install.packages("qtl")

library(qtl)

listeria <- read.cross("csvs", ".", "listeria\_gen.csv", "listeria\_phe.csv")

listeria

pull.map(listeria, 3)

out.2p <- scanone(listeria, model="2part", upper=TRUE)

summary(out.2p, thr=c(5,3,3), format="allpeaks")

# Plot all three LOD scores together

plot(out.2p, out.2p, out.2p, lodcolumn=c(2,3,1), lty=1, chr=c(1,5,13), col=c("red","blue","black"))