In [1]:
```
# Founders: real haplotype data (ch1to10.200SNP)
# "Sample animals for sire and dam candidates" & "Dams and Sires": dam size = N of dams
# One Dam -> 1 male & 1 female (1 dam -> 2 offsprings)
# selection: increase
# 5 generation selection: increase
# heritability = 0.3
# Phenotypes : all animals in G0 to G4
# Genotypes  : all progeny in G5 and all sires in each generation
# Change muAlpha = 0.2
# 10 chromosomes; 20 loci per chromosome = > 200 Loci (50 QTL & 150 Markers)
```

In [2]:
```
include("/home/nicole/Jupyter/XSimSel.jl")
```

Out[2]:
```
XSim
```

In [3]:
```
using DataFrames
```

In [4]:
```
using Distributions
```

In [5]:
```
using(Gadfly)
```

Initialize XSim

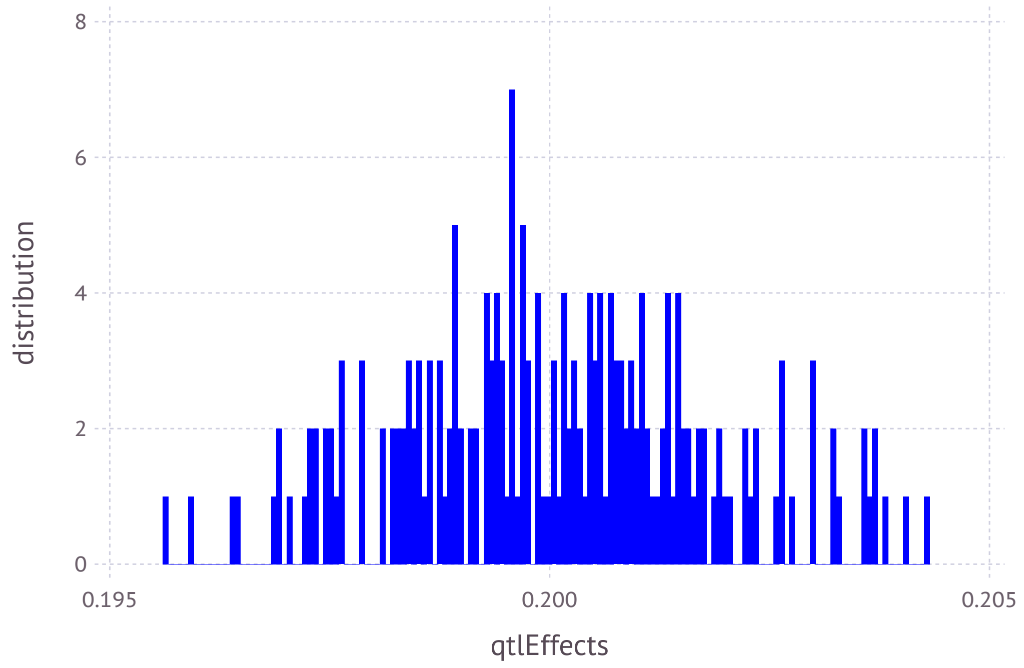
In [6]:
```
numChr    = 10
chrLength = 0.01
numLoci   = 20
nQTL      = 5
mutRate   = 0.0
locusInt  = chrLength/numLoci
mapPos    = collect(locusInt/2:locusInt:chrLength)
geneFreq  = fill(0.5,numLoci)
QTL = sample(1:numLoci,nQTL,replace=false)
qtlMarker = fill(false,numLoci)
qtlMarker[QTL] = true
mu = 100                                #  alpha ~ N(100,1)
Va = nQTL*numChr*0.5*mu*mu              # Va= nQTL*2pq*mean(alpha)^2
qtlEffects= rand(Normal(mu/sqrt(Va), sqrt(1/Va)),numLoci*numChr)  # Let alpha mu = 0.2
XSim.init(numChr,numLoci,chrLength,geneFreq,mapPos,qtlMarker,qtlEffects,mutRate)
```

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

```
Out[7]: 200-element Array{Float64,1}:
         0.202231
         0.199898
         0.199186
         0.203721
         0.199476
         0.200474
         0.200063
         0.200606
         0.200505
         0.20092
         0.19901
         0.20107
         0.200299
         ⋮
         0.199963
         0.200701
         0.200199
         0.200937
         0.201234
         0.201085
         0.199386
         0.201917
         0.199656
         0.203252
         0.19745
         0.198263
```

```
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]:  0.20006383331188526
```

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

```
Out[11]:  3.0249581858161443e-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
```

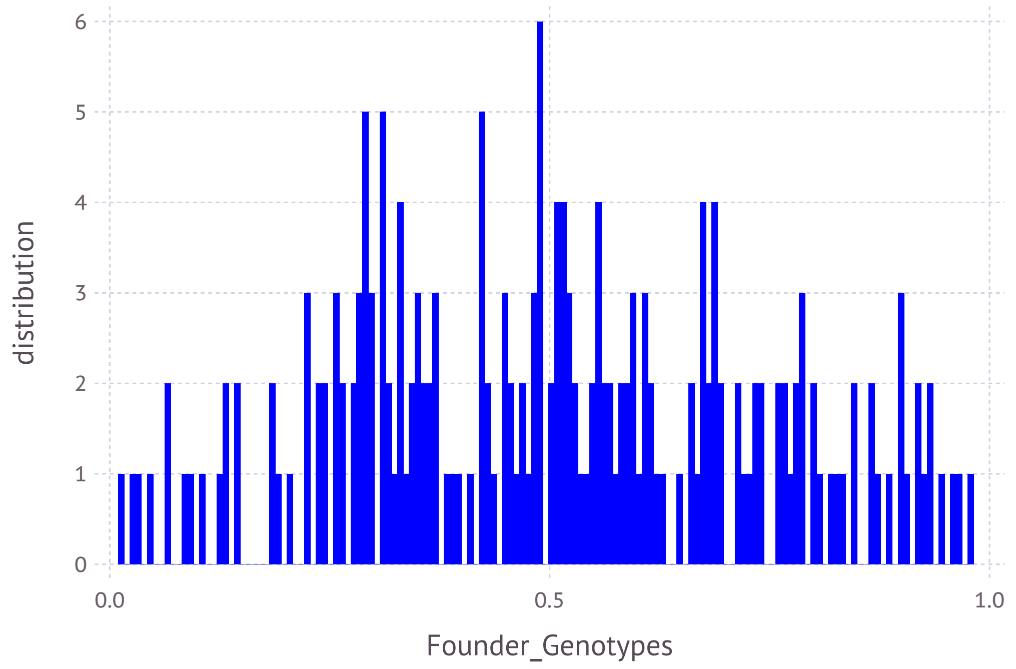
```
In [19]: gSPSire = XSim.getOurGenotypes(popSP[1])
         gSPDam = XSim.getOurGenotypes(popSP[2])
         gSP = [gSPSire;gSPSire];
```

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

```
Out[20]: 1x200 Array{Float64,2}:
          0.0655  0.831875  0.286625  0.94875  …  0.37275  0.373  0.897  0.552625
```

```
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);
```

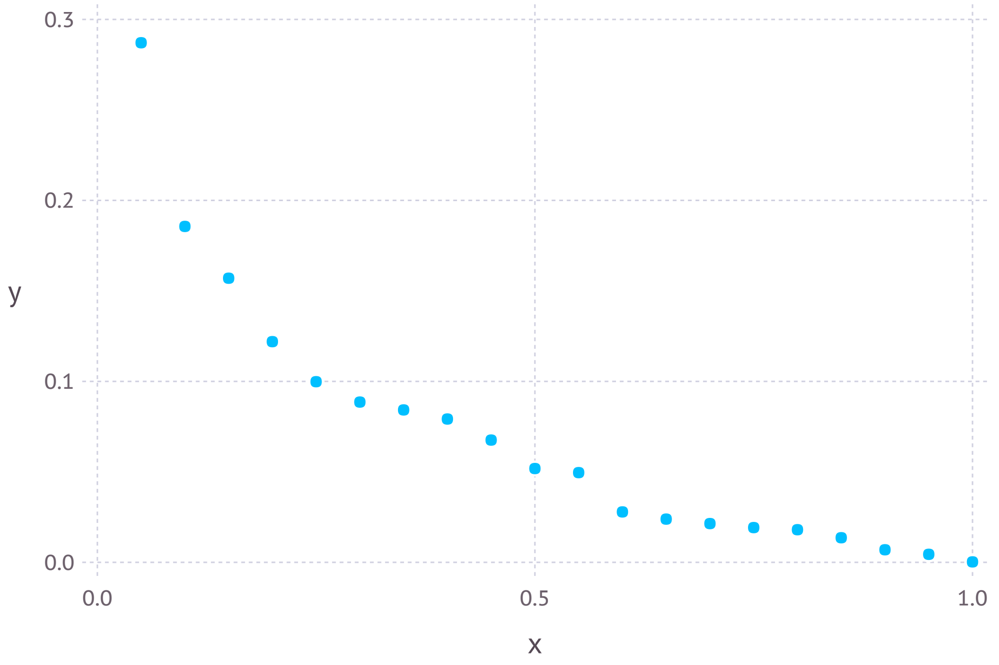
```
In [23]: for i=1:(nRows-20)
         LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
         end
```

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

```
Out[24]: 1x20 Array{Float64,2}:
          0.000268829  0.00446155  0.00697416  …  0.157034  0.185619  0.287133
```

```
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]:
```
11.238506942470075
```

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

Out[31]:
```
0.7315107459170033
```

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

Out[32]:
```
1.7068584071396744
```

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

Out[33]:
```
1.7068584071396744
```

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]: 13.27883951160792
```

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

Out[36]: 13.27472395435923
```

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

Out[37]: 0.4566575326907437
```

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

Out[38]: 0.44353840373937536
```

Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  33684  37036
 40723  34095  38894
 40724  36426  38701
 40725  36557  38535
 40726  33941  39653
 40727  34328  37622
 40728  35840  38381
 40729  34719  37144
 40730  36459  39796
 40731  36402  40634
 40732  34503  38422
 40733  34085  39307
 40734  35047  39666
     ⋮
 88710  74527  78955
 88711  75871  78642
 88712  75949  79737
 88713  75644  79765
 88714  75120  79440
 88715  75204  79713
 88716  76552  78752
 88717  73000  79800
 88718  74495  79081
 88719  75965  77942
 88720  76233  80591
 88721  74652  80276
```

In [40]:
```
PEDstream = open(PedAll, "w")
```

Out[40]:
```
IOStream(<file PedAll.txt>)
```

In [41]:
```
for i in 1:size(PED,1)
    @printf(PEDstream, "%19d%19d%19d \n", PED[i,1], PED[i,2], PED[i,3])
end
```

In [42]:
```
close(PEDstream)
```

Create matrix of ``genotype" covariates for all animals

```
In [43]: nObs = countlines(pedText)

Out[43]: 48000

In [44]: nMarker = numChr*numLoci

Out[44]: 200

In [45]: GT = convert(Array,readtable(genText,separator=' ',header=false))

Out[45]: 48000x201 Array{Int64,2}:
          40722  0  1  1  1  1  0  1  1  1  1  …  2  1  1  1  2  2  0  1  1  1  2  0
          40723  0  0  2  1  1  1  2  2  0  2     2  0  1  2  1  2  0  0  0  0  2  2
          40724  1  2  0  2  2  0  1  1  1  1     2  2  2  0  2  2  0  2  2  0  2  0
          40725  0  2  1  2  1  0  0  0  2  0     1  1  2  1  1  1  1  1  1  1  2  1
          40726  0  2  0  2  2  0  0  0  2  0     2  1  1  1  1  2  0  1  1  0  2  1
          40727  0  2  0  2  2  0  0  0  2  0  …  1  1  2  1  1  1  1  1  1  1  2  1
          40728  0  2  1  2  1  0  0  0  2  0     2  2  0  2  2  2  0  0  0  0  2  2
          40729  0  2  0  2  2  0  0  1  1  1     1  0  1  2  0  1  1  0  0  1  2  2
          40730  1  2  0  2  2  1  1  1  1  1     1  0  2  2  0  1  1  0  0  1  2  2
          40731  0  1  1  2  2  0  1  1  1  1     2  1  2  1  2  2  0  1  1  0  2  1
          40732  0  1  2  2  1  1  1  1  1  1  …  1  0  1  2  1  1  1  0  0  2  2  1
          40733  1  2  0  2  2  0  1  1  1  1     1  2  2  1  1  2  0  2  2  0  2  1
          40734  0  2  0  2  2  0  0  0  2  0     0  1  2  2  0  1  1  0  0  2  1  2
              ⋮              ⋮              ⋮  ⋱     ⋮              ⋮              ⋮
          88710  0  2  0  2  2  0  1  1  1  1     1  1  2  1  1  1  1  1  1  1  2  1
          88711  0  2  0  2  2  0  0  0  2  0     2  1  1  1  1  2  0  1  1  0  2  1
          88712  0  1  1  2  2  1  1  1  1  1  …  2  2  1  1  1  1  0  1  1  0  1  1
          88713  0  2  0  2  2  1  1  1  1  1     2  1  2  2  1  1  0  0  0  2  1  2
          88714  0  2  0  2  2  2  2  2  0  2     2  1  1  1  1  2  0  1  1  0  2  1
          88715  0  1  1  2  2  0  2  2  0  2     2  1  1  1  1  2  0  1  1  0  2  1
          88716  0  1  1  2  2  1  2  2  0  2     1  1  2  1  1  1  1  1  1  1  2  1
          88717  0  1  1  2  2  0  1  1  1  1  …  2  2  2  0  2  2  0  2  2  0  2  0
          88718  0  2  1  2  1  0  0  0  2  0     2  0  0  2  0  2  0  0  0  0  2  2
          88719  0  1  1  2  2  1  1  1  1  1     2  1  1  1  1  2  0  1  1  0  2  1
          88720  0  1  1  2  2  0  1  1  1  1     1  1  2  1  1  1  0  0  0  1  2  2
          88721  0  1  1  2  1  2  2  2  0  2     2  2  1  1  1  1  0  1  1  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]:
```
48000x200 Array{Int64,2}:
 0  1  1  1  1  0  1  1  1  1  1  0  1  …  2  1  1  1  2  2  0  1  1  1  2  0
 0  0  2  1  1  1  2  2  0  2  2  0  2     2  0  1  2  1  2  0  0  0  0  2  2
 1  2  0  2  2  0  1  1  1  1  1  0  0     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  1  2  1  0  0  0  2  0  0  1  0     1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  1  1  1  1  2  0  1  1  0  2  1
 0  2  0  2  2  0  0  0  2  0  0  2  1  …  1  1  2  1  1  1  1  1  1  1  2  1
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  2  0  2  2  2  0  0  0  0  2  2
 0  2  0  2  2  0  0  1  1  1  1  1  2     1  0  1  2  0  1  1  0  0  1  2  2
 1  2  0  2  2  1  1  1  1  1  1  1  1     1  0  2  2  0  1  1  0  0  1  2  2
 0  1  1  2  2  0  1  1  1  1  1  1  1     2  1  2  1  2  2  0  1  1  0  2  1
 0  1  2  2  1  1  1  1  1  1  1  1  0  …  1  0  1  2  1  1  1  0  0  2  2  1
 1  2  0  2  2  0  1  1  1  1  1  0  0     1  2  2  1  1  2  0  2  2  0  2  1
 0  2  0  2  2  0  0  0  2  0  0  1  1     0  1  2  2  0  1  1  0  0  2  1  2
 ⋮              ⋮              ⋮        ⋱        ⋮              ⋮
 0  2  0  2  2  0  1  1  1  1  1  0  1     1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  1  1  1  1  1  1  1  2  …  2  2  1  1  1  1  0  1  1  0  1  1
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  1  2  2  1  1  0  0  0  2  1  2
 0  2  0  2  2  2  2  2  0  2  2  0  2     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  0  2  2  0  2  2  0  1     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  1  2  2  0  2  2  0  2     1  1  2  1  1  1  1  1  1  1  2  1
 0  1  1  2  2  0  1  1  1  1  1  0  0  …  2  2  2  0  2  2  0  2  2  0  2  0
 0  2  1  2  1  0  0  0  2  0  0  2  1     2  0  0  2  0  2  0  0  0  0  2  2
 0  1  1  2  2  1  1  1  1  1  1  1  2     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  0  1  1  1  1  1  0  0     1  1  2  1  1  1  0  0  0  1  2  2
 0  1  1  2  1  2  2  2  0  2  2  0  1     2  2  1  1  1  1  0  1  1  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}:
          43040
          42170
          44091
          44038
          41472
          42771
          41411
          41411
          42084
          41153
          41450
          44352
          41759
              ⋮
          74527
          75871
          75949
          75644
          75120
          75204
          76552
          73000
          74495
          75965
          76233
          74652
```

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

```
Out[53]: 1000-element Array{Int64,1}:
          43040
          42170
          44091
          44038
          41472
          42771
          41411
          42084
          41153
          41450
          44352
          41759
          43144
              ⋮
          75566
          73991
          73906
          72899
          74412
          76676
          74378
          76490
          76012
          76007
          75927
          74018
```

```
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}:
          43040
          42170
          44091
          44038
          41472
          42771
          41411
          42084
          41153
          41450
          44352
          41759
          43144
              ⋮
          88710
          88711
          88712
          88713
          88714
          88715
          88716
          88717
          88718
          88719
          88720
          88721
```

```
In [56]: SOFF5ID= DataFrame()
         SOFF5ID[:ID] = SireOFF5ID;
```

```
In [57]: typeof(SOFF5ID)
```

```
Out[57]: DataFrames.DataFrame
```

```
In [58]: MT = readtable(GenAll,separator=' ',header=false);
```

```
In [59]: rename!(MT,:x1,:ID);
In [60]: GSOFF5 = join(SOFF5ID, MT, on = :ID, kind = :inner);
```

```
In [61]: size(GSOFF5)

Out[61]: (9000,201)
```

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

Out[62]: 9000
```

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

Out[63]: 201
```

```
In [64]: GSOFF5stream = open(Gen, "w")

Out[64]: IOStream(<file Gen.txt>)
```

```
In [65]: for i in 1:size(GSOFF5,1)
             for j in 1
                 @printf(GSOFF5stream, "%19d", GSOFF5[i,j])
             end
             for k in 2:size(GSOFF5,2)
                 @printf(GSOFF5stream, "%3d", GSOFF5[i,k])
             end
             @printf(GSOFF5stream, "\n")
         end
```

```
In [66]: close(GSOFF5stream)
```

Phenotypes - All animals

In [67]:
```
PBV = convert(Array,readtable(pheText,separator=' ',header=false))
```

Out[67]:
```
48000x3 Array{Real,2}:
 40722  11.043  10.888
 40723  10.505  11.703
 40724  11.462  12.513
 40725  10.03   10.285
 40726  12.991  11.7
 40727  10.792  11.696
 40728  10.816  11.497
 40729  11.25   11.901
 40730  11.44   10.49
 40731  10.916  12.305
 40732   9.104  10.281
 40733  12.773  12.7
 40734  11.093  11.099
     ⋮
 88710  14.93   13.916
 88711  13.499  13.913
 88712  10.757  13.51
 88713  15.599  14.124
 88714  14.215  14.12
 88715  12.104  13.914
 88716  12.998  14.315
 88717  12.648  13.507
 88718  14.453  14.523
 88719  14.451  13.908
 88720  13.142  14.114
 88721  13.495  13.711
```

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}:
            1
            4
            6
           17
           20
           21
           24
           26
           37
           40
           41
           44
           46
            ⋮
          157
          160
          161
          164
          166
          177
          180
          181
          184
          186
          197
          200
```

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

Out[83]:
```
150-element Array{Int64,1}:
   2
   3
   5
   7
   8
   9
  10
  11
  12
  13
  14
  15
  16
   ⋮
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 198
 199
```

Genotype codes: 0, 1, 2

In [84]:
```
IDgen = convert(Array,readtable(Gen,separator=' ',header=false));
```

```
In [85]: onlyID = IDgen[:,1]
         QTLMarker = IDgen[:, 2:end]
```

```
Out[85]: 9000x200 Array{Int64,2}:
 0  2  1  2  1  0  0  0  2  0  0  1  0  …  1  1  2  1  2  2  0  2  2  0  2  0
 1  2  0  2  2  1  1  1  1  1  1  0  1     2  2  2  0  2  2  0  2  2  0  2  0
 0  1  2  1  0  0  1  1  1  1  1  1  1     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     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  0  0  0  2  0  0  2  2  …  1  1  1  2  1  1  1  0  0  2  1  2
 1  2  0  2  2  1  2  2  0  2  2  0  1     2  2  2  1  2  2  0  1  1  1  2  1
 0  2  0  2  2  1  1  1  1  1  1  1  2     2  1  2  1  2  2  0  1  1  0  2  1
 0  1  1  2  2  0  1  1  1  1  1  0  0     1  1  2  2  1  1  1  0  0  1  2  2
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  1  1  1  1  2  0  1  1  0  2  1
 0  2  0  2  2  0  0  0  2  0  0  0  0  …  1  1  2  1  1  1  1  1  1  1  2  1
 0  1  1  2  2  0  1  1  1  1  1  1  1     2  2  2  0  2  2  0  2  2  0  2  0
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  1  1  1  2  0  1  1  0  2  1
 ⋮              ⋮              ⋮        ⋱           ⋮              ⋮
 0  2  0  2  2  0  1  1  1  1  1  0  1     1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  1  1  1  1  1  1  1  2  …  2  2  1  1  1  1  0  1  1  0  1  1
 0  2  0  2  2  1  1  1  1  1  1  0  1     2  1  2  2  1  1  0  0  0  2  1  2
 0  2  0  2  2  2  2  2  0  2  2  0  2     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  0  2  2  0  2  2  0  1     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  1  2  2  0  2  2  0  2     1  1  2  1  1  1  1  1  1  1  2  1
 0  1  1  2  2  0  1  1  1  1  1  0  0  …  2  2  2  0  2  2  0  2  2  0  2  0
 0  2  1  2  1  0  0  0  2  0  0  2  1     2  0  0  2  0  2  0  0  0  0  2  2
 0  1  1  2  2  1  1  1  1  1  1  1  2     2  1  1  1  1  2  0  1  1  0  2  1
 0  1  1  2  2  0  1  1  1  1  1  0  0     1  1  2  1  1  1  0  0  0  1  2  2
 0  1  1  2  1  2  2  2  0  2  2  0  1     2  2  1  1  1  1  0  1  1  0  1  1
```

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

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

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

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

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

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

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

Remove Fixed Gene from the panel

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

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

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

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

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

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

Check heritability

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

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

Out[99]: 0.3947976682360718
```

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

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

```
Out[100]: 0.6257993156015295
```

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

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

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

```
Out[102]: 50-element Array{Float64,1}:
           0.202231
           0.203721
           0.200474
           0.200169
           0.201008
           0.203583
           0.200296
           0.199718
           0.202225
           0.201023
           0.198464
           0.202664
           0.199375
           ⋮
           0.203272
           0.198944
           0.19643
           0.19914
           0.201982
           0.196954
           0.199432
           0.201461
           0.199287
           0.198541
           0.199656
           0.198263
```

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

```
Out[103]: 48000-element Array{Float64,1}:
           10.8291
           11.6183
           12.4307
           10.2231
           11.6234
           11.6313
           11.4238
           11.8387
           10.4238
           12.2408
           10.2302
           12.6239
           11.0193
            ⋮
           13.8201
           13.8266
           13.4273
           14.0335
           14.0156
           13.8325
           14.2362
           13.4332
           14.4291
           13.8301
           14.0288
           13.6318
```

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

```
Out[104]: 11.166503126061226
```

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

```
Out[105]: 11.737741580420865
```

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

```
Out[106]: 12.15188761624445
```

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

Out[107]: 12.513810620032293

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

Out[108]: 12.849328404937038

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

Out[109]: 13.192158153254328

In [110]: EAlphaG=onlyQTL*QTLo

Out[110]: 9000-element Array{Float64,1}:
           12.2228
           11.6276
           12.6198
           12.8269
           12.2261
           12.4292
           12.2152
           13.0283
           12.4234
           12.2272
           12.42
           12.4229
           11.828
             ⋮
           13.8201
           13.8266
           13.4273
           14.0335
           14.0156
           13.8325
           14.2362
           13.4332
           14.4291
           13.8301
           14.0288
           13.6318
```

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

Out[111]: 13.159539659740467

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

Out[112]: 1.9930365336792413

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

Out[113]: 12.326547522248301

In [114]: meanBreedingValueSelectedG0=meanEAlphaS0-meanEAlphaG0

Out[114]: 1.1600443961870752

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

Out[115]: 12.55709346541433

In [116]: meanBreedingValueSelectedG1=meanEAlphaS1-meanEAlphaG0

Out[116]: 1.3905903393531034

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

Out[117]: 12.909590146672342

In [118]: meanBreedingValueSelectedG2=meanEAlphaS2-meanEAlphaG0

Out[118]: 1.7430870206111155

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

Out[119]: 13.17377002489908

In [120]: meanBreedingValueSelectedG3=meanEAlphaS3-meanEAlphaG0

Out[120]: 2.0072668988378535
```

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

Out[121]: 13.525957398913983

In [122]: meanBreedingValueSelectedG4=meanEAlphaS4-meanEAlphaG0

Out[122]: 2.3594542728527568

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

Out[123]: 13.192158153254328

In [124]: meanBreedingValueSelectedG5=meanEAlphaS5-meanEAlphaG0

Out[124]: 2.0256550271931015
```