21_pemt_cage_clusters

Supplementary Figure 8

```
library(ComplexHeatmap)
library(circlize)
library(here); i_am("R/21_pemt_cage_clusters.Rmd")
```

```
cage_counts = read.delim(here("annotations/primary_cell.hCAGE_pemt.counts.tsv"), quote = "\'")
colnames(cage_counts)
```

```
##  [1] "X.chr"
##  [2] "start"
##  [3] "end"
##  [4] "Adipocyte...breast..donor1.CNhs11051.11376.118A8.hg38.nobarcode.bam"
##  [5] "Adipocyte...breast..donor2.CNhs11969.11327.117E4.hg38.nobarcode.bam"
##  [6] "Adipocyte...omental..donor1.CNhs11054.11473.119C6.hg38.nobarcode.bam"
##  [7] "Adipocyte...omental..donor2.CNhs12067.11474.119C7.hg38.nobarcode.bam"
##  [8] "Adipocyte...omental..donor3.CNhs12068.11475.119C8.hg38.nobarcode.bam"
##  [9] "Adipocyte...perirenal..donor1.CNhs12069.11476.119C9.hg38.nobarcode.bam"
## [10] "Adipocyte...subcutaneous..donor1.CNhs12494.11259.116F8.hg38.nobarcode.bam"
## [11] "Adipocyte...subcutaneous..donor2.CNhs11371.11336.117F4.hg38.nobarcode.bam"
## [12] "Adipocyte...subcutaneous..donor3.CNhs12017.11408.118E4.hg38.nobarcode.bam"
## [13] "Mesenchymal.Stem.Cells...adipose..donor1.CNhs11345.11537.120A7.hg38.nobarcode.bam"
## [14] "Mesenchymal.Stem.Cells...adipose..donor2.CNhs12101.11617.122A6.hg38.nobarcode.bam"
## [15] "Mesenchymal.Stem.Cells...adipose..donor3.CNhs12922.11698.123A6.hg38.nobarcode.bam"
## [16] "Mesenchymal.stem.cells...adipose..donor0.CNhs10844.11217.116B2.hg38.nobarcode.bam"
## [17] "Preadipocyte...breast..donor1.CNhs11052.11467.119B9.hg38.nobarcode.bam"
## [18] "Preadipocyte...breast..donor2.CNhs11971.11328.117E5.hg38.nobarcode.bam"
## [19] "Preadipocyte...omental..donor1.CNhs11065.11468.119C1.hg38.nobarcode.bam"
## [20] "Preadipocyte...omental..donor2.CNhs11902.11329.117E6.hg38.nobarcode.bam"
## [21] "Preadipocyte...omental..donor3.CNhs12013.11403.118D8.hg38.nobarcode.bam"
## [22] "Preadipocyte...perirenal..donor1.CNhs12065.11469.119C2.hg38.nobarcode.bam"
## [23] "Preadipocyte...subcutaneous..donor1.CNhs11081.11279.116I1.hg38.nobarcode.bam"
## [24] "Preadipocyte...subcutaneous..donor2.CNhs11981.11356.117H6.hg38.nobarcode.bam"
## [25] "Preadipocyte...subcutaneous..donor3.CNhs12038.11428.118G6.hg38.nobarcode.bam"
## [26] "Preadipocyte...visceral..donor1.CNhs11082.11280.116I2.hg38.nobarcode.bam"
## [27] "Preadipocyte...visceral..donor2.CNhs11982.11357.117H7.hg38.nobarcode.bam"
## [28] "Preadipocyte...visceral..donor3.CNhs12039.11429.118G7.hg38.nobarcode.bam"
## [29] "mesenchymal.precursor.cell...adipose..donor1.CNhs12363.11747.123G1.hg38.nobarcode.bam"
## [30] "mesenchymal.precursor.cell...adipose..donor2.CNhs12364.11748.123G2.hg38.nobarcode.bam"
## [31] "mesenchymal.precursor.cell...adipose..donor3.CNhs12365.11749.123G3.hg38.nobarcode.bam"
```

```
colnames(cage_counts) = gsub("\\.{1,3}","_",gsub("X.","", gsub(".CNhs.*.hg38.nobarcode.bam","", colnames
```

```
cage_counts = cage_counts[order(cage_counts$start, cage_counts$end),]
```

```
rownames(cage_counts) = paste0("c",nrow(cage_counts):1, "@PEMT")
cage_counts[,1:3] #TSS positions
```

```
##             chr    start      end
## c11@PEMT chr17 17506258 17506308
## c10@PEMT chr17 17507192 17507228
## c9@PEMT  chr17 17512559 17512569
## c8@PEMT  chr17 17518149 17518168
## c7@PEMT  chr17 17577141 17577174
## c6@PEMT  chr17 17577489 17577500
## c5@PEMT  chr17 17580960 17580978
## c4@PEMT  chr17 17582417 17582481
## c3@PEMT  chr17 17591658 17591723
## c2@PEMT  chr17 17592052 17592073
## c1@PEMT  chr17 17592119 17592147
```

```
countm = as.matrix(cage_counts[!colnames(cage_counts) %in% c("chr","start","end")])
countm[,1:5]
```

```
##          Adipocyte_breast_donor1 Adipocyte_breast_donor2
## c11@PEMT                       5                       5
## c10@PEMT                       2                       2
## c9@PEMT                        5                      44
## c8@PEMT                        2                       1
## c7@PEMT                       25                     640
## c6@PEMT                        1                       6
## c5@PEMT                        0                       1
## c4@PEMT                        2                       0
## c3@PEMT                      194                     199
## c2@PEMT                       13                      13
## c1@PEMT                        9                       7
##          Adipocyte_omental_donor1 Adipocyte_omental_donor2
## c11@PEMT                        6                        0
## c10@PEMT                        3                        0
## c9@PEMT                        10                        1
## c8@PEMT                         1                        0
## c7@PEMT                        73                        4
## c6@PEMT                         0                        0
## c5@PEMT                         3                        0
## c4@PEMT                         3                        0
## c3@PEMT                       290                       30
## c2@PEMT                        18                        0
## c1@PEMT                         9                        0
##          Adipocyte_omental_donor3
## c11@PEMT                        3
## c10@PEMT                        2
## c9@PEMT                         6
## c8@PEMT                         0
## c7@PEMT                        58
## c6@PEMT                         1
## c5@PEMT                         0
## c4@PEMT                         1
```
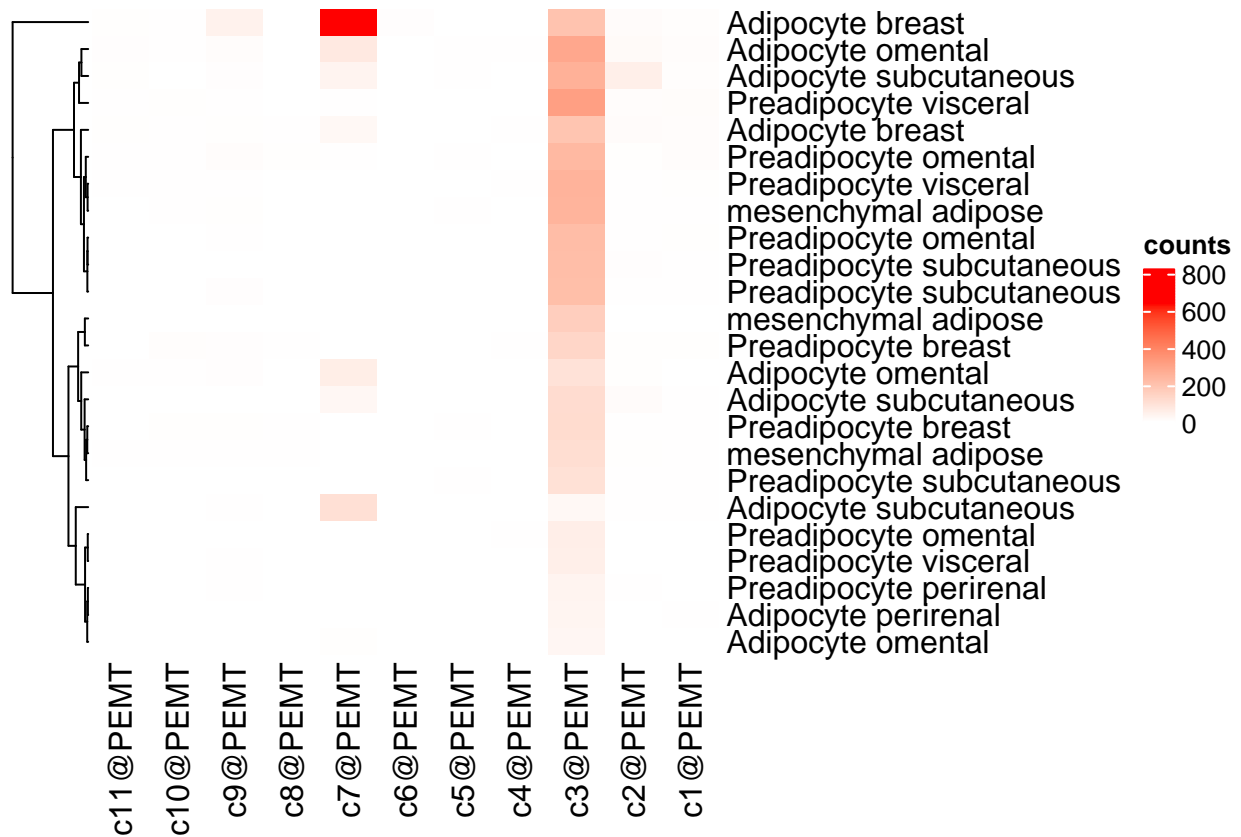
```
## c3@PEMT                            97
## c2@PEMT                             4
## c1@PEMT                             1
```

```r
#drop mesenchymal samples
countm=countm[,!grepl("Mesenchymal",colnames(countm))]
#drop doenstream PEMT
countm=countm[!grepl("PEMT@(8|9|10|11)",rownames(countm)),]
```

```r
samples = data.frame(sample =colnames(countm),
                     cell_type=gsub("_.*","",colnames(countm),),
                     donor=gsub(".*_","",colnames(countm)),
                     depot=gsub(".*_","",gsub("_donor.*","",colnames(countm))))
samples
```

```
##                                          sample    cell_type  donor         depot
## 1                       Adipocyte_breast_donor1    Adipocyte donor1        breast
## 2                       Adipocyte_breast_donor2    Adipocyte donor2        breast
## 3                      Adipocyte_omental_donor1    Adipocyte donor1       omental
## 4                      Adipocyte_omental_donor2    Adipocyte donor2       omental
## 5                      Adipocyte_omental_donor3    Adipocyte donor3       omental
## 6                     Adipocyte_perirenal_donor1    Adipocyte donor1     perirenal
## 7                  Adipocyte_subcutaneous_donor1    Adipocyte donor1 subcutaneous
## 8                  Adipocyte_subcutaneous_donor2    Adipocyte donor2 subcutaneous
## 9                  Adipocyte_subcutaneous_donor3    Adipocyte donor3 subcutaneous
## 10                    Preadipocyte_breast_donor1 Preadipocyte donor1        breast
## 11                    Preadipocyte_breast_donor2 Preadipocyte donor2        breast
## 12                   Preadipocyte_omental_donor1 Preadipocyte donor1       omental
## 13                   Preadipocyte_omental_donor2 Preadipocyte donor2       omental
## 14                   Preadipocyte_omental_donor3 Preadipocyte donor3       omental
## 15                 Preadipocyte_perirenal_donor1 Preadipocyte donor1     perirenal
## 16             Preadipocyte_subcutaneous_donor1 Preadipocyte donor1 subcutaneous
## 17             Preadipocyte_subcutaneous_donor2 Preadipocyte donor2 subcutaneous
## 18             Preadipocyte_subcutaneous_donor3 Preadipocyte donor3 subcutaneous
## 19                  Preadipocyte_visceral_donor1 Preadipocyte donor1      visceral
## 20                  Preadipocyte_visceral_donor2 Preadipocyte donor2      visceral
## 21                  Preadipocyte_visceral_donor3 Preadipocyte donor3      visceral
## 22 mesenchymal_precursor_cell_adipose_donor1   mesenchymal donor1       adipose
## 23 mesenchymal_precursor_cell_adipose_donor2   mesenchymal donor2       adipose
## 24 mesenchymal_precursor_cell_adipose_donor3   mesenchymal donor3       adipose
```
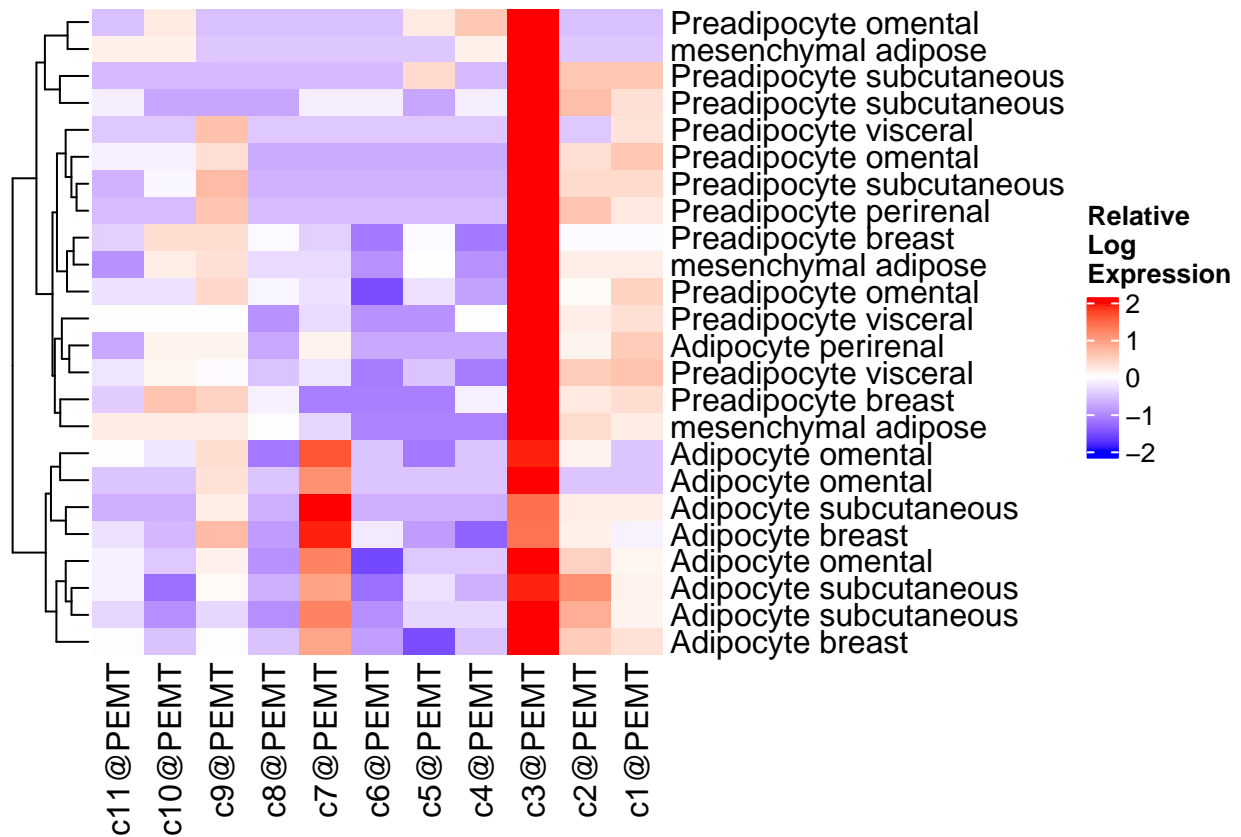
```r
colnames(countm) =paste(samples$cell_type, samples$depot)
```

```r
Heatmap(t(countm), cluster_columns = F, col = colorRamp2(c(0, max(countm)), c("white", "red")), name="co
```

Row labels (top to bottom):
- Adipocyte breast
- Adipocyte omental
- Adipocyte subcutaneous
- Preadipocyte visceral
- Adipocyte breast
- Preadipocyte omental
- Preadipocyte visceral
- mesenchymal adipose
- Preadipocyte omental
- Preadipocyte subcutaneous
- Preadipocyte subcutaneous
- mesenchymal adipose
- Preadipocyte breast
- Adipocyte omental
- Adipocyte subcutaneous
- Preadipocyte breast
- mesenchymal adipose
- Preadipocyte subcutaneous
- Adipocyte subcutaneous
- Preadipocyte omental
- Preadipocyte visceral
- Preadipocyte perirenal
- Adipocyte perirenal
- Adipocyte omental

Column labels:
c11@PEMT, c10@PEMT, c9@PEMT, c8@PEMT, c7@PEMT, c6@PEMT, c5@PEMT, c4@PEMT, c3@PEMT, c2@PEMT, c1@PEMT

Legend: counts — 800, 600, 400, 200, 0

```
Heatmap(t(scale(log(countm+0.5))), cluster_columns = F, col = colorRamp2(c(-2,0,2), c("blue","white", "
        name="Relative\nLog\nExpression")
```

```
pdf(file = here("R/plots/pemt_cage_enrichment.pdf"))
Heatmap(t(scale(log(countm+0.5))), cluster_columns = F, col = colorRamp2(c(-2,0,2), c("blue","white", ":
        name="Relative\nLog\nExpression")
dev.off()
```

```
## pdf
##   2
```