Electronic Supplementary Material (ESI) for Food & Function.

## Figure legends

Fig. S1. Transcriptomic analysis. (A) Volcano plot. The log2 FC indicates the mean expression level for each gene. Each dot represents one gene. After crocin-I administration, black dots represent no significant DEGs between CORT group and CORT-C20 group, the green dots represent down-regulated genes and red dots represent up-regulated genes; (B) GO classifications of the DEGs (FC>2, *p*<0.05) between CORT group and CORT-C20 group. All of the DEGs were assigned to three categories: cellular component, molecular function, and biological process. Top 20 most enriched GO terms of each category were list in Table. S4.

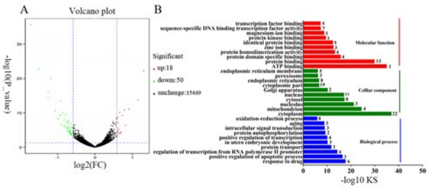

Fig. S2. Extended error bar plot comparing the differences in the mean proportions of significantly altered COG composition and the difference in the proportions of the means using STMAP version (2.1.3). Predictive functional profiling of microbial communities is related to carbohydrate transport and metabolism, coenzyme transport and metabolism, lipid transport and metabolism, transcription, cell wall/membrane/envelope biogenesis and post-translational modification, protein turnover, and chaperones.