Splicing Mouse embryo E8.5

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2024-05-22

```
library(Seurat)
```

```
## Loading required package: SeuratObject
```

```
## Loading required package: sp
```

```
##
## Attaching package: 'SeuratObject'
```

```
## The following objects are masked from 'package:base':
##
##     intersect, t
```

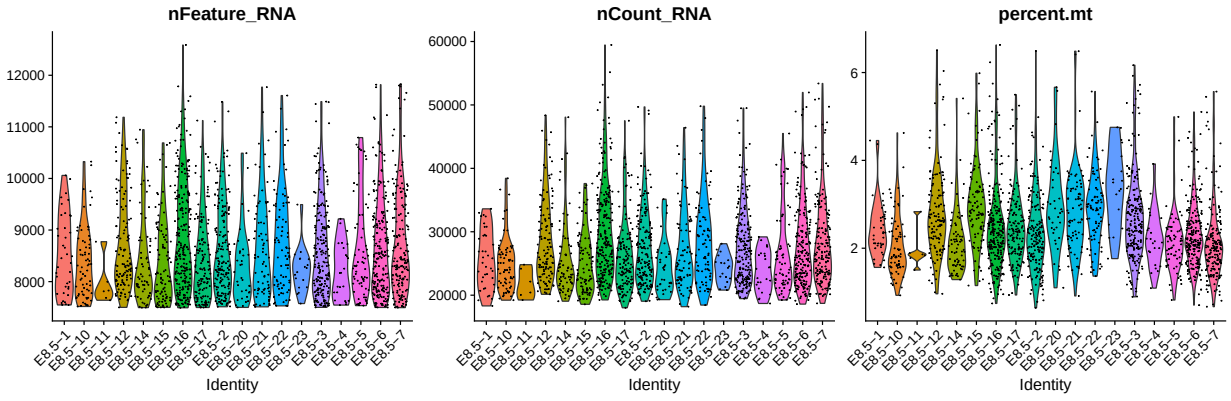
```
library(ggplot2)
library(sctransform)
library(here)
```

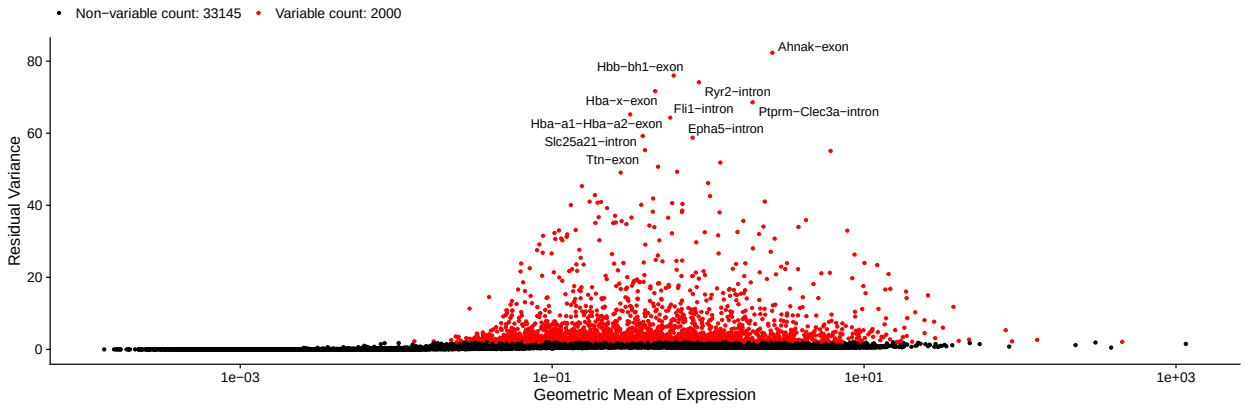
```
## here() starts at /home/1813928/projecticum/splicing
```

```
library(Matrix)
library(glmGamPoi)
```

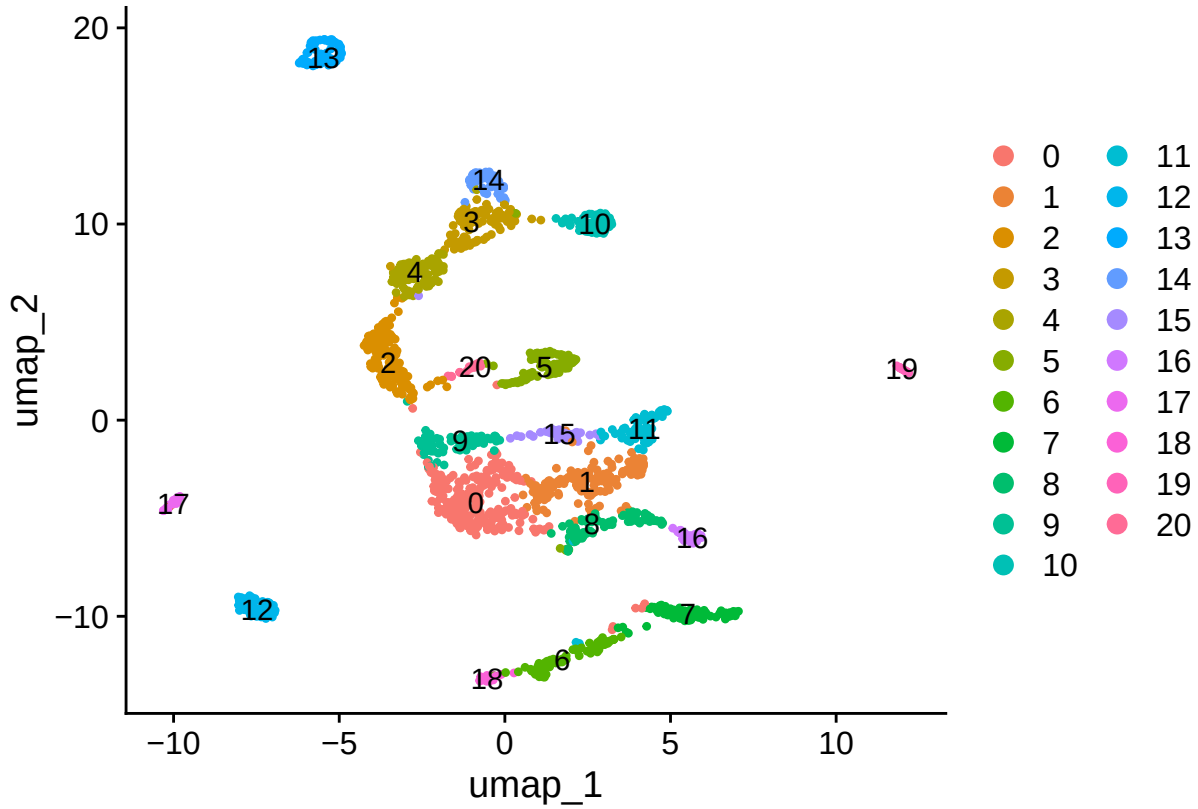
```
## Warning: Feature names cannot have underscores ('_'), replacing with dashes
## ('-')
```

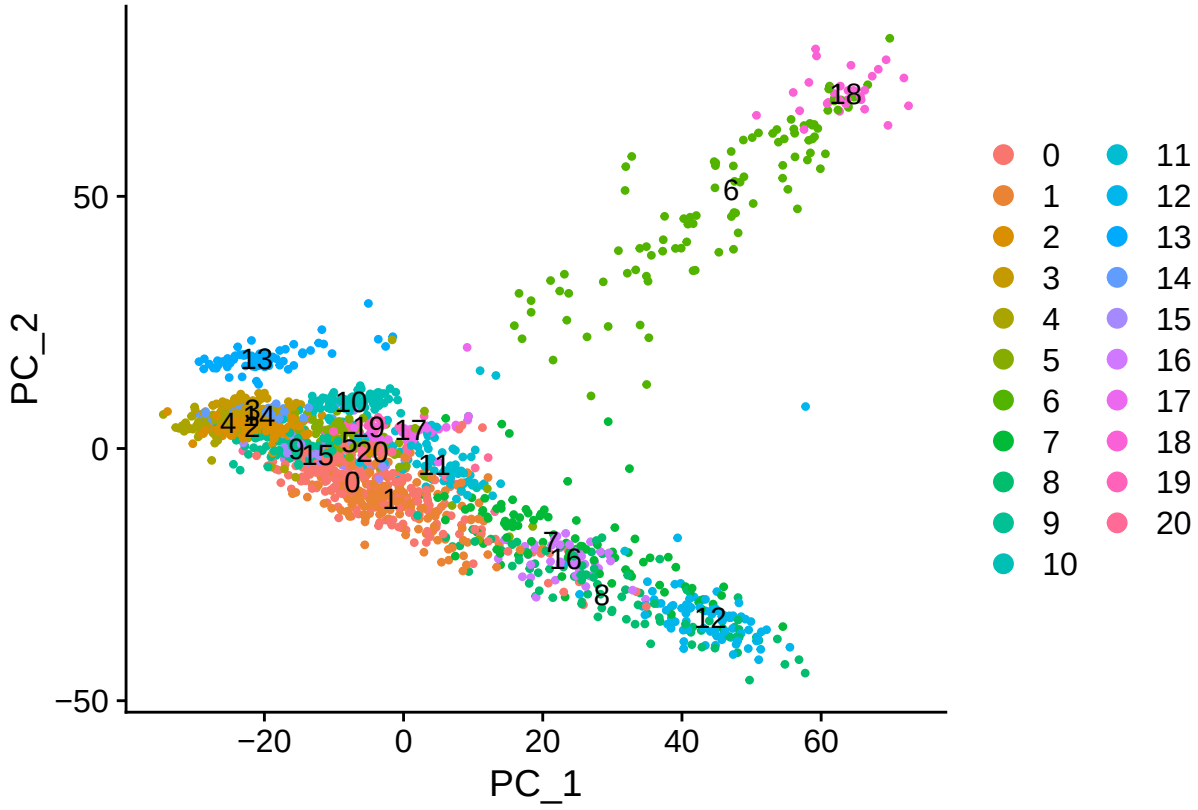
```
## An object of class Seurat
## 37864 features across 1817 samples within 1 assay
## Active assay: RNA (37864 features, 0 variable features)
##  1 layer present: counts
```






```
## Warning: The default method for RunUMAP has changed from calling Python UMAP via reticulate to the R
## To use Python UMAP via reticulate, set umap.method to 'umap-learn' and metric to 'correlation'
## This message will be shown once per session
```




PC_2
PC_1
50
0
−50
−20
0
20
40
60
0
1
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