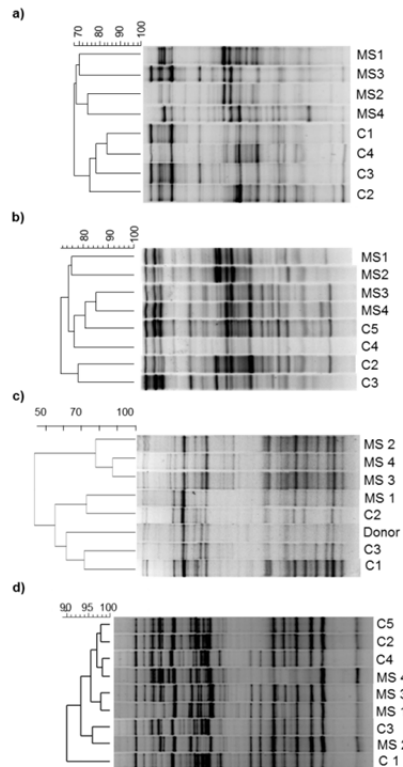


Supplementary Figure 1. DGGE profiles of fecal microbiota.

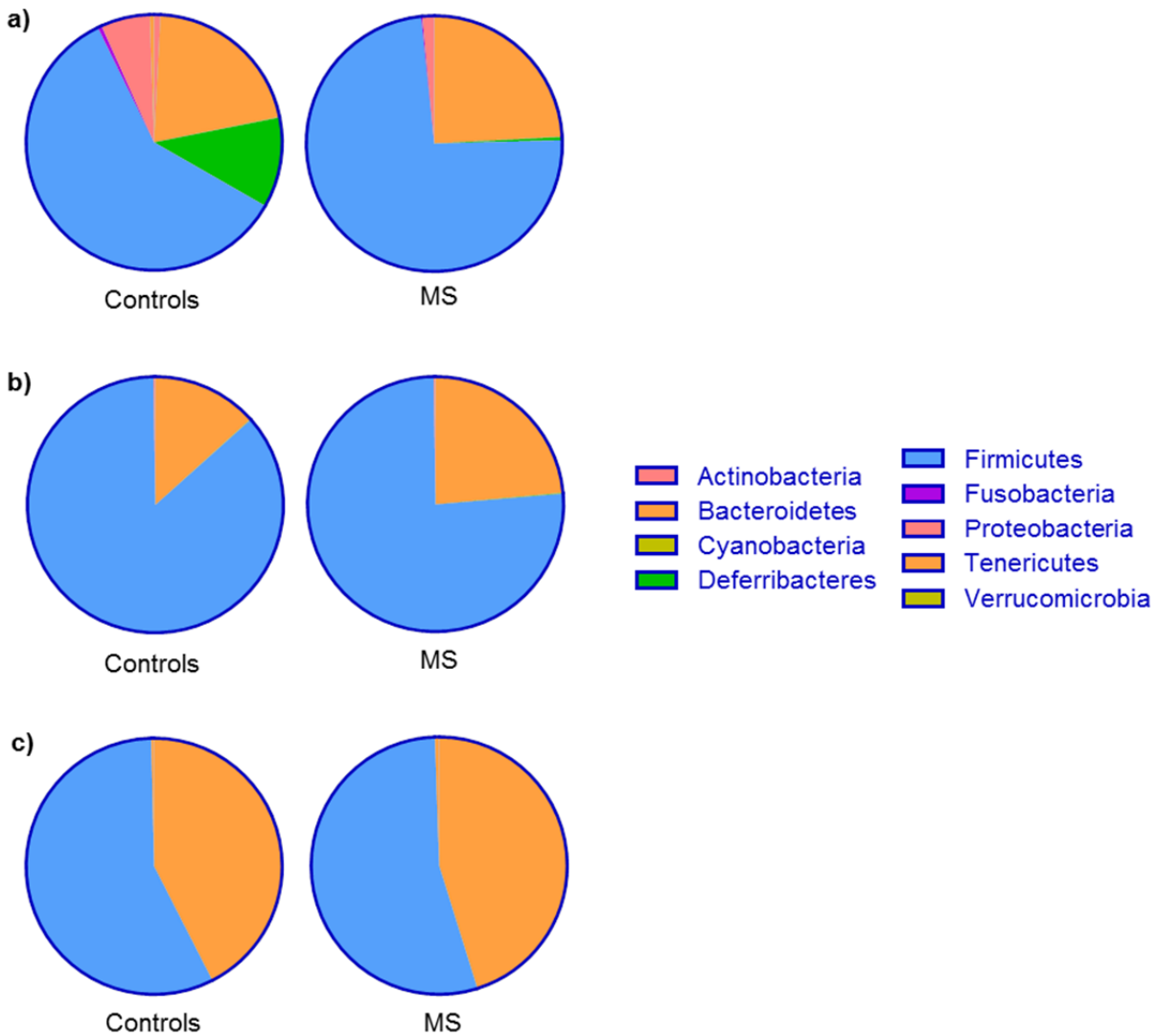


a,b) Dendrograms derived from DDGE analysis of 16S rDNA of colonic bacteria from adult SPF MS and control mice (a), and young (4 weeks old) SPF MS and control mice (b), based on Dice's similarity index and the unweighted-pair group method with the arithmetic average clustering algorithm.

c) Dendrogram derived from DGGE analysis of 16S rDNA of colonic bacteria from ex-germ free MS and ex-germ free control mice colonized by co-habitation based on Dice's similarity index and the weighted-pair group method with the arithmetic average clustering algorithm.

d) Dendrogram from DGGE analysis of 16S rDNA of colonic bacteria from ex-germ free mice colonized by gavage with MS or control microbiota based on Dice's similarity index and the unweighted-pair group method with the arithmetic average clustering algorithm.

Supplementary Figure 2. Taxonomic summary at phylum level of colonic microbiota.

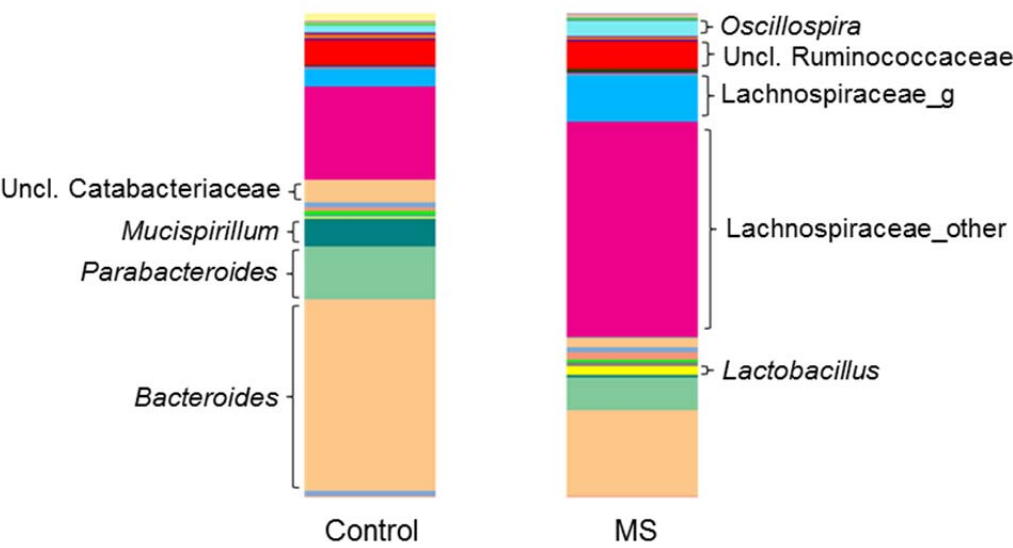


a) Taxonomic composition at phylum level of SPF MS and control mice.

b) Taxonomic composition at phylum level of germ-free MS and control mice colonized by cohabitation with a single SPF donor.

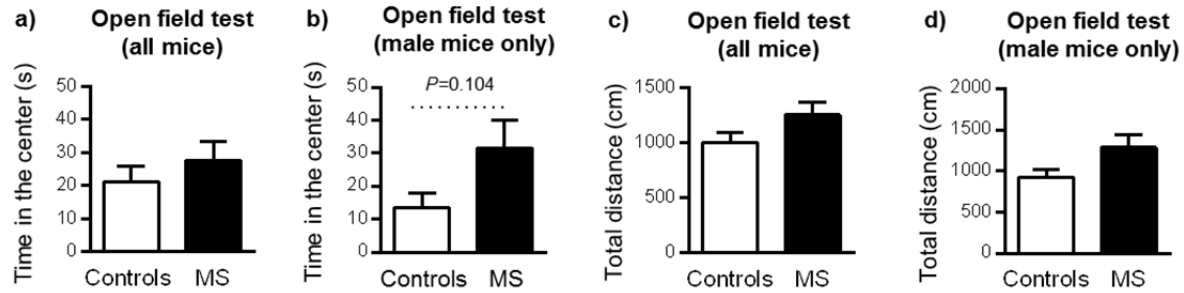
c) Taxonomic composition at phylum level of germ-free mice gavaged with fecal microbiota from MS or control mice.

Supplementary Figure 3. Taxonomic summary at genus level of SPF colonic microbiota.



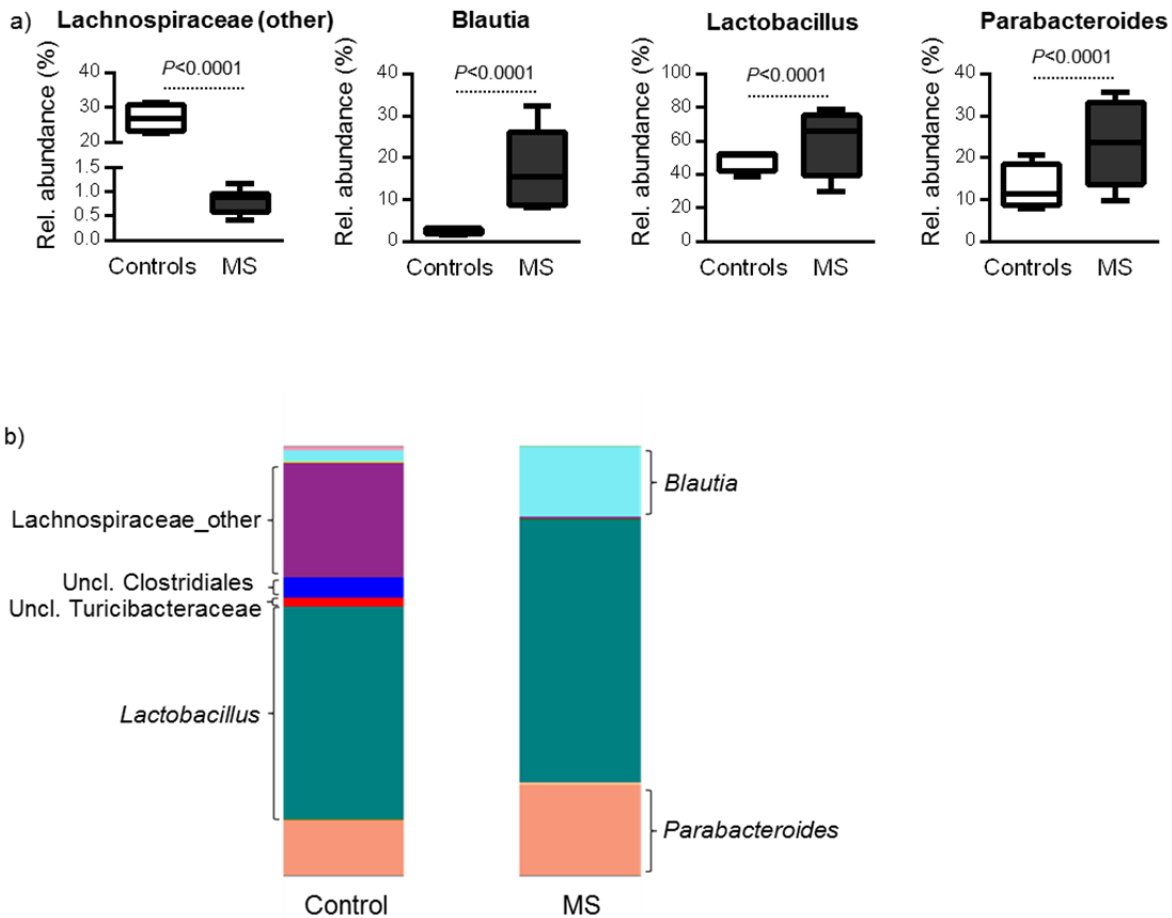
Taxonomic composition at genus level of SPF MS and control mice' colonic microbiota.

Supplementary Figure 4. Open field test shows no difference in behaviour between GF control and MS mice.



Total time spent in the center of the arena (a and b), and total distance travelled (c and d) during the open field test of all GF mice (a and c), and male mice only (b and d) (control, n=24 (12 males); MS, n=26 (17 males)). The graphs represent mean $\pm$ SEM. The assessment of the main effects (MS and gender) on all GF mice was performed with a two-way ANOVA, while the effect of MS on GF male mice only was performed with a one-way ANOVA.

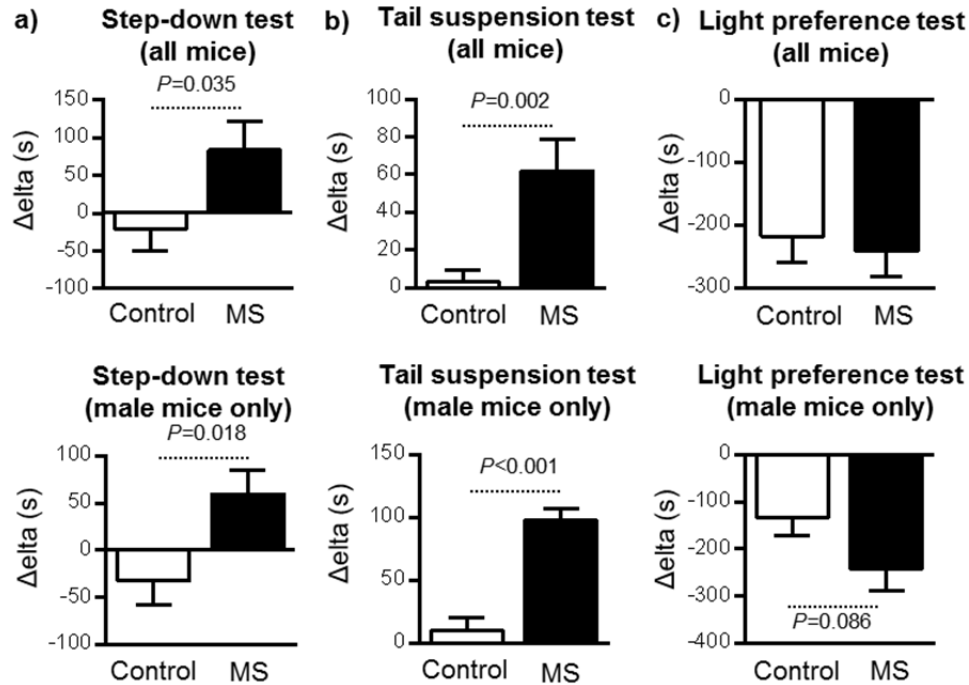
Supplementary Figure 5. Taxonomic differences in colonic microbiota composition of germ-free MS and control mice colonized through cohabitation with a single SPF donor mouse.



a) Main genera contributing to the taxonomic differences between germ-free MS and control mice colonized through cohabitation with a single SPF donor mouse. The P values obtained from multiple t test comparisons between groups (Controls vs MS) were corrected with the “False discovery rate” (FDR) method, accepting a 3% FDR.

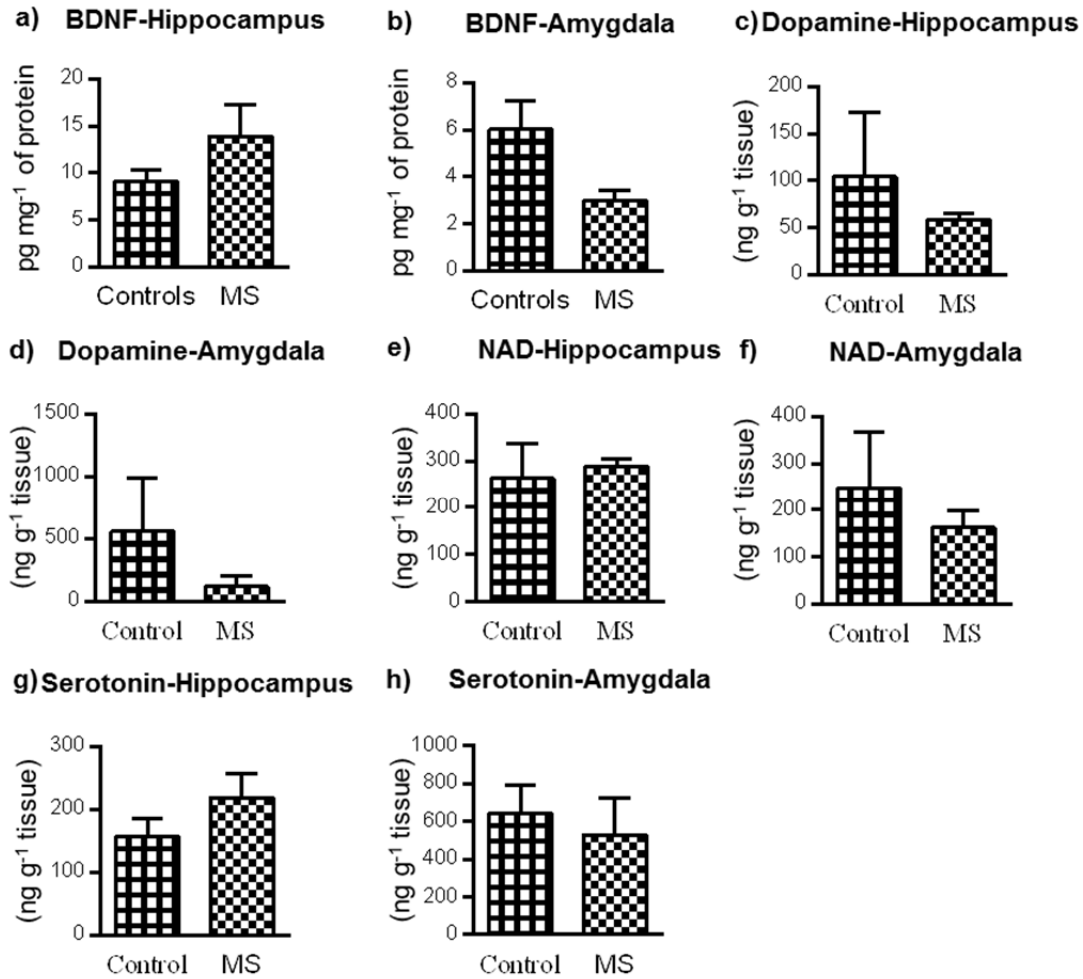
b) Taxonomic composition at genus level of germ-free MS and control mice colonized through cohabitation with a single SPF donor mouse.

Supplementary Figure 6. Colonization of adult germ-free mice induces anxiety-like behavior and behavioral despair in MS mice but not in controls.



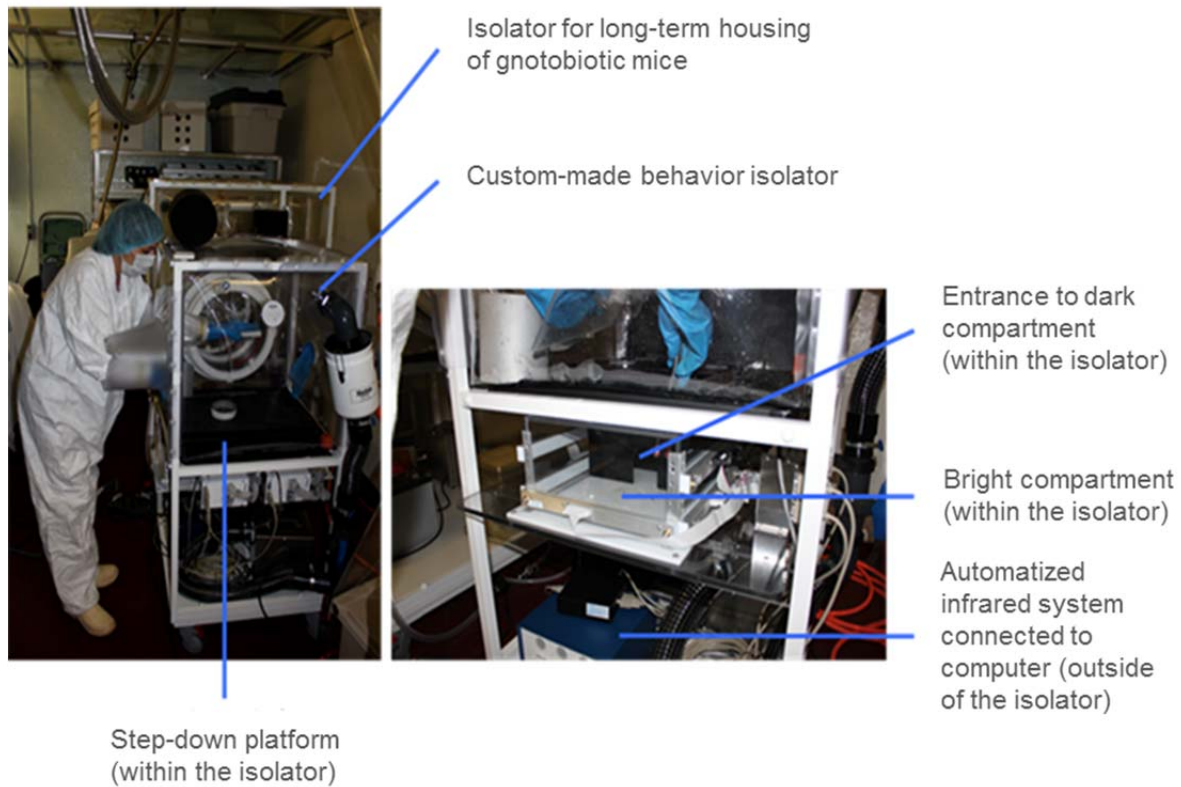
The graphs represent mean $\pm$ SEM of the difference (Δ) between the value obtained three weeks after colonization (T_1) and the value obtained in germ-free conditions (T_0) for each behavioral test applied, a) step-down test, b) tail suspension test, and c) light preference test. The upper panels represent all mice; the lower panels represent male mice only. MS, $n=11$, 7 males and 4 females; control, $n=16$, 9 males and 7 females. P values were calculated performing t-tests.

Supplementary Figure 7. BDNF and catecholamine levels in hippocampus and amygdala of colonized MS and control mice.



Total free BDNF levels in brain sections of hippocampus a) and amygdala b) of colonized GF control and MS mice. Dopamine c-d), noradrenaline (NAD) e-f), and serotonin g-h) levels in hippocampus and amygdala of colonized GF control and MS mice. (control, $n=5$ control; MS, $n=5$). The graphs represent mean $\pm$ SEM. The assessment of the main effects (MS and gender) on all colonized mice was performed with a two-way ANOVA.

Supplementary Figure 8. Customized equipment for behavioral testing within a gnotobiotic isolator at the Axenic Gnotobiotic Unit at McMaster University.



The picture shows the set-up for behavioral testing within a custom modified isolator in the germ-free facility at McMaster University.

Supplementary Table 1. OTUs' sequences found different between SPF MS and control mice.

Lachnospiraceae, g_

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>597 len=136 tot-seq=7

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Turicibacteraceae, g__

>506 len=160 tot-seq=10

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Oscillospira

>173 len=137 tot-seq=144

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Granulicatella

>762 len=160 tot-seq=5

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Lachnospiraceae

>22 len=135 tot-seq=11621

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>65 len=135 tot-seq=1773

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>205 len=134 tot-seq=92

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>209 len=136 tot-seq=89

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>279 len=136 tot-seq=42

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>327 len=135 tot-seq=30

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>859 len=138 tot-seq=4

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>791 len=135 tot-seq=4

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Ruminococcaceae

>139 len=138 tot-seq=272

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>377 len=138 tot-seq=23

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GCCACGGCTAACTACGTG

>719 len=137 tot-seq=5

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Lactobacillales

>903 len=160 tot-seq=4

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Clostridiales

>348 len=135 tot-seq=27

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CCGGCTAACTACGTG

>428 len=135 tot-seq=15

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>825 len=136 tot-seq=4

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Clostridia

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CCGGCTAACTACGTG

Firmicutes

>643 len=136 tot-seq=6

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>802 len=135 tot-seq=4

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>736 len=138 tot-seq=5

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T

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GCCCCGGCTAACTACGTG

Supplementary Table 2. OTUs' sequences found different between colonized MS and control mice.

Clostridium (Lachnospiraceae)

>10 len=138 tot-seq=410

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CCCCGGCTAACTACGTG

Atopobium (Coriobacteriaceae)

>122 len=140 tot-seq=5

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Lachnospiraceae

>4 len=134 tot-seq=11048

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>6 len=151 tot-seq=2686

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>7 len=135 tot-seq=1424

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CCGGCTAACTACGTG

>21 len=135 tot-seq=106

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CCGGCTAACTACGTG

>56 len=161 tot-seq=26

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>63 len=135 tot-seq=20

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Clostridiales

>5 len=135 tot-seq=2886

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>40 len=135 tot-seq=45

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