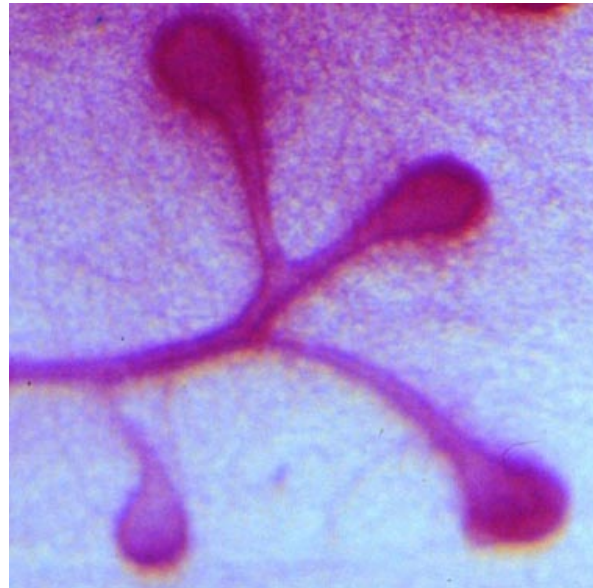


# Milk cell transcriptome opens a new dimension in the mammary gland biology research

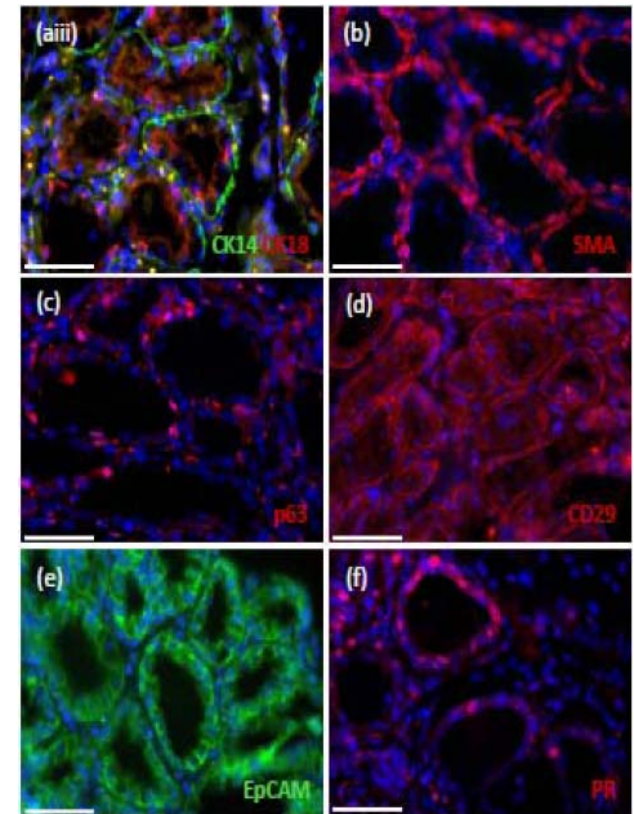
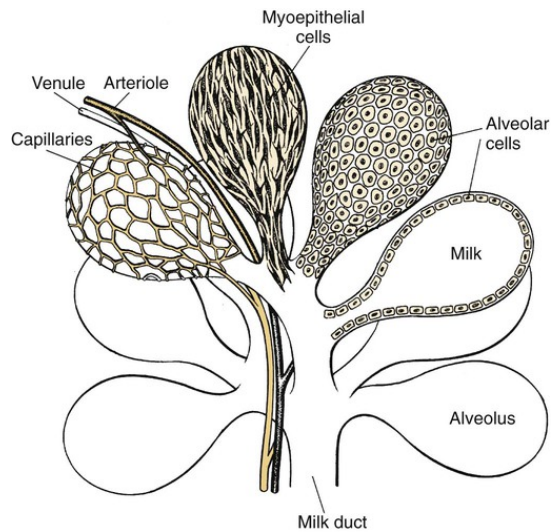


*M. Zorc and P. Dovc*

*<sup>1</sup>University of Ljubljana, Biotechnical Faculty, Jamnikarjeva 101, 1000 Ljubljana, Slovenia*

# Basic structure of the mammary gland is conserved among species

- Epithelial and myoepithelial cells build alveolar and ductal structures in the mammary gland.



Prpar et al., 2012

# Sources of biological material from mammary gland

Invasive collection methods:

- biopsies of the mammary gland tissue,
- laser capture microdissection

Non-invasive collection methods:

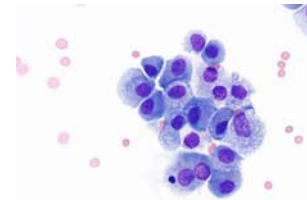
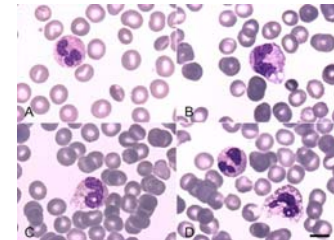
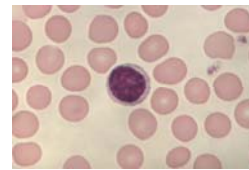
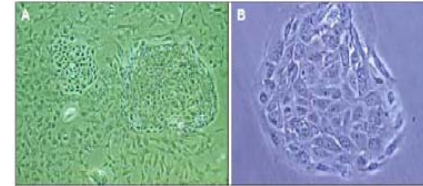
- milk somatic cells,
- milk fat globules
- antibody-captured milk mammary epithelial cells



# Major somatic cell types in milk

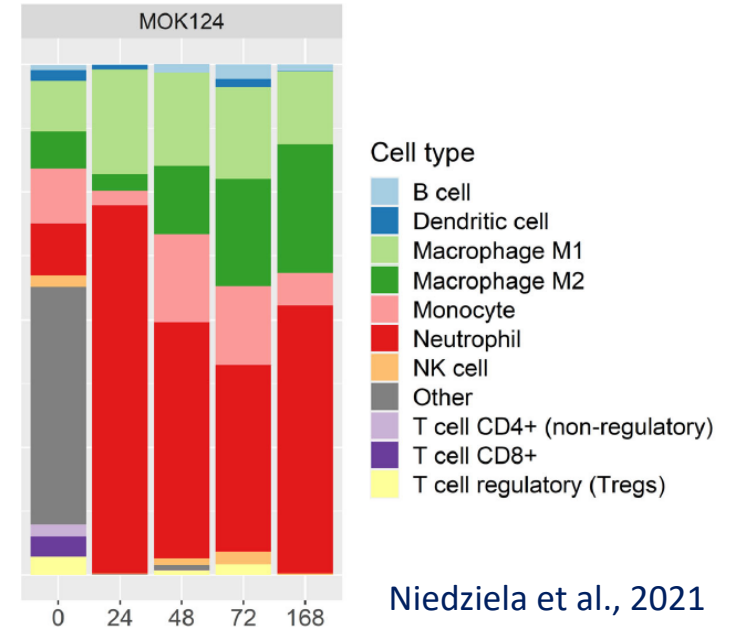
A consequence of the complex function of the mammary gland and intense secretion of milk is also the presence of somatic cells in milk.

- epithelial cells
- lymphocytes
- polymorphonuclear neutrophils (PMN)
- and macrophages.



# Somatic cell count and differential somatic cell count

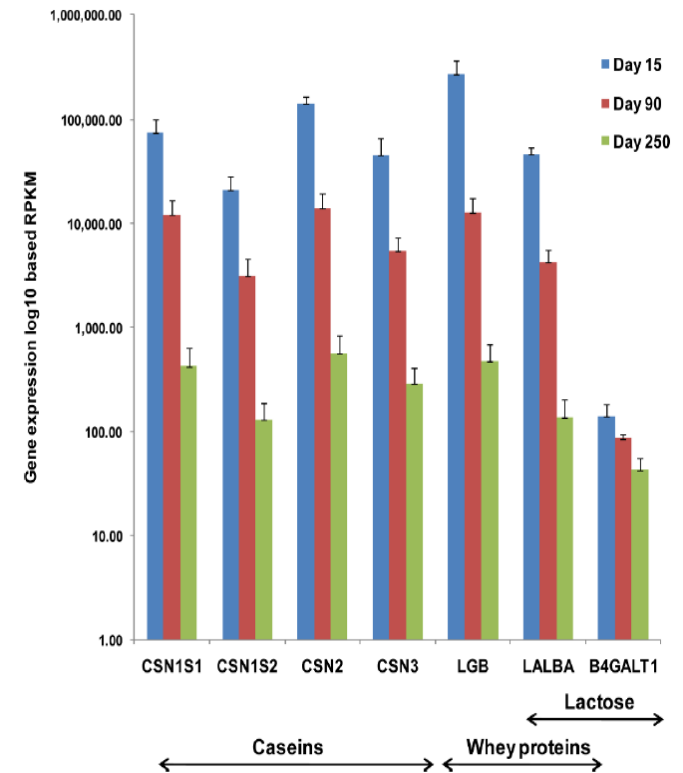
- The ratio of epithelial and immune cells differs among species. In cattle and sheep, the epithelial cell fraction represents only a relatively small part of somatic cells in milk, whereas, in porcine and goat milk, epithelial cells are the predominant cell type in milk.
- In the course of infection the proportion of different immune cells is changing.



- Somatic cell count (SCC) provides the cumulative number of somatic cells in milk.
- Differential somatic cell count (DSCC) allows differentiation between **PMN** and **lymphocytes** versus **macrophages**.

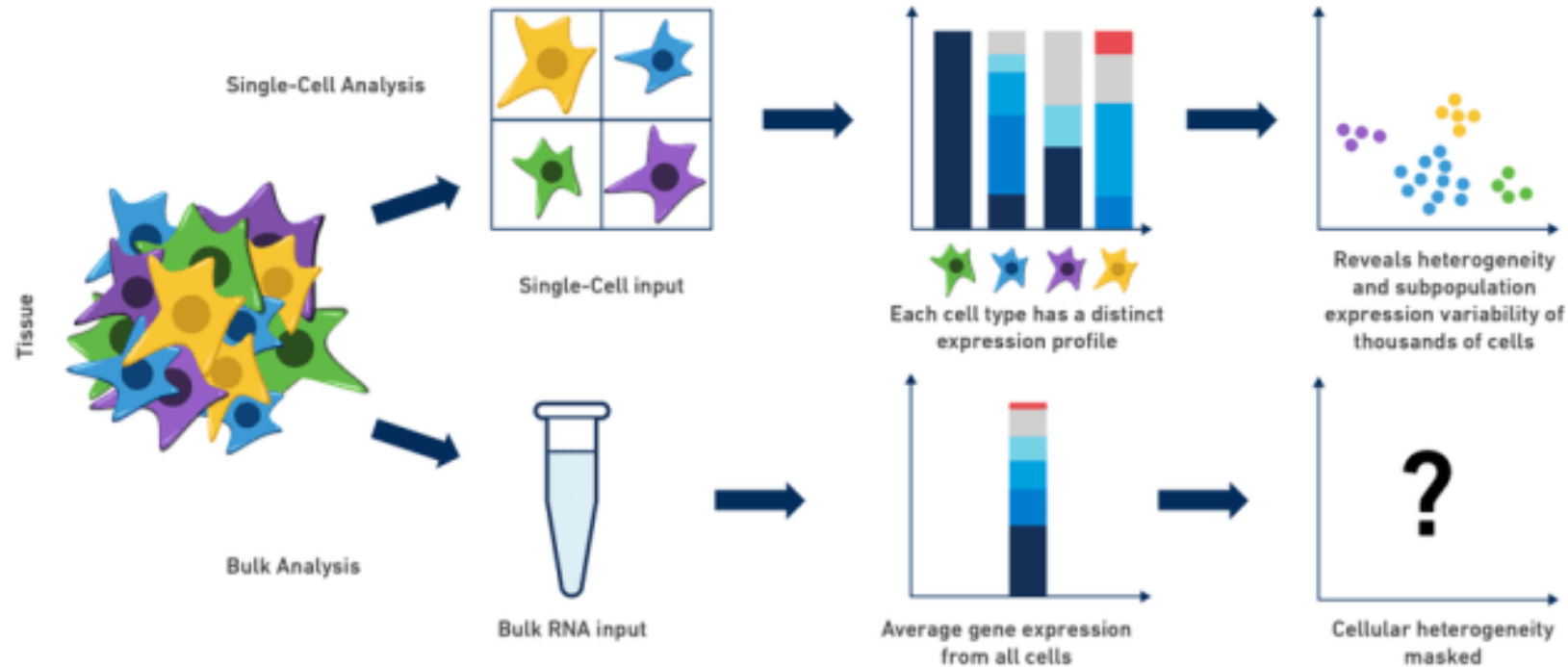
# Milk somatic cell transcriptome

- A total number of genes expressed in different lactation stages: 16,892 - 19,094
- 69% of annotated genes are expressed in milk somatic cells
- Approx. 9,000 genes expressed in all lactation stages
- 6,930 genes have a significant change in expression with the stage of lactation
- Genes encoding caseins, whey proteins and enzymes in lactose synthesis pathway show higher expression in early lactation.
- The majority of genes in the fat metabolism pathway have high expression in transition and peak lactation



Wickramasinghe et al.,  
2012

# Bulk vs. single cell transcriptome analysis



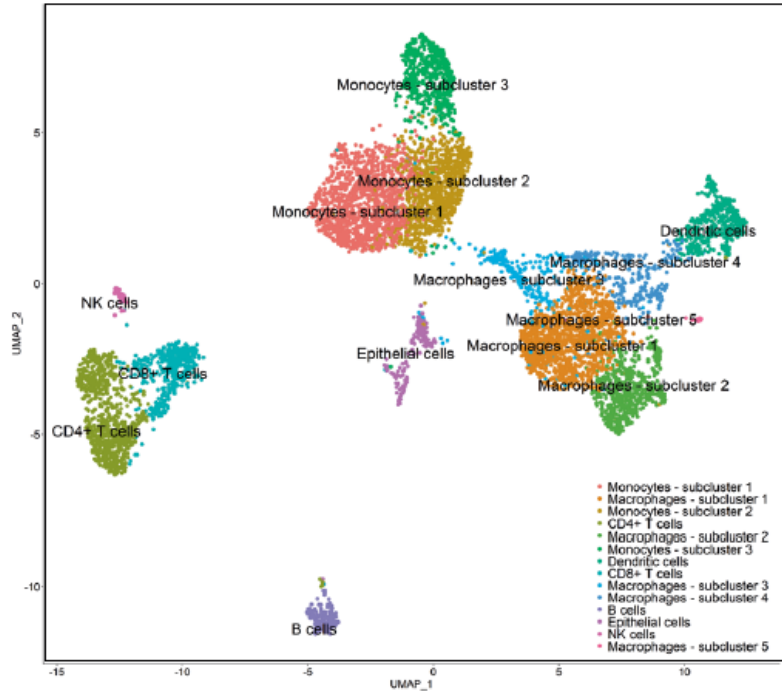
<https://www.10xgenomics.com/>



# Comparison of milk and pbMEC cell type clusters

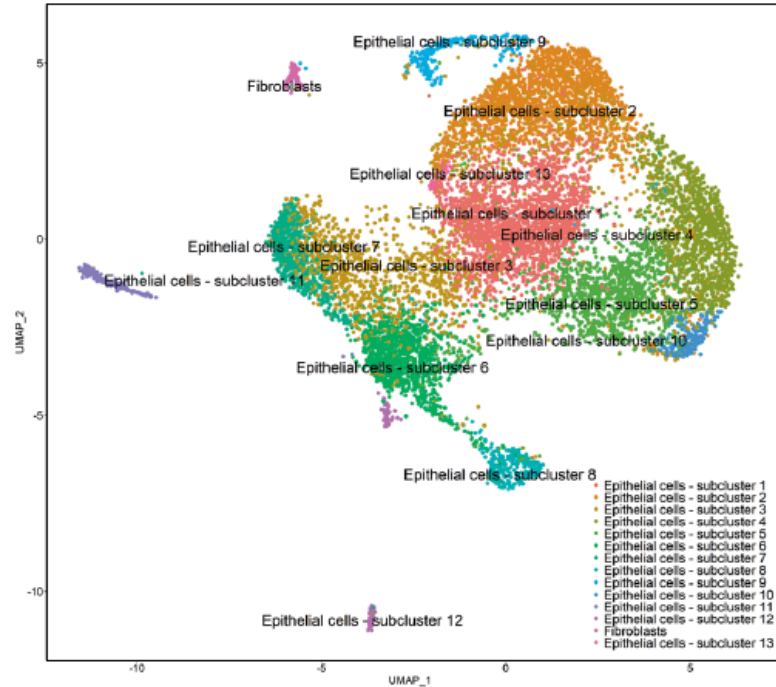
**a**

UMAP overview of 14 milk cell clusters



**b**

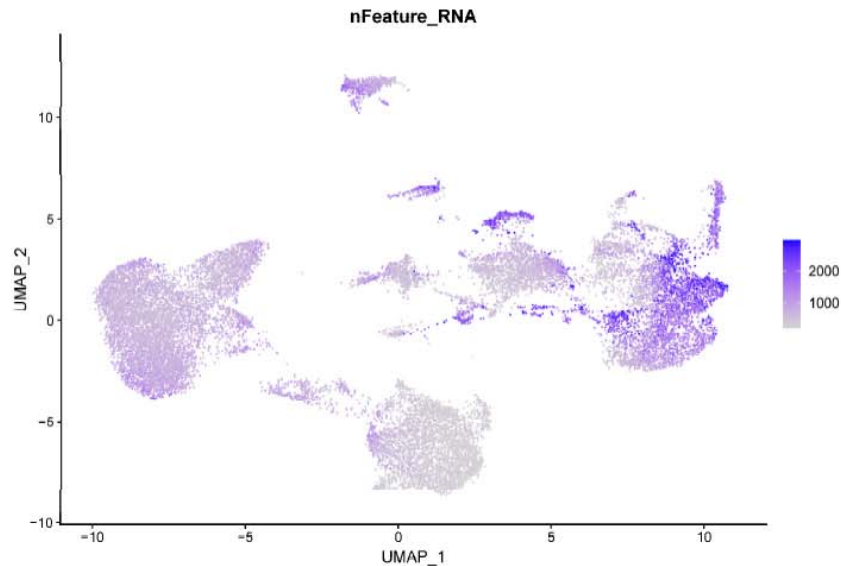
UMAP overview of 14 pbMECs clusters



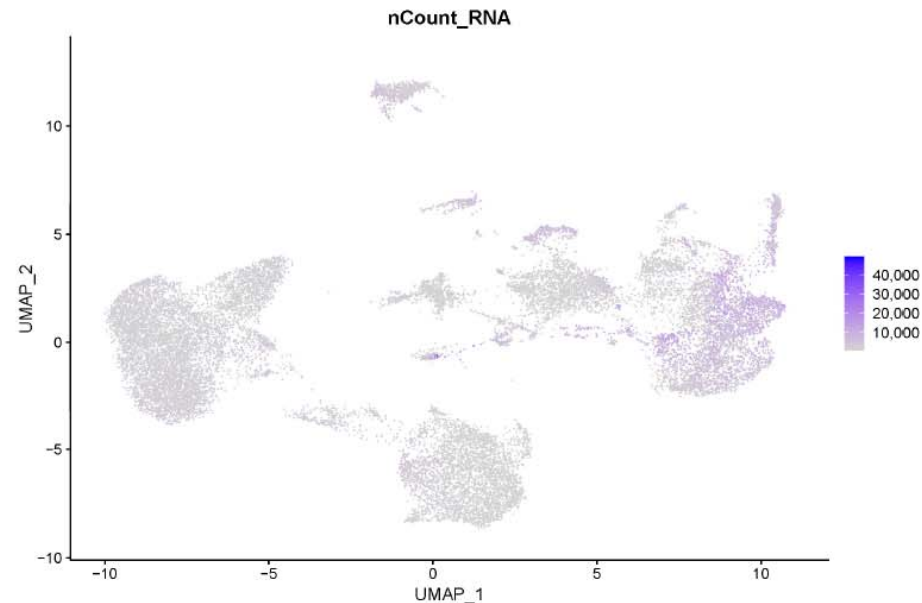
Becker et al., 2021



# ScRNA-seq quality control analysis



(a)

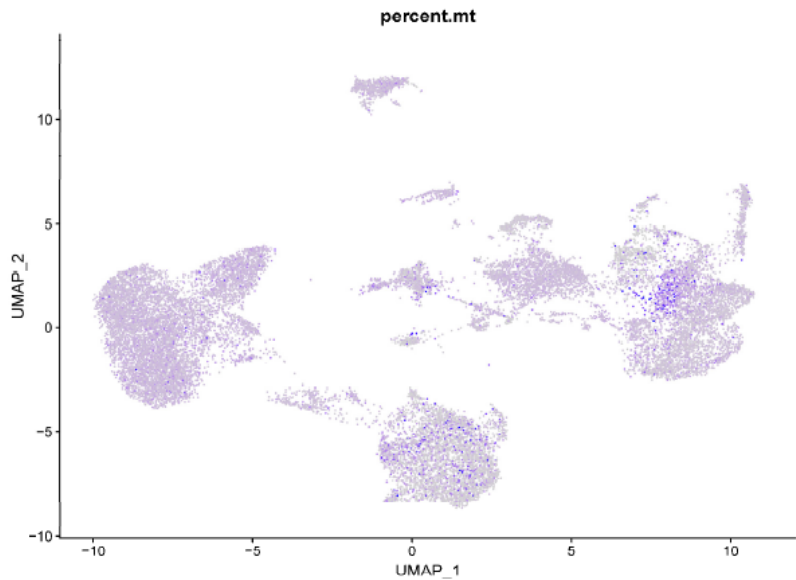


(b)

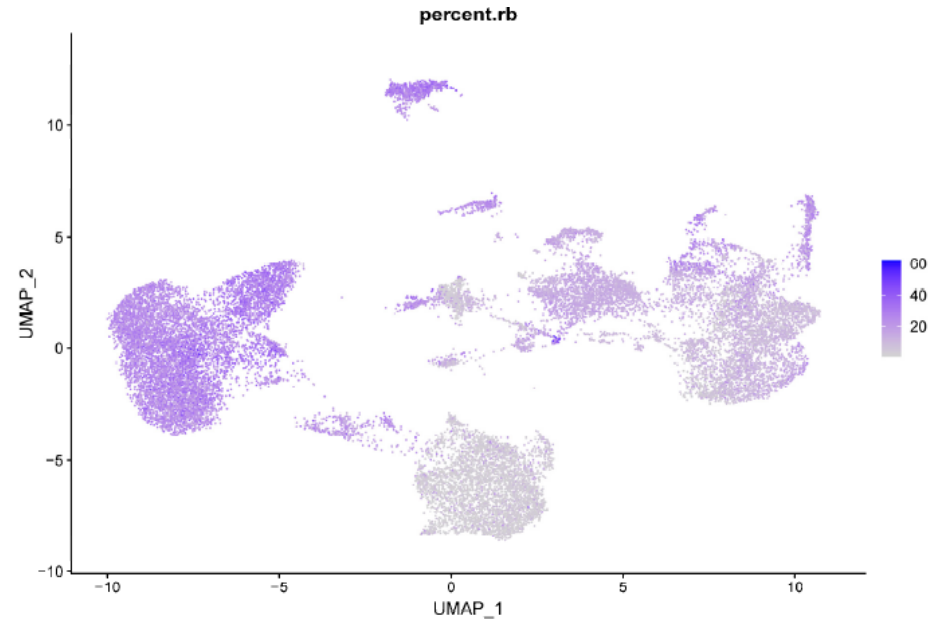
ScRNA-seq QC analysis of two somatic milk cell datasets after integration:

- a)** number of genes per cell
- b)** number of UMI reads per cell

# ScRNA-seq quality control analysis



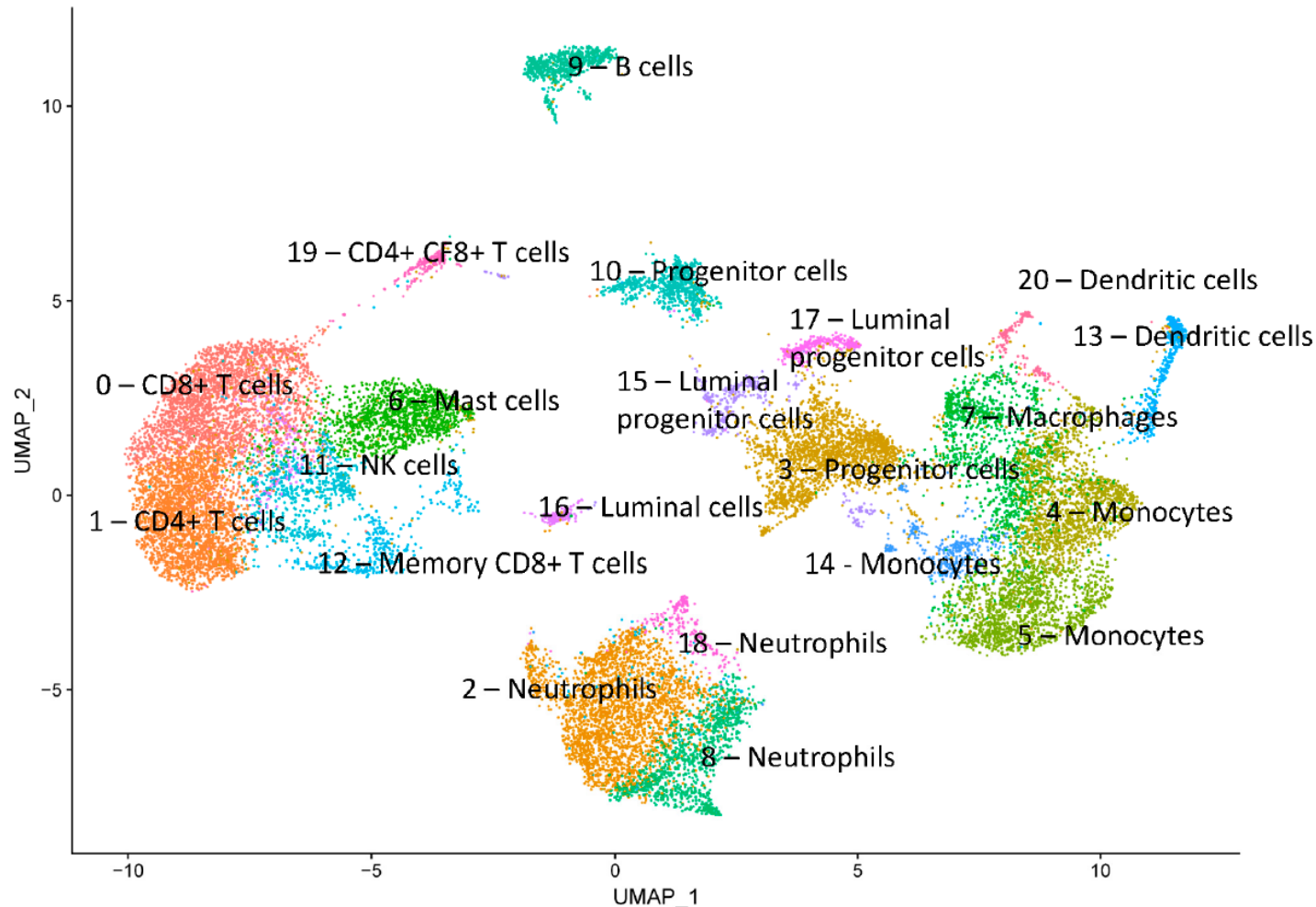
(c)



(d)

ScRNA-seq QC analysis of two somatic milk cell datasets after integration:  
**c)** percentage of cell counts mapping to mtDNA genes,  
**d)** percentage of cell counts mapping to ribosomal protein transcripts

# Annotated cell clusters from two bovine milk samples

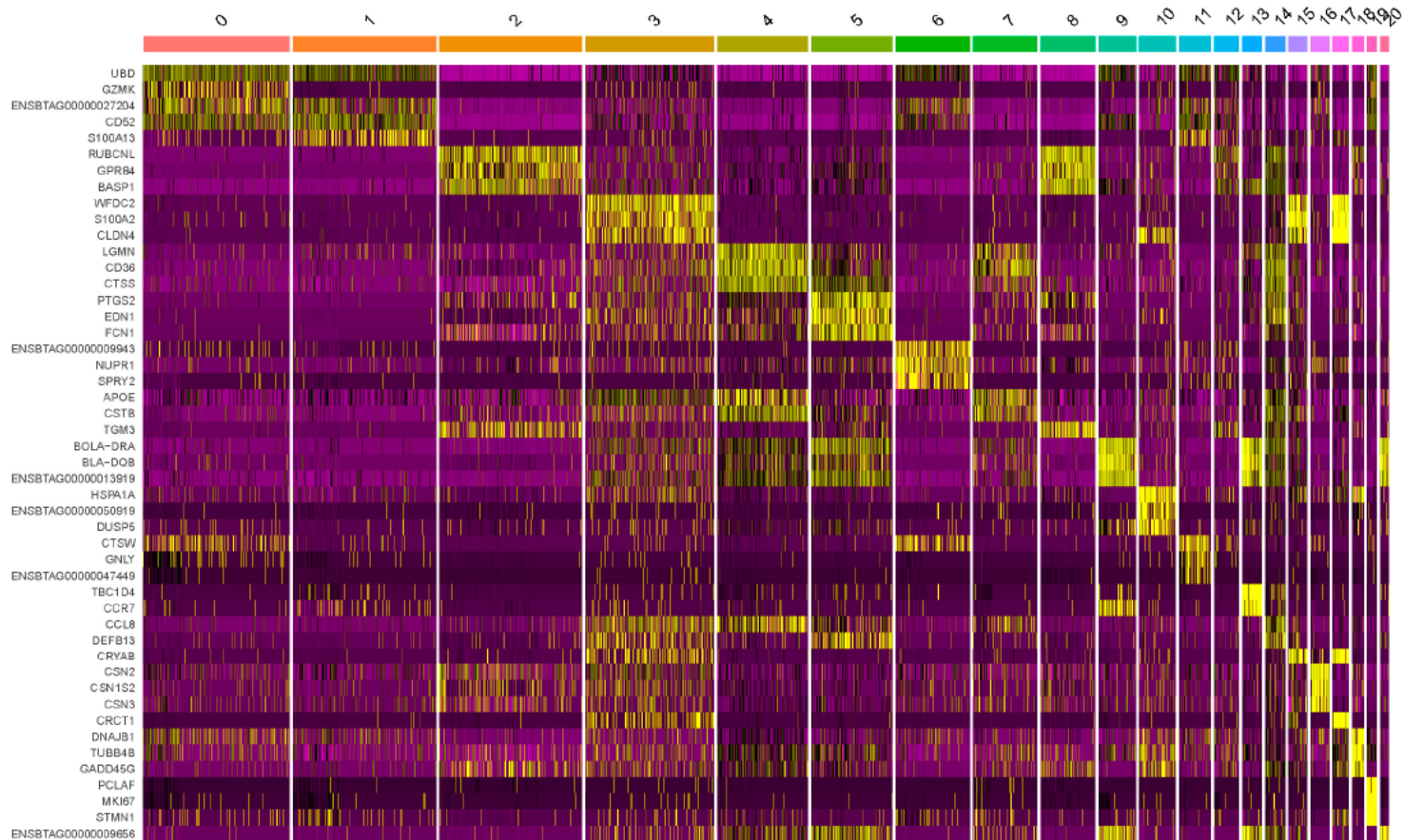


Zorc et al., 2024

# Annotation of milk somatic cell clusters

| Cluster | Cluster Annotation       | Marker Gene   |
|---------|--------------------------|---|
| 0       | CD8+ T cells             | <i>GZMK</i> , <i>ENSBTAG00000027204</i> , <i>CD52</i> , <i>ENSBTAG00000010828</i> , <i>FAM162A</i> , <i>RGS1</i> , <i>CCL5</i> , <i>ENSBTAG00000034609</i> , <i>ENSBTAG00000000432</i>  |
| 1       | CD4+ T cells             | <i>UBD</i> , <i>ICOS</i> , <i>ENSBTAG00000055140</i> , <i>GUCY1B1</i> , <i>ENSBTAG00000027204</i> , <i>CD4</i> , <i>S100A13</i> , <i>NCR3</i> , <i>ENSBTAG00000034609</i>   |
| 2       | Neutrophils              | <i>GPR84</i> , <i>BASP1</i> , <i>PLAU</i> , <i>PLEK</i> , <i>MARCKS</i> , <i>IL1B</i> , <i>DMXL2</i> , <i>IL1RN</i> , <i>BATF3</i>  |
| 3       | Progenitor cells         | <i>CCL2</i> , <i>APOE</i> , <i>S100A2</i> , <i>CLDN4</i> , <i>CD9</i> , <i>CCL8</i> , <i>CST6</i> , <i>CRYAB</i> , <i>CRCT1</i>   |
| 4       | Monocytes                | <i>CD36</i> , <i>CTSS</i> , <i>CTSB</i> , <i>LIPA</i> , <i>CCL8</i> , <i>GRN</i> , <i>CNDP2</i> , <i>TREM2</i> , <i>CD9</i>   |
| 5       | Monocytes                | <i>EDN1</i> , <i>FCN1</i> , <i>LYZ</i> , <i>CD14</i> , <i>ARAF</i> , <i>TNF</i> , <i>CXCL3</i> , <i>BOLA-DRA</i> , <i>DEFB13</i>  |
| 6       | Mast cells               | <i>NUPR1</i> , <i>KIT</i> , <i>ENSBTAG00000055197</i> , <i>SPRY2</i> , <i>CTSW</i> , <i>ENSBTAG00000000144</i> , <i>CD7</i> , <i>TNFRSF9</i> , <i>ENSBTAG00000034609</i>  |
| 7       | Macrophages              | <i>FABP5</i> , <i>CD36</i> , <i>CTSB</i> , <i>APOE</i> , <i>CSTB</i> , <i>CNDP2</i> , <i>CTSZ</i> , <i>ATOX1</i> , <i>CD9</i>   |
| 8       | Neutrophils              | <i>BASP1</i> , <i>ENSBTAG00000048980</i> ( <i>Chemokine interleukin-8-like domain-containing protein</i> ), <i>IFITM3</i> , <i>CXCR1</i> , <i>GPR84</i> , <i>SELL</i> , <i>ENSBTAG00000034366</i> , <i>TGM3</i> , <i>S100A9</i>   |
| 9       | B cells                  | <i>BLA-DQB</i> , <i>ENSBTAG00000013919</i> , <i>CD74</i> , <i>MS4A1</i> , <i>ENSBTAG00000055240</i> , <i>TNFRSF13C</i> , <i>CCR7</i> , <i>ENSBTAG00000009656</i> , <i>IRF4</i>  |
| 10      | Progenitor cells         | <i>TACSTD2</i> , <i>RASD1</i> , <i>ENSBTAG00000050919</i> , <i>DUSP5</i> , <i>EFNB2</i> , <i>ARC</i> , <i>KLF4</i> , <i>HSPA2</i> , <i>MAFB</i>   |
| 11      | NK cells                 | <i>GNLY</i> , <i>ENSBTAG00000047449</i> ( <i>Saposin B-type domain-containing protein</i> ), <i>CD52</i> , <i>UBD</i> , <i>S100A13</i> , <i>PRF1</i> , <i>GPR183</i> , <i>ENSBTAG00000000144</i> ( <i>Ig-like domain-containing protein</i> ), <i>ENSBTAG00000055197</i> ( <i>Immunoglobulin C1-set domain-containing protein</i> ) |
| 12      | Memory CD8+ T cells      | <i>RUBCNL</i> , <i>UBD</i> , <i>CD52</i> , <i>BASP1</i> , <i>PLAU</i> , <i>ENSBTAG00000027204</i> , <i>PLEK</i> , <i>IL1RN</i> , <i>ENSBTAG00000034609</i>  |
| 13      | Dendritic cells          | <i>CCR7</i> , <i>GPR183</i> , <i>LY75</i> , <i>BLA-DQB</i> , <i>TAMALIN</i> , <i>PKIB</i> , <i>ENSBTAG00000013919</i> , <i>BOLA-DRA</i> , <i>FSCN1</i>  |
| 14      | Monocytes                | <i>PTGS2</i> , <i>CCL2</i> , <i>CD36</i> , <i>CCL8</i> , <i>CTSS</i> , <i>RUBCNL</i> , <i>EDN1</i> , <i>CXCL5</i> , <i>DEFB13</i>   |
| 15      | Luminal progenitor cells | <i>CLU</i> , <i>CLDN3</i> , <i>CLDN4</i> , <i>CRYAB</i> , <i>KRT7</i> , <i>DSTN</i> , <i>WFDC2</i> , <i>KRT19</i> , <i>LTF</i>  |
| 16      | Luminal cells            | <i>CSN1S1</i> , <i>PAEP</i> , <i>CSN1S2</i> , <i>CSN3</i> , <i>GLYCAM1</i> , <i>LALBA</i> , <i>HSTN</i> , <i>SCGB1D</i> , <i>FABP3</i>  |
| 17      | Luminal progenitor cells | <i>CRCT1</i> , <i>AGPAT2</i> , <i>CLDN3</i> , <i>KRT7</i> , <i>CLDN4</i> , <i>DSTN</i> , <i>S100A2</i> , <i>CRYAB</i> , <i>WFDC2</i>  |
| 18      | Neutrophils              | <i>TUBB4B</i> , <i>GADD45G</i> , <i>DDIT4</i> , <i>GADD45A</i> , <i>HSPH1</i> , <i>HSPA1A</i> , <i>IER5L</i> , <i>ZFAND2A</i> , <i>LRIF1</i>  |
| 19      | CD4+ CD8+ T cells        | <i>PCLAF</i> , <i>MKI67</i> , <i>STMN1</i> , <i>TOP2A</i> , <i>DUT</i> , <i>HMGB2</i> , <i>CENPE</i> , <i>TMPO</i> , <i>DNMT1</i> , <i>UBE2C</i>  |
| 20      | Dendritic cells          | <i>BOLA-DRA</i> , <i>ENSBTAG00000013919</i> ( <i>BOLA-DRB3</i> ), <i>ENSBTAG00000009656</i> ( <i>BOLA-DQA2</i> ), <i>CD74</i> , <i>C3H1orf54</i> , <i>BLA-DQB</i> , <i>CST3</i> , <i>ENSBTAG00000037605</i> ( <i>BOLA-DQA1</i> ), <i>BOLA-DMA</i> , <i>PLAC8A</i>   |

# Specificity of marker gene expression

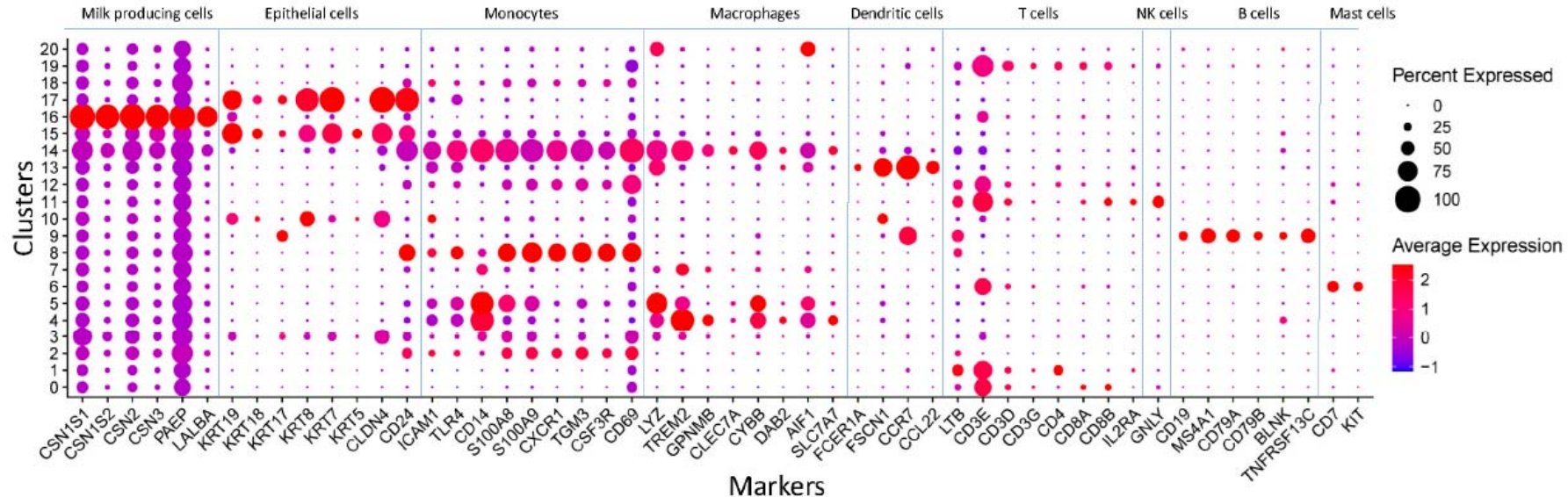


Zorc et al., 2024

Standardized expression of three major marker genes identified for each cell cluster. High expression of a particular gene is labeled with yellow and low expression with purple.

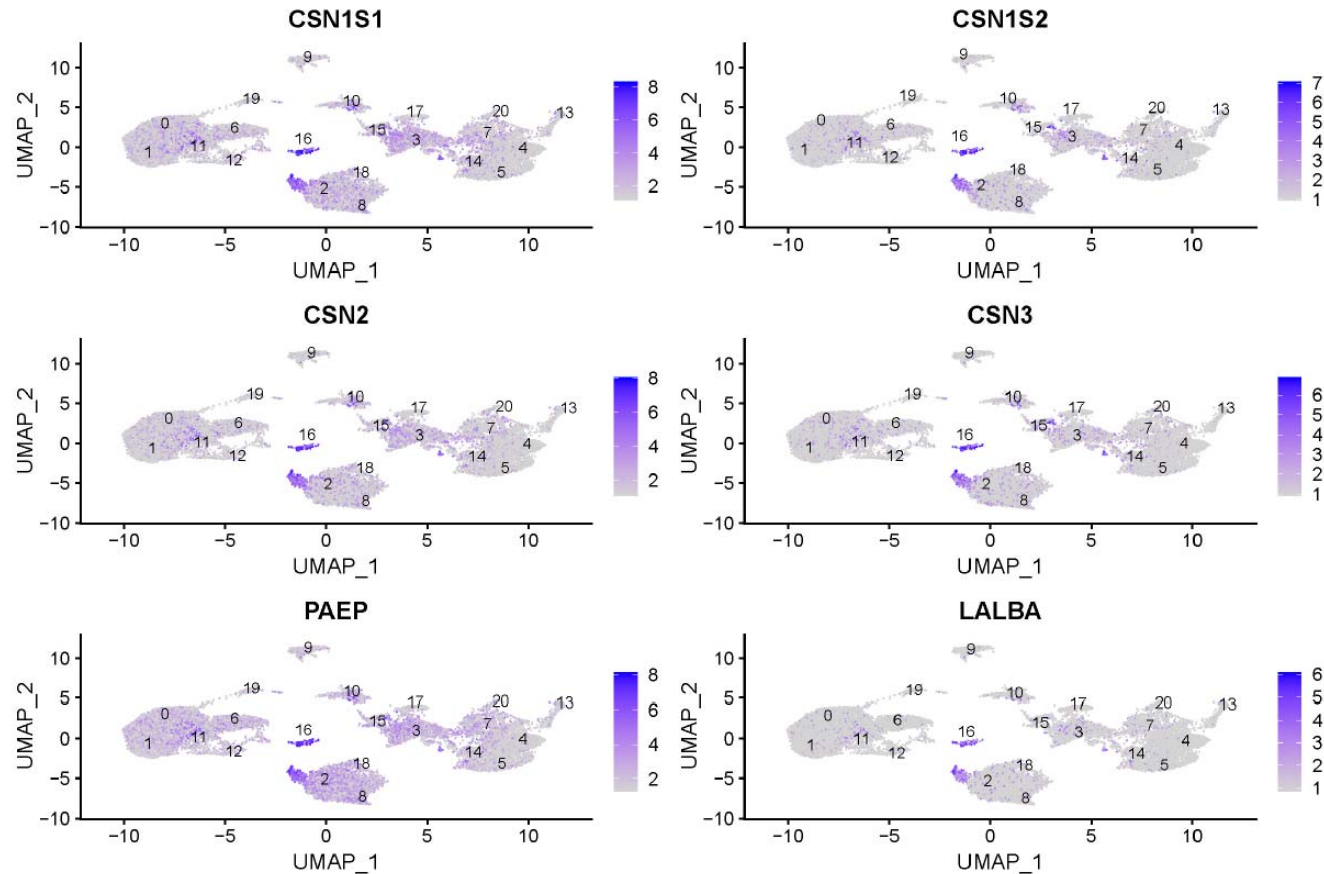


# Marker genes, used to determine cluster identity



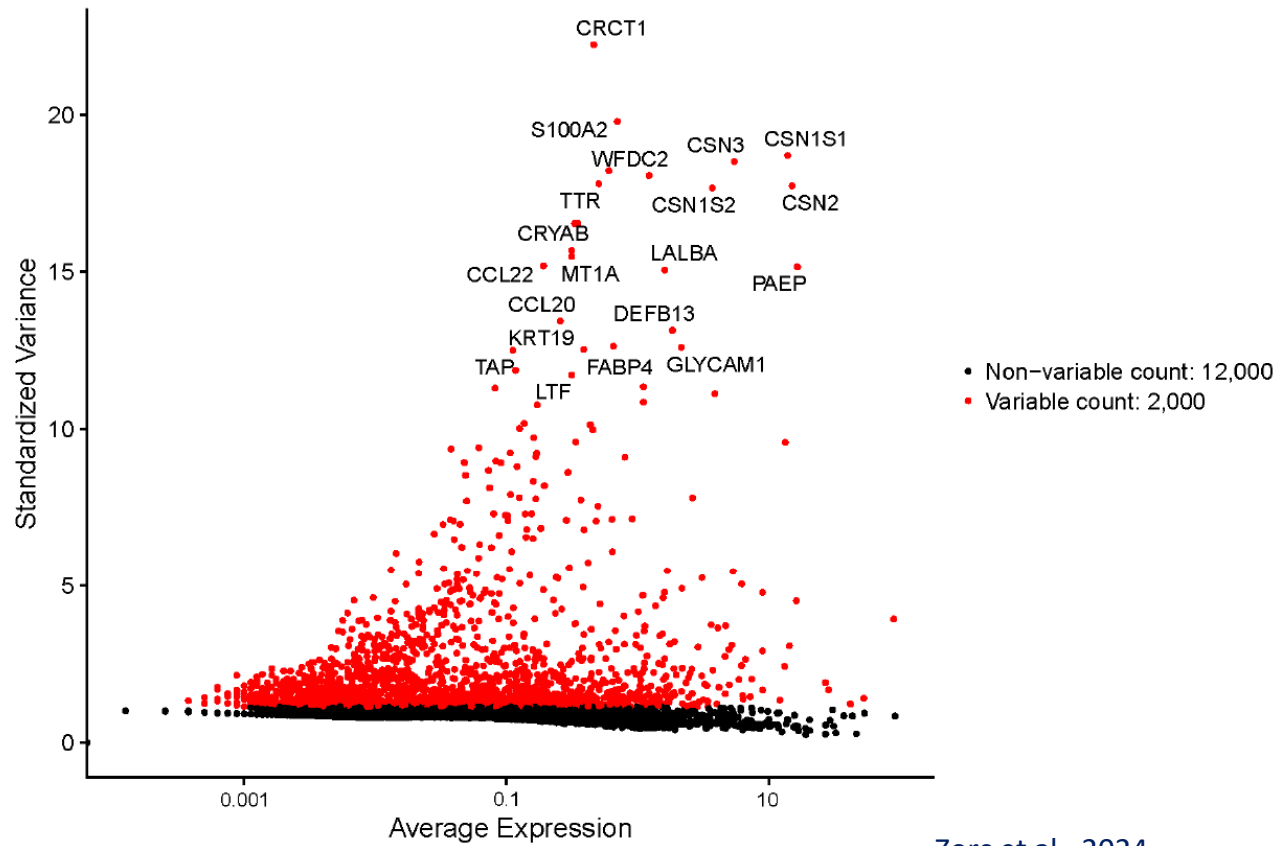
- The size of the circle corresponds to the percentage of cells in the cluster expressing the marker.
- Shading corresponds to the extent of expression.

# Expression of casein and whey protein genes in bovine somatic milk cell clusters





# Highly variable expressed genes in bovine milk somatic cells



Zorc et al., 2024

# Conclusions

- Our study aimed to capture a snapshot of cellular mechanisms driving milk synthesis and secretion at mid-lactation.
- Detection of highly variable expressed genes allowed identification of genes that strongly contribute to cell-to-cell variation within the cell population.
- Animal welfare arguments and the possibility of obtaining multiple samples from the same animal in the course of lactation are strong arguments for a non-invasive sampling approach.
- The identification of a considerably higher number of cell types in the milk somatic cell fraction compared to traditional expectations opens a new horizon for a more complex interpretation of the biological processes in the mammary gland.

**Thank you for your  
attention!**