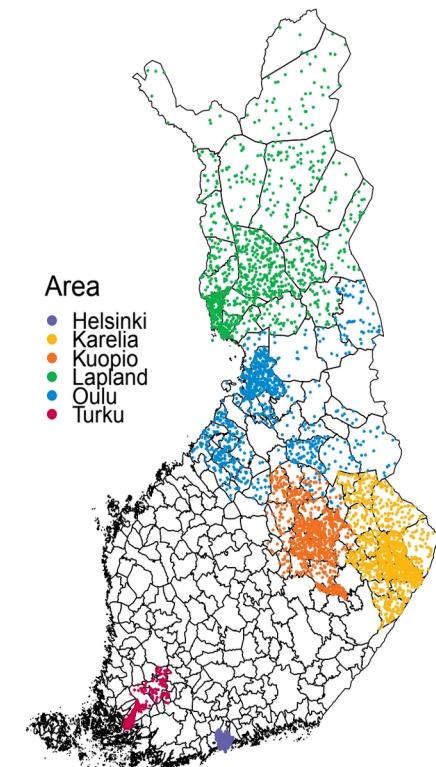


# Taxonomic Signatures of Long-Term Mortality Risk in Human Gut Microbiome

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IHMC 2021



# FINRISK 2002 cohort and follow-up register data

Prospective setup, data & methods

Long follow-up (now 18 years)

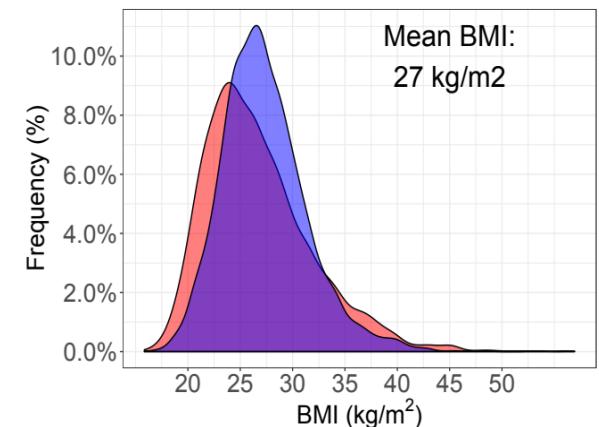
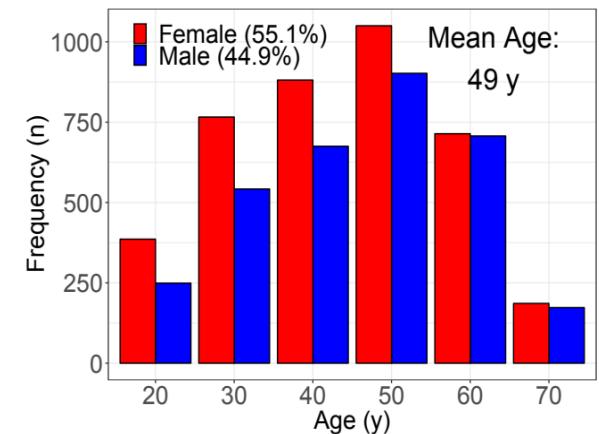
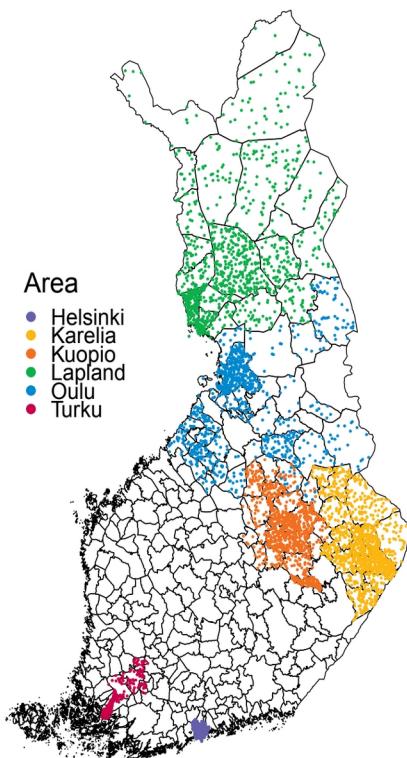
High quality register data

## FINRISK 2002 (THL)

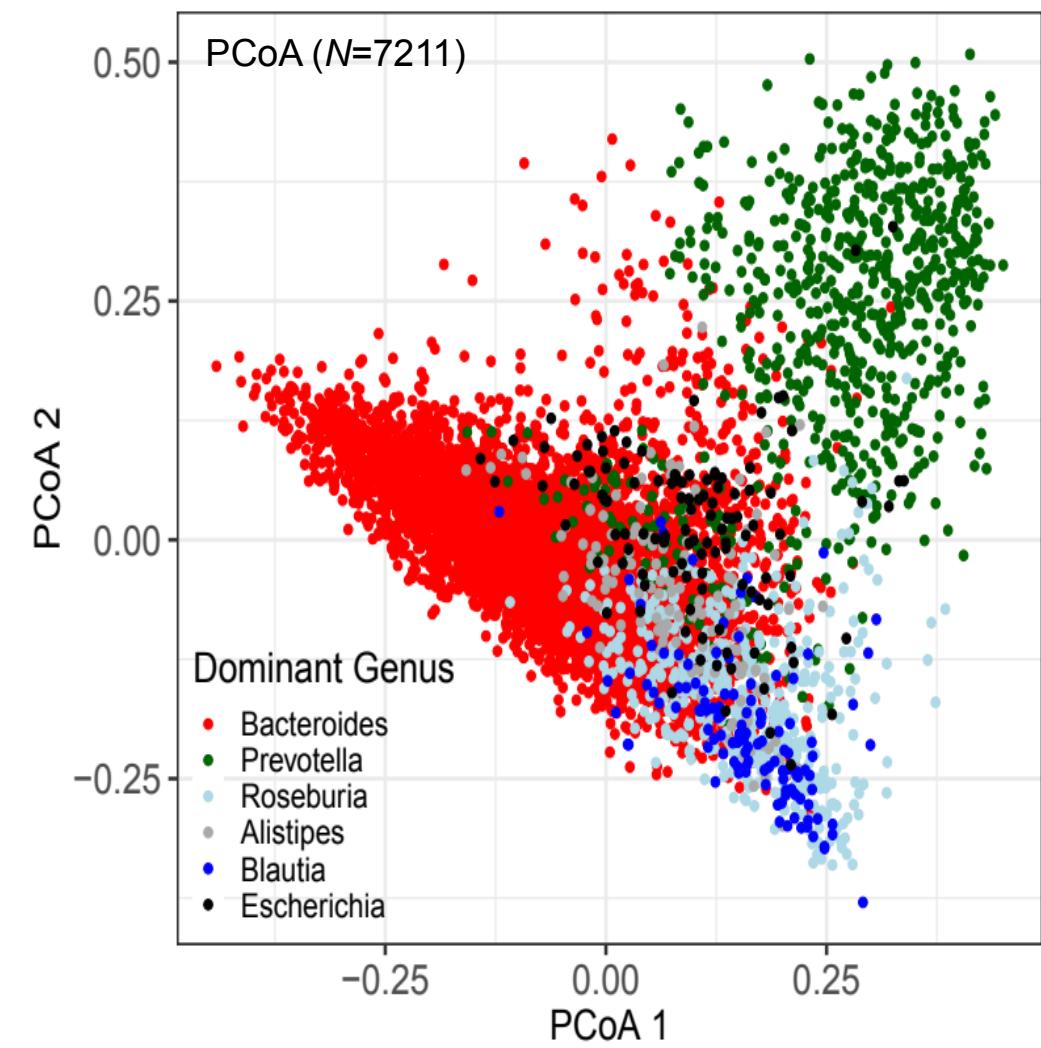
**2002** ~7200+ adult stool samples:  
omics and clinical measurements

**2016** ~15+ year follow up; 721  
(10%) deaths

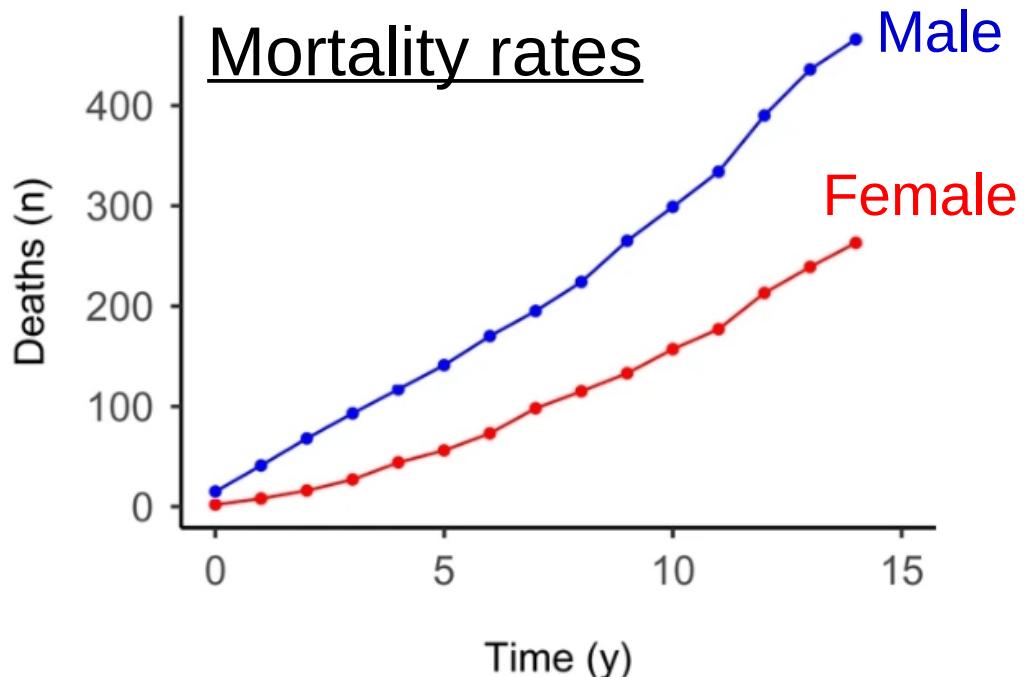
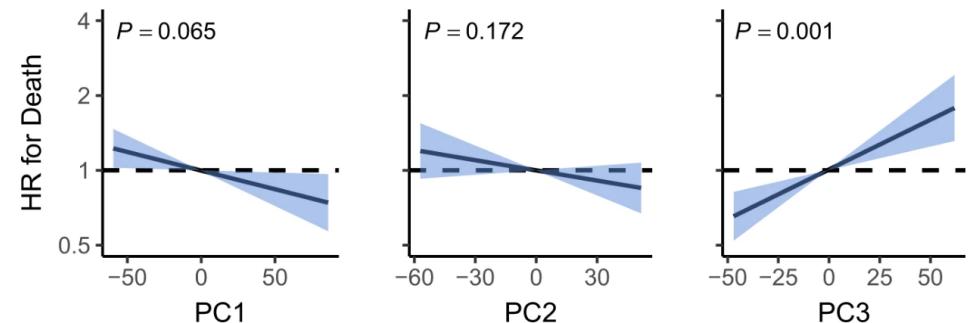
Shallow shotgun metagenome  
(~1M reads/sample)



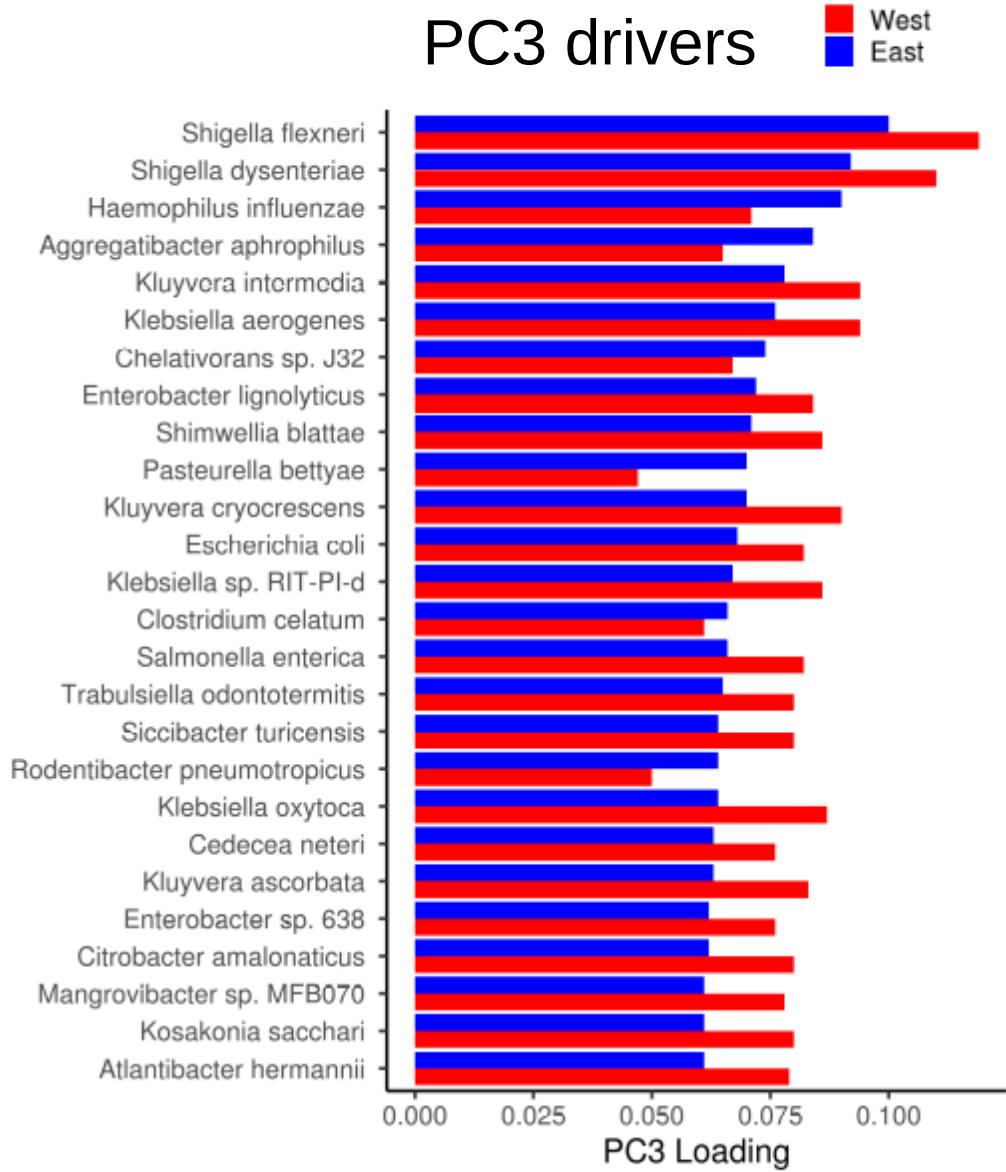
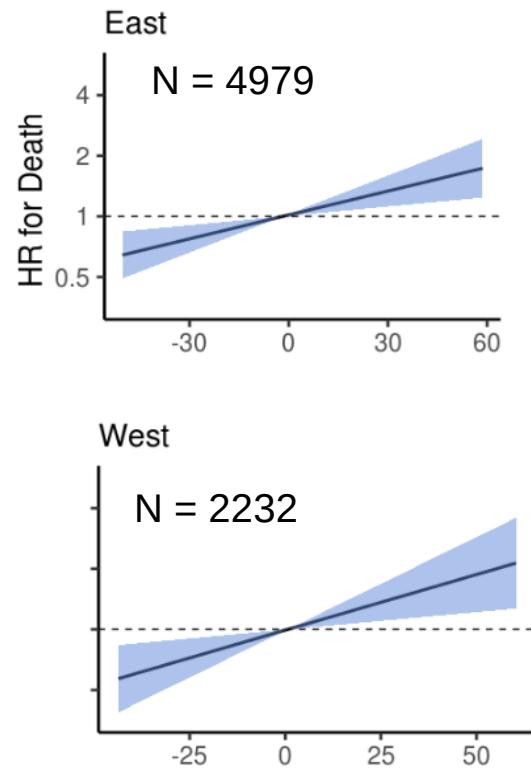
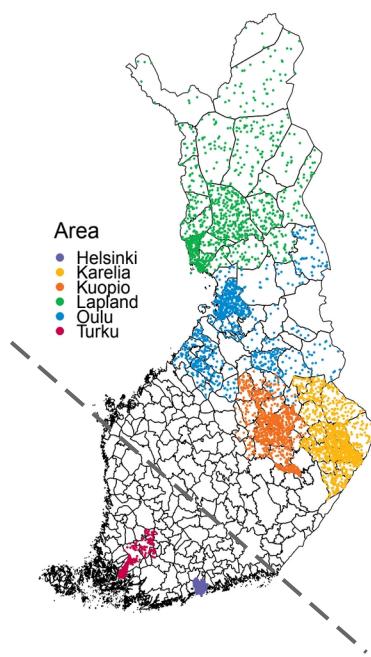
# Population landscape, dominance, and mortality



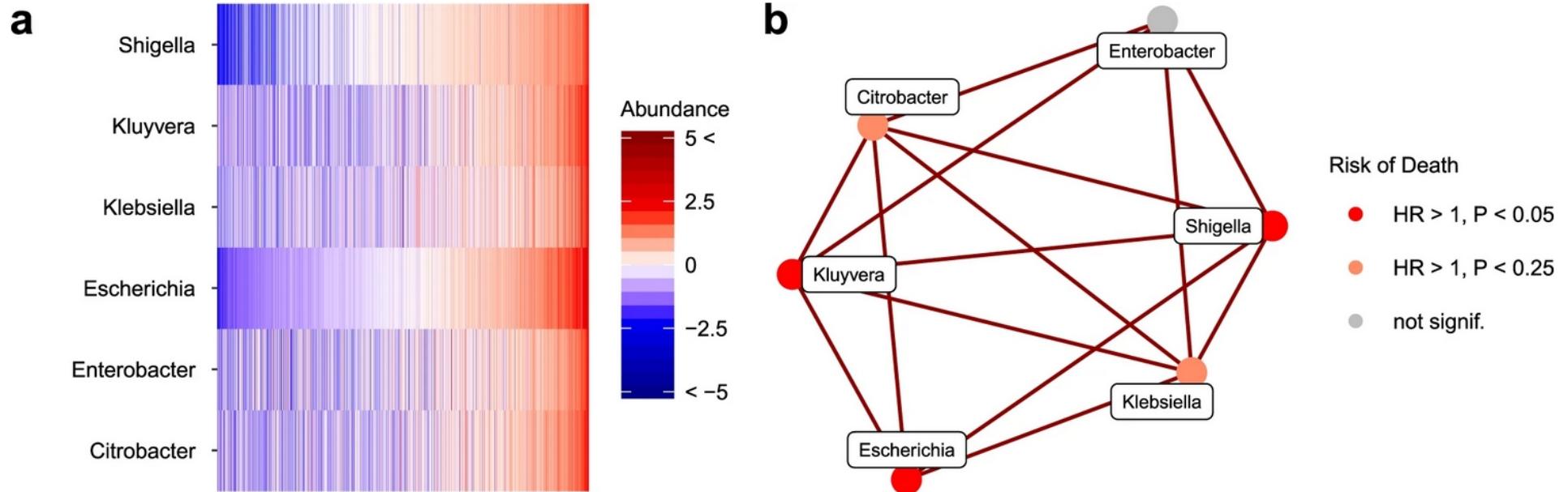
## Hazard ratios: PC1-3



# Association is robust in distinct sub-populations

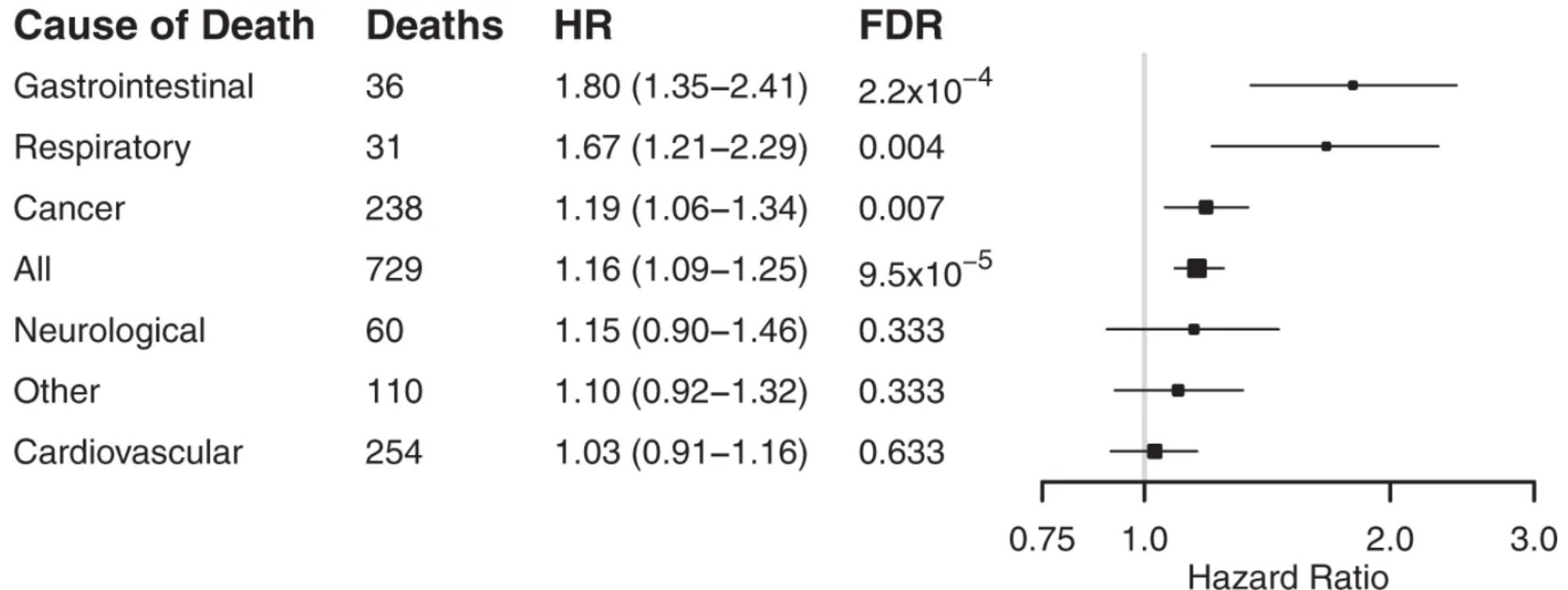


# Taxonomic subnetwork associated with mortality risk



Subnetwork identification with SPIEC-EASI

# Specific causes of death & Enterobacteriaceae abundance

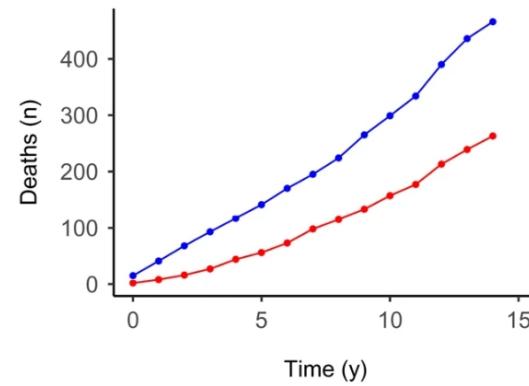
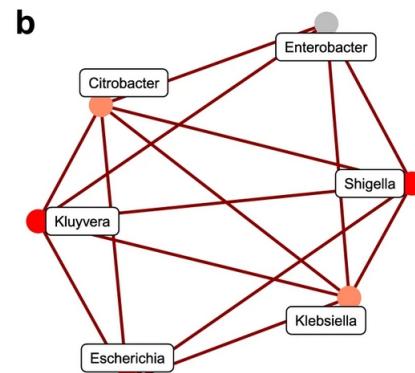
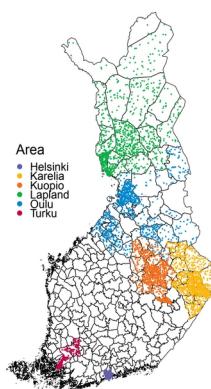


Cox hazard ratios & 95% confidence intervals  
per unit variance increase in Enterobacteriaceae (clr) abundance

Adjusted: age, bmi, sex, smoking, diabetes, antineoplastic and immunomodulating agents, systolic BP, antihypertensive medication

# Summary

fecal microbiome can predict mortality risk  
association is robust at multiple levels  
prospective population-level analysis



# Acknowledgments

Taxonomic signatures of cause-specific mortality risk in human gut microbiome  
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