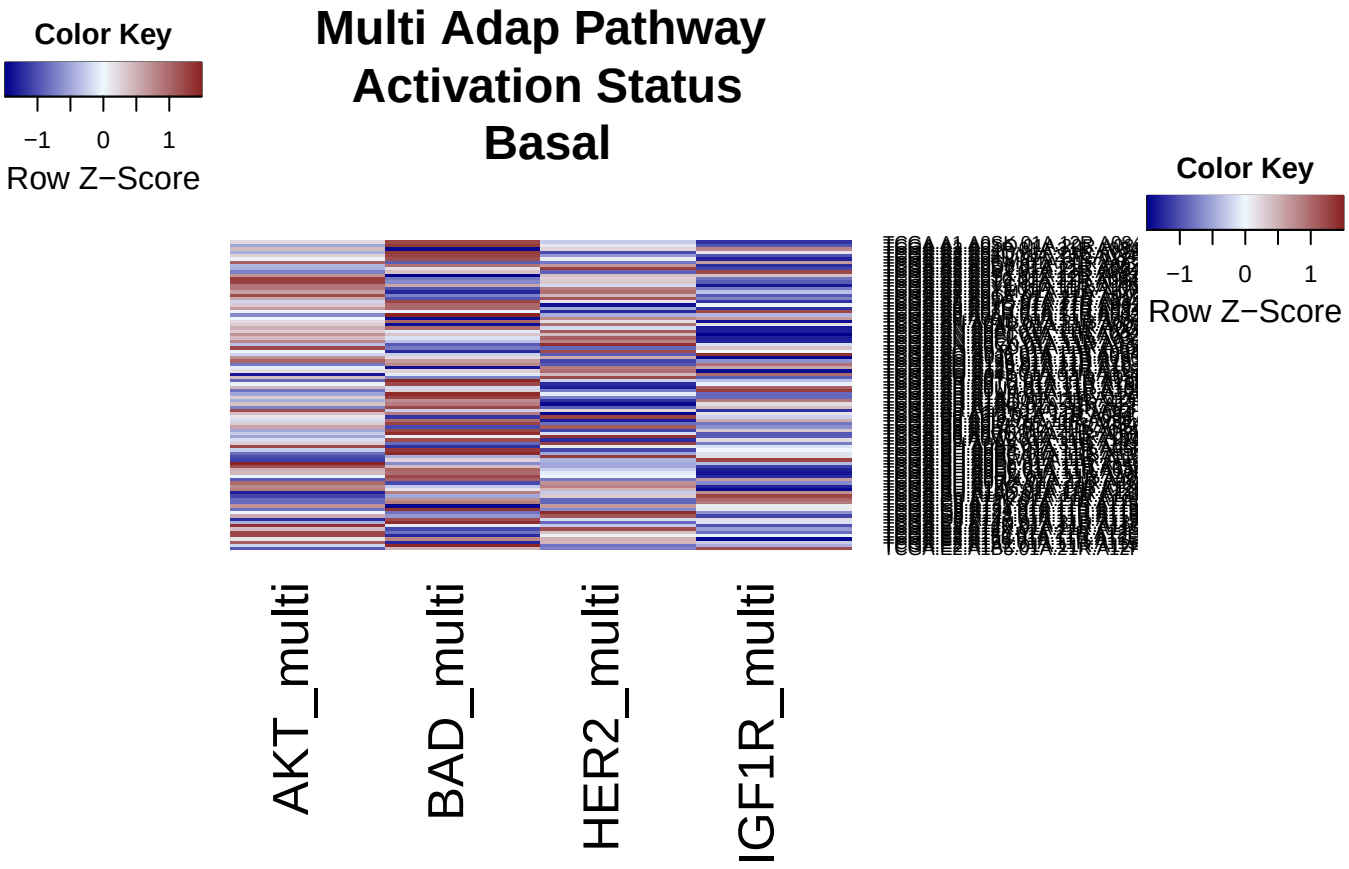
heatmaps using icbp breast cancer cell line dataset

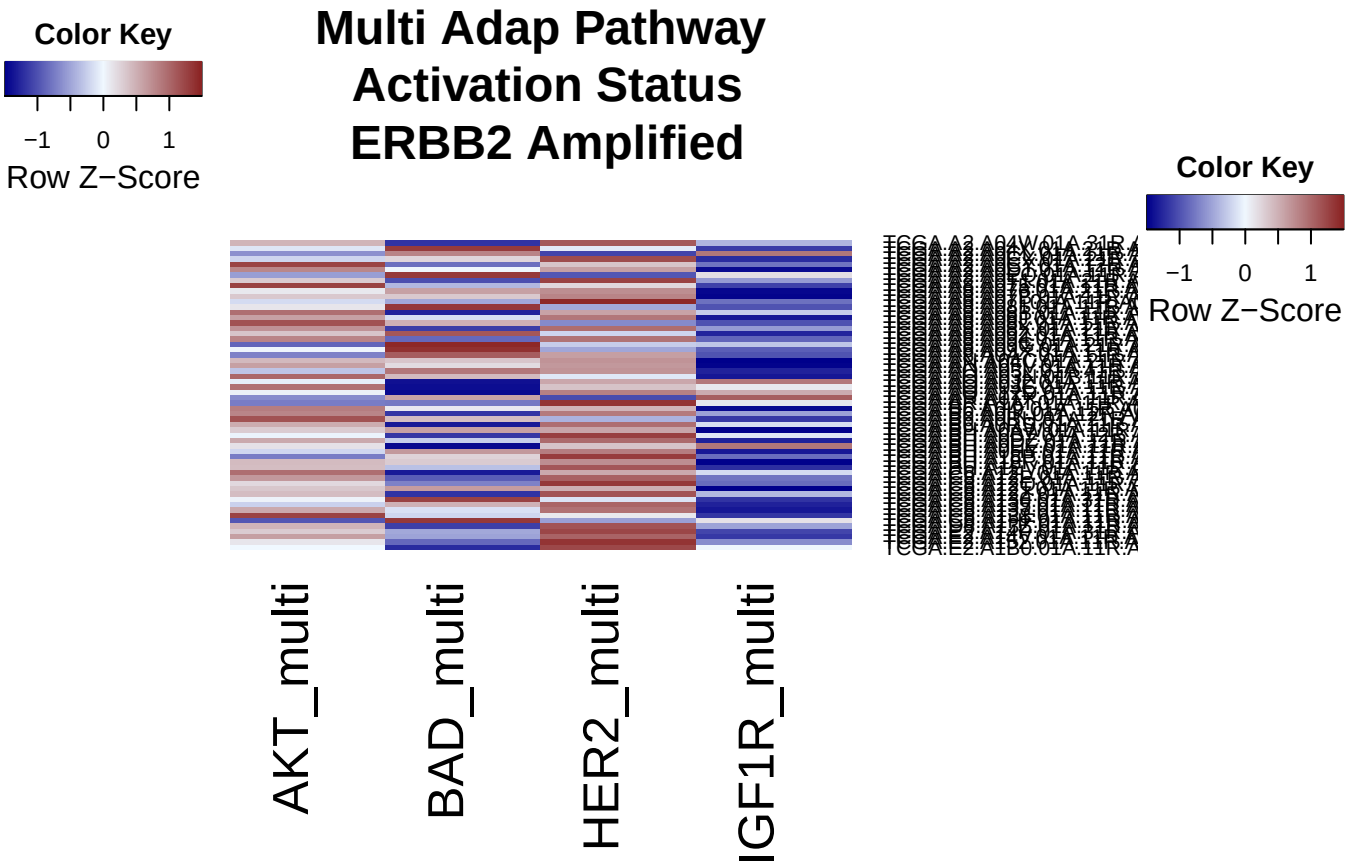
Creating heatmaps

Creating heatmaps for predictions and drug response correlatins with pathway activity within subtypes

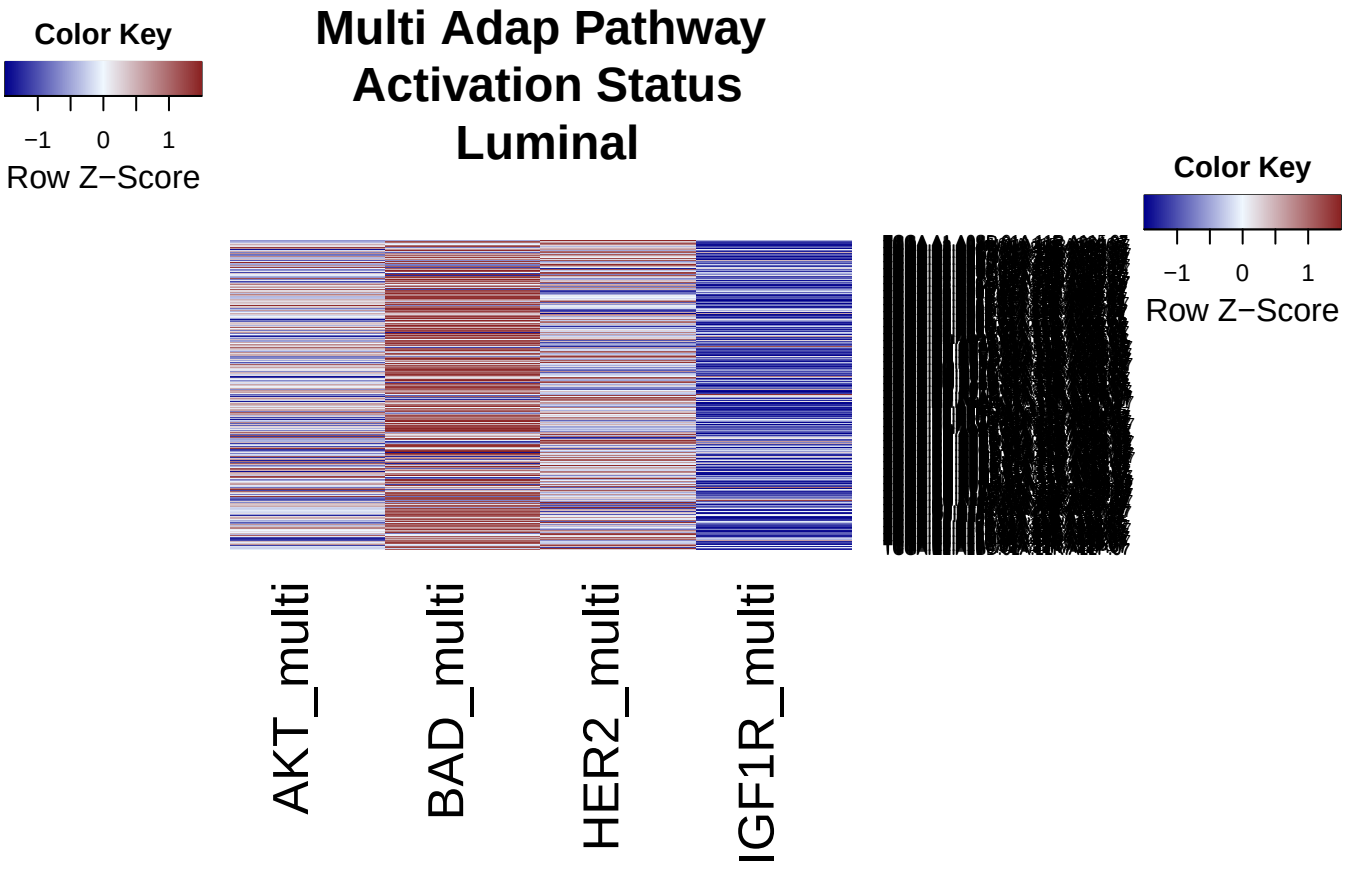
```
basal<-subset(pred_sub,pred_sub$PAM50.mRNA=="Basal-like")
prediction_heatmap(x=basal,type = "Basal")
```



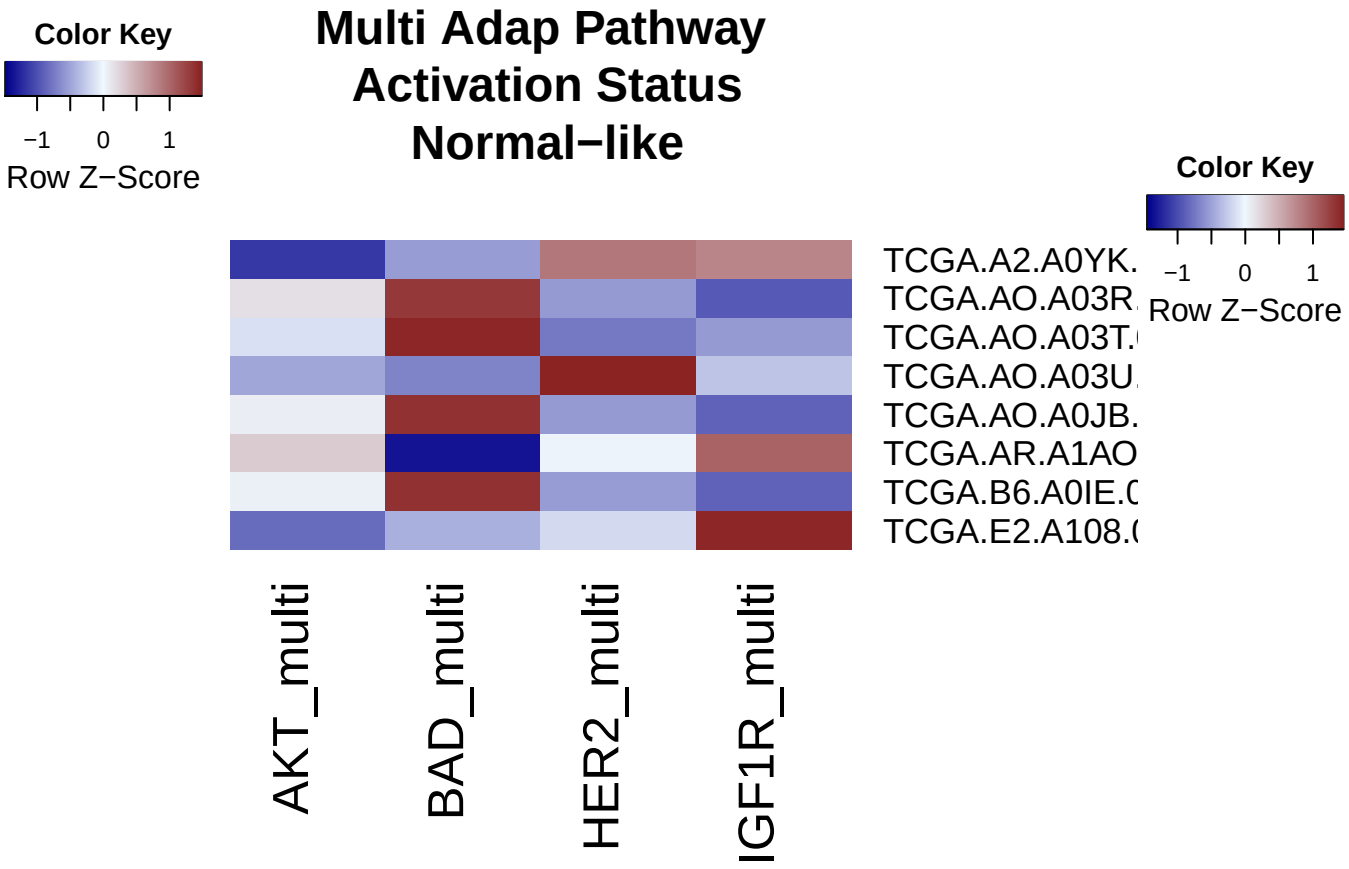

```
her<-subset(pred_sub,pred_sub$PAM50.mRNA=="HER2-enriched")
prediction_heatmap(x=her,type = "ERBB2 Amplified")
```




```
luminal<-subset(pred_sub,pred_sub$PAM50.mRNA=="Luminal A"|pred_sub$PAM50.mRNA=="Luminal B")
prediction_heatmap(x=luminal,type = "Luminal")
```

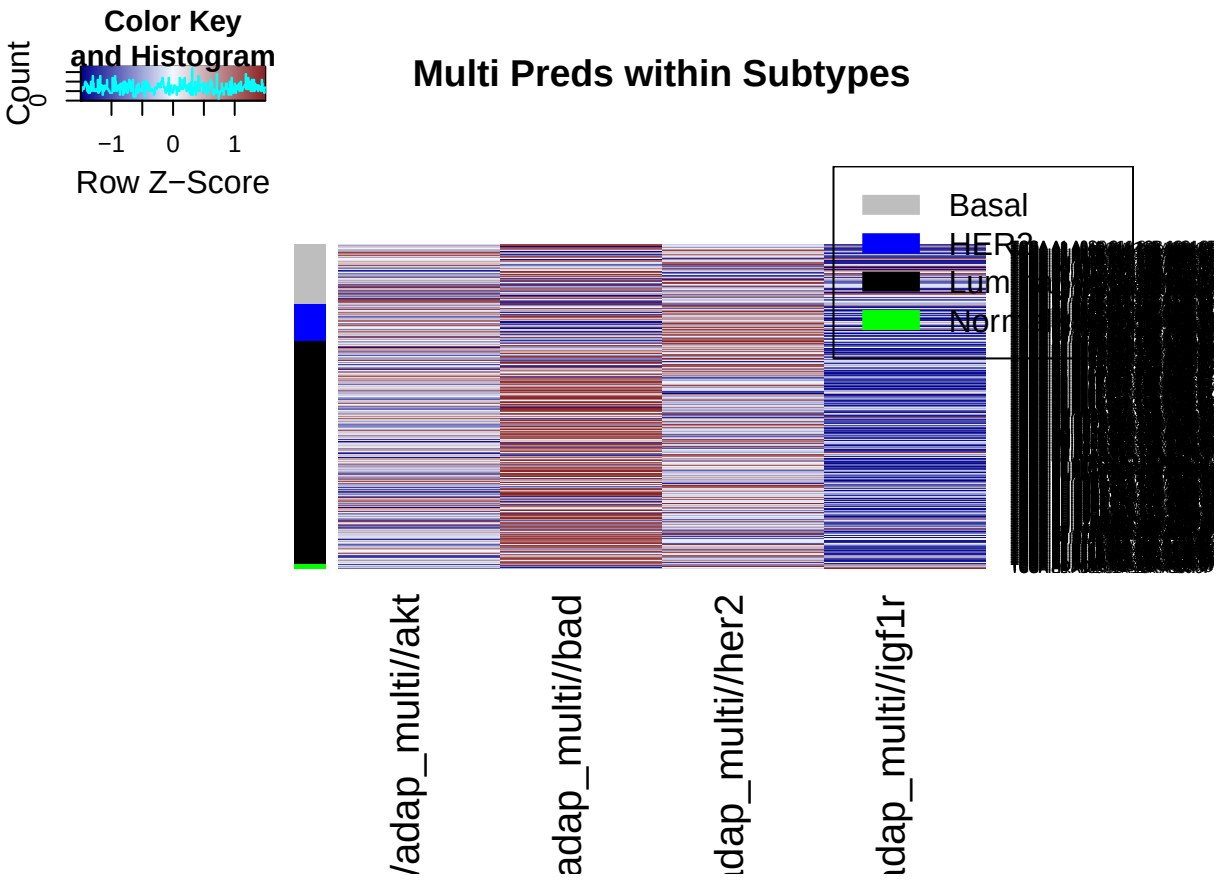



```
normal<-subset(pred_sub,pred_sub$PAM50.mRNA=="Normal-like")
prediction_heatmap(x=normal,type = "Normal-like")
```

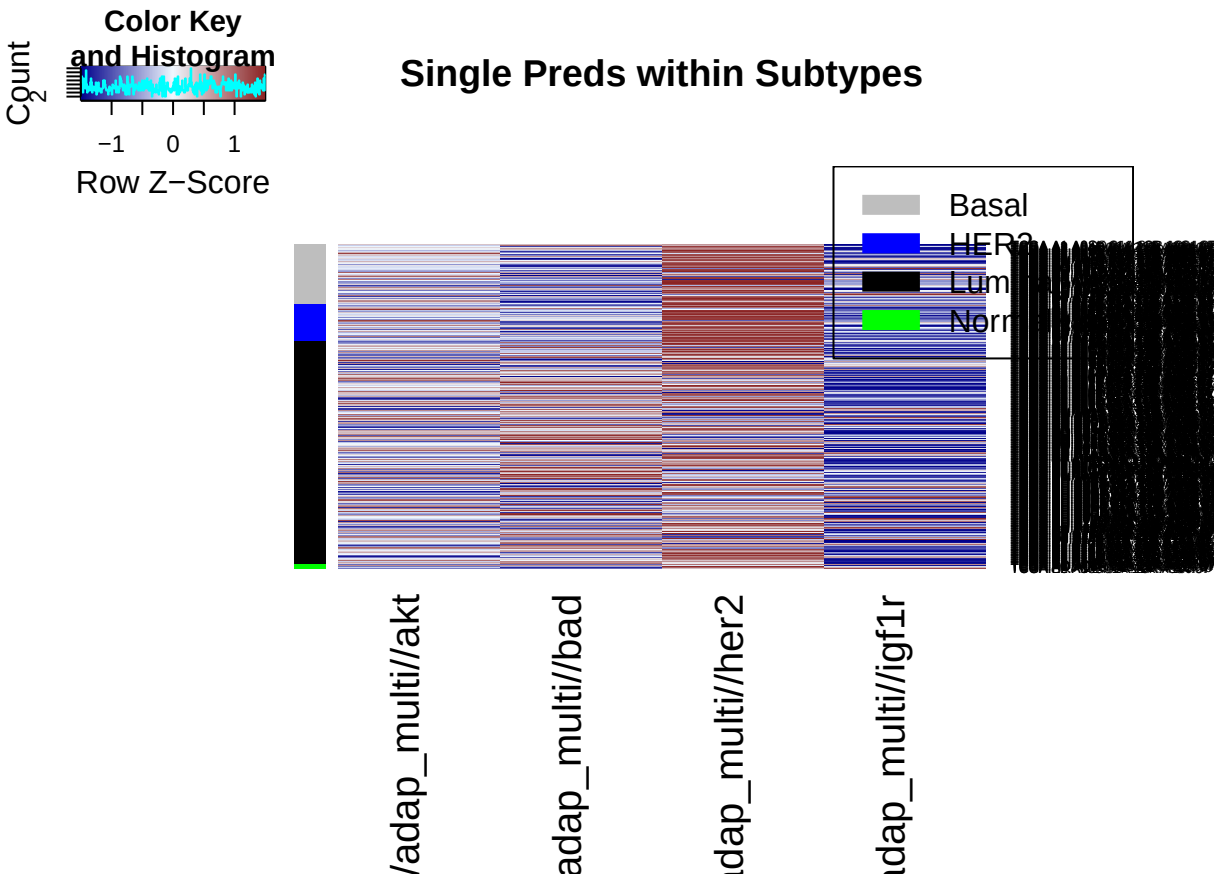


Now, trying to see patterns across all the subtypes in ICBP breast cancer cell lines

```
multi_4<- rbind(basal[,1:4],her[,1:4],luminal[,1:4],normal[,1:4])
heatmap.2(as.matrix(multi_4), RowSideColors = c(rep("gray", length(rownames(basal))),rep("blue", length
par(lend = 1)           # square line ends for the color legend
legend("topright",legend = c("Basal", "HER2", "Luminal","Normal-like"), col = c("gray", "blue", "black"
```




```
single_4<-rbind(basal[,c(9,11,13,15)],her[,c(9,11,13,15)],luminal[,c(9,11,13,15)],normal[,c(9,11,13,15)]
heatmap.2(as.matrix(single_4), RowSideColors = c(rep("gray", length(rownames(basal))),rep("blue", lengt
par(lend = 1)           # square line ends for the color legend
legend("topright",legend = c("Basal", "HER2", "Luminal","Normal-like"), col = c("gray", "blue", "black"
```



This analysis was run on Sat Jan 24 16:31:18 2015