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 = 0.1
# 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 = 0.115
XSim.init(numChr,numLoci,chrLength,geneFreq,mapPos,qtlMarker,qtlEffects,mutRate)
```

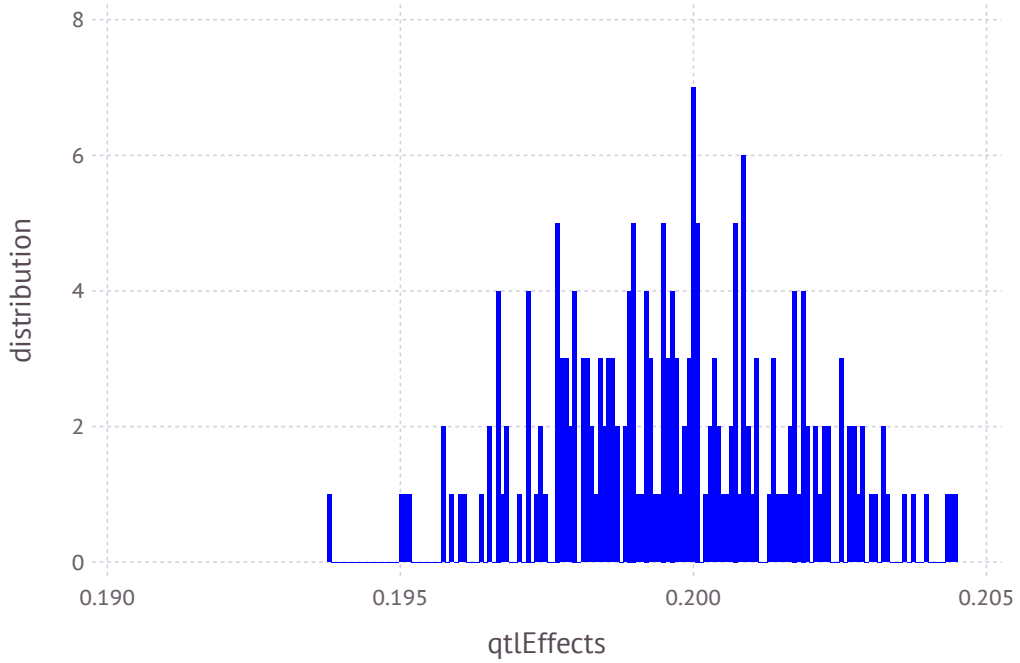
In [7]:
```
qtlEffects
```

Out[7]:
```
200-element Array{Float64,1}:
 0.200861
 0.198093
 0.197364
 0.199721
 0.195077
 0.199595
 0.199987
 0.199228
 0.196825
 0.202184
 0.203219
 0.198498
 0.199534
 ⋮
 0.199032
 0.199488
 0.196044
 0.200613
 0.200096
 0.199965
 0.198501
 0.200751
 0.199305
 0.201756
 0.200045
 0.202258
```

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]:
```
0.19969093241574648
```

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

Out[11]:
```
4.273562399395803e-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
```

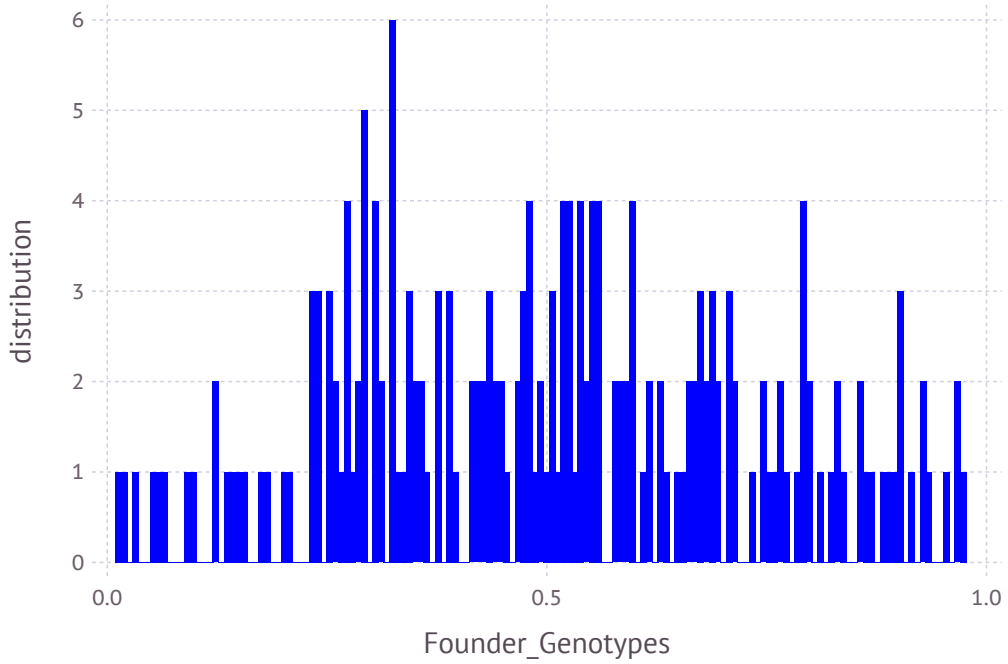
In [19]:
```
gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

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

Out[20]:
```
1x200 Array{Float64,2}:
 0.067  0.832375  0.283  0.952625  …  0.37575  0.390125  0.889625  0.551
```

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);
```

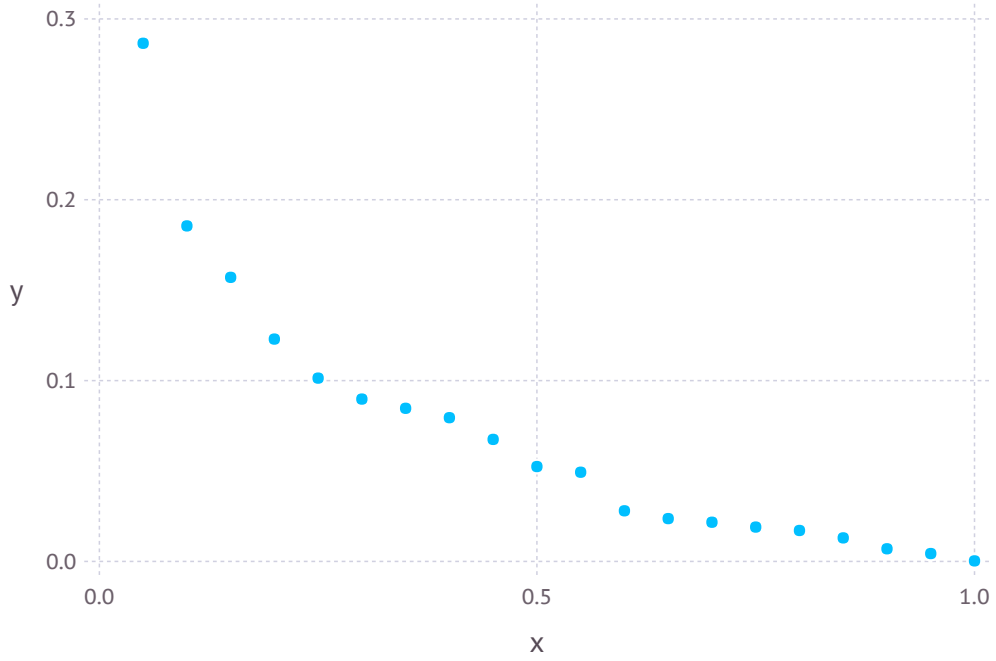
In [23]:
```
for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

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

Out[24]:
```
1x20 Array{Float64,2}:
 0.000311193  0.00437955  0.00698623  …  0.157091  0.185539  0.286512
```

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]:
```
9.663766860388161
```

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

Out[31]:
```
0.584396809619352
```

In [32]:
```
XSim.common.varRes = 9*varGen    #heritability = 0.1
```

Out[32]:
```
5.259571286574168
```

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

Out[33]:
```
5.259571286574168
```

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]: 11.1427461027958

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

Out[36]: 11.132343849577824

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

Out[37]: 0.6278243833312013

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

Out[38]: 0.602621532449843

Pedigree: All animals

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

Out[39]:
```
48000x3 Array{Int64,2}:
 40722  35894  40285
 40723  36216  36853
 40724  32813  39654
 40725  34917  38943
 40726  34233  38457
 40727  33049  38713
 40728  36604  39508
 40729  35726  40384
 40730  33023  38213
 40731  36353  37967
 40732  36041  40691
 40733  33414  36900
 40734  36076  39765
     ⋮
 88710  73114  78377
 88711  74523  80363
 88712  73553  77853
 88713  73701  77829
 88714  73846  78885
 88715  72782  79316
 88716  73958  77582
 88717  75410  79036
 88718  75870  78266
 88719  73784  79247
 88720  74839  80571
 88721  73153  79432
```

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	1	2	0	2	2	0	1	1	1	1	…	1	1	2	0	2	2	0	2	2	0	2	0
40723	0	2	1	2	1	0	0	0	2	0		1	0	2	2	1	1	1	0	0	1	2	2
40724	0	2	0	2	2	0	1	1	1	1		2	2	2	0	2	2	0	2	2	0	2	0
40725	1	2	0	2	2	0	2	2	0	2		1	1	2	2	1	1	1	0	0	1	2	2
40726	0	1	1	2	2	0	1	1	1	1		2	2	2	0	2	2	0	2	2	0	2	0
40727	0	2	0	2	2	1	1	1	1	1	…	2	1	2	2	2	1	1	0	0	1	2	2
40728	0	2	0	2	2	0	0	0	2	0		2	1	1	1	1	2	0	1	1	0	2	1
40729	0	2	0	2	2	0	0	0	2	0		1	0	1	2	1	1	2	1	1	1	2	2
40730	0	1	1	2	2	0	1	1	1	1		2	1	1	1	1	2	0	1	1	0	2	1
40731	0	1	1	2	2	0	1	1	1	1		2	2	2	0	2	2	0	2	2	0	2	0
40732	0	2	0	2	2	0	0	0	2	0	…	1	0	2	2	1	1	1	0	0	1	2	2
40733	0	2	0	2	2	1	1	1	1	1		1	0	1	2	0	1	1	0	0	1	2	2
40734	1	2	0	2	2	0	0	0	2	0		2	1	1	1	1	2	0	1	1	0	2	1
⋮				⋮				⋮	⋱			⋮				⋮				⋮			
88710	0	2	0	2	2	0	0	0	2	0		2	2	2	1	2	2	0	1	1	1	2	0
88711	0	2	0	2	2	0	0	0	2	0		1	0	2	2	1	1	1	0	0	1	2	2
88712	0	2	0	2	2	0	0	0	2	0	…	2	0	0	2	1	2	0	0	0	1	2	1
88713	0	1	1	2	2	1	2	2	1	1		2	1	1	1	2	2	0	1	1	1	2	0
88714	1	2	0	2	2	0	1	1	2	0		2	0	0	2	1	2	0	0	0	1	1	2
88715	1	2	0	2	2	0	1	1	1	1		2	1	2	1	1	2	0	1	1	0	1	1
88716	0	2	0	2	2	0	1	1	1	1		2	1	1	1	2	2	0	1	1	1	2	0
88717	1	2	0	2	2	1	1	0	2	0	…	2	1	0	2	2	2	0	0	0	1	2	1
88718	0	2	0	2	2	0	1	1	2	0		2	2	2	1	2	2	0	1	1	0	2	0
88719	0	2	0	2	2	0	0	0	2	0		2	1	1	1	2	2	0	1	1	1	2	0
88720	0	2	0	2	2	0	0	0	2	0		2	1	1	1	2	2	0	1	1	1	2	0
88721	0	2	0	2	2	1	1	1	1	1		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}:
 1  2  0  2  2  0  1  1  1  1  1  0  0  …  1  1  2  0  2  2  0  2  2  0  2  0
 0  2  1  2  1  0  0  0  2  0  0  1  0     1  0  2  2  1  1  1  0  0  1  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
 1  2  0  2  2  0  2  2  0  2  2  0  1     1  1  2  2  1  1  1  0  0  1  2  2
 0  1  1  2  2  0  1  1  1  1  1  0  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  2  2  1  1  0  0  1  2  2
 0  2  0  2  2  0  0  0  2  0  0  2  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  1  2  1  1  2  1  1  1  2  2
 0  1  1  2  2  0  1  1  1  1  1  0  0     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     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  …  1  0  2  2  1  1  1  0  0  1  2  2
 0  2  0  2  2  1  1  1  1  1  1  0  1     1  0  1  2  0  1  1  0  0  1  2  2
 1  2  0  2  2  0  0  0  2  0  0  1  0     2  1  1  1  1  2  0  1  1  0  2  1
 ⋮              ⋮              ⋮        ⋱        ⋮              ⋮
 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  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  0  0  2  0  0  1  1  …  2  0  0  2  1  2  0  0  0  1  2  1
 0  1  1  2  2  1  2  2  1  1  1  1  2     2  1  1  1  2  2  0  1  1  1  2  0
 1  2  0  2  2  0  1  1  2  0  0  2  1     2  0  0  2  1  2  0  0  0  1  1  2
 1  2  0  2  2  0  1  1  1  1  1  1  1     2  1  2  1  1  2  0  1  1  0  1  1
 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
 1  2  0  2  2  1  1  0  2  0  0  2  2  …  2  1  0  2  2  2  0  0  0  1  2  1
 0  2  0  2  2  0  1  1  2  0  0  1  1     2  2  2  1  2  2  0  1  1  0  2  0
 0  2  0  2  2  0  0  0  2  0  0  1  1     2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  0  0  0  2  0  0  1  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  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}:
 42213
 44033
 42804
 41513
 41767
 43441
 43305
 41438
 43163
 43980
 41595
 41117
 43163
    ⋮
 73114
 74523
 73553
 73701
 73846
 72782
 73958
 75410
 75870
 73784
 74839
 73153
```

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

Out[53]:
```
1000-element Array{Int64,1}:
 42213
 44033
 42804
 41513
 41767
 43441
 43305
 41438
 43163
 43980
 41595
 41117
 42008
    ⋮
 74071
 74782
 74984
 74008
 73255
 72877
 73545
 74847
 74329
 75159
 76248
 74945
```

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}:
 42213
 44033
 42804
 41513
 41767
 43441
 43305
 41438
 43163
 43980
 41595
 41117
 42008
     ⋮
 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   8.69    8.819
 40723   7.954   9.02
 40724   9.491  10.448
 40725   9.524  10.635
 40726  10.265   8.831
 40727  10.216   9.428
 40728  10.4    10.44
 40729   8.671   8.636
 40730   8.14    8.627
 40731   8.681   8.837
 40732   9.472  10.039
 40733   9.133   9.833
 40734  10.316   9.623
     ⋮
 88710  11.371  11.232
 88711  11.141  11.226
 88712   7.69   12.037
 88713  14.942  10.021
 88714  12.143  11.026
 88715  11.94   12.236
 88716  12.549  12.241
 88717   7.824  11.431
 88718   9.21   10.627
 88719   9.219  12.029
 88720   9.571  11.03
 88721  11.313  11.637
```

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
  14
  16
  18
  19
  22
  34
  36
  38
  39
  42
  54
  56
   ⋮
 158
 159
 162
 174
 176
 178
 179
 182
 194
 196
 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
   6
   7
   8
   9
  10
  11
  12
  13
  15
   ⋮
 185
 186
 187
 188
 189
 190
 191
 192
 193
 195
 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	0	0	…	2	2	2	1	2	2	0	1	1	1	2	0
0	2	0	2	2	0	0	0	2	0	0	0	0		1	1	2	2	1	1	1	0	0	2	2	1
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
1	2	0	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	2	2	2	0	2	2	0	2		2	1	1	1	2	2	0	1	1	1	2	0
0	2	0	2	2	0	0	0	2	0	0	0	0	…	1	1	2	2	0	1	1	1	0	1	2	2
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	0	1		2	1	2	2	2	2	0	0	0	0	2	1
0	1	1	1	1	0	1	1	1	1	1	1	2		1	1	2	2	1	1	1	0	0	1	2	2
2	2	0	2	2	0	2	2	0	2	2	0	0		2	2	2	1	2	2	0	1	1	1	2	0
0	1	1	2	2	0	1	1	1	1	1	0	1	…	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	1	1	2	1	2	0	0	0	0	2	2
1	2	0	2	2	0	0	0	2	0	0	2	1		1	1	2	2	1	1	1	0	0	2	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	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	0	0	2	0	0	1	1	…	2	0	0	2	1	2	0	0	0	1	2	1
0	1	1	2	2	1	2	2	1	1	1	1	2		2	1	1	1	2	2	0	1	1	1	2	0
1	2	0	2	2	0	1	1	2	0	0	2	1		2	0	0	2	1	2	0	0	0	1	1	2
1	2	0	2	2	0	1	1	1	1	1	1	1		2	1	2	1	1	2	0	1	1	0	1	1
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
1	2	0	2	2	1	1	0	2	0	0	2	2	…	2	1	0	2	2	2	0	0	0	1	2	1
0	2	0	2	2	0	1	1	2	0	0	1	1		2	2	2	1	2	2	0	1	1	0	2	0
0	2	0	2	2	0	0	0	2	0	0	1	1		2	1	1	1	2	2	0	1	1	1	2	0
0	2	0	2	2	0	0	0	2	0	0	1	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	2	2	0	2	2	0	2	2	0	2	0

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

Out[86]:
```
9000x50 Array{Int64,2}:
 2  2  1  0  0  2  2  2  1  0  1  1  0  …  1  0  0  2  2  0  2  0  2  1  1  2
 2  2  0  0  0  1  1  1  1  0  2  1  0     0  2  0  2  1  0  1  0  1  0  2  2
 2  2  0  0  0  2  0  2  2  2  1  0  1     2  0  0  2  0  2  0  1  2  2  0  2
 2  1  2  1  1  0  1  1  2  0  0  0  0     1  2  0  2  0  2  0  0  2  2  0  2
 2  2  0  0  0  2  0  2  2  2  1  1  0     1  2  1  2  1  1  1  1  2  1  1  2
 2  2  0  0  0  2  0  2  2  2  2  1  0  …  2  2  0  2  0  2  0  1  1  1  1  2
 2  1  1  1  0  2  0  2  2  2  1  1  0     1  2  0  2  0  2  0  0  1  1  1  2
 1  1  0  0  0  1  1  2  1  1  1  0  0     2  1  0  2  2  0  2  2  2  0  0  2
 1  1  1  1  0  1  0  2  1  2  2  1  0     1  2  0  2  1  1  1  1  1  0  1  2
 2  2  2  0  1  1  1  1  2  1  1  1  1     1  2  1  2  1  1  1  1  2  1  1  2
 1  1  0  0  0  1  0  2  2  2  1  2  0  …  1  1  0  2  0  2  0  1  2  2  0  2
 2  1  1  2  0  1  0  2  2  1  0  1  0     1  1  0  2  2  0  2  2  2  0  0  2
 2  0  2  1  0  2  1  1  1  1  1  1  0     1  1  1  1  2  0  1  0  1  0  2  2
 ⋮              ⋮              ⋮           ⋱        ⋮              ⋮
 2  1  1  1  0  1  1  1  1  1  1  2  0     1  2  1  2  2  0  2  0  2  1  1  2
 2  2  1  0  0  2  1  2  1  1  2  0  1     0  1  1  2  1  1  1  1  1  0  1  2
 2  1  1  1  0  1  1  1  2  1  1  2  0  …  1  2  0  2  1  1  1  1  2  0  1  2
 1  0  1  1  0  0  1  0  1  1  2  2  0     1  1  1  2  2  0  2  1  2  1  1  2
 2  0  2  1  0  2  0  2  2  2  2  1  1     2  2  1  2  1  1  1  1  2  0  1  1
 2  1  2  1  1  1  1  2  1  1  1  1  0     1  1  1  2  1  1  1  1  2  1  0  1
 2  2  0  1  0  2  0  2  2  2  1  1  0     1  2  0  2  1  1  1  1  2  1  1  2
 2  0  2  2  0  1  0  2  2  1  1  1  0  …  1  2  1  2  1  1  1  2  2  0  1  2
 2  1  1  1  0  2  1  2  1  1  1  1  1     1  1  0  2  0  2  0  1  2  1  0  2
 2  1  1  1  0  2  0  2  2  1  2  2  0     2  2  1  2  2  0  0  1  2  1  1  2
 2  1  1  1  0  1  2  2  0  0  2  1  0     1  2  0  2  0  2  0  1  2  1  1  2
 2  2  1  0  0  2  0  2  2  2  1  0  0     1  2  1  2  2  0  2  0  2  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]: 0.1543690591174735

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

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

Out[100]:
```
0.3975120474694069
```

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

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

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

Out[102]:
```
50-element Array{Float64,1}:
 0.198093
 0.198997
 0.201639
 0.202319
 0.20169
 0.202647
 0.196641
 0.200973
 0.201918
 0.196546
 0.198806
 0.198002
 0.198952
 ⋮
 0.203985
 0.2014
 0.197691
 0.199626
 0.198433
 0.198274
 0.200415
 0.201945
 0.199965
 0.200751
 0.201756
 0.200045
```

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

Out[103]:
```
48000-element Array{Float64,1}:
  8.79473
  8.98604
 10.3985
 10.5921
  8.8024
  9.38631
 10.396
  8.59241
  8.58496
  8.8033
  9.98903
  9.80066
  9.58769
  ⋮
 11.1817
 11.1835
 11.9842
  9.97964
 10.9912
 12.1964
 12.1908
 11.3992
 10.5873
 12.0052
 10.9806
 11.5957
```

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

Out[104]:
```
9.626440588060142
```

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

Out[105]:
```
10.121448978233257
```

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

Out[106]:
```
10.33425555559311
```

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

Out[107]:
```
10.598671596716464
```

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

Out[108]:
```
10.845569554220166
```

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

Out[109]:
```
11.09663616085411
```

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

Out[110]:
```
9000-element Array{Float64,1}:
 10.9902
 10.3831
  9.99824
  9.80474
 10.9953
 10.8003
 10.1971
  9.7938
 10.3982
 11.3828
 10.1798
 10.9947
 10.796
  ⋮
 11.1817
 11.1835
 11.9842
  9.97964
 10.9912
 12.1964
 12.1908
 11.3992
 10.5873
 12.0052
 10.9806
 11.5957
```

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

Out[111]: 11.074825135563698

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

Out[112]: 1.4483845475035562

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

Out[113]: 10.607222030470181

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

Out[114]: 0.9807814424100396

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

Out[115]: 10.556864200086855

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

Out[116]: 0.9304236120267131

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

Out[117]: 10.885132704654785

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

Out[118]: 1.2586921165946432

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

Out[119]: 11.101669142202331

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

Out[120]: 1.4752285541421895

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

Out[121]: 11.350796588787789

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

Out[122]: 1.7243560007276475

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

Out[123]: 11.09663616085411

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

Out[124]: 1.470195572793969