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 = 0.3
# 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 = 0.2
XSim.init(numChr,numLoci,chrLength,geneFreq,mapPos,qtlMarker,qtlEffects,mutRate)
```

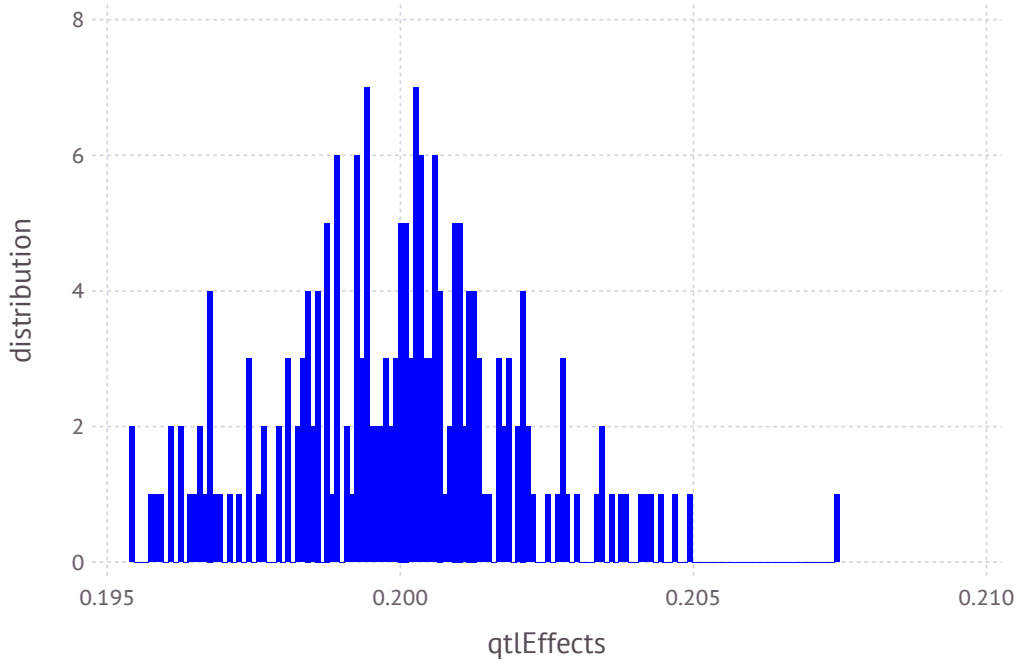
In [7]:
```
qtlEffects
```

Out[7]:
```
200-element Array{Float64,1}:
 0.203404
 0.199183
 0.202752
 0.203635
 0.200606
 0.200423
 0.198771
 0.20205
 0.199724
 0.198554
 0.198312
 0.198937
 0.199538
 ⋮
 0.199704
 0.200521
 0.200588
 0.20099
 0.196223
 0.199096
 0.200088
 0.198912
 0.199336
 0.201074
 0.196077
 0.199279
```

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]:
```
0.19997542938916765
```

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

Out[11]:
```
4.137626520300289e-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
```

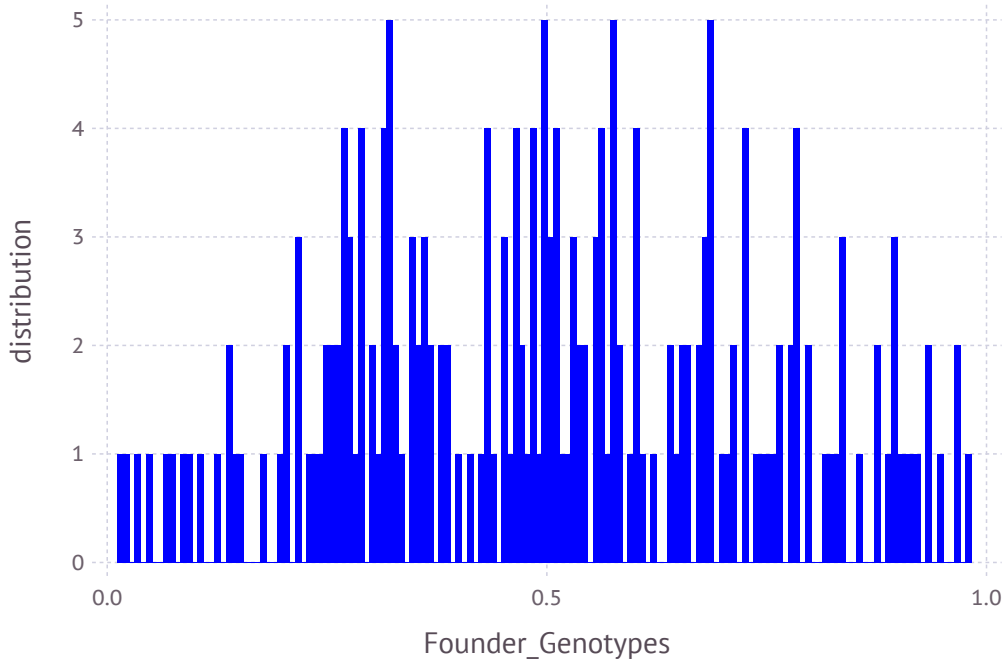
In [19]:
```
gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

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

Out[20]:
```
1x200 Array{Float64,2}:
 0.068375  0.839  0.28925  0.944375  …  0.362625  0.387  0.895375  0.555375
```

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);
```

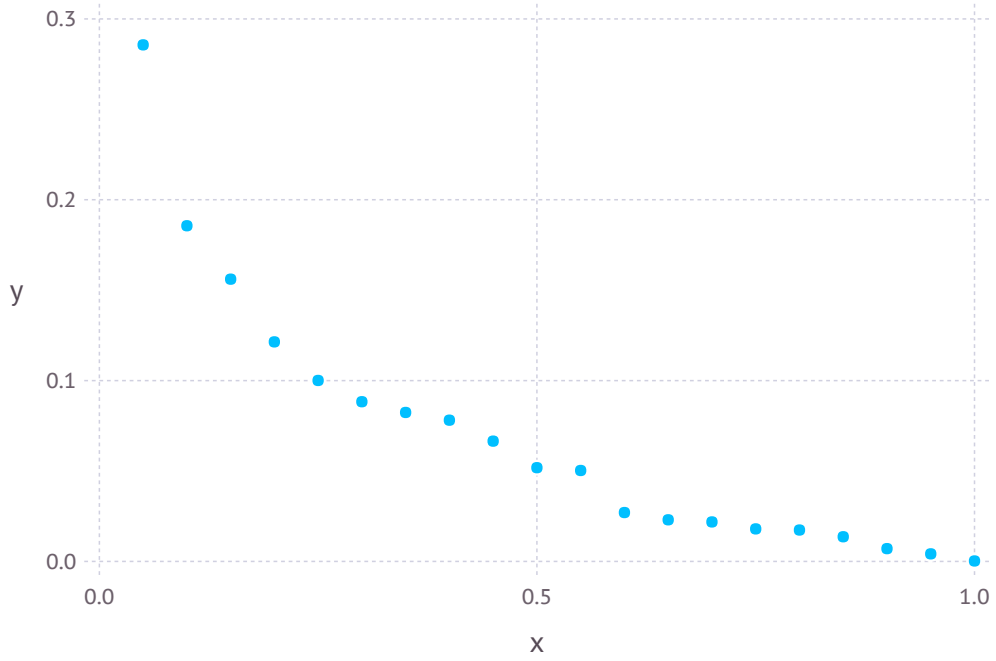
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.000255428  0.00421893  0.0071017  …  0.156088  0.185618  0.285661
```

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]:
```
10.232198059199094
```

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

Out[31]:
```
0.7544106344656164
```

In [32]:
```
XSim.common.varRes = (7*varGen)/3    #heritability = 0.3
```

Out[32]:
```
1.7602914804197718
```

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

Out[33]:
```
1.7602914804197718
```

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]: 12.718734004421915

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

Out[36]: 12.71129498176571

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

Out[37]: 0.7030267737001139

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

Out[38]: 0.694571139909399

Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  34327  37821
 40723  33128  37053
 40724  34005  39676
 40725  35285  39715
 40726  34726  39011
 40727  34107  39643
 40728  33862  39192
 40729  36399  38053
 40730  35560  37933
 40731  35139  37059
 40732  36185  36851
 40733  35478  38239
 40734  34521  37964
     ⋮
 88710  76666  78843
 88711  72765  80690
 88712  73327  79629
 88713  74648  79438
 88714  74559  79016
 88715  75106  78900
 88716  73117  77960
 88717  76264  79675
 88718  75325  76778
 88719  76503  78642
 88720  75396  79190
 88721  75438  80541
```

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	1	1	2	2	1	2	2	0	2	…	1	0	1	2	0	1	1	0	0	1	2	2
40723	0	0	2	1	1	0	2	2	0	2		1	1	2	2	0	1	1	0	0	2	1	2
40724	0	2	1	2	1	0	0	0	2	0		0	0	2	2	0	0	2	0	0	2	2	2
40725	0	1	1	1	1	0	1	1	1	1		2	1	1	2	1	1	1	0	0	1	2	2
40726	0	2	0	2	2	0	0	0	2	0		1	0	1	2	0	1	1	0	0	1	2	2
40727	0	2	0	2	2	0	0	0	2	0	…	2	2	2	0	2	2	0	2	2	0	2	0
40728	0	1	1	2	1	1	1	1	1	1		2	1	0	2	1	2	0	0	0	0	2	2
40729	1	1	1	1	1	0	1	1	1	1		2	2	2	1	2	2	0	1	1	1	2	0
40730	0	1	1	1	1	0	1	1	1	1		1	0	1	2	0	1	1	0	0	1	2	2
40731	0	1	1	1	1	0	1	1	1	1		2	1	0	2	1	2	1	0	0	2	0	2
40732	0	2	0	2	2	0	0	0	2	0	…	2	2	2	1	2	2	0	1	1	1	2	1
40733	0	1	1	2	2	1	2	2	0	2		2	2	2	0	2	2	0	2	2	0	2	0
40734	0	1	1	2	2	0	1	1	1	1		2	2	1	2	2	2	0	0	0	0	1	2
⋮				⋮				⋮	⋱			⋮					⋮					⋮	
88710	0	2	0	2	2	0	0	0	2	0		2	1	1	1	1	2	0	1	1	0	2	1
88711	0	2	0	2	2	0	0	0	2	0		2	1	2	1	1	1	0	1	1	0	2	1
88712	0	2	0	2	2	1	1	1	1	1	…	2	1	0	2	2	2	0	0	0	1	1	2
88713	0	2	0	2	2	0	0	0	2	0		2	0	1	2	0	0	0	0	0	0	2	2
88714	0	2	0	2	2	0	0	0	2	0		2	1	1	1	2	2	0	1	1	1	2	0
88715	0	2	0	2	2	1	1	1	1	1		1	0	1	2	0	1	1	0	0	1	2	2
88716	0	2	0	2	2	0	0	0	2	0		2	2	1	1	2	2	0	1	1	0	2	1
88717	0	2	1	2	1	1	1	1	1	1	…	2	1	1	1	1	2	0	1	1	0	2	1
88718	0	2	0	2	2	0	0	0	2	0		2	0	0	2	0	2	1	0	0	1	1	2
88719	0	2	0	2	2	1	1	1	1	1		2	1	0	2	2	2	0	0	0	1	2	1
88720	0	2	0	2	2	1	1	1	1	1		2	0	1	2	0	2	1	0	0	1	0	2
88721	0	2	0	2	2	0	0	0	2	0		2	1	2	1	1	1	0	1	1	0	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  1  1  2  2  1  2  2  0  2  2  0  2  …  1  0  1  2  0  1  1  0  0  1  2  2
 0  0  2  1  1  0  2  2  0  2  2  0  2     1  1  2  2  0  1  1  0  0  2  1  2
 0  2  1  2  1  0  0  0  2  0  0  2  1     0  0  2  2  0  0  2  0  0  2  2  2
 0  1  1  1  1  0  1  1  1  1  1  1  2     2  1  1  2  1  1  1  0  0  1  2  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  1  1  …  2  2  2  0  2  2  0  2  2  0  2  0
 0  1  1  2  1  1  1  1  1  1  1  0  0     2  1  0  2  1  2  0  0  0  0  2  2
 1  1  1  1  1  0  1  1  1  1  1  1  1     2  2  2  1  2  2  0  1  1  1  2  0
 0  1  1  1  1  0  1  1  1  1  1  0  1     1  0  1  2  0  1  1  0  0  1  2  2
 0  1  1  1  1  0  1  1  1  1  1  1  2     2  1  0  2  1  2  1  0  0  2  0  2
 0  2  0  2  2  0  0  0  2  0  0  0  0  …  2  2  2  1  2  2  0  1  1  1  2  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  1  1  2  2  0  1  1  1  1  1  0  1     2  2  1  2  2  2  0  0  0  0  1  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  2  0  2  2  0  0  0  2  0  0  2  2     2  1  2  1  1  1  0  1  1  0  2  1
 0  2  0  2  2  1  1  1  1  1  0  0  0  …  2  1  0  2  2  2  0  0  0  1  1  2
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  0  1  2  0  0  0  0  0  0  2  2
 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  0  1  2  0  1  1  0  0  1  2  2
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  2  1  1  2  2  0  1  1  0  2  1
 0  2  1  2  1  1  1  1  1  1  1  0  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     2  0  0  2  0  2  1  0  0  1  1  2
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  1  0  2  2  2  0  0  0  1  2  1
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  0  1  2  0  2  1  0  0  1  0  2
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  2  1  1  1  0  1  1  0  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}:
 41100
 42346
 42465
 44540
 42040
 41541
 44250
 44025
 44586
 43113
 40936
 44407
 43053
    ⋮
 76666
 72765
 73327
 74648
 74559
 75106
 73117
 76264
 75325
 76503
 75396
 75438
```

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

Out[53]:
```
1000-element Array{Int64,1}:
 41100
 42346
 42465
 44540
 42040
 41541
 44250
 44025
 44586
 43113
 40936
 44407
 43053
     ⋮
 73191
 73938
 75842
 76217
 75973
 76140
 76341
 74656
 76177
 76550
 73186
 74085
```

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}:
 41100
 42346
 42465
 44540
 42040
 41541
 44250
 44025
 44586
 43113
 40936
 44407
 43053
     ⋮
 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  11.49   11.002
 40723  12.095  11.392
 40724  11.043   9.401
 40725  10.373  10.198
 40726   8.753   9.207
 40727  10.626  10.198
 40728  11.966  11.208
 40729   9.752   9.597
 40730  11.435  10.398
 40731   8.825  10.205
 40732  11.132  10.8
 40733   8.437  10.195
 40734   9.426   9.999
    ⋮
 88710  14.425  13.203
 88711  10.857  12.991
 88712  14.644  13.595
 88713  14.597  15.195
 88714  13.24   13.398
 88715  12.463  12.994
 88716  12.29   12.202
 88717  14.685  13.996
 88718  12.652  13.196
 88719  12.144  12.194
 88720  15.5    12.994
 88721  12.414  12.792
```

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
   5
   7
  17
  20
  22
  25
  27
  37
  40
  42
  45
  47
   ⋮
 157
 160
 162
 165
 167
 177
 180
 182
 185
 187
 197
 200
```

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

Out[83]:
```
150-element Array{Int64,1}:
   1
   3
   4
   6
   8
   9
  10
  11
  12
  13
  14
  15
  16
   ⋮
 186
 188
 189
 190
 191
 192
 193
 194
 195
 196
 198
 199
```

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}:

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

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

Out[86]:
```
9000x50 Array{Int64,2}:
 2  2  1  1  0  2  1  1  2  1  2  0  0  …  2  0  1  0  1  2  2  1  2  1  0  1
 2  2  1  1  1  2  2  0  0  0  0  0  2     2  1  0  1  1  2  2  1  2  0  0  2
 1  2  1  0  2  1  1  0  1  1  2  1  1     2  1  2  1  1  2  1  0  1  1  1  1
 1  1  1  0  2  1  2  1  1  1  1  1  0     2  0  0  0  0  0  2  0  2  0  0  2
 2  2  1  0  1  2  1  1  1  0  1  1  1     2  1  1  2  1  2  1  1  1  1  1  1
 1  2  1  0  1  2  2  2  2  2  1  1  0  …  2  1  1  0  2  2  0  0  2  0  0  2
 1  1  1  0  2  1  1  1  1  1  1  1  1     2  0  0  0  1  2  1  2  2  2  0  2
 2  1  1  1  1  1  2  1  1  1  2  2  0     2  1  0  0  0  1  2  1  1  1  2  1
 2  2  1  1  1  1  1  1  1  1  0  0  1     2  0  2  1  2  2  2  0  1  1  1  1
 2  2  1  2  0  1  1  0  0  1  0  0  1     2  2  0  1  1  0  1  2  2  1  0  2
 2  2  0  1  1  1  1  0  0  2  2  1  0  …  2  0  1  0  0  2  2  0  0  2  2  0
 1  2  2  1  1  0  2  2  0  1  2  0  0     2  1  1  0  1  2  1  1  2  1  0  1
 2  2  1  1  2  1  2  2  1  1  2  0  0     2  0  0  0  1  1  1  1  2  1  0  1
 ⋮              ⋮              ⋮        ⋱     ⋮              ⋮
 2  2  0  2  0  1  1  2  2  1  2  1  0     2  1  2  2  2  2  2  1  1  2  1  1
 2  2  0  0  2  2  2  1  1  1  2  0  1     2  1  1  1  1  2  2  2  1  2  1  1
 2  2  1  2  2  0  0  0  0  2  2  2  0  …  2  2  2  0  2  2  2  2  2  2  0  2
 2  2  0  2  0  2  2  1  1  1  0  0  2     2  2  2  2  2  2  2  2  2  2  0  2
 2  2  0  1  1  1  2  1  0  2  2  0  0     2  1  2  2  1  2  2  1  1  2  1  0
 2  2  1  0  2  1  2  2  2  1  1  2  1     2  2  1  0  1  2  2  0  1  1  0  2
 2  2  0  1  1  2  1  2  2  1  2  1  0     2  0  0  0  0  1  2  1  1  2  1  1
 2  1  1  1  1  2  2  0  2  1  1  0  1  …  2  2  2  1  2  2  2  1  2  1  1  1
 2  2  0  1  1  1  2  1  0  1  1  1  2     2  1  1  1  1  2  0  1  2  1  0  2
 2  2  1  1  1  1  1  0  0  0  0  1  2     2  2  1  0  1  1  2  2  2  2  0  1
 2  2  1  1  1  0  2  2  2  0  0  0  2     2  1  2  1  2  2  2  1  2  1  0  2
 2  2  0  1  1  0  2  2  2  1  0  0  2     2  0  1  1  1  1  2  2  1  2  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]: 0.46117599619317917

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

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

Out[100]:
```
0.6774673222992164
```

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

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

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

Out[102]:
```
50-element Array{Float64,1}:
 0.199183
 0.200606
 0.198771
 0.201877
 0.198945
 0.197457
 0.198731
 0.200671
 0.20053
 0.200582
 0.197405
 0.200912
 0.199289
 ⋮
 0.200386
 0.199805
 0.201876
 0.197072
 0.200979
 0.19943
 0.202188
 0.200176
 0.199501
 0.201146
 0.199336
 0.199279
```

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

Out[103]:
```
48000-element Array{Float64,1}:
 10.994
 11.3877
  9.38226
 10.1875
  9.19603
 10.1981
 11.1865
  9.58896
 10.3979
 10.182
 10.8092
 10.1969
  9.99456
  ⋮
 13.1991
 12.9819
 13.6168
 15.2005
 13.3947
 12.9955
 12.1974
 13.9948
 13.1822
 12.1976
 12.9976
 12.7966
```

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

Out[104]:
```
10.225945841429708
```

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

Out[105]:
```
10.877263911109752
```

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

Out[106]:
```
11.337415180765166
```

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

Out[107]: 11.780683354505937

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

Out[108]: 12.290345626365287

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

Out[109]: 12.710724322744671

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

Out[110]:
```
9000-element Array{Float64,1}:
 11.7923
 11.987
 11.7847
 10.7835
 11.7843
 11.3923
 11.7949
 11.5937
 11.9928
 11.797
 10.7922
 11.7957
 11.3956
  ⋮
 13.1991
 12.9819
 13.6168
 15.2005
 13.3947
 12.9955
 12.1974
 13.9948
 13.1822
 12.1976
 12.9976
 12.7966
```

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

Out[111]: 12.664134985857116

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

Out[112]: 2.438189144427408

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

Out[113]: 11.495489990696244

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

Out[114]: 1.2695441492665367

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

Out[115]: 11.796846528704684

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

Out[116]: 1.5709006872749764

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

Out[117]: 12.233539436682486

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

Out[118]: 2.0075935952527786

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

Out[119]: 12.78792325166053

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

Out[120]: 2.5619774102308224

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

Out[121]: 13.143302246039516

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

Out[122]: 2.9173564046098086

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

Out[123]: 12.710724322744671

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

Out[124]: 2.4847784813149634