

# The human microbiome and colorectal cancer

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# Outline

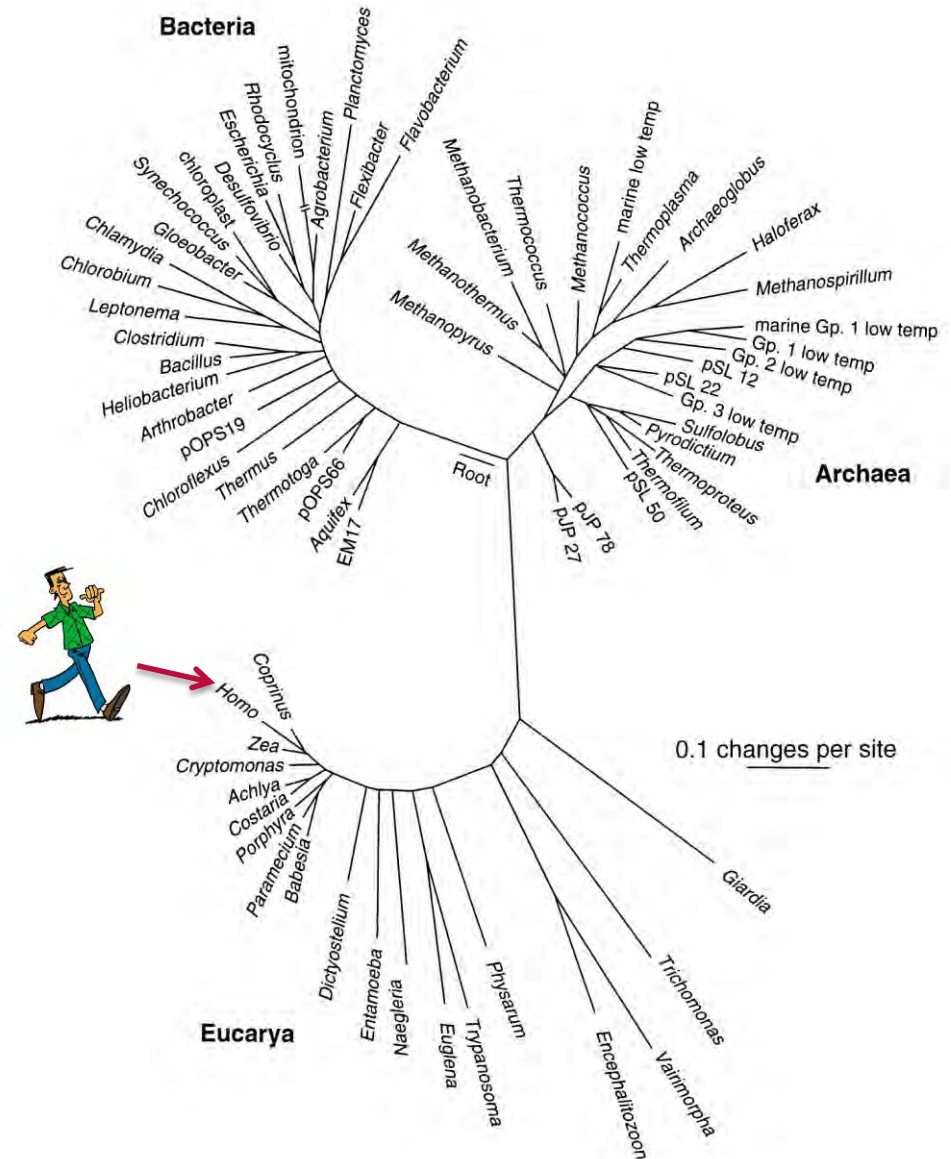
- Introduction to the human microbiome
- Technologies to assess the microbiome
- Human microbiome and colorectal cancer
- Future directions

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# Microbiota and the tree of life

- Microbes
  - Bacteria
  - Archaea
  - Fungi
  - Protists
  - Viruses
- Microbiome: collection of microbial genes

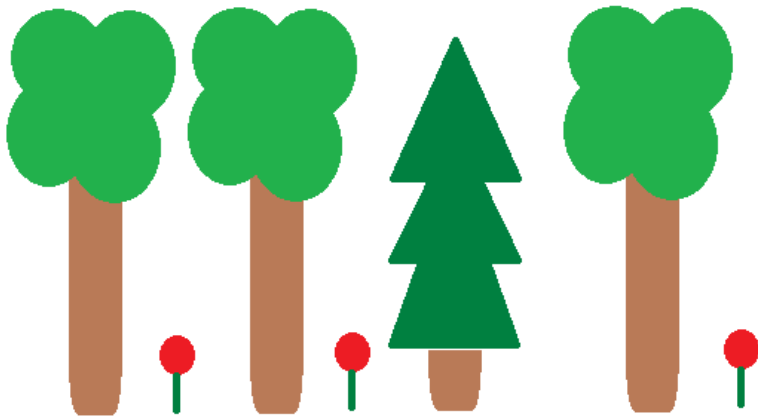


Kutschera (2011) *Biol Direct* & Pace (1997) *Science*

# Alpha and beta diversity

## Alpha diversity

- Counts (Taxonomy/OTUs)
- Shannon index
- Simpson index
- Chao1
- PD tree



Forest 1

Alpha diversity = 3

## Beta diversity

- Bray-Curtis
- UniFrac



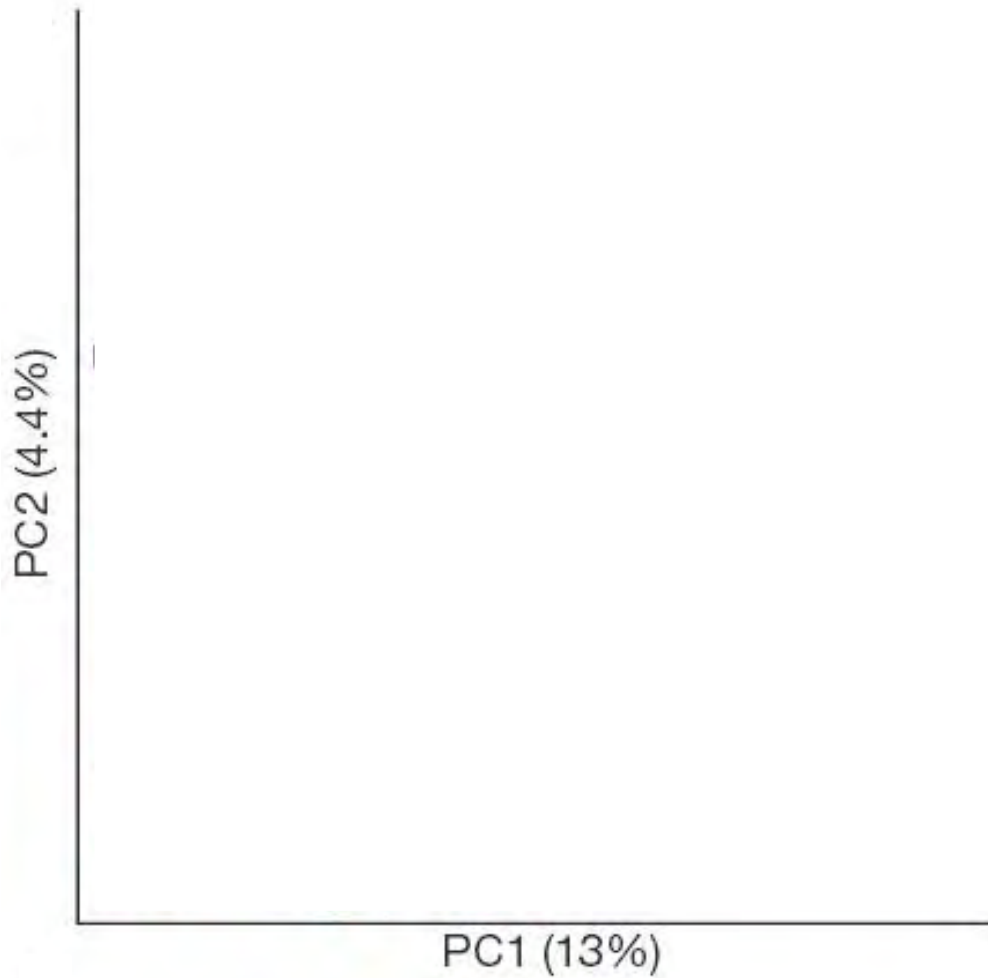
Forest 2

Alpha diversity = 6

Beta diversity

2 shared  
5 different

# PCoA plot: Clustering by body site



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# History of microbial research

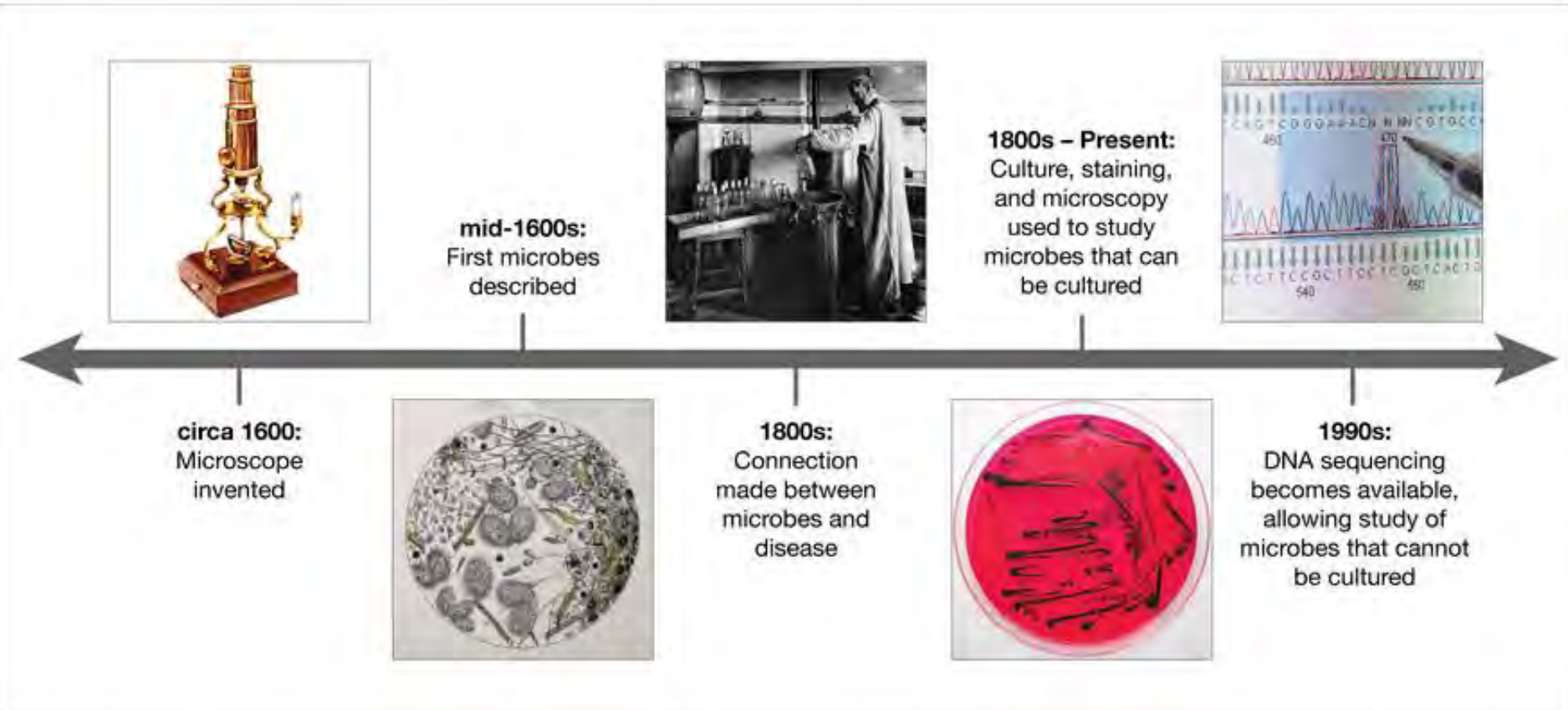
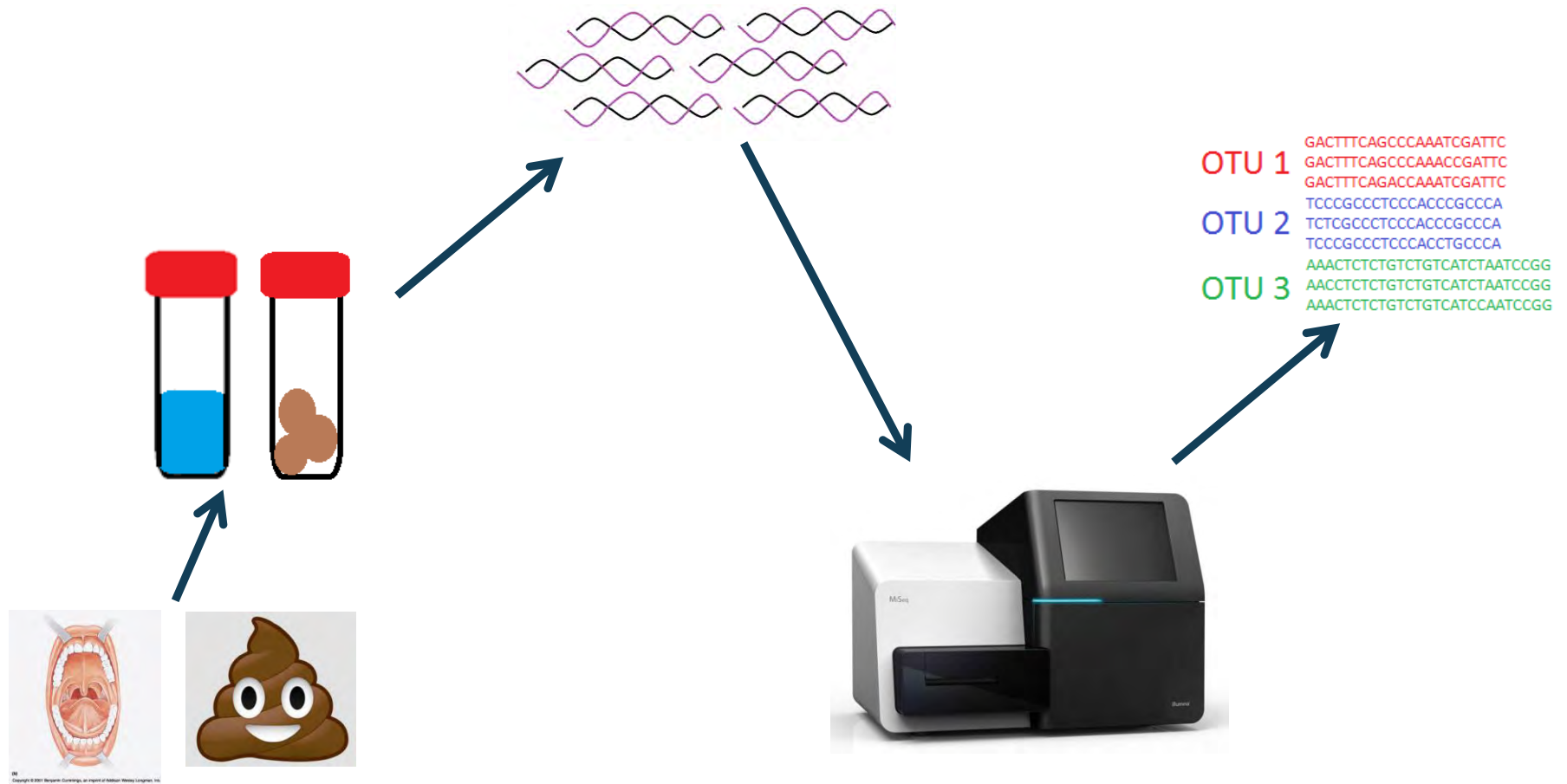


Image: <http://learn.genetics.utah.edu/content/microbiome/study/>



# Present day study



Images from: <http://legacy.owensboro.kctcs.edu/gcaplan/anat2/study%20guides/apii%20study%20guide%20k%20digestive%20anatomy.htm>, [http://davidql.github.io/scope\\_talk/emoji\\_poop.png](http://davidql.github.io/scope_talk/emoji_poop.png), <http://dnatech.genomecenter.ucdavis.edu/wp-content/uploads/2013/10/Miseq.png>, and reproductions from Morgan XC et al. (2012) *PLoS Comp Biol*

# Fecal collection methods



No Solution



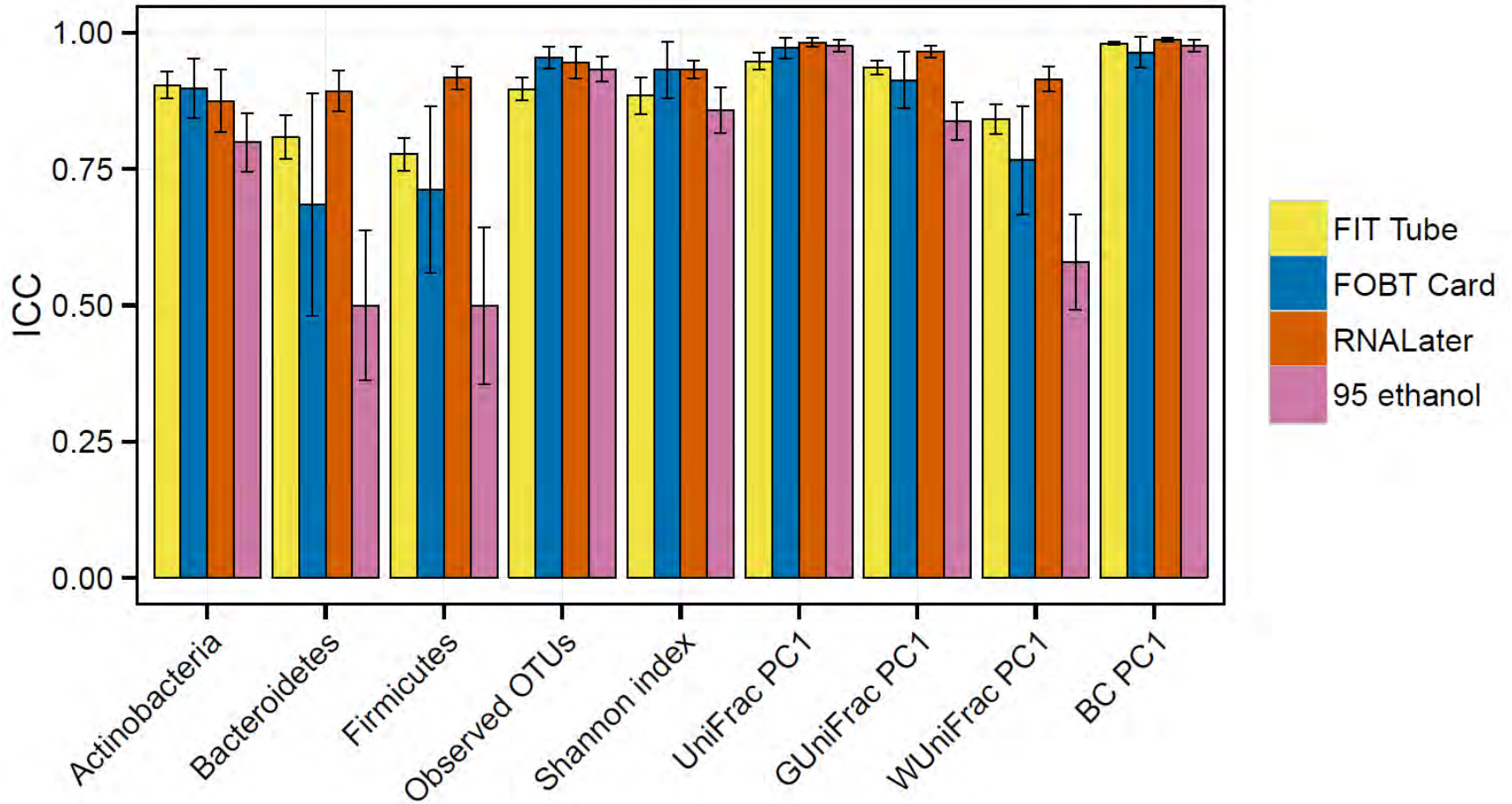
RNA later



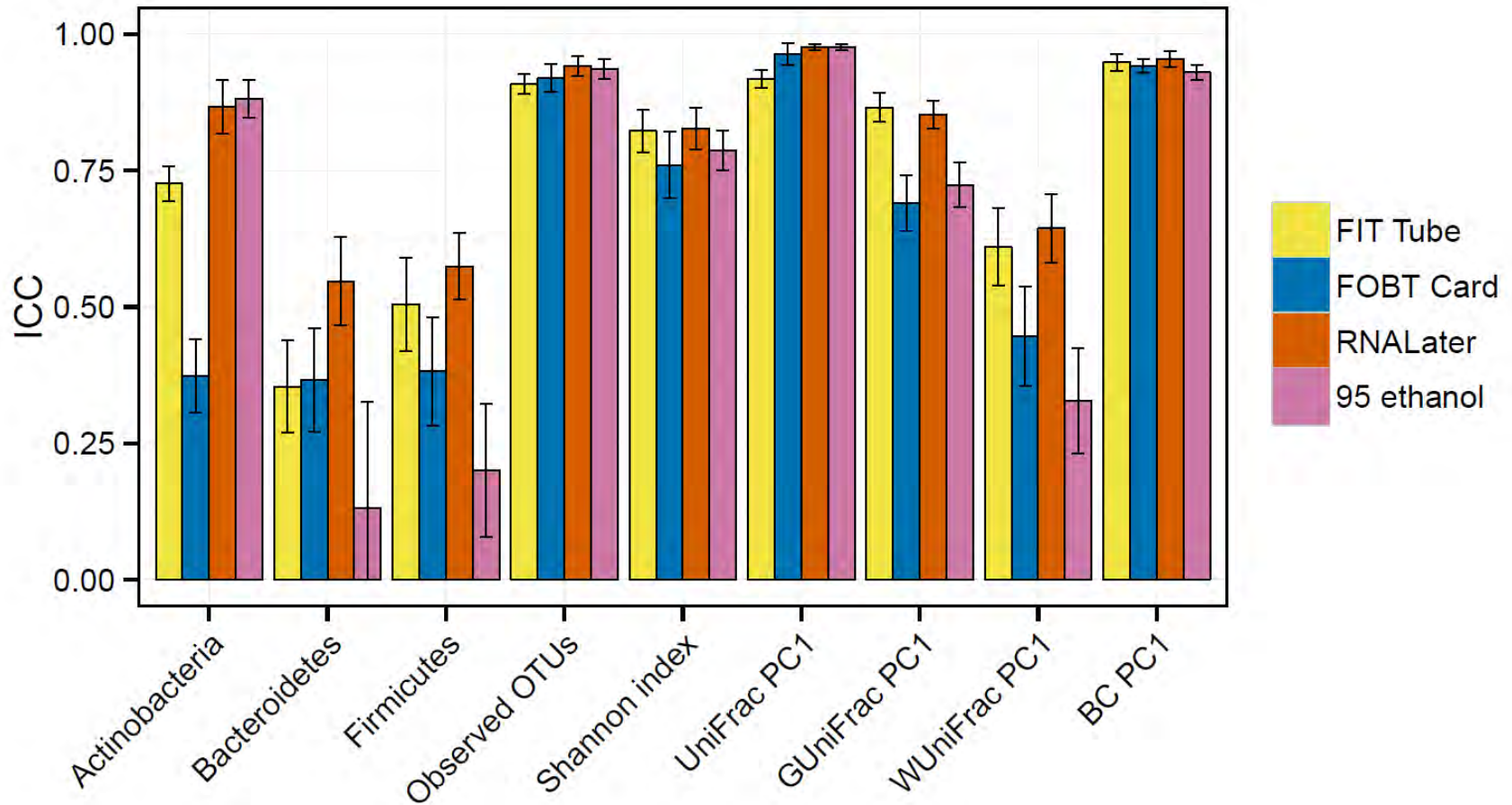
95% Ethanol



# Stability



# Accuracy



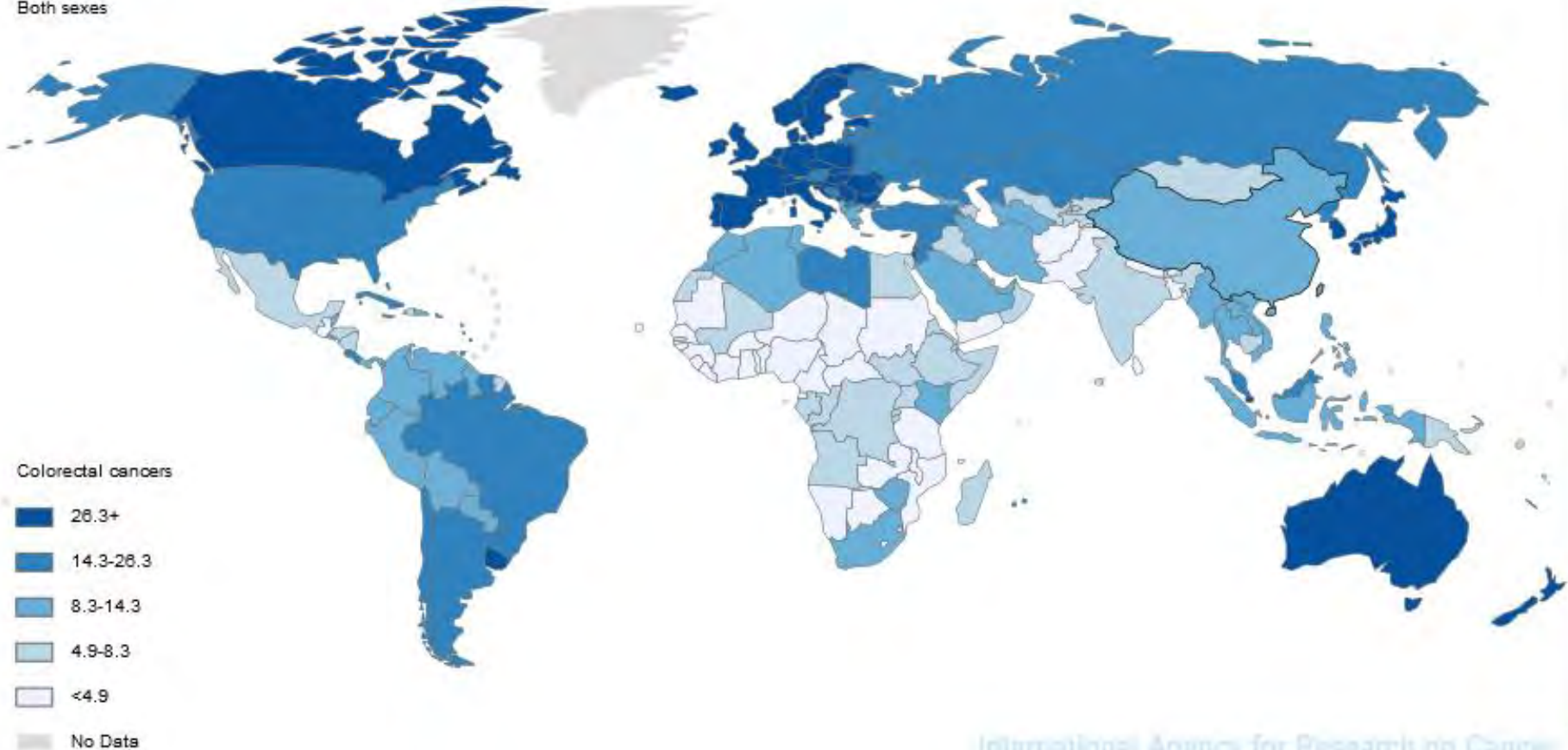
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# Colorectal cancer worldwide

Incidence ASR

Both sexes



International Agency for Research on Cancer

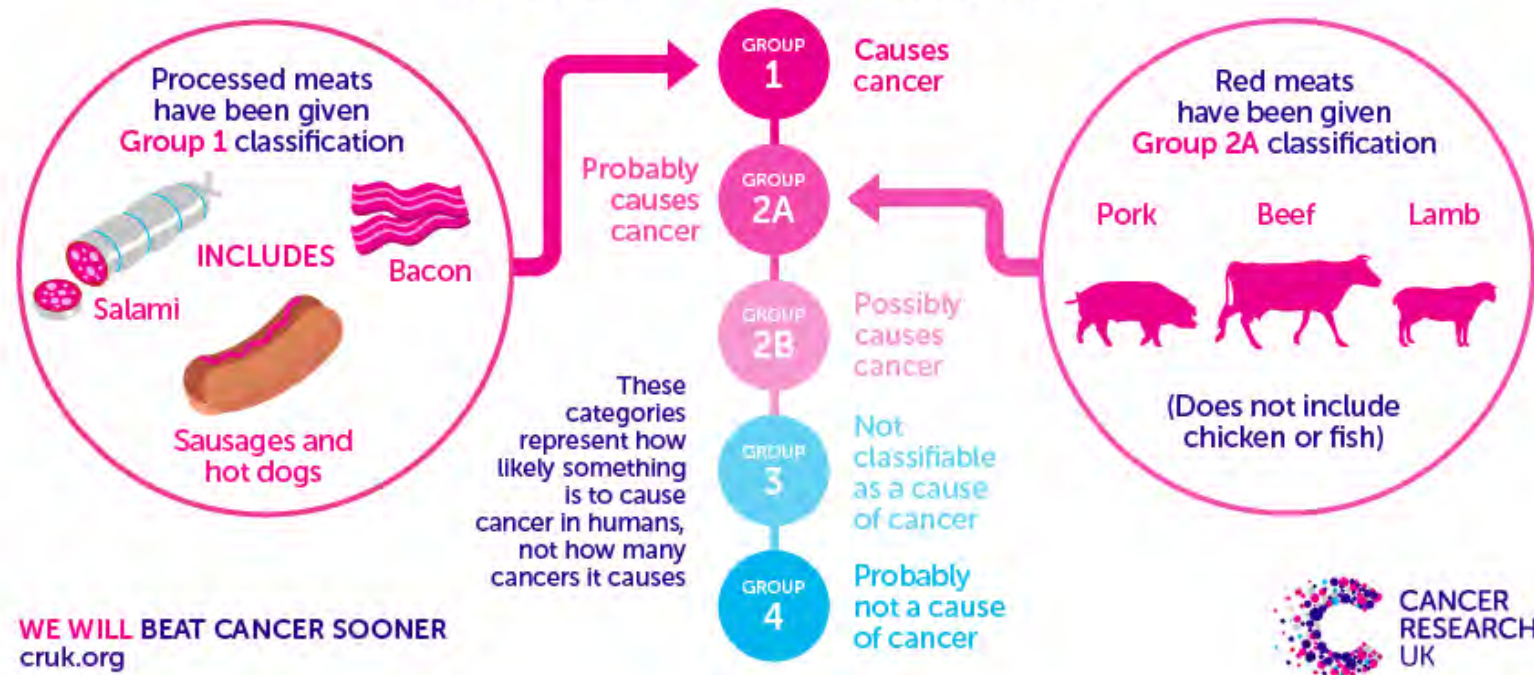


Source: GLOBOCAN 2012 (IARC)

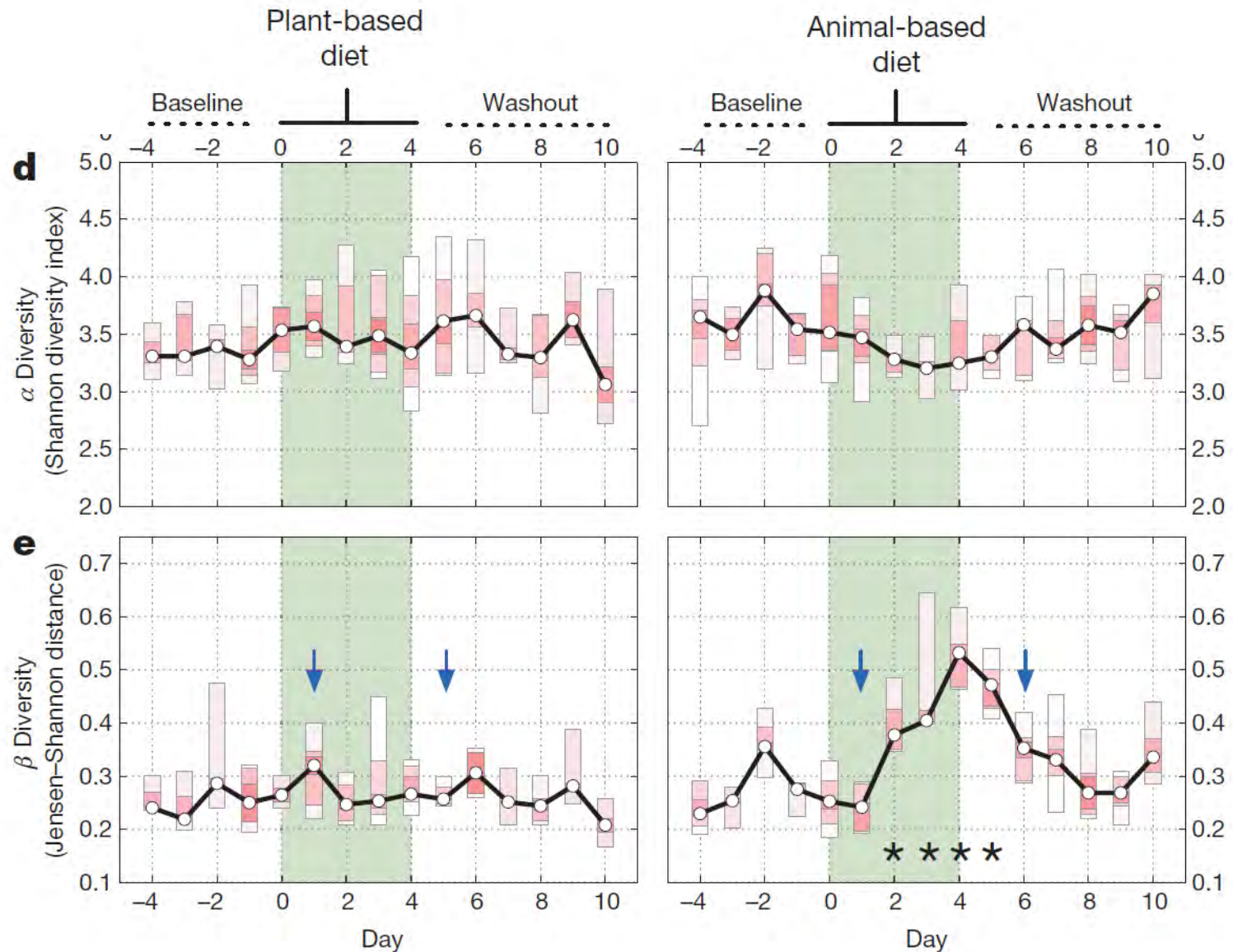
# Meat and colorectal cancer

## MEAT AND CANCER HOW STRONG IS THE EVIDENCE?

### IARC CARCINOGENIC CLASSIFICATION GROUPS

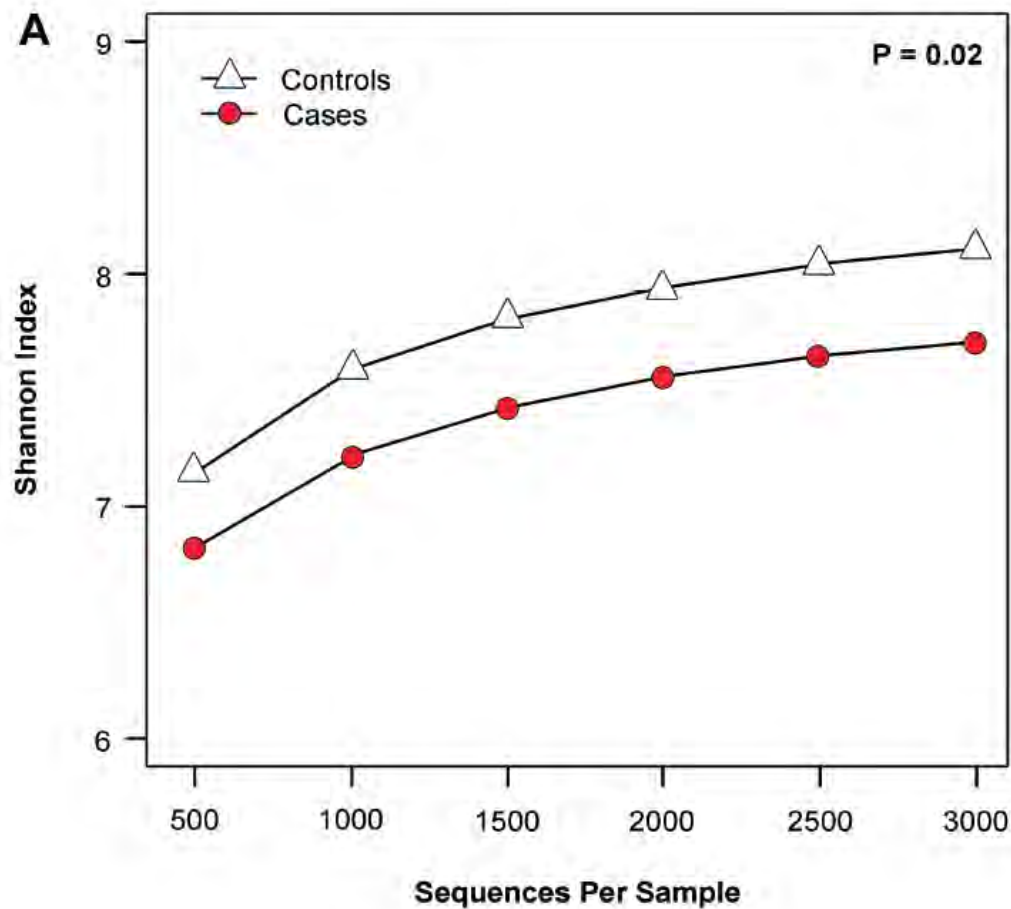


# Meat and the gut microbiome

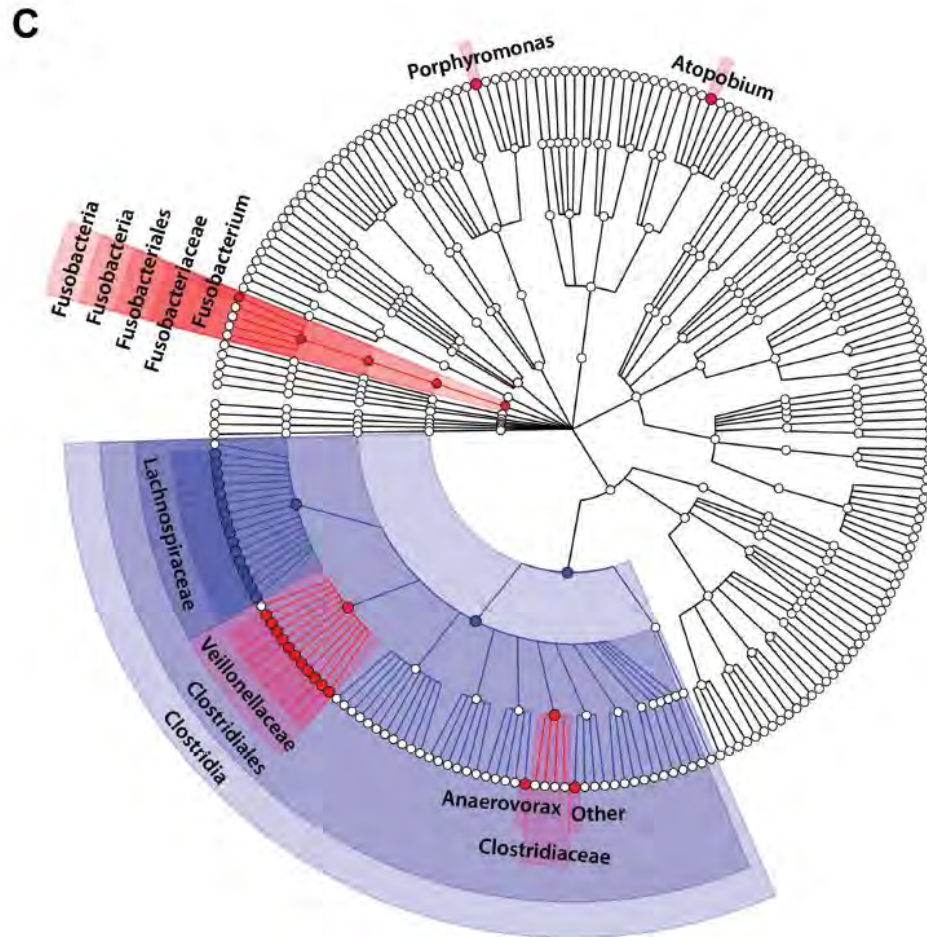




# Microbiome and colorectal cancer (U.S.)



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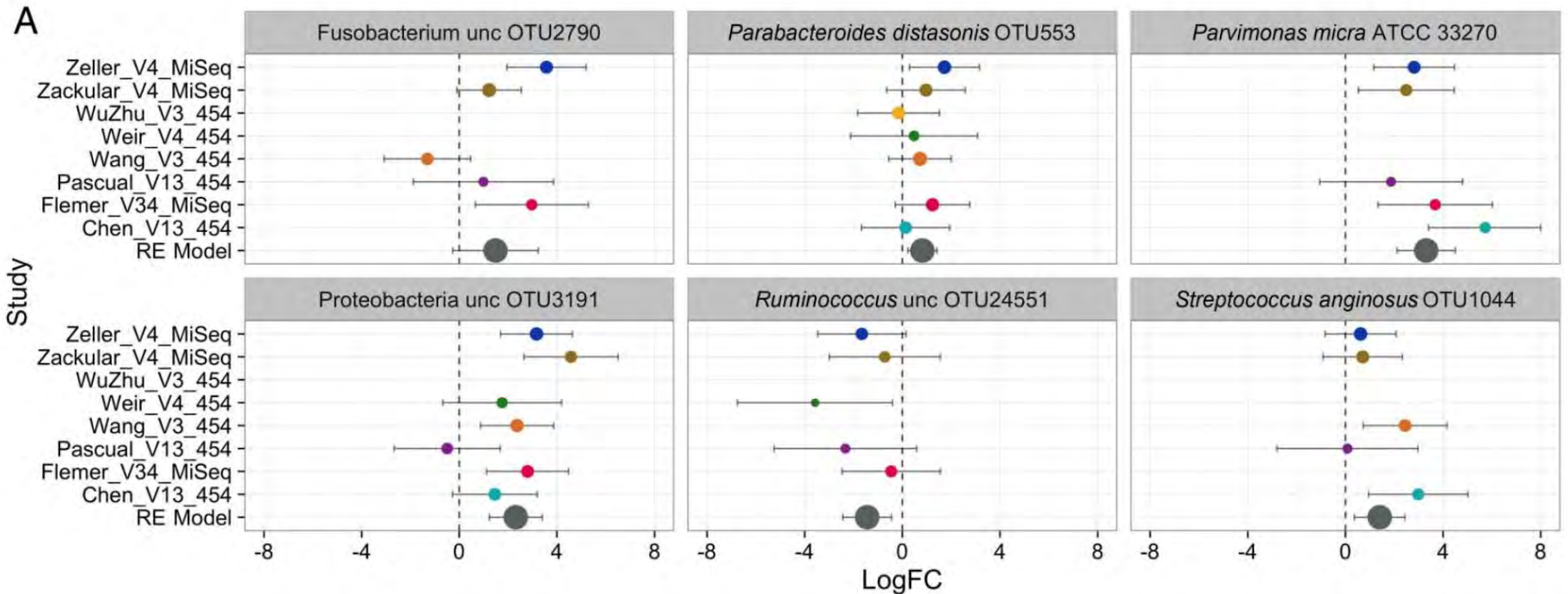
## Case enrichment

- *Fusobacterium*
- Veillonellaceae
- *Anaerovorax*
- *Porphyromonas*
- *Atopobium*

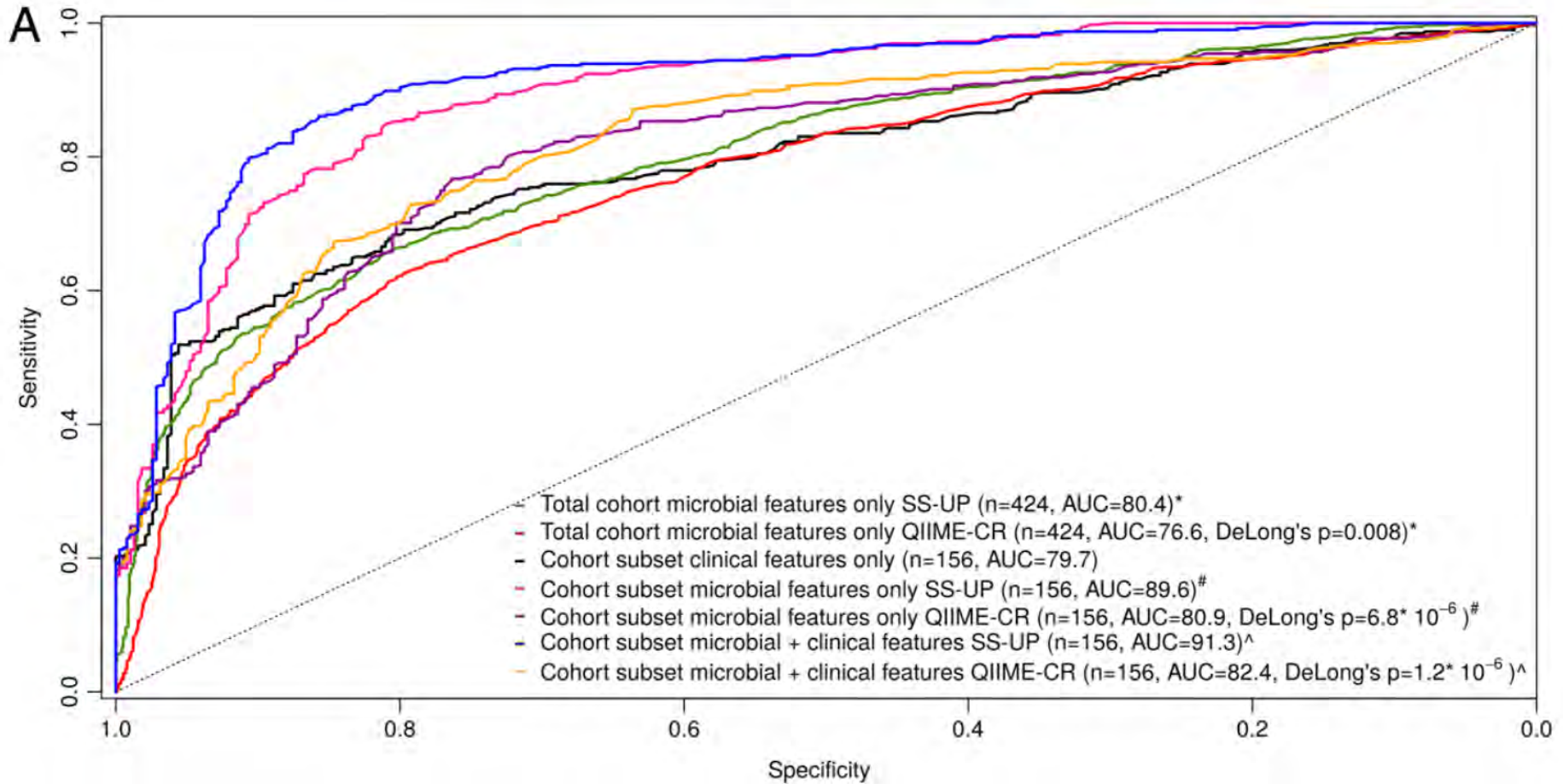
## Control enrichment

- Firmicutes overall
- Lachnospiraceae

# Meta-analysis of 16S rRNA gene studies



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# Potential mechanisms

# Conclusions

- There is promise for fecal microbial markers to enhance FOBT or FIT tests for colorectal cancer screening
- All previous studies have been cross-sectional
- Prospective studies (and studies with multiple serial samples) are needed to understand microbial associations with colorectal cancer etiology

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# Future directions

- Optimization of collection method for multiple technologies
- Collect fecal samples in prospective cohort studies
- Quality control standards to evaluate reproducibility
- Standardization of methods for extraction, sequencing, and bioinformatics for data pooling and meta-analyses



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[www.cancer.gov](http://www.cancer.gov)

[www.cancer.gov/espanol](http://www.cancer.gov/espanol)