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# Allele-specific expression may contribute to healthy aging, disease progression, and treatment outcomes

CanPath Webinar

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University of Toronto

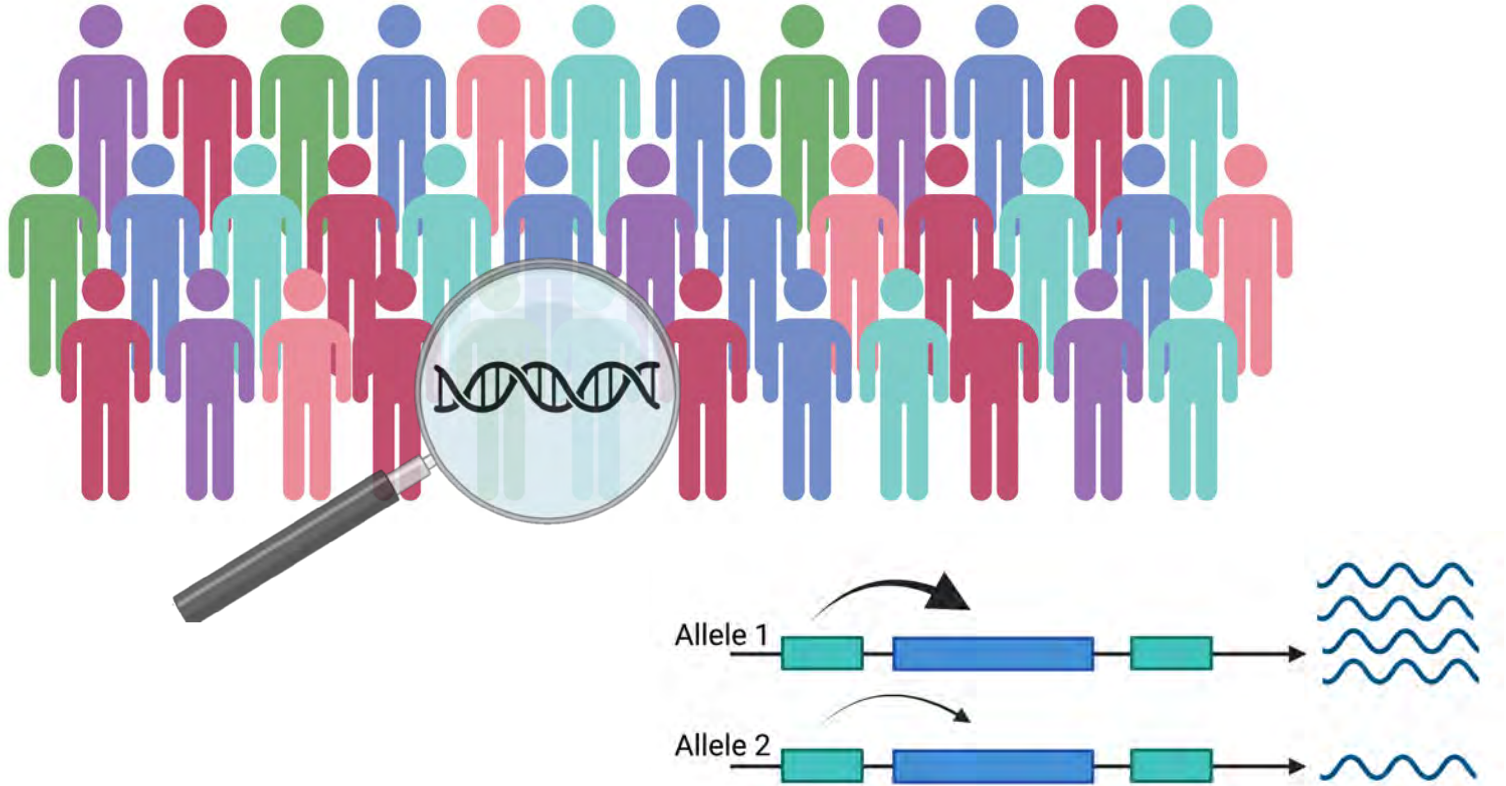
Ontario Institute for Cancer Research



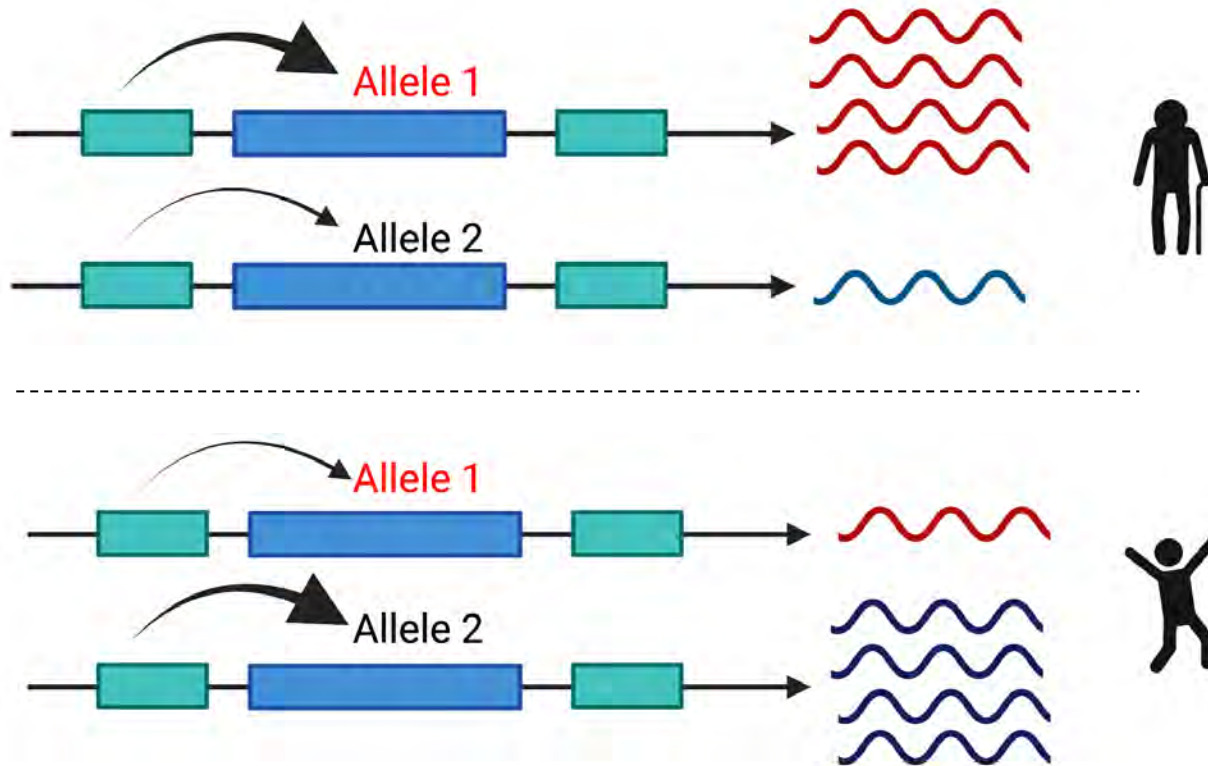
**AWADALLA LAB**

Pioneering Genomics for Precision Health.

# Why do individuals with the same genotype display highly variable phenotypes?



# Allele-specific approaches are used to investigate gene regulation

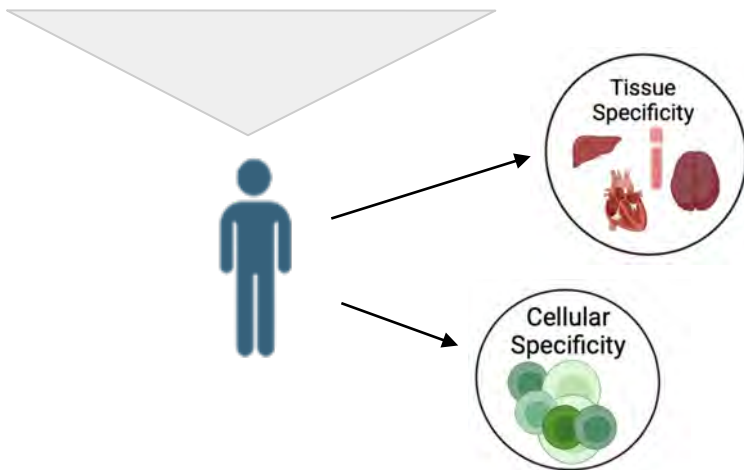


# Genetic and epigenetic factors influencing population variability of allele-specific expression

Inter-population variability



Inter-individual variability

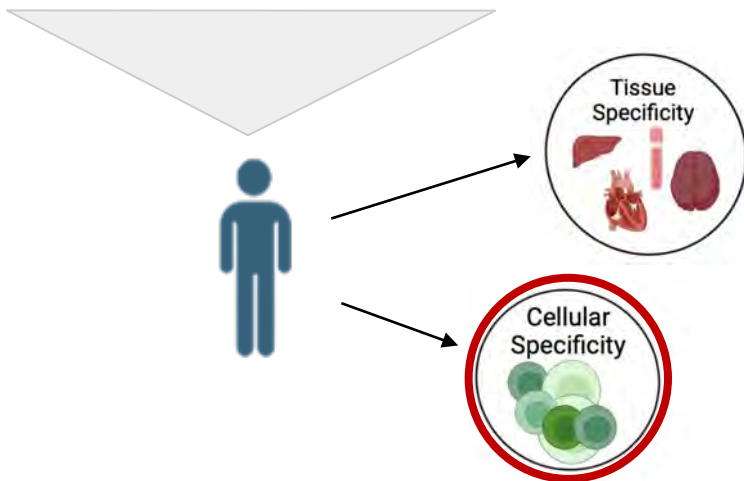


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Inter-population variability



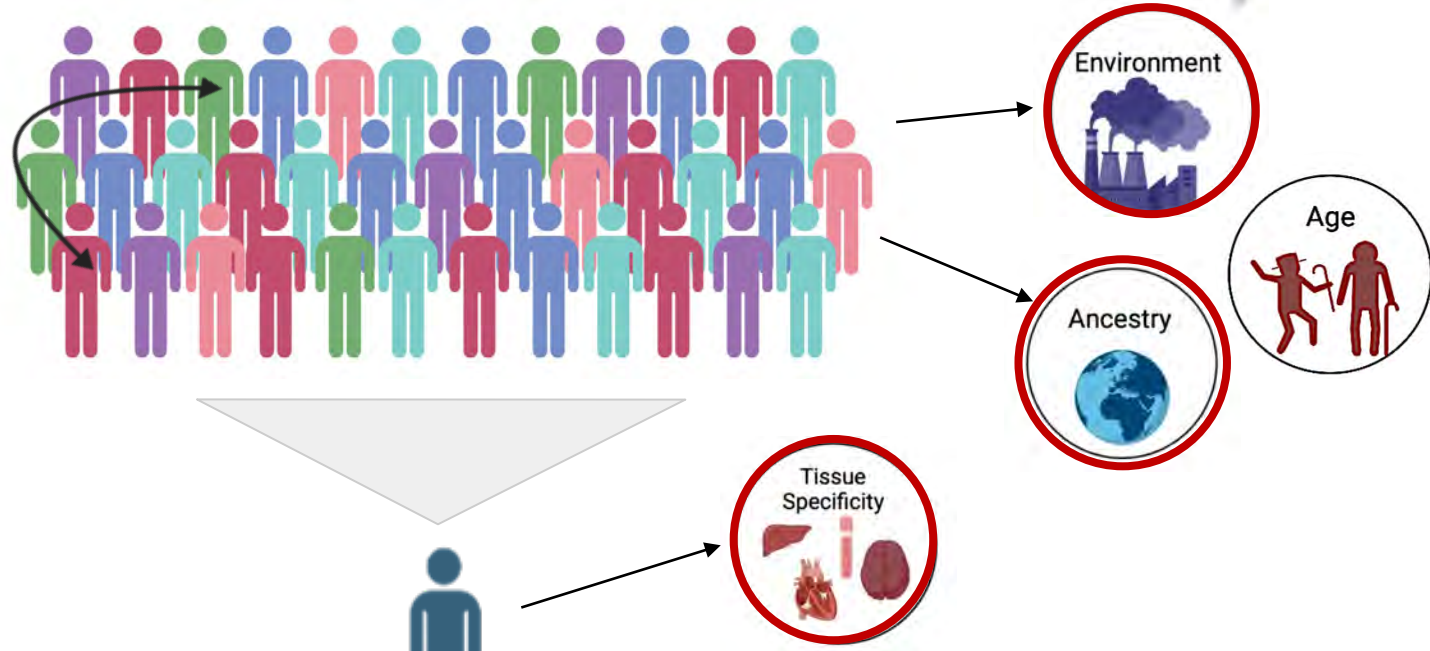
Inter-individual variability



# Genetic and epigenetic factors influencing population variability of allele-specific expression

Inter-population variability

Inter-individual variability



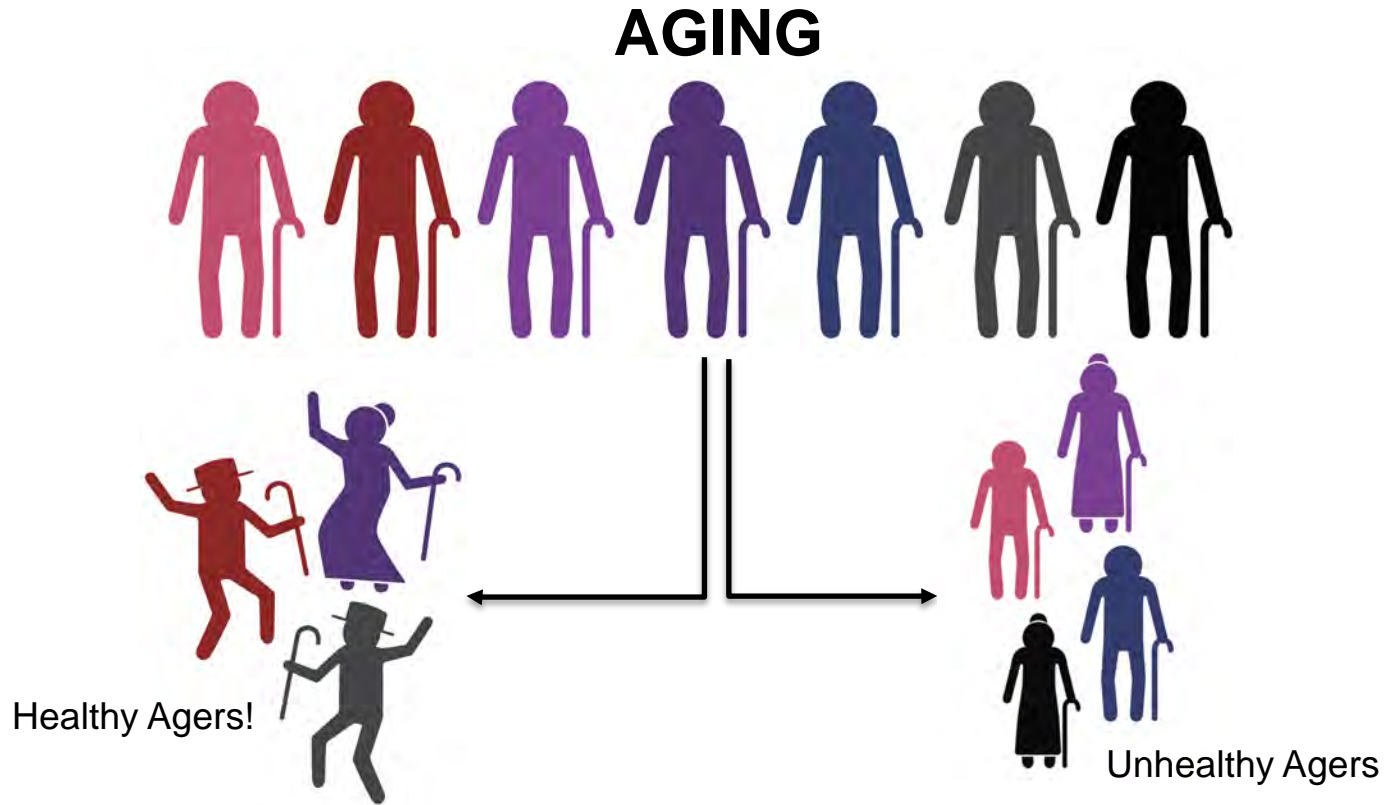
RESEARCH ARTICLE HUMAN GENETICS

**Recombination affects allele-specific expression of deleterious variants in human populations**

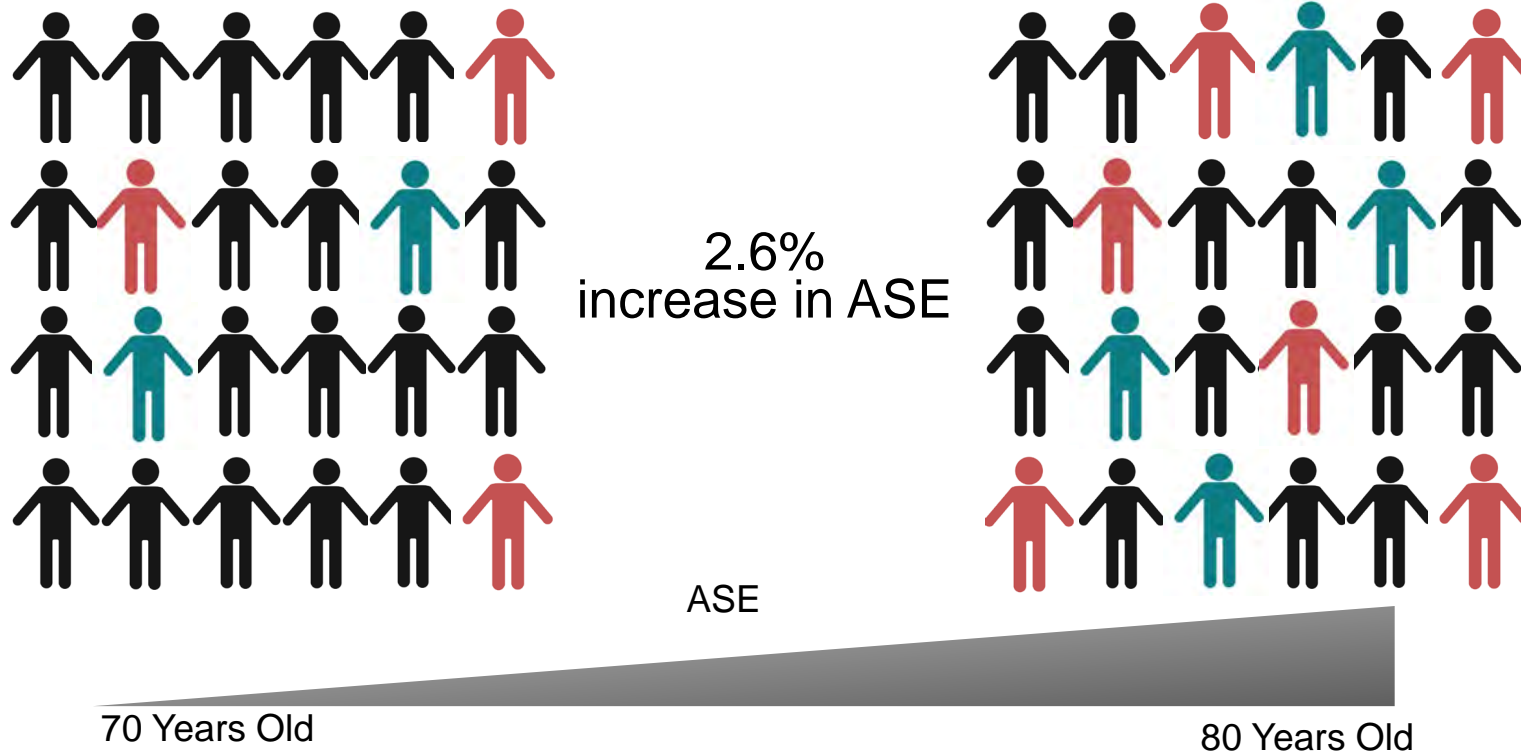
MICHELLE P. HARWOOD, ISABEL ALVES, HILARY EDGINGTON, MAWUSSE AGGRESTI, [...] AND PHILIP AWADALLA

+4 authors [Authors Info & Affiliations](#)

Why do individuals with the same genotype display highly variable phenotypes?



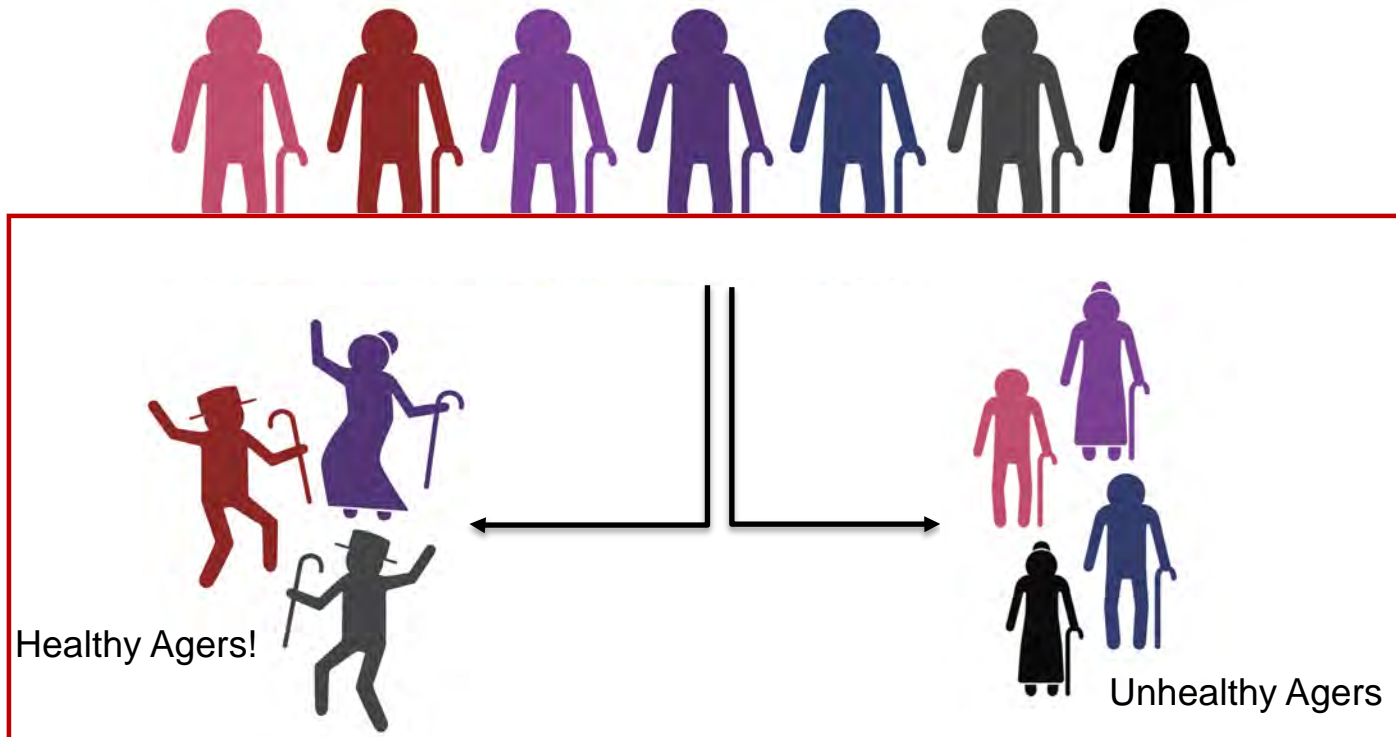
# ASE increases with age



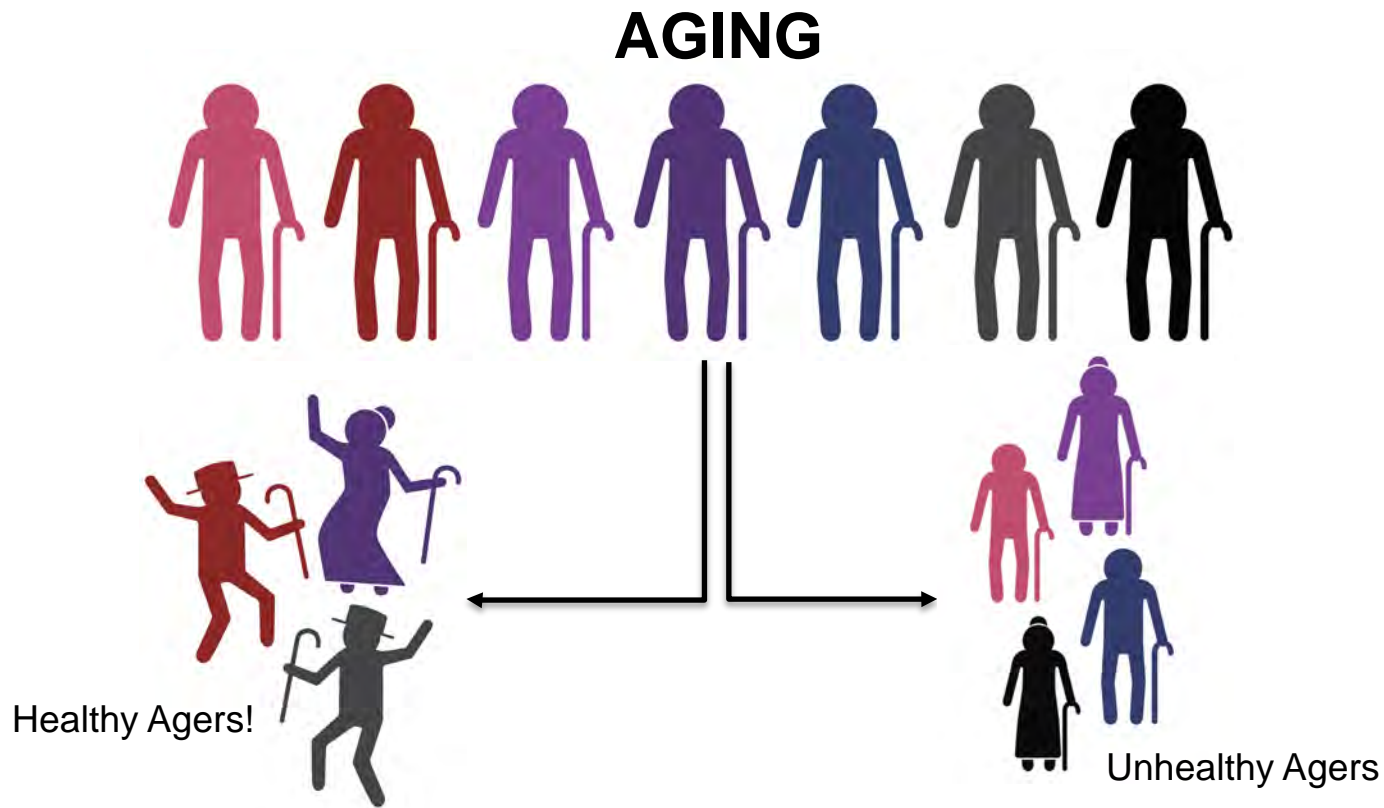


It remains unknown how increases in ASE impact aging processes

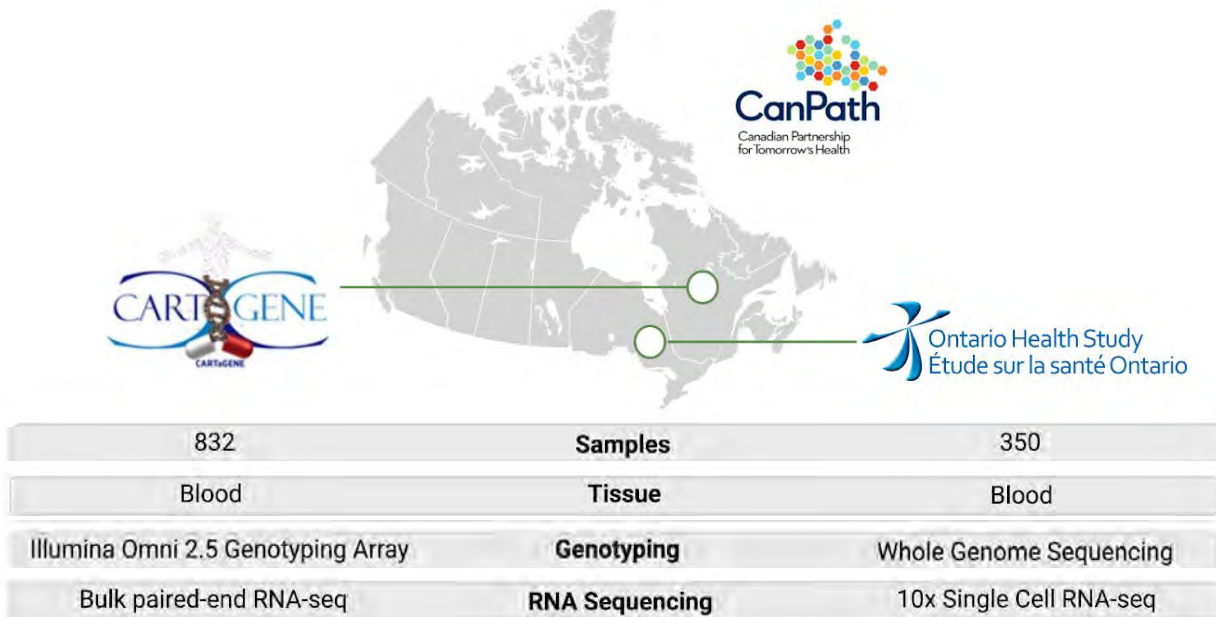
# AGING



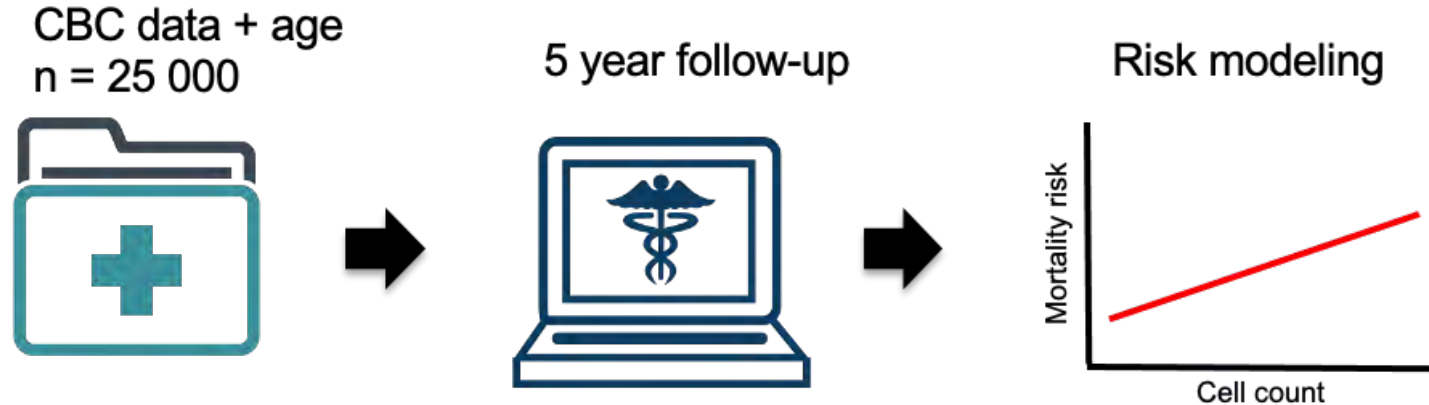
# Does ASE contribute to phenotypic variation observed during aging?



# Using population cohorts to investigate ASE



# Intermountain risk score predicts 5-year mortality

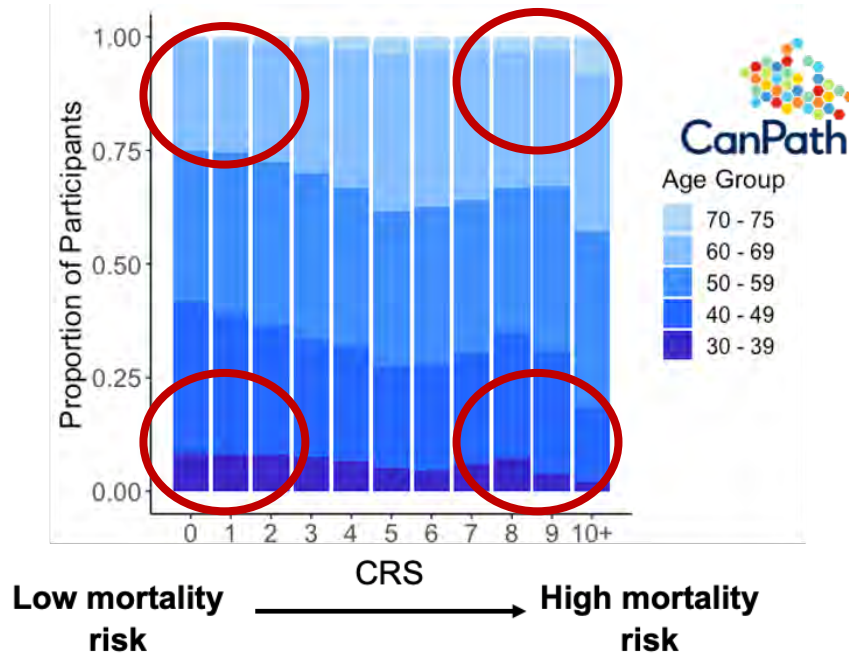


Low IRS = low mortality risk =  
healthy blood

Horne et al. (2009) Am J Med

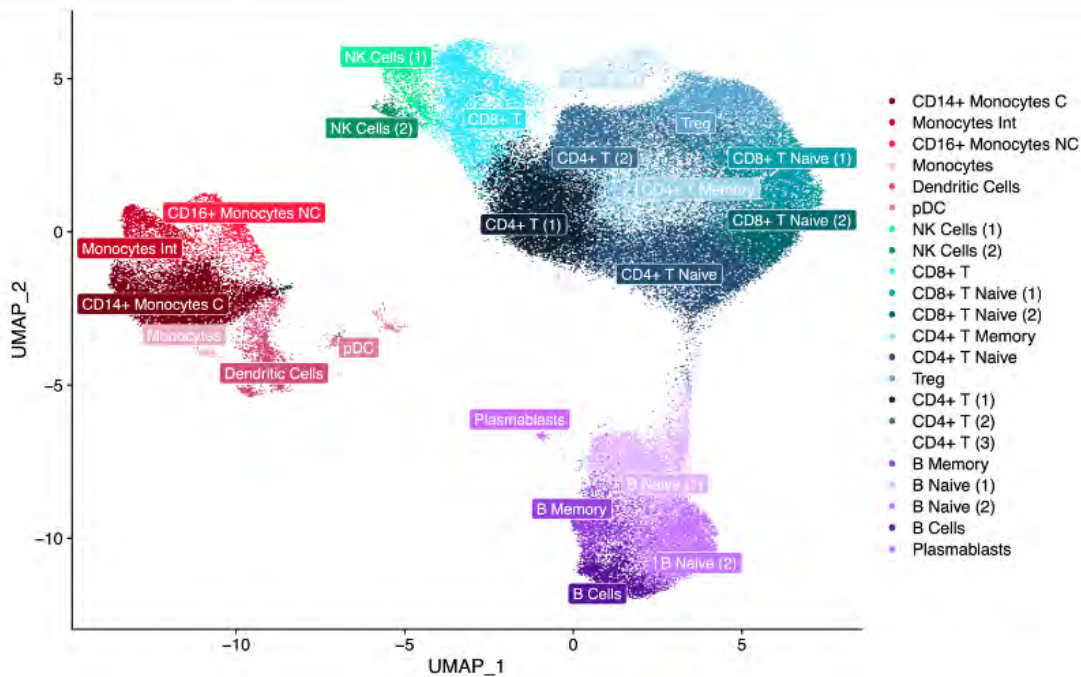
Dr. Elyssa Bader <sup>12</sup>

# OHS participant selection



- OHS participants used extreme sampling approach with respect to risk score and age
  - no self-reported disease

# OHS single-cell transcriptomics

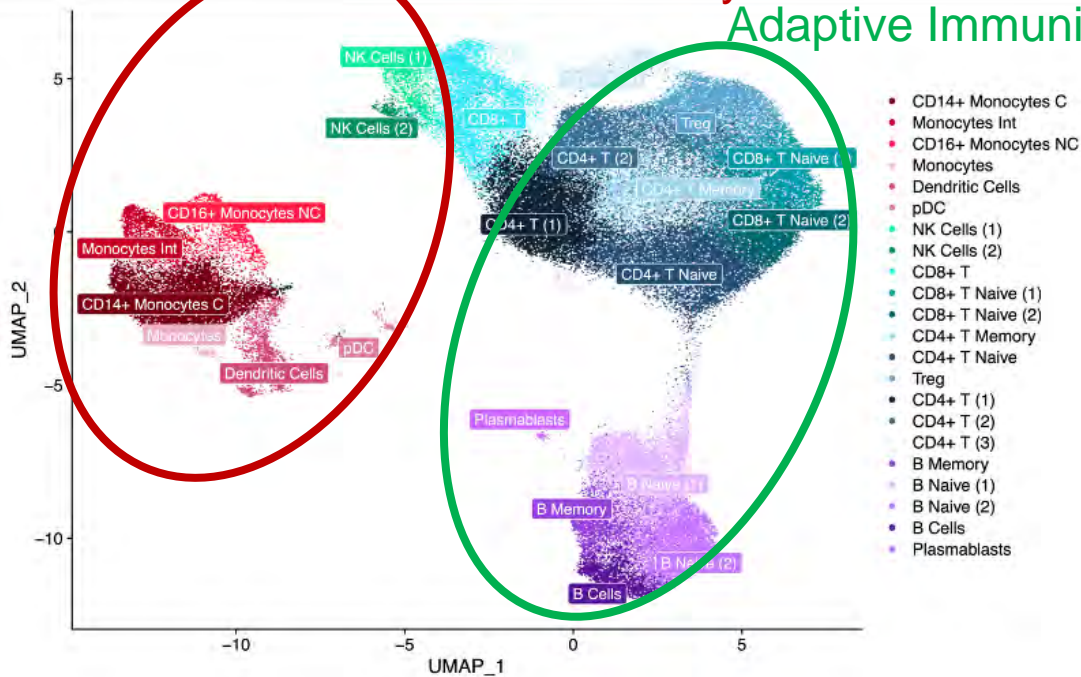


- OHS participants used extreme sampling approach with respect to risk score and age
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- 22 populations of blood cells identified from single-cell gene expression data

# OHS single-cell transcriptomics

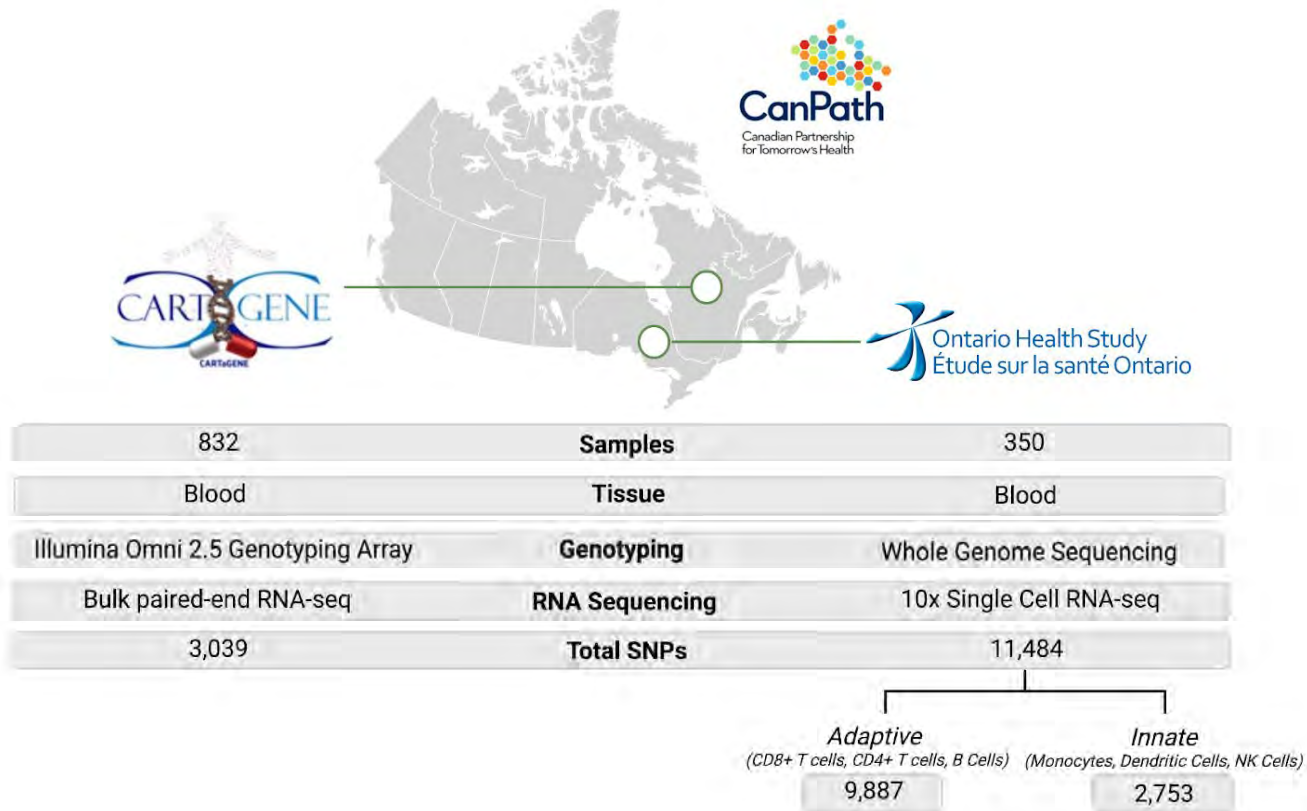
Innate Immunity

Adaptive Immunity



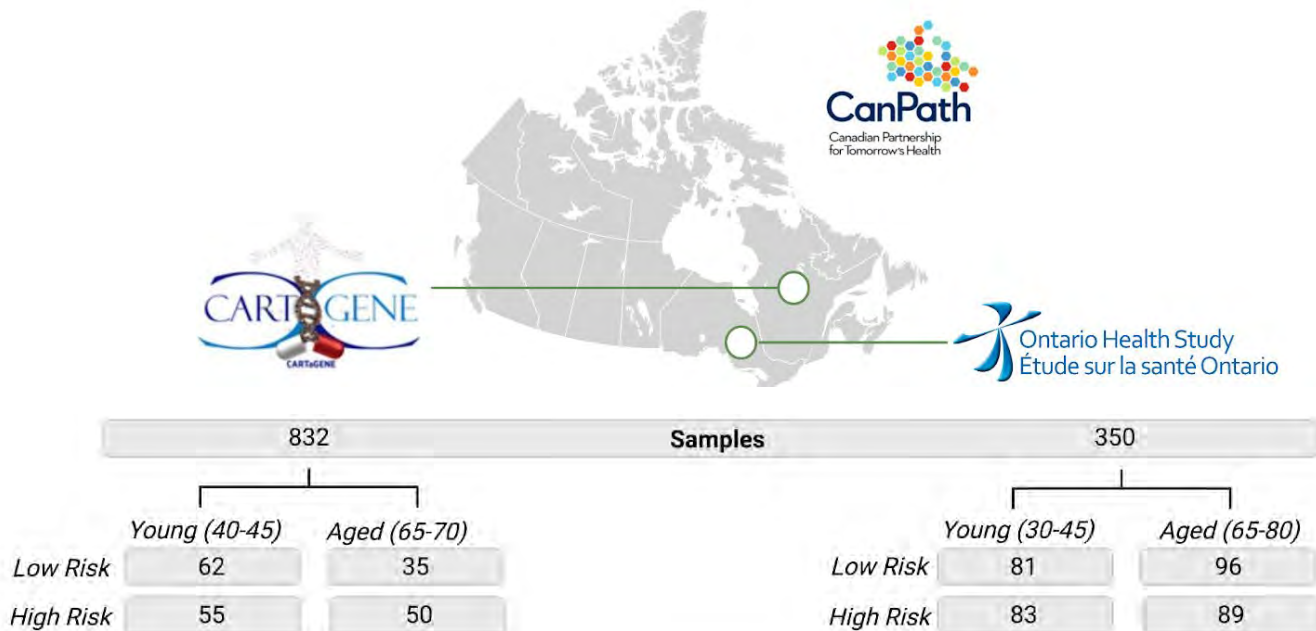
- OHS participants used extreme sampling approach with respect to risk score and age
  - no self-reported disease
- 22 populations of blood cells identified from single-cell gene expression data
- For ASE analyses, grouped cells based on adaptive vs innate immunity to improve detection at lower read depth

# Using population cohorts to investigate ASE





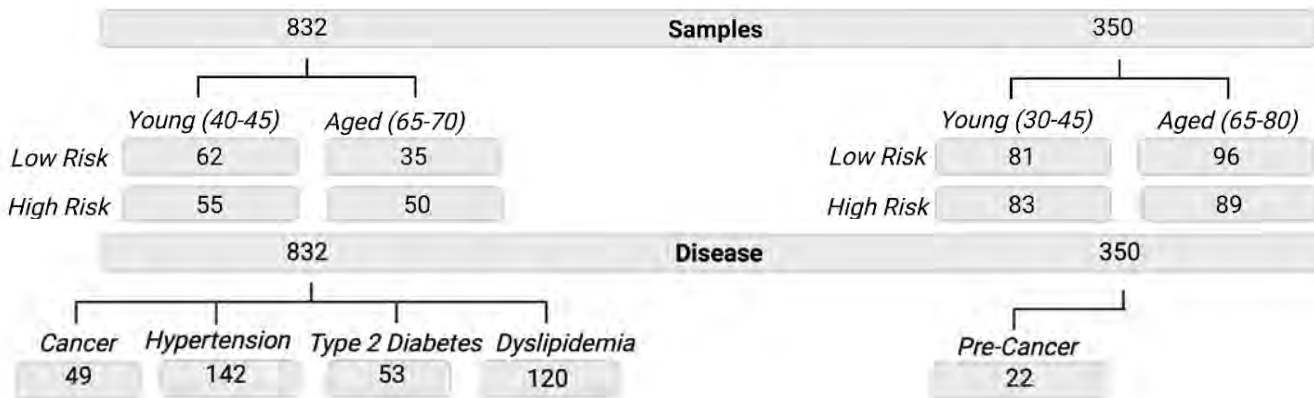
# Using population cohorts to investigate ASE



Modified the Intermountain Risk Score (Horne et al 2009) to exclude age

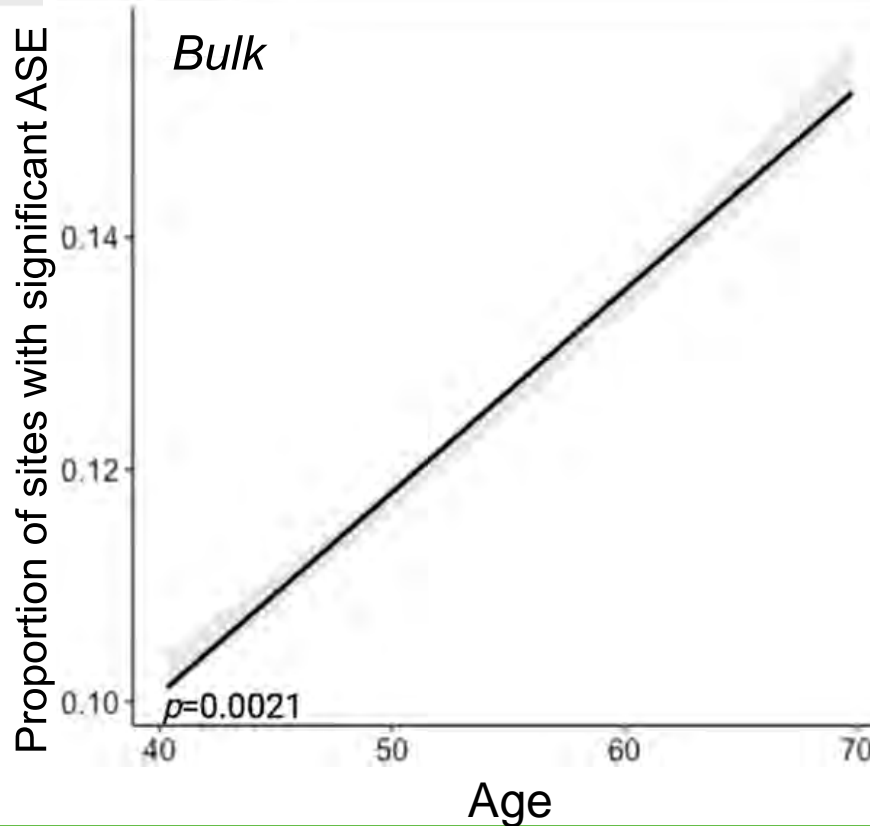
- Uses complete blood count variables that is predictive of mortality

# Using population cohorts to investigate ASE



# Aged individuals have larger proportion of ASE

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$$\frac{\# \text{ significant sites}}{\# \text{ heterozygote sites}}$$


- Confirmed that ASE **increases with age** (Balliu et al. 2019)

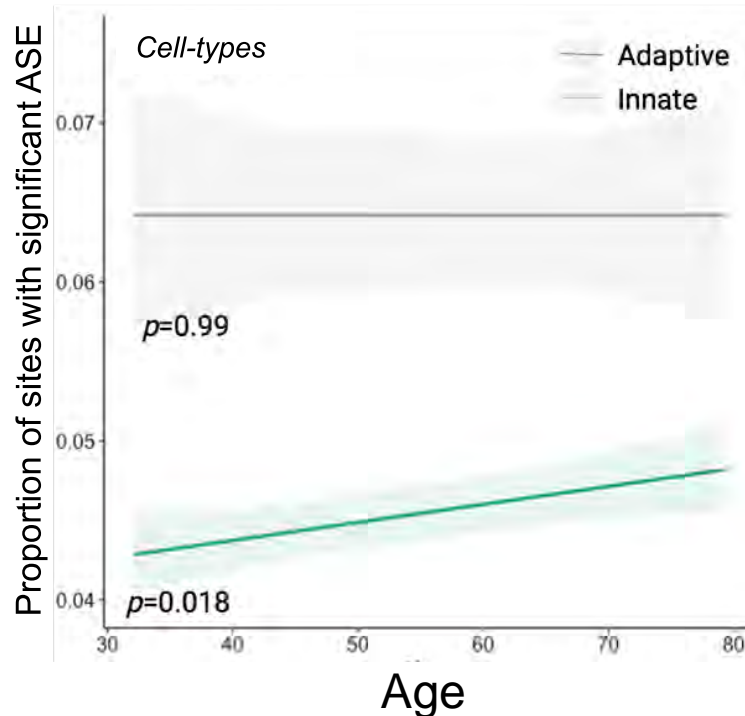
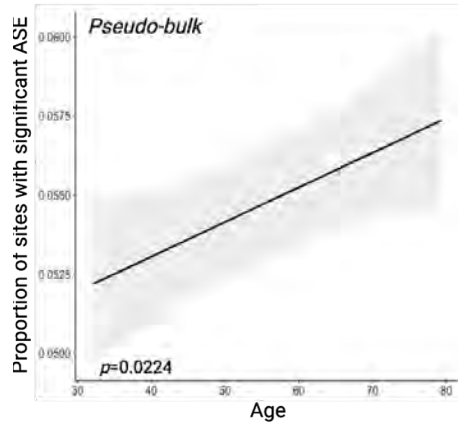
Binomial regression:

Proportion ASE ~ Age <sup>19</sup>

Collaborate. Translate. Change lives.

# Aged individuals have larger proportion of ASE

OHS



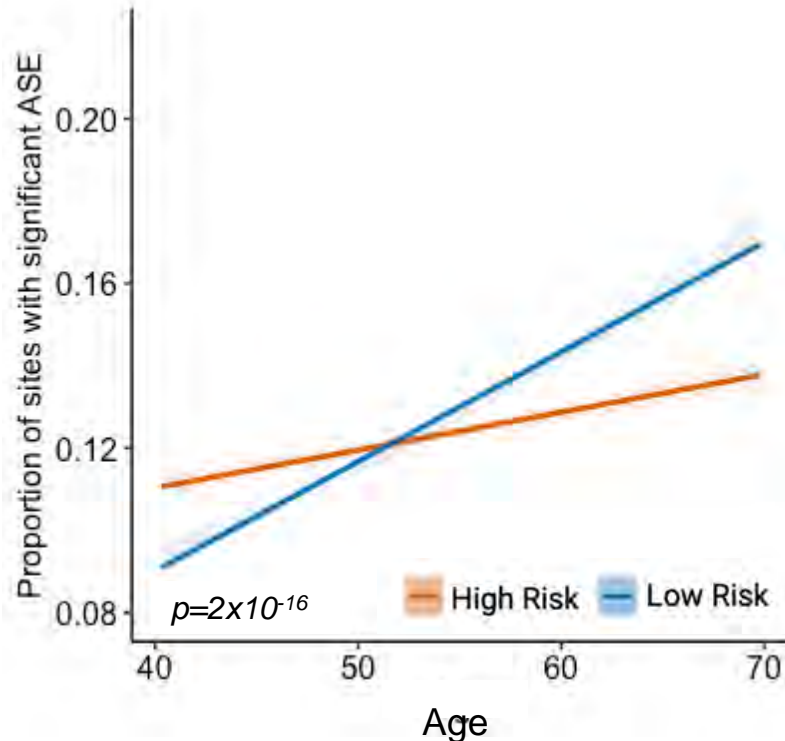
- Confirmed that ASE **increases with age** (Balliu et al. 2019)
- Replicated in OHS pseudo-bulk and **adaptive** immune cells

Binomial regression:

Proportion ASE ~ Age <sup>20</sup>

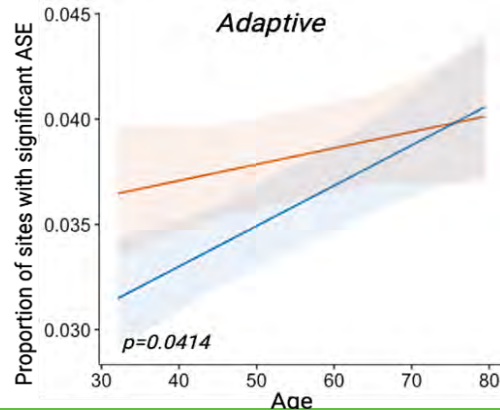
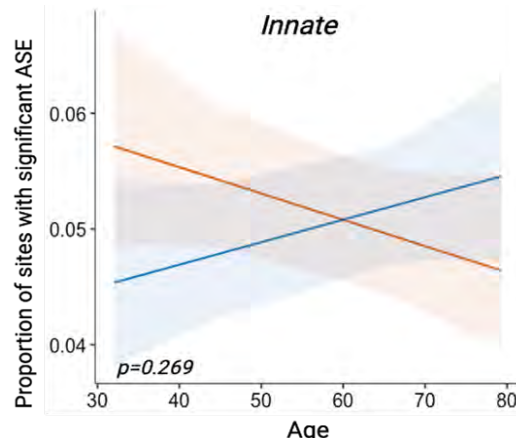
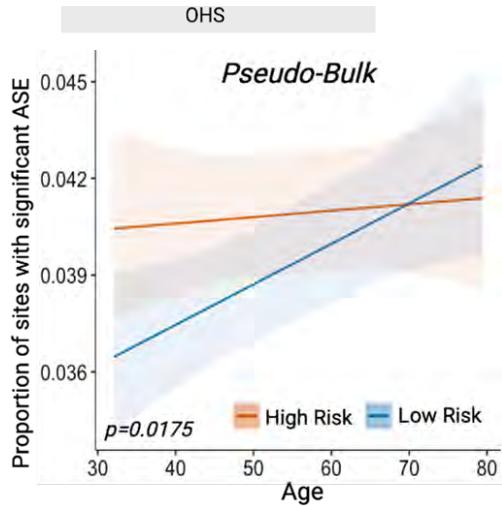
# Increased proportion of ASE in aged individuals is stronger in individuals who have a low health risk

CARTaGENE



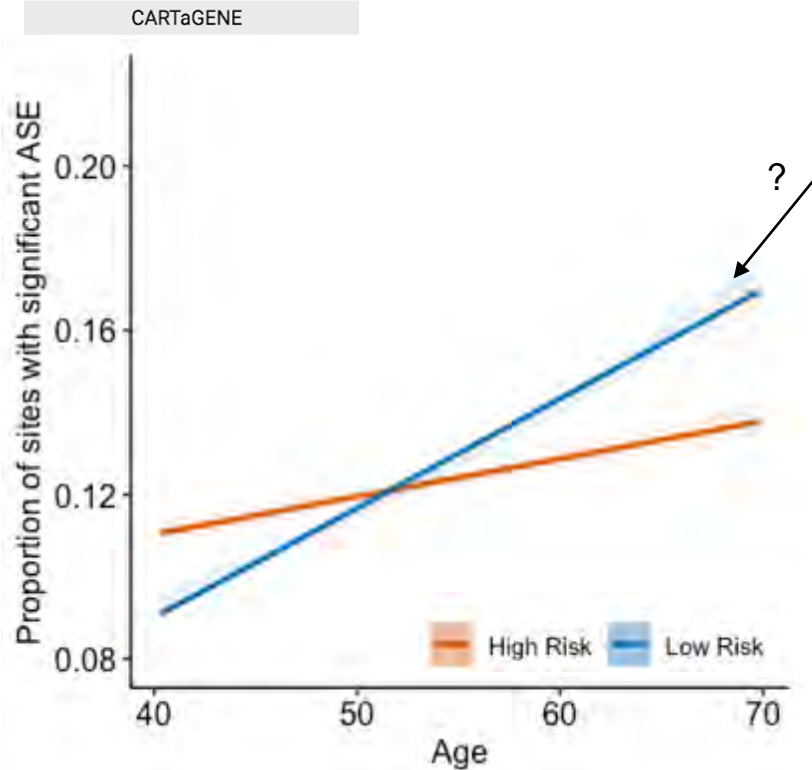
- Low risk individuals experience **larger increases** in ASE with age

# Increased proportion of ASE in aged individuals is stronger in individuals who have a low health risk



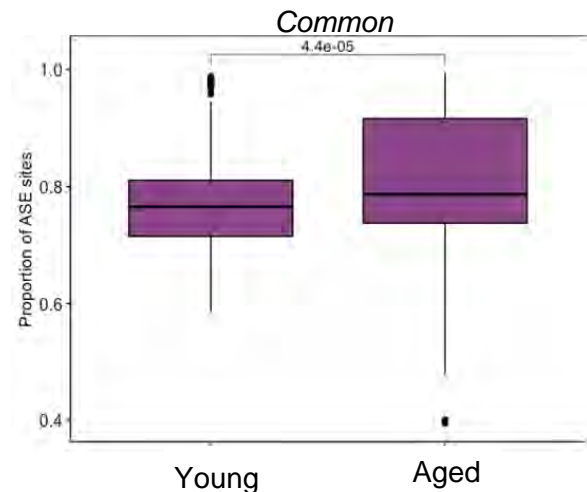
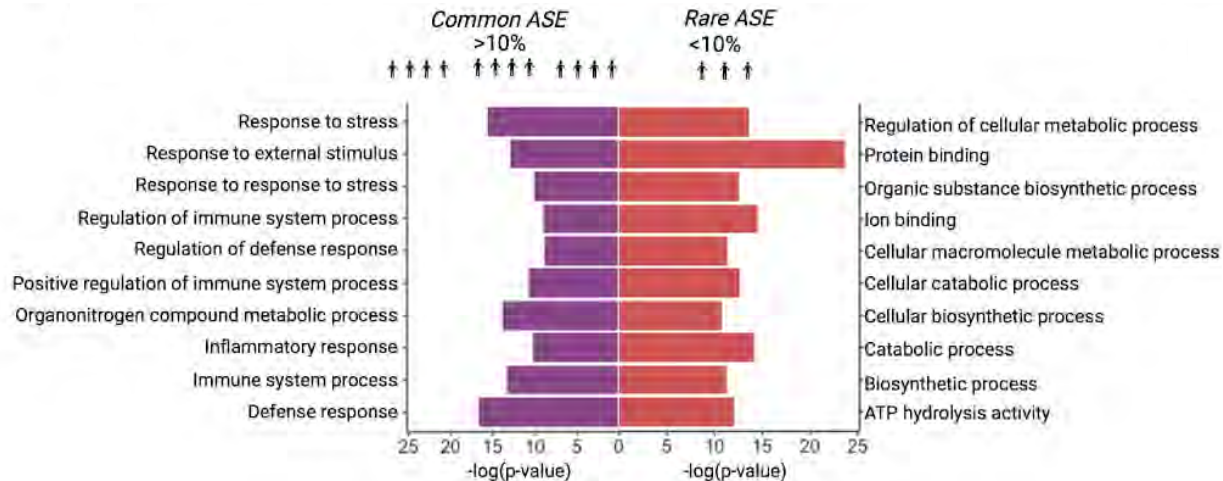
- Low risk individuals experience **larger increases** in ASE with age
- Replicated in OHS pseudo-bulk and **adaptive** immune cells

# What genes could be driving this?



# Older individuals have more common ASE events in genes involved in immune response

CARTaGENE

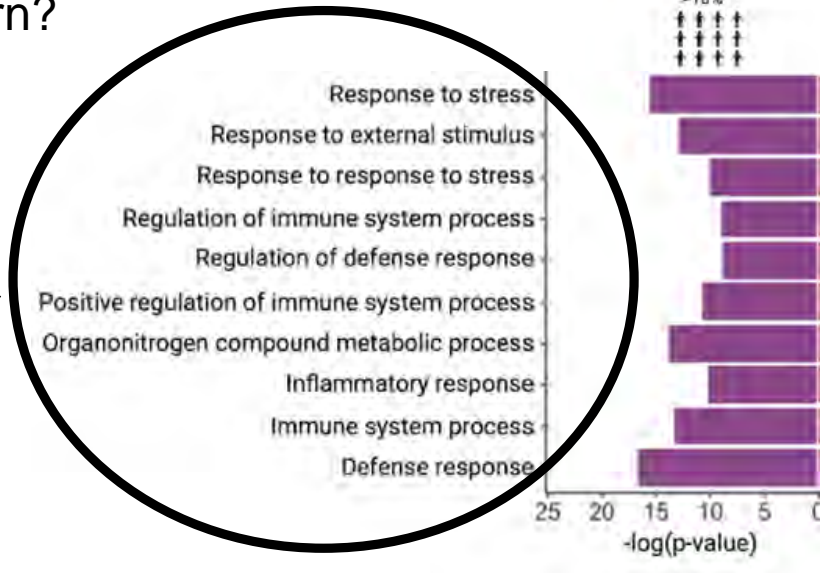
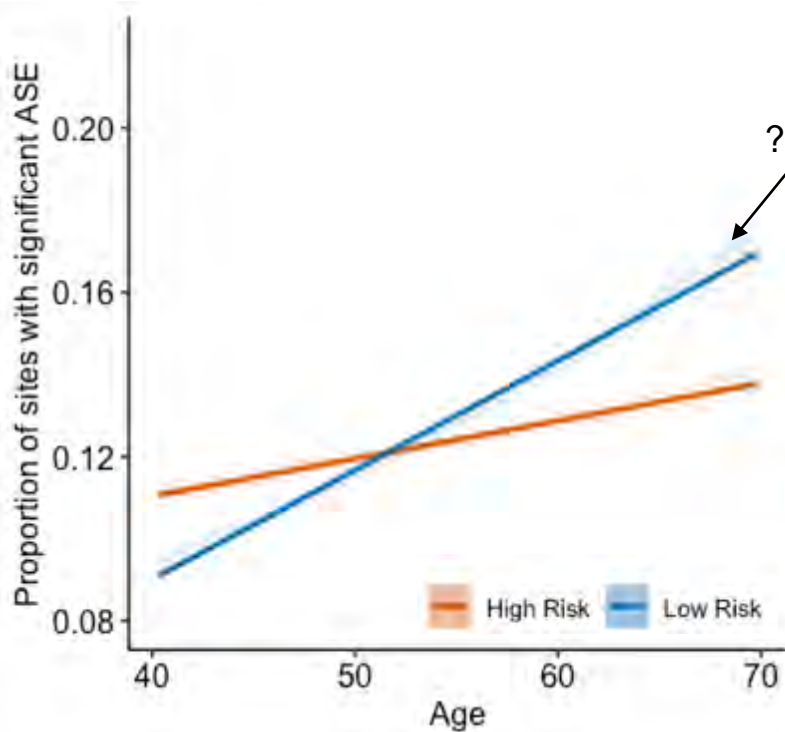


- **Aged** individuals have **more common** ASE events, which are involved in **immune response**



# Are immune genes driving this pattern?

CARTaGENE

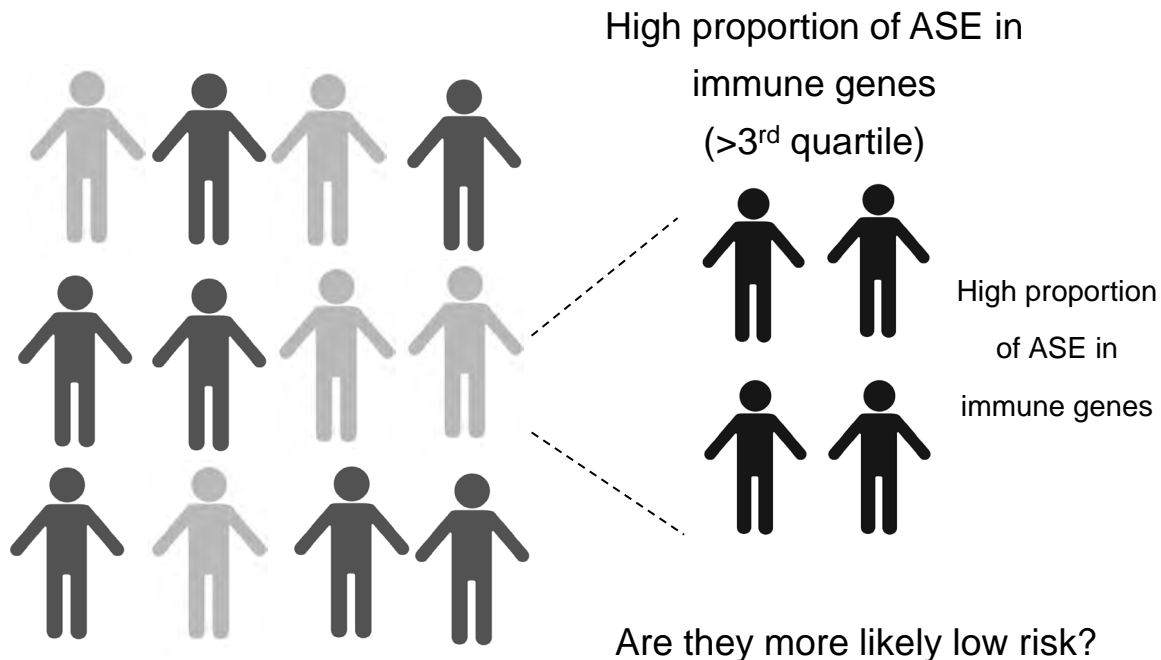


# Increased ASE in immune genes demonstrates lower health risk in aged individuals

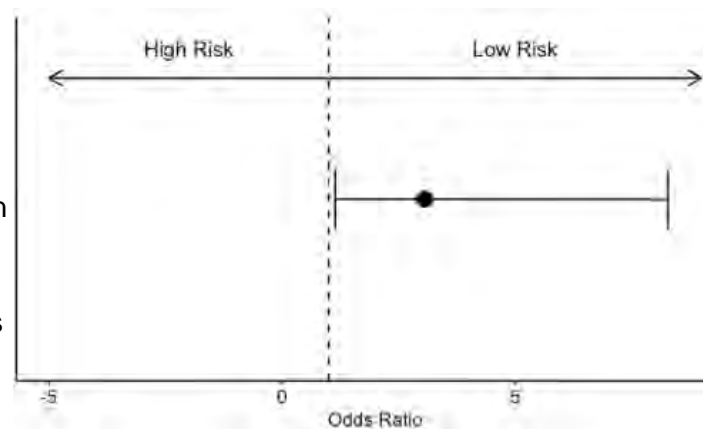
CARTaGENE

*Immune gene set (534 genes)*

# significant sites in immune  
# heterozygote sites in immun



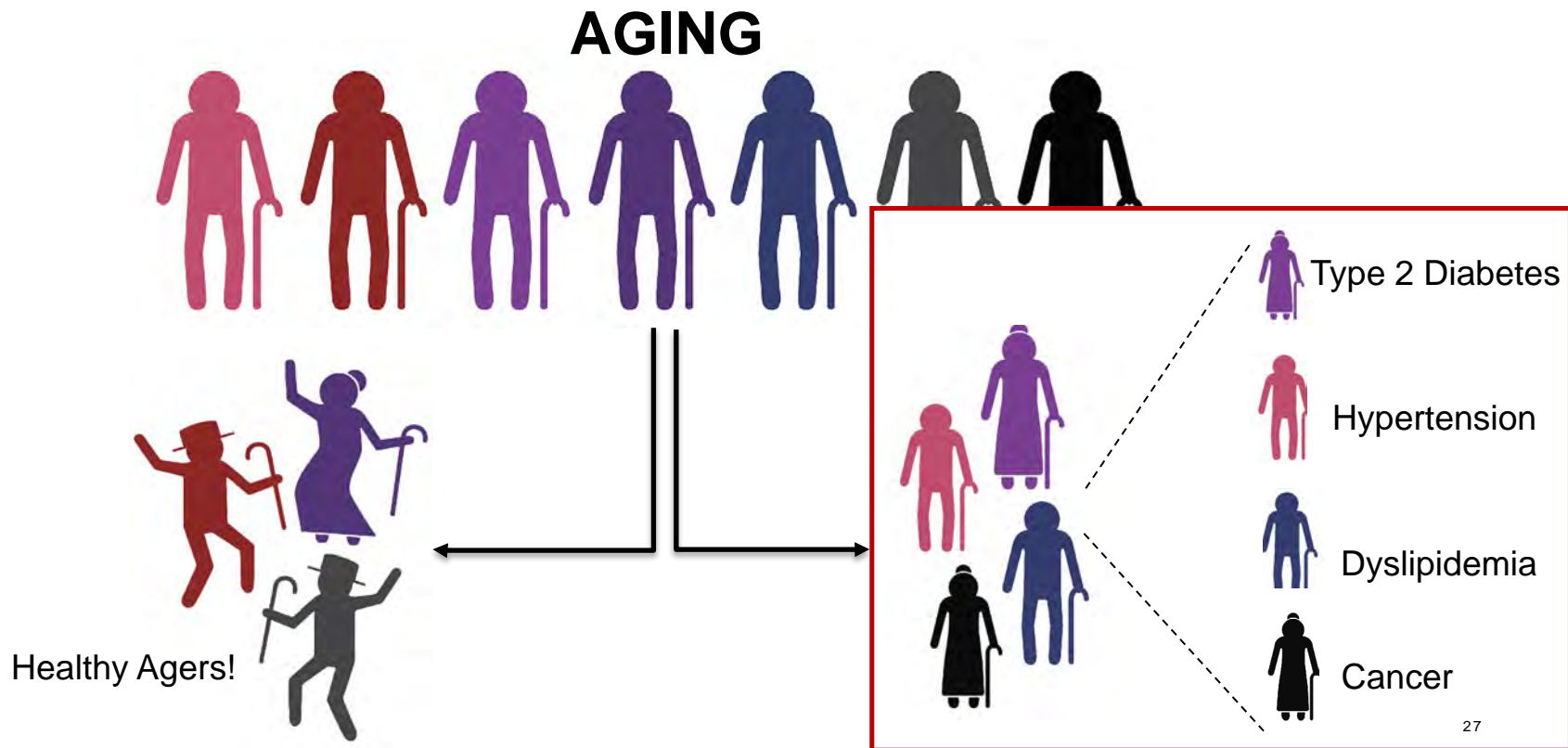
- Aged individuals with **high proportion of ASE in immune genes** are more likely to be **low risk**



logistic regression model:

$\log(\text{odds}) = \text{RiskScore} \sim \text{ASE in immune}$

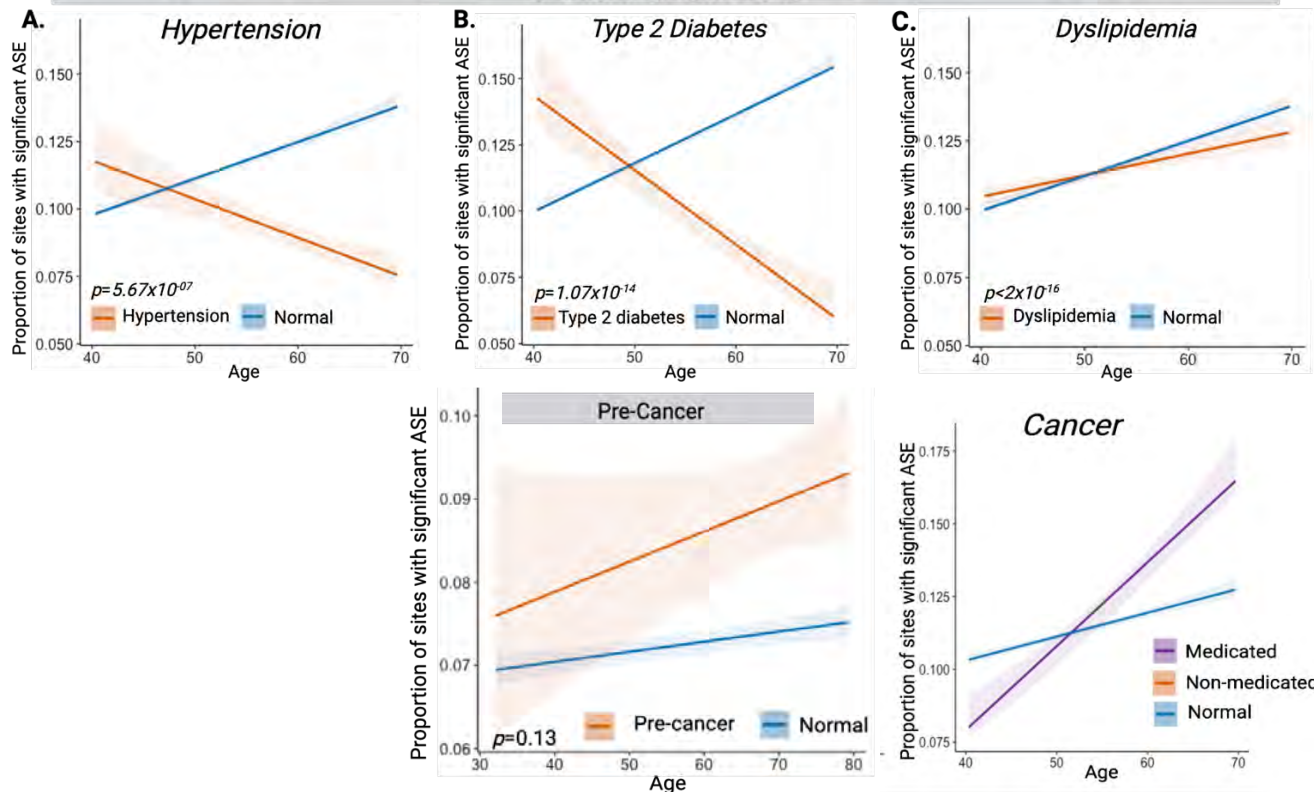
Do individuals with a known disease show consistent results with the risk score?



# Increased ASE during aging may reduce risk of cardiometabolic traits

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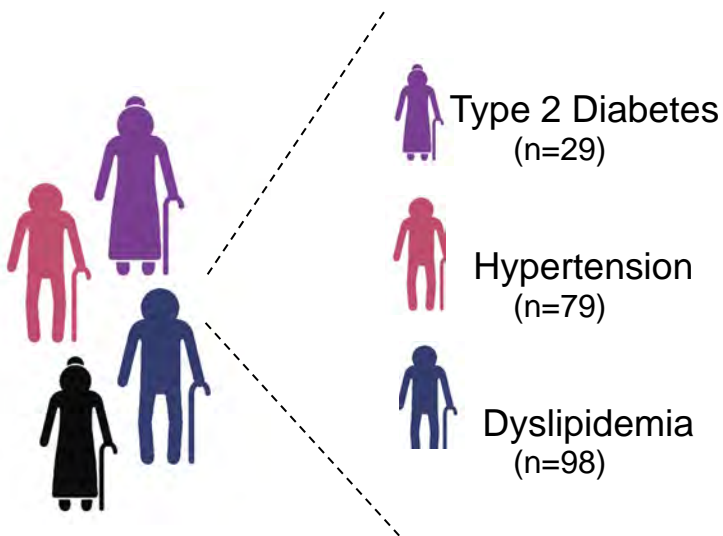
## Cardiometabolic Traits



- **Hypertension and T2D** individuals experience a **decrease** of ASE with age

- **Pre-cancer** individuals have increases of ASE with age—possible **tissue specificity or immune involvement?**
- **Consistent in cancer samples**, but individuals are treated and have no information on remission status

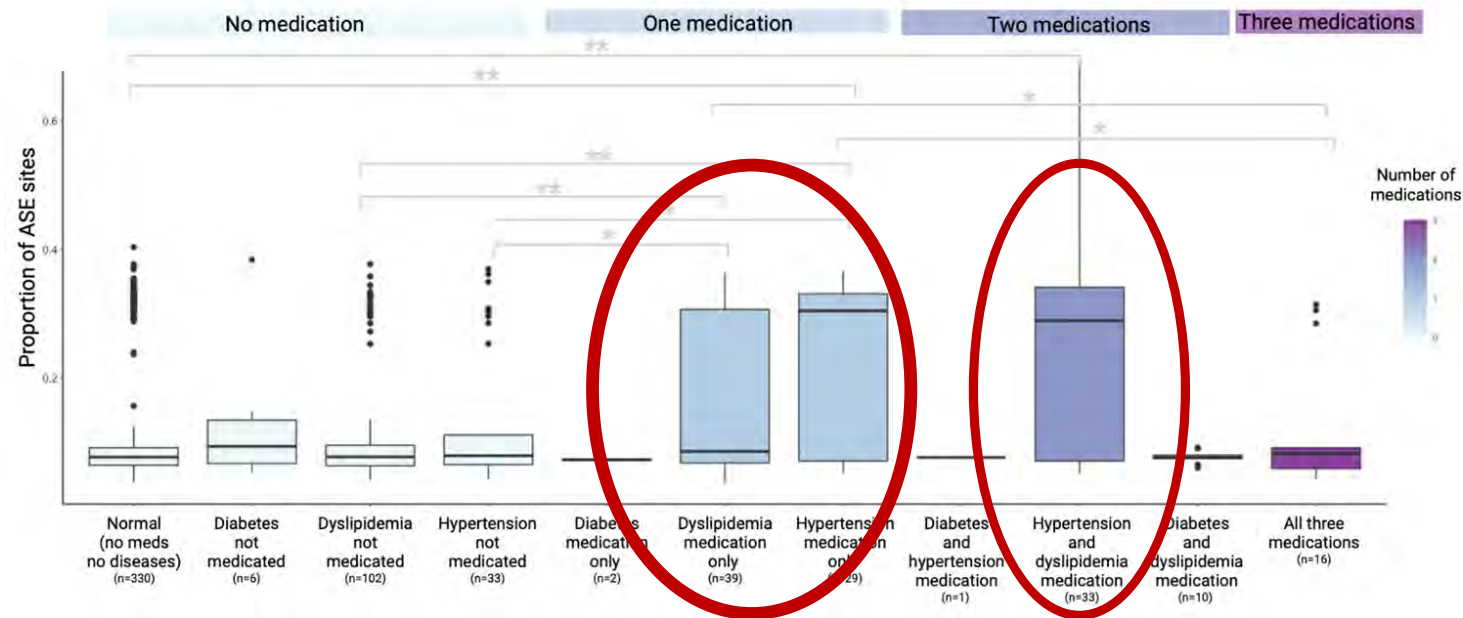
## Many studies exploring ASE with disease may ignore impact from medication



- CARTaGENE cohort has **treatment information for cardiometabolic disease**
- Overlapping disease/treatments, and different drug classes cause challenges with testing for associations
- **Response to treatment estimated** based on lab reported blood measurements

# Medication associated with increased ASE for hypertension and dyslipidemia

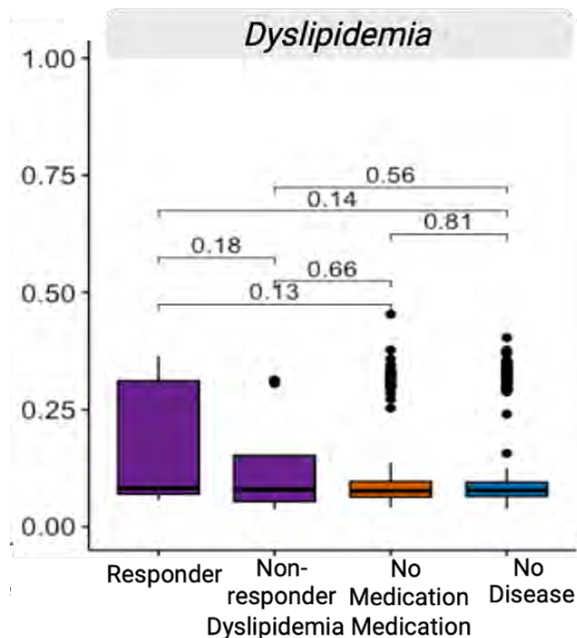
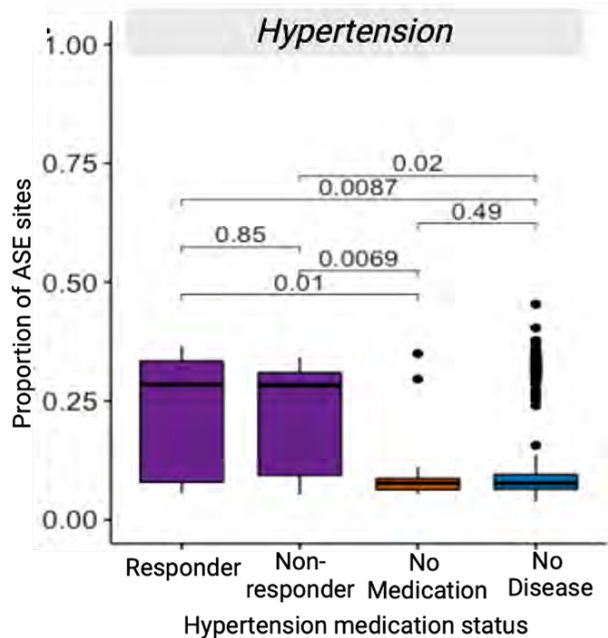
CARTaGENE



- **Hypertension and dyslipidemia** medications associated with **increased** ASE levels

# Medication associated with increased ASE for hypertension and dyslipidemia

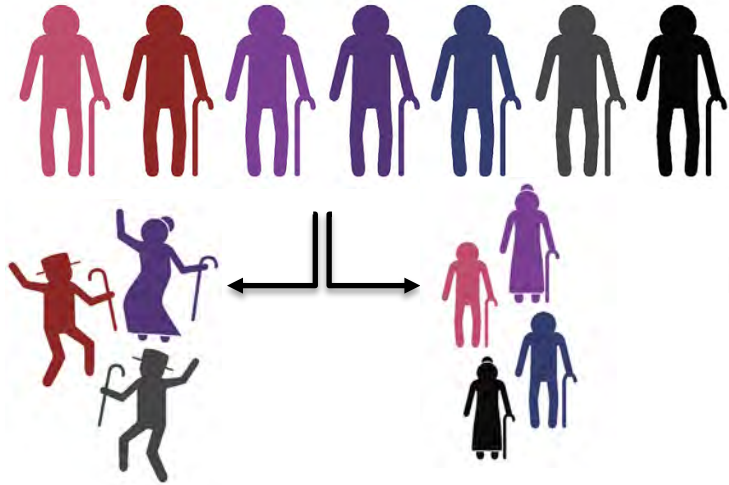
CARTaGENE



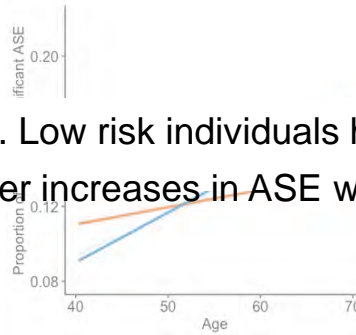
- **Hypertension and dyslipidemia** medications associated with **increased** ASE levels
- Increases in ASE observed in **both responders and non-responders**
- Identified genes with ASE differences specifically in non-responders

# Summary

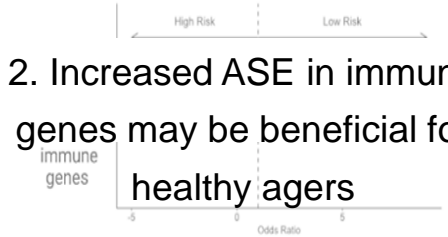
Does ASE contribute to phenotypic variation during aging?



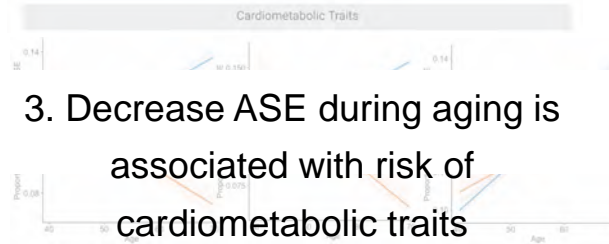
1. Low risk individuals have larger increases in ASE with age



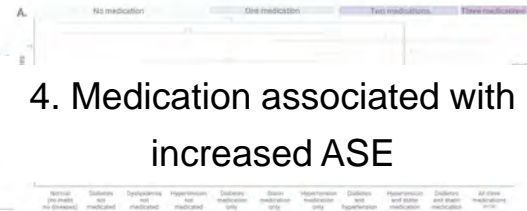
2. Increased ASE in immune genes may be beneficial for healthy agers



3. Decrease ASE during aging is associated with risk of cardiometabolic traits



4. Medication associated with increased ASE







# Acknowledgments

## Dr. Philip Awadalla

- **Mawussé Agbessi**
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- Tom Ouellette
- Yiran Shao
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- **Dr. David Soave**
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