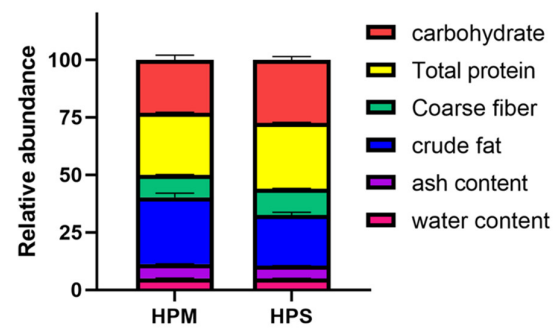


## Supporting Information

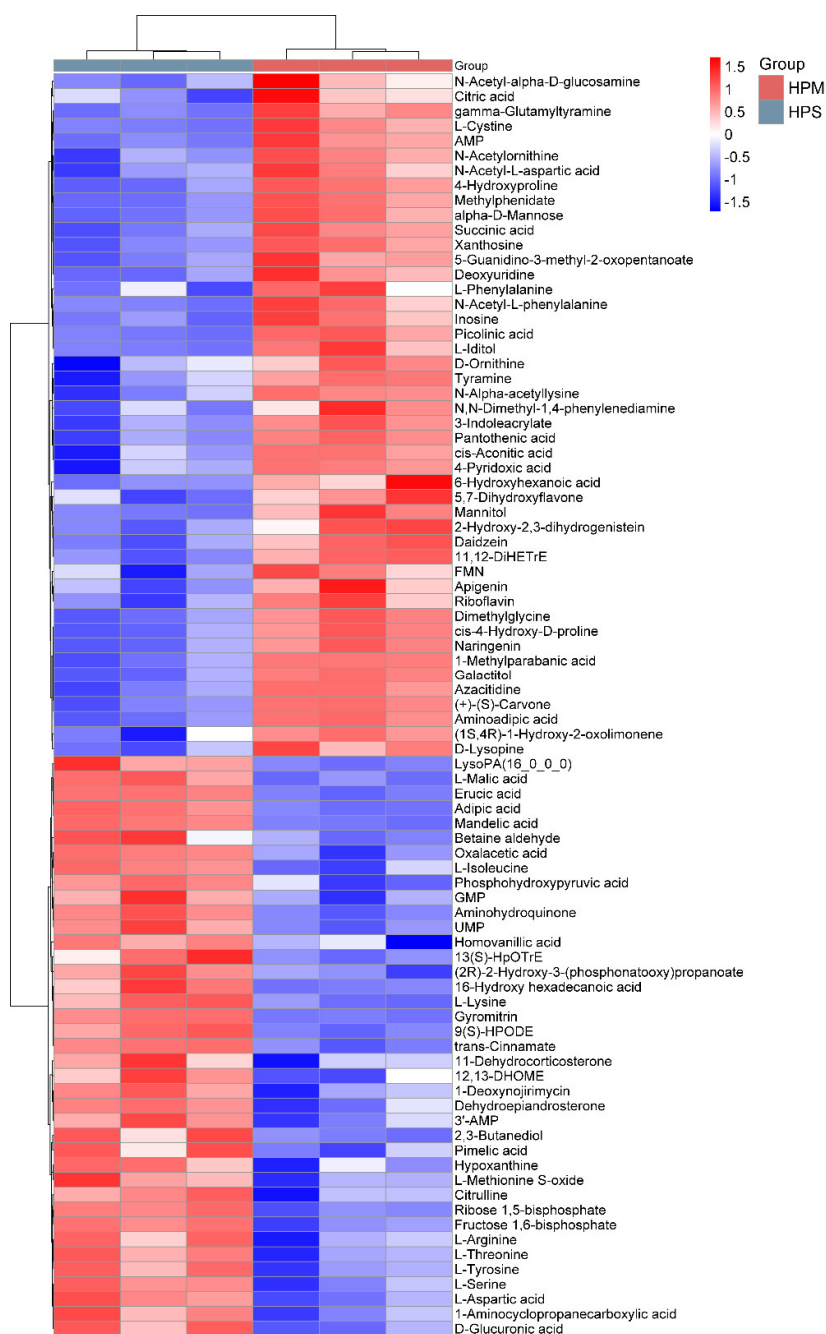
**Table S1.** Body and organ weight of mice.

group	Weight (g)	Organ index (%)				
		heart	liver	spleen	lung	kidney
Control	23.74±1.67	0.53±0.08	3.51±0.18	0.24±0.03	0.59±0.05	1.11±0.33
TAU	24.70±1.54	0.48±0.05	3.37±0.15	0.26±0.04	0.59±0.08	1.19±0.10
PHM-H	24.47±1.53	0.52±0.05	3.38±0.24	0.26±0.04	0.60±0.07	1.23±0.05
PHM-L	22.91±1.41	0.58±0.08	3.44±0.16	0.26±0.03	0.63±0.09	1.26±0.07
PHS-H	23.66±1.27	0.55±0.05	3.48±0.08	0.23±0.03	0.59±0.06	1.29±0.07
PHS-L	24.51±1.13	0.52±0.08	3.43±0.12	0.25±0.03	0.59±0.06	1.27±0.08

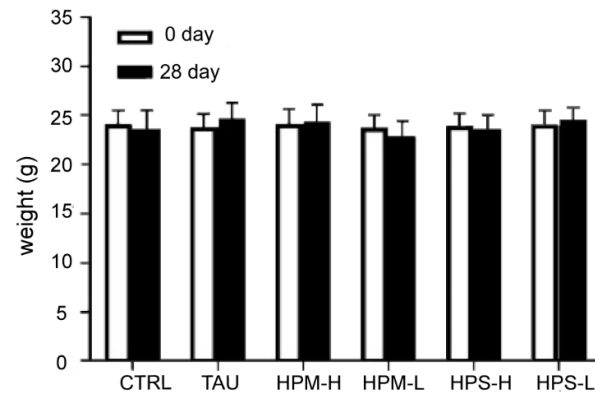
Values are expressed as means ± SD ( $n = 10$ ).



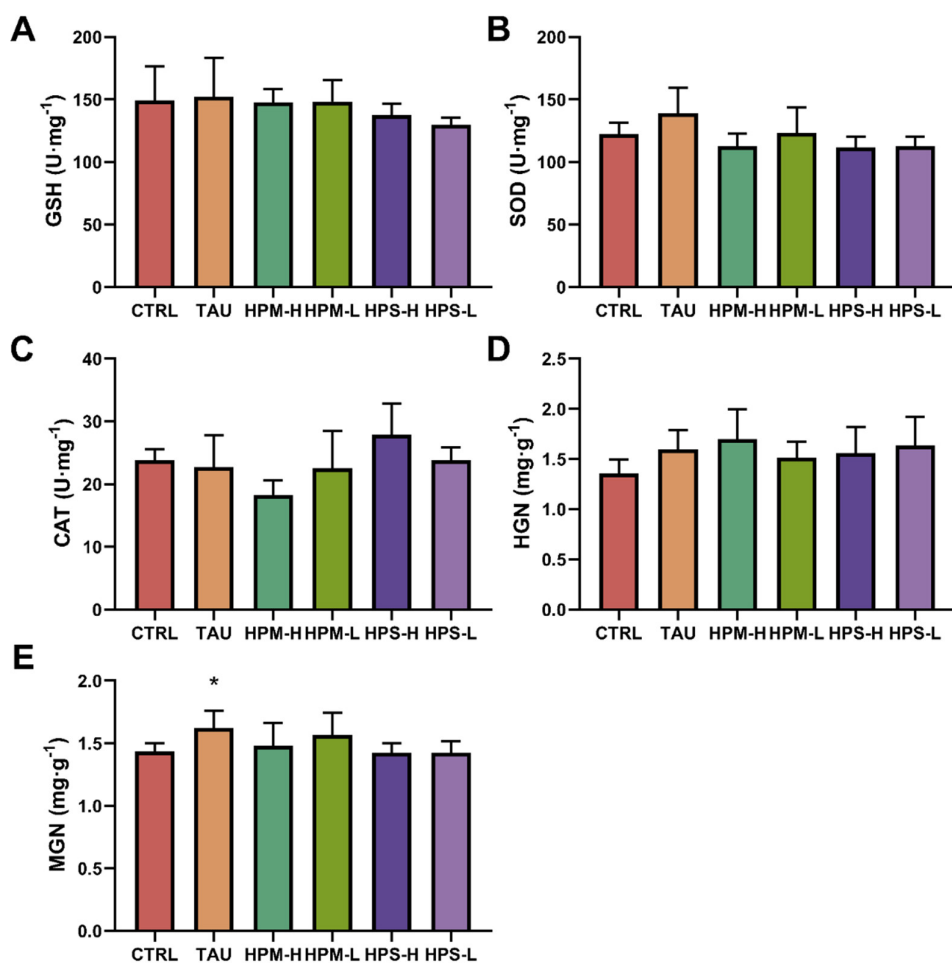
**Figure S1.** Contents of general components of mycelium and spores of *Paecilomyces hepiali*.



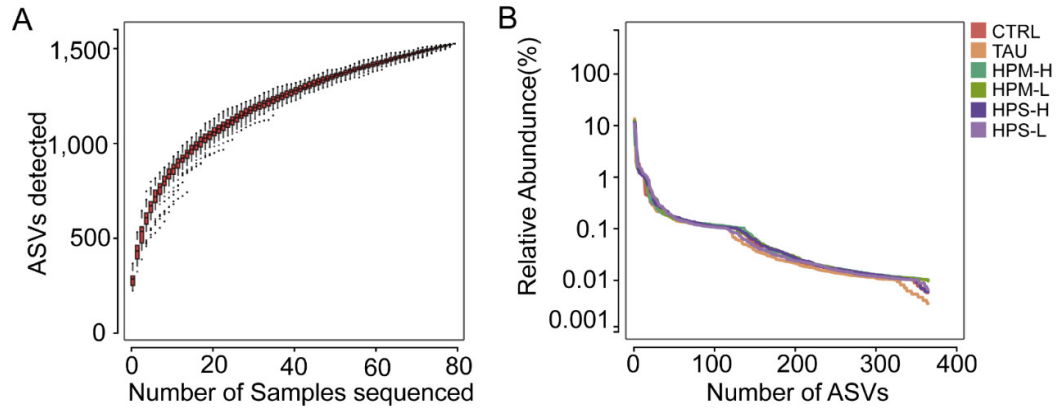
**Figure S2.** Heatmap comparison based on the 85 metabolites with significant differences. The intensity of the color of the heatmap represents the degree of relative abundance.



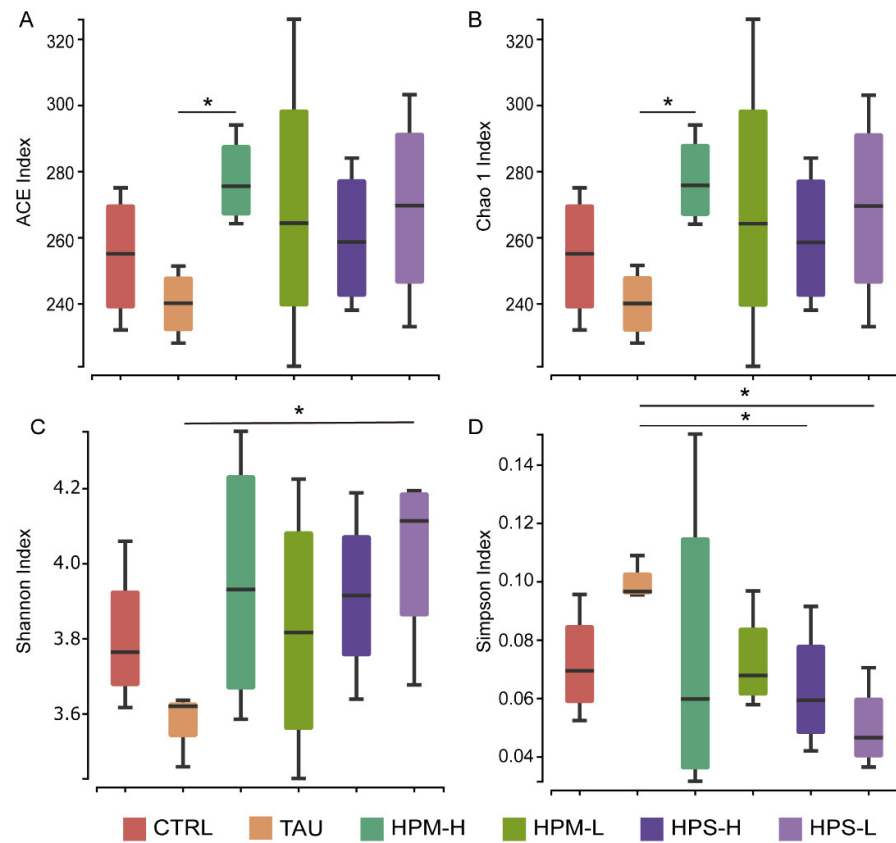
**Figure S3.** The body weight changes of mice on 0 day and 28 day. Data are mean  $\pm$  SD ( $n = 10$  per group).



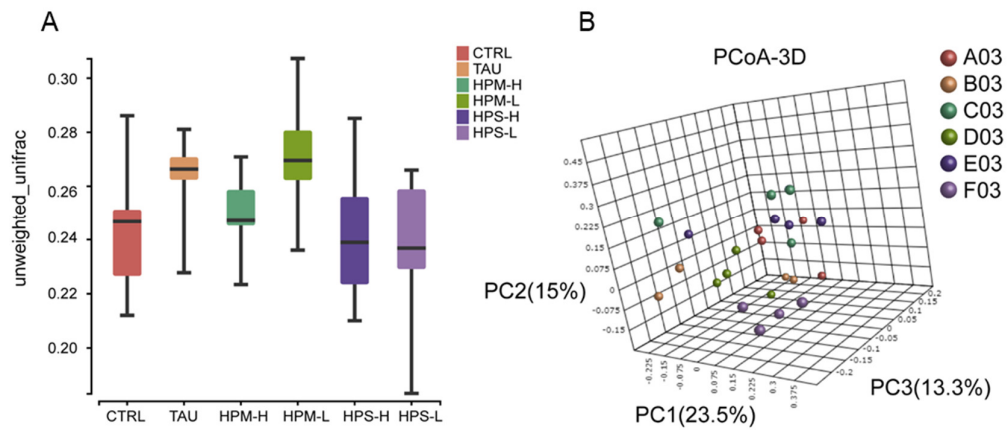
**Figure S4.** The anti-fatigue effect of the HP on mice in each group. (A) Glutathione peroxidase (GSH); (B) Superoxide dismutase (SOD); (C) Catalase (CAT); (D) Hepatic glycogen (HGN); (E) Muscle glycogen (MGN).



**Figure S5.** Evaluation of sequencing data of the different bacterial community groups. (A) ASVs accumulation curve; (B) Rank abundance curve.

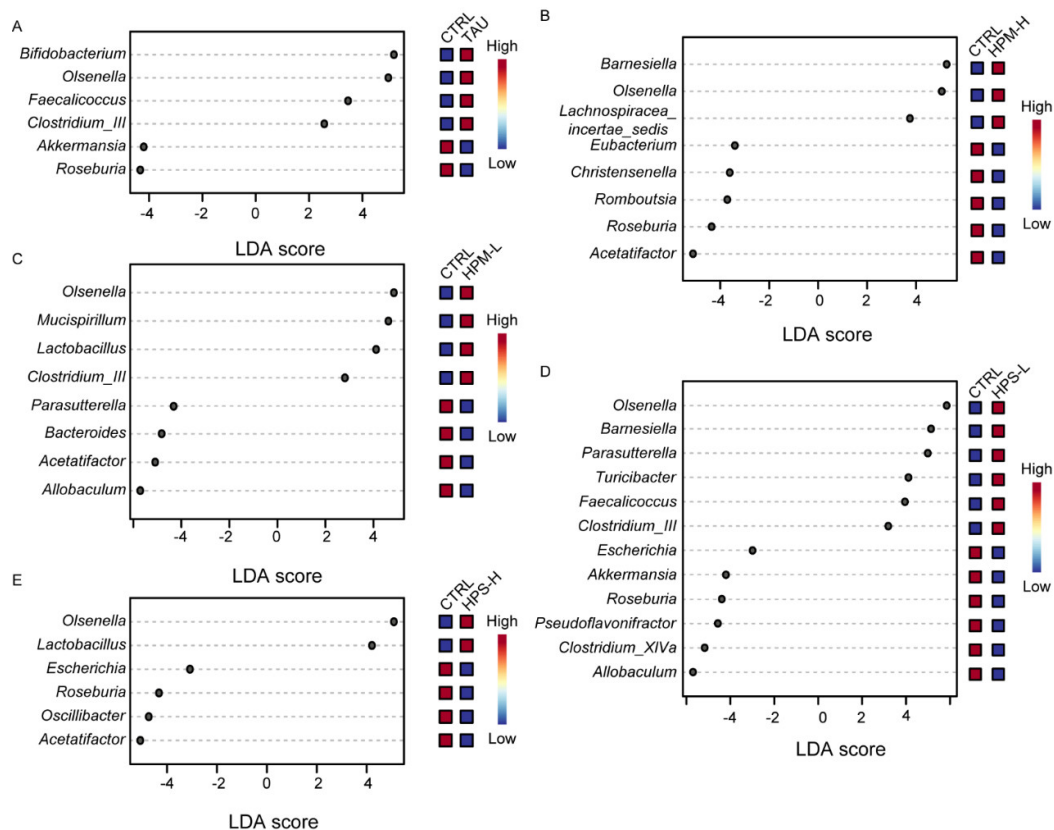


**Figure S6.** Alpha diversity of the gut microbiota. (A) ACE index; (B) Chao 1 index; (C) Shannon index; (D) Simpson index. Asterisk (\*) represents  $p < 0.05$ .

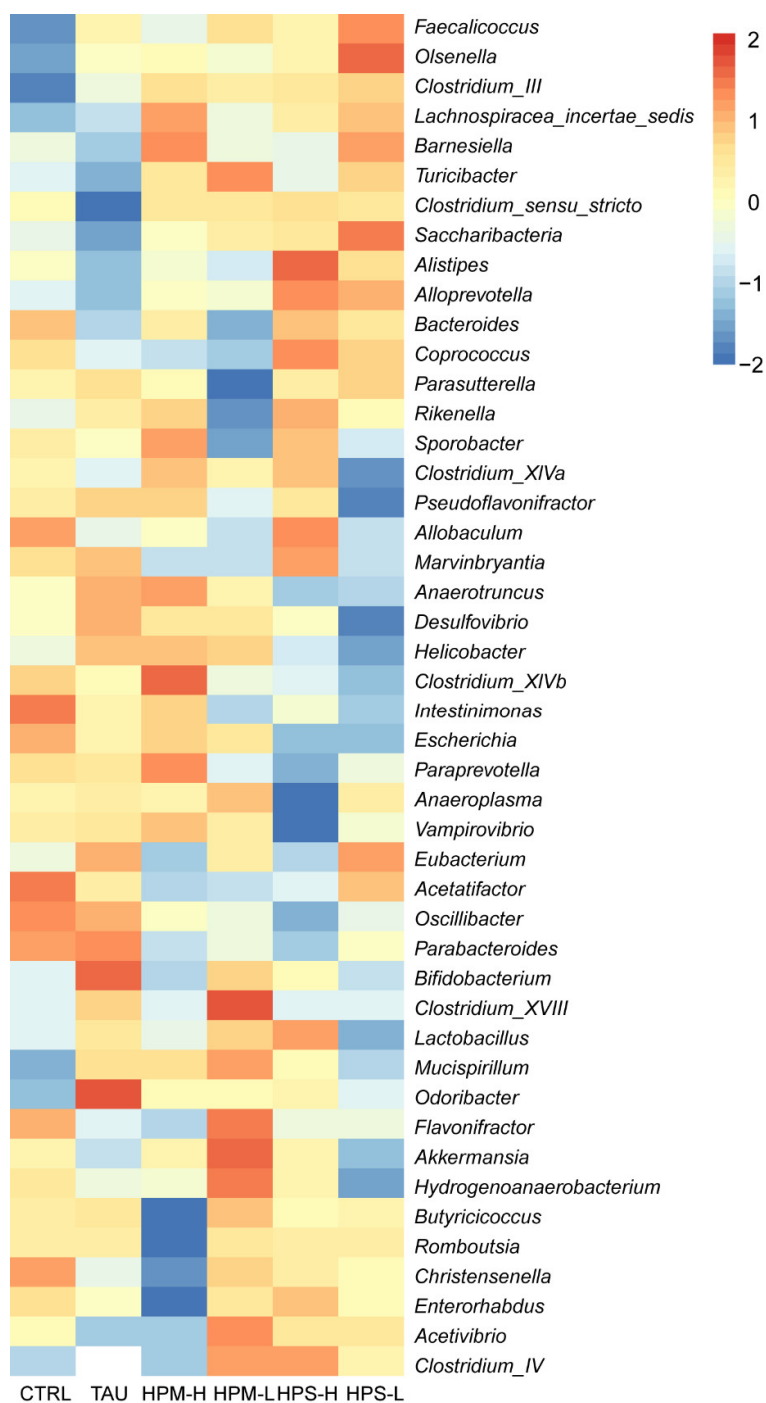


**Figure S7.** Beta diversity of the gut microbiota. (A) The intergroup differences of Beta diversity of the mice gut microbiota; (B) Principal Co-ordinates Analysis (PCoA) of the mice gut microbiota based on Bray–Curtis metrics.





**Figure S8.** Linear discriminant analysis (LDA) scores derived from LEfSe analysis. The biomarker taxa LDA score of  $> 2$  was shown (the length of the bar represents the LDA score). (A) CTRL Vs TAU; (B) CTRL Vs HPM-H; (C) CTRL Vs HPM-L; (D) CTRL Vs HPS-L; (E) CTRL Vs HPS-H.



**Figure S9.** Heatmap comparison based on the top relative abundance of 46 key genus. The intensity of the color of the heatmap represents the degree of relative abundance.