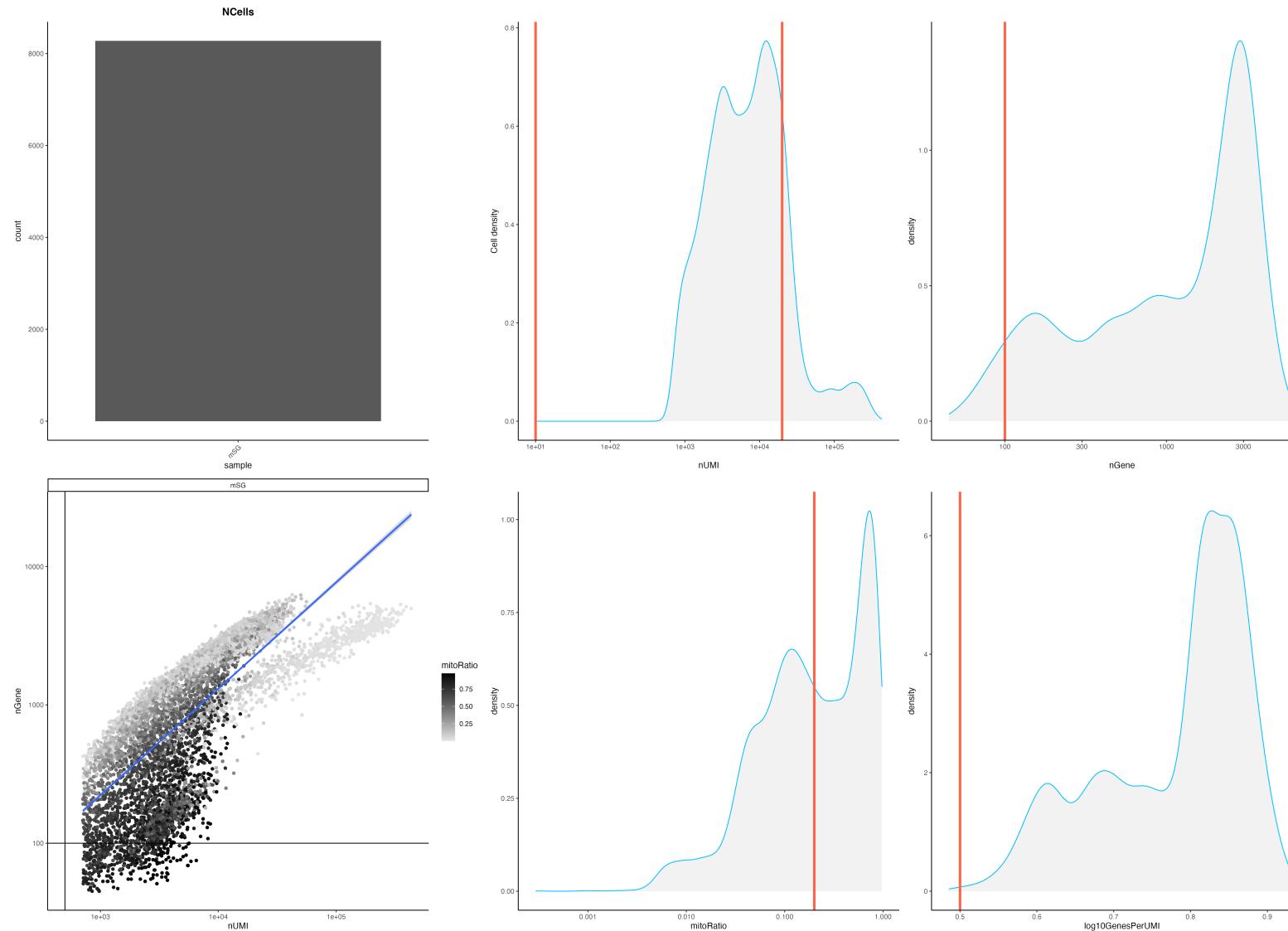


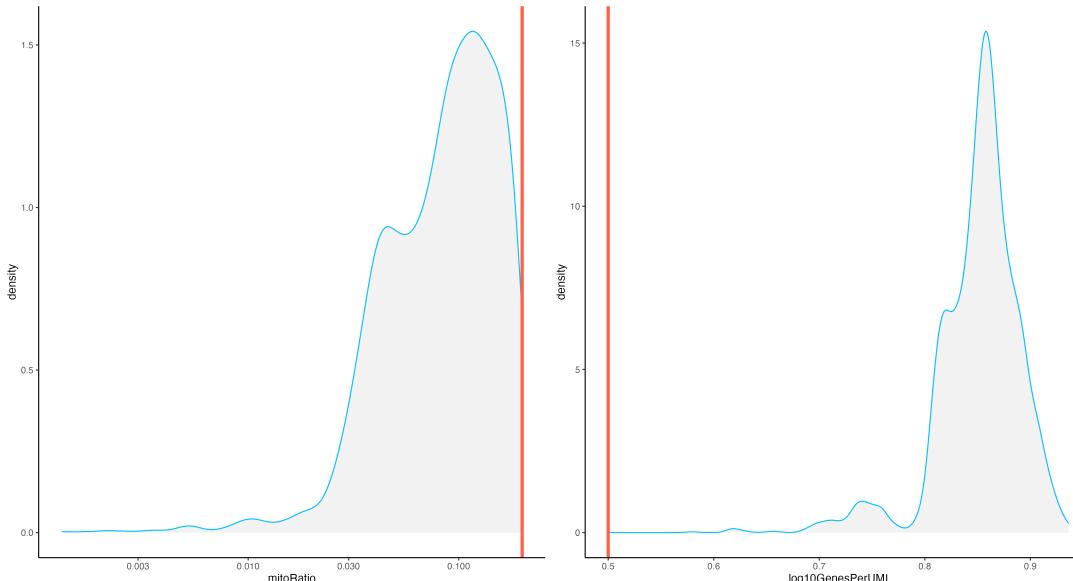
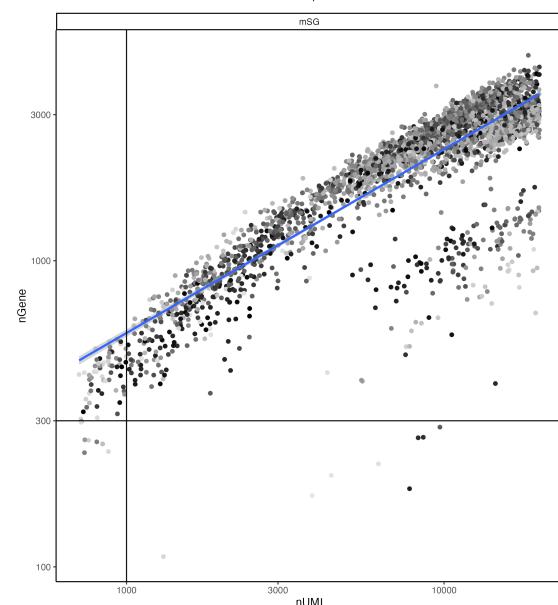
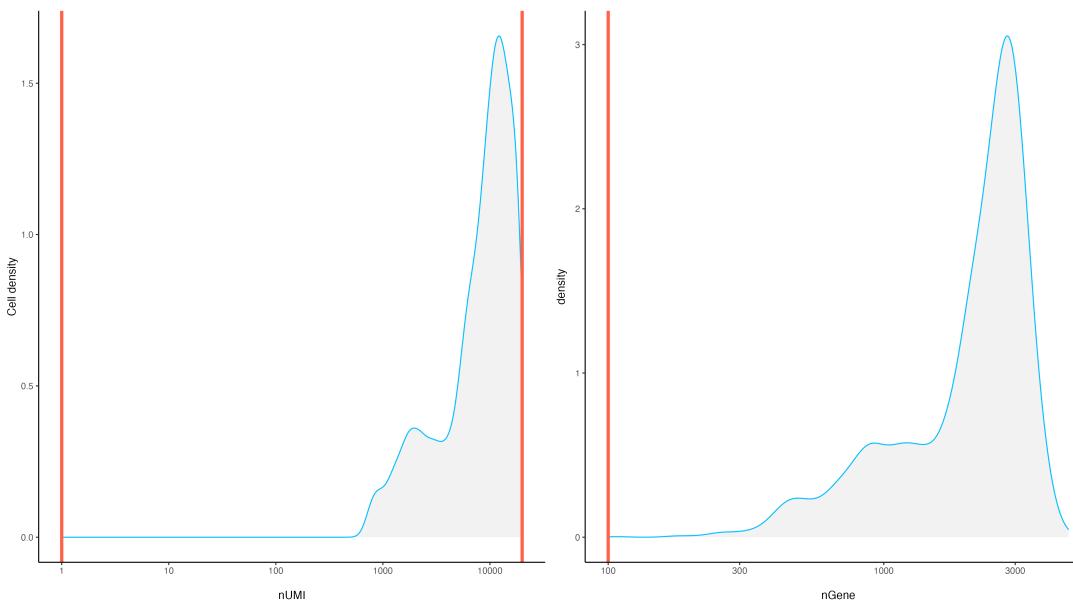
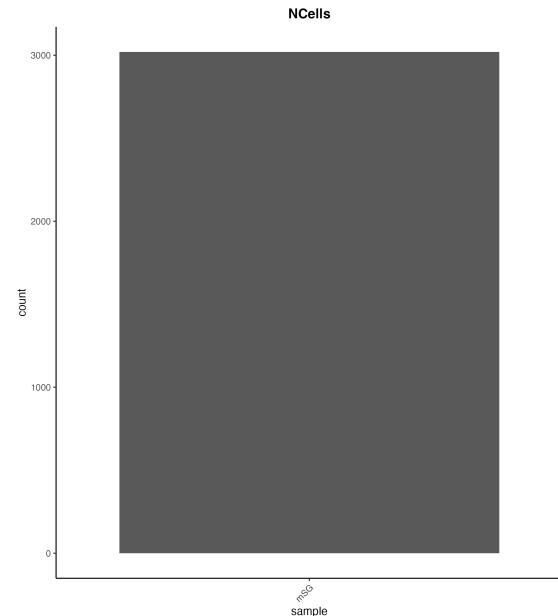
# **Dataset 1**

# Quality Control

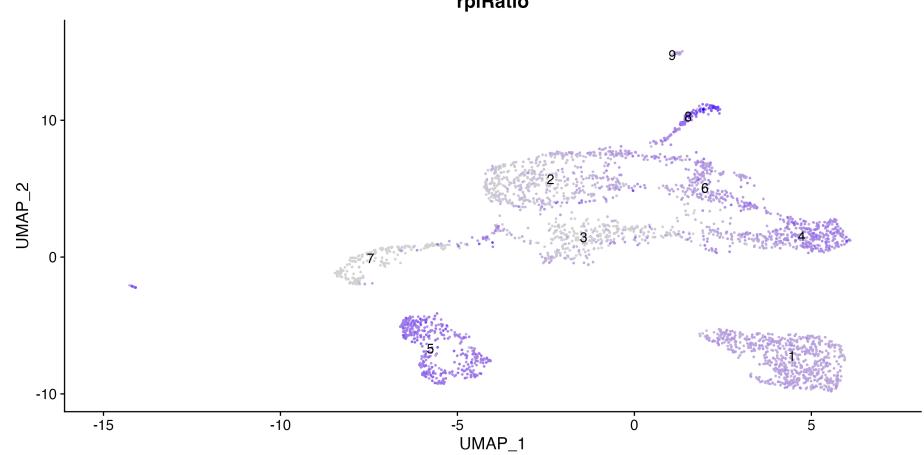
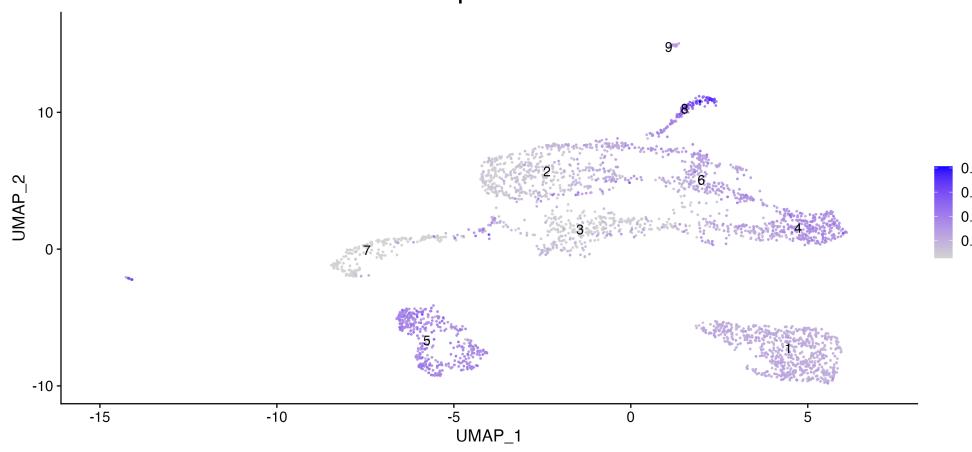
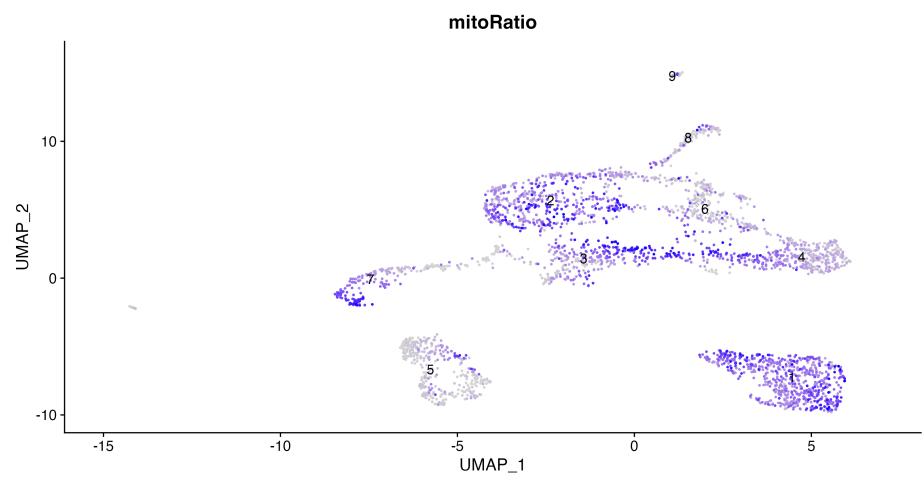
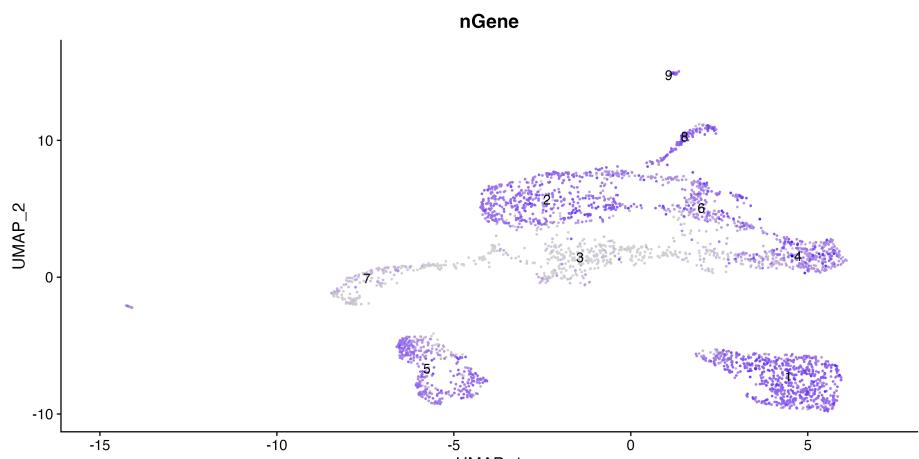
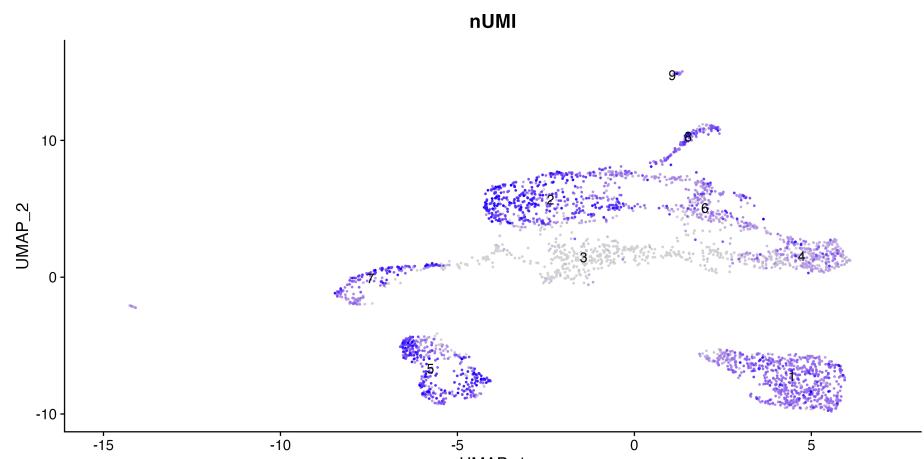


Before Quality Control  
Cell Size: 8277 cells

# Quality Control

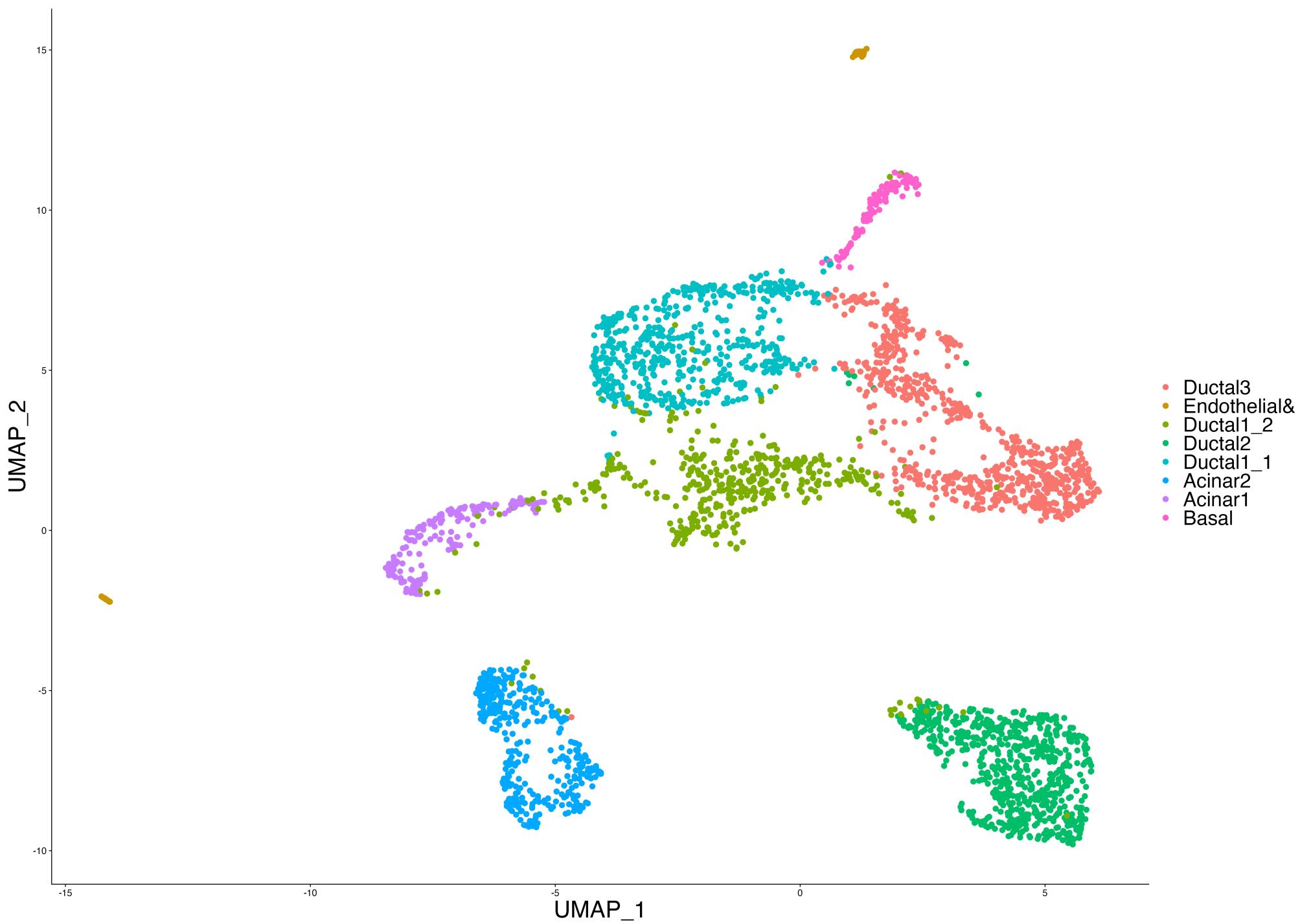


After Quality Control:  
Cell size: 3020 cells



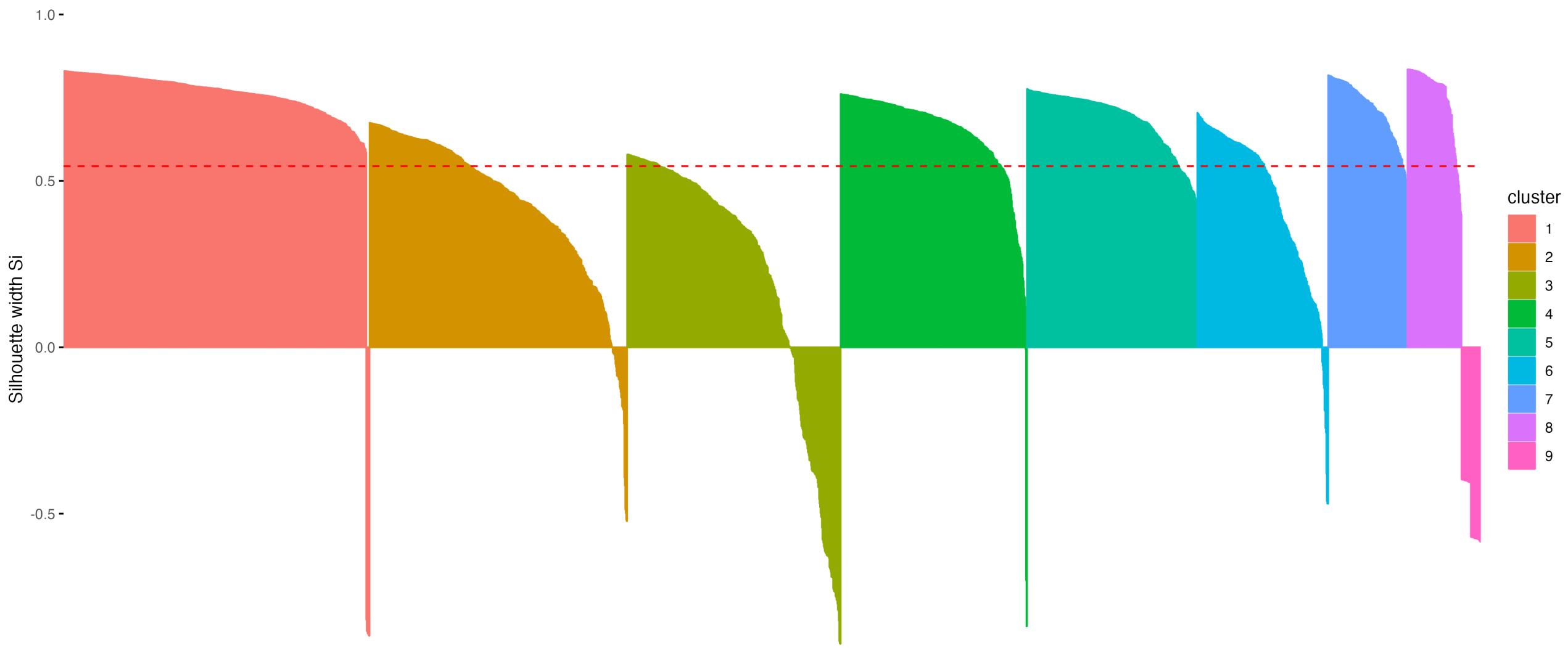
# Dataset 1: ful UMAP pl

res 0.5  
nUMI: <20000

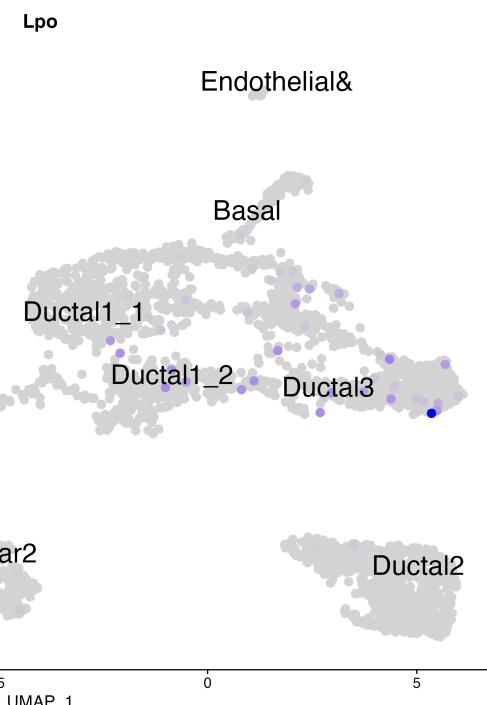
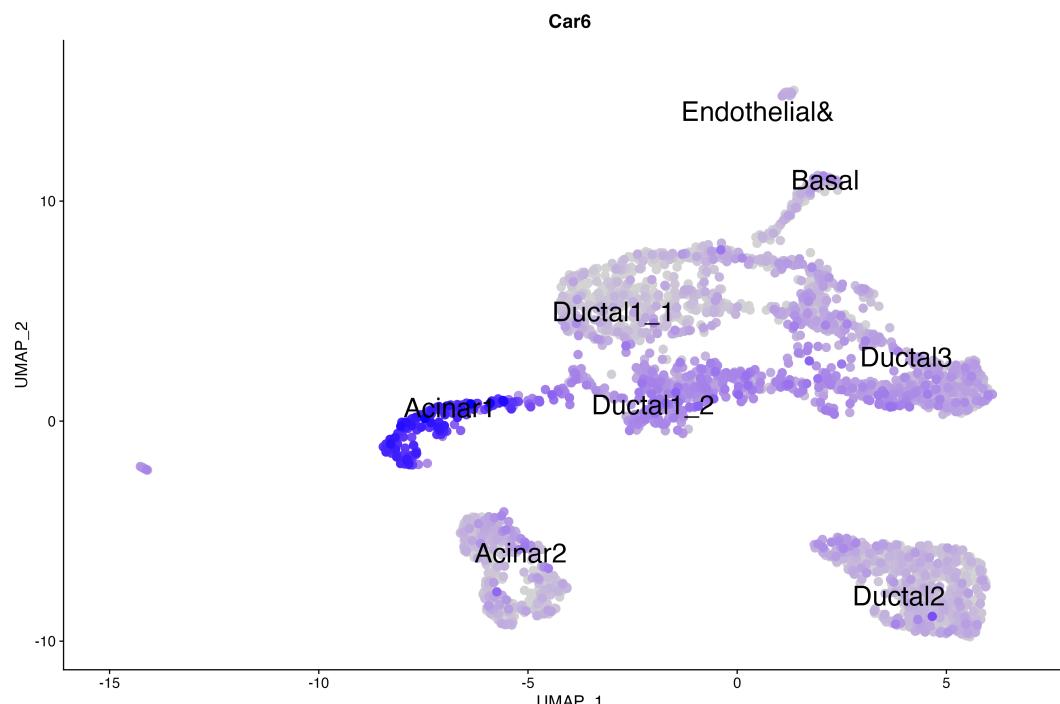


# Silhouette score plot

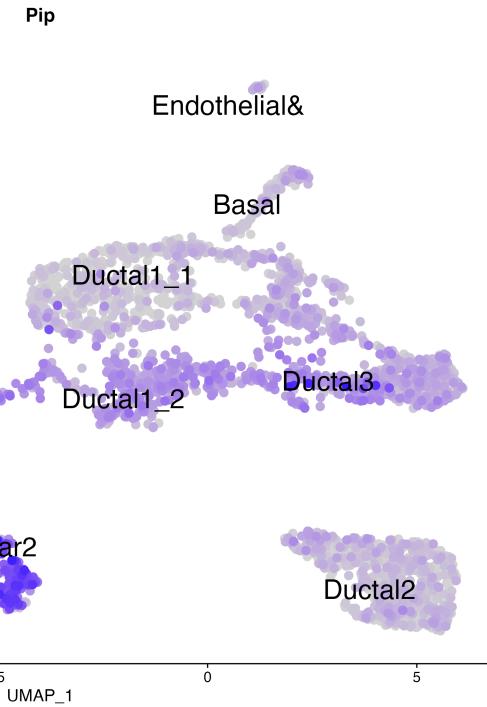
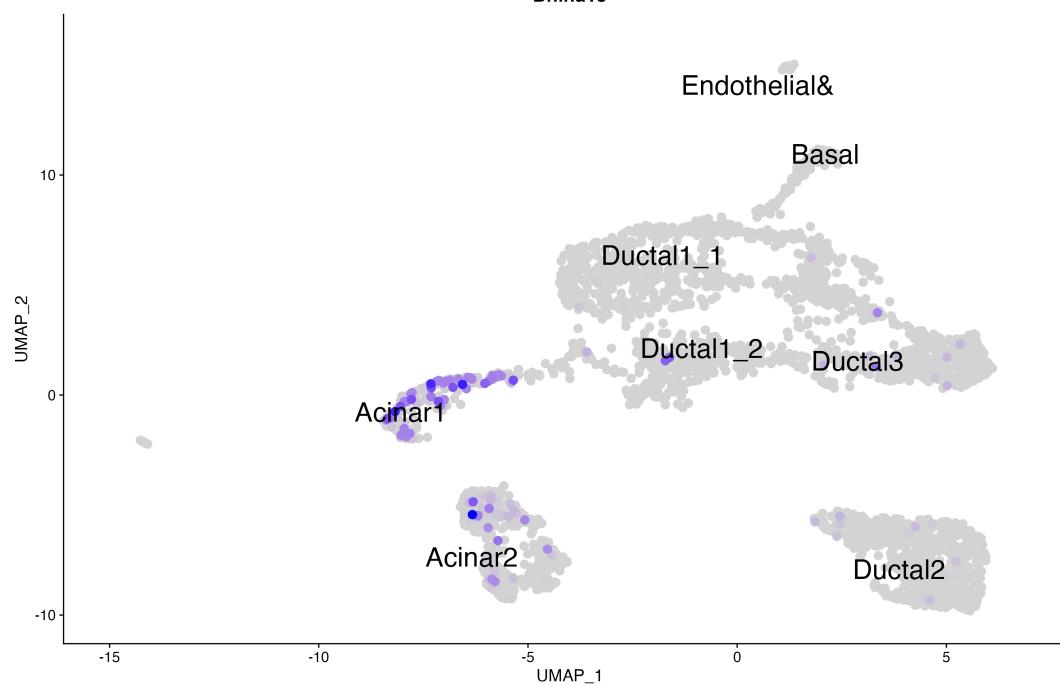
Clusters silhouette plot  
Average silhouette width: 0.54



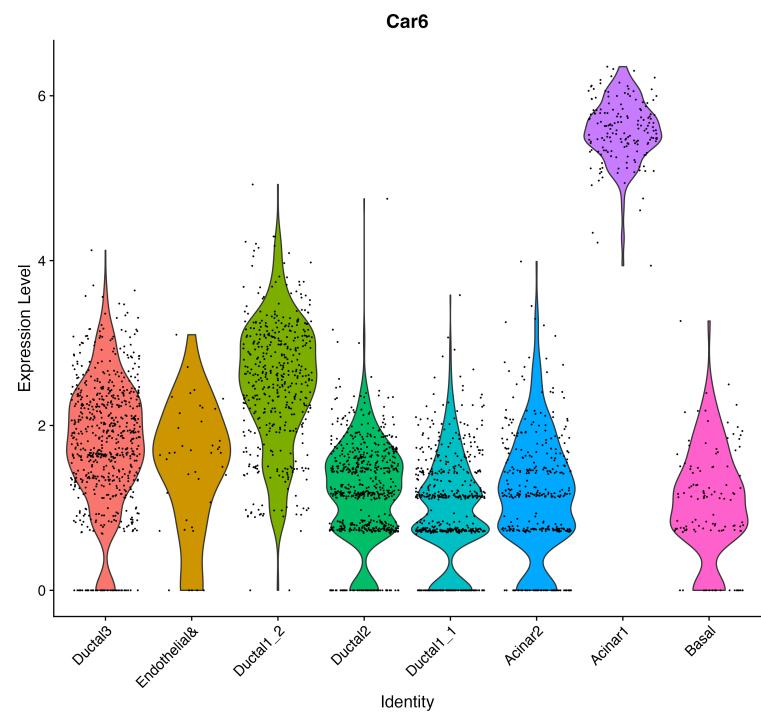
Acinar 1



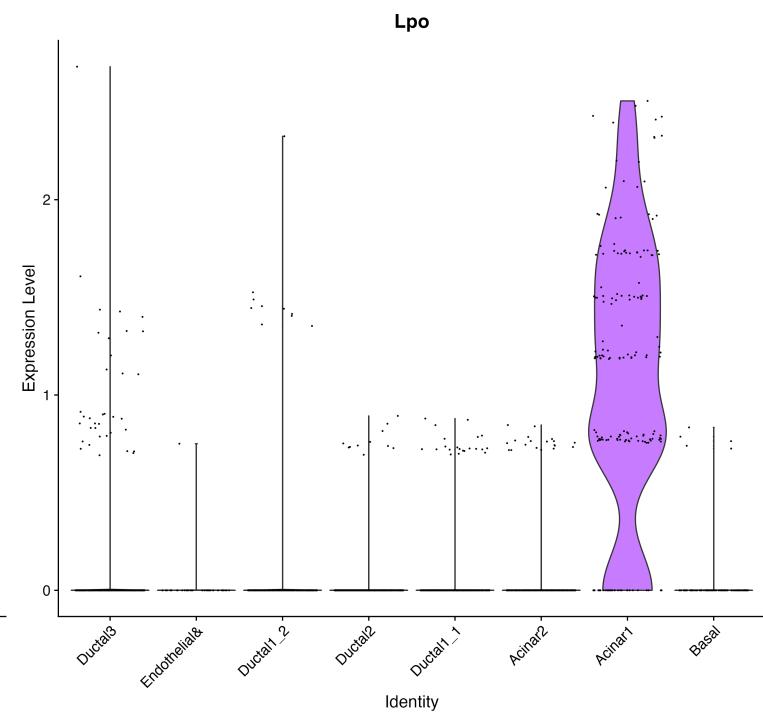
Bhlha15



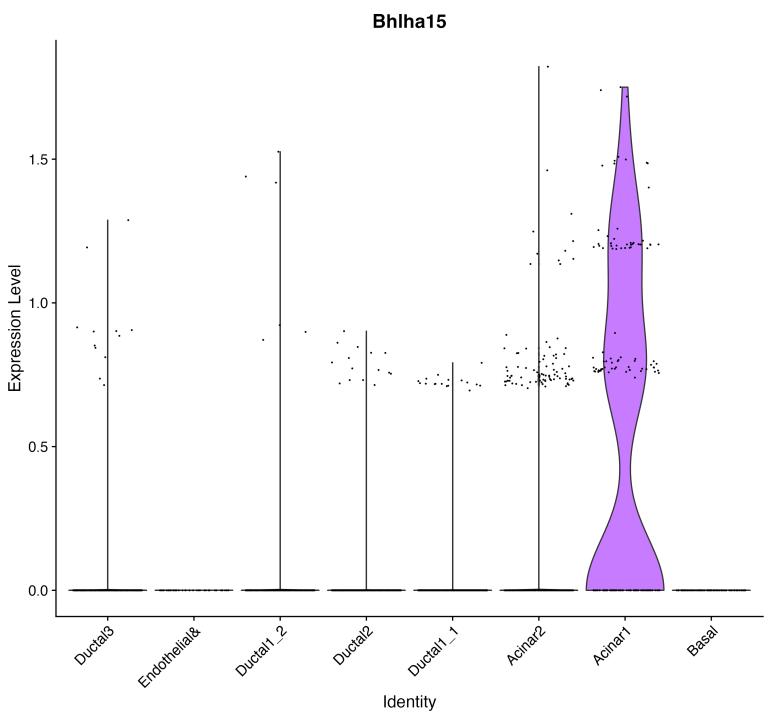
**Acinar 1**



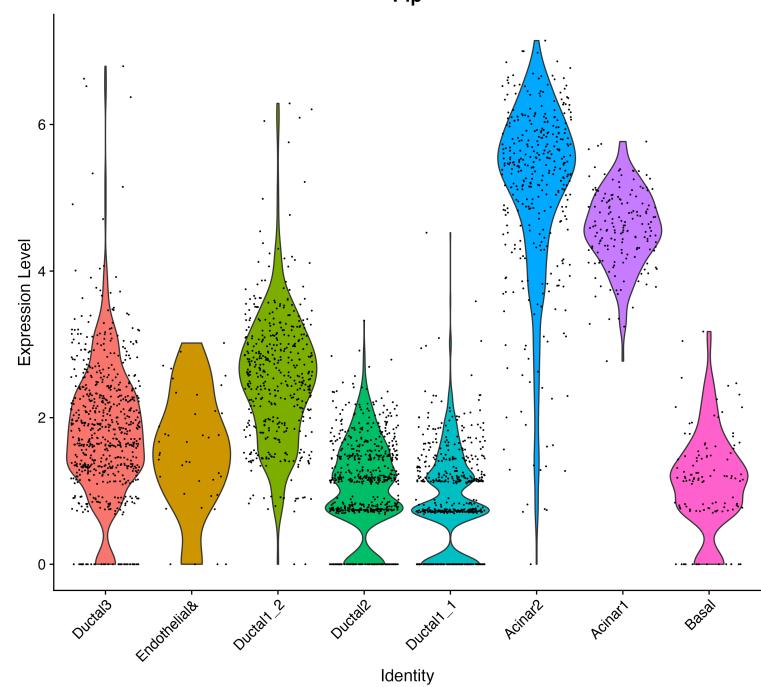
**Lpo**



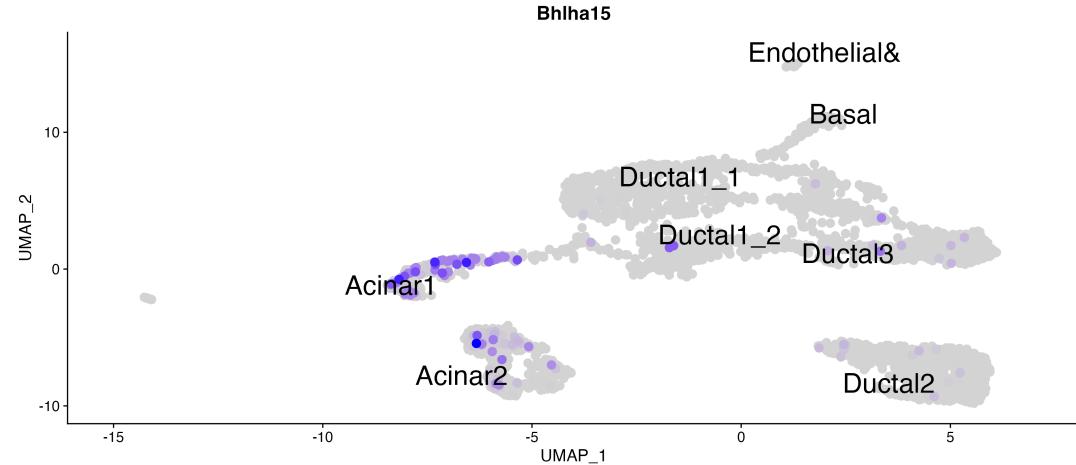
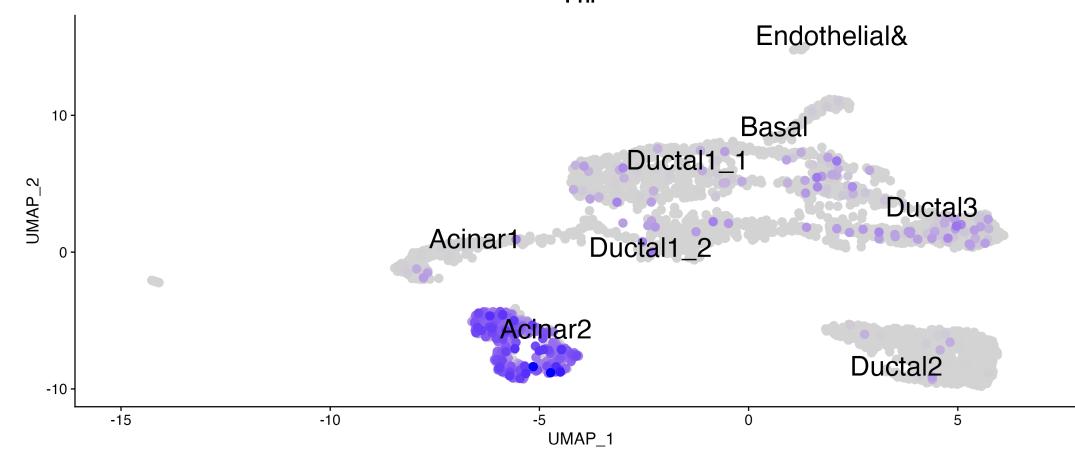
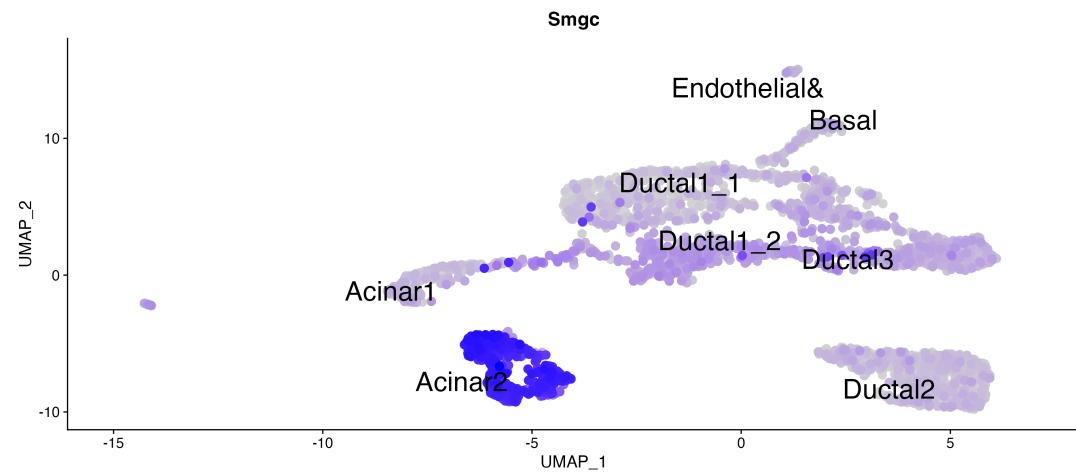
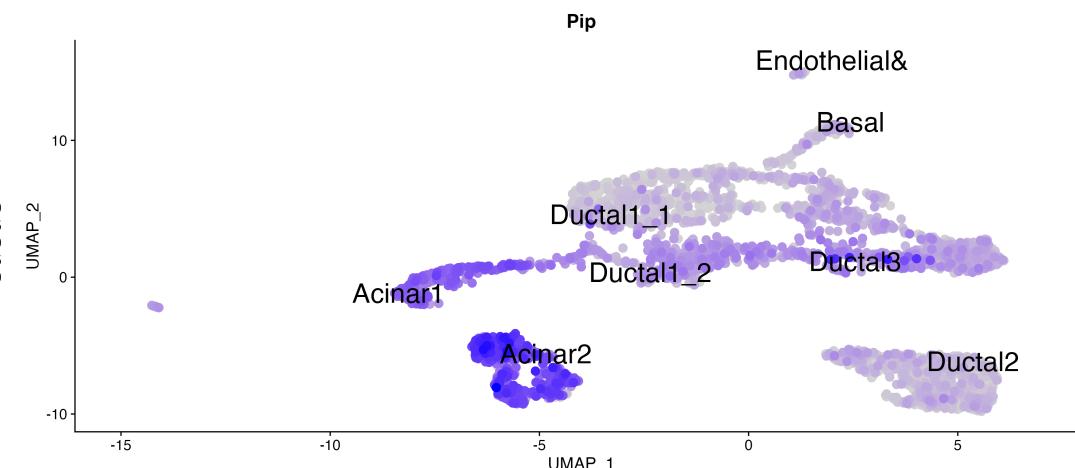
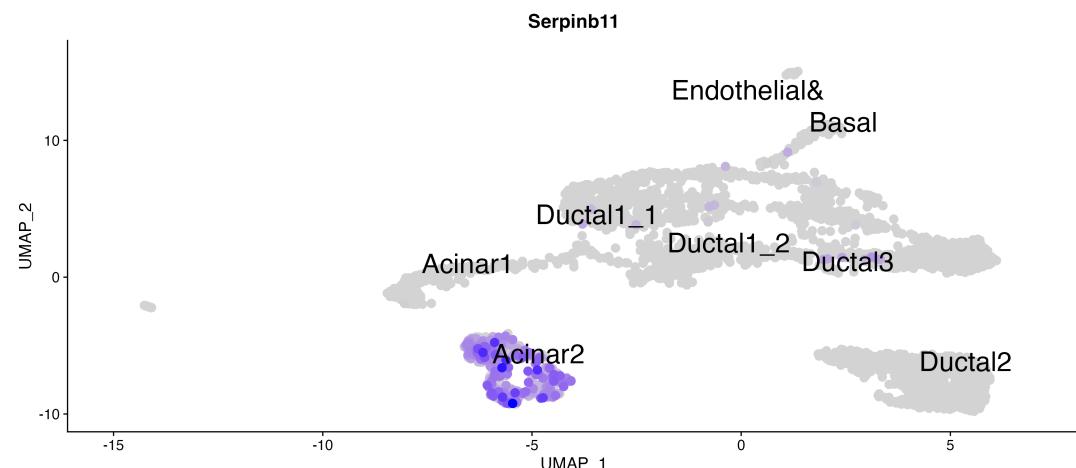
**Bhlha15**



**Pip**

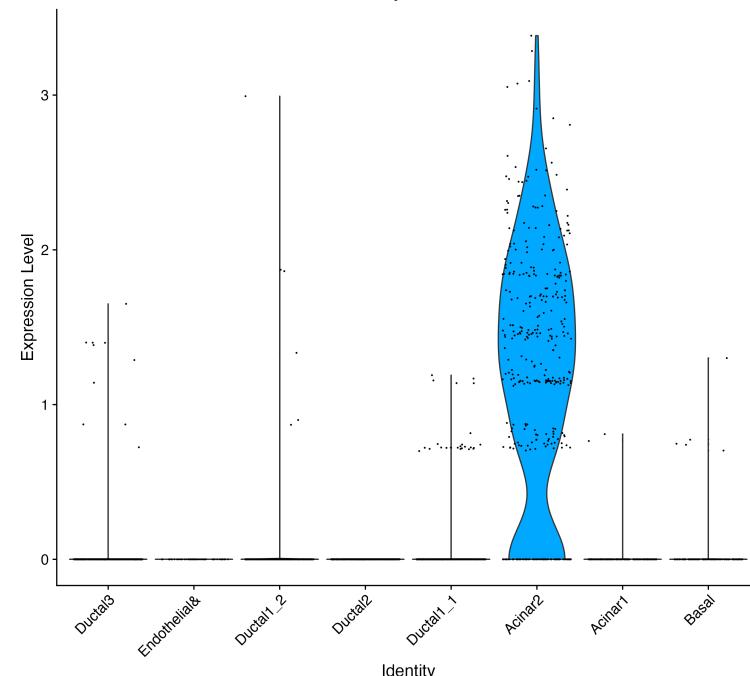


Acinar 2

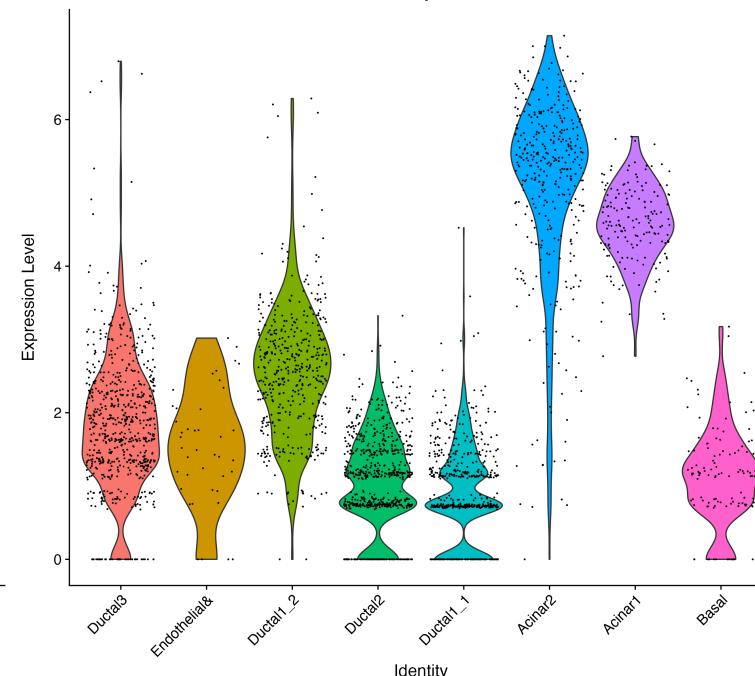


## Acinar 2

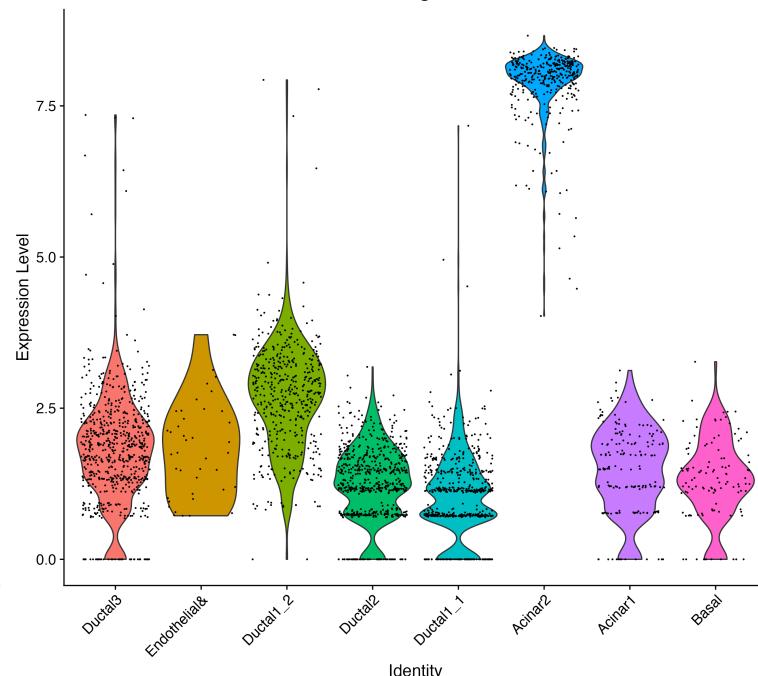
**Serpib11**



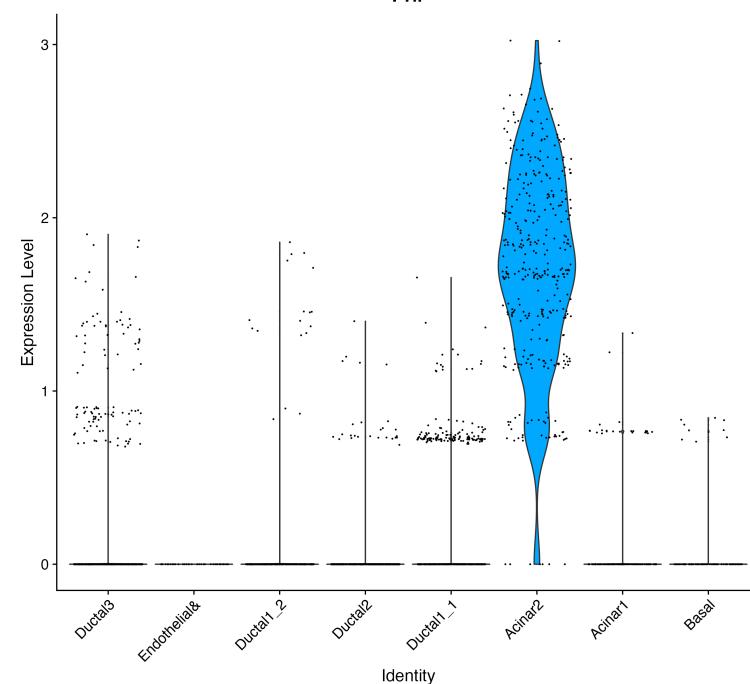
**Pip**



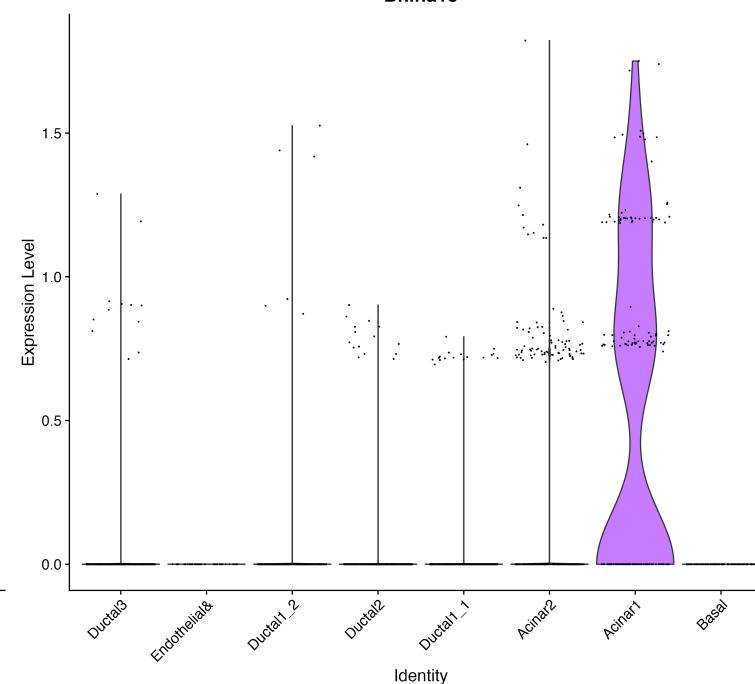
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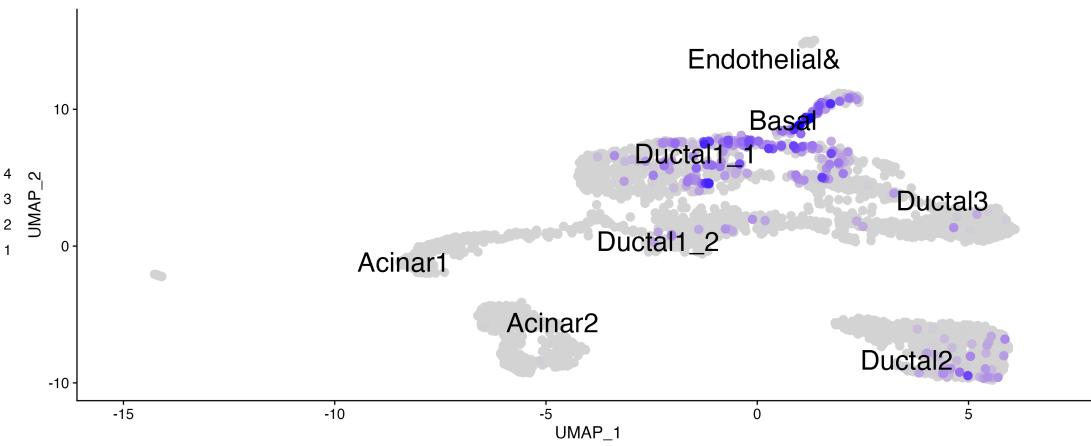
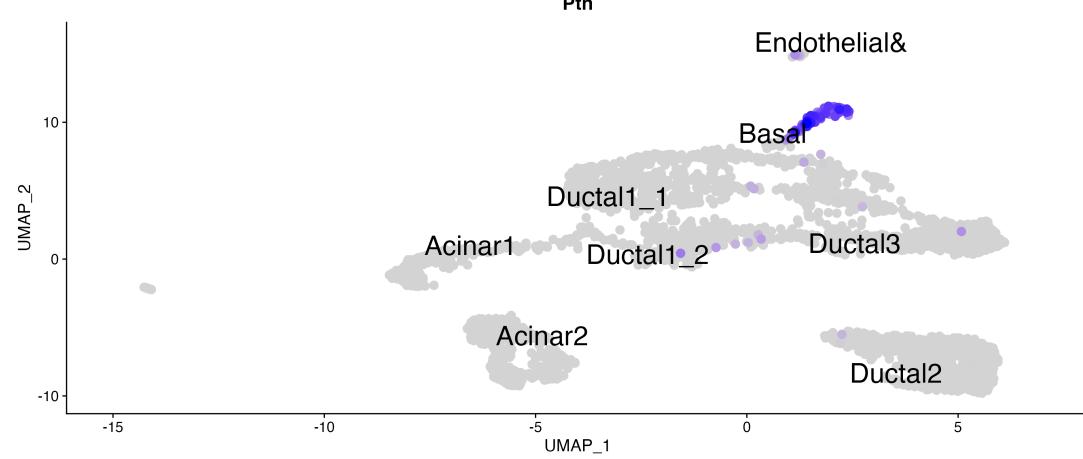
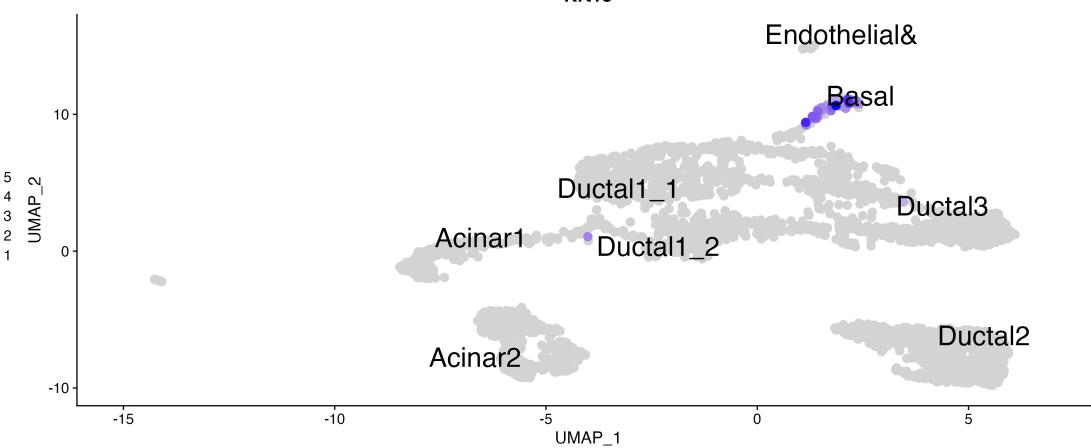
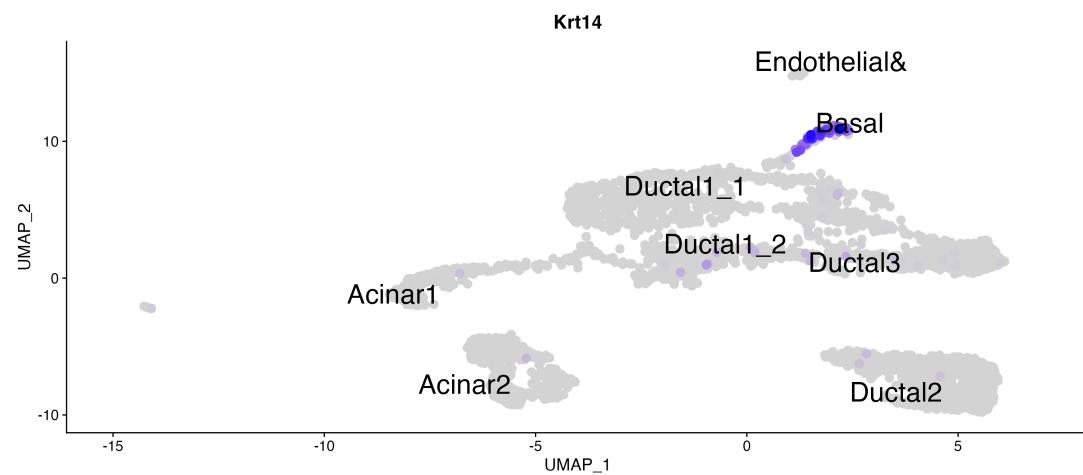
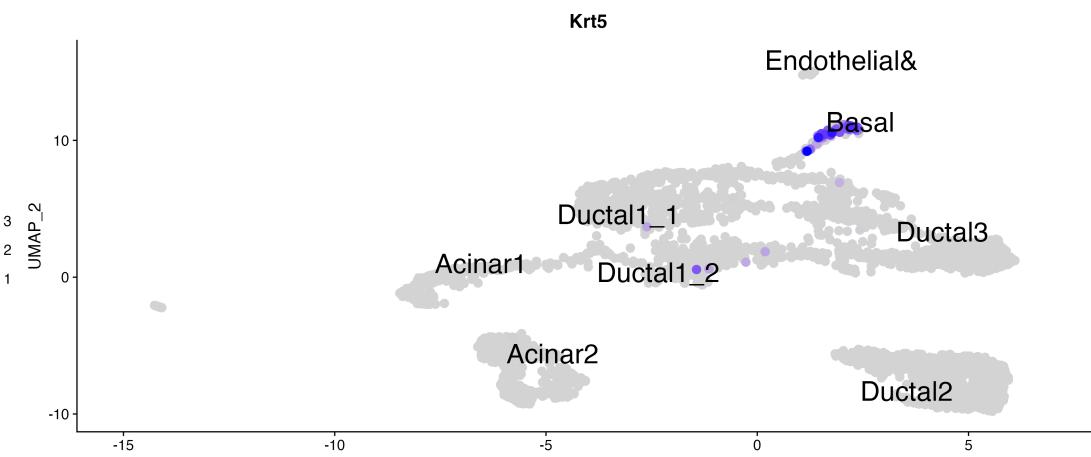
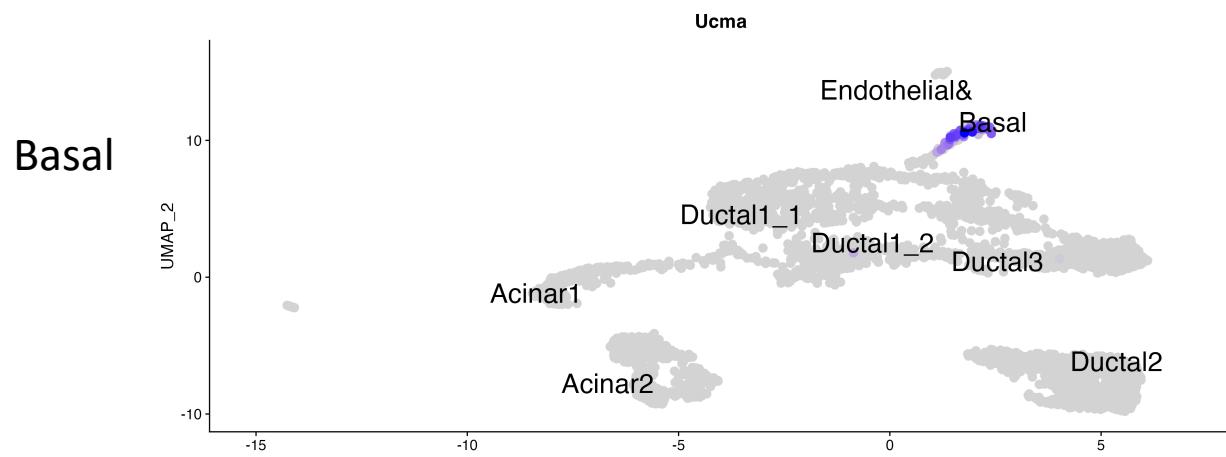


**Prlr**

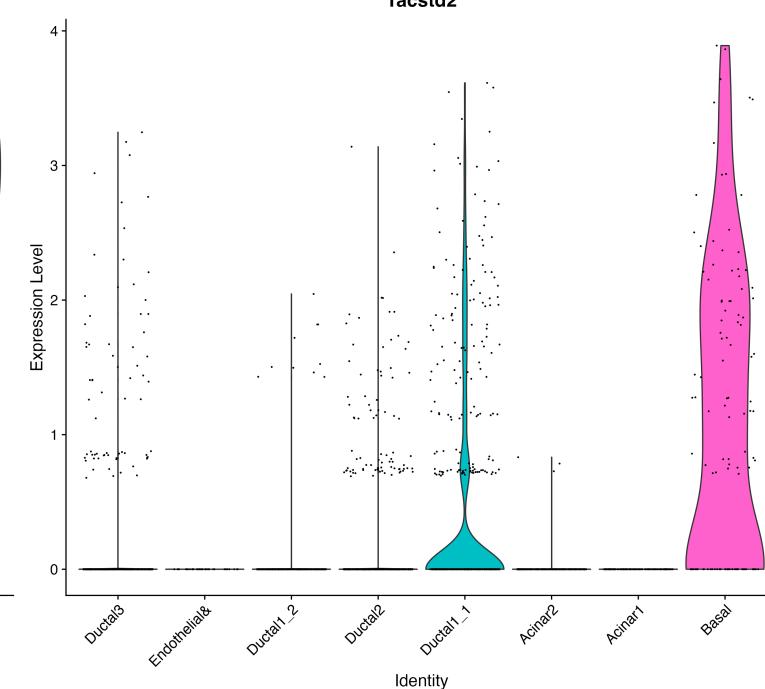
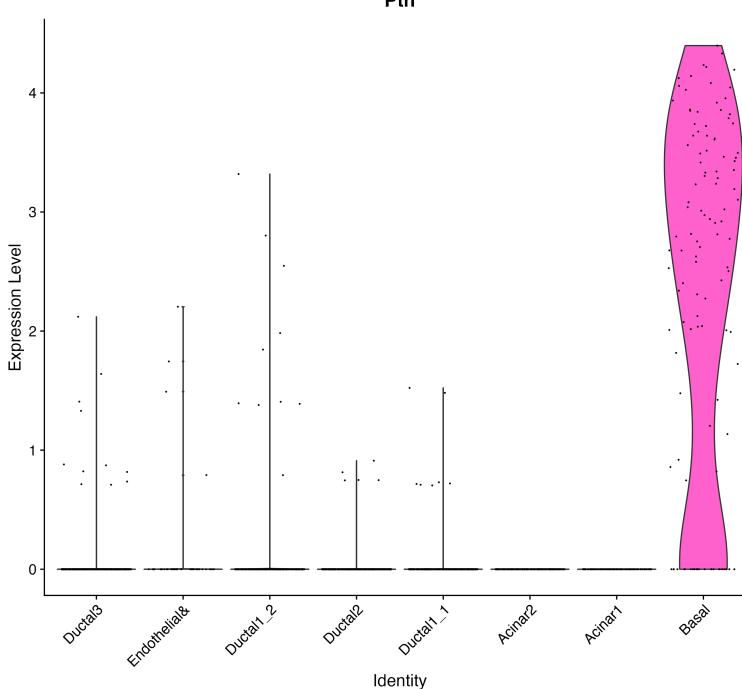
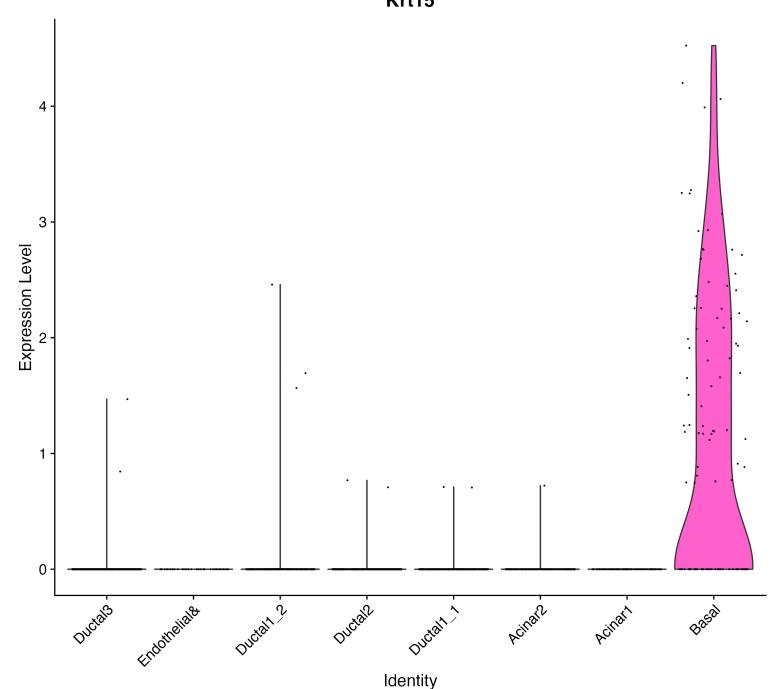
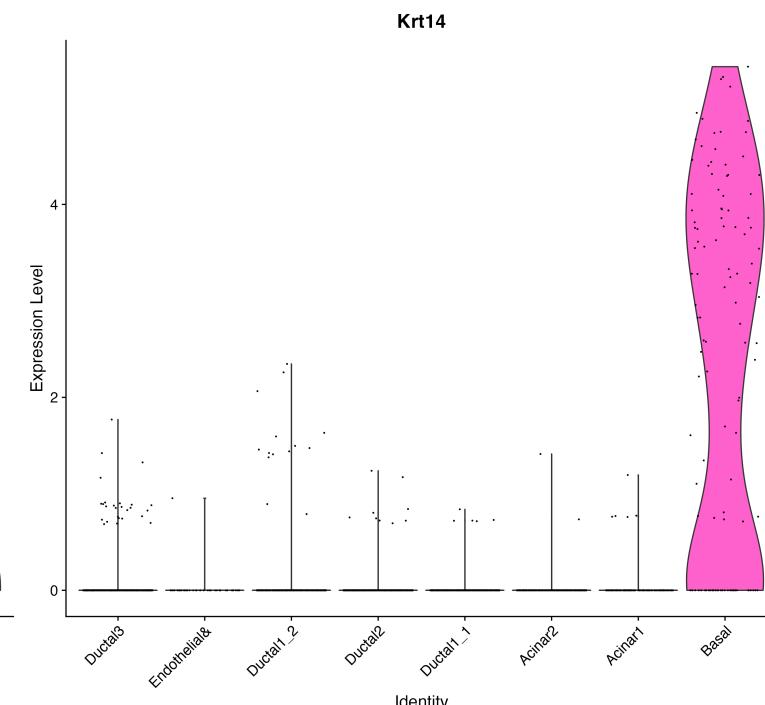
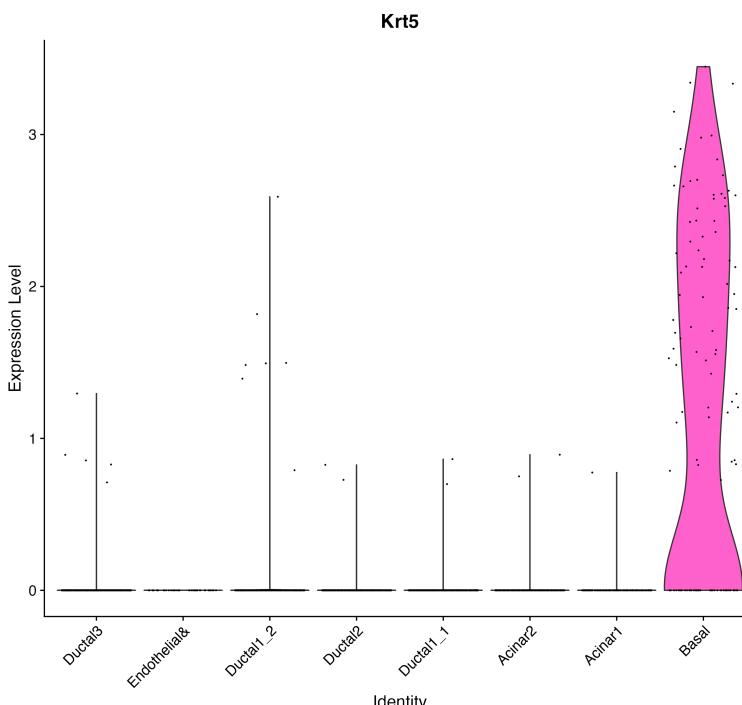
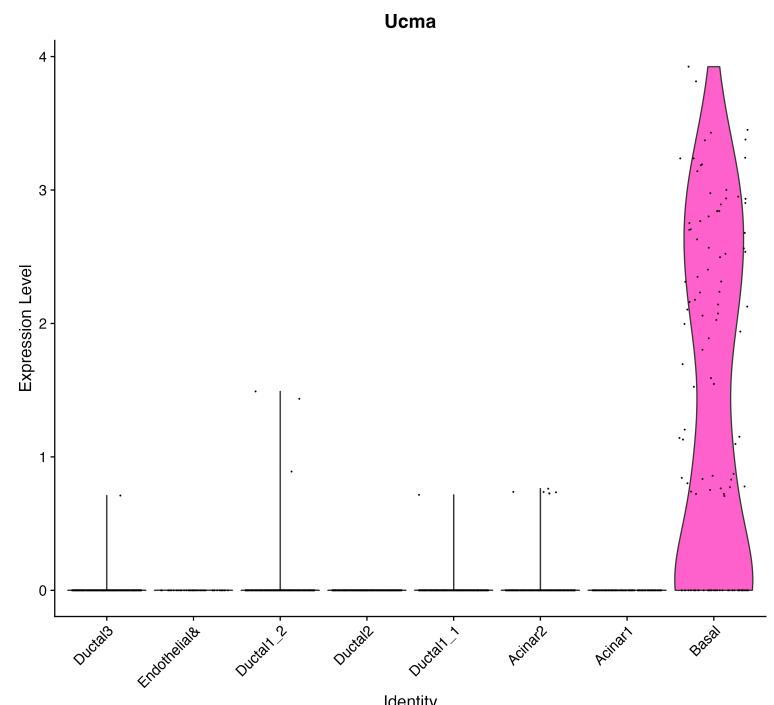


**Bhlha15**

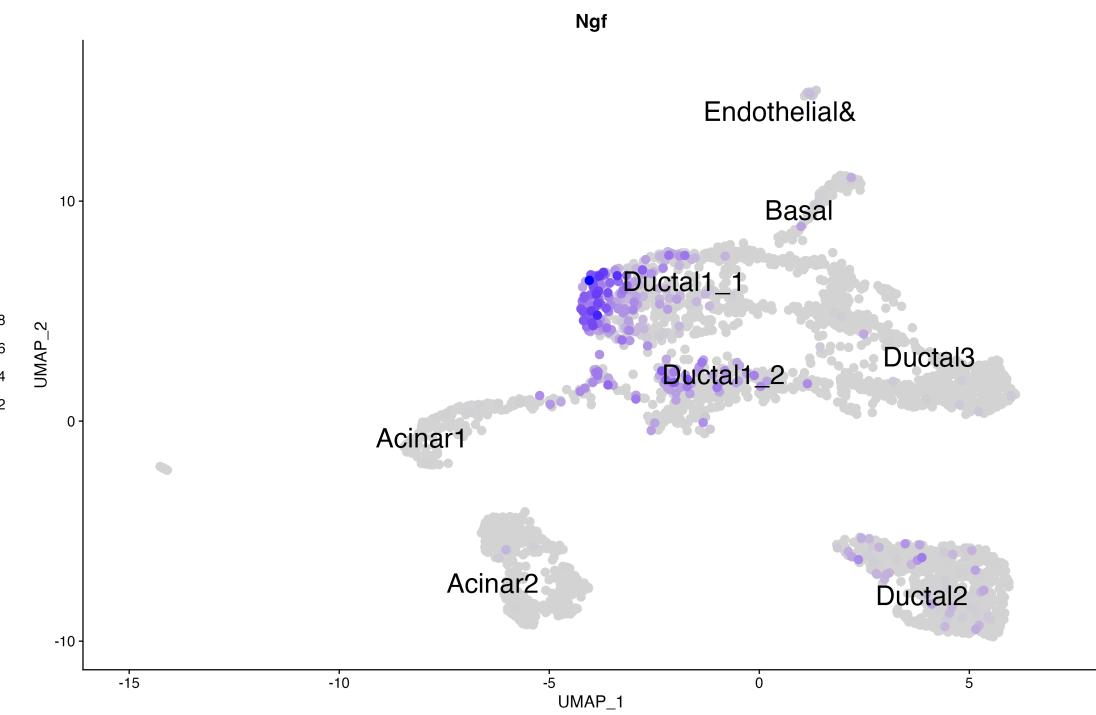
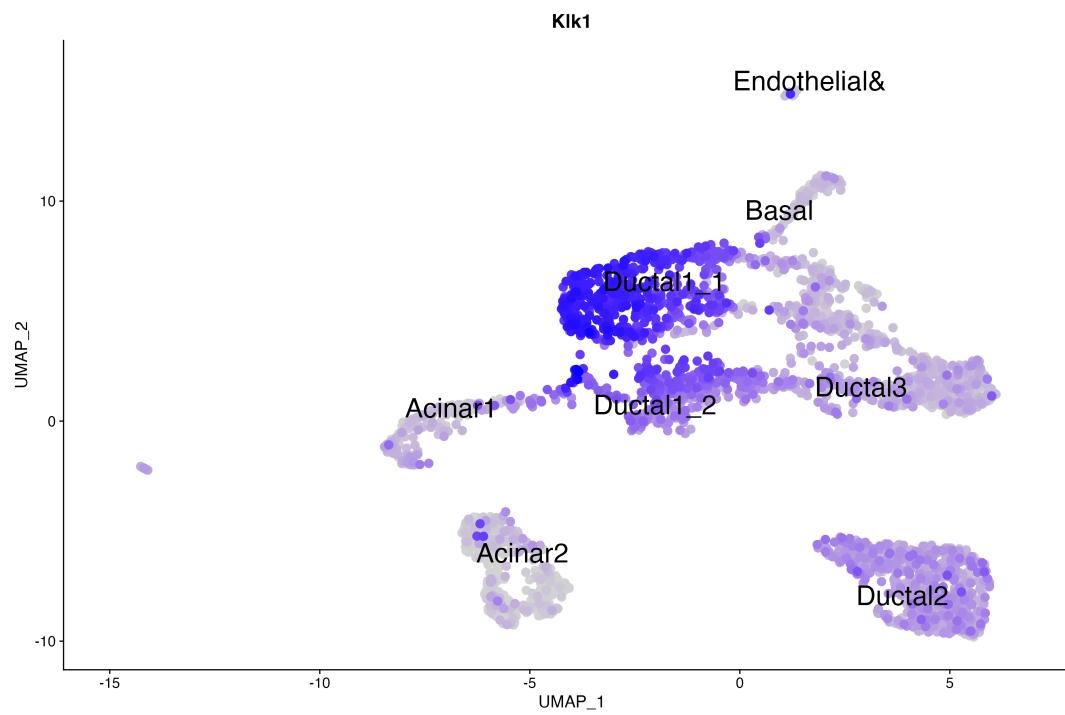




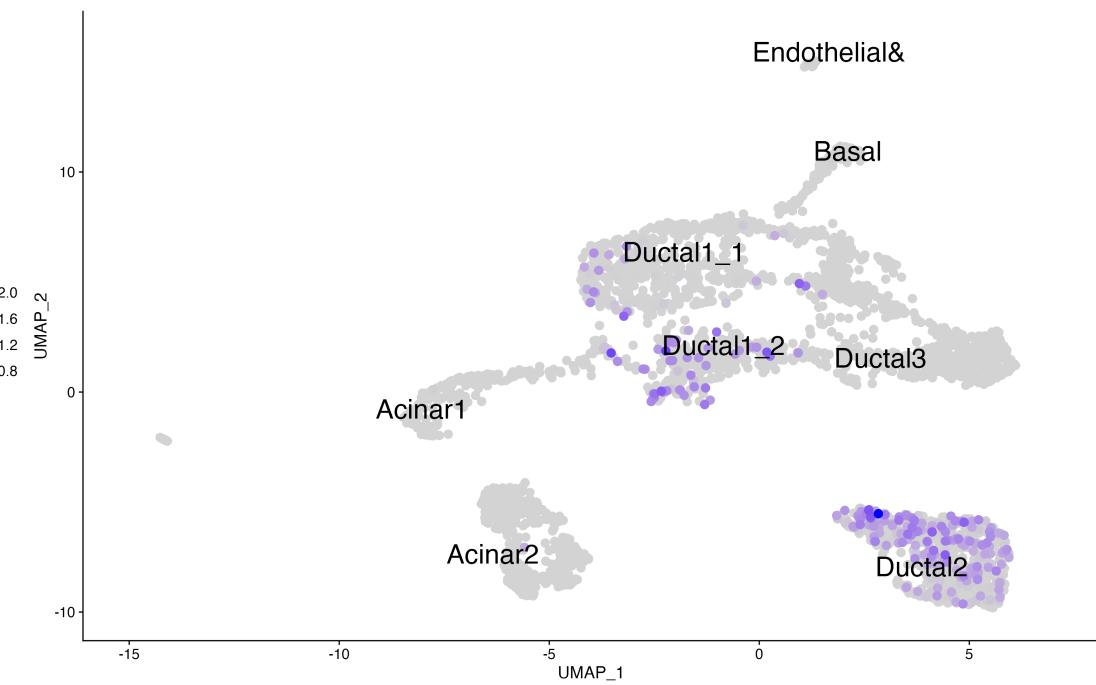
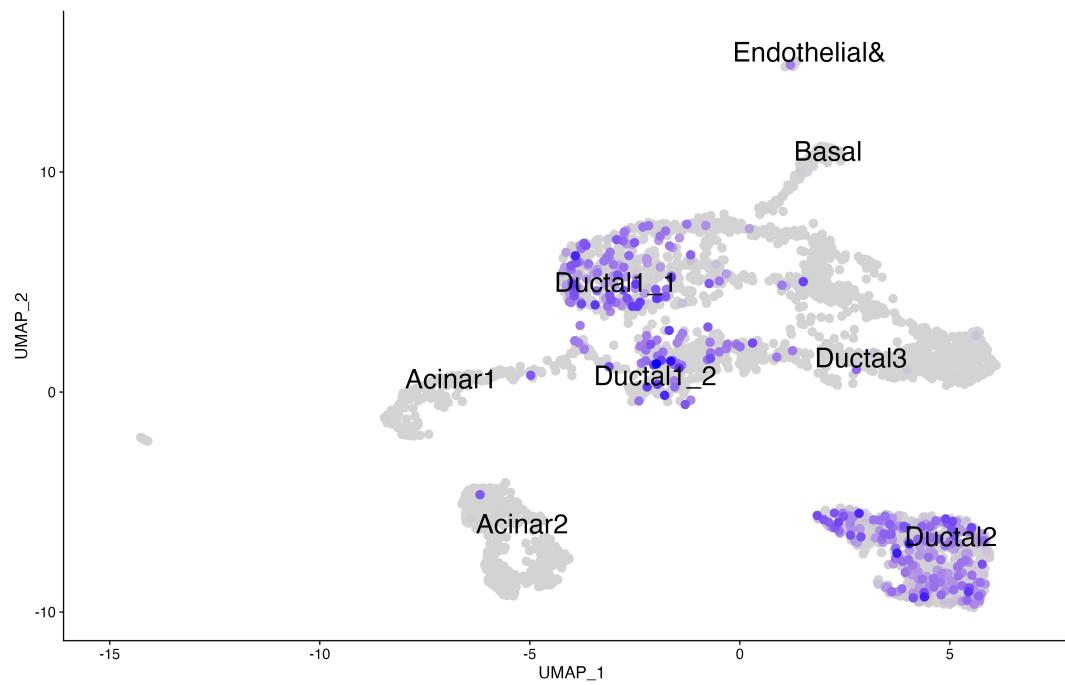
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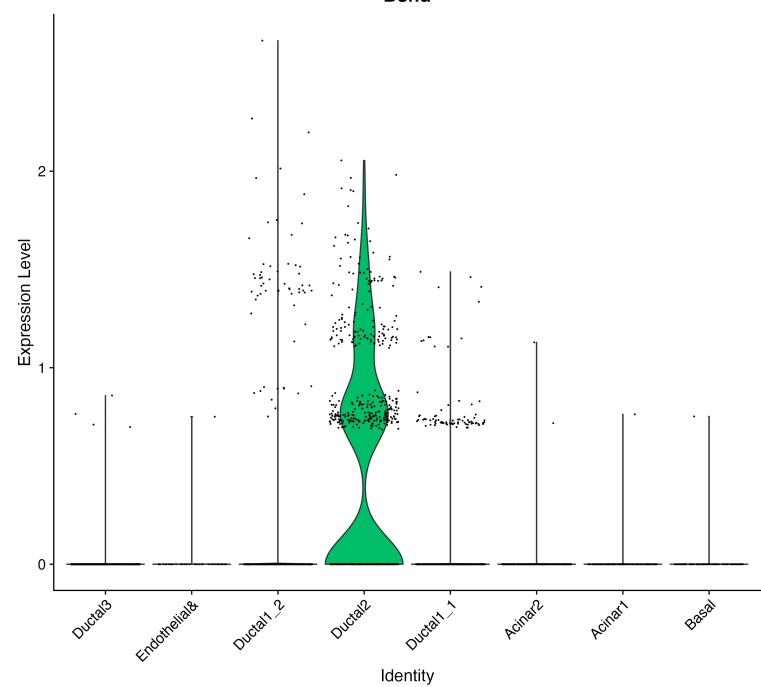
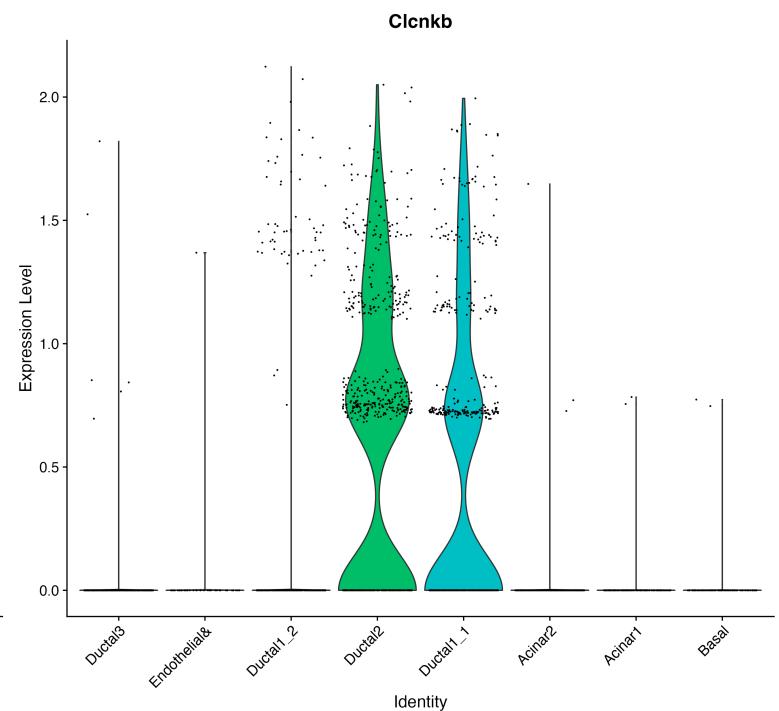
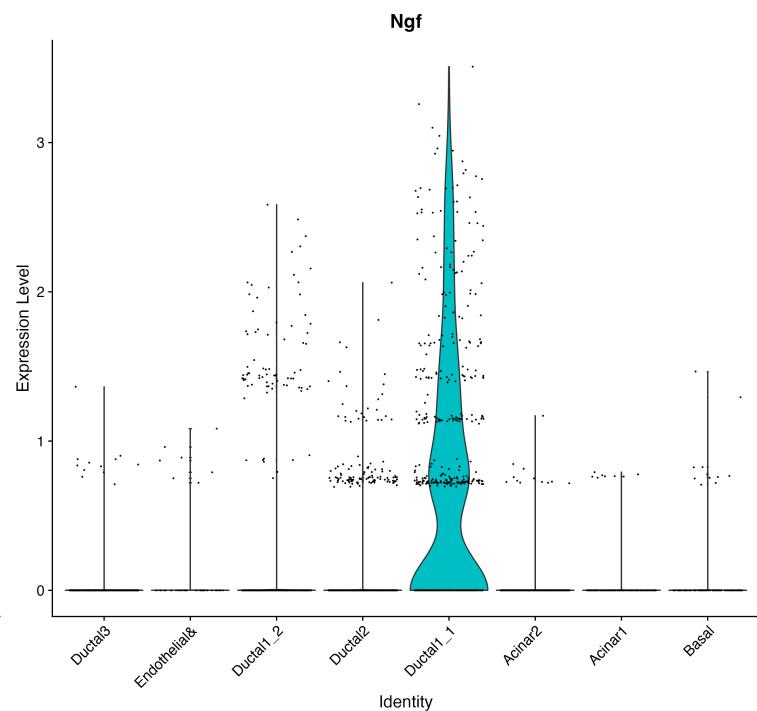
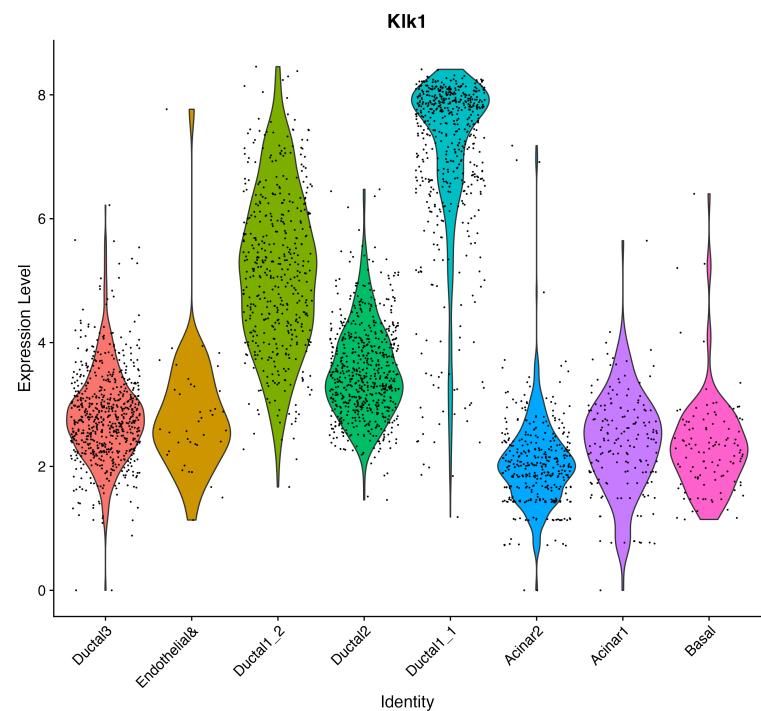
Ductal 1



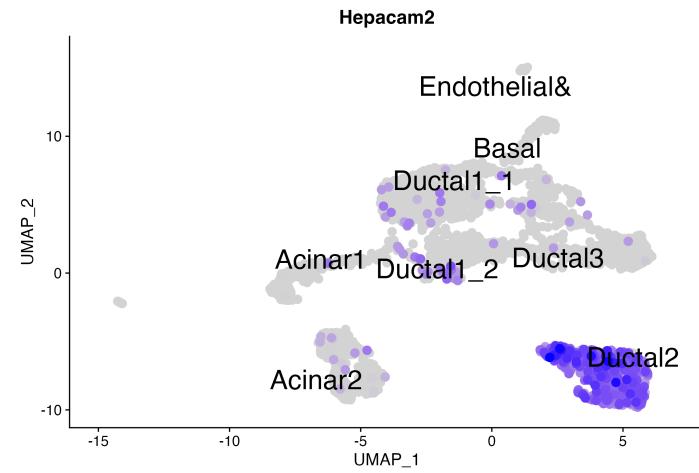
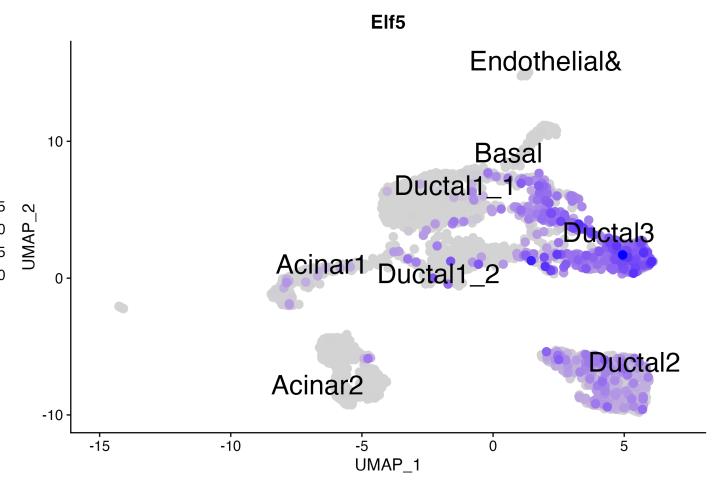
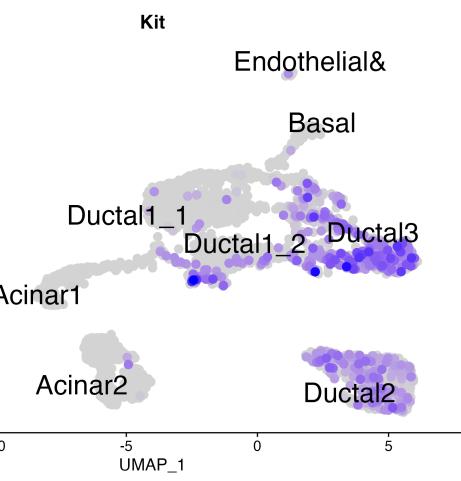
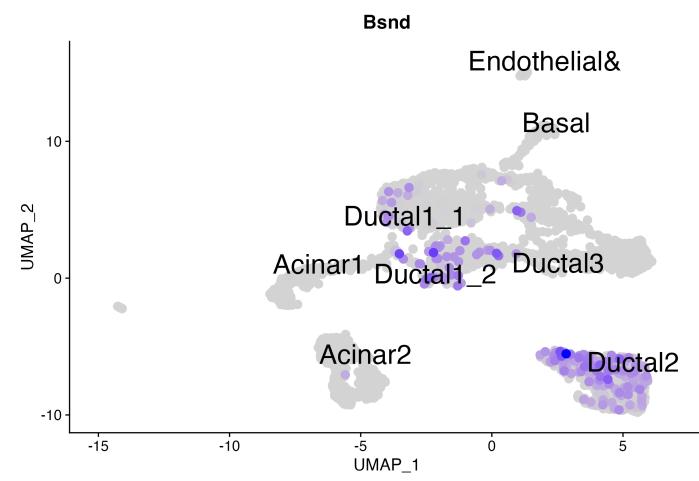
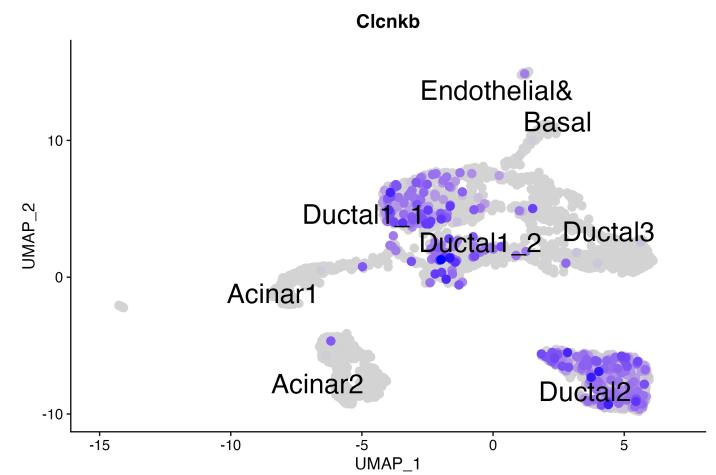
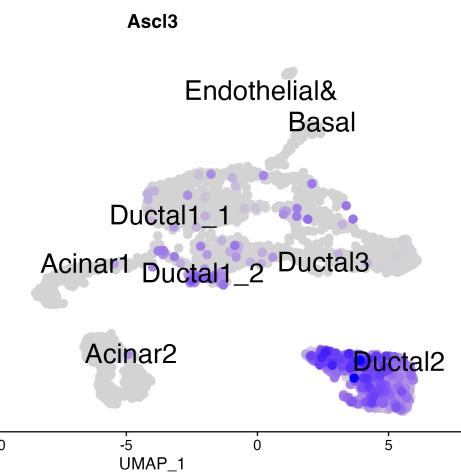
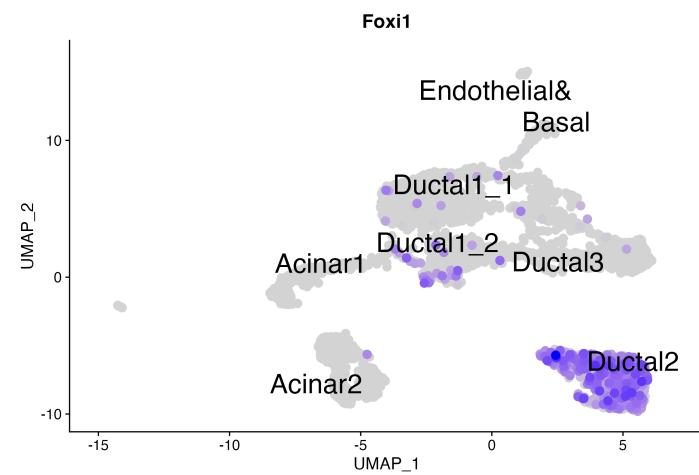
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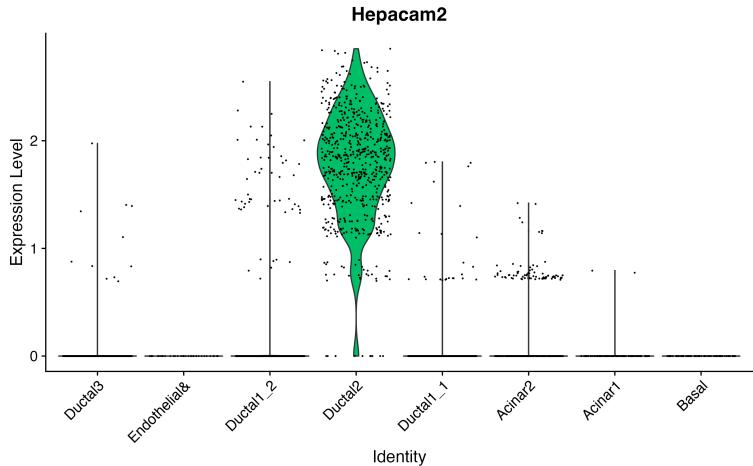
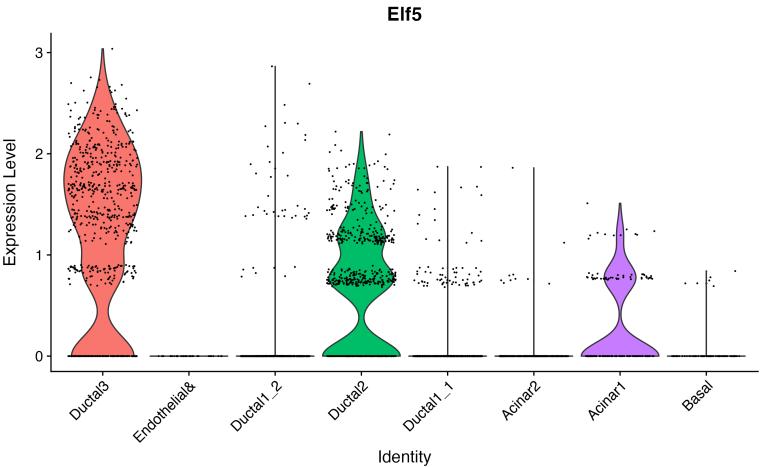
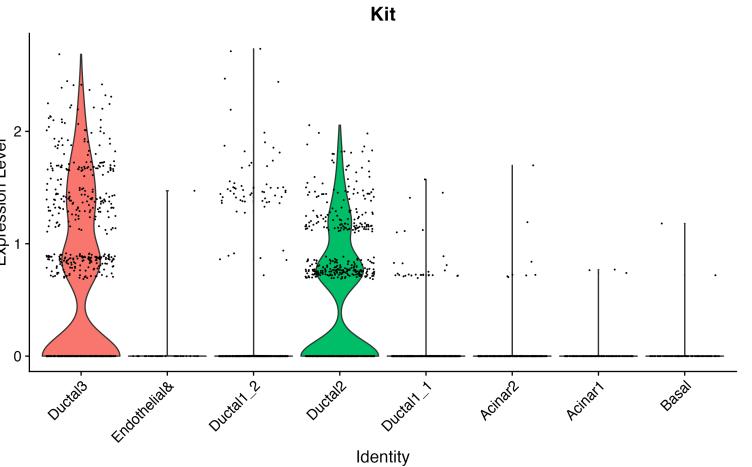
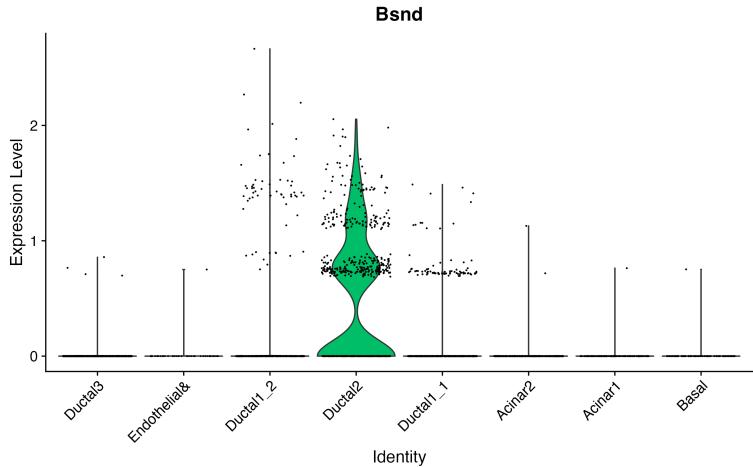
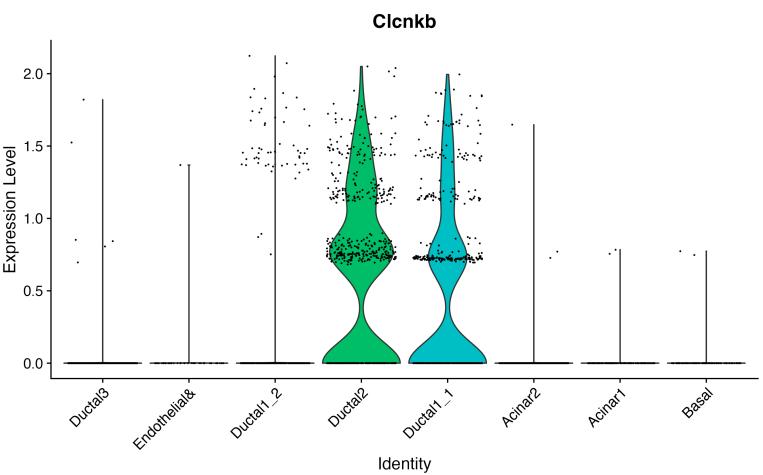
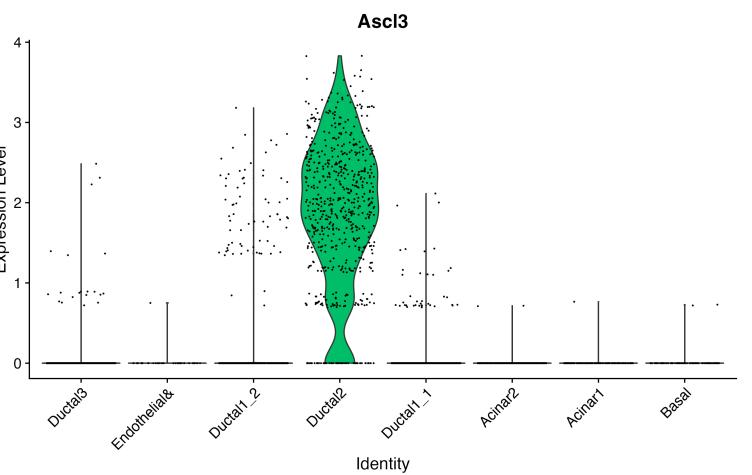
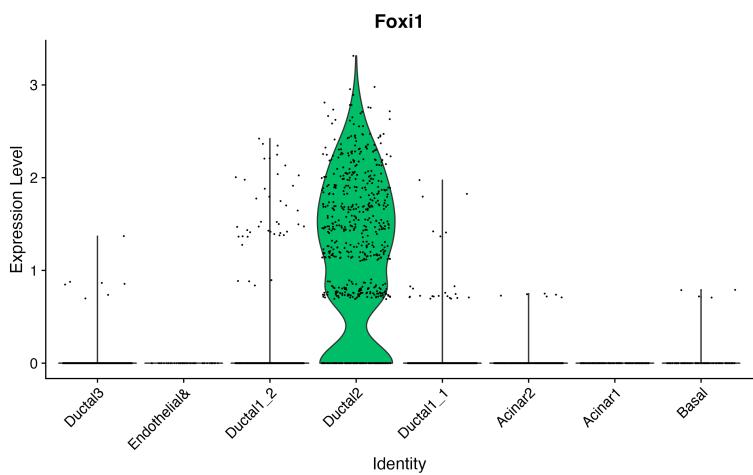
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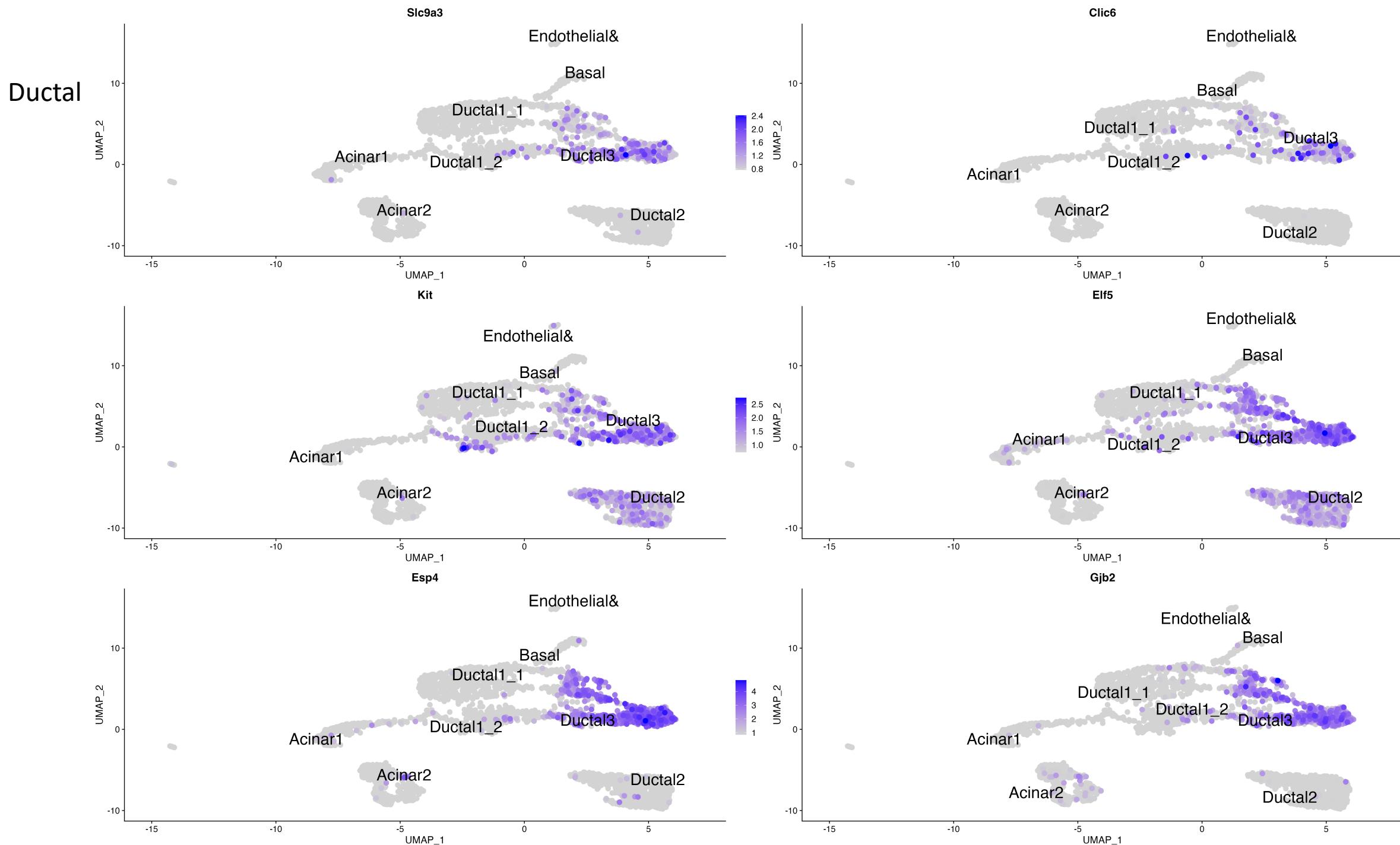


Ductal 2

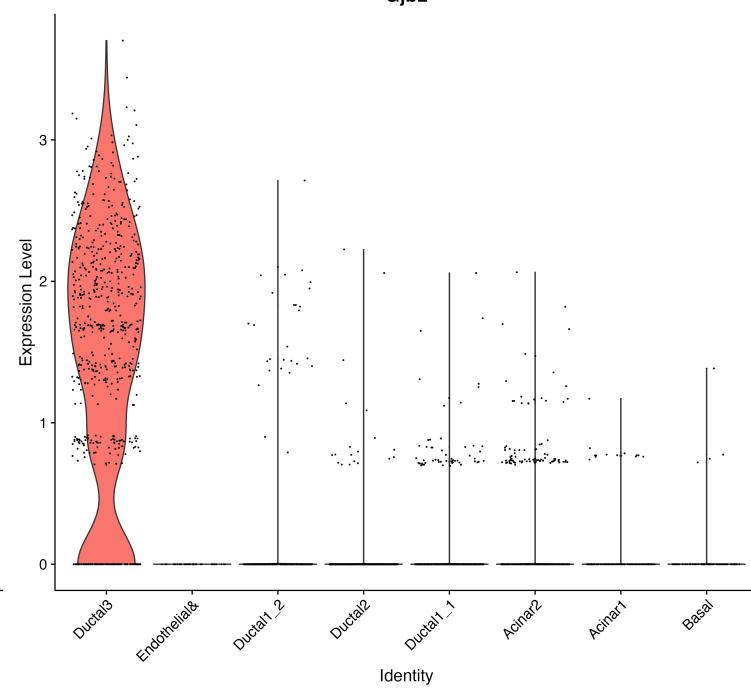
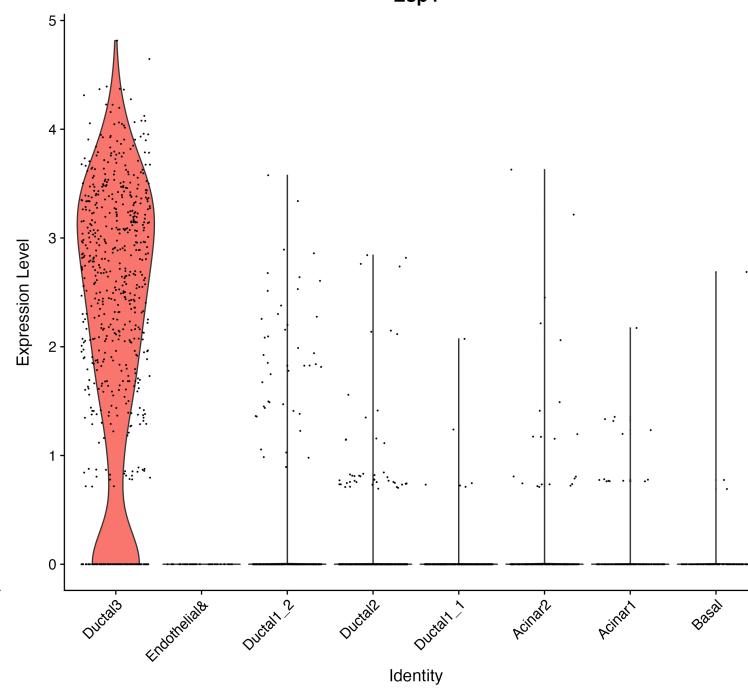
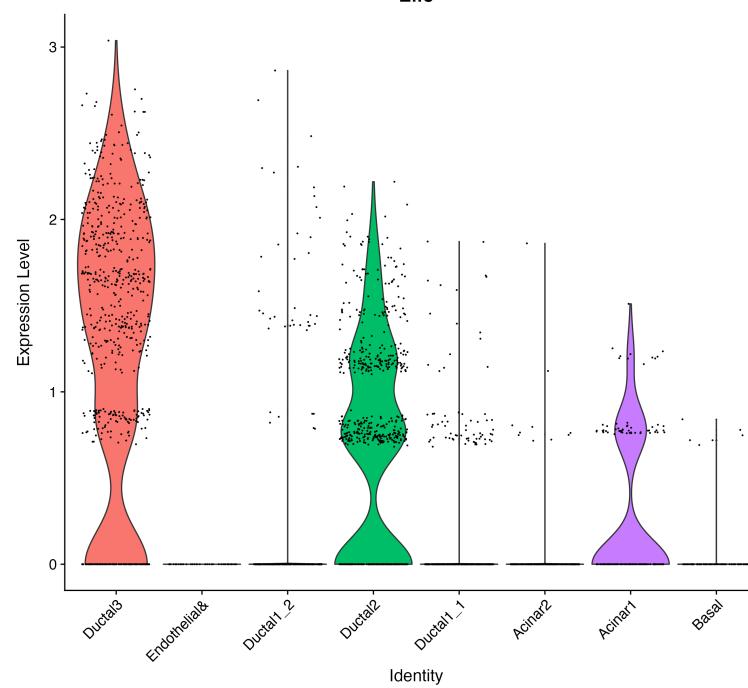
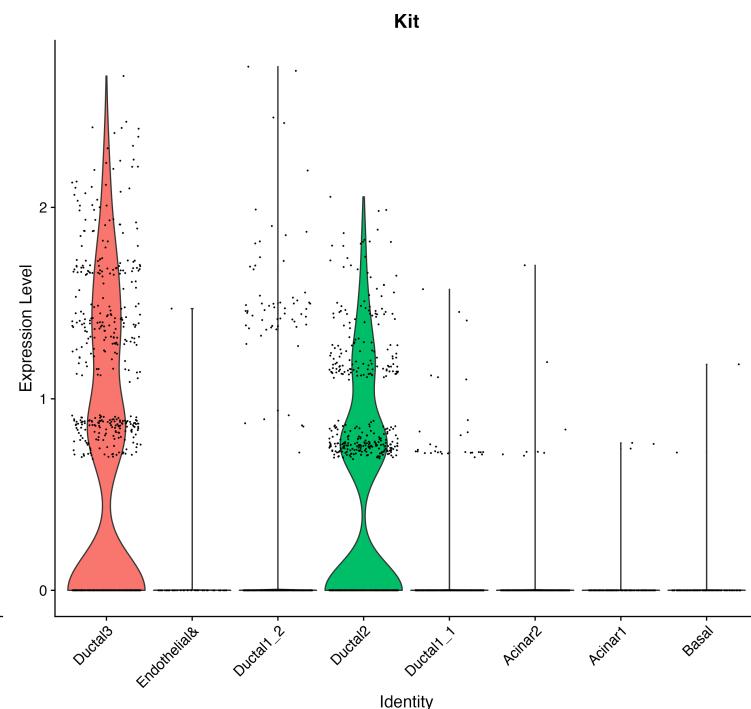
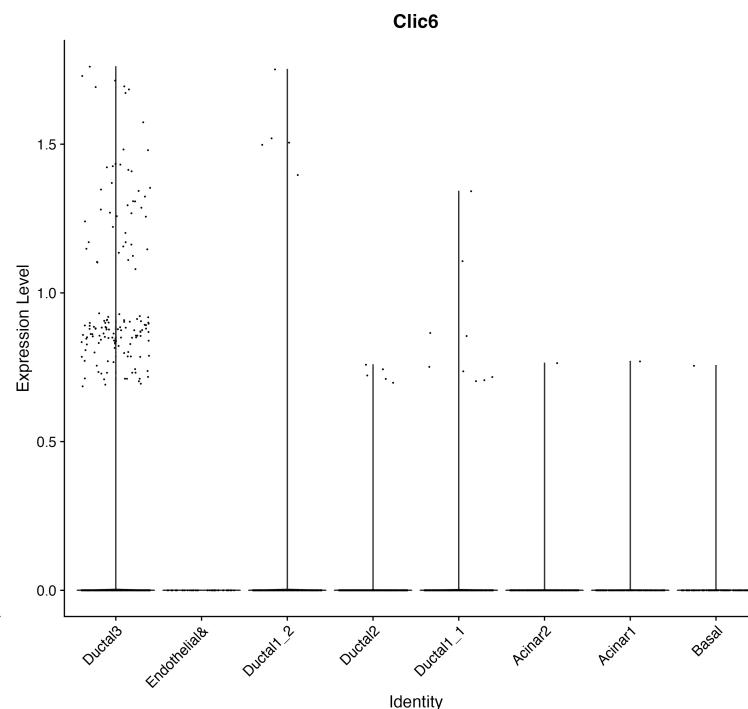
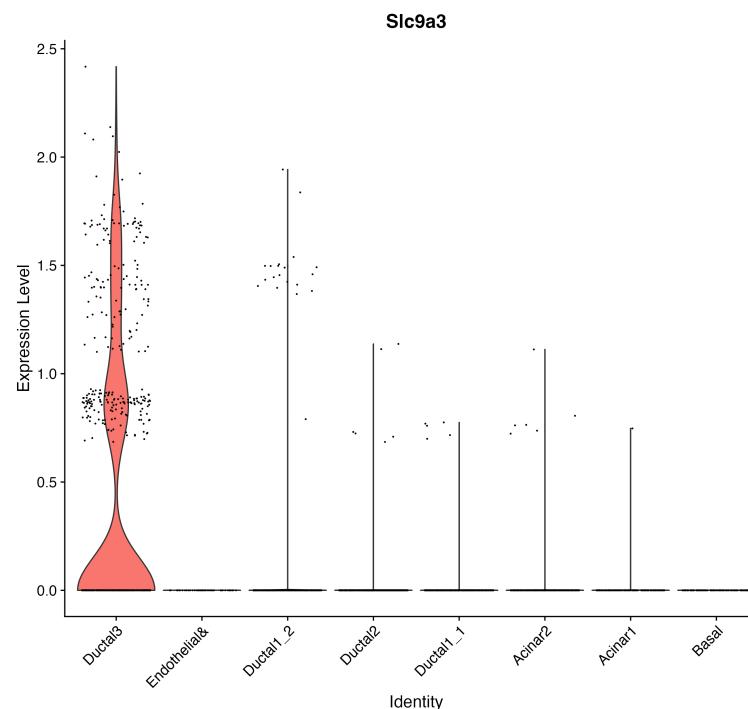


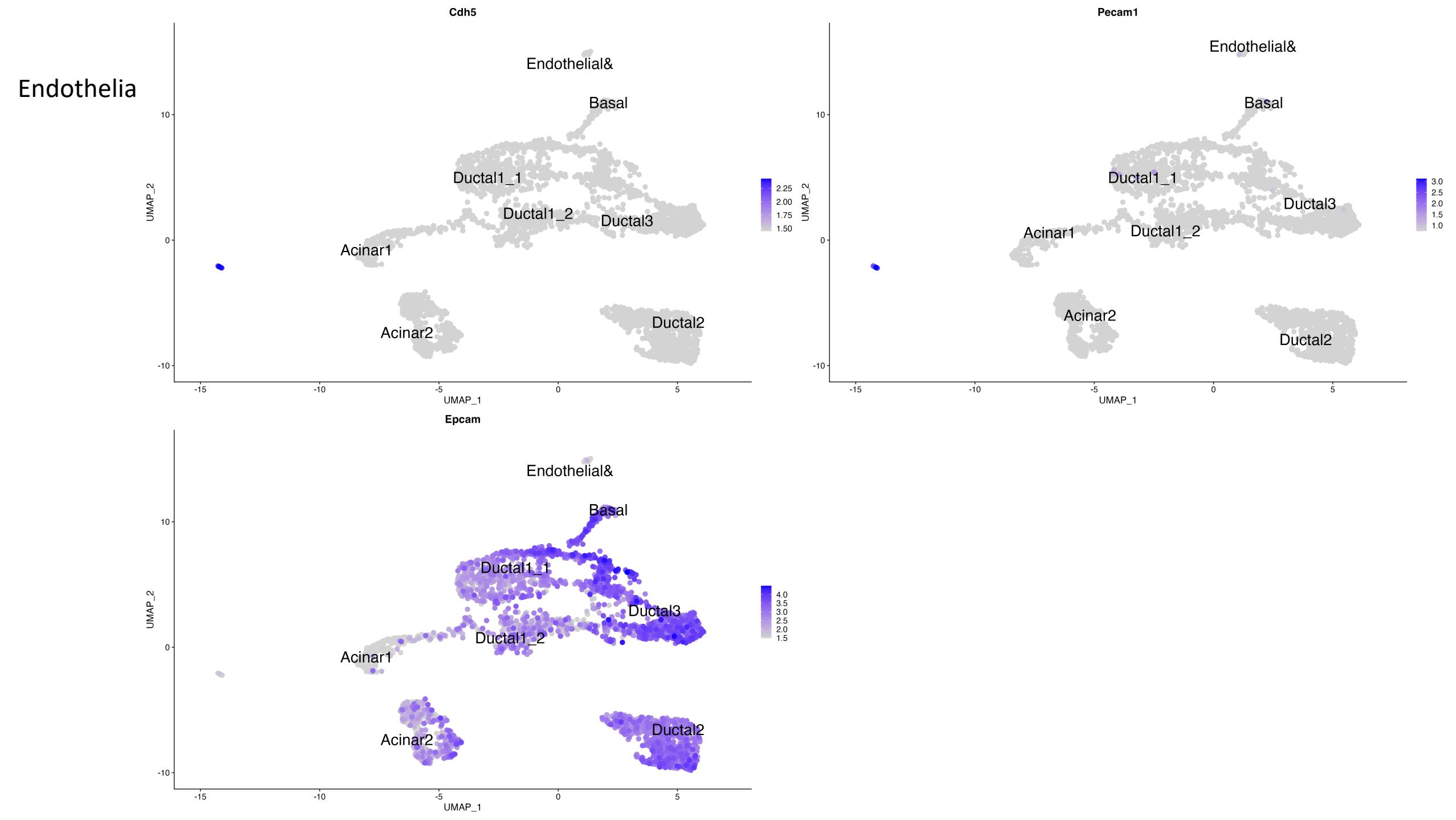
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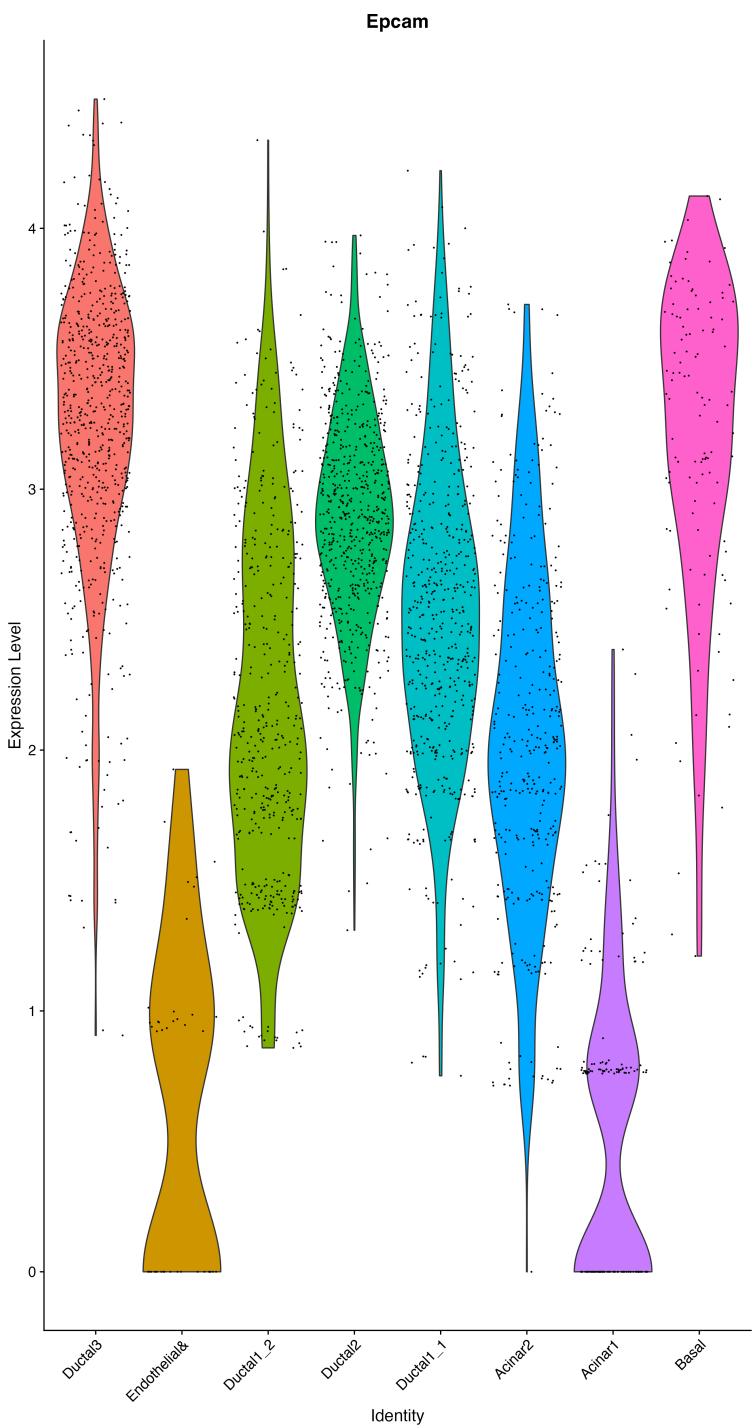
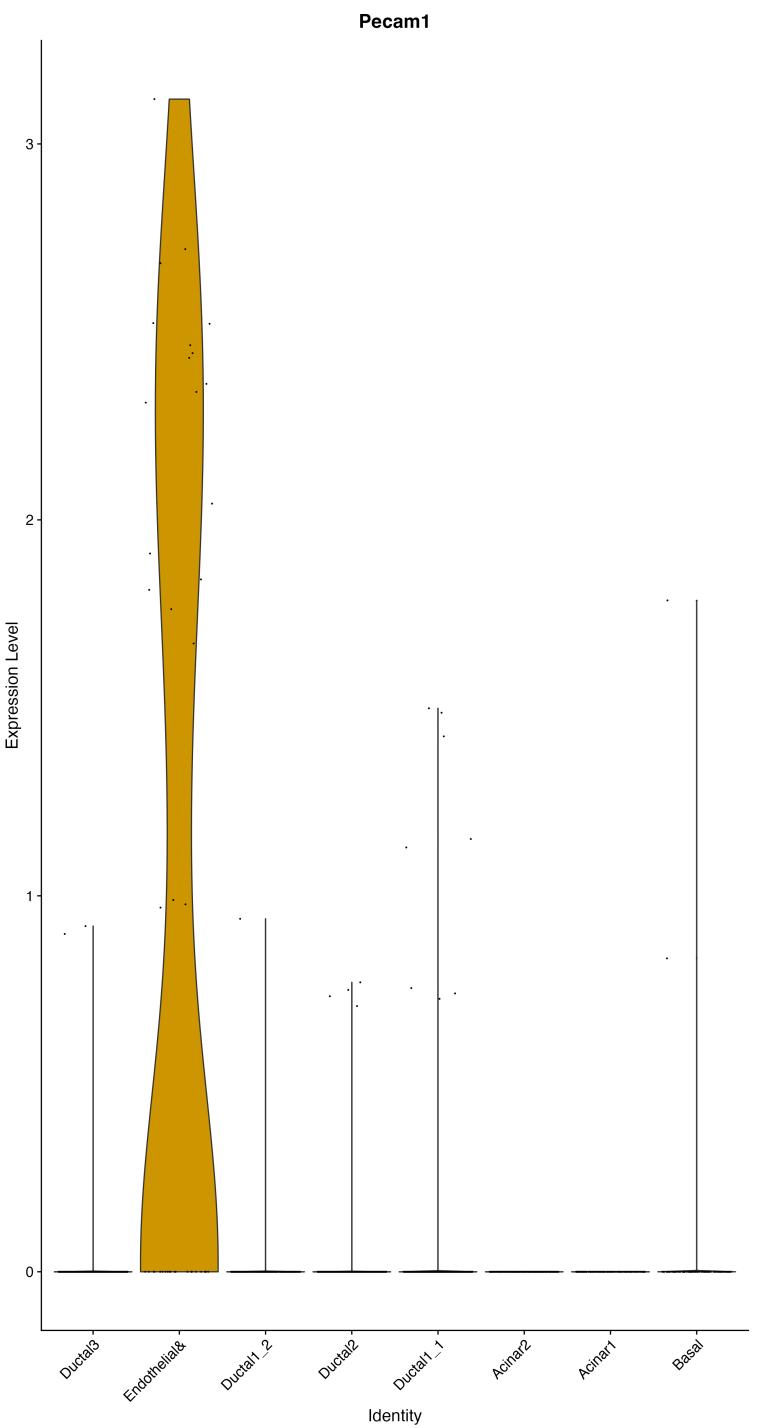
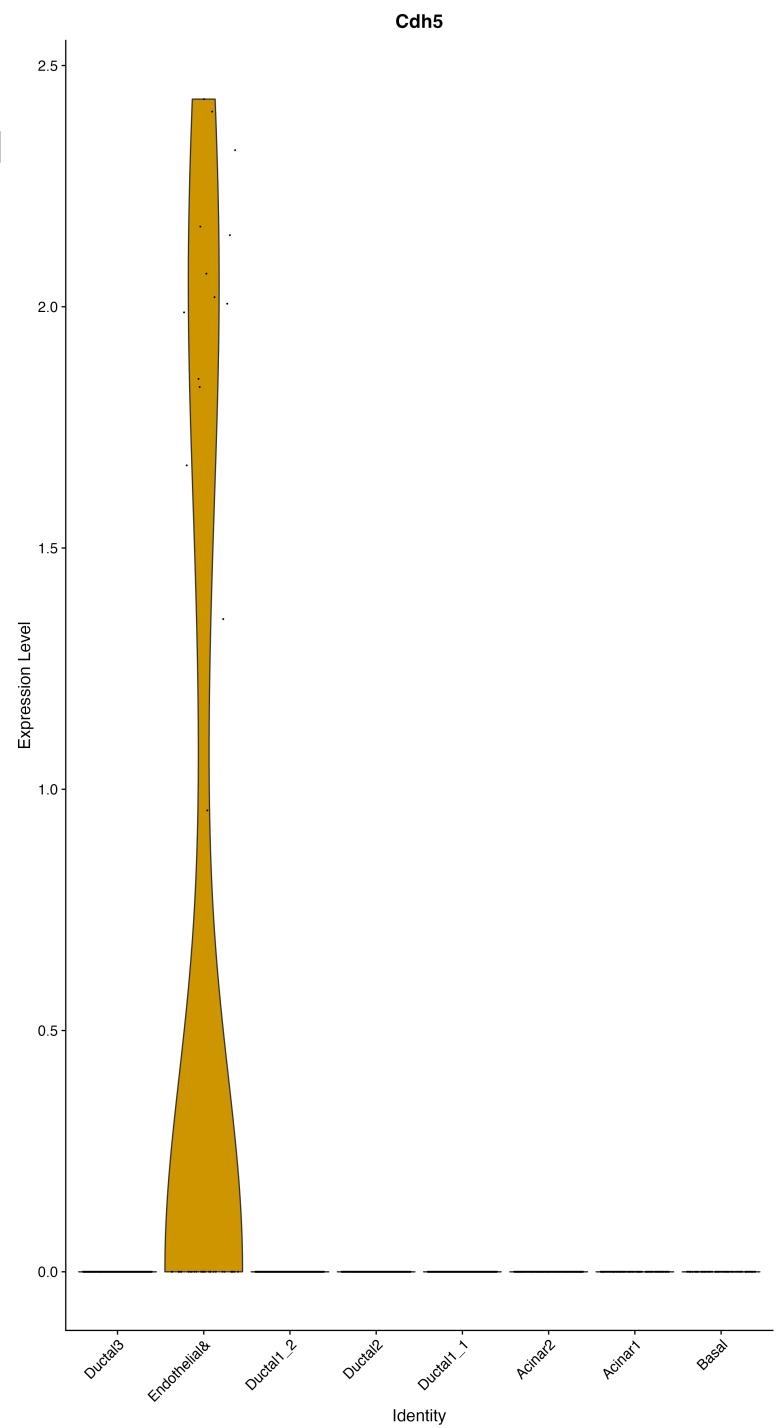


# Ductal 3



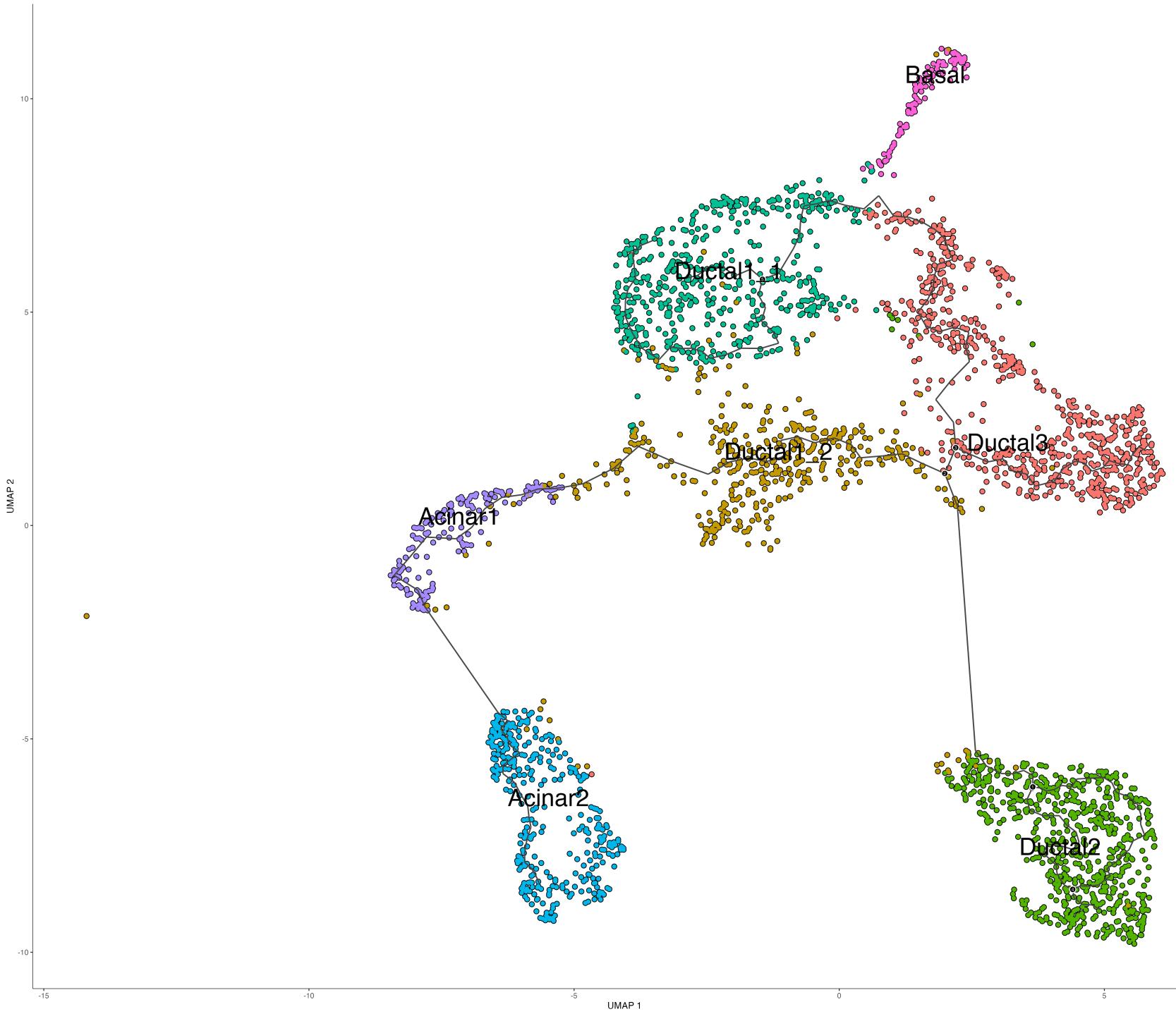


## Endothelial



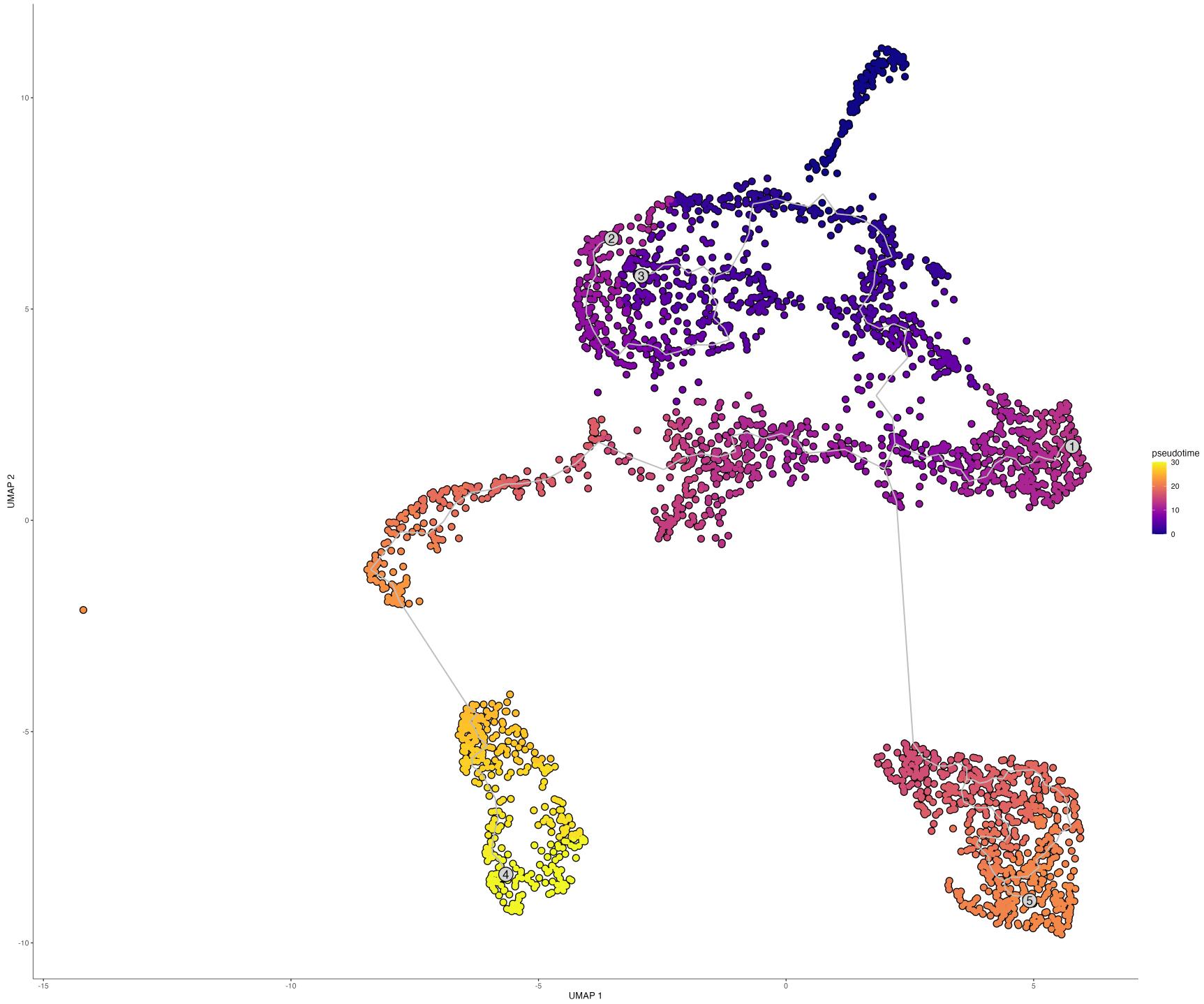
# Trajectory plot

## Without endothelial

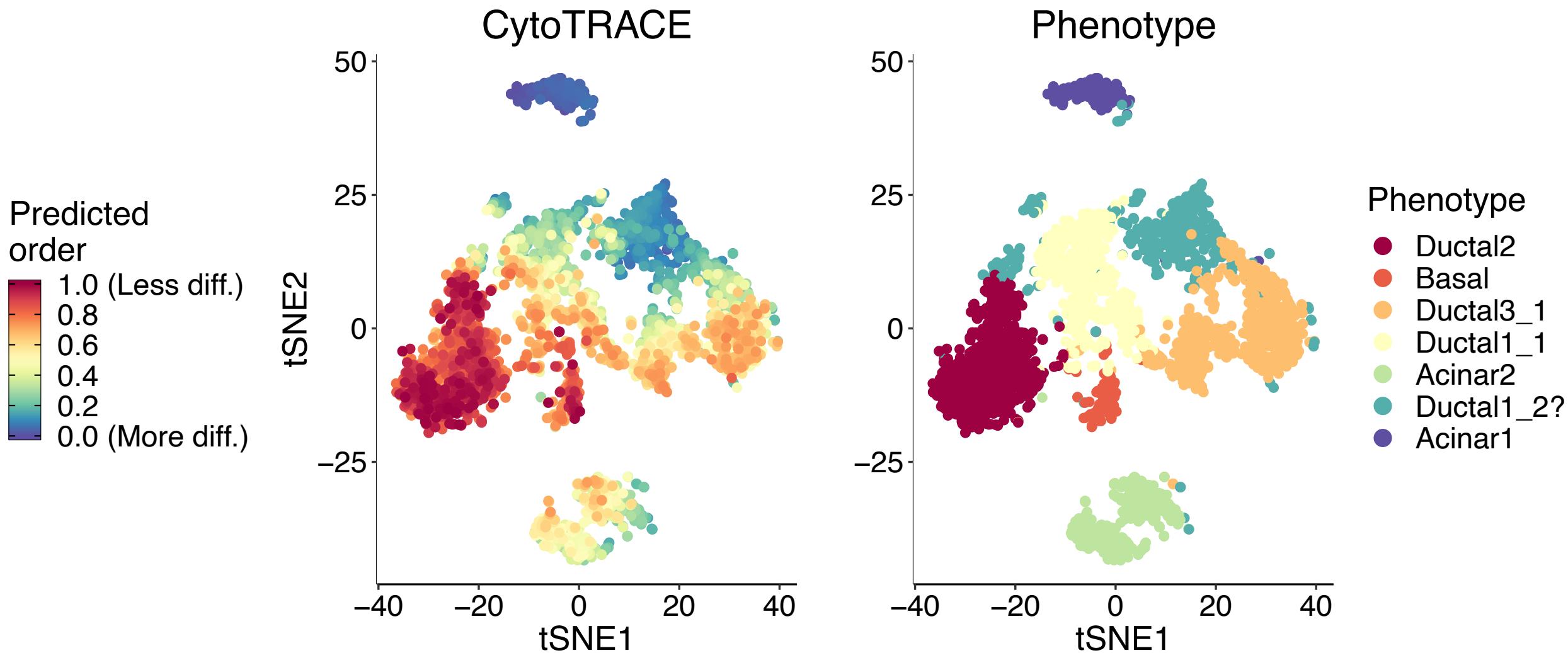


# Pseudotime plot

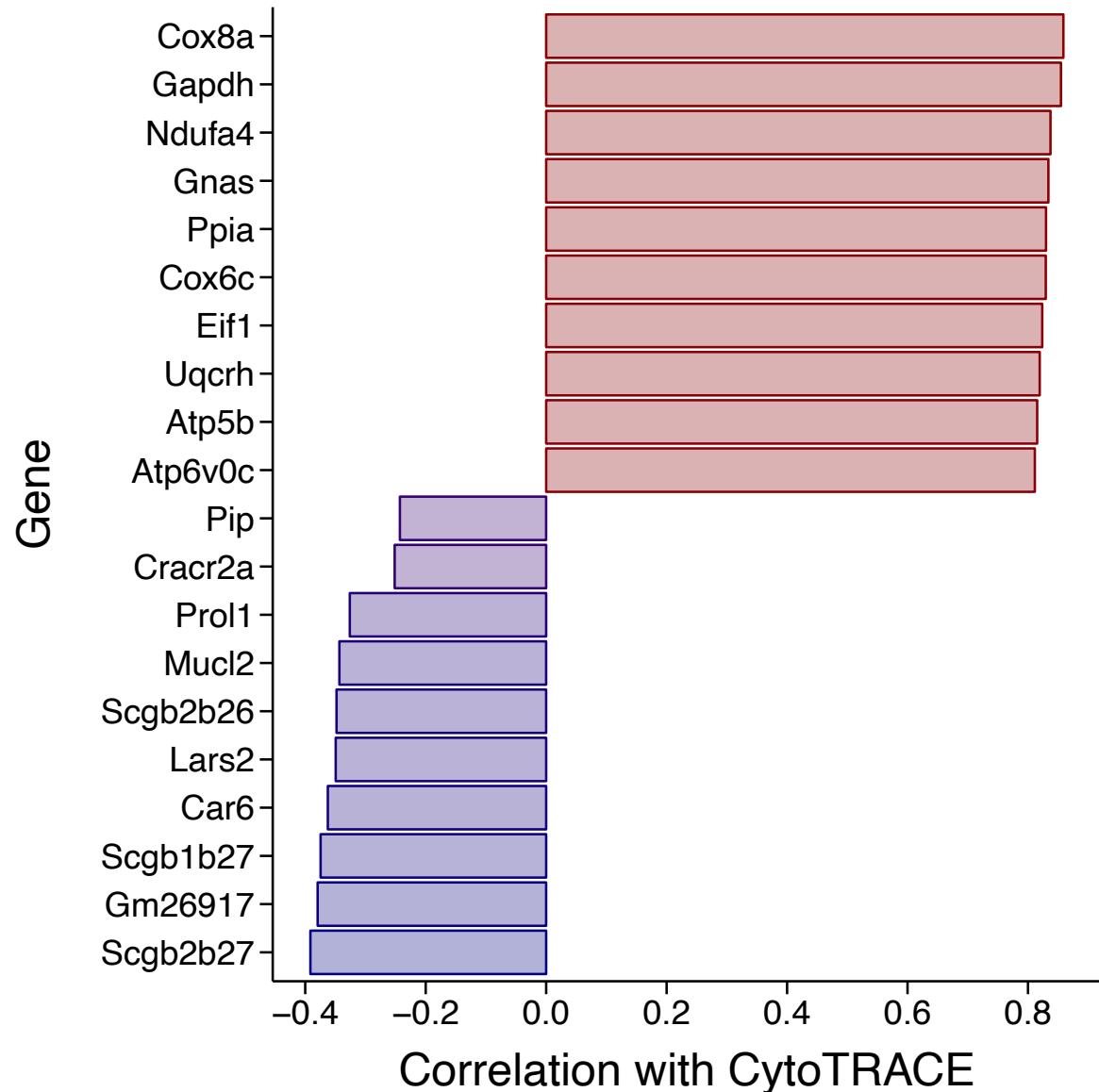
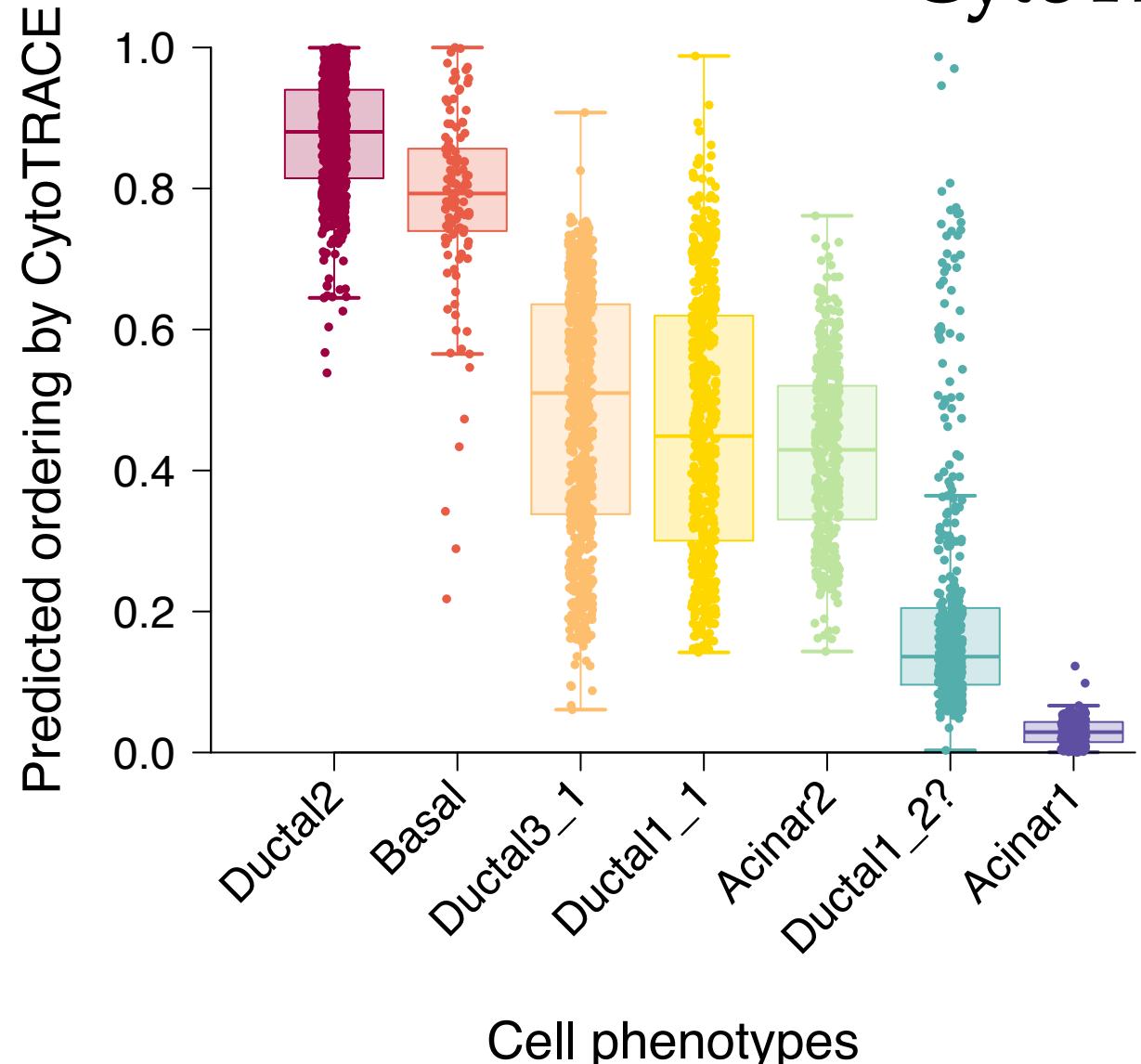
Without endothelial



# CytoTRACE



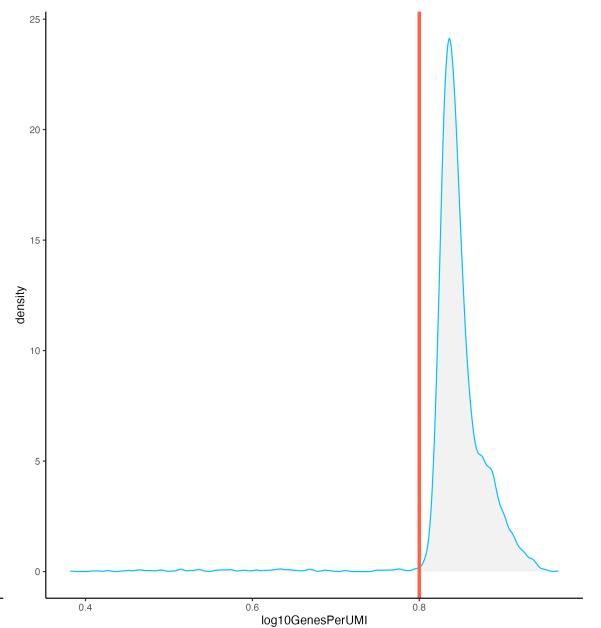
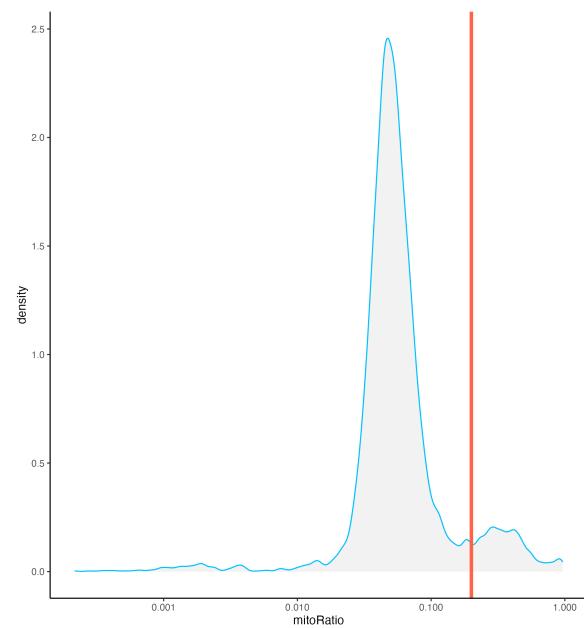
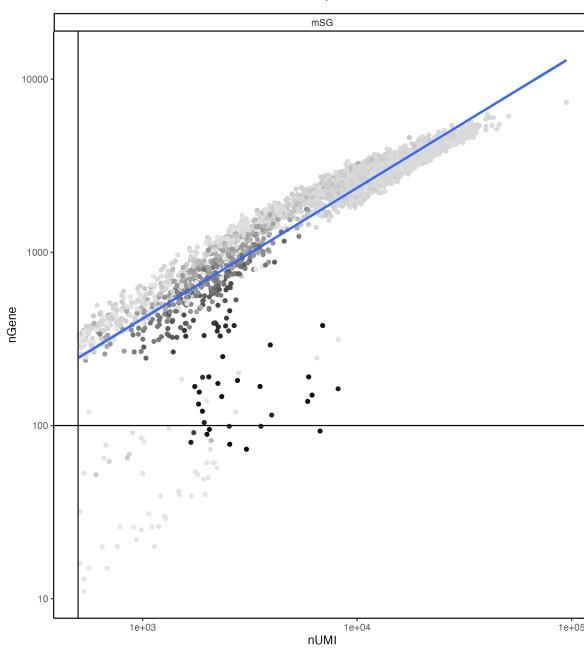
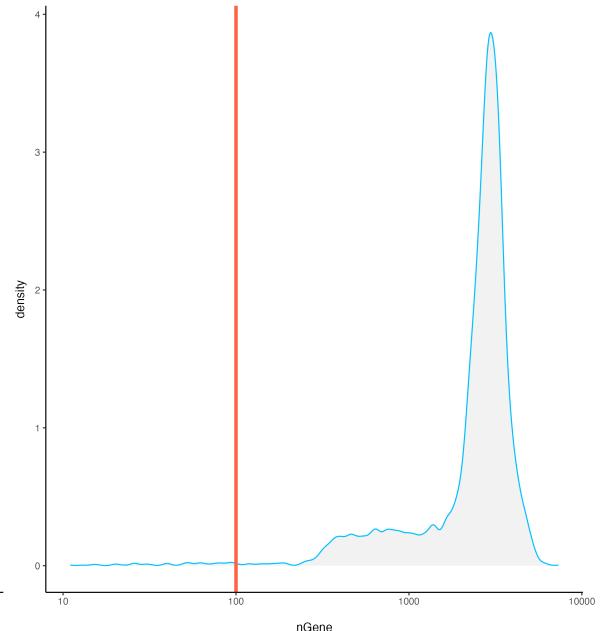
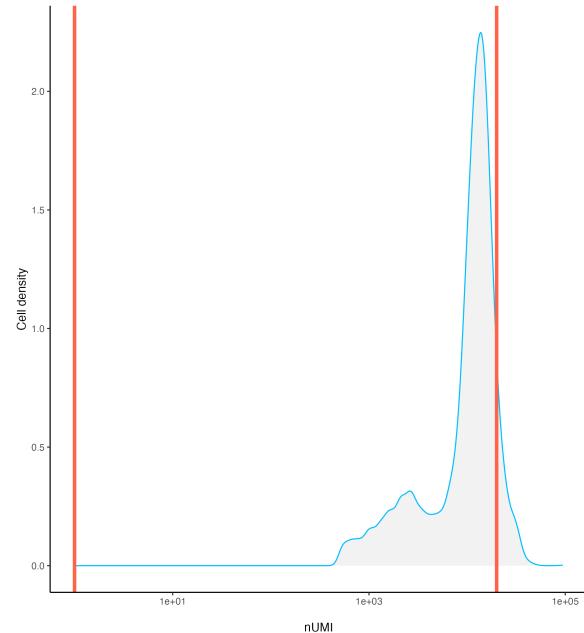
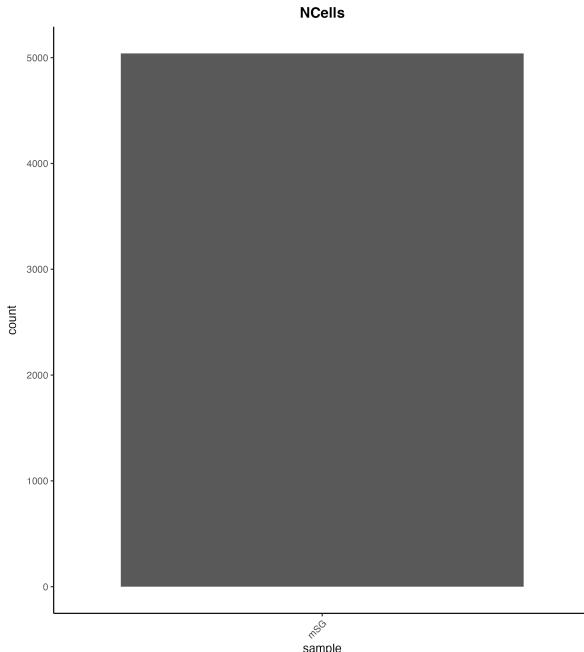
# CytoTRACE



# Gene Module (Dataset1)

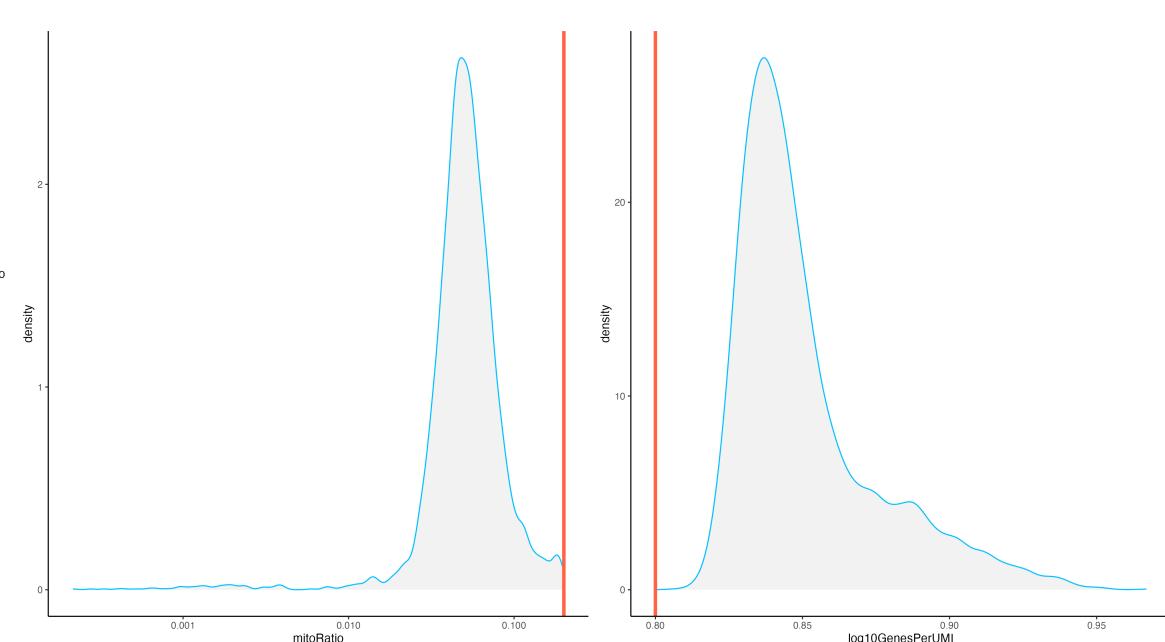
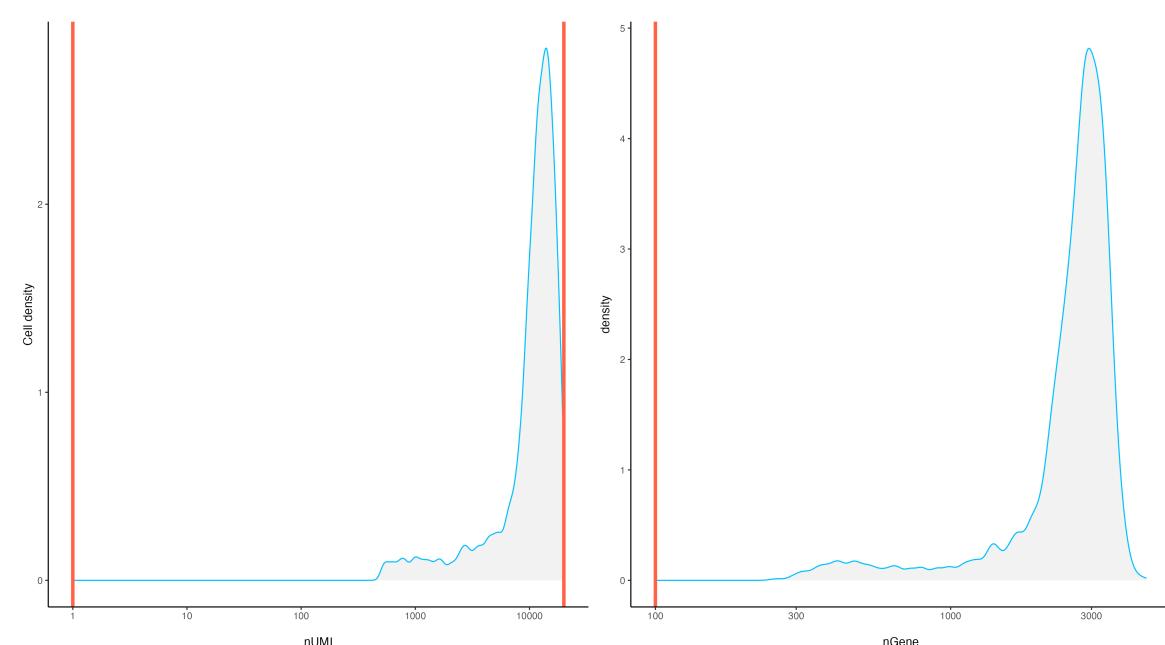
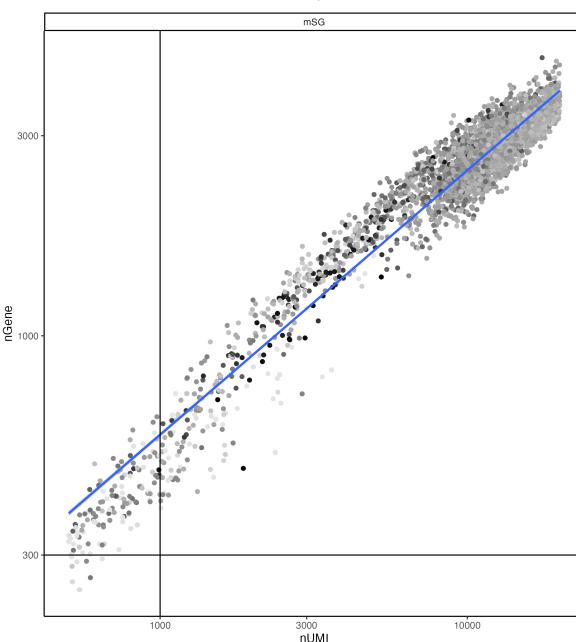
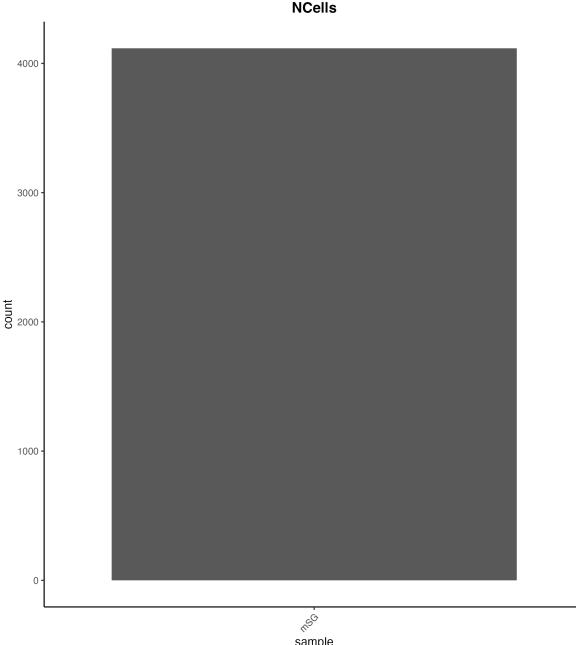


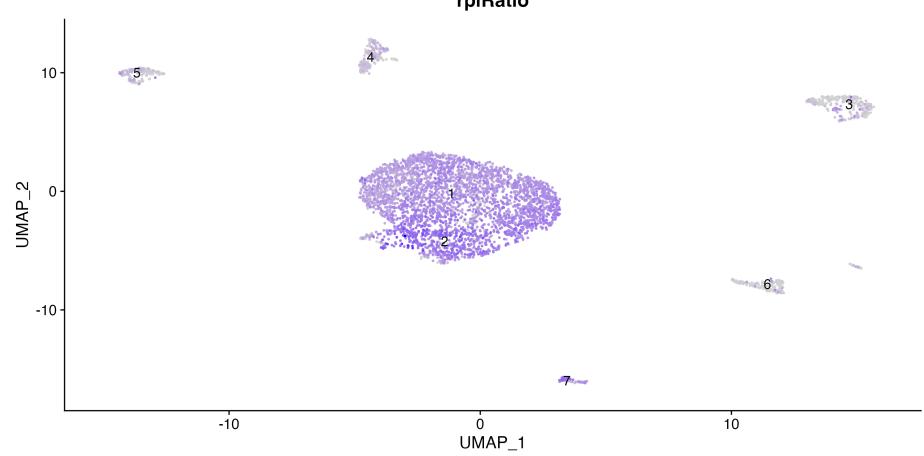
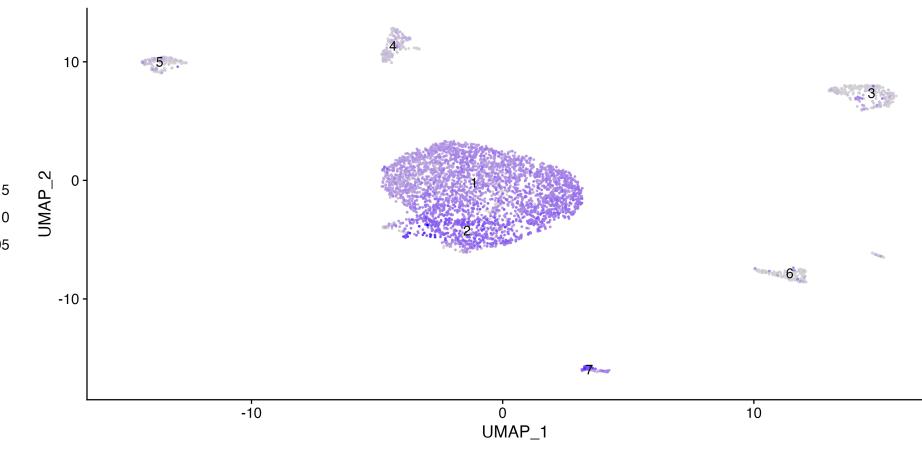
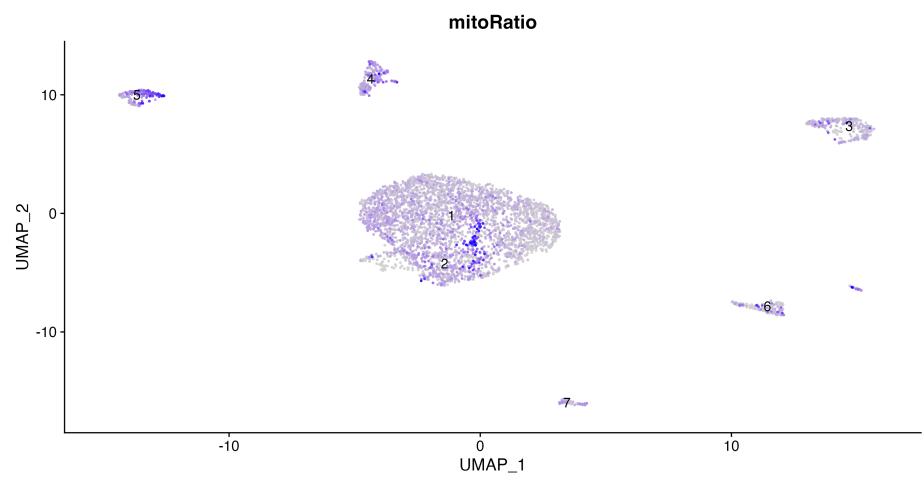
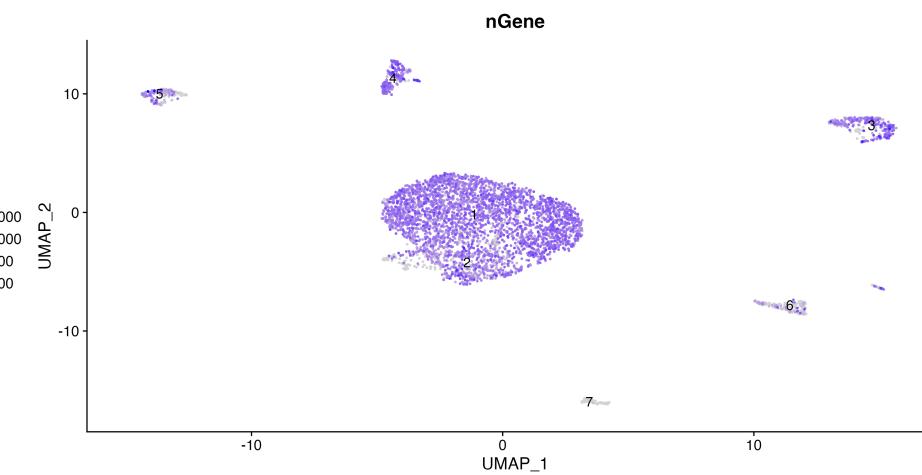
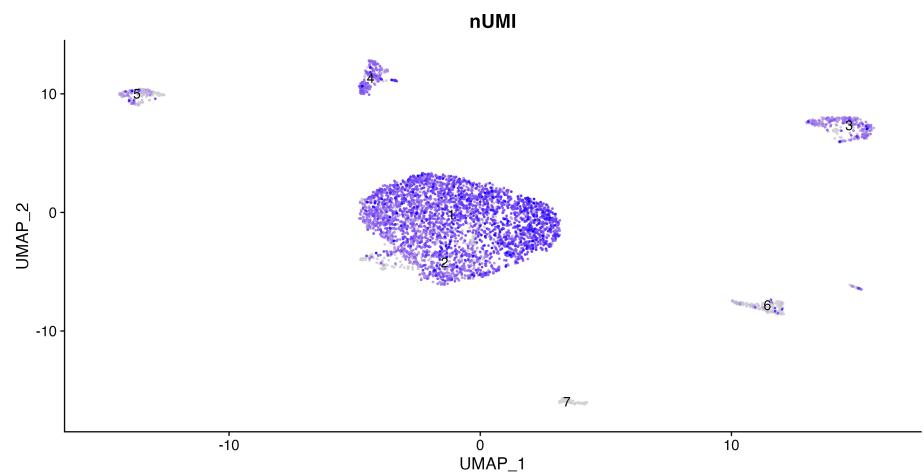
# Dataset2



# Quality Control

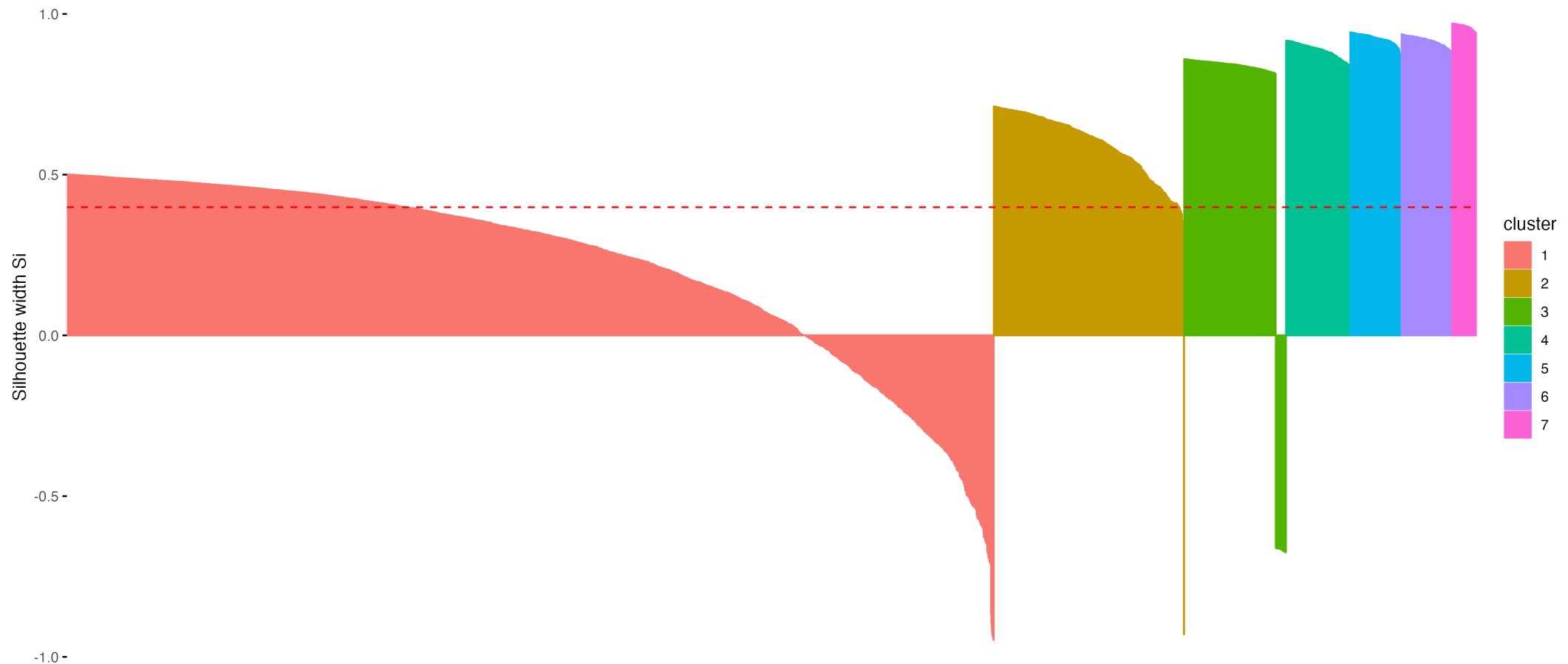
```
set.seed (12)
filtered_seurat <- subset(x = rare,
  subset= (nUMI >= 1) &
  (nUMI <=20000) &
  (nGene >= 100) &
  (log10GenesPerUMI > 0.8) &
  (mitoRatio < 0.20))
```

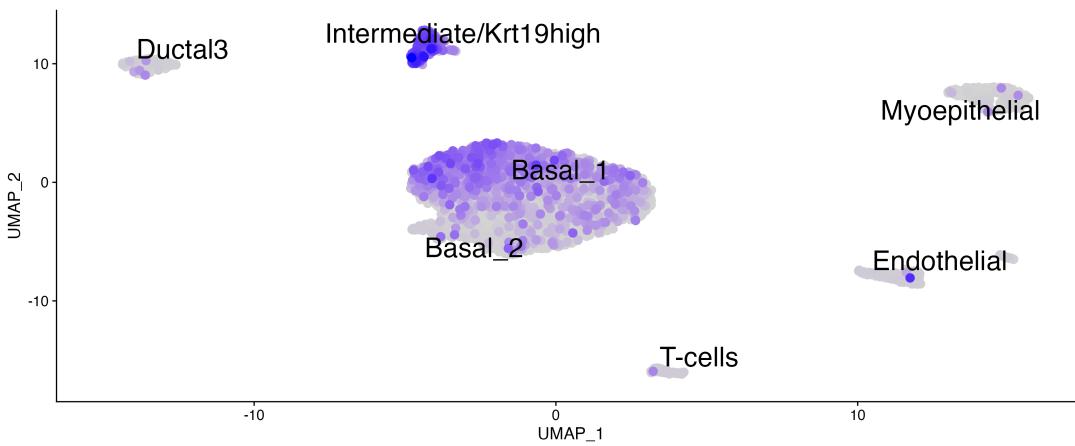
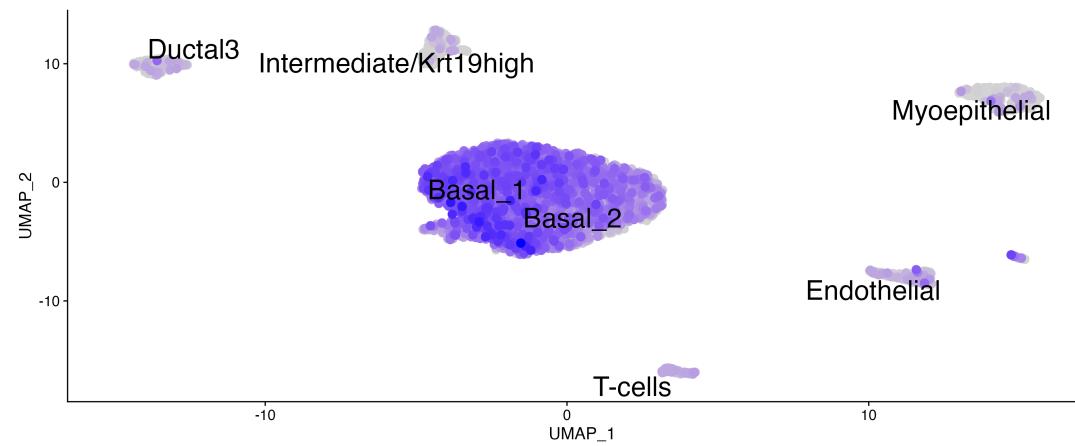
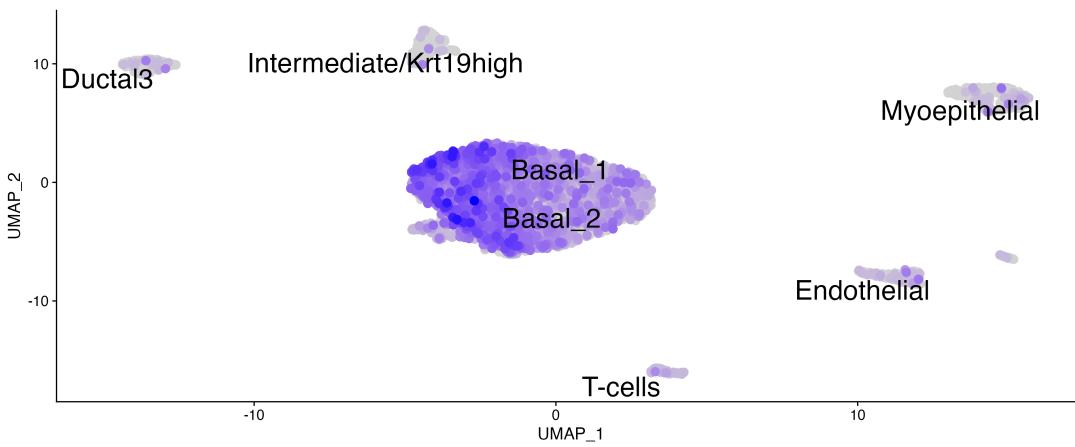
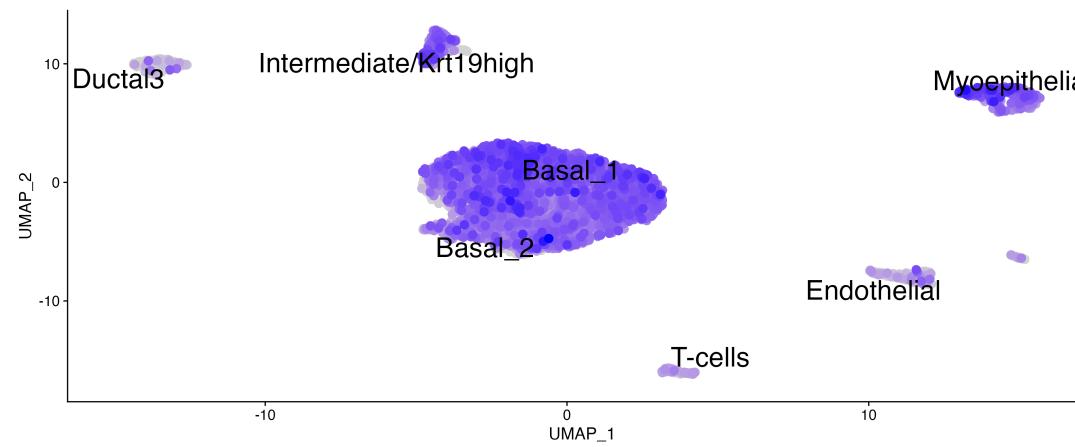
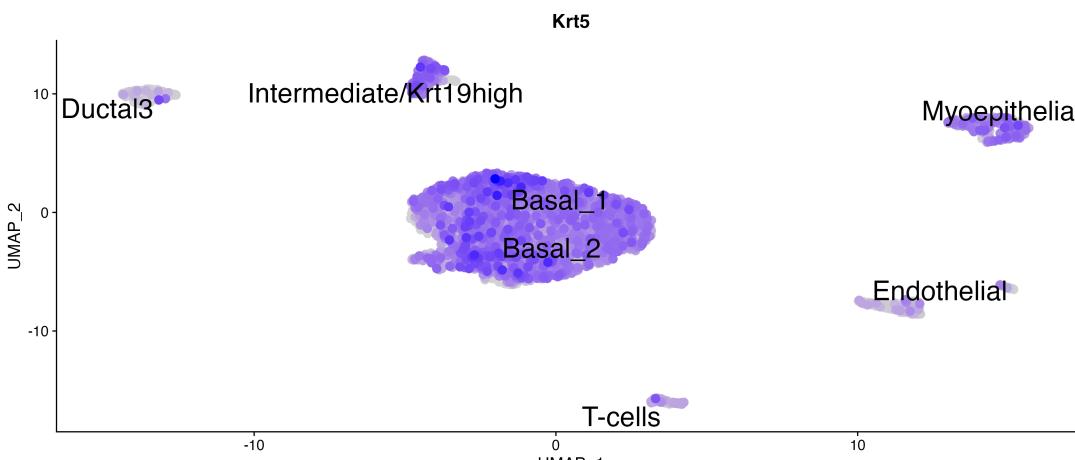
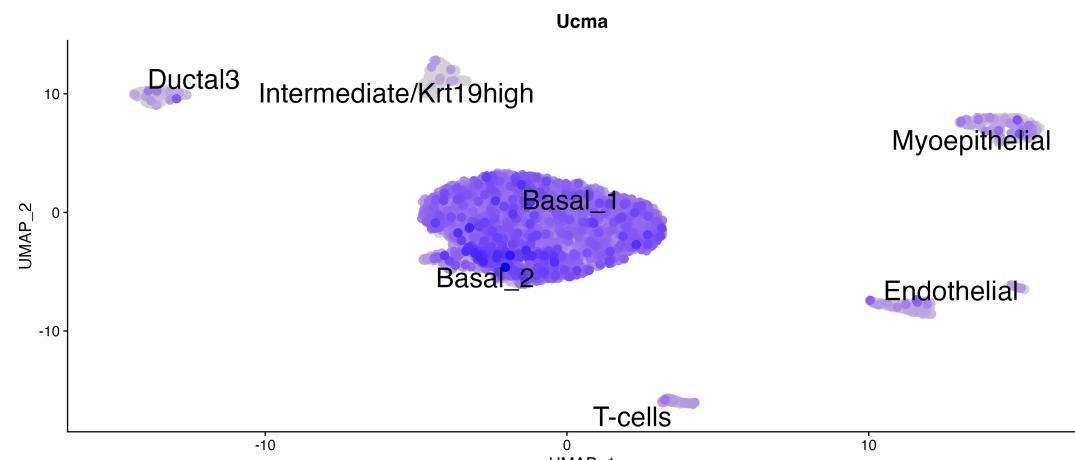




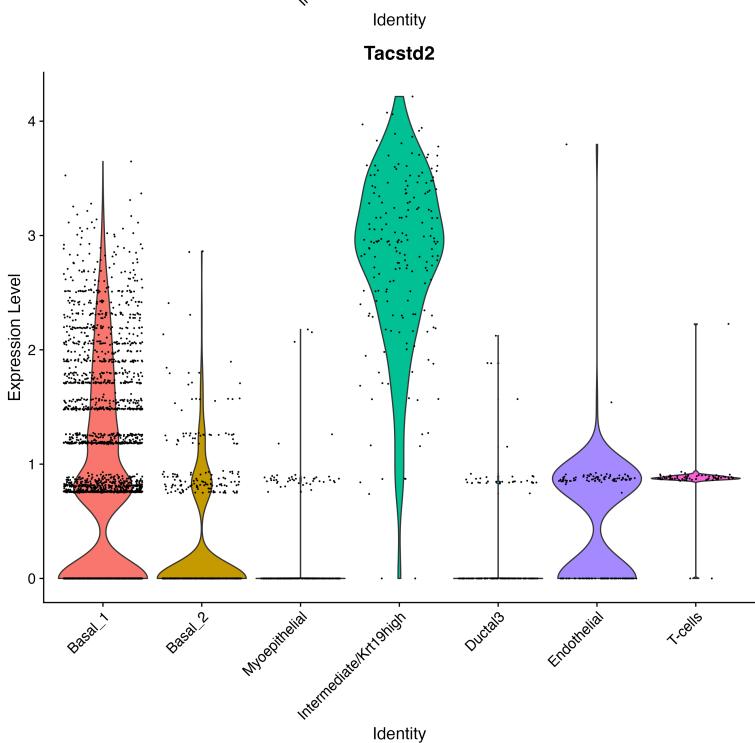
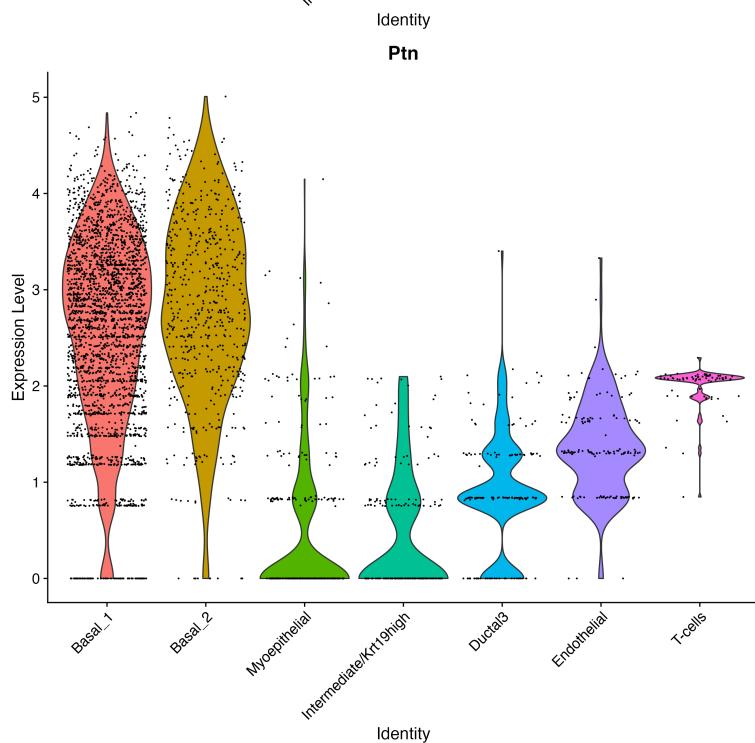
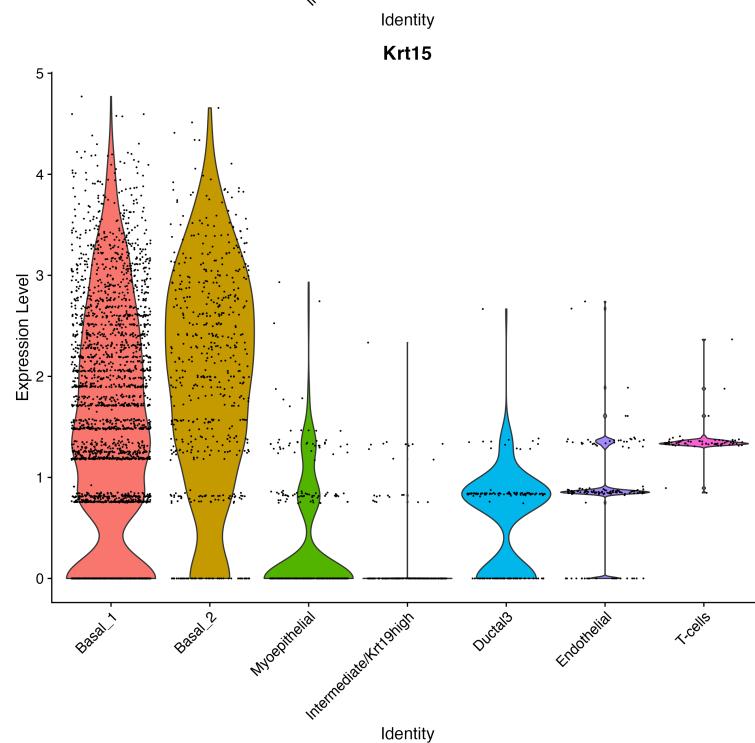
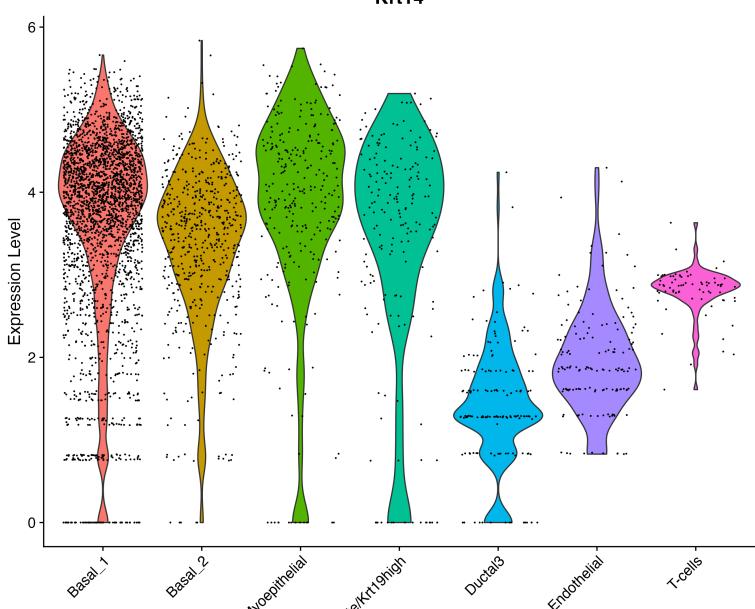
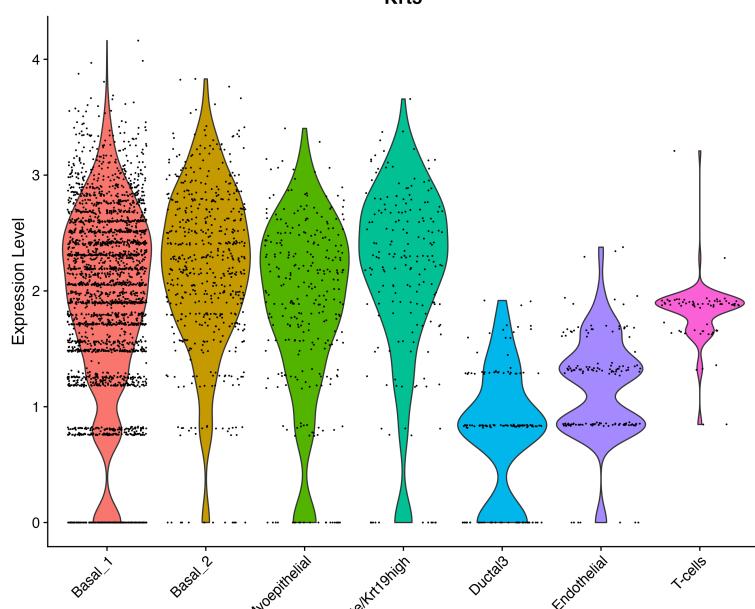
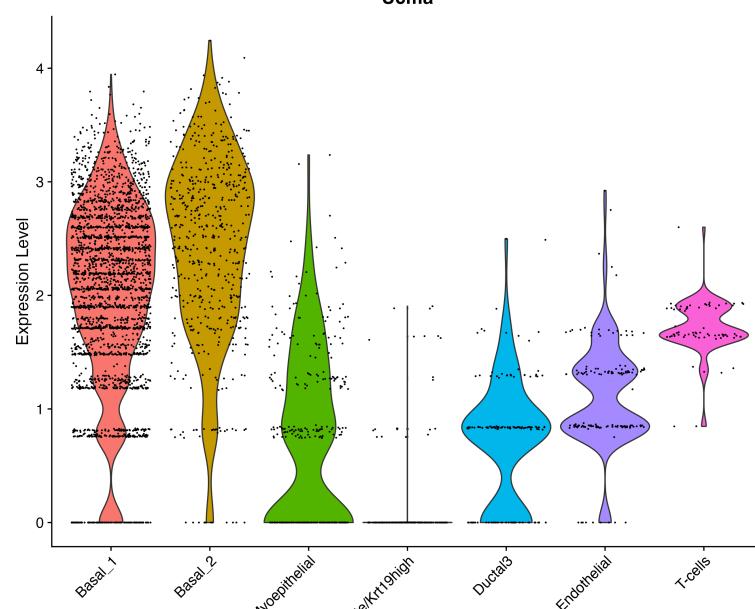
# Clustering – res 0.2

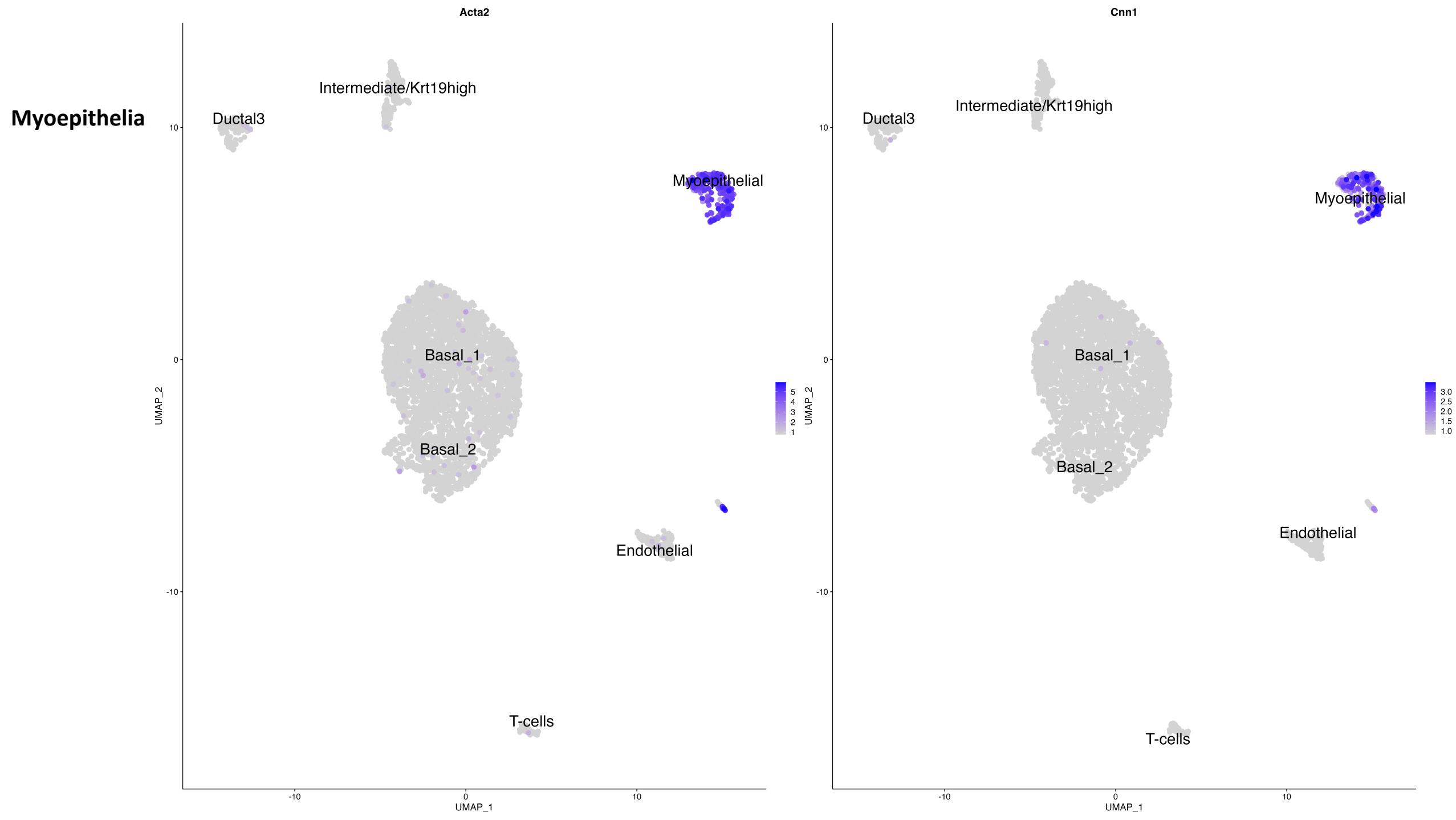
Clusters silhouette plot  
Average silhouette width: 0.4



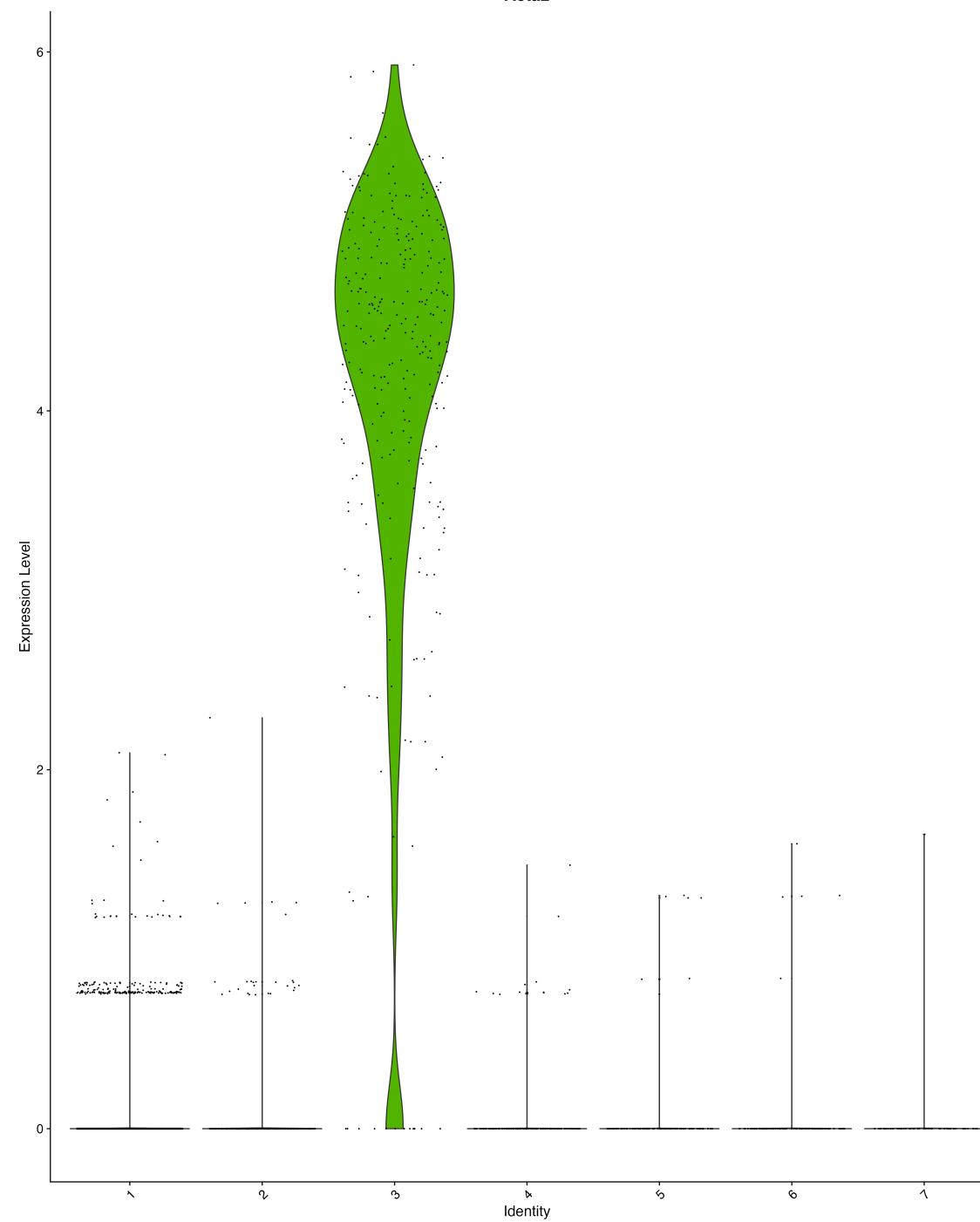
**Basal**

## Basal

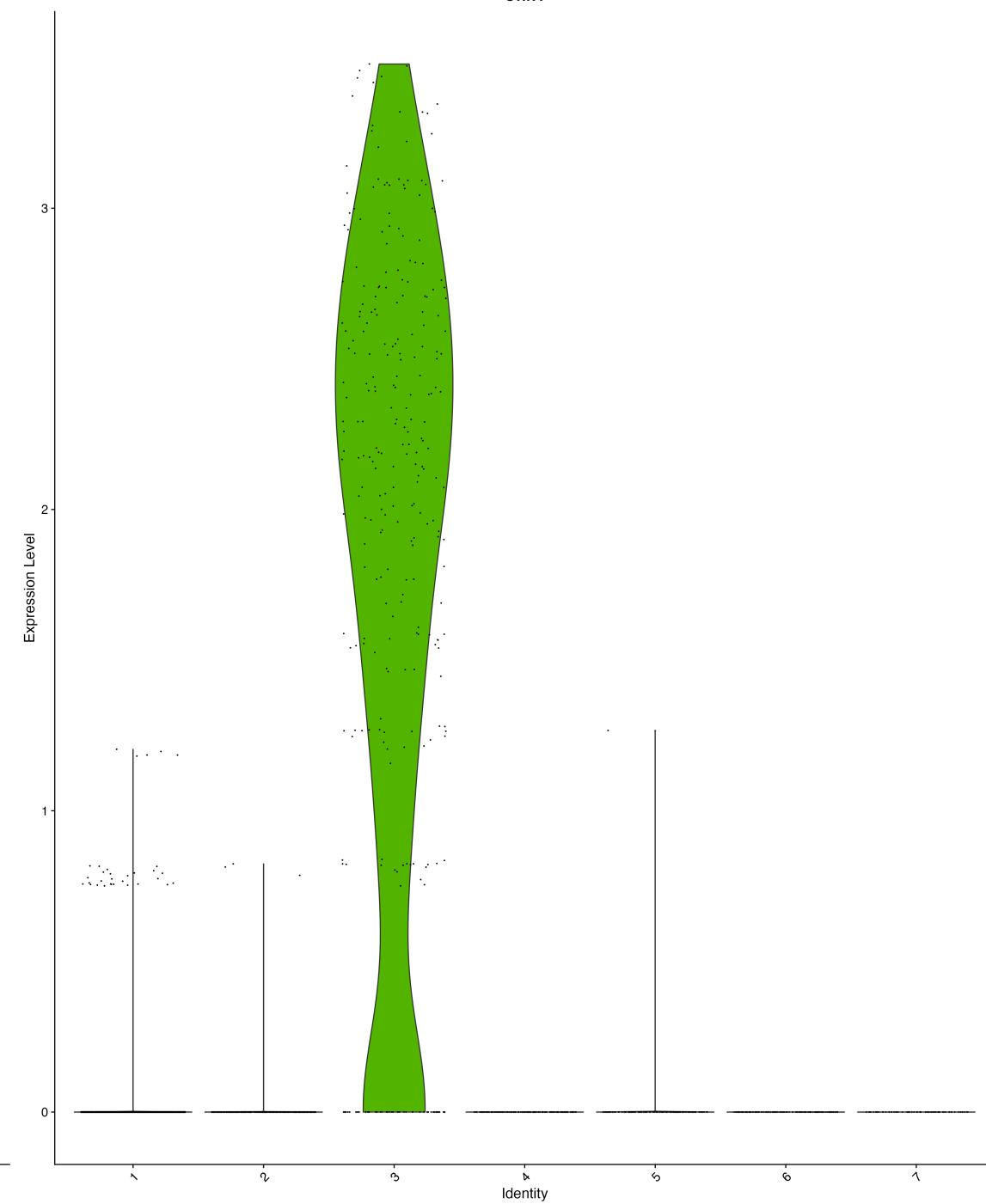


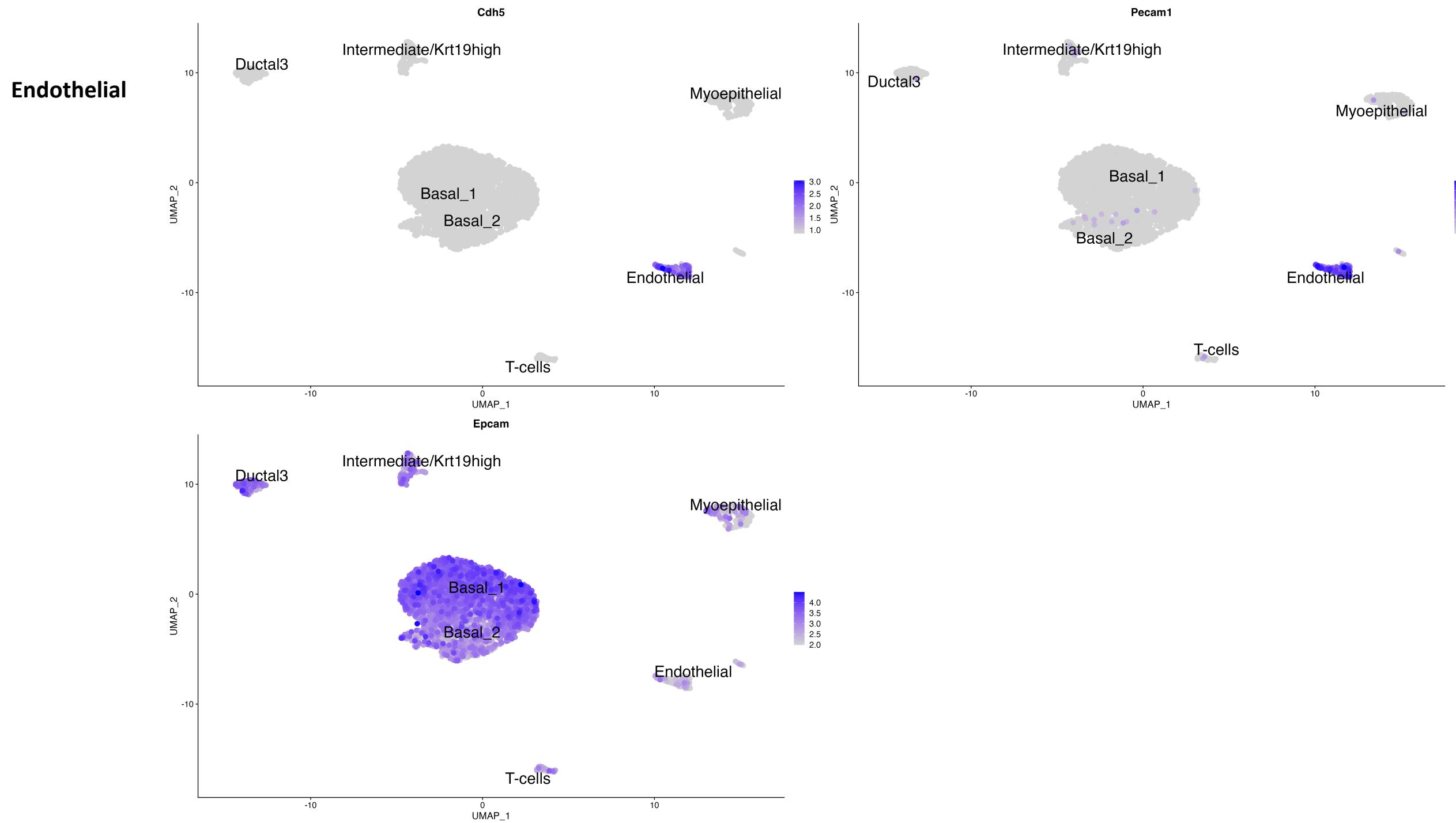


Acta2

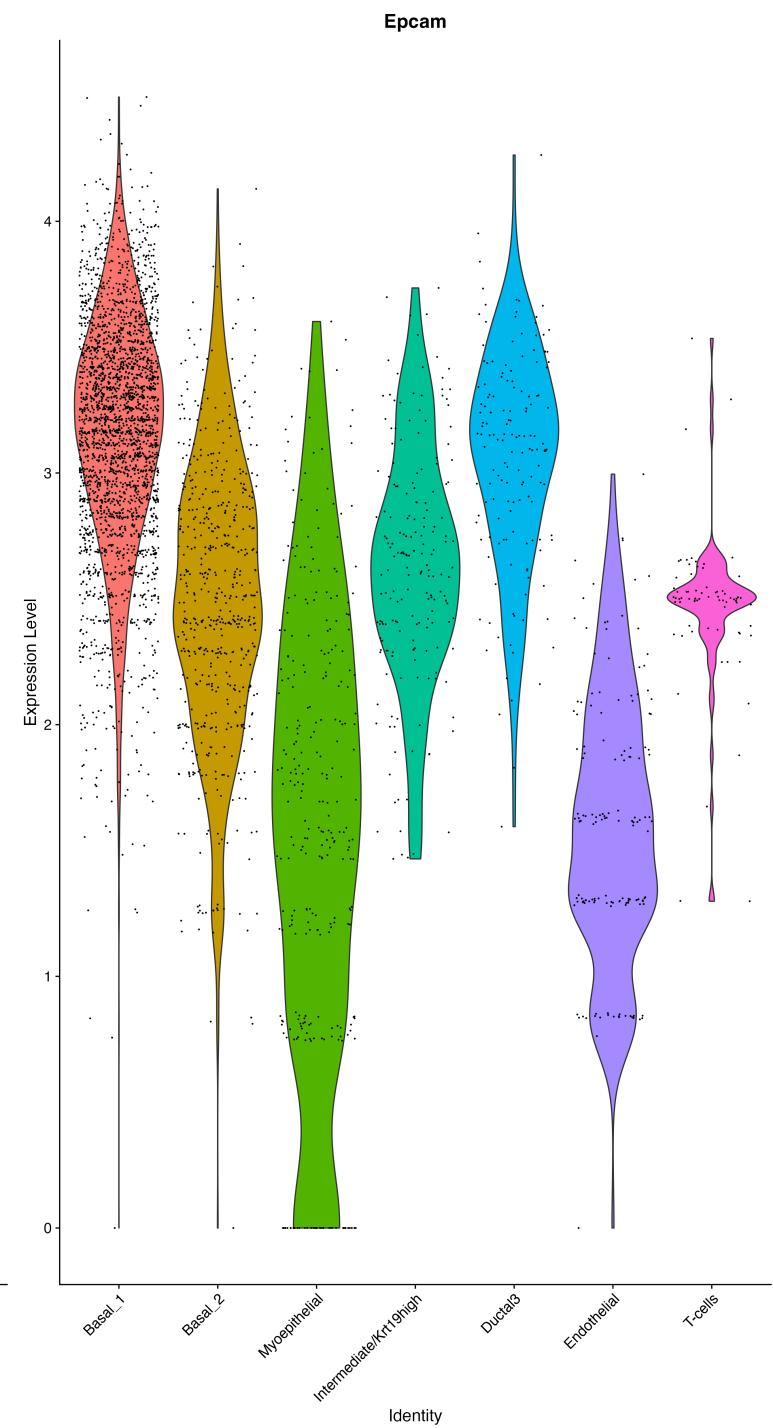
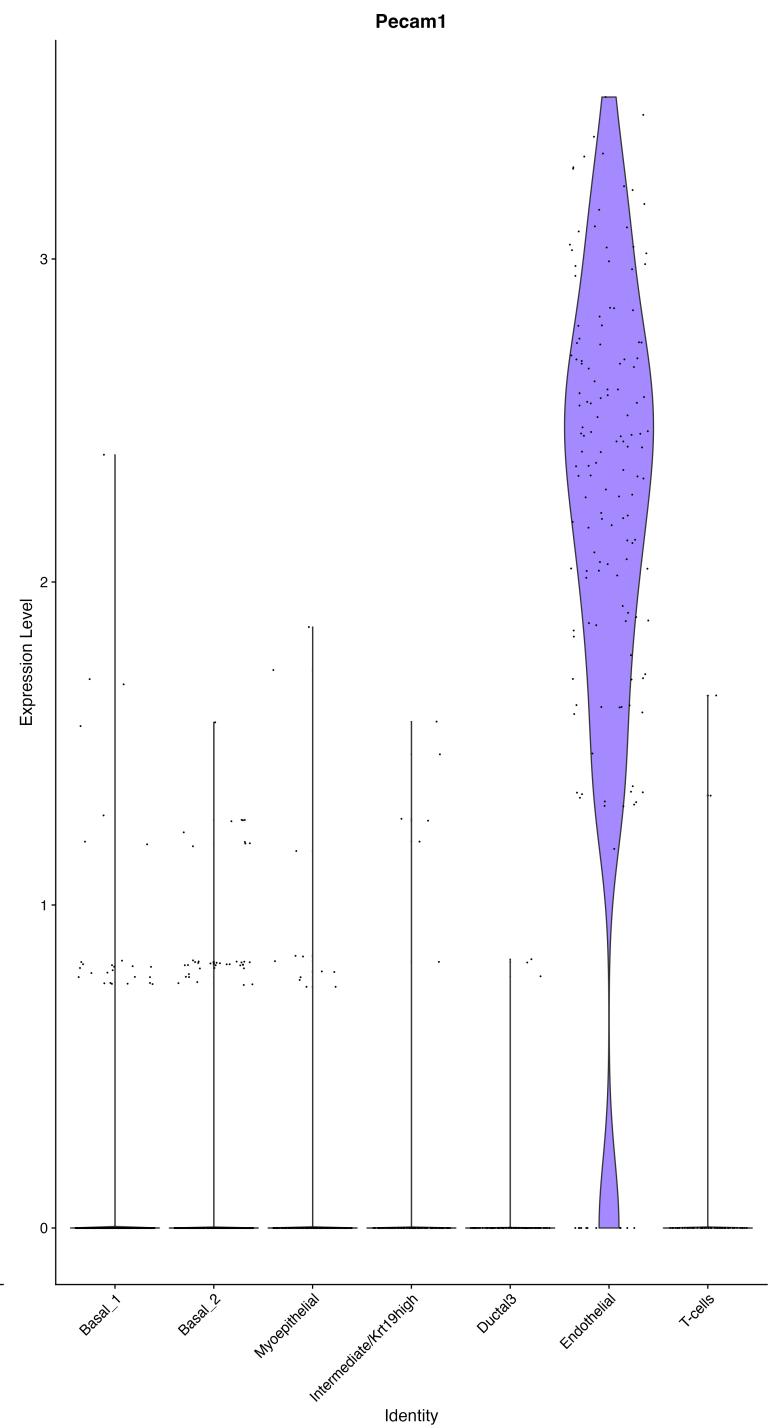
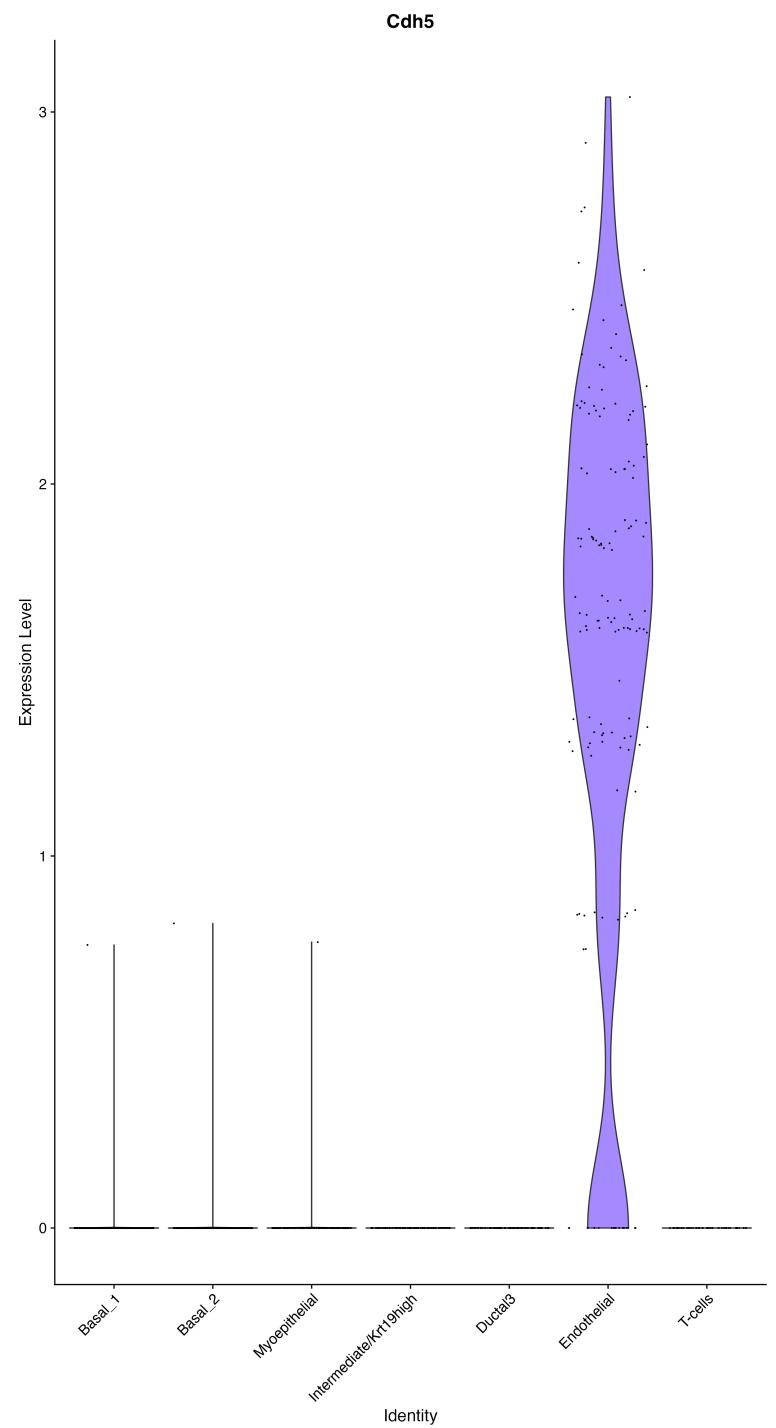
**Myoepithelial**

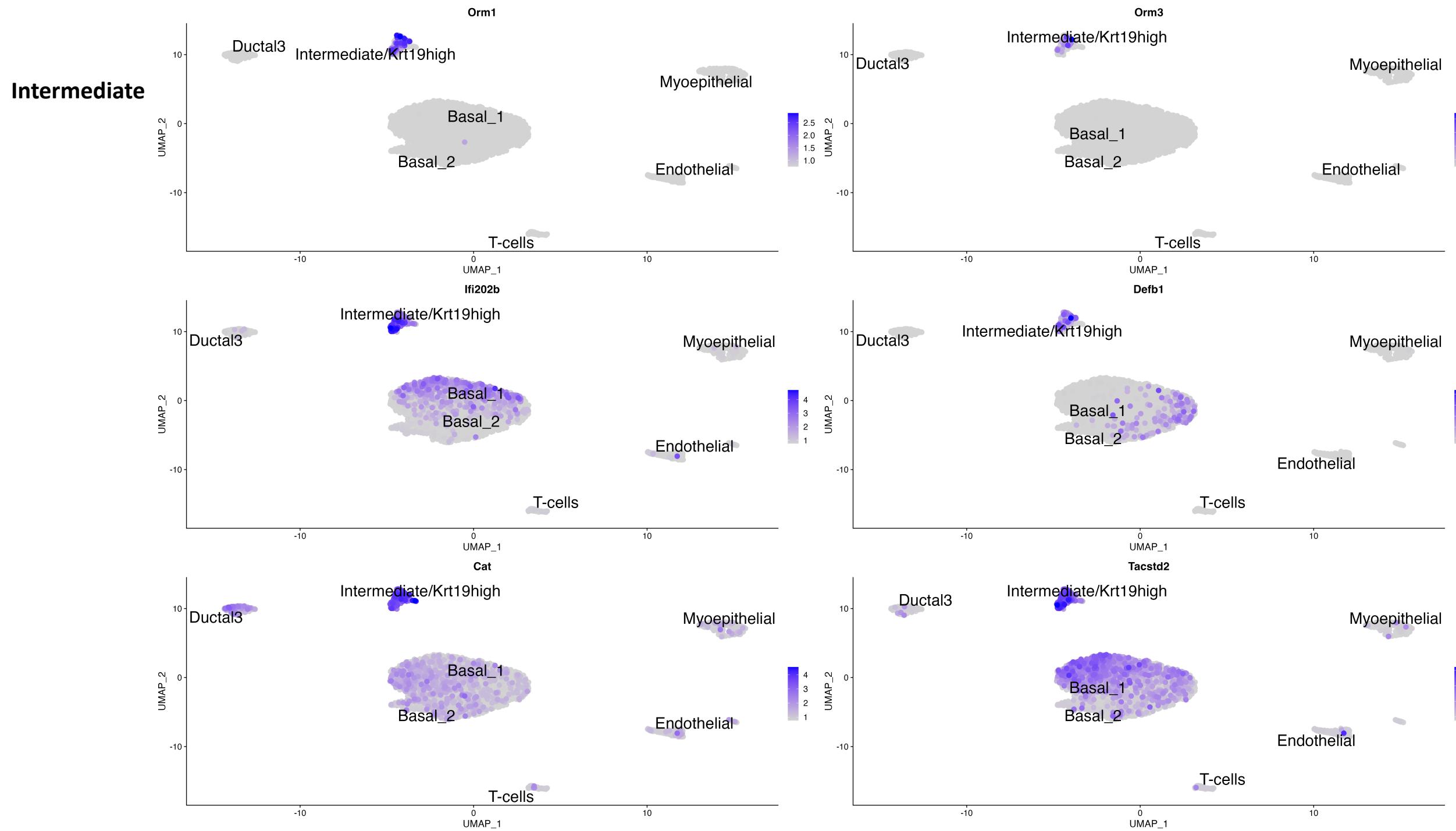
Cnn1



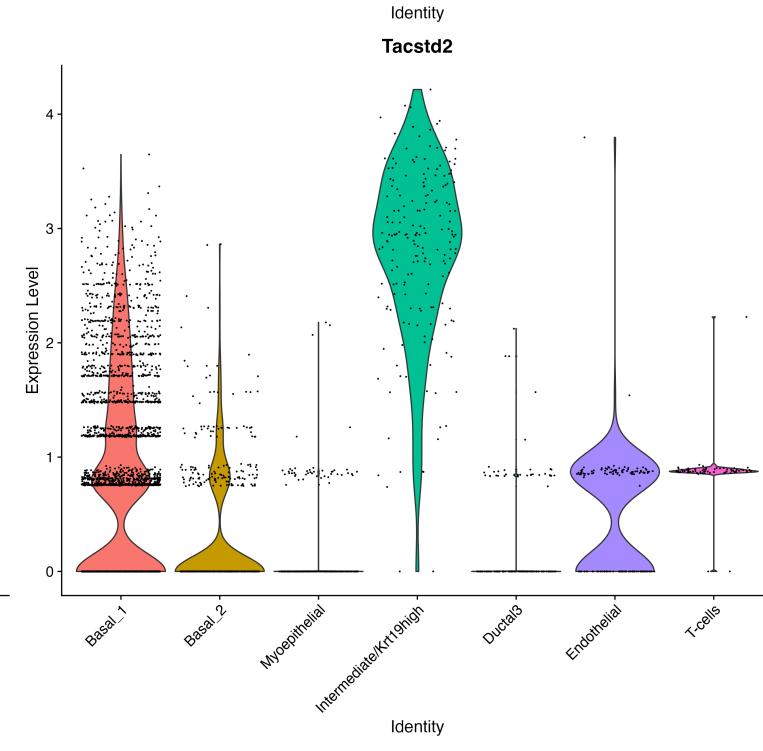
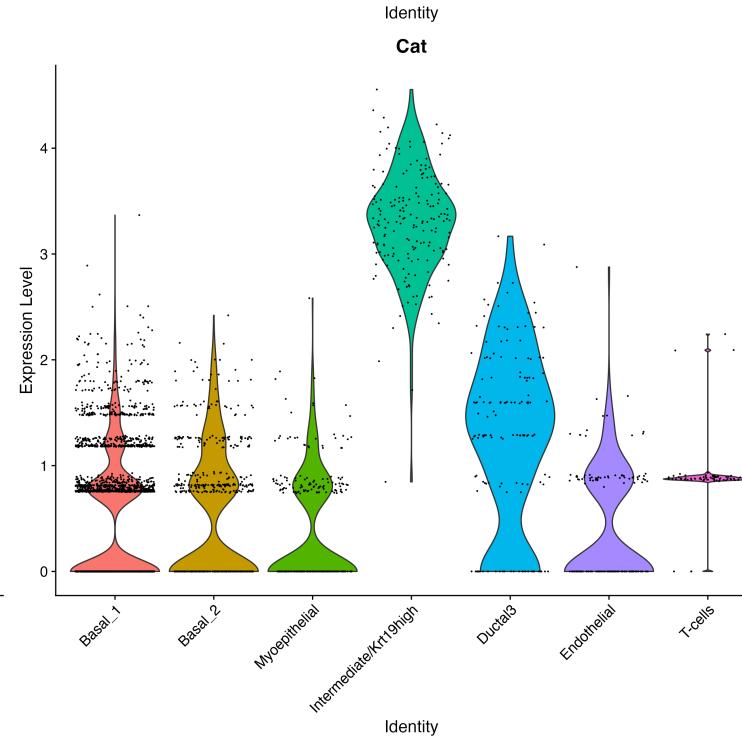
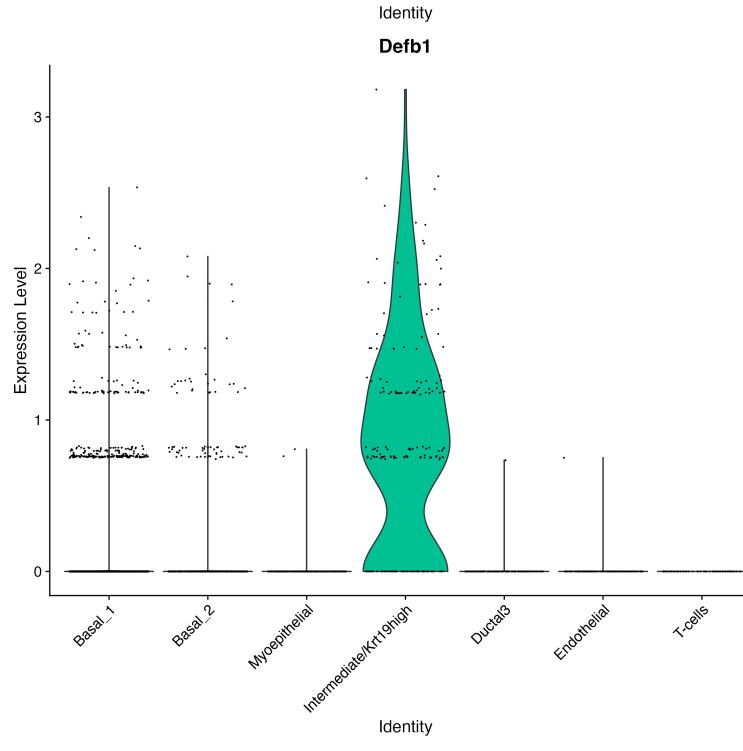
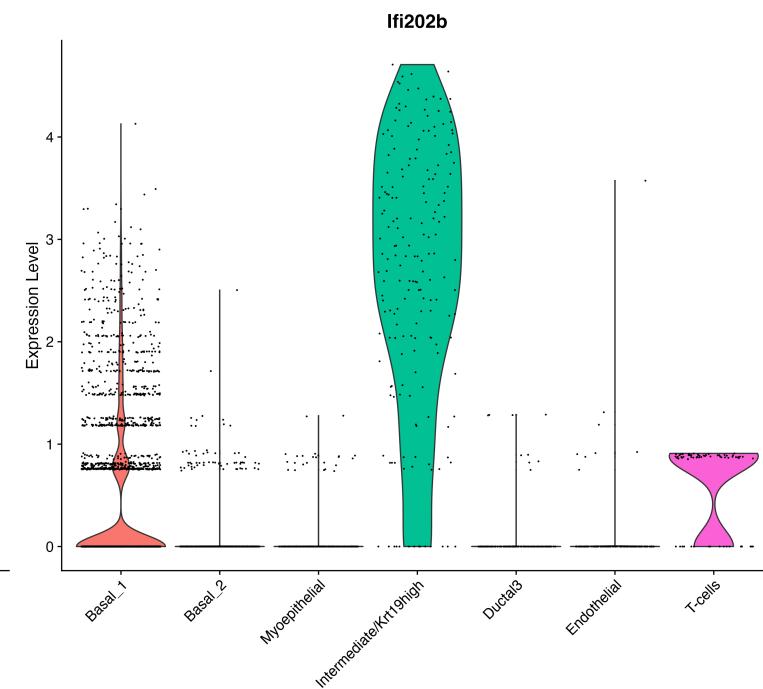
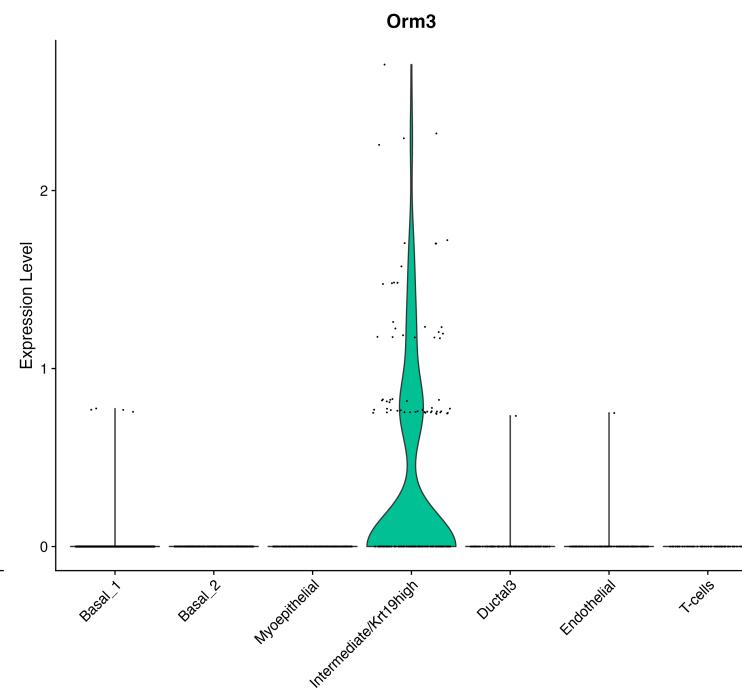
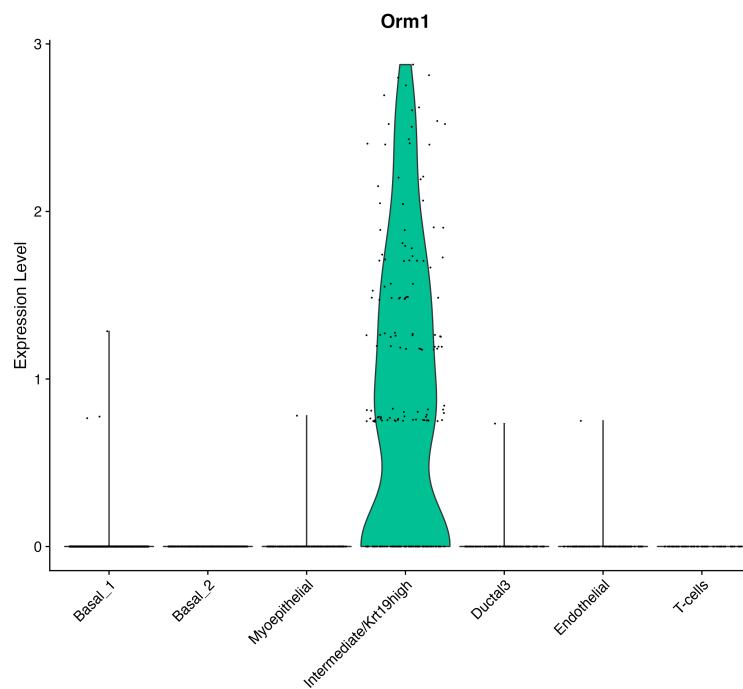


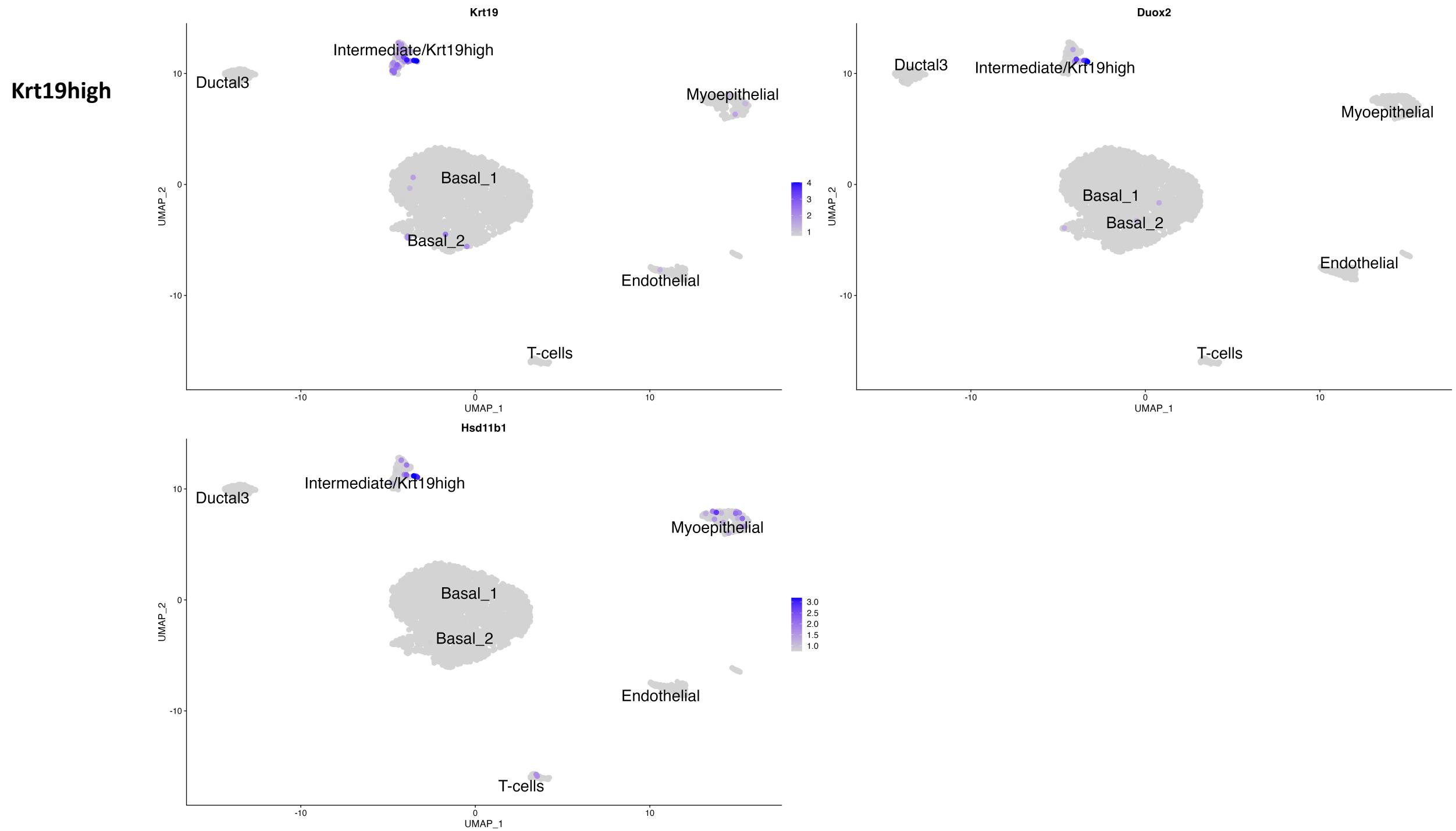
## Endothelial



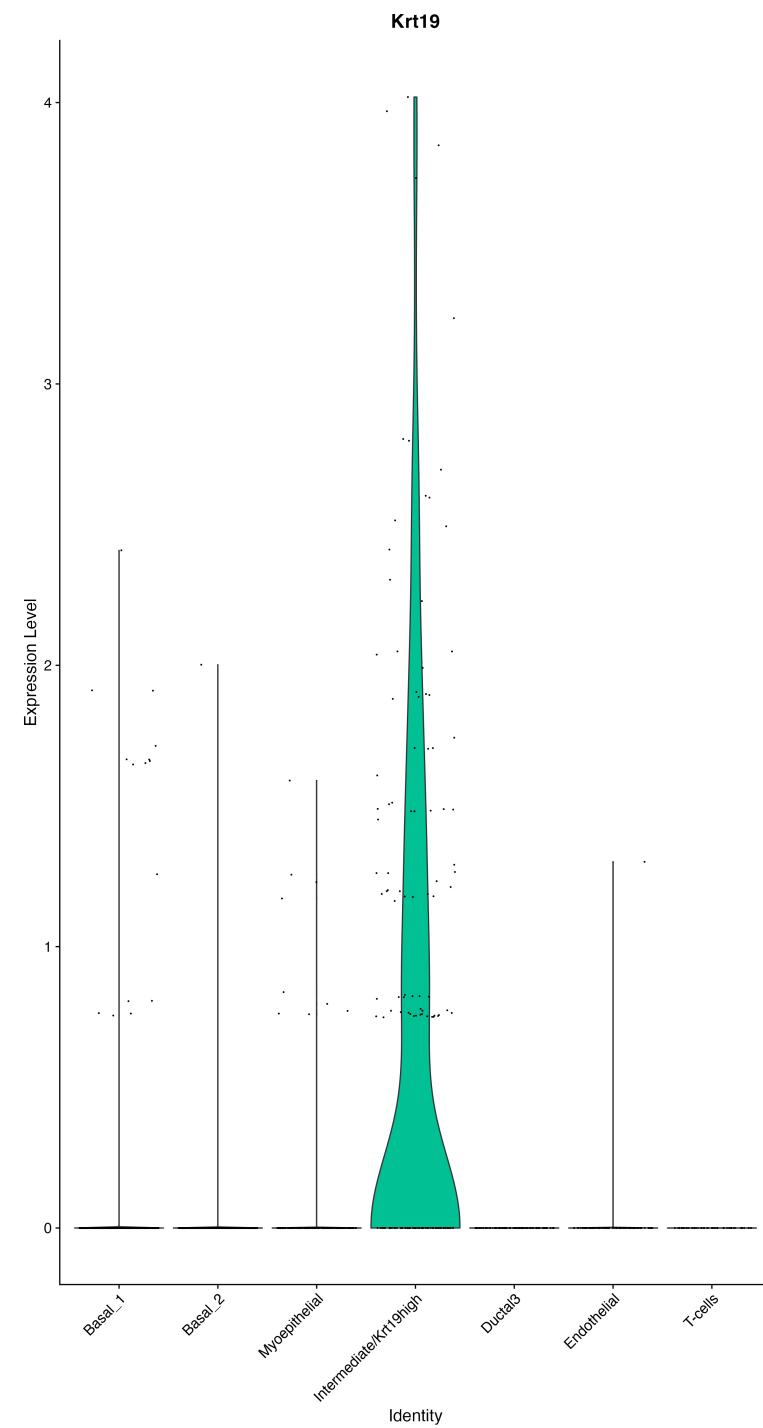


## Intermediate

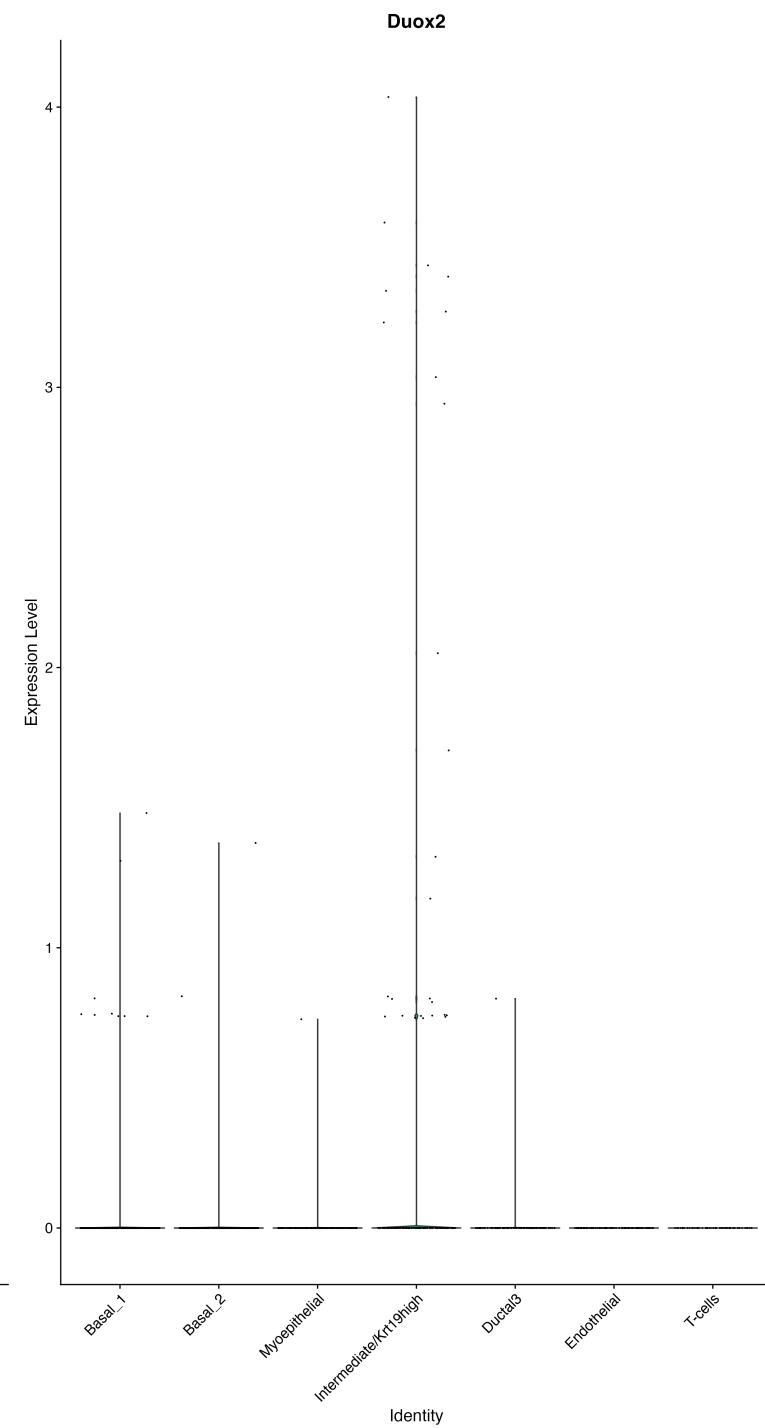




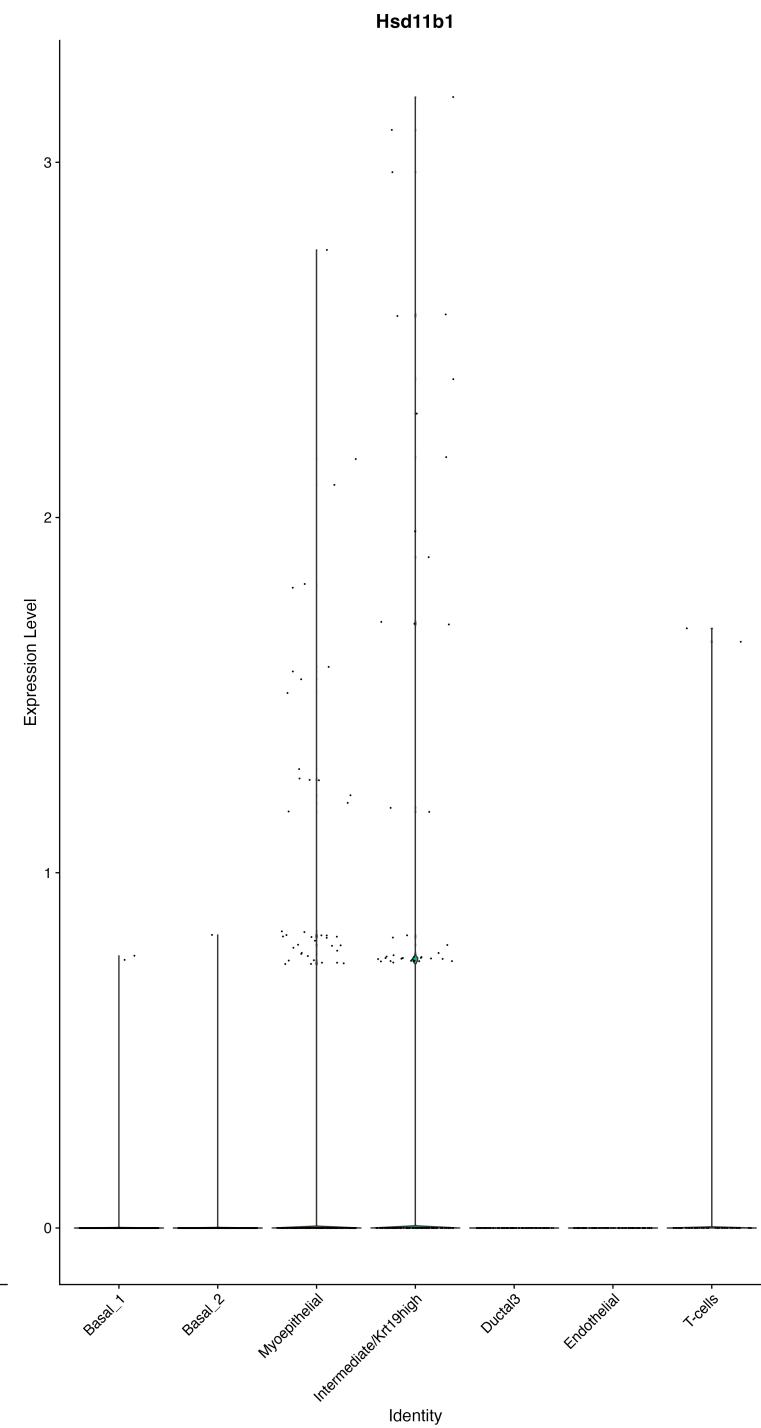
## Krt19high



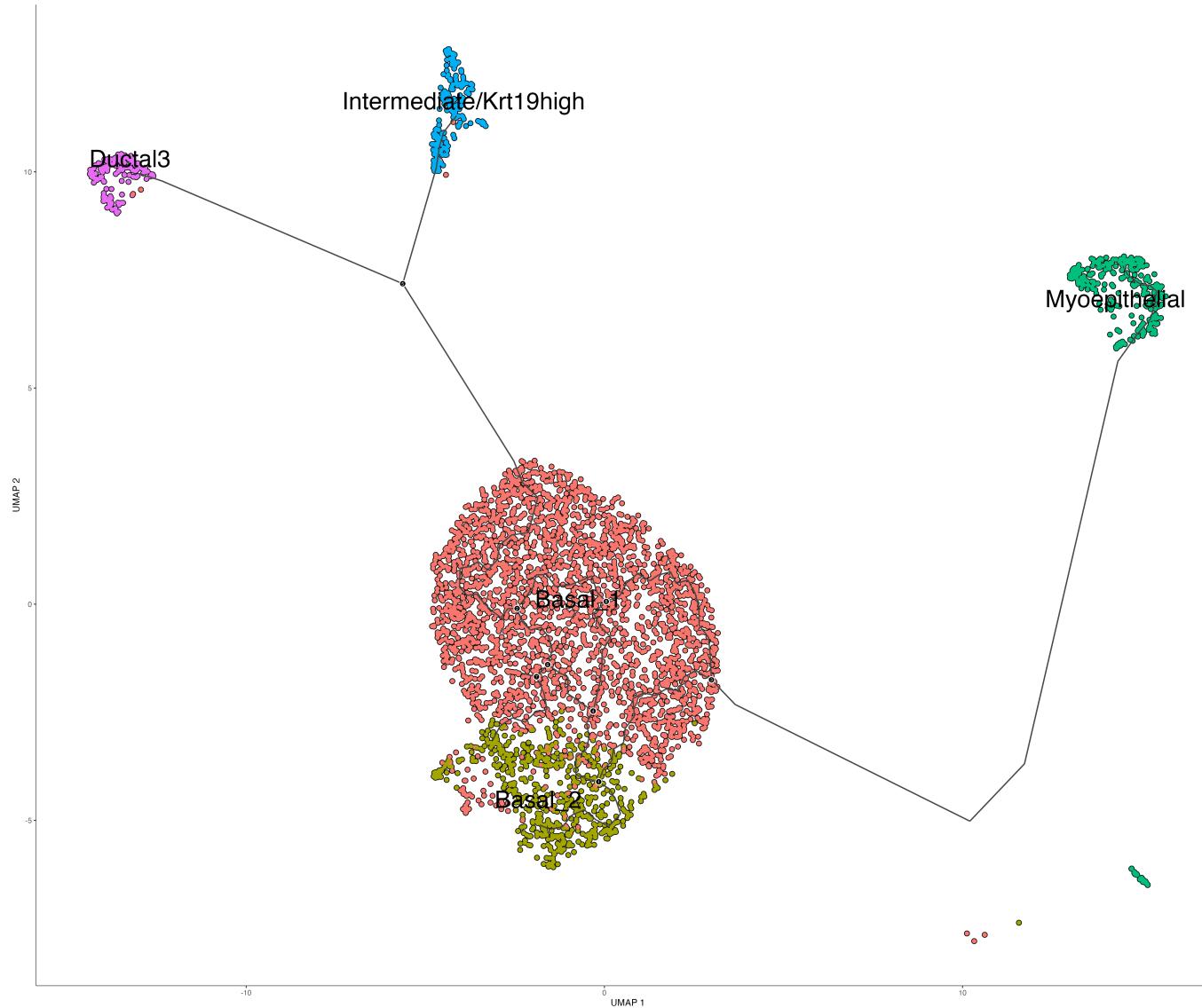
Duo2



Hsd11b1

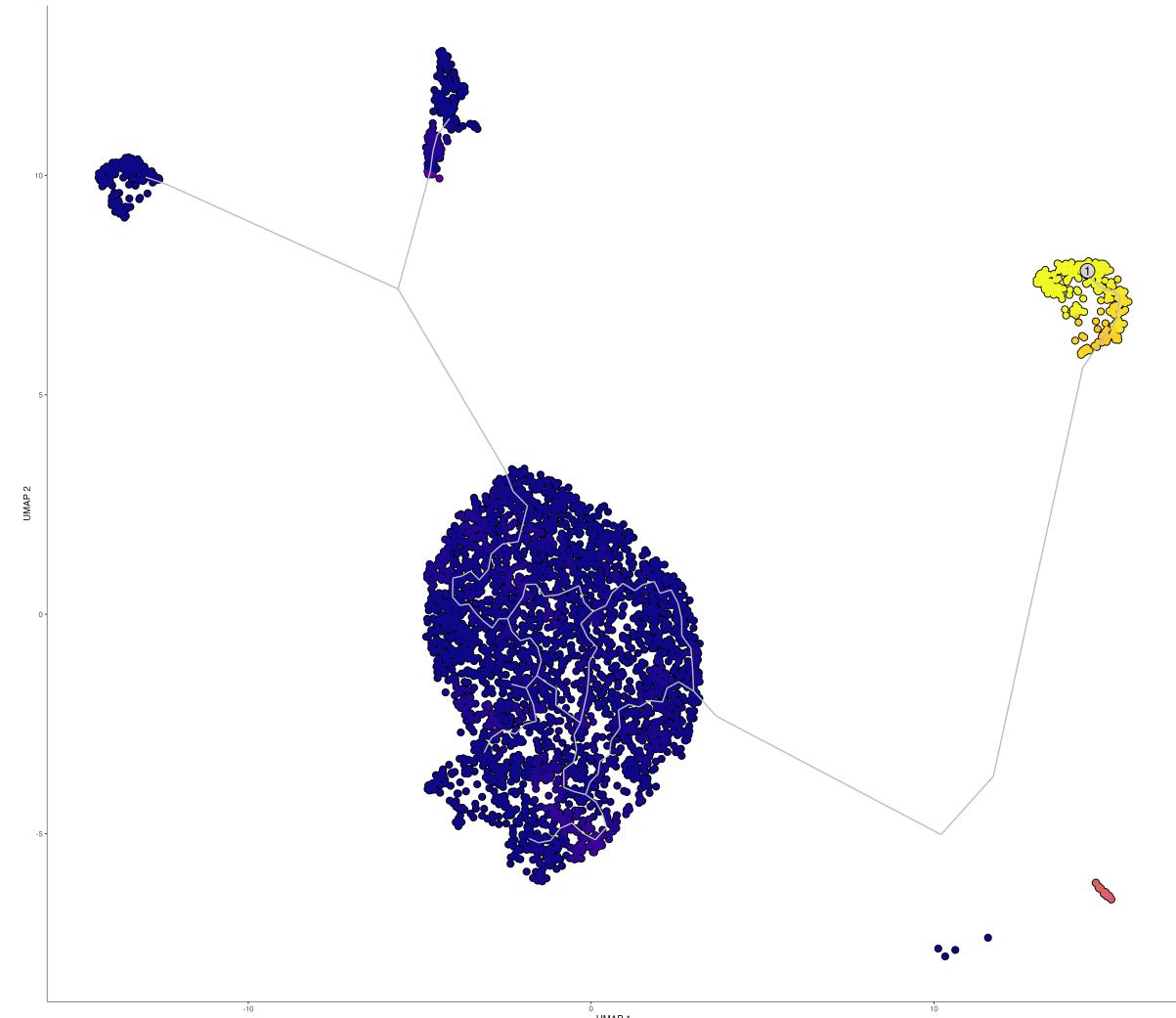


# Trajectory plot

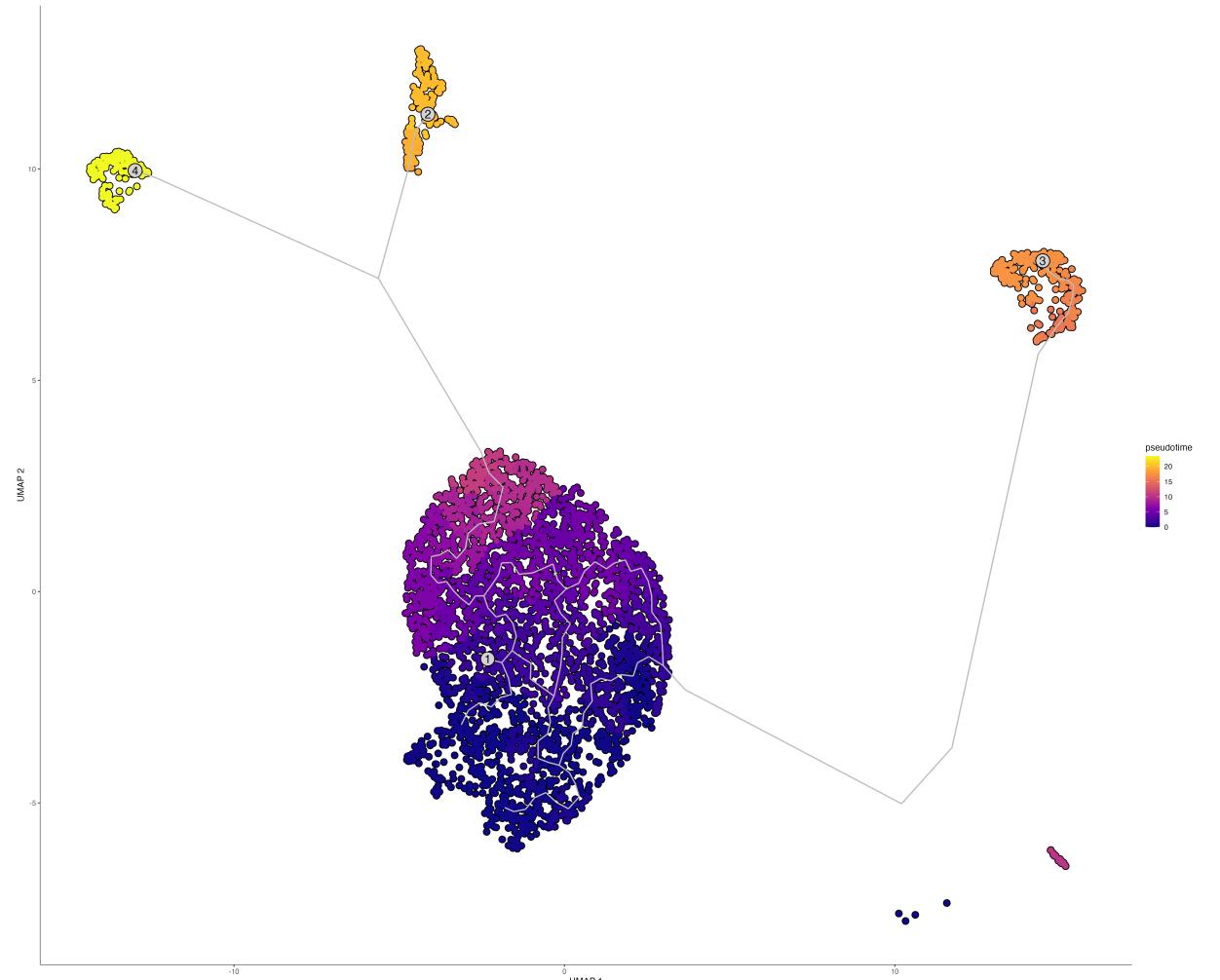


# Pseudotime plot

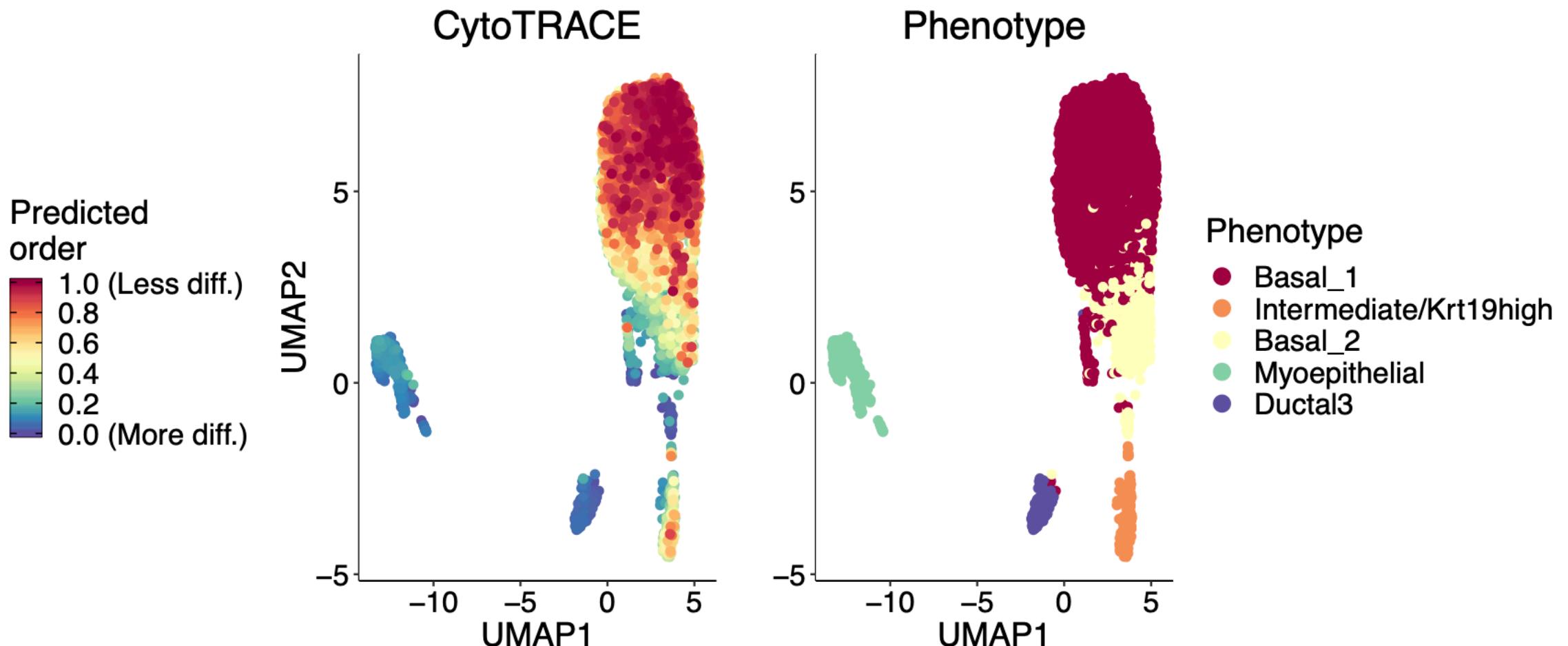
Start at Basal\_1



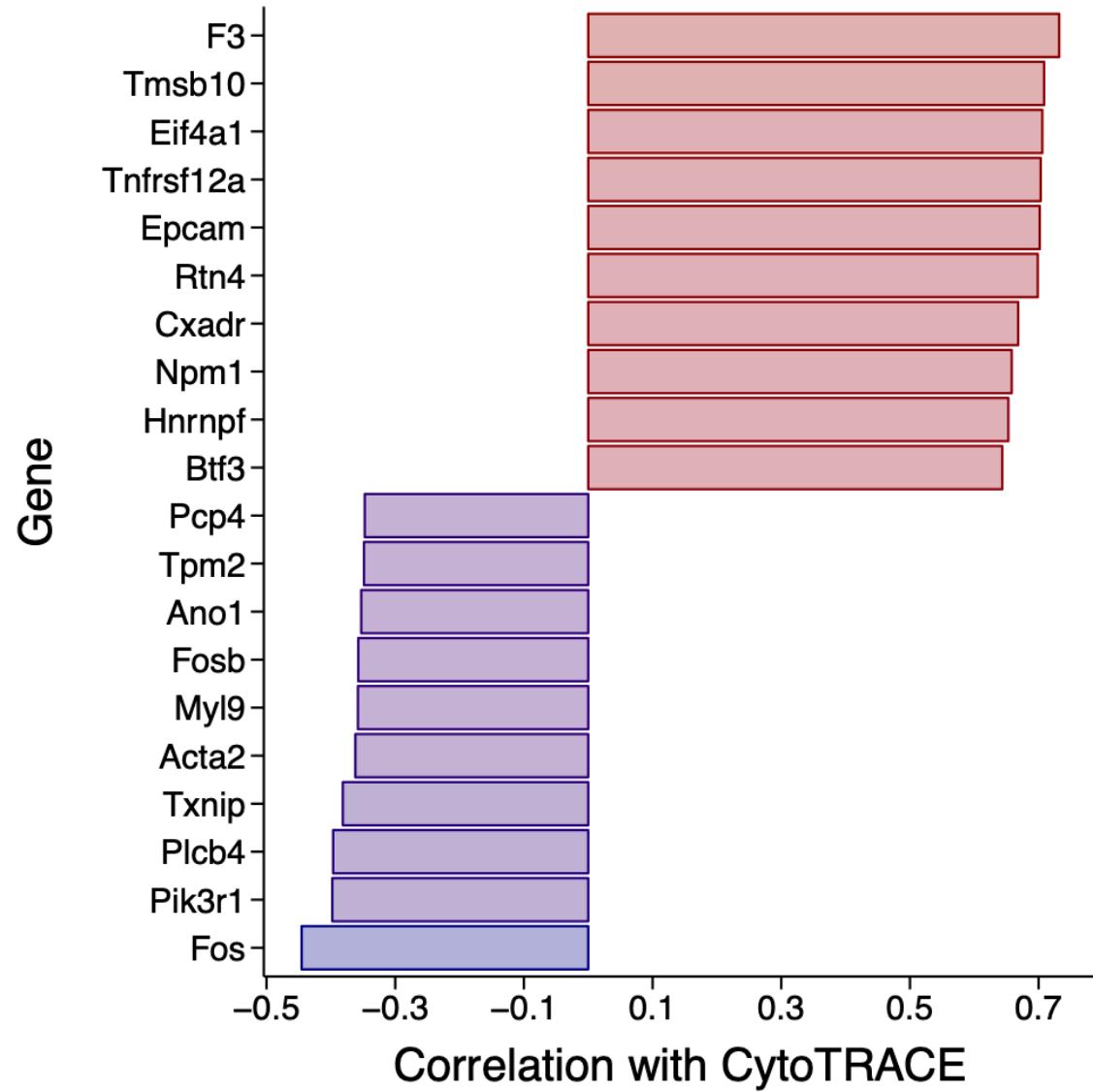
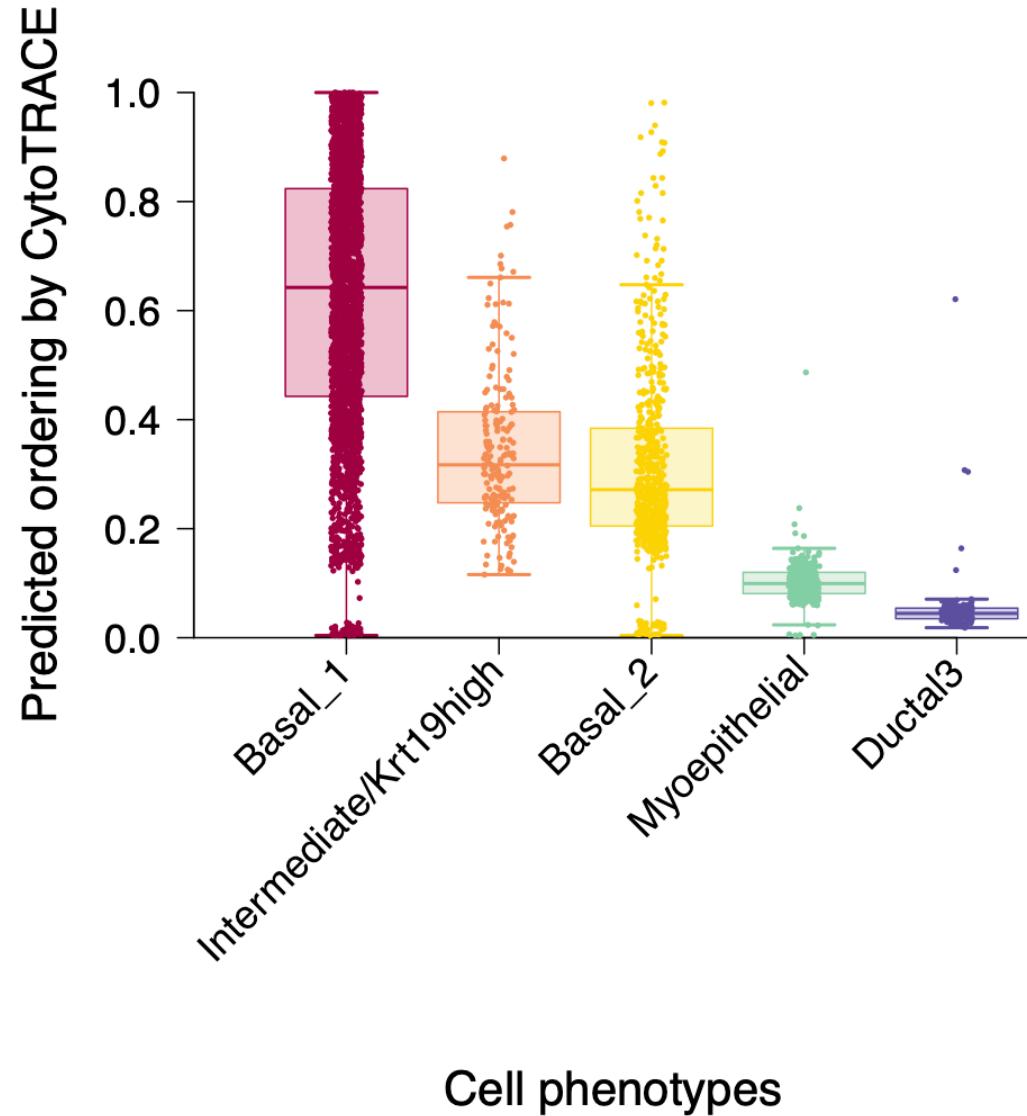
Start at Basal\_2



# CytoTRACE



# CytoTRACE



# Gene Module (Dataset2)

