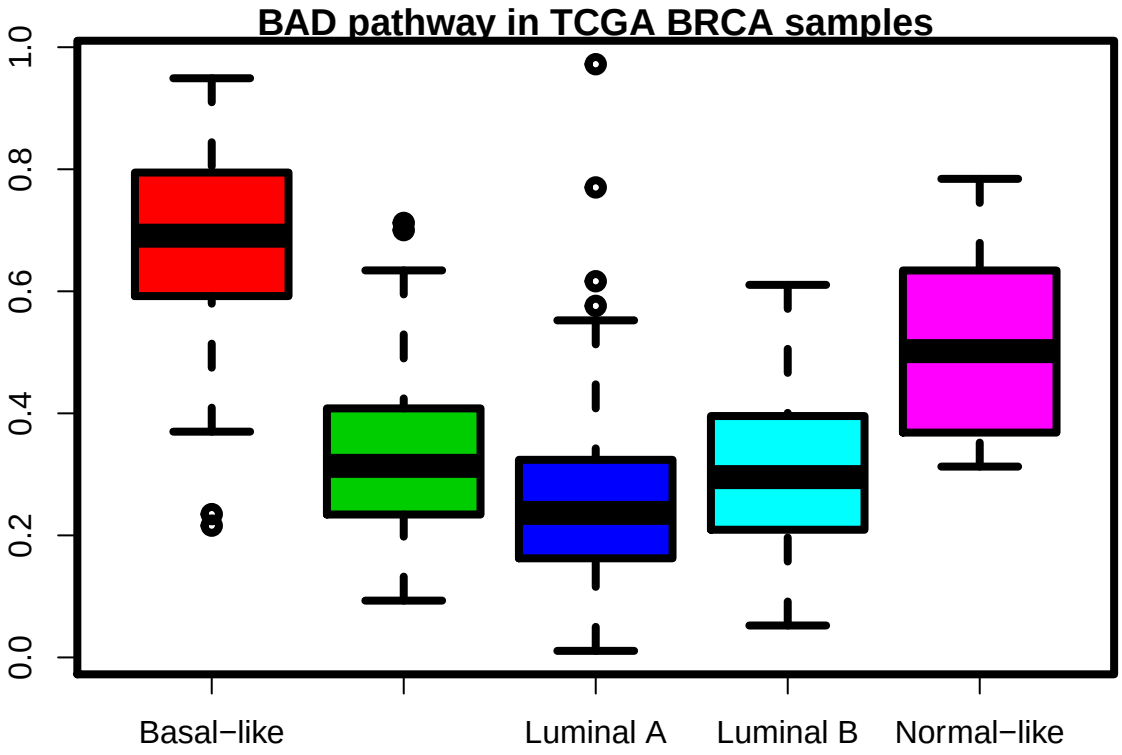
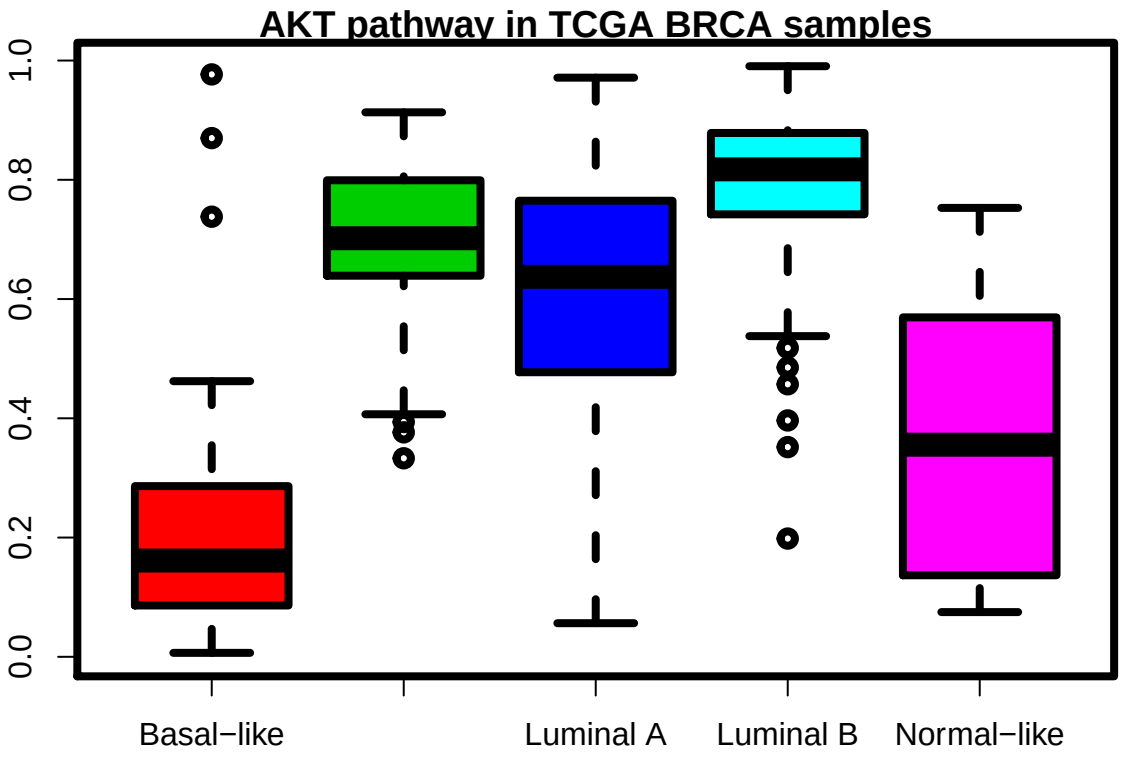
Heatmaps of pathway predictions in TCGA BRCA samples based on subtypes

Creating heatmaps for predictions within subtypes

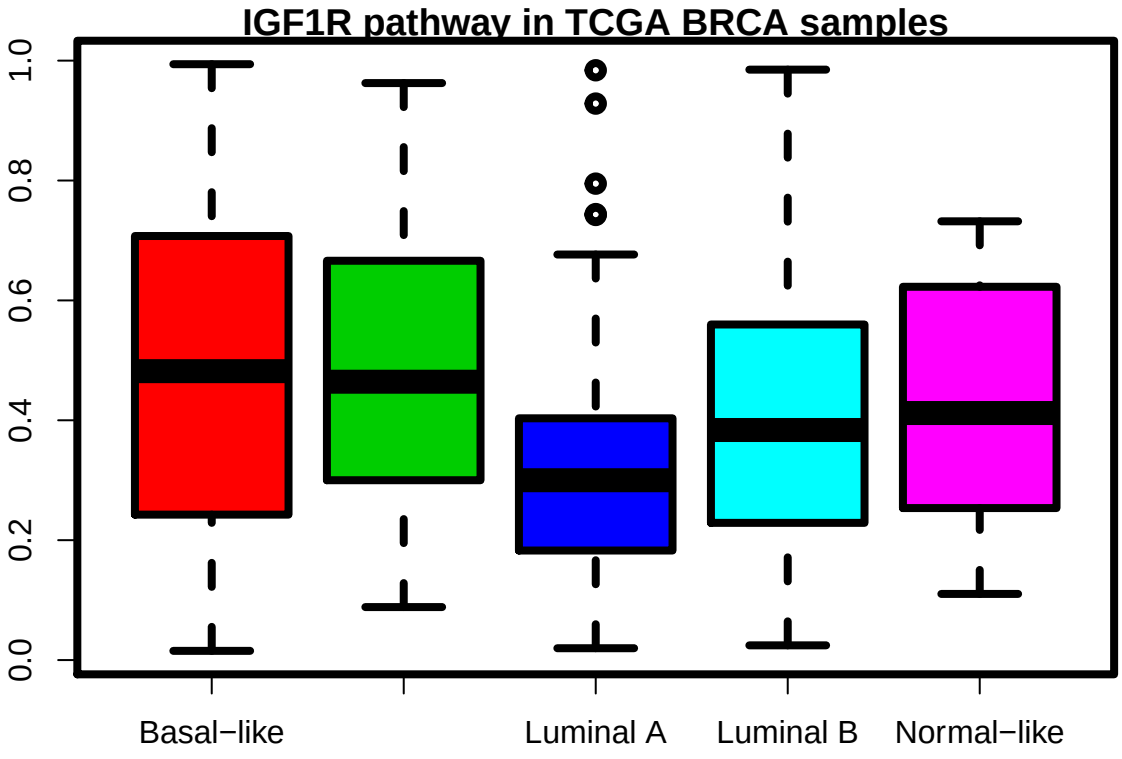
```
par(mar=c(5,5, 1, 0.5),lwd=4)
#pdf("~/Dropbox/bild_signatures/bild_signatures/Results/TCGA_predictions.pdf")
boxplot(pred_sub[,35]~pred_sub$PAM50.mRNA.x,main="BAD pathway in TCGA BRCA samples",col = 2:6)
```



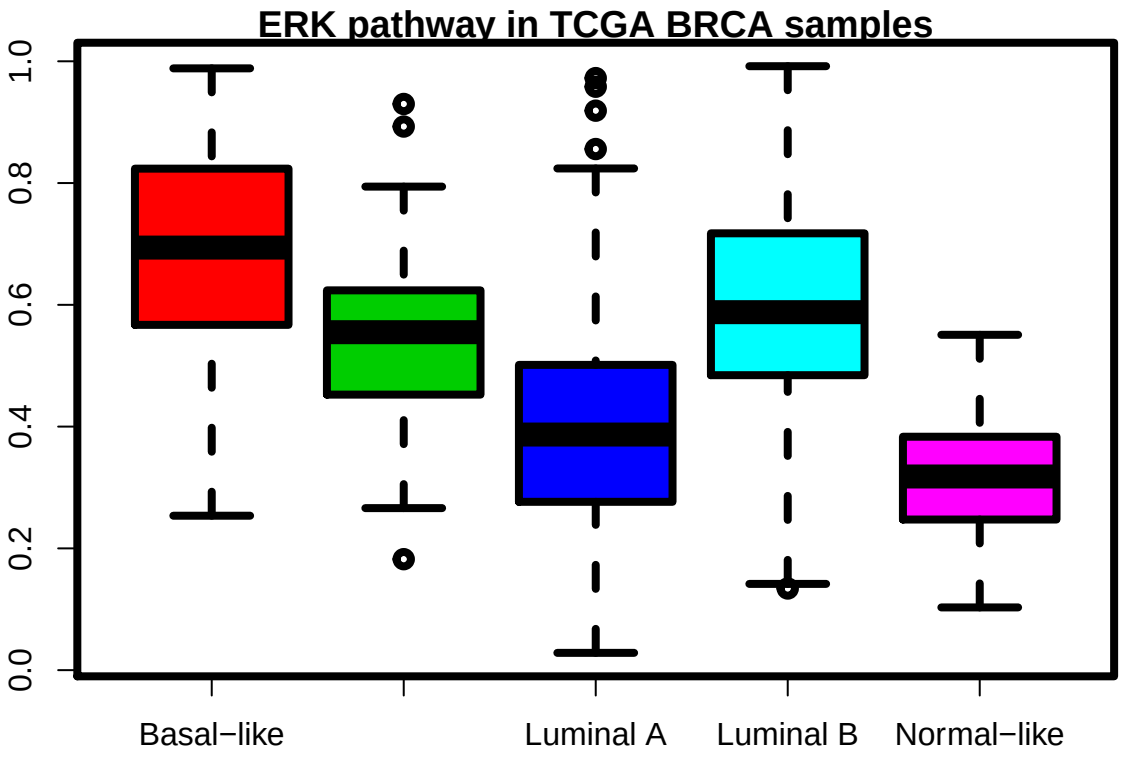

```
boxplot(pred_sub[,34]~pred_sub$PAM50.mRNA.x,main="AKT pathway in TCGA BRCA samples",col=2:6)
```



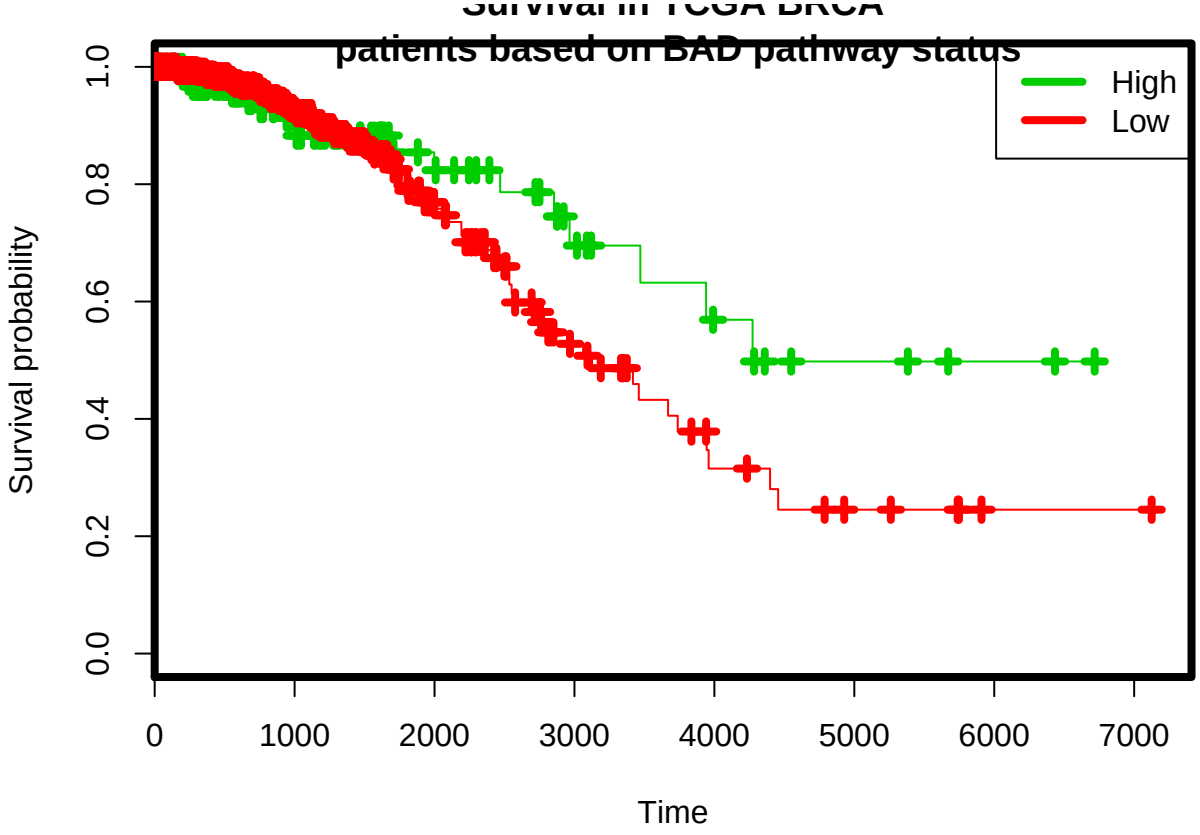

```
boxplot(pred_sub[,37]~pred_sub$PAM50.mRNA.x,main="IGF1R pathway in TCGA BRCA samples",col=2:6)
```



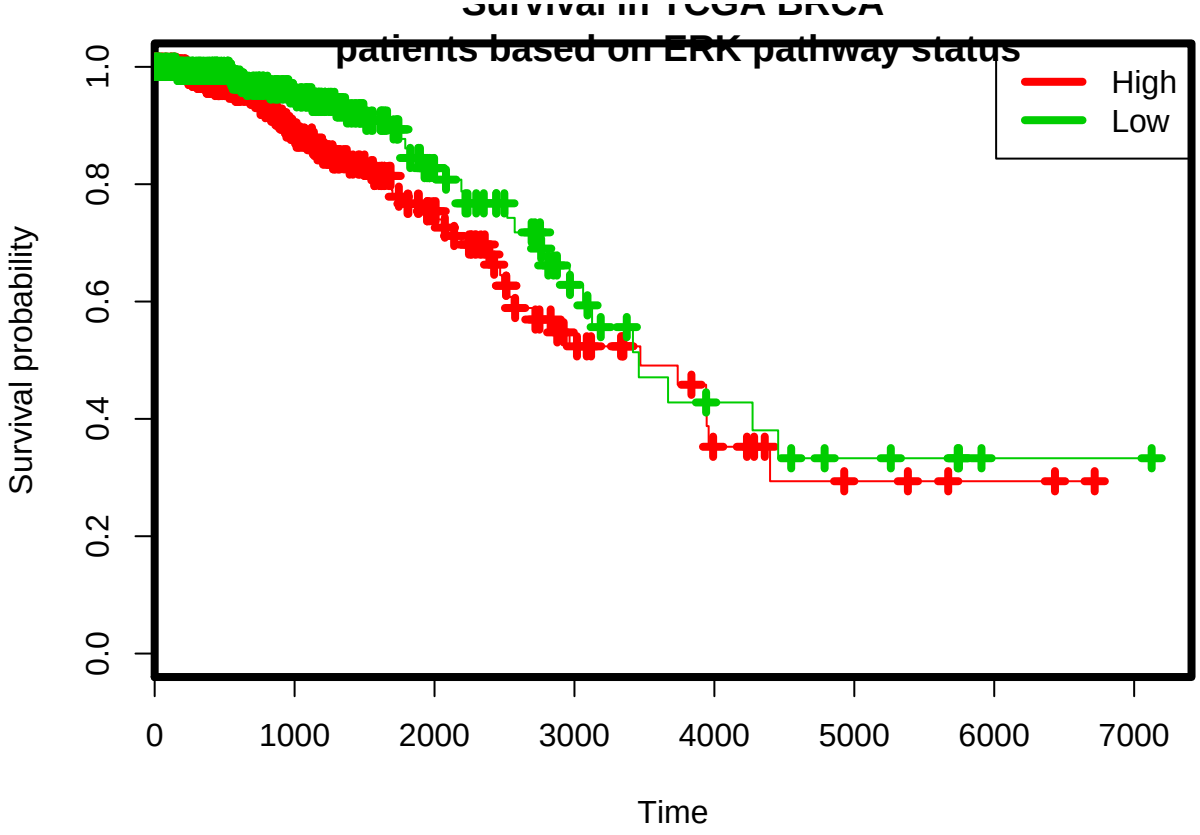

```
boxplot(pred_sub[,38]~pred_sub$PAM50.mRNA.x,main="ERK pathway in TCGA BRCA samples",col=2:6)
```



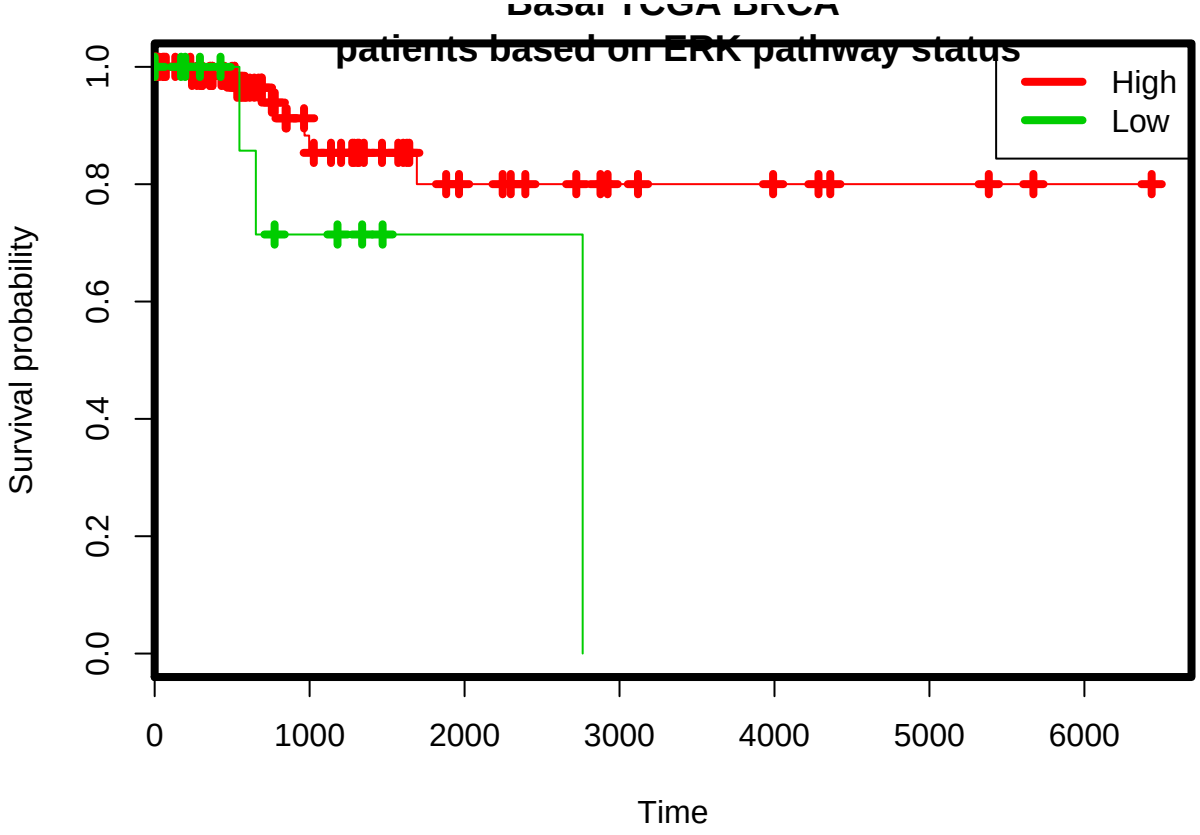

```
#boxplot(basal[,2],her[,2],luminal[,2],normal[,2])
#prediction_heatmap(x=basal,type = "Basal")
# her<-subset(pred_sub,pred_sub$PAM50.mRNA=="HER2-enriched")
# prediction_heatmap(x=her,type = "ERBB2 Amplified"
# prediction_heatmap(x=luminal,type = "Luminal")
# normal<-subset(pred_sub,pred_sub$PAM50.mRNA=="Normal-like")
# prediction_heatmap(x=normal,type = "Normal-like")
# surv<-read.table("~/Dropbox/Datasets/TCGA_BRCA_survival_tcga.txt",header=1,row.names=1,sep='\t')
best_predictors<-pred_sub[,c(34,35,37,38,145,150)]
# par(xpd=T)
#
# fit<-survfit(Surv(pred_sub$OS.Time,pred_sub$OS.event)~pred_sub$PAM50.mRNA.x)
# plot(fit,col=c(1:5), xlab="Time",ylab="Survival probability")
# legend(2.8,-1,c("Basal-like","HER2-enriched","Luminal A","Luminal B","Normal-like"),col=1:6,lwd=0.05,
bad_status<-best_predictors[,2]
for(i in 1:length(bad_status)){
  if(bad_status[i]<0.5){
    bad_status[i]="Low"}
  else{
    bad_status[i]="High"}
  }
pred_sub$bad_status<-bad_status
fit<-survfit(Surv(pred_sub$OS.Time,pred_sub$OS.event)~pred_sub$bad_status)
plot(fit,col=c(3:2), xlab="Time",ylab="Survival probability",main="Survival in TCGA BRCA\n patients bas
legend("topright",c("High","Low"),col=3:2,lwd=4,box.lwd = 1)
```



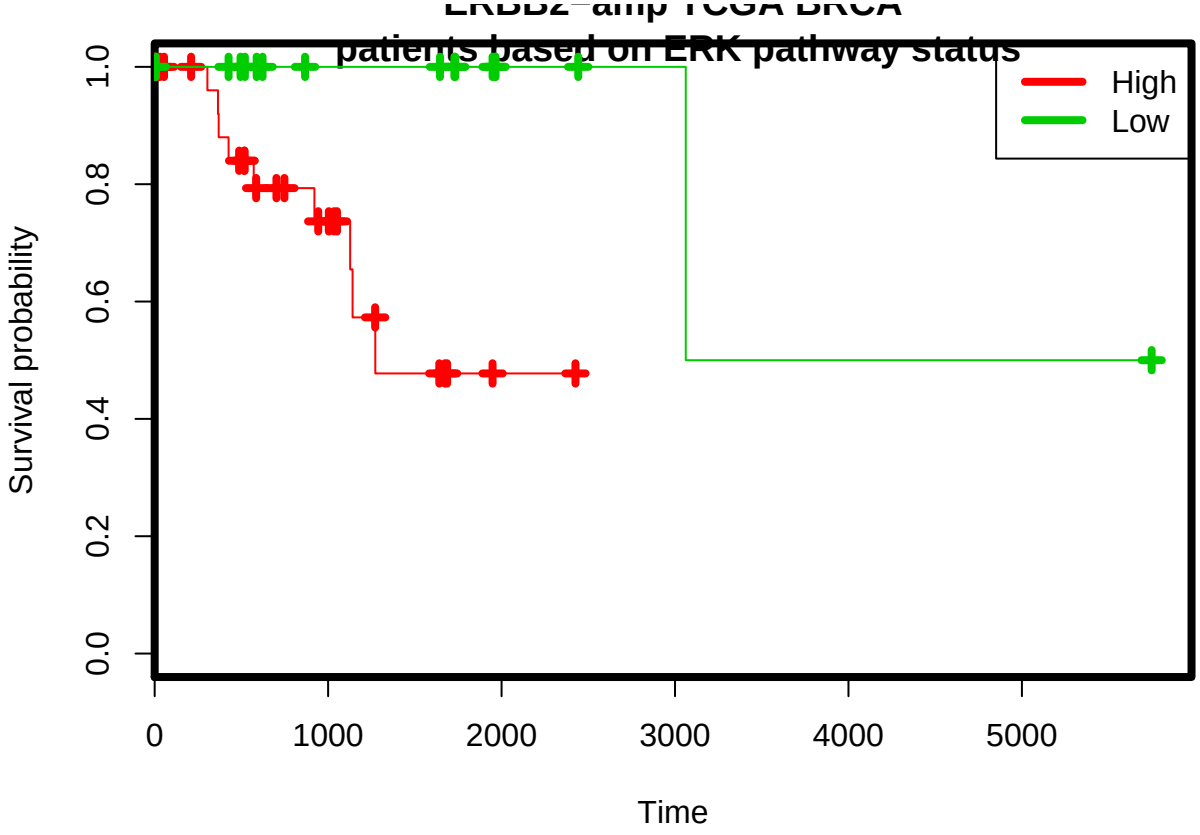

```
erk_status<-best_predictors[,4]
for(i in 1:length(erk_status)){
  if(erk_status[i]<0.5){
    erk_status[i]="Low"}
  else{
    erk_status[i]="High"}
  }
pred_sub$erk_status<-erk_status
fit<-survfit(Surv(pred_sub$OS.Time,pred_sub$OS.event)~pred_sub$erk_status)
plot(fit,col=c(2:3), xlab="Time",ylab="Survival probability",main="Survival in TCGA BRCA\n patients bas
legend("topright",c("High","Low"),col=2:3,lwd=4,box.lwd = 1)
```



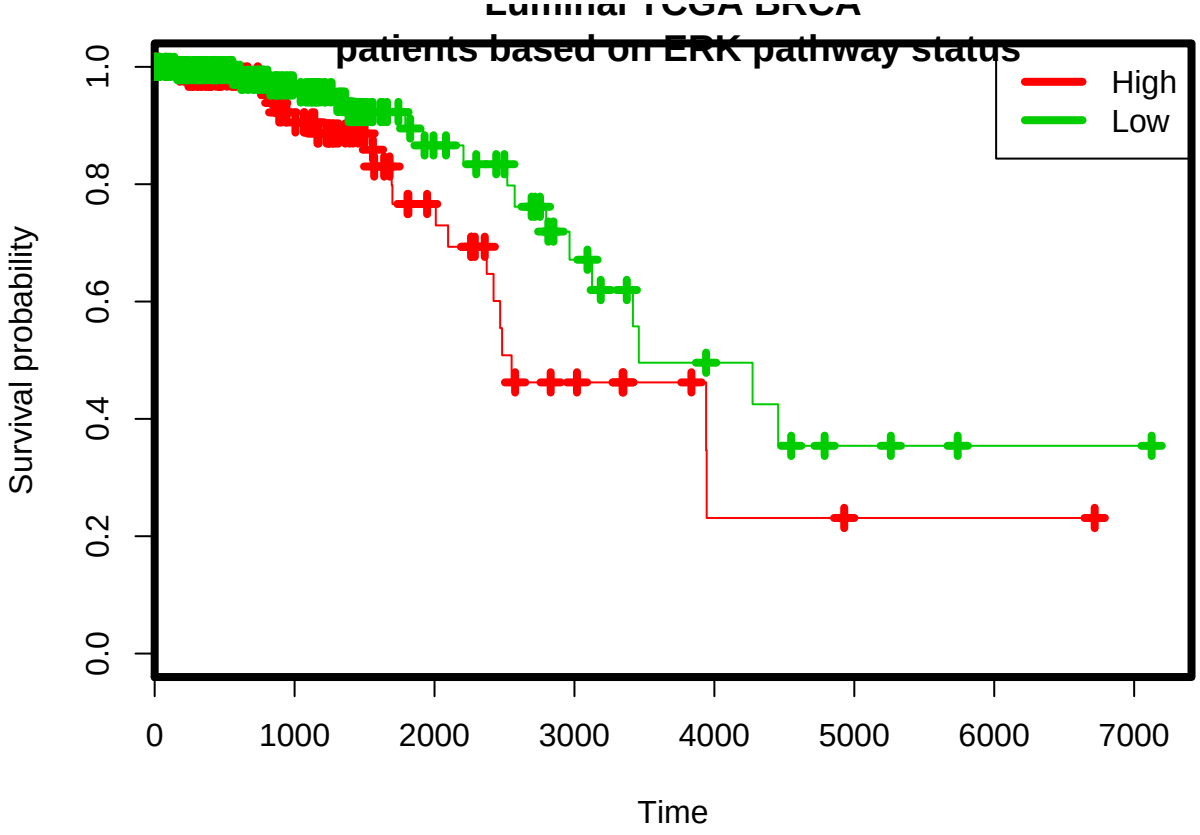

```
basal<-subset(pred_sub[,c(34,35,37,38,145,150,179,180,191,192)],pred_sub$PAM50.mRNA.x=="Basal-like")
her<-subset(pred_sub[,c(34,35,37,38,145,150,179,180,191,192)],pred_sub$PAM50.mRNA.x=="HER2-enriched")
luminal<-subset(pred_sub[,c(34,35,37,38,145,150,179,180,191,192)],pred_sub$PAM50.mRNA.x=="Luminal A"|pr
normal<-subset(pred_sub[,c(34,35,37,38,145,150,179,180,191,192)],pred_sub$PAM50.mRNA.x=="Normal-like")


fit<-survfit(Surv(basal$OS.Time,basal$OS.event)~basal$erk_status)
plot(fit,col=c(2:3), xlab="Time",ylab="Survival probability",main="Basal TCGA BRCA\n patients based on
legend("topright",c("High","Low"),col=2:3,lwd=4,box.lwd = 1)
```




```
fit<-survfit(Surv(her$OS.Time,her$OS.event)~her$erk_status)
plot(fit,col=c(2:3), xlab="Time",ylab="Survival probability",main="ERBB2-amp TCGA BRCA\n patients based
legend("topright",c("High","Low"),col=2:3,lwd=4,box.lwd = 1)
```




```
fit<-survfit(Surv(luminal$OS.Time,luminal$OS.event)~luminal$erk_status)
plot(fit,col=c(2:3), xlab="Time",ylab="Survival probability",main="Luminal TCGA BRCA\n patients based o
legend("topright",c("High","Low"),col=2:3,lwd=4,box.lwd = 1)
```




```
#dev.off()
#####Only 8 normal samples#####
# fit<-survfit(Surv(normal$OS.Time,normal$OS.event)~normal$erk_status)
# plot(fit,col=c(2:3), xlab="Time",ylab="Survival probability",main="Survival in TCGA BRCA\n patients b
# legend("topright",c("High","Low"),col=2:3,lwd=4,box.lwd = 1)
```

This analysis was run on Fri Mar 27 14:16:42 2015