



# ***Aging biomarkers in multimorbidity patients***

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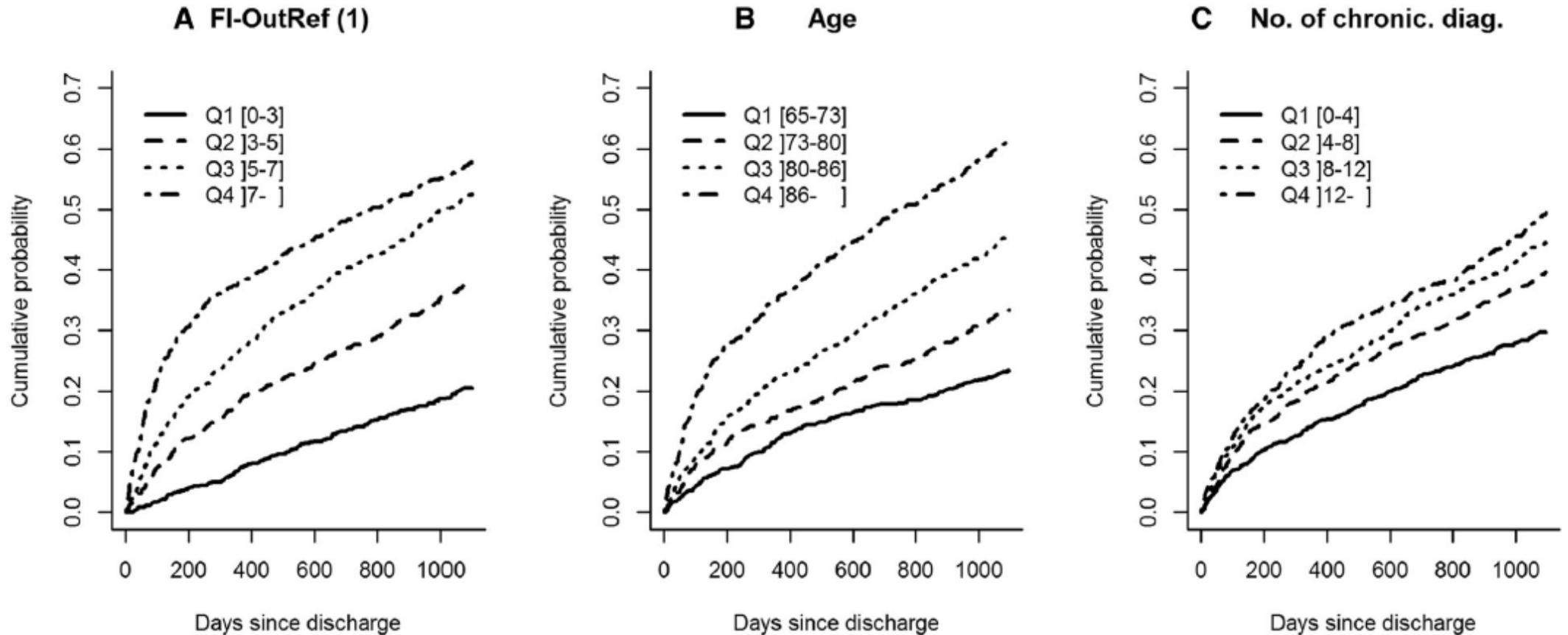


## AIM

**Introduce and implement prognostic biomarkers in routine clinical practice such as in emergency departments to predict short- or long-term all-cause mortality among acutely admitted patients**



# Cumulative incidence plots of mortality within 3 years post-discharge for 3172 patients without cancer diagnoses



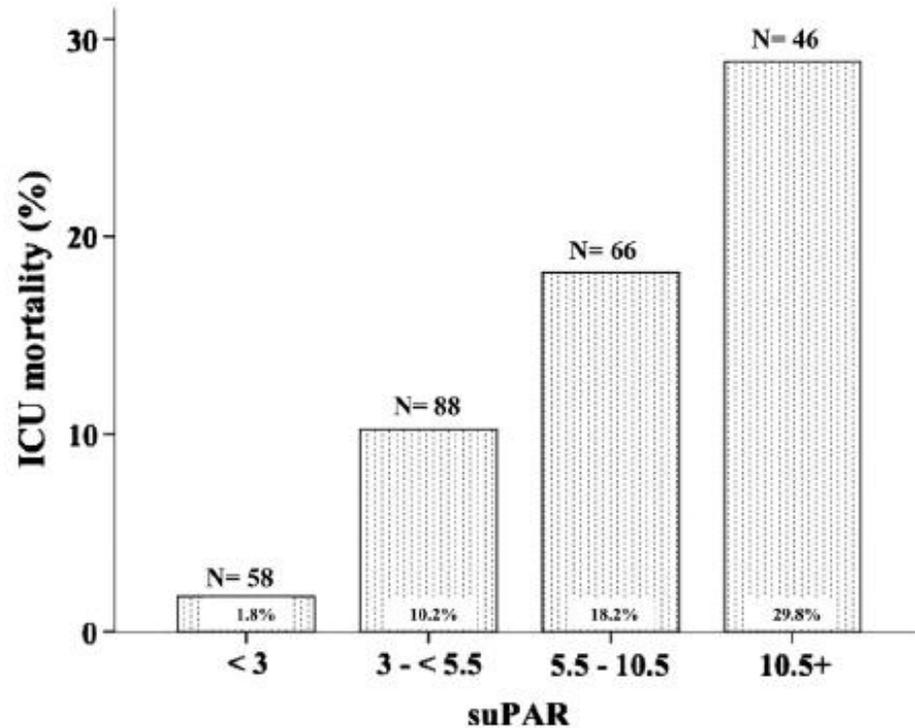


## For acutely admitted patients, the emergency department performs a standard panel of laboratory tests

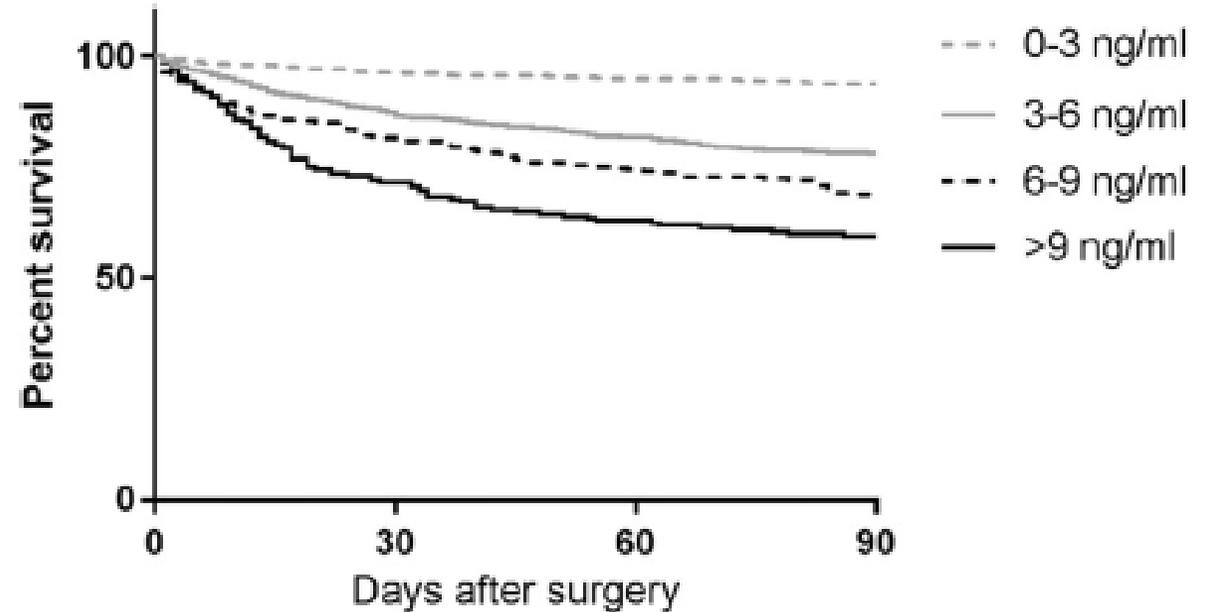
- C-reactive protein, leukocytes
- Differential blood count
- Hemoglobin
- Mean corpuscular hemoglobin concentration
- Mean corpuscular volume (MCV)
- Thrombocytes
- Creatinine
- Blood urea nitrogen (BUN)
- Sodium
- Potassium
- Albumin
- Alanine
- Aminotransferase
- Alkaline phosphatase
- Lactate dehydrogenase,
- Bilirubin
- Coagulation factors II, VII, and X
- (sUPAR)\*



## Intensive care unit mortality rates according to the 4 ranges of suPAR concentrations

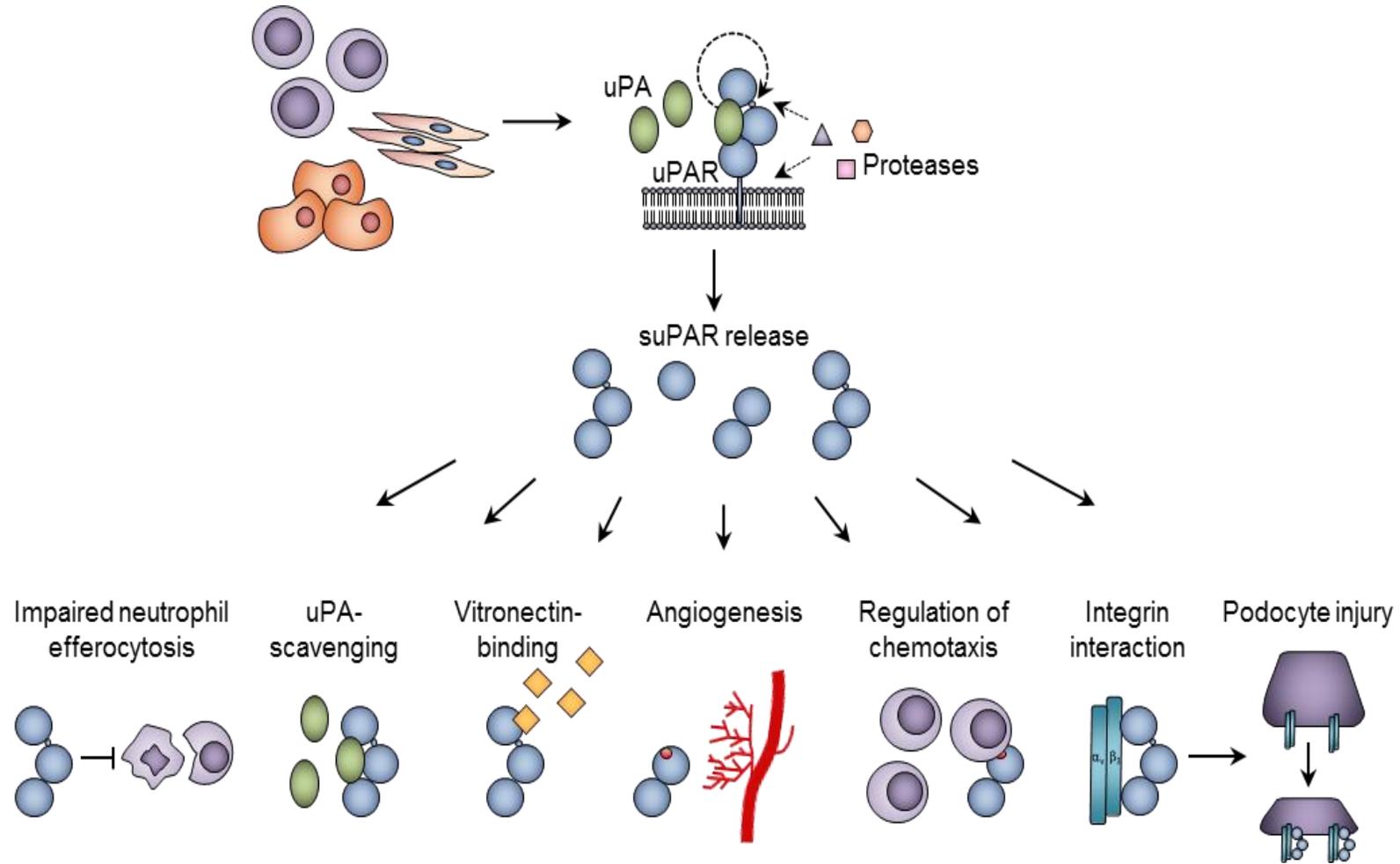


## 90-day post-operative mortality in acutely operated patients, stratified on suPAR concentrations



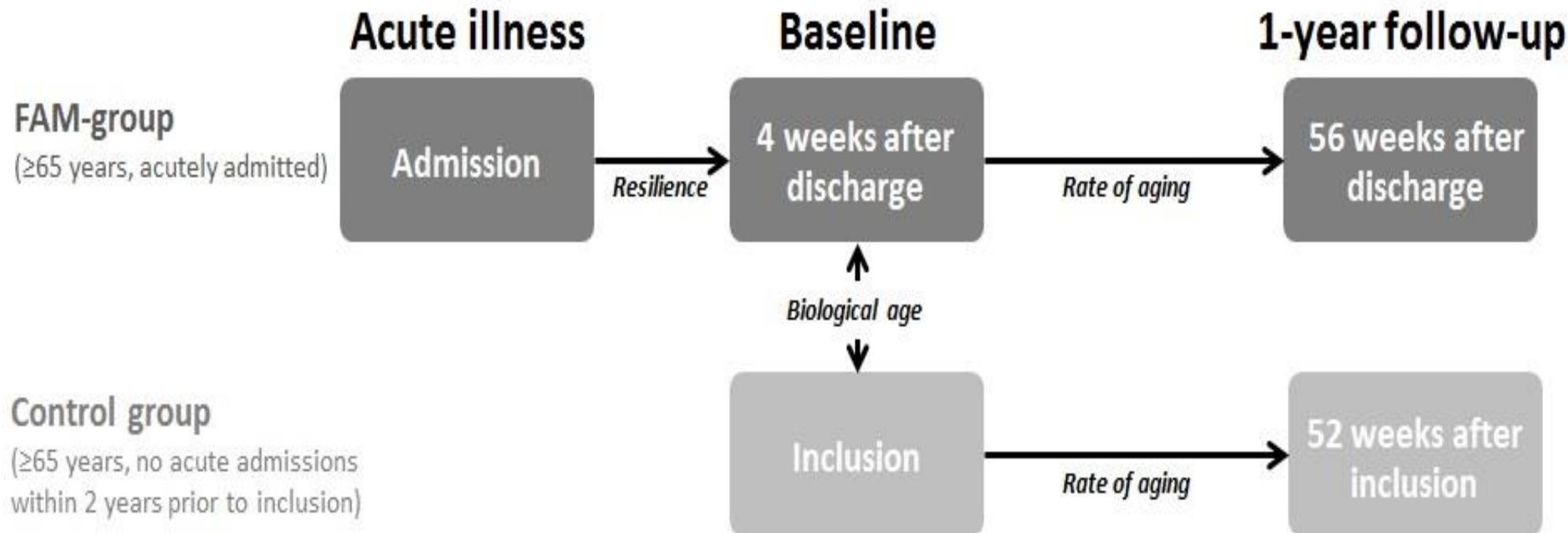


# Targets of suPAR





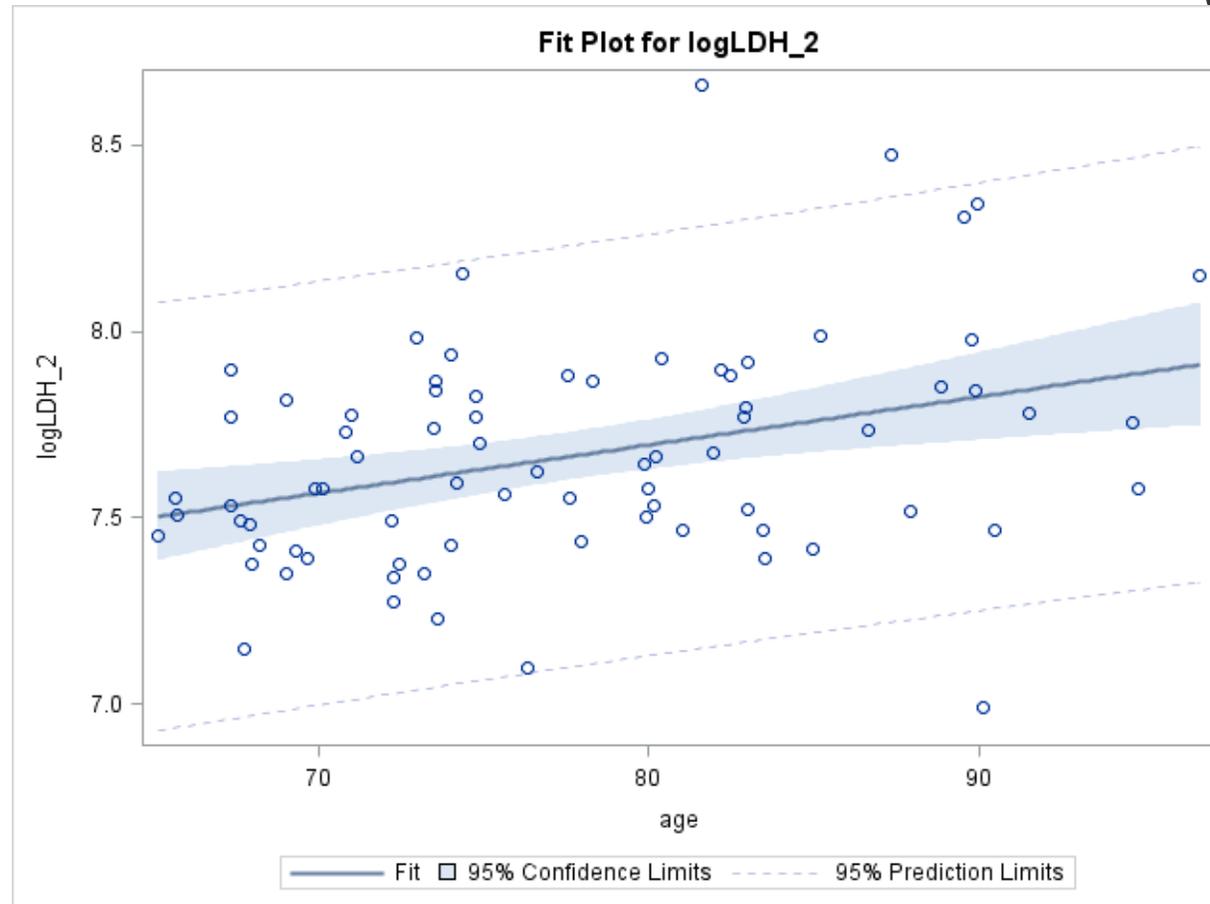
# Design of the FAM-CPH cohort



In dark grey, the FAM-group consists of acutely ill patients aged 65 and over ( $n=128$ ). In light grey, the Control group consists of citizen matched 1:1 on age, sex and municipality with patients from the FAM-group, but with no recent acute hospital admission ( $n=54$ ). In italics and arrows, the aspects of biological aging that we will investigate: resilience as the development in aging markers between acute illness and baseline, the biological age as the difference in aging markers between the groups at baseline, the rate of aging as the development in aging markers between baseline and the 1-year follow-up.



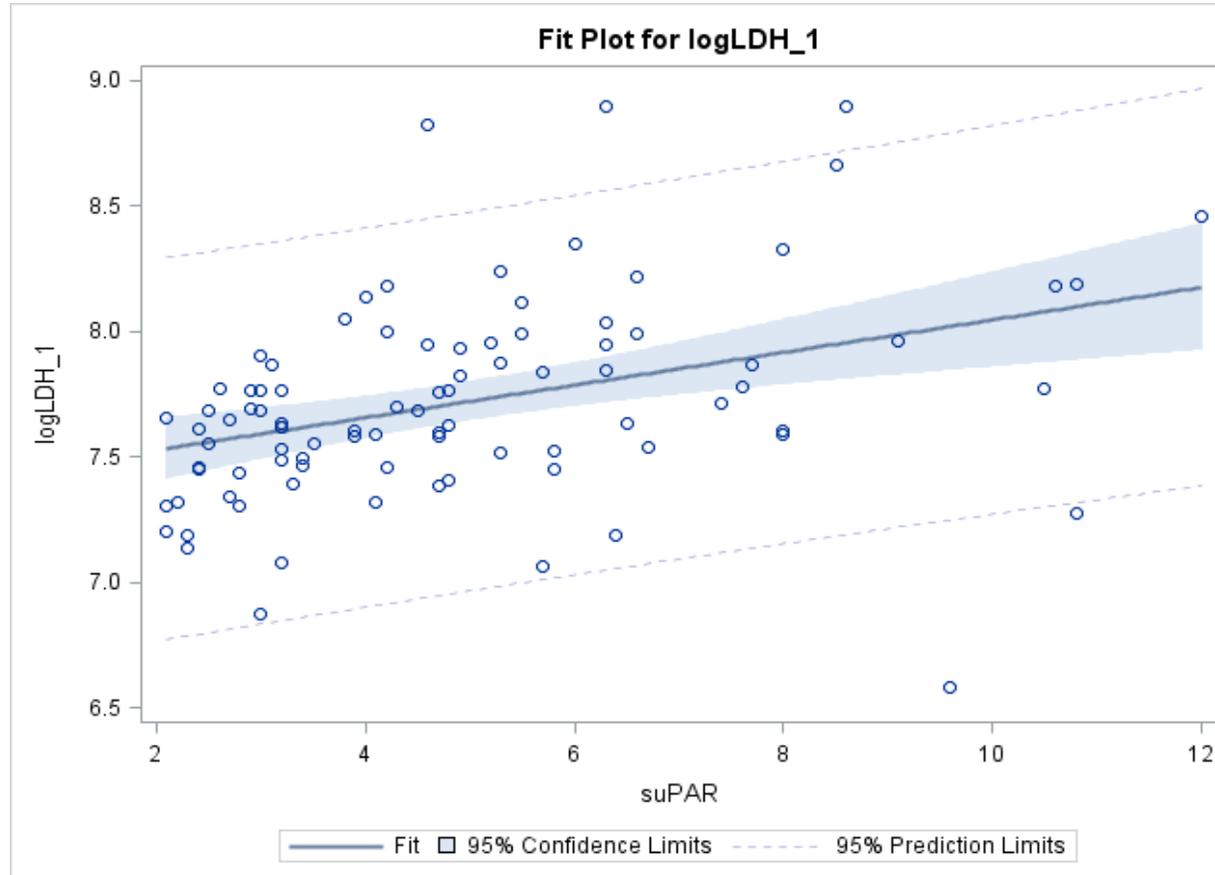
# Plasma LDH levels 4 weeks after discharge and age



Plasma LDH at 4-weeks after discharge and age, n= 77 – significant:  $p = 0.0019$



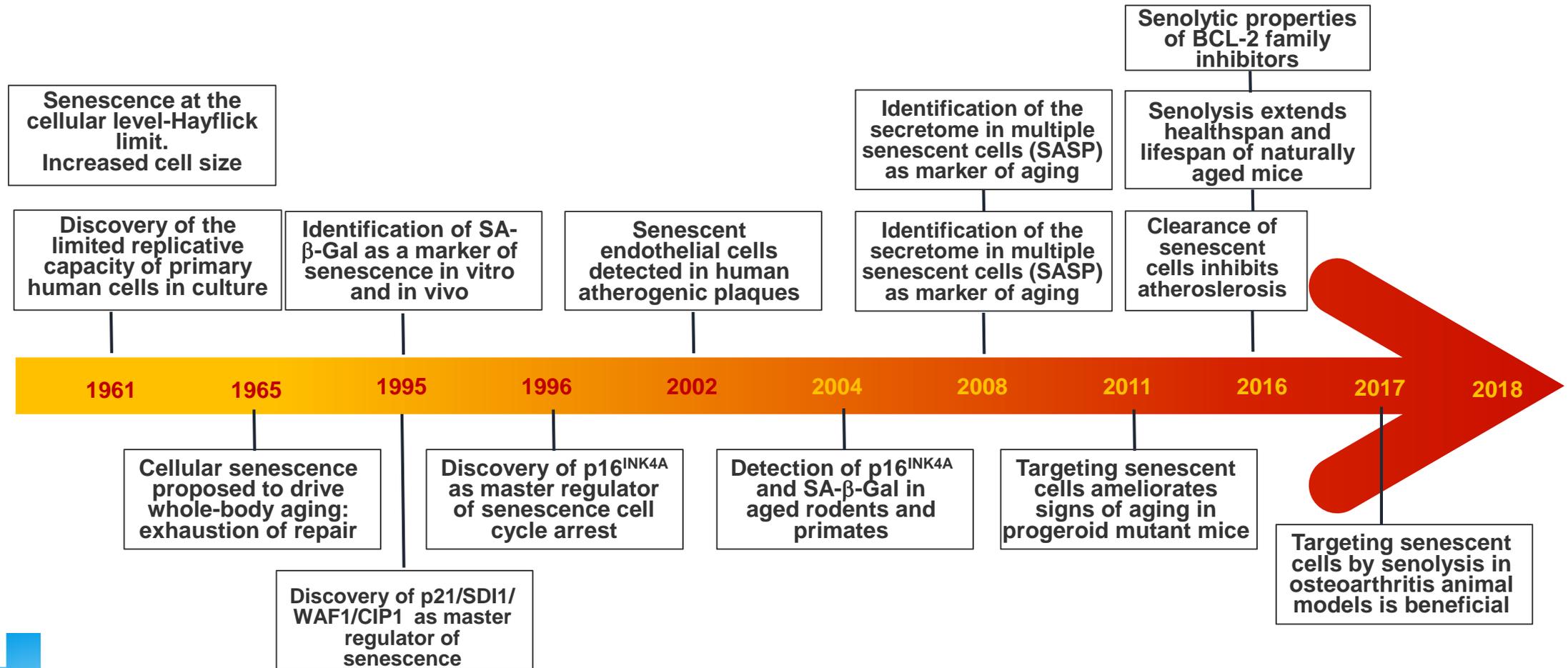
# Plasma LDH and suPAR levels at admission



Plasma LDH and suPAR levels at admission,  $n = 91$  – significant:  $p = 0.0003$ . The tissue-breakdown marker LDH (lactate dehydrogenase 1) [15] and the mortality marker suPAR (soluble urokinase-type plasminogen activator receptor) [16] are predictors of frailty and mortality.



# Timeline of milestones in aging biomarkers research





# Continuous proliferation leads to aging of cells in culture

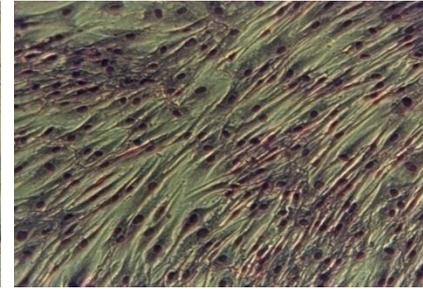
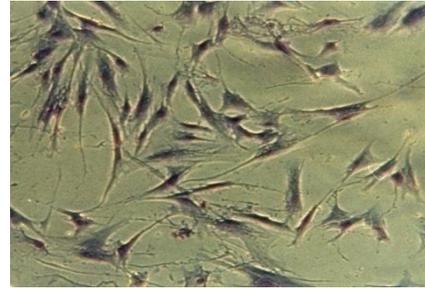
**Replicative senescence**

**Increased cell size as biomarker of aging**

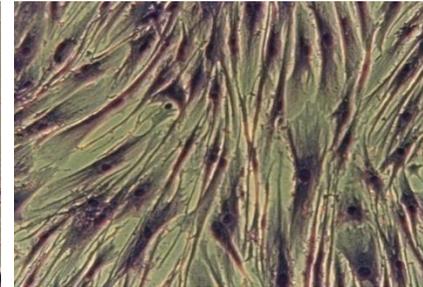
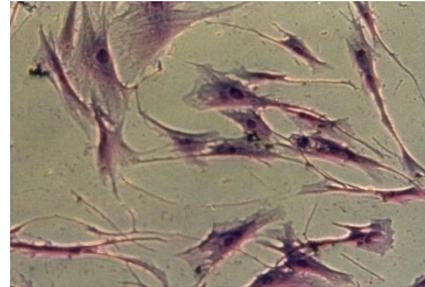
Sparse culture

Confluent culture

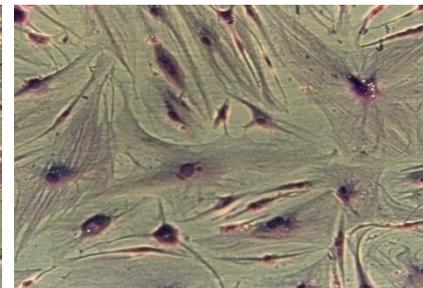
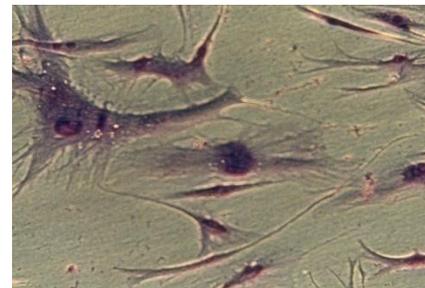
Human skin fibroblasts



young: less than 30% lifespan completed



middle aged: between 60 and 80% lifespan completed

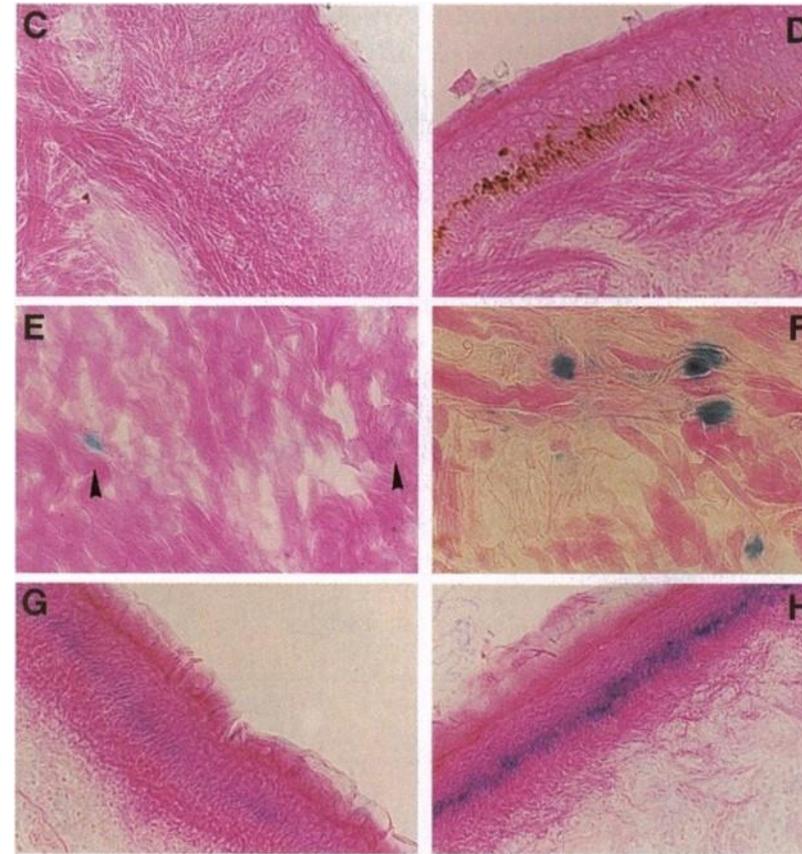
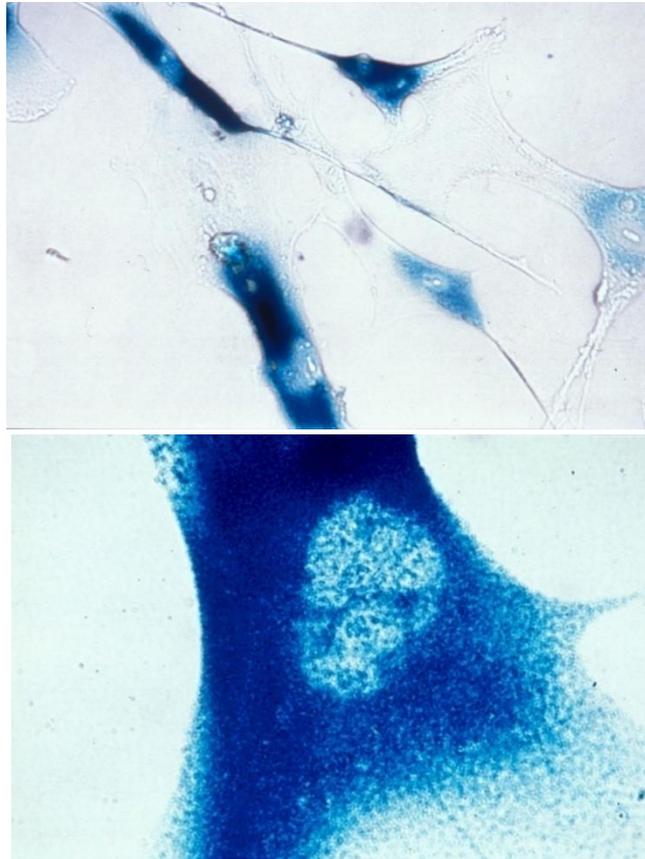


old: more than 95% lifespan completed

Senescence is the gradual and progressive slowing of cellular activity, including cell division, that occurs with aging. Cells lose the ability to divide over time



# SA- $\beta$ Gal: First commonly used senescence biomarker

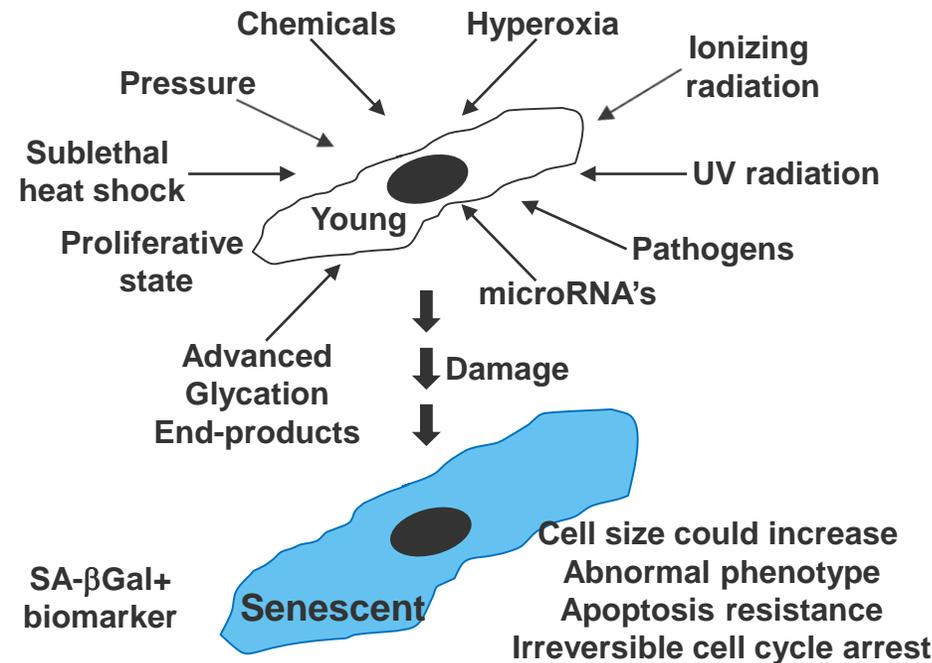


SA- $\beta$ Gal: Senescence-associated beta-galactosidase, a lysosomal marker that is specific for a pH 6.0 b-galactosidase



# Causes of aging of cells in cell culture

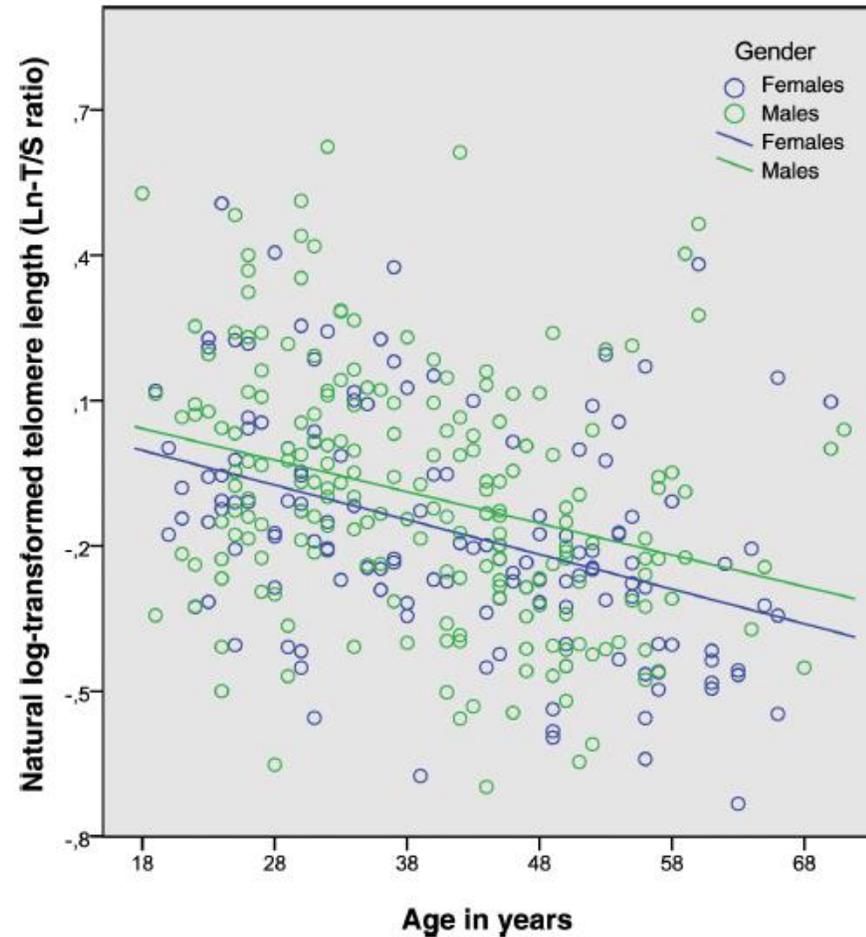
1. Replicative senescence
2. Stress-induced premature senescence (SIPS)
3. Oncogene-induced senescence (OIS)
4. Other....



1. The effects depend on dose and time of exposure
2. The SIPS cellular expression profiles are different from those of replicatively senescent cells



# Association of telomere length of peripheral blood leukocytes with age

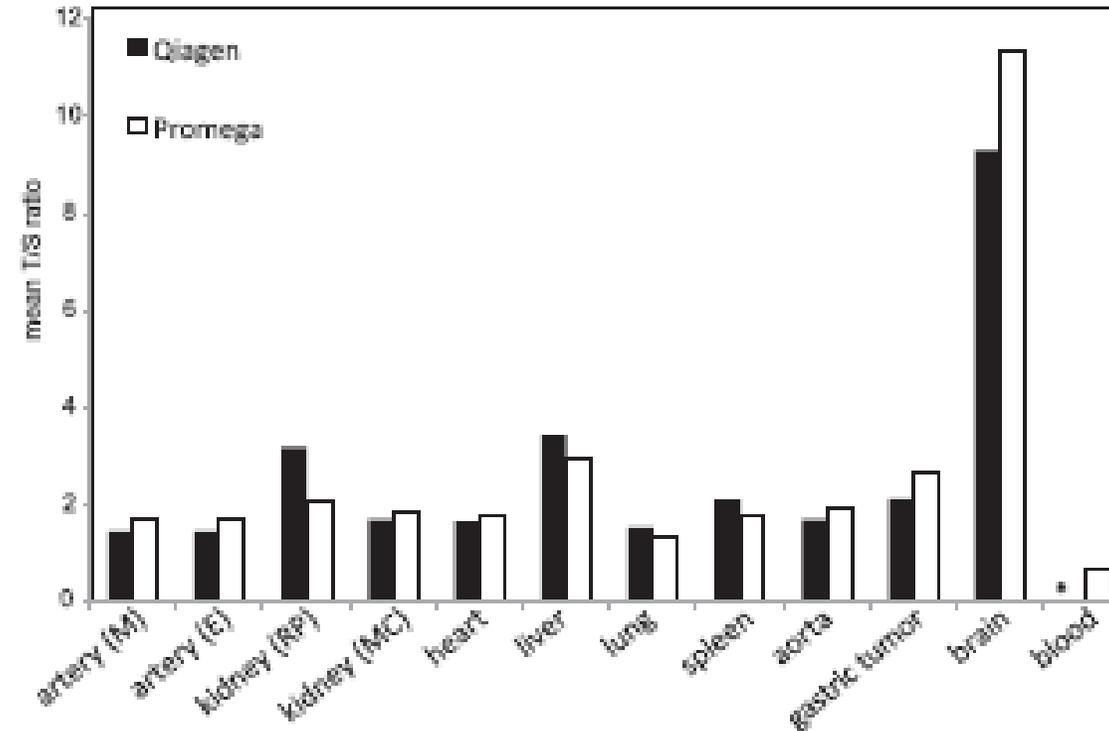


**Telomere length reduction in comparison with chronological age**

Age and natural log-transformed telomere length, males and females, n = 343.  
Regression lines for men (blue circles) and women (green circles)



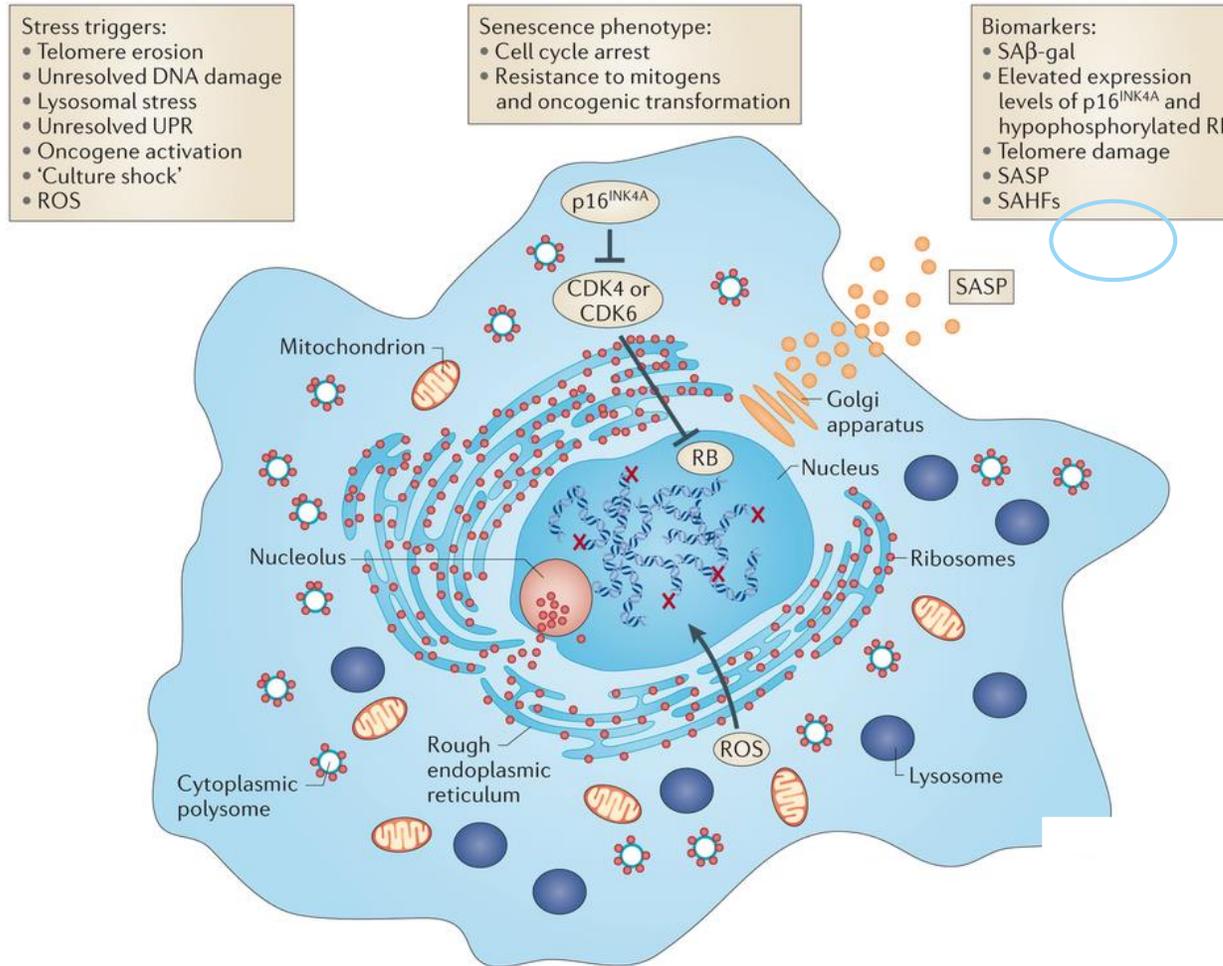
# Mean telomere length of 115 year old tissues



- Telomere lengths of healthy white blood cells were significantly shorter than in cells from other tissues
- The finite lifespan of hematopoietic stem cells may lead to hematopoietic clonal evolution at extreme ages.



# Senescence-associated secretory phenotype: SASP



**The Senescence-associated Secretory phenotype (SASP) consists of several secreted cytokines and chemokines that are involved in promoting a pro-inflammatory state**

Nature Reviews | Cancer



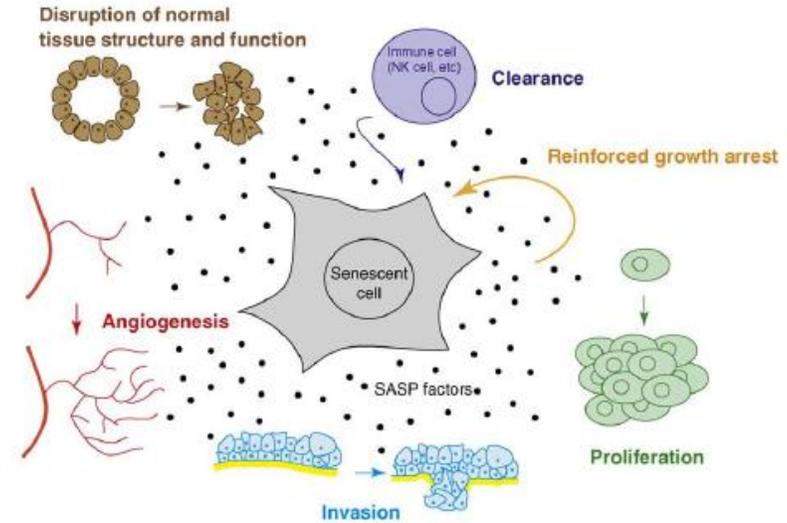
# Secretome from senescent cells (SASP)

## High increase (4+ fold)

Factor	Senescence inducer	Cell type	Reference
GM-CSF	OIS (RAS, MEK), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Acosta, Coppe
GRO $\alpha$	OIS (RAS, MEK), DDIS (XRA, BLEO), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3, prostate fibroblasts (PSC27, PSC31, and PSC32)	Acosta, Coppe, Bavik
GRO $\alpha$ , $\beta$ , $\gamma$	OIS (RAS, MEK), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Acosta, Rodier, Coppe
IGFBP-7	OIS (BRAF)	+ melanocytes	Wajsbeyee
IL-1 $\alpha$	OIS (RAS, MEK), DDIS (XRA, BLEO)	+ IMR-90, HCA2, PrECs, BPH1, RWPE1, PC3	Acosta, Coppe, Liu
IL-6	OIS (RAS, MEK), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Acosta, Rodier, Coppe
IL-7	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ	Coppe
IL-8	OIS (RAS, MEK), DDIS (XRA, BLEO), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3, prostate fibroblasts (PSC27, PSC31, and PSC32)	Acosta, Rodier, Coppe, Bavik
MCP-1	OIS (RAS, MEK), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Acosta, Rodier, Coppe, Liu
MCP-2	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ	Coppe
MIP-1 $\alpha$	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Coppe
MMP-1	OIS (RAS), DDIS (XRA, BLEO), REP	+ IMR-90, HCA2, WI-38, BJ	Coppe, Liu
MMP-10	OIS (RAS), DDIS (XRA, BLEO, ETOP), REP	+ IMR-90, HCA2, WI-38, BJ, hepatic myofibroblasts	Coppe, Krizhanovsky
MMP-3	OIS (RAS), DDIS (XRA, BLEO), REP	+ IMR-90, HCA2, WI-38, BJ	Coppe, Liu, Parrinella

## Intermediate increase (2-4 fold)

Factor	Senescence inducer	Cell type	Reference
Amphiregulin	OIS (RAS), DDIS (XRA, BLEO)	+ PrECs, BPH1, RWPE1, PC3, prostate fibroblasts (PSC27, PSC31, and PSC32)	Coppe, Bavik
ENA-78	OIS (RAS, MEK), DDIS (XRA)	+ IMR-90, PrECs, BPH1, PC3	Acosta, Coppe
Eotaxin-3	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2	Coppe
GCP-2	OIS (RAS), DDIS (XRA)	+ HCA2, PrECs, RWPE1, PC3	Coppe
GITR	OIS (RAS), DDIS (XRA)	+ HCA2, PrECs, BPH1, RWPE1, PC3	Coppe
HGF	OIS (RAS), DDIS (XRA, BLEO), REP	+ IMR-90, HCA2, WI-38, BJ, prostate fibroblasts (PSC27, PSC31, and PSC32)	Coppe, Bavik, Liu
ICAM-1	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Rodier, Coppe
IGFBP-2	DDIS (XRA, BLEO), REP	+ prostate fibroblasts (PSC27, PSC31, and PSC32)	Rodier, Coppe, Bavik
IGFBP-4	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ	Coppe
IGFBP-5	DDIS (BLEO), REP	+ prostate fibroblasts (PSC27, PSC31, and PSC32)	Bavik
IGFBP-6	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Coppe
IL-13	OIS (RAS), DDIS (XRA), REP	+ IMR-90, WI-38	Coppe
IL-15	OIS (RAS), DDIS (XRA, BLEO), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Coppe, Liu
MCP-4	OIS (RAS, MEK), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Acosta, Coppe
MIF	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Coppe
MIP-3 $\alpha$	OIS (RAS, MEK), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Acosta, Coppe
MMP-12	DDIS (XRA, ETOP)	+ IMR-90, HCA2, WI-38, BJ, hepatic myofibroblasts	Coppe, Krizhanovsky
MMP-13	DDIS (XRA, ETOP)	+ IMR-90, HCA2, WI-38, BJ, hepatic myofibroblasts	Coppe, Krizhanovsky
MMP-14	DDIS (XRA)	+ IMR-90, HCA2, WI-38, BJ	Coppe
NAP2	OIS (MEK)	+ IMR-90	Acosta
Oncostatin M	OIS (MEK), DDIS (XRA)	+ IMR-90, WI-38	Acosta, Coppe
Osteoprotegerin	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Rodier, Coppe
PLGF	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Coppe
RANTES	DDIS (BLEO)	+ HCA2	Liu
sgp130	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Rodier, Coppe
TIMP-2	OIS (RAS), DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ, PrECs, BPH1, RWPE1, PC3	Rodier, Coppe
TRAIL-R3	DDIS (XRA), REP	+ IMR-90, HCA2, WI-38, BJ	Rodier, Coppe



Senescence-messaging secretome (SMS)  
Senescence-associated secretory phenotype (SASP)





## *In vitro* cellular senescence biomarkers

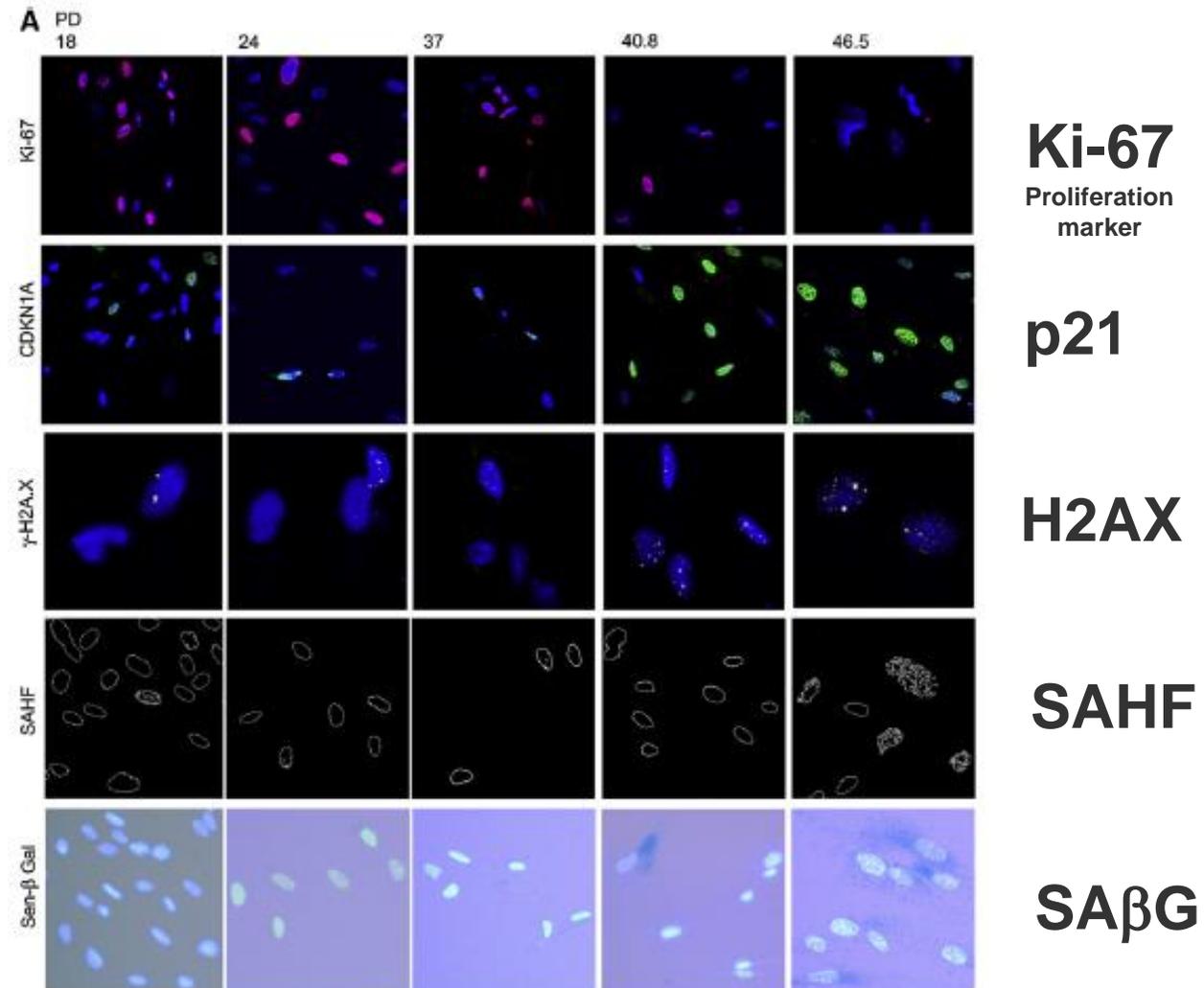
- SA- $\beta$ -Gal
- p53
- p21
- p16<sup>INK4a</sup>
- p14<sup>ARF</sup>
- p15<sup>INK4b</sup>
- DPP4
- Lipofuscin
- H2AX (SAHF)
- DEC1/DEC2
- DCR2
- H1/macroH2A/H3.3/H3metLys9
- Asf1a/HIRA
- HP1/HMGA
- SASP/SMS (*IL6/IL8*)
- Telomere-associated DNA damage foci(TAF)/DDR

DDR: DNA-damage response; SA- $\beta$ -Gal: senescence-associated  $\beta$ -Galactosidase; SAHF: senescence-associated heterochromatin foci; SASP: senescence-associated secretory phenotype; SMS: senescence-messaging secretome.



# Intracellular senescence biomarkers

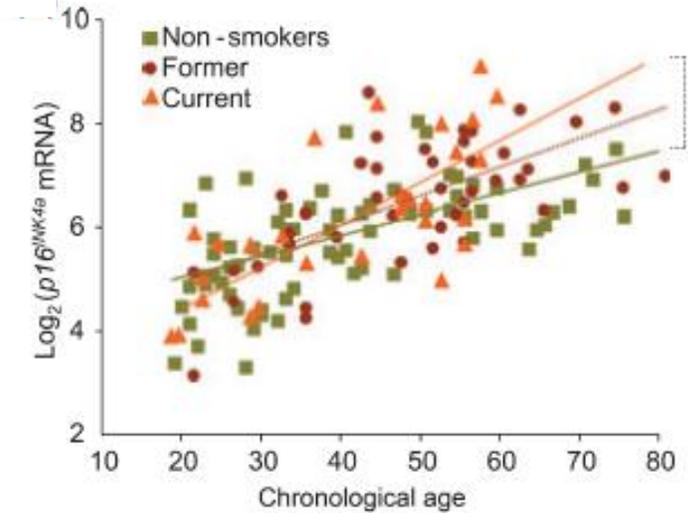
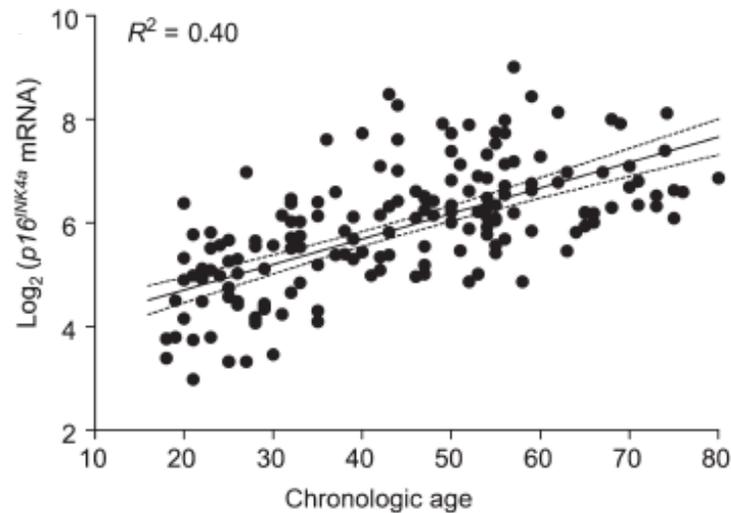
**Staining examples**  
(DAPI: counterstain)





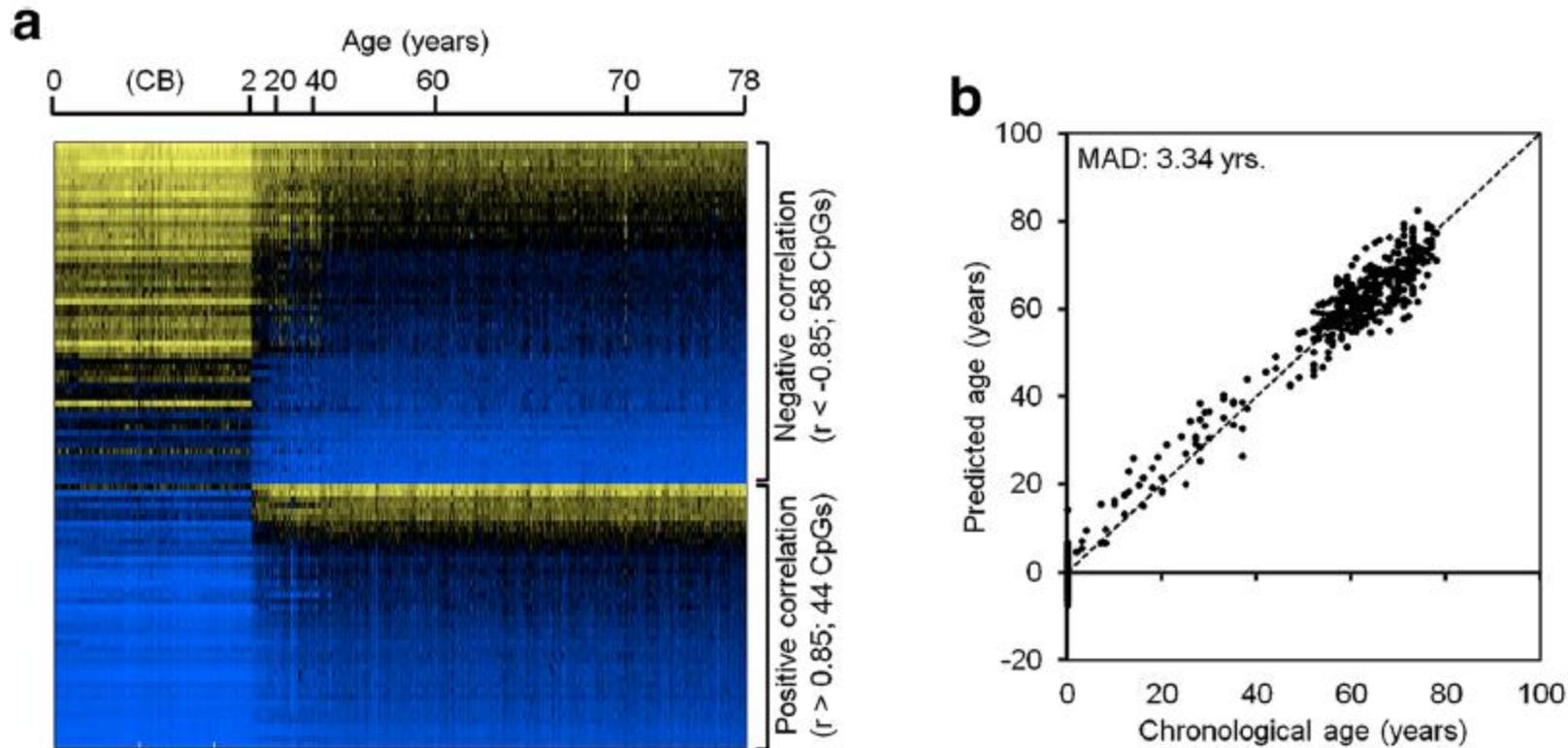
# Expression of p16<sup>INK4a</sup> in peripheral blood T lymphocytes is a biomarker of human aging

- Analyses of p16<sup>INK4a</sup> expression from human whole blood showed the highest expression in peripheral blood T lymphocytes (PBTL)
- Expression of p16<sup>INK4a</sup>, but not other INK4/ARF transcripts, appeared to exponentially increase with donor chronologic age (170 donors). Importantly, p16<sup>INK4a</sup> expression did not independently correlate with gender or body mass index, but was significantly associated with tobacco use and physical inactivity.
- p16<sup>INK4a</sup> expression was associated with plasma interleukin-6 concentration, a marker of human frailty.
- p16<sup>INK4a</sup> expression in PBTL is an easily measured, peripheral blood biomarker of molecular age.



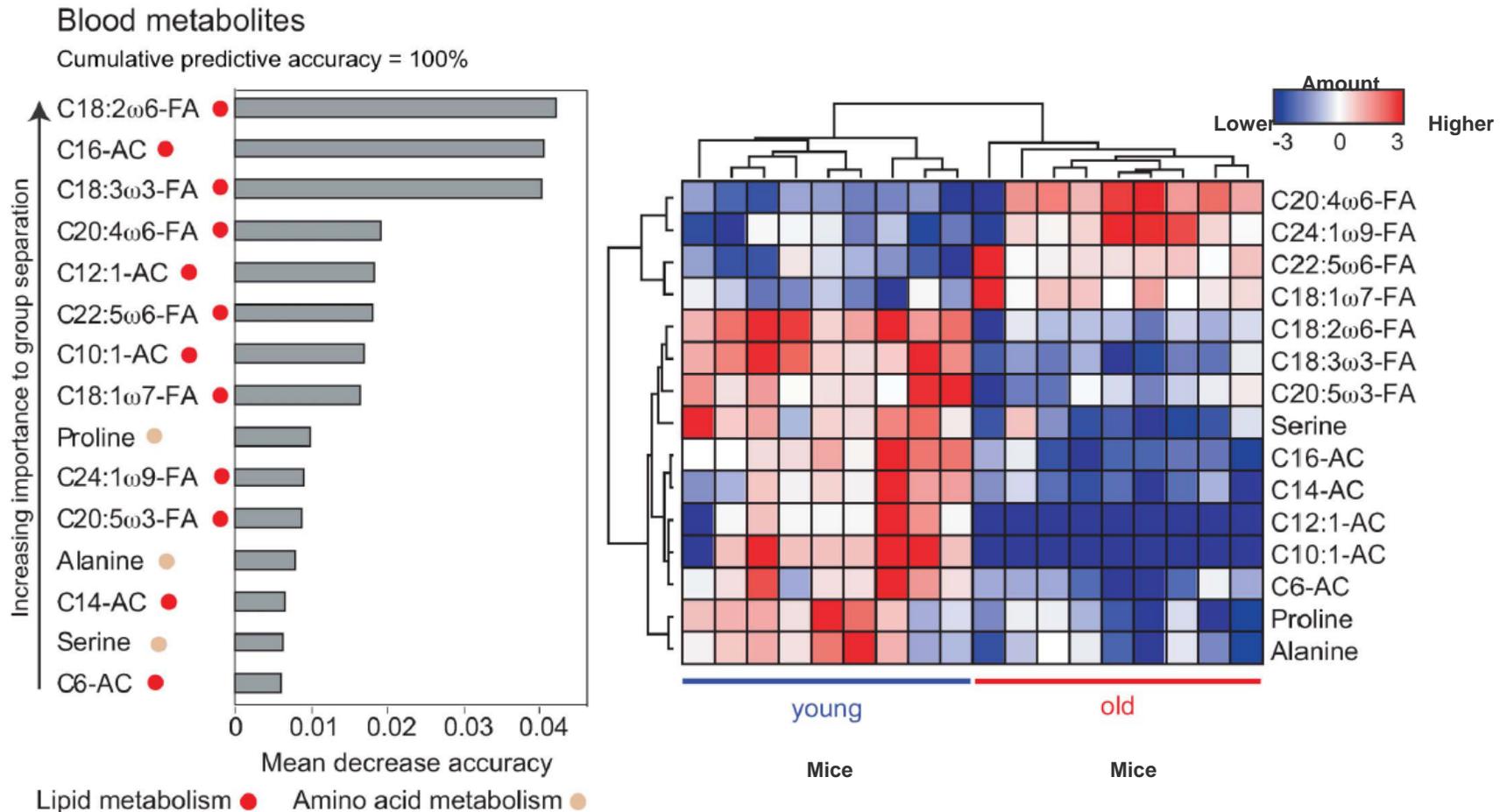


# DNA methylation is an epigenetic marker of age that is a reliable predictor of biological aging



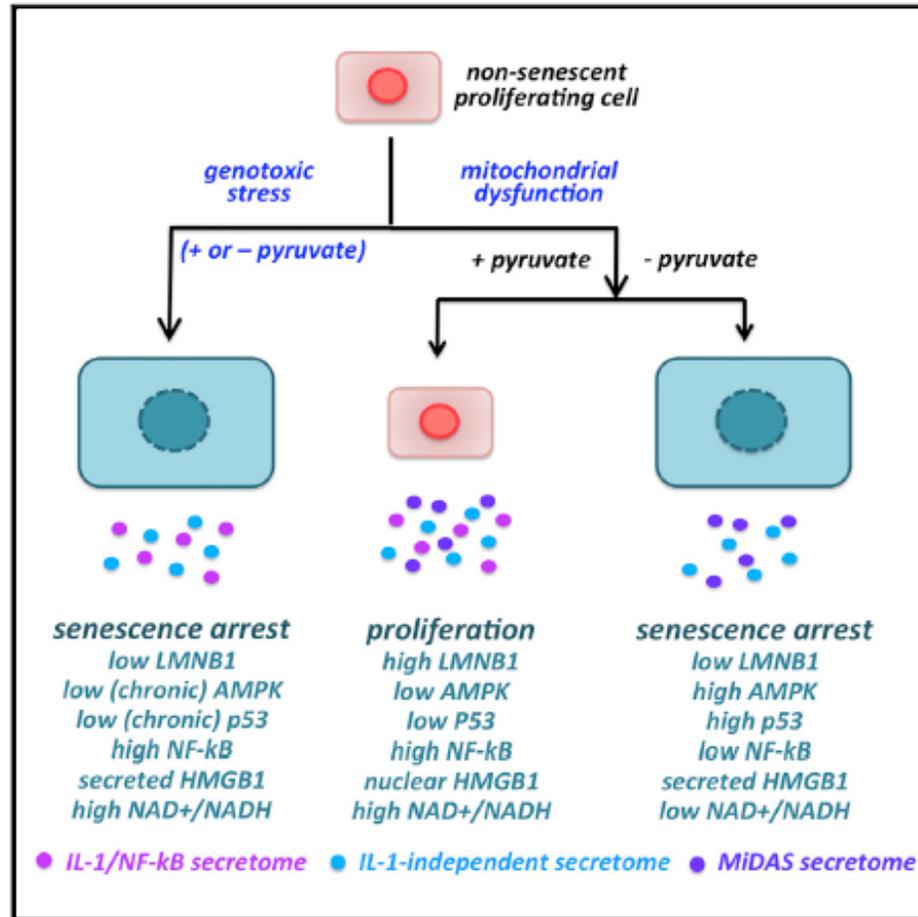


# Aging metabolome: Long-chain fatty acids as blood biomarkers of aging



Metabolite and pathway enrichment of targeted metabolomics and microarrays

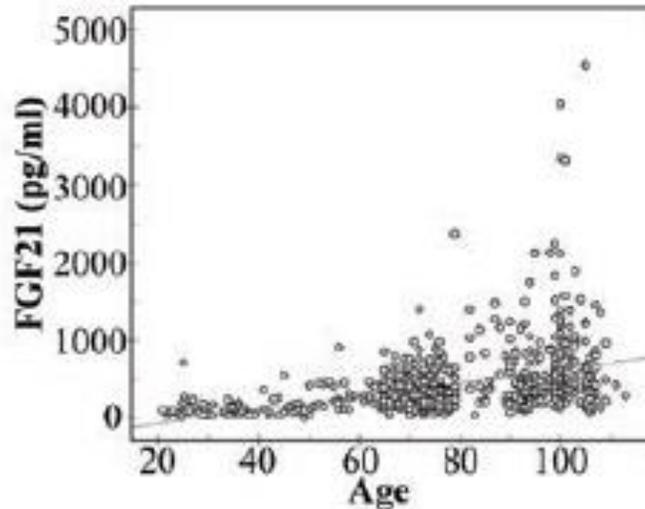
# Mitochondrial Dysfunction Induces Senescence with a Distinct Secretory Phenotype (mitSASP)



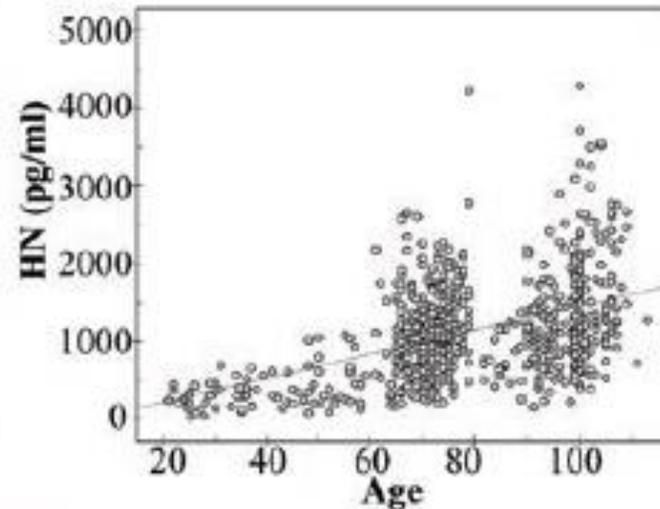
- Dysfunctional mitochondria cause cell senescence and a distinct secretory phenotype (MiDAS: Mitochondria Dysfunction Associated Senescence)
- This secretory phenotype can influence the differentiation of certain cell types
- An NAD-AMPK-p53 pathway controls the secretory and mitotic arrest phenotypes
- Mice with dysfunctional mitochondria and premature aging accumulate senescent cells

# Human aging and longevity are characterized by high levels of mitokines

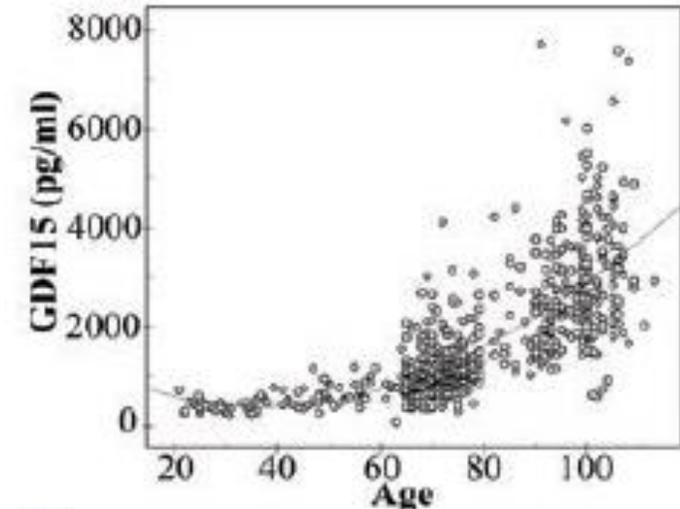
**FGF-21**



**Humanin**



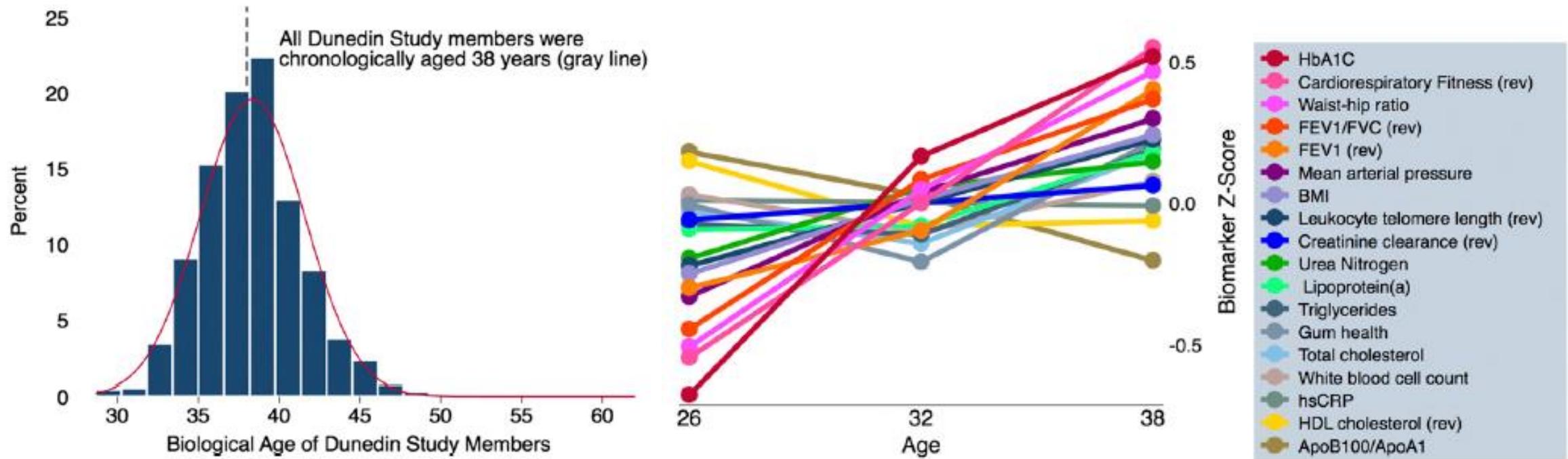
**GDF-15**



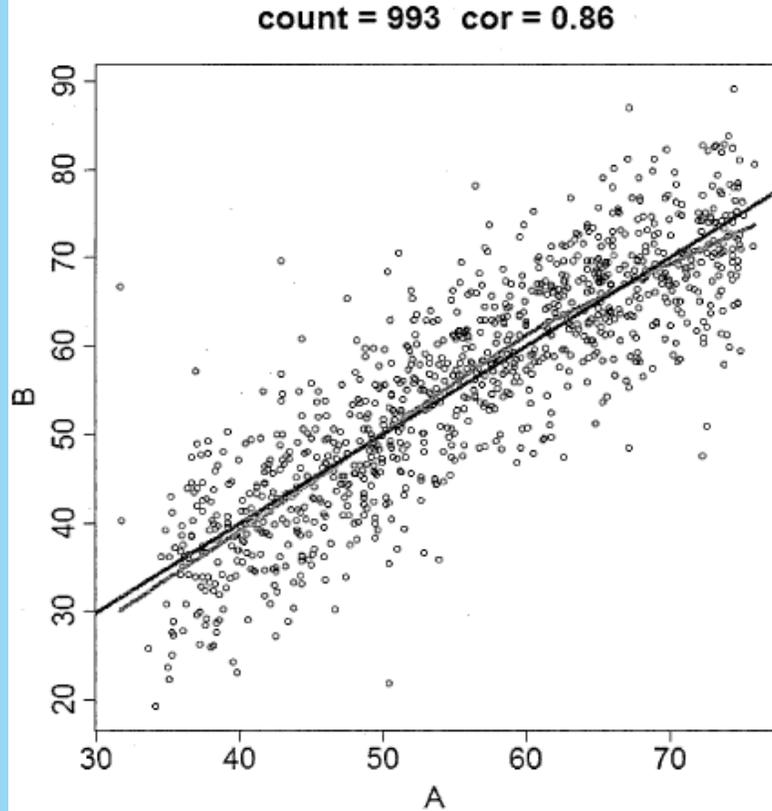
The mitokines are secreted in response to mitochondrial stress and are associated with worsened parameters (such as handgrip strength, insulin sensitivity, triglycerides), particularly in 70-year-old persons, and their levels are inversely correlated with survival in the oldest subjects.



# Quantification of biological aging in young adults



The science of healthspan extension may be focused on the wrong end of the lifespan; rather than only studying old humans, geroscience should also study the young  
 Various proposed approaches to quantifying biological aging may not measure the same aspects of the aging process.



## BioAge: Method for the determination of biological age in humans



Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

## Mechanisms of Ageing and Development

Journal homepage: [www.elsevier.com/locate/mechagedev](https://www.elsevier.com/locate/mechagedev)



### MARK-AGE biomarkers of ageing

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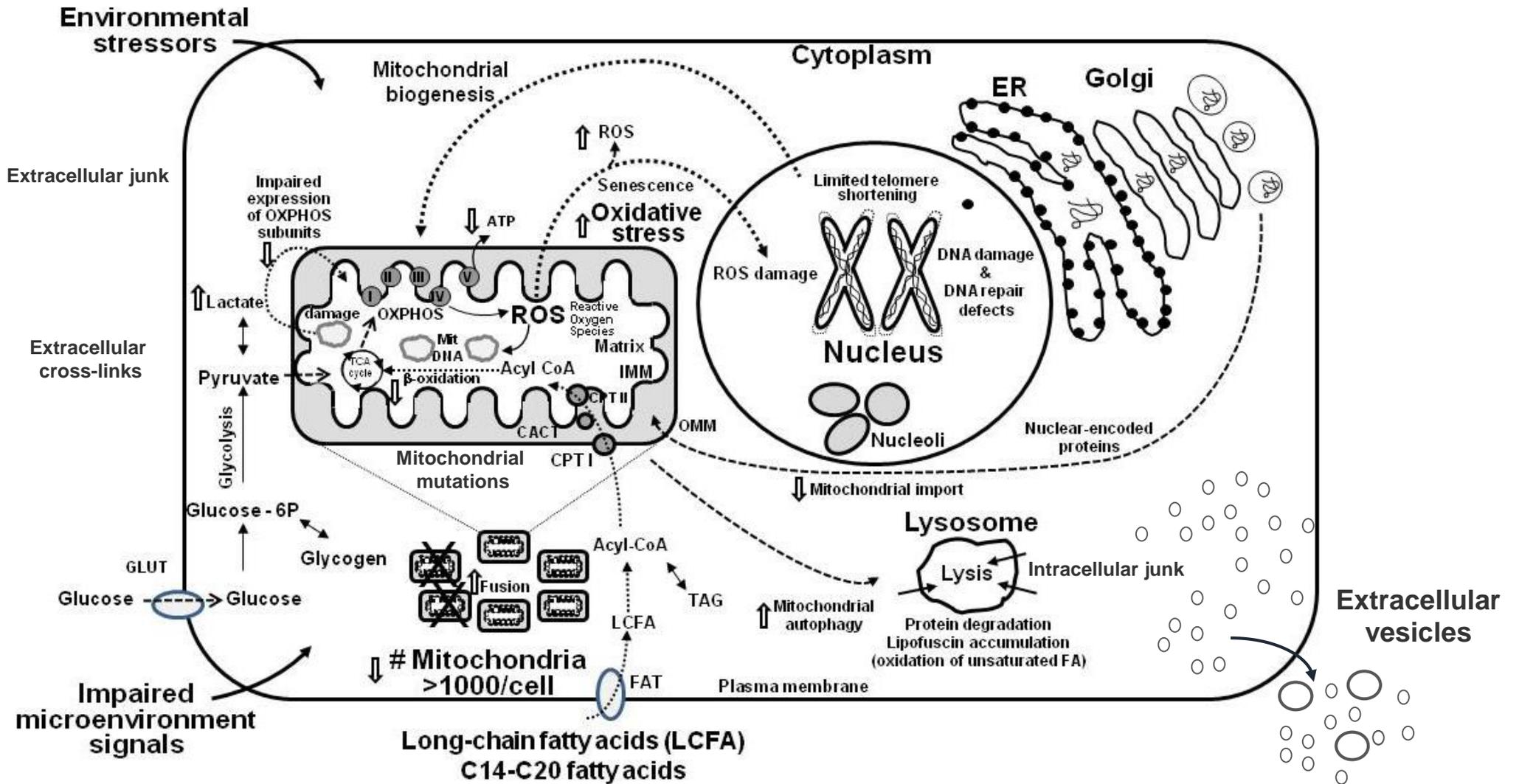
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# Causes of senescence and biomarker validation





Thank you!