```
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 = 0.2
        # 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

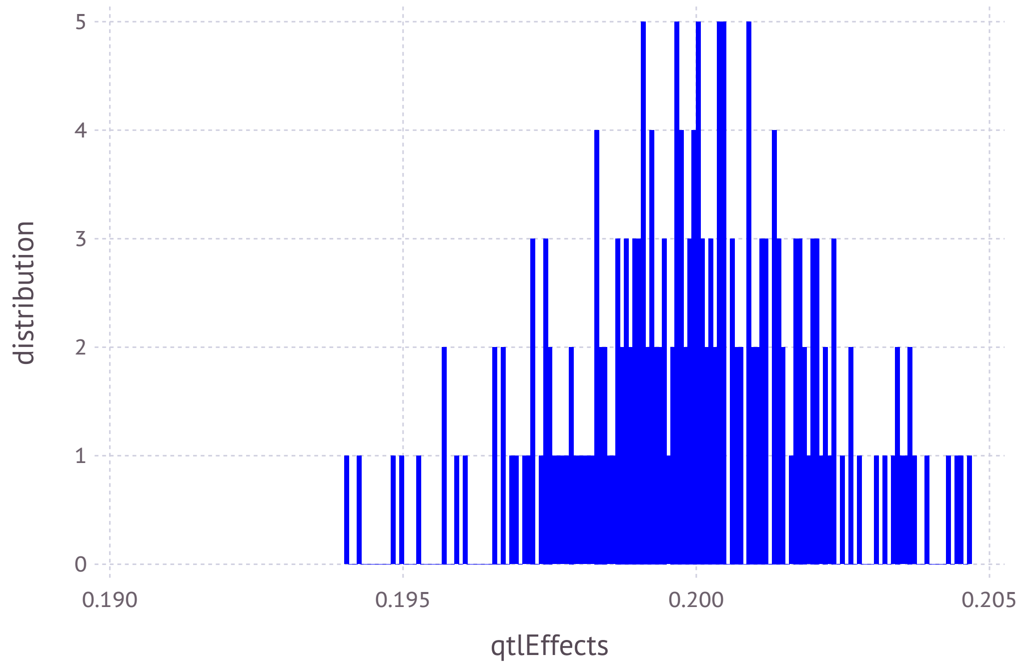
In [6]:
```
numChr    = 10
chrLength = 0.01
numLoci   = 20
nQTL      = 5
mutRate   = 0.0
locusInt  = chrLength/numLoci
mapPos    = collect(locusInt/2:locusInt:chrLength)
geneFreq  = fill(0.5,numLoci)
QTL = sample(1:numLoci,nQTL,replace=false)
qtlMarker = fill(false,numLoci)
qtlMarker[QTL] = true
mu = 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}:
  0.197414
  0.203425
  0.194
  0.202044
  0.196685
  0.198782
  0.200417
  0.200258
  0.199776
  0.20146
  0.196819
  0.201773
  0.199767
  ⋮
  0.200045
  0.199144
  0.202196
  0.200496
  0.198927
  0.199109
  0.199048
  0.200413
  0.199819
  0.20105
  0.201409
  0.203496
```

```
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]: 0.19991809195366528
```

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

```
Out[11]: 4.218543154341932e-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
```

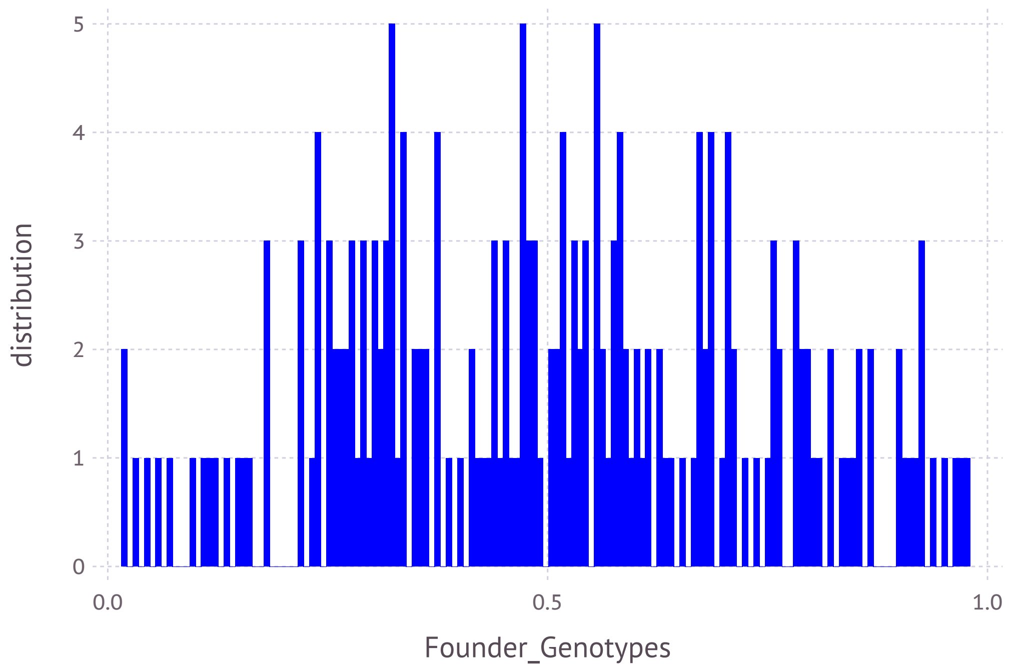
In [19]:
```
gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

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

Out[20]:
```
1x200 Array{Float64,2}:
 0.0575  0.8395  0.286875  0.949625  0.819375  …  0.372625  0.900625  0.54475
```

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);
```

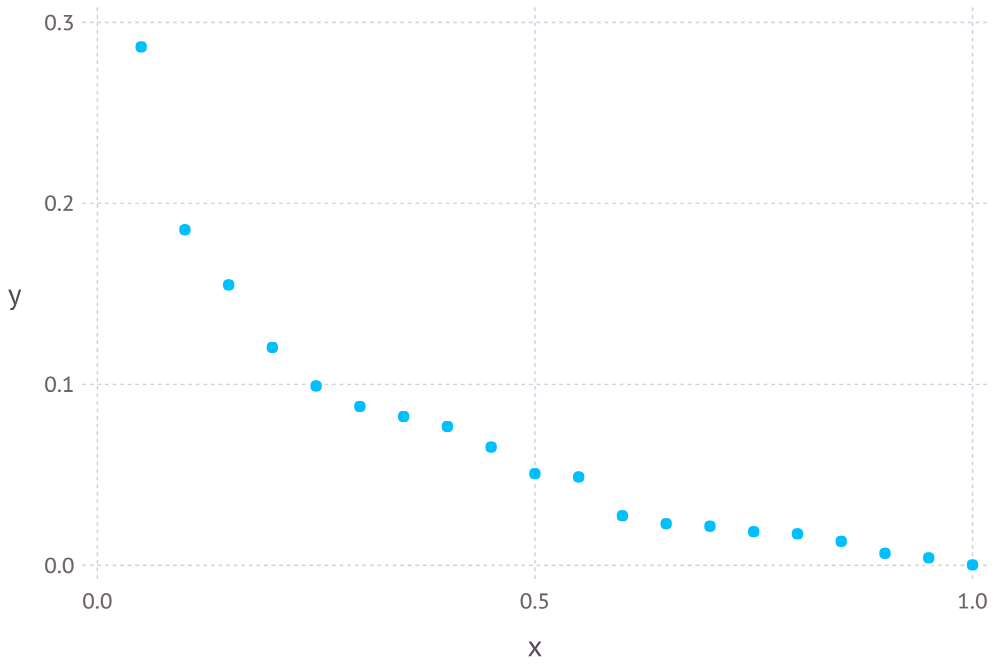
```
In [23]: for i=1:(nRows-20)
         LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
         end
```

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

```
Out[24]: 1x20 Array{Float64,2}:
          0.000282307  0.00415827  0.00667753  …  0.154987  0.185432  0.286476
```

```
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]: 9.017859058225335
```

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

Out[31]: 0.759279913948084
```

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

Out[32]: 0.759279913948084
```

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

Out[33]: 0.759279913948084
```

```
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]: 11.87982359659159
```

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

Out[36]: 11.894315463116778
```

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

Out[37]: 0.5752416102437536
```

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

Out[38]: 0.5692345352602364
```

## Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  36432  39072
 40723  32800  37060
 40724  35252  37650
 40725  34558  37706
 40726  33511  38834
 40727  32951  39852
 40728  34083  36870
 40729  32817  38184
 40730  33634  38956
 40731  33176  38911
 40732  35664  37834
 40733  32797  37666
 40734  34651  38589
     ⋮
 88710  76337  79832
 88711  75333  77245
 88712  76506  77397
 88713  74798  80201
 88714  73282  80392
 88715  75969  80343
 88716  76293  80210
 88717  73344  80599
 88718  74392  79424
 88719  76289  79252
 88720  75505  79640
 88721  74127  80510
```

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  1  1  2  0     1  1  2  1  1  1  1  1  1  1  2  1
          40724  1  2  0  2  2  0  0  0  2  0     1  0  2  2  1  0  2  0  0  2  2  2
          40725  0  0  2  1  1  0  2  2  0  2     2  1  1  1  2  2  0  1  1  1  2  0
          40726  0  2  1  2  1  0  0  0  2  0     2  0  2  1  1  1  0  1  1  0  2  1
          40727  0  2  1  2  1  0  0  0  2  0  …  1  1  2  1  1  1  1  1  1  1  2  2
          40728  0  2  0  2  2  0  1  1  1  1     2  2  2  0  2  2  0  1  1  1  2  1
          40729  0  2  0  2  2  0  0  0  2  0     1  1  2  1  1  1  1  1  1  1  2  1
          40730  0  1  2  2  1  0  1  1  1  1     1  0  2  2  0  0  1  0  0  1  2  2
          40731  0  1  1  2  2  1  1  1  1  1     1  0  2  2  1  1  1  0  0  1  2  2
          40732  0  2  0  2  2  0  0  0  2  0  …  2  1  0  2  0  1  0  0  0  0  2  2
          40733  0  2  0  2  2  0  0  0  2  0     2  0  0  2  2  2  0  0  0  2  2  0
          40734  0  2  1  2  1  0  0  0  2  0     2  1  2  1  0  1  0  0  0  0  2  2
              ⋮                 ⋮                 ⋮  ⋱     ⋮              ⋮              ⋮
          88710  0  1  1  2  2  0  1  1  2  0     1  1  2  1  1  1  1  0  0  2  2  2
          88711  0  2  1  2  1  0  0  0  2  0     2  1  1  1  2  2  0  1  1  1  2  0
          88712  0  1  2  1  0  0  1  1  1  1  …  2  0  1  2  2  1  0  0  0  1  1  2
          88713  0  2  1  2  1  0  0  0  2  0     2  1  1  1  2  2  0  1  1  1  2  0
          88714  0  1  1  2  2  1  2  2  0  2     2  1  1  1  1  2  0  1  1  0  2  1
          88715  0  2  1  2  1  0  0  0  2  0     2  2  2  0  2  2  0  2  2  0  2  0
          88716  0  2  0  2  2  1  1  1  1  1     2  1  1  1  2  2  0  1  1  1  2  0
          88717  0  2  0  2  2  1  1  0  2  0  …  2  2  2  1  2  2  0  1  1  0  2  1
          88718  0  0  2  2  2  2  2  2  0  2     2  0  0  2  2  2  0  0  0  2  1  1
          88719  0  2  0  2  2  1  1  1  1  1     2  1  2  1  1  2  0  1  1  0  1  1
          88720  0  2  1  2  1  0  0  0  2  0     2  2  2  0  2  2  0  2  2  0  2  0
          88721  0  0  2  1  1  1  2  2  0  2     1  0  0  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  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  1  1  2  0  0  1  1     1  1  2  1  1  1  1  1  1  1  2  1
 1  2  0  2  2  0  0  0  2  0  0  1  0     1  0  2  2  1  0  2  0  0  2  2  2
 0  0  2  1  1  0  2  2  0  2  2  0  1     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  0  2  1  1  1  0  1  1  0  2  1
 0  2  1  2  1  0  0  0  2  0  0  2  1  …  1  1  2  1  1  1  1  1  1  1  2  2
 0  2  0  2  2  0  1  1  1  1  1  1  2     2  2  2  0  2  2  0  1  1  1  2  1
 0  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  1  2  2  1  0  1  1  1  1  1  1  0     1  0  2  2  0  0  1  0  0  1  2  2
 0  1  1  2  2  1  1  1  1  1  1  1  2     1  0  2  2  1  1  1  0  0  1  2  2
 0  2  0  2  2  0  0  0  2  0  0  0  0  …  2  1  0  2  0  1  0  0  0  0  2  2
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  0  0  2  2  2  0  0  0  2  2  0
 0  2  1  2  1  0  0  0  2  0  0  2  1     2  1  2  1  0  1  0  0  0  0  2  2
 ⋮              ⋮              ⋮        ⋱        ⋮              ⋮
 0  1  1  2  2  0  1  1  2  0  0  1  1     1  1  2  1  1  1  1  0  0  2  2  2
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  1  1  1  2  2  0  1  1  1  2  0
 0  1  2  1  0  0  1  1  1  1  1  1  1  …  2  0  1  2  2  1  0  0  0  1  1  2
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  1  1  1  2  2  0  1  1  1  2  0
 0  1  1  2  2  1  2  2  0  2  2  0  1     2  1  1  1  1  2  0  1  1  0  2  1
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  1  1  0  2  0  0  1  0  …  2  2  2  1  2  2  0  1  1  0  2  1
 0  0  2  2  2  2  2  2  0  2  2  0  2     2  0  0  2  2  2  0  0  0  2  1  1
 0  2  0  2  2  1  1  1  1  1  1  0  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     2  2  2  0  2  2  0  2  2  0  2  0
 0  0  2  1  1  1  2  2  0  2  2  0  2     1  0  0  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}:
          43120
          41750
          40772
          43873
          43368
          42960
          43470
          41920
          41453
          43351
          43192
          43803
          44233
              ⋮
          76337
          75333
          76506
          74798
          73282
          75969
          76293
          73344
          74392
          76289
          75505
          74127
```

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

```
Out[53]: 1000-element Array{Int64,1}:
          43120
          41750
          40772
          43873
          43368
          42960
          43470
          41920
          41453
          43351
          43192
          43803
          44233
              ⋮
          73431
          75174
          75009
          74861
          74645
          76499
          75414
          74666
          73868
          76274
          74127
          74721
```

```
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}:
          43120
          41750
          40772
          43873
          43368
          42960
          43470
          41920
          41453
          43351
          43192
          43803
          44233
              ⋮
          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   8.879   8.615
 40723   8.761   7.998
 40724   4.84    7.222
 40725   8.2     8.782
 40726   8.477   8.796
 40727   8.424   9.395
 40728   8.653   9.213
 40729   7.941   8.991
 40730   7.608   8.189
 40731   8.908   8.189
 40732   6.922   7.805
 40733   8.774   9.206
 40734  10.505   8.812
     ⋮
 88710  11.607  11.393
 88711  12.44   12.197
 88712  13.32   13.211
 88713  13.244  13.024
 88714  12.151  12.026
 88715  12.308  11.587
 88716  12.583  13.223
 88717  13.565  13.017
 88718  12.351  12.4
 88719  13.239  13.024
 88720  12.741  13.211
 88721  11.306  12.991
```

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
            7
           13
           14
           15
           22
           27
           33
           34
           35
           42
           47
           53
            ⋮
          154
          155
          162
          167
          173
          174
          175
          182
          187
          193
          194
          195
```

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

```
Out[83]: 150-element Array{Int64,1}:
            1
            3
            4
            5
            6
            8
            9
           10
           11
           12
           16
           17
           18
            ⋮
          185
          186
          188
          189
          190
          191
          192
          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  2  2  1  1  1  1  1  1  1  1  1  …  2  2  2  1  2  2  0  1  1  1  2  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  0  2  1  0  1  1  0  0  1  1  2
 1  1  1  1  1  1  2  2  0  2  2  0  2     1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  1  1  1  1  1  1  0  1     1  1  2  2  1  1  1  0  0  1  1  2
 0  1  1  1  1  1  2  2  0  2  2  0  2     2  1  2  1  2  2  0  1  1  0  2  1
 0  2  1  2  1  0  0  0  2  0  0  1  0  …  2  0  0  2  1  2  0  0  0  1  2  1
 0  1  1  1  1  0  1  1  1  1  1  1  2     2  1  2  1  2  1  1  1  1  1  2  1
 0  2  0  2  2  0  1  1  1  1  1  0  0     0  0  2  2  1  1  2  0  0  1  1  1
 0  1  1  1  1  0  1  1  1  1  1  0  1     2  2  1  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  1  1  1  1  1  1  2     2  2  2  0  2  2  0  2  2  0  2  0
 0  1  2  2  1  1  1  1  1  1  1  1  1  …  2  2  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  1  1  1  1  1  1  0  1     2  2  1  1  1  2  0  1  1  0  2  1
 0  2  1  2  1  1  1  1  1  1  1  1  2     2  0  1  2  1  2  1  0  0  1  1  2
 ⋮              ⋮              ⋮        ⋱           ⋮              ⋮
 0  1  1  2  2  0  1  1  2  0  0  1  1     1  1  2  1  1  1  1  0  0  2  2  2
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  1  1  1  2  2  0  1  1  1  2  0
 0  1  2  1  0  0  1  1  1  1  1  1  1  …  2  0  1  2  2  1  0  0  0  1  1  2
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  1  1  1  2  2  0  1  1  1  2  0
 0  1  1  2  2  1  2  2  0  2  2  0  1     2  1  1  1  1  2  0  1  1  0  2  1
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  1  1  0  2  0  0  1  0  …  2  2  2  1  2  2  0  1  1  0  2  1
 0  0  2  2  2  2  2  2  0  2  2  0  2     2  0  0  2  2  2  0  0  0  2  1  1
 0  2  0  2  2  1  1  1  1  1  1  0  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     2  2  2  0  2  2  0  2  2  0  2  0
 0  0  2  1  1  1  2  2  0  2  2  0  2     1  0  0  2  2  2  0  0  0  1  1  2
```

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

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

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]:
```
0.6665351908242599
```

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

          WARNING: imported binding for cor overwritten in module Main

Out[100]: 0.8202612231656456
```

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

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

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

```
Out[102]: 50-element Array{Float64,1}:
           0.203425
           0.200417
           0.199767
           0.200007
           0.196678
           0.199639
           0.19815
           0.200396
           0.199319
           0.199465
           0.198467
           0.202607
           0.198323
           ⋮
           0.202007
           0.197973
           0.197109
           0.198981
           0.20031
           0.199954
           0.200612
           0.200031
           0.198282
           0.198927
           0.199109
           0.199048
```

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

```
Out[103]: 48000-element Array{Float64,1}:
            8.59032
            7.99375
            7.20132
            8.78943
            8.78608
            9.38873
            9.19509
            8.99747
            8.19816
            8.19291
            7.78251
            9.18473
            8.784
            ⋮
           11.3775
           12.1769
           13.1939
           12.9854
           11.9915
           11.5767
           13.1875
           12.9849
           12.3703
           12.9841
           13.1692
           12.9696
```

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

```
Out[104]: 9.007490766762167
```

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

```
Out[105]: 9.595749216814065
```

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

```
Out[106]: 10.16772169889899
```

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

Out[107]: 10.75444407207549

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

Out[108]: 11.338625613457358

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

Out[109]: 11.863299733957534

In [110]: EAlphaG=onlyQTL*QTLo

Out[110]: 9000-element Array{Float64,1}:
            9.57853
            9.392
           10.2001
            9.797
           10.7981
           10.5835
           11.3868
            9.18476
           10.778
            9.19177
            9.18499
           10.3828
            9.99471
            ⋮
           11.3775
           12.1769
           13.1939
           12.9854
           11.9915
           11.5767
           13.1875
           12.9849
           12.3703
           12.9841
           13.1692
           12.9696
```

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

Out[111]: 11.801298231616467

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

Out[112]: 2.7938074648543

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

Out[113]: 10.177388480189773

In [114]: meanBreedingValueSelectedG0=meanEAlphaS0-meanEAlphaG0

Out[114]: 1.1698977134276056

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

Out[115]: 10.719088773175919

In [116]: meanBreedingValueSelectedG1=meanEAlphaS1-meanEAlphaG0

Out[116]: 1.7115980064137517

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

Out[117]: 11.33691305303456

In [118]: meanBreedingValueSelectedG2=meanEAlphaS2-meanEAlphaG0

Out[118]: 2.3294222862723934

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

Out[119]: 11.913763868846445

In [120]: meanBreedingValueSelectedG3=meanEAlphaS3-meanEAlphaG0

Out[120]: 2.9062731020842776
```

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

Out[121]: 12.379276889193013

In [122]: meanBreedingValueSelectedG4=meanEAlphaS4-meanEAlphaG0

Out[122]: 3.371786122430846

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

Out[123]: 11.863299733957534

In [124]: meanBreedingValueSelectedG5=meanEAlphaS5-meanEAlphaG0

Out[124]: 2.855808967195367
```