

Family

- [Eubacterium] coprostanoligenes group
- Anaerofustaceae
- Bacteroidaceae
- Bifidobacteriaceae
- Butyrificoccaceae
- Christensenellaceae
- Clostridiaceae
- Defluviitaleaceae
- Enterobacteriaceae
- Enterococcaceae
- Erysipelatoclostridiaceae
- Erysipelotrichaceae
- Lachnospiraceae
- Monoglobaceae
- Muribaculaceae
- Oscillospiraceae
- Peptostreptococcaceae
- Ruminococcaceae
- Saccharimonadaceae
- Staphylococcaceae
- Sutterellaceae
- Tannerellaceae
- NA

Feature Value

- ASV301 Erysipelatoclostridiaceae
- ASV203 Frisingicoccus
- ASV16 Bifidobacterium
- ASV772 Butyrificoccus
- ASV10 Ruminococcus
- ASV335 Clostridia vadinBB60 group
- ASV324 Defluviitaleaceae UCG-011
- ASV274 Ruminococcaceae
- ASV49 [Eubacterium] coprostanoligenes group
- ASV1 Muribaculaceae
- ASV242 Erysipelatoclostridium
- ASV147 Lachnoclostridium
- ASV139 Lachnospiraceae UCG-006
- ASV196 UBA1819
- ASV428 Pygmaibacter
- ASV223 Dorea
- ASV355 Marvinbryantia
- ASV105 Bacteroides
- ASV73 Anaerostipes
- ASV36 NK4A214 group
- ASV665 Anaerofustis
- ASV313 Paludicola
- ASV200 Parasutterella
- ASV157 Parabacteroides
- ASV538 A2
- ASV334 Erysipelotrichaceae
- ASV524 Christensenellaceae R-7 group
- ASV512 Enterococcus
- ASV326 Gastranaerophilales
- 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

Family

# Significant metadata correlation heatmap

FDR-values: < 0.001 = \*\*\*, < 0.01 = \*\*, < 0.1 = \*

