

1 Additional file 17. Fig. S8. Correlation network between microbiome and functional genes in CON (a) and untreated (b) group. The node
 2 represented a microbial genus, its colour represents the bacterial phylum it belongs to and its size represents the number of direct edges that it has.
 3 The green edges indicated positive correlation and red edges indicated negative correlation (Spearman test). Only significant correlations (p value
 4 <0.05 after false discovery rate correction) are displayed.

