



The biological influences of social determinants of health: challenges, surprises and complexities



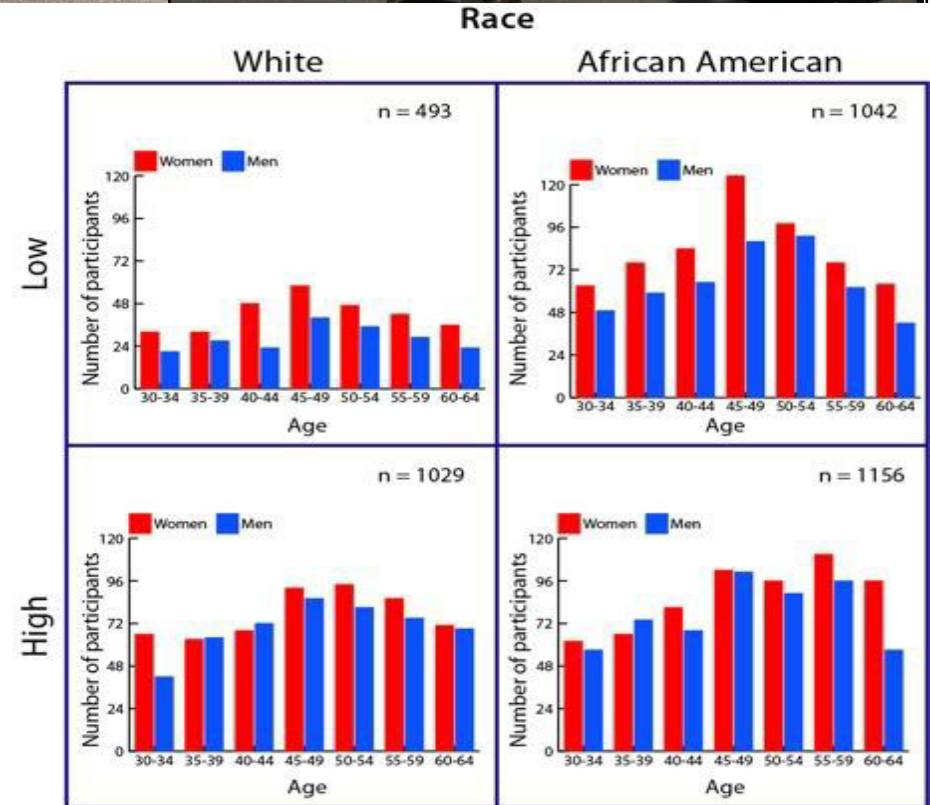
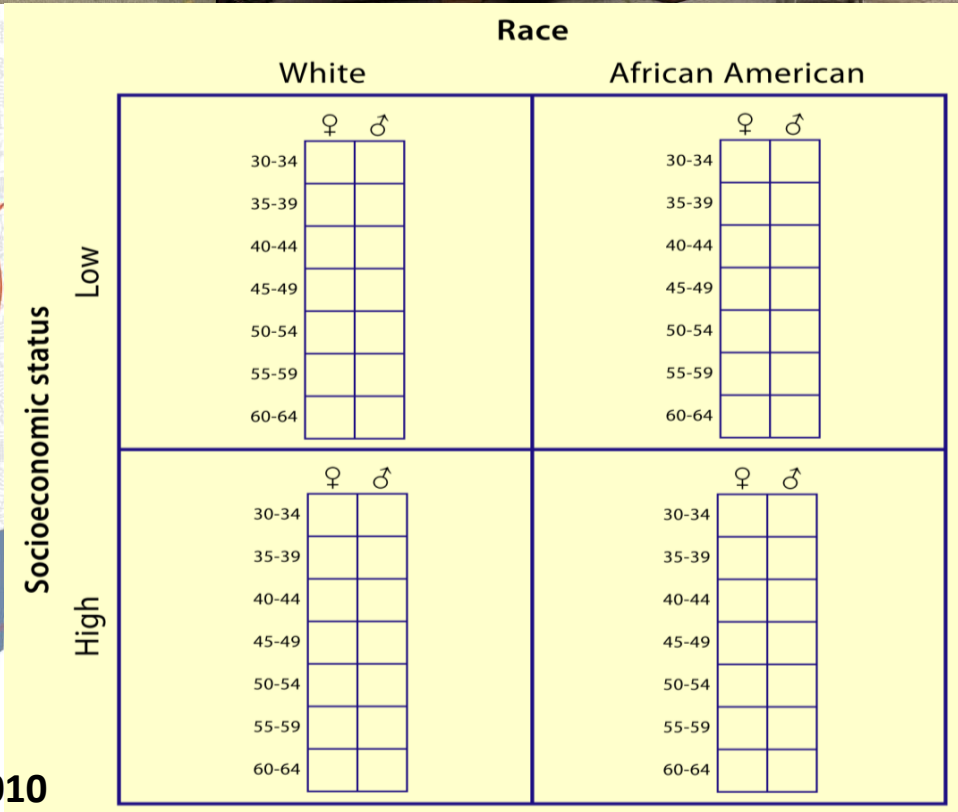
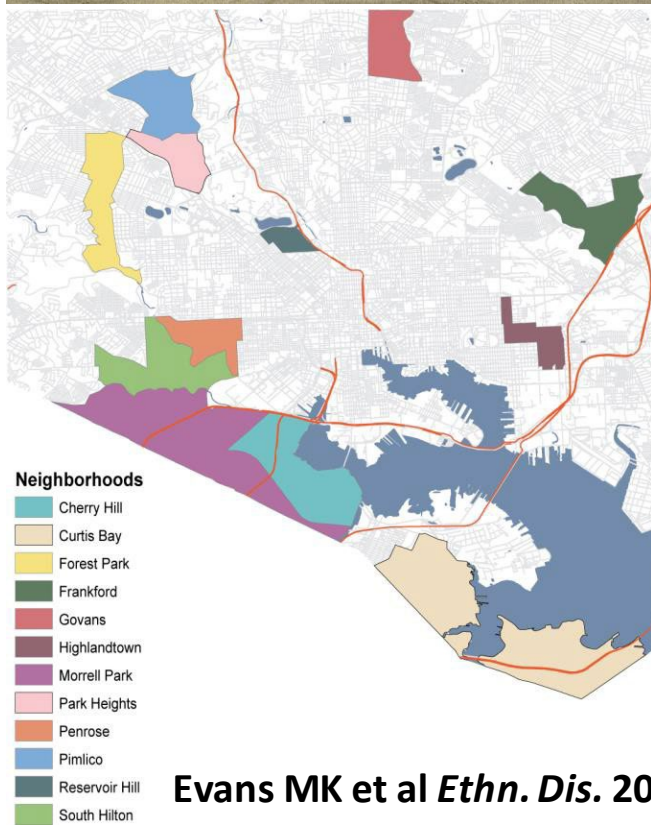
National Institute
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Deputy Scientific Director

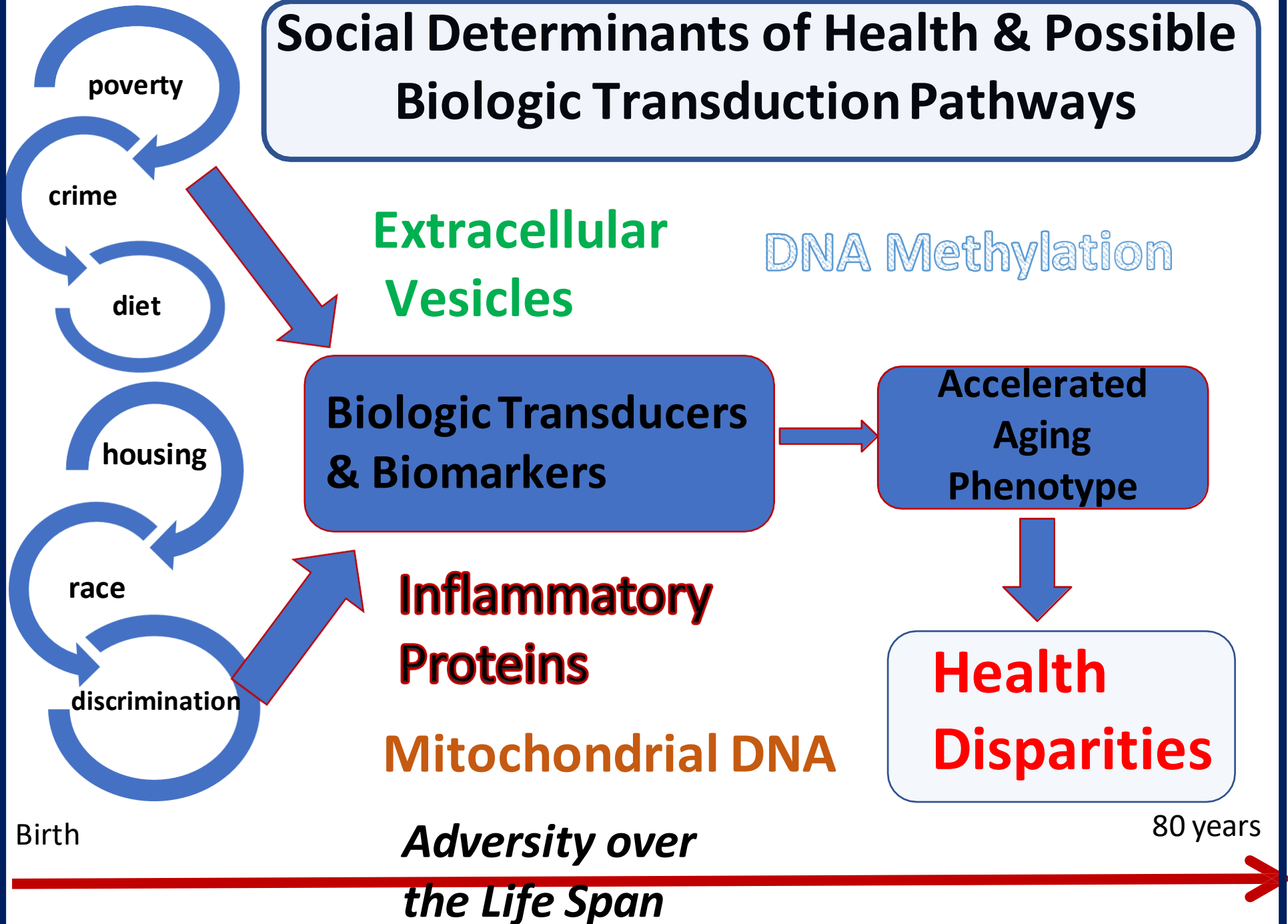
Chief, Health Disparities Research Section



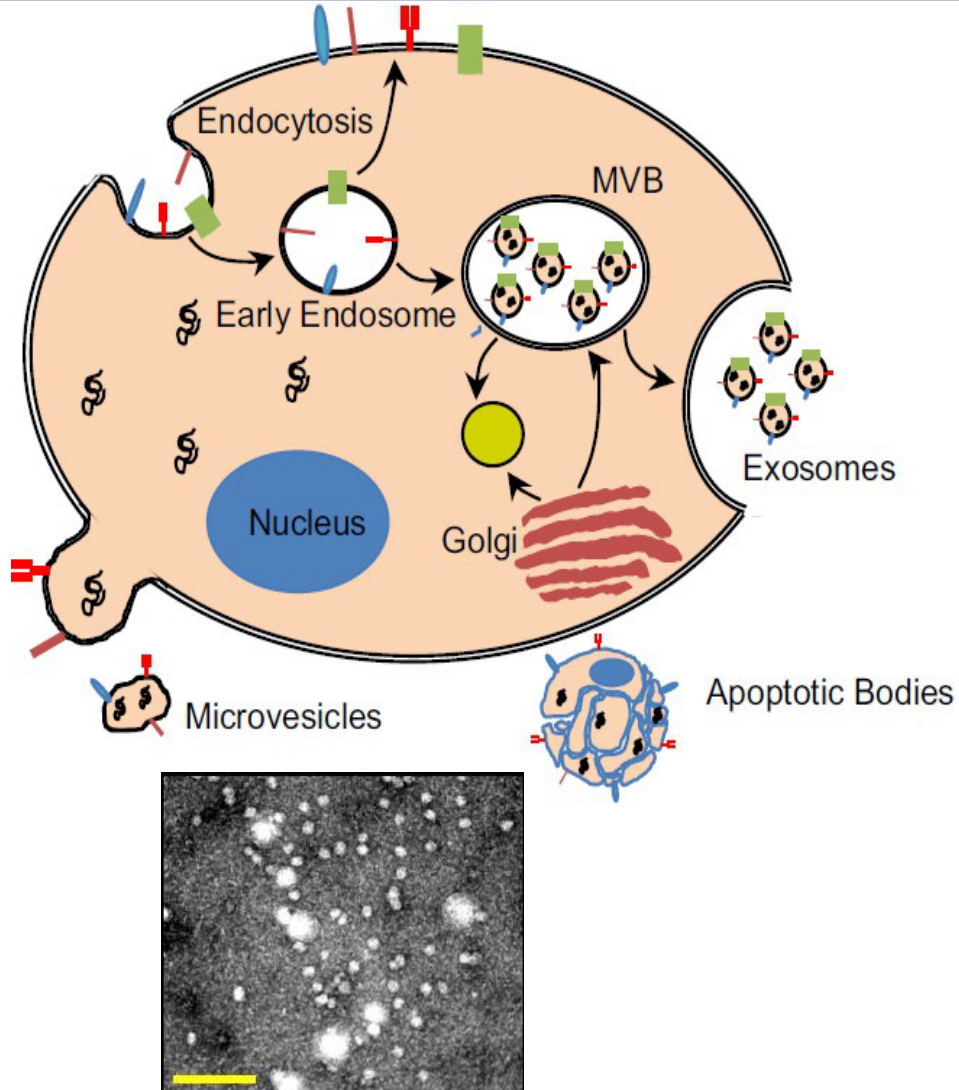


Evans MK et al *Ethn. Dis.* 2010

Social Determinants of Health & Possible Biologic Transduction Pathways

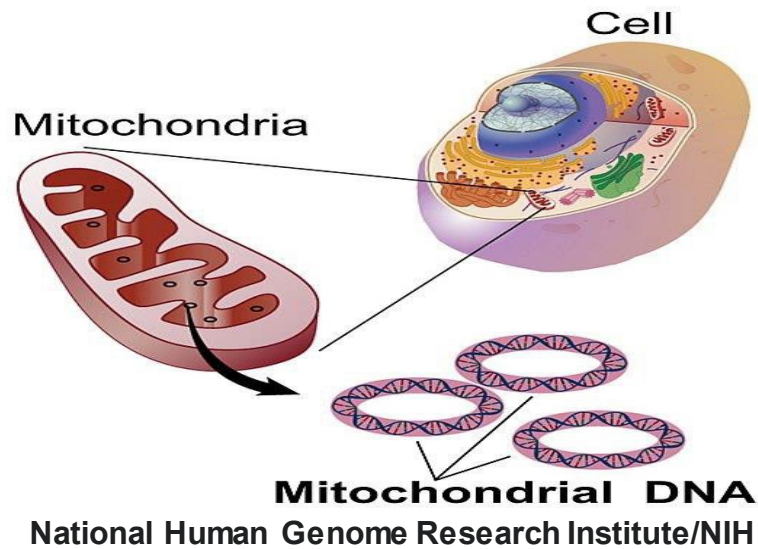


Extracellular Vesicles as Biomarkers of Health Disparities

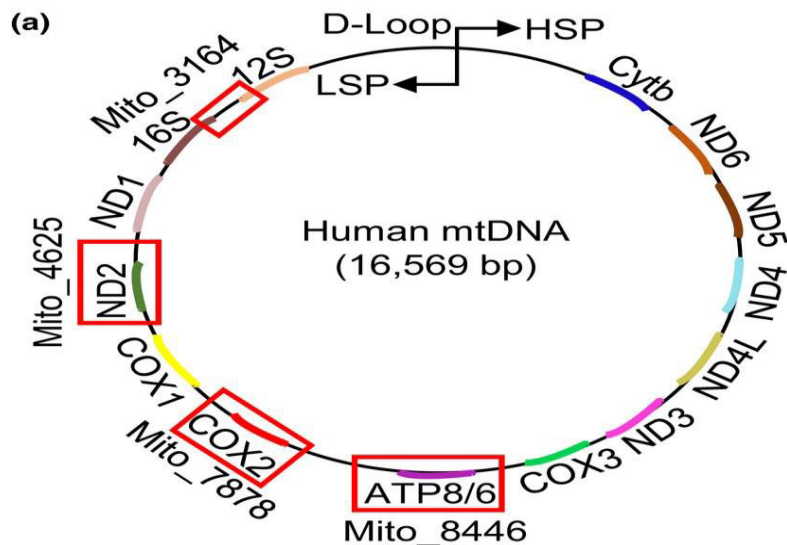


- Cells release lipid-bound extracellular vesicles (EVs): exosomes, microvesicles and apoptotic bodies into the extracellular space e.g. plasma, serum, urine
- Mediate intercellular communication
- Biomarkers and novel therapeutic modalities for chronic disease & cancer
- Contain molecular cargo, including RNAs (mRNA, microRNAs, and long noncoding RNAs), DNA, proteins, and lipids

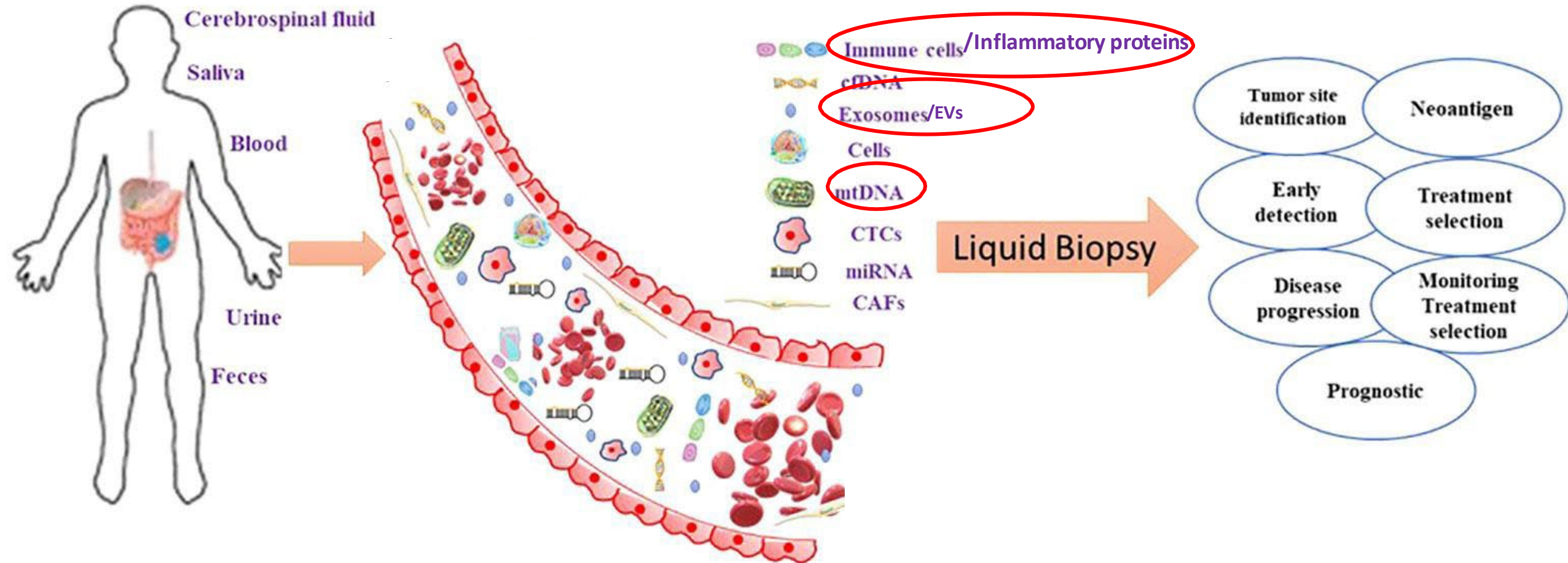
Circulating Cell Free Mitochondrial DNA as biomarkers of health disparities



- Released from cells under stress
- Mt and mtDNA may be mediators of stress relevant to SDOH
- Damage-associated molecular pattern molecules (DAMPs) associated with cancer and chronic inflammatory diseases
- Plasma mtDNA is present in EVs, EV-derived mtDNA declines with age, EVs affect mitochondrial energetics in an EV age-dependent manner. Lazo S, Noren Hooten N, Green J *Aging Cell* et al 2021



Liquid Biopsy in Cancer



Do social determinants of health influence liquid biopsy molecular and clinical assessments?

EVs, Inflammation, Poverty



A. Byppanahalli



M. Vannoy

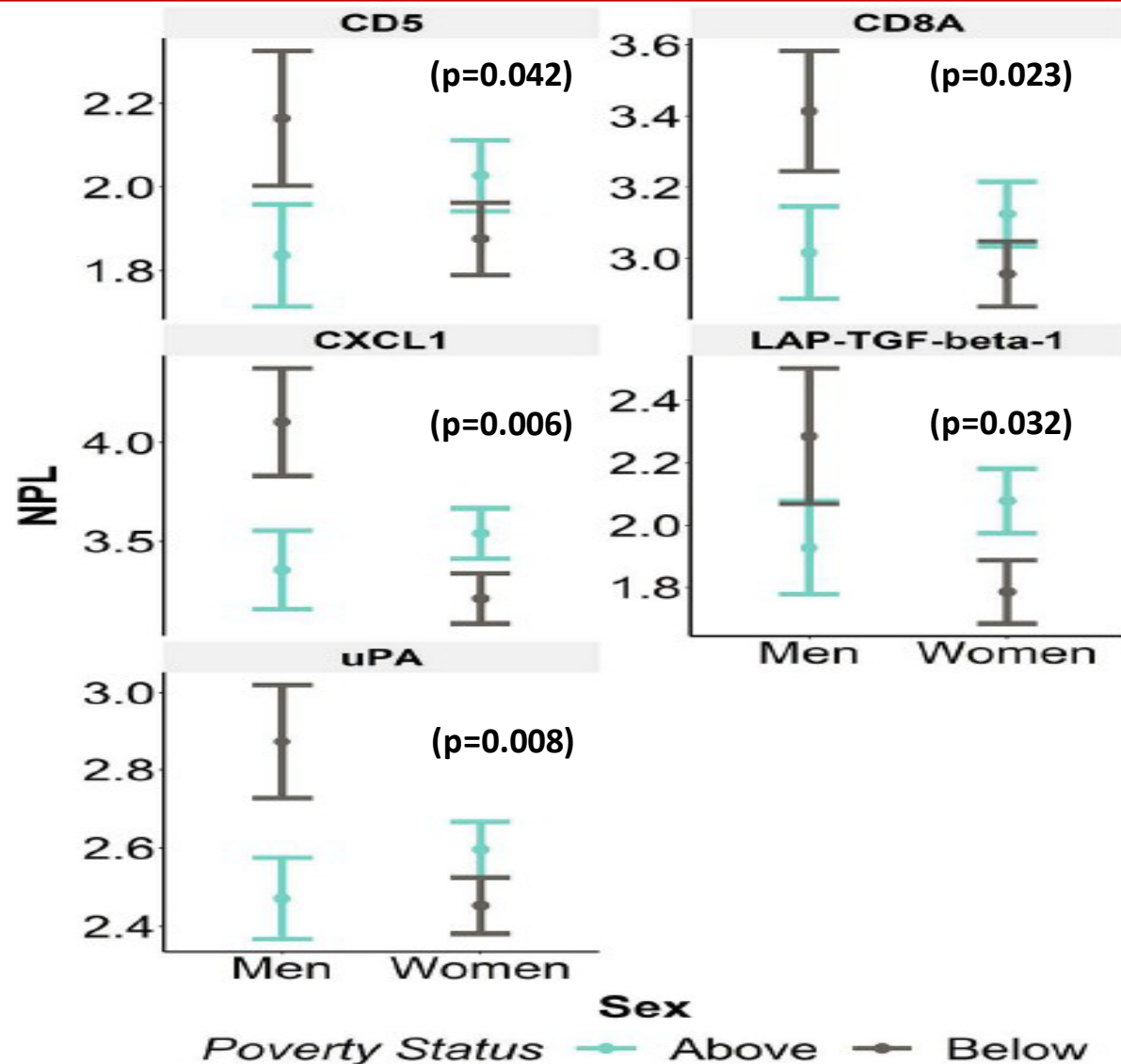


N. Noren Hooten

- We examined whether mitochondrial DNA (mtDNA) and inflammatory proteins in EVs may act as damage-associated molecular pattern (DAMP) molecules in frailty in the context of race, age and poverty status.

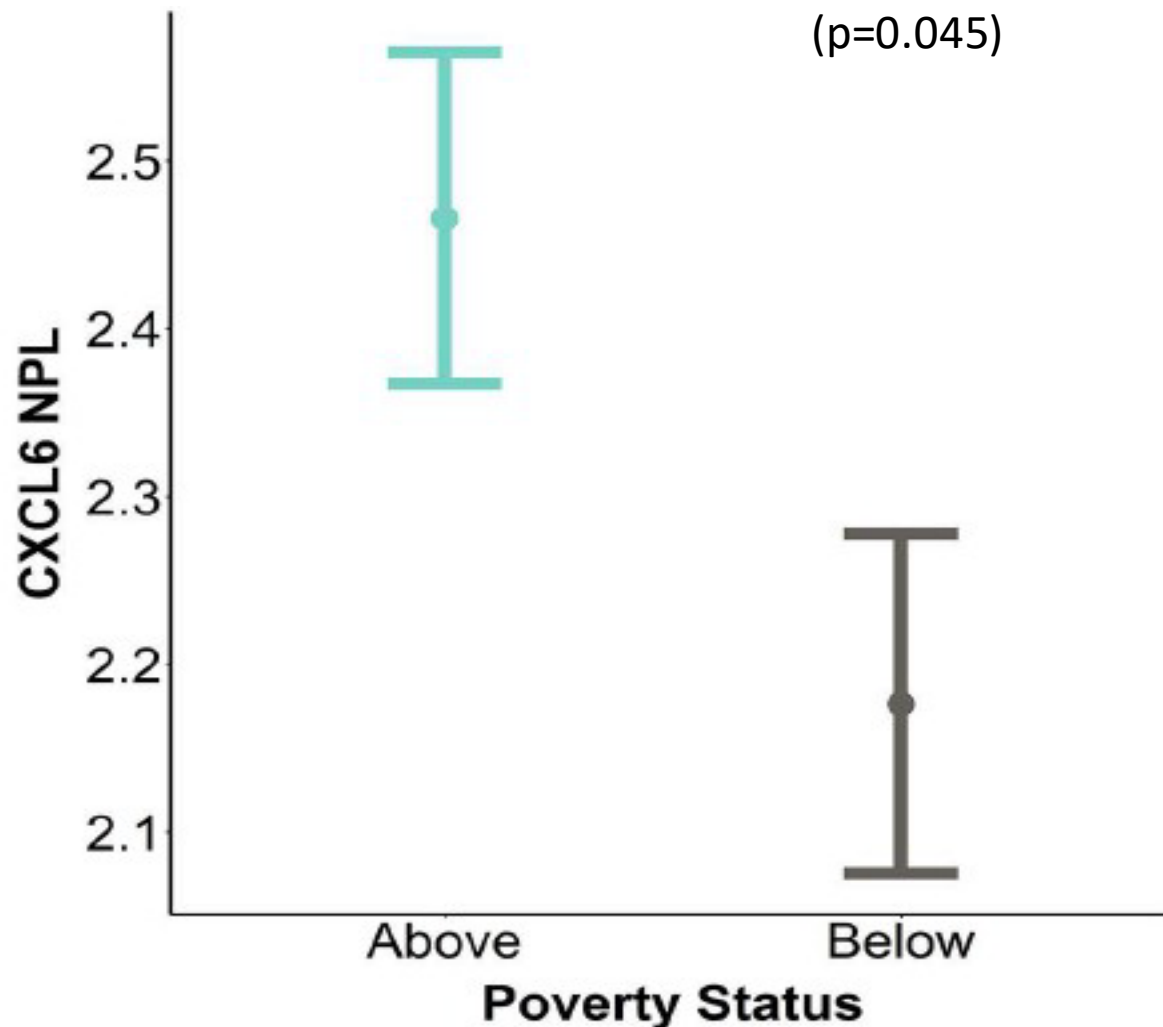
Characteristic	Frail, N = 87	Non-frail, N = 90	P-value
Age	50.66 (2.62)	50.06 (2.84)	0.15
Men (%)	24 (28%)	25 (28%)	> 0.9
AA (%)	41 (47%)	43 (48%)	> 0.9
Below Poverty (%)	43 (49%)	38 (42%)	0.3

EV inflammatory proteins are associated with sex and poverty status



- 5 proteins significant interactions between sex and poverty status
- All 5 proteins highest in men **below poverty**
- All proteins except **CD5** (*regulates antitumor immune response*) higher levels in men **below poverty** compared to women below poverty
- **CXCL1** (*role in inflammation, angiogenesis, tumorigenesis*) and **uPA** (*involved in cancer progression and tumor microenvironment remodeling*) - higher in men **below poverty** compared to men **above poverty**
- **LAP-TGF-beta-1** (*cytokine regulates cellular proliferation and differentiation*) - lower in women **below poverty** compared to women **above poverty**

CXCL6 levels were significantly different with poverty status



- **C-X-C motif chemokine ligand 6** (CXCL6) chemotactic for neutrophil granulocytes
- mediates inflammation, cell growth, promotes tumor growth, and metastasis,
- CXCL6 lower in individuals **below poverty** compared to **above poverty**



EV inflammatory proteins significantly altered by frailty status, sex, and poverty status

- Evs & EV mtDNA levels were significantly higher in frail individuals compared to non-frail individuals
- Five proteins had significant **interactions between sex and poverty** status: CD5, CD8A, CXCL1, LAP-TGF- β 1, Urokinase Type Plasminogen activator- immune response, inflammation, cancer
- In general, **all five proteins were highest in men living below poverty**
- CXCL6 levels were significantly different with poverty status

Does race associate with EVs, cell free circulating mtDNA or inflammatory protein levels?

Race, EVs, mtDNA, & inflammatory proteins

Characteristic	NT, N = 107	HTN, N = 108	p value
Age	52.6 (4.3)	53.1 (4.1)	0.3
AA (%)	54 (50%)	54 (50%)	>0.9
Men (%)	54 (50%)	54 (50%)	>0.9
Below poverty (%)	46 (43%)	47 (44%)	>0.9



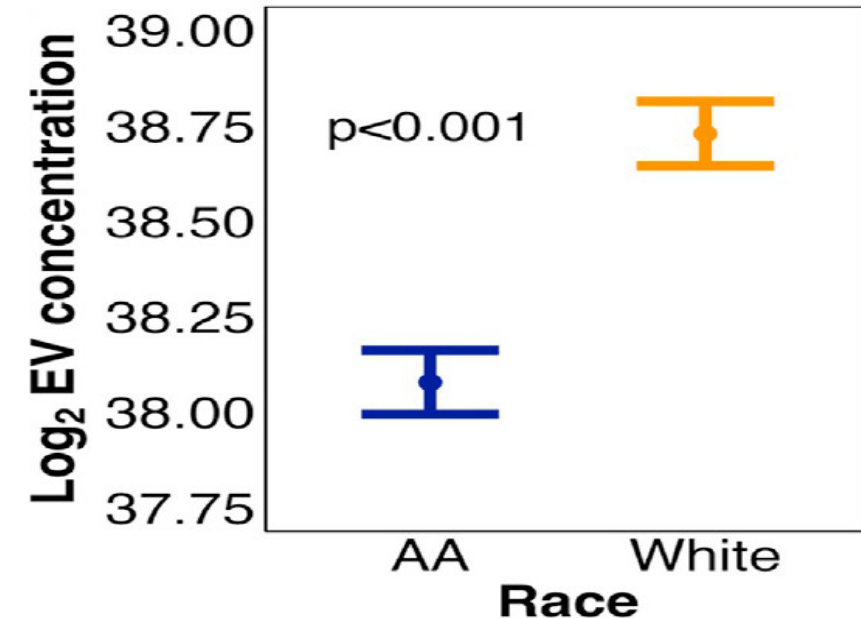
A. Byppanahalli



V. Omoniyi

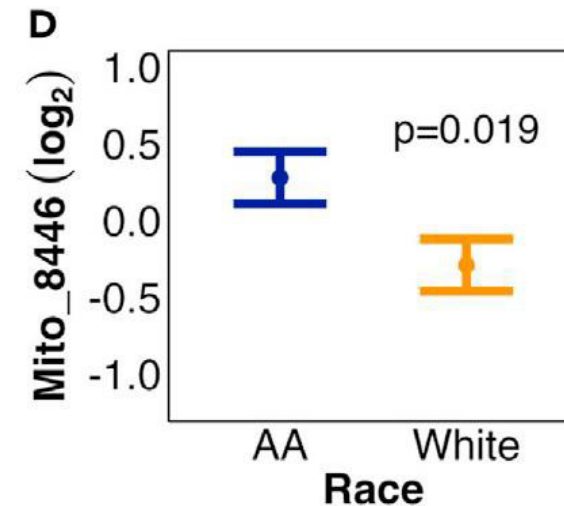
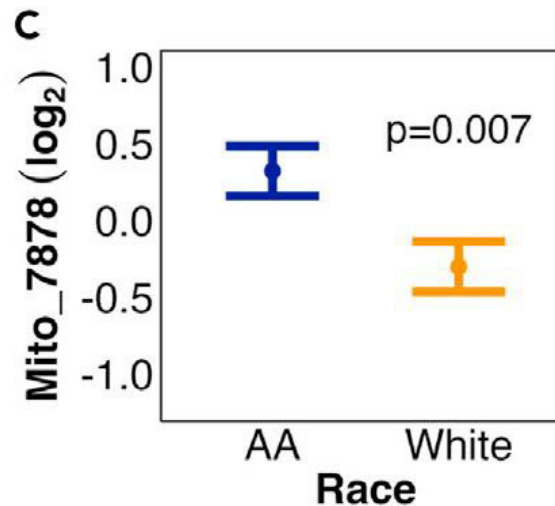
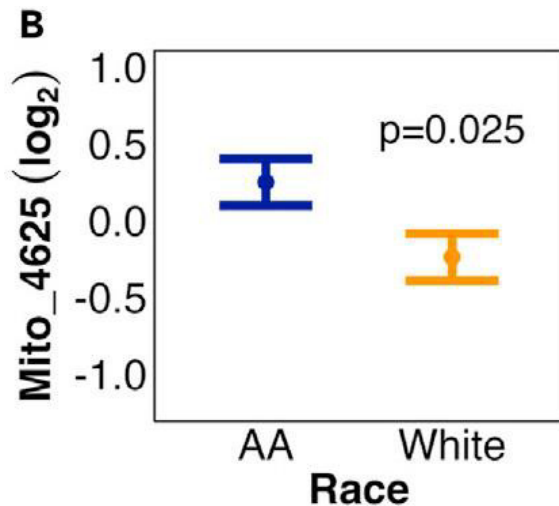


N. Noren Hooten

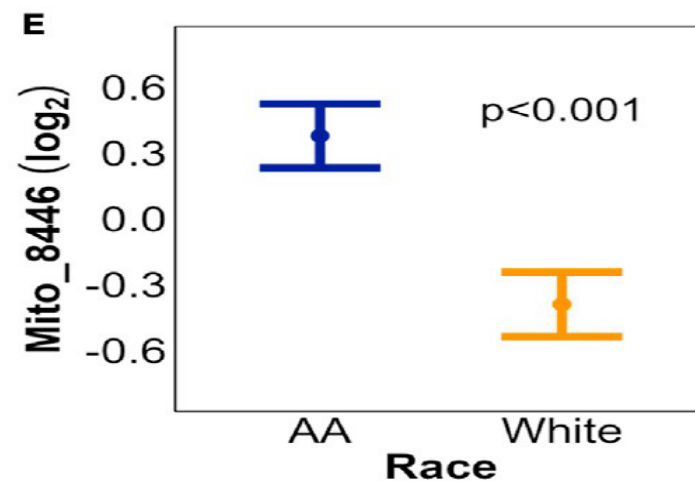
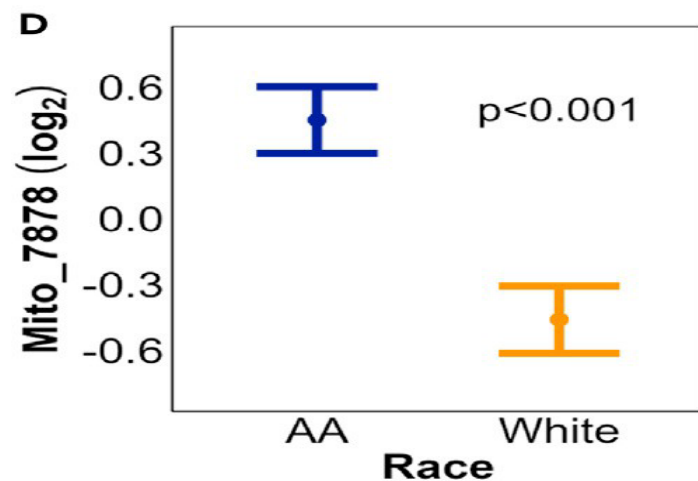
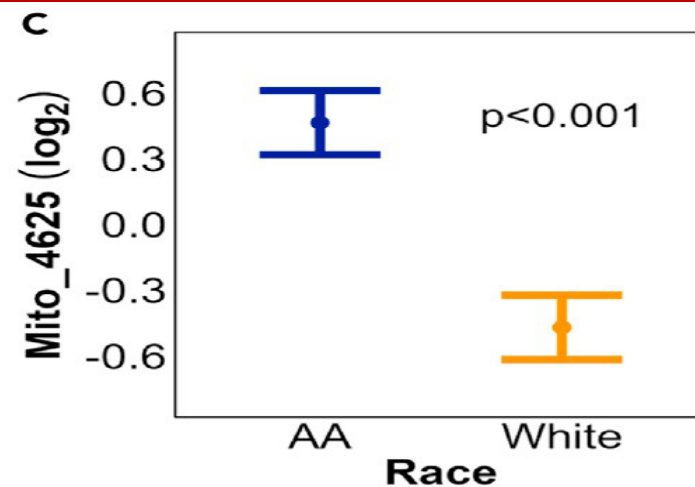
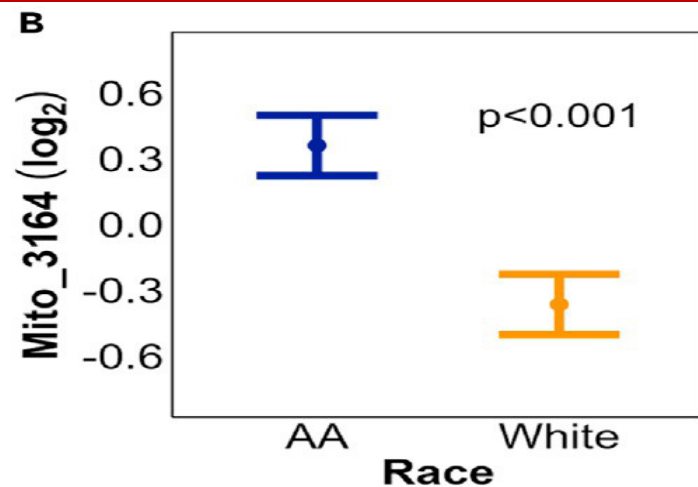


EV concentration was significantly higher in White participants compared with African American participants (p < 0.001)

Plasma mtDNA levels are significantly higher in African American participants



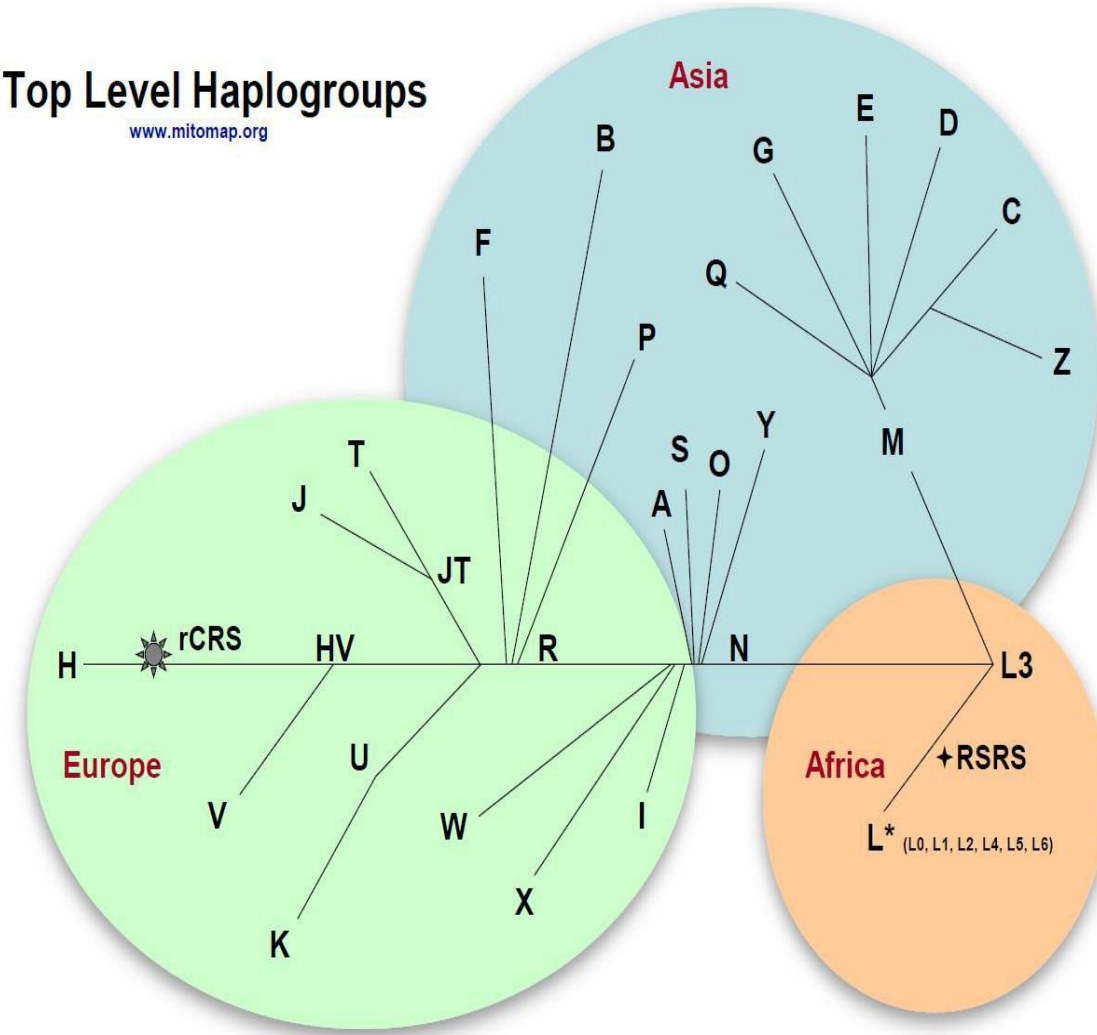
EV mtDNA levels are higher in African American participants



Race is a social construct

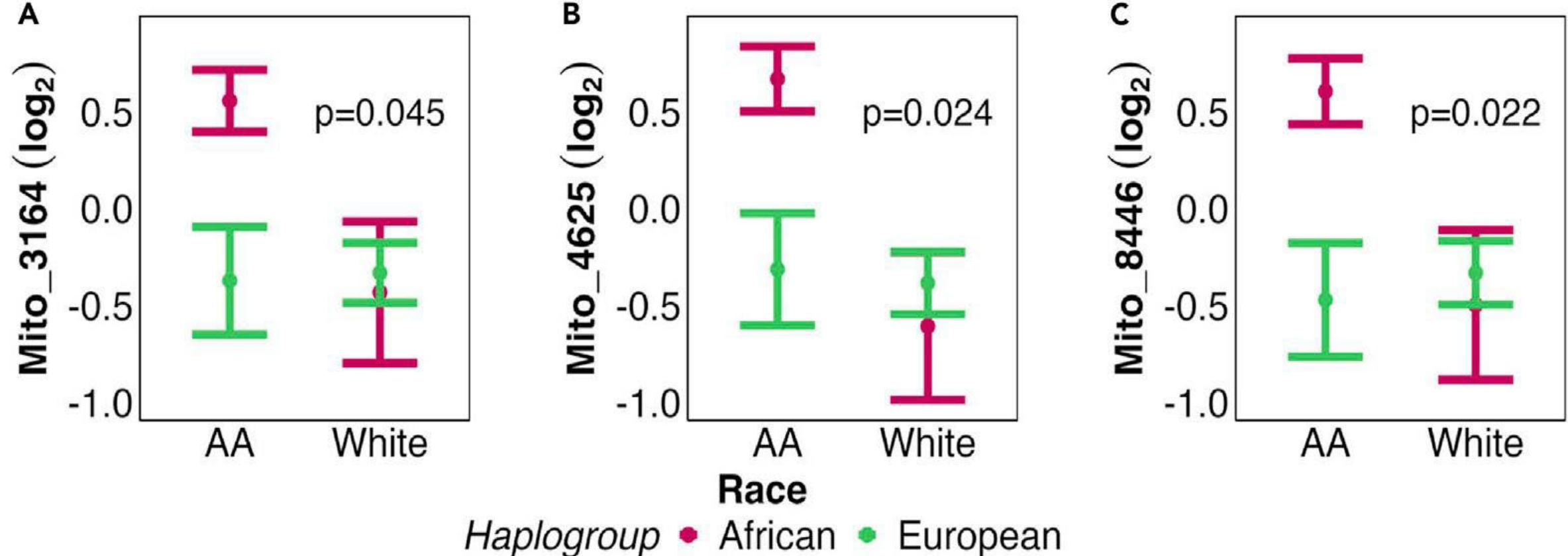
- “**Race is meaningful for health-** a *risk factor* for poor health outcomes in the context of social status, access to resources, ancestry, genomic variation” – (Moring A 2020)
- Mitochondrial haplogroups - genetic classifications within a population, defined by shared, inherited genetic markers or mutations - similar haplotypes defined by combinations of single nucleotide polymorphisms (SNPs) in mtDNA inherited from a common ancestor. (Wallace D 2012)
- mtDNA haplogroups - mitochondrial function, mtDNA damage, oxidative phosphorylation efficiency, ROS production, disease risk including cancer (Wallace DC 2013)

Top Level Haplogroups
www.mitomap.org

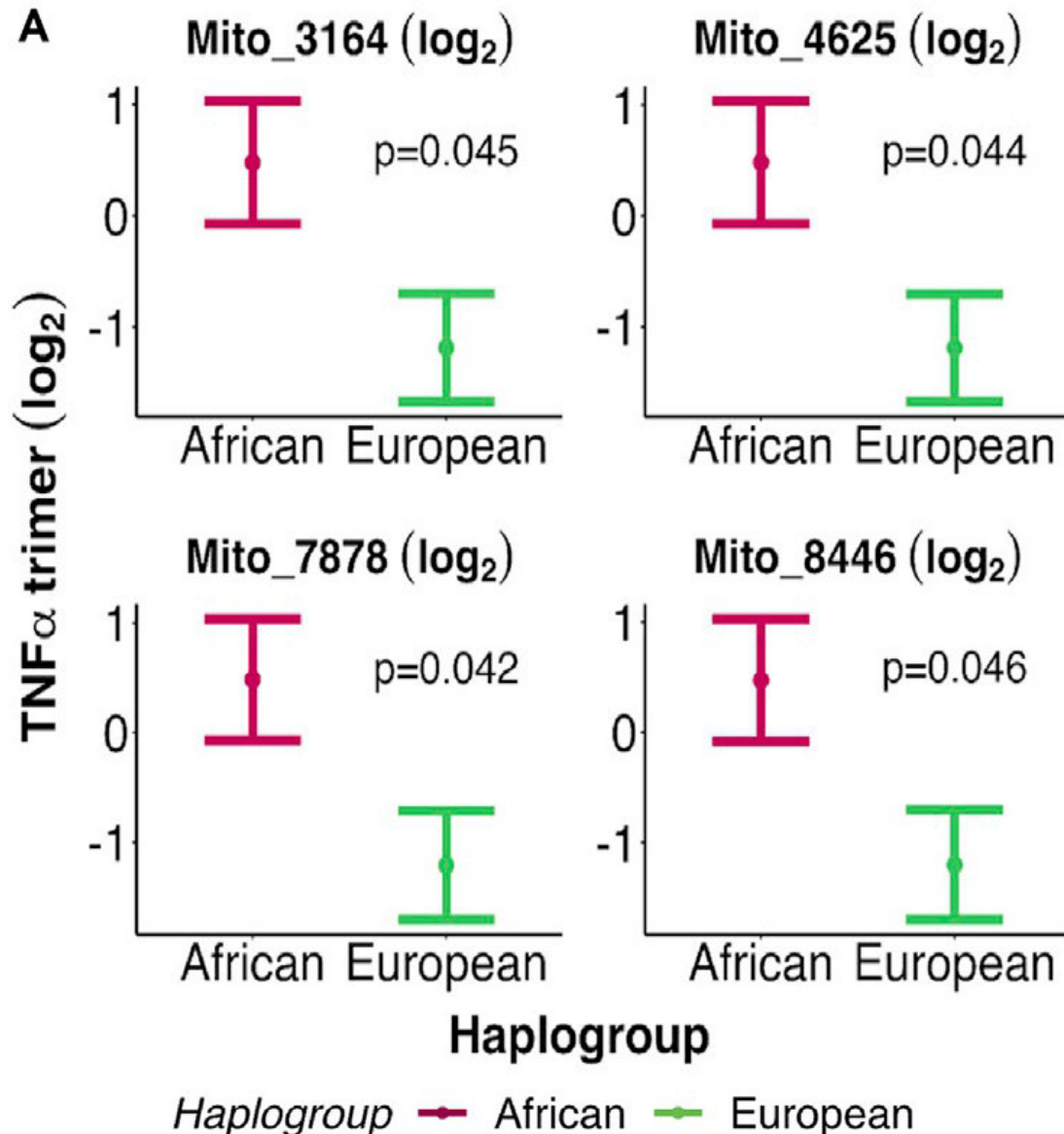


Higher EV mtDNA in African American participants with the African haplogroup

- Participants were grouped into mtDNA haplogroups: African (L0, 1, 2, 4, 5, 6, and L3), European (H, HV, J, K, T, U, and UK), and Other (B-P-F-R, M, and N-A-Y-W-I-X).
- There was concordance between race and mtDNA haplogroup for most participants (AAs 72%)

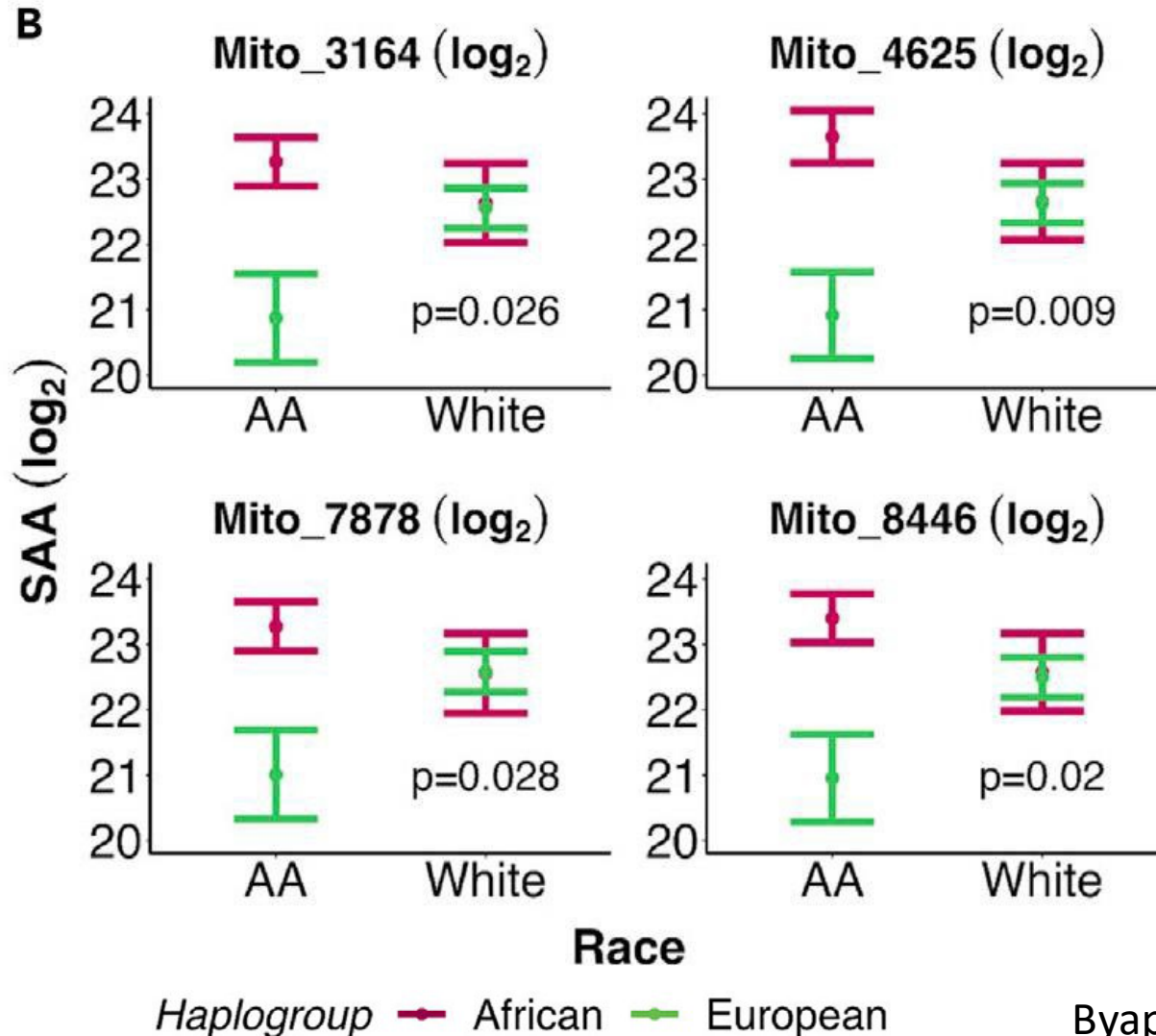


Inflammatory protein levels are associated with mitochondrial DNA haplogroup, race, and EV mtDNA



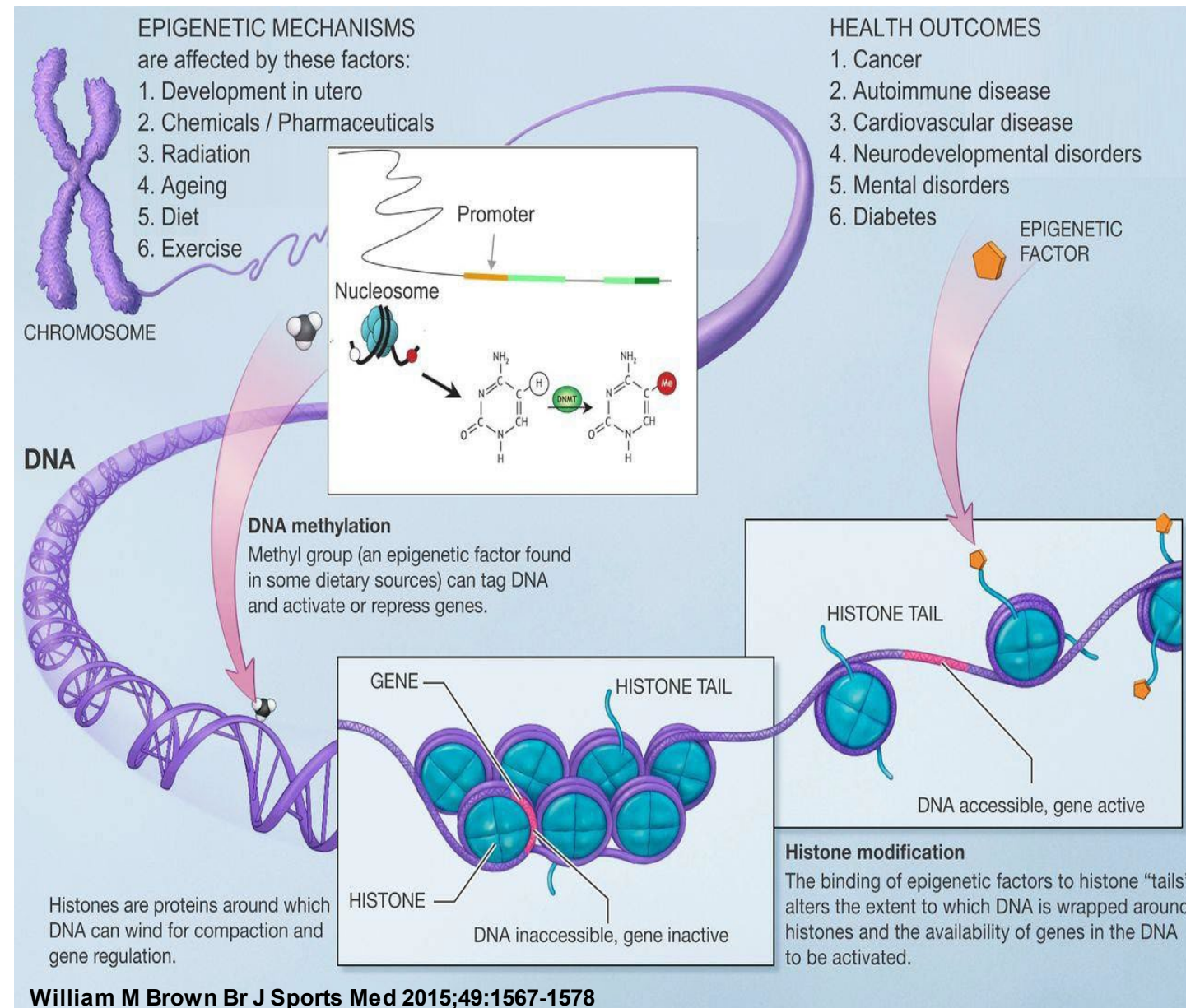
- Nine serum inflammatory proteins were assayed
- Linear regression used to analyze the relationship between each inflammatory protein, race, each EV mtDNA region, and mtDNA haplogroup.
- **TNF-a** – pro-inflammatory cytokine associated with cancer progression and treatment
- **TNF-a trimer levels** significantly different with haplogroup for each EV mtDNA region studied
- **TNF-a Levels were higher in those with African mt Haplogroups.**

Inflammatory protein levels are associated with mitochondrial DNA haplogroup, race, and EV mtDNA



- **Serum Amyloid A (SAA)**
- Acute phase protein secreted by cancer cells
- Cytokine-like protein involved in cell-cell communication, inflammation and neoplasia
- SAA levels significantly different with haplogroup and race for each EV mtDNA region

Race & Poverty: DNA methylation & Biological Aging



- DNA methylation (DNAm) is the most understood epigenetic marker.
- Hypermethylation generally triggers gene expression silencing, while the reverse is true for hypomethylation
- Epigenetic modifications are closely linked with aging & cancer
- Biological aging - changes over the lifespan in pathophysiologic and organismal function
- 'Slow agers' are those who maintain a 'healthy' phenotype despite advancing age
- 'Fast agers' develop age-associated disease earlier in the life span
- Biological age prediction algorithms based on DNAm at selected CpG sites = 'epigenetic age'
- Difference in epigenetic and chronological age - 'epigenetic age acceleration' reflecting the rate of biological aging



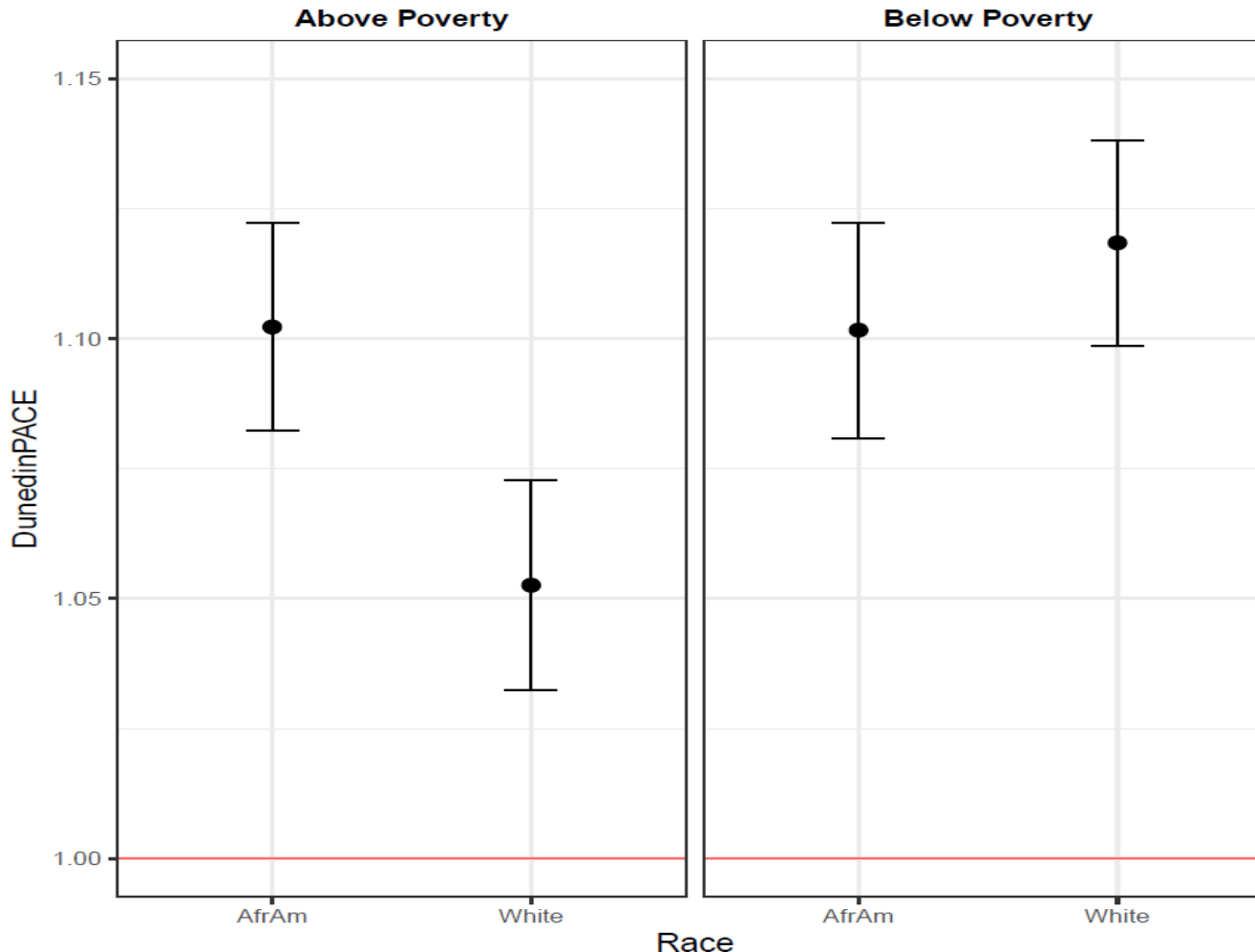
DunedinPACE Measure

- Pace of Aging Computed from the Epigenome -designed to measure aging.
- Detect the effects of interventions to slow aging
- Detect exposures that accelerate aging
- Tracks changes in 19 biomarkers of organ-system integrity in the 1000-member Dunedin Birth cohort in New Zealand



Botong Shen

DunedinPACE scores are associated with race and poverty status



- HANDLS participants aging 7% faster than the Dunedin Study cohort.
- Living below poverty and racial identity associated with faster biological aging
- White participants living above poverty had a DunedinPACE score near 1
- White participants' DunedinPACE scores differed based on poverty status, which was associated with faster biological aging.
- AA participants regardless of poverty status had DunedinPACE scores above one
- Unable to detect the effects of senolytics to slow aging in diverse populations

Shen B et al *JAMA Network Open* 2023