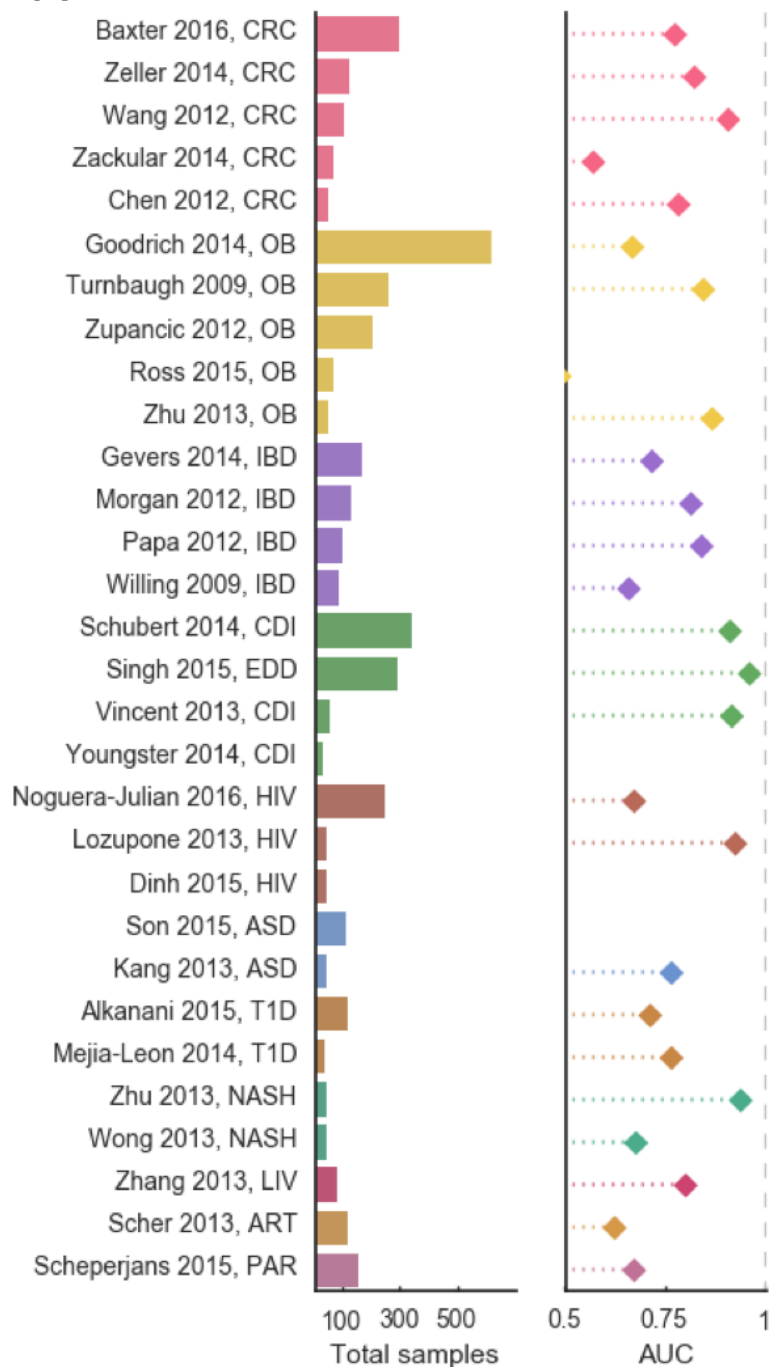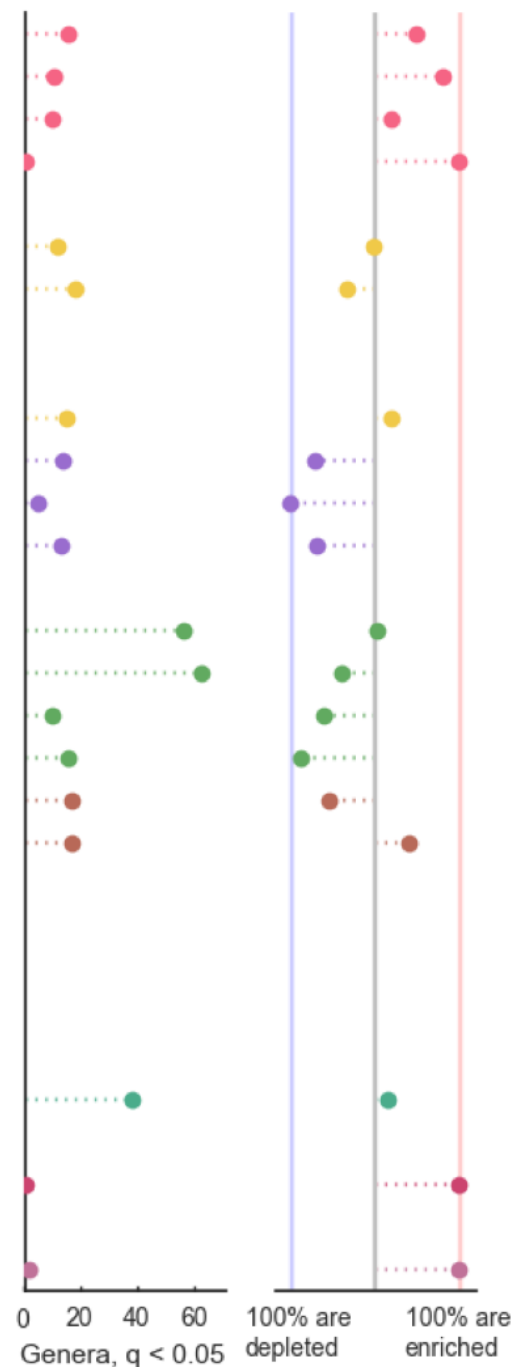# Meta-analysis of microbiome studies across diseases identifies universal and disease-specific patterns
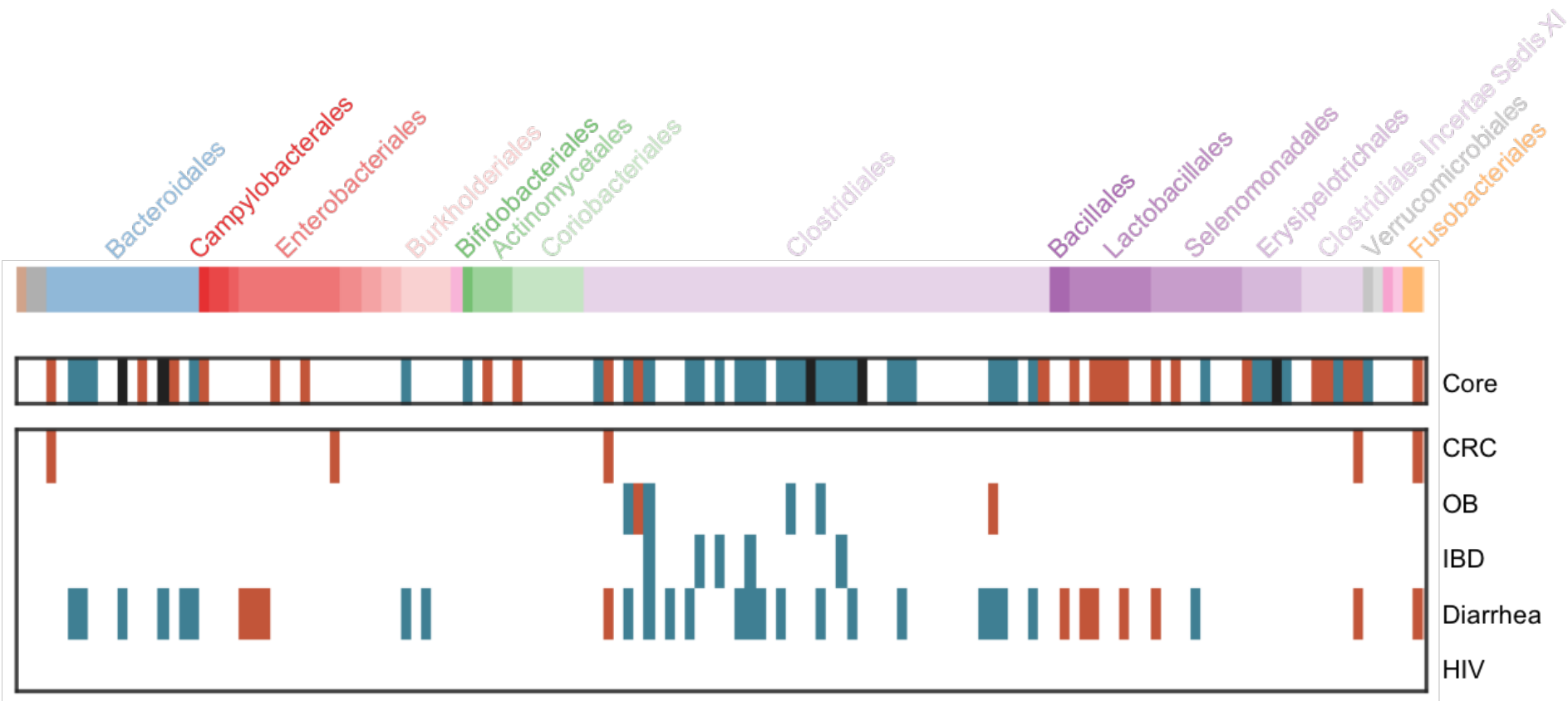
Claire Duvallet, Sean Gibbons,
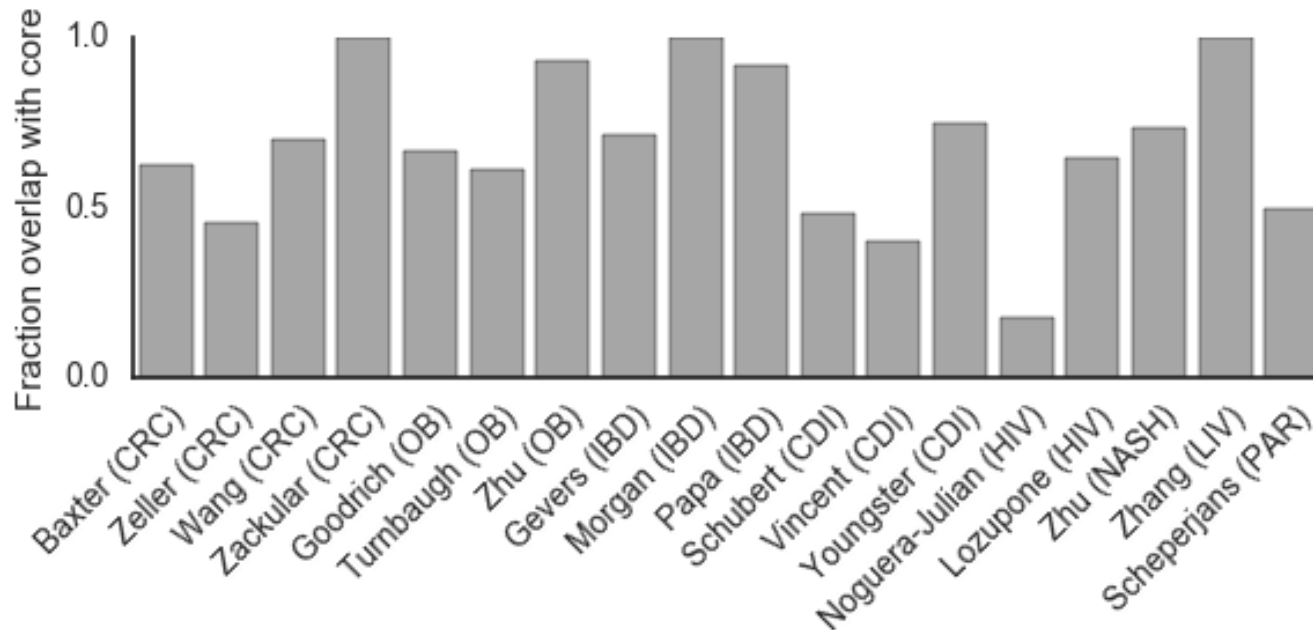Thomas Gurry, Rafael Irizarry, Eric Alm

A

Baxter 2016, CRC
Zeller 2014, CRC
Wang 2012, CRC
Zackular 2014, CRC
Chen 2012, CRC
Goodrich 2014, OB
Turnbaugh 2009, OB
Zupancic 2012, OB
Ross 2015, OB
Zhu 2013, OB
Gevers 2014, IBD
Morgan 2012, IBD
Papa 2012, IBD
Willing 2009, IBD
Schubert 2014, CDI
Singh 2015, EDD
Vincent 2013, CDI
Youngster 2014, CDI
Noguera-Julian 2016, HIV
Lozupone 2013, HIV
Dinh 2015, HIV
Son 2015, ASD
Kang 2013, ASD
Alkanani 2015, T1D
Mejia-Leon 2014, T1D
Zhu 2013, NASH
Wong 2013, NASH
Zhang 2013, LIV
Scher 2013, ART
Scheperjans 2015, PAR

B

100   300   500   0.5   0.75   1   0   20   40   60   100% are   100% are
Total samples   AUC   Genera, q < 0.05   depleted   enriched

core (top) = significant in 2 **diseases**

disease-associated (bottom) = significant in 2 **studies** (of the same disease)

For each dataset: $\dfrac{\text{\# of sig genera which are also "core" genera}}{\text{total number of significant genera}}$