

# Project02 - Group01

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## data loading

## data scaling

After checking for normalization, we scaled our data in the first place to provide the scaled data for further analysis.

## 3. Main questions

### Question 1: Predicted GI50-values

As we mentioned in our presentation, we want to create a model to predict GI50-values thus to predict, if Lapatinib is a good choice., The first linear model tries to predict the G-50 value under the data of the doubling time.

```
Fold_ChangeLap = select(Fold_Change, contains("Lapa"))
NegLogGI50Lap = NegLogGI50[,9,]
means = colMeans(Fold_ChangeLap)
Fold_Changemeans = as.data.frame(t(means))

a2 = gsub(x = colnames (Fold_Changemeans), pattern = "_lapatinib_10000nM_24h", replacement = "")
colnames(Fold_Changemeans) = a2

a3 = gsub(x = a2, pattern = "X7", replacement = "7")
colnames(Fold_Changemeans) = a3

a1 = gsub(x = colnames (NegLogGI50Lap), pattern = "-", replacement = ".")
colnames(NegLogGI50Lap) = a1

c1 = rbind(a1,NegLogGI50Lap)
c2 = rbind(a3,Fold_Changemeans)

c1 = t(c1)
c2 = t(c2)

c1 =as.data.frame(c1)
c2 =as.data.frame(c2)

c3 = subset(c1, `1` %in% intersect(c1$`1`, c2$V1))
c4 = as.numeric(as.character(c3$lapatinib))
adjustedNeglogI50Lap = as.data.frame(c4)

Fold_Changemeans = as.data.frame(t(Fold_Changemeans))

combined1 = cbind(adjustedNeglogI50Lap, Fold_Changemeans)

names1 = c( "NegLogI50Lap", "Fold_Changemeans")
colnames(combined1) = names1

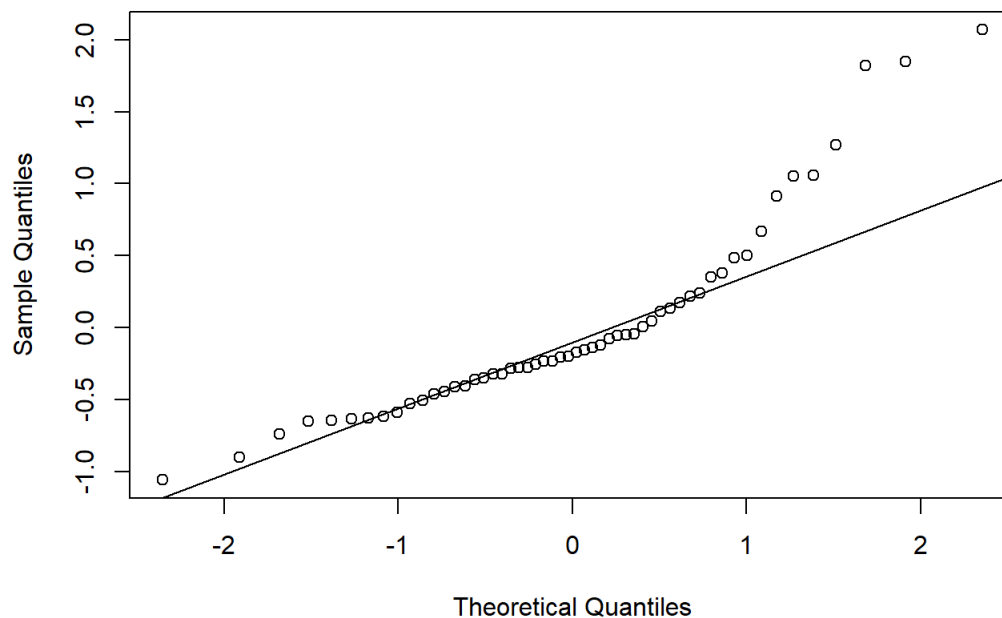
lmFold = lm(NegLogI50Lap ~ Fold_Changemeans, data = combined1)

summary(lmFold)
```

```
##
## Call:
## lm(formula = NegLogI50Lap ~ Fold_Changemeans, data = combined1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0574 -0.4099 -0.1873  0.2076  2.0682
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.464e+00  9.539e-02  57.281  <2e-16 ***
## Fold_Changemeans 1.913e+15  7.519e+14   2.544   0.014 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6822 on 52 degrees of freedom
## Multiple R-squared:  0.1107, Adjusted R-squared:  0.09355
## F-statistic:  6.47 on 1 and 52 DF,  p-value: 0.01398
```

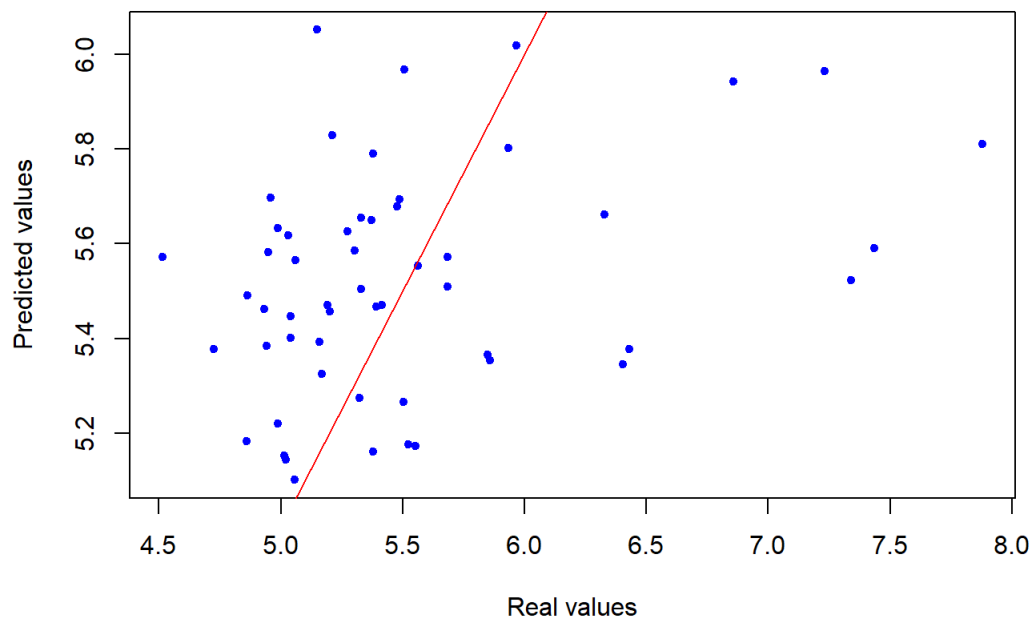
```
qqnorm(lmFold$residuals, main = "Test for normaldistribution of residuals")
qqline(lmFold$residuals)
```

### Test for normaldistribution of residuals



```
plot(combined1$NegLogI50Lap, lmFold$fitted.values, pch = 20, col = "blue", xlab = "Real values",
      ylab = "Predicted values", main = "Comparison: real and predicted values ~ linear regression (Fold_Changemeans)")
abline(0, 1, col = "red")
```

## Comparison: real and predicted values ~ linear regression (Fold\_Changemeans)



```
cor(combined1$NegLogI50Lap,combined1$Fold_Changemeans)
```

```
## [1] 0.3326477
```

```
#Split the data (Training - Testing)
```

```
n = nrow(combined1)
rmse1 = sqrt(1/n * sum(lmFold$residuals^2))
rmse1
```

```
## [1] 0.6694461
```

```
il.train = sample(1:nrow(combined1), 44)
```

```
dat1.train = combined1[il.train, ]
dat1.test = combined1[-il.train, ]
```

```
l1.train = lm(NegLogI50Lap ~ Fold_Changemeans, data = dat1.train)
summary(l1.train)
```

```
##
## Call:
## lm(formula = NegLogI50Lap ~ Fold_Changemeans, data = dat1.train)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0928 -0.4019 -0.2109  0.2030  2.0015
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.485e+00  1.082e-01  50.704  <2e-16 ***
## Fold_Changemeans 2.164e+15  9.354e+14   2.313   0.0257 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.699 on 42 degrees of freedom
## Multiple R-squared:  0.113, Adjusted R-squared:  0.09187
## F-statistic:  5.35 on 1 and 42 DF, p-value: 0.02569
```

```
n = nrow(dat1.train)
rmse1.train = sqrt(1/n * sum(l1.train$residuals^2))
rmse1.train
```

```
## [1] 0.6828938
```

```
pred1 = predict(l1.train, newdata = dat1.test)
```

```
n = nrow(dat1.test)
residuals = dat1.test$NegLogI50Lap - pred1
rmse1.test1 = sqrt(1/n * sum(residuals^2))
rmse1.test1
```

```
## [1] 0.6145976
```

The second linear model tries to predict the G-50 value under the data of the Foldchange-means.

```
NegLogGI50Lap = NegLogGI50[9,]

#Sort by Cellline-Name
df = arrange(Cellline_Annotation, Cell_Line_Name)
Doublingtime = cbind.data.frame (df$Cell_Line_Name, df$Doubling_Time)

c21 = as.data.frame(t(NegLogGI50Lap))

combined2 = cbind(c21, Doublingtime$`df$Doubling_Time`)
names2 = c( "NegLogI50Lap", "Doubling_Time")
colnames(combined2) = names2

combined2 =na.omit(combined2)

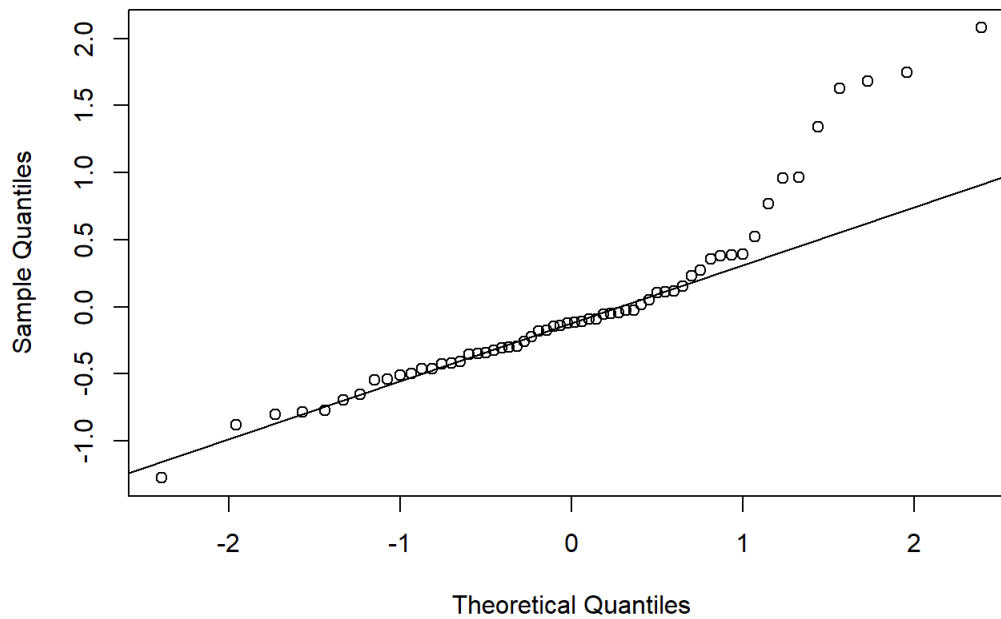
lmDouble = lm(NegLogI50Lap ~ Doubling_Time, data = combined2)

summary(lmDouble)
```

```
##
## Call:
## lm(formula = NegLogI50Lap ~ Doubling_Time, data = combined2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2751 -0.4124 -0.1210  0.1709  2.0784
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.147415   0.245361  20.979  <2e-16 ***
## Doubling_Time 0.010536   0.006391   1.649   0.105
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6741 on 58 degrees of freedom
## Multiple R-squared:  0.04476,    Adjusted R-squared:  0.0283
## F-statistic: 2.718 on 1 and 58 DF,  p-value: 0.1046
```

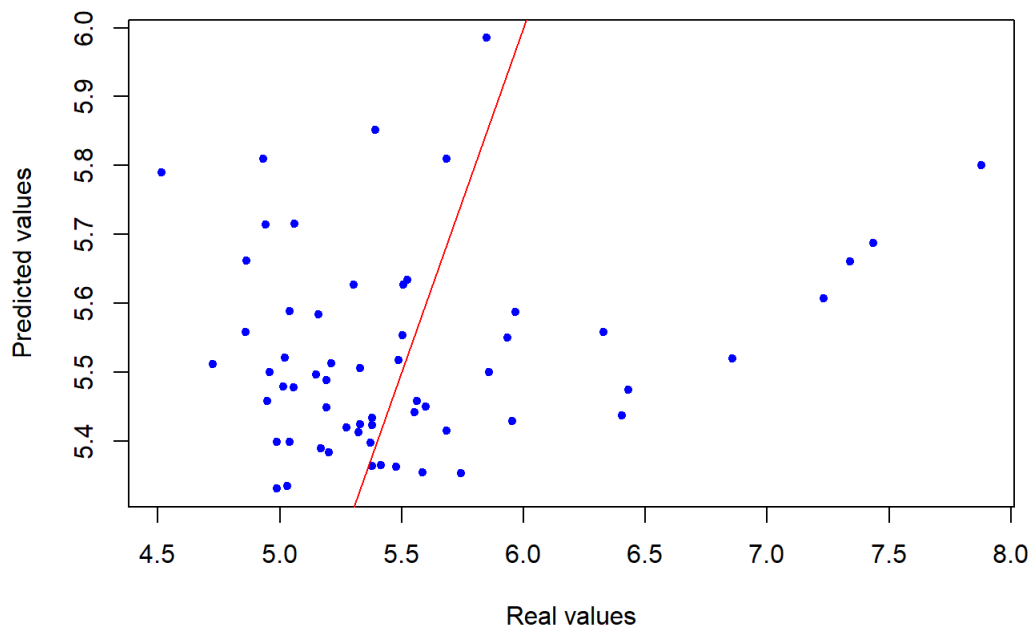
```
qqnorm(lmDouble$residuals, main = "Test for normaldistribution of residuals")
qqline(lmDouble$residuals)
```

## Test for normaldistribution of residuals



```
plot(combined2$NegLogI50Lap, lmDouble$fitted.values, pch = 20, col = "blue", xlab = "Real values",
     ylab = "Predicted values", main = "Comparison: real and predicted values ~ linear regression (Doubling-Time)")
abline(0, 1, col = "red")
```

## Comparison: real and predicted values ~ linear regression (Doubling-Tir



```
cor(combined2$NegLogI50Lap,combined2$Doubling_Time)
```

```
## [1] 0.2115772
```

```
#Split the data (Training - Testing)
```

```
n = nrow(combined2)
rmse2 = sqrt(1/n * sum(lmDouble$residuals^2))
rmse2
```

```
## [1] 0.6627233
```

```
i2.train = sample(1:nrow(combined2), 48)

dat2.train = combined2[i2.train, ]
dat2.test = combined2[-i2.train, ]

l2.train = lm(NegLogI50Lap ~ Doubling_Time, data = dat2.train)
summary(l2.train)
```

```
##
## Call:
## lm(formula = NegLogI50Lap ~ Doubling_Time, data = dat2.train)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.9740 -0.3577 -0.1473  0.1776  1.9844
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.010389    0.251749   19.902  <2e-16 ***
## Doubling_Time 0.014262    0.006528    2.185   0.034 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6345 on 46 degrees of freedom
## Multiple R-squared:  0.09402,    Adjusted R-squared:  0.07432
## F-statistic: 4.774 on 1 and 46 DF,  p-value: 0.03403
```

```
n = nrow(dat2.train)
rmse2.train = sqrt(1/n * sum(l2.train$residuals^2))
rmse2.train
```

```
## [1] 0.6211052
```

```
pred2 = predict(l2.train, newdata = dat2.test)

n = nrow(dat1.test)
residuals = dat2.test$NegLogI50Lap - pred2
rmse2.test = sqrt(1/n * sum(residuals^2))
rmse2.test
```

```
## [1] 0.8938786
```

As a last part, we did a multiple regression with both datasets to predict GI50-values.

```
b1 = gsub(x =Doublingtime$`df$Cell_Line_Name`, pattern = "-", replacement = ".")
Doublingtime1 = rbind(b1,Doublingtime$`df$Doubling_Time`)
Doublingtime1 = as.data.frame(t(Doublingtime1))

c31 = subset(Doublingtime1, b1 %in% intersect(Doublingtime1$b1, c2$V1))
c41 = as.numeric(as.character(c31$V2))
adjustedDoubling_Time = as.data.frame(c41)

combined3 = cbind(adjustedNeglogI50Lap, Fold_Changemeans, adjustedDoubling_Time)
names3 = c( "NegLogI50Lap", "Fold_Changemeans", "Doubling_Time")
colnames(combined3) = names3

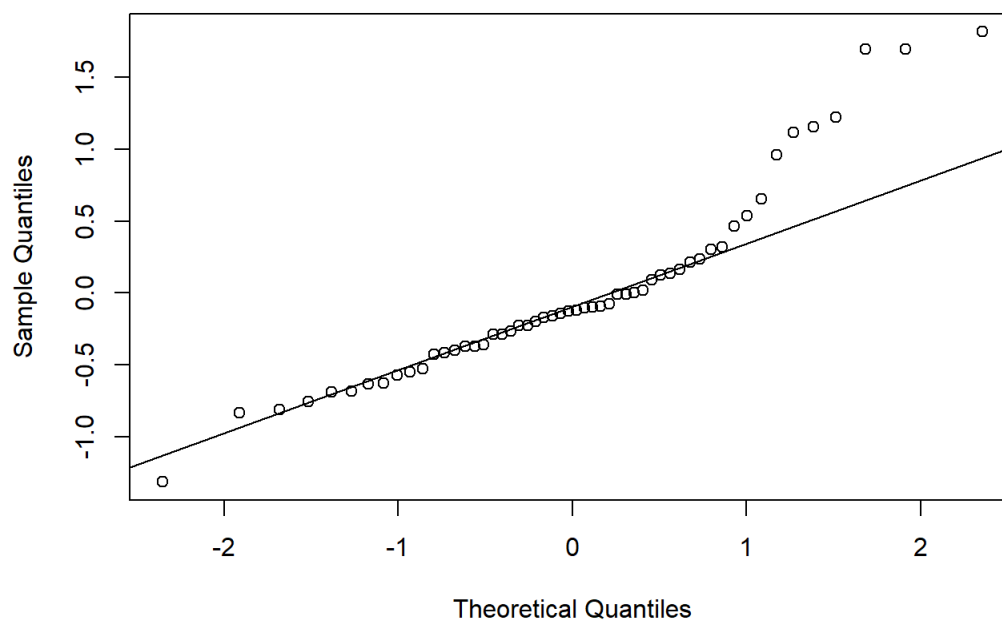
mlr = lm(NegLogI50Lap ~ ., data = combined3)

summary(mlr)
```

```
##
## Call:
## lm(formula = NegLogI50Lap ~ ., data = combined3)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3123 -0.3909 -0.1226  0.2003  1.8141
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.064e+00  2.655e-01  19.069  <2e-16 ***
## Fold_Changemeans 1.819e+15  7.429e+14   2.449   0.0178 *
## Doubling_Time    1.083e-02  6.717e-03   1.612   0.1130
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6719 on 51 degrees of freedom
## Multiple R-squared:  0.1538, Adjusted R-squared:  0.1206
## F-statistic: 4.635 on 2 and 51 DF,  p-value: 0.01415
```

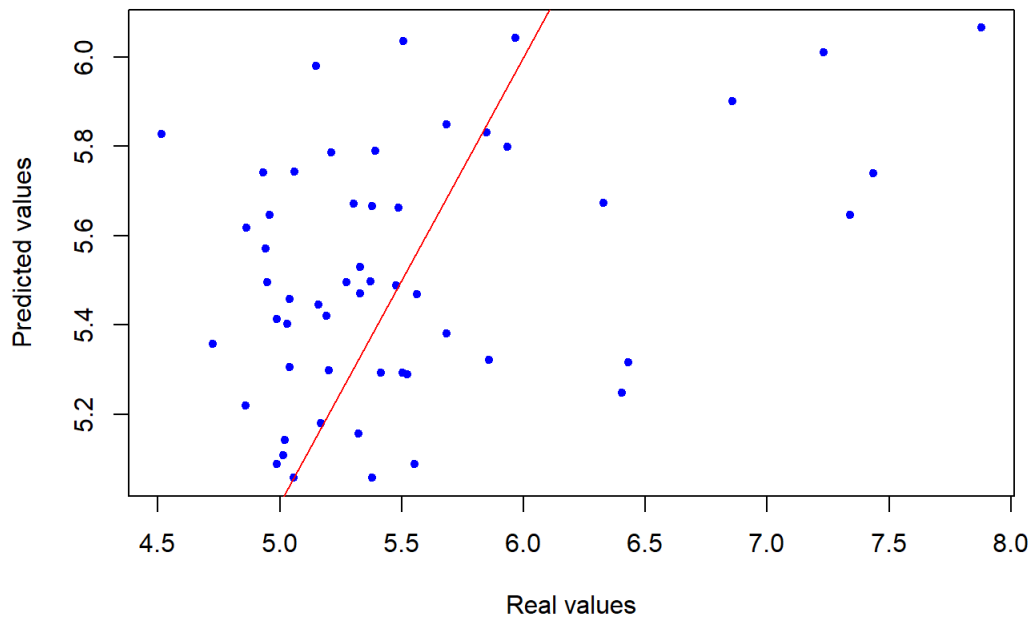
```
qqnorm(mlr$residuals, main = "Test for normaldistribution of residuals")
qqline(mlr$residuals)
```

### Test for normaldistribution of residuals



```
plot(combined3$NegLogI50Lap, mlr$fitted.values, pch = 20, col = "blue", xlab = "Real values",
      ylab = "Predicted values" , main = "Comparison: real and predicted values ~ multiple regression")
abline(0, 1, col = "red")
```

## Comparison: real and predicted values ~ multiple regression



```
#Split the data (Training - Testing)
```

```
n = nrow(combined3)
rmse3 = sqrt(1/n * sum(mlr$residuals^2))
rmse3
```

```
## [1] 0.6530072
```

```
i3.train = sample(1:nrow(combined2), 44)
```

```
dat3.train = combined3[i3.train, ]
dat3.test = combined3[-i3.train, ]
```

```
l3.train = lm(NegLogI50Lap ~ ., data = dat3.train)
summary(l3.train)
```

```
##
## Call:
## lm(formula = NegLogI50Lap ~ ., data = dat3.train)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4110 -0.4173 -0.1550  0.1519  1.7242
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.001e+00  3.341e-01  14.972  <2e-16 ***
## Fold_Changemeans 1.727e+15  1.003e+15   1.722   0.0935 .
## Doubling_Time    1.355e-02  8.286e-03   1.636   0.1104
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.734 on 37 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.1461, Adjusted R-squared:  0.09993
## F-statistic: 3.165 on 2 and 37 DF, p-value: 0.05384
```

```
n = nrow(dat3.train)
rmse3.train = sqrt(1/n * sum(l3.train$residuals^2))
rmse3.train
```



```
## [1] 0.6730553
```

```
pred3 = predict(l3.train, newdata = dat3.test)

n = nrow(dat3.test)
residuals = dat3.test$NegLogI50Lap - pred3
rmse3.test = sqrt(1/n * sum(residuals^2))
rmse3.test
```

```
## [1] 0.4813735
```

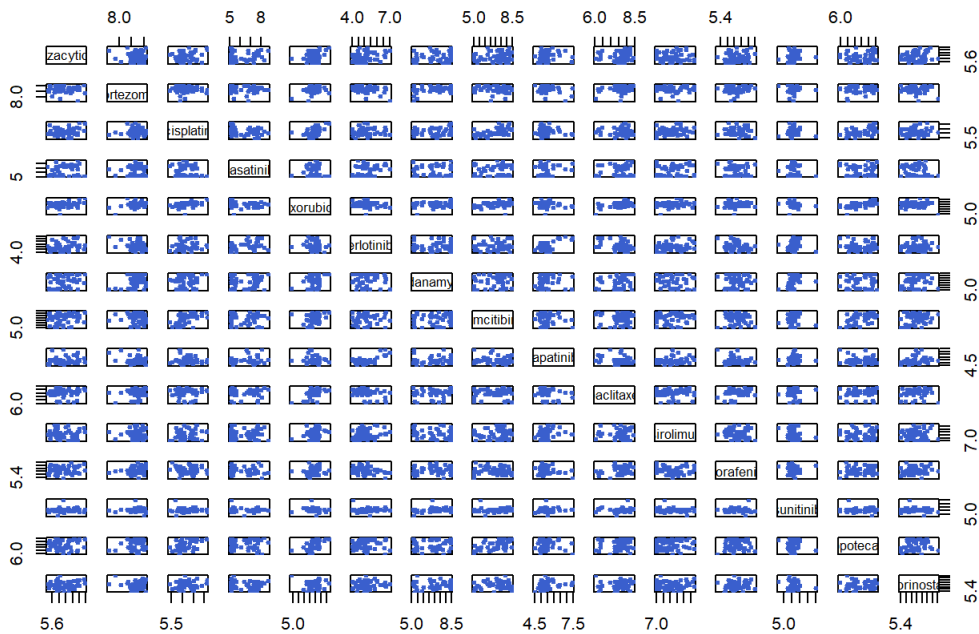
As you can see from the data, All three regression models are not really good. ##Question 2: Erlotinib vs Lapatinib

```
# correlation in general
n= as.data.frame(t(NegLogGI50))
rmv.rows = apply(n, 1, function(x) {
  sum(is.na(x))
})
NLGI50.all = n[-which(rmv.rows > 0), ] # Removing any row with 1 or more missing values
rm(rmv.rows, n, NegLogGI50)
cor.mat = as.data.frame(cor(NLGI50.all[, 1:ncol(NLGI50.all)], method = "pearson")) #Pearson correlation
round(cor.mat, 2) #round values
```

```
##          5-Azacytidine bortezomib cisplatin dasatinib doxorubicin
## 5-Azacytidine      1.00      -0.08      0.16      0.18      0.29
## bortezomib        -0.08      1.00      0.01     -0.10      0.32
## cisplatin          0.16      0.01      1.00     -0.24      0.52
## dasatinib          0.18     -0.10     -0.24      1.00     -0.08
## doxorubicin        0.29      0.32      0.52     -0.08      1.00
## erlotinib          0.27     -0.32      0.01      0.42     -0.17
## geldanamycin        0.23      0.36      0.19     -0.09      0.23
## gemcitibine         0.16     -0.08      0.53     -0.03      0.37
## lapatinib           0.14     -0.26     -0.07      0.19     -0.16
## paclitaxel          0.10      0.20      0.01     -0.10      0.55
## sirolimus          -0.05      0.01      0.27      0.07      0.17
## sorafenib           0.09      0.27     -0.01     -0.24      0.14
## sunitinib           0.12     -0.01     -0.05     -0.03     -0.14
## topotecan           0.14      0.13      0.55      0.02      0.60
## vorinostat          0.16     -0.02      0.07     -0.16     -0.06
##          erlotinib geldanamycin gemcitibine lapatinib paclitaxel
## 5-Azacytidine      0.27      0.23      0.16      0.14      0.10
## bortezomib        -0.32      0.36     -0.08     -0.26      0.20
## cisplatin          0.01      0.19      0.53     -0.07      0.01
## dasatinib          0.42     -0.09     -0.03      0.19     -0.10
## doxorubicin       -0.17      0.23      0.37     -0.16      0.55
## erlotinib          1.00     -0.01      0.01      0.65     -0.37
## geldanamycin       -0.01      1.00      0.12     -0.01      0.28
## gemcitibine         0.01      0.12      1.00     -0.15      0.03
## lapatinib           0.65     -0.01     -0.15      1.00     -0.24
## paclitaxel        -0.37      0.28      0.03     -0.24      1.00
## sirolimus           0.21     -0.21      0.05      0.21     -0.04
## sorafenib          -0.29      0.14     -0.01     -0.25      0.29
## sunitinib           0.06      0.24      0.06      0.12     -0.02
## topotecan          -0.02      0.21      0.63     -0.14      0.20
## vorinostat          0.12      0.20      0.18      0.26      0.09
##          sirolimus sorafenib sunitinib topotecan vorinostat
## 5-Azacytidine      -0.05      0.09      0.12      0.14      0.16
## bortezomib          0.01      0.27     -0.01      0.13     -0.02
## cisplatin           0.27     -0.01     -0.05      0.55      0.07
## dasatinib           0.07     -0.24     -0.03      0.02     -0.16
## doxorubicin         0.17      0.14     -0.14      0.60     -0.06
## erlotinib           0.21     -0.29      0.06     -0.02      0.12
## geldanamycin        -0.21      0.14      0.24      0.21      0.20
## gemcitibine          0.05     -0.01      0.06      0.63      0.18
## lapatinib            0.21     -0.25      0.12     -0.14      0.26
## paclitaxel          -0.04      0.29     -0.02      0.20      0.09
## sirolimus            1.00     -0.11     -0.20      0.03      0.02
## sorafenib           -0.11      1.00      0.05      0.16      0.10
## sunitinib           -0.20      0.05      1.00     -0.05     -0.13
## topotecan            0.03      0.16     -0.05      1.00      0.08
## vorinostat           0.02      0.10     -0.13      0.08      1.00
```

```
pairs(NLGI50.all[, 1:ncol(NLGI50.all)], pch = 20, cex = 0.8, col = "royalblue3", main = "Correlation_NegLogGI50")
```

## Correlation\_NegLogGI50



plot erlotinib all genes,

coloured by tissue

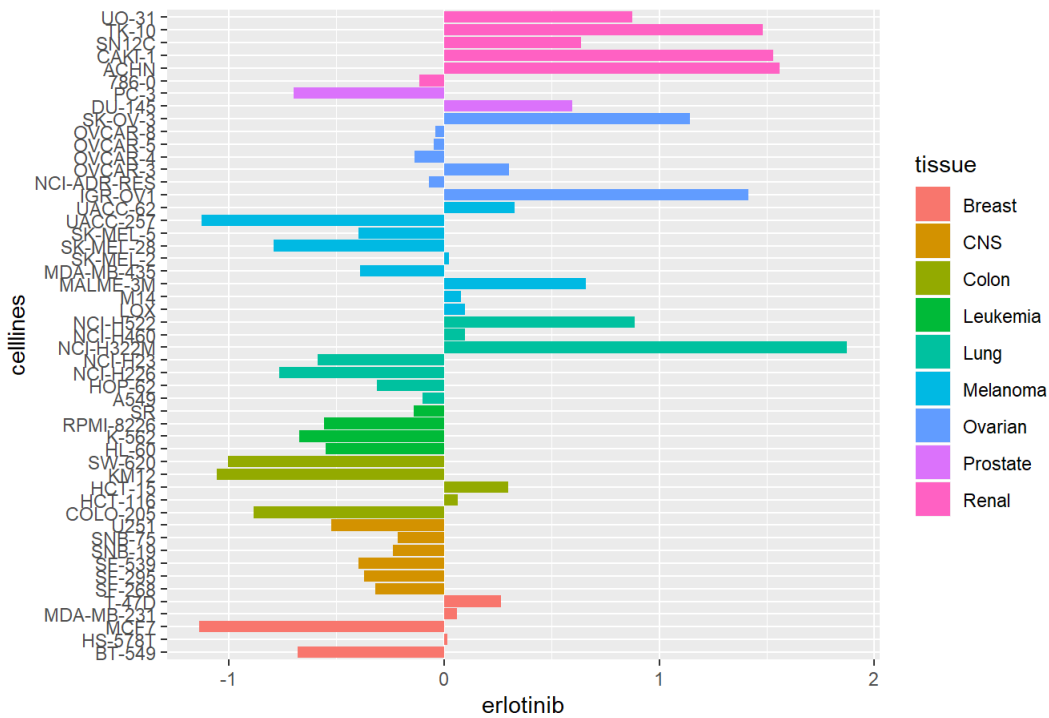
```
#differece
diff = data.frame(erlotinib = NLGI50.all$erlotinib - mean(NLGI50.all$erlotinib), lapatinib = NLGI50.all$lapatinib - mean(NLGI50.all$lapatinib))
diff$celllines = rownames(NLGI50.all)
#create vector to insert column tissue from Metadata

tissue = sapply(1:nrow(diff), function(x) {
  position = which(as.character(Metadata$cell) == diff[x, "celllines"])[1] #if tissue occurs several times, take the first
  out = as.character(Metadata[position, "tissue"]) #output the tissue at this position
  return(out)
})
diff$tissue = tissue
rm(tissue)

diff$celllines = factor(diff$celllines, levels = diff$celllines[order(diff$tissue)]) #Classified by tissue

ggplot(diff, aes(x = celllines, y = erlotinib, fill = tissue))+geom_bar(stat = "identity") + coord_flip()
+ labs(title = "Mean graph plot of NLGI50 values for Erlotinib")
```

Mean graph plot of NLGI50 values for Erlotinib



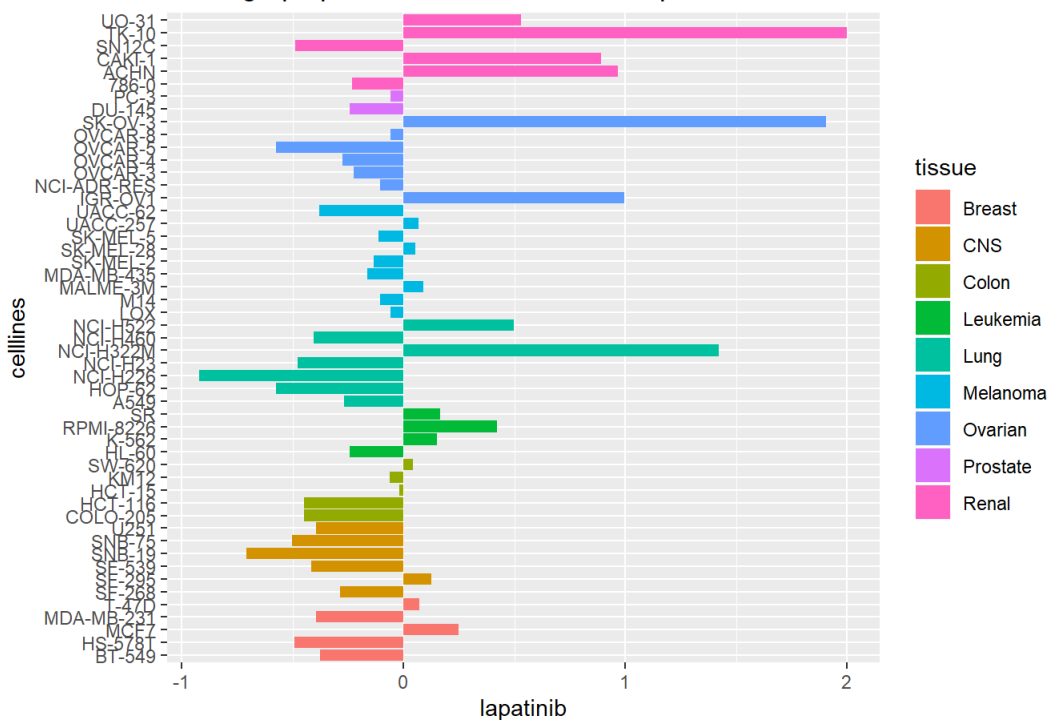
The difference from the

NegLogGI50 for a particular cell line and the mean NegLogGI50 is plotted here for Erlotinib.

plot lapatinib all genes, coloured by tissue

```
ggplot(diff, aes(x = celllines, y = lapatinib, fill = tissue)) + geom_bar(stat="identity") + coord_flip()
+ labs(title="Mean graph plot of NLGI50 values for Lapatinib")
```

Mean graph plot of NLGI50 values for Lapatinib



The difference from the

NegLogGI50 for a particular cell line and the mean NegLogGI50 is plotted here for Lapatinib.

correlation erlotinib , lapatinib

```
cor(NLGI50.all$erlotinib, NLGI50.all$lapatinib, method = "pearson")
```

```
## [1] 0.6528188
```

A Pearson correlation coefficient of ~ 0.65 confirms that these patterns are very similar

Lung genes

```

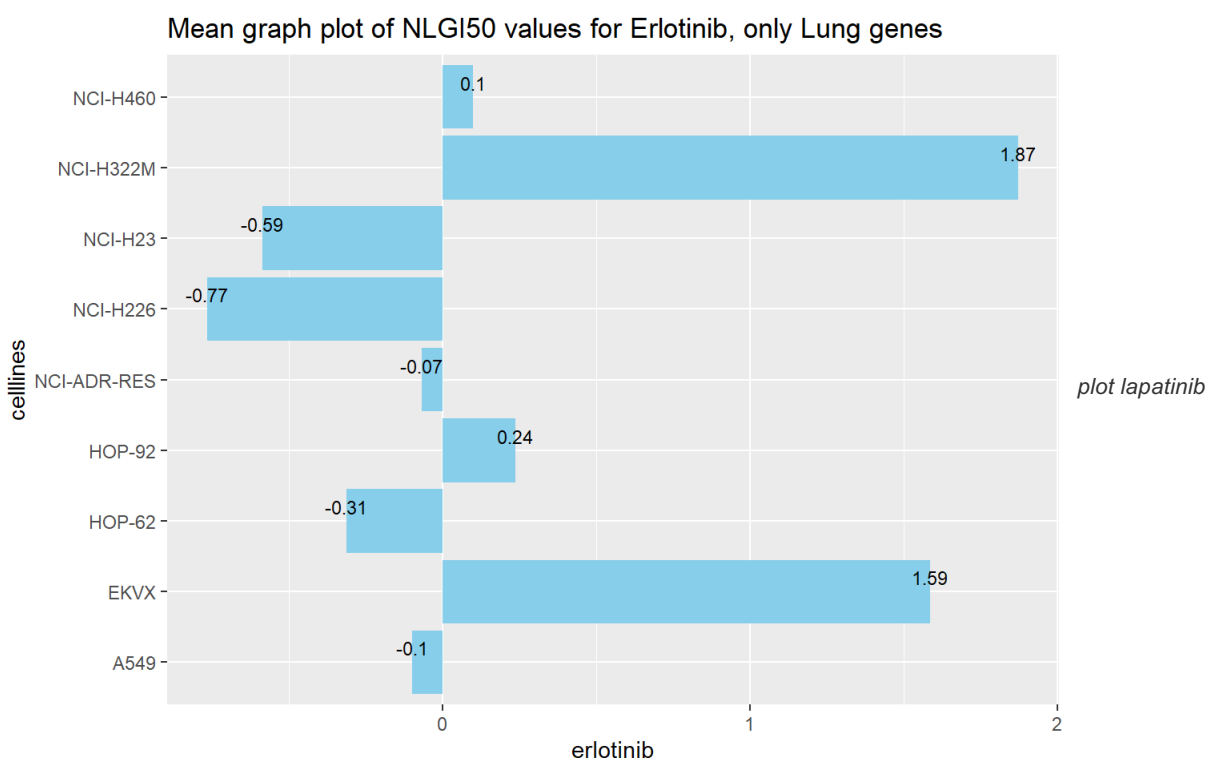
#only lung with mean all
### load data
Metadata_Lapatinib_treated = Metadata[which(Metadata$drug == "lapatinib" & Metadata$dose != "0nM"),]
NegLogGI50 = as.data.frame(readRDS(paste0(wd, "/Data/NegLogGI50.rds")))
#lung genes from Metadata
Lung_Metadata_L_treated = Metadata[which(Metadata$drug == "lapatinib" & Metadata$dose != "0nM" & Metadata$
tissue == "Lung"),]
celllines = Lung_Metadata_L_treated$cell
NegLogGI50.lung = as.data.frame(t(NegLogGI50[c("erlotinib", "lapatinib"), celllines]))

#Difference
dif.NegLogGI50.lung = data.frame(erlotinib = NegLogGI50.lung$erlotinib - mean(NLGI50.all$erlotinib), lap
atinib = NegLogGI50.lung$lapatinib - mean(NLGI50.all$lapatinib)) #erlotinib data - mean value, lapatinib
data - mean value
dif.NegLogGI50.lung$celllines = rownames(NegLogGI50.lung)

# PLOT

ggplot(dif.NegLogGI50.lung,aes(x = celllines, y = erlotinib)) + geom_bar(stat = "identity", fill = "skybl
ue") + geom_text(aes(label = round(erlotinib, 2)), vjust = -0.5, color = "black", size = 3) + coord_flip(
) + labs(title = "Mean graph plot of NLGI50 values for Erlotinib, only Lung genes")

```

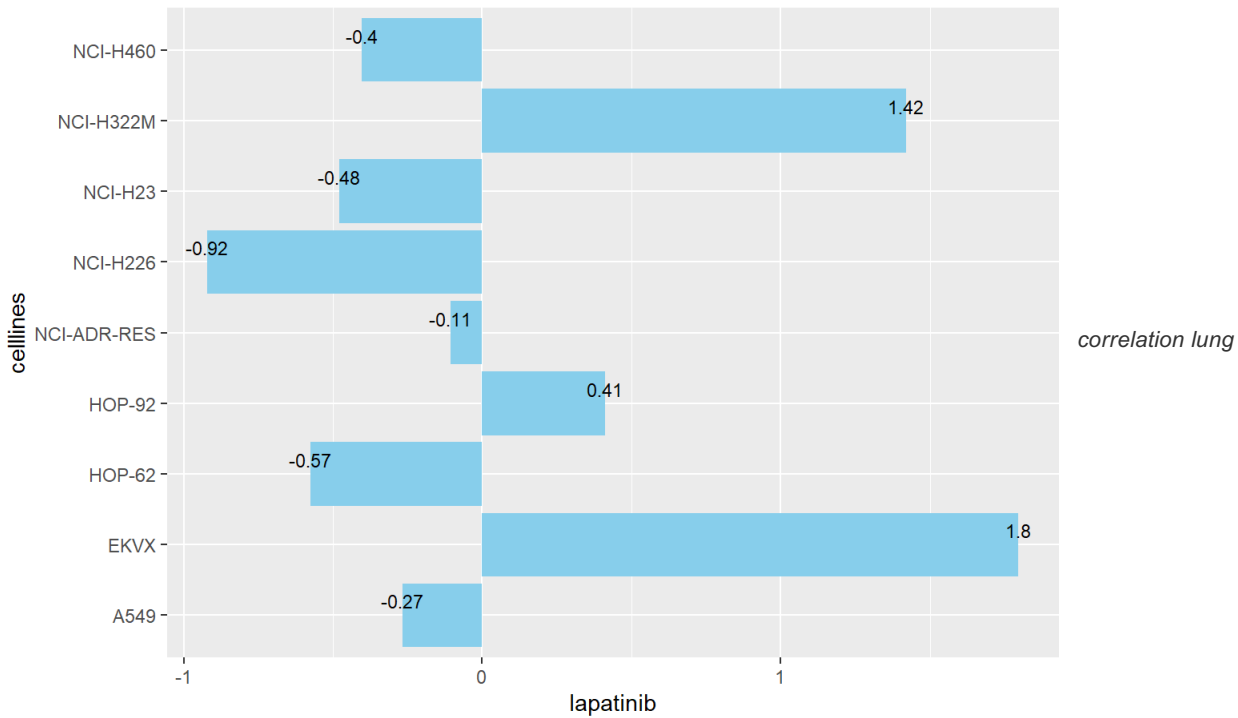


```

ggplot(dif.NegLogGI50.lung,aes(x = celllines, y = lapatinib)) + geom_bar(stat = "identity", fill = "skybl
ue") + geom_text(aes(label=round(lapatinib, 2)), vjust = -0.5, color = "black", size = 3) + coord_flip()
+ labs(title = "Mean graph plot of NLGI50 values for Lapatinib, only Lung genes")

```

Mean graph plot of NLGI50 values for Lapatinib, only Lung genes



```
cor(NegLogGI50.lung$erlotinib, NegLogGI50.lung$lapatinib, method = "pearson")
```

```
## [1] 0.9609488
```

A pearson correlation coefficient of ~ 0.96 suggests that Lapatinib has a similar effect on lung cancer as Erlotinib

## anova

<<<<<<< HEAD

## selection of Lapatinib and Erlotinib treated cells

```
lapa<-data.frame(Metadata[which(Metadata[, 'drug'] == "lapatinib"), ])
erlo<-data.frame(Metadata[which(Metadata[, 'drug'] == "erlotinib"), ])
el<-right_join(lapa,erlo, by="cell")
el
```

##	sample.x	cell	drug.x	dose.x	time.x
## 1	786-0_lapatinib_10000nM_24h	786-0	lapatinib	10000nM	24h
## 2	786-0_lapatinib_0nM_24h	786-0	lapatinib	0nM	24h
## 3	A498_lapatinib_10000nM_24h	A498	lapatinib	10000nM	24h
## 4	A498_lapatinib_0nM_24h	A498	lapatinib	0nM	24h
## 5	A549_lapatinib_10000nM_24h	A549	lapatinib	10000nM	24h
## 6	A549_lapatinib_0nM_24h	A549	lapatinib	0nM	24h
## 7	ACHN_lapatinib_10000nM_24h	ACHN	lapatinib	10000nM	24h
## 8	ACHN_lapatinib_0nM_24h	ACHN	lapatinib	0nM	24h
## 9	BT-549_lapatinib_10000nM_24h	BT-549	lapatinib	10000nM	24h
## 10	BT-549_lapatinib_0nM_24h	BT-549	lapatinib	0nM	24h
## 11	CAKI-1_lapatinib_10000nM_24h	CAKI-1	lapatinib	10000nM	24h
## 12	CAKI-1_lapatinib_0nM_24h	CAKI-1	lapatinib	0nM	24h
## 13	<NA>	CCRF-CEM	<NA>	<NA>	<NA>
## 14	DU-145_lapatinib_10000nM_24h	DU-145	lapatinib	10000nM	24h
## 15	DU-145_lapatinib_0nM_24h	DU-145	lapatinib	0nM	24h
## 16	EKVX_lapatinib_10000nM_24h	EKVX	lapatinib	10000nM	24h
## 17	EKVX_lapatinib_0nM_24h	EKVX	lapatinib	0nM	24h
## 18	HCC-2998_lapatinib_10000nM_24h	HCC-2998	lapatinib	10000nM	24h
## 19	HCC-2998_lapatinib_0nM_24h	HCC-2998	lapatinib	0nM	24h
## 20	HCT-116_lapatinib_10000nM_24h	HCT-116	lapatinib	10000nM	24h
## 21	HCT-116_lapatinib_0nM_24h	HCT-116	lapatinib	0nM	24h
## 22	HCT-15_lapatinib_10000nM_24h	HCT-15	lapatinib	10000nM	24h
## 23	HCT-15_lapatinib_0nM_24h	HCT-15	lapatinib	0nM	24h
## 24	<NA>	HL-60	<NA>	<NA>	<NA>

## 25	HOP-62_lapatinib_10000nM_24h	HOP-62	lapatinib	10000nM	24h
## 26	HOP-62_lapatinib_0nM_24h	HOP-62	lapatinib	0nM	24h
## 27	HOP-92_lapatinib_10000nM_24h	HOP-92	lapatinib	10000nM	24h
## 28	HOP-92_lapatinib_0nM_24h	HOP-92	lapatinib	0nM	24h
## 29	HS-578T_lapatinib_10000nM_24h	HS-578T	lapatinib	10000nM	24h
## 30	HS-578T_lapatinib_0nM_24h	HS-578T	lapatinib	0nM	24h
## 31	<NA>	HT29	<NA>	<NA>	<NA>
## 32	IGR-OV1_lapatinib_10000nM_24h	IGR-OV1	lapatinib	10000nM	24h
## 33	IGR-OV1_lapatinib_0nM_24h	IGR-OV1	lapatinib	0nM	24h
## 34	<NA>	K-562	<NA>	<NA>	<NA>
## 35	KM12_lapatinib_10000nM_24h	KM12	lapatinib	10000nM	24h
## 36	KM12_lapatinib_0nM_24h	KM12	lapatinib	0nM	24h
## 37	<NA>	LOX	<NA>	<NA>	<NA>
## 38	M14_lapatinib_10000nM_24h	M14	lapatinib	10000nM	24h
## 39	M14_lapatinib_0nM_24h	M14	lapatinib	0nM	24h
## 40	MALME-3M_lapatinib_10000nM_24h	MALME-3M	lapatinib	10000nM	24h
## 41	MALME-3M_lapatinib_0nM_24h	MALME-3M	lapatinib	0nM	24h
## 42	MCF7_lapatinib_10000nM_24h	MCF7	lapatinib	10000nM	24h
## 43	MCF7_lapatinib_0nM_24h	MCF7	lapatinib	0nM	24h
## 44	MDA-MB-231_lapatinib_10000nM_24h	MDA-MB-231	lapatinib	10000nM	24h
## 45	MDA-MB-231_lapatinib_0nM_24h	MDA-MB-231	lapatinib	0nM	24h
## 46	MDA-MB-435_lapatinib_10000nM_24h	MDA-MB-435	lapatinib	10000nM	24h
## 47	MDA-MB-435_lapatinib_0nM_24h	MDA-MB-435	lapatinib	0nM	24h
## 48	MDA-MB-468_lapatinib_10000nM_24h	MDA-MB-468	lapatinib	10000nM	24h
## 49	MDA-MB-468_lapatinib_0nM_24h	MDA-MB-468	lapatinib	0nM	24h
## 50	MOLT-4_lapatinib_10000nM_24h	MOLT-4	lapatinib	10000nM	24h
## 51	MOLT-4_lapatinib_0nM_24h	MOLT-4	lapatinib	0nM	24h
## 52	NCI-ADR-RES_lapatinib_10000nM_24h	NCI-ADR-RES	lapatinib	10000nM	24h
## 53	NCI-ADR-RES_lapatinib_0nM_24h	NCI-ADR-RES	lapatinib	0nM	24h
## 54	NCI-H226_lapatinib_10000nM_24h	NCI-H226	lapatinib	10000nM	24h
## 55	NCI-H226_lapatinib_0nM_24h	NCI-H226	lapatinib	0nM	24h
## 56	NCI-H23_lapatinib_10000nM_24h	NCI-H23	lapatinib	10000nM	24h
## 57	NCI-H23_lapatinib_0nM_24h	NCI-H23	lapatinib	0nM	24h
## 58	NCI-H322M_lapatinib_10000nM_24h	NCI-H322M	lapatinib	10000nM	24h
## 59	NCI-H322M_lapatinib_0nM_24h	NCI-H322M	lapatinib	0nM	24h
## 60	NCI-H460_lapatinib_10000nM_24h	NCI-H460	lapatinib	10000nM	24h
## 61	NCI-H460_lapatinib_0nM_24h	NCI-H460	lapatinib	0nM	24h
## 62	NCI-H522_lapatinib_10000nM_24h	NCI-H522	lapatinib	10000nM	24h
## 63	NCI-H522_lapatinib_0nM_24h	NCI-H522	lapatinib	0nM	24h
## 64	OVCAR-3_lapatinib_10000nM_24h	OVCAR-3	lapatinib	10000nM	24h
## 65	OVCAR-3_lapatinib_0nM_24h	OVCAR-3	lapatinib	0nM	24h
## 66	OVCAR-4_lapatinib_10000nM_24h	OVCAR-4	lapatinib	10000nM	24h
## 67	OVCAR-4_lapatinib_0nM_24h	OVCAR-4	lapatinib	0nM	24h
## 68	OVCAR-5_lapatinib_10000nM_24h	OVCAR-5	lapatinib	10000nM	24h
## 69	OVCAR-5_lapatinib_0nM_24h	OVCAR-5	lapatinib	0nM	24h
## 70	OVCAR-8_lapatinib_10000nM_24h	OVCAR-8	lapatinib	10000nM	24h
## 71	OVCAR-8_lapatinib_0nM_24h	OVCAR-8	lapatinib	0nM	24h
## 72	PC-3_lapatinib_10000nM_24h	PC-3	lapatinib	10000nM	24h
## 73	PC-3_lapatinib_0nM_24h	PC-3	lapatinib	0nM	24h
## 74	RPMI-8226_lapatinib_10000nM_24h	RPMI-8226	lapatinib	10000nM	24h
## 75	RPMI-8226_lapatinib_0nM_24h	RPMI-8226	lapatinib	0nM	24h
## 76	RXF-393_lapatinib_10000nM_24h	RXF-393	lapatinib	10000nM	24h
## 77	RXF-393_lapatinib_0nM_24h	RXF-393	lapatinib	0nM	24h
## 78	SF-268_lapatinib_10000nM_24h	SF-268	lapatinib	10000nM	24h
## 79	SF-268_lapatinib_0nM_24h	SF-268	lapatinib	0nM	24h
## 80	SF-295_lapatinib_10000nM_24h	SF-295	lapatinib	10000nM	24h
## 81	SF-295_lapatinib_0nM_24h	SF-295	lapatinib	0nM	24h
## 82	SF-539_lapatinib_10000nM_24h	SF-539	lapatinib	10000nM	24h
## 83	SF-539_lapatinib_0nM_24h	SF-539	lapatinib	0nM	24h
## 84	SK-MEL-2_lapatinib_10000nM_24h	SK-MEL-2	lapatinib	10000nM	24h
## 85	SK-MEL-2_lapatinib_0nM_24h	SK-MEL-2	lapatinib	0nM	24h
## 86	SK-MEL-28_lapatinib_10000nM_24h	SK-MEL-28	lapatinib	10000nM	24h
## 87	SK-MEL-28_lapatinib_0nM_24h	SK-MEL-28	lapatinib	0nM	24h
## 88	SK-MEL-5_lapatinib_10000nM_24h	SK-MEL-5	lapatinib	10000nM	24h
## 89	SK-MEL-5_lapatinib_0nM_24h	SK-MEL-5	lapatinib	0nM	24h
## 90	SK-OV-3_lapatinib_10000nM_24h	SK-OV-3	lapatinib	10000nM	24h
## 91	SK-OV-3_lapatinib_0nM_24h	SK-OV-3	lapatinib	0nM	24h
## 92	SN12C_lapatinib_10000nM_24h	SN12C	lapatinib	10000nM	24h
## 93	SN12C_lapatinib_0nM_24h	SN12C	lapatinib	0nM	24h
## 94	SNB-19_lapatinib_10000nM_24h	SNB-19	lapatinib	10000nM	24h
## 95	SNB-19_lapatinib_0nM_24h	SNB-19	lapatinib	0nM	24h
## 96	SNB-75_lapatinib_10000nM_24h	SNB-75	lapatinib	10000nM	24h
## 97	SNB-75_lapatinib_0nM_24h	SNB-75	lapatinib	0nM	24h

## 98	<NA>	SR	<NA>	<NA>	<NA>
## 99	SW-620_lapatinib_10000nM_24h	SW-620	lapatinib	10000nM	24h
## 100	SW-620_lapatinib_0nM_24h	SW-620	lapatinib	0nM	24h
## 101	T-47D_lapatinib_10000nM_24h	T-47D	lapatinib	10000nM	24h
## 102	T-47D_lapatinib_0nM_24h	T-47D	lapatinib	0nM	24h
## 103	TK-10_lapatinib_10000nM_24h	TK-10	lapatinib	10000nM	24h
## 104	TK-10_lapatinib_0nM_24h	TK-10	lapatinib	0nM	24h
## 105	U251_lapatinib_10000nM_24h	U251	lapatinib	10000nM	24h
## 106	U251_lapatinib_0nM_24h	U251	lapatinib	0nM	24h
## 107	UACC-257_lapatinib_10000nM_24h	UACC-257	lapatinib	10000nM	24h
## 108	UACC-257_lapatinib_0nM_24h	UACC-257	lapatinib	0nM	24h
## 109	UACC-62_lapatinib_10000nM_24h	UACC-62	lapatinib	10000nM	24h
## 110	UACC-62_lapatinib_0nM_24h	UACC-62	lapatinib	0nM	24h
## 111	UO-31_lapatinib_10000nM_24h	UO-31	lapatinib	10000nM	24h
## 112	UO-31_lapatinib_0nM_24h	UO-31	lapatinib	0nM	24h
## 113	786-0_lapatinib_10000nM_24h	786-0	lapatinib	10000nM	24h
## 114	786-0_lapatinib_0nM_24h	786-0	lapatinib	0nM	24h
## 115	A498_lapatinib_10000nM_24h	A498	lapatinib	10000nM	24h
## 116	A498_lapatinib_0nM_24h	A498	lapatinib	0nM	24h
## 117	A549_lapatinib_10000nM_24h	A549	lapatinib	10000nM	24h
## 118	A549_lapatinib_0nM_24h	A549	lapatinib	0nM	24h
## 119	ACHN_lapatinib_10000nM_24h	ACHN	lapatinib	10000nM	24h
## 120	ACHN_lapatinib_0nM_24h	ACHN	lapatinib	0nM	24h
## 121	BT-549_lapatinib_10000nM_24h	BT-549	lapatinib	10000nM	24h
## 122	BT-549_lapatinib_0nM_24h	BT-549	lapatinib	0nM	24h
## 123	CAKI-1_lapatinib_10000nM_24h	CAKI-1	lapatinib	10000nM	24h
## 124	CAKI-1_lapatinib_0nM_24h	CAKI-1	lapatinib	0nM	24h
## 125	<NA>	CCRF-CEM	<NA>	<NA>	<NA>
## 126	DU-145_lapatinib_10000nM_24h	DU-145	lapatinib	10000nM	24h
## 127	DU-145_lapatinib_0nM_24h	DU-145	lapatinib	0nM	24h
## 128	EKVX_lapatinib_10000nM_24h	EKVX	lapatinib	10000nM	24h
## 129	EKVX_lapatinib_0nM_24h	EKVX	lapatinib	0nM	24h
## 130	HCC-2998_lapatinib_10000nM_24h	HCC-2998	lapatinib	10000nM	24h
## 131	HCC-2998_lapatinib_0nM_24h	HCC-2998	lapatinib	0nM	24h
## 132	HCT-116_lapatinib_10000nM_24h	HCT-116	lapatinib	10000nM	24h
## 133	HCT-116_lapatinib_0nM_24h	HCT-116	lapatinib	0nM	24h
## 134	HCT-15_lapatinib_10000nM_24h	HCT-15	lapatinib	10000nM	24h
## 135	HCT-15_lapatinib_0nM_24h	HCT-15	lapatinib	0nM	24h
## 136	<NA>	HL-60	<NA>	<NA>	<NA>
## 137	HOP-62_lapatinib_10000nM_24h	HOP-62	lapatinib	10000nM	24h
## 138	HOP-62_lapatinib_0nM_24h	HOP-62	lapatinib	0nM	24h
## 139	HOP-92_lapatinib_10000nM_24h	HOP-92	lapatinib	10000nM	24h
## 140	HOP-92_lapatinib_0nM_24h	HOP-92	lapatinib	0nM	24h
## 141	HS-578T_lapatinib_10000nM_24h	HS-578T	lapatinib	10000nM	24h
## 142	HS-578T_lapatinib_0nM_24h	HS-578T	lapatinib	0nM	24h
## 143	<NA>	HT29	<NA>	<NA>	<NA>
## 144	IGR-OV1_lapatinib_10000nM_24h	IGR-OV1	lapatinib	10000nM	24h
## 145	IGR-OV1_lapatinib_0nM_24h	IGR-OV1	lapatinib	0nM	24h
## 146	<NA>	K-562	<NA>	<NA>	<NA>
## 147	KM12_lapatinib_10000nM_24h	KM12	lapatinib	10000nM	24h
## 148	KM12_lapatinib_0nM_24h	KM12	lapatinib	0nM	24h
## 149	<NA>	LOX	<NA>	<NA>	<NA>
## 150	M14_lapatinib_10000nM_24h	M14	lapatinib	10000nM	24h
## 151	M14_lapatinib_0nM_24h	M14	lapatinib	0nM	24h
## 152	MALME-3M_lapatinib_10000nM_24h	MALME-3M	lapatinib	10000nM	24h
## 153	MALME-3M_lapatinib_0nM_24h	MALME-3M	lapatinib	0nM	24h
## 154	MCF7_lapatinib_10000nM_24h	MCF7	lapatinib	10000nM	24h
## 155	MCF7_lapatinib_0nM_24h	MCF7	lapatinib	0nM	24h
## 156	MDA-MB-231_lapatinib_10000nM_24h	MDA-MB-231	lapatinib	10000nM	24h
## 157	MDA-MB-231_lapatinib_0nM_24h	MDA-MB-231	lapatinib	0nM	24h
## 158	MDA-MB-435_lapatinib_10000nM_24h	MDA-MB-435	lapatinib	10000nM	24h
## 159	MDA-MB-435_lapatinib_0nM_24h	MDA-MB-435	lapatinib	0nM	24h
## 160	MDA-MB-468_lapatinib_10000nM_24h	MDA-MB-468	lapatinib	10000nM	24h
## 161	MDA-MB-468_lapatinib_0nM_24h	MDA-MB-468	lapatinib	0nM	24h
## 162	MOLT-4_lapatinib_10000nM_24h	MOLT-4	lapatinib	10000nM	24h
## 163	MOLT-4_lapatinib_0nM_24h	MOLT-4	lapatinib	0nM	24h
## 164	NCI-ADR-RES_lapatinib_10000nM_24h	NCI-ADR-RES	lapatinib	10000nM	24h
## 165	NCI-ADR-RES_lapatinib_0nM_24h	NCI-ADR-RES	lapatinib	0nM	24h
## 166	NCI-H226_lapatinib_10000nM_24h	NCI-H226	lapatinib	10000nM	24h
## 167	NCI-H226_lapatinib_0nM_24h	NCI-H226	lapatinib	0nM	24h
## 168	NCI-H23_lapatinib_10000nM_24h	NCI-H23	lapatinib	10000nM	24h
## 169	NCI-H23_lapatinib_0nM_24h	NCI-H23	lapatinib	0nM	24h
## 170	NCI-H222M_lapatinib_10000nM_24h	NCI-H222M	lapatinib	10000nM	24h



##	170	NCI-H322M_lapatinib_10000nM_24h	NCI-H322M_lapatinib_10000nM_24h	24h
##	171	NCI-H322M_lapatinib_0nM_24h	NCI-H322M_lapatinib_0nM_24h	24h
##	172	NCI-H460_lapatinib_10000nM_24h	NCI-H460_lapatinib_10000nM_24h	24h
##	173	NCI-H460_lapatinib_0nM_24h	NCI-H460_lapatinib_0nM_24h	24h
##	174	NCI-H522_lapatinib_10000nM_24h	NCI-H522_lapatinib_10000nM_24h	24h
##	175	NCI-H522_lapatinib_0nM_24h	NCI-H522_lapatinib_0nM_24h	24h
##	176	OVCAR-3_lapatinib_10000nM_24h	OVCAR-3_lapatinib_10000nM_24h	24h
##	177	OVCAR-3_lapatinib_0nM_24h	OVCAR-3_lapatinib_0nM_24h	24h
##	178	OVCAR-4_lapatinib_10000nM_24h	OVCAR-4_lapatinib_10000nM_24h	24h
##	179	OVCAR-4_lapatinib_0nM_24h	OVCAR-4_lapatinib_0nM_24h	24h
##	180	OVCAR-5_lapatinib_10000nM_24h	OVCAR-5_lapatinib_10000nM_24h	24h
##	181	OVCAR-5_lapatinib_0nM_24h	OVCAR-5_lapatinib_0nM_24h	24h
##	182	OVCAR-8_lapatinib_10000nM_24h	OVCAR-8_lapatinib_10000nM_24h	24h
##	183	OVCAR-8_lapatinib_0nM_24h	OVCAR-8_lapatinib_0nM_24h	24h
##	184	PC-3_lapatinib_10000nM_24h	PC-3_lapatinib_10000nM_24h	24h
##	185	PC-3_lapatinib_0nM_24h	PC-3_lapatinib_0nM_24h	24h
##	186	RPMI-8226_lapatinib_10000nM_24h	RPMI-8226_lapatinib_10000nM_24h	24h
##	187	RPMI-8226_lapatinib_0nM_24h	RPMI-8226_lapatinib_0nM_24h	24h
##	188	RXF-393_lapatinib_10000nM_24h	RXF-393_lapatinib_10000nM_24h	24h
##	189	RXF-393_lapatinib_0nM_24h	RXF-393_lapatinib_0nM_24h	24h
##	190	SF-268_lapatinib_10000nM_24h	SF-268_lapatinib_10000nM_24h	24h
##	191	SF-268_lapatinib_0nM_24h	SF-268_lapatinib_0nM_24h	24h
##	192	SF-295_lapatinib_10000nM_24h	SF-295_lapatinib_10000nM_24h	24h
##	193	SF-295_lapatinib_0nM_24h	SF-295_lapatinib_0nM_24h	24h
##	194	SF-539_lapatinib_10000nM_24h	SF-539_lapatinib_10000nM_24h	24h
##	195	SF-539_lapatinib_0nM_24h	SF-539_lapatinib_0nM_24h	24h
##	196	SK-MEL-2_lapatinib_10000nM_24h	SK-MEL-2_lapatinib_10000nM_24h	24h
##	197	SK-MEL-2_lapatinib_0nM_24h	SK-MEL-2_lapatinib_0nM_24h	24h
##	198	SK-MEL-28_lapatinib_10000nM_24h	SK-MEL-28_lapatinib_10000nM_24h	24h
##	199	SK-MEL-28_lapatinib_0nM_24h	SK-MEL-28_lapatinib_0nM_24h	24h
##	200	SK-MEL-5_lapatinib_10000nM_24h	SK-MEL-5_lapatinib_10000nM_24h	24h
##	201	SK-MEL-5_lapatinib_0nM_24h	SK-MEL-5_lapatinib_0nM_24h	24h
##	202	SK-OV-3_lapatinib_10000nM_24h	SK-OV-3_lapatinib_10000nM_24h	24h
##	203	SK-OV-3_lapatinib_0nM_24h	SK-OV-3_lapatinib_0nM_24h	24h
##	204	SN12C_lapatinib_10000nM_24h	SN12C_lapatinib_10000nM_24h	24h
##	205	SN12C_lapatinib_0nM_24h	SN12C_lapatinib_0nM_24h	24h
##	206	SNB-19_lapatinib_10000nM_24h	SNB-19_lapatinib_10000nM_24h	24h
##	207	SNB-19_lapatinib_0nM_24h	SNB-19_lapatinib_0nM_24h	24h
##	208	SNB-75_lapatinib_10000nM_24h	SNB-75_lapatinib_10000nM_24h	24h
##	209	SNB-75_lapatinib_0nM_24h	SNB-75_lapatinib_0nM_24h	24h
##	210	<NA>	SR <NA> <NA>	<NA>
##	211	SW-620_lapatinib_10000nM_24h	SW-620_lapatinib_10000nM_24h	24h
##	212	SW-620_lapatinib_0nM_24h	SW-620_lapatinib_0nM_24h	24h
##	213	T-47D_lapatinib_10000nM_24h	T-47D_lapatinib_10000nM_24h	24h
##	214	T-47D_lapatinib_0nM_24h	T-47D_lapatinib_0nM_24h	24h
##	215	TK-10_lapatinib_10000nM_24h	TK-10_lapatinib_10000nM_24h	24h
##	216	TK-10_lapatinib_0nM_24h	TK-10_lapatinib_0nM_24h	24h
##	217	U251_lapatinib_10000nM_24h	U251_lapatinib_10000nM_24h	24h
##	218	U251_lapatinib_0nM_24h	U251_lapatinib_0nM_24h	24h
##	219	UACC-257_lapatinib_10000nM_24h	UACC-257_lapatinib_10000nM_24h	24h
##	220	UACC-257_lapatinib_0nM_24h	UACC-257_lapatinib_0nM_24h	24h
##	221	UACC-62_lapatinib_10000nM_24h	UACC-62_lapatinib_10000nM_24h	24h
##	222	UACC-62_lapatinib_0nM_24h	UACC-62_lapatinib_0nM_24h	24h
##	223	UO-31_lapatinib_10000nM_24h	UO-31_lapatinib_10000nM_24h	24h
##	224	UO-31_lapatinib_0nM_24h	UO-31_lapatinib_0nM_24h	24h
##		tissue.x	sample.y drug.y dose.y time.y	
##	1	Renal 786-0_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	2	Renal 786-0_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	3	Renal A498_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	4	Renal A498_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	5	Lung A549_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	6	Lung A549_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	7	Renal ACHN_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	8	Renal ACHN_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	9	Breast BT-549_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	10	Breast BT-549_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	11	Renal CAKI-1_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	12	Renal CAKI-1_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	13	<NA> CCRF-CEM_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	14	Prostate DU-145_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	15	Prostate DU-145_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	16	Lung EKVX_erlotinib_10000nM_24h	erlotinib 10000nM	24h
##	17	Lung EKVX_erlotinib_10000nM_24h	erlotinib 10000nM	24h

## 18	Colon	HCC-2998_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 19	Colon	HCC-2998_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 20	Colon	HCT-116_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 21	Colon	HCT-116_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 22	Colon	HCT-15_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 23	Colon	HCT-15_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 24	<NA>	HL-60_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 25	Lung	HOP-62_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 26	Lung	HOP-62_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 27	Lung	HOP-92_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 28	Lung	HOP-92_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 29	Breast	HS-578T_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 30	Breast	HS-578T_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 31	<NA>	HT29_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 32	Ovarian	IGR-OV1_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 33	Ovarian	IGR-OV1_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 34	<NA>	K-562_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 35	Colon	KM12_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 36	Colon	KM12_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 37	<NA>	LOX_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 38	Melanoma	M14_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 39	Melanoma	M14_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 40	Melanoma	MALME-3M_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 41	Melanoma	MALME-3M_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 42	Breast	MCF7_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 43	Breast	MCF7_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 44	Breast	MDA-MB-231_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 45	Breast	MDA-MB-231_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 46	Melanoma	MDA-MB-435_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 47	Melanoma	MDA-MB-435_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 48	Breast	MDA-MB-468_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 49	Breast	MDA-MB-468_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 50	Leukemia	MOLT-4_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 51	Leukemia	MOLT-4_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 52	Ovarian	NCI-ADR-RES_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 53	Ovarian	NCI-ADR-RES_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 54	Lung	NCI-H226_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 55	Lung	NCI-H226_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 56	Lung	NCI-H23_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 57	Lung	NCI-H23_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 58	Lung	NCI-H322M_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 59	Lung	NCI-H322M_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 60	Lung	NCI-H460_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 61	Lung	NCI-H460_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 62	Lung	NCI-H522_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 63	Lung	NCI-H522_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 64	Ovarian	OVCAR-3_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 65	Ovarian	OVCAR-3_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 66	Ovarian	OVCAR-4_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 67	Ovarian	OVCAR-4_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 68	Ovarian	OVCAR-5_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 69	Ovarian	OVCAR-5_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 70	Ovarian	OVCAR-8_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 71	Ovarian	OVCAR-8_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 72	Prostate	PC-3_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 73	Prostate	PC-3_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 74	Leukemia	RPMI-8226_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 75	Leukemia	RPMI-8226_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 76	Renal	RXF-393_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 77	Renal	RXF-393_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 78	CNS	SF-268_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 79	CNS	SF-268_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 80	CNS	SF-295_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 81	CNS	SF-295_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 82	CNS	SF-539_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 83	CNS	SF-539_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 84	Melanoma	SK-MEL-2_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 85	Melanoma	SK-MEL-2_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 86	Melanoma	SK-MEL-28_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 87	Melanoma	SK-MEL-28_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 88	Melanoma	SK-MEL-5_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 89	Melanoma	SK-MEL-5_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 90	Ovarian	SK-OV-3_erlotinib_10000nM_24h	erlotinib	10000nM	24h

## 91	Ovarian	SK-OV-3_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 92	Renal	SN12C_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 93	Renal	SN12C_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 94	CNS	SNB-19_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 95	CNS	SNB-19_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 96	CNS	SNB-75_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 97	CNS	SNB-75_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 98	<NA>	SR_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 99	Colon	SW-620_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 100	Colon	SW-620_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 101	Breast	T-47D_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 102	Breast	T-47D_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 103	Renal	TK-10_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 104	Renal	TK-10_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 105	CNS	U251_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 106	CNS	U251_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 107	Melanoma	UACC-257_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 108	Melanoma	UACC-257_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 109	Melanoma	UACC-62_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 110	Melanoma	UACC-62_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 111	Renal	UO-31_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 112	Renal	UO-31_erlotinib_10000nM_24h	erlotinib	10000nM	24h
## 113	Renal	786-0_erlotinib_0nM_24h	erlotinib	0nM	24h
## 114	Renal	786-0_erlotinib_0nM_24h	erlotinib	0nM	24h
## 115	Renal	A498_erlotinib_0nM_24h	erlotinib	0nM	24h
## 116	Renal	A498_erlotinib_0nM_24h	erlotinib	0nM	24h
## 117	Lung	A549_erlotinib_0nM_24h	erlotinib	0nM	24h
## 118	Lung	A549_erlotinib_0nM_24h	erlotinib	0nM	24h
## 119	Renal	ACHN_erlotinib_0nM_24h	erlotinib	0nM	24h
## 120	Renal	ACHN_erlotinib_0nM_24h	erlotinib	0nM	24h
## 121	Breast	BT-549_erlotinib_0nM_24h	erlotinib	0nM	24h
## 122	Breast	BT-549_erlotinib_0nM_24h	erlotinib	0nM	24h
## 123	Renal	CAKI-1_erlotinib_0nM_24h	erlotinib	0nM	24h
## 124	Renal	CAKI-1_erlotinib_0nM_24h	erlotinib	0nM	24h
## 125	<NA>	CCRF-CEM_erlotinib_0nM_24h	erlotinib	0nM	24h
## 126	Prostate	DU-145_erlotinib_0nM_24h	erlotinib	0nM	24h
## 127	Prostate	DU-145_erlotinib_0nM_24h	erlotinib	0nM	24h
## 128	Lung	EKVX_erlotinib_0nM_24h	erlotinib	0nM	24h
## 129	Lung	EKVX_erlotinib_0nM_24h	erlotinib	0nM	24h
## 130	Colon	HCC-2998_erlotinib_0nM_24h	erlotinib	0nM	24h
## 131	Colon	HCC-2998_erlotinib_0nM_24h	erlotinib	0nM	24h
## 132	Colon	HCT-116_erlotinib_0nM_24h	erlotinib	0nM	24h
## 133	Colon	HCT-116_erlotinib_0nM_24h	erlotinib	0nM	24h
## 134	Colon	HCT-15_erlotinib_0nM_24h	erlotinib	0nM	24h
## 135	Colon	HCT-15_erlotinib_0nM_24h	erlotinib	0nM	24h
## 136	<NA>	HL-60_erlotinib_0nM_24h	erlotinib	0nM	24h
## 137	Lung	HOP-62_erlotinib_0nM_24h	erlotinib	0nM	24h
## 138	Lung	HOP-62_erlotinib_0nM_24h	erlotinib	0nM	24h
## 139	Lung	HOP-92_erlotinib_0nM_24h	erlotinib	0nM	24h
## 140	Lung	HOP-92_erlotinib_0nM_24h	erlotinib	0nM	24h
## 141	Breast	HS-578T_erlotinib_0nM_24h	erlotinib	0nM	24h
## 142	Breast	HS-578T_erlotinib_0nM_24h	erlotinib	0nM	24h
## 143	<NA>	HT29_erlotinib_0nM_24h	erlotinib	0nM	24h
## 144	Ovarian	IGR-OV1_erlotinib_0nM_24h	erlotinib	0nM	24h
## 145	Ovarian	IGR-OV1_erlotinib_0nM_24h	erlotinib	0nM	24h
## 146	<NA>	K-562_erlotinib_0nM_24h	erlotinib	0nM	24h
## 147	Colon	KM12_erlotinib_0nM_24h	erlotinib	0nM	24h
## 148	Colon	KM12_erlotinib_0nM_24h	erlotinib	0nM	24h
## 149	<NA>	LOX_erlotinib_0nM_24h	erlotinib	0nM	24h
## 150	Melanoma	M14_erlotinib_0nM_24h	erlotinib	0nM	24h
## 151	Melanoma	M14_erlotinib_0nM_24h	erlotinib	0nM	24h
## 152	Melanoma	MALME-3M_erlotinib_0nM_24h	erlotinib	0nM	24h
## 153	Melanoma	MALME-3M_erlotinib_0nM_24h	erlotinib	0nM	24h
## 154	Breast	MCF7_erlotinib_0nM_24h	erlotinib	0nM	24h
## 155	Breast	MCF7_erlotinib_0nM_24h	erlotinib	0nM	24h
## 156	Breast	MDA-MB-231_erlotinib_0nM_24h	erlotinib	0nM	24h
## 157	Breast	MDA-MB-231_erlotinib_0nM_24h	erlotinib	0nM	24h
## 158	Melanoma	MDA-MB-435_erlotinib_0nM_24h	erlotinib	0nM	24h
## 159	Melanoma	MDA-MB-435_erlotinib_0nM_24h	erlotinib	0nM	24h
## 160	Breast	MDA-MB-468_erlotinib_0nM_24h	erlotinib	0nM	24h
## 161	Breast	MDA-MB-468_erlotinib_0nM_24h	erlotinib	0nM	24h
## 162	Leukemia	MOLT-4_erlotinib_0nM_24h	erlotinib	0nM	24h
## 163	Leukemia	MOLT-4_erlotinib_0nM_24h	erlotinib	0nM	24h

## 163	Leukemia	MOL1-4_erlotinib_0nM_24h	erlotinib	0nM	24h
## 164	Ovarian	NCI-ADR-RES_erlotinib_0nM_24h	erlotinib	0nM	24h
## 165	Ovarian	NCI-ADR-RES_erlotinib_0nM_24h	erlotinib	0nM	24h
## 166	Lung	NCI-H226_erlotinib_0nM_24h	erlotinib	0nM	24h
## 167	Lung	NCI-H226_erlotinib_0nM_24h	erlotinib	0nM	24h
## 168	Lung	NCI-H23_erlotinib_0nM_24h	erlotinib	0nM	24h
## 169	Lung	NCI-H23_erlotinib_0nM_24h	erlotinib	0nM	24h
## 170	Lung	NCI-H322M_erlotinib_0nM_24h	erlotinib	0nM	24h
## 171	Lung	NCI-H322M_erlotinib_0nM_24h	erlotinib	0nM	24h
## 172	Lung	NCI-H460_erlotinib_0nM_24h	erlotinib	0nM	24h
## 173	Lung	NCI-H460_erlotinib_0nM_24h	erlotinib	0nM	24h
## 174	Lung	NCI-H522_erlotinib_0nM_24h	erlotinib	0nM	24h
## 175	Lung	NCI-H522_erlotinib_0nM_24h	erlotinib	0nM	24h
## 176	Ovarian	OVCAR-3_erlotinib_0nM_24h	erlotinib	0nM	24h
## 177	Ovarian	OVCAR-3_erlotinib_0nM_24h	erlotinib	0nM	24h
## 178	Ovarian	OVCAR-4_erlotinib_0nM_24h	erlotinib	0nM	24h
## 179	Ovarian	OVCAR-4_erlotinib_0nM_24h	erlotinib	0nM	24h
## 180	Ovarian	OVCAR-5_erlotinib_0nM_24h	erlotinib	0nM	24h
## 181	Ovarian	OVCAR-5_erlotinib_0nM_24h	erlotinib	0nM	24h
## 182	Ovarian	OVCAR-8_erlotinib_0nM_24h	erlotinib	0nM	24h
## 183	Ovarian	OVCAR-8_erlotinib_0nM_24h	erlotinib	0nM	24h
## 184	Prostate	PC-3_erlotinib_0nM_24h	erlotinib	0nM	24h
## 185	Prostate	PC-3_erlotinib_0nM_24h	erlotinib	0nM	24h
## 186	Leukemia	RPMI-8226_erlotinib_0nM_24h	erlotinib	0nM	24h
## 187	Leukemia	RPMI-8226_erlotinib_0nM_24h	erlotinib	0nM	24h
## 188	Renal	RXF-393_erlotinib_0nM_24h	erlotinib	0nM	24h
## 189	Renal	RXF-393_erlotinib_0nM_24h	erlotinib	0nM	24h
## 190	CNS	SF-268_erlotinib_0nM_24h	erlotinib	0nM	24h
## 191	CNS	SF-268_erlotinib_0nM_24h	erlotinib	0nM	24h
## 192	CNS	SF-295_erlotinib_0nM_24h	erlotinib	0nM	24h
## 193	CNS	SF-295_erlotinib_0nM_24h	erlotinib	0nM	24h
## 194	CNS	SF-539_erlotinib_0nM_24h	erlotinib	0nM	24h
## 195	CNS	SF-539_erlotinib_0nM_24h	erlotinib	0nM	24h
## 196	Melanoma	SK-MEL-2_erlotinib_0nM_24h	erlotinib	0nM	24h
## 197	Melanoma	SK-MEL-2_erlotinib_0nM_24h	erlotinib	0nM	24h
## 198	Melanoma	SK-MEL-28_erlotinib_0nM_24h	erlotinib	0nM	24h
## 199	Melanoma	SK-MEL-28_erlotinib_0nM_24h	erlotinib	0nM	24h
## 200	Melanoma	SK-MEL-5_erlotinib_0nM_24h	erlotinib	0nM	24h
## 201	Melanoma	SK-MEL-5_erlotinib_0nM_24h	erlotinib	0nM	24h
## 202	Ovarian	SK-OV-3_erlotinib_0nM_24h	erlotinib	0nM	24h
## 203	Ovarian	SK-OV-3_erlotinib_0nM_24h	erlotinib	0nM	24h
## 204	Renal	SN12C_erlotinib_0nM_24h	erlotinib	0nM	24h
## 205	Renal	SN12C_erlotinib_0nM_24h	erlotinib	0nM	24h
## 206	CNS	SNB-19_erlotinib_0nM_24h	erlotinib	0nM	24h
## 207	CNS	SNB-19_erlotinib_0nM_24h	erlotinib	0nM	24h
## 208	CNS	SNB-75_erlotinib_0nM_24h	erlotinib	0nM	24h
## 209	CNS	SNB-75_erlotinib_0nM_24h	erlotinib	0nM	24h
## 210	<NA>	SR_erlotinib_0nM_24h	erlotinib	0nM	24h
## 211	Colon	SW-620_erlotinib_0nM_24h	erlotinib	0nM	24h
## 212	Colon	SW-620_erlotinib_0nM_24h	erlotinib	0nM	24h
## 213	Breast	T-47D_erlotinib_0nM_24h	erlotinib	0nM	24h
## 214	Breast	T-47D_erlotinib_0nM_24h	erlotinib	0nM	24h
## 215	Renal	TK-10_erlotinib_0nM_24h	erlotinib	0nM	24h
## 216	Renal	TK-10_erlotinib_0nM_24h	erlotinib	0nM	24h
## 217	CNS	U251_erlotinib_0nM_24h	erlotinib	0nM	24h
## 218	CNS	U251_erlotinib_0nM_24h	erlotinib	0nM	24h
## 219	Melanoma	UACC-257_erlotinib_0nM_24h	erlotinib	0nM	24h
## 220	Melanoma	UACC-257_erlotinib_0nM_24h	erlotinib	0nM	24h
## 221	Melanoma	UACC-62_erlotinib_0nM_24h	erlotinib	0nM	24h
## 222	Melanoma	UACC-62_erlotinib_0nM_24h	erlotinib	0nM	24h
## 223	Renal	UO-31_erlotinib_0nM_24h	erlotinib	0nM	24h
## 224	Renal	UO-31_erlotinib_0nM_24h	erlotinib	0nM	24h
##	tissue.y				
## 1	Renal				
## 2	Renal				
## 3	Renal				
## 4	Renal				
## 5	Lung				
## 6	Lung				
## 7	Renal				
## 8	Renal				
## 9	Breast				
## 10	Breast				

##	11	Renal
##	12	Renal
##	13	Leukemia
##	14	Prostate
##	15	Prostate
##	16	Lung
##	17	Lung
##	18	Colon
##	19	Colon
##	20	Colon
##	21	Colon
##	22	Colon
##	23	Colon
##	24	Leukemia
##	25	Lung
##	26	Lung
##	27	Lung
##	28	Lung
##	29	Breast
##	30	Breast
##	31	Colon
##	32	Ovarian
##	33	Ovarian
##	34	Leukemia
##	35	Colon
##	36	Colon
##	37	Melanoma
##	38	Melanoma
##	39	Melanoma
##	40	Melanoma
##	41	Melanoma
##	42	Breast
##	43	Breast
##	44	Breast
##	45	Breast
##	46	Melanoma
##	47	Melanoma
##	48	Breast
##	49	Breast
##	50	Leukemia
##	51	Leukemia
##	52	Ovarian
##	53	Ovarian
##	54	Lung
##	55	Lung
##	56	Lung
##	57	Lung
##	58	Lung
##	59	Lung
##	60	Lung
##	61	Lung
##	62	Lung
##	63	Lung
##	64	Ovarian
##	65	Ovarian
##	66	Ovarian
##	67	Ovarian
##	68	Ovarian
##	69	Ovarian
##	70	Ovarian
##	71	Ovarian
##	72	Prostate
##	73	Prostate
##	74	Leukemia
##	75	Leukemia
##	76	Renal
##	77	Renal
##	78	CNS
##	79	CNS
##	80	CNS
##	81	CNS
##	82	CNS
##	83	CNS

## 84 Melanoma  
## 85 Melanoma  
## 86 Melanoma  
## 87 Melanoma  
## 88 Melanoma  
## 89 Melanoma  
## 90 Ovarian  
## 91 Ovarian  
## 92 Renal  
## 93 Renal  
## 94 CNS  
## 95 CNS  
## 96 CNS  
## 97 CNS  
## 98 Leukemia  
## 99 Colon  
## 100 Colon  
## 101 Breast  
## 102 Breast  
## 103 Renal  
## 104 Renal  
## 105 CNS  
## 106 CNS  
## 107 Melanoma  
## 108 Melanoma  
## 109 Melanoma  
## 110 Melanoma  
## 111 Renal  
## 112 Renal  
## 113 Renal  
## 114 Renal  
## 115 Renal  
## 116 Renal  
## 117 Lung  
## 118 Lung  
## 119 Renal  
## 120 Renal  
## 121 Breast  
## 122 Breast  
## 123 Renal  
## 124 Renal  
## 125 Leukemia  
## 126 Prostate  
## 127 Prostate  
## 128 Lung  
## 129 Lung  
## 130 Colon  
## 131 Colon  
## 132 Colon  
## 133 Colon  
## 134 Colon  
## 135 Colon  
## 136 Leukemia  
## 137 Lung  
## 138 Lung  
## 139 Lung  
## 140 Lung  
## 141 Breast  
## 142 Breast  
## 143 Colon  
## 144 Ovarian  
## 145 Ovarian  
## 146 Leukemia  
## 147 Colon  
## 148 Colon  
## 149 Melanoma  
## 150 Melanoma  
## 151 Melanoma  
## 152 Melanoma  
## 153 Melanoma  
## 154 Breast  
## 155 Breast  
## 156 Breast

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## 156 Breast
## 157 Breast
## 158 Melanoma
## 159 Melanoma
## 160 Breast
## 161 Breast
## 162 Leukemia
## 163 Leukemia
## 164 Ovarian
## 165 Ovarian
## 166 Lung
## 167 Lung
## 168 Lung
## 169 Lung
## 170 Lung
## 171 Lung
## 172 Lung
## 173 Lung
## 174 Lung
## 175 Lung
## 176 Ovarian
## 177 Ovarian
## 178 Ovarian
## 179 Ovarian
## 180 Ovarian
## 181 Ovarian
## 182 Ovarian
## 183 Ovarian
## 184 Prostate
## 185 Prostate
## 186 Leukemia
## 187 Leukemia
## 188 Renal
## 189 Renal
## 190 CNS
## 191 CNS
## 192 CNS
## 193 CNS
## 194 CNS
## 195 CNS
## 196 Melanoma
## 197 Melanoma
## 198 Melanoma
## 199 Melanoma
## 200 Melanoma
## 201 Melanoma
## 202 Ovarian
## 203 Ovarian
## 204 Renal
## 205 Renal
## 206 CNS
## 207 CNS
## 208 CNS
## 209 CNS
## 210 Leukemia
## 211 Colon
## 212 Colon
## 213 Breast
## 214 Breast
## 215 Renal
## 216 Renal
## 217 CNS
## 218 CNS
## 219 Melanoma
## 220 Melanoma
## 221 Melanoma
## 222 Melanoma
## 223 Renal
## 224 Renal
```

```
rmv.rows = apply(el, 1, function(x) {
  sum(is.na(x))
}) # Go through each row and sum up all missing values
row.names(rmv.rows)
```

Create data frame with lapatinib and erlotinib data

```
fc<-(Treated-Untreated)
fc<-data.frame(scale(fc))
all<-data.frame(fc[grep("lapatinib|erlotinib", colnames(fc))])
```

since erlotinip contains more columns than lapatinib, we have to remove these columns

```
all.rmv<-all[, -which(colnames(all) %in% c(
  "CCRF.CEM_erlotinib_0nM_24h",
  "HL.60_erlotinib_0nM_24h",
  "HT29_erlotinib_0nM_24h",
  "K.562_erlotinib_0nM_24h",
  "LOX_erlotinib_0nM_24h",
  "SR_erlotinib_0nM_24h",
  "COLO.205_lapatinib_0nM_24h"))]
```

Checking the rows

```
la<-data.frame(all.rmv[grep("lapatinib", colnames(all.rmv))])
ncol(la)
```

```
## [1] 0
```

```
er<-data.frame(all.rmv[grep("erlotinib", colnames(all.rmv))])
ncol(er)
```

```
## [1] 0
```

```
erla<-data.frame(er,la)
ncol(all.rmv) #to prove if the columns are removed
```

```
## [1] 0
```

## Anova

p = 0.2 means that the result does not differ significantly. Thus, the two drugs did not differ significantly from each other.

```
``{r}
```

```
drug<-c(rep('Erlotinib',53), rep('Lapatinib',53))
```

```
expression_drug<-apply(erla, MARGIN = 2, sum)
```

```
df_drug<-data.frame(expression_drug, drug)
```

```
library(ggpubr)
```

```
ggboxplot (data = df_drug, x="drug", y="expression_drug",
color = "drug",
```

```
# add = "jitter", legend = "none")+ # rotate_x_text(angle = 45)+ # geom_hline(yintercept = mean(lapatinib$MCF7_lapatinib_0nM_24h),
linetype = 2)+ # Add horizontal line at base mean # stat_compare_means(method = "anova")+ # Add global annova p-value #
stat_compare_means(label = "p.signif", method = "t.test", # ref.group = ".all.", hide.ns = TRUE) # Pairwise comparison against all
```



## Question 3: Comparing lapatinib treated breast and cns celllines

```
L_fc <- select(Fold_Change, contains("Lapa"))
L_fc <- as.data.frame(t(L_fc))
rownames(Metadata) <- Metadata$sample

L_treated <- select(Treated, contains("Lapa"))
L_treated <- t(L_treated)
L_untreated <- select(Untreated, contains("Lapa"))
L_untreated <- t(L_untreated)

# selecting breast Lapatinib samples
breast <- Metadata[Metadata[, 'tissue']=="Breast",]
rownames(breast) <- breast$sample
rownames(breast) <- gsub(x = rownames(breast), pattern = "-", replacement = ".")

breastFC <- subset(L_fc, rownames(L_fc) %in% rownames(breast))
breastTreated <- subset(L_treated, rownames(L_treated) %in% rownames(breast))
breastUntreated <- subset(L_untreated, rownames(L_untreated) %in% rownames(breast))#

# selecting CNS Lapatinib samples
cns <- Metadata[Metadata[, 'tissue']=="CNS",]
rownames(cns) <- cns$sample
rownames(cns) <- gsub(x = rownames(cns), pattern = "-", replacement = ".")

cnsFC <- subset(L_fc, rownames(L_fc) %in% rownames(cns))
cnsTreated <- subset(L_treated, rownames(L_treated) %in% rownames(cns))
cnsUntreated <- subset(L_untreated, rownames(L_untreated) %in% rownames(cns))

#performing a paired t-test of treated and untreated samples
t_test_cns <- col_tpaired(cnsTreated, cnsUntreated, alternative = "two.sided", mu = 0, conf.level = 0.95)
t_test_breast <- col_tpaired(breastTreated, breastUntreated, alternative = "two.sided", mu = 0, conf.level = 0.95)

#obtaining Benjamini-Hochberg adjusted p-values
pval_cns <- t_test_cns$pvalue
pval_breast <- t_test_breast$pvalue

fdr_cns <- p.adjust(pval_cns, "BH")
fdr_breast <- p.adjust(pval_breast, "BH")

#obtaining mean FC values over all samples
breastFCm <- as.numeric(colMeans(breastFC))
cnsFCm <- as.numeric(colMeans(cnsFC))
genes <- colnames(breastFC)

## breast volcano plot
#creating a matrix containg all needed values for plotting
diff_df_breast <- data.frame(gene = genes, Fold = breastFCm, FDR = fdr_breast)
diff_df_breast$absFold <- abs(diff_df_breast$Fold)
head(diff_df_breast)
```

##	gene	Fold	FDR	absFold
## 1	A1CF	0.037268413	0.8765540	0.037268413
## 2	A2M	-0.032213825	0.7188608	0.032213825
## 3	A4GALT	0.006012452	0.9793436	0.006012452
## 4	A4GNT	-0.053969518	0.4235638	0.053969518
## 5	AAAS	0.081656784	0.5283372	0.081656784
## 6	AACS	0.023767096	0.8115022	0.023767096

```

# add a grouping column; default value is "not significant"
diff_df_breast$group <- "NotSignificant"

# change the grouping for the entries with significance but not a large enough Fold change
diff_df_breast[which(diff_df_breast['FDR'] < 0.5 & (diff_df_breast['absFold']) < 0.2 ), "group"] <- "Significant"

# change the grouping for the entries a large enough Fold change but not a low enough p value
diff_df_breast[which(diff_df_breast['FDR'] > 0.5 & (diff_df_breast['absFold']) > 0.2 ), "group"] <- "FoldChange"

# change the grouping for the entries with both significance and large enough fold change
diff_df_breast[which(diff_df_breast['FDR'] < 0.5 & (diff_df_breast['absFold']) > 0.2 ), "group"] <- "Significant&FoldChange"

# Find and label the top peaks.
top_peaks_breast <- diff_df_breast[with(diff_df_breast, order(Fold, FDR)),][1:10,]
top_peaks_breast <- rbind(top_peaks_breast, diff_df_breast[with(diff_df_breast, order(-Fold, FDR)),][1:10,])

# Add gene labels for all of the top genes we found
# creating an empty list, and filling it with entries for each row in the dataframe
# each list entry is another list with named items that will be used
a <- list()
for (i in seq_len(nrow(top_peaks_breast))) {
  m <- top_peaks_breast[i, ]
  a[[i]] <- list(
    x = m["Fold"],
    y = -log10(m["FDR"]),
    text = m["gene"],
    xref = "x",
    yref = "y",
    showarrow = TRUE,
    arrowhead = 0.5,
    ax = 20,
    ay = -40
  )
}

plot_breast <- plot_ly(data = diff_df_breast, x = diff_df_breast$Fold, y = -log10(diff_df_breast$FDR), type = "scatter", text = diff_df_breast$gene, mode = "markers", color = diff_df_breast$group) %>%
  layout(title = "Volcano Plot of Lapatinib breast cancer samples",
    xaxis = list(title = "log2 Fold Change"),
    yaxis = list(title = "FDR")) %>%
  layout(annotations = a)
plot_breast

```

```
###thresholds still need to be discussed
```

```
## CNS volcano plot
```

```
diff_df_cns <- data.frame(gene = genes, Fold = cnsFCm, FDR = fdr_cns)
diff_df_cns$absFold <- abs(diff_df_cns$Fold)
head(diff_df_cns)
```

```
##      gene      Fold      FDR      absFold
## 1  A1CF  0.066575311 0.5939566 0.066575311
## 2   A2M  0.038348381 0.6873009 0.038348381
## 3 A4GALT 0.000390011 0.9980719 0.000390011
## 4  A4GNT -0.018219799 0.8780106 0.018219799
## 5   AAAS 0.014723327 0.9008420 0.014723327
## 6   AACS 0.003887384 0.9870209 0.003887384
```

```
# add a grouping column; default value is "not significant"
```

```
diff_df_cns$group <- "NotSignificant"
```

```
# change the grouping for the entries with significance but not a large enough Fold change
```

```
diff_df_cns[which(diff_df_cns['FDR'] < 0.5 & (diff_df_cns['absFold']) < 0.2 ),"group"] <- "Significant"
```

```
# change the grouping for the entries a large enough Fold change but not a low enough p value
```

```
diff_df_cns[which(diff_df_cns['FDR'] > 0.5 & (diff_df_cns['absFold']) > 0.2 ),"group"] <- "FoldChange"
```

```
# change the grouping for the entries with both significance and large enough fold change
```

```
diff_df_cns[which(diff_df_cns['FDR'] < 0.5 & (diff_df_cns['absFold']) > 0.2 ),"group"] <- "Significant&FoldChange"
```

```
# Find and label the top peaks..
```

```
top_peaks_cns <- diff_df_cns[with(diff_df_cns, order(Fold, FDR)),][1:10,]
```

```
top_peaks_cns <- rbind(top_peaks_cns, diff_df_cns[with(diff_df_cns, order(-Fold, FDR)),][1:10,])
```

```
a <- list()
```

```
for (i in seq_len(nrow(top_peaks_cns))) {
```

```
  m <- top_peaks_cns[i, ]
```

```
  a[[i]] <- list(
```

```
    x = m[["Fold"]],
```

```
    y = -log10(m[["FDR"]]),
```

```
    text = m[["gene"]],
```

```
    xref = "x",
```

```
    yref = "y",
```

```
    showarrow = TRUE,
```

```
    arrowhead = 0.5,
```

```
    ax = 20,
```

```
    ay = -40
```

```
  )
```

```
}
```

```
plot_cns <- plot_ly(data = diff_df_cns, x = diff_df_cns$Fold, y = -log10(diff_df_cns$FDR), type = "scatter", text = diff_df_cns$gene, mode = "markers", color = diff_df_cns$group) %>%
```

```
  layout(title = "Volcano Plot of Lapatinib CNS cancer samples",
```

```
    xaxis = list(title = "log2 Fold Change"),
```

```
    yaxis = list(title = "FDR")) %>%
```

```
  layout(annotations = a)
```

```
plot_cns
```

```

# selectet top peak genes common in cns and breast tissue
tpb_comparison <- subset(top_peaks_breast, gene %in% top_peaks_cns$gene)
tpc_comparison <- subset(top_peaks_cns, gene %in% top_peaks_breast$gene)

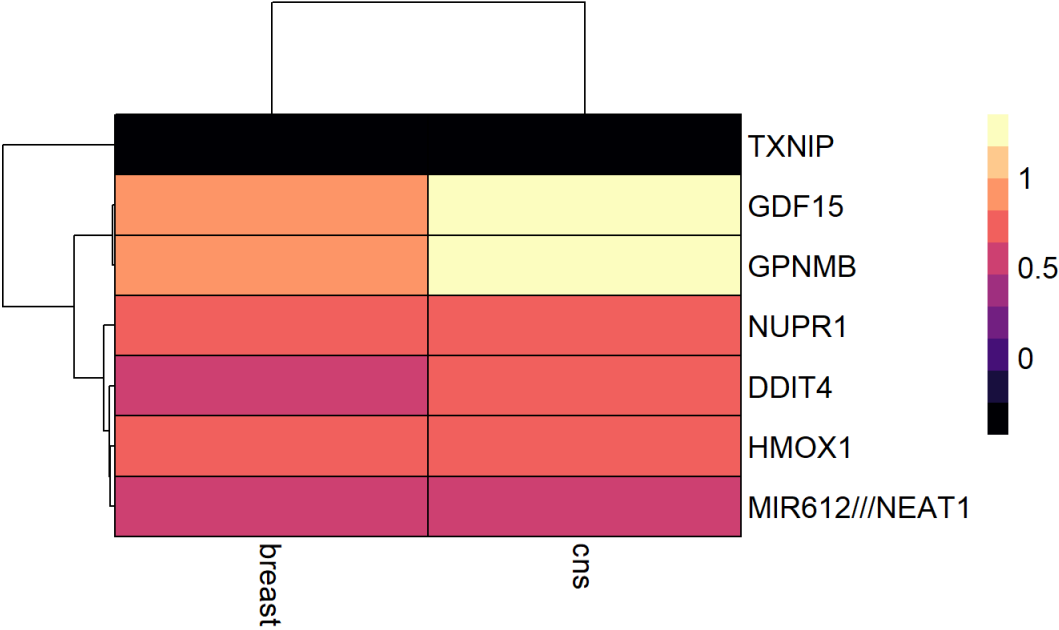
# order common genes alphabetically
tpb_comparison <- tpb_comparison[order(tpb_comparison$gene),]
tpc_comparison <- tpc_comparison[order(tpc_comparison$gene),]

## creating heat map of FCs to compare values
cor_mat <- cbind("breast" = tpb_comparison$Fold, "cns" = tpc_comparison$Fold)
rownames(cor_mat) <- tpb_comparison$gene
data <- read.delim

pheatmap(
  mat          = cor_mat,
  color        = magma(10),
  border_color = "black",
  show_colnames = TRUE,
  show_rownames = TRUE,
  drop_levels  = TRUE,
  fontsize     = 14,
  main         = "Comparison:
  FC levels of cns and breast top peak genes"
)

```

Comparison:  
FC levels of cns and breast top peak genes



===== still in progress >>>>>> cd0d16c457bb9d18b398e24c369d80b672402313