## test\_dcq.R

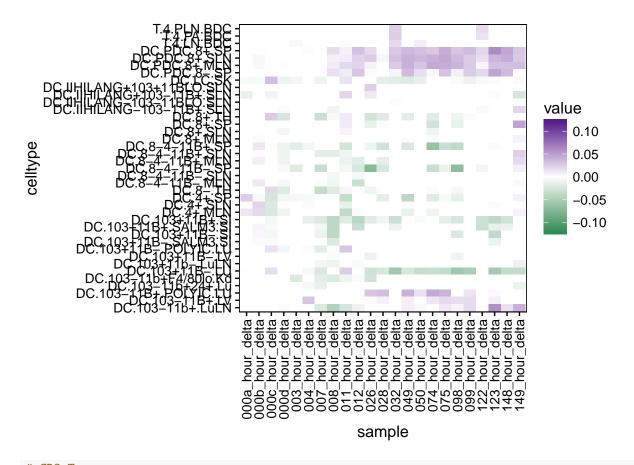
diez

Wed Jan 6 12:47:49 2016

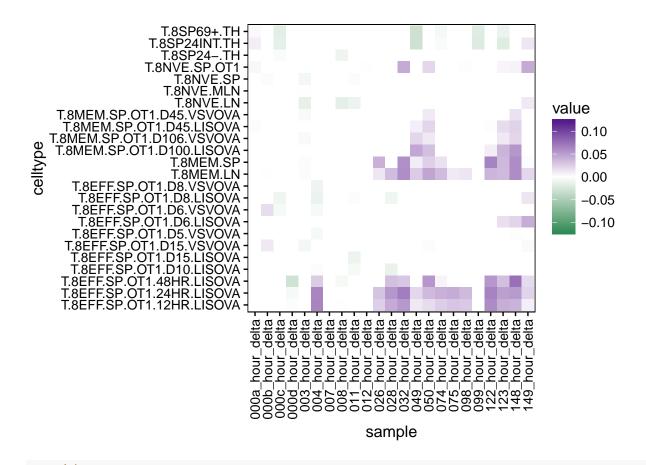
```
library(glmnet)
## Loading required package: Matrix
## Attaching package: 'Matrix'
## The following object is masked from 'package:tidyr':
##
##
       expand
## Loading required package: foreach
## Loaded glmnet 2.0-2
db <- read.table("data/CellSurfaceMarkersDict.txt", stringsAsFactors = FALSE)</pre>
#head(db)
rownames(db) <- db[,2]
#head(db)
x <- read.delim("data/immgenGeneExpressionData.txt", stringsAsFactors = FALSE, check.names = FALSE)
\#head(x)
x \leftarrow x[x[,1] \%in\% db[,1], ]
rownames(x) <- x[,1]</pre>
\#head(x)
x \leftarrow as.matrix(x[,-1])
\#head(x)
#x[1:10,1:10]
x <- x[order(rownames(x)), order(colnames(x))]</pre>
#x[1:10,1:10]
y <- read.delim("data/LungDataSet.txt", check.names = FALSE)
\#head(y)
library(limma)
y \leftarrow avereps(y[,-1], ID = y[,1])
\#head(y)
y <- y[rownames(y) %in% db[,2],]</pre>
rownames(y) <- db[rownames(y),1]</pre>
\#head(y)
y <- y[rownames(x),] # reorder
\#head(y)
#################
# test
\# fit2 <- glmnet(x, y[,1], family = c('gaussian'), alpha = .05, nlambda = 100, lambda.min = .2)
# foo <- fit2$beta[,100]
```

# barplot(foo[foo != 0])

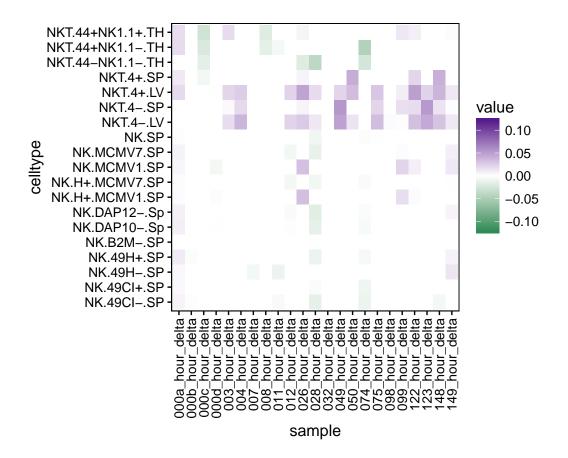
```
#################
## do all.
res <- lapply(1:ncol(y), function(k) {</pre>
     fit2 <- glmnet(x, y[,k], family = c('gaussian'), alpha = .05, nlambda = 100, lambda.min.ratio = .2)</pre>
      fit2$beta[,100]
})
res <- do.call(rbind, res)</pre>
rownames(res) <- colnames(y)</pre>
#head(res)
res <- res[, colSums(res) != 0]</pre>
d <- melt(res, varnames = c("sample", "celltype"))</pre>
head(d)
##
                                                 sample celltype
                                                                                                                                      value
## 1 000a_hour_delta B.FO.LN -0.0152802878
## 2 000b_hour_delta B.FO.LN 0.0000000000
## 3 000c_hour_delta B.FO.LN 0.0000000000
## 4 000d_hour_delta B.FO.LN 0.0000000000
## 5 003_hour_delta B.FO.LN -0.0003130248
## 6 004_hour_delta B.FO.LN 0.0000000000
\#ggplot(d,aes(x = sample, y = celltype,fill = value)) + geom\_tile() + scale\_fill\_gradient2(low = "seagrange") + geom\_tile() + 
 # DCs
ggplot(d %>% filter(grepl("DC", celltype)),aes(x = sample, y = celltype,fill = value)) + geom_tile() +
```



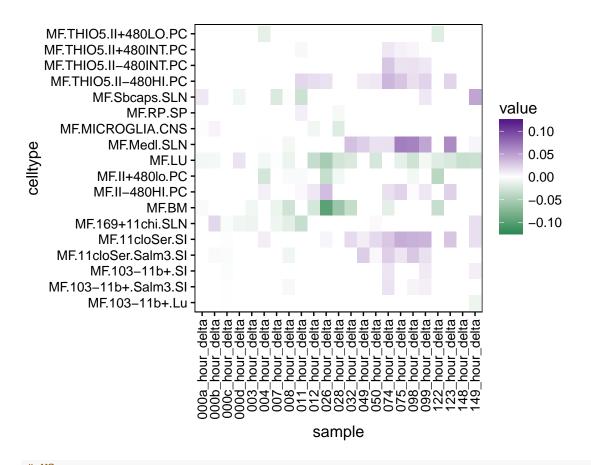
```
# CD8 T
ggplot(d %>% filter(grep1("T.8", celltype)),aes(x = sample, y = celltype,fill = value)) + geom_tile() +
```



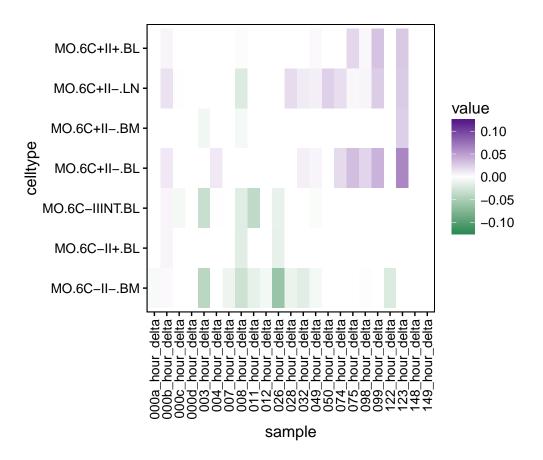
```
# NK(T)
ggplot(d %>% filter(grepl("NK", celltype)),aes(x = sample, y = celltype,fill = value)) + geom_tile() +
```



```
# MF
ggplot(d %>% filter(grepl("MF", celltype)),aes(x = sample, y = celltype,fill = value)) + geom_tile() +
```



```
ggplot(d %>% filter(grepl("MO", celltype)),aes(x = sample, y = celltype,fill = value)) + geom_tile() +
```



# SC
ggplot(d %>% filter(grepl("SC", celltype)),aes(x = sample, y = celltype,fill = value)) + geom\_tile() +

