
Cellular and transcriptional diversity over the course of human lactation

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10/01/2023

INTRODUCTION AND CONTEXT

Human breast milk (hBM) : What is it ?



- A dynamic fluid with millions of cells
- Water / Fat carbohydrates / protein / vitamins / minerals
- Blood cells / antibodies / enzymes

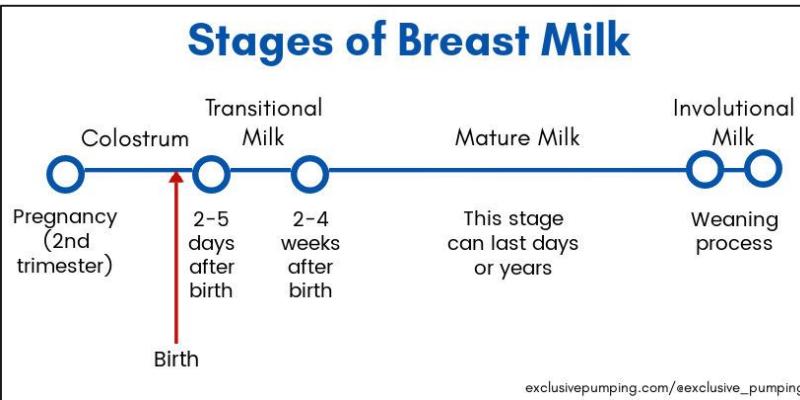
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→ Is there only one type of hBM along lactation time ?

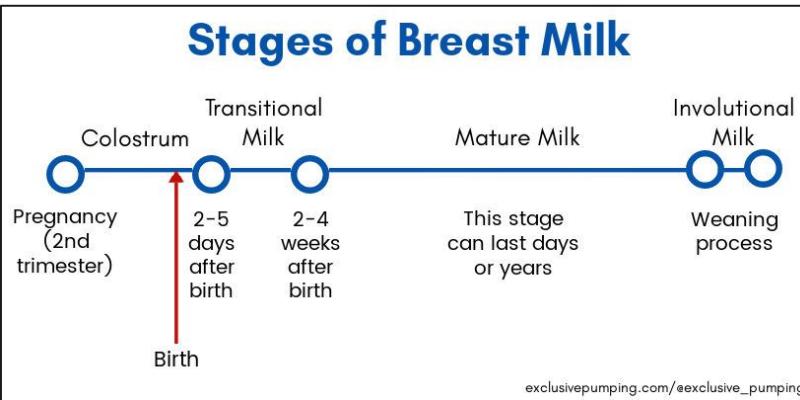
Human breast milk (hBM) : Different types over lactation



- 1) Colostrum
- 2) Transitional
- 3) Mature
- 4) Involution



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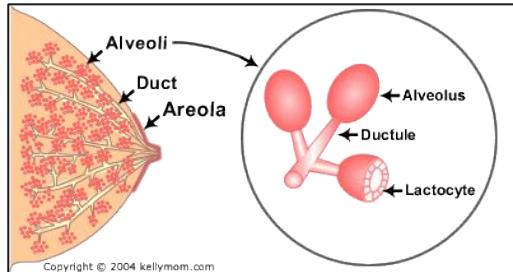
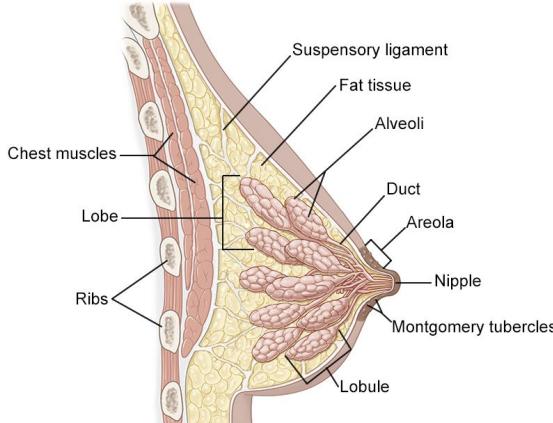


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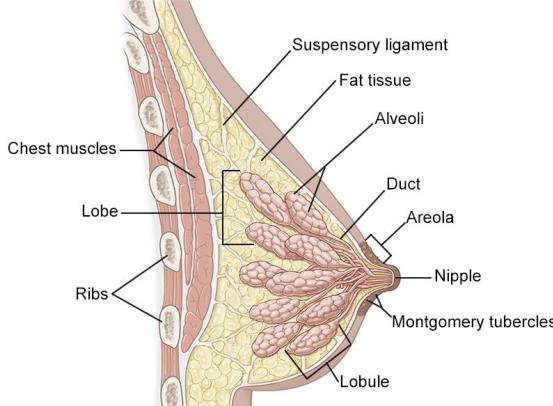


How is hBM produced in the human body?

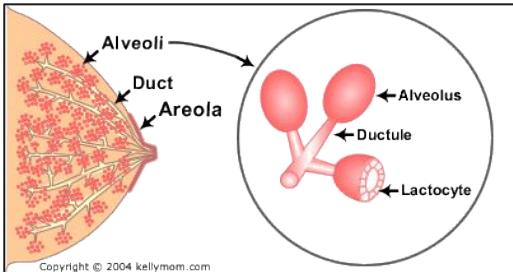
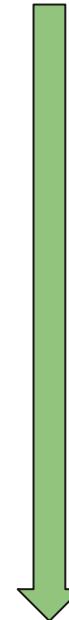
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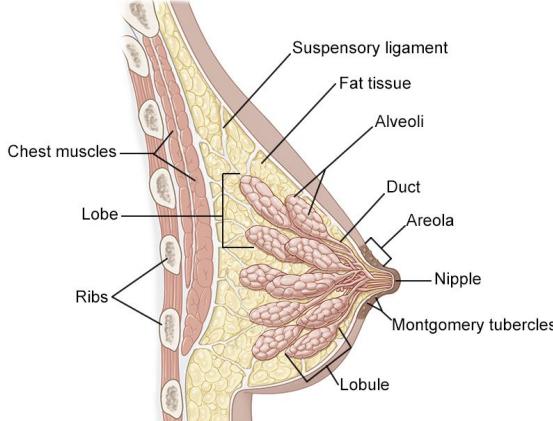
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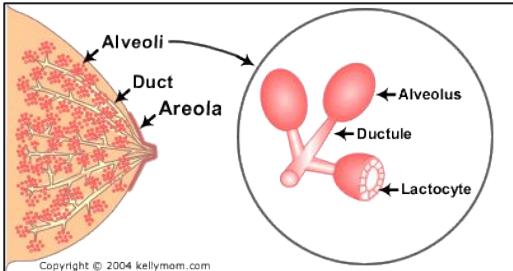
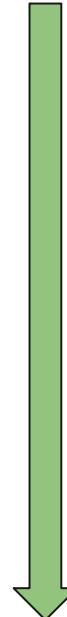


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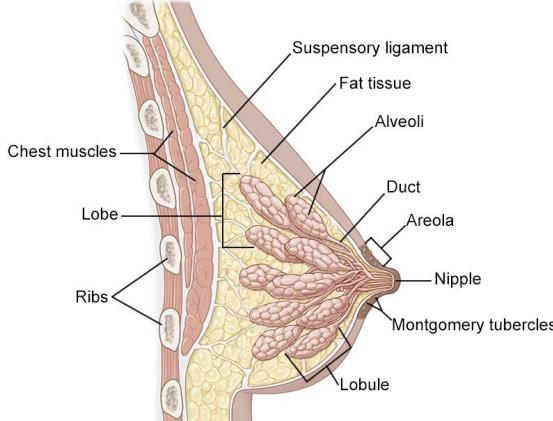


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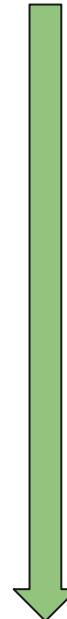
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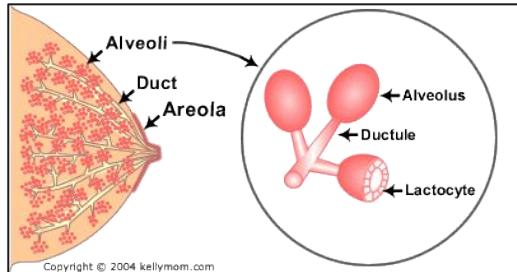
babycenter



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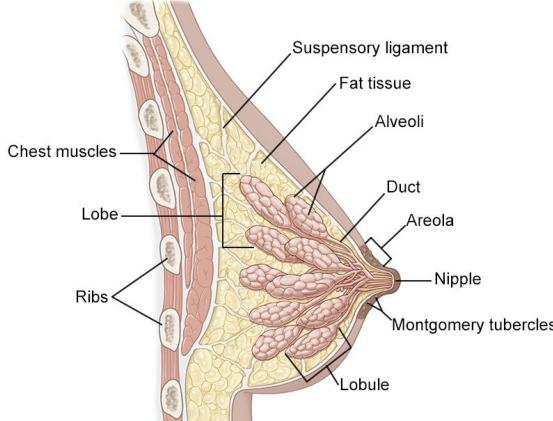
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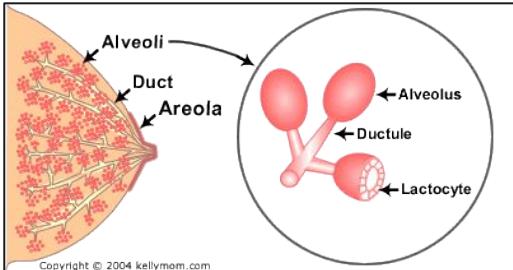


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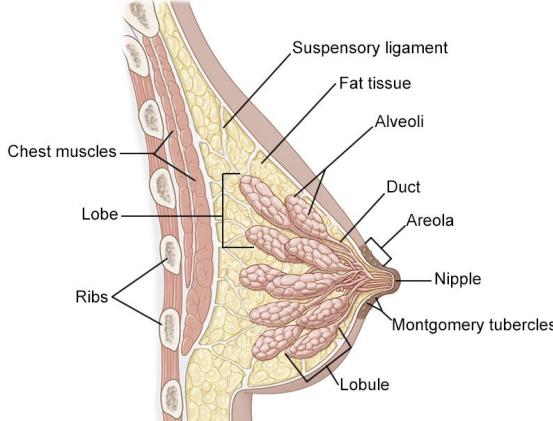
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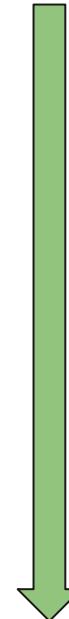
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babycenter



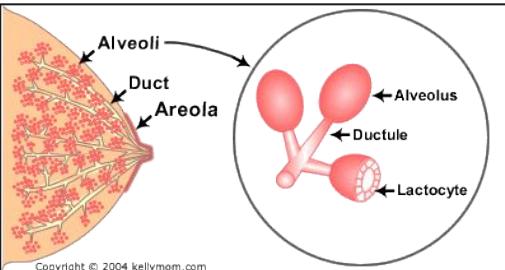
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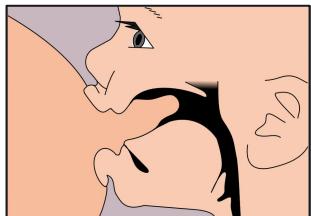
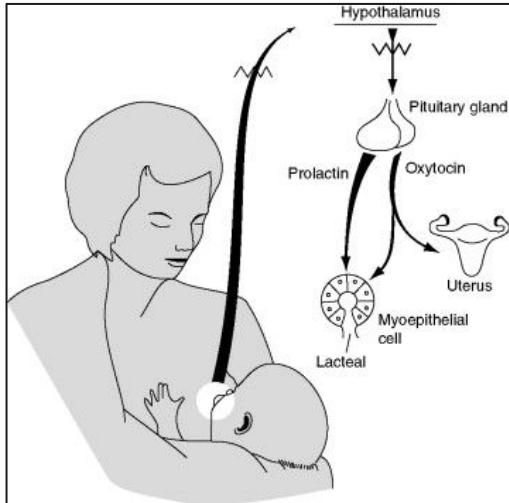
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How is hBM released for the infant?

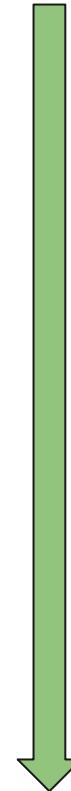
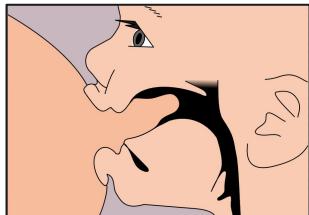
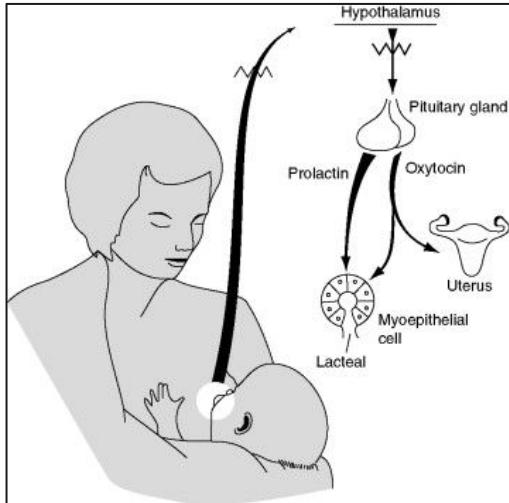


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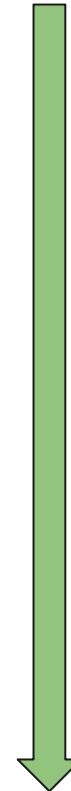
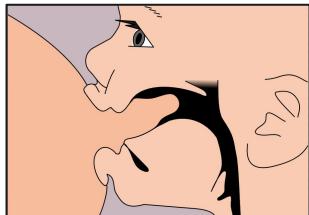
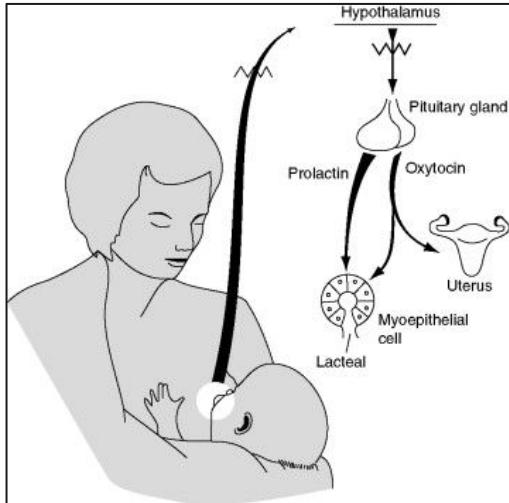


Human breast milk (hBM) : How is it released ?



1) Baby's sucking stimulates the pituitary gland

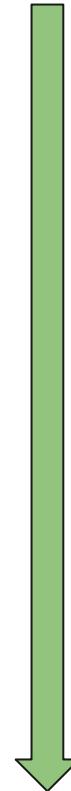
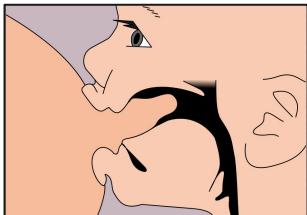
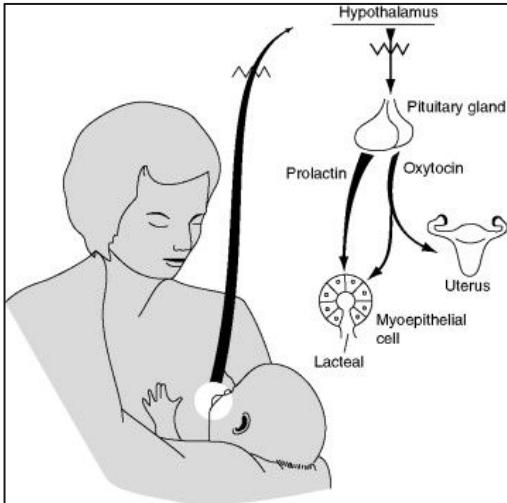
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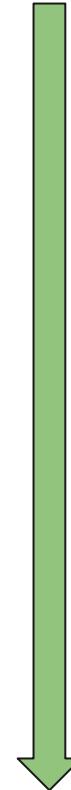
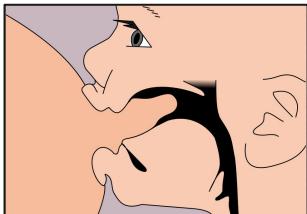
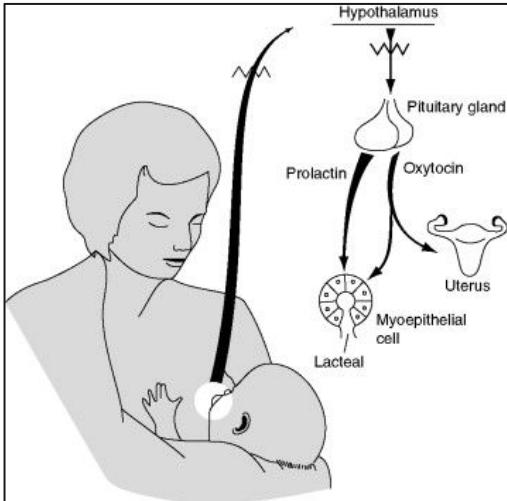
2) It releases prolactin and oxytocin

Human breast milk (hBM) : How is it released ?



- 1) Baby's sucking stimulates the pituitary gland
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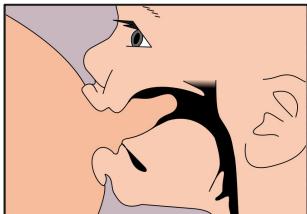
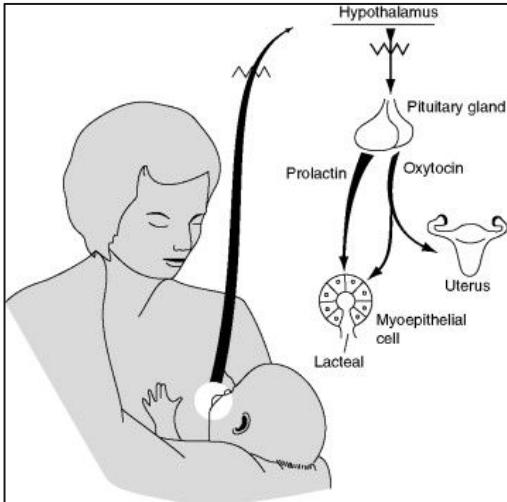
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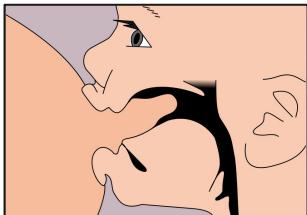
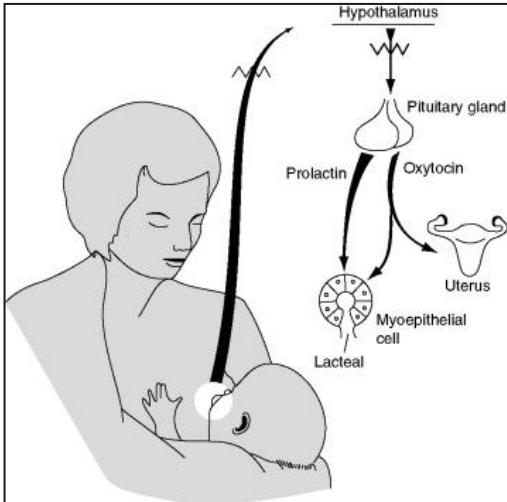
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What are hBM benefits ?

Human breast milk (hBM) : Its benefits

Long-term health benefits for both infants and nursing mothers

Infants

- decreased infection
- improved intestinal development
- improved regulation of weight

Nursing mothers

- decreased risk of ovarian and breast cancers

BREASTFEEDING

GOOD FOR BABY GOOD FOR MOM

Benefits for baby:

Prevents diarrhea,
ear infections,
pneumonia
and asthma

Cuts risk of
Sudden Infant
Death Syndrome

Lowers risk for obesity,
developing allergies

Benefits for mom:

Lessens risk of
breast cancer,
ovarian cancer

Prevents postpartum
depression,
Type 2 diabetes

Reduces stress

Sources: U.S. Surgeon General and National Institutes of Health

→ With all these benefits, it is important to better understand molecular and cellular features of hBM.

“ How a better understanding of cellular components and transcriptional diversity of the hBM across lactational time might help us to improve therapeutic support of healthy lactation and milk production ?”

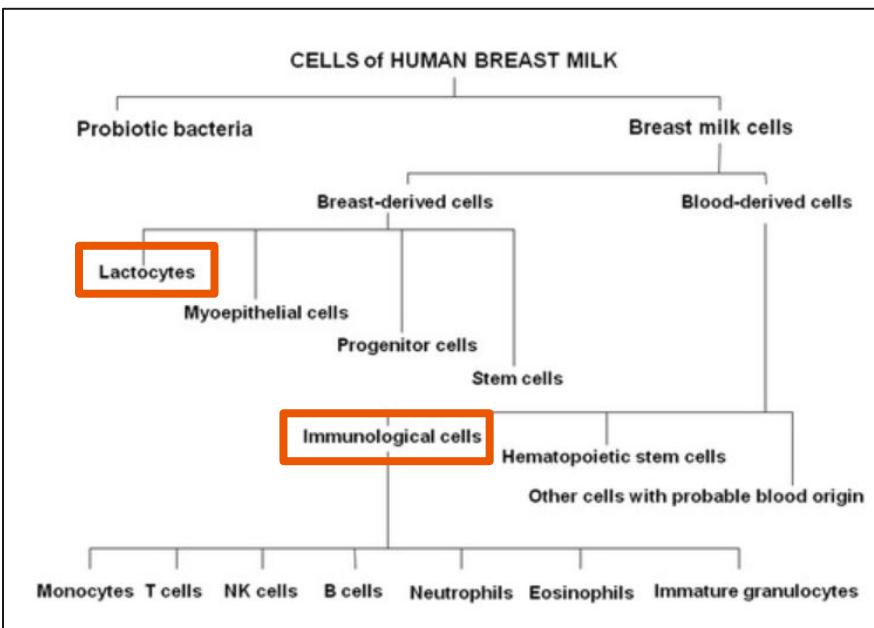
Challenges of the study

- 1) Provide a valuable single-cell characterization of hBM cells longitudinally (over the course of lactation)**
- 2) Influence of health and lifestyle on cells during lactation**
- 3) Genes that influence lactocyte functions over the course of lactation**

EXPERIMENTAL PROCESS



Cellular composition of human mammary gland

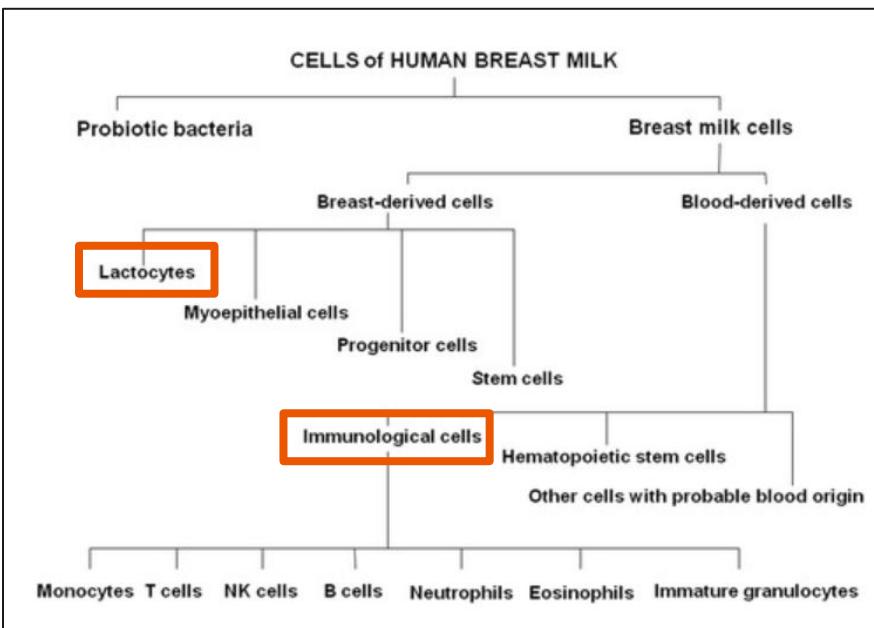


Cells of the mammary gland are responsible for synthesizing and transporting hBM

Collect cells in hBM → non-invasive method

Immune and Somatic cells

Cellular composition of human mammary gland



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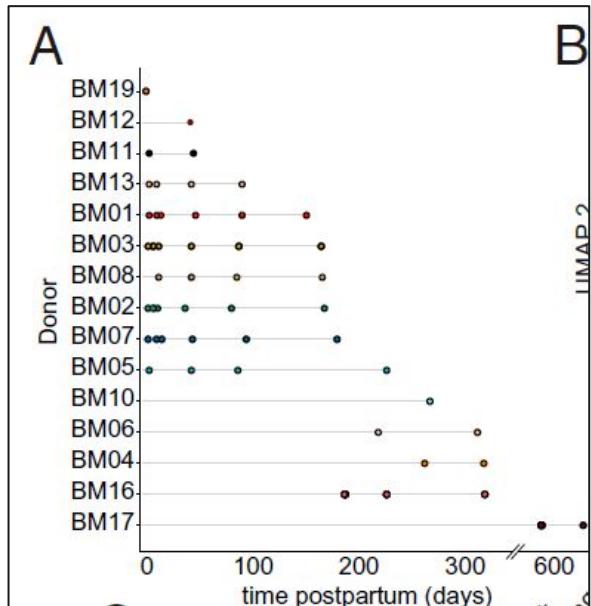
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Immune and Somatic cells

hBM has to be collected from donors



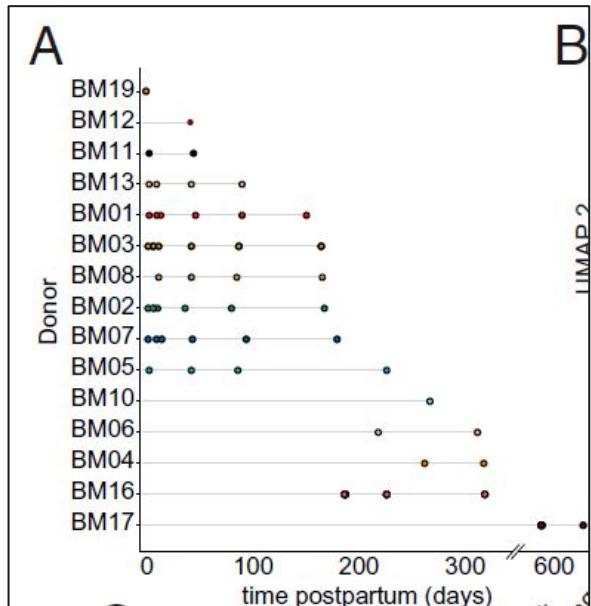
Cohort and samples at disposal



- 15 nursing mothers (ages 25-34, median 31 y)
- Samples at several time postpartum



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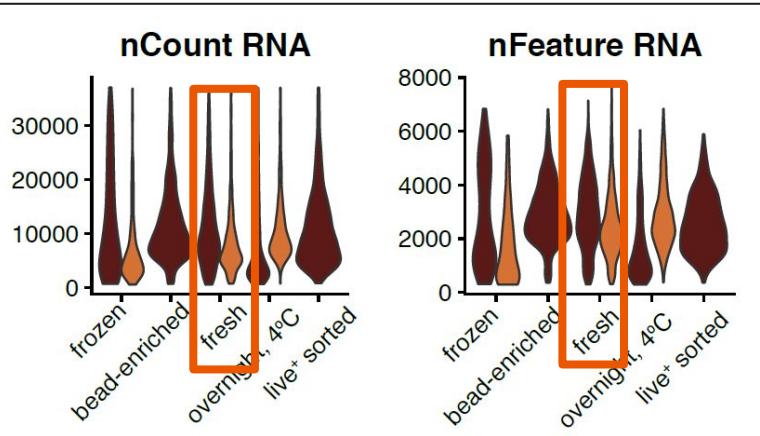


We have to isolate the cells



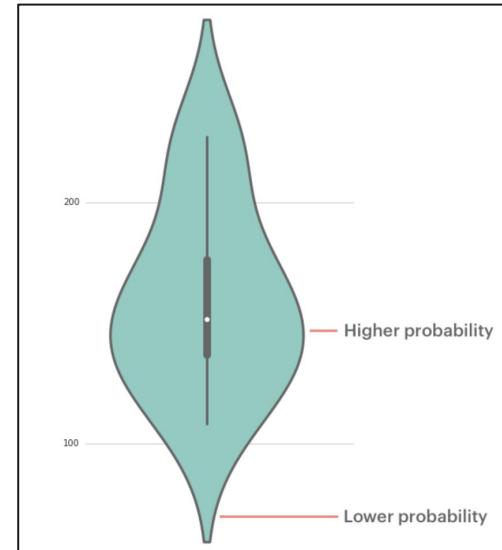
Experimental process

Cell isolation



Fresh milk → highest-quality data

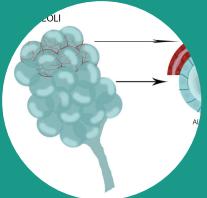
Cell isolation can impact the transcriptomes of isolated cells.



How to read a violin plot

Now, that these cells are isolated, they can be studied.

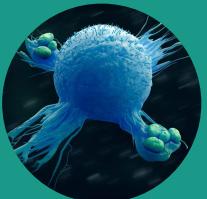
RESULTS



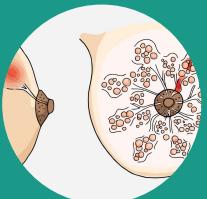
Cell types during lactation



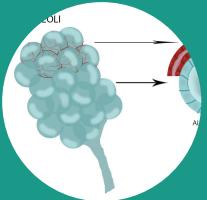
Cell frequencies during lactation



Macrophages in hBM



Epithelial cell subclusters



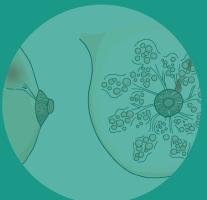
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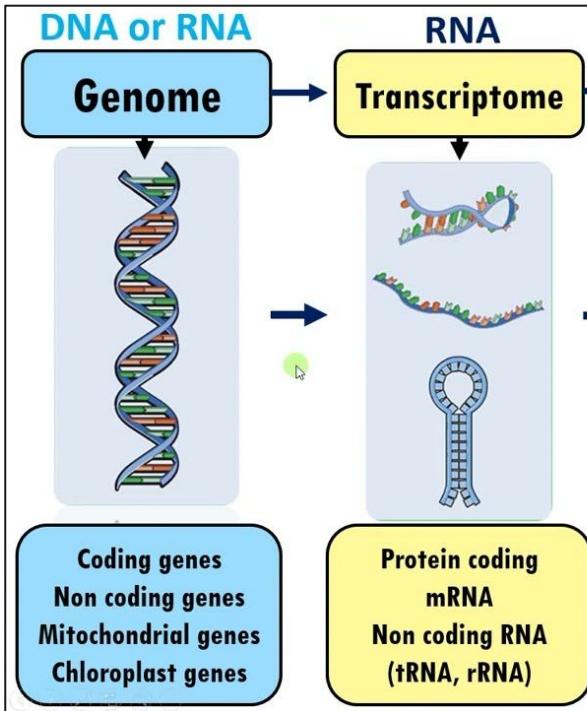


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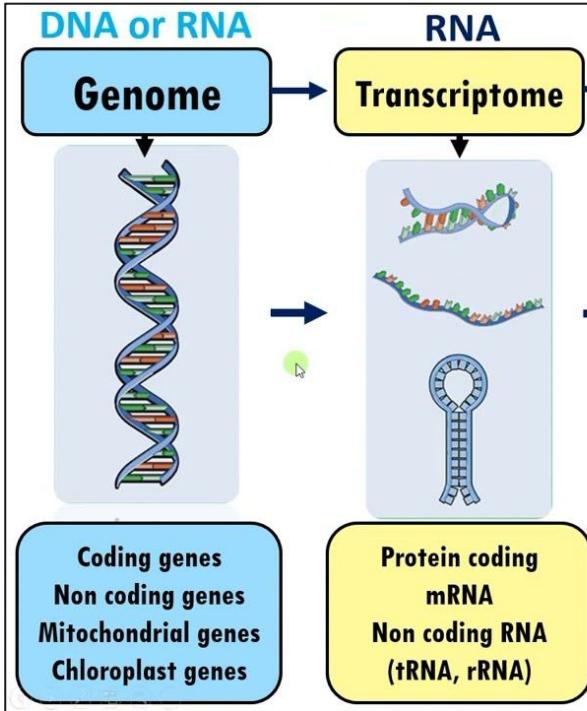
What is the transcriptome ?



The transcriptome is the **complete set of transcripts (RNA molecules)** produced by the genes in a cell or tissue.

It reflects **the patterns of gene expression** that are occurring within the cell or tissue at a given time and provides a **snapshot of the cellular state**.

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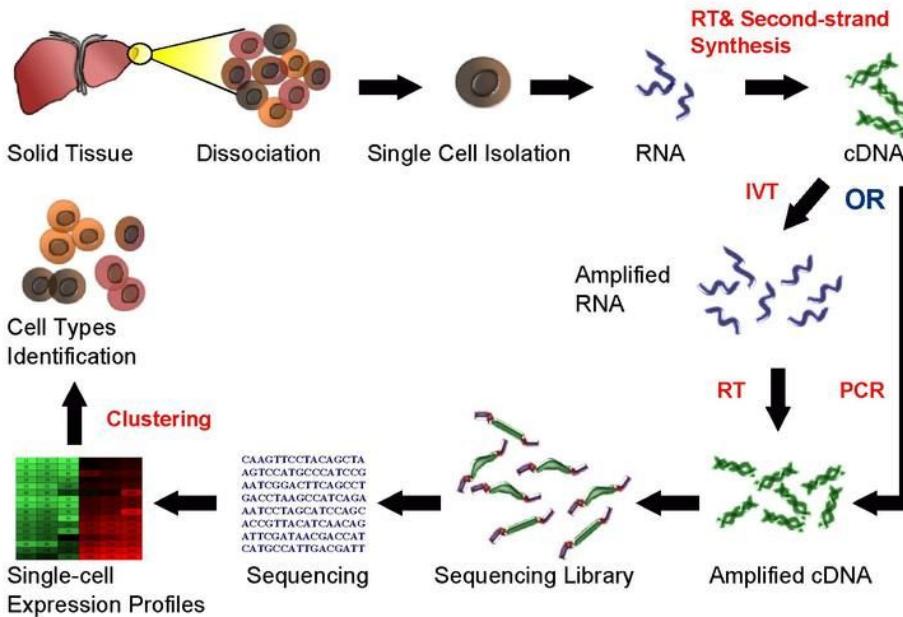
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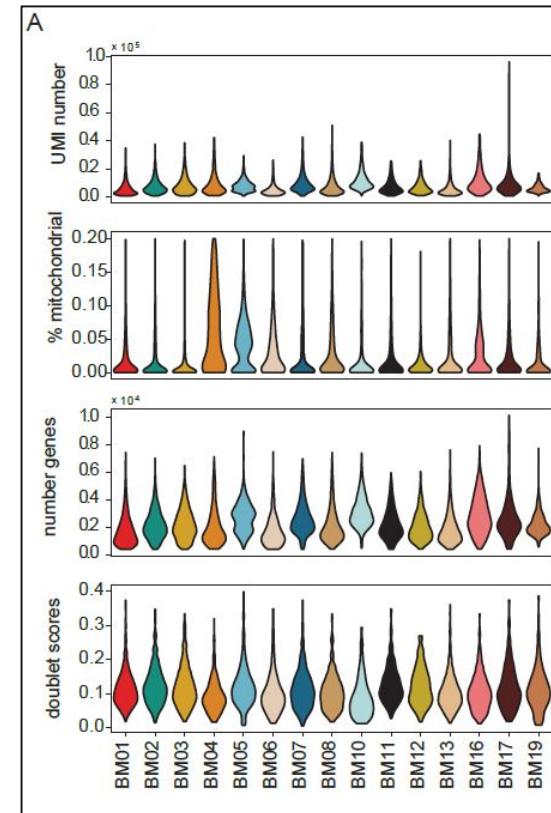
How to obtain the transcriptome of the cells ?

Generating scRNA-seq

Single Cell RNA Sequencing Workflow



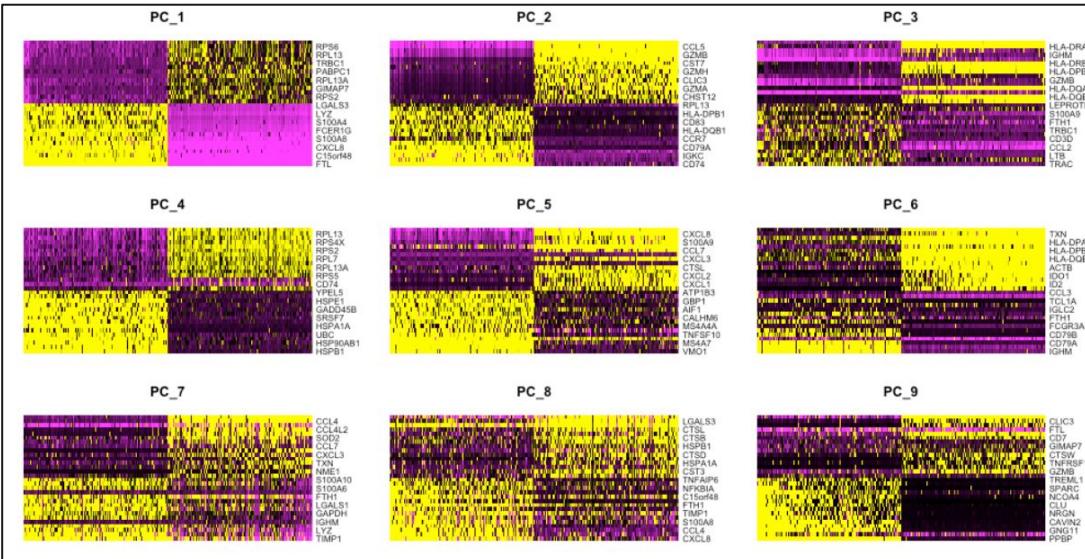
scRNA-SEQ Workflow



Results from our samples

How do you do clustering ?

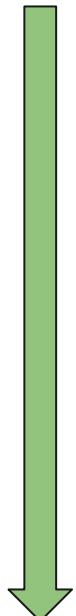
Clustering is the fact to divide cells into distinct groups based on gene expression



Use principal components

Uniform Manifold Approximation and Projection (UMAP)

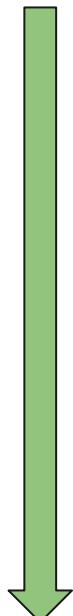
1) Obtain scRNA-seq data for the cells of interest



Uniform Manifold Approximation and Projection (UMAP)

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2) Identify the specific genes to use for the UMAP clustering



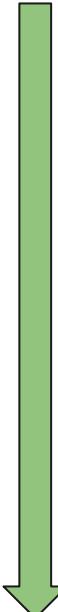
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 - 4) UMAP algorithm to reduce the dimensionality of the data
 - 5) K-means clustering

Clustering cell types with marker genes

B



UMAP 2

UMAP 1

Cell Types

- neutrophils
- B cells
- T cells
- dendritic cells
- GPNMB+ macrophages
- CSN1S1+ macrophages
- fibroblasts
- LC1
- LC2
- eosinophils

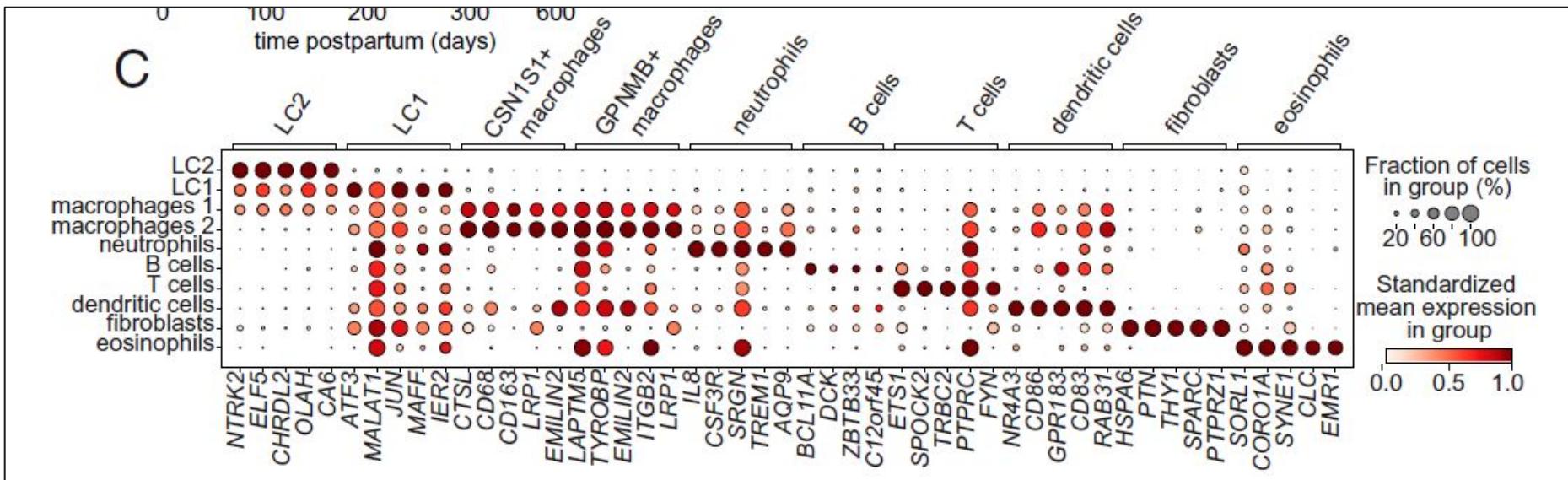
Lactation Stage (weeks)

- Early (3-6 days)
- Transitional (10-14 days)
- Mature (15-18 days)
- Late 1 (5-13 weeks)
- Late 2 (14-25 weeks)
- Late 3 (26 -33 weeks)
- Late 4 (34 - 90 weeks)

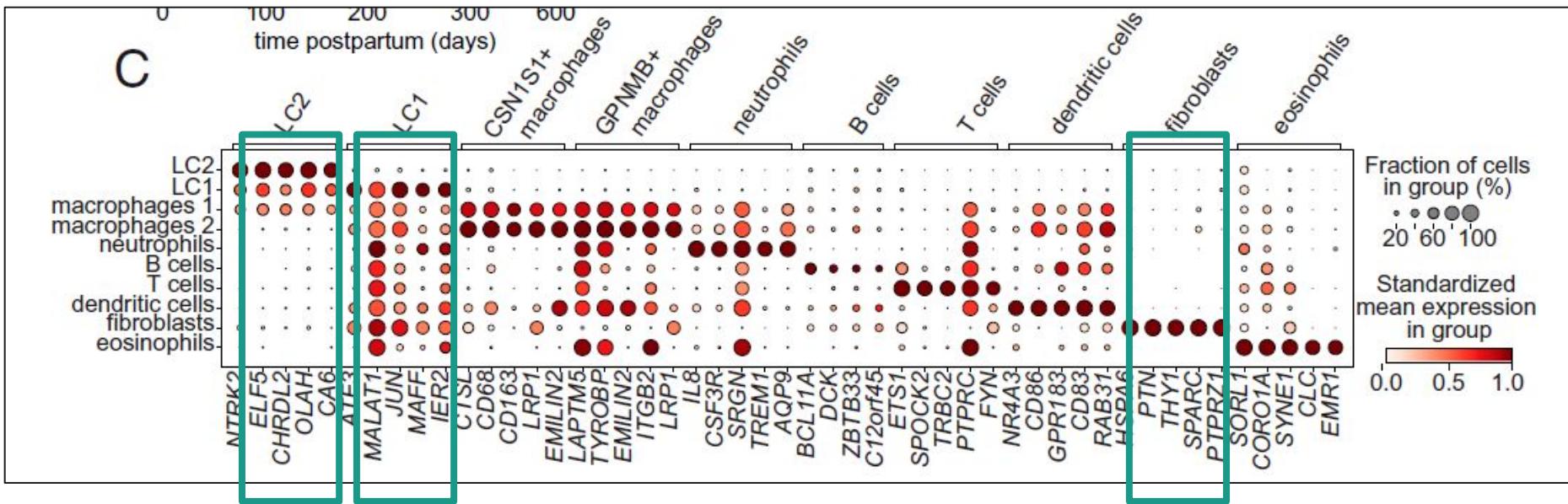
Donor (n = 15)

- BM01 ● BM06 ● BM12
- BM02 ● BM07 ● BM13
- BM03 ● BM08 ● BM16
- BM04 ● BM10 ● BM17
- BM05 ● BM11 ● BM19

Clustering cell types with marker genes

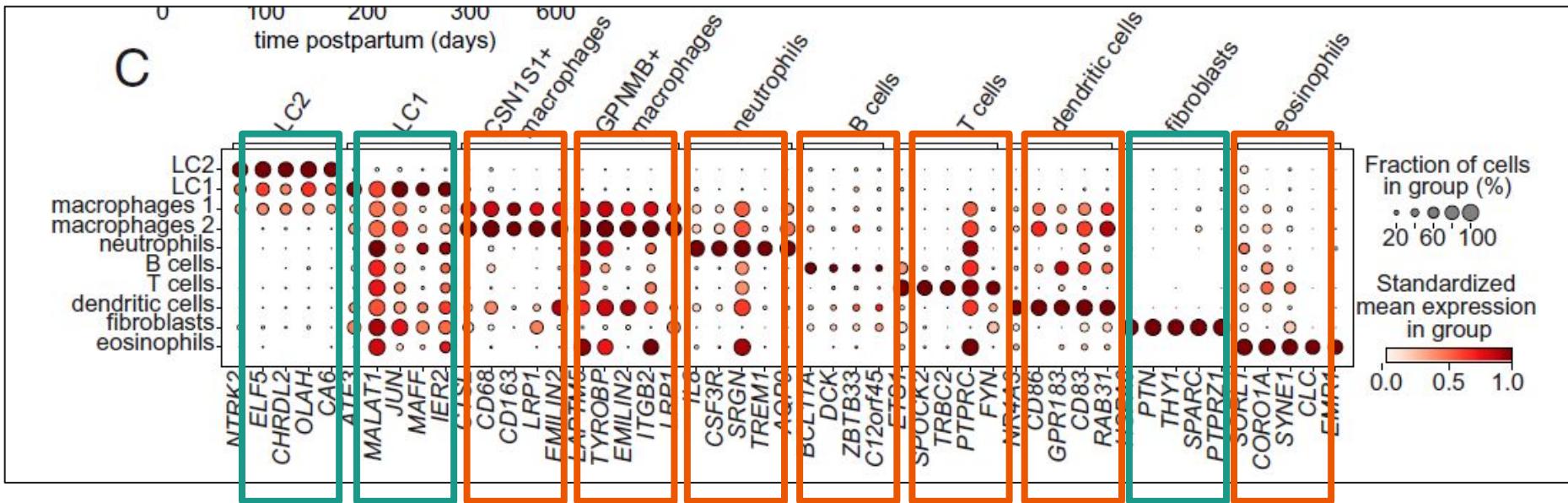


Clustering cell types with marker genes



- 7 immune cell clusters (green)
- 3 non-immune cell clusters (orange)

Clustering cell types with marker genes

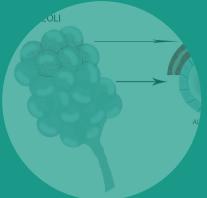


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Cell abundance

- Lactocyte epithelial cells are the most abundant cell types (LC1 and LC2) - **81.7 % of all cells per sample**
- Macrophages are the most abundant immune cell type - **50.5 % of immune cells**
- Identification of more immune clusters than previous studies

How these cells proportion evolves during the lactation, and how are they associated with maternal-infant metadata ?



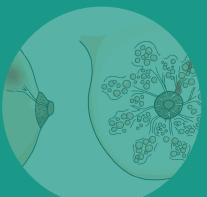
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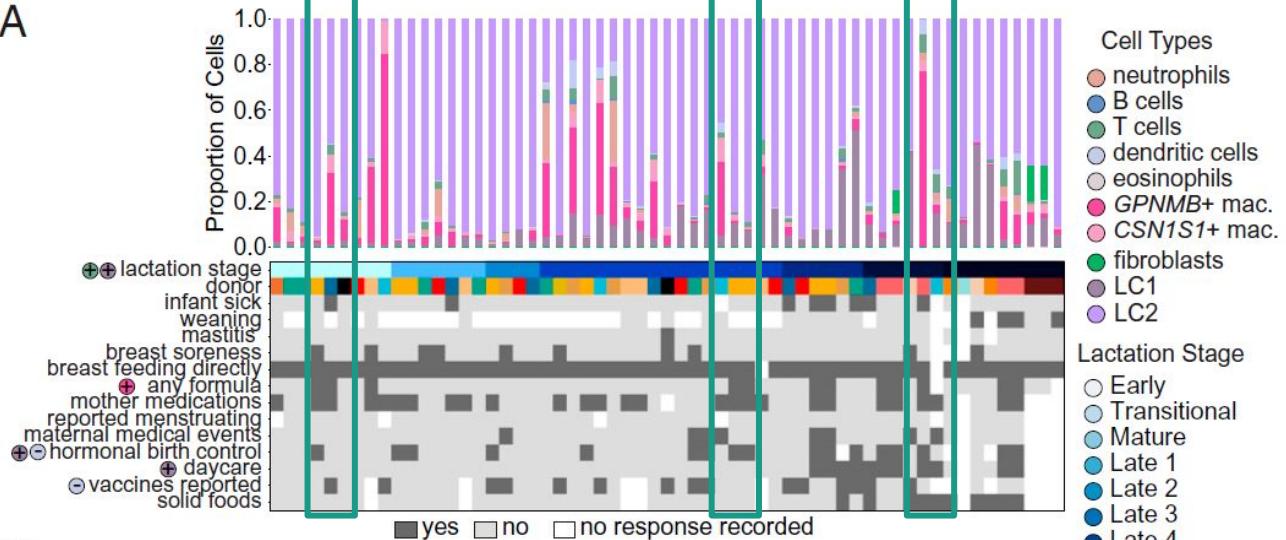
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Epithelial cell subclusters

Maternal-Infant Metadata

A



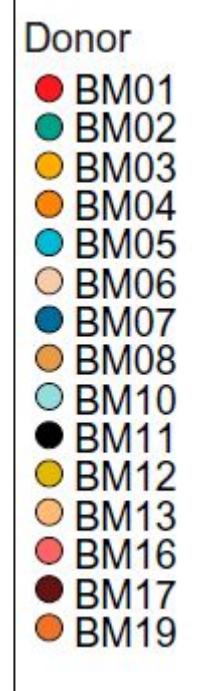
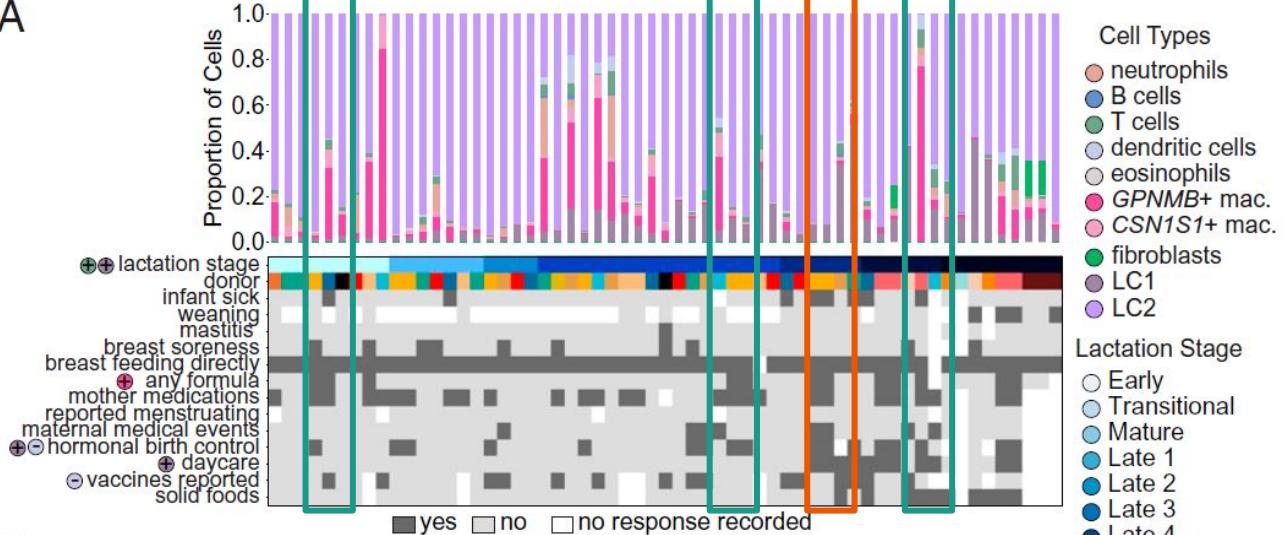
Donor

- BM01
- BM02
- BM03
- BM04
- BM05
- BM06
- BM07
- BM08
- BM10
- BM11
- BM12
- BM13
- BM16
- BM17
- BM19

- GPNMB+ associated with formula supplementation

Maternal-Infant Metadata

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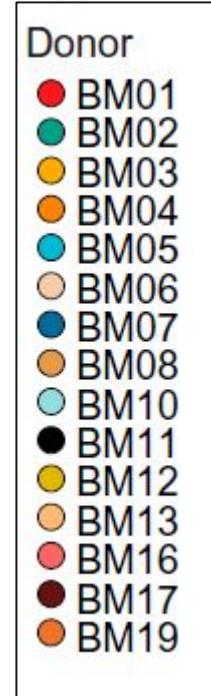
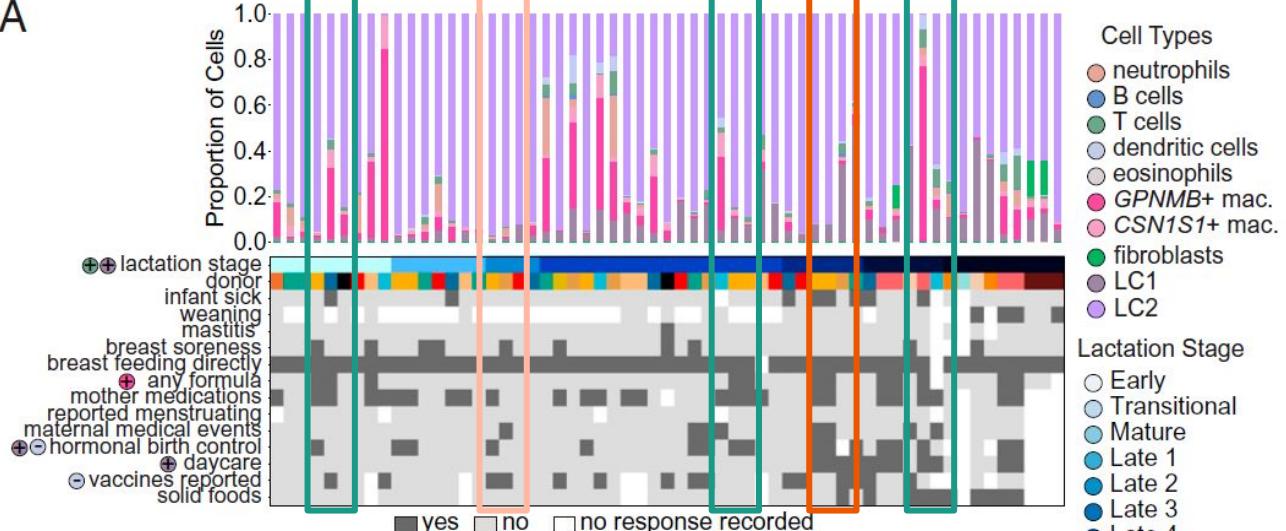


- GPNMB+ associated with formula supplementation

- LC1 associated positively with daycare and hormonal birth control

Maternal-Infant Metadata

A

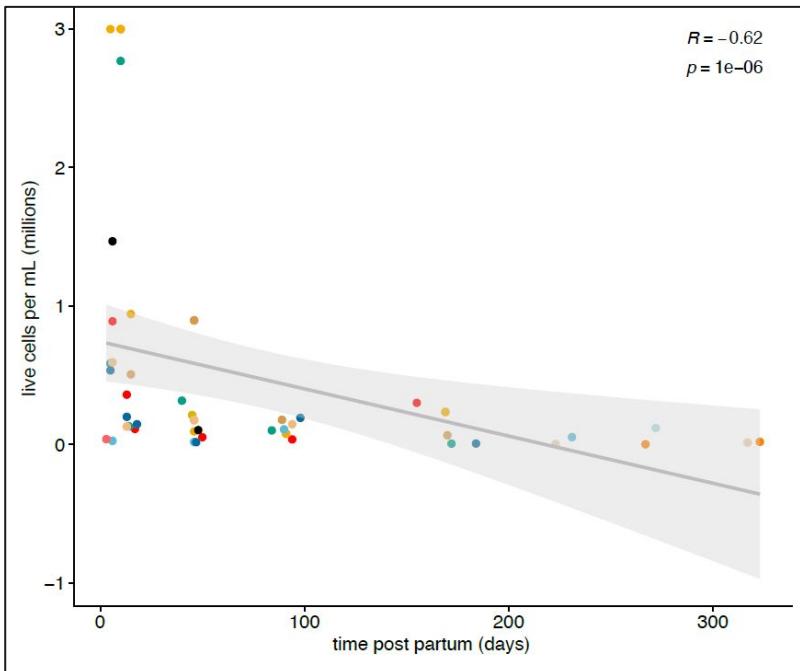


- GPNMB+ associated with formula supplementation

- LC1 associated positively with daycare and hormonal birth control

- Dendritic cells negatively associated with hormonal birth control and infant vaccinations

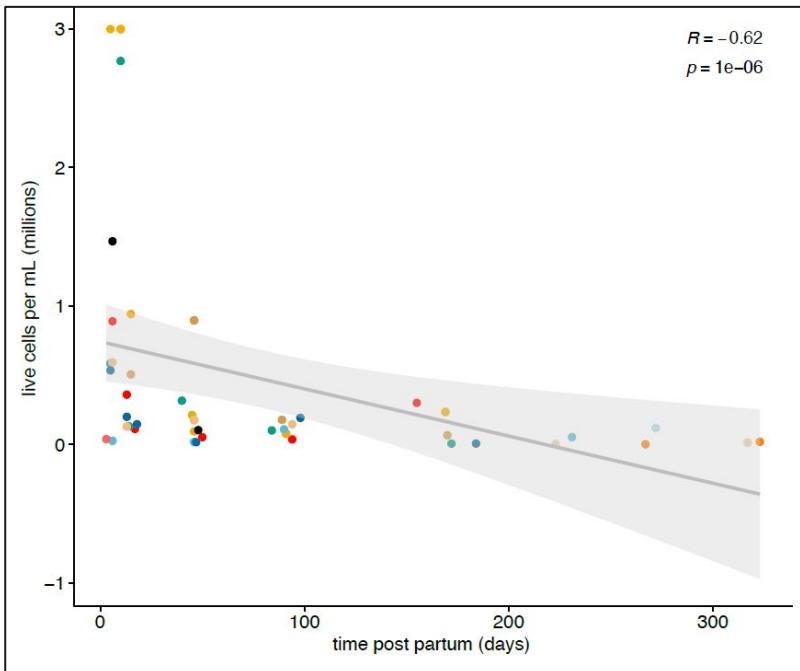
Cell-count evolution



- Total cell counts decrease over the course of lactation.

Donor
BM01
BM02
BM03
BM04
BM05
BM06
BM07
BM08
BM10
BM11
BM12
BM13
BM16
BM17
BM19

Cell-count evolution

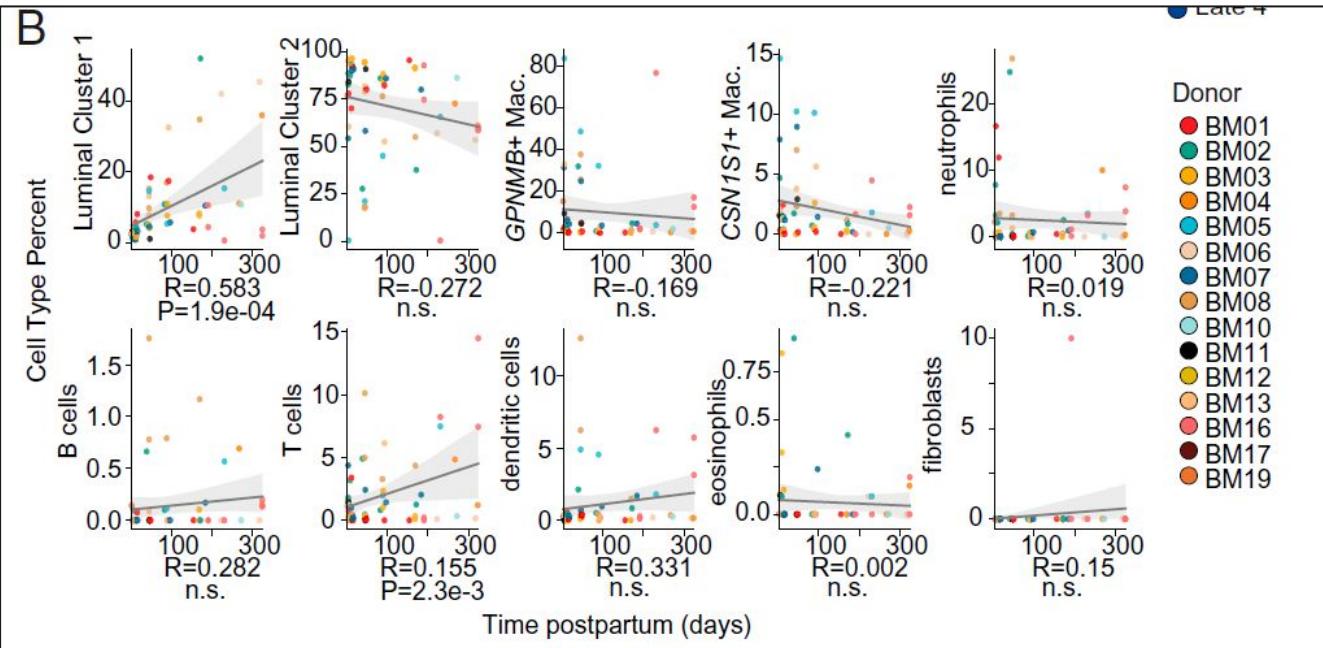


- Total cell counts decrease over the course of lactation.

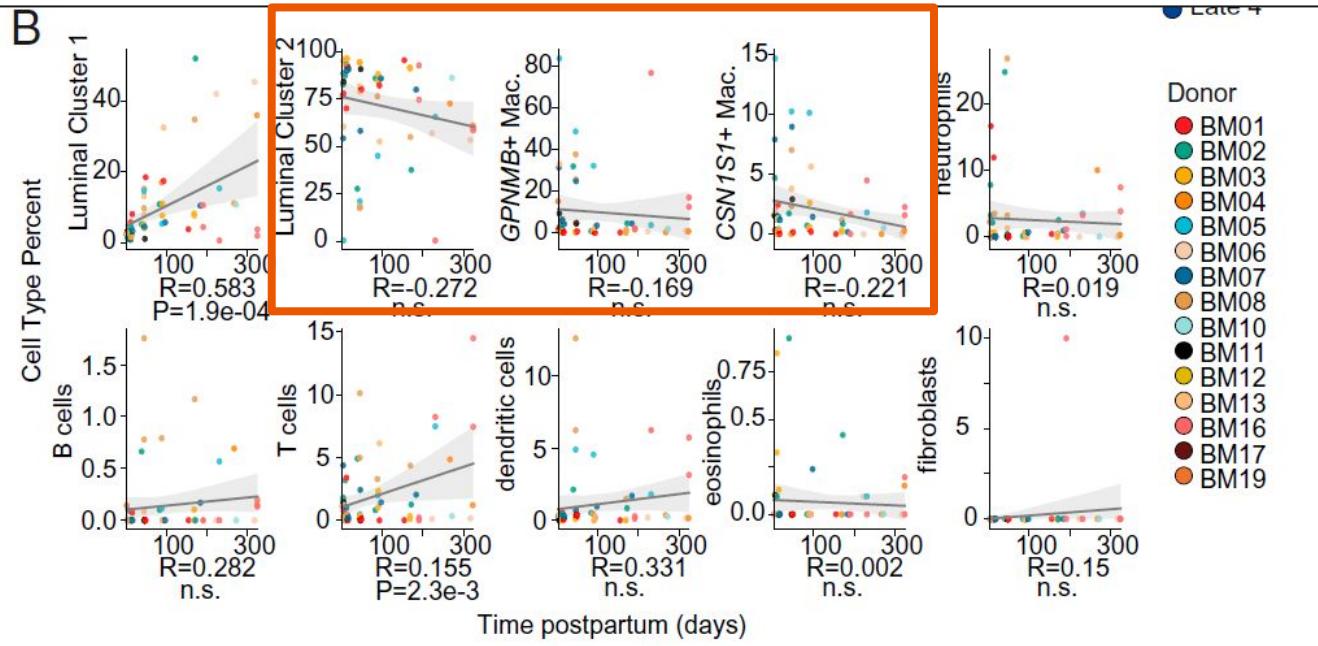
Donor
BM01
BM02
BM03
BM04
BM05
BM06
BM07
BM08
BM10
BM11
BM12
BM13
BM16
BM17
BM19

How do they specifically evolve ?

Cell-count per clusters

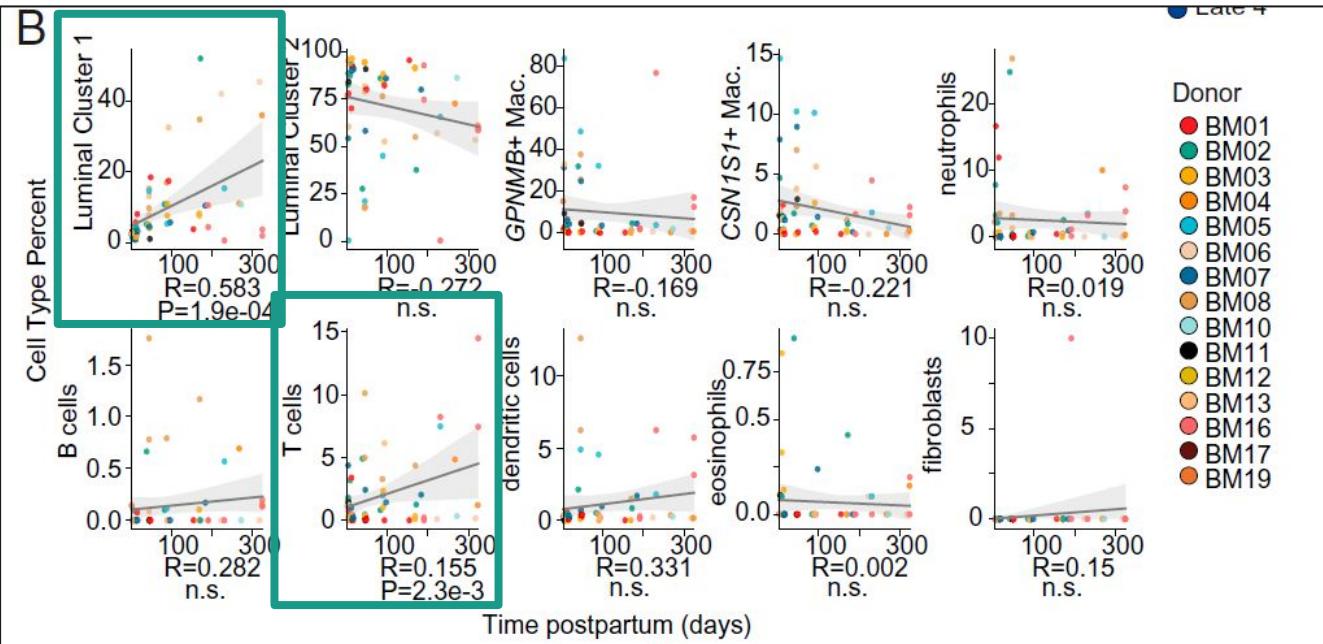


Cell-count per clusters



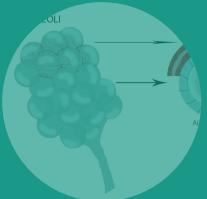
LC2 and macrophages remains constant

Cell-count per clusters



LC1 and T-cells are associated with postpartum as they increase.

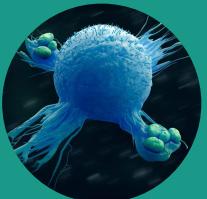
Macrophages appears as very important in the immune cells. It is therefore essential to understand better the functions of this cell in hBM.



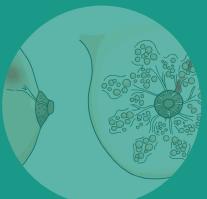
Cell types during lactation



Cell frequencies during lactation

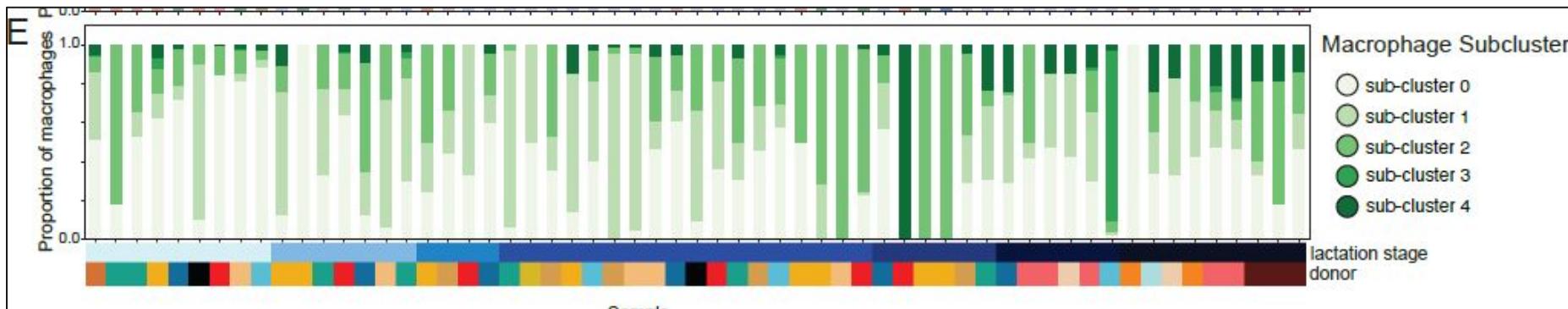


Macrophages in hBM



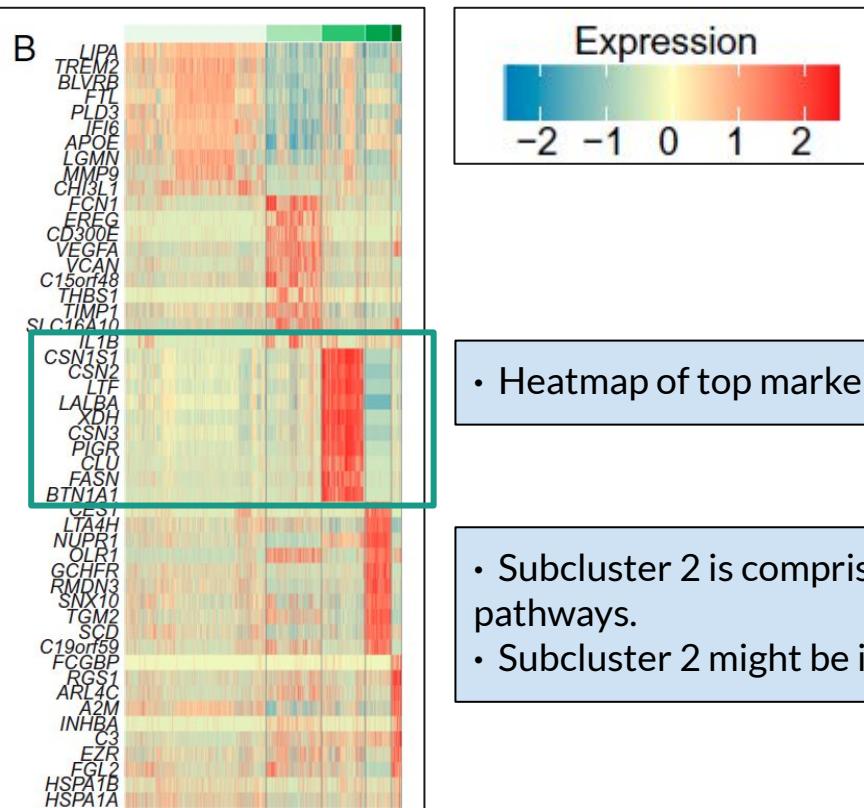
Epithelial cell subclusters

Identification of macrophages sub-clusters



- 5 macrophages subclusters

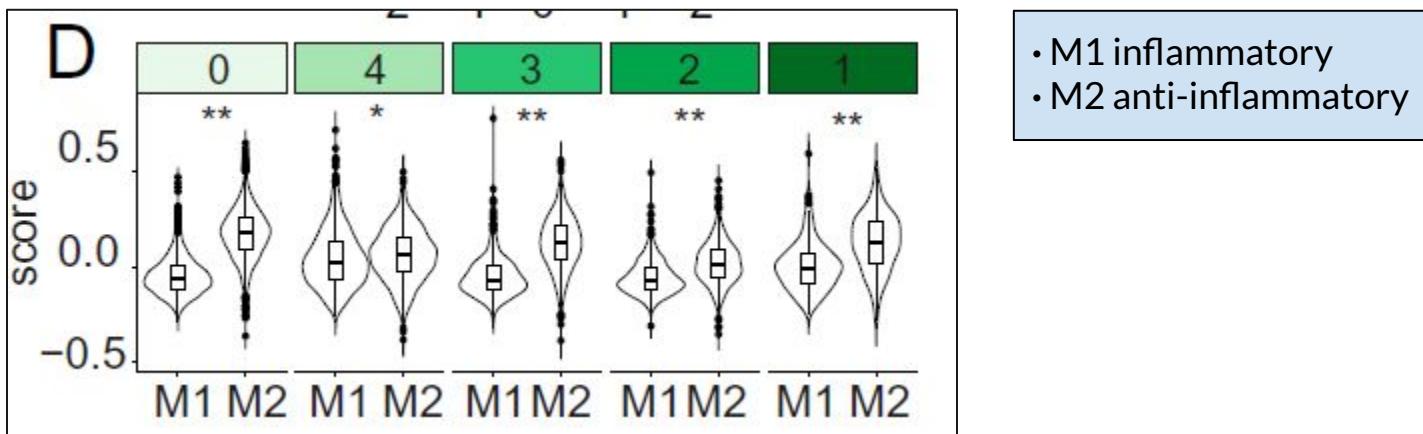
Functional enrichment of marker genes



- Heatmap of top marker genes for each identified macrophage subscluster

- Subcluster 2 is comprised almost entirely of CSN1S1+ related to structural pathways.
- Subcluster 2 might be important for **structural maintenance**

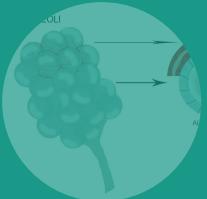
Identification of inflammatory clusters



Subclusters (except subcluster 1) scored higher for M2-gene sets

Macrophages seems to serve **immunosuppressive** and **tissue maintenance functions**

Now that we sought into macrophages and immune cells, let's focus on somatic cells and more especially epithelial cells that are primordial in the lactation process.



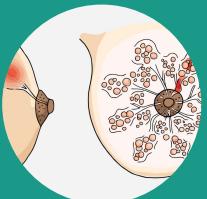
Cell types during lactation



Cell frequencies during lactation

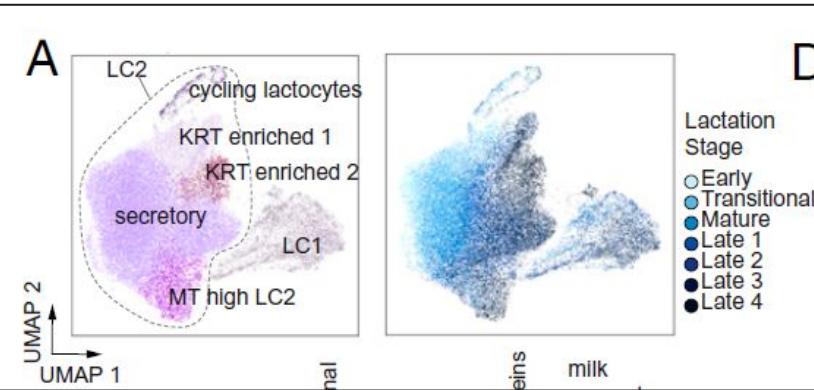


Macrophages in hBM



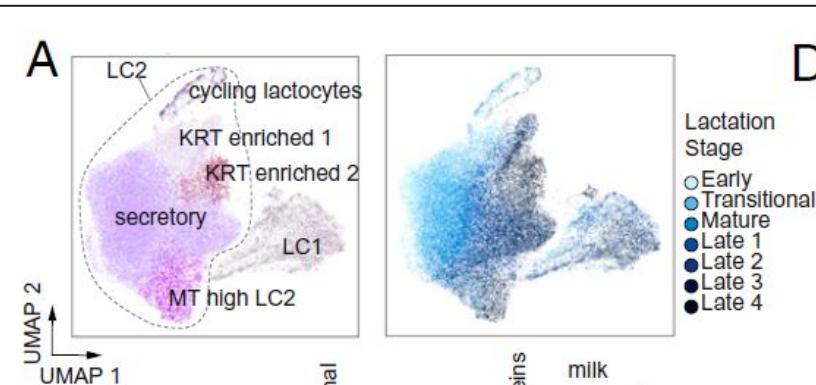
Epithelial cell subclusters

Subclusters of epithelial cells

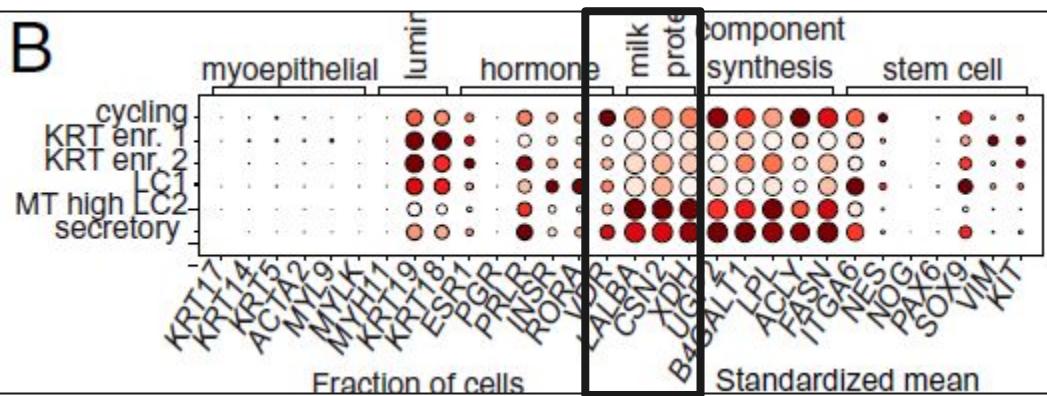


- 6 subclusters of epithelial cells

Subclusters of epithelial cells

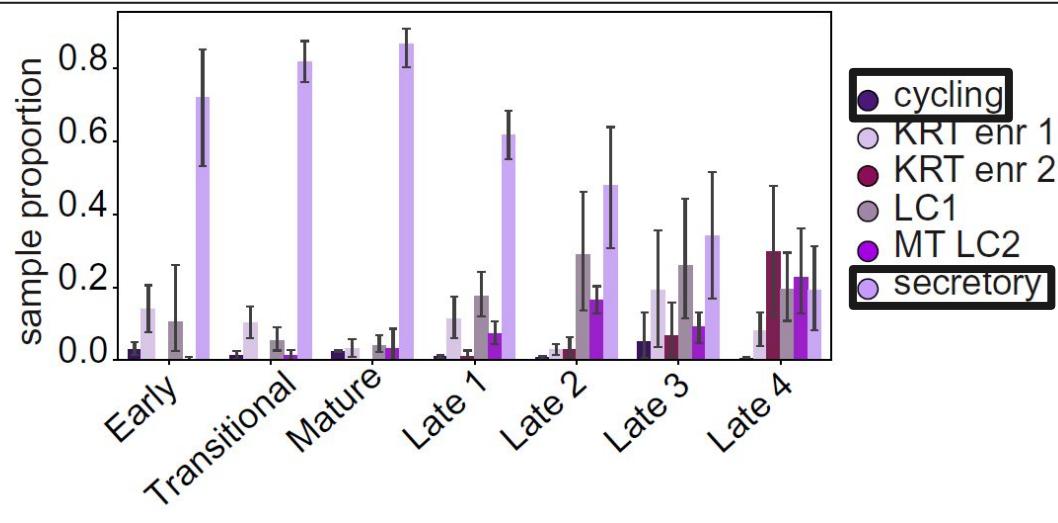


- 6 subclusters of epithelial cells



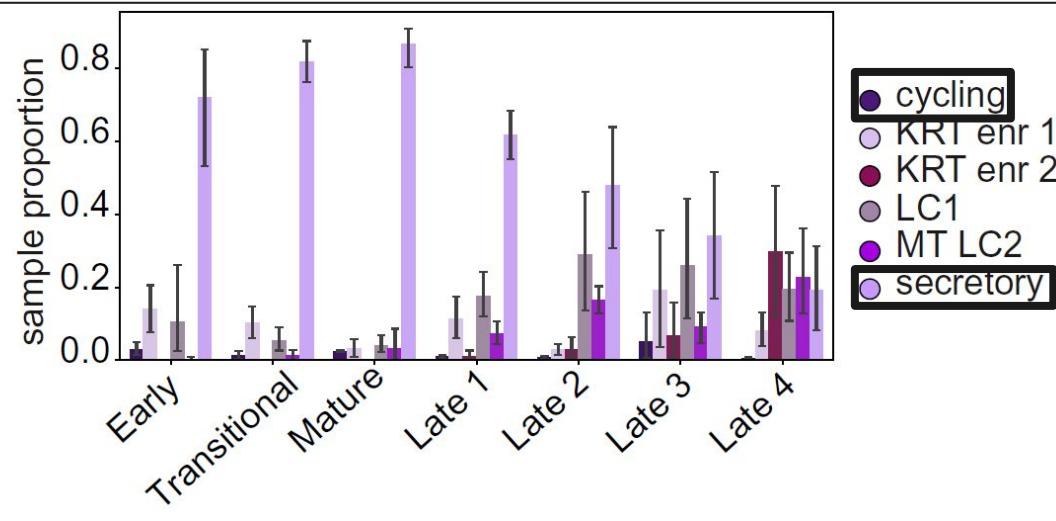
- Genes related to milk synthesis
- LALBA, CSN2, XDH

Subclusters over the course of lactation



- All subclusters except secretory and cycling lactocytes increase over the course of lactation

Subclusters over the course of lactation

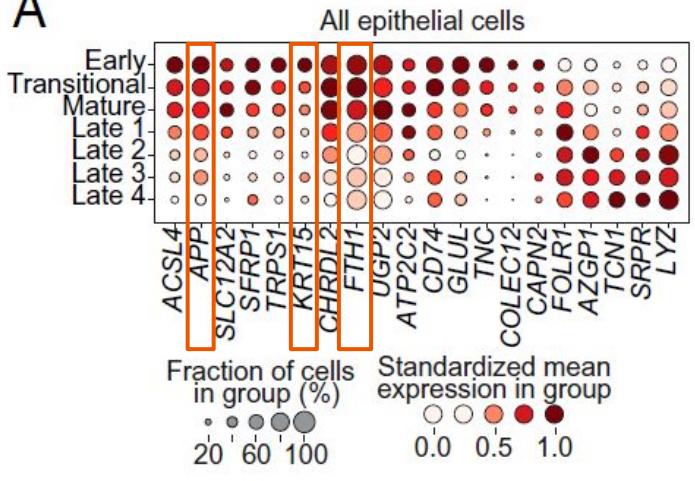


- All subclusters except secretory and cycling lactocytes increase over the course of lactation



Is there also changes in gene expression over the course of lactation ?

Gene expressions over the course of lactation

A

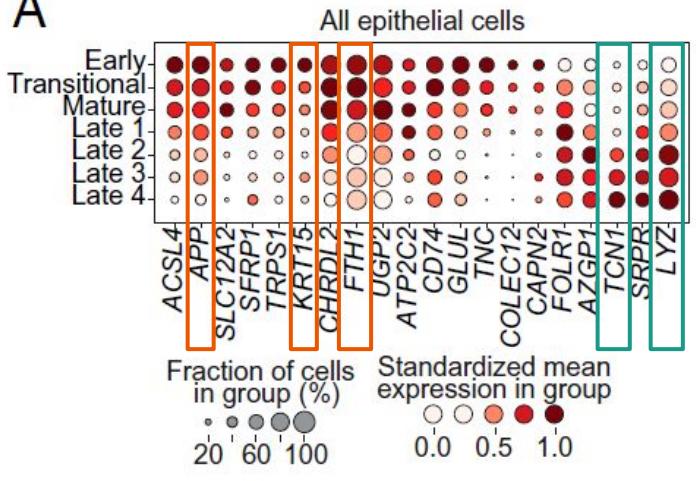
- Genes are differentially expressed over time



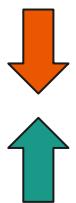
- APP, KRT15, FTH1 decrease

Gene expressions over the course of lactation

A



- Genes are differentially expressed over time



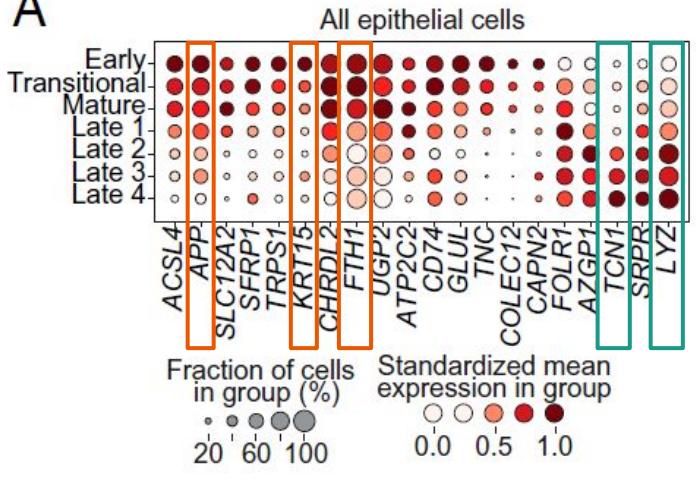
- APP, KRT15, FTH1 decrease



- LYZ, TCN1 increase

Gene expressions over the course of lactation

A



- Genes are differentially expressed over time



- APP, KRT15, FTH1 decrease



- LYZ, TCN1 increase

- Genes related to **metabolism** and **milk component biosynthesis** decrease



- Genes related to **structural pathways** and **signaling** increase



Now that we saw how the expression of epithelial cells over the course of lactation, which simple experiment could be led to pursue the study ?

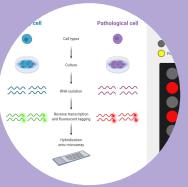
EXPERIMENT



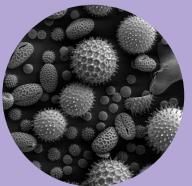
My thoughts

- 1) Improve the characterization of the cell transcriptomes**

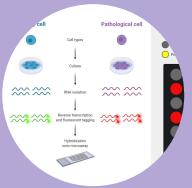
- 2) Obtain more quantitative data on the cells over the course of lactation**



Improve cell transcriptome



Quantitative data on the cells



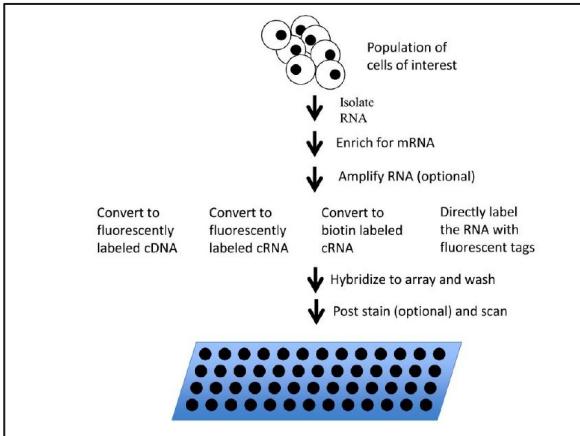
Improve cell transcriptome



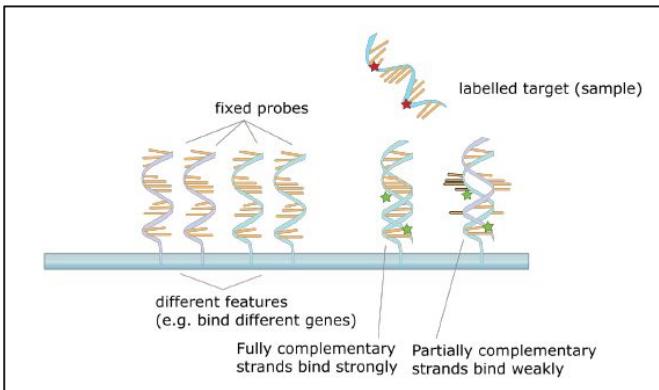
Quantitative data on the cells

Additional Experiment

DNA Micro-Array presentation



- DNA microarrays measure the expression levels of large number of genes simultaneously.



Advantages of sc SEQ-RNA compared to DNA Micro-Array

- 1) Higher sensitivity; able to detect lower levels of gene expression

Advantages of sc SEQ-RNA compared to DNA Micro-Array

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Advantages of sc SEQ-RNA compared to DNA Micro-Array

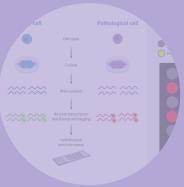
1) Higher sensitivity; able to detect lower levels of gene expression

2) Greater dynamic range;

3) Greater accuracy;

4) Greater flexibility;

5) Greater throughput; study many samples simultaneously

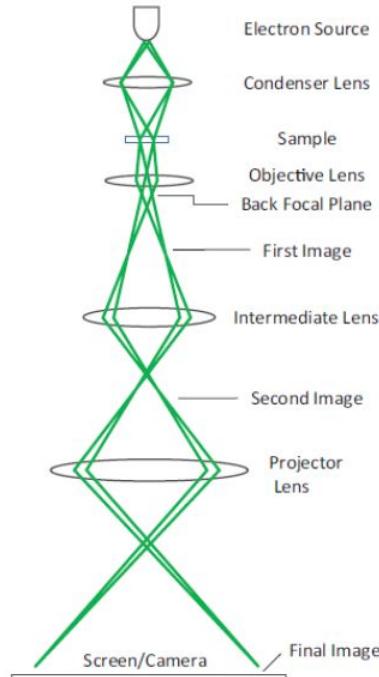


Improve cell transcriptome



Quantitative data on the cells

Transmission electron microscopy : principle



- E-beam with high acceleration voltage penetrating the sample → Ultrathin sections → Higher resolution + Ultrastructure
- 3 components
 - **Illumination system**; electron source, condenser lens
 - **Objective lens**
 - **Imaging system**; intermediate and projector lenses

Transmission electron microscopy : sample preparation

- 1) **Fixation;** preserve the sample by adding chemicals that stabilize the cellular structure. Done in formaldehyde or glutaraldehyde.

Transmission electron microscopy : sample preparation

- 1) **Fixation;** preserve the sample by adding chemicals that stabilize the cellular structure. Done in formaldehyde or glutaraldehyde.
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- 2) **Dehydration**; alcohol washes
- 3) **Embedding**; solid material such as resin (epoxy or acrylic)

Transmission electron microscopy : sample preparation

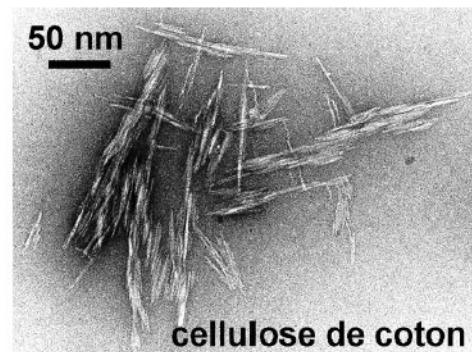
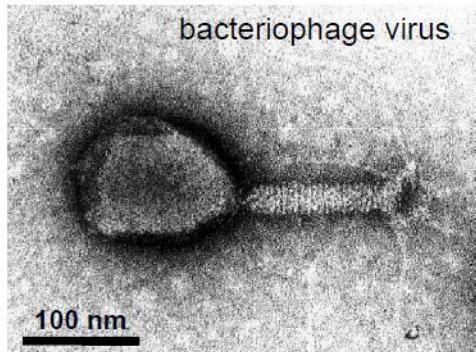
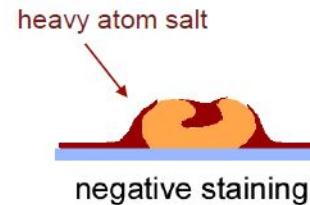
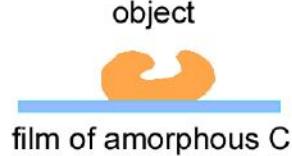
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- 3) **Embedding**; solid material such as resin (epoxy or acrylic)
- 4) **Sectioning**; Cut to be thin enough (~ 70-80 nm)

Transmission electron microscopy : sample preparation

- 1) **Fixation;** preserve the sample by adding chemicals that stabilize the cellular structure. Done in formaldehyde or glutaraldehyde.
- 2) **Dehydration;** alcohol washes
- 3) **Embedding;** solid material such as resin (epoxy or acrylic)
- 4) **Sectioning;** Cut to be thin enough (~ 70-80 nm)
- 5) **Staining;** Stained with heavy metals such as lead or uranyl acetate

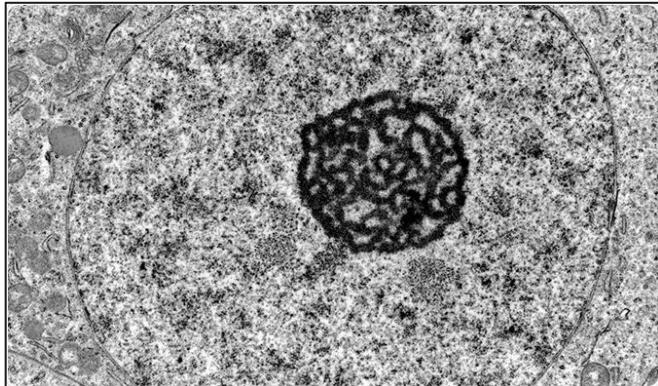
Transmission electron microscopy : contrast enhancement

TEM : Contrast enhancement of organic specimens



Negative staining with uranyl acetate

Transmission electron microscopy



- SEM can visualize many features of the cells
- Cell membrane / Cytoplasm / Nucleus / Cell junctions / Extracellular matrix

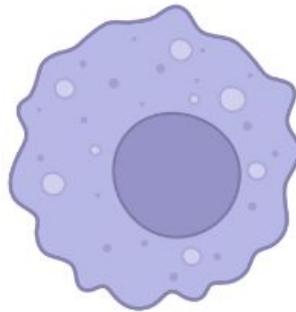
DISCUSSION

Size of the cohort



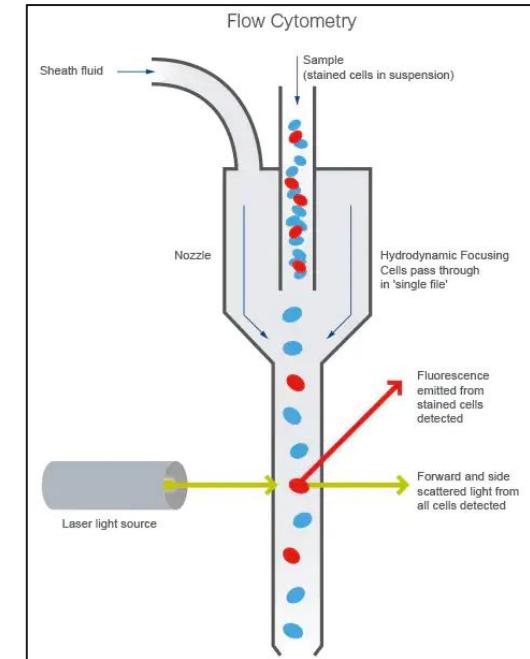
- Increase the size of the cohort to have more metadata

Macrophages characterization

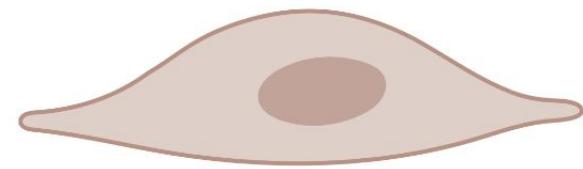


- More macrophages than previous studies

- Do more cell processing and potential use of flow cytometry



Epithelial cell characterization



- Influence of **daycare attendance** and **hormonal birth control** on epithelial cells concentration

- Identification of **key genes** in epithelial cell subclusters

- Decrease of milk transport, synthesis, and production over time.

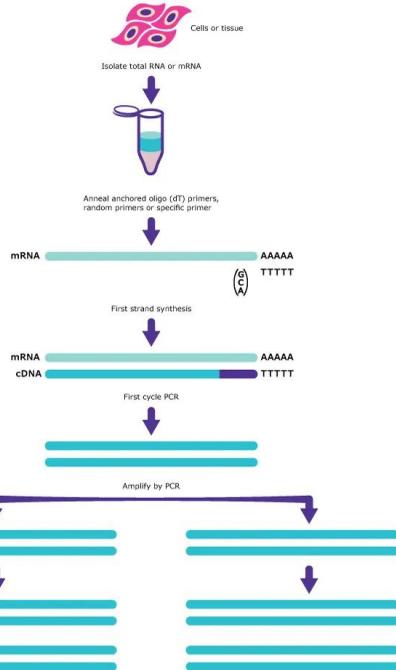
- **LC1 increase** (tight junction) // **secretory lactocyte decrease** (milk component synthesis and secretion)

- Fewer components are synthesized in the lactocytes themselves

Concerning the experiment

- qPCR is also an alternative to sc SEQ-RNA more precise than Micro-Array

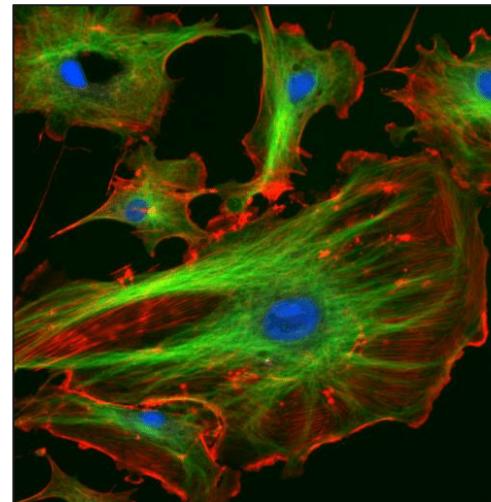
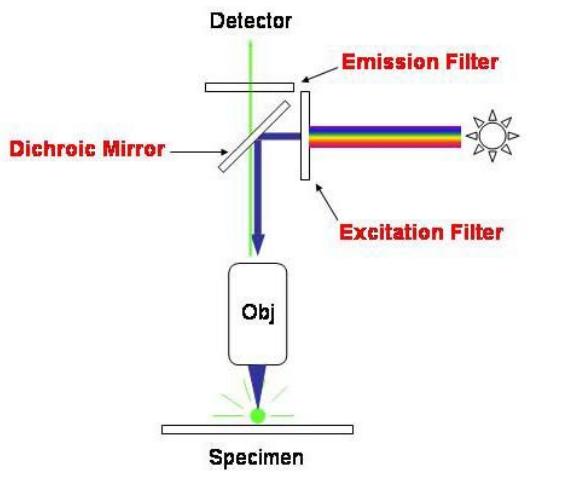
RT - PCR



- Sensitive and specific method to detect and quantify specific genes

Concerning the experiment

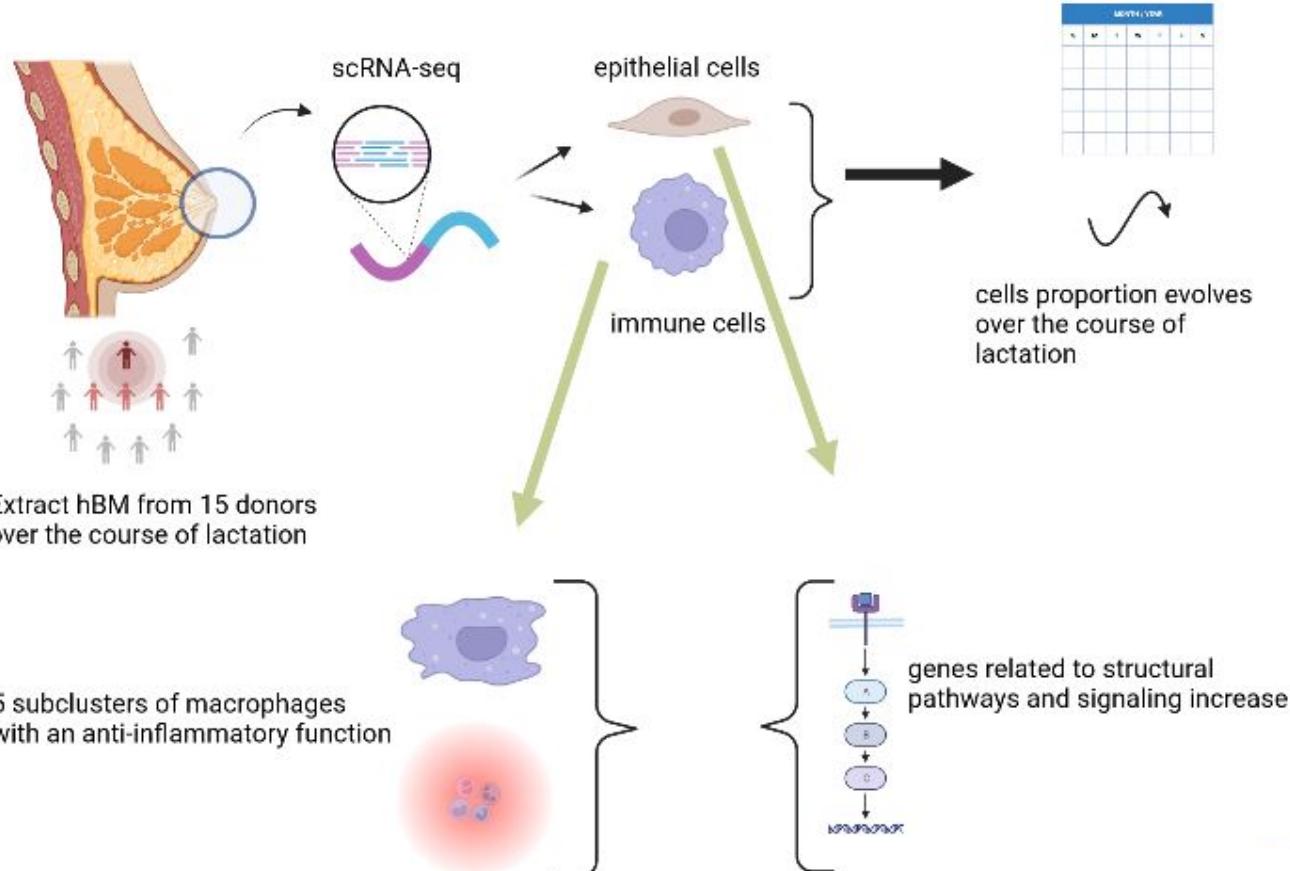
- TEM might be complicated to use



- Fluorescent microscopy or Confocal microscopy are easier to use

CONCLUSION

Conclusion



Conclusion



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Nutritional supplements and mother's milk composition: a systematic review of interventional studies

[Mojtaba Keikha](#), [Ramin Shayan-Moghadam](#), [Maryam Bahreynian](#)✉ & [Roya Kelishadi](#)✉

[International Breastfeeding Journal](#) **16**, Article number: 1 (2021) | [Cite this article](#)

9897 Accesses | **16** Citations | **4** Altmetric | [Metrics](#)

Impact of lifestyle on the hBM composition

Thank you !



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