



TARTU ÜLIKOOL

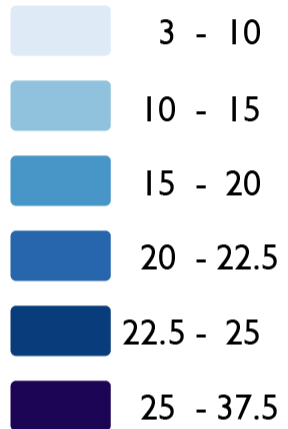
# **T cell aging**

**Pärt Peterson**

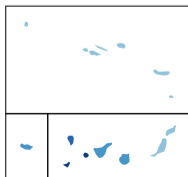
**Institute of Biomedicine and Translational Medicine  
University of Tartu, Estonia**

# Elderly population

% of population  
aged ≥65



Note:  
Data for the UK is from 2019.



Source: Eurostat, 2020

## Highest

1. Evrytania (37.4%)
2. Veurne (33.3%)
3. Suhl (32.7%)
4. Dessau-Roßlau (31.9%)
5. Ourense (31.5%)
6. Etelä-Savo (31.0%)
7. Creuse (31.0%)
8. Altenburger Land (30.9%)
9. Zamora (30.8%)
10. Alto Tâmega (30.6%)

# Most immunological variation occurs during life

- Human immunological variation is associated with age, CMV infection, stress, smoking, and metabolic health
- There are only few longitudinal studies of changes in the human immune system

## Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences

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<http://dx.doi.org/10.1016/j.cell.2014.12.020>

## Genetic Variants Regulating Immune Cell Levels in Health and Disease

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## Article

### Human Immune System Variation during 1 Year

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RESEARCH ARTICLE

Aging Cell  WILEY

### Identification of aging-associated immunotypes and immune stability as indicators of post-vaccination immune activation

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## Article

### Smoking changes adaptive immunity with persistent effects

<https://doi.org/10.1038/s41586-023-06968-8>

Received: 1 November 2022

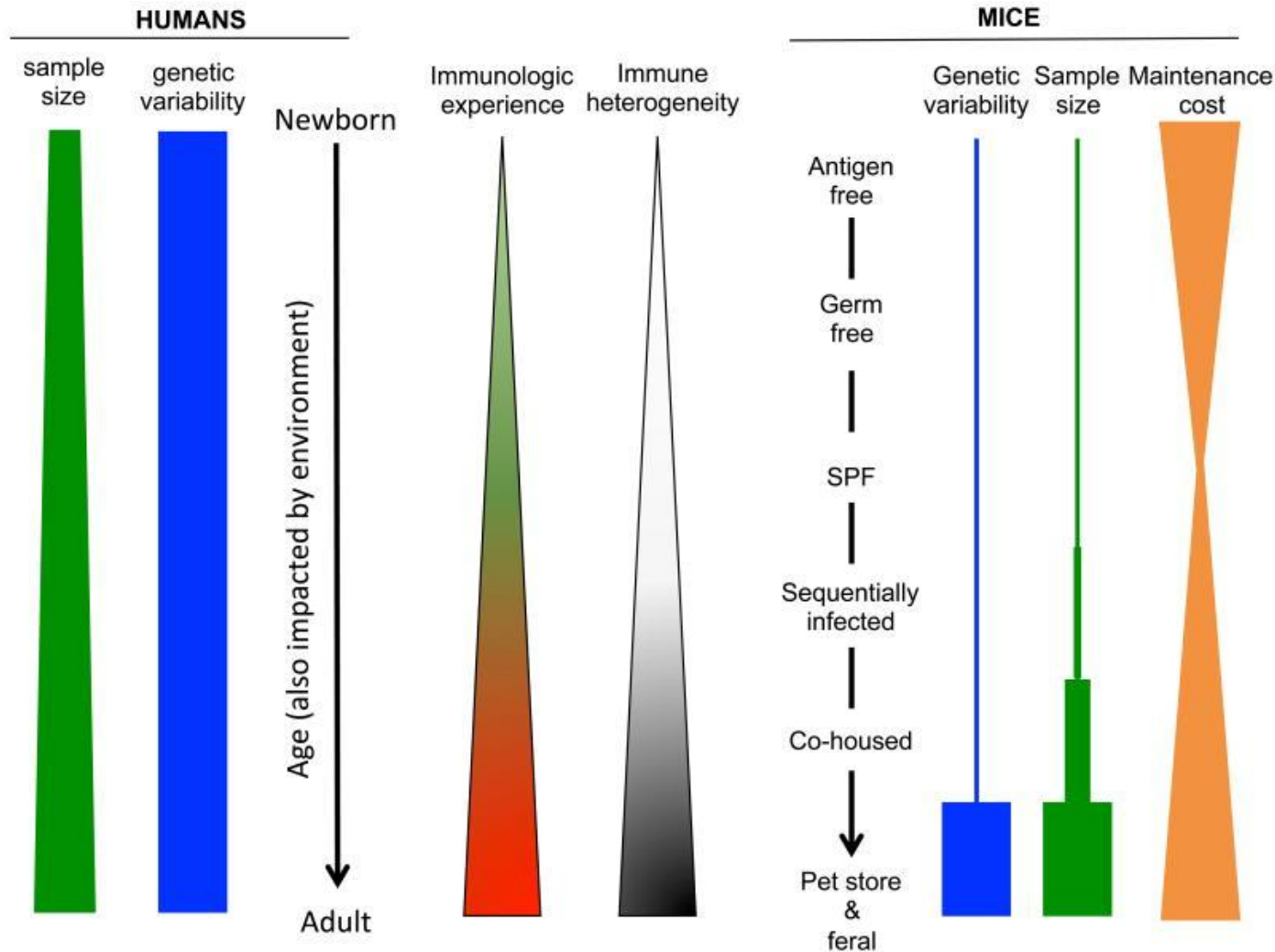
Accepted: 13 December 2023

Violaine Saint-André<sup>1,2,3</sup>, Bruno Charbit<sup>3</sup>, Anne Biton<sup>2</sup>, Vincent Rouilly<sup>4</sup>, Céline Posséme<sup>1</sup>, Anthony Bertrand<sup>1,5</sup>, Maxime Rotival<sup>6</sup>, Jacob Bergstedt<sup>6,7,8</sup>, Etienne Patin<sup>9</sup>, Matthew L. Albert<sup>9</sup>, Lluís Quintana-Murci<sup>6,10</sup>, Darragh Duffy<sup>1,3,11</sup> & The Milieu Intérieur Consortium\*

## **We know that age increases risk for immune-associated pathologies – but how?**

- Increased susceptibility to infections
- Decreased response to vaccination
- Increased risk for chronic inflammatory diseases; cardiovascular, type 2 diabetes, chronic kidney disease
- Increased risk for autoimmune diseases
- Increased risk for cancers

# Of mice and humans



## Brief Reviews

*The Journal of Immunology*

### Of Mice, Dirty Mice, and Men: Using Mice To Understand Human Immunology

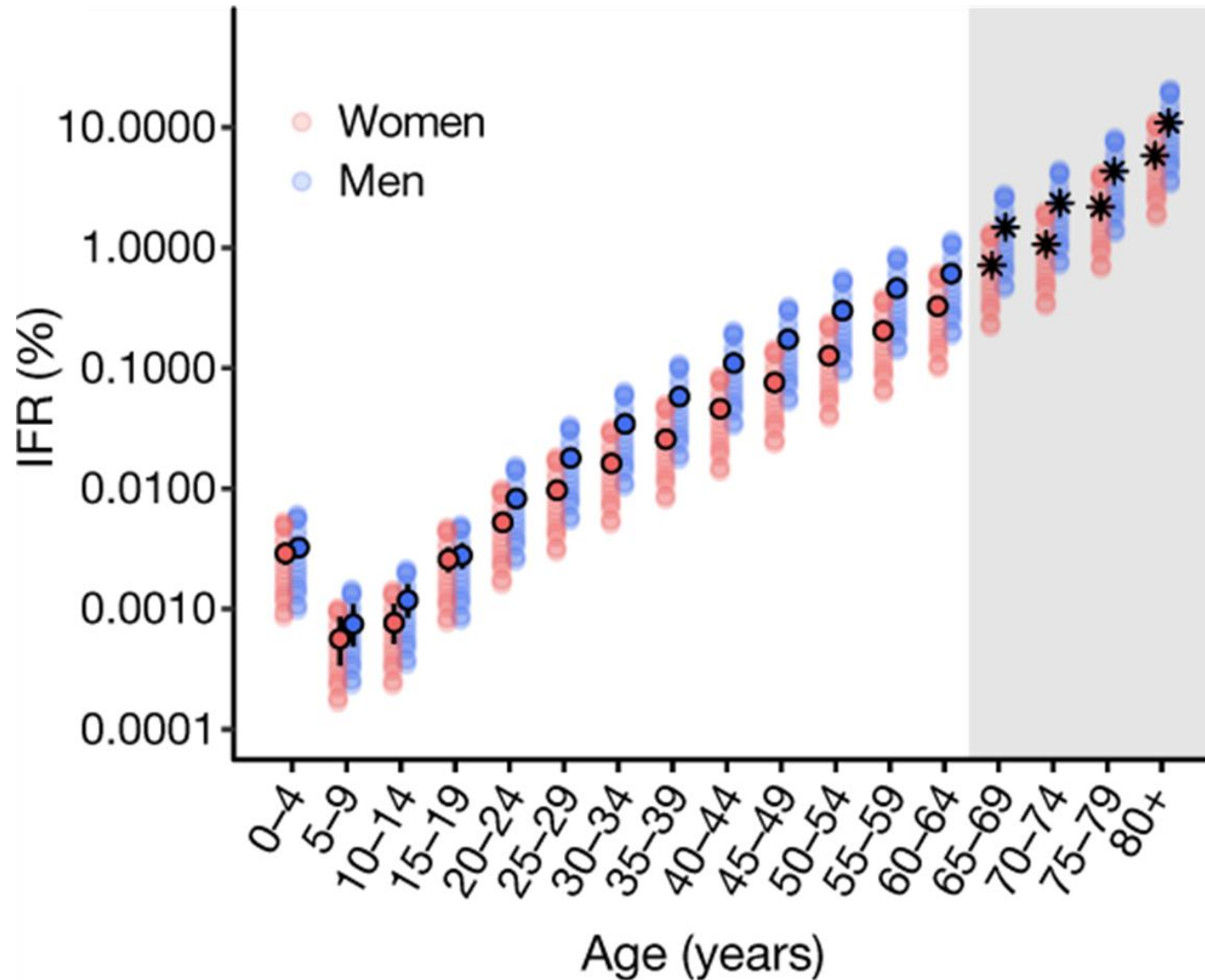
David Masopust,<sup>\*</sup> Christine P. Sivula,<sup>†</sup> and Stephen C. Jameson<sup>‡</sup>

Mouse models have enabled breakthroughs in our understanding of the immune system, but it has become increasingly popular to emphasize their shortcomings when translating observations to humans. This review provides a brief summary of mouse natural history, husbandry, and the pros and cons of pursuing basic research in mice versus humans. Opportunities are discussed for extending the predictive translational value of mouse research, with an emphasis on exploitation of a “dirty” mouse model that better mimics the diverse infectious history that is typical of most humans. *The Journal of Immunology*, 2017, 199: 383–388.

groups called demes that are composed of a dominant breeding male, a hierarchy of females, subordinate males, and juveniles. This results in a high degree of inbreeding that, combined with their high mutation rates, contributes to their ability to adapt quickly to environmental changes (3, 4). Mice are omnivorous, nocturnal, adapt well to temperature extremes, and with their ability to jump and chew through small openings, they are well poised to take advantage of human food sources in fields, homes, and granaries (5). Although such behaviors prove beneficial for the survival and propagation of the mouse, consumption and contamination of food stores have prompted the view of mice as a pest species. However, hobbyists took an interest in breeding and



## Infection fatality rate (IFR)



## SARS-CoV-2 fatality rate

Old individuals and old societies at risk

11% men and 6% women at age 80+

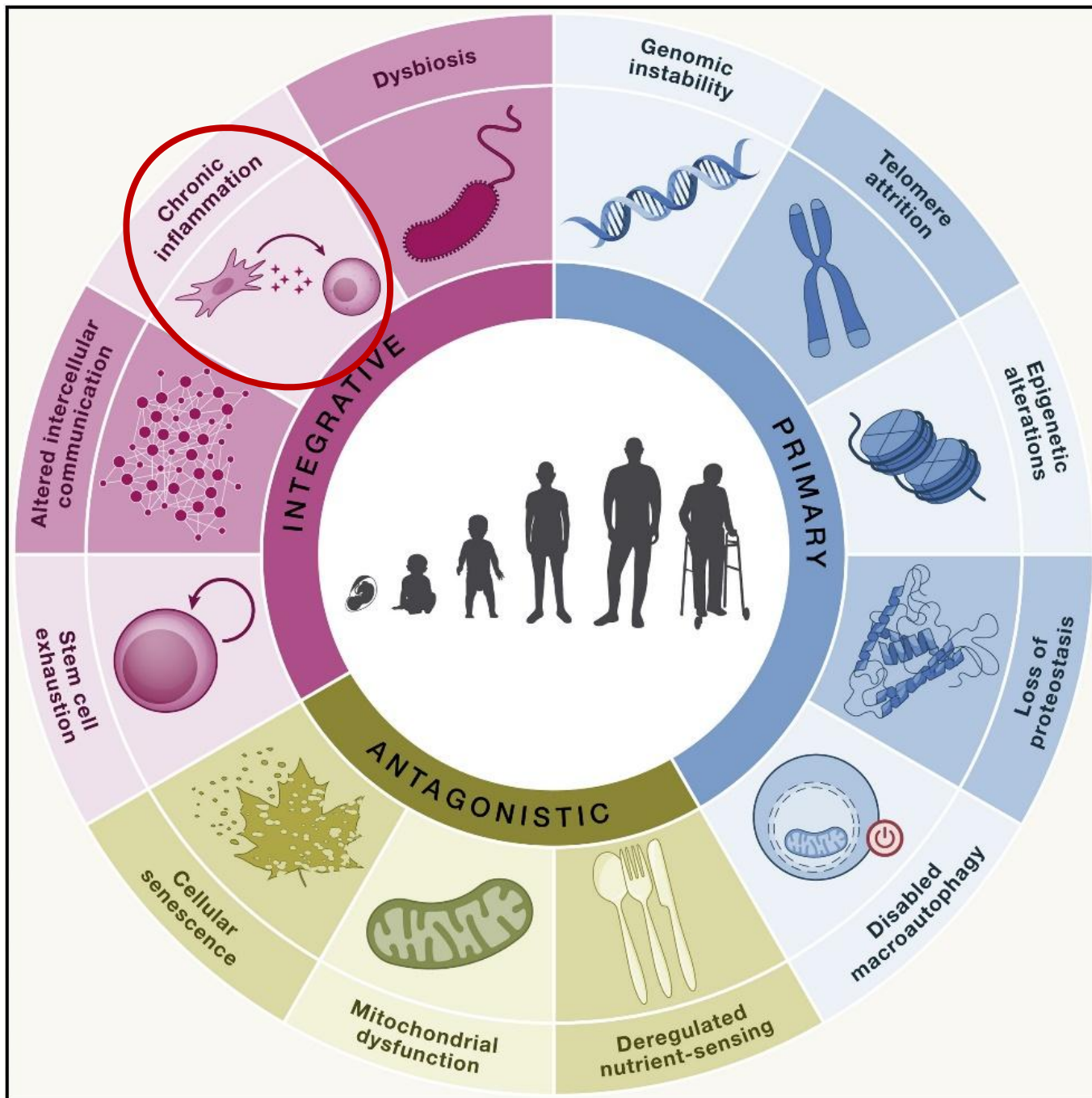
## Vaccination efficiency is decreased in older individuals



Edward Jenner (1796)





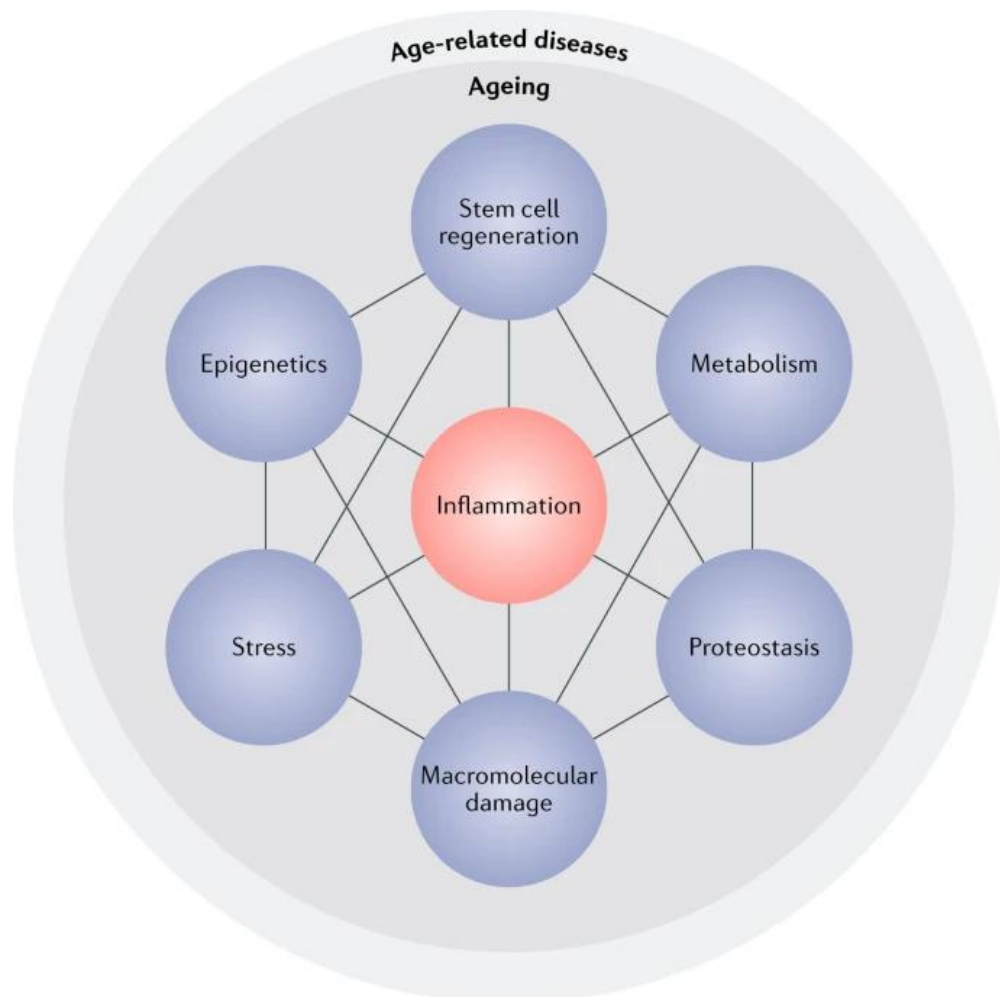


## Age associated changes in cells

- Chronic inflammation
- Imbalance of the intestinal microflora
- Genomic instability
- Telomere shortening
- Epigenetic changes
- Proteome instability
- Deficient macroautophagy
- Non-absorption of nutrients
- Errors in mitochondrial function
- Cellular senescence
- Stem cell insufficiency
- Changes in intercellular communication



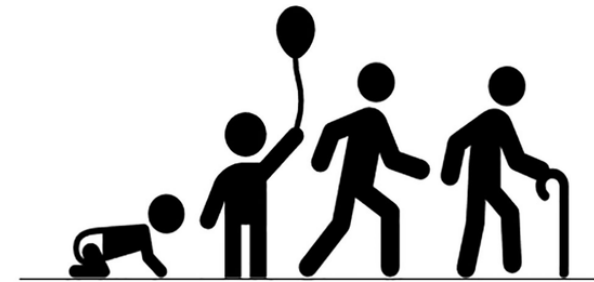
# Chronic immune inflammation is associated with chronic diseases



## Inflammageing: chronic inflammation in ageing, cardiovascular disease, and frailty

Luigi Ferrucci<sup>1</sup> \* and Elisa Fabbri<sup>2</sup>

**Abstract** | Most older individuals develop inflammageing, a condition characterized by elevated levels of blood inflammatory markers that carries high susceptibility to chronic morbidity, disability, frailty, and premature death. Potential mechanisms of inflammageing include genetic susceptibility, central obesity, increased gut permeability, changes to microbiota composition, cellular senescence, NLRP3 inflammasome activation, oxidative stress caused by dysfunctional mitochondria, immune cell dysregulation, and chronic infections. Inflammageing is a risk factor for cardiovascular diseases (CVDs), and clinical trials suggest that this association is causal.



Chronic activation of the immune system

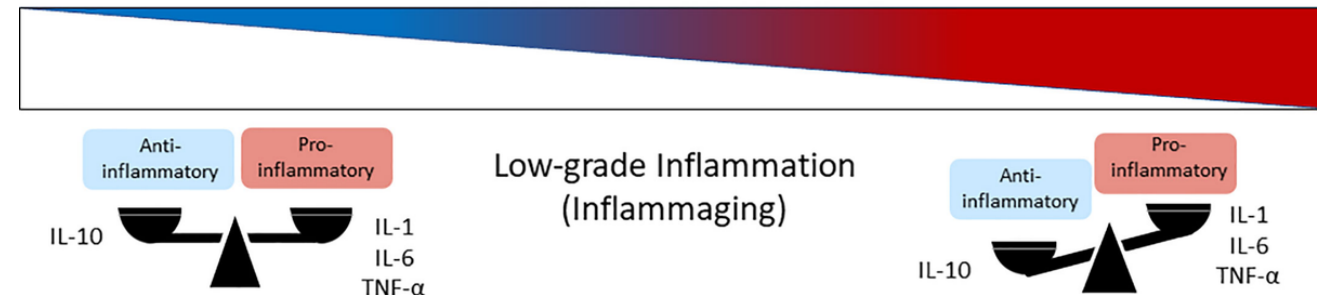
Chronic Infections

Antigenic Load

Increase of senescent cells  
SASP

Thymic Involution

Aging as a lifelong adaptive process



# Nonuniversality of inflammaging across human populations

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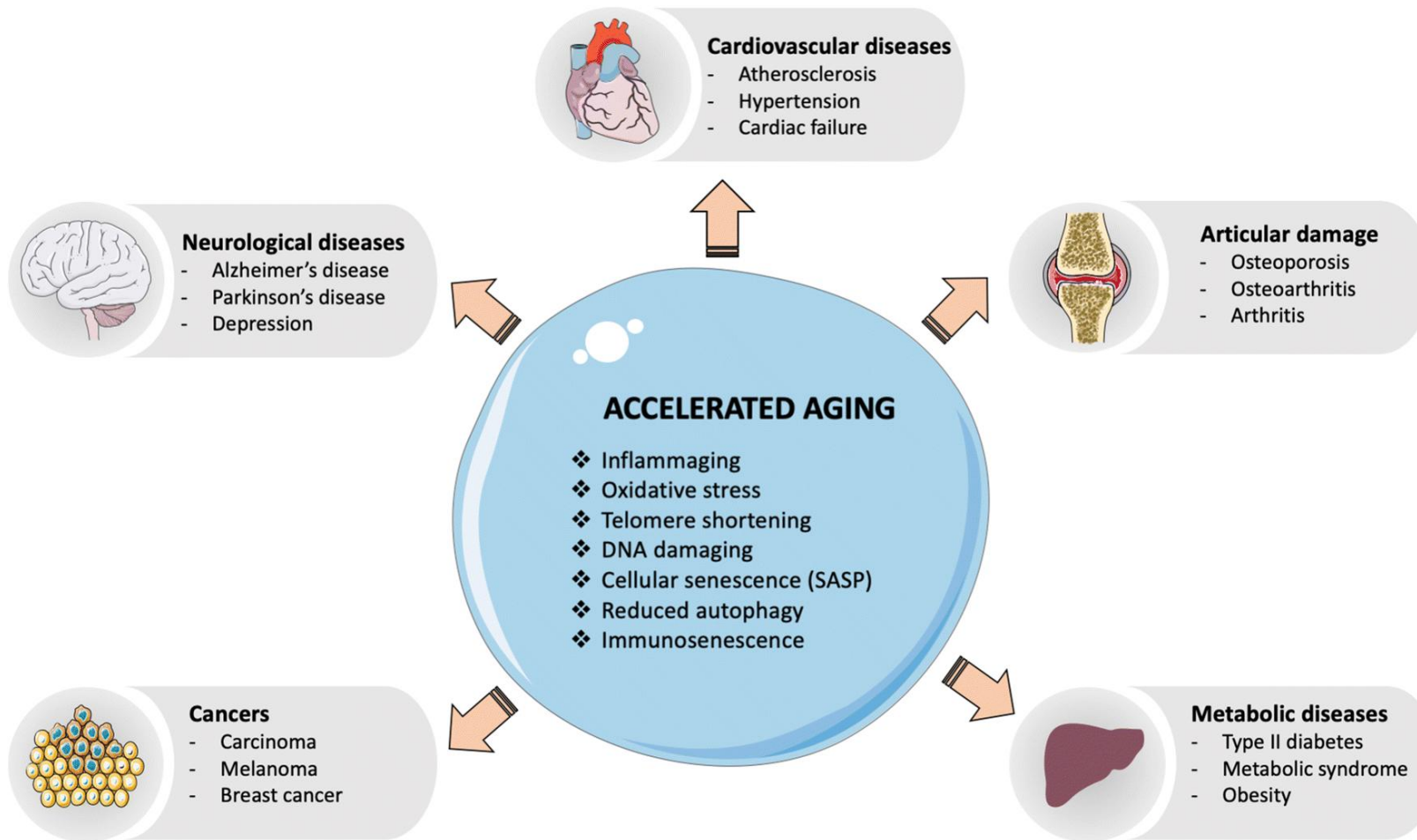


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Camille Daunizeau<sup>5</sup>, Luigi Ferrucci <sup>6</sup>, Stefania Bandinelli<sup>7</sup>,  
Benjamin C. Trumble<sup>8</sup>, Hillard S. Kaplan<sup>9</sup>, Jacob E. Aronoff<sup>8</sup>,  
Jonathan Stieglitz <sup>10</sup>, Thomas S. Kraft<sup>11</sup>, Amanda J. Lea<sup>3</sup>,  
Vivek V. Venkataraman<sup>12</sup>, Ian J. Wallace<sup>13</sup>, Yvonne A. L. Lim<sup>14</sup>, Kee Seong Ng<sup>15</sup>,  
Joe Poh Sheng Yeong<sup>16,17,18,19</sup>, Roger Ho<sup>20</sup>, Xinru Lim<sup>16</sup>, Ameneh Mehrjerd<sup>21</sup>,  
Eleftheria G. Charalambous <sup>21</sup>, Allison E. Aiello<sup>2,22</sup>, Graham Pawelec <sup>23,24</sup>,  
Claudio Franceschi <sup>25</sup>, Johannes Hertel <sup>21,26</sup>, Tamàs Fülöp<sup>1</sup>, Maël Lemoine<sup>27</sup>,  
Michael Gurven<sup>28</sup> & Alan A. Cohen <sup>1,2,29</sup>✉

# Chronic inflammation associated with multiple pathologies





# Clonally expanded CD8 T cells patrol the cerebrospinal fluid in Alzheimer's disease

<https://doi.org/10.1038/s41586-019-1895-7>

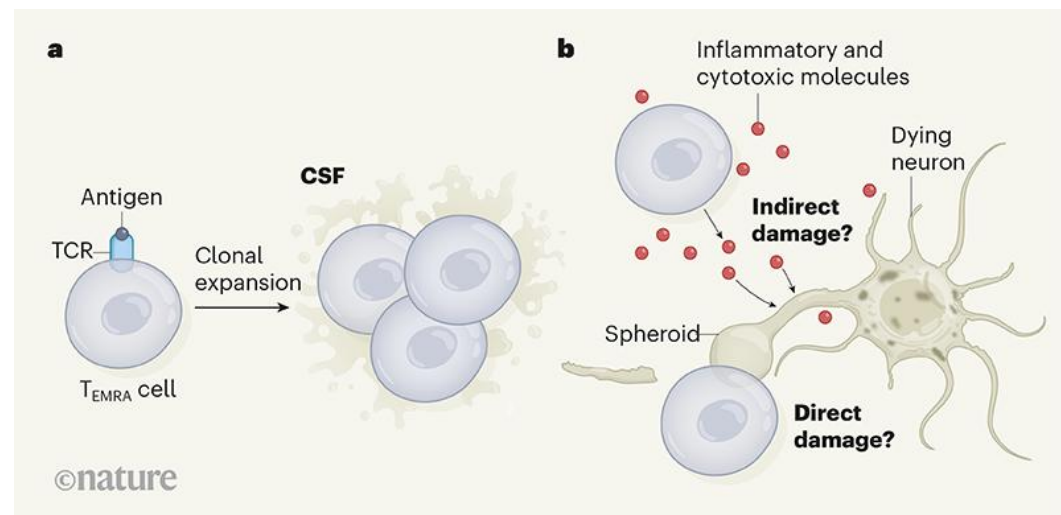
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David Gate<sup>1,2\*</sup>, Naresha Saligrama<sup>3</sup>, Olivia Leventhal<sup>1</sup>, Andrew C. Yang<sup>4,5</sup>, Michael S. Unger<sup>6,7</sup>, Jinte Middeldorp<sup>1,2,8</sup>, Kelly Chen<sup>1</sup>, Benoit Lehallier<sup>1,2</sup>, Divya Channappa<sup>1</sup>, Mark B. De Los Santos<sup>1</sup>, Alisha McBride<sup>1,2</sup>, John Pluvinage<sup>1,9,10</sup>, Fanny Elahi<sup>11</sup>, Grace Kyin-Ye Tam<sup>1,12</sup>, Yongha Kim<sup>1,12</sup>, Michael Greicius<sup>1,12</sup>, Anthony D. Wagner<sup>13,14</sup>, Ludwig Aigner<sup>6,7</sup>, Douglas R. Galasko<sup>15</sup>, Mark M. Davis<sup>3,16,17</sup> & Tony Wyss-Coray<sup>1,2,5,14,18\*</sup>

peripheral blood mononuclear cells and discovered an immune signature of Alzheimer's disease that consists of increased numbers of CD8<sup>+</sup> T effector memory CD45RA<sup>+</sup> (T<sub>EMRA</sub>) cells. In a second cohort, we found that CD8<sup>+</sup> T<sub>EMRA</sub> cells were negatively associated with cognition. Furthermore, single-cell RNA sequencing revealed that T cell receptor (TCR) signalling was enhanced in these cells. Notably, by using several strategies of single-cell TCR sequencing in a third cohort, we discovered clonally expanded CD8<sup>+</sup> T<sub>EMRA</sub> cells in the cerebrospinal fluid of patients with Alzheimer's disease. Finally, we used machine learning, cloning and peptide screens to demonstrate the specificity of clonally expanded TCRs in the cerebrospinal fluid of patients with Alzheimer's disease to two separate Epstein–Barr virus antigens. These



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DOI: 10.1002/alz.13136

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THE JOURNAL OF THE ALZHEIMER'S ASSOCIATION

## RESEARCH ARTICLE

### Early $\beta$ -amyloid accumulation in the brain is associated with peripheral T cell alterations

Christoph Gericke<sup>1</sup> | Tunahan Kirabali<sup>1</sup> | Roman Flury<sup>2</sup> | Anna Mallone<sup>1,3</sup> | Chiara Rickenbach<sup>1</sup> | Luka Kulic<sup>1,4</sup> | Vinko Tosevski<sup>5</sup> | Christoph Hock<sup>1,6,7</sup> | Roger M. Nitsch<sup>1,7</sup> | Valerie Treyer<sup>1,6,8</sup> | Maria Teresa Ferretti<sup>1,9</sup> | Anton Gietl<sup>1,6,10</sup>

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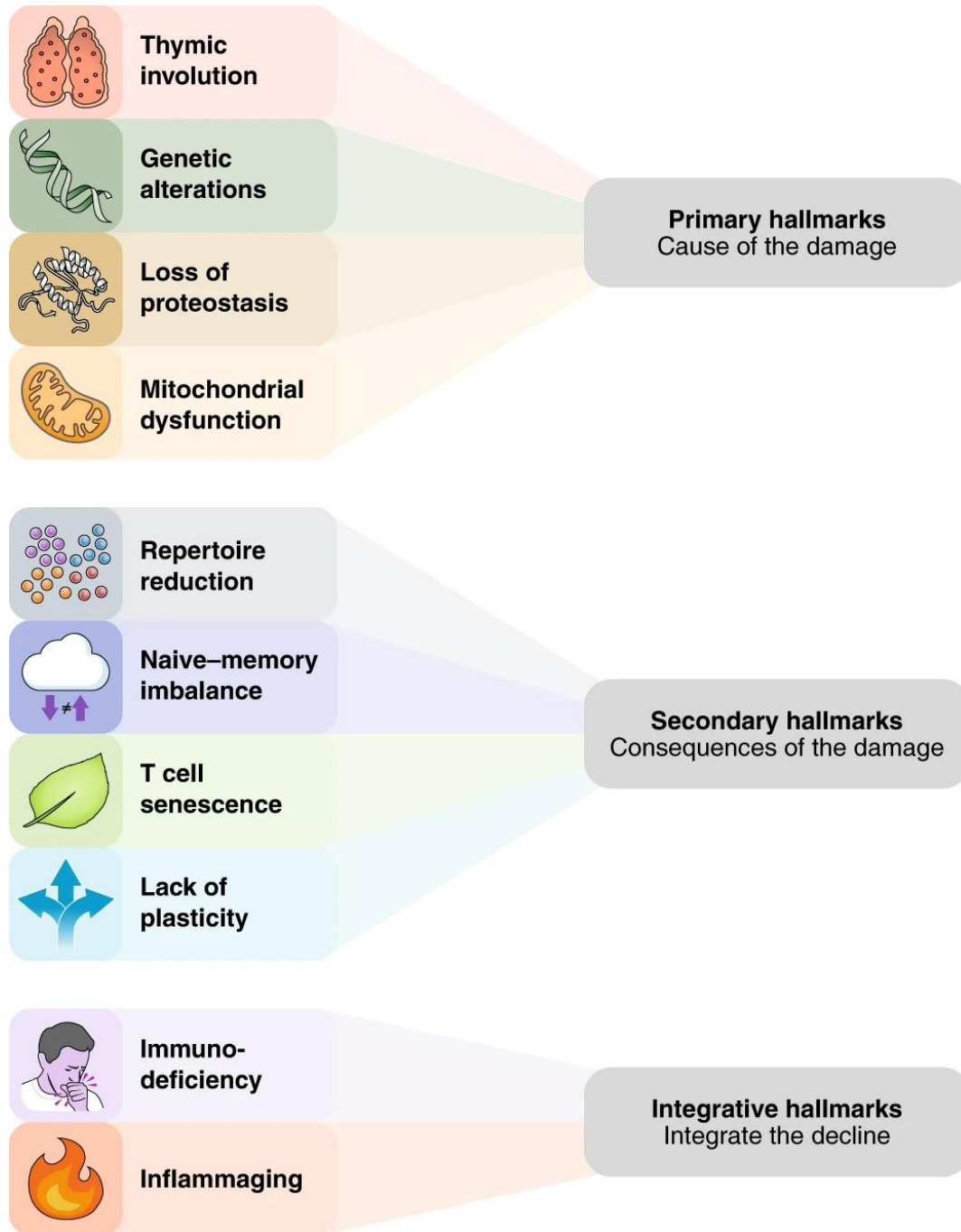
LETTER | Open Access |

### No increase of CD8<sup>+</sup> TEMRA cells in the blood of healthy adults at high genetic risk of Alzheimer's disease

Laura Deecke, Jan Homann, David Goldeck, Olena Ohlei, Valerija Dobricic, Johanna Drewelies, Ilja Demuth, Graham Pawelec, Lars Bertram, Christina M. Lill

First published: 25 January 2024 | <https://doi.org/10.1002/alz.13709>





## Hallmarks of T cells in aging

The hallmarks grouped into 3 categories, based on their hierarchical interconnections.

4 primary hallmarks account for the initial damage

- Thymic involution,
- Genetic and epigenetic alterations
- Loss of proteostasis
- Mitochondrial dysfunction

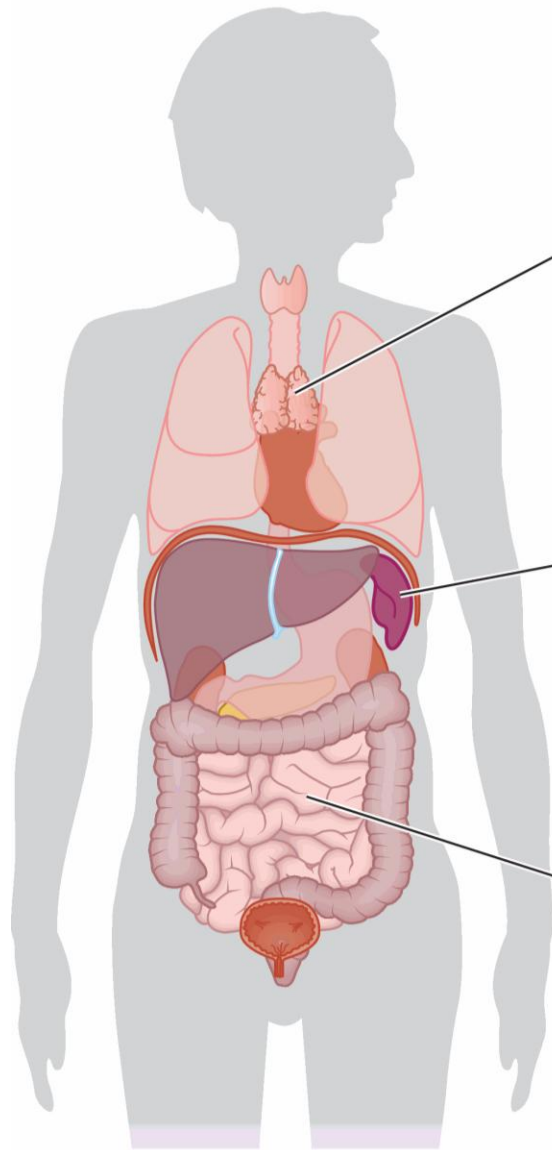
4 secondary hallmarks are consequences of primaries

- Reduction of the TCR repertoire
- Expansion of the memory pool
- Lack of effector plasticity
- T cell senescence

2 integrative hallmarks are the consequences of the T cell functional deficiencies

- Immunodeficiency
- Inflammaging

# Changes in T cells with aging



## Thymus

- Thymic involution
- Stroma deterioration
- Reduced T cell output

## Spleen and lymph nodes

- Forced homeostatic proliferation
- Naive to memory profile
- Defective GC responses:
  - Expansion of Tfh and Tfr
  - Diminished Tfh/Tfr ratio

## Nonlymphoid tissue

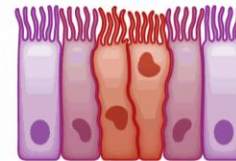
- Accumulation of:
- Extremely cytotoxic T cells
  - Exhausted T cells
  - Proinflammatory effector Tregs



T cell senescence



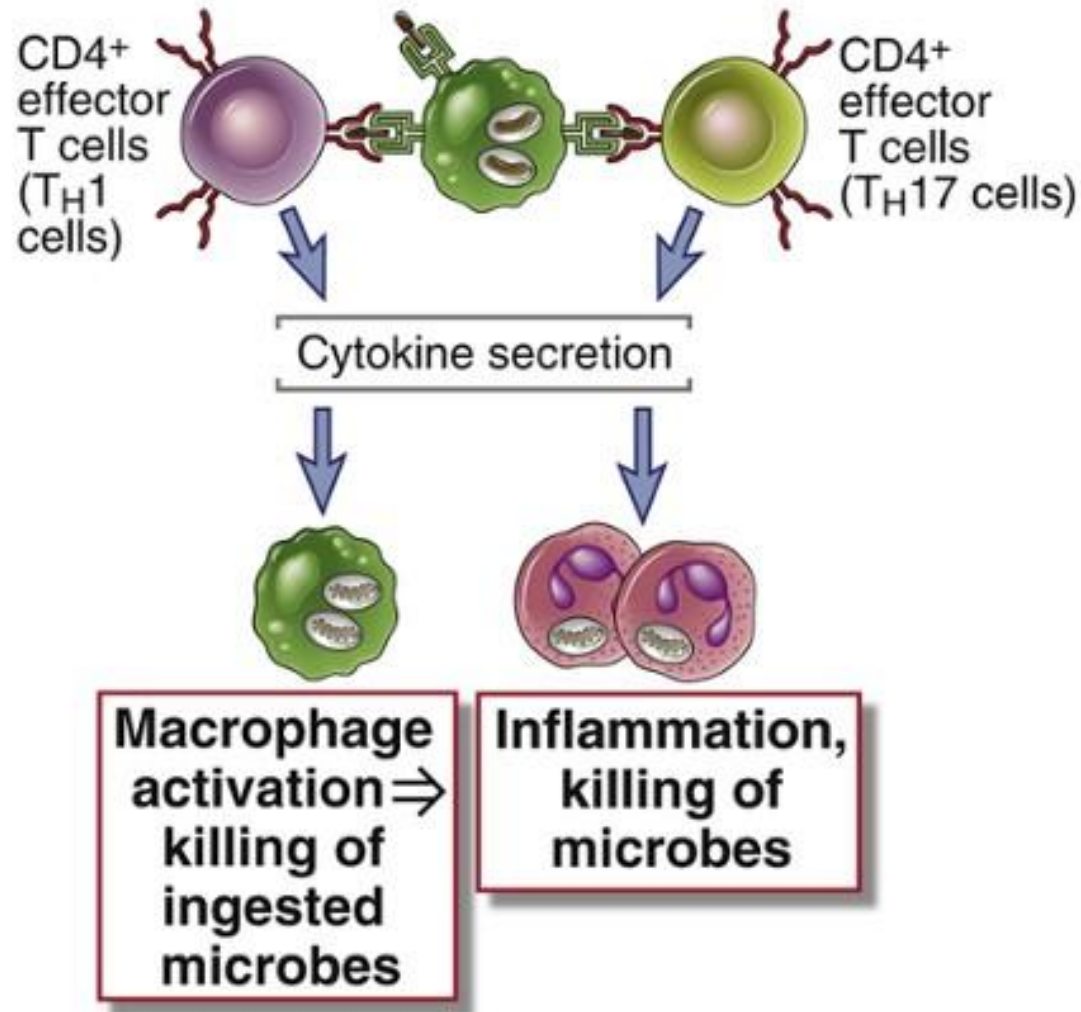
Impaired cellular immunity  
Poor humoral responses



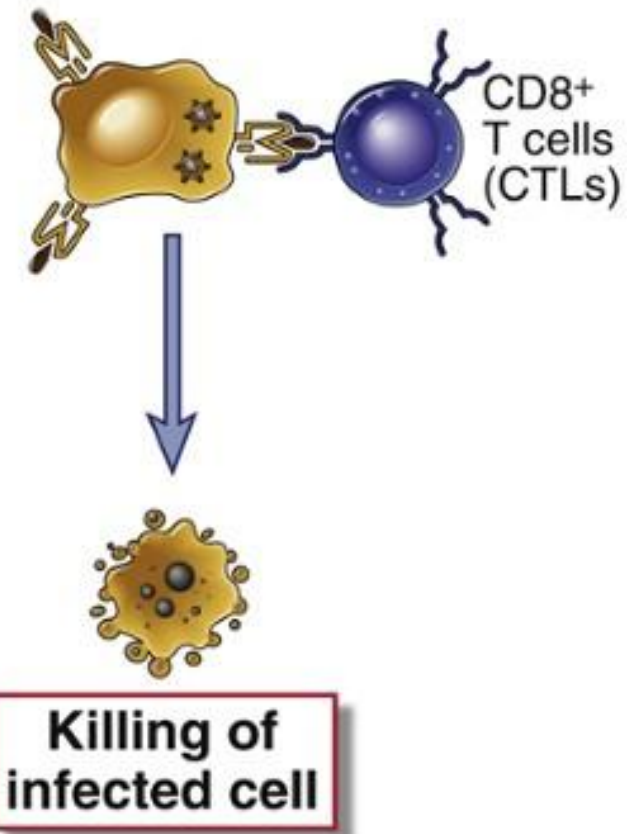
Tissue damage  
Inflammaging

## CD4+ and CD8+ T cells have different effector functions

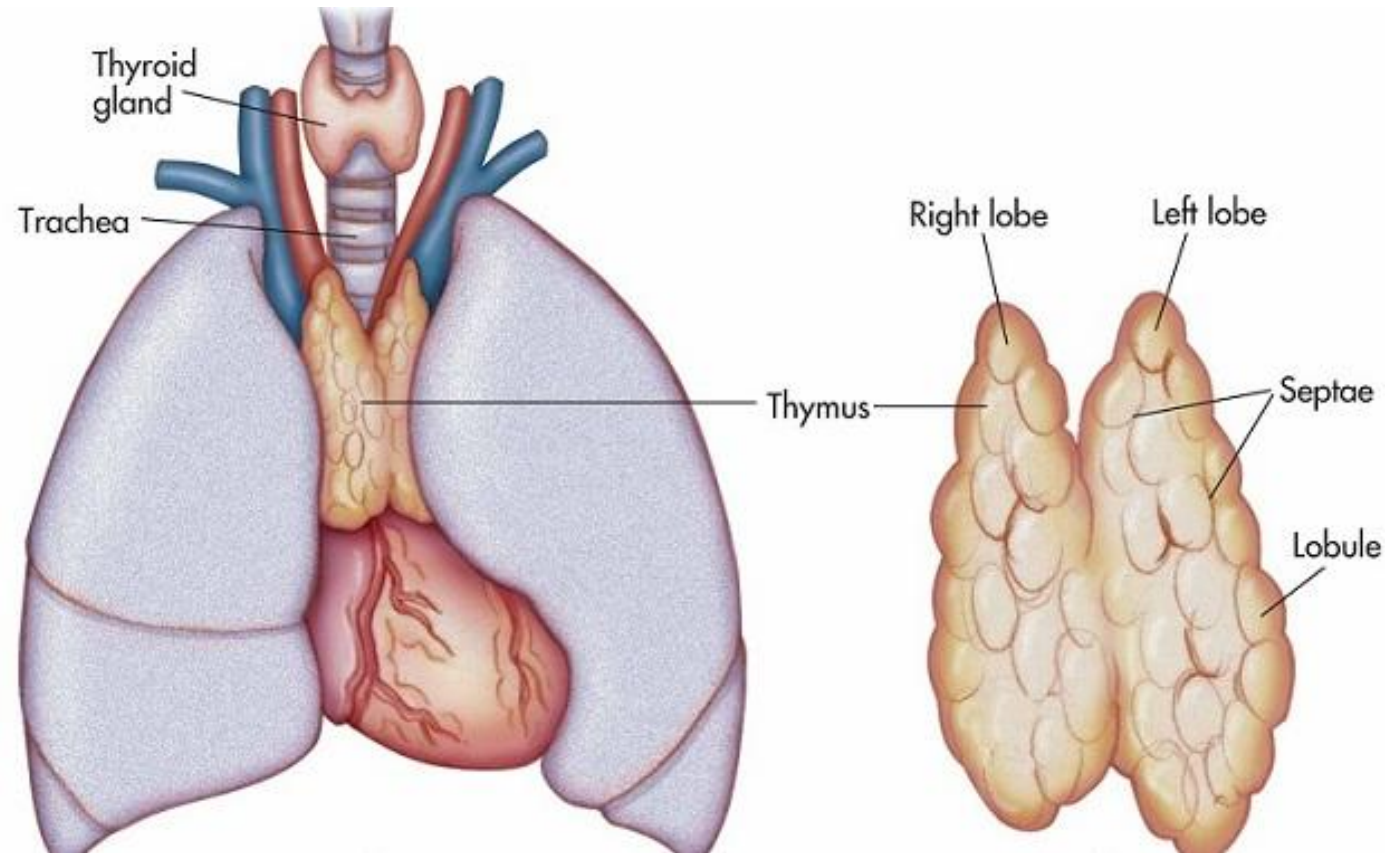
### A Phagocytes with ingested microbes in vesicles



### B Infected cell with microbes or antigens in cytoplasm



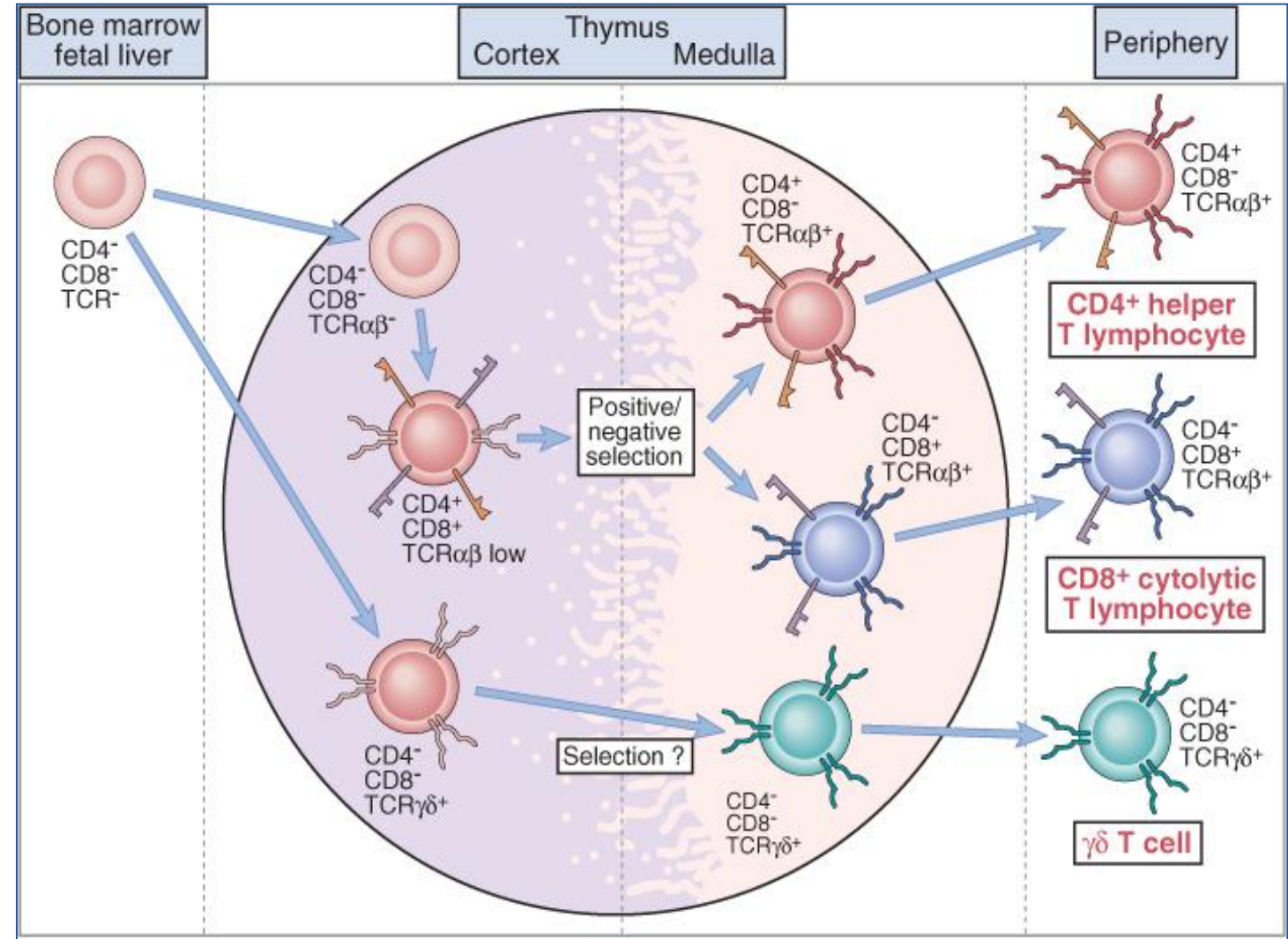
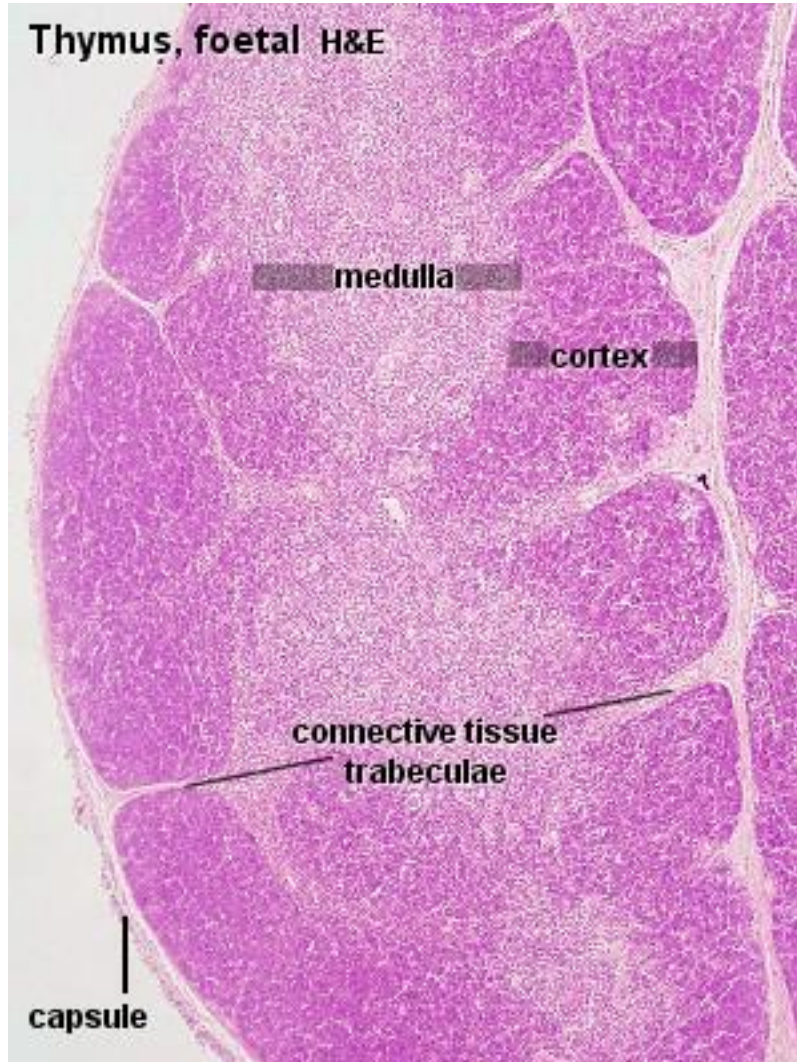
# The thymus



*Thymus vulgaris*

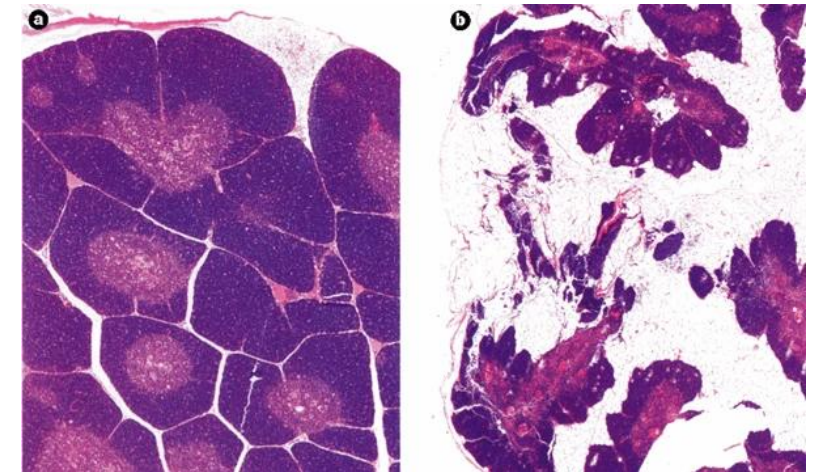
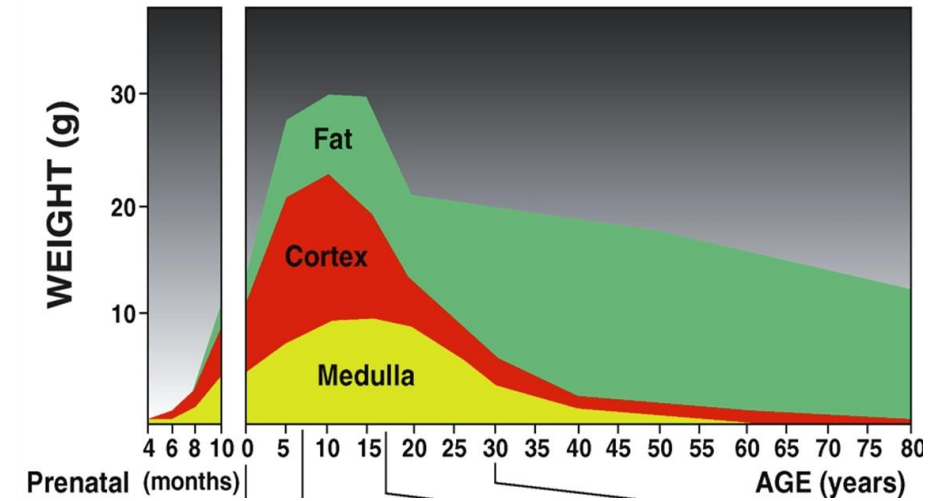
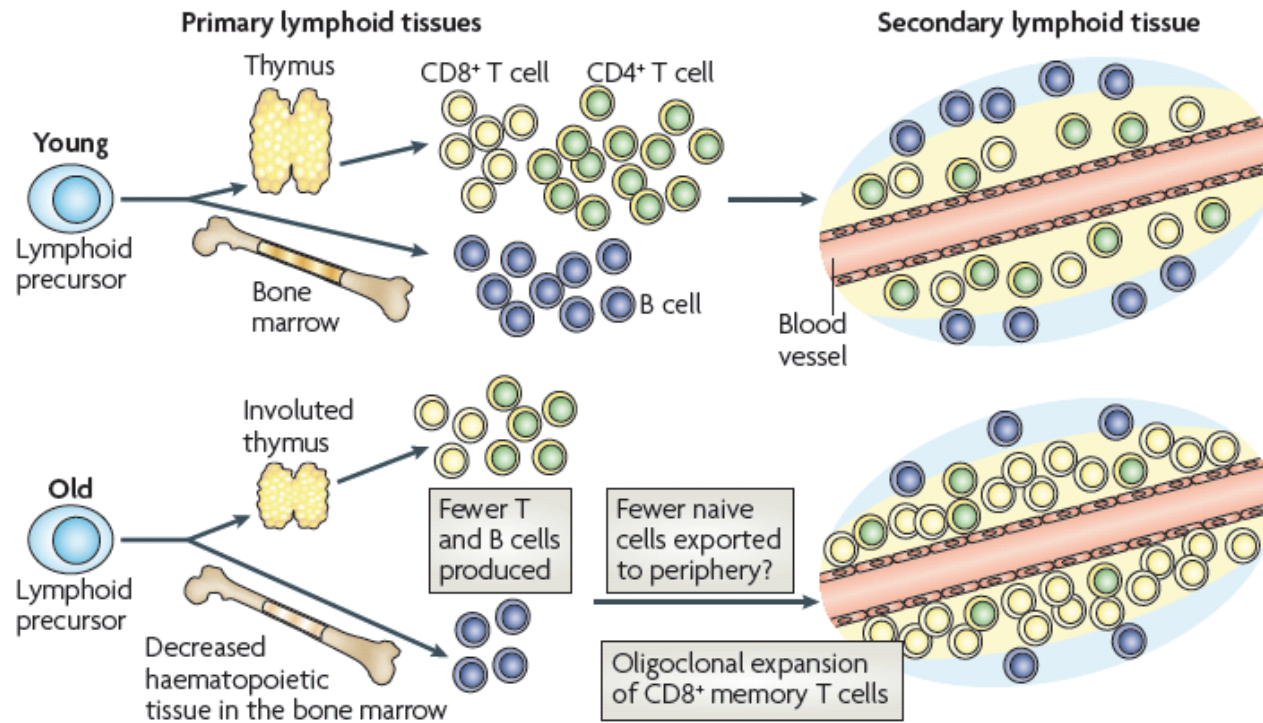


# T cells differentiate in the thymus





# Age-related changes in the thymus

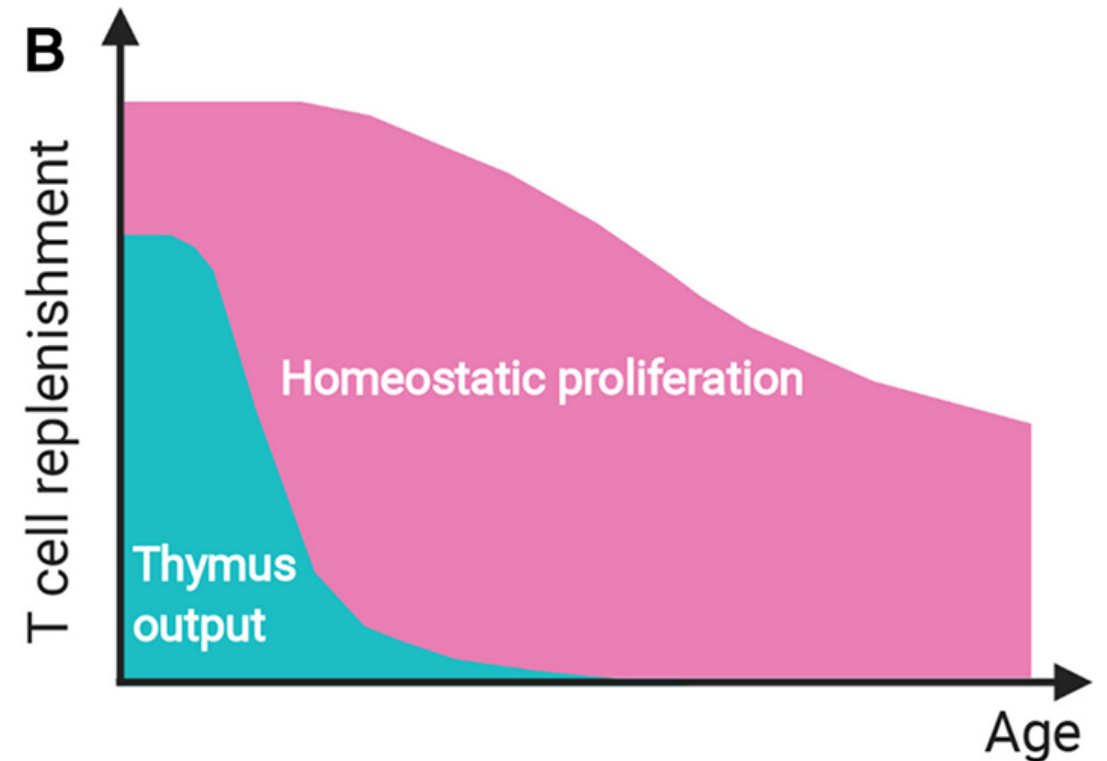
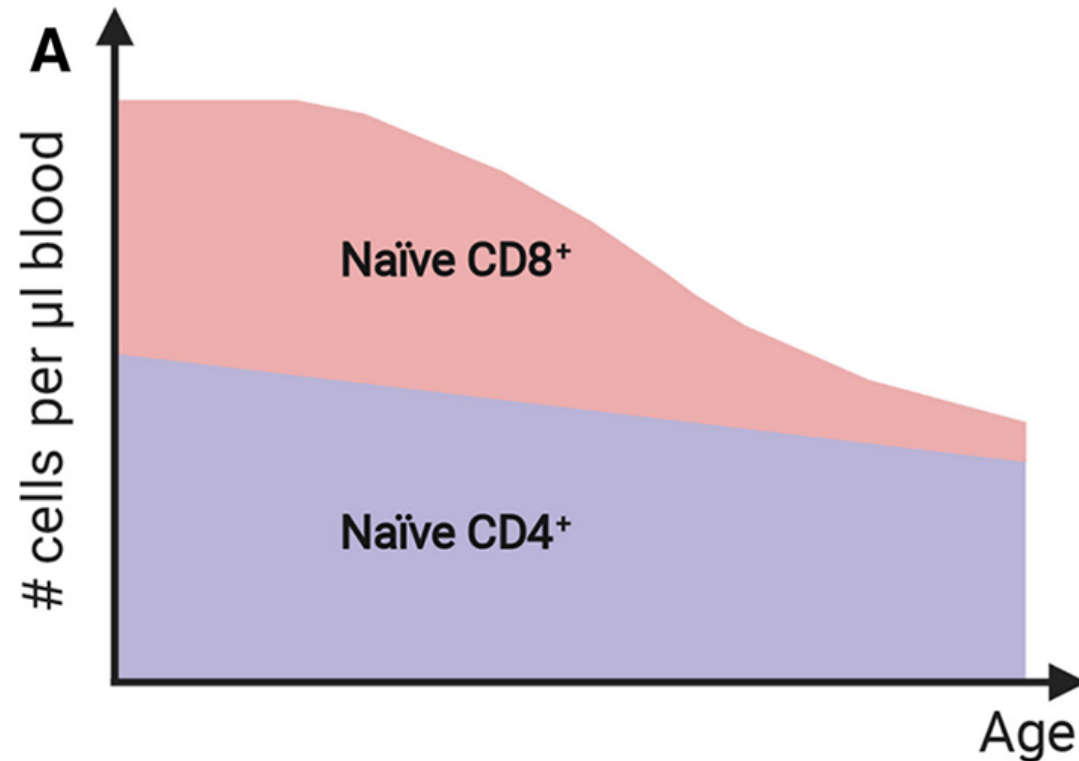


Young

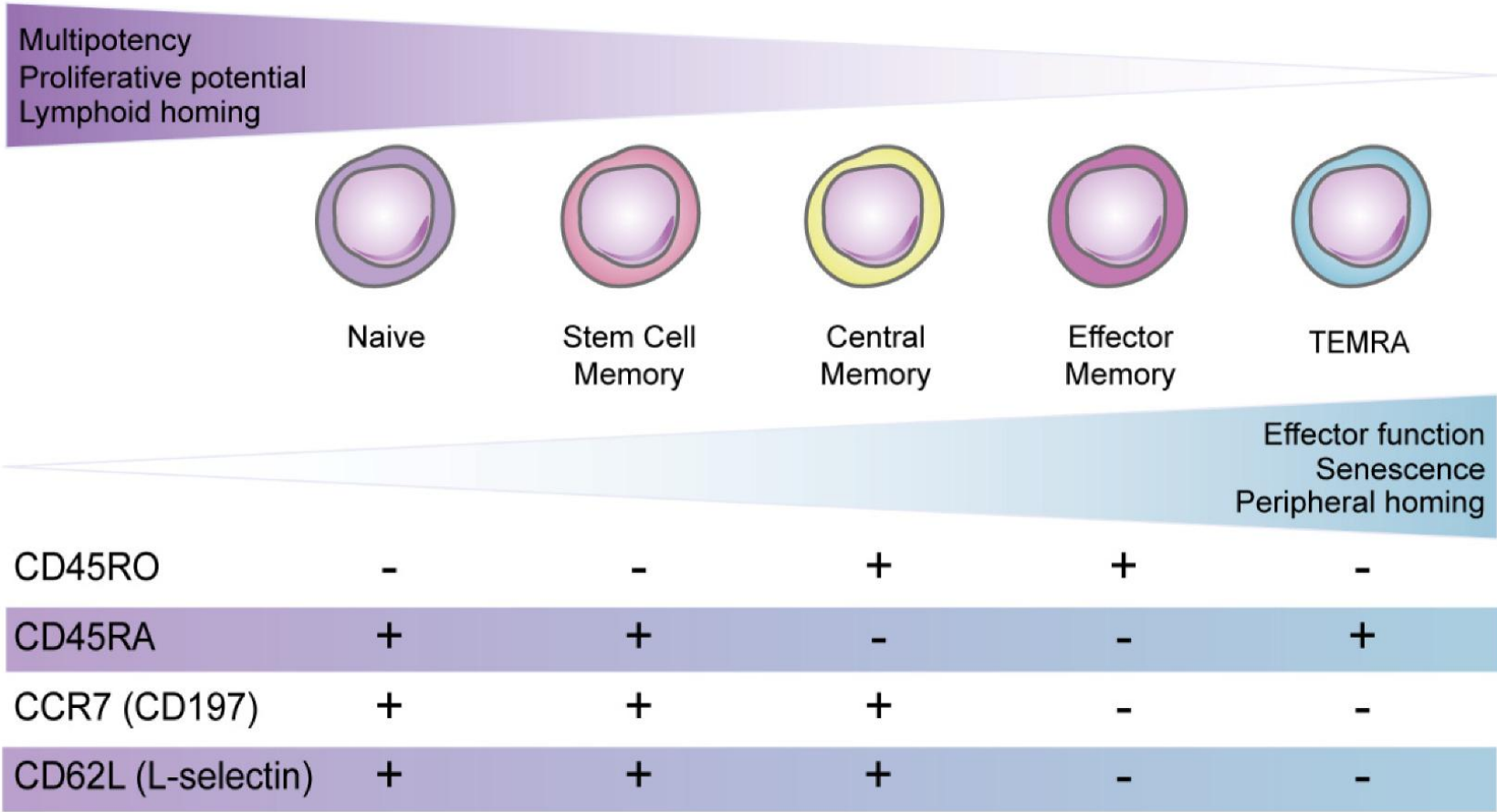
Old

- Thymus involutes and is replaced by adipose cells
- Less naïve T cells
- Oligoclonal expansion of T cells

## Aging mostly impacts on the numbers of naive CD8<sup>+</sup> T cells

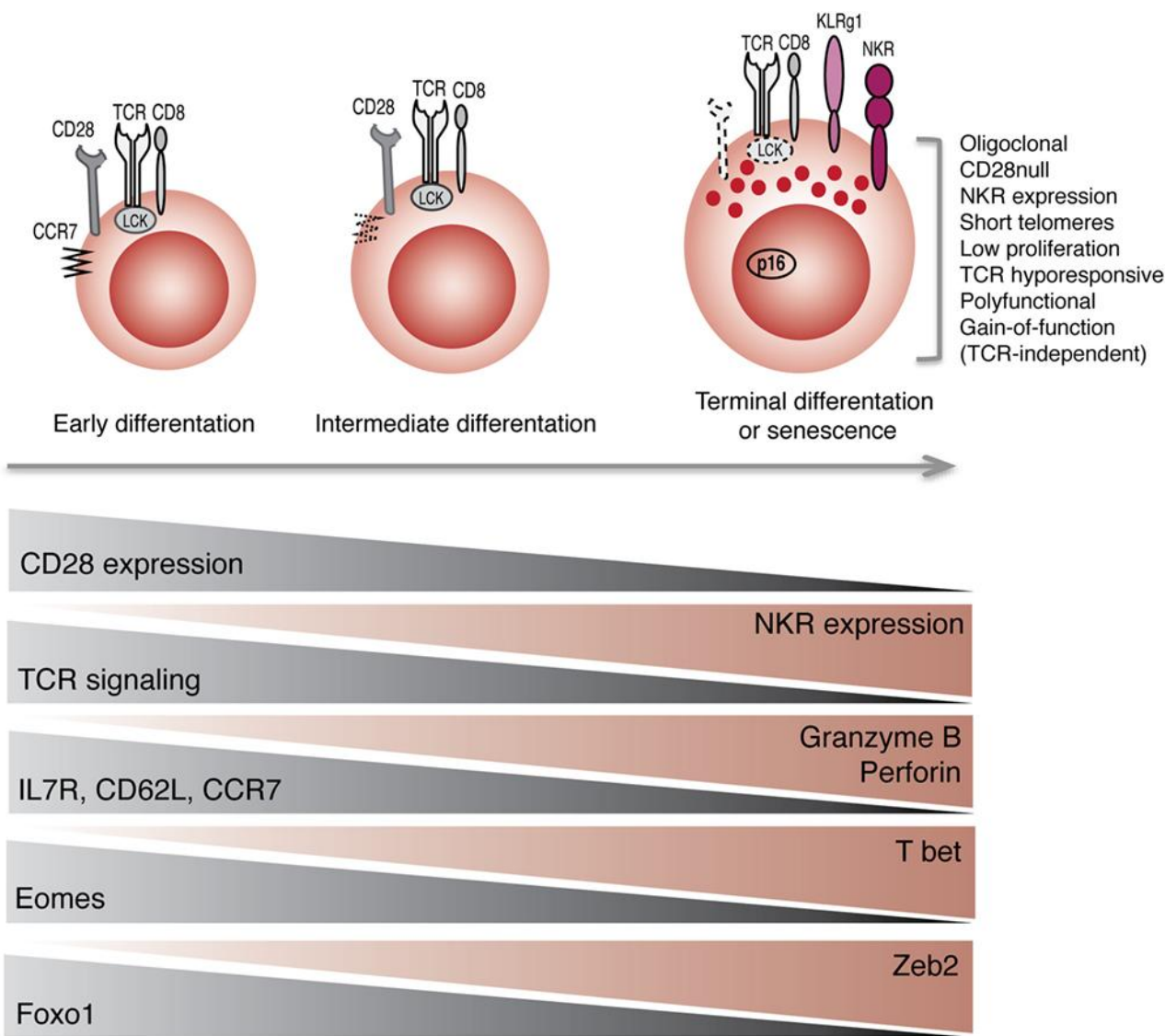


# T cells differentiate from naïve to terminally differentiated T cells (TEMRA)





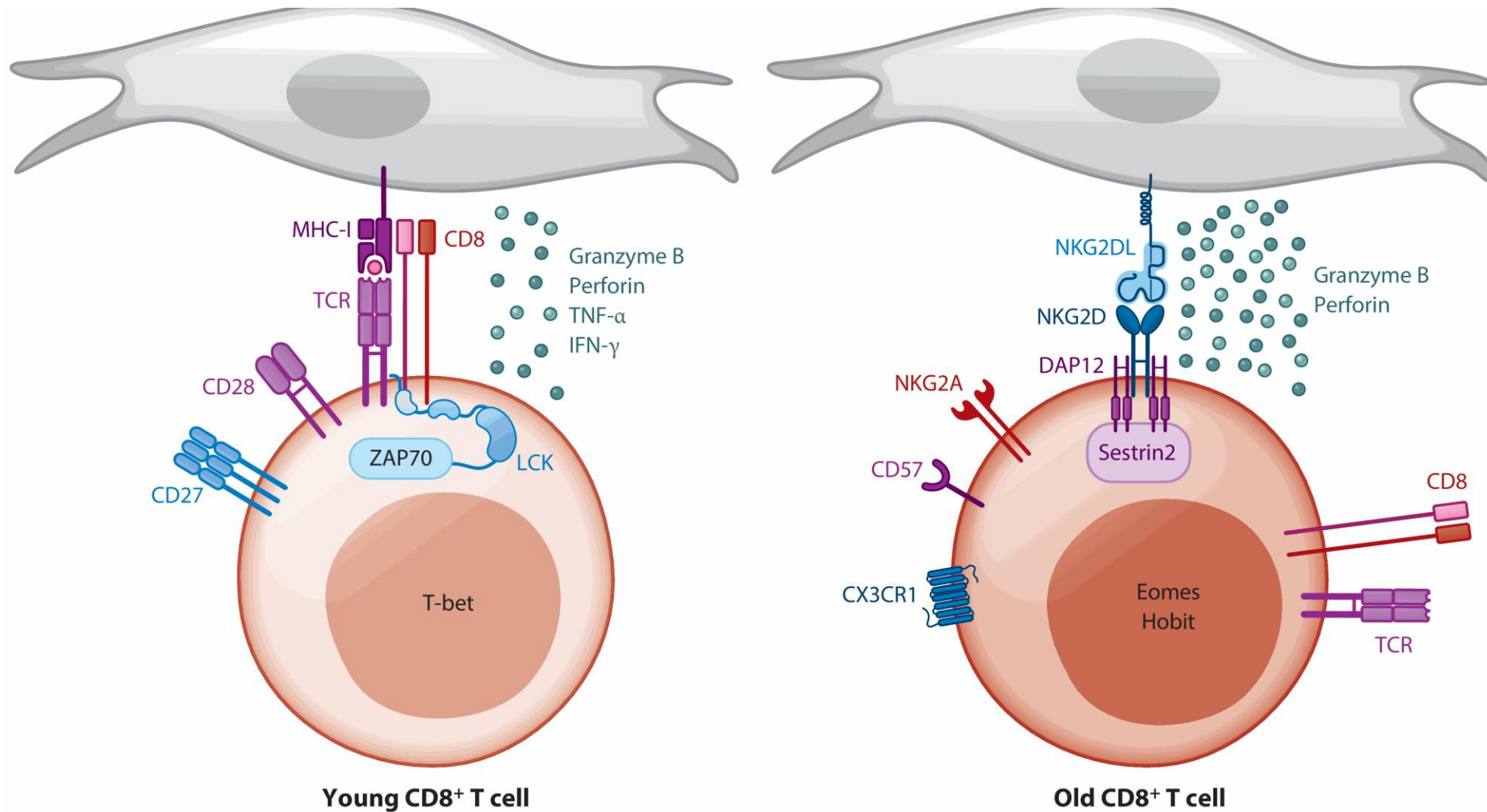
# Terminal differentiation of CD8+ T cells into NK-like T cells



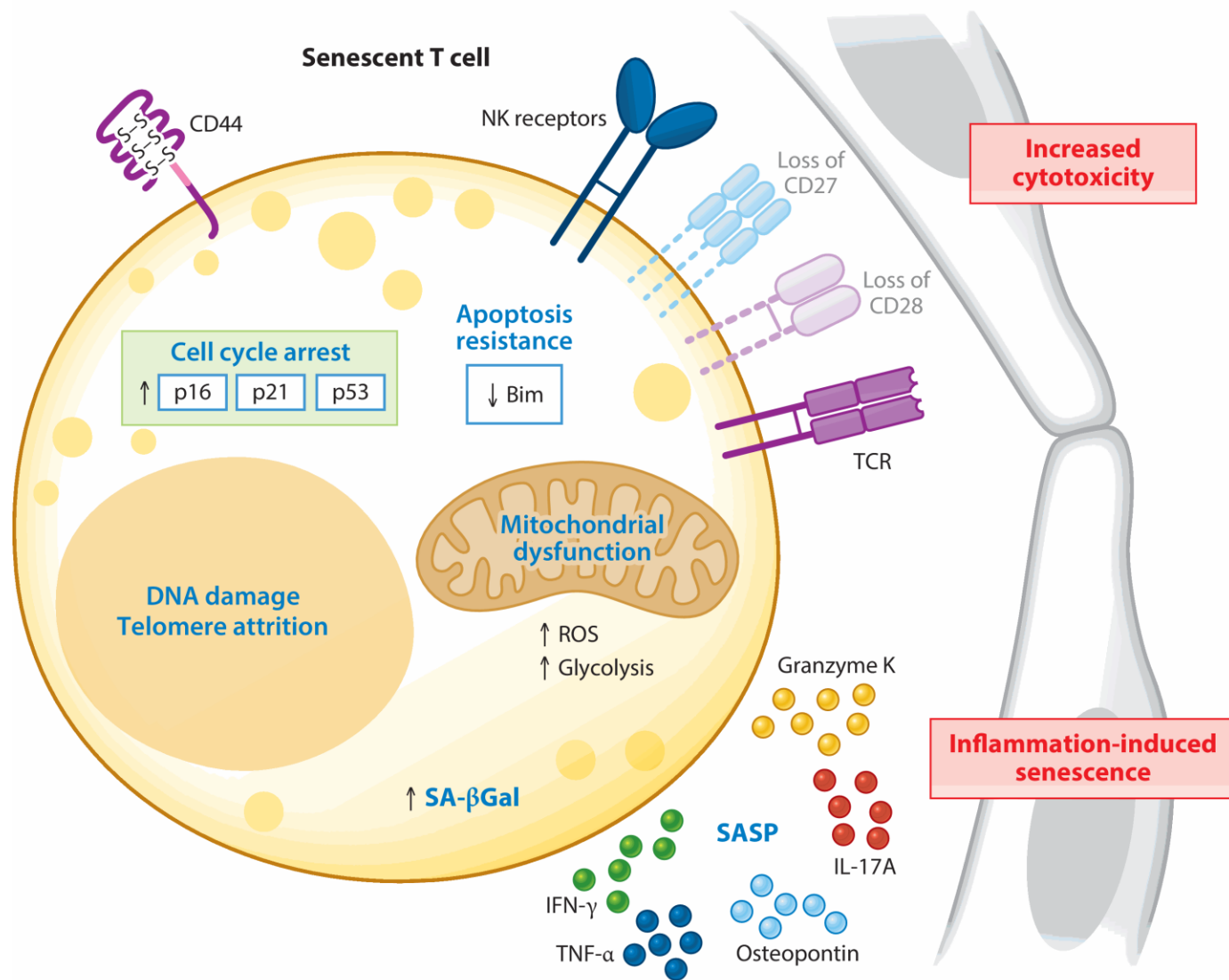
|   | Early differentiation | Intermediate differentiation | Terminal differentiation |
|---|-----------------------|------------------------------|--------------------------|
| <b>Phenotypic markers</b>                           |                       |                              |                          |
| CD28  | ++                    | +/-                          | -                        |
| CD27  | ++                    | +/-                          | -                        |
| CD45RA  | ++                    | +/-                          | +/-                      |
| CCR7  | ++                    | +                            | -                        |
| CD62L   | ++                    | +                            | -                        |
| CD57  | -                     | +/-                          | ++                       |
| KLRG1   | -                     | +/-                          | ++                       |
| Other NKR (KIR, NKG2, and CD56)                     | -                     | +/-                          | ++                       |
| <b>Functional features</b>                          |                       |                              |                          |
| Proliferation                                       | ++                    | +                            | -                        |
| Telomerase activity                                 | ++                    | +                            | -                        |
| Telomeres   | +++                   | ++                           | +                        |
| Cytotoxicity  | -                     | +                            | ++                       |
| Cytokine secretion (TNF- $\alpha$ , IFN- $\gamma$ ) | -                     | +                            | ++                       |
| <b>Signaling pathways</b>                           |                       |                              |                          |
| TCR signaling                                       | +                     | ++                           | +/-                      |
| IL-2 signaling                                      | +                     | ++                           | +/-                      |
| Pi3K-AKT-mTOR signaling                             | +                     | ++                           | +/-                      |
| p38MAPK activation                                  | -                     | -                            | +                        |

KLRG1, killer cell lectin-like receptor G1; NKR, natural killer receptor; KIR, killer cell immunoglobulin-like receptor; NKG2, natural killer receptor G2, TNF- $\alpha$ , tumor necrosis factor alpha; IFN- $\gamma$ , interferon gamma; PI3K, phosphatidylinositol-3 kinase; mTOR, mammalian target of rapamycin.

# T cells in aged individuals loose costimulatory and activate NK cell markers



# Intracellular changes in T cells



## Accumulation of SA-βGal-High Cells in Human Naïve T Cell Compartments Reveals a Stress-Adapted, Senescent-Like State

Andreea Cristina Alexandru<sup>1</sup>, Genesis Vega Hormazabal<sup>1</sup>, Hiroyuki Matsui<sup>1</sup>, Herbert Kasler<sup>1</sup>, Sierra Lore<sup>1</sup>, Carlos Galicia Aguirre<sup>1</sup>, Andrea Roberts<sup>1</sup>, Indra John Heckenbach<sup>2</sup>, Ritesh Tiwari<sup>1</sup>, Ryan Kwok<sup>1</sup>, Sydney Becker<sup>3</sup>, Eric Verdin<sup>4</sup>

Affiliations + expand

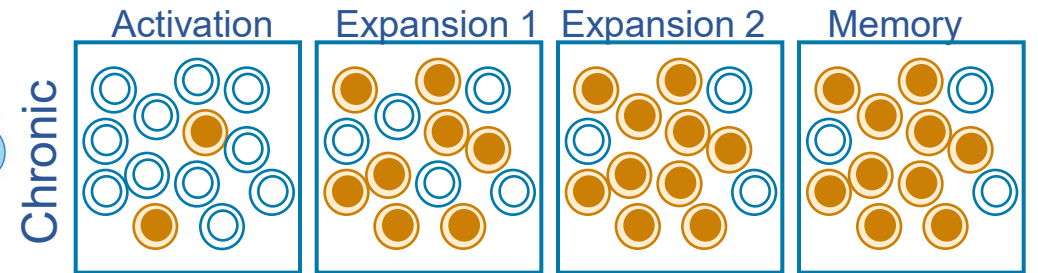
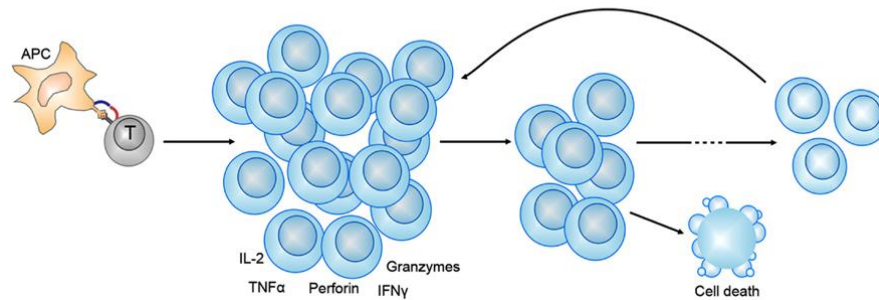
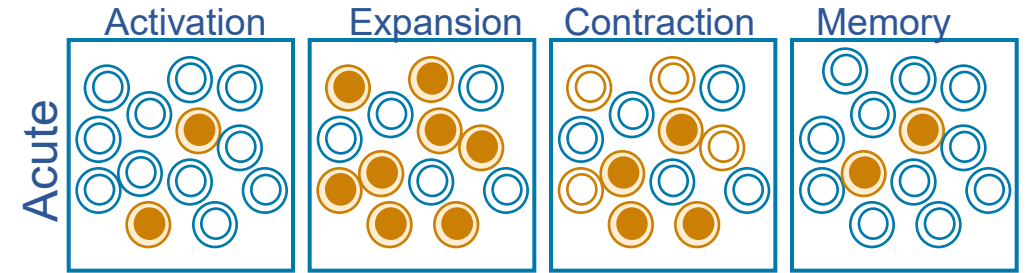
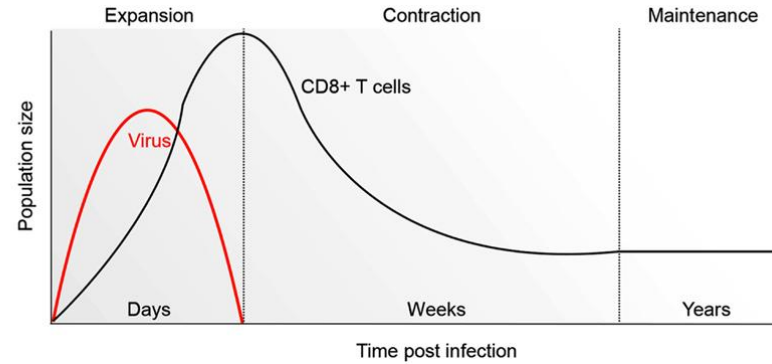
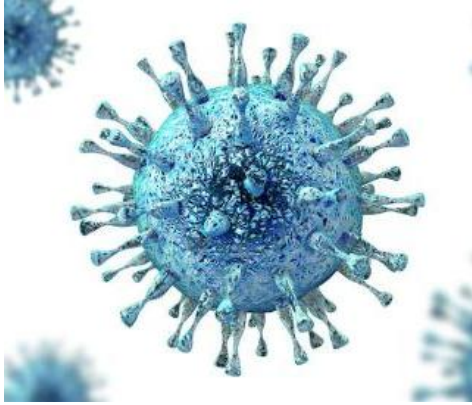
PMID: 40661537 PMCID: PMC12259081 DOI: 10.1101/2025.06.10.658841

### Abstract

Aging is associated with a decline in immune function termed immunosenescence, characterized by accumulation of senescent-like immune cells and chronic inflammation, known as inflammaging. While senescence-associated  $\beta$ -galactosidase (SA- $\beta$ Gal) activity is a well-established senescence marker, its functional significance and the precise cellular subsets affected within the T cell compartment remain unclear. Here, we identify and characterize a previously unrecognized subset of naïve CD4<sup>+</sup> and CD8<sup>+</sup> T cells displaying high SA- $\beta$ Gal activity that significantly increases with age. Despite exhibiting hallmark features of senescence such as DNA damage, nuclear envelope disruption, loss of heterochromatin, and pronounced dysregulation of autophagy and lysosomal pathways, these SA- $\beta$ Gal-high naïve T cells notably lack the canonical senescence marker p21CIP1 and retain robust proliferative capacity upon activation. Remarkably, naïve CD4<sup>+</sup> SA- $\beta$ Gal-high T cells acquire cytotoxic properties including NK-like features, granzyme secretion, and the ability to induce paracrine DNA damage in endothelial cells. Mechanistically, we demonstrate that impaired autophagic flux contributes significantly to this phenotype. Our findings address critical knowledge gaps regarding the nature and functional plasticity of senescence-like states in naïve T cells, highlighting a novel link between lysosomal-autophagic dysfunction, cellular stress adaptation, and inflammaging. Understanding this unique T cell population provides important insights into immune aging and offers potential targets to mitigate age-associated immune dysfunction and chronic inflammation.



# Cytomegalovirus (CMV) chronic infection associates with the accumulation of terminally differentiated T cells





# Age-related changes in gene expression of PBLs

A study of 15,000 people showed changes in the expression of 1500 genes, many of them related to immune functions

## ARTICLE

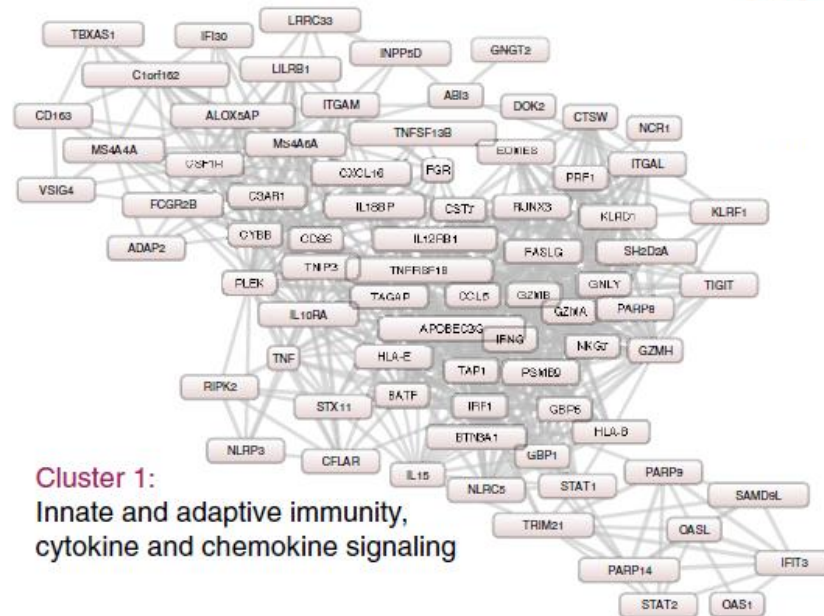
Received 16 Jan 2015 | Accepted 7 Sep 2015 | Published 22 Oct 2015

DOI: 10.1038/ncomms9570

## The transcriptional landscape of age in human peripheral blood

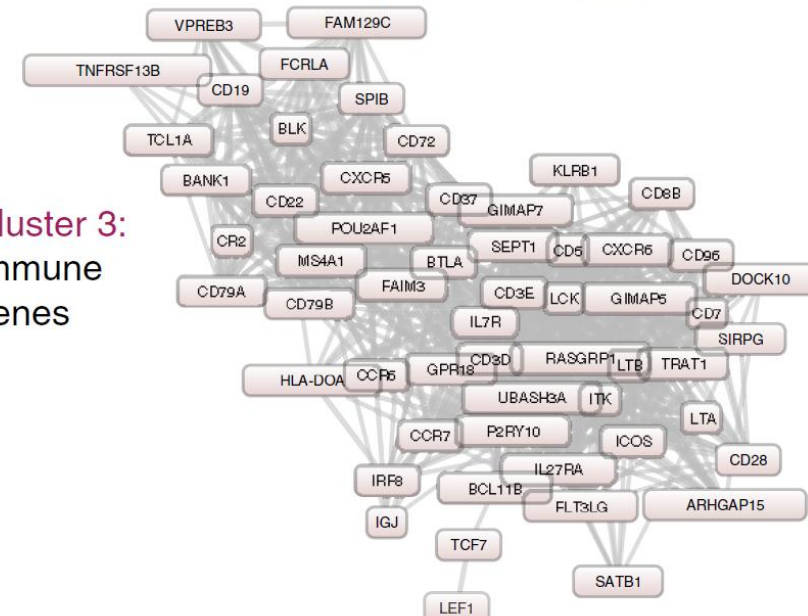
Marjolein J. Peters *et al.*<sup>#</sup>

### Upregulated immune genes

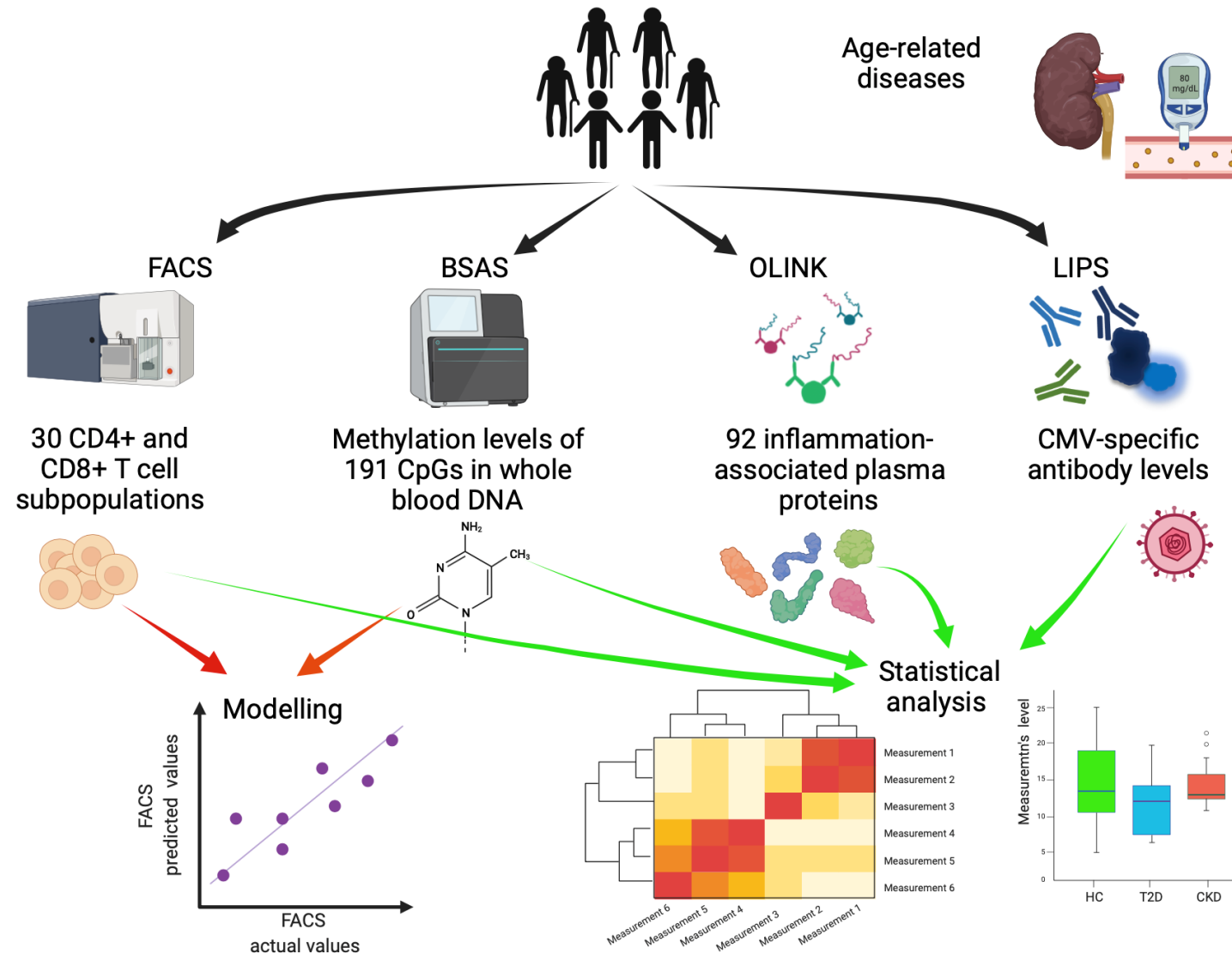


### Downregulated immune genes

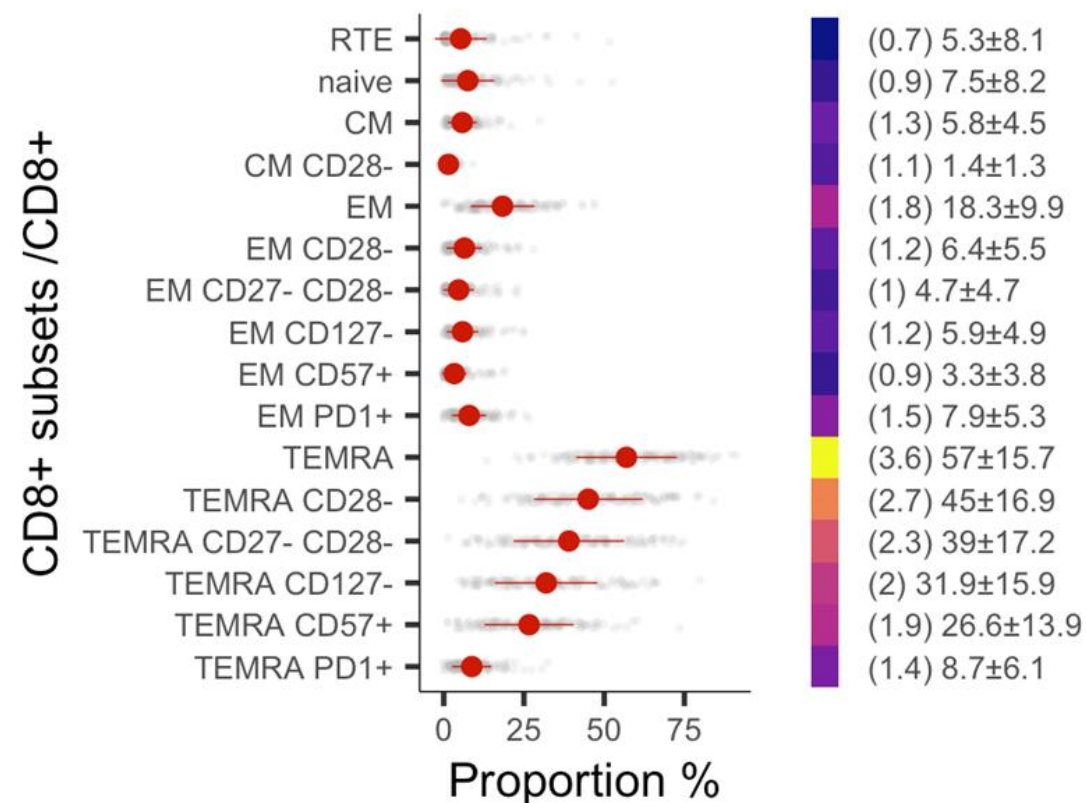
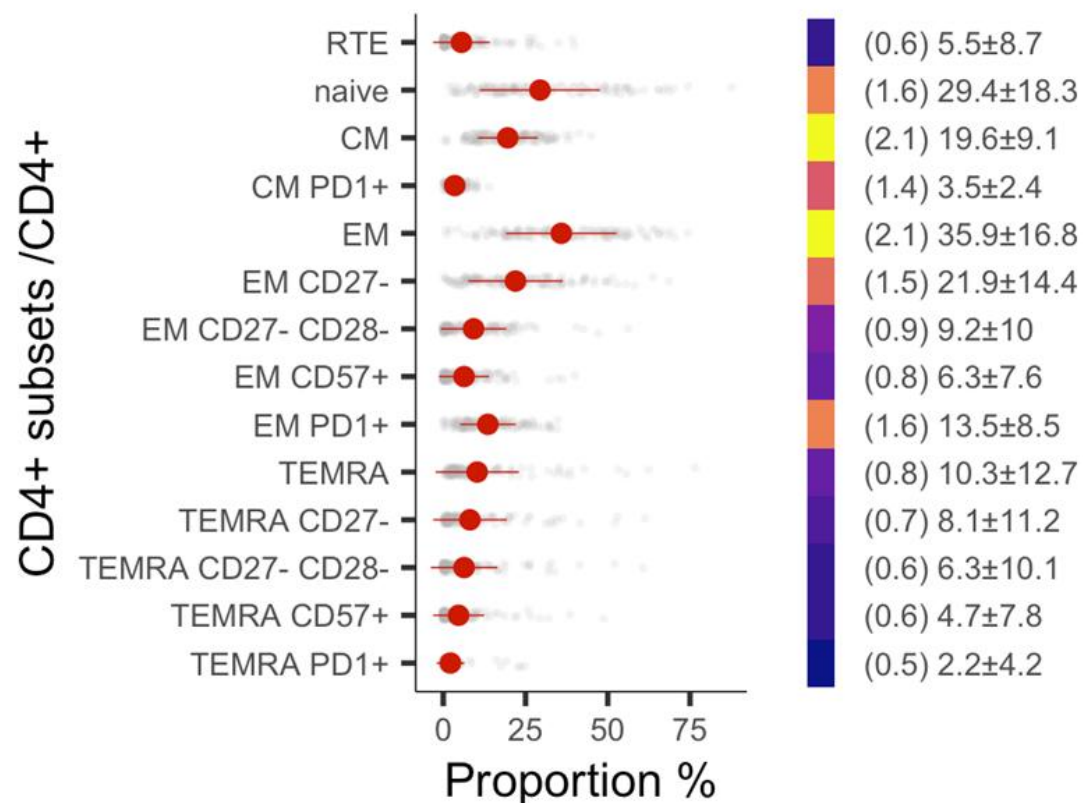
#### Cluster 3: Immune genes



# T cell profiling in old individuals (140 persons over 65 years)



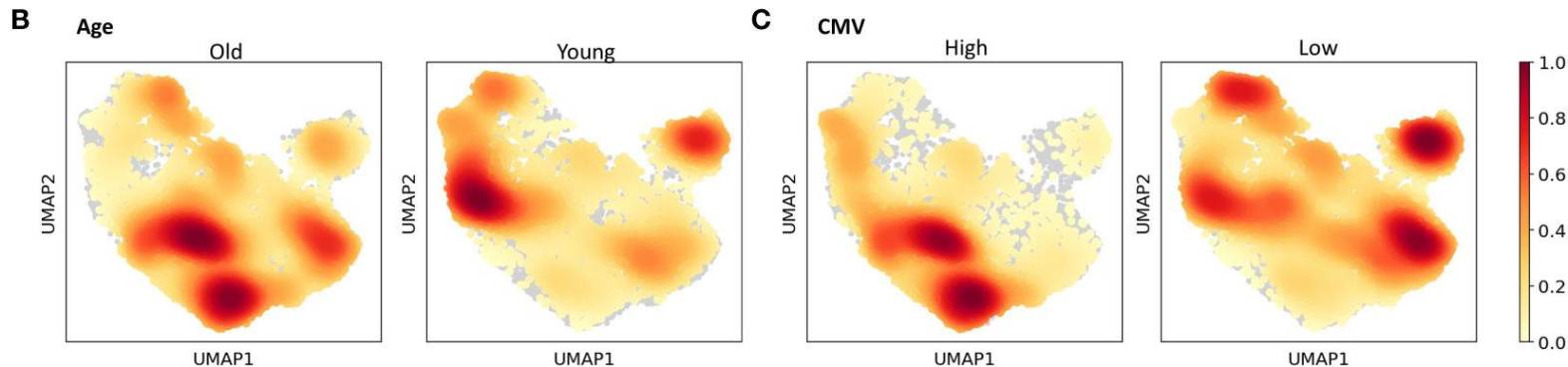
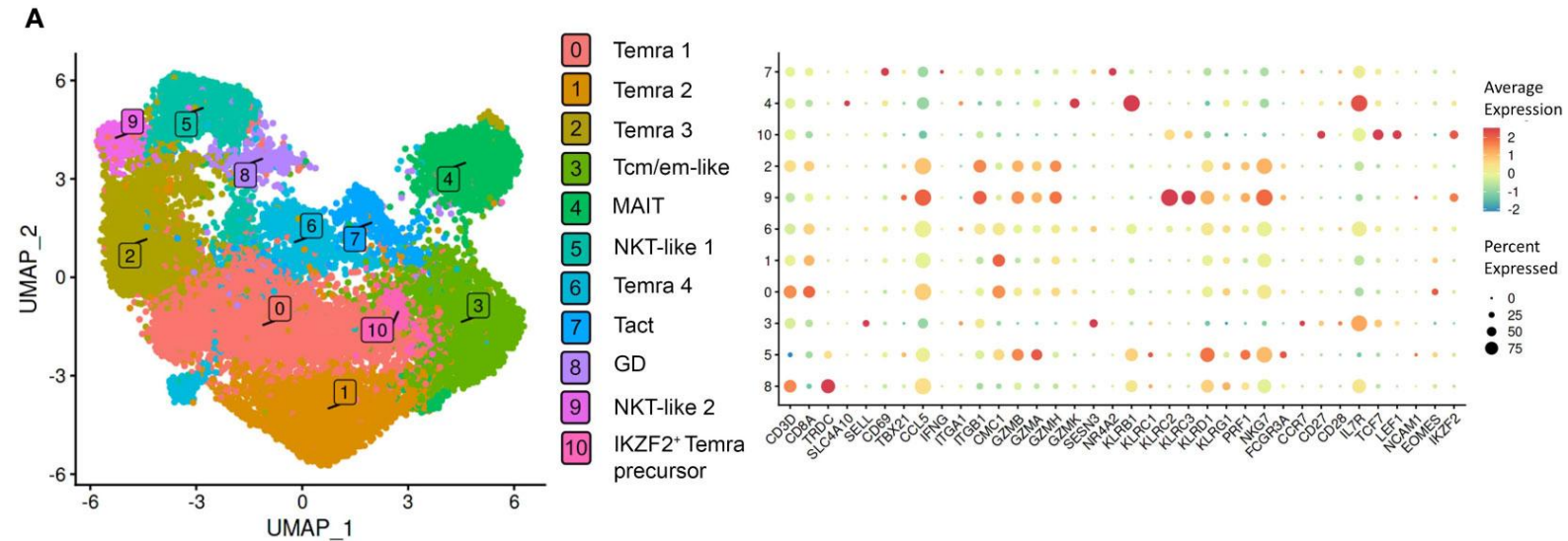
## Large and variable CD8+ TEMRA populations in old people



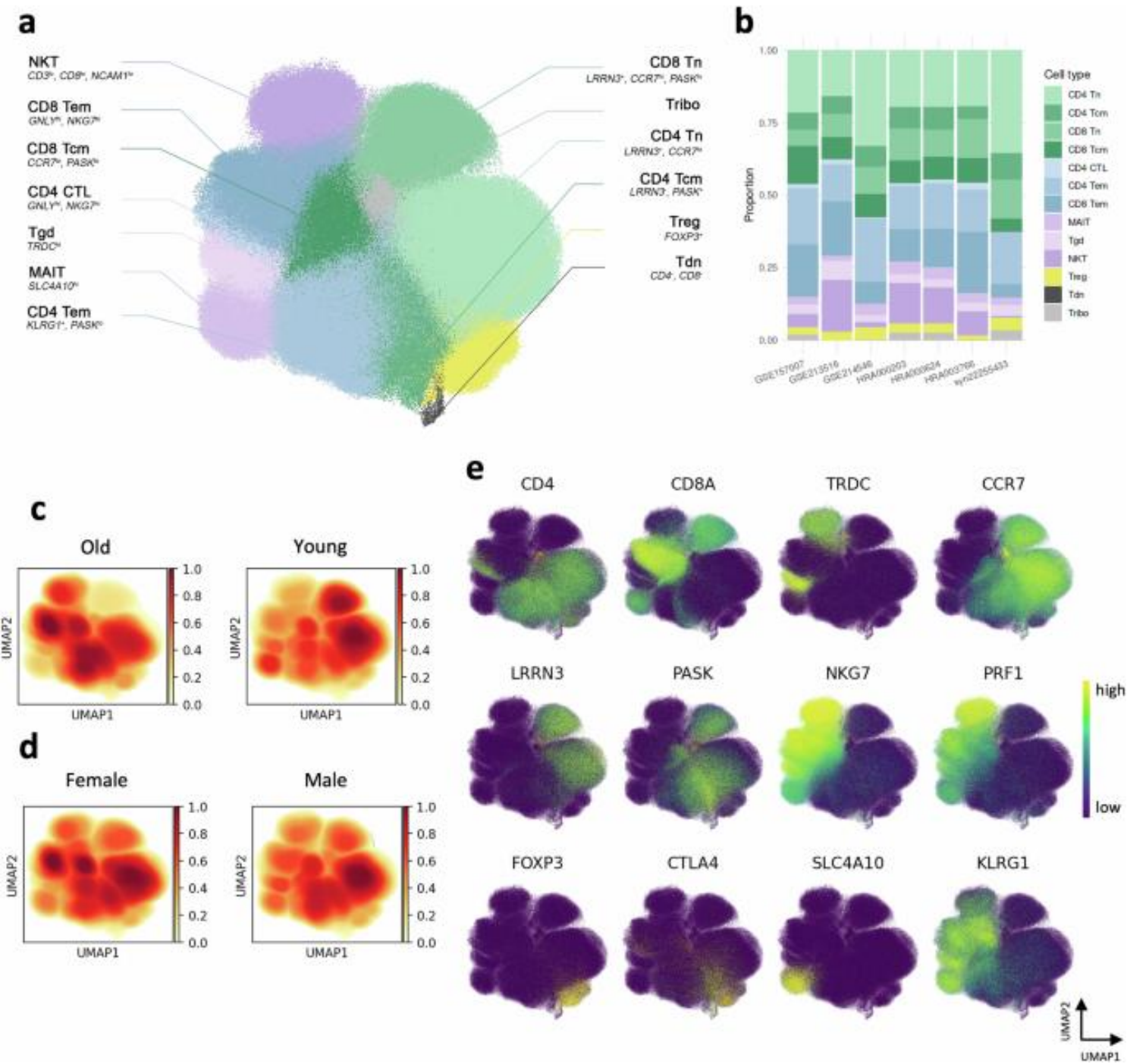


## Two CD8+ TEMRA cell subpopulations in old individuals

- Sorted CCR7<sup>lo</sup> CD45RA<sup>hi</sup> CD8+ TEMRA cells are heterogenous
- Five populations corresponding to CD8+ TEMRA cell subpopulations
  - Cluster 0: TEMRA1
  - Cluster 1: TEMRA2
  - Cluster 2: TEMRA3
  - Cluster 6: TEMRA4
  - Cluster 10: IKZF+ TEMRA precursor
- CD8+ TEMRA1 and 2 enriched in old and CMV<sup>+</sup> individuals
- CD8+ TEMRA1 and 2 express CMC1 and EOMES, high CD8A
- Compared to TEMRA3 and NKT –like cells TEMRA1 and 2 are lower in cytotoxic markers



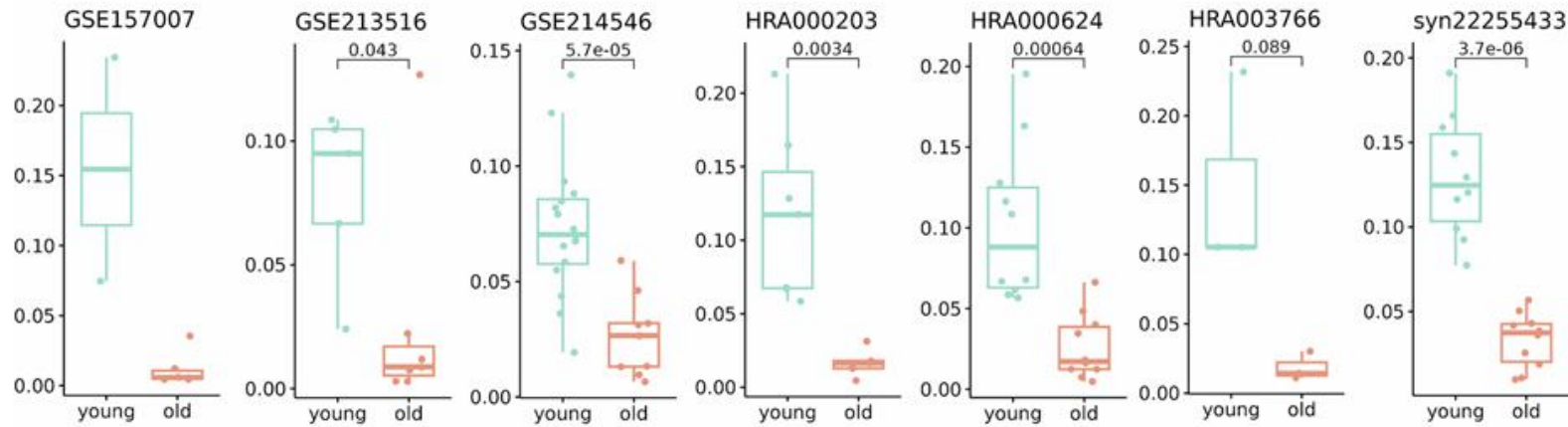
# Integrating data on T cells from seven scRNAseq studies



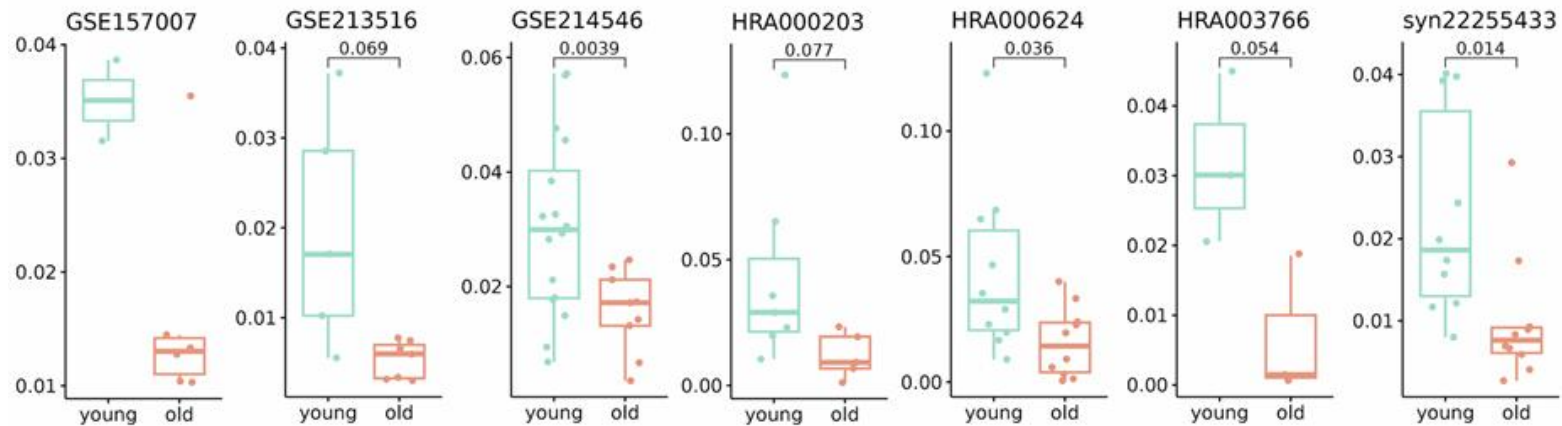
Filippov et al 2024. An integrated single-cell atlas of blood immune cells in aging. NPJ Aging.

# CD8+ T cells and MAIT cells are most consistently declining with age

## CD8 naïve cells

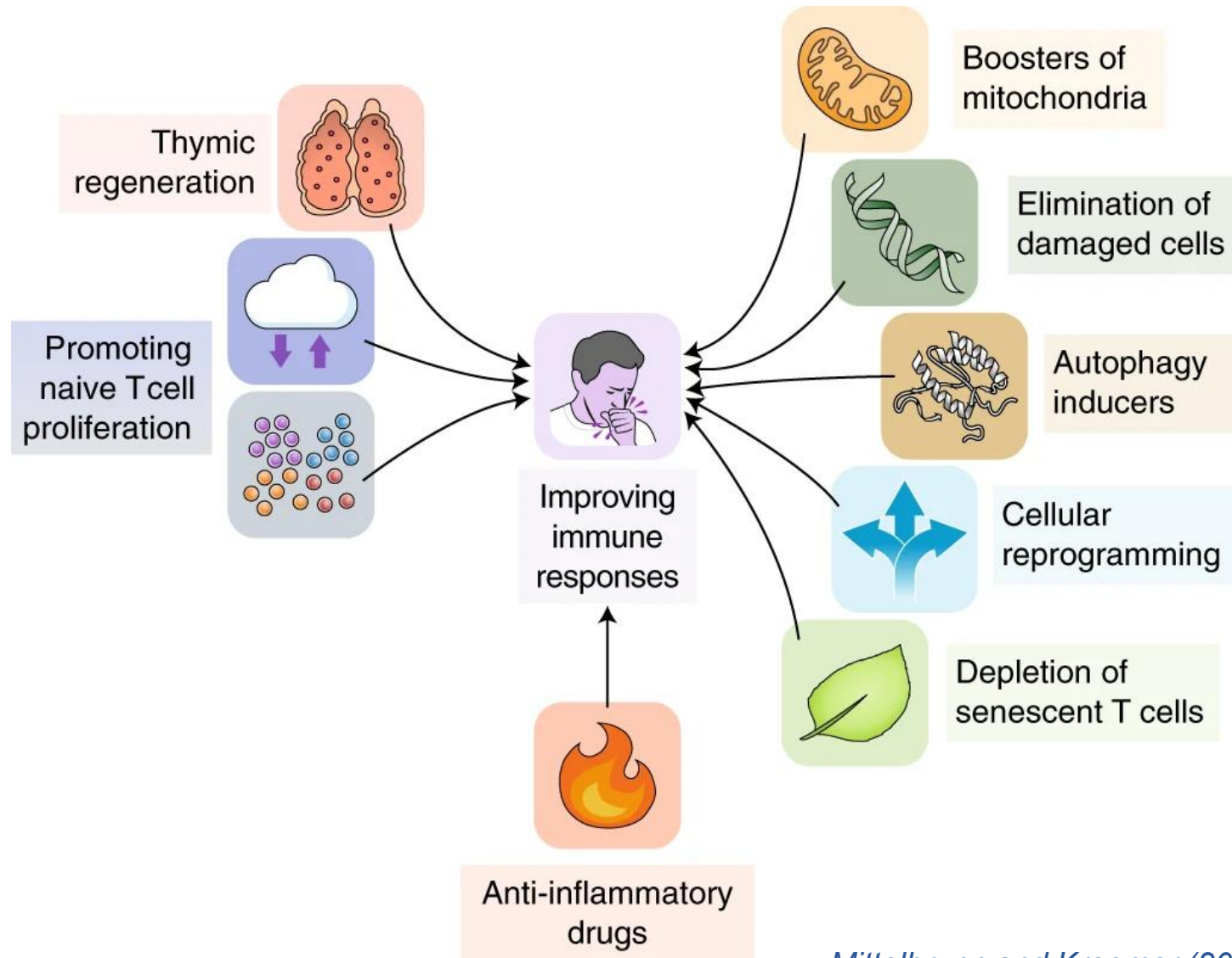


## MAIT cells





# The interventions we should focus on to improve our immune responses





TARTU ÜLIKOOL

Thank you!



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