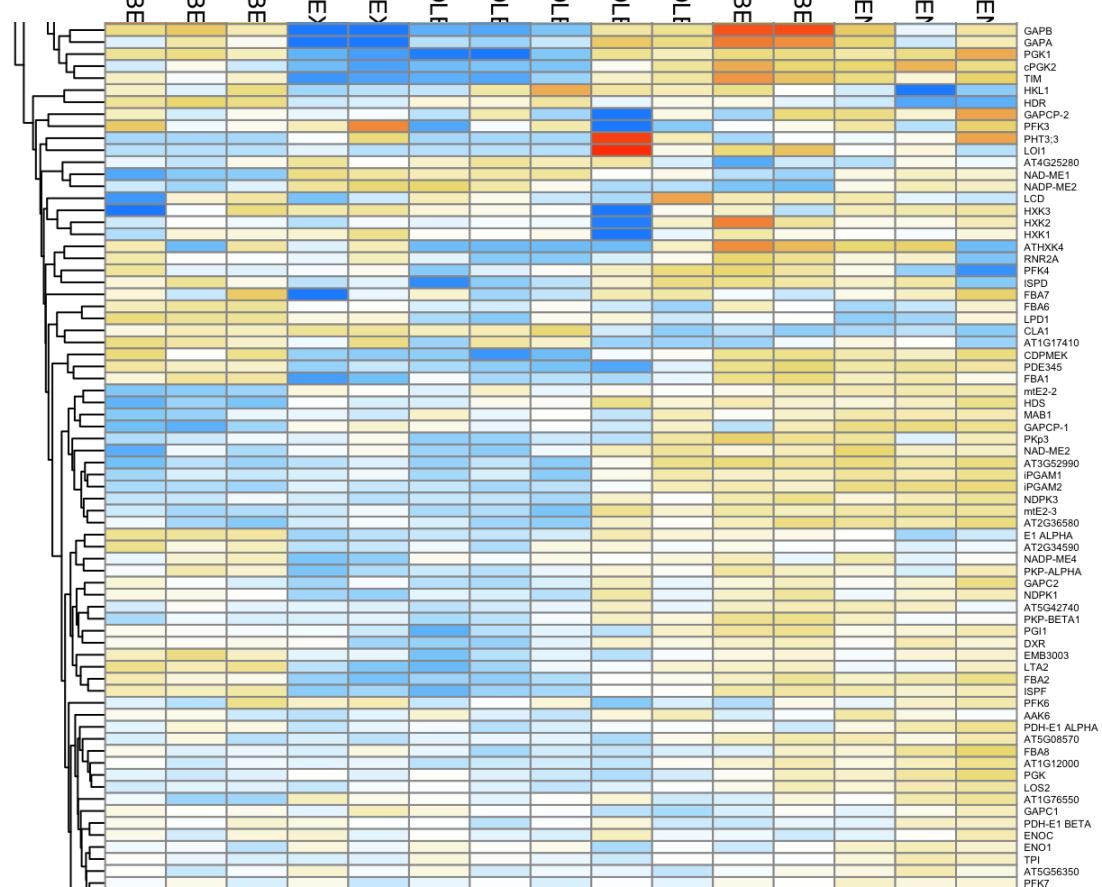
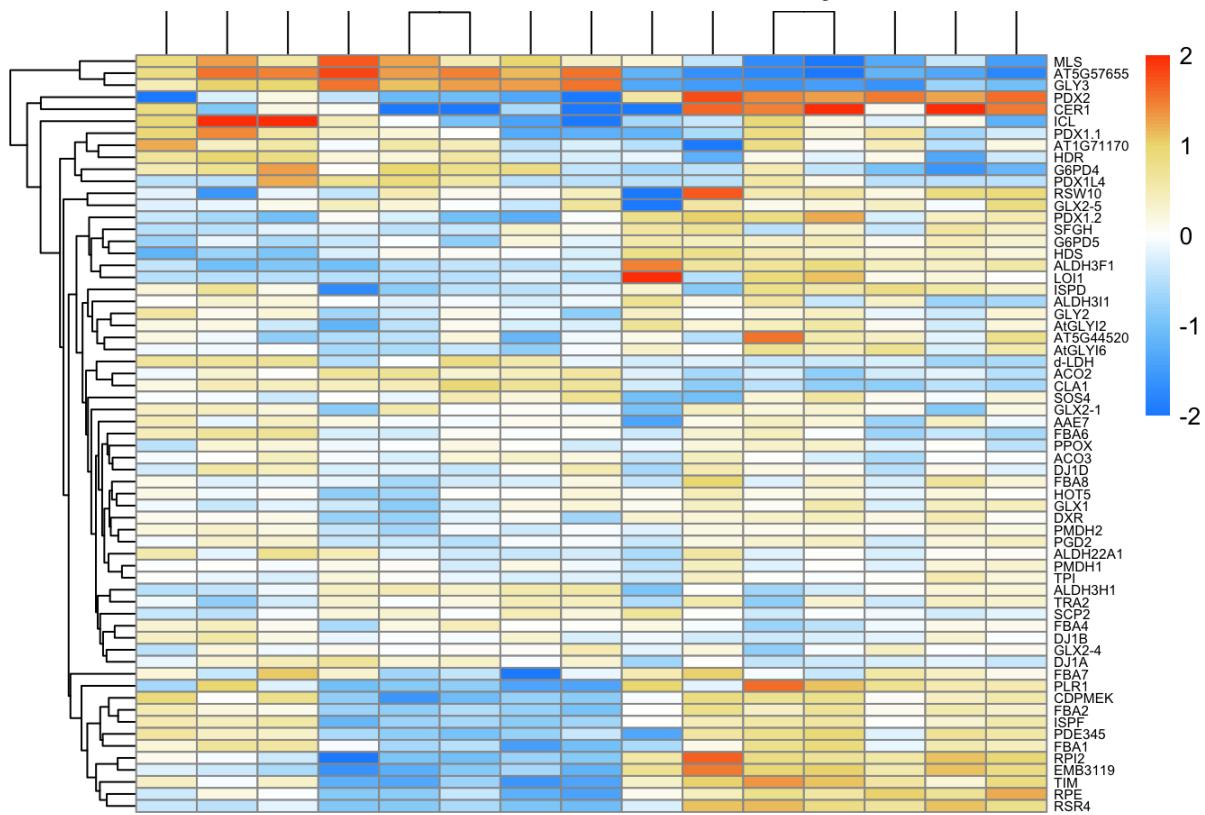
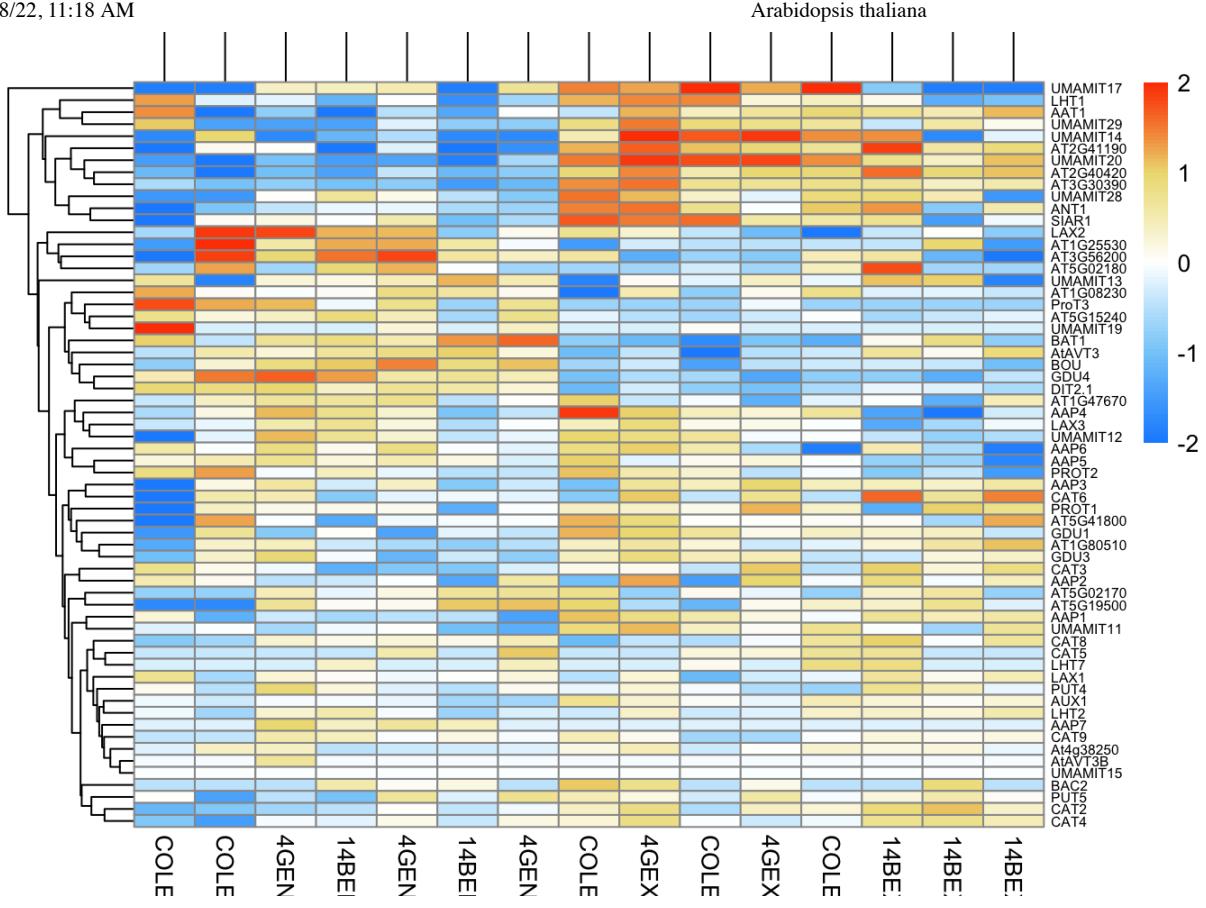
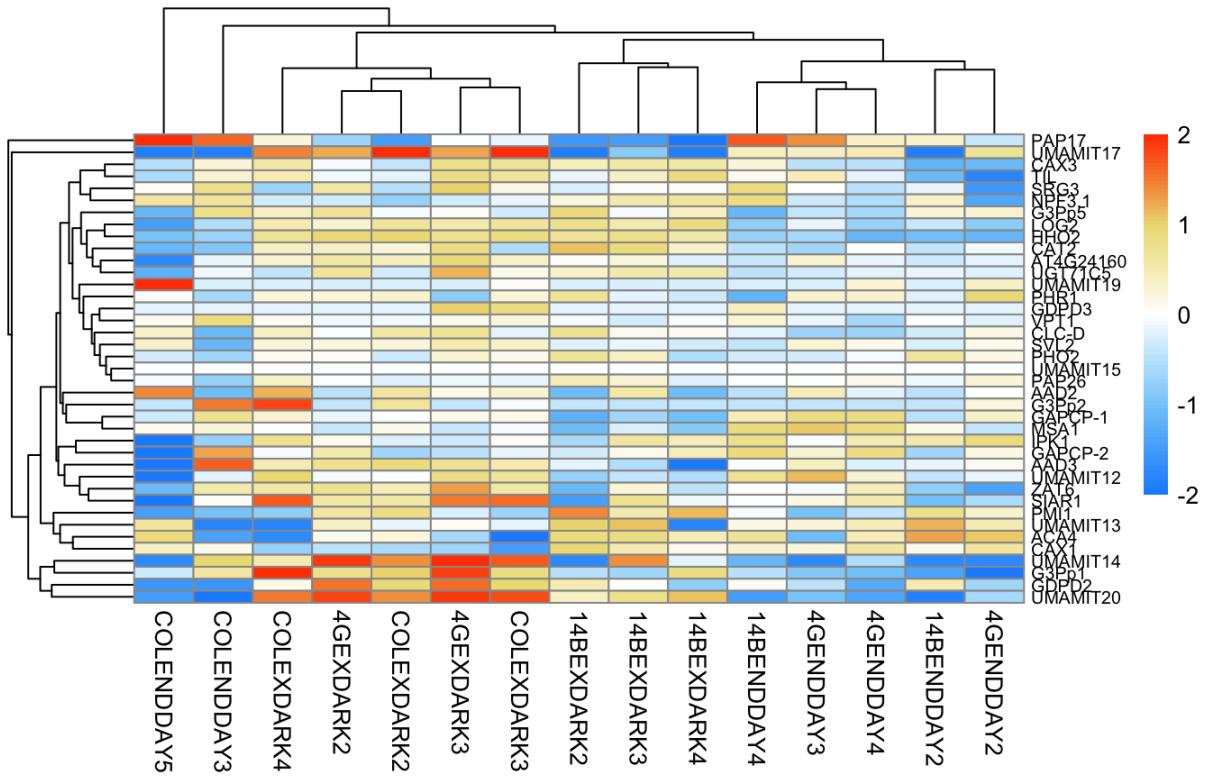


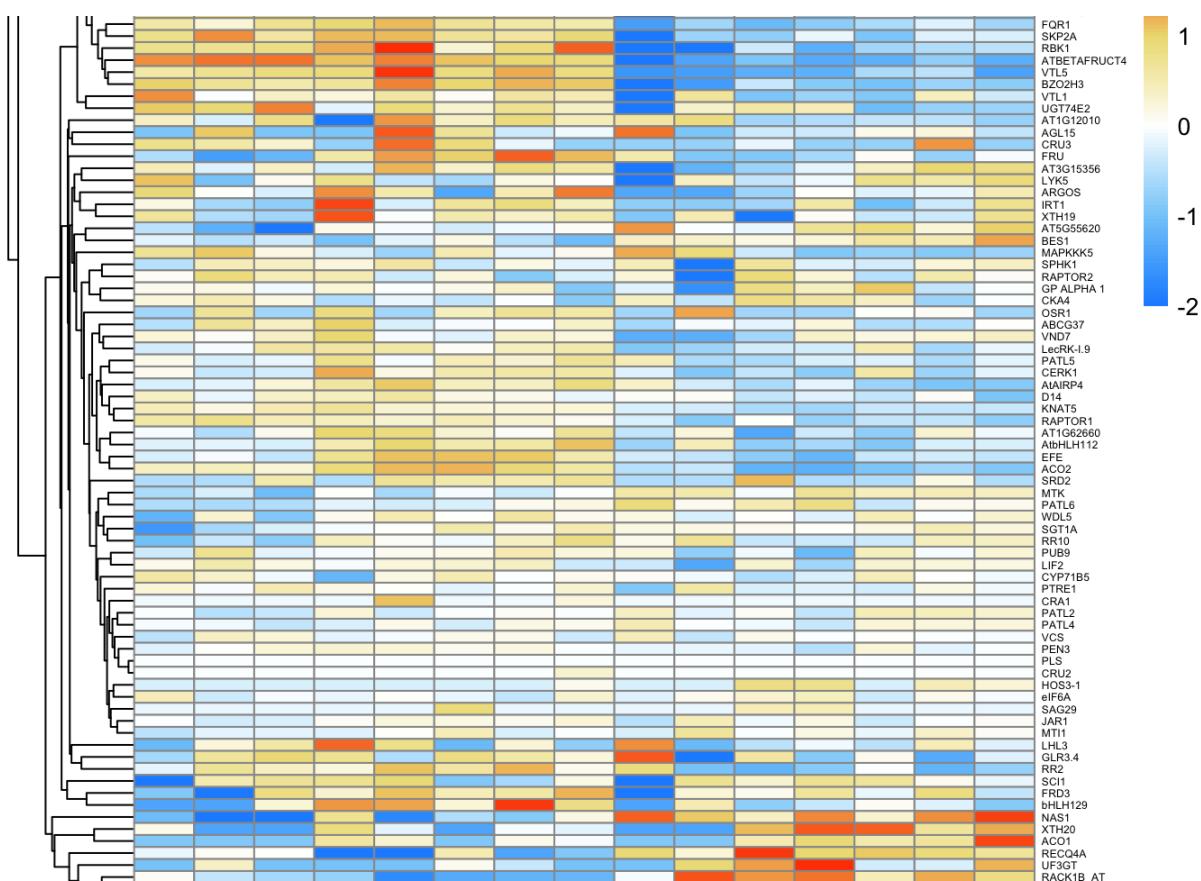
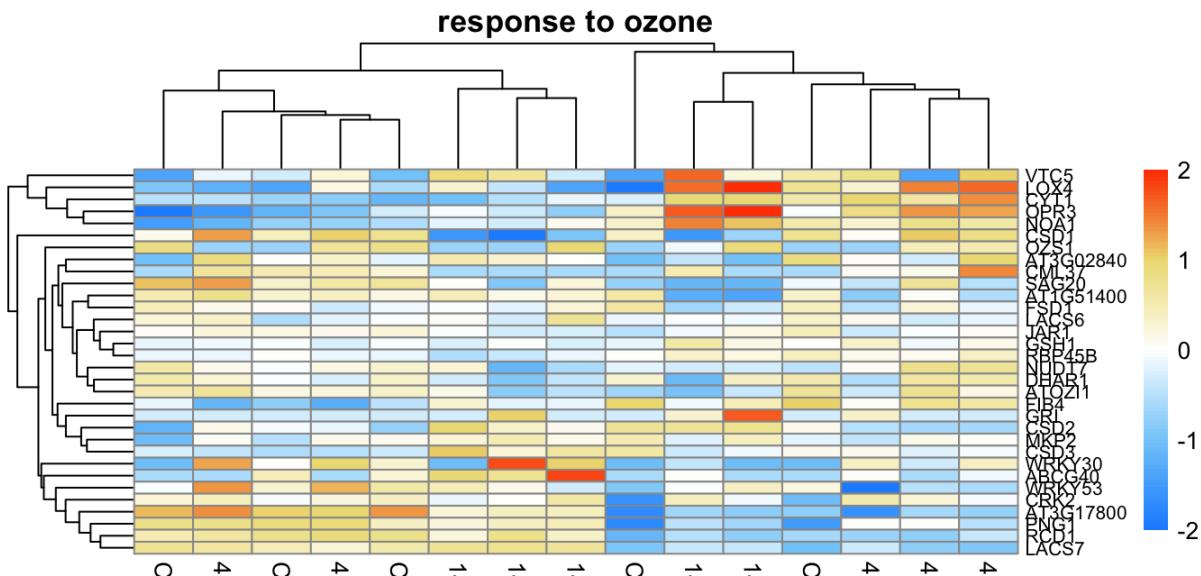
Arabidopsis thaliana





anion homeostasis

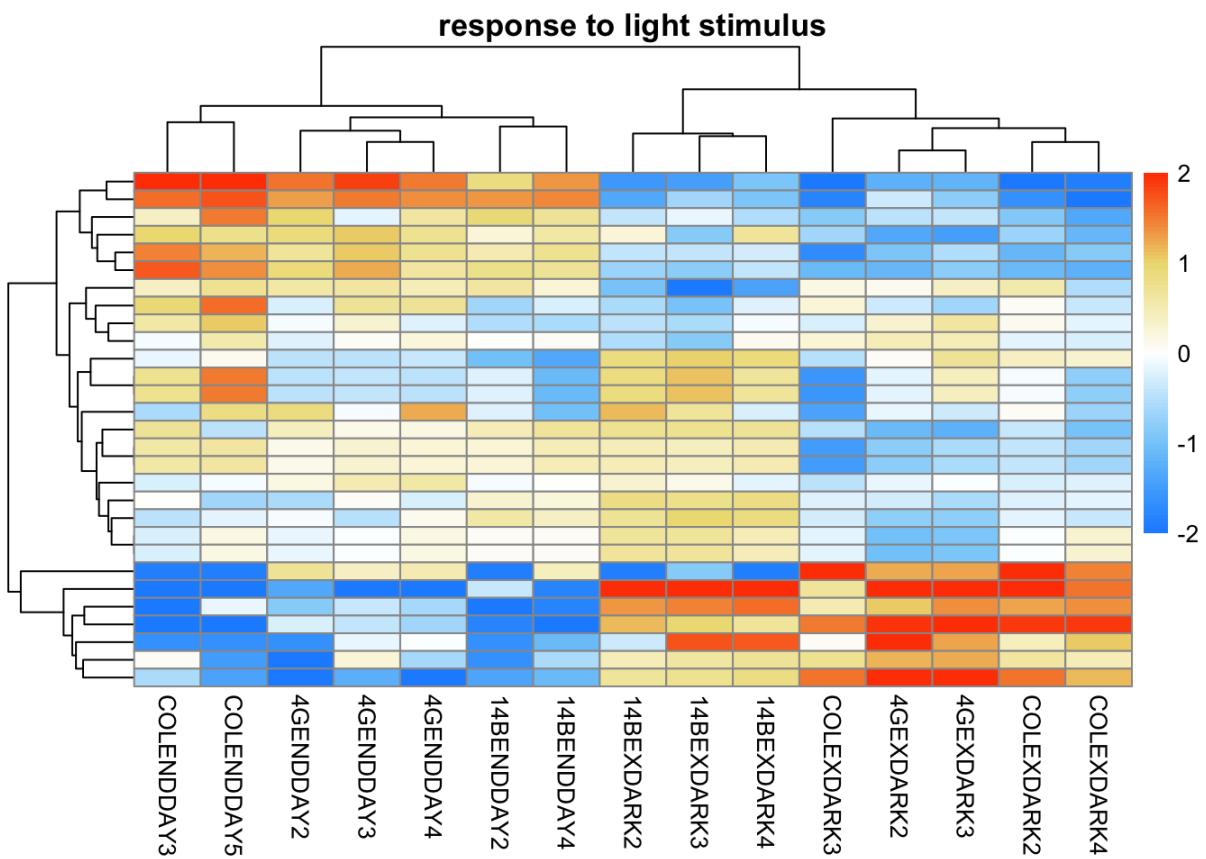




pHeatmaps for specific groups

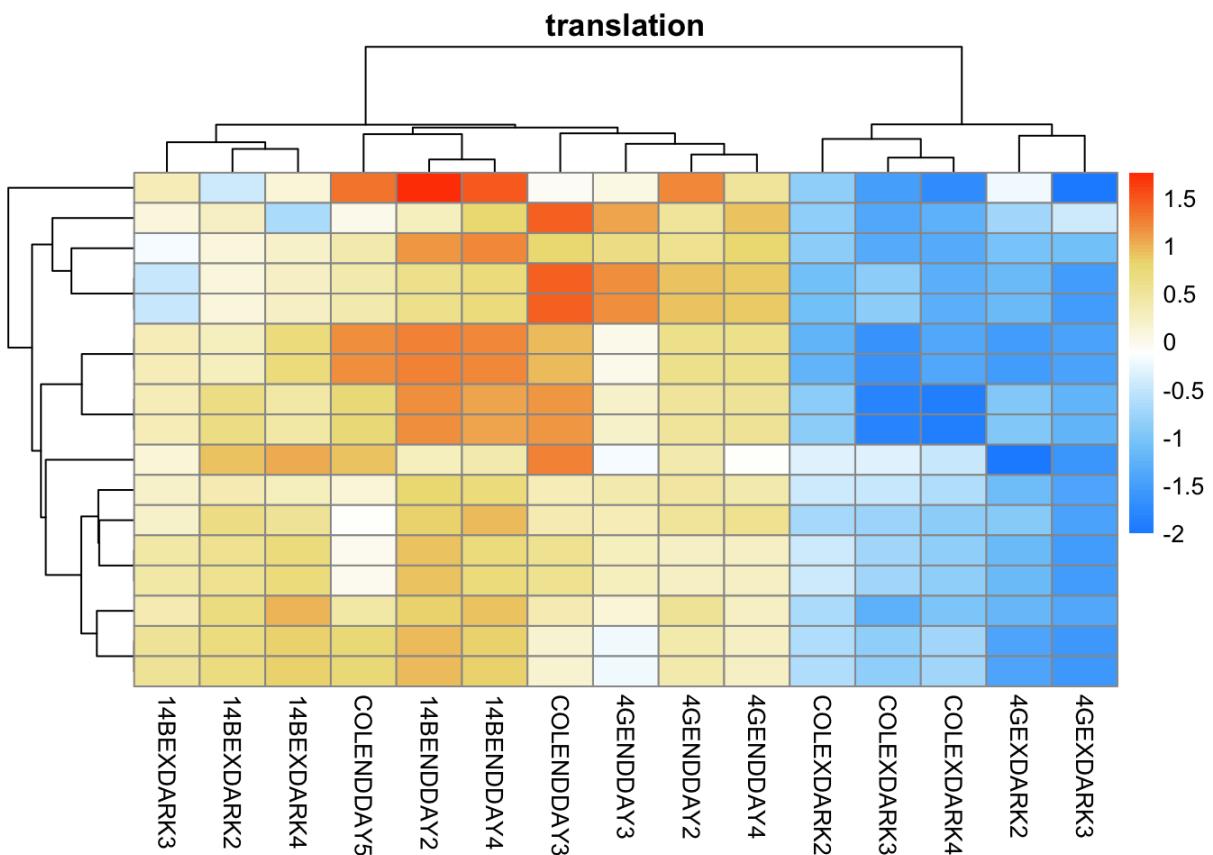
```
# "response to light stimulus"
temp_set <- goAssociations2 %>% filter(gene_ontology_name == "response to light stimulus")
lgGo <- lgNormRibo[temp_set$gene, ]

heatData = lgGo - rowMeans(lgGo)
heatData = as.data.frame(heatData)
heatData[heatData > 2] = 2; heatData[heatData < -2] = -2
fontsize_row = 10 - nrow(heatData) / 15
pheatmap(
  heatData,
  color = heatPalette,
  clustering_method = "average",
  main = "response to light stimulus",
  show_rownames = FALSE
)
```



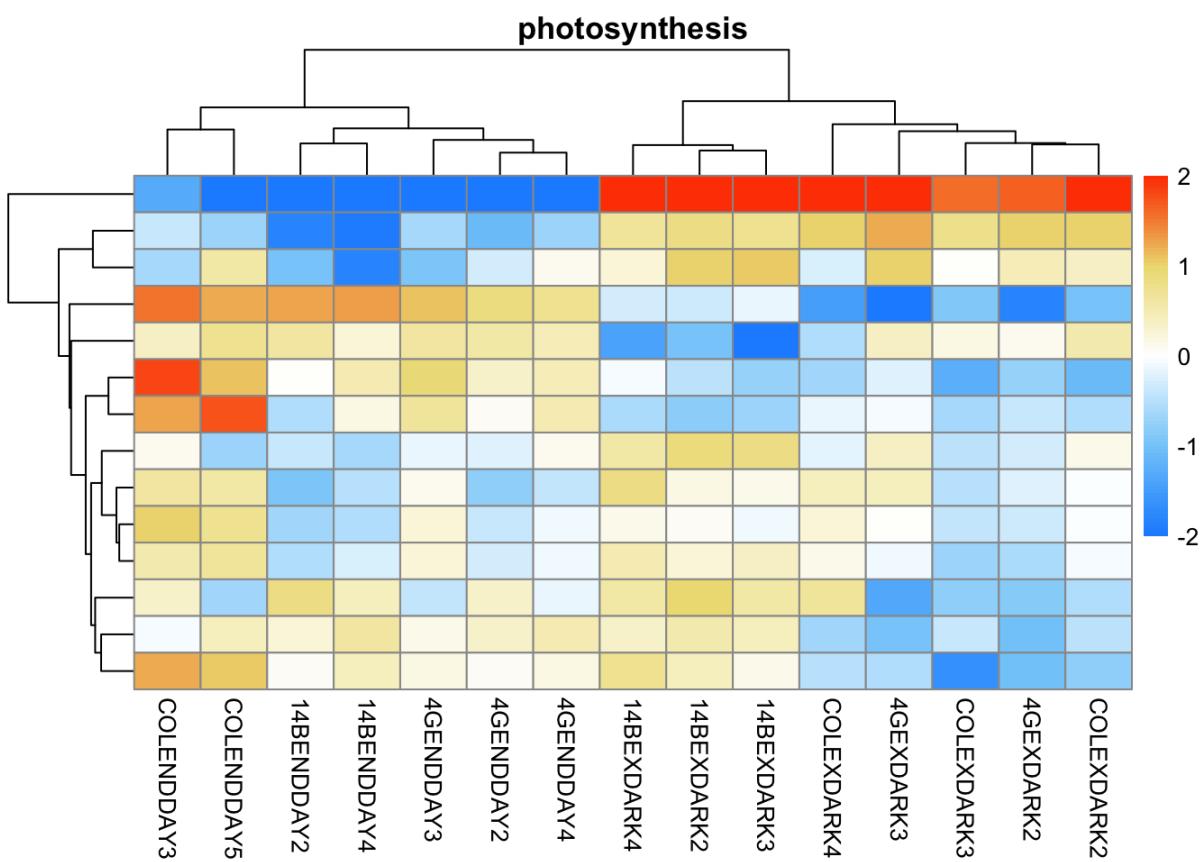
```
# "translation"
temp_set <- goAssociations2 %>% filter(gene_ontology_name == "translation")
lgGo <- lgNormRibo[temp_set$gene, ]

heatData = lgGo - rowMeans(lgGo)
heatData = as.data.frame(heatData)
heatData[heatData > 2] = 2; heatData[heatData < -2] = -2
fontsize_row = 10 - nrow(heatData) / 15
pheatmap(
  heatData,
  color = heatPalette,
  clustering_method = "average",
  main = "translation",
  show_rownames = FALSE
)
```



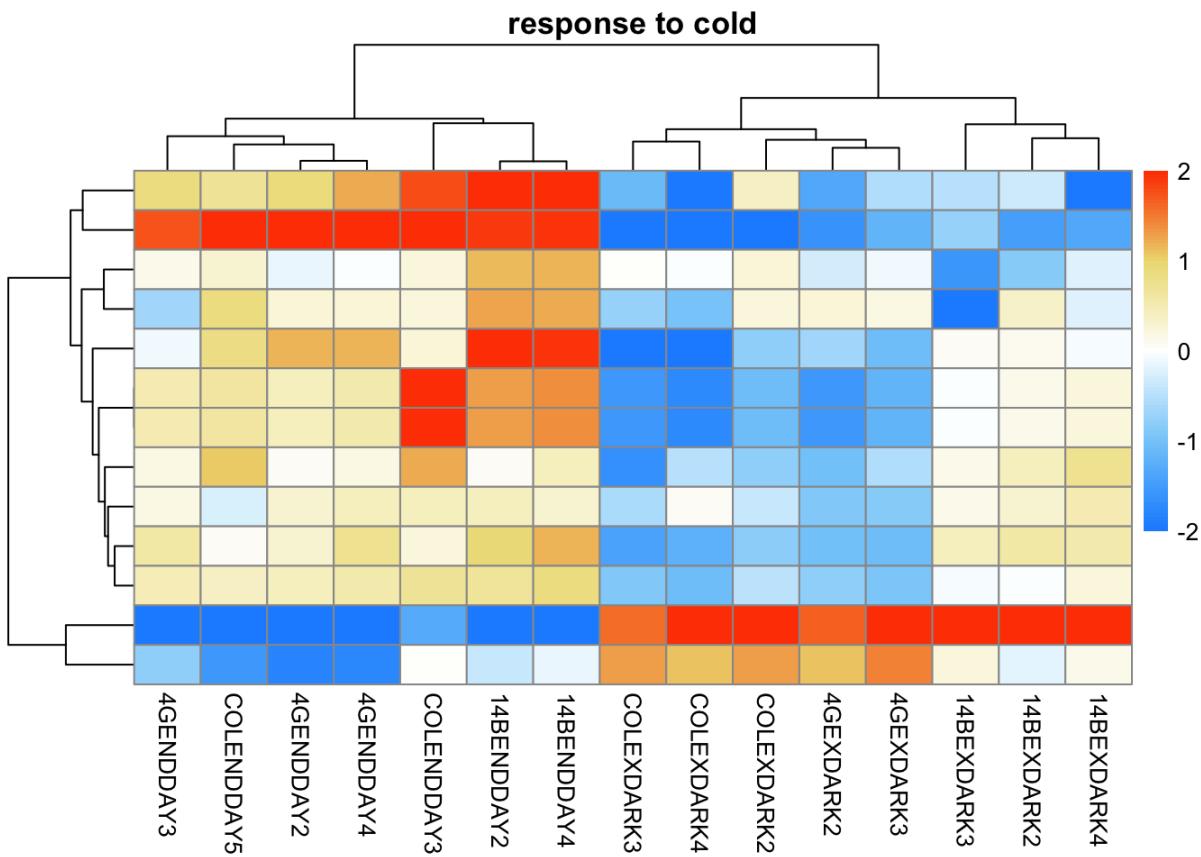
```
# "photosynthesis"
temp_set <- goAssociations2 %>% filter(gene_ontology_name == "photosynthesis")
lgGo <- lgNormRibo[temp_set$gene, ]

heatData = lgGo - rowMeans(lgGo)
heatData = as.data.frame(heatData)
heatData[heatData > 2] = 2; heatData[heatData < -2] = -2
fontsize_row = 10 - nrow(heatData) / 15
pheatmap(
  heatData,
  color = heatPalette,
  clustering_method = "average",
  main = "photosynthesis",
  show_rownames = FALSE
)
```



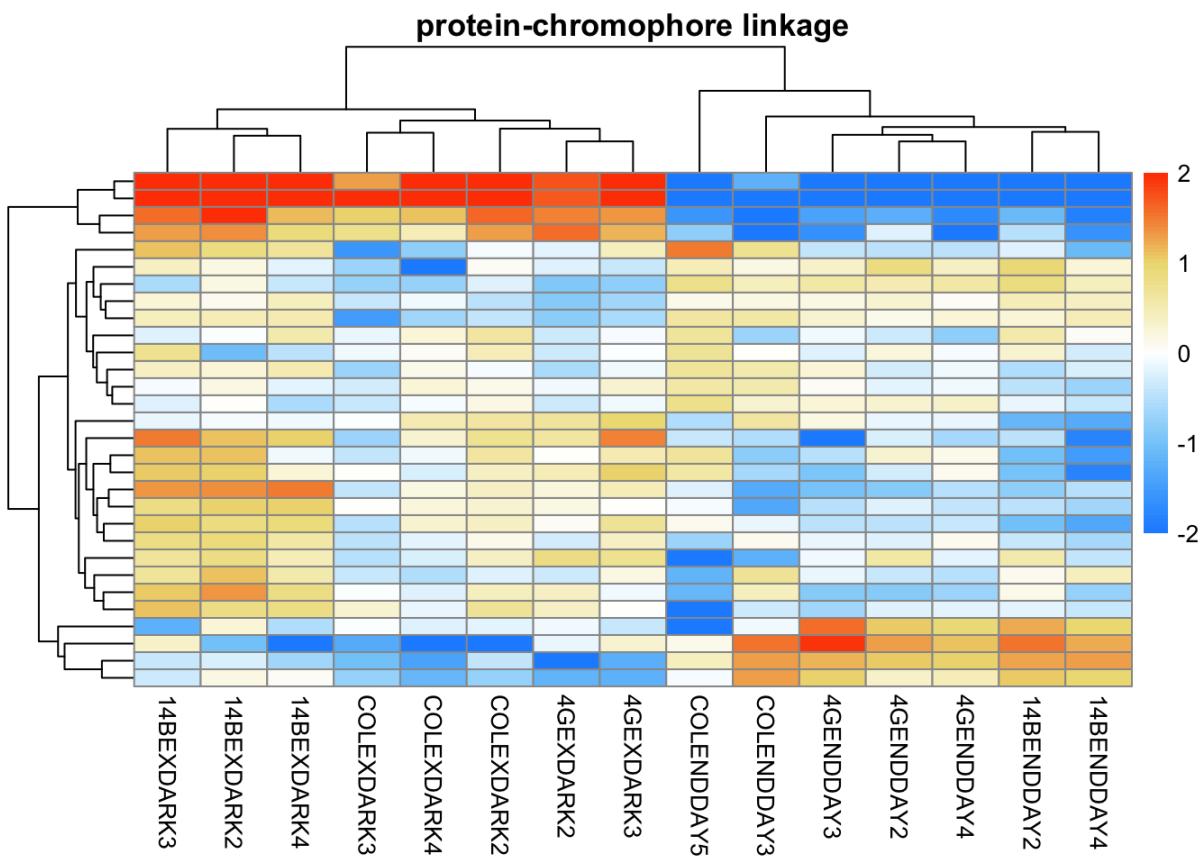
```
# "response to cold"
temp_set <- goAssociations2 %>% filter(gene_ontology_name == "response to cold")
lgGo <- lgNormRibo[temp_set$gene, ]

heatData = lgGo - rowMeans(lgGo)
heatData = as.data.frame(heatData)
heatData[heatData > 2] = 2; heatData[heatData < -2] = -2
fontsize_row = 10 - nrow(heatData) / 15
pheatmap(
  heatData,
  color = heatPalette,
  clustering_method = "average",
  main = "response to cold",
  show_rownames = FALSE
)
```



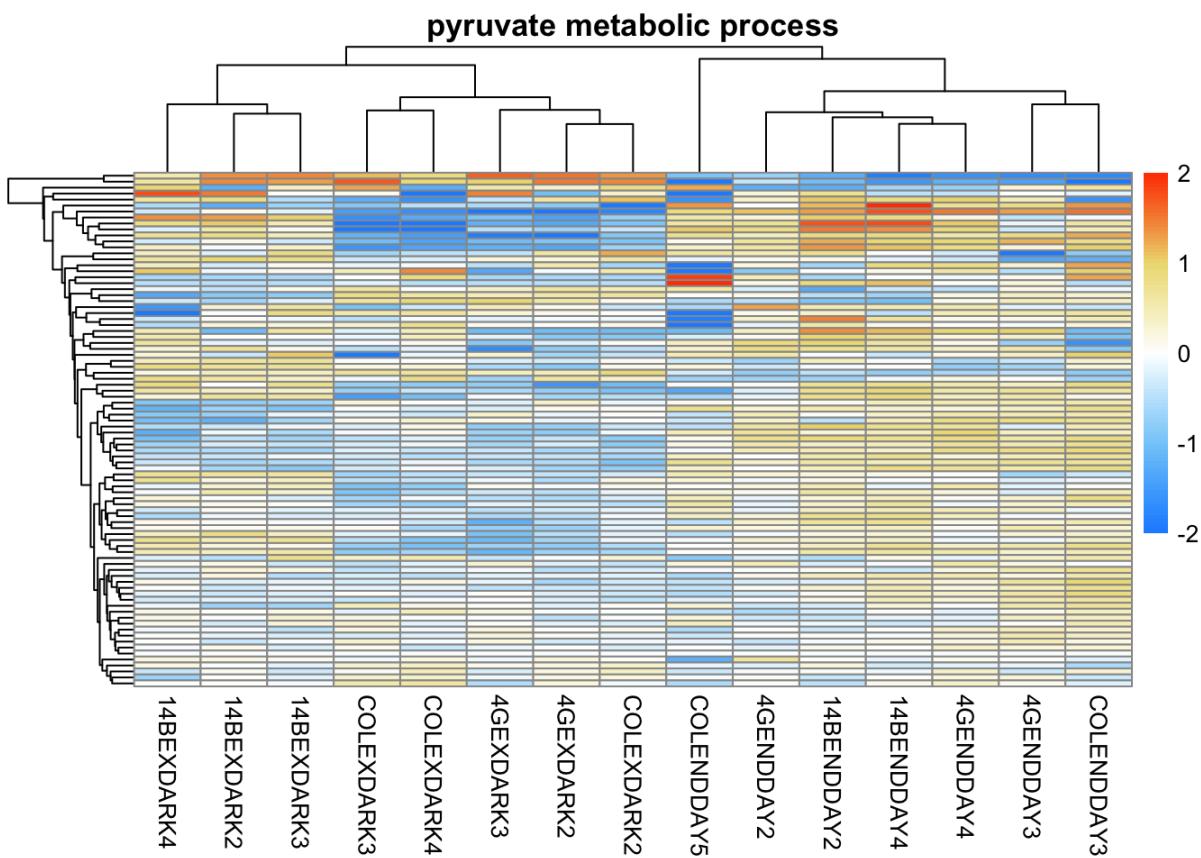
```
# "protein-chromophore linkage"
temp_set <- joined_set_ribo %>% filter(gene_ontology_name == "protein-chromophore linkage")
lgGo <- lgNormRibo[temp_set$gene, ]

heatData = lgGo - rowMeans(lgGo)
heatData = as.data.frame(heatData)
heatData[heatData > 2] = 2; heatData[heatData < -2] = -2
fontsize_row = 10 - nrow(heatData) / 15
pheatmap(
  heatData,
  color = heatPalette,
  clustering_method = "average",
  labels_row= geneNamesAndDescriptions[rownames(heatData), "symbol"],
  main = "protein-chromophore linkage",
  show_rownames = FALSE
)
```



```
# "pyruvate metabolic process"
temp_set <- joined_set_ribo %>% filter(gene_ontology_name == "pyruvate metabolic process")
lgGo <- lgNormRibo[temp_set$gene, ]

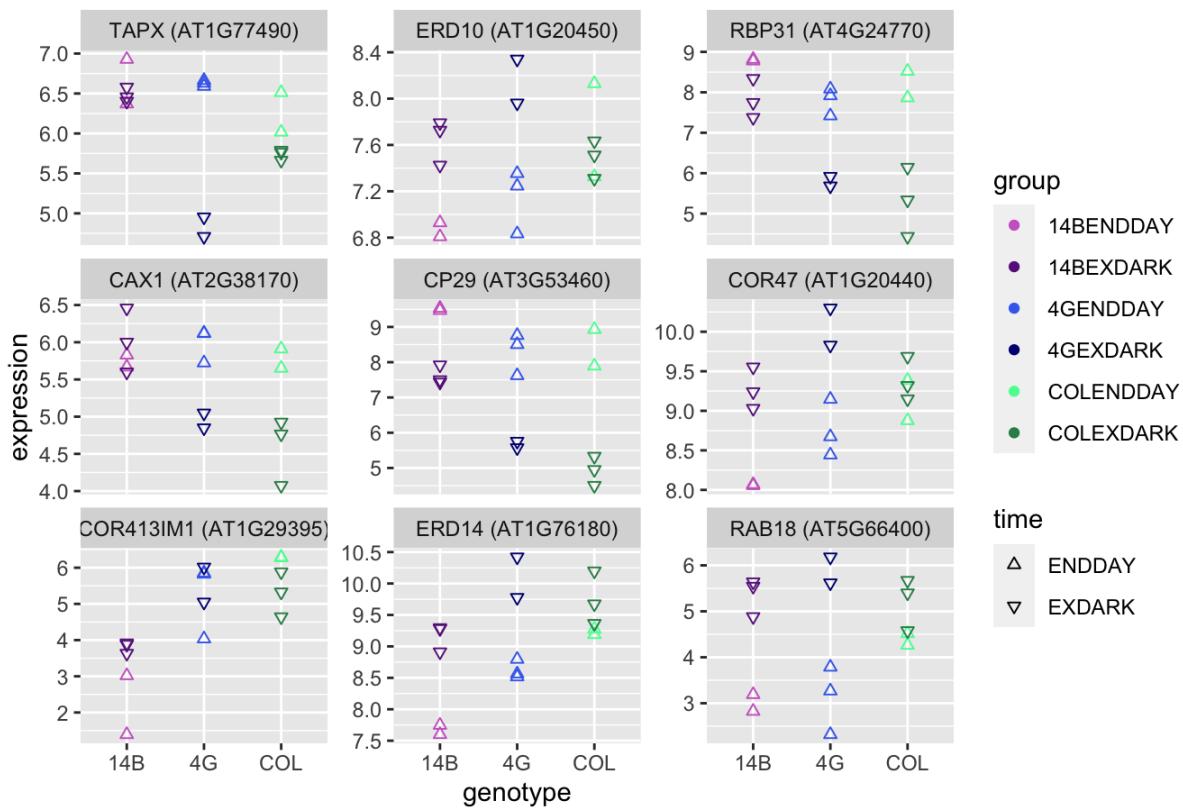
heatData = lgGo - rowMeans(lgGo)
heatData = as.data.frame(heatData)
heatData[heatData > 2] = 2; heatData[heatData < -2] = -2
fontsize_row = 10 - nrow(heatData) / 15
pheatmap(
  heatData,
  color = heatPalette,
  clustering_method = "average",
  labels_row= geneNamesAndDescriptions[rownames(heatData), "symbol"],
  main = "pyruvate metabolic process",
  show_rownames = FALSE
)
```



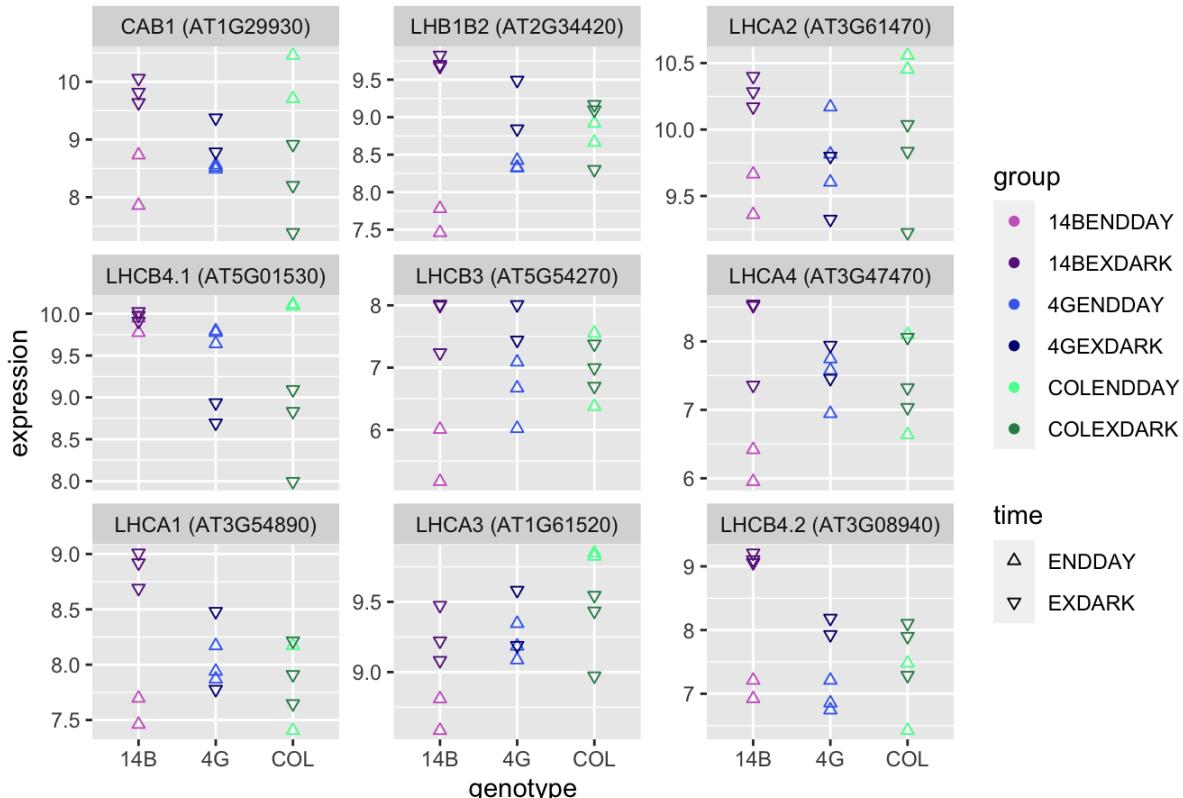
```
for (i in 1:length(ontology_names)){
  temp_set <- joined_set_ribo %>% filter(gene_ontology_name == ontology_names[i])
  lgGo <- lgNormRibo[temp_set$gene, ]

  DESeq_Results1 = DESeq_Results[temp_set$gene, ]
  DESeq_Results1 = DESeq_Results1[order(DESeq_Results1$pvalue), ]
  DESeq_Results1 = DESeq_Results1[1:9, ]
  lgGo1 <- lgNormRibo[rownames(DESeq_Results1), ]
  stripChart <- stripchart321g(data = lgGo1,
                                sampleAnnotation = sampleAnnotation2,
                                geneNames = geneNamesAndDescriptions,
                                colorValues = groupColors
                               )
  stripChart = stripChart + ggtitle(ontology_names[i])
  print(stripChart)
}
```

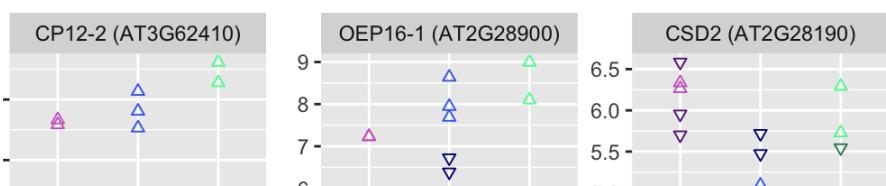
cold acclimation

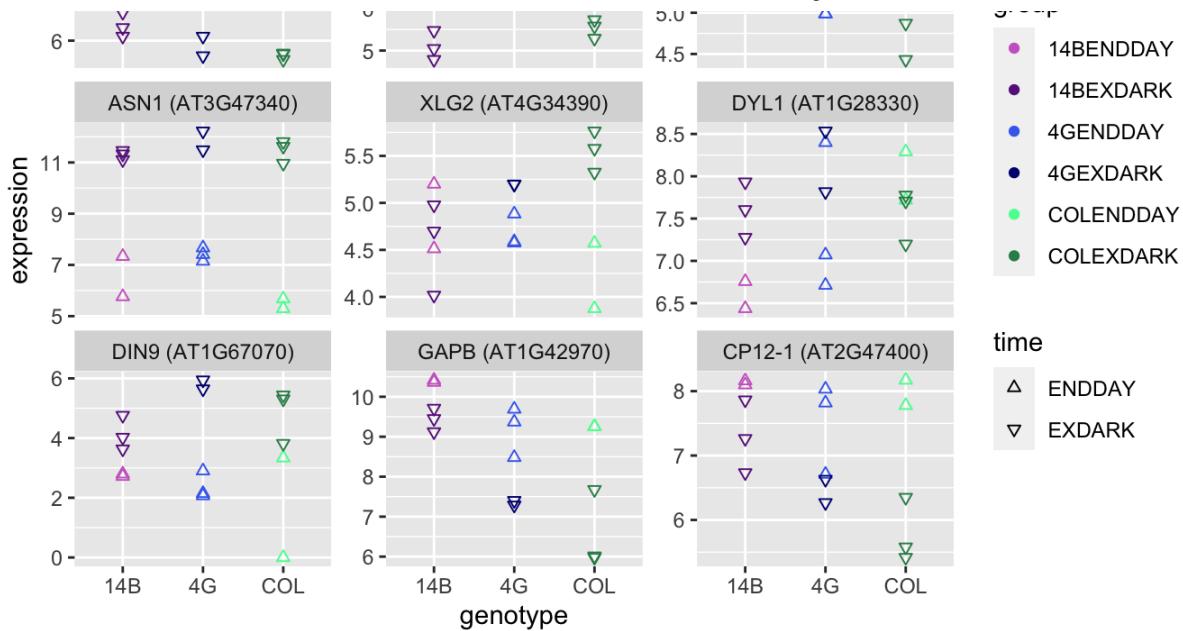


protein-chromophore linkage

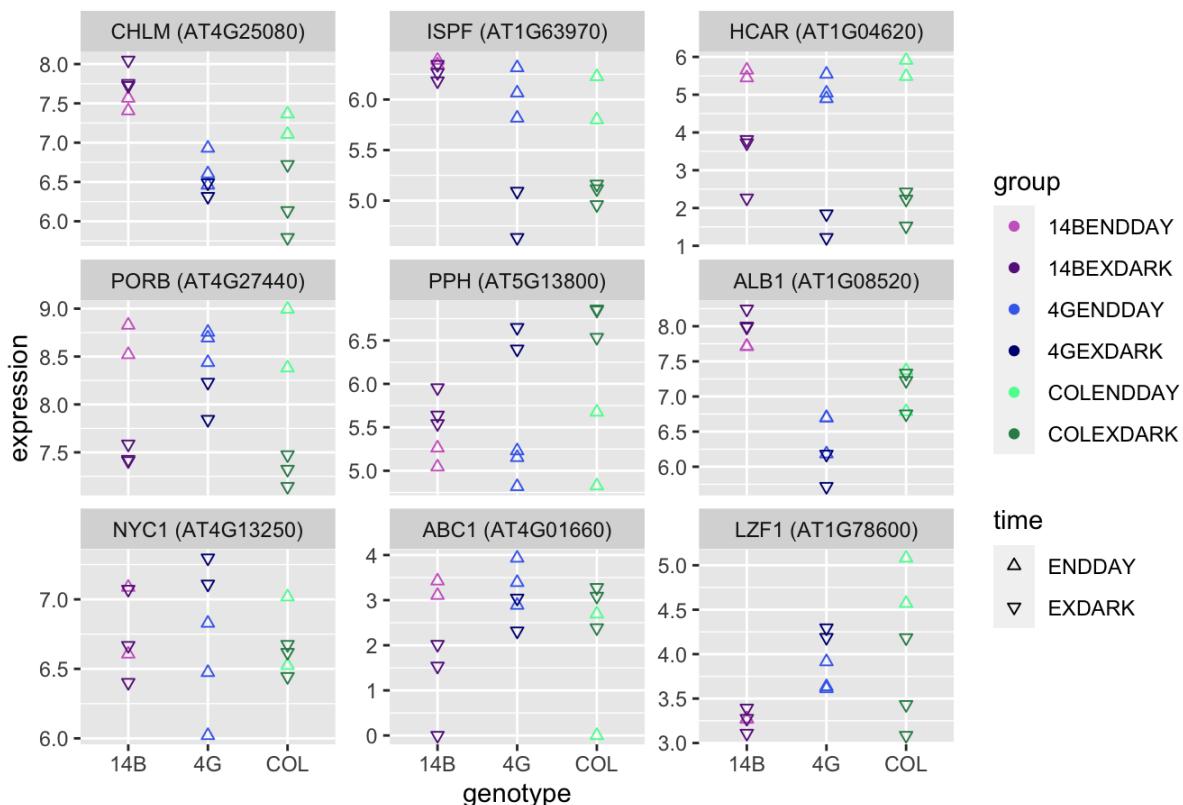


response to disaccharide

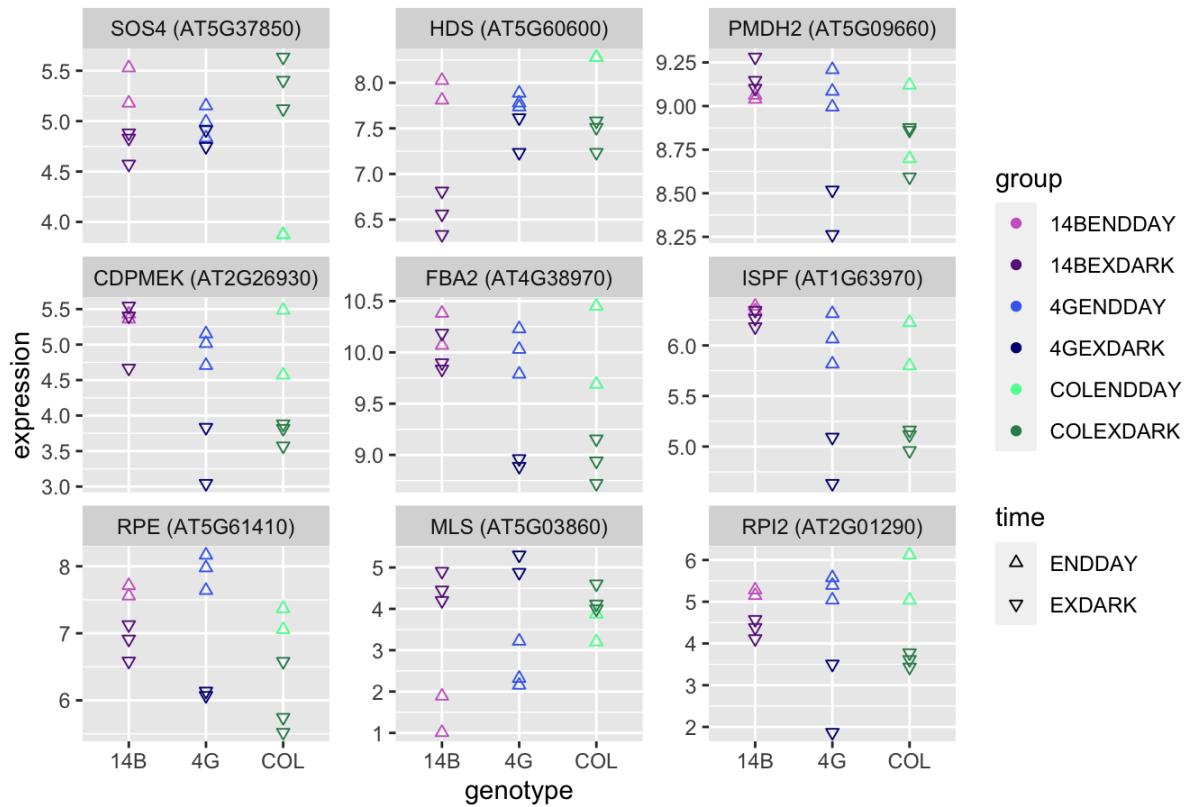




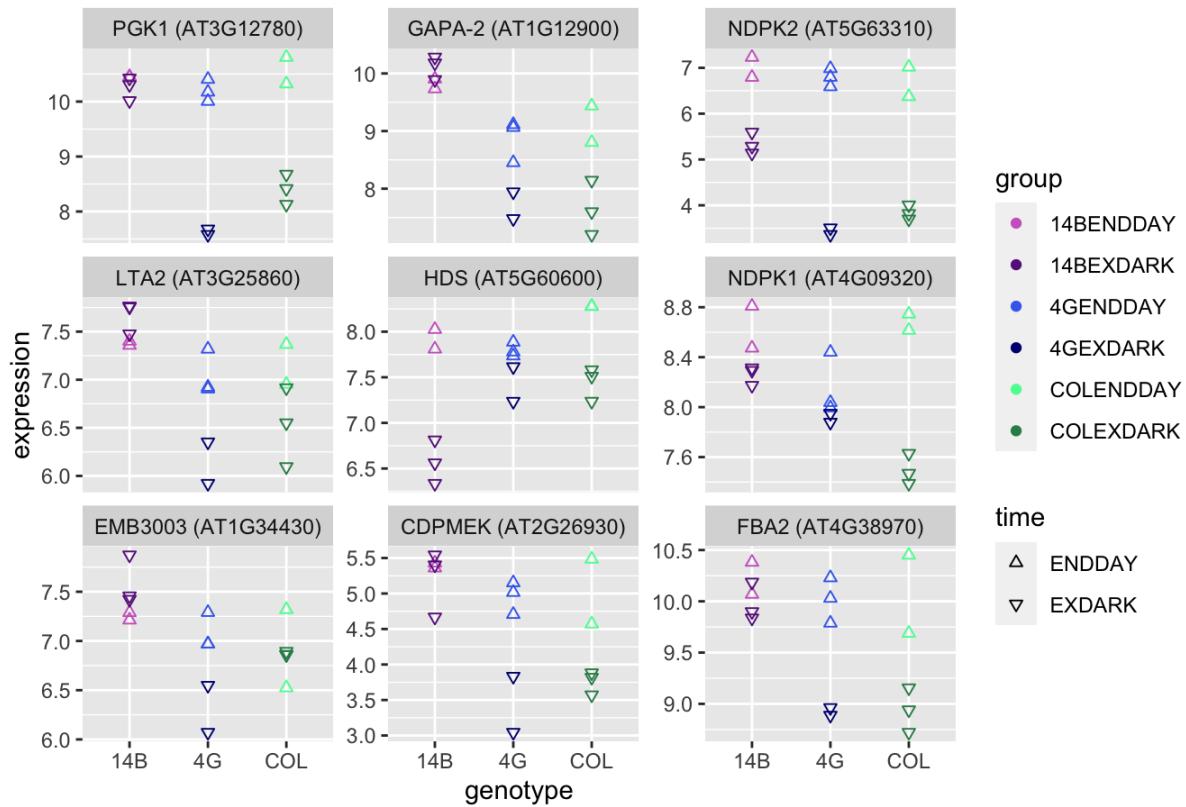
tetrapyrrole metabolic process



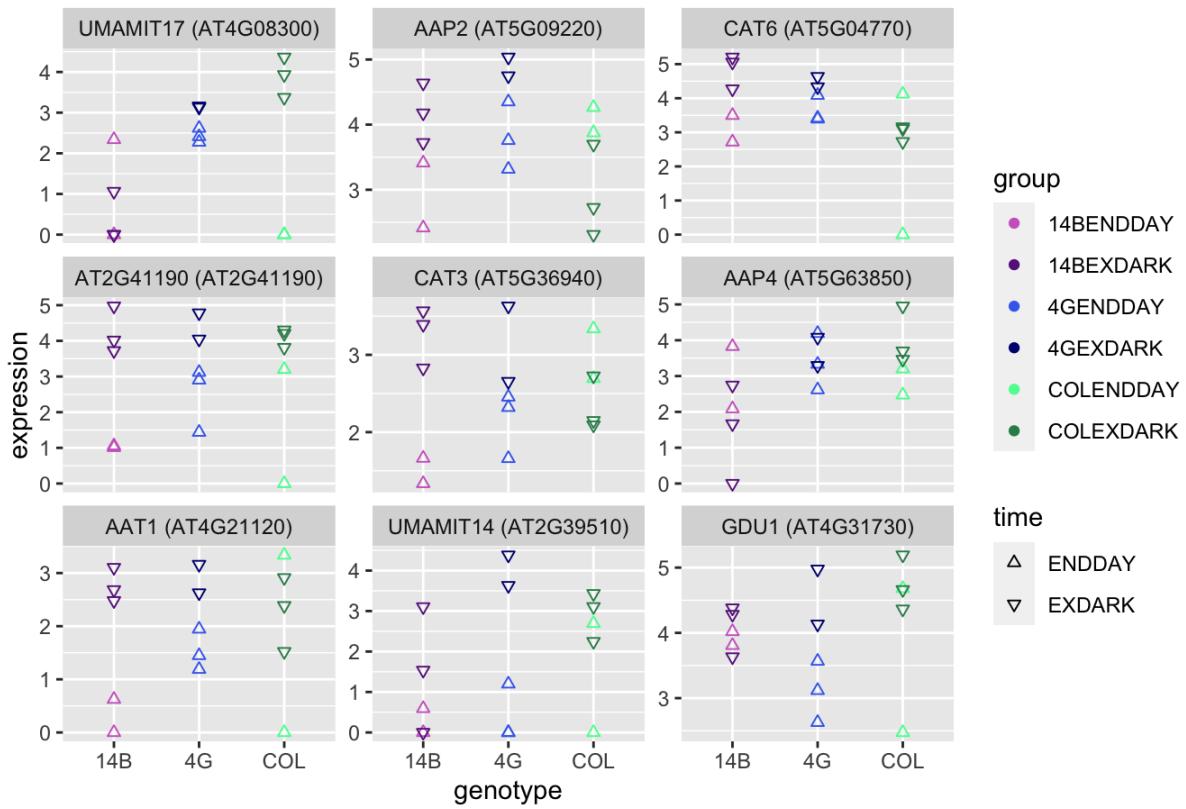
cellular aldehyde metabolic process



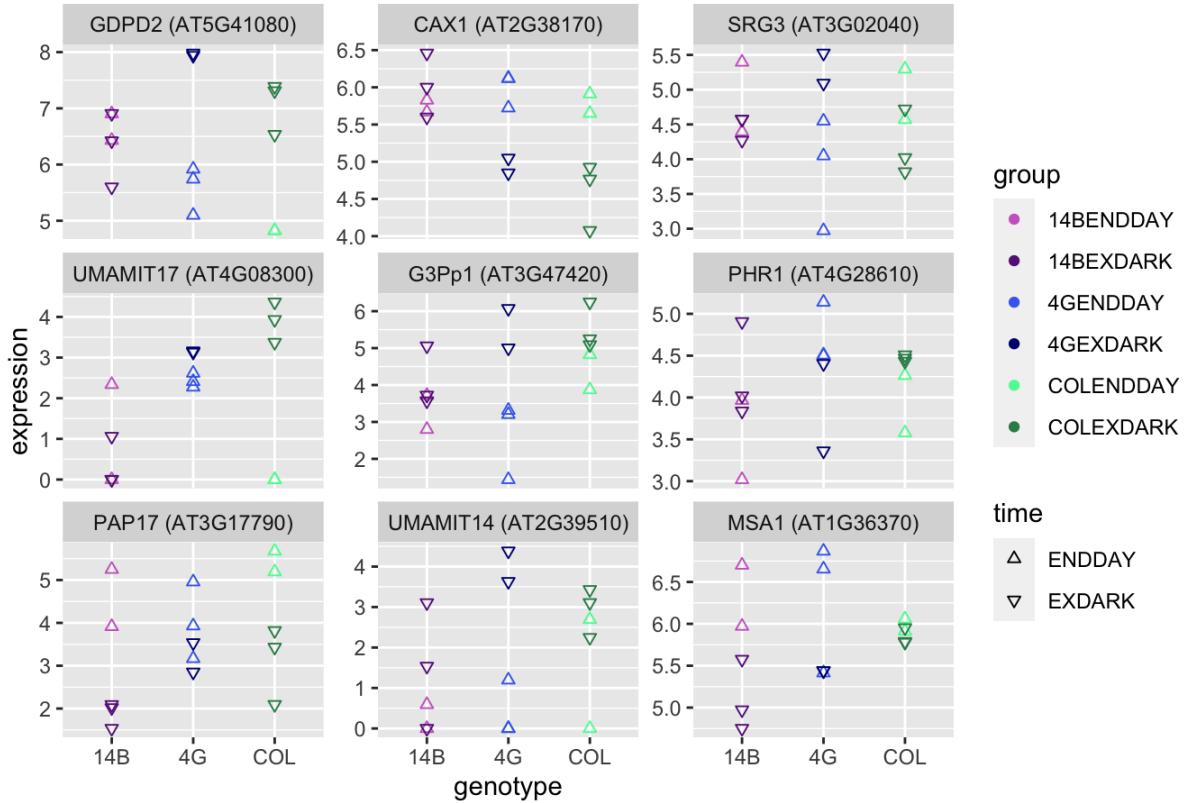
pyruvate metabolic process

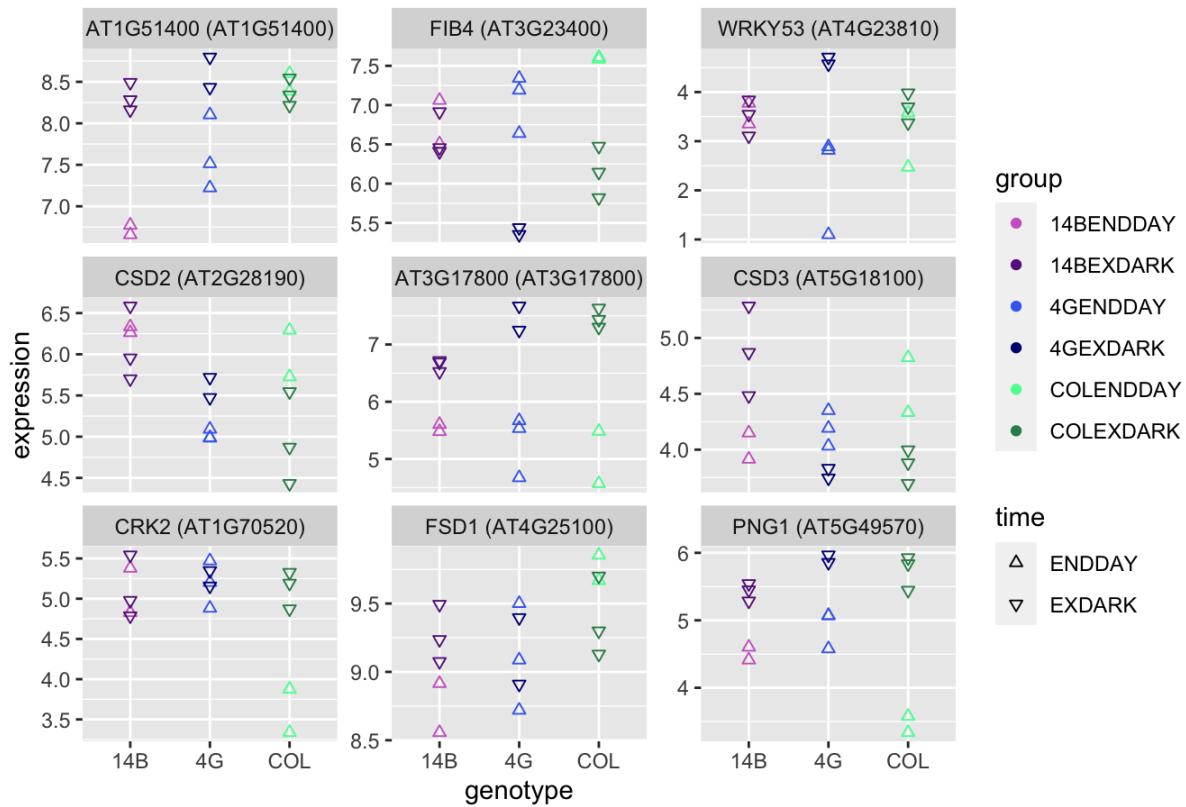
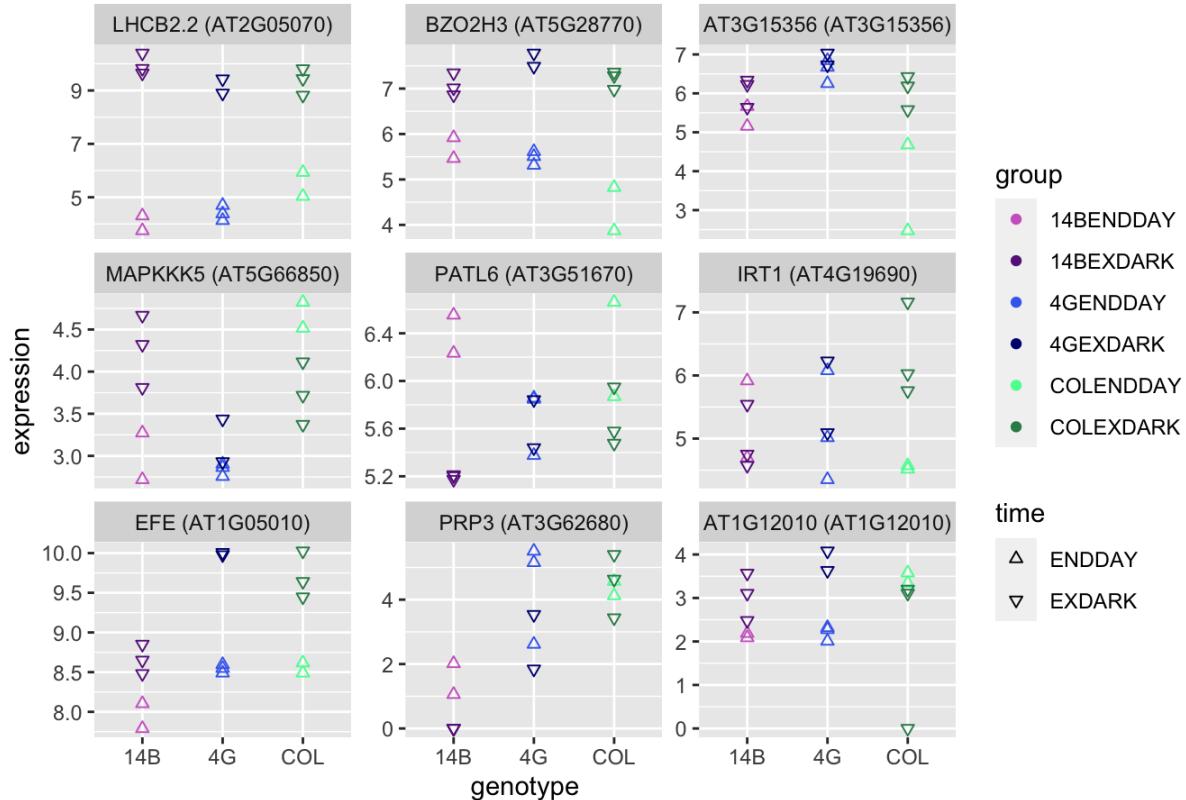


amino acid transport



anion homeostasis



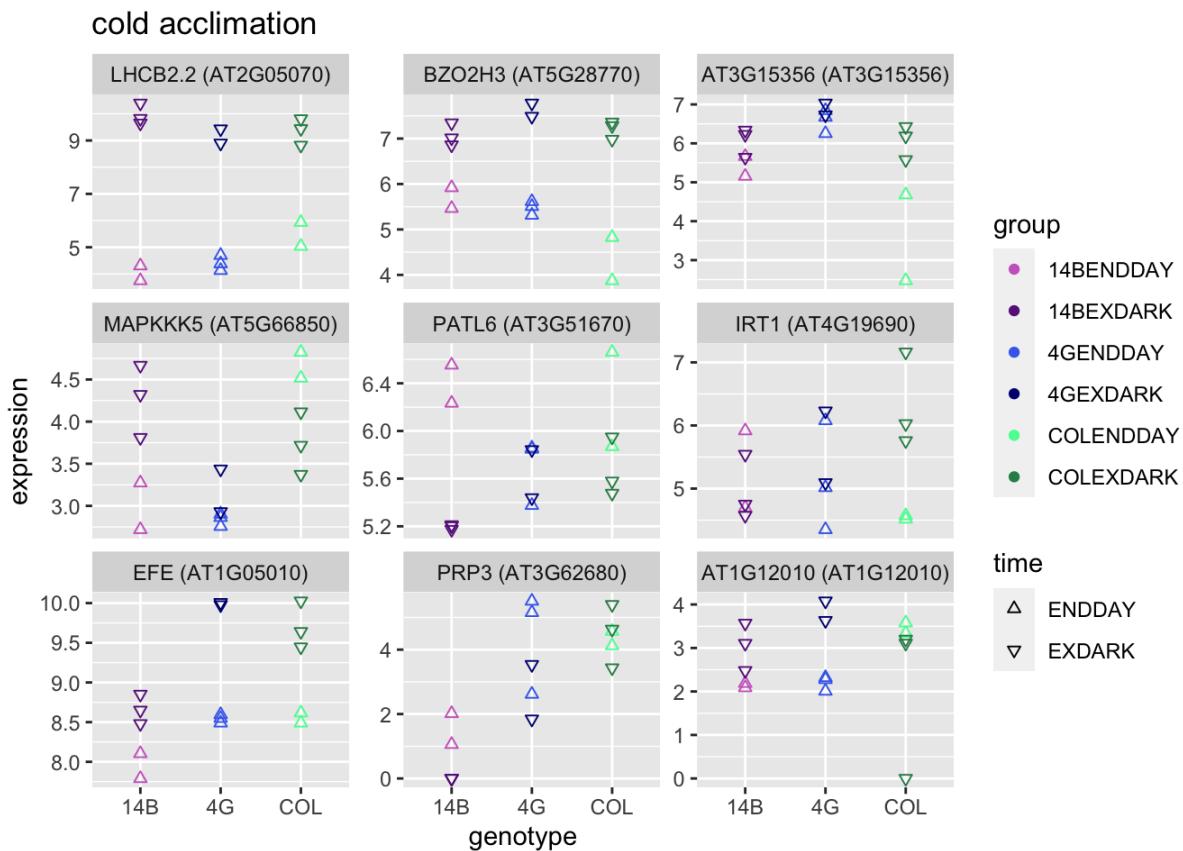
response to ozone**cellular response to endogenous stimulus**

```

lgNormRibo = log2(counts(DESeqDataSet, normalized=TRUE) + 1)

DESeq_Results1 = DESeq_Results[temp_set$gene, ]
DESeq_Results1 = DESeq_Results1[order(DESeq_Results1$pvalue), ]
DESeq_Results1 = DESeq_Results1[1:9, ]
lgGo1 <- lgNormRibo[rownames(DESeq_Results1), ]
stripChart <- stripchart321g(data = lgGo1,
                               sampleAnnotation = sampleAnnotation2,
                               geneNames = geneNamesAndDescriptions,
                               colorValues = groupColors
)
stripChart = stripChart + ggtitle("cold acclimation")
print(stripChart)

```



```

clean_DESeq_padj <- which(!is.na(DESeq_Results$padj))
clean_DESeq_Results <- DESeq_Results[clean_DESeq_padj, ]
significant_genes <- rownames(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1), ])
clean_DESeq_Results <- data.frame(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1),
])
clean_DESeq_Results$gene <- significant_genes
RNA_Result_groupings <- clean_DESeq_Results %>% inner_join(goAssociations2, by = "gene")
RNA_Result_groupings %>% group_by(gene_ontology_name) %>% summarize(count = n()) %>% arrange(desc(count)) %>%
  filter(count >= 6) %>%
knitr::kable(caption = "Distribution of Significant Genes Groupings For Ribo-Seq")

```

Distribution of Significant Genes Groupings For Ribo-Seq

gene_ontology_name	count
--------------------	-------

gene_ontology_name	count
response to light stimulus	17
translation	14
photosynthesis	13
response to cold	9
protein-chromophore linkage	8
pyruvate metabolic process	6

```

clean_DESeq_padj <- which(!is.na(DESeq_Results$padj))
clean_DESeq_Results <- DESeq_Results[clean_DESeq_padj, ]
significant_genes <- rownames(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1), ])
clean_DESeq_Results <- data.frame(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1),
])
clean_DESeq_Results$gene <- significant_genes
RNA_Result_groupings <- clean_DESeq_Results %>% inner_join(goAssociations2, by = "gene")
RNA_Result_groupings %>% group_by(gene_ontology_name) %>% summarize(count = n()) %>% arrange(desc(count)) %>
knitr::kable(caption = "Distribution of Significant Genes Groupings For Ribo-Seq")

```

Distribution of Significant Genes Groupings For Ribo-Seq

gene_ontology_name	count
response to light stimulus	17
translation	14
photosynthesis	13
response to cold	9
protein-chromophore linkage	8
pyruvate metabolic process	6
cold acclimation	5
response to abscisic acid	5
defense response	3
photosynthetic electron transport chain	3
regulation of transcription	3
response to red or far red light	3
translational elongation	3
anion homeostasis	2
carbohydrate metabolic process	2
circadian rhythm	2
NADH metabolic process	2
protein ubiquitination	2

gene_ontology_name	count
proton motive force-driven ATP synthesis	2
response to far red light	2
response to oxidative stress	2
response to ozone	2
tetrapyrrole metabolic process	2
transmembrane transport	2
cellular aldehyde metabolic process	1
cellular amino acid biosynthetic process	1
cellular amino acid metabolic process	1
cellular response to endogenous stimulus	1
developmental growth	1
exocytosis	1
gluconeogenesis	1
glucose metabolic process	1
glycerophospholipid catabolic process	1
inositol catabolic process	1
negative regulation of catalytic activity	1
negative regulation of translation in response to stress	1
peptidyl-cysteine S-nitrosylation	1
photosystem II oxygen evolving complex assembly	1
plastid translation	1
regulation of abscisic acid synthesis	1
regulation of defense response	1
response to disaccharide	1
response to heat	1
riboflavin biosynthetic process	1
thylakoid membrane organization	1
translational initiation	1
valine biosynthetic process	1

Comparison of two mutant types 14B and 4G ## translational Efficiency pt.2

```

start_time <- Sys.time()

riboCounts <- riboCounts %>% select(-contains("COL"))
rnaCounts <- rnaCounts %>% select(-contains("COL"))
sampleAnnotation <- sampleAnnotation %>% filter(!str_detect(group, 'COL'))
sampleAnnotation2 <- sampleAnnotation2 %>% filter(!str_detect(group, 'COL'))

# rna and ribo
sampleAnnotation$SeqType = "RNA"
sampleAnnotation2$SeqType = "Ribo"
combinedCounts = cbind(riboCounts, rnaCounts)
sampleAnnotation3 = rbind(sampleAnnotation, sampleAnnotation2)
colnames(combinedCounts) = rownames(sampleAnnotation3)

# time + genotype + time:genotype + SeqType + SeqType:time + SeqType:genotype + SeqType:time:genotype
pe

DESeqDataSet = DESeqDataSetFromMatrix(
  countData = combinedCounts,
  colData = sampleAnnotation3,
  design = ~ time * genotype * SeqType
)

```

```

## Warning in DESeqDataSet(se, design = design, ignoreRank): some variables in
## design formula are characters, converting to factors

```

```

DESeqDataSet_both = DESeq(
  DESeqDataSet,
  parallel=FALSE,
  test = "LRT",
  reduced = ~ (time + genotype + SeqType)^2
)

```

```

## estimating size factors

```

```

## estimating dispersions

```

```

## gene-wise dispersion estimates

```

```

## mean-dispersion relationship

```

```

## final dispersion estimates

```

```

## fitting model and testing

```

```

DESeq_Results_both <- results(DESeqDataSet_both)
clean_DESeq_padj <- which(!is.na(DESeq_Results_both$padj))
sum(DESeq_Results_both[clean_DESeq_padj, "padj"] <= 0.1)

```

```

## [1] 206

```

```
sum(DESeq_Results_both[clean_DESeq_padj, "padj"] <= 0.1) * 0.1
```

```
## [1] 20.6
```

```
end_time <- Sys.time()  
print(end_time - start_time)
```

```
## Time difference of 26.01305 secs
```

```
# rna  
DESeqDataSet = DESeqDataSetFromMatrix(  
  countData = rnaCounts,  
  colData = sampleAnnotation,  
  design = ~ time + genotype + time:genotype  
)
```

```
## Warning in DESeqDataSet(se, design = design, ignoreRank): some variables in  
## design formula are characters, converting to factors
```

```
DESeqDataSet = DESeq(  
  DESeqDataSet,  
  parallel=FALSE,  
  test = "LRT",  
  reduced = ~ time + genotype  
)
```

```
## estimating size factors
```

```
## estimating dispersions
```

```
## gene-wise dispersion estimates
```

```
## mean-dispersion relationship
```

```
## final dispersion estimates
```

```
## fitting model and testing
```

```
DESeq_Results_RNA <- results(DESeqDataSet)  
  
# ribo  
DESeqDataSet = DESeqDataSetFromMatrix(  
  countData = riboCounts,  
  colData = sampleAnnotation2,  
  design = ~ time + genotype + time:genotype  
)
```

```
## Warning in DESeqDataSet(se, design = design, ignoreRank): some variables in
## design formula are characters, converting to factors
```

```
DESeqDataSet = DESeq(
  DESeqDataSet,
  parallel=FALSE,
  test = "LRT",
  reduced = ~ time + genotype
)
```

```
## estimating size factors
```

```
## estimating dispersions
```

```
## gene-wise dispersion estimates
```

```
## mean-dispersion relationship
```

```
## final dispersion estimates
```

```
## fitting model and testing
```

```
DESeq_Results_ribo <- results(DESeqDataSet)
```

```
temp <- as.data.frame(DESeq_Results_both[clean_DESeq_padj,])
head(temp %>% filter(padj <= 0.1) %>% arrange(padj))
```

```
##          baseMean log2FoldChange      lfcSE      stat     pvalue      padj
## AT2G39010    708.7769     -1.548396  0.2576238  36.08845 1.885616e-09 1.046894e-05
## AT4G32260   1519.1830     -1.126996  0.1955850  33.32757 7.787065e-09 2.161689e-05
## AT3G60750   5367.2383     -1.101751  0.1943709  32.11992 1.449436e-08 2.682422e-05
## AT1G55480   299.8834      1.829006  0.3339363  31.29736 2.213803e-08 3.072758e-05
## AT2G37220  1993.9361     -1.074573  0.1949634  30.39901 3.517083e-08 3.303230e-05
## AT2G43030   999.6466     -1.708945  0.3107172  30.37016 3.569773e-08 3.303230e-05
```

```
clean_DESeq_padj <- which(!is.na(DESeq_Results_both$padj))
clean_DESeq_Results <- DESeq_Results_both[clean_DESeq_padj, ]
significant_genes <- rownames(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1), ])
clean_DESeq_Results <- data.frame(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1),
  ])
clean_DESeq_Results$gene <- significant_genes
RNA_Result_groupings <- clean_DESeq_Results %>% inner_join(goAssociations2, by = "gene")
RNA_Result_groupings %>% group_by(gene_ontology_name) %>% summarize(count = n()) %>% arrange(desc(count)) %>%
  filter(count >= 5) %>%
  knitr::kable(caption = "Distribution of Significant Genes Groupings For TE")
```

Distribution of Significant Genes Groupings For TE

gene_ontology_name	count
--------------------	-------

gene_ontology_name	count
response to light stimulus	14
translation	14
pyruvate metabolic process	9
response to cold	6
protein-chromophore linkage	5
translational elongation	5

```

clean_DESeq_padj <- which(!is.na(DESeq_Results_both$padj))
clean_DESeq_Results <- DESeq_Results_both[clean_DESeq_padj, ]
significant_genes <- rownames(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1), ])
clean_DESeq_Results <- data.frame(clean_DESeq_Results[which(clean_DESeq_Results[, "padj"] <= 0.1),
])
clean_DESeq_Results$gene <- significant_genes
RNA_Result_groupings <- clean_DESeq_Results %>% inner_join(goAssociations2, by = "gene")
RNA_Result_groupings %>% group_by(gene_ontology_name) %>% summarize(count = n()) %>% arrange(desc(count)) %>%
  knitr::kable(caption = "Distribution of Significant Genes Groupings For TE")

```

Distribution of Significant Genes Groupings For TE

gene_ontology_name	count
response to light stimulus	14
translation	14
pyruvate metabolic process	9
response to cold	6
protein-chromophore linkage	5
translational elongation	5
cellular aldehyde metabolic process	4
photosynthesis	4
proteolysis	4
cold acclimation	3
protein transport	3
response to abscisic acid	3
tetrapyrrole metabolic process	3
translational initiation	3
transmembrane transport	3
intracellular protein transport	2
NADH metabolic process	2
nitrate assimilation	2

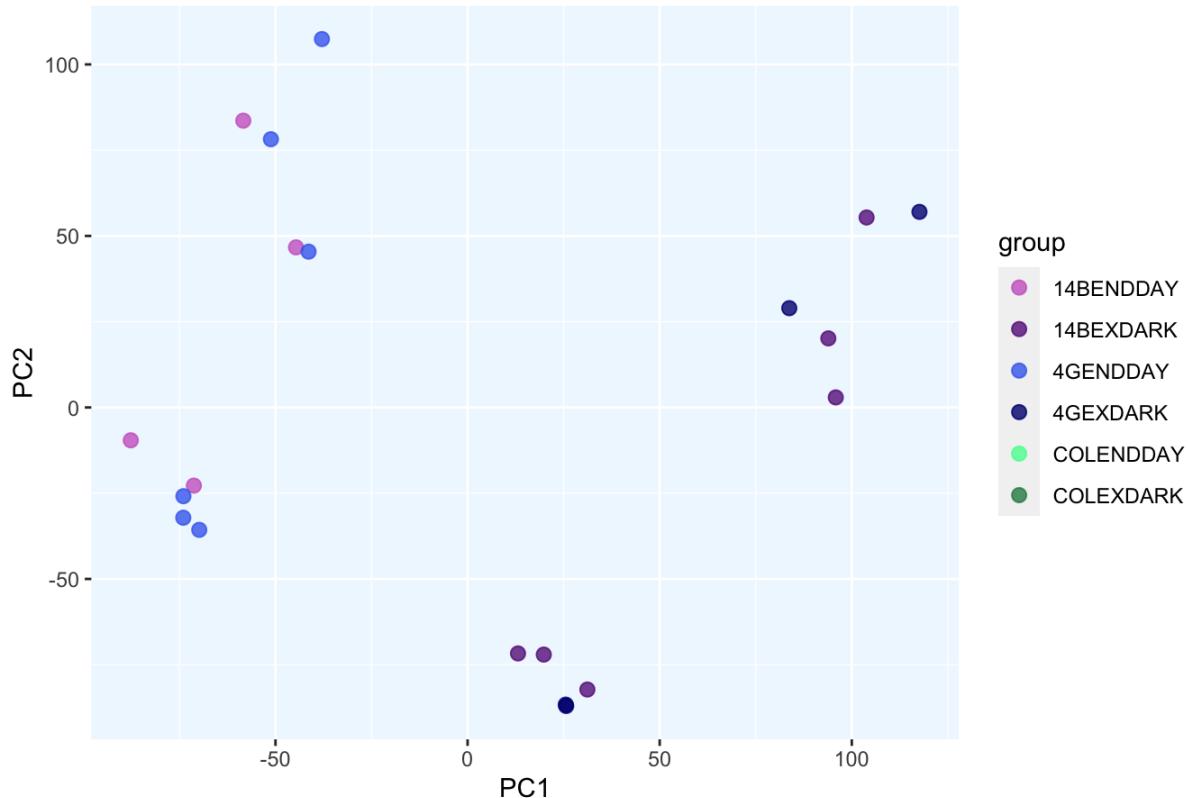
gene_ontology_name	count
protein folding	2
proton motive force-driven ATP synthesis	2
proton transmembrane transport	2
response to light intensity	2
valine biosynthetic process	2
amino acid transport	1
anion homeostasis	1
branched-chain amino acid biosynthetic process	1
carbohydrate metabolic process	1
cellular amino acid biosynthetic process	1
cellular response to abscisic acid stimulus	1
cellular response to endogenous stimulus	1
cysteine biosynthetic process	1
cytoplasmic translation	1
cytoplasmic translational elongation	1
defense response	1
fatty acid metabolic process	1
gibberellic acid mediated signaling pathway	1
gluconeogenesis	1
glucose metabolic process	1
protein autoubiquitination	1
protein ubiquitination	1
regulation of gene expression	1
response to disaccharide	1
response to far red light	1

```
lgNorm = log2(counts(DESeqDataSet_both, normalized=TRUE) + 1)
```

Overall PCA Plot

```
pca = prcomp(t(lgNorm))
pcaData = data.frame(pca$x[, 1:2])
pcaData$group = sampleAnnotation3[rownames(pcaData), "group"]
pcaData$sample = rownames(pcaData)
gg = ggplot(pcaData, aes(x=PC1, y=PC2, color=group, label=sample))
gg = gg + geom_point(size=2.5, alpha=0.8)
gg = gg + scale_color_manual(values=groupColors)
gg = gg + theme(panel.background = element_rect(fill = 'aliceblue')) + ggtitle("Overall PCA for Translational Efficiency")
print(gg)
```

Overall PCA for Translational Efficiency



```
exclusive = rownames(DESeq_Results_both)[which(DESeq_Results_both$padj < 0.1 & DESeq_Results_ribo$padj < 0.1 & DESeq_Results_RNA$padj > 0.1)]

both = rownames(DESeq_Results_both)[which(DESeq_Results_both$padj < 0.1 & DESeq_Results_ribo$padj < 0.1 & DESeq_Results_RNA$padj < 0.1)]

intensified = both[which(DESeq_Results_both[both,2]*DESeq_Results_RNA[both,2] > 0)]

buffered = both[which(DESeq_Results_both[both,2]*DESeq_Results_RNA[both,2] < 0)]
```

```
goAssociations2 %>% filter(gene %in% exclusive) %>% group_by(gene_ontology_name) %>% summarise(count = n()) %>%
  arrange(desc(count)) %>% knitr::kable(caption = "Gene Groupings for Exclusive TE Results")
```

Gene Groupings for Exclusive TE Results

gene_ontology_name	count
translation	8

gene_ontology_name	count
response to light stimulus	7
NADH metabolic process	2
protein-chromophore linkage	2
proton motive force-driven ATP synthesis	2
response to cold	2
cold acclimation	1
glucose metabolic process	1
photosynthesis	1
pyruvate metabolic process	1
tetrapyrrole metabolic process	1

```
goAssociations2 %>% filter(gene %in% both) %>% group_by(gene_ontology_name) %>% summarise(count = n()) %>% arrange(desc(count)) %>% knitr::kable(caption = "Gene Groupings for 'Both' TE Results")
```

Gene Groupings for 'Both' TE Results

gene_ontology_name	count
gluconeogenesis	1
pyruvate metabolic process	1
response to light stimulus	1

```
goAssociations2 %>% filter(gene %in% intensified) %>% group_by(gene_ontology_name) %>% summarise(count = n()) %>% arrange(desc(count)) %>% knitr::kable(caption = "Gene Groupings for Intensified TE Results")
```

Gene Groupings for Intensified TE Results

gene_ontology_name	count
gluconeogenesis	1
pyruvate metabolic process	1

```
goAssociations2 %>% filter(gene %in% buffered) %>% group_by(gene_ontology_name) %>% summarise(count = n()) %>% arrange(desc(count)) %>% knitr::kable(caption = "Gene Groupings for Buffered TE Results")
```

Gene Groupings for Buffered TE Results

gene_ontology_name	count
response to light stimulus	1

```
goAssociations2 %>% filter(gene %in% exclusive) %>%
  knitr::kable(caption = "Gene Groupings for Exclusive TE Results")
```

Gene Groupings for Exclusive TE Results

gene_ontology_primary_id	gene_ontology_name	gene
GO:0009631 (GO:0009631)	cold acclimation	AT1G77490
GO:0018298 (GO:0018298)	protein-chromophore linkage	AT3G47470
GO:0018298 (GO:0018298)	protein-chromophore linkage	AT5G01530
GO:0006090 (GO:0006090)	pyruvate metabolic process	AT1G12900
GO:0006412 (GO:0006412)	translation	AT3G27160
GO:0015986 (GO:0015986)	proton motive force-driven ATP synthesis	AT4G32260
GO:0006734 (GO:0006734)	NADH metabolic process	AT5G58330
GO:0006006 (GO:0006006)	glucose metabolic process	AT1G12900
GO:0006412 (GO:0006412)	translation	AT2G43030
GO:0006412 (GO:0006412)	translation	AT2G33800
GO:0009416 (GO:0009416)	response to light stimulus	AT5G01530
GO:0006412 (GO:0006412)	translation	AT3G15190
GO:0033013 (GO:0033013)	tetrapyrrole metabolic process	AT2G33430
GO:0009416 (GO:0009416)	response to light stimulus	AT4G25650
GO:0009416 (GO:0009416)	response to light stimulus	AT1G55480
GO:0009416 (GO:0009416)	response to light stimulus	AT3G50685
GO:0009416 (GO:0009416)	response to light stimulus	AT3G05350
GO:0015986 (GO:0015986)	proton motive force-driven ATP synthesis	AT4G32260
GO:0015979 (GO:0015979)	photosynthesis	AT1G55480
GO:0006412 (GO:0006412)	translation	AT2G43030
GO:0006734 (GO:0006734)	NADH metabolic process	AT5G58330
GO:0006412 (GO:0006412)	translation	AT2G33800
GO:0009409 (GO:0009409)	response to cold	AT1G32060
GO:0009416 (GO:0009416)	response to light stimulus	AT5G01530
GO:0006412 (GO:0006412)	translation	AT4G01310
GO:0009409 (GO:0009409)	response to cold	AT5G12250
GO:0009416 (GO:0009416)	response to light stimulus	AT4G25650
GO:0006412 (GO:0006412)	translation	AT3G15190

```
goAssociations2 %>% filter(gene %in% both) %>%
  knitr::kable(caption = "Gene Groupings for 'Both' TE Results")
```

Gene Groupings for 'Both' TE Results

gene_ontology_primary_id	gene_ontology_name	gene
GO:0006090 (GO:0006090)	pyruvate metabolic process	AT3G12780
GO:0006094 (GO:0006094)	gluconeogenesis	AT3G12780
GO:0009416 (GO:0009416)	response to light stimulus	AT1G51200

```
goAssociations2 %>% filter(gene %in% intensified) %>%
  knitr::kable(caption = "Gene Groupings for Intensified TE Results")
```

Gene Groupings for Intensified TE Results

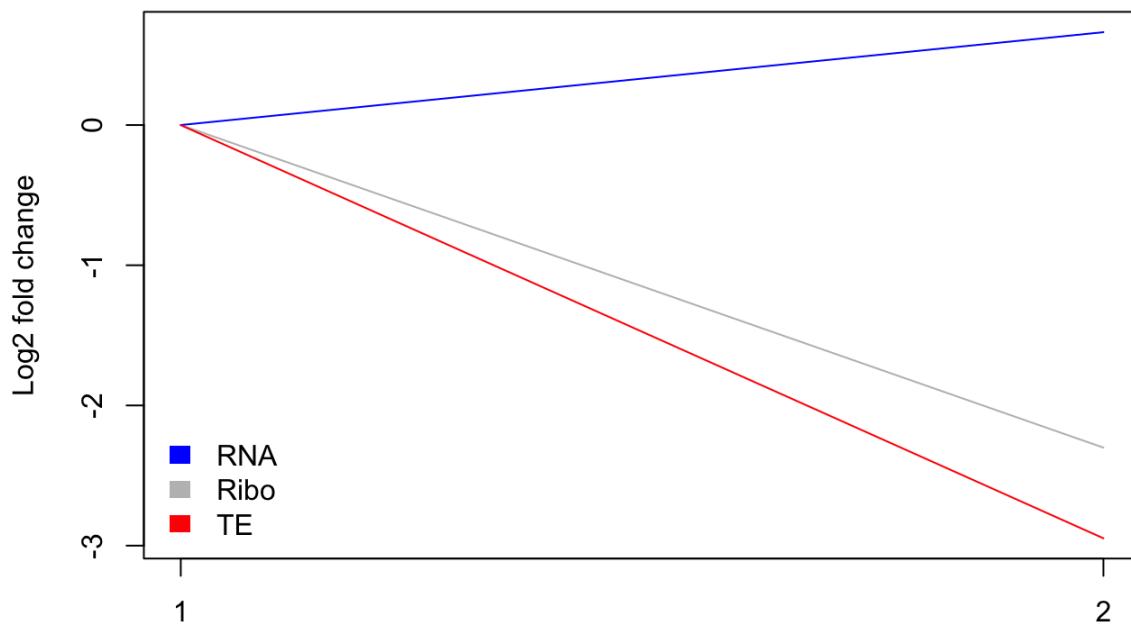
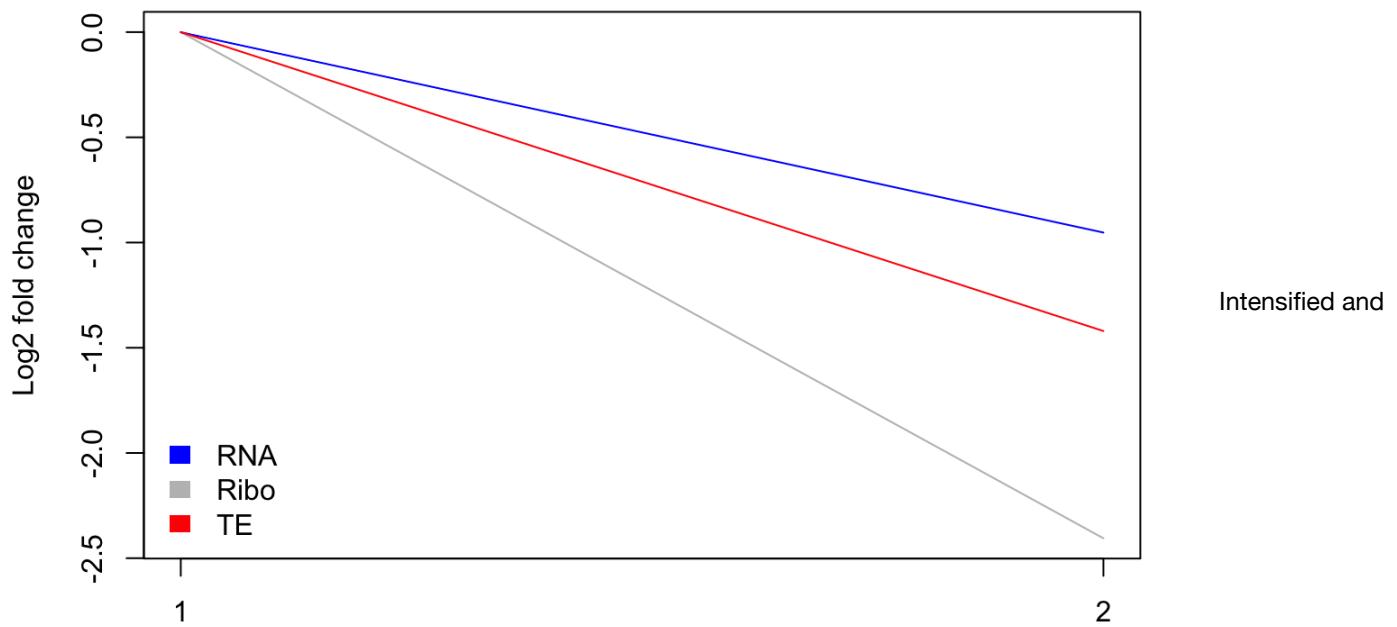
gene_ontology_primary_id	gene_ontology_name	gene
GO:0006090 (GO:0006090)	pyruvate metabolic process	AT3G12780
GO:0006094 (GO:0006094)	gluconeogenesis	AT3G12780

```
goAssociations2 %>% filter(gene %in% buffered) %>%
  knitr::kable(caption = "Gene Groupings for Buffered TE Results")
```

Gene Groupings for Buffered TE Results

gene_ontology_primary_id	gene_ontology_name	gene
GO:0009416 (GO:0009416)	response to light stimulus	AT1G51200

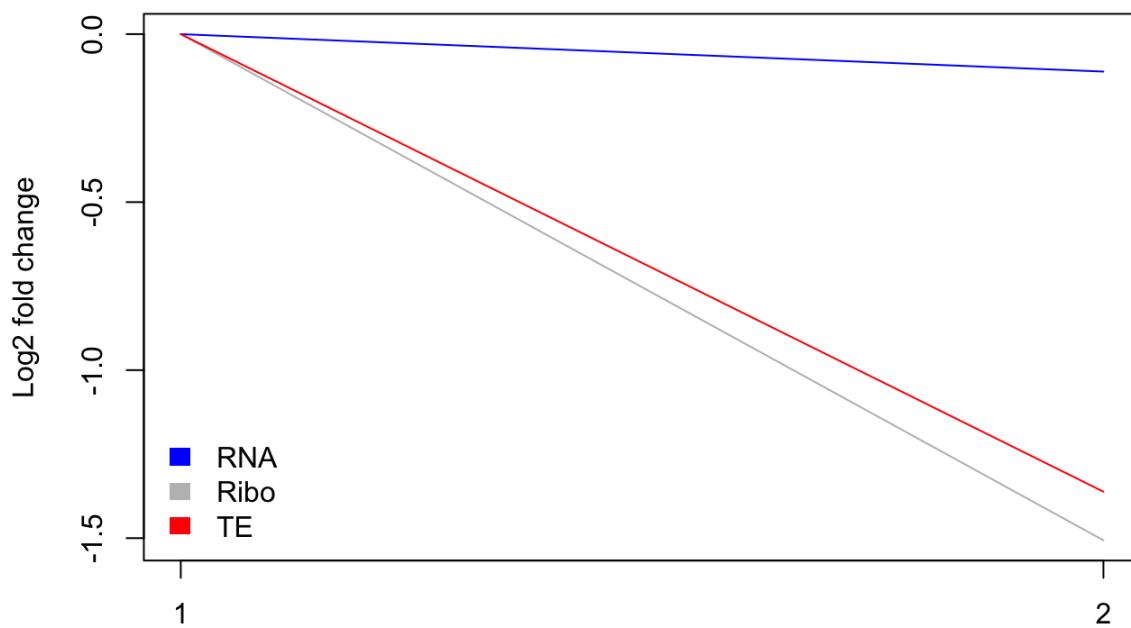
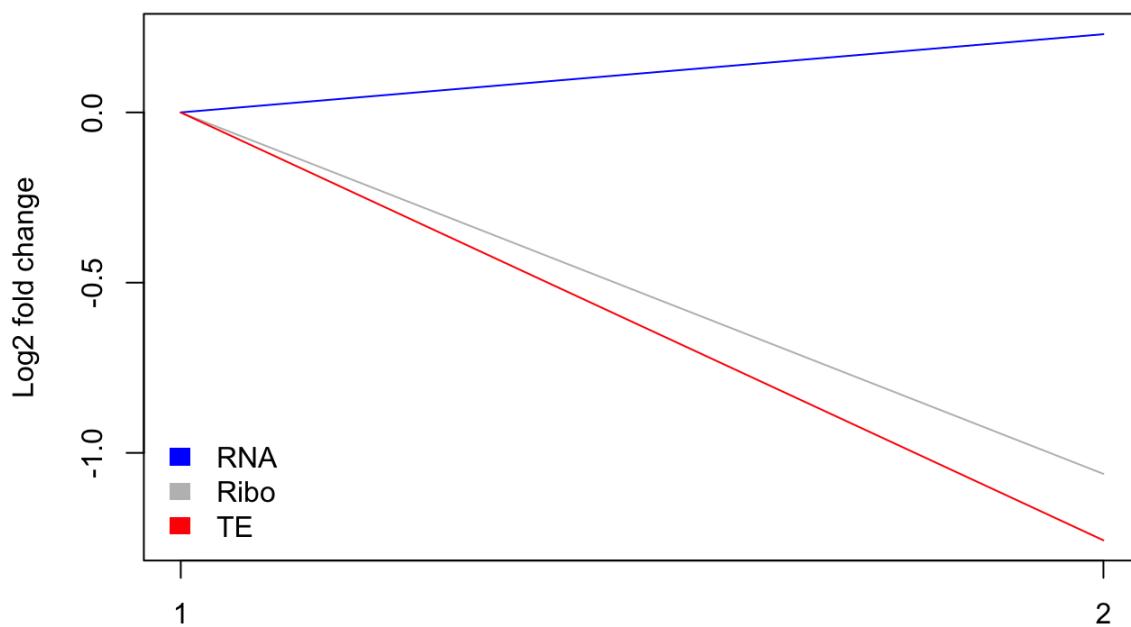
```
for (id in both){
  ymax=max(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)
  ymin=min(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)
  plot(c(0,1), c(0,DESeq_Results_ribo[id,2]), type="l",col="gray", ylim=c(ymin,ymax),
    ylab="Log2 fold change",xlab="",xaxt="n")
  lines(c(0,1), c(0,DESeq_Results_RNA[id,2]),type="l",col="blue")
  lines(c(0,1), c(0,DESeq_Results_both[id,2]), type="l",col="red")
  legend("bottomleft",c("RNA","Ribo","TE"),fill=c("blue","gray","red"), cex=1, border = NA, bty="n"
  )
  axis(1,at=c(0,1),labels=c(1,2),las=1)
  title(id)
}
```

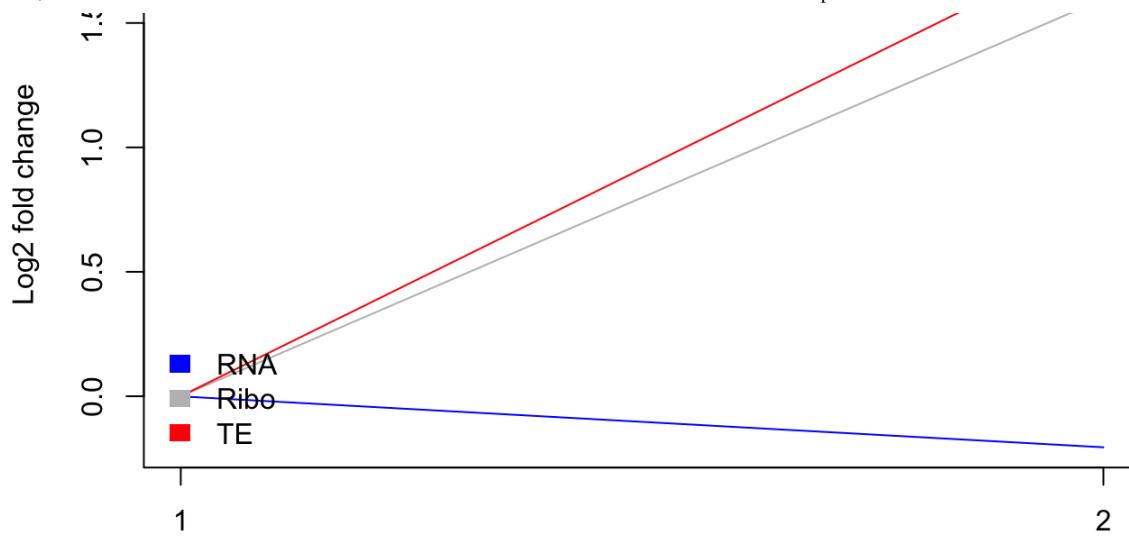
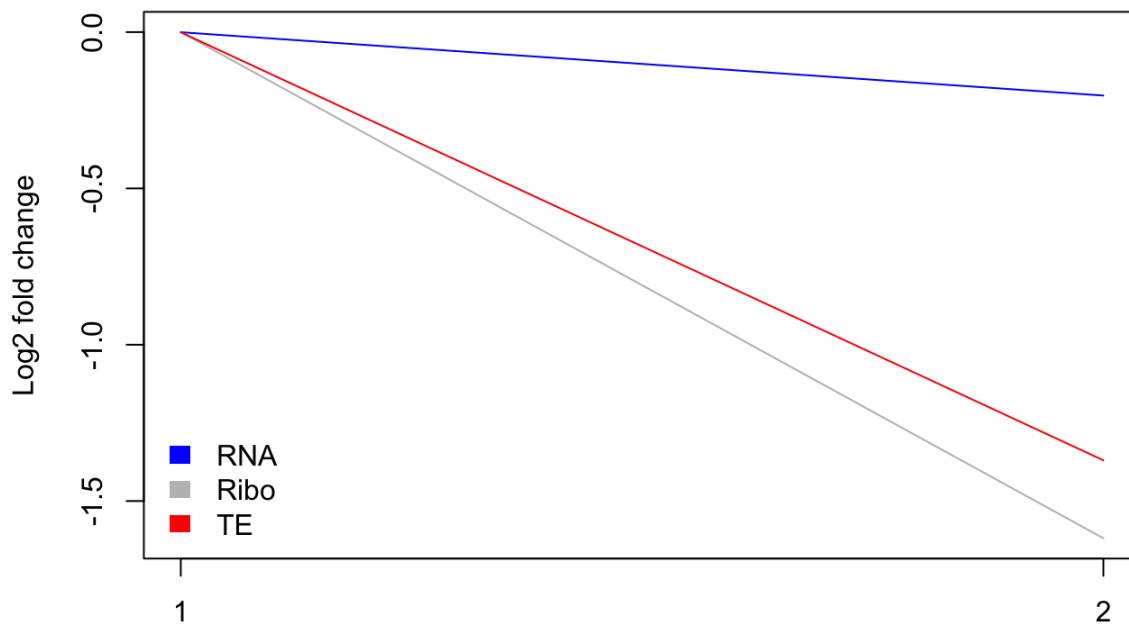
AT1G51200**AT3G12780**

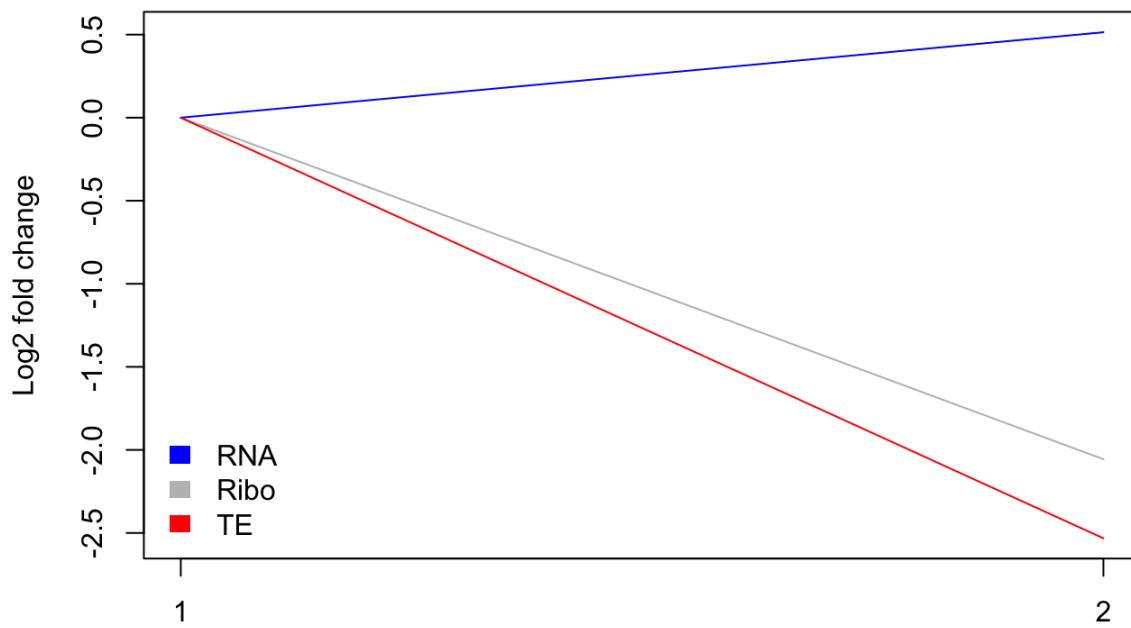
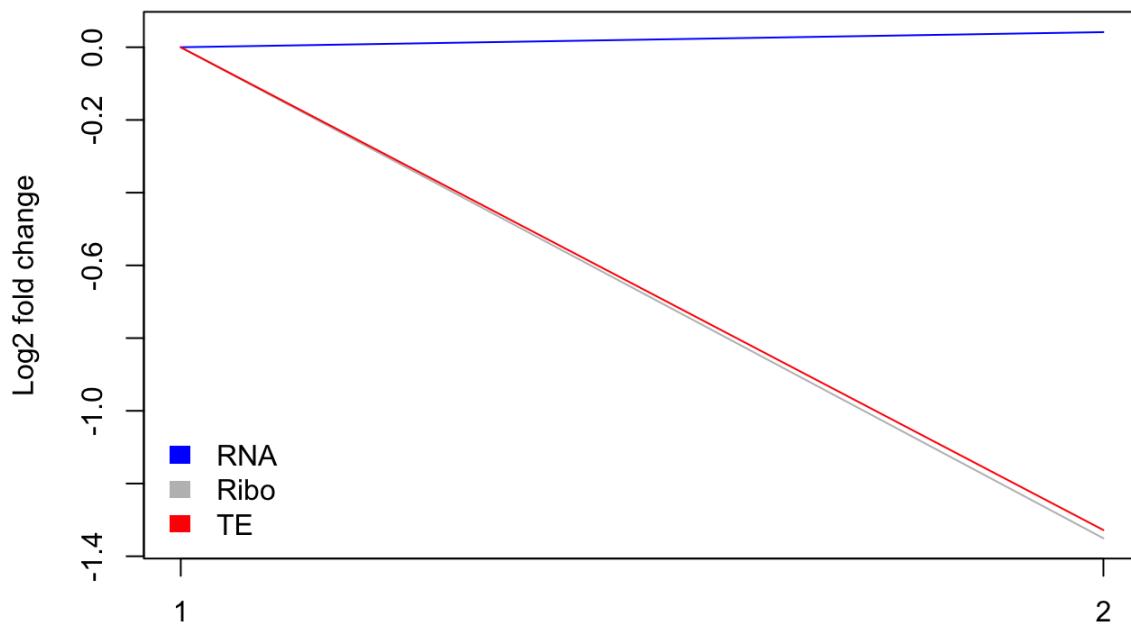
buffered: Genes regulated both by transcriptional and translational regulation (significant Δ RNA, Δ RPFs, and Δ TE) include intensified and buffered genes. These genes are both DTGs and DTEGs.

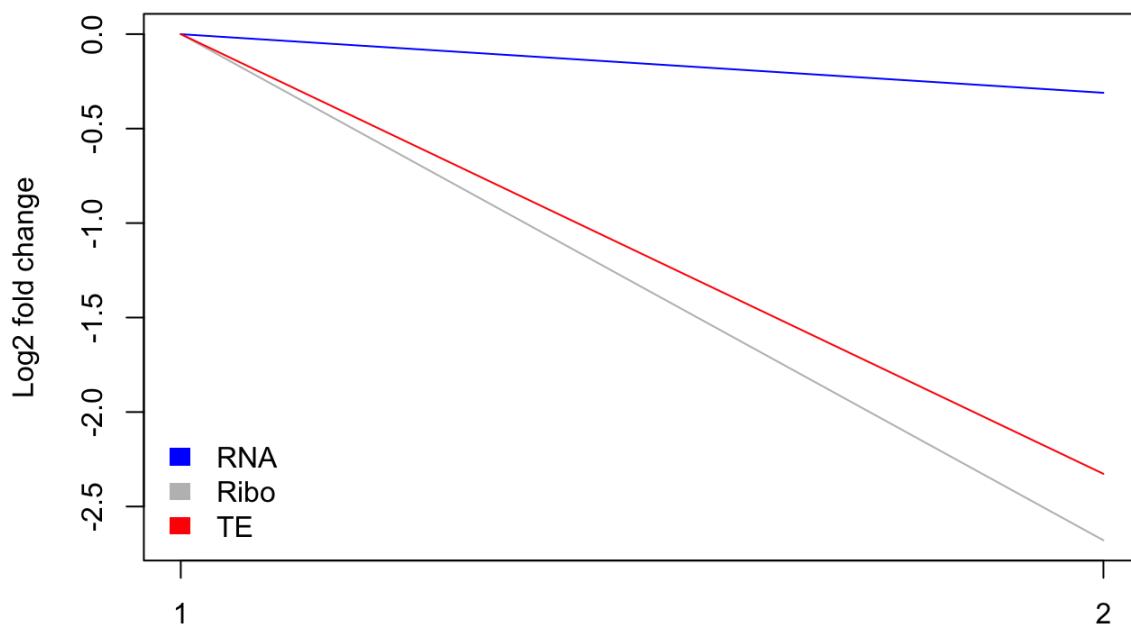
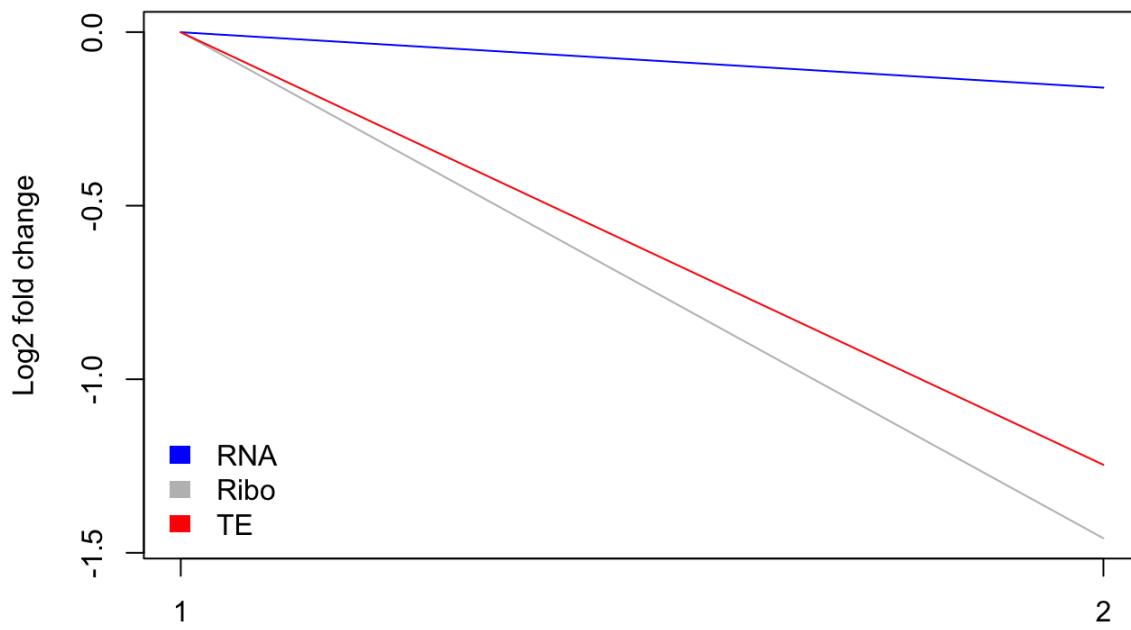
All lines going in the same direction \rightarrow change in translational efficiency is counteracting the change in RNA

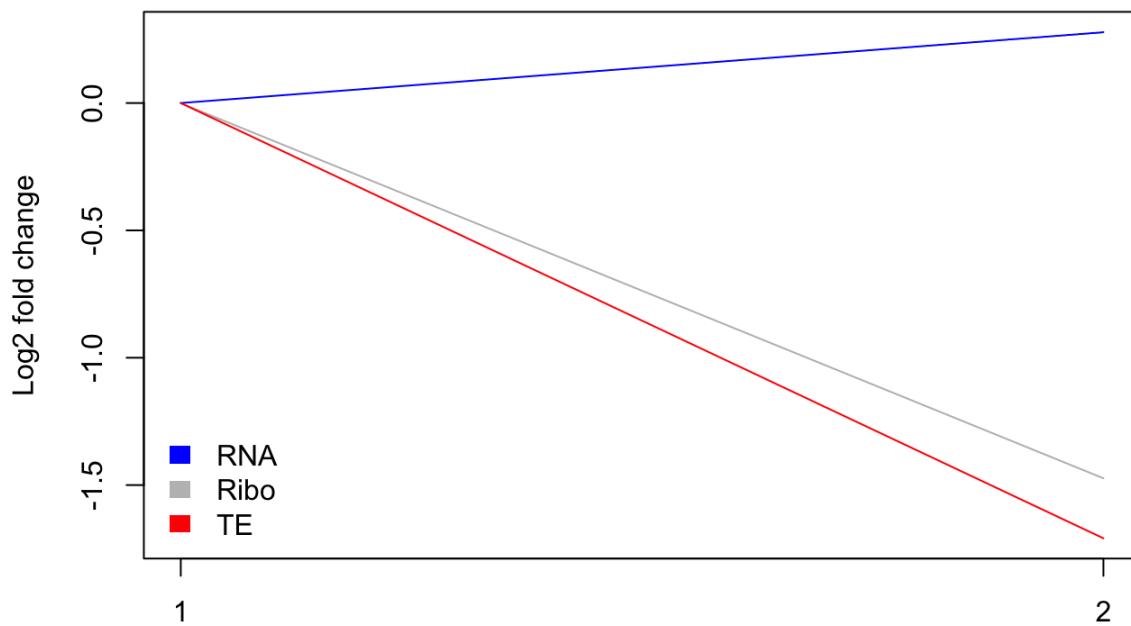
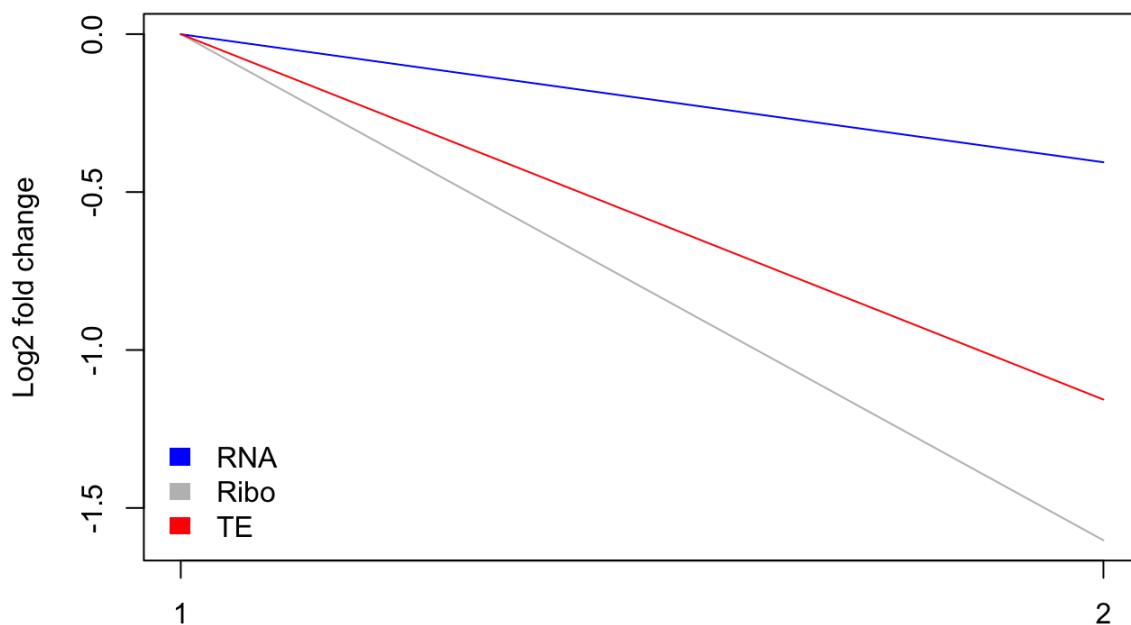
```
for (id in exclusive){  
  ymax=max(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)  
  ymin=min(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)  
  plot(c(0,1), c(0,DESeq_Results_ribo[id,2]), type="l",col="gray", ylim=c(ymin,ymax),  
       ylab="Log2 fold change",xlab="",xaxt="n")  
  lines(c(0,1), c(0,DESeq_Results_RNA[id,2]),type="l",col="blue")  
  lines(c(0,1), c(0,DESeq_Results_both[id,2]), type="l",col="red")  
  legend("bottomleft",c("RNA","Ribo","TE"),fill=c("blue","gray","red"), cex=1, border = NA, bty="n"  
)  
  axis(1,at=c(0,1),labels=c(1,2),las=1)  
  title(id)  
}
```

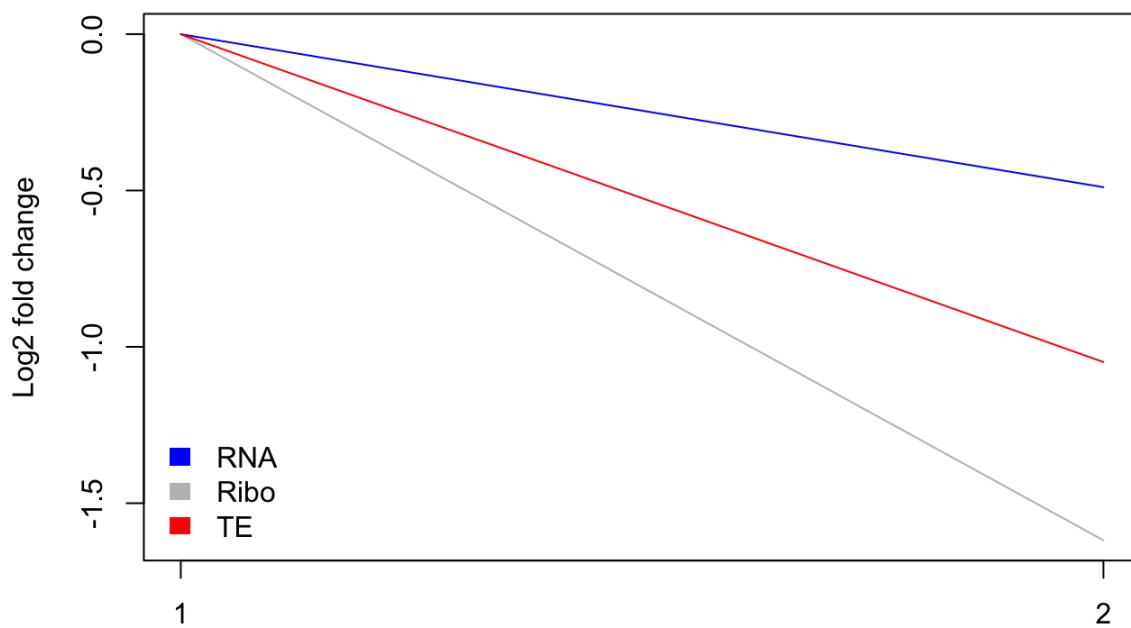
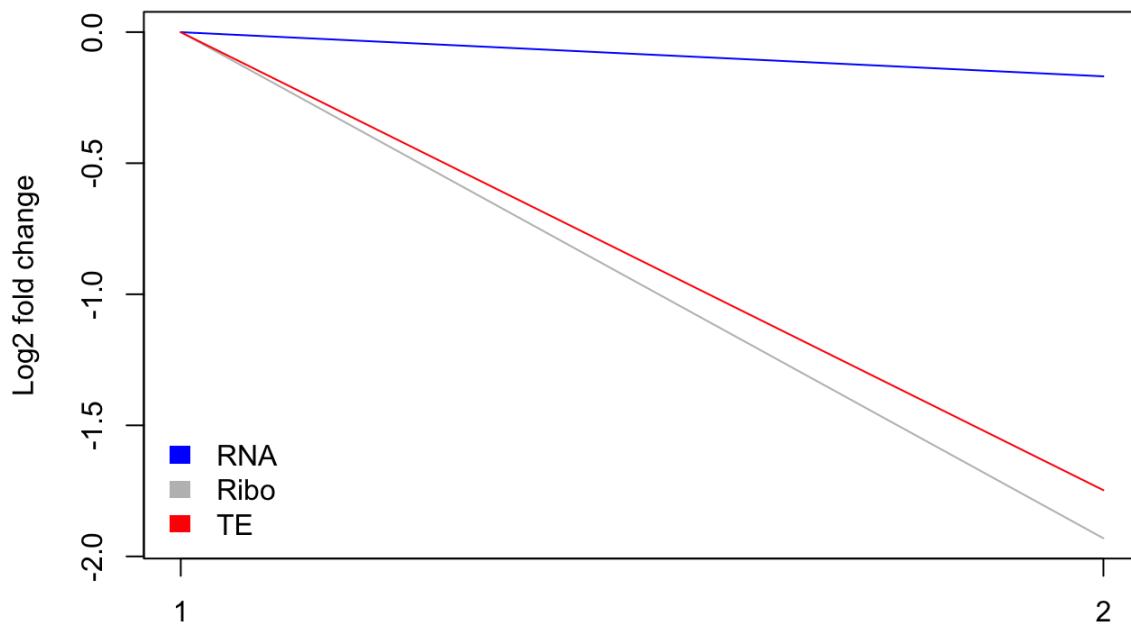
AT1G12900**AT1G32060****AT1G55480**

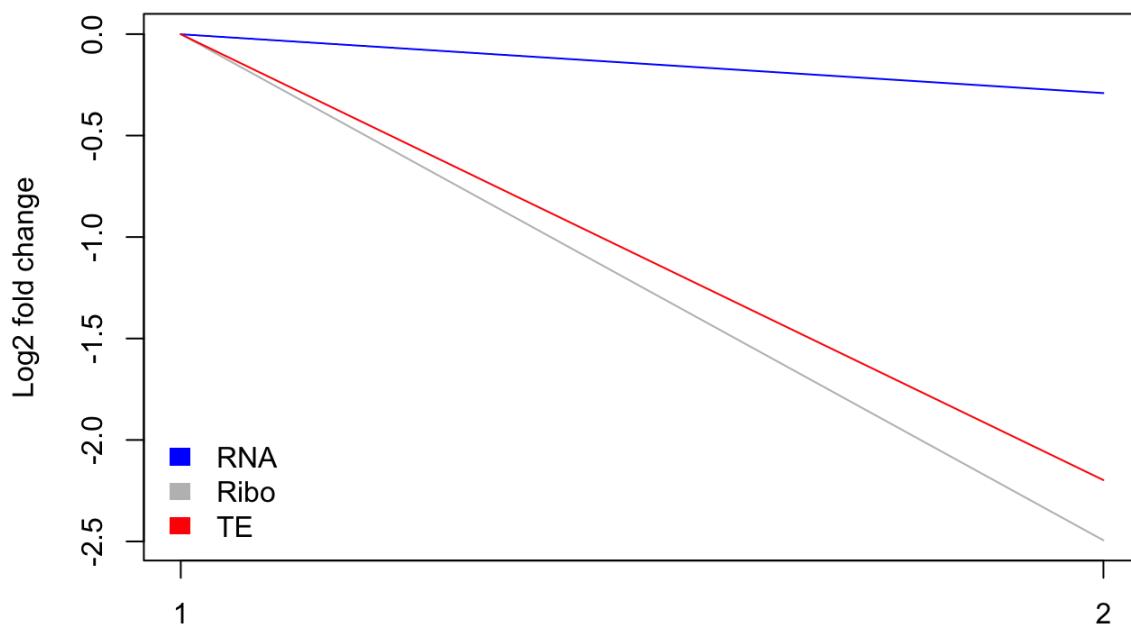
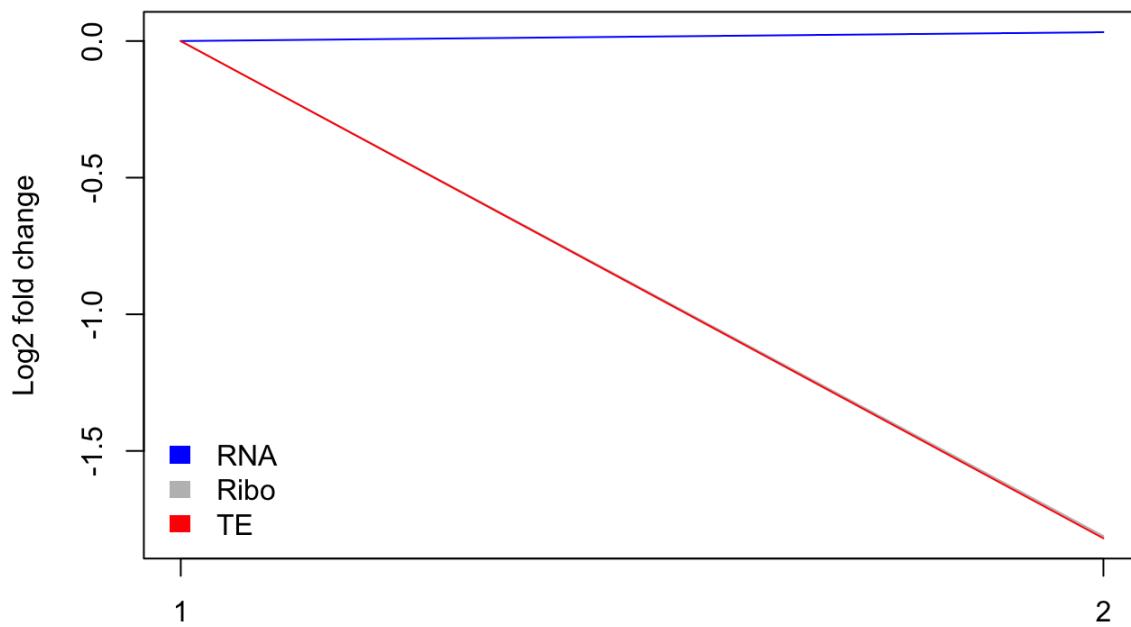
**AT1G77490**

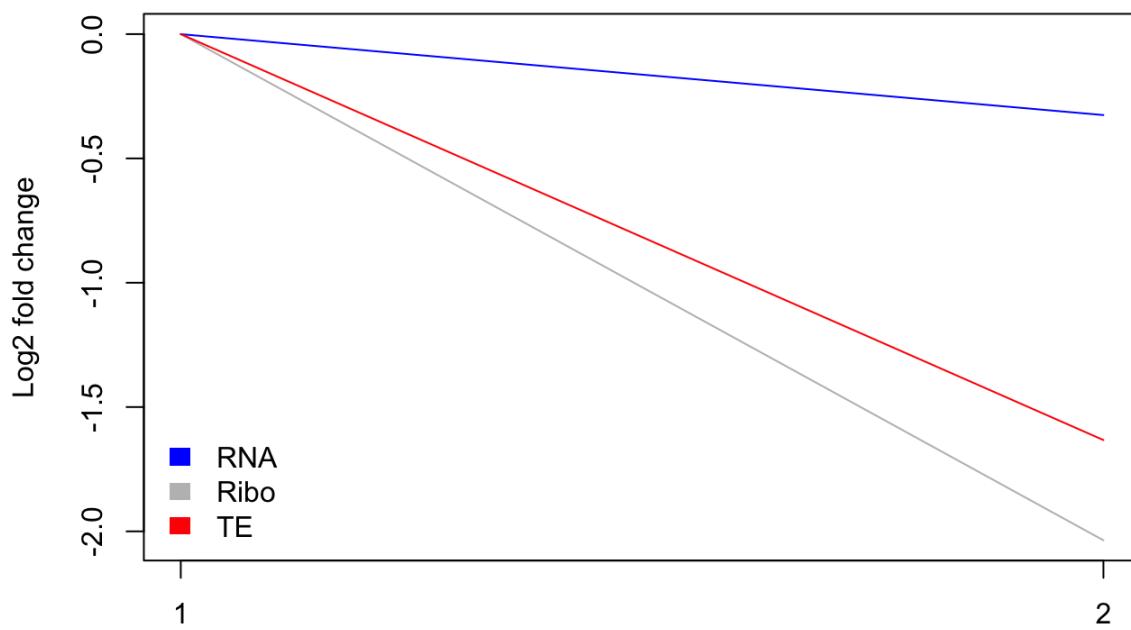
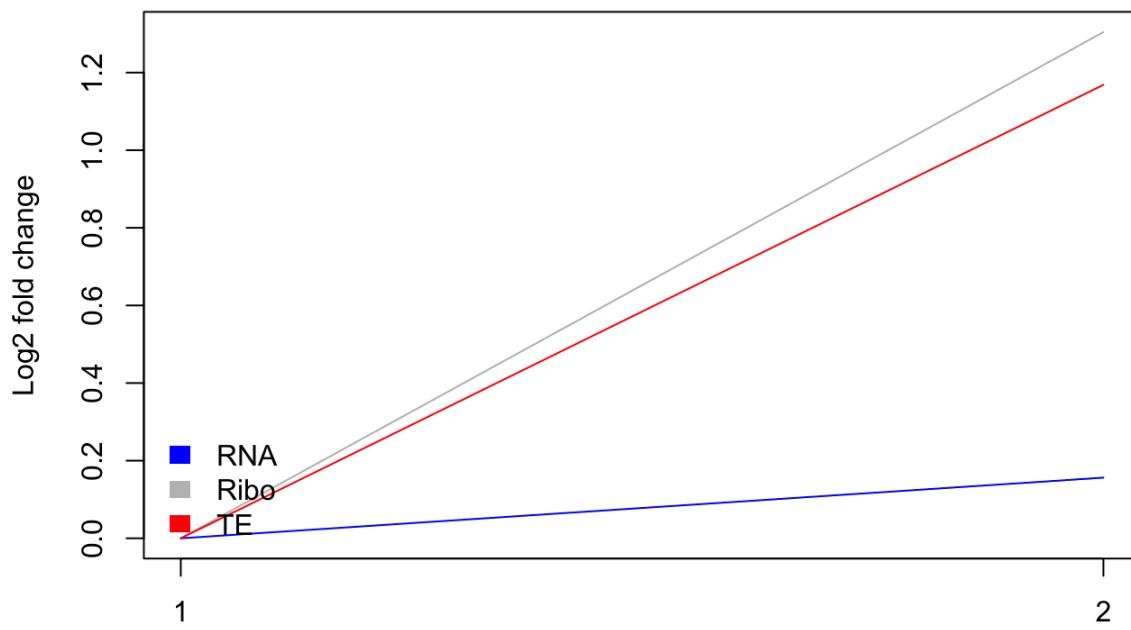
AT2G33430**AT2G33800**

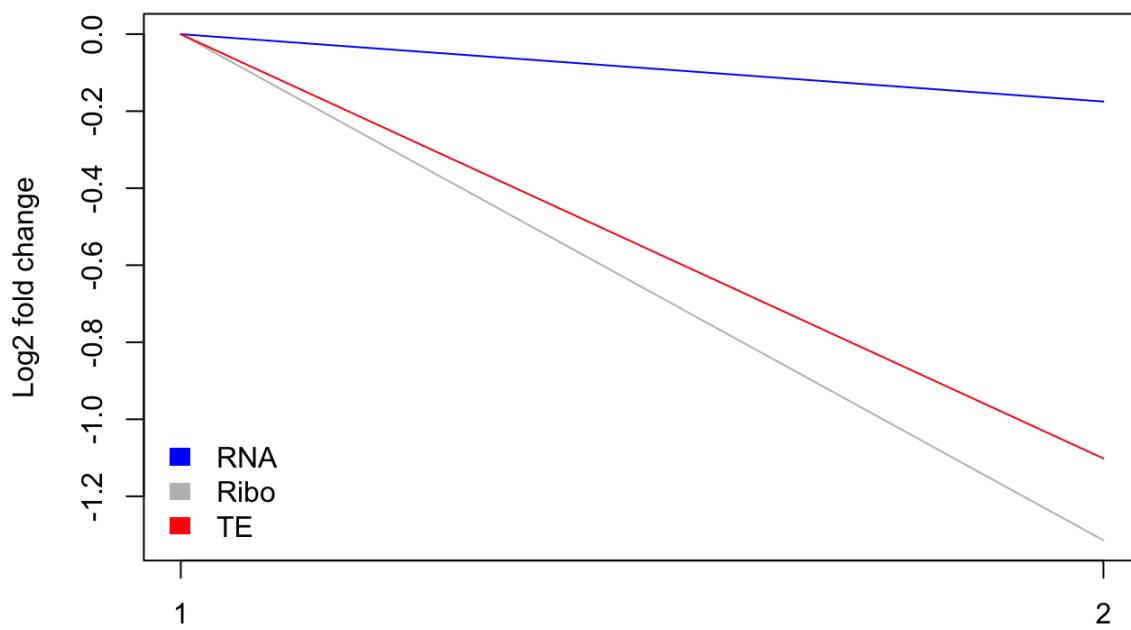
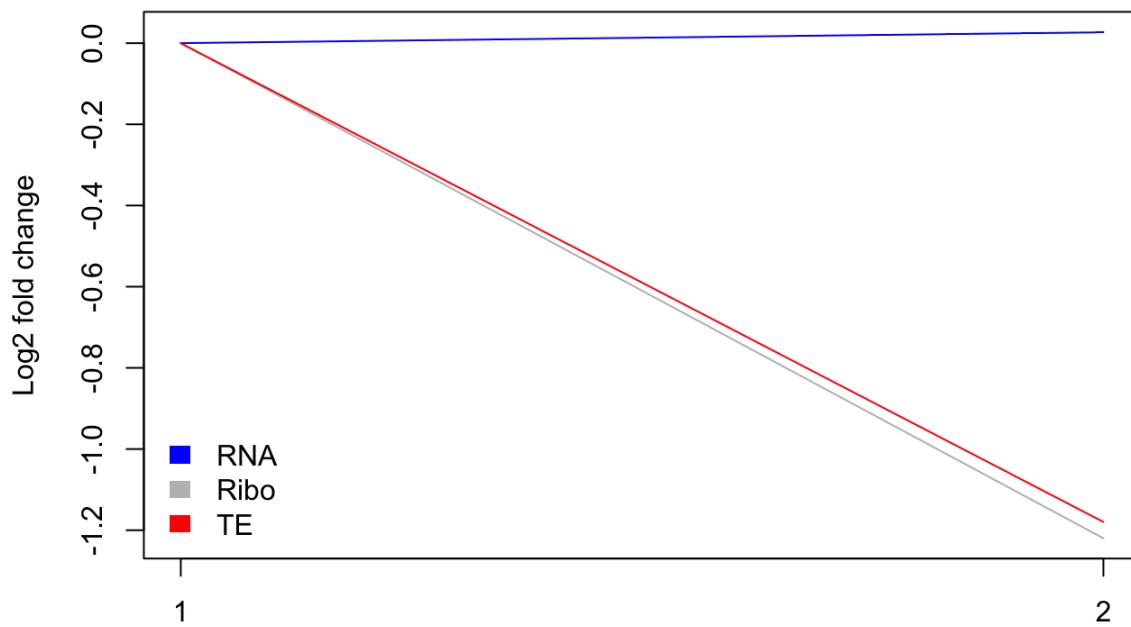
AT2G36145**AT2G42690**

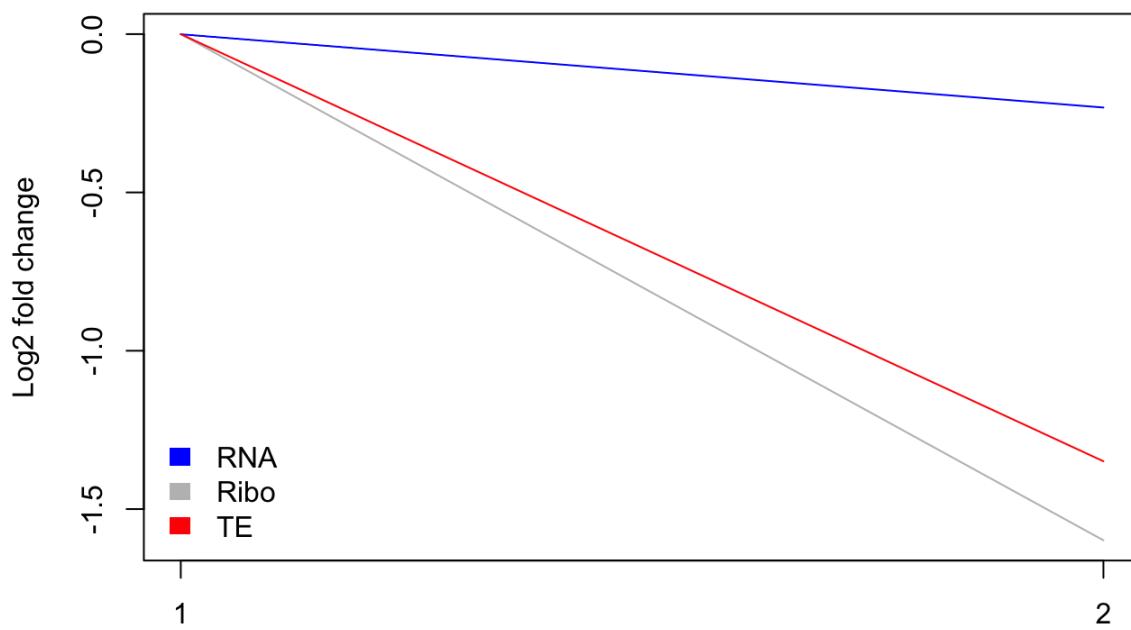
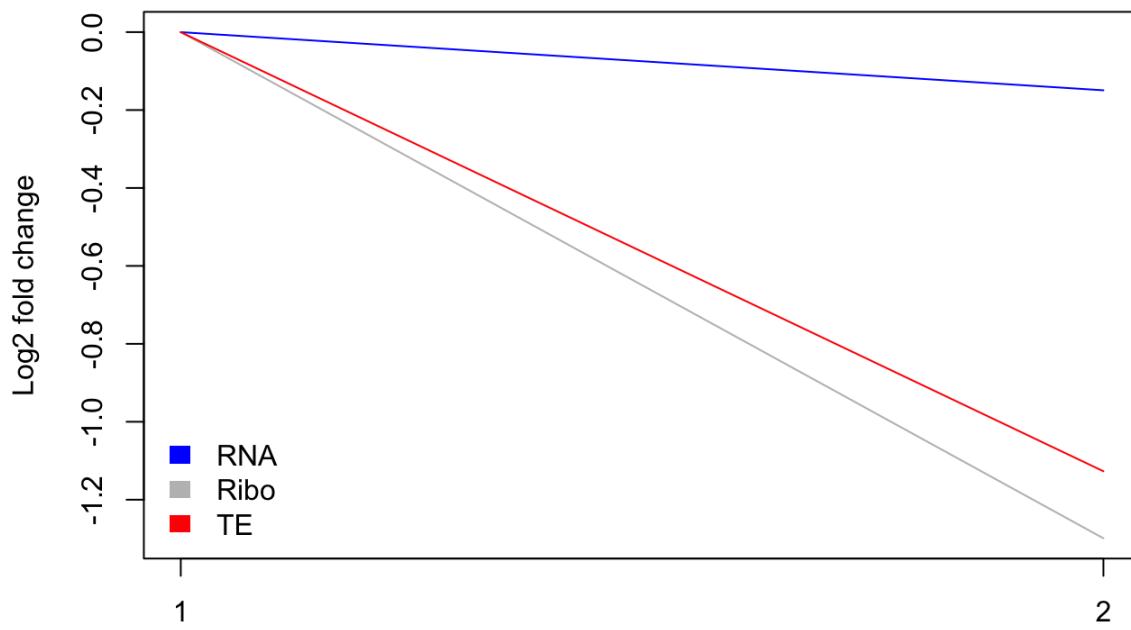
AT2G43030**AT3G05350**

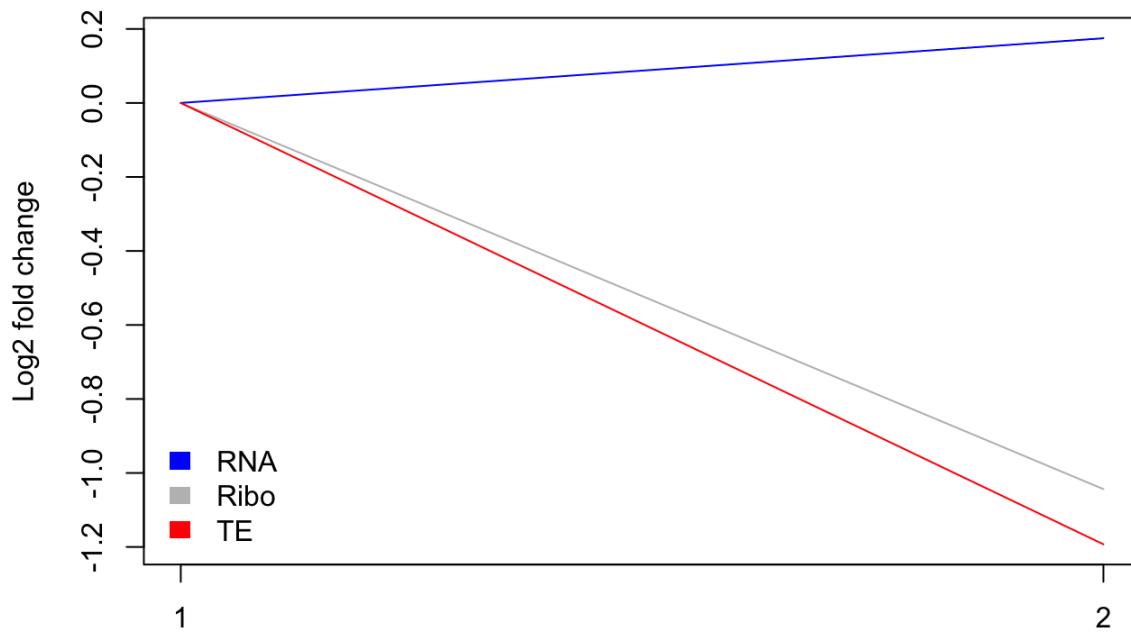
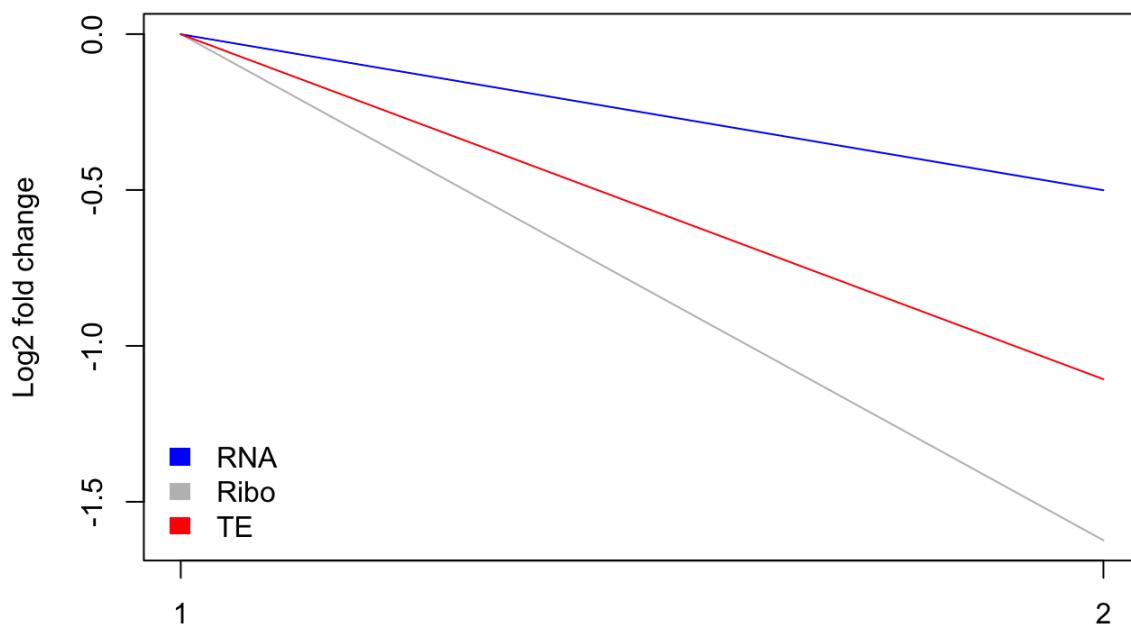
AT3G15190**AT3G24430**

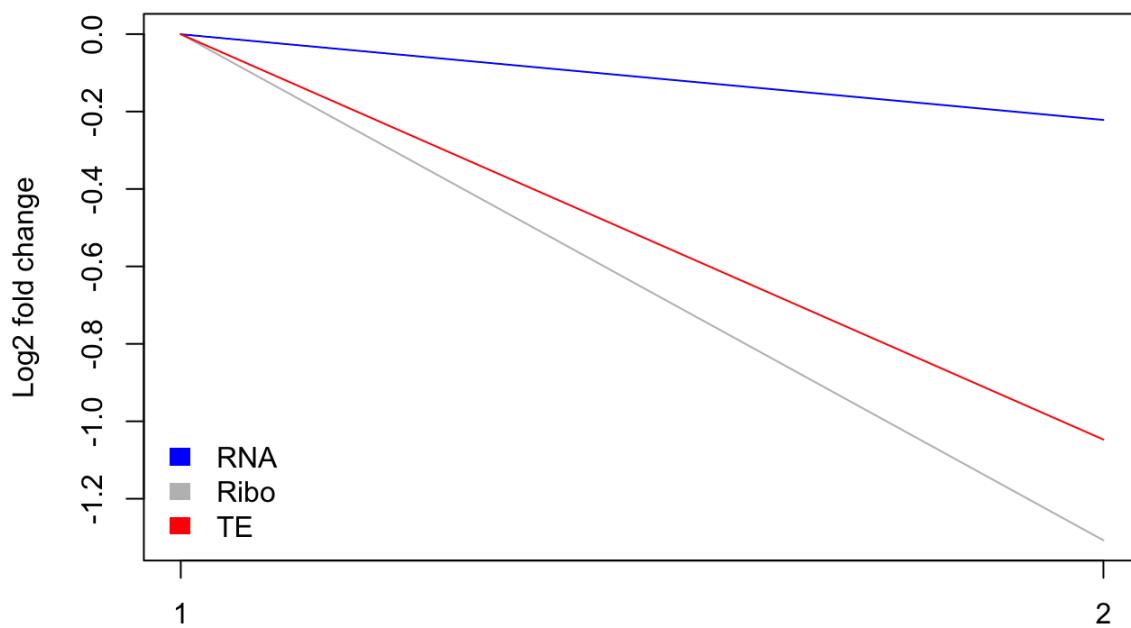
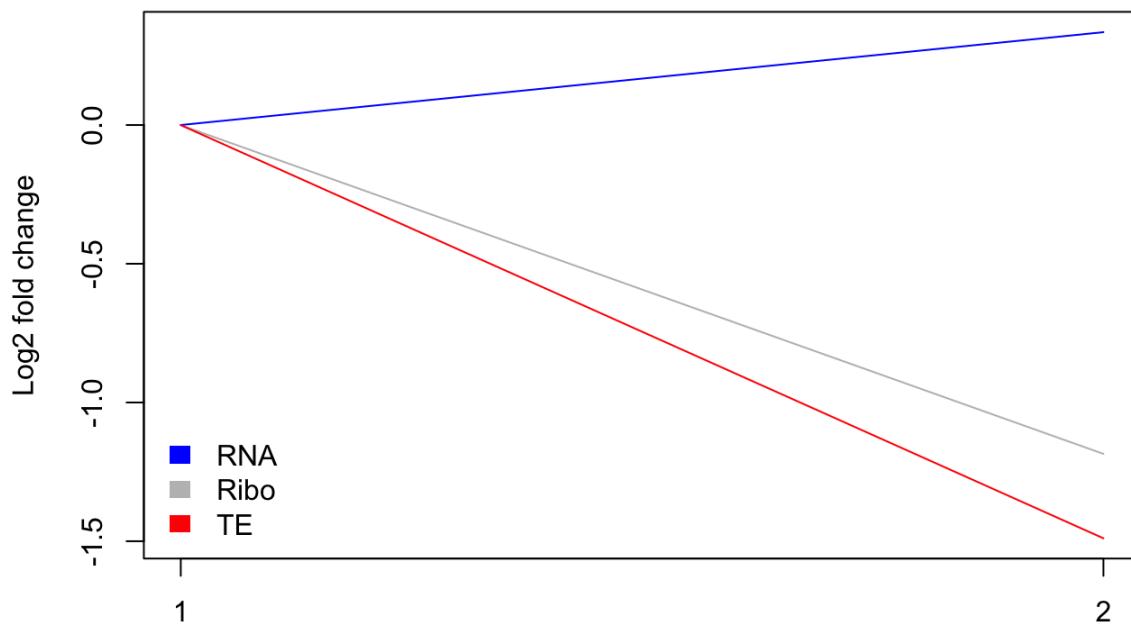
AT3G27160**AT3G47470**

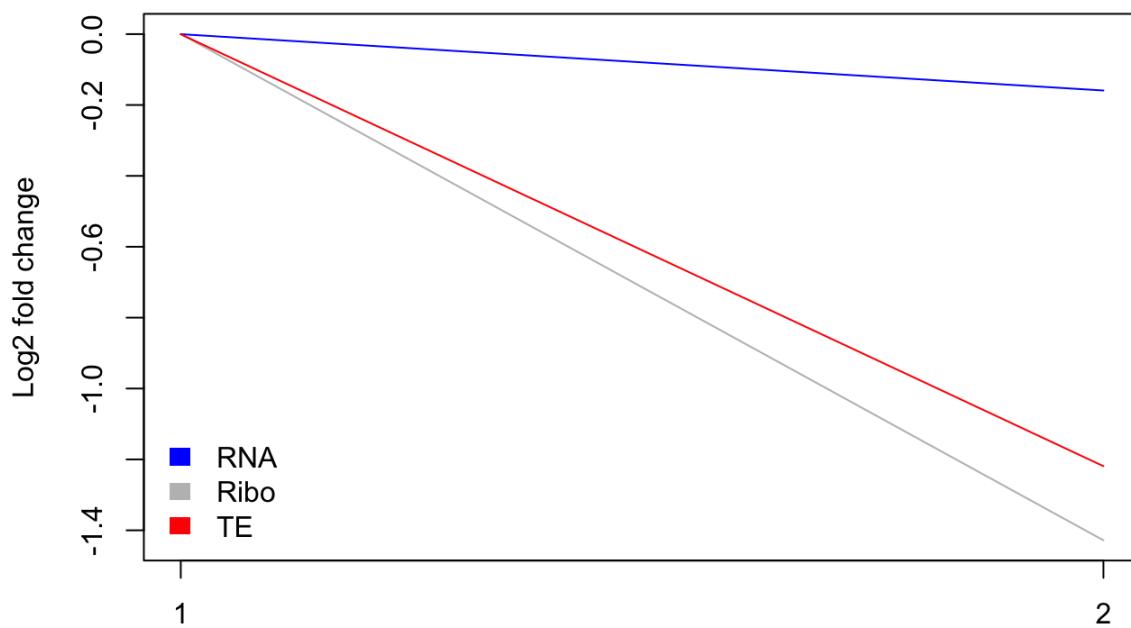
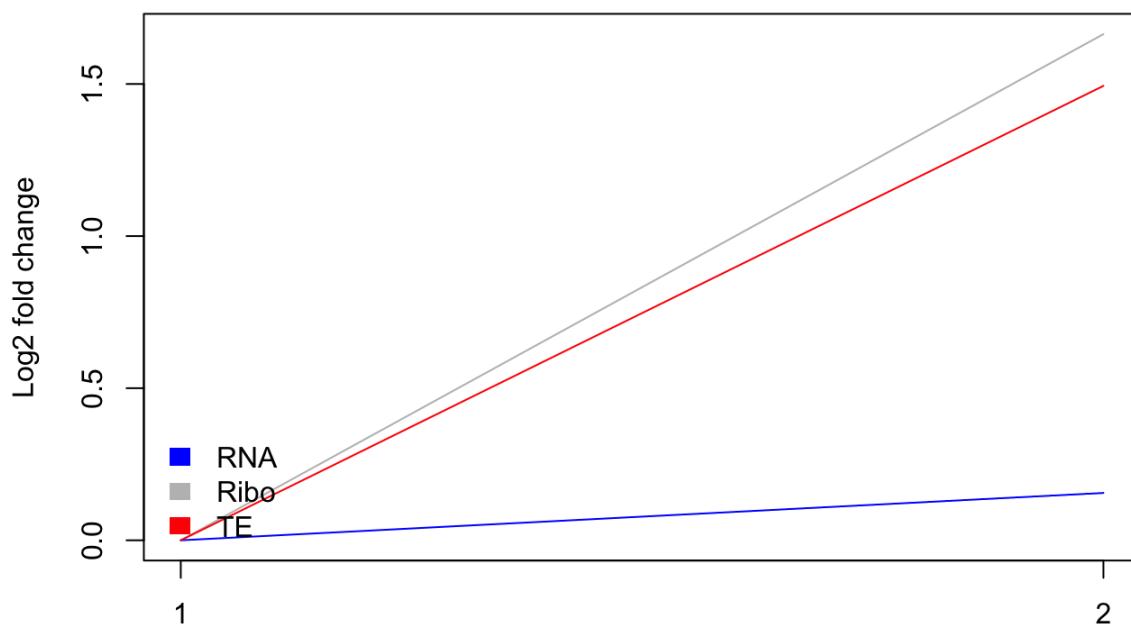
AT3G50685**AT3G56240**

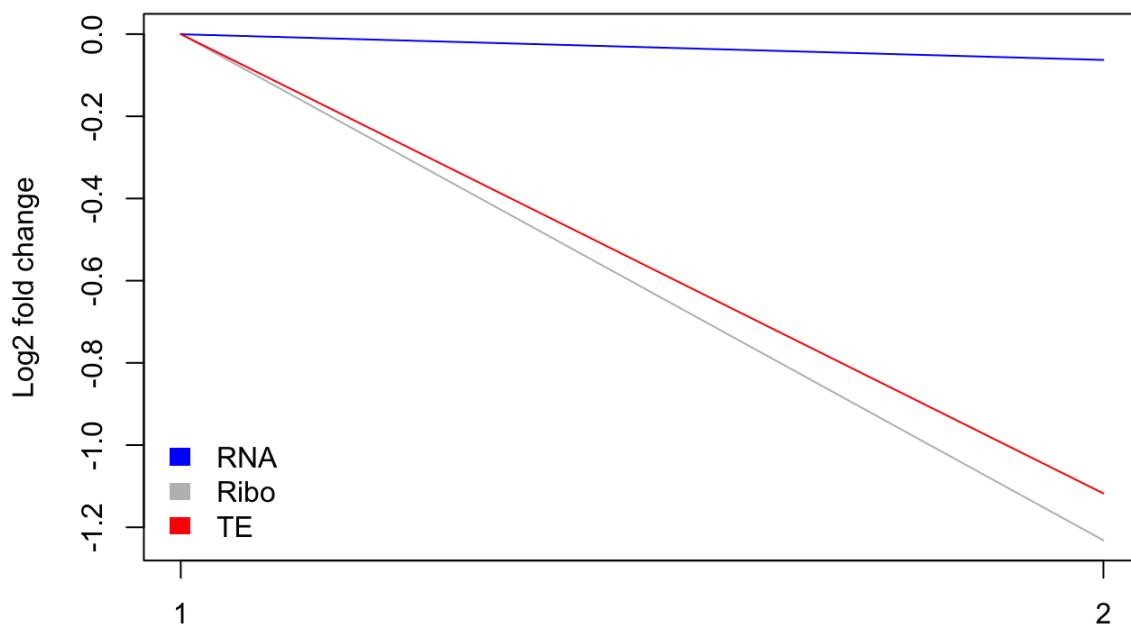
AT3G60750**AT4G01310**

AT4G25650**AT4G32260**

AT5G01530**AT5G03880**

AT5G05690**AT5G12250**

AT5G23120**AT5G50960**

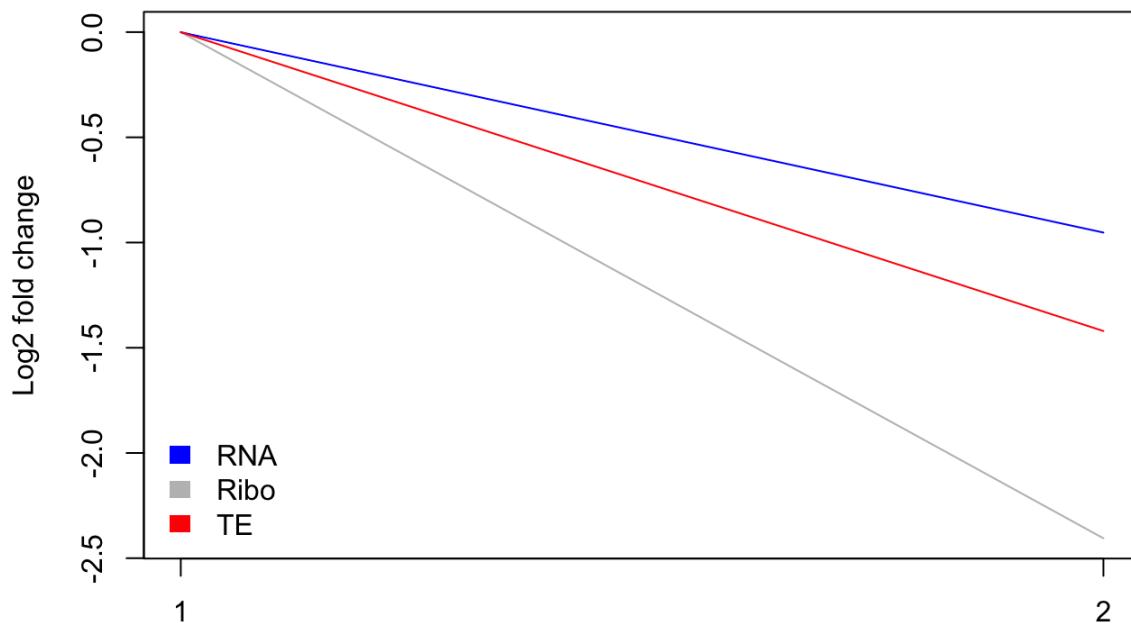
AT5G58330

exclusive focuses on findings that are translationally different only.

```

for (id in intensified){
  ymax=max(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)
  ymin=min(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)
  plot(c(0,1), c(0,DESeq_Results_ribo[id,2]), type="l",col="gray", ylim=c(ymin,ymax),
       ylab="Log2 fold change",xlab="",xaxt="n")
  lines(c(0,1), c(0,DESeq_Results_RNA[id,2]),type="l",col="blue")
  lines(c(0,1), c(0,DESeq_Results_both[id,2]), type="l",col="red")
  legend("bottomleft",c("RNA","Ribo","TE"),fill=c("blue","gray","red"), cex=1, border = NA, bty="n"
  )
  axis(1,at=c(0,1),labels=c(1,2),las=1)
  title(id)
}

```

AT3G12780

```

for (id in buffered){
  ymax=max(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)
  ymin=min(DESeq_Results_ribo[id,2],DESeq_Results_RNA[id,2],DESeq_Results_both[id,2],0)
  plot(c(0,1), c(0,DESeq_Results_ribo[id,2]), type="l",col="gray", ylim=c(ymin,ymax),
       ylab="Log2 fold change",xlab="",xaxt="n")
  lines(c(0,1), c(0,DESeq_Results_RNA[id,2]),type="l",col="blue")
  lines(c(0,1), c(0,DESeq_Results_both[id,2]), type="l",col="red")
  legend("bottomleft",c("RNA","Ribo","TE"),fill=c("blue","gray","red"), cex=1, border = NA, bty="n"
  )
  axis(1,at=c(0,1),labels=c(1,2),las=1)
  title(id)
}

```

AT1G51200