The NIA Biomarker Network Annual Meeting 2024

# RNA-based Indicators of Cellular Senescence Predict Aging Health Outcomes in the Health and Retirement Study

Qiao Wu

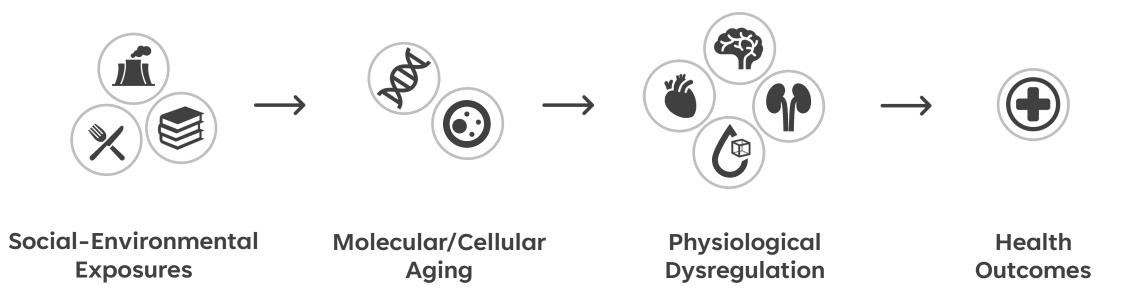
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### Acknowledgements

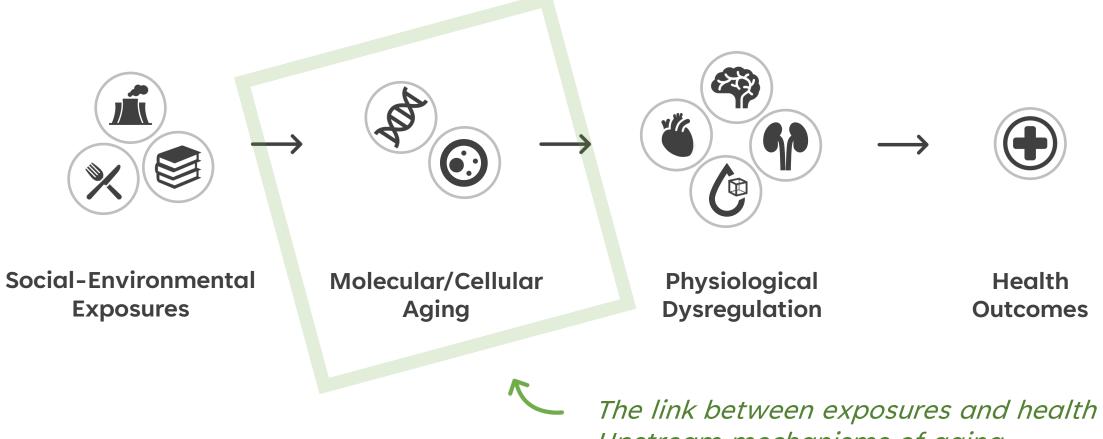
Thanks to my amazing collaborators: Jung Ki Kim, Eric Klopack, Bharat Thyagarajan, Steve Cole, Jessica Faul, and Eileen Crimmins

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#### **Age-Related Health Changes**

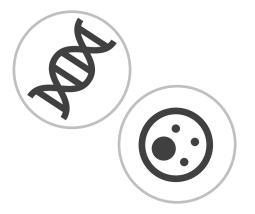


#### **Age-Related Health Changes**



Upstream mechanisms of aging

### Measuring Molecular/Cellular Aging



Molecular/Cellular Aging

#### Biological Hallmarks of Aging

- Genomic instability
- Telomere attrition
- Epigenetic alterations
- Mitochondrial dysfunction
- Cellular senescence

Etc.

(López-Otín et al. 2023)



### **Measuring Molecular/Cellular Aging**



Molecular/Cellular Aging Biological Hallmarks of Aging

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Etc.

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RNA-Sequencing-Based Transcriptomic Summary Measure

A common approach used in social and behavioral sciences



**Cellular Senescence** 

### **Cellular Senescence**

- One of the underlying mechanisms of aging
- Senescent cells accumulate with age
- Triggered by stress
- Stop multiplying
- Release pro-inflammatory signals



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2. Macromolecular

Damage (MD)

Stop multiplying

**1. Cell Cycle Arrest** (CCA)

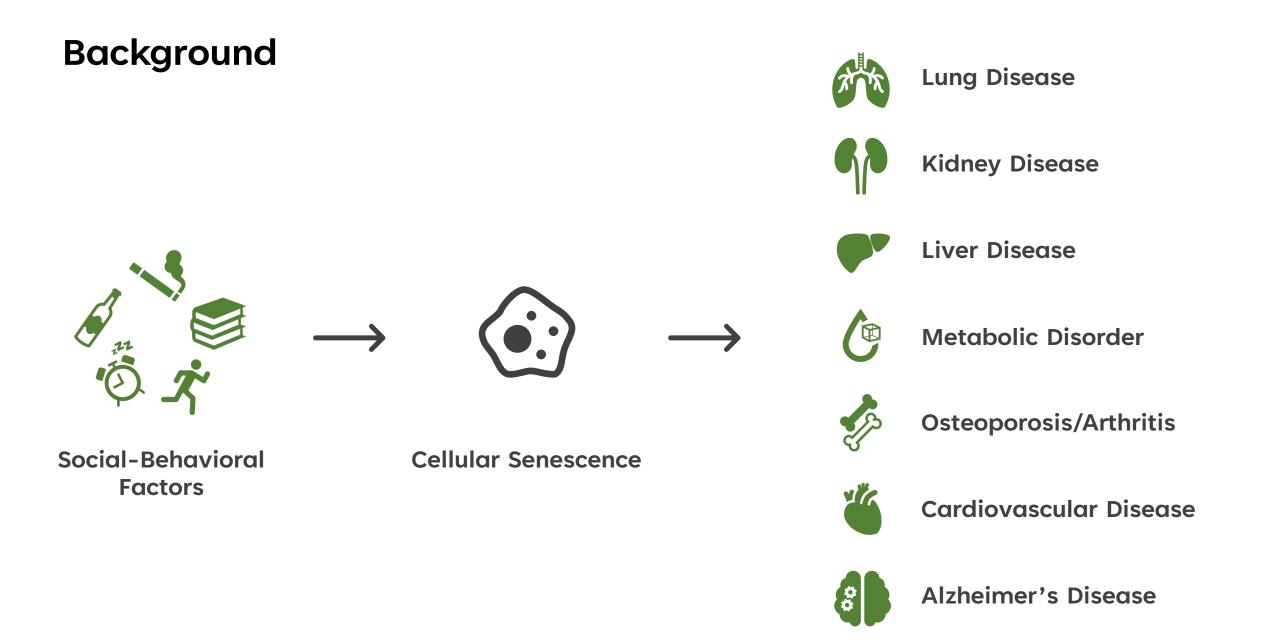


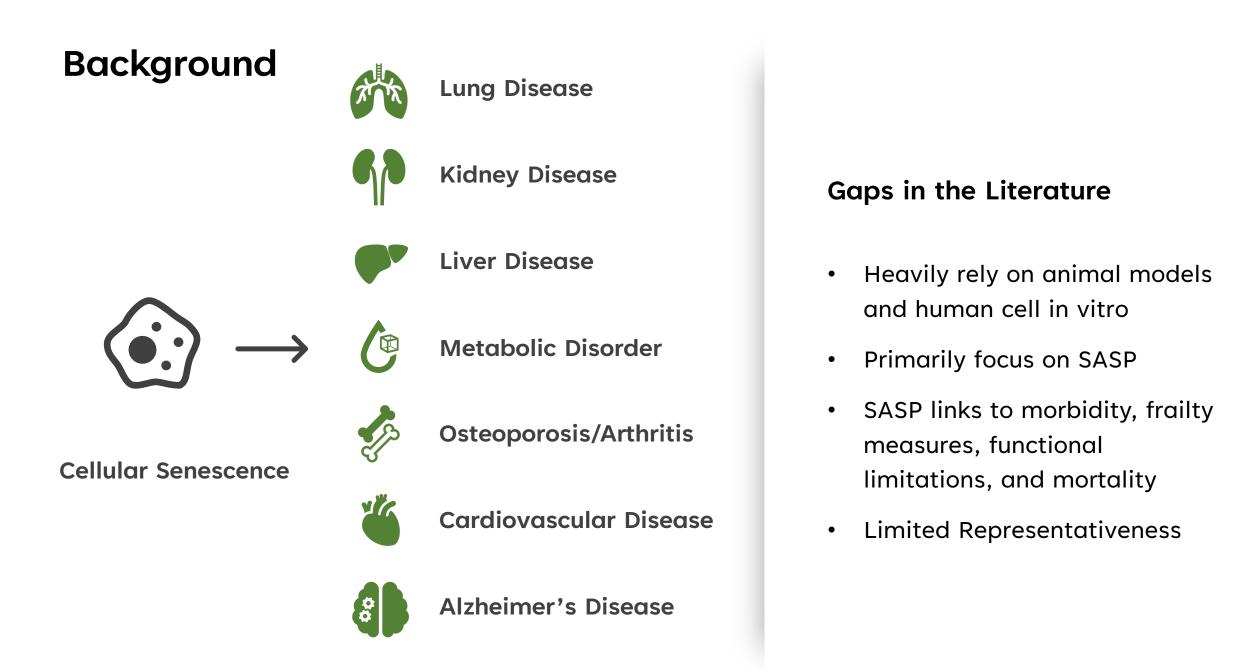
The Key Components of Cellular Senescence (Gorgoulis et al. 2019)

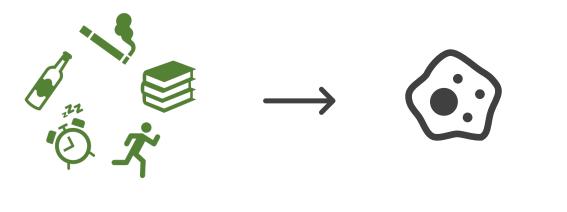
3. Senescence-Associated **Secretory Phenotype** (SASP)

Release pro-inflammatory

signals







Social-Behavioral Factors **Cellular Senescence** 

#### Gaps in the Literature

- In theory, obesity, high-fat diet, sleep deprivation, cigarette smoking, and alcohol abuse may all induce senescence.
- Very little direct evidence at population level.

#### **Research Questions**

- How do social-behavioral factors link to cellular senescence?
- How does cellular senescence measure aging?

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Social-Environmental Exposures

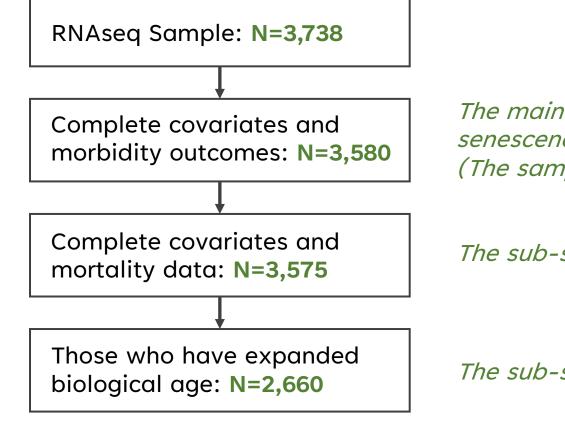
Molecular/Cellular Aging Physiological Dysregulation Health Outcomes

### **Research Questions**

- How do social-behavioral factors link to cellular senescence?
- How does cellular senescence measure aging?
  - How does cellular senescence link to **mortality** and **multimorbidity**?
  - How does cellular senescence link to physiological dysregulation?
  - How does cellular senescence link to other **molecular aging measures**?

# Methods – Data & Sample

- HRS Venous Blood Innovative Assays Sample A nationally representative sample of approximately 4,000 community-dwelling older adults.
- RNAseq data for about 3,700 HRS respondents



*The main analytical sample for the association between senescence scores and multimorbidity (The sample for epigenetic clocks is the same as this one)* 

The sub-samples for mortality analyses

The sub-sample for biological age analyses

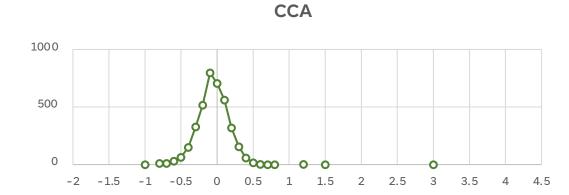
### **Methods – Cellular Senescence Measure**

#### Four RNA-Based Cellular Senescence Scores

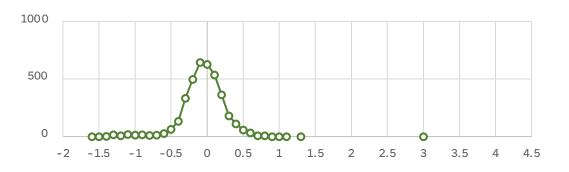
- 1. Cell Cycle Arrest Score (CCA) 22 genes
- 2. Macromolecular Damage Score (MD) 48 genes
- 3. Senescence-Associated Secretory Phenotype score (SASP) 44 genes
- 4. Senescence Summary Score 112 genes

Mean of the z-score standardized log2 transformation of the expression value of genes

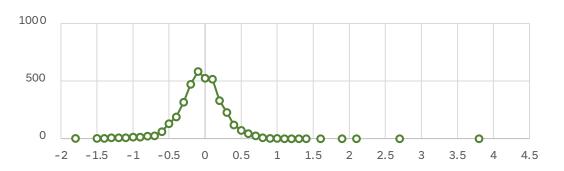
### Methods – Cellular Senescence Measure



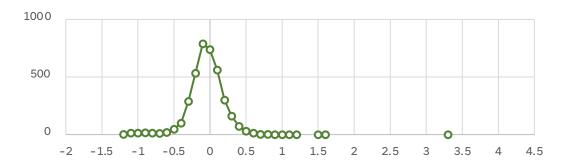
MD



SASP



Summary Score



# **Methods – Other Aging Measures**

#### **Molecular/Cellular Aging**

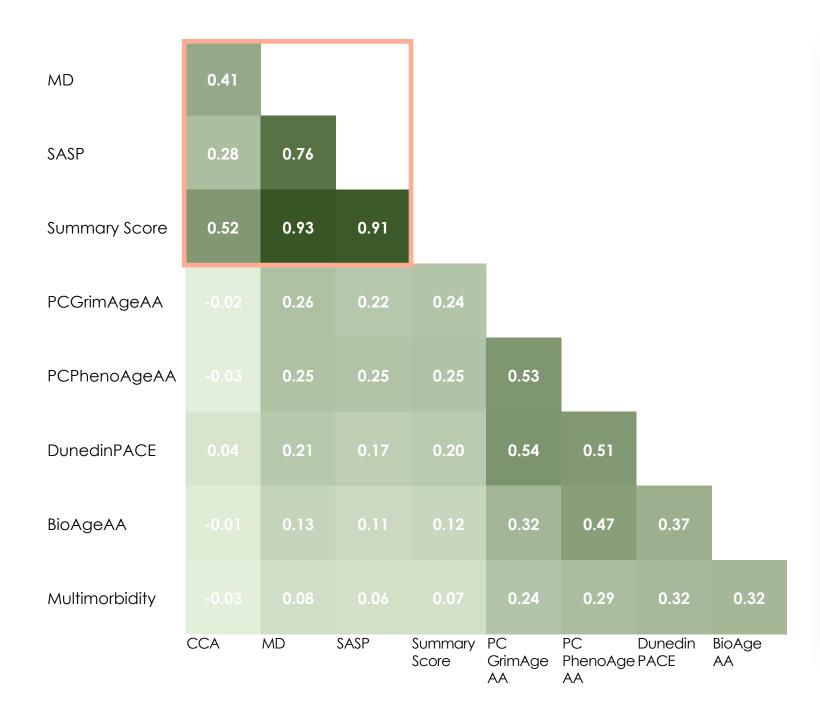
 Epigenetic Aging Measures – DNA-methylation-based measures, including age acceleration of the principal component versions of GrimAge and PhenoAge, and DunedinPACE.

#### **Physiological Dysregulation**

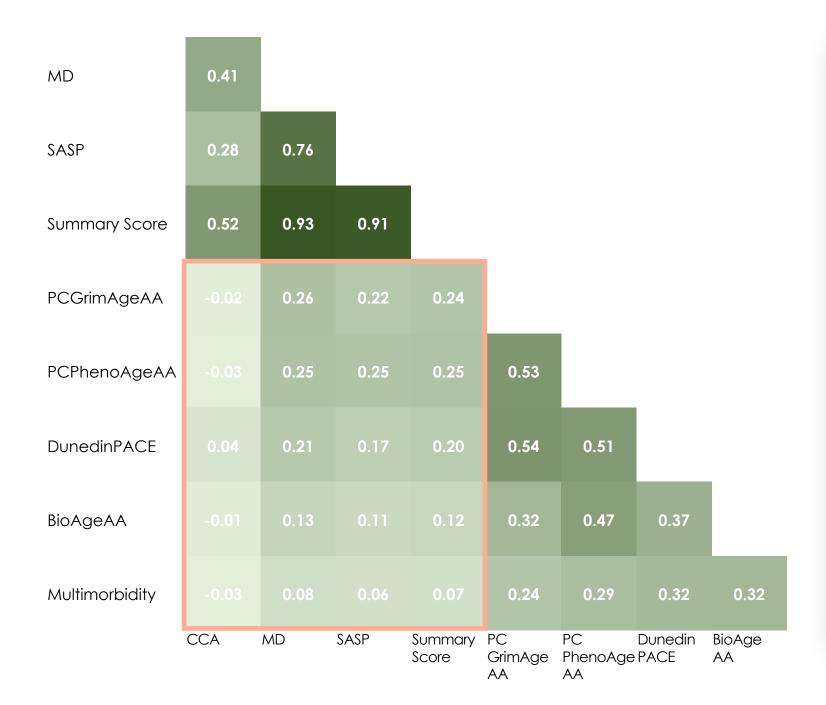
 Expanded Biological Age Acceleration (in years) – An overall measure of an individual's physiological status based on 22 biomarkers.

#### Health Outcomes

- **Multimorbidity (0-5)** The sum of the Doctor's diagnosis of cancer, diabetes, heart problems, lung disease, and stroke.
- Mortality Four-year mortality based on 2020 vital status.



- Senescence scores are correlated overall.
- The senescence summary score is mainly driven by MD and SASP.
- Correlations between senescence scores and other aging measures/outcomes are generally weak.



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### Methods – Social-Behavioral Measures

Age – Age Groups: 55-64, 65-74, 75-84, 85+

Education – Education Groups: Less than high school, high school, some college, college and higher Alcohol Consumption – Total Drinks Weekly: Days drinking per week \* number of drinks per day Smoking – Lifetime exposure to smoking: Average daily packs in a year \* years of smoking Body Mass Index (BMI) Categories – Based on measured values, and self-report is used when measured values are not available. Respondents are categorized into normal (BMI<25), overweight (25<=BMI<30), obesity I (30<=BMI<35), and obesity II (BMI>=35).

**Insomnia Symptoms** – A combined measure of sleep disturbance with non-restorative sleep

**Technical Controls** – Batch/Plate and cell type

#### **Sample Characteristics**

	Mean (SD) / Proportion		Mean (SD) / Proportion
	N=3,580		N=3,580
Senescence Scores		Total Drinks Weekly	2.9 (6.3)
Summary Score	0.0 (0.2)	Cumulative Packs Smoked	13.1 (20.7)
CCA Score	0.0 (0.2)	BMI	29.4 (6.6)
MD Score	0.0 (0.3)	Normal	23.8
SASP Score	0.0 (0.3)	Overweight	37.4
Age	68.6 (9.2)	– Obesity I	22.7
Aged 55-64	40.5	Obesity II	16.2
Aged 65-74	35.2	Insomnia Symptoms	20.4
Aged 75-84	17.2	4-Year Mortality (N=3,575)	9.8
Aged 85+	7.1	Multimorbidity	0.8 (1.0)
Female	54.4	Diabetes	25.5
Race Ethnicity		Cancer	14.6
Non-Hispanic White	77.5	Lung Disease	11.0
Non-Hispanic Black	10.2	Heart Problems	25.0
Hispanic	8.9	Stroke	8.1
Non-Hispanic Other	3.3	Expanded BioAge (N=2,660)	68.2 (11.7)
Education		Expanded BioAge AA (N=2,660)	0.0 (8.1)
Years of Education	13.3 (3.0)	PC GrimAge	77.3 (8.0)
Less than High School	14.0	PC PhenoAge	66.0 (10.6)
High School	29.9	DunedinPACE	1.0 (0.1)
Some College	25.9	PC GrimAge AA	0.0 (4.0)
College and Higher	30.2	PC PhenoAge AA	0.0 (6.5)

- A representative sample of older Americans.
- Includes people who regularly consume alcohol and smoke cigarettes.
- On average overweight.
- More than one-third are obese.
- About one-fifth have sleep problems.
- Around 10% died within 4 years. Many have chronic conditions.

#### Some social and behavioral factors are significantly associated with RNA scores

N=3,580	ССА	MD	SASP	Sum Score
Age: Ref - Aged 55-64			07 (01	
• •	0.04	0.01	0.02*	0.01
Aged 65-74	-0.04	0.01	0.03*	0.01
Aged 75-84	-0.06***	0.04**	0.07***	0.04***
Aged 85+	-0.07***	0.01	0.04**	0.01
Female	0.19***	0.05***	0.12***	0.12***
RE: Ref - Non-Hispanic White				
Non-Hispanic Black	0.12***	0.06***	0.03*	0.07***
Hispanic	-0.02	0.01	0.01	0.00
Non-Hispanic Other	0.00	0.01	0.00	0.01
Education: Ref - Less than High School				
High School	-0.03	-0.01	0.02	0.00
Some College	-0.01	-0.02	0.00	-0.01
College and Higher	-0.02	-0.06**	-0.01	-0.04*
BMI: Ref - Normal				
Overweight	0.01	0.03*	0.01	0.02
Obese I	0.01	0.06***	0.01	0.04**
Obese II	0.03	0.08***	0.06***	0.08***
Cumulative Packs Smoked	0.03	0.02	0.00	0.02
Total Drinks Weekly	0.03	-0.01	0.00	0.00
Insomnia Symptoms	0.01	0.02	0.00	0.01
Adjusted R2	0.22	0.66	0.55	0.60

\* p<0.05, \*\* p<0.01, \*\*\* p<0.001

Older ages Female sex

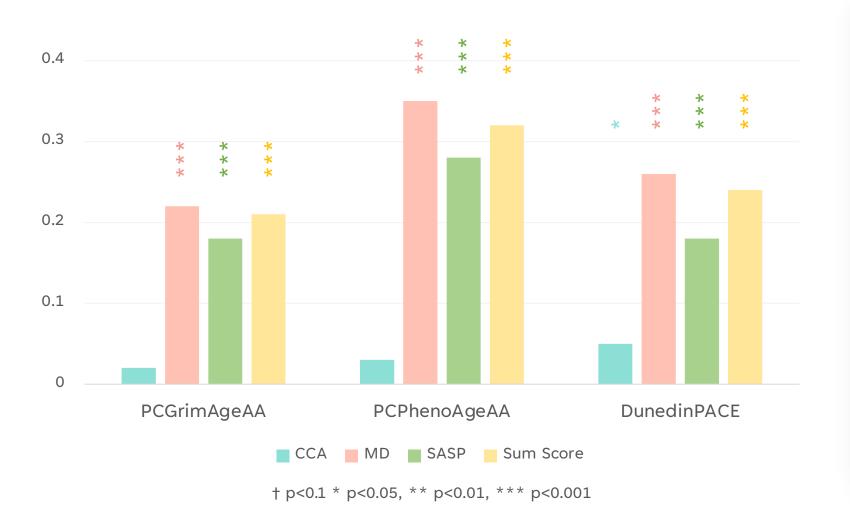
Non-Hispanic Blacks (Ref: Non-Hispanic Whites)

College and Higher (Ref: Less than high School)

Higher BMI Groups (Ref: Normal BMI)



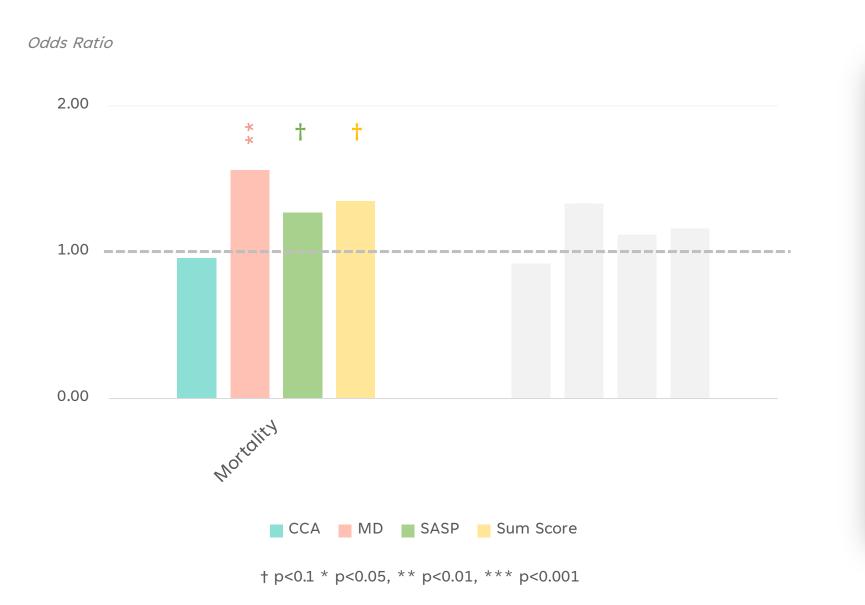
#### **Overall, our cellular senescence RNA scores are significantly associated with** *other upstream biological mechanisms - three epigenetic aging measures*



After controlling for covariates

MD, SASP, and the summary score are all significantly associated with the epigenetic measures. CCA is only associated with DunedinPACE.

#### The Macromolecular Damage score is significantly associated with *Four-Year Mortality*



Only MD is significantly associated with 4-yr mortality.

#### The Macromolecular Damage score is significantly associated with *Four-Year Mortality*



After controlling for PC GrimAge acceleration, the size of the coefficient reduced, and was only marginally significant.

# Overall, our cellular senescence RNA scores are significantly associated wit

multimorbidity and physiological dysregulation, with and without adjusted for epigenetic aging



All RNA scores are significantly associated with multimorbidity and biological age acceleration, except for the CCA score.

The associations remain significant after including the epigenetic aging measure (PC GrimAge AA) in the models.

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All RNA scores are significantly associated with multimorbidity and biological age acceleration, except for the CCA score.

The associations remain significant after including the epigenetic aging measure (PC GrimAge AA) in the models.

# Conclusion

- Social & behavioral factors: Older people, women, non-Hispanic Blacks, and those with high BMI have a higher level of cellular senescence. High education level (high SES) seems to be a protective factor.
- Other upstream aging measures: Our cellular senescence RNA scores are significantly associated with epigenetic age acceleration.
- Downstream aging measures: Cellular senescence summary score links to physiological dysregulation and multimorbidity, but not 4-year mortality, and the associations are driven by the MD and SASP scores, not the CCA score.
- Cellular senescence RNA scores capture multiple dimensions of aging in a useful way and add to our understanding of aging-related physiological changes and diseases.

# Thanks!

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