

SUPPLEMENTARY TABLES

Supplementary Table 1. Statistical analysis data of gut microbiota data at phylum.

Graph	Factor effect (Antibiotic)	Factor effect (MPTP)	Interaction effect (Antibiotic × MPTP)
<i>Bacteroidetes</i>	$F_{(1,36)} = 12.695, P = 0.001$	$F_{(1,36)} = 21.180, P < 0.001$	$F_{(1,36)} = 1.806, P = 0.187$
<i>Firmicutes</i>	$F_{(1,36)} = 14.284, P = 0.001$	$F_{(1,36)} = 20.353, P < 0.001$	$F_{(1,36)} = 2.272, P = 0.140$
<i>Proteobacteria</i>	$F_{(1,36)} = 40.495, P < 0.001$	$F_{(1,36)} = 1.034, P = 0.316$	$F_{(1,36)} = 0.190, P = 0.665$
<i>Deferribacteres</i>	$F_{(1,36)} = 10.911, P = 0.002$	$F_{(1,36)} = 3.872, P = 0.057$	$F_{(1,36)} = 3.948, P = 0.055$
<i>TM7</i>	$F_{(1,36)} = 10.916, P = 0.002$	$F_{(1,36)} = 10.916, P = 0.002$	$F_{(1,36)} = 10.916, P = 0.002$

Supplementary Table 2. Statistical analysis data of gut microbiota data at genus.

Graph	Factor effect (Antibiotic)	Factor effect (MPTP)	Interaction effect (Antibiotic × MPTP)
<i>lactobacillus</i>	$F_{(1,36)} = 40.826, P < 0.001$	$F_{(1,36)} = 0.743, P = 0.394$	$F_{(1,36)} = 0.744, P = 0.394$
<i>Mucispirillum</i>	$F_{(1,36)} = 10.835, P = 0.002$	$F_{(1,36)} = 3.818, P = 0.059$	$F_{(1,36)} = 3.893, P = 0.056$
<i>Candidatus Arthromitus</i>	$F_{(1,36)} = 10.302, P = 0.003$	$F_{(1,36)} = 1.204, P = 0.280$	$F_{(1,36)} = 0.796, P = 0.378$
<i>Parasutterella</i>	$F_{(1,36)} = 81.500, P < 0.001$	$F_{(1,36)} = 0.344, P = 0.561$	$F_{(1,36)} = 0.495, P = 0.486$
<i>Blautia</i>	$F_{(1,36)} = 11.239, P = 0.002$	$F_{(1,36)} = 1.430, P = 0.240$	$F_{(1,36)} = 1.542, P = 0.222$
<i>Robinsoniella</i>	$F_{(1,36)} = 11.589, P = 0.002$	$F_{(1,36)} = 0.211, P = 0.649$	$F_{(1,36)} = 0.211, P = 0.649$
<i>Escherichia</i>	$F_{(1,36)} = 8.289, P = 0.007$	$F_{(1,36)} = 2.245, P = 0.143$	$F_{(1,36)} = 2.399, P = 0.130$
<i>Dorea</i>	$F_{(1,36)} = 7.766, P = 0.008$	$F_{(1,36)} = 0.548, P = 0.464$	$F_{(1,36)} = 1.104, P = 0.300$
<i>Eubacterium</i>	$F_{(1,36)} = 8.529, P = 0.006$	$F_{(1,36)} = 3.508, P = 0.069$	$F_{(1,36)} = 1.747, P = 0.195$
<i>Asaccharobacter</i>	$F_{(1,36)} = 1.292, P = 0.263$	$F_{(1,36)} = 7.712, P = 0.009$	$F_{(1,36)} = 4.353, P = 0.044$
<i>Clostridium</i>	$F_{(1,36)} = 7.982, P = 0.008$	$F_{(1,36)} = 6.757, P = 0.013$	$F_{(1,36)} = 1.664, P = 0.205$
<i>Parabacteroides</i>	$F_{(1,36)} = 43.663, P < 0.001$	$F_{(1,36)} = 29.742, P < 0.001$	$F_{(1,36)} = 29.742, P < 0.001$
<i>Bacteroides</i>	$F_{(1,36)} = 19.018, P < 0.001$	$F_{(1,36)} = 12.176, P = 0.001$	$F_{(1,36)} = 7.447, P = 0.010$
<i>Enterococcus</i>	$F_{(1,36)} = 8.910, P = 0.005$	$F_{(1,36)} = 4.904, P = 0.033$	$F_{(1,36)} = 4.624, P = 0.038$

Supplementary Table 3. Statistical analysis data of gut microbiota data at species.

Graph	Factor effect (Antibiotic)	Factor effect (MPTP)	Interaction effect (Antibiotic × MPTP)
<i>Lactobacillus murinus</i>	F _(1,36) = 19.973, P < 0.001	F _(1,36) = 0.007, P = 0.935	F _(1,36) = 0.006, P = 0.936
<i>Lactobacillus johnsonii</i>	F _(1,36) = 21.666, P < 0.001	F _(1,36) = 1.126, P = 0.296	F _(1,36) = 1.126, P = 0.296
<i>Mucispirillum schaedleri</i>	F _(1,36) = 10.803, P = 0.002	F _(1,36) = 3.836, P = 0.058	F _(1,36) = 3.912, P = 0.056
<i>Candidatus Arthromitus sp. SFB-mouse</i>	F _(1,36) = 10.302, P = 0.003	F _(1,36) = 1.204, P = 0.280	F _(1,36) = 0.796, P = 0.378
<i>Escherichia coli</i>	F _(1,36) = 8.289, P = 0.007	F _(1,36) = 2.245, P = 0.143	F _(1,36) = 2.399, P = 0.130
<i>Blautia sp. Ser8</i>	F _(1,36) = 10.059, P = 0.003	F _(1,36) = 3.457, P = 0.071	F _(1,36) = 3.457, P = 0.071
<i>Robinsoniella peoriensis</i>	F _(1,36) = 11.921, P = 0.001	F _(1,36) = 0.239, P = 0.628	F _(1,36) = 0.239, P = 0.628
<i>Clostridium sp. Clone-27</i>	F _(1,36) = 6.957, P = 0.012	F _(1,36) = 9.366, P = 0.004	F _(1,36) = 6.036, P = 0.019
<i>Blautia sp. canine oral taxon 143</i>	F _(1,36) = 5.309, P = 0.027	F _(1,36) = 5.309, P = 0.027	F _(1,36) = 5.309, P = 0.027
<i>Parabacteroides distasonis</i>	F _(1,36) = 30.573, P < 0.001	F _(1,36) = 40.561, P < 0.001	F _(1,36) = 39.576, P < 0.001
<i>Blautia coccoides</i>	F _(1,36) = 26.794, P < 0.001	F _(1,36) = 6.406, P = 0.016	F _(1,36) = 6.406, P = 0.016
<i>Clostridium sp. HGF2</i>	F _(1,36) = 21.898, P < 0.001	F _(1,36) = 12.850, P = 0.001	F _(1,36) = 12.850, P = 0.001
<i>Clostridium bolteae</i>	F _(1,36) = 8.670, P = 0.006	F _(1,36) = 5.094, P = 0.030	F _(1,36) = 5.094, P = 0.030
<i>Lactobacillus intestinalis</i>	F _(1,36) = 23.328, P < 0.001	F _(1,36) = 8.172, P = 0.007	F _(1,36) = 8.105, P = 0.007
<i>Lactobacillus reuteri</i>	F _(1,36) = 23.676, P < 0.001	F _(1,36) = 8.288, P = 0.007	F _(1,36) = 8.214, P = 0.007
<i>Bacteroides acidifaciens</i>	F _(1,36) = 26.102, P < 0.001	F _(1,36) = 18.528, P < 0.001	F _(1,36) = 11.141, P = 0.002
<i>[Clostridium] cocleatum</i>	F _(1,36) = 14.097, P = 0.001	F _(1,36) = 9.975, P = 0.003	F _(1,36) = 9.975, P = 0.003
<i>Enterococcus casseliflavus</i>	F _(1,36) = 6.743, P = 0.014	F _(1,36) = 5.058, P = 0.031	F _(1,36) = 5.058, P = 0.031
<i>Bacteroides sp. TP-5</i>	F _(1,36) = 7.426, P = 0.010	F _(1,36) = 4.685, P = 0.037	F _(1,36) = 4.747, P = 0.036