

Supplementary Document 4. The detailed correlation analysis between EGFR expression and individual immune cell infiltration levels by the Spearman method.

The detailed correlation analysis between EGFR expression and individual immune cell infiltration levels by the Spearman method as follows:

```
library(limma)
library(ggplot2)
library(ggpubr)
library(ggExtra)

gene="EGFR"
pFilter=0.05
expFile="symbol.txt"
setwd("C:\\bio\\Gene\\17.cor")

rt=read.table(expFile, header=T, sep="\t", check.names=F)
rt=as.matrix(rt)
rownames(rt)=rt[,1]
exp=rt[,2:ncol(rt)]
dimnames=list(rownames(exp), colnames(exp))
data=matrix(as.numeric(as.matrix(exp)), nrow=nrow(exp),
dimnames=dimnames)
data=avereps(data)
data=data[rowMeans(data)>1,]

group=sapply(strsplit(colnames(data), "\\-"), "[", 4)
group=sapply(strsplit(group, ""), "[", 1)
group=gsub("2", "1", group)
data=data[,group==0]
data=log2(data+1)

x=as.numeric(data[gene,])
outTab=data.frame()
for(j in rownames(data)){
  if(gene==j){next}
  y=as.numeric(data[j,])
  corT=cor.test(x, y, method = 'Spearman')
  cor=corT$estimate
  pvalue=corT$p.value
  outTab=rbind(outTab, cbind(Query=gene, Gene=j, cor, pvalue))
  if((abs(cor)>corFilter) & (pvalue<pFilter)){
    df1=as.data.frame(cbind(x, y))
    p1=ggplot(df1, aes(x, y)) +
      xlab(paste0(gene, " expression"))+ ylab(paste0(j, "
expression"))+
      geom_point()+ geom_smooth(method="lm", formula=y~x) +
```

```
theme_bw()+
  stat_cor(method = 'pearson', aes(x =x, y =y))
  pdf(file=paste0("cor.", j, ".pdf"), width=5, height=4.6)
  print(p1)
  dev.off()
}
}

write.table(file="corResult.txt", outTab, sep="\t", quote=F,
row.names=F)
outTab=outTab[abs(as.numeric(outTab$cor))>corFilter &
as.numeric(outTab$pvalue)<pFilter, ]
write.table(file="corSig.txt", outTab, sep="\t", quote=F, row.names=F)
```