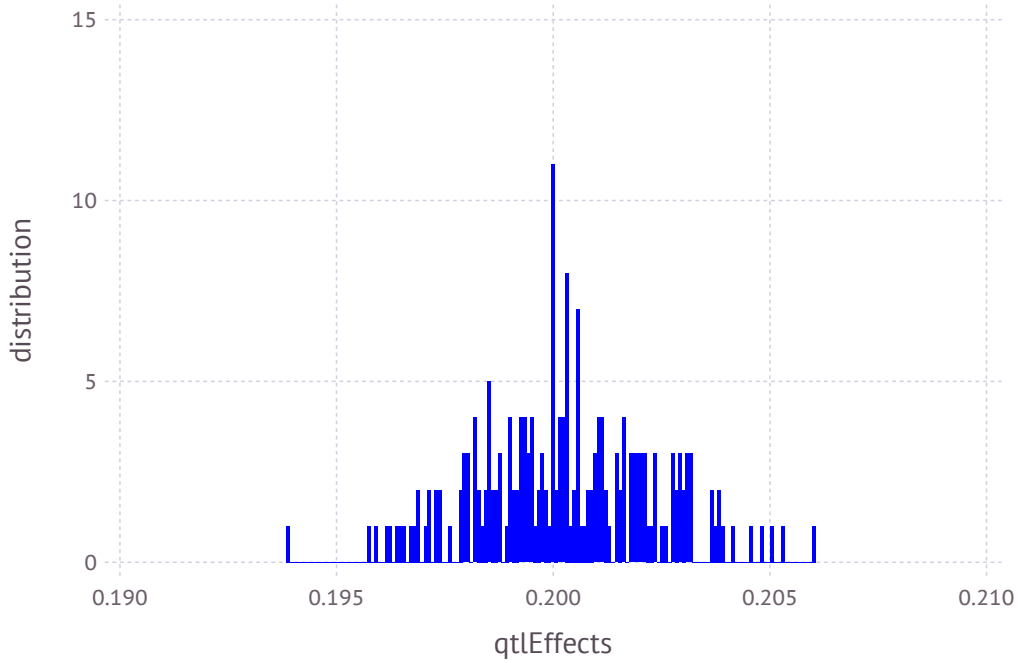
In [7]:
```
qtlEffects
```

Out[7]:
```
200-element Array{Float64,1}:
 0.195875
 0.20115
 0.199734
 0.199983
 0.2016
 0.199424
 0.199971
 0.198796
 0.198538
 0.196918
 0.201937
 0.196379
 0.198156
 ⋮
 0.198554
 0.201969
 0.203857
 0.200027
 0.200344
 0.20181
 0.199857
 0.20034
 0.200842
 0.193828
 0.201513
 0.19916
```

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]:
```
0.20027059005216008
```

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

Out[11]:
```
4.2427171412733505e-6
```

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
```

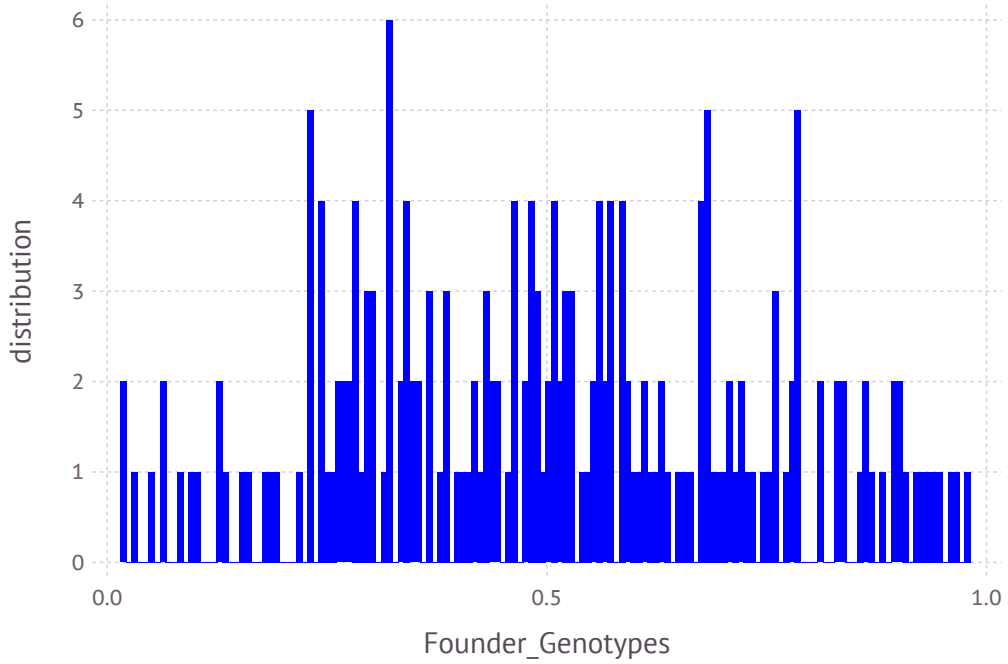
In [19]:
```
gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

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

Out[20]:
```
1x200 Array{Float64,2}:
 0.06625  0.829  0.28425  0.947  0.836625  …  0.384375  0.897125  0.5625
```

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);
```

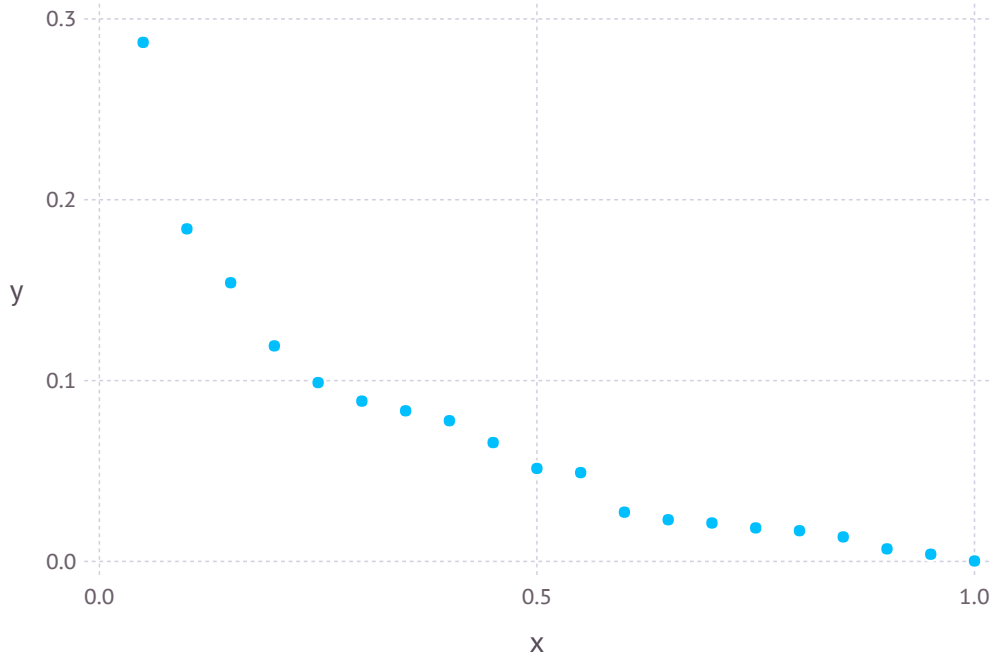
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.000268425  0.00397438  0.00695299  …  0.154149  0.183902  0.287029
```

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]:
```
9.244846051558397
```

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

Out[31]:
```
0.8658597703753241
```

In [32]:
```
XSim.common.varRes = 9*varGen    #heritability = 0.1
```

Out[32]:
```
7.792737933377917
```

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

Out[33]:
```
7.792737933377917
```

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]: 11.051727852517196

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

Out[36]: 11.054502225946253

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

Out[37]: 0.6866141836151588

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

Out[38]: 0.6869142805644659

Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  33145  39585
 40723  34015  39923
 40724  34667  38665
 40725  34416  39797
 40726  33055  38489
 40727  33851  38251
 40728  32995  37726
 40729  33366  40179
 40730  32881  39947
 40731  33328  38553
 40732  36684  38986
 40733  35623  38967
 40734  36414  39274
     ⋮
 88710  74139  80011
 88711  76231  78200
 88712  74613  79836
 88713  76027  77152
 88714  74612  79695
 88715  73379  80334
 88716  76572  78236
 88717  75660  78188
 88718  76229  77658
 88719  74527  79585
 88720  76056  77801
 88721  76511  80187
```

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

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

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}:
 43070
 42686
 41094
 43552
 41954
 43042
 41565
 41168
 42109
 41623
 41418
 44713
 41388
    ⋮
 74139
 76231
 74613
 76027
 74612
 73379
 76572
 75660
 76229
 74527
 76056
 76511
```

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

Out[53]:
```
1000-element Array{Int64,1}:
 43070
 42686
 41094
 43552
 41954
 43042
 41565
 41168
 42109
 41623
 41418
 44713
 41388
     ⋮
 74869
 74360
 75522
 74898
 76567
 75972
 74989
 73703
 76027
 74894
 74631
 76130
```

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}:
 43070
 42686
 41094
 43552
 41954
 43042
 41565
 41168
 42109
 41623
 41418
 44713
 41388
     ⋮
 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   8.896   9.794
 40723   8.56    9.402
 40724  11.488  10.595
 40725   9.83    9.799
 40726   7.849   8.606
 40727   8.261   9.6
 40728   7.705   8.599
 40729   9.14    9.395
 40730   6.625   7.604
 40731  10.634   9.399
 40732   8.458   8.999
 40733   9.928   9.997
 40734  10.557  10.191
     ⋮
 88710  11.611  11.997
 88711  14.166  11.598
 88712   6.598  11.998
 88713  12.722  10.801
 88714  11.369  10.796
 88715  10.297  10.998
 88716  14.44   11.596
 88717  14.244  12.188
 88718  13.066  11.397
 88719  12.758  10.603
 88720   7.908   9.799
 88721  12.064  12.797
```

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}:
   3
   5
   6
   7
   8
  23
  25
  26
  27
  28
  43
  45
  46
   ⋮
 147
 148
 163
 165
 166
 167
 168
 183
 185
 186
 187
 188
```

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

Out[83]:
```
150-element Array{Int64,1}:
   1
   2
   4
   9
  10
  11
  12
  13
  14
  15
  16
  17
  18
   ⋮
 189
 190
 191
 192
 193
 194
 195
 196
 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	1	1	1	0	0	0	2	0	0	1	1	…	1	1	2	1	0	0	1	0	0	1	2	2
1	2	0	2	2	0	0	0	2	0	0	2	1		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		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	1	1	2	1	2	0	1	1	1	2	1
0	2	1	2	1	0	1	1	2	0	0	2	1		1	0	1	2	0	1	1	0	0	1	2	2
0	2	0	2	2	0	1	1	2	0	0	2	2	…	2	1	2	0	2	2	0	2	2	0	2	0
1	2	0	2	2	1	1	1	1	1	1	0	1		1	1	2	1	1	1	1	1	1	1	2	1
0	1	1	2	2	0	2	2	1	1	1	1	2		2	2	1	2	1	1	1	0	0	2	2	1
0	2	1	2	1	0	0	0	2	0	0	2	0		2	2	2	0	2	2	0	2	2	0	2	0
0	2	1	2	1	0	1	1	2	0	0	2	1		1	1	2	1	1	1	1	1	1	1	2	1
1	2	0	2	2	1	1	1	1	1	1	0	1	…	2	1	1	1	1	2	0	1	1	0	2	1
0	1	1	2	2	1	2	2	0	2	2	0	1		1	0	2	2	0	1	1	0	0	1	1	2
0	2	0	2	2	0	1	1	2	0	0	2	2		2	2	2	0	2	2	0	2	2	0	2	0
⋮					⋮				⋮				⋱			⋮					⋮				
0	1	1	2	2	0	2	2	1	1	1	0	1		2	1	1	1	1	2	0	1	1	0	2	1
1	1	2	2	2	0	2	2	0	2	2	0	1		2	2	2	0	2	2	0	2	2	0	2	0
0	1	1	1	2	0	1	1	1	1	1	0	0	…	2	0	1	1	1	2	0	1	1	0	2	1
0	1	1	2	2	0	2	2	1	1	1	1	1		2	1	1	1	2	2	0	1	1	1	2	0
0	1	1	2	2	0	1	1	1	1	1	1	1		2	1	2	1	1	2	0	1	1	1	1	1
0	1	1	2	2	1	1	1	1	1	1	1	2		1	0	2	2	1	2	0	1	1	0	1	1
0	0	2	1	1	0	1	1	1	1	1	0	0		2	1	2	1	1	1	0	1	1	0	1	1
0	1	1	2	2	1	2	2	0	2	2	0	2	…	2	2	2	0	2	2	0	2	2	0	2	0
0	0	2	2	2	0	2	2	0	2	2	0	0		2	1	2	1	2	2	0	1	1	0	2	1
0	0	2	2	2	0	2	2	0	2	2	0	1		2	0	1	2	1	2	0	0	0	1	1	1
0	2	0	2	2	0	0	0	2	0	0	0	0		2	2	1	1	2	2	0	1	1	0	2	1
0	1	1	1	2	1	2	2	0	2	2	0	1		2	1	1	2	2	2	0	0	0	1	1	2

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

Out[86]:
```
9000x50 Array{Int64,2}:
 1  1  0  0  0  1  2  1  2  2  0  2  1  …  1  1  1  1  0  1  2  1  1  1  1  1
 0  2  0  0  0  1  1  1  1  1  2  0  0     2  0  0  0  1  1  1  2  0  2  2  2
 0  2  0  0  0  1  1  1  1  1  1  1  1     1  1  1  1  0  1  2  1  1  1  1  1
 1  1  0  0  0  1  0  1  1  1  2  0  1     0  1  1  0  2  2  2  1  2  0  1  0
 1  1  0  1  1  2  1  0  1  1  1  1  1     0  1  0  0  1  1  1  0  2  0  1  0
 0  2  0  1  1  2  0  0  1  1  1  0  0  …  2  0  0  1  1  1  2  2  0  2  2  2
 0  2  1  1  1  2  0  0  1  0  1  1  1     0  1  1  1  1  1  2  1  1  1  1  1
 1  2  0  2  2  2  1  1  2  1  2  0  0     0  1  0  0  2  1  2  2  1  2  1  1
 1  1  0  0  0  2  1  0  2  1  0  2  1     0  2  1  1  0  1  2  2  0  2  2  2
 1  1  0  1  1  2  2  0  2  2  2  0  1     1  0  0  1  1  0  2  1  1  1  1  1
 0  2  1  1  1  0  2  0  0  0  1  1  2  …  0  1  1  1  0  1  2  2  1  1  1  1
 1  2  1  2  2  1  1  0  1  0  1  1  2     0  0  0  0  1  0  2  1  2  0  0  0
 0  2  0  1  1  2  1  0  2  2  2  0  1     1  1  1  1  0  1  2  2  0  2  2  2
 ⋮              ⋮              ⋮        ⋱     ⋮              ⋮
 1  2  0  2  2  2  2  0  2  2  2  0  2     1  0  1  0  1  0  2  2  1  1  1  1
 2  2  0  2  2  2  1  0  2  2  0  0  1     1  1  1  2  0  1  2  2  0  2  2  2
 1  2  0  1  1  2  2  1  2  1  2  1  1  …  0  0  0  0  1  1  2  1  1  1  2  1
 1  2  0  2  2  0  2  0  0  0  0  1  2     0  1  0  0  2  0  2  2  1  1  1  1
 1  2  0  1  1  2  2  1  2  1  1  0  1     0  1  1  1  0  1  2  2  1  1  1  1
 1  2  1  1  1  2  1  0  1  1  2  0  0     2  0  1  0  1  1  2  1  2  0  0  0
 2  1  0  1  1  2  2  2  2  0  1  0  2     1  1  2  1  0  2  2  2  1  1  1  1
 1  2  1  2  2  1  1  1  2  2  0  1  1  …  0  1  0  0  1  1  2  2  0  2  2  2
 2  2  0  2  2  2  1  1  1  1  2  1  1     2  0  0  1  1  0  2  2  1  1  2  1
 2  2  0  2  2  1  2  0  1  1  1  0  0     0  0  0  1  1  0  2  2  2  0  1  0
 0  2  0  0  0  1  0  1  2  1  0  2  2     0  0  0  0  0  0  2  2  1  1  2  1
 1  2  1  2  2  2  2  0  2  2  0  1  1     0  1  1  1  0  1  2  2  1  1  2  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]: 0.14382557533889737

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

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

Out[100]:
```
0.3830423757141384
```

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

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

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

Out[102]:
```
50-element Array{Float64,1}:
 0.199734
 0.2016
 0.199424
 0.199971
 0.198796
 0.201458
 0.199531
 0.202397
 0.202257
 0.203069
 0.200324
 0.197315
 0.198552
 ⋮
 0.200725
 0.199465
 0.198996
 0.205035
 0.201482
 0.201846
 0.200851
 0.201826
 0.199975
 0.198903
 0.202321
 0.201185
```

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

Out[103]:
```
48000-element Array{Float64,1}:
  9.80662
  9.40416
 10.6164
  9.82305
  8.61598
  9.62679
  8.61817
  9.40662
  7.61127
  9.4132
  9.01317
 10.003
 10.2193
  ⋮
 12.0285
 11.6376
 12.027
 10.8077
 10.8294
 11.013
 11.6235
 12.2223
 11.4237
 10.6227
  9.8206
 12.8292
```

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

Out[104]:
```
9.261149160620839
```

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

Out[105]:
```
9.915795677162597
```

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

Out[106]:
```
10.180745549216091
```

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

Out[107]:
```
10.5135228858883
```

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

Out[108]:
```
10.81557090818261
```

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

Out[109]:
```
11.077552859306666
```

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

Out[110]:
```
9000-element Array{Float64,1}:
 10.8283
 10.2217
  9.61758
 10.025
  9.61017
 10.2256
 10.0189
 11.4254
 10.224
 11.0254
  9.81661
 10.2054
 10.0253
  ⋮
 12.0285
 11.6376
 12.027
 10.8077
 10.8294
 11.013
 11.6235
 12.2223
 11.4237
 10.6227
  9.8206
 12.8292
```

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

Out[111]: 11.054593130055375

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

Out[112]: 1.793443969434536

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

Out[113]: 10.574314274172618

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

Out[114]: 1.3131651135517792

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

Out[115]: 10.454069062103162

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

Out[116]: 1.1929199014823233

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

Out[117]: 10.82843130382898

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

Out[118]: 1.567282143208141

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

Out[119]: 11.148198427387342

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

Out[120]: 1.8870492667665033

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

Out[121]: 11.349563412733199

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

Out[122]: 2.0884142521123596

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

Out[123]: 11.077552859306666

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

Out[124]: 1.8164036986858267