

The figure is a scatter plot with $-\log_{10}(P)$ stool on the x-axis. The y-axis represents the relative abundance of bacterial taxa. A vertical dashed line at $x=0$ separates the two groups. Taxa are labeled with their names, and lines connect them to their respective data points. The taxa are distributed across the plot, with some showing significant enrichment in one group or the other.

$-\log_{10}(P)$ tissue

$-\log_{10}(P)$ stool

Key taxa labeled include: Anaerostipes, Gordonibacter, Holdemania, Clostridiaceae_noname, Coprobacillus, Coprobacter, Streptococcus, Adlercreutzia, Veillonella, Methanobrevibacter, Haemophilus, Desulfovibrio, Ruminococcaceae_noname, Blautia, Anaerotruncus, C2likevirus, Bilophila, Bacteroides, Sutterellaceae_unclassified, Escherichia, Erysipelotrichaceae_noname, Klebsiella, Mobiluncus, Parasutterella, Burkholderiales_noname, Pseudoflavonifractor, Lachnospiraceae_noname, Lactobacillus, Acidaminococcaceae_unclassified, Alistipes, Bacteroidales_noname, Roseburia, Eubacterium, Prevotella, Acidaminococcus, Porphyromonas, Clostridium, Sutterella, Coprococcus, Dialister, Collinsella, Faecalibacterium, Peptostreptococcaceae_noname, Akkermansia, Propionibacterium, Propionibacteriaceae, Parabacteroides, Subdoligranulum, Odoribacter, Clostridiales_noname, Dorea, Oscillibacter, Bacteroides, Sutterella, Collinsella, Faecalibacterium, Peptostreptococcaceae_noname, Akkermansia, Propionibacterium, Propionibacteriaceae, Parabacteroides, Subdoligranulum, Odoribacter, Clostridiales_noname, Dorea, Oscillibacter, Bacteroides, Sutterella, Collinsella, Faecalibacterium, Peptostreptococcaceae_noname, Akkermansia, Propionibacterium.