

## *Supplementary Material*

### **Supplementary Figures**

**FIGURE S1**| Impact of confounding variables on global gut microbial phenotypes. The global microbial phenotypes of two subtypes of MG groups were not clustered based on gender (n=44, HC Female; n=30, HC Male; n=13, OMG Female; n=18, OMG Male; n=26, GMG Female; n=13, GMG Male )(A-C) and medication (n=12, OMG IT; n=19, OMG Non\_IT; n=19, GMG IT; n=20, GMG Non\_IT. IT: immunosuppressive treatment )(D-E).

**FIGURE S2**| Discriminative OTUs observed in the pairwise comparisons among HC, OMG and GMG groups. Using LEfSe analysis , differential OTUs responsible for discrimination among the three groups were identified based on LDA score >2.5 and fold change >2. **(A-C)** Totally, 34 ,37 and 10 OTUs attributed to distinguish the OMG versus HCs, GMG versus HCs, and GMG and OMG, respectively. **(D)**15 OTUs were differentially expressed among the three groups.

**FIGURE S3**| Co-occurrence networks deduced from the relative abundance of differential OTUs between OMG and GMG. The differential OTUs between OMG and GMG groups were identified by LDA (LDA>2.5 and fold change>2). Totally, 10 OTUs were responsible for this discrimination. Compared to GMG group, the OMG group was mainly characterized by altered covarying OTUs belonging to Bacteroidaceae , Erysipelotrichaceae and Lachnospiraceae. Blue dots, increased microbes in OMG ;red dots, increased microbes in GMG. OTUs annotated to family level were marked. Edges between nodes indicate Spearman's correlation < - 0.35 (light blue), or >0.35 (light red), edges thickness indicate p value (p<0.05).

### **Supplementary Tables**

**TABLE S1**| The discriminative OTUs between two subtypes of MG patients and HCs.

**TABLE S2**| The discriminative OTUs between OMG and GMG patients.

**TABLE S3**| Differential metabolites between the two subtypes of MG patients and HCs.

**TABLE S4**| The discriminative OTUs and metabolites among the three groups.