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)
```

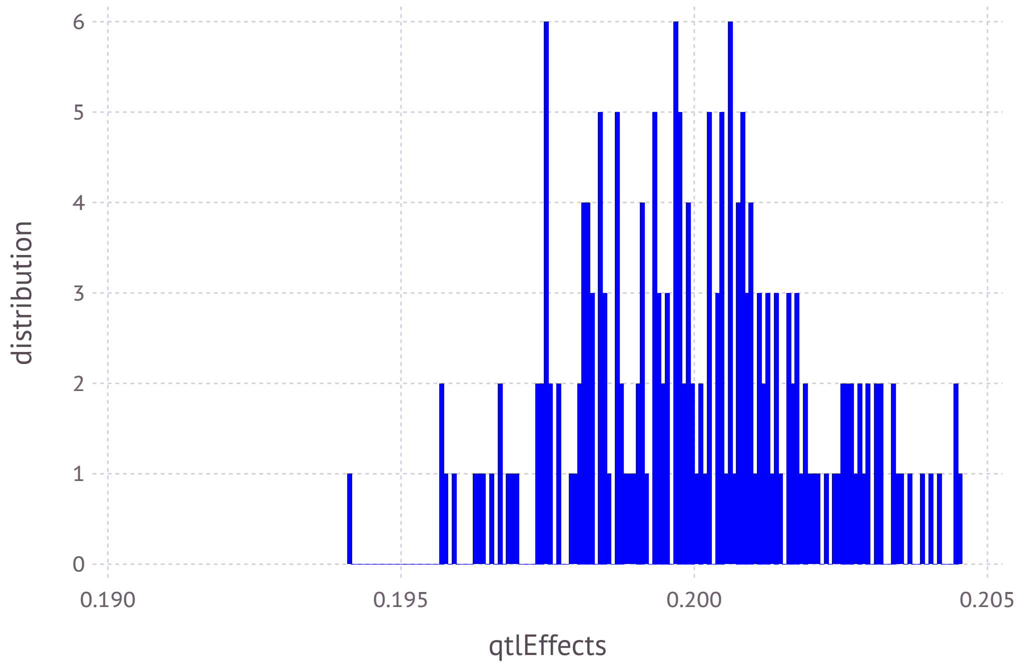
```
In [7]: qtlEffects
```

```
Out[7]: 200-element Array{Float64,1}:
          0.199093
          0.198196
          0.199915
          0.2005
          0.200892
          0.196811
          0.196524
          0.198152
          0.202258
          0.200555
          0.199922
          0.199812
          0.198402
          ⋮
          0.201463
          0.202471
          0.197298
          0.19748
          0.197985
          0.198225
          0.198431
          0.201419
          0.199661
          0.200979
          0.202853
          0.199392
```

```
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]:
```
0.20000669399769555
```

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

Out[11]:
```
4.030379102387221e-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
```

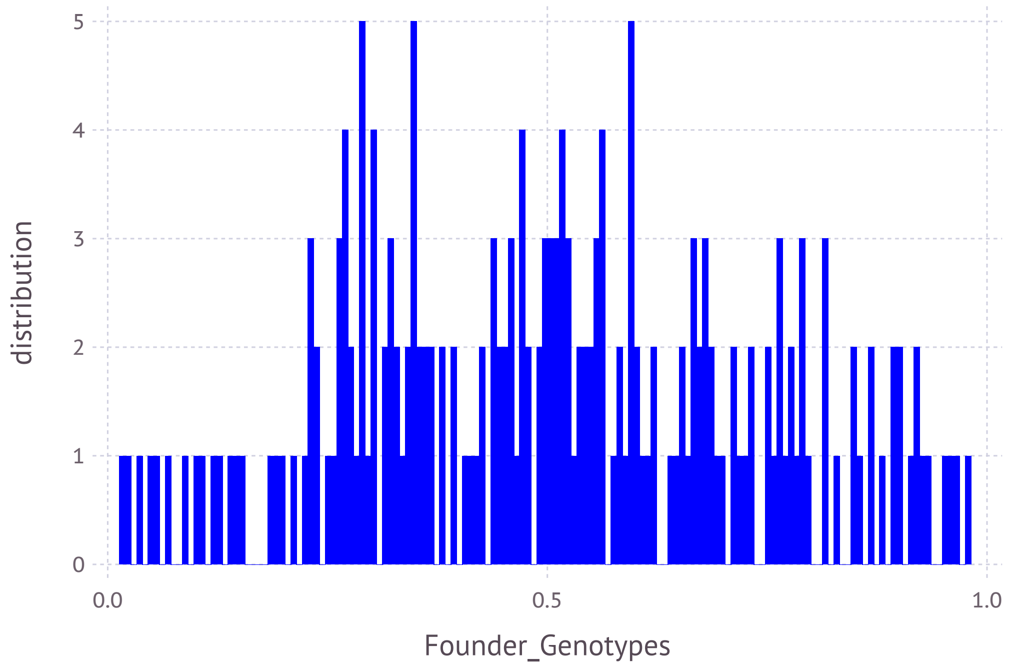
```
In [19]: gSPSire = XSim.getOurGenotypes(popSP[1])
         gSPDam = XSim.getOurGenotypes(popSP[2])
         gSP = [gSPSire;gSPSire];
```

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

```
Out[20]: 1x200 Array{Float64,2}:
          0.052125  0.846375  0.28825  0.953  …  0.360625  0.378625  0.89675  0.5535
```

```
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);
```

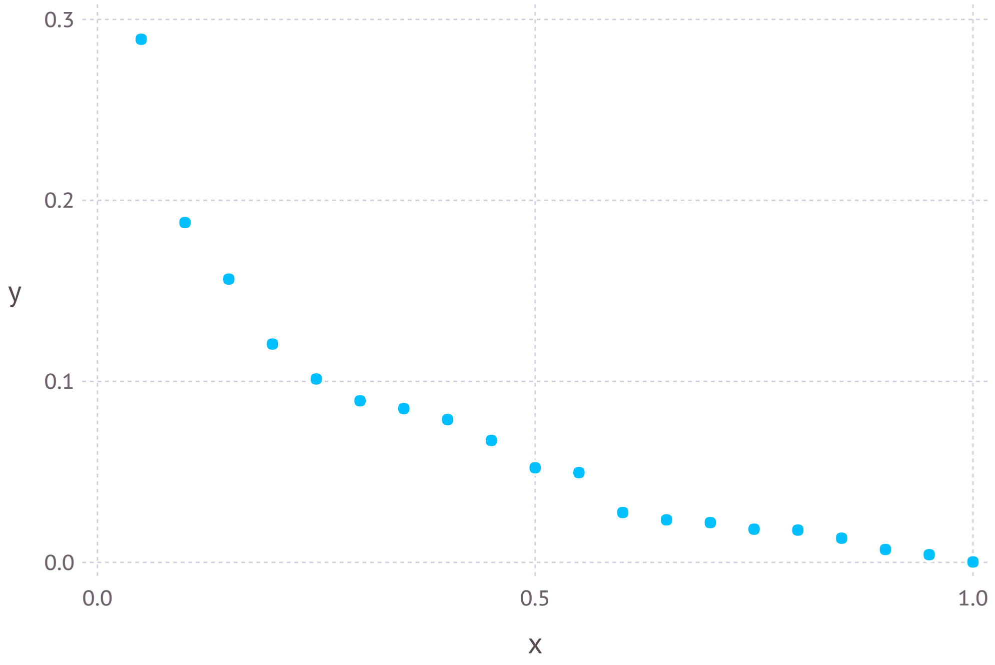
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.000234676  0.00426384  0.0071329  …  0.15651  0.187763  0.289037
```

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]:
```
8.778862573987976
```

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

Out[31]:
```
0.9332668891864851
```

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

Out[32]:
```
2.177622741435132
```

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

Out[33]:
```
2.177622741435132
```

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

```
Generation     7: sampling  4000 males and  4000 females
Generation     8: sampling  4000 males and  4000 females
Generation     9: sampling  4000 males and  4000 females
Generation    10: sampling  4000 males and  4000 females
Generation    11: sampling  4000 males and  4000 females
```

```
In [35]: ymRMP = XSim.getOurGenVals(popRMP[1])    # for males: pop[1]
         mean(ymRMP)

Out[35]: 11.21064566078809
```

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

Out[36]: 11.212202651770461
```

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

Out[37]: 0.6860659465557168
```

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

Out[38]: 0.6541821391923308
```

## Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  36243  36882
 40723  34196  38469
 40724  34861  38528
 40725  35507  39587
 40726  36594  37684
 40727  33553  40055
 40728  34459  38674
 40729  33491  38852
 40730  33273  37369
 40731  35636  39230
 40732  36243  38074
 40733  35925  38605
 40734  33696  40245
     ⋮
 88710  74915  79486
 88711  74917  76877
 88712  73438  78640
 88713  74042  77661
 88714  76361  79511
 88715  75574  80608
 88716  75683  78079
 88717  72928  79249
 88718  75797  78858
 88719  75763  80626
 88720  73017  80250
 88721  75471  80225
```

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

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

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

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

## Create matrix of ``genotype" covariates for all animals

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

Out[43]:
```
48000
```

In [44]:
```
nMarker = numChr*numLoci
```

Out[44]:
```
200
```

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

Out[45]:
```
48000x201 Array{Int64,2}:
 40722  0  2  0  2  2  0  0  0  2  0  …  2  1  0  2  2  2  1  1  1  0  2  2
 40723  0  2  0  2  2  0  0  0  2  0     2  1  1  1  1  2  0  1  1  0  2  1
 40724  0  2  1  2  1  1  1  1  1  1     1  1  2  1  1  1  1  1  1  1  2  1
 40725  0  2  0  2  2  0  0  0  2  0     2  0  2  2  1  1  1  1  1  0  2  2
 40726  1  2  0  2  2  0  1  1  1  1     2  1  1  2  2  2  0  0  0  1  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  1  1  2  2  1  1  1  1  1     2  0  1  2  1  1  1  0  0  2  2  1
 40729  0  2  0  2  2  1  1  1  1  1     2  1  1  1  2  2  0  1  1  1  2  0
 40730  0  2  0  2  2  0  0  0  2  0     2  1  1  1  1  2  1  1  1  1  1  1
 40731  0  2  0  2  2  0  0  0  2  0     2  2  1  2  1  1  0  1  1  0  1  1
 40732  0  2  0  2  2  0  1  1  1  1  …  2  1  1  1  2  2  0  1  1  1  1  1
 40733  0  1  2  1  0  0  1  1  1  1     2  1  2  0  1  2  1  1  1  1  1  1
 40734  0  2  0  2  2  0  0  0  2  0     2  1  1  1  2  2  0  1  1  1  1  1
     ⋮              ⋮              ⋮  ⋱        ⋮              ⋮              ⋮
 88710  0  2  1  2  1  0  0  0  2  0     1  0  2  2  1  0  1  0  0  1  2  2
 88711  1  2  0  2  2  1  2  2  0  2     1  0  2  2  1  1  1  1  1  1  2  1
 88712  0  1  2  2  1  0  1  1  1  1  …  1  1  2  2  1  1  1  0  0  1  2  2
 88713  0  2  0  2  2  0  0  0  2  0     2  2  2  1  2  2  0  1  1  1  2  0
 88714  0  2  0  2  2  2  2  2  0  2     1  1  2  1  1  1  1  1  1  1  2  1
 88715  1  2  0  2  2  0  1  1  1  1     2  2  1  1  2  2  0  1  1  0  2  1
 88716  0  1  1  2  2  1  1  1  1  1     1  0  1  2  0  1  1  0  0  1  2  2
 88717  0  2  0  2  2  1  1  1  1  1  …  2  2  1  1  2  2  0  0  0  1  2  2
 88718  0  2  1  1  1  0  1  1  1  1     2  2  2  1  2  2  0  1  1  0  2  0
 88719  1  2  1  2  1  0  1  1  1  1     2  2  2  1  2  2  0  1  1  1  2  0
 88720  0  1  1  2  2  1  1  1  1  1     2  2  1  1  1  1  0  1  1  0  1  1
 88721  0  2  0  2  2  0  0  0  2  0     2  2  2  0  2  2  0  2  2  0  2  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]: 48000x200 Array{Int64,2}:
 0  2  0  2  2  0  0  0  2  0  0  1  1  …  2  1  0  2  2  2  1  1  1  0  2  2
 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  1  2  1  1  1  1  1  1  1  1  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  0  2  2  1  1  1  1  1  0  2  2
 1  2  0  2  2  0  1  1  1  1  1  0  0     2  1  1  2  2  2  0  0  0  1  2  1
 0  2  0  2  2  0  0  0  2  0  0  1  1  …  1  1  2  1  1  1  1  1  1  1  2  1
 0  1  1  2  2  1  1  1  1  1  1  1  1     2  0  1  2  1  1  1  0  0  2  2  1
 0  2  0  2  2  1  1  1  1  1  1  1  2     2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  0  0  0  2  0  0  2  1     2  1  1  1  1  2  1  1  1  1  1  1
 0  2  0  2  2  0  0  0  2  0  0  0  0     2  2  1  2  1  1  0  1  1  0  1  1
 0  2  0  2  2  0  1  1  1  1  1  0  0  …  2  1  1  1  2  2  0  1  1  1  1  1
 0  1  2  1  0  0  1  1  1  1  1  1  1     2  1  2  0  1  2  1  1  1  1  1  1
 0  2  0  2  2  0  0  0  2  0  0  2  2     2  1  1  1  2  2  0  1  1  1  1  1
 ⋮              ⋮              ⋮        ⋱           ⋮              ⋮
 0  2  1  2  1  0  0  0  2  0  0  1  0     1  0  2  2  1  0  1  0  0  1  2  2
 1  2  0  2  2  1  2  2  0  2  2  0  1     1  0  2  2  1  1  1  1  1  1  2  1
 0  1  2  2  1  0  1  1  1  1  1  1  0  …  1  1  2  2  1  1  1  0  0  1  2  2
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  2  2  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  2  2  2  0  2  2  0  2     1  1  2  1  1  1  1  1  1  1  2  1
 1  2  0  2  2  0  1  1  1  1  1  1  1     2  2  1  1  2  2  0  1  1  0  2  1
 0  1  1  2  2  1  1  1  1  1  1  0  1     1  0  1  2  0  1  1  0  0  1  2  2
 0  2  0  2  2  1  1  1  1  1  1  1  2  …  2  2  1  1  2  2  0  0  0  1  2  2
 0  2  1  1  1  0  1  1  1  1  1  1  2     2  2  2  1  2  2  0  1  1  0  2  0
 1  2  1  2  1  0  1  1  1  1  1  1  0     2  2  2  1  2  2  0  1  1  1  2  0
 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  0  0  0  2  0  0  2  2     2  2  2  0  2  2  0  2  2  0  2  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}:
          40894
          42746
          44080
          44339
          41710
          42346
          42948
          43329
          42534
          44201
          42195
          42276
          43501
              ⋮
          74915
          74917
          73438
          74042
          76361
          75574
          75683
          72928
          75797
          75763
          73017
          75471
```

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

Out[53]: 1000-element Array{Int64,1}:
          40894
          42746
          44080
          44339
          41710
          42346
          42948
          43329
          42534
          44201
          42195
          42276
          43501
              ⋮
          73196
          74890
          73076
          75195
          76442
          74714
          73650
          75722
          76430
          76302
          76709
          76275
```

```
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}:
          40894
          42746
          44080
          44339
          41710
          42346
          42948
          43329
          42534
          44201
          42195
          42276
          43501
              ⋮
          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   9.822   9.359
          40723  10.423   8.971
          40724  10.863   9.361
          40725   9.466  10.155
          40726   9.634   9.166
          40727   9.518   8.965
          40728   9.792   9.964
          40729   7.927   7.776
          40730   9.087   8.775
          40731   7.674   8.168
          40732   8.814   7.37
          40733   9.387   8.774
          40734  11.417  11.359
              ⋮
          88710  11.156  11.545
          88711  14.537  12.353
          88712  11.264  11.357
          88713  11.744  11.553
          88714  11.727  12.552
          88715  16.062  13.544
          88716  11.26   10.769
          88717  10.695  12.153
          88718  12.145  12.154
          88719  12.757  11.749
          88720  11.542  11.75
          88721  12.023  12.55
```

```
In [68]: PBVstream = open(PheAll, "w")
```

```
Out[68]: IOStream(<file PheAll.txt>)
```

```
In [69]: for i in 1:size(PBV,1)
             @printf(PBVstream, "%19d %10.3f %10.3f \n", PBV[i,1], PBV[i,2], PBV[i,3])
         end
```

```
In [70]: close(PBVstream )
```

## Phenotypes - all animnls from G0 to G4

```
In [71]: OFFG0toG4 = PED[posOFF0S:posOFF4E,1]
```

```
Out[71]: 40000-element Array{Int64,1}:
          40722
          40723
          40724
          40725
          40726
          40727
          40728
          40729
          40730
          40731
          40732
          40733
          40734
              ⋮
          80710
          80711
          80712
          80713
          80714
          80715
          80716
          80717
          80718
          80719
          80720
          80721
```

```
In [72]: OFFG0toG4ID= DataFrame()
         OFFG0toG4ID[:ID] = OFFG0toG4;
```

```
In [73]: typeof(OFFG0toG4ID)
```

```
Out[73]: DataFrames.DataFrame
```

```
In [74]: AllPBV= readtable(pheText,separator=' ',header=false);
In [75]: rename!(AllPBV,:x1,:ID)
         head(AllPBV);
```

```
In [76]: OFFG0toG4PBV = join(OFFG0toG4ID, AllPBV, on = :ID, kind = :inner);
```

```
In [77]: Row = size(OFFG0toG4PBV,1)

Out[77]: 40000
```

```
In [78]: Col = size(OFFG0toG4PBV,2)

Out[78]: 3
```

```
In [79]: Phestream = open(Phe, "w")

Out[79]: IOStream(<file Phe.txt>)
```

```
In [80]: for i in 1:size(OFFG0toG4PBV,1)
             @printf(Phestream, "%19d %10.3f %10.3f \n", OFFG0toG4PBV[i,1], OFFG0toG4PBV[i,2], OFFG0toG4PBV[i,3])
         end
```

```
In [81]: close(Phestream)
```

# Get files with QTL only or Markers only

## QTL file and Markers file

```
In [82]: QTLPos = XSim.common.G.qtl_index
```

```
Out[82]: 50-element Array{Int64,1}:
            2
            6
           10
           18
           19
           22
           26
           30
           38
           39
           42
           46
           50
            ⋮
          158
          159
          162
          166
          170
          178
          179
          182
          186
          190
          198
          199
```

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

```
Out[83]: 150-element Array{Int64,1}:
            1
            3
            4
            5
            7
            8
            9
           11
           12
           13
           14
           15
           16
            ⋮
          185
          187
          188
          189
          191
          192
          193
          194
          195
          196
          197
          200
```

## Genotype codes: 0, 1, 2

```
In [84]: IDgen = convert(Array,readtable(Gen,separator=' ',header=false));
In [85]: onlyID = IDgen[:,1]
         QTLMarker = IDgen[:, 2:end]
```

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

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

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

```
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]:
```
0.42350681496224996
```

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

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

Out[100]:
```
0.6521422517846011
```

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

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

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

```
Out[102]: 50-element Array{Float64,1}:
           0.198196
           0.196811
           0.200555
           0.200371
           0.199711
           0.199032
           0.199989
           0.203437
           0.194087
           0.200264
           0.19847
           0.203418
           0.199324
           ⋮
           0.200957
           0.201083
           0.19993
           0.197468
           0.196887
           0.195775
           0.200946
           0.199491
           0.199526
           0.202471
           0.200979
           0.202853
```

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

Out[103]:
```
48000-element Array{Float64,1}:
  9.40518
  8.99907
  9.40224
 10.2136
  9.21708
  8.99432
 10.0017
  7.78719
  8.77528
  8.19562
  7.39102
  8.79432
 11.4115
  ⋮
 11.6128
 12.3861
 11.4047
 11.6157
 12.601
 13.6022
 10.7831
 12.2034
 12.2047
 11.8047
 11.7965
 12.6047
```

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

Out[104]:
```
8.807233451494575
```

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

Out[105]:
```
9.522621506091083
```

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

Out[106]:
```
10.004097920087974
```

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

Out[107]: 10.45596408393929

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

Out[108]: 10.892091025483325

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

Out[109]: 11.257011703318698

In [110]: EAlphaG=onlyQTL*QTLo

Out[110]: 9000-element Array{Float64,1}:
           11.4115
            8.80356
           10.9977
           10.6086
           10.61
           12.2069
           10.2093
            9.99962
           10.9943
            9.78812
           10.0038
            9.80186
            9.00192
            ⋮
           11.6128
           12.3861
           11.4047
           11.6157
           12.601
           13.6022
           10.7831
           12.2034
           12.2047
           11.8047
           11.7965
           12.6047
```

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

Out[111]: 11.219060335453037

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

Out[112]: 2.4118268839584616

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

Out[113]: 10.235894452352886

In [114]: meanBreedingValueSelectedG0=meanEAlphaS0-meanEAlphaG0

Out[114]: 1.4286610008583107

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

Out[115]: 10.494406898875582

In [116]: meanBreedingValueSelectedG1=meanEAlphaS1-meanEAlphaG0

Out[116]: 1.6871734473810065

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

Out[117]: 10.904459066858836

In [118]: meanBreedingValueSelectedG2=meanEAlphaS2-meanEAlphaG0

Out[118]: 2.0972256153642608

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

Out[119]: 11.297405803459236

In [120]: meanBreedingValueSelectedG3=meanEAlphaS3-meanEAlphaG0

Out[120]: 2.4901723519646612
```

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

Out[121]: 11.645080741092164

In [122]: meanBreedingValueSelectedG4=meanEAlphaS4-meanEAlphaG0

Out[122]: 2.8378472895975886

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

Out[123]: 11.257011703318698

In [124]: meanBreedingValueSelectedG5=meanEAlphaS5-meanEAlphaG0

Out[124]: 2.4497782518241227
```