

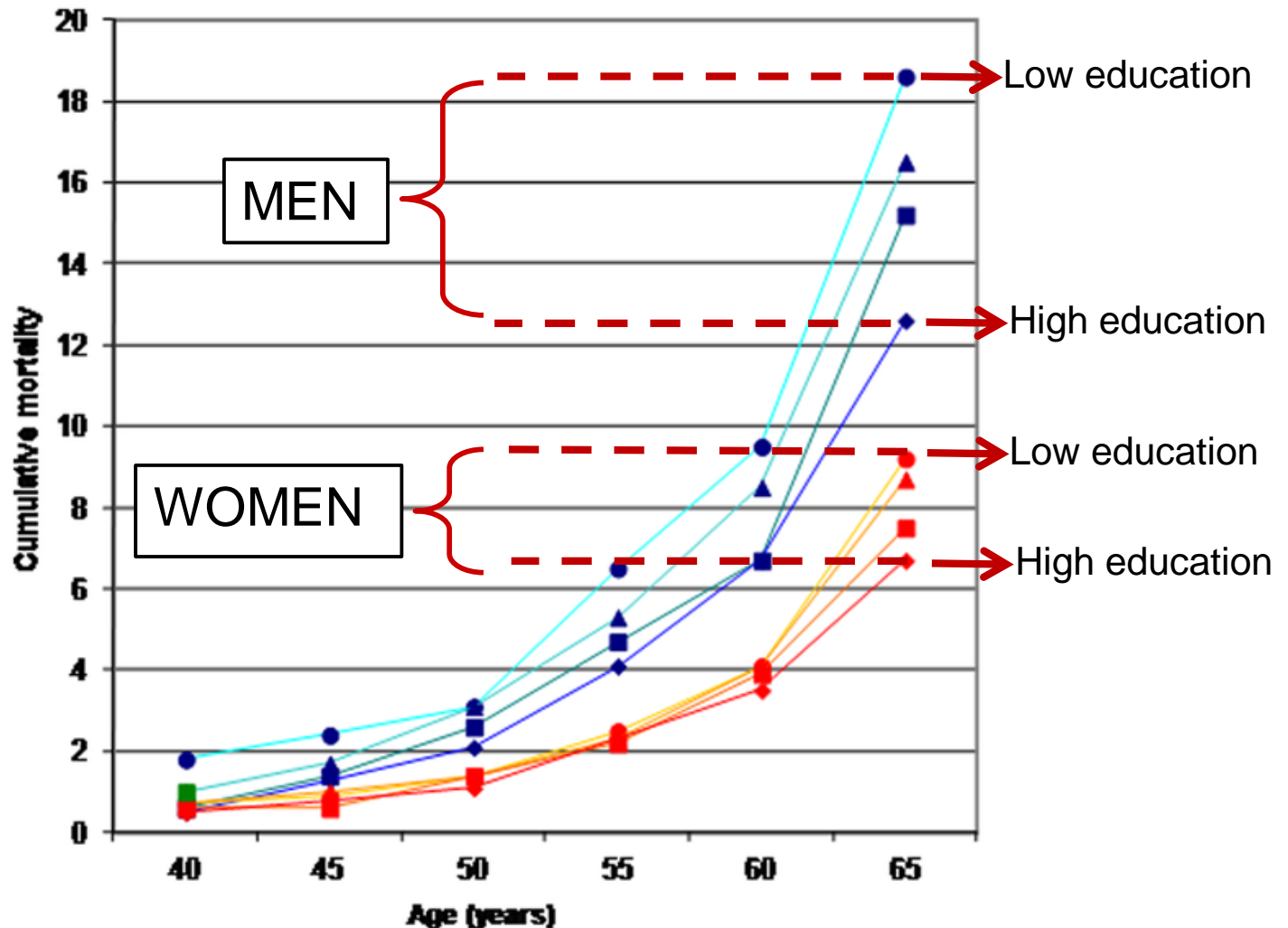
The biological consequences of social inequalities

Dr. PD Silvia STRINGHINI

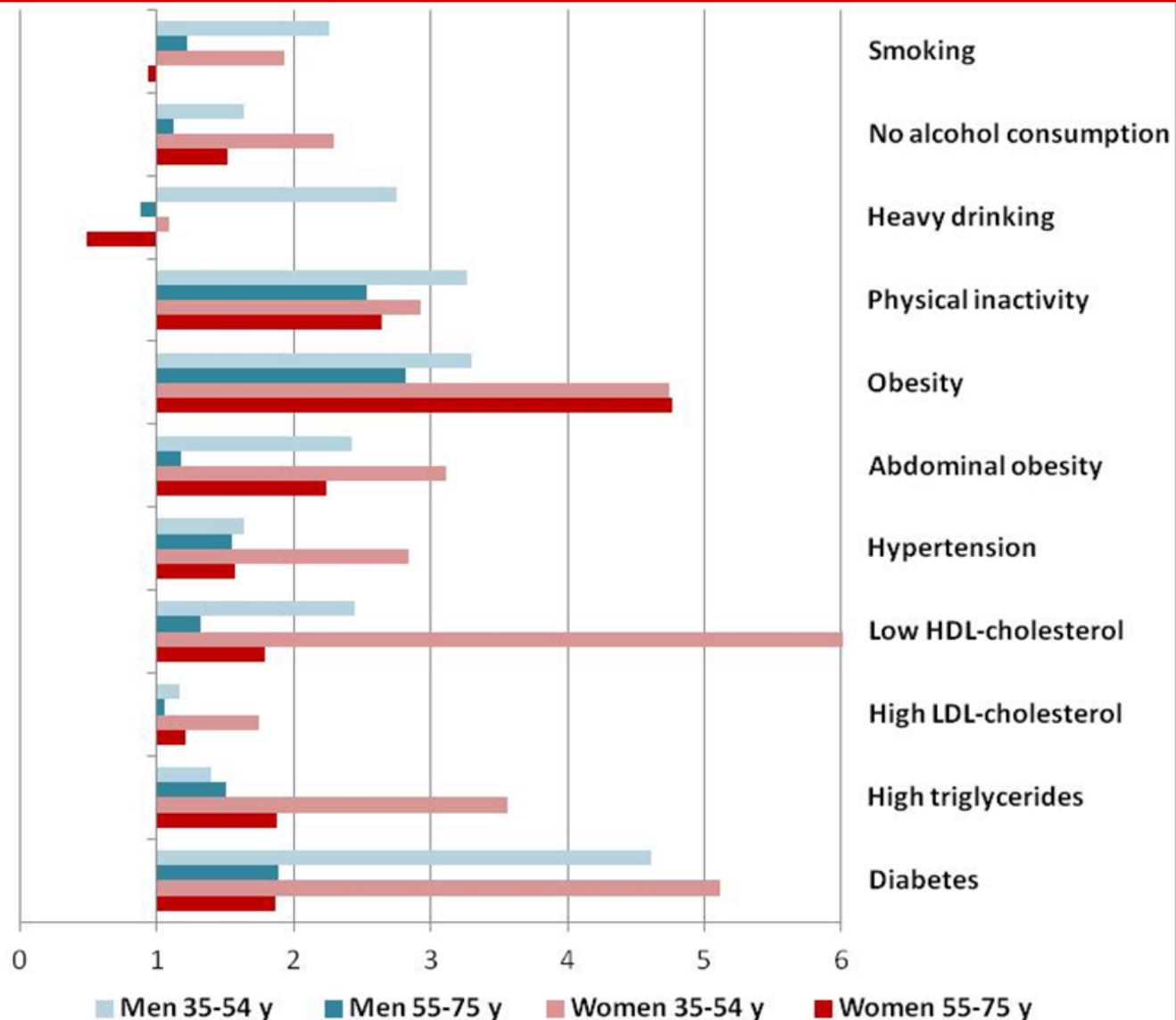
*Research Director
Geneva University Hospital/ Geneva University*

Educational inequalities in mortality

Education and cumulative mortality in Europe (EPIC, 371,295 participants, 9 countries)

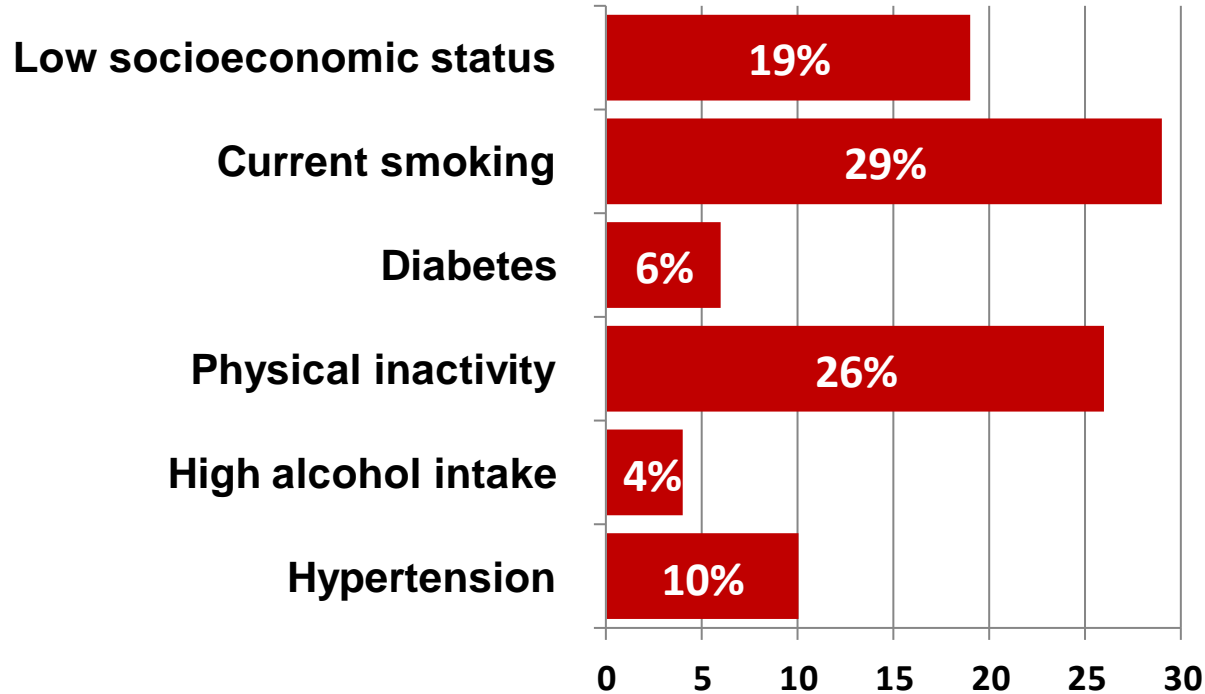


Educational inequalities in cardiovascular risk factors



Impact of social factors on premature mortality

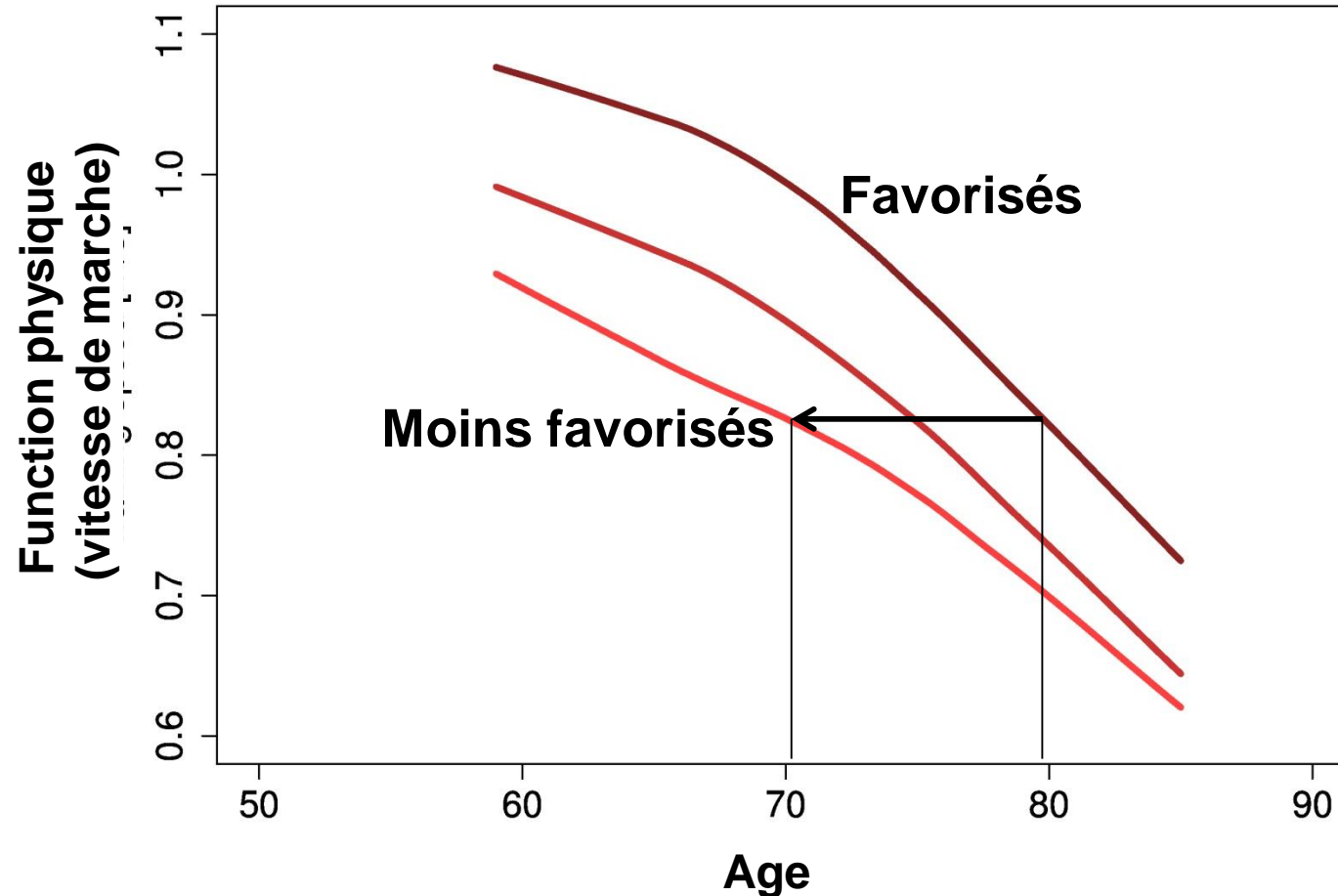
Risque attribuable dans la population à des facteurs de risque sélectionnés
(1.7 million de participants en 7 pays)



Stringhini S et al. *The Lancet*, 2017.

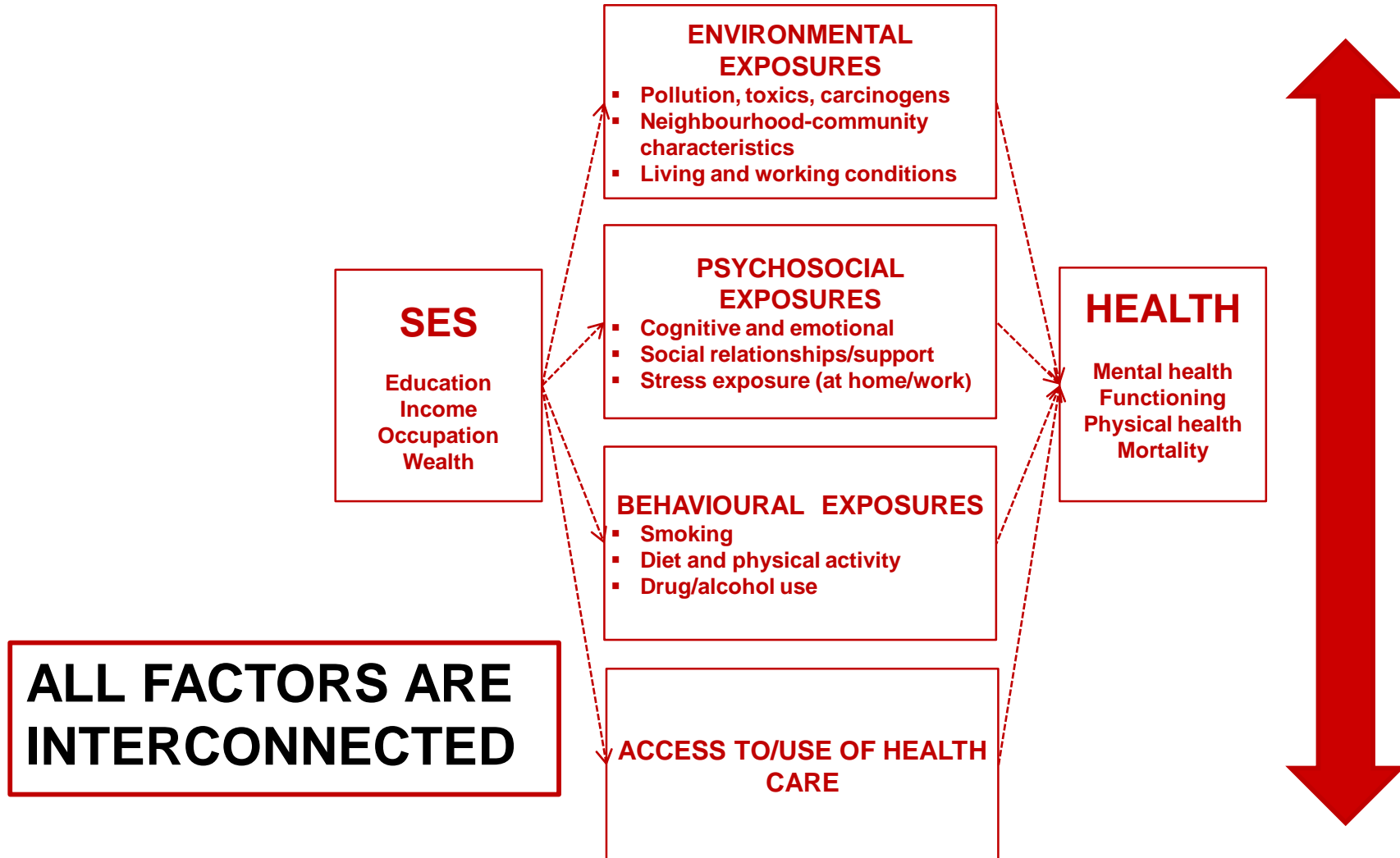
Social factors and trajectories of physical functioning

English Longitudinal Study of Ageing

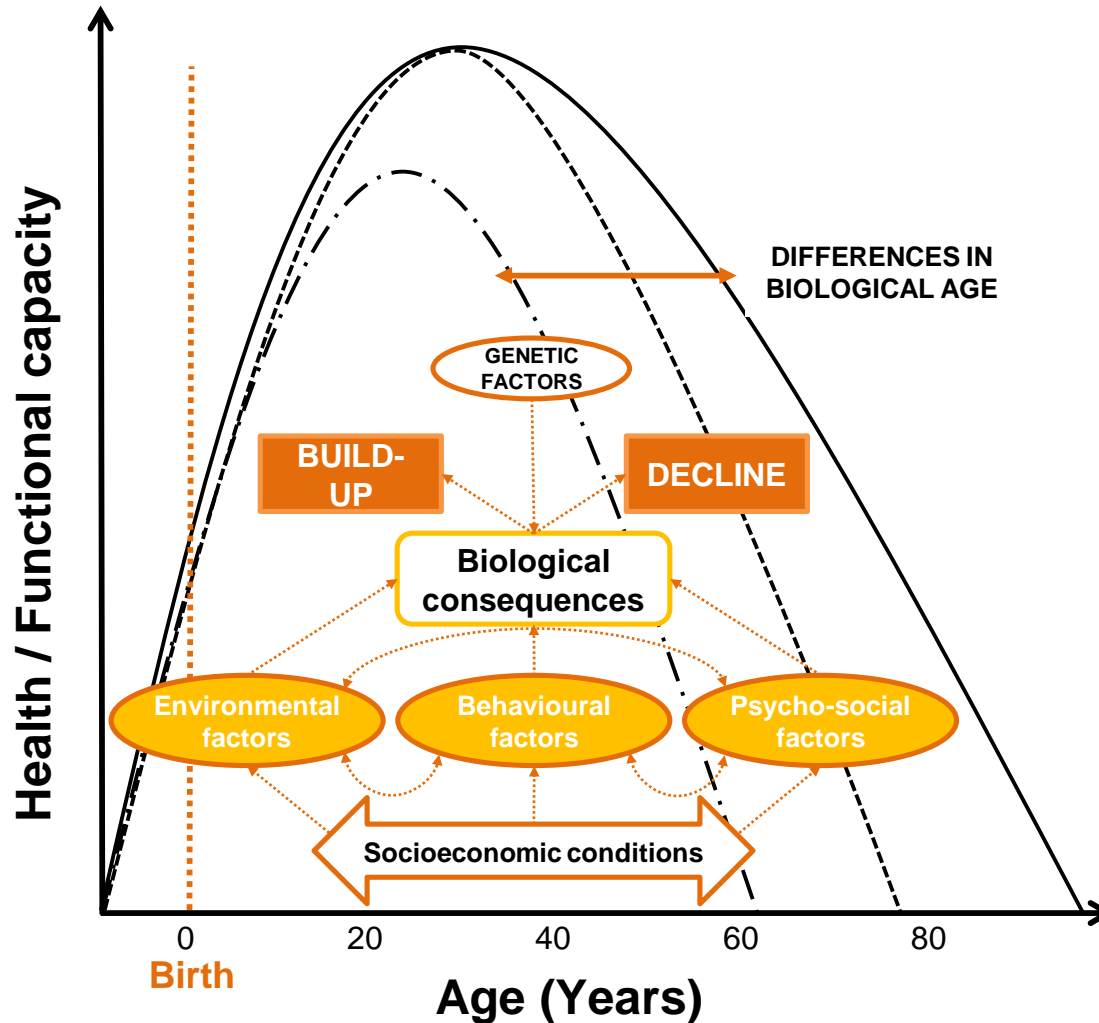


Stringhini S et al., BMJ 2018

Causal explanations for social inequalities in health



The lifecourse perspective



Models of lifecourse perspective

- **Latency model:**

- Exposure to adverse SES in critical/sensitive periods alters biological parameters permanently (fetal programming; traumatic events during first year etc.)

- **Cumulation model:**

- Cumulative effect of exposure to low SES (and its associated factors) across the lifecourse

- **Pathway model:**

- Low SES in early life influence social mobility pathways and behaviours

Embodiement

“we literally incorporate, biologically, the material and social world in which we live, from in utero to death; a corollary is that no aspect of our biology can be understood absent knowledge of history and individual and societal ways of living.”

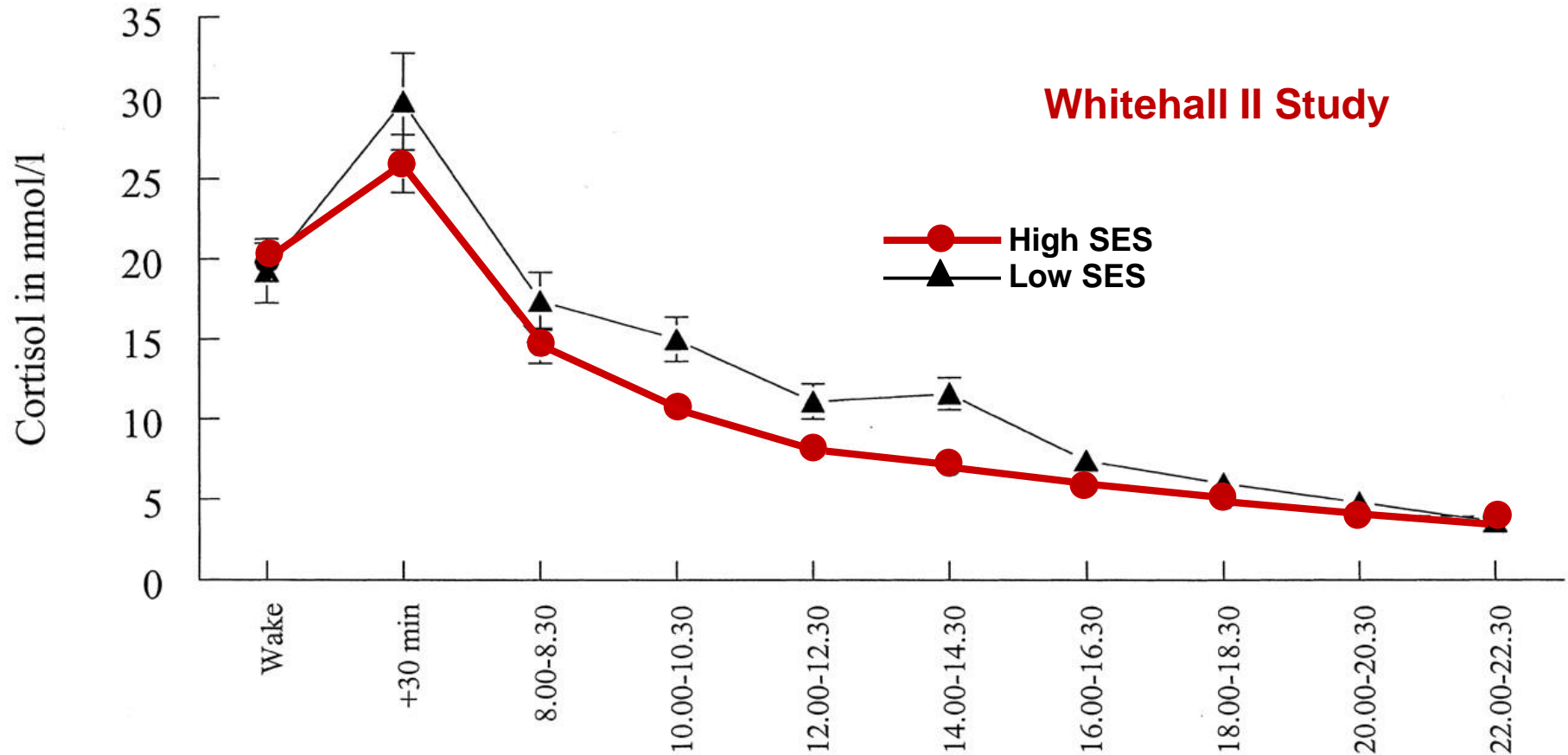
Nancy Krieger JECH 2001

SES and biomarkers

Hypothalamic-pituitary-adrenal axis	Cortisol - Saliva, urine Dehydroepiandrosterone sulfate - Blood
Sympathetic neuro-hormonal system	Norepinephrine/Epinephrine - Urine Alpha-amylase - Saliva
Parasympathetic neuro-hormonal system	Heart rate variability - Pulse rate recording
Inflammatory/Immune system	C-reactive protein - Blood Erythrocyte sedimentation rate - Blood Interleukins - Blood Lymphocyte number and function - Blood Circulating serum albumin - Blood, saliva
Cardiovascular	Diastolic/systolic blood pressure Resting heart rate
Glucose metabolism	Fasting glucose - Blood Glycosylated hemoglobin - Blood Fasting insulin - Blood
Lipid metabolism	Cholesterol and lipoprotein fractions - Blood BMI, waist to hip ratio Total body fat - DXA scan
Hematological	Serum hemoglobin - Blood Clotting factors and clotting time - Blood
Renal	Creatinine - Serum or 24h urine Urine albumin leakage - Urine Cystatin C - Serum or dried blood spot
Hepatic	Circulating serum albumin - Blood, saliva
Reproductive	Serum testosterone/estradiol - Blood Follicle-stimulating hormone - Blood
Pulmonary	Arterial oxygen saturation - Pulse oximeter Peak expiratory flow - Spirometer
Bone	Bone density - DXA scan Bone turnover markers - Blood, fasting urine
Muscle	Skeletal muscle mass - DXA scan, body impedance Grip strength - Dynamometer
DNA	Epigenetic markers

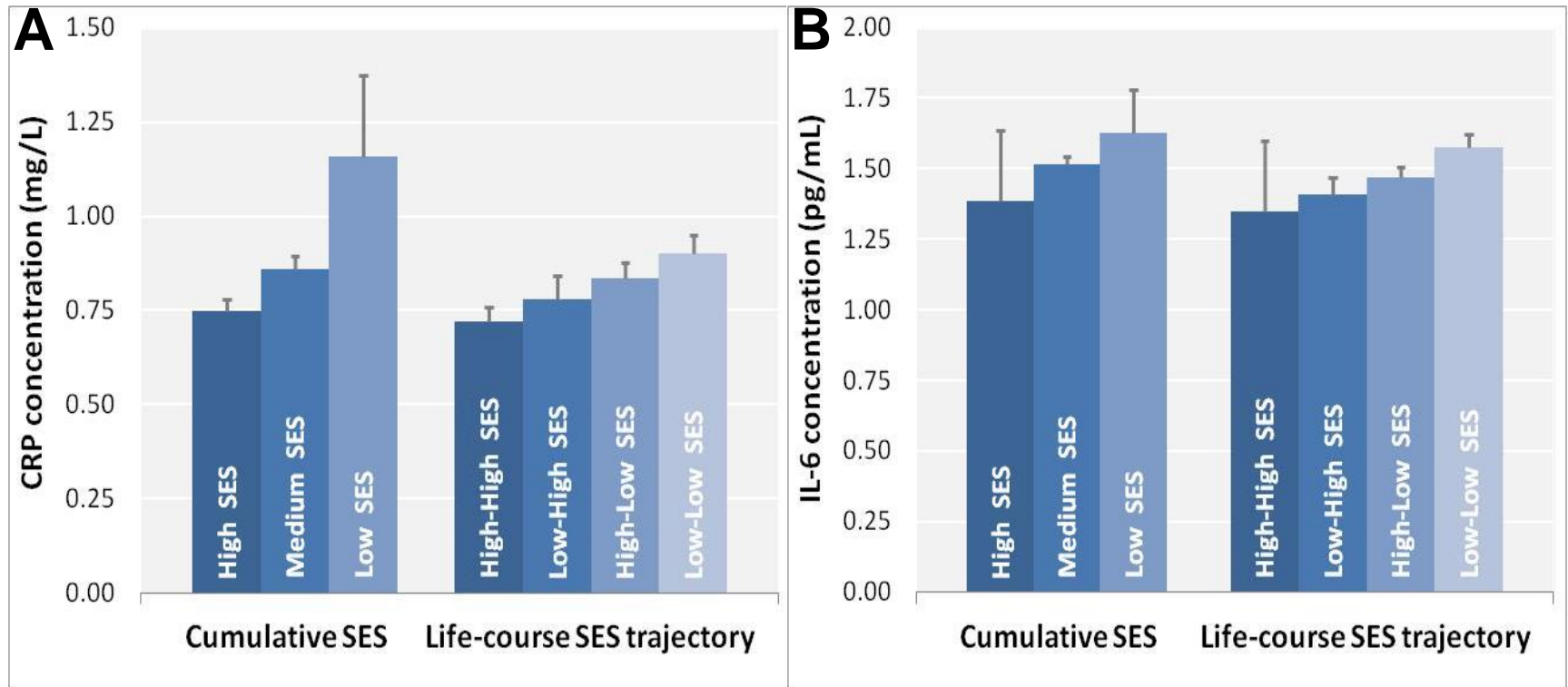
SES and HPA-axis dysregulation

Mean saliva-free cortisol sampled on waking up, 30 minutes later, and then at 2-hour intervals



SES and immune system biomarkers

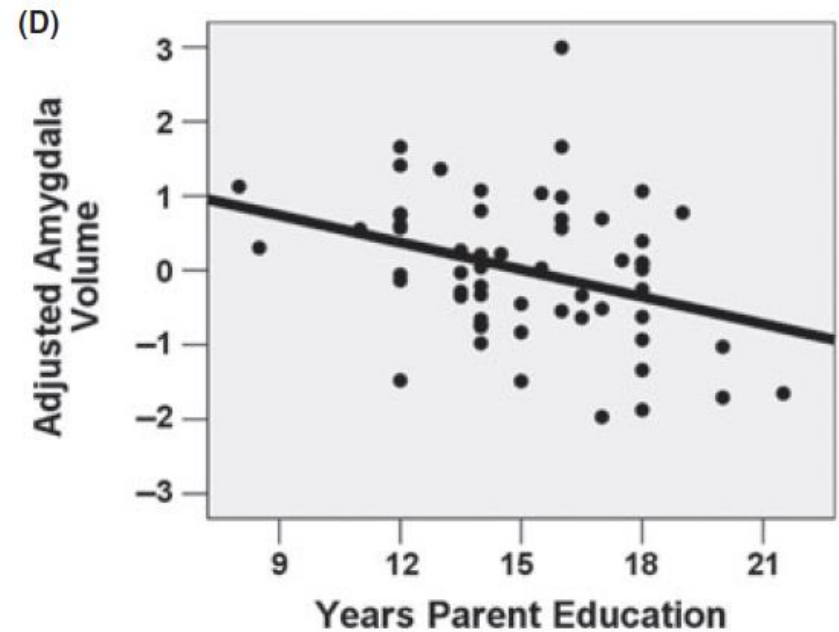
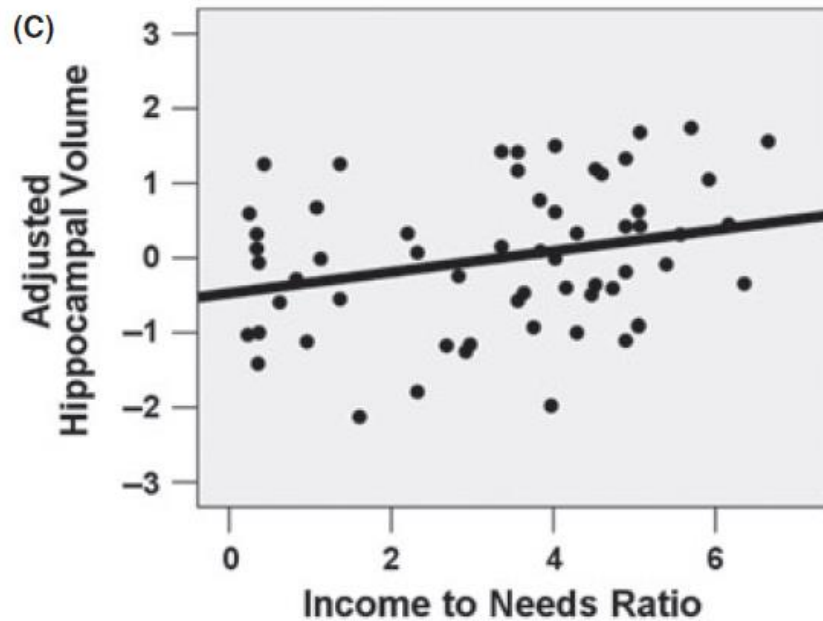
Lifecourse SES and CRP and IL-6 concentration



Whitehall II Study

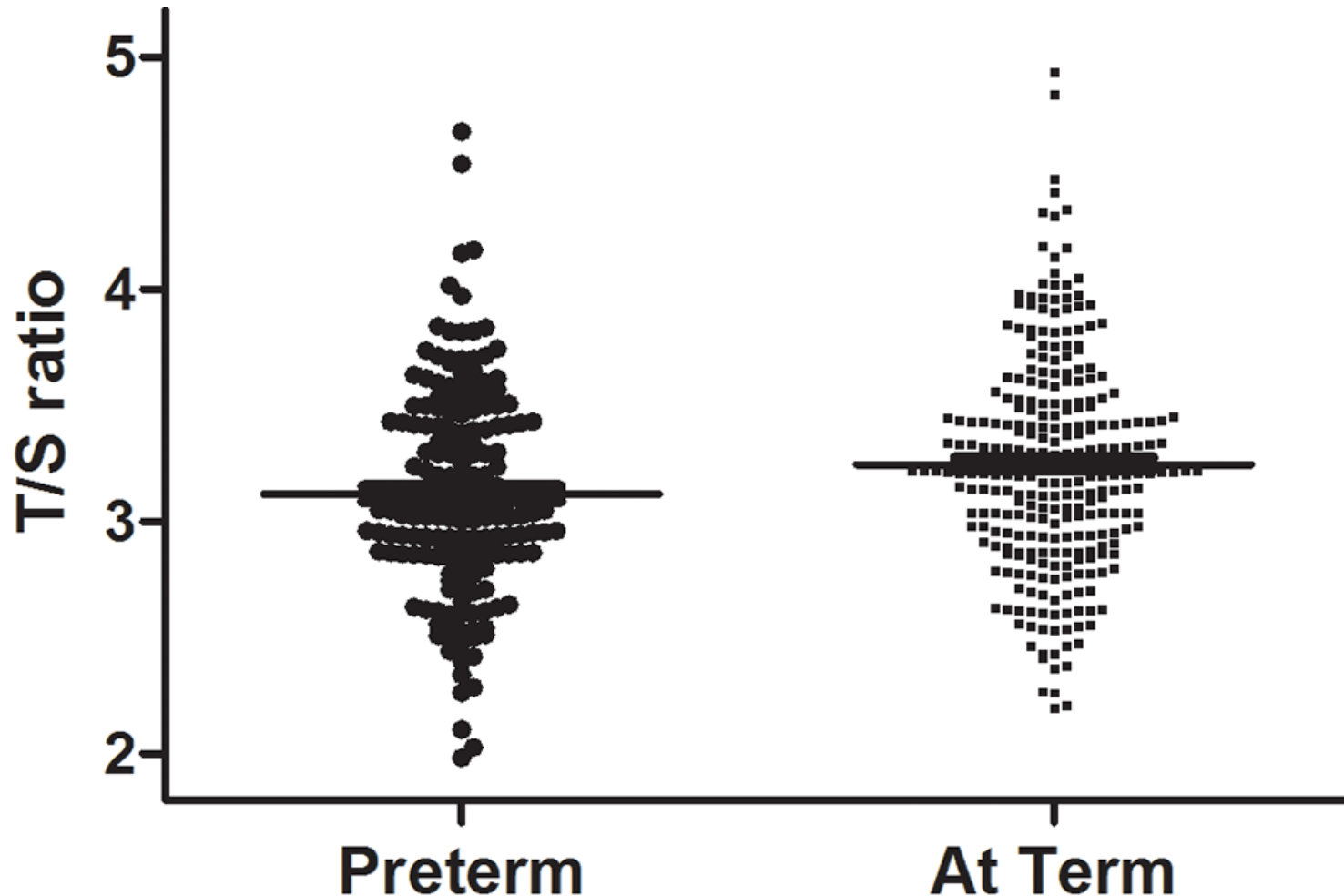
SES and neural structure

60 typically developing, native English speaking children (US)



Stressful events in early life generally related to lower hippocampal and higher amygdala volume

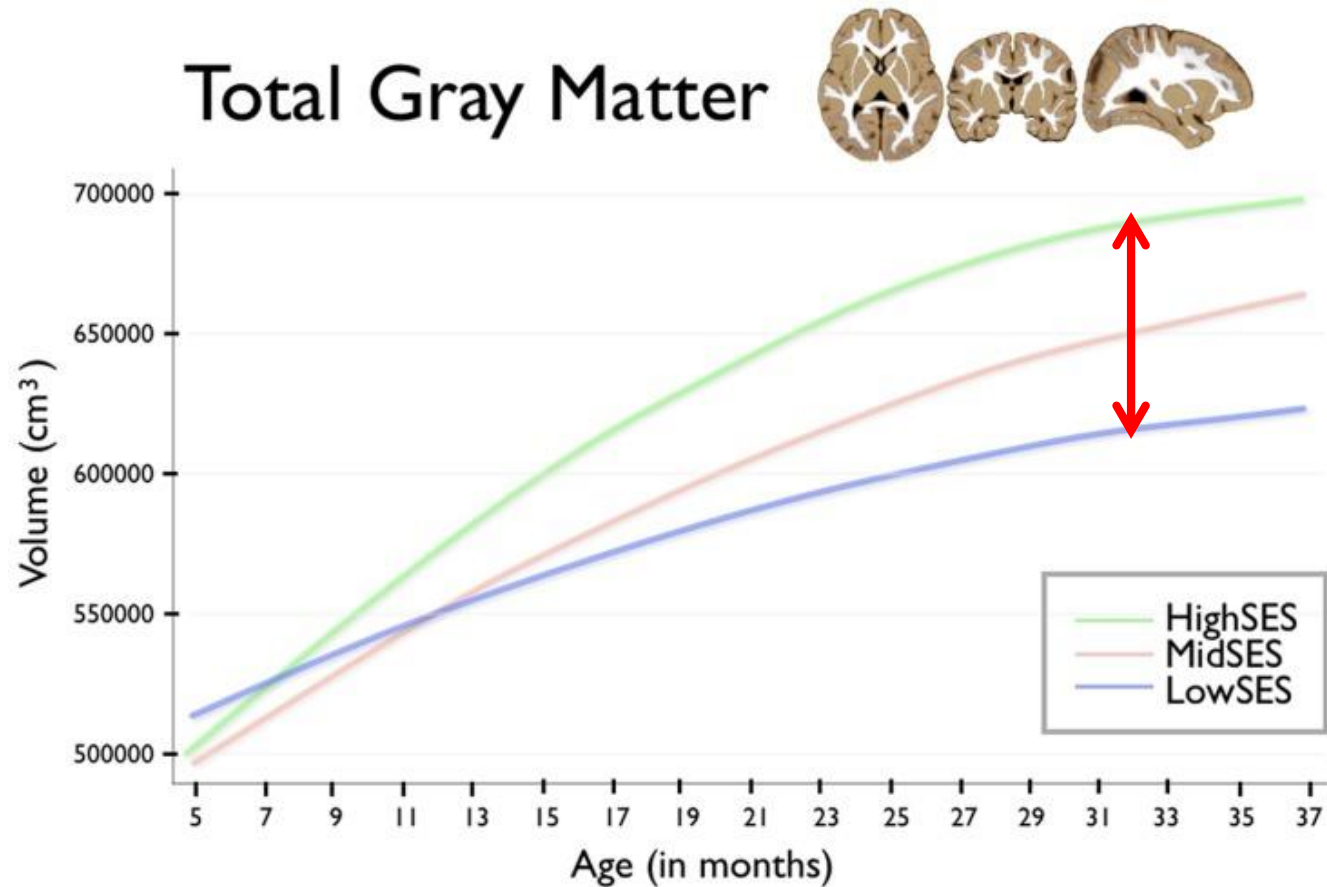
Preterm birth and telomere length



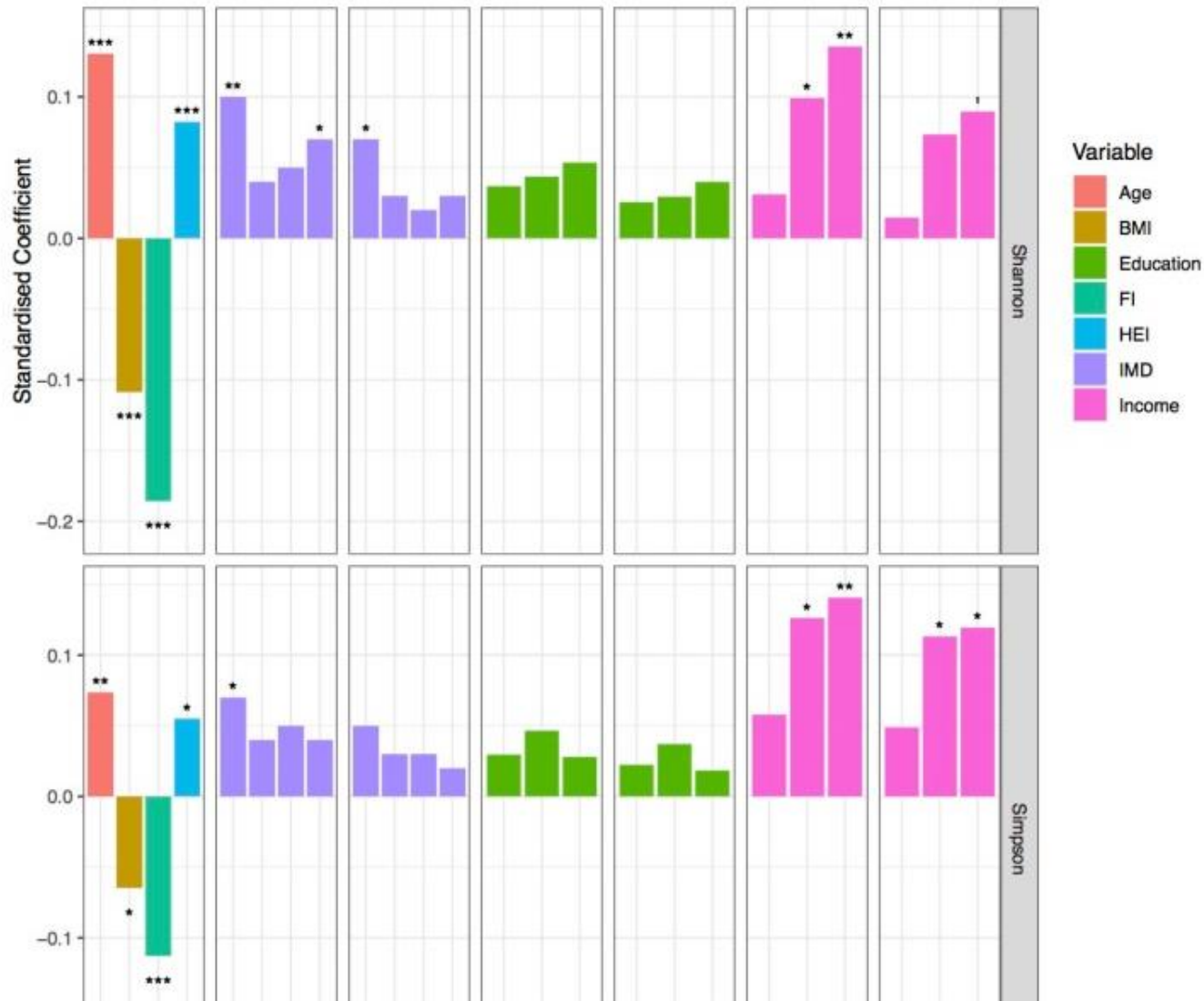
T/S ratio = Telomere to single-gene copy ratio. Preterm = gestational age <37 weeks. The horizontal bars represent the mean values.

Social factors and brain development

US NIH MRI Study of Normal Brain Development, N=55 healthy children



Social factors and gut microbiome



SES and gene regulation

Low early-life social class leaves a biological residue
manifested by decreased glucocorticoid and increased
proinflammatory signaling

Social
variation



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Original article



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Social Determinants

Life-course socioeconomic status and DNA methylation of genes regulating inflammation

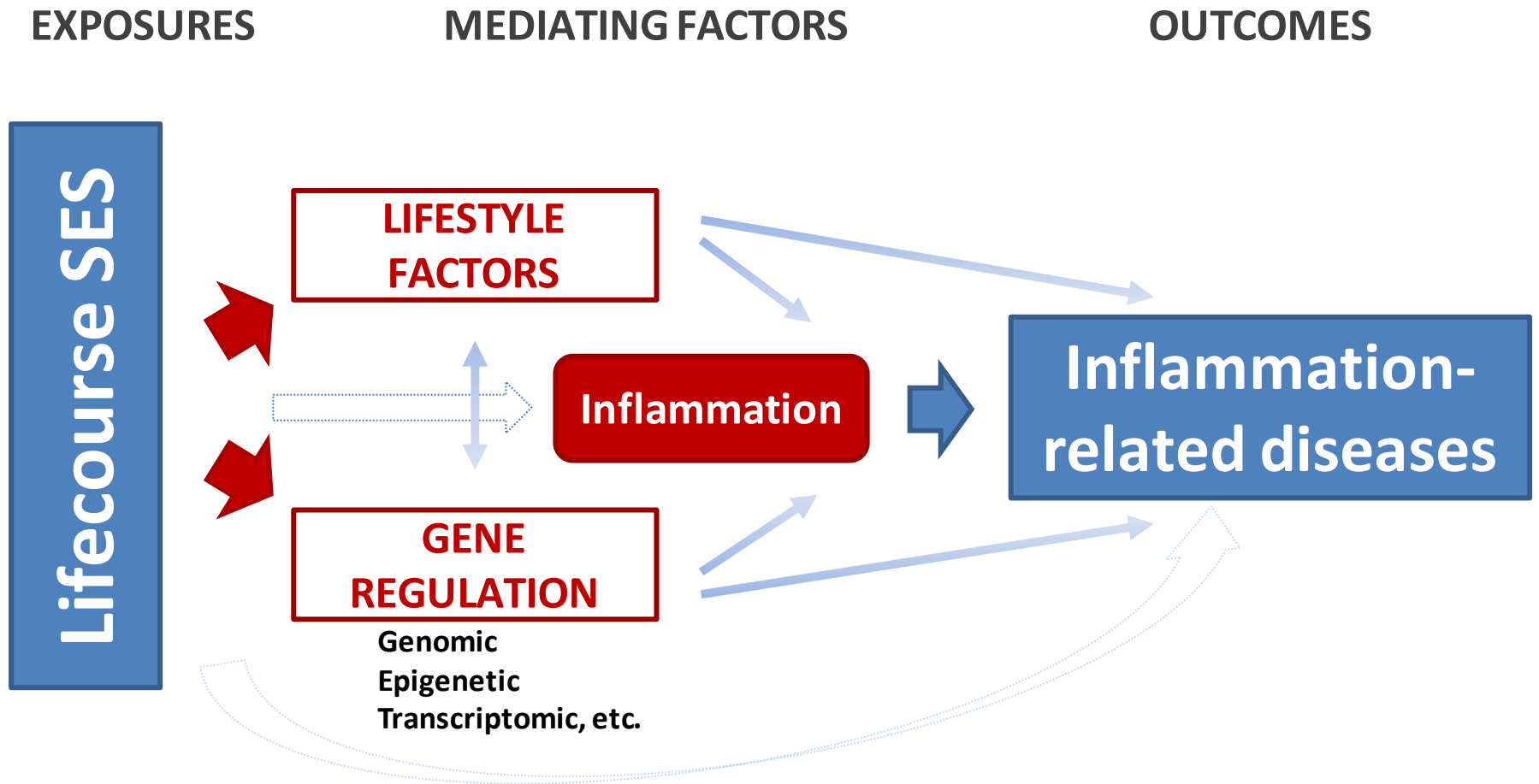
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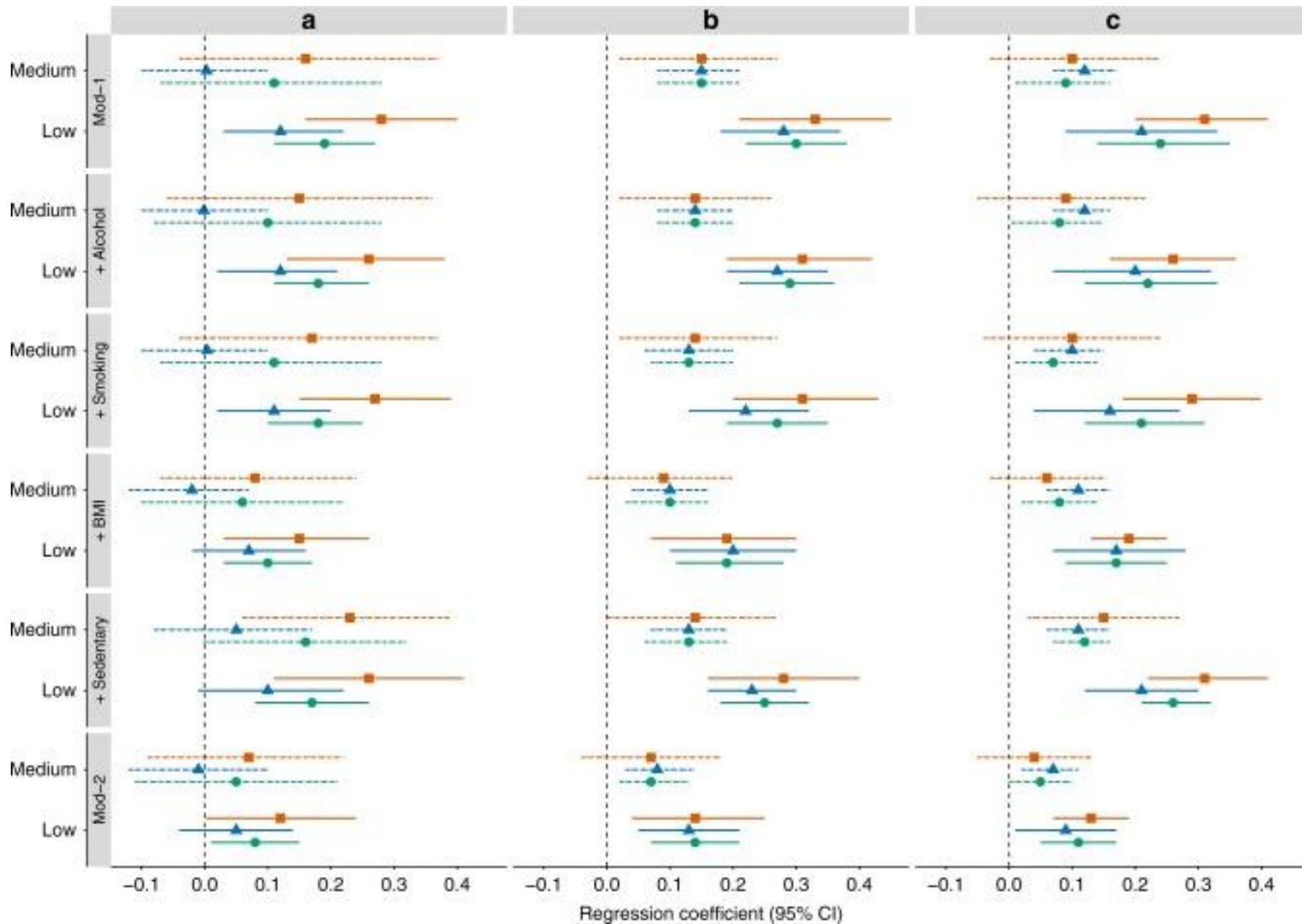
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SES and gene regulation

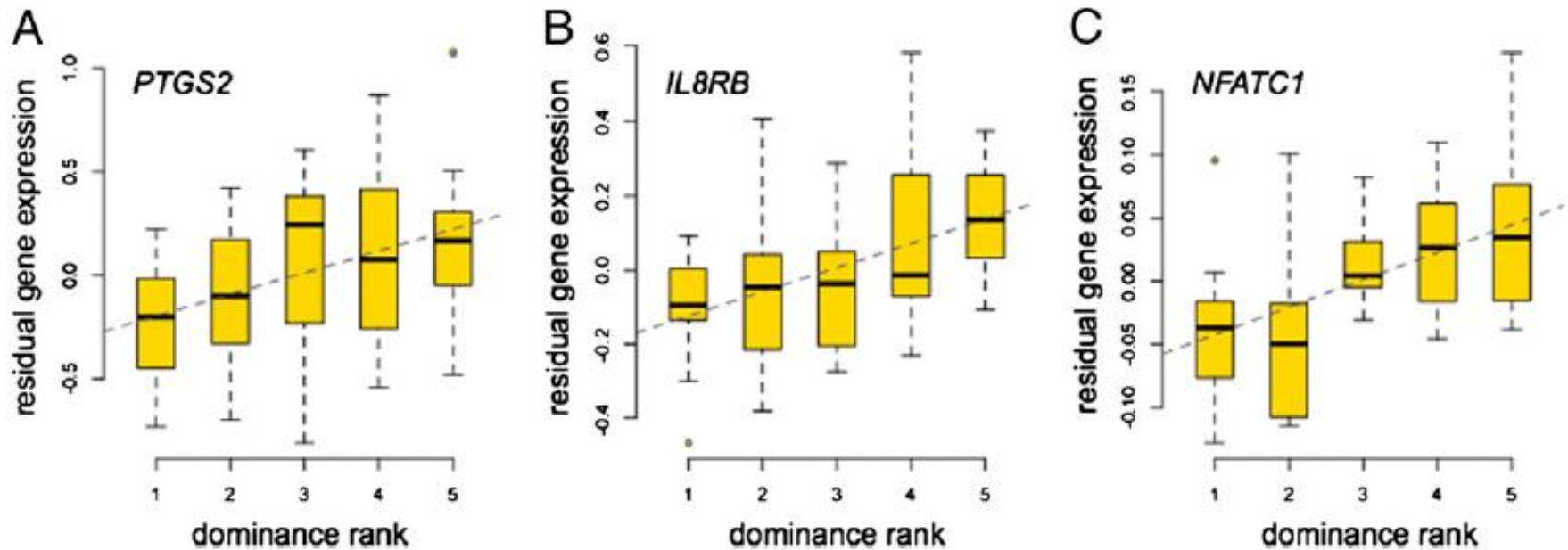


SES and inflammation

SES across the lifecourse and CRP among 23'000 participants in 6 cohorts



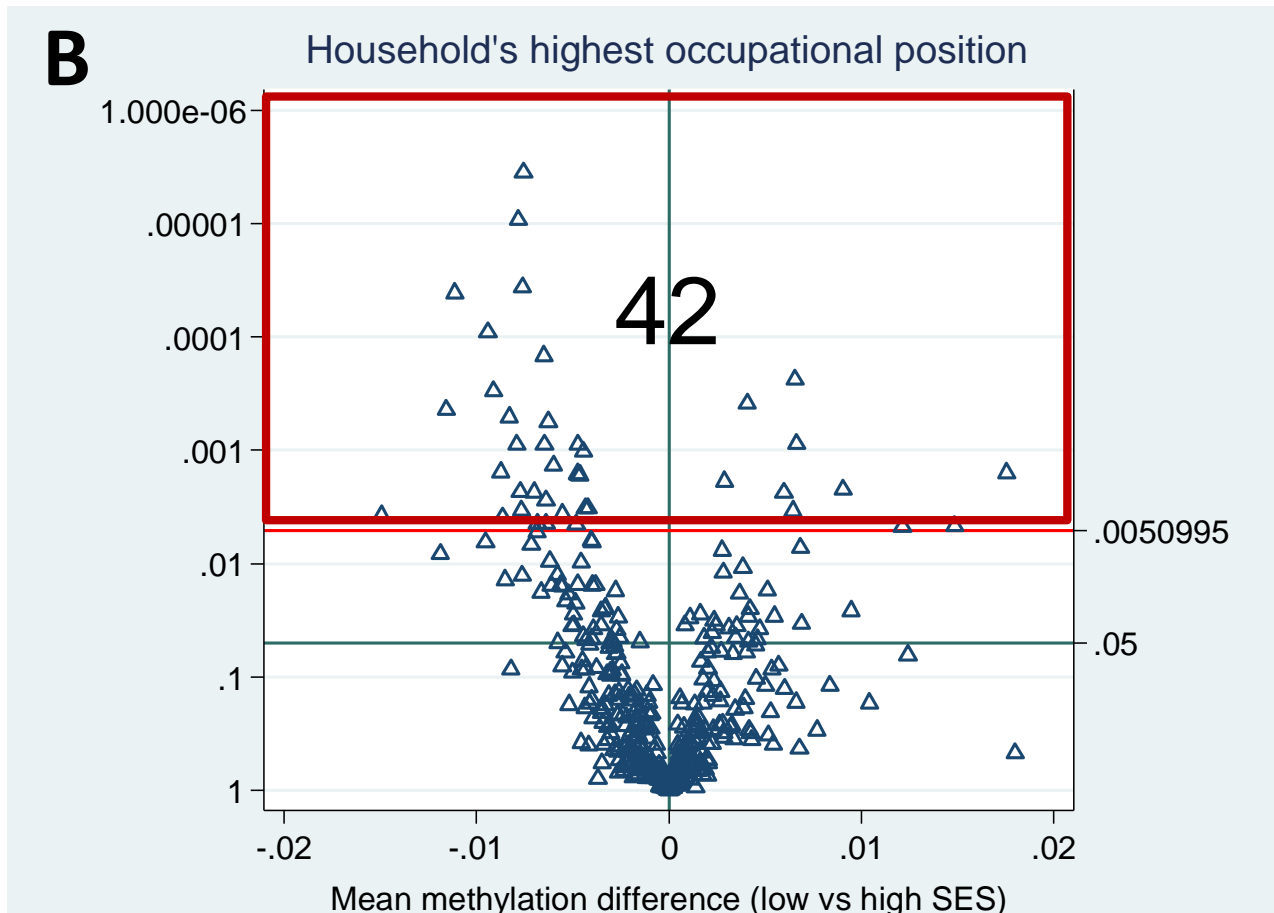
Dominance rank and proinflammatory genes expression (macaques)



Socioeconomic status and DNA methylation

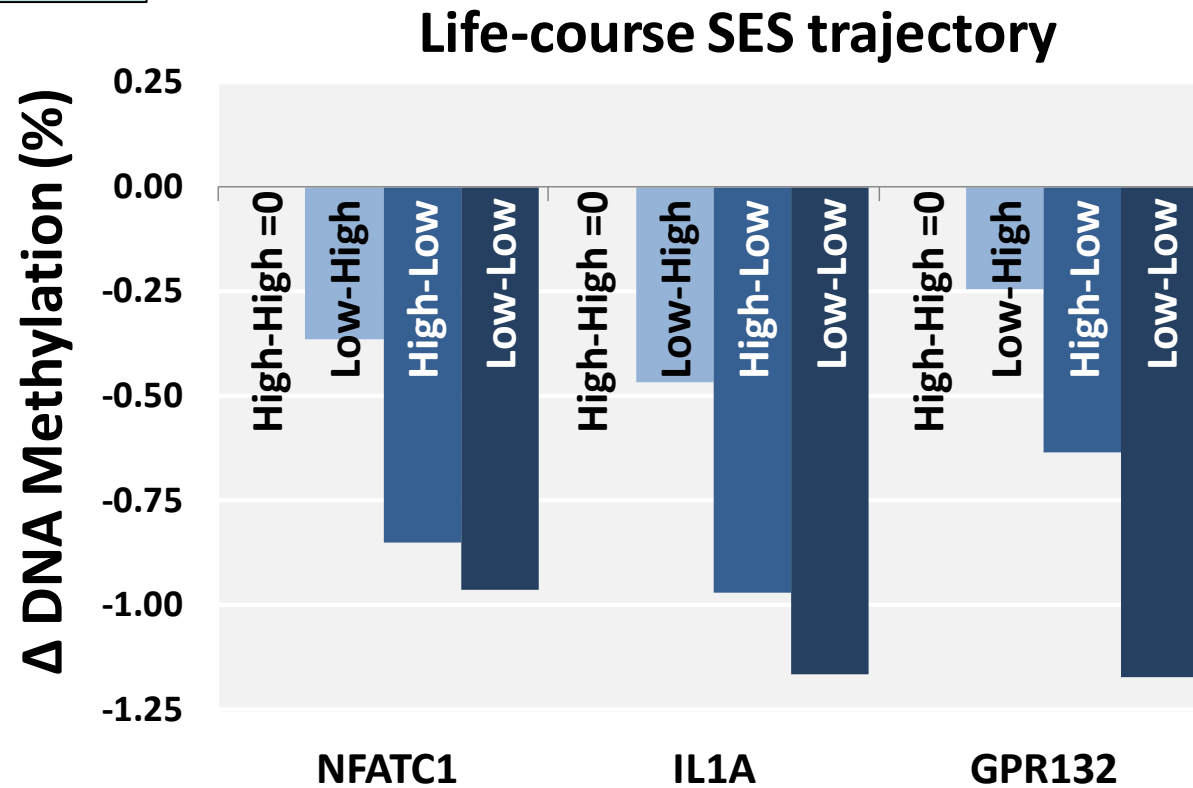
- **Population:** prospective cohort study of 857 individuals, sampled from the 47'749 participants of the EPIC-Italy study
- DNA extracted from white blood cells
- SES in early and adult life + lifecourse SES trajectories
- Genome wide methylation data available (450K)
- 17 genes (403 CpG sites) chosen on the basis of their involvement in SES-related inflammation in previous studies

Main results: household's occupation and DNA methylation

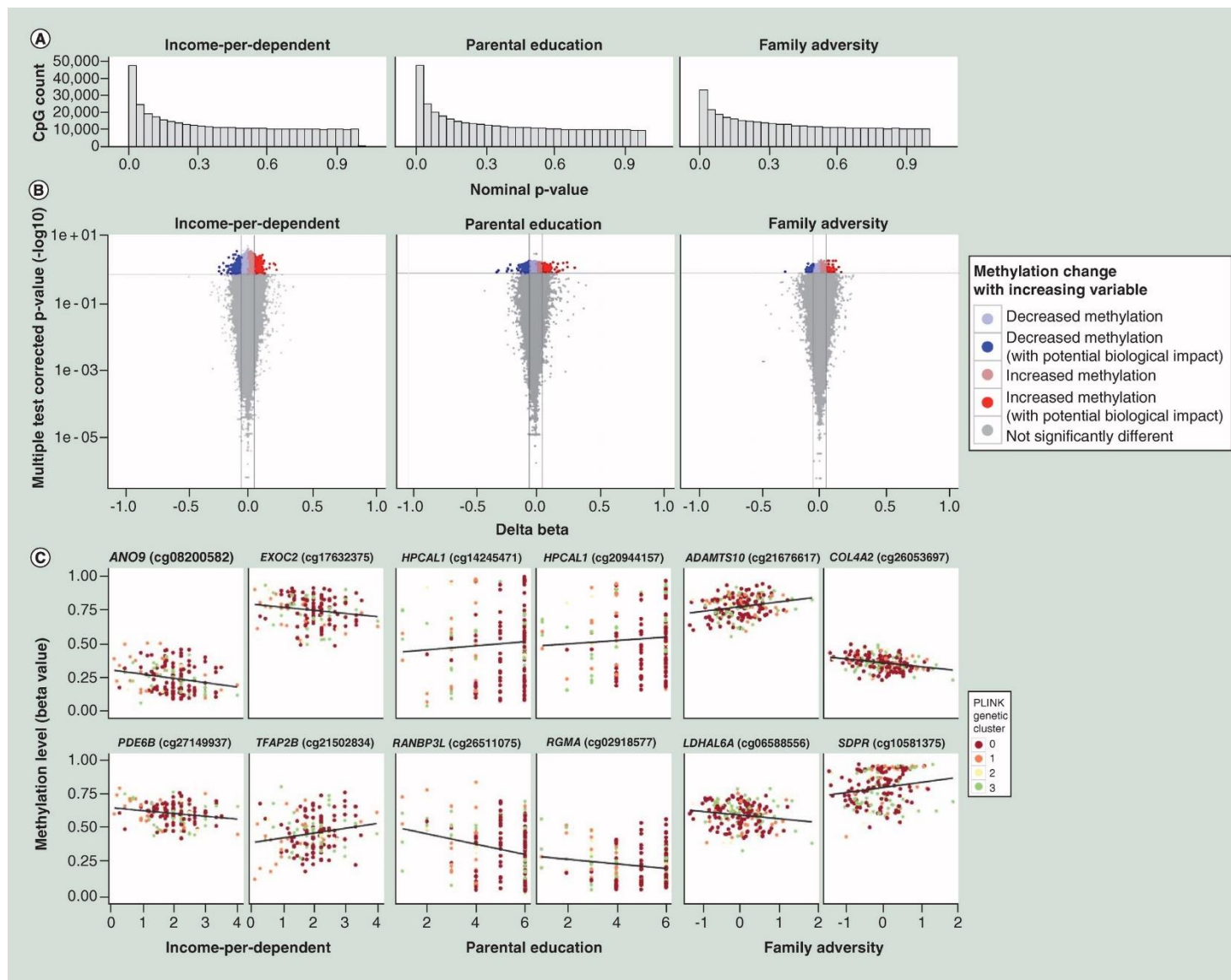


SES trajectory e DNA methylation of proinflammatory genes

EPIC ITALY

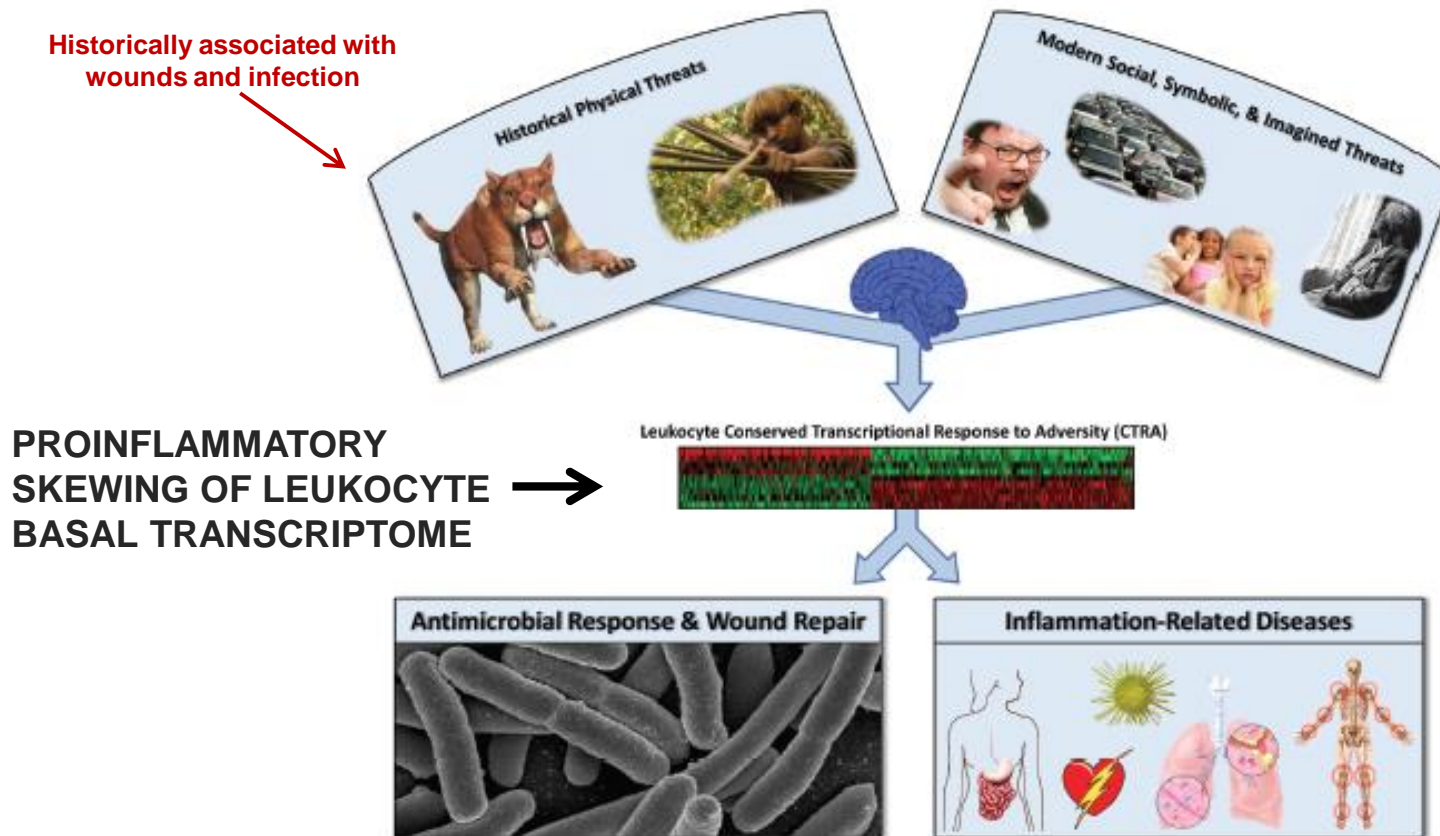


SES trajectory e DNA methylation of proinflammatory genes



Conserved transcriptional response to adversity (CTRA)

Neurobiological activation of leukocyte inflammatory genes and inhibition of innate antiviral genes in response to subjectively experienced physical or social threat



Human Social Genomics

- Socio-environmental conditions associated with hundreds of «socially-sensitive» genes
 - ✓ urbanity
 - ✓ low socioeconomic status
 - ✓ social isolation
 - ✓ social threat
 - ✓ low or unstable social status
- Majority of studies examined leukocytes or diseases tissues

Concept of the reactive genome

- Genes are unfolding in specific social and historical *milieu* → *change in paradigm where DNA not anymore the master of the cell but “sometimes comes to look like a servant, serving the proteins by being their memory”* (Morange, 2001, Shapiro, 2002)
- Heritability of non-genetic features (ie. Transgenerational transmission of epigenetic traits)
- Nature and nurture no longer understood as dichotomous elements

Challenges

- Few studies with biomarkers, fewer with repeated measures of biomarkers, very very few with epigenetics and/or transcriptomics measures with good exposure data
- When data exist, sample is small and not always exposure data is good enough (ie: SES indicators poorly collected)
- Concerning SES-epigenetics:
 - ✓ Need to replicate results on larger studies
 - ✓ Test whether SES differences in methylation translate into differences in gene expression and circulating molecules
 - ✓ Test whether this can partly explain social differences in health
 - ✓ Explore link between SES and gene-regulation in other tissues
- At this stage, no clear policy implications of this research if not for identification of exposures and of critical time windows

Conclusions

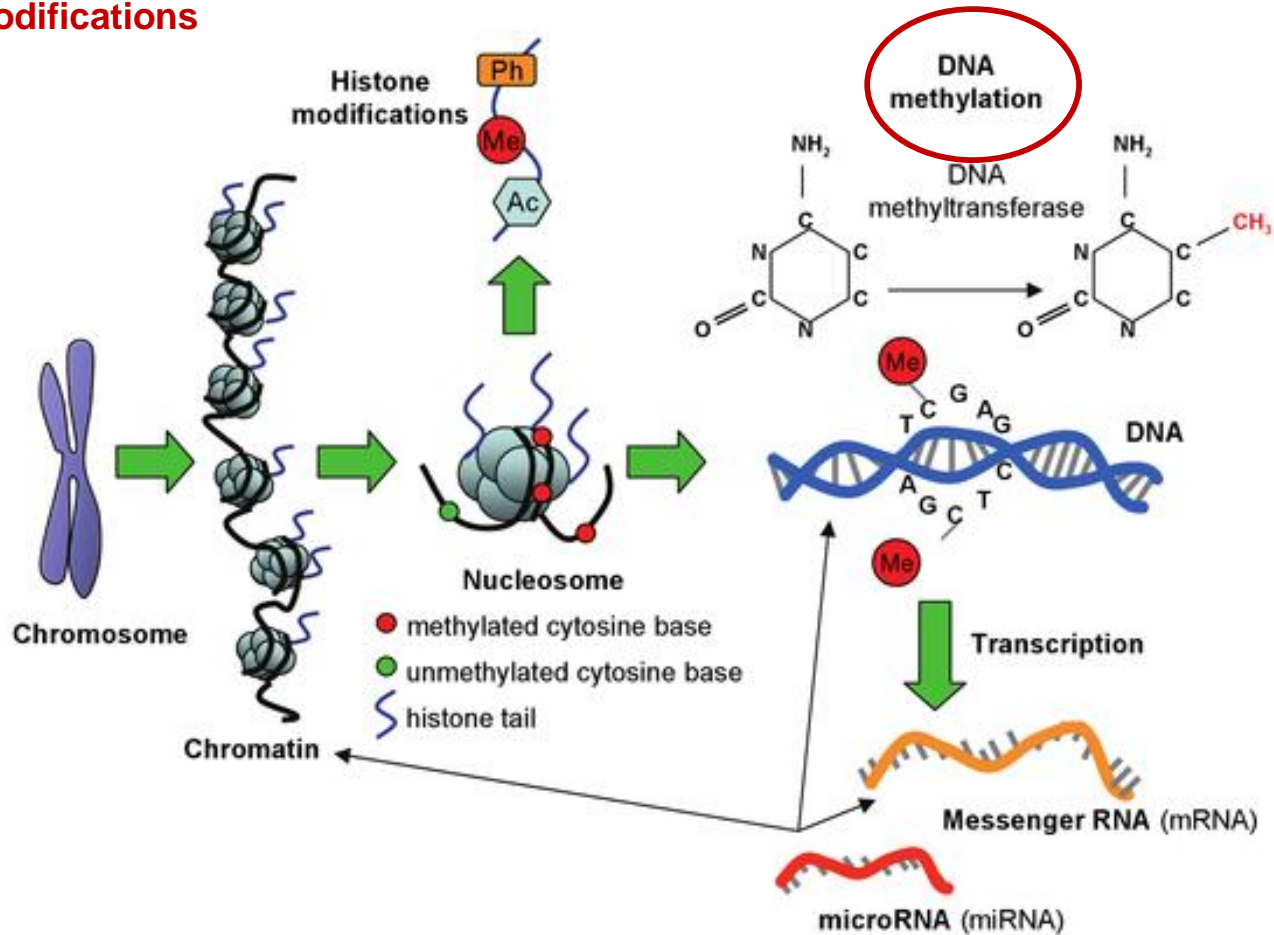
- Social factors are integrated biologically from birth (or earlier)
 - ✓ Various pathways of integration
 - ✓ Various windows of integration → of intervention?
 - ✓ Exposures from conception to old age
- Need better data and more interdisciplinary research
- Public health impact as well as phylosophycal/ethical implications not clear

**Thank you for
your attention!**



Epigenetics – DNA methylation

Epigenetic modifications



Relton CL, Davey Smith G (2010) Epigenetic Epidemiology of Common Complex Disease: Prospects for Prediction, Prevention, and Treatment. PLoS Med 7(10): e1000356. doi:10.1371/journal.pmed.1000356