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)
```

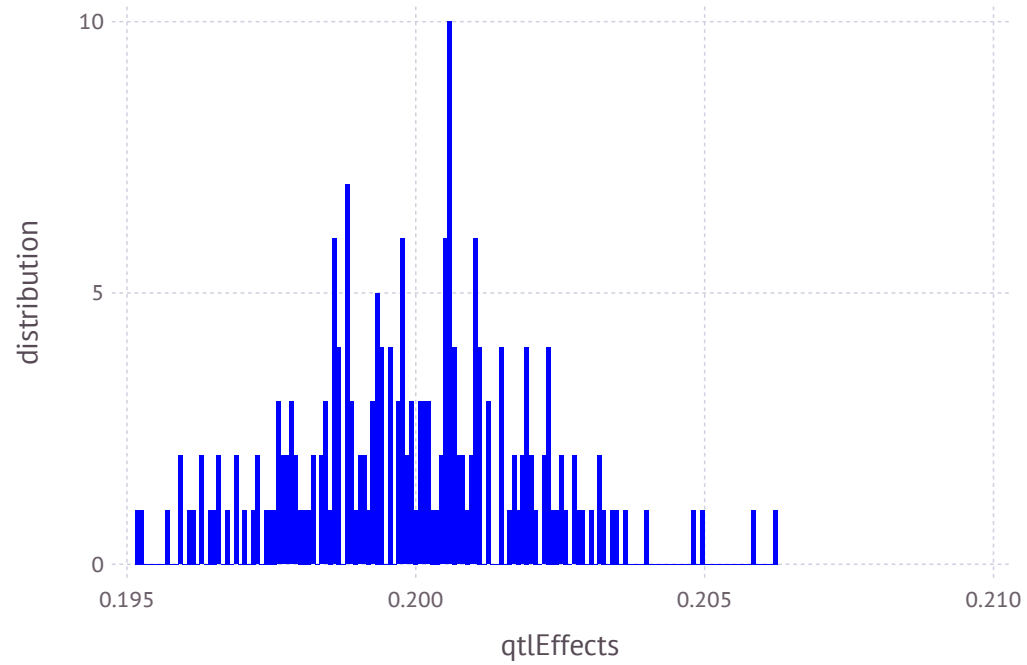
In [7]:
```
qtlEffects
```

Out[7]:
```
200-element Array{Float64,1}:
 0.201117
 0.198198
 0.199791
 0.198161
 0.2017
 0.2015
 0.19858
 0.197621
 0.195231
 0.198956
 0.195951
 0.197978
 0.198371
 ⋮
 0.199915
 0.201839
 0.204796
 0.200001
 0.201018
 0.201913
 0.201841
 0.202494
 0.202915
 0.199348
 0.198812
 0.197601
```

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]:
```
0.19991480222148758
```

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

Out[11]:
```
4.059871906510344e-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
```

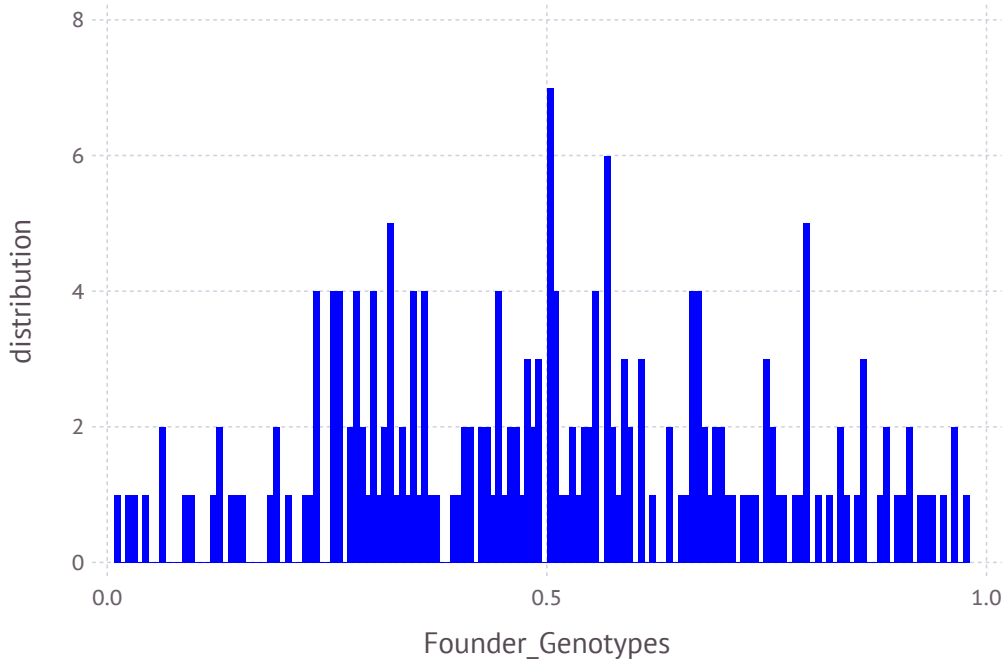
In [19]:
```
gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

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

Out[20]:
```
1x200 Array{Float64,2}:
 0.065  0.838125  0.284625  0.9505  0.82425  …  0.37175  0.887875  0.566375
```

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);
```

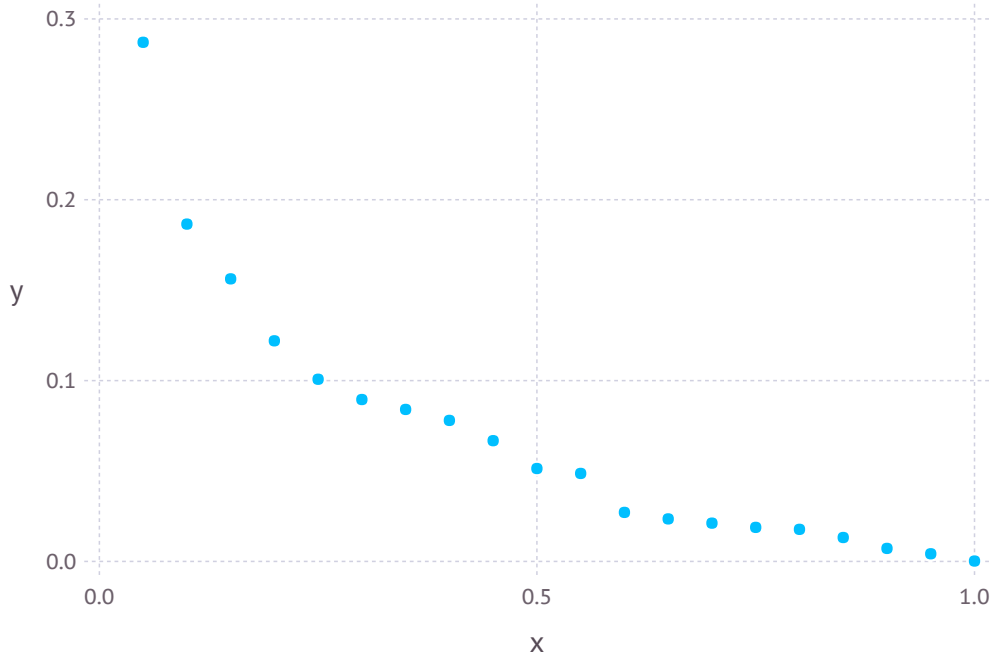
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.000222163  0.0042502  0.00722541  …  0.156248  0.186552  0.287093
```

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]:
```
10.388020136815136
```

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

Out[31]:
```
0.5059061614758548
```

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

Out[32]:
```
1.1804477101103277
```

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

Out[33]:
```
1.1804477101103277
```

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]: 12.361722714747374

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

Out[36]: 12.371588702507307

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

Out[37]: 0.49311363617683135

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

Out[38]: 0.46001816764891296

Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  34858  38369
 40723  34041  38272
 40724  34749  37640
 40725  36450  38755
 40726  33986  38073
 40727  35027  36935
 40728  36569  40111
 40729  35070  37015
 40730  35225  37576
 40731  36080  39505
 40732  34993  39630
 40733  36472  39511
 40734  34297  40135
     ⋮
 88710  76056  79378
 88711  73049  78735
 88712  74852  80016
 88713  74504  80390
 88714  74138  79746
 88715  76147  78666
 88716  75773  78169
 88717  76147  80651
 88718  73685  79265
 88719  73771  80047
 88720  76286  80498
 88721  76369  79251
```

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	2	2	1	1	1	1	1	…	2	2	2	0	2	2	0	2	2	0	2	0
40723	0	0	2	2	2	0	2	2	0	2		2	2	2	0	2	2	0	2	2	0	2	0
40724	0	2	0	2	2	0	0	0	2	0		2	2	1	1	2	2	0	1	1	0	2	1
40725	0	1	2	1	0	0	1	1	1	1		1	1	1	2	1	1	1	0	0	1	2	2
40726	0	2	1	2	2	2	2	2	1	1		1	0	2	2	1	1	1	0	0	1	2	2
40727	0	2	0	2	2	0	1	1	2	0	…	2	2	2	0	2	2	0	2	2	0	2	0
40728	0	2	1	2	1	0	0	0	2	0		1	1	2	1	1	1	1	1	1	1	2	1
40729	0	1	1	1	1	0	1	1	1	1		1	1	2	1	1	1	1	1	1	1	2	1
40730	0	1	2	2	1	1	1	1	1	1		2	2	1	1	2	2	0	0	0	1	2	2
40731	0	1	1	2	2	2	2	2	1	1		0	0	2	2	1	1	1	1	1	1	2	1
40732	0	2	0	2	2	1	1	1	1	1	…	2	1	1	1	2	2	0	0	0	2	1	1
40733	0	2	0	2	2	0	1	1	2	0		1	1	2	1	1	1	0	1	1	1	1	1
40734	0	2	1	2	1	0	0	0	2	0		2	2	2	1	2	2	0	0	0	2	1	2
⋮				⋮				⋮	⋱			⋮				⋮					⋮		
88710	0	2	0	2	2	1	1	1	1	1		1	1	1	2	1	1	1	0	0	1	2	2
88711	0	2	0	2	2	0	1	1	1	1		2	1	1	1	2	2	0	1	1	1	2	0
88712	0	2	0	2	2	1	1	1	1	1	…	2	1	1	1	1	2	0	1	1	0	2	1
88713	1	2	0	2	2	0	1	1	1	1		2	2	2	0	2	2	0	2	2	0	2	0
88714	0	1	1	2	2	0	0	0	2	0		2	2	2	0	2	2	0	2	2	0	2	0
88715	0	2	0	2	2	1	1	1	1	1		2	1	1	1	2	2	0	1	1	1	2	0
88716	1	1	1	2	2	0	2	2	0	2		2	2	0	2	2	2	0	0	0	0	2	2
88717	0	2	0	2	2	0	1	1	1	1	…	2	2	2	0	2	2	0	2	2	0	2	0
88718	0	1	1	2	2	2	2	2	0	2		2	2	1	1	2	2	0	1	1	0	2	1
88719	0	2	0	2	2	2	2	2	0	2		1	2	2	1	1	2	0	2	2	0	2	1
88720	0	0	2	2	2	0	2	2	0	2		2	1	2	1	2	2	0	1	1	1	1	1
88721	0	2	0	2	2	0	0	0	2	0		2	1	2	1	2	2	0	1	1	1	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  2  2  1  1  1  1  1  1  1  2  …  2  2  2  0  2  2  0  2  2  0  2  0
 0  0  2  2  2  0  2  2  0  2  2  0  2     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  1  1  2  2  0  1  1  0  2  1
 0  1  2  1  0  0  1  1  1  1  1  0  1     1  1  1  2  1  1  1  0  0  1  2  2
 0  2  1  2  2  2  2  2  1  1  1  0  1     1  0  2  2  1  1  1  0  0  1  2  2
 0  2  0  2  2  0  1  1  2  0  0  2  2  …  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  1  1  1  1  0  1  1  1  1  1  0  1     1  1  2  1  1  1  1  1  1  1  2  1
 0  1  2  2  1  1  1  1  1  1  1  1  1     2  2  1  1  2  2  0  0  0  1  2  2
 0  1  1  2  2  2  2  2  1  1  1  0  1     0  0  2  2  1  1  1  1  1  1  2  1
 0  2  0  2  2  1  1  1  1  1  1  1  2  …  2  1  1  1  2  2  0  0  0  2  1  1
 0  2  0  2  2  0  1  1  2  0  0  1  1     1  1  2  1  1  1  0  1  1  1  1  1
 0  2  1  2  1  0  0  0  2  0  0  1  0     2  2  2  1  2  2  0  0  0  2  1  2
 ⋮                 ⋮                 ⋮           ⋱        ⋮                 ⋮
 0  2  0  2  2  1  1  1  1  1  1  0  1     1  1  1  2  1  1  1  0  0  1  2  2
 0  2  0  2  2  0  1  1  1  1  1  0  1     2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  1  1  1  1  1  1  0  1  …  2  1  1  1  1  2  0  1  1  0  2  1
 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  1  1  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  1  1  1  1  1  1  0  1     2  1  1  1  2  2  0  1  1  1  2  0
 1  1  1  2  2  0  2  2  0  2  2  0  0     2  2  0  2  2  2  0  0  0  0  2  2
 0  2  0  2  2  0  1  1  1  1  1  0  1  …  2  2  2  0  2  2  0  2  2  0  2  0
 0  1  1  2  2  2  2  2  0  2  2  0  1     2  2  1  1  2  2  0  1  1  0  2  1
 0  2  0  2  2  2  2  2  0  2  2  0  2     1  2  2  1  1  2  0  2  2  0  2  1
 0  0  2  2  2  0  2  2  0  2  2  0  0     2  1  2  1  2  2  0  1  1  1  1  1
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  2  1  2  2  0  1  1  1  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}:
 43569
 44665
 41737
 41873
 41258
 41580
 41783
 41000
 44665
 44298
 41660
 42051
 44628
     ⋮
 76056
 73049
 74852
 74504
 74138
 76147
 75773
 76147
 73685
 73771
 76286
 76369
```

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

Out[53]:
```
1000-element Array{Int64,1}:
 43569
 44665
 41737
 41873
 41258
 41580
 41783
 41000
 44298
 41660
 42051
 44628
 43653
     ⋮
 74156
 74153
 75841
 73925
 74060
 76476
 76373
 73137
 75298
 75801
 72952
 75973
```

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}:
 43569
 44665
 41737
 41873
 41258
 41580
 41783
 41000
 44298
 41660
 42051
 44628
 43653
     ⋮
 88710
 88711
 88712
 88713
 88714
 88715
 88716
 88717
 88718
 88719
 88720
 88721
```

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

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

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

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

In [59]:
```
rename!(MT,:x1,:ID);
```

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

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

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

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

Out[62]:
```
9000
```

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

Out[63]:
```
201
```

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

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

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

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

Phenotypes - All animals

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

Out[67]:
```
48000x3 Array{Real,2}:
 40722   8.651   9.562
 40723  11.918  10.374
 40724  10.858  11.174
 40725   8.338   8.779
 40726  10.899  10.981
 40727  10.19    9.581
 40728   9.182   9.183
 40729  10.723  10.577
 40730  10.071  10.173
 40731  12.342  10.77
 40732   9.271   9.978
 40733  10.936  10.971
 40734  10.792  11.371
     ⋮
 88710  13.52   13.168
 88711  12.831  12.374
 88712  13.243  12.576
 88713  14.048  13.171
 88714  11.786  12.577
 88715  11.331  13.769
 88716  13.369  13.773
 88717  12.556  12.97
 88718  11.83   13.375
 88719  11.901  13.162
 88720  12.899  12.369
 88721  13.229  12.773
```

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
   4
   5
  10
  14
  22
  24
  25
  30
  34
  42
  44
  45
   ⋮
 150
 154
 162
 164
 165
 170
 174
 182
 184
 185
 190
 194
```

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

Out[83]:
```
150-element Array{Int64,1}:
   1
   3
   6
   7
   8
   9
  11
  12
  13
  15
  16
  17
  18
   ⋮
 187
 188
 189
 191
 192
 193
 195
 196
 197
 198
 199
 200
```

Genotype codes: 0, 1, 2

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

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

Out[85]: 9000x200 Array{Int64,2}:

0	2	0	2	2	0	0	0	2	0	0	1	1	…	1	1	2	2	1	1	1	0	0	2	2	1
0	1	2	2	1	0	1	1	1	1	1	1	0		2	2	2	1	2	2	0	1	1	1	2	1
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	2	0	2	2	0	0	0	2	0	0	2	2		2	1	0	2	0	2	0	0	0	0	2	2
0	2	1	2	1	1	1	1	1	1	1	1	2		2	1	2	1	2	2	0	1	1	1	1	1
0	2	1	2	1	0	0	0	2	0	0	1	0	…	2	0	0	2	1	2	1	0	0	2	1	1
0	1	1	2	2	0	1	1	1	1	1	1	2		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	0	2	2	1	1	1	0	0	1	2	2
0	2	0	2	2	0	1	1	1	1	1	1	2		2	2	2	0	2	2	0	2	2	0	2	0
0	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	2	…	2	1	2	2	2	2	1	0	0	1	1	2
0	2	1	2	1	0	0	0	2	0	0	2	2		2	1	1	2	2	1	1	0	0	1	2	2
1	1	1	2	2	1	1	1	1	1	1	1	1		2	1	1	1	1	2	0	1	1	0	2	1
⋮				⋮				⋮				⋱		⋮						⋮					
0	2	0	2	2	1	1	1	1	1	1	0	1		1	1	1	2	1	1	1	0	0	1	2	2
0	2	0	2	2	0	1	1	1	1	1	0	1		2	1	1	1	2	2	0	1	1	1	2	0
0	2	0	2	2	1	1	1	1	1	1	0	1	…	2	1	1	1	1	2	0	1	1	0	2	1
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	1	1	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	1	1	1	1	1	1	0	1		2	1	1	1	2	2	0	1	1	1	2	0
1	1	1	2	2	0	2	2	0	2	2	0	0		2	2	0	2	2	2	0	0	0	0	2	2
0	2	0	2	2	0	1	1	1	1	1	0	1	…	2	2	2	0	2	2	0	2	2	0	2	0
0	1	1	2	2	2	2	2	0	2	2	0	1		2	2	1	1	2	2	0	1	1	0	2	1
0	2	0	2	2	2	2	2	0	2	2	0	2		1	2	2	1	1	2	0	2	2	0	2	1
0	0	2	2	2	0	2	2	0	2	2	0	0		2	1	2	1	2	2	0	1	1	1	1	1
0	2	0	2	2	0	0	0	2	0	0	1	1		2	1	2	1	2	2	0	1	1	1	1	1

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

Out[86]:
```
9000x50 Array{Int64,2}:
 2  2  2  0  1  1  1  0  0  2  2  0  0  …  1  1  0  2  0  1  2  0  2  1  1  1
 1  2  1  1  2  1  1  1  0  0  0  2  0     1  0  1  2  0  2  2  0  2  1  2  2
 1  2  2  1  0  1  0  2  0  0  2  0  0     1  1  0  2  0  2  2  0  2  1  1  2
 2  2  2  0  0  1  1  1  0  1  2  0  1     0  2  1  2  1  1  2  0  2  1  1  2
 2  2  1  1  2  1  1  0  0  2  2  0  2     0  2  2  2  0  1  2  0  2  0  1  2
 2  2  1  0  2  1  0  2  0  1  2  0  0  …  0  0  0  2  0  2  2  2  1  2  0  2
 1  2  2  1  0  0  1  1  0  2  2  0  1     2  0  1  2  1  2  1  0  2  1  1  2
 2  2  2  0  2  2  0  2  0  0  2  0  1     0  1  0  2  0  2  2  1  2  2  0  1
 2  2  2  1  1  1  1  1  0  1  2  0  1     1  2  1  2  1  1  1  0  2  0  2  2
 2  2  2  0  2  1  1  1  0  0  2  0  1     2  0  0  2  0  2  2  0  2  1  1  2
 2  2  2  0  0  2  0  1  0  0  2  0  1  …  1  0  1  2  0  2  1  2  2  1  1  2
 2  2  1  0  1  1  1  1  0  1  1  0  1     0  1  0  2  0  2  2  2  2  1  1  1
 1  2  2  1  1  1  1  1  0  0  1  1  0     1  0  0  2  0  2  2  0  2  1  1  2
 ⋮              ⋮              ⋮          ⋱        ⋮              ⋮
 2  2  2  1  2  1  1  1  0  0  2  0  1     0  2  0  2  0  2  2  1  2  2  1  1
 2  2  2  1  2  1  1  1  0  2  2  0  1     0  0  1  2  0  2  2  2  1  1  1  2
 2  2  2  1  2  0  0  2  0  2  1  1  1  …  2  0  1  2  1  2  2  0  2  1  1  2
 2  2  2  1  2  1  0  2  0  2  2  0  2     2  0  1  2  0  1  2  0  2  0  2  2
 1  2  2  0  2  0  0  2  0  2  2  0  2     0  1  1  2  0  1  2  0  2  0  2  2
 2  2  2  1  2  0  1  1  0  2  2  0  1     2  1  2  2  1  1  2  2  1  2  1  2
 1  2  2  2  2  2  0  2  0  1  2  1  1     1  1  1  2  1  2  2  2  2  2  2  2
 2  2  2  1  2  2  0  2  0  1  2  0  1  …  1  1  1  2  0  2  2  0  2  0  2  2
 1  2  2  2  2  2  0  2  0  0  2  0  1     0  1  0  2  0  2  2  1  2  1  2  2
 2  2  2  2  2  1  1  1  0  0  2  0  1     0  1  2  2  1  1  1  1  2  1  2  2
 0  2  2  2  2  2  0  2  0  0  2  0  1     1  1  2  2  0  2  2  0  2  0  1  2
 2  2  2  0  1  0  1  1  0  2  2  0  2     1  1  1  2  1  2  2  1  2  0  1  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]: 0.45297287670910663

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

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

Out[100]:
```
0.6730160761287926
```

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

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

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

Out[102]:
```
50-element Array{Float64,1}:
 0.198198
 0.198161
 0.2017
 0.198956
 0.200629
 0.197405
 0.197776
 0.20235
 0.200165
 0.201091
 0.19981
 0.198822
 0.202739
 ⋮
 0.195909
 0.200232
 0.199936
 0.200501
 0.199418
 0.198591
 0.199079
 0.199801
 0.198456
 0.197876
 0.201839
 0.201913
```

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

Out[103]:
```
48000-element Array{Float64,1}:
  9.60049
 10.4088
 11.2014
  8.78143
 10.9836
  9.58784
  9.18068
 10.6056
 10.1963
 10.7775
  9.98727
 11.0089
 11.4021
  ⋮
 13.196
 12.3962
 12.597
 13.2162
 12.6222
 13.8005
 13.8134
 13.004
 13.41
 13.2103
 12.4074
 12.8143
```

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

Out[104]:
```
10.404778074747734
```

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

Out[105]:
```
10.830599481102556
```

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

Out[106]:
```
11.245043528638202
```

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

Out[107]:
```
11.6350074848879
```

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

Out[108]:
```
12.049391569494917
```

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

Out[109]:
```
12.394745661938472
```

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

Out[110]:
```
9000-element Array{Float64,1}:
 11.203
 10.5933
 10.1935
 11.8109
 12.4229
 11.3996
 11.1902
 11.8028
 12.2074
 11.1932
 11.397
 10.7991
 10.6058
  ⋮
 13.196
 12.3962
 12.597
 13.2162
 12.6222
 13.8005
 13.8134
 13.004
 13.41
 13.2103
 12.4074
 12.8143
```

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

Out[111]: 12.353487261879362

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

Out[112]: 1.9487091871316284

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

Out[113]: 11.25317774375598

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

Out[114]: 0.8483996690082467

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

Out[115]: 11.628308537038633

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

Out[116]: 1.2235304622908991

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

Out[117]: 12.01794705423602

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

Out[118]: 1.613168979488286

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

Out[119]: 12.475696757218122

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

Out[120]: 2.0709186824703885

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

Out[121]: 12.741970214783551

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

Out[122]: 2.3371921400358175

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

Out[123]: 12.394745661938472

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

Out[124]: 1.9899675871907387