

```
library(limma)
library(affy)
library("mgu74av2")
targets<-readTargets()
tab <- ReadAffy(filenamees=targets$filename)
reset<-rma(ab)
treatments <- factor(c(1,1,1,2,2,2,2,2,2),labels=c("normal","cancer"))
contrasts(treatments) <- cbind(CAvsNR=c(0,1))
design <- model.matrix(~treatments)
colnames(design) <- c("Cancer","Normal")
fit <- lmFit(eset,design)
cont.matrix <- cbind(Cancer=c(1,0),Normal=c(0,1))
fit2 <- contrasts.fit(fit, cont.matrix)
fit2 <- eBayes(fit2)
write.table(topTable(fit2, coef=2, adjust="fdr", n=24976), sep="\t", "allgenes.txt")
```