

Significant metadata correlation heatmap

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

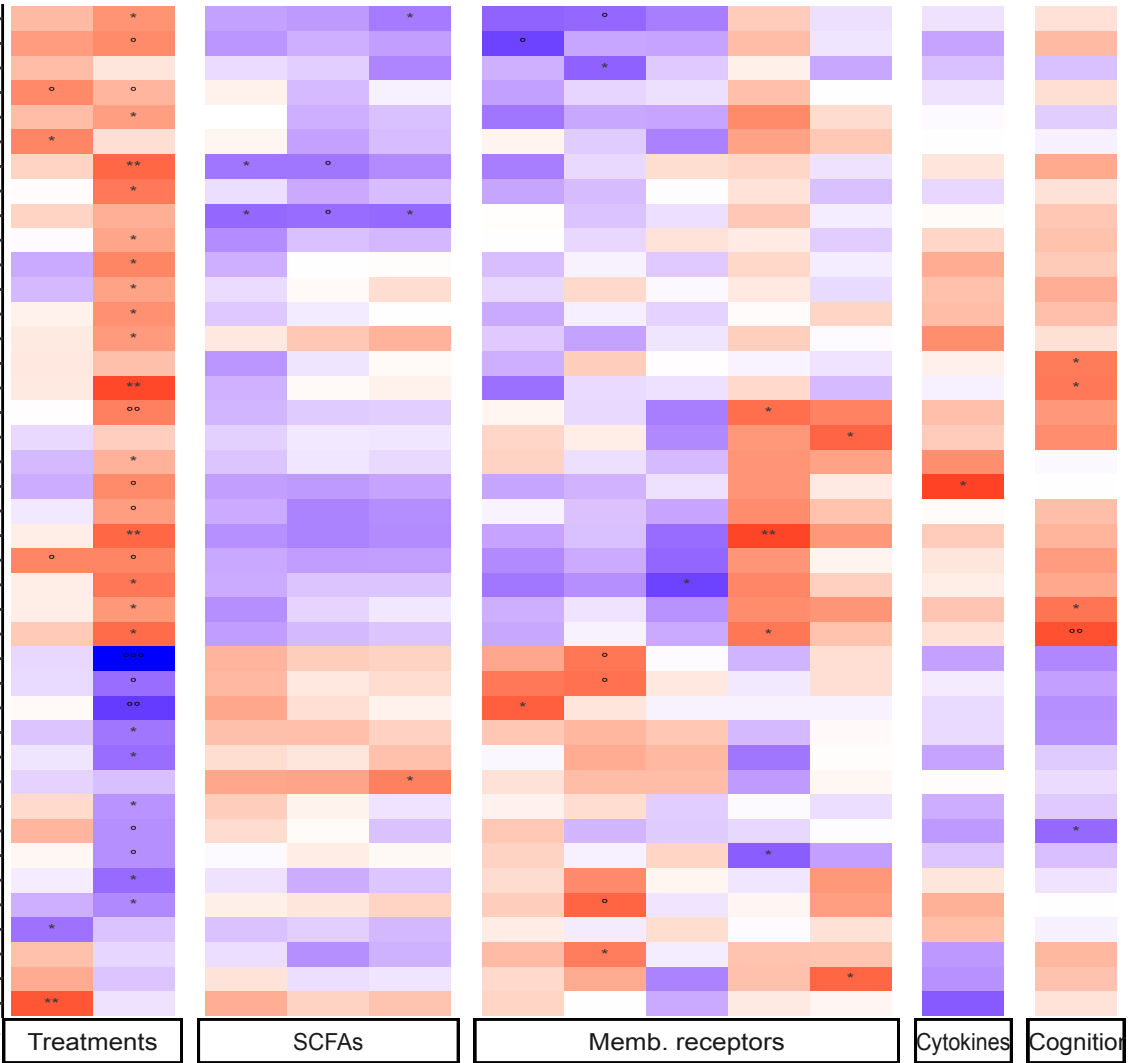
Family

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

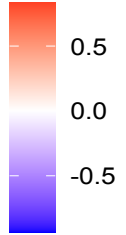
Feature Value

- Erysipelatoclostridiaceae
- Frisingicoccus
- Bifidobacterium
- Butyricicoccus
- Ruminococcus
- Clostridia vadinBB60 group
- Defluviitaleaceae UCG-011
- Ruminococcaceae
- [Eubacterium] coprostanoligenes group
- Muribaculaceae
- Erysipelatoclostridium
- Lachnoclostridium
- Lachnospiraceae UCG-006
- Ruminococcaceae UBA1819
- Pygmaibacter
- Dorea
- Marvinbryantia
- Bacteroides
- Anaerostipes
- Oscillospiraceae NK4A214 group
- Anaerofustis
- Paludicola
- Parasutterella
- Parabacteroides
- Lachnospiraceae A2
- Erysipelotrichaceae
- Christensenellaceae R-7 group
- Enterococcus
- Gastranaerophilales
- [Eubacterium] siraeum group
- Roseburia
- Lachnospiraceae NK4A136 group
- Candidatus Saccharimonas
- Clostridium sensu stricto 1
- Clostridia UCG-014
- Escherichia-Shigella
- Monoglobus
- Romboutsia
- Clostridia
- Jeotgalicoccus
- Oscillibacter

Family



Effect size



status

- Confounded
- * Deconfounded

Variables