





```

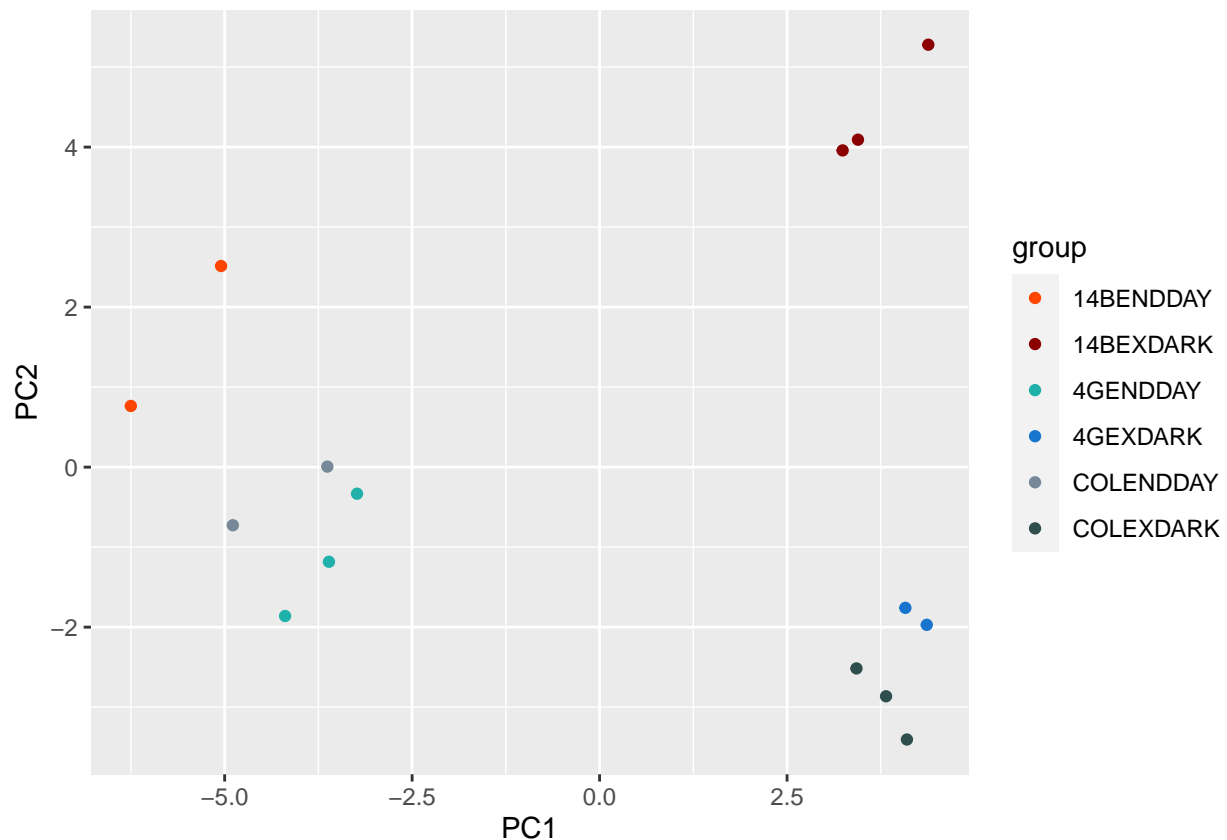
## Filtering counts for assigned geneset
lgNorm[rownames(lgNorm) %in% gene_vec,] %>% data.frame(check.names = FALSE) -> lgGo

## PCA on log normalized counts, assigned genes
pca_lggo <- prcomp(t(lgGo))

pca_lggo_dat <- data.frame(pca_lggo$x[,1:2])
pca_lggo_dat$group <- sampleAnnotation[rownames(pca_lggo_dat), "group"]
pca_lggo_dat$sample <- rownames(pca_lggo_dat)

pca_lggo_dat %>% ggplot(aes(x = PC1, y = PC2, color = group, label = sample)) + geom_point() + scale_color_manual(values = c("14BENDDAY", "14BEXDARK", "4GENDDAY", "4GEXDARK", "COLENDDAY", "COLEXDARK"))

```



```

## Clustered heatmap, assigned genes
library(pheatmap)
heatData <- lgGo - rowMeans(lgGo)
heatData[heatData > 2] = 2
heatData[heatData < -2] = -2

pdf("BI0321G-RNAseq.pdf", width = 24, height = 8)
pheatmap(heatData, color = heatPalette, clustering_method = "average", labels_row = geneNamesAndDescriptions, labels_col = sampleNames)
dev.off()
## pdf
## 3

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## Expression stripchart, assigned genes
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```
data.frame(results(dds)[5]) -> pmat
```

```
subset(pmat, rownames(pmat) %in% gene_vec) %>% arrange(pvalue) %>% head(9) %>% rownames -> top_9_exp
```

```
lgGo[rownames(lgGo) %in% top_9_exp,] -> l1l
```

```
stripchart321g(data = l1l, sampleAnnotation = sampleAnnotation) -> stripgg
```

```
stripgg
```

