

# multipathway\_ASSIGN

*Mumtahena Rahman*

*December 23, 2014*

Reading in the signature datasets...

Checking for correlation..

Now correlating multi pathway predictions with ICBP drugs..

Batch adjustment likely works better in this case without the EGFR signature...

Now including only AKT, HER2 and IGF1R signatures

Creating heatmaps

```
multi<-read.csv("~/Desktop/tmp/multi_icbp_expr/adap_multi/pathway_activity_testset.csv", row.names=1,header=1)
single<-read.csv("~/Desktop/tmp/single_pathway_results.csv", row.names=1,header=1)
comb<-cbind(multi,single)
dim(comb)
```

```
## [1] 55 8
```

```
library(gplots)
```

```
## Warning: package 'gplots' was built under R version 3.1.1
```

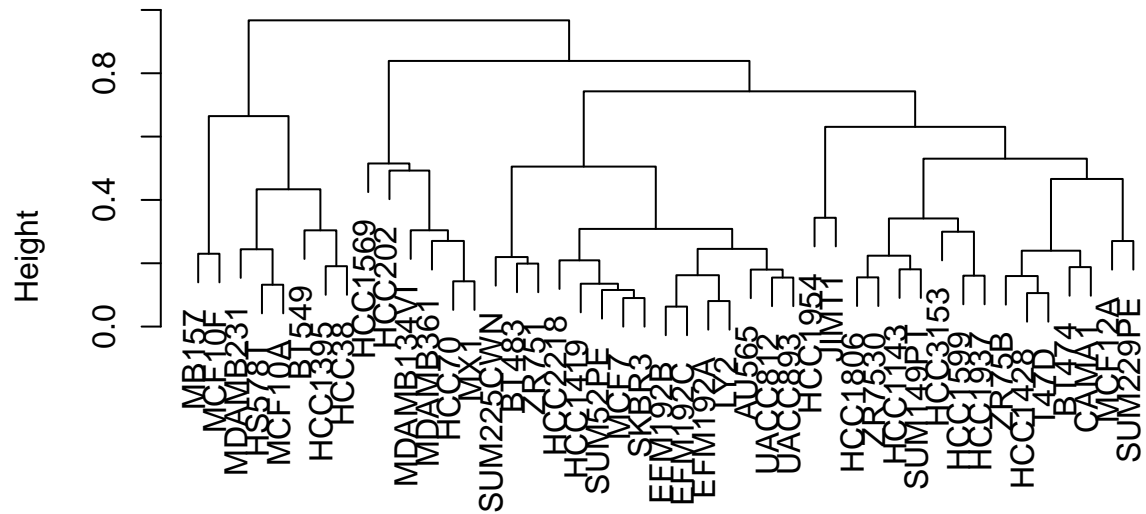
```
##
## Attaching package: 'gplots'
##
## The following object is masked from 'package:stats':
##
##      lowess
```

```
heatmap.2(as.matrix(comb[,1:4]),col=bluered,lmat=rbind( c(0, 3, 4), c(2,1,0 ) ), lwid=c(1.5, 4, 2 ), tr
```



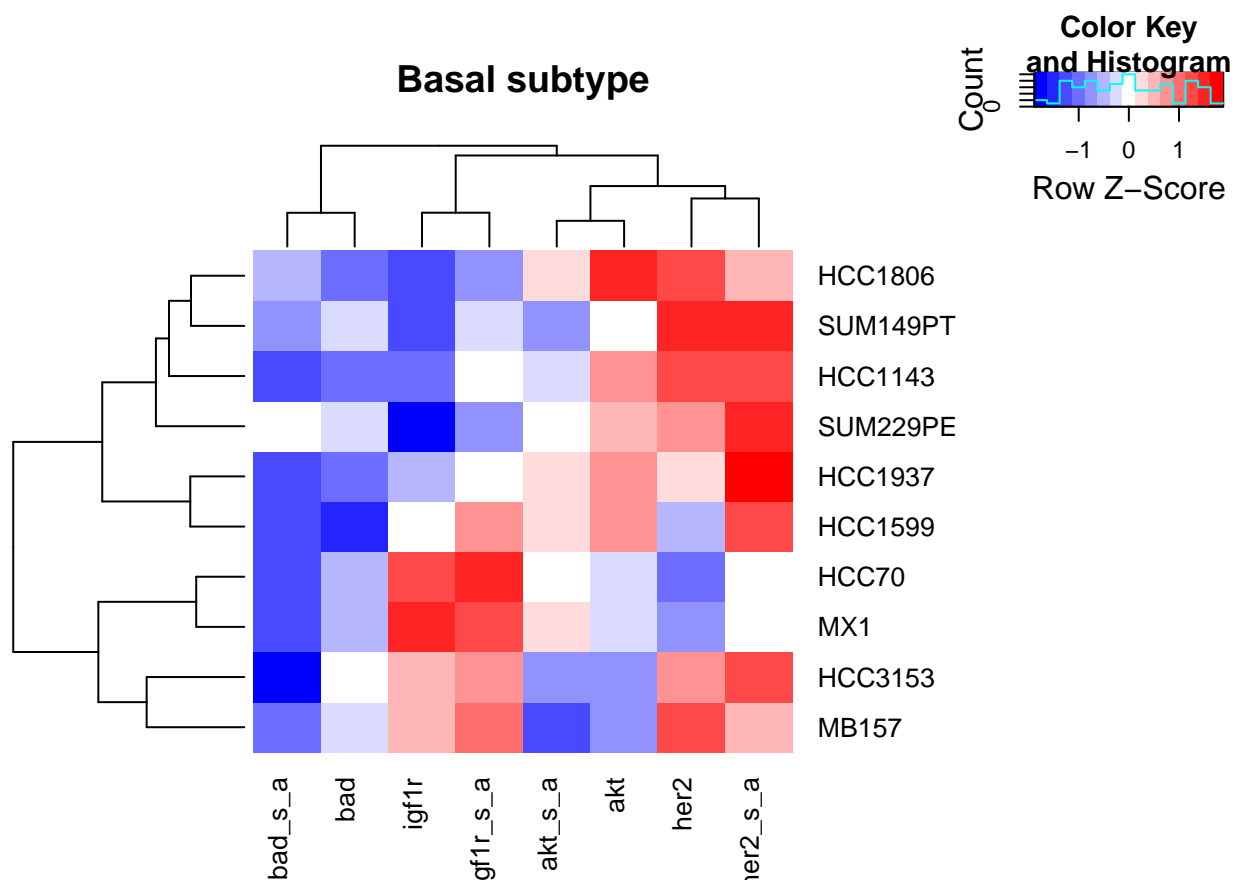


## Cluster Dendrogram

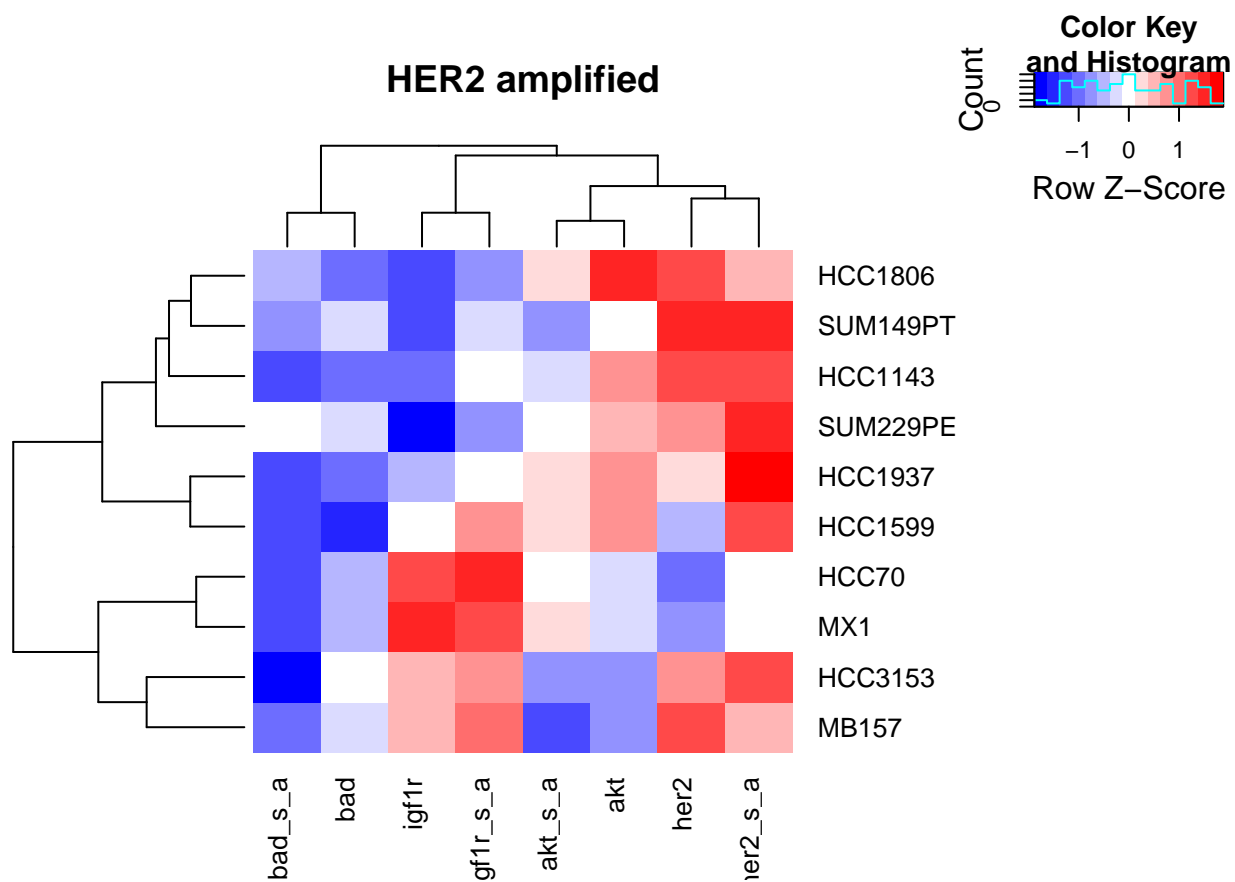


```
dist(comb_drug[, 1:8])
hclust (*, "complete")
```

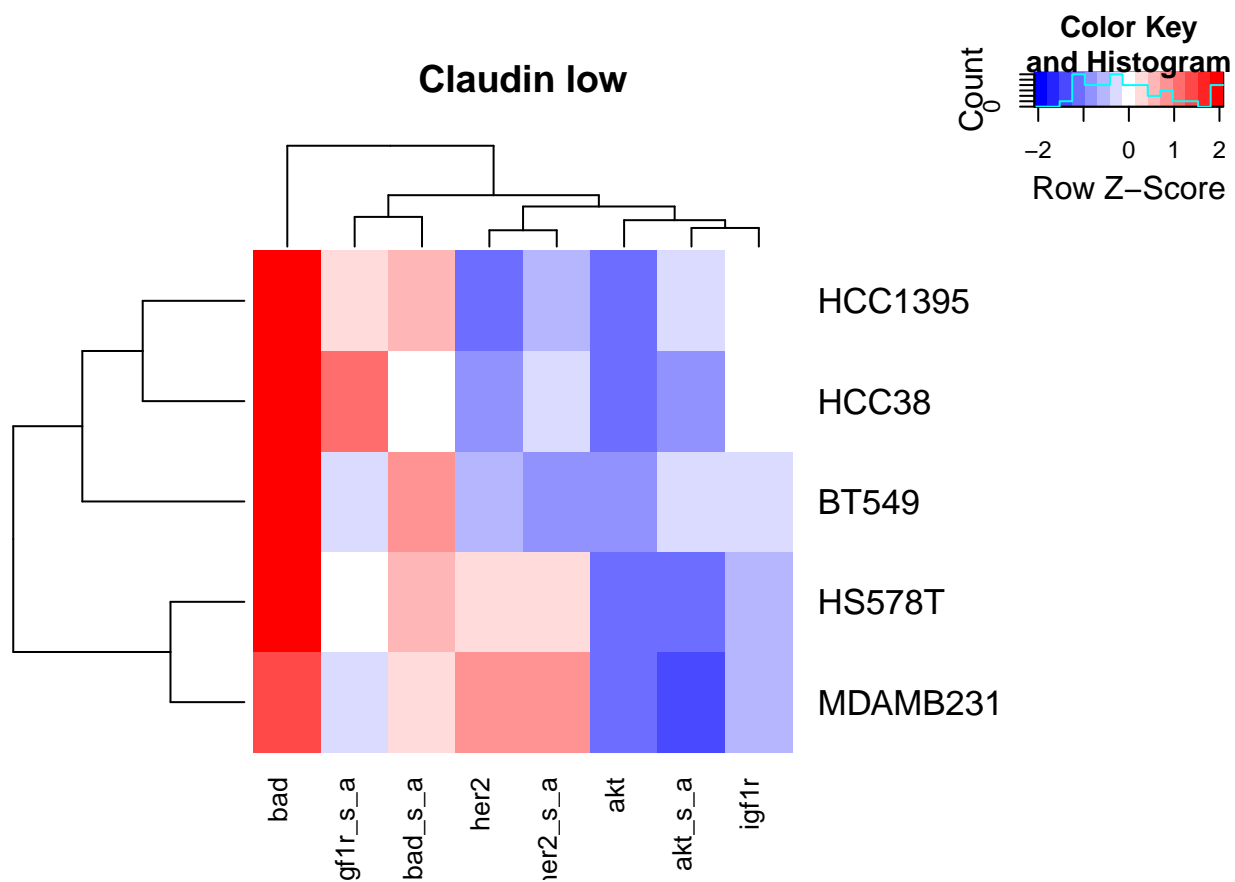
```
basal<-subset(comb_drug[,1:8],comb_drug$Transcriptional.subtype...ERBB2.status=="Basal")
heatmap.2(as.matrix(basal),col=bluered,lm=rbind( c(0, 3, 4), c(2,1,0) ), lwid=c(1.5, 4, 2 ), trace="")
```



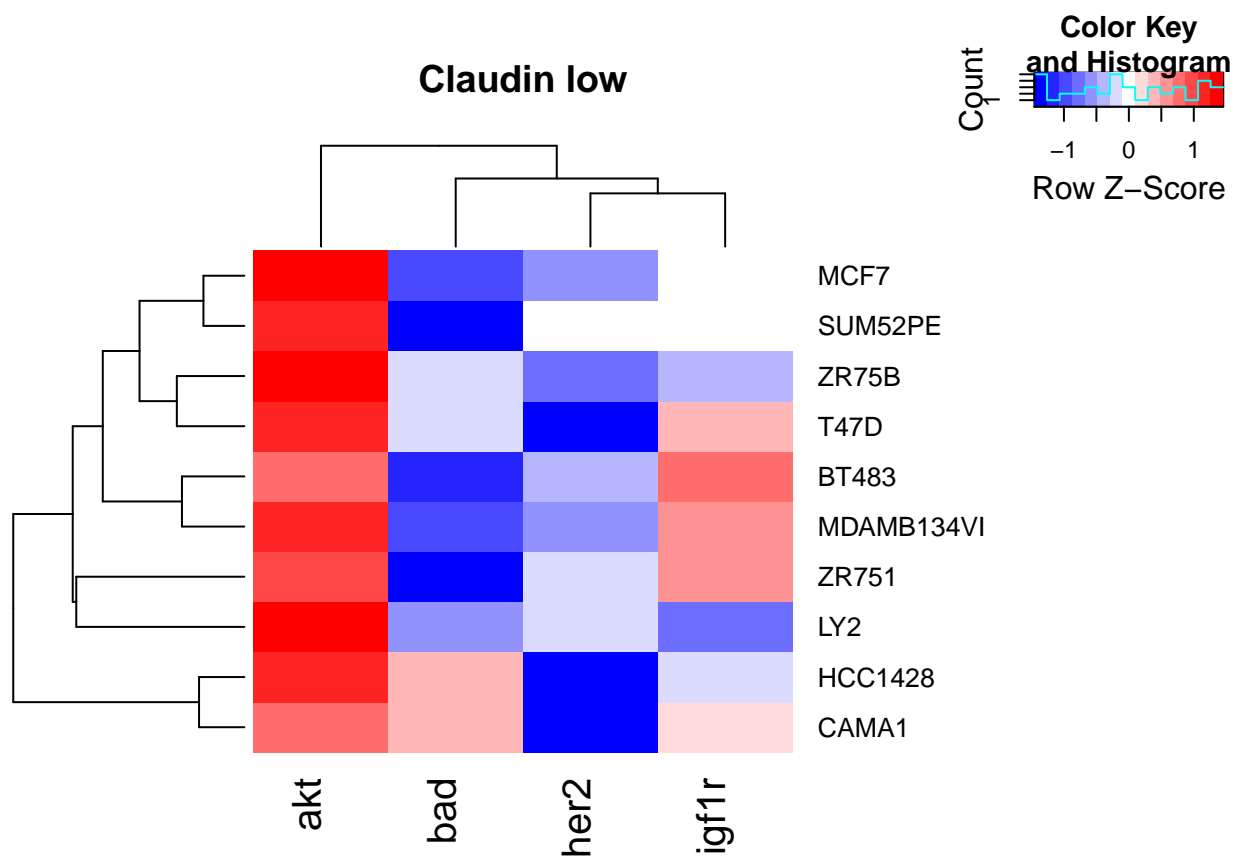
```
her<-subset(comb_drug[,1:8],comb_drug$Transcriptional.subtype...ERBB2.status=="ERBB2-amp"|comb_drug$Tra
heatmap.2(as.matrix(basal),col=bluered,lm=rbind( c(0, 3, 4), c(2,1,0) ), lwid=c(1.5, 4, 2 ), trace="")
```



```
claudin<-subset(comb_drug[,1:8],comb_drug$Transcriptional.subtype...ERBB2.status=="Claudin-low")
heatmap.2(as.matrix(claudin),col=bluered,lmat=rbind( c(0, 3, 4), c(2,1,0) ), lwid=c(1.5, 4, 2 ), trace=
```



```
luminal<-subset(comb_drug[,1:4],comb_drug$Transcriptional.subtype...ERBB2.status=="Luminal")
heatmap.2(as.matrix(luminal),col=bluered,lmat=rbind( c(0, 3, 4), c(2,1,0) ), lwid=c(1.5, 4, 2 ), trace=
```



This analysis was run on Mon Dec 29 01:01:20 2014