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Supplementary Information for

Mind the Gut: Alcohol Shifts Gut Microbial Networks and Ameliorates a Murine Model of Neuroinflammation in a Sex-Specific Pattern

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This PDF file includes:

Figures S1 to S3
Tables S1 to S3

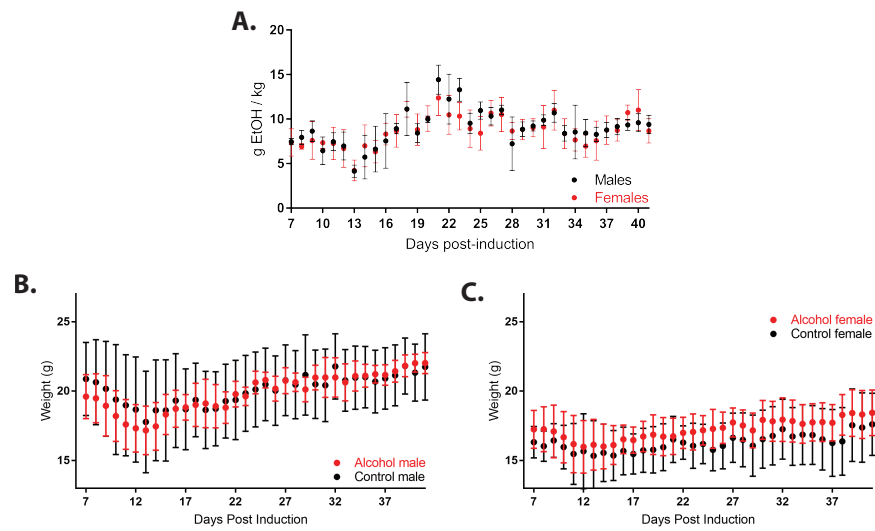


Fig. S1. Alcohol consumption and body weight A. Weight-adjusted alcohol consumption did not significantly differ between males and females throughout the experiment. Average body weight between the alcohol-consumers and controls were not significantly different within male (B.) or female (C.) groups ($n=10$ per group).

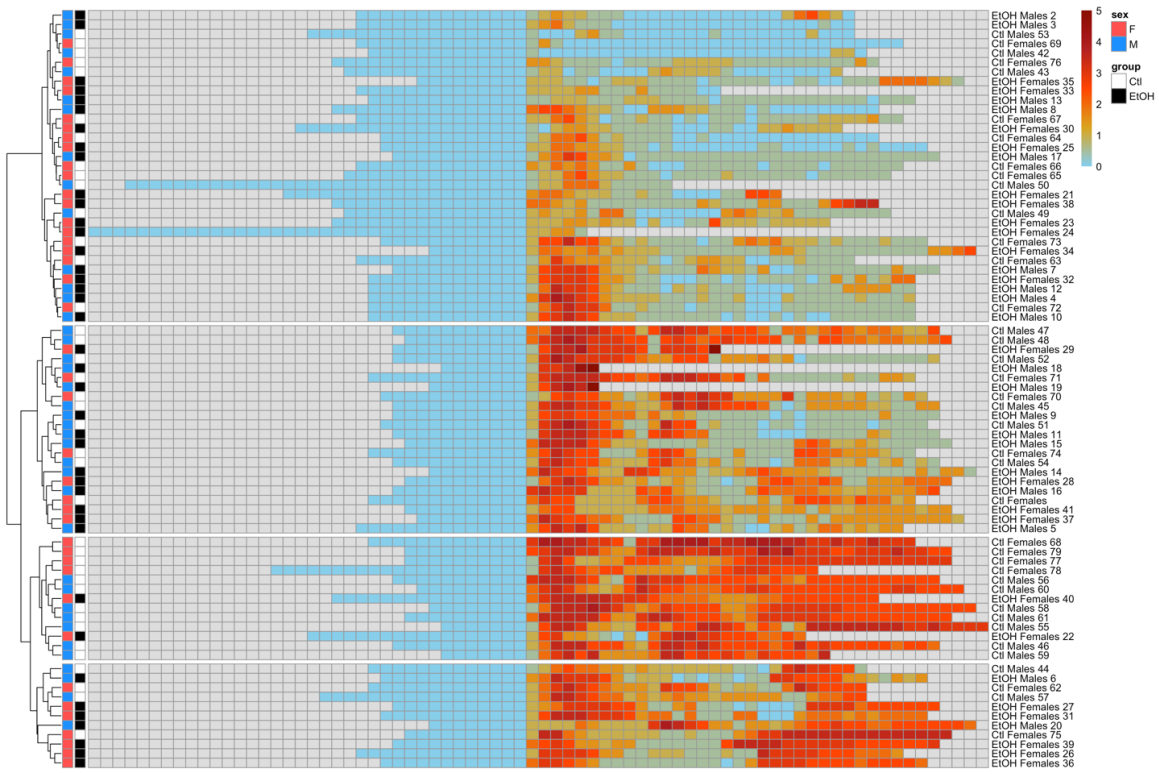


Fig. S2. Heat map of Clinical EAE scores aligned to first day of symptoms.

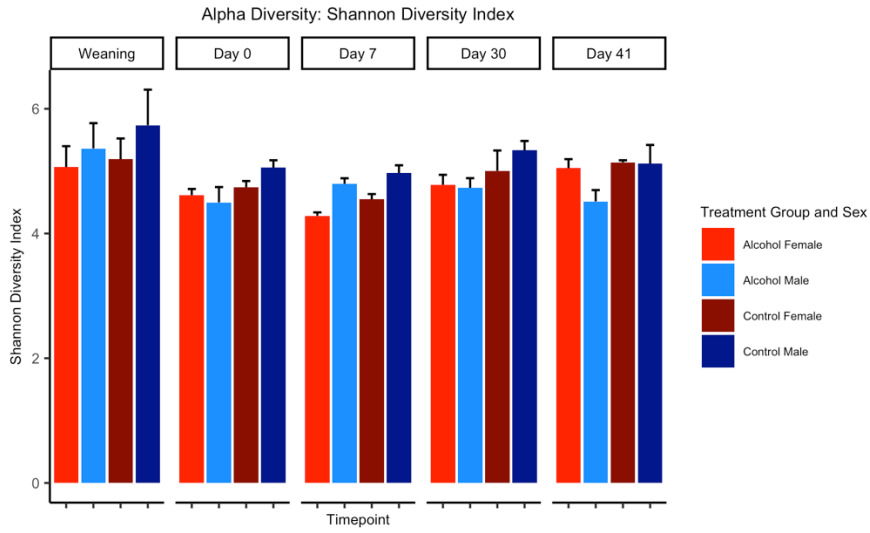


Fig. S3. Alpha Diversity Shannon Index for sex and treatment across experimental timepoints.

Table S1. Linear Mixed Effect Modeling statistical values with Benjamini Hochberg corrections for timepoints. (Green $p < 0.1$, yellow $p < 0.2$)

Taxon	p-value	FDR corrected
Bifidobacterium	2.680192e-05	9.689924e-05
Coriobacteriaceae_	5.407854e-02	7.905104e-02
Adlercreutzia	2.952043e-05	9.910431e-05
Bacteroides	1.714184e-13	8.056666e-12
Parabacteroides	3.614653e-02	5.480280e-02
Prevotella	3.376586e-01	3.870721e-01
Alistipes	8.740353e-01	8.740353e-01
Odoribacter	5.550392e-02	7.905104e-02
.Prevotella.	3.185435e-02	4.990514e-02
Enterococcus	7.268784e-01	7.426801e-01
Lactobacillus	1.492003e-04	3.245658e-04
Turicibacter	5.565890e-05	1.743979e-04
Clostridiales_	8.222074e-02	1.136581e-01
Clostridium	1.519244e-04	3.245658e-04
SMB53	2.965358e-04	6.059645e-04
Dehalobacterium	3.815148e-03	6.641184e-03
Lachnospiraceae_	2.175357e-01	2.690573e-01
Coprococcus	5.839290e-01	6.098814e-01
.Ruminococcus.	8.691999e-02	1.167211e-01
Peptostreptococcaceae_	1.943661e-03	3.513541e-03
Ruminococcaceae_	2.980132e-01	3.501656e-01
Anaerotruncus	1.628847e-01	2.069076e-01
Oscillospira	1.007715e-03	1.894504e-03
Ruminococcus	1.045183e-01	1.364544e-01
Allobaculum	9.876409e-05	2.730537e-04
Coprobacillus	1.356446e-02	2.198378e-02
Sutterella	5.351976e-04	1.048095e-03
Helicobacter	7.773077e-03	1.304766e-02
Enterobacteriaceae_	2.255812e-01	2.718542e-01
Aggregatibacter	5.562341e-01	5.941591e-01
Acinetobacter	4.037129e-01	4.412676e-01
Akkermansia	9.124310e-05	2.680266e-04

Table S2. Linear Mixed Effect Modeling statistical values with Benjamini Hochberg corrections for treatment group. (Green p < 0.1, yellow p < 0.2)

Taxon	p-value	FDR corrected
Adlercreutzia	0.5267904201	0.580820207
Bacteroides	0.6725767859	0.705385410
Parabacteroides	0.7550083140	0.772984702
Prevotella	0.3118806807	0.403037666
Alistipes	0.0231499191	0.099544652
Odoribacter	0.6670345477	0.705385410
.Prevotella.	0.0832501869	0.221785797
Enterococcus	0.8830634747	0.883063475
Lactobacillus	0.0220158054	0.099544652
Turicibacter	0.0676314843	0.193876922
Clostridiales.___	0.0156569091	0.084155887
Clostridium	0.0038040300	0.027262215
SMB53	0.0466897435	0.143404212
Dehalobacterium	0.0007129442	0.015328301
Lachnospiraceae.___	0.0080725224	0.049588352
Coprococcus	0.0001446390	0.006219478
.Ruminococcus.	0.1316652813	0.221785797
Peptostreptococcaceae.___	0.0931563002	0.221785797
Ruminococcaceae.___	0.0441126043	0.143404212
Anaerotruncus	0.3388848565	0.403037666
Oscillospira	0.0358071586	0.128308985
Ruminococcus	0.2420858441	0.325302853
Allobaculum	0.3467998522	0.403037666
Coprobacillus	0.2084144386	0.289090996
Sutterella	0.4671688950	0.528638486
Helicobacter	0.1619003377	0.240059121
Enterobacteriaceae.___	0.2079510294	0.289090996
Aggregatibacter	0.3388803556	0.403037666
Akkermansia	0.0325561659	0.127265012

Table S3. Linear Mixed Effect Modeling statistical values with Benjamini Hochberg corrections for treatment group and sex. (Green $p < 0.1$, yellow $p < 0.2$)

Taxon	p-value	FDR corrected
Adlercreutzia	0.664774509	0.93140369
Bacteroides	0.728182453	0.94884380
Parabacteroides	0.671477081	0.93140369
Prevotella	0.281187713	0.48364287
Alistipes	0.839006786	0.98055004
Odoribacter	0.155146543	0.29005658
.Prevotella.	0.048871089	0.12141657
Enterococcus	0.866532596	0.98055004
Lactobacillus	0.717041241	0.94884380
Turicibacter	0.528889520	0.78421550
Clostridiales.___	0.043111579	0.11586237
Clostridium	0.998412799	0.99841280
SMB53	0.025449636	0.07816674
Dehalobacterium	0.064739428	0.14346067
Lachnospiraceae.___	0.113609424	0.23262882
Coprococcus	0.012612298	0.07816674
.Ruminococcus.	0.774228450	0.97917127
Peptostreptococcaceae.___	0.203417205	0.36445583
Ruminococcaceae.___	0.066725894	0.14346067
Anaerotruncus	0.332704689	0.52986302
Oscillospira	0.855500845	0.98055004
Ruminococcus	0.154873169	0.29005658
Allobaculum	0.818789876	0.98055004
Coprobacillus	0.020335314	0.07816674
Sutterella	0.004888834	0.07816674
Helicobacter	0.050825542	0.12141657
Enterobacteriaceae.___	0.033245448	0.09530362
Aggregatibacter	0.345552650	0.53067014
Akkermansia	0.896955290	0.98895070