Meta-analysis of microbiome studies identifies disease-specific and shared responses

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Little generalized knowledge about human microbiome and disease

Many studies report associations between the human gut microbiome and disease. However, results from individual studies can be inconsistent and are difficult to compare because of a lack of standard methods.

We performed a meta-analysis of case-control studies to ask:

- Can we find **consistent biomarkers** across studies of the same disease?
- Are some bacteria associated with **general health and disease**?

MicrobiomeHD database includes 28 published case-control gut microbiome studies spanning 10 diseases

Conditions	Studies	Controls	Patients
Diarrhea	4	419	338
Obesity	5	627	543
Colorectal cancer	5	323	226
IBD	4	93	365
HIV	3	62	249
Autism	2	64	78
Type I Diabetes	2	63	78
Liver disease	3	63	84
Arthritis	1	28	86
Parkinson's	1	74	74

We reprocessed and analyzed each study independently and compared results across studies.

16S FASTQs → 100% OTUs → Genus-level

Data is available on Zenodo.org.

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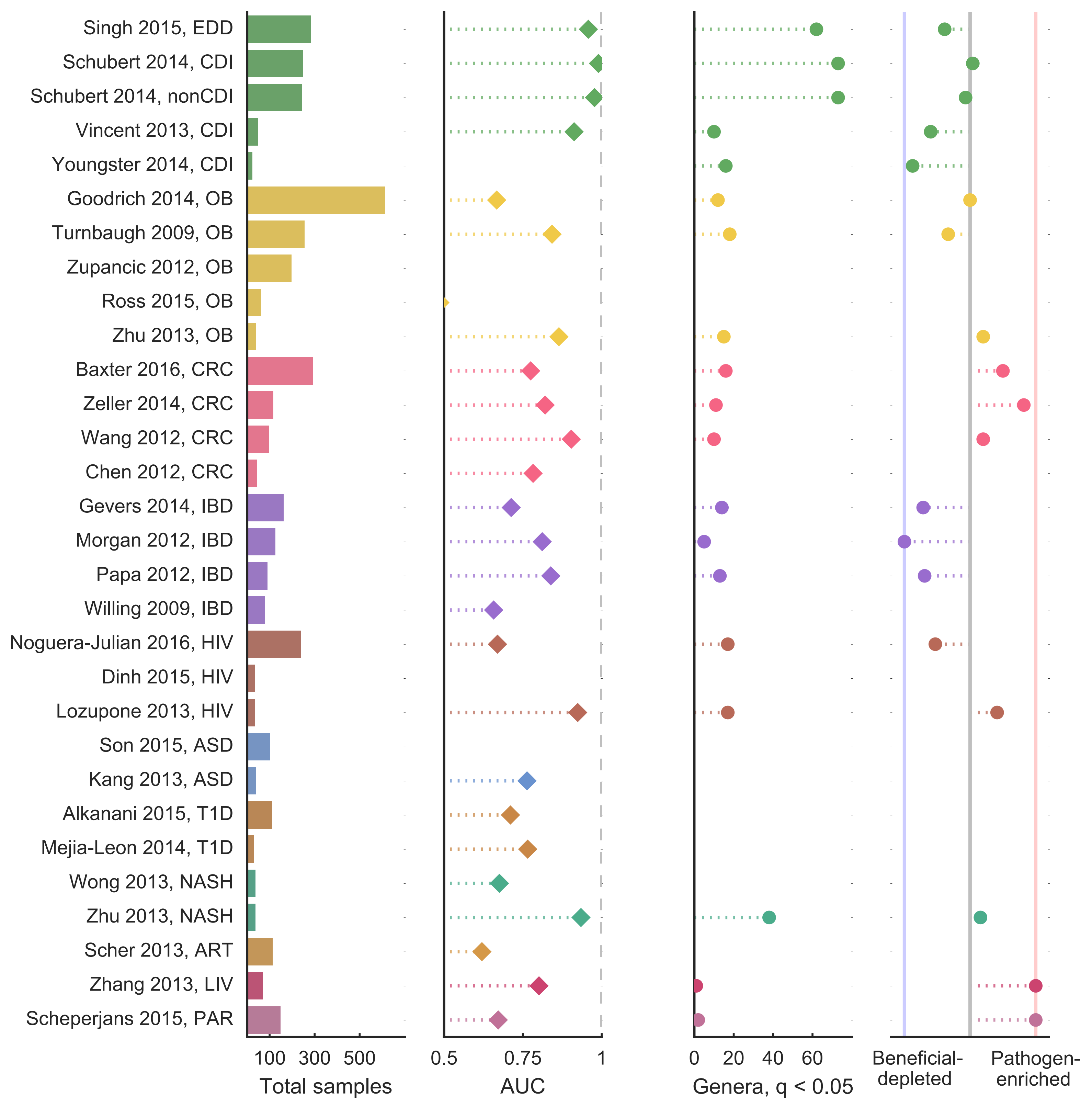
Directionality and extent of consistent disease-associated shifts can inform treatment strategies

Broad community restructuring (diarrhea): fecal transplants?

Enrichment of "pathogens" (colorectal cancer): targeted antimicrobials, diagnostics, or causality?

Depletion of health-associated bacteria (inflammatory bowel disease): probiotics?

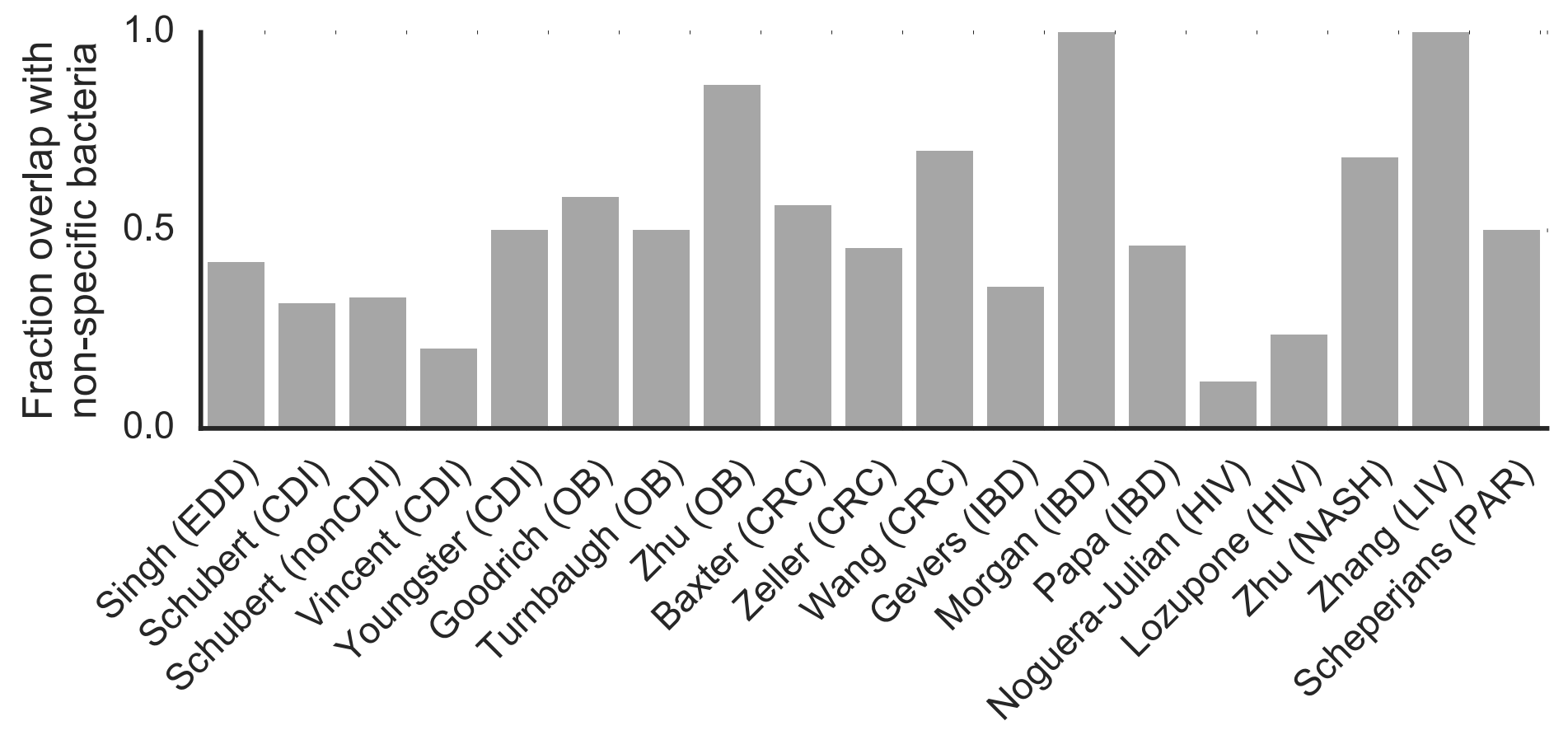


Bacteria associated with multiple diseases suggests a shared response to disease

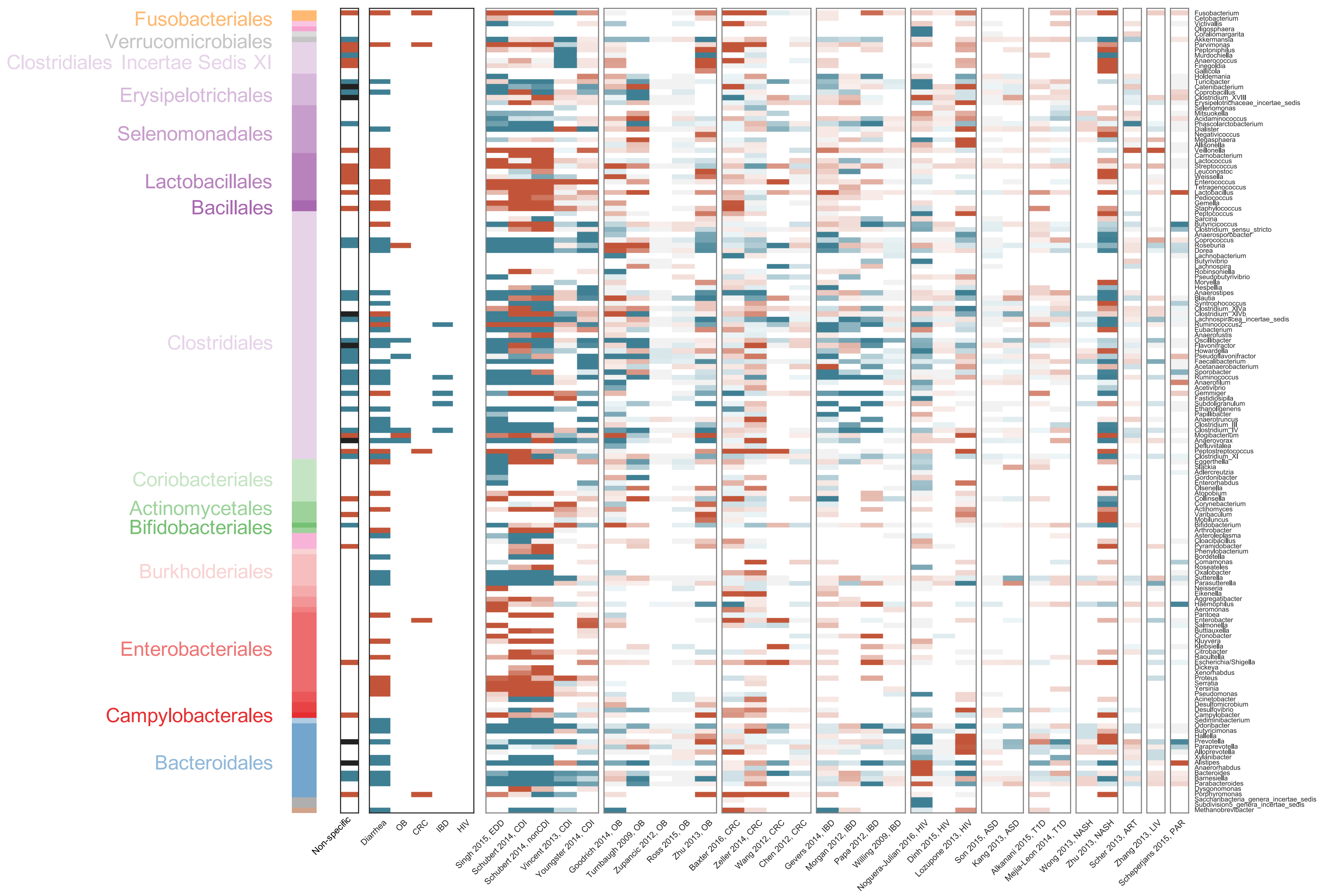
Non-specific bacteria	Health	Disease
Bacteroidetes	2	1
Firmicutes		
Clostridia	17	6
Bacilli	0	6
Other	3	1
Proteobacteria	0	2
Fusobacteria	0	1
Other	2	2

Lachnospiraceae and *Ruminococcaceae* are known short-chain fatty acid producers.

Lactobacillales are upper-gut bacteria which may indicate shorter stool transit times.



The majority of studies' associations overlap with the non-specific response.



From left:

Phylogeny colored by phylum and shaded by order

Non-specific bacteria are associated with at least **two diseases**.

Disease-associated bacteria are significant in **two studies** of the same disease.

Q values for all genera in all studies, grouped by disease.