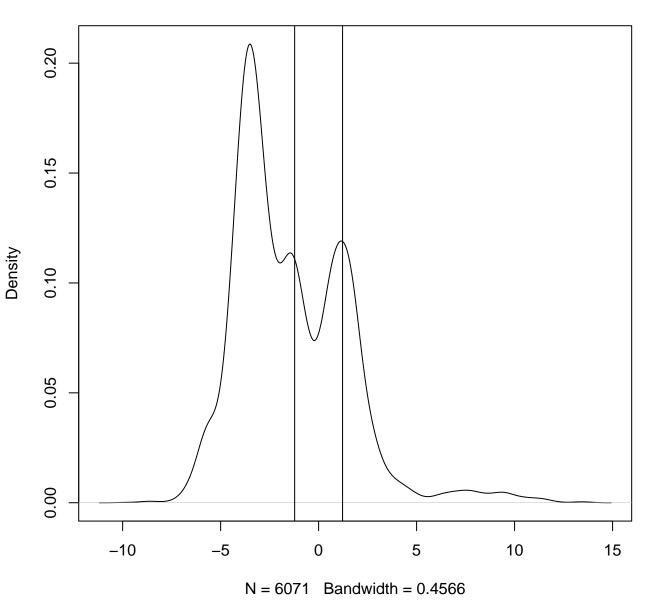
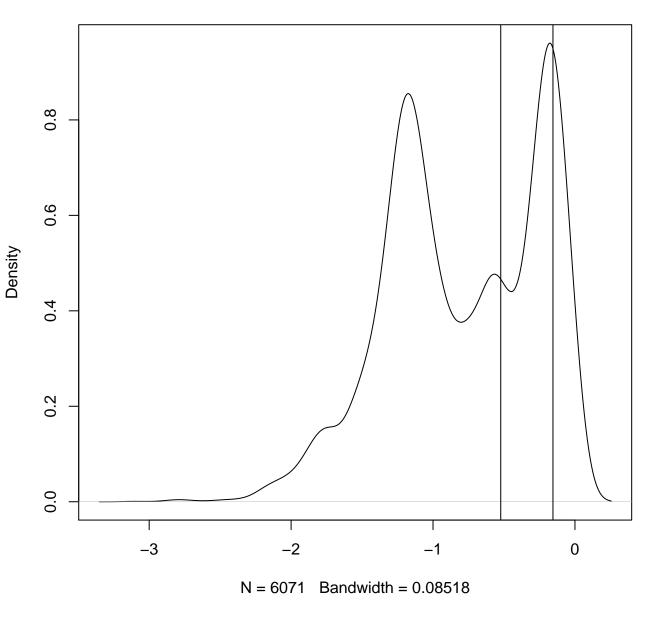
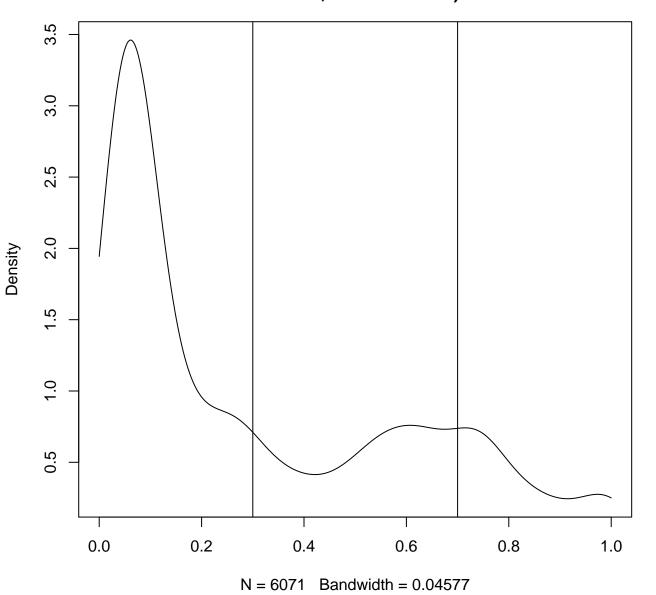


density.default(x = log2(p2r(colMeans(ratioCl[, !is.na(classIDs)]))))



density.default(x = log10((ratioCl[1, !is.na(classIDs)])), na.rm = TRUE)





density.default(x = log10((ratioCl[2, !is.na(classIDs)])), na.rm = TRUE)

