According to retention time (RT) and molecular weight of peak (Mp) data in Table S1 and

Figure S1, the standard curve is obtained, as LgMp= $0.0466 \, t_R^2 - 1.3722 t_R + 11.616$, $R^2 = 0.9996$.
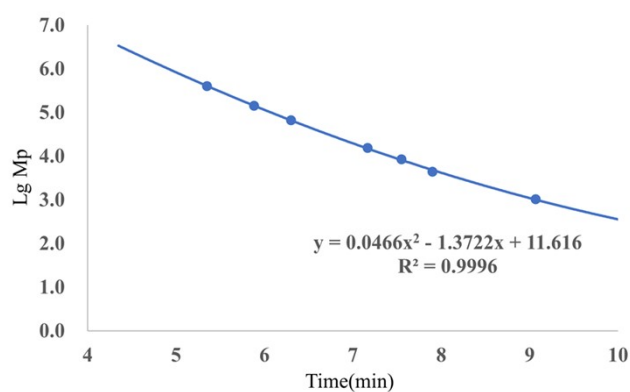

Figure S1. The standard curve of LgMp and time.

Table S1 The RT, Mp and Lg Mp of dextran standards.

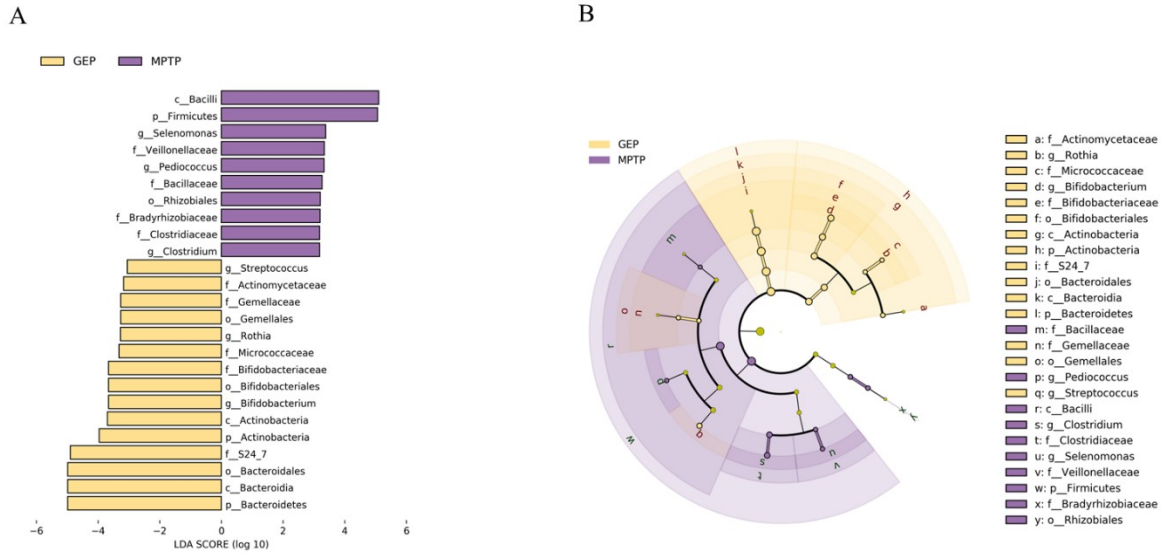| RT (min)	Mp (Da)	LgMp
5.350	401300	5.603
5.883	143000	5.155
6.300	66700	4.824
7.167	15400	4.188
7.550	8500	3.929
7.900	4410	3.644
9.067	1030	3.013

Figure S2. (A)The LDA effect value histogram of marker species in GEP and MPTP groups. (B) The difference taxa display diagram of taxonomic rank tree.
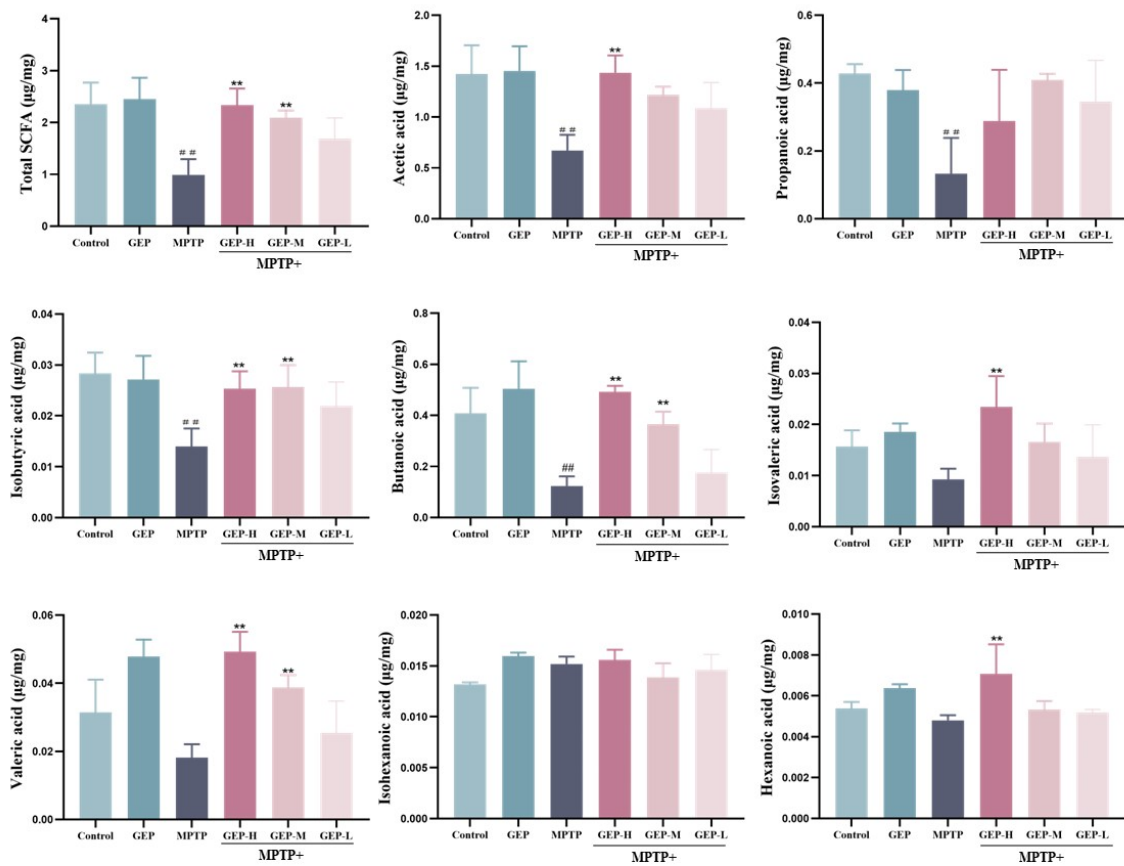

Figure S3. The content of SCFAs. Error bars indicate SEM, ## $p < 0.05$ vs. Con group, ** $p < 0.05$ vs. MPTP group.
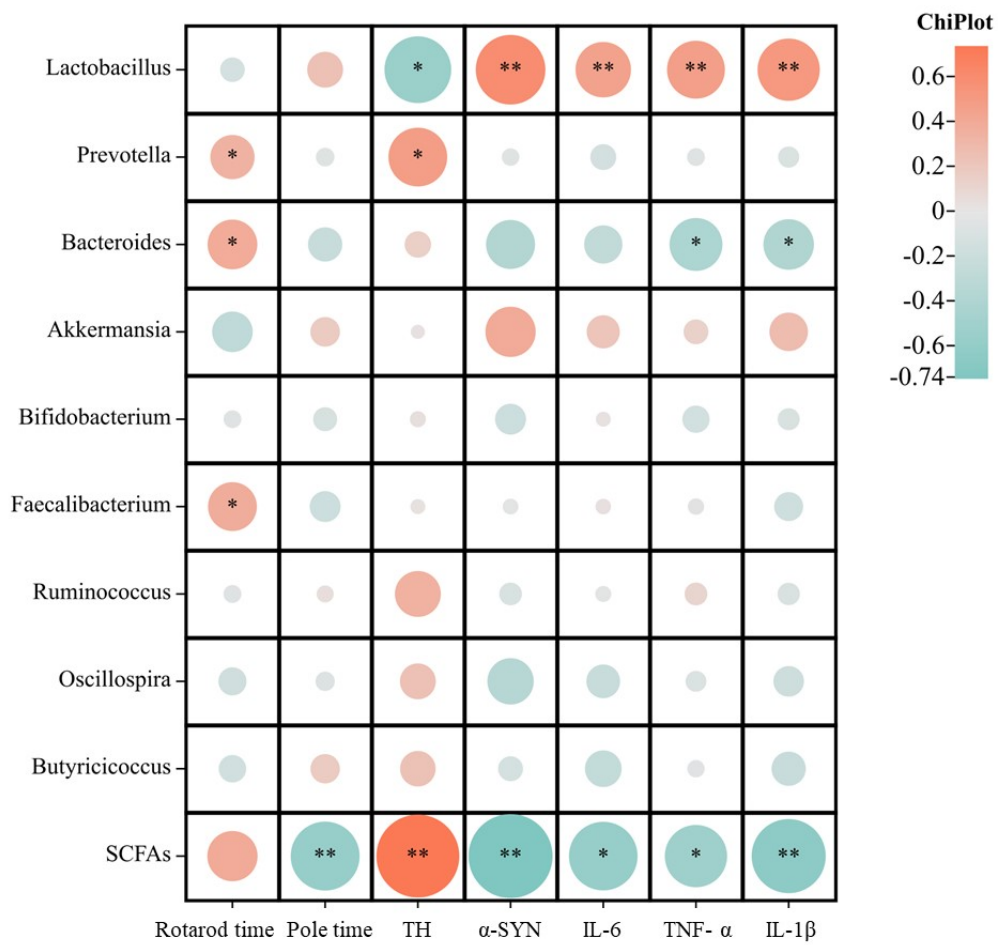
Figure S4. Correlation analysis of relative abundance of key bacteria and other parameters. The rValue was presented by circles with varied color depth (*$p < 0.05$, **$p < 0.005$).