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)
```

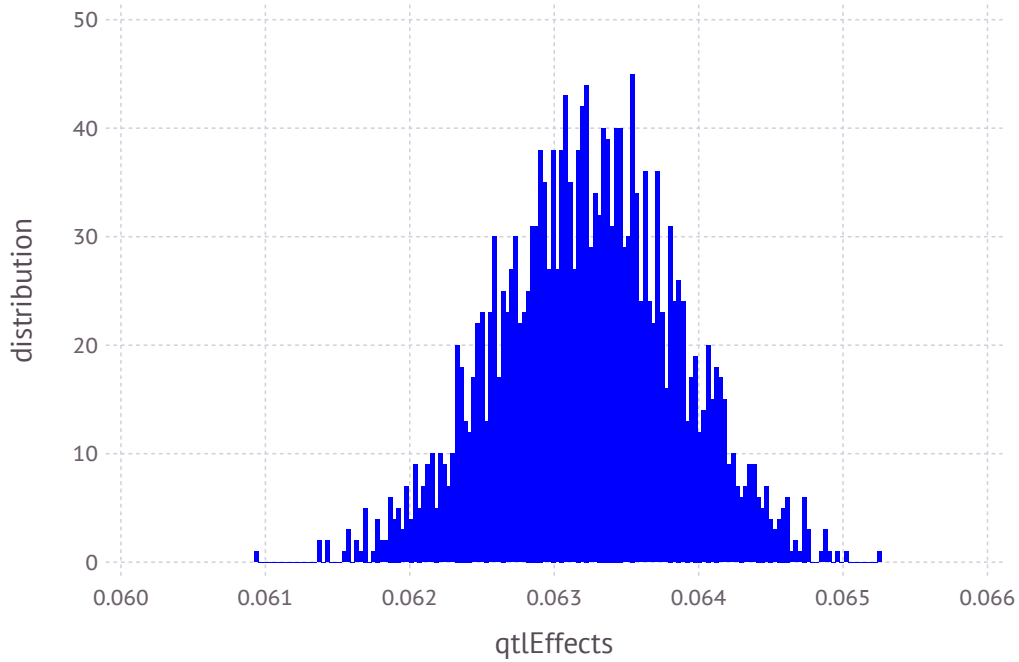
In [7]:
```
qtlEffects
```

Out[7]:
```
2000-element Array{Float64,1}:
 0.0635539
 0.0634522
 0.0626924
 0.0639808
 0.063187
 0.0628581
 0.0627233
 0.062301
 0.0634375
 0.0634917
 0.063584
 0.0625534
 0.0631722
 ⋮
 0.0623511
 0.063252
 0.0634503
 0.0625563
 0.0632967
 0.0626556
 0.062497
 0.0627981
 0.0636327
 0.062345
 0.0631688
 0.0636355
```

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]:
```
0.06323228843385383
```

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

Out[11]:
```
3.913078778677116e-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
```

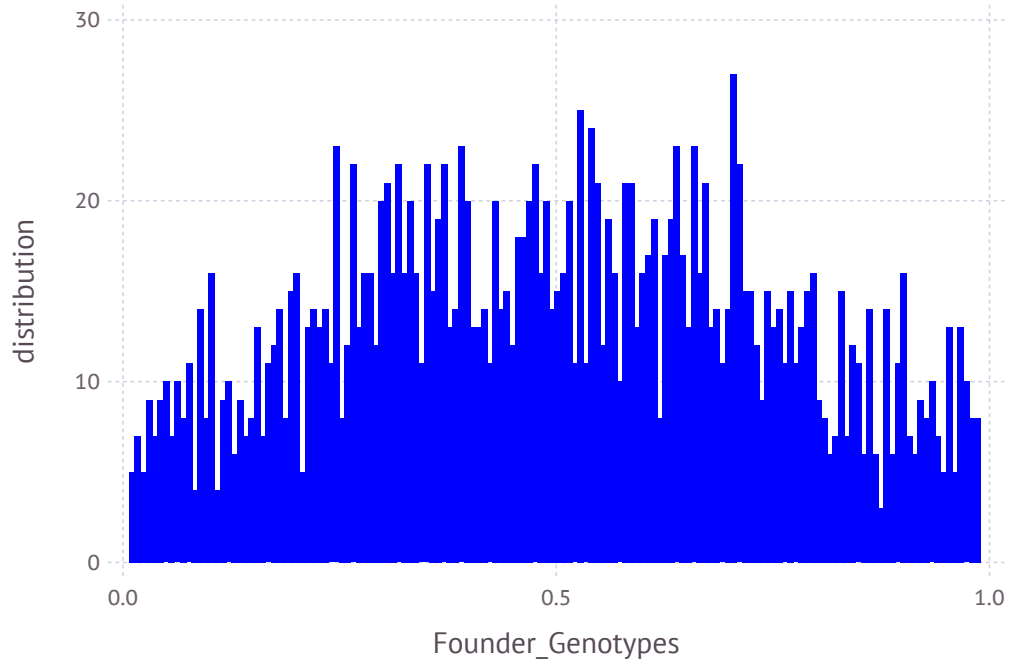
In [19]:
```
gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

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

Out[20]:
```
1x2000 Array{Float64,2}:
 0.063375  0.84  0.274875  0.956875  …  0.275875  0.362  0.443  0.273375
```

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);
```

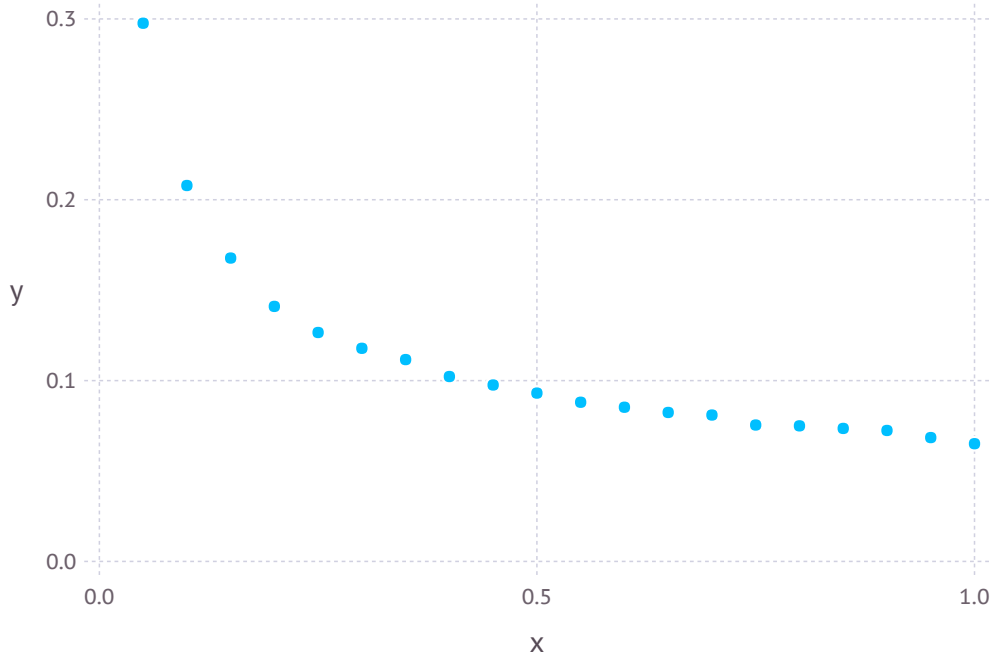
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.0651152  0.0685185  0.072441  0.073578  …  0.167767  0.207868  0.297608
```

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]:
```
31.92818230529562
```

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

Out[31]:
```
0.8060224711788292
```

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

Out[32]:
```
0.8060224711788292
```

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

Out[33]:
```
0.8060224711788292
```

In [34]:
```
popRMP = XSim.sampleSelNoLap(nSires, nDams, nGener,popSP[1],popSP[2],gen=popSP[3],fileName=fileName,direct
```

```
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]: 34.87992759783741

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

Out[36]: 34.88496641262051

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

Out[37]: 0.686357828213692

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

Out[38]: 0.6665716909390556

# Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  34072  36845
 40723  33719  40164
 40724  34837  36826
 40725  35873  40557
 40726  35202  40326
 40727  34556  40689
 40728  34766  40157
 40729  32776  39970
 40730  36629  40268
 40731  34503  39659
 40732  35979  40562
 40733  35053  38532
 40734  35010  38836
     ⋮
 88710  75775  79720
 88711  76228  78176
 88712  74533  80467
 88713  74883  80372
 88714  74023  79208
 88715  74023  77736
 88716  74196  78859
 88717  76651  78688
 88718  75832  80513
 88719  75316  78306
 88720  76640  80507
 88721  74297  80706
```

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 | 1 | 1 | 0 | 0 | 1 | 2 | 2 | 1 | 0 | 2 | 1 |
| 40723 | 0 | 2 | 0 | 2 | 2 | 0 | 1 | 1 | 2 | 0 | | 1 | 2 | 1 | 1 | 1 | 1 | 2 | 2 | 0 | 0 | 2 | 1 |
| 40724 | 0 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 40725 | 0 | 2 | 1 | 2 | 2 | 1 | 1 | 1 | 2 | 0 | | 2 | 1 | 2 | 2 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 |
| 40726 | 0 | 2 | 0 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 |
| 40727 | 0 | 2 | 0 | 2 | 2 | 0 | 1 | 1 | 2 | 0 | … | 2 | 1 | 2 | 2 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 0 |
| 40728 | 0 | 2 | 0 | 2 | 2 | 0 | 1 | 1 | 1 | 1 | | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| 40729 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 1 | 1 | 1 | 1 | 0 | 1 | 2 | 2 | 1 | 0 | 1 | 1 |
| 40730 | 0 | 0 | 2 | 2 | 2 | 1 | 2 | 2 | 0 | 2 | | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 2 | 1 | 0 |
| 40731 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 2 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 |
| 40732 | 1 | 1 | 1 | 2 | 1 | 2 | 2 | 2 | 0 | 2 | … | 1 | 2 | 1 | 1 | 0 | 1 | 2 | 2 | 1 | 0 | 1 | 1 |
| 40733 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 2 | 0 | 2 | 2 | 0 | 0 | 2 | 2 | 0 | 0 | 1 | 0 |
| 40734 | 0 | 1 | 1 | 2 | 1 | 1 | 2 | 1 | 1 | 1 | | 2 | 0 | 2 | 2 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 0 |
| ⋮ | | | | ⋮ | | | | ⋮ | ⋱ | | | ⋮ | | | | | | ⋮ | | | | | ⋮ |
| 88710 | 0 | 1 | 1 | 2 | 2 | 0 | 1 | 0 | 2 | 0 | | 2 | 0 | 2 | 0 | 1 | 1 | 2 | 2 | 1 | 0 | 2 | 1 |
| 88711 | 1 | 2 | 0 | 2 | 2 | 0 | 1 | 1 | 1 | 1 | | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| 88712 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | … | 2 | 0 | 2 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | 2 | 0 |
| 88713 | 1 | 2 | 0 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | | 2 | 0 | 2 | 1 | 0 | 0 | 2 | 2 | 0 | 0 | 2 | 1 |
| 88714 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 1 | 2 | 1 | 1 | 0 | 2 | 2 | 2 | 2 | 0 | 1 | 1 |
| 88715 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 2 | 1 | 2 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| 88716 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 2 | 2 | 0 | 0 | 0 |
| 88717 | 0 | 1 | 1 | 2 | 2 | 1 | 2 | 2 | 0 | 2 | … | 2 | 1 | 2 | 2 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 88718 | 0 | 2 | 1 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 1 | 0 | 2 | 1 | 0 | 1 | 2 | 2 | 1 | 0 | 1 | 0 |
| 88719 | 0 | 0 | 2 | 1 | 2 | 1 | 2 | 2 | 0 | 2 | | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| 88720 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 1 | 2 | 1 | 1 | 0 | 1 | 2 | 2 | 1 | 0 | 1 | 0 |
| 88721 | 0 | 2 | 0 | 2 | 2 | 0 | 0 | 0 | 2 | 0 | | 1 | 2 | 1 | 1 | 0 | 2 | 2 | 2 | 2 | 0 | 1 | 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]:
```
48000x2000 Array{Int64,2}:
 0  1  2  1  0  0  1  1  1  1  1  1  1  …  1  1  1  0  0  1  2  2  1  0  2  1
 0  2  0  2  2  0  1  1  2  0  0  2  2     1  2  1  1  1  1  2  2  0  0  2  1
 0  1  2  2  1  1  1  1  1  1  1  1  1     1  1  1  1  0  1  1  1  1  1  1  1
 0  2  1  2  2  1  1  1  2  0  0  0  0     2  1  2  2  0  1  1  1  0  1  1  0
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  1  1  1  1  1  1  1  0  1  1  1
 0  2  0  2  2  0  1  1  2  0  0  2  2  …  2  1  2  2  0  1  1  1  1  1  0  0
 0  2  0  2  2  0  1  1  1  1  1  1  2     2  0  2  2  0  0  0  0  0  2  0  0
 0  2  0  2  2  0  0  0  2  0  0  1  1     1  1  1  1  0  1  2  2  1  0  1  1
 0  0  2  2  2  1  2  2  0  2  2  0  1     1  1  1  1  0  0  0  0  0  2  1  0
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  2  1  1  1  1  1  0  1  1  1
 1  1  1  2  1  2  2  2  0  2  2  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  1  1     2  0  2  2  0  0  2  2  0  0  1  0
 0  1  1  2  1  1  2  1  1  1  1  2  1     2  0  2  2  0  0  1  1  0  1  0  0
 ⋮              ⋮              ⋮        ⋱     ⋮              ⋮
 0  1  1  2  2  0  1  0  2  0  0  1  1     2  0  2  0  1  1  2  2  1  0  2  1
 1  2  0  2  2  0  1  1  1  1  1  1  1     0  2  0  0  0  0  0  0  0  2  0  0
 0  2  0  2  2  0  0  0  2  0  0  1  1  …  2  0  2  0  0  0  2  2  0  0  2  0
 1  2  0  2  2  1  1  1  1  0  0  2  2     2  0  2  1  0  0  2  2  0  0  2  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     1  2  1  1  0  2  2  2  2  0  1  1
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  2  1  0  0  1  1  0  1  1  0
 0  2  0  2  2  0  0  0  2  0  0  1  0     2  2  2  2  0  2  2  2  2  0  0  0
 0  1  1  2  2  1  2  2  0  2  2  0  2  …  2  1  2  2  0  1  1  1  1  1  1  1
 0  2  1  2  2  0  0  0  2  0  0  1  1     1  0  2  1  0  1  2  2  1  0  1  0
 0  0  2  1  2  1  2  2  0  2  2  0  1     1  1  1  1  0  0  1  1  0  1  1  0
 0  2  0  2  2  0  0  0  2  0  0  0  0     1  2  1  1  0  1  2  2  1  0  1  0
 0  2  0  2  2  0  0  0  2  0  0  2  1     1  2  1  1  0  2  2  2  2  0  1  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}:
 42907
 42095
 41602
 42095
 41752
 44280
 44276
 42387
 41758
 40883
 40751
 41758
 44549
     ⋮
 75775
 76228
 74533
 74883
 74023
 74023
 74196
 76651
 75832
 75316
 76640
 74297
```

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

Out[53]:
```
1000-element Array{Int64,1}:
 42907
 42095
 41602
 41752
 44280
 44276
 42387
 41758
 40883
 40751
 44549
 42603
 40748
     ⋮
 74061
 74791
 74196
 76651
 74991
 75857
 75257
 74303
 75691
 72780
 72809
 73328
```

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}:
 42907
 42095
 41602
 41752
 44280
 44276
 42387
 41758
 40883
 40751
 44549
 42603
 40748
     ⋮
 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  31.326  30.371
 40723  32.558  32.971
 40724  30.828  31.694
 40725  30.998  31.686
 40726  34.145  32.705
 40727  32.668  32.062
 40728  32.133  30.918
 40729  29.981  30.315
 40730  31.676  32.949
 40731  30.991  31.379
 40732  32.255  33.454
 40733  32.407  32.304
 40734  32.395  31.95
     ⋮
 88710  34.544  35.547
 88711  35.849  35.43
 88712  34.22   34.717
 88713  35.643  36.319
 88714  36.418  35.738
 88715  35.402  36.125
 88716  38.162  37.148
 88717  35.251  35.427
 88718  35.323  34.607
 88719  37.046  36.498
 88720  35.227  35.233
 88721  37.215  36.048
```

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}:
    1
    5
    6
    9
   13
   14
   17
   18
   27
   36
   37
   38
   44
    ⋮
 1948
 1954
 1956
 1960
 1962
 1971
 1972
 1973
 1978
 1982
 1985
 1989
```

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

Out[83]:
```
1500-element Array{Int64,1}:
    2
    3
    4
    7
    8
   10
   11
   12
   15
   16
   19
   20
   21
    ⋮
 1988
 1990
 1991
 1992
 1993
 1994
 1995
 1996
 1997
 1998
 1999
 2000
```

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

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

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

In [87]:
```
onlyMar = QTLMarker[:,MarkerPos];
```

In [88]:
```
QTLstream = open(QTL, "w")
Marstream = open(Mar, "w");
```

In [89]:
```
for i in 1:size(onlyID,1)
    @printf(QTLstream, "%19d", onlyID[i])
    for j in 1:size(onlyQTL,2)
        @printf(QTLstream, "%3d", onlyQTL[i,j])
    end
    @printf(QTLstream, "\n")
end
```

In [90]:
```
for i in 1:size(onlyID,1)
    @printf(Marstream, "%19d", onlyID[i])
    for j in 1:size(onlyMar,2)
        @printf(Marstream, "%3d", onlyMar[i,j])
    end
    @printf(Marstream, "\n")
end
```

In [91]:
```
close(QTLstream)
close(Marstream)
```

# Remove Fixed Gene from the panel

In [92]:
```
VQM = var(QTLMarker,1)
QMnoFixed = QTLMarker[:,VQM .> 0]
VQ = var(onlyQTL,1)
QnoFixed = onlyQTL[:,VQ .> 0]
VM = var(onlyMar,1)
MnoFixed = onlyMar[:,VM .> 0];
```

In [93]:
```
GenNFstream = open(GenNF, "w")
QTLNFstream = open(QTLNF, "w")
MarNFstream = open(MarNF, "w");
```

In [94]:
```
for i in 1:size(onlyID,1)
    @printf(GenNFstream, "%19d", onlyID[i])
    for j in 1:size(QMnoFixed,2)
        @printf(GenNFstream, "%3d", QMnoFixed[i,j])
    end
    @printf(GenNFstream, "\n")
end
```

In [95]:
```
for i in 1:size(onlyID,1)
    @printf(QTLNFstream, "%19d", onlyID[i])
    for j in 1:size(QnoFixed,2)
        @printf(QTLNFstream, "%3d", QnoFixed[i,j])
    end
    @printf(QTLNFstream, "\n")
end
```

In [96]:
```
for i in 1:size(onlyID,1)
    @printf(MarNFstream, "%19d", onlyID[i])
    for j in 1:size(MnoFixed,2)
        @printf(MarNFstream, "%3d", MnoFixed[i,j])
    end
    @printf(MarNFstream, "\n")
end
```

In [97]:
```
close(GenNFstream)
close(QTLNFstream)
close(MarNFstream)
```

# Check heritability

In [98]:
```
P = AllPBV[:,2]
BV = AllPBV[:,3];
```

In [99]:
```
VP = var(P)
VBV = var(BV)
H = VBV/VP
```

Out[99]: 0.6647118497498843

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

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

Out[100]:
```
0.8217415323078527
```

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

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

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

Out[102]:
```
500-element Array{Float64,1}:
 0.0635539
 0.063187
 0.0628581
 0.0634375
 0.0631722
 0.063467
 0.0637923
 0.064768
 0.062225
 0.0635151
 0.0633426
 0.0630886
 0.0630776
 ⋮
 0.0643996
 0.0619074
 0.0621111
 0.0629117
 0.06402
 0.0635963
 0.063062
 0.063799
 0.0631486
 0.0627249
 0.062221
 0.0623511
```

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

Out[103]:
```
48000-element Array{Float64,1}:
 30.3177
 32.9015
 31.6328
 31.646
 32.6444
 32.0191
 30.8741
 30.2369
 32.8893
 31.3236
 33.4116
 32.277
 31.8854
  ⋮
 35.4884
 35.3673
 34.6642
 36.2596
 35.6736
 36.0698
 37.0909
 35.3779
 34.552
 36.4312
 35.188
 35.9962
```

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

Out[104]:
```
31.878739546507866
```

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

Out[105]:
```
32.57980221557168
```

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

Out[106]:
```
33.132279544590126
```

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

Out[107]:
```
33.72502680742494
```

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

Out[108]:
```
34.28794749293057
```

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

Out[109]:
```
34.83004284720865
```

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

Out[110]:
```
9000-element Array{Float64,1}:
 33.9325
 32.269
 33.912
 33.9224
 33.6109
 33.9801
 33.1506
 33.4025
 34.2427
 34.157
 31.5106
 33.3474
 33.0922
  ⋮
 35.4884
 35.3673
 34.6642
 36.2596
 35.6736
 36.0698
 37.0909
 35.3779
 34.552
 36.4312
 35.188
 35.9962
```

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

Out[111]: 34.771667493220605

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

Out[112]: 2.8929279467127387

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

Out[113]: 33.265734594835216

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

Out[114]: 1.3869950483273499

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

Out[115]: 33.68824874710843

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

Out[116]: 1.8095092006005657

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

Out[117]: 34.33843278238391

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

Out[118]: 2.4596932358760455

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

Out[119]: 34.8491824656282

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

Out[120]: 2.9704429191203374

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

Out[121]: 35.38172471662568

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

Out[122]: 3.5029851701178174

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

Out[123]: 34.83004284720865

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

Out[124]: 2.9513033007007863