Summarizing heatmap FDR-values: < 0.001 = ***, < 0.01 = **, < 0.1 = * ASV131 [Eubacterium] coprostanoligenes group -ASV28 [Eubacterium] coprostanoligenes group ASV208 Defluviitaleaceae UCG-011 ASV140 UBA1819 ASV351 Lachnoclostridium ASV429 Lachnospiraceae ASV184 Rhodospirillales ASV88 Lachnospiraceae ASV479 Anaerotruncus ASV238 [Eubacterium] xylanophilum group ASV483 Anaerofustis ASV36 Clostridia UCG-014 ASV183 Roseburia ASV127 caecimuris ASV103 Oscillospiraceae ASV252 Paludicola ASV132 Lachnospiraceae ASV345 Paludicola ASV335 Clostridia UCG-014 ASV583 Butyricicoccus Ds ASV115 UBA1819 ASV19 NK4A214 group 1.0 ASV564 Lachnoclostridium **ASV9 Ruminococcus** ASV365 A2 0.5 ASV226 Marvinbryantia ASV137 Ruminococcus Omics features ASV234 Enterorhabdus 0.0 ASV549 Enterorhabdus ASV125 Intestinimonas ASV494 Anaerotruncus -0.5ASV259 Lachnospiraceae ASV134 Dorea ASV253 Colidextribacter -1.0ASV522 Oscillospiraceae ASV355 Lachnospiraceae ASV102 Oscillospiraceae Confounding status ASV84 Enterorhabdus ASV83 Clostridia UCG-014 ASV690 Caldicoprobacter confounded ASV185 Lachnoclostridium ASV90 Clostridia UCG-014 deconfounded ASV41 [Eubacterium] coprostanoligenes group ASV24 Roseburia ASV172 Clostridia UCG-014 ASV10 Ruminococcus ASV209 Colidextribacter ASV359 Christensenellaceae R-7 group ASV193 Clostridia UCG-014 ASV203 Gastranaerophilales ASV171 Clostridia UCG-014 ASV149 Clostridia UCG-014 ASV393 Clostridia UCG-014 ASV112 Clostridia UCG-014 ASV25 Roseburia ASV298 Candidatus Saccharimonas ASV20 Clostridia UCG-014 ASV263 Monoglobus ASV394 Clostridia UCG-014 ASV116 Clostridia UCG-014 ASV364 Lachnospiraceae UCG-006 · ASV290 Roseburia · ASV101 Lachnospiraceae NK4A136 group

Antibiotic

TNFR1

Learning_index_Rmaze

Metadata variables