

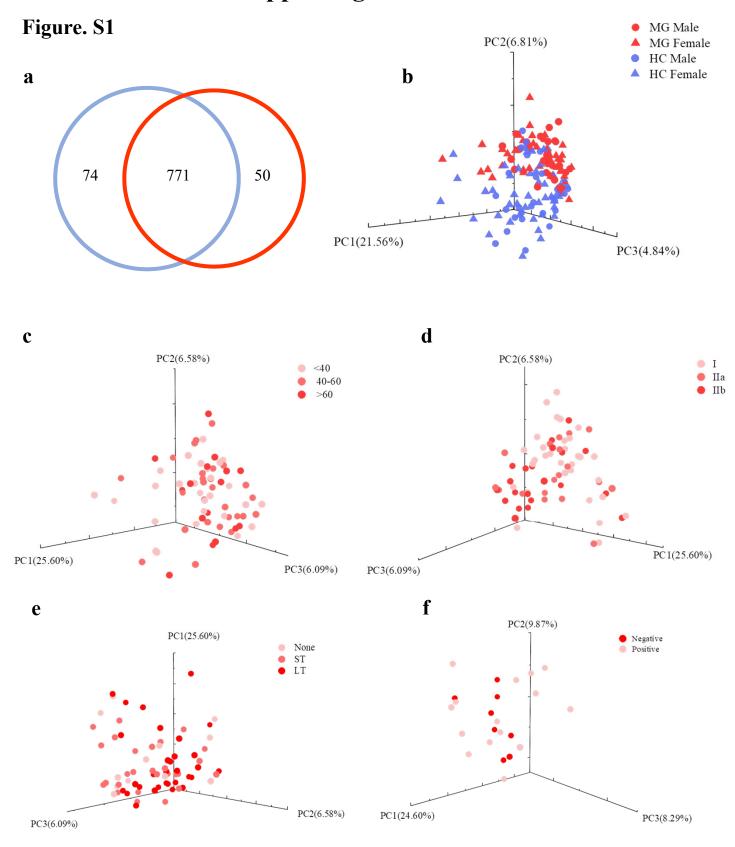
## **Supporting Information**

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Perturbed Microbial Ecology in Myasthenia Gravis: Evidence from the Gut Microbiome and Fecal Metabolome

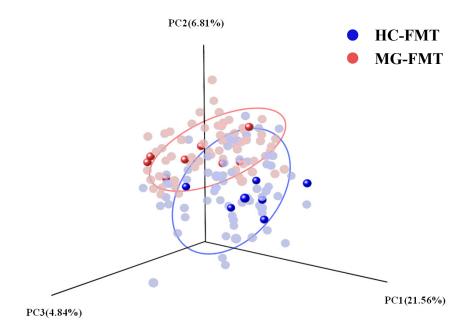
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## **Supporting Information**



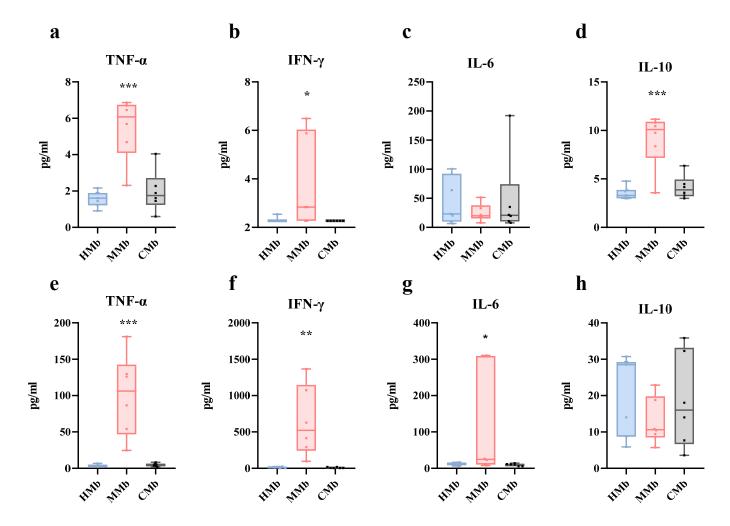
**Figure. S1.** (a) A Venn diagram showed that 771 of 895 OTUs were detected in the two groups, while 50 and 74 OTUs were unique to MG subjects (red circle, n=70) and HCs (blue circle, n=74), respectively. (b)The global microbial phenotypes were not clustered based on sex (n=44, HC Female; n=30, HC Male; n=39, MG Female; n=31, MG Male). (c-f) The global microbial phenotypes of MG groups were not clustered based on age (n=27, <40; n=26, 40-60; n=17, >60. MG), clinical classification, medication (n=30, LT; n=27, ST; n=12, None; LT: long term immunosuppressive treatment; ST: short term treatment; None: no treatment), and AChR antibody (n=15, Positive; n=8, Negative).

## Figure. S2



**Figure. S2** The samples used for fecal microbiota transplantation experiments (n=7-8 for every group) were mixed with the remaining samples (n=74, HC; n=70, MG group).

## Figure. S3



**Figure. S3**. The cytokine levels in serum and intestinal tissue among the three groups. (a-d) The serum levels of TNF- $\alpha$ , IFN- $\gamma$ , and IL-10 were significantly increased in MMb group relative to HMb group. These increased cytokines can be reversed in CMb group. (e-h) Compared to HMb group, the levels of TNF- $\alpha$ , IFN- $\gamma$ , and IL-6 were significantly un-regulated in MMb group; and these changes were reversed to normal level in CMb group. (male mice, HMb, n=7; MMb,n=6; CMb, n=6). \* P<0.05, \*\*P<0.01, \*\*\*P<0.001 by one way ANOVA.