**Supplementary data**

**Expression of SREBP2 and cholesterol metabolism related genes in TCGA glioma cohorts**

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**Supplementary methods:**

The complete R code is the following:

group <- read.csv("group.csv", header=T, row.names=1)

design=model.matrix(~0+factor(group$Disease))

colnames(design)=c('High','Low')

    fit=lmFit(sCLLex,design)

    cont.matrix=makeContrasts('High-Low',levels = design)

    fit2=contrasts.fit(fit,cont.matrix)

    fit2=eBayes(fit2)

    options(digits = 4)

    topTable(fit2,adjust='BH')