

# Seurat

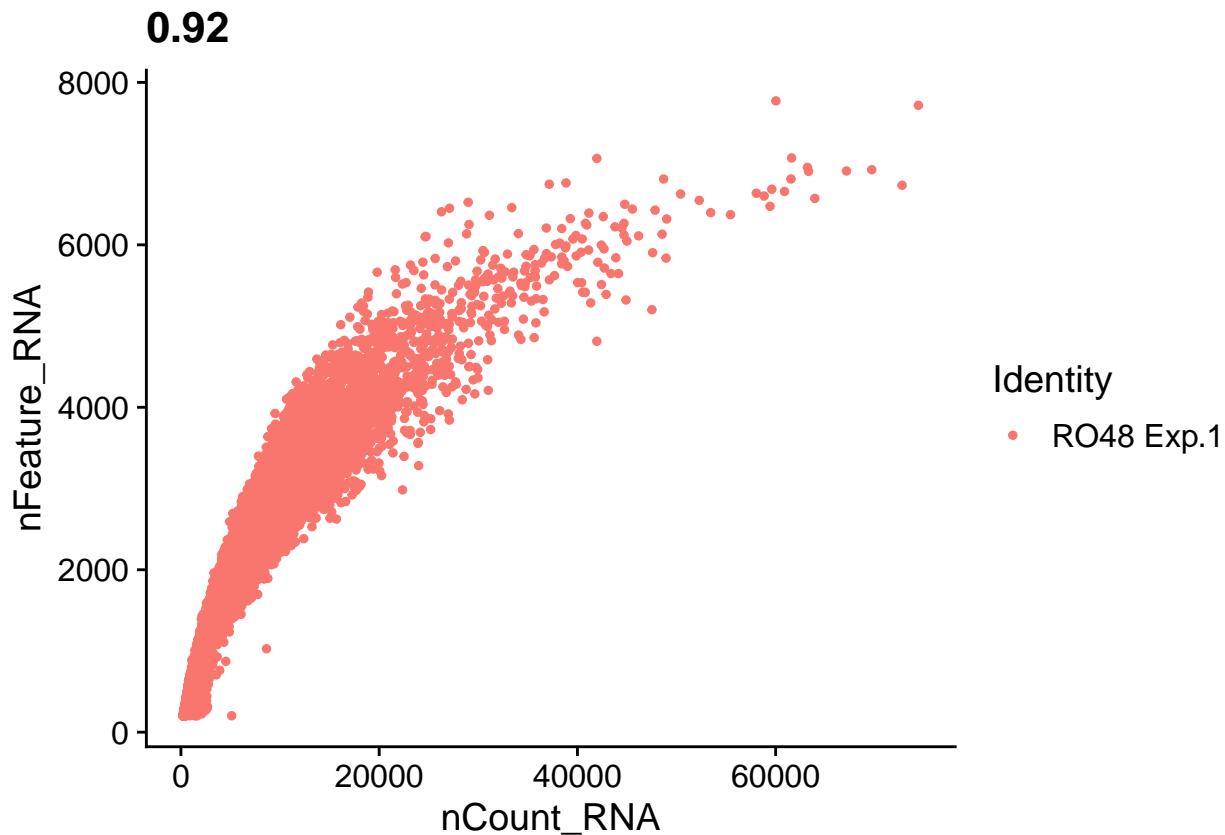
*programandoconro*

7/19/2019

```
##### Required packages #####
library(dplyr)
library(Seurat)
library(cowplot)

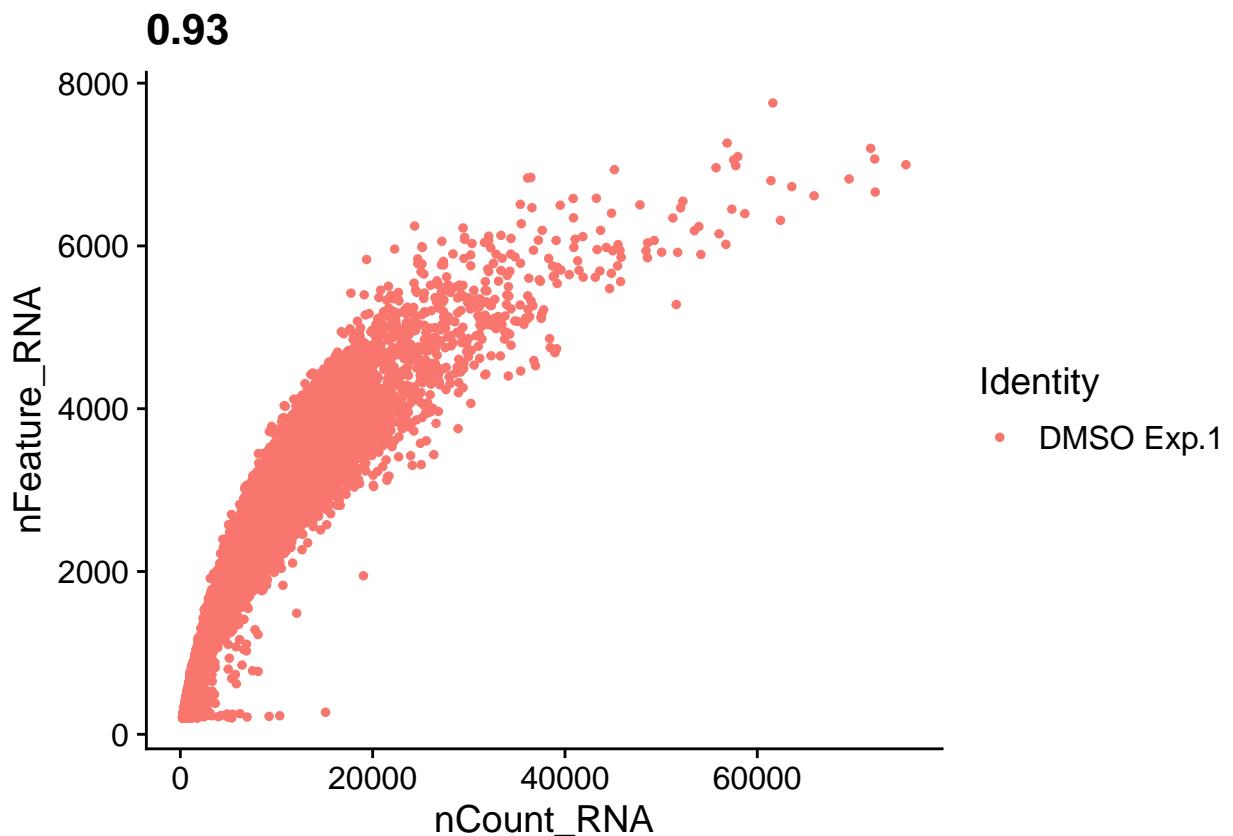
##### Exp_1 #####
R048_1 <- Read10X(data.dir = "~/Dropbox/DataScience/Fiver/R048_1/")%>%
  CreateSeuratObject(min.cells = 3, min.features = 200, project = "R048 Exp.1")

FeatureScatter(object = R048_1, feature1 = "nCount_RNA", feature2 = "nFeature_RNA")
```



```
DMSO_1 <- Read10X(data.dir = "~/Dropbox/DataScience/Fiver/DMSO_1/")%>%
  CreateSeuratObject(min.cells = 3, min.features = 200, project = "DMSO Exp.1")

FeatureScatter(object = DMSO_1, feature1 = "nCount_RNA", feature2 = "nFeature_RNA")
```

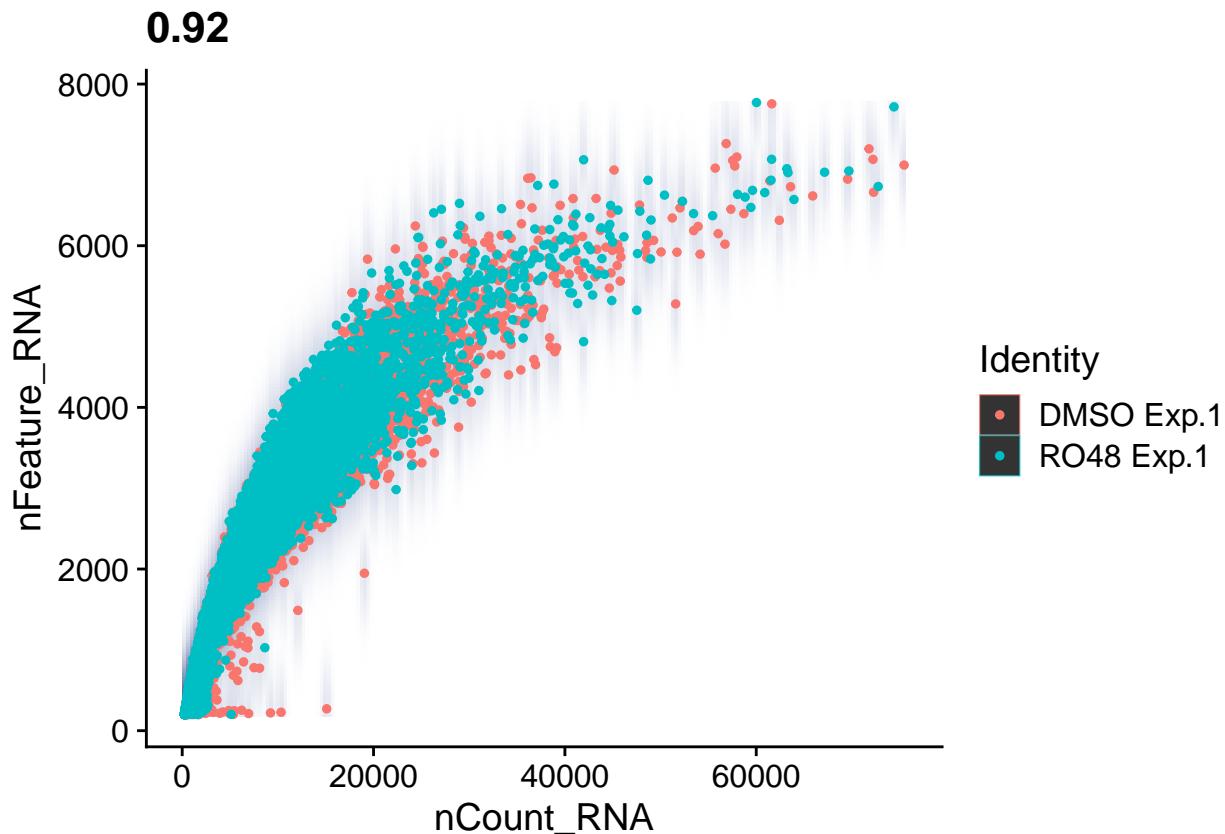


```

mix_1 <- merge (x= DMSO_1,y=R048_1)%>%
  NormalizeData(verbose = FALSE)%>%
  FindVariableFeatures(selection.method = "vst", nfeatures = 2000)

FeatureScatter(object = mix_1, feature1 = "nCount_RNA", feature2 = "nFeature_RNA",pt.size = 1,smo

```



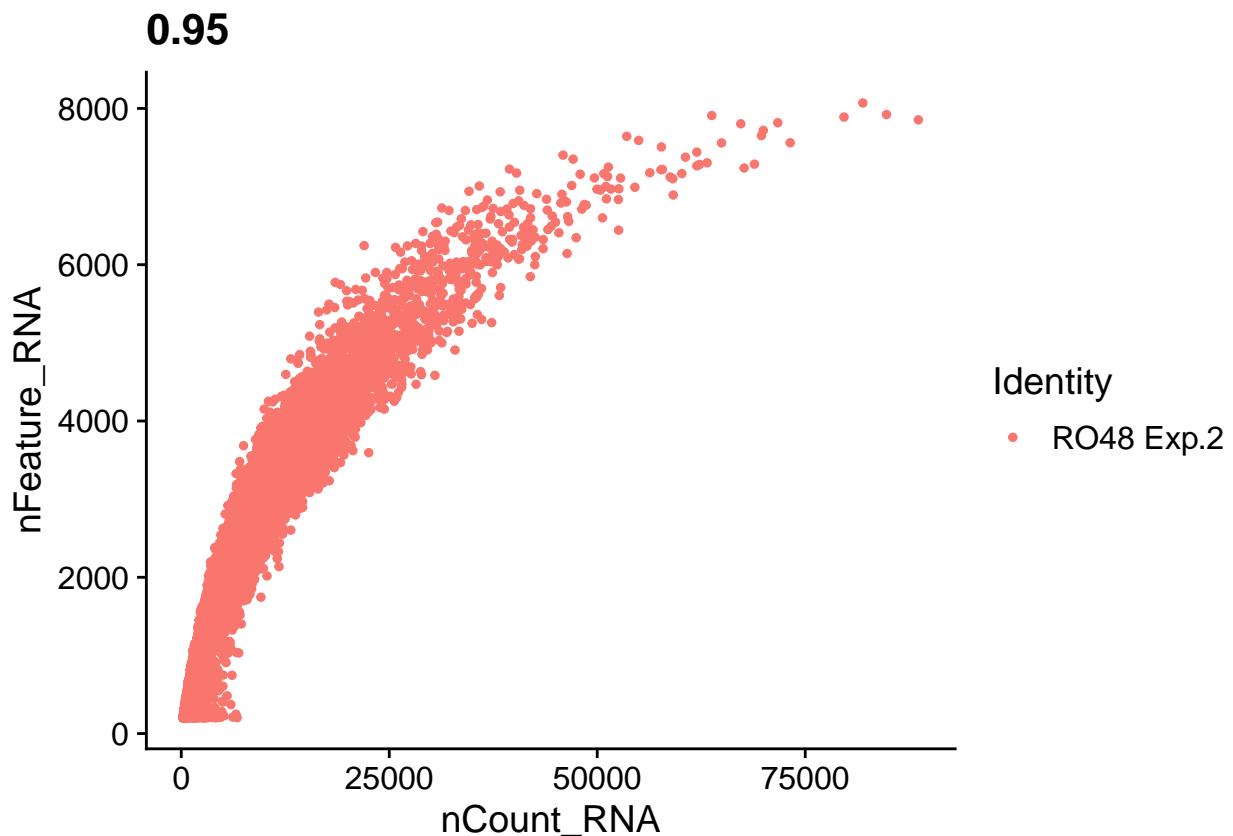
```

rm(R048_1,DMSO_1) #remove objects to reduce RAM load

##### Exp_2 #####
R048_2 <- Read10X(data.dir = "~/Dropbox/DataScience/Fiver/R048_2/")%>%
  CreateSeuratObject(min.cells = 3, min.features = 200, project = "R048 Exp.2")

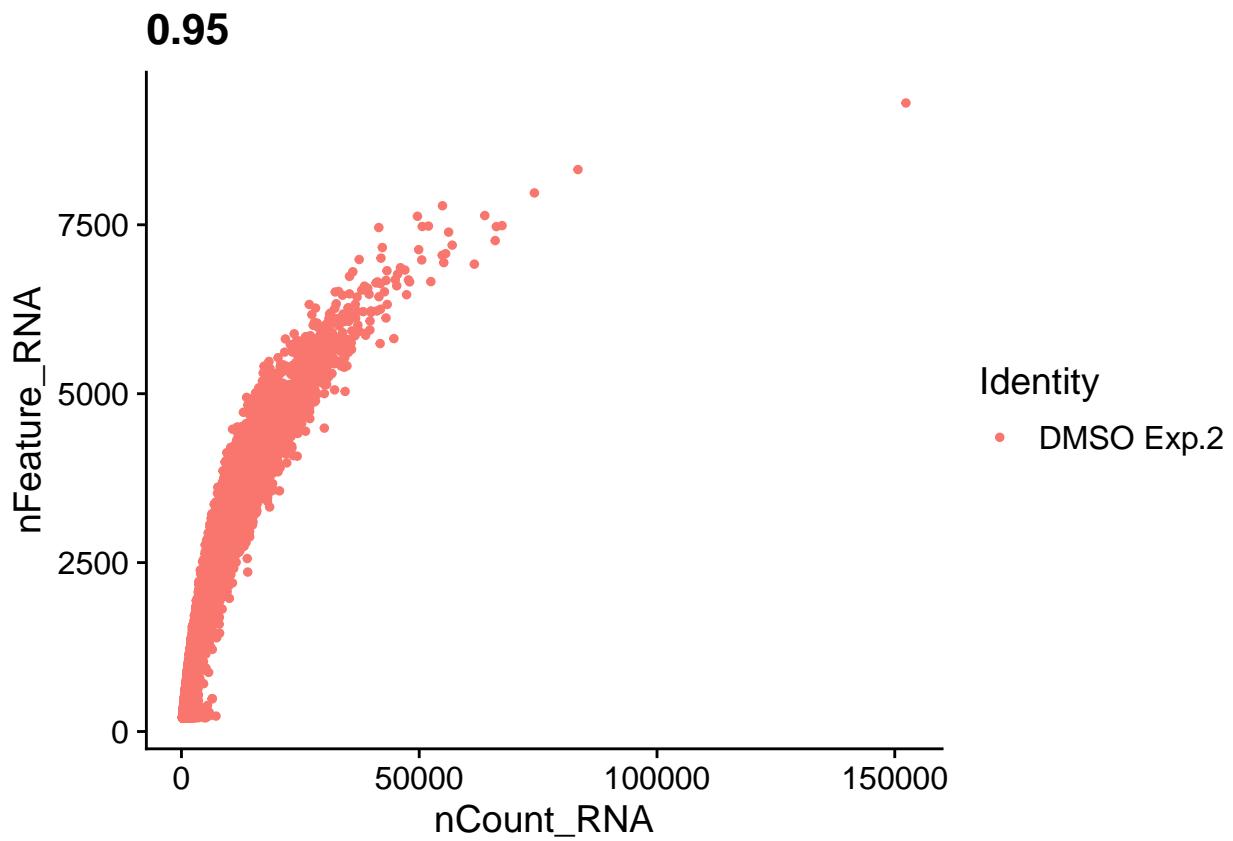
FeatureScatter(object = R048_2, feature1 = "nCount_RNA", feature2 = "nFeature_RNA")

```



```
DMSO_2 <- Read10X(data.dir = "~/Dropbox/DataScience/Fiver/DMSO_2/")%>%
  CreateSeuratObject(min.cells = 3, min.features = 200, project = "DMSO Exp.2")

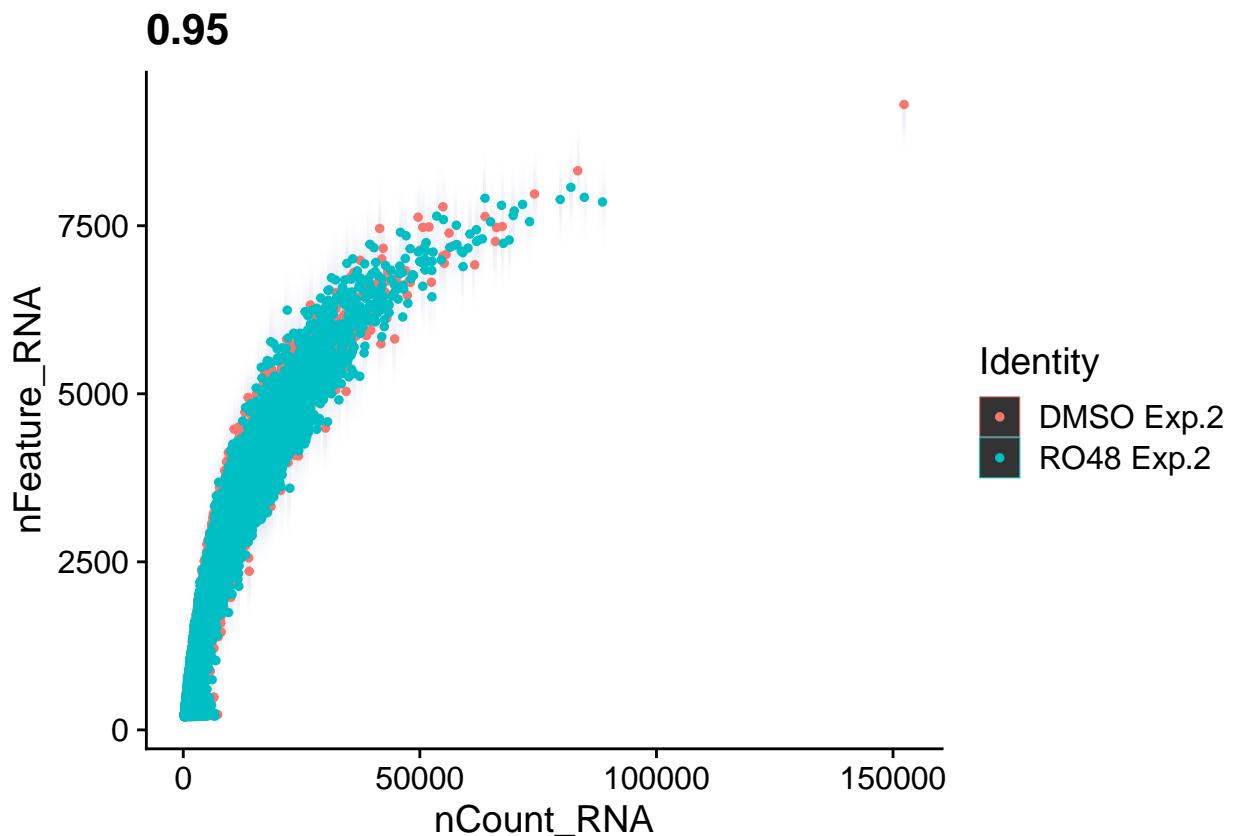
FeatureScatter(object = DMSO_2, feature1 = "nCount_RNA", feature2 = "nFeature_RNA")
```



```

mix_2 <- merge (x= DMSO_2,y=R048_2)%>%
  NormalizeData(verbose = FALSE)%>%
  FindVariableFeatures(selection.method = "vst", nfeatures = 2000)

FeatureScatter(object = mix_2, feature1 = "nCount_RNA", feature2 = "nFeature_RNA",pt.size = 1,smooth
  
```



rm(R048\_2,DMSO\_2)