## FDR-values: < 0.001 = \*\*\*, < 0.01 = \*\*, < 0.1 = \* ASV301 Erysipelatoclostridiaceae -ÁSV203 Frisingicoccus -ASV16 Bifidobacterium -ASV772 Butyricicoccus -ASV10 Ruminococcus -ASV335 Clostridia vadinBB60 group ASV324 Defluviitaleaceae UCG-011 -ASV274 Ruminococcaceae -ASV242 Erysipelatoclostridium -ASV147 Lachnoclostridium -Effect size ASV139 Lachnospiraceae UCG-006 -ASV196 UBA1819 -ASV428 Pygmaiobacter -0.5 ASV223 Dorea -ASV355 Marvinbryantia -0.0 Feature Value ASV105 Bacteroides -ASV73 Anaerostipes -ASV36 NK4A214 group --0.5ASV665 Anaerofustis -ASV313 Paludicola -ASV200 Parasutterella -ASV157 Parabacteroides -ASV538 A2 status ASV334 Erysipelotrichaceae -ASV524 Christensenellaceae R-7 group ASV512 Enterococcus - Confounded ASV326 Gastranaerophilales -Deconfounded ASV72 [Eubacterium] siraeum group - ASV44 Roseburia -ASV2 Lachnospiraceae NK4A136 group ASV468 Candidatus Saccharimonas -ASV35 Clostridium sensu stricto 1 - • ASV31 Clostridia UCG-014 -ASV509 Escherichia-Shigella -ASV399 Monoglobus -ASV24 Romboutsia -ASV328 Clostridia -ASV28 Jeotgalicoccus - • ASV100 Oscillibacter -Famil **SCFAs Treatments** ognitive tes Memb. receptors ytokines bra Fami CCL20 SCFA\_AA TNFR1 GAT1 NR2A NR2B Antibiotic SCFA\_BA NR1 SCFA

Variables

Significant metadata correlation heatmap