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; 200 loci per chromosome = > 2000 Loci (500 QTL & 1500 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

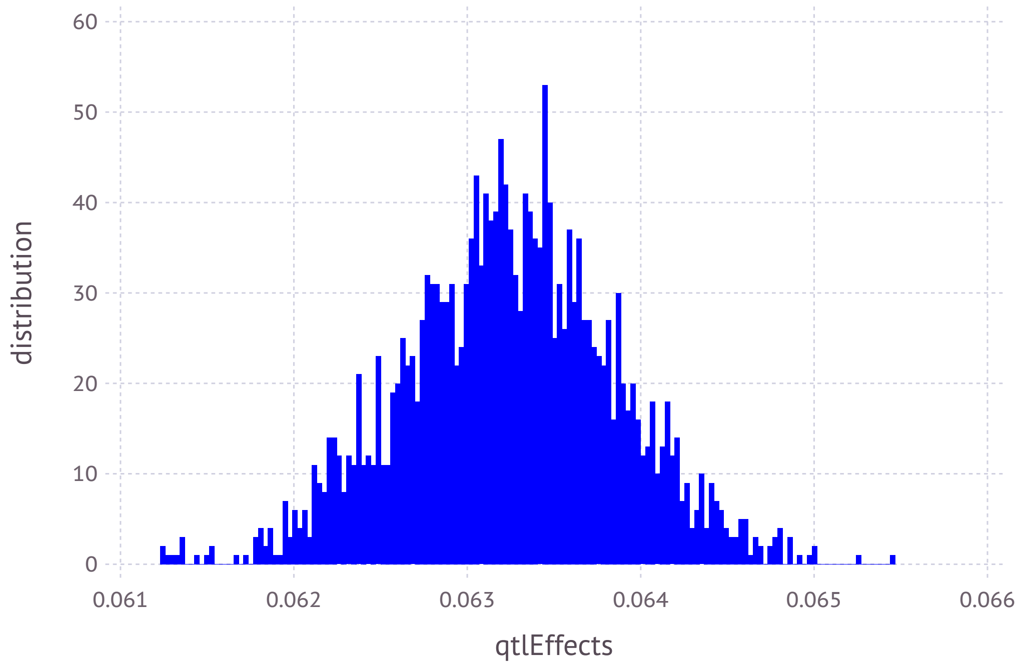
In [6]:
```
numChr    = 10
chrLength = 0.1
numLoci   = 200
nQTL      = 50
mutRate   = 0.0
locusInt  = chrLength/numLoci
mapPos    = collect(locusInt/2:locusInt:chrLength)
geneFreq  = fill(0.5,numLoci)
QTL = sample(1:numLoci,nQTL,replace=false)
qtlMarker = fill(false,numLoci)
qtlMarker[QTL] = true
mu = 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]: 2000-element Array{Float64,1}:
         0.0627749
         0.0628638
         0.0629075
         0.062677
         0.0639835
         0.063526
         0.0625823
         0.0640704
         0.0641861
         0.0639939
         0.0632457
         0.0627553
         0.0625641
         ⋮
         0.0633618
         0.0636531
         0.062245
         0.0635973
         0.0630348
         0.0640156
         0.0632495
         0.0630393
         0.0634654
         0.0627162
         0.0629547
         0.0630332
```

```
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]: 0.0632456152767019

In [11]: var(qtlEffects)

Out[11]: 3.783067315079925e-7
```

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/ch1to10.2000SNP.group1")
         dams  = XSim.sampleFounders("/home/nicole/Jupyter/HERdata/data/Clean/newdata/ch1to10.2000SNP.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
```

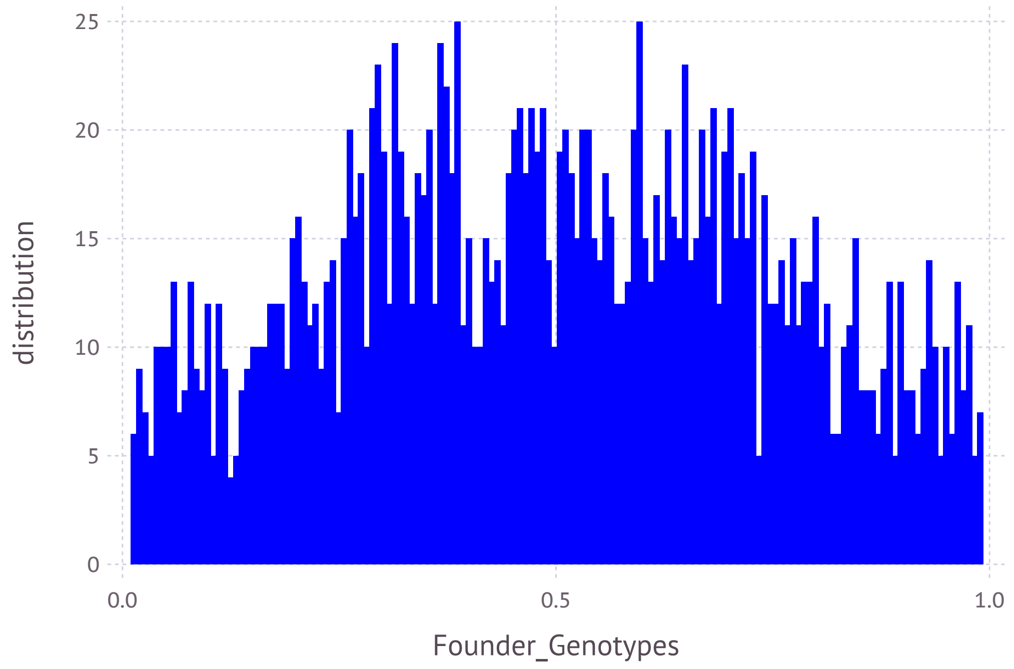
```
In [19]: gSPSire = XSim.getOurGenotypes(popSP[1])
         gSPDam = XSim.getOurGenotypes(popSP[2])
         gSP = [gSPSire;gSPSire];
```

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

```
Out[20]: 1x2000 Array{Float64,2}:
          0.06175  0.841125  0.28475  0.948875  …  0.273  0.34975  0.45625  0.27475
```

```
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);
```

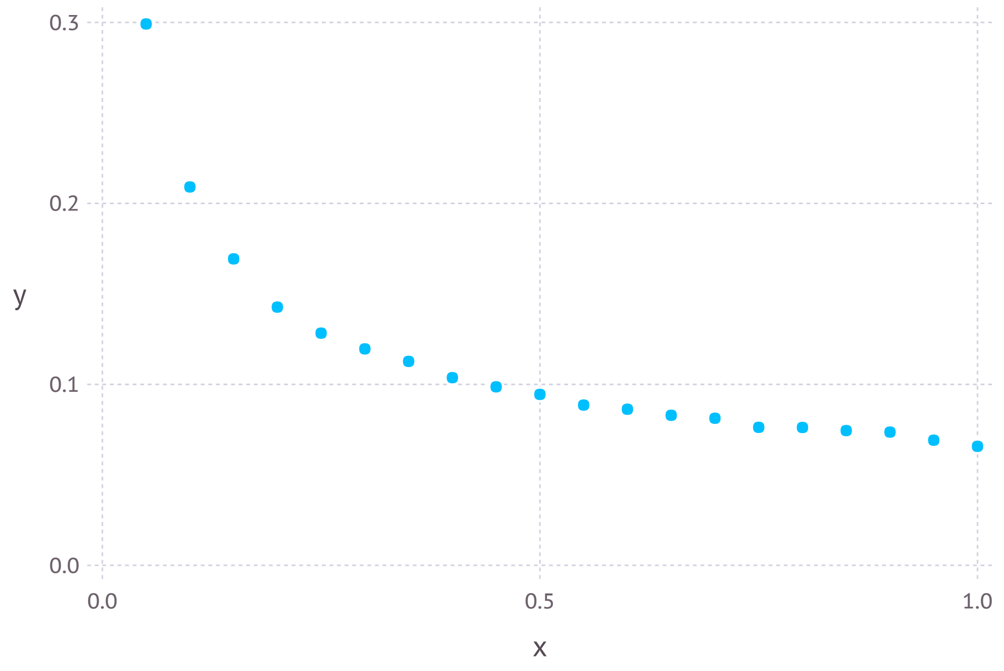
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.0657755  0.0691739  0.0736451  0.0744622  …  0.169373  0.209098  0.299148
```

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]:
```
30.945694572395936
```

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

Out[31]:
```
0.7195159400878134
```

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

Out[32]:
```
0.7195159400878134
```

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

Out[33]:
```
0.7195159400878134
```

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]: 33.47859783455852

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

Out[36]: 33.473292609001874

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

Out[37]: 0.565594683441546

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

Out[38]: 0.5560634653737103
```

## Pedigree: All animals

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

```
Out[39]: 48000x3 Array{Int64,2}:
          40722  35179  37398
          40723  34833  36783
          40724  35996  40565
          40725  34267  37196
          40726  33549  37454
          40727  35769  38022
          40728  33584  39281
          40729  35454  40586
          40730  32762  37750
          40731  34187  38228
          40732  33670  38493
          40733  34188  37684
          40734  34913  39289
              ⋮
          88710  76333  78038
          88711  76005  79728
          88712  73583  80586
          88713  76586  76921
          88714  73103  80088
          88715  76536  78916
          88716  76527  77255
          88717  76085  80647
          88718  76050  78199
          88719  73509  78347
          88720  75695  80711
          88721  74454  80573
```

```
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]:
```
2000
```

In [45]:
```
GT = convert(Array,readtable(genText,separator=' ',header=false))
```
Out[45]:
```
48000x2001 Array{Int64,2}:
 40722  0  1  2  1  0  0  1  1  1  1  …  1  2  1  1  1  1  2  2  1  0  1  1
 40723  0  1  2  2  1  0  0  0  2  0     2  0  2  2  0  0  0  0  0  2  0  0
 40724  0  2  1  2  1  0  0  0  2  0     1  1  1  1  0  1  1  1  1  1  1  1
 40725  0  1  2  1  0  0  1  1  1  1     1  1  1  1  0  1  1  1  1  1  1  1
 40726  0  2  1  2  1  0  0  0  2  0     1  1  1  1  1  2  2  2  1  0  1  1
 40727  0  2  0  2  1  0  0  0  2  0  …  1  2  1  1  0  1  2  2  1  0  1  1
 40728  0  2  0  2  2  0  0  0  2  0     2  1  2  1  0  1  2  2  1  0  1  0
 40729  0  2  1  2  1  0  1  1  1  1     2  2  2  2  0  2  2  2  1  0  1  1
 40730  0  2  0  2  2  0  1  1  2  0     1  2  1  1  1  2  2  2  1  0  1  1
 40731  0  2  0  2  2  0  0  0  2  0     2  1  2  2  1  1  1  1  0  1  1  1
 40732  0  1  1  2  2  1  1  1  1  1  …  2  2  2  2  0  2  2  2  2  0  0  0
 40733  0  2  0  2  2  0  0  0  2  0     0  2  1  0  0  2  2  2  2  0  1  1
 40734  0  2  0  2  2  0  0  0  2  0     1  2  1  1  0  1  2  2  1  0  1  1
     ⋮              ⋮              ⋮  ⋱     ⋮              ⋮              ⋮
 88710  0  2  0  2  2  0  0  0  2  0     2  1  2  2  0  0  2  2  1  0  1  0
 88711  0  2  0  2  2  0  0  0  2  0     2  0  2  2  0  0  0  0  0  2  0  0
 88712  0  2  0  2  2  0  1  1  2  0  …  2  1  2  2  0  0  1  1  1  1  0  0
 88713  0  0  2  2  2  0  2  1  1  1     0  2  0  0  0  1  2  2  1  0  2  2
 88714  0  2  1  2  1  0  0  0  2  0     0  2  0  0  1  1  2  2  0  0  2  1
 88715  0  1  1  2  2  0  1  1  1  1     0  2  0  0  1  1  1  1  0  1  1  1
 88716  0  2  0  2  2  0  0  0  2  0     1  2  1  1  0  1  2  2  1  0  1  1
 88717  0  1  1  1  1  0  1  1  1  1  …  1  2  1  1  0  2  2  2  2  0  1  1
 88718  1  2  0  2  2  0  1  1  1  1     1  1  1  1  0  0  0  0  0  2  0  0
 88719  0  2  0  2  2  0  0  0  2  0     1  1  1  0  0  0  2  2  0  0  2  0
 88720  0  1  1  2  2  0  1  1  1  1     0  2  0  0  1  2  2  2  1  0  2  2
 88721  0  2  0  2  2  0  0  0  2  0     1  1  1  1  0  0  0  0  0  2  0  0
```

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

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

## Create marker file for all animals

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

Out[48]:
```
48000x2000 Array{Int64,2}:
 0  1  2  1  0  0  1  1  1  1  1  1  1  …  1  2  1  1  1  1  2  2  1  0  1  1
 0  1  2  2  1  0  0  0  2  0  0  2  1     2  0  2  2  0  0  0  0  0  2  0  0
 0  2  1  2  1  0  0  0  2  0  0  2  1     1  1  1  1  0  1  1  1  1  1  1  1
 0  1  2  1  0  0  1  1  1  1  1  1  1     1  1  1  1  0  1  1  1  1  1  1  1
 0  2  1  2  1  0  0  0  2  0  0  2  2     1  1  1  1  1  2  2  2  1  0  1  1
 0  2  0  2  1  0  0  0  2  0  0  1  0  …  1  2  1  1  0  1  2  2  1  0  1  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  1  2  1  0  1  2  2  1  0  1  0
 0  2  1  2  1  0  1  1  1  1  1  1  1     2  2  2  2  0  2  2  2  1  0  1  1
 0  2  0  2  2  0  1  1  2  0  0  1  1     1  2  1  1  1  2  2  2  1  0  1  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  1  2  2  1  1  1  1  0  1  1  1
 0  1  1  2  2  1  1  1  1  1  1  1  2  …  2  2  2  2  0  2  2  2  2  0  0  0
 0  2  0  2  2  0  0  0  2  0  0  1  1     0  2  1  0  0  2  2  2  2  0  1  1
 0  2  0  2  2  0  0  0  2  0  0  0  1     1  2  1  1  0  1  2  2  1  0  1  1
 ⋮              ⋮              ⋮           ⋱        ⋮              ⋮
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  1  2  2  0  0  2  2  1  0  1  0
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  0  2  2  0  0  0  0  0  2  0  0
 0  2  0  2  2  0  1  1  2  0  0  2  1  …  2  1  2  2  0  0  1  1  1  1  0  0
 0  0  2  2  2  0  2  1  1  1  1  0  0     0  2  0  0  0  1  2  2  1  0  2  2
 0  2  1  2  1  0  0  0  2  0  0  1  0     0  2  0  0  1  1  2  2  0  0  2  1
 0  1  1  2  2  0  1  1  1  1  1  0  0     0  2  0  0  1  1  1  1  0  1  1  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     1  2  1  1  0  1  2  2  1  0  1  1
 0  1  1  1  1  0  1  1  1  1  1  1  2  …  1  2  1  1  0  2  2  2  2  0  1  1
 1  2  0  2  2  0  1  1  1  1  1  1  1     1  1  1  1  0  0  0  0  0  2  0  0
 0  2  0  2  2  0  0  0  2  0  0  0  0     1  1  1  0  0  0  2  2  0  0  2  0
 0  1  1  2  2  0  1  1  1  1  1  0  0     0  2  0  0  1  2  2  2  1  0  2  2
 0  2  0  2  2  0  0  0  2  0  0  1  1     1  1  1  1  0  0  0  0  0  2  0  0
```

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

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

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

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

## Genotypes - all sires and all offsprings in G5

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

```
Out[52]: 40000-element Array{Int64,1}:
          42691
          41167
          42115
          44577
          41515
          42100
          42821
          44517
          42001
          40984
          42251
          41267
          41372
              ⋮
          76333
          76005
          73583
          76586
          73103
          76536
          76527
          76085
          76050
          73509
          75695
          74454
```

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

Out[53]: 1000-element Array{Int64,1}:
          42691
          41167
          42115
          44577
          41515
          42100
          42821
          44517
          42001
          40984
          42251
          41267
          41372
              ⋮
          76552
          73591
          75549
          76427
          76418
          73265
          73847
          76586
          76050
          75658
          75373
          76459
```

```
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}:
          42691
          41167
          42115
          44577
          41515
          42100
          42821
          44517
          42001
          40984
          42251
          41267
          41372
              ⋮
          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]: (9000,2001)
```

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

Out[62]: 9000
```

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

Out[63]: 2001
```

```
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  31.393  31.491
          40723  29.856  29.906
          40724  32.591  32.616
          40725  34.087  31.167
          40726  32.895  31.304
          40727  31.03   31.492
          40728  29.93   29.984
          40729  30.504  29.485
          40730  29.438  29.402
          40731  30.81   30.289
          40732  30.855  30.211
          40733  29.39   29.897
          40734  28.38   29.782
              ⋮
          88710  32.837  34.211
          88711  33.626  33.888
          88712  34.529  34.079
          88713  33.037  33.314
          88714  33.181  33.643
          88715  34.287  33.777
          88716  35.029  34.772
          88717  35.21   35.151
          88718  35.132  34.323
          88719  32.558  34.138
          88720  36.668  36.485
          88721  34.247  33.697
```

```
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]: 500-element Array{Int64,1}:
            2
            7
           16
           23
           26
           27
           29
           31
           32
           37
           40
           43
           48
            ⋮
         1945
         1950
         1954
         1965
         1968
         1971
         1975
         1976
         1981
         1985
         1995
         2000
```

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

```
Out[83]: 1500-element Array{Int64,1}:
             1
             3
             4
             5
             6
             8
             9
            10
            11
            12
            13
            14
            15
             ⋮
          1987
          1988
          1989
          1990
          1991
          1992
          1993
          1994
          1996
          1997
          1998
          1999
```

## 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]: 9000x2000 Array{Int64,2}:
 0  1  2  1  0  0  1  1  1  1  1  1  1  …  1  1  1  1  0  1  1  1  1  1  1  1
 0  2  0  2  2  1  1  1  1  1  1  1  2     1  2  1  1  0  1  1  1  1  0  1  0
 1  2  1  2  1  1  1  1  1  1  1  1  1     0  2  0  0  0  0  2  2  1  0  1  0
 0  1  1  2  2  1  1  1  1  1  1  0  1     2  1  2  1  0  1  2  2  0  0  2  0
 0  2  0  2  2  0  1  1  2  0  0  1  1     1  1  1  1  0  1  2  2  1  0  1  1
 0  2  1  2  1  0  1  1  1  1  1  1  2  …  2  0  2  1  1  1  2  2  1  0  2  2
 0  2  0  2  2  0  0  0  2  0  0  2  2     2  1  2  2  0  1  2  2  1  0  1  0
 0  1  1  1  1  0  1  1  1  1  1  0  1     2  0  1  0  1  1  2  2  0  0  2  1
 0  2  0  2  2  0  0  0  2  0  0  2  2     1  1  1  0  1  1  2  2  1  0  2  2
 0  1  1  1  1  0  1  1  1  1  1  1  2     1  2  1  1  1  1  2  2  1  0  1  1
 0  1  1  2  1  1  1  1  1  1  1  0  0  …  1  0  2  2  1  2  2  2  1  0  1  1
 0  2  0  2  2  0  0  0  2  0  0  1  1     1  2  1  1  0  1  2  2  1  0  1  0
 0  2  0  2  2  0  0  0  2  0  0  2  2     1  2  1  1  0  2  2  2  1  0  2  1
 ⋮              ⋮              ⋮        ⋱           ⋮              ⋮
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  1  2  2  0  0  2  2  1  0  1  0
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  0  2  2  0  0  0  0  0  2  0  0
 0  2  0  2  2  0  1  1  2  0  0  2  1  …  2  1  2  2  0  0  1  1  1  1  0  0
 0  0  2  2  2  0  2  1  1  1  1  0  0     0  2  0  0  0  1  2  2  1  0  2  2
 0  2  1  2  1  0  0  0  2  0  0  1  0     0  2  0  0  1  1  2  2  0  0  2  1
 0  1  1  2  2  0  1  1  1  1  1  0  0     0  2  0  0  1  1  1  1  0  1  1  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     1  2  1  1  0  1  2  2  1  0  1  1
 0  1  1  1  1  0  1  1  1  1  1  1  2  …  1  2  1  1  0  2  2  2  2  0  1  1
 1  2  0  2  2  0  1  1  1  1  1  1  1     1  1  1  1  0  0  0  0  0  2  0  0
 0  2  0  2  2  0  0  0  2  0  0  0  0     1  1  1  0  0  0  2  2  0  0  2  0
 0  1  1  2  2  0  1  1  1  1  1  0  0     0  2  0  0  1  2  2  2  1  0  2  2
 0  2  0  2  2  0  0  0  2  0  0  1  1     1  1  1  1  0  0  0  0  0  2  0  0
```

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

```
Out[86]: 9000x500 Array{Int64,2}:
          1  1  0  0  1  1  1  2  2  1  0  1  2  …  2  0  2  1  1  1  1  1  1  1  1  1
          2  1  2  0  2  1  1  2  1  1  0  0  0     2  0  1  0  1  1  1  1  2  0  1  0
          2  1  1  0  0  1  1  1  2  1  0  1  1     2  0  1  1  2  1  2  2  2  0  2  0
          1  1  0  1  0  1  1  2  2  2  0  2  2     1  0  1  1  2  1  2  2  0  2  2  0
          2  1  1  0  0  0  2  2  2  1  1  2  1     1  1  1  1  1  1  1  1  2  1  2  1
          2  1  1  2  0  0  2  2  2  0  0  2  1  …  1  0  2  1  2  1  2  2  0  2  2  2
          2  0  2  0  2  2  0  2  0  0  0  0  0     2  0  2  1  1  1  1  2  1  1  2  0
          1  1  0  0  1  1  2  2  2  1  0  2  2     2  0  2  1  1  1  2  1  0  2  2  1
          2  0  2  0  2  2  0  2  0  0  0  0  1     1  0  2  1  1  0  2  1  1  1  2  2
          1  1  1  0  2  2  1  2  1  0  0  1  1     1  2  1  0  2  2  2  1  1  1  2  1
          1  1  1  1  0  1  1  2  2  2  0  2  1  …  1  0  2  2  0  0  2  1  1  2  2  1
          2  0  1  1  0  1  2  2  2  1  0  0  0     0  1  0  1  2  1  2  1  2  0  2  0
          2  0  2  0  2  2  0  2  0  0  0  0  0     2  1  2  1  0  0  1  2  2  1  2  1
          ⋮              ⋮              ⋮        ⋱        ⋮              ⋮
          2  0  0  0  0  0  2  2  2  1  1  2  1     2  0  2  2  0  0  1  1  2  1  2  0
          2  0  1  0  1  1  1  2  1  1  0  1  1     2  0  2  2  0  0  0  2  2  2  0  0
          2  1  1  1  1  1  2  2  2  0  1  2  0  …  1  1  1  1  1  1  1  1  2  1  1  0
          0  2  1  0  1  1  1  2  1  1  0  1  1     0  2  1  1  1  1  2  1  2  1  2  2
          2  0  0  0  0  0  1  2  2  2  0  1  2     1  1  1  0  1  1  1  2  2  0  2  1
          1  1  1  0  2  2  0  2  0  1  0  1  1     2  2  2  0  1  1  1  1  1  0  1  1
          2  0  0  0  0  0  2  2  2  2  0  2  2     2  0  1  0  1  1  2  0  2  0  2  1
          1  1  1  0  2  2  1  2  1  0  0  1  1  …  1  1  1  1  1  1  2  1  2  1  2  1
          2  1  2  1  1  2  1  2  2  1  0  1  0     2  0  2  1  0  0  0  2  2  1  0  0
          2  0  0  0  0  0  2  2  2  2  0  2  2     2  1  2  0  1  1  1  2  1  1  2  0
          1  1  1  0  1  1  1  2  1  2  0  2  2     0  2  1  1  1  1  2  1  2  1  2  2
          2  0  1  0  1  1  0  2  1  1  0  0  1     2  0  2  1  1  1  1  1  1  1  0  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]:
```
0.6417293508556361
```

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

          WARNING: imported binding for cor overwritten in module Main

Out[100]: 0.8012376219406415
```

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

Out[101]: 48000x500 Array{Int64,2}:
           1  1  0  1  2  1  1  1  1  0  0  1  0  …  1  1  1  0  1  1  1  1  1  1  2  1
           1  0  0  1  0  0  1  2  2  1  0  1  1     2  0  2  2  0  0  0  2  2  2  0  0
           2  0  1  1  0  1  1  2  2  1  0  0  1     2  0  2  2  0  0  1  2  2  2  1  1
           1  1  0  0  1  1  1  2  2  1  0  1  2     2  0  2  1  1  1  1  1  1  1  1  1
           2  0  1  1  1  1  2  2  2  1  0  2  1     2  1  2  1  0  0  0  2  2  1  2  1
           2  0  0  0  0  0  1  2  2  2  0  1  2  …  0  1  0  0  2  2  2  0  2  0  2  1
           2  0  0  0  1  1  1  2  1  1  0  1  1     2  0  1  0  2  2  2  1  1  1  2  0
           2  1  0  1  1  2  0  2  1  1  0  1  1     2  0  0  0  2  2  2  0  2  0  2  1
           2  1  1  0  0  0  2  2  2  1  1  2  1     1  2  1  0  1  1  1  1  2  0  2  1
           2  0  0  0  0  0  2  2  2  2  0  2  0     2  1  2  2  1  1  1  2  2  2  1  1
           1  1  1  1  1  2  0  2  1  1  0  1  1  …  1  0  1  1  1  1  2  0  2  0  2  0
           2  0  1  0  1  1  1  2  1  1  0  1  1     1  0  2  0  1  2  2  1  1  0  2  1
           2  0  1  0  1  1  1  2  1  0  1  1  0     1  1  1  0  1  1  2  0  2  0  2  1
           ⋮              ⋮              ⋮           ⋱        ⋮              ⋮
           2  0  0  0  0  0  2  2  2  1  1  2  1     2  0  2  2  0  0  1  1  2  1  2  0
           2  0  1  0  1  1  1  2  1  1  0  1  1     2  0  2  2  0  0  0  2  2  2  0  0
           2  1  1  1  1  1  2  2  2  0  1  2  0  …  1  1  1  1  1  1  1  1  2  1  1  0
           0  2  1  0  1  1  1  2  1  1  0  1  1     0  2  1  1  1  1  2  1  2  1  2  2
           2  0  0  0  0  0  1  2  2  2  0  1  2     1  1  1  0  1  1  1  2  2  0  2  1
           1  1  1  0  2  2  0  2  0  1  0  1  1     2  2  2  0  1  1  1  1  1  0  1  1
           2  0  0  0  0  0  2  2  2  2  0  2  2     2  0  1  0  1  1  2  0  2  0  2  1
           1  1  1  0  2  2  1  2  1  0  0  1  1  …  1  1  1  1  1  1  2  1  2  1  2  1
           2  1  2  1  1  2  1  2  2  1  0  1  0     2  0  2  1  0  0  0  2  2  1  0  0
           2  0  0  0  0  0  2  2  2  2  0  2  2     2  1  2  0  1  1  1  2  1  1  2  0
           1  1  1  0  1  1  1  2  1  2  0  2  2     0  2  1  1  1  1  2  1  2  1  2  2
           2  0  1  0  1  1  0  2  1  1  0  0  1     2  0  2  1  1  1  1  1  1  1  0  0
```

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

```
Out[102]: 500-element Array{Float64,1}:
           0.0628638
           0.0625823
           0.0633681
           0.0633933
           0.0631754
           0.062952
           0.0629863
           0.0624936
           0.0634755
           0.0642903
           0.0627095
           0.0634376
           0.0633124
           ⋮
           0.0627448
           0.0629601
           0.0641185
           0.063054
           0.0638493
           0.0627999
           0.0627494
           0.0631248
           0.0630126
           0.0638162
           0.0632495
           0.0630332
```

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

```
Out[103]: 48000-element Array{Float64,1}:
           31.5041
           29.9341
           32.6555
           31.1705
           31.3224
           31.4957
           29.9792
           29.476
           29.4034
           30.2966
           30.2347
           29.9161
           29.7857
            ⋮
           34.2261
           33.9091
           34.0875
           33.3288
           33.6389
           33.7705
           34.771
           35.1567
           34.3409
           34.1575
           36.4986
           33.709
```

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

```
Out[104]: 30.954580931054185
```

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

```
Out[105]: 31.50284322169989
```

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

```
Out[106]: 32.02664392482561
```

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

Out[107]: 32.52072838319532
```

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

Out[108]: 33.03988662569299
```

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

Out[109]: 33.486623379026575
```

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

Out[110]: 9000-element Array{Float64,1}:
           31.1705
           32.4488
           32.6288
           31.0576
           31.8737
           32.832
           32.7728
           32.1225
           32.1318
           31.8268
           32.5236
           32.4487
           30.7298
             ⋮
           34.2261
           33.9091
           34.0875
           33.3288
           33.6389
           33.7705
           34.771
           35.1567
           34.3409
           34.1575
           36.4986
           33.709
```

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

Out[111]: 33.435499717725506

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

Out[112]: 2.480918786671321

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

Out[113]: 32.07974698683219

In [114]: meanBreedingValueSelectedG0=meanEAlphaS0-meanEAlphaG0

Out[114]: 1.1251660557780063

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

Out[115]: 32.54217986500258

In [116]: meanBreedingValueSelectedG1=meanEAlphaS1-meanEAlphaG0

Out[116]: 1.5875989339483958

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

Out[117]: 33.00340028368407

In [118]: meanBreedingValueSelectedG2=meanEAlphaS2-meanEAlphaG0

Out[118]: 2.048819352629888

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

Out[119]: 33.5618632848723

In [120]: meanBreedingValueSelectedG3=meanEAlphaS3-meanEAlphaG0

Out[120]: 2.6072823538181176
```

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

Out[121]: 33.945361716193666

In [122]: meanBreedingValueSelectedG4=meanEAlphaS4-meanEAlphaG0

Out[122]: 2.9907807851394814

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

Out[123]: 33.486623379026575

In [124]: meanBreedingValueSelectedG5=meanEAlphaS5-meanEAlphaG0

Out[124]: 2.5320424479723904
```