

# 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

## Treatments

## SCFAs

## Memb. receptors

## Cytokines

## Cognition

Treated\_CCL  
Antibiotic

SCFA\_CA  
SCFA\_AA  
SCFA\_BA

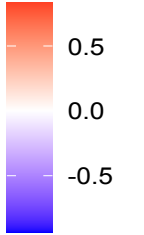
TNFR1  
NR1  
GAT1  
NR2A  
NR2B

CCL20

Learning\_index\_Rmaze

## Variables

## Effect size



## status

- Confounded
- \* Deconfounded