**Table S3.** OpenBugs code to test for contamination between samples.

model{

 for(i in 1:C){ # C=number collections

 for(k in 1:N[i]){ # N[i] = number inividuals in collection i

 z[i,k] ~ dbern(0.5) # z[i,k] = contamination indicator for individual k

 for(*l* in 1:L){ # L = number loci

 x[i,k,*l*,1:3] ~ dmulti(P[i,k,*l*,1:3],1) # Likelihood

 for(j in 1:3){ # P[i,k,*l*,j] = individual k's genotype frequency j

 P[i,k,*l*,j] <- pow(p1[i,*l*,j],z[i,k])\*pow(p0[i,*l*,j],1-z[i,k])

 }

 }

 }

 for(*l* in 1:L){

 pi[i,*l* ] ~ dbeta(0.5,0.5) # allele frequency = Prob(A)

 p0[i,*l* ,1] <- pow(q[i,*l*],2) # uncontaminated genotype 1

 p0[i,*l* ,2] <- 2\*q[i,*l*]\*(1-q[i,*l*]) # uncontaminated genotype 2

 p0[i,*l* ,3] <- pow(1-q[i,*l*],2) # uncontaminated genotype 3

 p1[i,*l* ,1] <- pow(q[i,*l*],4) # contaminated genotype 1

 p1[i,*l* ,2] <- 1-p1[i,*l*,1]-p1[i,*l*,3] # contaminated genotype 2

 p1[i,*l* ,3] <- pow(1-q[i,*l*],4) # contaminated genotype 3

 }

 }

}