

# Seurat pipeline 8 um data analysis

[Code ▾](#)

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## Seurat pipeline

Following Seurat “Analysis, visualization, and integration of Visium HD spatial datasets with Seurat” tutorial, available in: [https://satijalab.org/seurat/articles/visiumhd\\_analysis\\_vignette](https://satijalab.org/seurat/articles/visiumhd_analysis_vignette) ([https://satijalab.org/seurat/articles/visiumhd\\_analysis\\_vignette](https://satijalab.org/seurat/articles/visiumhd_analysis_vignette)).

And the “Visium HD Analysis” from Harvard Chan Bioinformatics Core (HBC) (<http://bioinformatics.sph.harvard.edu/>). Available in: [https://github.com/hbctraining/spatial\\_nanocourse/blob/main/lessons/visium\\_hd.md](https://github.com/hbctraining/spatial_nanocourse/blob/main/lessons/visium_hd.md) ([https://github.com/hbctraining/spatial\\_nanocourse/blob/main/lessons/visium\\_hd.md](https://github.com/hbctraining/spatial_nanocourse/blob/main/lessons/visium_hd.md))

Data used available in the 10X Genomics Data Base in: <https://www.10xgenomics.com/datasets/visium-hd-cytassist-gene-expression-human-breast-cancer-fresh-frozen> (<https://www.10xgenomics.com/datasets/visium-hd-cytassist-gene-expression-human-breast-cancer-fresh-frozen>)

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```
# Necessary packages CRAN
list.of.packages = c("Seurat","ggplot2", "dplyr", "patchwork","hdf5r","arrow","ape", "remotes", "devtools", "tictoc")

# Install necessary packages if needed
new.packages = list.of.packages[!(list.of.packages %in% installed.packages())]
if(length(new.packages)> 0) install.packages(new.packages)

# Load CRAN packages
invisible(lapply(list.of.packages, FUN=library, character.only=TRUE))
```

[Hide](#)

```
# Verify if Seurat packages are installed
if (!requireNamespace("SeuratDisk", quietly = TRUE)) {
  remotes::install_github("mojaveazure/seurat-disk")
}
```

[Hide](#)

```
if (!requireNamespace("SeuratData", quietly = TRUE)) {
  remotes::install_github("satijalab/seurat-data")
}

# Load Seurat packages
invisible(lapply(c("SeuratDisk", "SeuratData"), FUN=library, character.only=TRUE))

# Bioconductor packages
bioconductor.packages = c("G0.db", "org.Hs.eg.db", "limma")

if (!requireNamespace("BiocManager", quietly = TRUE)) {
  install.packages("BiocManager", repos = "https://cloud.r-project.org")
}
library(BiocManager)
```

[Hide](#)

```
new.packages.bio = bioconductor.packages[!(bioconductor.packages %in% installed.packages())]
if(length(new.packages.bio)> 0) BiocManager::install(new.packages.bio)

# Load Bioconductor packages
invisible(lapply(bioconductor.packages, FUN=library, character.only=TRUE))
```

[Hide](#)

```
# Measure run time notebook
tic("Total time Seurat pipeline")
```

[Hide](#)

```
# Load Visium HD data
localdir <- "../Data/Raw/raw_data_fresh_frozen/"
list.files(localdir)
```

```
[1] "binned_outputs"                "spatial"
[3] "Visium_HD_Human_Breast_Cancer_Fresh_Frozen_tissue_image.tif"
```

[Hide](#)

```
# Load a 10x Genomics 8 um Visium Spatial Experiment into a Seurat object
object <- Load10X_Spatial(data.dir = localdir, bin.size = 8)
object
```

```
An object of class Seurat
18085 features across 472859 samples within 1 assay
Active assay: Spatial.008um (18085 features, 0 variable features)
 1 layer present: counts
 1 spatial field of view present: slice1.008um
```

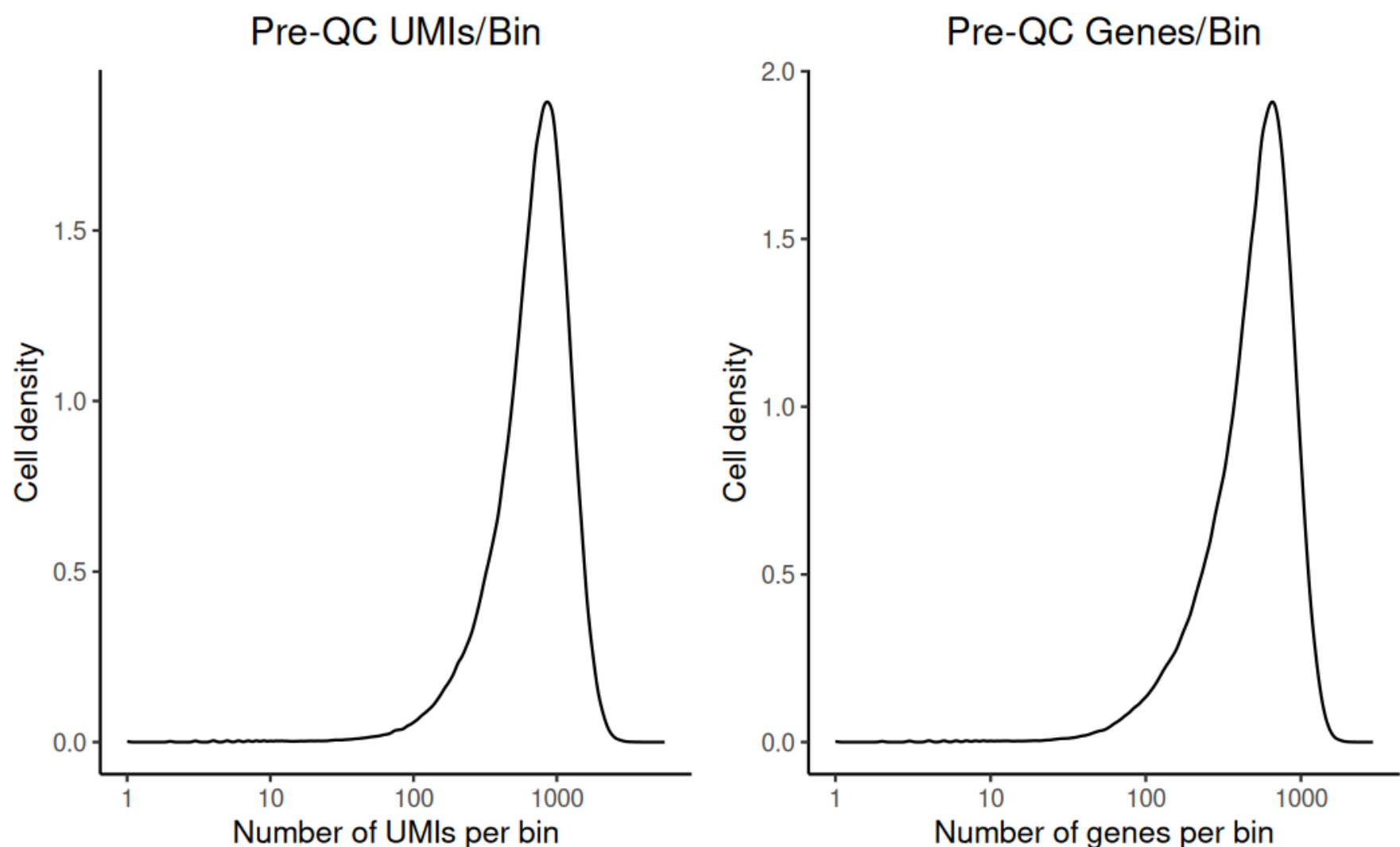
Hide

```
# Quality Control
# Pre-filtering
# Create a metadata object
object_meta <- object@meta.data

# Plot the number of UMIs (nUMI) and the number of genes (nGene)
# Create a plot for nUMI
dist_counts_before <- object_meta %>%
  ggplot(aes(x=nCount_Spatial.008um)) +
  geom_density(alpha = 0.2) +
  scale_x_log10() +
  theme_classic() +
  ylab("Cell density") +
  xlab("Number of UMIs per bin") +
  ggtitle('Pre-QC UMIs/Bin') +
  theme(plot.title = element_text(hjust = 0.5))

# Create a plot for nGene
dist_features_before <- object_meta %>%
  ggplot(aes(x=nFeature_Spatial.008um)) +
  geom_density(alpha = 0.2) +
  scale_x_log10() +
  theme_classic() +
  ylab("Cell density") +
  xlab("Number of genes per bin") +
  ggtitle('Pre-QC Genes/Bin') +
  theme(plot.title = element_text(hjust = 0.5))

dists_before <- dist_counts_before | dist_features_before
dists_before
```



Hide

```
# Good quality data, just one pick representing healthy cells with high number of genes and UMIs per bin.
```

[Hide](#)

```
# Apply filter to delete low quality bins and genes
print(paste("The number of initial bins and genes before filtering was:", nrow(object@meta.data), "and",nrow(object), "respectively." ))
```

```
[1] "The number of initial bins and genes before filtering was: 472859 and 18085 respectively."
```

[Hide](#)

```
# Create a filtered object, with with nUMI > 80 and nGene > 80, leaving the higher quality bins
object_filt <- subset(object, (nCount_Spatial.008um > 80) &
                        (nFeature_Spatial.008um > 80))

# Calculate the % of mitochondrial genes per bin
object_filt[["percent.mt"]] <- PercentageFeatureSet(object_filt, pattern = "^MT-")

# Apply filter keeping bins of < 30% mitochondrial genes
object_filt <- subset(object_filt, subset = percent.mt < 30)

# Obtain the count matrix
counts = GetAssayData(object_filt,layer = "counts")
# Filter genes that appear in at least 5 bins, high quality genes
hq_genes = rowSums(counts >0) >= 5
# Subset seurat object to keep only high quality genes
object_filt = subset(object_filt, features = names(hq_genes[hq_genes]))
print(paste("Resulting in" , nrow(object_filt@meta.data), "bins and",nrow(object_filt) , "genes after filtering for further processing."))
```

```
[1] "Resulting in 463329 bins and 16375 genes after filtering for further processing."
```

[Hide](#)

```
# Calculate statistics of filtered object
summary(object_filt$nCount_Spatial.008um, na.rm = T)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
82	506	747	787	1015	5670

[Hide](#)

```
summary(object_filt$nFeature_Spatial.008um, na.rm = T)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
81.0	355.0	544.0	560.5	735.0	2913.0

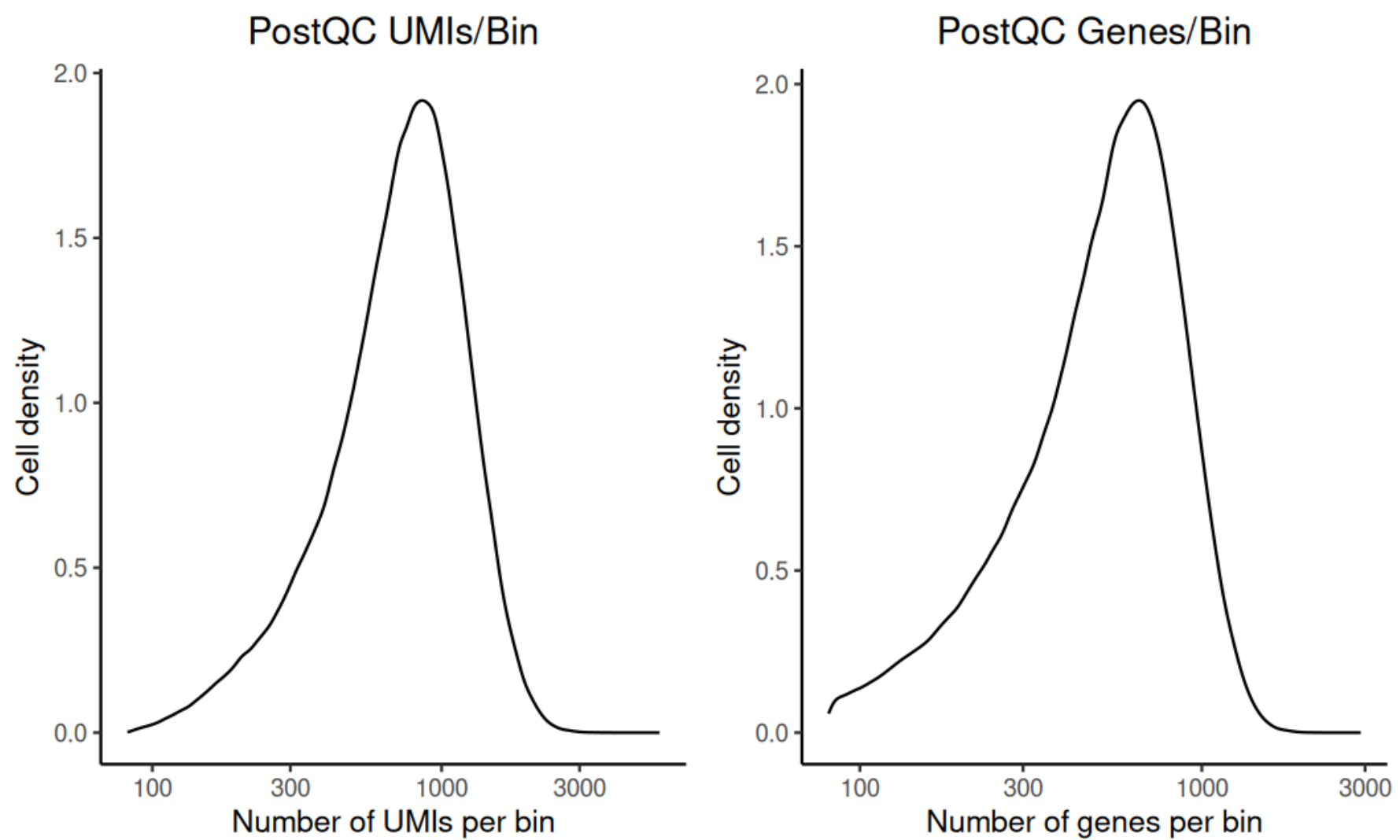
[Hide](#)

```
# Create a new metadata data frame with the filtered object
object_filt_meta <- object_filt@meta.data
```

```
# Plot nUMI
dist_counts_after <- object_filt_meta %>%
  ggplot(aes(x=nCount_Spatial.008um)) +
  geom_density(alpha = 0.2) +
  scale_x_log10() +
  theme_classic() +
  ylab("Cell density") +
  xlab("Number of UMIs per bin") +
  ggtitle('PostQC UMIs/Bin') +
  theme(plot.title = element_text(hjust = 0.5))
```

```
# Plot nGene
dist_features_after <- object_filt_meta %>%
  ggplot(aes(x=nFeature_Spatial.008um)) +
  geom_density(alpha = 0.2) +
  scale_x_log10() +
  theme_classic() +
  ylab("Cell density") +
  xlab("Number of genes per bin") +
  ggtitle('PostQC Genes/Bin') +
  theme(plot.title = element_text(hjust = 0.5))
```

```
# Combine plots side-by-side
dists_after <- dist_counts_after | dist_features_after
dists_after
```



Hide

```
# Visualizing Counts Data
# Visualize the number of UMIs and gene counts per bin as a distribution
# Violin plot of UMI counts
vln_counts_after <- VlnPlot(object_filt,
                           features = "nCount_Spatial.008um",
                           pt.size = 0,
                           group.by = 'orig.ident') +
  NoLegend() + scale_y_log10() + ggtitle('nUMI') + xlab('FF_breast') + ylim(c(80, 6000))
```

Warning: Default search for "data" layer in "Spatial.008um" assay yielded no results; utilizing "counts" layer in stead.Warning: The `slot` argument of `FetchData()` is deprecated as of SeuratObject 5.0.0. Please use the `layer` argument instead.Warning: `PackageCheck()` was deprecated in SeuratObject 5.0.0. Please use `rlang::check\_installed()` instead.Scale for y is already present. Adding another scale for y, which will replace the existing scale.Scale for y is already present. Adding another scale for y, which will replace the existing scale.

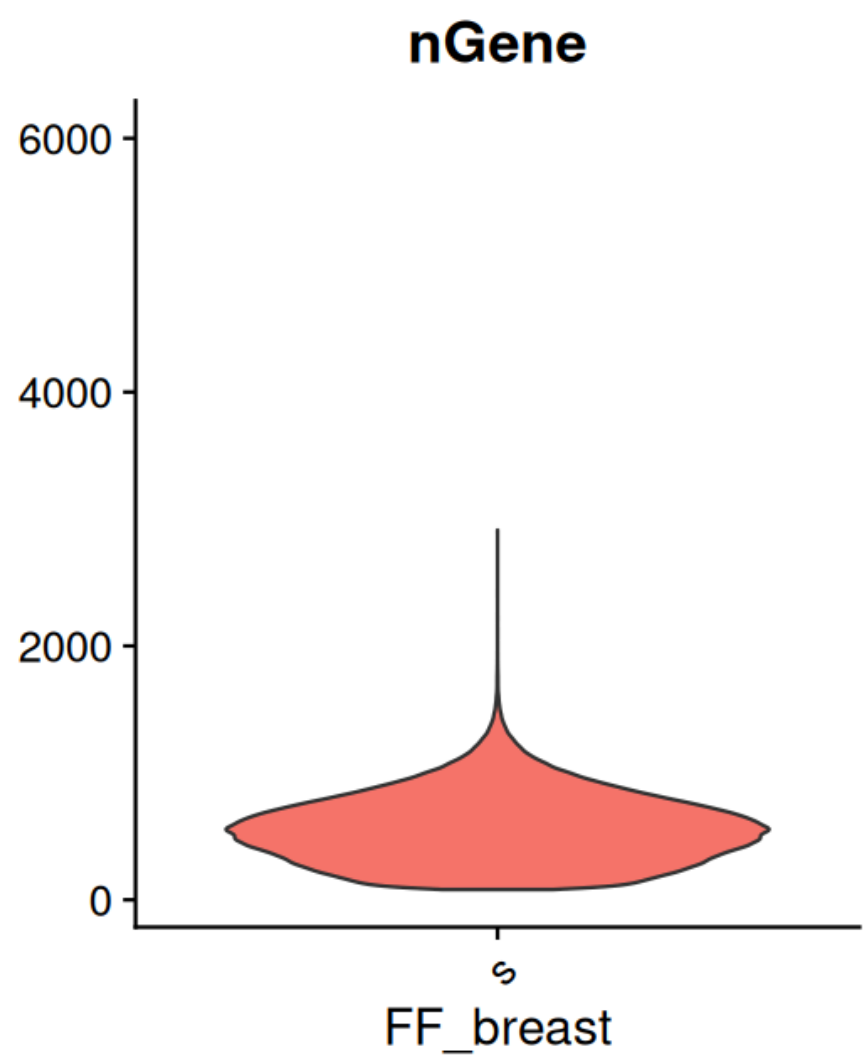
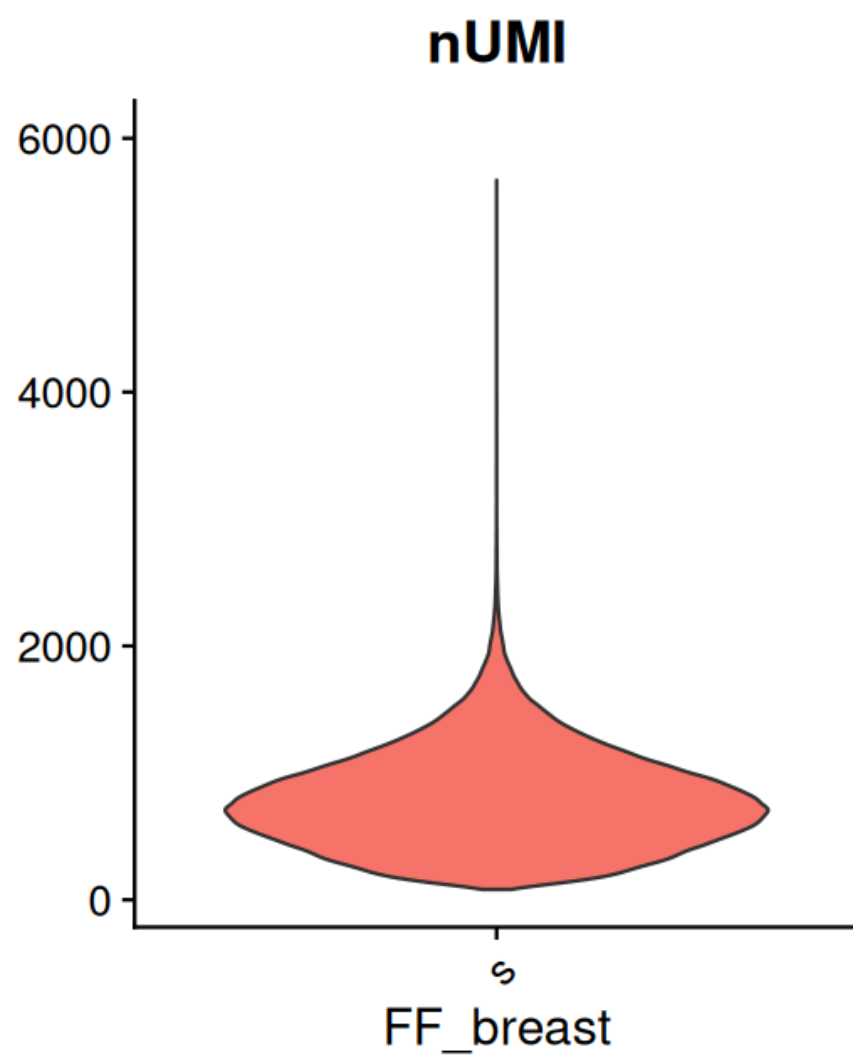
Hide

```
# Violin plot of gene counts
vln_features_after <- VlnPlot(object_filt,
                             features = "nFeature_Spatial.008um",
                             pt.size = 0,
                             group.by = 'orig.ident') +
  NoLegend() + scale_y_log10() + ggtitle('nGene') + xlab('FF_breast') + ylim(c(80, 6000))
```

Warning: Default search for "data" layer in "Spatial.008um" assay yielded no results; utilizing "counts" layer in stead.Scale for y is already present. Adding another scale for y, which will replace the existing scale.Scale for y is already present. Adding another scale for y, which will replace the existing scale.

Hide

```
# Plot both side by side
vln_counts_after | vln_features_after
```

[Hide](#)

```
# Visualizing UMI count across the tissue image
image_counts <- SpatialFeaturePlot(object_filt,
                                   feature = 'nCount_Spatial.008um',
                                   pt.size.factor = 8) +
  theme(legend.position = "top",
        legend.title = element_text(size = 10, hjust = 0, vjust = 1),
        legend.text = element_text(size = 6.5))

# Visualizing gene count across the image
image_features <- SpatialFeaturePlot(object_filt,
                                     features = "nFeature_Spatial.008um",
                                     pt.size.factor = 8) +
  theme(legend.position = "top",
        legend.title = element_text(size = 10, hjust = 0, vjust = 1))


# Plot the two side-by-side
image_counts | image_features
```

nCount\_Spatial.008um

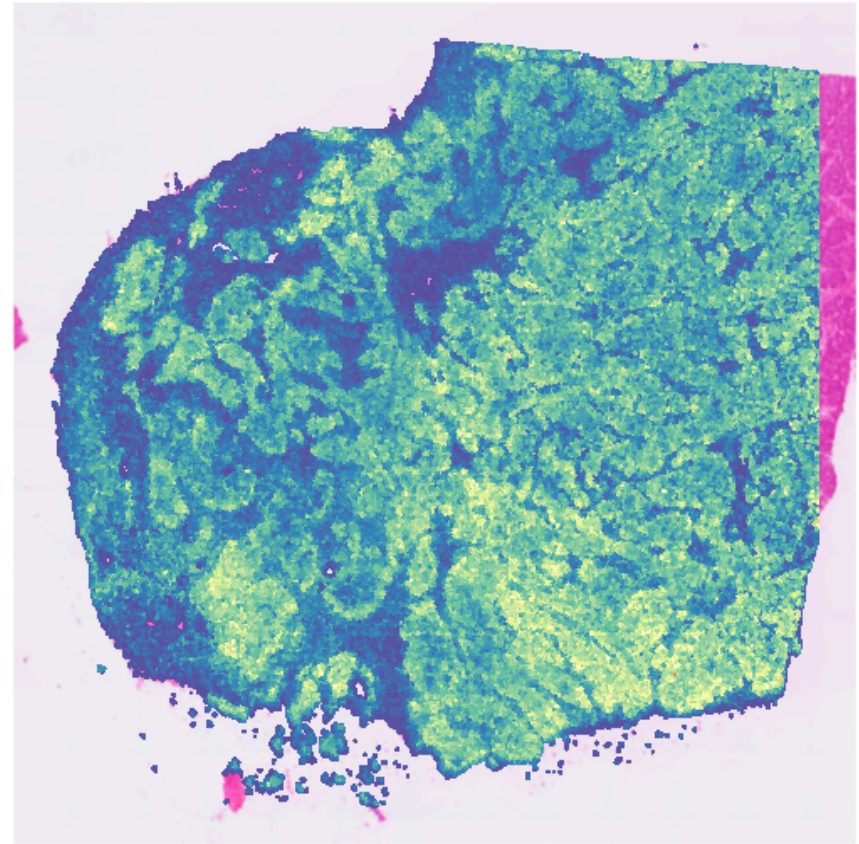
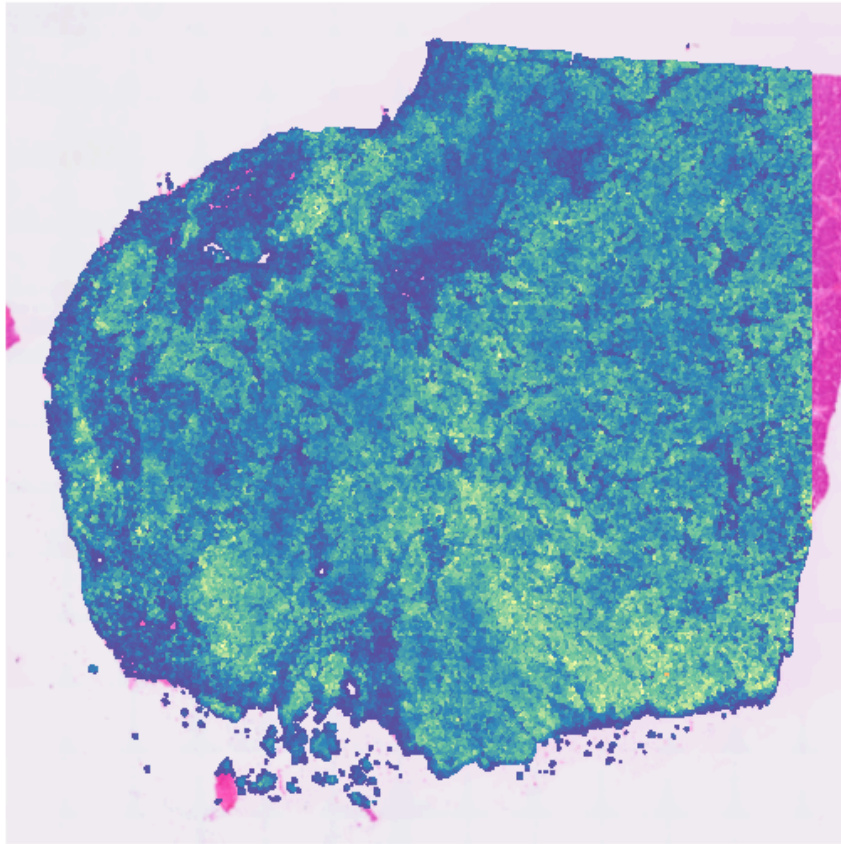


1000 2000 3000 4000 5000

nFeature\_Spatial.008um



1000 2000



Hide

```
# note that many spots have very few counts, in-part
# due to low cellular density in certain tissue regions
```

Hide

```
# Normalize dataset, use standard log-normalization for spatial data
object_filt <- NormalizeData(object_filt, assay = 'Spatial.008um')
```

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

Hide

object\_filt

```
An object of class Seurat
16375 features across 463329 samples within 1 assay
Active assay: Spatial.008um (16375 features, 0 variable features)
 2 layers present: counts, data
 1 spatial field of view present: slice1.008um
```

Hide

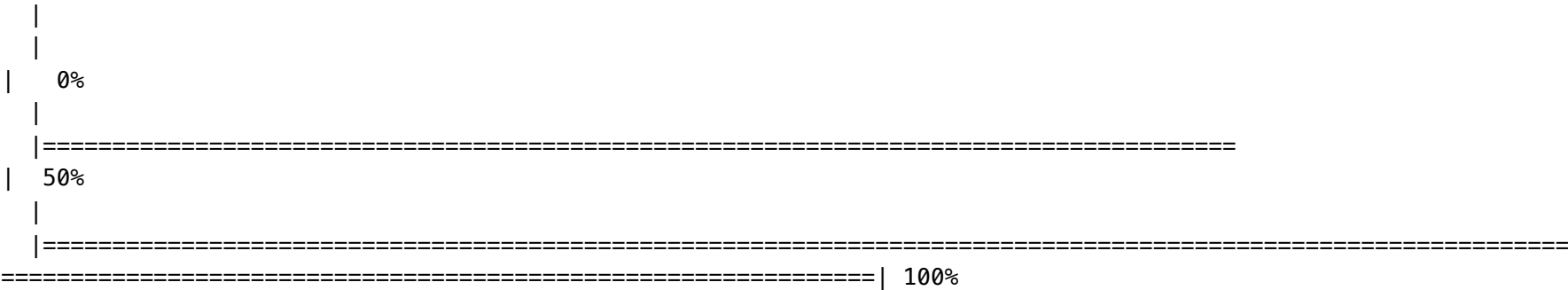
```
# Unsupervised clustering
# Define a set of highly variable genes, will help to quantify the variability and similarity between bins.
object_filt <- FindVariableFeatures(object_filt)
```

```
Finding variable features for layer counts
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%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Hide

```
object_filt <- ScaleData(object_filt)
```

Centering and scaling data matrix



Hide

```
# Select 50,000 cells and create a new 'sketch' assay
object_filt <- SketchData(
  object = object_filt,
  ncells = 50000,
  method = "LeverageScore",
  sketched.assay = "sketch",
  features = VariableFeatures(object_filt)
)
```

Calcuating Leverage Score  
Attempting to cast layer counts to dgCMatrix  
Attempting to cast layer data to dgCMatrix

Hide

object\_filt

An object of class Seurat  
32750 features across 463329 samples within 2 assays  
Active assay: sketch (16375 features, 2000 variable features)  
2 layers present: counts, data  
1 other assay present: Spatial.008um  
1 spatial field of view present: slice1.008um

Hide

```
# Observe the leverage score has been added as a column to the metadata of our object.
head(object_filt@meta.data)
```

	orig.ident	nCount_Spatial.008um	nFeature_Spatial.008um	percent.mt
	<chr>	<dbl>	<int>	<dbl>
s_008um_00269_00526-1	s	1479	1023	5.814740
s_008um_00260_00253-1	s	971	719	7.106076
s_008um_00433_00599-1	s	527	214	1.328273
s_008um_00266_00304-1	s	749	547	6.275033
s_008um_00359_00037-1	s	999	721	8.608609
s_008um_00469_00254-1	s	606	470	10.231023

6 rows | 1-5 of 5 columns

Hide

```
# Perform clustering workflow
object_filt <- FindVariableFeatures(object_filt)
```

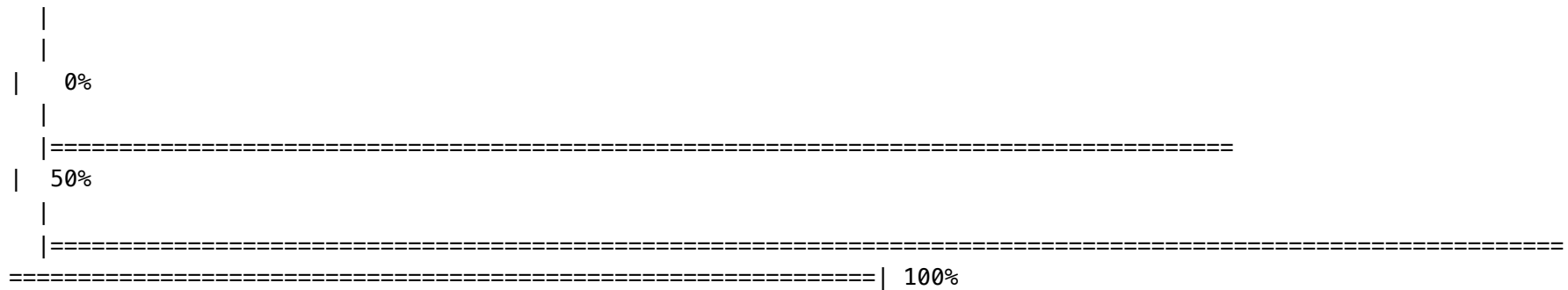
Finding variable features for layer counts  
Calculating gene variances  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Calculating feature variances of standardized and clipped values  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Hide

```
object_filt <- ScaleData(object_filt)
```



Centering and scaling data matrix



Hide

```
object_filt <- RunPCA(object_filt, assay = "sketch", reduction.name = "pca.sketch")
```

```
PC_ 1
Positive: AP0D, PIP, CLU, TSKU, ABCC11, PNMT, LTF, SULT1C3, MAB21L4, MPV17L
          S100A9, TAT, FABP7, PPP1R1B, UGT2B28, ANKRD30A, SCD, AQP3, ELF3, KRT8
          ZNF652, ARFGEF3, S100A7A, AR, TACSTD2, CLDN4, PEG10, ABCA12, CLDN3, IRX3
Negative: SPARC, COL1A1, COL3A1, COL1A2, IGKC, IGHG1, IGFBP7, COL4A1, COL6A2, FN1
          COL4A2, BGN, A2M, TIMP1, LUM, COL6A1, TAGLN, AEBP1, CALD1, APOE
          COL18A1, MMP2, COL6A3, ACTA2, DCN, PRSS23, THY1, COL5A2, COL5A1, PLVAP

PC_ 2
Positive: LYZ, APOE, IGKC, IGHG1, C1QC, C1QA, CD68, FTL, C3, C1QB
          CTSB, CTSZ, CTSS, GPNMB, LAPTM5, CTSD, IGHA1, TYROBP, LUM, SPI1
          MZB1, LSP1, MS4A6A, DCN, CYBB, MPEG1, CD4, LCP1, TRAC, IGHG3
Negative: PLVAP, MCAM, COL18A1, COL4A1, AQP1, COL4A2, VWF, CD34, ENG, PODXL
          RGS5, EGFL7, IGFBP7, CALCRL, CDH5, ESM1, PLPP1, ESAM, SLC9A3R2, KDR
          NOTCH3, CD93, RAMP2, SPARCL1, SEMA3F, EPAS1, OLFML2A, DLL4, A2M, EXOC3L2

PC_ 3
Positive: IGKC, IGHG1, IGHA1, IGLC1, IGHG3, MZB1, DERL3, IGHM, IGHD, TENT5C
          PIM2, TXNDC5, JCHAIN, POU2AF1, CD79A, FCRL5, ITM2C, SSR4, TNFRSF17, SEL1L3
          TXNDC11, CD27, DPEP1, LAX1, BMP6, BTG2, P2RX1, F13A1, CCR2, CPA3
Negative: CTSB, LYZ, APOE, CTSD, CXCL10, CTSZ, CXCL9, CD68, APOC1, LAPTM5
          LGMN, CXCL11, CTSL, GRN, LCP1, GPNMB, ACP5, S100A9, CTSS, FTL
          GBP1, IL4I1, TYROBP, LHFPL2, C3, SPI1, CLU, LIPA, TOP2A, SLC15A3

PC_ 4
Positive: LYZ, CD68, LAPTM5, LCP1, APOE, ENG, ITGAX, PLVAP, VWF, PLEK
          A2M, CTSZ, CTSS, CTSD, CALCRL, CD34, PECAM1, LSP1, EGFL7, SPI1
          CD4, RAMP2, CYBB, TNFAIP2, C1QC, CD83, IL4I1, MPEG1, CDH5, TRAC
Negative: AEBP1, COL1A2, CCN2, COL12A1, COMP, COL1A1, LUM, COL5A1, COL11A1, THBS2
          COL6A3, COL3A1, COL5A2, FN1, SFRP2, THBS1, FBN1, DCN, LRRC15, CTHRC1
          VCAN, POSTN, COL8A1, SULF1, C1S, EPYC, MXRA5, MMP11, BGN, C1R

PC_ 5
Positive: TOP2A, CDK1, TPX2, NUSAP1, ASPM, ANLN, HIST1H1B, HMGB2, MYBL2, MKI67
          KIFC1, TROAP, CIT, FAM83D, HIST1H1D, SPC24, ECT2, CENPF, CCNB1, IGKC
          FOXM1, UBE2C, CCNA2, CCNB2, IGHG1, CDCA3, PLK1, PRC1, SPAG5, GPM2
Negative: SULT1C3, SLC26A3, AP0D, TAT, TSKU, PIP, ACSM1, ECHDC2, MPV17L, FABP7
          ACSL3, ATP13A4, CYP1B1, ZBTB16, SLPI, ABCC11, AQP3, UGT2B28, GPCPD1, KYN
          HMGS2, THRSP, SORD, FM05, ZNF652, UGT2B11, MYCBP2, ABCA12, IRX3, SOD2
```

Hide

```
object_filt <- FindNeighbors(object_filt, assay = "sketch", reduction = "pca.sketch", dims = 1:50)
```

Computing nearest neighbor graph  
Computing SNN

Hide

```
# Find Clusters with Leiden algorithm
object_filt <- FindClusters(object_filt, cluster.name = "seurat_cluster.sketch", resolution = 0.65, algorithm = 4)
```

Warning: `random.seed` must be greater than 0 for leiden clustering, resetting `random.seed` to 1.3 singletons identified. 12 final clusters.

Hide

```
# Create a UMAP using the principal components as input
object_filt <- RunUMAP(object_filt, reduction = "pca.sketch", reduction.name = "umap.sketch", return.model = T, dims = 1:50)
```



Warning: The default method for RunUMAP has changed from calling Python UMAP via reticulate to the R-native UWOT using the cosine metric  
 To use Python UMAP via reticulate, set `umap.method` to 'umap-learn' and `metric` to 'correlation'

This message will be shown once per sessionUMAP will return its model

20:41:53 UMAP embedding parameters a = 0.9922 b = 1.112  
 20:41:53 Read 50000 rows and found 50 numeric columns  
 20:41:53 Using Annoy for neighbor search, n\_neighbors = 30  
 20:41:53 Building Annoy index with metric = cosine, n\_trees = 50  
 0% 10 20 30 40 50 60 70 80 90 100%  
 [----|----|----|----|----|----|----|----|----|----|  
 \*\*\*\*\*|  
 20:41:59 Writing NN index file to temp file /tmp/Rtmpyu4MmB/file29a6c692c2a  
 20:41:59 Searching Annoy index using 1 thread, search\_k = 3000  
 20:42:16 Annoy recall = 100%  
 20:42:17 Commencing smooth kNN distance calibration using 1 thread with target n\_neighbors = 30  
 20:42:19 Initializing from normalized Laplacian + noise (using RSpectra)  
 20:42:21 Commencing optimization for 200 epochs, with 2452432 positive edges  
 20:42:21 Using rng type: pcg  
 Using method 'umap'  
 0% 10 20 30 40 50 60 70 80 90 100%  
 [----|----|----|----|----|----|----|----|----|----|  
 \*\*\*\*\*|  
 20:42:35 Optimization finished

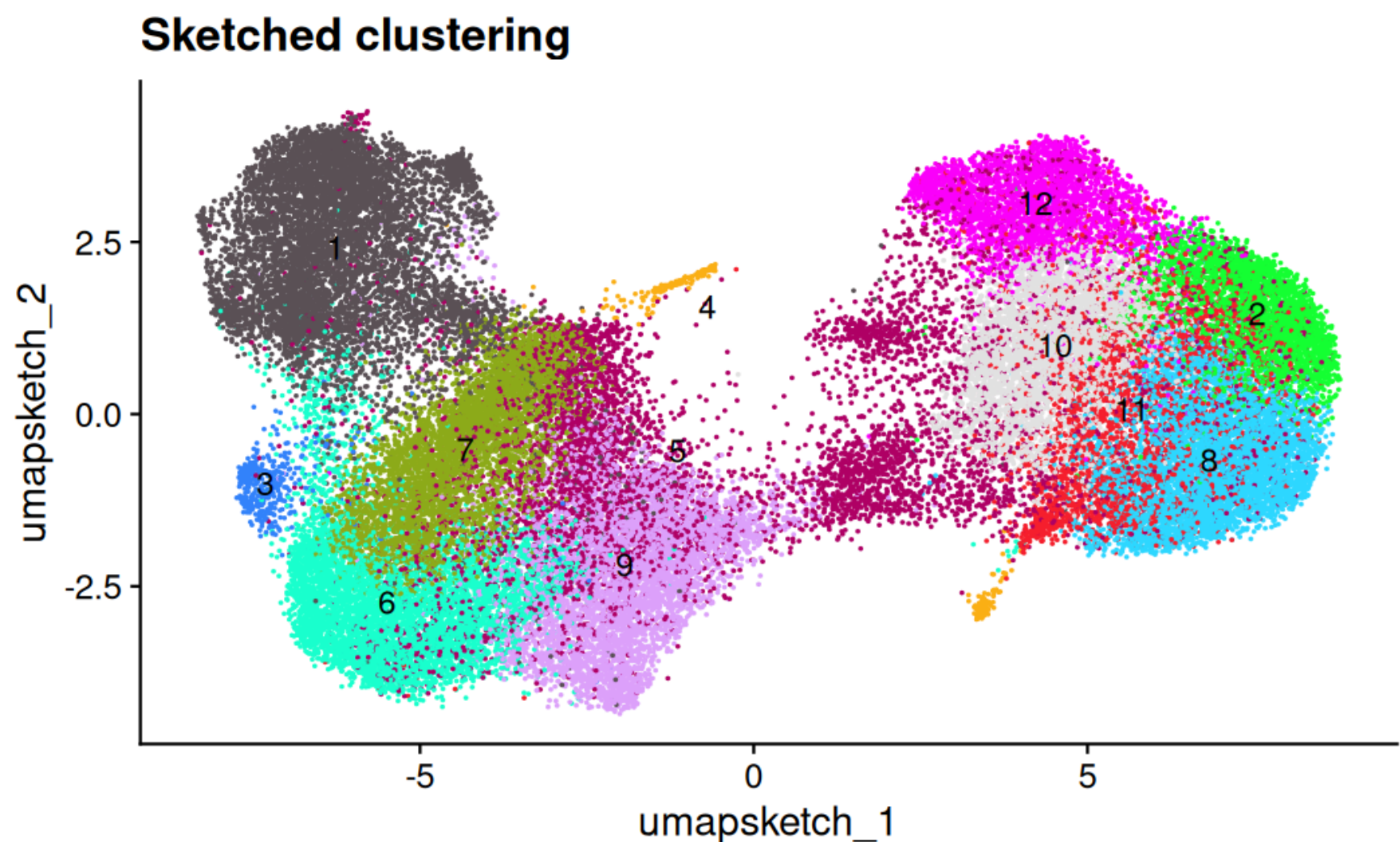
Hide

```
# Set color palette
color_pal <- Seurat::DiscretePalette(n = length(unique(object_filt$seurat_cluster.sketches)),
                                     palette = "polychrome")
names(color_pal) <- sort(unique(object_filt$seurat_cluster.sketches))

# Arrange so clusters get listed in numerical order
object_filt$seurat_cluster.sketches <- object_filt$seurat_cluster.sketches %>%
  as.numeric %>% as.factor()

Idents(object_filt) <- "seurat_cluster.sketches"

# Plot UMAP
DimPlot(object_filt, reduction = "umap.sketch", label = T, cols = color_pal) +
  ggtitle("Sketched clustering") +
  theme(legend.position = "none")
```



Hide

```
# Adjust MaxSize to run next step
options(future.globals.maxSize= 2000000000)

# Project the cluster labels, and dimensional reductions (PCA and UMAP) that we learned from the 50,000 sketched
cells
object_filt <- ProjectData(
  object = object_filt,
  assay = "Spatial.008um",
  full.reduction = "full.pca.sketch",
  sketched.assay = "sketch",
  sketched.reduction = "pca.sketch",
  umap.model = "umap.sketch",
  dims = 1:50,
  refdata = list(seurat_cluster.projected = "seurat_cluster.sketched")
)
```

```
full.pca.sketch is not in the object. Data from all cells will be projected to pca.sketch
Projecting cell embeddings
Finding sketch neighbors
Finding sketch weight matrix
0%   10   20   30   40   50   60   70   80   90  100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Transferring refdata from sketch
Projection to sketch umap
Running UMAP projection
20:46:09 Read 463329 rows
20:46:09 Processing block 1 of 1
20:46:09 Commencing smooth kNN distance calibration using 1 thread with target n_neighbors = 30
20:46:12 Initializing by weighted average of neighbor coordinates using 1 thread
20:46:14 Commencing optimization for 67 epochs, with 13899870 positive edges
Using method 'umap'
0%   10   20   30   40   50   60   70   80   90  100%
[----|----|----|----|----|----|----|----|----|----|
*****|
20:46:39 Finished
Warning: Keys should be one or more alphanumeric characters followed by an underscore, setting key from full.uma
p.sketch to fullumapsketch_
```

Hide

```
# Arrange so clusters get listed in numerical order
object_filt$seurat_cluster.projected <- object_filt$seurat_cluster.projected %>%
  as.numeric %>% as.factor()

object_filt
```

```
An object of class Seurat
32750 features across 463329 samples within 2 assays
Active assay: sketch (16375 features, 2000 variable features)
 3 layers present: counts, data, scale.data
 1 other assay present: Spatial.008um
 4 dimensional reductions calculated: pca.sketch, umap.sketch, full.pca.sketch, full.umap.sketch
 1 spatial field of view present: slice1.008um
```

Hide

```
head(object_filt@meta.data)
```

	orig.ident <chr>	nCount_Spatial.008um <dbl>	nFeature_Spatial.008um <int>	percent.mt <dbl>
s_008um_00269_00526-1	s	1479	1023	5.814740
s_008um_00260_00253-1	s	971	719	7.106076
s_008um_00433_00599-1	s	527	214	1.328273
s_008um_00266_00304-1	s	749	547	6.275033
s_008um_00359_00037-1	s	999	721	8.608609
s_008um_00469_00254-1	s	606	470	10.231023

6 rows | 1-5 of 9 columns

Hide

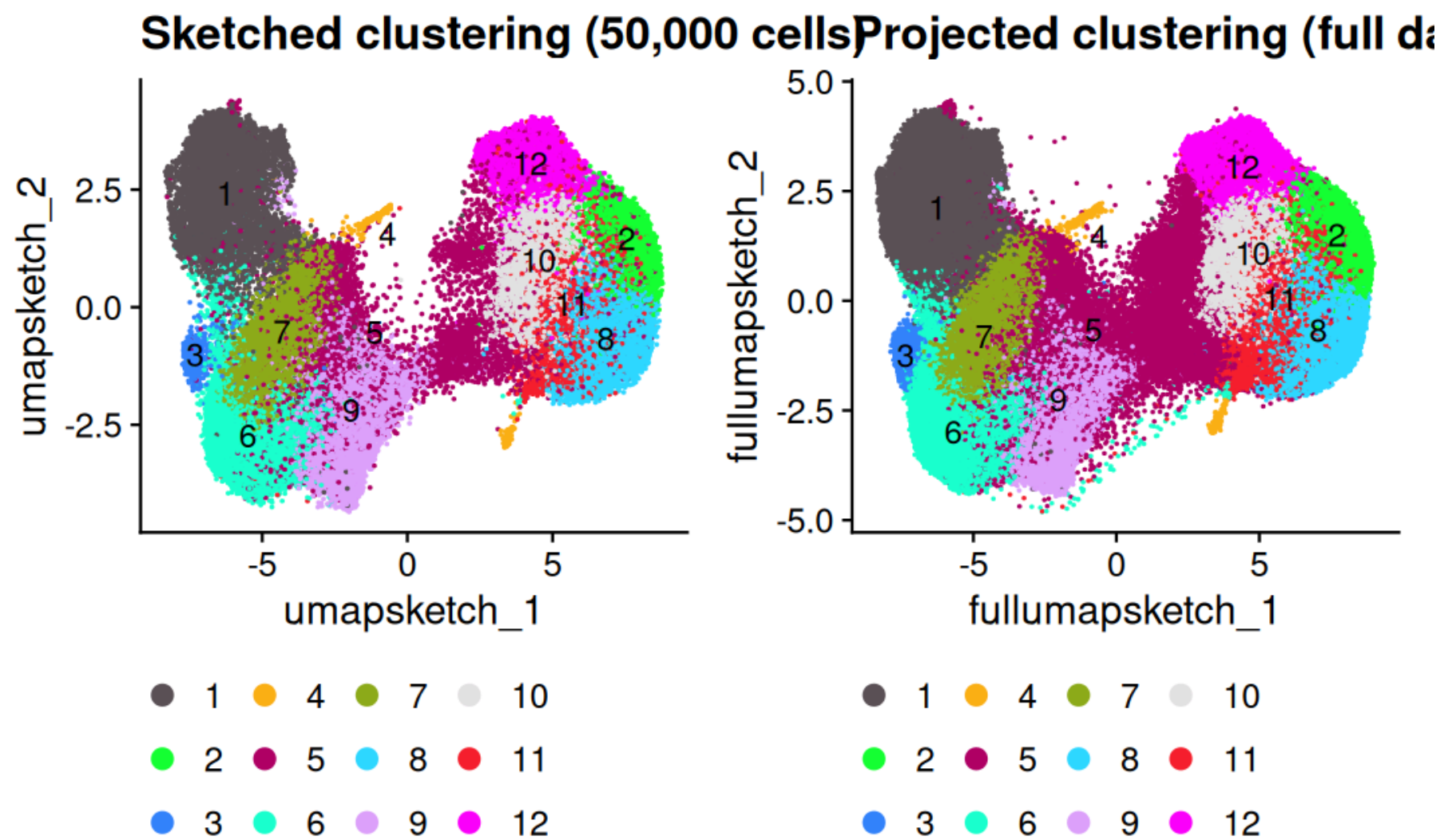
```
# Visualize the clustering results for the sketched cells, as well as the projected clustering results for the full dataset
DefaultAssay(object_filt) <- "sketch"
Idents(object_filt) <- "seurat_cluster.sketch"
p1 <- DimPlot(object_filt, reduction = "umap.sketch", label = T, raster = F, cols = color_pal) + ggtitle("Sketched clustering (50,000 cells)") + theme(legend.position = "bottom")

# switch to full dataset
DefaultAssay(object_filt) <- "Spatial.008um"
Idents(object_filt) <- "seurat_cluster.projected"
p2 <- DimPlot(object_filt, reduction = "full.umap.sketch", label = T, raster = F, cols = color_pal) + ggtitle("Projected clustering (full dataset)") + theme(legend.position = "bottom")

p_combinado <- p1 | p2
p_combinado
ggsave("p1.png", plot = p1, width = 8, height = 8, dpi = 300)
```

Hide

```
ggsave("p2.png", plot = p2, width = 8, height = 8, dpi = 300)
ggsave("p_combinado.png", plot = p_combinado, width = 12, height = 6, dpi = 300)
```



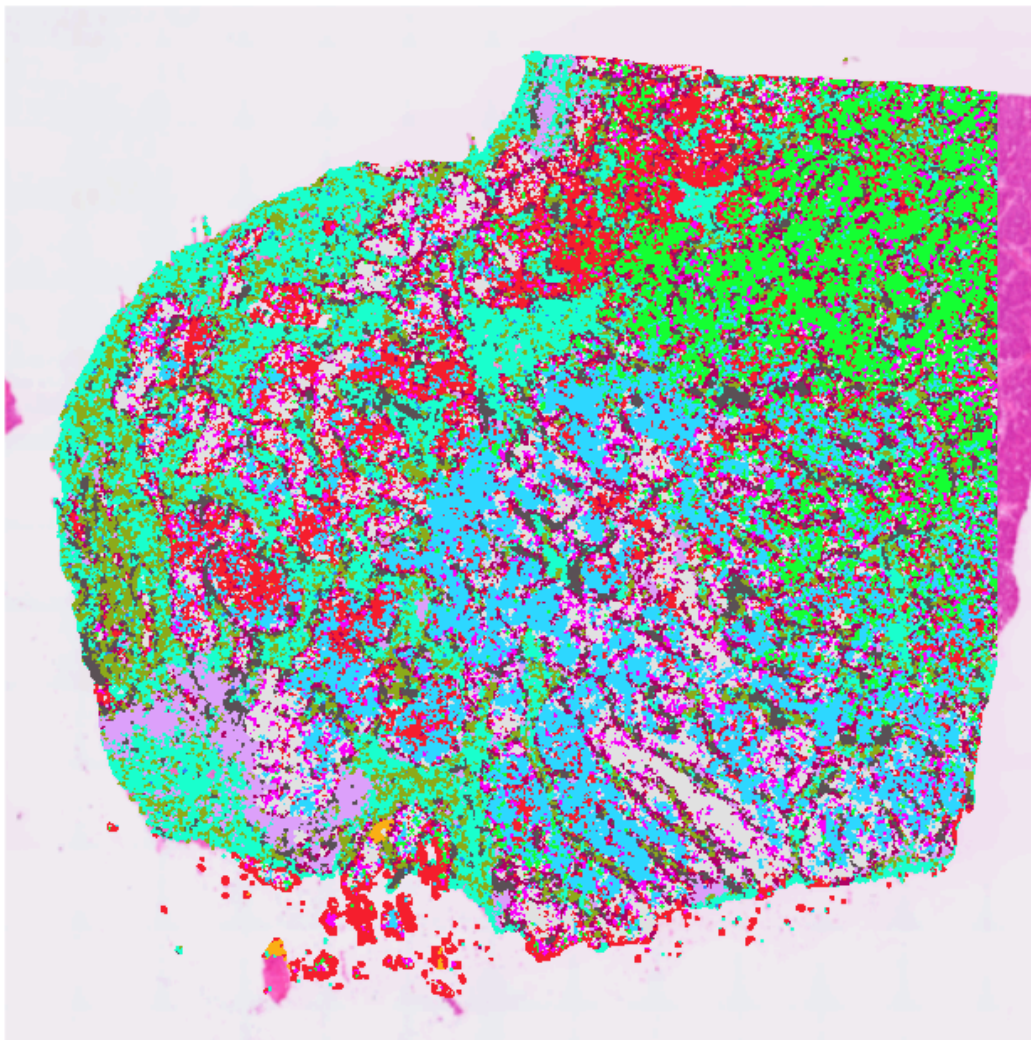
Hide

```
# Visualize the unsupervised clusters based on their spatial location.
image_seurat_clusters <- SpatialDimPlot(object_filt,
                                         group.by = 'seurat_cluster.projected',
                                         pt.size.factor = 6, cols = color_pal) +
  guides(fill=guide_legend(ncol=2))

image_seurat_clusters

ggsave("clusters_image_0.65.png", plot = image_seurat_clusters, width = 8, height = 6, dpi = 300)
```





seurat\_cluster.projected

- |     |      |
|-----|------|
| • 1 | • 7  |
| • 2 | • 8  |
| • 3 | • 9  |
| • 4 | • 10 |
| • 5 | • 11 |
| • 6 | • 12 |

Hide

```
# Find and visualize the top gene expression markers for each cluster
# Create downsampled object to make visualization easier
Idents(object_filt) <- "seurat_cluster.projected"
object_subset <- subset(object_filt, cells = Cells(object_filt[["Spatial.008um"]]), downsample = 1000)
```

Warning: Not validating Centroids objectsWarning: Not validating Centroids objectsWarning: Not validating FOV objectsWarning: Not validating FOV objectsWarning: Not validating FOV objectsWarning: Not validating FOV objectsWarning: Not validating FOV objectsWarning: Not validating Seurat objects

Hide

```
# Order clusters by similarity
DefaultAssay(object_subset) <- "Spatial.008um"
Idents(object_subset) <- "seurat_cluster.projected"
object_subset <- BuildClusterTree(object_subset, assay = "Spatial.008um", reduction = "full.pca.sketch", reorder = T)
```

Reordering identity classes and rebuilding tree

Hide

```
markers <- FindAllMarkers(object_subset, assay = "Spatial.008um", only.pos = TRUE)
```

Calculating cluster 1  
Warning: The `slot` argument of `GetAssayData()` is deprecated as of SeuratObject 5.0.0.  
Please use the `layer` argument instead. For a (much!) faster implementation of the Wilcoxon Rank Sum Test, (default method for FindMarkers) please install the presto package

```
install.packages('devtools')
devtools::install_github('immunogenomics/presto')
```

After installation of presto, Seurat will automatically use the more efficient implementation (no further action necessary).  
This message will be shown once per session

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Calculating cluster 9

	0 % ~calculating
+	1 % ~51s
+	2 % ~49s
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++++	7 % ~48s
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Calculating cluster 5

	0 % ~calculating
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Calculating cluster 4

	0 % ~calculating
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++	4 % ~01m 01s
+++	5 % ~01m 00s
+++	6 % ~60s
++++	7 % ~59s
++++	8 % ~59s
+++++	9 % ~58s
+++++	10% ~57s
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Calculating cluster 2

	0 % ~calculating
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++++++	100% elapsed=01m 01s

Calculating cluster 8



	0 % ~calculating
+	1 % ~01m 04s
+	2 % ~01m 02s
++	3 % ~01m 02s
++	4 % ~01m 01s
+++	5 % ~01m 00s
+++	6 % ~59s
++++	7 % ~59s
++++	8 % ~59s
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Calculating cluster 11

	0 % ~calculating
+	1 % ~59s
+	2 % ~59s
++	3 % ~58s
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+++	6 % ~57s
++++	7 % ~57s
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+++++	9 % ~56s
+++++	10% ~55s
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++++++	54% ~28s
++++++	55% ~28s
++++++	56% ~27s
++++++	57% ~27s
++++++	58% ~26s
++++++	59% ~25s
++++++	60% ~25s
++++++	61% ~24s
++++++	62% ~23s
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++++++	64% ~22s
++++++	65% ~22s
++++++	66% ~21s
++++++	67% ~20s
++++++	68% ~20s
++++++	69% ~19s
++++++	70% ~19s
++++++	71% ~18s
++++++	72% ~17s
++++++	73% ~17s
++++++	74% ~16s
++++++	75% ~15s
++++++	76% ~15s
++++++	77% ~14s
++++++	78% ~14s

++++++	79% ~13s
++++++	80% ~12s
++++++	81% ~12s
++++++	82% ~11s
++++++	83% ~10s
++++++	84% ~10s
++++++	85% ~09s
++++++	86% ~09s
++++++	87% ~08s
++++++	88% ~07s
++++++	89% ~07s
++++++	90% ~06s
++++++	91% ~06s
++++++	92% ~05s
++++++	93% ~04s
++++++	94% ~04s
++++++	95% ~03s
++++++	96% ~02s
++++++	97% ~02s
++++++	98% ~01s
++++++	99% ~01s
++++++	100% elapsed=01m 01s

Calculating cluster 10

	0 % ~calculating
+	1 % ~01m 14s
++	2 % ~01m 14s
++	3 % ~01m 14s
+++	4 % ~01m 13s
+++	5 % ~01m 12s
++++	6 % ~01m 11s
++++	7 % ~01m 11s
+++++	8 % ~01m 11s
+++++	9 % ~01m 10s
++++++	10% ~01m 09s
++++++	11% ~01m 08s
++++++	12% ~01m 07s
++++++	13% ~01m 06s
+++++++	14% ~01m 06s
+++++++	15% ~01m 05s
+++++++	16% ~01m 04s
+++++++	17% ~01m 03s
+++++++	18% ~01m 02s
+++++++	19% ~01m 02s
+++++++	20% ~01m 01s
+++++++	21% ~01m 00s
+++++++	22% ~59s
+++++++	23% ~58s
+++++++	24% ~58s
+++++++	25% ~57s
+++++++	26% ~56s
+++++++	27% ~55s
+++++++	28% ~55s
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+++++++	31% ~53s
+++++++	32% ~52s
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+++++++	37% ~48s
+++++++	38% ~47s
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+++++++	41% ~45s
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+++++++	46% ~41s
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+++++++	56% ~34s
+++++++	57% ~33s
+++++++	58% ~32s
+++++++	59% ~32s
+++++++	60% ~31s
+++++++	61% ~30s
+++++++	62% ~29s
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+++++++	66% ~26s
+++++++	67% ~25s
+++++++	68% ~25s
+++++++	69% ~24s
+++++++	70% ~23s
+++++++	71% ~22s
+++++++	72% ~22s
+++++++	73% ~21s
+++++++	74% ~20s
+++++++	75% ~19s
+++++++	76% ~19s
+++++++	77% ~18s
+++++++	78% ~17s
+++++++	79% ~16s

++++++	80% ~15s
++++++	81% ~15s
++++++	82% ~14s
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++++++	86% ~11s
++++++	87% ~10s
++++++	88% ~09s
++++++	89% ~08s
++++++	90% ~08s
++++++	91% ~07s
++++++	92% ~06s
++++++	93% ~05s
++++++	94% ~05s
++++++	95% ~04s
++++++	96% ~03s
++++++	97% ~02s
++++++	98% ~02s
++++++	99% ~01s
++++++	100% elapsed=01m 16s

Calculating cluster 12

	0 % ~calculating
+	1 % ~01m 14s
+	2 % ~01m 14s
++	3 % ~01m 13s
++	4 % ~01m 12s
+++	5 % ~01m 11s
+++	6 % ~01m 11s
++++	7 % ~01m 10s
++++	8 % ~01m 10s
+++++	9 % ~01m 09s
+++++	10% ~01m 08s
++++++	11% ~01m 08s
++++++	12% ~01m 07s
++++++	13% ~01m 06s
++++++	14% ~01m 05s
++++++	15% ~01m 04s
++++++	16% ~01m 04s
++++++	17% ~01m 03s
++++++	18% ~01m 02s
++++++	19% ~01m 02s
++++++	20% ~01m 01s
++++++	21% ~01m 00s
++++++	22% ~59s
++++++	23% ~58s
++++++	24% ~58s
++++++	25% ~57s
++++++	26% ~56s
++++++	27% ~55s
++++++	28% ~55s
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++++++	30% ~53s
++++++	31% ~52s
++++++	32% ~52s
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++++++	36% ~49s
++++++	37% ~48s
++++++	38% ~47s
++++++	39% ~46s
++++++	40% ~45s
++++++	41% ~45s
++++++	42% ~44s
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++++++	67% ~25s
++++++	68% ~24s
++++++	69% ~24s
++++++	70% ~23s
++++++	71% ~22s
++++++	72% ~21s
++++++	73% ~21s
++++++	74% ~20s
++++++	75% ~19s
++++++	76% ~18s
++++++	77% ~17s
++++++	78% ~17s



++++++	79% ~16s
++++++	80% ~15s
++++++	81% ~14s
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++++++	83% ~13s
++++++	84% ~12s
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++++++	89% ~08s
++++++	90% ~08s
++++++	91% ~07s
++++++	92% ~06s
++++++	93% ~05s
++++++	94% ~05s
++++++	95% ~04s
++++++	96% ~03s
++++++	97% ~02s
++++++	98% ~02s
++++++	99% ~01s
++++++	100% elapsed=01m 16s

Calculating cluster 7

	0 % ~calculating
+	1 % ~20s
++	2 % ~19s
++	3 % ~19s
+++	4 % ~18s
+++	5 % ~18s
++++	6 % ~18s
++++	7 % ~18s
+++++	8 % ~18s
+++++	9 % ~17s
++++++	10% ~17s
++++++	11% ~17s
+++++++	12% ~17s
+++++++	13% ~17s
++++++++	14% ~17s
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++++++++	18% ~16s
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++++++	94% ~01s
++++++	95% ~01s
++++++	96% ~01s
++++++	97% ~01s
++++++	98% ~00s
++++++	99% ~00s
++++++	100% elapsed=19s

Calculating cluster 3

	0 % ~calculating
+	1 % ~18s
++	2 % ~18s
++	3 % ~18s
+++	4 % ~18s
+++	5 % ~18s
++++	6 % ~17s
++++	7 % ~17s
+++++	8 % ~17s
+++++	9 % ~17s
++++++	10% ~17s
++++++	11% ~16s
++++++	12% ~16s
++++++	13% ~16s
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++++++	91% ~02s
++++++	92% ~01s
++++++	93% ~01s
++++++	94% ~01s
++++++	95% ~01s
++++++	96% ~01s
++++++	97% ~01s
++++++	98% ~00s
++++++	99% ~00s
++++++	100% elapsed=18s

Calculating cluster 6

	0 % ~calculating
+	1 % ~15s
++	2 % ~15s
++	3 % ~15s
+++	4 % ~14s
+++	5 % ~14s
++++	6 % ~14s
++++	7 % ~14s
+++++	8 % ~14s
+++++	9 % ~13s
++++++	10% ~13s
++++++	11% ~13s
++++++	12% ~13s
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+++++++	41% ~09s
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+++++++	71% ~04s
+++++++	72% ~04s
+++++++	73% ~04s
+++++++	74% ~04s
+++++++	75% ~04s
+++++++	76% ~04s
+++++++	77% ~03s
+++++++	78% ~03s
+++++++	79% ~03s

```
| ++++++ | 80% ~03s
| ++++++ | 81% ~03s
| ++++++ | 82% ~03s
| ++++++ | 83% ~03s
| ++++++ | 84% ~02s
| ++++++ | 85% ~02s
| ++++++ | 86% ~02s
| ++++++ | 87% ~02s
| ++++++ | 88% ~02s
| ++++++ | 89% ~02s
| ++++++ | 90% ~02s
| ++++++ | 91% ~01s
| ++++++ | 92% ~01s
| ++++++ | 93% ~01s
| ++++++ | 94% ~01s
| ++++++ | 95% ~01s
| ++++++ | 96% ~01s
| ++++++ | 97% ~00s
| ++++++ | 98% ~00s
| ++++++ | 99% ~00s
| ++++++ | 100% elapsed=15s
```

Hide

```
# Add entrez column with entrez Ids of genes
markers$entrez <- mapIds(org.Hs.eg.db,
                        keys = markers$gene,
                        column = "ENTREZID",
                        keytype = "SYMBOL",
                        multiVals = "first")
```

'select()' returned 1:1 mapping between keys and columns

Hide

```
# Select the 15 best ranked genes
markers %>%
  group_by(cluster) %>%
  dplyr::filter(avg_log2FC >= 1 , p_val_adj <= 0.05) %>%
  slice_head(n = 15) %>%
  ungroup() -> top15
```

Hide

```
# Manually annotating clusters using top 15 DEG from each cluster with CellMarkers BD, using tool CellMarker_anno
tation (http://www.bio-bigdata.center/CellMarker\_annotation.jsp)
```

Hide

```
markers %>%
  group_by(cluster) %>%
  dplyr::filter(avg_log2FC >= 1 , p_val_adj <= 0.05) %>%
  slice_head(n = 10) %>%
  ungroup() -> top10

object_subset <- ScaleData(object_subset, assay = "Spatial.008um", features = top10$gene)
```

Centering and scaling data matrix

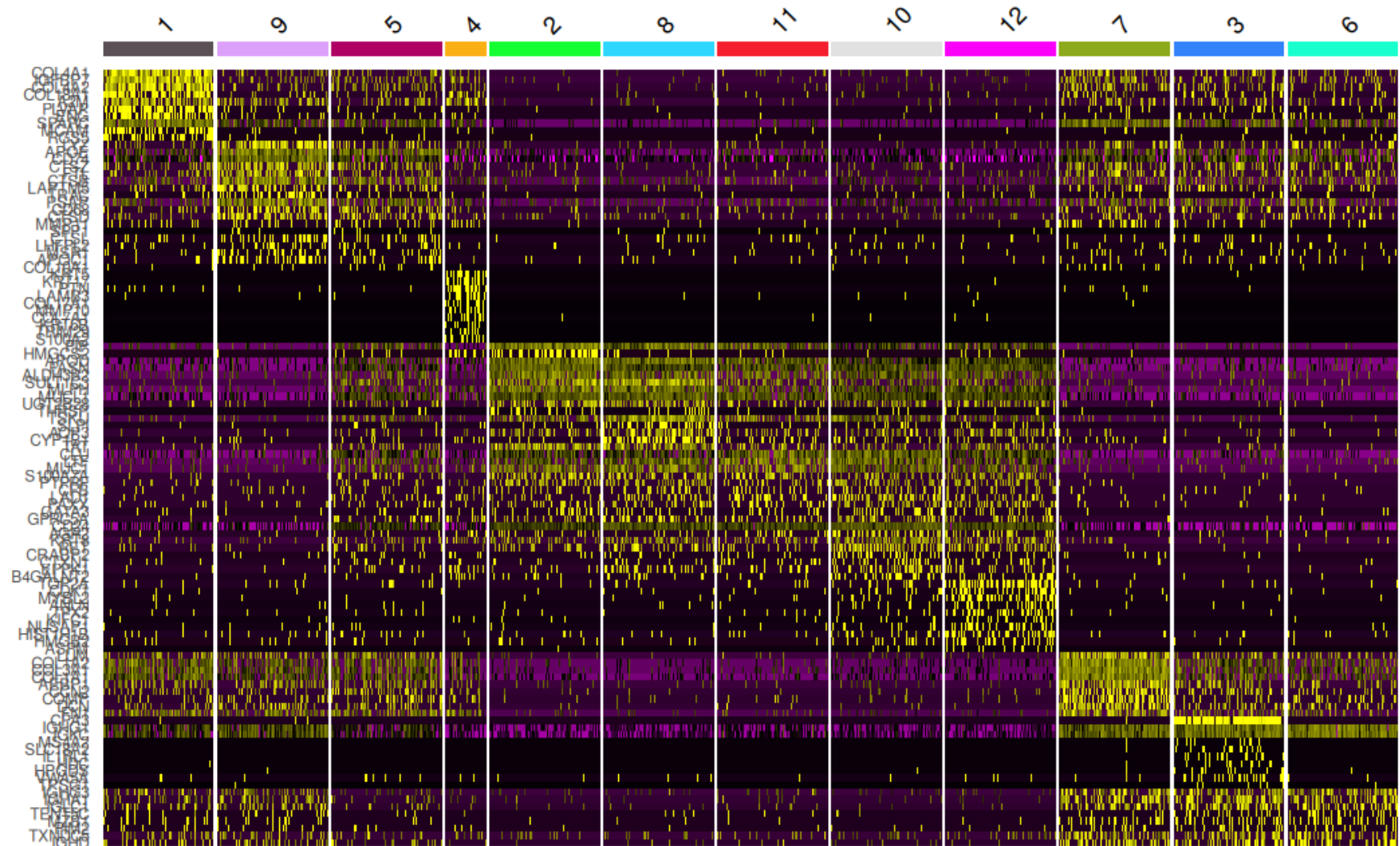
```
|
|
| 0%
|
|=====
=====| 100%
Warning: Different features in new layer data than already exists for scale.data
```

Hide

```
heatmap <- DoHeatmap(object_subset, assay = "Spatial.008um", features = top10$gene, size = 3, group.colors = colo
r_pal) + theme(axis.text = element_text(size = 5.5), legend.position = "none")
heatmap

ggsave("heatmap.png", plot=heatmap, width=16, height=10, dpi =600)
```

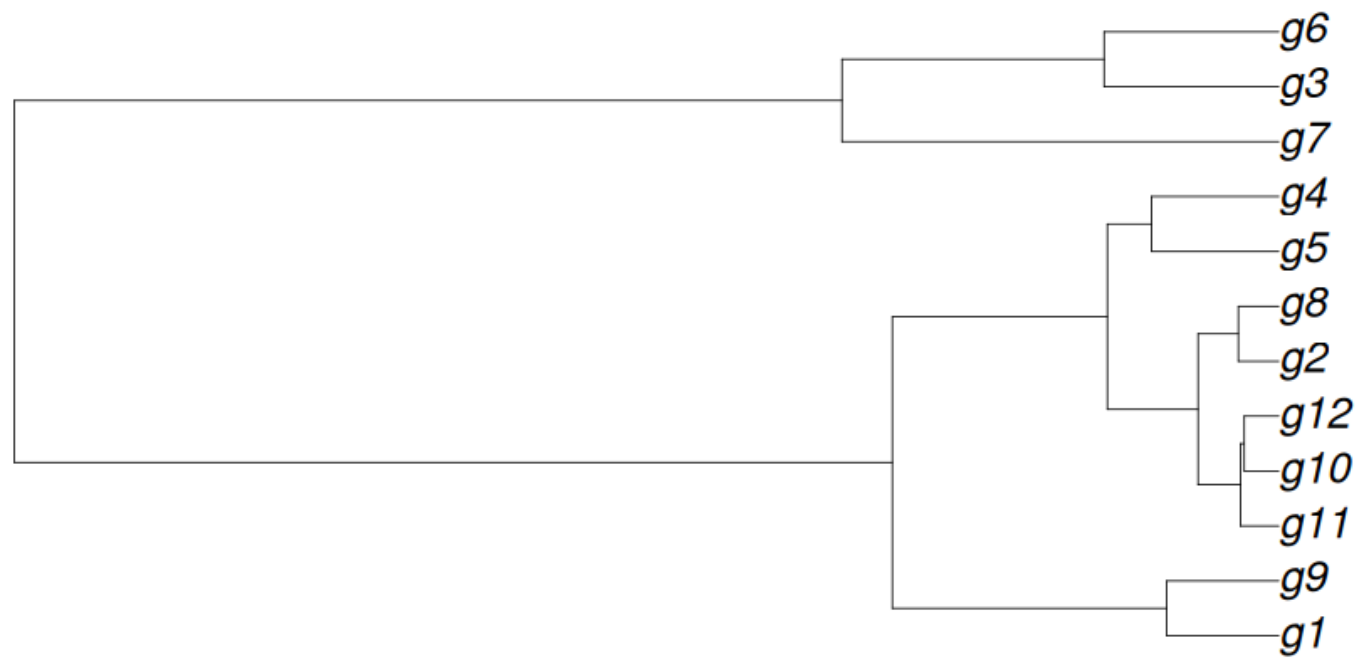




Hide

```
# Build Tree only based on the top 10 genes per cluster
object_subset10 = BuildClusterTree(object_subset, features = top10$gene, reorder.numeric = T)

# Plot dendrogram
data.tree <- Tool(object = object_subset10, slot = "BuildClusterTree")
ape::plot.phylo(x = data.tree, direction = "rightwards", edge.width=0.5)
```



Hide

```
# Assign cell types to metadata
clusters = object_filt@meta.data$seurat_cluster.projected

levels(clusters)
```

```
[1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12"
```

Hide

```
levels(clusters) = c("1.Célula madre hematopoyética/Pericito","2.Célula madre cancerosa","3.Mastocito/Célula plasmática", "4.Célula basal/Célula epitelial basal","5.Panmacrófago/Macrófago M1","6.Célula plasmática/Célula B","7.Miofibroblasto/Pericito","8.Célula progenitora epitelial/Célula B reguladora B10","9.Panmacrófago/Fibroblasto asoc. a cáncer","10.Célula progenitora epitelial/Fibroblasto asoc. a cáncer","11.Fibroblasto asoc. a cáncer/Célula epitelial luminal","12.Célula progenitora luminal")

object_filt@meta.data$seurat_cluster.projected = clusters

# Set color palette
color_pal <- Seurat::DiscretePalette(n = length(unique(object_filt$seurat_cluster.projected)),
                                     palette = "polychrome")
names(color_pal) <- sort(unique(object_filt$seurat_cluster.projected))
```

Hide

```
# Review the levels
levels(Ids(object_filt))
```

[1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12"

Hide

```
head(object_filt@meta.data)
```

	orig.ident <chr>	nCount_Spatial.008um <dbl>	nFeature_Spatial.008um <int>	percent.mt <dbl>
s_008um_00269_00526-1	s	1479	1023	5.814740
s_008um_00260_00253-1	s	971	719	7.106076
s_008um_00433_00599-1	s	527	214	1.328273
s_008um_00266_00304-1	s	749	547	6.275033
s_008um_00359_00037-1	s	999	721	8.608609
s_008um_00469_00254-1	s	606	470	10.231023

6 rows | 1-5 of 9 columns

Hide

```
levels(object_filt@meta.data$seurat_cluster.projected)
```

[1] "1.Célula madre hematopoyética/Pericito" "2.Célula madre cancerosa"

[3] "3.Mastocito/Célula plasmática" "4.Célula basal/Célula epitelial basal"

[5] "5.Panmacrófago/Macrófago M1" "6.Célula plasmática/Célula B"

[7] "7.Miofibroblasto/Pericito" "8.Célula progenitora epitelial/Célula B reguladora B10"

[9] "9.Panmacrófago/Fibroblasto asoc. a cáncer" "10.Célula progenitora epitelial/Fibroblasto asoc. a cáncer"

[11] "11.Fibroblasto asoc. a cáncer/Célula epitelial luminal" "12.Célula progenitora luminal"

Hide

```
# Assign cell types to object
levels(Ids(object_filt))
```

[1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12"

Hide

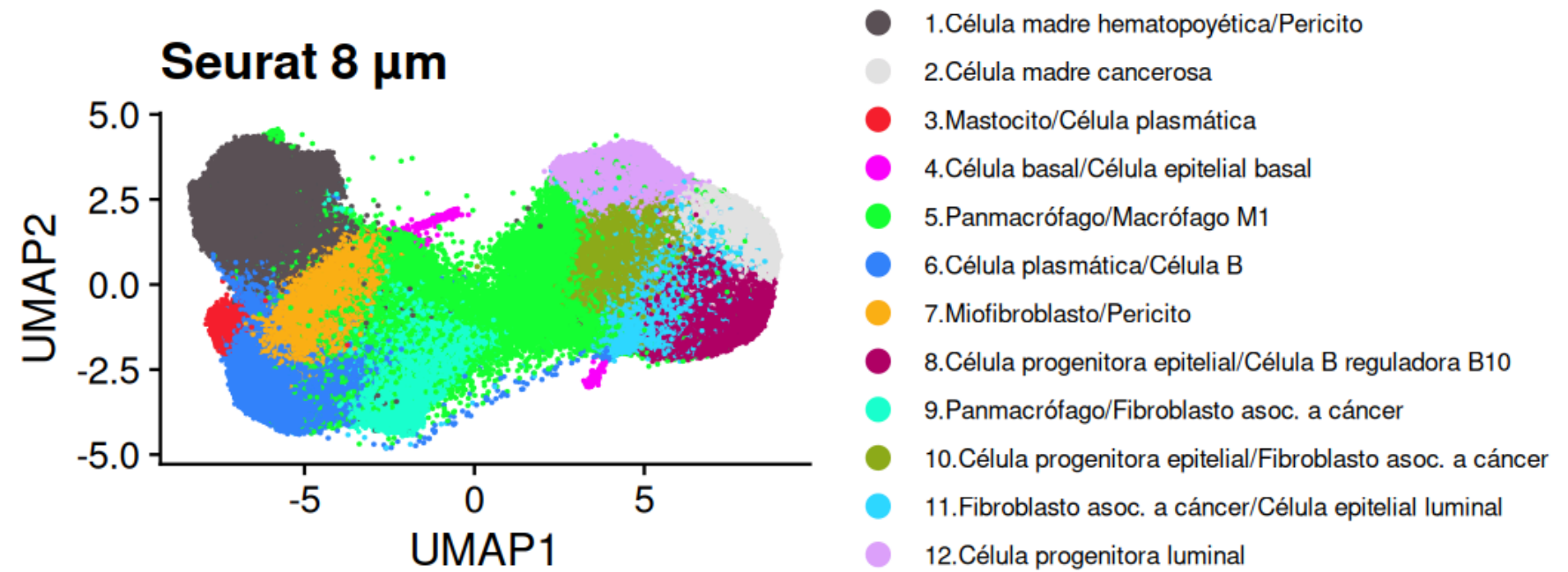
```
# Create new cluster names with cell types
new_cluster_names = c(
  "1" = "1.Célula madre hematopoyética/Pericito",
  "2" = "2.Célula madre cancerosa",
  "3" = "3.Mastocito/Célula plasmática",
  "4" = "4.Célula basal/Célula epitelial basal",
  "5" = "5.Panmacrófago/Macrófago M1",
  "6" = "6.Célula plasmática/Célula B",
  "7" = "7.Miofibroblasto/Pericito",
  "8" = "8.Célula progenitora epitelial/Célula B reguladora B10",
  "9" = "9.Panmacrófago/Fibroblasto asoc. a cáncer",
  "10" = "10.Célula progenitora epitelial/Fibroblasto asoc. a cáncer",
  "11" = "11.Fibroblasto asoc. a cáncer/Célula epitelial luminal",
  "12" = "12.Célula progenitora luminal"
)

# Assign cell types to clusters
names(new_cluster_names) = levels(object_filt)
object_filt = RenameIdents(object_filt, new_cluster_names)
levels(Idents(object_filt))
```

[1] "1.Célula madre hematopoyética/Pericito"	"2.Célula madre cancerosa"
[3] "3.Mastocito/Célula plasmática"	"4.Célula basal/Célula epitelial basal"
[5] "5.Panmacrófago/Macrófago M1"	"6.Célula plasmática/Célula B"
[7] "7.Miofibroblasto/Pericito"	"8.Célula progenitora epitelial/Célula B regula
dora B10"	
[9] "9.Panmacrófago/Fibroblasto asoc. a cáncer"	"10.Célula progenitora epitelial/Fibroblasto as
oc. a cáncer"	
[11] "11.Fibroblasto asoc. a cáncer/Célula epitelial luminal"	"12.Célula progenitora luminal"

Hide

```
# Plot UMAP
umap_cells = DimPlot(object_filt, reduction = "full.umap.sketch", label = TRUE, raster=F, pt.size = 0.02, label.s
size = 0, cols = color_pal)
umap_cells + coord_fixed(ratio = 1) +
  ggtitle("Seurat 8 µm") +
  xlab("UMAP1")+
  ylab("UMAP2")+
  theme(legend.text = element_text(size=8))
```

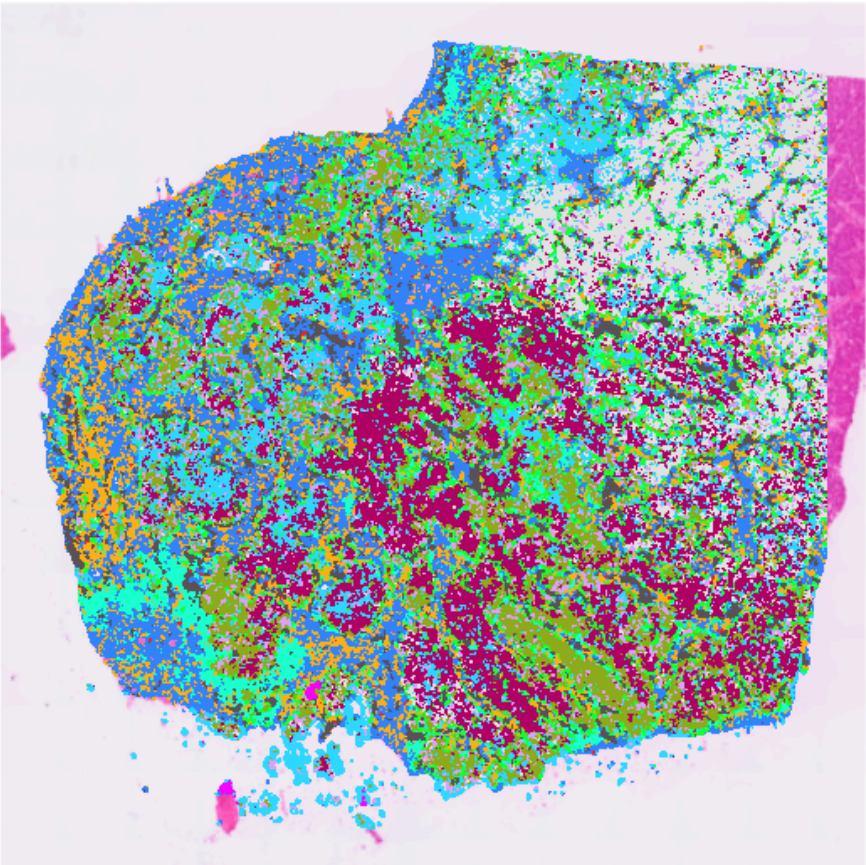


Hide

```
# Visualize the unsupervised clusters based on their spatial location.
image_seurat_clusters2 <- SpatialDimPlot(object_filt,
                                     group.by = 'seurat_cluster.projected',
                                     pt.size.factor = 6, cols = color_pal)

image_seurat_clusters2 + ggtitle("Seurat 8 μm") +
  theme(legend.title = element_blank(), legend.text = element_text(size=8))
```

Seurat 8 μm



- 1.Célula madre hematopoyética/Pericito
- 2.Célula madre cancerosa
- 3.Mastocito/Célula plasmática
- 4.Célula basal/Célula epitelial basal
- 5.Panmacrófago/Macrófago M1
- 6.Célula plasmática/Célula B
- 7.Miofibroblasto/Pericito
- 8.Célula progenitora epitelial/Célula B reguladora B10
- 9.Panmacrófago/Fibroblasto asoc. a cáncer
- 10.Célula progenitora epitelial/Fibroblasto asoc. a cáncer
- 11.Fibroblasto asoc. a cáncer/Célula epitelial luminal
- 12.Célula progenitora luminal

Hide

```
# Prepare objects to perform G0

# Define gene universe, all genes in markers
universe_genes = unique(na.omit(markers$entrez))

# Filter markers avg_log2FC > 1 and p_val_adj < 0.05
filtered_markers = markers %>%
  group_by(cluster) %>%
  dplyr::filter(avg_log2FC >= 1, p_val_adj <= 0.05)
```

Hide

```
# Run goana for each cluster with top 15 markers
go_results_list15 = list()

clusters15 = unique(top15$cluster)

for (cl in clusters15) {
  entrez_cl15 = top15 %>%
    filter(cluster == cl) %>%
    pull(entrez)

  go_r15 = goana(entrez_cl15, universe = universe_genes, species = "Hs")
  go_results_list15[[as.character(cl)]] = topG0(go_r15, number = 10, ontology = "BP")
  print(names(go_results_list15[cl]))
  print(go_results_list15[[cl]])
}
```

[1] "1"

	Term <chr>	O.. <chr>	N <dbl>	DE <dbl>	P.DE <dbl>
GO:0001525	angiogenesis	BP	404	10	1.089861e-11
GO:0048514	blood vessel morphogenesis	BP	468	10	4.685361e-11
GO:0001568	blood vessel development	BP	535	10	1.755911e-10

	Term<chr>	O.. <chr×dbl×dbl>	N	DE	P.DE <dbl>
GO:0001944	vasculature development	BP	557	10	2.611068e-10
GO:0035239	tube morphogenesis	BP	633	10	9.165101e-10
GO:0035295	tube development	BP	774	10	6.518964e-09
GO:0072359	circulatory system development	BP	800	10	8.984225e-09
GO:0048646	anatomical structure formation involved in morphogenesis	BP	803	10	9.316414e-09
GO:0003094	glomerular filtration	BP	22	3	3.174068e-06
GO:0097205	renal filtration	BP	25	3	4.728779e-06
1-10 of 10 rows					

[1] "9"

	Term<chr>	O.. <chr×dbl>	N	D.. <dbl>
GO:0009605	response to external stimulus	BP	1475	10
GO:0006952	defense response	BP	1138	9
GO:0009607	response to biotic stimulus	BP	996	8
GO:2000646	positive regulation of receptor catabolic process	BP	6	2
GO:0044419	biological process involved in interspecies interaction between organisms	BP	1096	8
GO:0002682	regulation of immune system process	BP	1102	8
GO:0050866	negative regulation of cell activation	BP	151	4
GO:0006955	immune response	BP	1154	8
GO:0002604	regulation of dendritic cell antigen processing and presentation	BP	10	2
GO:2000644	regulation of receptor catabolic process	BP	10	2
1-10 of 10 rows   1-5 of 5 columns				

[1] "5"

GO:0019886	
GO:0042157	
GO:0002495	
GO:0002504	
GO:0019882	
GO:0002478	
GO:0006898	
GO:0055094	
GO:0019884	
GO:0034381	
1-10 of 10 rows   1-1 of 5 columns	

[1] "4"

	Term<chr>	O... <chr×dbl>	N	DE <dbl>	P.DE <dbl>
GO:0008544	epidermis development	BP	225	6	3.058028e-07
GO:0031424	keratinization	BP	19	3	2.002136e-06
GO:0045109	intermediate filament organization	BP	22	3	3.174068e-06
GO:0045104	intermediate filament cytoskeleton organization	BP	38	3	1.715938e-05
GO:0045103	intermediate filament-based process	BP	38	3	1.715938e-05
GO:0009888	tissue development	BP	1291	8	1.111907e-04





GO:0042710
1-10 of 10 rows   1-1 of 5 columns

[1] "10"

	Term <chr>	O.. <chr>	N <dbl>	DE <dbl>	P.DE <dbl>
GO:0009888	tissue development	BP	1291	9	1.123814e-05
GO:0017038	protein import	BP	11	2	9.607215e-05
GO:0007155	cell adhesion	BP	1021	7	2.001726e-04
GO:1902533	positive regulation of intracellular signal transduction	BP	772	6	3.510740e-04
GO:0048799	animal organ maturation	BP	21	2	3.639223e-04
GO:0060429	epithelium development	BP	785	6	3.844648e-04
GO:0050793	regulation of developmental process	BP	1646	8	6.217095e-04
GO:0051094	positive regulation of developmental process	BP	904	6	8.225564e-04
GO:0030155	regulation of cell adhesion	BP	589	5	8.551243e-04
GO:0009653	anatomical structure morphogenesis	BP	1744	8	9.273109e-04
1-10 of 10 rows					

[1] "12"

	Term <chr>	Ont <chr>	N <dbl>	DE <dbl>	P.DE <dbl>
GO:0000280	nuclear division	BP	317	9	8.407861e-12
GO:0048285	organelle fission	BP	354	9	2.269782e-11
GO:0098813	nuclear chromosome segregation	BP	243	8	6.242417e-11
GO:0022402	cell cycle process	BP	972	11	1.729028e-10
GO:0051276	chromosome organization	BP	467	9	2.709723e-10
GO:0000819	sister chromatid segregation	BP	193	7	7.552913e-10
GO:0007059	chromosome segregation	BP	336	8	8.289123e-10
GO:0007049	cell cycle	BP	1223	11	2.089808e-09
GO:0140014	mitotic nuclear division	BP	228	7	2.425180e-09
GO:1903047	mitotic cell cycle process	BP	607	9	2.783825e-09
1-10 of 10 rows					

[1] "7"

	Term <chr>	Ont <chr>	N <dbl>	DE <dbl>	P.DE <dbl>
GO:0030199	collagen fibril organization	BP	62	7	8.298952e-13
GO:0001568	blood vessel development	BP	535	10	1.755911e-10
GO:0001944	vasculature development	BP	557	10	2.611068e-10
GO:0072359	circulatory system development	BP	800	10	8.984225e-09
GO:0045229	external encapsulating structure organization	BP	239	7	1.216970e-08
GO:0030198	extracellular matrix organization	BP	239	7	1.216970e-08
GO:0043062	extracellular structure organization	BP	239	7	1.216970e-08
GO:0048514	blood vessel morphogenesis	BP	468	8	5.271343e-08
GO:0071604	transforming growth factor beta production	BP	30	4	6.172500e-08
GO:0018149	peptide cross-linking	BP	9	3	1.749966e-07
1-10 of 10 rows					

[1] "3"

GO:0050853

GO:0002443

GO:0006958

GO:0019731

GO:0002460

GO:0016064

GO:0006956

GO:0019724

GO:0002455

GO:0002252

1-10 of 10 rows | 1-1 of 5 columns

[1] "6"

GO:0050853

GO:0050851

GO:0016064

GO:0019724

GO:0002429

GO:0002768

GO:0002250

GO:0002449

GO:0002460

GO:0002757

1-10 of 10 rows | 1-1 of 5 columns

Hide

```
# Report total run time Seurat pipeline
toc(quiet = FALSE)
```

Total time Seurat pipeline: 1474.222 sec elapsed