```
library(MASS)

#
# load data
#
nciRaw = scan("nci.data")
nci <- matrix(nciRaw,nrow=64,byrow=T)
p <- 6830


#
#PCA for entire data
#
pca <- prcomp(nci)
summary(pca)
plot(pca)


#
#PCA for the subset of data, containing NSCLC cancer, renal caner, melanoma cancer
#
nsclcID <- c(9:10,19,31:33,53:55)#9
renalID <- c(4,11:17)#8
melanomaID <- c(23,56,59:64)#8
nci1 <- nci[c(nsclcID,renalID,melanomaID),]
pca1 <- prcomp(nci1)
summary(pca1)
```