R Notebook

Code

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downloding and loading packages:

Hide

```
install.packages('patchwork')
```

```
Error in install.packages : Updating loaded packages
```

Step 1: loading the TSV file

	cell_091.133 <int>	cell_177.113 <int>	cell_289.088 <int>	cell_205.268 <int>	cell_162.063 <int>	cell_183.03 <int
A1BG	0	0	0	0	0	
A1CF	0	0	0	1	0	
A2M	0	0	0	0	0	
A2ML1	0	0	0	0	0	
A3GALT2	0	0	0	0	0	
A4GALT	0	0	0	0	0	

6 rows | 1-7 of 2000 columns

Step 2: creating Seurat object

project is titled ‘pdac1’. the Seurat object created here retains genes whcih are expressed in at least 3 cells, and it retains cells that express at least 200 features (genes)

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```
pdac1 <- CreateSeuratObject(counts = data, project = "pdac1", min.cells = 3, min.feature
s = 200)
pdac1
```

```
An object of class Seurat 
13248 features across 633 samples within 1 assay 
Active assay: RNA (13248 features, 0 variable features)
```

step 3: label mitochondrial genes

This code creates a column named “percent.mt” and isolates all the mitochondrial expression

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```
pdac1[["percent.mt"]] <- PercentageFeatureSet(object = pdac1, pattern = "^MT-")
```

step 4: visualize the distribution:

the code below creates a violin plot, which visualizes the feature data, count data, and percent of mitochondrial genes

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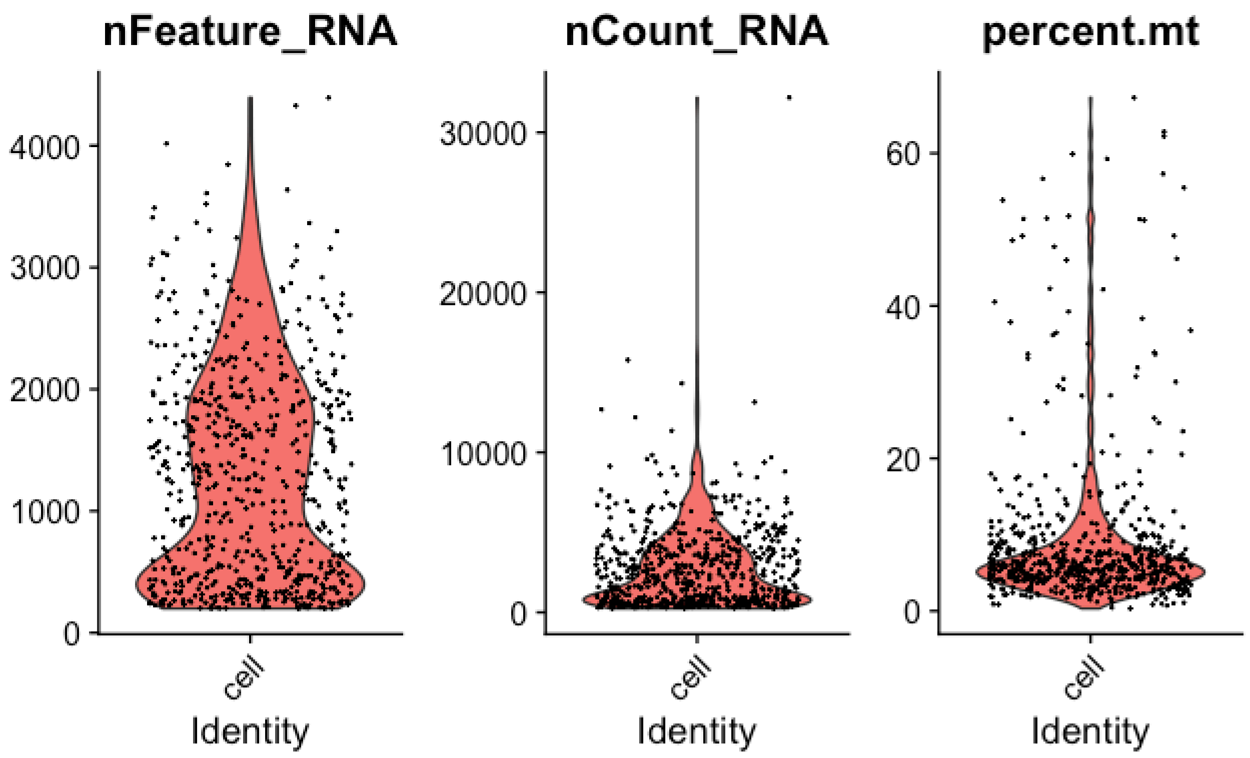
```
VlnPlot(object = pdac1, features = c("nFeature_RNA", "nCount_RNA", "percent.mt"), ncol =
3)
```



step 5: filter data

the code below uses the ‘subset’ function to select data which has features between 200 and 2500, while the percent mitochondrial expression is less than 5.

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```
pdac1 <- subset(x = pdac1, subset = nFeature_RNA > 200 & nFeature_RNA < 2500 & percent.m
t < 5)
```

step 6: normalize data

normalzing the data using Log method, and scaling the data by a vector of 10000

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```
pdac1 <- NormalizeData(object = pdac1, normalization.method = "LogNormalize", scale.fact
or = 10000)
```

```
Performing log-normalization
0%   10   20   30   40   50   60   70   80   90   100%
[----|----|----|----|----|----|----|----|----|----|
**************************************************|
```

step 7: calculate gene variation

the “FindVariableFeatures” function allows R to look through the seurat obect and use the vst method to filter out the top 2000 features/gene which have the most amount of variation across all the cells in the data

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```
pdac1 <- FindVariableFeatures(object = pdac1, selection.method = "vst", nfeatures = 200
0)
```

```
Calculating gene variances
0%   10   20   30   40   50   60   70   80   90   100%
[----|----|----|----|----|----|----|----|----|----|
**************************************************|
Calculating feature variances of standardized and clipped values
0%   10   20   30   40   50   60   70   80   90   100%
[----|----|----|----|----|----|----|----|----|----|
**************************************************|
```

step 8: scale data

scaling all the count data stored in the seurat object for all the genes (rows)

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```
all.genes <- rownames(x = pdac1)
pdac1 <- ScaleData(object = pdac1, features = all.genes)
```

```
Centering and scaling data matrix

  |
  |                                                                      |   0%
  |
  |=====                                                                 |   7%
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  |=======================================================               |  79%
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  |============================================================          |  86%
  |
  |=================================================================     |  93%
  |
  |======================================================================| 100%
```

step 9: PCA

performing principal component analysis on the seurat object, specifically using the features that show high variablility

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```
pdac1 <- RunPCA(object = pdac1, features = VariableFeatures(object = pdac1))
```

```
PC_ 1
Positive:  SPINK1, TM4SF1, DUOXA2, AQP3, APOL1, SOX4, GC, TSPAN8, SLPI, MMP7
	   DMBT1, DSTN, AGR2, SLC2A1, GABRP, ITGA2, EFNA1, AKR1B10, CYB5A, F3
	   CES1, TFF3, AKR1C3, ANKRD36C, MPZL2, FXYD3, FHL2, BAIAP2L1, EIF4A2, LIPH
Negative:  LAPTM5, TYROBP, ALOX5AP, FPR1, S100A9, BASP1, RGS2, S100A8, SLC2A3, LCP1
	   HCLS1, BCL2A1, FCGR3A, CSF3R, G0S2, FCGR3B, ARRB2, ST20, CD53, C5AR1
	   ARHGDIB, FCGR2A, ITGB2, OSM, FCER1G, SAMSN1, TNFRSF1B, AIF1, SLA, CD37
PC_ 2
Positive:  G0S2, CXCL8, CXCR2, S100A8, ST20, BCL2A1, S100A9, HCAR3, FFAR2, IL1R2
	   HCAR2, CMTM2, CSF3R, PROK2, FPR2, MMP9, SOD2, RIPOR2, FPR1, TLR4
	   CXCR1, MME, PLEK, ALPL, FAM177B, RHOH, MGAM, MMP25, AQP9, ALOX5AP
Negative:  MS4A7, SLCO2B1, HLA-DQB1, HLA-DPA1, TGFBI, HLA-DQA1, HLA-DRA, CD163, HLA-DQA
2, HLA-DRB1
	   HLA-DPB1, HLA-DRB5, LGALS1, C1QC, VIM, HLA-DQB2, NPC2, FCGR1A, C1QB, SDS
	   APOE, GPR183, CTSB, C1QA, CSF1R, CD74, MS4A4A, CPVL, CD4, GPX1
PC_ 3
Positive:  AQP3, DUOXA2, GC, TFF3, CES1, DMBT1, HLA-DRB1, AKR1B10, HLA-DRB5, CRP
	   HK2, CRISP3, NR4A1, SPINK1, CD74, CPM, ANKRD36, CTSS, FCGBP, REG1A
	   ANKRD36C, SGK1, F5, CYB5A, TSPAN8, AKR1C3, ANKRD36B, AGR2, CA12, ALDOB
Negative:  COL6A1, SERPINB5, COL6A2, COL17A1, MIA, MGP, CRABP2, SNCG, WNT11, PLAU
	   TIMP3, IGFBP2, S100P, DCBLD2, PCDH7, HMGA2, PODXL, LY6D, FSTL1, HIST1H2BD
	   VCAM1, TOMM70, TRIM29, RNASE1, DMKN, LYPD3, KRT16, PRODH, ZSCAN9, MUC16
PC_ 4
Positive:  CD2, SEPT6, CCL5, SPOCK2, IL2RB, CD3D, CD8A, CD7, CD8B, KLRC1
	   GZMB, RGS1, KLRC2, CD247, NPIPA7, IRF4, NPIPA3, NPIPA8, NPIPA2, SLAMF7
	   PRF1, FYN, CXCR3, RPL3, ZNF683, SIT1, TRAF3, LCK, CTLA4, NPIPA1
Negative:  S100A8, S100A9, PLAUR, SOD2, BCL2A1, FPR1, BASP1, ST20, IL1RN, FCN1
	   SLC11A1, FCGR3B, AQP9, S100P, C5AR1, FCGR3A, SLC2A3, G0S2, S100A12, CSF3R
	   PTGS2, MMP9, CXCL8, FAM177B, EMP1, RAB31, FFAR2, FCGR2A, SMAP2, GCA
PC_ 5
Positive:  ATP8A1, PALM, SLCO2A1, FGF2, REEP4, COL4A2, RBM43, RAD51D, ACE, HEG1
	   RASIP1, CYP1B1, SPARC, PCDH17, IGF2, PLEKHG1, SLC4A7, HTRA1, TCF4, AQP1
	   PTPRG, ZNF419, EFEMP1, MKL2, SLFN11, PODXL, ADGRL1, TTC27, ERMARD, FN1
Negative:  MSX2, MKI67, LPXN, ADCY7, TOP2A, RNF214, NUSAP1, SNAI2, UBE2C, CCNA2
	   CGRRF1, KIF14, CXCL14, MIS18BP1, CEP55, NCAPD2, NEURL1B, RACGAP1, CAD, RFWD3
	   HMMR, PRODH, UBE2T, UBFD1, NPIPA1, DIAPH3, NGEF, LGALS1, NPIPA3, MCM7
```

step 10: visualize PCA data

visualizing the 5 PC generated above by using ‘dims 1:5’

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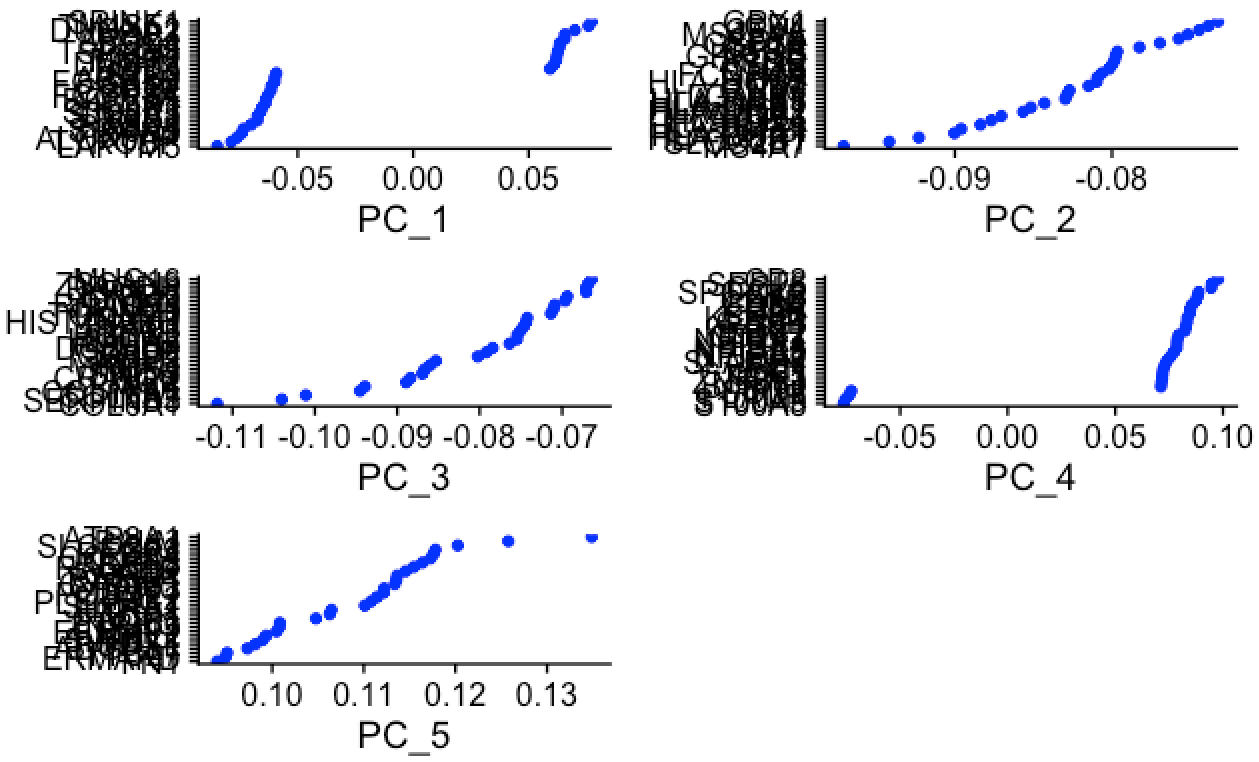
```
VizDimLoadings(object = pdac1, dims = 1:5, reduction = "pca")
```



the results of visualizing the variation from PC1 indicate that there could potentially be at least 2 different types of cells that are present as the data clusters in 2 groups

step 11: PCA heatmaps

dims = 1:10 specfies that I want 10 PCs and cells = 200 is for 200 cells

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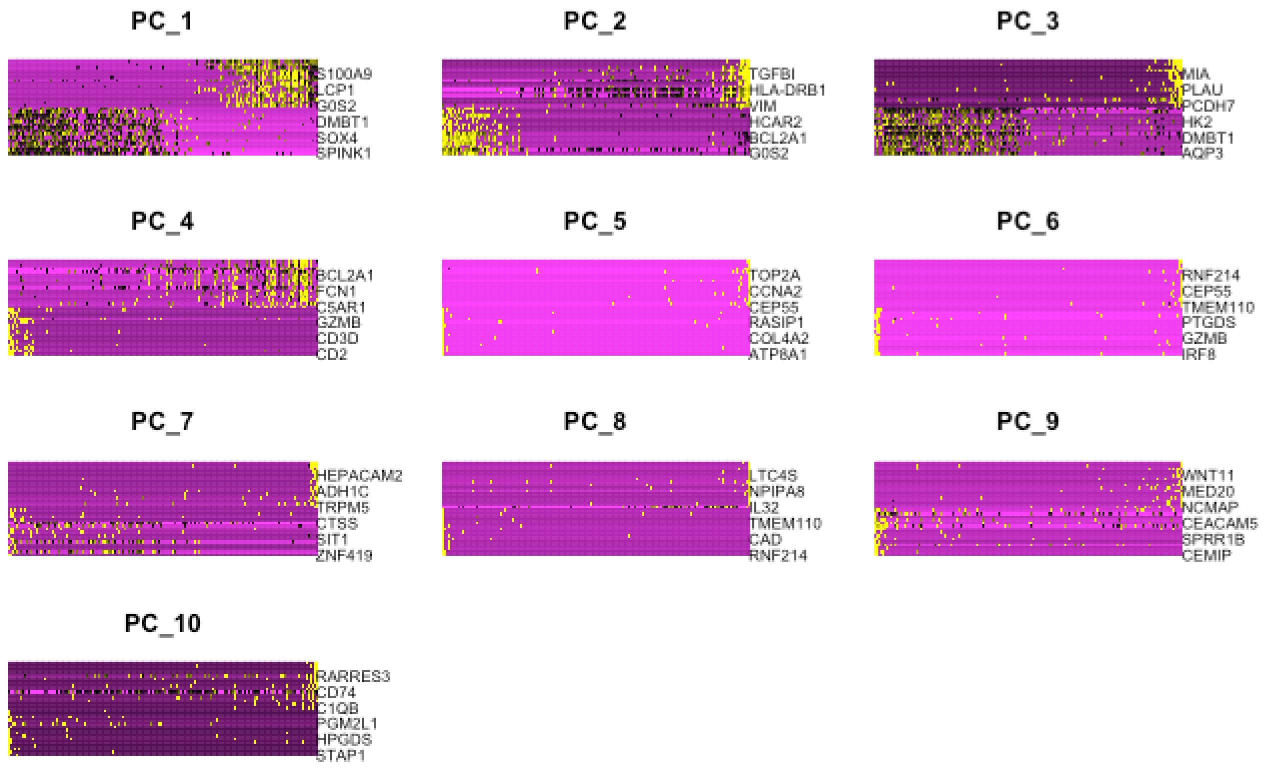
```
DimHeatmap(object = pdac1, dims = 1:10, cells = 200, balanced = TRUE)
```



step 12: dimensionality

num.replicate = 100 specifies that I want 100 replicates, and dims = 1:20 computes p-values for first 20 PCs

	orig.ident <fctr>	nCount_R... <dbl>	nFeature_RNA <int>	percent.mt <dbl>	RNA_snn_res.0.5 <fctr>	seurat_clus <fctr>
cell_091.133	cell	32176	1993	0.3170065	1	1
cell_143.259	cell	6459	2233	4.2885896	1	1
cell_057.153	cell	5026	2247	3.0839634	0	0
cell_169.242	cell	5416	2398	4.8929099	0	0
cell_058.010	cell	6806	2301	2.7622686	3	3
cell_189.209	cell	4386	2119	2.8727770	0	0
cell_023.156	cell	5060	2273	4.8616601	0	0
cell_018.217	cell	5391	2212	2.5041736	0	0
cell_312.307	cell	5615	2432	4.3811220	0	0
cell_318.085	cell	8606	2477	4.5317221	3	3

1-10 of 10 rows

plotting the results from JackStraw

This code below plots the results from JackStraw and gives the resulting p-value, which can tell us which PCs are showing significant variation in our data

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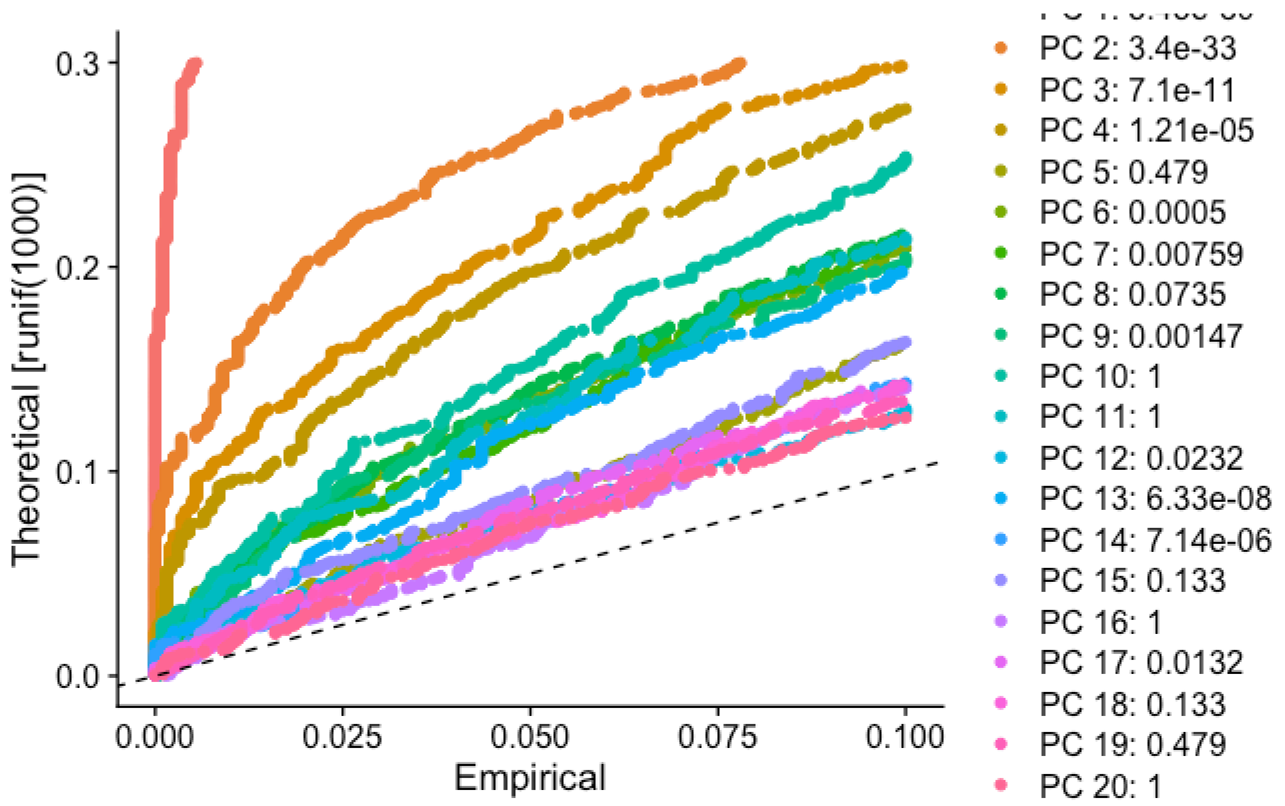
```
JackStrawPlot(object = pdac1, dims = 1:20)
```



graphing the results with Elbow plot:

Allows us to look at the amount of SD explained by each PC

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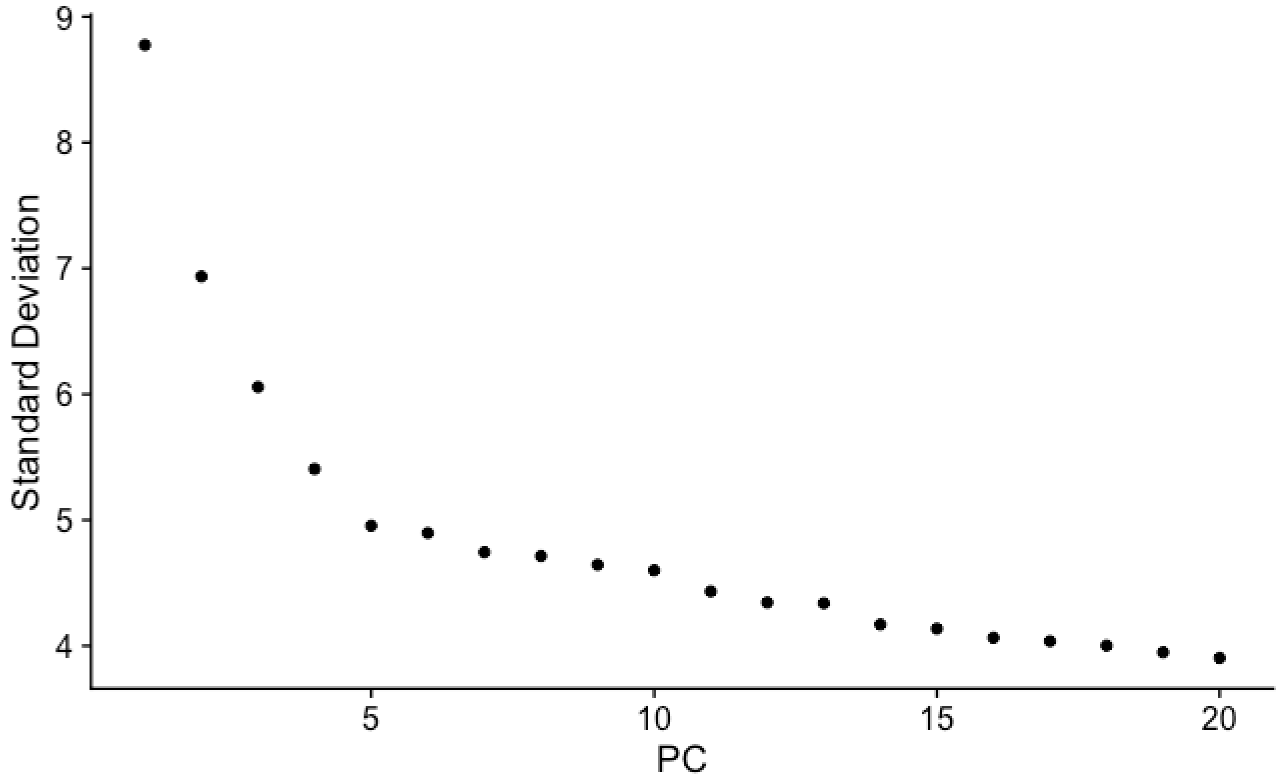
```
ElbowPlot(object = pdac1)
```



step 13: clustering

first 9 PCs capture most of the variation, so we can use that by specifying 1:9. The resolution = 0.5 can be increased if we want more clusters (or vice versa)

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```
pdac1 <- FindNeighbors(object = pdac1, dims = 1:9)
```

```
Computing nearest neighbor graph
Computing SNN
```

Hide

```
pdac1 <- FindClusters(object = pdac1, resolution = 0.5)
```

```
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

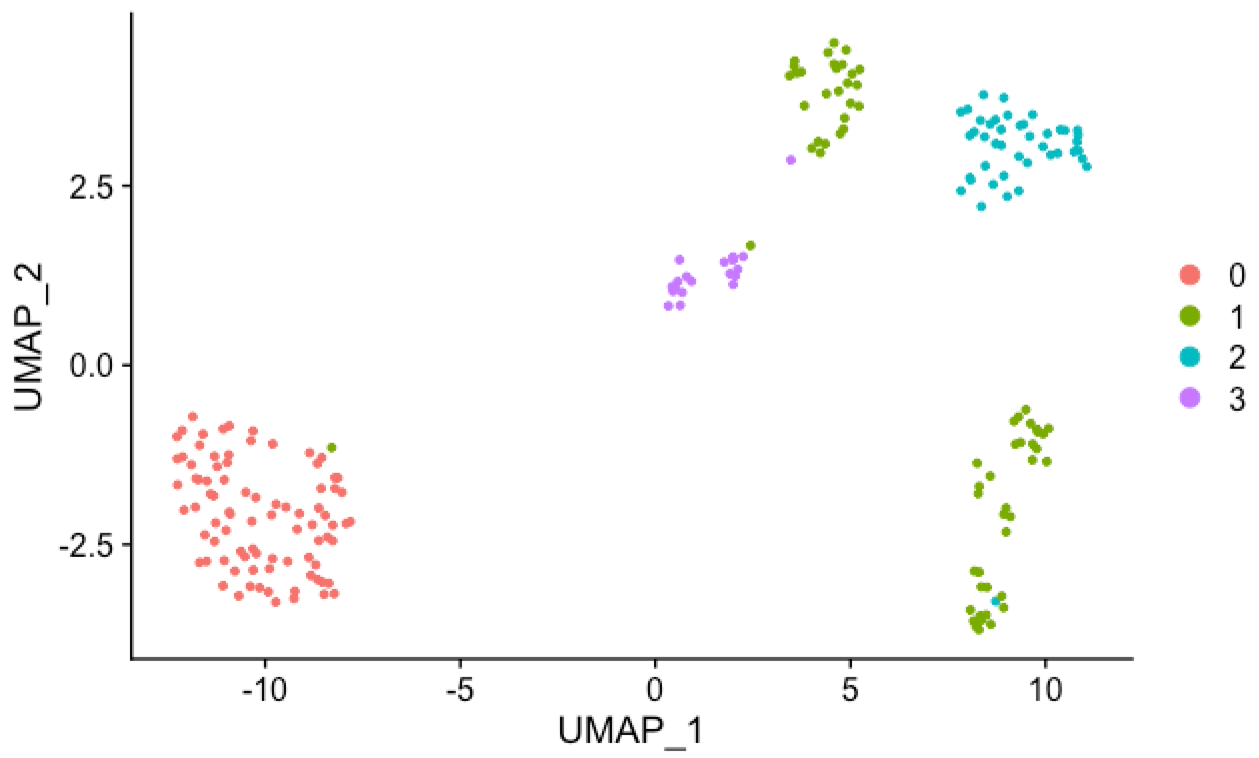
Number of nodes: 212
Number of edges: 5475

Running Louvain algorithm...
```

```
0%   10   20   30   40   50   60   70   80   90   100%
[----|----|----|----|----|----|----|----|----|----|
**************************************************|
Maximum modularity in 10 random starts: 0.7875
Number of communities: 4
Elapsed time: 0 seconds
```

step 14: UMAP on first 9 dimensions

installing UMAP; running first 9 dimensions; plotting the first 9 dimensions



4 distinct clusters are visible in the UMAP (visibly there are 5 but two of them are grouped in 1)

step 15: identify markers

the minimum number of cells that express the gene in at least 1 cluster is set at 25% (as per the Seurat markdown - I wasn't sure if this is something that needs to be altered). The log fold change threshold for the gene to be considered is also set at 0.25. In slice_max, I put n=1, specifying that I want 1 marker per cluster, which will then be used for plotting.

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```
pdac1.markers <- FindAllMarkers(object = pdac1, only.pos = TRUE, min.pct = 0.25, logfc.t
hreshold = 0.25)
```

```
Calculating cluster 0
```

```
|                                                  | 0 % ~calculating
|+                                                 | 1 % ~04s
|++                                                | 2 % ~03s
|++                                                | 3 % ~03s
|+++                                               | 4 % ~03s
|+++                                               | 5 % ~03s
|++++                                              | 6 % ~03s
|++++                                              | 7 % ~03s
|+++++                                             | 8 % ~03s
|+++++                                             | 9 % ~03s
|++++++                                            | 10% ~03s
|++++++                                            | 11% ~03s
|+++++++                                           | 12% ~03s
|+++++++                                           | 14% ~03s
|++++++++                                          | 15% ~03s
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|+++++++++                                         | 17% ~03s
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|++++++++++                                        | 19% ~03s
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|+++++++++++                                       | 21% ~03s
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|+++++++++++++                                     | 25% ~02s
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|+++++++++++++++++                                 | 32% ~02s
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|+++++++++++++++++++                               | 38% ~02s
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|+++++++++++++++++++++                             | 41% ~02s
|+++++++++++++++++++++                             | 42% ~02s
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|++++++++++++++++++++++                            | 44% ~02s
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|+++++++++++++++++++++++++                         | 50% ~02s
|++++++++++++++++++++++++++                        | 51% ~01s
|+++++++++++++++++++++++++++                       | 52% ~01s
```

```
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  |+++++++++++++++++++++++++++++++                   | 61% ~01s
  |++++++++++++++++++++++++++++++++                  | 62% ~01s
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  |+++++++++++++++++++++++++++++++++                 | 65% ~01s
  |+++++++++++++++++++++++++++++++++                 | 66% ~01s
  |++++++++++++++++++++++++++++++++++                | 67% ~01s
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  |+++++++++++++++++++++++++++++++++++               | 69% ~01s
  |+++++++++++++++++++++++++++++++++++               | 70% ~01s
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  |+++++++++++++++++++++++++++++++++++++             | 73% ~01s
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  |+++++++++++++++++++++++++++++++++++++++++++++++   | 94% ~00s
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  |++++++++++++++++++++++++++++++++++++++++++++++++  | 96% ~00s
  |+++++++++++++++++++++++++++++++++++++++++++++++++ | 97% ~00s
  |+++++++++++++++++++++++++++++++++++++++++++++++++ | 98% ~00s
  |++++++++++++++++++++++++++++++++++++++++++++++++++| 99% ~00s
  |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed=03s
```

```
Calculating cluster 1
```

```
  |                                                  |   0%, ~calculating
```

```
|                                                  | 0 % ~calculating
|+                                                 | 1 % ~02s
|++                                                | 2 % ~01s
|++                                                | 3 % ~01s
|+++                                               | 5 % ~01s
|+++                                               | 6 % ~01s
|++++                                              | 7 % ~01s
|++++                                              | 8 % ~01s
|+++++                                             | 9 % ~01s
|++++++                                            | 10% ~01s
|++++++                                            | 11% ~01s
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|++++++++++++++++++++++++                          | 47% ~00s
|++++++++++++++++++++++++                          | 48% ~00s
|+++++++++++++++++++++++++                         | 49% ~00s
|+++++++++++++++++++++++++                         | 50% ~00s
|++++++++++++++++++++++++++                        | 51% ~00s
|+++++++++++++++++++++++++++                       | 52% ~00s
|+++++++++++++++++++++++++++                       | 53% ~00s
|++++++++++++++++++++++++++++                      | 55% ~00s
|++++++++++++++++++++++++++++                      | 56% ~00s
|+++++++++++++++++++++++++++++                     | 57% ~00s
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  |+++++++++++++++++++++++++++++++                   | 60% ~00s
  |+++++++++++++++++++++++++++++++                   | 61% ~00s
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  |++++++++++++++++++++++++++++++++                  | 64% ~00s
  |+++++++++++++++++++++++++++++++++                 | 65% ~00s
  |+++++++++++++++++++++++++++++++++                 | 66% ~00s
  |++++++++++++++++++++++++++++++++++                | 67% ~00s
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  |++++++++++++++++++++++++++++++++++++              | 70% ~00s
  |++++++++++++++++++++++++++++++++++++              | 72% ~00s
  |+++++++++++++++++++++++++++++++++++++             | 73% ~00s
  |+++++++++++++++++++++++++++++++++++++             | 74% ~00s
  |++++++++++++++++++++++++++++++++++++++            | 75% ~00s
  |+++++++++++++++++++++++++++++++++++++++           | 76% ~00s
  |+++++++++++++++++++++++++++++++++++++++           | 77% ~00s
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  |+++++++++++++++++++++++++++++++++++++++++++++++++ | 97% ~00s
  |+++++++++++++++++++++++++++++++++++++++++++++++++ | 98% ~00s
  |++++++++++++++++++++++++++++++++++++++++++++++++++| 99% ~00s
  |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed=01s
```

```
Calculating cluster 2
```

```
  |                                                  | 0 % ~calculating  
  |+                                                 | 1 % ~01s          
  |++                                                | 3 % ~00s          
  |++                                                | 4 % ~00s          
  |+++                                               | 5 % ~00s          
  |++++                                              | 6 % ~00s          
  |++++                                              | 8 % ~01s          
  |+++++                                             | 9 % ~01s          
  |++++++                                            | 10% ~01s          
  |++++++                                            | 12% ~01s          
  |+++++++                                           | 13% ~01s          
  |++++++++                                          | 14% ~01s          
  |++++++++                                          | 15% ~01s          
  |+++++++++                                         | 17% ~01s          
  |+++++++++                                         | 18% ~01s          
  |++++++++++                                        | 19% ~01s          
  |+++++++++++                                       | 21% ~01s          
  |+++++++++++                                       | 22% ~01s          
  |++++++++++++                                      | 23% ~01s          
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  |+++++++++++++                                     | 26% ~01s          
  |++++++++++++++                                    | 27% ~01s          
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  |+++++++++++++++++++++                             | 41% ~00s          
  |++++++++++++++++++++++                            | 42% ~00s          
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  |+++++++++++++++++++++++                           | 45% ~00s          
  |++++++++++++++++++++++++                          | 46% ~00s          
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  |++++++++++++++++++++++++++                        | 51% ~00s          
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  |+++++++++++++++++++++++++++++                     | 56% ~00s          
  |+++++++++++++++++++++++++++++                     | 58% ~00s          
  |++++++++++++++++++++++++++++++                    | 59% ~00s          
  |+++++++++++++++++++++++++++++++                   | 60% ~00s          
  |+++++++++++++++++++++++++++++++                   | 62% ~00s          
  |++++++++++++++++++++++++++++++++                  | 63% ~00s          
  |+++++++++++++++++++++++++++++++++                 | 64% ~00s          
```

```
   |+++++++++++++++++++++++++++++++++                 | 65% ~00s
   |++++++++++++++++++++++++++++++++++                | 67% ~00s
   |++++++++++++++++++++++++++++++++++                | 68% ~00s
   |+++++++++++++++++++++++++++++++++++               | 69% ~00s
   |++++++++++++++++++++++++++++++++++++              | 71% ~00s
   |++++++++++++++++++++++++++++++++++++              | 72% ~00s
   |+++++++++++++++++++++++++++++++++++++             | 73% ~00s
   |++++++++++++++++++++++++++++++++++++++            | 74% ~00s
   |++++++++++++++++++++++++++++++++++++++            | 76% ~00s
   |+++++++++++++++++++++++++++++++++++++++           | 77% ~00s
   |++++++++++++++++++++++++++++++++++++++++          | 78% ~00s
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   |++++++++++++++++++++++++++++++++++++++++++        | 83% ~00s
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   |+++++++++++++++++++++++++++++++++++++++++++       | 86% ~00s
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   |+++++++++++++++++++++++++++++++++++++++++++++     | 90% ~00s
   |++++++++++++++++++++++++++++++++++++++++++++++    | 91% ~00s
   |+++++++++++++++++++++++++++++++++++++++++++++++   | 92% ~00s
   |+++++++++++++++++++++++++++++++++++++++++++++++   | 94% ~00s
   |++++++++++++++++++++++++++++++++++++++++++++++++  | 95% ~00s
   |+++++++++++++++++++++++++++++++++++++++++++++++++ | 96% ~00s
   |+++++++++++++++++++++++++++++++++++++++++++++++++ | 97% ~00s
   |++++++++++++++++++++++++++++++++++++++++++++++++++| 99% ~00s
   |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed=01s
```

```
Calculating cluster 3
```

```
|                                                  | 0 % ~calculating
|+                                                 | 1 % ~02s
|++                                                | 2 % ~02s
|++                                                | 3 % ~02s
|+++                                               | 4 % ~02s
|+++                                               | 5 % ~02s
|++++                                              | 6 % ~02s
|++++                                              | 7 % ~02s
|+++++                                             | 8 % ~02s
|+++++                                             | 9 % ~02s
|++++++                                            | 10% ~02s
|++++++                                            | 11% ~02s
|+++++++                                           | 12% ~02s
|+++++++                                           | 13% ~02s
|++++++++                                          | 14% ~02s
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|+++++++++                                         | 17% ~02s
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|+++++++++++++++++                                 | 33% ~02s
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|+++++++++++++++++++++++                           | 44% ~01s
|+++++++++++++++++++++++                           | 45% ~01s
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|+++++++++++++++++++++++++                         | 48% ~01s
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|++++++++++++++++++++++++++                        | 51% ~01s
```

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|++++++++++++++++++++++++++                        | 52% ~01s
|+++++++++++++++++++++++++++                       | 53% ~01s
|+++++++++++++++++++++++++++                       | 54% ~01s
|++++++++++++++++++++++++++++                      | 55% ~01s
|++++++++++++++++++++++++++++                      | 56% ~01s
|+++++++++++++++++++++++++++++                     | 57% ~01s
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|++++++++++++++++++++++++++++++                    | 59% ~01s
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|+++++++++++++++++++++++++++++++                   | 61% ~01s
|+++++++++++++++++++++++++++++++                   | 62% ~01s
|++++++++++++++++++++++++++++++++                  | 63% ~01s
|++++++++++++++++++++++++++++++++                  | 64% ~01s
|+++++++++++++++++++++++++++++++++                 | 65% ~01s
|+++++++++++++++++++++++++++++++++                 | 66% ~01s
|++++++++++++++++++++++++++++++++++                | 67% ~01s
|++++++++++++++++++++++++++++++++++                | 68% ~01s
|+++++++++++++++++++++++++++++++++++               | 69% ~01s
|+++++++++++++++++++++++++++++++++++               | 70% ~01s
|++++++++++++++++++++++++++++++++++++              | 71% ~01s
|++++++++++++++++++++++++++++++++++++              | 72% ~01s
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|+++++++++++++++++++++++++++++++++++++             | 74% ~01s
|++++++++++++++++++++++++++++++++++++++            | 75% ~01s
|++++++++++++++++++++++++++++++++++++++            | 76% ~01s
|+++++++++++++++++++++++++++++++++++++++           | 77% ~01s
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|++++++++++++++++++++++++++++++++++++++++++        | 83% ~00s
|++++++++++++++++++++++++++++++++++++++++++        | 84% ~00s
|+++++++++++++++++++++++++++++++++++++++++++       | 85% ~00s
|+++++++++++++++++++++++++++++++++++++++++++       | 86% ~00s
|++++++++++++++++++++++++++++++++++++++++++++      | 87% ~00s
|++++++++++++++++++++++++++++++++++++++++++++      | 88% ~00s
|+++++++++++++++++++++++++++++++++++++++++++++     | 89% ~00s
|+++++++++++++++++++++++++++++++++++++++++++++     | 90% ~00s
|++++++++++++++++++++++++++++++++++++++++++++++    | 91% ~00s
|++++++++++++++++++++++++++++++++++++++++++++++    | 92% ~00s
|+++++++++++++++++++++++++++++++++++++++++++++++   | 93% ~00s
|+++++++++++++++++++++++++++++++++++++++++++++++   | 94% ~00s
|++++++++++++++++++++++++++++++++++++++++++++++++  | 95% ~00s
|++++++++++++++++++++++++++++++++++++++++++++++++  | 96% ~00s
|+++++++++++++++++++++++++++++++++++++++++++++++++ | 97% ~00s
|+++++++++++++++++++++++++++++++++++++++++++++++++ | 98% ~00s
|++++++++++++++++++++++++++++++++++++++++++++++++++| 99% ~00s
|++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed=02s
```

Hide

```
pdac1.markers %>%
    group_by(cluster) %>%
    slice_max(n = 1, order_by = avg_log2FC)
```

p_val <dbl>	avg_log2FC <dbl>	pct.1 <dbl>	pct.2 <dbl>	p_val_adj <dbl>	cluster <fctr>	gene <chr>
1.260561e-30	3.830777	0.882	0.094	1.669991e-26	0	SPP1
1.053404e-11	2.997340	0.369	0.027	1.395550e-07	1	RGS1
1.967397e-29	5.863167	0.744	0.030	2.606407e-25	2	G0S2
2.631740e-15	4.856750	0.368	0.005	3.486529e-11	3	MGP

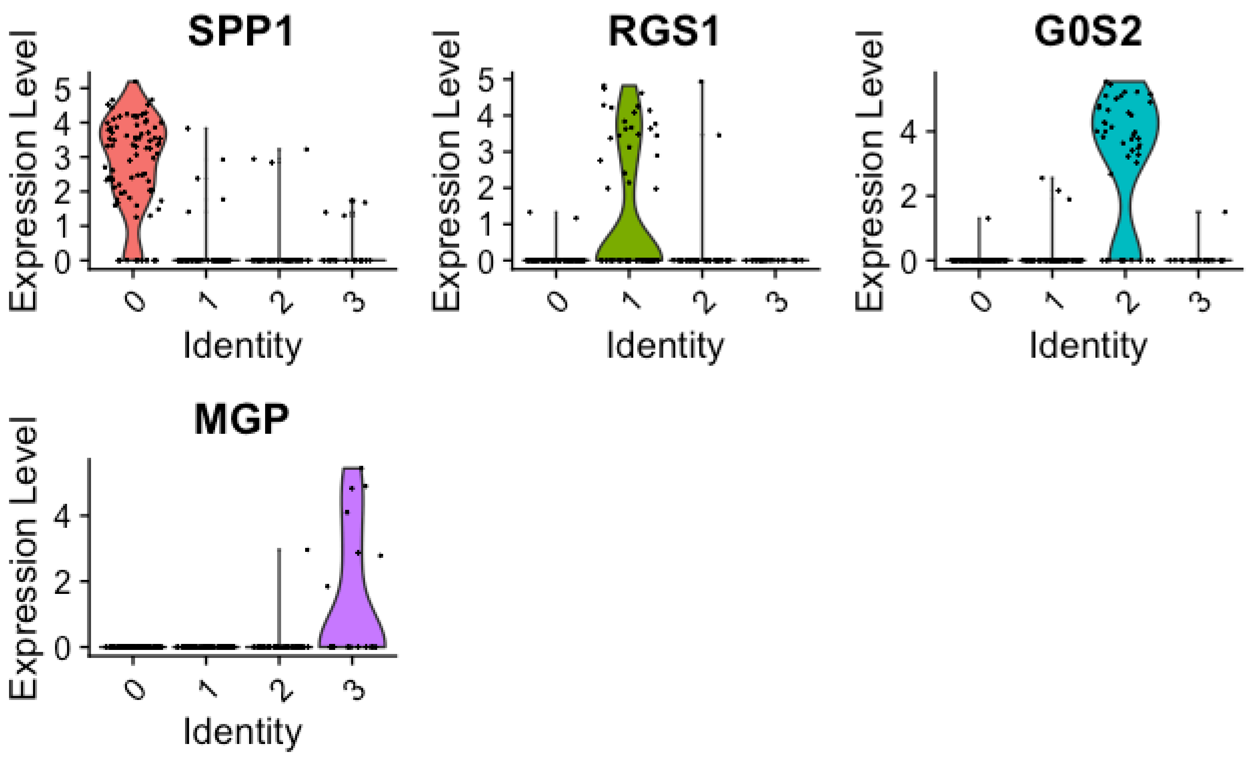
4 rows

step 16: violin plot from 1 feature from each cluster

I used the features obtained above to create this violon plot to see the distribution

Hide

```
VlnPlot(object = pdac1, features = c("SPP1", "RGS1", "G0S2", "MGP"))
```

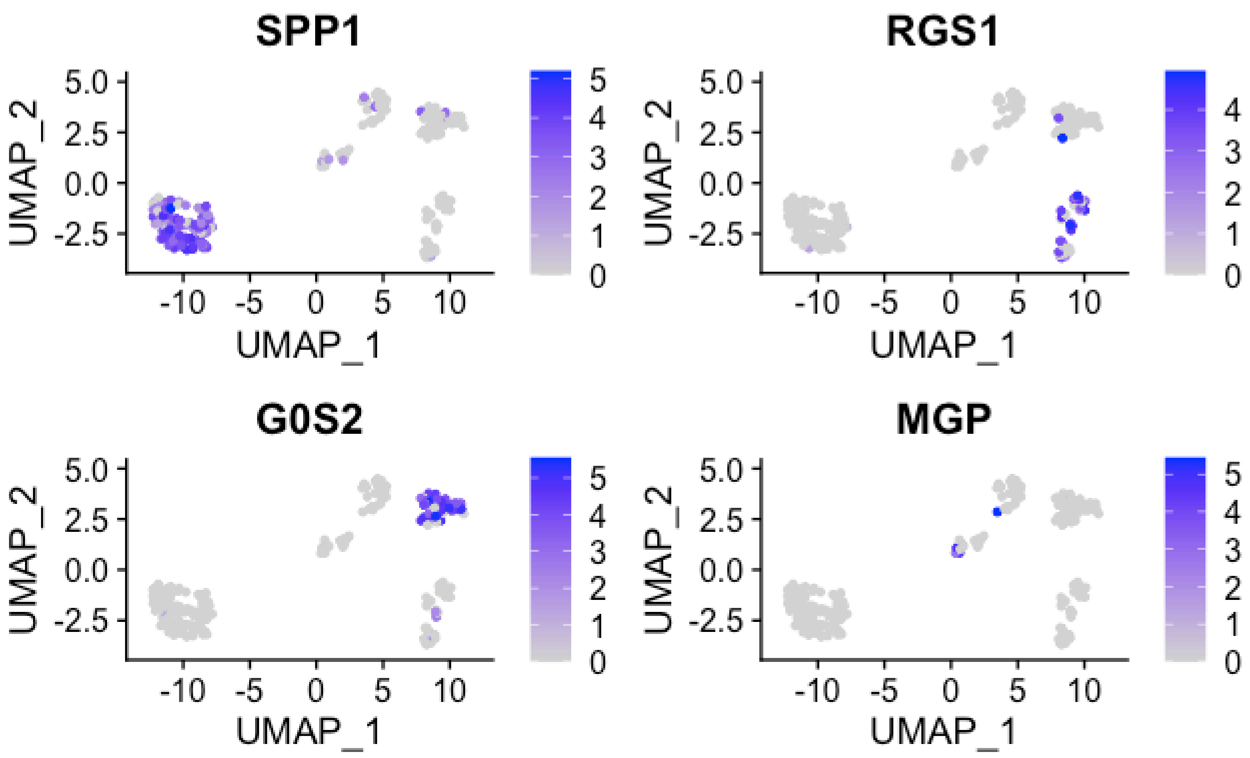


step 17: feature plot with the same features as step 16

Feature plot has been constructed with the same features as used in the creation of the violon plot above.

Hide

```
FeaturePlot(object = pdac1, features = c("SPP1", "RGS1", "G0S2", "MGP"))
```


SPP1
RGS1
G0S2
MGP
UMAP_1
UMAP_2