Coronavirus Liver and Blood Capillary Samples

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These samples are the headers added from three Gene Expression Omnibus studies at

* ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89166
* ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89160
* ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE100509

The first two studies are part of the same study that used human liver tumor samples in vitro to compare the effects of the coronavirus over time. The third study used human microvascular blood capillaries in vitro to study the effects of the coronavirus over time.

In the first two studies that used the liver tumor samples to examine the effects of the coronavirus in vitro, there were four groups inoculated or treated with the active coronavirus and four groups not inoculated with the active coranavirus, and two samples that were treated with heat inactivated coronavirus, and two samples that were treated with active coronavirus and IL-1alpha to see the gene expression changes over one hour’s time.

In the the third study that used blood capillaries, there were five samples followed over a 0,12,24,36, and 48 hour time intervals in groups A,B,C,D, and E that compared the time interval values of screening for changes in microarray analysis with a mock group of the same.

This following data is the data of all genes in common between these three studies, cleaned to remove missing values and with the attached gene symbols from the GEO platform for the probe IDs.

both <- read.csv('both\_clean\_liver\_capillary\_CoV.csv', sep=',', header=TRUE,   
 na.strings=c('',' '))

dim(both)

## [1] 21754 63

colnames(both)

## [1] "GENE\_SYMBOL"   
## [2] "LiverTumorSamples.GSM2359851\_CoV1"   
## [3] "LiverTumorSamples.GSM2359853\_CoV2"   
## [4] "LiverTumorSamples.GSM2359910\_CoV3"   
## [5] "LiverTumorSamples.GSM2359913\_CoV4"   
## [6] "LiverTumorSamples.GSM2359850\_ctrl1"   
## [7] "LiverTumorSamples.GSM2359852\_ctrl2"   
## [8] "LiverTumorSamples.GSM2359911\_ctrl3"   
## [9] "LiverTumorSamples.GSM2359914\_ctrl4"   
## [10] "LiverTumorSamples.GSM2359912\_Il1"   
## [11] "LiverTumorSamples.GSM2359917\_IL2"   
## [12] "LiverTumorSamples.GSM2359915\_inactiveHeatCoV1"  
## [13] "LiverTumorSamples.GSM2359916\_inactiveHeatCoV2"  
## [14] "capillarySamples.GSM2685693\_MERS\_CoV\_0hr\_A"   
## [15] "capillarySamples.GSM2685694\_MERS\_CoV\_0hr\_B"   
## [16] "capillarySamples.GSM2685695\_MERS\_CoV\_0hr\_C"   
## [17] "capillarySamples.GSM2685696\_MERS\_CoV\_0hr\_D"   
## [18] "capillarySamples.GSM2685697\_MERS\_CoV\_0hr\_E"   
## [19] "capillarySamples.GSM2685698\_ctrl\_0hr\_A"   
## [20] "capillarySamples.GSM2685699\_ctrl\_0hr\_B"   
## [21] "capillarySamples.GSM2685700\_ctrl\_0hr\_C"   
## [22] "capillarySamples.GSM2685701\_ctrl\_0hr\_D"   
## [23] "capillarySamples.GSM2685702\_ctrl\_0hr\_E"   
## [24] "capillarySamples.GSM2685703\_MERS\_CoV\_12hr\_A"   
## [25] "capillarySamples.GSM2685704\_MERS\_CoV\_12hr\_B"   
## [26] "capillarySamples.GSM2685705\_MERS\_CoV\_12hr\_C"   
## [27] "capillarySamples.GSM2685706\_MERS\_CoV\_12hr\_D"   
## [28] "capillarySamples.GSM2685707\_MERS\_CoV\_12hr\_E"   
## [29] "capillarySamples.GSM2685708\_ctrl\_12hr\_A"   
## [30] "capillarySamples.GSM2685709\_ctrl\_12hr\_B"   
## [31] "capillarySamples.GSM2685710\_ctrl\_12hr\_C"   
## [32] "capillarySamples.GSM2685711\_ctrl\_12hr\_D"   
## [33] "capillarySamples.GSM2685712\_ctrl\_12hr\_E"   
## [34] "capillarySamples.GSM2685713\_MERS\_CoV\_24hr\_A"   
## [35] "capillarySamples.GSM2685714\_MERS\_CoV\_24hr\_B"   
## [36] "capillarySamples.GSM2685715\_MERS\_CoV\_24hr\_C"   
## [37] "capillarySamples.GSM2685716\_MERS\_CoV\_24hr\_D"   
## [38] "capillarySamples.GSM2685717\_MERS\_CoV\_24hr\_E"   
## [39] "capillarySamples.GSM2685718\_ctrl\_24hr\_A"   
## [40] "capillarySamples.GSM2685719\_ctrl\_24hr\_B"   
## [41] "capillarySamples.GSM2685720\_ctrl\_24hr\_C"   
## [42] "capillarySamples.GSM2685721\_ctrl\_24hr\_D"   
## [43] "capillarySamples.GSM2685722\_ctrl\_24hr\_E"   
## [44] "capillarySamples.GSM2685723\_MERS\_CoV\_36hr\_A"   
## [45] "capillarySamples.GSM2685724\_MERS\_CoV\_36hr\_B"   
## [46] "capillarySamples.GSM2685725\_MERS\_CoV\_36hr\_C"   
## [47] "capillarySamples.GSM2685726\_MERS\_CoV\_36hr\_D"   
## [48] "capillarySamples.GSM2685727\_MERS\_CoV\_36hr\_E"   
## [49] "capillarySamples.GSM2685728\_ctrl\_36hr\_A"   
## [50] "capillarySamples.GSM2685729\_ctrl\_36hr\_B"   
## [51] "capillarySamples.GSM2685730\_ctrl\_36hr\_C"   
## [52] "capillarySamples.GSM2685731\_ctrl\_36hr\_D"   
## [53] "capillarySamples.GSM2685732\_ctrl\_36hr\_E"   
## [54] "capillarySamples.GSM2685733\_MERS\_CoV\_48hr\_A"   
## [55] "capillarySamples.GSM2685734\_MERS\_CoV\_48hr\_B"   
## [56] "capillarySamples.GSM2685735\_MERS\_CoV\_48hr\_C"   
## [57] "capillarySamples.GSM2685736\_MERS\_CoV\_48hr\_D"   
## [58] "capillarySamples.GSM2685737\_MERS\_CoV\_48hr\_E"   
## [59] "capillarySamples.GSM2685738\_ctrl\_48hr\_A"   
## [60] "capillarySamples.GSM2685739\_ctrl\_48hr\_B"   
## [61] "capillarySamples.GSM2685740\_ctrl\_48hr\_C"   
## [62] "capillarySamples.GSM2685741\_ctrl\_48hr\_D"   
## [63] "capillarySamples.GSM2685742\_ctrl\_48hr\_E"

Lets group the samples that are our columns with descriptive and GEO ID names into their respective groups, get the fold change between the controls from those groups, attach to the original data table, both, as a different names, then order by the genes that have the most fold change then the least fold change. Take the first 100 genes from both lists, combine into one table of 200 genes and the samples with their fold change values ordered, make into a transposed data frame so that the samples are the rows, the stats removed, and the 200 genes are the header columns to save as a machine learning ready file.

Liver tumor study control and CoV treated. Also, the IL-alpha treated and the inactive CoV treated tables are in this code block.

names <- both$GENE\_SYMBOL  
  
liverCtrl <- both[,c(6:9)]  
row.names(liverCtrl) <- names  
  
liverCoV <- both[,c(2:5)]  
row.names(liverCoV) <- names  
  
liverIL <- both[,10:11]  
row.names(liverIL) <- names  
  
liverIACoV <- both[,12:13]  
row.names(liverIACoV) <- names

Get the row means of those liver samples groups each.

liverCtrl$CtrlMeanLvr <- rowMeans(liverCtrl)  
liverCoV$CoVMeanLvr <- rowMeans(liverCoV)  
liverIL$ILMeanLvr <- rowMeans(liverIL)  
liverIACoV$IACoVMeanLvr <- rowMeans(liverIACoV)

Get the fold change values of those states as a ratio to the control group values.

fold1 <- as.data.frame(cbind(liverCtrl$CtrlMeanLvr,liverCoV$CoVMeanLvr,liverIL$ILMeanLvr,  
 liverIACoV$IACoVMeanLvr))  
row.names(fold1) <- names  
colnames(fold1) <- c('CtrlMeanLvr','CoVMeanLvr','ILMeanLvr','IACoVMeanLvr')  
  
fold1$FC\_CoV <- fold1$CoVMeanLvr/fold1$CtrlMeanLvr  
fold1$FC\_IL <- fold1$ILMeanLvr/fold1$CtrlMeanLvr  
fold1$FC\_IACov <- fold1$IACoVMeanLvr/fold1$CtrlMeanLvr

Most expressed in liver samples by fold change of the Coronavirus, inactive CoronaVirus, and the IL-alpha treated Coronavirus as tables.

mostCoV <- fold1[order(fold1$FC\_CoV, decreasing = TRUE)[0:100],]  
mostIL <- fold1[order(fold1$FC\_IL, decreasing = TRUE)[0:100],]  
mostIACoV <- fold1[order(fold1$FC\_IACov, decreasing = TRUE)[0:100],]

Least expressed in liver samples by fold change of the Coronavirus, inactive CoronaVirus, and the IL-alpha treated Coronavirus as tables.

leastCoV <- fold1[order(fold1$FC\_CoV, decreasing = FALSE)[0:100],]  
leastIL <- fold1[order(fold1$FC\_IL, decreasing = FALSE)[0:100],]  
leastIACoV <- fold1[order(fold1$FC\_IACov, decreasing = FALSE)[0:100],]

Gene Expressions with most changes in the liver samples.

changes <- rbind(mostCoV,mostIL,mostIACoV,leastCoV,leastIL,leastIACoV)  
Changes <- changes[!duplicated(row.names(changes)),]  
length(unique(row.names(Changes)))

## [1] 600

Get the magnitude of the fold change genes’ row means.

Changes$MagnitudeFCs <- abs(rowMeans(Changes[,5:7]))

Combine this to the samples data for the liver tumor group.

Changes$Gene <- row.names(Changes)  
combined1 <- merge(both, Changes, by.x='GENE\_SYMBOL', by.y='Gene')  
  
combined2 <- combined1[order(combined1$MagnitudeFCs, decreasing=TRUE),]  
  
CombinedLiver <- combined2[c(0:100,354:453),]

Machine Learning data for liver samples with 200 genes in the group of most gene expression changes.

names1 <- CombinedLiver$GENE\_SYMBOL  
names2 <- colnames(CombinedLiver)  
row.names(CombinedLiver) <- names1  
  
Combo\_lvr\_ML <- as.data.frame(t(CombinedLiver))  
  
colnames(Combo\_lvr\_ML) <- gsub('-','\_',colnames(Combo\_lvr\_ML))  
Combo1 <- Combo\_lvr\_ML[c(2:63),] #remove stats of fold change values and gene symbol row

Lets add a class field called Class\_Type to use machine learning on predicting class with these 200 genes and 62 mixed samples of capillary and liver tumor both inoculated with Coronavirus.

a <- rep('liver\_CoV', 4)  
b <- rep('liver\_Ctrl',4)  
c <- rep('liver\_CoV\_IL',2)  
d <- rep('liver\_IA\_CoV',2)  
e <- rep('capillary\_CoV\_0hr',5)  
f <- rep('capillary\_Ctrl\_0hr',5)  
g <- rep('capillary\_Cov\_12hr',5)  
h <- rep('capillary\_Ctrl\_12hr',5)  
i <- rep('capillary\_Cov\_24hr',5)  
j <- rep('capillary\_Ctrl\_24hr',5)  
k <- rep('capillary\_Cov\_36hr',5)  
l <- rep('capillary\_Ctrl\_36hr',5)  
m <- rep('capillary\_Cov\_48hr',5)  
n <- rep('capillary\_Ctrl\_48hr',5)  
  
type <- as.data.frame(c(a,b,c,d,e,f,g,h,i,j,k,l,m,n))  
colnames(type) <- 'Class\_Type'  
row.names(type) <- row.names(Combo1)  
type

## Class\_Type  
## LiverTumorSamples.GSM2359851\_CoV1 liver\_CoV  
## LiverTumorSamples.GSM2359853\_CoV2 liver\_CoV  
## LiverTumorSamples.GSM2359910\_CoV3 liver\_CoV  
## LiverTumorSamples.GSM2359913\_CoV4 liver\_CoV  
## LiverTumorSamples.GSM2359850\_ctrl1 liver\_Ctrl  
## LiverTumorSamples.GSM2359852\_ctrl2 liver\_Ctrl  
## LiverTumorSamples.GSM2359911\_ctrl3 liver\_Ctrl  
## LiverTumorSamples.GSM2359914\_ctrl4 liver\_Ctrl  
## LiverTumorSamples.GSM2359912\_Il1 liver\_CoV\_IL  
## LiverTumorSamples.GSM2359917\_IL2 liver\_CoV\_IL  
## LiverTumorSamples.GSM2359915\_inactiveHeatCoV1 liver\_IA\_CoV  
## LiverTumorSamples.GSM2359916\_inactiveHeatCoV2 liver\_IA\_CoV  
## capillarySamples.GSM2685693\_MERS\_CoV\_0hr\_A capillary\_CoV\_0hr  
## capillarySamples.GSM2685694\_MERS\_CoV\_0hr\_B capillary\_CoV\_0hr  
## capillarySamples.GSM2685695\_MERS\_CoV\_0hr\_C capillary\_CoV\_0hr  
## capillarySamples.GSM2685696\_MERS\_CoV\_0hr\_D capillary\_CoV\_0hr  
## capillarySamples.GSM2685697\_MERS\_CoV\_0hr\_E capillary\_CoV\_0hr  
## capillarySamples.GSM2685698\_ctrl\_0hr\_A capillary\_Ctrl\_0hr  
## capillarySamples.GSM2685699\_ctrl\_0hr\_B capillary\_Ctrl\_0hr  
## capillarySamples.GSM2685700\_ctrl\_0hr\_C capillary\_Ctrl\_0hr  
## capillarySamples.GSM2685701\_ctrl\_0hr\_D capillary\_Ctrl\_0hr  
## capillarySamples.GSM2685702\_ctrl\_0hr\_E capillary\_Ctrl\_0hr  
## capillarySamples.GSM2685703\_MERS\_CoV\_12hr\_A capillary\_Cov\_12hr  
## capillarySamples.GSM2685704\_MERS\_CoV\_12hr\_B capillary\_Cov\_12hr  
## capillarySamples.GSM2685705\_MERS\_CoV\_12hr\_C capillary\_Cov\_12hr  
## capillarySamples.GSM2685706\_MERS\_CoV\_12hr\_D capillary\_Cov\_12hr  
## capillarySamples.GSM2685707\_MERS\_CoV\_12hr\_E capillary\_Cov\_12hr  
## capillarySamples.GSM2685708\_ctrl\_12hr\_A capillary\_Ctrl\_12hr  
## capillarySamples.GSM2685709\_ctrl\_12hr\_B capillary\_Ctrl\_12hr  
## capillarySamples.GSM2685710\_ctrl\_12hr\_C capillary\_Ctrl\_12hr  
## capillarySamples.GSM2685711\_ctrl\_12hr\_D capillary\_Ctrl\_12hr  
## capillarySamples.GSM2685712\_ctrl\_12hr\_E capillary\_Ctrl\_12hr  
## capillarySamples.GSM2685713\_MERS\_CoV\_24hr\_A capillary\_Cov\_24hr  
## capillarySamples.GSM2685714\_MERS\_CoV\_24hr\_B capillary\_Cov\_24hr  
## capillarySamples.GSM2685715\_MERS\_CoV\_24hr\_C capillary\_Cov\_24hr  
## capillarySamples.GSM2685716\_MERS\_CoV\_24hr\_D capillary\_Cov\_24hr  
## capillarySamples.GSM2685717\_MERS\_CoV\_24hr\_E capillary\_Cov\_24hr  
## capillarySamples.GSM2685718\_ctrl\_24hr\_A capillary\_Ctrl\_24hr  
## capillarySamples.GSM2685719\_ctrl\_24hr\_B capillary\_Ctrl\_24hr  
## capillarySamples.GSM2685720\_ctrl\_24hr\_C capillary\_Ctrl\_24hr  
## capillarySamples.GSM2685721\_ctrl\_24hr\_D capillary\_Ctrl\_24hr  
## capillarySamples.GSM2685722\_ctrl\_24hr\_E capillary\_Ctrl\_24hr  
## capillarySamples.GSM2685723\_MERS\_CoV\_36hr\_A capillary\_Cov\_36hr  
## capillarySamples.GSM2685724\_MERS\_CoV\_36hr\_B capillary\_Cov\_36hr  
## capillarySamples.GSM2685725\_MERS\_CoV\_36hr\_C capillary\_Cov\_36hr  
## capillarySamples.GSM2685726\_MERS\_CoV\_36hr\_D capillary\_Cov\_36hr  
## capillarySamples.GSM2685727\_MERS\_CoV\_36hr\_E capillary\_Cov\_36hr  
## capillarySamples.GSM2685728\_ctrl\_36hr\_A capillary\_Ctrl\_36hr  
## capillarySamples.GSM2685729\_ctrl\_36hr\_B capillary\_Ctrl\_36hr  
## capillarySamples.GSM2685730\_ctrl\_36hr\_C capillary\_Ctrl\_36hr  
## capillarySamples.GSM2685731\_ctrl\_36hr\_D capillary\_Ctrl\_36hr  
## capillarySamples.GSM2685732\_ctrl\_36hr\_E capillary\_Ctrl\_36hr  
## capillarySamples.GSM2685733\_MERS\_CoV\_48hr\_A capillary\_Cov\_48hr  
## capillarySamples.GSM2685734\_MERS\_CoV\_48hr\_B capillary\_Cov\_48hr  
## capillarySamples.GSM2685735\_MERS\_CoV\_48hr\_C capillary\_Cov\_48hr  
## capillarySamples.GSM2685736\_MERS\_CoV\_48hr\_D capillary\_Cov\_48hr  
## capillarySamples.GSM2685737\_MERS\_CoV\_48hr\_E capillary\_Cov\_48hr  
## capillarySamples.GSM2685738\_ctrl\_48hr\_A capillary\_Ctrl\_48hr  
## capillarySamples.GSM2685739\_ctrl\_48hr\_B capillary\_Ctrl\_48hr  
## capillarySamples.GSM2685740\_ctrl\_48hr\_C capillary\_Ctrl\_48hr  
## capillarySamples.GSM2685741\_ctrl\_48hr\_D capillary\_Ctrl\_48hr  
## capillarySamples.GSM2685742\_ctrl\_48hr\_E capillary\_Ctrl\_48hr

Combo2 <- cbind(type,Combo1)  
Combo2[1:10,1:5]

## Class\_Type NEURL3 DUSP1  
## LiverTumorSamples.GSM2359851\_CoV1 liver\_CoV 1429.61750 8491.40875  
## LiverTumorSamples.GSM2359853\_CoV2 liver\_CoV 190.21750 2219.85650  
## LiverTumorSamples.GSM2359910\_CoV3 liver\_CoV 10.004148 11.494585  
## LiverTumorSamples.GSM2359913\_CoV4 liver\_CoV 11.245589 12.898250  
## LiverTumorSamples.GSM2359850\_ctrl1 liver\_Ctrl 34.57000 228.18775  
## LiverTumorSamples.GSM2359852\_ctrl2 liver\_Ctrl 17.25750 216.08550  
## LiverTumorSamples.GSM2359911\_ctrl3 liver\_Ctrl 3.708157 7.184185  
## LiverTumorSamples.GSM2359914\_ctrl4 liver\_Ctrl 4.757780 7.113854  
## LiverTumorSamples.GSM2359912\_Il1 liver\_CoV\_IL 4.879242 9.576161  
## LiverTumorSamples.GSM2359917\_IL2 liver\_CoV\_IL 5.1138565 9.5527540  
## ATF3 PCLO  
## LiverTumorSamples.GSM2359851\_CoV1 3608.28250 17.74792  
## LiverTumorSamples.GSM2359853\_CoV2 974.76937 613.28583  
## LiverTumorSamples.GSM2359910\_CoV3 8.337322 3.355859  
## LiverTumorSamples.GSM2359913\_CoV4 9.441972 2.741117  
## LiverTumorSamples.GSM2359850\_ctrl1 108.52250 13.80667  
## LiverTumorSamples.GSM2359852\_ctrl2 97.05125 12.88750  
## LiverTumorSamples.GSM2359911\_ctrl3 5.373051 3.904719  
## LiverTumorSamples.GSM2359914\_ctrl4 5.513552 3.621765  
## LiverTumorSamples.GSM2359912\_Il1 6.500059 3.653289  
## LiverTumorSamples.GSM2359917\_IL2 6.6111744 3.7909157

Write this ML ready file to csv.

write.csv(Combo2, 'ML\_ready\_CoV\_14\_classes.csv', row.names=TRUE)

Make a separate ML ready file with a smaller set of classes to classify by liver or capillary and control or CoronaVirus

a <- rep('liver', 4)  
b <- rep('liver',4)  
c <- rep('liver',2)  
d <- rep('liver',2)  
e <- rep('capillary',5)  
f <- rep('capillary',5)  
g <- rep('capillary',5)  
h <- rep('capillary',5)  
i <- rep('capillary',5)  
j <- rep('capillary',5)  
k <- rep('capillary',5)  
l <- rep('capillary',5)  
m <- rep('capillary',5)  
n <- rep('capillary',5)  
  
type <- as.data.frame(c(a,b,c,d,e,f,g,h,i,j,k,l,m,n))  
colnames(type) <- 'Class\_Type'  
row.names(type) <- row.names(Combo1)  
  
Combo3 <- cbind(type,Combo1)  
  
Combo3[1:10,1:5]

## Class\_Type NEURL3 DUSP1  
## LiverTumorSamples.GSM2359851\_CoV1 liver 1429.61750 8491.40875  
## LiverTumorSamples.GSM2359853\_CoV2 liver 190.21750 2219.85650  
## LiverTumorSamples.GSM2359910\_CoV3 liver 10.004148 11.494585  
## LiverTumorSamples.GSM2359913\_CoV4 liver 11.245589 12.898250  
## LiverTumorSamples.GSM2359850\_ctrl1 liver 34.57000 228.18775  
## LiverTumorSamples.GSM2359852\_ctrl2 liver 17.25750 216.08550  
## LiverTumorSamples.GSM2359911\_ctrl3 liver 3.708157 7.184185  
## LiverTumorSamples.GSM2359914\_ctrl4 liver 4.757780 7.113854  
## LiverTumorSamples.GSM2359912\_Il1 liver 4.879242 9.576161  
## LiverTumorSamples.GSM2359917\_IL2 liver 5.1138565 9.5527540  
## ATF3 PCLO  
## LiverTumorSamples.GSM2359851\_CoV1 3608.28250 17.74792  
## LiverTumorSamples.GSM2359853\_CoV2 974.76937 613.28583  
## LiverTumorSamples.GSM2359910\_CoV3 8.337322 3.355859  
## LiverTumorSamples.GSM2359913\_CoV4 9.441972 2.741117  
## LiverTumorSamples.GSM2359850\_ctrl1 108.52250 13.80667  
## LiverTumorSamples.GSM2359852\_ctrl2 97.05125 12.88750  
## LiverTumorSamples.GSM2359911\_ctrl3 5.373051 3.904719  
## LiverTumorSamples.GSM2359914\_ctrl4 5.513552 3.621765  
## LiverTumorSamples.GSM2359912\_Il1 6.500059 3.653289  
## LiverTumorSamples.GSM2359917\_IL2 6.6111744 3.7909157

write.csv(Combo3, 'ML\_ready\_CoV\_2\_classes.csv', row.names=TRUE)

a <- rep('CoV', 4)  
b <- rep('Ctrl',4)  
c <- rep('CoV\_IL',2)  
d <- rep('IA\_CoV',2)  
e <- rep('CoV',5)  
f <- rep('Ctrl',5)  
g <- rep('Cov',5)  
h <- rep('Ctrl',5)  
i <- rep('Cov',5)  
j <- rep('Ctrl',5)  
k <- rep('Cov',5)  
l <- rep('Ctrl',5)  
m <- rep('Cov',5)  
n <- rep('Ctrl',5)  
  
type <- as.data.frame(c(a,b,c,d,e,f,g,h,i,j,k,l,m,n))  
colnames(type) <- 'Class\_Type'  
row.names(type) <- row.names(Combo1)  
  
Combo4 <- cbind(type,Combo1)  
  
Combo4[1:10,1:5]

## Class\_Type NEURL3 DUSP1  
## LiverTumorSamples.GSM2359851\_CoV1 CoV 1429.61750 8491.40875  
## LiverTumorSamples.GSM2359853\_CoV2 CoV 190.21750 2219.85650  
## LiverTumorSamples.GSM2359910\_CoV3 CoV 10.004148 11.494585  
## LiverTumorSamples.GSM2359913\_CoV4 CoV 11.245589 12.898250  
## LiverTumorSamples.GSM2359850\_ctrl1 Ctrl 34.57000 228.18775  
## LiverTumorSamples.GSM2359852\_ctrl2 Ctrl 17.25750 216.08550  
## LiverTumorSamples.GSM2359911\_ctrl3 Ctrl 3.708157 7.184185  
## LiverTumorSamples.GSM2359914\_ctrl4 Ctrl 4.757780 7.113854  
## LiverTumorSamples.GSM2359912\_Il1 CoV\_IL 4.879242 9.576161  
## LiverTumorSamples.GSM2359917\_IL2 CoV\_IL 5.1138565 9.5527540  
## ATF3 PCLO  
## LiverTumorSamples.GSM2359851\_CoV1 3608.28250 17.74792  
## LiverTumorSamples.GSM2359853\_CoV2 974.76937 613.28583  
## LiverTumorSamples.GSM2359910\_CoV3 8.337322 3.355859  
## LiverTumorSamples.GSM2359913\_CoV4 9.441972 2.741117  
## LiverTumorSamples.GSM2359850\_ctrl1 108.52250 13.80667  
## LiverTumorSamples.GSM2359852\_ctrl2 97.05125 12.88750  
## LiverTumorSamples.GSM2359911\_ctrl3 5.373051 3.904719  
## LiverTumorSamples.GSM2359914\_ctrl4 5.513552 3.621765  
## LiverTumorSamples.GSM2359912\_Il1 6.500059 3.653289  
## LiverTumorSamples.GSM2359917\_IL2 6.6111744 3.7909157

write.csv(Combo4, 'ML\_ready\_CoV\_4\_classes.csv', row.names=TRUE)

We didn’t do any fold change or stat measures on the capillary samples, but we can plot them by using ggplot2 and group the sets by timed intervals for each group A through E and picking a handful of genes to compare over the 0,12,24,36, and 48 hour time intervals for the control group and the Coronavirus inoculated groups.

When the values are a ratio like this, it is easier to see the larger changes as in 9 compared to a low change like 0.0005, but this just means that compared to the control samples the inoculated Coronavirus had 9 times the gene expression values or had downregulated or suppressed gene expression values to 1/5000th the amount of the normal range of gene expression values respectively. \*\*\*

It makes sense to use some genes we already know have a higher magnitude of change, and we have a column for that in the CombinedLiver table called MagnitudeFCs that was already sorted from largest to smallest when made. We’ll just select the first five of those genes to compare in these capillary samples over time.

mostChanged <- CombinedLiver[1:5,c(1,71)]  
mostSuppressed <- CombinedLiver[196:200,c(1,71)]  
row.names(mostChanged)

## [1] "NEURL3" "DUSP1" "ATF3" "PCLO" "LHB"

row.names(mostSuppressed)

## [1] "RASSF7" "LOC100335030" "C2orf78" "DEFB1" "ZNF610"

capillary <- merge(mostChanged, CombinedLiver, by.x='GENE\_SYMBOL', by.y='GENE\_SYMBOL')  
capillary1 <- merge(mostSuppressed, CombinedLiver, by.x='GENE\_SYMBOL', by.y='GENE\_SYMBOL')  
capillaries <- rbind(capillary,capillary1)  
Capillaries <- capillaries[,c(1,15:64)]  
row.names(Capillaries) <- Capillaries$GENE\_SYMBOL  
  
Capillaries2 <- as.data.frame(t(Capillaries))  
Capillaries2 <- Capillaries2[-1,]  
row.names(Capillaries2) <- gsub('capillarySamples.','',row.names(Capillaries2))  
row.names(Capillaries2) <- gsub('GSM[0-9][0-9][0-9][0-9][0-9][0-9][0-9]\_','',row.names(Capillaries2))  
row.names(Capillaries2) <- gsub('MERS\_','', row.names(Capillaries2))

CoV <- grep('CoV', row.names(Capillaries2))  
ctrl <- grep('ctrl', row.names(Capillaries2))  
  
Capillaries2$Class <- 'CoV or ctrl'  
  
Capillaries2[CoV,11] <- 'Coronavirus'  
Capillaries2[ctrl,11] <- 'control'  
  
A <- grep('\_A', row.names(Capillaries2))  
B <- grep('\_B', row.names(Capillaries2))  
C <- grep('\_C', row.names(Capillaries2))  
D <- grep('\_D', row.names(Capillaries2))  
E <- grep('\_E', row.names(Capillaries2))  
  
Capillaries2$Group <- 'group'  
  
Capillaries2[A,12] <- 'A'  
Capillaries2[B,12] <- 'B'  
Capillaries2[C,12] <- 'C'  
Capillaries2[D,12] <- 'D'  
Capillaries2[E,12] <- 'E'  
  
hr0 <- grep('0hr', row.names(Capillaries2))  
hr12 <- grep('12hr', row.names(Capillaries2))  
hr24 <- grep('24hr', row.names(Capillaries2))  
hr36 <- grep('36hr', row.names(Capillaries2))  
hr48 <- grep('48hr', row.names(Capillaries2))  
  
Capillaries2$TimeInterval <- 'time'  
  
Capillaries2[hr0,13] <- '0 hr'  
Capillaries2[hr12,13] <- '12 hr'  
Capillaries2[hr24,13] <- '24 hr'  
Capillaries2[hr36,13] <- '36 hr'  
Capillaries2[hr48,13] <- '48 hr'  
  
Capillaries2

## ATF3 DUSP1 LHB NEURL3 PCLO C2orf78  
## CoV\_0hr\_A 10.290996 13.901505 9.093671 7.498965 6.468670 5.936451  
## CoV\_0hr\_B 9.780412 13.852933 9.128886 7.446590 6.476326 6.023280  
## CoV\_0hr\_C 9.574148 13.740905 8.662565 7.495092 6.463702 5.909934  
## CoV\_0hr\_D 9.848204 13.863910 8.729845 7.364854 6.572579 5.986079  
## CoV\_0hr\_E 10.114265 13.968982 8.738079 7.436675 6.625125 5.862801  
## ctrl\_0hr\_A 10.173291 14.398733 8.776979 7.267773 6.410249 6.016610  
## ctrl\_0hr\_B 10.132629 14.237192 9.610252 7.015544 6.467982 5.931786  
## ctrl\_0hr\_C 10.308477 14.382699 9.557514 7.440873 6.478339 5.853411  
## ctrl\_0hr\_D 9.888505 14.404923 9.602914 7.102155 6.489396 5.855096  
## ctrl\_0hr\_E 9.892730 14.120833 9.577233 6.936543 6.417981 5.942510  
## CoV\_12hr\_A 9.819186 11.303627 10.795022 12.768140 6.256646 5.865277  
## CoV\_12hr\_B 10.011539 11.577456 11.006393 12.402078 6.327304 5.922540  
## CoV\_12hr\_C 9.783105 11.626722 11.000187 12.532051 6.322820 5.988353  
## CoV\_12hr\_D 9.849858 11.692725 10.938022 12.668202 6.261566 5.901327  
## CoV\_12hr\_E 9.617070 12.220997 10.553798 12.273302 6.333485 5.898912  
## ctrl\_12hr\_A 7.825226 11.488735 9.286872 6.829080 6.528833 5.954890  
## ctrl\_12hr\_B 7.872041 11.710908 8.845744 6.784278 6.532492 5.862801  
## ctrl\_12hr\_C 7.989155 11.468072 9.267328 6.908973 6.489589 5.973506  
## ctrl\_12hr\_D 8.028735 11.407001 9.820556 6.615987 6.412667 5.928711  
## ctrl\_12hr\_E 8.154875 11.042038 9.741747 6.833504 6.431864 5.862305  
## CoV\_24hr\_A 12.356029 14.922819 10.081784 13.713997 6.330955 5.981748  
## CoV\_24hr\_B 12.393863 14.762759 10.125434 13.516154 6.376025 5.938335  
## CoV\_24hr\_C 12.347139 15.286795 9.988253 13.718699 6.398037 6.047165  
## CoV\_24hr\_D 12.280955 15.019195 9.580647 13.576554 6.441270 6.099102  
## CoV\_24hr\_E 12.187980 14.989084 9.508540 13.545156 6.428447 6.044217  
## ctrl\_24hr\_A 7.914153 12.020454 8.926344 6.410178 6.709108 6.033401  
## ctrl\_24hr\_B 8.179651 11.901618 9.159004 6.560892 6.642224 5.909934  
## ctrl\_24hr\_C 8.062523 11.831523 9.275883 6.568645 6.626875 5.938570  
## ctrl\_24hr\_D 8.045721 11.806023 9.273915 6.631753 6.618130 5.997365  
## ctrl\_24hr\_E 8.204591 11.942950 9.125971 6.562419 6.697083 5.919444  
## CoV\_36hr\_A 12.318180 14.508819 9.861903 13.561144 6.548994 6.087523  
## CoV\_36hr\_B 12.173687 14.540567 9.802688 13.549071 6.644295 5.999396  
## CoV\_36hr\_C 12.163530 14.579001 9.872176 13.449660 6.515321 5.933150  
## CoV\_36hr\_D 12.142847 14.514722 9.982218 13.712803 6.671993 6.001650  
## CoV\_36hr\_E 12.297080 14.374295 10.201176 13.521456 6.372439 6.051522  
## ctrl\_36hr\_A 7.940682 11.742312 9.321322 6.730998 6.678982 6.220477  
## ctrl\_36hr\_B 7.783378 11.751105 9.056790 6.621403 6.643658 6.125131  
## ctrl\_36hr\_C 7.810544 11.798201 9.151894 6.822530 6.618794 6.092605  
## ctrl\_36hr\_D 7.731982 11.876269 9.024215 6.685524 6.629717 6.098892  
## ctrl\_36hr\_E 7.734450 11.888111 8.922796 6.630443 6.673160 6.028326  
## CoV\_48hr\_A 11.205349 13.523040 9.679922 12.333937 6.529574 6.049019  
## CoV\_48hr\_B 11.253111 13.511350 9.912659 12.481150 6.549794 5.980606  
## CoV\_48hr\_C 10.944238 13.316529 9.850259 12.260608 6.708351 6.203350  
## CoV\_48hr\_D 10.983900 13.358680 9.899124 11.961065 6.599227 6.142515  
## CoV\_48hr\_E 11.255318 13.367467 10.184716 12.498831 6.679909 6.017946  
## ctrl\_48hr\_A 7.932607 12.174103 9.024090 6.757483 6.552106 6.016387  
## ctrl\_48hr\_B 7.668012 12.449589 8.985262 6.882334 6.700790 5.961156  
## ctrl\_48hr\_C 7.755264 12.365436 9.031925 6.844960 6.455577 6.003225  
## ctrl\_48hr\_D 7.725891 12.415529 8.940948 6.872043 6.533961 5.986534  
## ctrl\_48hr\_E 7.656200 12.455840 8.994880 6.868035 6.479109 6.091125  
## DEFB1 LOC100335030 RASSF7 ZNF610 Class Group  
## CoV\_0hr\_A 7.622403 8.114815 6.822339 7.227249 Coronavirus A  
## CoV\_0hr\_B 7.778352 8.270884 6.700971 7.428115 Coronavirus B  
## CoV\_0hr\_C 7.352772 8.308822 6.966246 7.481717 Coronavirus C  
## CoV\_0hr\_D 7.118591 8.246936 6.875601 7.426565 Coronavirus D  
## CoV\_0hr\_E 7.179596 8.214737 6.952108 7.420473 Coronavirus E  
## ctrl\_0hr\_A 7.331124 8.187333 6.964110 7.403619 control A  
## ctrl\_0hr\_B 7.872561 8.288294 6.910892 7.464914 control B  
## ctrl\_0hr\_C 7.584274 8.147007 6.994899 7.269174 control C  
## ctrl\_0hr\_D 7.650353 8.185575 7.033153 7.359418 control D  
## ctrl\_0hr\_E 7.847725 8.156999 7.056144 7.447995 control E  
## CoV\_12hr\_A 8.059324 7.868801 6.594891 8.147592 Coronavirus A  
## CoV\_12hr\_B 7.843962 7.735502 6.692292 8.178197 Coronavirus B  
## CoV\_12hr\_C 7.985707 7.820541 6.586602 8.121462 Coronavirus C  
## CoV\_12hr\_D 7.995350 7.717794 6.571151 8.224417 Coronavirus D  
## CoV\_12hr\_E 7.418830 7.832236 6.801301 8.247149 Coronavirus E  
## ctrl\_12hr\_A 8.009080 8.069778 6.880927 7.524340 control A  
## ctrl\_12hr\_B 8.055858 7.986788 6.895230 7.537055 control B  
## ctrl\_12hr\_C 7.952662 7.941232 6.903801 7.575149 control C  
## ctrl\_12hr\_D 8.277781 8.181431 6.745836 7.641494 control D  
## ctrl\_12hr\_E 8.235038 8.169354 6.554766 7.782781 control E  
## CoV\_24hr\_A 7.571666 8.536174 6.747448 8.938377 Coronavirus A  
## CoV\_24hr\_B 7.629778 8.509799 6.697222 8.733307 Coronavirus B  
## CoV\_24hr\_C 7.260831 8.425157 6.692222 9.019246 Coronavirus C  
## CoV\_24hr\_D 7.080690 8.584440 6.757083 9.012278 Coronavirus D  
## CoV\_24hr\_E 7.058040 8.736338 6.698612 9.092390 Coronavirus E  
## ctrl\_24hr\_A 7.563681 8.155811 6.789623 7.914991 control A  
## ctrl\_24hr\_B 7.729397 8.138252 6.704019 7.747434 control B  
## ctrl\_24hr\_C 7.946592 8.095640 6.643618 7.788730 control C  
## ctrl\_24hr\_D 7.625182 8.078397 6.716886 7.876311 control D  
## ctrl\_24hr\_E 7.486914 8.005603 6.680610 7.754600 control E  
## CoV\_36hr\_A 8.078504 8.482066 6.721733 8.534288 Coronavirus A  
## CoV\_36hr\_B 7.874253 8.583444 6.770072 8.659518 Coronavirus B  
## CoV\_36hr\_C 7.801655 8.552423 6.862404 8.572155 Coronavirus C  
## CoV\_36hr\_D 7.980233 8.606779 6.846841 8.654873 Coronavirus D  
## CoV\_36hr\_E 7.610937 8.589262 6.822339 8.589262 Coronavirus E  
## ctrl\_36hr\_A 7.737160 8.018402 6.849095 7.846848 control A  
## ctrl\_36hr\_B 7.704646 8.042240 6.771987 7.839025 control B  
## ctrl\_36hr\_C 7.652111 8.124825 6.842196 7.974192 control C  
## ctrl\_36hr\_D 7.564977 8.045657 6.925022 7.847725 control D  
## ctrl\_36hr\_E 7.592967 8.041310 6.908012 7.860321 control E  
## CoV\_48hr\_A 7.328972 8.062943 6.505043 7.678934 Coronavirus A  
## CoV\_48hr\_B 7.354622 8.098275 6.544158 7.742997 Coronavirus B  
## CoV\_48hr\_C 7.478970 8.024786 6.488793 7.725653 Coronavirus C  
## CoV\_48hr\_D 7.584650 7.979318 6.643906 7.822518 Coronavirus D  
## CoV\_48hr\_E 7.345740 8.128902 6.493502 9.374216 Coronavirus E  
## ctrl\_48hr\_A 7.551584 8.234894 6.812821 7.882805 control A  
## ctrl\_48hr\_B 7.634577 8.221036 6.918835 8.076742 control B  
## ctrl\_48hr\_C 7.580736 8.234032 6.851086 8.033925 control C  
## ctrl\_48hr\_D 7.753263 8.230602 6.913527 7.983884 control D  
## ctrl\_48hr\_E 7.731435 8.270651 6.878047 7.998738 control E  
## TimeInterval  
## CoV\_0hr\_A 0 hr  
## CoV\_0hr\_B 0 hr  
## CoV\_0hr\_C 0 hr  
## CoV\_0hr\_D 0 hr  
## CoV\_0hr\_E 0 hr  
## ctrl\_0hr\_A 0 hr  
## ctrl\_0hr\_B 0 hr  
## ctrl\_0hr\_C 0 hr  
## ctrl\_0hr\_D 0 hr  
## ctrl\_0hr\_E 0 hr  
## CoV\_12hr\_A 12 hr  
## CoV\_12hr\_B 12 hr  
## CoV\_12hr\_C 12 hr  
## CoV\_12hr\_D 12 hr  
## CoV\_12hr\_E 12 hr  
## ctrl\_12hr\_A 12 hr  
## ctrl\_12hr\_B 12 hr  
## ctrl\_12hr\_C 12 hr  
## ctrl\_12hr\_D 12 hr  
## ctrl\_12hr\_E 12 hr  
## CoV\_24hr\_A 24 hr  
## CoV\_24hr\_B 24 hr  
## CoV\_24hr\_C 24 hr  
## CoV\_24hr\_D 24 hr  
## CoV\_24hr\_E 24 hr  
## ctrl\_24hr\_A 24 hr  
## ctrl\_24hr\_B 24 hr  
## ctrl\_24hr\_C 24 hr  
## ctrl\_24hr\_D 24 hr  
## ctrl\_24hr\_E 24 hr  
## CoV\_36hr\_A 36 hr  
## CoV\_36hr\_B 36 hr  
## CoV\_36hr\_C 36 hr  
## CoV\_36hr\_D 36 hr  
## CoV\_36hr\_E 36 hr  
## ctrl\_36hr\_A 36 hr  
## ctrl\_36hr\_B 36 hr  
## ctrl\_36hr\_C 36 hr  
## ctrl\_36hr\_D 36 hr  
## ctrl\_36hr\_E 36 hr  
## CoV\_48hr\_A 48 hr  
## CoV\_48hr\_B 48 hr  
## CoV\_48hr\_C 48 hr  
## CoV\_48hr\_D 48 hr  
## CoV\_48hr\_E 48 hr  
## ctrl\_48hr\_A 48 hr  
## ctrl\_48hr\_B 48 hr  
## ctrl\_48hr\_C 48 hr  
## ctrl\_48hr\_D 48 hr  
## ctrl\_48hr\_E 48 hr

write.csv(Capillaries2,'FC\_10\_capillaries\_CoV.csv', row.names=TRUE)

The above table has 10 genes as the columns with the added Class (Coronavirus or control), Group (A,B,C,D,E), and TimeInterval (0,12,24,36,48 hours) fields to filter by and plot.

Lets make these group tables for the corona virus and see how they compare over time.

library(dplyr)  
  
A\_group <- filter(Capillaries2, Group=='A' & Class == 'Coronavirus')  
B\_group <- filter(Capillaries2, Group=='B' & Class == 'Coronavirus')  
C\_group <- filter(Capillaries2, Group=='C' & Class == 'Coronavirus')  
D\_group <- filter(Capillaries2, Group=='D' & Class == 'Coronavirus')  
E\_group <- filter(Capillaries2, Group=='E' & Class == 'Coronavirus')

Lets use the tidyr package to put the 10 genes into one Gene field.

library(tidyr)

We will do this for the A\_group table and ignore the Group and Class fields, because we made it only the A group of the Coronavirus class.

A\_group2 <- A\_group[,c(1,3,5,7,9,11:13)]  
A\_tidy <- gather(A\_group2, 'Gene','GeneExpression',1:5)

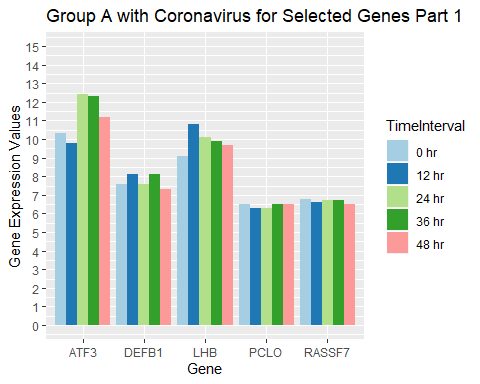
## Warning: attributes are not identical across measure variables;  
## they will be dropped

A\_tidy$GeneExpression <- round(as.numeric(A\_tidy$GeneExpression),1)  
A\_tidy$TimeInterval <- as.factor(A\_tidy$TimeInterval)  
A\_tidy$Gene <- as.factor(A\_tidy$Gene)  
A\_tidy

## Class Group TimeInterval Gene GeneExpression  
## 1 Coronavirus A 0 hr ATF3 10.3  
## 2 Coronavirus A 12 hr ATF3 9.8  
## 3 Coronavirus A 24 hr ATF3 12.4  
## 4 Coronavirus A 36 hr ATF3 12.3  
## 5 Coronavirus A 48 hr ATF3 11.2  
## 6 Coronavirus A 0 hr LHB 9.1  
## 7 Coronavirus A 12 hr LHB 10.8  
## 8 Coronavirus A 24 hr LHB 10.1  
## 9 Coronavirus A 36 hr LHB 9.9  
## 10 Coronavirus A 48 hr LHB 9.7  
## 11 Coronavirus A 0 hr PCLO 6.5  
## 12 Coronavirus A 12 hr PCLO 6.3  
## 13 Coronavirus A 24 hr PCLO 6.3  
## 14 Coronavirus A 36 hr PCLO 6.5  
## 15 Coronavirus A 48 hr PCLO 6.5  
## 16 Coronavirus A 0 hr DEFB1 7.6  
## 17 Coronavirus A 12 hr DEFB1 8.1  
## 18 Coronavirus A 24 hr DEFB1 7.6  
## 19 Coronavirus A 36 hr DEFB1 8.1  
## 20 Coronavirus A 48 hr DEFB1 7.3  
## 21 Coronavirus A 0 hr RASSF7 6.8  
## 22 Coronavirus A 12 hr RASSF7 6.6  
## 23 Coronavirus A 24 hr RASSF7 6.7  
## 24 Coronavirus A 36 hr RASSF7 6.7  
## 25 Coronavirus A 48 hr RASSF7 6.5

library(ggplot2)

ggplot(data = A\_tidy, aes(x=Gene, y=GeneExpression, fill=TimeInterval)) +  
 geom\_bar(stat='identity', position=position\_dodge())+  
 scale\_y\_continuous(breaks = seq(0, 15, by=1), limits=c(0,15))+  
 scale\_fill\_brewer(palette='Paired') +   
 ggtitle('Group A with Coronavirus for Selected Genes Part 1')+  
 xlab('Gene')+  
 ylab('Gene Expression Values')



The genes above for Part 1 of the group A samples of coronavirus in blood capillaries show some variation in gene expression values for some of these genes that had the most change in the liver tumor samples. Starting at the initial hour up to 48 hours after being inoculated in vitro, there is an increase then decrease for ATF3 and LHB genes, while a decrease then increase close to initial value with PCLO and slightly with RASSF7. For DEFB1, it has a cyclical increase, decrease, increase, then decrease to stabilize closer to the initial gene expressio value.

Now lets find the other five genes in the group A set of ten genes found to have the most change in the liver tumor samples, and examined here in the blood capillary samples.

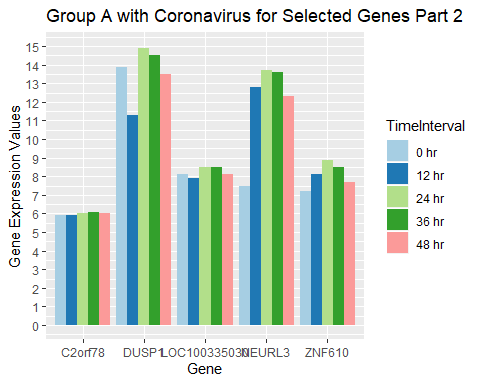
A\_group3 <- A\_group[,c(2,4,6,8,10,11:13)]  
A\_tidy1 <- gather(A\_group3, 'Gene','GeneExpression',1:5)

## Warning: attributes are not identical across measure variables;  
## they will be dropped

A\_tidy1$GeneExpression <- round(as.numeric(A\_tidy1$GeneExpression),1)  
A\_tidy1$TimeInterval <- as.factor(A\_tidy1$TimeInterval)  
A\_tidy1$Gene <- as.factor(A\_tidy1$Gene)  
A\_tidy1

## Class Group TimeInterval Gene GeneExpression  
## 1 Coronavirus A 0 hr DUSP1 13.9  
## 2 Coronavirus A 12 hr DUSP1 11.3  
## 3 Coronavirus A 24 hr DUSP1 14.9  
## 4 Coronavirus A 36 hr DUSP1 14.5  
## 5 Coronavirus A 48 hr DUSP1 13.5  
## 6 Coronavirus A 0 hr NEURL3 7.5  
## 7 Coronavirus A 12 hr NEURL3 12.8  
## 8 Coronavirus A 24 hr NEURL3 13.7  
## 9 Coronavirus A 36 hr NEURL3 13.6  
## 10 Coronavirus A 48 hr NEURL3 12.3  
## 11 Coronavirus A 0 hr C2orf78 5.9  
## 12 Coronavirus A 12 hr C2orf78 5.9  
## 13 Coronavirus A 24 hr C2orf78 6.0  
## 14 Coronavirus A 36 hr C2orf78 6.1  
## 15 Coronavirus A 48 hr C2orf78 6.0  
## 16 Coronavirus A 0 hr LOC100335030 8.1  
## 17 Coronavirus A 12 hr LOC100335030 7.9  
## 18 Coronavirus A 24 hr LOC100335030 8.5  
## 19 Coronavirus A 36 hr LOC100335030 8.5  
## 20 Coronavirus A 48 hr LOC100335030 8.1  
## 21 Coronavirus A 0 hr ZNF610 7.2  
## 22 Coronavirus A 12 hr ZNF610 8.1  
## 23 Coronavirus A 24 hr ZNF610 8.9  
## 24 Coronavirus A 36 hr ZNF610 8.5  
## 25 Coronavirus A 48 hr ZNF610 7.7

ggplot(data = A\_tidy1, aes(x=Gene, y=GeneExpression, fill=TimeInterval)) +  
 geom\_bar(stat='identity', position=position\_dodge())+  
 scale\_y\_continuous(breaks = seq(0, 15, by=1), limits=c(0,15))+  
 scale\_fill\_brewer(palette='Paired') +   
 ggtitle('Group A with Coronavirus for Selected Genes Part 2')+  
 xlab('Gene')+  
 ylab('Gene Expression Values')



The above genes in part 2 of the group A Coronavirus samples over 48 hours, shows that the gene expression values increase up to 24 hours then decrease to 48 hours for most of the genes above.