MERFISH example

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11/17/2020

MERFISH

[add description of data]

Load preprocessed data

```
col = MERFISH$col
pcs = MERFISH$pcs
vel = MERFISH$vel
```

Build VeloViz graph

```
curr = vel$current
proj = vel$projected

veloviz = buildVeloviz(
  curr = curr,
  proj = proj,
  normalize.depth = TRUE,
  use.ods.genes = FALSE,
  pca = TRUE,
  nPCs = 5,
  center = TRUE,
  scale = TRUE,
  k = 5,
  similarity.threshold = 0,
  distance.weight = 0.01,
  distance.threshold = 0.9,
  weighted = TRUE,
  seed = 0,
  verbose = FALSE
)
```

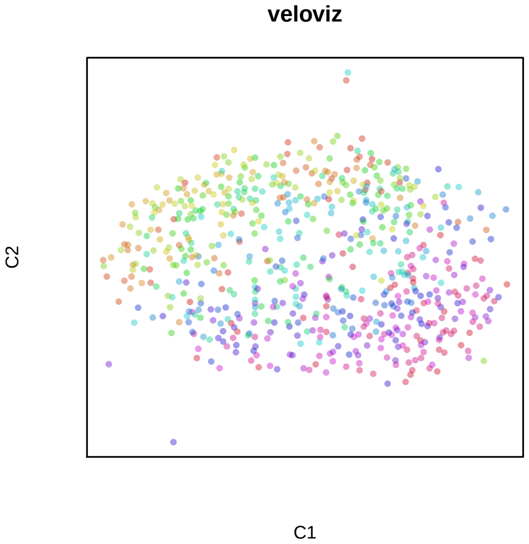
```
## Warning in if (!class(curr) %in% c("dgCMatrix", "dgTMatrix")) {: the condition
## has length > 1 and only the first element will be used
```

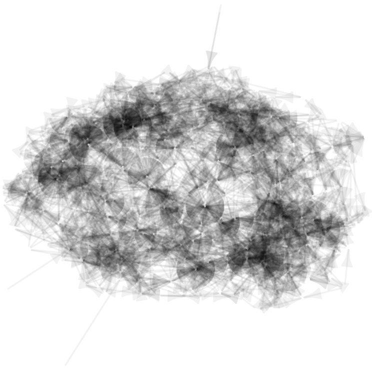
```
## Warning in if (!class(proj) %in% c("dgCMatrix", "dgTMatrix")) {: the condition
## has length > 1 and only the first element will be used
```

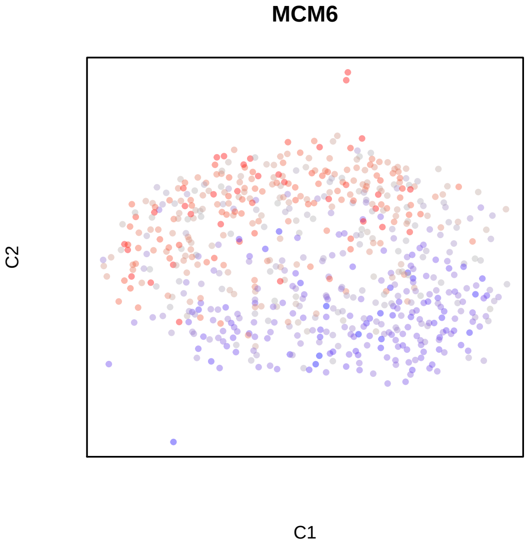
```
par(mfrow=c(3,2))
emb.veloviz = veloviz$fdg_coords
plotEmbedding(emb.veloviz, groups=col[rownames(emb.veloviz)], main='veloviz')
g = plotVeloviz(veloviz, clusters=col[rownames(emb.veloviz)], seed=0, verbose=TRUE)
```

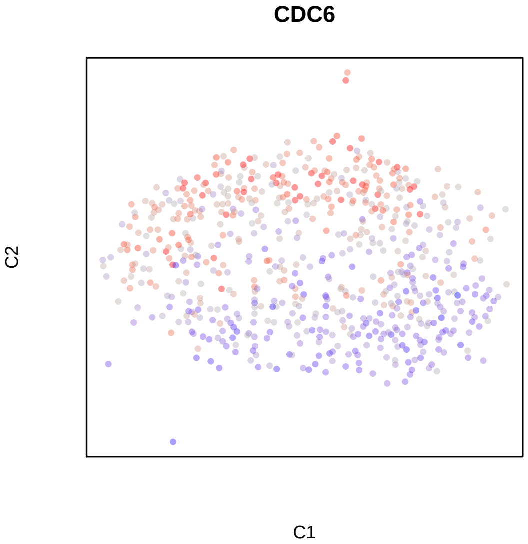
```
## Warning in if (!is.na(clusters) & is.na(col)) {: the condition has length > 1
## and only the first element will be used
## Using provided clusters...
```

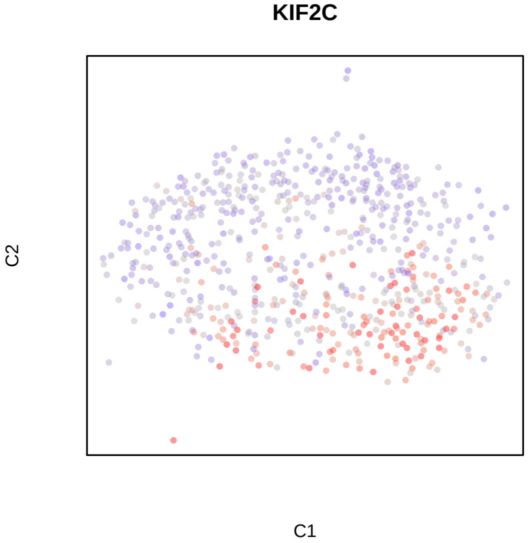
```
sapply(c('MCM6', 'CDC6', 'KIF2C', 'CCNF'), function(g) {
  gexp <- scale(curr[g,])[,1]
  plotEmbedding(emb.veloviz, col=gexp, main=g)
})
```

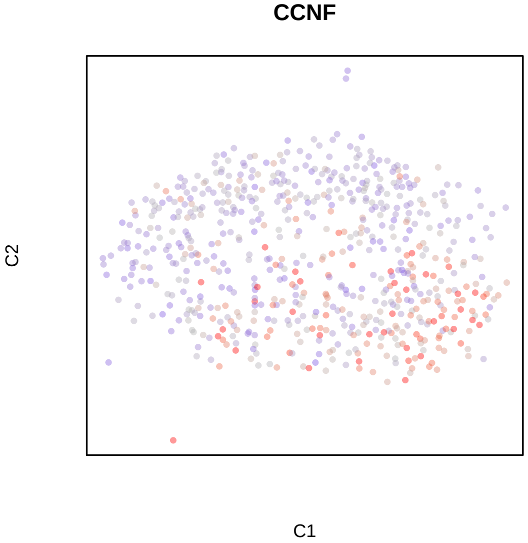

veloviz
C2
C1




MCM6
C2
C1


CDC6
C2
C1

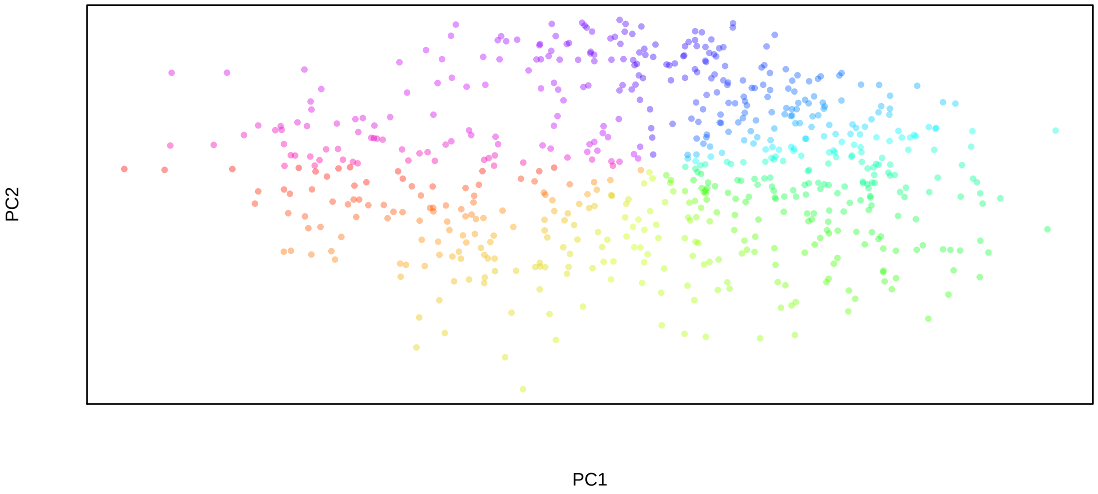

KIF2C
C2
C1


CCNF
C2
C1

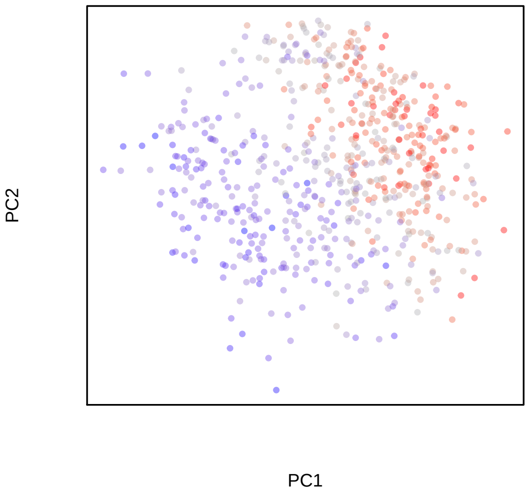
Compare to other embeddings

```r
#PCA
layout(matrix(c(1,1,2,3,4,5), 3, 2, byrow = TRUE))
emb.pcs = pcs[,1:2]
plotEmbedding(emb.pcs, col=col, main='PCA')
sapply(c('MCM6', 'CDC6', 'KIF2C', 'CCNF'), function(g) {
  gexp <- scale(curr[g,])[,1]
  plotEmbedding(emb.pcs, col=gexp, main=g)
})
```

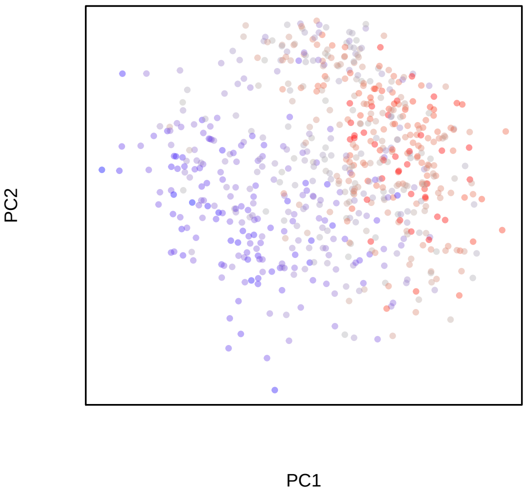
PCA



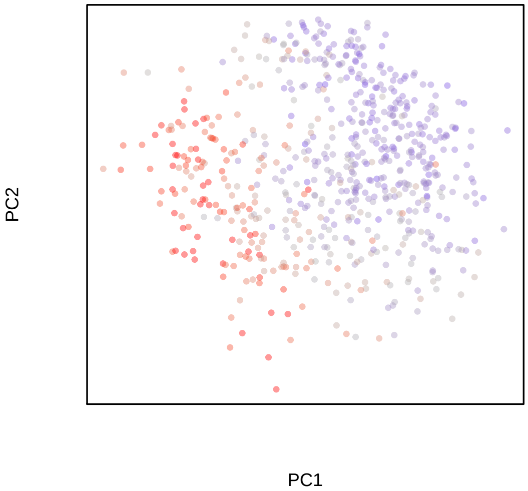
MCM6



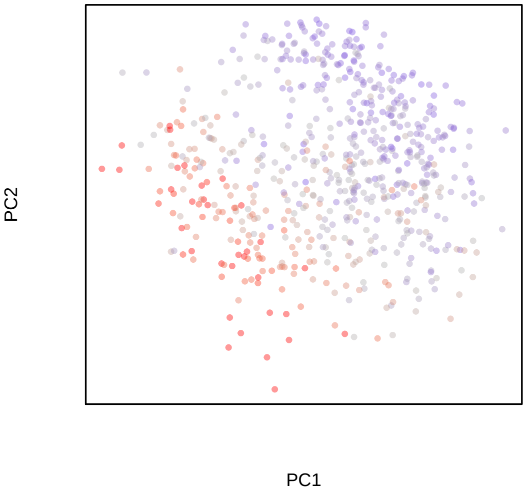
CDC6



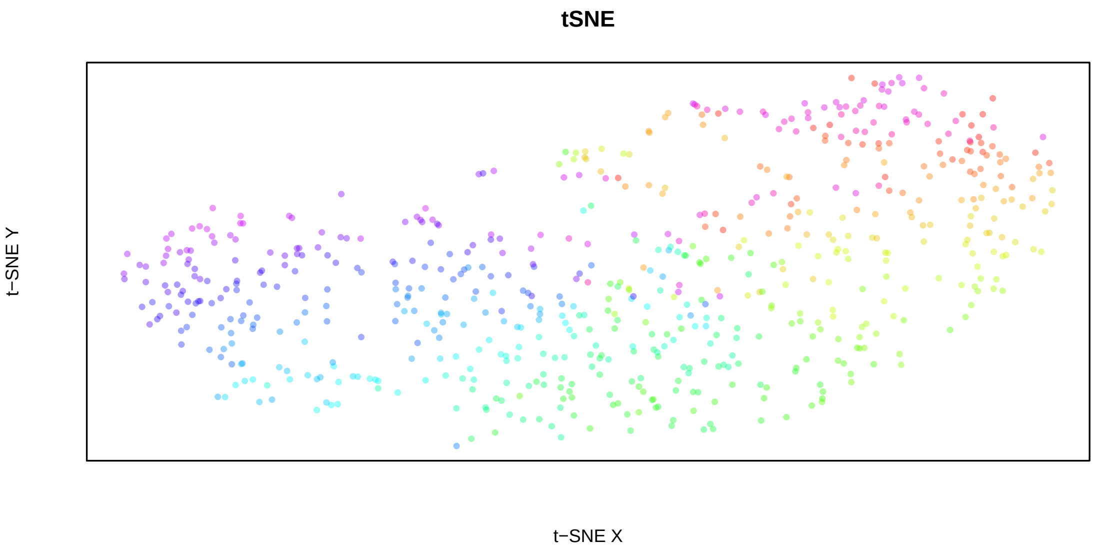
KIF2C

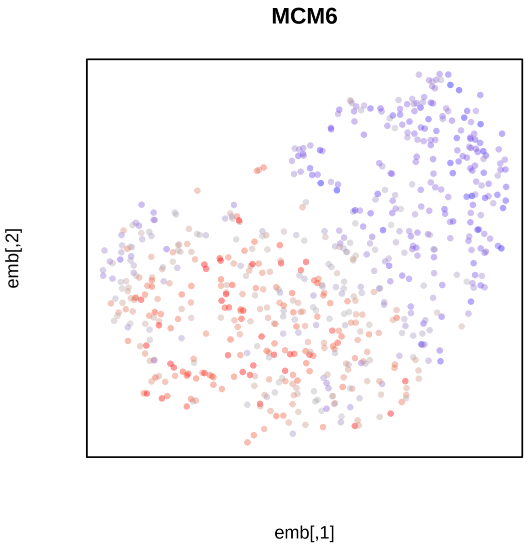


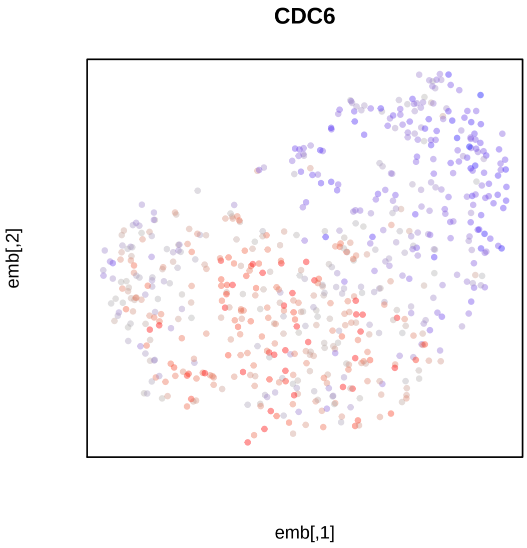
CCNF

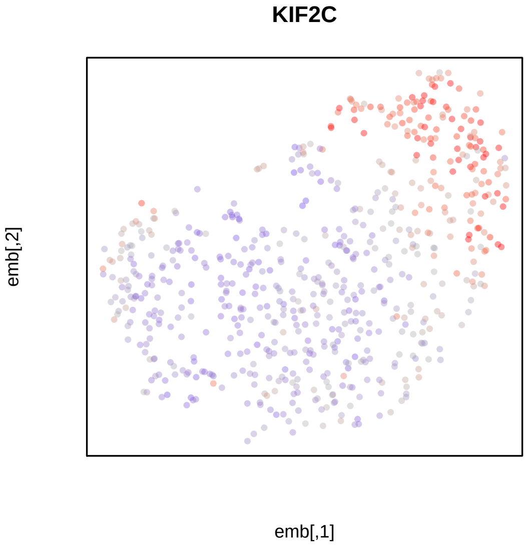


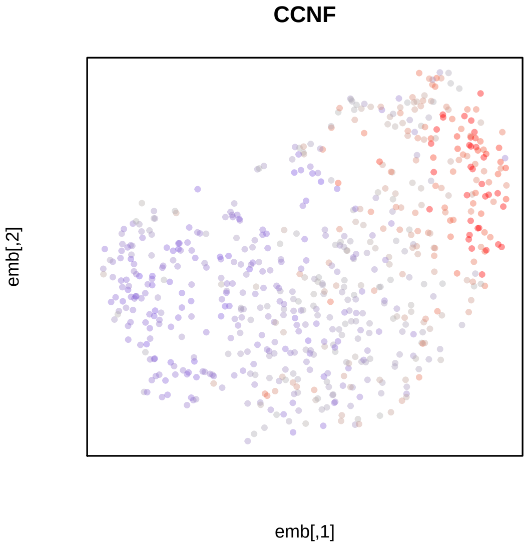
```r
#tSNE
set.seed(1)
layout(matrix(c(1,1,2,3,4,5), 3, 2, byrow = TRUE))
emb.tsne = Rtsne::Rtsne(pcs[,1:5], perplexity = 100)$Y
rownames(emb.tsne) = rownames(pcs)
plotEmbedding(emb.tsne, col=col, main='tSNE',
              xlab = "t-SNE X", ylab = "t-SNE Y")
sapply(c('MCM6', 'CDC6', 'KIF2C', 'CCNF'), function(g) {
  gexp <- scale(curr[g,])[,1]
  plotEmbedding(emb.tsne, col=gexp, main=g)
})
```


tSNE
t−SNE Y
t−SNE X

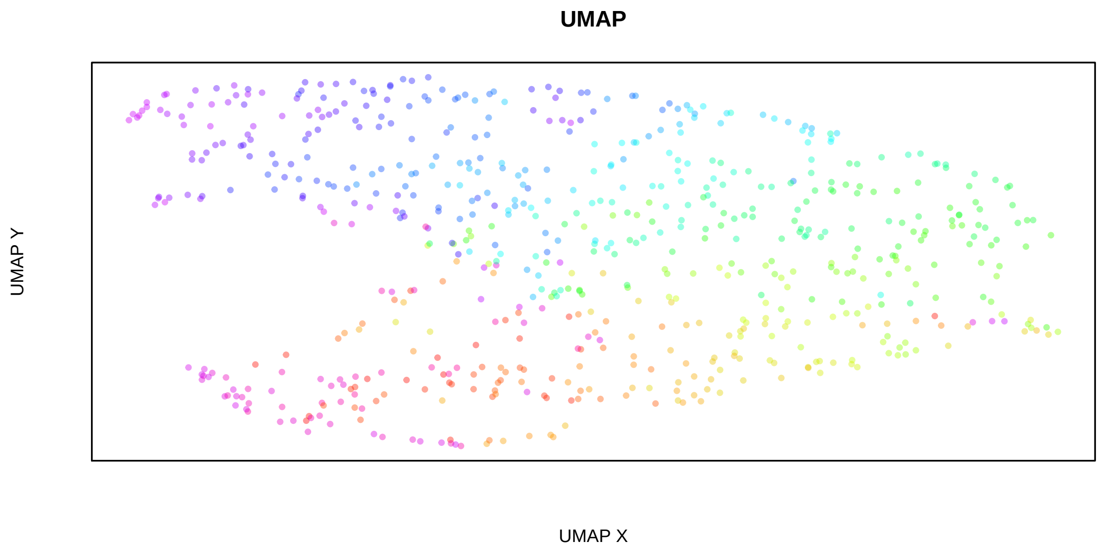

MCM6
emb[,2]
emb[,1]

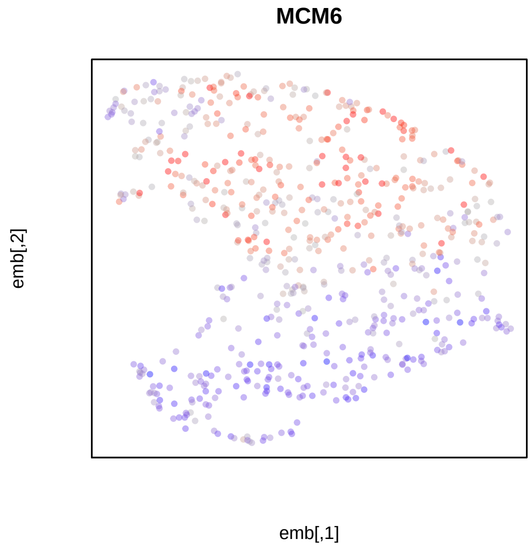

CDC6
emb[,2]
emb[,1]

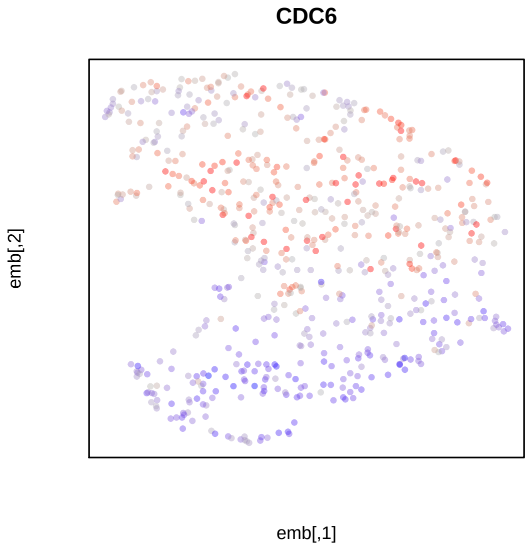

KIF2C
emb[,2]
emb[,1]

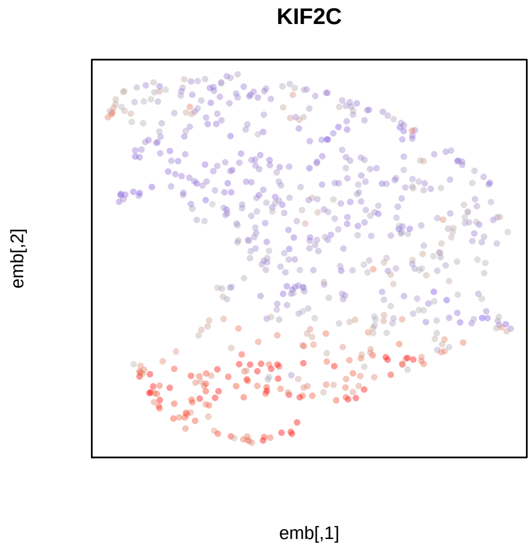

CCNF
emb[,2]
emb[,1]

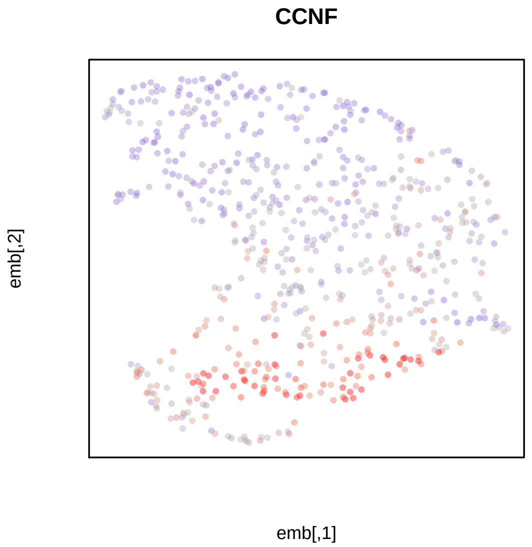
```r
#UMAP
set.seed(1)
layout(matrix(c(1,1,2,3,4,5), 3, 2, byrow = TRUE))
emb.umap = umap::umap(pcs[,1:5], min_dist = 0.3)$layout
rownames(emb.umap) = rownames(pcs)
plotEmbedding(emb.umap, col=col, main='UMAP',
              xlab = "UMAP X", ylab = "UMAP Y")
sapply(c('MCM6', 'CDC6', 'KIF2C', 'CCNF'), function(g) {
  gexp <- scale(curr[g,])[,1]
  plotEmbedding(emb.umap, col=gexp, main=g)
})
```


UMAP
UMAP Y
UMAP X

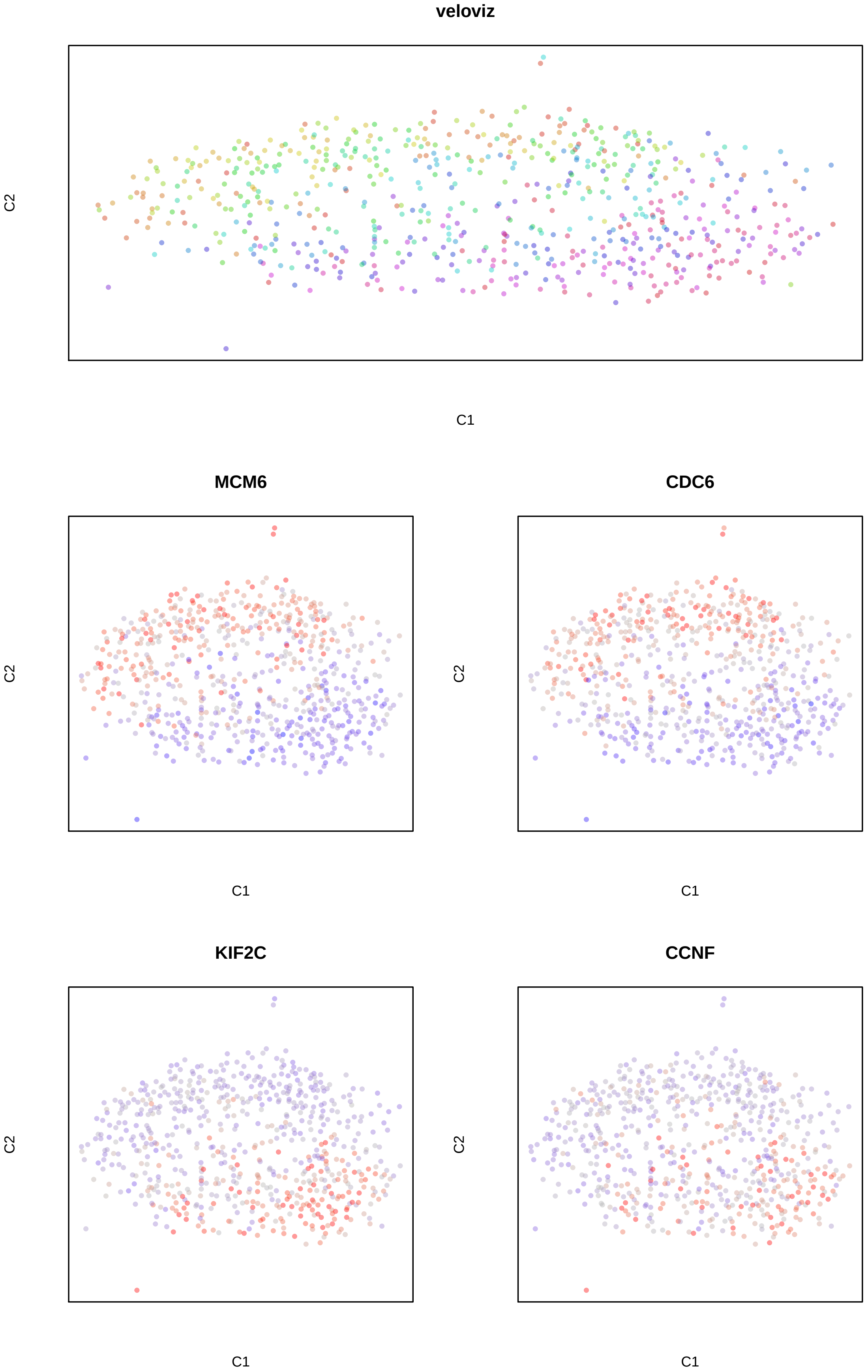

MCM6
emb[,2]
emb[,1]


CDC6
emb[,2]
emb[,1]


KIF2C
emb[,2]
emb[,1]


CCNF
emb[,2]
emb[,1]

```r
#veloviz
layout(matrix(c(1,1,2,3,4,5), 3, 2, byrow = TRUE))
plotEmbedding(emb.veloviz, groups=col[rownames(emb.veloviz)], main='veloviz')
sapply(c('MCM6', 'CDC6', 'KIF2C', 'CCNF'), function(g) {
  gexp <- scale(curr[g,])[,1]
  plotEmbedding(emb.veloviz, col=gexp, main=g)
})
```


veloviz
C2
C1
MCM6
C2
C1
CDC6
C2
C1
KIF2C
C2
C1
CCNF
C2
C1